

TRANSCRIPTIONAL PROFILING OF EARLY CARDIAC DEVELOPMENT

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TRANSCRIPTIONAL PROFILING OF EARLY CARDIAC DEVELOPMENT

by

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Cardiogenesis is an intricate process that spans nearly the entire developmental history of the mammal. A thorough comprehension of the molecular interactions that direct cardiac development will improve our ability to understand and treat cardiovascular diseases. The earliest stages of heart development are of particular interest because it is during these stages that patterning of cardiac structure appears critical. Traditionally, studies of these early developmental processes have been conducted on chicken, fish, or frog embryos due to ease of manipulation. More recently, however, the wide availability of tools designed to manipulate and isolate cell populations in the murine embryo, together with the advent of

technologies for studying gene expression at the transcriptome level, have allowed for detailed study of these events in mammalian systems.

I applied transgenic labeling and flow cytometry to isolate cardiac cell populations from early mouse embryos. Transcriptome analysis of these cell populations allowed me to characterize unique gene expression patterns and identify novel genetic pathways relevant to cardiac development. I undertook three interrelated studies. First, I completed a survey of the transcriptome of the developing heart at the cardiac crescent, linear heart tube, and looped heart tube stages to describe molecular signatures in the developing heart. I defined gene expression patterns unique to the cardiac crescent and looped heart, and identified novel markers of the developing heart. The second study focused on defining the transcriptional network of a key cardiac regulator, *Nkx2.5*. I identified transcripts misexpressed during the early development of *Nkx2.5* null embryos, including the *Nkx2.5* transcriptional targets *ETS-related transcription factor 71* and *vascular cell adhesion molecule*. Lastly, I characterized *Nkx2.5*-dependent left-right patterning in the cardiac crescent that revealed early specification of chamber myocardial lineages. In conclusion, these studies have elucidated the molecular profile of the developing heart and provided novel insights into the earliest stages of cardiac development.

TABLE OF CONTENTS

DEDICATION	ii
TITLE	iii
ACKNOWLEDGEMENTS	iv
ABSTRACT	vi
TABLE OF CONTENTS	viii
PUBLICATIONS	xi
LIST OF FIGURES	xii
LIST OF TABLES	xiv
LIST OF APPENDICES	xv
CHAPTER ONE. INTRODUCTION TO EVENTS IN EARLY CARIOGENESIS	1
Early morphogenetic events in cardiogenesis	1
Origins of the cardiac mesoderm	4
The primary heart field	4
The secondary heart field	6
Aims of dissertation research	6
CHAPTER TWO. MATERIALS AND METHODS	8
Generation and analysis of transgenic mice	8
Tissue immunohistochemistry	8
Flow cytometry	9

Genotyping of <i>Nkx2.5</i> mutant embryos	9
RNA amplification and GeneChip analysis	10
Semi-quantitative RT-PCR	11
<i>In situ</i> hybridization	11
Northern blot analysis	11
Generation and mutagenesis of reporter constructs	11
Tissue culture, transfection, and transcriptional activation assays	13
Preparation of nuclear extracts	15
Electrophoretic mobility shift assays	15

CHAPTER THREE. TRANSCRIPTIONAL PROFILING OF EARLY CARDIAC

DEVELOPMENT	17
Background	17
Results	21
Isolation of cardiac progenitors and early cardiac cells	21
Transcriptional profiling of cardiac development	24
Stage-specific gene expression programs	28
The stage-independent profile of the cardiac progenitor	32
Microarray analysis accurately identified cardiac transcripts	34
Discussion	39

CHAPTER FOUR. ANALYSIS OF THE NKX2.5 TRANSCRIPTIONAL NETWORK ..

Background	43
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Results	49
Isolation of <i>Nkx2.5</i> null cardiac cells	49
Analysis of the <i>Nkx2.5</i> null transcriptome	51
Putative downstream <i>Nkx2.5</i> targets include <i>etsrp71</i> and <i>VCAM</i>	53
Discussion	62
 CHAPTER FIVE. AN <i>NKX2.5</i> -DEPENDENT PATHWAY IS UPSTREAM OF LEFT- RIGHT ASYMMETRIC GENE EXPRESSION IN THE CARDIAC CRESCENT	66
Background	66
Results	70
Isolation of cells from the left and right sides of the cardiac crescent.....	70
The left side of the cardiac crescent is enriched for a cardiac structural program.....	70
<i>Nkx2.5</i> null mice have disrupted LR asymmetry in the cardiac crescent	72
Discussion	79
 CHAPTER SIX . CONCLUDING STATEMENTS	85
 APPENDICES	87
 BIBLIOGRAPHY	205
 VITAE	224

PRIOR PUBLICATIONS

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LIST OF FIGURES

FIGURE ONE. Schematic of mammalian cardiac development.....	2
FIGURE TWO. Cardiac progenitors are accurately labeled in transgenic <i>Nkx2.5-EYFP</i> embryos.....	22
FIGURE THREE. Staining of endocardium in <i>Nkx2.5-EYFP</i> transgenic embryonic hearts	23
FIGURE FOUR. Flow cytometry was used to isolate cardiac cells with high purity	25
FIGURE FIVE. Cardiac progenitor cells from sequential developmental stages exhibit distinct and shared gene expression profiles.....	29
FIGURE SIX. A shift in stage-specific transcription factor profile from a hematopoietic to a homeobox program occurs between E7.75 and E9.5.....	31
FIGURE SEVEN. Stage-independent enriched transcripts constitute a genetic profile of the cardiac progenitor cell population	33
FIGURE EIGHT. <i>In situ</i> hybridization confirms the cardiac expression of transcripts identified through array analysis.....	35
FIGURE NINE. <i>Phosphofructokinase-p</i> and <i>Calpain 6</i> are expressed in multiple lineages in the embryo and adult.....	37
FIGURE TEN. Confirmation of cardiac enrichment at E7.75.....	38
FIGURE ELEVEN. EYFP expression is preserved in <i>Nkx2.5</i> null embryos	50
FIGURE TWELVE. FACS analysis of null embryos reveals a reduction in live cell numbers and an increase in EYFP ⁺ cell numbers late in development.....	52

FIGURE THIRTEEN. Semi-quantitative RT-PCR confirms the pattern of enriched and depleted transcripts observed in null cardiac cells.....	55
FIGURE FOURTEEN. <i>Etsrp71</i> is expressed in the early developing heart	57
FIGURE FIFTEEN. The <i>Etsrp71</i> upstream enhancer exhibits transactivation in response to <i>Nkx2.5</i> that is sensitive to the deletion of NKEs.....	58
FIGURE SIXTEEN. EMSA demonstrates Nkx2.5 binding to NKEs in the <i>Etsrp71</i> enhancer.....	59
FIGURE SEVENTEEN. <i>VCAM</i> is a putative target of <i>Nkx2.5</i> regulation.....	61
FIGURE EIGHTEEN. Strategy used to isolate cells from the left and right sides of the cardiac crescent.....	71
FIGURE NINETEEN. Confirmation of transcripts enriched in the left and right sides of the cardiac crescent.....	77
FIGURE TWENTY. Comparison of fold change values between the wild type and <i>Nkx2.5</i> mutant crescents for selected transcripts enriched in the wild type state	78

LIST OF TABLES

TABLE ONE. Oligonucleotides used for semi-quantitative RT-PCR	12
TABLE TWO. Oligonucleotides used for mutagenesis of NKEs in the <i>Etsrp71</i> promoter utilizing the QuikChange system (Stratagene)	14
TABLE THREE. Oligonucleotides used for EMSA	14
TABLE FOUR. Affymetrix GeneChip analysis confirms the cardiac identity of sorted <i>Nkx2.5-EYFP</i> cell populations	27
TABLE FIVE. Transcripts depleted in early stage <i>Nkx2.5</i> null embryos include known downstream targets of <i>Nkx2.5</i>	54
TABLE SIX. Transcripts significantly enriched on the left side of the cardiac crescent with respect to the right.....	73
TABLE SEVEN. Transcripts significantly enriched on the right side of the cardiac crescent with respect to the left.....	75

LIST OF APPENDICES

APPENDIX A. Transcripts enriched in cardiac progenitors compared to non-cardiac age-matched embryonic cells (Affymetrix MgU74v2 GeneChip data).....	87
APPENDIX B. Annotated transcripts expressed in cardiac crescent stage (E7.75) cardiac progenitors (Affymetrix MgU74v2 GeneChip data)..	114
APPENDIX C. Transcripts enriched or depleted in <i>Nkx2.5</i> null cardiac cells at E8.0, E8.25, and E8.5 (Affymetrix MOE430v2 GeneChip data).....	166
APPENDIX D. Transcripts enriched or depleted in the left and right halves of the wild type and <i>Nkx2.5</i> null cardiac crescent (Affymetrix MOE430v2 GeneChip data).	174

CHAPTER ONE

Introduction to the Events of Early Cardiogenesis

Cardiac development spans nearly the entire ontogeny of the mammal, initiating shortly after the onset of gastrulation and terminating with the closure of the foramen ovale just before or after birth. A full understanding of this intricate process will inform our comprehension of both normal cardiac function and pathologic states. Developmental studies are also relevant to the emerging field of regenerative medicine, where recapitulation of embryonic pathways may be harnessed as an avenue to therapy. In this regard, understanding the earliest stages of cardiogenesis may be particularly critical.

Early Morphogenetic Events In Cardiac Development

The earliest morphologically distinct stage of mammalian cardiac development is evident around embryonic day 7.75 (E7.75) in the mouse, when specified cardiac precursors derived from the lateral plate mesoderm form a structure called the cardiac crescent (Figure 1, reviewed in Harvey, 2002, Brand, 2003). The apex of the crescent is cranial, with termini that extend laterally almost to the mid dorsoventral plane. The cells of the crescent exhibit a cubical morphology, visible through scanning electron microscopy, that distinguishes them from the surrounding mesoderm (Kaufmann, 1990). Crescent-stage progenitors are separated from the underlying endoderm by the nascent pericardial cavity. The cells of the cardiac crescent converge at the midline at E8.0 to form the linear heart

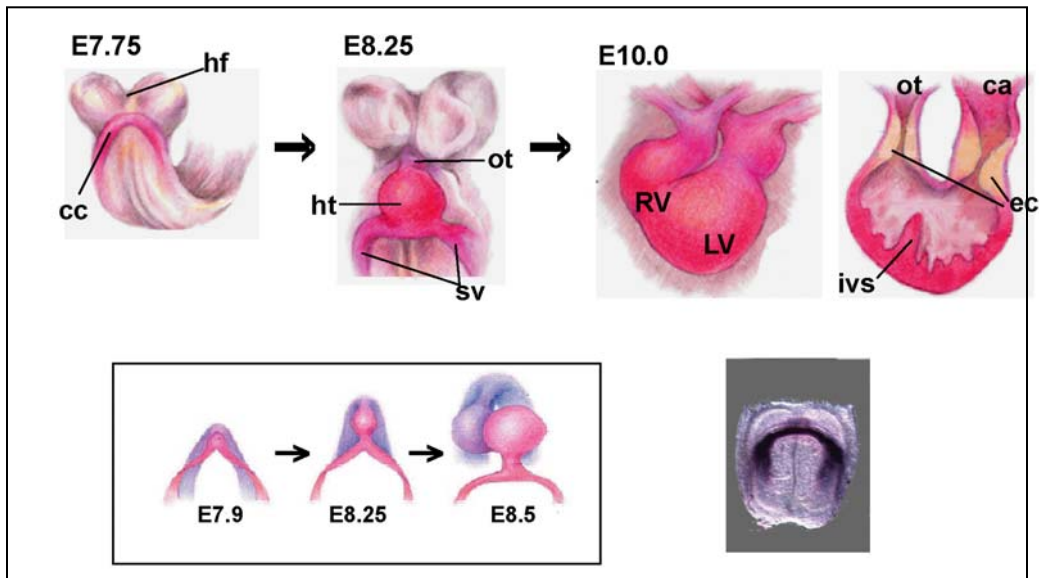


Figure 1. Schematic of mammalian cardiac development, depicting the cardiac crescent, at E7.75, the forming linear heart tube at E8.25, and the looped heart at E10. Left inset) A representation of the proposed positions of the primary (red) and secondary (blue) heart fields during early cardiac development. The secondary heart field contributes cells to the outflow tract and the right ventricle, while left ventricular precursors are derived from the primary heart fields. Right inset) Crescent stage embryo showing *in situ* hybridization for *tropomyosin alpha*, a cardiac and muscle specific marker. ca, common atrium; cc, cardiac crescent; ec, endocardial cushions; ivs, intraventricular septum; hf, headfold; ht, heart tube; LV, left ventricle; ot, outflow tract; RV, right ventricle; sv, sinus venosus. Schematics adapted from Harvey, 2002.

tube, which consists of an inner endocardial and outer myocardial cell layer separated by a specialized extracellular matrix termed the cardiac jelly. In the mouse, this endocardium appears to be derived from the cardiac crescent mesoderm (Stanley et al., 2002). At E8.0, the future outflow tract (aorta and pulmonary artery) is cranial and the sinus venosus (the vena cava and pulmonary vein) caudal. By E8.5, the heart begins to beat due to inherent cardiomyocyte automaticity.

