AN IN VIVO FUNCTIONAL GENOMICS SCREEN IDENTIFIES NEW REGULATORS OF TUMORIGENESIS IN NON-SMALL CELL LUNG CANCER

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DEDICATION

For Mom

네 보물 있는 그 곳에는 네 마음도 있느니라.

AN IN VIVO FUNCTIONAL GENOMICS SCREEN IDENTIFIES NEW REGULATORS OF TUMORIGENESIS IN NON-SMALL CELL LUNG CANCER

by

Suzie K. Hight

DISSERTATION

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AN IN VIVO FUNCTIONAL GENOMICS SCREEN IDENTIFIES FOXA1 AS A KEY REGULATOR OF TUMORIGENESIS IN A SUBSET OF NON-SMALL CELL LUNG CANCERS

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Cancer cells are characterized by the aberrant regulation of signaling pathways that govern responses to growth stimuli, resulting in dysregulated cellular proliferation. The accumulated genomic alterations that cause this malignant growth phenotype can also result in acquired vulnerabilities in the tumor. Loss-of-function screening using pooled short hairpin RNAs (shRNAs) is a powerful method for identifying new therapeutic targets in cancer. We have tested the use of parallel *in vitro* and *in vivo* screens using a mini-library of shRNAs to identify previously unknown acquired vulnerabilities in lung cancer. Using a mini-library of 1062 lentiviral shRNAs targeting nuclear hormone receptors and their coregulators (120 genes total),

we screened the lung adenocarcinoma cell line NCI-H1819 for dependency on these genes during *in vitro* and *in vivo* growth. We identified six genes required for survival *in vitro* (*BRCA1, CCND1, MED1, PHB, HNRNPU*, and *PELP1*), and three genes that were required for tumor survival *in vivo*, but not *in vitro*: *FOXA1, HDAC1*, and *NCOR2*. None of these genes were mutated by full exome sequencing of H1819, however *FOXA1* was found to be co-amplified with *NKX2-1* on chromosome 14q. Here we report that NSCLC cell lines and tumor samples have significantly higher FOXA1 expression compared to normal lung epithelial cells and tissues, and that 14q-amplified NSCLC cell lines are preferentially dependent on FOXA1 for clonogenicity and *in vivo* growth. Integrative transcriptomic and cistromic analyses identified a subset of direct FOXA1 targets as positive regulators of key growth signaling pathways, and negative regulators of several growth inhibitory mechanisms. This regulatory function appears to be partially independent of NKX2-1, and combing de novo motif discovery with expression analyses has identified several other putative FOXA1 coregulators. Our findings provide new insight into the functional consequences of 14q amplification in lung adenocarcinomas and suggest exploration of new transcriptional networks for potential therapeutic vulnerabilities.

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LIST OF ABBREVIATIONS

NSCLC – non-small cell lung cancer

SCLC – small cell lung cancer

ADC – adenocarcinoma

LUAD – lung adenocarcinoma

SCC – squamous cell carcinoma

DNA – deoxyribonucleic acid

gDNA – genomic DNA

RNA – ribonucleic acid

RNAi – RNA interference

siRNA - short interfering RNA

shRNA – short hairpin RNA

HBEC – human bronchial epithelial cell

HSAEC – human small airway epithelial cell

DEG(s) – differentially expressed gene(s)

ChIP – chromatin immunoprecipitation

TSS – transcription start site

IHC - immunohistochemistry

FDR – false discovery rate

RT-PCR – real-time PCR

RQ – relative quantitation

PCR – polymerase chain reaction

CN – copy number

Exp – expression

hi – high expression

lo – low expression

mRNA – messenger RNA

MTS – 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium

NOD/SCID – non-obese diabetic severe combined immunodeficiency mouse

CHAPTER ONE

FUNCTIONAL GENOMICS IN THE STUDY OF CANCER

We may therefore regard it as probable that individual chromosomes have different properties in vertebrates too, and it is this assumption that forms the basis of the tumour hypothesis I have put forward. A malignant tumour cell is – and here again I take up the ideas of Hansemann – a cell with a specific abnormal chromosome constitution.
— Theordor Boveri, *Concerning the Origin of Malignant Tumors, 1914*

1.1 A brief history of cancer genomics

It has now been over a century since abnormal mitoses in cancer cells were first reported by German pathologist David von Hansemann, followed nearly 25 years later by the publication of Theodor Boveri's seminal hypothesis that tumors actually arise from cells which harbor "chromosomal defects" (1-3). Based on his observations in sea urchin embryos harboring abnormal chromosome counts, Boveri made a number of stunningly accurate predictions that foreshadowed the next 100 years of cancer research. These included the concepts of cell cycle checkpoints (*Hemmungseinrichtung*, "inhibitory mechanism") oncogenes (*Teilungsfoerdernde Chromosomen*, "division-promoting chromosomes"), and tumor suppressors (*Teilungshemmende Chromosomen*, "division-inhibiting chromosomes") (2,3).

The publication of Boveri's work marked the beginning of the modern era of cancer research, in which we began to understand cancer as a genetic disease. Despite the accuracy of his postulations, it would be several more decades before experimental evidence would start to accumulate to support these theories. The first specific genetic abnormality found to be

consistently associated with neoplasia was discovered in 1960, when Nowell and Hungerford reported the identification of an abnormal “minute” chromosome, present only in the malignant cells of patients with chronic myelogenous leukemia (CML) (4,5). The abnormality, coined the Philadelphia chromosome and later confirmed to be the result of a translocation between chromosomes 9 and 22 (6), represented the first identified genetic signature for cancer. However, since no other specific signatures had been definitively identified by this point, it remained unknown for many decades whether the chromosomal abnormalities known to be associated with malignancy were merely the consequence, or in fact the cause of disease (7-9).

By the mid-1970s, however, circumstantial evidence had begun to accumulate to support the theory that cancer was caused by damaged genes. These were based mainly on the observation of aberrant chromosomal content in different leukemias (10), identification of hereditary predispositions to cancer (11), correlation between defective DNA repair mechanisms in human syndromes and cancer incidence (12,13), and detection of a clear relationship between carcinogenic substances and their mutagenic properties (14). By this point, work on the Rous sarcoma virus had also begun to point to the existence of viral genes with the capability to transform normal cells (15,16).

In 1976, work in the laboratories of Harold Varmus and Michael Bishop showed for the first time that normal avian cells contained a conserved gene – later termed *c-src* –that was homologous to the viral oncogene in avian sarcoma virus (17). The conservation of the gene

among related avian species not only suggested it was of cellular rather than viral origin, but that it may play a role in normal growth regulation. The discovery that cells harbored genes with intrinsic oncogenic potential had such an impact on the field that Bishop and Varmus were later awarded the Nobel Prize. In 1979, Robert Weinberg and colleagues reported a set of DNA transfection experiments which demonstrated the first proof-of-principle that chemically damaged DNA could in fact confer transformation on a recipient cell (18). This study finally provided definitive evidence for the causal relationship between genetic alterations and cancer, and led to refocused efforts to identify more proto-oncogenes and the precise mechanisms by which they become converted to bona fide oncogenes.

In subsequent years, the field moved at an extraordinary pace, and within less than a decade at least 30 cellular oncogenes had been identified, and several mechanisms of activation (19). One of the first proto-oncogenes to be linked to human tumors was the *H-ras* oncogene (20-22), and the discovery that human *HRAS* in bladder carcinoma cells carried a single point mutation in the G12 codon provided the first evidence for a mechanism of oncogene activation (23-25). Hybridization studies went on to show that the *c-abl* oncogene was the target of the t(8;21) translocation in CML (26), and that *c-myc* was translocated in Burkitt's lymphoma (27), confirming that translocation was another mechanism by which oncogenes could be activated. The discovery that promyelomyctic leukemia cells can harbor copy number gains of *c-myc* added gene amplification to the repertoire as well (28).

In the meantime, loss of function alleles and copy number loss were also beginning to be recognized for their role in oncogenesis. Their discovery lagged behind that of oncogenes in part because of the difficulty in studying a loss of function phenotype rather than gain of function. Early evidence for tumor suppressor genes came from somatic cell hybridization experiments, which showed that fusion of normal cells with tumor cells could result in non-tumorigenic hybrids (29). This suggested that the genetic information in normal cells was able to suppress the tumorigenic phenotype. In 1971, Alfred Knudson postulated that the hereditary patterns he observed in retinoblastoma patients would be consistent with two consecutive genetic alterations – an initial congenital lesion in one allele, and a second somatically acquired alteration in the other (30). This "two-hit" hypothesis was eventually proven correct by a series of genetic experiments which demonstrated inactivation or loss of both alleles at the *RB* gene locus (31-34). The "two-hit" model went on to guide discovery of many more tumor suppressors in different tissue types, including *TP53, APC,* and *BRCA1* (35-38).

By the early 1990s, several classes of structural genetic alterations had been implicated as activating mechanisms in oncogenesis, including point mutations, chromosomal translocations, inversions, amplifications, deletions, and loss of heterozygosity (39). Cancer was by then not only recognized as the direct consequence of genetic alterations, but also as a multistep process in which these alterations accumulate and lead to disease progression (40). In the meantime, evidence was also mounting to support the concept that some tumors exhibited "oncogene addiction" and/or "tumor suppressor hypersensitivity" (41). Studies in transgenic mouse models of *c-myc* driven malignancy showed that reversing activation of the oncogene

caused regression of both hematological and solid tumors (42-44). These studies provided proof of principle that some alterations were not only responsible for driving malignancy, but also represented an "Achilles Heel" of the tumors they drove. Further evidence soon followed to support an addiction model to other oncogenes as well, including *K-ras* (45)*, H-ras* (46), *BCR-ABL* (47)*,* and *erbB2* (48)*.* In fact, pre-clinical studies in *c-abl* led directly to the development of the first tyrosine kinase inhibitor imatinib (Gleevec; Novartis), which went on to show extraordinary efficacy in CML patients, effectively turning a once fatal disease into a chronic condition (49,50). Around the same time, the monoclonal antibody trastuzumab, designed to target *HER2* (*erbB2)* (Herceptin; Genentech) also showed remarkable responses in Her2-positive breast cancer patients (51,52). The advent and success of targeted therapies was the first major breakthrough in cancer treatment since the invention of chemotherapy more than a half-century earlier, prompting vigorous efforts to identify other oncogenic aberrations that could serve as potential therapeutic targets.

Around the same time, the complete sequence of the human genome was announced and the post-genomic era in biomedical research was officially born (53-56). Armed with high-throughput sequencing technologies, a reference human genome, and the inspiring success of the first targeted therapies, efforts in cancer research were immediately focused on sequencing known cancer-related genes in tumors. Sequencing of exons from select gene families rapidly led to the discovery of many activating somatic mutations in cancers, in genes such as the *BRAF* serine-threonine kinase (57), the *PIK3CA* lipid kinase subunit (58), and the *EGFR* (59-61), *ERBB2* (62)*, FGFR2* (63,64)*, JAK2* (65-69) and *ALK* receptor tyrosine kinases (70-72). Advances in

computational power and bioinformatics approaches also began to allow for large-scale systematic screens to be performed, and soon the first reports of whole-exome sequencing of human cancers were reported (73-75). These and subsequent studies which expanded to using massively parallel whole genome sequencing revealed that human cancers were much more genetically diverse and complex than previously anticipated (76,77). The Cancer Genome Atlas (TCGA) project was launched in 2005, and aimed to comprehensively characterize major tumor types via systematic molecular profiling of large tumor cohorts, and integrative analysis of these genome-wide datasets. This large-scale effort has now sequenced over 10,000 tumors in over 20 tumor types, identifying hundreds of new cancer-associated genomic alterations (78). While the US-based project is coming to a close, the International Cancer Genome Consortium will continue to expand the comprehensive catalogue to cover 50 different tumor types (79,80).

1.2 Cancer and functional genomics

Eventually the techniques of nucleic acid chemistry should allow us to itemize all the differences in nucleotide sequence and gene expression that distinguish a cancer cell from its normal counterpart, and perhaps at that point the steps involved in carcinogenesis will cease to be in doubt.
- John Cairns, *The Origin of Human Cancers*, 1981. *Nature*. 289:353-357.

The advent of genome-wide profiling technologies in combination with TCGA has yielded a vast wealth of knowledge about the complex molecular landscapes that exist in human tumors, and this knowledge in turn has impacted every area of cancer research. These integrative analyses have not only identified many new potential oncogenes and tumor suppressors, but have also allowed for the definition of new molecular subtypes in tumor types

that were previously only classified by histology (81,82), and even prediction of clinical response based on molecular signatures (83). Tumor sequencing projects have also revealed that in many tumor types, the oncogenic landscape is characterized by a "long tail" distribution of mutations (84). In lung adenocarcinomas, for example, mutations found in more than 10% of the population only comprise 5% of the total (Figure 1.1). In other words, while a handful of cancer genes are mutated at high frequency, many more genes are mutated at much lower frequencies in the patient population. This is clearly demonstrated by recent studies in non-small cell lung cancer, in which *EML4-ALK* fusions are found in only 4-6% of patients, and *ROS1* or *RET* fusions are found in only 1% of patients, each (85). Despite the low frequency of these mutations, they often respond dramatically to targeted therapies, confirming that mutation frequency alone is not sufficient to identify the best therapeutic targets (86-88). However, the genomic instability inherent in many tumors results in the accumulation of mutations and alterations that are not driving the tumor, but instead are collateral passengers. The identification of true drivers amongst the sea of passengers in the "long tail" distribution is a major hurdle in the post-genomic era of cancer research. As a proof of principle, Fröhling and colleagues showed that in AML, only a subset of acquired mutations in the *FLT3* gene are oncogenic (89). Given that the activating mutations in *FLT3* are known to be oncogenic in AML and other tumor types, this study highlighted the need for functional assessment of mutations, even when found in well established oncogenes. Thus, complementary studies exploring the biological function of the genes and mutations found in the "long tail" are required in order to define their role in oncogenesis and distinguish true drivers from passengers.

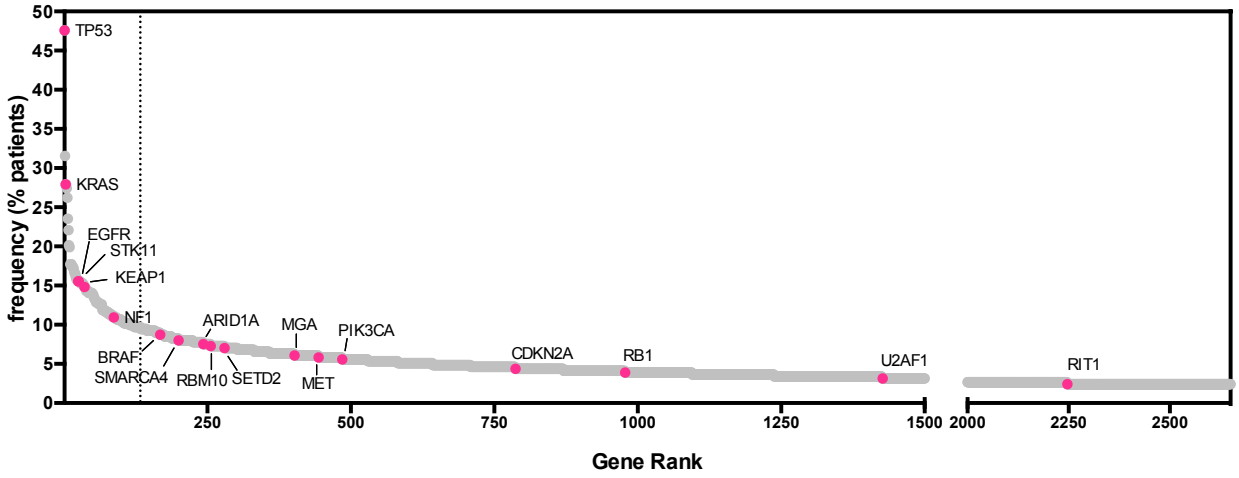


Figure 1.1. Prevalence of recurrent mutations in lung adenocarcinomas. Whole-exome sequencing across 412 tumor/normal pairs from the TCGA and Washington University datasets identified >100,000 mutations and 18 statistically significant mutated genes (pink). In lung adenocarcinomas, only 5% of mutations are found in more than 10% of the patient population (left of the dotted line), with the remaining 95% distributed in a "long tail" (90).

Direct targeting of oncogene addiction is a major strategy in the current development of cancer therapeutics, however there is also a growing body of evidence to suggest that acquisition of "driver" oncogenic alterations can create novel functional dependencies in other signaling pathways. These acquired vulnerabilities can be the downstream result of oncogene addiction (91), passenger alterations, haploinsufficiencies (92), or other synthetic lethal relationships (93,94). For example, Muller and colleagues showed that in a large homozygous deletion event that encompasses many genes, passenger loss of the essential gene *ENO1* in glioblastoma cells created a collateral dependency on *ENO2,* due to it's functionally redundant cellular roles (95). Similarly, Nijhawan and colleagues showed that partial loss of the 19S proteosome gene *PSMC2* can render cancer cells hypersensitive to *PSMC2* suppression (92). Other acquired vulnerabilities may create a synthetic lethal relationship between the oncogenotype and specific perturbagens such as drugs, antibodies, or RNAi reagents, and may

only be identified by functional studies. In the context of drug treatment, this type of interaction manifests as a genotype-dependent lethality similar to what is seen in oncogene addiction, except that the agent used does not directly target the primary oncogenic driver. The best example of this is the discovery that *BRCA*-deficient breast cancers are selectively sensitive to inhibition of PARP, due to their compromised repair of double-stranded DNA breaks (96-100). Notably, this discovery arose from hypothesis-driven functional experiments, and would not have been revealed by molecular profiling alone.

In the past, functional studies were done on a gene-by-gene basis and time consuming, but in the last decade the development of genome-wide tools for perturbation of mammalian gene function is now allowing for large-scale systematic interrogation of genes and signaling pathways (101). These screening technologies include the ability to perform systematic mutagenesis via transposon or retrovirus insertion (102,103), interrogate gain-of-function phenotypes using genome-wide ORF libraries (104,105), and high-throughput drug screening across large panels of cancer cell lines (106,107). They also include RNA interference (RNAi) technologies, which have revolutionized biomedical research with their ability to systematically interrogate the function of genes either on an individual or gene set basis (108). Recent advances in genome-editing using CRISPR-Cas9 (clustered regularly interspaced short palindromic repeats-CRISPR associated nuclease 9) constructs are also enabling systematic genetic manipulation in human cells (109), however RNAi currently remains the most ubiquitously used tool for this purpose.

RNAi is an endogenous gene-silencing process that is initiated by double-stranded RNA (108,110). First discovered in the nematode *Caenorhabditis elegans* (111), the phenomenon and cellular machinery were later confirmed to be widely conserved in most eukaryotes, including mammals (112-114). After discovering that the endogenous RNAi machinery could be specifically harnessed and redirected by introduction of exogenous RNA duplexes (siRNA) (115), RNAi became a ubiquitous tool in biological research for interrogating gene function (108). There are now several modes of introducing RNAi reagents into mammalian cells, including transfection of synthetic small interfering RNAs (siRNAs) or endoribonuclease-prepared siRNAs (esiRNAs), and viral delivery of short hairpin RNAs (shRNAs). Stable integration of shRNAs allows them to be processed through the DICER pathway before loading onto the RISC complex, a feature which allows for screens to be conducted in a high-throughput pooled format, since cells can be deconvoluted using either microarray hybridization or next-generation sequencing. It also allows for the use of long-term biological assays to investigate phenotypes that may more complex or revealed only in more physiological settings, such as survival *in vivo* (discussed below). Introduction of synthetic siRNAs, endoribonuclease-prepared siRNAs, or siRNA precursors that are designed to target specific mRNA transcripts allowed researchers to silence genes in a highly specific and targeted manner, and allowed for the first time the combination of genetic screens with phenotypic assays (116-118).

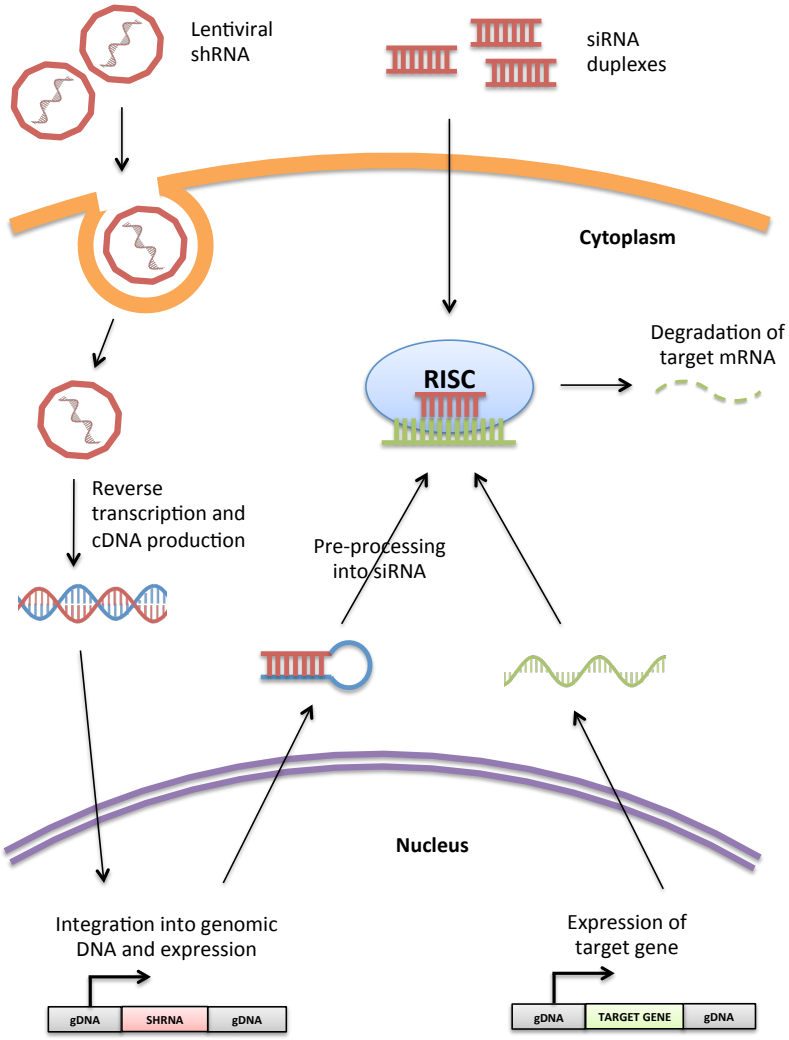


Figure 1.2. Exogenous RNA interference pathway. RNAi reagents can be introduced via either transduction of lentiviral short hairpin RNA (shRNA) constructs, or by lipogenic transfection of siRNA duplexes. Lentiviral transduction results in integration of the construct into the host genome, allowing for stable cell lines to be created, while transfection with siRNAs is typically used for transient assays. Stably expressed shRNAs are processed into siRNAs by DICER (not shown), and loaded into the RNA-induced silencing complex (RISC), which mediates target mRNA degradation based on complementarity to the siRNA sequence.

RNAi screening has made possible the identification of genes, signaling pathways and networks involved in a diverse array of biological processes, including regulatory pathways controlling cell growth and survival, and mechanisms of drug resistance in cancer (108). Gain-of-function shRNA screens are widely used to identify putative tumor suppressor genes, using

readouts such as anchorage-independent growth (119,120), or *in vivo* growth (121-123). Loss-of-function shRNA screening is likewise proving to be a powerful method for identifying oncogenotype-specific essential genes. Project Achilles is one such large-scale and systematic effort launched by the Broad Institute whose goal is to create comprehensive profiles for essential genes in multiple cancer types (124-126). Using genome-wide pooled shRNA libraries, over 216 cancer cell lines covering more than 10 different tumor types have been profiled (127). In Achilles 2.0, genome-wide RNAi screening across 102 cancer cell lines successfully identified multiple lineage-specific dependencies, including *PAX8* in ovarian cancer, and *NKX2-1* in NSCLC (125). Other efforts focused on specific cancer types and/or specific gene sets are able to screen at higher depth, and thus are revealing even more novel dependencies with greater precision (128).

While these studies are clearly shedding light on previously unknown context-dependent vulnerabilities, one limitation is that they are usually performed *in vitro,* under relatively low selection pressure. The nutrient-rich media typically used for culture of cancer cells are arguably highly artificial, and are not able to faithfully recapitulate the stressors and mitogenic signals encountered in the tumor microenvironment. Complex factors such as nutrient availability, low oxygen conditions, generation of reactive oxygen species, and tumor-stromal interactions are difficult to mimic outside of an organism (129,130). Thus standard screening methods may miss key vulnerabilities that might otherwise be detected in a more physiologically relevant setting. As discussed above, RNAi has proved amenable in the past for use in gain-of-function studies *in vivo,* successfully identifying many genes with tumor

suppressor functions. Loss-of-function studies require special consideration of library representation and engraftment efficiency if xenograft models are used, discussed in more detail in Appendix A, and elsewhere (131,132). Negative selection screens are thus more challenging, but have still been successfully employed to identify putative tumor vulnerabilities (133-136).

Synthetic lethal RNAi screens in particular have made notable strides in identifying mechanisms of drug sensitivity, or genes whose combinatorial inhibition synergize to effect tumor response. One of the first proof-of-principle genome-wide screens successfully identified a large panel of genes whose inhibition sensitized cells to paclitaxel by 1,000-fold (137), while later studies identified genes which can effect response to targeted therapies (138,139). Drug targets identified by RNAi screening have even led to direct translation to the clinic. In a true bench-to-bedside approach, Tyner and colleagues demonstrated that a kinome siRNA screen in primary leukemia samples could quickly identify drug targets in one third of patients (140). These findings were then able to direct personalized therapy for one patient, who exhibited a response to treatment. An shRNA kinome screen which identified EGFR inhibition as synergistic with BRAF(V600E) inhibition in colon cancer cell lines, has become the basis for a clinical trial which is currently ongoing (141,142). These studies raise the possibility that functional profiling could one day play a greater role in directing personalized medicine, and highlight the great utility of RNAi-based screening in identifying new potential therapeutic targets.

1.3 Lung cancer genomics

It has always been maintained that males are by far more frequently subject to lung tumors than females….The domestic life led by women, with their consequent retirement and immunity from the irritations and traumatisms which must be frequent in the more unprotected life of men (the abuse of tobacco and alcohol, the many trades and vocations which are accompanied by irritations of the respiratory organs, etc.) has been adduced in explanation of this fact. The entire subject is not yet ready for final judgment.
-Issac Adler, M.D. *Primary Malignant Growths of the Lung and Bronchi.* 1912

Lung cancer is the most common cancer worldwide, accounting for more deaths per year than breast, prostate, and colon cancer combined (133,134,136,143). The two main subtypes are small cell lung cancer and non-small cell lung cancer. Non-small cell lung cancer is further subdivided by histology, mainly into adenocarcinoma, large cell carcinoma, and squamous cell carcinoma. The most common of these is adenocarcinoma, accounting for ~80% of all non-small cell lung cancer diagnoses (Figure 1.3) (ref). While there is a strong correlation with lung cancer incidence and smoking (144), up to 20% of lung cancers are diagnosed in never-smokers every year (145-147). In lung adenocarcinomas, *KRAS* mutations are significantly correlated with smoking, while *EGFR* mutations are not, and many studies have confirmed that these mutations are mutually exclusive in patients (90,148). While there is a strong correlation with lung cancer incidence and smoking (144), up to 20% of lung cancers are diagnosed in never-smokers every year (145-147). Despite major advances in the last few decades in our understanding of the molecular mechanisms that drive this disease, the prognosis for newly diagnosed patients remains poor and underscores the urgent need for more effective therapies.

Sequencing efforts by TCGA and other groups have confirmed that lung cancer has one of the highest mutation burdens of all human cancers, with significantly more mutations associated with smoking history than non-smoking (90,148). In fact, the resolution that whole genome sequencing provides has allowed for identification of a highly specific mutational signature associated with tobacco use, characterized by high prevalence of C>A transversions (90,149-151).

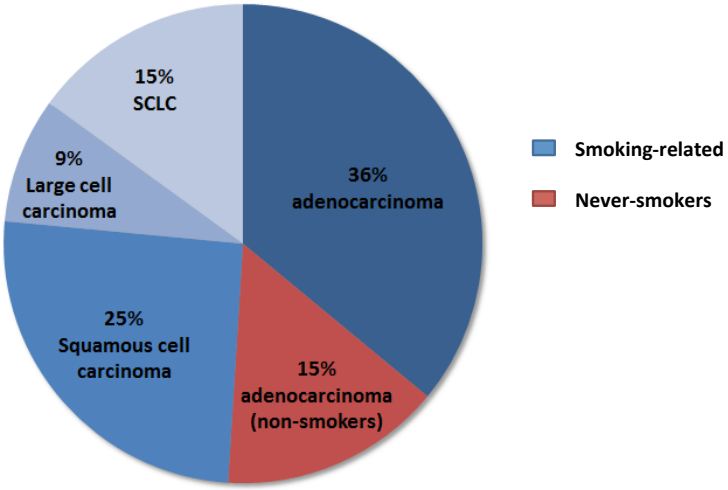


Figure 1.3. Relative frequency of lung cancer histology, and correlation with smoking. Lung cancer is divided into several different subtypes, of which adenocarcinoma is the most common. ~85% of all lung cancers are correlated with smoking history, while 15% of patients have never smoked. Adenocarcinoma is the most common histology found in never-smokers.

The scale of TCGA efforts in lung cancer was large enough to confirm the presence of oncogenic mutations in very small patient populations, confirming that mutation burden in lung cancer follows the "long tail" distribution seen in other cancers (Figure 1.1). Most lung adenocarcinomas are driven by oncogenic events within receptor tyrosine kinases or members of the RAS/RAF pathway (90). The most frequent culprits include point mutations in KRAS, BRAF, or EGFR, but alterations in many other genes in this same class are also detected (Figure

1.4). Despite this, it is estimated that up to ~25% of lung adenocarcinomas arise from a different oncogenic mechanism. Tyrosine kinase inhibition is one of the most developed targeted therapeutic strategies, however *EGFR* mutation and *ALK* rearrangement are currently the only driver alterations in lung cancers with FDA-approved targeted therapies available. This leaves up to 70% of lung cancers, even those with genetically defined oncogenic drivers, with no currently available targeted therapy (152). The standard first-line therapy for these patients continues to be platinum-based doublet chemotherapy, and poor prognosis with this regiment highlights the urgent need to identify new therapeutic strategies for this large patient population.

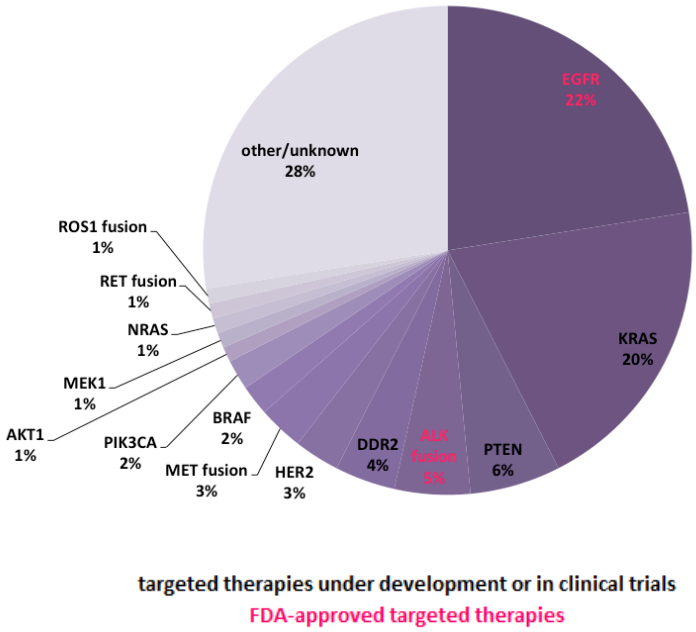


Figure 1.4. Prevalence of clinically actionable genetic alterations in lung adenocarcinomas. Many oncogenic mutations with potential for clinical action have been identified in lung adenocarcinomas. Despite the fact that there are ongoing efforts in both drug development and clinical trials to target many of these genes, only two of the lesions currently have an FDA-approved targeted therapy. Adapted from *www.mycancergenome.org/lungcancer*.

1.4 Nuclear hormone receptors and their co-regulators

It seems to me to be in the highest degree improbable that the relationship between the oöphorectomy and the atrophy of the cancer masses which I have described to you is other than causal. How removal of the ovaries can produce such an effect I do not know, but my working hypothesis is that the internal secretion of the ovaries in some cases favors the growth of the cancer, acting either upon the epithelial cells or upon the surrounding tissues; consequently, in these cases, removal of the ovaries will leave the tissues better able to cope with the parasitic cells.
- Stanley Boyd, F.R.C.S. *On oöphorectomy in the treatment of cancer.* 1897. *British Medical Journal.* 2(1918):890-896.

Nuclear receptors (NRs) are a class of ligand-activated transcription factors regulating a diverse array of biological processes, including development, reproduction, and lipid metabolism (153-156). Comprised of 48 members, this superfamily includes receptors that mediate the action of steroid hormones, thyroid hormones, vitamins A and D, cholesterol metabolites and other dietary lipids (156-158). Ligands can either be agonistic or antagonistic, allowing for gene regulation that is fine-tuned to internal and external environmental cues. There is also a large subset of NRs which are orphan receptors, for which the endogenous ligands are unknown (159). Notably, the presence of a specific and high-affinity binding site for small lipophilic ligands in NRs makes them easily "druggable", and agents that target nuclear receptor function are among the most widely used and successful currently on the market (160-163).

Deregulation of NHR function has been implicated in a variety of disease processes, including diabetes, atherosclerosis, metabolic disorders, and cancer (156,158). For example, it is now well established that the estrogen receptor has a driving role in significant portion of breast cancers, and the androgen receptor is similarly oncogenic in many prostate cancers (164-

166). The role of sex hormone signaling in non-reproductive cancers in still poorly understood, but gender-specific differences in both susceptibility and prognosis have long pointed to a possible endocrine component to this disease (167-172). Several studies have reported that, after controlling for number of cigarettes smoked, women have a higher risk of developing lung cancer than men (173-175). In addition, two-thirds of never-smokers diagnosed with lung cancer are women (176).

Studies in lung cancer cell lines have suggested that expression profiling of the NHR gene family can be used to distinguish between histological subtypes, with distinct signatures being associated SCLC, NSCLC, and normal epithelial cells (171,177). Subsets of NSCLC cell lines also display differential expression of several nuclear receptors: androgen receptor, estrogen receptor, vitamin D receptor, and peroxisome proliferator-activated receptor-γ, suggesting that a therapeutic window may exist for targeting certain receptors in some lung tumors (178).

Nuclear receptors require the presence of coregulator factors in their DNA-binding complex in order to achieve efficient transcriptional regulation. These can be divided into two major classes: coactivators, which interact with agonist-bound nuclear receptors to increase target gene expression, and corepressors, which associate with antagonist or unliganded receptors to decrease target gene expression. The interaction of nuclear receptors with different coregulator complexes directs the specificity of action, either in terms of transcriptional output and/or genomic binding location. While there are a huge number of proteins that fit into either the coactivator or corepressor class, curation of this list for genes

with either known or implied relevance to cancer led to identification of 72 key coregulators (Table 1.1). Interestingly, many coregulator complexes function as chromatin remodelers, either by direct modification of chromatin or effecting its reorganization (179). As these are associated with clear enzymatic activity (acetylation and de-acetylation of histones, methylation/ and demethylation of chromatin, etc.), understanding their function in disease may provide therapeutic opportunities that are distinct from targeting of their cognate nuclear receptors.

Differential expression and/or amplification of multiple coregulators has been implicated in tumorigenesis of many tumor types, including lung cancer (180). All of the SRC/NCOA family members have been found to be overexpressed in NSCLC (181), while loss of SIN3A, a component of the histone deacetylase complex suggests a possible role for tumor suppression in lung adenocarcinomas (182). Multiple members of the SWI/SNF chromatin remodeling complex, including SMARCA4/BRG1 and ARID1A/2, have been implicated as tumor suppressors in NSCLC (183), while overexpression of LSD1, a component of the NuRD chromatin remodeling complex, appears to promote growth in lung cancer cell lines (184-186).

Entrez Gene ID	Gene Symbol	Class	Gene Name
7421	VDR	NR	vitamin D (1,25- dihydroxyvitamin D3) receptor
5467	PPARD	NR	peroxisome proliferator-activated receptor delta
2100	ESR2	NR	estrogen receptor 2 (ER beta)
7068	THRB	NR	thyroid hormone receptor, beta
5914	RARA	NR	retinoic acid receptor, alpha
2104	ESRRG	NR	estrogen-related receptor gamma
2494	NR5A2	NR	nuclear receptor subfamily 5, group A, member 2
4306	NR3C2	NR	nuclear receptor subfamily 3, group C, member 2
6256	RXRA	NR	retinoid X receptor, alpha
5468	PPARG	NR	peroxisome proliferator-activated receptor gamma
7026	NR2F2	NR	nuclear receptor subfamily 2, group F, member 2
7376	NR1H2	NR	nuclear receptor subfamily 1, group H, member 2
8431	NR0B2	NR	nuclear receptor subfamily 0, group B, member 2
7181	NR2C1	NR	nuclear receptor subfamily 2, group C, member 1
3172	HNF4A	NR	hepatocyte nuclear factor 4, alpha
10062	NR1H3	NR	nuclear receptor subfamily 1, group H, member 3
2101	ESRRA	NR	estrogen-related receptor alpha
8013	NR4A3	NR	nuclear receptor subfamily 4, group A, member 3
6258	RXRG	NR	retinoid X receptor, gamma
5916	RARG	NR	retinoic acid receptor, gamma
5241	PGR	NR	progesterone receptor
8856	NR1I2	NR	nuclear receptor subfamily 1, group I, member 2
5465	PPARA	NR	peroxisome proliferator-activated receptor alpha
2103	ESRRB	NR	estrogen-related receptor beta
9971	NR1H4	NR	nuclear receptor subfamily 1, group H, member 4
4929	NR4A2	NR	nuclear receptor subfamily 4, group A, member 2
5915	RARB	NR	retinoic acid receptor, beta
9975	NR1D2	NR	nuclear receptor subfamily 1, group D, member 2
190	NR0B1	NR	nuclear receptor subfamily 0, group B, member 1
6095	RORA	NR	RAR-related orphan receptor A
6096	RORB	NR	RAR-related orphan receptor B
3174	HNF4G	NR	hepatocyte nuclear factor 4, gamma
7101	NR2E1	NR	nuclear receptor subfamily 2, group E, member 1
2063	NR2F6	NR	nuclear receptor subfamily 2, group F, member 6
6097	RORC	NR	RAR-related orphan receptor C
7025	NR2F1	NR	nuclear receptor subfamily 2, group F, member 1
3164	NR4A1	NR	nuclear receptor subfamily 4, group A, member 1
9572	NR1D1	NR	nuclear receptor subfamily 1, group D, member 1
9970	NR1I3	NR	nuclear receptor subfamily 1, group I, member 3
2908	NR3C1	NR	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
2516	NR5A1	NR	nuclear receptor subfamily 5, group A, member 1
10002	NR2E3	NR	nuclear receptor subfamily 2, group E, member 3
367	AR	NR	androgen receptor
7067	THRA	NR	thyroid hormone receptor, alpha
2099	ESR1	NR	estrogen receptor 1
6257	RXRB	NR	retinoid X receptor, beta
7182	NR2C2	NR	nuclear receptor subfamily 2, group C, member 2
2649	NR6A1	NR	nuclear receptor subfamily 6, group A, member 1
5300	PIN1	coreg	peptidylprolyl cis/trans isomerase, NIMA-interacting 1
3170	FOXA2	coreg	forkhead box A2
9759	HDAC4	coreg	histone deacetylase 4
672	BRCA1	coreg	breast cancer 1, early onset
51588	PIAS4	coreg	protein inhibitor of activated STAT, 4
10499	NCOA2	coreg	nuclear receptor coactivator 2
994	CDC25B	coreg	cell division cycle 25 homolog B (S. pombe)
3276	PRMT1	coreg	protein arginine methyltransferase 1
8648	NCOA1	coreg	nuclear receptor coactivator 1
1022	CDK7	coreg	cyclin-dependent kinase 7
10891	PPARGC1A	coreg	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
6597	SMARCA4	coreg	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4
2118	ETV4	coreg	ets variant 4

Table 1.1. The nuclear receptor superfamily, and select coregulators with known involvement in cancer.
(continued on next page)

Entrez Gene ID	Gene Symbol	Class	Gene Name
8031	NCOA4	coreg	nuclear receptor coactivator 4
23028	KDM1A	coreg	lysine (K)-specific demethylase 1A
6615	SNAI1	coreg	snail homolog 1 (Drosophila)
8202	NCOA3	coreg	nuclear receptor coactivator 3
4582	MUC1	coreg	mucin 1, cell surface associated
8819	SAP30	coreg	Sin3A-associated protein, 30kDa
8295	TRRAP	coreg	transformation/transcription domain-associated protein
7341	SUMO1	coreg	SMT3 suppressor of mif two 3 homolog 1 (S. cerevisiae)
8554	PIAS1	coreg	protein inhibitor of activated STAT, 1
5245	PHB	coreg	prohibitin
5469	MED1	coreg	mediator complex subunit 1
23054	NCOA6	coreg	nuclear receptor coactivator 6
9219	MTA2	coreg	metastasis associated 1 family, member 2
80324	PUS1	coreg	pseudouridylate synthase 1
2033	EP300	coreg	E1A binding protein p300
6907	TBL1X	coreg	transducin (beta)-like 1X-linked
23309	SIN3B	coreg	SIN3 transcription regulator homolog B (yeast)
55611	OTUB1	coreg	OTU domain, ubiquitin aldehyde binding 1
10197	PSME3	coreg	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)
29843	SENP1	coreg	SUMO1/sentrin specific peptidase 1
9584	RBM39	coreg	RNA binding motif protein 39
11331	PHB2	coreg	prohibitin 2
3148	HMGB2	coreg	high mobility group box 2
3065	HDAC1	coreg	histone deacetylase 1
8085	MLL2	coreg	myeloid/lymphoid or mixed-lineage leukemia 2
5925	RB1	coreg	retinoblastoma 1
10432	RBM14	coreg	RNA binding motif protein 14
5894	RAF1	coreg	v-raf-1 murine leukemia viral oncogene homolog 1
9439	MED23	coreg	mediator complex subunit 23
10498	CARM1	coreg	coactivator-associated arginine methyltransferase 1
51780	KDM3B	coreg	lysine (K)-specific demethylase 3B
9862	MED24	coreg	mediator complex subunit 24
9612	NCOR2	coreg	nuclear receptor corepressor 2
9112	MTA1	coreg	metastasis associated 1
10011	SRA1	coreg	steroid receptor RNA activator 1
7329	UBE2I	coreg	ubiquitin-conjugating enzyme E2I
898	CCNE1	coreg	cyclin E1
857	CAV1	coreg	caveolin 1, caveolae protein, 22kDa
221037	JMJD1C	coreg	jumonji domain containing 1C
27043	PELP1	coreg	proline, glutamate and leucine rich protein 1
1387	CREBBP	coreg	CREB binding protein
55818	KDM3A	coreg	lysine (K)-specific demethylase 3A
595	CCND1	coreg	cyclin D1
11315	PARK7	coreg	parkinson protein 7
1869	E2F1	coreg	E2F transcription factor 1
9611	NCOR1	coreg	nuclear receptor corepressor 1
675	BRCA2	coreg	breast cancer 2, early onset
3146	HMGB1	coreg	high mobility group box 1
10401	PIAS3	coreg	protein inhibitor of activated STAT, 3
142	PARP1	coreg	poly (ADP-ribose) polymerase 1
133522	PPARGC1B	coreg	peroxisome proliferator-activated receptor gamma, coactivator 1 beta
3169	FOXA1	coreg	forkhead box A1
8204	NRIP1	coreg	nuclear receptor interacting protein 1
90665	TBL1Y	coreg	transducin (beta)-like 1, Y-linked
6047	RNF4	coreg	ring finger protein 4
7337	UBE3A	coreg	ubiquitin protein ligase E3A
7041	TGFB1I1	coreg	transforming growth factor beta 1 induced transcript 1
8841	HDAC3	coreg	histone deacetylase 3
3192	HNRNPU	coreg	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)

Table 1.1 (continued from previous page). The nuclear receptor superfamily, and select coregulators with known involvement in cancer. EntrezGene IDs, official gene symbols, and names for the 48 nuclear receptor genes are listed, along with 72coregulators selected for their known relevance to cancer.

1.5 Goals of this study

Functional studies are essential in order to identify therapeutic vulnerabilities amidst the complex molecular landscape of lung tumors. RNAi screening technology is a useful tool for the systematic and high-throughput interrogation of gene function, and can be used to perform both gain-of-function and loss-of-function screens. In order to identify new acquired vulnerabilities in lung adenocarcinoma, we have utilized a parallel *in vitro* and *in vivo* screening strategy to interrogate the function of nuclear receptors and select coregulators in lung cancer. By exploiting *in vitro* and *in vivo* contexts in parallel, we aimed to discover novel tumor vulnerabilities that were not previously identified by standard *in vitro* screening methods. The identification of essential genes in cancer is a critical step towards the development of new therapeutic strategies, and our study will provide insight into new potential therapeutic targets in lung cancer.

CHAPTER TWO

A PARALLEL IN VITRO AND IN VIVO MINI-LIBRARY SCREEN

"They say that genius is an infinite capacity for taking pains," he remarked with a smile. "It's a very bad definition, but it does apply to detective work."
-- Sherlock Holmes, *A Study in Scarlet*

2.1 Introduction

Nuclear hormone receptors (NHRs) comprise a superfamily of ligand-dependent transcription factors that respond to a variety of endocrine cues in order to regulate diverse cellular processes. NHRs and their co-regulators are aberrantly regulated in many tumor types, the most well-known examples being estrogen-dependent breast cancers and androgen-dependent prostate cancers. We have previously shown that NHRs are aberrantly expressed in lung tumors, and that their expression signature has prognostic value in NSCLC (177). A large percentage of drugs are currently approved by the FDA target hormone receptors, making these genes attractive targets to explore for new cancer therapeutics. In order to interrogate the nuclear hormone receptor and co-regulator gene set for essential roles in lung tumorigenesis, we performed a parallel *in vitro* and *in vivo* shRNA screen in the lung adenocarcinoma cell line NCI-H1819.

2.2 Materials and Methods

2.2.1 Short hairpin library

Mini-library screens were performed using a custom-ordered shRNA library from the human MISSION lentiviral shRNA library (Sigma), originally developed by The RNAi Consortium (TRC). Short hairpins in the pLKO.1 vector are denoted as TRC1, while short hairpins cloned into a pLKO.1 derivative vector which harbors an upstream WPRE sequence are classified as TRC2 (Figure 2.1). A lentiviral shRNA mini-library comprised of both TRC1 and TRC2 vectors targeting 40 nuclear hormone receptors, 72 coregulator genes, and several control genes was selected (142 genes, 1062 shRNAs total). Arrayed glycerol stocks and pooled, high titer virus for the mini-library was obtained commercially (Sigma). A list of genes included in the library and the number shRNA clones per gene is included in Appendix C.

2.2.2 Parallel *in vitro* and *in vivo* mini-library screen

H1819 cells (2.3×10^6) were infected with the library pool at low MOI (≤ 0.5), in the presence of 4.0 ug/mL polybrene (3 replicates). Average library coverage was estimated to be ~800x across replicates. Transduced cells were selected in 1.0 ug/mL puromycin for 4 days, and then expanded for ~3-4 population doublings. At this point a reference sample was collected (t=0), and the remaining cells were either seeded into T175 flasks (1.5×10^6 cells per replicate) or resuspended in PBS and injected subcutaneously into female NOD-SCID mice (5×10^6 cells per injection). Cells maintained *in vitro* were cultured for 20 population doublings, and reference samples were harvested at incremental population doubling points (T=2, T=3), until

PD20 (T=4). Tumors were allowed to grow to a minimum volume of 300 mm^3 before harvesting. A detailed step-by-step protocol is included in Appendix A.

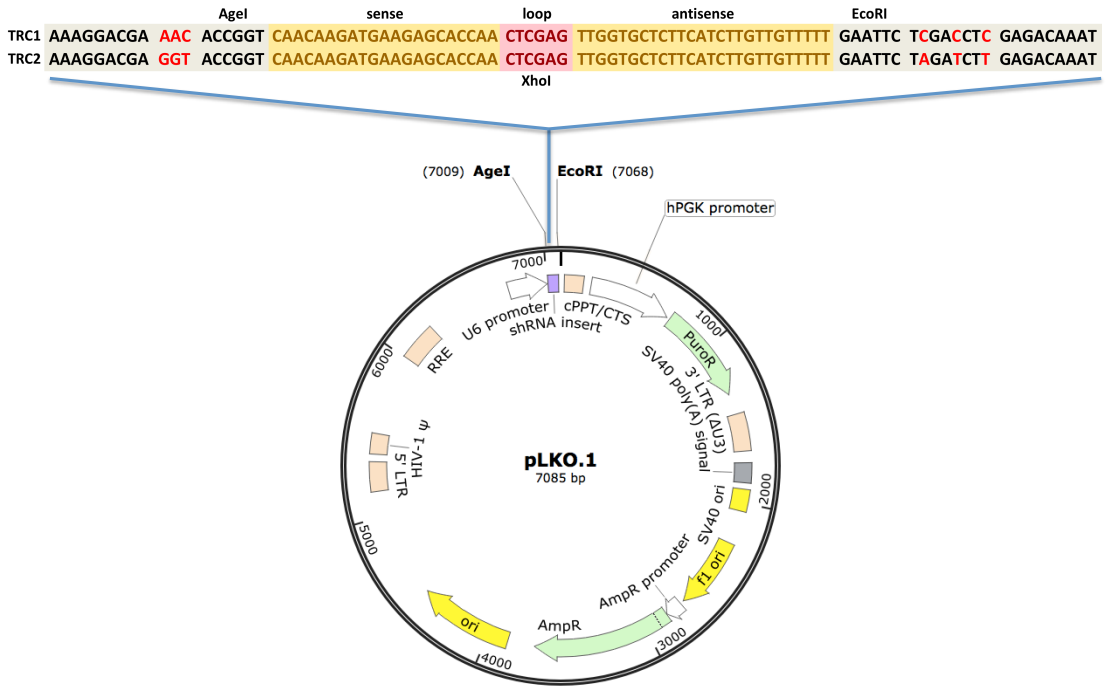


Figure 2.1. TRC library backbone. Short hairpin sequences are cloned into TRC vectors between the AgeI and EcoRI restriction sites. Puromycin is used as a selection marker. TRC2 vectors are identical to TRC1 vectors (pLKO.1), except that they contain the Woodchuck Hepatitis Post-Transcriptional Regulatory Element (WPRE) inserted between the puromycin resistance gene and the 3' LTR, and 6 nucleotides flanking either side of the shRNA (top of figure, mismatches shown in red). Figure made with SnapGene® software (GSL Biotech).

2.2.3 Preparation of TRC shRNAs for sequencing

Genomic DNA was extracted from cell pellets and tumors via PureGene Genomic DNA Purification Kit (Gentra). Short hairpins were PCR-amplified from gDNA using a common reverse primer and indexed forward primers, each containing the appropriate Illumina adapter sequences. The main analysis described in this study used primers which amplified TRC1

shRNAs (Figure 2.2). Sequences for primers which amplify both TRC1 and TRC2 constructs are listed in Appendix B, however these were developed later and not used in the present study. Sequences for all primers are listed in Table 2.1. To adequately cover the library, ~6 ug gDNA from each sample were used as input into each PCR and spread across multiple 50 uL reactions (~0.5 ug template/reaction). PCR reaction conditions were as follows: hot-start for 95°C for 15 min, then 94°C for 30 seconds, 66°C for 45 sec, 72°C for 60 sec, repeat for 33 cycles, and a final extension at 72°C for 5 min. PCR products were concentrated and gel purified, quantified by Picogreen assay, and sequenced on an Illumina HiSeq 2500 using a custom primer. A detailed discussion on sample preparation and protocol for TRC1/2 constructs is included in Appendix B.

Primer ID	Name	Sequence	Index
PR4231	TRC1-4nt-Index1	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGGCATGACGAAAC	GCAT
PR4232	TRC1-4nt-Index2	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGGCTAGACGAAAC	GCTA
PR4233	TRC1-4nt-Index3	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGTCGAGACGAAAC	TCGA
PR4234	TRC1-4nt-Index4	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGTCAGGACGAAAC	TCAG
PR4235	TRC1-4nt-Index5	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGCGATGACGAAAC	CGAT
PR4236	TRC1-4nt-Index6	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGCGTAGACGAAAC	CGTA
PR4237	TRC1-4nt-Index7	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGTGACGACGAAAC	TGAC
PR4238	TRC1-4nt-Index8	AATGATACGGCGACCACCGAGAAAGTATTTCGATTTCTTGGCTTTATATATCTTGTGGTGCAGACGAAAC	TGCA
PR4290	TRC1and2-Rev	CAAGCAGAAGACGGCATACGAGCTCTTCCGATCTCTTTTAAAATTGTGGATGAATACTGCCATTTGTCTC	n/a
PR4291	TRC1-Seq4nt	AGTATTTCGATTTCTTGGCTTTATATATCTTGTGG	n/a

Table 2.1. Primers used for TRC1 mini-library coverage. All sequences are shown 5’ to 3’. Index sequences used to multiplex sequencing samples are indicated on the right.

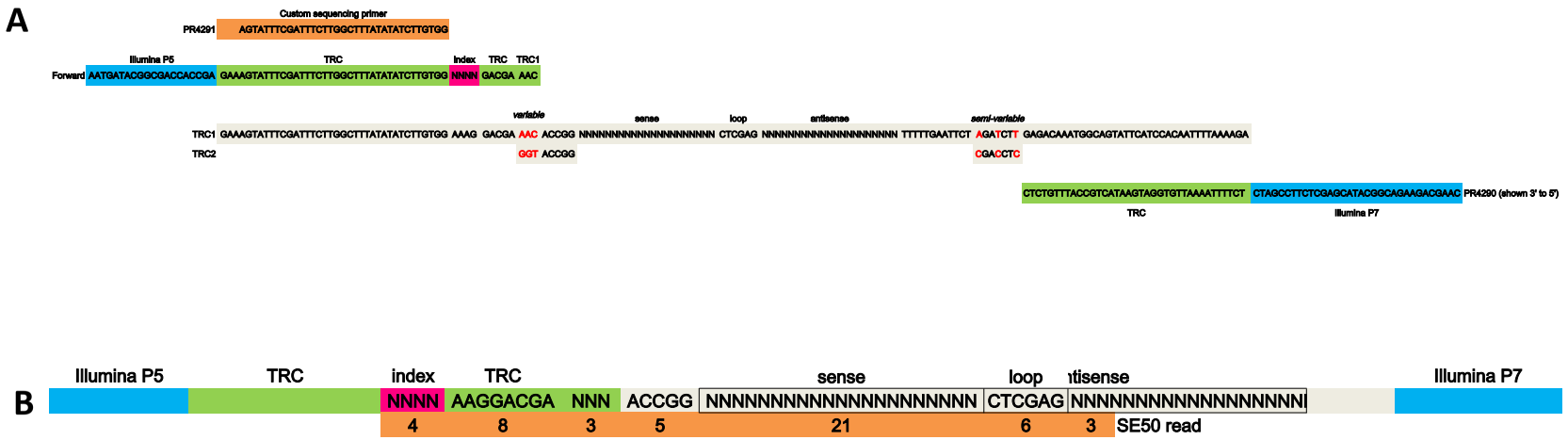


Figure 2.2. Primer design for TRC1 shRNAs. (A) TRC1 constructs were amplified from transduced gDNA using an indexed forward primer and universal reverse primer which contain the Illumina P5 and P7 adapter sequences, respectively. Illumina adapter sequences are highlighted in blue, and primer sequences which bind to TRC vector sequences are highlighted in green. Directionality of all sequences is 5' to 3', except the reverse primer, which is shown 3' to 5'. Index sequences were designed to have no complementarity to the vector sequence, to minimize primer-based bias in sequencing results. Differences in TRC1 and TRC2 vectors are indicated in red font. The resulting 207 bp PCR amplicons are sequenced on an Illumina HiSeq 2500 using the custom sequencing primer shown in orange. (B) Final PCR amplicon, with sequencing read out shown in orange. A single-end 50 bp read (SE50) begins at the index sequence, covers the whole sense region of the shRNA, and the first 6 nucleotides of the antisense region.

2.2.4 Analysis of shRNA abundance

Sequencing reads were mapped back to the shRNA library using Bowtie 2.0 via a local installation of Galaxy (187-189). Short hairpins which were not detected in all three replicates at T=0 were filtered out of all analyses. Relative abundance of each shRNA was calculated as a percentage of total mapped reads. Three different analyses were then calculated: $\log_2$ fold change in shRNA abundance at T=4 vs. T=0 ($\log_2$ T4/T0), tumors vs. T=0 ($\log_2$ tumors/T0), and tumors vs. T=4 ($\log_2$ tumors/T4).

2.2.5 Scoring of candidate genes

The tumors vs. PD20 (T=4) analysis was subjected to two independent statistical tests. In the first test, p-values were determined by a two-sided unpaired t-test comparing the $\log_2$ fold change of each shRNA to a set of negative control shRNAs (indicated in Appendix C). Genes for which 3 or more shRNAs passed $p \leq 0.05$ and $\log_2$ fold change of 2-fold or more were scored as hits. In the second test, the cumulative distribution of all shRNAs per gene $\log_2$ fold changes of all shRNAs against a particular gene was compared to the background distribution in a ranked Kolmogorov–Smirnov test. Genes for which $p<0.05$ were scored as hits. Genes which scored in both analyses are reported as final candidate hits.

2.3 Results

2.3.1 Parallel *in vitro* and *in vivo* NHR and coregulator screen

In order to investigate the role of hormone receptor pathways in lung tumorigenesis, we assembled a mini-library of 1062 shRNAs against 40 hormone receptors and 72 co-regulators, with an average coverage of ~7.4 shRNAs/ gene (details provided in Appendix C, Table C1). A well-known limitation of xenograft experiments is the unknown tumor-initiating capacity of individual cell lines. The lung adenocarcinoma cell line H1819 was chosen for this study because it harbors a large ALDH-positive subpopulation (~30%), a marker we have previously shown to correlate with tumor-initiating capacity (190,191). Since ALDH-positive subpopulations in NSCLC cell lines are enriched for cells capable of tumor-initiation, we reasoned that cell lines with a large ALDH-positive population would be able to maintain representation of the library during xenograft growth *in vivo*, due to high engraftment efficiency. H1819 cells were transduced with the library pool in triplicate, followed by selection for stably integrated cells in antibiotic (Figure 2.3A). Cell counts of the replicate infected flasks were then compared with a non-infected flask seeded at the same time confirmed an infection efficiency of ~30%, and an average library coverage of ~863-fold. After a brief period of expansion, reference samples were collected for each replicate, and then the remaining cells in each replicate were split between either continued *in vitro* culture or subcutaneous injection into two NOD-SCID mice. In order to maintain a high level of library representation in the tumors, 5 million cells were injected per mouse. For continued *in vitro* culture, cells were passaged for a total of ~20 population doublings with reference samples collected at various time points, while tumors were allowed to reach a volume of ~300 mm^3 before harvesting. Since tumors from the third

replicate were disparate in their growth rates, they were excluded from further downstream analysis (Figure 2.4). Genomic DNA was harvested from the first reference time point (T=0), PD20 time point (T=4) and tumors. Short hairpin sequences were then amplified by PCR and submitted for quantification by deep sequencing.

The PCR primers used in this study detected >97% of TRC1 library constructs in all three T=0 reference replicates, and >94% of these constructs were detected at all later time points, confirming good library representation throughout the screen. Subsequent analyses were restricted only to shRNAs detected in all three replicates at T=0. Relative abundance of each shRNA was calculated as a percentage of total mapped reads. The abundance of individual shRNAs correlated very well across *in vitro* replicates (Figure 2.3B). Interestingly, shRNAs in tumors from the same replicate infection also showed much higher correlation than tumors from different replicates, however Spearman correlation coefficients were still above 0.6 (data not shown). Thus these data confirmed good reproducibility among our screening replicates.

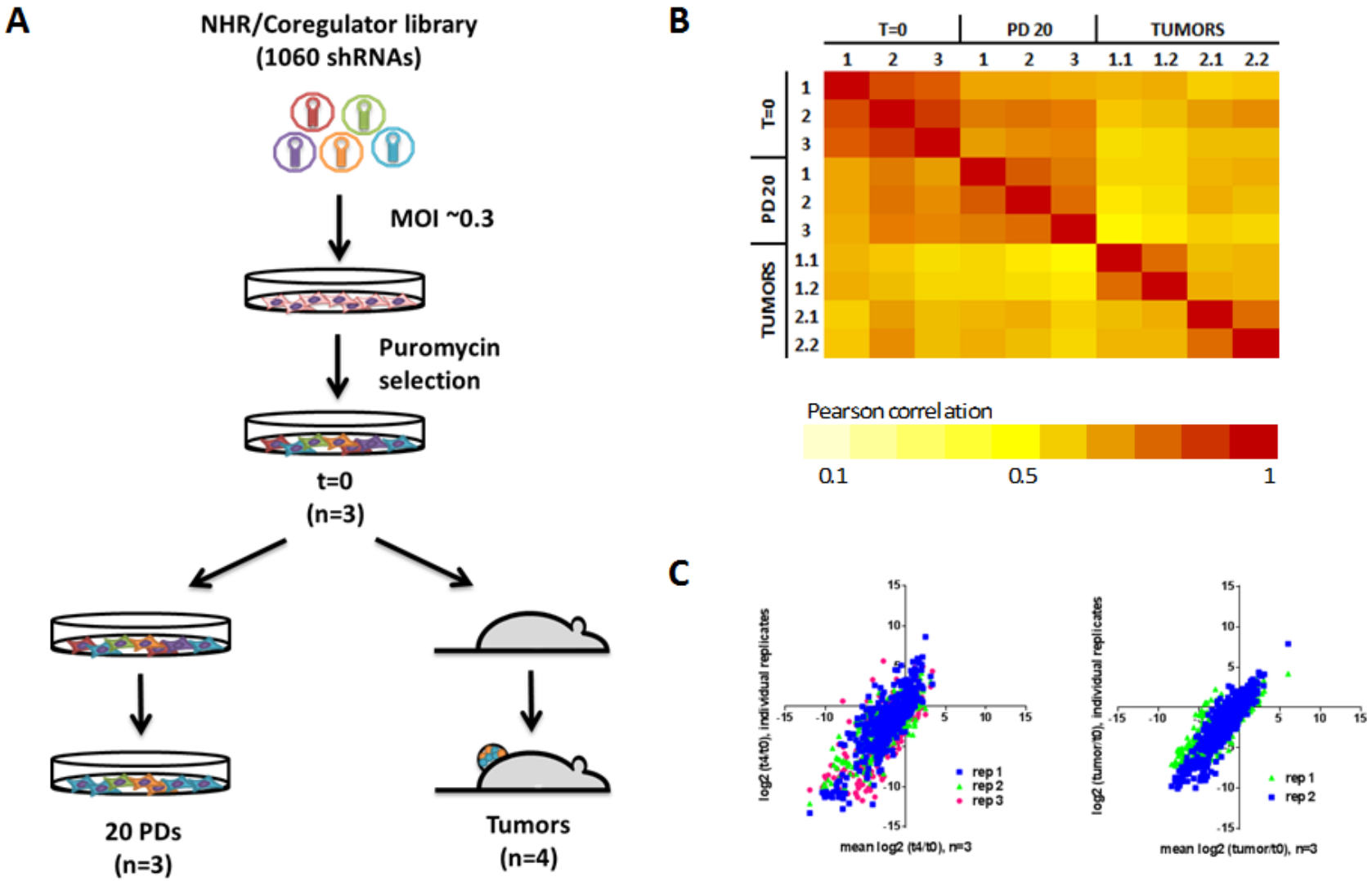

A
NHR/Coregulator library
(1060 shRNAs)
MOI ~0.3
Puromycin
selection
t=0
(n=3)
20 PDs
(n=3)
Tumors
(n=4)
B
T=0
PD 20
TUMORS
1 2 3 1 2 3 1.1 1.2 2.1 2.2
T=0
PD20
TUMORS
Pearson correlation
0.1
0.5
1
C
log2 (t4/t0), individual replicates
mean log2 (t4/t0), n=3
rep 1
rep 2
rep 3
log2 (tumor/t0), individual replicates
mean log2 (tumor/t0), n=3
rep 1
rep 2

Figure 2.3. Outline of parallel *in vitro* and *in vivo* screening strategy. (see previous page) (A) Experimental outline. Briefly, H1819 cells were infected with a pooled shRNA library against nuclear hormone receptors and coregulators at low MOI. After puromycin selection and expansion, a reference sample was collected (t=0), and the remaining cells were split into parallel *in vitro* and *in vivo* assays. Cells maintained *in vitro* were cultured for 20 population doublings, at which time a final reference sample was collected. Cells in the *in vivo* arm were injected subcutaneously into NOD-SCID mice, and tumors were harvested after surpassing a minimum volume of 300 mm^3. Short hairpins were PCR-amplified from gDNA and quantified by massively parallel sequencing. (B) Correlation map of shRNA abundance detected in each time point sampled. Pearson correlations between shRNA abundance detected at t=0, t=PD20, and in tumors reveal that *in vitro* replicates, and tumors derived from the same original *in vitro* replicate, correlate well. (C) Comparison of log2 fold changes observed between *in vitro* replicates and tumors. Plots of log2 fold changes in the *in vitro* screen (left) and log2 fold changes in the *in vivo* screen (right) confirm good correlation between experimental replicates.

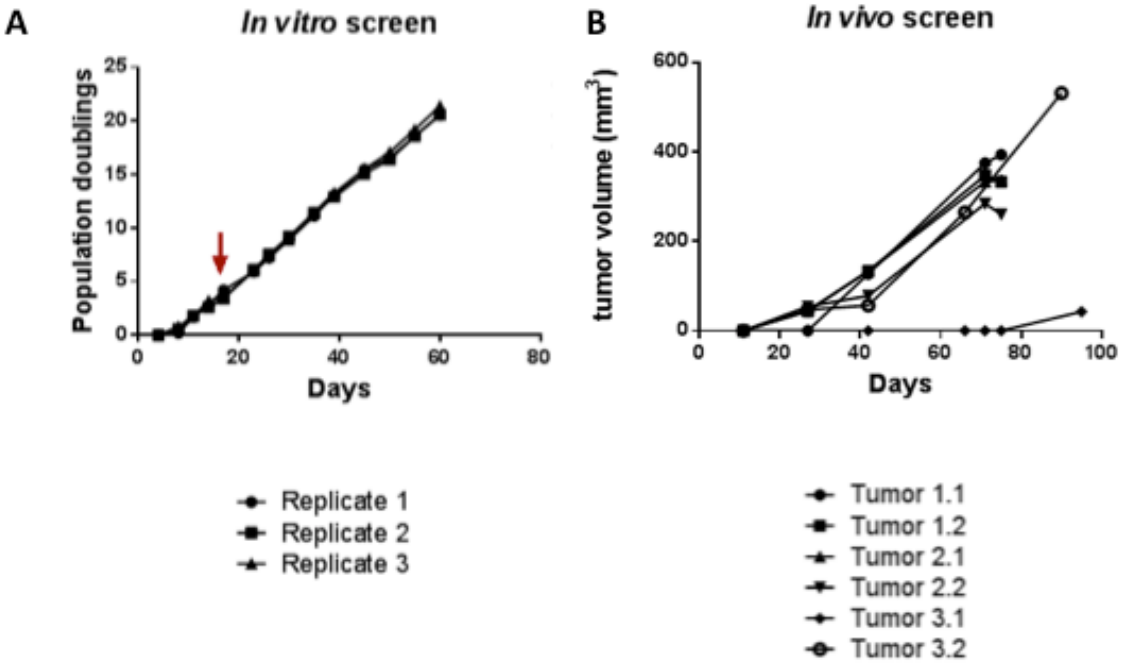


Figure 2.4. Growth curves during parallel *in vitro* and *in vivo* screening. (A) Three independent library transductions were performed, and after 4 population doublings (red arrow), cells were split parallel *in vitro* and *in vivo* screens. Cells were kept in continuous tissue culture for 20 population doublings (PDs). (B) For every biological replicate (independent viral transduction), two NOD-SCID mice were injected subcutaneously with 5 million cells each. Tumors were allowed to grow to at least 300 mm3 before harvest. Since the tumor 3.2 (*in vitro* replicate 3, tumor 2) exhibited significant delay in growth compared to the others, tumors from replicate 3 were not included in the final analysis.

2.3.2 Identification of candidate genes

To assess the ability of our screen to detect biologically meaningful relationships, two initial analyses were calculated from the relative shRNA abundance mapped reads: $\log_2$ fold change in shRNA abundance at PD 20 vs. T=0 ($\log_2$ T4/T0), and tumors vs. T=0 ($\log_2$ tumors/T0). Relative shRNA abundance in each time point, log fold changes, and t-test results are included in Appendix D. Fold changes between replicates correlated well (Figure 2.3C). Statistical filters were applied at both the shRNA and gene levels, identifying seven genes as being required for *in vitro* growth: *BRCA1, CCND1, MED1, PHB, HNRNPU, PELP1,* and *ALDH1A3,* and three genes required specifically for *in vivo* growth: *FOXA1, NCOR2,* and *HDAC1* (Figure 2.5, Table 2.2). The top scoring genes in each category by KS-test were *BRCA1* and *FOXA1.* Although no nuclear receptor genes passed filter, the identification of *ALDH1A3* (included in the library as a positive control) and *CCND1* as genes required for *in vitro* growth of H1819 are consistent with known oncogenic roles for these genes in lung cancer (190-193), demonstrating the utility of our method in reliably identifying essential genes in lung tumorigenesis.

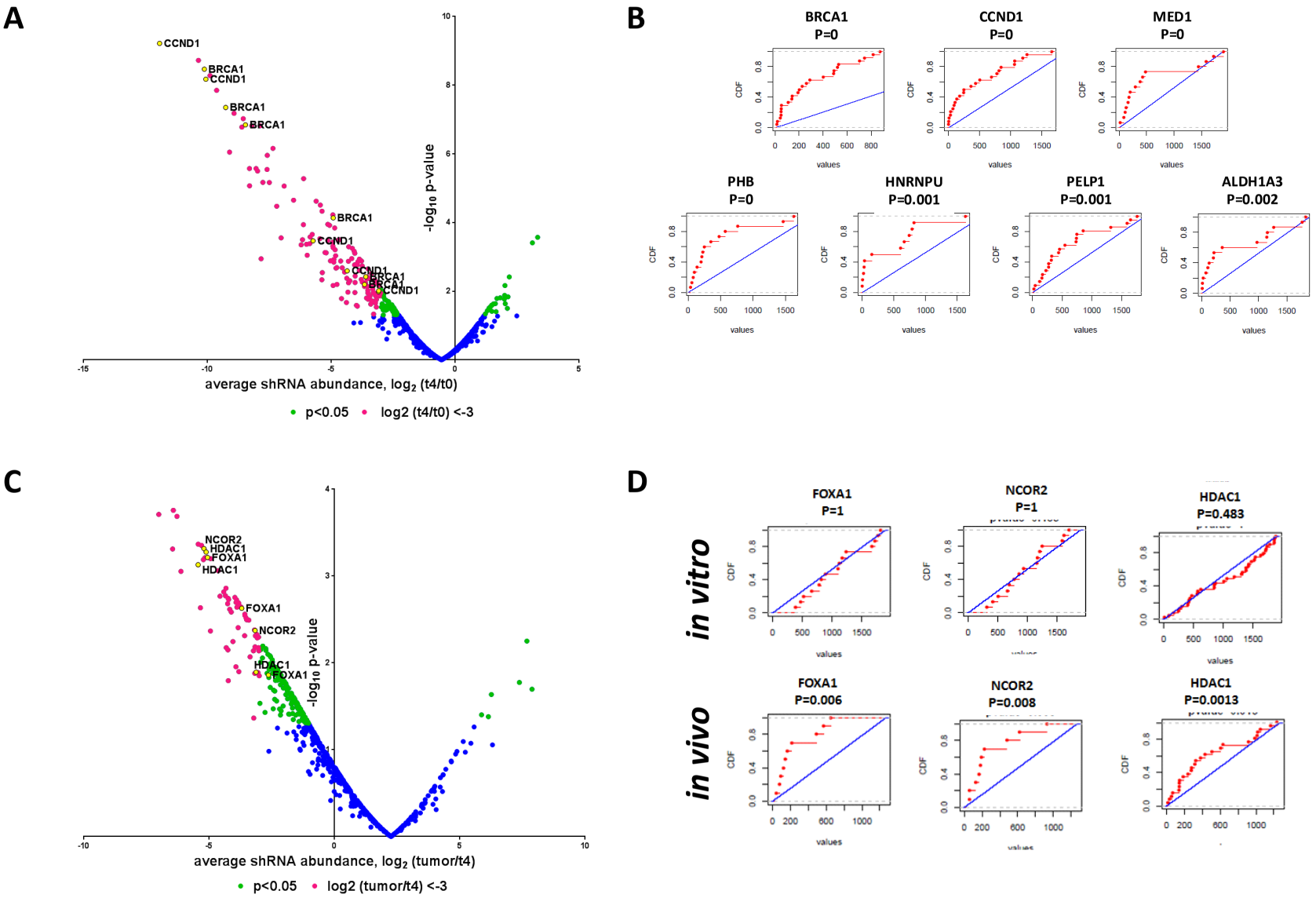

A
CCND1
BRCA1
CCND1
BRCA1
BRCA1
BRCA1
CCND1
BRCA1
CCND1
-log10 p-value
average shRNA abundance, log2 (t4/t0)
p<0.05
log2 (t4/t0) <-3
B
BRCA1
P=0
CCND1
P=0
MED1
P=0
PHB
P=0
HNRNPU
P=0.001
PELP1
P=0.001
ALDH1A3
P=0.002
CDF
values
C
NCOR2
HDAC1
FOXA1
HDAC1
FOXA1
NCOR2
HDAC1
FOXA1
-log10 p-value
average shRNA abundance, log2 (tumor/t4)
p<0.05
log2 (tumor/t4) <-3
D
in vitro
FOXA1
P=1
NCOR2
P=1
HDAC1
P=0.483
in vivo
FOXA1
P=0.006
NCOR2
P=0.008
HDAC1
P=0.0013
CDF
values

Figure 2.5. Identification of genes essential for *in vivo* tumorigenesis. (see previous page) (A) Volcano plot of log2 fold changes at PD 20 vs. t=0, with select genes passing a filter of ≥ 3 shRNAs with log2 < -2 and p<0.05 shown. (B) Cumulative distribution function plots for select genes which passed filter at both the shRNA level and exhibit p<0.05 by the K-S test. Plots for the *in vitro* distribution of each gene are shown on top, and plots for the *in vivo* distribution of each gene are shown on the bottom. (C) Volcano plot of log2 fold changes in tumors vs. PD 20, with select genes passing a filter of ≥ 3 shRNAs with log2 < -2 and p<0.05 shown. (D) Cumulative distribution function plots for genes which passed filter at both the shRNA level and exhibit p<0.05 by the K-S test. Plots for the *in vitro* distribution of each gene are shown on top, and plots for the *in vivo* distribution of each gene are shown on the bottom. K-S tests were performed by Elizabeth McMillan.

In vitro	***In vivo* only**
BRCA1	FOXA1
CCND1	NCOR2
MED1	HDAC1
PHB	
HNRNPU	
PELP1	
ALDH1A3	

Table 2.2. Genes required for viability in H1819 cells *in vitro,* or only *in vivo*.

2.4 Discussion

It is widely accepted that cell lines undergo different nutritional and stress-related selective pressures during growth *in vitro* and *in vivo,* yet there is conflicting evidence on how cell lines respond to these pressures. One recent study from Amgen and Cellecta used a barcoded library to demonstrate that that while minimal changes in clonal representation were

observed during *in vitro* culture, most of the cells in a xenograft tumor could be traced to less than 10% of the original population (194). By contrast, Porter et al observed clonal dominance during *in vitro* culture of the lung adenocarcinoma cell line HCC827, but wider clonal representation during *in vivo* growth (195). These phenomena are likely to be highly cell line specific, and underscore the importance of selecting a suitable experimental system for use in pooled shRNA screening *in vivo*.

Here we demonstrate that with the cell line H1819, we were able to maintain full representation of a 1062-member shRNA library both *in vitro* and *in vivo.* This was likely due to several key factors in experimental design: (1) Selection of a cell line with a high ALDH-positive subpopulation, (2) the use of high library representation (> 500 x) in the initial infection procedure, (3) continual passaging at subconfluency, and (4) the use of high cell number (and thus high library representation) at the point of injection into mice. The successful maintenance of library complexity using these experimental conditions suggests that other cell lines with unknown tumor-initiating capacity may also be successfully screened if high library representation can be achieved in the initial stages of the workflow.

CHAPTER THREE

IDENTIFICATION OF BRCA1 AS AN ESSENTIAL GENE IN A SUBSET OF NSCLCs

'"The more outre' and grotesque an incident is the more carefully it deserves to be examined, and the very point which appears to complicate a case is, when duly considered and scientifically handled, the one which is most likely to elucidate it."

-Sherlock Holmes*, The Hound of the Baskervilles*

3.1 Introduction

The identification of BRCA1 as an essential gene for *in vitro* growth in H1819 lung adenocarcinoma cells was initially surprising, given its generally known role as tumor suppressor in estrogen-dependent cancers. However, BRCA1 is absolutely required during embryonic development (196-198), and repression of BRCA1 in normal cells is known to induce growth arrest (199,200). In breast and ovarian cancers, BRCA1 is functions as a tumor suppressor that regulates genomic stability, but the role of BRCA1 in other tumor types is not well understood. In NSCLC, high expression of BRCA1 is thought to mediate resistance to cisplatin-based therapy, and is significantly correlated with worse overall survival (201-204). The correlation between BRCA1 expression and poor prognosis was also observed in our analyses of three independent tumor datasets: Director's Challenge (205), TCGA (90), and PROSPECT (MDACC) (Figure 3.1). These data suggest that, at least in lung cancer, BRCA1 may support oncogenic growth by promoting resistance to standard chemotherapies.

3.2 Materials and methods

3.2.1 Cell culture

All cell lines were obtained from either the NCI or Hamon Cancer Center libraries. Lung cancer cell lines were maintained in RPMI-1650 supplemented with 5% fetal bovine serum (Sigma), and passaged using standard trypsinization methods. Cell counts were performed on a Beckman Coulter Z2 Particle Count and Size Analyzer. Cell line identity was confirmed by DNA fingerprinting (PowerPlex 1.2 Kit, Promega) and mycoplasma-free status was verified by PCR (e-Myco Kit, Boca Scientific). All cell culture experiments were maintained in a humidified incubator at 37^{o}C, in 5% CO_2.

3.2.2 Generation of stable cell lines

Lentivirus for individual short hairpin constructs was prepared by transfection of 293T cells with packaging plasmids (pCMV-dR8.91 and pMD2-VSV-G) and the shRNA construct of interest using FuGene transfection reagent (Promega). Virus was harvested in R5 media over the course of 3 days, pooled, and then filtered through a 0.45 um filter prior to use. Cells were infected at high MOI ≥1 in the presence of 4 ug/mL polybrene, followed by selection in 1.0 ug/mL puromycin for at least 3 days. Growth assays and harvesting for molecular profiling were typically performed 5-7 days after initial infection.

3.2.3 Cell proliferation and clonogenicity assays

For MTS cell proliferation assays, cells were seeded in 100 uL media at 1000-4000 cells/well in triplicate, in three 96-well plates. At the desired time points, 20 uL MTS reagent (Promega) was added to each well and the plates were incubated at 37^{o}C for 1-3 hrs. Absorbance readings were taken at Day 1 and Day 5 or Day 7, and proliferation rate was estimated using the difference in absorbance between the end time point vs. reference. For clonogenicity assays, cells were plated at a density of 1000-2000 cells per well in 6-well dishes and allowed to incubate for 1-3 weeks before staining with crystal violet.

3.2.4 Quantitative RT-PCR

Total RNA was isolated from cell pellets using the RNeasy Plus Mini Kit (QIAGEN), and cDNAs were generated using the iScript cDNA Synthesis Kit (Bio-Rad). Gene-specific TaqMan probes were utilized for quantitative analyses of mRNA transcript levels, with the GAPDH gene used as an internal reference to normalize input cDNA (Applied Biosystems; BRCA1: Hs01556193_m1, GAPDH: Hs02758991_g1). PCR reactions were performed in triplicate, run on an ABI 7300 Real-Time PCR System, and analyzed with the SDS software (Applied Biosystems). The delta-delta-CT method was used to calculate relative mRNA expression levels.

3.2.5 Tumor cohorts and survival analyses

The Profiling of Resistance patterns and Oncogenic Signaling Pathways in Evaluation of Cancers of the Thorax (PROSPECT) cohort, also known as the UT Lung Cancer Specialized

Program of Research Excellence (UT Lung SPORE) cohort, consists of surgically resected tumors with both neoadjuvant and adjuvant treatment, representing 183 lung adenocarcinomas and 80 squamous cell carcinomas with detailed clinical annotations on treatment history (206). Genome-wide Illumina Human WG-6 V3 microarray expression profiles from this cohort were obtained as previously described (206), and were previously deposited in the GEO database as GSE42127. RNA-seq expression profiles for lung adenocarcinomas in The Cancer Genome Atlas (TCGA) cohort (n=126 lung adenocarcinomas) were accessed from the publically available database (90). The NCI Director's Challenge cohort is a clinically curated dataset on 443 early stage lung adenocarcinomas with whole-genome Affymetrix U133A microarray expression data publically available (205). Survival analyses were performed using in-house Visual Basic MicroArray Transformation in Microsoft Excel (MATRIX) v1.508 software (L. Girard, manuscript in preparation). Patient survival plots were generated using the R package "survival". Patients were stratified into two groups based on user-defined gene expression criteria, and survival data were then compared using log-rank test and Kaplan-Meier curves.

3.3 Results

3.3.1 BRCA1 is essential for viability in a subset of lung cancers

BRCA1 is absolutely required during embryonic development (196-198), and repression of BRCA1 in normal cells is known to induce growth arrest (199,200). In breast and ovarian cancers, BRCA1 is well characterized as a tumor suppressor that functions and genomic

instability. But the role of BRCA1 in other tumor types is not well understood. In NSCLC, high expression of BRCA1 is thought to mediate resistance to cisplatin-based therapy, and is significantly correlated with worse overall survival (201-204). The correlation between BRCA1 expression and poor prognosis was also observed in our analyses of three independent tumor datasets: Director's Challenge (205), TCGA (90), and PROSPECT (MDACC) (Figure 3.1). These data suggest that, at least in lung cancer, BRCA1 may support oncogenic growth by promoting resistance to standard chemotherapies.

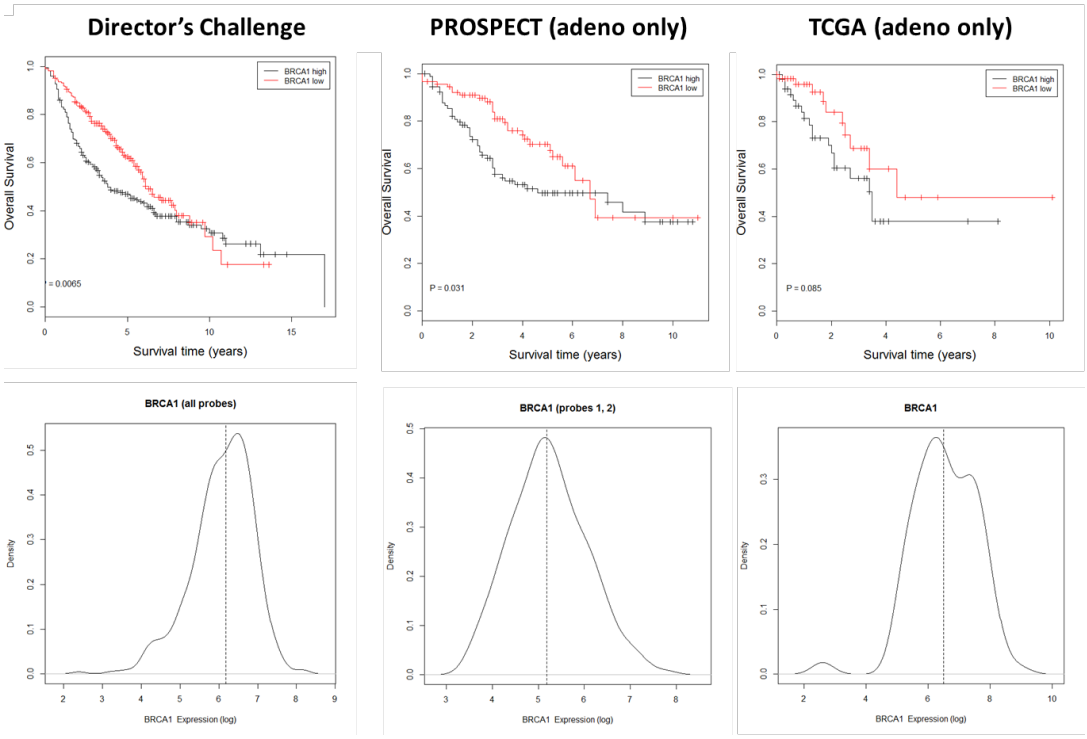


Figure 3.1. High expression of BRCA1 is significantly correlated with worse overall survival in lung adenocarcinoma patients. Kaplan-Meier overall survival curves in three independent tumor cohorts by BRCA1 expression (top panel). Patients were stratified by median expression (bottom panel).

In order to validate *BRCA1* as an essential *in vitro* hit in the lung adenocarcinoma cell line H1819, three individual shRNAs which scored as significantly depleted in the screen were tested for ability to knockdown BRCA1. Each shRNA was able to reduce BRCA1 mRNA levels and inhibit both bulk proliferation and colony formation in H1819 (Figure 3.2). We then screened the most potent shRNA against a panel of NSCLC and one breast cancer cell line, and found differential levels of sensitivity to BRCA1 inhibition as assayed by growth rate and clonogenicity (Figure 3.3A-D). Cell cycle analysis after knockdown of BRCA1 in HCC4017 revealed a significant sub-G0 shoulder, suggesting that suppression of BRCA1 expression induces apoptosis (Figure 3.3E). Viability and colony forming efficiency with shBRCA1 did not correlate with BRCA1 mRNA expression.

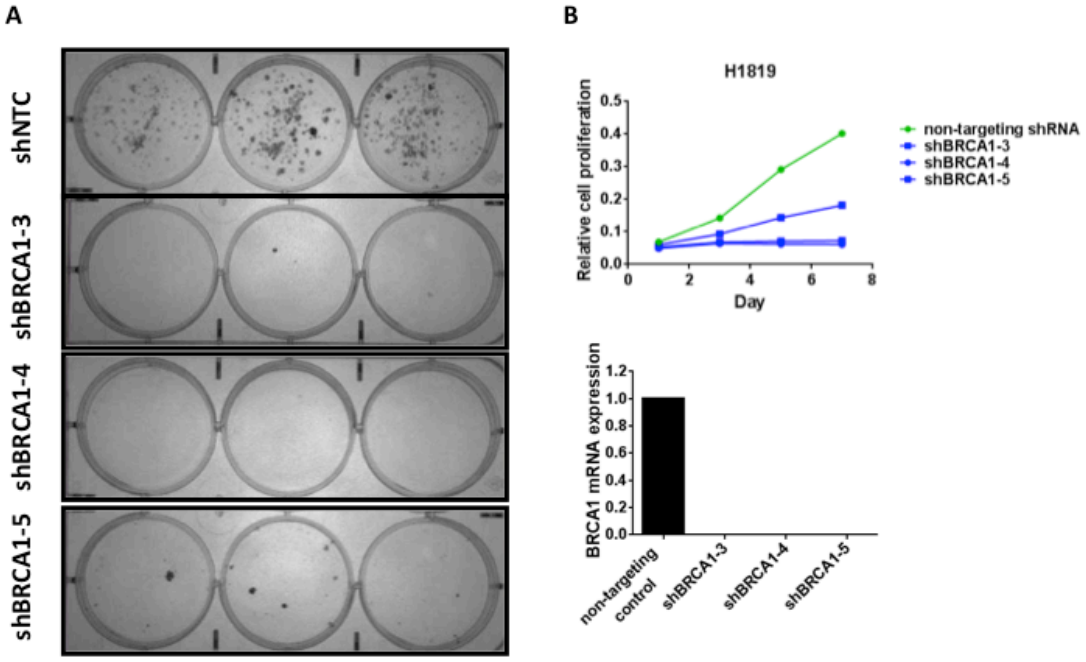


Figure 3.2. BRCA1 is required for viability in H1819. Knockdown of BRCA1 with individual shRNAs significantly reduces growth in H1819. (A) Colony formation assays with non-targeting and shBRCA1. (B) Short term cell proliferation was also measured by MTS assays. (C) BRCA1 mRNA expression levels were quantified by QPCR.

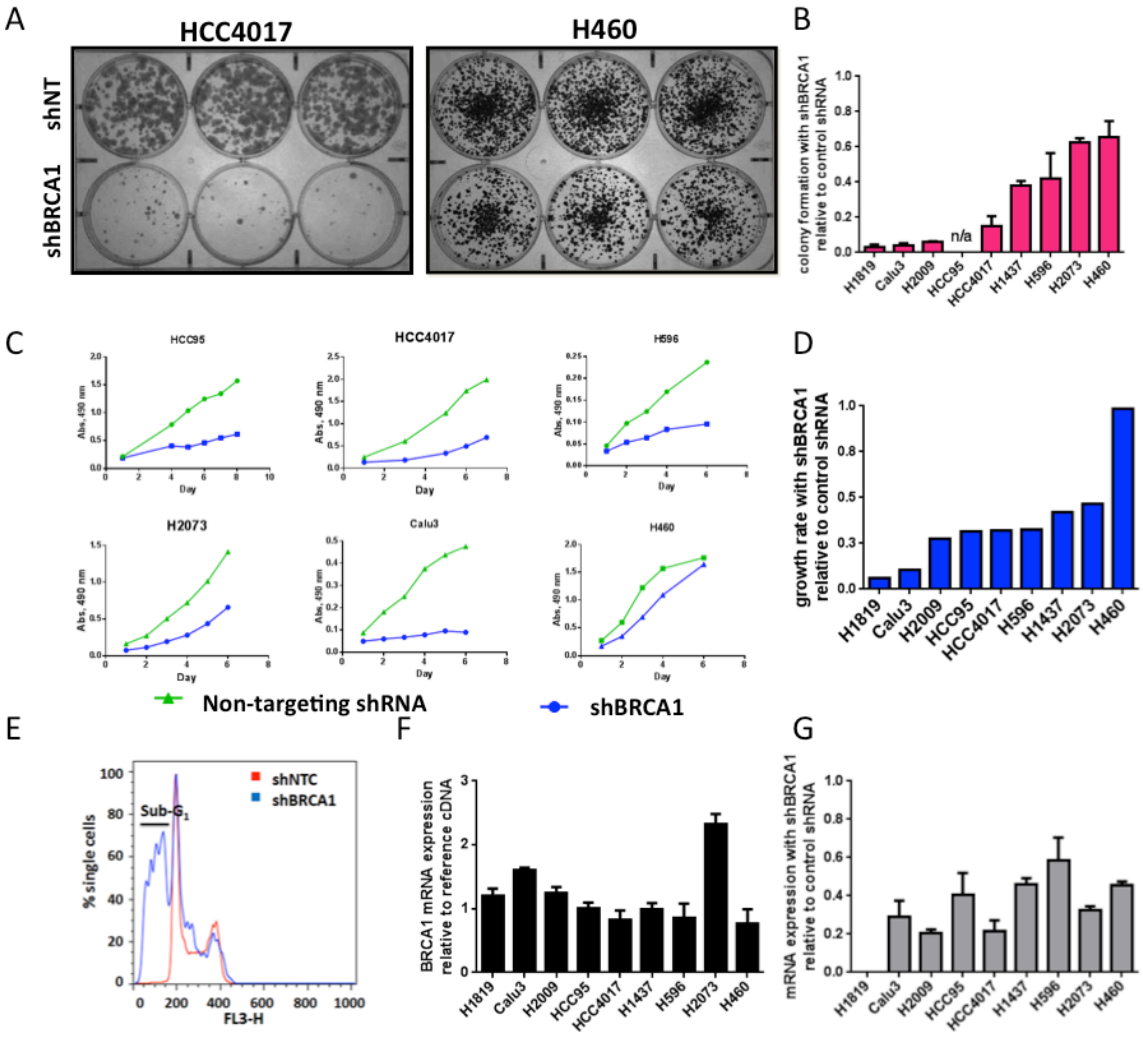


Figure 3.3. A panel of NSCLC cell lines exhibits differential dependencies on BRCA1. Representative colony formation assays (A) and MTS cell proliferation assays (C) are shown in the top left panels. Clonogenicity (B) and proliferation rates (D) relative to parental lines with non-targeting shRNAs are shown in the bottom panel. n/a = Parental cell line did not form colonies. (E) Knockdown of BRCA1 in HCC4017 increases the sub-G_1 fraction in propidium iodide cell cycle analysis. (F,G) QPCR quantitation of BRCA1 mRNA expression levels in parental cells with non-targeting shRNA (F), or shBRCA1 (G).

Notably, the BRCA1-mutant breast cancer cell line HCC1937 also appeared to be dependent on residual BRCA1 levels for viability, in that knockdown of BRCA1 completely

significantly reduced proliferation rate and completely abrogated colony formation (data not shown). Full-length BRCA1 is not expressed in this cell line (207,208), however studies on alternative splicing products for BRCA1 have revealed that an alternative splicing product of BRCA1 termed BRCA1-IRIS is retained and expressed HCC1937 (209). Full length BRCA1 comprises an uninterrupted open reading frame from exon 2 to exon 24 and is 1863 amino acids long, while the BRCA1-IRIS open reading frame terminates after exon 11 (Figure 3.4). BRCA1-IRIS expression has been confirmed in multiple adult mouse tissues and in breast and ovarian tumors (210,211), and overexpression of this isoform promotes transformation in normal mammary epithelial cells (210). Inhibition of BRCA1-IRIS can sensitize breast and ovarian cells to cisplatin, suggesting that it may be a viable therapeutic target (211,212). It is likely that BRCA1 expression detected at the mRNA level by qPCR is due to BRCA1-IRIS expression, and that reduction in viability observed after shBRCA1 is due to reduction of the BRCA1-IRIS transcript. The reagents used in this study do not distinguish between BRCA1 isoforms, thus it remains possible that the dependency observed in the cell lines tested may be due either in part or perhaps wholly on the pro-growth functions of BRCA1-IRIS. The expression of BRCA1-IRIS in lung tumors has not yet been explored, however future studies on expression levels and functional interactions with full-length BRCA1 may provide insight into the viability of this therapeutic strategy.

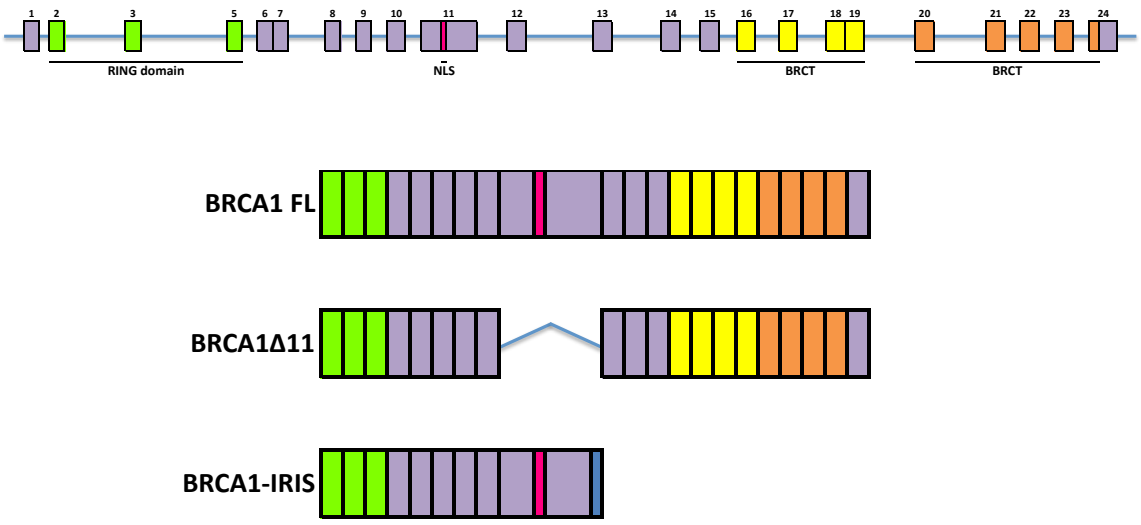


Figure 3.4. Structure of the human *BRCA1* gene and isoforms. The human *BRCA1* gene is comprised of 24 exons, with highly conserved motifs at both termini (top). Exons comprising the RING domain are shown in green, a nuclear localization signal (NLS) in pink, and tandem BRCT domains in yellow and orange. The three known protein products produced from this locus are full-length BRCA1 (BRCA1 FL), BRCA1Δ11, and BRCA1-IRIS (bottom). Full length BRCA1 comprises an uninterrupted open reading frame from exon 2 to exon 24 and is 1863 amino acids long. BRCA1Δ11 contains the same conserved motifs at both termini but lacks a nuclear localization signal in the final product and is expressed at low abundance. BRCA1-IRIS is a 1399 amino acid protein that contains the RING domain and NLS, and extends several codons into intron 11 (shown in blue) before termination.

3.3.2 BRCA1-independent lung cancers may be sensitive to PARP inhibition

The identification of NSCLC cell lines which were not sensitive to BRCA1 inhibition raised the intriguing possibility that requirement for BRCA1 may be context-dependent, and provide a potential therapeutic window. In order to investigate whether BRCA1 dependency could be correlated with pharmacological intervention, we performed correlation analyses on drug sensitivity profiles obtained in our group on a large panel of NSCLC cell lines across a diverse panel of pharmacological agents. Out of 48 agents analyzed, no correlations were found to be statistically significant, however filtering for $|\rho| \geq 0.7$ identified a negative correlation between

BRCA1 dependency and sensitivity to the PARP inhibitor olaparib (Figure 3.5). PARP inhibition is known to be synthetically lethal with BRCA1-deficiency in breast and ovarian cancers, due to the reliance of HR-deficient cells on base-excision repair pathways (96,97) (ref). This suggests that, similar to breast and ovarian cancers, lung cancers which do not require BRCA1 for viability may have lost HR pathway function and be sensitive to PARP inhibition.

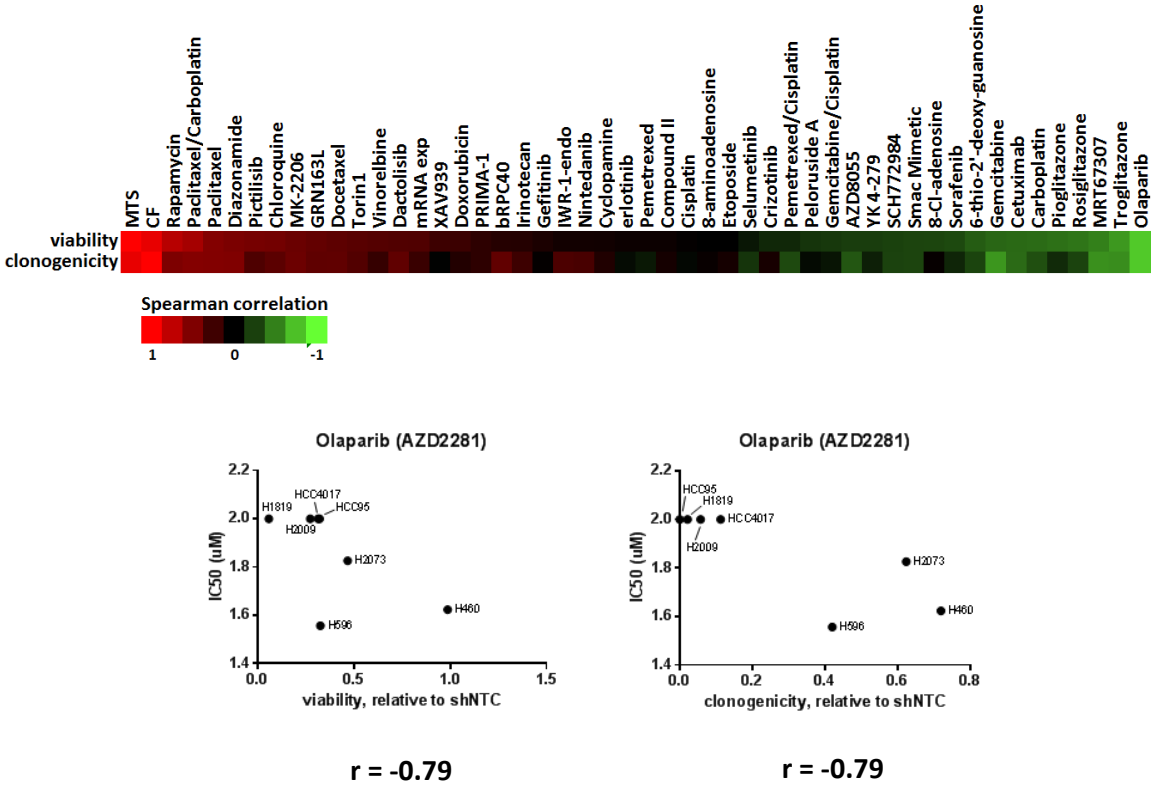


Figure 3.5. BRCA1 dependency may be correlated with sensitivity to olaparib. Median IC50 values for a select set of monotherapies screened across a panel of NSCLC cell lines were analyzed for correlation to BRCA1 dependency. No correlations reached statistical significance by t-test, however a trend was observed for sensitivity to olaparib.

3.3.3 Loss of STK11 may rescue lethality of BRCA1 inhibition in NSCLCs

In order to explore molecular mechanisms for putative HR deficiency in lung tumors, we compared mutation profiles of the tested cell lines. Whole exome sequencing data (Wheeler and colleagues at Baylor College of Medicine, unpublished data) was filtered for nuclear receptor and coregulator genes (see Table 1.1), driver genes in NSCLC, and genes known to be involved in DNA damage repair (see Appendix F). No *BRCA1/2* mutations were found in the panel of cell lines screened in this study. The cell line H595 exhibited reduced dependency on BRCA1 and harbors a mutation in a known phosphorylation site on ATR (S435T) (213), however the functional consequence of a serine-to-threonine transition at this site is not known. The two cell lines with the most extreme BRCA1-independent phenotypes also harbor mutations in *PARP1* (Figure 3.6). PARP mutations have not been previously implicated in any cancer types, thus the functional significance of the mutations seen here is also unknown. Interestingly, 3 out of 4 cell lines which are more BRCA1-independent harbor truncating mutations in *STK11* (Figure 3.6). We speculate that loss of LKB1/STK11 may be a novel mechanism by which lung tumor cells become deficient in DNA damage response, rendering inhibition of BRCA1 redundant in this context.

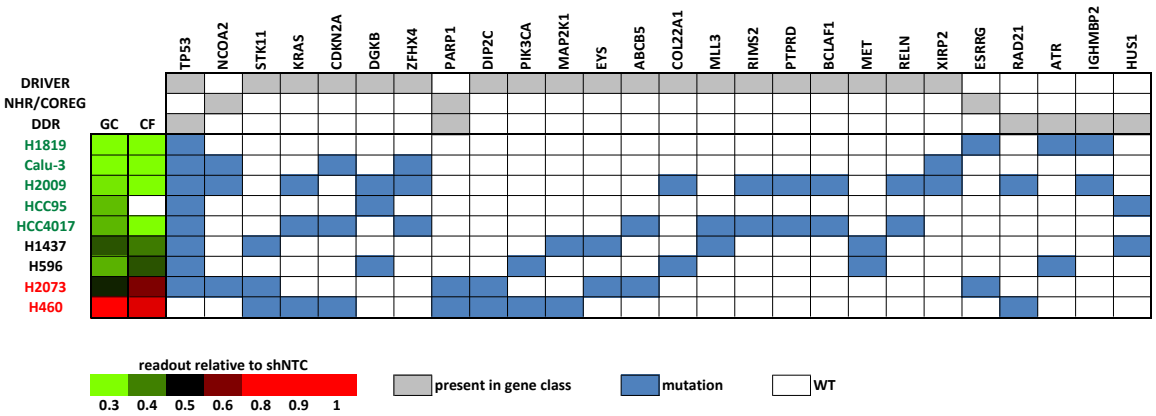


Figure 3.6. Mutation status for select genes across cell lines tested for dependency on BRCA1. Whole exome sequencing data was filtered for nuclear receptor and coregulator genes (see Table 1.1), driver genes in NSCLC (see Table 1.2), and genes known to be involved in DNA damage repair (ref). Genes with mutations in two or more cell lines in the panel are shown. BRCA1-dependent cell lines are indicated in green, and BRCA1-independent cell lines in red.

3.4 Discussion

BRCA1 is a well-characterized tumor suppressor with essential functions in homologous recombination (HR) repair of DNA double-strand breaks (DSBs). The high-fidelity nature of HR places BRCA1 in a caretaker role in maintaining genome integrity during cell proliferation. Inheritance of germline inactivating mutations in one allele of either *BRCA1* or *BRCA2* are associated with early-onset breast cancer and a lifetime risk of 50-80%, and a lifetime risk of 30-50% for ovarian cancer (214). Carriers also have an increased risk for pancreatic, stomach, laryngeal, fallopian tube and prostate cancers, although at much lower rates (214). The reasons for the tissue-tropism observed in BRCA1 mutation carriers are not well understood, but may be partly due to disruption of BRCA1-ER interactions which allow only estrogen-dependent tissues to continue proliferation in an HR-deficient context (215). This is in apparent

contradiction to the observation that BRCA1-mutant breast cancer tends to be ER-negative, (216), although there is evidence to suggest that loss of BRCA1 reduces expression of ERalpha (217).

Dependence upon BRCA1 for survival in lung cancer cell lines may reflect an essential role in cell proliferation that is not tumor-specific. Failure to repair DSBs that occur at replication forks during S phase results in activation of cell cycle checkpoints that induce growth arrest (ref). Thus it is possible that that BRCA1, as in the context of development, is simply an essential gene in estrogen-independent tissues such as the lung. Cell lines and tumors that are able to survive in the context of BRCA1-deficiency may arise from oncogenotypes which either rescue the growth arrest associated with BRCA1 depletion, or in which BRCA1 depletion is redundant. In mouse models of BRCA-deficiency, alterations in other DDR genes such as *TP53* Xu:2001ep}, *ATM* (218), or *CHEK2* (218) are able to rescue the lethality associated with BRCA1 depletion. Loss of *53BP1* has also been shown to rescue growth in *BRCA1*$^{\Delta 11/\Delta 11}$ MEFs (219). If a cell line already harbored a rescuing alteration, then depletion of BRCA1 would have little phenotypic effect in the assays used in this study. Alternatively, depletion of BRCA1 in certain oncogenic backgrounds may be redundant, if HR repair is already rendered defective by another mechanism.

The discovery that BRCA-deficient breast and ovarian cancers are sensitive to PARP inhibition (97,98), has spurred efforts to identify other DDR-related synthetic lethal relationships in other tumor types. While BRCA1/2 mutations result in tissue-specific cancers,

defects in other components of DNA damage response pathways are also known to drive genetic instability in solid tumors. For example, loss of function mutations in mismatch repair genes *MSH2* and *MLH1* are associated with hereditary non-polyposis colorectal cancer (HNPCC) (ref). In addition to BRCA1/2 mutations, HR-deficiencies caused by loss-of-function mutations in *PALB2, ATM, RAD51C*, or *RAD51D* are also associated with hereditary breast and ovarian cancers (ref). In lung cancer, defects in DDR as inferred by low BRCA1 or ERCC1 expression are correlated with response to platinum-based chemotherapies (201-203,220-225). In addition, a recent GWAS study identified a *BRCA2* variant as a risk factor for squamous cell carcinoma (226). Identification of new biomarkers for HR-deficiency may identify subsets of patients who can therapeutically benefit from PARP inhibition. Towards this end, Peng and colleagues recently reported that a 230-gene signature for HR-deficiency (HRD) could be used to identify HRD tumors in multiple tissue types, including lung (227). Other investigators have also recently identified putative HR-deficiencies in a subset of NSCLC cell lines (228). Expansion of this work to explore molecular correlates within these and more cell lines may reveal biomarkers for PARP sensitivity in human lung tumors.

Recently, several lines of evidence have suggested that LKB1/STK11 may play a role in DNA damage response. LKB1/STK11 localizes to the ends of DNA double-strand breaks (229), and is phosphorylated by ATM kinase in response to ionizing radiation (230). Depletion of LKB1 has been shown to inhibit HR-mediated repair of double-strand breaks (231), UVB-induced damage (232), and potentially non-homologous end joining (229). In addition, STK11 has been implicated in positive regulation of BRCA1 mRNA stability (231). Therefore, it is possible that

STK11-mutant cancer cells may exhibit intrinsic deficiencies in DNA damage response. Expansion of the screen for BRCA1-dependency and olaparib sensitivity to a larger panel of cell lines that include other STK11 and DDR gene mutants will be required to explore these putative associations. Future studies will include exploring the possible association between STK11 inactivation and olaparib sensitivity in lung tumors.

CHAPTER FOUR

IDENTIFICATION OF FOXA1 AS A KEY REGULATOR OF TUMORIGENESIS IN NSCLC

"It is of the highest importance in the art of detection to be able to recognize, out of a number of facts, which are incidental and which vital. Otherwise your energy and attention must be dissipated instead of being concentrated."
-Sherlock Holmes, The Reigate Puzzle

4.1 Introduction

Three genes were identified as essential *in vivo* but not *in vitro: FOXA1, HDAC1,* and *NCOR2.* All three of these genes are nuclear receptor coregulators, with known roles in chromatin remodeling or epigenetic regulation of gene expression. HDAC1 is an epigenetic regulator whose overexpression is thought to drive tumorigenesis in multiple tissue types, including lung (233,234). Inhibitors of class I histone deacetylases are actively being investigated for treatment of NSCLC in phase I and II clinical trials (235,236). NCOR2/SMRT is a is repressive co-regulatory factor for several transcription factors, including the retinoic acid receptor and thyroid hormone receptor, and functions in part by recruiting HDACs to promoter regions (237). FOXA1 is a pioneer transcription factor, able to bind condensed chromatin to allow a permissive state for other transcription factors to bind (238). It has well known roles as an essential co-regulator for estrogen and androgen receptors in breast and prostate cancers, respectively (239-242), but the role of FOXA1 in lung cancer is less well understood.

4.2 Methods

4.2.1 Cell culture, cell proliferation, and clonogenicity assays

Lung cancer cell lines were obtained from either the NCI or Hamon Cancer Center libraries and maintained as described in Chapter 3. HBECs were maintained in KSFM supplemented with bovine pituitary extract and EGF (Life Technologies), and passaged using trypsin followed by an equal volume of Trypsin Neutralizing Solution (Lifeline Cell Technologies). For MTS cell proliferation assays, cells were seeded in 100 uL media at 1000-4000 cells/well in triplicate, in three 96-well plates. At the desired time points, 20 uL MTS reagent (Promega) was added to each well and the plates were incubated at 37^{o}C for 1-3 hrs. Absorbance readings were taken at Day 1 to assess for equal seeding density, and at Day 5 or Day 7 as an end point. Proliferation rate was estimated using the ratio of the test sample absorbance to control sample absorbance at the end time point. Clonogenicity assays were performed as described in Chapter 3.

