# Mechanisms of Sensitization to Chemotherapy in Non-Small Cell Lung Cancer 

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## DEDICATION

For Martha, Charles C., James, Wanda, Michelle, James Jr, Charles T., and Manwe.

## by

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## DISSERTATION

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# Mechanisms of Sensitization to Chemotherapy in Non-Small Cell <br> Lung CANCER 

## RACHEL MARIE GREER, Ph.D.

The University of Texas Southwestern Medical Center at Dallas, 2011

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Lung cancer is the leading cause of cancer-related deaths world-wide for men and women, due in part to late detection of disease and inherent resistance to treatment. This body of work focuses on resistance to treatment, specifically chemotherapy and understanding ways to sensitize non-small cell lung cancers to existing chemotherapies. Using a large panel of non-small cell lung cancers, response to common platinum-based doublet chemotherapy was tested, and compared in a statistical fashion to each chemotherapy as a single agent, to understand the breadth of responses, and have a baseline of response to improve
upon. The rest of this work endeavors to make chemotherapies more effective at tumor kill by targeting tumor specific alterations. One such targeted approach focused on miR337, and its ability to influence paclitaxel sensitivity through introduction of miR337 mimics and antagomiRs was evaluated using MTS based assays; increasing miR337 levels in moderately paclitaxel-sensitive or completely paclitaxel resistant cells sensitized the cells at least ten-fold to paclitaxel. Nonsmall cell lung cancers have frequent mutations in p53 (>80\%). Targeting of the p53 promoter region with agRNAs, in p53-mutant containing cell lines induces cytotoxicity that is reminiscent of wild type p53 activity and is associated with large increases of the non-coding RNA lincRNAp21, and can cause large sensitizations to p53-dependent chemotherapies such as doxorubicin, indicating that these agRNAp53s could be of therapeutic importance in p53-mutant lung cancers. Re-engagement of the apoptotic pathway by a small molecule (JP1201) sensitizes non-small cell lung cancers to a variety of chemotherapies. Anti-mitotic chemotherapies have the most frequent sensitization across a large panel of nonsmall cell lung cancers, and the largest degree of sensitization by combination with JP1201, and this sensitization is dependent on activation of the ER stress pathway. Xenograft models using cell lines recapitulate the ability of JP1201 to sensitize non-small cell lung cancers to chemotherapy, indicating that combinations with JP1201 might be effective in patients.

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## LIST OF DEFINITIONS

| Abl | Abelson murine leukemia viral oncogene homolog |
| :--- | :--- |
| AC | Adenocarcinoma |
| agRNA | anti-gene ribonucleic acid |
| ALK | Anaplastic lymphoma kinase |
| ALL | Acute Lymphocytic Leukemia |
| AML | Acute Myeloid Leukemia |
| ANOVA | Apoptotic protease activating factor 1 |
| APAF | American Type Culture Collection |
| ASK1 | area under the curve |
| ATCC | alanine-valine-proline-phenylalalnine |
| AUC | BCL2-associated agonist of cell death |
| AVPF | BCL2 antagonist/killer 1 |
| BAD | BCL2-associated X protein |
| BAK | B-cell lymphoma 2 homase interacting death domain agonist |
| BAX | B-cell lymphoma extra large |
| BCL2 | BCL |


| BIM | BCL2-interacting mediator |
| :--- | :--- |
| BIR | Baculovirus inhibitor of apoptosis protein repeat |
| C. elegans | Caenorhabditis elegans, nematode |
| CDKN1A | Cyclin depdendent kinase inhibitor 1A (p21) |
| cDNA | complementary deoxyribonucleic acid |
| CI | Combination Index |
| cIAP1 | cellular inhibitor of apoptosis 1 |
| cIAP2 | cytadine triphosphate of apoptosis 2 |
| CT | deoxyribonucleic acid binding domain |
| CTP | database of transcription start sites |
| DBD | death inducing signaling complex |
| DBTSS | dimethyl sulfoxide |
| DISC | endoplasmic reticulum |
| DMSO | envidermal growth factor receptor |
| DNA | envinoderm microtubule-associated protein-like 4 |
| EGFR | ELISA |


| FACS | fluorescent-activated cell sorting |
| :---: | :---: |
| FADD | Fas-associated death domain |
| FBS | fetal bovine serum |
| FDA | Food and Drug Administration |
| FDG-PET | fludeoxyglucose-positron emission tomography |
| FITC | fluorescein isothiocyanate |
| G12V | glycine to valine mutation at residue 12 |
| GAPDH | glyceraldehyde 3-phosphate dehydrogenase |
| GDP | guanosine diphosphate |
| GI | gastrointestinal |
| GTP | guanosine triphosphate |
| GTPase | family of hydrolase enzymes that can bind to GTP and |
| catalyze its conversion to GDP |  |
| HBEC | Human bronchial epithelial cell |
| HSP90 | heat shock protein 90 |
| hTERT | Human telomerase enzyme |
| IACUC | Institutional Animal Care and Use Committees |
| IAP | inhibitor of apoptosis protein |
| $\mathrm{IC}_{50}$ | inhibitory concentration that kills 50\% of the population |
| ICAD | inhibitor of caspase activated DNase |
| IRB | Internal Review Board |


| IRE1 | inositol requiring enzyme 1 |
| :---: | :---: |
| JNK | c-Jun N -terminal kinase |
| KSFM | keratinocyte serum free media |
| LCC | large cell carcinoma |
| lincRNA | long non-coding ribonucleic acids |
| LKB1/STK11 | liver kinase b1 also known as serine/threonine-protein |
| kinase 11 |  |
| LOH | loss of heterozygosity |
| MDM2 | murine double minute oncogene |
| miRNA | micro-ribonucleic acid |
| mRNA | messenger-ribonucleic acid |
| MTS | 3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)- |
| 2-(4-sulfophenyl)-2H-tetrazolium, inner salt |  |
| NF-кB | nuclear factor kappa-light-chain-enhancer of activated B- |
| cells |  |
| NOD/SCID | non-obese diabetic/severe combined immunodeficient |
| mouse |  |
| Noxa | Latin for "an injury" BH3 only pro-apoptotic protein |
| NSAID | non-steroidal anti-inflammatory drug |
| NSCLC | non-small cell lung cancer |
| PAGE | poly-acrylamide gel electrophoresis |


| PARP | poly-ADP ribose polymerase |
| :---: | :---: |
| PDGFR | platelet-derived growth factor receptor |
| pri-miRNA | completely un-processed precursor miRNA directly |
| transcribed from DNA |  |
| PUMA | p53 upregulated modulator of apoptosis |
| qPCR | quantitative polymerase chain reaction |
| Ras | homologue of Rat-sarcoma viral protein, small GTPase |
| Rb | retinoblastoma gene/protein |
| RIPK1 | receptor interacting protein kinase 1 |
| RISC | RNA-induced silencing complex |
| RNAi | RNA interference |
| RPMI | Roswell park memorial institute medium |
| SCC | squamous cell carcinoma |
| SCLC | small cell lung cancer |
| SDS | sodium dodecyl-sulfate |
| SEM | standard error of the mean |
| shRNA | short hairpin-RNA |
| siRNA | small-interfering RNA |
| SMAC | second mitochondrial-derived activator of caspases |
| SPARC | secreted protein acidic and rich in cysteine |
| TGFb | transforming growth factor beta |

TKI

TNF
TNFR

TNFSFL
TNM

TP53

TP63
TP73

TRADD
TRAF

TRAIL

TSS

TUNEL
labeling
UPR

UTSW

VEGF

VEGFR

VIM

WRAP53

XIAP
tyrosine kinase inhibitor
tumor necrosis factor
tumor necrosis factor receptor
tumor necrosis factor super family of ligands
tumor, node, metastasis classification of malignant tumors
tumor protein 53 kilodaltons
tumor protein 63 kilodaltons
tumor protein 73 kilodaltons
TNF receptor associated death domain
TNF receptor associated factor
TNF-associated apoptosis inducing ligand
transcription start site
terminal deoxynucleotidyl transferase dUTP nick end
unfolded protein response
University of Texas Southwestern Medical Center
vascular endothelial growth factor
vascular endothelial growth factor receptor
vimentin

WD repeat containing, antisense to TP53
X-linked inhibitor of apoptosis protein

## CHAPTER ONE

## Introduction

### 1.1 CANCER

Contrary to popular belief, cancer has been a problem facing humans since antiquity. The first descriptions of cancer are from ancient Egypt, where women had growths in their breasts which ultimately was a death sentence for these women (Diamandopoulus, 1996). Hippocrates termed malignant tumors carcinos, Greek for crab or crayfish, owing to the appearance of the cut surface of a solid tumor with the veins stretched out on all sides as the crab has its feet (Karpozilos \& Pavlidis, 2004). He later added the Greek suffix -oma for swelling giving rise to the term carcinoma, which is now used to describe cancers arising from epithelial cell origin (Karpozilos \& Pavlidis, 2004).

The history of cancer treatments is also very ancient. Tales of treatments of breast cancer in Ancient Egypt with a tool called a fire drill, used to cauterize the ulcerated tumors abound. Hippocrates was well known for treating ailments according to the four humors (yellow bile, black bile, phlegm, blood), and cancer treatment was no different, depending on the humor of the patient, treatment consisted of diet, bloodletting, laxatives, and or plasters (Diamandopoulus, 1996; Karpozilos \& Pavlidis, 2004). Actually, this type of treatment for cancers was very popular until the discovery of cells.

Cancer remains a large problem, despite it affecting individuals for many centuries, one out of two men, and one out of three women in the US will be diagnosed with cancer in their lifetime. In fact, cancer is the number one cause of death in people under 85 years of age, and in people over 85 cancer is only second to heart disease in cause of death (Siegel, Ward, Brawley, \& Jemal, 2011).

There are many different terms used to describe cancers, such as malignant neoplasm, or tumor. Tumors are given specific names that are descriptive in a clinical or pathological fashion. Sarcomas are tumors that arise from mesenchymal tissues. Carcinoma is a term given to tumors arising from epithelial cell origin, with the exception of melanomas. An adenocarcinoma is a tumor of epithelia cell origin that has features resembling glands or ducts, while a squamous cell carcinoma is a tumor of epithelial cell origin that resembles differentiated squamous cell type. Lymphomas are tumors arising in the lymph system, usually in lymph nodes.

Leukemias are tumors that arise in blood precursor cells in bone marrow, there are two cell types that give rise to leukemias, lymphocytic or myeloid cells. Lymphocytes are a granular white blood cells, typically NK cells, T cells, B cells, and common precursor cells. Granular white blood cells; eosinophils, basophils, neutrophils, macrophages, dendritic cells; red blood cells, and platelets make up the cell types covered in the myeloid classification. Typically myeloblastic leukemias are characterized by accumulation of abnormal granulocytes in either
the blood or bone marrow. Most patients with CML (chronic mylogenous leukemia) have a $(9 ; 22)$ translocation with fusion of the Bcr and Abl genes which is often called the Philadelphia Chromosome. One of the great success stories of targeted therapy is CML with $(9 ; 22)$ translocation being treated with imatinib which can inhibit the progression of CML and in some patients lead to regrowth of normal bone marrow (Beran et al., 1998). CML is now treated with three different targeted therapies that all target the BCR-ABL fusion, imatinib, dasatinib, and nilotinib (Kimura, Ashihara, \& Maekawa, 2010).

### 1.2 Lung Cancer

Lung cancer is the leading cause of cancer related deaths, with over 200,000 deaths in 2009 (Ahmedin, Rebecca, Jiaquan, \& Elizabeth, 2010), lung cancer is the second most commonly diagnosed cancer in both men and women (Figure 1.1). The overall life time risk for being diagnosed with lung cancer in the United States is 1 out of 13 men will be diagnosed, and 1 in 16 women will be diagnosed in their lifetime with lung cancer (Ahmedin, et al., 2010; Jemal et al., 2009; Siegel, et al., 2011).

Smoking is a well-known factor associated with lung cancer development, because of this there have been many campaigns to warn the public of the harmful effects of smoking (Cardenas et al., 1997). With the decline in smoking due to these campaigns, there has been a decline in the incidence rate in men, there is still an increase in the incidence rate of women (Cardenas, et al., 1997; Pao et al.,

2004; Rudin et al., 2009; S. Sun, Schiller, \& Gazdar, 2007). There is no clear reason as to the increase in incidence in women; however, some possible causes will be discussed in the next section. Despite advances in both detection and treatment of cancer, the 5-year survival rate of lung cancer remains near 15\% of those diagnosed with the disease (Siegel, et al., 2011). This cause of this low survival rate can be attributed to at least two causes; late detection, and resistance to treatment.

One of the problems in detecting lung cancer at an early stage is there are no early screening procedures like there are for breast and prostate cancer; however, the National Lung Cancer Screening Trial has recently found that in a population of current and former heavy smokers that using low dose spiral CT as a screening technique results in a $20 \%$ decrease in lung cancer mortality from when the trial began in 2002 as compared to current and former heavy smokers that were screened with chest x-ray alone (Team). While this trial is promising, there are many factors that should be considered when evaluating this study, firstly is the large increase in false positive findings with CT screening, the less sophisticated CTs used on the trial than are routinely used across the country, this will likely result in a further increase in false positive rate with CT screening. Additionally, the trial only used three CT measurements in the study, but if people are routinely screened with CT every year, or two years or however often it is decided to do this, the long term effects of chronic exposure to X-rays on cancer
development is not known at this time. Additionally, who should be screened regularly was not addressed by this study. The NLCST only screened individuals that had smoked at least 30-pack years within the last fifteen years without a previous lung cancer diagnosis, so only high-risk patients were being screened. The utility of CT screening across non-smokers is not addressed even though never smokers account for at least $20 \%$ of lung cancer cases per year (S. Sun, et al., 2007).

### 1.2.1 Etiology

Smoking is one of the best characterized risk factors for developing lung cancer. In fact $85 \%$ of lung cancer in men world wide and $47 \%$ of cases of lung cancer in women is attributable to smoking (Parkin, Bray, Ferlay, \& Pisani, 2005). Smoking increases the risk of developing lung cancer by 10-20 fold (Parkin, et al., 2005). Studies done by the Environmental Protection Agency and others have shown that environmental tobacco smoke (ETS) accounts for roughly 3,000 lung cancer deaths per year in the US, and increases risk of developing lung cancer by 20-25\% (Cardenas, et al., 1997). However, most lung cancers that are not directly attributable to smoking cannot be explained by ETS alone. The other known risk factors for lung cancer include radioactive radon, cooking oil vapors, indoor coal and wood burning, genetic factors (Table 1.1), asbestos, and viral factors (S. Sun, et al., 2007). Other factors such as chromium, arsenic, cadmium,
silica, nickel, outdoor air pollutants, previous lung disease, and dietary factors have also been implicated in increasing risk of lung cancer (S. Sun, et al., 2007). Epidemiological studies from China, Taiwan, and Singapore have shown that cooking oil fumes, especially in the absence of fume extractors is significantly associated with increased risk of lung cancer in female never-smokers (S. Sun, et al., 2007).

### 1.2.2 PATHOLOGY

Lung cancer develops in the epithelium of the respiratory system, including bronchi, bronchioles, all the way to alveoli, which is distinct from mesotheliomas and sarcomas (stromal tumors). There are four major histological classes of lung cancer; however, lung cancer is usually broken into two classes, small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). SCLC is mainly associated with smoking, and it is characterized by small tumor cells that express neuroendocrine markers. NSCLC is a group of all the other kinds of lung cancer that cannot be classified as SCLC. There are at least three histologically distinct cancers within NSCLC, squamous cell carcinomas (SCC), adenocarcinomas (AC), and large cell carcinomas (LCC). Tumors that cannot be definitively identified as one particular type of NSCLC are generally called poorly differentiated, undifferentiated, or just NSCLC. It has recently been realized that not only are these histologically distinct tumors, but they respond
differently to different treatment regimens (Triano, Deshpande, \& Gettinger, 2010).

SCLC and SCC tend to occur in the central airways of the lung, while ACs tend to occur in the peripheral lung (S. Sun, et al., 2007). While all histological types of lung cancer are associated with smoking, the strongest associations are for SCLC or SCC. Adenocarcinomas are the prevalent form of lung cancer in never smokers. A rare global trend has been seen in lung cancer histological patterns in the recent history, with AC increasing while SCC has been decreasing. It has been postulated that this trend is due to the majority of cigarettes having a lower tar and nicotine content than was found in cigarettes of the past (S. Sun, et al., 2007). In theory smokers then compensate for the reduced nicotine by consuming more cigarettes, resulting in changes in the anatomic location and histological type of lung cancer. It has been shown in rodents that a nicotinederived carcinogen, NKK, readily induces KRAS mutation-associated adenocarcinomas, which supports the theory that changes in cigarettes leading to changes in smoking behavior (Hecht, 1999).

### 1.2.3 Tumor Staging

One important prognostic factor in cancer is the tumor stage at diagnosis. Tumor stage takes into account three factors, the size of the primary tumor, the extent to which lymph nodes are involved, and if the tumor has spawned distant metastases, and follows modified TNM classifications (Table 1.2) (Greene, 2004;

Ihde \& Minna, 1991a). When determining the stage of a non-small cell lung cancer (NSCLC) patient history, physical examination, routine laboratory evaluations, chest x-ray, and chest computed tomography scan with contrast media, are used. The added utility of FDF-PET in stage determination is being explored in clinical trials (Sieren, Ohno, Koyama, Sugimura, \& McLennan, 2010). Once the existence of a primary tumor has been established, further methods such as bronchoscopy, bronchial biopsy, medianoscopy for node biopsy, or fine needle aspiration guided by CT scan are used to obtain nodal samples for determining nodal involvement. Using all of these data, the tumor is then staged between stage 0 and stage IV (Table 1.2) which then helps determine the course of treatment. For SCLC a simple two stage system has been used; limited stage disease when the tumor is limited to one hemi thorax and regional lymph nodes, or extensive stage disease when the tumor is found beyond these boundaries.

### 1.2.4 TREATMENT

Treatments are generally based upon the staging criteria. Stage 0 is carcinoma in situ for which the suggested treatment options include surgical resection, or other endobronchial therapies. Stage I lung cancer is optimally treated with surgical resection of the primary lesion alone (Ihde \& Minna, 1991b). There have been three large randomized studies exploring the possibilities for benefit of adjuvant chemotherapy in early stage lung cancer (stage I - IIB), the summary of all three studies shows that there is no benefit to patients with stage

IA tumors, and marginal benefit (2-3\%) for patients with stage IB tumors due to limited risk of recurrence (Non-small Cell Lung Cancer Collaborative, 1995), for inoperable or where patients refused surgery with stage I disease, radiation with curative intent, clinical trials involving adjuvant chemotherapy, or endobronchial therapies are suggested as alternative treatment options. Stage II disease is still considered early stage lung cancer and as such the primary suggested therapy is surgery or surgery with adjuvant chemotherapy, curative radiotherapy, or experimental therapy in the setting of a clinical trial. Patients with surgically resectable stage IIIA disease are most often treated with surgery and adjuvant chemotherapy or can participate in clinical trials for which they are eligible. In some cases pre-operative chemotherapy may be used to make the tumor smaller for more effective surgical outcomes. In stage IIIA patients where surgery is not suggested and patients with stage IIIB disease, chemoradiation, radiation therapy, or enrollment into available clinical trials are the treatments used. Forty percent of newly diagnosed NSCLC patients present with stage IV disease, most of these patients will not benefit from surgery; instead chemotherapy, chemoradiation therapy, radiation therapy, or available clinical trials are the preferred treatment regimens for these patients.

### 1.2.5 Molecular oncogenic changes in Lung Cancer

Mutations leading to cancer tend to occur in two gene types, protooncogenes and tumor suppressor genes. Proto-oncogenes are genes which when activated, by point mutations, over expression, or chromosomal translocation that results in deregulation of activation or localization, lead to cancer formation. Some of the most famous oncogenes are Ras, Myc, EGFR, BCR-ABL, and the HPV encoded proteins E6/E7. Tumor suppressor genes are genes which act to control the development of cancer, these genes can directly regulate an oncogene, i.e. PTEN negatively regulates PI3K, are involved in DNA repair mechanisms, i.e. BRCA1, regulate the cell cycle, i.e. Rb or p53. p53, Kras, STK11/LKB1, and EGFR are some of the most commonly mutated genes in NSCLC (Figure 1.3) (Ding et al., 2008). Most TSG follow the two hit hypothesis in which both alleles of the gene must be inactivated whether by methylation, LOH coupled to inactivating mutation, or homozygous deletions. However, not all mutations that occur in cancer are necessary for the formation of cancer as will be discussed in the following section on Ras because sometimes Kras mutations are driver mutations and other times just passenger mutations. More detailed information follows for some of the most prevalent mutations found in lung cancer with emphasis for mutations that affect treatment either positively or negatively.

### 1.2.5.1 TP53

TP53 is the single most commonly mutated gene in human cancers, $50 \%$ of all cancers, and as such it is most likely the most heavily studied tumor
suppressor gene (Mitsudomi, Steinberg, et al., 1992). In lung cancer p53 is mutated in around 80\% of tumors. TP53 encodes a basally transcribed inducible transcription factor. Many types of cellular stresses are known to activate p53, such as irradiation, hypoxia, oxidative stress, osmotic shock, oncogene activation, and an array of chemotherapeutic agents. Upon activation, which consists of stabilization, post-translational modification, and binding to p53 response elements within the genome, p53 can activate apoptosis, senescence, or reversible cell cycle arrest by activating genes, such as CDKN1A, or repressing genes, such as VIM, gene transcription (Table 1.3). The majority of mutations in TP53 occur within the DNA binding domain (DBD), which can then be divided into two groups; those that affect direct interaction of p53 with DNA, or those that affect tertiary structure (Weisz, Oren, \& Rotter, 2007). Mutations in p53 not only result in the loss of wild type p53 transcriptional activity, dominant negative effects on wild type p53, but also gain of function activity that is through inhibition of p63 and p73 (Dittmer et al., 1993; Strano et al., 2007).
p53 also activates MDM2 which is responsible for keeping p53 levels low by promoting degradation of p53 by ubiquitination (Fesik, 2005). The regulation of p53 is very complex, and occurs at many levels. TP53 is located on chromosome 17p13.1 and shares exon 1 with that of another gene, WRAP53, that is transcribed from the opposite strand (Mahmoudi et al., 2009). WRAP53 RNA binds to p53 mRNA and stabilizes the mRNA, which provides another layer of
control, not to mention the large promoter region and long list of transcription factors that have been found bound to the promoter of TP53 (Table 1.4). In addition to ubiquitination, p53 can be acetylated or phosphorylated as well which can modulate both transcriptional and non-transcription activities of p53 (Van Dyke, 2007). Frequent LOH of 17p13 accompanied by point mutation of the other allele of p53 combined with the paucity of homozygous deletions of p53 when compared to other tumor suppressors suggests that mutations in p53 provides a dominant oncogenic activity that is important during tumorigenesis (Weisz, et al., 2007). Mutations in p53 not only lead to decreased ability to activate target genes, but also interferes with proper p63 and p73 signaling (S. W. Lowe, Cepero, \& Evan, 2004). Mutant p53 also has gain of function activity and was initially thought to be an oncogene instead of tumor suppressor.

In addition to uncoupling DNA damage from the cell cycle, mutations in p53 confer cancer cells with resistance to some chemotherapy because p53 can directly activate apoptosis through transcriptional activation of NOXA and PUMA as discussed in 1.4.3.

### 1.2.5.2 RAS

The RAS proto-oncogene family includes Kras, Nras, and Hras, which encode membrane bound small GTPases involved in signaling cascades controlling diverse cellular processes (Bos, 1989). Ras exists in two forms, inactive which is characterized by Ras being bound to GDP, or active which is
characterized by binding to GTP; mutations in codons $12,13,59$, or 61 abolishes the ability of Ras to bind GTP/GDP but also leads to intrinsic activation of Ras and thus oncogenic potential (Bos, 1989; Mitsudomi, Oyama, et al., 1992;

Wennerberg, Rossman, \& Der, 2005). The best characterized (and well known) Ras pathway is activation of Ras downstream of EGFR, which leads to recruitment and activation of Raf and thereby activating the ERK1/2 kinase cascade (Wennerberg, et al., 2005). Mutations in Ras gives cancer cells a growth advantage in that they no longer require growth signals such as EGF binding to EGFR to cause activation of the ERK kinase cascade, other downstream genes such as Braf can acquire mutations in place of Ras, as a result Ras and Raf mutations are mutually exclusive (Brose et al., 2002; Gandhi et al., 2009; Suzuki et al., 2006; Tam et al., 2006). If mutant Kras is expressed in normal immortalized HBECs it causes senescence in these cells, most likely through a p53 dependent mechanism; however, if p53 is first knocked down or neutralized by overexpression of mutant p53 then mutant Kras can be successful expressed in HBECs and confers a growth advantage to them (Sato et al., 2006).

Mutations in Ras not only remove the dependence of GTP for Ras signaling, but they also preclude the GTP binding pocket from being targeted by small molecules to inhibit mutant Ras signaling, as a result, a targeted therapeutic approach to mutant Ras tumors has as of yet been unsuccessful.

### 1.2.5.3 CDKN2A

The CDKN2A locus encodes three different tumor suppressor proteins, $\mathrm{p} 16, \mathrm{p} 14$, and p 15 . While these proteins are encoded by the same gene, alternative splicing results in proteins with very different functions. Both p16 and p15 act as cell cycle regulators by inhibiting activity of CDK4 which prohibits progression into S phase. p14ARF however acts to stabilize p53 by interacting with both p53 and MDM2 and preventing degradation of p53 via the ubiquitin proteolysis pathway. The CDKN2A locus is often hypermethylated in NSCLC (Minna, Fong, Zochbauer-Muller, \& Gazdar, 2002; Sato, et al., 2006; Toyooka et al., 2003).

### 1.2.5.4 STK11/LKB1

Serine/Threonine kinase 11 (STK11) which is also referred to as liver kinase B (LKB1) is a very frequent mutation in NSCLC ( $\sim 10 \%$ ). STK11 activates by phosphorylation a number of targets such as adenine monophosphate-activated protein kinase (AMPK). Not only does STK11 exert its tumor suppressive role by suppressing growth and proliferation while energy stores are low, but also regulating polarity of the cell (Gao, Ge, \& Ji, 2011).

### 1.2.5.5 EGFR

In the early part of the last decade mutations in EGFR were shown to be important not only in terms of response to treatment but also in defining a subtype of NSCLC, female never-smokers (Amann et al., 2005). EGFR is the receptor for epidermal growth factor (EGF), that is part of a normal kinase cascade that
includes Ras, Raf, and ERK, for this reason, mutations in EGFR, Ras, and Raf are all mutually exclusive, as it gives a cell no growth advantage to have multiple members of the same pathway mutated. EGFR is also a member, the founding member, of the ErbB receptors which also includes Her2/ErbB2, Her3/ErbB3, and Her4/ErbB4. Her2 is well known for being involved in breast cancer, and breast tumors with high Her2 levels are identified from initial biopsy and these patients then receive anti-Her2 therapy (trastuzamab, see section 1.5.4.2). There is increasing evidence that Her2, which has a non-functional ligand binding domain so, must heterodimerize with another ErbB family member, dimerizes with EGFR, and can provide EGFR-TKI mediated resistance.

### 1.2.5.6 PTEN

Another pathway that is often activated downstream of growth factor receptors such as EGFR is the PI3K pathway, and PTEN is a negative regulator of said pathway. PTEN mutations are quite common as well in lung cancer (Forgacs et al., 1998). Activating mutations are also found in lung cancers, suggesting that activation of the PI3K either by activating mutations or by loss of PTEN are oncogenic, and PI3K inhibitors are being developed.

### 1.3 Hallmarks of Cancer

Hanahan and Weinberg classify the major alterations that differentiate cancer cells from normal cells by the ten hallmarks of cancer (Figure 1.4) (Hanahan \& Weinberg, 2011). The first hallmark discovered by cancer
researchers was that cancer cells no longer rely on supply of growth signals from other tissues, cancer cells were able to secrete the growth signals that were necessary for them to continue to grow. Cancer cells also become insensitive to antigrowth signals, these can be both secreted signals, such as TGF $\beta$, or signals embedded within the surrounding stroma, such as SPARC. Antigrowth signals usually affect cells within the G1 phase, and as such the pathways that regulate insensitivity to antigrowth signals are involved in the cell cycle. Tumor suppressor genes such as Rb or $\mathrm{p} 15^{\mathrm{INK} 4 \mathrm{~B}}$ are inactivated to allow for this insensitivity. Consequently these mutations as well as others, such as expression of hTERT that is normally not expressed except in stem cell populations, confer upon cancers the ability to have limitless replicative potential. Additionally, in order to keep up with the high metabolic needs of tumors which have the ability to grow indefinitely, cancers also develop the ability to recruit nearby blood vessels to sprout new growth of smaller blood vessels to the tumor in a process known as angiogenesis, additionally cancer cells have deregulated cellular energetics usually by increased glycolysis and decreased mitochondrial function often referred to the Warburg effect (Warburg, 1956). An effect of limitless growth potential is that eventually the tumors overgrow the space they originated in, which leads to invasion of normal tissues, and eventually metastasis. And the final hallmark of cancer is the evasion of apoptosis.

Cancers have developed multiple strategies for evading apoptosis, primarily by over expression of the various anti-apoptotic proteins that have been previously described. Over expression of BCL-2 and BCL ${ }_{\text {XL }}$ makes it much less probably that the mitochondria will release the pro-apoptotic proteins that have become sequestered by high BCL-2 levels. Cancer also over express many of the IAP family members including (but not limited to) XIAP, cIAP1, cIAP2, and survivin (Nachmias, Ashhab, \& Ben-Yehuda, 2004; Richter \& Duckett, 2000; Salvesen \& Duckett, 2002; Srinivasula \& Ashwell, 2008; Y. Wei, Fan, \& Yu, 2008). XIAP inhibits apoptosis most directly through its regulation of caspase activity. cIAP1 and 2 are also known to localize to the TNFR and promote the pro-survival signaling and inhibit pro-apoptotic signaling through the TNFR (Kuai et al., 2003; Samuel et al., 2006; Wang, Mayo, Korneluk, Goeddel, \& Baldwin, 1998). Survivin is probably the most studied member of the IAP family; however, its role in binding caspases is completely unknown. Survivin does have a clear role in mitosis, and in cancer has been shown to allow cells to pass through mitosis that would normally trigger cell cycle checkpoints.

Cancers also avoid apoptosis through less direct means. TP53 is the most commonly mutated gene across all cancers because of its key role as a central hub for sensing damage to the genome. Mutations in TP53 that affect the DNA binding domain of p53, alter the ability of p53 to activate downstream targets
which includes proteins such as NOXA and PUMA, which are members of the BH3 only proteins (S. Lowe \& Lin, 2000).

### 1.4 Apoptosis

Apoptosis is an evolutionarily conserved process that was originally described by a series of distinct morphological events (Kerr, Wyllie, \& Currie, 1972). Characteristic features of apoptosis include cell shrinkage, nuclear fragmentation, loss of membrane architecture, membrane blebbing, as well as changes in plasma membrane lipid composition(Figure 1.5) (Kerr, et al., 1972). Our understanding of the biochemical processes involved in apoptosis comes from genetic studies in C. elegans. During development of C. elegans, it is critical for excess cells to die, a mutation in a gene called ced3 casuses accumulation of these excess cells in the adult animal, they also saw that ced3 shared homology with human IL-1 $\beta$ converting enzyme (ICE) (Yuan, Shaham, Ledoux, Ellis, \& Horvitz, 1993). These two proteins were the first to be discovered in a family of cysteine-dependent aspartate-directed proteases (caspases). The discovery of ced3 as a caspase was critical in bringing the field of apoptosis into mainstream science. Currently there are twelve caspases in the human genome; however, not all are known to be involved in apoptosis (caspase1, caspase-4, caspase-5, and caspase-11) (Yigong, 2004).

There are two classes of apoptogenic caspases, initiator caspases and effector/executioner caspases. Caspases are produced as inactive zymogens, and
most require processing for maximal enzymatic activity. Initiator caspases (caspase-2, $-8,-9$, and -10 ) rely on upstream signals for activation, which requires being a part of a large protein complex and auto proteolysis. Effector caspases (caspase-3, -6, and -7) require proteolytic cleavage by initiator caspases for maximal enzymatic activity, these caspases go on to cleave a number of proteins which facilitates the death of the cell such as PARP and ICAD (Figure 1.2).

Currently there are two well elucidated pathways that initiate apoptosis, the intrinsic and extrinsic pathways, and two less well understood pathways that are thought to initiate apoptosis, granzyme b initiated apoptosis and ER stress induced apoptosis.

### 1.4.2 Extrinsic Apoptotic Pathway

The extrinsic pathway or death receptor pathway is initiated when prodeath cytokines, the tumor necrosis factor super family ligands (TNFSFL) bind to their cognate receptors initiating a signaling cascade that results in caspase activation (Figure 1.3). Ligand binding occurs in a trimeric fashion, similarly for efficient receptor activation, the receptors also trimerize. In the case of FasL and TRAIL, ligand binding induces recruitment of fas-associated death domain (FADD). Recruitment of FADD induces recruitment of pro-caspase-8; these two proteins along with the receptor constitute the major components of the death inducing signaling complex (DISC). cFLIP can be a member of the DISC that acts in an inhibitory fashion, but is dispensable.

In the case of TNF $\alpha$, again ligands bind in a trimeric fashion, and studies have shown that there is equilibrium of trimerization of un-bound receptor, binding of TNF $\alpha$ results in the greatest down-stream signaling when the receptors are trimerized before ligand binding. Studies have also shown that in some cell types these pre-assembled trimers of TNFR are localized to lipid rafts, and that this localization also enhances downstream signaling. Upon ligand binding, the adaptor molecule tumor necrosis factor receptor associated death domain protein (TRADD) is recruited to the receptor, which causes recruitment of tumor necrosis factor receptor associated factor, TRAF1 and TRAF2, and receptor interacting protein kinase 1 (RIPK1). TRAF2 interacts with and helps to localize cIAP1 and cIAP2 to the TNFR complex. TRAF2, cIAP1, and cIAP2 all have RING domains, which allow them to act as ubiquitin E3 ligases. RIPK1 becomes ubiquitinated which allows RIPK1 to serve as a scaffold for TAB and TAK1 leading to downstream JNK activation, and is also involved in NF-кB signaling by activation of NIK. If RIPK1 does not become ubiquitinated, then TRADD as well as RIPK1 are allowed to dissociate from the active receptor, and form a secondary complex with FADD and caspases-8 which can lead to downstream activation. Regulation of the ability of TRADD and RIPK1 to dissociate from the receptor is a key switch between TNF $\alpha$ pro-survival signaling and TNF $\alpha$ apoptotic signaling.

### 1.4.3 Intrinsic Apoptotic Pathway

The intrinsic pathway is regulated by the mitochondria of a cell (Figure 1.4). Inside of the mitochondria are many key factors that are involved in both energy production and death induction, such as cytochrome c. Cytochrome c is not only a component of the electron transport chain, but when released into the cytosol, it binds with APAF1, together these act as scaffolds for caspases-9 and all three components are known as the apoptosome, and leads to activation of downstream executioner caspases. Activation of mitochondrial apoptosis is regulated by a family of both pro- anti-apoptotic proteins named for the founding member, BCL-2. There is a fine balance between the pro-apoptotic and antiapoptotic BCL-2 family members, and that balance regulates how a cell will respond to an intrinsic apoptogenic stress. Classification as a BCL-2 super family member relies on homology of BCL-2 homology (BH) domains. There are four distinct BH domains, $\mathrm{BH} 1, \mathrm{BH} 2, \mathrm{BH} 3$, and BH 4 . Anti-apoptotic BCL-2 family members (BCL-2, BCL ${ }_{\text {xL }}$, BCL-W, A1, MCL-1) contain all four BH domains. The pro-apoptotic proteins BAX and BAK contain BH1-3, and the pro-apoptotic BH3 only family members (BAD, BID, BIM, NOXA, PUMA) only contain the BH3 domain (P. Li, Nijhawan, \& Wang, 2004). BAX and BAK are required to initiate mitochondrial-induced apoptosis, and BCL-2, BCL ${ }_{\text {XL }}$ antagonize the ability of BAX and BAK to lead to mitochondrial release of cytochrome cas well as other pro-apoptotic proteins (M. C. Wei et al., 2001). The BH3 only proteins serve as upstream mediators of apoptosis, they sit and wait for a pro-apoptotic
signal, whether it's by cleavage (BID), phosphorylation (BAD), or transcriptional activation (PUMA and NOXA), and then they antagonize the ability of the antiapoptotic BCL-2 family members to bind BAX and BAK. The second mitochondrial activator of caspases (SMAC) is the natural antagonist of IAP inhibition of caspases by binding to IAPs in a competitive fashion to caspases. SMAC is localized in mitochondria, within the inter membrane space, and is released along with cytochrome c when BAX and BAK signal for initiation of apoptosis to ensure that apoptosis occurs (Du, Fang, Li, Li, \& Wang, 2000).

### 1.4.4 InHIBITORS OF APOPTOSIS

The inhibitor of apoptosis proteins (IAPs) are key players in the activation of apoptosis. IAPs are characterized by containing between one and three repeats of a zinc binding baculovirus IAP repeat (BIR) domains that bind to caspases, and are required for anti-apoptotic function. The human IAP family contains eight proteins, ML-IAP, ILP2, survivin, BRUCE, NIAP, cIAP1, cIAP2, and XIAP (Figure 1.5) (Nachmias, et al., 2004; Richter \& Duckett, 2000; Salvesen \& Duckett, 2002; Srinivasula \& Ashwell, 2008). XIAP, cIAP1, cIAP2, and survivin have been studied the most out of this family. While survivin contains one BIR domain, its role in direct caspase inhibition is controversial; however, survivin does regulate mitosis by direct interaction with tubulin, and is up-regulated in many cancers (Danial \& Korsmeyer, 2004; Salvesen \& Duckett, 2002). $\underline{\text { X}}$ chromosome encoded IAP (XIAP) binds to caspases-3 and -7 inhibiting each of
their catalytic activity through binding of BIR2 and the linker region between BIR1-BIR2 of XIAP to caspases-3 or -7 (Shi, 2004; Yuan, 2006). XIAP also binds to caspase 9 through its BIR3 domain and prevents its activation by cytochrome c. cIAP1 and cIAP2 can also bind to the same caspases but lack the ability to robustly inhibit enzymatic activity (Eckelman \& Salvesen, 2006; Holcik, Gibson, \& Korneluk, 2001). cIAP1 and cIAP2 were first identified for their ability to interact with tumor necrosis factor associated factors (TRAFs), most notably TRAF2 and TRAF1.

### 1.5 CHEMOTHERAPY

### 1.5.1 History

The first modern chemotherapeutic was isolated from nitrogen mustards as a result of chemical warfare used in World War I, and was further developed by Louis Goodman and Alfred Gilman (Brunton, Lazo, \& Parker, 2006; Chabner \& Roberts, 2005), which became a standard treatment for lymphomas. The next major advance came with Sydney Farber who was studying the effects of folic acid on leukemias. With the help of others he was the first to delve into rational drug design, making structural analogues of folic acid that could not be metabolized but could block enzymes that required folate, this drug is now commonly referred to as methotrexate, and is commonly used in the clinic as are other more recently designed folate analogues, see pemetrexed in next section.

Both academics and pharmaceutical companies have taken up the search for better treatments for cancer.

### 1.5.2 Single Agent Chemotherapies used to treat NSCLC

Platinum compounds are standard agents used to treat a variety of cancers. The oldest, cisplatin is a mainstay of doublet chemotherapy used to treat NSCLC, carboplatin is structurally very similar to cisplatin with the exception that the platinum atom is covalently linked to a cyclobutane 1,1 dicarboxylate ligand in place of two chlorines. As a result, DNA binding kinetics of carboplatin are slower than cisplatin, but the same DNA adducts are formed. Due to the decrease in reactivity, carboplatin has less severe side effects compared to cisplatin, with respect to nephrotoxicity and GI effects, but more severe myelosuppressive effects.

In the latter part of the $20^{\text {th }}$ century many new chemotherapies were found to exhibit single agent activity in NSCLC including vinorelbine, paclitaxel, docetaxel, gemcitabine, irinotecan, and pemetrexed (Kosmidis, 2002). Most of these agents are derivatives of older agents; however, these newer formulations are more selective in target binding leading to reduced toxicity.

Vinorelbine, a tubulin depolymerizing agent, is a semi-synthetic vinca alkaloid, and shows more selectivity for mitotic tubules compared to axonal tubules resulting in fewer dose limiting toxicities such as myelosuppression (granulocytopenia or thrombocytopenia) and mild neurotoxicity. Vinorelbine has
been used as a single agent to treat NSCLC and was a particularly good treatment for elderly patients; however, it is now rarely used as a single agent (Brunton, et al., 2006).

Paclitaxel and docetaxel are structurally related tubulin polymerizing agents that belong to the taxane group of anti-mitotics, and have similar toxicity profiles, neutropenia, mucositis, peripheral neuropathy, asthenia, peripheral edema, hair loss, cardiac toxicity (Brunton, et al., 2006). Paclitaxel is a natural product extracted from the rare Pacific Yew Tree, is administered to patients in an excipient known as cremaphor, a polyoxyethylated castor oil that causes some of the side effects felt by patients receiving paclitaxel such as severe anaphylactic hypersensitivity reactions, hyperlipidemia, abnormal lipoprotein patterns, aggregation of erythrocytes and peripheral neuropathy (Gelderblom, Verweij, Nooter, \& Sparreboom, 2001; McAuliffe, Roberts, \& Roberts, 2002). Docetaxel is a semi-synthetic analogue that is synthesized from precursor molecules extracted from the readily available and renewable European Yew Tree, and is administered in polysorbate 80, ethanol, and citric acid which are not known to cause as severe of side effects as cremaphor (Gelderblom, et al., 2001).

Gemcitabine is a cytosine analogue, as such it can replace CTP for most roles that CTP plays in the cell, most notably incorporation into DNA, causing strand termination after the next nucleotide being incorporated into the growing strand of DNA as such it is a very potent radiosensitizer and should not be
generally combined with radiotherapy (Brunton, et al., 2006). Gemcitabine is associated with myelosuppression, flu-like syndrome, asthenia, rarely interstitial pneumonitis and over many months of treatment can cause progressive hemolytic uremic syndrome (loss of red blood cells due to lysis and acute renal failure).

Doxorubicin is an anthracycline antibiotic isolated from the fungus Steptococcus peucetius var. caesius (Brunton, et al., 2006). It exerts anti-cancer activity though multiple ways, intercalating with DNA, forming a complex with topoisomerase II that prevents ligase activity of topoisomerase II, and stimulates the production of superoxide (Staquet, Rozencweig, Duarte-Karim, \& Kenis, 1977). Doxorubicin causes an array of toxicities in patients such as myelosuppression, thrombocytopenia, stomatitis, alopecia, and GI disturbances, but by far the most serious long term side effect is cardiomyopathy.

Another semi-synthetic compound that was found to have activity against lung cancer in this period is irinotecan, structurally related to camptothecin, and as such causes an accumulation of single stranded breaks in DNA leading to cell death. Currently irinotecan is not approved for NSCLC treatment, but has been explored as part of platinum based combination treatment (Pass, Pogrebniak, Steinberg, Mulshine, \& Minna, 1992). Pemetrexed is the newest of the antifolates. Folic acid is a critical co-factor for de novo purine and thymidylate synthesis, and the antifolates function at different steps in this pathway to disrupt de novo purine and thymidylate synthesis.

### 1.5.3 PLATINUM BASED DOUBLET CHEMOTHERAPY

A clinical strategy for improving the effectiveness of anti-neoplastic chemotherapy is to combine multiple cytotoxic agents with different mechanisms of action and non-overlapping toxicities (Pass et al., 2010). Platinum, the generic term for platinum containing drugs such as cisplatin or carboplatin, based doublet chemotherapies have been the mainstay for NSCLC treatment for the last three decades, and remains a standard of care for patients currently(Arriagada et al., 2004; Besse \& Le Chevalier, 2008; Carbone \& Minna, 1995; Cardenal et al., 1999; Clarke et al., 2002; Ettinger, 2002; Goffin, Lacchetti, Ellis, Ung, \& Evans, 2010; Heinemann et al., 2006; Ihde et al., 1980; Manegold et al., 2000).

Platinum was chosen as the basis for combinations because it was initially thought to be the most active out of cisplatin, vinblastine, and nitrogen mustards. It remains because clinical trials have not been able to show that any other chemotherapy is better to use for combinations (Dienstmann, Martinez, \& Felip, 2011; Pass, et al., 1992; Wu et al., 2011).

### 1.5.4 Molecularly Targeted Agents

Over the last two decades, a new approach to engineering treatments for cancer has emerged molecularly targeted agents. Molecularly targeted agents are attractive because in theory they should only act on tumor but not normal cells,
currently there are two types of MTAs, small molecule inhibitors, and antibody based therapy.

### 1.5.4.1 Tyrosine Kinase Inhibitors

With the discovery that a chromosomal fusion, the Philadelphia chromosome, found in $95 \%$ of CML patients, as well as in some cases of ALL and AML, resulted in the fusion of BCR and ABL genes and the product of this fusion was a constitutively active from of the Abl kinase leading to transformation (Buchdunger et al., 1996). Small molecule screens were conducted looking for an inhibitor for Abl, Novartis identified, characterized, and optimized a candidate drug which eventually became imatinib and in 2001 became the first FDA approved tyrosine kinase inhibitor (TKI) (Beran, et al., 1998; Buchdunger, et al., 1996; Kimura, et al., 2010).

Tyrosine kinases sit upstream of many key survival and proliferation pathways, and as such are attractive anti-cancer targets. EGFR is a tyrosine kinase that sits directly upstream of Ras, which is known to be mutated in many cancers, so controlling Ras activation in cancers is quite desirable. Targeting of EGFR by gefitinib or erlotinib results in dramatic regression of tumors in patients harboring EGFR mutations (Pao, et al., 2004). However, patients see recurrence of disease either from secondary EGFR mutations conferring resistance to TKIs or undefined acquired resistance (Benedettini et al., 2010; Pallis et al., 2011; Vikis et al., 2007). At present there are many TKIs in use in the clinic currently (Table
1.5) (Dienstmann, et al., 2011; Druker \& Lydon, 2000; Gerber \& Minna, 2010; Kimura, et al., 2010; Lowery \& Han, 2011).

One of the newest targets of TKIs is the anaplastic lymphoma kinase (ALK), which is found as part of a fusion product in glioblastomas, NSCLC, and anaplastic large-cell lymphomas (Gerber \& Minna, 2010; McDermott et al., 2008; Sabbatini et al., 2009; Settleman, 2009). Activation of ALK is regulated by protein tyrosine phosphatase $\zeta$, phosphatase activity is inactivated by binding of pleiotrophin to PTP $\zeta$, and fusions of Alk with other genes abrogate the requirement for $\mathrm{PTP} \zeta$ regulation. Pfizer recently got FDA approval for crizotinib for the treatment of late stage NSCLC with EML4-ALK fusions (Dienstmann, et al., 2011; McDermott, et al., 2008; Sabbatini, et al., 2009).

One of the problems that TKIs present is that most if not all target the ATP binding pocket of tyrosine kinases, so target specificity of a given TKI is a relative term (Scheffler, Di Gion, Doroshyenko, Wolf, \& Fuhr, 2011). Imatinib for example not only targets Abl, but also targets cKit and PDGFRb (Druker \& Lydon, 2000). Additionally no TKIs, perhaps except imatinib, are curative as single agents (Scheffler, et al., 2011).

### 1.5.4.2 Monoclonal Antibodies

An alternative to targeting enzymatic activity is targeting of membrane bound proteins with monoclonal antibodies, trastuzumab and bevacizumab being two such agents that are used in the clinic. Trastuzumab is a humanized mouse
monoclonal antibody that targets Her2 which is often found to be over expressed in breast cancer, and when used to treat breast cancer causes a decrease in proliferation signals and also induces an immune response against tumor cells that it is bound to (Kostyal et al., 2011). Bevacizumab is also a humanized monoclonal antibody targeting angiogenesis by disrupting VEGF-A from binding VEGFR1 and VEGFR2 (Pietras \& Hanahan, 2005). Similarly to TKIs, monoclonal antibody single agent treatment is not curative.

Cetuximab targets EFGR, as discussed earlier a target in NSCLC, but it also a target in colorectal cancer (Chung et al., 2005). Cetuximab is a monoclonal antibody that blocks signaling through EGFR homodimers, and is in use for colorectal cancer; however, it is not of much utility in NSCLCs because they also express HER2, and can signal efficiently with EGFR-HER heterodimers.

### 1.5.4.3 SMAC Mimetics or IAP inhibitors

With the advances in the understanding of the apoptotic process, targeted approaches to remove cancer cells resistance to apoptosis has moved into the mainstream of drug development. Removal of BCL-2 and IAP inhibition are the two major ways that this is being accomplished. BH3 only mimics such as ABT737 and ABT263 are being currently developed with ABT263 undergoing clinical trials currently (Fesik, 2005; Oltersdorf et al., 2005). IAPs are being targeted by deriving small molecule mimics of the four most N terminal amino acids of SMAC, AVPF (Bockbrader, Tan, \& Sun, 2005; Flygare \& Fairbrother,

2010; LaCasse et al., 2008; L. Li et al., 2004; Z. Liu et al., 2000; Schimmer et al., 2004; Haiying Sun et al., 2004; H. Sun, Z. Nikolovska-Coleska, C. Y. Yang, L. Xu, Y. Tomita, et al., 2004). Many labs and pharmaceutical companies are exploring this as a therapeutic strategy, but the initial work was done at UTSW by Xioadong Wang's lab (Table 1.6) (L. Li, et al., 2004). They showed that SMAC mimetic (compound 3 ) could bind to XIAP, induce activation of caspase-3 in cell free assays, and that the combination of SMAC mimetic with TNF $\alpha$ or TRAIL could induce caspase activation (L. Li, et al., 2004). In a large screen across 50 NSCLCs they also found that roughly $15 \%$ are sensitive to SMAC mimetic alone, which is due to an autocrine TNF $\alpha$ loop that is dependent on TNF $\alpha$, TNFR1, caspase-8, and RIPK1 (Gaither et al., 2007; Petersen et al., 2007; Varfolomeev et al., 2007; Vince et al., 2007).
1.6 RNAI

The RNA interference pathway (or RNAi) involves gene silencing as a result of complementarity between small duplex RNA molecules and mRNA. Small duplex RNAs that are expressed endogenously within a cell with the function of silencing genes are called microRNAs (miRNAs also referred to as miRs), which usually contain a 3 ' seed sequence of $\sim 8$ nucleotides that are complementary to the mRNA with additional regions of complementarity. Degree of complementarity determines the mechanism by which the gene is silenced. In the cases where the miRNA is $100 \%$ complementary to the mRNA, the target
mRNA is cleaved and then fully degraded; however, when there is less than full complementarity, the miRNA remains bound to the mRNA and physically blocks translation of the target mRNA. Pri-miRNAs are transcribed by RNA polymerase II and then processed by Drosha in the nucleus and then Dicer in the cytoplasm, to yield mature miRs (Figure 1.10) (Davidson \& McCray, 2011; Kuehbacher, Urbich, Zeiher, \& Dimmeler, 2007). Mature miRs are then loaded into a RNA induced silencing complex (RISC)

Synthetic small interfering RNAs (siRNAs) are designed to be completely complementary to the target mRNA, and function through endogenous RNAi machinery, after introduction into a cell; siRNAs are loaded into a RISC and then cause cleavage of a target mRNA through cleavage of the mRNA.

Transcription of genes can be altered by introduction of so called antigene RNAs (agRNA) (Janowski et al., 2005; Janowski et al., 2006; Ting, Schuebel, Herman, \& Baylin, 2005). While agRNAs are similar in chemistry to siRNAs; they differ in the intended target, siRNAs target mRNA, and agRNAs are designed to target the genomic DNA upstream of transcription start sites (TSS).

### 1.7 Hypothesis and Specific Aims

While both detection and resistance to treatment are key reasons for the lack of increases in long term survival of lung cancer patients, this work focuses on improving treatment. And not improving treatment by finding new and
exciting cancer-specific targets and targeting them by small molecules or antibodies, but improving treatment by rationally combining conventional chemotherapy with molecularly targeted techniques to further sensitize lung cancer cells to existing chemotherapies. I thus hypothesized that chemotherapy and molecularly targeted techniques can be combined in such a way that the result of the combination is greater than the sum of each agent alone that would be more effective than current combination regimens. Thus I set up three aims to assess this hypothesis.

Aim1: Systematically evaluate current combination chemotherapy regimens in preclinical models to find areas to exploit to make future combinations more effective.

Aim 2: Using molecular biology approaches, target cellular molecules implicated in drug resistance or cancer cell survival to sensitize NSCLC to conventional chemotherapies.

Aim 3: Evaluate, using small molecules, the ability of the re-engagement of the apoptotic pathway to sensitize NSCLCs to conventional and targeted chemotherapies.
1.7.1 AIM 1: SYSTEMATICALLY EVALUATE CURRENT COMBINATION CHEMOTHERAPY REGIMENS IN PRECLINICAL MODELS TO FIND AREAS TO EXPLOIT TO MAKE FUTURE COMBINATIONS MORE EFFECTIVE.

Platinum based chemotherapy combinations remain the mainstay of NSCLC treatment when chemotherapy is deemed necessary as part of the overall treatment plan. These combinations arose from combining two chemotherapies with different dose limiting toxicities at the highest tolerable dose of each drug. Using clinically relevant doses of gemcitabine + cisplatin, pemetrexed + cisplatin, and paclitaxel + carboplatin, equivalent molar ratios were calculated and used to create an in vitro dose response curve for each combination, which were used to screen a panel of 53 NSCLCs. From the dose response curves for each cell line, $\mathrm{IC}_{50} \mathrm{~S}$ were calculated and used with single agent $\mathrm{IC}_{50}$ s for each drug in the combination to compare the $\mathrm{IC}_{50} \mathrm{~s}$ by fold decrease, and were used to statistically analyze the effect of combining the two drugs by calculating CI values for each cell line tested. Finally using microarray data for these 53 cell lines signatures of synergy/antagonism were created and used to predict response using leave on out cross validation.

### 1.7.2 Aim 2: Using MOLECULAR BIOLOGY APPROACHES, TARGET CELLULAR

 MOLECULES IMPLICATED IN DRUG RESISTANCE OR CANCER CELL SURVIVAL to sensitize NSCLC to conventional chemotherapies.Altered levels of miRs were linked to resistance to gemcitabine, paclitaxel, and vinorelbine by miRNA profiling being correlated with drug response. Using mimics and inhibitors of miR19a, miR129, and miR337 the ability of altering
endogenous miR levels to affect response to gemcitabine or paclitaxel was tested using MTS based micro titer plate assays. Based on a paclitaxel synthetic lethal screen, the specificity of six hits was tested against a small panel of anti-mitotic agents that are structurally similar or act similarly to paclitaxel. Mutations in p53 are the most common mutation in lung cancer, targeting of mutant p53 would be a major step forward with regards to targeted treatment that would be relevant for more than a small subpopulation as is the case with EGFR-TKIs. Reactivation of wild type p53 activity was achieved by targeting of the promoter region of TP53 with agRNAs, specificity of the agRNAp53 were tested across a panel of tumor lines (NSCLC and others) with varying mutations in p53, homozygous deletions of p53, and wild type p53.
1.7.3 Aim 3: Evaluate, using small molecules, the ability of the reengagement of the apoptotic pathway to sensitize NSCLCs to CONVENTIONAL AND TARGETED CHEMOTHERAPIES.

Evasion of apoptosis is one of the hallmarks of cancer, and being able to re-engage the apoptotic pathway is an attractive method for sensitizing cancers to chemotherapy treatment. A small molecule SMAC mimetic (IAP antagonist) was used across a panel of NSCLCs with a panel of chemotherapeutics. Drug responses of JP1201 in combination with each chemotherapy was analyzed statistically using CI calculations to determine synergy, additively, or antagonism.

In vitro results of synergy were validated with two cell line xenograft models in NOD/SCID mice. Mechanisms of synergy were determined using siRNAs to perturb pathways suspected in synergy.

| Risk factor | Risk estimate (95\% CI) | Comments | Refs |
| :---: | :---: | :---: | :---: |
| Environmental ETS | 1.19 (90\% Cl: 1.04-1.35) | Meta-analysis of 11 US studies of spousal exposure (females only) | 48 |
|  | 1.21 (1.13-1.30) | Meta-analysis of 44 case-control studies worldwide of spousal exposure | 52 |
|  | 1.22 (1.13-1.33) | Meta-analysis of 25 studies worldwide of workplace exposure | 52 |
|  | 1.24 (1.18-1.29) | Meta-analysis of 22 studies worldwide of workplace exposure | 51 |
| Residential radon | $8.4 \%$ (3.0-15.8\%) per $100 \mathrm{~Bq} \mathrm{~m}^{3}$ increase in measured radon | Meta-analysis of 13 European studies | 56 |
|  | $11 \%$ (0-28\%) per $100 \mathrm{~Bq} \mathrm{~m}^{3}$ | Meta-analysis of 7 North American studies | 57 |
| Cooking oil vapours | 2.12 (1.81-2.47) | Meta-analysis of 7 studies from China and Taiwan (female never smokers) | 71 |
| Indoor coal and wood burning | 2.66 (1.39-5.07) | Meta-analysis of 7 studies from China and Taiwan (both sexes) | 71 |
|  | 1.22 (1.04-1.44) | Large case-control study ( 2,861 cases and 3,118 controls) from Eastern and Central Europe (both sexes) | 158 |
|  | 2.5 (1.5-3.6) | Large case-control study ( 1,205 cases and 1541 controls) from Canada (significant for women only) | 159 |
| Genetic factors: family history, CYP1A1 Ile 462 Val polymorphism, XRCC1 variants | 1.51 (1.11-2.06) | Meta-analysis of 28 case-control, 17 cohort and 7 twin studies | 99 |
|  | 2.99 (1.51-5.91) | Meta-analysis of 14 case-control studies of Caucasian never smokers | 103 |
|  | 2.04 (1.17-3.54) | Meta-analysis of 21 case-control studies of Caucasian and Asian never smokers (significant for Caucasians only) | 104 |
|  | No association | Meta-analysis of 13 case-control studies | 160 |
|  | No association overall; reduced risk 0.65 (0.46-0.83) with Arg194Trp polymorphism and 0.56 ( $0.36-0.86$ ) with Arg280His for heavy smokers | Large case-control study from Europe (2,188 cases and 2,198 controls) | 161 |
|  | Increased risk for never smokers 1.3 (1.01.8) and decreased risk for heavy smokers 0.5 (0.3-1.0) with Arg299GIn | Large case-control study from the US (1,091 cases and 1,240 controls) | 105 |
| Viral factors: HPV 16/18 | 10.12 (3.88-26.4) for never smoking women >60 years | Case-control ( 141 cases, 60 controls) study from Taiwan of never smoking women | 107 |
| Bq, becquerels; ETS, environmental tobacco smoke; EPA, Environment Protection Agency: HPV, human papillomavirus. |  |  |  |

## TABLE 1.1 Summary of selected studies of risk factors for lung cancer in

 never smokers.Factors associated with lung cancer in never smokers that have been studied.
Adapted from Sun et al., 2007.

Primary tumor cannot be assessed, or tumor proven by the
TX presence of malignant cells in sputum or bronchial washings but not visualized by imaging or bronchoscopy.
T0 No evidence of primary tumor.
Tis Carcinoma in situ.
Tumor $\leq 3 \mathrm{~cm}$ in greatest dimension, surrounded by lung or visceral
T1 pleura, without bronchoscopic evidence of invasion more proximal than the lobar bronchus (i.e., not in the main bronchus).
T1a $\quad$ Tumor $\leq 2 \mathrm{~cm}$ in greatest dimension.
T1b Tumor $>2 \mathrm{~cm}$ but $\leq 3$ in greatest dimension.
T2 Tumor $>3 \mathrm{~cm}$ but $\leq 7 \mathrm{~cm}$ or tumor with any of the following features ( T 2 tumors with these features are classified T 2 a if $\leq 5 \mathrm{~cm}$ ):

Involves main bronchus.
$\geq 2 \mathrm{~cm}$ distal to the carina.
Invades visceral pleura (PL1 or PL2).
Associated with atelectasis or obstructive pneumonitis that extends to the hilar region but does not involve the entire lung.
T2a Tumor $>3 \mathrm{~cm}$ but $\leq 5 \mathrm{~cm}$ in greatest dimension.
T2b Tumor $>5 \mathrm{~cm}$ but $\leq 7 \mathrm{~cm}$ in greatest dimension.
T3 Tumor $>7 \mathrm{~cm}$ or one that directly invades any of the following:
Parietal pleural (PL3) chest wall (including superior sulcus tumors), diaphragm, phrenic nerve, mediastinal pleura, or parietal pericardium.
Tumor in the main bronchus ( $<2 \mathrm{~cm}$ distal to the carina but without involvement of the carina).
Associated atelectasis or obstructive pneumonitis of the entire lung or separate tumor nodule(s) in the same lobe.
T4 Tumor of any size that invades any of the following: Mediastinum, heart, great vessels, trachea, recurrent laryngeal nerve, esophagus, vertebral body, carina, or separate tumor nodule(s) in a different ipsilateral lobe.

| N |  |  |
| :--- | :--- | :---: |
| classificatio <br> ns |  |  |
| NX | Regional lymph nodes cannot be assessed. |  |
| N0 | No regional lymph node metastases. |  |

Metastasis in ipsilateral peribronchial and/or ipsilateral hilar lymph
N1 nodes and intrapulmonary nodes, including involvement by direct extension.
Metastasis in ipsilateral mediastinal and/or subcarinal lymph node(s).
Metastasis in contralateral mediastinal, contralateral hilar, N3 ipsilateral or contralateral scalene, or supraclavicular lymph node(s).

M
Classificati
ons
M0 No distant metastasis.
M1 Distant metastasis.
Separate tumor nodule(s) in a contralateral lobe or tumor with
M1a pleural nodules or malignant pleural (or pericardial) effusion
M1b Distant metastasis.

TNM descriptors influence Staging

|  | Nodal Involvment |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
| Primary Tumor | N0 | N1 | N2 | N3 |
| T1a | IA | IIA | IIIA | IIIB |
| T1b | IA | IIA | IIIA | IIIB |
| T2a | IB | IIA | IIIA | IIIB |
| T2b | IIA | IIB | IIIA | IIIB |
| T3 | IIB | IIIA | IIIA | IIIB |
| T4 | IIIA | IIIA | IIIB | IIIB |
| M1a | IV | IV | IV | IV |
| M1b | IV | IV | IV | IV |

## TABLE 1.2 TNM Staging Guidelines.

Adapted from ("Lung," 2010)

| Gene Symbol | Transcriptional p53 effect | $\begin{aligned} & \text { p53 } \\ & \text { RE } \end{aligned}$ | Gene Symbol | Transcriptional p53 effect | $\begin{aligned} & \text { p53 } \\ & \text { RE } \end{aligned}$ |
| :---: | :---: | :---: | :---: | :---: | :---: |
| 14.3.3sigma | Activated | Yes | MCM4 | Repressed |  |
| AP-1 | Activated | Yes | MCM6 | Repressed | Yes |
| APAF1 | Activated | Yes | MCM7 | Repressed | Yes |
| ASK | Repressed |  | MDM2 | Activated | Yes |
| AURKB | Repressed |  | MSH2 | Activated | Yes |
| BAI1 | Activated | Yes | MSH2 | Repressed |  |
| BAX | Activated | Yes | MSH6 | Repressed |  |
| BTG2 | Activated | Yes | MYC | Repressed |  |
| BUB1 | Repressed |  | NEK2 | Repressed |  |
| BUB1B | Repressed |  | NOXA | Activated | Yes |
| CCNA2 | Repressed | Yes | p53AIP1 | Activated | Yes |
| CCNE2 | Repressed | Yes | P53DINP1 | Activated | Yes |
| CD95-Fas | Activated | Yes | P53R2 | Activated | Yes |
| CDC2 | Repressed |  | P53RDL1/UNC5B | Activated | Yes |
| CDC20 | Repressed | Yes | P53RFP | Activated | Yes |
| CDC25A | Repressed | Yes | PA26 | Activated | Yes |
| CDC6 | Repressed | Yes | PAI-1 | Activated | Yes |
| CDC7 | Repressed |  | PCNA | Activated | Yes |
| CDK4 | Repressed | Yes | PG13 | Activated | Yes |
| CDT1 | Repressed |  | PIDD | Activated | Yes |
| CENPF | Repressed |  | PIG3 | Activated | Yes |
| C-FOS | Activated | Yes | PIR121 | Activated | Yes |
| CHEK1 | Repressed | Yes | POLE2 | Repressed |  |
| CON-A | Activated | Yes | PRC1 | Repressed | Yes |
| CON-B | Activated | Yes | PRIM1 | Repressed |  |
| CON-C | Activated | Yes | PSF2 | Repressed |  |
| CSPG6 | Repressed |  | PTEN | Activated | Yes |
| CSR | Activated | Yes | PTGF- <br> beta/GDF15 | Activated | Yes |
| CyclinG | Activated | Yes | PUMA | Activated | Yes |
| DUT | Repressed |  | RAD54B | Repressed |  |
| EGFR | Activated | Yes | RFC3 | Repressed |  |
| FEN1 | Repressed |  | RGC | Activated | Yes |
| GADD45 | Activated | Yes | RPS27L | Activated | Yes |
| GML | Activated | Yes | RRM2 | Repressed | Yes |
| HCAP-G | Repressed |  | S100A2 | Activated | Yes |


| HGFIN | Activated | Yes | SEMA3F | Activated | Yes |
| :---: | :---: | :---: | :---: | :---: | :---: |
| HUNTINGTIN | Activated | Yes | SMC2L1 | Repressed |  |
| IGF-BP3 | Activated | Yes | SMC4L1 | Repressed |  |
| KAI1/CD82 | Activated | Yes | STK6 | Repressed |  |
| KIF23 | Repressed |  | TOP2A | Repressed |  |
| KILLER/DR5 | Activated | Yes | TOPK | Repressed |  |
| KNTC2 | Repressed |  | TPX2 | Repressed |  |
| MAD2L1 | Repressed | Yes | TYPE IV | COLLAGENASE | Activated |
| MASPIN/SERPINB5 | Activated | Yes | UBE2C | Repressed |  |
| MCM2 | Repressed | Yes | WAF1 | Activated | Yes |
| MCM3 | Repressed | Yes | WTH3 | Activated | Yes |

## TABLE 1.3 Transcriptional Targets of p53.

Sourced from (Olivier et al., 2002; Spurgers et al., 2006; Yu \& Zhang, 2005)

| Proteins found bound to promoter region of |  |
| :--- | :--- |
|  | p53 |
| pol2 | GATA |
| NFkB | IRF1 |
| TFR | MAX |
| YY1 | JUN |
| STAT3 | GABP |
| CEBPB | PAX5 |
| TAF1 | SIX5 |
| SP1 | TCF4 |
| TBP | p300 |
| POU2F2 | ELK4 |
| HEY1 | FOXA2 |
| AP2 $Y$ | FOXA1 |
| OCT2 | CFOS |
| RXR $\alpha$ | BCL3 |
| Sin3a | BCLAF1 |
| HMGn3 | EGR1 |
| CMYC | Er $\alpha$ |
| NF-YB | BRCA1 |
| ETS1 |  |

TABLE 1.4 Factors that have been found to regulate TP53 Transcription.
Data from ("Identification and analysis of functional elements in 1\% of the human genome by the ENCODE pilot project," 2007).

| Name | Agent Class | Target(s) | Tumor Types | FDA Approval |
| :---: | :---: | :---: | :---: | :---: |
| Bevacizumab (Avastin) | Monoclonal Antibody | VEGF | Colorectal cancer | 2004 |
|  |  |  | NSCLC | 2006 |
|  |  |  | Breast cancer | 2008 |
| $\begin{aligned} & \text { Cancertinib (CI- } \\ & 1033) \end{aligned}$ | Small <br> Molecule TKI | Pan-erbB | Phase II - SCC, ovarian, metastatic breast cancer |  |
| Cetuximab (Erbitux) | Monoclonal Antibody | EGFR | Colorectal cancer | 2004 |
|  |  |  | HNSCC <br> Phase III pancreatic cancer, NSCLC Phase II - HCC | 2006 |
| Crizotinib (Xalkori) | Small <br> Molecule TKI | ALK | NSCLC | 2011 |
| dasatinib <br> (Spryce) | Small <br> Molecule TKI | $\begin{gathered} \text { BCR-Abl, } \\ \text { Src } \end{gathered}$ | CML, ALL | 2010 |
| EKB-569 | Small <br> Molecule TKI | EGFR | Phase II - advanced colorectal cancer, NSCLC |  |
| Erlotinib <br> (Tarceva) | Small Molecule TKI | EGFR | NSCLC | 2004 |
|  |  |  | Phase II - HCC <br> Pancreatic cancer | 2005 |
| Gefitinib (Iressa) | Small <br> Molecule TKI | EGFR | NSCLC | 2003 |
|  |  |  | Phase I HCC |  |
| Imatinib <br> (Gleevec) | Small <br> Molecule TKI | $\begin{gathered} \text { KIT, } \\ \text { PDGFR, } \\ \text { BCR-ABL } \end{gathered}$ | CML, ALL, GIST | 2002 |
| Lapatinib (Tykerb) | Small <br> Molecule TKI | EGFR, HER-2 | Breast cancer | 2007 |
| Matuzumab <br> (EMD 72000) | Monoclonal Antibody | EGFR | Phase I/II - NSCLC, ovarian, pancreatic cancer |  |
| nilotinib <br> (Tasigna) | Small <br> Molecule TKI | $\begin{gathered} \text { BCR-Abl, } \\ \text { KIT, LCK, } \\ \text { EPHA, } \end{gathered}$ | CML | 2010 |



TABLE 1.5 TKIs.
Data sourced from (Lowery \& Han, 2011; O'Hare et al., 2009)

| SMAC <br> Compound | Pharmaceutical <br> Company | Clinical <br> Trial | Clinical Trial <br> $\#$ |
| :---: | :---: | :---: | :---: |
| AT-406 | Ascenta | Phase I | NCT01265199 |
| GDC0917 | Genentech | Phase I | NCT01078649 |
|  | Phase I | NCT01226277 |  |
| HGS1029 | Human Genome | Phase I | NCT00708006 |
|  | Sciences | Phase I | NCT01013818 |
| LCL161 | Novartis | Phase I | NCT01240655 |
|  |  | Phase I/II | NCT01188499 |
| TL32711 | TetraLogic | Phase I | NCT00993239 |
| JP1201 | Joyant | none |  |

TABLE 1.6 SMAC MIMETIC/IAP ANTAGONISTS IN DEVELOPMENT.

| Estimated New Cases* |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  |  |  | Males | Females |  |  |  |
| Prostate | 240,890 | 29\% |  |  | Breast | 230,480 | 30\% |
| Lung \& bronchus | 115,060 | 14\% |  |  | Lung \& bronchus | 106,070 | 14\% |
| Colon \& rectum | 71,850 | 9\% |  |  | Colon \& rectum | 69,380 | 9\% |
| Urinary bladder | 52,020 | 6\% |  |  | Uterine corpus | 46,470 | 6\% |
| Melanoma of the skin | 40,010 | 5\% |  |  | Thyroid | 36,550 | 5\% |
| Kidney \& renal petvis | 37,120 | 5\% |  |  | Non-Hodgkin lymphoma | 30,300 | 4\% |
| Non-Hodgkin lymphoma | 36,060 | 4\% |  |  | Melanoma of the skin | 30,220 | 4\% |
| Oral cavity \& pharynx | 27.710 | 3\% |  |  | Kidney \& renal pelvis | 23,800 | 3\% |
| Leukemia | 25,320 | 3\% |  |  | Ovary | 21.990 | 3\% |
| Pancreas | 22,050 | 3\% |  |  | Pancreas | 21,980 | 3\% |
| All Sites | 822,300 | 100\% |  |  | All Sites | 774,370 | 100\% |
| Estimated Deaths |  |  |  |  |  |  |  |
|  |  |  | Males | Females |  |  |  |
| Lung \& bronchus | 85,600 | 28\% |  |  | Lung \& bronchus | 71,340 | 26\% |
| Prostate | 33,720 | 11\% |  |  | Breast | 39.520 | 15\% |
| Colon \& rectum | 25,250 | 8\% |  |  | Colon \& rectum | 24,130 | 9\% |
| Pancreas | 19,360 | 6\% |  |  | Pancreas | 18,300 | 7\% |
| Liver \& intrahepatic bile duct | 13,260 | 4\% |  |  | Ovary | 15,460 | 6\% |
| Leukemia | 12,740 | 4\% |  |  | Non-Hodgkin lymphoma | 9,570 | 4\% |
| Esophagus | 11,910 | 4\% |  |  | Leukernia | 9,040 | 3\% |
| Urinary bladder | 10,670 | 4\% |  |  | Uterine Corpus | 8.120 | 3\% |
| Non-Hodgkin lymphoma | 9,750 | 3\% |  |  | Liver \& intrahepatic bile duct | 6,330 | 2\% |
| Kidney \& renal pelvis | 8.270 | 3\% |  |  | Brain \& other nervous system | 5,670 | 2\% |
| All Sites | 300,430 | 100\% |  |  | All Sites | 271,520 | 100\% |

FIGURE 1.1 Ten Leading Cancer Types for the Estimated New Cancer Cases and Deaths by Sex, United States, 2011.