The linear heart tube initiates looping morphogenesis at about E8.25, which initially brings the inflow and outflow portions of the heart into alignment and terminates with the emergence of a four-chambered structure at E10.5. During looping, cells from a secondary heart field migrate to the outflow (rostral) end of the heart tube and contribute to portions of the outflow tract and right ventricle (Kelly et al., 2001; Mjaatvedt et al., 2001, Waldo et al., 2001). The initial rightward bend that is formed by the primitive ventricular region of the looping heart tube appears to balloon away from the body as ventral regions of this bend differentiate into chamber myocardium (reviewed in Moorman and Christoffels, 2003). The endocardial cushions, precursors to the valves, form along the inner curvature of the late looping heart. Two other extracardiac populations migrate into the looping heart. Neural crest cells migrate into aortic and outflow tract regions where they will contribute to the cotruncus and great vessels (Kirby and Waldo, 1995). Cells of the proepicardial organ, which constitute the future epicardium, coronary vessels, and myofibroblast populations, begin to cover the surface of the myocardium at this time (Hiruma and Hirakow, 1989).

Origins Of The Cardiac Mesoderm

The Primary Heart Field

The origins of the specified cardiac precursors located in the cardiac crescent have been traced from gastrulation through cell labeling studies that, most recently, involve the use of lipophilic dyes. Gastrulation in the mouse embryo occurs at about E6.0 when cells of the epiblast invaginate at the primitive streak. Mesoderm is formed from the epiblast cell population that migrates through this region to a position between the remaining epiblast, now termed ectoderm, and the ventrally located hypoblast, which at this time becomes specified endoderm. In the chick, pre-cardiac mesoderm is initially located in the rostralmost region of the primitive streak (DeHaan, 1963; Garcia-Martinez and Schoenwolf, 1993). The pre-cardiac mesoderm thus migrates relatively early during gastrulation and is allocated to bilaterally paired primary heart fields that fuse at the midline 48 hours later to form the cardiac crescent (reviewed in Yutzey and Kirby, 2002). Separate primary heart fields are rarely evident in the mammal, perhaps due to differences in the timing of migration events. Cardiac crescent cells, in chick and mouse, express several markers of the cardiac lineage, including *Nkx2.5* and *alpha cardiac actin* (Lints et al., 1995; Schultheiss et al, 1995).

Conflicting data exist as to whether the primary heart fields are patterned prior to formation of the cardiac crescent. Labeling of precardiac mesoderm in the chick primitive streak indicated that ventricular progenitors are more rostral and atrial progenitors more caudal, suggesting that patterning in the primitive streak will be maintained in the AP patterning of

the linear heart tube (Garcia-Martinez and Schoenwolf, 1993). Studies of zebrafish blastulas have yielded similar findings, with ventricular myocardial progenitors located dorsally and marginally with respect to atrial myocardial progenitors prior to gastrulation (Keegan et al., 2004). Studies of patterning in the chick bilateral primary heart fields, however, did not find evidence of AP patterning until formation of the crescent (Redkar et al., 2001). Identification of molecular markers of the pre-crescent stage cardiac mesoderm would facilitate studies to address this question in murine embryos.

Signaling and induction of the heart field has been studied extensively in a variety of organisms. The endoderm that underlies the primary heart fields is a potent source of cardiac induction and expresses a variety of factors that have effects on cardiac specification or morphogenesis, including fibroblast growth factors and bone morphogenetic proteins (Nascone and Mercola, 1995; Schultheiss et al, 1997) *BMP2* is sufficient to induce cardiac fate in some contexts (Andree et al., 1998), although it likely cooperates with *fgf* factors *in vivo*, as explants of pre-specification mesoderm required both factors for cardiac differentiation (Barron et al, 2000). Inhibition of canonical *Wnt* signaling, which emanates from the forming notochord during the migration of the early heart fields, is also required for inducing the heart field (Marvin et al., 2001; Schneider et al., 2001). *Wnt 11*, a family member that signals independently of the β -*catenin* pathway, appears to induce cardiac fate in precardiac mesoderm and P19 cells (Pandur et al., 2002; Nakamura et al., 2003).

The Secondary Heart Field

More recently, a secondary heart field that contributes cells to the looping heart tube at the arterial pole has been described by several labs (Kelly et al., 2001; Mjaatvedt et al., 2001, Waldo et al., 2001). In the mouse, this population forms an inverted U-shaped region just medial to the primary heart field precursors of the cardiac crescent. These cells, which express *fgf10*, migrate into the heart during looping and contribute to regions of the right ventricle and outflow tract (Kelly et al., 2001). The transcription marker *islet 1* has been also been proposed as a marker of this lineage (Cai et al., 2002). *Isl1* null mice are embryonic lethal and lack the right ventricle, outflow tract, and most of the atria. However, lineage tracing indicated that the majority of the heart is derived from the *Isl1* positive population, suggesting that *Isl1* expression is not limited to the secondary heart field and may only be valid as an early marker of this population. The signaling events which direct the specification and migration of the secondary heart field remain an intense area of study.

Aims Of Dissertation Research

The basic goal of my Dissertation research was to identify novel pathways and processes directing early cardiac development through large-scale expression analyses of relevant cell populations. These studies were divided into three areas:

- 1) Transcriptional analysis of early cardiac development (Chapter 3).
- 2) Study of a key early transcriptional regulator, *Nkx2.5*, (Chapter 4)
- 3) Investigation of left-right patterning in the cardiac crescent (Chapter 5).

The topics outlined above provide one portion of a review of early cardiogenesis. Several other topics that are relevant to a full discussion of early cardiac morphogenesis will be presented in the introductory sections of each chapter.

CHAPTER TWO

Materials and Methods

Generation and Analysis of Transgenic Mice

The LacZ cassette of pNkx2.5-Hsp68-lacZ (Hsp106) was excised and replaced with Enhanced Yellow Fluorescent Protein (EYFP) cDNA isolated from the pEYFP plasmid (Clontech) by NcoI-NotI digestion. The resulting transgene was injected into C57BL/6/C3H blastocysts. Southern analysis of founder animals utilized an EYFP probe. PCR genotyping of F1 and further offspring was performed using primers that amplify a 688 bp fragment of EYFP (fwd 5'-GGGCGAGGAGCTGTTCACCGGGG; rev 5'-GCCGAGAGTGATCCCGGCGGCGG) at a 60°C annealing temperature. Transgenic mice from three founder lines were mated to C57BL/6 wild-type mice for analysis of embryonic fluorescence. Pregnant females were sacrificed between 7 and 15 days following plug appearance. Staging of embryos followed these criteria, based on Kaufman (1990): E8.0: 1-6 somites; E8.5: 7-12 somites, E9.0: 12-20 somites; E9.5: 21-28 somites; E10.5:> 30 somites. Crescent stage embryos (E7.75-E7.9) were designated by the presence of a headfold and cardiac crescent, and the absence of somites.

Tissue Immunohistochemistry

Embryos were fixed in 4% paraformaldehyde for 1-3 hours, paraffin embedded, and sectioned parasagittally. Deparaffinized tissue sections were permeabilized with 0.3% Triton X-100 for 3 minutes, blocked with 1.5% goat serum/1% bovine serum albumin for 30 minutes, then incubated in primary antibody (1:250 mouse monoclonal anti-desmin antibody

(Affinity Biolabs); 1:50 mouse monoclonal anti-PECAM (Santa Cruz)) at 4°C overnight. A 1:50 dilution of goat anti-mouse rhodamine (Jackson ImmunoResearch) was incubated on the slides at RT for 1 hour for detection. Slides were coverslipped with Vectashield (Vector Labs).

Flow Cytometry

Fluorescence-Activated Cell Sorting (FACS) was conducted on samples prepared in the following manner: embryos were digested with 0.25% Trypsin/EDTA (Invitrogen), neutralized in Dulbecco's Modified Eagle's Medium (Invitrogen) containing 5% fetal bovine serum (Hyclone) and 10mM HEPES (Invitrogen), rinsed and resuspended in PBS, and passed through a 70 µm nylon cell strainer (Falcon). Samples were sorted on a MoFlo flow cytometer (Cytomation, Inc.) utilizing Summit software. Samples from wild type and transgenic *Nkx2.5-EYFP* stage-matched embryos were used for gating on a minimum of 10,000 events. Samples intended for RNA isolation were collected directly into Tripure (Roche), with a fraction of each collected into PBS for post-sort assessment of purity.

Genotyping of *Nkx2.5* null embryos

In order to genotype embryos from *Nkx2.5* null heterozygote crosses, individual yolk sacs were collected prior to FACS analysis and digested by proteinase K for 48 hours in a standard buffer. A fraction of the EYFP – cells from each embryo was sorted into PBS and similarly digested overnight. Genotyping reactions utilized 1-5ul of the inactivated proteinase K digestion.

RNA Amplification and GeneChip Analysis

RNA was isolated with Tripure (Roche) following the manufacturer's protocol and subjected to two rounds of linear amplification following a modification of Affymetrix's Small Sample Target Labeling Protocol. First round cDNA synthesis utilizing Superscript II (Invitrogen) and a T7-promoter containing oligo dT (custom order) in a standard first strand synthesis reaction (Invitrogen protocol) yields a cDNA pool that is then amplified by *in vitro* transcription utilizing Ambion's Maxiscript Kit for the first round of expansion. This cRNA (complementary, or antisense, RNA) pool is subjected to a second round of cDNA synthesis utilizing both random primers and the same T7-oligodT, followed by a second round of *in vitro* transcription, this time incorporating biotinylated ribonucleotides to produce cRNA ready for chip hybridization to either the MgU74 or 430v2 Mouse Expression chip sets (Affymetrix). Microarray Suite (MAS) 5.0 and GeneChip Operating Software (GCOS) were used for normalization, scaling of chip intensities, and calculation of presence/absence calls and fold-change. User-definable parameters were kept at default settings. Representative samples were used for analysis, with replicates used to confirm reproducibility. Transcripts were scored as differentially expressed if they exhibited a signal log ratio greater than 2, a signal intensity >100 (for at least one side of the comparison), and the p-value of the fold change determination fell outside of a 95% confidence interval.

Semi-quantitative RT-PCR

RNA was isolated and amplified as described above in “RNA Analysis and Gene Chip Hybridization” section. cDNA was generated from 2 µg of cRNA utilizing Superscript II (Invitrogen) and random nonamers (Invitrogen) as primers during a two hour incubation at 42°C. PCR was performed on dilution series of the RT reaction; primer sequences and cycling conditions are listed in Table 1.

***In situ* hybridization**

In situ hybridization was performed according to Shelton et al.(2000). ³⁵S-labeled probes correspond to the following Genbank accession numbers: NM009627 (*Adr*), AK030851 (*Alcam*), NM031161 (*Cck*), AF079565 (*Capn6*), NM018870 (*Pgam2*), BC006926 (*PFK-C*). Whole mount *in situ* hybridizations followed the protocol of Correia and Conlon (2001). Both ³⁵S and digoxinin labeled probes were synthesized from plasmid DNA using the Maxiscript kit (Ambion).

Northern Blot Analysis

Clontech MTN blots (adult tissues) were used for Northern analysis. ³²P-labeled probes were generated using the Strip-EZ kit (Ambion), hybridized for 12-16 hours at 42°C, washed, and exposed to film for 24-72 hours.

Generation and Mutagenesis of Reporter Constructs

Reporter constructs were constructed in one or more of the following luciferase reporter vectors: pGL3 Basic (Promega), pGL4 Basic (Promega), or a pGL3-TATA in which a 53bp

Table 1. Oligonucleotides used for semi-quantitative RT-PCR

Primer	Sequence	Product Size	Cycling Conditions
ATP Syn rev	GCCTTCATCAAATTCATA	236 bp	56C, 18 cycles
ATPSyn for	GCACCTCATTATTGGTGTGT		
Bbx for	ATGCCTGCTGTGTCTGCGTTCTTC	438 bp	60C, 37 cycles
Bbx rev	CACCAGTCAAAAGCCTTCGGTTCC		
Dlx2 for	CCTCAACAATGTCTCCTACTCCGC	160 bp	60C, 25 cycles
Dlx2 rev	TGGGTATCTCGCCGCTTTTC		
Etsrp71 for	CGCTACTCCAAAATAACCACCG	246 bp	58C, 30 cycles
Etsrp71 rev	ACCACTCTTGAGCACGATGTCTG		
Flk-1 for	GCTTGGCCCGGGACATTTAT	550 bp	57C, 35 cycles
Flk-1 rev	ACTGGCCGGCTCTTTCGCTTACTG		
Gata1 rev	CAGAGGTCCAGGAAAAGGCATAAG	420 bp	57C, 30 cycles
Gata1for	CGAATGATTGTCAGCAAACGGG		
Myh 7 rev	CTTCTTGTCTTCTCTGTCTGGTAG	355 bp	57c, 20 cycles
Myh7 for	TAGAGGAGGCAGTACAGGAGTGTAG		
Odz4 for	TTATGATGTGCTGGCTGGACGC	440 bp	58C, 30 cycles
Odz4 rev	CAAAGATGGAACCACTGGAGGC		
Prrx1 rev	TCAGTCTCAGGTTGGCAATGC	206 bp	57C, 30 cycles
Prrx1for	ACGCTCTCTCCTCAAGTCCTACTC		
Rgs5 for	5CCACCGTTGGGTTTTTCAGC	370 bp	57C, 30 cycles
Rgs5 rev	GAGGTTACAATGACAGGAGGCATC		
Runx1 for	TCCCCGAGACGCAAGAAAGTC	500 bp	57C, 30 cycles
Runx1 rev	CATTGGTTGAGTGAGTCAGCCC		
Six1 rev	CGGTGTTCTCCCTTTCTTTGG	353 bp	60C, 25 cycles
Six1for	GCTGCCGTCGTTTGGTTTTACG		
Smpx for	TGTCCCCAAAGGTGAACAGTAGTC	260 bp	56C, 25 cycles
Smpx rev	GCTGATTTGCTCTACAAGGTGCC		
TdGF-1 for	TGGGGATACAGAACAGTAAGTCGC	246 bp	57C, 35 cycles
TdGF-1 rev	CCATCACAGCCAGGTAGAAAGGTC		
Tek for	GCTTGGCCCGGGACATTTAT	550 bp	57C, 35 cycles
Tek rev	ACTGGCCGGCTCTTTCGCTTACTG		
TenC for	CTATGACAAGGACACAGACTCAGCC	346 bp	57C, 20 cycles
TenC rev	CATCAAATGCCCAAGGAGAGC		
Tnnt for	GAAGGACCTGAATGAGCTACAGAC	336 bp	57C, 20 cycles
Tnnt rev	GATCTTCTTCTTCTCTCTCTCTGTC		
Tnnt2 for	GAAGGACCTGAATGAGCTACAGAC	250 bp	57C, 20 cycles
Tnnt2 rev	GATCTTCTTCTTCTCTCTCTCTGTC		
VCAM for	TGTGGAATGTGCCCCGAAAC	650 bp	57C, 35 cycles

minimal promoter from the Hsp70 gene has been cloned into the HindIII site of pGL3 Basic. Enhancer regions from *ETS-related protein 71* (*Etsrp71*) and *vascular cell adhesion molecule* (*VCAM*) were amplified from BAC clones containing the appropriate chromosomal regions by PCR utilizing a proofreading polymerase, LA Taq (Takara). PCR products were cloned into the pCRII vector using the TOPO-TA cloning kit (Invitrogen), sequenced, excised by digestion with XhoI and KpnI, and ligated into the XhoI, KpnI sites of the appropriate luciferase vector. *Nkx2.5* binding sites were deleted through oligonucleotide-directed mutagenesis using the QuikChange XL Kit (Stratagene). Mutagenic forward and reverse oligos (Table 2) were first incubated individually with 25 ng of vector template for a single primer extension reaction. Extension reactions were then combined for further cycling. Subsequent steps followed the QuikChange protocol.