4.2.2 Generation of stable cell lines

Lentivirus for individual short hairpin constructs was prepared as described in Chapter 3. Cells were infected at high MOI ≥1 in the presence of 4 ug/mL polybrene, followed by selection

in 1.0-2.0 ug/mL puromycin for at least 3 days. Growth assays and harvesting for molecular profiling were typically performed 1-2 weeks after initial infection.

4.2.3 Mouse xenograft experiments

Cells were counted and resuspended in PBS at a concentration of 1 injection/200 uL, and transported to the mouse facility on ice. 1-10x10^6 cells in 200 uL PBS were injected subcutaneously in the right flank female NOD-SCID mice using 27.5 gauge needles, and monitored for tumor formation for up to six months. All animal care was in accordance with institutional guidelines and approved IACUC protocols.

4.2.4 Quantitative RT-PCR

Total RNA, cDNAs, and PCR reactions were prepared as described in Chapter 3. Gene-specific TaqMan probes (Applied Biosystems) were utilized for quantitative analyses of mRNA transcript levels. Probes used in this study were: FOXA1 (Hs04187555_m1), GAPDH (Hs02758991_g1), IGFBP3 (Hs00365742_g1), THBS1 (Hs00962908_m1). The GAPDH gene was used as an internal reference to normalize input cDNA. PCR reactions were performed in triplicate, run on an ABI 7300 Real-time PCR System, and analyzed with the SDS software (Applied Biosystems). The delta-delta-CT method was used to calculate relative mRNA expression levels.

4.2.5 Western blotting

Cells were lysed in 0.1% SDS Lysis Buffer and protein concentration was quantified using Bio-Rad Protein Assay Dye Reagent Concentrate (Bio-Rad). Proteins were separated by SDS/polyacrylamide gel electrophoresis and electrotransferred to nitrocellulose membranes (Millipore). Membranes were blocked for 1 hour at room temperature (RT) in a 5% milk in TBST (Tris Buffered Saline with 1% Tween-20), incubated with primary antibody overnight at 4°C, and detected using horseradish peroxidase-conjugated secondary antibody (Cell Signaling) followed by chemiluminescence (Thermo Scientific). Primary antibodies used in this study are as follows: FOXA1 (Abcam, ab23738), Hsp90 (Santa Cruz, sc-13119), E-cadherin (BD Biosciences, BD610181), vimentin (BD Biosciences, BD550513).

4.2.6. Copy number analyses

To obtain copy number data on cell lines, genomic DNA was extracted using a DNeasy Blood and Tissue Kit (Qiagen) and quantified using UV spectroscopy. Whole-genome SNP array profiling of 75 NSCLC cell lines was performed at MD Anderson (J. Heymach) using the Illumina Human 1M-Duo DNA Analysis BeadChip (Illumina). Raw data was normalized using BeadStudio software, and Log R Ratios were then aggregated by gene using their mean values. The R package DNAcopy was used for segmentation into DNA regions of copy number alterations.

To obtain copy number data on primary lung adenocarcinomas in the PROSPECT tumor panel, snap-frozen tumor tissue was processed on a cryostat to generate multiple 5-micron thick shavings. Genomic DNA was extracted using the Qiagen QIAamp DNA Mini Kit (Qiagen) and quantified by Quant-iT PicoGreen dsDNA Assay kit (Life Technologies). Tumor DNA was labeled with Cy5 (red) and normal reference (Human Genomic DNA, Female, Promega, Inc., Cat #G1521) was labeled with Cy3 (green). Labeled DNA was hybridized on Agilent Human Genome CGH Microarray 244A using the Oligonucleotide Array-Based CGH for Genomic DNA Analysis protocol (Agilent) and scanned on an Agilent G2505C scanner. Normalized and background-corrected intensities were used to calculate log2 ratios (Cy5/Cy3) of test/reference for each probe. The array CGH data has been publically deposited in the GEO database as GSE74948.

4.2.7 Tumor cohorts and survival analyses

The tissue microarray (TMA) used for immunohistochemistry profiling was obtained from the PROSPECT study as described in Chapter 3. The Cancer Genome Atlas (TCGA) cohort was also described in Chapter 3. Survival analyses were performed using in-house Visual Basic MicroArray Transformation in Microsoft Excel (MATRIX) v1.508 software (L. Girard, manuscript in preparation). Patient survival plots were generated using the R package “survival”. Patients were stratified into two groups based on user-defined gene expression criteria, and survival data were then compared using log-rank test and Kaplan-Meier curves.

4.2.8 Microarray and RNA-Seq analyses

RNA for NSCLC cell lines analyzed by microarray was prepared using the RNeasy Mini Plus kit (QIAGEN). Microarray expression profiling on lung cancer cell lines was performed using Illumina HumanWG-6 V3 Expression BeadChips (Illumina Inc., San Diego, CA). The data have been previously deposited as part of GEO dataset GSE32036. Bead-level data were obtained and pre-processed using the R package mbcb for background correction and probe summarization (243). Pre-processed data were then quantile-normalized and log-transformed. Class comparison was performed using in-house MATRIX v1.508 software (L. Girard, manuscript in preparation). Two-sample t-tests and Significance of Microarray analyses (244) were used to assess statistical significance. Samples derived from squamous cell carcinomas and ASCL1-positive tumors were all omitted from expression analyses in both the cell line and tumor datasets.

RNA for cell lines analyzed by RNA-seq were prepared using either the RNeasy Mini or RNeasy Mini Plus kits (QIAGEN). Samples prepared using the RNeasy Mini kit were additionally treated with Dnase I (Life Technologies) prior to library preparation. Sequencing libraries were prepared and sequenced on a HiSeq 2500 machine according to manufacturer's guidelines (Illumina). Reads were mapped to the human genome with Tophat, (245) and differentially expressed genes were identified using Cuffdiff (246).

4.2.9 ChIP-seq analyses

Three or two 15 cm dishes of H1819 or H1781, respectively, were grown to 70-80% confluency prior to chromatin immunoprecipitation. Cross-linking was performed in 1% formaldehyde in RPMI for 10 minutes at room temperature, followed by reaction termination with 125mM glycine glycine for 5 minutes. Cells were harvested with a scraper in 5 mL ice-cold PBS supplemented with Complete Mini, EDTA-free Protease Inhibitor Cocktail (Roche), pelleted at 720 x g for 10 min at 4°C. Cross-linked cells were resuspended in 1 mL sonication buffer (1% SDS, 10 mM EDTA, 50 mM Tris-HCl, pH 8.1) and 4°C with a Bioruptor (Diagenode) (30 seconds ON and 30 seconds OFF at highest power for 15 minutes). Insoluble debri was pelleted at 20,000 x g for 10 min, and supernatant was stored at -80°C. GammaBind G Sepharose bead (GE Healthcare) was prepared in ChIP dilution buffer (0.01% SDS, 1.1% Triton X-100, 1.2 mM EDTA, 167 mM NaCl, 16.7 mM Tris-HCl, pH 8.1, plus protease inhibitors) and blocked in 50 mg/mL BSA (Ambion) for 1 hour at 4°C. Sheared chromatin was diluted 1:10 in ChIP dilution buffer and incubated with 100 uL blocked beads for 1 hour at 4°C for pre-clearing, and supernatant was then incubated with 5 ug FOXA1 antibody (Abcam, ab23738) overnight at 4°C. After incubation, the chromatin/antibody mixture was incubated with 80 uL blocked beads for 1 hr at 4°C. Beads were then serially washed for 10 min at 4°C in washing buffer 1 (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, 150 mM NaCl, pH 8.1, plus protease inhibitors), washing buffer 2 (0.1% SDS, 1% Triton X-100, 2 mM EDTA, 20 mM Tris-HCl, 500 mM NaCl, pH 8.1, plus protease inhibitors), washing buffer 3 (0.25 M LiCl, 1% NP-40, 1% sodium deoxycholate, 1 mM EDTA, 10 mM Tris-HCl, pH 8.1), and Tris-EDTA twice (10 mM Tris-HCl, 1 mM disodium EDTA, pH 8.0 - Sigma-Aldrich). Chromatin-antibody complexes were eluted were eluted twice in 100 uL ChIP elution buffer (100 mM NaCO3, 1% SDS) for 15 min at 65°C, adjusted to 200 mM NaCl, and

incubated overnight at 65°C. Following RNase and proteinase K treatment, ChIPed DNA was purified using a PCR purification kit (Qiagen) and eluted in 30x2uL EB using a Min-Elute column. Libraries were then prepared using a TruSeq ChIP Sample Prep Kit (Illumina) and sequenced according to manufacturer's guidelines (Illumina).

FOXA1-bound regions were identified as genomic regions with a significant read enrichment and binding peak profile in the FOXA1 reads over the input reads by using the Model-based Analysis of ChIP-Seq (MACS) software tool (v.1.4.2) (247). Using an in-house script, all genes whose TSSs were within +/-10 kb distance with respect to peak summit were called as target genes. If no gene was identified with in +/-10 kb distance, the nearest gene was considered as the putative target. De novo motif discovery analysis for shared FOXA1-bound regions was performed with the Hypergeometric Optimization of Motif EnRichment (HOMER) software tool (248,249).

4.2.10 Immunohistochemistry

Immunohistochemical (IHC) staining for FOXA1 was performed on TMA samples as follows: 5 µm-thick formalin-fixed, paraffin-embedded tissue sections were deparaffined, hydrated, heated in a Biocare decloaker for 30 minutes pretreated with Target Retreval Solution (Dako), and washed in Tris buffer. Peroxide blocking was performed with 3% H_2O_2 in methanol at room temperature for 15 minutes, followed by 35 minute incubations in Tris-buffered saline containing 15% FBS. Slides were incubated with the primary antibody against

FOXA1 (Abcam, ab23738, 1:500) at room temperature for 65 minutes, washed with Tris-buffered saline, followed by incubation with Envision Dual Link+ Polymer-Labeled System (Dako) for 30 minutes. Staining was developed with chromogen substrate (Dako) for 5 minutes and then counterstained with hematoxylin, dehydrated, and mounted. FOXA1 expression was quantitated using a four-value intensity score (0, 1, 2, and 3) and the percent of IHC+ tumor cells (0-100%). An H-score was calculated by adding the product of the percentage cells stained at a given staining intensity (0–100) and the staining intensity (0–3), as previously described (250).

4.2.11 Aldefluor assay and flow cytometry

The Aldefluor kit (Stem Cell Technologies) was used to profile and separate cells with high and low ALDH activity. Cells were processed as described previously (190) and profiled on a FACScan flow cytometer (BD Biosciences). Figures were produced using FlowJo software (Treestar).

4.3 Results

4.3.1 Selection of candidate genes for follow-up

None of the candidate genes have been identified as frequently mutated in lung cancer, and none were found to be mutated in H1819 by whole exome sequencing. However, analysis of high resolution SNP array profiling across a panel of NSCLC cell lines (n=63) and primary lung adenocarcinomas from TCGA (n=514) revealed that the *FOXA1* locus is highly amplified in a subset of cell lines and tumors, including in the cell line H1819 (Figure 6.1A). Copy number variation was observed for other candidate genes across the cell line panel, however none of the genes showed gain or loss in H1819 (data not shown). Notably, the *FOXA1* locus is located on 14q21.1, ~1 Mb downstream from *NKX2-1* on 14q13.3. *NKX2-1* is a known lineage-specific oncogene in lung cancer, and focal amplification peaking at the 14q13.3 band is one of the most frequently recurring genomic events observed in lung adenocarcinomas (90,251,252). In cell lines and tumors with amplification of *NKX2-1* of 4 or more copies, the amplicon extends to the *FOXA1* locus in 89% (8/9) and 79% of cases (27/34), respectively (Figure 4.1A). Amplification of *NKX2-1* is observed in ~12% of all patients (251-254), thus a co-amplification frequency of 79-89% in this cohort would represent ~9-11% of affected lung adenocarcinomas overall (Figure 4.1A). This is consistent with previously reported analyses of TCGA data (255). SNP array-derived copy number correlated well with FOXA1 mRNA expression levels as assessed by microarray and qPCR in cell lines and RNA-seq and IHC in tumors (Figure 4.1B,D,E,F,G). Comparison of FOXA1 mRNA expression in malignant versus non-malignant tissues also revealed that FOXA1 is more highly expressed in tumor cells compared to normal cells and tissue (Figure 4.1C). We also confirmed that FOXA1 amplification is correlated with overexpression at the mRNA and protein level in cell lines and primary lung adenocarcinomas (Figure 4.1D-G). Thus, lung adenocarcinomas harboring 14q amplification exhibit high

expression levels of FOXA1, and overall expression of FOXA1 is higher in tumors than in normal tissues. Taken together, these observations are consistent with a possible oncogenic role for FOXA1, thus it was prioritized for follow-up studies.

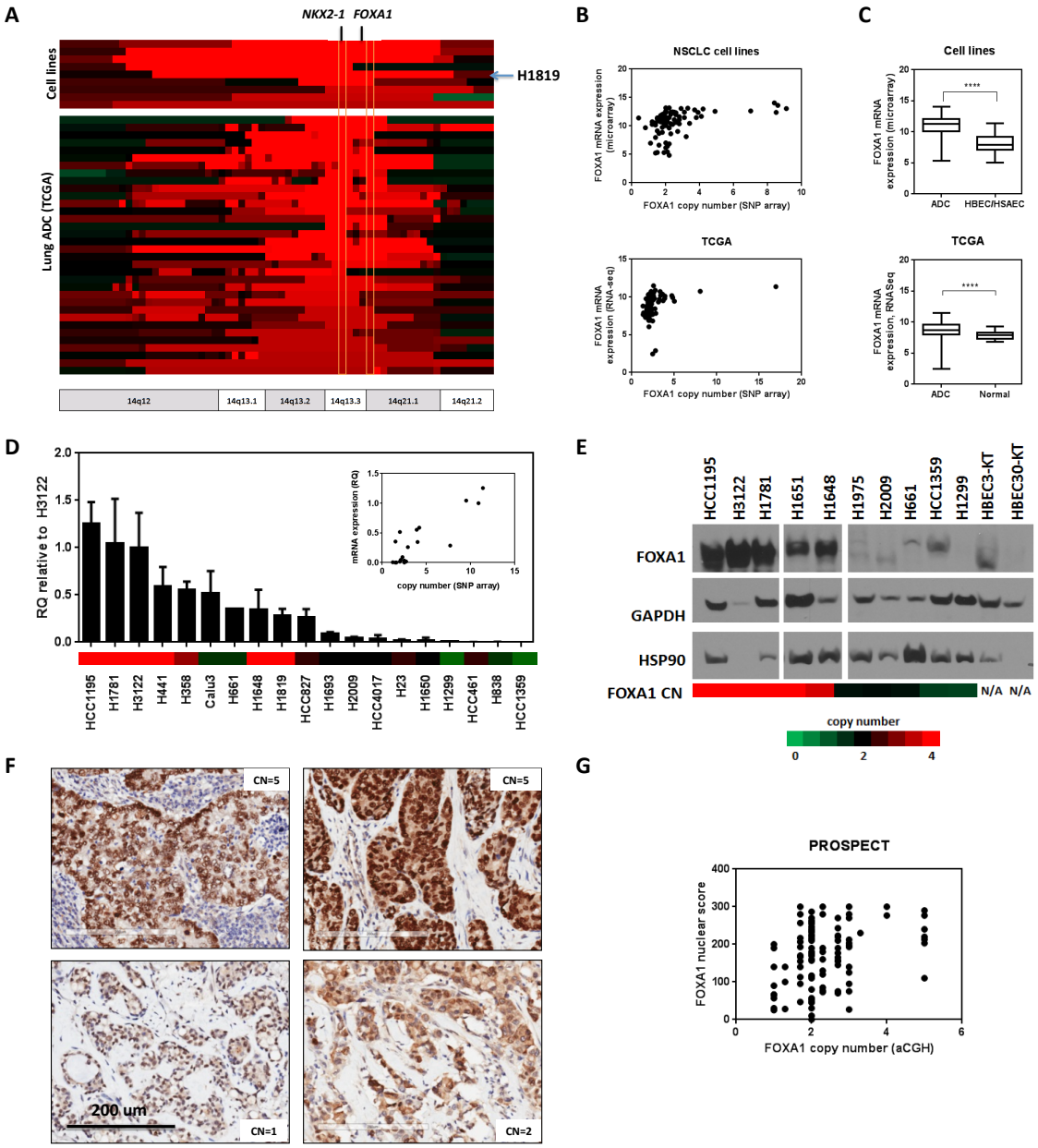


Figure 4.1. FoxA1 is amplified and overexpressed in NSCLCs. (A) Segmented copy number profiles of the genomic region on 14q that includes the *NKX2-1* and *FOXA1* gene loci (outlined in orange), from SNP array datasets on NSCLC cell lines (top) and primary lung adenocarcinomas from TCGA (bottom). Chromosome bands representing relative genomic location are indicated on the bottom. (B) Scatter plots comparing FOXA1 copy number with FOXA1 mRNA expression level in cell lines (top), and tumors (bottom). (C) Average FOXA1 expression levels in cell lines compared to HBEC and HSAEC cell lines (top), and in primary tumors compared to normal tissues (bottom). (D) FOXA1 mRNA levels measured by Q-RTPCR in a panel of NSCLC cell lines, with corresponding copy number shown on the bottom. Inset, Scatter plot comparing copy number levels in NSCLC cell lines with mRNA levels. (E) FOXA1 protein expression levels in a panel of cells lines, with copy number shown on the bottom. (F) Representative images of lung adenocarcinomas from the PROSPECT tumor array harboring 14q-ampflication and high

FOXA1 expression (top), or no amplification and low expression (bottom). (G) Scatter plot comparing FOXA1 copy number (aCGH) with quantified IHC staining for FOXA1 on PROSPECT tumor array specimens.

4.3.2 Validation of *FOXA1* as an essential gene for *in vivo* growth

In order to validate FOXA1 as required specifically *in vivo,* we tested three different shRNAs from the library for ability to knockdown FOXA1 in H1819: two which scored in the screen, and one that showed significant depletion but did not pass filter for fold depletion. All three shRNAs reduced FOXA1 mRNA levels, and fold mRNA reduction correlated with fold depletion observed in the screen (Figure 4.2A). Notably, levels of FOXA1 knockdown correlated with levels of depletion observed in the shRNA screen (Figure 4.2B). This direct functional link between expression of the shRNA target and phenotype suggests that the shRNA effects are on-target. Reduction in FOXA1 protein levels was confirmed using the shRNA which produced the highest levels of knockdown (Figure 4.2C), and this shRNA was used for all subsequent experiments. As observed in the screen, knockdown of FOXA1 did not have a significant impact on *in vitro* proliferation as measured by MTS (Figure 4.3A,B). However, a striking reduction in clonogenicity was observed when cells were plated at low density (Figure 4.3C). Finally, inhibition of FOXA1 nearly abolished the ability of H1819 cells to form tumors in mice (Figure 4.3D,E). Notably, tumors which did grow out from injection of H1819-shFOXA1 cells appeared to have arisen from cells that escaped FOXA1 inhibition and re-established FOXA1 expression levels comparable to those in H1819 tumors with non-targeting control (shNTC) (Figure 4.3F).

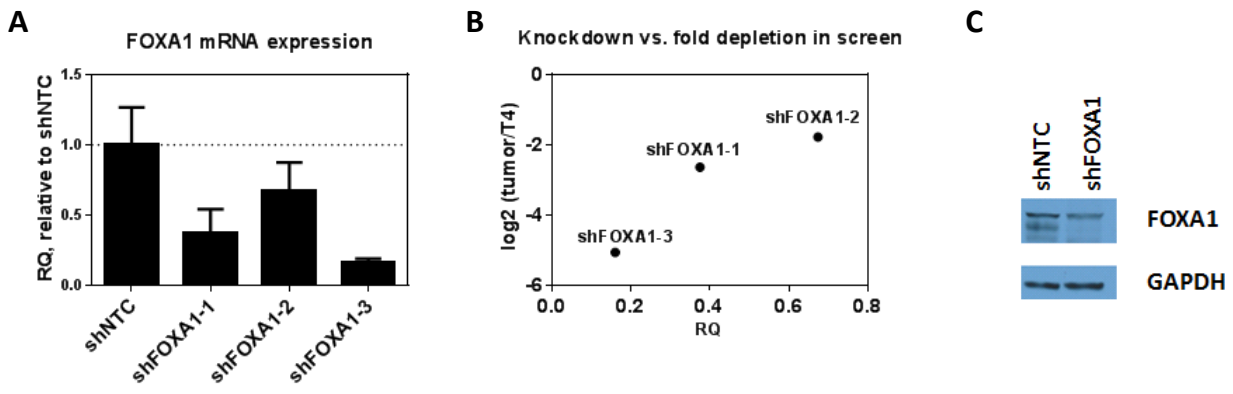


Figure 4.2. Knockdown of FOXA1 with individual short hairpins correlates with function in the screen. (A) Three short hairpins against FOXA1 exhibit varying ability to knockdown their target as assessed by QPCR for FOXA1 mRNA. (B) Level of knockdown as measured by Q-RTPCR correlates with the level of depletion observed for each shRNA in the screen. (C) Western blot showing knockdown of FOXA1 at the protein level with shFOXA1-3.

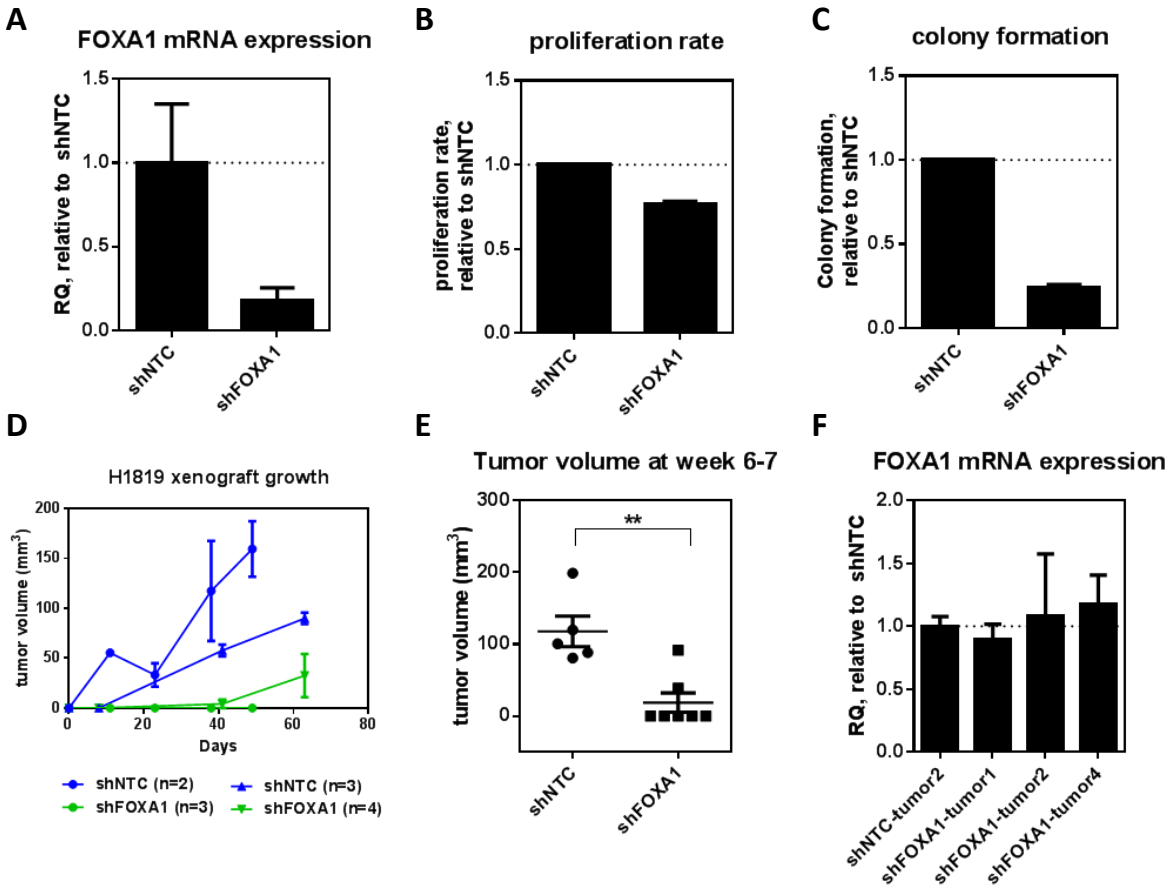


Figure 4.3. Knockdown of FOXA1 in H1819 reduces clonogenicity and xenograft growth. (A) QPCR for FOXA1 mRNA with shFOXA1. (B) Proliferation over 5 days as measured by MTS. (C) 2D colony formation assay. (D) Growth curves for H1819 xenografts. 10 million cells were injected subcutaneously into female NOD-SCID mice. (E) Tumor weights after a minimum of 50 days growth *in vivo.* (F) QPCR results for FOXA1 in H1819 xenograft tumors which grew out (harvested at 50 days or greater).

4.3.3 FOXA1 is required for clonogenicity in cell lines with amplification on 14q

To determine whether amplification and/or expression of *FOXA1* could serve as biomarkers for dependence on FOXA1, we expanded our analyses to a panel of NSCLC cell lines

representing a range of *FOXA1* copy number and expression levels. FOXA1 expression was reduced using the same lentiviral shRNA construct described above (Figure 4.4A). Knockdown of FOXA1 reduced bulk cell proliferation in some cell lines with high FOXA1 copy number, but not in most other cell lines tested (Figure 4.4B). Inhibition of FOXA1 significantly reduced clonogenicity in all cell lines that express FOXA1, and a good correlation with both expression and copy number was observed (Figure 4.4C-E). Notably, clonogenicity was not affected by knockdown of FOXA1 in the cell line H661, which harbors focal amplification of *NKX2-1* but not of *FOXA1*, suggesting that the requirement for FOXA1 in other 14q-amplified lines may be independent of NKX2-1. Knockdown of FOXA1 in H1299, a cell line with low levels of FOXA1, did not change *in vivo* growth rates (Figure 4.5). Taken together, these data suggest that dependency on FOXA1 follows a gene dosage-dependent model of oncogene addiction, where cells with higher copy number and higher expression exhibit dependency on the gene, and cells with low levels do not. We thus hypothesized that amplification of the 14q13.3-21.1 locus may serve as a biomarker for dependency in NSCLC tumors, and that this subset of tumors may be sensitive to inhibition of FOXA1 transcriptional targets.

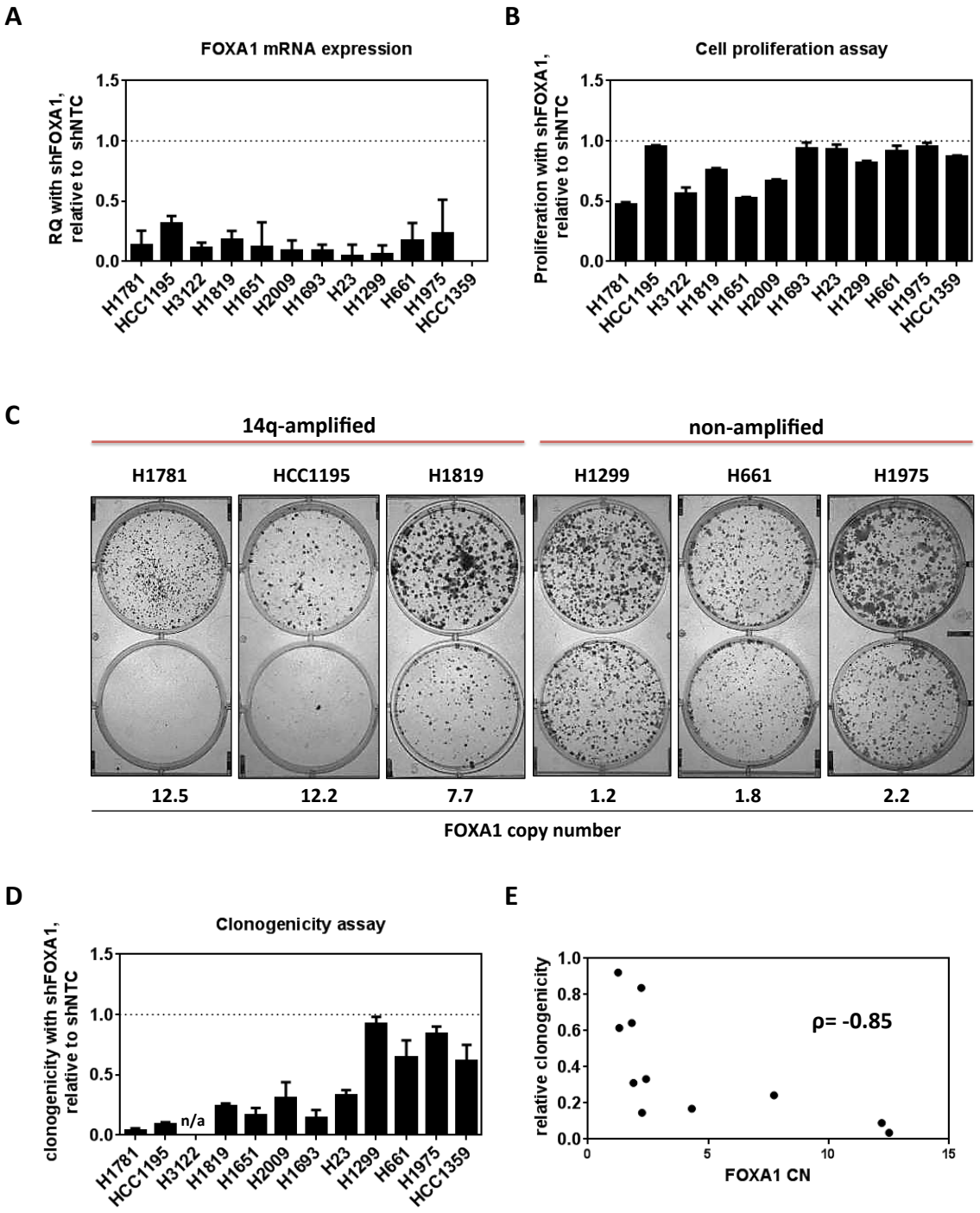


Figure 4.4. A panel of NSCLC cell lines exhibits differential dependencies on FOXA1. (A) Knockdown of FOXA1 in a panel of cell lines was verified by Q-RTPCR in all cell lines. (B) Proliferation rates after knockdown of FOXA1 as measured by MTS assay. (C) Representative colony formation assays in a panel of NSCLC cell lines with knockdown of FOXA1. (D) Quantitation of clonogenicity after knockdown of FOXA1. (E) Correlation between FOXA1 copy number (SNP array data) compared with clonogenicity relative to shNTC.

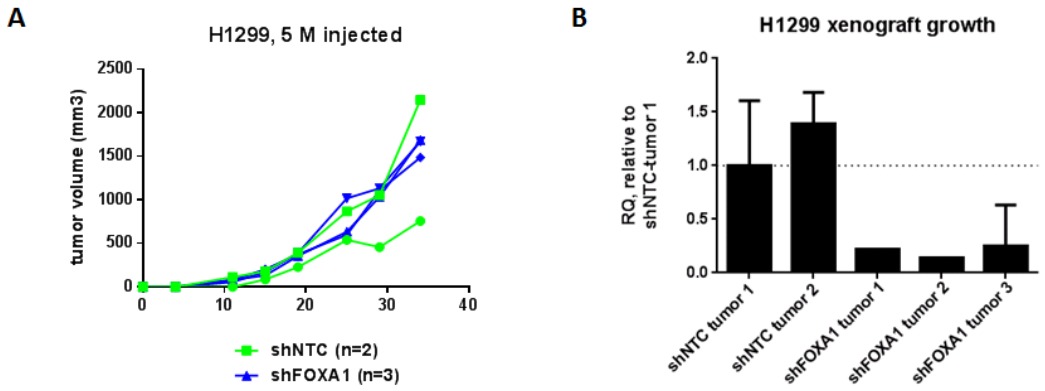


Figure 4.5. Inhibition of FOXA1 in a cell line with low copy number and low expression levels has no effect on xenograft growth rates. (A) Growth rate of H1299 xenograft tumors from subcutaneous injections of 5x10^^{6} cells with either non-targeting shRNA (shNTC) or shFOXA1. (B) QPCR for FOXA1 mRNA in xenograft tumors.

4.3.4 Identification of a FOXA1-associated gene signature

In order to identify genes regulated by FOXA1, we first used array-based expression profiles on cell lines and primary lung adenocarcinomas with high FOXA1 expression to derive a gene expression signature associated with FOXA1 dependency and expression. We compared genome-wide expression profiles between cell lines residing in the top and bottom 20th percentiles of FOXA1 expression in a select panel, and in PROSPECT lung adenocarcinomas in the top and bottom 10th percentiles of FOXA1 expression. More details on sample selection are included in Appendix E. SAM analysis identified 1214 differentially expressed genes (DEGs) in FOXA1^{hi} cell lines compared to FOXA1^{lo} (830 genes upregulated, 384 genes as downregulated; FDR<5.1%), and 458 DEGs in FOXA1^{hi} lung adenocarcinomas compared to FOXA1^{lo} (390 genes

upregulated, 68 genes downregulated; FDR<5.2%) (Figure 4.6A). Intersection of these datasets identified 153 shared overexpressed genes ($p< 5.679 \times 10^{-109}$), and 14 shared underexpressed genes ($p < 3.478 \times 10^{-11}$) (Figure 4.6B). Lists of differentially expressed and significant genes in the NSCLC cell line panel and the tumor panel are included in Appendix E. The full dataset is available upon request.

We found that FOXA1-associated genes fell into one of three main categories: Genes previously reported as part of an expression signature associated with NKX2-1 amplification (Class 1) (255), genes previously identified as part of an epithelial-to-mesenchymal gene signature by Byers and colleagues (Class 2) (9), and newly identified genes associated with FOXA1 (Class 3) (Figure 4.6C,D). Class 1 genes were expected, given frequent co-amplification of NKX2-1 and FOXA1. The identification of class 2 genes is also consistent with prior studies which implicate NKX2-1 and FOXA1 in positively regulating epithelial-specific markers (256), and which correlate NKX2-1 expression in lung tumors with differentiation state (257,258). Indeed, nearly all $FOXA1^{hi}$ cell lines were classified as epithelial by this signature (Figure 4.7A). Although FOXA1 and FOXA2 have been previously implicated in epithelial-to-mesenchymal transition in some contexts (10–12), we found no evidence of EMT after knockdown of FOXA1 as assessed by changes in E-cadherin and vimentin expression (Figure 4.7B). To look for potential gene sets of interest, the cell line dataset was filtered for nuclear hormone receptor and coregulator genes, genes involved in putative cancer stem cell maintenance, and statistically nominated driver genes in lung cancer (Figure 4.7A). Several genes in each category are upregulated in $FOXA1^{hi}$ cell lines, including the cancer stem cell marker *ALDH1A1.* This observation combined with the

difference between the bulk proliferation rates and tumor-initiating capacity of cells after FOXA1 inhibition suggested that FOXA1 may regulate the tumor-initiating population. However, no change in the percentage of ALDH-positive cells was observed after FOXA1 inhibition (Figure 4.7C).

To verify that this gene signature was representative of FOXA1-dependency and not just FOXA1 expression, we performed a smaller expression analysis using cell lines classified as either dependent or independent of FOXA1 based on their clonogenicity score after FOXA1 depletion. A two-sample t-test identified 329 genes as differentially expressed between the two classes ($p<0.05$, $|\log2|>2$), and there was good correlation among the most significant and differentially expressed genes between this and the previous analysis. For downstream analyses we used the gene signature derived from microarray expression data.

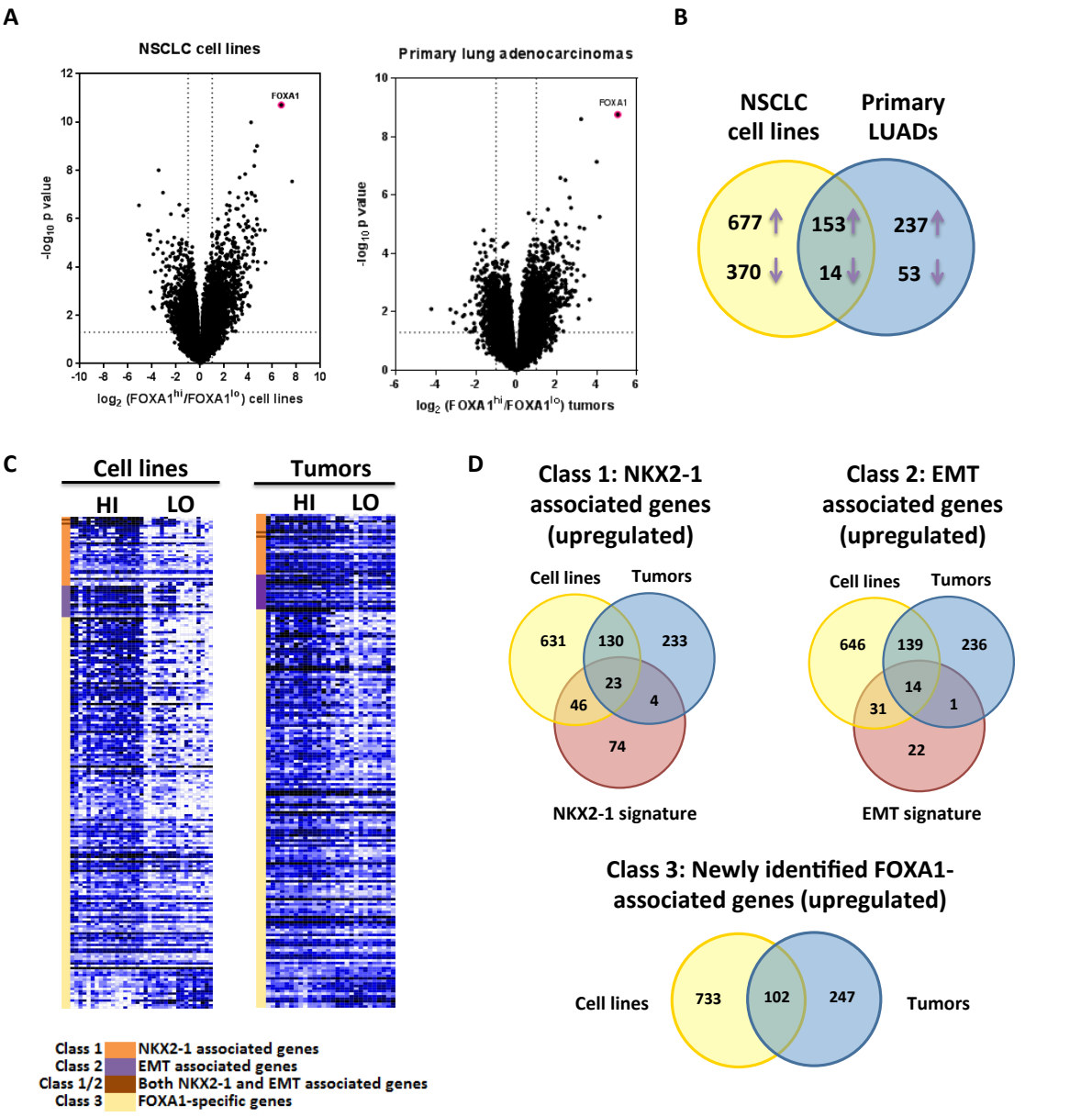


Figure 4.6. Identification of genes associated with FOXA1 expression in human lung adenocarcinomas. (A) Volcano plots showing $\log_2$ expression changes between cell lines (left) or primary lung adenocarcinomas (right) with high FOXA1 expression vs. low, plotted against –log10 p-value. (B) Venn diagram illustrating the intersection between DEGs in FOXA1 hi vs. lo cell lines and hi vs. lo tumors. (C) Expression heat maps showing differentially expressed genes in FOXA1 hi vs. lo cell lines (left) and FOXA1 hi vs. lo tumors (right), with gene classes indicated by a colored bar on the left. Genes previously identified as associated with NKX2-1 expression are indicated in orange (Class 1); genes previously identified as part of an EMT signature in lung cancer are indicated in purple (Class 2); genes falling into both of these categories are indicated in maroon; newly identified FOXA1-associated genes are indicated in yellow (Class 3). (D) Venn diagrams illustrating the intersection between upregulated genes in FOXA1 hi cell lines and tumors and genes in Class 1, Class 2, and the remaining genes in Class 3.

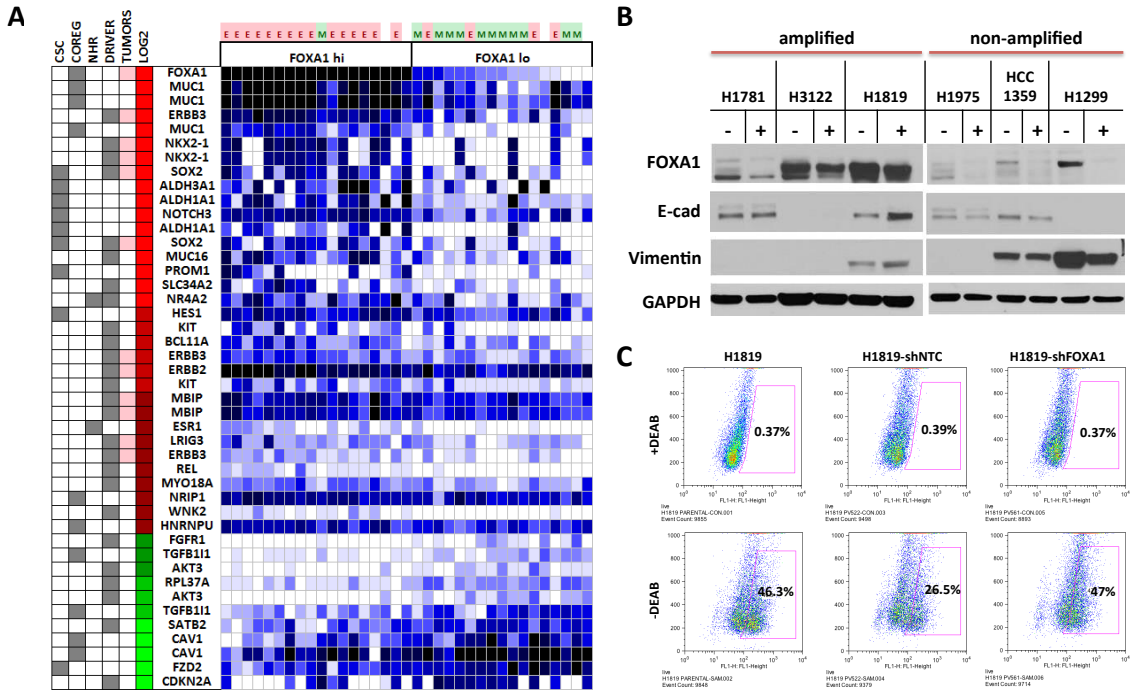


Figure 4.7. High FOXA1 expression is correlated but not functionally associated with expression of some markers of cancer stem cells and EMT. (A) Expression heat map showing nuclear receptor, coregulator, cancer stem cell, and driver genes which showed differential expression in FOXA1 hi vs. low cell lines (FDR<5.1%). Genes that were also significant in the tumor analysis are indicated by a pink bar in the "TUMOR" column. EMT status of cell lines is indicated as E, epithelial, or M, mesenchymal. (B) Western blotting for E-cadherin and vimentin with and without knockdown of FOXA1 in a panel of cell lines representing high (amplified) or low (non-amplified) FOXA1 copy number. (C) Flow cytometry analysis using the Aldefluor assay on H1819 cells alone, with non-targeting control shRNA (shNTC), or with shFOXA1. Baseline fluorescence was established by inhibiting ALDH activity with DEAB (top) and used to generate a gate to identify ALDH+ cells in samples that were not incubated with DEAB (bottom). In this experiment, introduction of a non-targeting shRNA may have adversely affected the ALDH- population, however this was not observed with shFOXA1.

4.3.5 Identification of genes regulated by FOXA1

Next we sought to identify downstream signaling targets of FOXA1 using RNA-seq based expression profiling on RNA from two replicate knockdown experiments each in H1819 and H1781. Surprisingly, no genes were identified as significant in experiments using H1819 (FDR<5%). We attribute this to the relatively small dynamic range in gene expression observed after knockdown of FOXA1. By contrast, the dynamic range of gene expression in H1781 was much larger, with 5363 genes scoring as significant (FDR<5%). The difference in dynamic ranges of differential gene expression may provide an explanation for why a FOXA1-knockdown associated growth defect was not observed in bulk culture for H1819, but was observed in H1781. Applying a 2-sample t-test and utilizing a cutoff of $p<0.05$ for differentially expressed genes in both cell lines resulted in a list of 179 DEGs in H1819 and 6218 genes in H1781 after FOXA1 knockdown (Figure 4.8A,B). Overlap analysis identified 70 genes whose directional expression was correlated between the two cell lines: 53 genes were downregulated in both cell lines after FOXA1 knockdown, and 17 genes were upregulated (Figure 4.8C,D). The full dataset is available upon request.

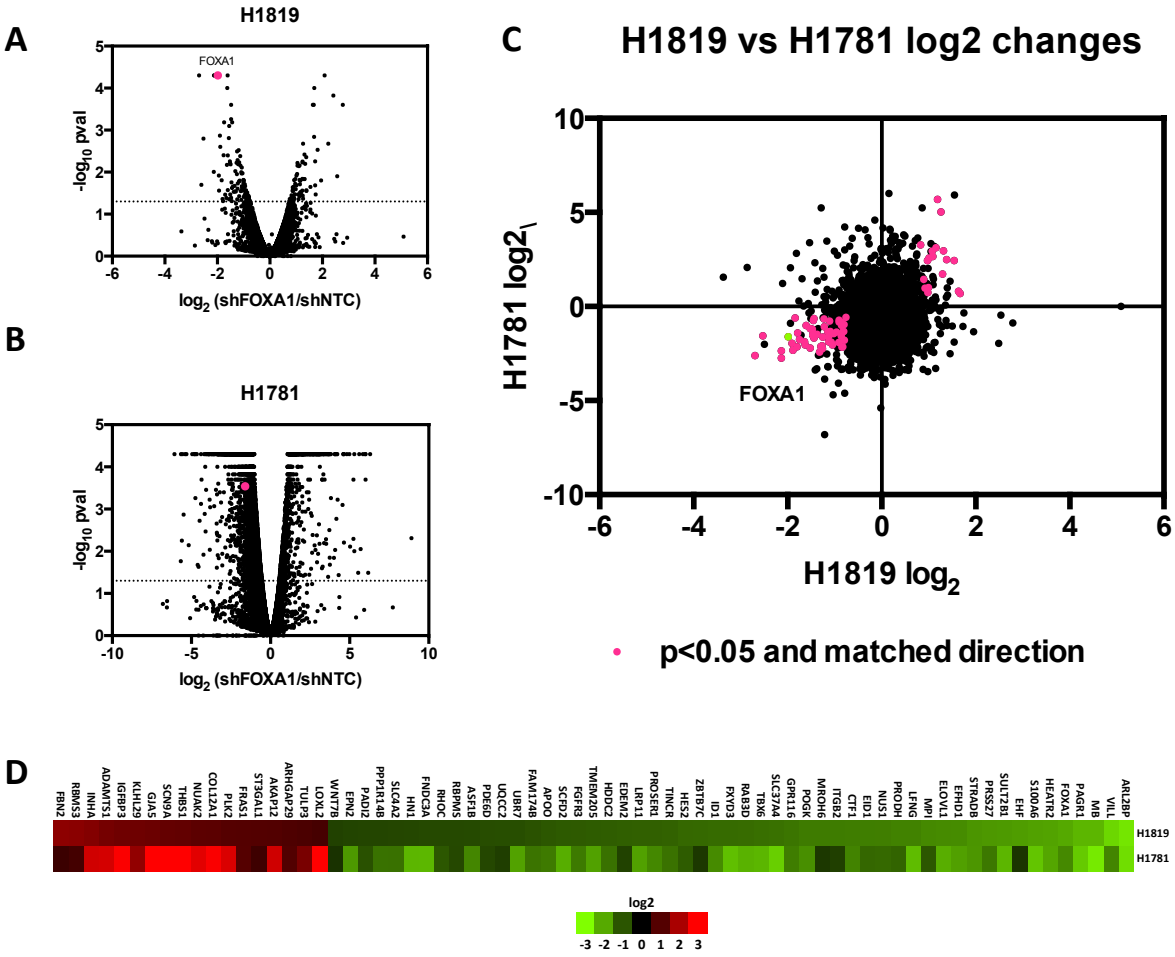


Figure 4.8. Identification of genes regulated by FOXA1. Volcano plots showing log2 expression changes between shFOXA1 and shNTC cells from 2 replicate experiments each in (A) H1819 and (B) H1781. (C) Log2 expression changes in H1819 compared to H1781. Significant genes ($p<0.05$) with matched directional expression are highlighted in pink. FOXA1 is indicated in green. (D) Heat map showing log2 fold changes in differentially expressed genes with matched directional expression. RNA-seq data processing was performed by Rahul Kollipara.

4.3.6 Characterization of the FOXA1 cistrome in 14q-amplified cells

We then sought to identify binding sites of FOXA1 on a genome-wide scale using chromatin immunoprecipitation with a FOXA1 antibody followed by massively parallel sequencing (Chip-seq) on two 14q-amplified cell lines: H1819 and H1781. A total of 15694 significant peaks were identified across the genome in H1819 cells, and 44238 peaks in H1781 cells, with 8974 peaks in shared genomic regions (Figure 4.9A,B). Genes with a transcription start site (TSS) within 10 kb of peak summits were then identified using an in-house script, and a total of 7034 genes were found to be common between the two cell lines. Intersection of this gene list with genes found differentially upregulated in FOXA1 hi cell lines and tumors identified 71 FOXA1-associated genes that also harbor a FOXA1-binding site, representing direct transcriptional targets of FOXA1 which may mediate downstream function in tumors with high FOXA1 expression (Figure 4.9C). De novo motif analysis within FOXA1-bound sequences revealed significant enrichment for the Forkhead motif in both cell lines (p= 1e-3695, Figure 4.9D). Several other motifs were also identified as significantly enriched at FOXA1 bound sites, including the AP-1, TEA, AP-2, and grainyhead binding sequences. The mRNA expression levels of several transcription factors associated with these motifs were correlated with FOXA1 expression (Figure 4.9E). The expression levels of several of the implicated transcription factors were also positively correlated with FOXA1 expression in the PROSPECT cohort, with GHLR2 among the top scoring genes (Figure 4.9F). Conversely, a negative correlation was observed for three other transcription factors, suggesting that these sites may be primed for transcription but are not active in FOXA1-amplified cell lines.

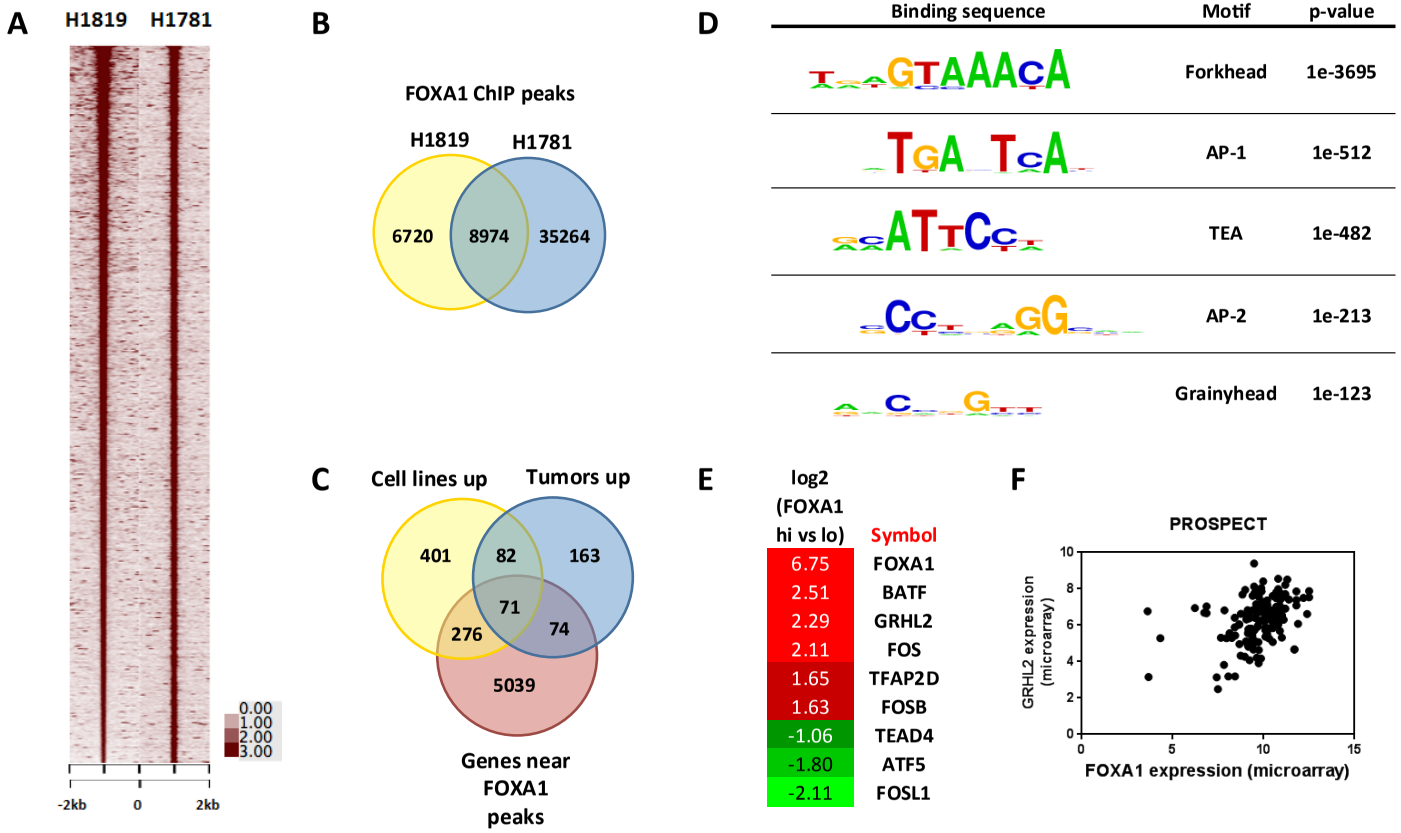


Figure 4.9. Identification of direct transcriptional targets of FOXA1and potential coregulators. (A) Heat maps showing FOXA1 chip peaks in H1819 and H1781, ranked by intensity. (B) Overlap between genomic regions with FOXA1 Chip peaks in H1819 and H1781. (C) Intersection between genes with a TSS within 10 kb of FOXA1 peak summits and genes that are upregulated in FOXA1 hi cell lines and tumors. (D) De novo motifs found in FOXA1-bound peaks shared between both cell lines. (E) Expression of select transcription factors associated with secondary motifs in FOXA1 hi cell lines compared to FOXA1 low cell lines. (F) One example of a transcription factor whose expression correlates to FOXA1 expression in lung tumors. Microarray-based expression of FOXA1 compared to expression of GRHL2 in PROSPECT lung adenocarcinomas. FOXA1 ChIP was performed by Paul Yenerall; ChIP-seq data processing was performed by

4.3.7 Integrative expression and cistromic analysis identifies direct FOXA1 targets

We then integrated these transcriptomic and cistromic analyses to derive a functional gene signature characterizing the FOXA1-driven pro-growth program in 14q-amplified cells. Genes near FOXA1 binding sites were compared with genes downregulated after FOXA1 knockdown and genes upregulated in FOXA1^{hi} cell lines. For the expression dataset, genes passing statistical filter by either t-test ($p<0.05$) or SAM analysis (FDR<5.1%) were included. Ten genes were at the intersection of all four datasets, and 21 intersected with 3 out of 4 datasets (Figure 4.10A), representing putative direct targets which are positively regulated by FOXA1. Conversely, genes near FOXA1 binding sites were compared with genes upregulated after FOXA1 knockdown and genes downregulated in FOXA1^{hi} cell lines, with the same statistical filters applied to the expression dataset as described above. One gene intersected all four datasets and 13 genes intersected with 3 out of 4 datasets, representing putative direct targets which are negatively regulated by FOXA1 (Figure 4.10B). In total, 45 genes were identified at the intersection of the expression and cistromic analyses, representing a FOXA1-associated gene signature in 14q-amplified cell lines (Figure 4.10C).

FOXA1 has previously been shown to cooperate with NKX2-1 to regulate expression of NKX2-1 transcriptional targets (255,256,258). NKX2-1 consensus motifs were not identified by de novo motif analysis of FOXA1-enriched peaks, but the large number of FOXA1 binding sites detected in the genomes of the cell lines analyzed here may confound the identification of some transcription factors whose motifs are present in lower abundance. In order to identify

genes which may be co-regulated by FOXA1 and NKX2-1, we intersected data from a previously published NKX2-1 ChIP performed in H1819 (255) with our FOXA1 ChIP dataset in H1819 and H1781. We identified peaks that were in overlapping genomic regions between the two datasets and cross-referenced nearby genes to our 45-gene signature (Figure 4.10C). Notably, only 16 of these genes were identified as co-occupied with FOXA1 and NKX2-1 in H1819, suggesting that even in 14q-amplified cells, at least part of FOXA1-driven growth is independent of its cooperation with NKX2-1. ChIP-seq data is available upon request.

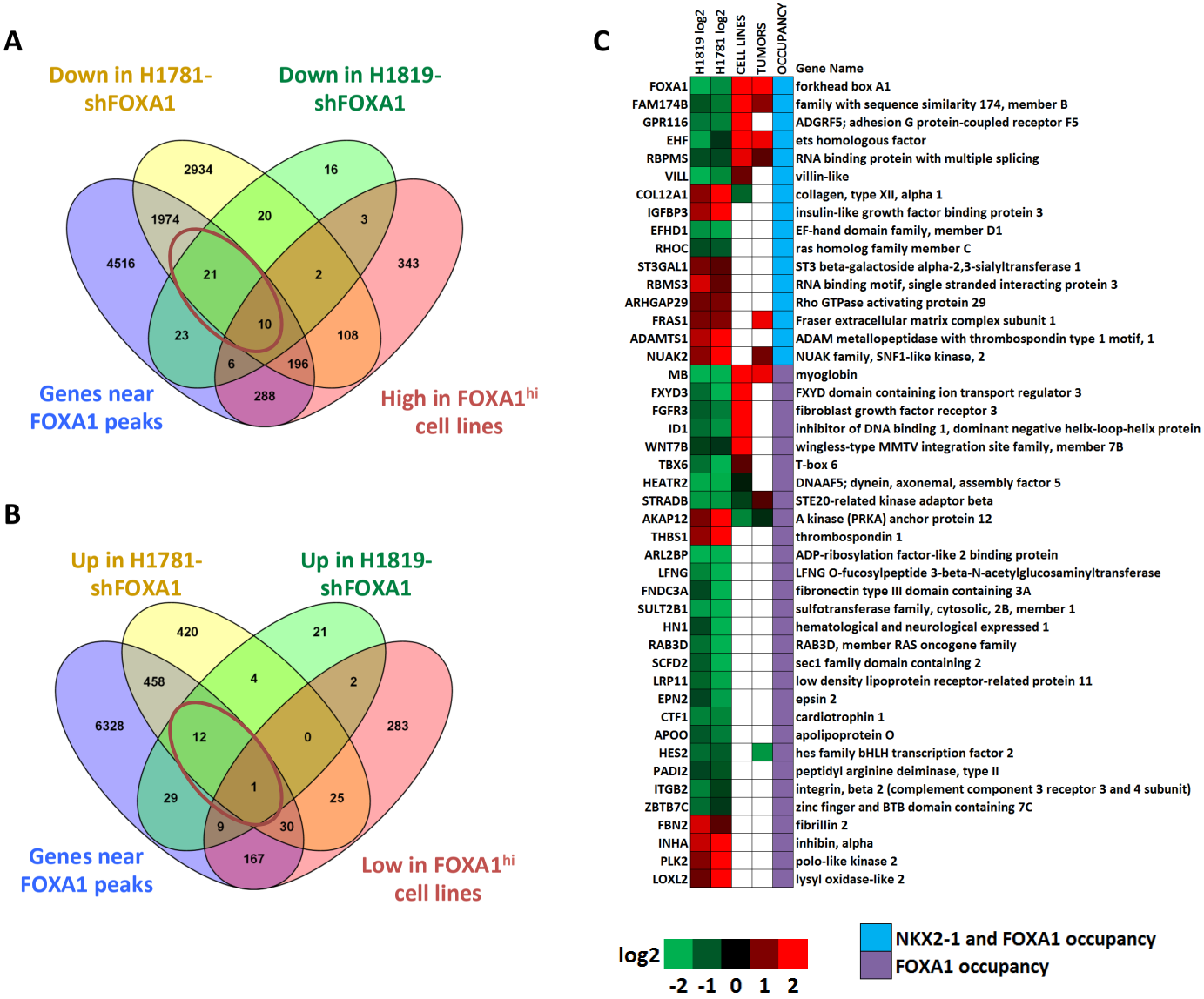


Figure 4.10. Identification of a 45-gene signature representative of the FOXA1-supported transcriptional program in 14q-amplified cells.
See next page for full legend.

Figure 4.10. Identification of a 45-gene signature representative of the FOXA1-driven transcriptional program in 14q-amplified cells. (see previous page) (A) Overlap of genes which are downregulated after FOXA1 inhibition in H1819 and H1781, with genes that are highly expressed in FOXA1hi cell lines, and genes near FOXA1 ChIP peaks. The intersection between 3 out of 4 and 4 out of 4 datasets is indicated in red. (B) Overlap of genes which are upregulated after FOXA1 inhibition in H1819 and H1781, with genes that are underexpressed in FOXA1hi cell lines and genes near FOXA1 Chip peaks. The intersection between 3 out of 4 and 4 out of 4 datasets is indicated in red. (C) Heat map table showing genes found at the intersections of overlap analyses shown in (A) and (B), and the corresponding log2 fold changes for all genes which scored as significant in the indicated expression dataset. Genes which scored as significant by t-test only in FOXA1hi vs. lo expression analyses are marked with an asterisk symbol (*). Genes which exhibited co-occupancy of both FOXA1 and NKX2-1 in ChIP analyses are indicated with a gray box at the right.

Strikingly, nearly all of the negatively regulated FOXA1 targets identified here are secreted extracellular proteins, and many of them have been implicated as tumor suppressors in various contexts. Conversely, several of the targets which are positively regulated by FOXA1 are involved in pro-growth signaling pathways. The identification of *FGFR3, WNT7B,* and *RHOC* were particularly intriguing since there are inhibitors available. In order to test whether this FOXA1 program is maintained other 14q-amplfiied lines, we tested for mRNA expression of a one NKX2-1/FOXA1 co-occupied gene (*IGFBP3*) and one FOXA1-only occupied gene (*THBS1*) in a panel of cell lines with and without FOXA1 knockdown. We found that expression of IGFBP3 and TBSP1 mRNA increases in 14q-amplified cell lines after FOXA1 inhibition, but not in non-amplified cell lines, even in cell lines with FOXA1 expression (Figure 4.11). This suggests that co-amplification of NKX2-1 and FOXA1 may have multiple consequences on downstream transcriptional targets, including some that are not co-regulated by NKX2-1. Taken together, these 45 genes comprise a FOXA1-associated gene signature which implicates FOXA1 in positive regulation of several growth signaling pathways and negative regulation of several tumor

suppressor pathways, and suggests that FOXA1 plays a neomorphic role in the context of 14q-amplification in lung adenocarcinomas.

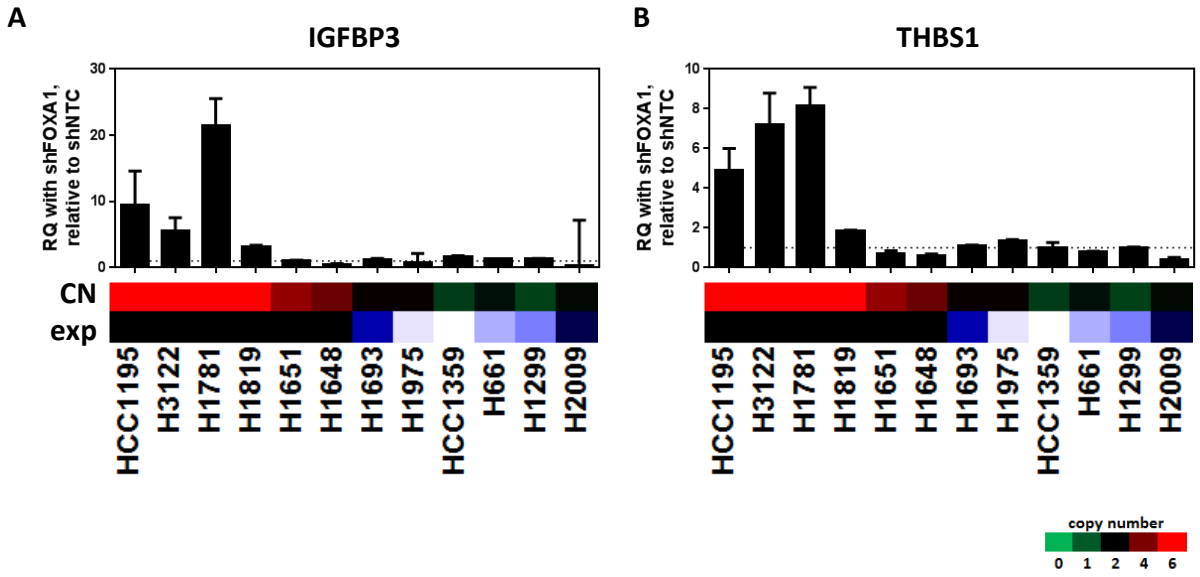


Figure 4.11. Genes identified as part of a FOXA1-supported transcriptional program are differentially regulated in 14q-amplified cells. QPCR for IGFBP3 (A) and THBS1 (B) in a panel of cell lines with and without FOXA1 knockdown. Quantification (RQ) is reported relative to cells with non-targeting shRNA (shNTC), and was normalized using GAPDH expression as in internal control.

4.3.8 FOXA1 expression is correlated with better prognosis in NSCLC patients

In order to assess whether FOXA1 expression can be used as a biomarker for clinical parameters, we performed immunohistochemistry staining for FOXA1 on a NSCLC tumor microarray cohort which is part of the PROSPECT dataset collected at MD Anderson Cancer Center (n=218; 152 adenocarcinoma, 66 squamous cell carcinomas). Broad expression across

most NSCLC tumors was confirmed, with higher expression in lung adenocarcinomas compared to squamous, and a small subset of tumors in each class that were negative for nuclear FOXA1 staining (Figure 4.12A, Figure 4.1F). Of note, cytoplasmic staining was observed in many tumors, especially in adenocarcinomas, with a small number showing exclusive cytoplasmic localization. Cytoplasmic staining for FOXA1 has been observed in other tumor types, but the functional significance remains unclear (259,260). Survival analyses using mRNA-based expression data in two independent tumor cohorts (TCGA and PROSPECT) did not reveal any correlation between FOXA1 mRNA expression and overall survival (data not shown). One prior study using IHC in NSCLCs reported no correlation with FOXA1 protein expression and survival in lung adenocarcinomas, but a strong positive correlation between FOXA1 expression and poor overall survival in squamous cell carcinomas (261). In the tumor microarray panel profiled here by IHC, survival analyses revealed that high FOXA1 expression trended towards improved survival in both lung adenocarcinomas and squamous cell carcinomas, though the difference did not reach significance (Figure 4.12B,C). No significant correlation was found with FOXA1 expression and stage or gender (Figure 4.13). We conclude that high FOXA1 expression trends towards better overall survival in NSCLC patients, which is consistent with previous reports correlating high NKX2-1 expression with better outcome (262,263)

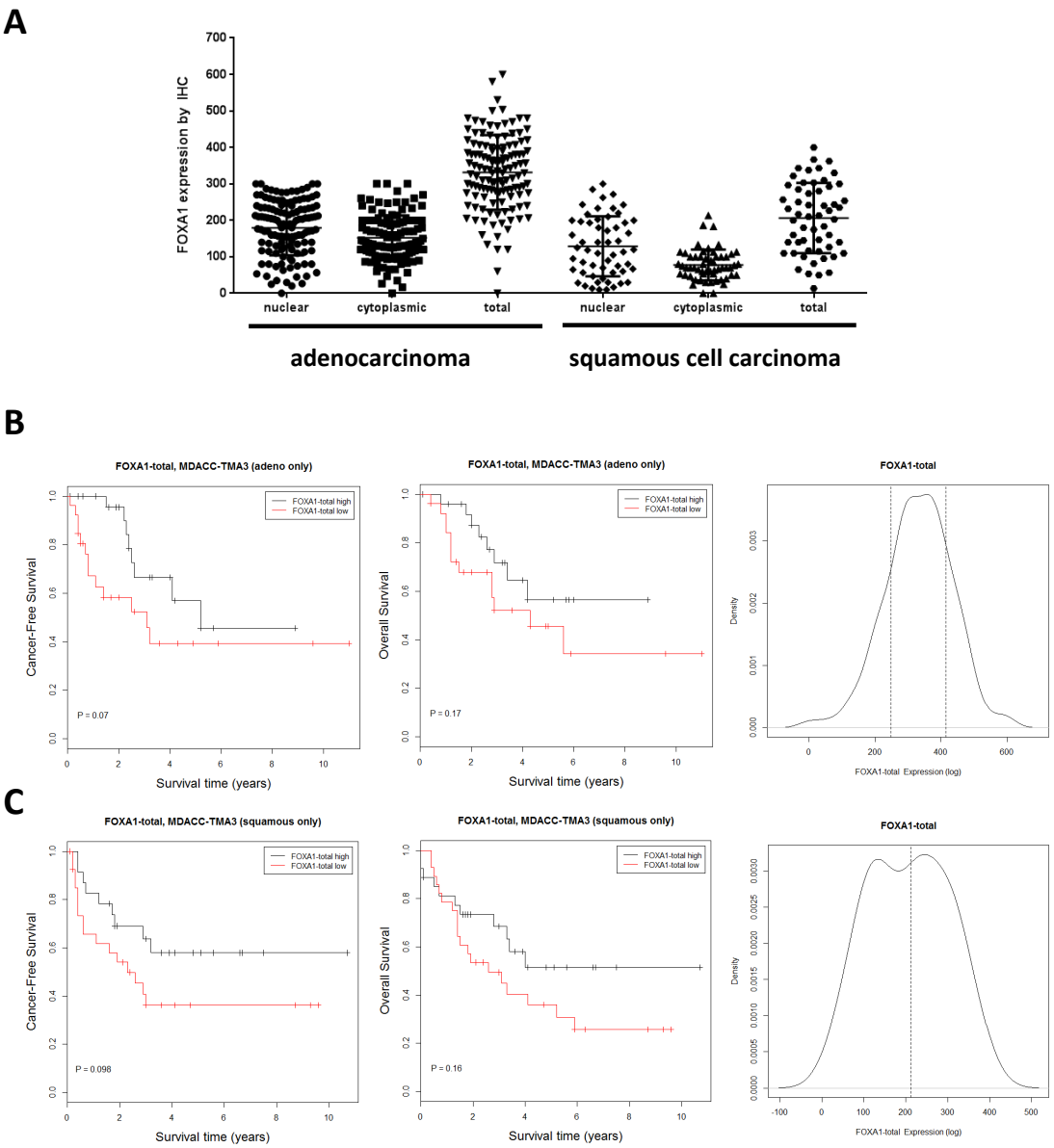


Figure 4.12. High FOXA1 expression in NSCLC tumors correlates with better prognosis. (A) Nuclear, cytoplasmic, and total FOXA1 protein expression levels in a tumor microarray panel (PROSPECT). (B) Progression-free survival and overall survival in lung adenocarcinoma patients, stratified by high vs. low FOXA1 expression (top and bottom quintiles of the overall distribution). (C) Progression-free survival and overall survival in lung squamous cell carcinoma patients, stratified by high vs. low FOXA1 expression (above and below the median of overall distribution).

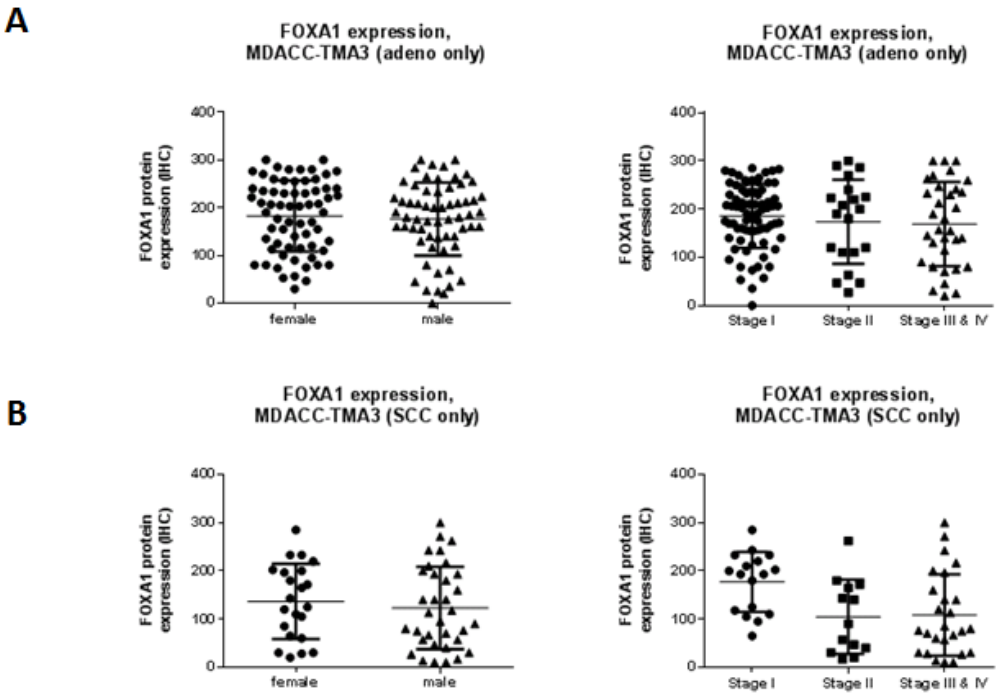


Figure 4.13. FOXA1 expression by IHC does not correlate with other clinical parameters. (A) Comparison of FOXA1 expression in female vs. male (left) and various stages (right) in adenocarcinomas. (B) Comparison of FOXA1 expression in female vs. male (left) and various stages (right) in squamous cell carcinomas.

4.4 Discussion

FoxA1/HNF3α is the founding member of the forkhead box superfamily of transcription factors, which are characterized by an evolutionarily conserved winged-helix DNA-binding domain. The *FOXA1* locus is located on chromosome 14q, near *NKX2-1*, a lung-specific lineage-survival transcription factor that is also the most frequently amplified gene in lung

adenocarcinomas (90,251-254). Cell lines harboring 14q amplification require NKX2-1 for survival (252-254), however the role of FOXA1 in lung cancer has not yet been systematically explored.

Here we used a parallel *in vitro* and *in vivo* functional genomics screen to identify FOXA1 as an essential gene in 14q-amplified lung adenocarcinomas. Importantly, this gene would not have been identified using standard *in vitro* methods, as a growth defect was only evident in clonogenicity and xenograft growth assays. Integrative transcriptomic and cistromic analyses identified genes which are positively or negatively regulated by FOXA1 only in the 14q-amplified context, suggesting that copy number gain at this locus creates a neomorphic phenotype in these cells. Notably, many of the genes whose expression increases after FOXA1 inhibition are secreted factors, suggesting a possible explanation as to why a growth defect was not observed in high density *in vitro* culture. We speculate that the functional effect of increased expression of anti-growth paracrine signals may be masked in the nutrient-rich environment of *in vitro* tissue culture, but that plating at low density or introduction to a stressful microenvironment in a xenograft setting exerted sufficient selective pressure to reveal FOXA1 functions in cell growth.

FOXA1 is able to bind to compacted chromatin as a “pioneer” factor, inducing a permissive state for transcription initiation with cooperating transcription factors (264) (265-267). In breast, prostate, and liver cancers, FOXA1 is known as a master regulator of steroid response, where it cooperates with ER and AR to globally direct hormone-dependent

transcription programs (268). In ER-positive breast cancers, FOXA1 is absolutely required for almost all ER-chromatin binding events, and depletion results in significant growth arrest (240). In prostate cancer, a large cohort of AR binding sites are pioneered by FOXA1, and depletion of FOXA1 results in redistribution of AR to new binding sites (269). FOXA1/2 also interact with ER and AR in the liver, where they are essential for gender-specific occurrences of hepatocellular carcinoma (270).

In lung tumors, the status of FOXA1 as a coregulator with ER or AR has not been explored, however several studies have linked FOXA1 function with the transcription factor NKX2-1. NKX2-1 and FOXA1 binding sites share a high degree of overlap in a 14q-amplified context (255), and the two transcription factors are able to physically interact to either positively or negatively regulate NKX2-1 target genes (255,256,258). In KRAS-driven mouse models of lung cancer, depletion of NKX2-1 results in redirection of FOXA1/2 to other de novo binding sites, including sites near gastric-specific genes (258). This suggests that recruitment of FOXA1 to specific sites can be dependent on other cis-acting transcription factors besides NKX2-1. We provide evidence that suggests that the 14q-amplified neomorphic function of FOXA1 is at least in part independent of its coregulatory roles with NKX2-1, as evidenced from the lack of shared binding regions near FOXA1-regulated genes. We identified other transcription factors whose expression correlated with FOXA1 in a panel of cell lines, and whose associated binding motifs were significantly enriched within FOXA1-binding sites. These transcription factors represent potential coregulatory factors by which FOXA1 is promoting pro-growth pathways.

Several genes which are positively regulated by FOXA1 in lung adenocarcinoma cells participate in pro-growth pathways, including *FGFR3, WNT7B,* and *RHOC*. Of these, FGFR3 was also found to be highly expressed in FOXA1^{hi} cell lines, suggesting a correlation between FOXA1 and FGFR signaling. FGFR inhibitors have been screened across a panels of lung cancer cell lines, however no drug sensitivity in 14q-amplified cell lines was observed. Given that the growth defect induced by FOXA1 inhibition only manifests in clonogenicity or *in vivo* growth assays, it is possible that 14q-amplified cells may still be sensitive to FGFR inhibition under more physiological conditions.

The role of FOXA1 in tumorigenesis is likely to be complex and highly context-dependent. In ER-positive breast cancer and androgen-dependent prostate cancer, FOXA1 clearly plays a role in driving tumor growth (240,269). However, in castration-resistant prostate cancers, FOXA1 appears to be able play either a pro-growth (260) or anti-metastatic role (271). Similarly, loss of FOXA1/2 appears to be required for the epithelial-to-mesenchymal transition in pancreatic cancer cells (259). One study using ChIP-seq and expression data linked loss of FOXA1 expression with EMT in the lung adenocarcinoma cell line A549 (272), although the significance of these findings are not clear given that A549 exhibits only low levels of FOXA1 expression and is already classified as a mesenchymal cell line (273).

Recurrent FOXA1 mutations have been identified in 3.4-5.2% of prostate tumors (241,274) and 1.8% of breast cancer patients (275), but not in other cancer types. Amplification however is observed in several tumor types, including esophageal (276,277), lung (261,277),

and thyroid (278). Specifically, co-amplification of NKX2-1 and FOXA1 is observed in 9-11% of lung adenocarcinomas (Figure 4.1 and reference (255). High FOXA1 expression is associated with good prognosis in breast cancer (279,280) and poor prognosis in prostate (260,269). One study reported that high FOXA1 expression in lung squamous cell carcinoma is correlated with poor outcome (261), however this is not consistent with our analyses of TCGA and PROSPECT datasets. Our findings that high FOXA1 expression trends towards better patient outcome are consistent with prior reports that high NKX2-1 expression correlates with better overall survival (262,263). Intriguingly, these same studies also reported that amplification of NKX2-1 appears to have the opposite effect, correlating with worse prognosis. These findings introduced the idea that 14q-amplification may create a hypermorphic or neomorphic oncogenic state that is distinct from contexts in which genes in this region are expressed at lower levels (Figure 4.14). In our studies, NKX2-1 and FOXA1 copy number followed expression trends. The reasons for this discrepancy are not known at this time, but it may arise from differences in the quantitation methods used (fluorescence in situ hybridization compared to SNP array). Future studies comparing FOXA1 and NKX2-1 genomic occupancy in cell lines without 14q amplification may shed more light on the distinct roles that these transcription factors play when highly overexpressed.

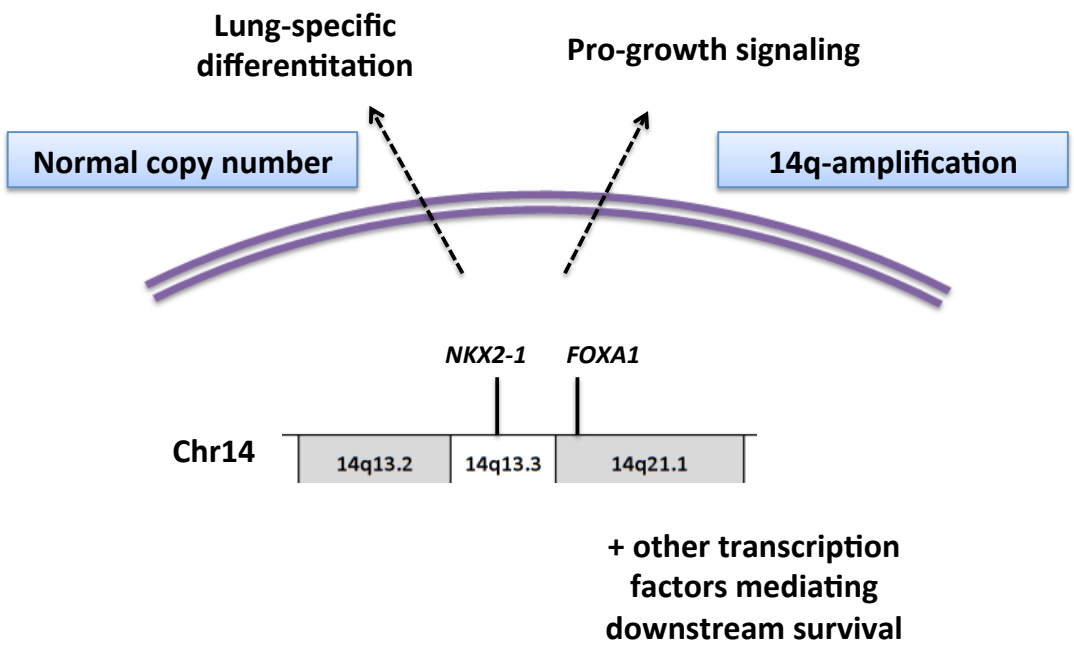


Figure 4.14 Model for neomorphic functions of 14q-amplification. In cells with normal copy number levels of at Chr14q, NKX2-1 and FOXA1 cooperate to regulate lung-specific epithelial markers and lung development. In cells with amplification at chr14q, overexpression of NKX2-1 and FOXA1 causes a gain-of-function neomorphic phenotype in which they cooperate with each other and possibly other transcription factors to mediate cell survival.

Here we provide evidence that amplification of FOXA1 on chromosome 14q drives a distinct transcriptional program that is unique to the 14q-amplified context, and that this appears to be in part independent of NKX2-1. In addition, the identification of genes regulated by FOXA1 in 14q-amplified cells has suggested a number of potential therapeutic targets. Further studies on the functional cooperation between FOXA1 and other co-regulating transcription factors may reveal important new vulnerabilities for 14q-amplified lung adenocarcinomas.

CHAPTER 5

CONCLUSIONS

"It is a capital mistake to theorize before one has data. Insensibly one begins to twist facts to suit theories, instead of theories to suit facts."
-Sherlock Holmes, *A Scandal in Bohemia*

This study sought to identify acquired vulnerabilities in lung cancer through the use of parallel *in vitro* and *in vivo* RNAi screening. We reasoned that important cancer vulnerabilities might be identified in a physiological context that might otherwise not be discoverable in cells cultured on plastic in nutrient-rich media. Negative selection screens conducted *in vivo* have successfully identified specific vulnerabilities in the past (134), and a similar parallel screening approach was recently employed by Possik and colleagues to identify a specific requirement for DDR kinases *in vivo* (136). Here we report the use of parallel screening to identify FOXA1 as an important regulator of tumorigenesis in 14q-amplified lung adenocarcinomas. Amplification of the 14q genomic region is one of the most frequent genomic events in lung adenocarcinomas, with NKX2-1 typically believed to be the target. The *FOXA1* locus is frequently co-amplified with *NKX2-1* in NSCLCs by virtue of genomic location. While FOXA1 is known to cooperate with NKX2-1 to regulate NKX2-1 transcriptional targets, we provide evidence that in the 14q-amplified context, the pro-growth functions of FOXA1 are only partially the result of cooperation with NKX2-1, and that other cooperating transcription factors are likely involved. Moreover, in the 14q-amplified context where FOXA1 is highly expressed, it appears to play a neomorphic role in oncogenesis that is not seen in cells without 14q-amplification. Future

studies comparing the FOXA1 cistrome in 14q-amplified cells compared to non-amplified may provide insight into the differences in FOXA1 functions in these two contexts.

Although focal amplification of the *NKX2-1* locus is the most frequently observed amplification event in lung adenocarcinomas, there currently there are no therapies available that specifically target tumors with this abnormality. Further functional studies on the FOXA1 transcriptional targets identified in this study may also identify therapeutic targets for which 14q-amplification can be used as a clinical biomarker. Taken together, our findings implicate FOXA1 as an oncogenic transcription factor that cooperates with multiple other transcription factors to regulate tumorigenesis in lung cancer. These results shed new light on the functional consequences of 14q-amplification in lung adenocarcinomas and suggest new avenues of exploration in the quest for identifying new therapeutic strategies.

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APPENDIX A

MINI-LIBRARY PARALLEL IN VITRO AND IN VIVO SHRNA SCREENING PROTOCOL

Mini-library parallel *in vitro* and *in vivo* shRNA screens
Suzie Hight, 7.1.14

Thought experiments / preparations required before beginning:

- Cell lines selected for screening should have the following features:
    - High viral transduction efficiency.
    - High engraftment efficiency, as evidenced by large stem cell population (i.e. ALDH activity), or robust tumor growth upon injection of very few cells.

- The *in vitro* portion of the screen extends for 20 PDs. The faster the cell line grows, the less time this will take.

- The larger the cell line is, the more flasks you will need to maintain the correct confluence throughout the screen.

- Before starting, determine the minimal amount of puromycin that will kill >90% of the cells over a period of 3-4 days.

- Before starting, verify the transduction efficiency of the cell lines you selected using the CSC virus pool in a 6-well format (see protocol for determination of viral titer).

- The number of cells required for the screen is determined by the size of the library used (number of clones) and desired representation (number of cells per clone). You will also need to consider engraftment efficiency for *in vivo* screens. I recommend a high representation for in vivo screens (1000 x).

  Example:
  Library size: 1000 clones
  Desired MOI: 0.3 → Corresponds to an infection efficiency of ~30%
  Desired representation: 1000
  (1000 clones) x (1000 x representation) = 1 million infected cells required
  (1 million cells)/(0.3 infection efficiency) = 3 million total cells required

The following protocol assumes a library size of 1000 clones using 1000 x representation, and describes 1 replicate. Screens should be performed in triplicate.

Day 0

1. Seed 4 sets of 3 million cells each in T75 or T175 flasks, such that they will be at ~30% confluency the next day.
   Note: You may need to spread this out over multiple flasks to achieve the correct confluency.

Day 1

1. Trypsinize and count the cells in Flask Set 4 to verify cell count. If you do not have at least 3 million cells, abort and re-seed flasks.

2. After verifying cell count, infect Flask Set 1 as follows:

Reagent	**Final conc**
virus	x uL (amount calculated to achieve 30% infection efficiency)
R5	9 mL/T75 or 12 mL/T175
polybrene	1 x (stock is 1000 x)

3. Treat Flask Set 2 as a mock, with polybrene and same volume of R5, but no virus.
4. Change the media on Flask Set 3 to just fresh R5.
5. Incubate overnight.

Day 2

1. After 8-16 hrs of incubation with virus, replace sup with fresh media.

Days 3-7

1. Incubate Flask Sets 1 and 2 with puro for 3-4 days, changing media if necessary. If cells near confluency, trypsinize and expand the population and continue puro selection.
2. Maintain cells in Flask Set 3 under the same conditions as Flask Sets 1 and 2, splitting if necessary, but without puro.
3. Puro selection is complete when all the cells in Flask Set 2 are dead.
4. Trypsinize and count the cells in Flask Sets 1 and 3. Calculate infection efficiency as follows:

   (# of cells in Flask Set 1) / (# cells in Flask Set 3) = fraction of cells infected
   (fraction of cells infected) * (# cells in Flask Set 4) = total number of cells infected

   Make sure this is the desired number before proceeding.

   The total number of cells infected = required unit of passage for the duration of the screen. This means that all cell pellets and all subsequent passages should contain at least this many cells. I usually multiply this number by 3 just to be safe.

Days 7 and on

1. If you have at least 2 x the minimal number of cells required, then pellet 50% of the culture and expand the rest.
2. Continue to expand the culture, always maintaining at subconfluency, until you have enough cells for pelleting, mouse injections with replicates, and continued culture.
3. When cells are ready for injection, trypsinze, count, and distribute as follows:

   At least 1 unit of passage for pelleting
   At least 1 unit of passage for continued culture
   5 million cells per mouse x at least 3
4. Inject cells subcutaneously into mice, save the pellet as time 0, and seed for continued culture.
5. Continue culturing cells, always keeping at subconfluency, and saving a pellet at least on every other passage. Cells must be counted at every passage to keep track of PDs.

$$\text{Population doubling} = \frac{\log_{10}\left(\frac{\text{final cell count}}{\text{initial cell count}}\right)}{\log_{10}(2)} \approx \frac{\log_{10}\left(\frac{\text{final cell count}}{\text{initial cell count}}\right)}{0.3}$$

6. Pellet all cells after 20 PDs have been reached.
7. Monitor xenograft growth in mice and sac when tumors reach pre-determined size.
8. Harvest all of the tumor for gDNA – do not reserve any portion for other analyses.

Prepare sequencing libraries: Two-step PCR reaction

1. Determine amount of gDNA needed to cover the library:

   (6 pg gDNA per diploid cell) * (minimal unit of passage) = pg gDNA template required

2. Prepare 1st PCR reaction:
   For every 50 uL PCR reaction, add 100 ng gDNA and 0.5 uM of each primer. Total input gDNA will need to be spread out over many reactions in a 96-well plate. Use 16 cycles. <insert PCR details>

3. Pool individual reactions together and use ammonium acetate precipitation to concentrate into a manageable volume. <insert details>

4. Purify product (183 bp) on a 2% agarose gel. This step is necessary to purify away the primers. Dissolve the agarose at room temperature – do not heat.

5. Input 1st PCR reaction product into 2nd PCR reaction, run for 16 cycles. <insert PCR details>

6. Purify product (257 bp) on 2% agarose gel. Dissolve the agarose at room temperature – do not heat.

7. Quantify by picogreen and QuBit assay. Accurate quantitation is essential.

8. Repeat for each T0 and T4 (late in vitro) replicate, and each tumor.

Quantification of shRNA abundance

1. Determine the number of reads required to cover the library:

   (library representation used) * (size of library) = number of shRNA reads required per sample

   For example: 1000 x representation * 1000 shRNAs = 1 million reads required

2. Check quality of reads using Fastq quality tools.

3. Map shRNA reads to library using Bowtie.

4. Calculate log2 fold differences between samples. Apply statistical tests as appropriate.

APPENDIX B

PREPARATION OF SHRNAS FOR SEQUENCING

Preparation of shRNAs for Miseq sequencing
Suzie Hight, 8.17.15

Background information:

- This protocol amplifies short hairpin sequences from transduced genomic DNA in two steps. The first step amplifies the short hairpin and adds partial Illumina adapter sequences, using a universal primer set. The second step increases amplification and completes the adapter sequences necessary for binding to the Illumina flow cell, adding index sequences. Thus the second PCR uses primers that are specific to each sample processed.
- Fewer cycles are used in order to minimize PCR-based bias in the final sample.
- The amplification primers used here should be compatible with either Miseq or Hiseq platforms, and allow for Illumina sequencing primers to be used. If the design is altered in such a way as to require a custom primer, note that Miseq sequencing primers must be more stable than Hiseq sequencing primers.

Prepare sequencing libraries: Two-step PCR reaction

9. Determine amount of gDNA needed to cover the library:

   (6 pg gDNA per diploid cell) * (minimal unit of passage) = pg gDNA template required

10. Determine the amount of gDNA needed to ensure full library coverage throughout sample preparation:

    (amount of gDNA needed to cover the library) / (% recovery expected after purification) = amount of gDNA needed for sample preparation
    Note: The expected % recovery will depend on the method used to purify the PCR reaction. QIAGEN kit stats are as follows:

	maximum binding capacity	**elution volume**	**% recovery**
QIAquick PCR Purification Kit	10 ug	30 uL	90-95% (100 bp-10 kb)
QIAGEN Minelute PCR Purification Kit	5 ug	10 uL	80% (70 bp-4kb)
QIAquick Gel Extraction Kit	10 ug	30 uL	70-80% (70 bp-10 kb)

11. Prepare 1st PCR reaction:

For every 50 uL PCR reaction, add 500 ng gDNA and 0.5 uM of each primer. Total input gDNA will need to be spread out over many reactions in a 96-well plate. Make up 1 more reaction than needed, to ensure adequate library coverage. Also include the following: 1) a separate 1 x reaction to be run for 33 cycles (positive control), and 2) a no-template water control reaction (negative control).

See below for primer sequences.

1st PCR setup

Reaction components	Stock conc	Final conc	1 x rxn, with 500 ng/uL gDNA	13 x rxn (scaled up to cover 1 M cells, plus 1)
2 X Hotstart MM	2x	1x	25 uL	325 uL
DMSO	1.0	0.5%	1 uL	13 uL
10 uM forward	10 uM	0.5 uM	2.5 uL	32.5 uL
10 uM reverse	10 uM	0.5 uM	2.5 uL	32.5 uL
template	n/a	500 ng	1.0 uL	13 uL
dH2O	n/a	to 50 uL	18 uL	234 uL

650 uL total, split between 13 50 uL rxns

1st PCR conditions

Step	Temp	Time
1	95°C	15 min
2	94°C	30 sec
3	54°C	45 sec
4	72°C	60 sec
5	Repeat 2-4 x 16 cycles	
6	72°C	5 min
7	4°C	hold

12. Pool individual reactions together and purify product (181 bp) on a 2% agarose gel. Use the positive control as a guide for where to cut the gel, as the product may not be visible at this step. Dissolve the agarose at room temperature – do not heat.

    Alternatively, use the QIAquick PCR Purification kit or QIAquick Minelute PCR Purification kit to pool reactions and elute into a smaller volume. Pros of using the

Mineulte kit are that you can elute into 10 uL (20 uL with 2 columns), for simplified input into the 2nd PCR. Cons of the Mineulte kit are that recovery is only 80%, so you require greater input into the 1st PCR.

13. Input 1st PCR reaction product into 2nd PCR reaction, run for 25 cycles. If 1st PCR reaction product volume is > 10 uL, adjust the volume or number of 2nd PCR reactions accordingly.

    See Miseq Primers spreadsheet for primer sequences.

2nd PCR setup

2nd PCR setup

Reaction components	Stock conc	Final conc	1 x rxn, with 10 uL PCR template
2 X Hotstart MM	2x	1x	25 uL
DMSO	1.0	0.5%	1 uL
10 uM forward	10 uM	0.5 uM	2.5 uL
10 uM reverse	10 uM	0.5 uM	2.5 uL
template - 1st PCR	n/a	n/a	10 uL
dH2O	n/a	to 50 uL	9 uL

50 uL total

1st PCR setup

Step	Temp	Time
1	95°C	15 min
2	94°C	30 sec
3	54°C	45 sec
4	72°C	60 sec
5	Repeat 2-4 x 25 cycles	
6	72°C	5 min
7	4°C	hold

14. Purify product (250 bp) on 2% agarose gel. Dissolve the agarose at room temperature – do not heat. Elute into water, not buffer.

    Alternatively, use the QIAquick PCR Purification kit.

15. Quantify by QuBit assay. Accurate quantitation is essential.

TRC1/2 primer design and sequences

1st PCR primers

PR ID	Name	Sequence
PR4439	PR4439-17-TRC1and2ForwardInner	ACACTCTTTCCCTACACGACGCTCTTCCGATCTVVBVBVTCTTGTGGAAAGGACGA
PR4441	PR4441-TRC1and2ReverseInner	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGAATACTGCCATTTGTCTC

2nd PCR primers

PR ID	Full sequence	Illumina P5 or P7 adapter	Index	Illumina partial read adapter	Forward or reverse
br_D701	CAAGCAGAAGACGGCATACGAGATcgagtaatGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	cgagtaat	GTGACTGGAGTTCAGACGTG	reverse
br_D702	CAAGCAGAAGACGGCATACGAGATtctccggaGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	tctccgga	GTGACTGGAGTTCAGACGTG	reverse
br_D703	CAAGCAGAAGACGGCATACGAGATaatgagcgGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	aatgagcg	GTGACTGGAGTTCAGACGTG	reverse
br_D704	CAAGCAGAAGACGGCATACGAGATggaatctcGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	ggaatctc	GTGACTGGAGTTCAGACGTG	reverse
br_D705	CAAGCAGAAGACGGCATACGAGATttctgaatGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	ttctgaat	GTGACTGGAGTTCAGACGTG	reverse
br_D706	CAAGCAGAAGACGGCATACGAGATacgaattcGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	acgaattc	GTGACTGGAGTTCAGACGTG	reverse
br_D707	CAAGCAGAAGACGGCATACGAGATagcttcagGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	agcttcag	GTGACTGGAGTTCAGACGTG	reverse
br_D708	CAAGCAGAAGACGGCATACGAGATgcgcattaGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	gcgcatta	GTGACTGGAGTTCAGACGTG	reverse
br_D709	CAAGCAGAAGACGGCATACGAGATcatagccgGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	catagccg	GTGACTGGAGTTCAGACGTG	reverse
br_D710	CAAGCAGAAGACGGCATACGAGATttcgcggaGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	ttcgcgga	GTGACTGGAGTTCAGACGTG	reverse
br_D711	CAAGCAGAAGACGGCATACGAGATgcgcgagaGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	gcgcgaga	GTGACTGGAGTTCAGACGTG	reverse
br_D712	CAAGCAGAAGACGGCATACGAGATctatcgctGTGACTGGAGTTCAGACGTG	CAAGCAGAAGACGGCATACGAGAT	ctatcgct	GTGACTGGAGTTCAGACGTG	reverse
br_D501	AATGATACGGCGACCACCGAGATCTACACtatagcctACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	tatagcct	ACACTCTTTCCCTACACGAC	forward
br_D502	AATGATACGGCGACCACCGAGATCTACACatagaggcACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	atagaggc	ACACTCTTTCCCTACACGAC	forward
br_D503	AATGATACGGCGACCACCGAGATCTACACcctatcctACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	cctatcct	ACACTCTTTCCCTACACGAC	forward
br_D504	AATGATACGGCGACCACCGAGATCTACACggctctgaACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	ggctctga	ACACTCTTTCCCTACACGAC	forward
br_D505	AATGATACGGCGACCACCGAGATCTACACaggcgaagACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	aggcgaag	ACACTCTTTCCCTACACGAC	forward
br_D506	AATGATACGGCGACCACCGAGATCTACACtaatcttaACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	taatctta	ACACTCTTTCCCTACACGAC	forward
br_D507	AATGATACGGCGACCACCGAGATCTACACcaggacgtACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	caggacgt	ACACTCTTTCCCTACACGAC	forward
br_D508	AATGATACGGCGACCACCGAGATCTACACgtactgacACACTCTTTCCCTACACGAC	AATGATACGGCGACCACCGAGATCTACAC	gtactgac	ACACTCTTTCCCTACACGAC	forward

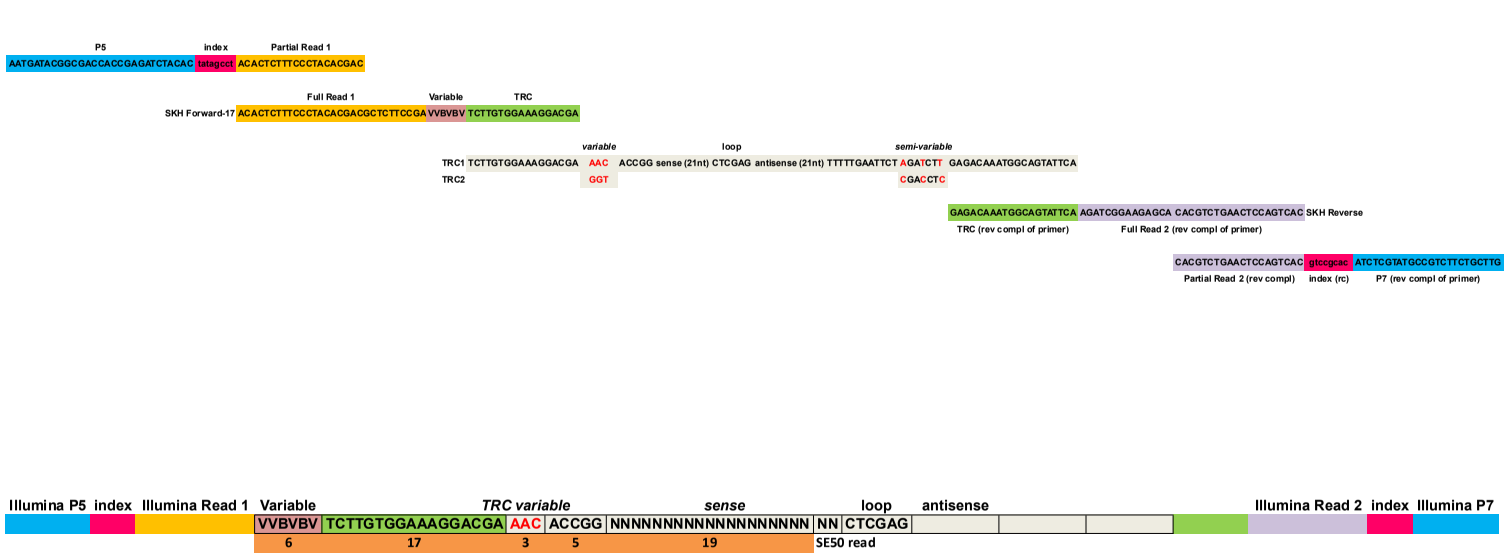


Figure B1. Primer design for TRC1 and TRC2 shRNAs. (A) TRC1 and TRC2 constructs are amplified from transduced gDNA using a nested PCR reaction. In the first reaction, universal forward and reverse primers contain partial sequences for Illumina read 1 and read 2 primers. The forward primer also contains a degenerate region, designed to be mismatched to TRC vector and used to introduce variability at the beginning of the sequencing read. Nucleotide codes follow IUPAC convention, i.e. V = A/C/G, B=C/G/T. In the second PCR reaction, indexed forward and reverse primers can be multiplexed to produce unique index combinations. Directionality of all sequences is 5' to 3', except the reverse primer, which is shown 3' to 5'. Differences in TRC1 and TRC2 vectors are indicated in red font. (B) The resulting 250 bp PCR amplicon is sequenced on either an Illumina HiSeq or Miseq using Illumina sequencing primers. Sequencing read out is shown in orange. A single-end 50 bp read (SE50) begins at the degenerate sequence, covers the first 19 nucleotides of the sense shRNA. Alternatively, longer read lengths could be used to cover both sense and antisense shRNAs.

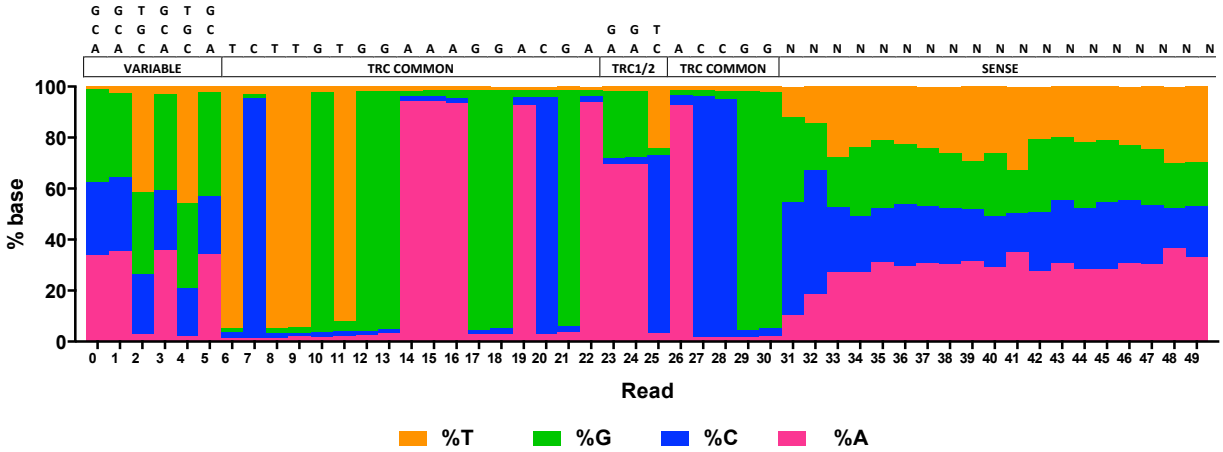


Figure B2. Base composition in the TRC1/2 PCR amplicon. Reads obtained in an SE50 Hiseq run on amplicons prepared using method described in this appendix. A custom pool of ~1500 shRNA plasmid constructs from TRC1 and TRC2 vectors was prepared by spotting from glycerol stocks onto LB-amp plates, allowing for colony growth overnight, and harvesting plasmid DNA directly from colonies.