* Estimates are rounded to the nearest 10 and exclude basal and squamous cell skin cancers and in situ carcinoma except urinary bladder. Adapted from (Siegel, et al., 2011).


FIGURE 1.2 Common somatic mutations in lung cancer.
Hight of the bars indicates the number of mutations for each gene in 188 tumor/normal pairs. Standard, gene-specific and category-based tests were used for this analysis. TP53, Kras, STK11/LKB1, and EGFR are the most common mutations found. Adapted from (Ding, et al., 2008).


## Figure 1.3 Hallmarks of Cancer.

The hallmarks of cancer include ten biological capabilities acquired during the multistep development of human tumors, giving a framework for rationalizing the complexity of cancer. They include sustaining proliferative signaling, evading growth suppressors, resisting cell death, being able to replicate indefinitely, inducing angiogenesis, activating invasion and metastisis, genetic instability, inflammation, evading immune destruction, and reprogramming of metabolic pathways. Modified from (Hanahan \& Weinberg, 2011).


FIGURE 1.4 Characteristics of apoptosis and necrosis highlighting the differences between the two forms of cell death.

Apoptosis is characterized by cellular shrinkage, chromatin condensation and fragmentation, membrane blebbing, and clearance by macrophages in the absence of inflammation. Necrosis is characterized by cell swelling, leakage of cytoplasmic contents, some membrane blebbing, cellular and nuclear lysis, and clearance through induction of inflammation. Modified from (Van Cruchten \& Van den Broeck, 2002).


## FIGURE 1.5 Human Caspase Family.

There are three functional groups within the caspases family, group I caspases are not believed to be involved in apoptosis, but are involved in the biogenesis of active IL-1b. Group II caspases are the initiator caspases, which are directly activated by cellular stresses, and activate downstream executioner caspases or other initiator caspases to amplify the apoptotic signal. Group III caspases are the executioner caspases which go on to cleave cellular substrates such as ICAD, PARP, as well as other targets and are responsible for the death of a cell. Adapted from (Lavrik \& Krammer, 2009).


## FIGURE 1.6 Extrinsic Apoptotic Pathway.

Activation of death receptors, TNFR1, DR4/DR5, FAS by binding of cognate ligands (TNF $\alpha$, TRAIL, FasL) activates the death inducing complex (DISC) which includes FADD and caspase-8. In some cases activation of caspase-8 is not sufficient for induction of apoptosis, but caspase-8 can cleave Bid to form t-Bid which amplifies the pro-death signal through the mitochondria resulting in apoptosis. Adapted from Cell Signaling


## FIGURE 1.7 Intrinsic Apoptotic Pathway.

The balance between the pro-apoptotic (BAX, BAK, Bad, $\mathrm{BCL}_{\mathrm{xs}}$, Bid, Bim, PUMA, and NOXA) and anti-apoptotic BCL-2 (BCL-2, BCL ${ }_{x L}$, MCL-1) family members determines if cytochrome c and other apoptogenic activators are released from the mitochondria. Release of cytochrome c leads to activation of caspase-9 through complex formation of APAF-1, cytochrome c, and caspase-9 (the apoptosome). Activation of caspase-9 is not dependent on caspase-9, and
results in activation of downstream caspase-3,-6, and -7 and ultimately cell death.
Adapted from Cell Signaling.


FIGURE 1.8 Human Inhibitors of Apoptosis Protein Family.
The human IAP family consists of 8 proteins, the best studied of this family are XIAP, cIAP1, and cIAP2. XIAP is the only IAP that can inhibit active caspases catalytic activity. cIAP1 and cIAP2 are recruited to the TNFR complex I by direct interactions with TRAF2, and regulate NF-кB and JNK activation by TNFR1, as well as inhibit activation of caspases-8 by inhibiting RIPK1 being incorporated
into complex II. Survivin regulates the cell cycle by direct tubulin interactions.
Adapted from (Srinivasula \& Ashwell, 2008).


FIGURE 1.9 The miRNA and siRNA pathways of RNAi in mammals.
Primary microRNAs (pri-miRNAs) are transcribed by RNA polymerases and are trimmed by the microprocessor complex (comprising Drosha and microprocessor complex subunit DCGR8) into ~70 nucleotide precursors, called pre-miRNAs (left side of the figure). miRNAs can also be processed from spliced short introns
(known as mirtrons). pre-miRNAs contain a loop and usually have interspersed mismatches along the duplex. pre-miRNAs associate with exportin 5 and are exported to the cytoplasm, where a complex that contains Dicer, TAR RNAbinding protein (TRBP) and PACT processes the pre-miRNAs into miRNAmiRNA* duplexes. The duplex associates with an Argonaute (AGO) protein within the precursor RNAi-induced silencing complex (pre-RISC). One strand of the duplex (the passenger strand) is removed. The mature RISC contains the guide strand, which directs the complex to the target mRNA for post-transcriptional gene silencing. The 'seed' region of a miRNA is indicated; in RNAi trigger design, the off-target potential of this sequence needs to be considered. Long dsRNAs (right side of the figure) are processed by Dicer, TRBP and PACT into small interfering RNAs (siRNAs). siRNAs are 20-24-mer RNAs and harbor 3'OH and 5' phosphate $\left(\mathrm{PO}_{4}\right)$ groups, with $3^{\prime}$ dinucleotide overhangs. Within the pre-RISC complex, an AGO protein cleaves the passenger siRNA strand. Then, the mature RISC, containing an AGO protein and the guide strand, associates with the target mRNA for cleavage. The inset shows the properties of siRNAs. The thermodynamic stability of the terminal sequences will direct strand loading. Like naturally occurring or artificially engineered miRNAs, the potential 'seed' region can be a source for miRNA-like off-target silencing. shRNA, short hairpin RNA. Adapted from (Davidson \& McCray, 2011).

## CHAPTER TWO

Materials and Methods

### 2.1 MATERIALS

### 2.1.1 Cell Lines

With the exception of A549, Calu1, Calu3, Calu6, SOAS-2, T47D, MIA PaCa2, MDA-MB-231, Panc1, MCF7, DU145, and Hs766 which were purchased from the American Type Culture Collection (ATCC), all tumor cell lines were established by Drs Minna and Gazdar and are deposited at the ATCC, or are available upon request (A. F. Gazdar et al., 1998; Phelps et al., 1996; Ramirez et al., 2004; Sato, et al., 2006). Lung cancer cell lines that were established at the National Cancer Institute are denoted with the prefix H and lung cancer cell lines that were established at the UTSW Hamon Center for Therapeutic Oncology Research are annotated as HCC (Adi F. Gazdar, Girard, Lockwood, Lam, \& Minna, 2010). Human bronchial epithelial cells were immortalized using ectopic expression of cdk4 and hTERT, denoted by -KT at the end of the name were established by our laboratories (Ramirez, et al., 2004). Defined oncogenic changes, Kras G12V and p53 shRNA, were introduced in HBEC3KT cells and tumorigenic clones (clone 1, clone 5) isolated by soft agar formation (Sato, et al., 2006)

### 2.1.2 SMALL MOLECULE DRUG LIBRARY

Cisplatin ( $1 \mathrm{mg} / \mathrm{mL}$; Teva Parenteral, Irvine, CA), carboplatin ( $10 \mathrm{mg} / \mathrm{mL}$; Bristol-Myers Squibb, New York City, New York), doxorubicin (2 mg/mL; Teva Parenteral, Irvine, CA), gemcitabine (Eli Lilly and Company, Indianapolis, IN), paclitaxel (Bristol-Myers Squibb, New York City, New York), pemetrexed (Eli Lilly and Company, Indianapolis, IN), vinorelbine (Pierre Fabre Company, Castres, France), and erlotinib (OSI Pharmaceuticals, Melville, NY) were purchased at the University of Texas Southwestern Medical Center Campus Pharmacy. Cisplatin, carboplatin, paclitaxel, and pemetrexed were stored as received at room temperature; pemetrexed was dissolved in $0.9 \%$ saline fresh each time before use; gemcitabine was dissolved in $0.9 \%$ saline at $38 \mathrm{mg} / \mathrm{mL}$ and stored at room temperature. Doxorubicin and vinorelbine were stored as received at $4^{\circ} \mathrm{C}$; erlotinib was dissolved in DMSO at $10 \mu \mathrm{M}$ and stored at $4^{\circ} \mathrm{C}$. SMAC mimetic (JP1201), diazonamide A (JP1036), and JP1798 (a diazonamide derivative) were obtained from Joyant pharmaceuticals, dissolved in DMSO at 10 $\mu \mathrm{M}$ and stored at $-20^{\circ} \mathrm{C}$, with the exception of JP 1798 which was stored at $4^{\circ} \mathrm{C}$. Peloruside A was obtained from Reata Pharmaceuticals, dissolved in DMSO at 10 $\mu \mathrm{M}$ and stored at $-20^{\circ} \mathrm{C}$.
2.2 Methods

### 2.2.1 Cell Culture

All cancer cell lines and tumorigenic HBEC clones were grown in RPMI1640 medium (Life Technologies Inc., Rockville, MD) supplemented with 5\%
fetal bovine serum (FBS). HBECs were grown in Keratinocyte Serum-Free Medium (KSFM) supplemented with bovine pituitary extract and recombinant human epidermal growth factor (Gibco, Carlsbad, CA). All cell lines were grown in a humidified atmosphere with $5 \% \mathrm{CO} 2$, at $37^{\circ} \mathrm{C}$, and have been DNA fingerprinted for provenance using the PowerPlex 1.2 kit (Promega) and confirmed to be the same as the DNA fingerprint library maintained by ATCC and the Minna/Gazdar lab (the primary source of the lines), and confirmed to be free of mycoplasma by the e-Myco kit (Boca Scientific).

### 2.2.2 DRUG RESPONSE CURVES

Cells were plated on day zero, so that by day 5, maximal MTS signal will be observed in the untreated cells. Chemotherapies were given on day one as fourfold dilutions with a maximum dose of 1000 nM for JP1306, JP1798, paclitaxel, peloruside, and vinorelbine, 2000 nM for gemcitabine and doxorubicin, or 100 $\mu \mathrm{M}$ for carboplatin, cisplatin, erlotinib, pemetrexed, and JP1201 alone. $10 \mu \mathrm{M}$ or 100 nM of JP1201 was used in combination assays as indicated. Cells were incubated for four days then relative cell number was determined with MTS (Promega, Madison, WI, final concentration $333 \mu \mathrm{~g} / \mathrm{ml}$ ), incubating for 1 to 3 hours at $37^{\circ} \mathrm{C}$, and reading absorbance at 490 nm plate reader (Spectra Max 190, Molecular Devices, Downington, PA). Each experiment contained eight replicates per concentration and the entire assay was performed in multiple replicates ( $\mathrm{n} \geq$
4). Drug sensitivity curves and $\mathrm{IC}_{50} \mathrm{~S}$ were calculated using in-house software (DIVISA).

### 2.2.3 Liquid Colony Formation Assay

Cells were seeded at 500 cells per well in 6 well dishes. The appropriate concentrations of drug were prepared from stock solutions in RPMI-1640 medium with $5 \%$ fetal bovine serum, for 10-14 days depending on the cell line. At the end of the assay, medium was aspirated and cells were fixed and stained with $0.5 \%$ methylene blue in $50 \%$ ethanol for 30 minutes. After staining, wells were washed and black and white images of the plates were taken using a ChemiDoc XRS+ imager (Quantity One software v4.6.5, BioRad, Hercules, CA). Colony counts are averages of triplicate wells done in duplicate over a two week period.

### 2.2.4 AnNexin V FACS Analysis

Induction of apoptosis was measured by flow cytometry using an Annexin V-FITC apoptosis kit (556547, BD Pharmingen) following the manufacturers guidelines. Cells were plated, allowed 24 hours to recover, and then given various doses of vinorelbine with or without $10 \mu \mathrm{M} \mathrm{JP1201}$. Florescence activated cell sorting (FACS) analysis was preformed 48 hours after treatment, all florescence activated cell sorting was performed on a FACScan (Becton-Dickinson, Franklin Lakes, NJ) or four laser BD LSR II (BD Biosciences, San Jose, CA) flow cytometers. Flow cytometry data was analyzed using FlowJo (FlowJo version 8.02 Treestar, Ashland, OR).
2.2.5 96-WELL TRANSFECTIONS WITH DRUG RESPONSE

For reverse transfection, $0.5 \mu \mathrm{l}$ of $20 \mu \mathrm{M}$ stock of each agRNA or siRNA in a volume of $20 \mu \mathrm{l}$ of serum free RPMI was delivered to each well of 96 well plate using a multichannel repeat pipetter. $0.25 \mu \mathrm{l}$ of either Dharmafect 1 or 3 (Dharmacon) in $9.75 \mu \mathrm{l}$ of RPMI was then delivered into each well again using multichannel repeat pipette. RNA-lipid complexes were allowed to form during a 20-30 minute incubation. Following the incubation 8,000 cells were added to each well in RPMI with 5\% FBS, total volume per well $100 \mu$ l. For dose response to agRNA, complexes were prepared at highest concentration (either 100 nM or 25 nM ) and then complexes were eight-fold serially diluted. Drugs were administered 24 hours after transfection as described in section 2.2.2.

### 2.2.6 Western Blot

siRNA mediated knockdowns were performed as reverse transfections with 25 nM final siRNA concentration, and a 1:2 lipid to oligo ratio. RNA-lipid complexes were formed in 6 well plates in a volume of 1 ml for a 20 minute incubation period, and then $5 \times 10^{5}$ cells were plated per well in RPMI with $5 \%$ FBS in a final volume of 3 ml . 48 hours later, cells were lysed in lysis buffer (40 $\mu \mathrm{M}$ HEPES-NaOH [pH 7.4], $150 \mu \mathrm{M} \mathrm{NaCl}, 0.5 \%$ Sodium deoxycholate, $1 \%$ Nonidet P-40, 0.1\% SDS, and Complete mini protease inhibitor [Roche, Mannheim, Germany]), protein concentration determined by Bradford assay (BioRad, Hercules, CA). Protein concentrations were normalized to total protein, and

SDS-PAGE, $10-15 \%$ acrylamide, was performed followed by western blotting of primary antibody (cIAP1, 3180A-100, BioVision, Mountain View, CA; cIAP2, sc-7944, Santa Cruz Biotechnology, Santa Cruz, CA; XIAP, 2042, Cell Signaling, Danvers, MA; HSP90, sc-7947, Santa Cruz Biotechnology). The membranes were then developed with peroxidase-labeled antibodies (Thermo Fisher Scientific, Waltham, MA) by Super Signal chemiluminescence substrate (Thermo Fisher Scientific, Waltham, MA). HSP90 levels were used as a control for equal protein loading.

### 2.2.7 ENZYME-LINKED IMMUNOSORBANT ASSAY (ELISA)

Roughly 100,000 cells were plated per well in a 6 well plate and allowed to adhere overnight. Media was removed and replaced with serum free media containing 2000 nM gemcitabine, 1000 nM vinorelbine, $10 \mu \mathrm{M}$ JP1201, or 1000 nM vinorelbine $+10 \mu \mathrm{M}$ JP1201. $300 \mu \mathrm{~L}$ conditioned media was removed at 12, 24, 48, 72, and 96 hours after drug treatment. ELISAs were performed per manufacturer instructions (Abcam, Cambridge, MA). Samples were run in triplicate and data shown is the average of at least two separate experiments.

### 2.2.8 Mouse Xenograft Treatment Studies

Mouse work followed an IACUC approved protocol. NCI-H1395 and NCI-H157 cells were gently trypsinized, washed, and counted using trypan blue exclusion to assess viability. Cell suspensions with viability greater than 95\% were used in animal studies. Subcutaneous tumors were established in

NOD/SCID mice as described (Dineen et al., 2010). Briefly, NCI-H1395 or NCIH157 cells ( $1 \times 10^{6}$ in $100 \mu \mathrm{~L}$ ) were injected subcutaneously on the left flank. Animals were monitored three times a week and tumors measured with digital calipers. Tumor volumes were calculated using the formula ( D * $2 \mathrm{~d} * 0.52$ ), where D is the largest diameter and d is the shortest (Euhus, Hudd, LaRegina, \& Johnson, 1986). At sacrifice, tumors were harvested and fixed in formalin. Treatment groups ( 8 mice per group) consisted of saline, $25 \mathrm{mg} / \mathrm{kg}$ gemcitabine, $2.4 \mathrm{mg} / \mathrm{kg}$ vinorelbine, $6 \mathrm{mg} / \mathrm{kg}$ JP1201, $6 \mathrm{mg} / \mathrm{kg}$ JP1201 + $25 \mathrm{mg} / \mathrm{kg}$ gemcitabine, $6 \mathrm{mg} / \mathrm{kg}$ JP1201 + $2.4 \mathrm{mg} / \mathrm{kg}$ vinorelbine, $12.5 \mathrm{mg} / \mathrm{kg}$ erlotinib, or $12.5 \mathrm{mg} / \mathrm{kg}$ erlotinib $+6 \mathrm{mg} / \mathrm{kg}$ JP1201; each injection given in a volume of 100 $\mu \mathrm{L}$ administered intraperitoneally (Bonfil, Russo, Binda, Delgado, \& Vincenti, 2002; Dineen, et al., 2010). Saline, gemcitabine, and JP1201 were given three times a week, vinorelbine was given twice a week to minimize toxicity, and erlotinib was given by oral gavage every 12 hours (Bonfil, et al., 2002; Dineen, et al., 2010).

### 2.2.9 QPCR ANALYSIS OF SIRNA KNOCKDOWN EFFICIENCY

Transfections were performed as described above with the exception of RNA-lipid complexes were formed in 6 well plates in a volume of 1 ml for a 20 minute incubation period, cells were plated at $70 \%$ confluency. 24 hours later, cells were harvested and total RNA prepared (RNeasy Plus Mini Kit, Qiagen, Hilden, Germany). cDNA was synthesized from $1 \mu$ g total RNA using the iScript
cDNA synthesis kit (BioRad, Hercules, CA). Gene specific TaqMan probes (Applied Biosystems, Foster City, CA) were used to quantitate GAPDH, cIAP1, cIAP2, XIAP, Caspase-3, $-4,-8$, and -9 , RIPK1, TNFR1, and TNF $\alpha$ levels in biological duplicates as well as duplicate samples of siRNA transfected H1395 cells. The $2^{-\Delta \Delta C T}$ method was used to calculate relative expression levels (Livak \& Schmittgen, 2001).

### 2.2.10 MicROSCOPY

Formalin-fixed tissues were embedded in paraffin and cut in $10 \mu \mathrm{~m}$ sections and stained with hematoxylin \& eosin. Immunofluorescent staining of xenograft tumor sections for rabbit anti- human TNF $\alpha$ (ab6671, Abcam, Cambridge, MA) was performed at $5 \mu \mathrm{~g} / \mathrm{mL}$ conjugated to rabbit-FITC secondary antibody (11-095-144, Jackson ImmunoResearch Laboratories Inc, West Grove, PA). Quantification of TNF $\alpha$ staining for each treatment group was performed by taking the average FITC signal across three fields each from three separate xenograft tumors. TUNEL staining was performed per manufacturer instructions (Promega, Madison, WI) on paraffin embedded tumor sections from three tumors per treatment group with data averaged from three images per slide, three slides per treatment group. Images of stained slides were taken using an Eclipse TE2000 epifluorescent microscope (Nikon). ImageJ (NIH) software was used to produce overlaid images of DAPI and antibody staining.
2.2.11 Luciferase Reporter Assay

Pathway analysis was performed using the Stress and Toxicity Cignal Finder 10 pathway reporter array (SA Biosciences, Fredrick, MD) following the manufacturer's instructions. Sixteen hours after cells were reverse transfected, they were treated with $1 \mu \mathrm{M}$ vinorelbine with $10 \mu \mathrm{M} \mathrm{JP1201} \mathrm{or} 10 \mu \mathrm{M} \mathrm{JP1201}$ as control, then incubated for an additional 24 hr. Luciferase activity was measured using the Dual Luciferase Assay system (Promega, Madison, WI) on a FLUOstar omega (BMG Biotech, Offenburg, Germany). Firefly luciferase was the experimental reporter and Renilla luciferase was the normalizing reporter, samples were further normalized to non-transfected control cells.

### 2.2.12 Microarray

Transcript expression data for most lung cancer cell lines has been previously generated in the Minna Lab by both Affymetrix (U133 plus 2.0 and U133AB chips) and Illumina (WG6-V2 and V3 BeadChips) array platforms. MATRIX (MicroArray Transformation in Microsoft Excel) software 1.482 is a Microsoft Visual Basic program with Microsoft Excel interface that was created by Dr. Luc Girard (luc.girard@utsouthwestern.edu) in the Minna Lab, was used to import and analyze microarray expression data. Three bioinformatics functions contained within MATRIX were used in these studies; gene correlation, subarray with a partial gene list, and class prediction. The gene correlation function calculates pearson correlations for sample properties (such as drug response to chemotherapy combinations) to gene expression. The subarray
with partial gene list function creates a new matrix (.mtx) file with a user defined gene list, which was used to create a subarray containing only genes that are involved in the NF- $\kappa \mathrm{B}$ and apoptosis pathways. The results from both of these two functions can be further clustered using hierarchical clustering analysis. The class prediction function takes class data input (synergism [given a value of 1] or antagonism [given a value of 0 ]) for a "training" set of cell lines and creates a signature based on gene expression patterns from the cell lines indicated, and then applies that signature to predict synergism or antagonism in a "test" set of cell lines, to which the training set can be added to see how accurate the predictions are.
2.3 Statistics

### 2.3.1 Combination Index

Combination indicies (CI) for the drug sensitivity data were calculated using the Chou-Talay method (Chou \& Rideout, 1991). Briefly, an effect level was chosen (40\%) and doses were calculated for each drug alone (where DX1 is the chemotherapy and DX2 is JP1201), then doses were measured for each drug in combination with JP1201 that gave the chosen effect level (D1, D2). CI were then calculated using the following equation:

Where CI<1 Synergy, CI=1 Additivity, and CI>1 Antagonism. Standard deviations were calculated based on drug sensitivity data. Data from the xenograft studies were analyzed using GraphPad software (GraphPad Prism version 5.02, San Diego, CA, www.graphpad.com). Results are expressed as mean $\pm$ SEM. Data was analyzed by t-test or ANOVA and results are considered significant at $\mathrm{p}<0.05$.

### 2.3.2 Analysis of Variance (ANOVA)

ANOVA is a statistical test to determine if more than two groups are different by calculating if the variance within a group is different between the variance between groups.

### 2.3.3 Pearson Correlation

Pearson correlation (r) is a statistic test for linear dependence of two variables, values range from -1 to 1 , is defined as the covariance of two variables divided by the product of their standard deviations, or for a given sample

## CHAPTER THREE

## PLATINUM BASED COMBINATION CHEMOTHERAPY

### 3.1 Introduction

Chemotherapy is a treatment option for tumors that are at least stage 2, which accounts for roughly $85 \%$ of NSCLC patients. The current mainstay of chemotherapy treatments for NSCLC consists of platinum based doublets, where either cisplatin or carboplatin are used in conjunction with a third generation chemotherapy agent, usually paclitaxel, gemcitabine, pemetrexed, vinorelbine, or docetaxel. These doublets arose from clinical trials where cisplatin was used in combination with new third generation chemotherapy and compared to best supportive care, or the third generation chemotherapy alone, or an older platinum based doublet (Non-small Cell Lung Cancer Collaborative, 1995; Pass, et al., 2010; Pass, et al., 1992). The most common rational for combining these agents was to pair chemotherapies that had different dose limiting toxicities. Since all these chemotherapies were already FDA approved, there was little to no preclinical testing to address these combinations.

Two major trends in therapeutic oncology research are developing new anti-cancer agents, or personalizing existing therapies. When references are made to personalized therapy what is meant is the ability to sample a patient's tumor and based on molecular profiling of that sample be able to determine which chemotherapeutic regimen that patient's tumor would respond best to.

In order to be able to personalize therapy, the range of responses for a particular cancer type need to be well defined in a large sample set, i.e. a large panel of cell lines. The responses then need to be correlated to other measurable parameters that also define the tumor state, such as mRNA gene expression profiles, protein expression and phosphorylation data, and other similar sets of data. The resulting correlations between expression profiles and response data (often called signatures of resistance or sensitivity) need then to be verified in a separate large sample set, to see how well the signatures predict response in a new set of samples. If the signatures predict response fairly accurately in the test set, then the signatures are then tested against different types of sets of data, response of cell line xenografts in mice, response of primary tumor samples grown solely as xenografts in mice, blinded retrospective analysis of patient data where expression profiles are available, etc.

In order to make combinations of chemotherapy more effective, it is important to know what effect current combinations have in the model system that will be used. To do this, three platinum based doublets were screened across a large panel of NSCLC cell lines, approximately 50 lines, initially using MTS based 96-well plate drug response assays to catalogue the responses to the combinations gemcitabine + cisplatin, paclitaxel + carboplatin, and pemetrexed + cisplatin.

### 3.2 Methods

In order to best model the combinations, gemcitabine + cisplatin, paclitaxel + carboplatin, and pemetrexed + cisplatin, the ratio of non-platinum agent to platinum agent was calculated for each combination, for example, gemcitabine + cisplatin is usually dosed at $1250 \mathrm{mg} / \mathrm{m}^{2}$ gemcitabine and 100 $\mathrm{mg} / \mathrm{m}^{2}$ cisplatin (Cardenal, et al., 1999).
molar ratio the corresponding amount of cisplatin was calculated at 140 nM .
Using these values the molar ration was calculated to verify these amounts.

With these ratios set for each combination, the non-platinum drug was set as the limiting reagent in each case; the highest concentration of platinum agent was calculated based on the in vitro highest dose of each non platinum agent (Table 3.1).

### 3.3 Results

A panel of 53 NSCLC cell lines was tested for drug response phenotypes to the combinations of gemcitabine with cisplatin, pemetrexed with cisplatin, and paclitaxel with carboplatin using an MTS based assay to determine cell viability relative to a control population of cells that had undergone the same handling as the drug treated cells. There was great heterogeneity in response to these combinations across the panel of cell lines (Table 3.2). When the data across the whole panel is shown as a dot plot where the $\mathrm{IC}_{50}$ for each cell line is a dot and the x -axis is the $\log _{10}$ of the concentration of chemotherapy, the overall spread of $\mathrm{IC}_{50}$ s of the panel of NSCLCs does not change; however, overall the spread shifts to the left with less cell lines being completely resistant to treatment (Figure 3.1). The combination of pemetrexed + cisplatin is the only combination in which no cell lines are resistant up to the highest dose of chemotherapy given.

Approximately 26\% of the cell lines tested responded better to the combination of gemcitabine + cisplatin than the drugs as single agents, while 8\% seemed to have a better response to either agent singularly.
$15 \%$ of cell lines respond better to the combination of paclitaxel + carboplatin than to either drug as a single agent. While 26\% of cell lines responded better to single agent paclitaxel or carboplatin treatment than to the combination, the majority of cell lines responded similarly to single agent paclitaxel as to the combination of paclitaxel + carboplatin.

Pemetrexed with cisplatin was the most "successful" combination regimen explored in this study in that over 50\% (52\%) of the cell lines tested responded better to the combination, than to either drug as a single agent. Conversely, this combination also has the highest rate of cell lines responding better to either agent as a single agent than the combination with $23 \%$ of cell lines responding better to single agent treatment. These data suggest that while pemetrexed given in combination with cisplatin can be a very successful treatment for some patients, it might also be detrimental to other patients, which encourages our goal of being able to predict which therapy is best suited for each patient.
$6 \%$ of the cell lines responded better to all three combinations. $4 \%$ of the cell lines responded better to both the combination of paclitaxel with carboplatin and pemetrexed with cisplatin, but not with gemcitabine with cisplatin. $20 \%$ of the cell lines responded better to the combination of cisplatin with gemcitabine or pemetrexed, but not to the combination of paclitaxel and carboplatin. These data suggest that combining DNA damage agents or drugs that result in similar cell cycle checkpoint/apoptototic stimuli are more commonly successful in treating
lung cancer than combining drugs that target different steps in the cell cycle or initiate apoptosis in different manners. Only one cell line tested responded better to these chemotherapies as single agents than to any of the combinations tested.

### 3.3.2 Statistical Analysis for Synergy

These data, along with single agent drug response data within the lab, were used to calculate the combination index (CI) at the $40 \%$ cell death as the effect level (Chou \& Rideout, 1991). 32\% of cell lines tested showed synergism to the combination of paclitaxel and carboplatin, while $34 \%$ of the cell lines show antagonism to the combination, and the remaining $34 \%$ show additivity or no real effect between the combination of these two agents (Figure 3.2). Surprisingly most of the cell lines (60\%) showed synergism to the combination of gemcitabine with cisplatin, while only $17 \%$ showed antagonism, and the remaining $23 \%$ showed additivity. The combination of pemetrexed with cisplatin showed synergism in $40 \%$ of the cell lines tested, and $38 \%$ of the cell lines showed antagonism, and only $22 \%$ showed additivity.

While it would be easy to assume that seemed to have a response as seen by $\mathrm{IC}_{50}$ directly or in fold change; however, that is just taking one variable into consideration while there are two drugs to consider for each combination. And while that assumption might work out decently well for the combinations of paclitaxel + carboplatin or gemcitabine + cisplatin because the platinum based
drug is given at a much lower level than single agent activity is seen on in vitro, the assumption does not work out well at all for the combination of pemetrexed + cisplatin because both agents are given on the micromolar $\left(1 \times 10^{-6} \mathrm{M}\right)$ scale as single agents as well as in the combination. Another factor to consider is the experimental error involved in the drug dilution and comparing drug data collected over time, there can be up to a fourfold variation in the drug responses seen, so when evaluating these data by fold decrease in $\mathrm{IC}_{50}$ of one chemotherapy anything over a fourfold decrease in $\mathrm{IC}_{50}$ is considered a real effect; however this consideration is not able to be applied to the CI data, which is why more cell lines seem to be responding synergistically to the combination.

### 3.3.3 Confirmation of MTS data using colony formation

Upon repeating drug treatment using colony formation as the readout instead of MTS for a subset of cell lines, $\mathrm{IC}_{50}$ values were similar between the two assays, cell lines were always more sensitive to paclitaxel + carboplatin in colony formation (Table 3.3). This is likely due to the longer time frame that cells are exposed to paclitaxel in colony formation making the cells seem more sensitive, but cell death from paclitaxel is highly time sensitive. Another factor at play is the short time span of the MTS assay and that during the 96 hours that cells are exposed to drug, most cell lines only go through two population doublings, or one for the extremely slow growing cell lines, which makes these
slow growing cell lines seem artificially resistant to paclitaxel in an MTS assay especially when compared to drug response determined by colony formation.

### 3.3.4 Predictive Value of Signatures of Synergy

Using synergy and antagonism as fixed integers of 1 and 0 respectively, the ability of these data to create signatures has been explored using MATRIX. Unfortunately, using microarray data for this is not predictive by leave one out cross validation or in a test set where the results are already known. Many statistical approaches using MATRIX were tried; random forest, k nearest neighbor, support vector, and penalized linear regression (Figure 3.6-3.8).

One of the possible reasons for the lack of predictability from these data is that most prediction algorithms use two groups to make the predictions, however these data don't fit a two group model, there isn't just a sensitive and resistant group, instead there is more a general continuum of response to the combinations.

### 3.4 Discussion

Most patients that are seen for advanced NSCLC are treated with a platinum based chemotherapy combination regimen as part of their treatment course. And with the 15\% 5-year survival rate, it is obvious that most of these patients either do not respond to treatment, or initially respond but progress and eventually the disease takes over. With the exception of the pemetrexed + cisplatin, these combinations are fairly toxic overall to the patient, with near MTD
doses of each chemotherapy given in the combination. Another drawback is that these large doses of chemotherapy often lead to chemotherapy induced leukemias. There is no basis on which a patient is given one of these platinum based regimens, it is purely at the doctor's discretion.

Single agent cisplatin and carboplatin tested across the 53 NSCLC panel yield one normal distribution of response, and when cisplatin is combined with gemcitabine at a fixed 7:100 molar ratio, the two distribution response to gemcitabine becomes one distribution in response to the combination. In fact response to gemcitabine across the panel of NSCLCs spans three orders of magnitude, while the combination of gemcitabine + cisplatin only spans $\sim 2$ orders of magnitude (Figure 3.1). Single agent paclitaxel and pemetrexed responses across the NSCLC panel results in two normal distributions, which are kept when combined with carboplatin and cisplatin respectively; however in all cases of the combination, the cell lines that were most sensitive to gemcitabine, paclitaxel, and pemetrexed as single agents are slightly less sensitive to that agent in the combination with platinum.

The majority of cell lines (68, and 60\% respectively) showed additivity or antagonism to the combinations of paclitaxel + carboplatin and pemetrexed + cisplatin, suggesting that many patients are not receiving added tumor kill from getting combination chemotherapy, or that they are receiving the wrong combination of chemotherapeutic agents.

This study endeavored to use cell lines as surrogates for tumors and catalogue the response to gemcitabine + cisplatin, paclitaxel + carboplatin, and pemetrexed + cisplatin, and then using mRNA expression data on the cell lines to build signatures of response to each combination, and be able to use said signatures to predict response of other cell lines, and hopefully be able to use these signatures clinically as a method of personalizing therapy. The signatures created are not predictive using a test set of NSCLCs that were not used in the initial training set but that drug response to the combinations has been performed. One concern is that the signatures are made from mRNA profiling that was performed with untreated cells, it could be that mRNA profiling after treatment would also be needed and then subtracted from untreated cells, giving a profile of gene changes from treatment and then signatures of synergistic cell lines vs antagonistic cell lines could be more informative. Another concern is that mRNA profiling is a static measure, but response to drugs is a dynamic process and would require a different measure of a cell's properties, such as epigenetic profile (ie catalogue of current epigenetic marks and protein levels of HATs, HDACs, HMT's HDMs, DNMTs) especially since epigenetics have been implicated in drug resistance (S. V. Sharma et al., 2010).

This startling result of high amounts of antagonism to conventional chemotherapy combinations on NSCLC cell lines emphasizes the need for improved combination strategy.

|  | Gemcitabine/Cisplatin |  | Paclitaxel/Carboplatin |  | Pemetrexed/Cisplatin |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Plate | Gemcitabin | Cisplati | Paclitaxe | Carboplati | Pemetrexe | Cisplati |
| Colum | e | n | l | n | d | n |
| $\mathrm{n} \#$ | nM | nM | nM | nM | $\mu \mathrm{M}$ | $\mu \mathrm{M}$ |
| 1 | - | - | - | - | - | - |
| 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0.12 | 0.009 | 0.06 | 0.2 | 0.06 | 0.018 |
| 5 | 0.48 | 0.034 | 0.24 | 0.9 | 0.24 | 0.07 |
| 6 | 1.96 | 0.14 | 0.98 | 3.4 | 0.98 | 0.3 |
| 7 | 7.8 | 0.6 | 3.9 | 13.7 | 3.9 | 1.2 |
| 8 | 31.2 | 2.2 | 15.6 | 54.7 | 15.6 | 4.7 |
| 9 | 125 | 8.75 | 62.5 | 219 | 62.5 | 18.63 |
| 10 | 500 | 35 | 250 | 875 | 250 | 74.5 |
| 11 | 2000 | 140 | 1000 | 3501 | 1000 | 298 |
| 12 | - | - | - | - | - | - |

TABLE 3.1 Drug dosages for agents in platinum based chemotherapy combination regimens.

|  | Carboplatin |  | Cisplatin |  | Gemcitabine |  | Gemcitabine/ Cisplatin |  | Paclitaxel |  | Paclitaxel/C arboplatin |  | Pemetrexed |  | Pemetrexed/ Cisplatin |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| Cell Line | IC50 | SD | IC50 | SD | IC50 | SD | IC50 | SD | IC50 | SD | IC50 | SD | IC50 | SD | IC50 | SD |
| A549 | 19.5 | 3.3 | 3 | 0.96 | 6.85 | 3.1 | 31 | 2 | 6.4 | 6.9 | 18 | 5.5 | 0.24 | 0.12 | 0.625 | 0.15 |
| Calu-1 | 99 | 3.3 | 4.15 | 3.1 | 53.5 | 960 | 215 | 160 | 7.8 | 0.91 | 11 | 1.6 | 1000 | 0 | 40 | 4 |
| Calu-3 | 42 | 17 | 1.9 | 0.45 | 13 | 26 | 6.3 | 0.52 | 1.49 | 0.94 | 1.87 | 1.2 | 1000 | 0 | 4.15 | 1.7 |
| Calu-6 | 27.5 | 6.1 | 0.91 | 0.15 | 13.5 | 5.6 | 8.35 | 3.5 | 12.6 | 9.9 | 3.1 | 1.5 | 0.068 | 520 | 0.055 | 0.006 |
| H1155 | 6.35 | 0.43 | 1.35 | 0.46 | 2.3 | 0.12 | 4.15 | 1.4 | 7.1 | 3.9 | 9.85 | 0.38 | 0.047 | 0.024 | 0.044 | 0.007 |
| H1299 | 29.5 | 10 | 2.05 | 0.96 | 2.45 | 2.6 | 9.9 | 8.2 | 7 | 6.2 | 9.1 | 2.6 | 0.19 | 580 | 0.22 | 0.013 |
| H1355 | 66.5 | 23 | 4.7 | 1.3 | 6 | 1.4 | 5.95 | 3.4 | 6.4 | 2.9 | 2.95 | 2.2 | 1000 | 0 | 7.85 | 1.3 |
| H1395 | 24 | 2.9 | 3.85 | 2.1 | 1070 | 1000 | 9.15 | 3.6 | 140 | 510 | 25.5 | 1.7 | 1000 | 0 | 4.5 | 1.1 |
| H157 | 28.5 | 10 | 2.5 | 1.2 | 5.6 | 3.4 | 6.5 | 0.68 | 2.05 | 1.5 | 3.35 | 1 | 0.215 | 0.13 | 0.535 | 0.36 |
| H1648 | 49.5 | 12 | 4.9 | 2.1 | 27 | 990 | 11.5 | 5.7 | 5.25 | 14 | 4.25 | 2.4 | 1000 | 350 | 22.5 | 5.3 |
| H1650 | 31.5 | 2.4 | 3.55 | 1.3 | 12.3 | 3.3 | 7.4 | 2.2 | 47.5 | 21 | 3.8 | 0.2 | 1000 | 0 | 6.5 | 0.82 |
| H1693 | 57.5 | 7.9 | 4.7 | 1.2 | 1.03 | 0.74 | 1.9 | 0.29 | 4.4 | 1.1 | 2.55 | 2.5 | 0.048 | 410 | 0.041 | 0.003 |
| H1770 | 19.5 | 2.9 | 1.9 | 4.4 | 13 | 3.8 | 8.35 | 4 | 7.65 | 410 | 3 | 0.44 | 0.54 | 1.3 | 2.65 | 2.5 |
| H1819 | 110 | 21 | 9.3 | 2.9 | 43 | 870 | 9.45 | 2.1 | 11 | 6.5 | 8.6 | 2.3 | 1000 | 0 | 0.052 | 0.005 |
| H1975 | 39 | 5.8 | 3.8 | 1.5 | 7.6 | 6 | 5.1 | 1.2 | 1.6 | 0.44 | 6.2 | 1 | 1000 | 520 | 5.1 | 0.93 |
| H1993 | 160 | 55 | 8.2 | 3 | 6.1 | 2.3 | 4.8 | 2.2 | 2.9 | 1.7 | 5.65 | 1.3 | 0.04 | 0.018 | 0.056 | 0.002 |
| H2009 | 32 | 16 | 5.05 | 11 | 4.3 | 21 | 5.45 | 2 | 1.8 | 1.5 | 3.3 | 1.4 | 0.038 | 460 | 17 | 20 |
| H2073 | 26 | 8.3 | 1.8 | 0.96 | 6.55 | 2.3 | 5.4 | 1.7 | 150 | 98 | 135 | 84 | 0.109 | 0.034 | 0.15 | 0.01 |
| H2077 | 32.5 | 13 | 2.85 | 0.38 | 37 | 24 | 23 | 9.1 | 3.85 | 1.8 | 0.895 | 0.23 | 0.024 | 0.008 | 0.043 | 0.015 |
| H2085 | 57.5 | 12 | 10 | 2.3 | 1170 | 710 | 93.5 | 21 | 1000 | 410 | 2.9 | 0.19 | 0.165 | 0.067 | 30 | 2.6 |
| H2086 | 50.5 | 14 | 4.2 | 0.79 | 74 | 6.2 | 135 | 950 | 1.2 | 0.06 | 2.15 | 0.5 | 1000 | 0 | 11.1 | 4.2 |
| H2087 | 5.45 | 5 | 0.62 | 0.27 | 6.1 | 10 | 10.5 | 1.2 | 0.64 | 0.82 | 4.45 | 2.1 | 1000 | 0 | 1.3 | 0.32 |
| H2106 | 58.5 | 9.8 | 4.25 | 1.1 | 39.5 | 13 | 41.5 | 6.5 | 0.5 | 0.23 | 0.615 | 0.51 | 0.35 | 13 | 0.51 | 0.23 |
| H2126 | 78 | 23 | 4.05 | 2.5 | 2000 | 580 | 23.5 | 1.7 | 10.7 | 38 | 8.55 | 0.99 | 1000 | 0 | 2.45 | 0.26 |
| H2170 | 14 | 0.58 | 1 | 0.21 | 7.3 | 0.49 | 6 | 1.6 | 2.8 | 3.6 | 3.9 | 0.18 | 0.14 | 550 | 0.18 | 0.083 |
| H2228 | 25.5 | 11 | 2.65 | 0.47 | 11.4 | 6.3 | 6.4 |  | 0.865 | 0.81 | 0.895 | 0.36 | 0.048 | 0.029 | 0.057 |  |
| H2347 | 43 | 6.5 | 3.5 | 1.3 | 30.5 | 23 | 14 | 4.4 | 2.3 | 2.4 | 3.65 | 0.28 | 0.2 | 520 | 10.4 | 8.2 |
| H2882 | 26 | 6.8 | 2 | 1.6 | 330 | 750 | 54 | 24 | 7.5 | 3.3 | 4.15 | 0.93 | 1000 | 170 | 13.5 | 2.9 |
| H2887 | 61 | 1.7 | 11 | 2.4 | 1020 | 1100 | 31 | 3.3 | 44 | 330 | 63 | 9.8 | 1000 |  | 79.5 | 36 |
| H322 | 129 | 66 | 18.5 | 2.4 | 2000 | 0 | 1010 | 1100 | 5.7 | 0.45 | 10 | 0.5 | 1000 | 460 | 22.5 | 12 |
| H3255 | 30.5 | 1.7 | 2.15 | 0.96 | 20 | 5 | 6.25 | 0.35 | 5.3 | 1.8 | 4.6 | 0.57 | 0.055 | 0.045 | 18.5 | 1.7 |
| H358 | 33.5 | 13 | 2.7 | 7 | 3.2 | 16 | 2.55 | 0.85 | 1.2 | 1.2 | 3.7 | 1.7 | 0.022 | 0.012 | 10.4 | 0.94 |
| H441 | 29.5 | 3.9 | 5.85 | 4.1 | 40 | 57 | 3.7 | 0.22 | 2.15 | 13 | 5.75 | 1.3 | 1000 | 0 | 12.5 | 11 |
| H460 | 22.5 | 37 | 4.7 | 5.3 | 3.2 | 1.4 | 2.4 | 0.64 | 4.6 | 2.1 | 6.5 | 0.7 | 1000 | 510 | 2.4 | 2.6 |
| H820 | 13.5 | 2.1 | 1.35 | 0.33 | 29.5 | 10 | 15.6 | 18 | 2.75 | 0.61 | 7.35 | 1.1 | 0.11 | 0.052 | 1.66 | 0.97 |
| HCC1171 | 83.5 | 3.6 | 8.8 | 12 | 9 | 870 | 1.8 | 0.17 | 1000 | 450 | 650 | 470 | 500 | 580 | 5.79 | 8.2 |
| HCC1195 | 65 | 17 | 5.9 | 1.5 | 2000 | 1100 | 84.5 | 17 | 26 | 490 | 6.2 | 2.4 | 1000 | 170 | 31.1 | 33 |
| HCC1359 | 70.5 | 26 | 7.3 | 2.5 | 42 | 19 | 49.5 | 8.1 | 54 | 500 | 15 | 3.7 | 1000 | 0 | 4.65 | 1.5 |
| HCC15 | 48.5 | 5.4 | 6.1 | 1.8 | 17 | 7 | 7.15 | 0.24 | 1.6 | 0.92 | 5.3 | 0.75 | 0.023 | 0.008 | 9.4 | 1.6 |
| HCC193 | 90.5 | 50 | 12 | 5 | 27 | 770 | 10.8 | 3 | 14 | 1.7 | 29.5 | 8.1 | 1000 | 0 | 0.049 | 0.012 |
| HCC2279 | 67 | 13 | 8.6 | 1.7 | 2000 | 0 | 50 | 40 | 7.3 | 2.9 | 7.25 | 0.81 | 1000 | 0 | 59.5 | 3.7 |
| HCC2935 | 260 | 18 | 43.5 | 7.3 | 2000 | 800 | 2000 | 0 | 1000 | 0 | 1000 | 480 | 1000 | 0 | 72.5 | 27 |
| HCC366 | 22.5 | 1.7 | 4 | 1.9 | 11 | 970 | 5.05 | 0.75 | 16.7 | 510 | 1000 | 500 | 1000 | 0 | 2.95 | 1.2 |
| HCC4006 | 72.5 | 5.7 | 14 | 4.9 | 110 | 8.2 | 12.5 | 2.4 | 1.95 | 0.41 | 3.8 | 0.15 | 1000 | 0 | 0.049 | 0.004 |
| HCC4011 | 53 | 6.2 | 5.9 | 0.98 | 18 | 16 | 6.2 | 0.63 | 4.4 | 1.6 | 1.83 | 1.1 | 1000 | 0 | 0.103 | 8.5 |
| HCC4017 | 23.5 | 3.6 | 3.8 | 0.89 | 12 | 6.9 | 32.5 | 1.3 | 6.1 | 510 | 6.1 | 0.5 | 0.037 | 500 | 0.048 | 0.002 |
| HCC44 | 61 | 2.6 | 4.4 | 0.95 | 72.5 | 270 | 120 | 8.2 | 5.7 | 7.2 | 12 | 1.2 | 1000 | 0 | 0.16 | 0.047 |
| HCC461 | 31.5 | 4 | 5.5 | 6.1 | 2000 | 1100 | 2.38 | 3.2 | 30.5 | 24 | 3.5 | 0.3 | 1000 | 0 | 3.55 | 1 |
| HCC515 | 59.5 | 16 | 2.6 | 1.6 | 1010 | 1100 | 1.55 | 0.24 | 1000 | 420 | 13.5 | 3.2 | 1000 | 0 | 0.195 | 0.042 |
| HCC78 | 20.5 | 3.6 | 0.65 | 0.84 | 16.5 | 2.1 | 2.75 | 0.36 | 2.4 | 1.5 | 3 | 0.15 | 0.028 | 0.002 | 0.023 | 0.006 |
| HCC827 | 36 | 7.9 | 2.7 | 4 | 7 | 12 | 13.5 | 25 | 2.2 | 0.89 | 6.95 | 0.29 | 0.073 | 0.028 | 0.151 | 0.31 |
| HCC95 | 18 | 3.4 | 2.2 | 1.4 | 2000 | 940 | 4.85 | 2.3 | 3.6 | 2.8 | 3.4 | 0.31 | 0.81 | 520 | 1.11 | 0.4 |

TABLE 3. $2 \mathrm{IC}_{50}$ s of NSCLC cell line panel to platinum based chemotherapy
combinations and each agent as a single agent.

| Cell Line | Gemcitabine/Cisplatin |  | Paclitaxel/Carboplatin |  | Pemetrexed/Cisplatin |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Gemcitabine $\mathrm{IC}_{50}$ | Cisplatin $\mathrm{IC}_{50}$ | Paclitaxel $\mathrm{IC}_{50}$ | Carboplatin $\mathrm{IC}_{50}$ | Pemetrexed $\mathrm{IC}_{50}$ | Cisplatin $\mathrm{IC}_{50}$ |
| HCC4017 | 6.91192771 | 0.96 | 3.010652 | 10.5 | 0.00372121 | 0.0011 |
| H2228 | 51.2 | 7.2 | 0.48 | 1.68 | 0.71 | 0.21 |
| H2087 | 183 | 25.6 | 0.68 | 2.38 |  |  |
| H1563 | 0.396 | 0.055 | 0.052 | 0.183 |  |  |
| H1355 |  |  | 0.0023 | 0.008 |  |  |
| HBEC30KT | 0.69 | 0.097 | 0.606905 | 2.12 | 0.005 | 0.0014 |
| HBEC34KT | 1.04 | 0.145 | 0.651926 | 2.28 | 0.005 | 0.0014 |

TABLE 3.3 $\mathrm{IC}_{50} \mathrm{~S}$ of platinum based chemotherapy combinations in colony formation.


FIGURE 3.1 NSCLC Cell Line Drug Response Phenotypes to Gemcitabine + Cisplatin, Paclitaxel + Carboplatin, Pemetrexed + Cisplatin, and to Each Agent as a Single Agent.

Plot of $\mathrm{IC}_{50}$ data for a panel of 53 NSCLC cell lines for carboplatin, cisplatin, gemcitabine, paclitaxel, pemetrexed, gemcitabine + cisplatin, paclitaxel + carboplatin, and pemetrexed + cisplatin on a log scale of concentration of chemotherapy. Each symbol represents the average $\mathrm{IC}_{50}$ value for several MTS concentration curve assays $(\mathrm{n} \geq 3)$ to determine drug response phenotype. These phenotypes were stable ( $r>0.70$ ) on tests performed at different times.


FIGURE 3.2 Combination Index Values for NSCLC Panel Treated with

Gemcitabine + Cisplatin, Paclitaxel + Carboplatin, or Pemetrexed +

Cisplatin. Combination Index calculated for gemcitabine + cisplatin, paclitaxel + carboplatin, and pemetrexed + cisplatin. Combination indices (CI) were calculated using the Chou-Talay method (Chou \& Rideout, 1991). Briefly, an effect level was chosen and doses were calculated for each drug alone, then doses were measured for each drug in combination that gave the chosen effect level. These were then plugged into the CI equation and standard deviations were calculated based on the drug sensitivity data; $\mathrm{CI}<1$ Synergy, CI=1 Additivity, CI>1 Antagonism. Green colored cells show synergy, red colored cells show antagonism, and black colored cells show additivity.


FIGURE 3.3 Hierarchical Clustering Analysis of mRNA Expression Data
that Correlates with Synergism or Antagonism to the Gemcitabine +
Cisplatin Combination.

Unsupervised clustering analysis is for both NSCLCs on the horizontal axis and genes on the vertical axis. Of approximately of 47,000 genes on the Illumina Human WG-6 v3, 567 genes correlate with synergy and antagonism ( $\mathrm{p} \leq 0.05$ ).

Each column is a cell line and each row a gene. Gene expression levels are indicated by the coloring with blue being high expression and white being no expression.


FIGURE 3.4 Hierarchical Clustering Analysis of mRNA Expression Data
that Correlates with Synergism or Antagonism to the Paclitaxel +
Carboplatin Combination.

Unsupervised clustering analysis is for both NSCLCs on the horizontal axis and genes on the vertical axis. Of approximately of 47,000 genes on the Illumina Human WG-6 v3, 387 genes correlate with synergy and antagonism ( $\mathrm{p} \leq 0.05$ ).

Each column is a cell line and each row a gene. Gene expression levels are indicated by the coloring with blue being high expression and white being no expression.


FIGURE 3.5 Hierarchical Clustering Analysis of mRNA Expression Data that Correlates with Sensitivity or Resistance to the Pemetrexed + Cisplatin Combination.

Unsupervised clustering analysis is for both NSCLCs on the horizontal axis and genes on the vertical axis. Of approximately of 47,000 genes on the Illumina Human WG-6 v3, 529 genes correlate with synergy and antagonism ( $\mathrm{p} \leq 0.05$ ). Each column is a cell line and each row a gene. Gene expression levels are indicated by the coloring with blue being high expression and white being no expression.


FIGURE 3.6 Hierarchical Clustering Analysis of mRNA Expression Data
Correlating Combination Effect of Gemcitabine + Cisplatin in an Effort to

Predict Response.

Unsupervised clustering analysis is for both 53 NSCLCs on the horizontal axis and 387 genes on the vertical axis. Each column is a cell line and each row a gene. Gene expression levels are indicated by the coloring with blue being high expression and white being no expression.


FIGURE 3.7 Hierarchical Clustering Analysis of mRNA Expression Data
Correlating Combination Effect of Paclitaxel + Carboplatin in an Effort to

## Predict Response.

Unsupervised clustering analysis is for both 53 NSCLCs on the horizontal axis and 567 genes on the vertical axis. Each column is a cell line and each row a gene. Gene expression levels are indicated by the coloring with blue being high expression and white being no expression.


FIGURE 3.8 Hierarchical Clustering Analysis of mRNA Expression Data Correlating Combination Effect of Pemetrexed + Cisplatin in an Effort to Predict Response.

Unsupervised clustering analysis is for both 53 NSCLCs on the horizontal axis and 529 genes on the vertical axis. Each column is a cell line and each row a gene. Gene expression levels are indicated by the coloring with blue being high expression and white being no expression.

## CHAPTER FOUR

## Targeted Molecular Biology Approaches to Rationally Designed

## Combinations

### 4.1 Introduction

Approximately only $10 \%$ of the human genome encodes for druggable target proteins half of which are relevant to disease, thus limiting the ability to selectively target cancer cells (Owens, 2007). However, advances in molecular techniques, including the discovery of the RNA interference (RNAi) pathway, have made it possible to modulate, at the expression level, any gene. In the RNAi pathway a double stranded RNA molecule, usually ~21-23 nt often called small interfering RNAs (siRNAs) that shares complementarity with a particular gene's mRNA, the degree of complementarity being the deciding factor to the type of inhibition of gene expression. If the siRNA shares $100 \%$ complementarity with the mRNA, it results in mRNA degradation; however if the siRNA does not share $100 \%$ complementarity with the mRNA, the mRNA is not degraded, but translation of the mRNA is blocked (Davidson \& McCray, 2011; X. Liu et al., 2011). Micro-RNAs (miRNA) are endogenously expressed double stranded RNA molecules that are transcribed from the genome and form stem loop structures. These pri-miRNAs are transcribed by RNA polymerase II, and are then processed
by drosha/pasha which are de-branching enzymes resulting in pre-miRNAs. The pre-miRNAs are then exported into the nucleus where they are further processed by dicer into mature miRNAs which get loaded into RNA induced silencing complexes (RISC). Most mammalian miRNA tend to not be 100\% complementary to the target mRNA; therefore, work by inhibiting translation, an additional benefit of not being completely complementary is that miRNAs are able to target multiple genes at once. Synthetic siRNAs are designed to have $100 \%$ complementarity to the target mRNA. Anti-gene RNAs (agRNA) are similar in chemistry to siRNAs; however, they differ in the intended target, siRNAs target mRNA, agRNAs are designed to target the genomic DNA upstream of transcription start sites (TSS) (Janowski, et al., 2005; Janowski, et al., 2006; Schwartz et al., 2008).

### 4.2 Altering miRNA levels can influence chemosensitivity in NSCLCs

Cancers not only have deregulation of mRNA and proteins, but also have a deregulation of miRNA expression which can act as oncogenes (oncomirs) or tumor suppressors (X. Liu, et al., 2011). Twenty three cell lines, 10 SCLC, 10 NSCLC, and 3 immortalized HBECs were profiled for miRNA expression on miRNA microarrays with probes for 136 nonredundant human and mouse miRNAs. A profile similarity search was used to identify miRNAs that might be involved in response to gemcitabine, paclitaxel and vinorelbine, three miRNAs were identified; miR19a, miR129, and miR337 (Figure 4.1). In cell lines that are
resistant to paclitaxel, gemcitabine, and vinorelbine express low levels of these miRNAs and conversely cell lines that are sensitive to paclitaxel and gemcitabine express higher levels of these miRNAs.

Could introduction of synthetic miRNA mimetics sensitize resistant cells to gemcitabine or paclitaxel? Conversely would introduction of antago-miRs (synthetic antagonists to miRNAs) into cells that are sensitive to paclitaxel or gemcitabine make these cells more resistant? Using H157, sensitive to paclitaxel and gemcitabine, H1819 and H2887, both of which are resistant to paclitaxel and gemcitabine the ability of altering miRNA levels to regulate response to gemcitabine and paclitaxel was tested. Since vinorelbine, gemcitabine, and paclitaxel were all inversely correlated with miR19a levels, H157 cells were transfected with mock control, a negative control miR, or a synthetic miR19a mimic, and then given a series of doses of gemcitabine, vinorelbine, and paclitaxel. In these cell lines, only treatment with paclitaxel after increase in miR19a levels selectively increased sensitivity to paclitaxel by a ten-fold leftwards shift in the drug response curve (Figure 4.2). To further explore the role of miR19a in response to paclitaxel treatment, and to investigate a potential role of miR337 in paclitaxel sensitivity, H157 cells were again transfected with a negative control miR, miR19a, or miR337, and again saw that increase of miR19a sensitized H157 cells to paclitaxel and saw a similar sensitization by miR337 to paclitaxel (Figure 4.3a). Additionally H157 cells were transfected with a negative
control antagomir, an inhibitor of miR19, or inhibitor of miR337, the inhibitor of both miR19a and miR337 desensitized H157 cells, meaning a right-ward shift in the drug response curve, to paclitaxel by $\sim 6$-fold (Figure 4.3b). In H1819 cells that were transfected with a negative control antagomir, an inhibitor of miR19, or inhibitor of miR337 the response to paclitaxel was not altered. However, H1819 cells that were transfected with either the miR19a or miR337 mimic were sensitized 20 fold to paclitaxel (a tenfold shift to the left) (Figure 4.4). Additionally, H2887 cells, which are also resistant to paclitaxel, were transfected with a negative control miR, miR19a, or miR337, treatment with miR19a and miR337 increased sensitivity to paclitaxel by 100 fold (a 100-fold shift to the left in the paclitaxel dose response curve, Figure 4.5). None of the cells $\mathrm{IC}_{50}$ s were altered with the miR129 mimic (Figure 4.6).
4.3 Evaluation of specificity of synthetic lethal sirnas for PACLITAXEL

Synthetic siRNAs tend to be designed with $100 \%$ complementarity to the target mRNA, with a 19-21 nt seed sequence, and a double dT overhang. A paclitaxel synthetic lethal screen was done on H 1155 cells with 1 nM dose of paclitaxel used (Whitehurst et al., 2007). Included in this study was confirmation that the candidate genes did not sensitize cells to any chemotherapeutic insult, by testing a few siRNAs and treated with gemcitabine or vinorelbine (Figure 4.7).

As was discussed in the introduction there are many antimitotics, including docetaxel, a structural relative of paclitaxel. Several new anti-mitotics were readily available to test against the paclitaxel synthetically lethal siRNAs, peloruside and diazonamide. Peloruside is a new tubulin binding drug that is water soluble, it binds to $\alpha$-tubulin as opposed to $\beta$-tubulin like the taxanes. Across a panel of 50 NSCLCs peloruside is slightly less potent than the taxanes in vitro. Diazonamide phenotypically acts as an anti-mitotic in that it causes a large $\mathrm{G}_{2} / \mathrm{M}$ block; however, it has yet to have been shown to directly bind to tubulin even though many groups have looked into it. The mechanism by which diazonamide works is still unknown; however, across a panel of NSCLCs diazonamide has a very large range of activity, and is more potent than the other anti-mitotics studied.

Ten of the top hits from the paclitaxel synthetic lethal screen were selected to test the hypothesis H1155 would be sensitized to docetaxel, but not peloruside, or diazonamide. For these experiments, H1155 cells were transfected with 20 nM siRNA, and eight wells per siRNA were treated with 1 nM paclitaxel, 1 nM peloruside, 1 nM docetaxel, and 0.1 nM diazonamide (Figure 4.8). Data was normalized to cells that were transfected with luciferase targeting siRNA treated with paclitaxel, peloruside, docetaxel, or diazonamide. Figure 4.9 shows that H1155 cells respond as reported to the indicated siRNAs (Whitehurst, et al., 2007). Not surprisingly, these cells also responded in the same manner to
docetaxel treatment as well as paclitaxel treatment. Additionally, these cells were not sensitized to peloruside at all by transfection of the indicated siRNAs (Figure 4.9). Most surprisingly however, is that two of the six siRNAs tested sensitized H1155 cells to diazonamide.

It was expected that these siRNAs would still be synthetically lethal to docetaxel because docetaxel is a structural analogue of paclitaxel, binds to the same site on tubulin and in theory should have the same activity within a cell. But diazonamide is not known to directly bind to tublin, even though it acts as an antimitotic (Williams et al., 2007). In fact, diazonamide’ s mechanism of action still remains elusive, but it is clear that diazonamide acts as an anti-mitotic, and clusters with vinorelbine across our panel of NSCLCs by IC 50 (Figure 4.10).

### 4.4 TARGETING MUTANT P53 In NSCLC using AgRNAs

While the definition of mutations in p53 is rather broad and encompasses p53 null cells, most mutations in p53 are within the DNA binding domain (mDBD-p53), and alter the ability of mDBD-p53 to bind to wild-type p53 response elements. This is not to say that mDBD-p53 is not able to regulate transcription as recent studies have shown that there is a specific subset of p53 target genes that are still regulated by mDBD-p53 (Strano, et al., 2007).

There are three documented TSS for TP53, one described in DBTSS, it is the most 3' TSS that is still upstream of the coding region of TP53, the TSS described by Lamb et al, and finally the most 5' one described by Bourdon et al
(Figure 4.11) (Bourdon et al., 2005; Lamb \& Crawford, 1986). Three agRNAs were designed to target the Lamb and Lane TSS, the agRNAs were designed to be complementary to the -7 nt , -9 nt , or -11 nt from TSS, the oligos targeted to the Lamb TSS (L) were termed L7, L9, and L11, and the oligos targeted to the most 5’ TSS were termed N7, N9, and N11. Transfection of H1355 (E285K) cells with L7, N7, or N9 decreases p53 levels, while control oligos do not affect p53 levels (Figure 4.12), but only transfection with N9 caused extensive cell death (data not shown). The induction of cell death was also found in other cell lines that transfection of N9 would cause cell death, so we chose to further pursue the cell death phenotype with N9. All control agRNAs were designed from the sequence of N9, a scrambled N9 (N9-scr), and a mismatch control with four mismatches (M4M), as well as siRNA that would target all potential isoforms of p53 (QsiR) (Table 4.1).

These new oligos were then tested again in H1355 cells, and similarly to the previous experiment, N7 and N9 transfection lowered p53 levels, and QsiR transfection lowered p53 levels so much that p53 could no longer be detected by western blot, while both scr and M4M transfection did not alter p53 levels and only N9 showed toxicity in H1355 (Figure 4.13). In quest of defining the p53 background necessary for N9-induced cytotoxicity, MIA PaCa2 (R248W), Panc1 (R273C, R273H), A549 (wt), and H1299 (null) were transfected with M4M, scr, QsiR, N7, andN9 (Figure 4.14). N7, N9, and QsiR decreased p53 levels in both

A549 and Panc1 cells; however, this was not seen in MIA PaCa2 cells. Most interestingly N9 caused toxicity in both Panc1 and MIA PaCa2 cells, but not in A549 nor H1299 cells. This suggests that knockdown of p53 is not required for cytotoxicity, but that mutant p53 is necessary for cytotoxicity. One possibility is that agRNA ${ }^{\mathrm{p} 53}$ was reactivating wild type p53 activity in these mutant cell lines.

To examine this possibility agRNA ${ }^{\mathrm{p} 53}$ was combined with doxorubicin, which normally causes activation of wild type p53, to see if a mutant-p53 containing cell line would be sensitized to doxorubicin. 100 pM N9 when combined with doxorubicin in H 1355 results in a 10 fold shift in $\mathrm{IC}_{50}$ of doxorubicin in the presence of N9 in these cells compared to 100 nM N7, M4M, and scr (Figure 4.15). Similarly in MIA PaCa2 that were transfected with 100 pM N9, there is a 6 fold shift in $\mathrm{IC}_{50}$ compared to cells transfected with 100 nM N7, M4M, or scr, and most strikingly in Panc1 cells (containing mutations in both alleles of p53) there is a 130 fold shift in $\mathrm{IC}_{50}$ in cells transfected with 100 pM N9 and treated with doxorubicin compared to cells transfected with 100 nM N7, M4M, or scr and treated with doxorubicin (Figure 4.16).

In order to be able to properly analyze the combination of N9 and doxorubicin, the death induced by agRNA ${ }^{\mathrm{p} 53}$ needed to be defined and catalogued. To do this, transfections with N9 were done as a concentration curve, to determine the $\mathrm{IC}_{50}$ of transfection with N9, in essence treating N9 as a drug. H1355 was found to be sensitive to N9 down to the picomolar range ( $\sim 10 \mathrm{pM}$ )
(Figure 4.17). These experiments showed that sensitivity (pM) to N9 was dependent on the tumor line expressing mutant p53 as A549 (wt), H358 (null), nor H1299 (null) did not respond to N9 (Figure 4.18). In addition to testing cells by MTS for cytotoxicity by transfection of N9, H1355 (E285K), MIA PaCa2 (R248W), and H1155 (R273H) were transfected with 25 nM N9, M4M, or QsiR, and then plated for colony formation with either 100 cells/well or 1000 cells/well, which confirmed that N9 induces cell death to such an extent that these cell lines ability to form colonies was inhibited after cells were treated with N9 (Figure 4.19). To evaluate how many agRNAs could induce cytotoxicity, agRNAs were used to walk the promoter of TP53 from -7 to -27 with respect to the Bourdan TSS skipping every other nucleotide. We found that N27 caused the greatest cytotoxicity in H2009 (Figure 4.20). From this point on, all experiments were done with N27 and scr and M4M versions of N27 were designed and synthesized (Table 4.1).

With these new N27 specific oligos, titration curves were done on H2009 (R273L), H358 (null), A549 (wt), H1355 (E285K), SAOS2 (null), MDA-MB-231 (R280K), and HBEC3-KT (wt) with N27 and (N27)M4M (Figure 4.21). H2009 has an IC50 $\sim 600 \mathrm{pM}$, H1355 has an $\mathrm{IC}_{50} \sim 400 \mathrm{pM}$, and MDA-MB-231 has an IC50 ~100 pM. The only other cell line where an $\mathrm{IC}_{50}$ can actually be measured is SAOS2 (20 nM), which due to the high concentration is likely due to off target effects.

To better define the mutations in p53 that result in cytotoxic activity of N27, H157 was used because it has premature stop codon resulting in truncated p53 protein, and H1373 (P47L) was used because it has a mutation in the N terminal transactivation domain. Using these cell lines, N27and M4M were titrated across these cell lines (Figure 4.22). Only H157 had a measurable $\mathrm{IC}_{50}$, 22.7 nM, whereas H 1373 did not respond to N 27 up to 25 nM , indicating that the cytotoxicity induced by agRNA ${ }^{\mathrm{p} 53}$ is dependent on mutant p 53 when the mutations are contained within the DBD.

There has been a novel form of p53 reported in which alternative splicing occurs between exon 7 and 9, resulting in the removal of part of the DBD, including residues 257-322 (Rohaly et al., 2005). Potentially agRNA ${ }^{\text {p53 }}$ could be inducing alternative splicing resulting specifically in an induction of $\Delta \mathrm{p} 53$; however we failed to reliably detect an increase in this isoform (Figures 4.12-14).

Alternatively agRNA ${ }^{\mathrm{p} 53}$ could be causing a change in the interactions between WRAP53 and p53 mRNA, because WRAP53 is known to regulate p53 response to DNA by agents such a camptothecin or mitomycin c (Mahmoudi, et al., 2009). However, after multiple transfections and q-RT-PCR runs for multiple cell lines, no clear response of WRAP53 was seen in response to N27 (Figure 4.23).

Regulation of pro-apoptosis genes that are thought to be p53 target genes have recently been described as being induced by a long non-coding RNA that is
a target of p53 (LincRNAp21) (Huarte et al., 2010). Using the q-RT-PCR primers previously described, I found that treatment with N27 causes a large induction in LincRNAp21 (Figure 4.24) (Huarte, et al., 2010).

### 4.5 DISCUSSION

### 4.5.1 ALTERING miRNA LEVELS INFLUENCES CHEMOSENSITIVITY IN NSCLCS

During the course of these experiments, the data within the miRNA database (miRbase) has constantly been changing, and as a result the entire sequence of miR19a changed during the course of these studies. Although the data with miR19a was quite promising, it was dropped because there was no way to be sure what the actual sequence of it is.