Tissue Culture, Transfection, and Transcriptional Activation Assays

COS-1 cells were maintained in Dulbecco's modified eagle medium, high glucose (Mediatech), containing 10% fetal bovine serum (Invitrogen), with 10 μ g penicillin and 100U streptomycin per mL (Invitrogen). C2C12 cells were maintained in similar media containing 20% fetal bovine serum. Transfection of plasmid DNA was accomplished using the Lipofectamine and PLUS reagents (Invitrogen). For transcriptional activation assays, COS-1 cells were plated in 6-well dishes at a density of 5 x10⁵ cells/well 24 hours before transfection. The following day, 1 μ g of DNA per well (200ng of luciferase reporter construct, 100ng of pCMV-lacZ control plasmid, 0-600 ng transcription factor expression constructs, and 100-600 ng of empty vector) was transfected following the manufacturer's

Table 2. Oligonucleotides used for mutagenesis of NKEs in the *Etsrp71* promoter utilizing the QuikChange (Stratagene) protocol.

Targeted NKE	Sequence (sense only - substitutions in bold, deletion site underlined)
Etsrp71 NKE 8911 4 substitutions	ATTATTTTCATGCAATAACTCACATTC GCTACCT ACTCGAAATTCTCCAATGGTTTCGG
Etsrp71 NKE 8911 deletion	ACATAAAATTATTTTCATGCAATAACTC <u>ATA</u> CTCGAAATTCTCCAATGGTTTCG
Etsrp71 NKE 9615 4 substitutions	CCCCCATCCCTGCAT CGAG CCCCAGGCTGCGACC
Etsrp71 NKE 9615 deletion	CCCATCCCTG <u>CCCC</u> AGGCTGC

Table 3. Oligonucleotides used for EMSA

Name	Sequence (sense strand - NKE in bold)
NKE positive control	TCGGGATCGCCCAGT CAAGTGC
NKE positive scrambled	TCGGGATCGCCCAGT GGACATC
Etsrp71	
NKE 8911	TAT GAACTGAATGT GAGTTATTGCATGAA ATAATTTT TAT
NKE 8911 scrambled	TAT GTAGATCAGAT GAGTTATTGCATTAAT GTATAA TAT
NKE 8911 short	TCGAGTAT GAACTGAATGT GAGTTAT
NKE 8911 short scrambled	TCGAGTAT GTAGATCAGAT GAGTTAT
NKE 9615	AGCCTGGGT CAAGTTG CAGGGATG
NKE 9615 scrambled	AGCCTGGGT GGATCAT CAGGGATG
VCAM	
NKE 917	GCTGAAATTTCAAT TAAGGT TATTGGCA
NKE 917 scrambled	GCTGAAATTTCAAG AGTTAT TATTGGCA
NKE 988	TGCAGAGCCAG CATAATTG AAAGCAGCCG
NKE 988 scrambled	TGCAGAGCCAG ACATTTG AAAGCAGCCG
NKE 1511	CTGCATAGAC CATAATT AAAACATCTATTA
NKE 1511 scrambled	CTGCATAGAC TATTA AAAAACATCTATTA

protocol. Cell extracts were prepared 36 hours post transfection in 250 μ l of CCLR lysis buffer (Promega) per well. Luciferase activity was quantitated by incubating 20 μ l of cell extract with 100 μ l of Luciferase Assay Reagent (Promega), then measuring light output at room temperature over a 10 second interval in a luminometer. Normalization of transfection efficiency was carried out by quantitating β -galactosidase expression by Western blot or activity through a colorimetric assay. Western detection utilized a 1/100 dilution of mouse monoclonal anti- β -galactosidase (Promega), incubated overnight at 4°C in 5% milk/Tris-buffered saline with 0.1% Tween. For colorimetric assays, 20 μ l of cell extract was incubated in a buffer containing 900 μ g/mL o-nitrophenyl- β -D-galactopyranoside (ONPG) for 30 min at 37°C, then the absorbance at 420nm recorded.

Preparation of Nuclear Extracts

COS-1 or C2C12 cells were transfected as described above. 36 hours post-transfection, cells were scraped in protein lysis buffer (20 mM HEPES, pH 7.6, 10 mM NaCl, 0.1% Triton X-100, 1 mM DTT, 20% glycerol and complete protease inhibitor (Roche)) and spun at 2640 rpm for 5 minutes at 4°C. The pellet was resuspended in lysis buffer supplemented with NaCl to a final concentration of 0.5 M and rocked at 4°C for 1 hour. Nuclear extracts were harvested by spinning the sample at 12000 rpm for 10 minutes at 4°C.

Electrophoretic Mobility Shift Assays

Single-stranded oligonucleotides containing wild type or mutated NKEs (Table 3) were annealed to their complementary strands and end-labeled with γ - 32 P by polynucleotide kinase

(Promega). COS-1 cell nuclear extracts (2-15 μ g) were incubated with 0.5 pmol of labeled oligonucleotide, 1 μ g of poly dI-dC and 1 μ g BSA in a buffer containing 20mM HEPES pH7.6, 50mM KCl, 10% glycerol, 0.2mM EDTA for 1 hour at 4°C. Competitors were added at a 5 to 100 molar excess; antibodies used for supershift were monoclonal anti-myc (Clone 9E10, Santa Cruz), rabbit polyclonal anti-myc (Santa Cruz, and polyclonal anti- β -galactosidase (Promega). DNA-protein complexes were resolved on 5% polyacrylamide gels at 4°C and visualized by a phosphorimager.

CHAPTER THREE

Transcriptional Profiling of Early Cardiac Development

Background

The transcriptional controls that underlie the complex and precise morphogenetic events of mammalian cardiac development remain an intense area of study. Several transcription factors expressed in the cardiac crescent, the earliest recognizable cardiac structure in the mammal, have essential functions during cardiogenesis. These include the homeobox transcription factors *Nkx2.5* and *homeodomain-only protein (HOP)*, the zinc-finger transcription factor *GATA4*, the basic helix loop helix factors *heart and neural crest derivatives-expressed 1* and *2 (Hand1* and *Hand2)*, the T-box factor *Tbx5*, and the MADS-box factors *serum response factor (SRF)* and *myocyte enhancer 2c (MEF2C)* (reviewed in Bruneau, 2002; Harvey 2002). Inactivation of any of these cardiac crescent-expressed factors, in the embryo or specifically in the heart, leads to severe disruptions in cardiac morphogenesis, typically during cardiac looping stages (Lyons et al., 1995; Lin et al., 1997; Tanaka et al., 1999; Srivastava et al., 1999; Bruneau et al., 2001; Chen et al., 2002; Shin et al., 2002; Niu et al., 2005; McFadden et al., 2005). No single transcription factor, however, has thus far been implicated as a master gene capable of directing specification of the cardiac lineage or differentiation of cardiac myocytes.

Transcriptional control of cardiac specification may involve the same factors that direct gastrulation and mesoderm allocation. *Nkx2.5*, whose *Drosophila* ortholog *tinman* is required for formation of the dorsal vessel (the *Drosophila* heart equivalent), (Bodmer,

1993), is essential for ventricular development but dispensable for the specification of cardiac progenitors in the mouse (Lyons et al., 1995; Tanaka et al., 1999). *Tinman* mutants, however, also fail to correctly develop visceral muscle in the midgut and exhibit mild disorganization of somatic muscle, implicating *tinman* in early specification of mesodermal lineages and suggesting that the cardiac defect is actually secondary to a more general mesoderm patterning defect. Mammalian cardiac specification may be similarly linked to gastrulation but involve factors other than *Nkx2.5*.

The predominant model for transcriptional control of cardiac differentiation involves combinatorial interactions between cardiac-specific transcription factors and more-broadly expressed factors that directly or functionally interact to activate or repress cardiac target genes (Nemer and Nemer, 2001). Direct binding interactions have been characterized between several pairs of factors, including *Nkx2.5* and *GATA4* (Durocher et al., 1997), *Hand2* and *GATA4* (Dai et al., 2002), *Hand2* and *MEF2C* (Zang et al., 2004), *GATA 4* and *MEF2C* (Marin et al., 2000), and *Nkx2.5* and *Tbx5* (Hiroi et al., 2001). SRF directly interacts with a variety of cardiac factors, among them *Nkx2.5*, *GATA4*, myocardin, and HOP (Chen et al., 1997; Wang et al., 2001; Sepulveda et al., 2002; Shin et al., 2002). Ternary complex formation has also been investigated. In the chick, expression of *SRF*, *Nkx2.5*, and *GATA4* overlap in a region where *alpha cardiac actin* is actively transcribed, and these factors act on the *acta1* promoter in a synergistic manner, with SRF serving as the DNA binding factor in the complex (Sepulveda et al., 2002). Similarly, *Nkx2.5*, *GATA4*, and *Tbx5* all bind to activate the *connexin 40* promoter (Linhares et al., 2004). Other

interactions recruit members of the general transcriptional machinery to cardiac promoters. Hand2 and MEF2C bind directly to the general transcriptional activator p300, and Hand2/GATA4 mediated *ANF* promoter activity is *p300* dependent in cultured cells (Dai et al., 2000). Competition may occur between transcription factors both for occupancy of DNA binding sites and for access to interaction domains on transcriptional co-factors. *Nkx2.5* competes with the transcriptional repressor *Hmx1* for occupancy of binding sites (Amendt et al., 1999). HOP and jumonji, an A/T rich interaction domain factor, can function as repressors that directly bind to SRF and Nkx2.5/GATA 4, respectively (Chin et al., 2002; Shen et al., 2002; Kim et al., 2004). Taken together, these data suggest that combinatorial interactions underpin the basic mechanisms of cardiac gene transcription. Further definition of these molecular pathways requires a comprehensive study of the transcriptional program of the developing heart.

The clinical relevance of studying the transcriptome of the early heart is two-fold. First, a comprehensive strategy may identify novel genes involved in cardiac development, and, consequently, candidate factors for involvement in congenital heart disease. Heterozygous mutations in *NKX2.5* and *GATA4*, among others, cause a variety of defects in human patients, including atrial and ventricular septal defects, Tetralogy of Fallot, persistent truncus arteriosus, and conduction system defects (Schott et al., 1998; Garg et al., 2003). Novel genes may reveal similar involvement. Second, the potential use of stem cell transplantation strategies for the cardiac repair would benefit from detailed knowledge of the early cardiac transcriptional program. An extensive transcriptional profile may allow for detailed

assessment of transplanted cell phenotype, and perhaps affect selection of transplant cell populations.

This study characterizes gene expression profiles of cell populations from three early stages of cardiogenesis. I utilized transgenic labeling of cardiac progenitors, fluorescence activated cell sorting (FACS) isolation, and oligonucleotide array analysis. Transgenic mice were generated that express EYFP in the developing heart, with expression initiating in the cardiac crescent. FACS was used to isolate pure populations of cells whose gene expression was analyzed by oligonucleotide array. Utilizing comparisons to embryonic stem (ES) cells, adult cardiomyocytes, and age-matched non-cardiac embryonic cells, I generated a transcriptional profile for the cardiac population that encompasses both stage-specific and stage-independent markers of this population. Results were confirmed using semi-quantitative RT-PCR and *in situ* hybridization of selected transcripts. These analyses have identified sets of genes previously uncharacterized in the heart whose pattern of regulation implies key global and stage-specific functions during cardiogenesis.