APPENDIX C

GENE COVERAGE IN THE NHR/COREG MINI-LIBRARY

Gene Symbol	Entrez Gene ID	Panel	Total shRNA count	TRC1 count	TRC2 count
non-targeting shRNA	n/a	Negative control	2	2	0
GFP	n/a	Negative control	1	1	0
VEGFA	7422	Negative control	5	2	3
ALDH1A1	216	Positive control	10	5	5
PLK1	5347	Positive control	8	6	2
UBB	7314	Positive control	5	3	2
UBC	7316	Positive control	6	4	2
ALDH1A3	220	Positive control	8	5	3
BRCA2	675	CoRegs	11	5	6
RB1	5925	CoRegs	12	7	5
UBE3A	7337	CoRegs	10	5	5
SRA1	10011	CoRegs	6	1	5
CCNE1	898	CoRegs	8	5	3
EP300	2033	CoRegs	12	8	4
PRMT1	3276	CoRegs	13	5	8
PARP1	142	CoRegs	12	5	7
CAV1	857	CoRegs	13	5	8
CDK7	1022	CoRegs	16	10	6
ETV4	2118	CoRegs	10	5	5
HMGB1	3146	CoRegs	8	5	3
HMGB2	3148	CoRegs	11	5	6
MUC1	4582	CoRegs	7	5	2
PHB	5245	CoRegs	9	5	4
RAF1	5894	CoRegs	10	10	0
RNF4	6047	CoRegs	9	4	5
SMARCA4	6597	CoRegs	14	5	9
UBE2I	7329	CoRegs	11	5	6
SUMO1	7341	CoRegs	10	10	0
MLL2	8085	CoRegs	10	5	5
NRIP1	8204	CoRegs	10	5	5
TRRAP	8295	CoRegs	14	7	7
NCOA1	8648	CoRegs	9	5	4
SAP30	8819	CoRegs	8	3	5
HDAC3	8841	CoRegs	14	14	0
JMJD1C	221037	CoRegs	8	5	3
CDC25B	994	CoRegs	10	5	5
CREBBP	1387	CoRegs	9	5	4
FOXA1	3169	CoRegs	9	5	4
MTA1	9112	CoRegs	11	5	6
MTA2	9219	CoRegs	10	5	5
MED1	5469	CoRegs	5	5	0
MED23	9439	CoRegs	10	5	5
RBM39	9584	CoRegs	10	5	5
HDAC1	3065	CoRegs	18	13	5
E2F1	1869	CoRegs	16	11	5
NCOA4	8031	CoRegs	9	5	4
TBL1X	6907	CoRegs	10	5	5
PSME3	10197	CoRegs	10	5	5
SNAI1	6615	CoRegs	8	4	4
HDAC4	9759	CoRegs	13	6	7
PIAS3	10401	CoRegs	10	5	5
PIN1	5300	CoRegs	9	5	4
NCOR1	9611	CoRegs	10	5	5
NCOR2	9612	CoRegs	10	5	5
RBM14	10432	CoRegs	4	4	0
NCOA3	8202	CoRegs	10	4	6
NCOA2	10499	CoRegs	10	5	5
PARK7	11315	CoRegs	4	4	0
PHB2	11331	CoRegs	9	5	4
BRCA1	672	CoRegs	13	8	5
PPARGC1A	10891	CoRegs	8	4	4
NCOA6	23054	CoRegs	10	5	5
PELP1	27043	CoRegs	7	7	0
SENP1	29843	CoRegs	9	5	4

Table C1. NHR/Coregulator shRNA library content. Continued on the next page. (1/2)

Gene Symbol	Entrez Gene ID	Panel	Total shRNA count	TRC1 count	TRC2 count
MED24	9862	CoRegs	10	5	5
KDM1A	23028	CoRegs	12	5	7
SIN3B	23309	CoRegs	10	5	5
PIAS4	51588	CoRegs	10	5	5
TGFB1I1	7041	CoRegs	8	4	4
PIAS1	8554	CoRegs	10	5	5
KDM3B	51780	CoRegs	12	5	7
OTUB1	55611	CoRegs	9	4	5
KDM3A	55818	CoRegs	14	5	9
FOXA2	3170	CoRegs	10	5	5
PUS1	80324	CoRegs	9	5	4
HNRNPU	3192	CoRegs	9	2	7
TBL1Y	90665	CoRegs	9	7	2
CCND1	595	CoRegs	13	8	5
PPARGC1B	133522	CoRegs	6	5	1
CARM1	10498	CoRegs	10	5	5
AR	367	NHR	7	3	4
ESR1	2099	NHR	5	5	0
NR3C1	2908	NHR	8	3	5
VDR	7421	NHR	9	5	4
HNF4A	3172	NHR	5	5	0
THRB	7068	NHR	5	5	0
NR0B1	190	NHR	5	5	0
NR3C2	4306	NHR	6	4	2
PGR	5241	NHR	5	5	0
RARA	5914	NHR	8	4	4
RARB	5915	NHR	4	4	0
RARG	5916	NHR	9	4	5
ESR2	2100	NHR	4	4	0
NR6A1	2649	NHR	3	3	0
NR4A1	3164	NHR	4	4	0
RORA	6095	NHR	5	5	0
RXRA	6256	NHR	8	5	3
THRA	7067	NHR	5	5	0
NR2E1	7101	NHR	5	5	0
NR2C1	7181	NHR	9	5	4
NR2C2	7182	NHR	9	5	4
NR5A2	2494	NHR	5	5	0
NR1I2	8856	NHR	5	5	0
HNF4G	3174	NHR	5	5	0
ESRRA	2101	NHR	9	5	4
ESRRB	2103	NHR	4	4	0
NR5A1	2516	NHR	5	5	0
PPARA	5465	NHR	10	5	5
RORC	6097	NHR	5	5	0
NR1I3	9970	NHR	5	5	0
NR1H4	9971	NHR	5	5	0
NR1D2	9975	NHR	9	5	4
NR2F6	2063	NHR	8	5	3
NR2F1	7025	NHR	10	5	5
NR1H3	10062	NHR	5	5	0
NR4A2	4929	NHR	6	3	3
PPARD	5467	NHR	5	5	0
RORB	6096	NHR	5	5	0
RXRG	6258	NHR	5	5	0
NR4A3	8013	NHR	5	5	0
NR1H2	7376	NHR	10	5	5
NR2E3	10002	NHR	5	5	0
NR2F2	7026	NHR	5	5	0
NR1D1	9572	NHR	5	5	0
NR0B2	8431	NHR	5	5	0
RXRB	6257	NHR	4	4	0
PPARG	5468	NHR	8	5	3
ESRRG	2104	NHR	5	5	0

Table C1. NHR/Coregulator shRNA library content. (2/2)

APPENDIX D

LOG2 FOLD CHANGES IN SHRNA ABUNDANCE AND STATISTICAL TEST RESULTS

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
SHC002	NON-MAMMALIAN SHRNA	0.004185	0.0349	0.019543	0.194637	0.007564	0.101101	0.104516	0.071778	0.09132	0.118067	0.095852	0.080876
SHC004	GFP	1.04166	1.612129	1.326894	2.12961	1.112848	1.621229	0.205837	0.156288	0.05877	0.11707	0.12151	0.009438
SHC016	NON-TARGETING SHRNA	0.310474	0.116677	0.213576	0.55253	0.183264	0.367897	0.120177	0.116174	0.116273	0.042575	0.072747	0.029113
TRCN0000000249	E2F1	0.010418	0.114077	0.062247	0.043257	0.111698	0.077477	0.076688	0.073821	0.101301	0.094499	0.037144	0.169702
TRCN0000000251	E2F1	0.547243	0.454938	0.50109	0.434447	0.397245	0.415846	0.191581	0.171992	0.238281	0.068669	0.013268	0.02149
TRCN0000000252	E2F1	0.187082	0.258674	0.222878	0.040633	0.054488	0.047561	0.102638	0.045374	0.079924	0.89476	0.108877	0.111368
TRCN0000000253,TRCN0000344500	E2F1,E2F1	0.021415	0.027305	0.02436	0.030587	0.008606	0.019596	0.05081	0.040274	0.03594	0.01434	0.030009	0.014883
TRCN0000000592	CDK7	0.271673	0.065763	0.168718	0.01267	0.083718	0.048194	0.087029	0.080572	0.035791	0.091253	0.050547	0.107157
TRCN0000000593	CDK7	2.23E-05	0.002532	0.001277	0.000323	0.000371	0.000347	0.021279	0.014529	0.017318	1.35E-05	9.46E-05	3.63E-05
TRCN0000000594	CDK7	0.048462	0.000821	0.024642	0.017755	0.012094	0.014925	0.051091	0.117409	0.065026	0.023554	0.052533	0.016226
TRCN0000000595	CDK7	0.001425	0.00024	0.000832	0.004402	0.002921	0.003661	0.077443	0.096361	0.094262	0.060539	0.065396	0.065412
TRCN0000000596	CDK7	0.098171	0.113427	0.105799	0.006416	0.005313	0.005865	0.119176	0.148803	0.198952	0.035779	0.05052	0.355159
TRCN0000001033,TRCN0000318418	PIN1,PIN1	0.566521	0.653392	0.609956	0.428938	0.424029	0.426484	0.36427	0.275324	0.222043	0.331159	0.25787	0.071475
TRCN0000001034,TRCN0000318360	PIN1,PIN1	0.071703	0.145248	0.108475	0.359969	0.915861	0.637915	0.42607	0.388171	0.429003	0.368669	0.310984	0.370695
TRCN0000001035	PIN1	0.133388	0.016082	0.074735	0.024196	0.023054	0.023625	0.046649	0.064991	0.030688	0.004277	0.031712	0.013975
TRCN0000001036,TRCN0000318359	PIN1,PIN1	0.021259	0.002464	0.011861	0.021473	0.070791	0.046132	0.033779	0.044579	0.079849	0.336116	0.044359	0.07721
TRCN0000001064	RAF1	0.014381	0.0349	0.024641	0.017096	0.005905	0.011501	0.130026	0.085452	0.116608	0.022194	0.019795	0.047008
TRCN0000001065	RAF1	0.009594	0.082872	0.046233	0.039116	0.008647	0.023882	0.114155	0.061456	0.106031	0.003543	0.00527	0.012778
TRCN0000001066	RAF1	6.68E-05	0.000582	0.000324	0.025539	0.091415	0.058477	0.002405	0.101204	0.115118	0.006951	0.014714	0.045847
TRCN0000001067	RAF1	1.425039	1.34011	1.382575	4.794219	6.716689	5.755454	1.362291	1.624106	1.349465	1.611076	1.268324	1.621845
TRCN0000001068	RAF1	4.45E-05	0.033977	0.017011	0.011476	0.019228	0.015352	0.025791	0.055989	0.038286	0.014656	0.016984	0.001525
TRCN0000001165	PPARGC1A	4.45E-05	0.000205	0.000125	0.002822	0.00145	0.002136	0.071597	0.084718	0.129569	0.007726	0.012796	0.031036
TRCN0000001166	PPARGC1A	0.355197	1.114318	0.734757	0.552766	0.314948	0.433857	0.360864	0.351908	0.398128	0.367281	0.3935	0.515096
TRCN0000001167	PPARGC1A	0.218915	0.168241	0.193578	0.050978	0.091619	0.071299	0.19762	0.169827	0.138619	0.208714	0.101716	0.046718
TRCN0000001168	PPARGC1A	2.23E-05	0.000171	9.67E-05	0.000385	0.071008	0.035697	0.035044	0.0238	0.008864	0.00877	0.000486	0.00029
TRCN0000001297	HNRNPU	0.169896	0.567167	0.368532	0.130517	0.129259	0.129888	0.666161	0.521124	0.666837	0.227358	0.108323	0.161208
TRCN0000001298,TRCN0000350256	HNRNPU,HNRNPU	6.68E-05	0.000137	0.000102	1.24E-05	0.000621	0.000317	0.046912	0.0368	0.111915	6.74E-06	1.35E-05	0.17816
TRCN0000001299,TRCN0000320513	HNRNPU,HNRNPU	2.23E-05	3.42E-05	2.82E-05	1.24E-05	0.000279	0.000146	0.011394	0.016523	0.04026	6.74E-06	1.35E-05	3.63E-05
TRCN0000001300	HNRNPU	2.23E-05	0.000103	6.25E-05	0.060913	0.001834	0.031373	0.061414	0.055977	0.112288	0.000862	0.016255	0.036663
TRCN0000001661	PPARD	0.069009	0.225929	0.147469	0.106221	0.113665	0.109943	0.096089	0.110719	0.092028	0.331637	0.050304	0.000218
TRCN0000001662	PPARD	0.014136	0.04869	0.031413	0.03433	0.026267	0.030298	0.085783	0.100152	0.030465	0.006823	0.011782	0.015645
TRCN0000001663	PPARD	0.003629	0.000445	0.002037	0.008952	0.000625	0.004789	0.050037	0.036507	0.053891	0.045923	0.131847	0.074887
TRCN0000001664	PPARD	0.315327	0.346131	0.330729	0.261978	0.484927	0.373453	0.256857	0.282013	0.506096	0.283835	0.122686	0.332544
TRCN0000001665	PPARA	0.151442	0.014747	0.083094	0.06468	0.045645	0.055163	0.09579	0.100996	0.124541	0.031462	0.059438	0.058443
TRCN0000001666	PPARA	0.316797	0.491652	0.404224	0.297153	0.572308	0.434731	0.245235	0.228274	0.131803	0.400077	0.330806	0.313377
TRCN0000001667	PPARA	0.145364	0.134812	0.140088	0.039477	0.071462	0.055469	0.148917	0.184038	0.232248	0.148714	0.082732	0.123529
TRCN0000001668	PPARA	0.182518	0.385514	0.284016	0.136684	0.2273	0.181992	0.071773	0.109508	0.102009	0.077384	0.116443	0.130353
TRCN0000001669	PPARA	0.046214	0.029768	0.037991	0.143721	0.054955	0.099338	0.905514	0.728338	0.918525	1.418117	1.080013	0.839327
TRCN0000001670	PPARG	0.000134	0.00024	0.000187	0.001032	0.002221	0.001627	0.031796	0.025011	0.030092	0.00879	0.004972	0.064251
TRCN0000001671	PPARG	2.23E-05	3.42E-05	2.82E-05	1.24E-05	4.17E-05	2.71E-05	1.76E-05	0.000453	0.000223	0.000108	6.76E-05	0.000145
TRCN0000001672	PPARG	0.002382	0.000684	0.001533	0.017221	0.005222	0.011221	0.128288	0.119048	0.090799	0.016489	0.008891	0.038188
TRCN0000001673	PPARG	0.041851	0.001369	0.02161	0.002251	0.000658	0.001454	0.021981	0.040641	0.03013	0.004674	0.001513	0.048061
TRCN0000001674	PPARG	0.012555	0.231199	0.121877	0.028896	0.006814	0.017855	0.08731	0.094062	0.044356	0.045202	0.111714	0.041527
TRCN0000002509,TRCN0000277862	CDC25B,CDC25B	2.23E-05	0.000137	7.96E-05	0.001517	0.000958	0.001238	0.052302	0.058619	0.048751	0.00716	0.019389	0.004501
TRCN0000002510,TRCN0000286048	CDC25B,CDC25B	0.083323	0.213304	0.148313	0.017631	0.001184	0.009407	0.125023	0.082382	0.044282	0.025366	0.05229	0.027515
TRCN0000002511,TRCN0000297052	CDC25B,CDC25B	0.022306	0.001642	0.011974	0.000709	0.000338	0.000523	0.029443	0.020559	0.038249	6.74E-06	0.000149	0.010382
TRCN0000002512,TRCN0000277861	CDC25B,CDC25B	0.076934	0.063163	0.070049	0.0046	0.008668	0.006634	0.08803	0.105289	0.097167	0.108428	0.014863	0.044504
TRCN0000002513,TRCN0000277863	CDC25B,CDC25B	2.092023	1.093275	1.592649	0.935836	0.241019	0.588428	0.006759	0.032067	0.020111	0.012084	0.022767	3.63E-05
TRCN0000003298	ESR1	0.044277	0.006364	0.025321	0.018452	0.027771	0.023111	0.122846	0.097498	0.163571	0.004782	0.028388	0.097574
TRCN0000003299	ESR1	0.042318	0.000205	0.021262	0.033335	0.030251	0.031793	0.013273	0.008965	0.011583	0.001731	0.000959	3.63E-05
TRCN0000003300	ESR1	0.125886	0.101314	0.1136	0.133028	0.028455	0.080742	0.25626	0.162379	0.116533	0.324464	0.070747	0.045121
TRCN0000003301	ESR1	0.058324	0.247007	0.152665	0.078631	0.105901	0.092266	0.295254	0.221634	0.315076	0.102346	0.061897	0.020546
TRCN0000003321	PGR	2.431749	3.17201	2.801879	3.215261	1.044245	2.129753	0.998144	0.983568	1.044295	1.174433	0.842964	0.756309
TRCN0000003323	PGR	0.039536	0.002908	0.021222	0.001828	0.000875	0.001351	0.036255	0.051635	0.025847	0.003994	0.000162	0.006861
TRCN0000003324	PGR	0.028873	0.150277	0.089575	0.003419	0.011644	0.007531	0.103744	0.105839	0.116906	0.000492	0.005053	0.034412
TRCN0000003325	ESR2	0.000267	0.005851	0.003059	0.008181	0.001538	0.00486	0.113014	0.0827	0.115044	0.037072	0.002256	0.007623
TRCN0000003326	ESR2	0.027403	0.032403	0.029903	0.138748	0.109447	0.124098	0.264249	0.340168	0.309639	0.497075	0.593566	0.987249
TRCN0000003327	ESR2	0.047995	0.037912	0.042953	0.027093	0.022666	0.02488	0.090137	0.05709	0.092698	0.187268	0.004932	0.012705
TRCN0000003328	ESR2	0.035996	0.103675	0.069836	0.388927	0.235273	0.3121	0.193424	0.214149	0.296753	0.178458	0.265234	0.351783
TRCN0000003343	VEGFA	0.074485	0.051427	0.062956	0.263408	0.113086	0.188247	0.032779	0.13365	0.134671	0.307975	0.194378	0.044068
TRCN0000003345	VEGFA	0.038534	0.157223	0.097879	0.272858	0.023383	0.148121	0.083272	0.076206	0.077317	0.042043	0.039238	0.040184
TRCN0000003368	UBE3A	0.001402	0.001334	0.001368	0.052557	0.046749	0.049653	0.095106	0.132574	0.104243	0.083931	0.244628	0.283829
TRCN0000003369	UBE3A	2.23E-05	0.003216	0.001619	0.010594	0.005472	0.008033	0.007304	0.121163	0.101897	0.030956	0.104215	0.132749
TRCN0000003370	UBE3A	0.418262	0.485322	0.451792	0.078867	0.10936	0.094113	0.245006	0.17626	0.128302	0.011242	0.053749	0.03336
TRCN0000003371	UBE3A	0.014759	0.010333	0.012546	0.001231	0.012752	0.006992	0.018347	0.019556	0.00149	0.067039	0.001838	0.010563
TRCN0000003372	UBE3A	0.476875	1.17317	0.825023	0.189962	0.157722	0.173842	0.724573	0.473145	0.454216	0.571347	0.308119	0.427105
TRCN0000003715,TRCN0000314658	AR,AR	0.000356	0.044823	0.02259	0.018613	0.024812	0.021713	0.252907	0.163969	0.169344	0.182869	0.381474	0.23359
TRCN0000003717	AR	0.106586	0.120338	0.113462	0.047994	0.083489	0.065742	0.182697	0.092545	0.048975	0.125826	0.151749	0.013939
TRCN0000003718,TRCN0000314657	AR,AR	0.023062	0.310478	0.16677	0.074379	0.02913	0.051754	0.042733	0.054681	0.018473	0.085999	0.108215	0.114018
TRCN0000004078,TRCN0000315113	NCOA1,NCOA1	0.073172	0.019127	0.046149	0.075162	0.022537	0.048849	0.135451	0.169081	0.228896	0.083015	0.192365	0.197617
TRCN0000004079	NCOA1	0.002003	0.002053	0.002028	0.022207	0.005063	0.013635	0.004266	0.192697	0.16778	0.044064	0.041954	0.089697
TRCN0000004080	NCOA1	0.063644	0.058989	0.061316	0.031681	0.047879	0.03978	0.220585	0.176761	0.276194	0.049371	0.034239	0.127631
TRCN0000004081	NCOA1	0.072682	0.092828	0.082755	0.032738	0.008497	0.020618	0.233577	0.118179	0.203496	0.128197	0.151249	0.097284
TRCN0000004082,TRCN0000315043	NCOA1,NCOA1	0.753179	0.835764	0.794472	1.37982	1.202942	1.291381	0.75161	0.567011	0.362636	0.252286	0.178624	0.120008
TRCN0000004115	PIAS4	0.005498	0.004756	0.005127	0.001803	0.001075	0.001439	0.074108	0.069283	0.120928	0.001515	0.003878	0.00127
TRCN0000004116	PIAS4	1.716925	1.256828	1.486877	0.344601	0.051509	0.198055	0.099635	0.060331	0.115342	0.257816	0.041116	0.057535
TRCN0000004117	PIAS4	0.553631	0.365326	0.459479	1.065632	1.780451	1.423041	0.256418	0.421302	0.389525	0.125988	0.070342	0.041818
TRCN0000004118	PIAS4	0.03564	0.038698	0.037169	0.000647	0.006626	0.003636	0.063415	0.071179	0.139661	0.003482	0.006769	7.26E-05
TRCN0000004119	PIAS4	0.018632	0.172278	0.095455	0.238802	0.05718	0.147991	0.070421	0.115342	0.115007	0.059071	0.047885	0.365105
TRCN0000004144	PIAS1	0.03426	0.005269	0.019764	0.002114	0.031493	0.016803	0.133415	0.114865	0.092474	0.027535	0.005688	3.63E-05
TRCN0000004145	PIAS1	6.68E-05	6.84E-05	6.76E-05	4.97E-05	0.000467	0.000258	0.011131	0.029095	0.044394	0.015081	0.00027	0.00294
TRCN0000004146	PIAS1	2.23E-05	0.000137	7.96E-05	0.000659	0.000271	0.000465	0.014204	0.015606	0.044245	0.011592	0.019416	0.004429
TRCN0000004147	PIAS1	0.001581	0.008657	0.005119	0.004439	0.003567	0.004003	0.010271	0.012732	0.009013	0.013882	0.011552	0.001924

Table D1. Abundance of individual shRNAs. See final page for full legend. (1/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000004211,TRCN0000273239	OTUB1,OTUB1	0.014113	0.000308	0.007211	0.003084	0.000979	0.002031	0.06547	0.063205	0.081115	0.019654	0.048858	0.062654
TRCN0000004213,TRCN0000273238	OTUB1,OTUB1	0.001135	0.038219	0.019677	0.040969	0.128113	0.084541	0.710158	0.557997	0.693279	0.120155	0.193271	0.153984
TRCN0000004214,TRCN0000273297	OTUB1,OTUB1	0.111995	0.080271	0.096133	0.14254	0.012156	0.077348	0.221322	0.181017	0.244724	0.039362	0.093811	0.090532
TRCN0000004215	OTUB1	0.182117	0.422262	0.30219	0.084475	0.22032	0.152397	0.211473	0.274565	0.276045	0.104145	0.228712	0.143276
TRCN0000004395	SENP1	0.001536	0.001061	0.001298	0.002126	0.000875	0.001501	0.004547	0.00976	0.005475	0.020658	0.018822	0.002033
TRCN0000004396	SENP1	4.45E-05	3.42E-05	3.94E-05	0.005732	0.001038	0.003385	0.000544	0.001627	0.013556	0.002728	0.000189	3.63E-05
TRCN0000004397	SENP1	0.179869	0.009683	0.094776	0.027628	0.056214	0.041921	0.099407	0.091823	0.06119	0.014421	0.025942	0.001343
TRCN0000004398	SENP1	0.065492	0.057791	0.061642	0.125543	0.05265	0.089097	0.174621	0.251854	0.190982	0.199021	0.166139	0.145127
TRCN0000004399	SENP1	0.098639	0.117806	0.108222	0.067602	0.314215	0.190908	0.135785	0.2158	0.194409	0.164663	0.045629	0.04356
TRCN0000004814,TRCN0000318714	HDAC1,HDAC1	0.274857	0.286834	0.280845	0.929383	0.431109	0.680246	0.983923	1.044339	1.018486	1.022843	0.893336	0.984164
TRCN0000004815	HDAC1	2.23E-05	3.42E-05	2.82E-05	1.24E-05	5.83E-05	3.54E-05	5.27E-05	0.003926	0.000708	6.74E-06	1.35E-05	3.63E-05
TRCN0000004816	HDAC1	0.122747	0.230412	0.176579	0.26776	0.142349	0.205054	0.993895	0.922026	0.561811	6.801336	6.486656	11.82583
TRCN0000004817,TRCN0000349639	HDAC1,HDAC1	0.13114	0.034935	0.083037	0.105811	0.094974	0.100393	0.15206	0.20944	0.205023	0.146848	0.238791	0.360531
TRCN0000004818,TRCN0000318655	HDAC1,HDAC1	2.23E-05	0.000103	6.25E-05	0.002798	0.000129	0.001463	0.027248	0.008035	0.012178	0.009908	0.017403	0.001452
TRCN0000004824	HDAC3	2.23E-05	3.42E-05	2.82E-05	0.004029	7.08E-05	0.00205	0.008849	0.00318	0.002197	0.000168	0.010742	3.63E-05
TRCN0000004825	HDAC3	0.023797	0.000513	0.012155	0.100091	0.087619	0.093855	0.099811	0.104164	0.081153	0.191262	1.218007	0.15874
TRCN0000004826	HDAC3	0.30462	0.506023	0.405321	3.840117	5.007676	4.423896	0.272202	0.579412	0.116049	0.323911	0.202107	0.071438
TRCN0000004827	HDAC3	0.007213	0.049271	0.028242	0.045818	0.040369	0.043094	0.095773	0.169277	0.214967	1.28507	1.486605	1.193941
TRCN0000004828	HDAC3	2.23E-05	3.42E-05	2.82E-05	0.000771	0.00015	0.00046	0.00323	0.010493	0.007039	2.69E-05	0.002824	3.63E-05
TRCN0000004829,TRCN0000314666	HDAC4,HDAC4	0.146745	0.00893	0.077838	0.024159	0.118657	0.071408	0.272869	0.215922	0.174037	0.101983	0.121983	0.099861
TRCN0000004830	HDAC4	0.090024	0.122836	0.10643	0.172841	0.387998	0.28042	0.075986	0.039173	0.00648	0.039598	0.019416	0.007006
TRCN0000004833	HDAC4	0.175105	0.281428	0.228267	0.211324	0.446695	0.329009	0.813867	0.607383	0.770968	0.513341	0.585946	0.530995
TRCN0000004918	PARK7	2.23E-05	3.42E-05	2.82E-05	0.000721	0.000329	0.000525	0.022842	0.018174	0.010167	0.014273	0.017349	3.63E-05
TRCN0000004919	PARK7	0.262146	0.056628	0.159387	0.064307	0.064657	0.064482	0.285054	0.201026	0.145844	0.151933	0.100054	0.090677
TRCN0000004920	PARK7	0.036686	0.063266	0.049976	0.033956	0.054759	0.044358	0.067822	0.072206	0.03985	0.03293	0.228603	0.071692
TRCN0000004921	PARK7	0.045791	0.026346	0.036069	0.052321	0.015473	0.033897	0.059658	0.054448	0.03918	0.060573	0.011363	0.039748
TRCN0000005096	NR2F2	0.004853	0.017963	0.011408	0.00087	0.009789	0.00533	0.068156	0.043551	0.037615	0.05672	0.017025	0.011943
TRCN0000005097	NR2F2	0.014514	0.036953	0.025734	0.02437	0.054192	0.039281	0.086011	0.102317	0.043872	0.06817	0.007567	0.002505
TRCN0000005098	NR2F2	6.68E-05	0.00787	0.003968	0.015841	0.005538	0.010689	0.064697	0.069565	0.021452	0.000465	0.001311	0.000472
TRCN0000005099	NR2F2	0.017608	0.006843	0.012226	0.196453	0.020928	0.108691	0.010025	0.101815	0.114336	0.016495	0.008647	0.091331
TRCN0000005100	NR2F2	0.083034	0.099056	0.091045	0.057083	0.066782	0.061933	0.185225	0.120063	0.138097	0.044077	0.018565	0.01815
TRCN0000005361	TRRAP	0.000223	0.001574	0.000898	0.004252	0.001225	0.002739	0.017241	0.018577	0.010279	4.71E-05	0.000149	3.63E-05
TRCN0000005363	TRRAP	0.072081	0.044755	0.058418	0.012533	0.014498	0.013516	0.264108	0.228825	0.203086	0.119434	0.094419	0.059895
TRCN0000005364	TRRAP	0.000824	0.003524	0.002174	0.000124	0.017111	0.008618	0.010622	0.021036	0.002458	0.000721	0.002783	0.026136
TRCN0000006485	CREBBP	0.111817	0.052009	0.081913	0.073322	0.11226	0.092791	0.188561	0.122509	0.122977	0.270027	0.121294	0.143966
TRCN0000006486	CREBBP	0.005677	0.000376	0.003026	0.005981	0.026296	0.016138	0.098687	0.05879	0.073332	0.146969	0.116741	0.073507
TRCN0000006487	CREBBP	0.652782	0.606174	0.629478	0.134794	0.034518	0.084656	0.126954	0.228128	0.232955	0.257041	0.392797	0.167343
TRCN0000006488	CREBBP	0.108411	0.359372	0.233892	0.076641	0.025658	0.05115	0.193547	0.14681	0.261223	0.328067	0.360761	0.189921
TRCN0000007166,TRCN0000280243	CARM1,CARM1	2.23E-05	0.004517	0.002269	0.002251	0.006926	0.004588	0.050265	0.067938	0.08268	0.00165	0.008256	0.003703
TRCN0000007167,TRCN0000280298	CARM1,CARM1	2.23E-05	3.42E-05	2.82E-05	0.000622	0.000229	0.000425	0.007497	0.01256	0.015717	0.00394	0.000189	0.004066
TRCN0000007168,TRCN0000280244	CARM1,CARM1	0.082299	0.01071	0.046504	0.028884	0.058085	0.043484	0.37721	0.300958	0.252135	0.034944	0.12124	0.222773
TRCN0000007169,TRCN0000280242	CARM1,CARM1	0.192424	0.257134	0.224779	0.143659	0.035343	0.089501	0.369695	0.201491	0.179921	0.050112	0.068761	0.039385
TRCN0000007205	UBE2I	0.011709	0.002772	0.00724	0.007448	0.001425	0.004437	0.066769	0.076096	0.038621	0.001576	0.025632	0.000617
TRCN0000007206	UBE2I	0.104048	0.000411	0.052229	8.7E-05	0.013965	0.007026	0.016556	0.021843	0.015977	0.000647	1.35E-05	3.63E-05
TRCN0000007207	UBE2I	0.130138	0.19907	0.164604	0.012844	0.140928	0.076886	0.056445	0.091139	0.119066	0.034486	0.014809	0.007151
TRCN0000007735	UBB	0.000735	0.000103	0.000419	0.000622	0.001109	0.000865	0.08947	0.060991	0.038658	0.004331	0.002486	0.007986
TRCN0000007737	UBB	2.23E-05	3.42E-05	2.82E-05	0.00046	0.000192	0.000326	0.004143	0.010628	0.015605	6.74E-06	0.000108	3.63E-05
TRCN0000007928	PARP1	1.385169	0.40399	0.89458	0.489366	2.84472	1.667043	0.816167	0.798661	0.767318	1.312322	0.909455	1.07927
TRCN0000007929,TRCN0000338406	PARP1,PARP1	0.070412	0.330939	0.200675	0.541451	0.181272	0.361362	0.269007	0.279164	0.298615	0.163256	0.277218	0.190938
TRCN0000007930	PARP1	1.04255	2.41573	1.72914	1.313672	1.153034	1.233353	0.37742	0.521527	0.601922	0.368265	0.146453	0.178305
TRCN0000007931	PARP1	0.111817	0.052009	0.081913	0.177628	0.102338	0.139983	0.113698	0.123035	0.091804	0.199473	0.114011	0.045811
TRCN0000007932,TRCN0000338467	PARP1,PARP1	0.010485	0.004311	0.007398	0.026509	0.081864	0.054186	0.062081	0.075937	0.088266	0.013518	0.022632	0.001379
TRCN0000007999,TRCN0000315311	CAV1,CAV1	0.441547	0.104736	0.273141	0.420508	0.185623	0.303066	0.230768	0.284349	0.274407	0.482378	0.215295	0.41636
TRCN0000008000,TRCN0000350508	CAV1,CAV1	0.096724	0.122049	0.109387	0.351141	0.407101	0.379121	0.159416	0.178987	0.186848	0.196138	0.205904	0.195693
TRCN0000008001	CAV1	0.008281	0.077602	0.042942	0.020031	0.001788	0.010909	0.070105	0.059597	0.09065	0.030754	0.011539	0.058733
TRCN0000008002,TRCN0000315310	CAV1,CAV1	0.012466	0.004243	0.008354	0.023525	0.008822	0.016173	0.081692	0.039943	0.010018	0.123839	0.078368	0.013721
TRCN0000008597	PPARGC1B	0.010663	0.036269	0.023466	0.004128	0.023996	0.014062	0.127674	0.059805	0.058621	0.002775	0.002621	0.008059
TRCN0000008598	PPARGC1B	0.102801	0.289811	0.196306	0.172754	0.165198	0.168976	0.259877	0.294904	0.203161	0.037699	0.091785	0.281942
TRCN0000008599	PPARGC1B	0.14601	0.039451	0.092731	0.000833	0.000671	0.000752	0.072896	0.039051	0.018919	0.007018	0.000459	0.003557
TRCN0000008600	PPARGC1B	0.001224	0.000103	0.000664	0.005135	0.001021	0.003078	0.025194	0.057432	0.084281	0.001428	0.028064	0.043015
TRCN0000008601	PPARGC1B	0.017074	0.031479	0.024277	0.064867	0.138856	0.101862	0.175551	0.111257	0.132436	0.043875	0.005283	0.030238
TRCN0000009823	BRCA1	0.010173	0.184733	0.097453	0.119675	0.082918	0.101296	0.205819	0.25534	0.250273	0.030761	0.042981	0.065739
TRCN0000009824	BRCA1	0.954686	0.478	0.716343	0.019235	0.059035	0.039135	0.264091	0.201197	0.189604	0.038824	0.033158	0.055285
TRCN0000009825,TRCN0000312567	BRCA2,BRCA2	0.006077	0.000753	0.003415	0.007585	0.032943	0.020264	0.181485	0.058325	0.150685	0.036709	0.019281	0.008785
TRCN0000009882	EP300	0.311855	0.003148	0.157501	0.025228	0.0029	0.014064	0.091436	0.063156	0.05404	0.068756	0.004445	3.63E-05
TRCN0000009883	EP300	0.0638	0.126018	0.094909	0.056884	0.116057	0.086471	0.225553	0.233619	0.23046	0.174349	0.223564	0.282849
TRCN0000009884	EP300	0.014047	0.000513	0.00728	0.018551	0.010181	0.014366	0.116911	0.040298	0.065026	0.178801	0.010012	0.015899
TRCN0000010305	BRCA1	0.052202	0.001163	0.026683	0.00041	0.00035	0.00038	0.012623	0.020547	0.029645	6.74E-06	2.7E-05	0.000181
TRCN0000010306	BRCA2	0.138041	0.288271	0.213156	0.021249	0.001275	0.011262	0.148935	0.071497	0.037951	0.02247	0.127172	0.01256
TRCN0000010315	CCND1	0.00345	0.000103	0.001777	0.000746	0.000517	0.000631	0.012518	0.028239	0.023202	0.007072	0.000284	0.000472
TRCN0000010316	CCND1	0.008838	0.039657	0.024247	0.011153	0.177542	0.094348	0.17355	0.175306	0.141524	0.02154	0.056114	0.005735
TRCN0000010317	CCND1	2.23E-05	0.000137	7.96E-05	2.49E-05	0.0009	0.000463	0.067629	0.059732	0.049198	6.74E-06	1.35E-05	3.63E-05
TRCN0000010327	E2F1	0.078025	0.084753	0.081389	1.531088	2.687235	2.109162	0.144756	0.30119	0.058881	0.161781	0.054317	0.18974
TRCN0000010328	E2F1	0.066739	0.164032	0.115385	0.043978	0.031693	0.037835	0.065435	0.050033	0.037243	0.021884	0.008729	0.040474
TRCN0000010417	RB1	0.307447	0.457744	0.382595	0.818947	0.420645	0.619796	0.171408	0.159517	0.170461	0.108462	0.151844	0.469031
TRCN0000010419,TRCN0000295842	RB1,RB1	0.214396	0.200541	0.207468	0.201016	0.377446	0.289231	0.131659	0.355052	0.227592	0.302991	0.148844	0.346555
TRCN0000010577,TRCN0000318417	PIN1,PIN1	0.253664	0.146069	0.199867	0.161551	0.133547	0.147549	0.320238	0.431172	0.417904	0.148458	0.502944	0.093618
TRCN0000010647	PPARD	0.063577	0.107781	0.085679	0.132369	0.060727	0.096548	0.292024	0.355125	0.2972	0.131181	0.080165	0.058261
TRCN0000010774	ESR1	0.210389	0.230035	0.220212	0.006316	0.002055	0.004185	0.093806	0.067045	0.021973	0.002101	0.01112	3.63E-05
TRCN0000010776	PGR	0.071369	0.011633	0.041501	0.003345	0.011523	0.007434	0.115226	0.128073	0.123051	0.098143	0.009066	0.020546
TRCN0000010853	PIAS1	0.223323	0.197941	0.210632	0.11485	0.437902	0.276376	0.43973	0.350502	0.389748	0.068938	0.053965	0.019493
TRCN0000011027	CREBBP	0.002738	0.007938	0.005338	0.001069	0.001004	0.001037	0.004214	0.003669	0.000633	0.002586	0.00281	0.006026
TRCN0000011071	CARM1	0.019723	0.001403	0.010563	0.020267	0.056038	0.038153	0.087749	0.057591	0.14562	0.03293	0.047156	0.09663

Table D1. Abundance of individual shRNAs. See final page for full legend. (2/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000011077,TRCN0000320445	UBE2I,UBE2I	0.000111	0.001266	0.000689	0.044724	0.004309	0.024517	0.027828	0.036507	0.016461	0.004607	0.001297	0.020546
TRCN0000011078	UBE2I	0.133855	0.083556	0.108706	0.095168	0.187856	0.141512	0.282982	0.204732	0.277535	0.238397	0.461382	0.164765
TRCN0000011102	UBB	0.009038	0.019811	0.014425	0.046912	0.118503	0.082708	0.008234	0.043368	0.008007	0.041706	0.014741	0.01187
TRCN0000011107	UBC	2.23E-05	3.42E-05	2.82E-05	1.24E-05	5.83E-05	3.54E-05	0.003213	0.001602	0.00283	6.74E-06	1.35E-05	3.63E-05
TRCN0000011108	UBC	0.079561	0.018443	0.049002	0.001504	0.012327	0.006916	0.027301	0.036348	0.093257	0.012488	0.020159	0.057681
TRCN0000011109	UBC	2.23E-05	3.42E-05	2.82E-05	3.73E-05	8.33E-05	6.03E-05	0.002967	0.002629	0.00797	0.001253	2.7E-05	3.63E-05
TRCN0000011111	UBC	0.011398	0.002977	0.007187	0.036928	0.085289	0.061109	0.101742	0.138334	0.084691	0.076367	0.041197	0.006352
TRCN0000011218	CAV1	0.057522	0.004038	0.03078	0.012396	0.030763	0.02158	0.204801	0.182485	0.195116	0.197984	0.245385	0.135072
TRCN0000013138	MLL2	0.011932	0.000855	0.006394	0.00056	0.011577	0.006068	0.072369	0.052626	0.078806	0.012851	0.008364	0.016408
TRCN0000013139	MLL2	0.040181	0.00414	0.022161	0.126874	0.045741	0.086307	0.055796	0.084865	0.106552	0.0267	0.295432	0.028677
TRCN0000013140	MLL2	0.015761	0.062445	0.039103	0.00695	0.004751	0.005851	0.115243	0.082969	0.055902	0.102845	0.020551	0.012959
TRCN0000013141	MLL2	0.103024	0.048108	0.075566	0.007846	0.030976	0.019411	0.195127	0.230207	0.218654	0.22494	0.112728	0.031472
TRCN0000013142	MLL2	0.014514	0.029529	0.022021	0.137579	0.072987	0.105283	0.03622	0.039246	0.014748	0.012501	0.005959	3.63E-05
TRCN0000013358,TRCN0000280439	MTA1,MTA1	0.012333	0.017313	0.014823	0.017395	0.009718	0.013557	0.003582	0.087066	0.074337	0.057622	0.072463	0.028967
TRCN0000013359	MTA1	0.001313	0.000719	0.001016	0.006018	0.017411	0.011715	0.00323	0.045117	0.079365	0.019964	0.022105	0.061528
TRCN0000013360	MTA1	6.68E-05	0.005543	0.002805	0.019359	0.000371	0.009865	0.042453	0.021036	0.006257	0.00749	0.000703	3.63E-05
TRCN0000013361	MTA1	0.01211	0.008759	0.010435	0.002611	0.007843	0.005227	0.066909	0.028166	0.020558	0.015377	0.015484	0.004174
TRCN0000013362	MTA1	4.45E-05	3.42E-05	3.94E-05	0.000249	0.000267	0.000258	0.009691	0.013771	0.011881	0.000626	4.05E-05	3.63E-05
TRCN0000013373	MTA2	0.012733	0.015842	0.014288	0.171809	0.333306	0.252557	0.010745	0.232433	0.3588	0.197445	0.18465	0.14059
TRCN0000013374	MTA2	0.000245	0.010128	0.005186	0.033807	0.01499	0.024399	0.231804	0.130923	0.12428	0.082173	0.22028	0.119826
TRCN0000013375	MTA2	0.001759	0.001403	0.001581	0.004688	0.001704	0.003196	0.006707	0.051244	0.04525	0.099679	0.0167	0.127159
TRCN0000013376	MTA2	0.012466	0.016116	0.014291	0.035473	0.249575	0.142524	0.306912	0.160593	0.184986	0.107977	0.141764	0.150173
TRCN0000013377	MTA2	1.101097	0.221002	0.661049	0.000472	0.051054	0.025763	0.068525	0.035418	0.049682	0.028943	0.001243	0.005881
TRCN0000013933,TRCN0000273927	ETV4,ETV4	0.121055	0.067098	0.094077	0.050282	0.043941	0.047111	0.176815	0.189542	0.209157	0.143622	0.183664	0.283575
TRCN0000013934	ETV4	0.007391	0.045987	0.026689	0.039813	0.00308	0.021446	0.078233	0.104506	0.080296	0.041336	0.037238	0.026209
TRCN0000013935	ETV4	0.03869	0.098029	0.068359	0.671694	0.82152	0.746607	0.34487	0.308161	0.239063	0.272014	0.18996	0.603087
TRCN0000013936	ETV4	0.145431	0.089715	0.117573	0.027317	0.003605	0.015461	0.192599	0.184051	0.27139	0.155658	0.122753	0.32336
TRCN0000013937,TRCN0000273925	ETV4,ETV4	0.002048	0.000171	0.00111	0.006503	0.024975	0.015739	0.002458	0.04771	0.019627	0.017068	0.034036	0.015319
TRCN0000014878	FOXA1	0.001736	0.060563	0.031149	0.032601	0.035306	0.033954	0.177465	0.278662	0.360997	0.366002	0.48873	1.256377
TRCN0000014879	FOXA1	0.008993	0.001677	0.005335	0.273878	0.041603	0.15774	0.591105	0.295944	0.267778	0.141527	0.229995	0.162769
TRCN0000014880	FOXA1	0.038467	0.105386	0.071926	0.032116	0.021216	0.026666	0.184382	0.145942	0.374367	0.452129	0.049912	0.233445
TRCN0000014881	FOXA1	0.026602	0.000924	0.013763	0.006117	0.001759	0.003938	0.150498	0.098856	0.211243	0.015121	0.03913	0.068643
TRCN0000014882	FOXA1	0.000111	0.000445	0.000278	0.004949	0.002125	0.003537	0.088715	0.109838	0.154745	0.014791	0.07476	0.021961
TRCN0000014913,TRCN0000329771	FOXA2,FOXA2	0.10082	0.122118	0.111469	0.636109	0.198454	0.417282	0.137506	0.124784	0.10726	0.232301	2.266713	0.22074
TRCN0000014914	FOXA2	0.016273	0.035277	0.025775	0.009437	0.006093	0.007765	0.098073	0.10694	0.053667	0.226388	0.021159	0.330729
TRCN0000014915	FOXA2	0.112574	0.035619	0.074096	0.009039	0.061031	0.035035	0.098775	0.073772	0.093406	0.235359	0.1197	0.007696
TRCN0000014916	FOXA2	0.006723	0.011086	0.008904	0.009773	0.051229	0.030501	0.106079	0.063645	0.091767	0.039591	0.037481	0.181064
TRCN0000014917	FOXA2	0.125752	0.238487	0.18212	0.256856	0.290894	0.273875	0.226572	0.179941	0.200032	0.02286	0.017268	0.032561
TRCN0000015548	SMARCA4	0.620325	1.179808	0.900067	0.570571	0.797604	0.684087	1.04402	0.983739	0.798938	0.753813	1.992454	1.028885
TRCN0000015549	SMARCA4	0.006522	0.025183	0.015853	0.004911	0.038015	0.021463	0.102023	0.02446	0.003873	0.049149	0.061748	0.005554
TRCN0000015550	SMARCA4	0.23492	0.25491	0.244915	0.06427	0.147012	0.105641	0.379229	0.291492	0.447103	0.264059	0.118375	0.478651
TRCN0000015551	SMARCA4	0.337254	0.198933	0.268094	0.159537	0.257084	0.208311	0.495473	0.665084	0.545052	0.426264	0.500687	0.291597
TRCN0000015552	SMARCA4	2.23E-05	0.000855	0.000439	1.24E-05	0.000517	0.000265	7.02E-05	0.010273	0.000596	1.35E-05	1.35E-05	0.00029
TRCN0000017055	RNF4	2.23E-05	3.42E-05	2.82E-05	1.24E-05	0.000167	8.96E-05	0.011535	0.013049	0.013743	6.74E-06	0.000527	3.63E-05
TRCN0000017056,TRCN0000284821	RNF4,RNF4	0.313034	0.29922	0.306127	0.086439	0.051317	0.068878	0.092981	0.064514	0.075156	0.024059	0.065153	0.05514
TRCN0000017057	RNF4	2.23E-05	0.000103	6.25E-05	0.000957	0.000408	0.000683	0.034447	0.021965	0.001415	0.001266	0.007404	3.63E-05
TRCN0000017093,TRCN0000274391	KDM3B,KDM3B	0.025199	0.014097	0.019648	0.16323	0.050654	0.106942	0.032937	0.041362	0.057205	0.003947	0.016282	0.004537
TRCN0000017094	KDM3B	0.166846	0.354377	0.260612	0.154116	0.268436	0.211276	0.220602	0.304639	0.334033	0.096783	0.094933	0.096231
TRCN0000017095,TRCN0000274439	KDM3B,KDM3B	0.183386	0.170568	0.176977	0.52903	0.446374	0.487702	0.184505	0.236946	0.201895	0.203042	0.234913	0.184767
TRCN0000017096	KDM3B	0.008148	0.003764	0.005956	0.003382	0.002721	0.003052	0.196426	0.147372	0.261856	0.027979	0.01493	0.108791
TRCN0000017097	KDM3B	0.188395	0.009649	0.099022	0.081018	0.06907	0.075044	0.111012	0.102696	0.166365	0.039847	0.033887	0.000944
TRCN0000018930	HMGB1	0.616586	1.198421	0.907503	1.821391	1.621191	1.721291	0.862078	1.127467	0.801992	0.541684	0.980553	0.729229
TRCN0000018931	HMGB1	2.23E-05	3.42E-05	2.82E-05	0.000385	1.67E-05	0.000201	0.00014	0.001199	0.000484	6.74E-06	1.35E-05	3.63E-05
TRCN0000018932	HMGB1	0.006879	0.016116	0.011497	0.011588	0.010485	0.011037	0.089294	0.144719	0.108899	0.02154	0.018241	0.026535
TRCN0000018933	HMGB1	0.047416	0.036064	0.04174	0.027852	0.016236	0.022044	0.215441	0.21646	0.286176	0.054005	0.012363	0.060693
TRCN0000018934	HMGB1	0.287501	0.08732	0.18741	0.167532	0.005305	0.086419	0.306385	0.268634	0.334405	0.469048	0.22532	0.212355
TRCN0000019009	HMGB2	0.035061	0.043044	0.039053	0.013951	0.065882	0.039916	0.095615	0.117837	0.106031	0.004142	0.076273	0.001851
TRCN0000019010	HMGB2	0.095077	0.068706	0.081891	0.199797	0.323208	0.261503	0.112259	0.200084	0.359656	0.139735	0.114281	0.085341
TRCN0000019011	HMGB2	0.031766	0.00284	0.017303	0.057531	0.03073	0.04413	0.118193	0.175746	0.408258	0.327488	0.301053	0.57608
TRCN0000019012	HMGB2	0.512493	0.252071	0.382282	0.53986	0.944382	0.742121	0.39747	0.568381	0.598645	0.984174	0.983215	0.636229
TRCN0000019013	HMGB2	0.024665	0.23989	0.132277	0.090803	0.028776	0.05979	0.106834	0.102537	0.099737	0.089468	0.160559	0.093363
TRCN0000019189	HNF4A	0.228821	0.388354	0.308587	0.327529	1.571403	0.949466	0.099706	0.214198	0.020782	0.115649	0.035968	0.125416
TRCN0000019190	HNF4A	0.00049	0.031102	0.015796	0.045644	0.018345	0.031994	0.056639	0.052149	0.023053	0.01238	0.007931	0.006389
TRCN0000019191	HNF4A	0.031833	0.024157	0.027995	0.046129	0.001696	0.023913	0.148198	0.07897	0.147669	0.000303	0.019078	0.014375
TRCN0000019192	HNF4A	2.23E-05	0.000342	0.000182	0.000448	0.000258	0.000353	0.004477	0.015434	0.005996	0.000101	0.013268	0.009692
TRCN0000019193	HNF4A	0.083189	0.066071	0.07463	0.082386	0.309877	0.196131	0.217582	0.196354	0.290459	0.179421	1.425748	0.270507
TRCN0000019194	MED23	0.340282	0.305858	0.32307	2.974233	0.716619	1.845426	0.190159	0.165094	0.074188	0.243301	0.128536	0.160119
TRCN0000019195	MED23	0.160034	0.153528	0.156781	0.101223	0.094878	0.098051	0.186963	0.247879	0.206438	0.158568	0.220456	0.120806
TRCN0000019196	MED23	0.052491	0.081948	0.06722	0.146183	0.068336	0.10726	0.139367	0.190948	0.206252	0.15163	0.221429	0.258238
TRCN0000019197	MED23	4.45E-05	3.42E-05	3.94E-05	0.026782	0.00711	0.016946	0.021051	0.026662	0.00514	0.000775	0.000878	3.63E-05
TRCN0000019198	MED23	0.085972	0.028297	0.057134	0.489279	0.062277	0.275778	0.012957	0.053763	0.033817	0.077593	0.260018	0.076375
TRCN0000019239	HNF4G	2.23E-05	6.84E-05	4.53E-05	0.001604	0.000171	0.000887	0.008357	0.012034	0.00283	0.003233	0.023456	3.63E-05
TRCN0000019240	HNF4G	0.002137	0.000787	0.001462	7.46E-05	3.33E-05	5.4E-05	0.017434	0.000697	0.000298	0.001967	0.001513	0.001089
TRCN0000019241	HNF4G	0.06242	0.056286	0.059353	0.174234	0.065265	0.119749	0.080182	0.059108	0.051097	0.095348	0.06568	0.023123
TRCN0000019242	HNF4G	0.088554	0.527853	0.308204	0.130641	0.04254	0.086591	0.095492	0.057041	0.029236	0.002916	0.00404	0.008349
TRCN0000019243	HNF4G	0.213261	0.037056	0.125158	0.091276	0.309381	0.200328	0.287476	0.277342	0.194744	0.040864	0.10277	0.165927
TRCN0000019319	NR3C1	0.007413	0.001711	0.004562	0.002835	0.034089	0.018462	0.054128	0.050914	0.024655	0.063725	0.044088	0.000799
TRCN0000019320	NR3C1	0.007101	0.002464	0.004782	0.003581	0.014465	0.009023	0.052372	0.056173	0.034487	0.002095	0.006837	3.63E-05
TRCN0000019321	NR3C1	2.23E-05	3.42E-05	2.82E-05	4.97E-05	0.0007	0.000375	0.00014	0.006274	0.003873	3.37E-05	0.001135	3.63E-05
TRCN0000019365	NR3C2	0.020836	0.367619	0.194227	0.117611	0.046941	0.082276	0.037115	0.039002	0.195452	0.030451	0.023997	0.024103
TRCN0000019366	NR3C2	0.004185	0.11784	0.061013	0.024395	0.01241	0.018403	0.219619	0.345023	0.206029	0.179172	0.440777	0.256132
TRCN0000019367	NR3C2	0.004875	0.002943	0.003909	0.000274	0.00035	0.000312	0.05311	0.017599	0.021824	0.009874	0.000378	0.003485
TRCN0000019368	NR3C2	0.525048	0.282454	0.403751	0.509484	0.195158	0.352321	0.347503	0.390176	0.538199	0.0659	0.125456	0.171481

Table D1. Abundance of individual shRNAs. See final page for full legend. (3/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000019425	NR4A1	0.080852	0.097105	0.088979	0.082274	0.084385	0.083329	0.179835	0.142603	0.220814	0.134589	0.161856	0.14382
TRCN0000019426	NR4A1	0.092316	0.110758	0.101537	0.02764	0.138294	0.082967	0.170899	0.153708	0.22033	0.110281	0.093149	0.171699
TRCN0000019427	NR4A1	0.00276	0.04691	0.024835	0.018452	0.014582	0.016517	0.100917	0.071093	0.036163	0.002304	0.024199	0.033432
TRCN0000019428	NR4A1	1.378113	1.461817	1.419965	0.48831	0.640682	0.564496	0.609452	0.497116	0.350978	1.062017	0.547613	3.963045
TRCN0000019479	NR4A2	0.031766	0.345104	0.188435	0.092196	0.01271	0.052453	0.127656	0.050266	0.138432	0.008682	0.073692	0.116087
TRCN0000019480	NR4A2	0.128847	0.368987	0.248917	0.267176	0.453913	0.360544	0.299819	0.304676	0.392393	0.173238	0.245817	0.493425
TRCN0000019483	NR4A2	0.47997	0.350202	0.415086	0.345943	0.724717	0.53533	0.285071	0.151127	0.094933	0.598195	0.166288	0.20691
TRCN0000019504	VDR	0.003784	0.001095	0.00244	0.277919	0.128326	0.203122	0.015011	0.111441	0.092326	0.070204	0.066964	0.033577
TRCN0000019505	VDR	0.07827	0.195511	0.13689	0.153917	0.110881	0.132399	0.325768	0.273795	0.320178	0.426769	0.401026	0.337226
TRCN0000019506,TRCN0000276542	VDR,VDR	0.142626	0.01988	0.081253	0.00179	0.006297	0.004044	0.082781	0.124184	0.101748	0.015344	0.016903	0.02149
TRCN0000019507	VDR	0.937389	0.288956	0.613172	0.016325	0.086344	0.051335	0.054549	0.05698	0.066889	0.049311	0.075962	0.036191
TRCN0000019508	VDR	0.052759	0.012113	0.032436	0.015492	0.041857	0.028675	0.119211	0.030967	0.013333	0.073741	0.024659	0.020328
TRCN0000019559	NR4A3	0.178199	0.021282	0.099741	0.292615	0.277238	0.284927	0.219303	0.14045	0.203459	0.173938	0.102851	0.13754
TRCN0000019560	NR4A3	0.100575	0.123247	0.111911	0.011974	0.018728	0.015351	0.080358	0.091261	0.044729	0.015451	0.37588	0.002868
TRCN0000019561	NR4A3	0.105228	0.095703	0.100465	0.089386	0.049354	0.06937	0.24318	0.164433	0.289043	0.10954	0.052952	0.137831
TRCN0000019562	NR4A3	0.044032	0.118935	0.081484	0.100415	0.109406	0.10491	0.193284	0.324207	0.263271	0.257627	0.418928	0.296353
TRCN0000019563	NR4A3	0.003673	0.000137	0.001905	0.001268	0.000654	0.000961	0.013817	0.037718	0.027113	0.011673	0.000284	0.000472
TRCN0000019599	NR5A1	1.341204	0.084377	0.712791	0.00756	0.02505	0.016305	0.200236	0.186276	0.109383	0.111446	0.058519	0.077319
TRCN0000019600	NR5A1	0.354039	2.511398	1.432719	0.125966	0.565519	0.345743	0.22931	0.288679	0.241931	0.222771	0.106728	0.18012
TRCN0000019601	NR5A1	0.23354	0.499556	0.366548	0.05487	0.024729	0.0398	0.347047	0.244822	0.227406	0.552555	0.131657	0.238527
TRCN0000019602	NR5A1	0.238772	0.203312	0.221042	0.05957	0.116736	0.088153	0.227994	0.155004	0.138134	0.121879	0.066045	0.037171
TRCN0000019603	NR5A1	0.149705	0.036166	0.092936	0.060453	0.054692	0.057573	0.267321	0.38559	0.261148	0.087259	0.260221	0.12803
TRCN0000019639,TRCN0000319399	NCOA2,NCOA2	4.45E-05	0.000376	0.00021	0.004936	0.058851	0.031894	0.058552	0.057738	0.039142	0.005712	0.009728	0.000617
TRCN0000019640	NCOA2	0.007034	0.019811	0.013423	0.075386	0.102892	0.089139	0.158697	0.257113	0.185098	0.072137	0.056492	0.026935
TRCN0000019641	NCOA2	0.339703	0.410491	0.375097	0.428802	0.24029	0.334546	0.441222	0.326409	0.337794	1.077441	0.711969	1.094987
TRCN0000019642,TRCN0000319400	NCOA2,NCOA2	0.378437	0.057723	0.21808	0.017581	0.014019	0.0158	0.142105	0.160385	0.120183	0.006035	0.030023	0.090314
TRCN0000019643	NCOA2	2.23E-05	0.000274	0.000148	0.199785	0.001329	0.100557	0.036887	0.050608	0.031806	0.005739	0.017687	0.007115
TRCN0000019649	MED24	0.162795	0.602718	0.382756	0.385284	0.213531	0.299408	0.236614	0.168641	0.139363	0.192225	0.160626	0.214242
TRCN0000019650	MED24	0.030832	0.342606	0.186719	0.077835	0.276096	0.176966	0.496825	0.472803	0.422038	0.291911	0.226563	0.255116
TRCN0000019651	MED24	0.03869	0.00024	0.019465	0.000796	0.004538	0.002667	0.016503	0.038072	0.047932	0.000283	0.002054	0.116632
TRCN0000019652	MED24	0.148882	0.027407	0.088144	0.126351	0.102313	0.114332	0.284053	0.221364	0.158469	0.290469	0.090244	0.098119
TRCN0000019653	MED24	0.094008	0.019469	0.056739	0.008803	0.006322	0.007562	0.058974	0.044138	0.024022	0.011504	0.002243	0.020219
TRCN0000019654	NR5A2	0.084725	0.08732	0.086023	0.48964	0.326725	0.408183	0.215441	0.220521	0.190312	0.201251	0.190244	0.208253
TRCN0000019655	NR5A2	0.257137	0.205092	0.231114	0.155571	0.260656	0.208113	0.40969	0.462945	0.534103	0.660418	0.560963	0.43491
TRCN0000019656	NR5A2	2.23E-05	3.42E-05	2.82E-05	0.000933	0.000408	0.00067	0.016802	0.025695	0.000968	6.74E-06	5.4E-05	3.63E-05
TRCN0000019657	NR5A2	0.000178	0.052761	0.02647	0.047982	0.002963	0.025472	0.197515	0.062642	0.052252	0.016724	0.034266	0.01158
TRCN0000019658	NR5A2	0.45733	0.217923	0.337627	0.155844	0.074587	0.115216	0.091278	0.071497	0.111655	0.025743	0.063302	0.020582
TRCN0000019699	NCOA3	0.219226	0.084138	0.151682	0.061074	0.24154	0.151307	0.089891	0.098	0.138805	0.040595	0.022943	0.04621
TRCN0000019700	NCOA3	0.283962	0.339116	0.311539	0.208426	0.054434	0.13143	0.259245	0.303233	0.463266	0.107081	0.294162	0.059133
TRCN0000019701	NCOA3	0.034638	0.066106	0.050372	0.011862	0.025163	0.018512	0.196233	0.147018	0.146961	0.029744	0.034711	0.035973
TRCN0000019703	NCOA3	0.005899	0.008622	0.007261	0.008455	0.002046	0.005251	0.162981	0.074836	0.123349	0.003765	0.004959	0.02276
TRCN0000019724	NCOA4	0.029006	0.081298	0.055152	0.06887	0.186369	0.127619	0.163033	0.134323	0.188152	0.094452	0.046548	0.059241
TRCN0000019725	NCOA4	2.23E-05	6.84E-05	4.53E-05	0.001703	0.015219	0.008461	0.000404	0.008439	0.002607	0.002842	0.004013	0.001379
TRCN0000019726	NCOA4	0.003584	0.005919	0.004752	0.021921	0.008718	0.015319	0.08013	0.115134	0.114709	0.042036	0.009472	0.018223
TRCN0000019727	NCOA4	2.23E-05	3.42E-05	2.82E-05	3.73E-05	5.42E-05	4.57E-05	0.001211	0.002617	0.001601	0.000115	0.000216	0.000181
TRCN0000019728	NCOA4	0.075198	0.066003	0.0706	0.015853	0.076542	0.046197	0.103638	0.094795	0.16089	0.042454	0.216308	0.244371
TRCN0000019739	NR6A1	0.000156	0.000103	0.000129	0.097493	0.059222	0.078358	0.000492	0.14467	0.099215	0.01725	0.027348	0.004973
TRCN0000019740	NR6A1	0.470731	2.574185	1.522458	0.297887	0.508706	0.403296	0.199183	0.212962	0.244575	0.98998	0.259829	0.240923
TRCN0000019743	NR6A1	0.028939	0.033498	0.031218	0.002387	0.015107	0.008747	0.013291	0.016498	0.012774	0.000687	6.76E-05	0.002142
TRCN0000019779,TRCN0000285495	NRIP1,NRIP1	4.45E-05	0.00089	0.000467	6.22E-05	0.000392	0.000227	0.033709	0.023873	0.011136	0.013141	0.000338	3.63E-05
TRCN0000019780	NRIP1	0.000178	0.020803	0.010491	0.002673	0.004751	0.003712	0.094474	0.114559	0.08119	0.012616	0.007931	0.003376
TRCN0000019781	NRIP1	0.006322	0.005509	0.005915	0.047882	0.051754	0.049818	0.198551	0.11407	0.136012	0.355764	0.171355	0.084107
TRCN0000019782	NRIP1	0.054027	0.281428	0.167728	0.081901	0.090057	0.085979	0.142825	0.074481	0.070315	0.059609	0.009107	0.0416
TRCN0000019783	NRIP1	0.281914	0.268631	0.275272	0.586014	0.57993	0.582972	0.615088	0.920448	0.787802	2.937308	3.655683	3.895673
TRCN0000019799	MED1	2.23E-05	0.008212	0.004117	0.019111	0.025075	0.022093	0.016539	0.021721	0.02607	0.001057	0.000567	0.000218
TRCN0000019800	MED1	0.001002	3.42E-05	0.000518	1.24E-05	0.005793	0.002903	0.014063	0.004354	0.000335	0.000283	1.35E-05	0.017097
TRCN0000019801	MED1	2.23E-05	3.42E-05	2.82E-05	2.49E-05	0.024804	0.012414	0.008023	0.002605	0.000298	0.001152	4.05E-05	3.63E-05
TRCN0000019802	MED1	4.45E-05	0.000103	7.36E-05	0.002586	0.056038	0.029312	0.037045	0.036641	0.06808	0.003664	0.000216	3.63E-05
TRCN0000019803	MED1	0.01999	0.037535	0.028763	0.006267	0.01289	0.009578	0.040504	0.069785	0.093219	0.082066	0.100864	0.099462
TRCN0000020099,TRCN0000281350	TGFB1I1,TGFB1I1	0.004675	0.001882	0.003278	0.117785	0.137298	0.127541	0.006812	0.168518	0.109644	0.180047	0.032036	0.232537
TRCN0000020100,TRCN0000281352	TGFB1I1,TGFB1I1	0.206137	0.459934	0.333035	0.090468	0.05688	0.073674	0.403492	0.495184	0.397532	0.078779	0.120686	0.090931
TRCN0000020101,TRCN0000281272	TGFB1I1,TGFB1I1	0.056053	0.029015	0.042534	0.006167	0.012806	0.009487	0.064258	0.080156	0.048677	0.000667	0.01012	0.049477
TRCN0000020103	TGFB1I1	0.031344	0.034182	0.032763	0.053403	0.031914	0.042658	0.13726	0.093499	0.085547	0.16306	0.096784	0.097538
TRCN0000020309	THRA	0.090469	0.220557	0.155513	0.164237	0.013352	0.088795	0.089874	0.033841	0.050204	0.02996	0.005715	0.014302
TRCN0000020310	THRA	0.010641	0.032642	0.021641	0.014063	0.00633	0.010196	0.294921	0.132207	0.092921	0.058471	0.052182	0.028895
TRCN0000020311	THRA	0.001469	0.000103	0.000786	0.008654	0.011081	0.009867	0.028337	0.042744	0.051023	0.001313	0.011377	0.036808
TRCN0000020312	THRA	1.440466	0.402143	0.921304	1.835951	0.305167	1.070559	0.336759	0.318459	0.319732	0.213651	0.240007	0.129373
TRCN0000020313	THRA	4.45E-05	0.000821	0.000433	0.002499	0.002784	0.002641	0.04391	0.04212	0.06741	0.001933	0.000189	0.011834
TRCN0000020344	THRB	0.003072	0.000479	0.001776	0.011327	0.04327	0.027298	0.15192	0.122949	0.064393	0.063732	0.014633	0.002069
TRCN0000020345	THRB	1.567754	1.28752	1.427637	0.225349	0.53173	0.378539	0.267725	0.193296	0.390791	0.075115	0.032468	0.08977
TRCN0000020346	THRB	0.187772	0.46445	0.326111	0.800458	0.54482	0.672639	0.432619	0.388378	0.267964	0.457665	0.556693	0.462643
TRCN0000020347	THRB	0.243268	0.037125	0.140196	0.052632	0.06301	0.057821	0.107044	0.08588	0.049422	0.015317	0.012714	0.002577
TRCN0000020348	THRB	0.038423	0.058783	0.048603	0.411768	0.989361	0.700564	0.308703	0.31786	0.354703	0.511462	1.122993	1.290354
TRCN0000020369	RARA	0.000623	0.000616	0.00062	0.000808	0.000133	0.000471	0.00553	0.008341	0.040558	0.012966	0.000284	3.63E-05
TRCN0000020370,TRCN0000275552	RARA,RARA	1.055751	2.691889	1.87382	0.287853	0.875854	0.581854	0.525565	0.418538	0.676669	0.794596	0.94114	1.293621
TRCN0000020371	RARA	0.022818	0.195066	0.108942	0.011029	0.025688	0.018358	0.110152	0.108787	0.11456	0.022093	0.028712	0.050457
TRCN0000020373,TRCN0000275554	RARA,RARA	0.280222	0.26237	0.271296	0.70207	0.248329	0.475199	0.461886	0.341329	0.487139	1.480791	0.67996	0.415416
TRCN0000020784	PIAS3	0.215108	0.038356	0.126732	0.115857	0.063923	0.08989	0.154834	0.203912	0.145136	0.241556	0.397742	0.190502
TRCN0000020785,TRCN0000274277	PIAS3,PIAS3	0.014514	0.016732	0.015623	0.316836	0.50796	0.412398	0.016117	0.375696	0.413882	1.160234	0.458072	0.377156
TRCN0000020786,TRCN0000274276	PIAS3,PIAS3	0.118072	0.031718	0.074895	0.03714	0.037544	0.037342	0.186788	0.164996	0.231205	0.025164	0.186569	0.279219
TRCN0000020787,TRCN0000274336	PIAS3,PIAS3	0.22261	0.058783	0.140697	0.149864	0.098308	0.124086	0.108554	0.122851	0.097986	0.063833	0.034684	0.038732
TRCN0000020788	PIAS3	0.115824	0.073428	0.094626	0.259865	0.148075	0.20397	0.194372	0.26894	0.337273	0.302156	0.33394	0.116813
TRCN0000021149	KDM3A	0.150284	0.07945	0.114867	0.125755	0.262381	0.194068	0.380475	0.363698	0.359656	0.353245	0.150776	0.058697

Table D1. Abundance of individual shRNAs. See final page for full legend. (4/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000021150	KDM3A	0.16905	0.140936	0.154993	0.116865	0.05288	0.084872	0.323608	0.286282	0.467549	0.078011	0.074314	0.120116
TRCN0000021151	KDM3A	0.073239	0.354582	0.21391	0.110324	0.15911	0.134717	0.179186	0.19211	0.181001	0.068015	0.026132	0.049658
TRCN0000021152,TRCN0000329990	KDM3A,KDM3A	0.002182	0.000582	0.001382	0.024333	0.105697	0.065015	0.177114	0.27876	0.360289	0.078455	0.078813	0.049332
TRCN0000021153	KDM3A	0.067384	0.011223	0.039303	0.026546	0.005576	0.016061	0.170021	0.15575	0.123163	0.123024	0.303904	0.04984
TRCN0000021195	RARB	0.000312	0.000103	0.000207	0.013055	0.015523	0.014289	0.006408	0.094392	0.019031	0.108112	0.212092	0.006352
TRCN0000021196	RARB	0.009216	0.007562	0.008389	0.032837	0.001621	0.017229	0.054145	0.0708	0.012774	0.052227	0.098486	0.006498
TRCN0000021197	RARB	0.039113	0.007904	0.023508	0.012135	0.040823	0.026479	0.167861	0.150332	0.20506	0.012737	0.038387	0.094416
TRCN0000021198	RARB	0.071436	0.059468	0.065452	0.019384	0.036089	0.027737	0.183259	0.187426	0.18156	0.267623	0.138873	0.160373
TRCN0000021229	RARG	0.109836	0.171526	0.140681	0.070773	0.013736	0.042254	0.433989	0.290416	0.275301	0.062506	0.089312	0.040111
TRCN0000021231	RARG	0.001937	0.006946	0.004441	0.011364	0.024071	0.017718	0.177588	0.138995	0.094448	0.130797	0.048966	0.109481
TRCN0000021232	RARG	0.233741	0.188942	0.211341	0.03336	0.028484	0.030922	0.306034	0.233668	0.209902	0.041053	0.140481	0.051401
TRCN0000021233	RARG	0.197388	0.004859	0.101124	0.024407	0.036802	0.030605	0.108449	0.065284	0.137613	0.472672	0.054263	0.080913
TRCN0000021604	NR1H4	2.23E-05	3.42E-05	2.82E-05	2.49E-05	0.000104	6.45E-05	0.004688	0.005186	0.003352	0.003711	0.000135	3.63E-05
TRCN0000021605	NR1H4	1.515174	1.554885	1.53503	1.220743	0.940744	1.080743	0.541963	0.637664	0.621586	1.425257	1.406805	0.771083
TRCN0000021606	NR1H4	0.00679	0.006946	0.006868	0.071108	0.009064	0.040086	0.050265	0.042218	0.057727	0.006237	0.020619	0.026898
TRCN0000021607	NR1H4	0.119675	0.09211	0.105893	0.025029	0.145591	0.08531	0.185892	0.131755	0.150909	0.057959	0.071612	0.044939
TRCN0000021608	NR1H4	0.789398	1.017726	0.903562	3.625785	1.389756	2.507771	0.38195	0.612275	0.491832	1.96785	1.26773	1.003076
TRCN0000021614	RXRA	0.022083	0.010025	0.016054	0.03796	0.027455	0.032707	0.032357	0.108371	0.032811	0.203642	0.295662	0.063307
TRCN0000021615	RXRA	0.058524	0.021796	0.04016	0.011912	0.027721	0.019816	0.105517	0.094587	0.19899	0.009975	0.0364	0.056265
TRCN0000021616	RXRA	0.005187	3.42E-05	0.002611	0.000721	0.001263	0.000992	0.019383	0.031431	0.00365	0.00029	0.024024	0.012632
TRCN0000021617	RXRA	2.23E-05	3.42E-05	2.82E-05	7.46E-05	0.0002	0.000137	0.005039	0.009662	0.009311	0.000512	0.001013	3.63E-05
TRCN0000021618	RXRA	0.050087	0.045918	0.048003	0.01211	0.001196	0.006653	0.069859	0.066042	0.061228	0.062836	0.075111	0.098445
TRCN0000021619	NR1I2	8.9E-05	0.045644	0.022867	0.000286	0.001729	0.001008	0.015029	0.016547	0.073108	0.042481	0.000919	0.001198
TRCN0000021620	NR1I2	0.00817	0.012181	0.010175	0.024308	0.032826	0.028567	0.009604	0.06038	0.021415	0.059596	0.021754	0.012705
TRCN0000021621	NR1I2	0.026335	0.047903	0.037119	0.097692	0.034918	0.066305	0.030918	0.06855	0.035269	0.02736	0.024294	0.051727
TRCN0000021622	NR1I2	0.005343	0.031171	0.018257	0.000137	0.002338	0.001237	0.034622	0.014835	0.003836	0.002014	0.000216	0.002977
TRCN0000021623	NR1I2	0.030876	6.84E-05	0.015472	0.003506	0.004622	0.004064	0.018294	0.043074	0.007933	0.004331	0.014633	0.00628
TRCN0000021624	RXRB	0.76894	0.66571	0.717325	0.677526	0.888502	0.783014	1.372931	1.35842	1.245743	0.865218	0.830007	1.219714
TRCN0000021625	RXRB	0.096991	0.166838	0.131915	0.217279	0.298462	0.257871	0.244409	0.232127	0.135081	0.206201	0.139859	0.020764
TRCN0000021627	RXRB	0.018632	0.014987	0.01681	0.080334	0.113777	0.097056	0.114453	0.133663	0.154857	0.007854	0.052155	0.055503
TRCN0000021628	RXRB	0.053515	0.122699	0.088107	0.02631	0.021404	0.023857	0.049914	0.032667	0.018361	0.060997	0.027239	0.020764
TRCN0000021634	NR1I3	0.101443	0.015397	0.05842	0.047136	0.019199	0.033168	0.056428	0.070898	0.022011	0.004459	0.001959	0.009982
TRCN0000021635	NR1I3	0.125085	0.045542	0.085313	0.134856	0.735147	0.435002	0.285686	0.272927	0.235078	0.129538	0.267612	0.17689
TRCN0000021636	NR1I3	0.502988	0.161466	0.332227	0.405837	0.047258	0.226547	0.043172	0.069944	0.05836	0.008426	0.215538	0.005735
TRCN0000021637	NR1I3	0.021259	0.045405	0.033332	0.002362	0.000454	0.001408	0.036448	0.025096	0.03553	0.001758	0.020038	0.001996
TRCN0000021638	NR1I3	0.014091	0.024396	0.019244	0.026434	0.073325	0.049879	0.09946	0.150124	0.095379	0.321924	0.09192	0.055357
TRCN0000021639	RXRG	2.23E-05	3.42E-05	2.82E-05	0.000187	0.000638	0.000412	0.002774	0.005247	0.001452	0.001563	0.003418	0.000181
TRCN0000021640	RXRG	0.010952	0.041641	0.026297	0.004165	0.001767	0.002966	0.072387	0.078872	0.06093	0.007355	0.060708	0.010273
TRCN0000021641	RXRG	0.002382	0.013481	0.007932	0.001306	0.002467	0.001886	0.096475	0.028386	0.064133	0.019331	0.020943	0.086866
TRCN0000021642	RXRG	2.23E-05	3.42E-05	2.82E-05	0.001243	0.000313	0.000778	0.008357	0.018602	0.007933	6.74E-06	9.46E-05	3.63E-05
TRCN0000021644	NR2C1	0.002204	0.040375	0.021289	0.007821	0.011714	0.009768	0.044314	0.101082	0.062755	0.028424	0.03813	0.006244
TRCN0000021645	NR2C1	6.68E-05	0.002772	0.001419	0.005446	0.000308	0.002877	0.002107	0.005516	0.001713	0.000404	0.009485	0.001053
TRCN0000021646	NR2C1	0.023997	0.015226	0.019612	0.024992	0.008968	0.01698	0.195935	0.179623	0.183459	0.128938	0.089325	0.042253
TRCN0000021647	NR2C1	0.038089	0.049853	0.043971	0.062517	0.006993	0.034755	0.188175	0.160239	0.136235	0.068312	0.05987	0.066792
TRCN0000021648	NR2C1	0.233785	0.43215	0.332968	0.291993	1.101138	0.696566	0.307561	0.331717	0.255413	0.166704	0.02601	0.064541
TRCN0000021654	NR2C2	0.142916	0.051324	0.09712	0.142254	0.702621	0.422438	0.27387	0.395802	0.354889	0.335806	0.311052	0.630094
TRCN0000021655	NR2C2	0.007903	0.018614	0.013258	0.00899	0.012048	0.010519	0.048738	0.022809	0.036535	0.005388	0.08792	0.028931
TRCN0000021656	NR2C2	0.076689	0.029289	0.052989	0.215128	0.055184	0.135156	0.104551	0.133296	0.095975	0.055932	0.054371	0.140009
TRCN0000021657	NR2C2	2.23E-05	6.84E-05	4.53E-05	3.73E-05	0.000392	0.000215	0.010587	0.027224	0.031247	0.010467	0.000338	3.63E-05
TRCN0000021658	NR2C2	0.192714	0.101143	0.146928	0.193208	0.209964	0.201586	0.244006	0.281512	0.287144	0.086336	0.049534	0.07064
TRCN0000021669	NR2E1	0.000646	0.000582	0.000614	0.29162	0.055722	0.173671	0.002792	0.147935	0.127371	0.130454	0.162586	0.067082
TRCN0000021670	NR2E1	0.084035	0.17594	0.129987	0.074354	0.084477	0.079415	0.254768	0.229791	0.148041	0.094594	0.107066	0.093146
TRCN0000021671	NR2E1	0.000223	0.005338	0.00278	0.042324	0.020362	0.031343	0.093596	0.072818	0.067559	0.152997	0.236737	0.073725
TRCN0000021672	NR2E1	0.255623	0.296244	0.275933	1.177772	0.550554	0.864163	0.250835	0.286172	0.354107	0.577079	0.318321	0.46326
TRCN0000021673	NR2E1	0.088821	0.378397	0.233609	0.046515	0.025158	0.035836	0.238721	0.1535	0.164875	0.389246	0.175962	0.166689
TRCN0000021686,TRCN0000319299	SAP30,SAP30	0.052803	0.202662	0.127733	0.310221	0.181847	0.246034	0.494209	0.498718	0.374665	0.93842	0.583487	0.553102
TRCN0000021687,TRCN0000319371	SAP30,SAP30	0.112262	0.018545	0.065404	0.209073	0.095995	0.152534	0.210156	0.17571	0.215526	0.344091	0.152911	0.303322
TRCN0000021688,TRCN0000319370	SAP30,SAP30	0.001825	0.00065	0.001238	0.003332	0.000954	0.002143	0.027371	0.058093	0.029199	0.009908	0.000486	3.63E-05
TRCN0000021699	NR2E3	0.117137	0.045131	0.081134	0.03336	0.068266	0.050813	0.32015	0.269123	0.235972	0.108361	0.133941	0.053216
TRCN0000021700	NR2E3	0.25077	0.137754	0.194262	0.131362	0.103392	0.117377	0.220672	0.293779	0.238355	0.021062	0.094473	0.05808
TRCN0000021701	NR2E3	0.061975	0.075002	0.068488	0.251186	0.431301	0.341244	0.298133	0.256465	0.238244	0.240896	1.436396	0.071547
TRCN0000021702	NR2E3	0.047015	0.02029	0.033653	0.023152	0.081789	0.05247	0.189263	0.092631	0.053295	0.028282	0.025929	0.024031
TRCN0000021703	NR2E3	0.001781	0.011189	0.006485	0.075373	0.062448	0.068911	0.001194	0.061212	0.011247	0.02742	0.065032	0.014266
TRCN0000021739	NR2F1	0.019701	0.000103	0.009902	0.000845	0.001175	0.00101	0.067875	0.066617	0.056498	0.011538	0.011607	0.004102
TRCN0000021740,TRCN0000322965	NR2F1,NR2F1	0.099707	0.02727	0.063489	0.184641	0.0739	0.12927	0.136593	0.084106	0.044915	0.041093	0.005945	0.086503
TRCN0000021741,TRCN0000322963	NR2F1,NR2F1	0.096457	0.115993	0.106225	0.029841	0.061989	0.045915	0.139279	0.120466	0.135192	0.264524	0.298769	0.138012
TRCN0000021742,TRCN0000323042	NR2F1,NR2F1	0.041962	0.031582	0.036772	0.04874	0.039027	0.043884	0.167247	0.140218	0.153963	0.122425	0.121983	0.051401
TRCN0000021743	NR2F1	0.186436	0.204407	0.195422	0.168825	0.359056	0.26394	0.489749	0.425485	0.300328	0.209825	0.289257	0.423402
TRCN0000021769	RBM39	0.039291	0.027886	0.033588	0.019533	0.037798	0.028666	0.022631	0.041754	0.022383	0.004419	0.031171	0.000363
TRCN0000021770	RBM39	6.68E-05	0.006912	0.003489	0.001803	0.000304	0.001054	0.027371	0.014334	0.001155	0.060074	0.001608	0.000145
TRCN0000021771	RBM39	0.327816	0.30863	0.318223	0.01446	0.004159	0.00931	0.080885	0.051281	0.13292	0.084019	0.012539	0.016408
TRCN0000021773	RBM39	0.007257	0.014371	0.010814	0.026583	0.015507	0.021045	0.139103	0.112615	0.220777	0.209495	0.20712	0.149556
TRCN0000022149	NR0B1	0.000178	0.012557	0.006368	0.003158	0.003159	0.003159	0.152868	0.10546	0.108005	0.014596	0.006999	0.00098
TRCN0000022150	NR0B1	0.020079	0.001232	0.010656	0.017482	0.012081	0.014781	0.300504	0.19211	0.2229	0.182054	0.195324	0.078009
TRCN0000022151	NR0B1	0.010574	0.085198	0.047886	0.065364	0.291532	0.178448	0.115928	0.165265	0.077168	0.033307	0.03559	0.03895
TRCN0000022152	NR0B1	0.168026	0.424725	0.296376	0.127868	0.147741	0.137805	0.273835	0.16891	0.057466	0.473002	0.548829	0.193188
TRCN0000022153	NR0B1	0.021526	0.12287	0.072198	0.021299	0.022404	0.021851	0.050494	0.06455	0.038398	0.0424	0.001797	0.011144
TRCN0000022154	RORA	0.08379	0.077157	0.080474	0.431102	0.054021	0.242562	0.082974	0.091481	0.080259	0.051439	0.034333	0.043088
TRCN0000022155	RORA	0.198012	0.138507	0.168259	0.15659	0.29297	0.22478	0.248518	0.360103	0.333437	0.391994	0.538615	0.459013
TRCN0000022156	RORA	0.201663	0.141518	0.17159	0.257801	0.041044	0.149423	0.240529	0.171197	0.196383	0.025204	0.066058	0.043996
TRCN0000022157	RORA	0.004118	0.000171	0.002145	0.106955	0.023479	0.065217	0.060325	0.054314	0.122045	0.013323	0.011404	3.63E-05
TRCN0000022158	RORA	0.01142	0.034045	0.022732	0.011588	0.023716	0.017652	0.143282	0.177899	0.183273	0.058175	0.245534	0.184839
TRCN0000022169	RORB	0.036219	0.007767	0.021993	0.045047	0.011127	0.028087	0.419065	0.404559	0.437866	0.29575	0.366355	0.550198

Table D1. Abundance of individual shRNAs. See final page for full legend. (5/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000022170	RORB	0.008838	0.005201	0.007019	0.006093	0.021245	0.013669	0.136189	0.078175	0.0562	0.067301	0.056776	0.158123
TRCN0000022171	RORB	0.519617	0.308596	0.414106	0.117586	0.171858	0.144722	0.257981	0.198054	0.335076	0.517814	0.400607	0.355485
TRCN0000022172	RORB	0.200661	0.083043	0.141852	0.028075	0.017445	0.02276	0.10564	0.114926	0.089718	0.06029	0.009701	0.00991
TRCN0000022173	RORB	0.046726	0.082085	0.064405	0.207009	0.156501	0.181755	0.33323	0.323706	0.436898	0.539758	0.554923	0.383872
TRCN0000022174	NR1D1	0.000156	0.019366	0.009761	0.008219	0.000104	0.004161	0.036852	0.007338	0.068192	4.04E-05	0.00431	0.028713
TRCN0000022175	NR1D1	2.23E-05	6.84E-05	4.53E-05	0.000137	0.000179	0.000158	0.026511	0.015899	0.005884	0.000337	0.007634	3.63E-05
TRCN0000022176	NR1D1	0.04519	0.122665	0.083927	0.529801	0.161427	0.345614	0.297835	0.361864	0.32908	0.409762	0.331103	0.514007
TRCN0000022177	NR1D1	0.014002	0.003045	0.008524	0.126165	0.018574	0.072369	0.050599	0.049703	0.032513	0.001152	0.023402	0.003521
TRCN0000022178	NR1D1	0.854801	0.361357	0.608079	0.266517	0.100346	0.183431	0.482147	0.476545	0.472614	0.600438	0.773893	0.648789
TRCN0000022179,TRCN0000330189	ESRRA,ESRRA	0.205469	0.117704	0.161586	0.068858	0.113615	0.091236	0.336249	0.327889	0.312767	0.42914	0.201459	0.266696
TRCN0000022180	ESRRA	0.058146	0.126839	0.092493	0.042983	0.024779	0.033881	0.108853	0.078199	0.137054	0.001361	0.017025	0.026717
TRCN0000022181,TRCN0000330191	ESRRA,ESRRA	0.059593	0.36471	0.212151	0.244223	0.020512	0.132367	0.213281	0.162526	0.198729	0.006251	0.030807	0.09968
TRCN0000022182	ESRRA	0.118451	0.139157	0.128804	0.079103	0.118961	0.099032	0.284299	0.311451	0.237909	0.491936	0.153871	0.163313
TRCN0000022183,TRCN0000353645	ESRRA,ESRRA	4.45E-05	0.000103	7.36E-05	1.24E-05	0.001096	0.000554	0.028565	0.001113	0.031172	3.37E-05	1.35E-05	3.63E-05
TRCN0000022189	NR1D2	0.231136	1.03367	0.632403	2.925965	0.236143	1.581054	0.395767	0.498254	0.342748	0.354396	0.317037	0.26194
TRCN0000022190	NR1D2	0.01654	0.003182	0.009861	0.007087	0.002588	0.004838	0.088943	0.034562	0.102679	0.091495	0.120483	0.006461
TRCN0000022191	NR1D2	6.68E-05	0.000411	0.000239	0.003407	0.000388	0.001897	0.044928	0.024008	0.025884	0.003361	0.003189	0.005118
TRCN0000022192	NR1D2	0.244315	0.014679	0.129497	0.019869	0.058272	0.039071	0.03845	0.03773	0.034971	0.044973	0.026307	0.019856
TRCN0000022193	NR1D2	0.110749	0.959695	0.535222	0.082572	0.620662	0.351617	0.270446	0.319205	0.257349	0.215678	0.181691	0.113328
TRCN0000022204	ESRRB	0.003629	0.000103	0.001866	0.015629	0.007793	0.011711	0.056674	0.080425	0.07322	0.011208	0.03363	0.006534
TRCN0000022205	ESRRB	0.182607	0.184665	0.183636	0.119513	0.168607	0.14406	0.290724	0.292788	0.32677	0.733741	0.736384	0.480611
TRCN0000022206	ESRRB	0.275881	0.397729	0.336805	0.564677	0.258243	0.41146	0.269182	0.261442	0.153628	0.14212	0.147263	0.222337
TRCN0000022207	ESRRB	4.45E-05	3.42E-05	3.94E-05	0.08246	0.003434	0.042947	0.019646	0.02753	0.048379	0.0026	0.002743	0.006135
TRCN0000022214,TRCN0000275310	NR1H2,NR1H2	0.013535	0.000513	0.007024	0.06851	0.030668	0.049589	0.137014	0.13617	0.262377	0.21223	0.362409	0.132132
TRCN0000022215,TRCN0000275326	NR1H2,NR1H2	0.004986	0.000342	0.002664	0.025265	0.230418	0.127841	0.036097	0.061101	0.029496	0.086127	0.236575	0.029693
TRCN0000022216	NR1H2	0.009795	0.002532	0.006163	0.195682	0.088386	0.142034	0.006022	0.277146	0.324834	0.380907	0.245074	0.127413
TRCN0000022217,TRCN0000282024	NR1H2,NR1H2	0.060172	0.026244	0.043208	0.06943	0.051538	0.060484	0.158521	0.124172	0.145918	0.084012	0.135914	0.072672
TRCN0000022218	NR1H2	1.471965	0.980601	1.226283	0.467956	0.488356	0.478156	0.359442	0.219811	0.31489	0.347977	0.225036	0.398283
TRCN0000022234	NR1H3	0.219939	0.120749	0.170344	0.476124	0.349683	0.412904	0.442486	0.419663	0.483042	0.114699	0.092393	0.079424
TRCN0000022235	NR1H3	0.064446	0.09933	0.081888	0.028896	0.013511	0.021203	0.046315	0.052271	0.058695	0.008554	0.060167	0.019094
TRCN0000022236	NR1H3	0.505793	0.778144	0.641968	0.126501	0.119428	0.122964	0.167019	0.223823	0.262377	0.142719	0.17807	0.277477
TRCN0000022237	NR1H3	0.122836	0.177445	0.150141	0.180401	0.704026	0.442213	0.044717	0.066287	0.004357	0.065234	0.121064	0.137649
TRCN0000022238	NR1H3	0.073884	0.049819	0.061852	0.012197	0.020403	0.0163	0.078286	0.076829	0.077987	0.040514	0.057762	0.062654
TRCN0000026415,TRCN0000276460	ALDH1A1,ALDH1A1	0.047082	0.081332	0.064207	0.112227	0.030943	0.071585	0.125619	0.163602	0.170238	0.402528	0.391716	0.33062
TRCN0000026417	ALDH1A1	4.45E-05	3.42E-05	3.94E-05	4.97E-05	0.000183	0.000117	0.000211	0.001847	0.00175	0.001388	8.11E-05	0.00029
TRCN0000026482,TRCN0000276459	ALDH1A1,ALDH1A1	0.002226	0.021693	0.01196	0.052421	0.007847	0.030134	0.064978	0.083593	0.058621	0.018772	0.038116	0.00922
TRCN0000026498,TRCN0000276461	ALDH1A1,ALDH1A1	0.22989	0.398481	0.314185	0.138947	0.111835	0.125391	0.165895	0.301349	0.556299	0.258152	0.409146	0.349568
TRCN0000026502	ALDH1A1	0.042318	0.156984	0.099651	0.134632	0.103846	0.119239	0.196128	0.181996	0.299732	0.062829	0.122294	0.073689
TRCN0000027144	ALDH1A3	0.000824	0.000308	0.000566	0.00092	0.000229	0.000575	0.021068	0.011411	0.054561	0.086807	0.027956	0.043923
TRCN0000027160	ALDH1A3	0.000312	3.42E-05	0.000173	0.000112	0.000117	0.000114	0.019471	0.008769	0.001192	6.74E-06	8.11E-05	3.63E-05
TRCN0000027171	ALDH1A3	2.23E-05	6.84E-05	4.53E-05	0.000535	0.000471	0.000503	0.01782	0.025487	0.062419	6.74E-06	0.000689	3.63E-05
TRCN0000027183	ALDH1A3	2.23E-05	0.000137	7.96E-05	0.00087	0.000433	0.000652	0.029004	0.030233	0.027783	0.002661	0.000162	7.26E-05
TRCN0000027212	ALDH1A3	4.253613	4.307234	4.280423	1.52982	1.329155	1.429487	0.248834	0.339434	0.180368	0.164192	0.162315	0.116958
TRCN0000029204,TRCN0000342682	PHB,PHB	0.005944	3.42E-05	0.002989	0.000435	0.000833	0.000634	0.019997	0.044346	0.00838	0.0007	4.05E-05	3.63E-05
TRCN0000029205	PHB	0.008504	0.014302	0.011403	0.020615	0.014419	0.017517	0.144388	0.111502	0.050502	0.044596	0.015984	0.0571
TRCN0000029206,TRCN0000342746	PHB,PHB	0.000134	6.84E-05	0.000101	3.73E-05	0.001259	0.000648	0.002019	0.003804	0.001192	5.39E-05	0.000162	3.63E-05
TRCN0000029207,TRCN0000342747	PHB,PHB	0.001581	6.84E-05	0.000824	0.003009	0.001088	0.002048	0.013817	0.015361	0.00149	4.04E-05	0.000162	0.002359
TRCN0000029208,TRCN0000342748	PHB,PHB	2.23E-05	3.42E-05	2.82E-05	1.24E-05	0.000158	8.54E-05	3.51E-05	0.007436	0.00041	6.74E-06	1.35E-05	3.63E-05
TRCN0000033644	ESRRG	0.423672	0.366729	0.3952	0.494191	0.23263	0.363411	0.255576	0.525258	0.40904	0.44699	0.493905	0.397811
TRCN0000033645	ESRRG	0.003473	0.000274	0.001873	0.002002	0.013569	0.007785	0.026002	0.019165	0.01013	0.002216	0.000324	0.016843
TRCN0000033646	ESRRG	0.016718	0.039862	0.02829	0.579847	0.744849	0.662348	0.014748	0.273024	0.1486	0.564834	0.405417	0.175002
TRCN0000033647	ESRRG	0.026513	0.062992	0.044752	0.026969	0.008364	0.017666	0.154711	0.142554	0.160033	0.114389	0.125699	0.352618
TRCN0000033648	ESRRG	0.001113	0.003866	0.00249	0.059856	0.007764	0.03381	0.025932	0.05166	0.02797	0.027528	0.069044	0.025737
TRCN0000033649	NR0B2	0.014314	0.001848	0.008081	0.003656	0.000113	0.001884	0.014186	0.007191	0.019962	0.003213	0.000784	3.63E-05
TRCN0000033650	NR0B2	0.00561	0.006843	0.006227	0.130927	0.002471	0.066699	0.049668	0.03987	0.039478	0.029017	0.06999	0.005989
TRCN0000033651	NR0B2	0.201618	0.072744	0.137181	0.021038	0.036119	0.028578	0.160961	0.138053	0.164167	0.051338	0.075044	0.0779
TRCN0000033653	NR0B2	0.115379	0.205365	0.160372	0.298596	0.628046	0.463321	0.493313	0.680665	0.747431	0.373599	0.137251	0.120951
TRCN0000033654	RORC	0.020591	0.056457	0.038524	0.038172	0.027259	0.032715	0.013536	0.017208	0.018994	0.003327	0.016011	0.03924
TRCN0000033655	RORC	0.045724	0.137652	0.091688	0.041168	0.014023	0.027596	0.160558	0.204903	0.14886	0.214924	0.123294	0.464857
TRCN0000033656	RORC	2.23E-05	0.000205	0.000114	0.017009	0.024275	0.020642	0.031989	0.038195	0.095901	0.001138	0.005026	0.004247
TRCN0000033657	RORC	0.113509	0.248649	0.181079	0.196092	0.183743	0.189918	0.065312	0.063633	0.036982	0.05577	0.036252	0.048097
TRCN0000033658	RORC	2.23E-05	3.42E-05	2.82E-05	0.000174	0.00225	0.001212	0.008094	0.023311	0.021303	4.04E-05	6.76E-05	0.00432
TRCN0000033659	NR2F6	0.046258	0.025491	0.035875	0.042063	0.020149	0.031106	0.110292	0.040127	0.084616	0.000896	0.001527	0.007187
TRCN0000033660,TRCN0000292069	NR2F6,NR2F6	2.23E-05	3.42E-05	2.82E-05	0.004638	0.00608	0.005359	0.000193	0.007619	0.006964	0.00163	0.005986	0.000181
TRCN0000033661,TRCN0000292068	NR2F6,NR2F6	0.002337	0.014165	0.008251	0.01175	0.034343	0.023047	0.186753	0.160336	0.141114	0.046098	0.024334	0.001416
TRCN0000033662,TRCN0000292067	NR2F6,NR2F6	0.000289	0.000445	0.000367	0.000236	0.000496	0.000366	0.003705	0.000709	0.000298	1.35E-05	8.11E-05	0.000762
TRCN0000033663	NR2F6	0.010529	0.044892	0.027711	0.039601	0.012948	0.026275	0.024141	0.035956	0.021117	0.04238	0.044953	0.041019
TRCN0000035929,TRCN0000290478	PRMT1,PRMT1	0.001914	0.000719	0.001316	0.018166	0.030072	0.024119	0.0148	0.072255	0.01594	0.001542	0.005067	0.004719
TRCN0000035930	PRMT1	0.82831	0.163895	0.496103	0.195495	0.362502	0.278999	0.739391	0.680396	0.764078	0.812324	1.046936	1.014474
TRCN0000035931,TRCN0000290479	PRMT1,PRMT1	0.000223	0.012968	0.006595	0.00046	0.000925	0.000693	0.031918	0.026001	0.003724	6.74E-06	0.002446	0.037607
TRCN0000035932	PRMT1	0.000868	0.000376	0.000622	0.031669	0.095183	0.063426	0.001053	0.08791	0.043723	0.024282	0.010728	0.001924
TRCN0000035933	PRMT1	0.087464	0.097482	0.092473	0.009661	0.006776	0.008219	0.068683	0.089622	0.117092	0.214493	0.191365	0.012487
TRCN0000039658,TRCN0000332899	E2F1,E2F1	0.002404	0.009512	0.005958	0.022082	0.014498	0.01829	0.012079	0.12323	0.080482	0.07405	0.029226	0.016153
TRCN0000039659,TRCN0000332897	E2F1,E2F1	0.001558	6.84E-05	0.000813	7.46E-05	0.000567	0.000321	0.034938	0.026478	0.040818	0.03165	0.00073	0.00461
TRCN0000039660,TRCN0000332963	E2F1,E2F1	2.23E-05	0.00284	0.001431	0.000647	7.92E-05	0.000363	0.001598	0.004464	0.000596	6.74E-06	0.000878	0.00127
TRCN0000039661,TRCN0000332898	E2F1,E2F1	0.016607	0.029836	0.023222	0.001641	0.01529	0.008466	0.108818	0.030172	0.039887	0.000828	0.011066	0.013104
TRCN0000039662	E2F1	0.032345	0.048484	0.040415	0.017034	0.000679	0.008857	0.059799	0.046927	0.0435	0.022503	0.025402	0.071293
TRCN0000039833	BRCA1	0.000156	0.094881	0.047519	0.017693	0.056172	0.036933	0.081692	0.074946	0.119774	0.002836	0.003472	0.040874
TRCN0000039834	BRCA1	0.001291	0.000103	0.000697	0.001455	0.002605	0.00203	0.074985	0.050963	0.025288	0.000108	0.000554	3.63E-05
TRCN0000039835	BRCA1	0.008237	0.015534	0.011885	0.006068	0.066865	0.036466	0.140332	0.114608	0.080222	0.003172	0.006769	0.002142
TRCN0000039836	BRCA1	0.059437	0.299357	0.179397	0.034964	0.048396	0.04168	0.086415	0.064648	0.114373	0.00943	0.024983	0.001343
TRCN0000039837	BRCA1	2.23E-05	0.002464	0.001243	3.73E-05	0.000167	0.000102	0.013536	0.010628	0.032104	6.74E-06	1.35E-05	3.63E-05
TRCN0000039884	EP300	0.000111	3.42E-05	7.28E-05	0.005732	0.004892	0.005312	0.000579	0.013967	0.010875	0.027744	0.001216	0.016952

Table D1. Abundance of individual shRNAs. See final page for full legend. (6/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000039885	EP300	0.007235	3.42E-05	0.003635	0.083231	0.011114	0.047173	0.014818	0.015092	0.01162	0.027481	0.029145	0.028205
TRCN0000039886	EP300	0.182162	0.222302	0.202232	0.155136	0.063369	0.109252	0.478706	0.237643	0.170126	0.607497	0.326901	0.211411
TRCN0000039887	EP300	0.012043	0.010915	0.011479	0.03045	0.030222	0.030336	0.090716	0.107527	0.064207	0.02874	0.006134	0.032888
TRCN0000040038	CCND1	2.23E-05	0.000376	0.000199	0.002101	0.000171	0.001136	0.017996	0.013539	0.007002	6.74E-05	0.004567	3.63E-05
TRCN0000040039	CCND1	0.003228	0.001916	0.002572	0.011688	0.006197	0.008942	0.169898	0.186986	0.265655	0.007106	0.047291	0.040837
TRCN0000040040	CCND1	0.156562	0.075276	0.115919	0.163566	0.114107	0.138836	0.198358	0.235882	0.251726	0.11253	0.18892	0.181028
TRCN0000040041	CCND1	0.009528	0.000342	0.004935	0.041777	0.000917	0.021347	0.032656	0.027493	0.017765	0.003004	0.009918	0.030347
TRCN0000040042,TRCN0000288598	CCND1,CCND1	0.002716	3.42E-05	0.001375	1.24E-05	0.000238	0.000125	0.017013	0.015924	0.015046	6.74E-06	1.35E-05	3.63E-05
TRCN0000040163,TRCN0000288710	RB1,RB1	0.138931	0.162424	0.150678	0.531479	0.206797	0.369138	0.399858	0.488726	0.5744	0.938339	1.482849	0.905538
TRCN0000040164	RB1	0.15349	0.255561	0.204525	0.118618	0.050588	0.084603	0.435007	0.152937	0.083797	0.529648	0.266274	0.26655
TRCN0000040165	RB1	0.008437	0.010847	0.009642	0.164846	0.291211	0.228029	0.006777	0.2107	0.135676	0.293009	0.218767	0.105996
TRCN0000040166	RB1	0.110793	0.287758	0.199276	0.087782	0.063236	0.075509	0.08861	0.053054	0.063574	0.050005	0.01285	0.020364
TRCN0000040167	RB1	0.30275	0.121433	0.212091	0.134682	0.564586	0.349634	0.167791	0.203827	0.19899	0.156069	0.083583	0.263501
TRCN0000040193,TRCN0000363564	BRCA2,BRCA2	0.084948	0.12092	0.102934	0.247879	0.168957	0.208418	0.264933	0.304358	0.239771	0.403236	0.190055	0.448413
TRCN0000040194	BRCA2	0.057856	0.08773	0.072793	0.05947	0.269541	0.164506	0.215792	0.264243	0.193589	0.183058	0.433251	0.055938
TRCN0000040197	BRCA2	0.005565	0.002156	0.00386	0.120122	0.003596	0.061859	0.204906	0.160483	0.122083	0.02286	0.034549	0.064432
TRCN0000045299	CCNE1	0.328595	0.079382	0.203988	0.058513	0.109089	0.083801	0.334511	0.378252	0.368781	0.050146	0.098824	0.088753
TRCN0000045300	CCNE1	0.03751	0.051632	0.044571	0.135901	0.244466	0.190183	0.22285	0.19436	0.136496	0.201224	0.062221	0.494587
TRCN0000045301	CCNE1	0.076066	0.100493	0.088279	0.157063	0.058189	0.107626	0.186103	0.222967	0.251465	0.121206	0.095933	0.093255
TRCN0000045302	CCNE1	0.053226	0.034285	0.043755	0.030102	0.072445	0.051274	0.160189	0.143606	0.091432	0.036486	0.058033	0.000218
TRCN0000045513,TRCN0000310619	PUS1,PUS1	0.150685	0.101896	0.12629	0.164821	0.146074	0.155448	0.20071	0.117727	0.166216	0.937113	0.041913	0.139973
TRCN0000045514	PUS1	0.000356	0.000342	0.000349	0.256545	0.50105	0.378798	0.000474	0.284068	0.082233	0.195404	0.241156	0.041382
TRCN0000045515,TRCN0000300401	PUS1,PUS1	2.23E-05	0.004174	0.002098	0.001442	0.028592	0.015017	0.044015	0.05698	0.078285	0.027723	0.006864	0.006933
TRCN0000045516,TRCN0000300402	PUS1,PUS1	0.01999	0.004209	0.012099	0.02917	0.023525	0.026347	0.01775	0.025011	0.017765	0.002351	0.003513	0.001162
TRCN0000045517,TRCN0000300403	PUS1,PUS1	0.024866	0.100322	0.062594	0.00368	0.009797	0.006739	0.163999	0.139655	0.136794	0.007665	0.005364	0.093291
TRCN0000046068,TRCN0000327856	KDM1A,KDM1A	0.007235	0.045302	0.026269	0.121875	0.037727	0.079801	0.120159	0.149586	0.092959	0.003987	0.037116	0.008458
TRCN0000046069,TRCN0000327857	KDM1A,KDM1A	0.109324	0.533498	0.321411	0.18004	0.077138	0.128589	0.688634	0.463398	0.447699	0.079499	0.176057	0.059604
TRCN0000046070	KDM1A	0.182629	0.287074	0.234852	0.093837	0.090544	0.092191	0.394837	0.300163	0.381816	0.329219	0.650667	0.42431
TRCN0000046071,TRCN0000327930	KDM1A,KDM1A	0.021949	0.000205	0.011077	0.000398	0.028492	0.014445	0.030812	0.038794	0.01527	0.002351	0.00027	0.000653
TRCN0000046072,TRCN0000327932	KDM1A,KDM1A	0.082076	0.088278	0.085177	0.261904	0.021441	0.141672	0.096422	0.224838	0.208077	0.017445	0.039413	0.03198
TRCN0000058069,TRCN0000290094	PSME3,PSME3	0.10899	0.487101	0.298046	0.131959	0.107222	0.119591	0.432742	0.204365	0.098284	0.041147	0.029023	0.027189
TRCN0000058070,TRCN0000307160	PSME3,PSME3	2.23E-05	3.42E-05	2.82E-05	0.006801	0.051063	0.028932	0.002932	0.014884	0.01013	0.00258	0.00023	0.000581
TRCN0000058071	PSME3	0.012577	0.129508	0.071043	0.110996	0.260202	0.185599	0.210647	0.257504	0.157501	0.162225	0.204701	0.039022
TRCN0000060653,TRCN0000299678	NCOR1,NCOR1	0.002426	3.42E-05	0.00123	0.00102	0.000296	0.000658	0.005934	0.017672	0.035791	0.000121	0.01285	0.014447
TRCN0000060654	NCOR1	0.091693	0.07791	0.084802	0.019695	0.023308	0.021502	0.22141	0.233631	0.313326	0.158547	0.157086	0.109408
TRCN0000060655	NCOR1	0.417951	0.110176	0.264063	0.176534	0.552855	0.364694	0.524091	0.548042	0.596298	0.706536	0.367963	2.114144
TRCN0000060656,TRCN0000310464	NCOR1,NCOR1	0.09196	0.026415	0.059188	0.038694	0.019991	0.029342	0.435973	0.366181	0.348818	0.206222	0.049304	0.034775
TRCN0000060657,TRCN0000299677	NCOR1,NCOR1	0.339302	0.429995	0.384648	0.033969	0.046349	0.040159	0.057867	0.045753	0.132287	0.010986	0.001608	0.034086
TRCN0000060703,TRCN0000298963	NCOR2,NCOR2	0.000913	0.000513	0.000713	0.004414	0.00055	0.002482	0.022122	0.033987	0.013743	0.005328	0.014903	0.021344
TRCN0000060704	NCOR2	0.767026	1.297443	1.032234	0.35635	0.357285	0.356817	0.991999	0.585014	0.53332	0.369268	0.43244	0.353707
TRCN0000060705,TRCN0000298965	NCOR2,NCOR2	4.45E-05	3.42E-05	3.94E-05	0.000112	0.000108	0.00011	0.020822	0.005968	3.72E-05	0.001475	0.004053	7.26E-05
TRCN0000060706,TRCN0000298964	NCOR2,NCOR2	0.011798	0.098851	0.055324	0.000821	0.000521	0.000671	0.075196	0.028851	0.035865	0.109479	0.009161	0.005626
TRCN0000060707,TRCN0000298889	NCOR2,NCOR2	0.006233	0.008246	0.00724	0.036083	0.007601	0.021842	0.27552	0.230549	0.316268	0.070393	0.18134	0.036808
TRCN0000060918,TRCN0000299608	PHB2,PHB2	0.050399	0.018614	0.034506	0.183497	0.016324	0.09991	0.065364	0.033718	0.072065	0.001354	0.019214	0.001379
TRCN0000060919,TRCN0000299607	PHB2,PHB2	2.23E-05	3.42E-05	2.82E-05	1.24E-05	8.33E-06	1.04E-05	0.004986	0.000844	0.009907	0.002445	6.76E-05	3.63E-05
TRCN0000060920	PHB2	2.23E-05	0.000103	6.25E-05	0.000137	2.92E-05	8.3E-05	0.006672	0.001211	0.000894	0.034062	0.000743	0.000907
TRCN0000060922,TRCN0000299609	PHB2,PHB2	0.30275	0.1124	0.207575	0.009673	0.005097	0.007385	0.085976	0.033816	0.085398	0.042683	0.018916	0.066538
TRCN0000063263,TRCN0000299538	NCOA6,NCOA6	0.359693	0.182577	0.271135	0.161999	0.800946	0.481472	0.126216	0.163259	0.051246	0.131127	0.06391	0.051945
TRCN0000063264	NCOA6	0.050421	0.86738	0.458901	0.039291	0.213894	0.126592	0.37505	0.261369	0.323381	0.132744	0.235535	0.067881
TRCN0000063265	NCOA6	0.000223	0.000137	0.00018	0.001853	0.006343	0.004098	0.00014	0.003168	0.00149	0.001266	0.00104	0.00029
TRCN0000063266	NCOA6	0.038333	0.070999	0.054666	0.002412	0.006989	0.0047	0.059957	0.053874	0.046666	0.035388	0.022375	0.004537
TRCN0000063267	NCOA6	0.077134	0.052214	0.064674	0.056909	0.071491	0.0642	0.201746	0.21624	0.23303	0.107587	0.121659	0.142078
TRCN0000063818	SNAI1	0.01467	0.029836	0.022253	0.135378	0.013661	0.074519	0.071755	0.057714	0.15359	0.006473	0.097824	0.000109
TRCN0000063819	SNAI1	0.065336	0.045542	0.055439	1.14578	1.547466	1.346623	0.014853	0.516623	0.206624	0.327899	0.221848	0.084579
TRCN0000063821	SNAI1	6.68E-05	3.42E-05	5.05E-05	0.000249	0.021895	0.011072	0.026054	0.008096	0.009162	0.030701	0.000689	0.005881
TRCN0000063822	SNAI1	4.45E-05	0.001779	0.000912	0.001592	0.000233	0.000912	0.009639	0.015899	0.009199	0.00421	0.008796	0.020328
TRCN0000072693	RBM14	4.45E-05	0.00065	0.000347	0.002089	0.046754	0.024421	0.056726	0.035932	0.030912	0.002243	0.000162	0.013177
TRCN0000072694	RBM14	0.037732	0.018408	0.02807	0.360143	0.052963	0.206553	0.096089	0.089157	0.213254	0.048361	0.101121	0.137069
TRCN0000072695	RBM14	0.000111	3.42E-05	7.28E-05	0.000485	0.004917	0.002701	0.012062	0.00905	0.013184	0.000283	0.003972	3.63E-05
TRCN0000072696	RBM14	0.163752	0.081127	0.122439	0.027404	0.070358	0.048881	0.118333	0.145905	0.114895	0.082941	0.153668	0.101495
TRCN0000107560	JMJD1C	2.23E-05	3.42E-05	2.82E-05	0.000224	0.000267	0.000245	0.01552	0.015618	0.013556	6.74E-06	2.7E-05	3.63E-05
TRCN0000107561	JMJD1C	0.017141	0.005577	0.011359	0.01875	0.002821	0.010786	0.092297	0.067987	0.094486	0.016307	0.026037	0.008567
TRCN0000107562	JMJD1C	0.115824	0.309588	0.212706	0.227898	0.029134	0.128516	0.085186	0.119476	0.176495	0.038446	0.271679	0.052381
TRCN0000107563	JMJD1C	0.07286	0.16434	0.1186	0.756878	0.105563	0.431221	0.303875	0.154527	0.207928	0.211873	0.124334	0.125598
TRCN0000107564	JMJD1C	0.004474	3.42E-05	0.002254	0.000162	0.000242	0.000202	0.010727	0.01459	0.018361	6.74E-06	1.35E-05	3.63E-05
TRCN0000107805	SIN3B	0.17633	0.213817	0.195073	0.168862	0.155168	0.162015	0.177974	0.284765	0.331724	0.280036	0.840573	0.687557
TRCN0000107806	SIN3B	0.232539	0.400534	0.316537	0.337924	0.199896	0.26891	0.747923	0.528523	0.414813	0.251962	0.204931	0.64868
TRCN0000107807	SIN3B	0.006678	0.001198	0.003938	0.049685	0.046341	0.048013	0.035974	0.02923	0.025809	0.018752	0.002365	0.005263
TRCN0000107808	SIN3B	0.041072	0.00349	0.022281	0.097667	0.0222	0.059933	0.041996	0.089585	0.109308	0.024497	0.050074	0.00824
TRCN0000107809	SIN3B	8.9E-05	0.001506	0.000797	0.305136	0.060752	0.182944	0.054918	0.056576	0.146328	0.007982	0.00735	0.00029
TRCN0000118647,TRCN0000310425	TBL1X,TBL1X	0.272274	0.041162	0.156718	0.002835	0.000929	0.001882	0.027757	0.038402	0.033035	0.006715	0.040373	0.053688
TRCN0000118648	TBL1X	0.032523	0.000855	0.016689	0.008355	0.005609	0.006982	0.058359	0.054815	0.107446	0.024531	0.022416	0.007623
TRCN0000118649,TRCN0000299525	TBL1X,TBL1X	0.035952	0.365326	0.200639	0.042001	0.062144	0.052072	0.169898	0.176003	0.09996	0.124634	0.435507	0.083018
TRCN0000118650,TRCN0000299582	TBL1X,TBL1X	0.219204	0.080066	0.149635	0.017544	0.010768	0.014156	0.087504	0.059866	0.076721	0.033846	0.013741	0.039966
TRCN0000118651,TRCN0000299581	TBL1X,TBL1X	2.23E-05	3.42E-05	2.82E-05	0.001131	0.001459	0.001295	0.029636	0.047893	0.039366	0.000822	0.042589	0.004646
TRCN0000121073	PLK1	2.23E-05	3.42E-05	2.82E-05	0.000112	1.67E-05	6.43E-05	0.000492	0.000856	0.002123	0.011673	0.000149	3.63E-05
TRCN0000121075	PLK1	4.45E-05	3.42E-05	3.94E-05	0.001815	0.001396	0.001606	0.006637	0.010677	0.001192	0.009544	0.002648	0.033541
TRCN0000121322	PLK1	0.075354	0.024773	0.050063	0.012993	0.103976	0.058484	0.090032	0.065529	0.054077	0.016596	0.122078	0.012088
TRCN0000121323	PLK1	4.45E-05	0.004003	0.002024	0.016512	0.022812	0.019662	0.023912	0.021048	0.01121	0.022732	0.009039	0.000181
TRCN0000121324,TRCN0000121324	PLK1,PLK1	0.000579	0.059023	0.029801	0.002362	0.004384	0.003373	0.021911	0.015373	0.001415	0.020914	0.009242	0.001162
TRCN0000122934	MUC1	1.079682	0.188018	0.63385	0.057419	0.685752	0.371585	0.372013	0.273257	0.317311	0.2328	0.102634	0.227818
TRCN0000122935	MUC1	0.061307	0.059262	0.060285	0.25892	0.067303	0.163111	0.634277	0.379145	0.332022	0.171022	0.201904	0.244335
TRCN0000122936	MUC1	0.154046	0.22959	0.191818	0.014324	0.009906	0.012115	0.093209	0.056907	0.189381	0.292867	0.045683	0.050457

Table D1. Abundance of individual shRNAs. See final page for full legend. (7/8)