Although miR129 expression correlated with response to chemotherapy (Figure 4.1), in our hands it does not appear to be functionally related with response to paclitaxel or gemcitabine. Only increasing miR129 levels was tested; however, it is still undetermined if inhibiting miR129 would affect chemotherapy response. This does seem unlikely, because even in the most sensitive line tested, H157, addition of miR19a or miR337 mimics further increased response to paclitaxel.

This study of miRNA induced sensitization to chemotherapy is completely void of any mechanistic data, and while mechanistic data is not per say necessary, it could be quite helpful in predicting possible side effects if increasing tumor
miR337 levels was to be pursued in vivo. However, that miR19a specifically sensitizes NSCLCs to paclitaxel, and that miR337 affects multiple NSCLC cell lines dose response curves to paclitaxel very similarly suggests that miR19a and miR337 act through a similar pathway that is dependent on microtubules. Using miRNA target prediction software, or alternatively there are websites (TargetScan www.targetscan.org) where miRNA target predictions are readily available, potential targets for miR337 need to be cross-referenced with proteins that are known to be involved in microtubule dynamics or paclitaxel sensitivity to narrow down the list of potential therapeutic targets of miR337. Alternatively, microarray run on samples from multiple cell lines whose miR337 levels have been altered, both my miR mimics and antagomiRs could shed light on the targets of miR337. One potential pitfall of the microarray experiment is there are likely to be confounding factors between antagomiRs and miR mimics so analysis of those samples would need to be run separately and the two lists compared looking for genes showing up on both lists. And once a potential target is found, it would need to be validated by a series of knockdown and over expression assays, looking to see if the knockdown of that gene would mimic miR337 mimic treatment in sensitizing NSCLCs to paclitaxel, and overexpression of the target gene would mimic miR337 inhibitor treatment in making NSCLCs more resistant to paclitaxel.

### 4.5.2 EVALUATION OF SPECIFICITY OF SYNTHETIC LETHAL sIRNAS

## FOR PACLITAXEL

That docetaxel and paclitaxel respond very similarly to the paclitaxel specific synthetic lethal siRNAs is a confirmation that these structurally related molecules act through the same pathway although docetaxel does so less effectively, but that diazonamide, an antimitotic with unknown mechanism of action, was sensitized to some, but not all of the 6 siRNAs is most remarkable. It implicates that the taxanes and diazonamide at some point are activating similar pathways that are not activated by vinorelbine. Testing more of the paclitaxel specific synthetic lethal siRNAs with diazonamide would be very interesting, and would give insight into the mechanism of diazonamide.

### 4.5.3 TARGETING MUTANT p53 IN NSCLC USING AGRNAS

The ability to reactive wild type p53 activity in cancers is something that researchers have been investigating since the discovery of p53 as such a major tumor suppressor. However, a way to therapeutically target p53 has remained elusive. In this work we used synthetic antigene-RNAs targeting 5' of the TSS of TP53, and found that two distinct sequences of agRNA targeting the 5' region of the TP53 promoter induce cytotoxicity in a p53-DBD-mutant specific fashion, as cells harboring wild-type p53, have homozygous deletions of the TP53 gene, truncation mutations of p53, or mutations outside of the DBD are not affected by agRNA treatment. While possible, it is not likely that this cytotoxicity is due to
simply decreasing mutant p53 levels as many cancers have homozygous deletions for p53, which effectively would be the same as removing mutant p53. The cytotoxicity specifically in the back ground of mutant-DBD-p53 suggests two things, the removal of mutant p53, and induction of wild-type p53 activity. This is because most mutants act in a dominant negative fashion by inhibiting wild-type p53 and also inhibiting p63 and p73, and that introduction of wild-type p53 into cancer cells causes cell death or differentiation (Baker, Markowitz, Fearon, Willson, \& Vogelstein, 1990; Goyette et al., 1992).

We also showed that N9 treatment sensitizes NSCLCs and pancreatic cancers with mutant p53 to doxorubicin, which is known to activate p53 in wild type cells and that apoptosis induced by doxorubicin is dependent on p53. These data further suggest that agRNA ${ }^{\mathrm{p} 53}$ is causing a re-activation of wild type p53 activity.

There was no appreciable change in WRAP53 levels after agRNA ${ }^{\mathrm{p} 53}$ treatment to suggest that the agRNAs were acting in a WRAP53 dependent fashion; however, WRAP53 levels after agRNA ${ }^{\text {p53 }}$ treatment and challenged with a DNA damaging agent was not tested in these studies.

There was a large induction of lincRNAp21 levels after agRNA treatment; however, the relevance of this observation has yet to be determined. The effect of over expression of lincRNAp21 needs to be evaluated as does the inhibition of lincRNAp21 expression, in cells with no other treatment, as well as in cells that
have been transfected with agRNA ${ }^{\text {p53 }}$ s, to see if knockdown of lincRNAp21 would oblate the cytotoxic effect of agRNA ${ }^{\mathrm{p} 53}$ in p53-DBD-mutant containing cells. If this is the case, then these agRNAs act through induction of lincRNAp21 which has been shown to positively regulate pro-apoptotic p53 target genes.

Target sequences of duplex RNAs

| Name | Target Sequence |
| :---: | :---: |
| p53-N $(-7)$ | AATGCACCCTCCTCCCCAACT |
| p53-N $(-9)$ | AATCTGCACCCTCCTCCCCAA |
| p53-N $(-11)$ | AAACTCTGCACCCTCCTCCCC |
| p53-N $(-15)$ | AACCTGACTCTGCACCCTCCT |
| p53-N $(-17)$ | AAATCCTGACTCTGCACCCTC |
| p53-N $(-19)$ | AAGAATCCTGACTCTGCACCC |
| p53-N $(-21)$ | AAGAGAATCCTGACTCTGCAC |
| p53-N $(-23)$ | AAGCGAGAATCCTGACTCTGC |
| p53-N $(-25)$ | AACGGCGAGAATCCTGACTCT |
| p53-N $(-27)$ | AAGTCGGCGAGAATCCTGACT |
| p53-N $(-29)$ | AAAGGTCGGCGAGAATCCTGA |
| p53-N $(-31)$ | AACCAGGTCGGCGAGAATCCT |
| N9-Scr | AAAGCTTCTCAAAAAGTTTTG |
| N27-Scr | AATGACTGTCGGCATCCAGAA |
| N27-M4M | AAGACGGAGAGACTCGTGACT |
| N9-M4M | AATGGACCCACCTGCCCATCT |
| p53 si-554 | AACCTACCAGGGCAGCTACGG |
| p53 QsiR | AAGGAAATTTGCGTGTGGAGT |
| p53 siR-788 | AATCTACTGGGACGGAACAGC |
| p53 siR-807 | AAAACAGCTTTGAGGTGCGTG |

TABLE 4. 1 agRNAs and siRNAs to study p53 activity.


FIGURE 4.1 Correlation of miRNAs expression with drug response to gemcitabine, paclitaxel, and vinorelbine in NSCLC.

Expression of miR19a, miR129, and miR337 correlate in a negative fashion with response to paclitaxel, gemcitabine, and vinorelbine. Data for this figure is not from the author, Rachel Greer, instead it is unpublished from Alex Pertsemlidus.


FIGURE 4.2 Alterations of miR19a levels can alter $\mathbf{H} 157$ response to chemotherapy.

H157 cells were transfected with mock reagents, negative control miR mimic (Dharmacon), or miR19a mimic. Twenty-four hours post transfection cells were treated with (A) gemcitabine, (B) paclitaxel, or (C) vinorelbine; after 96 hours post drug treatment, relative cell viability was determined using the MTS assay as described in methods.


FIGURE 4.3 Figure 4.3 Alterations of miR19a and miR337 alter H157 response to Paclitaxel.
(A) H157 cells were transfected with 20 nM negative control miR (Dharmacon), miR19a mimic, or miR337 mimic and 24 hours later were treated with 4-fold increasing concentrations of paclitaxel and relative cell viability was determined 96 hours after treatment with paclitaxel using the MTS assay as described in methods. (B) H 157 cells were transfected with 50 nM negative control antagomiR (Dharmacon), antagomiR19a, or antagomiR337. After 24 hours, cells were treated with 4-fold increasing concentrations of paclitaxel; relative cell viability was determined 96 hours later using the MTS assay as described in methods.


FIGURE 4.4 Alterations of miR19a and miR337 alter H1819 response to

## Paclitaxel.

(A) H 1819 cells were transfected with 20 nM negative control miR (Dharmacon), miR19a mimic, or miR337 mimic. After 24 hours cells were treated with 4-fold increasing concentrations of paclitaxel; relative cell viability was determined 96 hours after treatment with paclitaxel using the MTS assay as described in methods. (B) H 1819 cells were transfected with 50 nM negative control antagomiR (Dharmacon), antagomiR19a, or antagomiR337. After 24 hours, cells were treated with 4-fold increasing concentrations of paclitaxel; relative cell viability was determined 96 hours later using the MTS assay as described in methods.


FIGURE 4.5 Figure 4.5 Alterations of miR19a and miR337 alter H2887 response to Paclitaxel.

H2887 cells were transfected with 20 nM negative control miR (Dharmacon), miR19a mimic, or miR337 mimic. After 24 hours cells were treated with 4-fold increasing concentrations of paclitaxel; relative cell viability was determined 96 hours after treatment with paclitaxel using the MTS assay as described in methods.


FIGURE 4.6 Increasing miR129 Levels Does Not Affect Drug Response to

## Gemcitabine or Paclitaxel.

(A-B) H 157 and (C-D) H 1819 were transfected with 20 nM negative control miR (Dharmacon) or miR129 mimic. Twenty-four hours post transfection cells were treated with 4-fold increasing concentrations of (A, C) gemcitabine or (B, D) paclitaxel; relative cell viability was determined 96 hours after drug treatment using the MTS assay as described in methods.


FIGURE 4.7 Drug sensitivity profiles of Paclitaxel Synthetic Lethal siRNAs. (A-C) H1155 transfected with siRNAs targeting the indicated genes (DLNB1 and OR1A2 are control siRNAs) were exposed to (A) paclitaxel, (B) vinorelbine, or (C) gemcitabine 48 h after transfection at the indicated doses for 48 h . Results are viability normalized to siRNA-transfected samples in the absence of drug and are shown as means and s.e.m. Values are representative of three independent
experiments. Bars are cell viability obtained with Cell Titer Glo and are shown as means and s.e.m. Adapted from (Whitehurst, et al., 2007)

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\end{aligned}
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& 0.000000 \\
& 00000000 \\
& \text { ORODODOQ } \\
& \text { DOBODODR } \\
& 00000000 \\
& \text { OOODOROO } \\
& \text { OODODODO } \\
& 00000000 \\
& \text { DOEDOQDO }
\end{aligned}
$$

Blank

| Bells Only |
| :--- |
| Dharmafect 1 |
| Luciferase siRNA |
| Lun siRNA |
| TOX |
| ACRBP siRNA |
| ATP6VOD2 siRNA |
| FATE siRNA |
| FDG4 siRNA |
| FMR1NB siRNA |
| FMR |
| HS6T2 siRNA |
| Blank |

ADD DRUG
$(1 \mathrm{nM})$$\longrightarrow$

Day $0 \xrightarrow{24 \text { hours }}$ Day $1 \longrightarrow$ Day 5

FIGURE 4.8 Overall Scheme for Testing Paclitaxel Synthetic Lethal siRNAs

## Against other Anti-Mitotics.

Transfect cells with 20 nM of the indicated siRNAs on day zero; 24 hours later, treat with 50 uL of 2 nM paclitaxel, peloruside, docetaxel, or 0.2 nM diazonamide. Use MTS assay (as described in methods) to quantitate relative cell kill.


FIGURE 4.9 Figure 4.9 Paclitaxel-Specific Synthetic Lethals Are Not Completely Selective for Taxanes Only.

H1155 cells were transfected with 20 nM of the indicated siRNAs; 24 hours post transfection cells were treated with paclitaxel, docetaxel, peloruside (final concentration 1 nM ), or diazonamide (final concentration 0.1 nM ). Relative cell viability was determined 96 hours after drug treatment using the MTS assay; described in methods. Data was normalized to cells that were transfected with luciferase siRNA and treated with the test drug (paclitaxel, peloruside, docetaxel or diazonamide respectively). Data shown is the average of at least three separate experiments conducted on separate days.


FIGURE 4.10 Clustering of Chemotherapies by IC $_{50}$ across NSCLC Panel Roughly Clusters by Mechanism of Action.

Unsupervised clustering of chemotherapies based on response across a panel of 50 NSCLC (data collected by many members of the Minna lab). Diazonamide loosely clusters with vinorelbine and the taxanes for mechanism of action, strangely doxorubicin also clusters in the same group.


FIGURE 4.11 Design of agRNAs According to p53 Transcription Start Sites.
While there are four TSS associated with the TP53 gene, only the three upstream (5’) promoters were targeted using agRNAs, they were designed to be complementary to the + strand to the indicated regions, specific sequence information of agRNAs is in Table 4.1.


FIGURE 4.12 Targeting the 5' of the Transcription Start Site of p53 in H1355 Cells Results in Decreased p53 Expression.

Western blot analysis of lysates from H1355 cells transfected with mismatch (M4M-N9), scrambled N9 (N9-scr), L7, N7, and N9 collected 48 hours later.


FIGURE 4.13 Induction of lower molecular weight p53 bands is induced by agRNA ${ }^{\mathrm{p53}}$.

H1355 cells were transfected with mismatch control agRNAs (M3M, M4M), N9scr, QsiR, N7 or N9. Cells were harvested after 48 hours, cell lysates were analyzed using western blotting analysis for p53 (D01, Santa Cruz)and GAPDH (antibody specifics).


FIGURE 4.14 Figure 4.14 Western blot analysis of agRNA effects on p53 levels in p53 WT, mutant, and null cell lines.

A549, H1299, Mia PaCa2, and Panc1 cells were transfected with mismatch control agRNAs (M3M, M4M), N9-scr, QsiR, N7 or N9. Cells were harvested after 48 hours, cell lysates were analyzed using western blotting analysis for p53 (D01, Santa Cruz)and GAPDH (antibody specifics).


FIGURE 4.15H1355 Cells are Sensitized to a p53 Dependent Chemotherapy by Transfection with N9.

H1355 cells were reverse transfected with Dharmafect 1 lipid only, 100 nM N9M4M, 100 nM N7, or 100 nM N9; 24 hours later cells were treated with four-fold decreasing dilutions of doxorubicin. Relative cell viability was determined 96 hours after doxorubicin treatment was given using the MTS assay as described in methods.


FIGURE 4.16 Mutant-p53 containing cell lines are sensitized by agRNA ${ }^{\text {p53 }}$ to p53 inducing chemotherapy.
(A) Mia PaCa2 or (B) Panc1 cells were reverse transfected with Dharmafect 1 lipid only, 100 nM N9-M4M, 100 pM N9, as well as an untransfected control plate was plated in 96 well plate; 24 hours later cells were treated with four-fold decreasing dilutions of doxorubicin. Relative cell viability was determined 96 hours after doxorubicin treatment was given using the MTS assay as described in methods.


FIGURE 4.17 H1355 cells are killed selectively by N9.
H1355 cells were reverse transfected with 4-fold dilutions of siRNA:lipid or agRNA: lipid complexes with the indicated dsRNA oligo beginning at 100 nM on day zero, transfection complexes were handled in serum free RPMI, cells were plated in R5. Relative cell viability was determined 120 hours after transfection using the MTS assay as described in methods.


FIGURE 4.18 Figure 4.18 N9-induced cytotoxicity does not occur in wildtype p53 or p53 null cell lines.
(A) A549, (B) H358, and (C) H1299 cells were reverse transfected with 4-fold dilutions of siRNA:lipid or agRNA: lipid complexes with the indicated dsRNA oligo beginning at 100 nM on day zero, transfection complexes were handled in serum free RPMI, cells were plated in R5. Relative cell viability was determined 120 hours after transfection using the MTS assay as described in methods.


FIGURE 4.19 Colony Formation is inhibited in Cell Lines Harboring mutant-p53.

H1355, H1155, and MIA PaCa2 cells were transfected with 25 nM N9-M4M, si-p53-554, or N9. Twenty four hours after transfection the cells were split and plated for liquid colony formation assay with two wells per cell line per treatment plated at two different densities (A) 100 cells/well or (B) 1000 cells/well in a 6 well plate. Cells were allowed to grow undisturbed until colonies $>50$ cells/colony were visible, plates were then fixed and stained with $0.05 \%$ methylene blue and counted using ChemiDoc (BioRad, Hercules, CA).


All transfections done at 25 nM

FIGURE 4.20 Targeting 5' of the coding region of TP53 at multiple sites results in variable effects on p53 protein expression and cytotoxicity of cells. H2009 cells were transfected with 10 nM of the indicated dsRNA oligo, 96 hours post-transfection cells were harvested and viable cells were quantitated using the Trypan exclusion. Cell counts were normalized to control treated cells. H2009 cells were lysed and lysates analyzed by western blotting analysis. Changes in p53 protein expression were found after transfection with agRNAs ${ }^{\text {p53 }}$. Lipid is Dharmafect 1 alone. p53 has several lower molecular weight splice forms that are detectable by western blot. Data in this figure not produced by Rachel Greer.


FIGURE 4.21 Cells harboring mutant-p53 protein respond with cell death in response to agRNA ${ }^{\text {p53 }}$.
(A) A549, (B) H358, (C) H2009, (D) H1355, (E) HBEC3KT, (F) SAOS2, and (G) MDA-MB-231 cells were reverse transfected with N27-M4M, N27-scr, QsiR, and N27 as indicated as four-fold dilutions starting at 25 nM on day zero, transfection complexes were handled in serum free RPMI, cells were plated in R5. Relative cell viability was determined 120 hours after transfection using the MTS assay as described in methods.


FIGURE 4.22 Cytotoxicity induced by agRNA ${ }^{\text {p53 }}$ treatment is selective for cell lines with mutations within the DBD of p53.
(A) H157 and (B) H1373 cells were reverse transfected with N27-M4M or N27 as four-fold dilutions starting at 25 nM on day zero, transfection complexes were handled in serum free RPMI, cells were plated in R5. Relative cell viability was determined 120 hours after transfection using the MTS assay as described in methods.


FIGURE 4.23 WRAP53 levels do not correlate with cytotoxicity from agRNAp53 treatment.

H2009 cells were transfected with 20 nM luciferase siRNA, QsiR, N27, WRAP53 siRNA, or WRAP53a siRNA. Cells were harvested after 24 hours, RNA was isolated using the RNeasy Plus kit (Qiagen), cDNA made using iScript kit, and expression levels quantitated using Taqman probes (ABI) targeting the indicated gene (p53 or WRAP53).


FIGURE 4.24 LincRNAp21 levels are dramatically induced by agRNAp53 treatment.

H2009 cells were transfected with 20 nM luciferase siRNA, QsiR, N27, WRAP53 siRNA, or WRAP53a siRNA. Cells were harvested after 24 hours, RNA was isolated using the RNeasy Plus kit (Qiagen), cDNA made using iScript kit, and expression levels quantitated using syber green based pPCR.

## CHAPTER FIVE

## SMAC Mimetics as an Adjuvant Chemotherapy Combination

### 5.1 Introduction

Apoptosis is an evolutionarily conserved process that was originally described by a series of distinct morphological events (Kerr, et al., 1972). Characteristic features of apoptosis include cell shrinkage, nuclear fragmentation, loss of membrane architecture, membrane blebbing, as well as changes in plasma membrane lipid composition (Kerr, et al., 1972). Our understanding of the biochemical processes involved in apoptosis comes from genetic studies in C. elegans. During development of C. elegans, it is critical for excess cells to die, a mutation in a gene called ced3 casuses accumulation of these excess cells in the adult animal, they also saw that ced3 shared homology with human IL-1 $\beta$ converting enzyme (ICE) (Yuan, et al., 1993). These two proteins were the first to be discovered in a family of cysteine-dependent aspartate-directed proteases (caspases). The discovery of ced3 as a caspase was critical in bringing the field of apoptosis into mainstream science. There are twelve caspases in the human genome; however, not all are known to be involved in apoptosis (caspase-1[ICE], caspase-4, caspase-5, and caspase-11) (Yuan, 2006). There are two classes of apoptogenic caspases, initiator caspases and effector/executioner caspases.

Caspases are produced as inactive zymogens, and most require processing for maximal enzymatic activity. Initiator caspases (caspase-2, $-8,-9$, and -10 ) rely on upstream signals for activation, which requires being a part of a large protein complex and autoproteolysis. Effector caspases (caspase-3, -6, -7) require proteolytic cleavage by initiator caspases for maximal enzymatic activity, these caspases go on to cleave a number of proteins which facilitates the death of the cell such as PARP and ICAD (Yuan, 2006).

There are many pathways that can lead to apoptosis, one such pathway is the death receptor mediated (extrinsic) pathway. The death receptor mediated pathway is activated when a ligand (such as TNF $\alpha$, TRAIL, FasL, etc...) binds to its cognate receptor, which sounds simple enough, but nothing is ever that simple. TNF $\alpha$ binding to the TNF receptor (TNFR) is not sufficient for signaling of apoptosis; there is a fine balance of both pro-survival and pro-apoptotic signaling that can occur through TNFR (Kieser, 2008). Upon ligand binding, TNFR trimerizes and recruits TRADD, TRAF2, TRAF1, cIAP1, cIAP2, and RIPK1 (termed complex I). Complex I signals for cell survival through the JNK and canonical NF-кB pathways, and involvement of both cIAP1 and cIAP2 prevents dissociation of TRADD, TRAF2, and RIPK1 from TNFR1. In the absence of cIAPs, TRADD, TRAF2, and RIPK1 associate in the cytosol with FADD and caspase-8 resulting in caspase-8 activation, cFLIP can also prevent caspase-8 activation. Regulation of cell death from the TRAIL receptors (DR4 and DR5) is
more straightforward, with trimerization of the receptor recruiting directly FADD, caspase 8 or caspase 10, and/or cFLIP. However, there are decoy receptors for TRAIL (DcR1, DcR2, and OPG) which can bind to TRAIL and prevent activation of DR4 and DR5. Fas is the last member of the TNFR super family (TNFRSF) of receptors that is known to signal for apoptosis. Like DR4 and DR5, activation of Fas induces receptor trimerization, and recruitment of FADD, caspase-8 or -10, and/or cFLIP.

Another pathway that activates apoptosis is the mitochondrial (or intrinsic) pathway. Activation of mitochondrial apoptosis is regulated by a family of both pro- anti-apoptotic proteins named for the founding member, BCL-2. There is a fine balance between the pro-apoptotic and anti-apoptotic BCL-2 family members, and that balance regulates how a cell will respond to an intrinsic apoptogenic stress (P. Li, et al., 2004). Classification as a BCL-2 super family member relies on homology of BCL-2 homology (BH) domains. There are four distinct BH domains, $\mathrm{BH} 1, \mathrm{BH} 2, \mathrm{BH} 3$, and BH 4 . Anti-apoptotic BCL-2 family members (BCL-2, BCLxL, BCL-W, A1, MCL-1) contain all four BH domains. The pro-apoptotic proteins BAX and BAK contain BH1-3, and the pro-apoptotic BH3 only family members (BAD, BID, BIM, NOXA, PUMA) only contain the BH3 domain. BAX and BAK are required to initiate mitochondrial-induced apoptosis, and BCL-2, BCLxL, as well as others antagonize the ability of BAX and BAK to lead to mitochondrial release of cytochrome c as well as other pro-
apoptotic proteins (P. Li, et al., 2004). The BH3 only proteins serve as upstream mediators of apoptosis, they sit and wait for a pro-apoptotic signal, whether it's by cleavage (BID), phosphorylation (BAD), or transcriptional activation (PUMA and NOXA), and then they antagonize the ability of the anti-apoptotic BCL-2 familiy members to bind BAX and BAK. Upstream signals for mitochondrialinduced apoptosis include genotoxic stress, removal of growth factors, metabolic crisis, oxidative stress, chemotherapy, and others.

A less well known pathway that activates apoptosis is ER stress-induced apoptosis. The ER is the primary site for protein synthesis and folding for secreted, membrane bound, and some organelle targeted proteins, it comprises roughly one third of the newly translated proteins in a cell. With such responsibility for the normal functioning of a cell, the ER is primed to respond quickly when stresses alter cellular energy levels; redox state; intra-ER concentration of $\mathrm{Ca}^{2+}$; misfolded, unfolded, or excess protein in the ER lumen; lipid or glycolipid imbalances occur in the ER. So called ER stress can signal for three salvage pathways, the unfolded protein response (UPR), ER-associated degradation, and the control of protein translation (Figure 5.1) (Boyce \& Yuan, 2006). However, if these salvage attempts fail, the ER can directly signal for apoptosis. In mice, ER stress causes the release of $\mathrm{Ca}^{2+}$ in a BAX-BAK dependent fashion from the ER, PUMA and NOXA expression is induced in a p53dependent fashion, and directly activate mCaspase-12 (J. Li, Lee, \& Lee, 2006;

Moenner, Pluquet, Bouchecareilh, \& Chevet, 2007). The human gene encoding Caspase-12 contains a frame shift mutation which causes a premature stop codon preventing CASPASE-12 expression; however, further sequence analysis shows that even if CASPASE-12 were expressed that a protein coding mutation would obliterate enzymatic activity by mutation of the SGH box (mutated to SGS) (Fischer, Koenig, Eckhart, \& Tschachler, 2002). In light of these findings, an alternative caspase was explored, and it was found by multiple groups that CASPASE-4 is activated by ER stress (Figure 5.2) (Fischer, et al., 2002; Hitomi et al., 2004; Pei-Chun Liao, 2008).

The second mitochondrial activator of caspases (SMAC) is the natural antagonist of IAP inhibition of caspases by binding to IAPs in a competitive fashion to caspases. SMAC is localized in mitochondria, within the inter membrane space, and is released along with cytochrome c when BAX and BAK signal for initiation of apoptosis to ensure that apoptosis occurs. Evasion of apoptosis is one of the hallmarks of cancer; cancer cells have increased expression of BCL-2, BCL-xL, XIAP, surivivin, cFLIP, as well as other anti-apoptotic proteins. One targeted approach to overcome resistance to apoptosis has been target IAPs with a small molecule mimetic of SMAC. SMAC binds to IAPs using its 4 N-terminal residues, AVPI, so small molecules were designed to bind to bind BIR3 of XIAP in the same fashion as AVPI (L. Li, et al., 2004). In the initial paper from Xiaodong Wang’s lab it was shown that SMAC
mimetic could bind to XIAP, could induce activation of caspase-3 in cell free assays, and that the combination of SMAC mimetic with TNF $\alpha$ or TRAIL could induce caspase activation (L. Li, et al., 2004). In a large screen across 50 NSCLCs it was found that roughly $15 \%$ are sensitive to SMAC mimetic alone, which is due to an autocrine TNF $\alpha$ loop that is dependent on TNF $\alpha$, TNFR1, caspase-8, and RIPK1 (Petersen, et al., 2007). Two other studies that came out the same week as the Petersen paper from two other groups further showed that SMAC mimetics induce proteaosomal degradation of cIAP1 and cIAP2 but not XIAP, and that loss of cIAP1/2 from TNFR1 induces activation of both canonical and non-canonical NF-кB signaling that induces TNF $\alpha$ production (Varfolomeev, et al., 2007; Vince, et al., 2007).

While there is some single agent activity seen for SMAC mimetics, it is unlikely that any one molecule from this class of drugs would become FDA approved as a single agent, owing to the relatively low response rate in vitro. Therefore, the most likely route for SMAC mimetics to become used in the clinic is as part of a combination with one or more conventional chemotherapies; however the study of SMAC mimetics in combination with chemotherapy has been done on a limited basis. The first study published in 2005, explores compound 3 as a single agent as well as in combination with TRAIL or etoposide in a small panel of breast cancer cell lines (MDA-MB-231, MDA-MB-453, and T47D), and shows some single agent activity of compound 3 as well as synergy
between TRAIL or etoposide in combination (Bockbrader, et al., 2005). The next study was done on three colorectal carcinoma cell lines and found that cotreatment of NSAIDs with SMAC mimetics can sensitize colorectal carcinomas to NSAIDs by an increase in active caspase-3 (Bank, Wang, Du, Yu, \& Zhang, 2008). Another study found that H 460 cells can be sensitized to cisplatin by SMAC mimetics, by co-IPs of caspase-3 with XIAP, as well as propidium iodide staining, and caspase-3 activity assays (Checinska, Hoogeland, Rodriguez, Giaccone, \& Kruyt, 2007). A group in China found that using luteolin to inhibit SMAC mimetic induced NF-кB activation could synergistically kill a lung and colon cancer cell line, while not harming normal immortalized human bronchial epithelial cell lines (Bai et al., 2009). An Italian group studied three hematological tumor lines, all from different malignancies, in combination with cytarabine, idarubicine, etoposide, and imatinib, and found that SMAC mimetics can sensitize hematological tumor lines to these drugs (Servida et al., 2010). Another study showed that four melanoma cell lines can be sensitized to TRAIL and bortezomib by SMAC mimetics as measured by PARP cleavage, and cell viability assays (Lecis et al., 2010). Sun et al found that four head and neck squamous cell carcinoma cell lines could be sensitized to cisplatin or etoposide by either SMAC overexpression or SMAC mimetic treatment characterized by caspase-3 cleavage and cytochrome c release from the mitochondria (Q. Sun, Zheng, Zhang, \& Yu). Two similar studies from the same group found that
multiple pancreatic cancer cell lines (up to 8) can be sensitized to TRAIL, gemcitabine, and doxorubicin in vitro and in vivo (Awasthi et al., 2011; Dineen, et al., 2010). Probst et al find in a limited panel of cancer cell lines, consisting of 2 breast, 1 colon, 2 lung, 2 pancreatic, 1 prostate, and two melanoma cell lines, that JP1400 (a fourth generation compound 3 analogue) can sensitize to gemcitabine, paclitaxel, 5-FU, cisplatin and SN38, and claims that the sensitization is dependent on TNF $\alpha$ induction (Probst et al., 2010). Resistance to SMAC mimetics in this study was defined by induction of cell death by 100 nM JP1400. These ten cell lines were tested for $\mathrm{IC}_{50}$ to gemcitabine, paclitaxel, 5FU, cisplatin, etoposide, and SN38 with or without addition of 100 nM SMAC mimetic. Most of the figures in this study are from experiments done on A2058 cells, which were the model cell line of the Varfolomeev et al study, one of the initial studies showing single agent SMAC mimetic activity was dependent on TNF $\alpha$ signaling (Probst, et al., 2010; Varfolomeev, et al., 2007). The study by Dean et al. was done using a different type of SMAC mimetic, XAC 1396-11, which binds on XIAP near the BIR2 domain instead of BIR3 like most other SMAC mimetics, which is why there is some single agent activity seen of the SMAC mimetic in this study on H460 and A549 (Dean et al., 2009). This study also claims that synergy is seen between SMAC mimetic and vinorelbine, cisplatin, or the combination of vinorelbine and cisplatin; however, only a table summarizing calculated CI values is given, no raw data or drug response curves
are ever shown, with the exception of one western blot showing that 2.5 nM vinorelbine with $5 \mu \mathrm{M}$ SMAC mimetic causes an increase in PARP cleavage. These studies are very comprehensive in their experimental depth; however they are limited in by the small number of cell lines explored.

### 5.2 RESULTS

5.2.1 SMAC MIMETIC SYNERGIZES WITH CONVENTIONAL CHEMOTHERAPY IN NSCLC cell lines by MTS Assay.

While the ability to target patient populations that will respond to a targeted agent is an important strategy in designing clinical trials, for example (insert clinical trial where EGFR mutations was a selection criteria); the most likely route for a SMAC mimetic to get into the clinic is not by targeting patients that have circulating TNF $\alpha$ levels but instead as part of a combination chemotherapy regimen. Taking this into consideration, a sub-panel of the 50 NSCLCs studied in Petersen et al. were created by selecting NSCLCs that were resistant to SMAC mimetic (up to $100 \mu \mathrm{M}$ ), this panel included sixteen NSCLC cell lines resistant to JP1201 monotherapy, two immortalized human bronchial epithelial cells (HBECs), and two genetically modified malignant HBEC lines (Petersen, et al., 2007). These cell lines were used in combination studies where JP1201 (a second generation SMAC mimetic) was held at a constant concentration $(10 \mu \mathrm{M})$ and conventional chemotherapies were given
simultaneously at varying concentrations. Cells were considered to respond to the combination of JP1201 + chemotherapy if the $\mathrm{IC}_{50}$ decreased at least by 20 fold (Table 5.1). In combinations of JP1201 with doxorubicin, erlotinib, gemcitabine, paclitaxel, vinorelbine, or the combination of carboplatin + paclitaxel in at least one cell line showed at least a 20 -fold sensitization with co-treatment with JP1201, with some chemotherapies showing up to 31,000 fold decrease in $\mathrm{IC}_{50}$ in the presence of JP1201 (Table 5.1). There were three general phenotypes seen for the combination of JP1201 with doxorubicin, gemcitabine, erlotinib, paclitaxel, or vinorelbine, but only one phenotype seen for the combination of JP1201 with cisplatin (Figure 5.3). In the case of any single chemotherapy tested, there is substantial variability in the degree of response between cell lines to the combination with JP1201. Conversely, given any one cell line tested, there is heterogeneity of response between the combinations of JP1201 with the chemotherapies tested. All but one NSCLC line were sensitized to the combination of JP1201 + vinorelbine, while almost no cell lines were sensitized to the combination of JP1201 + cisplatin. Of importance, three NSCLCs with wild type EGFR were sensitized to the EGFR TKI, erlotinib.

One of the largest fold shifts in sensitivity identified by MTS assay was the combination of JP1201 with vinorelbine in H1819 cells (Figure 5.4). To confirm this shift in sensitivity, both colony formation and annexin V staining were used as alternative methods for measuring $\mathrm{IC}_{50}$. The combination of JP1201
with vinorelbine on H 1819 cells reduced colony formation greater than $50 \%$ at a dose of 500 pM vinorelbine and $10 \mu \mathrm{M} \mathrm{JP1201} \mathrm{(Figure} \mathrm{5.4)}$. 48 hours after drug treatment showed approximately a $20 \%$ increase in apoptosis induction when treated with a combination of $10 \mu \mathrm{M} \mathrm{JP1201} \mathrm{and} 50 \mathrm{pM}$ vinorelbine (compared to vehicle treated control cells), and 60\% increase with a combination of $10 \mu \mathrm{M} \mathrm{JP} 1201$ and 500 nM vinorelbine (Figure 5.4). These data support the MTS assay showing at least a 10,000 fold decrease in $\mathrm{IC}_{50}$ when JP1201 is combined with vinorelbine and paclitaxel in H1819. Furthermore, we confirmed the range of sensitization seen in mass culture MTS assays with similar results for other cell lines in colony formation assays (Table 5.2).

### 5.2.2 STATISTICAL ANALYSIS OF DRUG COMBINATIONS

Considering the possible outcomes when two drugs are combined, the ideal would be for the two drugs to yield synergy; synergy being where the effect of the drugs in combination is greater than the sum of the effect of each drug alone. The other possible outcomes would be additivity; which is where the effect of the drugs in combination is equal to the sum of the effect of each drug given alone, or antagonism; which is where the effect of the drugs in combination is less potent that the sum of each drug given alone. To quantitate the effects seen when JP1201 is combined with standard chemotherapy, combination indices (CI) were calculated for each cell line for each chemotherapy (Table 5.3) (Chou \& Rideout,
1991). Both paclitaxel and vinorelbine show greater frequency of synergy in combination with $10 \mu \mathrm{M} \mathrm{JP1201}$, while cisplatin shows no synergy in combination with $10 \mu \mathrm{M} \mathrm{JP1201}$.

### 5.2.3 JP1201 EXHIBITS GREAT SELECTIVITY IN CHEMOTHERAPY

 SENSITIZATION IN ISOGENIC CELL LINE PAIRSIncluded in this panel are several types of isogenic cell line pairs: a tumor /normal lung epithelial cell pair, HCC4017 and HBEC30KT established from the same patient; non-transformed HBEC transformed HBEC pair, HBEC3KT where defined oncogenic changes, Kras G12V and p53 shRNA, were introduced and tumorigenic clones (clone 1, clone 5) isolated by soft agar formation; and two sets of tumor lines that were each established from the same patient. These pairs were isolated before and after treatment of the same patients with cisplatin and etoposide: NCI-H1693 (before) and NCI-H1819 (after); NCI-H1993 (before) and NCI-H2073 (after) (Phelps, ramierez, sato). JP1201 sensitizes HCC4017 but not HBEC30KT to chemotherapy (Figure 5.5). HBEC3KT tumorigenic clones 1 and 5 are sensitized 10-20 fold to vinorelbine (20 fold) or paclitaxel (12-15 fold), while the parental HBEC3KT cells are not sensitized to chemotherapy (Figure 5.6). Surprisingly, H1819 and H2073; which were started from residual NSCLC cells harvested after neoadjuvant platinum and etoposide chemotherapy, were sensitized ~200 fold greater to chemotherapy than H1693 and H1993, which were
started from NSCLC samples from each respective patient prior to treatment (Table 5.1). Thus we found specificity of JP1201 sensitization for tumor compared to normal cells and even in tumor cells after neoadjuvant chemotherapy.

### 5.2.4 Combination of SMAC MIMETIC (JP1201) AND CHEMOTHERAPY

 CONTROL NSCLC XENOGRAFT GROWTHIn vitro, NCI-H1395 cells demonstrated a 134- and 33-fold increase in sensitivity to gemcitabine and vinorelbine, respectively, when co-treated with JP1201. In order to determine if this effect is observed in vivo, NCI-H1395 subcutaneous xenografts were treated with the same drug combinations. One of the challenges in treating lung cancer is that patients are typically diagnosed with late stage disease. In order to most closely mimic human disease, tumors were allowed to grow before treatment began. NCI-H1395 cells were injected subcutaneously on the left flank of NOD/SCID mice and tumors were allowed to establish for 40 days ( $\sim 150 \mathrm{~mm}^{3}$ ). The mice were then randomized based on tumor volume, and treated for three weeks with saline; $25 \mathrm{mg} / \mathrm{kg}$ gemcitabine; 2.4 $\mathrm{mg} / \mathrm{kg}$ vinorelbine; $6 \mathrm{mg} / \mathrm{kg}$ JP1201; $25 \mathrm{mg} / \mathrm{kg}$ gemcitabine and $6 \mathrm{mg} / \mathrm{kg} \mathrm{JP1201;}$ or $2.4 \mathrm{mg} / \mathrm{kg}$ vinorelbine and $6 \mathrm{mg} / \mathrm{kg}$ JP1201 starting on day 43 post tumor injection. Saline, gemcitabine, and JP1201 were given i.p. three times a week, vinorelbine was given i.p. twice a week; the animals were sacrificed 24 hours
after the last treatment. Tumors in mice treated with saline, gemcitabine, or JP1201 alone continued to grow exponentially during the three week treatment period. Tumors in mice treated with vinorelbine continued to grow, albeit at a decreased rate through the treatment period. Tumors of animals treated with JP1201 + gemcitabine showed an inhibition of tumor growth, while the tumors of animals treated with JP1201 + vinorelbine showed tumor regression (Figure 5.7). These data agree with the average tumor weights per treatment group (Figure 5.8). Tumors from the JP1201 + vinorelbine group showed a 70\% decrease in tumor burden as compared with the vinorelbine group. Similarly, tumors from the JP1201 + gemcitabine group showed a 60\% decrease in tumor burden as compared with the tumors treated with gemcitabine.

The induction of apoptosis in the xenografts was explored using terminal deoxynucleotidyl transferase dUTP nick end labeling (TUNEL) immunofluorescence on paraffin embedded tumor sections from three tumors per treatment group, the data are the average of three images per slide, three slides per treatment group. There is a marked increase in TUNEL staining in the JP1201 + gemcitabine and JP1201 + vinorelbine groups, up to $90 \%$ increase compared to single agent and vehicle control treated tumors (Figure 5.9).

I then wanted to know if the reduction in tumor growth would translate to an increase in survival in NSCLCs with very aggressive xenograft growth, to study this NCI-H157 was used, which was one of the NSCLCs that showed a
large sensitization to erlotinib with JP1201. Mice received treatment; saline, 2.4 $\mathrm{mg} / \mathrm{kg}$ vinorelbine, $12.5 \mathrm{mg} / \mathrm{kg}$ erlotinib, $6 \mathrm{mg} / \mathrm{kg}$ JP1201, $6 \mathrm{mg} / \mathrm{kg} \mathrm{JP1201}+2.4$ $\mathrm{mg} / \mathrm{kg}$ vinorelbine, or $6 \mathrm{mg} / \mathrm{kg} \mathrm{JP1201}+12.5 \mathrm{mg} / \mathrm{kg}$ erlotinib until tumor size reached the maximum allowable and mice were then sacrificed (Figure 5.10). The tumors of mice treated with saline continued to grow exponentially; median survival time was 19 days post tumor injection. Tumor growth was slowed by treatment with either vinorelbine or JP1201 and survival time was extended by 5 days compared to saline, however, the combination of JP1201 + vinorelbine further slowed tumor growth and extended median survival time by 15 days compared to control (Figure 5.11).

### 5.2.5 IAP SELECTIVE DEPENDENCE IN JP1201 AND CHEMOTHERAPY

 COMBINATIONSJP1201 is a pan-IAP inhibitor, which is known to inhibit cIAP1, cIAP2, and XIAP, its activity against the other five members of the IAP family have not been looked at (L. Li, et al., 2004). I thus wanted to see which of these three IAPs contributes to chemotherapy resistance by using siRNAs directed at cIAP1, cIAP2, or XIAP and assaying for sensitization to gemcitabine, paclitaxel, and vinorelbine in the presence of IAP knockdown. Knockdown of cIAP1 or cIAP2 in the presence of gemcitabine does not sensitize H1395, H358, H1819, or H2887 to gemcitabine; while the knockdown of XIAP in the presence of gemcitabine in all
four cell lines does sensitize the cell lines to gemcitabine, in a similar fashion to combination of JP1201 and gemcitabine treatment in these cells (Figure 5.12). Knockdown of cIAP1, cIAP2, or XIAP gave increasing sensitization to paclitaxel which is best seen in H358 cells where the largest sensitization to paclitaxel is seen out of H1395, H358, H1819, and H2887 cells, additionally the triple knockdown of cIAP1, cIAP2, and XIAP yields the greatest amount of sensitization to paclitaxel in all cell lines (Figure 5.13). In the presence of vinorelbine knockdown of any one of these IAPs results in sensitization to vinorelbine, and the triple knockdown giving further sensitization (Figure 5.16). Knockdowns were validated in H1395 cells (Table 5.4).
5.2.6 TNF $\alpha$ SIGNALING DOES IS NOT THE MECHANISM FOR JP1201-INDUCED SENSITIZATION TO CHEMOTHERAPY

Autocrine TNF $\alpha$ secretion has been shown to be strongly predictive of sensitivity to JP1201 as a single agent in a subset of NSCLC (Petersen et al., 2007). Using a sandwich ELISA, TNF $\alpha$ secretion induced by treatment with JP1201, gemcitabine, or vinorelbine (with and without JP1201) was measured 12 hours post treatment in eight cell lines. H2126 (a JP1201 sensitive line) secreted TNF $\alpha$ under all conditions tested, with increased production when treated with 20 nM vinorelbine (Figure 5.17). The other seven cell lines tested (H157, H1819, H2073, H2882, H1395, H358, and A549); however, showed no TNF $\alpha$ secretion
even after treatment with 20 nM vinorelbine. Induction of TRAIL by chemotherapy could be another mechanism for JP1201-mediated sensitization to chemotherapy; however TRAIL was not secreted in the same eight cell lines after JP1201, vinorelbine, or gemcitabine treatment (Figure 5.18).

To see if TNF $\alpha$ is being turned on at later time points that would coincide with the length of the MTS assay conditioned media was collected at $12,24,48,72$, and 96 hours post treatment in the same eight NSCLC lines. No detectable TNF $\alpha$ secretion was found under any conditions tested (Figure 5.19).

I then tried the approach of using TNF $\alpha(10 \mathrm{pg} / \mathrm{mL})$ in place of JP1201 in combinations with gemcitabine and vinorelbine, and found that no sensitization to gemcitabine or vinorelbine was seen. Finally; the combination of TNF $\alpha$ with gemcitabine or vinorelbine in the presence of XIAP knockdown showed no sensitization (Table 5.3).

### 5.2.7 Chronic JP1201 treatment induces TNFa secretion in vitro and

 IN VIVO IN JP1201-RESISTANT NSCLCs.Previous studies using pancreatic cancer mouse models showed an induction of TNF $\alpha$ in xenografts after treatment with either JP1201 alone or JP1201 + gemcitabine (Dineen, et al., 2010). It could be that the treatment with JP1201 is having an effect on the microenvironment that is causing TNF $\alpha$ secretion or it could be a direct effect of chronic JP1201 treatment on the tumor
cells themselves. To test the second hypothesis, and to be able to compare these results with TNF $\alpha$ staining from the current xenograft experiment, H1395 cells were treated for three weeks with either 100 nM or 1000 nM JP1201. H1395 cells (untreated, 100 nM JP1201 pre-treated, and 1000 nM JP1201 pre-treated) were plated before an acute 12hr treatment with the following: no treatment, 100 nM JP1201, 1000 nM JP1201, 20 nM gemcitabine, 20 nM paclitaxel, or 20 nM vinorelbine (Figure 5.20). Conditioned media was collected after 12 hours to measure TNF $\alpha$ secretion. The parental (no long term JP1201 treatment) H1395 did not show any induction of TNF $\alpha$ with any acute treatment (Figure 5.21). H1395 cells pretreated for three weeks with 100 nM JP1201 showed induction of TNF $\alpha$ when treated with 20 nM gemcitabine, paclitaxel or vinorelbine. H1395 cells pretreated for three weeks with 1000 nM JP1201 showed induction of TNF $\alpha$ under all acute treatment conditions (including untreated control) except low dose (100nM) JP1201.

Immunofluorescent staining of H1395 xenograft tumor sections for an antibody selective for human TNF $\alpha$ shows a significant increase in TNF $\alpha$ staining in JP1201, JP1201 + gemcitabine, and JP1201 + vinorelbine treated tumors compared with saline, gemcitabine, or vinorelbine treated tumors (Figure 5.22). TNF $\alpha$ staining was measured using three slides per animal, three images per slide, average FITC signal per image was averaged for each treatment group. These
data show that the tumors receiving combination treatment have the largest induction of TNF $\alpha$, with JP1201 + vinorelbine showing the most TNF $\alpha$ staining.

### 5.2.8 Inhibition of downstream TNFa signaling does not rescue

 NSCLCs From JP1201 + VINORELBINENCI-H1395 cells were transfected with siRNAs against luciferase, RIPK1, caspase 8, TNFR1, and caspase 3, then treated with JP1201 + vinorelbine. The knockdown of caspase 8, RIPK1, or TNFR1 did not protect the cells from JP1201 + vinorelbine, while the knockdown of caspase 3 offered some protection against JP1201 + vinorelbine (Figure 5.23). Analysis of knockdown was done by q-PCR, which showed fairly good (greater than 50\%) knockdown of each gene targeted (Table 5.4). These results suggest the effects of JP1201 + vinorelbine is dependent on an apoptotic pathway different from the TNF $\alpha$-RIPK1 pathway, indicating JP1201 sensitization to standard chemotherapies occurs by a TNF $\alpha$ independent mechanism.

### 5.2.9 CIAP1 REGULATES ACTIVATION OF APOPTOSIS AT THE ER MEMBRANE

The fact that both vinorelbine and paclitaxel are sensitized more often and to the greatest extent by JP1201 made me stop and consider what both agents share in common. Both agents are anti-mitotics, and while the general mechanism is quite clear, that they act by directly binding tubulin and thus alter tubulin dynamics. However, the complexity of the cellular response to such inhibition is
poorly understood, there are some reports in the literature where paclitaxel activates TNF $\alpha$, and caspase-8, -10 dependent apoptosis and other reports where paclitaxel acts through caspase-9 dependent apoptosis (Park et al., 2004; Zhang, Qiu, Jin, Guo, \& Guo, 2009). Scouring through the literature gave rise to the idea that anti-mitotics could potentially be interfering in ER to Golgi transport, on the assumption that binding of vinorelbine or paclitaxel would alter microtubule structure enough to disrupt dynein or kinesin progression down microtubules (PeiChun Liao, 2008). ER stress, such as inhibition of ER to Golgi transport, activates a multitude of signaling pathways, one such pathway is activation of CHOP by ATF4 and ATF6, treatment with paclitaxel and vinorelbine cause expression of CHOP in H2887 cells similar to treatment with tunicamycin, while treatment with gemcitabine does not cause expression of CHOP (Figure 5.24).

During times of ER stress, mammalian cells active IRE1 recruits TRAF2 and ASK1 which activates JNK (Boyce \& Yuan, 2006; Marciniak \& Ron, 2006). TRAF2 can activate JNK at the TNFR as well, and TRAF2 recruits cIAP1/2 to the TNFR, which left me wondering does TRAF2 recruit cIAP1/2 to the ER as well? I then looked for cIAP1 interactions with the IRE1 complex using monoclonal antibodies against ASK1 and TRAF2, as well as a polyclonal antibody against IRE1 and in all cases cIAP1 was pulled down from lysates from untreated H2887 cells (Figure 5.25).
5.2.10 ER STRESS INDUCED APOPTOSIS MEDIATED THROUGH CASPASE 4 AS MECHANISM FOR JP1201 + CHEMOTHERAPY SENSITIZATION

To better understand how NSCLCs are sensitized to the combination of JP1201 with vinorelbine, we used the Stress and Toxicity Cignal Finder 10pathway reporter array. H1395 cells were reverse transfected with a set of pathway specific firefly luciferase reporter constructs and control renilla luciferase constructs. Twenty four hours after transfection, cells were treated with $1 \mu \mathrm{M}$ JP1201, $1 \mu \mathrm{M}$ gemcitabine, $1 \mu \mathrm{M}$ vinorelbine, or JP1201 + vinorelbine for an additional 24 hours. Gemcitabine treatment induced p53 activity compared to un-treated control (Table 5.5). No significant pathway activity was activated by JP1201 or vinorelbine alone; however, the combination of JP1201 + vinorelbine resulted in ER stress activation (as a function of CBF/NF-Y transcriptional activity) and JNK activity (as a function of AP-1 transcriptional activity).

HCC4017, HBEC30KT, H1395, and H157 were reverse transfected with a set of pathway specific firefly luciferase reporter constructs and control renilla luciferase constructs, and cells were treated with JP1201 or the combination of JP1201 + vinorelbine for 24 hours after transfection. Activity of the indicated pathway was determined by firefly luciferase activity relative to control renilla luciferase activity (Table 5.6). Only the ER stress pathway was activated by combination therapy in all three NSCLC lines but not the normal cells. Caspase-4 is the putative initiator caspase for the ER stress induced apoptotic pathway
(Hitomi, et al., 2004; Pei-Chun Liao, 2008). Knockdown of caspase-4 protects H1395 cells against the effect to a greater extent than knockdown of caspase-3 or -9 (Figure 5.26). Additionally, using an antibody that only recognizes pro-caspase-4 but not activated caspase-4, we found that vinorelbine treatment resulted in to activation of caspase-4 over time, similarly to agents that are known to activate the ER stress pathway, thapsigargan and tunicamycin (Figure 5.27).

### 5.3 DIScussion

Evaluation of the apoptotic machinery in tumors has led to the development of therapeutic agents targeting this machinery, including SMAC mimetics (L. Li, et al., 2004; Oost et al., 2004; S. Sharma, Straub, \& Zawel, 2006; H. Sun et al., 2006; H. Sun, Z. Nikolovska-Coleska, C. Y. Yang, L. Xu, M. Liu, et al., 2004; H. Sun, Z. Nikolovska-Coleska, C. Y. Yang, L. Xu, Y. Tomita, et al., 2004; Zobel et al., 2006). This study addressed the utility of SMAC mimetic JP1201 in NSCLCs that do not express TNF $\alpha$ and are resistant to SMAC mimetic monotherapy. In a panel of NSCLC lines JP1201 frequently synergized with available chemotherapy agents, with considerable inter-tumor heterogeneity in NSCLC responses between drug combinations. In NSCLC xenografts, where JP1201 alone had little effect on tumor growth, the combination of vinorelbine or gemcitabine with JP1201 decreased tumor growth, which translated to an increase in survival of these mice. The frequent occurrence of synergy (particularly with paclitaxel and vinorelbine) suggests potential for JP1201 or similar drugs as a part
of combination chemotherapy for NSCLC. This agrees with the findings of Dean et al. (Dean, et al., 2009) who studied two NSCLC lines and found synergy with vinorelbine in combination with a different IAP antagonist that targeted XIAP. JP1201 sensitized many NSCLC lines to concentrations of vinorelbine (10-15 nM) and paclitaxel ( $\sim 100 \mathrm{nM}$ ) that are achievable in humans as steady state plasma (Leveque \& Jehl, 1996; Rowinsky, Jiroutek, Bonomi, Johnson, \& Baker, 1999). Also, three NSCLC lines, all wild-type for EGFR, were sensitized to the EGFR TKI, erlotinib at clinically achievable concentrations (Scheffler, et al., 2011). Studying a large panel of NSCLC lines, including the two studied by Dean et al., we found no synergy with JP1201 + cisplatin, while Dean using the BIR2 binding XIAP antagonist XAC 1296-11 saw synergy with cisplatin (Dean, et al., 2009). The reason for this discrepancy is not yet understood but suggests mechanistic specificity of the different SMAC mimetics. The lack of sensitization to cisplatin seen in this study correlates with p53 mutational status, indicating that p53 mutations may prevent cisplatin induced apoptotic signaling (Table 5.7).

Our panel includes three types of genetically paired cell lines, NSCLC lines started before (H1693 and H1993) and after etoposide/cisplatin treatment (H1819 and H2073), an isogenic HBEC3KT based system where oncogenic Kras and knockdown of p53 were introduced and tumorigenic clones were isolated from soft agar clones, and a tumor (HCC4017) and normal HBEC pair. Using these, we found sensitization by JP1201 to chemotherapy is specific for the
malignant phenotype, and NSCLC lines derived from samples after chemotherapy could be sensitized to chemotherapy more than NSCLCs that were chemo-naïve. Thus SMAC mimetic based combinations with chemotherapy may be effective in tumor cells resistant to chemotherapy alone.

XIAP is the only IAP with the ability to inhibit the enzymatic activity of an active caspase (Holcik, et al., 2001). Thus, it was reasonable to predict that stimulation of the intrinsic pathway of apoptosis would only require the inhibition of XIAP for apoptosis to occur (Yuan, 2006) such as was found in pancreatic cancer cell lines treated with JP1201 + gemcitabine (Dineen, et al., 2010). When we combine siRNA against cIAP1, cIAP2, or XIAP with gemcitabine, we see that the knockdown of XIAP mimics the combination of JP1201 + gemcitabine. By contrast we found knockdown of each cIAP1, cIAP2, or XIAP mimics to different degrees the effect seen when JP1201 is combined with paclitaxel or vinorelbine, suggesting unique roles for each IAP in sensitizing NSCLCs to anti-mitotics.

Inhibition of tubulin dynamics such as with vinorelbine can inhibit ER to Golgi transport, a trigger for ER stress-induced apoptosis (Boyce \& Yuan, 2006; Pei-Chun Liao, 2008). Analysis of pathways activated by the combination of JP1201 + vinorelbine in multiple cells lines revealed that the ER stress pathway is activated. Furthermore, western blotting, and siRNA-mediated rescue experiments also showed that caspase-4, the putative ER stress induced caspase, is activated after vinorelbine treatment, and knockdown of capsase-4 protected

NSCLCs from treatment of JP1201 + vinorelbine better than knockdown of the executioner caspase, caspase-3. There are reports that suggest cIAP1 is involved in a complex at the ER membrane that is responsible for activating apoptosis; however, further studies are needed to characterize the role of the ER stress pathway in sensitizing NSCLCs to chemotherapy by SMAC mimetics (Cheung, Lynn Kelly, Liston, \& Korneluk, 2006; Hitomi, et al., 2004; Szegezdi, Logue, Gorman, \& Samali, 2006).

We found JP1201 resistant NSCLC lines do no induce or secret TNF $\alpha$ after chemotherapy indicating the synergy seen between doxorubicin, gemcitabine, paclitaxel, or vinorelbine with JP1201 is TNF $\alpha$ independent. Studies adding recombinant TNF $\alpha$ with gemcitabine or vinorelbine also suggest that TNF $\alpha$ is not involved in the JP1201 induced sensitization to chemotherapy. This is further strengthened by the lack of additional sensitization when the combination of TNF $\alpha$ and gemcitabine or vinorelbine is given to cells where XIAP expression has been knocked down. The lack of protection of combinations of JP1201 + vinorelbine by the knockdown of caspase 8, RIPK1, or TNFR1 further suggests JP1201 is promoting apoptosis in a TNF $\alpha$ independent fashion (Petersen, et al., 2007; Varfolomeev, et al., 2007; Vince, et al., 2007).

In conclusion, we find that: a SMAC mimetic significantly sensitizes NSCLC lines to chemotherapy and EGFR targeted therapy; the sensitization varies between NSCLCs and between chemotherapeutic agents; the sensitization
is tumor specific and is stronger in NSCLCs that have progressed after neoadjuvant therapy; the required IAP target to be inhibited varied between chemotherapeutic agents; and the sensitization appeared to be TNF $\alpha$ independent, but dependent on two complementary apoptotic pathways, mitochondrial and ER Stress. These data strongly suggest the need to explore SMAC mimetics in combination with standard doublet chemotherapy as a new treatment approach for NSCLC patients.

| cell <br> line | Absolute fold decrease in $\mathrm{IC}_{50}$ of chemotherapy agents when combined with JP1201 |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Vinorel bine | Paclit axel | Doxoru bicin | Gemcita bine | Cispla tin | Erlotini b | Paclitax el/Carbo platin |
| H2073 | 31000 | 1 | 1 | 1 | 0.4 | 1 | 1 |
| H1819 | 4400 | 5600 | 1 | 6 | 0.7 | 4 | 18 |
| H2887 | 3600 | 22 | 7726 | 23 | 1 | 1 | 20 |
| H1993 | 270 | 6 | 1 | 2 | 0.4 | 0.7 | 5 |
| H358 | 397 | 17 | 13 | 4 | 1 | 6 | 12 |
| H441 | 181 | 3 | 4 | 16 | 0.5 | 4 | 2.8 |
| A549 | 100 | 4 | 5 | 2 | 0.7 | 18 | 4.6 |
| H2882 | 73 | 11 | 1 | 21 | 0.6 | 0.7 | 10 |
| H460 | 36 | 2 | 3 | 1 | 1.2 | 10 | 1.8 |
| H1395 | 33 | 43 | 10 | 134 | 1 | 0.4 | 23 |
| H1355 | 22 | 10 | 1 | 1 | 0.7 | 1 | NT |
| H157 | 16 | 32 | 3 | 2 | 1 | 111 | 15 |
| H1693 | 15 | 6 | 1 | 7 | 0.6 | NT | NT |
| H2009 | 12 | 4 | 1 | 3 | 1 | 1 | NT |
| H2087 | 1 | 4 | 4 | 1 | 1.4 | 1 | 3.6 |
| $\begin{aligned} & \text { HCC4 } \\ & 017 \end{aligned}$ | 25 | 10 | 6 | 15 | 0.7 | 1 | NT |
| $\begin{aligned} & \text { HBEC } \\ & \text { 30KT } \end{aligned}$ | 1 | 1 | 1 | 1 | 1 | 1 | NT |
| HBEC 3KT | 1 | 1 | 1 | 1 | 1 | 1 | NT |
| $\begin{aligned} & \text { HBEC } \\ & \text { 3KT } \\ & \text { clone1 } \end{aligned}$ | 20 | 12 | 3 | 7 | NT | NT | NT |
| $\begin{aligned} & \text { HBEC } \\ & \text { 3KT } \\ & \text { clone5 } \end{aligned}$ | 20 | 15 | 2 | 9 | NT | NT | NT |

TABLE 5.1 JP1201 Sensitizes NSCLC to doxorubicin, erlotinib, gemcitabine, paclitaxel, and vinorelbine in vitro.

Fold change is determined by dividing the median $\mathrm{IC}_{50}$ for each chemotherapy as a single agent $(\mathrm{n} \geq 4)$ by the median $\mathrm{IC}_{50}$ for each chemotherapy in combination with $10 \mu \mathrm{M}$ JP1201 ( $\mathrm{n} \geq 3$ ). NT represents instances where the combination was not tested.

| cell line | $\mathrm{IC}_{50}$ as determined by liquid colony formation |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | Gemcitabine | JP1201 + Gemcitabine | Paclitaxel | JP1201 + <br> Paclitaxel | Vinorelbine | JP1201 + <br> Vinorelbine | Erlotinib | JP1201 + Erlotinib |
| H157 | 1.7 | 0.05 | 0.27 | 0.1 | 0.3 | 0.03 | 5.2 | 0.9 |
| H1693 | 1.5 | 0.04 | 0.5 | 0.021 | 0.33 | 0.2 | - | - |
| H1819 | 1.6 | 0.06 | 1.2 | 0.03 | 0.43 | 0.1 | - | - |
| H1993 | 0.09 | 0.06 | 0.24 | 0.09 | 0.26 | 0.004 | 4.5 | 0.08 |
| H2009 | 0.09 | 0.07 | 0.02 | 0.009 | 0.43 | 0.038 | - | - |
| H2073 | 0.1 | 0.06 | 0.25 | 0.13 | 0.3 | 0.004 | 2.5 | 1.2 |
| HBEC3KT | 1.7 | 2.1 | 1.6 | 2.3 | 0.3 | 0.5 | - | - |
| $\begin{aligned} & \text { HBEC3KT } \\ & \text { RL53-S1 } \end{aligned}$ | 5.2 | 7.9 | 2.5 | 0.26 | 0.083 | 0.029 | - | - |
| $\begin{gathered} \text { HBEC3KT } \\ \text { RL53-S5 } \end{gathered}$ | 0.3 | 0.3 | 0.53 | 0.01 | 0.24 | 0.006 | - | - |
| HBEC30KT | 1.2 | 1.5 | 2.5 | 1.5 | 0.8 | 0.9 | - | - |
| HCC4017 | 21.3 | 7.7 | 2.3 | 0.11 | 11.8 | 1.6 | - | - |

## TABLE 5.2 Confirmation of NSCLC response to combination of 100 nM JP1201 with gemcitabine, paclitaxel, vinorelbine, or erlotinib.

Cells were seeded at 500 cells per well in 6 well dishes. The appropriate concentrations of drug were prepared from stock solutions in medium and given to cells for 10-28 days depending on the cell line. At the end of the assay, medium was aspirated and cells were fixed and stained with $0.5 \%$ methylene blue in $50 \%$ ethanol for 30 minutes. After staining, wells were washed and black and white images of the plates were taken using a ChemiDoc XRS imager and colonies counted (Quantity One software v4.6.5, BioRad, Hercules, CA). Colony counts are averages of triplicate wells done in triplicate over a two week period.

- indicates where no drug sensitivity data has been determined.

|  | Combination Indices of Chemotherapy with $\mathbf{1 0} \boldsymbol{\mu M}$ JP1201 |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| cell line | Vinorelbine | Paclitaxel | Gemcitabine | Doxorubicin | Cisplatin | Erlotinib |
| H2073 | $0.10 \pm 0.00$ | $1.58 \pm 0.54$ | $1.43 \pm 0.53$ | $1.05 \pm 0.59$ | $3.09 \pm 2.54$ | $0.83 \pm 0.01$ |
| H1819 | $0.10 \pm 0.00$ | $0.12 \pm 0.00$ | $0.27 \pm 0.1$ | $1.22 \pm 0.2$ | $1.74 \pm 0.29$ | $0.29 \pm 0.011$ |
| H2887 | $0.17 \pm 0.00$ | $0.23 \pm 0.002$ | $0.23 \pm 0.001$ | $0.17 \pm 0.03$ | $1.46 \pm 1.3$ | $1.00 \pm 0.24$ |
| H1993 | $0.27 \pm 0.001$ | $0.5 \pm 0.01$ | $0.87 \pm 0.01$ | $1.49 \pm 0.67$ | $1.55 \pm 1.37$ | $0.61 \pm 0.1$ |
| H358 | $0.10 \pm 0.001$ | $0.16 \pm 0.01$ | $0.35 \pm 0.04$ | $0.18 \pm 0.01$ | $1.01 \pm 1.23$ | $0.25 \pm 0.01$ |
| H441 | $0.11 \pm 0.22$ | $0.44 \pm 0.17$ | $0.17 \pm 0.02$ | $0.35 \pm 0.08$ | $2.32 \pm 1.95$ | $0.22 \pm 0.02$ |
| A549 | $0.11 \pm 0.01$ | $0.41 \pm 0.11$ | $0.79 \pm 0.48$ | $0.33 \pm 0.07$ | $1.59 \pm 0.7$ | $0.16 \pm 1.2$ |
| H2882 | $0.12 \pm 0.01$ | $0.20 \pm 0.02$ | $0.15 \pm 0.003$ | $1.20 \pm 1.13$ | $1.97 \pm 1.05$ | $1.37 \pm 0.3$ |
| H460 | $0.13 \pm 0.01$ | $0.72 \pm 0.08$ | $1.44 \pm 0.03$ | $0.43 \pm 0.02$ | $0.99 \pm 0.92$ | $0.21 \pm 0.05$ |
| H1395 | $0.13 \pm 0.01$ | $0.13 \pm 0.04$ | $0.10 \pm 0.01$ | $0.22 \pm 0.06$ | $0.99 \pm 0.1$ | $1.14 \pm 1.2$ |
| H1355 | $0.15 \pm 0.02$ | $0.21 \pm 0.03$ | $0.63 \pm 0.03$ | $0.93 \pm 0.03$ | $1.12 \pm 1.04$ | $1.07 \pm 1.1$ |
| H157 | $0.19 \pm 0.02$ | $0.16 \pm 0.02$ | $0.72 \pm 0.02$ | $0.45 \pm 0.03$ | $1.22 \pm 1.9$ | $0.13 \pm 0.001$ |
| H1693 | $0.19 \pm 0.01$ | $0.3 \pm 0.08$ | $0.27 \pm 0.03$ | $1.23 \pm 1.15$ | $1.22 \pm 1.01$ | NT |
| H2009 | $0.19 \pm 0.01$ | $0.34 \pm 0.01$ | $0.47 \pm 0.01$ | $0.93 \pm 0.41$ | $1.89 \pm 1.17$ | $1.12 \pm 0.4$ |
| H2087 | $2.42 \pm 1.37$ | $0.36 \pm 0.02$ | $0.90 \pm 0.36$ | $0.36 \pm 0.02$ | $0.92 \pm 0.87$ | $0.99 \pm 0.1$ |
| HCC4017 | $0.33 \pm 0.01$ | $0.23 \pm 0.03$ | $0.59 \pm 0.02$ | $1.05 \pm 0.21$ | $1.28 \pm 0.97$ | $1.13 \pm 0.2$ |
| HBEC30KT | $62.96 \pm 5.37$ | $15.65 \pm 1.3$ | $1.41 \pm 0.3$ | $0.80 \pm 0.17$ | $1.65 \pm 0.1$ | $2.35 \pm 0.1$ |
| HBEC3KT | $34.39 \pm 2.39$ | $2.54 \pm 1.1$ | $3.01 \pm 0.71$ | $1.3 \pm 0.02$ | $1.25 \pm 0.61$ | $5.19 \pm 1.1$ |
| HBEC3KT RL53 | $0.12 \pm 0.01$ | $0.21 \pm 0.08$ | $1.77 \pm 0.7$ | $1.20 \pm 0.1$ | NT | NT |
| S1 |  |  |  |  |  |  |

## TABLE 5.3 JP1201 can synergize with chemotherapy.

Combination indices (CI) were calculated using the Chou-Talay method (Chou \& Rideout, 1991). CI values that are less than $1 \pm 0.2$ indicate synergy, values that are equal to $1 \pm 0.2$ indicate additivity, and values that are greater than $1 \pm 0.2$ indicate antagonism. Error was calculated by propagating the error from the drug sensitivity phenotypes from MTS data. Data represents average of $\geq 3$ determinants.

|  | qRT-PCR mRNA levels relative to siLuc control (2- $\triangle \Delta C T$ values) |  |  |  |  |  |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | H1395 |  |  |  |  |  |  |  |  |  |  |  |
|  | siLuc | si-cIAP1 | si-cIAP2 | siXIAP | $\begin{gathered} \text { si- } \\ \text { cIAP1, } \\ \text { si- } \\ \text { cIAP2, } \\ \text { siXIAP } \\ \hline \end{gathered}$ | JP1201 | siCasp 3 | siCasp4 | siCasp9 | siCasp8 | siRIPK1 | siTNFR1 |
| cLAP1 | 1 | 0.132 | 1.23 | 0.79 | 0.139 | 1.28 | - | - | - | - | - | - |
| cLAP2 | 1 | 1.85 | 0.44 | 1.55 | 1.99 | 5.68 | - | - | - | - | - | - |
| XIAP | 1 | 0.67 | 1.3 | 0.1 | ND | 7.9 | - | - | - | - | - | - |
| Caspase 3 | 1 | $\therefore$ | - | - | - | - | 0.014 | 0.94 | 1.105 | 0.91 | - | - |
| Caspase 4 | 1 | - | - | - | - | - | 0.85 | 0.14 | 1.09 | 1.3 | - | - |
| Caspase 9 | 1 | - | - | - | - | - | 0.776 | 0.864 | 0.007 | 0.947 | - | - |
| Caspase 8 | 1 | - | - | - | - | - | 0.78 | 1.1 | 1.15 | 0.24 | - | - |
| TNFR1 | 1 | - | - | - | - | - | - | - | - | - | 1.36 | 0.358 |
| RIPK1 | 1 | - | - | - | - | - | - | - | \% | - | 0.123 | 1.31 |
| TNF $\alpha$ | ND** | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND | ND |

TABLE 5.4 Changes in mRNA expression after siRNA knockdown are validated by q-RTPCR. Studies of H1395 cells associated with Figures 5.21,

### 5.25.

H1395 cells were transfected with siRNAs against: firefly luciferase, cIAP1, cIAP2, XIAP, caspase-3, caspase-4, caspase-9, caspase 8, RIPK1, TNFR1, or pooled siRNAs of cIAP1, cIAP2, and XIAP, or treated with JP1201. 24 hours later, cells were harvested and total RNA prepared (RNeasy Plus Mini Kit, 74134, Qiagen, Hilden, Germany). cDNA was synthesized from $1 \mu \mathrm{~g}$ total RNA using the iScript cDNA synthesis kit (BioRad, Hercules, CA). Gene specific TaqMan probes (Applied Biosystems, Foster City, CA) were used to quantitate GAPDH, cIAP1, cIAP2, XIAP, Caspase-3, $-4,-8$, and -9 , RIPK1, TNFR1, and TNF $\alpha$ levels in biological duplicates as well as duplicate samples of siRNA transfected H1395 cells. The $2^{-\Delta \Delta C T}$ method was used to calculate relative expression levels (Livak \& Schmittgen, 2001). Expression of target genes were normalized to GAPDH
expression, and expression was normalized to H 1395 cells transfected with luciferase siRNA.