Results

Isolation of Cardiac Progenitors and Early Cardiac Cells

In order to label cardiac progenitor cells, I utilized transgenic mice in which a 6650 bp cardiac enhancer, located approximately 9700 bp upstream of the homeobox gene *Nkx2.5*, directs expression of EYFP in the embryonic heart (Figure 2A). This enhancer directs reporter gene expression in the developing heart between E7.75 and E10.5, as previously described using a LacZ transgenic reporter (Lien et al., 1999). This enhancer region does not direct reporter gene expression in the tongue, stomach, thyroid, or tooth primordium; these extracardiac sites of *Nkx2.5* expression are under the control of separate enhancer elements (Lien et al., 2001). The early myocardial expression pattern of *Nkx2.5* was recapitulated in embryos harboring the *Nkx2.5-EYFP* transgene, with fluorescence apparent in the cardiac crescent at E7.75 and throughout the developing myocardium of the linear and looping heart tube at E8.0 and E9.5 (Figure 2B). By midgestational age (E12.0), EYFP expression was not detectable using conventional microscopic techniques. Fluorescent cells were distributed throughout the myocardium in parasagittal sections of E8.5 and E9.5 transgenic embryos (Figure 2C). Immunostaining of transgenic embryo sections for desmin, an early cardiac-expressed intermediate filament protein, demonstrated that EYFP was uniformly expressed throughout the E8.5 heart tube myocardium compared to the heterogeneous desmin expression pattern observed. At E9.5, desmin and EYFP co-localized in the ventricular myocardial cells of the looped heart. EYFP expression did not significantly colocalize with CD31/PECAM (an endocardial and panendothelial marker (Baldwin et al., 1994)), further

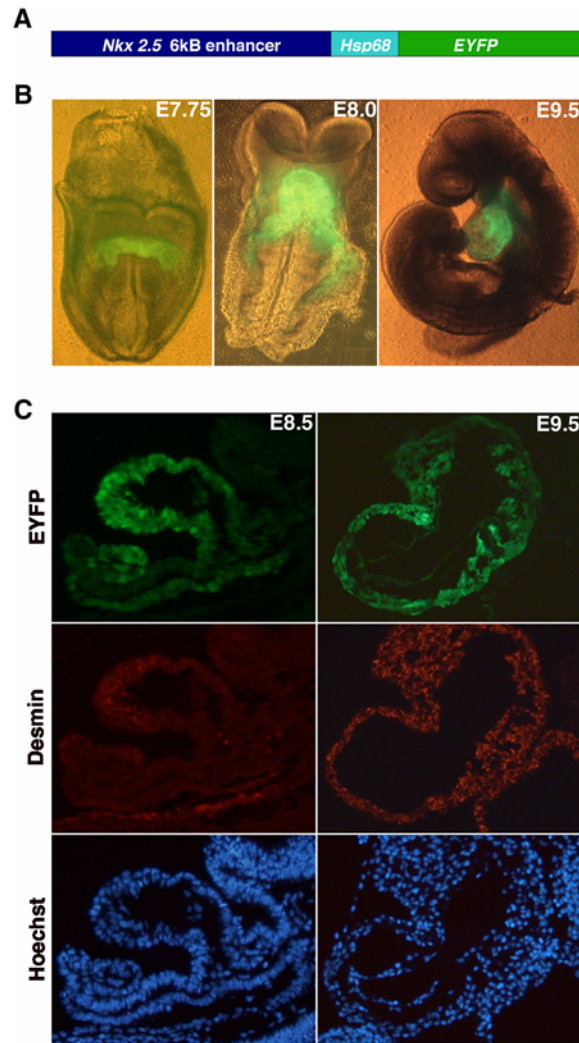


Figure 2. Cardiac progenitors are accurately labeled in transgenic *Nkx2.5-EYFP* embryos. A) The transgene contains a 6.6 kB region of the *Nkx2.5* enhancer, a basal *Hsp68* promoter, and an EYFP reporter. B) Whole-mount fluorescence microscopy of transgenic embryos confirmed that EYFP expression recapitulates the early cardiac expression pattern of *Nkx2.5*, with expression in the cardiac crescent at E7.75, the linear heart at E8.0, and the looping heart tube at E9.5. C) Parasagittal sections through transgenic E8.5 and E9.5 hearts revealed that EYFP signal was uniformly expressed throughout the myocardium and colocalized with desmin expression at E9.5. Nuclei were stained with Hoechst 33342.

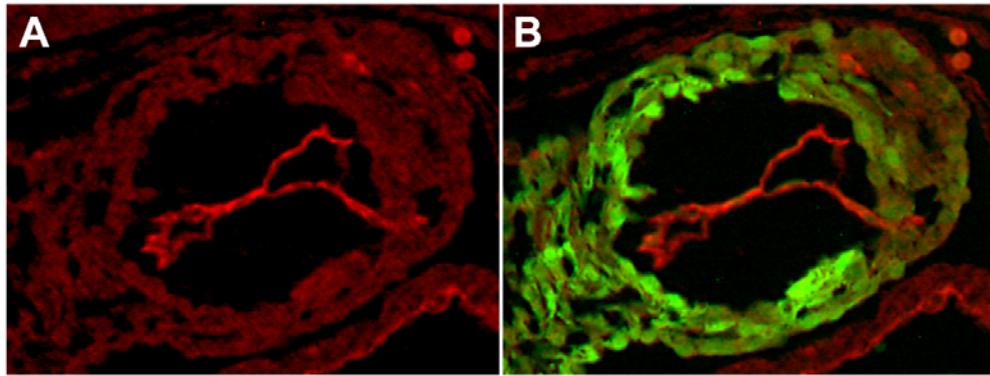
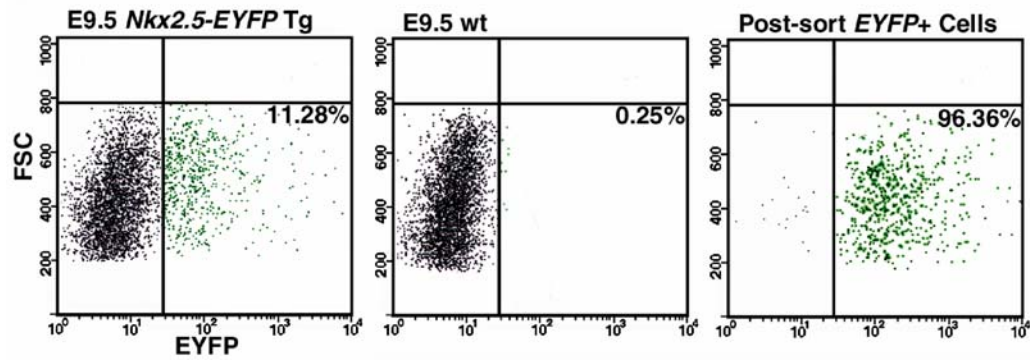


Figure 3. Staining of endocardium in *Nkx2.5-EYFP* transgenic embryonic hearts. A) Transverse sections through an E9.5 *Nkx2.5-EYFP* transgenic heart were immunostained for *CD31/PECAM*, a panendothelial and endocardial marker. B) Overlay of *CD31* immunostaining (red) and *EYFP* fluorescence (green).

supporting the use of this strategy to mark cardiac progenitors (Figure 3). Flow cytometric analysis of staged transgenic embryos revealed that EYFP⁺ cells comprised, on average, 1.8% of the live-gated cell population recovered from transgenic embryos at E7.75, 2.5% at E8.5, and 5.45% at E9.5. A second round of flow cytometry was used to assess the purity of cell separation; progenitor cell samples were typically found to contain 95-99% pure populations of EYFP⁺ cells (Figure 4).

Transcriptional Profiling of Cardiac Development

I utilized Affymetrix GeneChip analysis to characterize global patterns of gene expression in cardiac progenitor cell populations. Between 5,000-25,000 *Nkx2.5-EYFP*⁺ cells were isolated from pools of six to twelve staged transgenic embryos at E7.75, E8.5, and E9.5 and used for RNA isolation. Since cardiac progenitor cell numbers and RNA were limited, T7-based linear amplification was applied to generate sufficient amounts of cRNA for subsequent analysis with the Affymetrix MgU74v2 GeneChip set. Work done in the Garry lab has previously established that amplification of RNA from limited embryonic stem cell numbers (100 to 100,000 cells) using this T7-based protocol is linear and reproducible with minimal skewing of gene expression (Gallardo et al., 2003). Hybridization signals for cardiac progenitor cell samples were compared to those obtained from age-matched non-cardiac (EYFP⁻) embryonic cells that were collected from the same embryonic sample and analyzed in parallel. In E7.75 crescent-stage progenitors, a total of 11,070 features were present at a statistical significance level correlating to a 95% confidence bound, with 599 of these (5.41%) exhibiting 2-fold or greater differential expression when compared to age-

A**B**

Age	Number of Somite Pairs	Live Gated Cells/Embryo	EYFP+ Cells/Embryo	Percentage EYFP+	Theoretical RNA Yield (ng)*	Number of Samples Analyzed
E7.75	0	55000	1000	1.8	10	7
E8.5	7-12	160000	4000	2.5	35	2
E9.5	21-29	220000	12000	5.45	90	4

Figure 4. Flow cytometry was used to isolate cardiac cells with high purity. A) FACS profiles of an E9.5 *Nkx2.5-EYFP* transgenic embryo and a wild type littermate, with post-sort assessment of population purity. The percentage of EYFP+ cells in the live gate is shown in the upper right hand corner of the bottom right quadrant. B) Cell and theoretical mRNA yields from FACS separations of cardiac cells. *-calculation of RNA yield assumed 10ng total RNA per cell.

matched non-cardiac embryonic cells. At E8.5, 10,860 features were present in cardiac populations, with 844 (7.77%) differentially expressed, and at E9.5, 1,254 (13.13%) features were differentially expressed out of 9,551 deemed present. The increase in the percentage of features regulated as developmental time progresses likely reflects both cardiac and non-cardiac differentiation in the developing embryo as both EYFP+ and EYFP- populations exhibit the same stage-dependent trend when compared to a control ES cell population.

Examination of the transcripts differentially expressed in *Nkx2.5-EYFP+* cells when compared to stage-matched EYFP- cells confirmed the validity of this strategy in targeting cardiac cells. Cardiac-specific genes predicted to be present in the EYFP+ cell population were strongly enriched at all stages examined including the transcription factors *Nkx2.5*, *myocardin*, *MEF2C*, and *GATA4* (Table 4). Twenty-three cardiac structural genes were enriched in the EYFP+ cell population – most were significantly enriched only in progenitors from the heart tube and looped heart, although four genes (*Mylc*, *Mylc2a*, *Tnnc*, and *Tnnt2*) were also enriched in cardiac crescent-stage progenitors (Table 4 and Appendix 1). The array data are consistent with previously published work regarding the onset of expression or dynamic spatiotemporal regulation of known cardiac genes. For example, *MEF2A* is detectable in the cardiac region by *in situ* hybridization beginning at day E8.5 (Edmondson et al., 1994) and *Hand1*, although expressed in the cardiac crescent at E7.75, is also robustly expressed in other lineages (Srivastava et al, 1995), explaining the apparent depletion of these transcripts in E7.75 progenitors. The pattern of transcripts depleted in this cell population also corroborated cardiac identity. Consistently depleted transcripts included

Unigene No.	Symbol	Gene Name	E7.75	E8.5	E9.5
Mm.46514	Mylc2a	Myosin light chain, regulatory A *	13.93	73.52	45.25
Mm.712	Tnnc	Troponin C, cardiac/slow skeletal *	12.13	137.19	36.76
Mm.41974	Nkx2-5	NK2 transcription factor related, locus 5 *	8.00	21.10	9.20
Mm.7353	Mylc	Myosin light chain, alkali, cardiac ventricle *	6.06	78.80	222.90
Mm.32257	Myocd	Myocardin *	3.50	9.85	2.64
Mm.632	Tnnt2	Troponin T2, cardiac *	3.48	42.22	22.63
Mm.24001	Mef2c	Myocyte enhancer factor 2C *	3.48	2.14	8.57
Mm.1428	Gata4	GATA binding protein 4 *	2.83	3.48	9.85
Mm.30290	Capn6	Calpain 6 *	2.00	2.46	5.28
Mm.108076	Pfcp	Phosphofructokinase, platelet *	1.87	3.48	2.30
Mm.686	Actc1	Actin, alpha, cardiac*	nsc	68.59	32.00
Mm.604	Tnni3	Troponin I, cardiac*	nsc	3.25	4.92
Mm.221164	Myhca	Myosin heavy chain, cardiac muscle, fetal*	nsc	181.02	97.01
Mm.87279	Mef2a	Myocyte enhancer factor 2A*	nsc	2.64	2.00
Mm.4746	Hand1	Heart and neural crest derivatives expressed	-2.00	1.20	3.00
Mm.1306	Gbx2	Gastrulation brain homeobox 2	-2.83	-1.87	-6.06
Mm.913	T	Brachyury	-4.00	-18.38	-14.93
Mm.4875	Dll1	Delta-like 1	-6.06	-24.25	-55.72

Table 4. Affymetrix GeneChip analysis confirms the cardiac identity of sorted *Nkx2.5-EYFP* cell populations. RNA from sorted cells collected at the indicated stages of development was amplified and analyzed as described. MAS 5.0 software was used to determine presence/absence calls and fold-changes. Cell populations were compared to a control age-matched non-cardiac embryonic cell population for determination of cardiac enrichment. Asterisks indicate supporting *in situ* hybridization data, either previously published or performed in our laboratory. Nsc, no significant change.

markers of non-cardiac lineages, such as *Gbx2*, expressed in the neuroectoderm and pharyngeal endoderm (Wasserman et al., 1997) and *brachyury* and *Dll1*, expressed in early gastrulating but not differentiated mesoderm (Herrmann, 1991; Bettenhausen et al., 1993).