		SHRNA ABUNDANCE (% TOTAL READS)											
		TUMORS						T=0			T=4		
Oligo ID	GENE	Tumor 1.1	Tumor 1.2	Average	Tumor 2.1	Tumor 2.2	Average	T0 - rep1	T0 - rep2	T0 - rep3	T4 - rep1	T4 - rep2	T4 - rep3
TRCN0000122937	MUC1	0.001269	0.000582	0.000925	0.003668	0.095712	0.04969	0.001545	0.017379	0.010279	0.036136	0.034806	0.01354
TRCN0000122938	MUC1	0.209832	0.047184	0.128508	0.226953	0.133264	0.180108	0.179133	0.162269	0.226065	0.016084	0.016065	0.005554
TRCN0000128718	SUMO1	0.032701	0.062137	0.047419	0.000199	0.00025	0.000224	0.028706	0.016131	0.041861	0.000869	0.003054	3.63E-05
TRCN0000129359	SUMO1	0.003139	0.000103	0.001621	0.120993	0.069445	0.095219	0.009235	0.025182	0.033481	0.00617	0.008701	3.63E-05
TRCN0000146543	SUMO1	2.23E-05	0.000137	7.96E-05	0.011762	0.000925	0.006344	0.022385	0.01256	0.065548	0.000162	0.011066	0.006026
TRCN0000147057	SUMO1	0.489809	0.389756	0.439783	0.3612	0.371437	0.366318	0.468418	0.481988	0.384721	0.479509	2.327164	0.914032
TRCN0000147601	SUMO1	0.015894	0.24971	0.132802	0.152189	0.076229	0.114209	0.128973	0.226526	0.280962	0.118673	0.079394	0.072201
TRCN0000148311	SUMO1	3.201245	0.368919	1.785082	0.262886	0.362106	0.312496	0.454197	0.457393	0.600134	0.91593	0.637223	1.267811
TRCN0000148589	SUMO1	0.021014	0.069048	0.045031	0.156118	0.42032	0.288219	0.156994	0.163015	0.373436	0.14707	0.31801	0.347318
TRCN0000148613	SUMO1	0.249591	0.128516	0.189053	0.058302	0.357701	0.208001	0.345835	0.279017	0.207146	0.072212	0.080232	0.004465
TRCN0000150166	SUMO1	2.23E-05	0.000376	0.000199	0.016984	0.099179	0.058082	0.00374	0.045716	0.044766	0.00718	0.056371	0.094416
TRCN0000150216	SUMO1	0.01723	0.005509	0.011369	0.004165	0.011981	0.008073	0.041943	0.040543	0.091804	0.004041	0.021686	0.001162
TRCN0000151254	TBL1Y	0.010997	0.000205	0.005601	0.071656	0.040461	0.056058	0.03536	0.017085	0.046926	0.014663	0.049655	0.035211
TRCN0000152203	TBL1Y	0.489698	0.923871	0.706784	0.760123	2.036681	1.398402	1.013471	1.128898	1.056585	1.413072	1.577025	0.918642
TRCN0000152673	TBL1Y	0.009372	0.007733	0.008552	0.06233	0.004413	0.033372	0.091348	0.051843	0.01743	0.001132	0.009255	0.004828
TRCN0000153227	TBL1Y	0.039736	0.031239	0.035488	0.052644	0.021779	0.037211	0.124724	0.091897	0.171132	0.008669	0.016538	0.033614
TRCN0000154186	TBL1Y	0.141714	0.041915	0.091814	0.043928	0.079888	0.061908	0.156168	0.165608	0.082009	0.20284	0.389689	0.111005
TRCN0000156393	TBL1Y	0.014603	0.078081	0.046342	0.009387	0.027963	0.018675	0.050037	0.048443	0.085696	0.372373	0.047169	0.00853
TRCN0000157198	TBL1Y	0.847633	0.255116	0.551374	0.214793	0.370237	0.292515	0.217442	0.199375	0.194409	0.509771	0.05383	0.026281
TRCN0000159193	PELP1	0.020792	1.054405	0.537599	0.115758	0.050217	0.082987	0.033937	0.043967	0.026368	0.012535	0.005526	0.000907
TRCN0000159617	PELP1	2.23E-05	6.84E-05	4.53E-05	0.00179	0.004872	0.003331	0.025422	0.043661	0.063164	0.000377	0.01239	3.63E-05
TRCN0000159673	PELP1	2.23E-05	3.42E-05	2.82E-05	0.000584	0.00353	0.002057	0.004126	0.017954	0.001452	0.00031	0.015592	7.26E-05
TRCN0000159883	PELP1	0.013112	0.001677	0.007394	0.001703	0.009568	0.005636	0.043822	0.047661	0.037653	0.005873	0.013809	0.001851
TRCN0000161421	PELP1	2.23E-05	3.42E-05	2.82E-05	1.24E-05	2.5E-05	1.87E-05	0.006145	0.001773	0.00216	6.74E-06	1.35E-05	3.63E-05
TRCN0000161584	PELP1	0.004675	0.031239	0.017957	0.078469	0.019807	0.049138	0.144546	0.131889	0.12361	0.010292	0.038792	0.02178
TRCN0000166488	PELP1	0.081342	0.20386	0.142601	0.35119	0.218724	0.284957	0.222235	0.185212	0.355559	0.371707	0.272503	0.847749
TRCN0000179333	SRA1	0.253308	0.251318	0.252313	0.048852	0.040353	0.044602	0.385602	0.253542	0.31381	0.187672	0.148696	0.520468
TRCN0000194993	HDAC3	0.221163	0.145898	0.18353	0.136734	0.037869	0.087301	0.208997	0.222954	0.19709	0.136098	0.142778	0.169085
TRCN0000195103,TRCN0000318656	HDAC1,HDAC1	0.006322	0.011565	0.008944	0.219903	0.104046	0.161975	0.183733	0.178253	0.172547	0.104037	0.034495	0.032089
TRCN0000195159	TRRAP	0.252061	0.110073	0.181067	0.53792	0.510372	0.524146	0.162893	0.176774	0.123796	0.130669	0.053884	0.004465
TRCN0000195333	HDAC3	0.04283	0.021796	0.032313	0.039278	0.173183	0.106231	0.199358	0.128159	0.13549	0.085959	0.014822	0.018622
TRCN0000195435	TRRAP	0.046347	0.118901	0.082624	0.042959	0.121166	0.082062	0.099881	0.12109	0.24789	0.024639	0.032982	0.045992
TRCN0000195467,TRCN0000349638	HDAC1,HDAC1	0.001202	0.000205	0.000704	0.008753	0.018553	0.013653	0.007409	0.114217	0.090352	0.045828	0.016119	3.63E-05
TRCN0000195502	RAF1	0.000534	0.016526	0.00853	0.008778	7.92E-05	0.004429	0.012132	0.005381	0.004506	6.74E-06	0.000203	3.63E-05
TRCN0000195646	RAF1	0.212504	0.069288	0.140896	0.439507	0.116332	0.27792	0.354754	0.229143	0.346807	0.166953	0.208903	0.349822
TRCN0000195672	HDAC1	0.000378	0.017416	0.008897	0.016301	0.001804	0.009053	0.115278	0.099638	0.10942	0.025225	0.071112	0.013213
TRCN0000195712	HDAC1	0.064446	0.099364	0.081905	0.024954	0.016986	0.02097	0.137541	0.155958	0.102307	0.366022	0.249114	0.207999
TRCN0000195727	TRRAP	2.23E-05	6.84E-05	4.53E-05	0.000746	0.000396	0.000571	0.040012	0.02358	0.044431	2.02E-05	0.001824	3.63E-05
TRCN0000196264	RAF1	0.017965	0.052111	0.035038	0.07137	0.210031	0.1407	0.15501	0.213855	0.248486	0.146033	0.279569	0.339767
TRCN0000196267	HDAC3	0.728358	0.915077	0.821718	0.285279	0.264411	0.274845	0.185559	0.218821	0.402113	0.032209	0.146453	0.046936
TRCN0000196306,TRCN0000230910	CDK7,CDK7	0.180804	0.192911	0.186857	0.411382	0.224567	0.317974	0.146986	0.170964	0.143982	0.018092	0.013282	0.010055
TRCN0000196691	CDK7	2.23E-05	6.84E-05	4.53E-05	0.006727	0.01619	0.011458	0.011236	0.017391	0.028156	0.004398	0.00277	0.007478
TRCN0000196829	HDAC3	0.525738	2.241775	1.383757	0.289793	1.611377	0.950585	0.296149	0.371538	0.314182	0.119535	0.052033	0.104834
TRCN0000196877	HDAC1	0.001647	0.015876	0.008762	0.063773	0.013144	0.038458	0.11412	0.088852	0.064207	0.100413	0.1768	0.084107
TRCN0000196925	HDAC3	0.104716	0.121844	0.11328	0.052781	1.103321	0.578051	0.11268	0.140524	0.125807	0.069996	0.028334	0.031835
TRCN0000196969	RAF1	0.000178	0.000103	0.00014	0.000833	0.015678	0.008255	0.00992	0.023298	0.010093	0.002425	0.004675	0.030528
TRCN0000196998	HDAC1	9.115329	0.323788	4.719559	0.337439	0.433643	0.385541	0.22845	0.274492	0.411983	0.116996	0.104864	0.150717
TRCN0000197115	RAF1	0.021326	0.000479	0.010903	0.019583	0.107897	0.06374	0.175639	0.162807	0.128563	0.034762	0.013931	0.103854
TRCN0000197171	HDAC3	0.020903	0.010744	0.015823	0.032489	0.005613	0.019051	0.079585	0.090613	0.111543	0.002297	0.001054	0.017968
TRCN0000197176	HDAC1	0.003784	0.013413	0.008599	0.000323	0.000683	0.000503	0.034903	0.040873	0.046963	0.000606	0.002797	0.04886
TRCN0000197198	HDAC1	0.014225	0.046945	0.030585	0.057879	0.014415	0.036147	0.082833	0.07837	0.047299	0.10568	0.008661	0.001996
TRCN0000199110	HDAC4	8.9E-05	0.000308	0.000198	0.000995	0.000246	0.00062	0.038151	0.015312	0.02391	0.083224	0.002459	0.002251
TRCN0000199182	HDAC3	1.939491	0.195306	1.067398	0.316127	0.179563	0.247845	0.119246	0.114327	0.081339	0.021197	0.010066	0.038841
TRCN0000199964	HDAC3	0.147613	0.153015	0.150314	0.144318	0.11384	0.129079	0.162348	0.122607	0.133479	0.0339	0.028131	0.045702
TRCN0000218391,TRCN0000219664	CDK7,CDK7	0.098995	0.988608	0.543801	0.066035	0.033685	0.04986	0.083852	0.078052	0.087558	0.017405	0.059086	0.051836
TRCN0000219663,TRCN0000230908	CDK7,CDK7	0.329151	0.232533	0.280842	0.635823	0.413023	0.524423	0.154307	0.127658	0.134112	0.155065	0.115457	0.05082

Table D1. Abundance of individual shRNAs at screening time points. Relative abundance of shRNAs is shown as % of total reads in each condition. T0= time zero reference, T4=PD20 *in vitro* time point. Clones for which reads were detected at T0 but not in T4 or in tumors were adjusted to the lowest read abundance found in that condition to allow for log2 calculations, and are highlighted in yellow. (8/8)

		LOG2 CALCULATIONS																
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)						IN VIVO LOG2 - T4				
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val		REP1	REP2	AVG	STDEV	p-val
SHC002	NON-MAMMALIAN SHRNA	0.17588	0.417254	-0.17521	0.139307	0.297922	0.406576	-2.41902	0.494171	-0.96242	2.059936	0.16109		-2.5949	0.076917	-1.25899	1.889259	0.045996
SHC004	GFP	-0.81413	-0.36313	-2.63852	-1.27193	1.204794	0.411817	2.68848	3.374807	3.031644	0.485306	0.096294		3.502609	3.737939	3.620274	0.166403	0.375585
SHC016	NON-TARGETING SHRNA	-1.49707	-0.67533	-1.9978	-1.39007	0.667698	0.324313	0.829589	1.663019	1.246304	0.589324	0.786225		2.326661	2.338348	2.332504	0.008264	0.958923
TRCN0000000249	E2F1	0.301295	-0.99092	0.744356	0.018245	0.901599	0.503274	-0.301	0.069748	-0.11562	0.262155	0.383562		-0.60229	1.060665	0.229187	1.175887	0.206611
TRCN0000000251	E2F1	-1.48023	-3.69627	-3.47096	-2.88248	1.219603	0.014917	1.387119	1.273711	1.330415	0.080191	0.730335		2.867347	4.969979	3.918663	1.486786	0.298214
TRCN0000000252	E2F1	3.123943	1.262772	0.478644	1.621786	1.358702	0.022953	1.118695	0.06792	0.593308	0.74301	0.779357		-2.00525	-1.19485	-1.60005	0.573037	0.026171
TRCN0000000253,TRCN0000344500	E2F1,E2F1	-1.82506	-0.42442	-1.27191	-1.1738	0.705455	0.462527	-1.0606	-1.03926	-1.04993	0.015091	0.114021		0.764464	-0.61483	0.074816	0.97531	0.17447
TRCN0000000592	CDK7	0.068366	-0.67265	1.58208	0.325933	1.149219	0.316092	0.955042	-0.74142	0.106811	1.19958	0.502792		0.886676	-0.06877	0.408952	0.675604	0.241103
TRCN0000000593	CDK7	-10.6253	-7.2632	-8.89809	-8.92888	1.681288	6.6E-08	-4.05845	-5.38753	-4.72299	0.939803	0.000668		6.566898	1.875663	4.221281	3.317204	0.269269
TRCN0000000594	CDK7	-1.11708	-1.16024	-2.00271	-1.42667	0.499329	0.300847	-1.05195	-2.97578	-2.01387	1.360354	0.032929		0.065123	-1.81555	-0.87521	1.329834	0.064604
TRCN0000000595	CDK7	-0.35528	-0.55924	-0.52711	-0.48054	0.109663	0.929813	-6.54023	-4.71797	-5.6291	1.288531	0.000249		-6.18495	-4.15873	-5.17184	1.43275	0.000616
TRCN0000000596	CDK7	-1.73591	-1.55848	0.83604	-0.81945	1.436438	0.763584	-0.17177	-4.66523	-2.4185	3.177357	0.035976		1.564135	-3.10675	-0.77131	3.302816	0.101775
TRCN0000001033,TRCN0000318418	PIN1,PIN1	-0.13749	-0.09449	-1.63534	-0.62244	0.877461	0.934599	0.743697	0.631362	0.68753	0.079432	0.838752		0.881183	0.725848	0.803516	0.109838	0.347482
TRCN0000001034,TRCN0000318360	PIN1,PIN1	-0.20877	-0.31985	-0.21075	-0.24646	0.063568	0.709927	-1.97373	0.716673	-0.62853	1.9024	0.235876		-1.76496	1.036524	-0.36422	1.980948	0.121938
TRCN0000001035	PIN1	-3.44714	-1.03521	-1.13479	-1.87238	1.364693	0.146741	0.679945	-1.45992	-0.38999	1.513115	0.298431		4.12709	-0.42471	1.85119	3.218609	0.813896
TRCN0000001036,TRCN0000318359	PIN1,PIN1	3.314742	-0.00714	-0.04849	1.086373	1.929935	0.09287	-1.50987	0.049415	-0.73023	1.10258	0.18819		-4.82461	0.05655	-2.38403	3.451502	0.021091
TRCN0000001064	RAF1	-2.55059	-2.11	-1.31068	-1.99042	0.628548	0.099341	-2.3997	-2.89338	-2.64654	0.349086	0.010835		0.150894	-0.78337	-0.31624	0.660628	0.113168
TRCN0000001065	RAF1	-5.00992	-3.54381	-3.0528	-3.86884	1.018244	0.001163	-1.304	-1.36364	-1.33382	0.042175	0.075831		3.705927	2.180167	2.943047	1.078875	0.655185
TRCN0000001066	RAF1	1.53102	-2.78199	-1.32822	-0.85973	2.194339	0.750106	-2.89113	-0.79132	-1.84123	1.484786	0.043465		-4.42215	1.990663	-1.21574	4.534543	0.089218
TRCN0000001067	RAF1	0.24199	-0.35672	0.265249	0.050172	0.352573	0.469048	0.021322	1.825284	0.923303	1.275594	0.998308		-0.22067	2.182006	0.980669	1.698947	0.424316
TRCN0000001068	RAF1	-0.81533	-1.72096	-4.65031	-2.39554	2.004508	0.063801	-0.60044	-1.8667	-1.23357	0.895383	0.092739		0.214893	-0.14574	0.034578	0.255003	0.162728
TRCN0000001165	PPARGC1A	-3.21217	-2.72703	-2.06168	-2.66696	0.577593	0.020186	-9.16287	-5.30945	-7.23616	2.724783	0.000105		-5.9507	-2.58242	-4.26656	2.381733	0.002081
TRCN0000001166	PPARGC1A	0.02543	0.161162	0.371609	0.186067	0.174428	0.375315	1.025812	0.30202	0.663916	0.511798	0.824082		1.000382	0.140858	0.57062	0.607775	0.281498
TRCN0000001167	PPARGC1A	0.078794	-0.73952	-1.56907	-0.74327	0.823938	0.821629	-0.02982	-1.25211	-0.64097	0.864295	0.206734		-0.10861	-0.51259	-0.3106	0.285657	0.112318
TRCN0000001168	PPARGC1A	-1.99856	-5.6126	-4.93182	-4.18099	1.920452	0.001124	-8.50185	0.584839	-3.95851	6.42526	0.030775		-6.50329	6.197441	-0.15293	8.980776	0.384409
TRCN0000001297	HNRNPU	-1.55091	-2.26629	-2.04841	-1.9552	0.366686	0.104076	-0.85408	-2.00436	-1.42922	0.813369	0.069426		0.696825	0.26193	0.479377	0.307518	0.256091
TRCN0000001298,TRCN0000350256	HNRNPU,HNRNPU	-12.7659	-11.4113	0.670766	-7.83547	7.397687	0.001136	-8.84774	-6.86052	-7.85413	1.405171	2.41E-05		3.918142	4.550775	4.234458	0.447339	0.209502
TRCN0000001299,TRCN0000320513	HNRNPU,HNRNPU	-10.7242	-10.256	-10.1152	-10.3651	0.318869	1.88E-09	-8.65644	-6.8241	-7.74027	1.295666	2.55E-05		2.067806	3.431948	2.749877	0.964594	0.746658
TRCN0000001300	HNRNPU	-6.15449	-1.784	-1.61481	-3.18443	2.573537	0.017486	-9.94154	-0.8353	-5.38842	6.439082	0.008816		-3.78705	0.948694	-1.41918	3.348677	0.054215
TRCN0000001661	PPARD	1.787164	-1.13816	-8.72292	-2.69131	5.424451	0.161929	0.617974	-0.01015	0.303914	0.444148	0.599269		-1.16919	1.128015	-0.02059	1.62437	0.166483
TRCN0000001662	PPARD	-3.65219	-3.08752	-0.96142	-2.56704	1.418887	0.034117	-1.44934	-1.72489	-1.58712	0.194841	0.052399		2.202851	1.362628	1.78274	0.594127	0.756189
TRCN0000001663	PPARD	-0.12379	1.852623	0.474675	0.734503	1.013501	0.145135	-4.61871	-2.93046	-3.77459	1.193771	0.002557		-4.49492	-4.78309	-4.639	0.203763	0.000866
TRCN0000001664	PPARD	0.144086	-1.2008	-0.60587	-0.55419	0.673929	0.998867	0.364683	0.405161	0.384922	0.028622	0.64562		0.220597	1.605958	0.913278	0.979598	0.389523
TRCN0000001665	PPARA	-1.60629	-0.76485	-1.09152	-1.15422	0.424209	0.471389	-0.20513	-0.87253	-0.53883	0.471927	0.230409		1.401158	-0.10769	0.646736	1.066915	0.307348
TRCN0000001666	PPARA	0.706114	0.535214	1.249516	0.830281	0.372988	0.108505	0.720994	0.929352	0.825173	0.147332	0.93145		0.01488	0.394138	0.204509	0.268176	0.19424
TRCN0000001667	PPARA	-0.00198	-1.15349	-0.91082	-0.68876	0.607025	0.870699	-0.08818	-1.73024	-0.90921	1.161112	0.149696		-0.0862	-0.57675	-0.33148	0.346868	0.109941
TRCN0000001668	PPARA	0.108611	0.08859	0.353732	0.183644	0.14764	0.376691	1.984467	0.732838	1.358653	0.885036	0.717206		1.875856	0.644248	1.260052	0.870878	0.518756
TRCN0000001669	PPARA	0.647168	0.568368	-0.13009	0.361817	0.427819	0.278275	-4.57501	-2.87419	-3.7246	1.202661	0.002747		-5.22218	-3.44256	-4.33237	1.258382	0.001377
TRCN0000001670	PPARG	-1.85491	-2.33055	1.094318	-1.03038	1.85535	0.606898	-7.4132	-3.9426	-5.6779	2.454081	0.00045		-5.55829	-1.61205	-3.58517	2.790411	0.00486
TRCN0000001671	PPARG	2.617825	-2.74376	-0.62197	-0.2493	2.700148	0.76748	0.685631	-4.06406	-1.68922	3.358541	0.092657		-1.93219	-1.32031	-1.62625	0.432669	0.025166
TRCN0000001672	PPARG	-2.95985	-3.7431	-1.24957	-2.65084	1.275165	0.026467	-6.38677	-3.40724	-4.897	2.106845	0.000908		-3.42692	0.335865	-1.54553	2.660689	0.039899
TRCN0000001673	PPARG	-2.2334	-4.74715	0.673687	-2.10229	2.712794	0.145148	-0.02459	-4.80435	-2.41447	3.379799	0.03931		2.208808	-0.05721	1.075802	1.602313	0.456875
TRCN0000001674	PPARG	-0.94976	0.248136	-0.09509	-0.26557	0.616878	0.730871	0.4812	-2.39729	-0.95805	2.035402	0.161234		1.430964	-2.64543	-0.60723	2.882445	0.110119
TRCN0000002509,TRCN0000277862	CDC25B,CDC25B	-2.86886	-1.59611	-3.43706	-2.63401	0.942676	0.024258	-9.36055	-5.56563	-7.46309	2.68342	8.13E-05		-6.49169	-3.96952	-5.2306	1.783448	0.000646
TRCN0000002510,TRCN0000286048	CDC25B,CDC25B	-2.30122	-0.65579	-0.68648	-1.2145	0.941255	0.440568	0.246459	-3.13048	-1.44201	2.387855	0.094551		2.547681	-2.47469	0.036496	3.551351	0.223616
TRCN0000002511,TRCN0000297052	CDC25B,CDC25B	-12.0938	-7.1119	-1.88135	-7.02903	5.106749	0.00028	-1.29802	-5.29642	-3.29722	2.827293	0.010091		10.79582	1.815488	6.305655	6.350055	0.087826
TRCN0000002512,TRCN0000277861	CDC25B,CDC25B	0.300673	-2.82457	-1.12654	-1.21681	1.564577	0.462525	-0.32964	-3.98827	-2.15895	2.587036	0.039714		-0.63032	-1.16369	-0.897	0.377154	0.058322
TRCN0000002513,TRCN0000277863	CDC25B,CDC25B	0.838075	-0.49415	-9.11382	-2.9233	5.402372	0.12262	7.880318	4.197692	6.039005	2.60401	0.002906		7.042243	4.691842	5.867043	1.661984	0.039592
TRCN0000003298	ESR1	-4.68302	-1.7801	-0.74535	-2.40282	2.041361	0.063894	-2.27846	-2.07677	-2.17761	0.142616	0.021611		2.404564	-0.29667	1.053947	1.910061	0.454868
TRCN0000003299	ESR1	-2.93879	-3.22415	-8.31777	-4.82691	3.026545	0.000928	0.679765	1.826383	1.253074	0.810781	0.783313		3.618558	5.050536	4.334547	1.012561	0.193713
TRCN0000003300	ESR1	0.340447	-1.19862	-1.36888	-0.74235	0.941587	0.82377	-1.17365	-1.00798	-1.09081	0.117144	0.107696		-1.51409	0.190643	-0.66172	1.205431	0.080715
TRCN0000003301	ESR1	-1.5285	-1.84024	-3.93879	-2.43584	1.310889	0.043935	-0.95159	-1.26431	-1.10795	0.221127	0.10535		0.576913	0.575932	0.576422	0.000693	0.280756
TRCN0000003321	PGR	0.234644	-0.22255	-0.46548	-0.15113	0.355486	0.627954	1.489075	1.11459	1.301832	0.264801	0.748972		1.254431	1.337142	1.295787	0.058486	0.529416
TRCN0000003323	PGR	-3.18221	-8.31498	-1.91355	-4.47025	3.389519	0.002767	-0.77262	-5.25578	-3.0142	3.170072	0.01711		2.409593	3.0592	2.734396	0.459342	0.75195
TRCN0000003324	PGR	-7.72105	-4.38849	-1.76435	-4.62463	2.985362	0.001327	-0.21186	-3.8128	-2.01233	2.546255	0.047406		7.509194	0.575684	4.042439	4.902731	0.36886
TRCN0000003325	ESR2	-1.60808	-5.19576	-3.91568	-3.57318	1.818198	0.004205	-5.20727	-4.08898	-4.64813	0.790749	0.000706		-3.59919	1.106778	-1.2462	3.32762	0.064114
TRCN0000003326	ESR2	0.911567	0.803164	1.672829	1.129187	0.473917	0.055989	-3.14353	-1.45477	-2.29915	1.194136	0.020908		-4.0551	-2.25793	-3.15652	1.270789	0.004874
TRCN0000003327	ESR2	1.054911	-3.53307	-2.86714	-1.78177	2.479096	0.228403	-1.06936	-1.19827	-1.13381	0.091156	0.101261		-2.12427	2.334796	0.105265	3.153034	0.225036
TRCN0000003328	ESR2	-0.11619	0.30865	0.245424	0.145963	0.229218	0.401546	-1.46974	0.543394	-0.46317	1.423497	0.271358		-1.35355	0.234744	-0.5594	1.123092	0.089616
TRCN0000003343	VEGFA	3.231983	0.540405	-1.61163	0.720253	2.42681	0.209838	0.941588	0.494163	0.717876	0.316377	0.859316		-2.29039	-0.04624	-1.16832	1.586856	0.048301
TRCN0000003345	VEGFA	-0.98597	-0.95765	-0.94416	-0.96259	0.021338	0.619764	0.233156	0.958802	0.595979	0.513109	0.779685		1.219123	1.916455	1.567789	0.493089	0.651778
TRCN0000003368	UBE3A	-0.18032	0.883792	1.445068	0.71618	0.825556	0.14587	-6.11893	-1.41683	-3.76788	3.324883	0.007387		-5.93861	-2.30063	-4.11962	2.572442	0.002596
TRCN0000003369	UBE3A	2.083549	-0.21739	0.381588	0.74925	1.193716	0.146073	-2.17326	-3.91494	-3.0441	1.231552	0.007197		-4.25681	-3.69755	-3.97718	0.395455	0.001758
TRCN0000003370	UBE3A	-4.4459	-1.71339	-1.94337	-2.70089	1.515596	0.026298	0.88284	-0.90523	-0.0112	1.264358	0.446419		5.328742	0.808155	3.068448	3.196537	0.636041
TRCN0000003371	UBE3A	1.869454	-3.41172	2.825943	0.427891	3.359419	0.387571	-0.54829	-1.48392	-1.01611	0.661591	0.122879		-2.41775	1.927799	-0.24497	3.072765	0.161455
TRCN0000003372	UBE3A	-0.34276	-0.61879	-0.08879	-0.35011	0.265079	0.805785	0.187304	-1.4445	-0.6286	1.153862	0.215486		0.530065	-0.82571	-0.14782	0.958679	0.138058
TRCN0000003715,TRCN0000314658	AR,AR	-0.46779	1.218165	0.464021	0.404798	0.844537	0.266119	-3.48487	-2.9168	-3.20083	0.401688	0.004821		-3.01708	-4.13496	-3.57602	0.790464	0.002832
TRCN0000003717	AR	-0.53802	0.713462	-1.81289	-0.54582	1.263193	0.993412	-0.68724	-0.49335	-0.5903	0.137103	0.213625		-0.14922	-1.20681	-0.67802	0.747828	0.076221
TRCN0000003718,TRCN0000314657	AR,AR	1.008957	0.984793	2.625808	1.539853	0.940542	0.02356	1.964422	-0.07936	0.942533	1.445169	0.98915		0.955465	-1.06415	-0.05434	1.428083	0.157928
TRCN0000004078,TRCN0000315113	NCOA1,NCOA1	-0.70633	0.186135	-0.21198	-0.24406	0.447094	0.709823	-1.55339	-1.7913	-1.67234	0.168226	0.046129		-0.84707	-1.97743	-1.41225	0.799291	0.033129
TRCN0000004079	NCOA1	3.368529	-2.19947	-0.90344	0.088542	2.913531	0.545642	-1.07277	-3.82095	-2.44686	1.943256	0.021265		-4.4413	-1.62148	-3.03139	1.993912	0.006674
TRCN0000004080	NCOA1	-2.15959	-2.36811	-1.11371	-1.88047	0.672168	0.126429	-1.84699	-2.15169	-1.99934	0.215458	0.028328		0.312599	0.216422	0.264511	0.068007	0.206138
TRCN0000004081	NCOA1	-0.86553	0.355952	-1.06473	-0.52477	0.769202	0.973204	-1.49697	-2.51903	-2.008	0.722702	0.02932		-0.63144	-2.87498	-1.75321	1.586421	0.025043
TRCN0000004082,TRCN0000315043	NCOA1,NCOA1	-1.57493	-1.66645	-1.59539	-1.61226	0.048037	0.209199	0.080011	1.187466	0.633738	0.783089	0.805778		1.654937	2.853917	2.254427	0.847807	0.999819
TRCN0000004115	PIAS4	-5.61176	-4.15918	-6.57261	-5.44785	1.215035	3.08E-05	-3.85336	-5.58934	-4.72135	1.22752	0.000739		1.758401	-1.43015	0.164124	2.254648	0.213108
TRCN0000004116	PIAS4	1.371611	-0.5532	-1.00339	-0.06166	1.261495	0.574482	3.899484	1.714927	2.807205	1.544715	0.148649		2.527874	2.268129	2.398001	0.183667	0.92444
TRCN0000004117	PIAS4	-1.02521	-2.5824	-3.21954	-2.27572	1.128852	0.059132	0.841499	1.756051	1.298775	0.646686	0.752828		1.866712	4.338455	3.102584	1.747786	0.592362
TRCN0000004118	PIAS4	-4.18674	-3.39437	-10.9097	-6.16359	4.12928	0.000315	-0.77073	-4.2909	-2.53081	2.489137	0.023415		3.416009	-0.89653	1.259739	3.049426	0.560042
TRCN0000004119	PIAS4	-0.25356	-1.26826	1.666595	0.048257	1.490526	0.502013	0.438829	0.359595	0.399212	0.056027	0.654289		0.692389	1.627858	1.160123	0.661477	0.476764
TRCN0000004144	PIAS1	-2.27659	-4.33577	-11.3149	-5.97574	4.737064	0.000895	-2.75494	-2.77313	-2.76403	0.012864	0.008962		-0.47835	1.562644	0.542149	1.443198	0.284304
TRCN0000004145	PIAS1	0.438125	-6.75044	-3.91632	-3.40955	3.620979	0.023913	-7.36319	-6.81594	-7.08956	0.386967	3.71E-05		-7.80131	-0.06549	-3.9334	5.470051	0.01108
TRCN0000004146	PIAS1	-0.29314	0.315201	-3.32059	-1.09951	1.947411	0.560446	-7.47994	-5.0689	-6.27442	1.704864	0.000146		-7.1868	-5.3841	-6.28545	1.274702	0.000205
TRCN0000004147	PIAS1	0.434661	-0.1402	-2.22795	-0.6445	1.401108	0.917362	-1.00472	-1.66923	-1.33698	0.469881	0.07674		-1.43938	-1.52903	-1.48421	0.063389	0.02936
TRCN0000004211,TRCN0000273239	OTUB1,OTUB1	-1.73598	-0.37144	-0.37258	-0.82667	0.787491	0.74542	-3.18261	-4.95946	-4.07104	1.256423	0.001749		-1.44663	-4.58802	-3.01732	2.221299	0.007247
TRCN0000004213,TRCN0000273238	OTUB1,OTUB1	-2.56324	-1.52964	-2.17065	-2.08784	0.521756	0.078915	-5.17353	-2.72253	-3.94803	1.733116	0.002505		-2.61029	-1.1929	-1.90159	1.002245	0.019274
TRCN0000004214,TRCN0000273297	OTUB1,OTUB1	-2.49126	-0.94829	-1.43466	-1.62474	0.788848	0.214153	-1.20304	-1.22669	-1.21487	0.016722	0.090093		1.288216	-0.27839	0.504911	1.107761	0.269463
TRCN0000004215	OTUB1	-1.02188	-0.26362	-0.94611	-0.74387	0.417631	0.81777	0.514983	-0.84931	-0.16716	0.964702	0.370326		1.536865	-0.58569	0.475587	1.500874	0.268083
TRCN0000004395	SENP1	2.183629	0.947504	-1.42932	0.56727	1.836243	0.234926	-1.8083	-2.70123	-2.25477	0.631394	0.020051		-3.99193	-3.64873	-3.82033	0.242669	0.002064
TRCN0000004396	SENP1	2.325407	-3.10416	-8.5448	-3.10785	5.435104	0.099334	-3.78917	1.057214	-1.36598	3.426911	0.136747		-6.11458	4.161373	-0.9766	7.266193	0.192031
TRCN0000004397	SENP1	-2.7852	-1.82355	-5.50967	-3.37281	1.91202	0.00717	-0.06883	-1.1312	-0.60001	0.751214	0.216175		2.716376	0.692351	1.704364	1.431202	0.723606
TRCN0000004398	SENP1	0.188697	-0.6002	-0.39612	-0.26921	0.409474	0.732097	-1.50225	-1.49914	-1.5007	0.002199	0.059354		-1.69095	-0.89895	-1.29495	0.56003	0.037237
TRCN0000004399	SENP1	0.278196	-2.24168	-2.15802	-1.37383	1.431311	0.3597	-0.32732	-0.17681	-0.25207	0.106428	0.326346		-0.60552	2.064864	0.729672	1.888247	0.346231
TRCN0000004814,TRCN0000318714	HDAC1,HDAC1	0.055968	-0.22532	-0.04946	-0.07293	0.142104	0.561721	-1.80877	-0.61846	-1.21361	0.841675	0.09479		-1.86474	-0.39315	-1.12894	1.040572	0.046957
TRCN0000004815	HDAC1	-2.96714	-8.18266	-4.28493	-5.14491	2.712027	0.000335	-0.89933	-6.79359	-3.84646	4.167869	0.01093		2.067806	1.389073	1.72844	0.479937	0.728911
TRCN0000004816	HDAC1	2.774653	2.814596	4.395712	3.32832	0.924604	0.000269	-2.49278	-2.1688	-2.33079	0.229086	0.017229		-5.26743	-4.9834	-5.12541	0.200841	0.000529
TRCN0000004817,TRCN0000349639	HDAC1,HDAC1	-0.05032	0.189212	0.814338	0.317743	0.446428	0.301535	-0.87281	-1.06089	-0.96685	0.132988	0.128286		-0.82249	-1.2501	-1.0363	0.302362	0.049582
TRCN0000004818,TRCN0000318655	HDAC1,HDAC1	-1.45951	1.114936	-3.06822	-1.1376	2.110077	0.541462	-8.76914	-2.45702	-5.61308	4.463345	0.002019		-7.30963	-3.57195	-5.44079	2.642939	0.000739
TRCN0000004824	HDAC3	-5.7156	1.756212	-5.91965	-3.29301	4.373946	0.046451	-8.29165	-0.63354	-4.4626	5.415098	0.011646		-2.57605	-2.38976	-2.4829	0.13173	0.009207
TRCN0000004825	HDAC3	0.938281	3.547599	0.967953	1.817944	1.497999	0.015564	-3.03763	-0.15034	-1.59399	2.04162	0.070663		-3.97591	-3.69794	-3.83693	0.196553	0.002023
TRCN0000004826	HDAC3	0.250922	-1.51947	-0.69997	-0.65617	0.886008	0.903017	0.574389	2.932655	1.753522	1.667546	0.510172		0.323467	4.452125	2.387796	2.919402	0.936816
TRCN0000004827	HDAC3	3.746088	3.134567	2.473545	3.118067	0.636432	0.000389	-1.76178	-1.97383	-1.8678	0.149945	0.034426		-5.50787	-5.1084	-5.30813	0.282465	0.000443
TRCN0000004828	HDAC3	-6.90574	-1.89371	-7.59925	-5.46623	3.113267	0.000295	-6.83793	-4.51027	-5.6741	1.645904	0.000279		0.067806	-2.61657	-1.27438	1.898137	0.045297
TRCN0000004829,TRCN0000314666	HDAC4,HDAC4	-1.41989	-0.82383	-0.8014	-1.01504	0.350789	0.577835	-1.80967	-1.59635	-1.70301	0.150838	0.044047		-0.38978	-0.77252	-0.58115	0.270637	0.083155
TRCN0000004830	HDAC4	-0.9403	-1.01259	0.112509	-0.61346	0.629749	0.942253	0.486093	2.839657	1.662875	1.664221	0.556579		1.426398	3.852252	2.639325	1.715338	0.806727

Table D2. Log fold changes in shRNA abundance. See final page for full legend. (1/7)

		LOG2 CALCULATIONS														
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)					IN VIVO LOG2 - T4			
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val	REP1	REP2	AVG	STDEV	p-val
TRCN0000004833	HDAC4	-0.66487	-0.05184	-0.53797	-0.41823	0.323585	0.87036	-1.83407	-0.88448	-1.35928	0.671466	0.075592	-1.1692	-0.83264	-1.00092	0.237984	0.051548
TRCN0000004918	PARK7	-0.67841	-0.06702	-8.12976	-2.9584	4.488953	0.080571	-9.65977	-5.11289	-7.38633	3.215133	0.000133	-8.98136	-5.04587	-7.01362	2.782814	0.000195
TRCN0000004919	PARK7	-0.9078	-1.00661	-0.68561	-0.86667	0.164402	0.703783	-0.8387	-1.64041	-1.23956	0.566897	0.088951	0.069095	-0.63381	-0.28236	0.497027	0.11658
TRCN0000004920	PARK7	-1.04236	1.662649	0.847238	0.489176	1.387595	0.246775	-0.44053	-0.70294	-0.57173	0.185554	0.21901	0.601832	-2.36559	-0.88188	2.098282	0.07195
TRCN0000004921	PARK7	0.021942	-2.26051	0.020792	-0.73926	1.317441	0.831549	-0.72598	-0.68372	-0.70485	0.02988	0.183448	-0.74792	1.576788	0.414435	1.643815	0.255579
TRCN0000005096	NR2F2	-0.26498	-1.35509	-1.6552	-1.09176	0.731562	0.523419	-2.57877	-3.03058	-2.80467	0.319479	0.008548	-2.31378	-1.67549	-1.99464	0.451343	0.016417
TRCN0000005097	NR2F2	-0.33538	-3.75727	-4.1306	-2.74109	2.091746	0.032542	-1.74086	-1.38113	-1.561	0.254365	0.054589	-1.40548	2.376138	0.485331	2.674005	0.297813
TRCN0000005098	NR2F2	-7.1211	-5.73002	-5.50649	-6.1192	0.874835	5.25E-06	-4.02713	-2.70216	-3.36464	0.936891	0.004202	3.093973	3.027862	3.060917	0.046748	0.595931
TRCN0000005099	NR2F2	0.718455	-3.55754	-0.32411	-1.0544	2.229578	0.605148	0.286335	0.094271	0.190303	0.13581	0.533827	-0.43212	3.651809	1.609844	2.887774	0.701194
TRCN0000005100	NR2F2	-2.07117	-2.69313	-2.92765	-2.56398	0.442601	0.025349	-1.02463	-0.95502	-0.98983	0.049225	0.124109	1.04654	1.738114	1.392327	0.489016	0.572155
TRCN0000005361	TRRAP	-8.5144	-6.96571	-8.14553	-7.87521	0.80896	1.51E-07	-4.26253	-2.76196	-3.51224	1.061064	0.003529	4.251872	4.203749	4.22781	0.034028	0.209761
TRCN0000005363	TRRAP	-1.14491	-1.27709	-1.76159	-1.39453	0.324679	0.315855	-2.17665	-4.08153	-3.12909	1.346959	0.006614	-1.03173	-2.80444	-1.91809	1.253496	0.01961
TRCN0000005364	TRRAP	-3.8815	-2.91792	3.410455	-1.12966	3.961259	0.637324	-2.28865	-1.28746	-1.78805	0.707947	0.040537	1.592854	1.630466	1.61166	0.026596	0.671455
TRCN0000006485	CREBBP	0.518074	-0.01438	0.22734	0.243679	0.266601	0.340929	-1.20287	-0.40083	-0.80185	0.567129	0.163722	-1.72094	-0.38645	-1.0537	0.943628	0.05065
TRCN0000006486	CREBBP	0.574578	0.989663	0.003455	0.522565	0.495157	0.206558	-5.02716	-1.86508	-3.44612	2.235926	0.006181	-5.60173	-2.85474	-4.22824	1.942416	0.001855
TRCN0000006487	CREBBP	1.017695	0.783942	-0.47725	0.441463	0.804165	0.247865	2.309852	-1.43016	0.439848	2.644585	0.718792	1.292157	-2.2141	-0.46097	2.479296	0.118901
TRCN0000006488	CREBBP	0.761307	1.297093	-0.45988	0.53284	0.900492	0.211427	0.273157	-1.52114	-0.62399	1.268763	0.219303	-0.48815	-2.81824	-1.65319	1.647621	0.028348
TRCN0000007166,TRCN0000280243	CARM1,CARM1	-4.92885	-3.04077	-4.48092	-4.15018	0.986534	0.000565	-4.46918	-3.88818	-4.17868	0.410831	0.001223	0.459666	-0.84741	-0.19387	0.92424	0.131153
TRCN0000007167,TRCN0000280298	CARM1,CARM1	-0.92797	-6.0531	-1.95075	-2.97727	2.712385	0.029106	-8.05246	-4.88375	-6.46811	2.240615	0.000164	-7.12449	1.169344	-2.97757	5.864624	0.029162
TRCN0000007168,TRCN0000280244	CARM1,CARM1	-3.43225	-1.3117	-0.17863	-1.64086	1.651601	0.239157	-3.01993	-2.791	-2.90547	0.161877	0.007294	0.412324	-1.47931	-0.53349	1.337584	0.094191
TRCN0000007169,TRCN0000280242	CARM1,CARM1	-2.8831	-1.55106	-2.19163	-2.2086	0.666184	0.061428	-0.71783	-1.17073	-0.94428	0.320252	0.133062	2.165273	0.380323	1.272798	1.26215	0.528548
TRCN0000007205	UBE2I	-5.40473	-1.56989	-5.96774	-4.31412	2.393188	0.00134	-3.20503	-4.10031	-3.65267	0.633058	0.002617	2.199699	-2.53042	-0.16536	3.344702	0.181356
TRCN0000007206	UBE2I	-4.67833	-10.6587	-8.78184	-8.03964	3.058514	2.67E-06	1.657493	-1.6364	0.010544	2.329137	0.489481	6.335819	9.022343	7.679081	1.899659	0.005596
TRCN0000007207	UBE2I	-0.71085	-2.62161	-4.05746	-2.46331	1.67891	0.048024	1.54407	-0.24534	0.649363	1.265307	0.819809	2.25492	2.376267	2.315593	0.085805	0.967856
TRCN0000007735	UBB	-4.36865	-4.61663	-2.27524	-3.7535	1.286208	0.00184	-7.73958	-6.13959	-6.93959	1.131361	5.37E-05	-3.37093	-1.52297	-2.44695	1.306707	0.010849
TRCN0000007737	UBB	-9.26482	-6.61944	-8.74781	-8.21069	1.402097	1.53E-07	-7.19701	-5.02741	-6.11221	1.534141	0.00016	2.067806	1.592035	1.829921	0.336421	0.779088
TRCN0000007928	PARP1	0.685186	0.187419	0.492158	0.454921	0.250964	0.232064	0.132346	1.061636	0.596991	0.657107	0.781154	-0.55284	0.874217	0.160689	1.009082	0.190881
TRCN0000007929,TRCN0000338406	PARP1,PARP1	-0.72051	-0.01009	-0.64518	-0.45859	0.390238	0.909125	-0.42278	0.372331	-0.02522	0.562228	0.427236	0.29773	0.38242	0.340075	0.059885	0.222517
TRCN0000007930	PARP1	-0.03543	-1.83231	-1.75523	-1.20765	1.015909	0.447541	2.195811	1.241771	1.718791	0.674608	0.507254	2.23124	3.074079	2.652659	0.595978	0.793398
TRCN0000007931	PARP1	0.810978	-0.10989	-1.00288	-0.1006	0.906965	0.595191	-0.47305	0.186187	-0.14343	0.466151	0.37305	-1.28403	0.296076	-0.49398	1.117302	0.096227
TRCN0000007932,TRCN0000338467	PARP1,PARP1	-2.19925	-1.74643	-5.99975	-3.31514	2.335934	0.011176	-3.06893	-0.48687	-1.7779	1.825792	0.051894	-0.86968	1.25956	0.194941	1.505599	0.204477
TRCN0000007999,TRCN0000315311	CAV1,CAV1	1.063723	-0.40135	0.601516	0.421295	0.74898	0.25576	0.243207	0.091965	0.167586	0.106945	0.521463	-0.82052	0.493318	-0.1636	0.929021	0.135499
TRCN0000008000,TRCN0000350508	CAV1,CAV1	0.299071	0.202114	0.066724	0.189303	0.116702	0.372981	-0.54336	1.082801	0.269718	1.149873	0.588919	-0.84244	0.880687	0.019125	1.218432	0.167441
TRCN0000008001	CAV1	-1.18872	-2.36873	-0.62612	-1.39452	0.889349	0.327721	-0.70713	-2.44969	-1.57841	1.232176	0.059842	0.481586	-0.08096	0.200314	0.397778	0.193891
TRCN0000008002,TRCN0000315310	CAV1,CAV1	0.6002	0.972297	0.453776	0.675424	0.26732	0.149664	-3.28957	-1.30433	-2.29695	1.403779	0.022146	-3.88977	-2.27663	-3.0832	1.140667	0.005156
TRCN0000008597	PPARGC1B	-5.52381	-4.51194	-2.86281	-4.29952	1.343159	0.000507	-2.44381	-2.08848	-2.26615	0.251255	0.019007	3.079999	2.423453	2.751726	0.464248	0.74336
TRCN0000008598	PPARGC1B	-2.78524	-1.68392	0.472774	-1.33213	1.657252	0.39443	-0.40472	-0.80342	-0.60407	0.281925	0.210398	2.380518	0.880497	1.630507	1.060675	0.685021
TRCN0000008599	PPARGC1B	-3.37663	-6.40947	-2.41098	-4.06569	2.086404	0.001712	0.347203	-5.69847	-2.67563	4.274933	0.042372	3.723829	0.710999	2.217414	2.130392	0.981386
TRCN0000008600	PPARGC1B	-4.14109	-1.03316	-0.97035	-2.0482	1.812766	0.118096	-5.24684	-4.22177	-4.73431	0.724835	0.000622	-1.10575	-3.18861	-2.14718	1.472801	0.015708
TRCN0000008601	PPARGC1B	-2.00041	-4.39638	-2.13087	-2.84256	1.347232	0.017439	-2.85426	-0.12729	-1.49077	1.92826	0.078837	-0.85384	4.269095	1.707626	3.622464	0.756767
TRCN0000009823	BRCA1	-2.7422	-2.57066	-1.92868	-2.41385	0.428832	0.036449	-1.0786	-1.33384	-1.20622	0.180481	0.091431	1.663601	1.236826	1.450213	0.301775	0.597089
TRCN0000009824	BRCA1	-2.76603	-2.6012	-1.77804	-2.38176	0.529291	0.039993	1.439617	-2.36208	-0.46123	2.688207	0.317155	4.205646	0.239117	2.222382	2.804759	0.984483
TRCN0000009825,TRCN0000312567	BRCA2,BRCA2	-2.30566	-1.59693	-4.10042	-2.66767	1.290408	0.025615	-5.73182	-1.52522	-3.62852	2.974519	0.007192	-3.42616	0.071715	-1.67722	2.47337	0.033089
TRCN0000009882	EP300	-0.41128	-3.82856	-10.5398	-4.92656	5.152779	0.006794	0.784525	-2.16689	-0.69118	2.086966	0.224973	1.195801	1.66167	1.428736	0.329419	0.587569
TRCN0000009883	EP300	-0.37149	-0.06347	0.295516	-0.04648	0.333828	0.541994	-1.24885	-1.43388	-1.34136	0.130834	0.075089	-0.87736	-1.3704	-1.12388	0.348635	0.044894
TRCN0000009884	EP300	0.612942	-2.00896	-2.03205	-1.14269	1.520468	0.511387	-4.00534	-1.48806	-2.7467	1.779987	0.013193	-4.61828	0.520909	-2.04869	3.633955	0.031349
TRCN0000010305	BRCA1	-10.872	-9.57048	-7.3517	-9.26473	1.779965	4.45E-08	1.079805	-5.75605	-2.33812	4.833678	0.075243	11.95183	3.814429	7.883128	5.75401	0.020066
TRCN0000010306	BRCA2	-2.72863	0.83082	-1.59531	-1.16437	1.818434	0.509368	0.517226	-2.66639	-1.07458	2.251158	0.14552	3.245856	-3.49721	-0.12568	4.76807	0.233909
TRCN0000010315	CCND1	-0.82376	-6.63697	-5.61965	-4.36013	3.104537	0.002555	-2.81686	-5.48303	-4.14994	1.885269	0.002065	-1.9931	1.153934	-0.41958	2.225288	0.119231
TRCN0000010316	CCND1	-3.01025	-1.64345	-4.62501	-3.0929	1.492498	0.010422	-2.83947	-0.89382	-1.86664	1.375781	0.040839	0.170779	0.749628	0.460204	0.409308	0.251768
TRCN0000010317	CCND1	-13.2936	-12.1101	-10.4044	-11.936	1.452417	6.04E-10	-9.73133	-7.01287	-8.3721	1.922242	1.99E-05	3.562233	5.097206	4.329719	1.08539	0.195505
TRCN0000010327	E2F1	0.16041	-2.4712	1.688142	-0.20755	2.103945	0.716982	-0.83072	2.807923	0.988602	2.572909	0.962567	-0.99113	5.279127	2.143999	4.433741	0.952905
TRCN0000010328	E2F1	-1.58019	-2.51908	0.12004	-1.32641	1.337737	0.383422	0.818337	-0.40315	0.207594	0.863722	0.549785	2.398531	2.115929	2.25723	0.19983	0.998701
TRCN0000010417	RB1	-0.66024	-0.07112	1.460239	0.242959	1.094575	0.360578	1.158386	1.958084	1.558235	0.565471	0.594281	1.818628	2.029205	1.923917	0.1489	0.82673
TRCN0000010419,TRCN0000295842	RB1,RB1	1.202467	-1.25422	0.606635	0.184959	1.28148	0.402806	0.656085	-0.29581	0.18014	0.673088	0.532295	-0.54638	0.958419	0.206018	1.064055	0.200485
TRCN0000010577,TRCN0000318417	PIN1,PIN1	-1.10909	0.222135	-2.15832	-1.01509	1.193009	0.595171	-0.68011	-1.54707	-1.11359	0.613033	0.106785	0.428985	-1.7692	-0.67011	1.554352	0.083283
TRCN0000010647	PPARD	-1.15453	-2.14729	-2.35082	-1.88421	0.640068	0.124893	-1.76907	-1.87901	-1.82404	0.077738	0.036702	-0.61454	0.268283	-0.17313	0.624252	0.131903
TRCN0000010774	ESR1	-5.48021	-2.59197	-9.24158	-5.77125	3.334343	0.000221	1.231135	-4.00169	-1.38528	3.700168	0.143815	6.711342	-1.40972	2.650809	5.74246	0.849662
TRCN0000010776	PGR	-0.2315	-3.82031	-2.58234	-2.21139	1.822936	0.08597	-1.47324	-4.10674	-2.78999	1.862169	0.012809	-1.24174	-0.28643	-0.76409	0.675503	0.068862
TRCN0000010853	PIAS1	-2.67324	-2.69931	-4.32151	-3.23136	0.944192	0.005558	-1.0619	-0.34279	-0.70234	0.508485	0.186434	1.611348	2.356524	1.983936	0.526919	0.858227
TRCN0000011027	CREBBP	-0.7041	-0.38461	3.250572	0.72062	2.196819	0.197345	0.341263	-1.82324	-0.74099	1.530531	0.195325	1.045366	-1.43863	-0.19663	1.756447	0.141002
TRCN0000011071	CARM1	-1.41399	-0.28842	-0.59166	-0.76469	0.582389	0.799549	-3.05436	-0.59407	-1.82421	1.739689	0.04754	-1.64037	-0.30564	-0.97301	0.943796	0.055511
TRCN0000011077,TRCN0000320445	UBE2I,UBE2I	-2.59459	-4.81478	0.319751	-2.36321	2.575076	0.087156	-5.3366	-0.57441	-2.9555	3.367379	0.020241	-2.74201	4.240376	0.749182	4.937294	0.447676
TRCN0000011078	UBE2I	-0.24734	1.172228	-0.75226	0.057543	0.997811	0.477642	-1.38028	-0.53281	-0.95655	0.599254	0.132824	-1.13294	-1.70504	-1.41899	0.404535	0.031975
TRCN0000011102	UBB	2.340571	-1.55677	0.56795	0.450583	1.951321	0.291275	0.808831	0.931396	0.870114	0.086666	0.961992	-1.53174	2.488168	0.478215	2.842504	0.300837
TRCN0000011107	UBC	-8.89787	-6.88965	-6.28493	-7.35749	1.367852	6.93E-07	-6.83007	-5.50058	-6.16532	0.940089	0.000117	2.067806	1.389073	1.72844	0.479937	0.728911
TRCN0000011108	UBC	-1.12845	-0.85042	-0.69312	-0.89066	0.220437	0.682674	0.84388	-2.39391	-0.77501	2.289461	0.210583	1.972328	-1.54349	0.214419	2.486059	0.229138
TRCN0000011109	UBC	-1.2439	-6.60442	-7.77847	-5.20893	3.483636	0.000762	-6.71525	-5.44589	-6.08057	0.897571	0.000127	-5.47135	1.158534	-2.15641	4.688037	0.039757
TRCN0000011111	UBC	-0.41389	-1.74755	-3.73681	-1.96608	1.672204	0.132579	-3.82334	-1.17871	-2.50103	1.870034	0.019213	-3.40945	0.568838	-1.42031	2.813074	0.047265
TRCN0000011218	CAV1	-0.04884	0.427268	-0.53061	-0.05073	0.47894	0.547107	-2.73416	-3.08002	-2.90709	0.244558	0.007308	-2.68532	-3.50728	-3.0963	0.581217	0.004701
TRCN0000013138	MLL2	-2.49346	-2.65356	-2.26395	-2.47032	0.195834	0.030991	-3.50067	-3.11643	-3.30855	0.271697	0.004076	-1.00721	-0.46287	-0.73504	0.384908	0.070145
TRCN0000013139	MLL2	-1.06334	1.799593	-1.8936	-0.38578	1.937583	0.857762	-1.33216	0.024321	-0.65392	0.959174	0.204899	-0.26882	-1.77527	-1.02205	1.065223	0.053151
TRCN0000013140	MLL2	-0.16422	-2.01335	-2.10893	-1.42883	1.096231	0.315813	-1.55935	-3.82591	-2.69263	1.602702	0.013372	-1.39513	-1.81256	-1.60385	0.295169	0.025671
TRCN0000013141	MLL2	0.205122	-1.03009	-2.79651	-1.20716	1.508628	0.466518	-1.36861	-3.568	-2.4683	1.555204	0.018112	-1.57373	-2.53791	-2.05582	0.681777	0.015568
TRCN0000013142	MLL2	-1.53472	-2.7195	-8.66636	-4.30686	3.821629	0.005706	-0.71788	1.423645	0.352884	1.514284	0.643221	0.816845	4.143149	2.479997	2.352052	0.889524
TRCN0000013358,TRCN0000280439	MTA1,MTA1	4.007952	-0.26487	-1.35966	0.794477	2.836275	0.208572	2.049159	-2.68312	-0.31698	3.346227	0.397116	-1.95879	-2.41826	-2.18852	0.324889	0.013021
TRCN0000013359	MTA1	2.627593	-1.02929	-0.36725	0.410352	1.94851	0.310233	-1.66889	-1.94536	-1.80712	0.195497	0.037758	-4.29648	-0.91607	-2.60627	2.390309	0.011868
TRCN0000013360	MTA1	-2.50283	-4.90398	-7.42932	-4.94538	2.463506	0.000374	-3.91983	-1.09244	-2.50613	1.999268	0.019992	-1.417	3.811547	1.197275	3.697139	0.554255
TRCN0000013361	MTA1	-2.12141	-0.86314	-2.30004	-1.76153	0.78314	0.163853	-2.68082	-2.42989	-2.55535	0.177439	0.012278	-0.55941	-1.56675	-1.06308	0.712296	0.049135
TRCN0000013362	MTA1	-3.95154	-8.40826	-8.35442	-6.90474	2.557687	8.65E-06	-7.9435	-5.73985	-6.84167	1.558217	7.29E-05	-3.99196	2.668415	-0.66177	4.709594	0.149926
TRCN0000013373	MTA2	4.19974	-0.33202	-1.35169	0.838678	2.955078	0.20157	0.411133	0.119798	0.265465	0.206005	0.575903	-3.78861	0.451817	-1.66839	2.998432	0.038289
TRCN0000013374	MTA2	-1.49616	0.750622	-0.05265	-0.26606	1.138492	0.739643	-5.48202	-2.42385	-3.95293	2.162454	0.003067	-3.98586	-3.17447	-3.58016	0.573739	0.002747
TRCN0000013375	MTA2	3.893608	-1.6175	1.49063	1.255579	2.763064	0.094741	-2.08501	-4.00305	-3.04403	1.356263	0.007484	-5.97862	-2.38555	-4.18208	2.540681	0.002408
TRCN0000013376	MTA2	-1.5071	-0.17992	-0.30079	-0.6626	0.733847	0.896087	-4.42465	-0.1722	-2.29843	3.006931	0.039001	-2.91755	0.007714	-1.45492	2.068473	0.03841
TRCN0000013377	MTA2	-1.24343	-4.83252	-3.0787	-3.05155	1.794697	0.013789	3.270066	-0.45917	1.405447	2.63697	0.722163	4.513495	4.373343	4.443419	0.099102	0.167918
TRCN0000013933,TRCN0000273927	ETV4,ETV4	-0.29997	-0.04545	0.439145	0.031241	0.375479	0.483159	-0.91033	-2.00837	-1.45935	0.776429	0.066167	-0.61036	-1.96292	-1.28664	0.956403	0.038871
TRCN0000013934	ETV4	-0.92039	-1.48874	-1.61529	-1.34147	0.370117	0.346961	-1.55156	-2.28479	-1.91818	0.518471	0.032697	-0.63117	-0.79606	-0.71361	0.11659	0.07142
TRCN0000013935	ETV4	-0.34237	-0.69799	1.334975	0.098205	1.085733	0.452183	-2.33484	1.276664	-0.52909	2.553718	0.28965	-1.99247	1.974653	-0.00891	2.805178	0.193649
TRCN0000013936	ETV4	-0.30722	-0.58434	0.252772	-0.21293	0.426448	0.682048	-0.71204	-3.57341	-2.14273	2.023293	0.033292	-0.40482	-2.98907	-1.69695	1.827341	0.027957
TRCN0000013937,TRCN0000273925	ETV4,ETV4	2.795743	-0.48722	-0.35756	0.650318	1.859123	0.204636	-1.14749	-1.59994	-1.37372	0.31993	0.072098	-3.94324	-1.11272	-2.52798	2.001478	0.011585
TRCN0000014878	FOXA1	1.044316	0.810518	1.799211	1.218015	0.516727	0.045764	-2.51025	-3.03688	-2.77357	0.372384	0.008992	-3.55457	-3.8474	-3.70099	0.207064	0.002347
TRCN0000014879	FOXA1	-2.06234	-0.36372	-0.71821	-1.04809	0.896071	0.561012	-6.79178	-0.90777	-3.84977	4.16062	0.010845	-4.72944	-0.54405	-2.63675	2.959513	0.013778
TRCN0000014880	FOXA1	1.294033	-1.54793	-0.68137	-0.31176	1.456589	0.78571	-1.35811	-2.45231	-1.90521	0.773717	0.034396	-2.65214	-0.90438	-1.77826	1.235855	0.022942
TRCN0000014881	FOXA1	-3.31509	-1.33706	-1.62171	-2.09129	1.069358	0.087119	-3.45089	-4.64979	-4.05034	0.84775	0.001584	-0.1358	-3.31273	-1.72426	2.24643	0.029761
TRCN0000014882	FOXA1	-2.58444	-0.55505	-2.81685	-1.98544	1.244199	0.113658	-8.31765	-4.95672	-6.63718	2.376538	0.00015	-5.73221	-4.40167	-5.06744	0.941541	0.00061
TRCN0000014913,TRCN0000329771	FOXA2,FOXA2	0.756509	4.183102	1.041236	1.993616	1.901488	0.013239	-0.30285	1.741594	0.719372	1.445639	0.866219	-1.05936	-2.44151	-1.75043	0.977328	0.022864
TRCN0000014914	FOXA2	1.206871	-2.33744	2.623535	0.497655	2.555398	0.304713	-1.92789	-3.78368	-2.85579	1.312243	0.009652	-3.13476	-1.44624	-2.2905	1.193963	0.012703
TRCN0000014915	FOXA2	1.252647	0.698276	-3.60141	-0.55016	2.656954	0.997775	-0.41474	-1.07427	-0.7445	0.466355	0.175884	-1.66739	-1.77254	-1.71997	0.074356	0.022306
TRCN0000014916	FOXA2	-1.42188	-0.76388	0.980455	-0.40177	1.241428	0.861936	-3.57447	-1.06119	-2.31783	1.777154	0.024061	-2.15259	-0.29731	-1.22495	1.311884	0.043531
TRCN0000014917	FOXA2	-3.30905	-3.38136	-2.61902	-3.10314	0.420822	0.00647	-0.31508	0.605992	0.145456	0.651297	0.513533	2.993966	3.987355	3.49066	0.702432	0.423772
TRCN0000015548	SMARCA4	-0.46987	1.018199	0.364927	0.304418	0.745878	0.314949	-0.21405	-0.52409	-0.36907	0.219238	0.28339	0.255825	-1.54229	-0.64323	1.271462	0.082951
TRCN0000015549	SMARCA4	-1.05366	1.335963	0.519944	0.267416	1.21466	0.350905	-2.68609	-0.18858	-1.43733	1.766002	0.081535	-1.63243	-1.52455	-1.57849	0.076285	0.026308
TRCN0000015550	SMARCA4	-0.52221	-1.30008	0.098367	-0.57464	0.700699	0.979389	-0.63078	-1.46429	-1.04754	0.589375	0.116955	-0.10858	-0.1642	-0.13639	0.039331	0.135334
TRCN0000015551	SMARCA4	-0.21706	-0.40963	-0.90242	-0.5097	0.353469	0.958196	-0.88607	-1.6748	-1.28043	0.557717	0.083821	-0.66901	-1.26517	-0.96709	0.42155	0.053923

Table D2. Log fold changes in shRNA abundance. See final page for full legend. (2/7)

		LOG2 CALCULATIONS															
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)						IN VIVO LOG2 - T4					
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val		REP1	REP2	AVG	STDEV	p-val	
TRCN0000015552	SMARCA4	-2.38217	-9.57048	-1.037	-4.32989	4.588052	0.010656	2.643562	-5.27898	-1.31771	5.60208	0.237263		5.025737	4.291501	4.658619	0.519183	0.134779	
TRCN0000017055	RNF4	-10.7419	-4.63017	-8.56448	-7.97886	3.097675	3.16E-06	-8.67412	-7.18686	-7.93049	1.051651	1.9E-05		2.067806	-2.55669	-0.24444	3.270009	0.166711	
TRCN0000017056,TRCN0000284821	RNF4,RNF4	-1.95035	0.014229	-0.44681	-0.79431	1.027354	0.777963	1.71912	0.094439	0.90678	1.148823	0.987355		3.669466	0.08021	1.874838	2.537988	0.81685	
TRCN0000017057	RNF4	-4.7657	-1.56877	-5.28493	-3.87313	2.012452	0.002477	-9.10733	-5.00741	-7.05737	2.899088	0.000143		-4.34164	-3.43863	-3.89014	0.63852	0.001976	
TRCN0000017093,TRCN0000274391	KDM3B,KDM3B	-3.06086	-1.34507	-3.65618	-2.68737	1.199969	0.023539	-0.74529	1.370447	0.312576	1.496055	0.619933		2.315568	2.715522	2.515545	0.28281	0.863065	
TRCN0000017094	KDM3B	-1.18863	-1.68212	-1.79541	-1.55539	0.322637	0.235225	0.240454	-0.52797	-0.14376	0.543359	0.373724		1.42908	1.154152	1.291616	0.194404	0.527856	
TRCN0000017095,TRCN0000274439	KDM3B,KDM3B	0.138119	-0.01243	-0.1279	-0.00074	0.133393	0.505113	-0.0601	1.041444	0.490672	0.77891	0.714632		-0.19822	1.053871	0.427826	0.885362	0.247585	
TRCN0000017096	KDM3B	-2.81155	-3.30315	-1.26721	-2.46064	1.062361	0.038024	-5.04358	-5.59374	-5.31866	0.389021	0.000279		-2.23203	-2.2906	-2.26131	0.041413	0.011879	
TRCN0000017097	KDM3B	-1.47816	-1.59957	-7.46166	-3.51313	3.420063	0.01718	-0.1649	-0.45257	-0.30873	0.203417	0.305082		1.313265	1.146996	1.23013	0.11757	0.502287	
TRCN0000018930	HMGB1	-0.67037	-0.20142	-0.13721	-0.33633	0.291057	0.793021	0.074085	0.610406	0.342245	0.379236	0.621246		0.744451	0.811823	0.778137	0.047639	0.339432	
TRCN0000018931	HMGB1	-4.38217	-6.47094	-3.73744	-4.86352	1.428906	0.000144	-2.31437	-2.57561	-2.44499	0.184725	0.014487		2.067806	3.895332	2.981569	1.292256	0.639674	
TRCN0000018932	HMGB1	-2.05154	-2.98802	-2.037	-2.35885	0.54492	0.042345	-2.95728	-3.71288	-3.33508	0.534286	0.004041		-0.90574	-0.72486	-0.8153	0.127905	0.06363	
TRCN0000018933	HMGB1	-1.99611	-4.12998	-2.23729	-2.78779	1.168608	0.018295	-2.36779	-3.29566	-2.83172	0.656101	0.00856		-0.37168	0.834325	0.231324	0.852772	0.203373	
TRCN0000018934	HMGB1	0.61439	-0.25366	-0.65512	-0.09813	0.64889	0.587822	-0.70915	-1.63623	-1.17269	0.655546	0.098576		-1.32354	-1.38256	-1.35305	0.041739	0.034196	
TRCN0000019009	HMGB2	-4.52871	-0.62754	-5.83981	-3.66535	2.711266	0.007212	-1.29182	-1.56174	-1.42678	0.190866	0.06637		3.236895	-0.9342	1.151347	2.949411	0.516222	
TRCN0000019010	HMGB2	0.315868	-0.80802	-2.0753	-0.85582	1.196303	0.727081	-0.45504	0.386219	-0.03441	0.594862	0.423313		-0.77091	1.194235	0.211662	1.389567	0.206044	
TRCN0000019011	HMGB2	1.470298	0.776523	0.496787	0.914536	0.501215	0.091426	-2.77203	-1.99365	-2.38284	0.550402	0.016393		-4.24233	-2.77017	-3.50625	1.040975	0.003178	
TRCN0000019012	HMGB2	1.308067	0.790649	0.087846	0.728854	0.612453	0.137989	-0.05621	0.384797	0.164293	0.311839	0.5205		-1.36428	-0.40585	-0.88507	0.677709	0.060051	
TRCN0000019013	HMGB2	-0.25592	0.646957	-0.09527	0.098588	0.481647	0.43659	0.3082	-0.77818	-0.23499	0.768187	0.339132		0.564123	-1.42514	-0.43051	1.40662	0.106058	
TRCN0000019189	HNF4A	0.214006	-2.57416	2.593344	0.077731	2.586445	0.535037	1.629933	2.148174	1.889053	0.366452	0.419718		1.415926	4.722331	3.069129	2.337981	0.617332	
TRCN0000019190	HNF4A	-2.19378	-2.71701	-1.85137	-2.25405	0.435955	0.053308	-1.84221	-0.70482	-1.27352	0.804259	0.0867		0.351572	2.012186	1.181879	1.174232	0.49074	
TRCN0000019191	HNF4A	-8.93352	-2.04936	-3.36075	-4.78121	3.655298	0.002045	-2.40428	-1.72353	-2.06391	0.481369	0.026203		6.529235	0.325828	3.427532	4.386471	0.534354	
TRCN0000019192	HNF4A	-5.46964	-0.21815	0.692775	-1.665	3.32624	0.326799	-4.61885	-5.45035	-5.0346	0.587963	0.000411		0.850788	-5.23221	-2.19071	4.301326	0.033915	
TRCN0000019193	HNF4A	-0.27821	2.860191	-0.10267	0.826437	1.763468	0.145047	-1.54373	-0.00164	-0.77268	1.090422	0.177839		-1.26551	-2.86183	-2.06367	1.128766	0.016289	
TRCN0000019194	MED23	0.355537	-0.36111	1.109884	0.368103	0.735578	0.281262	0.764644	3.482595	2.12362	1.921882	0.354749		0.409108	3.843707	2.126407	2.428628	0.937152	
TRCN0000019195	MED23	-0.23766	-0.16915	-0.77302	-0.39327	0.330646	0.846683	-0.254	-1.33804	-0.79602	0.76653	0.167318		-0.01635	-1.16889	-0.59262	0.814973	0.084235	
TRCN0000019196	MED23	0.121672	0.213661	0.324292	0.219875	0.101453	0.354064	-1.05193	-0.83207	-0.942	0.155463	0.132861		-1.1736	-1.04573	-1.10967	0.090417	0.04536	
TRCN0000019197	MED23	-4.7643	-4.92398	-7.14553	-5.61127	1.331105	2.39E-05	-9.06259	-0.65383	-4.85821	5.945892	0.010759		-4.29829	4.270148	-0.01407	6.058799	0.303196	
TRCN0000019198	MED23	2.582201	2.273914	1.175366	2.010494	0.739486	0.006839	2.14063	2.358811	2.249721	0.154277	0.273154		-0.44157	0.084897	-0.17834	0.372269	0.129985	
TRCN0000019239	HNF4G	-1.3701	0.962806	-6.28493	-2.23074	3.699723	0.166503	-7.52586	-3.76143	-5.64364	2.661855	0.000538		-6.15576	-4.72423	-5.43999	1.01224	0.000428	
TRCN0000019240	HNF4G	-3.148	1.118234	1.869886	-0.05329	2.706317	0.627715	-3.57587	-3.69115	-3.63351	0.081514	0.002538		-0.42787	-4.80938	-2.61863	3.098197	0.014715	
TRCN0000019241	HNF4G	0.24992	0.152103	-1.14392	-0.2473	0.778035	0.716794	-0.43397	1.018593	0.292312	1.027116	0.599532		-0.68389	0.86649	0.091301	1.096284	0.178789	
TRCN0000019242	HNF4G	-5.03308	-3.81958	-1.80806	-3.55357	1.62888	0.003815	1.690434	0.602211	1.146322	0.769489	0.85264		6.723511	4.421793	5.572652	1.627561	0.054638	
TRCN0000019243	HNF4G	-2.81453	-1.43225	-0.23103	-1.4926	1.292805	0.290515	-1.19969	-0.4693	-0.83449	0.516465	0.156183		1.614837	0.962954	1.288895	0.460951	0.52769	
TRCN0000019319	NR3C1	0.235483	-0.20766	-4.94826	-1.64014	2.873467	0.308462	-3.56868	-1.4635	-2.51609	1.488583	0.016572		-3.80416	-1.25585	-2.53	1.801929	0.010991	
TRCN0000019320	NR3C1	-4.64395	-3.03846	-9.89187	-5.85809	3.5844	0.000263	-3.45299	-2.63821	-3.0456	0.576139	0.006181		1.190963	0.400252	0.795608	0.559116	0.346887	
TRCN0000019321	NR3C1	-2.06025	-2.46673	-6.73744	-3.75481	2.591023	0.005388	-2.31437	-4.06472	-3.18954	1.237683	0.005864		-0.25412	-1.59799	-0.92605	0.950256	0.058577	
TRCN0000019365	NR3C2	-0.28551	-0.7007	-3.01952	-1.33524	1.473323	0.384015	2.387663	1.076931	1.732297	0.926827	0.503987		2.673171	1.777635	2.225403	0.63324	0.984559	
TRCN0000019366	NR3C2	-0.29366	0.353356	0.314045	0.12458	0.36274	0.417156	-1.84782	-4.2287	-3.03826	1.683539	0.008468		-1.55416	-4.58206	-3.06811	2.14105	0.006697	
TRCN0000019367	NR3C2	-2.42722	-5.53973	-2.6468	-3.53792	1.737091	0.004291	-3.76415	-5.81874	-4.79144	1.452814	0.000742		-1.33692	-0.27901	-0.80796	0.748057	0.06585	
TRCN0000019368	NR3C2	-2.39867	-1.63695	-1.65009	-1.89524	0.436034	0.119205	0.21644	-0.14724	0.034602	0.257158	0.453496		2.615109	1.489713	2.052411	0.795775	0.894295	
TRCN0000019425	NR4A1	-0.41811	0.182709	-0.61856	-0.28466	0.416974	0.746172	-1.01514	-0.7751	-0.89512	0.169733	0.141824		-0.59703	-0.95781	-0.77742	0.255112	0.06659	
TRCN0000019426	NR4A1	-0.63196	-0.72257	-0.35979	-0.57144	0.188814	0.982136	-0.75113	-0.88958	-0.82036	0.097895	0.156997		-0.11917	-0.16701	-0.14309	0.033823	0.134358	
TRCN0000019427	NR4A1	-5.45317	-1.55475	-0.11327	-2.37373	2.762546	0.09271	-2.0227	-2.1058	-2.06425	0.058759	0.025582		3.430466	-0.55105	1.439708	2.815357	0.626917	
TRCN0000019428	NR4A1	0.801222	0.139575	3.497155	1.479317	1.778538	0.038614	1.220271	0.183379	0.701825	0.733193	0.850082		0.419049	0.043805	0.231427	0.265338	0.199665	
TRCN0000019479	NR4A2	-3.87808	0.551945	-0.25397	-1.19337	2.359686	0.516937	0.561807	0.06146	0.311633	0.353799	0.603157		4.439884	-0.49049	1.974699	3.486298	0.872551	
TRCN0000019480	NR4A2	-0.79134	-0.30969	0.330532	-0.25683	0.5628	0.722422	-0.26843	0.242902	-0.01276	0.361564	0.43124		0.522912	0.552591	0.537751	0.020986	0.270472	
TRCN0000019483	NR4A2	1.069295	0.13792	1.124026	0.77708	0.554205	0.123857	0.542089	1.824666	1.183377	0.906919	0.829148		-0.52721	1.686746	0.57977	1.565501	0.296602	
TRCN0000019504	VDR	2.225528	-0.73482	-1.45924	0.010489	1.952176	0.548673	-2.62129	0.866073	-0.87761	2.465938	0.192662		-4.84682	1.600896	-1.62296	4.559222	0.062206	
TRCN0000019505	VDR	0.389612	0.550599	0.074841	0.338351	0.241986	0.28815	-1.25082	-1.0482	-1.14951	0.143274	0.099096		-1.64044	-1.5988	-1.61962	0.029439	0.025068	
TRCN0000019506,TRCN0000276542	VDR,VDR	-2.43166	-2.87713	-2.24329	-2.51736	0.32549	0.027957	-0.02687	-4.94067	-2.48377	3.474581	0.037617		2.404791	-2.06355	0.170621	3.159593	0.238621	
TRCN0000019507	VDR	-0.14566	0.414832	-0.88613	-0.20565	0.652551	0.678418	3.490662	-0.15053	1.670068	2.574708	0.58072		3.636318	-0.56536	1.53548	2.971033	0.670655	
TRCN0000019508	VDR	-0.69299	-0.32861	0.608463	-0.13771	0.6714	0.620826	-1.87787	-0.11093	-0.9944	1.249414	0.13512		-1.18488	0.217679	-0.4836	0.991759	0.096292	
TRCN0000019559	NR4A3	-0.33435	-0.44951	-0.56488	-0.44958	0.115265	0.899974	-1.13667	1.020531	-0.05807	1.52537	0.431591		-0.80232	1.470039	0.333861	1.606798	0.236021	
TRCN0000019560	NR4A3	-2.37871	2.042205	-3.96324	-1.43325	3.112359	0.421733	0.47784	-2.57167	-1.04692	2.156332	0.147717		2.856552	-4.61388	-0.87866	5.282392	0.140933	
TRCN0000019561	NR4A3	-1.15057	-1.63474	-1.06839	-1.28457	0.306033	0.381183	-1.27533	-1.24512	-1.26023	0.021363	0.08438		-0.12476	0.389624	0.132432	0.363724	0.180635	
TRCN0000019562	NR4A3	0.414564	0.369788	0.170766	0.318372	0.129777	0.297973	-1.24613	-1.62776	-1.43695	0.269851	0.065577		-1.6607	-1.99755	-1.82912	0.238189	0.019707	
TRCN0000019563	NR4A3	-0.24334	-7.0545	-5.84436	-4.38073	3.633818	0.004177	-2.85863	-5.29417	-4.0764	1.722183	0.002104		-2.6153	1.760331	-0.42748	3.094036	0.136271	
TRCN0000019599	NR5A1	-0.84536	-1.67047	-0.50049	-1.00544	0.601191	0.588991	1.831775	-3.51407	-0.84115	3.780084	0.256866		2.677134	-1.8436	0.416766	3.196643	0.296098	
TRCN0000019600	NR5A1	-0.04174	-1.43552	-0.42563	-0.6343	0.719938	0.922758	2.643381	0.260233	1.451807	1.68514	0.673896		2.685124	1.695753	2.190439	0.699591	0.966226	
TRCN0000019601	NR5A1	0.670988	-0.89494	0.068881	-0.05169	0.789898	0.553612	0.078872	-2.62091	-1.27102	1.909032	0.10516		-0.59212	-1.72596	-1.15904	0.801752	0.044335	
TRCN0000019602	NR5A1	-0.90354	-1.23079	-1.89382	-1.34272	0.504538	0.348294	-0.04467	-0.81422	-0.42945	0.544155	0.265388		0.858868	0.416563	0.637715	0.312757	0.298303	
TRCN0000019603	NR5A1	-1.6152	-0.56733	-1.02839	-1.07031	0.525192	0.536029	-1.52427	-2.74361	-2.13394	0.862209	0.024868		0.090937	-2.17628	-1.04267	1.603166	0.055682	
TRCN0000019639,TRCN0000319399	NCOA2,NCOA2	-3.35773	-2.56925	-5.98709	-3.97136	1.789638	0.001621	-8.1201	-0.85625	-4.48818	5.13632	0.009694		-4.76238	1.713005	-1.52469	4.578787	0.068376	
TRCN0000019640	NCOA2	-1.13745	-2.18628	-2.78076	-2.03483	0.832056	0.093381	-3.56351	-1.52828	-2.54589	1.439129	0.015642		-2.42606	0.658004	-0.88403	2.180763	0.072835	
TRCN0000019641	NCOA2	1.288032	1.125135	1.696697	1.369955	0.294456	0.030831	-0.23424	0.035525	-0.09936	0.190753	0.390412		-1.52227	-1.08961	-1.30594	0.305938	0.036311	
TRCN0000019642,TRCN0000319400	NCOA2,NCOA2	-4.55746	-2.41741	-0.41221	-2.46236	2.072988	0.057456	0.617896	-3.34353	-1.36282	2.801153	0.116366		5.175353	-0.92612	2.124614	4.314396	0.944153	
TRCN0000019643	NCOA2	-2.68433	-1.5167	-2.16039	-2.12047	0.584836	0.074003	-7.96142	0.990577	-3.48542	6.330017	0.044903		-5.27709	2.507276	-1.38491	5.504381	0.098231	
TRCN0000019649	MED24	-0.29974	-0.07024	0.62039	0.083469	0.478937	0.447063	0.69389	0.828159	0.761024	0.094942	0.888017		0.993629	0.898402	0.946016	0.067336	0.394835	
TRCN0000019650	MED24	-0.76721	-1.06132	-0.72622	-0.85158	0.182793	0.71741	-1.41187	-1.41777	-1.41482	0.004173	0.067351		-0.64466	-0.35645	-0.50055	0.203798	0.09088	
TRCN0000019651	MED24	-5.86637	-4.21239	1.282905	-2.93195	3.742685	0.05786	0.238082	-3.83545	-1.79868	2.880419	0.069699		6.104456	0.376947	3.240702	4.04996	0.590796	
TRCN0000019652	MED24	0.032227	-1.29452	-0.6916	-0.6513	0.66429	0.906418	-1.68822	-0.95319	-1.32071	0.519742	0.078857		-1.72045	0.341324	-0.68956	1.457891	0.080552	
TRCN0000019653	MED24	-2.3579	-4.29858	-0.24863	-2.3017	2.025559	0.077689	-0.05574	-2.5451	-1.30042	1.760247	0.097946		2.302162	1.753473	2.027817	0.387981	0.880773	
TRCN0000019654	NR5A2	-0.0983	-0.21306	0.129969	-0.06046	0.174617	0.551868	-1.3245	0.888301	-0.2181	1.564689	0.364311		-1.22621	1.101364	-0.06242	1.645841	0.159888	
TRCN0000019655	NR5A2	0.688847	0.277063	-0.2964	0.22317	0.49483	0.356222	-0.82593	-1.15347	-0.9897	0.231611	0.124524		-1.51477	-1.43054	-1.47265	0.059564	0.029756	
TRCN0000019656	NR5A2	-11.2845	-8.89309	-4.73744	-8.30503	3.312931	2.67E-06	-9.21674	-5.2602	-7.23847	2.797696	0.000111		2.067806	3.632888	2.850347	1.10668	0.699042	
TRCN0000019657	NR5A2	-3.56194	-0.87038	-2.17389	-2.20207	1.346001	0.074294	-2.89955	-1.29821	-2.09888	1.132317	0.02761		0.662396	-0.42783	0.117286	0.770903	0.180326	
TRCN0000019658	NR5A2	-1.82608	-0.17563	-2.43958	-1.48043	1.170886	0.291804	1.887086	0.688383	1.287734	0.847611	0.76144		3.713167	0.864015	2.288591	2.014654	0.983049	
TRCN0000019699	NCOA3	-1.14688	-2.09474	-1.58679	-1.60947	0.474336	0.214007	0.754798	0.626633	0.690716	0.090626	0.840881		1.901676	2.721371	2.311523	0.579611	0.970142	
TRCN0000019700	NCOA3	-1.27561	-0.04381	-2.96982	-1.42975	1.469078	0.3305	0.265097	-1.20613	-0.47052	1.040313	0.259889		1.540706	-1.16231	0.189196	1.911323	0.210744	
TRCN0000019701	NCOA3	-2.7219	-2.08251	-2.03044	-2.27828	0.385063	0.050046	-1.96188	-2.98945	-2.47566	0.7266	0.014647		0.760017	-0.90694	-0.07346	1.178715	0.151664	
TRCN0000019703	NCOA3	-5.43585	-3.91568	-2.43817	-3.9299	1.498889	0.001402	-4.48842	-3.83319	-4.16081	0.46332	0.001262		0.947423	0.082486	0.514954	0.611603	0.266857	
TRCN0000019724	NCOA4	-0.78751	-1.52893	-1.66722	-1.32788	0.47306	0.356634	-1.56368	-0.07386	-0.81877	1.053466	0.166723		-0.77618	1.455069	0.339447	1.577728	0.236768	
TRCN0000019725	NCOA4	2.815362	-1.07236	-0.91836	0.274879	2.20147	0.395124	-3.1546	0.003851	-1.57538	2.233363	0.076295		-5.96996	1.076215	-2.44687	4.982401	0.033738	
TRCN0000019726	NCOA4	-0.9307	-3.60355	-2.65418	-2.39614	1.354982	0.048807	-4.07582	-2.90988	-3.49285	0.824439	0.003411		-3.14512	0.693669	-1.22573	2.714434	0.05659	
TRCN0000019727	NCOA4	-3.40324	-3.5977	-3.14134	-3.38076	0.229007	0.00305	-5.42289	-5.83849	-5.63069	0.293875	0.000189		-2.01966	-2.2408	-2.13023	0.156369	0.013853	
TRCN0000019728	NCOA4	-1.28758	1.190198	0.603	0.168538	1.294766	0.413658	-0.55381	-1.037	-0.79541	0.341669	0.163364		0.733775	-2.2272	-0.74671	2.093726	0.083032	
TRCN0000019739	NR6A1	5.132962	-2.40328	-4.31835	-0.52956	4.996494	0.986649	-1.92744	-0.88462	-1.40603	0.737384	0.071151		-7.0604	1.518661	-2.77087	6.06631	0.037135	
TRCN0000019740	NR6A1	2.313307	0.286963	-0.02171	0.859521	1.26844	0.119087	2.934237	0.921241	1.927739	1.423403	0.420692		0.620931	0.634278	0.627605	0.009438	0.29484	
TRCN0000019743	NR6A1	-4.2739	-7.93198	-2.57643	-4.92743	2.736935	0.000538	1.231998	-0.91547	0.158265	1.518488	0.536801		5.505897	7.01651	6.261203	1.068165	0.023096	
TRCN0000019779,TRCN0000285495	NRIP1,NRIP1	-1.35907	-6.14311	-8.26101	-5.2544	3.535753	0.000746	-6.17336	-6.71687	-6.44511	0.38432	7.46E-05		-4.81429	-0.57375	-2.69402	2.998511	0.013153	
TRCN0000019780	NRIP1	-2.9047	-3.85239	-4.58796	-3.78168	0.843854	0.001316	-3.17079	-4.94774	-4.05927	1.256495	0.001777		-0.26609	-1.09536	-0.68073	0.586379	0.075255	
TRCN0000019781	NRIP1	0.841411	0.587066	-0.69343	0.245015	0.822609	0.350678	-5.06887	-1.19517	-3.13202	2.739121	0.011929		-5.91028	-1.78224	-3.84626	2.91897	0.003921	
TRCN0000019782	NRIP1	-1.26064	-3.03185	-0.75726	-1.68325	1.194737	0.203478	0.23187	0.207105	0.219487	0.017512	0.549707		1.49251	3.238957	2.365734	1.234925	0.942592	
TRCN0000019783	NRIP1	2.25563	1.989732	2.305967	2.183777	0.169921	0.00384	-1.15993	-0.65891	-0.90942	0.354276	0.139833		-3.41556	-2.64864	-3.0321	0.542294	0.005034	
TRCN0000019799	MED1	-3.96714	-5.25833	-6.90325	-5.37624	1.471605	4.66E-05	-2.00615	0.024512	-0.99082	1.435892	0.139516		1.960992	5.282841	3.621917	2.348902	0.40727	
TRCN0000019800	MED1	-5.63552	-8.33196	5.672654	-2.76494	7.43051	0.248816	-4.76287	-0.585	-2.67393	2.954199	0.023724		0.872648	7.746965	4.309807	4.860877	0.303183	
TRCN0000019801	MED1	-2.80037	-6.00598	-3.037	-3.94779	1.78637	0.001708	-8.15042	2.252667	-2.94888	7.356092	0.099298		-5.35005	8.258645	1.454299	9.622798	0.779189	
TRCN0000019802	MED1	-3.33774	-7.40505	-10.8731	-7.20528	3.771628	3.34E-05	-8.97565	-0.32196	-4.6488	6.119079	0.014304		-5.63791	7.08309	0.722591	8.995104	0.575896	
TRCN0000019803	MED1	1.018723	0.531431	0.093513	0.547889	0.462824	0.196105	-0.49385	-2.8651	-1.67948	1.676725	0.057218		-1.51258	-3.39653	-2.45455	1.332158	0.010807	
TRCN0000020099,TRCN0000281350	TGFB1I1,TGFB1I1	4.724139	-2.39513	1.084642	1.137882	3.559935	0.155833	-1.05512	-0.40194	-0.72853	0.461869	0.179643		-5.77926	1.993193	-1.89303	5.495955	0.064262	
TRCN0000020100,TRCN0000281352	TGFB1I1,TGFB1I1	-2.35666	-2.03671	-2.12822	-2.17386	0.16479	0.062735	-0.27687	-2.74874	-1.5128	1.747876	0.073261		2.079798	-0.71203	0.683884	1.974121	0.334521	
TRCN0000020101,TRCN0000281272	TGFB1I1,TGFB1I1	-6.59045	-2.98557	0.023522	-3.18416	3.311454	0.029012	-0.59525	-3.07883	-1.83704	1.756153	0.046907		5.995192	-0.09326	2.950966	4.305186	0.708665	
TRCN0000020103	TGFB1I1	0.248497	0.049816	0.189241	0.162518	0.102001	0.389998	-2.06678	-1.13213	-1.59945	0.660901	0.053222		-2.31528	-1.18194	-1.74861	0.801389	0.022468	

Table D2. Log fold changes in shRNA abundance. See final page for full legend. (3/7)

		LOG2 CALCULATIONS														
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)					IN VIVO LOG2 - T4				
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val	REP1	REP2	AVG	STDEV	p-val
TRCN0000020309	THRA	-1.58488	-2.56582	-1.81156	-1.98742	0.513575	0.098475	0.791065	1.391716	1.09139	0.424724	0.888008	2.375945	3.95754	3.166743	1.118356	0.556028
TRCN0000020310	THRA	-2.33453	-1.34118	-1.6852	-1.78697	0.504436	0.15058	-3.76845	-3.69667	-3.73256	0.050758	0.002206	-1.43392	-2.35549	-1.89471	0.651649	0.018709
TRCN0000020311	THRA	-4.43127	-1.90963	-0.47112	-2.27067	2.004608	0.081912	-5.17212	-2.11498	-3.64355	2.161724	0.004593	-0.74085	-0.20535	-0.4731	0.378657	0.094105
TRCN0000020312	THRA	-0.65646	-0.40803	-1.30532	-0.78994	0.4633	0.775289	1.451963	1.749184	1.600574	0.210167	0.567826	2.108423	2.157214	2.132819	0.034501	0.935604
TRCN0000020313	THRA	-4.50556	-7.79875	-2.51005	-4.93812	2.67075	0.000487	-6.66451	-3.9951	-5.32981	1.887563	0.000477	-2.15896	3.803649	0.822346	4.216199	0.444162
TRCN0000020344	THRB	-1.25323	-3.07075	-4.95984	-3.09461	1.853418	0.012979	-6.41892	-2.17117	-4.29505	3.003613	0.003236	-5.16569	0.899581	-2.13306	4.288795	0.035668
TRCN0000020345	THRB	-1.83359	-2.5737	-2.1221	-2.17646	0.373041	0.06336	2.414806	0.969629	1.692217	1.021895	0.526613	4.248393	3.543332	3.895863	0.498553	0.292518
TRCN0000020346	THRB	0.081195	0.519419	0.787861	0.462825	0.356716	0.229668	-0.40773	0.792369	0.192317	0.848601	0.541261	-0.48893	0.27295	-0.10799	0.538731	0.140945
TRCN0000020347	THRB	-2.80504	-2.75585	-4.26121	-3.27403	0.855274	0.004799	0.389242	-0.57072	-0.09074	0.678793	0.39866	3.194284	2.185129	2.689707	0.71358	0.775195
TRCN0000020348	THRB	0.728409	1.820886	1.863084	1.470793	0.64327	0.025571	-2.6671	1.140126	-0.76349	2.692117	0.228804	-3.39551	-0.68076	-2.03814	1.919619	0.01951
TRCN0000020369	RARA	1.22926	-4.87754	-10.1258	-4.59136	5.682933	0.01642	-3.15798	-4.1471	-3.65254	0.699414	0.002652	-4.38724	0.730441	-1.8284	3.618747	0.03885
TRCN0000020370,TRCN0000275552	RARA,RARA	0.596352	1.160051	0.934893	0.900099	0.28793	0.092479	1.83404	0.475298	1.154669	0.960776	0.848245	1.237688	-0.69375	0.271968	1.365735	0.218322
TRCN0000020371	RARA	-2.31786	-1.92176	-1.18297	-1.80753	0.576003	0.145405	-0.01593	-2.56701	-1.29147	1.803881	0.100049	2.30193	-0.64524	0.828343	2.083967	0.381426
TRCN0000020373,TRCN0000275554	RARA,RARA	1.680758	0.994285	-0.22978	0.815089	0.96779	0.122036	-0.76767	0.477369	-0.14515	0.880377	0.378074	-2.44843	-0.51692	-1.48267	1.365787	0.032765
TRCN0000020784	PIAS3	0.641634	0.963886	0.3924	0.665973	0.286519	0.152776	-0.28894	-1.18171	-0.73533	0.631284	0.179687	-0.93057	-2.1456	-1.53809	0.859151	0.028821
TRCN0000020785,TRCN0000274277	PIAS3,PIAS3	6.16967	0.286008	-0.13406	2.107207	3.52446	0.03164	-0.04494	0.134471	0.044767	0.12686	0.458014	-6.21461	-0.15154	-3.18307	4.287237	0.013175
TRCN0000020786,TRCN0000274276	PIAS3,PIAS3	-2.89197	0.177276	0.272226	-0.81416	1.800066	0.776383	-1.31845	-2.14357	-1.73101	0.583451	0.043473	1.573521	-2.32085	-0.37366	2.753736	0.135571
TRCN0000020787,TRCN0000274336	PIAS3,PIAS3	-0.76605	-1.82455	-1.33906	-1.30989	0.529854	0.368615	0.374174	0.014427	0.1943	0.254379	0.536433	1.140225	1.83898	1.489603	0.494095	0.615658
TRCN0000020788	PIAS3	0.636469	0.312308	-1.52971	-0.19365	1.168366	0.678292	-1.03851	-0.39893	-0.71872	0.452256	0.181929	-1.67498	-0.71123	-1.19311	0.681473	0.042228
TRCN0000021149	KDM3A	-0.10714	-1.27033	-2.61526	-1.33091	1.255159	0.377361	-1.72784	-0.90618	-1.31701	0.581	0.079674	-1.6207	0.364151	-0.62828	1.403503	0.085575
TRCN0000021150	KDM3A	-2.0525	-1.94573	-1.96068	-1.98631	0.057814	0.095699	-1.06204	-1.75407	-1.40806	0.489339	0.069307	0.990459	0.191656	0.591057	0.56484	0.286726
TRCN0000021151	KDM3A	-1.39752	-2.87807	-1.86589	-2.04716	0.756736	0.089634	0.255553	-0.512	-0.12822	0.542742	0.380421	1.653075	2.36607	2.009573	0.504164	0.871464
TRCN0000021152,TRCN0000329990	KDM3A,KDM3A	-1.17473	-1.82251	-2.86857	-1.95527	0.854688	0.111197	-7.00216	-2.10019	-4.55117	3.466223	0.003207	-5.82743	-0.27767	-3.05255	3.924272	0.012918
TRCN0000021153	KDM3A	-0.46677	0.964382	-1.3052	-0.26919	1.147616	0.742552	-2.11298	-3.2776	-2.69529	0.823511	0.010779	-1.64621	-4.24198	-2.9441	1.835487	0.007026
TRCN0000021195	RARB	4.076448	1.167959	-1.58297	1.220478	2.830076	0.103591	-4.95118	-2.72371	-3.83745	1.575053	0.00271	-9.02762	-3.89167	-6.45965	3.631666	0.000487
TRCN0000021196	RARB	-0.05204	0.476176	-0.97525	-0.1837	0.734618	0.660785	-2.69028	-2.03889	-2.36458	0.460607	0.016675	-2.63825	-2.51506	-2.57665	0.087105	0.00826
TRCN0000021197	RARB	-3.72019	-1.96948	-1.11894	-2.26954	1.326327	0.063824	-2.83603	-2.50521	-2.67062	0.233924	0.010368	0.884157	-0.53573	0.174213	1.004013	0.193464
TRCN0000021198	RARB	0.546318	-0.43256	-0.17901	-0.02175	0.508034	0.524957	-1.48538	-2.75645	-2.12092	0.898782	0.025516	-2.0317	-2.32389	-2.17779	0.206612	0.013125
TRCN0000021229	RARG	-2.7956	-1.70119	-2.77892	-2.42524	0.627097	0.03673	-1.62523	-2.78095	-2.20309	0.817218	0.022275	1.170366	-1.07976	0.045304	1.591079	0.177394
TRCN0000021231	RARG	-0.4412	-1.50517	0.213077	-0.57777	0.867228	0.976636	-5.32141	-2.97178	-4.14659	1.661438	0.001866	-4.88021	-1.46661	-3.17341	2.413779	0.006525
TRCN0000021232	RARG	-2.89813	-0.73409	-2.02985	-1.88736	1.089036	0.134002	-0.53412	-2.91776	-1.72594	1.685492	0.053752	2.364014	-2.18367	0.09017	3.215701	0.223884
TRCN0000021233	RARG	2.123825	-0.26677	-0.76618	0.363624	1.544695	0.313111	-0.1009	-1.09298	-0.59694	0.70151	0.216342	-2.22472	-0.82621	-1.52547	0.988896	0.029659
TRCN0000021604	NR1H4	-0.33696	-5.26222	-6.52886	-4.04268	3.27114	0.005594	-7.37506	-6.32848	-6.85177	0.740047	5.16E-05	-7.0381	-1.06626	-4.05218	4.222733	0.005671
TRCN0000021605	NR1H4	1.394955	1.141554	0.310931	0.949147	0.567047	0.085417	1.501999	0.761155	1.131577	0.523856	0.861399	0.107044	-0.3804	-0.13668	0.344674	0.135857
TRCN0000021606	NR1H4	-3.01062	-1.03391	-1.10173	-1.71542	1.122189	0.189106	-2.87166	-0.07476	-1.47321	1.977704	0.081706	0.138963	0.959149	0.549056	0.579959	0.275537
TRCN0000021607	NR1H4	-1.68136	-0.87959	-1.74763	-1.43619	0.48317	0.295513	-0.81187	-0.62707	-0.71947	0.130672	0.180038	0.869492	0.252519	0.561006	0.436266	0.277807
TRCN0000021608	NR1H4	2.365165	1.049997	1.028194	1.481119	0.765684	0.025729	1.24224	2.034155	1.638197	0.559969	0.549238	-1.12293	0.984158	-0.06938	1.489933	0.15638
TRCN0000021614	RXRA	2.653869	1.447972	0.948182	1.683341	0.876864	0.01626	-1.01115	-1.72829	-1.36972	0.507095	0.073381	-3.66502	-3.17626	-3.42064	0.345603	0.003215
TRCN0000021615	RXRA	-3.40297	-1.3777	-1.82239	-2.20102	1.064403	0.068507	-1.39364	-2.25495	-1.8243	0.609038	0.037963	2.009324	-0.87726	0.566033	2.041122	0.302817
TRCN0000021616	RXRA	-6.06443	-0.38774	1.791229	-1.55365	4.055535	0.422499	-2.89237	-4.98582	-3.93909	1.48029	0.002274	3.172065	-4.59807	-0.713	5.494316	0.167584
TRCN0000021617	RXRA	-3.29915	-3.25312	-8.00279	-4.85169	2.72903	0.000623	-7.47928	-6.1367	-6.80799	0.949347	5.77E-05	-4.18012	-2.88357	-3.53185	0.916797	0.003027
TRCN0000021618	RXRA	-0.15286	0.185635	0.685143	0.239306	0.421571	0.345401	-0.54133	-3.31126	-1.9263	1.958642	0.043935	-0.38847	-3.4969	-1.94268	2.197992	0.023166
TRCN0000021619	NR1I2	1.499096	-4.17071	-5.93145	-2.86769	3.882869	0.068927	0.605529	-4.03744	-1.71595	3.283072	0.087699	-0.89357	0.133278	-0.38014	0.726089	0.105907
TRCN0000021620	NR1I2	2.633564	-1.47281	-0.75321	0.135849	2.192804	0.477206	0.083432	-1.07971	-0.49814	0.822468	0.247205	-2.55013	0.393091	-1.07852	2.081173	0.058046
TRCN0000021621	NR1I2	-0.17638	-1.49655	0.552521	-0.37347	1.038658	0.833869	0.263715	-0.04803	0.107842	0.220437	0.490298	0.440094	1.448522	0.944308	0.713066	0.397395
TRCN0000021622	NR1I2	-4.10362	-6.10059	-0.36595	-3.52339	2.911019	0.011352	-0.92326	-3.58371	-2.25349	1.881221	0.027244	3.180354	2.516884	2.848619	0.469144	0.695979
TRCN0000021623	NR1I2	-2.07864	-1.55759	-0.33709	-1.32444	0.893881	0.368592	-0.24171	-3.40587	-1.82379	2.2374	0.054961	1.836929	-1.84828	-0.00568	2.605836	0.189179
TRCN0000021624	RXRB	-0.66612	-0.71073	-0.03046	-0.46911	0.380531	0.919181	-0.93656	-0.79482	-0.86569	0.100226	0.14754	-0.27044	-0.08408	-0.17726	0.131771	0.129565
TRCN0000021625	RXRB	-0.24525	-0.73094	-2.70169	-1.22596	1.300891	0.445419	-0.88969	0.151734	-0.36898	0.736401	0.288527	-0.64445	0.882675	0.119113	1.07984	0.183751
TRCN0000021627	RXRB	-3.86526	-1.35772	-1.48031	-2.23443	1.41367	0.070883	-2.7674	-0.46171	-1.61456	1.630372	0.061926	1.097854	0.89601	0.996932	0.142725	0.412926
TRCN0000021628	RXRB	0.289285	-0.26212	0.177423	0.068198	0.291476	0.455437	0.819811	-0.45342	0.183195	0.900312	0.537144	0.530526	-0.19131	0.16961	0.510413	0.188432
TRCN0000021634	NR1I3	-3.66164	-5.17741	-1.14073	-3.3266	2.039091	0.008741	0.050065	-1.09596	-0.52295	0.810365	0.239421	3.711706	4.081448	3.896577	0.261447	0.291188
TRCN0000021635	NR1I3	-1.14106	-0.02837	-0.41029	-0.52657	0.565384	0.974662	-1.74359	0.672509	-0.53554	1.708438	0.25688	-0.60253	0.700881	0.049175	0.921651	0.169377
TRCN0000021636	NR1I3	-2.35716	1.623671	-3.34701	-1.36017	2.63105	0.431713	2.943988	1.695543	2.319766	0.882784	0.257704	5.301153	0.071872	2.686512	3.69766	0.80779
TRCN0000021637	NR1I3	-4.37386	-0.32474	-4.15349	-2.9507	2.276811	0.023325	-0.12893	-4.15541	-2.14217	2.847152	0.04469	4.244927	-3.83067	0.207129	5.710309	0.337023
TRCN0000021638	NR1I3	1.694537	-0.70771	-0.7849	0.067308	1.40975	0.48546	-2.36973	-1.58964	-1.97968	0.551605	0.029933	-4.06427	-0.88193	-2.4731	2.250251	0.013161
TRCN0000021639	RXRG	-0.82797	-0.61807	-3.00048	-1.48217	1.319071	0.296796	-6.61815	-3.6705	-5.14432	2.084303	0.000665	-5.79017	-3.05243	-4.4213	1.935879	0.00152
TRCN0000021640	RXRG	-3.2989	-0.37763	-2.5683	-2.08161	1.520232	0.100854	-1.46085	-4.73286	-3.09685	2.31366	0.010202	1.83805	-4.35523	-1.25859	4.379309	0.082569
TRCN0000021641	RXRG	-2.31924	-0.43871	0.437731	-0.77341	1.408632	0.802922	-3.60448	-3.91154	-3.75801	0.217125	0.002143	-1.28524	-3.47283	-2.37904	1.546863	0.012278
TRCN0000021642	RXRG	-10.277	-7.61968	-7.77171	-8.55613	1.492249	9.44E-08	-8.20919	-4.57961	-6.3944	2.566498	0.000222	2.067806	3.04007	2.553938	0.687494	0.844018
TRCN0000021644	NR2C1	-0.64064	-1.40653	-3.32927	-1.79215	1.385174	0.172031	-1.05761	-3.37137	-2.21449	1.636075	0.026641	-0.41697	-1.96484	-1.1909	1.094513	0.044025
TRCN0000021645	NR2C1	-2.38217	0.782113	-0.70259	-0.76755	1.583144	0.811217	-0.57005	-0.93891	-0.75448	0.260823	0.172212	1.812127	-1.72102	0.045554	2.498312	0.195901
TRCN0000021646	NR2C1	-0.60369	-1.00783	-2.11833	-1.24329	0.784289	0.416873	-3.32058	-3.40307	-3.36182	0.058327	0.003738	-2.71689	-2.39524	-2.55606	0.22744	0.008486
TRCN0000021647	NR2C1	-1.46187	-1.42031	-1.02835	-1.30351	0.239198	0.368633	-2.09746	-2.20494	-2.1512	0.076001	0.022452	-0.63559	-0.78462	-0.71011	0.105385	0.071696
TRCN0000021648	NR2C1	-0.88358	-3.67282	-1.98454	-2.18031	1.404885	0.079287	0.114507	1.070308	0.592408	0.675853	0.778317	0.998092	4.743126	2.870609	2.648139	0.709834
TRCN0000021654	NR2C2	0.294139	-0.34763	0.8282	0.258238	0.588734	0.337289	-1.49565	0.093959	-0.70085	1.124023	0.195905	-1.78979	0.441585	-0.6741	1.57782	0.083174
TRCN0000021655	NR2C2	-3.17711	1.946586	-0.33668	-0.5224	2.566892	0.975777	-1.87817	-1.11665	-1.49741	0.538473	0.06107	1.298943	-3.06324	-0.88215	3.084528	0.087198
TRCN0000021656	NR2C2	-0.90247	-1.29372	0.544782	-0.55047	0.968481	0.997624	-0.98044	0.019998	-0.48022	0.707418	0.251057	-0.07797	1.313723	0.617875	0.984077	0.29816
TRCN0000021657	NR2C2	-0.01642	-6.33261	-9.74953	-5.36619	4.938001	0.002868	-7.86705	-6.98766	-7.42735	0.621829	2.74E-05	-7.85064	-0.65504	-4.25284	5.088053	0.007072
TRCN0000021658	NR2C2	-1.49888	-2.50671	-2.02322	-2.00961	0.504055	0.093689	-0.7318	-0.4818	-0.6068	0.176776	0.209183	0.767079	2.024913	1.395996	0.889423	0.576597
TRCN0000021669	NR2E1	5.54633	0.136235	-0.92504	1.585843	3.470686	0.074595	-2.18564	0.231394	-0.97712	1.709102	0.148478	-7.73197	0.095159	-3.81841	5.534616	0.012572
TRCN0000021670	NR2E1	-1.42937	-1.10182	-0.66844	-1.06654	0.38169	0.537003	-0.97081	-1.53284	-1.25182	0.397412	0.086388	0.458556	-0.43102	0.013769	0.629024	0.160914
TRCN0000021671	NR2E1	0.708992	1.700923	0.126012	0.845309	0.796256	0.110974	-5.0732	-1.21615	-3.14467	2.727348	0.011669	-5.78219	-2.91707	-4.34963	2.025947	0.001685
TRCN0000021672	NR2E1	1.20203	0.1536	0.387636	0.581089	0.550336	0.185022	0.13758	1.594422	0.866001	1.030143	0.960146	-1.06445	1.440822	0.188186	1.771495	0.207801
TRCN0000021673	NR2E1	0.705357	0.197028	0.015789	0.306058	0.357479	0.306592	-0.03123	-2.09874	-1.06498	1.461949	0.126938	-0.73659	-2.29577	-1.51618	1.102506	0.030394
TRCN0000021686,TRCN0000319299	SAP30,SAP30	0.925113	0.226475	0.561944	0.571178	0.349411	0.18585	-1.95199	-1.01937	-1.48568	0.659466	0.06285	-2.87711	-1.24584	-2.06147	1.153478	0.01639
TRCN0000021687,TRCN0000319371	SAP30,SAP30	0.71133	-0.2005	0.492993	0.334608	0.476101	0.293063	-1.68401	-0.20406	-0.94404	1.046485	0.140915	-2.39534	-0.00356	-1.19945	1.691245	0.04745
TRCN0000021688,TRCN0000319370	SAP30,SAP30	-1.466	-6.90002	-9.65171	-6.00591	4.16546	0.00043	-4.46686	-4.76047	-4.61366	0.207613	0.000671	-3.00086	2.139549	-0.43066	3.634819	0.149569
TRCN0000021699	NR2E3	-1.5629	-1.00667	-2.14869	-1.57275	0.571075	0.231276	-1.98036	-2.40501	-2.19269	0.300269	0.021286	-0.41746	-1.39834	-0.9079	0.693584	0.058575
TRCN0000021700	NR2E3	-3.38919	-1.63675	-2.037	-2.35432	0.918303	0.046561	-0.1839	-1.32358	-0.75374	0.805873	0.177557	3.205293	0.313173	1.759233	2.045038	0.756502
TRCN0000021701	NR2E3	-0.30755	2.48562	-1.73547	0.147534	2.147028	0.46745	-2.12203	0.412041	-0.85499	1.791858	0.175868	-1.81448	-2.07358	-1.94403	0.18321	0.017212
TRCN0000021702	NR2E3	-2.74241	-1.83693	-1.14912	-1.90949	0.799119	0.121274	-2.4916	-0.81999	-1.6558	1.182003	0.053058	0.250816	1.016938	0.633877	0.54173	0.298451
TRCN0000021703	NR2E3	4.52153	0.087335	0.342977	1.650614	2.48957	0.039403	2.441415	0.170921	1.306168	1.605482	0.759162	-2.08011	0.083586	-0.99826	1.529967	0.057865
TRCN0000021739	NR2F1	-2.55649	-2.52096	-3.78383	-2.95376	0.71908	0.010247	-2.77711	-6.04298	-4.41004	2.309315	0.001858	-0.22062	-3.52201	-1.87132	2.334438	0.025909
TRCN0000021740,TRCN0000322965	NR2F1,NR2F1	-1.7329	-3.82243	0.945545	-1.5366	2.390044	0.325653	-1.10531	0.620105	-0.2426	1.220051	0.345224	0.627592	4.44254	2.535066	2.697576	0.865547
TRCN0000021741,TRCN0000322963	NR2F1,NR2F1	0.925425	1.310403	0.029785	0.755204	0.657059	0.13136	-0.39085	-1.39159	-0.89122	0.707625	0.14646	-1.31628	-2.70199	-2.00913	0.979845	0.016984
TRCN0000021742,TRCN0000323042	NR2F1,NR2F1	-0.45008	-0.20099	-1.58272	-0.7446	0.736444	0.819525	-2.18531	-1.67591	-1.93061	0.360198	0.031664	-1.73523	-1.47492	-1.60507	0.184063	0.025549
TRCN0000021743	NR2F1	-1.22286	-0.55675	0.495491	-0.42804	0.866375	0.88253	-1.32545	-0.68889	-1.00717	0.450114	0.122638	-0.1026	-0.13214	-0.11737	0.020892	0.138127
TRCN0000021769	RBM39	-2.35666	-0.42168	-5.9463	-2.90821	2.803305	0.035213	0.569676	-0.54257	0.013551	0.786479	0.448744	2.926335	-0.1209	1.402719	2.154718	0.597763
TRCN0000021770	RBM39	1.134086	-3.15617	-2.9912	-1.67109	2.430758	0.26835	-2.97168	-3.76607	-3.36888	0.56172	0.003866	-4.10577	-0.6099	-2.35783	2.471949	0.015885
TRCN0000021771	RBM39	0.05485	-2.03202	-3.01813	-1.6651	1.569004	0.225542	1.976101	-2.46161	-0.24275	3.137933	0.41551	1.921251	-0.42959	0.745831	1.662296	0.346433
TRCN0000021773	RBM39	0.59076	0.879073	-0.56191	0.302643	0.762472	0.316349	-3.68519	-2.41984	-3.05252	0.894736	0.006503	-4.27595	-3.29892	-3.78743	0.690869	0.002221
TRCN0000022149	NR0B1	-3.38865	-3.9134	-6.78395	-4.69533	1.827728	0.000316	-4.58537	-5.06131	-4.82334	0.336541	0.000518	-1.19671	-1.14791	-1.17231	0.03451	0.042174
TRCN0000022150	NR0B1	-0.72301	0.023938	-1.51469	-0.73792	0.769422	0.826012	-4.8177	-3.70007	-4.25888	0.790282	0.001179	-4.09469	-3.72401	-3.90935	0.262109	0.001876
TRCN0000022151	NR0B1	-1.79933	-2.21525	-0.98638	-1.66699	0.625035	0.193889	-1.27555	0.110721	-0.58241	0.980243	0.224903	0.523775	2.325973	1.424874	1.274347	0.593363
TRCN0000022152	NR0B1	0.788541	1.700106	1.749226	1.412624	0.54103	0.028825	0.114122	-0.29363	-0.08975	0.288321	0.395192	-0.67442	-1.99373	-1.33408	0.932894	0.036724
TRCN0000022153	NR0B1	-0.25203	-5.16672	-1.78474	-2.40116	2.514664	0.079142	0.515865	-1.5627	-0.52342	1.46977	0.253626	0.767897	3.604021	2.185959	2.005442	0.965501
TRCN0000022154	RORA	-0.68979	-1.41387	-0.89737	-1.00034	0.372863	0.590097	-0.04413	1.406808	0.681337	1.025971	0.838417	0.645654	2.820681	1.733167	1.537976	0.738477
TRCN0000022155	RORA	0.657483	0.580846	0.46112	0.566483	0.098966	0.185817	-0.56266	-0.67989	-0.62128	0.082896	0.205013	-1.22014	-1.26074	-1.24044	0.028705	0.038972
TRCN0000022156	RORA	-3.25447	-1.37384	-2.15824	-2.26218	0.944613	0.057876	-0.48724	-0.19626	-0.34175	0.205759	0.293029	2.767225	1.177584	1.972404	1.124046	0.854204
TRCN0000022157	RORA	-2.17886	-2.2518	-11.7152	-5.38194	5.484852	0.004653	-4.81393	0.263927	-2.275	3.590587	0.050538	-2.63507	2.515728	-0.05967	3.642162	0.208432
TRCN0000022158	RORA	-1.30039	0.464864	0.012277	-0.27442	0.916884	0.742992	-2.65603	-3.33313	-2.99458	0.478781	0.006571	-1.35564	-3.79799	-2.57681	1.727004	0.010249
TRCN0000022169	RORB	-0.5028	-0.14311	0.32946	-0.10548	0.417402	0.590434	-4.25207	-3.84837	-4.05022	0.285457	0.001437	-3.74927	-3.70526	-3.72727	0.03112	0.002272
TRCN0000022170	RORB	-1.0169	-0.46142	1.492407	0.004695	1.317993	0.526553	-4.27815	-2.51581	-3.39698	1.246163	0.00439	-3.26125	-2.05439	-2.65782	0.853381	0.007954