*     - indicates where no gene expression data has been determined.
** ND indicates where gene expression was not detected

Fold change in relative luciferase activity of treated H1395 cells compared to untreated control

| Pathway | JP1201 | Gemcitabine | Vinorelbine | Vinorelbine + <br> JP1201 |
| :--- | :--- | :--- | :--- | :--- |
| 1 | 0.9 | 1.1 | 0.8 | 1.3 |
| 2 | 0.8 | $\underline{\mathbf{2 . 6}}$ | 0.7 | 1.1 |
| 3 | 0.8 | 0.9 | 0.9 | 1.1 |
| 4 | 0.9 | 0.8 | 1.1 | 1.1 |
| 5 | 1.4 | 1.7 | 0.8 | $\underline{\mathbf{3 . 5}}$ |
| 6 | 0.6 | 0.8 | 1.1 | 1.1 |
| 7 | 0.8 | 1.3 | 1 | 1 |
| 8 | 1.1 | 0.8 | 1.4 | 1.1 |
| 9 | 1.3 | 0.9 | 0.8 | $\underline{\mathbf{2 . 5}}$ |
| 10 | 1.2 | 1.3 | 0.7 | $\mathbf{1 . 3}$ |

TABLE 5.5 Analysis of pathways activated by JP1201 + chemotherapy using

## Cignal finder assay system (SABiosciences).

The combination of JP1201 + vinorelbine selectively activates the ER stress pathway. H1395 cells were reverse transfected with firefly luciferase reporter constructs that contain response elements for the indicated pathways and control renilla luciferase constructs, then treated with $10 \mu \mathrm{M} \mathrm{JP1201} ,1 \mu \mathrm{M}$ gemcitabine, $1 \mu \mathrm{M}$ vinorelbine, or JP1201 + vinorelbine for 24 hours, luciferase activity was assayed, firefly luciferase activity was normalized to renilla luciferase activity for each sample, and normalized to un-transfected cells.

* Pathways are: 1) oxidative stress, 2) p53, 3) NF-кB, 4) hypoxia, 5) ER stress, 6) heavy metals, 7) heat shock, 8) the glucocorticoid receptor, 9) the JNK pathway, or 10) the xenobiotic receptor
** Bolded and underlined values have $\mathrm{p}<0.001$ by two-way ANOVA.

| Pathway | Fold change in relative luciferase activity of cells treated with JP1201 + vinorelbine compared to JP1201 alone |  |  |  |
| :---: | :---: | :---: | :---: | :---: |
|  | H1395 | H157 | HCC4017 | HBEC30KT |
| 1 | 3.4 | 0.7 | 1.1 | 0.4 |
| 2 | 1.7 | 2.6 | 0.4 | 0.4 |
| 3 | 2.2 | 0.9 | 1.1 | 1.5 |
| 4 | $\underline{2.5}$ | 0.8 | 0.6 | 0.7 |
| 5 | 4.4 | $\underline{2.1}$ | 3.8 | 0.5 |
| 6 | 1.7 | $\underline{2.8}$ | 0.4 | 0.4 |
| 7 | 1.7 | $\underline{3.5}$ | 0.7 | 0.5 |
| 8 | 0.9 | 1.3 | 0.3 | 0.4 |
| 9 | 4.7 | 1.1 | 0.5 | 0.9 |
| 10 | 0.8 | 1.3 | 0.7 | 0.7 |

TABLE 5.6 Analysis of pathways activated by JP1201 + chemotherapy using

## Cignal finder assay system (SABiosciences).

ER stress pathway is activated by the combination of vinorelbine + JP1201. H1395, H157, HCC4017, and HBEC30KT cells were reverse transfected with the indicated firefly luciferase reporter construct, treated with JP1201 + vinorelbine. Firefly luciferase activity was normalized to renilla luciferase for each sample, and to JP1201 treated cells.

* Pathways are: 1) oxidative stress, 2) p53, 3) NF-кB, 4) hypoxia, 5) ER stress, 6) heavy metals, 7) heat shock, 8) the glucocorticoid receptor, 9) the JNK pathway, or 10 ) the xenobiotic receptor
** Bolded and underlined values have $\mathrm{p}<0.001$ by two-way ANOVA.

|  | Analysis of Oncogenotype and Drug Response Phenotypes of Combination Therapy with JP1201 |  |  |  |  |  |  |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
|  | (Pearson r values) |  |  |  |  |  |  |
|  | Vinorelbi ne | Paclitaxel | $\begin{aligned} & \text { Doxorubi } \\ & \text { cin } \end{aligned}$ | Gemcitabine | $\begin{aligned} & \text { Cispla } \\ & \text { tin } \end{aligned}$ | Erlotinib | Paclitax el/Carbo platin |
| p53 | 0.17 | -0.33 | -0.2 | -0.28 | -0.51 | 0.16 | -0.39 |
| Braf | -0.1 | -0.07 | -0.08 | 0.64* | 0.61 | -0.13 | 0.2 |
| $\begin{gathered} \text { SMARC } \\ \text { A4 } \end{gathered}$ | -0.07 | 0.46 | -0.11 | -0.15 | -0.15 | 0.63 | 0.19 |
| STK11 | 0.27 | -0.17 | -0.17 | 0.19 | -0.17 | 0.35 | -0.13 |
| PI3K | -0.07 | -0.05 | -0.05 | -0.1 | 0.33 | 0 | -0.35 |
| Kras | -0.26 | -0.25 | 0.21 | -0.21 | 0.14 | 0.31 | -0.12 |

## TABLE 5.7 Pearson correlations of gene mutation and absolute fold decrease

 in drug IC ${ }_{50}$ when combined with JP1201.There are significant negative and positive correlations with various oncogene and tumor suppression gene mutations.

* Bold figures identify significant Pearson correlations ( $\mathrm{p}<0.05$ ).



## FIGURE 5.1 Mammalian ESR signaling.

Unfolded protein in the ER lumen titrates BiP away from three sentinels of ER stress: PERK, IRE1 and ATF6. Activated PERK phosphorylates the translation initiation factor eIF2 to slow global protein synthesis temporarily and upregulate certain stress-inducible messages, such as ATF4. Activated IRE1 splices the mRNA for XBP-1 to allow the translation of mature XBP-1 protein, a transcription factor that mediates the transcriptional upregulation of numerous genes involved in mammalian ER function and the secretory pathway in general. Similarly, during ER stress ATF6 traffics to the Golgi, where it is cleaved by

S1P/S2P proteases and thereby released from the membrane to activate a distinct but overlapping set of genes in the nucleus. Adapted from Boyce et al., 2006.


FIGURE 5. 2 Simplified depiction of selected apoptotic pathways induced by

## ER stress.

Physiological or experimentally induced ER stress leads to the activation of PERK and, eventually, the GADD34/PP1 phosphatase complex, which dephosphorylates eIF2alpha, promoting apoptosis. Genetic strategies or chemicals (e.g., salubrinal) that enforce eIF2alpha phosphorylation protect cells from ER stress-induced apoptosis. Caspase-12 (mice) or -4 (humans) is associated with the cytoplasmic face of the ER membrane and can be activated by ER stress in several ways, including via IRE1 and TRAF2, or by cleavage by calpain, itself activated by the release of calcium from ER stores. Bcl-2 family members also
reside in the ER membrane and influence apoptosis induced by ER stress, both through the regulation of calcium flux and amplification of the apoptotic signal via the mitochondrial pathway (not shown). Adapted from Boyce et al., 2006.


FIGURE 5.3 Drug sensitivity profiles of chemotherapy in combination with
JP1201 have three distinct phenotypes.
(A) NCI-H2087 (B) NCI-H157 and (C) NCI-H460 were treated with cisplatin (black circles) or cisplatin in combination with $10 \mu \mathrm{M} \mathrm{JP} 1201$ (open circles). (D) NCI-H2887 (E) NCI-H358 and (F) NCI-H157 were treated with doxorubicin (black circles) or doxorubicin in combination with $10 \mu \mathrm{M} \mathrm{JP} 1201$ (open circles). (G) NCI-H1395 (H) NCI-H441 and (I) NCI-H460 were treated with gemcitabine (black circles) or gemcitabine in combination with $10 \mu \mathrm{M} \mathrm{JP1201} \mathrm{(open} \mathrm{circles)}$. (J) NCI-H1819 (K) NCI-H2882 and (L) NCI-H460 were treated with paclitaxel (black circles) or paclitaxel in combination with $10 \mu \mathrm{M} \mathrm{JP1201} \mathrm{(open} \mathrm{circles)}$. (M) NCI-H2073 (N) A549 and (O) NCI-H2087 were treated with vinorelbine (black circles) or vinorelbine in combination with $10 \mu \mathrm{M} \mathrm{JP1201}$ (open circles). (P) NCI-H157 (Q) A549 and (R) NCI-H2073 (bottom) were treated with erlotinib (black circles) or erlotinib in combination with $10 \mu \mathrm{M} \mathrm{JP} 1201$ (open circles).


## FIGURE 5.4 JP1201 Can Synergize with Chemotherapy In Vitro.

(A) Cell viability curves of NCI-H1819 treated with vinorelbine alone (black circles), in combination with $10 \mu \mathrm{M} \mathrm{JP} 1201$ (open circles), or JP1201 alone (black triangles), data is representative of at least three replicates of independently preformed 96 well plate assay. (B) Colony forming efficiency expressed as a percent of untreated NCI-H1819 in the presence of vinorelbine alone (black circles), in combination with $10 \mu \mathrm{M} \mathrm{JP} 1201$ (open circles), or JP1201 alone (black triangles) for two weeks, data is representative of two independent assays performed 3 weeks apart. (C) Number of Annexin V positive NCI-H1819 cells which were treated with vinorelbine alone (black circles), or vinorelbine with 10 $\mu \mathrm{M} \mathrm{JP1} 201$ (open circles) 48 hours after drug treatment as determined by FACS analysis.


FIGURE 5.5 JP1201 Specifically Sensitizes Tumorgenic Cell Lines in a Tumor/Normal Isogenic System.

Colony forming efficiency expressed as a percent of untreated HCC4017 (circles)
and HBEC30KT (triangles) in the presence of paclitaxel alone (solid line), or in combination with 100 nM JP1201 (dashed line), data is representative of two independent assays.


FIGURE 5.6 JP1201 Specifically Sensitizes Tumorgenic Cell lines in an Isogenic System.

Colony forming efficiency expressed as a percent of untreated HBEC3KT RL53 clone1 (diamonds) and HBEC3KT (squares) in the presence of paclitaxel alone (solid line), or in combination with 100 nM JP1201 (dashed line), data is representative of two independent assays.


FIGURE 5.7 JP1201 in Combination with Gemcitabine or Vinorelbine Is Effective in Controlling NCI-H1395 Xenograft Growth.

Tumor growth curves during the course of treatment, treatment began on day 41, saline, $25 \mathrm{mg} / \mathrm{kg}$ gemcitabine and $6 \mathrm{mg} / \mathrm{kg} \mathrm{JP1201}$ were given thrice weekly, 2.4 $\mathrm{mg} / \mathrm{kg}$ vinorelbine given twice weekly.


FIGURE 5.8 JP1201 in Combination with Gemcitabine or Vinorelbine Results in Smaller Overall NCI- H1395 Tumor Size.

Tumor weights of xenografts were harvested 24 hours after the final treatments, treatment began on day 41, saline, $25 \mathrm{mg} / \mathrm{kg}$ gemcitabine and $6 \mathrm{mg} / \mathrm{kg}$ JP1201 were given thrice weekly, $2.4 \mathrm{mg} / \mathrm{kg}$ vinorelbine given twice weekly. Treatment was given for three weeks.


FIGURE 5.9 JP1201 in Combination with Gemcitabine or Vinorelbine Is Effective in Controlling NCI-H1395 Xenograft Growth by Inducing Apoptosis.

Induction of apoptosis was analyzed using TUNEL immunofluorescence. Data from a minimum of three tumors per treatment group were normalized to the saline group, and are representative of at least two independent assays, ${ }^{* * *}$ p < 0.0001.


FIGURE 5.10 JP1201 in Combination with Vinorelbine Is Effective in

## Controlling NCI-H157 Xenograft Growth.

Tumor growth curves for xenografts, animals were sacrificed throughout the study due to tumor burden. Treatment began on day 14, saline and $6 \mathrm{mg} / \mathrm{kg}$ JP1201 were given thrice weekly, $2.4 \mathrm{mg} / \mathrm{kg}$ vinorelbine given twice weekly.


FIGURE 5.11 JP1201 in Combination with Vinorelbine Extends Survival Time of Mice Carrying NCI-H157 Xenografts.

Kaplen-Meyer survival curves. Animals had median survival times of 19, 24, 24, and 35 days respectively for saline, vinorelbine, JP1201, and JP1201 with vinorelbine.


FIGURE 5.12 siRNA Mediated Knockdown of XIAP Can Mimic JP1201

## When Co-Treated with Gemcitabine in NSCLCs.

Knockdown of XIAP is sufficient and necessary to mimic combination of JP1201 with gemcitabine On day zero (A) NCI-H1395, (B) NCI-H358, (C) NCI-H1819, and (D) NCI-H2887 cells were transfected in 96 well format with firefly luciferase siRNA, cIAP1 siRNA, cIAP2 siRNA, XIAP siRNA, or cIAP1, cIAP2, and XIAP siRNAs as indicated and on day one treated with increasing amounts of gemcitabine.


FIGURE 5.13 siRNA Mediated Knockdown of cIAP1, cIAP2, and XIAP Are All Required to Mimic JP1201 When Co-Treated with Paclitaxel in NSCLCs. Knockdown of cIAP1, cIAP2, and XIAP gives maximal sensitization to paclitaxel. On day zero (A) NCI-H1395, (B) NCI-H358, (C) NCI-H1819, and (D) NCI-H2887 cells were transfected in 96 well format with firefly luciferase siRNA, cIAP1 siRNA, cIAP2 siRNA, XIAP siRNA, or cIAP1, cIAP2, and XIAP siRNAs as indicated and on day one treated with increasing amounts of paclitaxel.


FIGURE 5.14 siRNA Mediated Knockdown of cIAP1, cIAP2, or XIAP Can Mimic JP1201 When Co-Treated with Vinorelbine in NSCLCs.

Knockdown of cIAP1, cIAP2, or XIAP mimics the sensitization to vinorelbine seen when treated with JP1201. On day zero (A) NCI-H1395, (B) NCI-H358, (C) NCI-H1819, and (D) NCI-H2887 cells were transfected in 96 well format with firefly luciferase siRNA, cIAP1 siRNA, cIAP2 siRNA, XIAP siRNA, or cIAP1,
cIAP2, and XIAP siRNAs as indicated and on day one treated with increasing amounts of vinorelbine.


FIGURE 5.15 ELISA Analysis Shows that TNF $\alpha$ Is Not Induced in JP1201Resistant Cell Lines by Vinorelbine Treatment.

Conditioned medium samples were taken from NCI-H2126 (a JP1201 sensitive NSCLC line), and seven other NSCLC cell lines (JP1201 resistant) 12 hrs after being placed in RPMI with the following treatments: untreated, 100 nM JP1201, 500 nM gemcitabine, 100 nM vinorelbine, and 100 nM vinorelbine with 100 nM JP1201, to test if treatment with chemotherapy can cause TNF $\alpha$ secretion.


FIGURE 5.16 ELISA Analysis Shows that TRAIL Is Not Induced in JP1201Resistant Cell Lines by Vinorelbine Treatment.

Conditioned medium samples were taken from NCI-H2126 (a JP1201 sensitive NSCLC line), and seven other NSCLC cell lines (JP1201 resistant) 12 hrs after being placed in RPMI with the following treatments: untreated, 100 nM JP1201, 500 nM gemcitabine, 100 nM vinorelbine, and 100 nM vinorelbine with 100 nM JP1201, to test if treatment with chemotherapy can cause TRAIL secretion.


FIGURE 5.17 ELISA Analysis Shows that TNF $\alpha$ Is Not Induced in JP1201Resistant Cell Lines by Vinorelbine Treatment.

Conditioned medium samples were taken from NCI-H2126 (a JP1201 sensitive NSCLC line), and eight other NSCLC cell lines (JP1201 resistant) 12, 24, 48, 72, and 96 hrs after being placed in RPMI with the following treatments: untreated, $10 \mu \mathrm{M}$ JP1201, 2000 nM gemcitabine, 1000 nM vinorelbine, and 1000 nM vinorelbine with $10 \mu \mathrm{M} \mathrm{JP1201}$, to test if treatment with chemotherapy can cause TNF $\alpha$ secretion.


FIGURE 5.18 Scheme for Testing if Chronic JP1201 Treatment Induces TNF $\alpha$ Expression in NCI-H1395 Cells In Vitro.

NCI-H1395 cells were treated for three weeks with either 100 nM or 1000 nM JP1201, which was given to the cells three times a week in mass culture. Parental (untreated) NCI-H1395 cells as well as the pretreated 100 nM NCI-H1395, and 1000 nM NCI-H1395 cells were plated in six well plates at time zero and were treated for twelve hours with no treatment, 100 nM JP1201, 1000 nM JP1201, 20 nM gemcitabine, 20 nM paclitaxel, or 20 nM vinorelbine.

conditioned media from H1395 cells
FIGURE 5.19 Chronic JP1201 Treatment Induces TNF $\alpha$ Expression in NCIH1395 Cells In Vitro.

NCI-H1395 cells were treated for three weeks with either 100 nM or 1000 nM JP1201, which was given to the cells three times a week in mass culture. Parental (untreated) NCI-H1395 cells as well as the pretreated 100 nM NCI-H1395, and 1000 nM NCI-H1395 cells were plated in six well plates at time zero and were treated for twelve hours with no treatment, 100 nM JP1201, 1000 nM JP1201, 20 nM gemcitabine, 20 nM paclitaxel, or 20 nM vinorelbine. Conditioned media was collected and analyzed for TNF $\alpha$ secretion by competitive ELISA.


FIGURE 5.20 Chronic JP1201 Treatment Induces TNFa Expression in NCIH1395 Cells In Vivo.

Formalin fixed, paraffin embedded sections of NCI-H1395 xenograft tumors were stained with a human specific antibody against TNF $\alpha$ for three tumors within each treatment group. Average level of TNF $\alpha$ staining in NCI-H1395 xenografts by treatment group. Data from a minimum of three tumors per treatment group were normalized to saline group, and are representative of at least two independent assays, * p < 0.01, *** p < 0.0001. GEM, gemcitabine; VIN, vinorelbine; JP, JP1201; JPG, gemcitabine and JP1201; JPV, vinorelbine and JP1201.


FIGURE 5.21 Synergy of Vinorelbine and JP1201 Does Not Act Through TNF $\alpha /$ RIPK1-Dependent Pathway.

Knockdown of caspase 3 protects H1395 cells from the effects of JP1201 + vinorelbine. H1395 cells were transfected with siRNAs that are specific for the indicated target in 96 well plates and treated with vinorelbine $+10 \mu \mathrm{M} \mathrm{JP1201}$, the MTS assay was used to produce drug response curves for each transfection.


FIGURE 5.22 CHOP Expression is Induced by Vinorelbine and Paclitaxel Treatment Similarly to Known ER Antagonist Tunicamycin.

NCI-H1395 cells were treated with $1 \mu \mathrm{M}$ tunicamycin, 100 nM paclitaxel, 100 nM vinorelbine, or 500 nM gemcitabine for the indicated hours, at which point cells were harvested and lysates made. Cell lysates were analyzed by western blotting for CHOP (612201, BioLegend) or HSP90 (sc-13119, Santa Cruz) as a loading control.


FIGURE 5.23 cIAP1 Co-immunoprecipitates with IRE1, ASK1, and TRAF2.
NCI-H358, NCI-H2887, and NCI-H1819 cell pellets were lysed using IP lysis buffer, and pre-cleared using protein A/G-agarose and a control antibody (targeting VEGF, obtained from RAB) lysates were then incubated at 4C for 2 hours with an antibody against IRE1 (sc-20790, Santa Cruz), ASK1 (sc-5294 Santa Cruz), or TRAF2 (sc-7346, Santa Cruz), protein A/G-agarose was added and incubated overnight at 4C. Pellets were spun down and washed 5 times with 1000 fold excess lysis buffer. 1X SDS buffer was added to pellets which was then
boiled for 5 minutes at 94C, and then analyzed by western blot analysis for cIAP1/2 (sc-12410, Santa Cruz).


FIGURE 5.24 Treatment with Vinorelbine + JP1201 abolishes the ability of cIAP1 and cIAP2 to be Co-immunoprecipitated with IRE1 and ASK1.

NCI-H1395 cells were treated with DMSO, $1 \mu \mathrm{M}$ JP1201, $1 \mu \mathrm{M}$ vinorelbine, or 1 $\mu \mathrm{M}$ JP1201 $+1 \mu \mathrm{M}$ vinorelbine. After 12 hours of treatment, cells were lysed using IP lysis buffer and pre-cleared using protein A/G-agarose and a control antibody (targeting VEGF, obtained from RAB) lysates were then incubated at $4^{\circ} \mathrm{C}$ for 2 hours with an antibody against IRE1 (sc-20790, Santa Cruz) or ASK1 (sc-5294 Santa Cruz), protein A/G-agarose was added and incubated overnight at $4^{\circ} \mathrm{C}$. Pellets were spun down and washed 5 times with 1000 fold excess lysis buffer. 1X SDS buffer was added to pellets which was then boiled for 5 minutes at $94^{\circ} \mathrm{C}$, and then analyzed by western blot analysis for cIAP1/2 (sc sc-12410, Santa Cruz), cIAP1 (3180A-100, BioVision) and cIAP2 (sc-7944, Santa Cruz).


FIGURE 5.25 Caspase-4, -9, and -3 are Activated in Response to JP1201 + Vinorelbine Treatment in NCI-H1395 Cells.

Determination of which caspases are involved in cell kill induced by vinorelbine + JP1201. NCI-H1395 cells were transfected with siRNAs that are specific for the indicated target in a 96 well plate format and treated with vinorelbine $+10 \mu \mathrm{M}$ JP1201, the MTS assay was used to produce drug response curves for each transfection. Validation of knockdowns are found in Table 5.5.


FIGURE 5.26 Pro-caspase-4 Protein Levels Decline After Vinorelbine
Treatment, Similarly to Known ER Antagonists Tunicamycin and

## Thapsigargin.

NCI-H1395 cells were treated with 300 nM thapsigargin, $1 \mu \mathrm{M}$ tunicamycin, 500 nM gemcitabine, or 100 nM vinorelbine for the indicated hours at which point cells were harvested and lysed. Cell lysates were then analyzed at 50 ug per well by western blot analysis probing for pro-caspase-4 (sc-56056, Santa Cruz) and HSP90 (sc-13119, Santa Cruz) as a loading control.

## CHAPTER 6

## Conclusions and Future Works

The work presented in this work shows that using targeted approaches that NSCLCs can be sensitized to conventional chemotherapies, whether it's by altering miRNA levels to modulate chemosensitivity, reactivating wild type p53 activity in mutant p53 background, or relieving negative inhibition on the apoptotic pathway. The broad range of approaches contained in this work leaves many avenues to pursue in the future, identification miR337 target genes that are responsible for increased sensitivity to paclitaxel, the mechanism by which agRNA ${ }^{\text {p53 }}$ induces lincRNAp21 expression, exploring the role of ER stress induced apoptosis in cancer, among others.

### 6.1 Platinum-Based Combination Chemotherapy

The initial study on platinum based chemotherapy combinations in a panel of NSCLCs highlights the inefficiency with which cancers are treated in the clinic (Figure 3.2). More often than not it would seem that patients are undergoing combination chemotherapy when a single agent would be just as effective at killing the actual tumor cells. However, as the lack of success in this study of defining signatures that would predict synergy or antagonism indicates, predicting response to treatment has not been successful as a method for personalizing therapy yet. There are several caveats to the experimental approaches used here that may contribute to the lack of predictability of the signatures derived herein
(Figure 3.3-5). One such caveat is that the signatures were created using genomewide mRNA microarray expression profiling, and while this encompasses the expression levels of every gene at the mRNA level, these expression profiles were taken from cells with no treatment, so the ability of the cells to respond to stress is not really evaluated by this approach. Perhaps it would be more informative to profile the epigenetic profile of these cells by histone modifications or by protein array of epigenetic regulating enzymes (S. V. Sharma, et al., 2010).

Another caveat is that this analysis is based on the analysis of the two drugs as a combination compared to each drug as a single agent, instead of simply identifying responders and non-responders, and the MATRIX program used to analyze gene expression correlations with response is designed to make these correlations on a $1 / 0$ scale. So the program is designed to analyze simply two groups and make correlations based on these two simple groups; however, response to chemotherapy is more of a continuum than two distinct populations of resonse (Figure 3.1), which is highlighted even more when you consider combination index, which loosely groups cell lines as antagonistic, additive, or synergistic. For these analyses, additive cell lines were simply ignored and signatures derived from antagonistic or synergistic cell lines across three platinum based combinations. And while analyses like this are often done, it completely ignores a real biological response to drug and as a result ignores some of the complexity within cancer cells that is regulating response to drugs, and thereby it
should be no surprise that the signatures made with such parameters is not predictive of a large panel of NSCLCs.

### 6.2 Targeted Molecular Biology Approaches to Rationally Designed

## Combinations

In this study where increasing endogenous miR337 levels by transfection of a synthetic mimic of miR337, NSCLCs were sensitized to paclitaxel, both in already fairly sensitive cell line H157 and in resistant cell lines H1819, H2887. Conversely it was shown that a sensitive cell line H157 could be made more resistant to paclitaxel by antagonizing miR337 activity using a miR337-specific antagomiR. While these data are encouraging,, there is a lot left unexamined before altering miR337 levels could become a potential therapeutic option for altering NSCLC response in mice, much less patients. The mRNA targets of miR337 are unknown, so the tumor selectivity of increasing miR337 levels sensitizing cells to paclitaxel has not been shown. If increasing miR337 levels sensitizes all cells, not just tumor cells to paclitaxel, it would not be useful as a cancer therapy, which is the goal of this entire body of work. Additionally, this work only showed that increasing miR337 levels was effective in vitro models, mouse studies need to be done showing that the synthetic miR337 mimic can also sensitize tumor cells in a living animal occurs. In addition to showing that the miR337 mimic could be effective in vivo, the in vivo properties; aka absorption, clearance, metabolism need to be evaluated to determine if use of the miR337
mimic would achieve such a standard state plasma level as to be effective at sensitizing tumor cells to paclitaxel, as well as to determine appropriate scheduling of dosing to keep a certain steady state plasma level.

Similar future works are also necessary for the taxane-specific synthetic lethal siRNAs, as considering to advance them as therapeutics to use in conjunction with paclitaxel or docetaxel, showing tumor specificity of sensitization, and in vivo efficacy of this sensitization. To further the analysis of diazonamide being sensitized by the "paclitaxel-specific" synthetic lethals, all 87 hits need to be tested with diazonamide initially in H 1155 cells, the cell line used in the screen, and then take the best hits from that and screen them across multiple cell lines, maintaining diazonamide at an $\mathrm{IC}_{10}$ dose for each cell line.

The work on targeting the 5' from the TSS of TP53, shows that these agRNAs specifically cause cytotoxicity in cancer cell lines containing mutant p53 protein, specifically only mutants where the mutation lies within the DBD. Some of the experiments that need to be done to confirm this specificity is to take a cell line that has DBD-mutant-p53, and over express mutant p53 from an artificial promoter, and then test across a dilution range of agRNA looking for loss of cytotoxicity. The companion experiment to this, where mutant p53 is expressed from the endogenous TP53 promoter is not possible in this system; however, using HBECs that are over expressing a mutant version of p53, while still expressing wild type p53 is underway. The mechanism by which these
$\operatorname{agRNA}{ }^{\mathrm{p} 53}$ s induce cytotoxicity is still under investigation. Analyzing mRNA from both mutant p53 and wild type p53 containing cells where N27 has been transfected in for induction of pro-apoptotic p53 target genes is planned. As well as performing ChIP on lysates from cells transfected with N27 and N27-M4M using p53 as the immunoprecipitate target, looking for enrichment of p53 at proapoptotic target genes (PUMA, NOXA) as well as at the lincRNAp21 locus are planned experiments to better elucidate the mechanism by which these agRNA ${ }^{\text {p53 }}$ induce cytotoxicity.

### 6.3 SMAC Mimetics as an Adjuvant Chemotherapy Combination

The work on using SMAC mimetic JP1201 is by far the furthest along of the projects within this body of work. However, as the most likely route of using SMAC mimetics in the clinic is as a part of chemotherapy combination therapy, and that most patients treated with chemotherapy for NSCLC are treated with a platinum based doublet, it is not likely that simply the combination of vinorelbine + JP1201 would likely be given to patients. Patients in Canada and Europe are routinely treated with the combination of cisplatin + vinorelbine, so further studies into using JP1201 in combination with cisplatin + vinorelbine in the in vitro system used here would be very necessary for planning a clinical trial.

That ER stress is inducing apoptosis in response to chemotherapy has never been described before, so the role of ER stress induced apoptosis is largely unexplored within cancer, and yields an as yet unexplored target for cancer
therapies. In addition to implicating ER stress as a dominant apoptogenic trigger, this work also shows that cIAP1/2 can negatively regulate apoptosis at an as yet un-described site within the cell.

### 6.4 Perspectives

It has long been known that each patient with cancer is different from every other patient with respect to presentation of disease, prognosis, response and tolerance to treatment, risk of recurrence, secondary malignancy, and long term complications from treatment; however, it has only been recently that clinicians and scientists have begun to explore the molecular heterogeneity of cancers. Identifying breast cancer patient subpopulations with overexpression of HER2 (ErbB2) and correlating that with increased chance of response to trastuzumab is one example of using knowledge of the heterogeneity of cancers to help personalize treatment, or cater treatment options to the molecular profile of an individual patient (Schilsky, 2010). And while trastuzumab is effective in HER2+ breast cancers, it is only in about $30 \%$ of this breast cancer subpopulation that it effectively controls disease, which points to a down fall of targeted therapies being the mainstay of cancer treatments based on molecularly defined subpopulations.

Another example that illustrates this is erlotinib used to treat NSCLC patients with activating mutations in EGFR. Erlotinib was showed to give a survival benefit in this selected population as a monotherapy, most if not all of
these patients have recurrence of disease due to resistance to erlotinib therapy. There have been numerous ways found that the tumors develop resistance to erlotinib, such as T790M mutations within EGFR that block binding of erlotinib into the ATP binding pocket of EGFR, upregulation of alternative growth factor receptors (MET, HER2 partnering with EGFR) to circumvent EGFR blockage, or downstream pathway activating mutations (Kobayashi 2005, engelman, 2007 2008, oreily 2006). These examples suggest that merely designing targeted agents to mutant proteins within a tumor are not sufficient for irradication of disease, with the exception of imatinib which controls CML for $90 \%$ of cases; however increasing evidence is coming to light showing that leukemia cells are developing resistance to imatinib (Kimura, et al., 2010).

Another approach to personalizing therapy is to use genome wide expression data, whether it's from microarray expression profiling, or protein arrays, to create signatures that are predictive of response to a given therapy. Usually these types of signatures are based off of cell line panels where multiple agents can be tested within the same cancer sample, which has its own set of caveats. Cell lines have shorter doubling times than tumor cells, and as a result have more opportunity to obtain genomic changes as a result of genomic instability (Adi F. Gazdar, Gao, \& Minna, 2010). Additionally, cell lines are thought to only represent tumor cell subpopulations and not recapitulate the heterogeneity of the parent tumor, as well as lacking important interactions with
other cell types, such as stromal, inflammatory, immune, and vascularization (Adi F. Gazdar, Gao, et al., 2010). Although cell lines have the potential for loss of tumor heterogeneity, acquired mutations not relevant to the tumor in vivo, lack of tumor-associated immune and stromal cells; cell lines represent a basis for performing multiple assays on the same oncogenic background to be able to make comparisons between response to different therapies, whereas with a real patient, each sequential treatment alters the tumor, so comparisons between treatments in patients that receive multiple rounds of treatment cannot really be made. So while cell lines might not be ideal, they still provide a useful tool in creating signatures that can be later refined using xenograft data, and retrospective profiling of biopsy samples, such as from the BATTLE trial at MD Anderson (Printz, 2010).

The approach of introducing small duplex RNA molecules (miRNA, siRNA, or agRNA) into cancer cells to alter gene expression and thereby response to chemotherapy is quite ingenious; however, being able to treat a patient with such molecules is a bit more difficult. There are mechanisms in place throughout the human body to prevent foreign RNA or DNA molecules from entering cells and having an effect. One could imagine that foreign DNA/RNA being able to readily be taken up by cells could be detrimental to an organism, essentially viruses are clever ways of introducing DNA/RNA into a cell, and even injection of viral DNA/RNA directly into a cell can cause immune responses, such as the interferon response (Sledz, Holko, de Veer, Silverman, \& Williams, 2003).

Additionally there are circulating DNases and RNases in blood to protect from systemic distribution of foreign DNAs/RNAs.

In tissue culture, lipids (usually cationic lipids to counteract the overall negative charge of the ribo-phosphate backbone of nucleic acids) are complexed with the nucleic acids to facilitate passive transport through the cell membrane; however these lipids often show toxicity even just in cell culture, and would likely be very toxic to a mouse, much less a human at the levels that would be needed to afford sufficient knockdown of the target gene in the desired location. There are many groups around the world working on the technical side of delivery; lipids, liposomes, cationic polymers, and direct conjugation of lipid moieties to the sugar-phosphate backbone are all currently being evaluated (Whitehead, Langer, \& Anderson, 2009).

Another thing to be considered is the specificity of the target gene, which is even more important for the context of altering miRNA levels to achieve a clinical outcome. As far as we know miRNAs target multiple different mRNA targets, thus is goes to reason that altering the miRNA in a cancer might result in sensitization to chemotherapy (Figure 4.2-6), but will it have the same effect on normal cells, and not just normal cells in the same organ as the tumor but normal cells throughout the entire body? With miRNAs altering the expression of multiple genes, how does one determine which gene is important in the alteration of chemosensitivity, and will the changes in gene expression due to alterations in
miRNA level be the same throughout the body or will there be tissue specific changes that might or might not cause negative side effects just from the miRNA treatment? These are all things that need to be considered as RNAi mediated therapies make their ways into the clinics.

SMAC mimetics/IAP antagonists are much closer to being used in patients, in fact there are many clinical trials that have been completed or are underway evaluating the safety and determining dosing and safety of said molecules (Table 6.1). The studies understanding single agent SMAC mimetic induced apoptosis will no doubt be used to design clinical trials where one of the inclusion criteria is detectable serum TNF $\alpha$; however, the levels of serum TNF $\alpha$ that coincide with SMAC mimetic tumor-lethality still need to be determined. The work presented here has shown that SMAC mimetics in combination with chemotherapy is a valid therapeutic strategy, and suggests that in clinical trials it would be best paired with an anti-mitotic, preferably vinorelbine, and that it is still effective when combined with an anti-mitotic as part of a platinum-based doublet.

Overall the studies presented herein show major advances in rationally designing combination chemotherapy strategies at different stages of preclinical development, with one such strategy being ready to begin being translated to the clinic as part of a clinical trial.

| SMAC Mimetic | Trial Name | Pharmaceutical Company | Phase | NTC Number | Condition | Intervention |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| AT-406 | Oral AT-406 in Combination With Daunorubicin and Cytarabine in Patients With Poor-nisk AML | Ascenta | Phase I | NCT01265199 | Acute Myelogenous Leukemia (AML) | AT-406 + daunorubicin/cytarabine |
|  | Study of Safety and Tolerability of AT-406 in Patients With Advanced Solid Tumors and Lymphomas |  | Phase I | NCT01078649 | Solid Tumors, Lymphomas | AT-406 |
| GDC0917 | GDC-0917 Administered to Patients With Refractory Solid Tumors or Lymphoma | Genentech | Phase I | NCT01226277 | Solid Tumors | GDC0917 |
| HGS1029 | HGS1029 in Subjects With Advanced Solid Tumors | HGS | Phase I | NCT00708006 | Advanced Solid Tumors | HGS1029 |
|  | HGS1029 in Subjects With Relapsed or Refractory Lymphoid Malignancies |  | Phase I | NCT01013818 | Lymphoid Malignancies | HGS1029 |
| LCL161 | fety and Efficacy of LCL161 in Patients With Solid Tum | Novartis | Phase I | NCT01098838 | Advanced Solid Tumors | LCL161 |
|  | LCL161 in Combination With Weekly Paclitaxel in Adult Patients With Advanced Solid Tumors |  | Phase I | NCT01240655 | Solid Tumors | LCL161 |
| TL32711 | Docetaxel + carboplatin with TL32711, in Subjects With Advanced or Metastatic Solid Tumors | TetraL ogic | Phase IIII | NCT01188499 | Advanced Solid Tumors | (Paclitaxel/Carboplatin, Irinotecan, Docetaxel, Gemcitabine, Liposomal doxorubicin) + TL32711 |
|  | TL32711 in Adults With Refractory Solid Tumors or Lymphoma |  | Phase I | NCT00993239 | Solid Tumors, Lymphomas | TL32711 |

TABLE 6.1 U.S.Clinical Trials involving SMAC mimetics.

## APPENDIX A. 1188 GENES CORRELATING WITH SYNERGY TO

GEMCITABINE + CISPLATIN

| Gene ID | Symbol | Synergy Correlation | Correlation $P$ value | Up or Down regulated |
| :---: | :---: | :---: | :---: | :---: |
| 106 | CARS | -0.37 | 0.042 | D |
| 118 | GABARAPL2 | -0.45 | 0.014 | D |
| 136 | FUBP1 | -0.39 | 0.034 | D |
| 198 |  | -0.39 | 0.035 | D |
| 206 | DARC | -0.39 | 0.032 | D |
| 243 | ZBTB2 | -0.42 | 0.019 | D |
| 280 | HSD11B1 | -0.38 | 0.040 | D |
| 283 | GLIS1 | -0.43 | 0.018 | D |
| 298 | MAPKAP1 | -0.51 | 0.004 | D |
| 322 | KCNJ8 | -0.50 | 0.005 | D |
| 405 | SCML2 | -0.43 | 0.018 | D |
| 415 | BBS7 | -0.45 | 0.014 | D |
| 467 | HSPD1 | -0.45 | 0.012 | D |
| 496 | HSPE1 | -0.58 | 0.001 | D |
| 516 | C12orf29 | -0.46 | 0.011 | D |
| 572 | WHSC1 | -0.37 | 0.043 | D |
| 621 | SAA1 | -0.52 | 0.003 | D |
| 778 | DNTTIP2 | -0.45 | 0.013 | D |
| 813 | KDELC1 | -0.39 | 0.034 | D |
| 815 | ANAPC7 | -0.37 | 0.047 | D |
| 855 | DPH5 | -0.44 | 0.015 | D |
| 869 | GGH | -0.36 | 0.048 | D |
| 886 | S1PR1 | -0.52 | 0.003 | D |
| 953 | ACCN1 | -0.37 | 0.047 | D |
| 957 | DHX36 | -0.41 | 0.025 | D |
| 959 | LAS1L | -0.37 | 0.046 | D |
| 977 | CPSF6 | -0.48 | 0.007 | D |
| 980 | CCDC144NL | -0.36 | 0.049 | D |
| 989 | UBE2N | -0.39 | 0.034 | D |
| 1035 | RPRD1A | -0.40 | 0.030 | D |
| 1055 | TMEFF2 | -0.52 | 0.003 | D |
| 1062 | AMZ2 | -0.47 | 0.009 | D |


| 1066 | OR4P4 | -0.42 | 0.022 | D |
| :---: | :---: | :---: | :---: | :---: |
| 1067 | HIPK1 | -0.40 | 0.030 | D |
| 1075 | ASCC3 | -0.61 | 0.000 | D |
| 1076 | RAD17 | -0.45 | 0.012 | D |
| 1082 | PRPSAP2 | -0.41 | 0.024 | D |
| 1083 | EBNA1BP2 | -0.38 | 0.040 | D |
| 1115 | MRPL44 | -0.40 | 0.029 | D |
| 1165 | ZNF182 | -0.47 | 0.008 | D |
| 1242 | TSPAN4 | -0.51 | 0.004 | D |
| 1247 | GPM6A | -0.38 | 0.038 | D |
| 1266 | RPL23 | -0.48 | 0.007 | D |
| 1284 | RFXAP | -0.37 | 0.045 | D |
| 1286 | SRSF1 | -0.40 | 0.030 | D |
| 1359 | CAPN7 | -0.42 | 0.019 | D |
| 1380 | C18orf21 | -0.48 | 0.008 | D |
| 1399 | SEPT7 | -0.41 | 0.023 | D |
| 1489 | XCL1 | -0.42 | 0.020 | D |
| 1512 | PTMA | -0.43 | 0.017 | D |
| 1514 | IPO8 | -0.40 | 0.030 | D |
| 1531 | RABEPK | -0.53 | 0.003 | D |
| 1585 | POSTN | -0.41 | 0.026 | D |
| 1618 | RAD51C | -0.39 | 0.036 | D |
| 1642 | ZNF331 | -0.39 | 0.036 | D |
| 1661 | SUMO2 | -0.39 | 0.031 | D |
| 1708 | SYN3 | -0.39 | 0.032 | D |
| 1790 | CXCL5 | -0.37 | 0.044 | D |
| 1793 | CEMP1 | -0.41 | 0.024 | D |
| 1974 | IQCB1 | -0.57 | 0.001 | D |
| 1994 | PRTG | -0.44 | 0.015 | D |
| 2065 | FCRL3 | -0.41 | 0.026 | D |
| 2249 | SNRPF | -0.37 | 0.047 | D |
| 2254 | RPS28 | -0.40 | 0.030 | D |
| 2273 | ZNF772 | -0.44 | 0.016 | D |
| 2289 | USP33 | -0.43 | 0.017 | D |
| 2292 | CLIP3 | -0.53 | 0.003 | D |
| 2300 | TBCB | -0.41 | 0.024 | D |
| 2316 | PRDM10 | -0.39 | 0.035 | D |
| 2416 | MRPL48 | -0.37 | 0.046 | D |


| 2435 | NTRK1 | -0.47 | 0.008 | D |
| :---: | :---: | :---: | :---: | :---: |
| 2442 |  | -0.41 | 0.023 | D |
| 2443 | MMP19 | -0.40 | 0.027 | D |
| 2456 | NRXN3 | -0.38 | 0.038 | D |
| 2476 | PRRG3 | -0.42 | 0.022 | D |
| 2490 | PAPPA | -0.39 | 0.032 | D |
| 2614 | C12orf24 | -0.42 | 0.020 | D |
| 2634 | OR2M4 | -0.39 | 0.034 | D |
| 2637 | RTN4 | -0.39 | 0.034 | D |
| 2714 | TNNI3K | -0.49 | 0.006 | D |
| 2766 | RPL5 | -0.45 | 0.012 | D |
| 2783 | NCF1C | -0.43 | 0.017 | D |
| 2807 | CYBB | -0.38 | 0.037 | D |
| 2831 | EXOSC10 | -0.52 | 0.003 | D |
| 2836 | NXPH2 | -0.50 | 0.005 | D |
| 2846 | RSPH9 | -0.42 | 0.020 | D |
| 2890 | PHYHIPL | -0.50 | 0.005 | D |
| 2907 | MSH6 | -0.37 | 0.046 | D |
| 2932 | ZNF673 | -0.43 | 0.018 | D |
| 2956 |  | -0.38 | 0.036 | D |
| 3002 | ASAP1 | -0.42 | 0.020 | D |
| 3017 | SNX16 | -0.37 | 0.046 | D |
| 3024 | TXNL1 | -0.49 | 0.006 | D |
| 3025 | EIF3M | -0.47 | 0.009 | D |
| 3063 | SMCP | -0.40 | 0.029 | D |
| 3067 | PCDHB6 | -0.49 | 0.006 | D |
| 3085 | SRGAP2 | -0.38 | 0.039 | D |
| 3138 | SPATS1 | -0.44 | 0.016 | D |
| 3140 | TAF9 | -0.57 | 0.001 | D |
| 3145 | SRSF11 | -0.45 | 0.014 | D |
| 3152 | ZNF280A | -0.43 | 0.018 | D |
| 3192 | PSMG1 | -0.42 | 0.021 | D |
| 3295 | SULT1A4 | -0.62 | 0.000 | D |
| 3300 | FPR1 | -0.55 | 0.002 | D |
| 3310 | CDKN1B | -0.42 | 0.019 | D |
| 3338 | COPS3 | -0.41 | 0.024 | D |
| 3451 | IGF2BP1 | -0.49 | 0.006 | D |
| 3453 | ZNF286A | -0.50 | 0.005 | D |


| 3542 | AQR | -0.39 | 0.033 | D |
| :---: | :---: | :---: | :---: | :---: |
| 3582 | FLCN | -0.41 | 0.024 | D |
| 3587 | SPCS2 | -0.40 | 0.028 | D |
| 3599 | SF3B3 | -0.39 | 0.033 | D |
| 3635 | ARL6 | -0.37 | 0.042 | D |
| 3658 | FAM72D | -0.42 | 0.020 | D |
| 3672 | SCRG1 | -0.41 | 0.026 | D |
| 3683 | HS2ST1 | -0.43 | 0.019 | D |
| 3740 | EBF1 | -0.41 | 0.024 | D |
| 3795 | FAM83G | -0.63 | 0.000 | D |
| 3798 | ZNF804B | -0.51 | 0.004 | D |
| 3892 | SGCB | -0.41 | 0.026 | D |
| 3977 | FADS3 | -0.38 | 0.040 | D |
| 4005 | RPL26 | -0.59 | 0.001 | D |
| 4019 | FLJ16423 | -0.39 | 0.034 | D |
| 4080 | MOSPD2 | -0.54 | 0.002 | D |
| 4090 | RAB12 | -0.44 | 0.016 | D |
| 4094 | OR52D1 | -0.37 | 0.046 | D |
| 4113 | MRPL52 | -0.39 | 0.031 | D |
| 4119 | ANP32A | -0.56 | 0.001 | D |
| 4133 | KDM3A | -0.42 | 0.020 | D |
| 4197 | EYA4 | -0.55 | 0.002 | D |
| 4261 | UNC93A | -0.43 | 0.017 | D |
| 4309 | C1S | -0.37 | 0.043 | D |
| 4358 | MTHFD2 | -0.40 | 0.027 | D |
| 4481 | CRHR1 | -0.39 | 0.031 | D |
| 4483 | FXYD1 | -0.37 | 0.042 | D |
| 4484 | MATN1 | -0.37 | 0.044 | D |
| 4514 | TGIF1 | -0.40 | 0.030 | D |
| 4536 | GORAB | -0.37 | 0.045 | D |
| 4556 | SF1 | -0.62 | 0.000 | D |
| 4563 | OR52A5 | -0.36 | 0.047 | D |
| 4565 | RPS6 | -0.39 | 0.032 | D |
| 4566 | R3HDM1 | -0.49 | 0.006 | D |
| 4568 | GSK3A | -0.40 | 0.027 | D |
| 4581 | GOPC | -0.51 | 0.004 | D |
| 4603 | GLI1 | -0.37 | 0.043 | D |
| 4621 |  | -0.39 | 0.031 | D |


| 4624 | RPSA | -0.37 | 0.047 | D |
| :---: | :---: | :---: | :---: | :---: |
| 4802 | EXOSC2 | -0.36 | 0.048 | D |
| 4810 | SSX2IP | -0.36 | 0.048 | D |
| 4823 | ZKSCAN5 | -0.38 | 0.039 | D |
| 4849 | TRAPPC2L | -0.48 | 0.007 | D |
| 4858 | EXOSC3 | -0.46 | 0.011 | D |
| 4877 | FSD1 | -0.51 | 0.004 | D |
| 4893 | RPL17 | -0.45 | 0.014 | D |
| 4943 | TRIM69 | -0.37 | 0.043 | D |
| 4977 | IL1F8 | -0.41 | 0.026 | D |
| 5052 | CWC22 | -0.52 | 0.003 | D |
| 5059 | PES1 | -0.40 | 0.027 | D |
| 5083 | HNRNPC | -0.44 | 0.014 | D |
| 5104 | ATF7 | -0.45 | 0.013 | D |
| 5220 | DACT1 | -0.40 | 0.027 | D |
| 5231 | RNASEH1 | -0.36 | 0.048 | D |
| 5278 | C5orf34 | -0.52 | 0.003 | D |
| 5364 | MPHOSPH10 | -0.37 | 0.047 | D |
| 5367 | GPR62 | -0.44 | 0.015 | D |
| 5467 | SULT1E1 | -0.36 | 0.050 | D |
| 5485 | ID2 | -0.37 | 0.046 | D |
| 5528 | KIF21A | -0.40 | 0.028 | D |
| 5550 | MCTS1 | -0.38 | 0.036 | D |
| 5566 | U2AF2 | -0.41 | 0.023 | D |
| 5582 | ATG3 | -0.44 | 0.014 | D |
| 5621 | C2orf57 | -0.38 | 0.038 | D |
| 5708 | NXF5 | -0.38 | 0.040 | D |
| 5712 | GPR19 | -0.42 | 0.020 | D |
| 5734 | PIGF | -0.38 | 0.036 | D |
| 5753 | SLC38A2 | -0.41 | 0.024 | D |
| 5754 | USP10 | -0.37 | 0.046 | D |
| 5781 | ZNF711 | -0.39 | 0.035 | D |
| 5783 | RNASE13 | -0.39 | 0.034 | D |
| 5797 | MCRS1 | -0.48 | 0.008 | D |
| 5806 | RBM24 | -0.55 | 0.002 | D |
| 5822 | BOLA2 | -0.40 | 0.031 | D |
| 5830 | SYNE2 | -0.45 | 0.012 | D |
| 5881 |  | -0.37 | 0.043 | D |


| 5910 | RAB21 | -0.42 | 0.021 | D |
| :---: | :---: | :---: | :---: | :---: |
| 5931 | MAPK7 | -0.43 | 0.017 | D |
| 5974 | PEMT | -0.45 | 0.012 | D |
| 5975 | GRIA3 | -0.38 | 0.038 | D |
| 5991 | PSMB7 | -0.62 | 0.000 | D |
| 6012 | PTGES3 | -0.39 | 0.035 | D |
| 6013 | CCDC59 | -0.37 | 0.046 | D |
| 6040 | ZCCHC3 | -0.44 | 0.014 | D |
| 6081 | NME1 | -0.51 | 0.004 | D |
| 6083 | PAPSS1 | -0.42 | 0.020 | D |
| 6127 | WTAP | -0.37 | 0.045 | D |
| 6129 | HLCS | -0.47 | 0.009 | D |
| 6132 | SLC35F1 | -0.38 | 0.038 | D |
| 6134 | STARD6 | -0.38 | 0.040 | D |
| 6159 | EIF5A | -0.39 | 0.033 | D |
| 6177 | HIAT1 | -0.39 | 0.033 | D |
| 6189 | MRGPRX1 | -0.37 | 0.047 | D |
| 6254 | ZNF831 | -0.39 | 0.035 | D |
| 6260 | NDUFAF4 | -0.49 | 0.007 | D |
| 6294 | RASSF2 | -0.42 | 0.022 | D |
| 6323 | CCNH | -0.51 | 0.004 | D |
| 6350 | METTL6 | -0.40 | 0.028 | D |
| 6351 | FLCN | -0.37 | 0.042 | D |
| 6360 | C10orf129 | -0.46 | 0.011 | D |
| 6438 | METTL1 | -0.37 | 0.043 | D |
| 6474 | ZCRB1 | -0.41 | 0.024 | D |
| 6494 | ZNF454 | -0.37 | 0.042 | D |
| 6530 | CCDC25 | -0.40 | 0.030 | D |
| 6705 | BAZ2A | -0.38 | 0.038 | D |
| 6717 | EIF3A | -0.54 | 0.002 | D |
| 6859 | CSRP2BP | -0.65 | 0.000 | D |
| 6912 | RBBP7 | -0.39 | 0.032 | D |
| 6917 | ZFP1 | -0.58 | 0.001 | D |
| 6951 | QTRT1 | -0.46 | 0.010 | D |
| 6977 | NOL8 | -0.41 | 0.024 | D |
| 7061 | MC5R | -0.66 | 0.000 | D |
| 7076 | BOLL | -0.39 | 0.035 | D |
| 7090 | RNF212 | -0.37 | 0.046 | D |


| 7163 | RPL14 | -0.49 | 0.006 | D |
| :---: | :---: | :---: | :---: | :---: |
| 7172 | FBXO40 | -0.37 | 0.042 | D |
| 7215 | DNAJC18 | -0.38 | 0.039 | D |
| 7329 | SPRR2F | -0.41 | 0.025 | D |
| 7350 | HAUS1 | -0.41 | 0.026 | D |
| 7367 | RAD51C | -0.44 | 0.014 | D |
| 7411 | RAD1 | -0.44 | 0.014 | D |
| 7431 | KRTAP10-11 | -0.65 | 0.000 | D |
| 7442 | MPHOSPH6 | -0.42 | 0.021 | D |
| 7517 | RPSA | -0.54 | 0.002 | D |
| 7525 |  | -0.39 | 0.032 | D |
| 7572 | OR2J2 | -0.40 | 0.026 | D |
| 7577 | AGTPBP1 | -0.37 | 0.041 | D |
| 7640 | EYA4 | -0.51 | 0.004 | D |
| 7643 | CHD1 | -0.39 | 0.032 | D |
| 7644 | GNAS | -0.38 | 0.038 | D |
| 7653 | TSNAXIP1 | -0.38 | 0.038 | D |
| 7664 | TBX18 | -0.40 | 0.028 | D |
| 7676 | RAN | -0.39 | 0.036 | D |
| 7698 | GPR55 | -0.48 | 0.007 | D |
| 7725 | FADS1 | -0.60 | 0.000 | D |
| 7736 | H3F3A | -0.36 | 0.047 | D |
| 7749 | KRT82 | -0.38 | 0.036 | D |
| 7838 | RPS15A | -0.36 | 0.050 | D |
| 7868 | KCNH1 | -0.39 | 0.034 | D |
| 7882 | RORB | -0.42 | 0.022 | D |
| 7920 | VCP | -0.40 | 0.029 | D |
| 7928 | PSMG1 | -0.48 | 0.007 | D |
| 7949 |  | -0.55 | 0.002 | D |
| 8004 | CCDC34 | -0.41 | 0.026 | D |
| 8005 | KIF18A | -0.42 | 0.020 | D |
| 8032 | ZDHHC2 | -0.38 | 0.040 | D |
| 8084 | RTN3 | -0.40 | 0.028 | D |
| 8093 | ANKRD19 | -0.41 | 0.025 | D |
| 8116 | VHL | -0.38 | 0.040 | D |
| 8124 | OR1D2 | -0.57 | 0.001 | D |
| 8148 | RANBP10 | -0.41 | 0.025 | D |
| 8149 | TCEAL5 | -0.47 | 0.009 | D |


| 8173 | C1D | -0.44 | 0.015 | D |
| :---: | :---: | :---: | :---: | :---: |
| 8208 | TRMT61B | -0.44 | 0.015 | D |
| 8210 | TRA2B | -0.39 | 0.034 | D |
| 8246 | RFX5 | -0.41 | 0.023 | D |
| 8324 | GPR34 | -0.41 | 0.025 | D |
| 8342 | TMTC4 | -0.37 | 0.044 | D |
| 8346 | NACA2 | -0.37 | 0.043 | D |
| 8348 | FAM101A | -0.53 | 0.003 | D |
| 8397 | AKT3 | -0.59 | 0.001 | D |
| 8442 | HNRPDL | -0.44 | 0.015 | D |
| 8444 | PPHLN1 | -0.57 | 0.001 | D |
| 8447 | KIF5C | -0.40 | 0.029 | D |
| 8451 | C4orf43 | -0.36 | 0.049 | D |
| 8456 | RTP3 | -0.38 | 0.038 | D |
| 8496 | PSMD14 | -0.37 | 0.043 | D |
| 8545 | AADACL4 | -0.46 | 0.011 | D |
| 8608 | CHST5 | -0.45 | 0.012 | D |
| 8637 | RNGTT | -0.38 | 0.041 | D |
| 8662 | XAGE1D | -0.52 | 0.003 | D |
| 8678 | RPF1 | -0.45 | 0.012 | D |
| 8687 | FAM49B | -0.40 | 0.029 | D |
| 8898 | STC1 | -0.39 | 0.034 | D |
| 8900 | TMEM225 | -0.40 | 0.027 | D |
| 8916 | RPL7 | -0.44 | 0.015 | D |
| 8926 | CCDC129 | -0.47 | 0.009 | D |
| 8944 | R3HDM2 | -0.39 | 0.031 | D |
| 8998 | BEST3 | -0.38 | 0.037 | D |
| 9005 | MRPS23 | -0.51 | 0.004 | D |
| 9088 | MARS | -0.39 | 0.035 | D |
| 9182 | SPECC1 | -0.46 | 0.011 | D |
| 9250 | CPEB3 | -0.41 | 0.023 | D |
| 9253 | RPL7A | -0.37 | 0.042 | D |
| 9272 | C20orf27 | -0.38 | 0.037 | D |
| 9275 | SLITRK5 | -0.57 | 0.001 | D |
| 9316 | MTF2 | -0.36 | 0.049 | D |
| 9363 | C16orf73 | -0.47 | 0.009 | D |
| 9368 | TRIM35 | -0.37 | 0.045 | D |
| 9402 | SPECC1 | -0.46 | 0.010 | D |


| 9440 | NEGR1 | -0.47 | 0.008 | D |
| :---: | :---: | :---: | :---: | :---: |
| 9506 | CHAC2 | -0.42 | 0.022 | D |
| 9551 | KCTD12 | -0.37 | 0.044 | D |
| 9560 | CRX | -0.44 | 0.016 | D |
| 9566 | PAGE5 | -0.38 | 0.040 | D |
| 9603 | NME7 | -0.41 | 0.023 | D |
| 9635 | VCAM1 | -0.46 | 0.011 | D |
| 9659 | PODNL1 | -0.39 | 0.033 | D |
| 9696 | HOXD9 | -0.44 | 0.014 | D |
| 9705 | LRRC4C | -0.44 | 0.014 | D |
| 9707 | C18orf32 | -0.56 | 0.001 | D |
| 9766 | C9orf5 | -0.42 | 0.022 | D |
| 9903 | SLC39A6 | -0.42 | 0.021 | D |
| 9913 | MAK16 | -0.38 | 0.038 | D |
| 9918 | CIT | -0.36 | 0.048 | D |
| 9989 | CNOT7 | -0.40 | 0.028 | D |
| 10057 | RPS13 | -0.45 | 0.012 | D |
| 10078 | NCRNA00152 | -0.43 | 0.019 | D |
| 10089 | SEMG2 | -0.43 | 0.017 | D |
| 10122 | STX8 | -0.51 | 0.004 | D |
| 10136 | FAM18B2 | -0.36 | 0.050 | D |
| 10151 | AKNAD1 | -0.46 | 0.011 | D |
| 10156 | UTP15 | -0.36 | 0.049 | D |
| 10160 | C11orf58 | -0.49 | 0.006 | D |
| 10190 | PPAP2C | -0.38 | 0.038 | D |
| 10197 | DEFB108B | -0.44 | 0.014 | D |
| 10217 | KCNT2 | -0.48 | 0.007 | D |
| 10320 | ZFPM2 | -0.42 | 0.021 | D |
| 10375 | IFT74 | -0.41 | 0.025 | D |
| 10415 | ZNF271 | -0.44 | 0.014 | D |
| 10475 | SYT4 | -0.37 | 0.045 | D |
| 10476 | MAP3K15 | -0.43 | 0.017 | D |
| 10511 | LYPD6B | -0.43 | 0.017 | D |
| 10536 | MGA | -0.45 | 0.012 | D |
| 10546 | ITPRIPL1 | -0.40 | 0.027 | D |
| 10584 | ATP5G2 | -0.40 | 0.030 | D |
| 10595 | DNAJC7 | -0.40 | 0.028 | D |
| 10626 | LAP3 | -0.39 | 0.032 | D |


| 10676 | SREK1 | -0.45 | 0.013 | D |
| :---: | :---: | :---: | :---: | :---: |
| 10716 | TDP2 | -0.47 | 0.008 | D |
| 10736 | TIMM10 | -0.39 | 0.034 | D |
| 10785 | FAM35A | -0.43 | 0.018 | D |
| 10847 | MGC45800 | -0.49 | 0.006 | D |
| 10874 | SIGLEC12 | -0.43 | 0.017 | D |
| 10962 | HERPUD2 | -0.45 | 0.013 | D |
| 10967 | LILRA2 | -0.41 | 0.025 | D |
| 10998 | FREM2 | -0.42 | 0.022 | D |
| 11012 | PRKDC | -0.37 | 0.046 | D |
| 11016 | RBMS1 | -0.39 | 0.034 | D |
| 11037 | NETO1 | -0.44 | 0.014 | D |
| 11041 | PDP2 | -0.37 | 0.046 | D |
| 11059 | RECK | -0.44 | 0.016 | D |
| 11069 | MRRF | -0.38 | 0.036 | D |
| 11142 | SRR | -0.38 | 0.041 | D |
| 11268 | TRAPPC1 | -0.36 | 0.049 | D |
| 11274 | GTF2H1 | -0.43 | 0.017 | D |
| 11312 | FBN2 | -0.53 | 0.003 | D |
| 11338 | FECH | -0.44 | 0.015 | D |
| 11359 | ELP3 | -0.39 | 0.035 | D |
| 11363 | HCCS | -0.37 | 0.044 | D |
| 11464 | SCO1 | -0.43 | 0.018 | D |
| 11484 | RXRG | -0.45 | 0.012 | D |
| 11522 | HEATR1 | -0.37 | 0.047 | D |
| 11528 | HDGFRP3 | -0.43 | 0.019 | D |
| 11622 | PTH2R | -0.39 | 0.032 | D |
| 11631 | DACT1 | -0.39 | 0.035 | D |
| 11656 |  | -0.48 | 0.008 | D |
| 11713 | FOXS1 | -0.43 | 0.018 | D |
| 11722 | CDKL3 | -0.36 | 0.048 | D |
| 11755 | C3orf26 | -0.39 | 0.035 | D |
| 11767 | TROVE2 | -0.37 | 0.047 | D |
| 11768 |  | -0.42 | 0.022 | D |
| 11772 | OFD1 | -0.38 | 0.039 | D |
| 11823 | ROBO1 | -0.71 | 0.000 | D |
| 11885 | CDH4 | -0.40 | 0.028 | D |
| 11886 | OR4C45 | -0.54 | 0.002 | D |


| 11905 | AOX1 | -0.37 | 0.046 | D |
| :---: | :---: | :---: | :---: | :---: |
| 11946 | NOVA1 | -0.42 | 0.020 | D |
| 12045 | LDHAL6B | -0.44 | 0.015 | D |
| 12047 | APOC2 | -0.37 | 0.045 | D |
| 12066 | DCP1B | -0.36 | 0.048 | D |
| 12092 | SCN9A | -0.48 | 0.007 | D |
| 12159 | PGA3 | -0.45 | 0.012 | D |
| 12206 | GPAM | -0.49 | 0.006 | D |
| 12209 | C9orf50 | -0.37 | 0.044 | D |
| 12217 | PFAS | -0.49 | 0.006 | D |
| 12243 | LARP4 | -0.40 | 0.029 | D |
| 12255 |  | -0.40 | 0.029 | D |
| 12347 | CCDC77 | -0.42 | 0.019 | D |
| 12387 | HK1 | -0.41 | 0.023 | D |
| 12431 | TSEN15 | -0.39 | 0.033 | D |
| 12492 | C6orf58 | -0.37 | 0.045 | D |
| 12503 | OR52W1 | -0.43 | 0.017 | D |
| 12560 | HIST1H4C | -0.38 | 0.040 | D |
| 12588 | NUP37 | -0.41 | 0.026 | D |
| 12590 | TOP3A | -0.36 | 0.049 | D |
| 12597 | DNM1L | -0.44 | 0.016 | D |
| 12618 | RPL14 | -0.41 | 0.023 | D |
| 12625 | COX10 | -0.37 | 0.046 | D |
| 12652 | EIF1AX | -0.50 | 0.005 | D |
| 12742 | WNK3 | -0.44 | 0.014 | D |
| 12750 | KIF3A | -0.43 | 0.018 | D |
| 12762 | TAF1B | -0.37 | 0.043 | D |
| 12770 | YSK4 | -0.44 | 0.014 | D |
| 12794 | PPP1R1C | -0.43 | 0.017 | D |
| 12796 | DOT1L | -0.38 | 0.036 | D |
| 12929 | NAE1 | -0.37 | 0.047 | D |
| 12941 | ASTN2 | -0.53 | 0.002 | D |
| 12961 | SMC3 | -0.49 | 0.006 | D |
| 12995 |  | -0.42 | 0.020 | D |
| 13002 | SGK196 | -0.43 | 0.017 | D |
| 13018 | CLEC18A | -0.43 | 0.019 | D |
| 13055 | POLR1E | -0.42 | 0.022 | D |
| 13076 | TMEM19 | -0.38 | 0.037 | D |


| 13087 | TEAD4 | -0.37 | 0.043 | D |
| :---: | :---: | :---: | :---: | :---: |
| 13130 | RAB6A | -0.39 | 0.032 | D |
| 13131 | CDH7 | -0.40 | 0.029 | D |
| 13168 | PAICS | -0.45 | 0.012 | D |
| 13192 | FLJ35409 | -0.63 | 0.000 | D |
| 13226 | TRMT6 | -0.46 | 0.011 | D |
| 13259 | DUSP11 | -0.44 | 0.015 | D |
| 13306 | PPAT | -0.47 | 0.009 | D |
| 13335 | GFRA4 | -0.38 | 0.039 | D |
| 13345 | ATP6V1C2 | -0.37 | 0.044 | D |
| 13367 | SOX5 | -0.37 | 0.047 | D |
| 13482 | ZZZ3 | -0.39 | 0.036 | D |
| 13560 | AASDH | -0.48 | 0.008 | D |
| 13584 | MUTED | -0.39 | 0.032 | D |
| 13590 | TRPC1 | -0.39 | 0.031 | D |
| 13622 | TBX18 | -0.40 | 0.030 | D |
| 13640 | GPHA2 | -0.40 | 0.029 | D |
| 13679 | PDE1A | -0.42 | 0.019 | D |
| 13710 | SNX24 | -0.38 | 0.038 | D |
| 13764 | LUZP4 | -0.40 | 0.027 | D |
| 13802 | C3orf75 | -0.36 | 0.048 | D |
| 13839 | FGF4 | -0.38 | 0.038 | D |
| 13847 | ANKRD17 | -0.40 | 0.028 | D |
| 13909 | DYNC2H1 | -0.47 | 0.010 | D |
| 13942 | LIN28B | -0.37 | 0.042 | D |
| 13993 | TCP1 | -0.37 | 0.043 | D |
| 14009 | SET | -0.41 | 0.023 | D |
| 14054 | ATP2B1 | -0.48 | 0.008 | D |
| 14068 | CALB2 | -0.38 | 0.038 | D |
| 14123 | STK4 | -0.37 | 0.044 | D |
| 14134 | DNAJC10 | -0.38 | 0.040 | D |
| 14185 | DHX37 | -0.39 | 0.033 | D |
| 14196 | ZNF23 | -0.39 | 0.033 | D |
| 14223 | PARD3B | -0.37 | 0.046 | D |
| 14238 | GNAI1 | -0.40 | 0.029 | D |
| 14241 | AIFM3 | -0.43 | 0.019 | D |
| 14305 | PHF8 | -0.39 | 0.032 | D |
| 14355 | SLBP | -0.43 | 0.017 | D |


| 14356 | PHF3 | -0.43 | 0.016 | D |
| :---: | :---: | :---: | :---: | :---: |
| 14365 | SEZ6L2 | -0.43 | 0.018 | D |
| 14374 | DPH5 | -0.39 | 0.032 | D |
| 14464 | UBA2 | -0.40 | 0.031 | D |
| 14472 | HNRNPH3 | -0.52 | 0.003 | D |
| 14479 | CCDC104 | -0.44 | 0.015 | D |
| 14490 | PRAMEF10 | -0.40 | 0.028 | D |
| 14581 | CRELD1 | -0.37 | 0.046 | D |
| 14590 | OR2V2 | -0.46 | 0.012 | D |
| 14603 | SEPT1 | -0.46 | 0.011 | D |
| 14618 | USP9X | -0.38 | 0.038 | D |
| 14651 |  | -0.37 | 0.043 | D |
| 14750 | KCNMB3 | -0.37 | 0.042 | D |
| 14751 | ACOX3 | -0.44 | 0.016 | D |
| 14769 | ROBO1 | -0.45 | 0.012 | D |
| 14856 | ATP5I | -0.48 | 0.007 | D |
| 14879 | CNTROB | -0.41 | 0.025 | D |
| 14960 | USP9X | -0.39 | 0.031 | D |
| 14971 | RPS10 | -0.44 | 0.015 | D |
| 15024 | NME1 | -0.43 | 0.018 | D |
| 15037 | ACVR2A | -0.36 | 0.049 | D |
| 15088 | ELOVL2 | -0.38 | 0.040 | D |
| 15112 | MLH1 | -0.55 | 0.002 | D |
| 15114 | ZNF804A | -0.42 | 0.021 | D |
| 15118 | AGTRAP | -0.37 | 0.047 | D |
| 15165 | PRR5L | -0.37 | 0.043 | D |
| 15192 | RPL9 | -0.48 | 0.007 | D |
| 15206 | PLOD2 | -0.39 | 0.032 | D |
| 15226 | TRIM37 | -0.51 | 0.004 | D |
| 15249 | CDO1 | -0.43 | 0.018 | D |
| 15250 | UCHL1 | -0.37 | 0.044 | D |
| 15335 | TIPRL | -0.37 | 0.042 | D |
| 15382 | EFHA2 | -0.48 | 0.007 | D |
| 15427 | C4orf46 | -0.42 | 0.022 | D |
| 15442 | IGFL2 | -0.41 | 0.023 | D |
| 15474 | UBE2D2 | -0.45 | 0.014 | D |
| 15511 | CDK7 | -0.38 | 0.040 | D |
| 15543 | RAB11FIP2 | -0.44 | 0.016 | D |