Stage-Specific Gene Expression Patterns

Cardiac progenitor cell populations isolated at sequential stages of early cardiac development exhibit both distinct and shared patterns of transcript enrichment. Following the removal of the redundancy of array features, 318 transcripts were enriched two-fold or greater at two stages while only 35 exhibited enrichment in cardiac progenitor cell populations at all three stages (Figure 5). Pairwise comparisons revealed that progenitor cell populations from the linear and looped heart (E8.5 and E9.5) shared a much higher percentage of enriched transcripts with each other than either one compared with cells isolated from the cardiac crescent. 41% of the transcripts enriched in either the E8.5 or E9.5 populations were enriched in both populations. In contrast, only 4.5% of transcripts enriched at E8.5 and 4.0% of enriched E9.5 transcripts were also enriched at E7.75. The majority of transcripts (61.5%) enriched at the cardiac crescent stage were stage-specific, that is, they were enriched in crescent-stage progenitors but not in progenitors from the heart tube or looped heart. Approximately half of these transcripts were not present in either EYFP+ or EYFP- cell

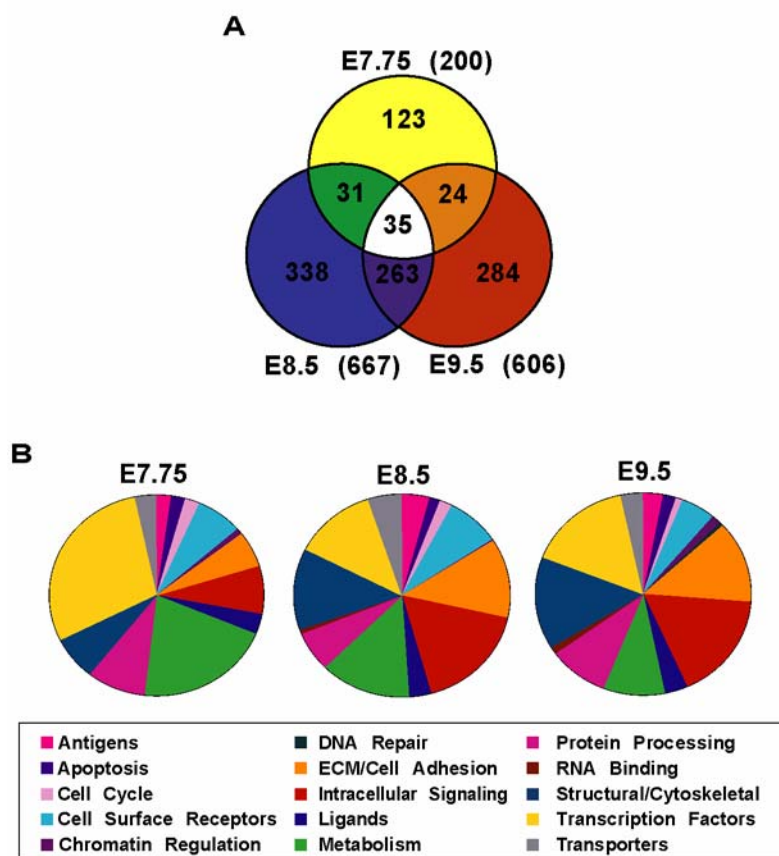


Figure 5. Cardiac progenitor cells from sequential developmental stages exhibit distinct and shared gene expression profiles. A) The Venn diagram illustrates the numbers of shared and stage-specific array features that are enriched two-fold or greater in the cell populations studied when compared to age-matched non-cardiac embryonic cells. B) Annotated transcripts enriched at each stage were classified according to Gene Ontology categories. While the percentage of structural and cell adhesion genes enriched in cardiac cells increased throughout the developmental period examined, the percentage of enriched genes encoding transcription factors is highest in the cardiac crescent.

populations at E8.5 and E9.5, potentially indicating a set of genes involved in early cardiac patterning but not differentiation.

To further characterize this molecular program, I categorized transcripts enriched in cardiac progenitors using Gene Ontology annotations. Transcription factors comprised a greater percentage of the enriched transcripts at the crescent stage compared to later developmental stages (Fig. 2B). Half of the twenty-eight transcription factors enriched at E7.75 were stage-specific, that is, they were not enriched at E8.5 or E9.5 (Appendix 1). This group of crescent stage-specific factors appeared to be enriched for markers of the hematopoietic and vascular programs (Figure 6A). For example, *Tal 1*, *T-cell acute lymphoblastic lymphoma 1*, exhibited 25-fold enrichment in the cardiac crescent when compared to age-matched non-cardiac embryonic cells. Tal1 (also known as SCL) is a basic helix-loop-helix transcription factor expressed in vascular endothelium and hematopoietic progenitors, and is considered a marker of the hemangioblast population (Visvader et al., 1991; Green et al., 1992; Hwang et al., 1993; Chung et al., 2002). Additional crescent stage-restricted enriched transcription factors are similarly implicated in hematopoietic and vascular developmental programs. The set of stage-restricted transcription factor genes in the looped heart (E9.5) contained multiple genes encoding homeodomain-containing proteins, including *Msx2* (*Msh-like homeobox 2*), *Prrx1* (*Pair-related homeobox 1*), *Dlx2* (*distalless homeobox 2*), and *Six2* (*sine-oculis-related homeobox 2*). I confirmed the stage-specific cardiac enrichment of these genes by performing semi-quantitative RT-PCR on independently collected and amplified EYFP+ cardiac progenitor cell populations and stage-matched EYFP- cells (Figure 6B).

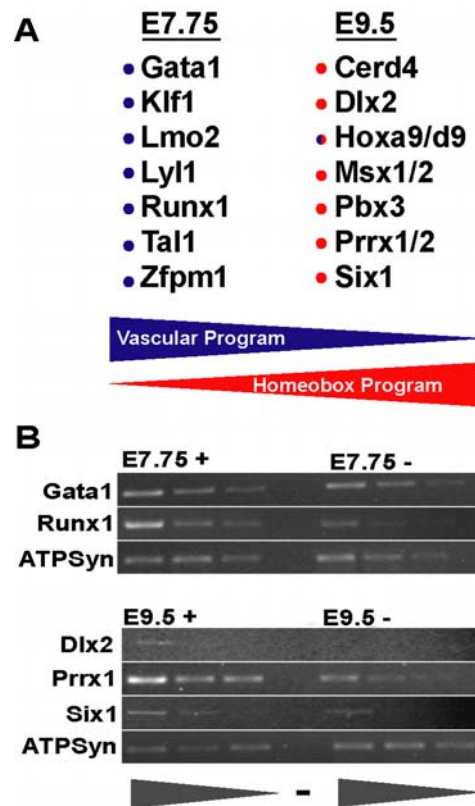


Figure 6. A shift in stage-specific transcription factor profile from a hematopoietic to a homeobox program occurs between E7.75 and E9.5. A) Genes enriched in a stage-specific fashion in cardiac progenitor cell populations are listed by symbol. Blue dots indicate transcripts that have a role in hematopoietic or vascular endothelial development; red dots label homeodomain-containing genes. *Hoxa9* (blue/red dot) is a homeobox-containing gene that functions in hematopoiesis and/or vasculogenesis. B) Semi-quantitative RT-PCR performed on independently collected EYFP⁺ cardiac progenitor cell populations and EYFP⁻ stage-matched controls confirmed the cardiac enrichment of several stage-specific transcription factors. ATP Synthase was used as a control for the amount of input cDNA.

The Stage-Independent Transcriptional Profile of the Cardiac Progenitor

While stage-specific differential expression patterns identified genes likely to function in temporally restricted processes, I predicted that transcripts enriched in progenitor cell populations throughout all stages studied would highlight molecular pathways that functioned throughout early cardiac development. Of the thirty-five transcripts enriched in the cardiac progenitor cell population at all developmental stages studied, twenty-eight represented annotated transcripts. (ESTs were excluded from this analysis). In order to distinguish between markers enriched in the heart only during development and those that also serve as markers in the adult heart, I compared each transcript's expression level in cardiac progenitor populations to SM1 ES cells and adult mouse cardiomyocytes (ACMs) (Figure 7). As expected, cardiac transcriptional regulators (*GATA4*, *Hop*, *MEF2C*, *myocardin*) and myocardial structural genes (*Myla*, *Mylc2a*, *Tncc*, *Tnni1*, *Tnnt2*) were consistently enriched in the cardiac progenitor cell population when compared to ES cells. However, when compared to ACMs, several transcripts exhibited no change in expression, or, in the case of some structural proteins, were depleted, consistent with higher expression levels in the mature adult cardiomyocyte. This myocardial program was complemented by the expression of genes critical to vascular and endocardial development. Transcripts encoding the VEGF receptors *Kdr* (*kinase insert domain receptor*, also called *Flk-1*) and *neuropilin* (*Nrp*), and the angiopoietin 1 and 2 receptor, *Tek* (*endothelial-specific receptor tyrosine kinase*, also called *Tie2*) were all enriched in the cardiac progenitor cell population. Enriched signaling genes include both predicted and novel sequences. BMPs are implicated in the specification and maintenance of cardiac progenitors. *Bmp2* was enriched in cardiac

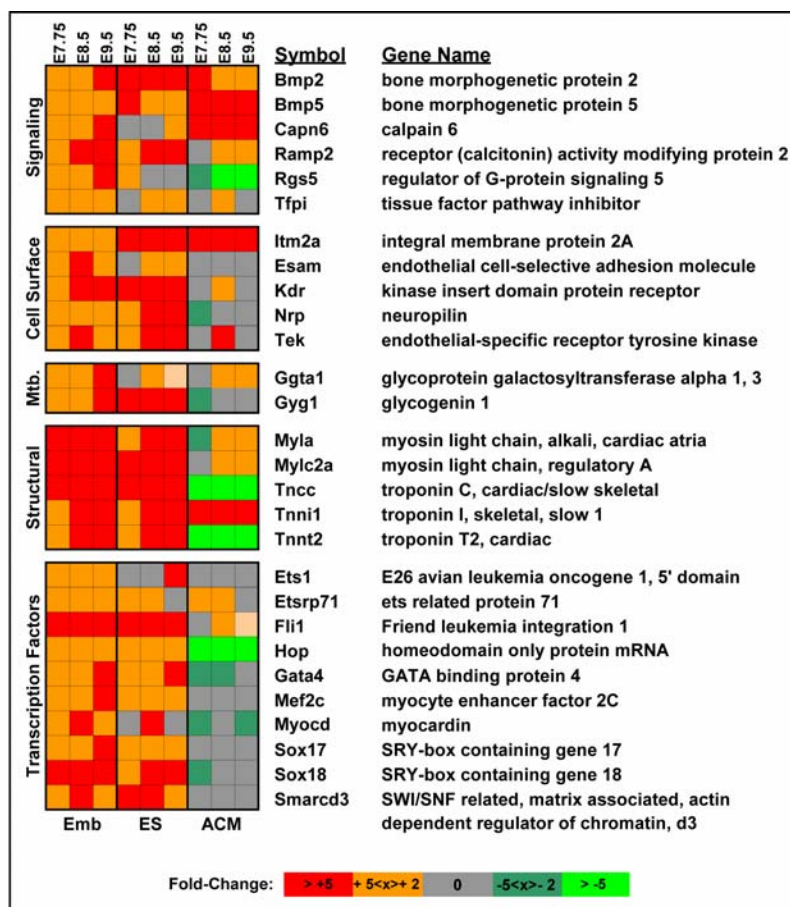


Figure 7. Stage-independent enriched transcripts constitute a genetic profile of the early cardiac cell population. The 28 annotated transcripts that are enriched in the cardiac cell pool throughout early development represent a genetic profile of this cell population. Fold change levels for each gene are represented by color code. Depicted are comparisons to a stage-matched EYFP- embryonic sample (Emb), embryonic stem cells (ES), and adult mouse cardiomyocytes (ACMs).

progenitor cells at all stages, reflecting the critical role of this morphogen in patterning the heart-forming field (Zhang et al., 1995). *Bmp5* is also highly enriched across these comparisons. Additional genes not previously shown to function in cardiac development include *Rgs5* (*regulator of G-protein signaling 5*), *Ramp2* (*receptor modifying calcitonin activity 2*), and *Capn 6* (*calpain 6*). This pattern of enriched genes serves to distinguish the early cardiac population from a diverse range of cell types.