Table D2. Log fold changes in shRNA abundance. See final page for full legend. (4/7)

		LOG2 CALCULATIONS															
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)					IN VIVO LOG2 - T4				
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val	REP1	REP2	AVG	STDEV	p-val
TRCN0000022171	RORB	1.005169	1.016293	0.085303	0.702255	0.534325	0.144538	0.682737	-0.45261	0.115062	0.802813	0.499722	-0.32243	-1.4689	-0.89567	0.810679	0.059907
TRCN0000022172	RORB	-0.80917	-3.56638	-3.17847	-2.518	1.492549	0.039312	0.425231	-2.33614	-0.95545	1.952581	0.159324	1.234401	1.230239	1.23232	0.002943	0.5031
TRCN0000022173	RORB	0.695796	0.777605	-0.18667	0.428909	0.534676	0.247597	-2.37127	-0.83269	-1.60198	1.08794	0.056359	-3.06706	-1.61029	-2.33868	1.030092	0.011723
TRCN0000022174	NR1D1	-9.8327	-0.76764	-1.24789	-3.94941	5.100735	0.027327	-1.91662	-0.81831	-1.36747	0.776622	0.075553	7.916074	-0.05068	3.932698	5.633344	0.425017
TRCN0000022175	NR1D1	-6.29865	-1.05842	-7.34078	-4.89929	3.366853	0.001192	-9.19137	-6.65303	-7.9222	1.794882	2.8E-05	-2.89272	-5.59461	-4.24366	1.910521	0.001807
TRCN0000022176	NR1D1	0.460274	-0.12817	0.643352	0.325153	0.403117	0.296932	-1.8273	-0.06629	-0.94679	1.245225	0.143926	-2.28757	0.061882	-1.11285	1.661316	0.051982
TRCN0000022177	NR1D1	-5.45718	-1.08669	-3.20693	-3.25027	2.185564	0.011519	-2.56955	0.542046	-1.01375	2.200233	0.155292	2.887623	1.628739	2.258181	0.890166	0.998217
TRCN0000022178	NR1D1	0.316542	0.699521	0.457086	0.49105	0.193735	0.216074	0.334785	-1.37737	-0.52129	1.210678	0.247737	0.018243	-2.07689	-1.02933	1.481485	0.055515
TRCN0000022179,TRCN0000330189	ESRRA,ESRRA	0.351918	-0.70272	-0.22989	-0.19357	0.528258	0.666254	-1.05723	-1.84552	-1.45138	0.557411	0.065429	-1.40914	-1.1428	-1.27597	0.188332	0.037471
TRCN0000022180	ESRRA	-6.32202	-2.19953	-2.35893	-3.62682	2.335464	0.005685	-0.23497	-1.20667	-0.72082	0.687094	0.183847	6.087048	0.99286	3.539954	3.602135	0.471172
TRCN0000022181,TRCN0000330191	ESRRA,ESRRA	-5.09263	-2.39936	-0.99543	-2.82914	2.082134	0.026836	-0.00766	-0.29612	-0.15189	0.20397	0.367586	5.084964	2.10324	3.594102	2.108398	0.410666
TRCN0000022182	ESRRA	0.791063	-1.01729	-0.54276	-0.25633	0.937586	0.727372	-1.14223	-1.65303	-1.39763	0.361193	0.069777	-1.93329	-0.63574	-1.28452	0.917504	0.038813
TRCN0000022183,TRCN0000353645	ESRRA,ESRRA	-9.72825	-6.36403	-9.74609	-8.61279	1.947504	1.65E-07	-8.60062	-1.00583	-4.80322	5.370327	0.00815	1.127627	5.358196	3.242912	2.991464	0.561229
TRCN0000022189	NR1D2	-0.15929	-0.65223	-0.38791	-0.39981	0.246685	0.852609	0.676193	1.665935	1.171064	0.699854	0.835987	0.835481	2.318163	1.576822	1.048414	0.659706
TRCN0000022190	NR1D2	0.040815	1.801566	-3.99015	-0.71592	2.96909	0.878279	-3.17308	-2.83684	-3.00496	0.237755	0.006326	-3.21389	-4.63841	-3.92615	1.007285	0.002007
TRCN0000022191	NR1D2	-3.74064	-2.91243	-2.33832	-2.99713	0.704987	0.009145	-7.55634	-3.66155	-5.60895	2.754036	0.000596	-3.8157	-0.74912	-2.28241	2.168402	0.015847
TRCN0000022192	NR1D2	0.226094	-0.52025	-0.81659	-0.37025	0.537282	0.826105	1.751876	0.05038	0.901128	1.203139	0.983659	1.525781	0.570629	1.048205	0.675395	0.434273
TRCN0000022193	NR1D2	-0.32646	-0.813	-1.18322	-0.77423	0.429693	0.789563	0.984795	0.139521	0.562158	0.597699	0.758373	1.311257	0.952518	1.131887	0.253667	0.463542
TRCN0000022204	ESRRB	-2.33816	-1.25788	-3.4862	-2.36074	1.114333	0.048627	-4.92497	-2.77977	-3.85237	1.516883	0.002593	-2.58681	-1.5219	-2.05435	0.753007	0.015703
TRCN0000022205	ESRRB	1.335619	1.330602	0.556592	1.074271	0.44833	0.063355	-0.6628	-1.02319	-0.843	0.254829	0.152678	-1.99842	-2.35379	-2.17611	0.251282	0.01317
TRCN0000022206	ESRRB	-0.92148	-0.82809	0.533312	-0.40542	0.814305	0.86105	0.32333	0.654259	0.488795	0.234003	0.710038	1.244808	1.482354	1.363581	0.167971	0.558512
TRCN0000022207	ESRRB	-2.91771	-3.32725	-2.97931	-3.07476	0.220821	0.006743	-8.96297	0.641563	-4.1607	6.791428	0.030308	-6.04526	3.968808	-1.03822	7.081012	0.178353
TRCN0000022214,TRCN0000275310	NR1H2,NR1H2	0.631303	1.412214	-0.98967	0.351284	1.225179	0.305686	-4.28589	-1.45732	-2.87161	2.0001	0.012082	-4.9172	-2.86954	-3.89337	1.447914	0.002284
TRCN0000022215,TRCN0000275326	NR1H2,NR1H2	1.254591	1.95302	0.009596	1.072402	0.984438	0.070524	-3.76004	1.065076	-1.34748	3.411873	0.139057	-5.01463	-0.88794	-2.95129	2.918009	0.009792
TRCN0000022216	NR1H2	5.983051	-0.17743	-1.35019	1.485144	3.93919	0.107771	0.033486	-0.96441	-0.46546	0.705621	0.255715	-5.94956	-0.78698	-3.36827	3.650495	0.008502
TRCN0000022217,TRCN0000282024	NR1H2,NR1H2	-0.916	0.13035	-1.00568	-0.59711	0.631593	0.957857	-1.87532	-1.03772	-1.45652	0.59227	0.065145	-0.95931	-1.16807	-1.06369	0.147614	0.047867
TRCN0000022218	NR1H2	-0.04677	0.033893	0.338946	0.108691	0.203444	0.426392	1.770461	1.121216	1.445838	0.459086	0.65987	1.817227	1.087323	1.452275	0.51612	0.598886
TRCN0000022234	NR1H3	-1.94778	-2.18338	-2.6045	-2.24522	0.332699	0.053779	-1.37718	-0.02343	-0.7003	0.957251	0.192925	0.570594	2.159957	1.365275	1.123849	0.565698
TRCN0000022235	NR1H3	-2.43679	0.20296	-1.62014	-1.28466	1.351474	0.409602	0.822164	-1.30173	-0.23979	1.501822	0.353828	3.258954	-1.50469	0.87713	3.368408	0.433272
TRCN0000022236	NR1H3	-0.22683	-0.32991	0.080724	-0.15867	0.213635	0.633344	1.942493	-0.86412	0.539189	1.984572	0.761612	2.169325	-0.5342	0.817561	1.911683	0.374044
TRCN0000022237	NR1H3	0.544778	0.868975	4.981374	2.131709	2.4732	0.014573	1.747407	2.737943	2.242675	0.700415	0.28037	1.202629	1.868969	1.535799	0.471173	0.636779
TRCN0000022238	NR1H3	-0.95033	-0.41153	-0.31583	-0.55923	0.342065	0.993985	-0.33995	-2.23675	-1.28835	1.34124	0.091789	0.610383	-1.82522	-0.60742	1.722229	0.091116
TRCN0000026415,TRCN0000276460	ALDH1A1,ALDH1A1	1.68003	1.259619	0.95762	1.29909	0.362819	0.036899	-0.96826	-1.19247	-1.08036	0.158538	0.109388	-2.64829	-2.45208	-2.55019	0.138737	0.008523
TRCN0000026417	ALDH1A1	2.719363	-4.50967	-2.59159	-1.46063	3.744869	0.447172	-2.41994	-3.98597	-3.20295	1.107353	0.005535	-5.1393	0.523704	-2.3078	4.004348	0.027441
TRCN0000026482,TRCN0000276459	ALDH1A1,ALDH1A1	-1.79138	-1.13297	-2.66854	-1.86429	0.770379	0.132651	-2.44179	-1.47199	-1.95689	0.685749	0.031472	-0.65041	-0.33902	-0.49472	0.220182	0.091501
TRCN0000026498,TRCN0000276461	ALDH1A1,ALDH1A1	0.637953	0.44118	-0.67029	0.136282	0.705404	0.415567	0.921346	-1.265	-0.17183	1.545982	0.382696	0.283394	-1.70618	-0.71139	1.406842	0.078161
TRCN0000026502	ALDH1A1	-1.64229	-0.57355	-2.02415	-1.41333	0.751916	0.313519	-0.97684	-0.61004	-0.79344	0.259363	0.163367	0.665454	-0.03649	0.314482	0.49635	0.218275
TRCN0000027144	ALDH1A3	2.042747	1.292754	-0.3129	1.007534	1.203444	0.086033	-5.21863	-4.31156	-4.76509	0.641399	0.000586	-7.26138	-5.60431	-6.43284	1.171725	0.000175
TRCN0000027160	ALDH1A3	-11.4972	-6.7571	-5.037	-7.76377	3.34569	6.78E-06	-6.81492	-6.26158	-6.53825	0.391274	6.73E-05	4.682298	0.495522	2.58891	2.960497	0.842722
TRCN0000027171	ALDH1A3	-11.3694	-5.20895	-10.7478	-9.10873	3.391586	8.87E-07	-8.6183	-5.66372	-7.14101	2.089209	7.34E-05	2.751135	-0.45477	1.148182	2.266917	0.497848
TRCN0000027183	ALDH1A3	-3.44646	-7.54273	-8.58004	-6.52308	2.714436	2.24E-05	-8.50994	-5.53536	-7.02265	2.103348	8.36E-05	-5.06348	2.007376	-1.52805	4.999847	0.076433
TRCN0000027212	ALDH1A3	-0.5998	-1.06433	-0.62495	-0.76303	0.26124	0.799102	4.1045	2.074296	3.089398	1.435571	0.100071	4.704299	3.138627	3.921463	1.107098	0.291507
TRCN0000029204,TRCN0000342682	PHB,PHB	-4.83529	-10.0954	-7.85079	-7.59383	2.639469	2.85E-06	-2.74209	-6.12744	-4.43477	2.393806	0.001892	2.093195	3.967987	3.030591	1.325678	0.617943
TRCN0000029205	PHB	-1.69497	-2.80234	0.177157	-1.44005	1.506017	0.326701	-3.66246	-2.67023	-3.16634	0.701612	0.0053	-1.96749	0.13211	-0.91769	1.484644	0.062874
TRCN0000029206,TRCN0000342746	PHB,PHB	-5.22766	-4.55204	-5.037	-4.9389	0.348332	5.97E-05	-4.32125	-2.55346	-3.43736	1.250022	0.004154	0.90641	1.998583	1.452497	0.772283	0.60061
TRCN0000029207,TRCN0000342747	PHB,PHB	-8.41743	-6.56589	0.663436	-4.7733	4.798498	0.006327	-4.06684	-2.90676	-3.4868	0.820303	0.003437	4.350592	3.659132	4.004862	0.488936	0.263387
TRCN0000029208,TRCN0000342748	PHB,PHB	-2.38217	-9.10416	-3.49644	-4.99426	3.602619	0.001304	-0.31437	-6.44418	-3.37927	4.334432	0.020053	2.067806	2.659978	2.363892	0.418728	0.942504
TRCN0000033644	ESRRG	0.806491	-0.08879	-0.04016	0.225846	0.503441	0.354761	0.628834	-0.53142	0.048705	0.820427	0.466451	-0.17766	-0.44263	-0.31014	0.187366	0.112172
TRCN0000033645	ESRRG	-3.55259	-5.88506	0.733514	-2.90138	3.356997	0.049301	-3.79501	-1.2996	-2.54731	1.764523	0.017353	-0.24243	4.585458	2.171516	3.413829	0.961744
TRCN0000033646	ESRRG	5.259258	0.570376	0.235939	2.021858	2.808653	0.023052	0.939791	1.278559	1.109175	0.239546	0.875735	-4.31947	0.708183	-1.80564	3.555085	0.038996
TRCN0000033647	ESRRG	-0.43562	-0.18154	1.139732	0.17419	0.845779	0.394621	-1.78954	-3.01243	-2.40099	0.864716	0.016763	-1.35392	-2.8309	-2.09241	1.044384	0.01557
TRCN0000033648	ESRRG	0.086198	0.414842	-0.12003	0.128216	0.271705	0.413714	-3.38064	-0.6116	-1.99612	1.958007	0.0399	-3.46684	-1.03008	-2.24846	1.723046	0.014762
TRCN0000033649	NR0B2	-2.14254	-3.19792	-9.10309	-4.81452	3.751315	0.002133	-0.8119	-1.93244	-1.37217	0.792339	0.075181	1.330639	1.265484	1.298061	0.046072	0.530366
TRCN0000033650	NR0B2	-0.77545	0.811849	-2.72053	-0.89471	1.769207	0.709477	-2.99583	0.742363	-1.12674	2.643304	0.148749	-2.22039	-0.06949	-1.14494	1.520915	0.049078
TRCN0000033651	NR0B2	-1.64861	-0.87942	-1.07548	-1.20117	0.399703	0.437741	-0.23064	-2.27224	-1.25144	1.44363	0.098344	1.417975	-1.39282	0.01258	1.987529	0.178709
TRCN0000033653	NR0B2	-0.40101	-2.31013	-2.62751	-1.77955	1.20435	0.169768	-1.62108	-0.55493	-1.08801	0.75388	0.112066	-1.22007	1.755193	0.267562	2.103827	0.231392
TRCN0000033654	RORC	-2.02439	-0.10397	1.046793	-0.36052	1.551585	0.829756	1.50892	0.926901	1.217911	0.41155	0.80393	3.533315	1.030867	2.282091	1.769498	0.986145
TRCN0000033655	RORC	0.420734	-0.73284	1.642826	0.443573	1.187998	0.259221	-0.80829	-2.89243	-1.85036	1.47371	0.042789	-1.22902	-2.15959	-1.69431	0.65801	0.023613
TRCN0000033656	RORC	-4.8126	-2.92579	-4.497	-4.07846	1.01064	0.000686	-8.13518	-0.88778	-4.51148	5.124689	0.009407	-3.32258	2.038012	-0.64228	3.79051	0.126946
TRCN0000033657	RORC	-0.22785	-0.81173	0.379123	-0.22015	0.595462	0.6903	1.471207	1.577524	1.524366	0.075178	0.611392	1.699054	2.389252	2.044153	0.488044	0.889421
TRCN0000033658	RORC	-7.64584	-8.43064	-2.30206	-6.12618	3.33495	0.000115	-8.16299	-4.26525	-6.21412	2.756116	0.000308	-0.51716	4.165381	1.824112	3.311054	0.802946
TRCN0000033659	NR2F6	-6.9439	-4.71597	-3.55739	-5.07242	1.721162	0.00012	-1.62029	-0.36737	-0.99383	0.885953	0.129375	5.323607	4.348606	4.836107	0.68943	0.112068
TRCN0000033660,TRCN0000292069	NR2F6,NR2F6	3.077257	-0.34816	-5.26197	-0.84429	4.191693	0.817036	-2.7738	-0.50771	-1.64075	1.602369	0.059312	-5.85106	-0.15955	-3.0053	4.024502	0.014064
TRCN0000033661,TRCN0000292068	NR2F6,NR2F6	-2.01835	-2.72003	-6.6392	-3.79253	2.490131	0.004545	-4.50034	-2.79848	-3.64941	1.203395	0.003047	-2.48198	-0.07845	-1.28022	1.699553	0.043435
TRCN0000033662,TRCN0000292067	NR2F6,NR2F6	-8.10327	-3.12925	1.355313	-3.2924	4.731404	0.056432	-3.33503	-0.95433	-2.14468	1.683404	0.029827	4.768246	2.174915	3.47158	1.833762	0.447473
TRCN0000033663	NR2F6	0.811912	0.322175	0.957898	0.697328	0.332991	0.143552	0.198966	-0.45258	-0.1268	0.46071	0.38018	-0.61295	-0.77475	-0.69385	0.114413	0.073035
TRCN0000035929,TRCN0000290478	PRMT1,PRMT1	-3.26236	-3.83394	-1.7561	-2.9508	1.073383	0.011823	-3.49087	-1.58295	-2.53691	1.3491	0.015432	-0.22851	2.250985	1.011238	1.753267	0.436229
TRCN0000035930	PRMT1	0.135719	0.621726	0.40894	0.388795	0.243629	0.262726	-0.5757	-1.28612	-0.93091	0.502342	0.136752	-0.71142	-1.90784	-1.30963	0.846001	0.037446
TRCN0000035931,TRCN0000290479	PRMT1,PRMT1	-12.2103	-3.41031	3.335948	-4.09489	7.795706	0.083956	-2.27489	-5.23041	-3.75265	2.08987	0.00384	9.935426	-1.8201	4.057665	8.31241	0.489434
TRCN0000035932	PRMT1	4.526718	-3.03461	-4.5063	-1.00473	4.846562	0.742751	-0.75944	-0.47096	-0.6152	0.203986	0.206992	-5.28616	2.563651	-1.36125	5.550652	0.101289
TRCN0000035933	PRMT1	1.642914	1.094404	-3.22912	-0.16394	2.668662	0.703938	0.429084	-3.4469	-1.50891	2.740731	0.095734	-1.21383	-4.5413	-2.87756	2.352877	0.008768
TRCN0000039658,TRCN0000332899	E2F1,E2F1	2.615989	-2.07605	-2.31683	-0.5923	2.781063	0.969772	-1.01958	-2.75221	-1.8859	1.225152	0.038402	-3.63557	-0.67616	-2.15587	2.09262	0.017857
TRCN0000039659,TRCN0000332897	E2F1,E2F1	-0.14259	-5.18149	-3.14635	-2.82348	2.534922	0.035412	-5.42478	-6.36752	-5.89615	0.666613	0.000147	-5.28219	-1.18602	-3.23411	2.896431	0.007252
TRCN0000039660,TRCN0000332963	E2F1,E2F1	-7.88997	-2.34562	1.092279	-3.04777	4.532103	0.0724	-0.15885	-3.62082	-1.88983	2.447982	0.053841	7.73112	-1.2752	3.227959	6.368432	0.659695
TRCN0000039661,TRCN0000332898	E2F1,E2F1	-7.03725	-1.44705	-1.60589	-3.3634	3.182638	0.019049	-2.22837	-1.8335	-2.03094	0.279217	0.027102	4.808876	-0.38645	2.211215	3.673647	0.980354
TRCN0000039662	E2F1	-1.40997	-0.88548	0.71275	-0.52757	1.105696	0.976394	-0.56523	-2.40557	-1.4854	1.301312	0.069186	0.844741	-1.52009	-0.33767	1.672187	0.120587
TRCN0000039833	BRCA1	-4.84844	-4.43181	-1.55106	-3.61044	1.795595	0.003788	-0.7817	-1.02096	-0.90133	0.169178	0.140611	4.066739	3.410848	3.738794	0.463785	0.338487
TRCN0000039834	BRCA1	-9.44253	-6.52347	-9.44427	-8.47009	1.685823	1.43E-07	-6.74953	-4.65012	-5.69983	1.484503	0.00025	2.693005	1.873348	2.283177	0.579585	0.985053
TRCN0000039835	BRCA1	-5.46711	-4.08155	-5.22716	-4.92528	0.740471	7.3E-05	-3.56159	-1.65207	-2.60683	1.350236	0.013958	1.905525	2.429485	2.167505	0.370496	0.953978
TRCN0000039836	BRCA1	-3.19599	-1.37166	-6.41204	-3.6599	2.552013	0.006366	1.053803	-0.63327	0.210267	1.19294	0.557026	4.249796	0.738393	2.494094	2.482937	0.88354
TRCN0000039837	BRCA1	-10.9728	-9.61944	-9.78855	-10.1269	0.737386	3.4E-09	-3.44504	-6.70318	-5.07411	2.303851	0.000825	7.527719	2.916263	5.221991	3.260792	0.106835
TRCN0000039884	EP300	5.581509	-3.52172	0.64045	0.900078	4.557167	0.28067	-2.99327	-1.39461	-2.19394	1.130424	0.024018	-8.57478	2.127113	-3.22383	7.567383	0.043166
TRCN0000039885	EP300	0.891079	0.949453	1.279364	1.039966	0.20937	0.067066	-2.02751	1.64418	-0.19167	2.596279	0.412296	-2.91859	0.694727	-1.11193	2.555003	0.061565
TRCN0000039886	EP300	0.343738	0.460058	0.313444	0.372413	0.077399	0.269859	-1.24313	-1.12113	-1.18213	0.086264	0.094485	-1.58686	-1.58119	-1.58403	0.004013	0.026129
TRCN0000039887	EP300	-1.65828	-4.13166	-0.96518	-2.25171	1.66456	0.074688	-2.98236	-1.8256	-2.40398	0.817952	0.016546	-1.32408	2.306061	0.490992	2.566895	0.296294
TRCN0000040038	CCND1	-8.06165	-1.56779	-7.59159	-5.74035	3.621174	0.000341	-6.49643	-3.57495	-5.03569	2.0658	0.00075	1.56522	-2.00716	-0.22097	2.526055	0.152053
TRCN0000040039	CCND1	-4.57949	-1.9833	-2.70159	-3.08813	1.340565	0.00967	-6.04565	-4.38614	-5.21589	1.173448	0.00039	-1.46616	-2.40284	-1.9345	0.662338	0.017882
TRCN0000040040	CCND1	-0.81779	-0.32029	-0.47564	-0.53791	0.254528	0.985385	-0.77499	-0.76468	-0.76984	0.007291	0.168076	0.042798	-0.44439	-0.2008	0.344495	0.126774
TRCN0000040041	CCND1	-3.44236	-1.47102	0.772509	-1.38029	2.1089	0.390262	-2.72624	-0.36504	-1.54564	1.669618	0.068759	0.716126	1.105982	0.911054	0.27567	0.383255
TRCN0000040042,TRCN0000288598	CCND1,CCND1	-11.3025	-10.2027	-8.69522	-10.0668	1.308959	6.71E-09	-3.62907	-6.99325	-5.31116	2.378831	0.000653	7.673457	3.209499	5.441478	3.156495	0.084272
TRCN0000040163,TRCN0000288710	RB1,RB1	1.230622	1.601273	0.656721	1.162872	0.475907	0.051773	-1.40802	-0.40487	-0.90644	0.709339	0.143471	-2.63864	-2.00614	-2.32239	0.447249	0.01123
TRCN0000040164	RB1	0.283995	0.799972	1.66944	0.917803	0.700198	0.093406	-1.08876	-0.85416	-0.97146	0.165884	0.127538	-1.37276	-1.65414	-1.51345	0.198967	0.028438
TRCN0000040165	RB1	5.434162	0.054206	-0.35616	1.710735	3.231104	0.053307	0.508654	0.114026	0.31134	0.279044	0.602598	-4.92551	0.05982	-2.43284	3.52516	0.020587
TRCN0000040166	RB1	-0.8254	-2.04574	-1.64239	-1.50451	0.621744	0.263653	1.16923	0.509181	0.839205	0.466725	0.941244	1.994634	2.554925	2.274779	0.396185	0.989445
TRCN0000040167	RB1	-0.10448	-1.28606	0.405117	-0.32848	0.867553	0.790806	0.33802	0.778503	0.558262	0.311468	0.754479	0.442505	2.064563	1.253534	1.146969	0.519151
TRCN0000040193,TRCN0000363564	BRCA2,BRCA2	0.605993	-0.67935	0.903173	0.276604	0.841112	0.332995	-1.36391	-0.54629	-0.9551	0.578146	0.132895	-1.9699	0.133065	-0.91842	1.487023	0.062843
TRCN0000040194	BRCA2	-0.23734	0.713336	-1.79109	-0.43837	1.264259	0.895303	-1.56776	-0.68373	-1.12575	0.625105	0.105072	-1.33042	-1.39707	-1.36374	0.047123	0.033775
TRCN0000040197	BRCA2	-3.16404	-2.21569	-0.922	-2.10058	1.125446	0.086624	-5.73006	-1.37536	-3.55271	3.079236	0.008369	-2.56601	0.840335	-0.86284	2.408652	0.077658
TRCN0000045299	CCNE1	-2.73785	-1.93641	-2.05489	-2.24305	0.432584	0.054672	-0.71357	-2.17431	-1.44394	1.032898	0.070077	2.02428	-0.2379	0.893192	1.5996	0.392376
TRCN0000045300	CCNE1	-0.14727	-1.64326	1.857367	0.02228	1.756461	0.531607	-2.32189	-0.03135	-1.17662	1.619661	0.112406	-2.17462	1.611913	-0.28135	2.677486	0.146599
TRCN0000045301	CCNE1	-0.61864	-1.21673	-1.43111	-1.08883	0.421066	0.520196	-1.07595	-1.0508	-1.06338	0.017783	0.111872	-0.45731	0.16593	-0.14569	0.440697	0.134908
TRCN0000045302	CCNE1	-2.13435	-1.30718	-8.71355	-4.05169	4.058415	0.010949	-1.87224	-1.48582	-1.67903	0.273242	0.045861	0.262103	-0.17864	0.041731	0.311654	0.164127
TRCN0000045513,TRCN0000310619	PUS1,PUS1	2.223109	-1.48997	-0.24791	0.161742	1.890132	0.445223	-0.66837	0.400988	-0.13369	0.756151	0.38092	-2.89148	1.890957	-0.50026	3.381694	0.133906
TRCN0000045514	PUS1	8.68725	-0.23627	-0.99071	2.486756	5.383019	0.052379	-0.44107	0.41519	-0.01294	0.605468	0.433551	-9.12832	0.651462	-4.23843	6.91535	0.016011

Table D2. Log fold changes in shRNA abundance. See final page for full legend. (5/7)

		LOG2 CALCULATIONS																
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)						IN VIVO LOG2 - T4				
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val		REP1	REP2	AVG	STDEV	p-val
TRCN0000045515,TRCN0000300401	PUS1,PUS1	-0.66689	-3.05335	-3.49712	-2.40579	1.522186	0.050961	-4.39069	-1.92383	-3.15726	1.744336	0.00735		-3.7238	1.129521	-1.29714	3.431816	0.062552
TRCN0000045516,TRCN0000300402	PUS1,PUS1	-2.91666	-2.83175	-3.93485	-3.22775	0.613834	0.004939	-0.55287	0.075111	-0.23888	0.444052	0.333493		2.363785	2.906859	2.635322	0.384011	0.801628
TRCN0000045517,TRCN0000300403	PUS1,PUS1	-4.41925	-4.70238	-0.55219	-3.22461	2.318705	0.013403	-1.3896	-4.37321	-2.8814	2.109732	0.012473		3.029655	0.329176	1.679415	1.909527	0.71727
TRCN0000046068,TRCN0000327856	KDM1A,KDM1A	-4.91335	-2.01084	-3.45822	-3.4608	1.451252	0.004204	-2.19354	-0.90649	-1.55002	0.91008	0.059059		2.719804	1.104351	1.912077	1.142298	0.823691
TRCN0000046069,TRCN0000327857	KDM1A,KDM1A	-3.11472	-1.39621	-2.90904	-2.47332	0.938458	0.035494	-1.09932	-1.84948	-1.4744	0.530448	0.063118		2.015405	-0.45327	0.781066	1.745618	0.358988
TRCN0000046070	KDM1A	-0.26221	1.116173	0.152242	0.335402	0.707209	0.297381	-0.74951	-1.70305	-1.22628	0.674258	0.091502		-0.4873	-2.81922	-1.65326	1.648921	0.028353
TRCN0000046071,TRCN0000327930	KDM1A,KDM1A	-3.71235	-7.16548	-4.54656	-5.14146	1.801795	0.000113	-1.4759	-1.42525	-1.45057	0.035813	0.063911		2.236449	5.74023	3.988339	2.477547	0.301766
TRCN0000046072,TRCN0000327932	KDM1A,KDM1A	-2.46655	-2.51212	-2.70186	-2.56018	0.124799	0.024736	-0.1789	-0.66633	-0.42261	0.344659	0.26584		2.287651	1.845799	2.066725	0.312436	0.901007
TRCN0000058069,TRCN0000290094	PSME3,PSME3	-3.39464	-2.81588	-1.85396	-2.68816	0.77824	0.02019	-0.53797	-0.77304	-0.65551	0.166218	0.196154		2.856663	2.042834	2.449749	0.575464	0.897709
TRCN0000058070,TRCN0000307160	PSME3,PSME3	-0.18468	-6.01788	-4.12447	-3.44234	2.975825	0.01402	-6.69807	0.958901	-2.86959	5.414298	0.055223		-6.51339	6.976782	0.231694	9.538995	0.480626
TRCN0000058071	PSME3	-0.37683	-0.33108	-2.01298	-0.90696	0.958114	0.678125	-1.56807	-0.47241	-1.02024	0.774748	0.123388		-1.19124	-0.14133	-0.66628	0.742393	0.077202
TRCN0000060653,TRCN0000299678	NCOR1,NCOR1	-5.61313	-0.45978	-1.30877	-2.46056	2.763007	0.079417	-2.27001	-4.74788	-3.50894	1.752117	0.004553		3.343119	-4.28809	-0.47249	5.396083	0.198074
TRCN0000060654	NCOR1	-0.4818	-0.57268	-1.51795	-0.85748	0.573786	0.715139	-1.38455	-3.44172	-2.41314	1.454637	0.019012		-0.90275	-2.86905	-1.8859	1.390381	0.020807
TRCN0000060655	NCOR1	0.430947	-0.57473	1.825968	0.560729	1.205598	0.210216	-0.98893	-0.5876	-0.78827	0.283785	0.164634		-1.41988	-0.01287	-0.71638	0.994905	0.074441
TRCN0000060656,TRCN0000310464	NCOR1,NCOR1	-1.08004	-2.89278	-3.32634	-2.43305	1.191627	0.042339	-2.88087	-3.6415	-3.26119	0.537848	0.004497		-1.80083	-0.74872	-1.27478	0.743951	0.038628
TRCN0000060657,TRCN0000299677	NCOR1,NCOR1	-2.39713	-4.83062	-1.95644	-3.0614	1.547956	0.011598	2.732716	-0.18813	1.272293	2.065349	0.787015		5.12985	4.642492	4.886171	0.344614	0.104607
TRCN0000060703,TRCN0000298963	NCOR2,NCOR2	-2.05385	-1.18936	0.635191	-0.86934	1.372787	0.719595	-4.95547	-3.77541	-4.36544	0.834431	0.001035		-2.90162	-2.58604	-2.74383	0.223148	0.006844
TRCN0000060704	NCOR2	-1.42567	-0.43597	-0.59245	-0.81803	0.532016	0.750188	0.05736	-0.71328	-0.32796	0.544928	0.300683		1.483029	-0.27731	0.602857	1.244751	0.297539
TRCN0000060705,TRCN0000298965	NCOR2,NCOR2	-3.81928	-0.55815	0.962996	-1.13814	2.443323	0.557451	-9.04686	-5.76007	-7.40347	2.324113	6.62E-05		-5.22759	-5.20192	-5.21475	0.018148	0.000482
TRCN0000060706,TRCN0000298964	NCOR2,NCOR2	0.541926	-1.65505	-2.67227	-1.2618	1.642788	0.43691	-0.44274	-5.42664	-2.93469	3.524149	0.022381		-0.98467	-3.77159	-2.37813	1.970653	0.013555
TRCN0000060707,TRCN0000298889	NCOR2,NCOR2	-1.96865	-0.34638	-3.10305	-1.80603	1.385512	0.167565	-5.25011	-3.3999	-4.325	1.308293	0.001273		-3.28145	-3.05352	-3.16749	0.161171	0.004229
TRCN0000060918,TRCN0000299608	PHB2,PHB2	-5.59337	-0.81141	-5.70719	-4.03733	2.794305	0.003603	-0.92164	1.567099	0.322727	1.759807	0.631641		4.671729	2.378507	3.525118	1.621553	0.424158
TRCN0000060919,TRCN0000299607	PHB2,PHB2	-1.0281	-3.64283	-8.09229	-4.2544	3.571584	0.004968	-7.46412	-6.34457	-6.90434	0.791641	4.95E-05		-6.43602	-2.70174	-4.56888	2.640536	0.001705
TRCN0000060920	PHB2	2.352036	-0.70423	0.02189	0.556566	1.596745	0.227796	-6.73908	-3.86718	-5.30313	2.030741	0.000534		-9.09112	-3.16295	-6.12703	4.191846	0.00088
TRCN0000060922,TRCN0000299609	PHB2,PHB2	-1.01027	-0.83808	-0.36003	-0.73613	0.336896	0.824631	1.271626	-2.19503	-0.4617	2.451297	0.307129		2.281899	-1.35695	0.462475	2.573054	0.289151
TRCN0000063263,TRCN0000299538	NCOA6,NCOA6	0.055067	-1.35305	0.019539	-0.42615	0.802918	0.880312	1.103114	1.560287	1.331701	0.32327	0.730098		1.048047	2.913338	1.980693	1.31896	0.859314
TRCN0000063264	NCOA6	-1.49844	-0.15015	-2.25216	-1.30025	1.064929	0.388944	0.291098	-1.0459	-0.3774	0.9454	0.289145		1.789538	-0.89575	0.446893	1.898787	0.26868
TRCN0000063265	NCOA6	3.172414	-1.60625	-2.35893	-0.26426	2.999944	0.787092	0.355782	0.371419	0.363601	0.011057	0.632808		-2.81663	1.977672	-0.41948	3.390085	0.14464
TRCN0000063266	NCOA6	-0.76064	-1.26767	-3.36239	-1.7969	1.379252	0.170267	-0.13328	-3.51872	-1.826	2.393869	0.05754		0.627366	-2.25105	-0.81184	2.035347	0.076723
TRCN0000063267	NCOA6	-0.90704	-0.82979	-0.71383	-0.81689	0.09725	0.748737	-1.64128	-1.75199	-1.69663	0.078281	0.044401		-0.73424	-0.92219	-0.82821	0.132906	0.062703
TRCN0000063818	SNAI1	-3.47061	0.761277	-10.4619	-4.3904	5.667828	0.021326	-1.68906	0.368702	-0.66018	1.45506	0.214072		1.781546	-0.39258	0.694485	1.537336	0.328638
TRCN0000063819	SNAI1	4.464412	-1.21954	-1.28864	0.652076	3.301761	0.287633	1.900132	1.382162	1.641147	0.366261	0.546006		-2.56428	2.601705	0.018712	3.652903	0.223388
TRCN0000063821	SNAI1	0.236735	-3.55449	-0.63967	-1.31914	1.984847	0.418799	-9.01104	0.451578	-4.27973	6.691081	0.02619		-9.24777	4.006071	-2.62085	9.371884	0.104079
TRCN0000063822	SNAI1	-1.19512	-0.85401	1.143912	-0.30174	1.263537	0.773237	-3.40192	-4.12307	-3.7625	0.509924	0.002198		-2.2068	-3.26905	-2.73793	0.751126	0.007172
TRCN0000072693	RBM14	-4.66056	-7.79189	-1.23015	-4.56086	3.282007	0.002078	-7.35163	-0.55713	-3.95438	4.804436	0.013872		-2.69107	7.234755	2.271843	7.018618	0.99413
TRCN0000072694	RBM14	-0.99052	0.18166	-0.63767	-0.48218	0.601362	0.932287	-1.77532	1.212086	-0.28162	2.112416	0.357881		-0.7848	1.030427	0.122814	1.283558	0.187026
TRCN0000072695	RBM14	-5.41402	-1.18794	-8.50461	-5.03552	3.672991	0.001309	-7.37305	-1.74436	-4.5587	3.980082	0.00443		-1.95902	-0.55642	-1.25772	0.99179	0.040331
TRCN0000072696	RBM14	-0.5127	0.074788	-0.17891	-0.20561	0.29465	0.674529	0.049209	-1.57769	-0.76424	1.150392	0.180976		0.561905	-1.65248	-0.54529	1.565805	0.095465
TRCN0000107560	JMJD1C	-11.1701	-9.17477	-8.5448	-9.62988	1.370535	1.41E-08	-9.10227	-5.99274	-7.54751	2.198769	5.26E-05		2.067806	3.182031	2.624919	0.787876	0.808145
TRCN0000107561	JMJD1C	-2.50081	-1.3847	-3.46327	-2.44959	1.040231	0.03873	-3.02243	-2.65614	-2.83928	0.259002	0.008085		-0.52162	-1.27144	-0.89653	0.530208	0.058757
TRCN0000107562	JMJD1C	-1.14777	1.185184	-1.75252	-0.5717	1.551261	0.983326	1.320172	0.105229	0.712701	0.859094	0.857898		2.467941	-1.07995	0.693993	2.508741	0.350896
TRCN0000107563	JMJD1C	-0.52028	-0.31364	-0.72727	-0.5204	0.206818	0.968416	-1.35737	1.480566	0.061599	2.006723	0.502493		-0.83709	1.794204	0.478557	1.860606	0.275826
TRCN0000107564	JMJD1C	-10.6372	-10.0766	-8.98245	-9.89875	0.841593	5.24E-09	-2.2505	-6.17687	-4.21369	2.776359	0.003113		8.3867	3.89974	6.14322	3.172759	0.041614
TRCN0000107805	SIN3B	0.653945	1.5616	1.051497	1.089014	0.454989	0.061292	0.132348	-0.81365	-0.34065	0.668919	0.297639		-0.5216	-2.37525	-1.44842	1.310727	0.033786
TRCN0000107806	SIN3B	-1.56968	-1.36683	0.645045	-0.76382	1.224323	0.808269	-1.24052	-0.97484	-1.10768	0.18786	0.105295		0.329163	0.391983	0.360573	0.04442	0.227133
TRCN0000107807	SIN3B	-0.93994	-3.62781	-2.29381	-2.28719	1.343952	0.061784	-3.19145	0.715983	-1.23773	2.762969	0.133966		-2.25151	4.343798	1.046144	4.663587	0.531154
TRCN0000107808	SIN3B	-0.77764	-0.8392	-3.7296	-1.78215	1.686825	0.187664	-0.91445	-0.57991	-0.74718	0.236559	0.173804		-0.13681	0.25929	0.06124	0.280084	0.167425
TRCN0000107809	SIN3B	-2.78253	-2.94432	-8.97695	-4.90127	3.530574	0.001428	-6.10605	1.69313	-2.20646	5.514854	0.106906		-3.32352	4.637448	0.656962	5.629256	0.446621
TRCN0000118647,TRCN0000310425	TBL1X,TBL1X	-2.04735	0.072185	0.700612	-0.42485	1.439827	0.884882	2.497227	-4.35078	-0.92678	4.842272	0.286601		4.544574	-4.42296	0.060805	6.341007	0.329392
TRCN0000118648	TBL1X	-1.25036	-1.29006	-3.81711	-2.11918	1.470589	0.091969	-1.80603	-2.97279	-2.38941	0.825025	0.016928		-0.55566	-1.68273	-1.1192	0.796956	0.046386
TRCN0000118649,TRCN0000299525	TBL1X,TBL1X	-0.44697	1.307096	-0.26793	0.197398	0.965187	0.383667	0.239932	-1.75701	-0.75854	1.412051	0.188088		0.686901	-3.06411	-1.1886	2.652363	0.058018
TRCN0000118650,TRCN0000299582	TBL1X,TBL1X	-1.37036	-2.12322	-0.94083	-1.47814	0.598516	0.27612	0.774035	-2.08031	-0.65314	2.018325	0.232912		2.144391	0.042913	1.093652	1.485969	0.461498
TRCN0000118651,TRCN0000299581	TBL1X,TBL1X	-5.17254	-0.16934	-3.08276	-2.80821	2.51287	0.036037	-10.0355	-5.20877	-7.62212	3.412994	0.000125		-4.86293	-5.03942	-4.95118	0.124798	0.000628
TRCN0000121073	PLK1	4.569526	-2.52608	-5.86989	-1.27548	5.330889	0.622909	-4.12172	-3.7352	-3.92846	0.273312	0.001697		-8.69125	-1.20912	-4.95018	5.290665	0.004289
TRCN0000121075	PLK1	0.524207	-2.01136	4.814745	1.109198	3.450447	0.156608	-7.39722	-2.73322	-5.06522	3.297944	0.001598		-7.92142	-0.72186	-4.32164	5.09086	0.006669
TRCN0000121322	PLK1	-2.43957	0.897599	-2.16145	-1.23447	1.851658	0.464424	-0.84669	-0.16408	-0.50538	0.482679	0.240574		1.592881	-1.06167	0.265603	1.877054	0.226101
TRCN0000121323	PLK1	-0.07301	-1.2194	-5.9487	-2.41437	3.114591	0.100605	-3.56255	-0.09827	-1.83041	2.449617	0.058229		-3.48953	1.121133	-1.1842	3.260234	0.067101
TRCN0000121324,TRCN0000121324	PLK1,PLK1	-0.0672	-0.73415	-0.28493	-0.36209	0.340103	0.81733	0.443698	-2.18821	-0.87226	1.861043	0.174062		0.510898	-1.45407	-0.47158	1.389439	0.101284
TRCN0000122934	MUC1	-0.67626	-1.41274	-0.47801	-0.85567	0.492515	0.715871	0.768789	0.443436	0.606113	0.230059	0.785258		1.44505	1.856179	1.650615	0.290712	0.690467
TRCN0000122935	MUC1	-1.89094	-0.90908	-0.44242	-1.08081	0.739371	0.531958	-3.39525	-1.21689	-2.30607	1.540333	0.022728		-1.50432	-0.30782	-0.90607	0.846054	0.059374
TRCN0000122936	MUC1	1.651698	-0.31694	-1.90817	-0.19114	1.783264	0.693703	1.041192	-2.23183	-0.59532	2.314378	0.260053		-0.61051	-1.91489	-1.2627	0.922339	0.039813
TRCN0000122937	MUC1	4.547756	1.001995	0.397503	1.982418	2.242113	0.017017	-0.73966	1.515611	0.387977	1.594714	0.665095		-5.28741	0.513616	-2.3869	4.101946	0.026287
TRCN0000122938	MUC1	-3.47729	-3.33636	-5.3471	-4.05358	1.122429	0.000785	-0.47917	0.15048	-0.16435	0.445229	0.363955		2.998124	3.486841	3.242482	0.345575	0.518072
TRCN0000128718	SUMO1	-5.04602	-2.40128	-10.1714	-5.87291	3.950521	0.000412	0.724138	-6.16708	-2.72147	4.872827	0.051661		5.77016	-3.7658	1.002181	6.742941	0.583755
TRCN0000129359	SUMO1	-0.58189	-1.53304	-9.84918	-3.98804	5.09813	0.025815	-2.51046	1.918867	-0.2958	3.132007	0.395132		-1.92857	3.45191	0.76167	3.804573	0.411483
TRCN0000146543	SUMO1	-7.11349	-0.18273	-3.44332	-3.57985	3.467397	0.015759	-8.13622	-0.98547	-4.56085	5.056348	0.008602		-1.02273	-0.80274	-0.91273	0.155559	0.056945
TRCN0000147057	SUMO1	0.033761	2.271505	1.248434	1.184567	1.120238	0.057055	-0.091	-0.3959	-0.24345	0.215593	0.330099		-0.12477	-2.6674	-1.39608	1.797916	0.03886
TRCN0000147601	SUMO1	-0.12007	-1.51256	-1.96029	-1.19764	0.959678	0.452643	0.042209	-0.988	-0.47289	0.728466	0.253676		0.162283	0.524568	0.343425	0.256174	0.223636
TRCN0000148311	SUMO1	1.011921	0.478364	1.078983	0.856422	0.329121	0.102133	1.974602	-0.5496	0.712503	1.784877	0.864862		0.962681	-1.02796	-0.03264	1.407595	0.161203
TRCN0000148589	SUMO1	-0.0942	0.96407	-0.1046	0.255088	0.614018	0.339644	-1.80171	0.822162	-0.48977	1.855355	0.275875		-1.7075	-0.14191	-0.92471	1.107044	0.059586
TRCN0000148613	SUMO1	-2.25978	-1.7981	-5.53588	-3.19792	2.037846	0.011645	-0.87129	-0.42376	-0.64753	0.316454	0.198923		1.388491	1.374342	1.381416	0.010005	0.566127
TRCN0000150166	SUMO1	0.941107	0.302242	1.076625	0.773325	0.413559	0.123066	-4.22974	0.345384	-1.94218	3.235098	0.065885		-5.17084	0.043143	-2.56385	3.686845	0.019108
TRCN0000150216	SUMO1	-3.37555	-0.90267	-6.30438	-3.52753	2.70406	0.009528	-1.88329	-2.32823	-2.10576	0.31462	0.024276		1.492262	-1.42556	0.033352	2.06321	0.183934
TRCN0000151254	TBL1Y	-1.2699	1.539181	-0.41437	-0.04836	1.439862	0.570462	-2.65831	1.71416	-0.47208	3.091805	0.331416		-1.38842	0.174979	-0.60672	1.105487	0.084928
TRCN0000152203	TBL1Y	0.47953	0.482291	-0.20183	0.253329	0.394185	0.336777	-0.51996	0.308864	-0.10555	0.586069	0.390866		-0.99949	-0.17343	-0.58646	0.584118	0.083637
TRCN0000152673	TBL1Y	-6.33499	-2.48578	-1.85209	-3.55762	2.426051	0.007122	-3.41698	-0.63553	-2.02626	1.966784	0.038381		2.918001	1.850248	2.384125	0.755016	0.932238
TRCN0000153227	TBL1Y	-3.84679	-2.47421	-2.34798	-2.88966	0.8313	0.01249	-1.81335	-1.30427	-1.55881	0.359978	0.055066		2.033443	1.169942	1.601692	0.610587	0.6683
TRCN0000154186	TBL1Y	0.377241	1.234556	0.43677	0.682856	0.478713	0.149632	-0.76631	-1.41956	-1.09294	0.461917	0.108786		-1.14355	-2.65412	-1.89884	1.06813	0.019506
TRCN0000156393	TBL1Y	2.895679	-0.03846	-3.32853	-0.1571	3.113802	0.715655	-0.11067	-1.37517	-0.74292	0.894139	0.181448		-3.00635	-1.33672	-2.17153	1.180608	0.014516
TRCN0000157198	TBL1Y	1.22922	-1.88899	-2.88699	-1.18225	2.147186	0.513282	1.342401	0.553026	0.947713	0.558173	0.985213		0.113182	2.442016	1.277599	1.646735	0.536389
TRCN0000159193	PELP1	-1.43694	-2.99205	-4.86075	-3.09658	1.714299	0.011824	3.985579	0.916465	2.451022	2.170191	0.253514		5.422518	3.908515	4.665516	1.070561	0.137942
TRCN0000159617	PELP1	-6.07467	-1.81716	-10.7649	-6.21892	4.475625	0.000446	-9.13089	-3.71231	-6.4216	3.831512	0.000559		-3.05622	-1.89515	-2.47568	0.821002	0.009749
TRCN0000159673	PELP1	-3.73513	-0.20344	-4.32241	-2.75366	2.227989	0.034201	-7.19089	-3.12562	-5.15825	2.874574	0.001079		-3.45576	-2.92218	-3.18897	0.377292	0.004169
TRCN0000159883	PELP1	-2.89939	-1.7872	-4.34615	-3.01091	1.283113	0.011297	-2.5672	-3.0801	-2.82365	0.362675	0.008343		0.332197	-1.2929	-0.48035	1.149114	0.097952
TRCN0000161421	PELP1	-9.83339	-7.03614	-5.89499	-7.58817	2.026402	1.1E-06	-7.76558	-6.56584	-7.16571	0.848341	3.82E-05		2.067806	0.470296	1.269051	1.12961	0.525298
TRCN0000161584	PELP1	-3.81195	-1.7655	-2.50472	-2.69406	1.03628	0.021713	-3.0089	-1.42441	-2.21665	1.120408	0.023182		0.803047	0.341093	0.57207	0.326651	0.280251
TRCN0000166488	PELP1	0.742078	0.557091	1.253546	0.850905	0.360756	0.103636	-0.6401	0.621565	-0.00927	0.892134	0.439575		-1.38218	0.064474	-0.65885	1.02294	0.079562
TRCN0000179333	SRA1	-1.0389	-0.76986	0.72992	-0.35961	0.953104	0.820213	-0.6119	-2.50703	-1.55947	1.340063	0.062783		0.427002	-1.73717	-0.65508	1.530301	0.084396
TRCN0000194993	HDAC3	-0.61884	-0.64298	-0.22111	-0.49431	0.236907	0.943213	-0.18746	-1.35268	-0.77007	0.823929	0.174011		0.431374	-0.7097	-0.13916	0.806858	0.138051
TRCN0000195103,TRCN0000318656	HDAC1,HDAC1	-0.82051	-2.36946	-2.42683	-1.87227	0.911299	0.133559	-4.36061	-0.13816	-2.24939	2.985722	0.041138		-3.5401	2.231299	-0.6544	4.080993	0.133087
TRCN0000195159	TRRAP	-0.318	-1.71396	-4.79319	-2.27505	2.289749	0.091084	0.152605	1.568067	0.860336	1.000883	0.956322		0.470609	3.282029	1.876319	1.987975	0.812085
TRCN0000195333	HDAC3	-1.21365	-3.1121	-2.86312	-2.39629	1.031734	0.043688	-2.62518	-0.27074	-1.44796	1.664843	0.078556		-1.41153	2.84136	0.714914	3.007249	0.371549
TRCN0000195435	TRRAP	-2.01929	-1.87633	-2.43024	-2.10862	0.287557	0.073442	-0.27365	-0.56129	-0.41747	0.203395	0.266759		1.745649	1.315044	1.530346	0.304484	0.633658
TRCN0000195467,TRCN0000349638	HDAC1,HDAC1	2.628893	-2.82491	-11.2814	-3.82579	7.008935	0.08206	-3.39626	-3.06446	-3.23036	0.234614	0.004552		-6.02515	-0.23956	-3.13235	4.091032	0.012778
TRCN0000195502	RAF1	-10.8147	-4.7307	-6.95587	-7.50043	3.078348	6.83E-06	-0.50812	-0.28106	-0.39459	0.160558	0.274328		10.3066	4.449644	7.37812	4.141491	0.016784
TRCN0000195646	RAF1	-1.08737	-0.13341	0.012489	-0.40277	0.59736	0.856998	-1.33219	0.27842	-0.52689	1.138875	0.244426		-0.24482	0.41183	0.083506	0.464321	0.172112
TRCN0000195672	HDAC1	-2.19222	-0.48661	-3.04983	-1.90956	1.304777	0.134456	-3.69562	-3.46031	-3.57797	0.166392	0.002754		-1.5034	-2.97369	-2.23855	1.039656	0.013162
TRCN0000195712	HDAC1	1.412072	0.675649	1.023674	1.037132	0.368396	0.068368	-0.74784	-2.89474	-1.82129	1.518086	0.04508		-2.15991	-3.57039	-2.86515	0.997356	0.006423
TRCN0000195727	TRRAP	-10.9514	-3.6923	-10.2574	-8.30036	4.005753	8.52E-06	-9.78523	-5.368	-7.57661	3.123448	0.000103		1.166172	-1.6757	-0.25476	2.009506	0.136965
TRCN0000196264	RAF1	-0.08607	0.386572	0.451385	0.250631	0.293383	0.337121	-2.14537	-0.60401	-1.37469	1.089905	0.07802		-2.0593	-0.99058	-1.52494	0.7557	0.028972
TRCN0000196267	HDAC3	-2.52633	-0.57931	-3.09884	-2.06816	1.320773	0.097785	2.146767	0.328869	1.237818	1.285448	0.797487		4.673095	0.908184	2.790639	2.662194	0.746114
TRCN0000196306,TRCN0000230910	CDK7,CDK7	-3.02229	-3.68616	-3.83989	-3.51611	0.434516	0.002231	0.346256	0.895215	0.620736	0.388172	0.795267		3.368544	4.581372	3.974958	0.857599	0.274182
TRCN0000196691	CDK7	-1.35316	-2.65046	-1.91275	-1.97212	0.650682	0.103694	-7.95297	-0.60195	-4.27746	5.197956	0.01239		-6.5998	2.048509	-2.27565	6.115281	0.05637
TRCN0000196829	HDAC3	-1.30889	-2.836	-1.58349	-1.90946	0.814069	0.121584	2.224193	1.355307	1.78975	0.614395	0.470185		3.533081	4.191307	3.862194	0.465436	0.301785

Table D2. Log fold changes in shRNA abundance. See final page for full legend. (6/7)

		LOG2 CALCULATIONS															
		IN VITRO LOG2 (T4/T0)						IN VIVO LOG2 (TUMOR/T0)					IN VIVO LOG2 - T4				
Oligo ID	GENE	REP1	REP2	REP3	AVG	stdev	p-val	REP1	REP2	AVG	stdev	p-val	REP1	REP2	AVG	STDEV	p-val
TRCN0000196877	HDAC1	-0.1846	0.992648	0.389494	0.399181	0.588684	0.262645	-3.70318	-1.20811	-2.45564	1.764281	0.019738	-3.51858	-2.20075	-2.85966	0.931841	0.006399
TRCN0000196925	HDAC3	-0.6869	-2.31021	-1.98252	-1.65988	0.858407	0.202	0.007658	2.040384	1.024021	1.437354	0.936116	0.694555	4.350596	2.522575	2.585211	0.870598
TRCN0000196969	RAF1	-2.03243	-2.31718	1.596809	-0.9176	2.182191	0.704764	-6.143	-1.49683	-3.81991	3.28534	0.006783	-4.11057	0.820352	-1.64511	3.486688	0.044885
TRCN0000196998	HDAC1	-0.96542	-1.38825	-1.45074	-1.26813	0.264014	0.391296	4.368701	0.49012	2.42941	2.742571	0.282642	5.33412	1.878366	3.606243	2.443587	0.414927
TRCN0000197115	RAF1	-2.33703	-3.54684	-0.30792	-2.06393	1.636642	0.108326	-4.00988	-1.35289	-2.68138	1.878775	0.014991	-1.67285	2.193954	0.260553	2.734242	0.245708
TRCN0000197171	HDAC3	-5.1148	-6.42589	-2.63406	-4.72492	1.925747	0.000328	-2.33044	-2.24982	-2.29013	0.057005	0.018213	2.784362	4.176074	3.480218	0.984089	0.430453
TRCN0000197176	HDAC1	-5.84742	-3.86924	0.057106	-3.21985	3.005353	0.022067	-2.02119	-6.34341	-4.1823	3.056269	0.003827	3.826235	-2.47417	0.676035	4.455056	0.409089
TRCN0000197198	HDAC1	0.351423	-3.17771	-4.56626	-2.46418	2.535298	0.071012	-1.4374	-1.11643	-1.27692	0.226958	0.082673	-1.78883	2.061274	0.136224	2.722432	0.219151
TRCN0000199110	HDAC4	1.125277	-2.63846	-3.40924	-1.64081	2.4263	0.280775	-7.58648	-4.62559	-6.10604	2.093664	0.000221	-8.71176	-1.98714	-5.34945	4.755025	0.002319
TRCN0000199182	HDAC3	-2.49203	-3.50558	-1.06637	-2.35466	1.225394	0.05113	3.162082	1.116276	2.139179	1.446603	0.333805	5.654116	4.621853	5.137984	0.72992	0.080475
TRCN0000199964	HDAC3	-2.25974	-2.12379	-1.5463	-1.97661	0.378811	0.099418	-0.11112	0.074218	-0.01845	0.131052	0.427376	2.148625	2.198009	2.173317	0.03492	0.956959
TRCN0000218391,TRCN0000219664	CDK7,CDK7	-2.26837	-0.40162	-0.75628	-1.14209	0.991377	0.492825	2.697168	-0.64656	1.025306	2.36437	0.939596	4.96554	-0.24494	2.3603	3.684365	0.952468
TRCN0000219663,TRCN0000230908	CDK7,CDK7	0.007067	-0.14492	-1.39997	-0.51261	0.772229	0.961679	0.863952	2.038452	1.451202	0.830497	0.660044	0.856885	2.183376	1.52013	0.937971	0.632566

Table D2. Log fold changes in shRNA abundance *in vitro* and *in vivo*. Log2 changes between tumor and T4 were used to identify genes essential only *in vivo.* Significance was scored as p<0.05, with non-significant values shown in pink. (7/7)

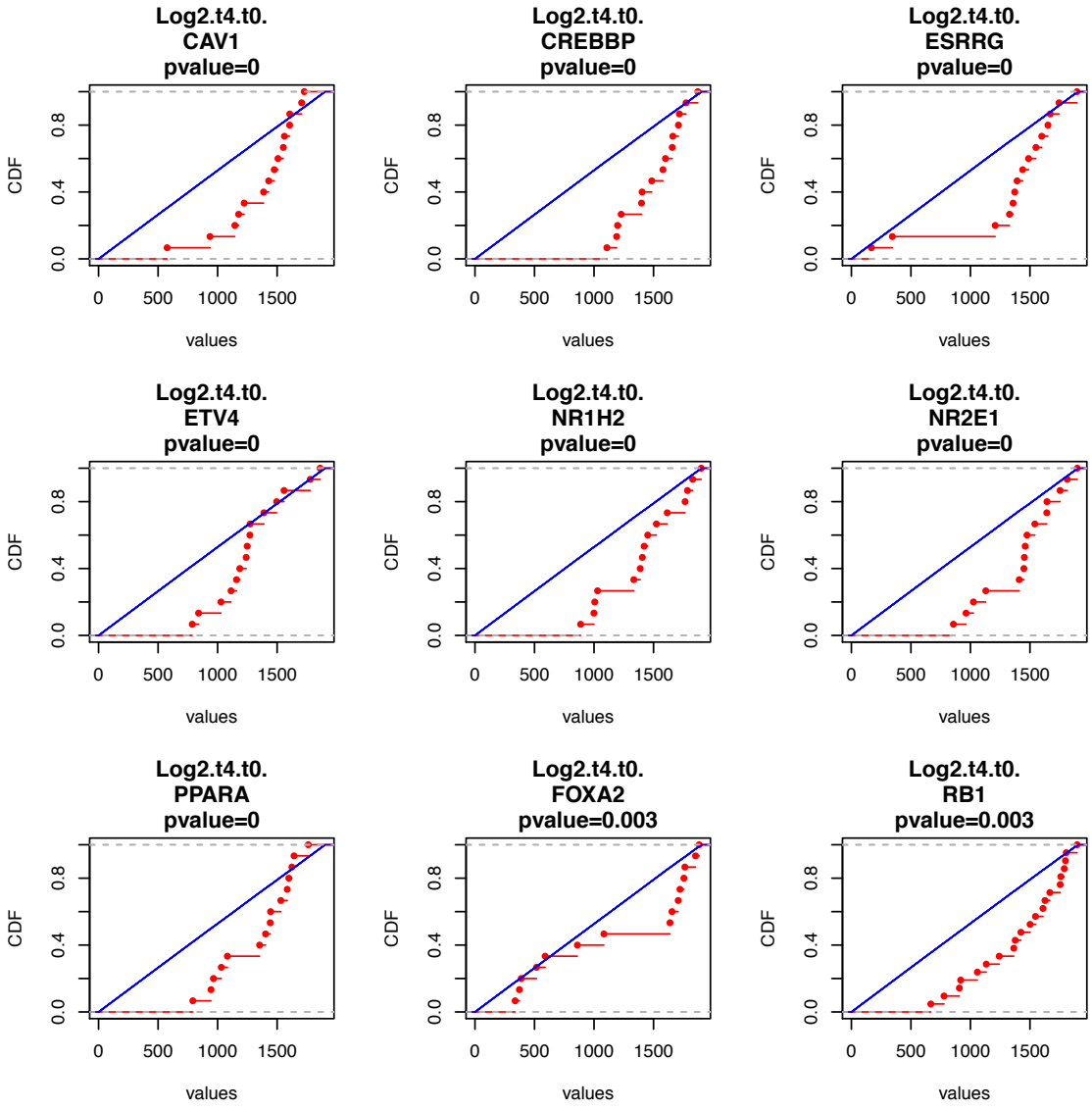


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (1/14)

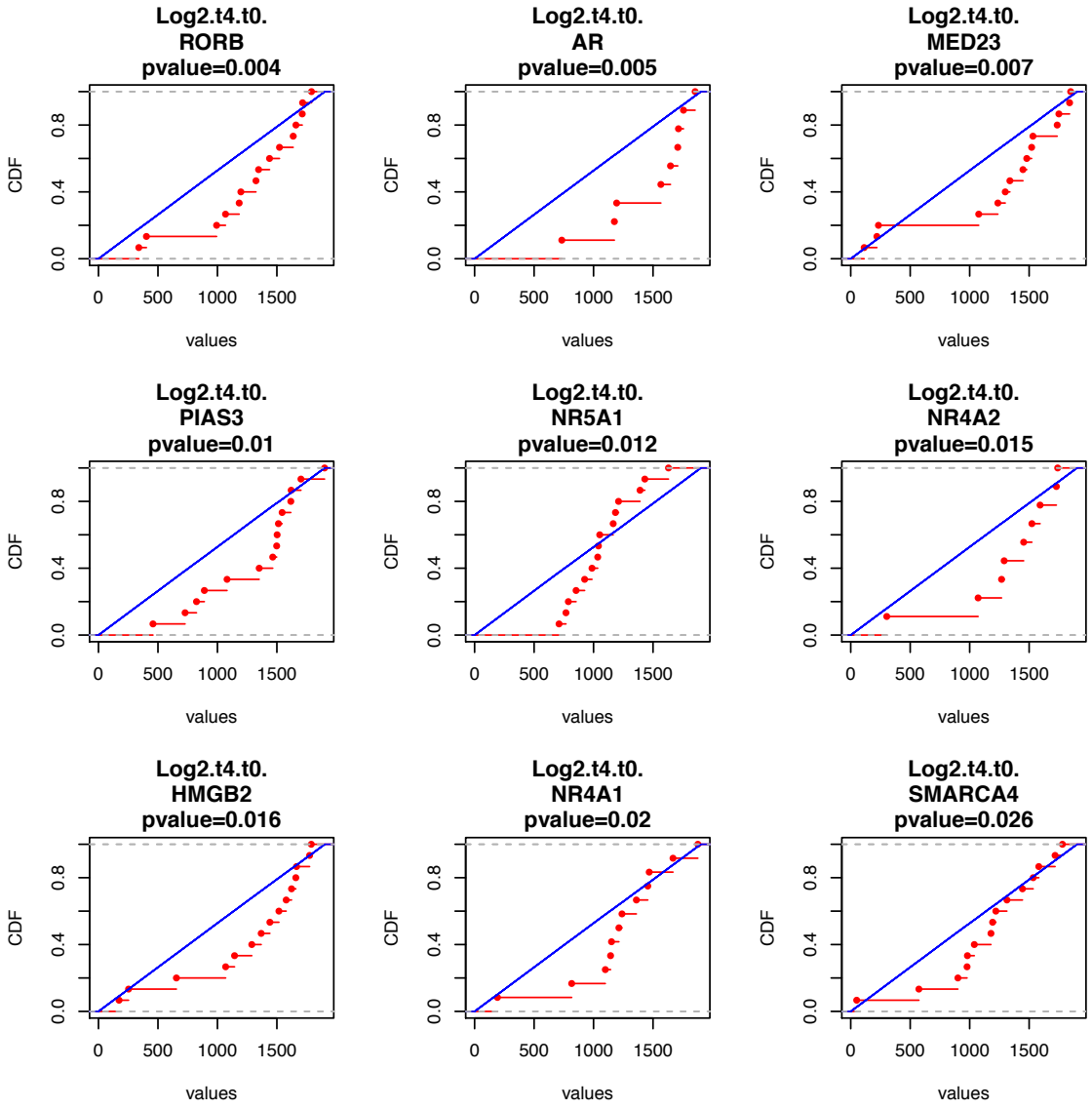


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (2/14)

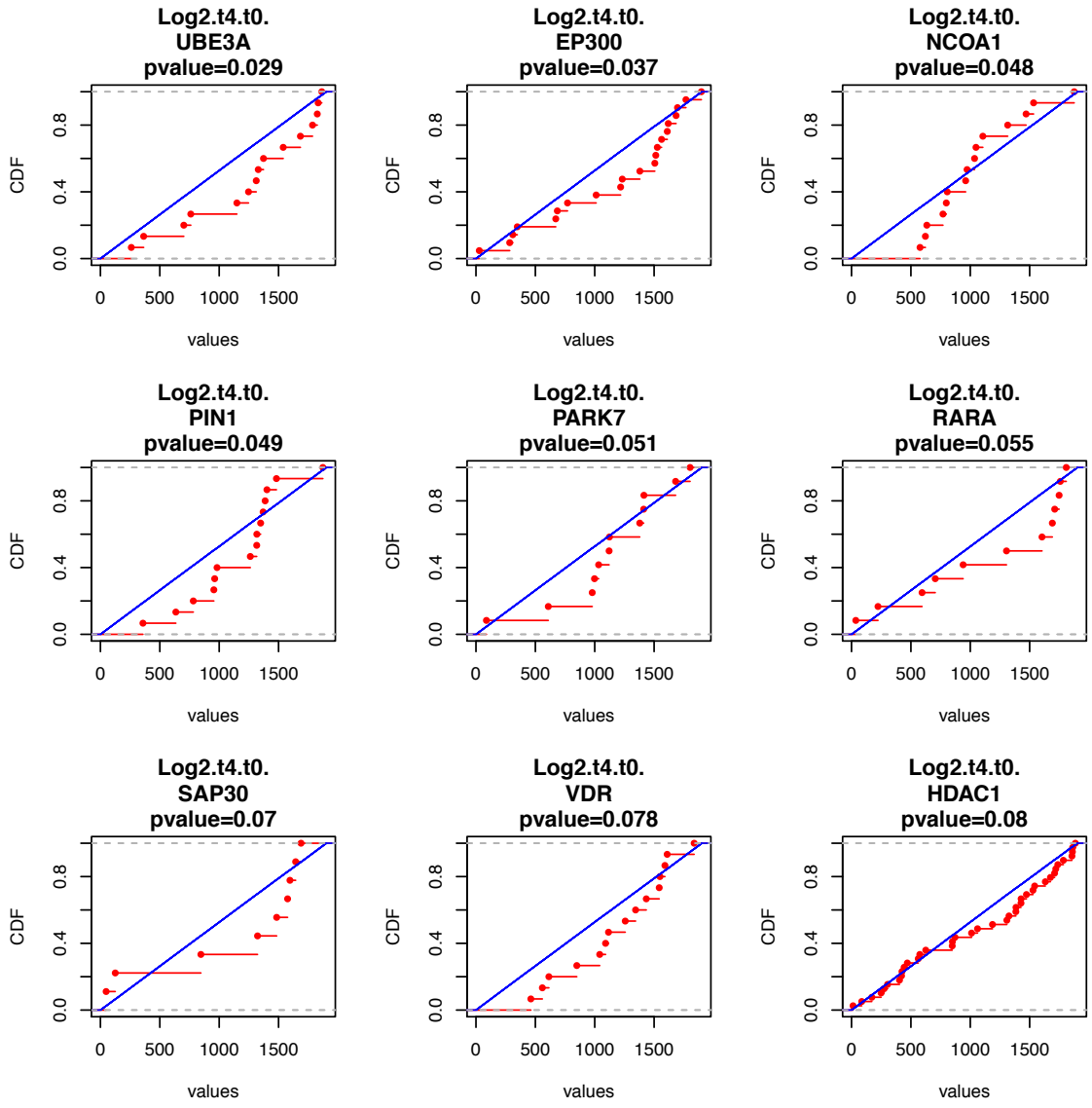


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (3/14)

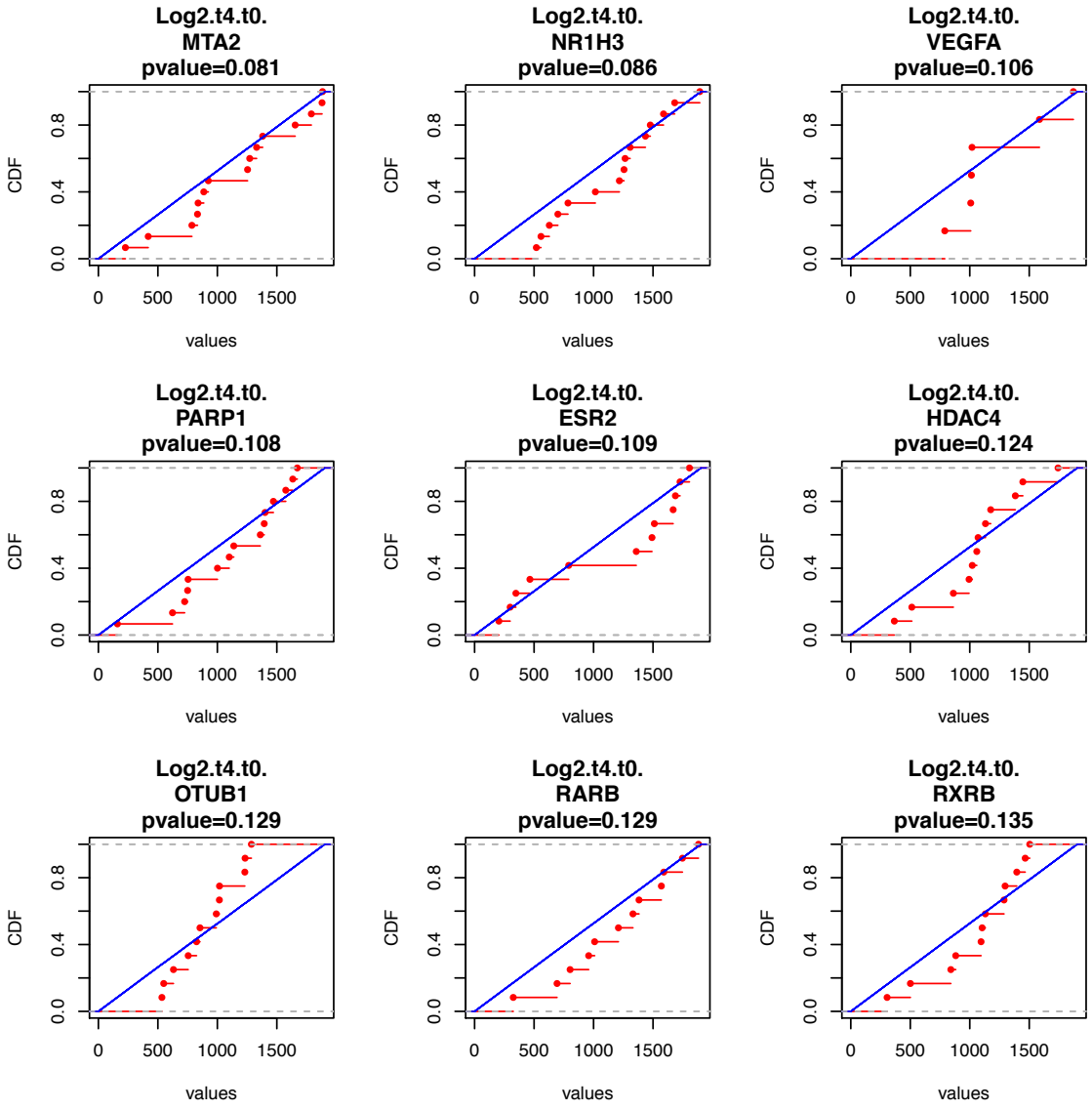


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (4/14)

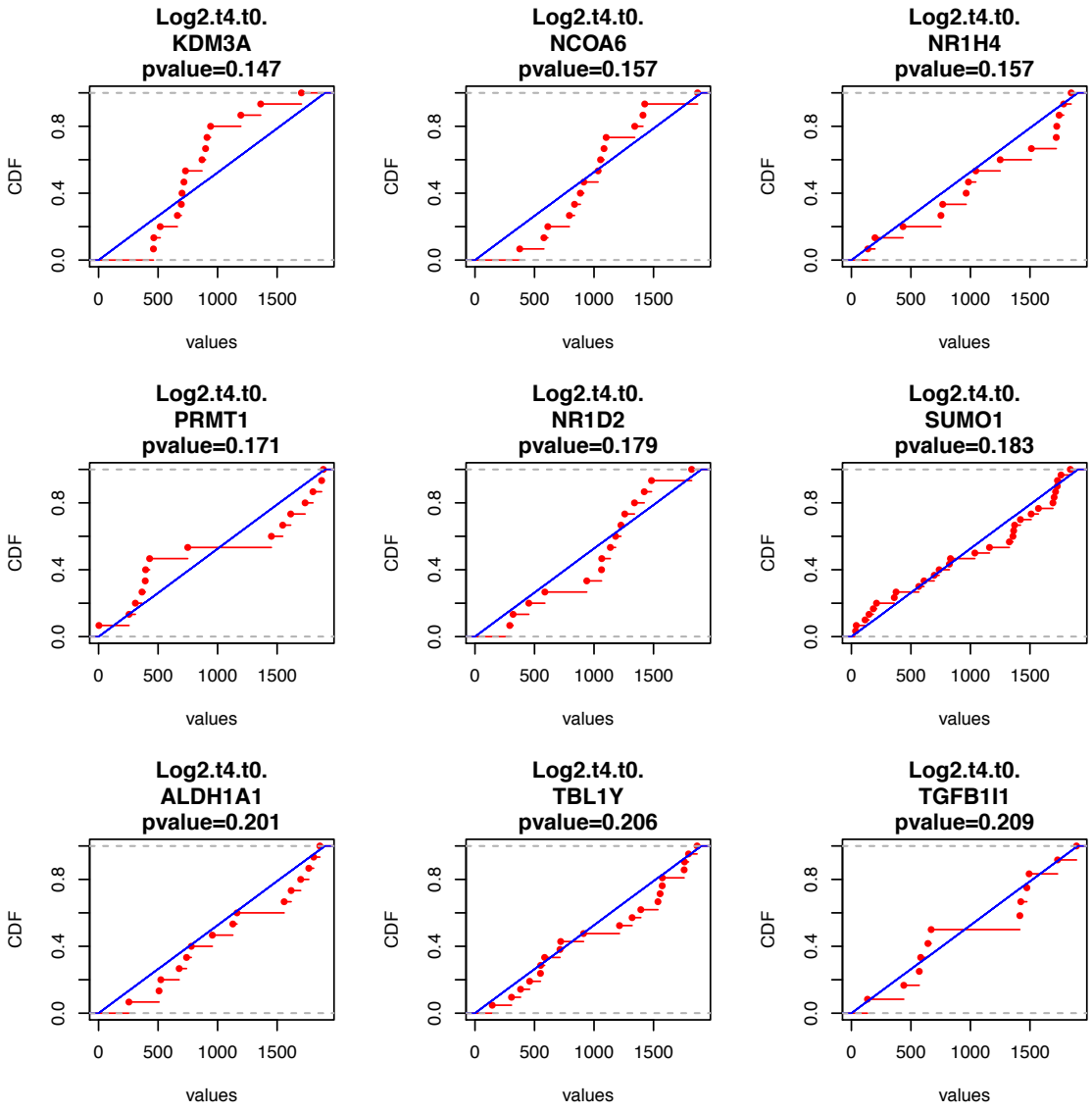


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (5/14)

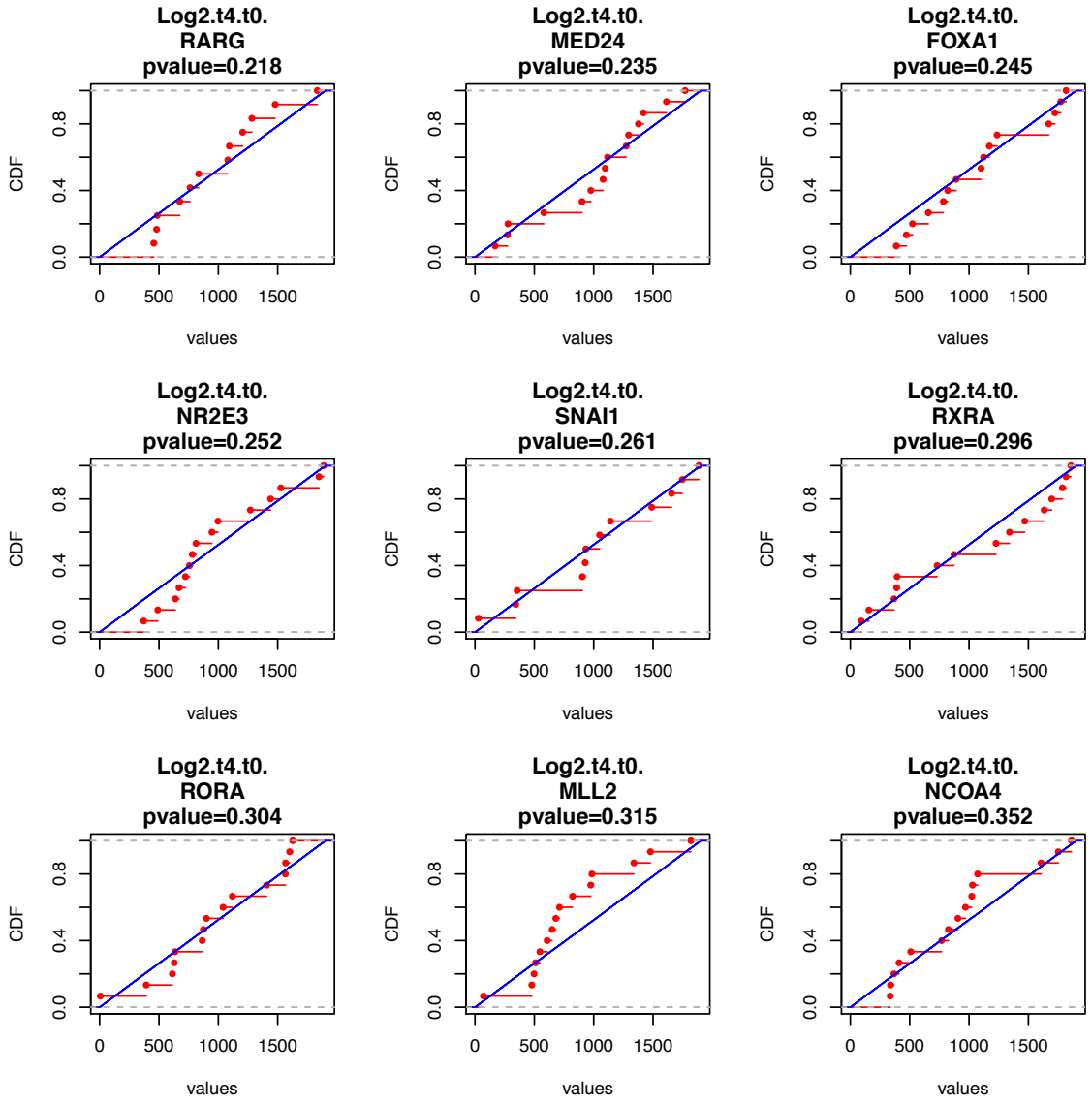


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (6/14)

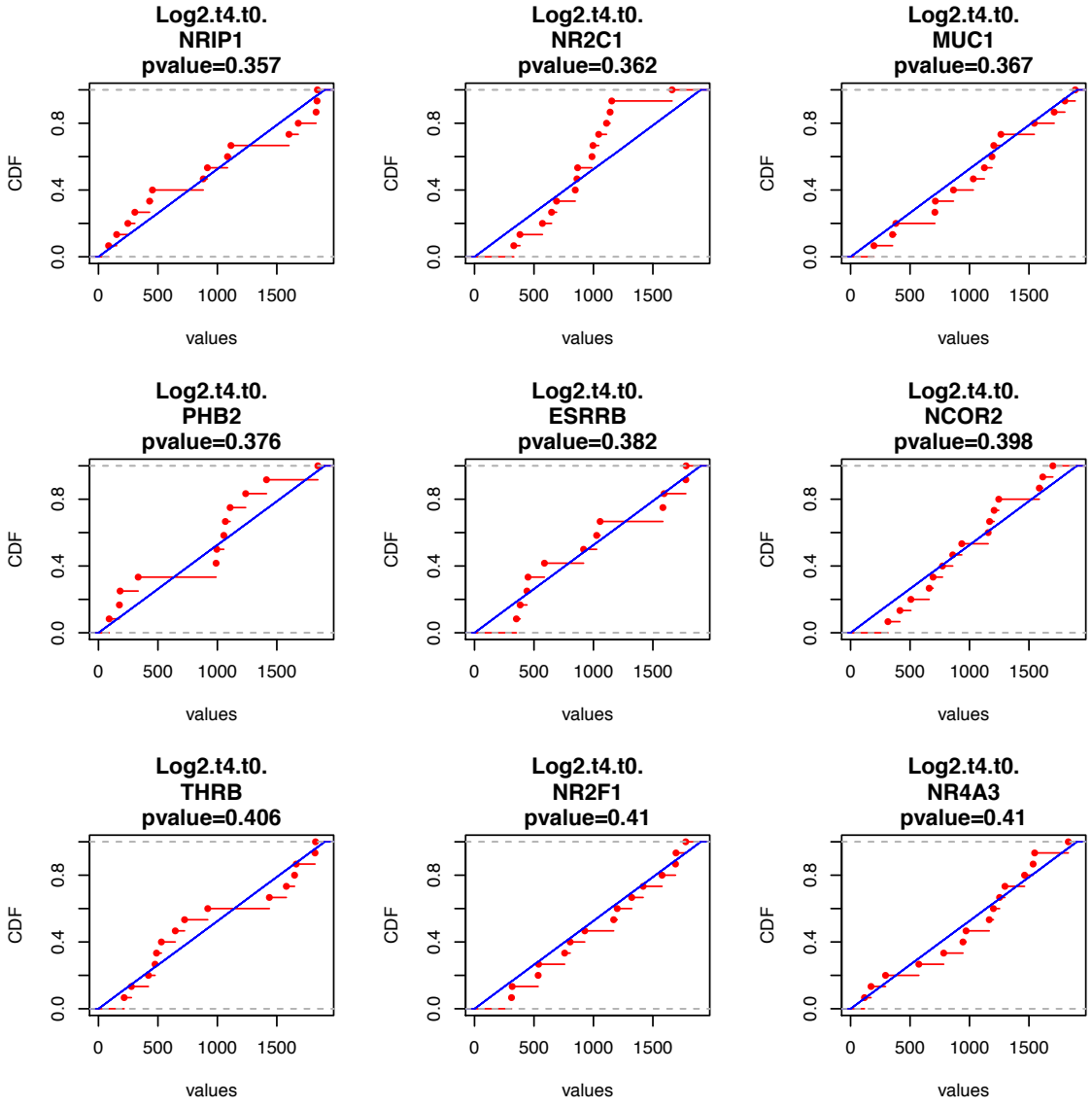


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (7/14)

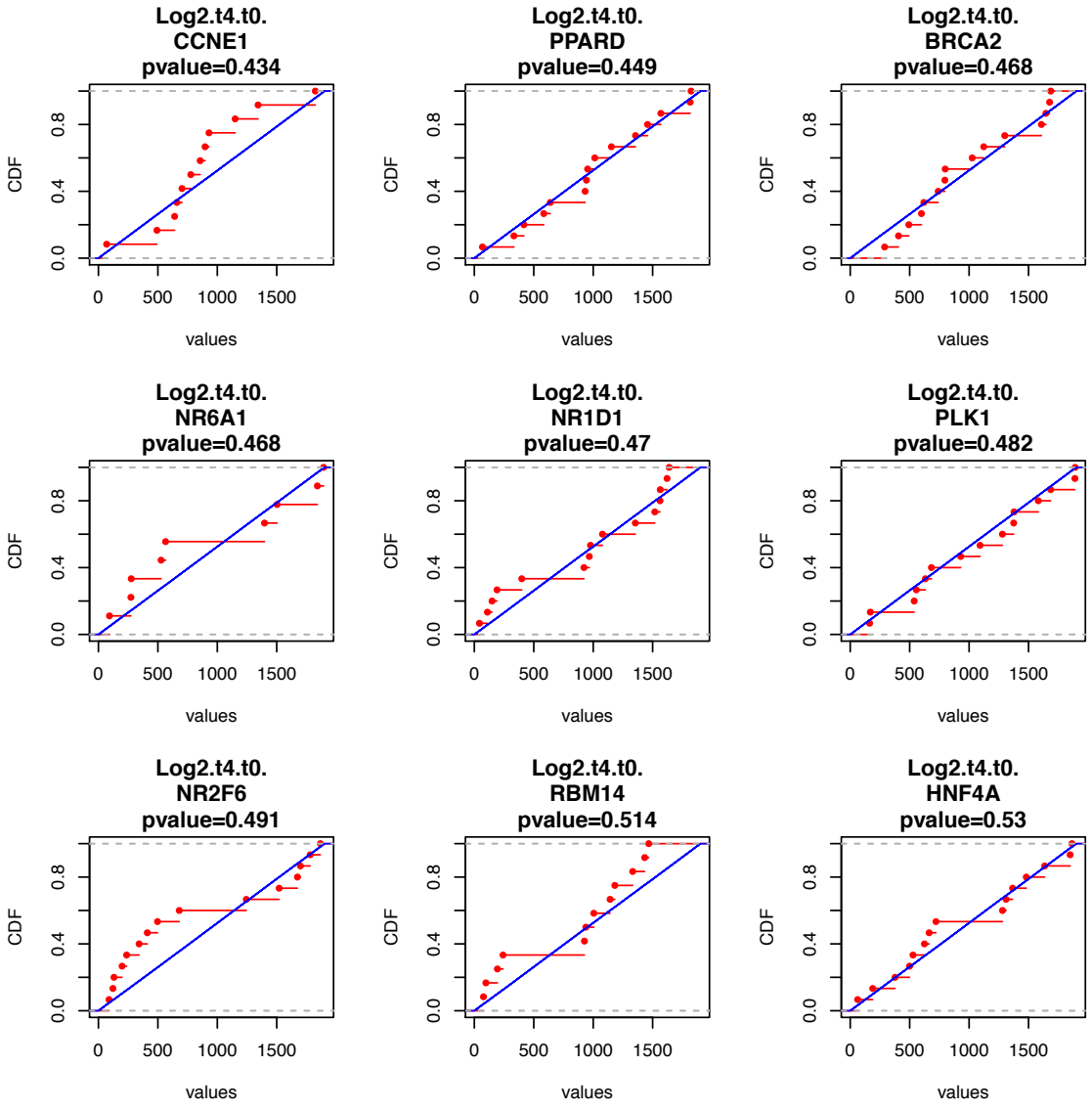


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (8/14)

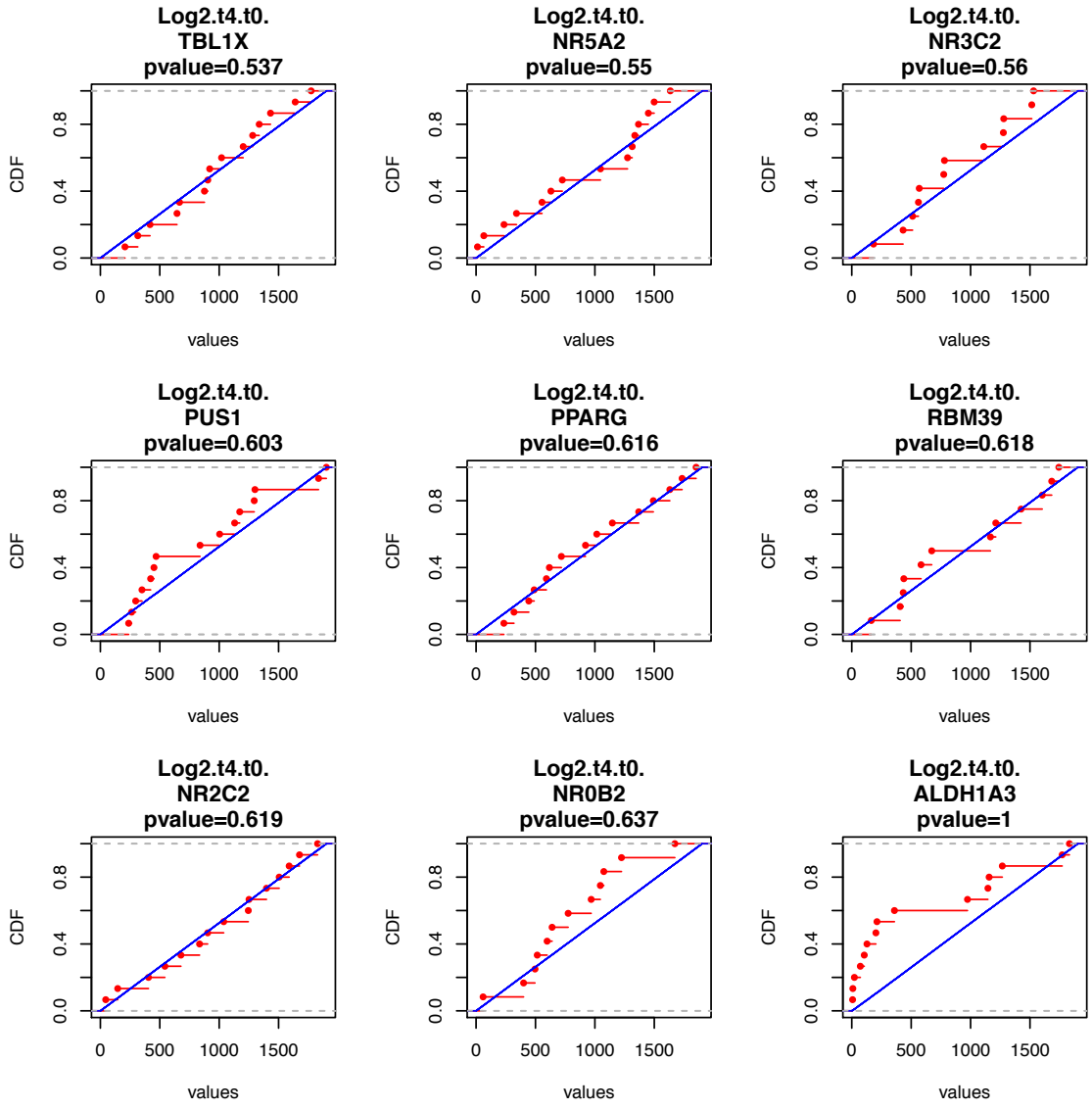


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (9/14)

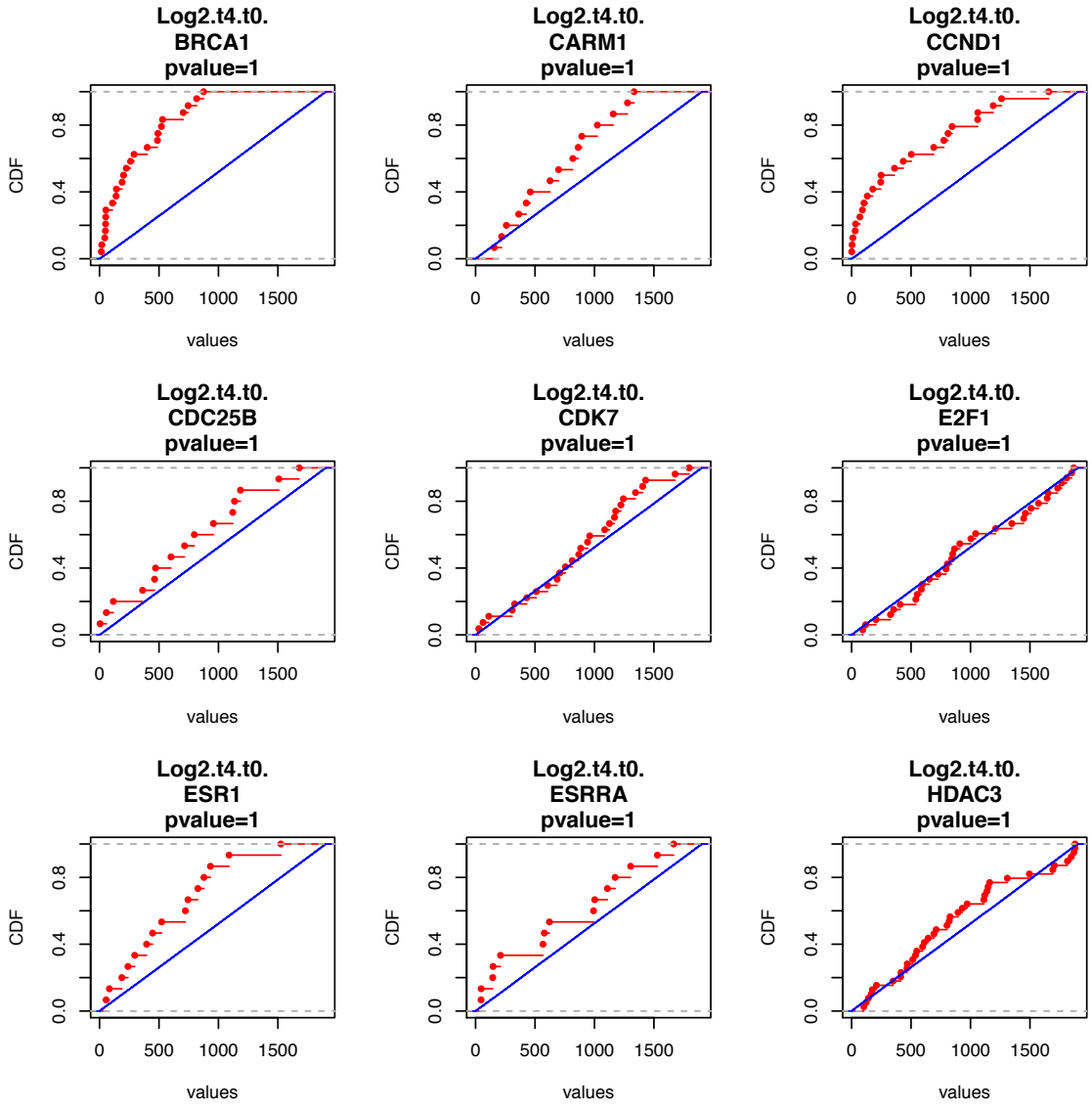


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (10/14)

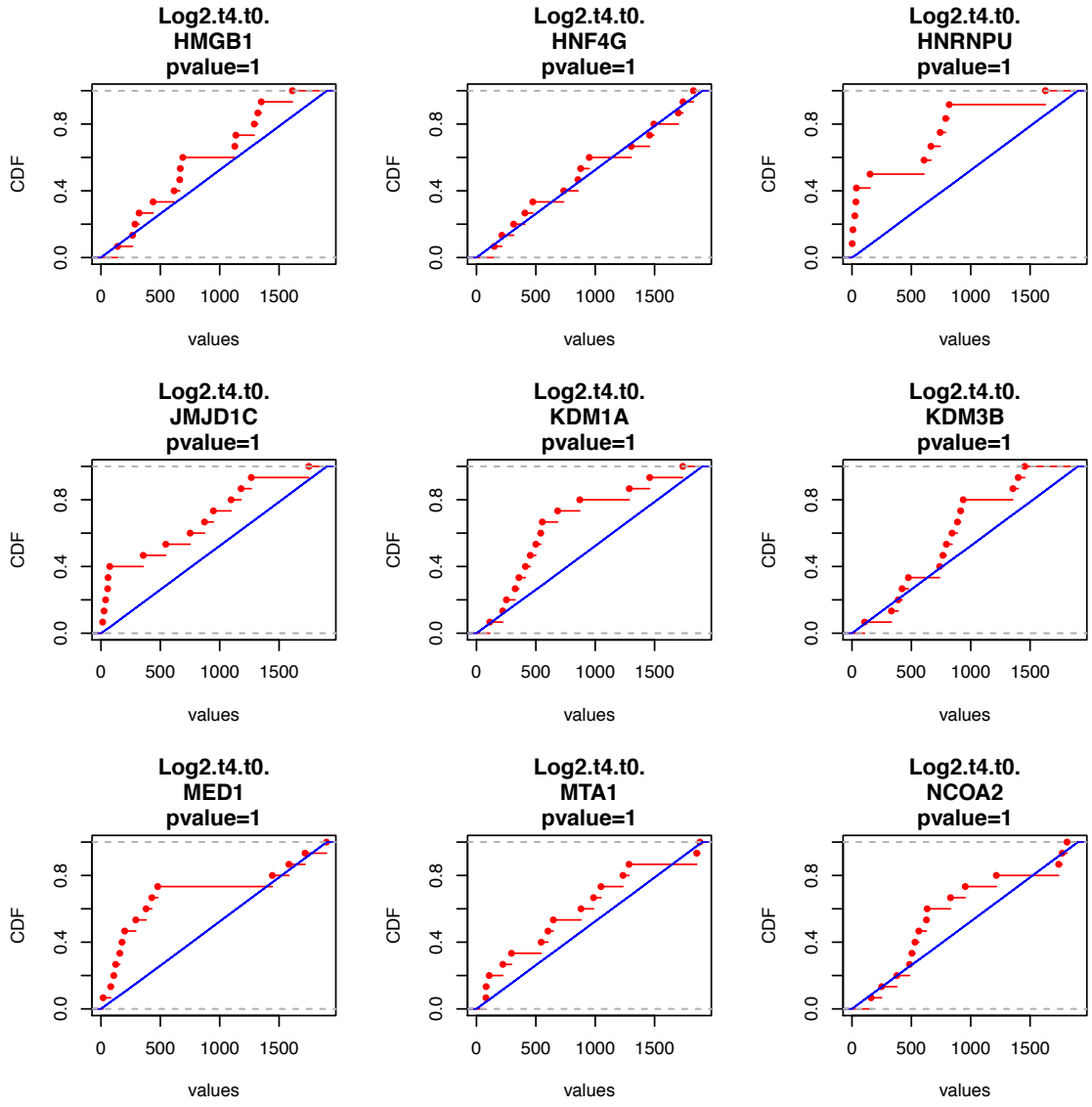


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (11/14)

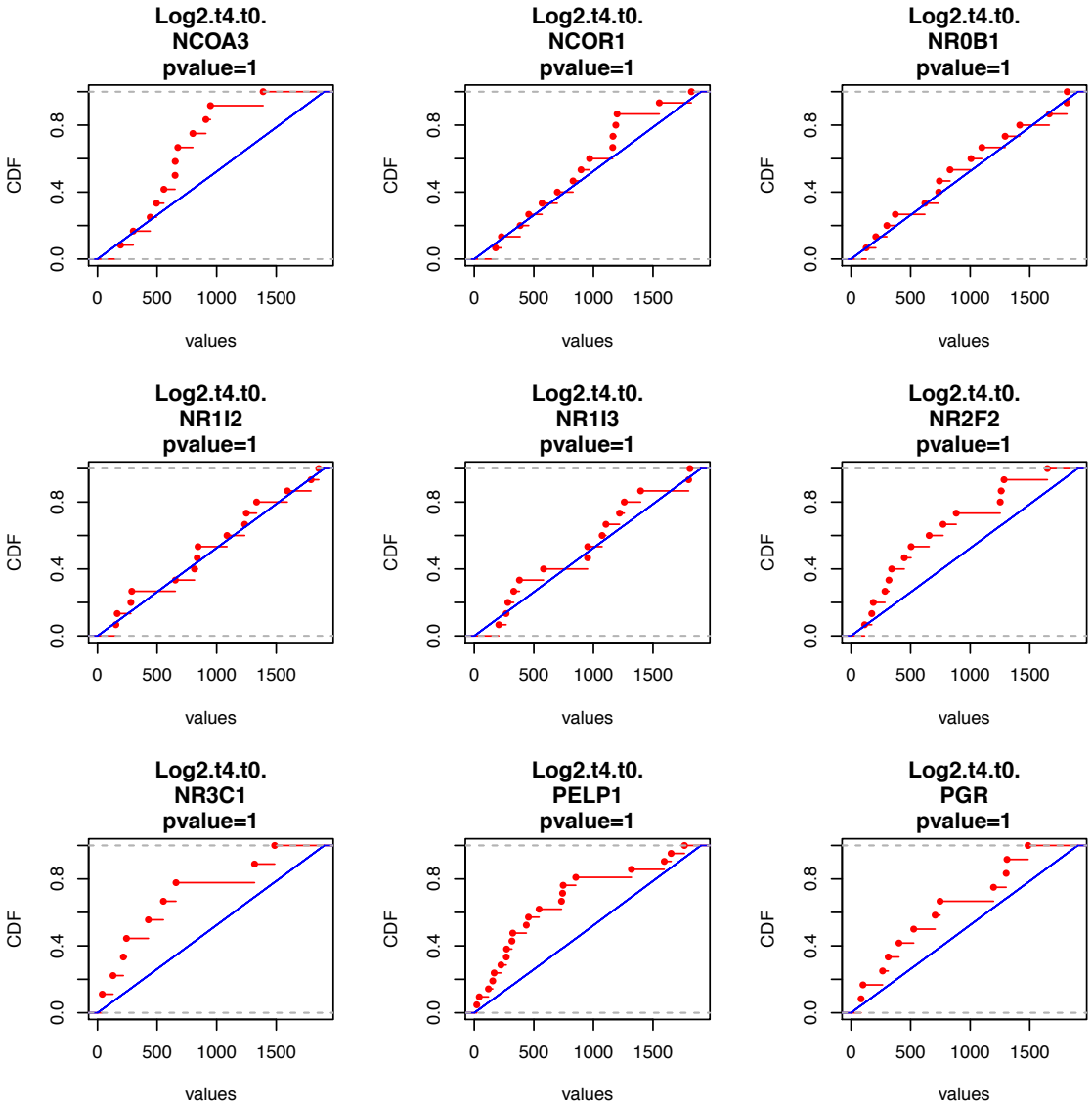


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (12/14)

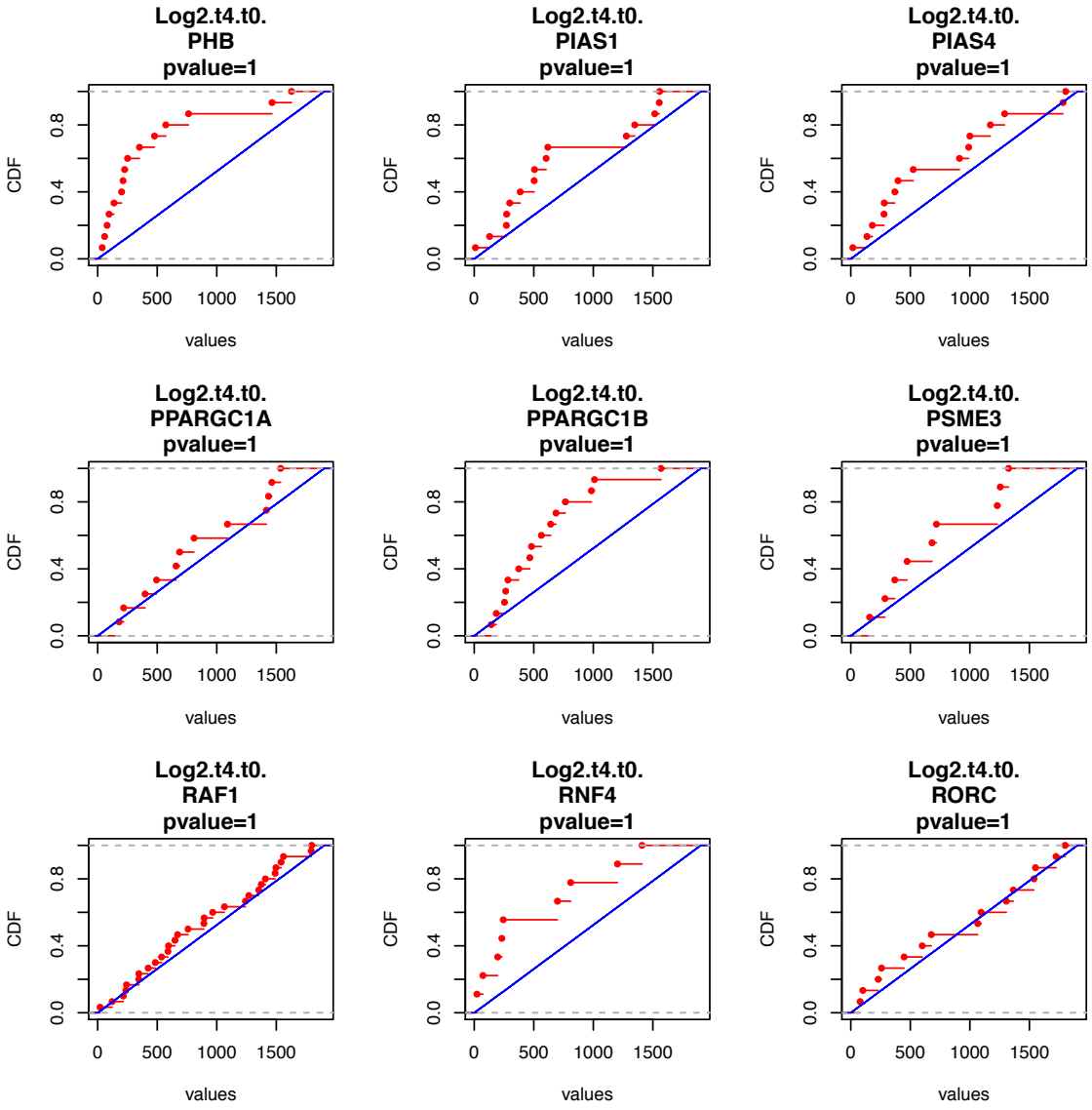


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. See final page for full legend. (13/14)

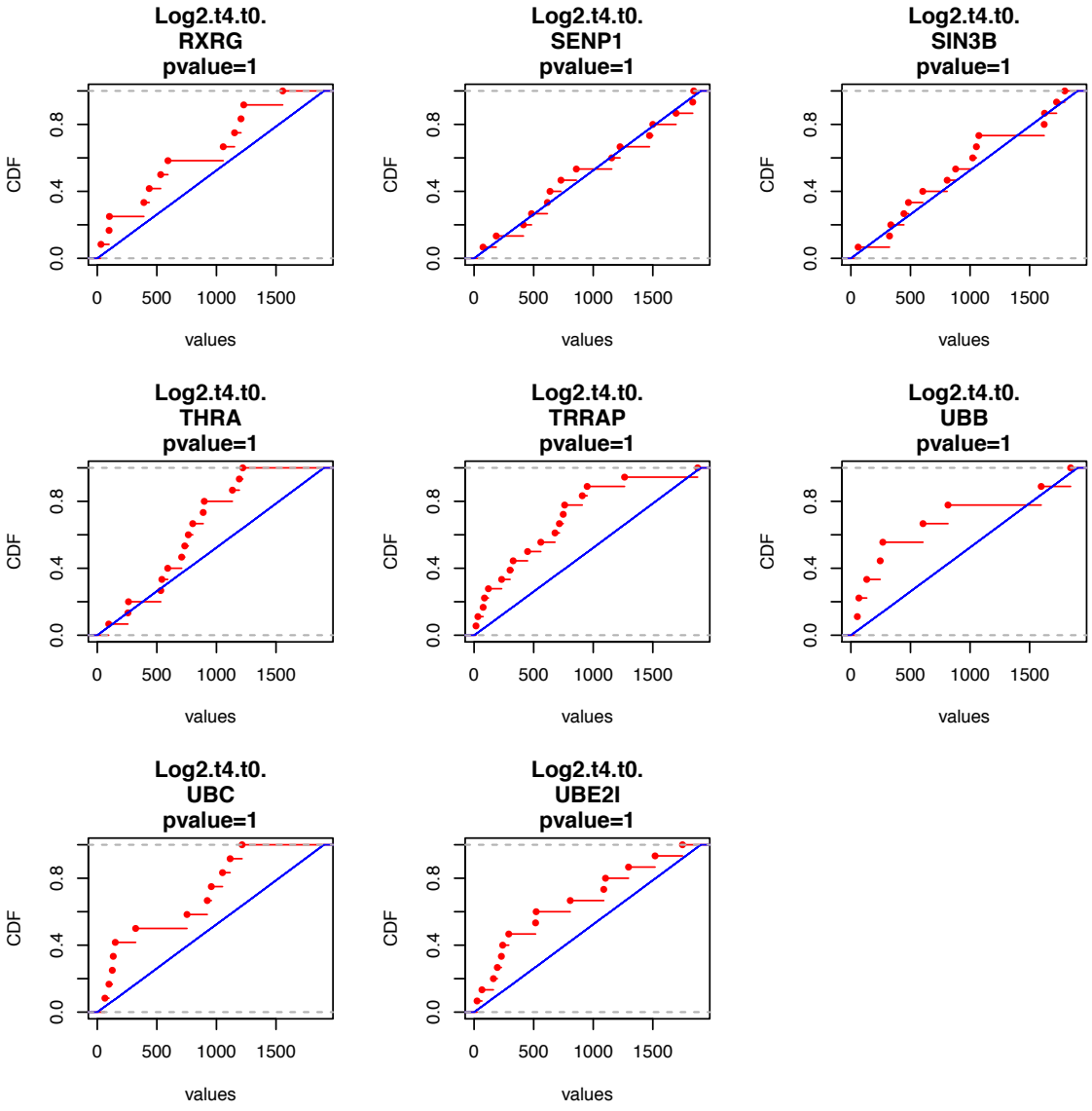


Figure D1. Cumulative distribution function plots with p-values for ranked Dmax KS-test. Individual shRNAs are shown in red, with rank transformed background shRNAs shown in blue. KS-test p-value is shown above each plot (14/14).