| 15558 | IL17A | -0.44 | 0.015 | D |
| :---: | :---: | :---: | :---: | :---: |
| 15559 | LRRC40 | -0.37 | 0.043 | D |
| 15576 | CEP290 | -0.37 | 0.043 | D |
| 15618 | ANK2 | -0.46 | 0.010 | D |
| 15683 | STAT1 | -0.45 | 0.013 | D |
| 15692 | SPG7 | -0.50 | 0.005 | D |
| 15823 | NLGN2 | -0.48 | 0.008 | D |
| 15844 | SLC7A7 | -0.37 | 0.047 | D |
| 15869 | EMG1 | -0.38 | 0.039 | D |
| 15881 | C12orf68 | -0.41 | 0.024 | D |
| 15892 | HCFC1 | -0.45 | 0.012 | D |
| 15909 | ITSN1 | -0.37 | 0.044 | D |
| 15943 | EEF1E1 | -0.38 | 0.038 | D |
| 15963 | AKAP3 | -0.50 | 0.005 | D |
| 15968 | UTP18 | -0.51 | 0.004 | D |
| 16013 | GTDC1 | -0.51 | 0.004 | D |
| 16019 | C7orf69 | -0.45 | 0.012 | D |
| 16074 | ABL1 | -0.40 | 0.026 | D |
| 16094 | BDNF | -0.51 | 0.004 | D |
| 16109 | SERTAD3 | -0.38 | 0.036 | D |
| 16120 | C19orf30 | -0.36 | 0.049 | D |
| 16210 | EXOSC10 | -0.38 | 0.037 | D |
| 16216 | SPATA22 | -0.40 | 0.027 | D |
| 16299 | SCG2 | -0.48 | 0.007 | D |
| 16306 | AMMECR1L | -0.38 | 0.037 | D |
| 16316 | AGTRAP | -0.47 | 0.009 | D |
| 16337 | RPL21 | -0.41 | 0.025 | D |
| 16369 | MAP3K12 | -0.63 | 0.000 | D |
| 16478 | ZEB2 | -0.47 | 0.010 | D |
| 16479 | RAD52 | -0.44 | 0.016 | D |
| 16498 | FGF5 | -0.48 | 0.007 | D |
| 16515 | LONRF1 | -0.38 | 0.038 | D |
| 16591 | DCAF6 | -0.41 | 0.026 | D |
| 16596 | IL16 | -0.37 | 0.046 | D |
| 16615 | OR8J1 | -0.55 | 0.002 | D |
| 16703 | CLCN5 | -0.40 | 0.028 | D |
| 16743 | MRPL47 | -0.43 | 0.018 | D |
| 16765 | TPRKB | -0.60 | 0.000 | D |


| 16853 | CD3EAP | -0.40 | 0.028 | D |
| :---: | :---: | :---: | :---: | :---: |
| 16884 | NARS | -0.43 | 0.018 | D |
| 16952 | CHRNE | -0.39 | 0.031 | D |
| 16997 | GPR149 | -0.40 | 0.031 | D |
| 17027 | SEMA4B | -0.38 | 0.040 | D |
| 17030 | PA2G4 | -0.37 | 0.046 | D |
| 17033 | NXT2 | -0.38 | 0.039 | D |
| 17034 | MPDZ | -0.38 | 0.040 | D |
| 17056 | COX8C | -0.37 | 0.047 | D |
| 17057 | C12orf11 | -0.38 | 0.039 | D |
| 17062 | CCT7 | -0.48 | 0.007 | D |
| 17089 | HSDL1 | -0.51 | 0.004 | D |
| 17257 | OR8J3 | -0.48 | 0.008 | D |
| 17270 | SEC31B | -0.46 | 0.010 | D |
| 17322 | KARS | -0.41 | 0.024 | D |
| 17335 | TPTE | -0.39 | 0.035 | D |
| 17342 | GDNF | -0.45 | 0.012 | D |
| 17377 | ARHGAP12 | -0.46 | 0.011 | D |
| 17413 | MRFAP1L1 | -0.46 | 0.010 | D |
| 17440 | EPHA6 | -0.40 | 0.030 | D |
| 17443 | PROL1 | -0.47 | 0.008 | D |
| 17481 | OR14A16 | -0.44 | 0.016 | D |
| 17487 | RBM34 | -0.37 | 0.046 | D |
| 17489 | RASSF2 | -0.45 | 0.014 | D |
| 17532 | DICER1 | -0.39 | 0.035 | D |
| 17545 | LOC728643 | -0.42 | 0.021 | D |
| 17559 | GABRR2 | -0.47 | 0.009 | D |
| 17567 | SCARF2 | -0.40 | 0.030 | D |
| 17610 | ASAH1 | -0.37 | 0.043 | D |
| 17687 | MAP1LC3A | -0.41 | 0.026 | D |
| 17716 | CCDC22 | -0.37 | 0.041 | D |
| 17726 | RABL5 | -0.43 | 0.019 | D |
| 17753 | FCAMR | -0.37 | 0.047 | D |
| 17770 | LSM6 | -0.49 | 0.006 | D |
| 17801 | KCTD16 | -0.38 | 0.039 | D |
| 17809 | ADPRH | -0.36 | 0.048 | D |
| 17844 | CCDC61 | -0.42 | 0.021 | D |
| 17855 | SYNE1 | -0.40 | 0.030 | D |


| 17858 | ATP6V1C1 | -0.37 | 0.047 | D |
| :---: | :---: | :---: | :---: | :---: |
| 17877 | RNMTL1 | -0.38 | 0.036 | D |
| 17882 | WDR11 | -0.51 | 0.004 | D |
| 17897 | SAMD14 | -0.37 | 0.043 | D |
| 17940 | GPR149 | -0.39 | 0.034 | D |
| 18085 | FBXO5 | -0.56 | 0.001 | D |
| 18121 | TOPORS | -0.39 | 0.036 | D |
| 18148 | OSBPL11 | -0.39 | 0.035 | D |
| 18162 | TRUB2 | -0.51 | 0.004 | D |
| 18178 | CDK5RAP2 | -0.40 | 0.028 | D |
| 18186 | BAI3 | -0.38 | 0.036 | D |
| 18187 | HOXA7 | -0.47 | 0.008 | D |
| 18218 | PPM1D | -0.45 | 0.013 | D |
| 18222 | ICOSLG | -0.41 | 0.026 | D |
| 18229 | NETO1 | -0.55 | 0.002 | D |
| 18237 | CLEC4E | -0.47 | 0.009 | D |
| 18334 | PIP5K1B | -0.47 | 0.009 | D |
| 18357 | G3BP1 | -0.49 | 0.006 | D |
| 18447 | POLA1 | -0.38 | 0.039 | D |
| 18672 | UBE2CBP | -0.56 | 0.001 | D |
| 18710 | GPR155 | -0.38 | 0.036 | D |
| 18733 | KIAA1632 | -0.41 | 0.025 | D |
| 18745 | ZNF620 | -0.38 | 0.036 | D |
| 18829 | TRIM58 | -0.41 | 0.026 | D |
| 18838 | RAP1B | -0.41 | 0.023 | D |
| 18871 | L1CAM | -0.41 | 0.024 | D |
| 18896 | DCAF16 | -0.45 | 0.014 | D |
| 18898 | SMURF2 | -0.38 | 0.036 | D |
| 18915 | LUC7L3 | -0.44 | 0.014 | D |
| 18923 | OR51T1 | -0.40 | 0.027 | D |
| 18924 | MRPL18 | -0.43 | 0.017 | D |
| 18927 | BATF3 | -0.40 | 0.030 | D |
| 18962 | HMGB2 | -0.37 | 0.044 | D |
| 18964 | PLXDC2 | -0.37 | 0.046 | D |
| 19006 | PCDH10 | -0.44 | 0.015 | D |
| 19018 | NOP56 | -0.51 | 0.004 | D |
| 19025 | RAD51C | -0.39 | 0.035 | D |
| 19045 | LIAS | -0.40 | 0.028 | D |


| 19050 | LRRC59 | -0.55 | 0.002 | D |
| :---: | :---: | :---: | :---: | :---: |
| 19051 | VSTM2A | -0.46 | 0.011 | D |
| 19058 | PKIA | -0.46 | 0.011 | D |
| 19084 | DRG2 | -0.50 | 0.005 | D |
| 19111 | ISCA1 | -0.36 | 0.049 | D |
| 19121 | ARL6IP1 | -0.47 | 0.008 | D |
| 19122 | SLC39A10 | -0.37 | 0.046 | D |
| 19153 | PMS1 | -0.68 | 0.000 | D |
| 19302 | CLDN17 | -0.48 | 0.007 | D |
| 19324 | ZBTB11 | -0.50 | 0.004 | D |
| 19340 | C18orf55 | -0.37 | 0.043 | D |
| 19403 | NFAM1 | -0.41 | 0.026 | D |
| 19430 | EIF1B | -0.38 | 0.039 | D |
| 19496 | SNX12 | -0.41 | 0.025 | D |
| 19586 | IBSP | -0.43 | 0.018 | D |
| 19625 | PIGL | -0.37 | 0.044 | D |
| 19670 | NKAP | -0.42 | 0.023 | D |
| 19686 | RPL7A | -0.45 | 0.013 | D |
| 19727 | CPNE7 | -0.44 | 0.016 | D |
| 19735 | GPT | -0.37 | 0.047 | D |
| 19824 | FBXO10 | -0.38 | 0.041 | D |
| 19833 | C1QTNF1 | -0.42 | 0.020 | D |
| 19874 | THBS4 | -0.55 | 0.001 | D |
| 19885 | FTCD | -0.40 | 0.029 | D |
| 19965 |  | -0.41 | 0.024 | D |
| 19970 | CLTA | -0.38 | 0.036 | D |
| 20025 | SLC38A10 | -0.43 | 0.018 | D |
| 20042 | MYBBP1A | -0.37 | 0.045 | D |
| 20080 | ARHGEF4 | -0.40 | 0.028 | D |
| 20083 | TSR2 | -0.37 | 0.046 | D |
| 20113 | KPNA2 | -0.52 | 0.003 | D |
| 20151 | ELMO2 | -0.40 | 0.030 | D |
| 20155 | CD47 | -0.36 | 0.047 | D |
| 20178 | SLC6A15 | -0.40 | 0.031 | D |
| 20224 | SMARCAD1 | -0.39 | 0.033 | D |
| 20228 | FTCD | -0.46 | 0.011 | D |
| 20310 | PSMD7 | -0.45 | 0.013 | D |
| 20318 | RFC1 | -0.37 | 0.046 | D |


| 20341 | IL17RC | -0.42 | 0.021 | D |
| :---: | :---: | :---: | :---: | :---: |
| 20379 | DYNC1LI1 | -0.57 | 0.001 | D |
| 20454 | SUV39H2 | -0.38 | 0.040 | D |
| 20480 | MCFD2 | -0.41 | 0.026 | D |
| 20524 | ZNF567 | -0.45 | 0.012 | D |
| 20608 | LEPROTL1 | -0.48 | 0.008 | D |
| 20682 | ROD1 | -0.38 | 0.039 | D |
| 20712 | FXYD7 | -0.43 | 0.016 | D |
| 20717 | TAF1C | -0.39 | 0.034 | D |
| 20781 | ZNF385D | -0.40 | 0.029 | D |
| 20828 | KIAA0368 | -0.39 | 0.035 | D |
| 20896 | EPN2 | -0.36 | 0.049 | D |
| 20949 | PAICS | -0.42 | 0.020 | D |
| 20964 | ITSN1 | -0.39 | 0.031 | D |
| 20983 | RPL9 | -0.46 | 0.011 | D |
| 21070 | TPSAB1 | -0.50 | 0.005 | D |
| 21097 | IGDCC4 | -0.39 | 0.033 | D |
| 21150 | TXNDC3 | -0.39 | 0.035 | D |
| 21197 | NSMCE4A | -0.39 | 0.035 | D |
| 21273 | NAE1 | -0.51 | 0.004 | D |
| 21288 | LIN7C | -0.52 | 0.004 | D |
| 21312 | KSR2 | -0.41 | 0.024 | D |
| 21352 | ARL6 | -0.58 | 0.001 | D |
| 21386 | MSL2 | -0.52 | 0.003 | D |
| 21462 | MYO1A | -0.36 | 0.049 | D |
| 21488 | PIK3C3 | -0.48 | 0.007 | D |
| 21501 | PHLPP2 | -0.47 | 0.009 | D |
| 21538 | INTS9 | -0.44 | 0.015 | D |
| 21616 | PNMAL1 | -0.45 | 0.013 | D |
| 21648 | GPR4 | -0.44 | 0.015 | D |
| 21697 | PITPNA | -0.46 | 0.010 | D |
| 21744 | PAQR9 | -0.37 | 0.044 | D |
| 21758 | FAM26F | -0.39 | 0.031 | D |
| 21766 | RAP1B | -0.40 | 0.027 | D |
| 21803 | TRIM74 | -0.39 | 0.032 | D |
| 21818 | NAA50 | -0.37 | 0.041 | D |
| 21828 | DEFB114 | -0.47 | 0.008 | D |
| 21853 | ATMIN | -0.41 | 0.024 | D |


| 21861 | NRXN3 | -0.38 | 0.038 | D |
| :---: | :---: | :---: | :---: | :---: |
| 21894 | LSM5 | -0.37 | 0.046 | D |
| 21901 | TRMT11 | -0.42 | 0.021 | D |
| 21921 | CLGN | -0.58 | 0.001 | D |
| 22014 | DCUN1D4 | -0.38 | 0.036 | D |
| 22108 | BRAP | -0.36 | 0.049 | D |
| 22152 | EYA4 | -0.70 | 0.000 | D |
| 22159 | OR52L1 | -0.37 | 0.047 | D |
| 22195 | C10orf85 | -0.43 | 0.017 | D |
| 22207 | UMOD | -0.42 | 0.021 | D |
| 22295 | PPP2CB | -0.36 | 0.049 | D |
| 22300 | RPL13P5 | -0.41 | 0.024 | D |
| 22331 | KPNB1 | -0.48 | 0.007 | D |
| 22463 | AMN1 | -0.38 | 0.039 | D |
| 22470 | PCNA | -0.53 | 0.002 | D |
| 22483 | APBB1 | -0.38 | 0.040 | D |
| 22552 | HDAC2 | -0.38 | 0.041 | D |
| 22564 | PFN1 | -0.40 | 0.029 | D |
| 22614 | AKAP12 | -0.36 | 0.048 | D |
| 22644 | PAQR3 | -0.38 | 0.040 | D |
| 22735 | PDCL3 | -0.46 | 0.010 | D |
| 22736 | BMP6 | -0.38 | 0.038 | D |
| 22740 | PHF23 | -0.38 | 0.040 | D |
| 22769 | HUWE1 | -0.52 | 0.003 | D |
| 22784 | EFTUD2 | -0.39 | 0.032 | D |
| 22910 | MRPL52 | -0.49 | 0.006 | D |
| 22917 | C3orf31 | -0.37 | 0.046 | D |
| 22939 | OR8B12 | -0.37 | 0.046 | D |
| 22951 | NECAB1 | -0.55 | 0.002 | D |
| 22995 | TAF9 | -0.44 | 0.016 | D |
| 23023 | BNC2 | -0.45 | 0.013 | D |
| 23036 | ODZ3 | -0.44 | 0.015 | D |
| 23125 | ARID2 | -0.36 | 0.049 | D |
| 23130 | POLR2G | -0.45 | 0.012 | D |
| 23159 | CCT2 | -0.40 | 0.029 | D |
| 23189 | ZNF607 | -0.42 | 0.022 | D |
| 23190 | DACT1 | -0.41 | 0.024 | D |
| 23191 | CEP57 | -0.37 | 0.042 | D |


| 23203 | NCRNA00188 | -0.46 | 0.010 | D |
| :---: | :---: | :---: | :---: | :---: |
| 23246 | CSTF1 | -0.50 | 0.005 | D |
| 23404 | UBQLN1 | -0.37 | 0.044 | D |
| 23417 | RBBP4 | -0.40 | 0.029 | D |
| 23449 | FECH | -0.41 | 0.023 | D |
| 23485 | ATF1 | -0.41 | 0.024 | D |
| 23497 | LOXL3 | -0.39 | 0.032 | D |
| 23510 | MAPKAP1 | -0.39 | 0.032 | D |
| 23553 | BVES | -0.37 | 0.046 | D |
| 23579 | BHLHB9 | -0.41 | 0.023 | D |
| 23587 | BTG3 | -0.36 | 0.049 | D |
| 23612 | FSD1 | -0.46 | 0.011 | D |
| 23617 | CERKL | -0.37 | 0.042 | D |
| 23645 | NSFL1C | -0.39 | 0.036 | D |
| 23659 | HNRNPA1 | -0.37 | 0.044 | D |
| 23665 | AMTN | -0.43 | 0.017 | D |
| 23671 | LYNX1 | -0.39 | 0.034 | D |
| 23688 | UNC5D | -0.42 | 0.021 | D |
| 23710 | GYPA | -0.43 | 0.017 | D |
| 23734 | BDNF | -0.40 | 0.028 | D |
| 23738 | ADNP2 | -0.37 | 0.047 | D |
| 23740 | WFDC8 | -0.52 | 0.003 | D |
| 23803 | CDK4 | -0.51 | 0.004 | D |
| 23855 | MBLAC2 | -0.36 | 0.049 | D |
| 23887 | UBE2C | -0.36 | 0.050 | D |
| 23924 | CTU2 | -0.50 | 0.005 | D |
| 23961 | POU4F1 | -0.38 | 0.037 | D |
| 23994 | CETP | -0.41 | 0.023 | D |
| 24031 | MSC | -0.41 | 0.025 | D |
| 24057 | PLXNA2 | -0.37 | 0.044 | D |
| 24058 | NAA25 | -0.50 | 0.005 | D |
| 24132 | CYP26A1 | -0.38 | 0.040 | D |
| 24135 | ARHGAP8 | -0.43 | 0.017 | D |
| 24186 | NUDT11 | -0.43 | 0.018 | D |
| 24202 | NOC3L | -0.47 | 0.010 | D |
| 24204 | RCN1 | -0.52 | 0.003 | D |
| 24216 | TMEM14B | -0.48 | 0.007 | D |
| 24259 | NME1 | -0.38 | 0.036 | D |


| 24264 | ZNF625 | -0.43 | 0.017 | D |
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| 24276 | DVL2 | -0.43 | 0.019 | D |
| 24285 | ZNF442 | -0.45 | 0.013 | D |
| 24362 | C10orf118 | -0.41 | 0.024 | D |
| 24377 | ITLN1 | -0.38 | 0.039 | D |
| 24470 | DCN | -0.57 | 0.001 | D |
| 24478 | OR2M7 | -0.42 | 0.020 | D |
| 24481 | ERI1 | -0.37 | 0.047 | D |
| 24483 | METTL11A | -0.40 | 0.029 | D |
| 24503 | BCAT1 | -0.41 | 0.024 | D |
| 238 | COPB2 | 0.44 | 0.016 | U |
| 318 | GLIS2 | 0.37 | 0.046 | U |
| 484 | FCRL3 | 0.36 | 0.048 | U |
| 508 | TRAM1 | 0.38 | 0.037 | U |
| 539 | GPR83 | 0.47 | 0.009 | U |
| 550 | S100A16 | 0.55 | 0.002 | U |
| 591 | MT1H | 0.37 | 0.045 | U |
| 983 | FAM134B | 0.37 | 0.043 | U |
| 984 | TMEM8A | 0.41 | 0.026 | U |
| 998 | RFNG | 0.36 | 0.050 | U |
| 1018 | TCL6 | 0.39 | 0.035 | U |
| 1030 | SGSM3 | 0.46 | 0.010 | U |
| 1114 | SHH | 0.46 | 0.010 | U |
| 1124 | EIF2C2 | 0.43 | 0.019 | U |
| 1270 | ZFYVE21 | 0.37 | 0.042 | U |
| 1384 | KRTAP17-1 | 0.39 | 0.035 | U |
| 1414 | MID2 | 0.39 | 0.035 | U |
| 1461 | CAPN13 | 0.38 | 0.038 | U |
| 1627 | RNF208 | 0.41 | 0.024 | U |
| 1641 | ESYT2 | 0.45 | 0.012 | U |
| 1668 | HYOU1 | 0.38 | 0.036 | U |
| 1749 | STEAP4 | 0.44 | 0.014 | U |
| 1756 | KDELR3 | 0.45 | 0.012 | U |
| 1850 | MOSPD3 | 0.39 | 0.033 | U |
| 1915 | C1orf65 | 0.36 | 0.050 | U |
| 1935 | IFNA1 | 0.51 | 0.004 | U |
| 2053 | MALL | 0.46 | 0.011 | U |
| 2066 | ATG4A | 0.36 | 0.049 | U |


| 2183 | RAP1A | 0.47 | 0.009 | U |
| :---: | :---: | :---: | :---: | :---: |
| 2233 | LST1 | 0.37 | 0.044 | U |
| 2385 | TMEM134 | 0.40 | 0.029 | U |
| 2388 | TMEM61 | 0.49 | 0.005 | U |
| 2547 | CA3 | 0.46 | 0.010 | U |
| 2590 | SYTL2 | 0.37 | 0.043 | U |
| 2689 | FOXA1 | 0.47 | 0.008 | U |
| 2691 | LYPD5 | 0.39 | 0.035 | U |
| 2716 | GMPPA | 0.36 | 0.049 | U |
| 2743 | TLR5 | 0.37 | 0.046 | U |
| 2794 | GAD1 | 0.42 | 0.020 | U |
| 2886 | CORO6 | 0.40 | 0.028 | U |
| 2936 | TTC6 | 0.43 | 0.019 | U |
| 2945 | PPARA | 0.37 | 0.047 | U |
| 2981 | PDIA2 | 0.39 | 0.033 | U |
| 2997 | HRCT1 | 0.41 | 0.024 | U |
| 3040 | FUT3 | 0.40 | 0.030 | U |
| 3087 | PVRL1 | 0.38 | 0.037 | U |
| 3120 | MCTP2 | 0.36 | 0.049 | U |
| 3249 | MLL3 | 0.38 | 0.041 | U |
| 3326 | C19orf10 | 0.44 | 0.014 | U |
| 3349 | ARHGEF35 | 0.42 | 0.020 | U |
| 3360 | LDLRAP1 | 0.36 | 0.049 | U |
| 3373 | MAP4K4 | 0.49 | 0.007 | U |
| 3375 | KIAA1147 | 0.38 | 0.039 | U |
| 3537 | COPE | 0.39 | 0.033 | U |
| 3695 | RORA | 0.37 | 0.042 | U |
| 3709 | PXMP4 | 0.45 | 0.013 | U |
| 3806 | SLC8A3 | 0.44 | 0.015 | U |
| 3820 | GPRC5C | 0.40 | 0.027 | U |
| 3835 | TMPRSS15 | 0.39 | 0.031 | U |
| 3887 | TXK | 0.46 | 0.010 | U |
| 3894 | NUDT16P1 | 0.37 | 0.047 | U |
| 3917 | IER3 | 0.47 | 0.009 | U |
| 3973 | NDRG1 | 0.53 | 0.003 | U |
| 3992 | SYN1 | 0.40 | 0.029 | U |
| 3994 | ICA1L | 0.48 | 0.008 | U |
| 4025 | AES | 0.46 | 0.011 | U |


| 4031 | SYNGR1 | 0.38 | 0.041 | U |
| :---: | :---: | :---: | :---: | :---: |
| 4074 | PARM1 | 0.39 | 0.033 | U |
| 4097 | BACE2 | 0.42 | 0.021 | U |
| 4166 | SPINT2 | 0.46 | 0.010 | U |
| 4222 | CYP7A1 | 0.37 | 0.044 | U |
| 4242 | PPFIA1 | 0.40 | 0.027 | U |
| 4317 | FAM83H | 0.42 | 0.021 | U |
| 4328 | LGMN | 0.39 | 0.031 | U |
| 4346 | ST3GAL1 | 0.43 | 0.019 | U |
| 4387 | RALY | 0.39 | 0.034 | U |
| 4528 | MYO1D | 0.51 | 0.004 | U |
| 4583 | CCNDBP1 | 0.39 | 0.032 | U |
| 4598 | RGR | 0.40 | 0.031 | U |
| 4694 | FGD4 | 0.37 | 0.045 | U |
| 4734 | NET1 | 0.44 | 0.015 | U |
| 4765 | LGALS9B | 0.38 | 0.038 | U |
| 4800 | HTRA4 | 0.38 | 0.040 | U |
| 4804 | ALG1L | 0.38 | 0.038 | U |
| 4805 | GAD1 | 0.51 | 0.004 | U |
| 4927 | HRCT1 | 0.38 | 0.039 | U |
| 4930 | ANK3 | 0.49 | 0.006 | U |
| 4937 | KIAA1217 | 0.45 | 0.012 | U |
| 5046 | PTPN3 | 0.39 | 0.035 | U |
| 5057 | LRRC45 | 0.42 | 0.019 | U |
| 5061 | RPS6KA2 | 0.39 | 0.033 | U |
| 5065 | KDELR2 | 0.38 | 0.039 | U |
| 5118 | WNT7B | 0.40 | 0.027 | U |
| 5146 | CBX7 | 0.39 | 0.035 | U |
| 5152 | MGST2 | 0.48 | 0.008 | U |
| 5327 | LOC401296 | 0.36 | 0.050 | U |
| 5400 | SLC35B2 | 0.41 | 0.026 | U |
| 5491 | SERPINB10 | 0.37 | 0.042 | U |
| 5500 | STAT6 | 0.37 | 0.047 | U |
| 5533 | LGALS3 | 0.44 | 0.015 | U |
| 5556 | CALML5 | 0.37 | 0.046 | U |
| 5568 | ASL | 0.54 | 0.002 | U |
| 5573 | RNF19A | 0.50 | 0.005 | U |
| 5606 | CLDN16 | 0.37 | 0.043 | U |


| 5613 | FAM53B | 0.42 | 0.020 | U |
| :---: | :---: | :---: | :---: | :---: |
| 5697 | ACHE | 0.39 | 0.033 | U |
| 5714 | C11orf63 | 0.53 | 0.003 | U |
| 5735 | TMEM63A | 0.36 | 0.048 | U |
| 5774 | CHPF2 | 0.49 | 0.007 | U |
| 5803 | LMF2 | 0.40 | 0.027 | U |
| 5994 | TMUB1 | 0.43 | 0.019 | U |
| 6005 | ADCK2 | 0.41 | 0.025 | U |
| 6055 | INSIG1 | 0.36 | 0.048 | U |
| 6079 | C2orf50 | 0.48 | 0.008 | U |
| 6142 | APH1A | 0.37 | 0.043 | U |
| 6145 | ARTN | 0.37 | 0.047 | U |
| 6179 | NPDC1 | 0.41 | 0.025 | U |
| 6235 | CNOT4 | 0.38 | 0.038 | U |
| 6266 | LRRC14B | 0.48 | 0.008 | U |
| 6271 | PCDHGC3 | 0.43 | 0.017 | U |
| 6304 | C16orf82 | 0.59 | 0.001 | U |
| 6307 | MKRN1 | 0.41 | 0.026 | U |
| 6324 | MYO5C | 0.51 | 0.004 | U |
| 6325 | RNF39 | 0.43 | 0.019 | U |
| 6418 | CALML4 | 0.39 | 0.031 | U |
| 6488 | CAMKK2 | 0.41 | 0.024 | U |
| 6543 | FAM189A2 | 0.47 | 0.009 | U |
| 6649 | ARID1A | 0.39 | 0.031 | U |
| 6818 | C20orf54 | 0.47 | 0.009 | U |
| 6828 | RFNG | 0.36 | 0.050 | U |
| 6862 | AFTPH | 0.49 | 0.006 | U |
| 6932 | CDK2AP2 | 0.53 | 0.003 | U |
| 6964 | VWA1 | 0.37 | 0.047 | U |
| 7074 | PALMD | 0.41 | 0.026 | U |
| 7128 | GPR32 | 0.39 | 0.032 | U |
| 7355 | BACE2 | 0.37 | 0.045 | U |
| 7375 | GRIK1 | 0.47 | 0.009 | U |
| 7379 | MS4A6A | 0.47 | 0.009 | U |
| 7416 | PTPN6 | 0.36 | 0.050 | U |
| 7490 | KCNK17 | 0.40 | 0.028 | U |
| 7494 | KCNC4 | 0.45 | 0.012 | U |
| 7718 | ZNF645 | 0.42 | 0.022 | U |


| 7828 | KCNK10 | 0.46 | 0.010 | U |
| :---: | :---: | :---: | :---: | :---: |
| 7834 | TRIM26 | 0.39 | 0.033 | U |
| 7896 | FAM133A | 0.36 | 0.050 | U |
| 7929 | RHEB | 0.37 | 0.043 | U |
| 7933 | XBP1 | 0.39 | 0.033 | U |
| 7963 | FASTK | 0.42 | 0.022 | U |
| 8038 | ZSCAN16 | 0.40 | 0.029 | U |
| 8053 | STAP2 | 0.46 | 0.011 | U |
| 8079 | AKT1 | 0.47 | 0.008 | U |
| 8127 | GPAA1 | 0.37 | 0.046 | U |
| 8177 | ADCK5 | 0.37 | 0.043 | U |
| 8220 | ADAM22 | 0.37 | 0.046 | U |
| 8495 | MB | 0.38 | 0.036 | U |
| 8513 | HRH3 | 0.39 | 0.034 | U |
| 8569 | WDR60 | 0.46 | 0.010 | U |
| 8587 | WDR45L | 0.36 | 0.049 | U |
| 8756 | SUN2 | 0.45 | 0.012 | U |
| 8779 | FAIM | 0.43 | 0.019 | U |
| 8792 | ARSJ | 0.38 | 0.036 | U |
| 8794 | BHLHE40 | 0.38 | 0.040 | U |
| 8805 | NOMO1 | 0.40 | 0.028 | U |
| 8992 | WDR24 | 0.40 | 0.030 | U |
| 9060 | CSMD2 | 0.43 | 0.019 | U |
| 9178 | MSRB2 | 0.37 | 0.042 | U |
| 9180 | KIAA2013 | 0.37 | 0.046 | U |
| 9197 | PKP3 | 0.36 | 0.048 | U |
| 9222 | OR5H2 | 0.52 | 0.003 | U |
| 9248 | ACTR3B | 0.40 | 0.027 | U |
| 9258 | SPHK1 | 0.50 | 0.005 | U |
| 9273 | ARCN1 | 0.49 | 0.007 | U |
| 9312 | GPM6B | 0.41 | 0.023 | U |
| 9435 | S100A6 | 0.49 | 0.006 | U |
| 9465 | ZNF141 | 0.41 | 0.025 | U |
| 9619 | SLC25A24 | 0.46 | 0.010 | U |
| 9645 | PRAMEF7 | 0.41 | 0.025 | U |
| 9661 | VEGFA | 0.36 | 0.048 | U |
| 9684 | BLVRA | 0.46 | 0.011 | U |
| 9827 | NET1 | 0.39 | 0.034 | U |


| 9849 | TMF1 | 0.43 | 0.019 | U |
| :---: | :---: | :---: | :---: | :---: |
| 9924 | ENPP4 | 0.38 | 0.041 | U |
| 9939 | CARD14 | 0.40 | 0.029 | U |
| 10188 | TRAK1 | 0.37 | 0.041 | U |
| 10291 | APOBEC3B | 0.43 | 0.018 | U |
| 10300 | SMAD1 | 0.38 | 0.038 | U |
| 10325 | MTSS1 | 0.50 | 0.005 | U |
| 10359 | MAL2 | 0.39 | 0.033 | U |
| 10487 | THNSL2 | 0.37 | 0.047 | U |
| 10498 | ZNF688 | 0.39 | 0.032 | U |
| 10667 | NCRNA00257 | 0.39 | 0.033 | U |
| 10703 | S100A14 | 0.45 | 0.012 | U |
| 10718 | C6orf89 | 0.47 | 0.008 | U |
| 10744 | ACTG1 | 0.40 | 0.029 | U |
| 10793 | KDELR3 | 0.44 | 0.014 | U |
| 10900 | STK39 | 0.37 | 0.047 | U |
| 11217 | PPP1R13B | 0.42 | 0.020 | U |
| 11225 | SLC37A3 | 0.39 | 0.032 | U |
| 11235 | LRRC45 | 0.40 | 0.028 | U |
| 11295 | PEX6 | 0.43 | 0.017 | U |
| 11296 | SPO11 | 0.39 | 0.034 | U |
| 11475 | TCF20 | 0.40 | 0.028 | U |
| 11542 | RTN2 | 0.42 | 0.021 | U |
| 11553 | TMPRSS13 | 0.41 | 0.024 | U |
| 11555 | SH3PXD2A | 0.43 | 0.019 | U |
| 11601 | OR4D5 | 0.38 | 0.038 | U |
| 11613 | TUBG2 | 0.39 | 0.031 | U |
| 11615 | C9orf153 | 0.41 | 0.023 | U |
| 11682 | AGPAT2 | 0.44 | 0.015 | U |
| 11700 | DGAT1 | 0.43 | 0.017 | U |
| 11736 | SLC26A5 | 0.48 | 0.007 | U |
| 11776 | GUSB | 0.37 | 0.045 | U |
| 11791 | OR2A9P | 0.39 | 0.035 | U |
| 11806 | PDZD2 | 0.42 | 0.021 | U |
| 11808 | SFN | 0.48 | 0.007 | U |
| 11955 | CORO1B | 0.65 | 0.000 | U |
| 12055 | FAM174B | 0.41 | 0.024 | U |
| 12090 | CDCA7L | 0.37 | 0.045 | U |


| 12138 | UNC13A | 0.55 | 0.002 | U |
| :---: | :---: | :---: | :---: | :---: |
| 12204 | B3GNT7 | 0.51 | 0.004 | U |
| 12212 | OR5H1 | 0.37 | 0.045 | U |
| 12232 | GAD1 | 0.37 | 0.044 | U |
| 12253 | GMPR | 0.42 | 0.022 | U |
| 12258 | OR6C2 | 0.41 | 0.026 | U |
| 12361 | AGPAT2 | 0.49 | 0.006 | U |
| 12428 | KLHDC9 | 0.45 | 0.012 | U |
| 12495 | MAPK3 | 0.38 | 0.037 | U |
| 12725 | MAGEA5 | 0.41 | 0.025 | U |
| 12727 | EDA | 0.37 | 0.047 | U |
| 12756 | TAPBP | 0.37 | 0.047 | U |
| 12917 | PPP2R2B | 0.47 | 0.009 | U |
| 12940 | XKRX | 0.39 | 0.031 | U |
| 12990 | ABCC9 | 0.41 | 0.026 | U |
| 13077 | DNAJC5 | 0.44 | 0.014 | U |
| 13215 | RREB1 | 0.38 | 0.038 | U |
| 13316 | SPDYA | 0.41 | 0.025 | U |
| 13324 | ATP2B3 | 0.38 | 0.039 | U |
| 13347 | TRIM41 | 0.44 | 0.016 | U |
| 13358 | ZNF654 | 0.37 | 0.047 | U |
| 13528 | ARHGEF5 | 0.39 | 0.032 | U |
| 13617 | RHOD | 0.45 | 0.014 | U |
| 13704 | REM1 | 0.37 | 0.047 | U |
| 13707 | RMND5B | 0.40 | 0.028 | U |
| 13874 | FMN2 | 0.37 | 0.041 | U |
| 13965 | MT1F | 0.44 | 0.016 | U |
| 14003 | NAV2 | 0.38 | 0.037 | U |
| 14014 | CD109 | 0.38 | 0.040 | U |
| 14095 | EXOC5 | 0.38 | 0.039 | U |
| 14105 | APOOL | 0.41 | 0.025 | U |
| 14109 | CHPF | 0.41 | 0.024 | U |
| 14193 | SRXN1 | 0.38 | 0.040 | U |
| 14211 | TPH2 | 0.43 | 0.018 | U |
| 14335 | CRYBA2 | 0.43 | 0.018 | U |
| 14367 | SEC24C | 0.42 | 0.020 | U |
| 14390 | CD99 | 0.47 | 0.010 | U |
| 14407 | TMC6 | 0.40 | 0.029 | U |


| 14416 | OR5AN1 | 0.45 | 0.013 | U |
| :---: | :---: | :---: | :---: | :---: |
| 14429 | PSG4 | 0.44 | 0.014 | U |
| 14546 | RAB27A | 0.42 | 0.021 | U |
| 14844 | LGMN | 0.36 | 0.048 | U |
| 14886 | MAPK1 | 0.37 | 0.046 | U |
| 14896 | LGR4 | 0.43 | 0.019 | U |
| 14913 | FCAR | 0.45 | 0.013 | U |
| 14984 | ALS2CL | 0.38 | 0.037 | U |
| 15068 | LMBR1 | 0.37 | 0.043 | U |
| 15208 | SNX31 | 0.45 | 0.012 | U |
| 15213 | MAX | 0.43 | 0.017 | U |
| 15246 | SGMS2 | 0.44 | 0.015 | U |
| 15315 | ZFP64 | 0.38 | 0.040 | U |
| 15357 | ACP6 | 0.41 | 0.024 | U |
| 15424 | SLC26A5 | 0.44 | 0.015 | U |
| 15461 | LSR | 0.47 | 0.009 | U |
| 15622 | CAMK1D | 0.47 | 0.009 | U |
| 15787 | CHI3L2 | 0.50 | 0.005 | U |
| 15791 | ITPKB | 0.50 | 0.005 | U |
| 15868 | GIPC1 | 0.40 | 0.031 | U |
| 16066 | CLSTN1 | 0.42 | 0.022 | U |
| 16091 | TRIOBP | 0.44 | 0.015 | U |
| 16102 | EHHADH | 0.47 | 0.010 | U |
| 16123 | GALNT12 | 0.45 | 0.013 | U |
| 16159 | BRP44L | 0.40 | 0.027 | U |
| 16209 | GRAMD3 | 0.42 | 0.022 | U |
| 16238 | RTN3 | 0.37 | 0.043 | U |
| 16244 | DKK2 | 0.38 | 0.040 | U |
| 16246 | C13orf39 | 0.37 | 0.044 | U |
| 16325 | UBE2H | 0.42 | 0.021 | U |
| 16326 | C11orf75 | 0.51 | 0.004 | U |
| 16365 | ERLEC1 | 0.39 | 0.035 | U |
| 16398 | MB | 0.36 | 0.050 | U |
| 16490 | OPLAH | 0.40 | 0.028 | U |
| 16512 | TMEM62 | 0.40 | 0.027 | U |
| 16527 | IL17RE | 0.36 | 0.049 | U |
| 16639 | AQP7 | 0.40 | 0.030 | U |
| 16851 | RREB1 | 0.45 | 0.012 | U |


| 17014 | PLEK2 | 0.41 | 0.023 | U |
| :---: | :---: | :---: | :---: | :---: |
| 17036 | ALAS2 | 0.36 | 0.049 | U |
| 17148 | MCEE | 0.37 | 0.042 | U |
| 17206 | STAP2 | 0.43 | 0.017 | U |
| 17211 | CORO1B | 0.69 | 0.000 | U |
| 17253 | NRTN | 0.37 | 0.042 | U |
| 17284 | LRP5 | 0.43 | 0.019 | U |
| 17292 | CRAMP1L | 0.46 | 0.010 | U |
| 17362 | AKAP8L | 0.47 | 0.008 | U |
| 17437 | MBIP | 0.36 | 0.049 | U |
| 17439 | RPS6KA2 | 0.45 | 0.012 | U |
| 17539 | OR6N2 | 0.37 | 0.045 | U |
| 17649 | PILRA | 0.39 | 0.035 | U |
| 17684 | PC | 0.39 | 0.035 | U |
| 17720 | PPP1R14C | 0.37 | 0.046 | U |
| 17728 | ATL1 | 0.38 | 0.041 | U |
| 17735 | BDH1 | 0.48 | 0.008 | U |
| 17836 | AKR1A1 | 0.44 | 0.015 | U |
| 17850 | ALG11 | 0.38 | 0.041 | U |
| 17853 | GH2 | 0.39 | 0.034 | U |
| 17892 | STARD10 | 0.41 | 0.026 | U |
| 17933 | CBR3 | 0.40 | 0.027 | U |
| 17974 | TRIOBP | 0.37 | 0.042 | U |
| 17975 | GADD45G | 0.36 | 0.048 | U |
| 18058 | LOC399744 | 0.42 | 0.020 | U |
| 18067 | KCNG2 | 0.37 | 0.046 | U |
| 18091 | CASP14 | 0.44 | 0.015 | U |
| 18154 | XBP1 | 0.46 | 0.011 | U |
| 18209 | C11orf80 | 0.36 | 0.048 | U |
| 18220 | SLC22A12 | 0.37 | 0.041 | U |
| 18231 | TMEM134 | 0.37 | 0.044 | U |
| 18372 | MPG | 0.37 | 0.043 | U |
| 18751 | KIAA0513 | 0.39 | 0.031 | U |
| 18775 | SLC25A41 | 0.44 | 0.016 | U |
| 18856 | FERMT1 | 0.39 | 0.036 | U |
| 18865 | PC | 0.41 | 0.025 | U |
| 18873 | TPCN2 | 0.36 | 0.048 | U |
| 18982 | PCDHA@ | 0.40 | 0.030 | U |


| 18990 | ANXA11 | 0.42 | 0.021 | U |
| :---: | :---: | :---: | :---: | :---: |
| 19012 | VAMP8 | 0.43 | 0.017 | U |
| 19057 | SUMO1 | 0.36 | 0.047 | U |
| 19065 |  | 0.42 | 0.020 | U |
| 19081 | STAP2 | 0.40 | 0.029 | U |
| 19110 | AK5 | 0.42 | 0.020 | U |
| 19134 | MASP1 | 0.39 | 0.032 | U |
| 19189 | SUSD4 | 0.38 | 0.038 | U |
| 19257 | TAS2R46 | 0.40 | 0.030 | U |
| 19389 | SAMD10 | 0.39 | 0.034 | U |
| 19395 | RBBP8 | 0.41 | 0.023 | U |
| 19604 | TMEM198 | 0.37 | 0.044 | U |
| 19606 | NET1 | 0.47 | 0.009 | U |
| 19765 | ITPR3 | 0.37 | 0.044 | U |
| 19771 | AES | 0.48 | 0.007 | U |
| 19898 | AKT1 | 0.45 | 0.014 | U |
| 19960 | STX10 | 0.43 | 0.017 | U |
| 20007 | MGAT4A | 0.47 | 0.009 | U |
| 20087 | GGA1 | 0.40 | 0.028 | U |
| 20088 | NCRNA00086 | 0.57 | 0.001 | U |
| 20150 | CD1B | 0.40 | 0.030 | U |
| 20162 | TRAK1 | 0.48 | 0.007 | U |
| 20193 | LGALS8 | 0.45 | 0.013 | U |
| 20270 | LONRF2 | 0.38 | 0.037 | U |
| 20328 | UGT2B17 | 0.39 | 0.033 | U |
| 20429 | GPC4 | 0.40 | 0.030 | U |
| 20450 | PCDHA@ | 0.37 | 0.044 | U |
| 20475 | PTK6 | 0.53 | 0.003 | U |
| 20510 | PAX9 | 0.46 | 0.010 | U |
| 20514 | FAM110C | 0.40 | 0.030 | U |
| 20553 | TSC22D3 | 0.38 | 0.040 | U |
| 20568 | CCDC120 | 0.42 | 0.022 | U |
| 20569 | TSC22D3 | 0.41 | 0.025 | U |
| 20577 | ARHGAP26 | 0.36 | 0.048 | U |
| 20606 | DRD1 | 0.37 | 0.041 | U |
| 20618 | RSBN1 | 0.41 | 0.026 | U |
| 20705 | TBC1D8B | 0.38 | 0.036 | U |
| 20803 | EPDR1 | 0.40 | 0.026 | U |


| 20877 | NTN3 | 0.39 | 0.033 | U |
| :---: | :---: | :---: | :---: | :---: |
| 20945 | OCIAD2 | 0.39 | 0.034 | U |
| 21035 | APOL5 | 0.40 | 0.030 | U |
| 21043 | DAB2IP | 0.37 | 0.046 | U |
| 21108 | ARHGAP1 | 0.37 | 0.042 | U |
| 21165 | MGMT | 0.39 | 0.032 | U |
| 21181 | ATP9A | 0.48 | 0.008 | U |
| 21199 | COPG | 0.39 | 0.033 | U |
| 21336 | SLC24A2 | 0.40 | 0.030 | U |
| 21526 | CRELD2 | 0.39 | 0.031 | U |
| 21630 | CUL9 | 0.43 | 0.017 | U |
| 21695 | CD6 | 0.40 | 0.029 | U |
| 21984 | DCXR | 0.38 | 0.039 | U |
| 22005 | DYX1C1 | 0.37 | 0.046 | U |
| 22008 | CSPG4P1Y | 0.47 | 0.009 | U |
| 22113 | RNF135 | 0.54 | 0.002 | U |
| 22290 | EVPL | 0.42 | 0.020 | U |
| 22310 | FBXL16 | 0.55 | 0.002 | U |
| 22362 | SLC16A5 | 0.36 | 0.050 | U |
| 22398 | FAM46C | 0.47 | 0.008 | U |
| 22430 | FLJ43763 | 0.37 | 0.044 | U |
| 22646 | STXBP2 | 0.37 | 0.046 | U |
| 22872 | SLMO2 | 0.44 | 0.015 | U |
| 22902 | DNAJC3 | 0.39 | 0.035 | U |
| 23008 | DHRS3 | 0.43 | 0.017 | U |
| 23034 | ZNF829 | 0.38 | 0.038 | U |
| 23077 | ARL6IP6 | 0.39 | 0.034 | U |
| 23082 | LILRB5 | 0.43 | 0.017 | U |
| 23112 | LYST | 0.39 | 0.034 | U |
| 23206 | MST1R | 0.47 | 0.008 | U |
| 23264 | WDR91 | 0.38 | 0.037 | U |
| 23309 | SLC45A4 | 0.39 | 0.033 | U |
| 23312 | RNF19A | 0.39 | 0.035 | U |
| 23339 | C1orf146 | 0.48 | 0.007 | U |
| 23341 | AGFG2 | 0.40 | 0.029 | U |
| 23371 | KLHDC9 | 0.47 | 0.009 | U |
| 23438 | GJB3 | 0.39 | 0.031 | U |
| 23448 | ARID5A | 0.38 | 0.037 | U |


| 23610 | CHST15 | 0.48 | 0.008 | U |
| :---: | :---: | :---: | :---: | :---: |
| 23810 | SERINC3 | 0.36 | 0.049 | U |
| 23943 | HIST1H4D | 0.40 | 0.028 | U |
| 23948 | UPP1 | 0.41 | 0.024 | U |
| 23956 | GSTT1 | 0.36 | 0.050 | U |
| 24028 | GPR160 | 0.40 | 0.030 | U |
| 24040 | GPR172B | 0.41 | 0.025 | U |
| 24063 | GPRC5C | 0.49 | 0.006 | U |
| 24171 | HDAC11 | 0.38 | 0.036 | U |
| 24175 | TAPBP | 0.40 | 0.027 | U |
| 24198 | GCAT | 0.42 | 0.020 | U |
| 24252 | OSM | 0.40 | 0.027 | U |
| 24345 | UPP1 | 0.41 | 0.025 | U |
| 24445 | EDARADD | 0.41 | 0.026 | U |
| 24458 |  | 0.52 | 0.003 | U |
| 24466 | GNA11 | 0.38 | 0.039 | U |

## APPENDIX B. 1030 GENES CORRELATING WITH SYNERGISM TO

## PACLITAXEL + CARBOPLATIN

| Gene ID | Symbol | Synergy Correlation | Correlation $P$ value | Up or down regulated |
| :---: | :---: | :---: | :---: | :---: |
| 980 | CCDC144NL | -0.52 | 0.006 | D |
| 1585 | POSTN | -0.56 | 0.003 | D |
| 3300 | FPR1 | -0.42 | 0.031 | D |
| 20341 | IL17RC | -0.46 | 0.019 | D |
| 23246 | CSTF1 | -0.45 | 0.021 | D |
| 2053 | MALL | -0.41 | 0.038 | D |
| 6324 | MYO5C | -0.45 | 0.022 | D |
| 9197 | PKP3 | -0.41 | 0.036 | D |
| 11808 | SFN | -0.48 | 0.013 | D |
| 12725 | MAGEA5 | -0.51 | 0.008 | D |
| 14003 | NAV2 | -0.44 | 0.025 | D |
| 19765 | ITPR3 | -0.47 | 0.017 | D |
| 20475 | PTK6 | -0.39 | 0.049 | D |
| 22005 | DYX1C1 | -0.45 | 0.022 | D |
| 23610 | CHST15 | -0.50 | 0.010 | D |
| 24466 | GNA11 | -0.40 | 0.041 | D |
| 83 | ZNF365 | -0.40 | 0.042 | D |
| 147 | TRADD | -0.41 | 0.040 | D |
| 164 | C2orf53 | -0.43 | 0.027 | D |
| 253 | SULT1A1 | -0.42 | 0.032 | D |
| 293 | NRN1L | -0.41 | 0.040 | D |
| 368 | GLA | -0.40 | 0.042 | D |
| 414 | C6orf201 | -0.46 | 0.017 | D |
| 433 | SYNPO2 | -0.49 | 0.012 | D |
| 449 | NOL3 | -0.48 | 0.014 | D |
| 463 | VCL | -0.45 | 0.023 | D |
| 479 | GAS6 | -0.41 | 0.036 | D |
| 507 | PACRG | -0.39 | 0.048 | D |
| 511 | GABRB2 | -0.40 | 0.043 | D |
| 566 | PTER | -0.59 | 0.001 | D |
| 573 | SLC16A3 | -0.46 | 0.019 | D |
| 594 | ASB9 | -0.44 | 0.026 | D |


| 599 | GALNTL4 | -0.44 | 0.026 | D |
| :---: | :---: | :---: | :---: | :---: |
| 602 | LCK | -0.50 | 0.010 | D |
| 640 | GPR107 | -0.41 | 0.039 | D |
| 641 | CTTN | -0.41 | 0.038 | D |
| 721 | HS6ST1 | -0.46 | 0.017 | D |
| 725 | LCA10 | -0.39 | 0.046 | D |
| 803 | AK4 | -0.44 | 0.025 | D |
| 806 | PKM2 | -0.42 | 0.034 | D |
| 818 | C13orf15 | -0.43 | 0.027 | D |
| 988 | SLC7A5 | -0.48 | 0.012 | D |
| 1014 | SULT1A3 | -0.41 | 0.035 | D |
| 1048 | ABCC3 | -0.50 | 0.010 | D |
| 1095 | STARD13 | -0.41 | 0.040 | D |
| 1138 | SLC6A15 | -0.39 | 0.046 | D |
| 1167 | C9orf84 | -0.43 | 0.027 | D |
| 1307 | NLN | -0.39 | 0.046 | D |
| 1339 | KRT81 | -0.40 | 0.044 | D |
| 1342 | G6PD | -0.57 | 0.003 | D |
| 1367 | WDR53 | -0.43 | 0.027 | D |
| 1370 | CELA3A | -0.41 | 0.037 | D |
| 1464 | TSPAN7 | -0.42 | 0.034 | D |
| 1475 |  | -0.42 | 0.033 | D |
| 1492 | KLK3 | -0.42 | 0.031 | D |
| 1507 | C22orf40 | -0.39 | 0.050 | D |
| 1574 | SCRT1 | -0.40 | 0.045 | D |
| 1606 | CDC6 | -0.40 | 0.045 | D |
| 1687 | IKBKG | -0.43 | 0.029 | D |
| 1729 | WISP3 | -0.40 | 0.043 | D |
| 1838 | INO80E | -0.41 | 0.040 | D |
| 1870 | NOXO1 | -0.42 | 0.033 | D |
| 1959 | COBL | -0.50 | 0.010 | D |
| 2116 |  | -0.44 | 0.023 | D |
| 2161 | ZNF773 | -0.42 | 0.031 | D |
| 2282 | FAM125B | -0.40 | 0.043 | D |
| 2345 | GPA33 | -0.43 | 0.028 | D |
| 2351 | RUSC1 | -0.40 | 0.042 | D |
| 2391 | HPD | -0.39 | 0.047 | D |
| 2401 | LAMB3 | -0.41 | 0.040 | D |


| 2432 | TXNRD1 | -0.40 | 0.041 | D |
| :---: | :---: | :---: | :---: | :---: |
| 2440 | MSN | -0.40 | 0.044 | D |
| 2462 | PCID2 | -0.39 | 0.050 | D |
| 2572 | TENC1 | -0.39 | 0.047 | D |
| 2591 | LAMP2 | -0.39 | 0.049 | D |
| 2643 | NQO1 | -0.41 | 0.040 | D |
| 2645 | SLC11A1 | -0.44 | 0.024 | D |
| 2653 | CKS2 | -0.47 | 0.015 | D |
| 2669 | XIRP1 | -0.45 | 0.021 | D |
| 2677 | SUPT16H | -0.46 | 0.017 | D |
| 2711 | TSKU | -0.40 | 0.041 | D |
| 2722 | OR56A4 | -0.47 | 0.016 | D |
| 2747 | PRKAR1B | -0.47 | 0.016 | D |
| 2753 | GPR126 | -0.52 | 0.006 | D |
| 2769 | CNGA2 | -0.44 | 0.025 | D |
| 2855 | TRIM47 | -0.40 | 0.042 | D |
| 2880 | PRICKLE3 | -0.40 | 0.041 | D |
| 2897 | LMX1A | -0.43 | 0.028 | D |
| 3045 | RABGGTA | -0.39 | 0.049 | D |
| 3234 | C9orf140 | -0.55 | 0.004 | D |
| 3308 | CCL2 | -0.44 | 0.023 | D |
| 3445 | PLAC1 | -0.47 | 0.015 | D |
| 3541 | EFHD2 | -0.48 | 0.013 | D |
| 3600 | BCAN | -0.54 | 0.005 | D |
| 3754 | CSNK1D | -0.41 | 0.039 | D |
| 3966 | ACER3 | -0.41 | 0.036 | D |
| 3967 | TSPO | -0.41 | 0.039 | D |
| 3982 | SLC5A2 | -0.43 | 0.029 | D |
| 4013 | ALAS2 | -0.40 | 0.044 | D |
| 4112 | RAB20 | -0.46 | 0.018 | D |
| 4199 | RAB11FIP5 | -0.40 | 0.043 | D |
| 4295 | DSCAM | -0.42 | 0.033 | D |
| 4304 | MYLK | -0.43 | 0.030 | D |
| 4333 | POLE3 | -0.56 | 0.003 | D |
| 4351 | FHOD3 | -0.57 | 0.002 | D |
| 4354 | FADD | -0.41 | 0.037 | D |
| 4370 | STEAP3 | -0.41 | 0.038 | D |
| 4404 | DHRS4 | -0.42 | 0.033 | D |


| 4477 | OR14J1 | -0.46 | 0.017 | D |
| :---: | :---: | :---: | :---: | :---: |
| 4529 | IGSF11 | -0.42 | 0.033 | D |
| 4542 | AP2B1 | -0.45 | 0.022 | D |
| 4679 | PCDHGC3 | -0.52 | 0.007 | D |
| 4700 | MICAL2 | -0.44 | 0.024 | D |
| 4773 | SEPX1 | -0.43 | 0.027 | D |
| 4897 | SLC2A9 | -0.39 | 0.048 | D |
| 4944 | ZDHHC9 | -0.45 | 0.020 | D |
| 5021 | SEL1L3 | -0.44 | 0.024 | D |
| 5098 | MYH6 | -0.50 | 0.009 | D |
| 5128 | HSD3B7 | -0.45 | 0.020 | D |
| 5213 | MYH9 | -0.51 | 0.008 | D |
| 5326 | PRAMEF17 | -0.42 | 0.032 | D |
| 5394 |  | -0.46 | 0.018 | D |
| 5457 | CRTAC1 | -0.39 | 0.047 | D |
| 5466 | CORO2B | -0.45 | 0.020 | D |
| 5490 | FBXW2 | -0.49 | 0.010 | D |
| 5524 | DIRC1 | -0.55 | 0.004 | D |
| 5579 | GABPB1 | -0.44 | 0.026 | D |
| 5608 | OR2D3 | -0.54 | 0.005 | D |
| 5614 | CFI | -0.44 | 0.025 | D |
| 5629 | UBE3C | -0.40 | 0.044 | D |
| 5658 | HMCN2 | -0.53 | 0.005 | D |
| 5715 | LAMB4 | -0.40 | 0.043 | D |
| 5717 | SPRR2B | -0.41 | 0.037 | D |
| 5767 | SNRPN | -0.48 | 0.013 | D |
| 5857 | EPB41L4B | -0.43 | 0.030 | D |
| 5861 | LOC400940 | -0.45 | 0.023 | D |
| 5869 | ZDHHC16 | -0.45 | 0.023 | D |
| 5903 | SIGLEC7 | -0.45 | 0.020 | D |
| 5922 | LIMCH1 | -0.43 | 0.029 | D |
| 5934 | CD99L2 | -0.40 | 0.043 | D |
| 5990 | SLC6A8 | -0.52 | 0.007 | D |
| 6060 | MAPK9 | -0.49 | 0.011 | D |
| 6092 | PCDHA@ | -0.40 | 0.045 | D |
| 6112 | SLC25A43 | -0.57 | 0.003 | D |
| 6150 | RPL39 | -0.40 | 0.040 | D |
| 6220 | CD151 | -0.49 | 0.010 | D |
|  |  |  |  |  |


| 6223 | FBXO32 | -0.41 | 0.036 | D |
| :---: | :---: | :---: | :---: | :---: |
| 6255 | PARVA | -0.49 | 0.011 | D |
| 6283 | NCAPG2 | -0.41 | 0.038 | D |
| 6316 | C9orf95 | -0.46 | 0.019 | D |
| 6361 | ADAM15 | -0.45 | 0.020 | D |
| 6434 | ASTN1 | -0.49 | 0.011 | D |
| 6464 | IL25 | -0.41 | 0.035 | D |
| 6517 | OSBPL7 | -0.51 | 0.008 | D |
| 6540 | TMEM156 | -0.41 | 0.036 | D |
| 6542 | PITX1 | -0.42 | 0.032 | D |
| 6562 | AR | -0.53 | 0.006 | D |
| 6662 | MORN1 | -0.52 | 0.006 | D |
| 6673 | KCND3 | -0.42 | 0.031 | D |
| 6816 | EMX2 | -0.44 | 0.026 | D |
| 6855 | TENC1 | -0.66 | 0.000 | D |
| 6894 | NEDD9 | -0.39 | 0.049 | D |
| 6926 |  | -0.41 | 0.037 | D |
| 6930 | TNFAIP2 | -0.41 | 0.036 | D |
| 6943 | MYO1C | -0.49 | 0.011 | D |
| 7020 | FBXL13 | -0.41 | 0.035 | D |
| 7085 | CYB5A | -0.45 | 0.023 | D |
| 7104 | TMOD3 | -0.49 | 0.012 | D |
| 7194 | PRSS23 | -0.51 | 0.007 | D |
| 7227 | KLF10 | -0.40 | 0.040 | D |
| 7286 | C15orf52 | -0.42 | 0.034 | D |
| 7312 | TELO2 | -0.42 | 0.031 | D |
| 7576 | C6orf10 | -0.46 | 0.018 | D |
| 7579 | MAP4 | -0.49 | 0.011 | D |
| 7619 | ENPEP | -0.49 | 0.012 | D |
| 7776 | C1orf49 | -0.42 | 0.033 | D |
| 7893 | PDK1 | -0.43 | 0.028 | D |
| 7931 | PARP4 | -0.40 | 0.046 | D |
| 7989 | KRT1 | -0.45 | 0.022 | D |
| 8114 | OR9G4 | -0.54 | 0.004 | D |
| 8128 | SNRPN | -0.49 | 0.011 | D |
| 8417 | TNXB | -0.43 | 0.029 | D |
| 8446 | CPN2 | -0.41 | 0.035 | D |
| 8515 | DPF3 | -0.40 | 0.044 | D |


| 8548 | INVS | -0.40 | 0.040 | D |
| :---: | :---: | :---: | :---: | :---: |
| 8641 | TUBGCP2 | -0.49 | 0.010 | D |
| 8657 | CASP10 | -0.56 | 0.003 | D |
| 8672 | CAV2 | -0.41 | 0.035 | D |
| 8690 | NOVA1 | -0.43 | 0.030 | D |
| 8757 | KRTAP27-1 | -0.45 | 0.021 | D |
| 8771 | NPRL3 | -0.45 | 0.022 | D |
| 8796 | TAF1L | -0.40 | 0.042 | D |
| 8866 | LRP12 | -0.42 | 0.032 | D |
| 8911 | CES1 | -0.42 | 0.032 | D |
| 8928 | TFAP4 | -0.42 | 0.031 | D |
| 8979 | MAP6D1 | -0.39 | 0.046 | D |
| 9165 | MAP1B | -0.46 | 0.019 | D |
| 9443 | ABCB6 | -0.42 | 0.033 | D |
| 9458 | CCDC157 | -0.49 | 0.011 | D |
| 9472 | GRB10 | -0.41 | 0.036 | D |
| 9494 | FLJ41170 | -0.43 | 0.029 | D |
| 9509 | PLCB4 | -0.40 | 0.045 | D |
| 9519 | SCUBE1 | -0.42 | 0.034 | D |
| 9558 | TBC1D9B | -0.44 | 0.025 | D |
| 9570 | UBA1 | -0.43 | 0.026 | D |
| 9587 | VCL | -0.45 | 0.022 | D |
| 9717 | HPS6 | -0.39 | 0.048 | D |
| 9762 | CHRFAM7A | -0.41 | 0.037 | D |
| 9774 | KCNK4 | -0.46 | 0.018 | D |
| 9780 | S100A2 | -0.52 | 0.006 | D |
| 9832 | SLC9A3R2 | -0.41 | 0.036 | D |
| 9892 | MRPL43 | -0.52 | 0.007 | D |
| 9947 | INF2 | -0.45 | 0.021 | D |
| 9948 | HILS1 | -0.51 | 0.008 | D |
| 9957 | RNASEH2C | -0.58 | 0.002 | D |
| 9985 | TBC1D24 | -0.42 | 0.032 | D |
| 10039 | CFHR2 | -0.51 | 0.008 | D |
| 10088 | ARMCX5 | -0.41 | 0.035 | D |
| 10130 | ADK | -0.41 | 0.035 | D |
| 10175 | GCNT2 | -0.40 | 0.044 | D |
| 10268 | EMD | -0.56 | 0.003 | D |
| 10349 | TIAL1 | -0.39 | 0.046 | D |


| 10393 | FAM129B | -0.41 | 0.036 | D |
| :---: | :---: | :---: | :---: | :---: |
| 10486 | NOL6 | -0.45 | 0.023 | D |
| 10516 | DDIT4 | -0.42 | 0.034 | D |
| 10551 | LRSAM1 | -0.40 | 0.043 | D |
| 10611 |  | -0.42 | 0.033 | D |
| 10613 | PILRB | -0.52 | 0.006 | D |
| 10677 | PPP1R2P9 | -0.52 | 0.006 | D |
| 10790 | TNKS1BP1 | -0.39 | 0.047 | D |
| 10850 | COL8A1 | -0.41 | 0.038 | D |
| 10923 | SGPL1 | -0.44 | 0.025 | D |
| 10925 | MPP6 | -0.39 | 0.050 | D |
| 10942 | ERCC6L | -0.51 | 0.008 | D |
| 10974 | SMU1 | -0.61 | 0.001 | D |
| 11033 | ME1 | -0.61 | 0.001 | D |
| 11176 | RNPS1 | -0.41 | 0.037 | D |
| 11271 | GIMAP7 | -0.50 | 0.009 | D |
| 11353 | ADAM15 | -0.47 | 0.015 | D |
| 11468 | PARD3B | -0.53 | 0.005 | D |
| 11486 | MYEOV2 | -0.49 | 0.011 | D |
| 11491 | CNDP1 | -0.52 | 0.006 | D |
| 11495 | TRIM54 | -0.50 | 0.009 | D |
| 11676 | CDH22 | -0.43 | 0.028 | D |
| 11723 | IDS | -0.40 | 0.042 | D |
| 11779 | FAM151A | -0.42 | 0.035 | D |
| 11801 | AR | -0.41 | 0.038 | D |
| 11878 | AIMP1 | -0.58 | 0.002 | D |
| 11899 | PALLD | -0.57 | 0.002 | D |
| 11981 | COL8A1 | -0.40 | 0.045 | D |
| 12011 | KRT7 | -0.42 | 0.034 | D |
| 12025 | ME3 | -0.43 | 0.028 | D |
| 12128 | LASS1 | -0.55 | 0.004 | D |
| 12149 | IL7R | -0.41 | 0.038 | D |
| 12190 | KRT6A | -0.48 | 0.012 | D |
| 12201 | TMEM119 | -0.40 | 0.045 | D |
| 12221 | PRDM1 | -0.54 | 0.005 | D |
| 12254 |  | -0.45 | 0.021 | D |
| 12271 | GCLC | -0.46 | 0.019 | D |
| 12313 | FAM46D | -0.58 | 0.002 | D |


| 12359 | SLC25A33 | -0.46 | 0.018 | D |
| :---: | :---: | :---: | :---: | :---: |
| 12379 | C9orf25 | -0.45 | 0.022 | D |
| 12487 | SLC7A3 | -0.53 | 0.005 | D |
| 12561 | CNTN1 | -0.40 | 0.041 | D |
| 12583 | C9orf78 | -0.43 | 0.030 | D |
| 12585 | TRIM6 | -0.41 | 0.037 | D |
| 12591 | LAMP2 | -0.52 | 0.006 | D |
| 12709 | CHST3 | -0.49 | 0.010 | D |
| 12757 | SLAMF9 | -0.48 | 0.014 | D |
| 13044 | HSD17B6 | -0.41 | 0.039 | D |
| 13063 | IRAK1 | -0.46 | 0.017 | D |
| 13095 | TUBB3 | -0.43 | 0.029 | D |
| 13129 | CNTN4 | -0.42 | 0.033 | D |
| 13141 | IP6K3 | -0.46 | 0.017 | D |
| 13154 | ELFN2 | -0.41 | 0.039 | D |
| 13177 | RAB44 | -0.49 | 0.011 | D |
| 13220 | BTNL8 | -0.50 | 0.009 | D |
| 13225 | TRAF3IP2 | -0.47 | 0.015 | D |
| 13317 | PSMD10 | -0.40 | 0.042 | D |
| 13322 | RGS12 | -0.45 | 0.022 | D |
| 13372 | FAM129B | -0.42 | 0.034 | D |
| 13379 | PLSCR4 | -0.48 | 0.013 | D |
| 13438 | TMEM100 | -0.39 | 0.049 | D |
| 13448 | PATZ1 | -0.39 | 0.046 | D |
| 13461 | MAZ | -0.45 | 0.021 | D |
| 13541 | LRRFIP2 | -0.40 | 0.045 | D |
| 13717 | DEFB118 | -0.40 | 0.043 | D |
| 13738 | G6PD | -0.48 | 0.012 | D |
| 13741 | DRGX | -0.44 | 0.023 | D |
| 13742 | FLJ39061 | -0.42 | 0.032 | D |
| 13752 | FAM113B | -0.41 | 0.036 | D |
| 13915 | CTSZ | -0.40 | 0.041 | D |
| 13980 | NOXO1 | -0.48 | 0.013 | D |
| 14012 | BRCC3 | -0.47 | 0.015 | D |
| 14040 | SPINLW1 | -0.39 | 0.046 | D |
| 14146 | CYP4B1 | -0.43 | 0.030 | D |
| 14315 | RCOR1 | -0.46 | 0.019 | D |
| 14330 | RAPH1 | -0.47 | 0.015 | D |


| 14358 | GAS6 | -0.39 | 0.047 | D |
| :---: | :---: | :---: | :---: | :---: |
| 14363 | KRT86 | -0.43 | 0.029 | D |
| 14447 | TXN | -0.42 | 0.034 | D |
| 14535 | GEMIN7 | -0.48 | 0.012 | D |
| 14582 | ASB9 | -0.47 | 0.016 | D |
| 14595 | FGFRL1 | -0.43 | 0.027 | D |
| 14602 | THADA | -0.39 | 0.047 | D |
| 14636 | CCNY | -0.46 | 0.019 | D |
| 14644 | MBL2 | -0.42 | 0.031 | D |
| 14757 | LIMS3 | -0.43 | 0.027 | D |
| 14857 | RNF216 | -0.49 | 0.010 | D |
| 14869 | CDH24 | -0.59 | 0.002 | D |
| 14978 | OPN1LW | -0.46 | 0.019 | D |
| 15006 | TPSG1 | -0.40 | 0.045 | D |
| 15034 | IFNA21 | -0.46 | 0.019 | D |
| 15041 | MCCD1 | -0.43 | 0.030 | D |
| 15072 | C8orf34 | -0.46 | 0.018 | D |
| 15161 | MOCOS | -0.44 | 0.026 | D |
| 15346 | HTATIP2 | -0.39 | 0.047 | D |
| 15440 | PILRB | -0.39 | 0.048 | D |
| 15455 | CHRNB3 | -0.46 | 0.017 | D |
| 15615 | LRP8 | -0.42 | 0.032 | D |
| 15627 | PRPS1 | -0.44 | 0.023 | D |
| 15662 | IMPDH1 | -0.52 | 0.007 | D |
| 15752 | ZNF484 | -0.44 | 0.025 | D |
| 15762 | RGP1 | -0.40 | 0.042 | D |
| 15865 | WDR5 | -0.50 | 0.009 | D |
| 15901 | EYA1 | -0.40 | 0.041 | D |
| 15989 | RAPH1 | -0.43 | 0.030 | D |
| 16032 | C10orf93 | -0.46 | 0.017 | D |
| 16061 | CDH7 | -0.46 | 0.017 | D |
| 16075 | C1orf124 | -0.42 | 0.031 | D |
| 16222 | PRR4 | -0.43 | 0.027 | D |
| 16224 | C1orf61 | -0.44 | 0.026 | D |
| 16226 | SH3BP4 | -0.41 | 0.037 | D |
| 16247 | KIAA1715 | -0.41 | 0.039 | D |
| 16250 | HAPLN3 | -0.60 | 0.001 | D |
| 16354 | FLYWCH2 | -0.45 | 0.020 | D |


| 16390 | INF2 | -0.48 | 0.013 | D |
| :---: | :---: | :---: | :---: | :---: |
| 16391 | TCEAL4 | -0.41 | 0.037 | D |
| 16445 | ERCC6L | -0.41 | 0.040 | D |
| 16468 | OR2K2 | -0.39 | 0.049 | D |
| 16536 | PRSS3 | -0.45 | 0.020 | D |
| 16565 | FARSB | -0.39 | 0.048 | D |
| 16593 | ACTL6A | -0.39 | 0.048 | D |
| 16633 | C9orf89 | -0.44 | 0.024 | D |
| 16674 | ANKZF1 | -0.44 | 0.023 | D |
| 16709 | MECP2 | -0.46 | 0.018 | D |
| 16718 | PHLDB1 | -0.46 | 0.019 | D |
| 16732 | NAAA | -0.45 | 0.021 | D |
| 16764 | GABRE | -0.44 | 0.024 | D |
| 16897 | FLNB | -0.40 | 0.044 | D |
| 16905 | TMEM187 | -0.40 | 0.040 | D |
| 16910 | RNF41 | -0.45 | 0.020 | D |
| 16989 | TSC22D1 | -0.49 | 0.010 | D |
| 17018 | DIAPH2 | -0.43 | 0.027 | D |
| 17043 | PPP1R8 | -0.42 | 0.034 | D |
| 17064 | ALPK2 | -0.39 | 0.047 | D |
| 17098 | PDE5A | -0.41 | 0.040 | D |
| 17110 | COL18A1 | -0.45 | 0.022 | D |
| 17210 | DEFB112 | -0.43 | 0.030 | D |
| 17261 | MPP1 | -0.41 | 0.039 | D |
| 17267 | AKR1B10 | -0.42 | 0.035 | D |
| 17410 | DUX4 | -0.53 | 0.006 | D |
| 17427 | NQO1 | -0.43 | 0.027 | D |
| 17615 | CD99L2 | -0.40 | 0.043 | D |
| 17664 | GPX3 | -0.42 | 0.033 | D |
| 17820 | AGTR2 | -0.46 | 0.019 | D |
| 17870 | MFGE8 | -0.42 | 0.034 | D |
| 18006 | SH3RF2 | -0.44 | 0.024 | D |
| 18072 | PRKACB | -0.55 | 0.004 | D |
| 18157 | MAP1B | -0.42 | 0.032 | D |
| 18431 | HSD11B1 | -0.41 | 0.038 | D |
| 18463 | CYB5A | -0.45 | 0.020 | D |
| 18466 | HNRNPAB | -0.39 | 0.049 | D |
| 18530 | C5orf44 | -0.39 | 0.047 | D |