Microarray Analysis Accurately Identified Cardiac Transcripts

I verified the GeneChip results by two methods. Selected transcripts that exhibited high levels of cardiac enrichment at E9.5 were analyzed through *in situ* hybridization. I confirmed cardiac expression and enrichment at E9.5 for transcripts encoding the neuroendocrine peptides adrenomedullin and cholecystokinin, the calcium-activated protease calpain 6, and the glycolytic enzymes phosphoglycerase mutase 2 and phosphofructokinase-platelet (Figure 8). *Capn6* and *Pfkp* also exhibited enrichment at E8.5, as did *Alcam*, a cell surface receptor. Spatiotemporal expression patterns conformed to predictions based on array data. The expression patterns of *Capn6* and *Pfkp* were examined in greater detail (Figure 9). *Capn 6* is expressed in the E11.5 embryonic heart but not in the E15.5 or adult heart, while *Pfkp* is abundantly expressed in the developing and adult heart. Low-abundance transcripts were verified with semi-quantitative RT-PCR performed on independently collected samples of EYFP⁺ cardiac progenitors and EYFP⁻ stage-matched cells from E7.75 embryos. Cardiac enrichment was confirmed for all transcripts (Figure 10). The robust early cardiac expression

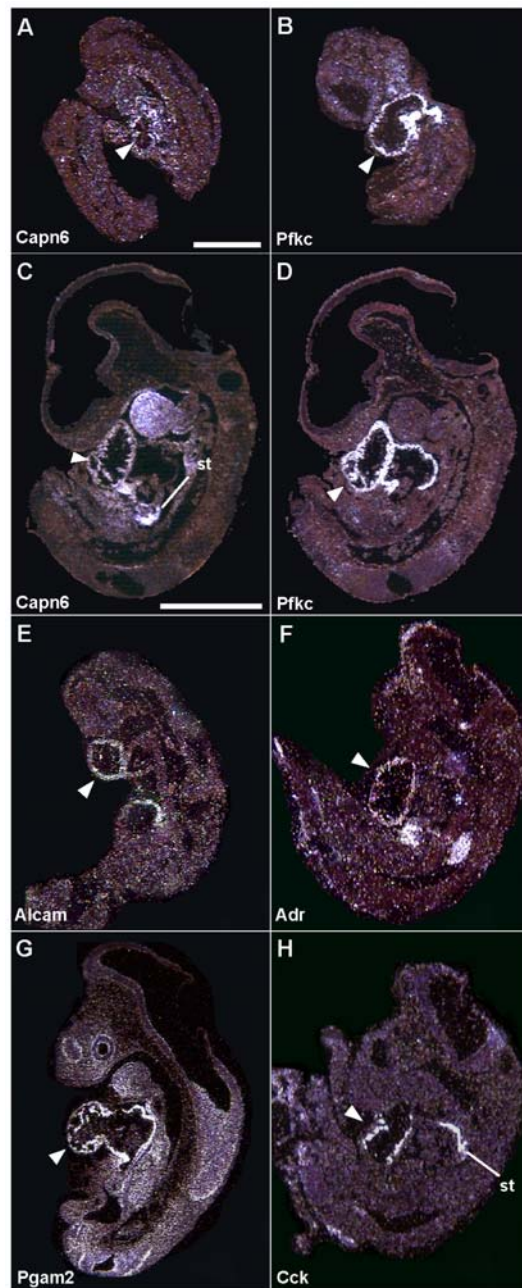


Figure 8. *In situ* hybridization confirms the cardiac expression of transcripts identified through array analysis. The embryonic expression patterns of *Alcam* (*Acm*), *Adrenomedullin* (*Adr*), *Calpain 6* (*Capn6*), *Cholecystokinin* (*Cck*), *Phosphofructokinase-platelet* (*Pfkfb*), and *Phosphoglycerate mutase 2* (*Pgk2*) were evaluated by *in situ* hybridization at E8.5 (A, B, E) and E9.5 (C, D, F-H). Cardiac expression indicated by closed arrowhead. *Capn6* and *Cck* also exhibited expression at/near the septum transversum (st).

of these transcripts confirmed our methodology in targeting transcripts specific to the cardiac progenitor cell pool and identified several novel markers of this population.

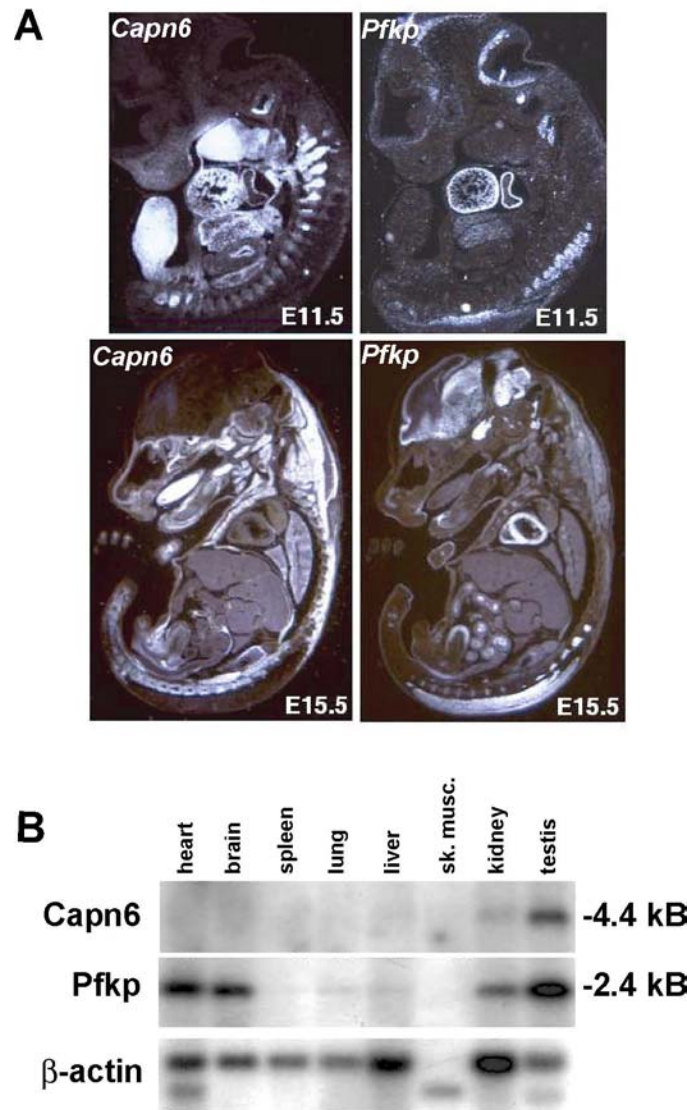


Figure 9. *Phosphofructokinase-p* and *Calpain 6* are expressed in multiple lineages in the embryo and adult. A) The expression patterns of *Capn6* (left panels) and *Pfkp* (right panels) were assessed by *in situ* hybridization at E11.5 and E15. *Capn6* is expressed in the heart at E11.5 but not at E15.5. Expression is also evident in the limb buds at E11.5, and later, in axial skeletal muscle and the tongue. *Pfkp* continues to be expressed in the heart as well as in neural lineages (brain, dorsal root ganglia). B) Western analysis of *Capn6* and *Pfkp* expression in adult murine tissues. *Capn6* protein is limited primarily to the testis; *Pfkp* is present in the adult heart. β -actin was used as a loading control.

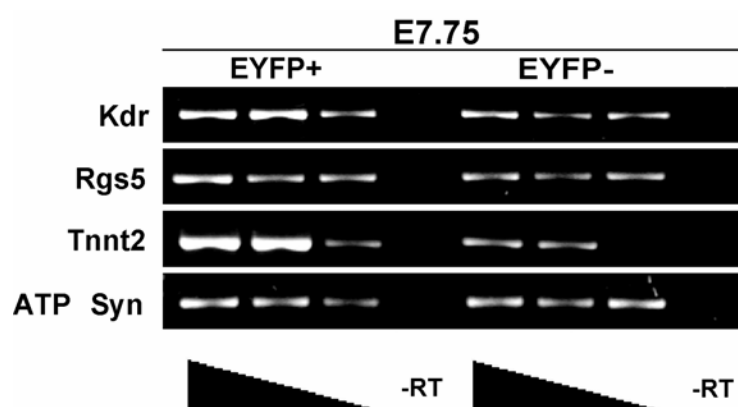


Figure 10. Confirmation of cardiac enrichment at E7.75. Semi-quantitative RT-PCR was performed on independently collected sets of EYFP+ and EYFP- cells from cardiac crescent stage (E7.75) embryos. Genes tested are *Kdr* (*kinase domain receptor*), *Rgs5* (*regulator of G-protein signaling 5*), and *Tnnt2* (*troponin T, cardiac*). *ATP Synthase* (*ATPSyn*) was used as a control for amount of input RNA.

Discussion

In this study, I applied transgenic technology and FACS to accurately isolate cardiac progenitor cells from murine embryos at three critical stages of early heart development: the cardiac crescent at E7.75, the linear heart at E8.5, and the looped heart at E9.5. RNA amplification followed by microarray analysis was used to define the dynamic transcriptional program of this progenitor cell population. I identified stage-specific and stage-independent sets of genes that were enriched in cardiac progenitor cell populations and used this information to identify novel cardiac genes and correlate waves of gene expression to key stages of cardiogenesis.

The Cardiac Crescent Stage Transcriptome is Enriched for Hematopoietic Markers

Gene expression patterns reflected a major shift in the transcriptional profile of the cardiac progenitor cell population between the cardiac crescent and heart tube stages. The expression profile of transcription factor genes in the crescent provided evidence of shared identity between cardiac crescent stage progenitors and a vascular/hematopoietic (or hemangioblast) cell type. Hemangioblasts comprise a transient embryonic cell population that serve as precursors of hematopoietic and vascular cells (Sabin, 1922; reviewed by Choi, 2000; Mikkola and Orkin, 2002). A related cell population is the mesoangioblast, an angioblast-derived progenitor with shared vascular and mesodermal potential (Minasi et al., 2002; Cossu and Bianco, 2003). Clonal populations of mesoangioblasts isolated from embryonic dorsal aorta exhibit cardiomyogenic differentiation capability (Minasi et al.,

2002). Both the crescent-stage cardiac progenitor and the mesoangioblast cell populations consist of mesodermally-derived cells that give rise to endothelial (endocardium or aortic endothelium) as well as mesodermal (myocardium or pericytes) cell types, a differentiation capability potentially reflected in shared transcriptional identity.

Furthermore, it has been observed that the differentiation of mesoderm to cardiac or hematopoietic lineages may represent antagonistic fates (Olson 2001). Anterior mesoderm becomes specified to a cardiac fate in response to inductive signals from the anterior endoderm – specifically, BMP signaling (Schultheiss et al., 1997) and Wnt inhibition (Marvin et al., 2001; Schneider et al., 2001; Tzahor et al., 2001). Explant and transplant models have demonstrated that the potential of anterior mesoderm (which normally will differentiate into cardiac and head mesoderm) and posterior mesoderm (which forms blood and vasculature) are determined by the signals each receives from the adjacent endoderm, rather than intrinsic differences between the two tissues (Nascone et al., 1995; Schultheiss et al., 1995). When misexpressed in *Xenopus*, *Wnt3a* and *Wnt8* ablated cardiac specification of anterior mesoderm and promoted the formation of primitive blood cells in the region. Similarly, expression of the Wnt inhibitor *crescent* in posterior mesoderm promoted cardiac cell differentiation at the expense of blood cell development (Marvin et al., 2001; Schneider et al., 2001). Features of the hemangioblast-like transcriptional program present in cardiac progenitors may reflect the potential of the anterior mesoderm from which the cardiac mesoderm originates.

The specific role of these hematopoietic/vascular factors in the cardiac crescent is unclear. Several of these hemangioblast transcription factors function in vasculogenesis. For example, a compartment-specific rescue of the *Tall*-null hematopoietic phenotype revealed that *Tall* also functioned in the development of mature vessels from primitive endothelial precursors in the yolk sac (Robb et al., 2004). *Tall* may play an analogous role in early endocardial development. *Tall* may also function in delaying myogenesis; *Tall* suppressed myotube fusion in 10T1/2 cells transfected with *MyoD* via a C-terminal domain that interacts with other bHLH factors (Galdfarb et al., 1995). Other factors may have broader roles. For example, *GATA1* is highly expressed in the testis and may regulate early spermatogenesis (Ito et al., 1993) suggestive of a general role in progenitor cell function.

The Looped Heart Expresses a Homeodomain-Protein Program.

I also identified a set of homeodomain-containing proteins, some of which were previously uncharacterized in the looped heart. Three of the genes found to be cardiac-enriched --*Dlx2*, *Hoxa9*, and *Hoxd9*-- have not exhibited cardiac phenotypes in gene disruption model (Qiu et al., 1995; Fromental-Ramain et al., 1996). The high degree of redundancy among homeobox-containing paralogs may obscure the functional significance of one particular gene in a tissue. This is observed in the *Prrx2* mutant, which exhibits no defects on its own but exacerbates the *Prrx1* null phenotype (Bergwerff et al., 1999). Since the induction of this homeobox transcriptional program correlates to E9.5, a stage during which chamber morphogenesis is active – and as some of these factors have already been described to play

roles in these processes- it is possible that the novel cardiac homeobox genes and their interacting partners may prove to play key roles in chamber and lineage-specific pathways.

Transcriptome Analysis Identified Novel Cardiac Transcripts

Analysis of stage-independent enriched transcripts has identified several novel markers of the cardiac progenitor cell population, including signaling and cell surface proteins whose cardiac expression pattern had not been previously demonstrated by *in situ* hybridization. Previously published studies on the roles of these markers in other cell populations may provide clues as to their roles in cardiac development. *Alcam* is expressed in a variety of cell types, including metastatic tumors of multiple origin, epiblast tissue, and mesenchymal stem cells (Swart et al., 2002). *Alcam* expression occurs primarily in the migrating cell populations of these tissues. Several of these genes may also represent target genes of cardiac transcription factor pathways – for example, GATA and Nkx2.5 binding sites are present in the 5' regulatory upstream region of the mouse *PFK-C* gene (Gunasekera et al., 2000).

In summary, this study has defined a stage-independent gene-specific transcriptional program of the cardiac progenitor cell population. Stage-specific enriched transcripts are implicated in the regulation of cardiac developmental processes. Further studies in the Garry lab will focus on characterizing the mechanisms by which these factors participate in cardiac development.

CHAPTER FOUR

Analysis of the *Nkx2.5* Transcriptional Network

Background

Nkx2.5 was independently identified by two labs conducting screens for murine orthologs of the *Drosophila* homeodomain transcription factor *tinman* (Komuro and Izumo; 1993 Lints et al., 1993). *Tinman*, previously named *msh-2* or *NK4*, is expressed transiently throughout the mesoderm and then specifically in the cardioblasts of the developing dorsal vessel, the *Drosophila* heart (Bodmer et al. 1990). *Tinman* expression is induced by the *GATA*-factor *pannier*, which is expressed in a less restricted pattern throughout the mesoderm and endoderm. Flies bearing a truncated DNA-binding deficient form of tinman fail to specify cardiac mesoderm and lack a dorsal vessel (Bodmer, 1993), leading to interest in a mammalian *Nkx2.5* ortholog.