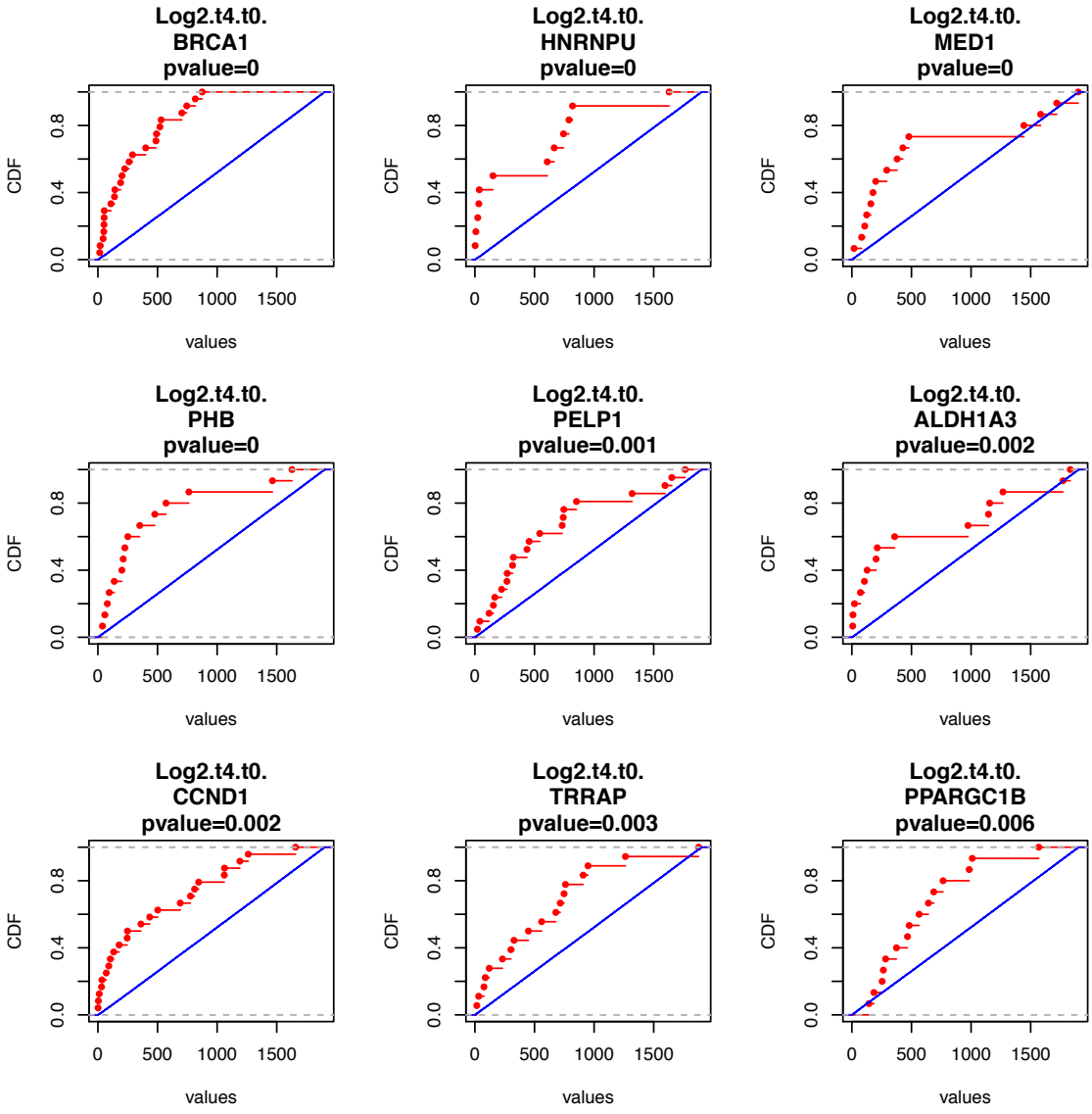


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (1/14)

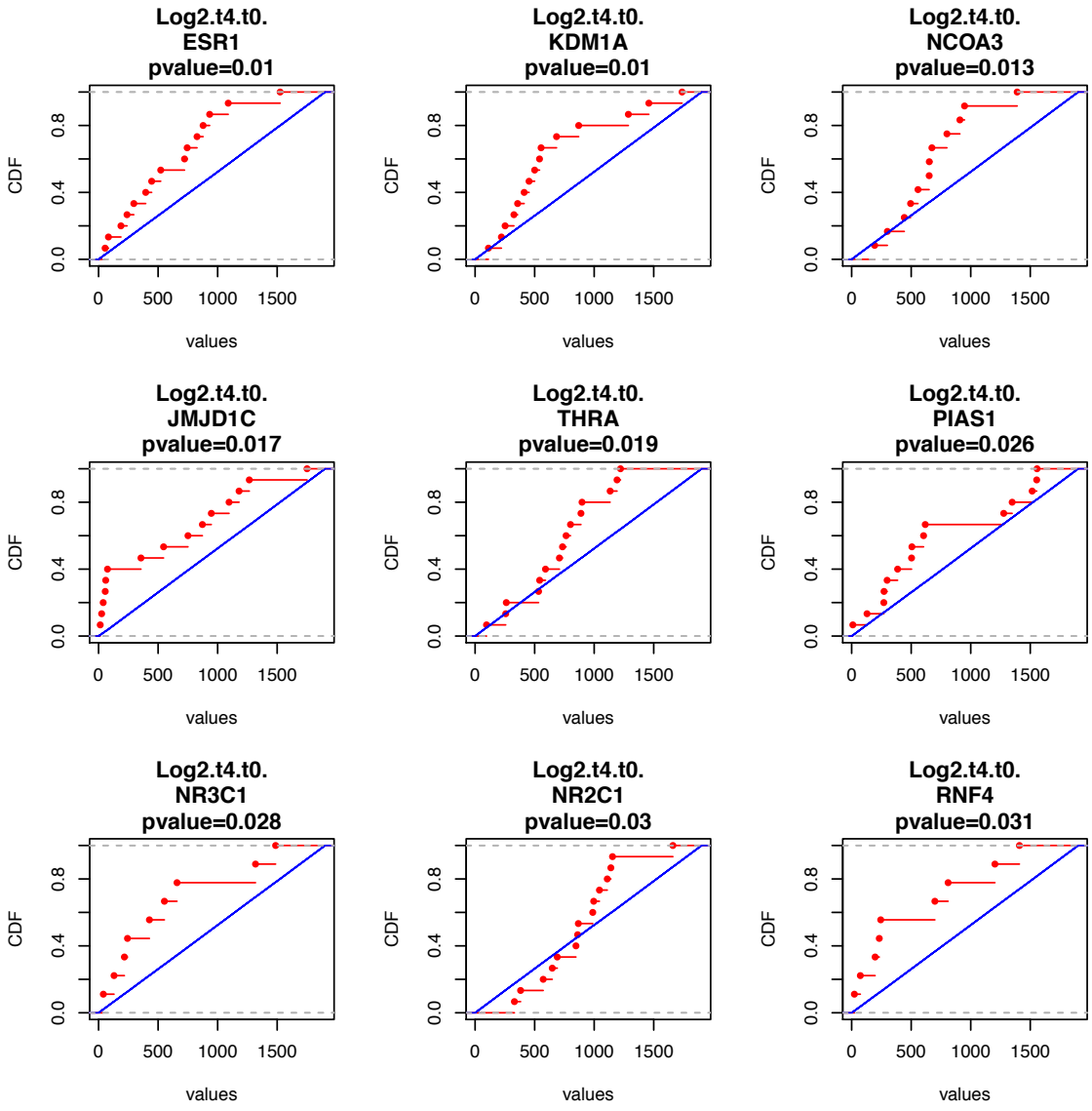


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (2/14)

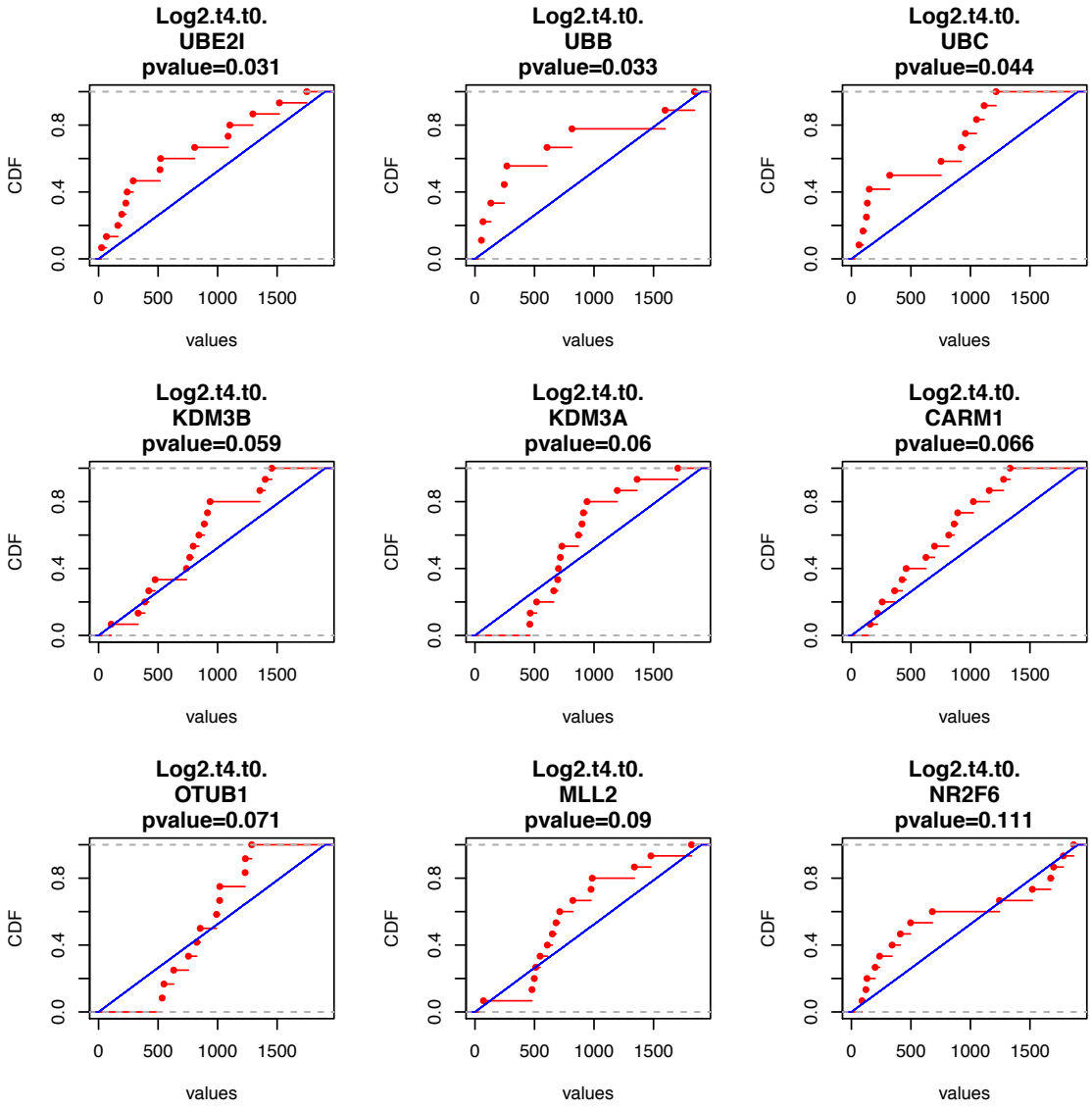


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (3/14)

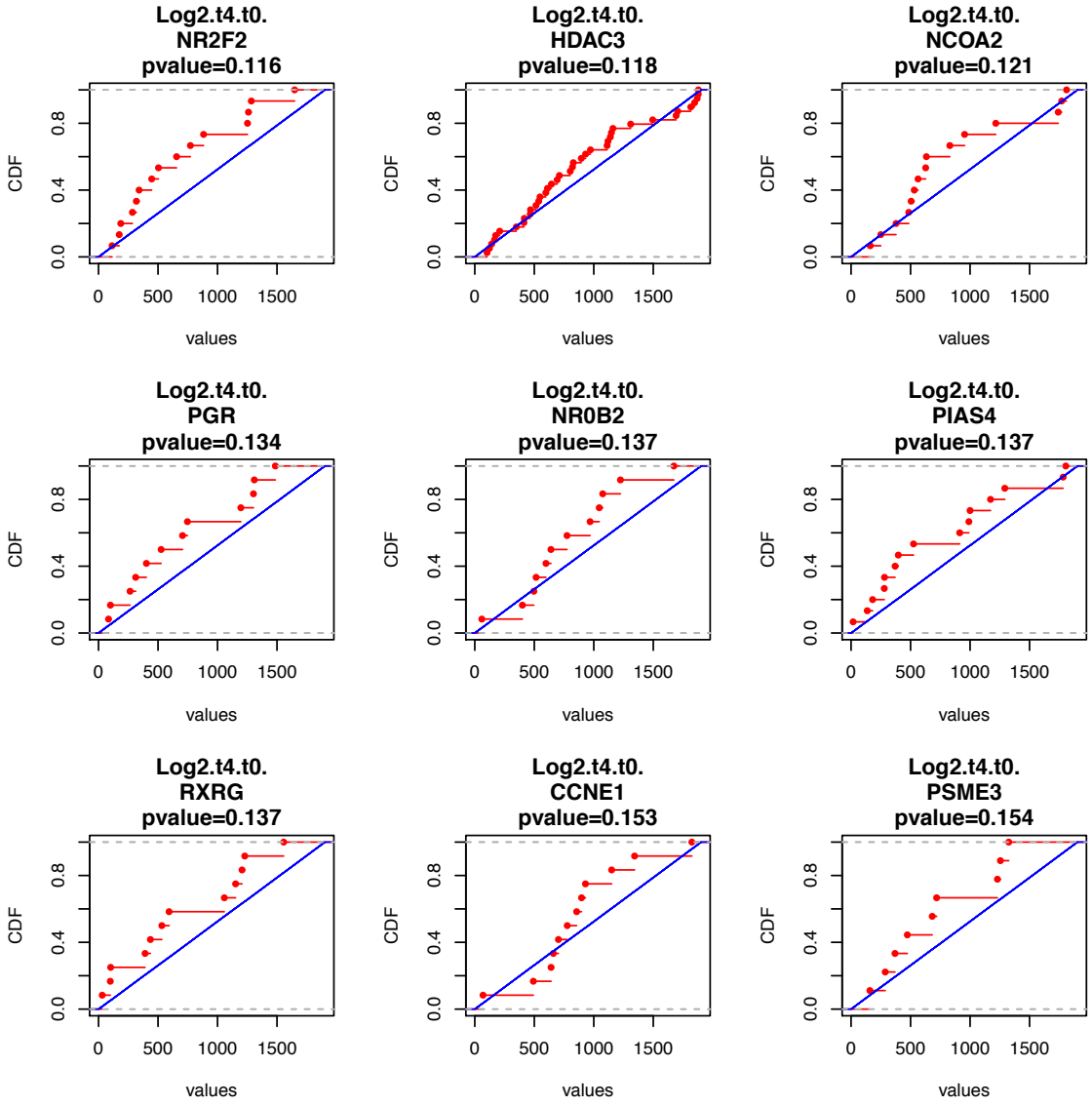


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (4/14)

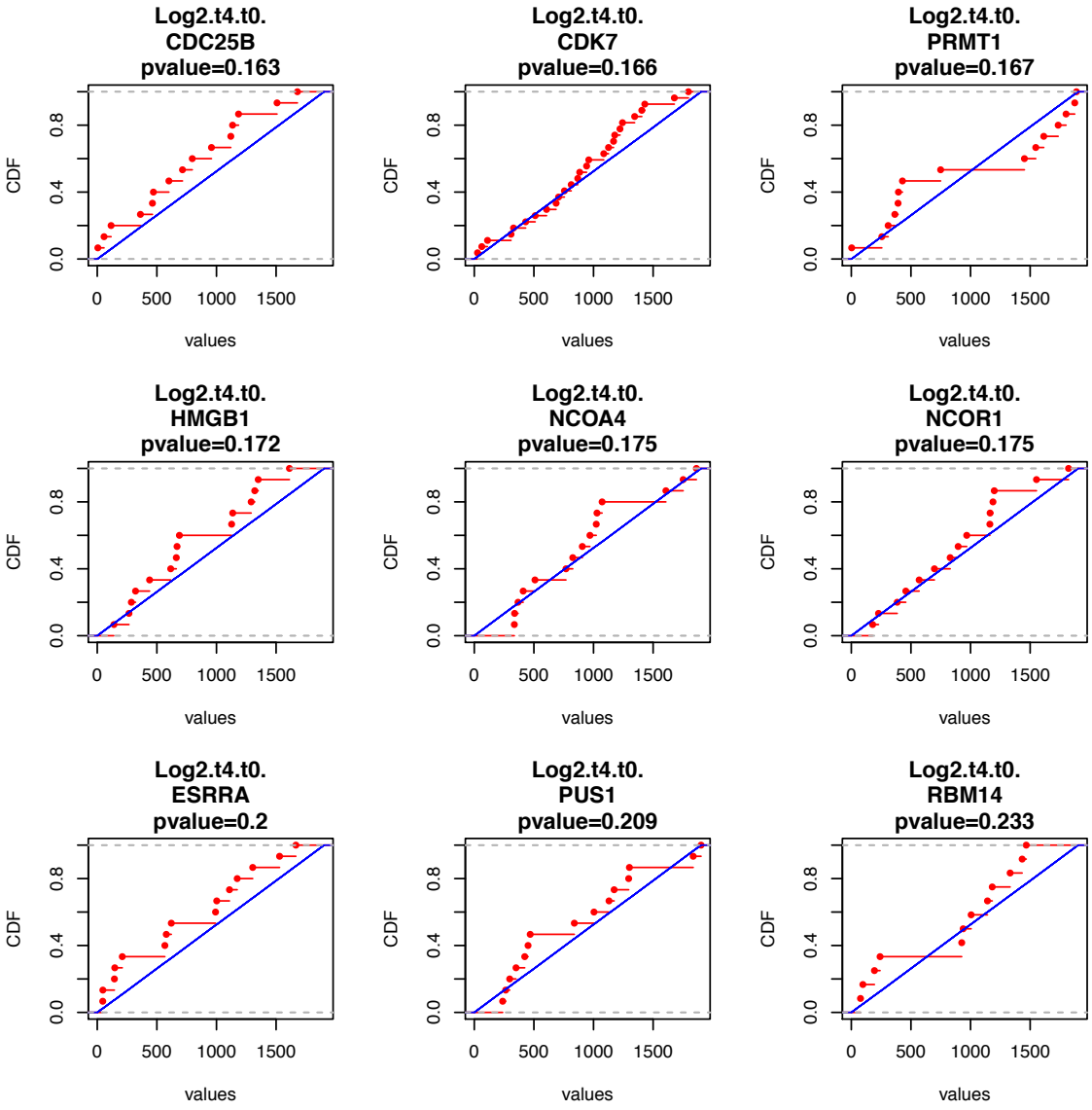


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (5/14)

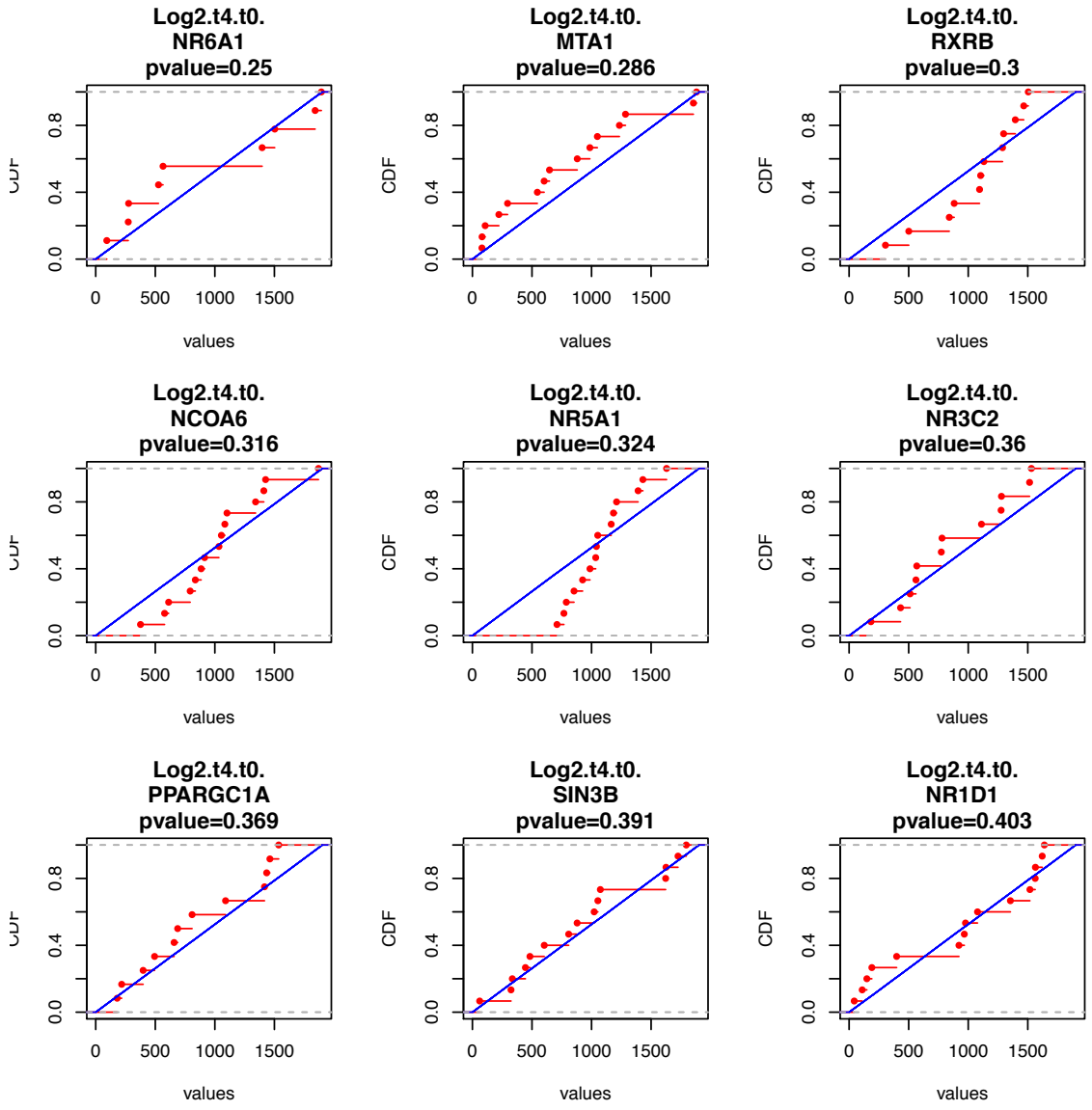


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (6/14)

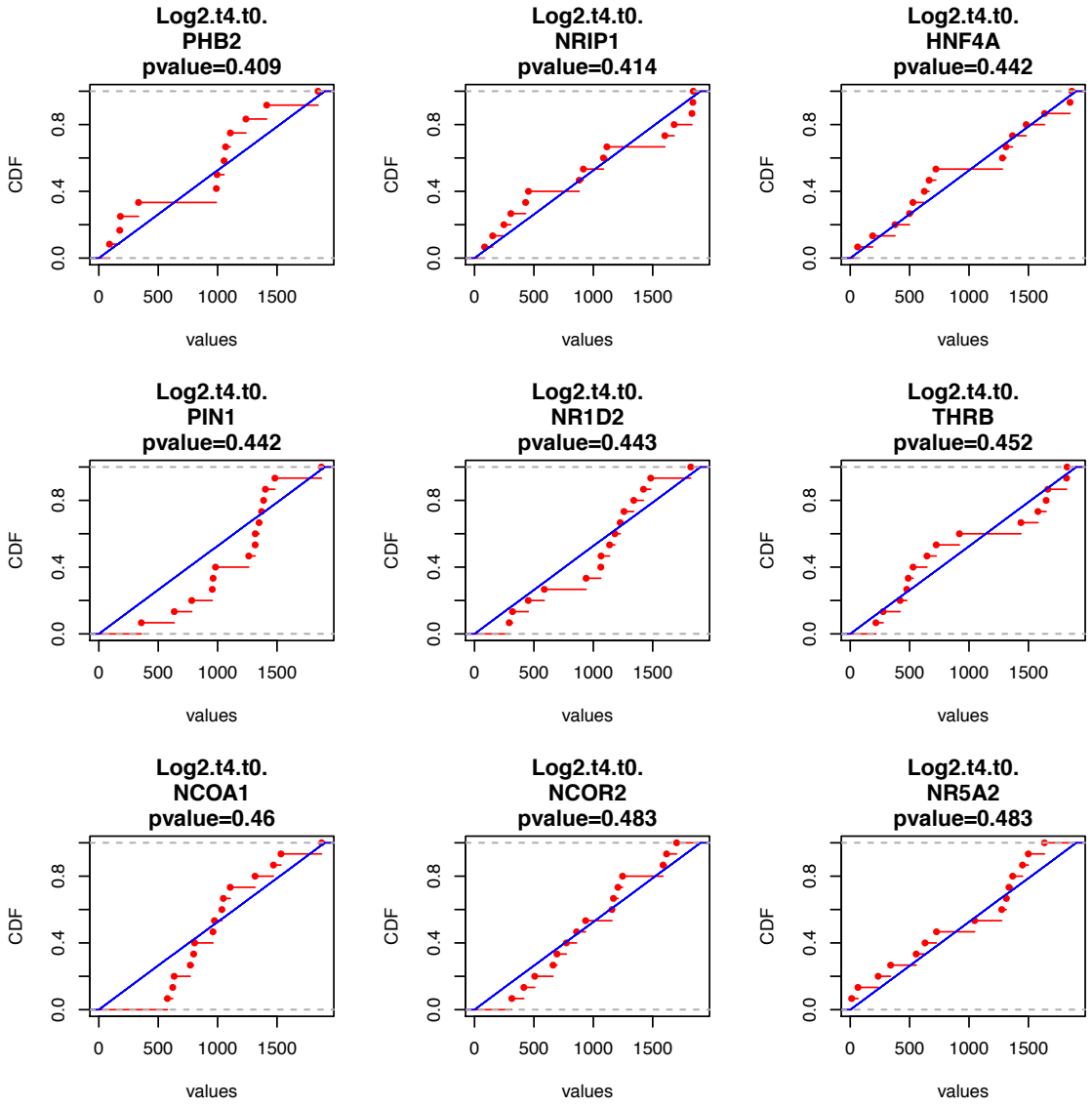


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (7/14)

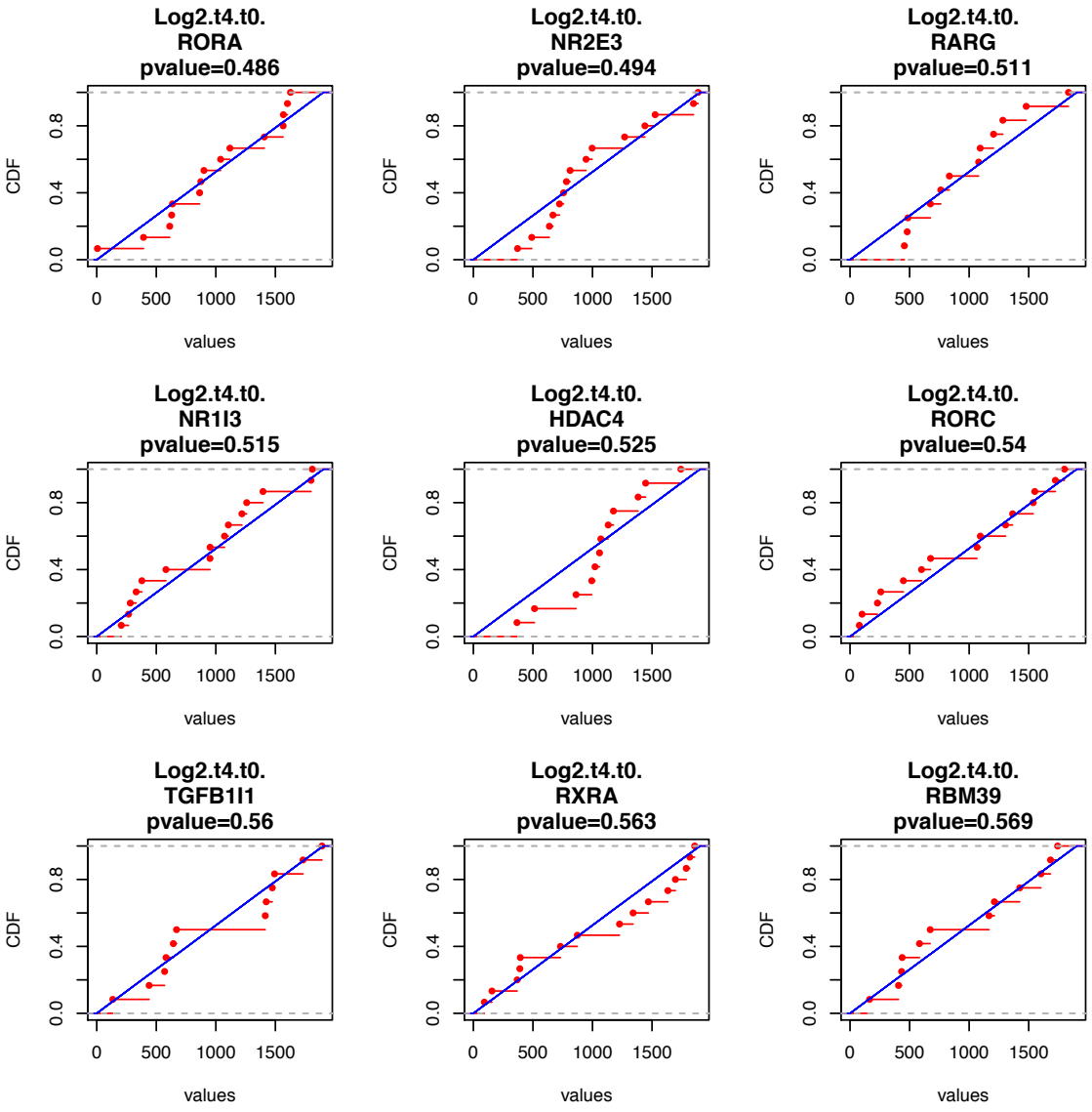


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (8/14)

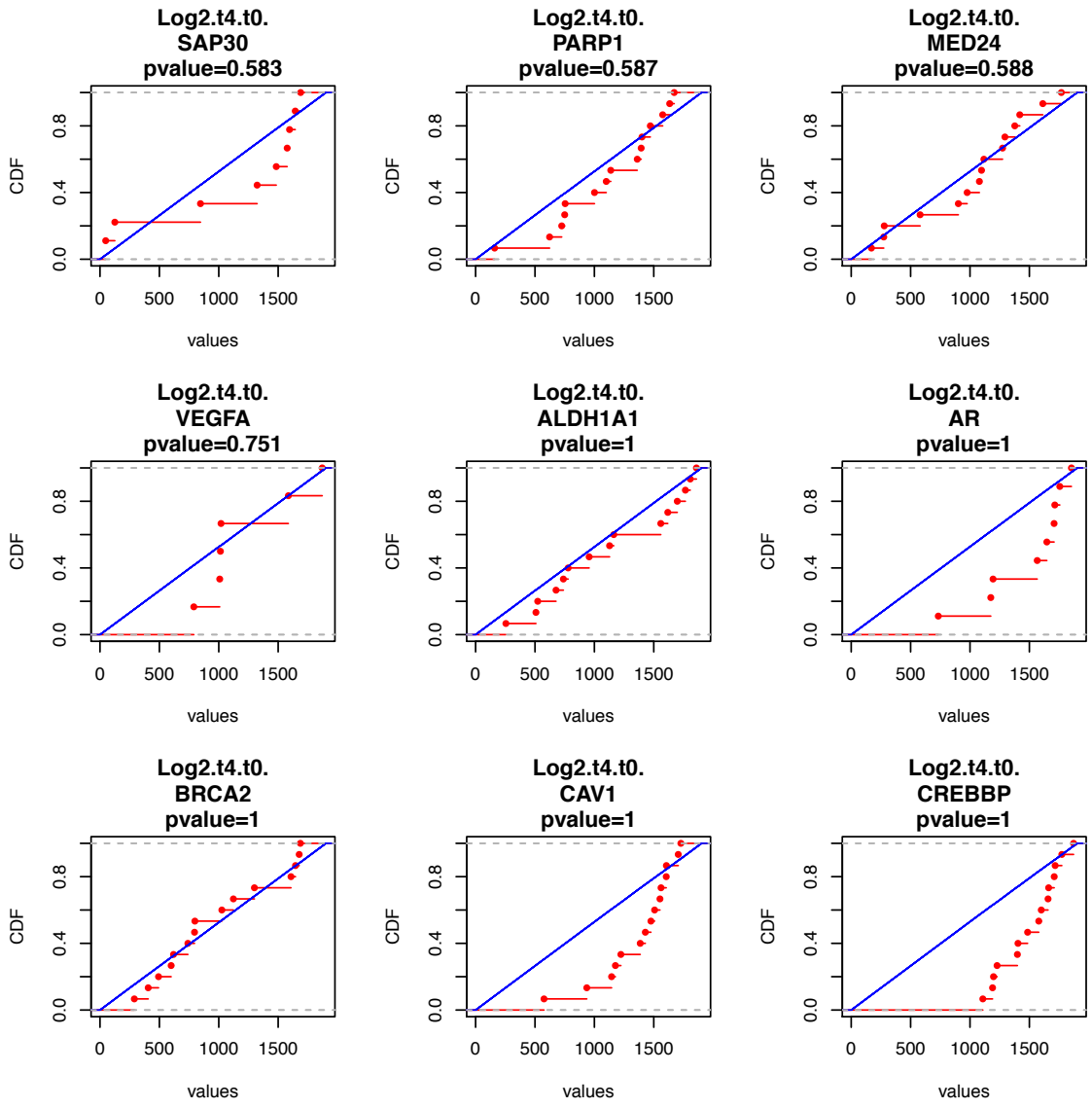


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (9/14)

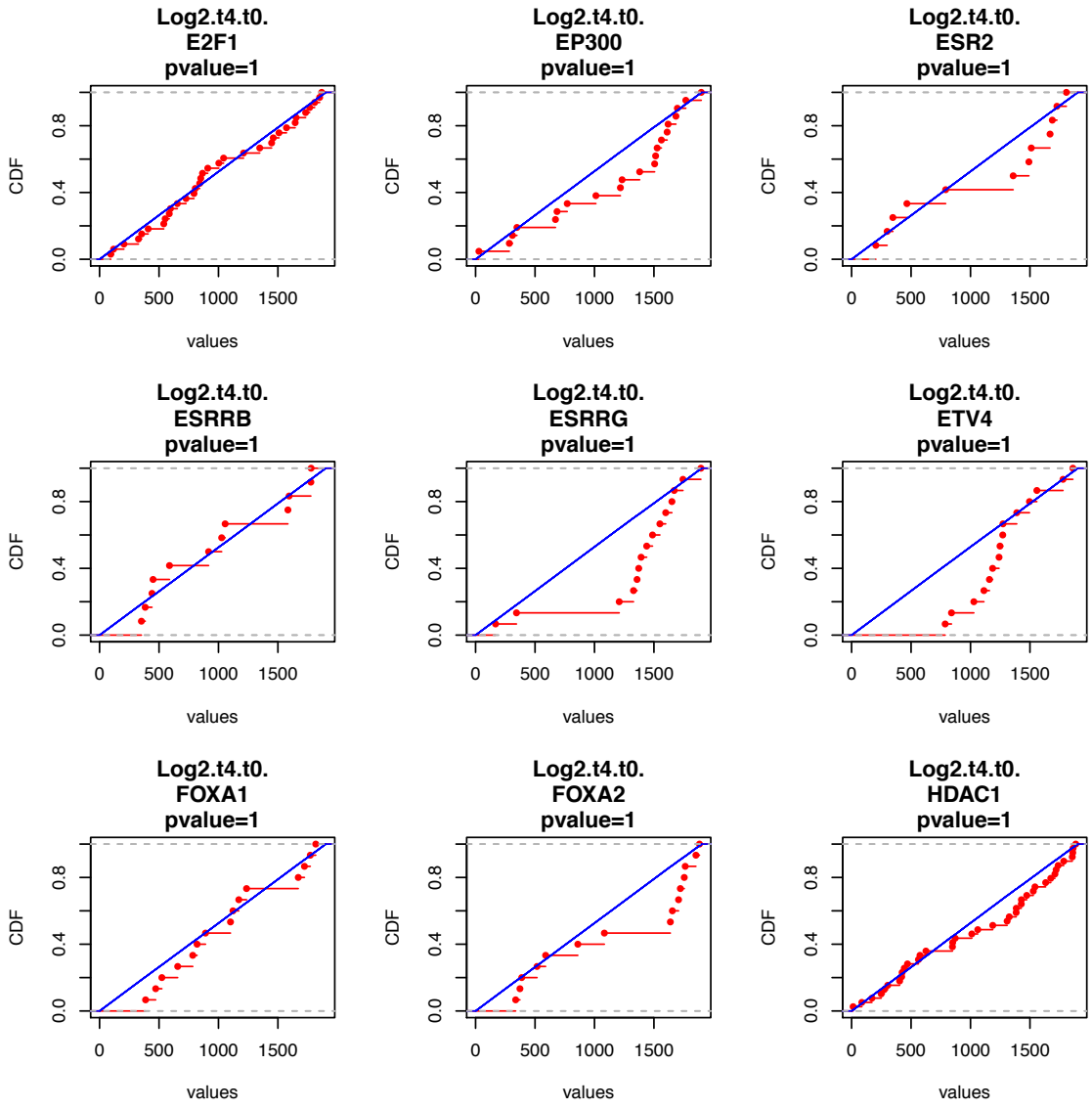


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (10/14)

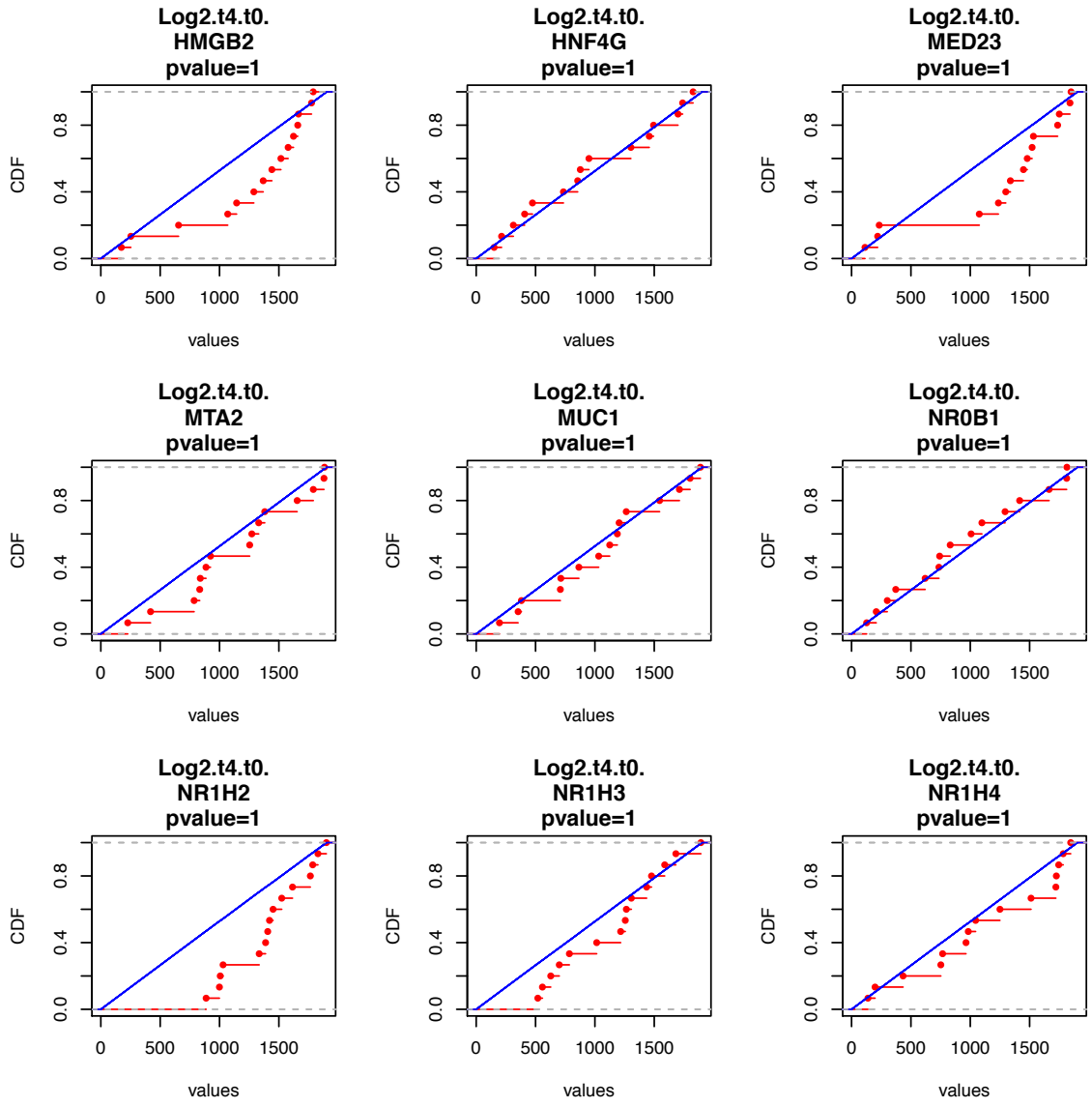


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (11/14)

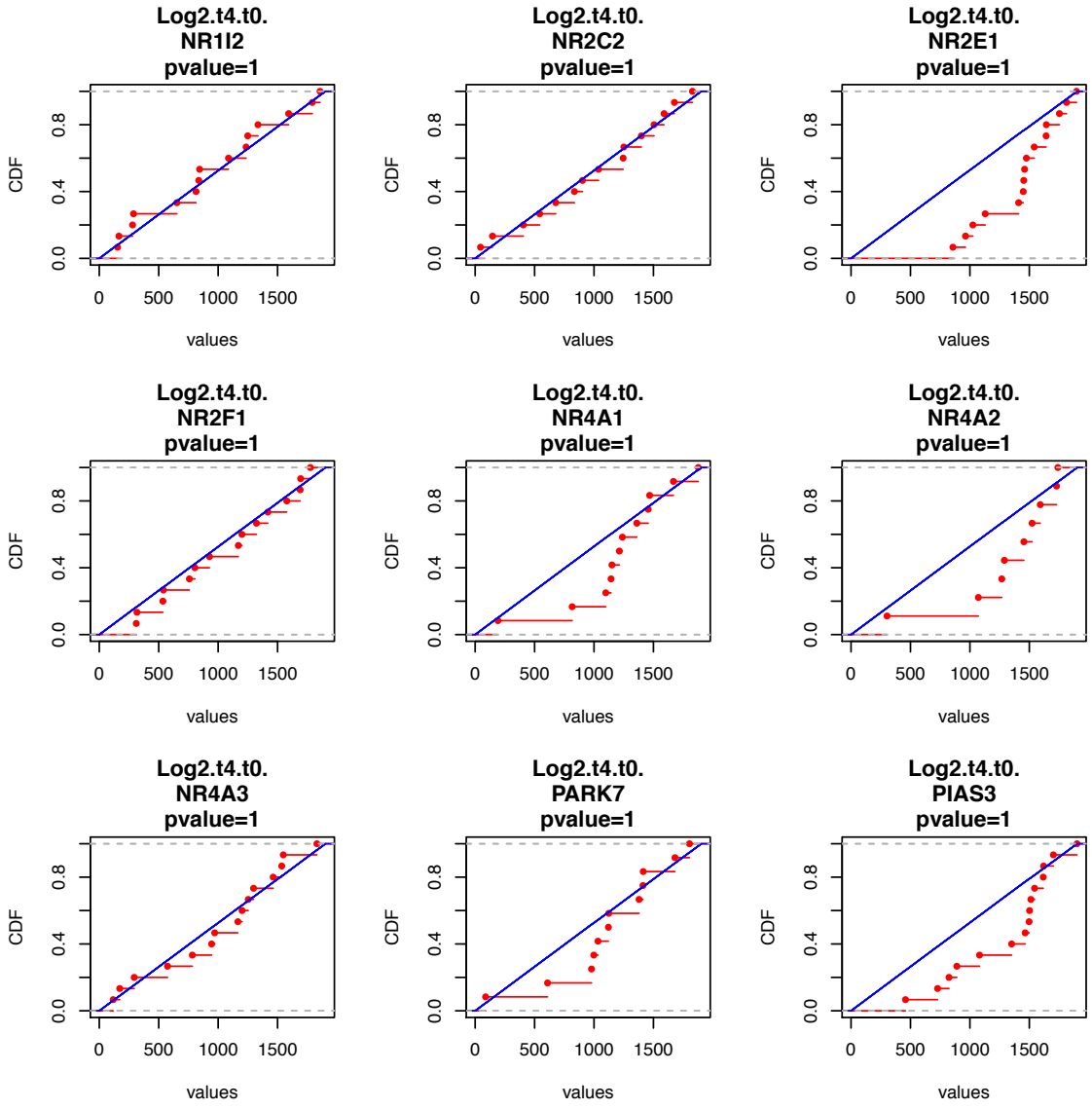


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (12/14)

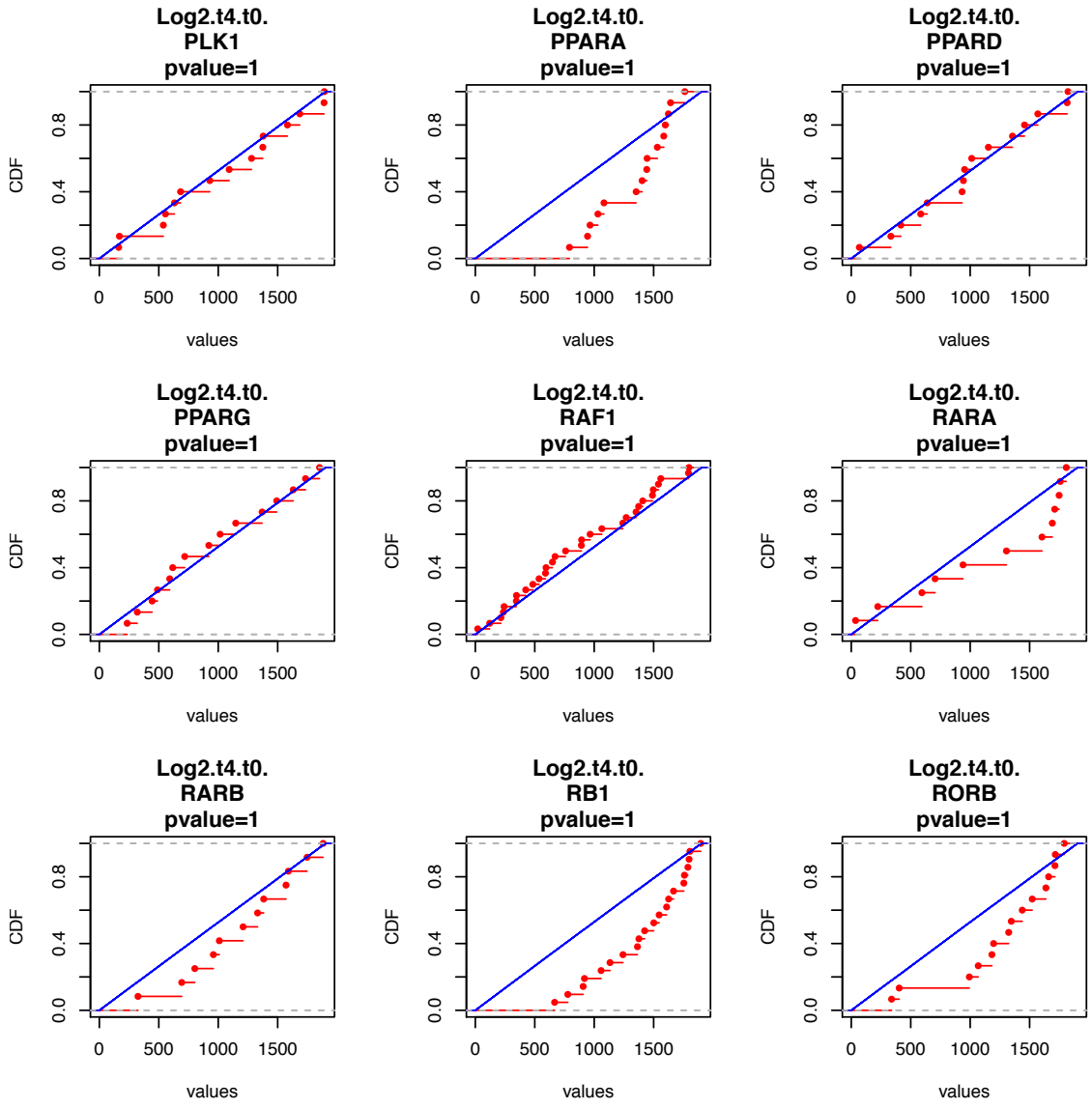


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. See final page for full legend. (13/14)

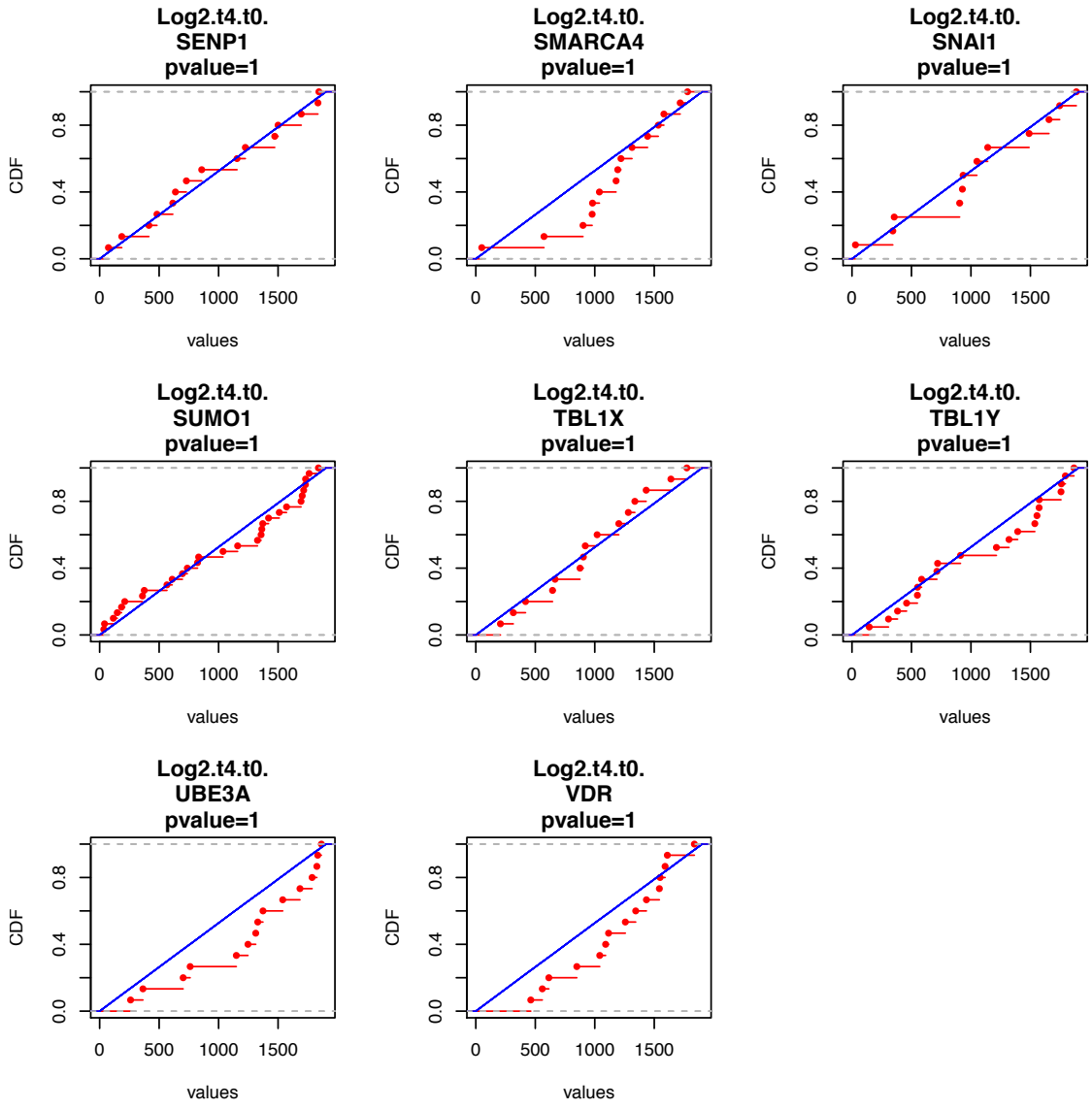
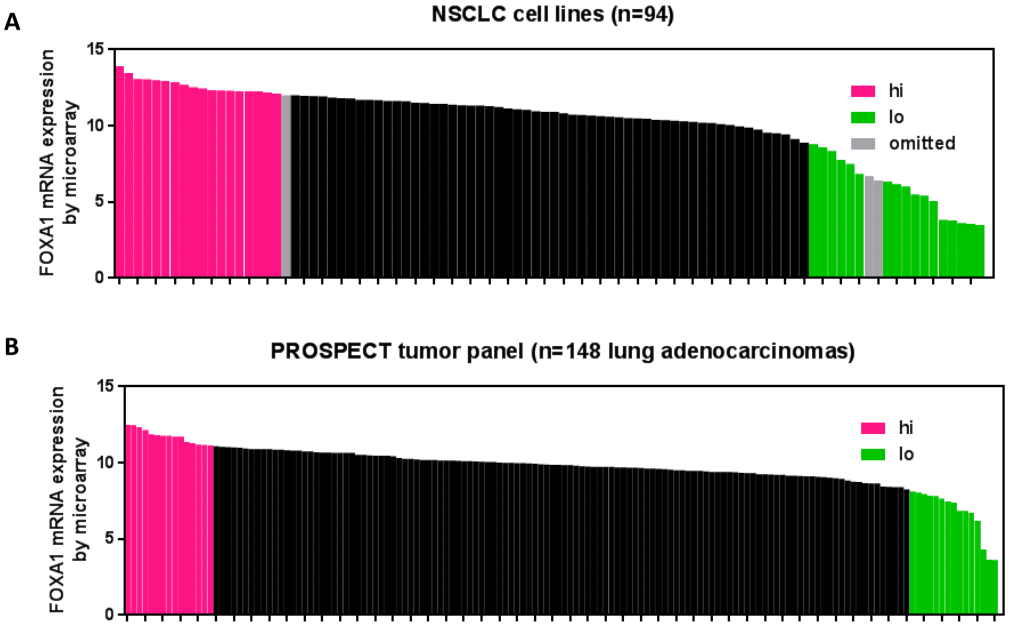


Figure D2. Cumulative distribution function plots with p-values for ranked Dmin KS-test. Individual shRNAs are shown in red, with rank transformed background shRNAs shown in blue. KS-test p-value is shown above each plot. (14/14)

APPENDIX E

SUPPLEMENTARY DATA FOR FOXA1-ASSOCIATED GENE SIGNATURE



C

Sample	FOXA1 hi/lo
H1781	HI
HCC1195	HI
H2126	HI
H1437	HI
H3255	HI
HCC4006	HI
H441	HI
HCC2935	HI
H1819	HI
H1734	HI
H1993	HI
H2087	HI
H1648	HI
H2122	HI
H3122	HI
H1651	HI
HCC515	HI
H1793	HI
H1570	
HCC2374	
HCC827	
H1755	
H820	
H322	
PC-9	
HCC1833	
HOP-62	
HCC78	
H2250	
HCC193	
H820	
H1838	
H969	
HCC44	
H460	
HCC3051	
Calu-3	
H2342	
HCC2279	
HCC4011	
H522	
HCC4019	
H1944	
H2009	
H2887	
H358	
H1373	
H1355	

Sample	FOXA1 hi/lo
H2030	
H1666	
H1155	
H2258	
HCC1171	
H2023	
EKVX	
H1395	
HCC1438	
H2347	
H2077	
HCC2429	
H2291	
H2172	
H2228	
H1792	
H324	
H1563	
H1573	
HCC4018	
H1693	
DFCI024	
A549	
DFCI032	
HCC4017	
HCC2108	
H2882	
H1568	LO
H1650	LO
Calu-6	LO
H2073	LO
HCC364	LO
H2086	LO
H2106	
H23	
H1299	LO
HCC461	LO
H650	LO
H661	LO
H2405	LO
H2085	LO
SK-LU-1	LO
H1975	LO
H838	LO
HCC1359	LO
HOP-92	LO

D

Sample	FOXA1 hi/lo
2274-T	hi
2278-T	hi
1736-T	hi
157-T	hi
1551-T	hi
1908-T	hi
1346-T	hi
432-T	hi
2313-T	hi
386-T	hi
2293-T	hi
15-T	hi
1311-T	hi
566-T	hi
1761-T	hi
2193-T	
1168-T	
2259-T	
814-T	
2249-T	
1325-T	
1353-T	
1956-T	
539-T	
426-T	
471-T	
1714-T	
1041-T	
1718-T	
850-T	
1921-T	
1405-T	
1872-T	
1913-T	
1723-T	
2382-T	
259-T	
819-T	
1323-T	
1161-T	
296-T	
475-T	
724-T	
1549-T	
1937-T	
2305-T	
764-T	
1305-T	
2157-T	
590-T	
2076-T	
1038-T2	
546-T	
717-T	
2207-T	
1498-T	
1465-T	
1890-T	
1376-T	
633-T2	
363-T	
952-T	
1930-T	
2172-T	
534-T	
830-T	
1793-T	
1454-T	
495-T	
2192-T	
630-T	
2264-T	
593-T	
1401-T	
1357-T	
309-T	
2185-T	

Sample	FOXA1 hi/lo
1462-T	
1240-T	
2281-T	
1218-T	
1805-T	
2279-T	
2296-T	
1496-T	
1266-T	
2308-T	
482-T	
2237-T	
1289-T	
759-T3	
619-T2	
2214-T	
940-T	
1980-T	
2242-T	
2275-T	
1282-T	
1853-T	
1380-T	
1898-T2	
1434-T	
2230-T	
1601-T	
1671-T	
1727-T	
1662-T	
2302-T	
2287-T	
2309-T	
1936-T	
1944-T	
2269-T	
2190-T	
1607-T	
1964-T	
412-T	
1867-T	
1858-T2	
1933-T	
1729-T	
1894-T	
1354-T	
2138-T	
1238-T	
96-T	
1834-T	
2204-T	
1804-T	
2045-T	
1284-T	
1476-T	
1987-T	
650-T2	lo
2024-T	lo
999-T	lo
1443-T	lo
2442-T	lo
404-T	lo
922-T2	lo
697-T	lo
399-T	lo
2247-T	lo
1502-T2	lo
2155-T	lo
1255-T	lo
2212-T	lo
1237-T	lo

Figure E1. Selection of FOXA1 hi and FOXA1 lo samples used to derive the FOXA1-associated signature. (A) NSCLC cell lines in the top and bottom 20th percentiles of FOXA1 expression were classified as FOXA1 hi and lo, respectively. Some cell lines falling within these percentiles were omitted from analysis (gray). (B) Lung adenocarcinomas in the top and bottom 10th percentiles of FOXA1 expression were classified as FOXA1 hi and lo, respectively. (C) NSCLC cell lines and (D) PROSPECT tumors included in percentile calculations.

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Bi-pers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
38441	7400377	19q13.2	1.281	7.65	0.000	U	0.000	U	P	x	x	x		CEACAM6
4397	830056	14q21.1	2.869	6.75	0.000	U	0.000	U			x	x	x	FOXA1
8259	1510424	4p16.1	0.806	5.45	0.000	U	0.000	U			x			S100P
24179	4610520	15q22.2	0.951	5.39	0.000	U	0.000	U			x	x		GCNT3
19704	3850246	4q12	0.939	4.97	0.000	U	0.000	U			x	x		HOPX
16567	3170594	8q24.12	0.830	4.78	0.000	U	0.000	U		x	x			MAL2
337	50195	1q22	0.734	4.78	0.000	U	0.000	U	P	x				RAB25
8893	1690400	1q41	1.016	4.76	0.000	U	0.000	U			x			CAPN8
920	1110685	9q22.2	1.706	4.74	0.000	U	0.000	U			x			SYK
17725	3400097	3q29	1.136	4.72	0.000	U	0.000	U			x			MUC20
36892	7040487	12p13.31	1.078	4.67	0.000	U	0.000	U	P	x	x	x		SCNN1A
19017	3780082	1p34.2	1.103	4.65	0.000	U	0.000	U		x				TMEM125
19590	3840491	14q22.3	1.502	4.56	0.000	U	0.000	U			x			PELI2
6452	1240037	4q13.3	1.125	4.56	0.000	U	0.000	U						PARM1
8238	1510300	1q32.1	1.140	4.53	0.000	U	0.000	U	P		x	x		ELF3
14312	2680241	3q13.33	1.337	4.51	0.000	U	0.000	U						ILDR1
20019	3890228	11q23.3	1.085	4.50	0.000	U	0.000	U		x				MPZL2
3902	6700754	14q23.1	0.852	4.47	0.000	U	0.000	U	P	x				TMEM30B
26515	5080373	17p13.1	0.854	4.45	0.000	U	0.000	U	P	x	x			CLDN7
32789	6330201	20p11.23	0.859	4.41	0.000	U	0.000	U			x			OVOL2
37694	7200601	1q22	1.027	4.39	0.000	U	0.000	U		x	x			MUC1
30817	6020224	9q22.32	0.927	4.34	0.000	U	0.000	U	P					FBP1
14710	2710735	17p11.2	0.903	4.33	0.000	U	0.000	U			x			RASD1
16386	3140463	7p21.1	1.205	4.31	0.000	U	0.000	U			x			AGR2
13658	2600170	16p13.12	1.267	4.27	0.000	U	0.000	U						PLA2G10
9779	1850300	14q32.12	1.742	4.24	0.000	U	0.000	U			x			TC2N
6778	1300113	16q22.1	0.792	4.20	0.001	U	0.000	U		x	x	x		CDH1
5133	990619	16p11.2	0.643	4.19	0.001	U	0.000	U	P	x	x	x		PRSS8
2994	540546	12q13.13	0.868	4.11	0.000	U	0.000	U			x	x		KRT4
31197	6060630	17q21.2	0.574	4.10	0.004	U	0.001	U		x	x	x		KRT19
13563	2570538	13q32.1	0.874	4.06	0.000	U	0.000	U						SOX21
19586	3840470	17q25.1	1.447	4.05	0.000	U	0.000	U			x	x		ST6GALNAC1
4770	870376	9q31.3	0.930	4.00	0.000	U	0.000	U			x			C9orf152
23195	4390398	9q34.11	0.521	3.99	0.004	U	0.001	U						LCN2
3287	610437	Yq11.222	0.792	3.99	0.000	U	0.000	U						CD24
39295	7650026	1q22	1.070	3.97	0.000	U	0.000	U		x	x			MUC1
23711	4560288	12q13.2	0.995	3.96	0.000	U	0.000	U		x	x	x		ERBB3
37190	7100435	9q21.32	1.178	3.95	0.000	U	0.000	U			x			RASEF
32323	6270138	1p32.1	0.637	3.90	0.001	U	0.000	U		x	x	x		TACSTD2
18499	3460739	2q37.3	0.767	3.89	0.000	U	0.000	U	P					RAB17
10078	1980246	15q21.2	1.421	3.88	0.000	U	0.000	U	P		x	x		MYO5C
4009	730491	1q32.1	0.899	3.87	0.000	U	0.000	U	P	x	x	x		C1orf116
2756	520128	1q22	1.143	3.84	0.000	U	0.000	U		x	x			MUC1
38723	7550292	1q21.3	0.908	3.83	0.000	U	0.000	U	P					SELENBP1
19260	3800465	15q26.1	1.098	3.81	0.000	U	0.000	U			x	x	x	FAM174B
38757	7550445	19q13.2	1.043	3.79	0.000	U	0.000	U			x			CXCL17
2935	540204	2p24.2	0.937	3.78	0.000	U	0.000	U	P		x			KCNS3
2245	430541	11q24.3	1.444	3.75	0.000	U	0.000	U		x	x	x		TMEM45B
19192	3800161	12q13.13	0.620	3.75	0.001	U	0.000	U			x			KRT7
18300	3450524	19p13.3	0.919	3.73	0.000	U	0.000	U		x	x	x		TJP3
21153	4060497	14q13.3	0.601	3.71	0.002	U	0.000	U	P					NKX2-1
23757	4560543	12q21.1	0.839	3.68	0.000	U	0.000	U			x			TSPAN8
13423	2510669	16q24.1	1.152	3.64	0.000	U	0.000	U	P		x			ATP2C2
11262	2120452	2q37.3	0.627	3.61	0.002	U	0.000	U						MLPH
37372	7150634	3q29	0.726	3.61	0.000	U	0.000	U			x			APOD
29873	5860093	15q22.2	1.070	3.61	0.000	U	0.000	U						C2CD4B
37101	7100021	1q32.1	0.838	3.58	0.000	U	0.000	U			x	x		C1orf106
26639	5090278	14q23.3	0.548	3.56	0.003	U	0.001	U						GPX2
20209	3930424	21q22.12	0.724	3.54	0.001	U	0.000	U			x			CLIC6
26649	5090347	Yq11.222	0.734	3.54	0.000	U	0.000	U						CD24
24422	4670138	15q21.2	1.322	3.54	0.000	U	0.000	U						SLC27A2
19129	3780603	6p12.3	0.491	3.51	0.009	U	0.002	U	P		x	x	x	GPR116
4898	940242	14q13.3	0.595	3.51	0.002	U	0.000	U	P					NKX2-1
6424	1230672	21q22.3	0.659	3.48	0.005	U	0.001	U						TFF1
6093	1170349	1q32.1	0.551	3.48	0.003	U	0.001	U						LAD1
38467	7400524	19p13.3	0.967	3.46	0.000	U	0.000	U		x				CRB3
39086	7570484	21q22.3	0.494	3.44	0.006	U	0.002	U						TFF3
22682	4260278	11q24.3	0.728	3.43	0.000	U	0.000	U		x				ST14
21395	4120193	2q11.1	0.612	3.39	0.001	U	0.000	U						PROM2
33179	6370553	7q34	0.644	3.37	0.001	U	0.000	U		x				EPHA1
11075	2100296	19q13.33	0.529	3.35	0.005	U	0.001	U						NAP5A
35431	6760072	14q13.3	0.582	3.34	0.002	U	0.000	U						SFTA3
13364	2510358	1p34.1	0.983	3.33	0.000	U	0.000	U			x			TSPAN1
30002	5860767	15q15.1	0.774	3.32	0.000	U	0.000	U			x	x		SFXN1
10224	1990142	20q11.21	0.767	3.31	0.002	U	0.000	U						C20orf114
22642	4260088	17q25.1	1.282	3.28	0.000	U	0.000	U						C17orf28
4945	940487	19p13.3	0.713	3.28	0.000	U	0.000	U						FUT3
29989	5860689	22q11.21	0.674	3.24	0.000	U	0.000	U	P					PRODH
9691	1820632	1q31.1	0.599	3.22	0.001	U	0.000	U						PTGS2
29795	5820491	6q23.3	0.929	3.21	0.000	U	0.000	U			x			MAP7
7753	1450348	19q13.42	0.797	3.20	0.000	U	0.000	U		x	x			TMC4
9387	1770603	11q12.1	0.431	3.20	0.015	U	0.005	U						TCN1
12497	2360632	19q13.2	1.137	3.20	0.000	U	0.000	U						CEACAM5
24476	4670402	19p13.3	0.908	3.18	0.000	U	0.000	U		x				CRB3
23156	4390221	1p35.3	0.981	3.18	0.000	U	0.000	U	P					SMPDL3B
1002	130324	21q22.3	0.821	3.18	0.000	U	0.000	U						TMPRSS2
28785	5570114	9q22.2	1.287	3.17	0.000	U	0.000	U	P					GADD45G
25008	4810026	11q23.3	0.884	3.16	0.000	U	0.000	U		x				MPZL2
7627	1440474	3q21.2	0.630	3.15	0.001	U	0.000	U						ALG1L
12772	2450411	10q21.3	0.694	3.15	0.000	U	0.000	U			x	x		DNAJC12
1150	150202	11q23.3	1.134	3.14	0.000	U	0.000	U		x				MPZL2
11441	2140541	9q34.3	0.733	3.14	0.000	U	0.000	U						LRRC26
6468	1240093	1q21.3	0.772	3.13	0.000	U	0.000	U		x				S100A14
26754	5130156	3q26.33	0.558	3.10	0.002	U	0.000	U			x	x		SOX2
3376	620102	2q13	0.717	3.10	0.001	U	0.000	U	P					MAL1
27890	5360301	12p12.3	0.517	3.09	0.005	U	0.001	U	P		x	x		LMO3
19175	3800088	11q22.2	0.459	3.08	0.011	U	0.003	U			x	x		MMP7
2419	450750	2p23.1	1.026	3.06	0.000	U	0.000	U			x			CAPN13
4866	940075	6q21.31	0.654	3.06	0.001	U	0.000	U			x			SPDEF
462	60014	8q24.21	0.837	3.05	0.000	U	0.000	U			x	x		FAM84B
7175	1400474	17q11.2	0.802	3.03	0.000	U	0.000	U			x	x		MYO1D
394	50446	2q14.2	0.784	3.02	0.000	U	0.000	U			x	x		INHBB
38582	7510367	3q26.2	1.106	3.01	0.000	U	0.000	U						GPR160
22040	4210228	7q21.3	0.575	3.00	0.004	U	0.001	U			x			PON3
10163	1980670	1q21.3	0.677	3.00	0.001	U	0.000	U			x			CGN
39343	7650286	11q22.3	0.856	2.98	0.000	U	0.000	U			x	x		EXPH5
28027	5390220	1q21.3	0.351	2.96	0.045	U								S100A9
34402	6550528	Xp11.3	0.692	2.95	0.000	U	0.000	U						MAOA
30392	5900368	10q11.23	0.874	2.95	0.000	U	0.000	U						MSMB
15135	2810451	15q21.3	0.522	2.94	0.005	U	0.001	U			x			WDR72
22540	4250364	4q34.1	0.596	2.93	0.001	U	0.000	U	P		x			HPGD
28679	5560369	17q11.2	0.409	2.93	0.020	U	0.006	U			x			ALDH3A1
15958	3120053	1p32.1	0.978	2.92	0.000	U	0.000	U						HOXK1
20913	4050121	7p21.3	0.884	2.92	0.000	U	0.000	U						ICA1
16057	3120475	6q23.3	0.895	2.92	0.000	U	0.000	U			x			MAP7
36920	7040670	1p36.22	0.738	2.91	0.000	U	0.000	U			x			DHRS3
4028	730592	7p21.3	0.705	2.90	0.000	U	0.000	U			x			SCIN
38998	7570053	12q13.12	1.038	2.90	0.000	U	0.000	U						RND1
21327	4070647	11q13.2	0.552	2.89	0.003	U	0.001	U						ALDH3B2
23102	4290706	20q13.12	0.545	2.89	0.003	U	0.001	U			x	x		EYA2

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Bi-pers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
1714	270615	17q21.33	0.586	2.88	0.002	U	0.000	U						ABCC3
2008	380026	1q32.1	0.802	2.88	0.000	U	0.000	U	P	x	x	x		C1orf116
29465	5720465	10q21.3	0.653	2.88	0.000	U	0.000	U			x	x		DNAJC12
34121	6510754	9q21.13	0.553	2.87	0.003	U	0.001	U			x			ALDH1A1
29370	5700753	19q13.2	0.638	2.87	0.001	U	0.000	U			x			CEACAM1
33652	6420736	10q21.3	0.660	2.86	0.000	U	0.000	U			x	x		DNAJC12
37867	7210632	10p15.1	0.452	2.86	0.011	U	0.003	U						AKR1C3
27915	5360424	6p27	0.634	2.85	0.001	U	0.000	U						RPS6KA2
32534	6280440	22q13.2	0.864	2.85	0.000	U	0.000	U						BIK
32515	6280332	17p13.2	0.881	2.84	0.000	U	0.000	U						CXCL16
15868	3060343	20q13.2	0.941	2.84	0.000	U	0.000	U						BCAS1
3546	630315	2q31.1	0.446	2.84	0.014	U	0.004	U						DHRS9
2330	450246	10q22.3	0.449	2.84	0.017	U	0.005	U						SFTPA1
36012	6860689	17p13.1	0.554	2.83	0.002	U	0.000	U						DNAH2
21313	4070575	2p21	0.545	2.83	0.004	U	0.001	U						EPCAM
38640	7510634	17q25.1	0.586	2.82	0.004	U	0.001	U						GPRC5C
12913	2470348	3q12.2	0.967	2.81	0.000	U	0.000	U						NFKBIZ
35200	6650504	1p22.1	0.880	2.81	0.000	U	0.000	U	P					ABCA4
262	20546	7q11.23	0.737	2.81	0.000	U	0.000	U						CLDN3
9421	1770754	4p13	0.698	2.80	0.001	U	0.000	U						LIMCH1
8002	1470731	13q22.3	0.780	2.80	0.000	U	0.000	U	P		x	x		SCEL
971	130181	10q23.31	0.654	2.79	0.001	U	0.000	U		x	x			ANKRD22
35134	6650202	6p12.3	0.556	2.79	0.002	U	0.000	U		x	x	x		GPR110
28375	5490437	6q25.1	0.681	2.79	0.001	U	0.000	U			x			PPP1R14C
30178	5890100	3q11.1	0.863	2.79	0.000	U	0.000	U						STX19
17698	3390692	8q24.13	0.522	2.78	0.008	U	0.001	U						FAM83A
12225	2340692	19p13.12	0.991	2.78	0.000	U	0.000	U						NOTCH3
16079	3120598	10p15.1	0.438	2.78	0.014	U	0.005	U						AKR1C4
20626	4010296	14q11.2	0.457	2.77	0.015	U	0.005	U	P					RNASE1
3947	730164	2q32.2	0.699	2.77	0.000	U	0.000	U			x	x		SLC40A1
17908	3420176	17q25.3	0.983	2.77	0.000	U	0.000	U			x	x		ZNF750
10978	2070575	3q13.11	0.714	2.77	0.001	U	0.000	U	P		x	x		ALCAM
8967	1710019	7p21.3	0.858	2.77	0.000	U	0.000	U						ICA1
18480	3460646	13q22.3	0.710	2.76	0.000	U	0.000	U	P		x	x		SCEL
11448	2140601	16p12.3	0.870	2.76	0.000	U	0.000	U	P		x	x		TMC5
26614	5090132	11p13	0.701	2.75	0.000	U	0.000	U			x	x	x	EHF
25863	4890241	16p21	0.723	2.75	0.001	U	0.000	U			x	x		GPR56
37424	7160102	7q31.32	0.695	2.75	0.000	U	0.000	U	P					CADPS2
37305	7150270	9q34.3	0.626	2.75	0.001	U	0.000	U						LRRC26
22189	4220189	8q24.21	0.691	2.74	0.000	U	0.000	U						GSDMC
10418	2000270	16q22.2	0.626	2.73	0.002	U	0.000	U						MARVELD3
39200	7610338	16q22.1	0.522	2.72	0.007	U	0.001	U		x	x			CDH3
12213	2340632	1p31.3	0.950	2.72	0.000	U	0.000	U		x	x			INADL
5760	1070477	9q21.13	0.522	2.72	0.005	U	0.001	U			x			ALDH1A1
2982	540465	6p21.1	0.884	2.71	0.000	U	0.000	U			x			ENPP5
23027	4290307	10q25.3	0.794	2.71	0.000	U	0.000	U						C10orf81
13033	2480228	8p22	0.785	2.71	0.002	U	0.000	U						FGL1
26491	5080273	3q26.33	0.582	2.70	0.001	U	0.000	U			x	x		SOX2
26244	4920561	22q12.3	0.639	2.69	0.001	U	0.000	U			x		x	MB
27700	5340129	10p15.1	0.368	2.68	0.044	U								AKR1C2
36677	7000255	6p12.3	0.555	2.68	0.002	U	0.001	U		x	x	x		GPR110
34744	6580689	Xp22.33	0.727	2.68	0.001	U	0.000	U						ARSD
766	70630	6p22.3	0.701	2.68	0.000	U	0.000	U			x	x		RNF144B
4401	830082	19q13.33	0.837	2.67	0.000	U	0.000	U						FUT2
12341	2350537	11q22.2	0.438	2.67	0.015	U	0.005	U			x	x		MMP7
11880	2260477	1q31.1	0.501	2.67	0.006	U	0.001	U						PTGS2
28437	5490768	16q21	0.694	2.66	0.001	U	0.000	U		x	x			GPR56
37231	7100685	3p21.31	0.563	2.66	0.003	U	0.001	U			x			MST1R
13673	2600240	16p13.3	0.810	2.66	0.000	U	0.000	U						RAB26
17963	3420452	7p21.1	0.845	2.65	0.000	U	0.000	U	P		x	x		TSPAN13
12714	2450162	6p21.33	0.710	2.65	0.003	U	0.000	U						SFTA2
10090	1980309	4q13.3	0.392	2.65	0.032	U								IL8
25154	4810730	11p11.2	0.605	2.65	0.002	U	0.000	U						SYT13
29206	5690647		0.796	2.64	0.001	U	0.000	U	P					SLC44A4
37571	7200044	6q14.1	0.793	2.63	0.000	U	0.000	U			x			SH3BGRL2
30365	5900243	17q12	0.840	2.62	0.000	U	0.000	U			x			GRB7
19159	3800017	8p22	0.845	2.62	0.000	U	0.000	U			x	x		MTUS1
18924	3710397	1q22	0.703	2.62	0.003	U	0.000	U			x	x		EFNA1
26708	5090671	19p13.11	0.514	2.62	0.005	U	0.001	U			x	x		GDF15
12288	2350243	1q21.1	1.034	2.61	0.000	U	0.000	U	P					FMO5
27416	5290273	7p21.1	0.834	2.61	0.000	U	0.000	U			x	x		AGR3
15499	2900681	3q21.2	0.639	2.61	0.001	U	0.000	U						ALG1L
3837	670372	20q13.2	0.856	2.61	0.000	U	0.000	U						BCAS1
3227	610189	7p12.1	0.483	2.61	0.012	U	0.003	U			x	x		COBL
35273	6660131	7p21.1	0.786	2.60	0.001	U	0.000	U	P		x	x		TSPAN13
19177	3800095	8q24.12	0.732	2.60	0.000	U	0.000	U						DEPDC6
4744	870202	3q26.33	0.519	2.59	0.004	U	0.001	U						TNFSF10
2909	540091	7q21.12	0.860	2.59	0.000	U	0.000	U			x	x		STEAP4
28907	5570731	8p11.21	0.409	2.58	0.023	U	0.008	U			x			C8orf4
36407	6960367	6p12.3	0.539	2.58	0.003	U	0.001	U		x	x	x		GPR110
21572	4150270	10q23.31	0.610	2.55	0.001	U	0.000	U		x	x			ANKRD22
13615	2600019	22q12.3	0.745	2.55	0.000	U	0.000	U			x		x	MB
6597	1240730	19q13.2	0.441	2.55	0.020	U	0.005	U		x	x	x		SPINT2
35933	6860347	1p12	0.569	2.55	0.002	U	0.000	U			x			FAM46C
13153	2490070	19p13.2	0.542	2.55	0.003	U	0.001	U			x			MUC16
29850	5860010	4q21.23	0.555	2.54	0.003	U	0.001	U		x				CD51
36180	6940039	11q24.1	0.777	2.54	0.000	U	0.000	U	P		x	x		SORL1
18594	3520431	16q12.1	0.977	2.54	0.000	U	0.000	U	P		x			TOX3
22795	4280019	6p21.31	0.548	2.53	0.003	U	0.001	U			x			MAPK13
21970	4200674	2q35	0.409	2.52	0.022	U	0.008	U						IGFBP2
32015	6220195	14q24.3	0.626	2.51	0.003	U	0.001	U			x			BATF
35765	6840228	17q25.1	0.560	2.51	0.003	U	0.001	U		x				EVPL
31060	6040647	19p13.12	0.775	2.50	0.000	U	0.000	U						HSH2D
4488	840019	3q26.2	0.640	2.47	0.002	U	0.000	U			x	x		HS6ST2
21704	4180142	15q21.2	1.121	2.47	0.000	U	0.000	U						KIAA1370
4975	940639	12p12.3	0.398	2.46	0.023	U	0.008	U			x			ERP27
22895	4280468	17q25.1	1.141	2.46	0.000	U	0.000	U			x			LGL2
19770	3850561	1q23.3	0.762	2.45	0.001	U	0.000	U			x			F11R
10834	2060687	19q13.12	0.659	2.45	0.000	U	0.000	U			x	x	x	FXYD3
30393	5900376	13q21.2	0.638	2.43	0.002	U	0.000	U						PCDH20
3519	630181	9q34.3	0.961	2.43	0.000	U	0.000	U						NOXA1
17637	3390372	12q12	0.650	2.42	0.001	U	0.000	U			x			CNTN1
24001	4590377	1q21.1	0.892	2.42	0.000	U	0.000	U			x			ANKRD35
15319	2850576	1q22	0.729	2.42	0.000	U	0.000	U						SEMA4A
13415	2510605	8p24.13	0.474	2.41	0.012	U	0.003	U						FAM83A
17589	3360750	5q14.3	0.591	2.41	0.002	U	0.000	U			x	x		GPR98
38456	7640452	4p15.1	0.561	2.40	0.007	U	0.002	U			x			PROM1
5865	1090307	14q11.2	0.549	2.39	0.007	U	0.002	U	P					RNASE1
964	130148	11p15.3	0.657	2.39	0.001	U	0.000	U						GALNTL4
18103	3440341	20q13.32	0.573	2.39	0.007	U	0.002	U						PHACTR3
33840	6480066	19q13.12	0.643	2.38	0.001	U	0.000	U						HPN
10079	1980255	6p22.1	0.646	2.38	0.001	U	0.000	U						RNF39
6043	1170047	14q32.33	0.439	2.37	0.014	U	0.004	U						CRIP1
25367	4850142	15q21.2	1.061	2.37	0.000	U	0.000	U						KIAA1370
17731	3400121	11p15.5	0.760	2.37	0.000	U	0.000	U						ANO9
25725	4880370	17q21.2	0.710	2.37	0.002	U	0.000	U			x			JUP
8832	1690066	21q22.3	0.440	2.37	0.021	U	0.006	U			x	x		MX1
3179	610010	6p21.33	0.706	2.36	0.004	U	0.001	U	P					SLC44A4
13040	2480274	11q24.1	0.707	2.34	0.000	U	0.000	U	P		x	x		SORL1
5831	1090048	1p13.1	0.390	2.34	0.025	U	0.009	U			x	x		VTCN1

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (1/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Bypro EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
2305	450133	20q11.21	0.782	2.34	0.001	U	0.000	U						C20orf70
36631	7000026	3q13.2	0.865	2.34	0.000	U	0.000	U			X			SIDT1
668	70167	8q21.11	0.405	2.34	0.026	U	0.010	U			X			LY96
36250	6940379	11q23.3	0.825	2.33	0.000	U	0.000	U	x					MPZL2
26490	5080259	2p24.2	1.382	2.33	0.000	U	0.000	U	P		X			KCNS3
10499	2000630	4q35.1	0.526	2.33	0.004	U	0.001	U			X			SORBS2
35103	6650068	11q13.4	0.446	2.32	0.015	U	0.005	U	P		X			FOLR1
32105	6220593	2q11.2	0.730	2.32	0.000	U	0.000	U			X			MGAT4A
14712	2710739	19q13.33	0.893	2.32	0.000	U	0.000	U			X			FAM83E
4941	940474	Xq22.1	0.441	2.32	0.013	U	0.004	U						SRPX2
887	110471	3q29	0.534	2.31	0.008	U	0.002	U			X			MUC4
15914	3060605	19q13.33	0.583	2.31	0.002	U	0.000	U						PRRG2
34060	6510403	6q12	0.648	2.31	0.001	U	0.000	U						LGSN
9765	1850201	19q13.12	0.450	2.31	0.013	U	0.004	U						C19orf46
8473	1570661	1p32.1	0.553	2.30	0.003	U	0.001	U			X			CYP22
19871	3870291	2q32.2	0.830	2.30	0.000	U	0.000	U			X			MFSD6
31452	6110338	8q22.3	0.530	2.29	0.004	U	0.001	U		x	X	X		GRHL2
24730	4760095	19q13.11	0.556	2.29	0.008	U	0.002	U						CRLF1
17600	3390187	1q22	0.615	2.29	0.005	U	0.001	U			X	X		EPHA1
1062	130609	19q13.2	0.529	2.28	0.004	U	0.001	U						FCGBP
13842	2630292	3q27.2	0.821	2.28	0.000	U	0.000	U						LIPH
11643	2230008	4q31.3	0.472	2.28	0.029	U								FGG
19478	3830743	9q34.12	0.625	2.28	0.001	U	0.000	U						FIBCD1
32799	6330270	Xq26.2	0.420	2.27	0.017	U	0.006	U	P					GPC4
17351	3360553	20p12.3	0.975	2.27	0.000	U	0.000	U			X			GPCPD1
32938	6350161	13q14.13	0.403	2.27	0.022	U	0.007	U						LCP1
4981	940674	7p22.3	0.762	2.27	0.000	U	0.000	U						TMEM184A
16191	3130296	1p21.1	0.797	2.27	0.001	U	0.000	U						AMY2A
32622	6290161	10q21.2	0.476	2.27	0.010	U	0.003	U			X			SLC16A9
21378	4120131	19p13.3	0.575	2.25	0.002	U	0.000	U						KISS1R
18441	3460440	11q23.3	0.752	2.25	0.000	U	0.000	U			X	X		TMPRSS13
9526	1780537	7p12.3	0.675	2.24	0.003	U	0.001	U			X			ABCA13
14930	2760274	7q33	0.433	2.24	0.019	U	0.007	U						AKR1B10
26684	5090500	12q21.32	0.848	2.24	0.000	U	0.000	U			X	X		KITLG
969	130167	Xp11.21	1.109	2.23	0.000	U	0.000	U			X			FAAH2
18356	3460053	1q42.2	0.635	2.23	0.001	U	0.000	U			X			SIPA1L2
15482	2900600	2q11.2	0.817	2.22	0.000	U	0.000	U						C2orf15
33405	6400131	20q13.2	0.567	2.22	0.004	U	0.001	U			X	X		CYP24A1
10508	2000685	1p35.3	0.724	2.22	0.000	U	0.000	U	P					SMPDL3B
1318	160242	13q14.11	0.542	2.22	0.003	U	0.001	U						C13orf15
32932	6350138	14q13.3	0.933	2.22	0.000	U	0.000	U						PAX9
4774	870390	8q24.12	0.700	2.21	0.000	U	0.000	U						DEPDC6
23401	4490037	4p15.2	0.509	2.21	0.009	U	0.002	U	P		X	X		SLC34A2
27320	5270619	9q22.31	0.574	2.21	0.002	U	0.001	U			X			FGD3
33448	6400364	2q24.1	0.501	2.20	0.008	U	0.002	U						NR4A2
8342	1570079	20p12.3	0.815	2.19	0.000	U	0.000	U			X			PLCB1
33598	6420392	4p11	0.531	2.19	0.017	U	0.003	U						OCIAD2
8601	1580475	13q22.2	1.115	2.18	0.000	U	0.000	U	P		X	X		LMO7
28280	5490019	5q33.1	0.427	2.17	0.018	U	0.006	U			X			GPX3
4792	870468	12q15	0.662	2.17	0.000	U	0.000	U						KCNMB4
14736	2750092	7q31.1	0.637	2.17	0.001	U	0.000	U			X	X		NRCAM
5877	1090390	12q24.13	0.435	2.17	0.020	U	0.007	U						OAS1
807	110100	15q21.3	0.454	2.16	0.014	U	0.004	U						CGNL1
37783	7210240	4q31.3	0.499	2.16	0.023	U	0.008	U						FGB
23008	4290209	17q25.3	0.653	2.16	0.001	U	0.000	U						TMC6
10439	2000364	4p14	0.488	2.16	0.007	U	0.002	U						TMEM156
19633	3840709	11q13.4	0.418	2.15	0.023	U	0.009	U	P		X			FOLR1
2424	460010	Xp11.4	0.480	2.15	0.015	U	0.005	U						TSPAN7
2839	520553	8q22.3	0.554	2.15	0.003	U	0.001	U	P		X	X		NCALD
19648	3840767	Xp11.4	0.537	2.15	0.009	U	0.002	U						TSPAN7
21943	4200541	12q13.11	0.436	2.15	0.014	U	0.004	U						FAM113B
36869	7040386	6p24.1	0.723	2.13	0.000	U	0.000	U			X			EDN1
482	60093	8q22.3	0.496	2.12	0.006	U	0.002	U	P		X	X		NCALD
10682	2030735	15q15.1	0.716	2.12	0.000	U	0.000	U			X			BUB1B
933	110754	8q22.1	0.651	2.12	0.000	U	0.000	U			X			ESRP1
20680	4010519	7q34	0.755	2.12	0.001	U	0.000	U						PIP
36035	6900053	11p15.4	0.931	2.12	0.000	U	0.000	U			X	X		PPFIBP2
9095	1710630	3q27.3	0.515	2.12	0.005	U	0.001	U			X	X		ST6GAL1
30554	5910402	17q11.2	0.382	2.12	0.031	U								KRT19P3
844	110280	15q15.1	0.572	2.11	0.002	U	0.000	U			X			BMF
3533	630243	17q21.32	0.856	2.11	0.000	U	0.000	U			X	X		PRR15L
34136	6520064	2p22.1	0.630	2.11	0.001	U	0.000	U						TMEM178
22794	4280017	14q24.3	0.528	2.11	0.008	U	0.001	U						FOS
20534	3990670	12q21.32	0.869	2.10	0.000	U	0.000	U			X	X		KITLG
35281	6660162	19p13.3	0.468	2.10	0.009	U	0.003	U						LRG1
19809	3850767	16p11.2	0.486	2.10	0.007	U	0.002	U						SBK1
10739	2060228	17q22	0.791	2.10	0.000	U	0.000	U			X	X		RNF43
28372	5490431	Xq22.11	1.125	2.10	0.000	U	0.000	U			X			SAT1
12430	2360273	2q36.3	0.561	2.10	0.002	U	0.001	U						SLC16A14
24626	4730360	1q31.1	0.825	2.09	0.000	U	0.000	U			X			PLA2G4A
39330	7650209	15q15.1	0.596	2.09	0.001	U	0.000	U			X			BMF
36245	6940364	3q24	0.571	2.09	0.006	U	0.002	U			X			CP
31051	6040603	10p13	0.483	2.09	0.010	U	0.003	U			X	X		FAM107B
25852	4890181	1p36.12	0.686	2.09	0.000	U	0.000	U						RAP1GAP
2437	460082	1q32.1	0.448	2.08	0.016	U	0.005	U						GOLT1A
30633	5960091	11q23.3	0.710	2.08	0.001	U	0.000	U						TMPRSS4
18049	3440095	19q13.2	0.416	2.08	0.019	U	0.006	U						PSG3
29442	5720373	11p15.5	0.803	2.07	0.000	U	0.000	U						ANO9
21025	4050674	15q23	0.796	2.07	0.000	U	0.000	U			X	X		LOC145837
5066	990280	9q33.3	0.640	2.07	0.001	U	0.000	U						RALGPS1
2851	520609	1p13.3	0.439	2.06	0.024	U	0.009	U						KIAA1324
7842	1470014	16p13.3	0.512	2.06	0.006	U	0.002	U						ZG16B
34157	6520139	4p16.3	0.386	2.06	0.027	U					X		X	FGFR3
28030	5390240	19q13.12	0.786	2.05	0.000	U	0.000	U		x	X		X	FXYD3
25631	4860681	4q32.1	0.467	2.05	0.011	U	0.003	U	P		X	X		GUCY1A3
18742	3610338	11q23.1	0.719	2.05	0.000	U	0.000	U						C11orf52
37206	7100541	Xq22.3	0.738	2.04	0.001	U	0.000	U						NUP62CL
908	110630	3q26.1	0.691	2.04	0.004	U	0.001	U						C3orf57
3161	580692	20q11.21	0.572	2.03	0.002	U	0.000	U					X	ID1
22988	4290114	1p36.11	0.612	2.03	0.001	U	0.000	U		x				C1orf172
6840	1300392	8q24.3	0.599	2.03	0.002	U	0.000	U						FAM83H
32406	6270615	17q12	0.636	2.03	0.001	U	0.000	U						GSDMB
34811	6590240	8q24.3	0.543	2.02	0.004	U	0.001	U		x				EPPK1
6111	1170477	17q25.1	0.487	2.02	0.011	U	0.003	U						GPRC5C
9940	1940301	5q13.2	0.677	2.01	0.001	U	0.000	U						MARVELD2
9065	1710468	15q15.1	0.727	2.01	0.000	U	0.000	U			X	X		SPINT1
28048	5390333	17q11.2	0.354	2.01	0.043	U								TMEM98
37501	7160468	2q31.1	0.431	2.01	0.021	U	0.008	U						DHRS9
31378	6110022	8p22	0.690	2.01	0.005	U	0.001	U						FGL1
26384	5050537	8q24.3	0.527	2.01	0.012	U	0.003	U						OPLAH
9710	1820743	8q21.13	0.540	2.01	0.004	U	0.001	U			X			ZNF704
38908	7560376	16p13.3	0.786	2.00	0.000	U	0.000	U						CCDC64B
28105	5390608	17q12	0.679	2.00	0.001	U	0.000	U						GSDMB
8115	1500500	22q13.31	0.563	1.99	0.004	U	0.001	U					X	WNT7B
5279	1010528	3q29	0.719	1.99	0.000	U	0.000	U			X	X		HES1
6846	1300408	3q13.33	0.495	1.99	0.013	U	0.004	U						HCLS1
14948	2760368	1q32.2	0.587	1.99	0.002	U	0.000	U						IRF6
22345	4230195	11p15.1	0.622	1.99	0.002	U	0.000	U			X	X		NAV2
12900	2470296	6p22.1	0.857	1.99	0.000	U	0.000	U						ZSCAN16
36542	6980301	7q31.1	0.567	1.99	0.003	U	0.001	U			X	X		NRCAM

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Bypro EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
8795	1660647	14q22.3	0.764	1.98	0.000	U	0.000	U			X	X		LGALS3
37295	7150209	20p13	0.555	1.98	0.003	U	0.001	U						SLC4A11
2351	450368	17q12	0.773	1.97	0.000	U	0.000	U			X			GRB7
210	20274	19q13.12	0.619	1.97	0.001	U	0.000	U						HPN
15893	3060471	6p21.1	0.568	1.97	0.002	U	0.001	U	P		X	X		ENPP4
16933	3290048	1p33	0.627	1.97	0.001	U	0.000	U			X			CYP4X1
7855	1470053	6q23.3	0.951	1.97	0.000	U	0.000	U						KIAA1244
22929	4280615	16q22.2	0.502	1.97	0.008	U	0.002	U						MARVELD3
38333	7380626	4p14	0.653	1.97	0.002	U	0.000	U			X	X		RBM47
33698	6450162	9q34.3	0.515	1.96	0.006	U	0.002	U						C9orf169
1831	290435	2q23.3	0.703	1.96	0.000	U	0.000	U		x				KRTCAP3
2004	380019	4q24	0.507	1.96	0.007	U	0.002	U						DDIT4L
9460	1780224	2q11.2	0.405	1.96	0.029	U								C2orf55
6251	1190524	16q23.1	0.661	1.95	0.001	U	0.000	U						FAZH
19530	3840192	2q31.1	0.637	1.95	0.001	U	0.000	U						GAD1
2971	540403	22q11.23	0.602	1.95	0.002	U	0.001	U			X	X		LRP5L
23774	4560632	4p15.33	0.595	1.94	0.001	U	0.000	U			X	X		HS3ST1
22187	4220184	13q34	0.428	1.94	0.015	U	0.005	U						LOC100289410
29862	5860050		0.539	1.94	0.003	U	0.001	U						LOC388564
8173	1510019	4q31.1	0.580	1.94	0.015	U	0.003	U						MGST2
1793	290239	11p15.1	0.612	1.94	0.002	U	0.000	U			X	X		NAV2
7178	1400484	Xq27.1	0.441	1.94	0.043	U								LDOC1
8968	1710020	14q24.2	0.403	1.94	0.031	U								SMOC1
33475	6400465	12p13.31	0.671	1.93	0.002	U	0.000	U						PTPN6
4381	780767	20p13	0.645	1.93	0.001	U	0.000	U	P					ProSAPiP1
26444	5080044	3p22.1	0.672	1.93	0.001	U	0.000	U						ENTPD3
17083	3290731	14q23.1	0.550	1.93	0.002	U	0.001	U			X	X		PRKCH
30494	5910128	2p11.2	0.615	1.93	0.007	U	0.001	U						VAMP8
31629	6130458	2q11.1	0.503	1.92	0.008	U	0.003	U						LOC400986
1903	360128	4q12	0.463	1.91	0.011	U	0.004	U			X			KIT
34031	6510270	10q22.3	0.412	1.91	0.021	U	0.008	U	P					SFTPD
37299	7150240	4q31.3	0.592	1.91	0.002	U	0.000	U	P		X	X		TRIM2
37906	7320041	10q26.13	0.585	1.91	0.004	U	0.001	U			X			CHST15
17661	3390484	1p35.2	0.462	1.90	0.009	U	0.003	U		x	X			SERINC2
36624	6980762	12q13.2	0.605	1.88	0.006	U	0.002	U			X	X		MUCL1
35248	6650750	17q21.33	0.625	1.88	0.001	U	0.000	U		x				EPN3
20227	3930523	1p36.13	0.526	1.88	0.004	U	0.001	U						CLCNKA
14349	2680411	1p13.3	0.442	1.87	0.014	U	0.004	U			X			PTGFRN
26394	5050577	9q34.3	0.598	1.86	0.003	U	0.001	U			X			PNPLA7
29676	5810689	11p13	0.572	1.86	0.002	U	0.001	U			X	X		PRRG4
11427	2140463	21q22.3	0.698	1.86	0.000	U	0.000	U			X	X		SLC37A1
2082	380424	1q31.3	0.402	1.86	0.027	U								CFH
2683	510546	16p13.3	0.544	1.86	0.003	U	0.001	U		x				PRSS22
4595	840253	12q24.12	0.535	1.86	0.005	U	0.001	U			X			ALDH2
26151	4920121	16q22.1	0.543	1.86	0.004	U	0.001	U						ELMO3
28230	5420482		0.687	1.85	0.001	U	0.000	U						AIF1L
38438	7400372	17q11.1	0.566	1.85	0.002	U	0.001	U			X			WSB1
25425	4850504	3p22.1	0.655	1.85	0.001	U	0.000	U						ENTPD3
23600	4540376	4q22.1	0.696	1.85	0.000	U	0.000	U			X	X		FAM13A
14752	2750170	4q35.1	0.477	1.85	0.008	U	0.002	U			X			SORBS2
33234	6380066	2q36.3	0.780	1.84	0.000	U	0.000	U			X			COL4A3
125	10592	11p15.5	0.572	1.84	0.002	U	0.000	U						EFCAB4A
29742	5820195	1p36.13	0.534	1.83	0.004	U	0.001	U						CLCNKA
5011	990044	7q34	0.855	1.83	0.000	U	0.000	U						KIAA1147
3925	730072	11p15.1	0.889	1.83	0.000	U	0.000	U			X	X		PLEKHA7
16612	3180025	4q31.3	0.558	1.83	0.026	U	0.010	U						FGG
13515	2570288	2p25.3	0.586	1.82	0.002	U	0.000	U		x				SH3YL1
30317	5900008	19q13.41	0.504	1.82	0.014	U	0.005	U						KLK11
30088	5870431	4p14	0.662	1.82	0.000	U	0.000	U						NSUN7
1092	130750	16p11.2	0.619	1.82	0.004	U	0.001	U			X	X		YPEL3
32999	6350446	Xq22.3	0.547	1.82	0.003	U	0.001	U	P		X	X		TSC22D3
6536	1240440	1q21.1	0.435	1.82	0.021	U	0.006	U			X			TXNIP
31574	6130156	8p11.23	0.915	1.81	0.000	U	0.000	U	P		X	X		RAB11FIP1
21622	4150519	15q25.1	0.741	1.81	0.000	U	0.000	U						FAM108C1
38997	7570050	Xq28	0.609	1.81	0.001	U	0.000	U						HMGB3
21570	4150255	4q22.1	0.765	1.80	0.000	U	0.000	U			X	X		FAM13A
21285	4070369	16q22.2	0.616	1.80	0.001	U	0.000	U						MARVELD3
10425	2000292	5q35.3	0.538	1.80	0.018	U	0.006	U						SCGB3A1
10719	2060121	1p36.11	0.761	1.80	0.000	U	0.000	U	P					FUCA1
32853	6330550	1q32.2	0.576	1.80	0.003	U	0.001	U						SERTAD4
17406	3370056	12q13.13	0.434	1.80	0.041	U					X	X		KRT8
7963	1470551	4p15.2	0.460	1.79	0.013	U	0.004	U						SEL1L3
17145	3310307	21q22.11	0.430	1.79	0.018	U	0.007	U						C21orf63
12663	2370671	7q31.31	0.470	1.79	0.008	U	0.003	U						TSPAN12
32283	6250672	5q11.2	0.726	1.79	0.000	U	0.000	U						CCNO
25071	4810343	1q23.1	0.807	1.79	0.000	U	0.000	U			X	X		ETV3
38159	7330544	17q11.2	0.437	1.78	0.015	U	0.005	U						ALDOC
17290	3360279	1q31.3	0.452	1.78	0.014	U	0.005	U						CFH
36612	6980689	2p22.1	0.649	1.78	0.000	U	0.000	U						TMEM178
13181	2490240	10q26.2	0.394	1.78	0.026	U	0.010	U	P					PTPRE
22193	4220209	11q13.3	0.651	1.77	0.001	U	0.000	U			X			SHANK2
27105	5260403	2p11.2	0.563	1.77	0.003	U	0.001	U	P					ST3GAL5
34693	6580450	2p16.1	0.533	1.77	0.003	U	0.001	U						BCL11A
26457	5080112	1q41	0.613	1.77	0.001	U	0.000	U			X			MARK1
21272	4070300	22q13.33	0.706	1.77	0.000	U	0.000	U						PANK2
13368	2510369	8p12	0.784	1.76	0.000	U	0.000	U		x	X	X	X	RBPMS
5479	1030753	1p36.32	0.697	1.76	0.000	U	0.000	U						ARHGEF16
17268	3360148	21q22.11	0.468	1.76	0.011	U	0.004	U						CLDN8
33415	6400176	11p15.5	0.398	1.76	0.030	U				P				IRF7
10447	2000390	9q21.11	0.375	1.76	0.031	U					X			FAM189A2
3893	670707	1p32.3	0.591	1.75	0.002	U	0.001	U			X	X		TMEM61
13447	2570010	7p21.3	0.476	1.75	0.007	U	0.003	U						VWDE
10766	2060347	1q42.2	0.637	1.75	0.001	U	0.000	U						CAPN9
37819	7210392	6p12.2	0.674	1.75	0.005	U	0.001	U						GSTA2
13567	2570551	17q21.2	0.556	1.74	0.006	U	0.001	U			X			JUP
17097	3310025	4p11	0.496	1.74	0.015	U	0.004	U						OCIAD2
11788	2230746	10q24.2	0.345	1.74	0.049	U								ABCC2
13474	2570100	19p13.3	0.607	1.74	0.002	U	0.000	U						ABCA7
16087	3120615	9q21.11	0.775	1.73	0.000	U	0.000	U			X	X		TJP2
20704	4010647	9q34.12	0.553	1.73	0.003	U	0.001	U						AIF1L
22990	4290133	6p21.31	0.581	1.73	0.002	U	0.001	U						PACSIN1
12860	2470093	9q21.11	0.674	1.73	0.001	U	0.000	U			X	X		TJP2
17553	3370736	6p22.3	0.483	1.72	0.009	U	0.003	U			X			SOX4
1552	240608	11p11.2	0.762	1.72	0.000	U	0.000	U						TPS3I11
12770	2450400	2p22.3	0.551	1.72	0.004	U	0.001	U			X			RASGRP3
13823	2630204	6q23.1	0.504	1.72	0.016	U	0.005	U						ENPP3
34247	6520561	4q21.1	0.664	1.71	0.001	U	0.000	U		x				SHROOM3
12484	2360563	4p14	0.562	1.71	0.002	U	0.001	U						NSUN7
26353	5050390	11q12.2	0.551	1.71	0.002	U	0.001	U						SYT7
3738	650639	2p24.1	0.383	1.71	0.038	U								NR4A2
18819	3610672	6p24.3	0.456	1.70	0.013	U	0.004	U		x				DSP
37749	7210093	11q13.4	0.580	1.70	0.001	U	0.000	U			X	X		PGM2L1
37754	7210113	2q24.3	0.370	1.70	0.037	U								NOSTRIN
28160	5420152	12q13.13	0.972	1.70	0.000	U	0.000	U			X			AMHR2
13632	2600070	11q14.2	0.504	1.70	0.007	U	0.002	U						RAB38
23057	4290431	5q32	0.365	1.70	0.039	U								DPYSL3
38010	7320551	8q12.1	0.629	1.69	0.001	U	0.000	U						LYN
20043	3890382	2p11.2	0.563	1.69	0.002	U	0.001	U	P					ST3GAL5
9128	1740020	1q42.12	0.764	1.69	0.000	U	0.000	U	P		X			TMEM63A
24657	4730482	16q21	0.411	1.69	0.021	U	0.009	U			X	X		CDH5