| 18538 | TYRO3 | -0.45 | 0.022 | D |
| :---: | :---: | :---: | :---: | :---: |
| 18578 | C1orf35 | -0.47 | 0.016 | D |
| 18673 | GLDN | -0.41 | 0.037 | D |
| 18678 | C17orf54 | -0.40 | 0.041 | D |
| 18680 | MARCH10 | -0.49 | 0.010 | D |
| 18837 | RBM18 | -0.46 | 0.019 | D |
| 18864 | C20orf71 | -0.39 | 0.048 | D |
| 18911 | RGR | -0.41 | 0.037 | D |
| 18917 | SLC11A1 | -0.39 | 0.049 | D |
| 18981 | MAML1 | -0.53 | 0.005 | D |
| 19085 | SYCP3 | -0.58 | 0.002 | D |
| 19138 | BCL9L | -0.44 | 0.025 | D |
| 19171 | GRB10 | -0.47 | 0.017 | D |
| 19359 | TRIM6 | -0.43 | 0.028 | D |
| 19409 | CMTM4 | -0.42 | 0.031 | D |
| 19429 | C3orf70 | -0.43 | 0.030 | D |
| 19431 | RPS6KA4 | -0.51 | 0.008 | D |
| 19475 | GCGR | -0.43 | 0.028 | D |
| 19520 | PRPF4 | -0.54 | 0.004 | D |
| 19584 | TRERF1 | -0.41 | 0.036 | D |
| 19682 |  | -0.39 | 0.049 | D |
| 19740 | KCNAB1 | -0.40 | 0.045 | D |
| 19750 | STBD1 | -0.49 | 0.012 | D |
| 19781 | CDC42EP2 | -0.42 | 0.033 | D |
| 19783 | DYNLT3 | -0.46 | 0.017 | D |
| 19841 | POLR2L | -0.40 | 0.045 | D |
| 19846 | IGSF1 | -0.43 | 0.029 | D |
| 19924 | OR6C74 | -0.41 | 0.038 | D |
| 19929 | ITIH3 | -0.41 | 0.039 | D |
| 20021 | PLCE1 | -0.39 | 0.048 | D |
| 20068 | PPIE | -0.43 | 0.027 | D |
| 20095 |  | -0.44 | 0.023 | D |
| 20101 | KLHL14 | -0.40 | 0.044 | D |
| 20108 | EFEMP1 | -0.44 | 0.023 | D |
| 20238 | PDZD7 | -0.43 | 0.028 | D |
| 20312 | PSRC1 | -0.41 | 0.038 | D |
| 20320 | SDPR | -0.40 | 0.042 | D |
| 20324 | SLC16A9 | -0.45 | 0.022 | D |


| 20380 | SUN5 | -0.56 | 0.003 | D |
| :---: | :---: | :---: | :---: | :---: |
| 20386 | SERPINB5 | -0.48 | 0.014 | D |
| 20398 | PDLIM3 | -0.40 | 0.045 | D |
| 20403 | ANXA7 | -0.39 | 0.050 | D |
| 20458 | CD151 | -0.50 | 0.009 | D |
| 20516 | NCRNA00152 | -0.40 | 0.043 | D |
| 20645 | CSRP1 | -0.40 | 0.041 | D |
| 20706 | NAA20 | -0.39 | 0.048 | D |
| 20736 | STOML3 | -0.41 | 0.037 | D |
| 20744 | F8 | -0.42 | 0.033 | D |
| 20799 | GJB5 | -0.44 | 0.025 | D |
| 20804 | CASP1 | -0.43 | 0.029 | D |
| 20818 |  | -0.41 | 0.038 | D |
| 20836 | SULT1A2 | -0.44 | 0.025 | D |
| 20855 | RGS20 | -0.41 | 0.039 | D |
| 20895 | ANO1 | -0.41 | 0.037 | D |
| 21007 | FAM69C | -0.45 | 0.021 | D |
| 21033 | LEFTY2 | -0.39 | 0.048 | D |
| 21053 | PTGR1 | -0.43 | 0.028 | D |
| 21115 | ADAM15 | -0.45 | 0.021 | D |
| 21154 | COL4A6 | -0.41 | 0.037 | D |
| 21167 | PHACTR4 | -0.46 | 0.019 | D |
| 21216 | PORCN | -0.44 | 0.024 | D |
| 21239 | LPA | -0.49 | 0.011 | D |
| 21251 | ANKS3 | -0.47 | 0.015 | D |
| 21259 | IL17D | -0.44 | 0.025 | D |
| 21285 | COMMD10 | -0.40 | 0.041 | D |
| 21423 | CD151 | -0.42 | 0.034 | D |
| 21447 | LOC440944 | -0.46 | 0.019 | D |
| 21461 | MAP4 | -0.46 | 0.019 | D |
| 21481 | JAG2 | -0.41 | 0.036 | D |
| 21617 | CTSW | -0.39 | 0.048 | D |
| 21763 | APTX | -0.43 | 0.030 | D |
| 21890 | CDON | -0.40 | 0.041 | D |
| 22043 | DHDPSL | -0.41 | 0.036 | D |
| 22231 | SYT8 | -0.42 | 0.031 | D |
| 22267 | BICD2 | -0.45 | 0.021 | D |
| 22367 | CRYBA4 | -0.45 | 0.022 | D |


| 22427 | FOXK1 | -0.45 | 0.023 | D |
| :---: | :---: | :---: | :---: | :---: |
| 22452 | TSPO | -0.46 | 0.019 | D |
| 22510 | NEIL3 | -0.39 | 0.047 | D |
| 22515 | EFEMP1 | -0.46 | 0.017 | D |
| 22532 | EPHX1 | -0.48 | 0.012 | D |
| 22540 | RPL39L | -0.41 | 0.036 | D |
| 22602 | MID1 | -0.47 | 0.015 | D |
| 22604 | PHOX2B | -0.44 | 0.023 | D |
| 22679 | FOSL1 | -0.41 | 0.036 | D |
| 22692 | UBE2A | -0.44 | 0.024 | D |
| 22694 |  | -0.46 | 0.017 | D |
| 22768 | DKC1 | -0.58 | 0.002 | D |
| 22861 | C9orf24 | -0.39 | 0.048 | D |
| 22915 | TMEM31 | -0.39 | 0.047 | D |
| 22933 | PLEKHG5 | -0.54 | 0.005 | D |
| 22973 | MGC44328 | -0.42 | 0.031 | D |
| 23143 | HES2 | -0.39 | 0.048 | D |
| 23169 | CCDC136 | -0.46 | 0.017 | D |
| 23329 | STX17 | -0.45 | 0.020 | D |
| 23331 | NCS1 | -0.44 | 0.023 | D |
| 23360 | MYLK | -0.40 | 0.040 | D |
| 23373 | UBN1 | -0.48 | 0.013 | D |
| 23385 | GPC1 | -0.40 | 0.044 | D |
| 23399 | C12orf50 | -0.42 | 0.034 | D |
| 23445 | TPP2 | -0.42 | 0.032 | D |
| 23522 | PGM2L1 | -0.50 | 0.010 | D |
| 23545 | EIF6 | -0.42 | 0.035 | D |
| 23564 | RFC4 | -0.41 | 0.038 | D |
| 23639 | CDH24 | -0.39 | 0.047 | D |
| 23827 | ARAP3 | -0.40 | 0.043 | D |
| 23879 | NINJ1 | -0.43 | 0.028 | D |
| 23974 | C1S | -0.40 | 0.045 | D |
| 24088 | KCTD5 | -0.40 | 0.042 | D |
| 24127 | HYDIN | -0.45 | 0.021 | D |
| 24149 | DENND2C | -0.52 | 0.007 | D |
| 24169 | CAPN9 | -0.40 | 0.046 | D |
| 24236 | DAOA | -0.45 | 0.022 | D |
| 24274 | HMGB3 | -0.43 | 0.029 | D |


| 24344 | UNKL | -0.40 | 0.043 | D |
| :---: | :---: | :---: | :---: | :---: |
| 24370 |  | -0.48 | 0.013 | D |
| 24425 | SLC6A10P | -0.52 | 0.007 | D |
| 24429 | GCK | -0.45 | 0.021 | D |
| 24497 | STUB1 | -0.45 | 0.022 | D |
| 1284 | RFXAP | 0.43 | 0.027 | U |
| 4133 | KDM3A | 0.42 | 0.033 | U |
| 4536 | GORAB | 0.59 | 0.001 | U |
| 5220 | DACT1 | 0.47 | 0.016 | U |
| 7329 | SPRR2F | 0.45 | 0.022 | U |
| 7572 | OR2J2 | 0.45 | 0.021 | U |
| 7882 | RORB | 0.41 | 0.040 | U |
| 8608 | CHST5 | 0.41 | 0.038 | U |
| 8900 | TMEM225 | 0.43 | 0.030 | U |
| 9316 | MTF2 | 0.40 | 0.043 | U |
| 13259 | DUSP11 | 0.46 | 0.017 | U |
| 14618 | USP9X | 0.39 | 0.049 | U |
| 16369 | MAP3K12 | 0.58 | 0.002 | U |
| 17770 | LSM6 | 0.39 | 0.047 | U |
| 19430 | EIF1B | 0.45 | 0.020 | U |
| 20224 | SMARCAD1 | 0.46 | 0.017 | U |
| 21488 | PIK3C3 | 0.41 | 0.039 | U |
| 23189 | ZNF607 | 0.41 | 0.039 | U |
| 4025 | AES | 0.41 | 0.038 | U |
| 4583 | CCNDBP1 | 0.48 | 0.013 | U |
| 9312 | GPM6B | 0.47 | 0.014 | U |
| 12204 | B3GNT7 | 0.39 | 0.046 | U |
| 24445 | EDARADD | 0.40 | 0.045 | U |
| 3 | PHF7 | 0.39 | 0.049 | U |
| 18 | GNG5 | 0.41 | 0.036 | U |
| 55 | TM2D1 | 0.46 | 0.019 | U |
| 116 | NDUFAF3 | 0.43 | 0.030 | U |
| 218 | LAIR2 | 0.42 | 0.035 | U |
| 277 | NDRG4 | 0.43 | 0.028 | U |
| 320 | ZNF74 | 0.39 | 0.048 | U |
| 397 | ACBD4 | 0.44 | 0.024 | U |
| 416 | COL8A2 | 0.46 | 0.019 | U |
| 514 | CHST11 | 0.45 | 0.021 | U |


| 544 | TERF1 | 0.39 | 0.048 | U |
| :---: | :---: | :---: | :---: | :---: |
| 554 | OR2T35 | 0.46 | 0.017 | U |
| 601 | PDE1B | 0.45 | 0.021 | U |
| 648 | STAT2 | 0.45 | 0.022 | U |
| 687 | SMARCB1 | 0.42 | 0.034 | U |
| 738 | B3GALT5 | 0.45 | 0.021 | U |
| 761 | ARSB | 0.41 | 0.036 | U |
| 797 |  | 0.48 | 0.013 | U |
| 817 | TRIM39 | 0.44 | 0.023 | U |
| 888 | TBC1D15 | 0.47 | 0.014 | U |
| 902 | ZNF627 | 0.40 | 0.043 | U |
| 922 | PPM1F | 0.42 | 0.034 | U |
| 968 | ZACN | 0.48 | 0.013 | U |
| 1096 | HMGB3L1 | 0.48 | 0.014 | U |
| 1203 | ADNP | 0.49 | 0.011 | U |
| 1217 | B3GNT2 | 0.40 | 0.043 | U |
| 1257 | LACRT | 0.51 | 0.007 | U |
| 1300 | SCMH1 | 0.43 | 0.030 | U |
| 1324 | OR2W3 | 0.42 | 0.032 | U |
| 1350 | HIST1H2BG | 0.46 | 0.018 | U |
| 1364 | NLRP12 | 0.67 | 0.000 | U |
| 1418 | CNTN4 | 0.56 | 0.003 | U |
| 1462 | HIST1H2BC | 0.39 | 0.047 | U |
| 1481 | TRIM9 | 0.48 | 0.013 | U |
| 1493 | PLIN2 | 0.41 | 0.039 | U |
| 1649 | AKIRIN1 | 0.40 | 0.044 | U |
| 1670 | GNL2 | 0.47 | 0.015 | U |
| 1750 | WFIKKN1 | 0.39 | 0.048 | U |
| 1797 | UTY | 0.45 | 0.021 | U |
| 1804 | KIF19 | 0.46 | 0.018 | U |
| 1833 | NDNL2 | 0.45 | 0.021 | U |
| 1865 | TTC21A | 0.43 | 0.026 | U |
| 1890 | PRRX1 | 0.43 | 0.030 | U |
| 1948 | ZSCAN29 | 0.49 | 0.012 | U |
| 1982 | WAC | 0.46 | 0.017 | U |
| 1985 | PGS1 | 0.43 | 0.030 | U |
| 2041 | LANCL3 | 0.58 | 0.002 | U |
| 2141 | KRT23 | 0.42 | 0.033 | U |


| 2164 | NMS | 0.43 | 0.027 | U |
| :---: | :---: | :---: | :---: | :---: |
| 2202 | TOE1 | 0.49 | 0.012 | U |
| 2369 |  | 0.43 | 0.030 | U |
| 2418 | ZNF16 | 0.41 | 0.037 | U |
| 2602 | SGK2 | 0.39 | 0.047 | U |
| 2661 | SLC22A6 | 0.58 | 0.002 | U |
| 2868 | USP6 | 0.56 | 0.003 | U |
| 2878 | MS4A14 | 0.56 | 0.003 | U |
| 2908 | C11orf57 | 0.47 | 0.015 | U |
| 2914 |  | 0.43 | 0.027 | U |
| 2920 | MAP2K7 | 0.44 | 0.024 | U |
| 2927 | C14orf101 | 0.44 | 0.026 | U |
| 2928 | ECSIT | 0.41 | 0.039 | U |
| 2946 | ASB8 | 0.46 | 0.017 | U |
| 2991 | PHTF2 | 0.45 | 0.020 | U |
| 3042 | CLDN14 | 0.44 | 0.023 | U |
| 3047 | PRTFDC1 | 0.46 | 0.017 | U |
| 3048 | C13orf26 | 0.39 | 0.049 | U |
| 3070 | NFATC1 | 0.52 | 0.006 | U |
| 3080 | BCL7A | 0.47 | 0.016 | U |
| 3107 | SF3B4 | 0.43 | 0.030 | U |
| 3336 | PHF2 | 0.45 | 0.021 | U |
| 3424 | HAMP | 0.41 | 0.038 | U |
| 3432 | TTLL1 | 0.47 | 0.015 | U |
| 3742 | BEX4 | 0.40 | 0.043 | U |
| 3773 |  | 0.54 | 0.005 | U |
| 3882 | VPS28 | 0.56 | 0.003 | U |
| 3891 | FAM92B | 0.39 | 0.046 | U |
| 3922 | KRTAP4-4 | 0.39 | 0.046 | U |
| 3933 | PPFIA2 | 0.42 | 0.031 | U |
| 3939 | PLAGL1 | 0.43 | 0.030 | U |
| 3981 | LRRC48 | 0.46 | 0.018 | U |
| 4009 | RERE | 0.49 | 0.010 | U |
| 4021 | CHD3 | 0.51 | 0.007 | U |
| 4033 | COMMD3 | 0.41 | 0.036 | U |
| 4043 | ABAT | 0.54 | 0.004 | U |
| 4064 | PTCH2 | 0.42 | 0.035 | U |
| 4092 | C10orf53 | 0.48 | 0.013 | U |


| 4117 | GPR137B | 0.43 | 0.027 | U |
| :---: | :---: | :---: | :---: | :---: |
| 4134 | PIK3CA | 0.39 | 0.046 | U |
| 4234 | TTLL3 | 0.46 | 0.019 | U |
| 4239 | ARHGAP21 | 0.41 | 0.037 | U |
| 4321 | TRMT2A | 0.42 | 0.034 | U |
| 4344 | DNMT3A | 0.46 | 0.018 | U |
| 4472 | PTOV1 | 0.45 | 0.022 | U |
| 4523 | FDXR | 0.43 | 0.028 | U |
| 4564 | ZFAT | 0.44 | 0.024 | U |
| 4649 | SOCS7 | 0.40 | 0.041 | U |
| 4735 | CYS1 | 0.46 | 0.018 | U |
| 4754 | SDC1 | 0.41 | 0.039 | U |
| 4757 | DRAM2 | 0.39 | 0.047 | U |
| 4760 | CCR10 | 0.44 | 0.023 | U |
| 4768 | OR2B2 | 0.39 | 0.049 | U |
| 4794 | LTK | 0.55 | 0.003 | U |
| 4880 | DLX1 | 0.39 | 0.048 | U |
| 4882 | ERCC1 | 0.49 | 0.010 | U |
| 4890 | BLOC1S1 | 0.44 | 0.025 | U |
| 4911 | HIST1H2BE | 0.41 | 0.038 | U |
| 4942 | GTPBP1 | 0.46 | 0.018 | U |
| 4968 | C18orf8 | 0.40 | 0.045 | U |
| 4981 | TMEM35 | 0.42 | 0.031 | U |
| 4994 | C19orf43 | 0.58 | 0.002 | U |
| 5006 | PDE9A | 0.43 | 0.028 | U |
| 5076 | ACP1 | 0.42 | 0.034 | U |
| 5078 | PCBP1 | 0.61 | 0.001 | U |
| 5090 | RANBP2 | 0.40 | 0.044 | U |
| 5121 | GDF7 | 0.45 | 0.020 | U |
| 5131 | SYF2 | 0.39 | 0.049 | U |
| 5147 | VARS2 | 0.41 | 0.040 | U |
| 5163 | CDNF | 0.55 | 0.004 | U |
| 5262 | GGA3 | 0.39 | 0.050 | U |
| 5317 | USP44 | 0.44 | 0.025 | U |
| 5320 | C1orf86 | 0.39 | 0.050 | U |
| 5356 | HCST | 0.39 | 0.046 | U |
| 5392 |  | 0.44 | 0.026 | U |
| 5477 | ATP6V0A1 | 0.50 | 0.009 | U |


| 5785 | HSPC159 | 0.45 | 0.022 | U |
| :---: | :---: | :---: | :---: | :---: |
| 5851 | KRTAP19-2 | 0.43 | 0.030 | U |
| 5860 | SCGBL | 0.43 | 0.028 | U |
| 5862 | CTSE | 0.42 | 0.031 | U |
| 5905 | TNKS2 | 0.39 | 0.046 | U |
| 5947 | TAAR2 | 0.42 | 0.033 | U |
| 5948 | LOC374491 | 0.45 | 0.021 | U |
| 5959 | HIF3A | 0.41 | 0.040 | U |
| 6086 | ZNF428 | 0.41 | 0.039 | U |
| 6090 | HIST2H2AA3 | 0.53 | 0.006 | U |
| 6321 | DEDD | 0.45 | 0.022 | U |
| 6468 | WFDC8 | 0.39 | 0.049 | U |
| 6596 | SCYL3 | 0.59 | 0.002 | U |
| 6623 | SERPING1 | 0.39 | 0.050 | U |
| 6650 | NBAS | 0.58 | 0.002 | U |
| 6659 | CCK | 0.49 | 0.011 | U |
| 6660 | CUL7 | 0.52 | 0.007 | U |
| 6667 | HSD17B7 | 0.50 | 0.010 | U |
| 6678 | SEPHS2 | 0.41 | 0.038 | U |
| 6745 | UBE2E1 | 0.43 | 0.028 | U |
| 6804 | MTMR14 | 0.50 | 0.009 | U |
| 6827 | SLC12A5 | 0.42 | 0.035 | U |
| 6911 | ALS2CR8 | 0.41 | 0.035 | U |
| 6933 | FBXO11 | 0.42 | 0.034 | U |
| 6935 | B3GNT3 | 0.42 | 0.033 | U |
| 6939 | ALLC | 0.47 | 0.016 | U |
| 6978 | COL3A1 | 0.40 | 0.041 | U |
| 6980 | TNFRSF8 | 0.45 | 0.022 | U |
| 6991 | ATP5S | 0.42 | 0.033 | U |
| 7019 | PRDM16 | 0.52 | 0.007 | U |
| 7068 | SH2D4B | 0.42 | 0.033 | U |
| 7071 | PRKAG1 | 0.42 | 0.034 | U |
| 7129 | HIST1H3D | 0.41 | 0.040 | U |
| 7173 | ARNT | 0.48 | 0.014 | U |
| 7199 | EIF3L | 0.54 | 0.004 | U |
| 7226 | ADCY6 | 0.41 | 0.036 | U |
| 7267 | RGPD1 | 0.49 | 0.011 | U |
| 7284 | HSD17B14 | 0.58 | 0.002 | U |


| 7376 | HCST | 0.51 | 0.008 | U |
| :---: | :---: | :---: | :---: | :---: |
| 7380 | PLCG1 | 0.42 | 0.032 | U |
| 7410 | CACNB4 | 0.42 | 0.031 | U |
| 7455 | SAP30L | 0.42 | 0.032 | U |
| 7556 | TCEAL6 | 0.56 | 0.003 | U |
| 7601 |  | 0.50 | 0.010 | U |
| 7625 | ESCO1 | 0.66 | 0.000 | U |
| 7646 | ARL6IP4 | 0.39 | 0.046 | U |
| 7689 | FLRT3 | 0.63 | 0.001 | U |
| 7731 | NIPBL | 0.54 | 0.004 | U |
| 7769 | SLC22A17 | 0.44 | 0.024 | U |
| 7782 | DPM1 | 0.55 | 0.004 | U |
| 7788 | DDT | 0.43 | 0.030 | U |
| 7802 | TOM1 | 0.61 | 0.001 | U |
| 7803 | MTRR | 0.46 | 0.017 | U |
| 7967 | NKG7 | 0.41 | 0.040 | U |
| 8066 | FRG1 | 0.45 | 0.021 | U |
| 8103 | NPAS4 | 0.39 | 0.050 | U |
| 8207 | CLEC2B | 0.43 | 0.028 | U |
| 8235 | ZNF644 | 0.40 | 0.042 | U |
| 8327 | GOLGA6A | 0.48 | 0.013 | U |
| 8431 | SH3YL1 | 0.41 | 0.037 | U |
| 8437 | GSTTP2 | 0.41 | 0.036 | U |
| 8493 | CEP76 | 0.41 | 0.037 | U |
| 8561 | ARID4A | 0.47 | 0.017 | U |
| 8680 | FTMT | 0.40 | 0.044 | U |
| 8733 | HBA1 | 0.41 | 0.040 | U |
| 8832 | EEF1B2 | 0.41 | 0.037 | U |
| 8834 | C8orf30A | 0.41 | 0.038 | U |
| 8843 | ZNF749 | 0.43 | 0.029 | U |
| 8891 | ITSN1 | 0.43 | 0.026 | U |
| 8919 | YPEL5 | 0.39 | 0.049 | U |
| 8972 | RPL41 | 0.40 | 0.045 | U |
| 9063 | MYL4 | 0.60 | 0.001 | U |
| 9090 | ZNF320 | 0.40 | 0.041 | U |
| 9110 | OR5M9 | 0.49 | 0.012 | U |
| 9114 | ATXN7L2 | 0.41 | 0.036 | U |
| 9123 | QARS | 0.48 | 0.012 | U |


| 9138 | ENOSF1 | 0.43 | 0.027 | U |
| :---: | :---: | :---: | :---: | :---: |
| 9249 | RGAG4 | 0.39 | 0.048 | U |
| 9366 | FAM175A | 0.40 | 0.042 | U |
| 9383 | FARP1 | 0.44 | 0.023 | U |
| 9476 | PHF20L1 | 0.53 | 0.005 | U |
| 9599 | TDRKH | 0.51 | 0.008 | U |
| 9649 | MED9 | 0.62 | 0.001 | U |
| 9710 | POMGNT1 | 0.42 | 0.030 | U |
| 9716 | QPRT | 0.40 | 0.041 | U |
| 9742 | CCDC8 | 0.39 | 0.049 | U |
| 9791 | CAND2 | 0.41 | 0.038 | U |
| 9942 | PTPN13 | 0.46 | 0.018 | U |
| 10103 | AP1G2 | 0.43 | 0.030 | U |
| 10119 | ADAM10 | 0.40 | 0.045 | U |
| 10147 | RRP36 | 0.40 | 0.044 | U |
| 10157 | POLR2B | 0.44 | 0.026 | U |
| 10229 | PTPN12 | 0.40 | 0.042 | U |
| 10233 | SCAP | 0.41 | 0.039 | U |
| 10263 | OR51B5 | 0.42 | 0.034 | U |
| 10355 | FLJ33360 | 0.47 | 0.016 | U |
| 10424 | ELMO2 | 0.44 | 0.024 | U |
| 10437 | SCYL3 | 0.52 | 0.006 | U |
| 10468 | PIGU | 0.44 | 0.023 | U |
| 10490 | ARHGEF1 | 0.48 | 0.014 | U |
| 10500 | IMMT | 0.41 | 0.037 | U |
| 10541 | TGFBR3 | 0.42 | 0.033 | U |
| 10612 | PCMTD1 | 0.41 | 0.036 | U |
| 10642 | C12orf23 | 0.44 | 0.025 | U |
| 10660 | NFYC | 0.46 | 0.018 | U |
| 10682 | C14orf166 | 0.43 | 0.030 | U |
| 10728 | ALKBH7 | 0.57 | 0.002 | U |
| 10773 | TBKBP1 | 0.51 | 0.008 | U |
| 10804 | RBMXL3 | 0.41 | 0.038 | U |
| 10846 | PPIL2 | 0.39 | 0.048 | U |
| 11011 | SDHD | 0.42 | 0.033 | U |
| 11021 | ACBD5 | 0.43 | 0.028 | U |
| 11068 | SEMA5A | 0.39 | 0.047 | U |
| 11072 | MDH1 | 0.39 | 0.046 | U |


| 11115 | NIPSNAP3A | 0.50 | 0.009 | U |
| :---: | :---: | :---: | :---: | :---: |
| 11180 | WAC | 0.45 | 0.022 | U |
| 11190 | CIB2 | 0.41 | 0.037 | U |
| 11315 | KCND3 | 0.52 | 0.007 | U |
| 11418 | SPATA6 | 0.40 | 0.043 | U |
| 11425 | MSMP | 0.43 | 0.027 | U |
| 11472 | PPM1B | 0.46 | 0.018 | U |
| 11511 | SRGAP2 | 0.40 | 0.041 | U |
| 11513 | C19orf53 | 0.39 | 0.049 | U |
| 11608 | RAD23A | 0.43 | 0.027 | U |
| 11669 | TSHR | 0.47 | 0.015 | U |
| 11683 | RS1 | 0.50 | 0.009 | U |
| 11826 | PQLC2 | 0.48 | 0.012 | U |
| 11860 | PRSS48 | 0.47 | 0.016 | U |
| 11888 | MRPL45 | 0.51 | 0.008 | U |
| 11895 | SIRPB1 | 0.40 | 0.044 | U |
| 11904 | LILRA1 | 0.46 | 0.019 | U |
| 11944 | HTR7 | 0.56 | 0.003 | U |
| 11961 | SIK2 | 0.40 | 0.041 | U |
| 11966 | SF3B14 | 0.40 | 0.045 | U |
| 11997 | RCOR3 | 0.39 | 0.050 | U |
| 12002 | C19orf56 | 0.46 | 0.017 | U |
| 12039 | FAM110B | 0.40 | 0.043 | U |
| 12086 | NCRNA00115 | 0.41 | 0.037 | U |
| 12129 | ZNF791 | 0.58 | 0.002 | U |
| 12132 | CSAG1 | 0.40 | 0.041 | U |
| 12188 | MRPS21 | 0.41 | 0.038 | U |
| 12210 | ERCC1 | 0.45 | 0.020 | U |
| 12225 | SLC26A6 | 0.43 | 0.029 | U |
| 12288 | FAM81B | 0.56 | 0.003 | U |
| 12297 | SNRNP35 | 0.44 | 0.025 | U |
| 12344 | PEBP1 | 0.46 | 0.019 | U |
| 12380 | MS4A5 | 0.43 | 0.026 | U |
| 12398 | OR11H12 | 0.46 | 0.019 | U |
| 12509 | TNFRSF6B | 0.39 | 0.046 | U |
| 12606 | NLRP10 | 0.39 | 0.047 | U |
| 12666 | C2orf76 | 0.39 | 0.048 | U |
| 12714 | DOK1 | 0.52 | 0.006 | U |


| 12748 | FBXW8 | 0.47 | 0.016 | U |
| :---: | :---: | :---: | :---: | :---: |
| 12833 | TMEM91 | 0.43 | 0.028 | U |
| 12863 | OR2L8 | 0.39 | 0.047 | U |
| 12870 | TADA3 | 0.47 | 0.017 | U |
| 12886 | ACSL4 | 0.41 | 0.037 | U |
| 12921 | DERL2 | 0.44 | 0.023 | U |
| 12966 | CBY1 | 0.42 | 0.030 | U |
| 12971 | B4GALT6 | 0.53 | 0.005 | U |
| 13021 | APOL2 | 0.44 | 0.023 | U |
| 13104 | KIR2DS4 | 0.39 | 0.047 | U |
| 13117 | RNF170 | 0.43 | 0.027 | U |
| 13126 | MASP1 | 0.45 | 0.020 | U |
| 13155 | LIG4 | 0.43 | 0.027 | U |
| 13231 | ATP5F1 | 0.41 | 0.039 | U |
| 13310 | DCAF6 | 0.41 | 0.037 | U |
| 13354 | ATP5L | 0.47 | 0.015 | U |
| 13390 | KISS1R | 0.43 | 0.027 | U |
| 13536 | HELQ | 0.42 | 0.031 | U |
| 13557 | CCDC121 | 0.41 | 0.037 | U |
| 13639 | SFSWAP | 0.46 | 0.018 | U |
| 13652 | THRB | 0.40 | 0.043 | U |
| 13745 | BRWD1 | 0.63 | 0.001 | U |
| 13828 | TMED5 | 0.42 | 0.035 | U |
| 13929 | SPN | 0.41 | 0.035 | U |
| 13941 | C6orf81 | 0.42 | 0.033 | U |
| 13956 | CEACAM20 | 0.50 | 0.009 | U |
| 13960 | PFDN5 | 0.42 | 0.035 | U |
| 13988 | ABCC6 | 0.43 | 0.030 | U |
| 14031 | PDK2 | 0.41 | 0.038 | U |
| 14084 | NUPL1 | 0.40 | 0.042 | U |
| 14099 | CYP7B1 | 0.39 | 0.049 | U |
| 14119 | KLHDC3 | 0.43 | 0.027 | U |
| 14167 | COIL | 0.44 | 0.025 | U |
| 14253 | NAA38 | 0.54 | 0.004 | U |
| 14257 | PAK7 | 0.54 | 0.005 | U |
| 14262 | F8A1 | 0.40 | 0.046 | U |
| 14272 | GP1BA | 0.51 | 0.008 | U |
| 14277 | CBY1 | 0.40 | 0.044 | U |


| 14395 | FAM69B | 0.43 | 0.028 | U |
| :---: | :---: | :---: | :---: | :---: |
| 14414 | COLQ | 0.42 | 0.031 | U |
| 14482 | C1orf129 | 0.56 | 0.003 | U |
| 14501 | UBE2V1 | 0.46 | 0.019 | U |
| 14593 | CDC42SE1 | 0.56 | 0.003 | U |
| 14634 | PLA2G5 | 0.47 | 0.015 | U |
| 14683 | RGS1 | 0.41 | 0.039 | U |
| 14684 | BEX4 | 0.39 | 0.047 | U |
| 14733 | PI15 | 0.56 | 0.003 | U |
| 14773 | RSRC2 | 0.43 | 0.027 | U |
| 14787 | CDC42SE1 | 0.57 | 0.002 | U |
| 14799 | NLRP3 | 0.46 | 0.019 | U |
| 14807 | PCSK6 | 0.48 | 0.014 | U |
| 14928 | SIRT4 | 0.41 | 0.037 | U |
| 15020 | SHOC2 | 0.43 | 0.029 | U |
| 15110 | C1orf103 | 0.44 | 0.024 | U |
| 15171 | OSTC | 0.43 | 0.028 | U |
| 15419 | BTG1 | 0.40 | 0.046 | U |
| 15423 | GREB1 | 0.39 | 0.050 | U |
| 15451 | AMIGO1 | 0.48 | 0.014 | U |
| 15498 |  | 0.44 | 0.023 | U |
| 15566 | FBXO7 | 0.47 | 0.017 | U |
| 15599 | NID1 | 0.47 | 0.014 | U |
| 15666 | TMEM151A | 0.52 | 0.006 | U |
| 15769 |  | 0.49 | 0.012 | U |
| 15795 | DPP4 | 0.45 | 0.020 | U |
| 15878 | RNMT | 0.53 | 0.006 | U |
| 15941 | CTRB1 | 0.56 | 0.003 | U |
| 16016 | ARL1 | 0.42 | 0.032 | U |
| 16079 | RERG | 0.46 | 0.018 | U |
| 16086 | ABHD8 | 0.43 | 0.028 | U |
| 16105 | ZBTB17 | 0.50 | 0.009 | U |
| 16113 | MZF1 | 0.43 | 0.027 | U |
| 16125 | MFSD9 | 0.40 | 0.043 | U |
| 16180 | RFT1 | 0.39 | 0.046 | U |
| 16330 | KCNJ12 | 0.43 | 0.028 | U |
| 16343 | NCRNA00052 | 0.42 | 0.031 | U |
| 16350 | IGDCC3 | 0.41 | 0.039 | U |


| 16364 | PI4KA | 0.43 | 0.029 | U |
| :---: | :---: | :---: | :---: | :---: |
| 16389 | KIAA1143 | 0.53 | 0.006 | U |
| 16413 |  | 0.64 | 0.000 | U |
| 16448 | CLPS | 0.47 | 0.015 | U |
| 16509 | TSPAN11 | 0.50 | 0.009 | U |
| 16647 | SALL3 | 0.39 | 0.048 | U |
| 16660 | PSD3 | 0.41 | 0.039 | U |
| 16667 | RPS27 | 0.40 | 0.044 | U |
| 16687 | MFAP2 | 0.43 | 0.029 | U |
| 16811 | HAVCR2 | 0.40 | 0.044 | U |
| 16830 | NEK5 | 0.41 | 0.039 | U |
| 16834 | ALOX15 | 0.50 | 0.010 | U |
| 16838 | AKT3 | 0.40 | 0.044 | U |
| 16870 | HPCAL4 | 0.42 | 0.033 | U |
| 17047 | LSP1 | 0.44 | 0.025 | U |
| 17126 | SERHL2 | 0.61 | 0.001 | U |
| 17135 | PDZD9 | 0.52 | 0.007 | U |
| 17173 | C14orf4 | 0.48 | 0.012 | U |
| 17244 | H2AFJ | 0.57 | 0.003 | U |
| 17319 | EGFL8 | 0.39 | 0.050 | U |
| 17374 | SMCR8 | 0.42 | 0.032 | U |
| 17379 | CEACAM1 | 0.52 | 0.006 | U |
| 17421 | C16orf78 | 0.57 | 0.002 | U |
| 17546 | C6orf162 | 0.42 | 0.033 | U |
| 17575 | MINA | 0.67 | 0.000 | U |
| 17641 | BACH1 | 0.41 | 0.040 | U |
| 17652 | C2orf42 | 0.46 | 0.019 | U |
| 17713 | ZNF580 | 0.44 | 0.025 | U |
| 17761 | GPRC5D | 0.44 | 0.023 | U |
| 17816 | MLLT10 | 0.40 | 0.043 | U |
| 17823 | KCNMA1 | 0.44 | 0.023 | U |
| 17913 | PPP1R1C | 0.49 | 0.012 | U |
| 17994 | HIST1H1C | 0.44 | 0.025 | U |
| 18004 | IQUB | 0.47 | 0.016 | U |
| 18012 | B3GALT5 | 0.43 | 0.030 | U |
| 18227 | SHOX | 0.40 | 0.041 | U |
| 18276 | VPS28 | 0.59 | 0.002 | U |
| 18288 | SERHL2 | 0.41 | 0.037 | U |


| 18316 | KIAA1409 | 0.39 | 0.048 | U |
| :---: | :---: | :---: | :---: | :---: |
| 18394 | CPSF3 | 0.52 | 0.006 | U |
| 18484 | TRIM24 | 0.39 | 0.050 | U |
| 18488 | FBXO25 | 0.50 | 0.010 | U |
| 18492 | C22orf28 | 0.55 | 0.003 | U |
| 18503 | LTB4R2 | 0.41 | 0.037 | U |
| 18565 | CPB2 | 0.51 | 0.008 | U |
| 18608 | HIST1H2AJ | 0.49 | 0.012 | U |
| 18625 | CAMP | 0.39 | 0.047 | U |
| 18663 | ZNF643 | 0.44 | 0.023 | U |
| 18703 | IZUMO1 | 0.50 | 0.010 | U |
| 18708 | PAIP2 | 0.48 | 0.012 | U |
| 18823 | MED13 | 0.51 | 0.008 | U |
| 18906 | FGF11 | 0.49 | 0.012 | U |
| 18922 | NBR2 | 0.58 | 0.002 | U |
| 18932 | OR11H4 | 0.46 | 0.017 | U |
| 18948 | FUZ | 0.54 | 0.004 | U |
| 19061 | SYT11 | 0.51 | 0.007 | U |
| 19078 | METTL14 | 0.43 | 0.030 | U |
| 19108 | MOGAT1 | 0.39 | 0.047 | U |
| 19136 | SLC35C2 | 0.42 | 0.031 | U |
| 19154 | TMEM130 | 0.41 | 0.040 | U |
| 19212 | EGR2 | 0.40 | 0.044 | U |
| 19220 | GABRG2 | 0.52 | 0.007 | U |
| 19296 | HORMAD2 | 0.41 | 0.035 | U |
| 19463 | HIST2H2AC | 0.48 | 0.012 | U |
| 19489 | ZNF653 | 0.42 | 0.033 | U |
| 19561 | INPP5F | 0.43 | 0.029 | U |
| 19688 | STAG3L1 | 0.42 | 0.033 | U |
| 19745 | PCM1 | 0.44 | 0.024 | U |
| 19766 | MRPL10 | 0.47 | 0.015 | U |
| 19788 | ADAMTS5 | 0.40 | 0.042 | U |
| 19836 | LAIR2 | 0.45 | 0.022 | U |
| 19902 | CFDP1 | 0.40 | 0.040 | U |
| 20043 | DHTKD1 | 0.50 | 0.010 | U |
| 20045 | DTX3 | 0.40 | 0.041 | U |
| 20058 | LZTFL1 | 0.45 | 0.020 | U |
| 20071 | INGX | 0.44 | 0.025 | U |


| 20137 | PKIG | 0.43 | 0.027 | U |
| :---: | :---: | :---: | :---: | :---: |
| 20201 | TMEM120A | 0.41 | 0.037 | U |
| 20313 | AUP1 | 0.41 | 0.035 | U |
| 20343 | CRH | 0.43 | 0.029 | U |
| 20465 | ZSCAN2 | 0.48 | 0.014 | U |
| 20499 | H2AFB2 | 0.45 | 0.021 | U |
| 20520 | OR5H6 | 0.39 | 0.050 | U |
| 20525 | SON | 0.40 | 0.043 | U |
| 20526 | FAM84A | 0.43 | 0.028 | U |
| 20539 | IMPA1 | 0.39 | 0.048 | U |
| 20708 | CAV3 | 0.42 | 0.031 | U |
| 20761 | SRSF5 | 0.40 | 0.044 | U |
| 20765 | NEUROD4 | 0.50 | 0.009 | U |
| 20770 | WBP1 | 0.43 | 0.027 | U |
| 20795 | OR2F1 | 0.47 | 0.016 | U |
| 20908 | HSPBAP1 | 0.46 | 0.018 | U |
| 20915 | DENND4A | 0.47 | 0.017 | U |
| 20937 | CHGB | 0.45 | 0.021 | U |
| 20950 | LRRC17 | 0.40 | 0.045 | U |
| 20968 | TIFA | 0.43 | 0.029 | U |
| 20982 | CAPN3 | 0.39 | 0.050 | U |
| 21018 | ADAM32 | 0.39 | 0.047 | U |
| 21055 | DHPS | 0.58 | 0.002 | U |
| 21120 | ZNF335 | 0.48 | 0.012 | U |
| 21147 | SLC17A1 | 0.48 | 0.013 | U |
| 21163 | SH3BGRL | 0.44 | 0.023 | U |
| 21194 | FAM195B | 0.40 | 0.043 | U |
| 21224 | PPAN | 0.49 | 0.011 | U |
| 21265 | ARID3A | 0.56 | 0.003 | U |
| 21296 | SNF8 | 0.39 | 0.048 | U |
| 21355 | ROCK1 | 0.39 | 0.050 | U |
| 21366 | SLC2A10 | 0.44 | 0.024 | U |
| 21418 | C1orf114 | 0.41 | 0.038 | U |
| 21441 | CAMKK2 | 0.46 | 0.017 | U |
| 21472 | WSB2 | 0.46 | 0.018 | U |
| 21479 | FLJ41649 | 0.52 | 0.006 | U |
| 21544 | CNTFR | 0.44 | 0.026 | U |
| 21774 | MAGEB3 | 0.40 | 0.042 | U |


| 21785 | ATG13 | 0.51 | 0.008 | U |
| :---: | :---: | :---: | :---: | :---: |
| 21908 | C9orf24 | 0.42 | 0.033 | U |
| 21940 | MC4R | 0.49 | 0.010 | U |
| 22058 | WAC | 0.58 | 0.002 | U |
| 22095 | CHP | 0.42 | 0.031 | U |
| 22166 | IGFBPL1 | 0.47 | 0.015 | U |
| 22355 | UMODL1 | 0.40 | 0.044 | U |
| 22421 | NCALD | 0.51 | 0.008 | U |
| 22546 | ATP5S | 0.50 | 0.010 | U |
| 22603 | RRAGB | 0.40 | 0.044 | U |
| 22631 | PDGFRA | 0.43 | 0.029 | U |
| 22639 | C4orf38 | 0.59 | 0.002 | U |
| 22713 | OR5K2 | 0.49 | 0.010 | U |
| 22716 | EFTUD1 | 0.52 | 0.007 | U |
| 22748 | DOCK3 | 0.47 | 0.016 | U |
| 22771 | IRF4 | 0.44 | 0.026 | U |
| 22789 | FGF1 | 0.39 | 0.046 | U |
| 22907 | AGL | 0.42 | 0.032 | U |
| 22914 | MLC1 | 0.43 | 0.030 | U |
| 22946 | NEURL2 | 0.51 | 0.007 | U |
| 23053 | CDC20B | 0.41 | 0.036 | U |
| 23069 | DDA1 | 0.42 | 0.034 | U |
| 23090 | FOXD4L3 | 0.45 | 0.022 | U |
| 23138 | RBMXL2 | 0.39 | 0.046 | U |
| 23183 | C7orf62 | 0.42 | 0.032 | U |
| 23221 | ANKHD1 | 0.58 | 0.002 | U |
| 23232 | CDKL5 | 0.45 | 0.020 | U |
| 23236 | PMS2CL | 0.45 | 0.022 | U |
| 23267 | TGM6 | 0.45 | 0.020 | U |
| 23513 | C1QL2 | 0.39 | 0.049 | U |
| 23558 | USF2 | 0.49 | 0.011 | U |
| 23570 | ZNF546 | 0.39 | 0.050 | U |
| 23630 | GTSF1L | 0.50 | 0.009 | U |
| 23634 | HEMGN | 0.41 | 0.037 | U |
| 23732 | SVOPL | 0.39 | 0.046 | U |
| 23751 | MLANA | 0.47 | 0.015 | U |
| 23775 | WDR88 | 0.47 | 0.015 | U |
| 23781 |  | 0.40 | 0.041 | U |


| 23830 | PAPOLG | 0.40 | 0.044 | U |
| :---: | :---: | :---: | :---: | :---: |
| 23874 | YIPF3 | 0.49 | 0.011 | U |
| 23936 | SNAPC3 | 0.46 | 0.017 | U |
| 23940 | FAM19A2 | 0.50 | 0.010 | U |
| 23986 | DQX1 | 0.57 | 0.002 | U |
| 24006 | SCAMP5 | 0.46 | 0.019 | U |
| 24152 | S100A7A | 0.54 | 0.004 | U |
| 24283 | C22orf15 | 0.46 | 0.018 | U |
| 24382 | GAL3ST3 | 0.47 | 0.016 | U |
| 24518 | ENOX1 | 0.41 | 0.039 | U |

## APPENDIX C. 1403 GENES CORRELATE WITH SYNERGY TO

## PEMETREXED + CISPLATIN

| Gene <br> ID | Symbol | Synergy <br> Correlation | Correlation <br> P value | Up or <br> Down <br> regulated |
| :---: | :---: | :---: | :---: | :---: |
| 602 | LCK | -0.52 | 0.004 | D |
| 1492 | KLK3 | -0.41 | 0.032 | D |
| 5490 | FBXW2 | -0.43 | 0.021 | D |
| 8928 | TFAP4 | -0.38 | 0.047 | D |
| 10039 | CFHR2 | -0.46 | 0.014 | D |
| 14869 | CDH24 | -0.38 | 0.046 | D |
| 15865 | WDR5 | -0.48 | 0.010 | D |
| 16674 | ANKZF1 | -0.42 | 0.026 | D |
| 17110 | COL18A1 | -0.41 | 0.031 | D |
| 19520 | PRPF4 | -0.38 | 0.043 | D |
| 22267 | BICD2 | -0.41 | 0.031 | D |
| 9316 | MTF2 | -0.60 | 0.001 | D |
| 13259 | DUSP11 | -0.42 | 0.025 | D |
| 416 | COL8A2 | -0.43 | 0.023 | D |
| 6991 | ATP5S | -0.50 | 0.007 | D |
| 7455 | SAP30L | -0.38 | 0.047 | D |
| 8066 | FRG1 | -0.40 | 0.034 | D |
| 10103 | AP1G2 | -0.39 | 0.041 | D |
| 11966 | SF3B14 | -0.39 | 0.038 | D |
| 17546 | C6orf162 | -0.48 | 0.010 | D |
| 106 | CARS | -0.39 | 0.038 | D |
| 243 | ZBTB2 | -0.55 | 0.002 | D |
| 415 | BBS7 | -0.44 | 0.019 | D |
| 496 | HSPE1 | -0.51 | 0.005 | D |
| 1266 | RPL23 | -0.54 | 0.003 | D |
| 1399 | SEPT7 | -0.59 | 0.001 | D |
| 1512 | PTMA | -0.62 | 0.000 | D |
| 1661 | SUMO2 | -0.62 | 0.000 | D |
| 2254 | RPS28 | -0.42 | 0.025 | D |
| 2273 | ZNF772 | -0.41 | 0.029 | D |
| 2300 | TBCB | -0.42 | 0.028 | D |
| 2416 | MRPL48 | -0.55 | 0.002 | D |
|  |  |  |  |  |


| 2476 | PRRG3 | -0.40 | 0.033 | D |
| :---: | :---: | :---: | :---: | :---: |
| 2766 | RPL5 | -0.52 | 0.005 | D |
| 2831 | EXOSC10 | -0.48 | 0.010 | D |
| 2956 |  | -0.46 | 0.013 | D |
| 3024 | TXNL1 | -0.54 | 0.003 | D |
| 3140 | TAF9 | -0.46 | 0.014 | D |
| 3145 | SRSF11 | -0.49 | 0.009 | D |
| 3310 | CDKN1B | -0.47 | 0.012 | D |
| 3683 | HS2ST1 | -0.52 | 0.005 | D |
| 4005 | RPL26 | -0.39 | 0.043 | D |
| 4481 | CRHR1 | -0.41 | 0.030 | D |
| 4563 | OR52A5 | -0.49 | 0.008 | D |
| 4566 | R3HDM1 | -0.51 | 0.005 | D |
| 4603 | GLI1 | -0.51 | 0.005 | D |
| 4858 | EXOSC3 | -0.39 | 0.041 | D |
| 5083 | HNRNPC | -0.49 | 0.008 | D |
| 5278 | C5orf34 | -0.44 | 0.019 | D |
| 5550 | MCTS1 | -0.43 | 0.022 | D |
| 5712 | GPR19 | -0.68 | 0.000 | D |
| 5806 | RBM24 | -0.47 | 0.011 | D |
| 5881 |  | -0.42 | 0.026 | D |
| 5991 | PSMB7 | -0.41 | 0.030 | D |
| 6012 | PTGES3 | -0.54 | 0.003 | D |
| 6083 | PAPSS1 | -0.53 | 0.004 | D |
| 6177 | HIAT1 | -0.69 | 0.000 | D |
| 6260 | NDUFAF4 | -0.47 | 0.012 | D |
| 6323 | CCNH | -0.55 | 0.003 | D |
| 6530 | CCDC25 | -0.44 | 0.019 | D |
| 6912 | RBBP7 | -0.50 | 0.006 | D |
| 6917 | ZFP1 | -0.39 | 0.042 | D |
| 6977 | NOL8 | -0.50 | 0.007 | D |
| 7163 | RPL14 | -0.40 | 0.036 | D |
| 7172 | FBXO40 | -0.50 | 0.007 | D |
| 7411 | RAD1 | -0.46 | 0.014 | D |
| 7431 | KRTAP10-11 | -0.46 | 0.014 | D |
| 7643 | CHD1 | -0.48 | 0.010 | D |
| 7698 | GPR55 | -0.39 | 0.041 | D |
| 7736 | H3F3A | -0.38 | 0.048 | D |


| 7838 | RPS15A | -0.39 | 0.039 | D |
| :---: | :---: | :---: | :---: | :---: |
| 8451 | C4orf43 | -0.38 | 0.045 | D |
| 8637 | RNGTT | -0.41 | 0.032 | D |
| 8687 | FAM49B | -0.63 | 0.000 | D |
| 8916 | RPL7 | -0.68 | 0.000 | D |
| 9253 | RPL7A | -0.44 | 0.018 | D |
| 9272 | C20orf27 | -0.46 | 0.015 | D |
| 10078 | NCRNA00152 | -0.42 | 0.026 | D |
| 10160 | C11orf58 | -0.43 | 0.023 | D |
| 10197 | DEFB108B | -0.40 | 0.037 | D |
| 10595 | DNAJC7 | -0.38 | 0.044 | D |
| 10676 | SREK1 | -0.64 | 0.000 | D |
| 10736 | TIMM10 | -0.38 | 0.048 | D |
| 10962 | HERPUD2 | -0.42 | 0.024 | D |
| 11012 | PRKDC | -0.41 | 0.030 | D |
| 11363 | HCCS | -0.49 | 0.008 | D |
| 11656 |  | -0.44 | 0.019 | D |
| 12045 | LDHAL6B | -0.38 | 0.045 | D |
| 12750 | KIF3A | -0.38 | 0.044 | D |
| 13055 | POLR1E | -0.45 | 0.017 | D |
| 13130 | RAB6A | -0.41 | 0.032 | D |
| 14068 | CALB2 | -0.39 | 0.039 | D |
| 14223 | PARD3B | -0.38 | 0.044 | D |
| 14355 | SLBP | -0.42 | 0.027 | D |
| 14356 | PHF3 | -0.58 | 0.001 | D |
| 14490 | PRAMEF10 | -0.38 | 0.046 | D |
| 15335 | TIPRL | -0.63 | 0.000 | D |
| 15474 | UBE2D2 | -0.41 | 0.030 | D |
| 15559 | LRRC40 | -0.59 | 0.001 | D |
| 16216 | SPATA22 | -0.45 | 0.015 | D |
| 16591 | DCAF6 | -0.50 | 0.007 | D |
| 16743 | MRPL47 | -0.56 | 0.002 | D |
| 17057 | C12orf11 | -0.55 | 0.002 | D |
| 17062 | CCT7 | -0.49 | 0.008 | D |
| 17443 | PROL1 | -0.55 | 0.003 | D |
| 17487 | RBM34 | -0.40 | 0.037 | D |
| 18162 | TRUB2 | -0.59 | 0.001 | D |
| 18178 | CDK5RAP2 | -0.39 | 0.039 | D |


| 18334 | PIP5K1B | -0.39 | 0.042 | D |
| :---: | :---: | :---: | :---: | :---: |
| 18357 | G3BP1 | -0.54 | 0.003 | D |
| 18672 | UBE2CBP | -0.50 | 0.007 | D |
| 18962 | HMGB2 | -0.41 | 0.029 | D |
| 19111 | ISCA1 | -0.41 | 0.033 | D |
| 19153 | PMS1 | -0.52 | 0.004 | D |
| 20113 | KPNA2 | -0.42 | 0.026 | D |
| 20682 | ROD1 | -0.57 | 0.002 | D |
| 20828 | KIAA0368 | -0.41 | 0.032 | D |
| 20983 | RPL9 | -0.66 | 0.000 | D |
| 21288 | LIN7C | -0.39 | 0.041 | D |
| 21616 | PNMAL1 | -0.40 | 0.036 | D |
| 21766 | RAP1B | -0.42 | 0.024 | D |
| 21894 | LSM5 | -0.71 | 0.000 | D |
| 21901 | TRMT11 | -0.39 | 0.039 | D |
| 22295 | PPP2CB | -0.59 | 0.001 | D |
| 22300 | RPL13P5 | -0.42 | 0.026 | D |
| 22470 | PCNA | -0.43 | 0.022 | D |
| 22552 | HDAC2 | -0.43 | 0.022 | D |
| 22784 | EFTUD2 | -0.38 | 0.047 | D |
| 22910 | MRPL52 | -0.41 | 0.029 | D |
| 23417 | RBBP4 | -0.59 | 0.001 | D |
| 23659 | HNRNPA1 | -0.38 | 0.049 | D |
| 23803 | CDK4 | -0.55 | 0.002 | D |
| 23994 | CETP | -0.43 | 0.024 | D |
| 24031 | MSC | -0.45 | 0.017 | D |
| 24216 | TMEM14B | -0.39 | 0.040 | D |
| 18067 | KCNG2 | -0.44 | 0.018 | D |
| 15 | CD164 | -0.45 | 0.018 | D |
| 36 | UBLCP1 | -0.38 | 0.043 | D |
| 88 | RASSF4 | -0.38 | 0.044 | D |
| 126 | ARPC5 | -0.43 | 0.023 | D |
| 150 | RNF157 | -0.46 | 0.014 | D |
| 194 | TEKT5 | -0.52 | 0.005 | D |
| 268 | DDHD2 | -0.43 | 0.022 | D |
| 269 | PDE9A | -0.55 | 0.002 | D |
| 276 | LCE1B | -0.50 | 0.007 | D |
| 338 | URM1 | -0.39 | 0.039 | D |


| 360 | C11orf76 | -0.45 | 0.016 | D |
| :---: | :---: | :---: | :---: | :---: |
| 384 | ACAP2 | -0.40 | 0.036 | D |
| 393 | UPF3A | -0.43 | 0.021 | D |
| 419 | SLC22A24 | -0.38 | 0.048 | D |
| 426 | TMEM8A | -0.49 | 0.008 | D |
| 503 | EML4 | -0.40 | 0.036 | D |
| 533 | SYMPK | -0.50 | 0.007 | D |
| 555 | FBXL5 | -0.39 | 0.041 | D |
| 632 | OLFML1 | -0.38 | 0.043 | D |
| 671 | MED21 | -0.43 | 0.021 | D |
| 772 | KLHL7 | -0.57 | 0.001 | D |
| 810 | POTEE | -0.46 | 0.014 | D |
| 893 | OR11A1 | -0.38 | 0.049 | D |
| 907 | CAND1 | -0.42 | 0.026 | D |
| 944 | TCF7 | -0.38 | 0.048 | D |
| 964 | PAIP2 | -0.39 | 0.039 | D |
| 974 | MRPL3 | -0.42 | 0.028 | D |
| 982 | MYO18A | -0.43 | 0.022 | D |
| 993 | ZNF230 | -0.43 | 0.024 | D |
| 1006 | GADL1 | -0.63 | 0.000 | D |
| 1052 | C15orf21 | -0.60 | 0.001 | D |
| 1063 | SLC25A16 | -0.38 | 0.048 | D |
| 1157 | LHFPL2 | -0.40 | 0.033 | D |
| 1243 | C9orf82 | -0.46 | 0.013 | D |
| 1277 | TSC22D1 | -0.38 | 0.048 | D |
| 1297 | HSPA4 | -0.40 | 0.036 | D |
| 1375 | GPR25 | -0.40 | 0.033 | D |
| 1393 | RAB5C | -0.38 | 0.045 | D |
| 1402 | PBLD | -0.39 | 0.038 | D |
| 1429 | CXCR7 | -0.38 | 0.048 | D |
| 1476 | PAK4 | -0.47 | 0.011 | D |
| 1478 | DOC2A | -0.50 | 0.007 | D |
| 1505 | SPAST | -0.48 | 0.009 | D |
| 1570 | CCNB1IP1 | -0.50 | 0.007 | D |
| 1629 | CNTFR | -0.40 | 0.034 | D |
| 1643 | ANKHD1 | -0.51 | 0.005 | D |
| 1663 | CLCN3 | -0.38 | 0.047 | D |
| 1696 | PJA2 | -0.39 | 0.038 | D |


| 1709 | CDH6 | -0.40 | 0.034 | D |
| :---: | :---: | :---: | :---: | :---: |
| 1714 | LOC151121 | -0.39 | 0.038 | D |
| 1840 | TFEC | -0.41 | 0.032 | D |
| 1891 | DENND1A | -0.40 | 0.033 | D |
| 1972 | SEPT6 | -0.38 | 0.046 | D |
| 1976 | CHRAC1 | -0.38 | 0.044 | D |
| 1986 | HECA | -0.46 | 0.015 | D |
| 2016 | USP25 | -0.39 | 0.040 | D |
| 2043 | BNIP3L | -0.42 | 0.024 | D |
| 2088 | ARHGAP6 | -0.44 | 0.020 | D |
| 2133 | STK33 | -0.47 | 0.011 | D |
| 2211 | TBX19 | -0.39 | 0.042 | D |
| 2237 | COMMD8 | -0.51 | 0.005 | D |
| 2256 | PSMD8 | -0.45 | 0.015 | D |
| 2303 | CORO1C | -0.39 | 0.039 | D |
| 2314 | ORM1 | -0.38 | 0.044 | D |
| 2319 | FAM47B | -0.49 | 0.009 | D |
| 2321 | TMEM169 | -0.40 | 0.033 | D |
| 2323 | ACTN2 | -0.39 | 0.040 | D |
| 2339 | KRTAP19-6 | -0.46 | 0.013 | D |
| 2357 | PPP6C | -0.43 | 0.021 | D |
| 2373 | C2 | -0.41 | 0.031 | D |
| 2426 | VDAC3 | -0.39 | 0.038 | D |
| 2450 | TBC1D13 | -0.53 | 0.004 | D |
| 2560 | TSPAN32 | -0.43 | 0.022 | D |
| 2568 | CCBL2 | -0.38 | 0.049 | D |
| 2597 | INPP5F | -0.38 | 0.048 | D |
| 2695 | SEZ6L | -0.39 | 0.039 | D |
| 2723 | FAM104A | -0.44 | 0.018 | D |
| 2752 | IL5RA | -0.52 | 0.005 | D |
| 2789 | CLU | -0.39 | 0.043 | D |
| 2835 | ADAMTS10 | -0.38 | 0.045 | D |
| 2865 | SPDYE3 | -0.46 | 0.013 | D |
| 2912 | PDS5B | -0.38 | 0.048 | D |
| 2913 | CYP2S1 | -0.55 | 0.002 | D |
| 3076 | TMEM183A | -0.38 | 0.045 | D |
| 3099 | PRKD2 | -0.51 | 0.006 | D |
| 3112 | RPL37A | -0.45 | 0.017 | D |


| 3168 | CYTH2 | -0.46 | 0.015 | D |
| :---: | :---: | :---: | :---: | :---: |
| 3182 | SLC5A7 | -0.45 | 0.017 | D |
| 3257 | C20orf112 | -0.50 | 0.007 | D |
| 3297 | GRIK2 | -0.39 | 0.039 | D |
| 3315 | PLCG1 | -0.41 | 0.028 | D |
| 3348 | RRM2B | -0.39 | 0.042 | D |
| 3465 | FBXO17 | -0.38 | 0.045 | D |
| 3491 | MED1 | -0.54 | 0.003 | D |
| 3497 | SLC12A3 | -0.40 | 0.037 | D |
| 3656 | GPBP1 | -0.62 | 0.000 | D |
| 3660 | METTL2B | -0.46 | 0.013 | D |
| 3670 | CEP68 | -0.38 | 0.048 | D |
| 3678 | TIAL1 | -0.42 | 0.028 | D |
| 3694 | TATDN1 | -0.55 | 0.003 | D |
| 3745 | ITM2C | -0.42 | 0.027 | D |
| 3751 | BRIX1 | -0.53 | 0.004 | D |
| 3889 | EMILIN2 | -0.45 | 0.017 | D |
| 3900 | REXO4 | -0.39 | 0.038 | D |
| 3923 | HTR1E | -0.41 | 0.031 | D |
| 4012 | LIPK | -0.40 | 0.034 | D |
| 4017 | SLC26A1 | -0.48 | 0.009 | D |
| 4047 | CCL13 | -0.39 | 0.039 | D |
| 4075 | TMEM30A | -0.46 | 0.014 | D |
| 4081 | OR1G1 | -0.46 | 0.014 | D |
| 4327 | SOX30 | -0.40 | 0.036 | D |
| 4339 | TEX11 | -0.39 | 0.042 | D |
| 4373 | RGAG4 | -0.41 | 0.032 | D |
| 4374 | TGIF2 | -0.42 | 0.028 | D |
| 4388 | HSDL2 | -0.54 | 0.003 | D |
| 4397 | KCNAB2 | -0.39 | 0.041 | D |
| 4438 | UBR5 | -0.56 | 0.002 | D |
| 4448 | CCL21 | -0.42 | 0.028 | D |
| 4456 | FGFR1OP2 | -0.48 | 0.009 | D |
| 4459 | LUC7L2 | -0.41 | 0.029 | D |
| 4515 | TAAR9 | -0.56 | 0.002 | D |
| 4522 | ZNF396 | -0.39 | 0.038 | D |
| 4539 | LRRC32 | -0.42 | 0.028 | D |
| 4548 | EFHA1 | -0.41 | 0.030 | D |


| 4555 | CSF3R | -0.42 | 0.024 | D |
| :---: | :---: | :---: | :---: | :---: |
| 4558 | PDLIM1 | -0.43 | 0.024 | D |
| 4571 | CDC26 | -0.52 | 0.005 | D |
| 4611 | KAT5 | -0.40 | 0.033 | D |
| 4623 | POP4 | -0.63 | 0.000 | D |
| 4666 | RASSF3 | -0.40 | 0.034 | D |
| 4748 | BID | -0.39 | 0.040 | D |
| 4777 | XAGE2B | -0.39 | 0.040 | D |
| 4824 | AGL | -0.44 | 0.018 | D |
| 4839 | IL16 | -0.39 | 0.040 | D |
| 5031 | SPRR2G | -0.48 | 0.010 | D |
| 5043 | CFHR1 | -0.38 | 0.045 | D |
| 5074 | KCNK7 | -0.43 | 0.022 | D |
| 5153 | LRCH4 | -0.40 | 0.035 | D |
| 5158 | DYRK1B | -0.45 | 0.017 | D |
| 5200 | TMEM67 | -0.52 | 0.004 | D |
| 5307 | ZDHHC11 | -0.46 | 0.013 | D |
| 5358 | PAIP1 | -0.57 | 0.002 | D |
| 5359 | MAP3K10 | -0.43 | 0.024 | D |
| 5396 | EPB41 | -0.39 | 0.042 | D |
| 5402 | CD3D | -0.40 | 0.033 | D |
| 5409 | AMICA1 | -0.55 | 0.003 | D |
| 5456 | AP2A1 | -0.42 | 0.027 | D |
| 5596 | TMEM128 | -0.39 | 0.040 | D |
| 5617 | NAGS | -0.40 | 0.034 | D |
| 5620 | TREML4 | -0.39 | 0.042 | D |
| 5671 | SKP2 | -0.38 | 0.048 | D |
| 5741 | C9orf21 | -0.38 | 0.048 | D |
| 5794 | TOMM40 | -0.51 | 0.006 | D |
| 5808 | KCNA10 | -0.42 | 0.027 | D |
| 5843 | C3orf67 | -0.47 | 0.013 | D |
| 5879 | YWHAG | -0.54 | 0.003 | D |
| 5883 | GALR1 | -0.50 | 0.007 | D |
| 5887 | SLC17A5 | -0.47 | 0.013 | D |
| 5920 | TMEM160 | -0.56 | 0.002 | D |
| 5942 | SAMD4B | -0.42 | 0.027 | D |
| 5957 | C14orf73 | -0.48 | 0.010 | D |
| 5967 | ALKBH4 | -0.39 | 0.041 | D |


| 5976 | PCGF6 | -0.43 | 0.021 | D |
| :---: | :---: | :---: | :---: | :---: |
| 6010 | HNRNPUL1 | -0.50 | 0.007 | D |
| 6011 | DDX17 | -0.41 | 0.031 | D |
| 6017 | METTL7A | -0.38 | 0.044 | D |
| 6024 | SLC43A2 | -0.46 | 0.015 | D |
| 6128 | C4orf33 | -0.41 | 0.030 | D |
| 6137 | SLC6A5 | -0.41 | 0.031 | D |
| 6154 | MRPS12 | -0.52 | 0.004 | D |
| 6190 | KAZ | -0.42 | 0.027 | D |
| 6311 | SERPINB9 | -0.46 | 0.013 | D |
| 6326 | XKRY | -0.46 | 0.013 | D |
| 6343 | LIMK1 | -0.41 | 0.029 | D |
| 6362 | HOMEZ | -0.39 | 0.041 | D |
| 6407 | TRIM10 | -0.41 | 0.031 | D |
| 6458 | XRN1 | -0.44 | 0.020 | D |
| 6467 | PAK1IP1 | -0.49 | 0.008 | D |
| 6520 | MTA2 | -0.38 | 0.047 | D |
| 6665 | TTTY14 | -0.38 | 0.043 | D |
| 6801 | ZNF451 | -0.44 | 0.018 | D |
| 6844 | TM7SF3 | -0.42 | 0.026 | D |
| 6879 | RBX1 | -0.45 | 0.016 | D |
| 6910 | TGS1 | -0.41 | 0.028 | D |
| 7003 | TAOK2 | -0.44 | 0.018 | D |
| 7059 | SRPK2 | -0.71 | 0.000 | D |
| 7062 | MLC1 | -0.38 | 0.045 | D |
| 7079 | BASP1 | -0.38 | 0.048 | D |
| 7093 | ERMN | -0.55 | 0.002 | D |
| 7106 | HSPD1 | -0.42 | 0.027 | D |
| 7176 | TMEM199 | -0.44 | 0.019 | D |
| 7242 | BRD9 | -0.43 | 0.023 | D |
| 7245 | EDDM3B | -0.39 | 0.040 | D |
| 7318 | TTC35 | -0.58 | 0.001 | D |
| 7334 | OVOS2 | -0.43 | 0.023 | D |
| 7335 | USP32 | -0.40 | 0.036 | D |
| 7396 | GPATCH8 | -0.47 | 0.012 | D |
| 7425 | RAD21 | -0.49 | 0.008 | D |
| 7448 | MAGI2 | -0.44 | 0.019 | D |
| 7449 | CPNE5 | -0.47 | 0.012 | D |


| 7469 | ASB16 | -0.48 | 0.010 | D |
| :---: | :---: | :---: | :---: | :---: |
| 7497 | VASP | -0.46 | 0.013 | D |
| 7582 | PCDHGC3 | -0.49 | 0.008 | D |
| 7637 | GJA9 | -0.44 | 0.020 | D |
| 7818 | ISM2 | -0.38 | 0.048 | D |
| 7840 | AKAP7 | -0.39 | 0.039 | D |
| 7865 | EGR3 | -0.48 | 0.009 | D |
| 7897 | PBLD | -0.40 | 0.036 | D |
| 7898 | NAA38 | -0.47 | 0.012 | D |
| 7918 | TSC22D2 | -0.44 | 0.020 | D |
| 7925 | FLOT2 | -0.39 | 0.041 | D |
| 7942 | DGKB | -0.38 | 0.048 | D |
| 7947 | PSORS1C1 | -0.46 | 0.013 | D |
| 7969 | TRIM33 | -0.41 | 0.030 | D |
| 8013 | CLEC18B | -0.43 | 0.023 | D |
| 8034 | DUS4L | -0.38 | 0.044 | D |
| 8042 | TBPL1 | -0.42 | 0.026 | D |
| 8075 | KATNAL1 | -0.40 | 0.035 | D |
| 8126 | SORD | -0.64 | 0.000 | D |
| 8134 | DBI | -0.48 | 0.010 | D |
| 8146 |  | -0.50 | 0.007 | D |
| 8153 | STX6 | -0.42 | 0.025 | D |
| 8223 | SSX5 | -0.38 | 0.048 | D |
| 8224 | ARRB1 | -0.57 | 0.002 | D |
| 8243 | SLC25A17 | -0.38 | 0.044 | D |
| 8244 | C14orf104 | -0.61 | 0.001 | D |
| 8285 | CAPN10 | -0.56 | 0.002 | D |
| 8287 | EIF3E | -0.45 | 0.016 | D |
| 8301 | SIRPG | -0.49 | 0.009 | D |
| 8304 | MRPL55 | -0.57 | 0.002 | D |
| 8326 | NUP62 | -0.55 | 0.003 | D |
| 8384 | CLASRP | -0.40 | 0.033 | D |
| 8389 | C9orf102 | -0.42 | 0.028 | D |
| 8497 | NCL | -0.40 | 0.036 | D |
| 8499 | C19orf2 | -0.51 | 0.005 | D |
| 8505 | POLR2K | -0.39 | 0.040 | D |
| 8531 | SACM1L | -0.44 | 0.018 | D |
| 8532 | SURF2 | -0.38 | 0.045 | D |