Nkx2.5 is one of the earliest markers of cardiac lineage in the mammal, expressed in the primary heart field, that is, cardiac progenitors of the cardiac crescent, at around E7.75 (Lints, et al. 1993). *Nkx2.5* continues to be expressed in the myocardium of the developing heart, though not in the mature endocardium, epicardium, or endocardial cushions, and is strongly expressed throughout the myocardium of the adult heart. *Nkx2.5* is also transiently expressed in regions of the developing stomach, thyroid, and pharyngeal endoderm, and in the developing and adult tongue and spleen (Lints et al, 1993; Komuro and Izumo, 1993). Protein detection generally agrees with RNA expression, with the exception of the thyroid,

where *Nkx2.5* protein was not detected (Kasahara et al, 1998). The human ortholog of *Nkx2.5* is expressed specifically in the fetal and adult heart; tongue and spleen were not tested (Shiojama et al., 1996).

Nkx2.5 also appears to mark cells of the secondary heart field. Shortly before the appearance of the cardiac crescent, *Nkx2.5* is expressed in two bands in the far anterior and lateral mesoderm. The expression of *Nkx2.5* at this early stage (prior to foregut closure and the appearance of the cardiac crescent) does not correspond well to the location of the paired primary heart fields as described by lineage mapping experiments (Eisenberg, 1999) and likely represents early expression in cells of the secondary heart field. The expression of *Nkx2.5* in the region of pharyngeal endoderm that apposes the cardiac mesoderm between E8.0 and E9.0 may label endodermal tissue that serves as a cardiac inducer. Alternatively, the proximity of this tissue to the anterior heart field described by Kelly et al. (2001) suggests that *Nkx2.5* marks at least a subset of the cells that will contribute to the secondary heart field.

Despite the promising finding of early and specific expression of *Nkx2.5* in the cardiac lineage, its ablation did not lead to a failure of cardiac specification, as might have been predicted from the *Drosophila tinman* data. Murine embryos homozygous for either a truncated (Lyons et al., 1995) or complete null allele (Tanaka et al., 1999) of *Nkx2.5* exhibited lethality at E10.5 and were severely growth retarded. Both nulls exhibited a phenotype of defective morphogenesis during cardiac looping, deficient ventricular

trabeculation, and failure to form endocardial cushions. The expression levels of several cardiac proteins normally expressed in the developing ventricles, such as *atrial natriuretic factor*, *Hand1* (*eHAND*), and *myosin light chain 2v* (*mylpc*) were greatly reduced. Tanaka et al. additionally reported that *Msx2*, a transcript normally restricted to the AV region, was expressed throughout the atrial and ventricular regions in the *Nkx2.5* null background. It is clear from the severe cardiac phenotype exhibited by these embryos that *Nkx2.5* plays a critical role in cardiac morphogenesis, however, *Nkx2.5* is not a master regulator of cardiac mesoderm specification in the mammal.

The importance of *Nkx2.5* in cardiac development is further highlighted by the association of *NKX2.5* mutations with human congenital heart defects, described both in family association studies (Schott et al, 1998; Benson et al., 1999; Gutierrez-Roelens et al., 2002; Wantanabe et al., 2002) and in screening of CHD patients (Ikeda et al., 2002; McElhinney et al., 2003).

The most commonly associated defects are atrial septal defect (61 patients) and progressive AV block (58 patients), with other abnormalities, including ventricular septal defects, Tetralogy of Fallot, double outlet right ventricle, tricuspid valve defects, and atrial fibrillation, occurring at smaller frequency among patients with *NKX2.5* mutations.

The mechanisms through which mutations in *Nkx2.5* cause adult cardiac disease appear to involve early roles in morphogenesis as well as later functions in maintaining myocyte lineage identity. Mice heterozygous for null alleles of *Nkx2.5* exhibit increased frequency of patent foramen ovale at birth, a typically asymptomatic condition that involves incomplete

closure of the foramen ovale (Biben et al., 2000). While not as severe as the type of ASD observed in human patients, it represents a related defect. In a separate study, *Nkx2.5* null heterozygotes were found to suffer from conduction system dysplasia and a prolonged PR interval (Jay et al., 2004). Similarly, conditional knockout of *Nkx2.5* in ventricular lineages beginning at E13.5 resulted in a variety of conduction system defects similar to those observed in human patients bearing *NKX2.5* mutations (Pashmforousch et al, 2004). The conditional null animals exhibit hypoplastic AV nodes at birth, extensive fibrosis in the conduction system, disorganization of surviving conduction system myocytes, and progressive heart block. Adult null hearts are hypertrabeculated, the result of persistent myocyte mitosis in adult life. This suggests distinct roles for *Nkx2.5* in different myocyte lineages, perhaps involving survival of conduction system myocytes and differentiation of the working myocardium. There may also be direct transcriptional involvement of *Nkx2.5* in conduction system development. *Connexins 43* and *45* are depleted in *Nkx2.5* null embryos (Dupays et al., 2005). Similarly, overexpression of *NKX2.5* in mouse C2C12 myoblasts results in increased expression of several neuronal markers expressed in the developing conduction system (Riazi et al., 2005).

More thorough knowledge of *Nkx2.5* transcriptional targets would augment our understanding of the *Nkx2.5* null phenotype, and of the role of *NKX2.5* mutations in human congenital heart defects. *Nkx2.5* binds to two consensus binding sites in enhancer regions of its transcriptional targets, a low affinity site (consensus C(A/T)TAATTN) which contains the TAAT core typical of most homeodomain recognition sequences (Gehring et al., 1994), and a

high affinity site (consensus TNAAGTG) unique to the NK2 family (Chen and Schwartz, 1995). NK2 family members, including *Nkx2.5*, contain a characteristic tyrosine residue at amino acid position 54 in the homeodomain. This unique feature of NK2 homeodomains serves as a contact point for the “AAG” sequence in the high affinity binding site of Nkx2.5 proteins (Viglino et al., 1993; Tsao et al., 1994). *Nkx2.5* binds to single NKEs (Nkx2.5 recognition elements) as a monomer and to palindromic sets of NKEs as a homodimer (Kasahara et al., 2001). Direct and indirect transcriptional targets of *Nkx2.5* have been characterized through a number of methods. Targets include genes dependent on *Nkx2.5* binding as well as those for which *Nkx2.5* serves as a component in a cardiac transcription factor complex (Durocher et al., 1997, Sepulveda et al., 2002; Small and Krieg, 2003; Stennard et al., 2003; Linhares et al., 2004). Most downstream targets were identified through candidate gene approaches (Lyons et al, 1995; Chen and Schwartz, 1996; Zou et al., 1997; Rivkees et al., 1999; Tanaka et al, 1999; Ganga et al., 2000; Linhares et al., 2004). These include *alpha cardiac actin*, *adenosine a1 receptor*, *ankyrin repeat domain protein 1*, *atrial natriuretic factor*, *brain natriuretic peptide*, *connexin 43*, *Hand 1*, *homeodomain only protein*, *myosin light chain 2v*, *paired related transcription factor 2c*, and *procollagen lysyl hydroxylase*. Further transcriptional targets (*chisel* and *myocardin*) were identified through differential screens of total RNA from *Nkx2.5* null embryos (Palmer et al., 2001; Ueyama et al., 2003). I hypothesized that additional downstream targets of *Nkx2.5* could be identified by utilizing an unbiased transcriptome-wide analysis of cardiac progenitors, not total embryonic RNA, from *Nkx2.5* null embryos.

The *Nkx2.5*-EYFP transgenic line was crossed to a previously developed *Nkx2.5* loss-of-function mouse (Lyons et al., 1995) and fluorescent-activated cell sorting (FACS) utilized to isolate cardiac progenitor cell populations from individual *Nkx2.5* null embryos prior to the onset of lethality. Transcriptional profiles of cardiac progenitors from the early heart tube of *Nkx2.5* null mice were compared to age-matched wild type heart tubes to identify differentially expressed genes. A set of transcripts depleted at two early stages in the null included known downstream targets of *Nkx2.5* such as *ANF*, *Ankrd1*, and *Mlc2v*, and represent novel putative transcriptional targets of *Nkx2.5*. RT-PCR confirmed transcript depletion in *Nkx2.5* null embryos; *Nkx2.5* overexpression in cell culture demonstrated transcript induction. Transcriptional activation assays demonstrated that enhancer regions upstream of these genes were responsive to *Nkx2.5* and that this response was dependant on intact NKEs. These results define the transcriptional profile of *Nkx2.5* null cardiac progenitors and identify novel members of the *Nkx2.5* transcriptional network.

Results

Isolation of *Nkx2.5* Null Cardiac Cells

Nkx2.5 null cardiac cells were generated by crossing the *Nkx2.5-EYFP* transgenic mouse lines described in Chapter 3 with a previously generated *Nkx2.5* loss of function mouse line (Lyons et al., 1995). This allele was created by inserting a neomycin expression cassette into exon 2 of the *Nkx2.5* genomic locus. The insertion disrupts the DNA recognition locus (helix III) of the *Nkx2.5* homeodomain and results in a functional null allele whose phenotype is identical to that of a full deletion of the *Nkx2.5* coding sequence (Tanaka et al., 1999). For brevity, the *Nkx2.5* functional null will be referred to from this point on as an *Nkx2.5* null.

Mice heterozygous for the *Nkx2.5* null allele were crossed into one of two *Nkx2.5-EYFP* transgenic lines, and the resulting heterozygous null/transgenic females mated to *Nkx2.5* null heterozygous males. Embryos were collected at embryonic day 8.0 (E8.0), E8.5, E9.5, and E10.5. At early stages of development (E8.0-E8.5), the homozygous null embryos were morphologically indistinguishable from wild-type littermates (Figure 11). By E9.5, however, the growth deficit and dysmorphic cardiac morphogenesis characteristic of this line were apparent. No *Nkx2.5* homozygous null embryos were recovered after E11.0. Mendelian ratios were observed for embryos collected at E8.0 and E8.5, and no differences were observed in the ratios of *Nkx2.5* null state between transgenic and non- transgenic littermates. Previously published data on this particular *Nkx2.5* null mouse line reported that no

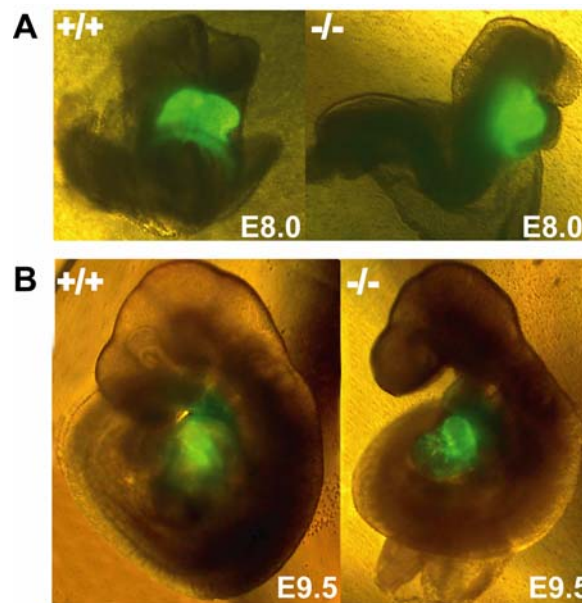


Figure 11. EYFP expression is preserved in *Nkx2.5* null embryos. *Nkx2.5* +/- mice were crossed to *Nkx2.5-EYFP* transgenic lines. E8.0 null embryos are morphologically normal at E8.0 but exhibit growth defects by E9.5. A) E8.0 wt (2 somites); B) E8.0 null (4 somites); C) E9.5 wt (24 somites); D) E9.5 null (24 somites).

homozygous null embryos were recovered with more than 24 somites (Lyons et al., 1995), in contrast with our findings. However, E10.5 homozygous null embryos were recovered in the study of Tanaka et al., suggesting that differences observed in embryo recovery may be due to strain differences impacting the expressivity of the null phenotype.

Flow cytometric separation was utilized to isolate EYFP⁺ cardiac cells from *Nkx2.5* homozygous null embryos and their wild type littermates. Null homozygous and wild type embryos exhibited comparable fluorescence profiles at E8.0 and E8.5, but by E9.5, FACS profiles revealed reduction in the number of live-gated cells obtained from homozygous null embryos (Figure 12). Additional differences were observed in the number of EYFP⁺ cells recovered from embryos of comparable stages. At E9.5, homozygous null embryos contained larger percentage of EYFP⁺ cells in relation to total live gated cells than did wild type littermates. This finding is consistent with previously reported observations of increased lacZ reporter activity in *Nkx2.5* enhancer reporter mice crossed into an *Nkx2.5* null background (Schwartz and Olson, 1999). The absence of *Nkx2.5* likely results in a loss of autoregulatory repressor activity on the *Nkx2.5* transgene enhancer fragment.