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (2/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
32251	6250484	1q31.3	0.487	1.69	0.011	U	0.004	U						CFH
37627	7200324	7q22.1	0.412	1.69	0.027	U								AZGP1
16084	3120608	12q13.2	0.702	1.69	0.000	U	0.000	U		x	X	X		ERBB3
7469	1430497	6q14.1	0.603	1.69	0.001	U	0.000	U	P		X	X		MYO6
24696	4730692	19q13.12	0.571	1.69	0.002	U	0.001	U			X			LSR
21640	4150598	10q11.23	0.673	1.69	0.005	U	0.001	U						MSMB
19372	3830193	7q31.31	0.475	1.69	0.008	U	0.003	U						TSPAN12
22352	4230228	17q21.32	0.497	1.68	0.010	U	0.004	U			X	X		CDK5RAP3
26451	5080075	10q22.1	0.701	1.68	0.000	U	0.000	U			X			TSPAN15
27106	5260408	17p13.3	0.410	1.68	0.022	U	0.008	U	P					RPH3AL
19466	3830681	12q13.13	0.494	1.68	0.018	U	0.006	U						KRT6A
5385	1030278	10q24.2	0.474	1.68	0.010	U	0.004	U						PYROXD2
9856	1850674	6p22.1	0.599	1.68	0.007	U	0.002	U						TRIM31
33208	6370703	2q37.1	0.429	1.68	0.047	U								UGT1A1
5387	1030286	22q12.3	0.566	1.67	0.007	U	0.002	U						SLC5A1
25263	4830424	6p22.3	0.777	1.67	0.000	U	0.000	U			X	X		MYLIP
32784	6330187	3q23	0.848	1.67	0.000	U	0.000	U						PLS1
7502	1430673	20p13	0.515	1.67	0.006	U	0.002	U						SDCBP2
13477	2570112	10q25.3	0.412	1.67	0.037	U					X	X		ABLIM1
36790	7040035	12q24.13	0.423	1.67	0.026	U								OAS1
36135	6900538	10q21.3	0.550	1.66	0.002	U	0.001	U			X	X		DNAJC12
38460	7400475	14q11.2	0.789	1.66	0.000	U	0.000	U						RPGRIP1
19163	3800035	12q13.3	0.857	1.66	0.000	U	0.000	U	P					GLS2
1942	360377	2p13.3	0.372	1.66	0.044	U								TGFA
2892	540020	1q43	0.627	1.65	0.001	U	0.000	U			X			LGALS8
30552	5910398	4q24	0.542	1.65	0.004	U	0.001	U			X	X		NPNT
96	10427	6q12.3	0.598	1.65	0.009	U	0.003	U						TFAP2D
23457	4490333	6q22.31	0.491	1.65	0.007	U	0.002	U			X			FAM184A
16679	3180347	3q12.3	0.623	1.65	0.001	U	0.000	U						LOC285359
27276	5270414	9q31.1	0.825	1.65	0.000	U	0.000	U						LOC441461
31042	6040546	5q13.2	0.563	1.65	0.003	U	0.001	U			X	X		OCLN
22157	4220053	17q21.32	0.536	1.65	0.003	U	0.001	U						SKAP1
30783	6020070	1q41	0.594	1.65	0.003	U	0.001	U						SUSD4
8156	1500703	1p13.3	0.455	1.64	0.012	U	0.004	U						DENND2D
909	110634	17q21.2	0.718	1.64	0.000	U	0.000	U			X			JUP
23125	4390059	11q13.4	0.499	1.64	0.007	U	0.002	U			X			P2RY6
2966	540379	Xq13.1	0.598	1.64	0.001	U	0.000	U	P					DLG3
29132	5690270	12p13.1	0.483	1.63	0.011	U	0.003	U						GPRC5A
20108	3890735	2q31.1	0.403	1.63	0.024	U			P					HOXD1
13008	2480092	16q13	0.610	1.63	0.003	U	0.001	U			X	X		CCL22
8311	1510731	8q24.3	0.501	1.63	0.007	U	0.002	U						KIAA1875
6000	1110465	17q22	0.767	1.63	0.000	U	0.000	U			X	X		YPEL2
37456	7160239	19q13.32	0.501	1.63	0.007	U	0.002	U			X			FOSB
15414	2900274	16p13.3	0.404	1.63	0.025	U	0.009	U			X			VASN
22183	4220168	2q22.1	0.381	1.62	0.032	U				x	X			HNMT
34751	6580717	17p13.2	0.738	1.62	0.000	U	0.000	U						ZNFN1D15
26940	5220398	3p21.31	0.533	1.62	0.015	U	0.003	U						P4HTM
23241	4390646	8q24.13	0.739	1.62	0.000	U	0.000	U			X			ZHX2
6026	1110678	17p13.2	0.818	1.61	0.000	U	0.000	U			X			ATP2A3
28632	5560148	7q11.23	0.494	1.61	0.006	U	0.002	U						MLXIPL
31179	6060482	1q24.2	0.624	1.61	0.001	U	0.000	U						ATP1B1
20921	4050156	17q12	0.617	1.60	0.001	U	0.000	U						ERBB2
25147	4810703	1q42.2	0.392	1.60	0.040	U								KCNK1
33002	6350470	5q32	0.388	1.60	0.031	U								STK32A
22942	4280678	5p12	0.557	1.60	0.003	U	0.001	U						SEPP1
32536	6280458	3q27.3	0.764	1.60	0.000	U	0.000	U			X	X		BCL6
2657	510427		0.741	1.60	0.000	U	0.000	U						LOC285141
18592	3520424	12q23.1	0.549	1.60	0.004	U	0.001	U						SLC5A8
20638	4010356	Xq22.1	0.537	1.60	0.006	U	0.002	U						KRBOX
24108	4610161	2p25.1	0.432	1.60	0.032	U					X			KCNF1
4298	780348	12q24.31	0.637	1.59	0.001	U	0.000	U						LOC338799
25685	4880133	3q27.2	0.747	1.59	0.000	U	0.000	U			X	X		MAP3K13
21773	4180452	1q24.2	0.630	1.59	0.001	U	0.000	U						ATP1B1
29204	5690639	14q32.12	0.526	1.59	0.004	U	0.001	U						FBLN5
18976	3710671	17q21.2	0.392	1.59	0.025	U	0.010	U			X	X		KRT15
35855	6840739	3q23	0.680	1.59	0.000	U	0.000	U						PLS1
36754	7000619	19p13.3	0.533	1.59	0.004	U	0.001	U			X	X		VAV1
29308	5700431	16p13.3	0.596	1.59	0.003	U	0.001	U						WDR90
23282	4480112	9q21.11	0.416	1.59	0.026	U								PGM5
35540	6760669	4q28.1	0.388	1.59	0.031	U					X	X		SPRY1
17089	3290747	17p13.2	0.606	1.58	0.002	U	0.001	U			X			ATP2A3
33644	6420687	20q11.21	0.526	1.58	0.023	U	0.008	U						PLUNC
31647	6130609	13q13.3	0.839	1.58	0.000	U	0.000	U						SMAD9
27405	5290209	8p12	0.982	1.58	0.000	U	0.000	U			X	X		KIF13B
33856	6480131	1q22	0.553	1.57	0.002	U	0.001	U						ADAM15
17303	3360349	4q31.3	0.559	1.57	0.007	U	0.001	U			X			FHDC1
15498	2900674	1p13.1	0.450	1.57	0.023	U	0.007	U			X			IGSF3
32394	6270554	1q43	0.585	1.57	0.002	U	0.001	U			X			LGALS8
22962	4290017	1q32.1	0.472	1.57	0.008	U	0.003	U			X			PLEKHA6
30611	5910746	20q12	0.425	1.57	0.021	U	0.009	U						PRO0628
422	50600	1q32.1	0.443	1.57	0.045	U								PIGR
21984	4200743	3p21.31	0.724	1.57	0.000	U	0.000	U						NBEAL2
10751	2060291	9q33.2	0.606	1.57	0.002	U	0.000	U			X			STOM
10085	1980288	15q25.1	0.403	1.56	0.028	U	0.010	U	P		X			CTSH
30507	5910170	7q35	0.515	1.56	0.004	U	0.002	U						CTAGE6P
6323	1230164		0.534	1.56	0.005	U	0.002	U						MTRNR2L1
10143	1980553	1q22	0.617	1.56	0.001	U	0.000	U						ADAM15
1579	240768	9q22.33	0.528	1.56	0.004	U	0.001	U						CORO2A
22244	4220468	1q24.2	0.648	1.56	0.001	U	0.000	U						ATP1B1
17261	3360112	9q21.13	0.503	1.56	0.009	U	0.002	U			X	X		TMEM2
11923	2260731	5q15	0.364	1.56	0.038	U								ERAP2
30999	6040348	1p35.3	0.966	1.55	0.000	U	0.000	U	P					SMPDL3B
23412	4490079	2q31.1	0.407	1.55	0.021	U	0.009	U						DHRS9
25766	4880544	9q22.33	0.548	1.55	0.003	U	0.001	U						GALNT12
7771	1450400	5p15.33	0.371	1.55	0.040	U								ZDHHC11
7826	1450672	19q21.2	0.847	1.54	0.000	U	0.000	U			X			ANK3
13239	2490520	6p12.2	0.550	1.54	0.012	U	0.004	U						GSTA2
35816	6840468	12q23.1	0.633	1.54	0.014	U	0.005	U						HAL
23811	4570075	2q11.1	0.536	1.54	0.011	U	0.004	U						LOC400986
33886	6480274		0.516	1.54	0.007	U	0.003	U						LOC400986
7426	1430332	1q23.3	0.580	1.54	0.003	U	0.001	U			X	X		PVRL3
3806	670202	2q31.2	0.786	1.54	0.000	U	0.000	U			X			SESTD1
38729	7550324	Xp22.2	0.545	1.54	0.003	U	0.001	U			X	X		SHROOM2
26255	4920632	Xq23	0.641	1.54	0.005	U	0.001	U						SLC6A14
4444	830274	1q32.2	0.542	1.54	0.008	U	0.002	U			X	X		CD55
17222	3310692	4q28.1	0.395	1.54	0.026	U					X	X		SPRY1
28648	5560221	11q13.4	0.490	1.53	0.007	U	0.003	U						STARD10
30384	5900343	1p36.11	0.960	1.53	0.000	U	0.000	U	P					CNKSR1
32793	6330224	14q12	0.674	1.53	0.001	U	0.000	U						ADCY4
31887	6200286	1p34.3	0.478	1.53	0.008	U	0.003	U						RHBDL2
19837	3870102	2q22.1	0.376	1.53	0.035	U				x	X			HNMT
28005	5390121	16p11.2	0.503	1.53	0.005	U	0.002	U						GDPD3
164	20017	16q22.1	0.596	1.53	0.003	U	0.001	U						PDXDC2P
31824	6200014	6p22.1	0.550	1.53	0.003	U	0.001	U						ZNF165
19645	3840753	8q21.13	0.364	1.53	0.049	U								HEY1
35424	6760037	11q14.1	0.395	1.53	0.030	U					X			SYTL2
31328	6100494	Xq26.2	0.518	1.52	0.004	U	0.001	U			X	X		HS6ST2
26550	5080576	4q12	0.468	1.52	0.010	U	0.004	U			X			KIT
25287	4830520	12q13.13	0.459	1.52	0.020	U	0.006	U			X			KRT80
2107	380561	10p12.31	0.492	1.52	0.009	U	0.003	U						NEBL

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
18892	3710196	6p21.33	0.701	1.51	0.000	U	0.000	U			X	X		DDR1
6451	1240026	Xq13.1	0.735	1.51	0.000	U	0.000	U	P					DLG3
16526	3170431		0.483	1.51	0.009	U	0.003	U						SAP25
29928	5860373	11p15.5	0.754	1.51	0.000	U	0.000	U						SIGIRR
14409	2680725	3q22.1	0.580	1.51	0.001	U	0.001	U			X			ACPP
37859	7210600	16p13.3	0.457	1.51	0.010	U	0.004	U						PISD27
36646	7000121	1p31.3	0.761	1.51	0.000	U	0.000	U		x	X			INADL
20763	4040176	20q13.33	0.528	1.51	0.012	U	0.003	U			X			LAMA5
9425	1780019	2p21	0.499	1.51	0.006	U	0.002	U						PLEKHH2
27082	5260309	9q21.11	0.602	1.51	0.002	U	0.000	U			X	X		TJP2
28241	5420538	8q22.1	0.499	1.51	0.007	U	0.003	U						TPS3INP1
36083	6900301	4p14	0.846	1.50	0.000	U	0.000	U						C4orf34
31596	6130292	5q13.2	0.429	1.50	0.018	U	0.008	U						GUSBP3
3503	630091	6q22.32	0.648	1.50	0.000	U	0.000	U						NCOA7
32466	6280093	1p34.1	0.530	1.50	0.004	U	0.001	U			X			ZSWIM5
33429	6400243	10q25.3	0.426	1.49	0.023	U	0.008	U			X	X		ABLIM1
35509	6760482	22q13.31	0.423	1.49	0.019	U	0.007	U						ARHGAP8
38252	7380239	Xq26.3	0.445	1.49	0.013	U	0.005	U			X			FGF13
28211	5420377	14q22.3	0.557	1.49	0.005	U	0.001	U			X	X		LGALS3
18445	3460451	10q24.33	0.399	1.49	0.030	U								SH3PXD2A
37339	7150451	6q12	0.475	1.49	0.010	U	0.004	U						LGSN
34461	6560093	3q13.33	0.425	1.49	0.018	U	0.007	U			X	X		SLC15A2
29366	5700735	3q21.1	0.509	1.49	0.007	U	0.002	U						PARP9
23649	4540689	13q34	0.750	1.48	0.001	U	0.000	U						ANKRD10
10546	2030091	19q13.42	0.551	1.48	0.002	U	0.001	U						EPS8L1
14936	2760301	3p21.31	0.549	1.48	0.007	U	0.002	U						P4HTM
34164	6520176	7p15.3	0.435	1.48	0.013	U	0.005	U			X	X		STK31
20196	3930377	6p22.2	0.446	1.48	0.012	U	0.005	U						TRIM38
21259	4070242	2p25.3	0.569	1.48	0.002	U	0.001	U						TTC15
4054	730709	4q28.1	0.378	1.48	0.032	U					X	X		SPRY1
24828	4760634	11q23.1	0.617	1.48	0.001	U	0.001	U						C11orf93
29690	5810762	9q21.11	0.393	1.48	0.038	U								PGM5
8670	1660025	1q32.1	0.468	1.48	0.011	U	0.003	U						CDK18
37970	7320370	2q32.2	0.431	1.48	0.019	U	0.007	U			X			STAT4
5539	1050253	1p32.3	0.379	1.48	0.030	U								ACDT11
5500	1050082	7q34	1.002	1.48	0.000	U	0.000	U						KIAA1147
23190	4390372	1q21.3	0.516	1.47	0.004	U	0.001	U						BNIPL
22154	4220041	5q23.3	0.628	1.47	0.001	U	0.000	U			X			SLC12A2
14704	2710717	13q13.1	0.854	1.47	0.000	U	0.000	U						EEF1DP3
5906	1090561	6p12.2	0.543	1.47	0.020	U	0.007	U						GSTA1
4828	870670	11p15.3	0.476	1.47	0.015	U	0.006	U			X	X		MICALCL
30612	5910753	19p13.3	0.496	1.47	0.006	U	0.002	U		x				STAP2
19275	3800538	3p23	0.665	1.47	0.000	U	0.000	U						ACPL2
12025	2320408	1p36.11	0.459	1.47	0.015	U	0.006	U						C1orf63
38339	7380670	6q23.3	0.464	1.47	0.011	U	0.004	U			X			MYB
31681	6180048	6p24.2	0.491	1.47	0.006	U	0.002	U			X	X		NEDD9
19707	3850259	8q12.1	0.527	1.47	0.004	U	0.001	U			X			SDR16C5
6137	1170630	5q13.2	0.766	1.46	0.000	U	0.000	U						ANKRA2
17185	3310484	7q32.1	0.411	1.46	0.024	U	0.010	U						C7orf54
36729	7000474	14q13.2	0.517	1.46	0.005	U	0.002	U						RALGAPA1
10296	1990471	1p33	0.489	1.46	0.008	U	0.003	U	P					FAAH
27054	5260176	6p12.2	0.535	1.46	0.007	U	0.002	U						GSTA1
17624	3390326	6q14.2	0.672	1.46	0.001	U	0.000	U			X	X		ME1
37771	7210184		0.607	1.46	0.002	U	0.001	U						NDUFB4
5684	1070152	3p21.1	0.393	1.46	0.030	U								IL17RB
25384	4850224	9p24.1	0.377	1.46	0.045	U								INSL4
19019	3780092	6p12.3	0.411	1.46	0.028	U	0.010	U		x	X	X		TNFRSF21
32452	6280048	1q42.2	0.418	1.46	0.019	U	0.008	U						FAM89A
23688	4560129	14q32.12	0.909	1.45	0.000	U	0.000	U			X	X		LGMN
15430	2900348	19q13.2	0.769	1.45	0.000	U	0.000	U			X			ZFP36
36154	6900674	13q34	0.617	1.45	0.003	U	0.001	U						ANKRD10
30984	6040286	2q37.3	0.782	1.45	0.000	U	0.000	U			X			PER2
24589	4730180	5q34	0.526	1.45	0.015	U	0.006	U						ATP10B
11794	2260020	9p24.2	0.598	1.45	0.002	U	0.001	U						SLC1A1
30004	5870010	7q11.23	0.517	1.44	0.005	U	0.002	U						MLXIPL
37764	7000156	5q31.3	0.529	1.44	0.008	U	0.003	U						PCDHB9
39426	7650767	1q23.2	0.376	1.44	0.034	U								IGSF9
21589	4150356	7q35	0.480	1.44	0.015	U	0.004	U						ARHGEF5
24486	4670441	14q32.12	0.527	1.44	0.004	U	0.001	U						FBLN5
27583	5310328	3q26.2	0.553	1.44	0.007	U	0.002	U						LRRC31
8399	1570300	13q12.12	0.811	1.44	0.001	U	0.000	U			X			SPATA13
14966	2760437	1p36.11	0.383	1.44	0.028	U								SYTL1
33032	6350632	Xq22.3	0.544	1.43	0.003	U	0.001	U	P		X	X		TSC22D3
20596	4010139	4q24	0.549	1.43	0.002	U	0.001	U			X	X		BANK1
30438	5900603	20q11.21	0.607	1.43	0.008	U	0.002	U						C20orf186
34809	6590228	11q12.2	0.731	1.43	0.001	U	0.000	U						CD6
29829	5820671	19p13.3	0.596	1.43	0.010	U	0.003	U						FUT6
29163	5690400	22q11.23	0.494	1.43	0.006	U	0.002	U						GSTTP2
36602	6980632	19q13.33	0.468	1.43	0.011	U	0.004	U						LMTK3
142	10673	22q13.33	0.668	1.43	0.000	U	0.000	U			X			PLXNB2
80	10358	16p11.2	0.489	1.43	0.008	U	0.003	U						SPN
29619	5810424	12p13.31	0.604	1.42	0.004	U	0.001	U						C1RL
26427	5050735	15q15.2	0.906	1.42	0.000	U	0.000	U			X	X		TMEM62
18134	3440452	1q22	0.754	1.42	0.000	U	0.000	U						ADAM15
1056	130577	5q13.2	0.922	1.42	0.000	U	0.000	U			X			CCDC125
27490	5290630	4q31.3	0.624	1.42	0.017	U	0.006	U						FGB
20275	3940014	11q25	0.446	1.42	0.013	U	0.005	U						GLB1L2
17263	3360131	8q24.3	0.514	1.42	0.005	U	0.002	U						NAPRT1
15462	2900474	19q13.2	0.400	1.42	0.024	U	0.010	U						RINL
10906	2070246	1p36.32	0.529	1.42	0.005	U	0.002	U						MMEL1
1990	360706	13q34	0.611	1.41	0.005	U	0.001	U						GRTP1
8776	1660521	1q21.3	0.632	1.41	0.005	U	0.002	U						SPRR2D
27913	5360411	14q13.3	0.658	1.41	0.001	U	0.000	U	P					MBIP
26110	4900711	2q35	0.526	1.41	0.008	U	0.003	U						ABCA12
7339	1410609	9q22.33	0.537	1.41	0.005	U	0.002	U						CORO2A
6858	1300452	14q32.12	0.851	1.41	0.000	U	0.000	U			X	X		LGMN
4619	840364	22q11.23	0.420	1.41	0.023	U	0.008	U						SGSM1
38373	7400053	11p15.4	0.542	1.41	0.006	U	0.001	U						SLC22A18
21094	4060259	20q13.32	0.572	1.41	0.009	U	0.003	U						PHACTR3
16466	3170093	14q24.1	0.628	1.41	0.001	U	0.000	U			X	X		KIAA0247
29588	5810278	11q14.1	0.374	1.41	0.039	U					X			SYTL2
35843	6840639	1p22.3	0.566	1.40	0.002	U	0.001	U						COL24A1
28774	5570070	1p36.12	0.509	1.40	0.006	U	0.002	U						PLA2G2D
25737	4880408	9q22.2	1.059	1.40	0.000	U	0.000	U						SEMA4D
6489	1240201	21q22.2	0.381	1.40	0.039	U								BACE2
5510	1050113	11p13	0.591	1.40	0.008	U	0.003	U						ELF5
3276	610392	1p31.3	0.513	1.40	0.006	U	0.002	U			X	X	X	RBPMS
20798	4040360	9q31.3	0.471	1.40	0.010	U	0.004	U						ZNF483
3002	540608	11q13.2	0.731	1.39	0.000	U	0.000	U		x				SSH3
21889	4200253	14q21.2	0.654	1.39	0.000	U	0.000	U			X	X		C14orf28
33246	6380112	22q13.31	0.698	1.39	0.001	U	0.000	U						GRAMD4
29930	5860377	21q22.2	0.364	1.39	0.040	U								ABCG1
26502	5080301	19q13.42	0.705	1.39	0.000	U	0.000	U						EPS8L1
32849	6330484	1q21.3	0.562	1.39	0.005	U	0.002	U						CTSS
5078	990349	15q26.2	0.418	1.39	0.018	U	0.008	U						MCTP2
12989	2480014	16p11.2	0.483	1.39	0.009	U	0.004	U						SULT1A2
35393	6660671	1q42.2	0.365	1.39	0.043	U								KCNK1
20021	3890246	20p13	0.608	1.38	0.003	U	0.001	U						SDCBP2
12421	2360201	11q13.2	0.424	1.38	0.019	U	0.008	U						ALDH3B2
34771	6590041	14q11.2	0.492	1.38	0.006	U	0.002	U						ANG

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (3/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 sig=if	SAM P value (FDR=5.1%)	1531 sig=if	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
32208	6250300	7p22.1	0.425	1.38	0.016	U	0.007	U						RAC1
36272	6940465	14q13.2	0.568	1.38	0.002	U	0.001	U						RALGAPA1
2785	520259	7p15.3	0.446	1.38	0.012	U	0.005	U			X	X		STK31
6596	1240725	17q12	0.403	1.38	0.024	U					X			SLFN5
8136	1570064	1p35.1	0.552	1.38	0.006	U	0.001	U			X			KIAA1522
23323	4480341	1p32.3	0.845	1.37	0.000	U	0.000	U			X	X		DHCR24
31202	6060661	16p13.3	0.615	1.37	0.001	U	0.001	U			X			CLDN9
3734	650619	9q33.3	0.474	1.37	0.015	U	0.006	U						FAM125B
28731	5560630	8p22	0.549	1.37	0.004	U	0.001	U			X	X		PSD3
24578	4730131	2q13	0.488	1.37	0.007	U	0.002	U						PSD4
14190	2650482	10q26.2	0.389	1.37	0.027	U				P				PTPRE
16296	3140047	17q21.33	0.442	1.37	0.017	U	0.007	U						LUC7L3
2586	510092	16p13.3	0.398	1.37	0.034	U								RHBDL1
37030	7050433	8q21.11	0.360	1.36	0.041	U								RDH10
38388	7400114	5q13.2	0.910	1.36	0.000	U	0.000	U						ANKRA2
20778	4040242	1q42.2	0.546	1.36	0.004	U	0.001	U						FAM89A
15883	3060437	12p12.3	0.376	1.36	0.037	U				P	X	X		LMO3
27137	5260575	12q24.31	0.444	1.36	0.016	U	0.007	U			X			DENR
10384	2000102	15q15.3	0.554	1.36	0.005	U	0.001	U						ELL3
18165	3440630	1p36.31	0.506	1.36	0.008	U	0.003	U						ESPN
25632	4860685	7p14.3	0.596	1.36	0.002	U	0.001	U						LOC401321
11992	2320273	19p13.3	0.583	1.36	0.001	U	0.001	U						REEP6
22774	4260687	5q21.1	0.638	1.36	0.001	U	0.000	U			X	X		SLCO4C1
27208	5270132	3q13.11	0.661	1.35	0.001	U	0.000	U			X	X		CBLB
16517	3170349	1q41	0.601	1.35	0.003	U	0.001	U			X			CAPN8
19536	3840215	9q34.11	0.642	1.35	0.001	U	0.000	U			X			FAM102A
29060	5670687	16q13	0.417	1.35	0.022	U	0.009	U			X			PLLP
11881	2260482	12p13.31	0.634	1.35	0.001	U	0.000	U						PTPN6
13988	2640324	13q12.3	0.382	1.35	0.030	U					X	X		SLC46A3
19841	3870114	10p12.31	0.487	1.35	0.008	U	0.003	U						NEBL
34880	6590538	3q22.1	0.520	1.35	0.019	U	0.007	U						TF
1289	160121	14q23.2	0.361	1.35	0.045	U					X	X		SYNE2
38053	7320753		0.566	1.34	0.005	U	0.002	U						TMPRSS4
20910	4050102	8p11.23	0.852	1.34	0.000	U	0.000	U	P		X	X		RAB11FIP1
25252	4830372	14q12.33	0.478	1.34	0.008	U	0.003	U						ADSSL1
6978	1340288	11q24.3	0.495	1.34	0.006	U	0.002	U			X			ARHGAP32
23768	4560600	3q26.1	0.587	1.34	0.007	U	0.002	U						C3orf57
21517	4150014	19q13.2	0.464	1.34	0.010	U	0.004	U			X			CEACAM1
16960	3290156	7q35	0.486	1.34	0.006	U	0.003	U						CTAGE6P
4827	870669	11p15.5	0.452	1.34	0.011	U	0.005	U						LRRC56
33441	6400326	16p11.2	0.462	1.34	0.011	U	0.004	U						SULT1A2
4537	830735	7p22.3	0.364	1.34	0.037	U								ADAP1
7883	1470176	16p12.3	0.408	1.34	0.034	U								SYT17
30529	5910291	13q12.2	0.499	1.34	0.006	U	0.002	U						RASL11A
9075	1710520	19p13.2	0.692	1.34	0.001	U	0.000	U						HOOK2
5416	1030431	4q35.1	0.599	1.33	0.001	U	0.001	U	P					ACSL1
9758	1850164	17q21.33	0.450	1.33	0.014	U	0.005	U			X	X		ACSF2
28882	5570593	1p36.33	0.433	1.33	0.018	U	0.008	U			X			KIAA1751
6252	1190528	12p13.2	0.450	1.33	0.017	U	0.007	U			X	X		MANSC1
21235	4070138	1p35.3	0.514	1.33	0.004	U	0.002	U			X	X		PTPRU
20215	3930446	12q24.13	0.705	1.33	0.001	U	0.000	U			X			RASAL1
8861	1690384	8q22.2	0.551	1.33	0.002	U	0.001	U			X			RNF19A
22868	4280328		0.499	1.33	0.006	U	0.002	U						SPAG5
32163	6250091	8q24.13	0.647	1.33	0.001	U	0.000	U			X			ZHX2
2856	520634	4p13	0.776	1.33	0.000	U	0.000	U			X	X		ATP8A1
19059	3780273	7p21.3	0.691	1.33	0.000	U	0.000	U						ICA1
24821	4760600	16p13.11	0.704	1.33	0.001	U	0.000	U						PDXDC1
38458	7400468	14q11.2	0.597	1.32	0.003	U	0.001	U						AP1G2
31048	6040598	17q12	0.769	1.32	0.000	U	0.000	U						GSDMB
18713	3610192	7q21.3	0.533	1.32	0.004	U	0.001	U						LOC441268
8991	1710113	14q11.2	0.594	1.32	0.003	U	0.001	U						PPP1R3E
14321	2680288	14q21.1	0.679	1.32	0.000	U	0.000	U						TRAPPC6B
10253	1990278	1q23.3	0.407	1.32	0.029	U								FCGR2A
33833	6480041	14q13.3	0.610	1.32	0.002	U	0.001	U	P					MBIP
24527	4670671	1q21.2	0.683	1.32	0.000	U	0.000	U			X			ACP6
29091	5690066	22q12.1	0.768	1.31	0.000	U	0.000	U						XBP1
29478	5720537	3q23	0.640	1.31	0.001	U	0.000	U						ACPL2
36708	7000397	9p24.3	0.397	1.31	0.032	U					X			KANK1
26052	4900411	17q25.3	0.760	1.31	0.000	U	0.000	U						C17orf55
8013	1500014	7p21.3	0.576	1.31	0.002	U	0.001	U			X			COL28A1
30575	5910521	3q25.31	0.699	1.31	0.000	U	0.000	U						PLCH1
21091	4060242	9q34.3	0.451	1.31	0.016	U	0.007	U						LOC286254
16792	3190112	6p25.2	0.446	1.31	0.013	U	0.005	U			X	X		SERPINB1
4784	870437	19q13.33	0.423	1.30	0.016	U	0.007	U			X			TRPM4
14221	2650612	18q11.2	0.360	1.30	0.039	U								LAMA3
21238	4070164	1p21.1	0.501	1.30	0.019	U	0.007	U						AMY1C
23848	4570279	1p34.2	0.729	1.30	0.000	U	0.000	U			X			BMPBB
31001	6040356	19p13.2	0.571	1.30	0.002	U	0.001	U						KIAA1545
6155	1170736	16q21	0.566	1.30	0.002	U	0.001	U						MMP15
800	110064	1q25.3	0.499	1.30	0.005	U	0.002	U						RNASEL
22270	4220605	21q22.2	0.388	1.30	0.028	U					X	X		ETS2
11231	2120326	2q24.3	0.403	1.30	0.025	U					X	X		GRB14
38506	7400747	1q42.2	0.423	1.29	0.017	U	0.007	U						FAM89A
26227	4920458	1q21.3	0.537	1.29	0.003	U	0.001	U						CREB3L4
29055	5670673	11q13.4	0.490	1.29	0.007	U	0.003	U			X	X		ARRB1
34176	6520241	22q13.33	0.509	1.29	0.005	U	0.002	U						FAM116B
18590	3520398	1p36.11	0.408	1.29	0.023	U	0.010	U						IL28RA
3468	620619	2q11.2	0.454	1.29	0.012	U	0.005	U			X	X		TBC1D8
28984	5670328	2q37.1	0.448	1.29	0.040	U								UGT1A1
5917	1090682	6q22.1	0.786	1.29	0.000	U	0.000	U						FRK
18893	3710202	3p21.31	0.436	1.29	0.019	U	0.008	U						MST1
38741	7550368		0.443	1.28	0.013	U	0.005	U	P					FLJ22184
18508	3520020	5q33.3	0.476	1.28	0.012	U	0.005	U						CYFIP2
36139	6900563	1q42.12	0.443	1.28	0.013	U	0.005	U			X			EPHX1
27366	5290068	17q12	0.645	1.28	0.001	U	0.000	U						SLFN13
17360	3360601	17q25.3	0.628	1.28	0.001	U	0.000	U			X			TMEM105
30065	5870301	16q24.1	0.516	1.28	0.005	U	0.002	U						KIAA0513
16753	3180672	16p13.13	0.582	1.28	0.003	U	0.001	U			X	X		LITAF
32691	6290519	9q33.2	0.399	1.28	0.026	U					X			STOM
23528	4540017	12q23.1	0.776	1.27	0.000	U	0.000	U						GOLGA2B
26663	5090408	3p14.1	0.450	1.27	0.016	U	0.007	U			X			LRIG1
22490	4250136	14q12	0.472	1.27	0.010	U	0.004	U						LTB4R
4364	780681	14q13.3	0.517	1.27	0.004	U	0.002	U						SLC25A21
22643	4260092	22q11.23	0.380	1.27	0.031	U								GGT1
34889	6590592	2p24.1	0.414	1.27	0.025	U	0.010	U	P		X	X		SOC1
4642	840446	17q23.3	0.501	1.27	0.006	U	0.002	U						CYB561
28560	5550544	1p32.3	0.690	1.27	0.002	U	0.001	U			X			LDLRAD1
35629	6770326	19q13.43	0.482	1.27	0.009	U	0.004	U						NLRP8
26468	5080154	6p22.3	0.620	1.26	0.001	U	0.000	U			X	X		ATXN1
4607	840309	7q32.1	0.438	1.26	0.018	U	0.008	U						LEP
5034	990131	4q32.1	0.485	1.26	0.011	U	0.005	U	P		X	X		GUCY1A3
36910	7040603	14q32.12	0.627	1.26	0.005	U	0.002	U			X	X		CATSPER3
34634	6580113	3q12.3	0.429	1.26	0.038	U					X			ZFLD1
15998	3120187	12p13.31	0.347	1.26	0.050	U					X	X		PLEKHG6
6470	1240097	14q13.1	0.493	1.26	0.009	U	0.004	U						BAZ1A
34507	6560307	17q21.31	0.570	1.25	0.002	U	0.001	U						ARL17B
28401	5490593	3p29	0.447	1.25	0.012	U	0.005	U						BOH1
11721	2230376	4p14	0.649	1.25	0.001	U	0.000	U						C4orf34
27012	5260019	16q22.1	0.557	1.25	0.003	U	0.001	U						CES8
21744	4180364	9q21.33	0.658	1.25	0.001	U	0.000	U			X			GOLM1

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 sig=if	SAM P value (FDR=5.1%)	1531 sig=if	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
21540	4150102	Xp22.11	0.455	1.25	0.025	U	0.010	U						PDK3
27081	5260307		0.482	1.25	0.007	U	0.003	U			X			PPP1R9A
22300	4230017	5q21.1	0.445	1.25	0.016	U	0.007	U			X			ST8SIA4
28727	5560603	16p11.2	0.480	1.25	0.010	U	0.003	U						SULT1A3
12219	2340673	10q26.2	0.356	1.25	0.043	U				P				PTPRE
9652	1820414	13q12.12	0.471	1.25	0.028	U								ATP12A
4389	830022	5q23.3	0.388	1.25	0.028	U					X			SLC12A2
12713	2450156	22q12.1	0.822	1.24	0.000	U	0.000	U						XBP1
19952	3870706	15q26.1	0.481	1.24	0.010	U	0.004	U			X			FURIN
27675	5310767	11q13.2	0.456	1.24	0.013	U	0.006	U			X			LRP5
137	10634	14q23.2	0.455	1.24	0.011	U	0.005	U			X	X		SYNE2
28806	5570195	21q22.2	0.397	1.24	0.024	U								BRWD1
22315	4230075		0.378	1.24	0.032	U								GGT2
13506	2570240	8q13.2	0.370	1.24	0.046	U								SULF1
33510	6400703	3q26.32	0.499	1.24	0.007	U	0.003	U						KCNMB3
5451	1030605	15q22.2	0.815	1.23	0.002	U	0.001	U			X	X		C2CD4A
12858	2470088	4q22.1	0.704	1.23	0.000	U	0.000	U			X	X		FAM13A
15867	3060341	3q29	0.488	1.23	0.008	U	0.003	U						LOC440993
19881	3870347	17p13.1	0.481	1.23	0.017	U	0.007	U						MFSD6L
32429	6270725	16p11.2	0.439	1.23	0.018	U	0.007	U						SULT1A1
35385	6660630	8q22.1	0.508	1.23	0.006	U	0.002	U						TP53INP1
25073	4810348	1p36.31	0.403	1.23	0.029	U								RNF207
8701	1660161	6q23.2	0.417	1.23	0.022	U								SLC2A12
17259	3360095	6q25.1	0.706	1.23	0.000	U	0.000	U						ESR1
9270	1740767	11q24.1	0.449	1.23	0.017	U	0.008	U						C11orf63
29239	5700056	6p21.32	0.417	1.23	0.023	U	0.009	U						HSD17B8
15552	2940192	9q34.11	0.622	1.23	0.002	U	0.001	U						LOC389791
12921	2470379	19p13.3	0.363	1.23	0.044	U				x				STAP2
16491	3170201	1q31.3	0.505	1.22	0.005	U	0.002	U						DENND1B
25948	4890703	17q21.33	0.450	1.22	0.012	U	0.005	U						MIB1D1
8747	1660397	12q13.3	0.635	1.22	0.003	U	0.001	U						STAT6
33948	6480593	11q23.1	0.424	1.22	0.020	U	0.009	U			X			ARHGAP20
21479	4120593	7p22.3	0.449	1.22	0.011	U	0.005	U						MICALL2
20952	4050300	12q13.11	0.447	1.22	0.013	U	0.006	U			X	X		RAPGEF3
7894	1470215	10p11.23	0.376	1.22	0.035	U								MAP3K8
15425	2900328	9q21.3	0.528	1.21	0.005	U	0.002	U						PTPLAD2
11307	2120687	20q13.12	0.602	1.21	0.002	U	0.001	U	P					WFDC2
14263	2680044	15q21.3	0.403	1.21	0.021	U	0.010	U						RAB27A
25572	4860408	2q33.2	0.540	1.21	0.003	U	0.001	U			X	X		RAPH1
15094	2810280	3p25.1	0.463	1.21	0.011	U	0.005	U						SLC6A6
12976	2470722	10q25.3	0.465	1.21	0.012	U	0.005	U						TDRD1
32475	6280138	2p21	0.404	1.21	0.028	U					X			PPM1B
25717	4880333	17q11.2	0.474	1.21	0.013	U	0.004	U						FLJ40504
28570	5550603	6p21.1	0.435	1.21	0.016	U	0.007	U			X			USP49
4734	870161	21q21.3	0.357	1.21	0.043	U					X	X		CXADR
15585	2940372	5q23.1	0.463	1.20	0.012	U	0.005	U						DTWD2
9116	1710735	14q23.1	0.540	1.20	0.003	U	0.001	U			X			DAAM1
31632	6130484	14q13.1	0.445	1.20	0.013	U	0.006	U			X	X		EGLN3
23639	4540630	12q14.1	0.435	1.20	0.019	U	0.009	U			X	X		LRIG3
21074	4060139	Xq28	0.448	1.20	0.014	U	0.006	U						PLXNB3
21947	4200551	3q21.3	0.461	1.20	0.014	U	0.006	U						RPL32P3
17140	3310279	17q12	0.561	1.20	0.002	U	0.001	U						TBC1D3G
32355	6270347	3p22.1	0.709	1.20	0.000	U	0.000	U			X	X		TRAK1
6367	1230369	4q12	0.415	1.20	0.023	U					X	X		HOPX
6265	1190634	17q25.3	0.404	1.20	0.021	U	0.010	U						GAA
3499	630066	11q13.2	0.471	1.20	0.012	U	0.005	U			X			LRP5
4428	830201	11q13.5	0.538	1.19	0.003	U	0.001	U	N		X	X		TSKU
1337	160333	6q23.2	0.431	1.19	0.025	U	0.009	U						C6orf192
32635	6290241	2p21	0.508	1.19	0.005	U	0.002	U						EPCAM
23770	4560609	11p14.1	0.426	1.19	0.018	U	0.008	U			X	X		LGR4
11759	2230594	1q25.3	0.389	1.19	0.034	U					X	X		LAMC2
4169	770494	3q22.3	0.486	1.19	0.007	U	0.003	U	P		X	X		TSC22D3
23348	4480463	8p22	0.600	1.19	0.036	U								FGL1
510	60220	16p13.3	0.464	1.19	0.015	U	0.007	U						C16orf79
26838	5130661	5p15.2	0.553	1.19	0.007	U	0.003	U						FAM105A
11540	2190228	2q36.1	0.530	1.19	0.005	U	0.002	U						SGPP2
2531	460564	1p31.1	0.396	1.19	0.027	U								FAM73A
1106	150041	12p13.2	0.401	1.19	0.027	U					X	X		MANSC1
4478	830440	1q41	0.364	1.19	0.041	U					X	X		TLR5
29018	5670475	15q15.1	0.376	1.18	0.046	U								GCHFR
9841	1850564	3p14.3	0.432	1.18	0.018	U	0.008	U			X	X		LMOD3
22439	4230678	1q21.2	0.408	1.18	0.026	U								HIST2H2BE
9839	1850546	9q34.11	0.487	1.18	0.007	U	0.003	U			X			FAM102A
20737	4040066		0.568	1.18	0.002	U	0.001	U						LOC644334
14229	2650653	Xq26.3	0.430	1.18	0.014	U	0.007	U			X			ZNF750
9210	1740451	2q11.2	0.442	1.18	0.035	U								IL1R2
23087	4290605	9q31.1	0.430	1.18	0.034	U								SLC44A1
5589	1050482	1q32.2	0.651	1.17	0.001	U	0.000	U			X			CD46
20917	4050136	20q13.12	0.698	1.17	0.002	U	0.001	U	P					WFDC2
7825	1450671	7p22.2	0.494	1.17	0.009	U	0.004	U						CARD11
11261	2120451	1q32.2	0.822	1.17	0.000	U	0.000	U			X			CD46
30884	6020543	17q11.2	0.660	1.17	0.000	U	0.000	U			X	X		CPD
21834	4200019	11q12.1	0.494	1.17	0.006	U	0.003	U			X	X		CTNND1
20533	3950661	14q13.2	0.480	1.17	0.007	U	0.003	U						FAM117A1
25836	4890102	2q33.3	0.502	1.17	0.005	U	0.002	U			X	X		FZD5
3229	610201	2q37.3	0.484	1.17	0.007	U	0.003	U						HES6
38414	7400259	4p16.3	0.467	1.17	0.008	U	0.004	U						IDUA
33767	6450482	6q23.3	0.417	1.17	0.012	U	0.005	U						IL20RA
4647	840475	22q11.22	0.344	1.17	0.049	U					X			GGTLC2
21660	4150692	3q21.1	0.511	1.17	0.004	U	0.002	U						PARP14
11650	2230026	13q22.1	0.439	1.16	0.013	U	0.006	U			X	X		KLF5
30103	5870491	6p12.3	0.616	1.16	0.001	U	0.001	U			X			CYP39A1
12767	2450392	16q24.3	0.531	1.16	0.003	U	0.001	U						FAM157C
21045	4060017	3p14.3	0.466	1.16	0.012	U	0.006	U			X			IL17RD
25119	4810520	8q24.13	0.517	1.16	0.007	U	0.002	U			X	X		TRIB1
3085	580270	16p13.3	0.399	1.16	0.029	U								NOXO1
15023	2760709	2q21.2	0.376	1.16	0.032	U								LYPD1
8932	1690608	17p11.2	0.598	1.15	0.001	U	0.001	U						ALDH3A2
30548	5910382	14q11.2	0.416	1.15	0.018	U	0.009	U						ANG
22425	4230609	Xp22.33	0.411	1.15	0.022	U	0.010	U						ARSD
26116	4900747	11q21	0.555	1.15	0.003	U	0.001	U						C11orf75
952	130086	17q23.3	0.463	1.15	0.011	U	0.004	U						CYB561
38044	7320717	12q21.33	0.444	1.15	0.016	U	0.007	U			X	X		GALNT4
12209	2340608	9q21.2	0.591	1.15	0.001	U	0.001	U			X	X		GNA14
37358	7150554	10q24.1	0.556	1.15	0.003	U	0.001	U			X			LCOR
7514	1430735	10p15.1	0.530	1.15	0.004	U	0.002	U						NET1
30391	5900367	5q32	0.362	1.15	0.042	U					X	X		ARHGEF37
29208	5690671	15q14	0.407	1.15	0.033	U								GOLGA8B
4638	840437	17q11.2	0.461	1.15	0.028	U					X			LGALS9
22733	4260482	12q13.2	0.567	1.15	0.002	U	0.001	U	x	X	X			ERBB3
9862	1850709	10q21.2	0.734	1.15	0.000	U	0.000	U			X			ANK3
25819	4890041	11p15.5	0.450	1.15	0.012	U	0.005	U						DUSP8
32735	6290735	3q27.1	0.594	1.15	0.001	U	0.001	U			X	X		EPHB3
33453	6400376	15q22.2	0.587	1.15	0.002	U	0.001	U			X	X		VPS13C
37125	7100121	2q22.1	0.377	1.15	0.034	U				x	X			HNMT
36961	7050082	19p13.2	0.342	1.15	0.049	U								ACP5
24464	4670343	14q32.33	0.451	1.14	0.018	U	0.008	U	P					JAG2
18455	3460504	4q23	0.599	1.14	0.001	U	0.001	U			X			DAPP1
16828	3190338	9q32	0.821	1.14	0.000	U	0.000	U						HOMD3
25879	4890324	1p22.2	0.652	1.14	0.001	U	0.000	U						LRRC8B

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (4/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	STAT1 signif	SAM P value (FDR<5.1%)	1531 signif	NKX2-1 assoc	Beyers ESAT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET		Symbol
10462	2000441	17q12	0.575	1.14	0.002	U	0.001	U							PGAP3
8330	1570039	7q22.1	0.476	1.14	0.012	U	0.006	U							PILRB
7338	1410603	12q15	0.536	1.14	0.004	U	0.001	U			X	X			RAB3IP
37287	7150181	15q15.3	0.398	1.14	0.026	U									STRC
24687	4730670	6p12.1	0.620	1.14	0.001	U	0.000	U							GCLC
24529	4670681	18p11.22	0.463	1.14	0.013	U	0.006	U							RAB12
36320	6940730	4q28.1	0.377	1.14	0.038	U									LOC285419
28124	5390725	17q25.1	0.407	1.14	0.022	U									SSTR2
4460	830356	2p13.1	0.513	1.14	0.006	U	0.003	U							SLC4A5
12994	2480037	3p22.3	0.514	1.13	0.005	U	0.002	U			X				CMTM8
6225	1190367	6p21.33	0.422	1.13	0.029	U					X				IER3
13528	2570356	4q28.1	0.404	1.13	0.026	U									LOC285419
14893	2760102	2q37.3	0.475	1.13	0.009	U	0.004	U							ANKMY1
31833	6200041	21q22.2	0.529	1.13	0.006	U	0.003	U							BRWD1
3331	610634	3q22.3	0.453	1.13	0.015	U	0.007	U							ESYT3
5204	1010154	17q25.1	0.456	1.13	0.011	U	0.005	U							LOC643008
9698	1820682	1q25.3	0.530	1.13	0.004	U	0.002	U							RNASEL
37629	7200328	13q14.11	0.400	1.13	0.034	U									NCRNA00284
22405	4230500	1p21.3	0.418	1.13	0.036	U									SLC44A3
21295	4070427	9q33.2	0.404	1.13	0.028	U					X	X			TTLL11
14071	2640735	3p26.1	0.607	1.12	0.002	U	0.001	U			X				BHLHE40
7237	1410050	14q13.1	0.453	1.12	0.012	U	0.005	U							C14orf147
11582	2190452	22q13.33	0.542	1.12	0.003	U	0.002	U			X	X			PIM3
20548	3990739	6p21.2	0.492	1.12	0.008	U	0.004	U	P		X				KCNK5
10066	1980180	9p21.13	0.533	1.12	0.004	U	0.001	U							C9orf95
16435	3140707	3q21.1	0.519	1.12	0.006	U	0.003	U							PARP9
10942	2070402	Xq21.1	0.408	1.12	0.043	U									CYSLTR1
30900	6020619	16q13	0.392	1.12	0.030	U					X				PLLP
18526	3520093	11q13.1	0.524	1.12	0.006	U	0.002	U	P		X	X			LTBP3
1636	270224	14q32.12	0.676	1.12	0.000	U	0.000	U			X				MOAP1
30706	5960440	12q13.11	0.397	1.12	0.024	U									VDR
11067	2100241	2q33.2	0.498	1.11	0.005	U	0.002	U			X	X			RAPH1
37400	7160010	8q22.2	0.730	1.11	0.000	U	0.000	U			X				RNF19A
5734	1070368	17q21.31	0.504	1.11	0.005	U	0.002	U							C17orf69
32512	6280309	14q13.3	0.729	1.11	0.000	U	0.000	U			X				MIPOL1
11673	2230114	11p13	0.487	1.11	0.009	U	0.004	U			X	X			PRRG4
32017	6220202	14q24.3	0.464	1.11	0.010	U	0.005	U			X				PTGR2
197	20170	12q13.13	0.494	1.11	0.006	U	0.003	U							ZNF385A
11758	2230592	2p16.1	0.972	1.11	0.000	U	0.000	U			X				REL
1078	130681	14q11.2	0.682	1.11	0.003	U	0.001	U							RNASE6
22645	4260097	14q24.2	0.416	1.11	0.041	U									SMOC1
19334	3830044	13q34	0.506	1.11	0.005	U	0.002	U							GRTP1
21692	4180086	14q32.33	0.779	1.11	0.000	U	0.000	U							KIAA0284
7291	1410358	4q32.3	0.540	1.11	0.005	U	0.002	U			X	X			SH3RF1
38287	7380390	17q21.31	0.417	1.11	0.022	U									LOC90586
21958	4200605	7q36.1	0.418	1.11	0.021	U					X				XRCC2
24763	4760296	4p15.2	0.373	1.10	0.044	U			P		X	X			SLC34A2
8165	1500747	22q13.1	0.561	1.10	0.005	U	0.002	U			X				CBX7
4156	770441	6q14.1	0.519	1.10	0.007	U	0.003	U							DOPEY1
16895	3390626	3q21.1	0.475	1.10	0.008	U	0.004	U							MAGT1
33633	6420632	3q27.1	0.651	1.10	0.000	U	0.000	U			X				MCCC1
24512	4670577	2p15	0.447	1.10	0.015	U	0.008	U			X	X			TMEM17
21038	4050746	16q22.2	0.625	1.10	0.002	U	0.001	U			X	X			ZFHX3
36587	6980546	22q13.1	0.377	1.10	0.037	U									CACNA1I
19455	3830615	1q21.2	0.402	1.10	0.022	U									FAM91A2
21674	4150753	7p14.3	0.420	1.10	0.022	U									FKBP14
9959	1940402	19p13.3	0.413	1.10	0.024	U									PLIN5
39246	7610528	19p13.11	0.423	1.10	0.022	U									ZNF14
31395	6110091	17q11.1	0.497	1.09	0.008	U	0.004	U			X				WSB1
10918	2070315	20p13	0.366	1.09	0.039	U									C20orf54
12643	2370564	12q13.13	0.532	1.09	0.013	U	0.006	U			X				KRT78
31831	6200026	9q22.33	0.449	1.09	0.023	U									NR4A3
11655	2230044	13q32.3	0.451	1.09	0.015	U	0.007	U	P		X	X			DOCK9
14908	2760156	1q21.3	0.515	1.09	0.004	U	0.002	U							FAM63A
35148	6650278	19q13.2	0.427	1.09	0.019	U	0.008	U							KCNK6
4598	840270	7q22.1	0.495	1.09	0.010	U	0.005	U							PILRB
17289	3360273	22q11.23	0.584	1.09	0.002	U	0.001	U							POM121L8P
31753	6180414	6q12	0.438	1.09	0.017	U	0.009	U			X				PTP4A1
24260	4640132	8q13.1	0.392	1.09	0.027	U									C8orf45
23395	4490010	14q23.1	0.401	1.09	0.022	U					X				DAAM1
38946	7560520	3q22.3	0.356	1.09	0.041	U									MIG2
17423	3370128	9q32	0.389	1.09	0.028	U					X	X			TNFSF15
2911	540095	19p12	0.363	1.09	0.037	U					X				ZNF254
6143	1170673	19p13.3	0.433	1.09	0.019	U	0.009	U							TNFSF14
7643	1440575	17q22	0.421	1.08	0.019	U	0.010	U			X	X			DSRPL7
24984	4780671	14q22.1	0.576	1.08	0.002	U	0.001	U			X				ERO1L
2741	520059	3q27.1	0.450	1.08	0.012	U	0.006	U			X	X			LAMP3
1606	270093	17q11.2	0.484	1.08	0.009	U	0.004	U			X				MYO18A
5859	1090286	17q11.2	0.506	1.08	0.005	U	0.002	U							NEK8
4861	940048	14q11.2	0.471	1.08	0.011	U	0.006	U							NGDN
9205	1740438	2p15	0.449	1.08	0.011	U	0.005	U							OTX1
34916	6590709	8q24.3	0.718	1.08	0.000	U	0.000	U							RHPN1
12961	2470609	17q24.3	0.506	1.08	0.005	U	0.002	U							SLC39A11
2692	510605	9q32	0.769	1.08	0.000	U	0.000	U							WDR31
18128	3440431	19p12	0.384	1.08	0.034	U									ZNF682
12379	2350722	15q15.1	0.410	1.08	0.030	U									JMJD7
6690	1260438	8p11.21	0.543	1.07	0.004	U	0.002	U							IKBKB
31699	6180133	6q13.1	0.748	1.07	0.000	U	0.000	U	P		X				ITPR3
25452	4850646	9q34.3	0.565	1.07	0.002	U	0.001	U							ARRDC1
20540	3990703	1q32.1	0.449	1.07	0.016	U	0.008	U							IL10
29792	5820482	5p12	0.553	1.07	0.003	U	0.002	U							LOC153684
34467	6560131	6q13	0.386	1.07	0.032	U					X				FAM135A
8818	1660762	7q11.21	0.417	1.07	0.023	U									NCRNA00174
25945	4890674	2q37.2	0.414	1.07	0.034	U					X	X			SH3BP4
18716	3610202	5q33.2	0.378	1.07	0.032	U					X	X			GALNT10
7754	1450349	5q12.1	0.392	1.07	0.045	U									LOC728153
38514	7510025	15q24.3	0.640	1.06	0.001	U	0.000	U	P		X	X			TSPAN3
434	50647	1q41	0.653	1.06	0.013	U	0.006	U							FAM177B
23400	4490025	1q32.1	0.482	1.06	0.012	U	0.006	U							KIF21B
35486	6760364	10q24.1	0.866	1.06	0.000	U	0.000	U			X				LCOR
27547	5310132	19p13.3	0.358	1.06	0.043	U			x						STAP2
38253	7380240	13q32.3	0.732	1.06	0.000	U	0.000	U							LOC100129122
7712	1450136	11q22.3	0.510	1.06	0.013	U	0.006	U							LOC643733
33030	6350626	5q13.23	0.539	1.06	0.004	U	0.002	U							CCDC120
4905	940288	14q13.1	0.574	1.05	0.005	U	0.002	U							BAZ1A
28086	5390497	7q31.1	0.484	1.05	0.012	U	0.006	U							C7orf53
27711	5340162	10q25.3	0.564	1.05	0.002	U	0.001	U			X				KIAA1598
14189	2650477	17q11.2	0.418	1.05	0.021	U	0.010	U							TRAF4
5964	1110180	15q22.2	0.371	1.05	0.036	U					X				RORA
4582	840176	16q22.1	0.572	1.05	0.002	U	0.001	U							HSD11B2
33490	6400564	15q22.2	0.401	1.05	0.025	U					X				RORA
2280	430768	6p22.1	0.482	1.05	0.007	U	0.003	U	P		X	X			PRSS16
39143	7610050	3q27.1	0.448	1.05	0.020	U	0.008	U							ABCC5
33962	6480674	1q22	0.493	1.05	0.006	U	0.003	U							HCN3
21964	4200646	7q31.1	0.441	1.05	0.017	U	0.009	U							IFRD1
34619	6580047	19p13.12	0.449	1.05	0.012	U	0.006	U							LOC113230
36825	7040181	1q32.2	0.510	1.05	0.005	U	0.002	U							PFKFB2
11493	2190022	14q21.1	0.416	1.05	0.020	U	0.010	U							TRAPPC6B
7417	1430278	1q21.3	0.428	1.05	0.021	U					X				CTSK
19907	3870450	1p34.2	0.384	1.05	0.035	U									DEM1

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	STAT1 signif	SAM P value (FDR<5.1%)	1531 signif	NKX2-1 assoc	Beyers ESAT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET		Symbol
11594	2190541	7q22.1	0.409	1.05	0.027	U						X	X		GATS
16002	3120196	17p11.2	0.472	1.05	0.010	U	0.005	U							ALDH3A2
16243	3130544	19p12	0.495	1.05	0.009	U	0.004	U							ZNF486
29002	5670435	22q13.1	0.377	1.05	0.039	U									DMC1
2234	430465	Xq28	0.424	1.04	0.016	U	0.008	U							G6PD
23191	4390382	16q24.1	0.567	1.04	0.003	U	0.001	U							KIAA0182
38593	7510408	21q11.2	0.529	1.04	0.007	U	0.002	U				X	X		NRIP1
37274	7150132	14q21.1	0.610	1.04	0.002	U	0.001	U							PNN
3266	610354	Xq26.1	0.732	1.04	0.000	U	0.000	U							ZDHHC9
21726	4180289	16q22.1	0.464	1.04	0.013	U	0.007	U							HSF4
37427	7160128	3q29	0.487	1.04	0.011	U	0.006	U							SDHAP2
3775	670059	9q22.31	0.979	1.04	0.000	U	0.000	U							WNK2
34877	6590523	3q13.31	0.563	1.04	0.003	U	0.001	U							ZDHHC23
18213	3450092	2p14	0.394	1.04	0.028	U				P					PELI1
19243	3800402	11q24.2	0.436	1.04	0.021	U									ESAM
4434	830224	22q11.23	0.353	1.04	0.043	U									GGT1
24420	4670131	5p15.1	0.382	1.04	0.040	U						X	X		MYO10
5237	1010328	6p24.2	0.373	1.04	0.041	U						X	X		NEDD9
7149	1400376	Xp22.2	0.399	1.04	0.034	U						X	X		WWC3
11734	2230431	7q32.1	0.485	1.04	0.012	U	0.006	U							IRF5
31549	6130020	1q24.2	0.449	1.04	0.016	U	0.008	U				X	X		BLZF1
26506	5080328	21q22.12	0.478	1.04	0.012	U	0.005	U				X			DOPEY2
6075	1170220	2p15	0.402	1.04	0.032	U									AHSA2
4764	870338	5q31.2	0.383	1.04	0.030	U									EGR1
20201	3930392	14q11.2	0.478	1.03	0.007	U	0.004	U							ANG
11703	2230288	22q12.3	0.460	1.03	0.013	U	0.005	U							TST
28986	5670341	19p13.3	0.453	1.03	0.013	U	0.006	U							C19orf21
36317	6940709	2q33.2	0.464	1.03	0.015	U	0.008	U							ICA1L
6558	1240528	2q13	0.452	1.03	0.013	U	0.007	U							ILIF5
8392	1570279	14q13.2	0.460	1.03	0.013	U	0.007	U							SRP54
1660	270347	16p11.2	0.427	1.03	0.020	U	0.009	U							SULT1A3
12759	2450367	3p14.1	0.381	1.03	0.035	U						X			LRIG1
33663	6450022	6p22.2	0.403	1.03	0.046	U						X			LRRC16A
21247	4070193	3q23	0.372	1.03	0.033	U						X			MBNL3
1147	150184	20q13.33	0.629	1.03	0.004	U	0.002	U							CDH26
704	70343	10q24.1	0.541	1.03	0.004	U	0.002	U				X			FRAT1
4615	840349	11q13.1	0.542	1.03	0.003	U	0.002	U							OVOL1
6955	1340154	17q13.2	0.392	1.03	0.041	U									GGT6
17917	3420228	14q32.33	0.607	1.03	0.001	U	0.001	U	P						PPP1R13B
37388	7150711	19q13.31	0.452	1.03	0.015	U	0.008	U							ZNF223
27298	5270504	12q13.12	0.514	1.02	0.017	U	0.008	U							FAIM2
25463	4850703	2q36.3	0.449	1.02	0.020	U	0.010	U							SLC16A14
28130	5390747	14q23.3	0.469	1.02	0.016	U	0.008	U				X			SPTB
7784	1450451	21q22.12	0.386	1.02	0.028	U						X			DOPEY2
38232	7380142	Xq24	0.382	1.02	0.034	U						X	X		KLHL13
21918	4200438	10q25.3	0.497	1.02	0.025	U									VWA2
26844	5130692	22q13.1	0.480	1.02	0.015	U	0.007	U							DDX17
28209	5420373	19p13.3	0.452	1.02	0.013	U	0.007	U							FUT6
12721	2450187	3p22.3	0.692	1.02	0.000	U	0.000	U				X	X		GPD1L
7305	1410400	1q44	0.498	1.02	0.007	U	0.004	U							HNRNPU
17930	3420328	1q23.3	0.447	1.02	0.015	U	0.008	U							HSD17B7
34659	6580270	12q13.13	0.612	1.02	0.005	U	0.001	U							KRT18
16665	3180259	16p11.2	0.437	1.02	0.018	U	0.008	U							SULT1A3
15097	3120184	12q21.31	0.458	1.02	0.013	U	0.006	U				X			TMTC2
13152	2490068	14q24.1	0.384	1.02	0.028	U									PLEKHH1
38874	7560242	1p35.2	0.374	1.02	0.042	U						X	X		PTP4A2
23242	4390661	12q24.33	0.383	1.01	0.035	U									DDX51
21250	4070201	20p13	0.440	1.01	0.013	U	0.007	U							FAM110A
18957	3710563	2q12.1	0.394	1.01	0.029	U						X	X		SLC9A2
32142	6250020	19q13.33	0.465	1.01	0.014	U	0.007	U							SYNGR4
20435	3990040	2q11.2	0.573	1.01	0.040	U									IL1R2
2098	380494	9q21.11	0.439	1.01	0.039	U									PGM5
17249	3360064	15q15.1	0.393	1.01	0.027	U									PLA2G4F
3754	650730	1q42.2	0.542	1.01	0.005	U	0.002	U							FAM89A
31777	6180543	3q23	0.567	1.01	0.002	U	0.001	U							GK5
12915	2470358	6q23.3	0.633	1.01	0.001	U	0.001	U				X			IFNGR1
18800	3610059	2q12.2	0.569	1.01	0.003	U	0.001	U				X	X		KIF16B
8658	1580725	14q12	0.531	1.01	0.006	U	0.003	U							NUBPL
2654	510400	12q21.31	0.628	1.01	0.002	U	0.001	U				X			RASSF9
16305	3140092	3p22.1	0.636	1.01	0.001	U	0.000	U				X	X		TRAK1
20918	4050138	9q14.3	0.360	1.01	0.045	U						X	X		GPR98
4205	770682	5q31.2	0.448	1.01	0.023	U									MGC29506
23256	4390768	5q31.3	0.353	1.01	0.043	U									PCDHA1
24363	4640639	14q12	0.538	1.01	0.003	U	0.002	U				X			KHNYN
5090	990392	4p14	-0.500	-1.01	0.006	D	0.003	D				X			APBB2
20874	4040739	20q13.12	-0.710	-1.01	0.001	D	0.000	D							JPH2
10670	2030681	3p25.2	-0.479	-1.01	0.011	D	0.005	D							RPL32
4279	780270	17q25.3	-0.409	-1.01	0.020	D									TIMP2
22235	4220417	3p21.31	-0.376	-1.01	0.049	D									UCN2
33976	6480754	17q25.3	-0.439	-1.01	0.015	D									FAM195B
17984	3420554	8p21.1	-0.455	-1.02	0.010	D	0.005	D	N						P8K
34830	6590341	18p11.22	-0.532	-1.02	0.005	D	0.002	D							RAB31
18478	3460634	3p21.2	-0.656	-1.02	0.001	D	0.000	D							RRP9
6196	1190162	4q12	-0.519	-1.02	0.004	D	0.002	D							SGCB
37455	7160228	16q22.1	-0.607	-1.02	0.001	D	0.001	D							SLC12A4
15799	2970730	19q13.42	-0.358	-1.02	0.050	D						X			MYADM
38254	7380241	17q21.31	-0.441	-1.02	0.015	D									PLCD3
18533	3520121	19q13.42	-0.439	-1.02	0.013	D									RPL28
14498	2690402	3p14.3	-0.635	-1.02	0.006	D	0.003	D							ABHD6
27759	5340403	22q13.1	-0.541	-1.02	0.007	D	0.002	D							APOBEC3F
25478	4850762	10p12.2	-0.593	-1.02	0.007	D	0.002	D							C10orf67
9266	1740722	3p21.1	-0.613	-1.02	0.001	D	0.001	D							GLTBD1
10587	2030278	6p21.1	-0.513	-1.02	0.007	D	0.003	D							PPP2R5D
296	20753	12p11.22	-0.559	-1.02	0.006	D	0.002	D				X	X		REP15
8280	1510553	14q23.1	-0.477	-1.02	0.020	D									DACT1
13052	2480341	3p21.31	-0.563	-1.02	0.002	D	0.001	D							CDC25A
22960	4290010	1p21.2	-0.633	-1.03	0.001	D	0.001	D				X	X		DPYS
33028	6350608	14q24.3	-0.596	-1.03	0.002	D	0.001	D							PNMA1
10018	1940743	16q24.3	-0.449	-1.03	0.011	D	0.006	D							RPL13
11898	2260577	5p13.3	-0.501	-1.03	0.005	D	0.003	D				X			RUSC2
12716	2450167	3p21.2	-0.404	-1.03	0.027	D						X			RPL29
23985	4590280	1q21.3	-0.380	-1.03	0.034	D									SHC1
26798	5130435	6q21	-0.631	-1.03	0.002	D	0.001	D				X			LAMA4
23631	4540593	2q36.3	-0.367	-1.03	0.040	D						X			SLC19A3
37761	7210142	3p27.3	-0.451	-1.03	0.030	D						X			TWIST2
28292	5490053	13q14.2	-0.555	-1.03	0.002	D	0.001	D							DLEU1
38175	7330619	19p13.3	-0.529	-1.03	0.005	D	0.002	D							FSD1
23605	4540392	8p12	-0.639	-1.03	0.002	D	0.001	D							GSR
18678	3610059	2q33.2	-0.534	-1.03	0.006	D	0.002	D							ICA1L
1702	270546	17q12	-0.581	-1.03	0.002	D	0.001	D							PIP4K2B
36321	6940731	4q35.1	-0.438	-1.03	0.013	D									C4orf38
6591	1240674	9q33.3	-0.438	-1.03	0.020	D									DENND1A
17384	3360717	1p36.22	-0.424	-1.03	0.019	D									PIK3CD
18427	3460376	19q13.32	-0.437	-1.03	0.016	D						X			RTN2
13426	2510672	18q21.2	-0.355	-1.03	0.049	D									TCF4
6425	1230673	19p13.2	-0.615	-1.04	0.001	D	0.001	D							PPAN
17619	3390291	20q11.23	-0.622	-1.04	0.002	D	0.001	D							MANBAL
9440	1780088	19q13.3	-0.709	-1.04	0.002	D	0.000	D							TBXA2R
12001	2320307	20q11.22	-0.565	-1.04	0.003	D	0.001	D							CEP250
27990	5390066	13q34	-0.524	-1.04	0.007	D	0.002	D							FAM70B

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (5/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 sig=#	SAM P value (FDR=5.1%)	1531 sig=#	NKX2-1 amp	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TxMSET	Symbol
5650	1070019	19q13.2	-0.657	-1.04	0.003	D	0.001	D						FBXO17
33211	6370711	19q13.32	-0.488	-1.04	0.007	D	0.003	D						MEIS3
37273	7150128	3p24.3	-0.492	-1.04	0.006	D	0.003	D						SGOL1
25528	4860220	1q32.1	-0.679	-1.04	0.001	D	0.000	D						SRGAP2
21904	4220367	3p21.31	-0.367	-1.04	0.037	D								C3orf54
11560	2190356	3q26.2	-0.373	-1.04	0.043	D								EIF5A2
33705	6450192	Xq26.3	-0.361	-1.04	0.039	D								FAM127C
1648	270292	20p13	-0.382	-1.04	0.030	D								FKBP1A
35938	6860369	2q33.3	-0.422	-1.04	0.038	D								GPR1
32723	6290678	7q11.23	-0.349	-1.04	0.050	D								POMZP3
3996	730440	19q13.32	-0.413	-1.04	0.018	D								RELB
13588	2570661	6p21.1	-0.422	-1.04	0.020	D								TRERF1
2448	460121	14q22.1	-0.474	-1.04	0.018	D					x			TRIM9
11542	2190241	19q13.11	-1.110	-1.04	0.000	D	0.000	D						AP1M1
35418	6760008	5q35.3	-0.599	-1.04	0.001	D	0.001	D						DBN1
32906	6350037	12p11.21	-0.800	-1.04	0.000	D	0.000	D						DNM1L
34873	6590504	11q13.1	-0.703	-1.04	0.000	D	0.000	D						FIBP
6601	1240739	1p34.2	-0.562	-1.04	0.002	D	0.001	D						LEPRE1
23496	4490577	12q13.12	-0.640	-1.04	0.001	D	0.000	D			x	x		TUBA1A
3683	650300	11q12.2	-0.799	-1.05	0.000	D	0.000	D						CCDC86
23506	4490673	7p21.1	-0.470	-1.05	0.010	D	0.004	D						TWIST1
5324	1030026	17p11.2	-0.364	-1.05	0.037	D								CENPV
26941	5220400	19q13.32	-0.527	-1.05	0.004	D	0.002	D			x			CD3EAP
29357	5700689	20q11.22	-0.568	-1.05	0.002	D	0.001	D						CEP250
9418	1770746	1p21.2	-0.445	-1.05	0.013	D	0.006	D						EXTL2
35140	6650240	15q23	-0.484	-1.05	0.007	D	0.003	D						HEXA
24622	4730348	5q33.3	-0.458	-1.05	0.013	D	0.006	D						THG1L
31763	6180450	10q24.33	-0.416	-1.05	0.047	D								CALHM3
6557	1240523	12q13.2	-0.411	-1.05	0.026	D								RPL41
36829	7040195	1p34.1	-0.389	-1.05	0.026	D								ST3GAL3
4287	780315	1q21.3	-0.488	-1.05	0.031	D								ADAMTSL4
27007	5220754	3p25.3	-0.661	-1.05	0.000	D	0.000	D						ATG7
24369	4640673	13q12.3	-0.448	-1.05	0.011	D	0.006	D						B3GALTL
16988	3290286	12p13.33	-0.591	-1.06	0.001	D	0.001	D						TEAD4
11798	2260039	19p13.3	-0.552	-1.06	0.003	D	0.001	D						C19orf28
27130	5260538	9q31.1	-0.577	-1.06	0.001	D	0.001	D						C9orf30
24865	4780059	6p21.32	-0.575	-1.06	0.002	D	0.001	D			x			PPT2
23627	4540543	6p21.1	-0.719	-1.06	0.000	D	0.000	D						SUPT3H
5497	1050072	Xq21.31	-0.434	-1.06	0.035	D					x			KLHL4
16005	3120221	22q13.1	-0.576	-1.06	0.002	D	0.001	D						APOBEC3C
3064	580154	16q22.1	-0.613	-1.06	0.001	D	0.001	D						COG8
38586	7510379	13q12.12	-0.366	-1.06	0.044	D			N					SACS
16378	3140431	19q13.12	-0.352	-1.06	0.044	D								APLP1
17873	3420022	15q25.1	-0.428	-1.06	0.023	D								CIB2
39382	7650487	6p21.33	-0.412	-1.06	0.027	D					x			MICA
88	10379	9q34.11	-0.441	-1.07	0.013	D	0.006	D			x			STGALS6ALC4
38350	7380709	20q13.12	-0.536	-1.07	0.003	D	0.001	D						YWHAB
33411	6400161	17q24.1	-0.388	-1.07	0.027	D								CCDC46
4639	840433	6p21.1	-0.583	-1.07	0.006	D	0.002	D						RSPH9
19832	3870092	19q13.33	-0.516	-1.07	0.004	D	0.002	D						AKT1S1
16663	3180253	20q13.12	-0.640	-1.07	0.001	D	0.000	D						ELMO2
2947	540279	10p11.22	-0.451	-1.07	0.011	D	0.005	D						LOC338620
31853	6200133	6p25.2	-0.518	-1.07	0.004	D	0.002	D						PECI
8272	1510471	4q12	-0.645	-1.07	0.000	D	0.000	D						SGCB
34364	6550358	19p13.11	-0.446	-1.07	0.012	D	0.006	D						UBA52
9660	1820450	19q13.42	-0.449	-1.07	0.021	D								OSCAR
14535	2690608	2p25.3	-0.415	-1.07	0.020	D								RPS7
6334	1230215	1p21.3	-0.395	-1.07	0.027	D								SNX7
34146	6520100	3q28	-0.395	-1.08	0.028	D								CCDC50
26165	4920189	18q21.2	-0.551	-1.08	0.003	D	0.001	D						C18orf54
14219	2650608	4q27	-0.552	-1.08	0.002	D	0.001	D						CCNA2
24936	4780414	3p25.2	-0.545	-1.08	0.003	D	0.001	D						RPL32
32499	6280240	1p36.11	-0.601	-1.08	0.001	D	0.001	D						SH3BGRL3
24795	4760458	5q35.1	-0.509	-1.08	0.004	D	0.002	D						UBTD2
9693	1820646	9q31.2	-0.413	-1.08	0.027	D					x			ZNF462
2835	520528	5q35.1	-0.569	-1.09	0.002	D	0.001	D						CCDC99
11398	2140360	14q32.33	-0.496	-1.09	0.009	D	0.004	D			x			INF2
27687	5340059	3q13.33	-0.582	-1.09	0.002	D	0.001	D			x			LRRC58
17250	3360066	8q23.1	-0.358	-1.09	0.048	D					x	x		ANGPT1
37511	7160504	2q37.3	-0.372	-1.09	0.034	D								GPC1
16180	3130240	4q12	-0.531	-1.09	0.026	D								PDGFRA
17846	3400672	18q22.1	-0.390	-1.09	0.030	D								SERPINB8
22527	4250309	14q23.2	-0.383	-1.09	0.040	D								SNAPC1
26953	5220452	1p35.1	-0.422	-1.09	0.027	D								SYNC
34869	6590484	12q21.2	-0.470	-1.09	0.009	D	0.004	D						NAP1L1
28684	5560398	1q42.11	-0.702	-1.10	0.000	D	0.000	D						DEGS1
8520	1580088	19q13.12	-0.410	-1.10	0.021	D								HCST
15026	2760735	15q26.3	-0.405	-1.10	0.021	D					x			SYNM
24850	4780010	17q21.31	-0.446	-1.10	0.017	D								ARL4D
29506	5720692	10q22.1	-0.409	-1.10	0.037	D								COL13A1
21701	4180133	13q12.11	-0.511	-1.11	0.004	D	0.002	D						SKA3
17734	3400133	16p13.3	-0.604	-1.11	0.001	D	0.001	D						TCEB2
24940	4780437	4q25	-0.451	-1.11	0.014	D	0.006	D			x	x		ANK2
27671	5310747	9p22.3	-0.464	-1.11	0.010	D	0.004	D						PSIP1
2352	450369	3p14.2	-0.504	-1.11	0.006	D	0.003	D			x	x		PTPRG
30447	5900672	17p13.3	-0.579	-1.11	0.003	D	0.001	D						RTN4RL1
27022	5260047	8q21.13	-0.381	-1.11	0.030	D					x			FABP5
32118	6220671	19q13.31	-0.396	-1.11	0.024	D								PLAUR
2519	460484	4q31.1	-0.651	-1.12	0.001	D	0.000	D			x	x		CCRN4L
25355	4850091	12p13.31	-0.717	-1.12	0.000	D	0.000	D						EMG1
5499	1050079	7q35	-0.373	-1.12	0.037	D					x	x		TPK1
33501	6400646	11q13.1	-0.449	-1.12	0.014	D	0.006	D						CCDC85B
1720	270653	1p36.11	-0.462	-1.12	0.009	D	0.004	D						CLIC4
22783	4260731	1p36.11	-0.466	-1.12	0.010	D	0.004	D			x			STMN1
28959	5670187	11p15.1	-0.347	-1.12	0.048	D								DKFZp686O24166
28779	5570088	1p36.22	-0.891	-1.12	0.000	D	0.000	D						SRM
33394	6400082	12p11.23	-0.689	-1.13	0.000	D	0.000	D						C12orf11
27619	5310471	20q13.12	-0.679	-1.13	0.041	D								UBE2C
834	110239	7q21.3	-0.466	-1.13	0.037	D								CALCR
37378	7150671	10q24.32	-0.559	-1.13	0.003	D	0.001	D						ARL3
4762	870328	19p13.2	-0.683	-1.13	0.000	D	0.000	D						ECSIT
33764	6450471		-0.674	-1.13	0.003	D	0.001	D						FGFR1
38431	7400343	12q24.33	-0.444	-1.13	0.012	D	0.006	D						STX2
36584	6980541	17q25.3	-0.473	-1.13	0.008	D	0.004	D						TIMP2
9341	1770376	18q22.1	-0.353	-1.13	0.048	D								SERPINB8
13538	2570400		-0.396	-1.13	0.026	D								TMLHE
15615	2940504	7q21.3	-0.487	-1.13	0.018	D	0.006	D			x			PEG10
25114	4810487	11q22.3	-0.416	-1.13	0.021	D								ELMOD1
31902	6200367	21q22.3	-0.447	-1.13	0.028	D								FTCD
28198	5420347	16p13.3	-0.659	-1.13	0.001	D	0.000	D						HCFC1R1
13857	2630370	7p22.3	-0.526	-1.13	0.006	D	0.002	D			x	x		MAD1L1
12871	2470142	19q13.12	-0.351	-1.13	0.045	D								ZFP82
28934	5670095	10q11.21	-0.451	-1.13	0.015	D								ZNF239
14510	2690458	1q43	-0.518	-1.14	0.005	D	0.002	D			x			EXO1
2807	520367	20q13.12	-0.899	-1.14	0.000	D	0.000	D						IFTS2
34197	6520356	1q42.13	-0.431	-1.14	0.019	D								GJC2
39104	7570601	4p15.33	-0.405	-1.14	0.029	D								LOC285548
26601	5090070	14q11.2	-0.396	-1.14	0.030	D								MMP14
19774	3850593	1p21.3	-0.417	-1.14	0.019	D								SNX7
20520	3990598	11q13.1	-0.660	-1.14	0.001	D	0.000	D						DRAP1

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 sig=#	SAM P value (FDR=5.1%)	1531 sig=#	NKX2-1 amp	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TxMSET	Symbol
28722	5560576	15q21.3	-0.519	-1.14	0.004	D	0.002	D			x			NEDD4
32416	6270674	12p12.1	-0.751	-1.14	0.000	D	0.000	D						RECQL
38180	7330653	1p36.33	-0.650	-1.15	0.001	D	0.000	D						C1orf86
39009	7570092	5q35.3	-0.629	-1.15	0.001	D	0.000	D						DBN1
33839	6480064	9p13.2	-0.799	-1.15	0.000	D	0.000	D						POLR1E
36270	6940458	19q13.41	-0.392	-1.15	0.027	D								ZNF175
26090	4900626	19q13.2	-0.642	-1.15	0.001	D	0.000	D						EID2B
1899	360110	10p15.1	-0.558	-1.15	0.002	D	0.001	D			x	x		KLF6
2403	450653	1q41	-0.650	-1.15	0.001	D	0.000	D			x	x		PTPN14
9467	1780259	4q25	-0.628	-1.16	0.001	D	0.000	D						CCDC109B
13784	2630020	6p21.1	-0.463	-1.16	0.011	D	0.004	D						SUPT3H
31746	6180373	2q32.2	-0.593	-1.16	0.002	D	0.001	D			x	x		TMEM194B
9645	1820376	16p11.2	-0.742	-1.16	0.000	D	0.000	D						TGFB1I1
26037	4900341	4p15.2	-0.459	-1.16	0.049	D								GBA3
36222	6940215	3q22.3	-0.490	-1.16	0.007	D	0.003	D						MRAS
22551	4250398	20q13.12	-1.050	-1.16	0.000	D	0.000	D						STK4
32815	6330338	12q13.13	-0.403	-1.16	0.028	D								ITGA5
15824	3060095	6q13	-0.408	-1.17	0.024	D					x	x	x	COL12A1
5753	1070451	4q27	-0.646	-1.17	0.001	D	0.000	D			x			ANXA5
13354	2510324	9p13.3	-0.761	-1.17	0.000	D	0.000	D						NUDT2
12865	2470114	2q37.3	-0.481	-1.17	0.032	D					x			COL6A3
37379	7150673	Xp21.1	-0.351	-1.17	0.048	D					x			PRRG1
14713	2710746	16q23.1	-0.718	-1.17	0.000	D	0.000	D			x			BCAR1
10750	2060288	Xp11.23	-0.654	-1.17	0.001	D	0.000	D						PLP2
22704	4260368	20q13.12	-0.703	-1.17	0.047	D								UBE2C
314	50088	16p13.3	-0.502	-1.18	0.006	D	0.002	D						HCFC1R1
7493	1430626	8p21.2	-0.668	-1.18	0.000	D	0.000	D						KCTD9
36005	6860671	Xq22.1	-0.551	-1.18	0.005	D	0.002	D						RPL36A
20995	4050519	1q43	-0.748	-1.18	0.001	D	0.000	D						CEP170
29162	5690398	1q25.1	-0.537	-1.18	0.010	D	0.003	D						TNFSF4
26703	5090626	2q24.2	-0.482	-1.18	0.035	D								FAP
37703	7200639	16q22.1	-0.445	-1.18	0.023	D								RRAD
38427	7400327	2q13	-0.529	-1.18	0.003	D	0.001	D						SEPT10
1400	160605	13q34	-0.566	-1.18	0.003	D	0.001	D						RASA3
28654	5560246	15q22.2	-0.400	-1.18	0.023	D					x			TPM1
14109	2650112	Xq13.2	-0.423	-1.19	0.016	D								SLC16A2
2405	450671		-0.485	-1.19	0.012	D	0.004	D						ANXA6
8545	1580195	19p13.3	-0.553	-1.19	0.007	D	0.002	D						LPPR3
15315	2850551	21q22.12	-0.567	-1.19	0.002	D	0.001	D						RCAN1
31844	6200072	12p13.1	-0.392	-1.19	0.032	D					x			GPR19
29316	5700458	15q24.1	-0.406	-1.19	0.033	D								LOXL1
21219	4070053	1p22.1	-0.486	-1.20	0.006	D	0.003	D	N		x			BCAR3
36067	6900196	20q13.13	-0.608	-1.20	0.009	D	0.002	D						KCNB1
16625	3180070	1p13.2	-0.558	-1.20	0.007	D	0.002	D						OLFML3
15022	2760706	16q22.1	-0.474	-1.20	0.010	D	0.004	D						GFOD2
28866	5570520	16q22.1	-0.491	-1.20	0.023	D								RRAD
1729	270703	2q32.3	-0.515	-1.20	0.027	D								TMEFF2
12309	2350379	19q13.42	-0.369	-1.20	0.035	D								TNNT1
20895	4050040	16q24.3	-0.487	-1.20	0.013	D	0.005	D						TUBB3
24526	4670670	3p21.31	-0.749	-1.21	0.000	D	0.000	D						CDC25A
13856	2630369	15q15.1	-0.711	-1.21	0.000	D	0.000	D						CHST14
35597	6770168	3p22.3	-0.506	-1.21	0.008	D	0.003	D						CRTAP
14287	2680131	12p11.23	-0.547	-1.21	0.004	D	0.001	D						PPFIBP1
34958	6620170	16p13.3	-0.480	-1.21	0.034	D								HBA2
15873	3060377	17p11.2	-0.495	-1.21	0.023	D								MFAP4
8817	1660750	Xq22.2	-0.407	-1.21	0.027	D								WIBP5
20091	3890632	12p11.21	-0.651	-1.22	0.000	D	0.000	D						DNM1L
6140	1170653	7p22.3	-0.440	-1.22	0.013	D	0.005	D			x	x		PDGFA
22507	4250204	12q23.1	-0.487	-1.22	0.007	D	0.003	D						SLC25A3
36942	7050014	16q23.1	-0.591	-1.22	0.001	D	0.001	D						TMEM231
18033	3440025	6q26	-0.426	-1.22	0.019	D								AGPAT4
32189	6250192	2q37.3	-0.410	-1.22	0.041	D					x			COL6A3
18779	3610474	19q13.32	-0.418	-1.22	0.022	D								ERCC1
14674	2710524	5q13.2	-0.420	-1.22	0.019	D								MAP1B
17918	3420241	12p13.31	-0.360	-1.22	0.041	D								SLC2A14
22008	4210066	16q24.3	-0.917	-1.22	0.000	D	0.000	D			x			DEF8
33717	6450274	5q14.3	-0.652	-1.22	0.000	D	0.000	D						POLR3G
28331	5490246	1q43	-0.766	-1.23	0.000	D	0.000	D						AKT3
29957	5690519	5q24.2	-0.562	-1.23	0.009	D	0.002	D						CSF2RA
12887	2470215	5q33.1	-0.535	-1.23	0.004	D	0.001	D			x			NDST1
7629	1440482	3p25.3	-0.655	-1.23	0.001	D	0.000	D						OGG1
1773	290132	20q11.23	-0.645	-1.23	0.002	D	0.001	D						C20orf117
27372	5290086	7p14.3	-0.543	-1.23	0.004	D	0.001	D						FKBP9
20828	4040491	19p11.22	-0.487	-1.23	0.014	D	0.005	D			x			ITGB1
27127	5260494	Xq28	-0.404	-1.23	0.026	D								TMLHE
4016	730528	19q13.31	-0.360	-1.24	0.039	D								PLAUR
569	60470	6q24.2	-0.387	-1.24	0.028	D								STX11
8964	1690768	19p13.22	-0.733	-1.24	0.001	D	0.000	D		x				ZER1
26036	4900338	7q36.3	-0.513	-1.24	0.005	D	0.002	D						C7orf13
25563	4860368	3q22.3	-0.443	-1.24	0.014	D	0.006	D						TMEM22
31938	6200561	1p35.1	-0.412	-1.24	0.021	D								CCDC28B
30628	5960068	5q32	-0.473	-1.25	0.021	D								PDGFRB
17003	3420347	3q21.2	-0.478	-1.25	0.011	D	0.005	D			x	x		HEG1
11483	2140753	3p22.1	-0.503	-1.25	0.006	D	0.002	D						RPL14
24439	4670204	3q13.31	-0.431	-1.25	0.044	D								GAP43
5798	1070678	16q24.1	-0.897	-1.26	0.000	D	0.000	D						CDTL1
26132	4920047	12q13.12	-0.389	-1.26	0.036	D								C1QL4
15639	2940630	22q12.2	-0.723	-1.26	0.001	D	0.000	D						SLC35E4
24362	4640634	20q13.12	-0.547	-1.26	0.002	D	0.001	D						SNX21
4977	940670	6p12.2	-0.590	-1.26	0.001	D	0.001	D			x	x		TRAM2
28549	5550500	17q25.1	-0.405	-1.26	0.023	D								MXRA7
14994	2760544	19q13.11	-0.544	-1.27	0.004	D	0.002	D						PBX4
7917	1470348	14q32.31	-0.525	-1.27	0.006	D	0.002	D						RAGE
27973	5360743	1p35.2	-0.397	-1.27	0.025	D					x			COL16A1
15019	2760689	Xq13.3	-0.422	-1.27	0.018	D								MAGEE1
3307	610519	15q22.2	-0.414	-1.28	0.019	D					x			TPM1
20981	4050446	11q13.1	-0.694	-1.28	0.000	D	0.000	D						C11orf68
13822	2630202	8q22.3	-0.666	-1.28	0.001	D	0.000	D						FLJ45248
20914	4050128	20q13.12	-0.571	-1.28	0.002	D	0.001	D						SULF2
29346	5700646	3p22.3	-0.505	-1.29	0.005	D	0.002	D						CRTAP
38241	7510181	4q25	-0.479	-1.29	0.007	D	0.003	D			x			ELOVL6
17714	3400048	19q13.42	-0.592	-1.29	0.010	D	0.004	D						IL11
15404	2900220	12p12.1	-0.529	-1.29	0.005	D	0.001	D						BHLHE41
25283	4830497	20q11.21	-0.687	-1.29	0.000	D	0.000	D						POFUT1
10658	2030598	1q42.12	-0.522	-1.29	0.018	D	0.005	D						CNIH3
38634	7510603	12q15	-0.478	-1.29	0.014	D	0.004	D						CPEB1
24436	4670192	15q26.1	-0.559	-1.29	0.003	D	0.001	D						KIF7
20980	4050441	2q12.3	-0.540	-1.29	0.011	D	0.003	D						SH3RF3
15432	2900358	19p13.3	-0.564	-1.30	0.003	D	0.001	D						C19orf28
8021	1500047	11q13.2	-0.605	-1.30	0.002	D	0.001	D						RIN1
11520	2190128	6q24.3	-0.623	-1.30	0.001	D	0.000	D						RAB12
37773	7210192	20q13.12	-0.408	-1.30	0.021	D				N				ADA
14987	2760520	18q21.2	-0.567	-1.31	0.002	D	0.001	D						C18orf54
13045	2480296	13q14.3	-0.768	-1.31	0.000	D	0.000	D						SUGT1
8485	1570709	3q33.1	-0.393	-1.31	0.029	D								FZD7
19777	3850603	2q35	-0.425	-1.31	0.041	D								PTPRN
33846	6480092	16q22.1	-0.637	-1.31	0.001	D	0.001	D			x			FAM65A
32711	6290609	19p13.3	-0.500	-1.31	0.007	D	0.003	D						RPS15
24818	4760593	11p13	-0.404	-1.31	0.025	D					x			CD59
8536	1580156	19p13.3	-0.512	-1.32	0.008	D	0.002	D						FSD1

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (6/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Bryers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
12006	2320343	Xq28	-0.352	-1.32	0.050	D								MAMLD1
4600	840278	21q21.3	-0.465	-1.32	0.022	D								JAM2
19558	3840367	2p11.2	-0.459	-1.32	0.016	D	0.005	D						CAPG
5649	1070014	5q32	-0.378	-1.32	0.044	D								CSF1R
27532	5310050	3p21.31	-0.703	-1.33	0.001	D	0.000	D						CCDC71
28920	5670040	4q25	-0.603	-1.33	0.001	D	0.001	D			X			ELOVL6
4040	730632	11p15.5	-0.451	-1.33	0.012	D	0.005	D						LSP1
20659	4010414	12p11.23	-0.660	-1.33	0.001	D	0.000	D						PPFIBP1
13894	2630563	8p21.3	-0.732	-1.33	0.000	D	0.000	D						SLC39A14
7751	1450341	2q31.1	-0.563	-1.34	0.003	D	0.001	D						DLX1
38822	7560037	6p21.33	-0.538	-1.34	0.003	D	0.001	D						KIAA1949
30211	5890242	Xq21.1	-0.449	-1.34	0.024	D								SH3BGRL
32753	6330037	12p12.1	-0.553	-1.35	0.004	D	0.001	D			X			ITPR2
7509	1430711	13q22.1	-0.484	-1.35	0.008	D	0.003	D			X			KLF12
17902	3420154	1q44	-0.557	-1.35	0.015	D	0.004	D						NLRP3
5175	1010035	1q44	-0.596	-1.35	0.009	D	0.002	D						NLRP3
24724	4760056	6q14.1	-0.351	-1.35	0.048	D								ELOVL4
39142	7610044	1p36.31	-0.671	-1.35	0.001	D	0.000	D			X			ACOT7
20059	3890458	20q13.32	-0.716	-1.35	0.002	D	0.000	D						MGC4294
12623	2370471	7q35	-0.831	-1.35	0.000	D	0.000	D						ORI6B1
580	60524	9q33.3	-0.545	-1.35	0.003	D	0.001	D						DENND1A
2388	450553	11q12.3	-0.605	-1.36	0.001	D	0.000	D			X			AHNAK
5952	1110112	12p12.1	-0.827	-1.36	0.000	D	0.000	D						RECQL
8421	1570382	3p14.1	-0.418	-1.36	0.043	D					X			ADAMTS9
7882	1470626	19p13.12	-0.565	-1.36	0.002	D	0.001	D						CD97
29457	5720438	5q11.2	-0.645	-1.36	0.001	D	0.000	D						GPX8
21790	4180544	5p15.2	-0.799	-1.37	0.000	D	0.000	D			X			ROPN1L
9716	1820768	8q21.3	-0.535	-1.37	0.005	D	0.002	D			X			TMEM64
35836	6840600	1q25.3	-0.351	-1.37	0.049	D								GLT25D2
23743	4560471	9q21.13	-0.626	-1.38	0.001	D	0.000	D						GDA
25397	4850327	4q32.1	-0.523	-1.38	0.004	D	0.002	D			X	X		PDGFC
2729	520014	19p13.11	-0.432	-1.38	0.016	D								ISYNA1
13799	2630102	1p35.1	-0.384	-1.38	0.030	D								CCDC28B
762	70603	3q28	-0.484	-1.38	0.017	D								CCDC50
9705	1820722	10p12.1	-0.522	-1.39	0.018	D	0.005	D						APBB1IP
29486	5720575	10p12.31	-0.575	-1.39	0.003	D	0.001	D						C10orf114
23739	4560450	12q21.2	-0.578	-1.39	0.002	D	0.001	D						E2F7
29853	5860021	2q31.1	-0.667	-1.39	0.001	D	0.000	D						SPC25
8146	1500661	13q14.2	-0.499	-1.39	0.005	D	0.002	D			X			DLEU2
6344	1230270	19q13.11	-0.435	-1.40	0.014	D	0.006	D			X	X		WTIP
39171	7610168	9p22.2	-1.016	-1.40	0.000	D	0.000	D						CNTLN
4467	830377	1q21.3	-0.517	-1.40	0.005	D	0.002	D			X			S100A13
28721	5560575	20q11.23	-0.539	-1.40	0.009	D	0.002	D			X			TGM2
3122	580465	14q24.3	-0.569	-1.40	0.004	D	0.001	D						VASH1
28594	5550743	19q13.43	-0.364	-1.40	0.041	D								ZNF814
27703	5340136	12q24.33	-0.595	-1.41	0.005	D	0.001	D						GALNT9
21677	4180008	3q23	-0.589	-1.41	0.005	D	0.002	D						TRPC1
6069	1170180	19q13.11	-0.485	-1.41	0.007	D	0.002	D			X	X		WTIP
7167	1400446	9p22.1	-0.456	-1.42	0.011	D	0.004	D						PLIN2
8090	1500390	21q22.3	-0.476	-1.42	0.009	D	0.004	D						C21orf56
3482	620717	17q12	-0.466	-1.42	0.029	D								CCL5
36268	6940446	15q25.2	-0.451	-1.43	0.012	D	0.005	D						MEX3B
19875	3870301	8p21.3	-0.780	-1.43	0.002	D	0.001	D			X	X		SORBS3
30196	5890168	Xq28	-0.460	-1.43	0.010	D	0.004	D						TMLHE
2468	460204	9p22.1	-0.347	-1.43	0.047	D								PLIN2
37397	7150762	20q13.13	-0.541	-1.43	0.023	D	0.006	D			X			PTGIS
1959	360475	19q13.31	-0.445	-1.44	0.012	D	0.005	D						PLAUR
15196	2810767	19p13.3	-0.449	-1.44	0.019	D	0.006	D						EBI3
10301	1990484	15q14	-0.629	-1.44	0.001	D	0.000	D						GPR176
7913	1470324	6q21	-0.356	-1.44	0.041	D			N					POPDC3
33616	6420500	22q13.1	-0.365	-1.44	0.046	D					X	X		MGAT3
39291	7650017	11q13.5	-0.480	-1.44	0.009	D	0.003	D						SERPINH1
18923	3710386	2q13	-0.540	-1.45	0.004	D	0.001	D						SEPT10
7348	1410706	12q23.1	-0.555	-1.45	0.002	D	0.001	D						IKBIP
38797	7550685	5q13.2	-0.432	-1.45	0.014	D	0.006	D						MAP1B
30597	5910619	12q24.33	-0.617	-1.46	0.001	D	0.000	D						STX2
11241	2120360	Xp11.23	-0.680	-1.46	0.004	D	0.001	D						SYNJ
35594	6770138	2q36.3	-0.521	-1.46	0.010	D	0.002	D						WDR69
26248	4920593	1p32.3	-0.601	-1.46	0.001	D	0.000	D						CDKN2C
11143	2100673	1q23.1	-0.736	-1.47	0.000	D	0.000	D						KIRREL
20127	3930040	2p22.3	-0.618	-1.47	0.001	D	0.000	D			X			CRIM1
21733	4180324	1p36.11	-0.398	-1.47	0.025	D								FAM46B
21048	4060026	1p21.3	-0.618	-1.48	0.010	D	0.002	D						FLJ35409
37503	7160471	12q14.3	-0.576	-1.48	0.004	D	0.001	D			X	X		MSRB3
3274	610379	22q13.1	-0.531	-1.48	0.004	D	0.001	D						APOBEC3F
10534	2030041	2p25.1	-0.635	-1.48	0.001	D	0.000	D			X	X		ASAP2
8189	1510075	20q13.33	-0.465	-1.48	0.044	D								KCNQ2
32401	6270600	8q21.3	-0.527	-1.49	0.006	D	0.002	D			X			TMEM64
28622	5560110	17p13.1	-0.496	-1.50	0.006	D	0.002	D						DLG4
32370	6270411	9q21.33	-0.737	-1.50	0.004	D	0.001	D						GAS1
3772	670041	6q25.1	-0.433	-1.50	0.024	D			N		X			AKAP12
30408	5900452	Xp11.23	-0.497	-1.51	0.008	D	0.003	D			X			CHST7
31238	6100072	7q34	-0.432	-1.51	0.016	D	0.006	D						DENND2A
34620	6580048	Xp11.22	-0.427	-1.51	0.016	D	0.006	D						FGD1
38133	7530379	12p13.31	-0.794	-1.51	0.000	D	0.000	D			X			PTMS
38657	7510731	Xq22.2	-0.503	-1.51	0.025	D								WBP5
22974	4290050	1p36.31	-0.872	-1.52	0.000	D	0.000	D			X			ACOT7
16121	3130010	16q24.3	-0.957	-1.52	0.000	D	0.000	D			X			DEF8
12052	2320598	Xp11.3	-0.433	-1.52	0.031	D								NDP
26080	4900592	15q25.2	-0.451	-1.52	0.021	D								CPEB1
20429	3940762	15q22.2	-0.621	-1.52	0.002	D	0.001	D						APH1B
9144	1740100	11p13	-0.593	-1.53	0.008	D	0.001	D			X	X		PAX6
13199	2490328	11q24.2	-0.374	-1.53	0.044	D					X			SLC37A2
37909	7320059	19q13.3	-0.519	-1.53	0.005	D	0.001	D						FSD1
38978	7560706	9q32	-0.672	-1.53	0.001	D	0.000	D						NCRNA00256B
23618	4540465	11q22.1	-0.489	-1.54	0.007	D	0.003	D						C11orf70
33351	6380646	3p24.3	-0.559	-1.55	0.017	D	0.004	D			X			ZNF385D
28539	5550452	10q22.3	-0.371	-1.55	0.038	D								KCNMA1
34999	6620370	12q23.1	-0.630	-1.56	0.001	D	0.000	D						IKBIP
17321	3360431	2q31.1	-0.603	-1.56	0.001	D	0.000	D			X	X		ZAK
11324	2140022	5q33.3	-0.622	-1.57	0.002	D	0.000	D						ADRA1B
72	10324	5q23.1	-0.796	-1.57	0.000	D	0.000	D						PRR16
26364	5050441	2q22.3	-0.680	-1.57	0.002	D	0.000	D						ZEB2
27783	5340504	6q23.2	-0.542	-1.57	0.003	D	0.001	D						AKAP7
19295	3800634	15q14	-0.730	-1.57	0.000	D	0.000	D						AVEN
35688	6770603	17q22	-0.524	-1.57	0.012	D	0.003	D						NOG
24402	4670059	2q31.1	-0.488	-1.57	0.007	D	0.003	D			X	X		ZAK
1033	130445	1p34.2	-0.624	-1.58	0.001	D	0.000	D						HYI
26747	5130110	11q13.1	-0.635	-1.58	0.001	D	0.000	D						SNX15
33667	6450041	6p22.3	-0.685	-1.58	0.001	D	0.000	D						RBM24
8332	1570047	22q11.21	-0.468	-1.58	0.040	D								SLC7A4
13049	2480327	20q11.23	-0.573	-1.59	0.002	D	0.001	D						MYL9
23694	4560164	5q35.3	-0.709	-1.59	0.000	D	0.000	D						PDLIM7
23766	4560592	4p15.31	-0.395	-1.59	0.029	D					X	X		SLIT2
11574	2190408	19q13.12	-0.397	-1.60	0.026	D								UPK1A
38096	7330189	5q31.2	-0.610	-1.60	0.002	D	0.000	D						REEP2
2213	430376		-0.530	-1.61	0.003	D	0.001	D						ASMTL
34939	6620050	12p13.31	-0.459	-1.61	0.015	D	0.004	D						IFFO1
5244	1010349		-0.604	-1.62	0.001	D	0.000	D						ASMTL
35590	6770121	17q21.31	-0.516	-1.62	0.005	D	0.001	D						C1QL1

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Bryers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
65	10286	1q21.3	-0.572	-1.62	0.009	D	0.002	D						ADAMTSL4
3409	620274	16q22.2	-0.893	-1.62	0.000	D	0.000	D						ATXN1L
37095	7050768	3p25.3	-0.514	-1.62	0.009	D	0.003	D						OXTR
5866	1090326	3p25.2	-0.463	-1.62	0.017	D	0.005	D			X			TIMP4
11460	2140678	2q31.1	-0.615	-1.63	0.001	D	0.000	D	N		X			ITGA6
20184	3930343	13q12.3	-0.589	-1.63	0.008	D	0.002	D						ALOX5AP
27142	5260605	15q26.3	-0.492	-1.63	0.006	D	0.002	D						LOC400464
34732	6580639	1p36.31	-0.820	-1.64	0.000	D	0.000	D			X			ACOT7
33462	6400403	8q11.23	-0.426	-1.64	0.016	D	0.006	D			X	X		RGS20
12957	2470600	13q12.3	-0.612	-1.64	0.001	D	0.000	D						KATNAL1
28609	5560056	4q28.1	-0.755	-1.64	0.000	D	0.000	D						NUDT6
10596	2030309	11q12.1	-0.535	-1.64	0.010	D	0.002	D						SERPING1
16023	3120326	8q23.1	-0.377	-1.64	0.035	D					X	X		ANGPT1
20119	3930008	3p22.1	-0.380	-1.64	0.033	D								RPL14
21133	4060437	11q22.1	-0.483	-1.65	0.008	D	0.003	D						C11orf70
33487	6400553	7q21.13	-0.568	-1.65	0.002	D	0.001	D			X	X		CDK14
1856	290593	4q27	-0.531	-1.65	0.005	D	0.001	D			X			FGF2
1128	150100	1q21.3	-0.500	-1.65	0.010	D	0.003	D						S100A3
26926	5220333	14q32.13	-0.648	-1.67	0.001	D	0.000	D						C14orf139
10396	2000148	10q23.31	-0.395	-1.67	0.037	D								IFIT1
28899	5570682	11q24.1	-0.484	-1.68	0.010	D	0.003	D						ASAM
37596	7200167	6q23.1	-0.487	-1.69	0.006	D	0.002	D			X	X		EPB41L2
21429	4120369	22q13.1	-0.584	-1.69	0.003	D	0.001	D						APOBEC3G
9931	1940274	14q32.12	-0.471	-1.69	0.014	D	0.005	D						IFI27L2
37454	7160224	15q22.2	-0.642	-1.70	0.002	D	0.000	D						APH1B
12704	2450114	1q41	-0.858	-1.70	0.000	D	0.000	D			X	X		PTPN14
31755	6180427	1q32.2	-0.380	-1.70	0.040	D								G0S2
15602	2940446	20q11.23	-0.370	-1.70	0.040	D					X			TGM2
29675	5810687	15q23	-0.454	-1.71	0.011	D	0.004	D						LARP6
18005	3420672	2q31.1	-0.410	-1.71	0.026	D								DLX1
35075	6620711	10q25.3	-0.523	-1.72	0.007	D	0.002	D			X	X		AFAP1L2
27064	5260215	10p13	-0.598	-1.72	0.001	D	0.000	D						OPTN
31258	6100180	11q13.1	-0.394	-1.72	0.035	D								EFEMP2
30925	6020746	16q21	-0.569	-1.72	0.003	D	0.001	D						CMTM3
18407	3460296	15q25.2	-0.478	-1.73	0.009	D	0.003	D						HDGFRP3
2678	510520	10q11.22	-0.426	-1.73	0.022	D								ARHGAP22
24523	4670653	Xp21.3	-0.435	-1.73	0.022	D								IL1RAPL1
9045	1710386	8p21.3	-1.077	-1.73	0.000	D	0.000	D						C8orf58
23404	4490044	11q13.2	-0.623	-1.73	0.001	D	0.000	D						LRFN4
21696	4180110	2q35	-0.909	-1.73	0.000	D	0.000	D			X			RPL37A
24382	4640743	1p21.3	-0.699	-1.74	0.001	D	0.000	D						CNN3
17773	3400326	4q34.3	-0.602	-1.74	0.001	D	0.000	D						MGC45800
3403	620239	21q22.12	-0.715	-1.74	0.001	D	0.000	D						RCAN1
11163	2100767	18p11.32	-0.479	-1.74	0.036	D								COLEC12
1926	360270	12q21.2	-0.660	-1.74	0.001	D	0.000	D			X	X		NAV3
23965	4590133	10p25.3	-0.425	-1.74	0.027	D					X	X		AFAP1L2
21339	4070719	15q21.1	-0.372	-1.74	0.040	D								C15orf48
16449	3170019	19q13.3	-0.378	-1.74	0.036	D								FSD1
8786	1660575	6p21.32	-0.865	-1.75	0.000	D	0.000	D			X			PPT2
1313	160209	13q33.1	-0.866	-1.75	0.000	D	0.000	D	N					KDELC1
20448	3990152	1q32.1	-0.706	-1.75	0.000	D	0.000	D						DYRK3
16570	3170605	12q23.1	-0.569	-1.75	0.002	D	0.001	D						IKBIP
6948	1340100	2q33.1	-0.605	-1.76	0.001	D	0.000	D						LOC100288092
37473	7160343	3q21.1	-0.592	-1.76	0.004	D	0.001	D			X	X		MYLK
33617	6420520	20q13.12	-0.424	-1.76	0.017	D								CD40
39158	7610128	1p31.3	-0.407	-1.76	0.035	D								KANK4
733	70465	2q37.3	-0.616	-1.76	0.008	D	0.001	D						ESPNL
21827	4180747	5p15.31	-0.401	-1.77	0.028	D								SNORD123
4275	780240	12q24.11	-0.621	-1.77	0.001	D	0.000	D						C12orf24
30115	5870561	1q43	-0.927	-1.78	0.000	D	0.000	D						AKT3
5200	1010139	13q13.3	-0.465	-1.78	0.010	D	0.004	D			X	X		LHFP
36626	7000008	19q13.12	-0.505	-1.80	0.005	D	0.001	D						APLP1
122	10561	12q23.3	-0.479	-1.80	0.010	D	0.003	D						GLTSD2
8439	1570484	19q13.33	-0.752	-1.80	0.000	D	0.000	D						ATF5
347	50255	8q11.21	-0.455	-1.82	0.023	D	0.006	D	N					SNAI2
1957	360471	6q15	-0.727	-1.82	0.000	D	0.000	D						MAP3K7
23719	4560328	7p22.1	-0.592	-1.83	0.001	D	0.000	D	N					FSCN1
4197	770639	5q35.3	-0.817	-1.83	0.000	D	0.000	D						PDLIM7
18289	3450458	1p36.12	-0.491	-1.84	0.008	D	0.002	D						SH2D5
5710	1070279	6q21.1	-0.393	-1.84	0.025	D								DLK2
31307	6100433	20q13.33	-0.463	-1.85	0.013	D	0.004	D						SOX18
13253	2490598	5q33.1	-0.685	-1.85	0.000	D	0.000	D						ANXA6
7540	1440088	16p11.2	-0.461	-1.86	0.009	D	0.003	D						ASPHD1
28474	5550142	9q33.3	-0.400	-1.86	0.012	D					X	X		LHX2
25101	4810445	3q23	-0.394	-1.86	0.024	D					X	X		PCOLCE2
4363	780678	1q21.3	-0.651	-1.86	0.004	D	0.001	D						ADAMTSL4
27235	5270241	5q35.1	-0.793	-1.88	0.000	D	0.000	D						STK10
38087	7330142	9p11.2	-0.553	-1.88	0.003	D	0.001	D						TGFB1I1
22075	4210403	5p13.2	-0.385	-1.88	0.032	D					X	X		SLC1A3
27632	5310554	Xq28	-0.585	-1.91	0.001	D	0.000	D						MPP1
9885	1940048	19q13.33	-0.533	-1.93	0.005	D	0.001	D						CLEC11A
9271	1770008	10p13	-0.635	-1.93	0.001	D	0.000	D						FRMD4A
30087	5870424	19q12	-0.526	-1.93	0.010	D	0.002	D						TSH23
4188	770603	11p14.1	-0.463	-1.94	0.012	D	0.004	D			X	X		BDNF
38353	7380719	12q13.13	-0.357	-1.94	0.043	D								IGFBP6
3062	580148	7q11.23	-0.735	-1.95	0.000	D	0.000	D						CLIP2
11169	2120021	2q32.2	-0.428	-1.95	0.036	D								COL3A1
8042	1500139	17p12	-0.364	-1.95	0.041	D								HS3ST3A1
20080	3890551	16q21	-0.571	-1.96	0.006	D	0.001	D						CMTM3
17802	3400458	12q14.3	-0.537	-1.98	0.004	D	0.001	D			X	X		MSRB3
24302	4640328	19q13.33	-0.650	-1.99	0.001	D	0.000	D						MAMSTR
20297	3940097	1q21.1	-0.577	-2.00	0.002	D	0.001	D	x					LIX1L
37612	7200243	18q21.33	-0.450	-2.00	0.017	D	0.005	D						SERPINB7
5971	1110228	11q23.3	-0.743	-2.00	0.000	D	0.000	D						TMEM136
20242	3930592	6p22.3	-0.482	-2.01	0.007	D	0.002	D			X			CAP2
34506	6560301	12q24.12	-0.584	-2.01	0.003	D	0.001	D						SH2B3
19021	3780095	2q33.1	-0.577	-2.02	0.009	D	0.001	D						AOX1
21518	4150017	1p36.11	-0.715	-2.02	0.000	D	0.000	D						PAQR7
10170	1980682	2q33.1	-0.643	-2.02	0.001	D	0.000	D						SATB2
22161	4220068	19q13.3	-0.557	-2.02	0.041	D								CD70
3110	580403	7p15.3	-0.364	-2.03	0.039	D					X			DFNA5
4015	730523	7q11.23	-0.779	-2.05	0.000	D	0.000	D						CLIP2
23858	4570358	17q21.2	-0.519	-2.05	0.004	D	0.001	D						CNTNAP1
3177	580767	17p13.3	-0.655	-2.05	0.001	D	0.000	D						FAM101B
29397	5720129	19p13.2	-0.571	-2.06	0.002	D	0.001	D			X	X		NFIX
21837	4200025	11q23.3	-0.399	-2.06	0.023	D								OAF
9014	1710242	1p13.3	-0.359	-2.07	0.044	D								C1orf59
37211	7100561	1p34.3	-0.731	-2.08	0.000	D	0.000	D						FAM176B
27608	5310437	20q11.23	-0.560	-2.08	0.002	D	0.001	D						MYL9
2373	450463	18q21.33	-0.623	-2.09	0.004	D	0.001	D						SERPINB7
15733	2970301	8q22.1	-0.812	-2.10	0.000	D	0.000	D						FAM92A1
36400	6960332	11q13.1	-0.421	-2.11	0.018	D	0.006	D						FOSL1
9437	1780075	4p15.31	-0.500	-2.12	0.006	D	0.002	D						NKX3-2
26603	5090079	17q25.3	-0.512	-2.13	0.009	D	0.002	D						C1QTNF1
39071	7570408	17q12	-0.526	-2.13	0.008	D	0.002	D						CCL5
23865	4570398	5q13.3	-0.635	-2.14	0.001	D	0.000	D						F2R
31830	6200025	1p13	-0.773	-2.14	0.001	D	0.000	D						C11orf41
34929	6620014	9p21.3	-0.355	-2.15	0.048	D								CDKN2A
13488	2570154	12p13.31	-0.526	-2.15	0.029	D								MFAP5
19193	3800168	12p13.31	-0.447	-2.15	0.013	D	0.004	D			X			SLC2A3

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. See last page for full legend. (7/8)