| 8576 | GNPTAB | -0.40 | 0.033 | D |
| :---: | :---: | :---: | :---: | :---: |
| 8583 | NCBP1 | -0.38 | 0.048 | D |
| 8612 | SUMO1 | -0.48 | 0.010 | D |
| 8623 | ARL5A | -0.42 | 0.027 | D |
| 8653 | SSX3 | -0.43 | 0.024 | D |
| 8664 | KSR1 | -0.42 | 0.028 | D |
| 8718 | PRMT2 | -0.40 | 0.033 | D |
| 8722 | ZNF80 | -0.51 | 0.006 | D |
| 8741 | FKBP5 | -0.43 | 0.023 | D |
| 8750 | XPA | -0.51 | 0.005 | D |
| 8765 | RUFY4 | -0.42 | 0.027 | D |
| 8809 | SMARCE1 | -0.38 | 0.048 | D |
| 8880 | GPBP1L1 | -0.47 | 0.012 | D |
| 8903 | ITM2C | -0.42 | 0.024 | D |
| 8983 | SPAG1 | -0.40 | 0.036 | D |
| 8997 |  | -0.50 | 0.007 | D |
| 8999 | HIF1A | -0.46 | 0.014 | D |
| 9073 | UBE2U | -0.40 | 0.035 | D |
| 9105 | FCGR2C | -0.39 | 0.040 | D |
| 9116 | TARS | -0.52 | 0.005 | D |
| 9117 | UTP6 | -0.47 | 0.011 | D |
| 9172 | TTBK1 | -0.43 | 0.023 | D |
| 9218 | CALM3 | -0.43 | 0.022 | D |
| 9247 | C6orf225 | -0.53 | 0.003 | D |
| 9269 | SPPL3 | -0.53 | 0.004 | D |
| 9271 | POLR2J2 | -0.40 | 0.036 | D |
| 9330 | PSMB1 | -0.38 | 0.044 | D |
| 9335 | DCAF13 | -0.52 | 0.004 | D |
| 9351 | PHF2 | -0.39 | 0.040 | D |
| 9367 | PDE6G | -0.45 | 0.016 | D |
| 9370 | STK38L | -0.61 | 0.001 | D |
| 9424 | EXOSC5 | -0.43 | 0.021 | D |
| 9473 | PTK2B | -0.40 | 0.037 | D |
| 9582 | C7orf11 | -0.40 | 0.035 | D |
| 9654 | DDHD1 | -0.43 | 0.022 | D |
| 9677 | SRPK2 | -0.38 | 0.048 | D |
| 9694 | ENY2 | -0.46 | 0.013 | D |
| 9697 | AGL | -0.46 | 0.013 | D |


| 9763 | UNC119 | -0.41 | 0.029 | D |
| :---: | :---: | :---: | :---: | :---: |
| 9779 | FGFR2 | -0.41 | 0.028 | D |
| 9788 | SHMT1 | -0.41 | 0.032 | D |
| 9805 | SCRIB | -0.42 | 0.025 | D |
| 9836 | KCNQ2 | -0.40 | 0.035 | D |
| 9838 | GLUD2 | -0.40 | 0.034 | D |
| 9847 | CELSR1 | -0.45 | 0.016 | D |
| 9868 | PABPC1 | -0.54 | 0.003 | D |
| 9872 | TAF1A | -0.43 | 0.021 | D |
| 9910 | MFAP4 | -0.39 | 0.041 | D |
| 9916 | MYO7B | -0.38 | 0.046 | D |
| 9940 | SIAH3 | -0.43 | 0.021 | D |
| 9999 | ABHD12B | -0.39 | 0.043 | D |
| 10003 | FAM117B | -0.40 | 0.036 | D |
| 10072 | RFC2 | -0.38 | 0.048 | D |
| 10090 | C15orf40 | -0.40 | 0.034 | D |
| 10092 | BRPF1 | -0.37 | 0.049 | D |
| 10123 | HYAL1 | -0.42 | 0.028 | D |
| 10206 | ZNF146 | -0.42 | 0.026 | D |
| 10240 | ZNF92 | -0.45 | 0.016 | D |
| 10246 | ARHGAP18 | -0.41 | 0.030 | D |
| 10396 | NAIP | -0.40 | 0.033 | D |
| 10409 | CASP4 | -0.41 | 0.031 | D |
| 10514 | MRPS27 | -0.48 | 0.010 | D |
| 10523 | GRK5 | -0.42 | 0.028 | D |
| 10670 | AKAP9 | -0.38 | 0.046 | D |
| 10681 | DPYSL2 | -0.41 | 0.030 | D |
| 10782 | OR5M8 | -0.38 | 0.049 | D |
| 10812 | TIMM8A | -0.39 | 0.039 | D |
| 10820 | RPS20 | -0.43 | 0.023 | D |
| 10830 | PAX2 | -0.51 | 0.005 | D |
| 10841 | SMC2 | -0.39 | 0.042 | D |
| 10891 | CBWD1 | -0.39 | 0.041 | D |
| 10908 | RASL11B | -0.42 | 0.026 | D |
| 10920 | WDR3 | -0.44 | 0.018 | D |
| 10933 | KRT85 | -0.38 | 0.047 | D |
| 11019 | C2orf69 | -0.45 | 0.016 | D |
| 11065 | C13orf33 | -0.46 | 0.015 | D |


| 11075 | TLR8 | -0.38 | 0.046 | D |
| :---: | :---: | :---: | :---: | :---: |
| 11125 | LCE1D | -0.37 | 0.050 | D |
| 11160 | ICK | -0.39 | 0.041 | D |
| 11161 | SMARCD1 | -0.38 | 0.046 | D |
| 11197 | HAT1 | -0.41 | 0.029 | D |
| 11294 | ANXA4 | -0.38 | 0.046 | D |
| 11399 | NSUN2 | -0.40 | 0.036 | D |
| 11437 | CSF2RB | -0.45 | 0.015 | D |
| 11439 | NUDT15 | -0.43 | 0.021 | D |
| 11441 | CREB3L3 | -0.43 | 0.024 | D |
| 11446 | CCDC34 | -0.51 | 0.005 | D |
| 11480 | N6AMT2 | -0.42 | 0.026 | D |
| 11516 | H2AFV | -0.39 | 0.042 | D |
| 11592 |  | -0.46 | 0.014 | D |
| 11594 | TDGF3 | -0.42 | 0.028 | D |
| 11623 | NUMBL | -0.49 | 0.009 | D |
| 11626 | LIG4 | -0.39 | 0.040 | D |
| 11629 | TSPAN11 | -0.51 | 0.006 | D |
| 11663 | EPHA10 | -0.68 | 0.000 | D |
| 11757 | SH2B2 | -0.43 | 0.021 | D |
| 11774 | C10orf120 | -0.41 | 0.030 | D |
| 11830 | DISC1 | -0.43 | 0.023 | D |
| 11853 | AHNAK | -0.51 | 0.006 | D |
| 11859 | C6orf211 | -0.43 | 0.022 | D |
| 11884 | ARFGEF1 | -0.59 | 0.001 | D |
| 11897 | TIAF1 | -0.38 | 0.049 | D |
| 11921 | GRM6 | -0.46 | 0.014 | D |
| 11922 | RPL18 | -0.51 | 0.005 | D |
| 11973 | ST6GALNAC6 | -0.44 | 0.020 | D |
| 12050 | OVOS2 | -0.51 | 0.006 | D |
| 12064 | NCK1 | -0.38 | 0.046 | D |
| 12083 | XPO4 | -0.54 | 0.003 | D |
| 12094 | C11orf73 | -0.58 | 0.001 | D |
| 12160 | GPR151 | -0.44 | 0.019 | D |
| 12279 | KIR2DL5A | -0.39 | 0.038 | D |
| 12330 | MTDH | -0.41 | 0.032 | D |
| 12338 | TMEM167A | -0.62 | 0.000 | D |
| 12489 | EHMT2 | -0.48 | 0.010 | D |


| 12582 | DEDD2 | -0.38 | 0.047 | D |
| :---: | :---: | :---: | :---: | :---: |
| 12607 | SMAD7 | -0.60 | 0.001 | D |
| 12626 | E2F3 | -0.47 | 0.012 | D |
| 12645 | U2AF1 | -0.48 | 0.010 | D |
| 12707 | FAM103A1 | -0.45 | 0.017 | D |
| 12712 | PRR3 | -0.48 | 0.010 | D |
| 12717 | HEBP2 | -0.38 | 0.045 | D |
| 12751 | CTR9 | -0.44 | 0.019 | D |
| 12765 | OSBPL8 | -0.51 | 0.006 | D |
| 12768 | SGK3 | -0.42 | 0.025 | D |
| 12802 | PUS7 | -0.47 | 0.011 | D |
| 12830 | CTCFL | -0.40 | 0.037 | D |
| 12864 | PLEKHO2 | -0.48 | 0.009 | D |
| 12947 | PGBD1 | -0.40 | 0.034 | D |
| 12989 | CD86 | -0.52 | 0.004 | D |
| 13149 | C4orf41 | -0.43 | 0.022 | D |
| 13222 | ZNRD1 | -0.40 | 0.035 | D |
| 13294 | ICK | -0.42 | 0.028 | D |
| 13318 | DDX4 | -0.38 | 0.049 | D |
| 13389 | PCDH8 | -0.53 | 0.004 | D |
| 13418 | ITGAE | -0.41 | 0.030 | D |
| 13473 | REG3A | -0.48 | 0.009 | D |
| 13506 | LAIR1 | -0.50 | 0.007 | D |
| 13599 | ABL1 | -0.43 | 0.024 | D |
| 13609 | C22orf9 | -0.46 | 0.015 | D |
| 13628 | LGALS12 | -0.56 | 0.002 | D |
| 13642 | PI4K2B | -0.45 | 0.016 | D |
| 13674 | LOC84856 | -0.47 | 0.012 | D |
| 13695 | NUP62 | -0.41 | 0.030 | D |
| 13750 | LRRC37B | -0.44 | 0.018 | D |
| 13779 | BPI | -0.41 | 0.030 | D |
| 13795 | CHRNA2 | -0.38 | 0.045 | D |
| 13803 | CMTM2 | -0.43 | 0.023 | D |
| 13804 | MTPN | -0.42 | 0.024 | D |
| 13805 | ELOVL5 | -0.40 | 0.033 | D |
| 13820 | MRPL13 | -0.39 | 0.039 | D |
| 13851 | IFT122 | -0.42 | 0.025 | D |
| 13911 | TOP1MT | -0.54 | 0.003 | D |


| 13926 | C19orf2 | -0.44 | 0.020 | D |
| :---: | :---: | :---: | :---: | :---: |
| 13970 | PMPCB | -0.37 | 0.050 | D |
| 14033 | BDH2 | -0.49 | 0.008 | D |
| 14046 | SREBF1 | -0.44 | 0.020 | D |
| 14157 | SSRP1 | -0.39 | 0.040 | D |
| 14183 | EFS | -0.39 | 0.039 | D |
| 14326 | RNF166 | -0.43 | 0.022 | D |
| 14383 | STRN4 | -0.39 | 0.042 | D |
| 14476 | ELK4 | -0.38 | 0.045 | D |
| 14583 | KCNJ10 | -0.38 | 0.046 | D |
| 14591 | DEK | -0.42 | 0.026 | D |
| 14611 | MRPL32 | -0.41 | 0.032 | D |
| 14667 | KIF21B | -0.39 | 0.040 | D |
| 14674 | GFRA2 | -0.46 | 0.015 | D |
| 14744 | ECE2 | -0.47 | 0.012 | D |
| 14794 | LSM2 | -0.53 | 0.004 | D |
| 14795 | UFM1 | -0.39 | 0.042 | D |
| 14800 | GSR | -0.43 | 0.022 | D |
| 14843 | HOXD12 | -0.38 | 0.044 | D |
| 14863 | FSCN1 | -0.38 | 0.043 | D |
| 14867 | NDUFA8 | -0.43 | 0.022 | D |
| 14871 | PTTG2 | -0.50 | 0.007 | D |
| 14877 | GDA | -0.45 | 0.017 | D |
| 14907 | EEF1G | -0.44 | 0.019 | D |
| 15016 | WRB | -0.47 | 0.012 | D |
| 15070 | PNMA2 | -0.44 | 0.020 | D |
| 15091 | AAMP | -0.41 | 0.032 | D |
| 15096 | OR10G4 | -0.42 | 0.025 | D |
| 15169 | CTNNA2 | -0.42 | 0.026 | D |
| 15204 | DYRK1B | -0.39 | 0.041 | D |
| 15234 | ZFYVE27 | -0.41 | 0.031 | D |
| 15242 | HIATL1 | -0.51 | 0.005 | D |
| 15298 | CAPZB | -0.43 | 0.021 | D |
| 15309 | CTRC | -0.41 | 0.030 | D |
| 15333 | SEPT4 | -0.40 | 0.037 | D |
| 15383 | NOX1 | -0.44 | 0.020 | D |
| 15389 | SARS2 | -0.55 | 0.002 | D |
| 15403 | LMX1A | -0.56 | 0.002 | D |


| 15436 | CLTC | -0.47 | 0.012 | D |
| :---: | :---: | :---: | :---: | :---: |
| 15493 | ACSM2B | -0.41 | 0.031 | D |
| 15517 | EIF3K | -0.51 | 0.006 | D |
| 15575 | DIS3L2 | -0.51 | 0.005 | D |
| 15658 | FAM8A1 | -0.39 | 0.042 | D |
| 15668 | ACTL6B | -0.44 | 0.018 | D |
| 15809 | GMNN | -0.41 | 0.031 | D |
| 15815 | MYLIP | -0.42 | 0.027 | D |
| 15846 | PLXDC1 | -0.38 | 0.044 | D |
| 15877 | CAMK2A | -0.39 | 0.042 | D |
| 15910 | FLJ42102 | -0.49 | 0.008 | D |
| 15918 | PAOX | -0.41 | 0.032 | D |
| 15948 | DCD | -0.44 | 0.020 | D |
| 16000 | FAM172A | -0.38 | 0.044 | D |
| 16084 | LDHAL6A | -0.45 | 0.018 | D |
| 16088 | CTBP2 | -0.41 | 0.031 | D |
| 16095 | FBL | -0.62 | 0.000 | D |
| 16101 | MAFF | -0.38 | 0.043 | D |
| 16112 | NKX6-2 | -0.39 | 0.040 | D |
| 16117 | SYNCRIP | -0.39 | 0.042 | D |
| 16155 | SIRT2 | -0.42 | 0.026 | D |
| 16202 | CCHCR1 | -0.43 | 0.022 | D |
| 16280 | TCF3 | -0.42 | 0.024 | D |
| 16293 | MED23 | -0.39 | 0.039 | D |
| 16356 | HTATSF1 | -0.38 | 0.043 | D |
| 16538 | ATXN1 | -0.57 | 0.002 | D |
| 16578 | SMR3A | -0.52 | 0.005 | D |
| 16630 | DSG4 | -0.44 | 0.018 | D |
| 16654 | HSPA4 | -0.40 | 0.037 | D |
| 16665 | PLAA | -0.42 | 0.026 | D |
| 16673 | PPP2R3A | -0.40 | 0.037 | D |
| 16698 | ELOVL7 | -0.39 | 0.038 | D |
| 16713 | OR6B3 | -0.42 | 0.027 | D |
| 16757 | PIPOX | -0.45 | 0.015 | D |
| 16785 | SERF1B | -0.39 | 0.042 | D |
| 16803 | KRT73 | -0.39 | 0.040 | D |
| 16832 | RAD1 | -0.47 | 0.012 | D |
| 16888 | PIGX | -0.39 | 0.040 | D |


| 16892 | NR1I3 | -0.44 | 0.020 | D |
| :---: | :---: | :---: | :---: | :---: |
| 17003 | MYBPC2 | -0.38 | 0.047 | D |
| 17029 | COL9A1 | -0.44 | 0.018 | D |
| 17100 | HIST1H2BB | -0.45 | 0.015 | D |
| 17102 | C22orf42 | -0.46 | 0.014 | D |
| 17130 | PRR18 | -0.45 | 0.016 | D |
| 17134 | FBXO30 | -0.58 | 0.001 | D |
| 17203 | TDRD7 | -0.42 | 0.026 | D |
| 17262 | PHF20L1 | -0.39 | 0.039 | D |
| 17278 | FAM162A | -0.41 | 0.029 | D |
| 17281 | PSIP1 | -0.42 | 0.025 | D |
| 17290 | NAA35 | -0.41 | 0.031 | D |
| 17296 | FOXN3 | -0.38 | 0.049 | D |
| 17310 | RALGAPA2 | -0.46 | 0.013 | D |
| 17344 | ABHD15 | -0.41 | 0.029 | D |
| 17345 | ANKRD55 | -0.38 | 0.044 | D |
| 17347 | MOG | -0.42 | 0.026 | D |
| 17371 | STRBP | -0.39 | 0.038 | D |
| 17376 | GHRHR | -0.46 | 0.013 | D |
| 17383 | PPP2R3B | -0.38 | 0.045 | D |
| 17388 | CCL23 | -0.39 | 0.042 | D |
| 17389 | GALNT9 | -0.42 | 0.028 | D |
| 17390 | GNLY | -0.41 | 0.031 | D |
| 17422 | C2orf65 | -0.52 | 0.005 | D |
| 17431 | RAB2A | -0.43 | 0.023 | D |
| 17499 | COX7A1 | -0.43 | 0.021 | D |
| 17527 | MOV10L1 | -0.51 | 0.005 | D |
| 17597 | OR1L6 | -0.46 | 0.014 | D |
| 17600 | CMTM1 | -0.41 | 0.029 | D |
| 17689 | EED | -0.38 | 0.045 | D |
| 17732 | HLA-C | -0.39 | 0.040 | D |
| 17733 | CCDC132 | -0.40 | 0.033 | D |
| 17740 | GJA3 | -0.40 | 0.036 | D |
| 17776 | AATK | -0.42 | 0.027 | D |
| 17808 | LTF | -0.38 | 0.049 | D |
| 17834 | OTUD6B | -0.50 | 0.006 | D |
| 17843 | CIC | -0.38 | 0.044 | D |
| 17846 | IKZF4 | -0.58 | 0.001 | D |


| 17854 | CASP6 | -0.48 | 0.010 | D |
| :---: | :---: | :---: | :---: | :---: |
| 17905 | RPS11 | -0.38 | 0.047 | D |
| 17923 | RAMP2 | -0.40 | 0.034 | D |
| 17952 | C6orf120 | -0.44 | 0.020 | D |
| 17987 | ING3 | -0.49 | 0.008 | D |
| 18059 | ING1 | -0.44 | 0.018 | D |
| 18060 | ECHS1 | -0.37 | 0.049 | D |
| 18064 | ANKRD27 | -0.59 | 0.001 | D |
| 18107 | TNFRSF9 | -0.45 | 0.016 | D |
| 18111 | PRR3 | -0.42 | 0.026 | D |
| 18143 | AZU1 | -0.49 | 0.009 | D |
| 18204 | SNTA1 | -0.43 | 0.021 | D |
| 18206 | MDGA1 | -0.38 | 0.046 | D |
| 18323 | EED | -0.46 | 0.013 | D |
| 18350 | SF1 | -0.38 | 0.044 | D |
| 18360 | CPSF4 | -0.38 | 0.048 | D |
| 18364 | TMEM183B | -0.40 | 0.035 | D |
| 18398 | GPX1 | -0.41 | 0.030 | D |
| 18585 | GGN | -0.41 | 0.031 | D |
| 18592 | HNRNPK | -0.55 | 0.002 | D |
| 18619 | CDK12 | -0.40 | 0.037 | D |
| 18641 | SNRPD2 | -0.51 | 0.005 | D |
| 18668 | ABCG1 | -0.41 | 0.032 | D |
| 18690 | EFCAB2 | -0.54 | 0.003 | D |
| 18702 | FAM163B | -0.43 | 0.022 | D |
| 18706 | C9orf9 | -0.38 | 0.048 | D |
| 18730 | IKBKAP | -0.48 | 0.010 | D |
| 18758 | TOP1MT | -0.44 | 0.020 | D |
| 18768 | SULT1C3 | -0.40 | 0.033 | D |
| 18787 | FBXO24 | -0.63 | 0.000 | D |
| 18807 | CYP21A2 | -0.41 | 0.032 | D |
| 18809 | NKX6-1 | -0.47 | 0.011 | D |
| 18876 | BTNL8 | -0.45 | 0.016 | D |
| 18879 | BEND4 | -0.43 | 0.024 | D |
| 18897 |  | -0.41 | 0.029 | D |
| 18907 | LOH12CR1 | -0.40 | 0.033 | D |
| 18969 | SEPT4 | -0.48 | 0.009 | D |
| 19024 | PIH1D1 | -0.39 | 0.042 | D |


| 19030 | ANKRD13B | -0.45 | 0.015 | D |
| :---: | :---: | :---: | :---: | :---: |
| 19090 | PDGFRB | -0.39 | 0.040 | D |
| 19130 | KCNQ3 | -0.39 | 0.040 | D |
| 19151 | DBR1 | -0.43 | 0.023 | D |
| 19160 | IGSF10 | -0.43 | 0.024 | D |
| 19176 | PPP4R2 | -0.39 | 0.038 | D |
| 19192 | SARS | -0.40 | 0.034 | D |
| 19242 | PPP1R14A | -0.43 | 0.023 | D |
| 19244 | ZNF3 | -0.39 | 0.040 | D |
| 19256 | NNT | -0.48 | 0.010 | D |
| 19294 | PPP2R4 | -0.45 | 0.015 | D |
| 19375 | TALDO1 | -0.39 | 0.038 | D |
| 19398 | CNGA3 | -0.40 | 0.034 | D |
| 19406 | ZFR | -0.53 | 0.004 | D |
| 19425 | ABCG1 | -0.38 | 0.047 | D |
| 19452 | RPL13 | -0.41 | 0.032 | D |
| 19513 | OR1S2 | -0.54 | 0.003 | D |
| 19521 | RHOJ | -0.51 | 0.005 | D |
| 19550 | DNAH7 | -0.42 | 0.026 | D |
| 19695 | ABLIM1 | -0.58 | 0.001 | D |
| 19705 | TOP1MT | -0.47 | 0.013 | D |
| 19709 | PTER | -0.39 | 0.041 | D |
| 19725 | EGLN3 | -0.49 | 0.008 | D |
| 19741 | SPRR4 | -0.44 | 0.019 | D |
| 19751 | NEDD9 | -0.50 | 0.006 | D |
| 19805 | SLC2A6 | -0.38 | 0.049 | D |
| 19806 | FAM108B1 | -0.53 | 0.004 | D |
| 19813 | GDI2 | -0.46 | 0.014 | D |
| 19849 | CUL3 | -0.40 | 0.033 | D |
| 19869 | TBX5 | -0.39 | 0.038 | D |
| 19872 | NLK | -0.48 | 0.010 | D |
| 19903 | ZBTB3 | -0.41 | 0.030 | D |
| 19993 | PCMT1 | -0.51 | 0.006 | D |
| 20011 | PSMD11 | -0.38 | 0.047 | D |
| 20054 | RAB14 | -0.38 | 0.046 | D |
| 20057 | OR4F15 | -0.40 | 0.035 | D |
| 20103 | ITGB1BP3 | -0.56 | 0.002 | D |
| 20148 | ARL5A | -0.50 | 0.007 | D |


| 20197 | RPL23AP64 | -0.55 | 0.003 | D |
| :---: | :---: | :---: | :---: | :---: |
| 20202 | PPP2R5C | -0.41 | 0.032 | D |
| 20230 | SEMA4D | -0.42 | 0.026 | D |
| 20335 | C17orf50 | -0.45 | 0.017 | D |
| 20349 | ARL4A | -0.41 | 0.030 | D |
| 20371 | HRSP12 | -0.52 | 0.005 | D |
| 20461 | SULF2 | -0.38 | 0.044 | D |
| 20504 | ITPA | -0.39 | 0.042 | D |
| 20554 | MDK | -0.45 | 0.015 | D |
| 20581 | CWC27 | -0.61 | 0.001 | D |
| 20785 | C19orf12 | -0.50 | 0.007 | D |
| 20805 | CST11 | -0.43 | 0.024 | D |
| 20814 | PRMT1 | -0.47 | 0.012 | D |
| 21046 | CCNB1IP1 | -0.49 | 0.009 | D |
| 21064 | FKBP3 | -0.50 | 0.007 | D |
| 21082 | MRPS28 | -0.38 | 0.046 | D |
| 21179 | FAM122A | -0.42 | 0.025 | D |
| 21204 | CHEK2 | -0.38 | 0.043 | D |
| 21238 | KLHL25 | -0.41 | 0.032 | D |
| 21252 | PRKD2 | -0.47 | 0.011 | D |
| 21310 | KLF8 | -0.43 | 0.021 | D |
| 21349 | TLR1 | -0.48 | 0.010 | D |
| 21353 | SPACA4 | -0.41 | 0.031 | D |
| 21368 | SMNDC1 | -0.41 | 0.032 | D |
| 21372 | IQGAP1 | -0.40 | 0.036 | D |
| 21426 | RBPJL | -0.42 | 0.027 | D |
| 21473 | ARMC8 | -0.52 | 0.004 | D |
| 21506 | EPB41L1 | -0.38 | 0.044 | D |
| 21536 | HNRPLL | -0.41 | 0.029 | D |
| 21546 | BCAT2 | -0.42 | 0.027 | D |
| 21554 | RAET1G | -0.41 | 0.029 | D |
| 21586 | C14orf19 | -0.41 | 0.030 | D |
| 21597 | ENTPD2 | -0.43 | 0.023 | D |
| 21611 | SNX16 | -0.45 | 0.016 | D |
| 21622 | SLCO2B1 | -0.40 | 0.035 | D |
| 21637 | OR8D4 | -0.43 | 0.022 | D |
| 21669 | LPHN1 | -0.39 | 0.038 | D |
| 21724 | TCF7 | -0.43 | 0.021 | D |


| 21734 | GRXCR2 | -0.42 | 0.027 | D |
| :---: | :---: | :---: | :---: | :---: |
| 21737 | NAP1L1 | -0.40 | 0.033 | D |
| 21761 | RAB24 | -0.38 | 0.044 | D |
| 21769 | RAD23B | -0.40 | 0.037 | D |
| 21800 | OR4C13 | -0.41 | 0.029 | D |
| 21815 | ARPP19 | -0.56 | 0.002 | D |
| 21819 | LPHN3 | -0.45 | 0.016 | D |
| 21863 | WDR75 | -0.40 | 0.036 | D |
| 21898 | GNA13 | -0.38 | 0.049 | D |
| 21903 | PEX5 | -0.42 | 0.024 | D |
| 21906 | CCDC97 | -0.38 | 0.044 | D |
| 21907 | PITX2 | -0.48 | 0.010 | D |
| 21918 | NRAP | -0.48 | 0.010 | D |
| 21920 | TRIM36 | -0.40 | 0.035 | D |
| 21930 | OR51M1 | -0.52 | 0.004 | D |
| 21949 | ZNHIT3 | -0.44 | 0.018 | D |
| 21953 | UEVLD | -0.70 | 0.000 | D |
| 21997 | DGKZ | -0.51 | 0.006 | D |
| 22004 | INTS8 | -0.48 | 0.011 | D |
| 22075 | YY1 | -0.41 | 0.031 | D |
| 22099 | LMOD1 | -0.41 | 0.032 | D |
| 22169 | TOX4 | -0.50 | 0.007 | D |
| 22226 | CYP2S1 | -0.41 | 0.031 | D |
| 22241 | USP8 | -0.42 | 0.025 | D |
| 22243 | TLK1 | -0.50 | 0.007 | D |
| 22265 | MYL6B | -0.42 | 0.024 | D |
| 22314 | TSSK4 | -0.39 | 0.041 | D |
| 22379 | RPL12 | -0.39 | 0.043 | D |
| 22511 | CHCHD5 | -0.40 | 0.037 | D |
| 22574 | ACTR3 | -0.44 | 0.018 | D |
| 22697 | NOP2 | -0.38 | 0.045 | D |
| 22700 | TERF1 | -0.45 | 0.016 | D |
| 22717 | ADIPOR2 | -0.38 | 0.043 | D |
| 22727 | SPIC | -0.42 | 0.026 | D |
| 22786 | MRPS12 | -0.46 | 0.014 | D |
| 22793 | SLMO1 | -0.52 | 0.005 | D |
| 22795 | ATP11A | -0.41 | 0.031 | D |
| 22814 | SSX3 | -0.46 | 0.015 | D |


| 22842 | FAM153C | -0.55 | 0.003 | D |
| :---: | :---: | :---: | :---: | :---: |
| 22905 | SNCG | -0.44 | 0.018 | D |
| 22919 | AMY2B | -0.43 | 0.023 | D |
| 22931 | C9orf41 | -0.39 | 0.040 | D |
| 22978 | C1orf212 | -0.50 | 0.007 | D |
| 22984 | ZNF226 | -0.38 | 0.048 | D |
| 23088 | SPINT4 | -0.41 | 0.029 | D |
| 23092 | TUBB2B | -0.40 | 0.036 | D |
| 23131 | PFKM | -0.48 | 0.010 | D |
| 23154 | RTCD1 | -0.38 | 0.048 | D |
| 23187 | PMFBP1 | -0.37 | 0.049 | D |
| 23224 | CASQ1 | -0.41 | 0.029 | D |
| 23253 | C7orf49 | -0.38 | 0.048 | D |
| 23285 | LCOR | -0.40 | 0.036 | D |
| 23298 | FOLR4 | -0.47 | 0.011 | D |
| 23421 | CUL4A | -0.42 | 0.025 | D |
| 23429 | ABCD4 | -0.49 | 0.009 | D |
| 23530 | DDX59 | -0.45 | 0.017 | D |
| 23547 | KBTBD7 | -0.47 | 0.011 | D |
| 23618 | C6orf106 | -0.41 | 0.032 | D |
| 23649 | CLEC1A | -0.37 | 0.050 | D |
| 23709 | SNX4 | -0.47 | 0.011 | D |
| 23724 | SGK2 | -0.42 | 0.028 | D |
| 23729 | REEP2 | -0.41 | 0.032 | D |
| 23767 | PYHIN1 | -0.47 | 0.012 | D |
| 23776 | OR2W5 | -0.42 | 0.026 | D |
| 23796 | CNBP | -0.45 | 0.017 | D |
| 23880 | ZFAND1 | -0.49 | 0.008 | D |
| 23902 | BTN1A1 | -0.42 | 0.025 | D |
| 23907 | P2RY10 | -0.44 | 0.019 | D |
| 23908 | ZNF707 | -0.39 | 0.039 | D |
| 23938 | RABL2A | -0.53 | 0.004 | D |
| 24007 | CLDN18 | -0.38 | 0.049 | D |
| 24017 | LOC401589 | -0.38 | 0.047 | D |
| 24157 | NKAIN4 | -0.45 | 0.017 | D |
| 24230 | KRTAP20-2 | -0.40 | 0.036 | D |
| 24244 | ITCH | -0.40 | 0.036 | D |
| 24248 | ELMO1 | -0.41 | 0.030 | D |


| 24270 | DHFRL1 | -0.42 | 0.024 | D |
| :---: | :---: | :---: | :---: | :---: |
| 24286 | LOC441956 | -0.57 | 0.001 | D |
| 24386 | HTR3D | -0.44 | 0.019 | D |
| 24389 | PABPN1 | -0.50 | 0.007 | D |
| 24393 | HIST1H2BL | -0.37 | 0.050 | D |
| 24394 | SLC22A2 | -0.40 | 0.036 | D |
| 24433 | SLCO1A2 | -0.49 | 0.008 | D |
| 24457 | MOBKL2C | -0.40 | 0.034 | D |
| 566 | PTER | 0.38 | 0.047 | U |
| 5326 | PRAMEF17 | 0.41 | 0.033 | U |
| 13225 | TRAF3IP2 | 0.38 | 0.044 | U |
| 19409 | CMTM4 | 0.38 | 0.045 | U |
| 24236 | DAOA | 0.41 | 0.030 | U |
| 1324 | OR2W3 | 0.40 | 0.035 | U |
| 11418 | SPATA6 | 0.60 | 0.001 | U |
| 16667 | RPS27 | 0.38 | 0.049 | U |
| 19463 | HIST2H2AC | 0.37 | 0.049 | U |
| 19489 | ZNF653 | 0.44 | 0.020 | U |
| 21055 | DHPS | 0.44 | 0.018 | U |
| 22748 | DOCK3 | 0.50 | 0.007 | U |
| 23090 | FOXD4L3 | 0.38 | 0.045 | U |
| 23183 | C7orf62 | 0.42 | 0.027 | U |
| 23236 | PMS2CL | 0.54 | 0.003 | U |
| 4261 | UNC93A | 0.38 | 0.045 | U |
| 9250 | CPEB3 | 0.45 | 0.016 | U |
| 13076 | TMEM19 | 0.43 | 0.021 | U |
| 16703 | CLCN5 | 0.41 | 0.030 | U |
| 539 | GPR83 | 0.47 | 0.012 | U |
| 983 | FAM134B | 0.40 | 0.037 | U |
| 1756 | KDELR3 | 0.40 | 0.034 | U |
| 2385 | TMEM134 | 0.48 | 0.009 | U |
| 2590 | SYTL2 | 0.42 | 0.025 | U |
| 2716 | GMPPA | 0.51 | 0.005 | U |
| 3326 | C19orf10 | 0.53 | 0.004 | U |
| 3537 | COPE | 0.39 | 0.039 | U |
| 4346 | ST3GAL1 | 0.43 | 0.021 | U |
| 5568 | ASL | 0.40 | 0.037 | U |
| 5714 | C11orf63 | 0.58 | 0.001 | U |


| 6179 | NPDC1 | 0.49 | 0.008 | U |
| :---: | :---: | :---: | :---: | :---: |
| 7933 | XBP1 | 0.50 | 0.007 | U |
| 8805 | NOMO1 | 0.42 | 0.027 | U |
| 9465 | ZNF141 | 0.46 | 0.014 | U |
| 9849 | TMF1 | 0.40 | 0.035 | U |
| 10487 | THNSL2 | 0.54 | 0.003 | U |
| 11955 | CORO1B | 0.47 | 0.012 | U |
| 12138 | UNC13A | 0.48 | 0.010 | U |
| 12727 | EDA | 0.49 | 0.008 | U |
| 13316 | SPDYA | 0.42 | 0.027 | U |
| 14896 | LGR4 | 0.46 | 0.014 | U |
| 14984 | ALS2CL | 0.38 | 0.043 | U |
| 17211 | CORO1B | 0.38 | 0.044 | U |
| 18154 | XBP1 | 0.48 | 0.011 | U |
| 18231 | TMEM134 | 0.49 | 0.009 | U |
| 18751 | KIAA0513 | 0.46 | 0.013 | U |
| 18865 | PC | 0.40 | 0.035 | U |
| 20007 | MGAT4A | 0.41 | 0.028 | U |
| 20270 | LONRF2 | 0.39 | 0.042 | U |
| 20514 | FAM110C | 0.51 | 0.005 | U |
| 22872 | SLMO2 | 0.49 | 0.009 | U |
| 23810 | SERINC3 | 0.41 | 0.031 | U |
| 17 | OR1J2 | 0.49 | 0.009 | U |
| 63 | PDIA6 | 0.56 | 0.002 | U |
| 91 | OR8H2 | 0.39 | 0.040 | U |
| 112 | HIST2H2BF | 0.53 | 0.003 | U |
| 115 | OGDH | 0.46 | 0.013 | U |
| 292 | LPGAT1 | 0.38 | 0.045 | U |
| 305 | BOLA2 | 0.44 | 0.020 | U |
| 430 | CLCNKB | 0.38 | 0.045 | U |
| 440 | CD8B | 0.39 | 0.039 | U |
| 441 | OR4C11 | 0.38 | 0.043 | U |
| 488 | RABEP2 | 0.48 | 0.010 | U |
| 683 | AIM2 | 0.43 | 0.021 | U |
| 700 | NBPF1 | 0.42 | 0.026 | U |
| 716 | ACBD5 | 0.41 | 0.032 | U |
| 724 | MAN2C1 | 0.39 | 0.040 | U |
| 752 | SLITRK2 | 0.43 | 0.024 | U |


| 780 | ANKRD36B | 0.39 | 0.039 | U |
| :---: | :---: | :---: | :---: | :---: |
| 802 | GPR89B | 0.44 | 0.018 | U |
| 854 | TCEAL8 | 0.38 | 0.047 | U |
| 934 | SETD3 | 0.38 | 0.044 | U |
| 1069 | MUTYH | 0.39 | 0.041 | U |
| 1183 | AMPH | 0.47 | 0.011 | U |
| 1241 | KCNRG | 0.38 | 0.048 | U |
| 1261 | PDLIM5 | 0.63 | 0.000 | U |
| 1279 | MTX1 | 0.38 | 0.048 | U |
| 1301 | TMCO4 | 0.42 | 0.026 | U |
| 1401 | ALG9 | 0.47 | 0.012 | U |
| 1451 | MT2A | 0.42 | 0.026 | U |
| 1474 | PARD6A | 0.46 | 0.014 | U |
| 1500 | ROPN1B | 0.45 | 0.017 | U |
| 1520 | PRSS50 | 0.46 | 0.013 | U |
| 1564 | WDR45 | 0.42 | 0.027 | U |
| 1635 | RRM2 | 0.44 | 0.019 | U |
| 1669 | TMEM79 | 0.38 | 0.045 | U |
| 1683 | TAOK2 | 0.38 | 0.048 | U |
| 1733 | PRDX5 | 0.39 | 0.038 | U |
| 1758 | SOS2 | 0.39 | 0.043 | U |
| 1836 | MAPK10 | 0.40 | 0.037 | U |
| 1911 | ETFDH | 0.45 | 0.016 | U |
| 1942 | ACADVL | 0.52 | 0.004 | U |
| 1991 | RBPMS | 0.47 | 0.011 | U |
| 2007 | SLC10A7 | 0.41 | 0.032 | U |
| 2087 | ZNF2 | 0.38 | 0.045 | U |
| 2262 | MRGPRX2 | 0.39 | 0.038 | U |
| 2305 | OR6C1 | 0.40 | 0.033 | U |
| 2497 | FBXO15 | 0.42 | 0.025 | U |
| 2663 | HGF | 0.46 | 0.015 | U |
| 2826 | USP1 | 0.47 | 0.012 | U |
| 2898 | PTPRC | 0.42 | 0.028 | U |
| 2931 | DEDD | 0.39 | 0.038 | U |
| 2994 | NR1I2 | 0.39 | 0.040 | U |
| 3006 | PPM1G | 0.39 | 0.042 | U |
| 3171 | DRP2 | 0.41 | 0.031 | U |
| 3177 | FAM21C | 0.39 | 0.040 | U |


| 3185 | TCTN3 | 0.41 | 0.032 | U |
| :---: | :---: | :---: | :---: | :---: |
| 3203 | IFI6 | 0.38 | 0.045 | U |
| 3291 | CCL1 | 0.41 | 0.029 | U |
| 3311 | COG7 | 0.38 | 0.047 | U |
| 3329 | SEC61A1 | 0.42 | 0.027 | U |
| 3352 | STT3B | 0.50 | 0.006 | U |
| 3399 | POLD4 | 0.38 | 0.046 | U |
| 3459 | HM13 | 0.46 | 0.013 | U |
| 3486 | VPS13C | 0.38 | 0.046 | U |
| 3571 | ZNF354C | 0.40 | 0.035 | U |
| 3617 | UBFD1 | 0.43 | 0.021 | U |
| 3721 | C15orf48 | 0.40 | 0.034 | U |
| 3733 | GPHN | 0.39 | 0.042 | U |
| 3799 | MT1G | 0.39 | 0.040 | U |
| 3808 | ADAM3A | 0.46 | 0.014 | U |
| 3844 | ACADVL | 0.38 | 0.044 | U |
| 3879 | ZCCHC13 | 0.52 | 0.005 | U |
| 3901 | LCLAT1 | 0.40 | 0.037 | U |
| 3949 | WDR83 | 0.41 | 0.029 | U |
| 3955 | AMBN | 0.37 | 0.050 | U |
| 4042 | GNAT2 | 0.50 | 0.006 | U |
| 4071 | PHKB | 0.43 | 0.023 | U |
| 4105 | PATZ1 | 0.39 | 0.040 | U |
| 4141 | ACADVL | 0.44 | 0.019 | U |
| 4150 | TBC1D29 | 0.43 | 0.023 | U |
| 4320 | SOBP | 0.44 | 0.019 | U |
| 4334 | SPCS1 | 0.40 | 0.037 | U |
| 4349 | ANKRD23 | 0.39 | 0.041 | U |
| 4375 | PMVK | 0.47 | 0.011 | U |
| 4395 | REEP1 | 0.40 | 0.034 | U |
| 4458 | RPN1 | 0.43 | 0.023 | U |
| 4526 | YME1L1 | 0.41 | 0.030 | U |
| 4547 | AMFR | 0.44 | 0.018 | U |
| 4557 |  | 0.38 | 0.043 | U |
| 4647 | THSD1 | 0.42 | 0.026 | U |
| 4651 | USF1 | 0.38 | 0.045 | U |
| 4720 | C1orf228 | 0.44 | 0.020 | U |
| 4846 | PIGF | 0.52 | 0.005 | U |


| 4857 | CSTF1 | 0.51 | 0.006 | U |
| :---: | :---: | :---: | :---: | :---: |
| 4870 | BEX5 | 0.48 | 0.010 | U |
| 4904 | ERBB2IP | 0.38 | 0.048 | U |
| 4974 | CALCA | 0.43 | 0.021 | U |
| 5164 | LARP1B | 0.42 | 0.025 | U |
| 5181 | RMI1 | 0.44 | 0.018 | U |
| 5190 | UHRF1 | 0.41 | 0.030 | U |
| 5234 | NBPF1 | 0.42 | 0.024 | U |
| 5248 | GLYATL1 | 0.39 | 0.042 | U |
| 5325 | RAG1AP1 | 0.58 | 0.001 | U |
| 5391 | WDFY3 | 0.51 | 0.005 | U |
| 5453 | DHPS | 0.39 | 0.040 | U |
| 5507 | MTPAP | 0.39 | 0.042 | U |
| 5518 | CKLF | 0.38 | 0.045 | U |
| 5543 | ATP6V1D | 0.37 | 0.050 | U |
| 5611 | ARPP21 | 0.44 | 0.020 | U |
| 5699 | FAM98B | 0.44 | 0.021 | U |
| 5731 | ARL5B | 0.46 | 0.013 | U |
| 5737 | C18orf25 | 0.48 | 0.010 | U |
| 5752 | HAO1 | 0.39 | 0.042 | U |
| 5766 | KCNAB3 | 0.40 | 0.036 | U |
| 5770 | TMSB15A | 0.41 | 0.030 | U |
| 5773 | LGALS13 | 0.44 | 0.020 | U |
| 5838 | SMARCA2 | 0.40 | 0.036 | U |
| 5846 | C15orf24 | 0.38 | 0.043 | U |
| 5928 | GYS2 | 0.43 | 0.023 | U |
| 5978 | POGZ | 0.40 | 0.033 | U |
| 5984 | CES3 | 0.40 | 0.035 | U |
| 6200 | MS4A1 | 0.43 | 0.021 | U |
| 6215 | PSMA1 | 0.41 | 0.029 | U |
| 6258 | CSTL1 | 0.45 | 0.017 | U |
| 6264 | AGER | 0.38 | 0.043 | U |
| 6272 | UBASH3B | 0.42 | 0.027 | U |
| 6313 | DHX32 | 0.40 | 0.033 | U |
| 6373 | UNC5A | 0.43 | 0.023 | U |
| 6461 | WIPI2 | 0.43 | 0.024 | U |
| 6491 | SPEF1 | 0.44 | 0.019 | U |
| 6516 | MMP17 | 0.53 | 0.003 | U |


| 6546 | OR4E2 | 0.39 | 0.042 | U |
| :---: | :---: | :---: | :---: | :---: |
| 6632 | ZBTB25 | 0.50 | 0.007 | U |
| 6668 | CHRM5 | 0.47 | 0.012 | U |
| 6725 | KRTAP5-4 | 0.38 | 0.046 | U |
| 6753 | LPAL2 | 0.39 | 0.043 | U |
| 6764 | ACVR1B | 0.39 | 0.040 | U |
| 6836 | TRPC4 | 0.42 | 0.025 | U |
| 6885 | IGHMBP2 | 0.47 | 0.013 | U |
| 6889 | ZNF568 | 0.52 | 0.004 | U |
| 7052 | PCDHA@ | 0.49 | 0.008 | U |
| 7153 | SLPI | 0.46 | 0.013 | U |
| 7387 | SRFBP1 | 0.38 | 0.045 | U |
| 7399 | SPINK1 | 0.47 | 0.011 | U |
| 7418 | EFCAB6 | 0.39 | 0.039 | U |
| 7444 | GSTO2 | 0.52 | 0.005 | U |
| 7513 | PATZ1 | 0.43 | 0.023 | U |
| 7514 | SLC22A8 | 0.38 | 0.048 | U |
| 7530 | ECHDC2 | 0.40 | 0.036 | U |
| 7551 | CASP9 | 0.49 | 0.008 | U |
| 7616 | UHMK1 | 0.44 | 0.020 | U |
| 7634 | KCNK10 | 0.42 | 0.024 | U |
| 7691 | TYMP | 0.38 | 0.045 | U |
| 7813 | ZNF274 | 0.45 | 0.016 | U |
| 7827 | TEX11 | 0.39 | 0.040 | U |
| 7899 | CHORDC1 | 0.40 | 0.034 | U |
| 8003 | LILRB3 | 0.44 | 0.018 | U |
| 8029 | SRGAP1 | 0.39 | 0.038 | U |
| 8070 | C9orf116 | 0.39 | 0.042 | U |
| 8082 | SPHK1 | 0.39 | 0.041 | U |
| 8098 | XDH | 0.45 | 0.017 | U |
| 8140 | ELMOD2 | 0.38 | 0.048 | U |
| 8171 | SUV420H1 | 0.38 | 0.045 | U |
| 8197 | PLEKHH1 | 0.42 | 0.027 | U |
| 8312 | OLIG3 | 0.39 | 0.041 | U |
| 8385 | OGFOD1 | 0.42 | 0.026 | U |
| 8443 | C21orf58 | 0.40 | 0.037 | U |
| 8480 | ATF7IP | 0.38 | 0.044 | U |
| 8482 | STT3A | 0.58 | 0.001 | U |


| 8502 | CYFIP1 | 0.46 | 0.015 | U |
| :---: | :---: | :---: | :---: | :---: |
| 8568 | SH3GL2 | 0.46 | 0.014 | U |
| 8591 | TTC8 | 0.45 | 0.017 | U |
| 8606 | PRDX5 | 0.41 | 0.032 | U |
| 8617 | MAPT | 0.39 | 0.039 | U |
| 8639 | CYB5D2 | 0.47 | 0.012 | U |
| 8660 | PSMD4 | 0.39 | 0.040 | U |
| 8674 | ANK3 | 0.46 | 0.013 | U |
| 8735 | SLC35F4 | 0.44 | 0.019 | U |
| 8742 | MYPN | 0.44 | 0.021 | U |
| 8785 | CD300E | 0.42 | 0.025 | U |
| 8789 | NR1D2 | 0.41 | 0.029 | U |
| 8852 | LIF | 0.42 | 0.026 | U |
| 8868 | LRPAP1 | 0.39 | 0.041 | U |
| 8933 | DPAGT1 | 0.62 | 0.000 | U |
| 8953 | CHP2 | 0.43 | 0.021 | U |
| 9031 | C1orf77 | 0.45 | 0.017 | U |
| 9058 | TBC1D23 | 0.41 | 0.030 | U |
| 9099 | MPDU1 | 0.38 | 0.044 | U |
| 9100 | TM2D3 | 0.48 | 0.010 | U |
| 9129 | MFAP3 | 0.39 | 0.042 | U |
| 9205 | TRMT2B | 0.42 | 0.026 | U |
| 9261 | MTX1 | 0.40 | 0.037 | U |
| 9304 | TRIP11 | 0.40 | 0.033 | U |
| 9401 | FBF1 | 0.40 | 0.036 | U |
| 9499 | PHYH | 0.42 | 0.028 | U |
| 9557 | DPM3 | 0.51 | 0.006 | U |
| 9567 | PCBP4 | 0.38 | 0.049 | U |
| 9581 | H2AFY2 | 0.42 | 0.028 | U |
| 9673 | CYP27B1 | 0.51 | 0.006 | U |
| 9674 | SHANK1 | 0.46 | 0.014 | U |
| 9808 | ABHD2 | 0.38 | 0.043 | U |
| 9893 | GINS3 | 0.39 | 0.043 | U |
| 9943 | HK3 | 0.40 | 0.037 | U |
| 9956 | HIPK3 | 0.50 | 0.006 | U |
| 10043 | PPOX | 0.41 | 0.028 | U |
| 10058 | OPRM1 | 0.40 | 0.037 | U |
| 10105 | SIL1 | 0.47 | 0.011 | U |


| 10145 | ATP5J | 0.38 | 0.043 | U |
| :---: | :---: | :---: | :---: | :---: |
| 10248 | AGR2 | 0.46 | 0.014 | U |
| 10311 | FOXJ1 | 0.50 | 0.006 | U |
| 10318 | MYOF | 0.47 | 0.012 | U |
| 10344 | CDC42BPA | 0.49 | 0.009 | U |
| 10383 | BTBD7 | 0.41 | 0.031 | U |
| 10411 | SYNJ2BP | 0.41 | 0.032 | U |
| 10432 | PDXDC1 | 0.47 | 0.012 | U |
| 10446 | STEAP2 | 0.49 | 0.009 | U |
| 10477 | FAM134B | 0.40 | 0.035 | U |
| 10503 |  | 0.41 | 0.031 | U |
| 10534 | FAM115C | 0.45 | 0.018 | U |
| 10643 | PPP2R5B | 0.39 | 0.038 | U |
| 10748 | PIGO | 0.40 | 0.033 | U |
| 10766 | PRDX5 | 0.40 | 0.033 | U |
| 10776 | RAPH1 | 0.40 | 0.037 | U |
| 10779 | DOCK5 | 0.44 | 0.018 | U |
| 10849 | BANP | 0.39 | 0.041 | U |
| 10859 | GALC | 0.43 | 0.022 | U |
| 10929 | LDHD | 0.38 | 0.048 | U |
| 11020 | EIF4E3 | 0.42 | 0.027 | U |
| 11053 | C9orf86 | 0.39 | 0.038 | U |
| 11102 | CASC4 | 0.40 | 0.034 | U |
| 11143 | CHKB | 0.48 | 0.009 | U |
| 11172 | FRAT1 | 0.39 | 0.039 | U |
| 11173 | SMCR7 | 0.45 | 0.017 | U |
| 11179 | TPM3 | 0.49 | 0.008 | U |
| 11187 | SLC38A7 | 0.45 | 0.017 | U |
| 11240 | TSPAN13 | 0.38 | 0.049 | U |
| 11245 | AKD1 | 0.52 | 0.005 | U |
| 11290 | ZGPAT | 0.40 | 0.036 | U |
| 11301 | C21orf119 | 0.43 | 0.023 | U |
| 11358 | GALC | 0.39 | 0.039 | U |
| 11366 | CLCC1 | 0.38 | 0.048 | U |
| 11383 | HBB | 0.44 | 0.018 | U |
| 11412 | RIMS2 | 0.39 | 0.040 | U |
| 11633 | SLC16A7 | 0.41 | 0.030 | U |
| 11690 | MPV17 | 0.55 | 0.002 | U |


| 11728 | LOC441268 | 0.37 | 0.049 | U |
| :---: | :---: | :---: | :---: | :---: |
| 11754 | PEG3 | 0.38 | 0.048 | U |
| 11777 | ARFGEF2 | 0.40 | 0.033 | U |
| 11896 | AKAP2 | 0.37 | 0.050 | U |
| 11906 | OSBP2 | 0.46 | 0.014 | U |
| 12026 | ZXDA | 0.39 | 0.041 | U |
| 12059 | VPS45 | 0.46 | 0.015 | U |
| 12063 | PLEKHB2 | 0.42 | 0.025 | U |
| 12116 | LRRC36 | 0.45 | 0.017 | U |
| 12183 | FAM91A2 | 0.50 | 0.007 | U |
| 12184 | XAGE2B | 0.39 | 0.038 | U |
| 12241 | CTBP1 | 0.39 | 0.041 | U |
| 12353 | ARHGEF4 | 0.40 | 0.034 | U |
| 12391 | GSC2 | 0.44 | 0.018 | U |
| 12457 | RIOK1 | 0.43 | 0.022 | U |
| 12491 | MFSD10 | 0.40 | 0.033 | U |
| 12543 | PIGO | 0.47 | 0.011 | U |
| 12558 | NCRNA00175 | 0.37 | 0.050 | U |
| 12581 | DRD2 | 0.46 | 0.013 | U |
| 12598 |  | 0.45 | 0.016 | U |
| 12642 | ARMCX2 | 0.49 | 0.007 | U |
| 12697 | NCKAP1 | 0.44 | 0.020 | U |
| 12708 | DHRS7 | 0.39 | 0.042 | U |
| 12713 | PDLIM5 | 0.55 | 0.002 | U |
| 12729 | TNPO1 | 0.47 | 0.012 | U |
| 12734 | FAM46A | 0.40 | 0.036 | U |
| 12747 | RPS27 | 0.50 | 0.007 | U |
| 12760 | DEFB110 | 0.40 | 0.035 | U |
| 12965 | PIP | 0.47 | 0.011 | U |
| 13062 | DNASE1L1 | 0.44 | 0.020 | U |
| 13261 | PHYH | 0.39 | 0.042 | U |
| 13295 | TMED10 | 0.39 | 0.043 | U |
| 13314 | FGF12 | 0.39 | 0.041 | U |
| 13349 | C16orf93 | 0.44 | 0.019 | U |
| 13373 | C15orf48 | 0.45 | 0.017 | U |
| 13397 | C9orf23 | 0.41 | 0.032 | U |
| 13449 | FGF12 | 0.40 | 0.033 | U |
| 13478 | WDR20 | 0.49 | 0.008 | U |


| 13531 | GK | 0.41 | 0.031 | U |
| :---: | :---: | :---: | :---: | :---: |
| 13551 | COPA | 0.42 | 0.024 | U |
| 13600 | APPL2 | 0.38 | 0.046 | U |
| 13601 | FAM189B | 0.40 | 0.034 | U |
| 13620 | HSF4 | 0.44 | 0.019 | U |
| 13629 | SLC39A9 | 0.51 | 0.006 | U |
| 13678 | VPREB1 | 0.49 | 0.008 | U |
| 13760 | TMEM48 | 0.43 | 0.022 | U |
| 13811 | PBLD | 0.43 | 0.023 | U |
| 13831 | WDR73 | 0.39 | 0.040 | U |
| 13860 | GPR155 | 0.44 | 0.021 | U |
| 13871 | CRIPAK | 0.41 | 0.032 | U |
| 13943 | ARFIP1 | 0.40 | 0.035 | U |
| 13971 | AADAT | 0.38 | 0.045 | U |
| 14092 | CTAG2 | 0.40 | 0.033 | U |
| 14137 | BOLA1 | 0.43 | 0.024 | U |
| 14172 | FGF14 | 0.39 | 0.039 | U |
| 14208 | MAST4 | 0.40 | 0.036 | U |
| 14218 | HAX1 | 0.39 | 0.042 | U |
| 14242 | SIM2 | 0.38 | 0.047 | U |
| 14320 | LAIR1 | 0.45 | 0.017 | U |
| 14332 |  | 0.53 | 0.004 | U |
| 14345 | CDK8 | 0.39 | 0.042 | U |
| 14353 | BMP2 | 0.44 | 0.020 | U |
| 14401 | AOC2 | 0.40 | 0.035 | U |
| 14405 | IL24 | 0.38 | 0.045 | U |
| 14443 | BMPR1A | 0.54 | 0.003 | U |
| 14452 | CERKL | 0.39 | 0.041 | U |
| 14460 | PIWIL1 | 0.41 | 0.030 | U |
| 14470 | C1orf58 | 0.45 | 0.017 | U |
| 14494 | CYS1 | 0.49 | 0.009 | U |
| 14515 | NBR1 | 0.45 | 0.015 | U |
| 14549 | KDELR3 | 0.39 | 0.040 | U |
| 14613 | AKTIP | 0.41 | 0.030 | U |
| 14664 | TTC13 | 0.40 | 0.034 | U |
| 14699 | C15orf26 | 0.42 | 0.026 | U |
| 14703 | ZNF586 | 0.50 | 0.006 | U |
| 14711 | GPR171 | 0.44 | 0.019 | U |


| 14756 | LMLN | 0.49 | 0.009 | U |
| :---: | :---: | :---: | :---: | :---: |
| 14762 | C16orf75 | 0.40 | 0.035 | U |
| 14775 | ANAPC11 | 0.46 | 0.013 | U |
| 14797 | TSPYL2 | 0.52 | 0.004 | U |
| 14840 | MANF | 0.43 | 0.022 | U |
| 14880 | DPP3 | 0.49 | 0.009 | U |
| 14905 | GEM | 0.41 | 0.030 | U |
| 14910 | SLCO4A1 | 0.44 | 0.019 | U |
| 14911 | MAP2K3 | 0.41 | 0.030 | U |
| 14934 | MSR1 | 0.39 | 0.042 | U |
| 14968 | HERPUD1 | 0.46 | 0.013 | U |
| 15138 | ANGPTL4 | 0.52 | 0.004 | U |
| 15157 | AMFR | 0.42 | 0.025 | U |
| 15316 | PLSCR2 | 0.39 | 0.041 | U |
| 15445 | SRSF5 | 0.47 | 0.012 | U |
| 15582 | GBA | 0.60 | 0.001 | U |
| 15629 | ZNF274 | 0.38 | 0.044 | U |
| 15645 | ERO1L | 0.39 | 0.042 | U |
| 15705 | RNF207 | 0.52 | 0.005 | U |
| 15761 | ZMAT1 | 0.40 | 0.035 | U |
| 15764 | FAM20C | 0.43 | 0.021 | U |
| 15777 | PI4KB | 0.38 | 0.044 | U |
| 15820 | GMPPB | 0.39 | 0.041 | U |
| 15940 | ENTPD8 | 0.38 | 0.044 | U |
| 15944 | PSEN1 | 0.55 | 0.003 | U |
| 15947 | MBTPS2 | 0.49 | 0.008 | U |
| 15953 | ZRANB3 | 0.49 | 0.008 | U |
| 15974 | SLC35A2 | 0.40 | 0.035 | U |
| 16033 | NEK9 | 0.40 | 0.035 | U |
| 16037 | FAM20C | 0.43 | 0.024 | U |
| 16060 | ORAOV1 | 0.38 | 0.047 | U |
| 16077 | OR5A2 | 0.38 | 0.043 | U |
| 16118 | SPO11 | 0.42 | 0.027 | U |
| 16150 | DUSP8 | 0.47 | 0.011 | U |
| 16179 | SLC35A2 | 0.37 | 0.049 | U |
| 16187 | HSF4 | 0.42 | 0.025 | U |
| 16188 | HIST2H4A | 0.42 | 0.026 | U |
| 16220 |  | 0.41 | 0.031 | U |


| 16256 | MMEL1 | 0.48 | 0.009 | U |
| :---: | :---: | :---: | :---: | :---: |
| 16258 | GPS2 | 0.40 | 0.034 | U |
| 16272 | ZDHHC9 | 0.43 | 0.024 | U |
| 16273 | HTR4 | 0.38 | 0.045 | U |
| 16460 |  | 0.54 | 0.003 | U |
| 16500 | TULP4 | 0.44 | 0.019 | U |
| 16545 | ATP2C1 | 0.45 | 0.017 | U |
| 16557 | EPS8L1 | 0.42 | 0.028 | U |
| 16590 | VWA5A | 0.38 | 0.044 | U |
| 16694 | GDF15 | 0.39 | 0.043 | U |
| 16752 | KRTAP13-4 | 0.38 | 0.044 | U |
| 16772 | PKD1L2 | 0.43 | 0.021 | U |
| 16815 | NUDT9 | 0.39 | 0.041 | U |
| 16875 | RBFOX1 | 0.38 | 0.045 | U |
| 16966 | PIGO | 0.44 | 0.019 | U |
| 17060 | EMR3 | 0.41 | 0.032 | U |
| 17094 | SLC30A8 | 0.45 | 0.016 | U |
| 17170 | TTLL1 | 0.37 | 0.049 | U |
| 17182 | SLC35B1 | 0.41 | 0.031 | U |
| 17193 | NBPF1 | 0.43 | 0.024 | U |
| 17219 | COG1 | 0.45 | 0.016 | U |
| 17229 | LCMT2 | 0.39 | 0.038 | U |
| 17241 | CRLF2 | 0.40 | 0.036 | U |
| 17328 | CLDN14 | 0.42 | 0.025 | U |
| 17348 | ITGA2B | 0.42 | 0.026 | U |
| 17492 | RORC | 0.46 | 0.013 | U |
| 17564 | GPR108 | 0.38 | 0.049 | U |
| 17613 | ATF6 | 0.43 | 0.022 | U |
| 17654 | FLG2 | 0.41 | 0.029 | U |
| 17719 | ADAR | 0.49 | 0.008 | U |
| 17724 | CCDC62 | 0.39 | 0.041 | U |
| 17752 | ENTPD8 | 0.45 | 0.016 | U |
| 17817 | TMED3 | 0.41 | 0.032 | U |
| 17869 | BTNL3 | 0.58 | 0.001 | U |
| 17918 | EIF2C4 | 0.38 | 0.049 | U |
| 17920 | FBXO44 | 0.41 | 0.028 | U |
| 17976 | ITGBL1 | 0.39 | 0.042 | U |
| 18050 | MUTYH | 0.38 | 0.047 | U |


| 18098 | SLC39A1 | 0.51 | 0.005 | U |
| :---: | :---: | :---: | :---: | :---: |
| 18151 | TK2 | 0.38 | 0.048 | U |
| 18202 | IRX3 | 0.45 | 0.015 | U |
| 18340 | ZNF562 | 0.42 | 0.028 | U |
| 18341 | TOM1L1 | 0.39 | 0.043 | U |
| 18343 | COQ2 | 0.44 | 0.018 | U |
| 18392 | GRID2 | 0.54 | 0.003 | U |
| 18424 | ANKRD36 | 0.50 | 0.007 | U |
| 18474 | PURG | 0.37 | 0.050 | U |
| 18522 | MYST4 | 0.42 | 0.025 | U |
| 18543 | CHKB | 0.50 | 0.007 | U |
| 18582 | AGAP4 | 0.41 | 0.031 | U |
| 18599 | FUT6 | 0.40 | 0.035 | U |
| 18627 | C2CD4B | 0.38 | 0.046 | U |
| 18669 | DOK5 | 0.41 | 0.031 | U |
| 18802 | PPP2R5A | 0.43 | 0.024 | U |
| 18828 | KIAA0913 | 0.47 | 0.013 | U |
| 18980 | OTOA | 0.41 | 0.032 | U |
| 18998 | KIAA1530 | 0.43 | 0.024 | U |
| 19043 | ANG | 0.45 | 0.017 | U |
| 19159 | C5orf25 | 0.37 | 0.049 | U |
| 19175 | PSMD4 | 0.48 | 0.010 | U |
| 19188 | LPPR1 | 0.41 | 0.029 | U |
| 19191 | ZDHHC13 | 0.41 | 0.030 | U |
| 19229 | MOBKL2C | 0.46 | 0.013 | U |
| 19243 | SELS | 0.41 | 0.031 | U |
| 19264 | CLK2P | 0.38 | 0.046 | U |
| 19353 | PDLIM5 | 0.54 | 0.003 | U |
| 19400 | COQ6 | 0.47 | 0.011 | U |
| 19421 | ZNF490 | 0.39 | 0.042 | U |
| 19422 | AHR | 0.46 | 0.015 | U |
| 19453 | ST3GAL1 | 0.47 | 0.011 | U |
| 19531 | PHF11 | 0.38 | 0.046 | U |
| 19558 | AP3D1 | 0.41 | 0.030 | U |
| 19581 | C20orf46 | 0.40 | 0.034 | U |
| 19655 | KRTCAP2 | 0.61 | 0.001 | U |
| 19757 | NFYA | 0.39 | 0.041 | U |
| 19758 | TLL2 | 0.39 | 0.039 | U |


| 19870 | TTC13 | 0.38 | 0.049 | U |
| :---: | :---: | :---: | :---: | :---: |
| 20006 | KRTAP12-4 | 0.38 | 0.047 | U |
| 20019 | ZC3H14 | 0.39 | 0.038 | U |
| 20074 | MPP5 | 0.41 | 0.032 | U |
| 20098 | GPHN | 0.46 | 0.015 | U |
| 20147 | DMP1 | 0.49 | 0.008 | U |
| 20164 | PCK1 | 0.38 | 0.049 | U |
| 20179 |  | 0.48 | 0.009 | U |
| 20182 | TLX2 | 0.40 | 0.036 | U |
| 20198 | MAP4K3 | 0.49 | 0.008 | U |
| 20214 | FAM3B | 0.48 | 0.011 | U |
| 20232 | TPM3 | 0.42 | 0.028 | U |
| 20265 | USF1 | 0.41 | 0.030 | U |
| 20277 | BCL6 | 0.41 | 0.030 | U |
| 20327 | RCE1 | 0.42 | 0.025 | U |
| 20390 | DPAGT1 | 0.54 | 0.003 | U |
| 20478 | ZNF672 | 0.41 | 0.032 | U |
| 20515 | TNFRSF6B | 0.39 | 0.038 | U |
| 20927 | NDEL1 | 0.42 | 0.027 | U |
| 20931 | FAM134B | 0.41 | 0.032 | U |
| 20995 | VPS53 | 0.39 | 0.042 | U |
| 20998 | MCOLN1 | 0.57 | 0.002 | U |
| 21008 | KCNH7 | 0.44 | 0.019 | U |
| 21013 | BCAP31 | 0.41 | 0.032 | U |
| 21036 | FBXW7 | 0.44 | 0.019 | U |
| 21049 | CTAG2 | 0.43 | 0.024 | U |
| 21132 | GPATCH2 | 0.43 | 0.021 | U |
| 21214 | MTMR1 | 0.38 | 0.047 | U |
| 21283 | MYOF | 0.42 | 0.027 | U |
| 21370 | USP53 | 0.55 | 0.003 | U |
| 21419 | OR2T3 | 0.39 | 0.042 | U |
| 21432 | C17orf77 | 0.45 | 0.015 | U |
| 21470 | IGSF5 | 0.38 | 0.043 | U |
| 21537 | GALNTL1 | 0.38 | 0.049 | U |
| 21547 | TLE2 | 0.42 | 0.028 | U |
| 21557 | SIL1 | 0.41 | 0.029 | U |
| 21641 | PACRG | 0.41 | 0.031 | U |
| 21658 | MIA3 | 0.53 | 0.003 | U |


| 21726 | PCDHGC3 | 0.40 | 0.033 | U |
| :---: | :---: | :---: | :---: | :---: |
| 21757 | SRD5A3 | 0.41 | 0.032 | U |
| 21811 | COQ6 | 0.45 | 0.016 | U |
| 22031 | TRIM15 | 0.49 | 0.008 | U |
| 22080 | SYTL2 | 0.40 | 0.034 | U |
| 22103 | DPP3 | 0.39 | 0.040 | U |
| 22292 | CTSA | 0.38 | 0.046 | U |
| 22497 | KITLG | 0.39 | 0.038 | U |
| 22616 | GNL3 | 0.45 | 0.017 | U |
| 22622 | RHBDF2 | 0.44 | 0.019 | U |
| 22635 | C16orf58 | 0.38 | 0.044 | U |
| 22707 | ANXA11 | 0.45 | 0.016 | U |
| 22708 | THSD4 | 0.43 | 0.024 | U |
| 22719 | ZSCAN10 | 0.39 | 0.043 | U |
| 22801 | CRCP | 0.38 | 0.044 | U |
| 22967 | ANG | 0.39 | 0.042 | U |
| 23037 | TNKS | 0.46 | 0.014 | U |
| 23099 | XPNPEP1 | 0.44 | 0.019 | U |
| 23346 | SLC12A4 | 0.40 | 0.036 | U |
| 23370 | MGST3 | 0.38 | 0.044 | U |
| 23379 | EXD2 | 0.50 | 0.007 | U |
| 23410 | MAP2K3 | 0.39 | 0.039 | U |
| 23446 | SCAMP3 | 0.44 | 0.020 | U |
| 23501 | INTS3 | 0.59 | 0.001 | U |
| 23546 | RBM11 | 0.39 | 0.038 | U |
| 23557 | GPR37 | 0.55 | 0.002 | U |
| 23560 | GNPTG | 0.43 | 0.023 | U |
| 23577 | TMEM205 | 0.42 | 0.028 | U |
| 23600 | NCSTN | 0.59 | 0.001 | U |
| 23605 | MFSD8 | 0.44 | 0.020 | U |
| 23661 | DPM3 | 0.49 | 0.008 | U |
| 23791 | PPM1B | 0.38 | 0.048 | U |
| 23801 | MCL1 | 0.50 | 0.006 | U |
| 23947 | CTTN | 0.51 | 0.005 | U |
| 23982 | PTPRH | 0.56 | 0.002 | U |
| 24083 | TMEM161B | 0.41 | 0.032 | U |
| 24309 | NPC1 | 0.38 | 0.046 | U |
| 24328 | SIAH1 | 0.47 | 0.012 | U |


| 24441 | NLRP12 | 0.41 | 0.031 | U |
| :---: | :---: | :---: | :---: | :---: |
| 24444 | MUC1 | 0.40 | 0.037 | U |
| 24459 | LAMB2 | 0.48 | 0.010 | U |

## APPENDIX D. 567 GENES THAT CORRELATE WITH SYNERGISM TO

GEMCITABINE + CISPLATIN AND MET REQUIREMENTS FOR

## CLUSTERING.

Genes are listed as they appear in signature in Figure 3.3.