Gene ID	V4 Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1874 signif	SAM P value (FDR=5.1%)	1531 signif	NKX2-1 assoc	Byers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
30744	5960653	8q21.3	-0.902	-2.15	0.000	D	0.000	D						TMEM55A
16842	3190379	1p22.1	-0.609	-2.16	0.001	D	0.000	D			X	X		TGFBR3
962	130138	20q13.32	-0.615	-2.16	0.004	D	0.001	D						APCDD1L
22121	4210630	17q12	-0.498	-2.17	0.007	D	0.002	D						ARHGAP23
24329	4640446	Xq26.3	-0.669	-2.22	0.001	D	0.000	D			X			FHL1
33876	6480204	11q23.3	-0.569	-2.22	0.013	D	0.002	D						THY1
36941	7050010	9p22.3	-0.877	-2.23	0.000	D	0.000	D			X	X		BNC2
21233	4070133	11p15.3	-0.429	-2.24	0.018	D	0.006	D			X			DKK3
8996	1710142	1q23.3	-0.720	-2.24	0.005	D	0.001	D						RGS4
37459	7160253	6q21	-0.702	-2.25	0.001	D	0.000	D			X			LAMA4
23449	4490292	2q32.2	-0.380	-2.25	0.034	D					X			COL5A2
37767	7210170	6q22.1	-0.531	-2.26	0.003	D	0.001	D			X			DSE
30573	5910500	1q22	-0.497	-2.26	0.007	D	0.002	D						SYT11
17050	3290577	2q21.1	-0.816	-2.26	0.000	D	0.000	D						CCDC74A
31194	6060612	7q21.3	-0.453	-2.28	0.024	D	0.006	D						COL1A2
26822	5130563	5q35.3	-0.547	-2.28	0.004	D	0.001	D						GFPT2
22982	4290088	12q14.3	-0.523	-2.29	0.004	D	0.001	D			X	X		MSRB3
20198	3930382	10p13	-0.816	-2.32	0.000	D	0.000	D						NMT2
37463	7160292	16q22.1	-0.928	-2.32	0.000	D	0.000	D						ST3GAL2
26068	4900520	2q36.1	-0.482	-2.36	0.016	D	0.003	D						SCG2
12582	2370300	2q31.1	-0.487	-2.37	0.008	D	0.002	D						CYBRD1
25191	4830113	4q21.22	-0.459	-2.37	0.010	D	0.003	D			X	X		PLAC8
20862	4040671	7q21.3	-0.393	-2.37	0.037	D								COL1A2
28074	5390451	11p15.3	-0.439	-2.37	0.016	D	0.005	D			X			DKK3
22247	4220482	6q16.3	-0.586	-2.38	0.003	D	0.000	D			X			LIN28B
6172	1190047	12p11.21	-0.677	-2.39	0.001	D	0.000	D						DENND5B
29061	5670706	10p13	-0.516	-2.41	0.005	D	0.001	D						FAM171A1
20276	3940017	5q23.2	-0.439	-2.41	0.020	D	0.005	D						LOX
4987	940706	Xp22.2	-0.632	-2.41	0.001	D	0.000	D			X			AP1S2
28524	5550379	7q31.2	-0.574	-2.41	0.002	D	0.000	D						CAV1
29867	5860066	10p13	-1.078	-2.43	0.000	D	0.000	D						NMT2
15327	2850619	7q22.1	-0.643	-2.43	0.001	D	0.000	D						VGF
32894	6330730	8q11.21	-0.478	-2.44	0.013	D	0.003	D	N					SNAI2
5701	1070215	7q31.2	-0.562	-2.45	0.003	D	0.001	D						CAV1
13210	2490372	4q21.22	-0.480	-2.49	0.007	D	0.002	D			X	X		PLAC8
29409	5720180	17q21.31	-0.797	-2.49	0.000	D	0.000	D			X			FZD2
7725	1450193	22q13.1	-0.526	-2.50	0.004	D	0.001	D						LGALS1
6166	1190026	22q13.1	-0.652	-2.51	0.001	D	0.000	D						APOBEC3G
39102	7570598	21q22.3	-0.579	-2.52	0.003	D	0.001	D						COL6A1
11330	2140047	19q13.2	-0.739	-2.54	0.000	D	0.000	D			X	X		FBXO17
12782	2450465	2q31.1	-0.507	-2.56	0.006	D	0.002	D						CYBRD1
37111	7100064	19q13.2	-0.742	-2.56	0.000	D	0.000	D			X	X		FBXO17
36186	6940059	2q31.1	-0.557	-2.56	0.007	D	0.001	D						LOC375295
7160	1400427	20q13.13	-0.619	-2.61	0.001	D	0.000	D						KCNG1
32132	6220746	12q21.2	-0.537	-2.62	0.005	D	0.001	D						GLIPR1
22364	4230328	7q33	-0.669	-2.66	0.001	D	0.000	D			X			CALD1
28579	5550671	9p21.3	-0.429	-2.66	0.017	D	0.005	D						CDKN2A
25396	4850301	17q21.2	-0.807	-2.66	0.000	D	0.000	D						PTRF
22932	4280632	13q34	-0.579	-2.68	0.002	D	0.000	D						GAS6
29662	5810612	15q26.1	-0.474	-2.68	0.010	D	0.002	D						ANPEP
23954	4590092	2q31.2	-0.954	-2.71	0.000	D	0.000	D						OSBPL6
23171	4390301	17p11.2	-0.577	-2.72	0.004	D	0.001	D						TRPV2
21522	4150048	8q21.13	-0.588	-2.78	0.003	D	0.001	D			X			FABP5
782	70730	13q34	-0.581	-2.80	0.002	D	0.000	D						GAS6
29994	5860717	11q24.2	-0.834	-2.81	0.000	D	0.000	D						ROBO3
26351	5050382	5q33.1	-0.476	-2.81	0.011	D	0.002	D						SPARC
14788	2750356	21q22.3	-0.803	-2.84	0.000	D	0.000	D						COL6A2
5696	1070192	Xp22.2	-0.720	-2.85	0.000	D	0.000	D			X			AP1S2
5239	1010333	4p16.2	-0.639	-2.85	0.001	D	0.000	D						MSX1
3487	620750	7q33	-0.656	-2.88	0.001	D	0.000	D			X			CALD1
2865	520682	7q32.2	-0.594	-2.91	0.003	D	0.000	D						CPA4
14131	2650220	3q13.33	-0.624	-2.96	0.001	D	0.000	D			X			FSTL1
1890	360047	9q21.33	-0.772	-2.97	0.001	D	0.000	D						GAS1
19258	3800452	19q13.33	-1.160	-3.08	0.000	D	0.000	D						EMP3
4149	770408	7q22.1	-0.742	-3.08	0.000	D	0.000	D						SERPINE1
2784	520255	18p11.21	-0.813	-3.08	0.000	D	0.000	D			X			TUBB6
33215	6370731	7p12.3	-0.719	-3.09	0.002	D	0.000	D						SUN3
25645	4860743	1p36.12	-1.083	-3.10	0.000	D	0.000	D			X	X		FAM43B
26205	4920369	9q34.3	-0.551	-3.12	0.003	D	0.001	D						COL5A1
14245	2650730	8p21.2	-0.673	-3.12	0.001	D	0.000	D	N					STC1
38726	7550307	11p15.4	-0.522	-3.16	0.005	D	0.001	D						PRKCDBP
29685	5810743	12q23.3	-0.799	-3.25	0.000	D	0.000	D			X	X		C12orf75
2644	510368	13q32.3	-0.988	-3.28	0.000	D	0.000	D						ZIC2
12591	2370348	19p13.12	-1.283	-3.45	0.000	D	0.000	D						SYDE1
8347	1570092	18p11.21	-1.026	-3.51	0.000	D	0.000	D			X			TUBB6
17656	3390458	21q22.3	-0.876	-3.54	0.000	D	0.000	D						COL6A2
33353	6380669	5q31.2	-0.763	-3.75	0.000	D	0.000	D			X			SPOCK1
36943	7050019	10p13	-0.500	-3.82	0.005	D	0.001	D		x				VIM
20281	3940044	2q35	-0.955	-3.88	0.000	D	0.000	D						MARCH4
4507	830593	10p13	-0.510	-3.93	0.005	D	0.001	D		x				VIM
8504	1580025	7q21.3	-0.612	-4.12	0.001	D	0.000	D						GNG11
33966	6480703	19q13.2	-0.912	-4.14	0.000	D	0.000	D		x				AXL
36957	7050066	4q35.1	-0.895	-4.19	0.000	D	0.000	D						ODZ3
24321	4640403	19q13.2	-0.913	-4.34	0.000	D	0.000	D		x				AXL
16177	3130220	3p21.31	-1.112	-5.08	0.000	D	0.000	D	N					TMEM158

Table E1. Differentially expressed genes in FOXA1 hi vs. lo NSCLC cell lines. Genes which passed significance by either 2-sample t-test ($p<0.05$) or SAM analysis (FDR<5.1%) are shown. "S2N", signal to noise; "NKX2-1 assoc", genes previously identified as associated with NKX2-1 expression (255); "Byers EMT", genes previously identified as part of an EMT signature (273); "FOXA1 peak", genes with TSSs called within +/- 10kb of FOXA1-binding sites that were present in both H1819 and H1781; "NKX2-1/FOXA1 peak", genes with TSSs called within +/- 10kb of binding sites co-occupied with NKX2-1 and FOXA1. (8/8)

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 sig=if	SAM P value (FDR=5.2%)	S37 sig=if	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
5452	830056	14q21.1	2.483	5.05	0.000	U	0.000	U			X	X	x	FOXA1
33178	5130156	3q26.33	1.210	4.15	0.000	U	0.000	U			X	X		SOX2
24278	3840470	17q25.1	1.376	4.00	0.000	U	0.000	U			X	X		ST6GALNAC1
16099	2480228	8p22	0.580	3.66	0.004	U	0.000	U						FGL1
3006	450750	2p23.1	0.967	3.38	0.000	U	0.000	U			X			CAPN13
26080	4050674	15q23	0.750	3.37	0.001	U	0.000	U			X	X		LOC145837
23065	3520431	16q12.1	1.587	3.23	0.000	U	0.000	U	P		X			TOX3
32837	5080273	3q26.33	1.091	3.15	0.000	U	0.000	U			X	X		SOX2
41668	6420687	20q11.21	0.565	3.10	0.016	U	0.002	U						BPIFA1
44235	6840154	11q12.3	0.582	3.09	0.006	U	0.001	U						SCGB2A1
15654	2370678	12q24.31	0.930	3.09	0.000	U	0.000	U						
5568	830491	Xq26.2	0.856	3.05	0.000	U	0.000	U			X	X		HS6ST2
30661	4760095	19p13.11	0.845	3.04	0.000	U	0.000	U						CRLF1
26243	4060497	14q13.3	0.698	3.01	0.001	U	0.000	U	P					NKX2-1
6104	940242	14q13.3	0.632	2.94	0.002	U	0.000	U	P					NKX2-1
47581	7400377	19q13.2	0.642	2.89	0.002	U	0.000	U	P		X	X		CEACAM6
48268	7570050	Xq28	0.773	2.83	0.000	U	0.000	U						HMGB3
48381	7570484	21q22.3	0.639	2.79	0.002	U	0.000	U						TFF3
15170	2350243	1q21.1	0.617	2.78	0.003	U	0.000	U	P					FMO5
21550	3360750	5q14.1	0.885	2.77	0.000	U	0.000	U			X	X		GPR98
24967	3930064	8q11.23	0.755	2.75	0.000	U	0.000	U			X	X		FAM150A
15440	2360632	19q13.2	0.784	2.75	0.001	U	0.000	U						CEACAM5
38442	6040546	5q13.2	1.141	2.73	0.000	U	0.000	U						
6839	1050113	11p13	0.592	2.71	0.003	U	0.000	U						ELF5
25660	4010519	7q34	0.709	2.70	0.002	U	0.000	U						PIP
43831	6760072	14q13.3	0.619	2.69	0.002	U	0.000	U						SFTA3
40589	6330187	3q23	1.334	2.66	0.000	U	0.000	U						PLS1
3538	520609	1p13.3	0.791	2.66	0.000	U	0.000	U						KIAA1324
38864	6130022	8p22	0.565	2.63	0.006	U	0.001	U						FGL1
33152	5130053	4q13.3	0.972	2.60	0.000	U	0.000	U			X			SLC4A4
14111	2140541	9q34.3	0.617	2.60	0.002	U	0.000	U						LRRC26
6061	940075	6p21.31	0.594	2.57	0.003	U	0.000	U			X			SPDEF
3918	610010	6p21.33	0.765	2.54	0.000	U	0.000	U	P					SLC44A4
29999	4610520	15q22.2	0.546	2.54	0.006	U	0.001	U			X	X		GCNT3
12408	1940747	17q12	0.576	2.53	0.004	U	0.001	U						PPP1R1B
36179	5690647		0.790	2.50	0.000	U	0.000	U	P					SLC44A4
8148	1240746	20q13.12	0.672	2.47	0.001	U	0.000	U			X	X		WFDC3
12584	1980670	1q21.3	0.686	2.47	0.002	U	0.000	U			X			CGN
26453	4070575	2q21	1.166	2.47	0.000	U	0.000	U						EPCAM
5936	870376	9q31.3	0.624	2.47	0.002	U	0.000	U			X			C9orf152
25955	4050138	5q14.3	1.012	2.46	0.000	U	0.000	U			X	X		GPR98
12573	1980608	16p12.2	0.751	2.45	0.001	U	0.000	U						CRYM
44379	6840739	3q23	1.280	2.45	0.000	U	0.000	U						PLS1
1242	130324	21q22.3	0.690	2.45	0.001	U	0.000	U						TMPRSS2
18711	2810543	12q13.12	0.642	2.43	0.005	U	0.000	U						AQP5
7619	1190064	4q13.2	0.575	2.43	0.006	U	0.001	U						UGT2B7
28303	4280048	20q13.12	0.679	2.42	0.001	U	0.000	U			X	X		WFDC3
44063	6770270	11q12.3	0.803	2.40	0.000	U	0.000	U			X			ASRGL1
845	70209	17q21.31	0.834	2.39	0.000	U	0.000	U			X			ETV4
46200	7150270	9q34.3	0.566	2.35	0.006	U	0.001	U						LRRC26
47985	7550445	19q13.2	0.624	2.34	0.003	U	0.000	U			X			CXCL17
4584	650431	4q13.3	0.450	2.34	0.046	U								ALB
32780	5080044	3p22.1	0.814	2.33	0.000	U	0.000	U						ENTPD3
15780	2450411	10q21.3	0.586	2.32	0.003	U	0.001	U			X	X		DNAJC12
36487	5720465	10q21.3	0.648	2.27	0.001	U	0.000	U			X	X		DNAJC12
20501	3170594	8q24.12	0.769	2.27	0.001	U	0.000	U		x	X			MAL2
19127	2900681	3q21.2	0.685	2.27	0.001	U	0.000	U						ALG11
27988	4250364	4q34.1	0.450	2.25	0.021	U			P		X			HPGD
34157	5310328	3q26.2	0.572	2.21	0.006	U	0.001	U						
20754	3180731	12q12.3	0.664	2.20	0.001	U	0.000	U			X	X		MGST1
36403	5720112	17p22	1.377	2.20	0.000	U	0.000	U						TOM1L1
40394	6290161	10q21.2	0.589	2.19	0.003	U	0.001	U			X			SLC16A9
24941	3890735	2q31.1	0.477	2.19	0.015	U	0.003	U	P					HOXD1
40162	6270743	21q22.3	0.599	2.18	0.004	U	0.001	U						FAM3B
23242	3610338	11q23.1	0.889	2.18	0.000	U	0.000	U						C11orf52
41675	6420736	10q21.3	0.559	2.17	0.005	U	0.001	U			X	X		DNAJC12
3770	580132	8q22.1	0.922	2.17	0.000	U	0.000	U			X			LAPTM4B
24557	3850767	16p11.2	0.842	2.16	0.000	U	0.000	U						SBK1
9614	1450408	14q23.1	0.547	2.13	0.006	U	0.001	U			X	X		SIX1
6377	990577	17q21.31	0.788	2.13	0.001	U	0.000	U			X			ETV4
12085	1850201	19q13.12	0.735	2.11	0.001	U	0.000	U						SYNE4
21859	3390411	20q13.31	0.646	2.10	0.005	U	0.001	U			X	X		TFAP2C
5719	840324	13q32.1	0.411	2.10	0.038	U								CLDN10
17661	2680241	3q13.33	0.835	2.09	0.000	U	0.000	U						ILDR1
46240	7150437	11q12	1.066	2.09	0.000	U	0.000	U						MDK
17072	2630204	6q23.2	0.613	2.07	0.004	U	0.001	U						ENPP3
29507	4560717	11p11.2	0.982	2.07	0.000	U	0.000	U						MDK
357	20653	14q23.1	0.856	2.07	0.000	U	0.000	U			X			SIX4
37158	5860767	15q15.1	0.788	2.06	0.000	U	0.000	U			X	X		SPINT1
10183	1510300	1q32.1	0.768	2.06	0.002	U	0.000	U	P		X	X		ELF3
43513	6650348	8q22.1	0.878	2.06	0.000	U	0.000	U			X			LAPTM4B
534	50600	1q32.1	0.395	2.04	0.041	U								PIGR
2784	430541	11q24.3	0.628	2.04	0.002	U	0.000	U		x	X	X		TMEM45B
44979	6960735	19p13.11	0.633	2.04	0.002	U	0.000	U						TMEM59L
29410	4560288	12q13.2	0.734	2.03	0.001	U	0.000	U		x	X	X		ERBB3
43379	6620630	Xp21.1	0.875	2.03	0.000	U	0.000	U						XK
3973	610201	2q37.3	0.647	2.02	0.001	U	0.000	U						HES6
29281	4540440		0.915	2.01	0.000	U	0.000	U						
25611	4010356	Xq22.1	0.544	2.01	0.006	U	0.001	U						XKRX
8371	1300113	16q22.1	0.977	2.00	0.000	U	0.000	U		x	X	X		CDH1
7495	1170131	4q12	0.576	2.00	0.006	U	0.001	U			X	X		HOPX
34558	5360347	16q22.1	0.731	2.00	0.000	U	0.000	U						NQO1
15650	2370671	7q31.31	0.998	2.00	0.000	U	0.000	U						TSPAN12
23568	3780082	1p34.2	0.602	1.99	0.009	U	0.001	U		x				TMEM125
28055	4250626	19p13.3	0.722	1.99	0.001	U	0.000	U			X	X		PPAP2C
40593	6330201	20p11.23	0.809	1.99	0.002	U	0.000	U			X			OVOL2
29799	4590438	16p13.3	0.540	1.98	0.009	U	0.002	U						ZG16B
32866	5080373	17q11.2	0.920	1.97	0.000	U	0.000	U	P	x	X			CLDN7
38784	6100446	1p22.3	0.642	1.97	0.002	U	0.000	U						
26723	4150044	Xq13.1	0.905	1.97	0.000	U	0.000	U	P					DLG3
40854	6350470	5q32	0.699	1.97	0.001	U	0.000	U						STK32A
21164	3310022	16q12.2	0.555	1.96	0.007	U	0.001	U						IRX5
26895	4150672	18q12.1	0.693	1.96	0.003	U	0.000	U			X			DSG2
38605	6060458	5q31.2	0.405	1.96	0.035	U								GFRA3
34979	5420450	4q13.2	0.440	1.96	0.031	U								UGT2B7
8585	1340154	17p13.2	0.584	1.95	0.005	U	0.001	U						GGT6
15716	2450162	6p21.33	0.414	1.95	0.032	U								SFTA2
43554	6650477	13q32.1	0.451	1.93	0.031	U								CLDN10
32803	5080131	12p12.3	0.692	1.90	0.001	U	0.000	U			X	X		MGST1
17893	2690379	1q32.2	0.473	1.89	0.015	U	0.004	U			X	X		C4BPB
37868	5910521	2q31.31	0.759	1.89	0.000	U	0.000	U						PLCH1
47742	7510259	13q14.3	0.717	1.89	0.001	U	0.000	U			X			ATP7B
433	50195	1q22	0.775	1.89	0.001	U	0.000	U	P	x				RAB25
28576	4290307	10p25.3	0.572	1.87	0.004	U	0.001	U			X	X		PLEKHS1
12305	1940301	5q13.2	0.808	1.87	0.000	U	0.000	U						MARVELD2
19621	3060343	20q13.2	0.603	1.87	0.003	U	0.001	U						BCAS1
26412	4070358	2q31.1	0.917	1.87	0.000	U	0.000	U						KLHL23
32521	4920561	22q12.3	0.544	1.87	0.006	U	0.001	U			X		x	MB
46049	7100435	9q21.32	0.513	1.86	0.009	U	0.002	U			X			RASEF
38958	6110338	8q22.3	0.666	1.86	0.001	U	0.000	U		x	X	X		GRHL2

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 sig=if	SAM P value (FDR=5.2%)	S37 sig=if	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
25145	3940014	11q25	0.574	1.86	0.004	U	0.001	U						GLB1L2
30974	4780563	9q22.33	0.428	1.86	0.031	U								GABBR2
5979	870524	17q21.32	0.387	1.85	0.044	U								HOXB8
37646	5900376	13q21.2	0.440	1.85	0.026	U								PCDH20
15729	2450201	13q32.1	0.773	1.85	0.000	U	0.000	U			X	X		ABCC4
2028	270358	4q21.21	0.647	1.84	0.003	U	0.000	U			X	X	x	FRAS1
20268	3140463	7p21.1	0.566	1.84	0.004	U	0.001	U			X			AGR2
23114	3520632	17q12	0.521	1.84	0.010	U	0.002	U			X			HNF1B
4689	670100	16p12.2	0.532	1.84	0.008	U	0.002	U						SCNN1G
32993	5090132	11p13	0.599	1.83	0.003	U	0.001	U			X	X	x	EHF
5004	730592	7p21.3	0.490	1.83	0.017	U					X			SCIN
21640	3370327	1q41	0.703	1.83	0.001	U	0.000	U						MARC1
19107	2900600	2q11.2	0.942	1.83	0.000	U	0.000	U						C2orf15
9741	1470121	8p21.1	0.686	1.83	0.001	U	0.000	U						FZD3
42388	6520561	4q21.1	0.887	1.83	0.000	U	0.000	U			x			SHROOM3
8385	1300162	15q15.1	0.717	1.82	0.001	U	0.000	U			X			PPP1R14D
36440	5720288		0.458	1.82	0.018	U								
7219	1090048	1p13.1	0.385	1.82	0.044	U					X	X		VTCN1
4259	620577	10q25.2	0.580	1.82	0.004	U	0.001	U			X			ACSL5
20423	3170292	1p22.3	0.890	1.81	0.000	U	0.000	U			X	X		DDAH1
27010	4180364	9q21.33	0.850	1.81	0.000	U	0.000	U			X			GOLM1
47768	7510367	3q26.2	0.732	1.81	0.000	U	0.000	U						GPR160
28221	4260482	12q13.2	0.881	1.80	0.000	U	0.000	U			x	X	X	ERBB3
17001	2600707	4q22.3	0.763	1.80	0.002	U	0.000	U				X	X	BMPR1B
21395	3360148	21q22.11	0.444	1.80	0.022	U								CLDN8
33788	5270403	Xq26.3	0.725	1.80	0.001	U	0.000	U						
27519	4220041	5q23.3	0.690	1.79	0.001	U	0.000	U			X			SLC12A2
3031	460082	1q32.1	0.528	1.79	0.007	U	0.002	U						GOLT1A
10535	1580139	6q16.2	0.602	1.79	0.003	U	0.001	U						FAXC
33177	5130154	6q25.2	0.467	1.79	0.020	U								RGS17
5460	830082	19q13.33	0.505	1.78	0.010	U	0.002	U						FUT2
36569	5810047	5q13.3	0.672	1.77	0.004	U	0.000	U			X			F2RL1
28454	4280615	16q22.2	0.841	1.77	0.001	U	0.000	U						MARVELD3
13936	2120612		0.633	1.77	0.002	U	0.000	U						
29019	4490037	4p15.2	0.418	1.76	0.030	U				P	X	X		SLC34A2
17414	2650075	Xp11.21	0.505	1.76	0.037	U								PAGE5
24647	3870347	17p13.1	0.594	1.76	0.006	U	0.001	U						MFSD6L
40607	6330270	Xq26.2	0.553	1.75	0.006	U	0.001	U	P					GPC4
2923	450368	17q12	0.552	1.75	0.010	U	0.002	U			X			GRB7
10461	1570661	1p32.1	0.710	1.74	0.001	U	0.000	U			X			CYP2J2
27561	4220184	13q34	0.722	1.74	0.001	U	0.000	U						MCF2L-AS1
26332	4070070	11q24.2	0.464	1.74	0.017	U								VSIG2
39497	6200309	1p34.3	0.629	1.73	0.002	U	0.000	U						DNAJ11
19312	2940632	1q41	0.579	1.72	0.004	U	0.001	U						KCTD14
21804	3390187	1q22	0.727	1.72	0.001	U	0.000	U			X	X		EFNA1
39972	6250672	5q11.2	0.776	1.72	0.000	U	0.000	U						CCNO
28724	4390221	1p35.3	0.793	1.71	0.001	U	0.000	U	P					SMPDL3B
28160	4260278	11q24.3	0.732	1.71	0.001	U	0.000	U		x				ST14
8668	1340463	6p22.1	0.790	1.71	0.000	U	0.000	U						ZSCAN31
40766	6350138	14q13.3	0.681	1.71	0.003	U	0.000	U						PAX9
23744	3800017	8p22	0.899	1.70	0.000	U	0.000	U			X	X		MTUS1
26022	4050398	19q13.41	0.405	1.70	0.049	U								KLK12
5434	780767	20p13	0.571	1.70	0.010	U	0.002	U						LZTS3
20374	3170102	12q24.22	0.929	1.70	0.000	U	0.000	U			X			C12orf49
28951	4480463	8p22	0.471	1.69	0.022	U								FGL1
32805	5080136	1q41	0.597	1.69	0.006	U	0.001	U						ESRRG
44358	6840619	1p34.2	0.580	1.69	0.004	U	0.001	U						RIMKLA
336	20546	7q11.23	0.458	1.68	0.025	U								CLDN3
19656	3060471	6p21.1	0.778	1.68	0.000	U	0.000	U	P		X	X		ENPP4
15064	2340608	8q21.2	0.860	1.68	0.000	U	0.000	U			X	X		GNA14
38453	6040600	17q11.2	0.717	1.68	0.001	U	0.000	U						TMEM98
44574	6860689	17p13.1	0.439	1.67	0.023	U								DNAH2
33116	5090671	19p13.11	0.462	1.67	0.020	U					X	X		GDF15
20278	3140494	9p24.2	0.610	1.66	0.003	U	0.001	U			X			GLIS3
37614	5900243	17q12	0.456	1.66	0.019	U					X			GRB7
9435	1440474	3q21.2	0.544	1.65	0.008	U	0.002	U						ALG11
6512	1010326	20p11.1	0.833	1.64	0.001	U	0.000	U						LOC284801
46822	7210377	7q31.33	0.396	1.63	0.040	U					X			GPR37
46826	7210392	6p12.2	0.461	1.63	0.018	U								GSTA2
19884	3120608	12q13.2	0.646	1.62	0.001	U	0.000	U		x	X	X		ERBB3
2835	430768	6q22.1	0.753	1.62	0.000	U	0.000	U	P		X	X		PRSS16
3611	540131	12q24.33	0.803	1.62	0.000	U	0.000	U						PXMP2
17694	2680372	8p21.3	0.755	1.62	0.000	U	0.000	U			X	X		SH2D4A
42896	6580270	12q13.13	0.636	1.62	0.004	U	0.001	U						KRT18
24741	3870707	19q13.41	0.700	1.61	0.001	U	0.000	U			X			ZNF702P
13206	2060040	17p12	0.522	1.61	0.012	U	0.003	U			X			ADORA2B
25168	3940079	3q13.2	0.645	1.61	0.003	U	0.000	U			X			C3orf52
25960	4050156	17q12	0.590	1.61	0.003	U	0.001	U						ERBB2
35666	5570139	2p22.2	0.458	1.61	0.018	U								QPCT
22283	3420541	17q11.2	0.743	1.60	0.000	U	0.000	U						TMEM97
7047	1070152	3p21.1	0.515	1.60	0.010	U	0.002	U						IL17RB
6539	1010431	16p12.2	0.618	1.60	0.004	U	0.001	U						CRYM
38312	6040044	9q22.33	0.910	1.60	0.000	U	0.000	U						CORO2A
30357	4920402	19p13.3	0.708	1.59	0.001	U	0.000	U			x			CRB3
38801	6100494	Xq26.2	0.596	1.59	0.003	U	0.001	U			X	X		HS6ST2
26611	4120392	10q22.1	0.417	1.58	0.035	U								PLA2G12B
38246	6020543	17q11.2	1.064	1.58	0.000	U	0.000	U			X	X		CPD
12972	2000630	4q35.1	0.638	1.58	0.003	U	0.000	U			X			SORBS2
37832	5910382	14q11.2	0.515	1.58	0.009	U	0.002	U						ANG
46435	7160402	1q23.3	0.530	1.58	0.007	U	0.002	U						KLHDC9
46788	7210255	12q24.13	0.795	1.58	0.001	U	0.000	U			X	X		IQCD
7714	1190524	16q23.1	0.646	1.58	0.003	U	0.001	U						FA2H
42654	6560093	3q13.33	0.557	1.57	0.006	U	0.001	U			X	X		SLC15A2
43649	6660131	7p21.1	0.827	1.57	0.000	U	0.000	U	P		X	X		TSPAN13
44873	6940364	3q24	0.456	1.57	0.019	U					X			CP
46537	7200044	6q14.1	0.668	1.57	0.001	U	0.000	U			X			SH3BGRL2
4041	610437	Yq11.222	0.556	1.57	0.006	U	0.001	U						CD24
8882	1400543		0.511	1.57	0.013	U	0.003	U						
12907	2000390	9q21.11	0.428	1.57	0.028	U					X			FAM189A2
21966	3400097	3q29	0.486	1.57	0.014	U	0.004	U			X			MUC20
27783	4230332	4p15.33	0.658	1.56	0.001	U	0.000	U			X	X		HS3ST1
24798	3890164	7p14.2	0.591	1.56	0.003	U	0.001	U			X			KIAA0895
33945	5290246	1q25.3	0.803	1.56	0.000	U	0.000	U						XPR1
9717	1470053	6q23.3	0.636	1.56	0.002	U	0.000	U						KIAA1244
3023	460050	19p12	0.778	1.56	0.000	U	0.000	U						RPSAP58
48640	7650064	21q22.3	0.492	1.55	0.017	U					X	X		UMODL1
34766	5390386	13q13.3	0.542	1.55	0.006	U	0.001	U			X	X		FREM2
29314	4540630	12q14.1	0.578	1.55	0.004	U	0.001	U			X	X		LRIG3
40159	6270735	16p12.2	0.393	1.55	0.044	U								SCNN1G
4355	630243	17q21.32	0.574	1.55	0.005	U	0.001	U			X	X		PRR15L
19126	2900674	1p13.1	0.521	1.54	0.010	U	0.002	U			X			IGSF3
17243	2640142	17p13.3	0.687	1.54	0.001	U	0.000	U						C17orf97
13843	2120240	12p12.3	0.617	1.54	0.004	U	0.001	U	P		X	X		LMO3
14015	2140154	18q22.3	0.776	1.54	0.000	U	0.000	U						CYB5A
580	60014	8p24.21	0.763	1.52	0.000	U	0.000	U			X	X		FAM84B
4759	670372	20q13.2	0.519	1.52	0.009	U	0.002	U						BCAS1
24081	3830491	20q11.21	0.607	1.52	0.019	U	0.004	U						BPIFB2
45712	7040682	18q21.2	0.398	1.52	0.039	U					X			RAB27B
36671	5810414	18q22.3	0.713	1.52	0.001	U	0.000	U						CYB5A
742	60603	4q32.1	0.548	1.52	0.006	U	0.001	U						GLRB

Table E2. Differentially expressed genes in FOXA1 hi vs. lo primary LUADs. See last page for full legend. (1/5)

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	S37 signif	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
47816	7510544	12q13.12	0.472	1.51	0.015	U					X			DNAJC22
16049	2480037	3p22.3	0.796	1.51	0.000	U	0.000	U			X			CMTM8
11226	1710575	1p13.2	0.573	1.51	0.005	U	0.001	U						BCL2L15
40464	6290452	8p22	0.869	1.51	0.000	U	0.000	U						NAT1
5838	870014	10p14	0.577	1.51	0.005	U	0.001	U						PROSER2
1371	150041	12p13.2	0.573	1.50	0.004	U	0.001	U			X	X		MANSC1
28528	4290114	1p36.11	0.824	1.50	0.001	U	0.000	U		x				C1orf172
43218	6620014	9p21.3	0.387	1.50	0.047	U								CDKN2A
31947	4880554	14q11.2	0.624	1.50	0.005	U	0.001	U						SALL2
24660	3870382	13q22.3	0.835	1.50	0.000	U	0.000	U						SLAIN1
9082	1410609	9q22.33	0.762	1.50	0.002	U	0.000	U						COX20A
45062	6960367	6p12.3	0.454	1.49	0.019	U				x	X	X		GPR110
42630	6560017	9p24.2	0.566	1.49	0.004	U	0.001	U			X			GLIS3
47946	7550292	1q21.3	0.391	1.49	0.045	U				P				SELENBP1
12574	1980609	11p11.2	0.393	1.49	0.043	U								LRP4
16369	2490520	6p12.2	0.397	1.49	0.040	U								GSTA2
45671	7040487	12q13.31	0.469	1.48	0.026	U				P	x	X	X	SCNN1A
31542	4850504	3p22.1	0.468	1.48	0.016	U								ENTPD3
17092	2630292	3q27.2	0.595	1.48	0.003	U	0.001	U						LIPH
30673	4760154	8q22.1	0.704	1.47	0.001	U	0.000	U			X	X		CCNE2
12924	2000440	1q21.3	0.497	1.47	0.012	U	0.003	U						ENSA
9279	1430681	17q11.2	0.661	1.47	0.002	U	0.000	U						TLCD1
15424	2360563	4p14	0.625	1.46	0.002	U	0.001	U						NSUN7
48722	7650431	18q12.2	0.571	1.46	0.006	U	0.001	U						SLC39A6
1357	130754	7q11.32	0.429	1.45	0.026	U					X	X		PTPRZ1
46892	7210674	16q24.3	0.499	1.45	0.011	U	0.003	U						DBNDD1
23954	3830044	13q34	0.708	1.45	0.001	U	0.000	U						GRTP1
37266	5870431	4p14	0.656	1.45	0.001	U	0.000	U						NSUN7
47453	7380647	4q21.1	0.520	1.45	0.010	U	0.002	U						CDK12
3922	610020	4p14	0.514	1.45	0.033	U								CHRNA9
47966	7550368		0.485	1.44	0.016	U				P				FLJ22184
27831	4230500	1p21.3	0.740	1.44	0.000	U	0.000	U						SLC44A3
38340	6040156	6p24.2	0.801	1.44	0.000	U	0.000	U						C6orf52
36086	5690270	12p13.1	0.515	1.44	0.012	U	0.003	U						GPRC5A
14974	2340241	18p11.21	0.549	1.44	0.007	U	0.002	U						IMPA2
39229	6180047	4q21.1	0.859	1.44	0.000	U	0.000	U						STBD1
23199	3610167	12q24.23	0.756	1.44	0.001	U	0.000	U						VSIG10
43702	6660347	6p22.2	0.649	1.44	0.001	U	0.000	U						ZNF322
38942	6110279	10p15.1	0.475	1.43	0.019	U								NET1
34333	5340228	2q24.1	0.603	1.43	0.003	U	0.001	U		x	X	X		GALNT5
19028	2900291	20q13.12	0.810	1.43	0.000	U	0.000	U						ACOT8
45785	7050192	1q21.3	0.886	1.43	0.000	U	0.000	U						GOLPH3L
17511	2650441		0.716	1.43	0.005	U	0.001	U						
44382	6840747	4q35.1	0.873	1.42	0.000	U	0.000	U						SLC25A4
44121	6770463	17q21.31	0.727	1.42	0.000	U	0.000	U						CCDC103
38360	6040240	18q21.31	0.778	1.42	0.000	U	0.000	U			X			ATP9B1
33040	5090347	Yq11.222	0.395	1.42	0.039	U								CD24
24589	3870100	1q23.3	0.519	1.42	0.009	U	0.002	U						KLHDC9
35965	5670594	15q25.2	0.477	1.42	0.024	U								NMB
13188	2030735	15q15.1	0.594	1.42	0.003	U	0.001	U	P					PAK6
35785	5570653	11q13.1	0.579	1.42	0.004	U	0.001	U						TM7SF2
13953	2120687	20q13.12	0.831	1.42	0.000	U	0.000	U	P					WFDC2
48690	7650286	11q22.3	0.594	1.41	0.003	U	0.001	U			X	X		EXPH5
43477	6650202	6p12.3	0.440	1.41	0.023	U				x	X	X		GPR110
30104	4640161	17p13.3	0.654	1.41	0.001	U	0.000	U						C17orf97
216	20044		0.496	1.41	0.014	U								
42809	6560674	6p22.3	0.658	1.41	0.002	U	0.000	U						DCDC2
38125	6020070	1q41	0.436	1.41	0.024	U								SUSD4
30128	4640242	3q22.3	0.854	1.40	0.000	U	0.000	U						CEP70
9142	1430129	Xq13.1	0.467	1.40	0.016	U								KIF4A
22942	3460739	2q37.3	0.464	1.40	0.029	U				P				RAB17
41704	6450075	20q13.31	0.472	1.40	0.021	U					X	X		TFAP2C
10721	1660079	16p12.2	0.376	1.40	0.049	U				P		X		SCNN1B
27042	4180452	1q24.2	0.946	1.40	0.000	U	0.000	U						ATP1B1
39022	6110592	1q21.23	0.726	1.39	0.001	U	0.000	U			X	X		ABHD11
12481	1980246	15q21.2	0.527	1.39	0.009	U	0.002	U	P		X	X		MYO5C
17549	2650605	4q32.1	0.452	1.39	0.022	U					X			FAM198B
43017	6580754	19p13.3	0.658	1.39	0.003	U	0.001	U			X	X		PPAP2C
23320	3610615	6q22.31	0.513	1.39	0.009	U	0.003	U			X			PKIB
39704	6220397	11q23.3	0.703	1.39	0.001	U	0.000	U			X	X		SCD
2936	450414	12q14.1	0.552	1.38	0.008	U	0.002	U			X			PPM1H
47953	7550324	Xp22.2	0.695	1.38	0.001	U	0.000	U			X	X		SHROOM2
24456	3850370	9q34.3	0.550	1.38	0.005	U	0.002	U						AGPAT2
2466	360706	11p34	0.576	1.38	0.006	U	0.001	U						GRTP1
14535	2260010	1q22	0.583	1.37	0.004	U	0.001	U						RIT1
6076	940148	11p13	0.546	1.37	0.006	U	0.002	U			X			ABTB2
24208	3840192	2q31.1	0.398	1.37	0.039	U								GAD1
24527	3850661	3p21.31	0.862	1.37	0.000	U	0.000	U						TCAIM
19632	3060392		0.639	1.37	0.002	U	0.001	U						
44787	6940037	2q37.1	0.389	1.37	0.050	U								HTR2B
674	60349	6p21.31	0.764	1.37	0.001	U	0.000	U		x				MAPK13
44788	6940039	11q24.1	0.511	1.36	0.010	U	0.003	U	P		X	X		SORL1
13972	2140038	1q22	0.532	1.36	0.007	U	0.002	U						SLC50A1
46743	7210093	11q13.4	0.607	1.36	0.003	U	0.001	U			X	X		PGM2L1
32797	5080112	1q41	0.653	1.36	0.002	U	0.000	U			X			MARK1
26633	4120465	4q25	0.713	1.36	0.001	U	0.000	U						GAR1
22233	3420356	2p23.3	0.428	1.36	0.026	U					X			EFR3B
47456	7380670	9q23.3	0.555	1.36	0.005	U	0.001	U			X			MYB
14538	2260020	9p24.2	0.554	1.36	0.010	U	0.002	U						SLC1A1
16106	2480274	11q24.1	0.516	1.35	0.009	U	0.003	U	P		X	X		SORL1
20311	3140646	6p12.3	0.646	1.35	0.003	U	0.001	U			X	X		CD2AP
12936	2000471	6p12.1	0.533	1.35	0.008	U	0.002	U			X			BMP5
33920	5290148	16q11.2	0.568	1.35	0.006	U	0.001	U			X			GPT2
43001	6580689	Xp22.33	0.647	1.35	0.002	U	0.000	U						ARSD
3684	540465	6p21.1	0.576	1.35	0.004	U	0.001	U		x				ENPP5
13459	2070246	1p36.32	0.495	1.35	0.012	U	0.004	U						MMEL1
43012	6580735	16p12.3	0.453	1.34	0.022	U								ACSM3
13823	2120161	9q34.3	0.491	1.34	0.012	U	0.004	U						C9orf116
32417	4920156	2p13.3	0.926	1.34	0.000	U	0.000	U						GFPT1
34115	5310142	12q13.2	0.410	1.34	0.035	U								METTL7B
46187	7150209	20p13	0.421	1.34	0.031	U								SLC4A11
18226	2750170	4q35.1	0.547	1.33	0.010	U	0.003	U			X			SORBS2
43439	6650079	3p14.2	0.515	1.33	0.009	U	0.003	U						C3orf14
38996	6110470	2q37.3	0.448	1.33	0.037	U								DTYMK
39877	6250300	7p22.1	0.527	1.33	0.011	U	0.003	U						RAC1
6654	1030133	14q24.3	0.617	1.33	0.004	U	0.001	U						ZC2HC1C
1417	150184	20q13.33	0.560	1.33	0.006	U	0.002	U						CDH26
14222	2190228	2q36.1	0.825	1.32	0.000	U	0.000	U						SGPP2
36978	5860050		0.593	1.32	0.003	U	0.001	U						TMEM238
47619	7400524	19p13.3	0.528	1.32	0.008	U	0.002	U		x				CRB3
26350	4070132	4q12	0.551	1.31	0.008	U	0.002	U						PPAT
33593	5260408	17p13.3	0.635	1.31	0.002	U	0.001	U	P					RPH3AL
30292	4670138	15q21.2	0.574	1.31	0.004	U	0.001	U						SLC27A2
6200	940639	12p12.3	0.392	1.31	0.042	U					X			ERP27
5573	830523	6p24.1	0.588	1.30	0.006	U	0.001	U			X	X		GPR126
27634	4220468	1q24.2	0.876	1.30	0.000	U	0.000	U						ATP1B1
43709	6660369	6p24.3	0.468	1.30	0.016	U					X	X		GCNT2
15998	2470528	9q34.3	0.579	1.30	0.004	U	0.001	U						C9orf116
46483	7160603	16p13.11	0.847	1.30	0.000	U	0.000	U	P		X			ABCC6
5882	870161	21q21.1	0.473	1.29	0.023	U					X	X		CXADR

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	S37 signif	NKX2-1 assoc	Beyers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
17932	2690541	18q12.2	0.651	1.29	0.003	U	0.001	U			X	X		TPGS2
9591	1450348	19q13.42	0.413	1.29	0.035	U				x	X			TMC4
33004	5090181	2p22.3	0.549	1.29	0.006	U	0.002	U						DPY30
29048	4490164	12q13.13	0.446	1.29	0.022	U								GALNT6
47100	7320717	12q21.33	0.665	1.29	0.001	U	0.000	U						POC1B
122	10427	6p12.3	0.512	1.29	0.024	U								TFAP2D
44764	6900711			1.29	0.000	U								
16818	2600019	22q12.3	0.528	1.29	0.008	U	0.002	U			X		x	MB
12242	1940068	7q11.23	0.634	1.28	0.005	U	0.001	U			X	X		ABHD11
34578	5360411	14q13.3	0.624	1.28	0.002	U	0.001	U	P					MBIP
27478	4210634	1q25.2	0.672	1.28	0.001	U	0.000	U						QSOX1
24514	3850600		0.565	1.28	0.009	U	0.002	U						
41594	6420349	15q22.31	0.811	1.28	0.001	U	0.000	U			X			PTPLAD1
12073	1850156	8p23.1	0.602	1.28	0.004	U	0.001	U						CLDN23
7941	1230719	1q23.2	0.700	1.28	0.001	U	0.000	U						PIGM
9112	1430014	8q21.11	0.632	1.27	0.005	U	0.001	U			X	X		HNF4G
1488	150458	11p11.2	0.737	1.27	0.000	U	0.000	U						MDK
21165	3310025	4p11	0.469	1.27	0.020	U								OCIAD2
47911	7550139	8q21.11	0.997	1.27	0.000	U	0.000	U						STAU2
16711	2570347	11q13.5	0.521	1.27	0.013	U	0.004	U			X			B3GNT6
24883	3890484	14q11.2	0.535	1.27	0.007	U	0.002	U						ANG
39927	6250468	12q21.33	0.420	1.26	0.029	U			P		X	X		DUSP6
2707	430209	5q12.3	0.701	1.26	0.001	U	0.000	U						NLN
14291	2190524	9q32	0.630	1.26	0.003	U	0.001	U						RNF183
24473	3850438	11p11.2	0.610	1.26	0.004	U	0.001	U						C11orf49
39720	6220451	4q35.1	0.902	1.26	0.000	U	0.000	U						SLC25A4
30216	4640630	2q24.2	0.555	1.25	0.007	U	0.002	U	P		X	X		CD302
38930	6110215	12q24.11	0.544	1.25	0.006	U	0.002	U			X	X		C12orf76
32677	5050431	13q13.3	0.415	1.25	0.032	U								DCLK1
3065	460193	6p21.1	0.541	1.25	0.008	U	0.002	U						MAD2L1BP
41887	6480041	14q13.3	0.624	1.25	0.003	U	0.001	U	P					MBIP
36845	5820324	12q24.33	0.691	1.25	0.001	U	0.000	U						PXMP2
27857	4230609	Xp22.33	0.597	1.25	0.003	U	0.001	U						ARSD
10353	1570224	15q25.1	0.436	1.25	0.028	U								CHRNA5
24423	3850246	4q12	0.468	1.24	0.016	U					X	X		HOPX
17520	2650477	17q11.2	0.641	1.24	0.002	U	0.001	U						TRAF4
14122	2140601	16p12.3	0.381	1.24	0.046	U			P		X	X		TMC5
12874	2000270	16q22.2	0.585	1.24	0.009	U	0.002	U						MARVELD3
8101	1240541	11q13.2	0.558	1.24	0.010	U	0.003	U						RBM4
15249	2350554	5p15.2	0.768	1.23	0.000	U	0.000	U			X			DNAH5
14906	2320730	4q25	0.639	1.23	0.002	U	0.001	U						CASP6
27330	4210072	11q14.1	0.514	1.23	0.009	U	0.003	U						AQP11
25484	3990661	14q13.2	0.563	1.23	0.006	U	0.002	U						FAM177A1
12382	1940632	7q36.3	0.410	1.23	0.034	U								NCAPG2
28468	4280674	2q32.1	0.390	1.23	0.048	U								TFPI
6622	1030026	17p11.2	0.581	1.22	0.004	U	0.001	U						CENPV
13966	2120743	6p12.2	0.537	1.22	0.016	U								GSTA2
23606	3780221	16q12.2	0.584	1.22	0.004	U	0.001	U			X	X		CRNDE
9238	1430497	6q14.1	0.573	1.22	0.005	U	0.002	U	P		X	X		MYO6
25503	3990739	6p21.2	0.381	1.22	0.048	U			P		X			KCNK5
41802	6450440	9q31.3	0.622	1.22	0.004	U	0.001	U						PTGR1
41606	6420392	4p11	0.692	1.22	0.001	U	0.000	U						OCIAD2
8142	1240730	19q13.2	0.575	1.21	0.007	U	0.002	U		x	X	X		SPINT2
22530	3440703	17q24.2	0.654	1.21	0.001	U	0.000	U			X	X		C17orf58
7626	1190091	9p24.3	0.483	1.21	0.017	U					X	X		DMRT2
27567	4220209	11q13.3	0.424	1.21	0.031	U					X			SHANK2
22577	3450114	9q34.3	0.392	1.21	0.045	U								FAM69B
127	10440	2q33.1	0.622	1.21	0.002	U	0.001	U						MARS2
18863	2850390	11p11.2	0.541	1.21	0.008	U	0.002	U						MDK
15928	2470255	Xq22.1	0.536	1.21	0.007	U	0.002	U						TSPAN6
36282	5700343	7q21.3	0.446	1.20	0.041	U					X			BAIAP2L1
38919	6110181	13q32.1	0.376	1.20	0.050	U					X	X		ABCC4
29370	4560092	1p22.1	0.514	1.20	0.018	U					X			FNBP1L
12022	1820743	8q21.13	0.629	1.20	0.002	U	0.001	U			X			ZNF704
28421	4230484	6q16.2	0.518	1.20	0.009	U	0.003	U						FAXC
12759	1990577	1p22.1	0.477	1.20	0.020	U								GCLM
33536	5260176	6p12.2	0.396	1.20	0.040	U								GSTA1
7523	1170326	14q21.3	0.503	1.20	0.012	U	0.004	U						POLE2
23456	3710397	1q22	0.565	1.19	0.010	U	0.003	U			X	X		EFNA1
18783	2850056	10p13	0.618	1.19	0.003	U	0.001	U			X			PITH
36463	5720392	14q23.3	0.570	1.19	0.004	U	0.001	U						RAB15
47609	7400475	14q11.2	0.491	1.19	0.012	U								RPGRIP1
35609	5560706	10q21.3	0.403	1.19	0.036	U								STOX1
21229	3310291	6q16.1	0.615	1.19	0.011	U	0.002	U						POU3F2
45617	7040286	10q25.2	0.418	1.19	0.033	U					X			ACSL5
4790	670475	4p14	0.554	1.19	0.005	U	0.002	U			X			C4orf19
27768	4230259	Xq28	0.682	1.19	0.001	U	0.000	U						BRCC3
268	20259	1p21.3	0.643	1.18	0.003	U	0.001	U						LOC100507670
19914	3120730	2q31.1	0.400	1.18	0.045	U								LRP2
17377	2640725	4q26	0.513	1.18	0.009	U	0.003	U			X	X		ARSJ
18210	2750129	6q25.1	0.521	1.18	0.008	U	0.003	U						C6orf211
9915	1500041	17p13.2	0.424	1.18	0.037	U								EMC6
40262	6370379	2p11.2	0.397	1.18	0.041	U								LONRF2
10603	1580400	7q34	0.743	1.18	0.000	U	0.000	U						TTC26
33317	5220035	1q21.3	0.703	1.18	0.001	U	0.000	U						TUFT1
19686	3060605	19q13.33	0.567	1.18	0.007	U	0.002	U						PRRG2
24284	3840491	14q22.3	0.540	1.17	0.006	U	0.002	U			X			PELI2
20564	3180048	2q34	0.505	1.17	0.010	U	0.004	U						IDH1
29837	4590619	8p21.2	0.423	1.17	0.029	U					X	X		PNMA2
8141	1240725	17q12	0.441	1.17	0.029	U					X			SLFN5
40196	6280093	1p34.1	0.396	1.17	0.042	U					X			ZSWIM5
6458	1010114	3p14.3	0.405	1.17	0.039	U								ACOX2
21269	3310440	16p12.3	0.696	1.17	0.002	U	0.000	U						COQ7
8559	1340039	2q32.1	0.393	1.17	0.041	U								TFPI
9520	1450072	2p21	0.535	1.16	0.013	U	0.004	U						PIGF
5019	730671	11p15	0.677	1.16	0.001	U	0.000	U			X			ACAD8
37176	5870100	2q24.1	0.698	1.16	0.001	U	0.000	U			X			PKP4
45381	7000161	15q15.1	0.400	1.16	0.045	U								OIP5
45843	7050433	8q21.11	0.469	1.16	0.016	U								RDH10
6547	1010470	9q34.3	0.396	1.16	0.043	U								SAPCD2
12431	1980082	1q22	0.661	1.16	0.001	U	0.000	U						SCAMP3
23144	3520754	2q33.1	0.496	1.16	0.012	U								SGOL2
38992	6110451	4q35.1	0.508	1.16	0.010	U	0.003	U						SNX25
38277	6020674	4q32.3	0.733	1.16	0.000	U	0.000	U						TMEM192
7315	1090577	17q21.31	0.543	1.16	0.018	U								VPS25
45752	7050068	8q24.13	0.422	1.16	0.034	U					X			SQLE
3631	540204	2p24.2	0.519	1.15	0.010	U	0.003	U	P		X			KCNS3
45345	7000026	3q13.2	0.485	1.15	0.013	U					X			SIDT1
45631	7040333	14q11.2	0.486	1.15	0.014	U								ANG
35190	5490593	3q29	0.535	1.15	0.007	U	0.002	U						BDH1
45745	7050047	19q13.41	0.496	1.15	0.031	U								KLK12
9073	1410564	10p12.1	0.436	1.15	0.025	U				x	X	X		MPP7
25861	4040563	7q11.21	0.583	1.15	0.004	U	0.001	U						CCT6P3
8794	1400192		0.430	1.15	0.026	U								
32403	4920102	1q32.1	0.401	1.14	0.040	U					X	X		MFSD4
32287	4900397	4q21.21	0.604	1.14	0.007	U	0.002	U			X			BMP3
3581	540017	1p34.2	0.760	1.14	0.001	U	0.000	U						C1orf210
1362	150019	13q22.3	0.458	1.14	0.020	U								SLAIN1
11689	1780133	13q32.3	0.489	1.14	0.014	U								TMTC4
5616	830687	7p14.3	0.521	1.14	0.008	U	0.003	U			X	X		CHN2

Table E2. Differentially expressed genes in FOXA1 hi vs. lo primary LUADs. See last page for full legend. (2/5)

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	537 signif	NKX2-1 assoc	Bayers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
25485	3990670	12q21.32	0.438	1.14	0.024	U					X	X		KITLG
34935	5420289	1p34.3	0.754	1.14	0.001	U	0.000	U			X	X		OSCP1
36893	5820491	6q23.3	0.580	1.14	0.006	U	0.002	U			X			MAP7
24319	3840632	16p12.3	0.492	1.14	0.012	U								ACSM3
275	20286	2p21	0.536	1.14	0.007	U	0.002	U						EPCAM
5495	830215	22q13.2	0.706	1.14	0.002	U	0.001	U						MCAT
41432	6400411	14q12	0.783	1.14	0.000	U	0.000	U						TM9SF1
4151	620102	2q13	0.412	1.14	0.035	U				P				MALL
25475	3990619	17q21.2	0.412	1.14	0.033	U								TOP2A
9768	1470209	1q24.1	0.812	1.13	0.000	U	0.000	U						TMCO1
7715	1190528	12p13.2	0.456	1.13	0.026	U					X	X		MANSC1
23767	3800095	8q24.12	0.537	1.13	0.006	U	0.002	U			X			DEPTOR
40251	6280309	14q13.3	0.610	1.13	0.007	U	0.002	U			X			MIPOL1
6332	990382	1q31.3	0.427	1.13	0.027	U								C1orf53
7881	1230477	16q12.2	0.398	1.13	0.038	U								IRX5
26338	4070091	1q21.3	0.436	1.13	0.025	U								RORC
37277	5870474	5q15	0.702	1.12	0.001	U	0.000	U			X	X		RHOBTB3
45571	7040114	5q13.2	0.598	1.12	0.003	U	0.001	U			X			MCC2
35232	5550014	1q21.3	0.492	1.12	0.012	U					X			TARS2
4166	620161	1q22	0.490	1.12	0.013	U								EFNA4
35500	5560255	17q23.1	0.737	1.12	0.001	U	0.000	U						PTRH2
6471	1010154	17q25.1	0.635	1.12	0.007	U	0.002	U						SMIM5
24712	3870592		0.576	1.12	0.005	U	0.002	U						
24640	3870309	5q12.3	0.396	1.12	0.039	U					X	X		RGS7BP
28415	4280468	17q25.1	0.436	1.12	0.032	U					X			LLGL2
14963	2340180	1q23.2	0.505	1.12	0.014	U					X			TAGLN2
32929	5080647	17q12	0.491	1.12	0.013	U								PIGW
23867	3800465	15q26.1	0.677	1.11	0.001	U	0.000	U			X	X	x	FAM174B
30416	4670671	1q21.2	0.569	1.11	0.004	U	0.002	U			X			ACP6
29818	4590541	20q13.33	0.463	1.11	0.018	U								CDH26
6281	990164	14q32.2	0.504	1.11	0.021	U								DEGS2
38724	6100239	5q11.2	0.523	1.11	0.027	U								SETD9
23711	3780619	6p12.2	0.582	1.11	0.006	U	0.002	U						TMEM14A
25794	4040296	1p34.3	0.605	1.11	0.003	U	0.001	U						MYCBP
15214	2350438	6p24.3	0.599	1.11	0.003	U	0.001	U						SNRNP48
26493	4070736	1q23.2	0.504	1.11	0.017	U					X			TAGLN2
19739	3120053	1p32.1	0.573	1.11	0.005	U	0.002	U						HOOK1
40550	6330047	11p14.1	0.382	1.11	0.048	U								HSP90AA2
44057	6770242	1p35.1	0.520	1.11	0.010	U	0.003	U						MARCKSL1
43253	6620133	10q23.31	0.461	1.11	0.019	U								PANK1
25534	4010075	1q25.3	0.601	1.11	0.003	U	0.001	U						XPR1
32025	4890102	2q33.3	0.490	1.10	0.013	U					X	X		FZD5
26812	4150360	14q22.2	0.512	1.10	0.009	U	0.003	U			X			WDHD1
7552	1170477	17q25.1	0.504	1.10	0.011	U								GPRC5C
5314	780296	14q12	0.660	1.10	0.005	U	0.001	U						TM9SF1
34623	5360612		0.492	1.10	0.012	U								
26751	4150131	11p11.2	0.413	1.10	0.036	U								MAPK8IP1
22369	3440095	19q13.2	0.427	1.10	0.027	U								PSG3
28840	4390754	16p13.3	0.397	1.10	0.045	U				P				PPL
44384	6840753	14q24.3	0.673	1.10	0.001	U	0.000	U			X			SPTLC2
42452	6550048	11q13.4	0.532	1.10	0.007	U	0.003	U						DHCR7
15253	2350575	17q21.32	0.388	1.10	0.044	U								HOXB3
46716	7200762	20q11.23	0.556	1.10	0.007	U	0.002	U						NDRG3
16708	2570332	9q31.3	0.484	1.10	0.016	U								PTGR1
42583	6550554	1p34.3	0.576	1.09	0.004	U	0.001	U			X	X		OSCP1
4558	650324	11p15.1	0.465	1.09	0.018	U								ZDHHC13
41833	6450592	13q13.3	0.450	1.09	0.020	U					X	X		NBEA
24054	3830400	1p34.3	0.564	1.09	0.005	U	0.002	U			X	X		OSCP1
47447	7380626	4p14	0.485	1.09	0.015	U					X	X		RBM47
42196	6510576	Xp22.2	0.563	1.09	0.005	U	0.002	U						CTPS2
43207	6590731	6p22.3	0.662	1.09	0.002	U	0.001	U						DTNBP1
20341	3140768	17p13.2	0.577	1.09	0.004	U	0.001	U						EMC6
48333	7570315	17q12	0.434	1.09	0.031	U								MRPL45
2641	380725	1q22	0.618	1.09	0.003	U	0.001	U						MTX1
27273	4200612	6p21.2	0.593	1.09	0.007	U	0.002	U						PPIL1
24462	3850392	4q32.3	0.694	1.09	0.001	U	0.000	U						TMEM192
6864	1050201	1p44	0.596	1.09	0.003	U	0.001	U						ZNF670
10363	1570273	18q21.31	0.438	1.08	0.024	U					X	X		NEDD4L
11203	1710468	15q15.1	0.572	1.08	0.004	U	0.002	U			X	X		SPINT1
30598	4730605	20q13.2	0.430	1.08	0.026	U			N					AURKA
38688	6100079	22q13.2	0.393	1.08	0.043	U								CENPM
29290	4540484	12q22	0.456	1.08	0.019	U								FGD6
30665	4760113	16p12.3	0.530	1.08	0.009	U	0.003	U						KNOP1
42413	6520681	17q25.3	0.700	1.08	0.001	U	0.000	U						PYCR1
39480	6200241	1q23.3	0.593	1.08	0.003	U	0.001	U						SDHC
32054	4890224	Xp11.23	0.577	1.08	0.004	U	0.001	U						SLC35A2
29458	4560484	11q13.2	0.535	1.08	0.008	U	0.003	U						DPP3
41273	6380563	22q12.2	0.596	1.08	0.006	U	0.002	U						UQCR10
11928	1820343	3p14.3	0.441	1.07	0.026	U					X	X		WNT5A
46238	7150427	Xq22.1	0.520	1.07	0.020	U								ARMCX3
31161	4810543	3p24.1	0.605	1.07	0.001	U	0.001	U						CMC1
18990	2900142	1q21.3	0.479	1.07	0.015	U								TDRKH
24580	3870072	2q32.1	0.450	1.07	0.021	U					X	X		GULP1
15041	2340524	1p21.3	0.547	1.07	0.010	U	0.003	U						ALG14
15302	2360020	11q12.2	0.508	1.07	0.010	U	0.004	U						FADS1
48741	7650484	1q22	0.757	1.07	0.000	U	0.000	U						CCT3
22595	3450176	17q24.2	0.600	1.06	0.003	U	0.001	U			X	X		C17orf58
36735	5810689	11p13	0.413	1.06	0.032	U					X	X		PRRG4
32497	4920458	1q21.3	0.530	1.06	0.008	U	0.003	U						CRE BL4
39957	6250594	3p21.31	0.526	1.06	0.011	U	0.004	U						IP6K2
40792	6350239	11p15.2	0.550	1.06	0.007	U	0.002	U						RRAS2
31662	4860195	Xp11.23	0.805	1.06	0.000	U	0.000	U						SLC35A2
37089	5860445	7q21.12	0.462	1.06	0.021	U								SRI
3717	540647	1p21.3	0.553	1.06	0.007	U	0.002	U						TMEM56
22907	3460605	21q22.3	0.620	1.06	0.003	U	0.001	U			X	X		C2CD2
4876	730072	11p15.1	0.479	1.06	0.020	U					X	X		PLEKHA7
21210	3310181	6p21.2	0.563	1.06	0.007	U	0.002	U						C6orf89
6309	990280	9q33.3	0.559	1.06	0.005	U	0.002	U						RALGPS1
6602	1010730	1p32.3	0.444	1.06	0.022	U								SCP2
3545	520647	19q13.43	0.417	1.06	0.031	U								ZIK1
41984	6480440	6p22.3	0.659	1.05	0.001	U	0.001	U			X			MRS2
16576	2510593	11q12.3	0.456	1.05	0.020	U					X			PLA2G16
5757	840446	17q21.3	0.905	1.05	0.000	U	0.000	U						CYB561
38167	6020224	9q22.32	0.456	1.05	0.025	U				P				FBP1
32077	4890324	1p22.2	0.970	1.05	0.000	U	0.000	U						LRRC8B
4851	670754	14q23.1	0.462	1.05	0.021	U			P	x				TMEM30B
25201	3940193	1q22	0.602	1.05	0.003	U	0.001	U			X	X		PMF1
9818	1470414	21q22.3	0.564	1.05	0.023	U					X	X		UMOD L1
22089	3400577	20q11.22	0.470	1.05	0.016	U					X			EIF2S2
32272	4900338	7q36.3	0.418	1.05	0.030	U								C7orf13
11964	1820471	6p21.33	0.561	1.05	0.005	U	0.002	U						FKBPL
36936	5820671	19q13.3	0.417	1.05	0.046	U								FUT6
4796	670494	8p21.3	0.552	1.05	0.005	U	0.002	U						LOC389641
9305	1440014	18q21.1	0.452	1.05	0.020	U								MYO5B
40672	6330504	1q32.2	0.439	1.05	0.025	U								SERTAD4
18862	2850382	13q32.3	0.613	1.05	0.003	U	0.001	U						TMTC4
5802	840634	1p34.2	0.448	1.05	0.021	U								ZMYND12
31272	4830195	15q21.3	0.497	1.05	0.017	U								
27228	4200437	1q21.3	0.387	1.05	0.043	U								ENSA
29835	4590612	7q36.3	0.449	1.05	0.039	U								LMBR1

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	537 signif	NKX2-1 assoc	Bayers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
40140	6270670	2q34	0.647	1.04	0.001	U	0.001	U						IDH1
6561	1010528	3q29	0.438	1.04	0.026	U					X	X		HES1
3522	520544	5p13.2	0.435	1.04	0.024	U								AMACR
46728	7210041	2q14.2	0.628	1.04	0.004	U	0.001	U						C1QL2
11182	1710397	11q24.2	0.687	1.04	0.002	U	0.001	U						HYLS1
30886	4780201	17q25.3	0.513	1.04	0.009	U	0.004	U						LRRC45
9899	1470746	9q31.3	0.566	1.04	0.006	U	0.002	U						PTPN3
28748	4390326	16p23.3	0.456	1.04	0.022	U								SDR42E1
39447	6200114	15q21.1	0.506	1.04	0.030	U								SLC28A2
42051	6480747	14q12	0.686	1.04	0.001	U	0.000	U						TM9SF1
44966	6940753	3q22.1	0.384	1.04	0.047	U								TMEM108
7874	1230450	11q23.2	0.503	1.04	0.013	U								TTC12
45547	7040039	6p22.2	0.392	1.04	0.049	U								ZNF322
15724	2450187	3p22.3	0.486	1.04	0.019	U					X	X		GPD1L
6264	990100	1q44	0.463	1.04	0.023	U					X			TFB2M
45696	7040609	14q21.1	0.404	1.04	0.037	U								GEMIN2
38639	6060661	16p13.3	0.436	1.03	0.025	U					X			CLDN9
38264	6020619	16q13	0.412	1.03	0.033	U					X			PLLP
6748	1030484	4q12	0.540	1.03	0.010	U	0.003	U			X			SPINK2
20149	3140039	14q13.2	0.466	1.03	0.024	U								BRM S1L
13585	2070730	14q11.2	0.446	1.03	0.039	U								NGDN
721	60520	1q23.3	0.471	1.03	0.028	U								PCP4L1
39415	6200017	11p15.5	0.618	1.03	0.003	U	0.001	U						POLR2L
3346	510605	9q32	0.655	1.03	0.002	U	0.001	U						WDR31
25346	3990017	7q31.2	0.477	1.03	0.018	U								
32770	5080017	20p13	0.529	1.03	0.009	U	0.003	U			X			GNRH2
36375	5700753	19q13.2	0.442	1.03	0.024	U					X			CEACAM1
46355	7160102	7q31.32	0.484	1.03	0.014	U				P				CADPS2
10541	1580161	16q12.1	0.437	1.03	0.033	U								NETO2
24920	3890647	12p12.3	0.438	1.02	0.024	U					X	X		MGST1
36054	5690132	16p13.3	0.465	1.02	0.017	U								FAM195A
6735	1030440	17q25.1	0.616	1.02	0.003	U	0.001	U						METTL23
30076	4640070	10q23.33	0.480	1.02	0.014	U								PIP5L
42016	6480593	11q23.1	0.416	1.02	0.032	U					X			ARHGAP20
39101	6130156	8p11.23	0.472	1.02	0.015	U				P	X	X		RAB11FIP1
15886	2470093	9q21.11	0.555	1.02	0.008	U	0.003	U			X	X		TJP2
33566	5260309	9q21.11	0.610	1.02	0.002	U	0.001	U			X	X		TJP2
3609	540113	9q22.32	0.557	1.02	0.009	U	0.003	U			X			CDC14B
1156	110754	8q22.1	0.433	1.02	0.027	U					X			ESRP1
33755	5270296	1q44	0.590	1.02	0.004	U	0.001	U			X			TFB2M
42766	6560497	19q13.33	0.638	1.02	0.002	U	0.001	U						BCAT2
34105	5310110	1q21.3	0.530	1.02	0.007	U	0.003	U						HAX1
1330	130647	7q21.2	0.586	1.02	0.005	U	0.002	U						PEX1
23331	3610671	4q21.22	0.393	1.02	0.041	U								SCD5
22780	3460121	1q42.3	0.499	1.02	0.014	U								TOMM20
34638	5360678	11q13.4	0.402	1.01	0.036	U								DHCR7
38559	6060278	11q23.3	0.471	1.01	0.032	U								HMBS
34441	5340692	9q33.3	0.655	1.01	0.002	U	0.001	U						STRBP
10375	1570309	1q32.3	0.434	1.01	0.027	U					X	X		NEK2
13580	2070707	17q25.3	0.412	1.01	0.035	U					X			AFMID
29895	4610102	11q22.2	0.525	1.01	0.013	U					X			TMEM123
282	20324	14q11.2	0.476	1.01	0.017	U								ANG
38392	6040356	19p13.2	0.413	1.01	0.032	U								CAMSAP3
617	60138	1p31.1	0.615	1.01	0.002	U	0.001	U						CTH
12513	1980370	7q22.1	0.663	1.01	0.001	U	0.001	U						FAM185A
32250	4900240	17q12	0.571	1.01	0.005	U	0.002	U						FBXL20
5835	840768	17q11.2	0.810	1.01	0.000	U	0.000	U						SDF2
33592	5260403	2p11.2	0.417	1.01	0.030	U				P				ST3GAL5
34753	5390333	17q11.2	0.671	1.01	0.002	U	0.001	U						TMEM98
27747	4230167	6q14.1	0.412	1.01	0.036	U								
42256	6520075	16p12.3	0.892	1.01	0.000	U	0.000	U						GDE1
29142	4490615	15q24.3	0.660	1.00	0.001		0.001	U	P		X	X		TSPAN3
38313	6040048	15q22.31	0.589	1.00	0.004		0.001	U			X			PTPLAD1
35601	5560670	16p13.3	0.516	1.00	0.009		0.004	U						ALG1
40519	6290709	4q25	0.722	1.00	0.001		0.000	U						HADH
46412	7160328	10q22.1	0.526	1.00	0.008		0.003	U						LRRC20
7777	1230068	20q13.33	0.585	1.00	0.004		0.002	U						PPP1R3D
6087	940180	1q32.1	0.529	1.00	0.010		0.004	U						RBBP5
39853	6250192	2q37.3	-0.630	-1.01	0.002	D						X		COL6A3
667	60328	16q22.1	-0.578	-1.01	0.005	D						X		IL34
27670	4220632	3q23	-0.505	-1.01	0.010	D								ATP1B3
29014	4490020	Xp22.33	-0.519	-1.01	0.012	D								MXRA5
35559	5560474	17q21.31	-0.551	-1.01	0.005	D								RAMP2
8838	1400373	8q24.22	-0.557	-1.01	0.007	D								SLA
9325	1440088	16p11.2	-0.408	-1.01	0.036	D								ASPHD1
14859	2320546	9q34.11	-0.565	-1.01	0.008	D								DNM1
34822	5390600	22q13.31	-0.454	-1.01	0.031	D								LOC100506737
11207	1710484	1q32.1	-0.692	-1.01	0.001	D								FMOD
11285	1740050		-0.402	-1.01	0.038	D								GVINP1
6699	1030296	14q32.2	-0.434	-1.02	0.025	D								BCL11B
42184	6510524	22q13.1	-0.486	-1.02	0.019	D								CYTH4
30652	4760056	6q14.1	-0.433	-1.02	0.026	D								ELOVL4
2800	430605	11q13.2	-0.446	-1.02	0.026	D								RBM14
3998	610301	3q13.2	-0.510	-1.02	0.013	D						X	X	PHLDB2
46441	7160435	10q26.3	-0.636	-1.02	0.003	D								EBF3
30339	4670343	14q32.33	-0.464	-1.02	0.017	D				P				JAG2
27663	4220603	11p11.2	-0.497	-1.02	0.016	D								SPI1
46823	7210382	19q13.12	-0.617	-1.02	0.004	D								USF2
2967	450553	11q12.3	-0.667	-1.02	0.001	D						X		AHNAK
17245	2640161	21q22.3	-0.430	-1.03	0.026	D						X	X	PRMT2
6615	1030008	14q24.3	-0.638	-1.03	0.002	D						X	X	TGFB3
48705	7650358	5q31.1	-0.511	-1.03	0.009	D						X		TGFBI
29348	4560020	10q11.21	-0.419	-1.03	0.030	D								CXCL12
40524	6290725	6q21	-0.445	-1.03	0.022	D								FYN
4868	730047	14q32.13	-0.396	-1.03	0.039	D								SERPINA1
20150	3140041	2q37.1	-0.405	-1.03	0.040	D								SP140
16595	2510672	18q21.2	-0.583	-1.03	0.004	D								TCF4
37017	5860192	5p13.2	-0.449	-1.03	0.025	D								
9500	1450008	15q25.1	-0.464	-1.03	0.018	D								IL16
5815	840682	19q13.3	-0.526	-1.03	0.008	D						X	X	DAPK3
25819	4040397	22q13.1	-0.510	-1.03	0.010	D						X		PDGFB
33382	5220309	12q24.31	-0.795	-1.03	0.000	D	0.000	D				X		RILPL1
42495	6550204	6q22.33	-0.495	-1.03	0.012	D						X		RSPO3
18512	2760537	16q13	-0.431	-1.03	0.027	D								MT1JP
33701	5270097		-0.405	-1.03	0.038	D								
7588	1170673	19p13.3	-0.568	-1.04	0.008	D								TNFSF14
13697	2100431	19q13.33	-0.608	-1.04	0.004	D						X		RCN3
47696	7510079	16q13	-0.489	-1.04	0.017	D								CETP
8008	1240192	19p13.3	-0.504	-1.04	0.010	D								CSNK1G2
39346	6180497	15q11.2	-0.392	-1.04	0.040	D								GOLGA8DP
14566	2260113	19q13.12	-0.442	-1.04	0.036	D								HCST
39266	6180168	22q12.3	-0.458	-1.04	0.023	D								NCF4
21311	3310615	10q24.32	-0.465	-1.04	0.020	D								NFKB2
9338	1440129		-0.394	-1.04	0.041	D								
15595	2370438	12p13.31	-0.442	-1.04	0.022	D				P				A2M
37934	5960068	5q32	-0.576	-1.04	0.004	D								PDGFRB
5295	780189	7q36.1	-0.602	-1.05	0.004	D								ZNF786
5921	870324	19q13.2	-0.445	-1.05	0.021	D						X	X	ARHGEF1
15295	2350747	5q32	-0.450	-1.05	0.020	D						X		ABLIM3
43994	6770017	13q22.1	-0.536	-1.05	0.009	D						X		KLF12

Table E2. Differentially expressed genes in FOXA1 hi vs. lo primary LUADs. See last page for full legend. (3/5)

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	S37 signif	NKX2-1 seroc	Bayers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
3461	520292	16q24.3	-0.448	-1.05	0.021	D					X			MC1R
46584	7200240	Xq28	-0.523	-1.05	0.009	D								ARHGAP4
46865	7210551	8q12.3	-0.507	-1.05	0.010	D								BHLHE22
12956	2000564	6q22.31	-0.471	-1.05	0.016	D								CEP85L
45054	6960332	11q13.1	-0.381	-1.05	0.046	D								FOSL1
6801	1030743	6p21.33	-0.426	-1.05	0.027	D								LTA
27932	4250136	14q12	-0.443	-1.05	0.025	D								LTB4R
30273	4670082	1q23.3	-0.418	-1.05	0.036	D								RGS5
45862	7050484	7q34	-0.780	-1.05	0.000	D	0.000	D						ZYX
2135	290022		-0.462	-1.05	0.026	D								
23511	3710601	19p13.3	-0.436	-1.05	0.027	D								DENND1C
9828	1470450		-0.389	-1.05	0.046	D								
14582	2260168		-0.670	-1.05	0.001	D								
47073	7320594	7q34	-0.731	-1.06	0.001	D	0.000	D						ZYX
40763	6350131	16q22.1	-0.480	-1.06	0.015	D								CTRL
46114	7100731	17q25.1	-0.542	-1.06	0.008	D								CYGB
21697	3370544	17q24.3	-0.493	-1.06	0.014	D								KCNJ16
41	10136	15q24.1	-0.466	-1.06	0.018	D								PML
1064	110349	19q13.32	-0.554	-1.06	0.006	D								SYMPK
5193	770575	11p15.5	-0.385	-1.06	0.048	D								TSPAN32
311	20441	3p22.2	-0.490	-1.06	0.014	D								
1076	110397		-0.387	-1.06	0.047	D								
35511	5560300	19p13.2	-0.581	-1.06	0.007	D								COL5A3
4104	610678	19q13.2	-0.489	-1.06	0.013	D					X			ERF
24340	3840719	12q24.31	-0.848	-1.06	0.000	D	0.000	D			X			SNRNP35
25885	4040671	7q21.3	-0.424	-1.06	0.028	D								COL1A2
25040	3930367	5p13.1	-0.718	-1.06	0.001	D	0.000	D						DAB2
33266	5130563	5q35.3	-0.417	-1.06	0.031	D								GFPT2
28606	4290440	19p13.11	-0.469	-1.06	0.016	D								SIN3B
37264	5870424	19q12	-0.519	-1.06	0.008	D								TSHZ3
10901	1690053	17q25.1	-0.411	-1.06	0.038	D								TTYH2
48730	7650451	1p36.11	-0.389	-1.06	0.046	D								ZNF683
44671	6900300		-0.446	-1.06	0.021	D								
3331	510520	10q11.22	-0.631	-1.07	0.003	D								ARHGAP22
25517	4010025	1p35.1	-0.558	-1.07	0.005	D								LCK
46073	7100544		-0.578	-1.07	0.004	D								
47429	7380546	19q13.12	-0.583	-1.07	0.004	D					X			FXYD5
16318	2490328	11q24.2	-0.667	-1.07	0.001	D					X			SLC37A2
37683	5900543	17q22	-0.588	-1.07	0.006	D								SEPT4
33915	5290132	21q22.3	-0.493	-1.07	0.012	D								COL18A1
5642	840025	6q21	-0.524	-1.07	0.008	D								FYN
156	10561	12q23.3	-0.436	-1.07	0.024	D								GLT8D2
37194	5870164	8q24.22	-0.408	-1.07	0.038	D								SLA
8790	1400176		-0.583	-1.07	0.004	D								
1264	130390	11p15.4	-0.450	-1.08	0.021	D								OLFML1
48406	7570608	2q31.1	-0.610	-1.08	0.012	D			N		X			ITGA6
43979	6760719	2p23.3	-0.555	-1.08	0.007	D								EMILIN1
3845	580431	1q24.2	-0.525	-1.08	0.008	D								PRRX1
16785	2570661	6p21.1	-0.615	-1.08	0.002	D								TRERF1
28418	4280474	Xp11.21	-0.415	-1.08	0.031	D								TRO
20866	3190411	13q13.1	-0.752	-1.09	0.000	D	0.000	D			X	X		STARD13
23458	3710400	11q12.3	-0.483	-1.09	0.014	D					X			AHNAK
43291	6620292	10q22.1	-0.716	-1.09	0.001	D	0.000	D			X			C10orf54
14654	2260471	4p16.1	-0.501	-1.09	0.015	D								ABLIM2
10386	1570348	12p13.32	-0.676	-1.09	0.001	D	0.000	D						CCND2
7150	1070541	17p13.1	-0.593	-1.09	0.004	D								MYH3
5061	770056	1q42.13	-0.651	-1.09	0.002	D								TRIM17
4956	730379		-0.658	-1.09	0.001	D								
20820	3190239	10q26.11	-0.617	-1.09	0.002	D								GRK5
20800	3190148	10q22.1	-0.433	-1.10	0.026	D					X			DDIT4
36843	5820309	11p15.4	-0.642	-1.10	0.003	D			P		X			STS
2760	430431	19p13.3	-0.513	-1.10	0.014	D					X			TRIP10
19056	2900390	1p21.2	-0.472	-1.10	0.015	D					X			VCAM1
15372	2360356	19p13.3	-0.540	-1.10	0.008	D								FSTL3
28458	4280632	13q34	-0.594	-1.10	0.004	D								GAS6
5718	840309	7q32.1	-0.589	-1.10	0.005	D								LEP
38026	5960411	Xq13.1	-0.564	-1.10	0.007	D								
16024	2470689	17q25.1	-0.464	-1.10	0.017	D					X			SPHK1
27208	4200367	3p21.31	-0.466	-1.10	0.017	D								FAM212A
41876	6480014	15q22.31	-0.563	-1.11	0.009	D								IGDCC4
8891	1400592	11q13.5	-0.554	-1.11	0.005	D								LRRC32
19340	2940746	11q23.2	-0.712	-1.11	0.001	D	0.000	D						NNMT
40293	6280504		-0.497	-1.11	0.013	D								
30307	4670192	15q26.1	-0.639	-1.11	0.002	D								KIF7
2648	360719	11p13	-0.569	-1.11	0.004	D								CD44
32336	4900612	3p21.1	-0.405	-1.11	0.035	D								DNAH1
19986	3130196	19q13.11	-0.603	-1.11	0.003	D								KCTD15
21880	3390487	9p13.3	-0.390	-1.11	0.045	D								RECK
5599	830615	3q29	-0.467	-1.11	0.027	D								ZDHHC19
40433	6290356	17p13.3	-0.478	-1.11	0.016	D					X			SERPINF1
966	70730	13q34	-0.602	-1.11	0.003	D								GAS6
1020	110180	12q13.3	-0.456	-1.12	0.024	D								ARHGAP9
32813	5080167	9q34.3	-0.607	-1.12	0.003	D								NOTCH1
10507	1580048		-0.386	-1.12	0.046	D					X	X		CAST
44666	6900286	Xq28	-0.522	-1.12	0.010	D					X			GAB3
24627	3870253	10q11.21	-0.509	-1.12	0.010	D								CXCL12
26607	4120379	1p22.1	-0.390	-1.12	0.043	D								GFI1
6888	1050309	1q41	-0.737	-1.12	0.000	D	0.000	D						HLX
32072	4890292	20q13.2	-0.524	-1.12	0.008	D								TSHZ2
1498	150491		-0.449	-1.12	0.022	D								
6005	870632	2p13.3	-0.481	-1.12	0.017	D								
14350	2230010	6q22.31	-0.596	-1.12	0.003	D								CEP85L
22721	3450692	9q22.33	-0.607	-1.12	0.010	D								FOXE1
41855	6450685	3q21.3	-0.549	-1.13	0.006	D					X	X		PLXNA1
29326	4540682	19p13.3	-0.491	-1.13	0.012	D								PALM
8418	1300286	3q21.1	-0.524	-1.13	0.008	D					X	X		MYLK
28551	4290201	1q32.1	-0.452	-1.13	0.043	D					X			IL24
10319	1570092	18q11.21	-0.613	-1.13	0.003	D					X			TUBB6
28277	4260725	17q23.3	-0.389	-1.13	0.046	D								CD79B
6543	1010446	22q12.3	-0.465	-1.13	0.021	D					X	X		C1QTNF6
22887	3460520	12p13.32	-0.772	-1.13	0.000	D	0.000	D						CCND2
17876	2690324	10q25.1	-0.931	-1.13	0.000	D	0.000	D						ITPRIP
16055	2480050	8p23.1	-0.479	-1.13	0.017	D								SOX7
36353	5700670	2q31.1	-0.510	-1.14	0.009	D					X			WIPF1
23170	3610072	22q13.2	-0.430	-1.14	0.028	D								A4GALT
35126	5490341	12p13.31	-0.622	-1.14	0.003	D								CLEC2D
29150	4490673	7p21.1	-0.475	-1.14	0.016	D								TWIST1
295	20370		-0.581	-1.14	0.008	D								
12835	2000110	19q13.42	-0.652	-1.14	0.001	D								BRSK1
42203	6510608	12q23.3	-0.378	-1.14	0.048	D								BTBD11
45808	7050300	2p21	-0.470	-1.14	0.016	D								ZFP36L2
8627	1340326	22q13.2	-0.426	-1.15	0.028	D								MEI1
26467	4070619	1p32.3	-0.674	-1.15	0.001	D								PCSK9
13403	2070053	5q34	-0.462	-1.15	0.033	D								SLIT3
13165	2030612	11p13	-0.536	-1.15	0.012	D					X			LDLRAD3
45621	7040296	15q23	-0.593	-1.15	0.004	D								CELF6
22635	3450338	6p21.32	-0.490	-1.15	0.012	D								HLA-DOB
21532	3360678	11q13.1	-0.580	-1.15	0.005	D								NRXN2
8413	1300270	5q31.3	-0.648	-1.15	0.003	D								PCDHB19P
5646	840040	19q13.42	-0.554	-1.15	0.005	D								SSC5D

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	S37 signif	NKX2-1 seroc	Bayers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
7829	1230278	16q22.1	-0.436	-1.16	0.025	D								PDXDC2P
31050	4810110	Xp11.23	-0.616	-1.16	0.003	D				X				RBM3
35460	5560110	17p13.1	-0.518	-1.16	0.009	D								DLG4
1511	150551	12q13.12	-0.603	-1.16	0.003	D								FMNL3
23181	3610102	20q11.21	-0.539	-1.16	0.006	D								FOXS1
29454	4560471	9q21.13	-0.591	-1.16	0.007	D								GDA
40623	6330338	12q13.13	-0.503	-1.16	0.011	D								ITGA5
47	10161	19p13.3	-0.713	-1.16	0.001	D	0.000	D						MOB3A
12098	1850259	19p13.3	-0.524	-1.16	0.008	D								NFIC
12260	1940129	20p13	-0.780	-1.16	0.000	D	0.000	D						SIRPA
7950	1230746	9q21.33	-0.613	-1.16	0.002	D								ZCCHC6
35451	5560075	15q26.1	-0.523	-1.17	0.008	D					X	X		MFGE8
12786	1990717	1p36.11	-0.696	-1.17	0.001	D	0.000	D						C1orf63
3456	520273	19p13.12	-0.433	-1.17	0.030	D								RASAL3
43230	6620050	12p13.31	-0.646	-1.17	0.001	D								IFFO1
33741	5270241	5q35.1	-0.723	-1.18	0.000	D	0.000	D						STK10
8075	1240450	12p13.31	-0.410	-1.18	0.041	D					X			CD27
3453	520255	18p11.21	-0.407	-1.19	0.048	D					X			TUBB6
27774	4230292	6q13	-0.499	-1.19	0.023	D								CD109
43708	6660368	19p13.2	-0.398	-1.19	0.041	D								MAP4K1
47950	7550307	11p15.4	-0.626	-1.19	0.002	D								PRKCDBP
15669	2370747	11q23.3	-0.413	-1.19	0.045	D								TRIM29
36584	5810095	18q21.33	-0.543	-1.19	0.015	D								SERPINB2
27418	4210403	5p13.2	-0.465	-1.19	0.022	D					X	X		SLC1A3
30026	4610615	10q11.21	-0.403	-1.19	0.036	D								CXCL12
40599	6330224	14q12	-0.455	-1.20	0.020	D								ADCY4
41848	6450661	9q13	-0.396	-1.20	0.041	D								ANKRD20A1
23445	3710343	3p21.1	-0.436	-1.20	0.035	D								ITIH4
47554	7400279	13q13.3	-0.401	-1.20	0.044	D								CCNA1
35795	5570682	11q24.1	-0.551	-1.20	0.006	D								CLMP
29062	4490221	7q22.1	-0.401	-1.20	0.037	D								RELN
24062	3830433		-0.514	-1.20	0.010	D								
2928	450379	6q21	-0.567	-1.21	0.005	D					X	X		PRDM1
3486	520382	2q33.1	-0.526	-1.21	0.008	D								CLK1
20097	3130609	2q37.1	-0.564	-1.21	0.008	D								INPP5D
20702	3180528	20q13.12	-0.561	-1.21	0.006	D					X	X		MMP9
11524	1770224	12q12	-0.618	-1.22	0.003	D					X	X		PRICKLE1
36839	5820292	17q21.32	-0.705	-1.22	0.001	D	0.000	D						CDK12
41825	6450541	12q24.23	-0.924	-1.22	0.000	D	0.000	D						PXN
19670	3060524	5q13.2	-0.548	-1.22	0.006	D								SMAA4
31001	4780678	2q11.2	-0.393	-1.22	0.049	D								ZAP70
7492	1170112	16q22.1	-0.568	-1.22	0.005	D								LCAT
32619	5050193	16q22.1	-0.489	-1.22	0.016	D								RLTPR
23173	3610082	1q32.1	-0.533	-1.22	0.007	D								PTPN7
41474	6400603	7q22.1	-0.400	-1.22	0.037	D								PVRIG
41255	6380484	14q32.13	-0.456	-1.22	0.019	D								SERPINA1
17315	2640463		-0.568	-1.22	0.004	D								
31153	4810497	19q13.12	-0.389	-1.23	0.045	D								DMKN
40344	6280750	7q34	-0.510	-1.23	0.015	D								IL23A
47087	7320669	11p13	-0.385	-1.23	0.044	D								PAMR1
7127	1070450	9q33.2	-0.534	-1.23	0.009	D								PTGS1
31436	4850092	16p12.3	-0.600	-1.23	0.011	D								ACSM5
45734	7050010	9p22.3	-0.542	-1.23	0.006	D					X	X		BNC2
9797	1470332	19q13.12	-0.695	-1.23	0.001	D	0.000	D			X			FXYD5
17321	2640482	10q22.2	-0.506	-1.23	0.011	D								BMS1P4
38568	6060324	20q13	-0.426	-1.23	0.039	D								PRND
5973	870500	3p25.3	-0.453	-1.23	0.020	D								TTLL3
38314	6040053	3p21.1	-0.630	-1.24	0.002	D								STAB1
8453	1300411	10q22.1	-0.687	-1.24	0.001	D	0.000	D						UNC5B
29193	4540070	1p12.3	-0.647	-1.24	0.004	D								MROH7
47187	7330292	3p25.1	-0.617	-1.24	0.002	D					X			FBLN2
21449	3360373	12p12.1	-0.450	-1.24	0.021	D					X			SSPN
22349	3440025	6q26	-0.692	-1.24	0.001	D	0.000	D						AGPAT4
21063	3290402	11q12.1	-0.589	-1.24	0.003	D								APLNR
47109	7320747	15q24.1	-0.580	-1.24	0.004	D								PSTPIP1
30156	4640367	22q12.2	-0.509	-1.24	0.020	D								SFI1
17648	2680189	12q13.31	-0.417	-1.25	0.034	D								LAG3
3910	580739	22q13.31	-0.448	-1.25	0.025	D					X			FBLN1
843	70196	1p34.3	-0.589	-1.25	0.003	D								COL8A2
11941	1820386	22q13.31	-0.998	-1.25	0.000	D	0.000	D	N					PARVB
46178	7150181	15q15.3	-0.458	-1.25	0.023	D								STRC
23665	3780441	3q13.2	-0.521	-1.26	0.015	D					X	X		PHLDB2
40085	6270437	11p13	-0.526	-1.26	0.011	D					X			FJX1
2762	430438	22q12.1	-0.408	-1.26	0.034	D								MIAT
29698	4570768	9q33.2	-0.702	-1.26	0.001	D	0.000	D						TRAF1
43631	6660050	15q14	-0.391	-1.26	0.043	D								GOLGA8B
46886	7210647	5p15.33	-0.477	-1.26	0.015	D								NKD2
1075	110390	1p36.21	-0.585	-1.26	0.004	D								SLC25A34
3367	510703	2p24.1	-0.690	-1.27	0.001	D	0.000	D			X	X		KLHL29
29600	4570358	17q21.2	-0.630	-1.27	0.002	D								CNTNAP1
15579	2370373	8p21.3	-0.516	-1.27	0.013	D								EGR3
3842	580403	7p15.3	-0.457	-1.27	0.023	D					X			DFNA5
12233	1940041	22q12.3	-0.481	-1.27	0.018	D								NCF4
25950	4050128	20q13.12	-0.563	-1.27	0.005	D								SULF2
45287	6980546	22q13.1	-0.425	-1.28	0.028	D								CACNA1I
2401	360379	6q25.2	-0.499	-1.28	0.016	D								VIP
33819	5270519	18q21.31	-0.496	-1.28	0.012	D					X			AUPK2
6941	1050500	8p24.3	-0.505	-1.28	0.012	D					X			PLEC
4990	730523	7q11.23	-0.659	-1.28	0.002	D								CLIP2
41629	6420500	22q13.1	-0.559	-1.29	0.006	D					X	X		MGAT3
25998	4050300	12q13.11	-0.449	-1.29	0.022	D					X	X		RAPGEF3
3775	580148	7q11.23	-0.709	-1.29	0.001	D	0.000	D						CLIP2
6420	990743	19q13.12	-0.410	-1.29	0.036	D								DMKN
41942	6480246	20q13.33	-0.531	-1.29	0.015	D								STMN3
12721	1990427	1p36.21	-0.496	-1.30	0.014	D					X	X		KAZN
44762	6900707	8p23.1	-0.467	-1.30	0.042	D								DEFB103A
12118	1850349	Xq12	-0.507	-1.30	0.010	D								HEPH
16557	2510520	1q25.2	-0.772	-1.30	0.001	D	0.000	D						ABL2
21185	3310097	17p25.3	-0.540	-1.31	0.006	D								TSPAN10
17113	2630373	7p12.2	-0.402	-1.31	0.043	D								
10698	1580762	18q21.33	-0.494	-1.31	0.036	D								SERPINB13
34708	5390148	13q12.11	-0.717	-1.31	0.001	D	0.000	D			X	X		MPHOSPH8
18701	2810482	11q12.3	-0.489	-1.31	0.013	D					X			AHNAK
20453	3170431		-0.462	-1.31	0.022	D								SAP25
47885	7550048	9q34.11	-0.434	-1.32	0.024	D								CERCAM
35970	5670605	19p13.3	-0.617	-1.32	0.005	D								MATK
40686	6330575	20p13	-0.534	-1.32	0.008	D								HSPA12B
26101	4050717	8p23.3	-0.469	-1.32	0.017	D								MYOM2
8175	1260066	19q12	-0.651	-1.32	0.001	D	0.000	D						
33233	5130435	6q21	-0.515	-1.33	0.009	D					X			LAMA4
40081	6270411	9q21.33	-0.440	-1.33	0.029	D								GAS1
47292	7380047	17q21.1	-0.712	-1.33	0.001	D	0.000	D						THRA
14988	2340324		-0.435	-1.34	0.027	D					X	X		TGFBR2
8428	1300327	12p13.31	-0.587	-1.34	0.003	D								C1S
24482	3850468	19p13.43	-0.466	-1.34	0.017	D								PEG3
1394	150100	1q21.3	-0.414	-1.34	0.031	D								S100A3
15494	2370070	16p11.2	-0.667	-1.34	0.001	D	0.000	D						SNX29P2
31933	4880497		-0.527	-1.34	0.007	D								
45408	7000270	1q23.1	-0.460	-1.34	0.020	D								PYHIN1
38488	6040736	8p11.23	-0.599	-1.35	0.003	D								GPR124

Table E2. Differentially expressed genes in FOXA1 hi vs. lo primary LUADs. See last page for full legend. (4/5)

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	537 signif	NKX2-1 assoc	Byers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
20156	3140064	22q13.33	-0.556	-1.35	0.008	D								C22orf34
46462	7160504	2q37.3	-0.567	-1.35	0.007	D								GPC1
20909	3190592	22q13.31	-0.613	-1.36	0.007	D								KIAA1644
21744	3370730	19q13.42	-0.614	-1.36	0.003	D								CDC42EP5
44079	6770333	14q32.13	-0.375	-1.36	0.049	D								SERPINA1
43028	6590026	18q11.2	-0.527	-1.36	0.010	D								ZNF521
23368	3710048	13q33.3	-0.510	-1.37	0.009	D					X			FAM155A
1313	130576	10q22.1	-0.640	-1.37	0.002	D								UNC5B
7585	1170653	7p22.3	-0.587	-1.37	0.004	D					X	X		PDGFA
23537	3710735	11q13.1	-0.593	-1.37	0.004	D								RASGRP2
42821	6560722	11q13.1	-0.478	-1.37	0.018	D								RASGRP2
36406	5720129	19p13.2	-0.470	-1.38	0.016	D					X	X		NFIX
22394	3440184	13q13.1	-0.673	-1.38	0.001	D	0.000	D			X	X		STARD13
4643	650689	19q13.12	-0.680	-1.38	0.001	D	0.000	D						CLIP3
11041	1690630	3p29	-0.669	-1.39	0.001	D	0.000	D						FAM43A
19992	3130220	3p21.31	-0.406	-1.39	0.035	D			N					TMEM158
34285	5340064	4p16.1	-0.488	-1.39	0.013	D								CPZ
12878	2000286		-0.509	-1.39	0.010	D								
38181	6020286	5q11.2	-0.513	-1.39	0.014	D								FST
31344	4830471	4q27	-0.516	-1.39	0.009	D								TNIP3
46895	7210682	17p13.1	-0.499	-1.40	0.011	D								ACAP1
11914	1820279	11p11.2	-0.603	-1.40	0.003	D					X			TSPAN18
44804	6940088	12q13.2	-0.626	-1.40	0.002	D								DGKA
16865	2600154	19q13.12	-0.391	-1.40	0.043	D								HSPB6
26113	4050768	3q21.3	-0.581	-1.41	0.004	D								CHST13
9454	1440564	1p36.11	-0.664	-1.41	0.001	D	0.000	D						RUNX3
12713	1990397	2q37.1	-0.608	-1.41	0.002	D								SP110
2319	360047	9q21.33	-0.543	-1.42	0.006	D								GAS1
42626	6550762	3p25.1	-0.668	-1.42	0.001	D	0.000	D			X			FBLN2
29523	4570008	3p22.2	-0.606	-1.42	0.003	D								EXOG
23807	3800273	17p13.2	-0.663	-1.42	0.001	D	0.000	D						LOC728392
12842	2000133		-0.578	-1.42	0.005	D								
36392	5720059	6p24.1	-0.796	-1.43	0.000	D	0.000	D			X			GFOD1
29868	4610010	19q13.42	-0.551	-1.43	0.006	D								LILRB5
27887	4230739	4p16.1	-0.470	-1.44	0.033	D					X	X		SORCS2
28318	4280093	14q11.2	-0.682	-1.45	0.001	D	0.000	D						LOC440157
20347	3170020	12q13.2	-0.653	-1.45	0.001	D	0.000	D						DGKA
38113	6020037	19p13.3	-0.406	-1.46	0.036	D								ISRG1
37163	5870020	15q26.3	-0.582	-1.46	0.005	D								LOC100128108
26775	4150204	9q34.11	-0.409	-1.46	0.036	D								PRRX2
32898	5080523	19q13.33	-0.741	-1.47	0.000	D	0.000	D						EHD2
41041	6370435	11q24.3	-0.618	-1.49	0.003	D					X	X		ETS1
7444	1110592	5q33.3	-0.783	-1.49	0.000	D	0.000	D						EBF1
42015	6480592	18q11.2	-0.407	-1.49	0.036	D								LAMA3
21121	3290639		-0.483	-1.49	0.014	D								RAB7B
15568	2370348	19p13.12	-0.896	-1.49	0.000	D	0.000	D						SYDE1
3553	520682	7q32.2	-0.493	-1.50	0.043	D								CPVL
22215	3420288	1p36.21	-0.551	-1.50	0.006	D								PDPN
34846	5390703	22q11.21	-0.626	-1.50	0.002	D								SCARF2
32740	5050671	8q21.3	-0.527	-1.50	0.015	D								
37938	5960086		-0.510	-1.51	0.009	D								
32472	4920369	9q34.3	-0.647	-1.51	0.002	D	0.000	D						COL5A1
17552	2650612	18q11.2	-0.452	-1.51	0.020	D								LAMA3
33638	5260605	15q26.3	-0.723	-1.51	0.001	D	0.000	D						LOC100128108
12244	1940072	17q21.1	-0.586	-1.51	0.004	D								RAPGEFL1
28982	4480615	1q23.1	-0.743	-1.52	0.002	D	0.000	D						PEAR1
14227	2190255	20q13.33	-0.450	-1.52	0.034	D								
16266	2490113	11q13.2	-0.673	-1.53	0.001	D	0.000	D						CD248
37148	5860717	11q24.2	-0.845	-1.54	0.000	D	0.000	D						ROBO3
461	50309	10q26.3	-0.493	-1.54	0.013	D								DPYSL4
12297	1940274	14q32.12	-0.652	-1.54	0.001	D	0.000	D						IFI27L2
29368	4560088	10p14	-0.481	-1.54	0.015	D								PRKCQ-AS1
45012	6960142	17q21.33	-0.567	-1.56	0.006	D								COL1A1
33631	5260561	Xp11.21	-0.643	-1.56	0.002	D	0.000	D						TRO
15997	2470524	19q13.31	-0.467	-1.57	0.018	D								LYPD3
6147	940427	15q24.1	-0.544	-1.57	0.007	D								ISLR
26609	4120386	7q22.1	-0.696	-1.57	0.001	D	0.000	D						PCOLCE
1082	110424	7p14.1	-0.742	-1.58	0.000	D	0.000	D						GLI3
40669	6330487	20q13.12	-0.478	-1.59	0.017	D								SULF2
17198	2630746	7q31.1	-0.915	-1.60	0.000	D	0.000	D	N		X	X		LAMB1
9461	1440601	1q24.2	-0.834	-1.60	0.000	D	0.000	D						PRRX1
32723	5050600	9q22.3	-0.728	-1.60	0.000	D	0.000	D						MGC24103
22750	3460026	17p13.1	-0.573	-1.60	0.024	D								SLC13A5
29419	4560128	7p22.1	-0.605	-1.60	0.003	D			N					FSCN1
24555	3850754	19p13.11	-0.471	-1.61	0.020	D								KIAA1683
18269	2750356	21q22.3	-0.695	-1.62	0.001	D	0.000	D						COL6A2
37668	5900468	2q37.3	-0.999	-1.62	0.000	D	0.000	D						HDAC4
36973	5860039	16q22.2	-0.480	-1.62	0.023	D								CALB2
5003	730577	20p13	-0.529	-1.63	0.008	D					X			CPXM1
20549	3180010	17q25.1	-0.408	-1.63	0.037	D								SDK2
40898	6350682	1q42.13	-0.521	-1.63	0.011	D								TRIM17
32976	5090079	17q25.3	-0.635	-1.64	0.002	D	0.000	D						C1QTNF1
29672	4570669	2q36.3	-0.567	-1.64	0.011	D								DNER
705	60452	11q13.3	-0.474	-1.65	0.029	D								GAL
4593	650452	1p36.32	-0.572	-1.65	0.004	D								PLCH2
16383	2490593	3p21.31	-0.448	-1.66	0.021	D			N		X			COL7A1
787	70035	4q35.2	-0.534	-1.66	0.008	D								ZFP42
47152	7330132	10q11.22	-0.445	-1.67	0.031	D								ANXA8L2
32389	4920066	10p14	-0.584	-1.68	0.004	D					X			SFMBT2
28718	4390193	4p16.1	-0.525	-1.68	0.008	D								CPZ
18302	2750475	4p16.3	-0.660	-1.68	0.001	D	0.000	D						NSG1
45970	7100136	1p36.31	-0.435	-1.69	0.030	D					X		x	HES2
34656	5360743	1p35.2	-0.803	-1.70	0.000	D	0.000	D			X			COL16A1
10207	1510392	7q31.1	-0.721	-1.72	0.000	D	0.000	D	N		X	X		LAMB1
28577	4290315	19q13.2	-0.693	-1.73	0.001	D	0.000	D			X			LTBP4
16664	2570154	12p13.31	-0.435	-1.74	0.026	D								MFAP5
22260	3420446	1p34.3	-0.459	-1.75	0.024	D								GJB3
446	50255	8q11.21	-0.544	-1.75	0.012	D			N					SNAI2
17630	2680131	12p11.23	-0.738	-1.76	0.000	D	0.000	D						PPFIBP1
32479	4920390	9q22.31	-0.838	-1.79	0.000	D	0.000	D						ROR2
2311	290767	19q13.12	-0.733	-1.79	0.002	D	0.000	D						KRTDAP
2276	290593	4q27	-0.777	-1.80	0.001	D	0.000	D			X			FGF2
14135	2140678	2q31.1	-0.601	-1.80	0.006	D			N		X			ITGA6
10787	1660341	14q11.2	-0.563	-1.81	0.005	D								FLJ39632
32515	4920528		-0.519	-1.85	0.010	D								
21387	3360113	14q32.2	-0.510	-1.87	0.011	D								MEG3
42122	6510274	10q22.1	-0.655	-1.87	0.001	D	0.000	D			X			CDH23
46586	7200242	20q13.12	-0.704	-1.89	0.001	D	0.000	D						SULF2
3864	580491	7q32.1	-0.556	-1.92	0.006	D								FLNC
21873	3390458	21q22.3	-0.811	-1.93	0.000	D	0.000	D						COL6A2
17614	2680072	9q34.3	-0.685	-1.96	0.001	D	0.000	D						OLFM1
40780	6350184	20q13.33	-0.661	-1.98	0.003	D	0.000	D						
23021	3520246	5q31.1	-0.590	-2.01	0.003	D				P				CXCL14
48401	7570598	21q22.3	-0.919	-2.03	0.000	D	0.000	D						COL6A1
44401	6860047	19q13.33	-0.412	-2.04	0.034	D								SNAI-A1
12340	1940450	12p11.23	-0.748	-2.05	0.000	D	0.000	D						PPFIBP1
38262	6020605	19q13.32	-0.421	-2.05	0.043	D					X	X		IGFL1
13847	2120270	10q24.33	-0.570	-2.09	0.024	D								CDL17A1
9826	1470441	17q21.2	-0.420	-2.09	0.038	D								KRT17
29232	4540246	17q21.2	-0.409	-2.13	0.046	D								KRT16

Gene ID	Probe ID	UCSC Cytoband	S2N	FOXA1 hi vs FOXA1 lo	T-test P value	1086 signif	SAM P value (FDR=5.2%)	537 signif	NKX2-1 assoc	Byers EMT	FOXA1 PEAK	NKX2-1/FOXA1 PEAK	FOXA1 TARGET	Symbol
37369	5890064	7q33	-0.708	-2.17	0.001	D	0.000	D			×			CALD1
40720	6330730	8q11.21	-0.718	-2.19	0.001	D	0.000	D	N					SNAI2
43895	6760341	12q13.13	-0.621	-2.22	0.012	D								KRT6B
8920	1400711	10q11.22	-0.394	-2.28	0.048	D								ANXA8L2
12837	2000114	12q13.13	-0.774	-2.30	0.004	D	0.000	D						KRT6B
32302	4900458	17q21.2	-0.508	-2.49	0.039	D								KRT14
47213	7330398		-0.550	-2.54	0.006	D								HLA-DRB1
24270	3840445	17q21.2	-0.489	-2.57	0.012	D								KRT17
6329	990372	10q24.33	-0.555	-2.65	0.014	D								COL17A1
2765	430446	12q13.13	-0.609	-2.98	0.010	D					X	X		KRT81
15158	2350196	12q13.13	-0.486	-3.12	0.023	D								KRT6B
36927	5820626	12q13.13	-0.714	-3.27	0.008	D								KRT6C
24127	3830681	12q13.13	-0.553	-4.22	0.008	D								KRT6A

Table E2. Differentially expressed genes in FOXA1 hi vs. lo primary LUADs. Genes which passed significance by either 2-sample t-test (p<0.05) or SAM analysis (FDR<5.2%) are shown. "S2N", signal to noise; "NKX2-1 assoc", genes previously identified as associated with NKX2-1 expression (255); "Byers EMT", genes previously identified as part of an EMT signature (273); "FOXA1 peak", genes with TSSs called within +/- 10kb of FOXA1-binding sites that were present in both H1819 and H1781; "NKX2-1/FOXA1 peak", genes with TSSs called within +/- 10kb of binding sites co-occupied with NKX2-1 and FOXA1. (5/5)

APPENDIX F

LUNG CANCER DRIVER GENES AND DNA DAMAGE GENES

Entrez Gene IDs	Gene	LCMC	Ding	Weir	Govindan	TCGA-Sq	COSMIC	Rudin-SCLC	Broad-Ad	TCGA-Ad
7157	TP53	x	x		x	x	x	x	x	x
1956	EGFR	x	x	x	x	x	x		x	x
3845	KRAS	x	x	x	x		x		x	x
5925	RB1		x	x		x	x	x	x	x
673	BRAF	x			x	x	x		x	x
4763	NF1		x		x	x			x	x
1029	CDKN2A		x	x		x			x	x
6794	STK11		x		x		x		x	x
5290	PIK3CA	x				x			x	x
5728	PTEN	x		x		x			x	
324	APC	x	x		x	x				
595	CCND1			x		x			x	x
5789	PTPRD		x	x		x				x
2064	ERBB2			x			x		x	x
7080	NKX2-1			x			x		x	x
4233	MET	x			x					x
238	ALK	x			x		x			
3717	JAK2	x			x					x
9817	KEAP1					x			x	x
6657	SOX2					x	x	x		
6597	SMARCA4					x	x		x	
4609	MYC			x		x			x	
53353	LRP1B		x		x	x				
898	CCNE1			x					x	x
4193	MDM2			x					x	x
7015	TERT			x					x	x
3815	KIT	x				x				
4851	NOTCH1	x				x				
1499	CTNNB1	x							x	
207	AKT1	x					x			
4893	NRAS	x	x							
8289	ARID1A								x	x
29072	SETD2								x	x
7307	U2AF1								x	x
8241	RBM10								x	x
55294	FBXW7					x			x	
4089	SMAD4					x			x	
4780	NFE2L2					x	x			
2260	FGFR1				x	x				
5156	PDGFRA		x			x				
472	ATM		x						x	
6098	ROS1				x		x			
3791	KDR		x				x			
2042	EPHA3		x		x					
2066	ERBB4		x		x					
4058	LTK		x		x					
4170	MCL1								x	x
1019	CDK4			x						x
2322	FLT3	x								
5604	MAP2K1	x								
23269	MGA									x
6016	RIT1									x
23520	ANP32C					x				
121549	ASCL4					x				
53335	BCL11A					x				
598	BCL2L1					x				
1021	CDK6					x				
1387	CREBBP					x				
64478	CSMD1					x				
8452	CUL3					x				
346007	EYS					x				
139285	FAM123B					x				
27086	FOXP1					x				
3105	HLA-A					x				
3265	HRAS					x				
8085	MLL2					x				
4853	NOTCH2					x				
5173	PDYN					x				
5966	REL					x				
7128	TNFAIP3					x				
8626	TP63					x				
7248	TSC1					x				
9686	VGLL4					x				

Table F1. Driver genes in lung cancer. See last page for full legend. (1/2)

Entrez Gene IDs	Gene	LCMC	Ding	Weir	Govindan	TCGA-Sq	COSMIC	Rudin-SCLC	Broad-Ad	TCGA-Ad
54904	WHSC1L1					x				
51741	WWOX					x				
107	ADCY1							x		
9774	BCLAF1							x		
201229	C17orf108							x		
9425	CDYL							x		
26047	CNTNAP2							x		
169044	COL22A1							x		
1284	COL4A2							x		
22982	DIP2C							x		
1993	ELAVL2							x		
2899	GRIK3							x		
2918	GRM8							x		
8570	KHSRP							x		
55605	KIF21A							x		
57088	PLSCR4							x		
11228	RASSF8							x		
9699	RIMS2							x		
862	RUNX1T1							x		
23314	SATB2							x		
121256	TMEM132D							x		
57683	ZDBF2							x		
8019	BRD3								x	
867	CBL								x	
9811	CTIF								x	
2261	FGFR3								x	
57120	GOPC								x	
5518	PPP2R1A								x	
1399	CRKL								x	
8314	BAP1						x			
80304	C2orf44						x			
8030	CCDC6						x			
972	CD74						x			
27436	EML4						x			
7430	EZR						x			
2263	FGFR2						x			
3799	KIF5B						x			
121227	LRIG3						x			
4610	MYCL1						x			
5979	RET						x			
6385	SDC4						x			
10568	SLC34A2						x			
10342	TFG						x			
7170	TPM3						x			
340273	ABCB5				x					
1080	CFTR				x					
1602	DACH1				x					
1969	EPHA2				x					
2043	EPHA4				x					
3702	ITK				x					
3718	JAK3				x					
5649	RELN				x					
405	ARNT			x						
26053	AUTS2			x						
1030	CDKN2B			x						
51562	MBIP			x						
5144	PDE4D			x						
7422	VEGFA			x						
2044	EPHA5		x							
2264	FGFR4		x							
2778	GNAS		x							
3624	INHBA		x							
4914	NTRK1		x							
4916	NTRK3		x							
5063	PAK3		x							
10991	SLC38A3		x							
51364	ZMYND10		x							
896	CCND3									x
1018	CDK3									x
7994	KAT6A									x
7012	TERC									x
7764	ZNF217									x

Table F1. Driver genes in lung cancer. Literature sources are indicated in columns: LCMC, Lung Cancer Mutation Consortium; Ding, (148); Weir, (251), Govindan, (149); TCGA-Sq (281); COSMIC, Catalogue of Somatic Mutations in Cancer (282); Rudin-SCLC, (283); Broad-Ad, (150); TCGA-Ad, (90). (2/2)

Apoptosis	Cell cycle		DNA Repair				
	Cell Cycle Arrest	Cell Cycle Checkpoint	Damaged DNA Binding	Base-excision Repair	Double-strand Break Repair	Mismatch Repair	Other
ABL1	CHEK1	ATR	ANKRD17	APEX1	CIB1	ABL1	ATM
BRCA1	CHEK2	BRCA1	BRCA1	MBD4	FEN1	ANKRD17	ATRX
CIDEA	DDIT3	FANCG	DDB1	MPG	XRCC6	EXO1	BTG2
GADD45A	GADD45A	NBN	DMC1	MUTYH	XRCC6BP1	MLH1	CCNH
GADD45G	GML	RAD1	ERCC1	NTHL1	MRE11A	MLH3	CDK7
GML	GTSE1	RBBP8	FANCG	OGG1	NBN	MSH2	CRY1
IP6K3	HUS1	SMC1A	FEN1	UNG	PRKDC	MSH3	ERCC2
PCBP4	MAP2K6	TP53	MPG		RAD21	MUTYH	GTF2H1
AIFM1(PDCD8)	MAPK12		MSH2		RAD50	N4BP2	GTF2H2
PPP1R15A	PCBP4		MSH3			PMS1	IGHMBP2
RAD21	PPP1R15A		N4BP2			PMS2	LIG1
TP53	RAD17		NBN			PMS2P3	MNAT1
TP73	RAD9A		OGG1			TP73	PCNA
	SESN1		PMS2P3			TREX1	RPA1
	ZAK		PNKP				SUMO1
			RAD1				BRCC3
			RAD18				PIAS1
			RAD51				PIAS4
			RAD51B				
			REV1				
			SEMA4A				
			XPA				
			XPC				
			XRCC1				
			XRCC2				
			XRCC3				

Table F2. Genes involved in DNA damage response. Source: http://www.sabiosciences.com/rt_pcr_product/HTML/PAHS-029A.html