| Symbol | Correl | Gene <br> ID |
| :---: | :---: | :---: |
| CARS |  | 106 |
| BDNF | 0.846 | 16094 |
| ZEB2 | 0.803 | 16478 |
| CLGN | 0.782 | 21921 |
| BNC2 | 0.770 | 23023 |
| C1S | 0.453 | 4309 |
| BVES | 0.851 | 23553 |
| BDNF | 0.550 | 23734 |
| BCAT1 | 0.691 | 24503 |
| AOX1 | 0.635 | 11905 |
| SCG2 | 0.647 | 16299 |
| IGF2BP1 | 0.186 | 3451 |
| KIAA0368 | 0.690 | 20828 |
| RBM24 | 0.496 | 5806 |
| FBN2 | 0.765 | 11312 |
| ROBO1 | 0.861 | 11823 |
| EYA4 | 0.776 | 22152 |
| CDKL3 | 0.588 | 11722 |
| TRPC1 | 0.866 | 13590 |
| HUWE1 | 0.662 | 22769 |
| S1PR1 | 0.353 | 886 |
| ANK2 | 0.897 | 15618 |
| FBXO5 | 0.846 | 18085 |
| FLJ35409 | 0.782 | 13192 |
| ZNF23 | 0.766 | 14196 |
| ELOVL2 | 0.682 | 15088 |
| WDR11 | 0.783 | 17882 |
| PIK3C3 | 0.574 | 21488 |
| RTN4 | 0.444 | 2637 |
|  |  |  |


| SNX24 | 0.820 | 13710 |
| :---: | :---: | :---: |
| PKIA | 0.752 | 19058 |
| WNK3 | 0.710 | 12742 |
| DCAF6 | 0.759 | 16591 |
| TMEFF2 | 0.328 | 1055 |
| KCNT2 | 0.742 | 10217 |
| SCN9A | 0.745 | 12092 |
| C7orf69 | 0.881 | 16019 |
| RECK | 0.648 | 11059 |
| GNAI1 | 0.736 | 14238 |
| ATP5I | 0.032 | 14856 |
| FTCD | 0.651 | 19885 |
| FTCD | 0.946 | 20228 |
| ZBTB2 | 0.255 | 243 |
| NDUFAF4 | 0.739 | 6260 |
| FGF5 | 0.802 | 16498 |
| SLC39A10 | 0.708 | 19122 |
| HS2ST1 | 0.669 | 3683 |
| PLOD2 | 0.762 | 15206 |
| SGCB | 0.625 | 3892 |
| NME7 | 0.839 | 9603 |
| FADS3 | 0.739 | 3977 |
| HNRPDL | 0.564 | 8442 |
| AMN1 | 0.723 | 22463 |
| AMZ2 | 0.486 | 1062 |
| FAM49B | 0.839 | 8687 |
| NXT2 | 0.802 | 17033 |
| OSBPL11 | 0.797 | 18148 |
| EIF1AX | 0.693 | 12652 |
| HERPUD2 | 0.682 | 10962 |
| DUSP11 | 0.853 | 13259 |
| ARL6IP1 | 0.695 | 19121 |
| LSM5 | 0.825 | 21894 |
| PHF3 | 0.618 | 14356 |
| LIN7C | 0.816 | 21288 |
| MCTS1 | 0.685 | 5550 |
| C12orf11 | 0.829 | 17057 |
| NKAP | 0.732 | 19670 |


| RPL23 | 0.558 | 1266 |
| :---: | :---: | :---: |
| RPL9 | 0.938 | 20983 |
| SUMO2 | 0.806 | 1661 |
| TXNL1 | 0.935 | 3024 |
| G3BP1 | 0.878 | 18357 |
| PAPSS1 | 0.858 | 6083 |
| OR52A5 | 0.686 | 4563 |
| CDKN1B | 0.690 | 3310 |
| RTN3 | 0.913 | 8084 |
| GOPC | 0.778 | 4581 |
| EXOSC10 | 0.789 | 2831 |
| SRSF11 | 0.877 | 3145 |
| C4orf46 | 0.843 | 15427 |
| AMMECR1L | 0.809 | 16306 |
| PTMA | 0.501 | 1512 |
| SLBP | 0.748 | 14355 |
| HMGB2 | 0.769 | 18962 |
| VHL | 0.633 | 8116 |
| BTG3 | 0.802 | 23587 |
| MTF2 | 0.720 | 9316 |
| TAF9 | 0.606 | 3140 |
| IFT74 | 0.866 | 10375 |
| TAF9 | 0.846 | 22995 |
| LSM6 | 0.721 | 17770 |
| RAP1B | 0.683 | 21766 |
| NAA50 | 0.774 | 21818 |
| CCNH | 0.547 | 6323 |
| DNM1L | 0.827 | 12597 |
| ANP32A | 0.521 | 4119 |
| MRPL47 | 0.837 | 16743 |
| HNRNPC | 0.813 | 5083 |
| MAK16 | 0.671 | 9913 |
| MRPL52 | 0.754 | 22910 |
| CCDC25 | 0.638 | 6530 |
| PPP2CB | 0.901 | 22295 |
| SNX12 | 0.692 | 19496 |
| LAS1L | 0.516 | 959 |
| C20orf27 | 0.727 | 9272 |


| MRPL48 | 0.509 | 2416 |
| :---: | :---: | :---: |
| RPL7 | 0.778 | 8916 |
| TRUB2 | 0.871 | 18162 |
| RPL14 | 0.734 | 7163 |
| RPL13P5 | 0.859 | 22300 |
| POLR1E | 0.840 | 13055 |
| CCDC77 | 0.681 | 12347 |
| EMG1 | 0.745 | 15869 |
| RPL9 | 0.655 | 15192 |
| LIAS | 0.829 | 19045 |
| C12orf29 | 0.422 | 516 |
| LARP4 | 0.814 | 12243 |
| ATP2B1 | 0.716 | 14054 |
| GPAM | 0.730 | 12206 |
| PPM1D | 0.762 | 18218 |
| EIF1B | 0.800 | 19430 |
| AKAP12 | 0.780 | 22614 |
| SLC39A6 | 0.542 | 9903 |
| UTP15 | 0.743 | 10156 |
| NME1 | 0.917 | 24259 |
| FAM72D | 0.625 | 3658 |
| PES1 | 0.812 | 5059 |
| SSX2IP | 0.804 | 4810 |
| CHAC2 | 0.556 | 9506 |
| FAM35A | 0.851 | 10785 |
| CD3EAP | 0.691 | 16853 |
| DPH5 | 0.717 | 14374 |
| GGH | 0.377 | 869 |
| RAD1 | 0.688 | 7411 |
| RPSA | 0.635 | 7517 |
| UBA2 | 0.807 | 14464 |
| UTP18 | 0.815 | 15968 |
| RPL21 | 0.798 | 16337 |
| CPSF6 | 0.277 | 977 |
| RABL5 | 0.725 | 17726 |
| ZCRB1 | 0.764 | 6474 |
| TRMT6 | 0.827 | 13226 |
| DICER1 | 0.842 | 17532 |


| ARID2 | 0.819 | 23125 |
| :---: | :---: | :---: |
| ZNF331 | 0.065 | 1642 |
| SMURF2 | 0.679 | 18898 |
| PMS1 | 0.756 | 19153 |
| TIMM10 | 0.617 | 10736 |
| GPT | 0.676 | 19735 |
| FBXO10 | 0.352 | 19824 |
| FLCN | 0.413 | 3582 |
| NOVA1 | 0.603 | 11946 |
| NOL8 | 0.285 | 6977 |
| BHLHB9 | 0.690 | 23579 |
| ICOSLG | 0.537 | 18222 |
| GABARAPL2 | $0.039$ | 118 |
| C11orf58 | 0.799 | 10160 |
| NME1 | 0.815 | 15024 |
| GLI1 | 0.637 | 4603 |
| C19orf30 | 0.541 | 16120 |
| IL16 | 0.852 | 16596 |
| TDP2 | 0.658 | 10716 |
| KPNA2 | 0.829 | 20113 |
| H3F3A | 0.397 | 7736 |
| NACA2 | 0.639 | 8346 |
| ZNF385D | 0.739 | 20781 |
| MCFD2 | 0.737 | 20480 |
| UCHL1 | 0.570 | 15250 |
| ISCA1 | 0.563 | 19111 |
| MBLAC2 | 0.746 | 23855 |
| OR4P4 | 0.211 | 1066 |
| HAUS1 | 0.808 | 7350 |
| SEPT7 | 0.617 | 1399 |
| SMC3 | 0.806 | 12961 |
| EIF3M | 0.796 | 3025 |
| FSD1 | 0.463 | 4877 |
| FSD1 | 0.895 | 23612 |
| NUDT11 | 0.815 | 24186 |
| DACT1 | 0.469 | 5220 |
| DACT1 | 0.962 | 11631 |


| LRRC4C | 0.847 | 9705 |
| :---: | :---: | :---: |
| ZNF607 | 0.791 | 23189 |
| SLITRK5 | 0.689 | 9275 |
| ZNF804A | 0.857 | 15114 |
| NETO1 | 0.835 | 11037 |
| DNAJC18 | 0.529 | 7215 |
| RPL14 | 0.706 | 12618 |
| TIPRL | 0.786 | 15335 |
| KIF5C | 0.622 | 8447 |
| THBS4 | 0.811 | 19874 |
| METTL6 | 0.339 | 6350 |
| BMP6 | 0.729 | 22736 |
| STC1 | 0.629 | 8898 |
| CLIP3 | $0.020$ | 2292 |
| CD47 | 0.736 | 20155 |
| CEP57 | 0.542 | 23191 |
| RBBP4 | 0.802 | 23417 |
| EYA4 | 0.527 | 4197 |
| EYA4 | 0.957 | 7640 |
| SCARF2 | 0.628 | 17567 |
| LUC7L3 | 0.769 | 18915 |
| C18orf32 | 0.558 | 9707 |
| ATMIN | 0.654 | 21853 |
| MAP1LC3A | 0.584 | 17687 |
| NXPH2 | 0.406 | 2836 |
| ZFPM2 | 0.802 | 10320 |
| XAGE1D | 0.780 | 8662 |
| DCN | 0.721 | 24470 |
| PDE1A | 0.603 | 13679 |
| NRXN3 | 0.738 | 21861 |
| ITLN1 | 0.768 | 24377 |
| MAPKAP1 | 0.327 | 298 |
| DCP1B | 0.541 | 12066 |
| RNF212 | 0.328 | 7090 |
| KDELC1 | 0.101 | 813 |
| ITSN1 | 0.702 | 15909 |
| LYPD6B | 0.573 | 10511 |


| IPO8 | 0.368 | 1514 |
| :---: | :---: | :---: |
| TRIM37 | 0.610 | 15226 |
| ODZ3 | 0.654 | 23036 |
| MPDZ | 0.627 | 17034 |
| ZNF673 | 0.487 | 2932 |
| PHLPP2 | 0.823 | 21501 |
| KDM3A | 0.613 | 4133 |
| KIF18A | 0.715 | 8005 |
| C10orf118 | 0.518 | 24362 |
| ASAP1 | 0.428 | 3002 |
| RBBP7 | 0.836 | 6912 |
| ZDHHC2 | 0.603 | 8032 |
| PHF23 | 0.415 | 22740 |
| USP9X | 0.444 | 14960 |
| RPRD1A | 0.223 | 1035 |
| FADS1 | 0.752 | 7725 |
| C18orf21 | 0.530 | 1380 |
| ZNF271 | 0.804 | 10415 |
| HSD11B1 | $0.010$ | 280 |
| FOXS1 | 0.929 | 11713 |
| PCDH10 | 0.870 | 19006 |
| FPR1 | 0.550 | 3300 |
| VCAM1 | 0.864 | 9635 |
| EBF1 | 0.498 | 3740 |
| CDH4 | 0.338 | 11885 |
| MSC | 0.779 | 24031 |
| PRR5L | 0.635 | 15165 |
| CXCL5 | 0.395 | 1790 |
| PAPPA | 0.750 | 2490 |
| SPECC1 | 0.587 | 9402 |
| C1QTNF1 | 0.629 | 19833 |
| CETP | 0.701 | 23994 |
| CALB2 | 0.570 | 14068 |
| AGTRAP | 0.700 | 15118 |
| AGTRAP | 0.921 | 16316 |
| SAA1 | 0.498 | 621 |
| POSTN | 0.789 | 1585 |


| KCTD12 | 0.865 | 9551 |
| :---: | :---: | :---: |
| SPRR2F | 0.822 | 7329 |
| PTH2R | 0.801 | 11622 |
| RORB | 0.792 | 7882 |
| FAM101A | 0.819 | 8348 |
| C16orf73 | 0.322 | 9363 |
| MRFAP1L1 | 0.648 | 17413 |
| PNMAL1 | 0.488 | 21616 |
| LAP3 | 0.147 | 10626 |
| C6orf58 | 0.526 | 12492 |
| STAT1 | 0.691 | 15683 |
| TCP1 | 0.418 | 13993 |
| BATF3 | 0.464 | 18927 |
| FUBP1 | 0.290 | 136 |
| RAB12 | 0.717 | 4090 |
| MAP3K12 | 0.719 | 16369 |
| KIF21A | 0.645 | 5528 |
| MPHOSPH6 | 0.747 | 7442 |
| SCML2 | 0.455 | 405 |
| CLCN5 | 0.661 | 16703 |
| POU4F1 | 0.764 | 23961 |
| TAF1B | 0.431 | 12762 |
| PIGL | 0.627 | 19625 |
| MOSPD2 | 0.604 | 4080 |
| ANKRD19 | 0.776 | 8093 |
| ATP6V1C1 | 0.785 | 17858 |
| SLC35F1 | 0.608 | 6132 |
| AGTPBP1 | 0.730 | 7577 |
| TPTE | 0.914 | 17335 |
| CDO1 | 0.788 | 15249 |
| LIN28B | 0.830 | 13942 |
| TBX18 | 0.632 | 7664 |
| TBX18 | 0.646 | 13622 |
| TRIM58 | 0.742 | 18829 |
| SPG7 | 0.173 | 15692 |
| ZNF442 | 0.793 | 24285 |
| TOP3A | 0.405 | 12590 |
| C12orf24 | 0.402 | 2614 |


| TMTC4 | 0.722 | 8342 |
| :---: | :---: | :---: |
| ADPRH | 0.756 | 17809 |
| RAB6A | 0.490 | 13130 |
| SNX16 | 0.402 | 3017 |
| ZFP1 | 0.801 | 6917 |
| SRR | 0.791 | 11142 |
| PRKDC | 0.743 | 11012 |
| LOC728643 | 0.824 | 17545 |
| HNRNPA1 | 0.934 | 23659 |
| ZNF286A | 0.597 | 3453 |
| CDK5RAP2 | 0.766 | 18178 |
| RPL7A | 0.503 | 9253 |
| PFAS | 0.852 | 12217 |
| CNTROB | 0.605 | 14879 |
| DYNC2H1 | 0.420 | 13909 |
| LONRF1 | 0.702 | 16515 |
| LOXL3 | 0.616 | 23497 |
| PAQR3 | 0.558 | 22644 |
| ZNF280A | 0.123 | 3152 |
| CDK4 | 0.832 | 23803 |
| MYBBP1A | 0.620 | 20042 |
| METTL1 | 0.387 | 6438 |
| MAP3K15 | 0.542 | 10476 |
| CPNE7 | 0.688 | 19727 |
| SLC6A15 | 0.482 | 20178 |
| KCNJ8 | 0.191 | 322 |
| FLCN | 0.680 | 6351 |
| ATP5G2 | 0.521 | 10584 |
| IGDCC4 | 0.627 | 21097 |
| ZCCHC3 | 0.364 | 6040 |
| NSFL1C | 0.875 | 23645 |
| RASSF2 | 0.466 | 6294 |
| RASSF2 | 0.924 | 17489 |
| SLC7A7 | 0.639 | 15844 |
| IGFL2 | 0.683 | 15442 |
| FXYD7 | 0.831 | 20712 |
| CYP26A1 | 0.864 | 24132 |
| C12orf68 | 0.338 | 15881 |


| ID2 | 0.320 | 5485 |
| :---: | :---: | :---: |
| HDGFRP3 | 0.261 | 11528 |
| PLXDC2 | 0.508 | 18964 |
| S100A16 | 0.045 | 550 |
| CD99 | 0.738 | 14390 |
| SPINT2 | 0.587 | 4166 |
| FAM83H | 0.839 | 4317 |
| MGMT | 0.882 | 21165 |
| SFN | 0.840 | 11808 |
| MGST2 | 0.759 | 5152 |
| LGALS8 | 0.911 | 20193 |
| ATP9A | 0.757 | 21181 |
| ZSCAN16 | 0.754 | 8038 |
| APOBEC3B | 0.624 | 10291 |
| VAMP8 | 0.848 | 19012 |
| STXBP2 | 0.904 | 22646 |
| NUDT16P1 | 0.495 | 3894 |
| BDH1 | 0.665 | 17735 |
| WNT7B | 0.238 | 5118 |
| UBE2H | 0.718 | 16325 |
| PLEK2 | 0.583 | 17014 |
| MID2 | 0.408 | 1414 |
| EXOC5 | 0.654 | 14095 |
| KDELR3 | 0.466 | 1756 |
| KDELR3 | 0.940 | 10793 |
| AES | 0.787 | 19771 |
| C19orf10 | 0.407 | 3326 |
| GGA1 | 0.774 | 20087 |
| XBP1 | 0.581 | 7933 |
| XBP1 | 0.986 | 18154 |
| BACE2 | 0.516 | 4097 |
| BACE2 | 0.983 | 7355 |
| ST3GAL1 | 0.716 | 4346 |
| NOMO1 | 0.530 | 8805 |
| FAM46C | 0.716 | 22398 |
| FAM133A | 0.573 | 7896 |
| TMEM8A | 0.404 | 984 |
| CHPF | 0.673 | 14109 |


| RPS6KA2 | 0.813 | 17439 |
| :---: | :---: | :---: |
| MALL | 0.588 | 2053 |
| KIAA0513 | 0.814 | 18751 |
| MST1R | 0.842 | 23206 |
| TRIOBP | 0.537 | 17974 |
| PTK6 | 0.753 | 20475 |
| STAT6 | 0.434 | 5500 |
| BHLHE40 | 0.918 | 8794 |
| S100A6 | 0.826 | 9435 |
| OCIAD2 | 0.942 | 20945 |
| MSRB2 | 0.829 | 9178 |
| DHRS3 | 0.847 | 23008 |
| SH3PXD2A | 0.671 | 11555 |
| OPLAH | 0.779 | 16490 |
| TSC22D3 | 0.795 | 20553 |
| TSC22D3 | 0.925 | 20569 |
| VEGFA | 0.371 | 9661 |
| STK39 | 0.573 | 10900 |
| NAV2 | 0.716 | 14003 |
| PC | 0.645 | 17684 |
| PC | 0.963 | 18865 |
| ARSJ | 0.372 | 8792 |
| ITPR3 | 0.706 | 19765 |
| TRIOBP | 0.606 | 16091 |
| MPG | 0.797 | 18372 |
| PXMP4 | 0.545 | 3709 |
| CDCA7L | 0.705 | 12090 |
| CHST15 | 0.822 | 23610 |
| SLC16A5 | 0.667 | 22362 |
| KIAA1217 | 0.402 | 4937 |
| GPRC5C | 0.302 | 3820 |
| GPRC5C | 0.971 | 24063 |
| CBR3 | 0.797 | 17933 |
| BLVRA | 0.721 | 9684 |
| EPDR1 | 0.769 | 20803 |
| IER3 | 0.594 | 3917 |
| CD109 | 0.755 | 14014 |
| HRCT1 | 0.460 | 2997 |


| GMPR | 0.735 | 12253 |
| :---: | :---: | :---: |
| GRAMD3 | 0.604 | 16209 |
| SGMS2 | 0.324 | 15246 |
| UPP1 | 0.597 | 24345 |
| CAPN13 | $0.157$ | 1461 |
| SYTL2 | 0.816 | 2590 |
| LGALS3 | 0.642 | 5533 |
| ALS2CL | 0.747 | 14984 |
| PAX9 | 0.752 | 20510 |
| CD6 | 0.761 | 21695 |
| MYO5C | 0.609 | 6324 |
| MB | 0.752 | 8495 |
| MB | 0.934 | 16398 |
| LGMN | 0.453 | 4328 |
| LGMN | 0.934 | 14844 |
| FUT3 | 0.648 | 3040 |
| SAMD10 | 0.751 | 19389 |
| MCTP2 | 0.514 | 3120 |
| CLSTN1 | 0.698 | 16066 |
| RPS6KA2 | 0.249 | 5061 |
| ACP6 | 0.799 | 15357 |
| VWA1 | 0.638 | 6964 |
| FOXA1 | 0.530 | 2689 |
| FAM174B | 0.864 | 12055 |
| TMC6 | 0.794 | 14407 |
| C11orf75 | 0.515 | 16326 |
| GALNT12 | 0.665 | 16123 |
| CCDC120 | 0.787 | 20568 |
| MYO1D | 0.642 | 4528 |
| THNSL2 | 0.813 | 10487 |
| MAL2 | 0.826 | 10359 |
| LSR | 0.899 | 15461 |
| ENPP4 | 0.586 | 9924 |
| RHOD | 0.851 | 13617 |
| AFTPH | 0.790 | 6862 |
| GADD45G | 0.836 | 17975 |
| CRELD2 | 0.722 | 21526 |


| TMEM62 | 0.534 | 16512 |
| :---: | :---: | :---: |
| ALG1L | 0.545 | 4804 |
| EVPL | 0.764 | 22290 |
| TMEM63A | 0.421 | 5735 |
| PKP3 | 0.805 | 9197 |
| PTPN6 | 0.462 | 7416 |
| S100A14 | 0.750 | 10703 |
| TMPRSS13 | 0.856 | 11553 |
| STARD10 | 0.877 | 17892 |
| PPP1R14C | 0.681 | 17720 |
| ANK3 | 0.604 | 4930 |
| GPR160 | 0.753 | 24028 |
| PPP1R13B | 0.620 | 11217 |
| FAM189A2 | 0.711 | 6543 |
| GPC4 | 0.807 | 20429 |
| KLHDC9 | 0.588 | 12428 |
| KLHDC9 | 0.939 | 23371 |
| EHHADH | 0.508 | 16102 |
| ESYT2 | 0.016 | 1641 |
| LDLRAP1 | 0.613 | 3360 |
| CBX7 | 0.788 | 5146 |
| ADCK5 | 0.575 | 8177 |
| MBIP | 0.727 | 17437 |
| ATL1 | 0.564 | 17728 |
| RNF208 | 0.433 | 1627 |
| STEAP4 | 0.723 | 1749 |
| TMEM61 | 0.802 | 2388 |
| XKRX | 0.724 | 12940 |
| AKR1A1 | 0.668 | 17836 |
| NPDC1 | 0.517 | 6179 |
| AGPAT2 | 0.641 | 11682 |
| AGPAT2 | 0.930 | 12361 |
| TRAK1 | 0.668 | 10188 |
| TRAK1 | 0.839 | 20162 |
| LRP5 | 0.678 | 17284 |
| TMEM134 | 0.575 | 2385 |
| TMEM134 | 0.978 | 18231 |
| C11orf80 | 0.735 | 18209 |
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| NDRG1 | 0.381 | 3973 |
| :---: | :---: | :---: |
| CDK2AP2 | 0.784 | 6932 |
| LGR4 | 0.617 | 14896 |
| TPCN2 | 0.578 | 18873 |
| DNAJC3 | 0.694 | 22902 |
| PARM1 | 0.336 | 4074 |
| RNF19A | 0.703 | 5573 |
| RNF19A | 0.869 | 23312 |
| GPAA1 | 0.683 | 8127 |
| MGAT4A | 0.804 | 20007 |
| DGAT1 | 0.699 | 11700 |
| SLC45A4 | 0.787 | 23309 |
| NRTN | 0.522 | 17253 |
| TLR5 | 0.305 | 2743 |
| RTN2 | 0.670 | 11542 |
| SUN2 | 0.612 | 8756 |
| STAP2 | 0.520 | 8053 |
| STAP2 | 0.974 | 17206 |
| STAP2 | 0.946 | 19081 |
| ARHGEF5 | 0.713 | 13528 |
| NET1 | 0.405 | 4734 |
| NET1 | 0.874 | 9827 |
| NET1 | 0.942 | 19606 |
| GSTT1 | 0.654 | 23956 |
| TAPBP | 0.377 | 12756 |
| LGALS9B | 0.432 | 4765 |
| ANXA11 | 0.638 | 18990 |
| C20orf54 | 0.570 | 6818 |
| FERMT1 | 0.670 | 18856 |
| TRIM41 | 0.614 | 13347 |
| STX10 | 0.737 | 19960 |
| LRRC45 | 0.280 | 5057 |
| LRRC45 | 0.801 | 11235 |
| RNF39 | 0.570 | 6325 |
| ALG11 | 0.653 | 17850 |
| ADCK2 | 0.401 | 6005 |
| RMND5B | 0.619 | 13707 |
| PEX6 | 0.529 | 11295 |


| MT1H | 0.237 | 591 |
| :---: | :---: | :---: |
| MT1F | 0.760 | 13965 |
| MTSS1 | 0.729 | 10325 |
| KCNK10 | 0.340 | 7828 |
| CUL9 | 0.571 | 21630 |
| WDR24 | 0.482 | 8992 |
| TMEM198 | 0.751 | 19604 |
| FBXL16 | 0.724 | 22310 |
| ZNF688 | 0.638 | 10498 |
| HDAC11 | 0.714 | 24171 |
| FAM134B | 0.065 | 983 |
| COPE | 0.729 | 3537 |
| LONRF2 | 0.570 | 20270 |
| ATG4A | 0.532 | 2066 |
| TBC1D8B | 0.772 | 20705 |
| PTPN3 | 0.654 | 5046 |
| PVRL1 | 0.301 | 3087 |
| SUSD4 | 0.699 | 19189 |
| GAD1 | 0.378 | 2794 |
| GAD1 | 0.976 | 4805 |
| ITPKB | 0.784 | 15791 |
| GAD1 | 0.642 | 12232 |
| APOOL | 0.232 | 14105 |
| RAB27A | 0.643 | 14546 |
| ARHGEF35 | $0.050$ | 3349 |
| GCAT | 0.466 | 24198 |
| RORA | 0.007 | 3695 |
| RREB1 | 0.510 | 13215 |
| FAM110C | 0.674 | 20514 |
| C11orf63 | 0.532 | 5714 |
| ZNF654 | 0.554 | 13358 |
| LOC399744 | 0.585 | 18058 |
| SLC25A24 | 0.160 | 9619 |
| ARTN | 0.400 | 6145 |
| PDZD2 | 0.618 | 11806 |
| GPR172B | 0.619 | 24040 |
| OR2A9P | 0.213 | 11791 |


| MAX | 0.515 | 15213 |
| :---: | :---: | :---: |
| ZFP64 | 0.478 | 15315 |
| OSM | 0.652 | 24252 |
| SHH | 0.393 | 1114 |
| CAMKK2 | 0.589 | 6488 |
| INSIG1 | 0.412 | 6055 |
| HYOU1 | 0.454 | 1668 |
| KIAA1147 | 0.669 | 3375 |
| CARD14 | 0.482 | 9939 |
| LYST | 0.741 | 23112 |
| ACTR3B | 0.271 | 9248 |

## APPENDIX E. 387 GENES THAT CORRELATE WITH SYNERGY TO

## PACLITAXEL + CARBOPLATIN AND MET REQUIREMENTS FOR

## CLUSTERING.

Genes are listed as they are clustered in Figure 3.4

| Symbol | Correlation | Gene <br> ID |
| :---: | :---: | :---: |
| PHF7 |  | 3 |
| CLEC2B | 0.736 | 8207 |
| C4orf38 | 0.517 | 22639 |
| IMPA1 | 0.534 | 20539 |
| GPR137B | 0.278 | 4117 |
| NBAS | 0.765 | 6650 |
| HSPC159 | 0.567 | 5785 |
| CUL7 | 0.654 | 6660 |
| ERCC1 | 0.299 | 4882 |
| ERCC1 | 0.977 | 12210 |
| TGFBR3 | 0.709 | 10541 |
| KCNMA1 | 0.460 | 17823 |
| FAM110B | 0.514 | 12039 |
| RERG | 0.663 | 16079 |
| LAIR2 | 0.042 | 218 |
| CACNB4 | 0.873 | 7410 |
| LAIR2 | 0.708 | 19836 |
| HPCAL4 | 0.665 | 16870 |
| ARHGAP21 | 0.316 | 4239 |
| CEACAM1 | 0.622 | 17379 |
| RGPD1 | 0.488 | 7267 |
| ZNF580 | 0.678 | 17713 |
| FUZ | 0.682 | 18948 |
| NEURL2 | 0.593 | 22946 |
| PDE1B | 0.436 | 601 |
| SGK2 | 0.708 | 2602 |
| HAVCR2 | 0.812 | 16811 |
| MSMP | 0.634 | 11425 |
|  |  |  |


| KRT23 | 0.487 | 2141 |
| :---: | :---: | :---: |
| VARS2 | 0.670 | 5147 |
| C6orf81 | 0.470 | 13941 |
| DDT | 0.041 | 7788 |
| TIFA | 0.677 | 20968 |
| C9orf24 | 0.527 | 21908 |
| B3GNT2 | 0.241 | 1217 |
| DNMT3A | 0.571 | 4344 |
| PDE9A | 0.771 | 5006 |
| LTB4R2 | 0.884 | 18503 |
| QPRT | 0.414 | 9716 |
| DHTKD1 | 0.657 | 20043 |
| SNRNP35 | 0.591 | 12297 |
| MFSD9 | 0.599 | 16125 |
| FAM69B | 0.560 | 14395 |
| KISS1R | 0.405 | 13390 |
| ZSCAN29 | -0.065 | 1948 |
| C14orf101 | 0.488 | 2927 |
| ESCO1 | 0.686 | 7625 |
| ARHGEF1 | 0.773 | 10490 |
| SCYL3 | 0.658 | 6596 |
| SEPHS2 | 0.219 | 6678 |
| POMGNT1 | 0.775 | 9710 |
| ZNF16 | 0.629 | 2418 |
| MTF2 | 0.668 | 9316 |
| PHTF2 | 0.273 | 2991 |
| C1orf103 | 0.691 | 15110 |
| PRTFDC1 | 0.549 | 3047 |
| ARID4A | 0.523 | 8561 |
| NUPL1 | 0.761 | 14084 |
| CAMKK2 | 0.396 | 21441 |
| ZNF643 | 0.481 | 18663 |
| CAND2 | 0.293 | 9791 |
| PI4KA | 0.842 | 16364 |
| BRWD1 | 0.688 | 13745 |
| ROCK1 | 0.464 | 21355 |
| DCAF6 | 0.536 | 13310 |
| UBE2V1 | 0.728 | 14501 |


| NID1 | 0.670 | 15599 |
| :---: | :---: | :---: |
| BEX4 | 0.499 | 3742 |
| BEX4 | 0.941 | 14684 |
| CCR10 | 0.345 | 4760 |
| MFAP2 | 0.880 | 16687 |
| DLX1 | 0.704 | 4880 |
| SYT11 | 0.632 | 19061 |
| CDNF | 0.545 | 5163 |
| ATP5S | 0.540 | 6991 |
| ATP5S | 0.762 | 22546 |
| PRRX1 | 0.109 | 1890 |
| OR51B5 | 0.764 | 10263 |
| HBA1 | 0.207 | 8733 |
| RGS1 | 0.823 | 14683 |
| C6orf162 | 0.436 | 17546 |
| FDXR | 0.376 | 4523 |
| CSAG1 | 0.549 | 12132 |
| NCRNA00115 | 0.435 | 12086 |
| PLCG1 | 0.212 | 7380 |
| ZNF335 | 0.750 | 21120 |
| PTPN13 | 0.730 | 9942 |
| ZNF320 | 0.509 | 9090 |
| TERF1 | 0.500 | 544 |
| ARNT | 0.681 | 7173 |
| PIK3C3 | 0.774 | 21488 |
| C12orf23 | 0.599 | 10642 |
| OSTC | 0.678 | 15171 |
| WSB2 | 0.791 | 21472 |
| TMEM91 | 0.485 | 12833 |
| ZNF428 | 0.497 | 6086 |
| TMEM120A | 0.620 | 20201 |
| C2orf76 | 0.625 | 12666 |
| SHOC2 | 0.681 | 15020 |
| ATP5L | 0.616 | 13354 |
| SIRT4 | 0.661 | 14928 |
| TRIM9 | 0.289 | 1481 |
| B4GALT6 | 0.865 | 12971 |
| YPEL5 | 0.651 | 8919 |


| ELMO2 | 0.751 | 10424 |
| :---: | :---: | :---: |
| ABAT | 0.568 | 4043 |
| CCDC8 | 0.845 | 9742 |
| SEMA5A | 0.895 | 11068 |
| TRIM24 | 0.804 | 18484 |
| SVOPL | 0.780 | 23732 |
| EGR2 | 0.700 | 19212 |
| SERPING1 | 0.769 | 6623 |
| ADAM10 | 0.836 | 10119 |
| ARID3A | 0.727 | 21265 |
| COL3A1 | 0.725 | 6978 |
| IGDCC3 | 0.866 | 16350 |
| NDNL2 | 0.235 | 1833 |
| NFATC1 | 0.770 | 3070 |
| CHP | 0.689 | 22095 |
| USF2 | 0.701 | 23558 |
| CCK | 0.521 | 6659 |
| CIB2 | 0.783 | 11190 |
| ADCY6 | 0.682 | 7226 |
| TOM1 | 0.595 | 7802 |
| ENOSF1 | 0.323 | 9138 |
| TMEM151A | 0.724 | 15666 |
| CHGB | 0.785 | 20937 |
| CAMP | 0.551 | 18625 |
| PCMTD1 | 0.101 | 10612 |
| BTG1 | 0.741 | 15419 |
| SLC35C2 | 0.637 | 19136 |
| MRPL45 | 0.524 | 11888 |
| RNF170 | 0.681 | 13117 |
| MAP3K12 | 0.568 | 16369 |
| RRAGB | 0.708 | 22603 |
| HIST1H2BG | -0.002 | 1350 |
| HIST1H3D | 0.683 | 7129 |
| HIST1H2BC | 0.721 | 1462 |
| HIST1H1C | 0.937 | 17994 |
| HIST1H2BE | 0.898 | 4911 |
| HIST2H2AA3 | 0.740 | 6090 |
| HIST2H2AC | 0.989 | 19463 |


| PPP1R1C | 0.646 | 17913 |
| :---: | :---: | :---: |
| TDRKH | 0.517 | 9599 |
| H2AFJ | 0.738 | 17244 |
| ABHD8 | 0.648 | 16086 |
| LZTFL1 | 0.738 | 20058 |
| C14orf4 | 0.676 | 17173 |
| PDGFRA | 0.657 | 22631 |
| KDM3A | -0.055 | 4133 |
| LSM6 | 0.675 | 17770 |
| SPRR2F | 0.395 | 7329 |
| FRG1 | 0.588 | 8066 |
| SH3YL1 | 0.166 | 8431 |
| DPP4 | 0.699 | 15795 |
| SLC2A10 | 0.560 | 21366 |
| DUSP11 | 0.516 | 13259 |
| PLIN2 | -0.113 | 1493 |
| DTX3 | 0.652 | 20045 |
| ECSIT | 0.368 | 2928 |
| SCAMP5 | 0.791 | 24006 |
| DOCK3 | 0.718 | 22748 |
| PPAN | 0.562 | 21224 |
| TTC21A | 0.033 | 1865 |
| SLC12A5 | 0.722 | 6827 |
| HSD17B14 | 0.560 | 7284 |
| FGF11 | 0.696 | 18906 |
| EGFL8 | 0.484 | 17319 |
| TTLL1 | 0.356 | 3432 |
| HCST | 0.605 | 5356 |
| FAM195B | 0.771 | 21194 |
| GLA | -0.387 | 368 |
| CDC6 | 0.720 | 1606 |
| ACER3 | 0.482 | 3966 |
| POLR2L | 0.697 | 19841 |
| SLC6A8 | 0.456 | 5990 |
| SLC6A10P | 0.948 | 24425 |
| KRT6A | 0.466 | 12190 |
| SLC7A5 | 0.235 | 988 |
| DHRS4 | 0.714 | 4404 |
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| FAM125B | 0.624 | 2282 |
| :---: | :---: | :---: |
| HSD17B6 | 0.692 | 13044 |
| NCAPG2 | -0.049 | 6283 |
| MAP6D1 | 0.726 | 8979 |
| ERCC6L | 0.647 | 10942 |
| ERCC6L | 0.849 | 16445 |
| ZNF484 | 0.652 | 15752 |
| PHLDB1 | 0.650 | 16718 |
| CDH24 | 0.319 | 14869 |
| IL17D | 0.724 | 21259 |
| TYRO3 | 0.565 | 18538 |
| TELO2 | 0.382 | 7312 |
| ABCB6 | 0.721 | 9443 |
| ME3 | 0.815 | 12025 |
| RGS12 | 0.518 | 13322 |
| GAS6 | 0.046 | 479 |
| GAS6 | 0.990 | 14358 |
| UNKL | 0.480 | 24344 |
| SLC6A15 | 0.459 | 1138 |
| RAB11FIP5 | 0.393 | 4199 |
| PALLD | 0.692 | 11899 |
| LAMP2 | 0.660 | 12591 |
| SLC25A43 | 0.649 | 6112 |
| CHST3 | 0.743 | 12709 |
| MICAL2 | 0.391 | 4700 |
| RGS20 | 0.765 | 20855 |
| CAV2 | 0.733 | 8672 |
| MECP2 | 0.501 | 16709 |
| MPP1 | 0.709 | 17261 |
| RPS6KA4 | 0.799 | 19431 |
| S100A2 | 0.652 | 9780 |
| ANO1 | 0.700 | 20895 |
| TSPAN7 | 0.200 | 1464 |
| COL4A6 | 0.750 | 21154 |
| CES1 | 0.596 | 8911 |
| NOVA1 | 0.450 | 8690 |
| TSC22D1 | 0.700 | 16989 |
| AR | 0.663 | 6562 |


| PORCN | 0.746 | 21216 |
| :---: | :---: | :---: |
| CNTN1 | 0.447 | 12561 |
| FPR1 | 0.167 | 3300 |
| C1S | 0.682 | 23974 |
| CD99L2 | 0.626 | 5934 |
| CD99L2 | 0.952 | 17615 |
| HPD | 0.158 | 2391 |
| NQO1 | 0.732 | 2643 |
| NEDD9 | 0.409 | 6894 |
| CCL2 | 0.478 | 3308 |
| DHDPSL | 0.774 | 22043 |
| PTGR1 | 0.598 | 21053 |
| SLC11A1 | 0.424 | 2645 |
| TSKU | 0.672 | 2711 |
| AKR1B10 | 0.731 | 17267 |
| HSD11B1 | 0.517 | 18431 |
| KRT81 | 0.269 | 1339 |
| MID1 | 0.780 | 22602 |
| KRT86 | 0.763 | 14363 |
| CSRP1 | 0.387 | 20645 |
| PCID2 | 0.511 | 2462 |
| UBA1 | 0.732 | 9570 |
| TMOD3 | 0.583 | 7104 |
| GCNT2 | 0.683 | 10175 |
| TENC1 | 0.494 | 2572 |
| ALPK2 | 0.935 | 17064 |
| SNRPN | 0.447 | 5767 |
| SNRPN | 0.996 | 8128 |
| EFHD2 | 0.147 | 3541 |
| CDC42EP2 | 0.789 | 19781 |
| PRR4 | 0.762 | 16222 |
| MYH9 | 0.572 | 5213 |
| C15orf52 | 0.747 | 7286 |
| MFGE8 | 0.551 | 17870 |
| CCDC136 | 0.599 | 23169 |
| ARAP3 | 0.756 | 23827 |
| CD151 | 0.552 | 6220 |
| CD151 | 0.809 | 21423 |
|  |  |  |


| PLSCR4 | 0.592 | 13379 |
| :---: | :---: | :---: |
| PLCE1 | 0.510 | 20021 |
| PARVA | 0.432 | 6255 |
| MAP1B | 0.581 | 9165 |
| MAP1B | 0.970 | 18157 |
| GABRE | 0.658 | 16764 |
| COL18A1 | 0.580 | 17110 |
| FHOD3 | 0.227 | 4351 |
| C9orf25 | 0.648 | 12379 |
| STEAP3 | 0.378 | 4370 |
| FOSL1 | 0.826 | 22679 |
| MAP4 | 0.695 | 7579 |
| VCL | 0.699 | 9587 |
| PITX1 | 0.356 | 6542 |
| DIAPH2 | 0.793 | 17018 |
| LRP8 | 0.691 | 15615 |
| DDIT4 | 0.440 | 10516 |
| MPP6 | 0.280 | 10925 |
| TMEM100 | 0.621 | 13438 |
| RGP1 | 0.694 | 15762 |
| GLDN | 0.336 | 18673 |
| NOL3 | 0.278 | 449 |
| RAB20 | 0.579 | 4112 |
| CFI | 0.401 | 5614 |
| FAM113B | 0.794 | 13752 |
| GRB10 | 0.692 | 9472 |
| GRB10 | 0.977 | 19171 |
| FGFRL1 | 0.693 | 14595 |
| SULT1A3 | 0.320 | 1014 |
| SULT1A2 | 0.836 | 20836 |
| KRT7 | 0.730 | 12011 |
| MOCOS | 0.626 | 15161 |
| COBL | 0.593 | 1959 |
| ADAM15 | 0.705 | 6361 |
| ADAM15 | 0.972 | 11353 |
| ADAM15 | 0.969 | 21115 |
| SEPX1 | 0.664 | 4773 |
| NCS1 | 0.673 | 23331 |
|  |  |  |


| NINJ1 | 0.740 | 23879 |
| :---: | :---: | :---: |
| SEL1L3 | 0.132 | 5021 |
| HSD3B7 | 0.804 | 5128 |
| HTATIP2 | 0.781 | 15346 |
| ITPR3 | 0.596 | 19765 |
| DYNLT3 | 0.870 | 19783 |
| LIMCH1 | 0.428 | 5922 |
| MYO5C | 0.715 | 6324 |
| ASB9 | 0.416 | 594 |
| ASB9 | 0.942 | 14582 |
| GALNTL4 | 0.702 | 599 |
| NAV2 | 0.760 | 14003 |
| ABCC3 | 0.337 | 1048 |
| EPHX1 | 0.801 | 22532 |
| CYB5A | 0.663 | 7085 |
| CYB5A | 0.976 | 18463 |
| G6PD | 0.570 | 1342 |
| G6PD | 0.965 | 13738 |
| GPR126 | 0.357 | 2753 |
| ME1 | 0.721 | 11033 |
| SDPR | 0.542 | 20320 |
| C9orf84 | 0.573 | 1167 |
| STBD1 | 0.885 | 19750 |
| IDS | 0.787 | 11723 |
| MYLK | 0.678 | 23360 |
| FBXO32 | 0.474 | 6223 |
| TRIM47 | 0.499 | 2855 |
| PRKAR1B | 0.424 | 2747 |
| COL8A1 | 0.654 | 10850 |
| C9orf140 | 0.423 | 3234 |
| FBXL13 | 0.593 | 7020 |
| C1orf61 | 0.811 | 16224 |
| GCGR | 0.761 | 19475 |
| PRICKLE3 | 0.180 | 2880 |
| PRSS3 | 0.728 | 16536 |
| PLAC1 | 0.598 | 3445 |
| HMGB3 | 0.767 | 24274 |
| IL7R | 0.575 | 12149 |


| MALL | -0.002 | 2053 |
| :---: | :---: | :---: |
| TNFAIP2 | 0.764 | 6930 |
| HAPLN3 | 0.771 | 16250 |
| CHST15 | 0.417 | 23610 |
| MSN | 0.440 | 2440 |
| TSPO | 0.799 | 3967 |
| TSPO | 0.986 | 22452 |
| NQO1 | 0.832 | 17427 |
| C9orf89 | 0.599 | 16633 |
| SLC16A9 | 0.192 | 20324 |
| RPL39L | 0.677 | 22540 |
| SLC16A3 | -0.015 | 573 |
| LAMB3 | 0.682 | 2401 |
| PKP3 | 0.710 | 9197 |
| SFN | 0.789 | 11808 |
| ELFN2 | 0.464 | 13154 |
| SERPINB5 | 0.844 | 20386 |
| TMEM187 | 0.607 | 16905 |
| C9orf95 | 0.388 | 6316 |
| PTK6 | 0.699 | 20475 |
| KLK3 | 0.251 | 1492 |
| PRSS23 | 0.834 | 7194 |
| FLNB | 0.699 | 16897 |
| GPC1 | 0.732 | 23385 |
| KLF10 | 0.467 | 7227 |
| INF2 | 0.772 | 9947 |
| INF2 | 0.941 | 16390 |
| TUBB3 | 0.709 | 13095 |
| CTSZ | 0.233 | 13915 |
| EFEMP1 | 0.518 | 20108 |
| EFEMP1 | 0.951 | 22515 |
| NAAA | 0.228 | 16732 |
| JAG2 | 0.657 | 21481 |
| LCK | 0.317 | 602 |
| MAPK9 | 0.867 | 6060 |
| C13orf15 | 0.590 | 818 |
| TMEM156 | 0.804 | 6540 |
| FAM129B | 0.615 | 10393 |


| FAM129B | 0.879 | 13372 |
| :---: | :---: | :---: |
| ADK | 0.429 | 10130 |
| COMMD10 | 0.733 | 21285 |
| TRIM6 | 0.450 | 12585 |
| PGM2L1 | 0.640 | 23522 |
| TRIM6 | 0.638 | 19359 |
| SLC9A3R2 | -0.190 | 9832 |
| KCTD5 | 0.661 | 24088 |
| SH3RF2 | 0.534 | 18006 |
| PDLIM3 | 0.638 | 20398 |
| GPX3 | 0.576 | 17664 |
| NOXO1 | 0.499 | 1870 |
| NOXO1 | 0.920 | 13980 |
| PILRB | 0.707 | 15440 |
| BCL9L | 0.697 | 19138 |
| HES2 | 0.635 | 23143 |
| C8orf34 | 0.348 | 15072 |

## APPENDIX F. 529 GENES THAT CORRELATE WITH SYNERGY TO

## PEMETREXED + CISPLATIN, AND MET REQUIREMENTS FOR

## CLUSTERING.

Genes are listed as they are shown in the cluster in Figure 3.5

| Symbol | Correlation | Gene <br> ID |
| :---: | :---: | :---: |
| CD164 |  | 15 |
| H3F3A | 0.759 | 7736 |
| ZFP1 | 0.695 | 6917 |
| RAD1 | 0.753 | 7411 |
| SLC43A2 | 0.517 | 6024 |
| FLOT2 | 0.630 | 7925 |
| MYLIP | 0.519 | 15815 |
| NEDD9 | 0.649 | 19751 |
| METTL7A | 0.451 | 6017 |
| DCAF6 | 0.626 | 16591 |
| MFAP4 | 0.598 | 9910 |
| CLEC1A | 0.786 | 23649 |
| PDGFRB | 0.706 | 19090 |
| SYMPK | 0.180 | 533 |
| PAK4 | 0.721 | 1476 |
| CLASRP | 0.842 | 8384 |
| SIRT2 | 0.813 | 16155 |
| SAMD4B | 0.554 | 5942 |
| C19orf12 | 0.773 | 20785 |
| SUMO1 | 0.692 | 8612 |
| ZBTB2 | 0.435 | 243 |
| TXNL1 | 0.728 | 3024 |
| SEPT7 | 0.640 | 1399 |
| NNT | 0.796 | 19256 |
| BID | 0.725 | 4748 |
| PTMA | 0.619 | 1512 |
| SMAD7 | 0.756 | 12607 |
| ANKRD27 | 0.473 | 18064 |
| LSM5 | 0.776 | 21894 |
|  |  |  |


| COL8A2 | 0.208 | 416 |
| :---: | :---: | :---: |
| SH2B2 | 0.631 | 11757 |
| NLK | 0.634 | 19872 |
| TMEM128 | 0.649 | 5596 |
| ARFGEF1 | 0.695 | 11884 |
| RRM2B | 0.293 | 3348 |
| C7orf11 | 0.718 | 9582 |
| CYP2S1 | 0.180 | 2913 |
| CYP2S1 | 0.793 | 22226 |
| PNMAL1 | 0.609 | 21616 |
| PRKD2 | 0.346 | 3099 |
| PRKD2 | 0.826 | 21252 |
| VASP | 0.566 | 7497 |
| DEDD2 | 0.404 | 12582 |
| LRCH4 | 0.452 | 5153 |
| ANXA4 | 0.651 | 11294 |
| EGLN3 | 0.561 | 19725 |
| C6orf120 | 0.342 | 17952 |
| ACAP2 | 0.230 | 384 |
| MRPL47 | 0.808 | 16743 |
| DBR1 | 0.599 | 19151 |
| TMEM8A | 0.529 | 426 |
| RPL23AP64 | 0.912 | 20197 |
| TMEM199 | 0.744 | 7176 |
| RPL23 | 0.649 | 1266 |
| SUMO2 | 0.852 | 1661 |
| RPL9 | 0.792 | 20983 |
| HNRNPA1 | 0.857 | 23659 |
| PABPC1 | 0.665 | 9868 |
| ZNHIT3 | 0.731 | 21949 |
| GPBP1 | 0.579 | 3656 |
| POLR2J2 | 0.817 | 9271 |
| DUSP11 | 0.684 | 13259 |
| HIF1A | 0.516 | 8999 |
| C4orf41 | 0.686 | 13149 |
| EXOSC10 | 0.456 | 2831 |
| TATDN1 | 0.858 | 3694 |
| RPL7 | 0.866 | 8916 |


| ZFAND1 | 0.903 | 23880 |
| :---: | :---: | :---: |
| RTCD1 | 0.678 | 23154 |
| MTF2 | 0.718 | 9316 |
| INTS8 | 0.783 | 22004 |
| C14orf104 | 0.766 | 8244 |
| XPO4 | 0.864 | 12083 |
| UFM1 | 0.783 | 14795 |
| SACM1L | 0.778 | 8531 |
| CTCFL | 0.822 | 12830 |
| ARPP19 | 0.697 | 21815 |
| PAK1IP1 | 0.571 | 6467 |
| PRR3 | 0.830 | 18111 |
| SRSF11 | 0.645 | 3145 |
| CUL4A | 0.801 | 23421 |
| PRKDC | 0.747 | 11012 |
| ELOVL5 | 0.476 | 13805 |
| G3BP1 | 0.798 | 18357 |
| RAP1B | 0.850 | 21766 |
| ACTR3 | 0.613 | 22574 |
| CDKN1B | 0.459 | 3310 |
| PAPSS1 | 0.811 | 6083 |
| YY1 | 0.918 | 22075 |
| FAM103A1 | 0.847 | 12707 |
| WRB | 0.720 | 15016 |
| FAM8A1 | 0.759 | 15658 |
| ATXN1 | 0.462 | 16538 |
| FGFR1OP2 | 0.585 | 4456 |
| TM7SF3 | 0.806 | 6844 |
| EHMT2 | 0.775 | 12489 |
| ZNF226 | 0.583 | 22984 |
| SPAST | 0.184 | 1505 |
| TTC35 | 0.707 | 7318 |
| FAM49B | 0.797 | 8687 |
| DCAF13 | 0.587 | 9335 |
| HRSP12 | 0.754 | 20371 |
| USP8 | 0.504 | 22241 |
| C6orf211 | 0.686 | 11859 |
| FAM108B1 | 0.746 | 19806 |


| RAD21 | 0.545 | 7425 |
| :---: | :---: | :---: |
| SLBP | 0.782 | 14355 |
| HMGB2 | 0.848 | 18962 |
| AHNAK | 0.676 | 11853 |
| KBTBD7 | 0.798 | 23547 |
| TSC22D1 | 0.438 | 1277 |
| FBXO30 | 0.805 | 17134 |
| CCNH | 0.667 | 6323 |
| ISCA1 | 0.706 | 19111 |
| TAF9 | 0.673 | 3140 |
| PCGF6 | 0.789 | 5976 |
| OSBPL8 | 0.757 | 12765 |
| NAP1L1 | 0.868 | 21737 |
| GNA13 | 0.898 | 21898 |
| GMNN | 0.702 | 15809 |
| NDUFAF4 | 0.640 | 6260 |
| WDR3 | 0.781 | 10920 |
| PRR3 | 0.459 | 12712 |
| C12orf11 | 0.714 | 17057 |
| NOP2 | 0.635 | 22697 |
| MRPL48 | 0.309 | 2416 |
| NUP62 | 0.699 | 8326 |
| C11orf73 | 0.756 | 12094 |
| EED | 0.762 | 17689 |
| OVOS2 | 0.734 | 12050 |
| SARS2 | 0.710 | 15389 |
| FBL | 0.870 | 16095 |
| TGS1 | 0.725 | 6910 |
| CAPN10 | 0.819 | 8285 |
| C1orf212 | 0.719 | 22978 |
| RPL14 | 0.608 | 7163 |
| GSR | 0.732 | 14800 |
| RPL13 | 0.620 | 19452 |
| RPL13P5 | 0.881 | 22300 |
| TIPRL | 0.495 | 15335 |
| SLMO1 | 0.683 | 22793 |
| USP25 | 0.129 | 2016 |
| PDS5B | 0.716 | 2912 |


| BNIP3L | 0.450 | 2043 |
| :---: | :---: | :---: |
| HS2ST1 | 0.705 | 3683 |
| ATP5S | 0.727 | 6991 |
| TMEM169 | 0.274 | 2321 |
| NAGS | 0.661 | 5617 |
| C9orf82 | 0.109 | 1243 |
| CCBL2 | 0.605 | 2568 |
| TGIF2 | 0.702 | 4374 |
| HNRNPUL1 | 0.727 | 6010 |
| CXCR7 | 0.076 | 1429 |
| GRK5 | 0.542 | 10523 |
| KLK3 | 0.378 | 1492 |
| RASL11B | 0.560 | 10908 |
| PPP2CB | 0.663 | 22295 |
| TUBB2B | 0.461 | 23092 |
| PTK2B | 0.402 | 9473 |
| DPYSL2 | 0.687 | 10681 |
| PNMA2 | 0.782 | 15070 |
| EMILIN2 | 0.110 | 3889 |
| PDLIM1 | 0.620 | 4558 |
| CARS | 0.154 | 106 |
| SLCO1A2 | 0.711 | 24433 |
| MCTS1 | 0.436 | 5550 |
| SOX30 | 0.480 | 4327 |
| LGALS12 | 0.491 | 13628 |
| ABCG1 | 0.633 | 18668 |
| ABCG1 | 0.920 | 19425 |
| RNF157 | 0.370 | 150 |
| SORD | 0.740 | 8126 |
| C6orf162 | 0.683 | 17546 |
| KRTAP19-6 | 0.599 | 2339 |
| ABCD4 | 0.706 | 23429 |
| OR52A5 | 0.422 | 4563 |
| RBPJL | 0.647 | 21426 |
| SNCG | 0.507 | 22905 |
| TFAP4 | 0.402 | 8928 |
| EXOSC5 | 0.743 | 9424 |
| CALB2 | 0.559 | 14068 |


| SLC2A6 | 0.616 | 19805 |
| :---: | :---: | :---: |
| CCNB1IP1 | 0.416 | 1570 |
| CCNB1IP1 | 0.966 | 21046 |
| ORM1 | 0.694 | 2314 |
| KIF21B | 0.705 | 14667 |
| TNFRSF9 | 0.620 | 18107 |
| TOP1MT | 0.395 | 18758 |
| TOP1MT | 0.762 | 19705 |
| PFKM | 0.743 | 23131 |
| CORO1C | 0.507 | 2303 |
| C9orf21 | 0.768 | 5741 |
| KATNAL1 | 0.589 | 8075 |
| DSG4 | 0.759 | 16630 |
| RPL7A | 0.419 | 9253 |
| MRPS12 | 0.752 | 22786 |
| CCDC34 | 0.483 | 11446 |
| TIMM8A | 0.541 | 10812 |
| SURF2 | 0.390 | 8532 |
| C20orf27 | 0.609 | 9272 |
| BEND4 | 0.305 | 18879 |
| PPP1R14A | 0.651 | 19242 |
| RAET1G | 0.482 | 21554 |
| FBXO17 | 0.361 | 3465 |
| SGK3 | 0.656 | 12768 |
| SEPT4 | 0.597 | 15333 |
| SLCO2B1 | 0.611 | 21622 |
| UPF3A | 0.084 | 393 |
| SKP2 | 0.725 | 5671 |
| CDK5RAP2 | 0.542 | 18178 |
| CCDC25 | 0.516 | 6530 |
| OTUD6B | 0.666 | 17834 |
| NAA35 | 0.520 | 17290 |
| HSDL2 | 0.527 | 4388 |
| MRPL52 | 0.742 | 22910 |
| NUDT15 | 0.656 | 11439 |
| KPNA2 | 0.710 | 20113 |
| SMC2 | 0.520 | 10841 |
| PSIP1 | 0.761 | 17281 |


| PGBD1 | 0.581 | 12947 |
| :---: | :---: | :---: |
| KIAA0368 | 0.542 | 20828 |
| TRMT11 | 0.706 | 21901 |
| C9orf9 | 0.301 | 18706 |
| DENND1A | 0.430 | 1891 |
| SRPK2 | 0.443 | 7059 |
| PUS7 | 0.717 | 12802 |
| TRUB2 | 0.696 | 18162 |
| MRPS28 | 0.790 | 21082 |
| FKBP5 | 0.561 | 8741 |
| KAT5 | -0.009 | 4611 |
| AP2A1 | 0.564 | 5456 |
| N6AMT2 | 0.646 | 11480 |
| CETP | 0.497 | 23994 |
| RASSF4 | 0.012 | 88 |
| EML4 | 0.547 | 503 |
| COL18A1 | 0.629 | 17110 |
| MYO18A | 0.488 | 982 |
| TIAF1 | 0.933 | 11897 |
| DYRK1B | 0.758 | 5158 |
| DYRK1B | 0.846 | 15204 |
| ICK | 0.473 | 11160 |
| TDRD7 | 0.643 | 17203 |
| CDH24 | 0.399 | 14869 |
| MED21 | 0.399 | 671 |
| HECA | 0.692 | 1986 |
| XRN1 | 0.752 | 6458 |
| LHFPL2 | 0.434 | 1157 |
| C4orf33 | 0.043 | 6128 |
| SPAG1 | 0.424 | 8983 |
| SRD5A3 | 0.179 | 21757 |
| CHRAC1 | -0.225 | 1976 |
| ZNF707 | 0.634 | 23908 |
| PRMT2 | 0.382 | 8718 |
| RBBP4 | 0.648 | 23417 |
| TIMM10 | 0.164 | 10736 |
| PTER | 0.593 | 19709 |
| STK33 | 0.182 | 2133 |


| CPSF4 | 0.724 | 18360 |
| :---: | :---: | :---: |
| RABL2A | 0.565 | 23938 |
| TSC22D2 | 0.372 | 7918 |
| CASP6 | 0.704 | 17854 |
| C7orf49 | 0.575 | 23253 |
| KCNQ3 | 0.470 | 19130 |
| KLF8 | 0.684 | 21310 |
| TSPAN32 | -0.043 | 2560 |
| SSX5 | 0.736 | 8223 |
| CEP68 | 0.413 | 3670 |
| GPX1 | 0.546 | 18398 |
| GRIK2 | 0.465 | 3297 |
| PLCG1 | 0.565 | 3315 |
| ITM2C | -0.363 | 3745 |
| ITM2C | 0.967 | 8903 |
| BASP1 | 0.487 | 7079 |
| CD3D | 0.273 | 5402 |
| ARRB1 | 0.619 | 8224 |
| PIGX | 0.541 | 16888 |
| RAMP2 | 0.666 | 17923 |
| LIMK1 | 0.320 | 6343 |
| ST6GALNAC6 | 0.503 | 11973 |
| HIST2H2BF | -0.210 | 112 |
| ANKRD36B | 0.538 | 780 |
| ANKRD36 | 0.871 | 18424 |
| CASC4 | 0.651 | 11102 |
| ZDHHC9 | 0.817 | 16272 |
| UNC5A | 0.347 | 6373 |
| ALS2CL | 0.656 | 14984 |
| CTTN | 0.742 | 23947 |
| XDH | 0.449 | 8098 |
| ARHGEF4 | 0.391 | 12353 |
| PAOX | 0.132 | 15918 |
| FAM134B | 0.535 | 983 |
| FAM134B | 0.947 | 20931 |
| LDHD | 0.663 | 10929 |
| FAM134B | 0.403 | 10477 |
| VPS13C | 0.397 | 3486 |


| GALC | 0.637 | 10859 |
| :---: | :---: | :---: |
| GALC | 0.871 | 11358 |
| ANG | 0.783 | 19043 |
| ANG | 0.920 | 22967 |
| PHYH | 0.467 | 9499 |
| PHYH | 0.896 | 13261 |
| HERPUD1 | 0.674 | 14968 |
| ROPN1B | 0.518 | 1500 |
| SLPI | 0.712 | 7153 |
| GNPTG | 0.719 | 23560 |
| CSTF1 | 0.320 | 4857 |
| LAMB2 | 0.767 | 24459 |
| XBP1 | 0.785 | 7933 |
| XBP1 | 0.982 | 18154 |
| AGR2 | 0.802 | 10248 |
| C2CD4B | 0.824 | 18627 |
| C9orf86 | 0.655 | 11053 |
| GDF15 | 0.299 | 16694 |
| IRX3 | 0.590 | 18202 |
| BCL6 | 0.666 | 20277 |
| KDELR3 | 0.164 | 1756 |
| KDELR3 | 0.826 | 14549 |
| SOS2 | 0.513 | 1758 |
| LGR4 | 0.725 | 14896 |
| PHKB | 0.667 | 4071 |
| NOMO1 | 0.510 | 8805 |
| MIA3 | 0.732 | 21658 |
| ANGPTL4 | 0.683 | 15138 |
| SUV420H1 | 0.357 | 8171 |
| SLC39A9 | 0.723 | 13629 |
| LMLN | 0.744 | 14756 |
| ATP5J | 0.410 | 10145 |
| ARFIP1 | 0.631 | 13943 |
| TAOK2 | 0.109 | 1683 |
| ATF7IP | 0.641 | 8480 |
| PC | 0.729 | 18865 |
| SYTL2 | 0.145 | 2590 |
| PDXDC1 | 0.813 | 10432 |


| RNF207 | 0.693 | 15705 |
| :---: | :---: | :---: |
| KITLG | 0.513 | 22497 |
| C16orf93 | 0.523 | 13349 |
| CMTM4 | 0.718 | 19409 |
| CES3 | 0.531 | 5984 |
| HIPK3 | 0.524 | 9956 |
| ANXA11 | 0.739 | 22707 |
| ZMAT1 | 0.493 | 15761 |
| ECHDC2 | 0.329 | 7530 |
| MUC1 | 0.791 | 24444 |
| DUSP8 | 0.574 | 16150 |
| LONRF2 | 0.296 | 20270 |
| COG7 | 0.394 | 3311 |
| FRAT1 | 0.624 | 11172 |
| ENTPD8 | 0.703 | 15940 |
| PIP | 0.568 | 12965 |
| FUT6 | 0.699 | 18599 |
| DOK5 | 0.625 | 18669 |
| SLC35A2 | 0.247 | 16179 |
| ZSCAN10 | 0.743 | 22719 |
| PTPRH | 0.450 | 23982 |
| ST3GAL1 | 0.459 | 4346 |
| ST3GAL1 | 0.762 | 19453 |
| NPDC1 | 0.583 | 6179 |
| AKAP2 | 0.489 | 11896 |
| FAM20C | 0.656 | 15764 |
| FAM20C | 0.821 | 16037 |
| ACADVL | 0.427 | 1942 |
| ACADVL | 0.865 | 4141 |
| AHR | 0.716 | 19422 |
| GPHN | 0.446 | 3733 |
| GPATCH2 | 0.814 | 21132 |
| GPHN | 0.563 | 20098 |
| WDFY3 | 0.604 | 5391 |
| PSEN1 | 0.738 | 15944 |
| PATZ1 | 0.630 | 7513 |
| CHKB | 0.764 | 11143 |
| SYNJ2BP | 0.721 | 10411 |


| EXD2 | 0.855 | 23379 |
| :---: | :---: | :---: |
| TMED10 | 0.625 | 13295 |
| ANKRD23 | 0.166 | 4349 |
| LOC441268 | 0.640 | 11728 |
| HSF4 | 0.751 | 13620 |
| HSF4 | 0.733 | 16187 |
| NBPF1 | 0.665 | 5234 |
| NBPF1 | 0.956 | 17193 |
| CRIPAK | 0.563 | 13871 |
| KIAA1530 | 0.874 | 18998 |
| LPGAT1 | -0.288 | 292 |
| MAST4 | 0.626 | 14208 |
| FAM46A | 0.448 | 12734 |
| DNASE1L1 | 0.558 | 13062 |
| ABHD2 | 0.608 | 9808 |
| CRLF2 | 0.656 | 17241 |
| C9orf23 | 0.526 | 13397 |
| MBTPS2 | 0.624 | 15947 |
| PARD6A | 0.193 | 1474 |
| HIST2H2AC | 0.755 | 19463 |
| UHMK1 | 0.642 | 7616 |
| FGF12 | 0.709 | 13314 |
| RIMS2 | 0.517 | 11412 |
| FBXO15 | 0.183 | 2497 |
| C21orf119 | 0.736 | 11301 |
| LRPAP1 | 0.624 | 8868 |
| FAM110C | 0.688 | 20514 |
| THNSL2 | 0.383 | 10487 |
| ZDHHC13 | 0.655 | 19191 |
| THSD4 | 0.518 | 22708 |
| PIGO | 0.212 | 10748 |
| TMEM205 | 0.764 | 23577 |
| PIGO | 0.530 | 16966 |
| DOCK3 | 0.586 | 22748 |
| TMEM134 | 0.367 | 2385 |
| TMEM134 | 0.981 | 18231 |
| C1orf228 | 0.755 | 4720 |
| DPP3 | 0.495 | 14880 |


| RCE1 | 0.752 | 20327 |
| :---: | :---: | :---: |
| IFI6 | 0.592 | 3203 |
| CORO1B | 0.699 | 11955 |
| FOXJ1 | 0.648 | 10311 |
| MGST3 | 0.804 | 23370 |
| ZNF586 | 0.659 | 14703 |
| POLD4 | 0.262 | 3399 |
| GSTO2 | 0.628 | 7444 |
| TCEAL8 | 0.072 | 854 |
| ARFGEF2 | 0.702 | 11777 |
| BEX5 | 0.151 | 4870 |
| EIF4E3 | 0.692 | 11020 |
| TMSB15A | 0.525 | 5770 |
| NR1D2 | 0.517 | 8789 |
| RBPMS | 0.246 | 1991 |
| KIAA0513 | 0.623 | 18751 |
| C20orf46 | 0.600 | 19581 |
| CYB5D2 | 0.559 | 8639 |
| SYTL2 | 0.670 | 22080 |
| GPR37 | 0.716 | 23557 |
| SPINK1 | 0.422 | 7399 |
| VWA5A | 0.632 | 16590 |
| ELMOD2 | 0.404 | 8140 |
| ARMCX2 | 0.669 | 12642 |
| CTSA | 0.438 | 22292 |
| TSPAN13 | 0.463 | 11240 |
| TLE2 | 0.818 | 21547 |
| EPS8L1 | 0.707 | 16557 |
| MGAT4A | 0.693 | 20007 |
| C1orf58 | -0.039 | 14470 |
| IGSF5 | 0.634 | 21470 |
| ERO1L | 0.534 | 15645 |
| RBM11 | 0.522 | 23546 |
| OGDH | 0.177 | 115 |
| LIF | 0.627 | 8852 |
| SLCO4A1 | 0.723 | 14910 |
| TK2 | 0.436 | 18151 |
| FAM21C | 0.466 | 3177 |


| ZC3H14 | 0.582 | 20019 |
| :---: | :---: | :---: |
| VPS53 | 0.585 | 20995 |
| PBLD | 0.318 | 13811 |
| AMPH | 0.420 | 1183 |
| MAP2K3 | 0.583 | 23410 |
| SRGAP1 | 0.363 | 8029 |
| USP53 | 0.614 | 21370 |
| MYPN | 0.289 | 8742 |
| IL24 | 0.688 | 14405 |
| MSC | 0.861 | 24031 |
| GK | 0.542 | 13531 |
| SIM2 | 0.739 | 14242 |
| C15orf48 | 0.252 | 3721 |
| C15orf48 | 0.960 | 13373 |
| GEM | 0.421 | 14905 |
| C11orf63 | 0.432 | 5714 |
| MCOLN1 | 0.663 | 20998 |
| UBASH3B | 0.700 | 6272 |
| SPHK1 | 0.706 | 8082 |
| PPP2R5B | 0.408 | 10643 |
| MYOF | 0.382 | 21283 |
| CDC42BPA | 0.504 | 10344 |
| C5orf25 | 0.724 | 19159 |
| CLCC1 | 0.406 | 11366 |
| TCTN3 | 0.285 | 3185 |
| OSBP2 | 0.617 | 11906 |
| TYMP | 0.482 | 7691 |
| NPC1 | 0.623 | 24309 |
| TOM1L1 | 0.595 | 18341 |
| TNFRSF6B | 0.388 | 20515 |
| GPR89B | 0.165 | 802 |
| DPM3 | 0.632 | 9557 |
| DPM3 | 0.945 | 23661 |
| CASP9 | 0.451 | 7551 |
| DPAGT1 | 0.708 | 8933 |
| C9orf116 | 0.225 | 8070 |
| HIST2H4A | 0.657 | 16188 |
| FAM91A2 | 0.636 | 12183 |


| TMEM79 | 0.274 | 1669 |
| :---: | :---: | :---: |
| C16orf75 | 0.609 | 14762 |
| ARL5B | 0.388 | 5731 |
| SH3GL2 | 0.308 | 8568 |
| RAPH1 | 0.789 | 10776 |
| FAM3B | 0.672 | 20214 |
| MUTYH | 0.075 | 1069 |
| PMVK | 0.601 | 4375 |
| MAPT | 0.741 | 8617 |
| BOLA1 | 0.724 | 14137 |
| HAX1 | 0.692 | 14218 |
| RAG1AP1 | 0.610 | 5325 |
| FAM189B | 0.476 | 13601 |
| COQ2 | 0.621 | 18343 |
| PLEKHH1 | 0.093 | 8197 |
| CYP27B1 | 0.647 | 9673 |
| MT2A | 0.583 | 1451 |
| MT1G | 0.728 | 3799 |
| BMP2 | 0.548 | 14353 |
| SETD3 | 0.169 | 934 |
| CDK8 | 0.622 | 14345 |
| RRM2 | 0.497 | 1635 |
| TMEM48 | 0.743 | 13760 |
| PPM1G | 0.443 | 3006 |
| UHRF1 | 0.639 | 5190 |
| PDLIM5 | 0.483 | 12713 |
| PDLIM5 | 0.770 | 19353 |
| FSCN1 | 0.559 | 14863 |
| GDA | 0.808 | 14877 |
| REEP1 | -0.447 | 4395 |
| GALNTL1 | 0.669 | 21537 |
| H2AFY2 | 0.570 | 9581 |
| DOCK5 | 0.502 | 10779 |
| CTAG2 | 0.579 | 14092 |
| CTAG2 | 0.945 | 21049 |
| POGZ | 0.249 | 5978 |
| ZBTB25 | 0.600 | 6632 |
| TRIP11 | 0.723 | 9304 |


| TTC8 | 0.705 | 8591 |
| :---: | :---: | :---: |
| KIAA0913 | 0.472 | 18828 |
| SLC38A7 | 0.571 | 11187 |
| CLCN5 | 0.610 | 16703 |
| FGF12 | 0.309 | 13449 |
| GNL3 | 0.670 | 22616 |

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