Analysis of the *Nkx2.5* Null Transcriptome

EYFP⁺ cardiac cells isolated from homozygous null embryos and their age-matched wild type littermates were subjected to transcriptional analysis with the Affymetrix Mouse Expression 430v2 GeneChips. In order to identify putative downstream targets of *Nkx2.5*, I focused on the E8.0, E8.25 and E8.5 timepoints, prior to the lethality due to the null

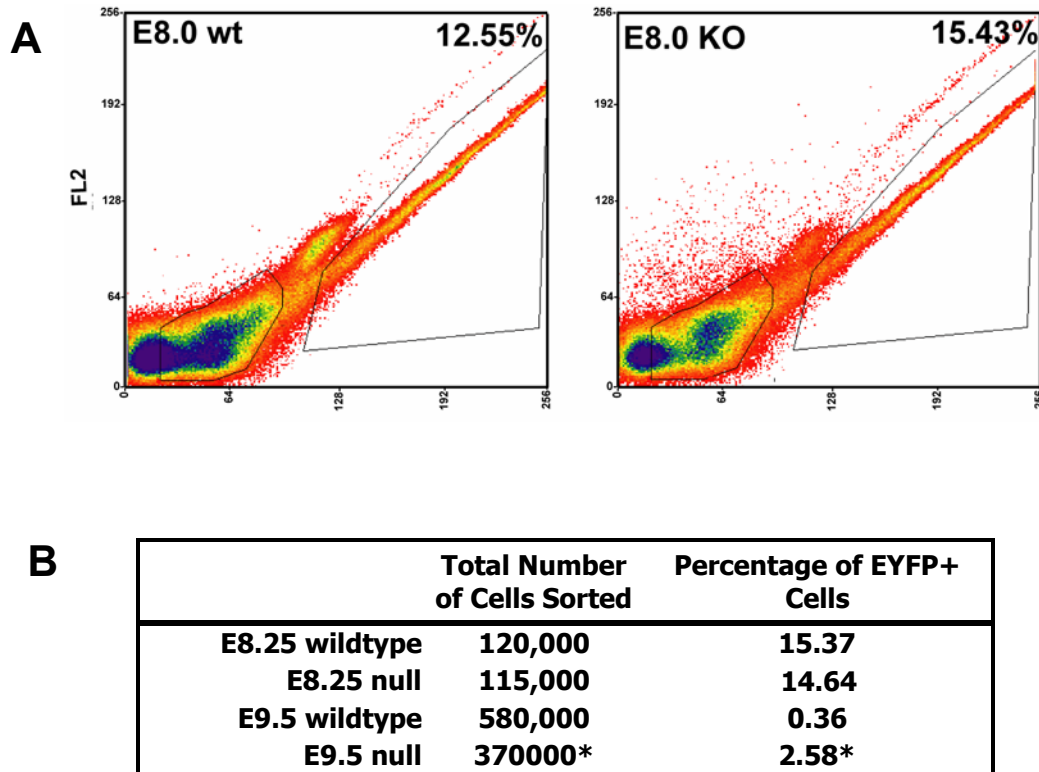


Figure 12. FACS analysis of null embryos reveals a reduction in live cell numbers and an increase in EYFP+ cell numbers late in development. A) FACS profiles of *Nkx2.5* null embryos at E8.25 are comparable to wild type, both in percentage of cells collected and fluorescence profile. The percentage of EYFP+ cells in the live gate is shown in the upper right hand corner of each plot. B) Number of live gated cells in *Nkx2.5* null embryos and their wild type littermates. By E9.5, EYFP+ cells comprise a greater percentage of the null embryo.

phenotype and, presumably, timepoints at which the contribution of transcripts dysregulated by secondary effects would be minimal. Fifty transcripts were depleted in *Nkx2.5* null cardiac cells at E8.0; 42 at E8.25, and 68 at E8.5. The E8.0 and E8.5 samples were hybridized to the full 430v2 chip set while the E8.25 sample was only hybridized to the A chip. Only six transcripts were dysregulated at all three early timepoints – this set includes the known *Nkx2.5* targets *atrial natriuretic factor*, *ankyrin repeat domain 1*, *myosin light chain a*, *natriuretic peptide precursor type B*, and *small muscle protein, X-linked*, and the novel putative targets *RIO kinase 2* and *VCAM* (Table 5). Five transcripts were depleted only at the earlier stages (E8.0 and E8.25), including *aldo-keto reductase family1 E1*, *ets-related protein 71* and *homeobox a9*. An additional 4 transcripts were depleted at both E8.0 and E8.5 but not assessed at E8.25 since the relevant features are on the “B” chip. The number of enriched transcripts also increased over developmental time – counting only A chip, 108 transcripts are enriched at E8.0; 141 at E8.5; 151 at E9.5. Semi-quantitative RT-PCR on independent samples was used to confirm array results (Figure 13).

Putative Downstream Targets of *Nkx2.5* Include *Etsrp71* and *VCAM*

Two approaches were used to identify NKEs in the genomic loci of putative *Nkx2.5* target genes. First, I used rVISTA (<http://rvista.dcode.org/>), a software package that identifies matches to the transcription factor binding site position weight matrices defined in the TRANSFAC database that occur in evolutionarily conserved regions of genomic DNA. Alignments for rVISTA analysis were generated through the linked ECR browser (<http://ecrbrowser.dcode.org/>), which uses the blastz algorithm to create alignments. The

			E8.0			E8.25			E8.5
Symbol	Gene Name	Signal Null	Fold Change	Signal wt	Signal Null	Fold Change	Signal wt	Signal Null	Fold Change
Acp1	acid phosphatase 1, soluble	38.3	-2.00	95.1	15.3	-1.15	24.9	124.3	-1.87
Akr1e1	Aldo-keto reductase family1, E1	149.7	-1.87	382.9	93	-2.83	333.8	137.3	-1.41
ANF	atrial natriuretic factor	22.7	-4.92	177.6	28.3	-16.00	714.9	41.8	-5.66
Carp	cardiac responsive adriamycin protein	369	-2.00	807.4	966.7	-1.07	1038.4	693.6	-2.46
Ckb	creatine kinase, brain	194.5	-1.52	236.9	183.1	-2.14	401.6	229.3	-1.87
EST	RIKEN 1700029I01 gene	15.7	-9.85	166.3	27.7	-3.03	132.4	77.9	1.00
EST	BG066277	48.3	-2.64	131.5	43	-2.64	119.6	50.6	-1.52
EST	BG070258	2198.6	-2.30	4388.9	na	na	na	2036	-2.14
EST	RIKEN 2700050F09	273.7	-2.00	877	na	na	na	744.4	-2.14
EST	RIKEN 0610033H09 gene	218.7	-1.87	619.7	na	na	na	146.8	-4.00
etsrp71	ets-related protein 71	374.4	-1.87	847.7	473.4	-2.14	1199.9	497.2	-1.41
Hox a9	homeobox a9	133.5	-2.00	160	52.2	-6.96	310	88.3	-1.41
Mylpc	myosin light chain, cardiac ventricles	101.4	-4.00	498.4	175.8	-10.56	1294.4	179	-11.31
Nppb	natriuretic peptide precursor type B	42.7	-5.66	230.2	68.3	-3.03	334.3	83.6	-5.66
Pim1	proviral integration site 1	492	1.32	320.3	58.4	-7.46	298.4	191.4	-2.14
Rapgef5	Rap1 guanine nuclear exchange factor 5	405.8	-2.00	617.6	na	na	na	282.5	-2.30
Riok2	RIO kinase 2	42.2	-2.83	154.7	43.8	-3.25	169.4	83.7	-2.63
Smpx	small muscle protein, X-linked	56	-2.00	117.8	46.5	-3.48	194.2	68.5	-6.06
Tctex1	t-complex testis expressed 1	20	-5.66	129	89.6	-2.46	235.9	35.5	-2.64
Vcam	vascular cell adhesion molecule	124.2	-2.83	377.4	158.5	-2.64	310.7	179.1	-2.64

Table 5. Transcripts depleted in early stage *Nkx2.5* null embryos include known downstream targets of *Nkx2.5*. Listed are transcripts that were depleted in at least two of the three early embryonic timepoints tested (E8.0, E8.25, E8.5). Colored boxes indicate statistically significant depletion; na, not assayed.

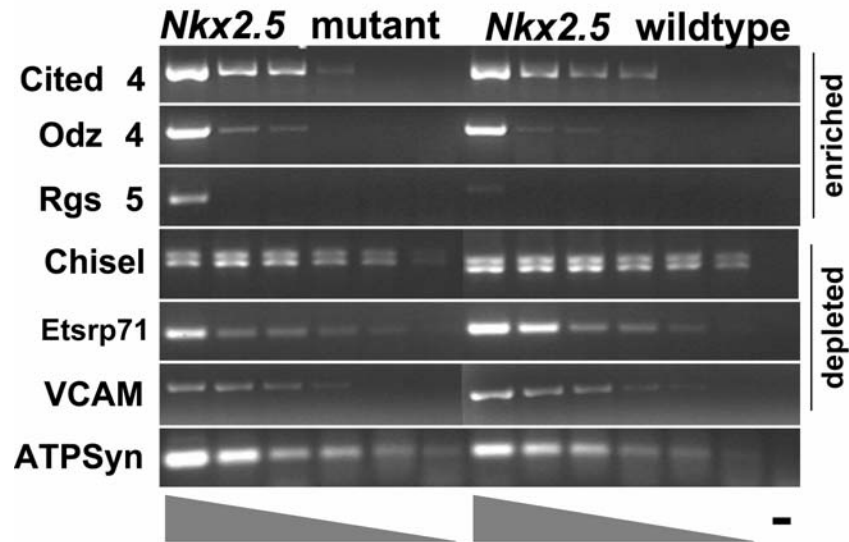


Figure 13. Semi-quantitative RT-PCR confirms the pattern of enriched and depleted transcripts observed in null cardiac cells. cDNA was generated from an independently collected set of wild type and null E8.0 EYFP⁺ cells, and PCR performed on a dilution series of the RT reaction. *Cited 4*, *Odz 4*, and *Rgs 5* all showed enrichment in the null; *Chisel* (*Smpx*), *Etsrp71*, and *VCAM* were depleted in the null. *ATP Synthase* is a loading control.

second approach involved use of the software package CONSITE (<http://mordor.gb.ki.se/cgi-bin/CONSITE/consite>), which includes a unique set of experimentally verified position weight matrices. Pre-calculated alignments for CONSITE analysis were obtained from the University of Santa Cruz Genome Browser (<http://genome.ucsc.edu>). Comparisons of the matches obtained with each method yielded candidate regions for further testing. These included a 1.5 kB fragment upstream of the *Etsrp71* promoter, which contains two NKEs conserved between mouse and human. A 2.5 kB upstream enhancer from the *VCAM* locus contains 4 conserved NKEs; a 1 kB intronic enhancer located between exons 2 and 3 of the *VCAM* locus contains 3 NKEs, one a palindromic sequence.

Characterization of *Etsrp71* confirmed expression in early cardiac lineages (Figure 14). The *Etsrp71* 2.5 kB upstream enhancer demonstrated a small but consistent transcriptional response to *Nkx2.5* levels in C2C12 myoblasts (not shown) and COS-1 cells (Figure 15A). The response was dose-dependant and statistically significant when compared to the level of transactivation observed with the empty vector. (Figure 15B) Several factors were tested for synergistic or additive effects on transactivation, including *GATA4*, *Tbx5*, *Pitx2c*, and *MEF2c*. These factors demonstrated little activity on the *Etsrp71* enhancer. To confirm that intact NKEs were required for activity, I undertook mutagenesis of the two NKEs in the *Etsrp71* enhancer. Enhancers in which NKEs were deleted showed a three to four-fold reduction in the level of *Nkx2.5* transactivation (Figure 14B). Both NKEs were also tested for their ability to interact specifically with *Nkx2.5* *in vitro* by EMSA (Figure 16). Both

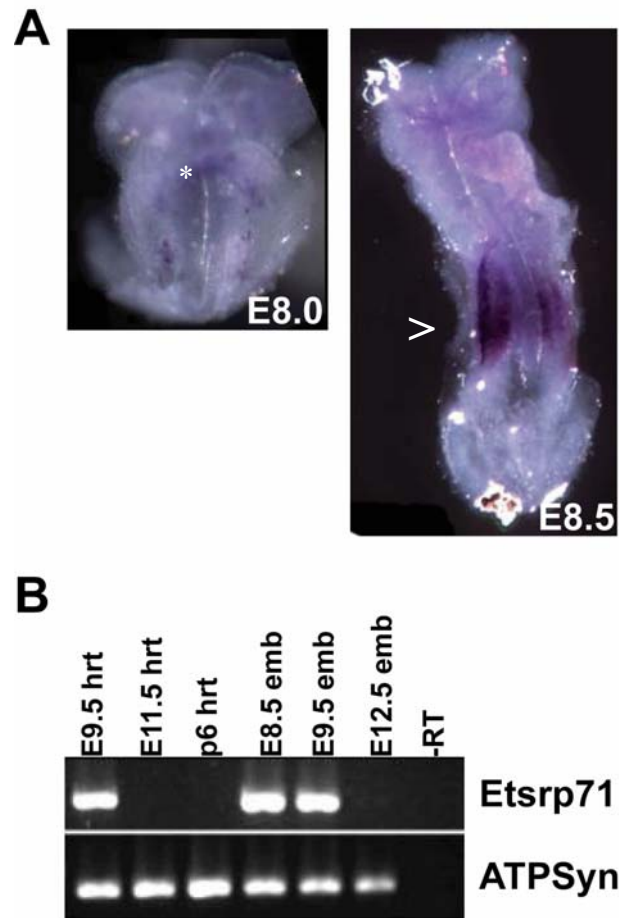


Figure 14. *Etsrp71* is expressed in the early developing heart. A) Whole mount *in situ* hybridization of *Etsrp71* reveals expression in the late cardiac crescent/forming heart tube at E8.0 (asterisk). By E8.5, expression in the heart is diminished and there is strong signal in the presomitic mesoderm (arrowhead). B) RT-PCR on a panel of embryonic cDNA samples shows that *Etsrp71* is expressed in the early embryo and heart, but expression in the heart is lost by E11.5.

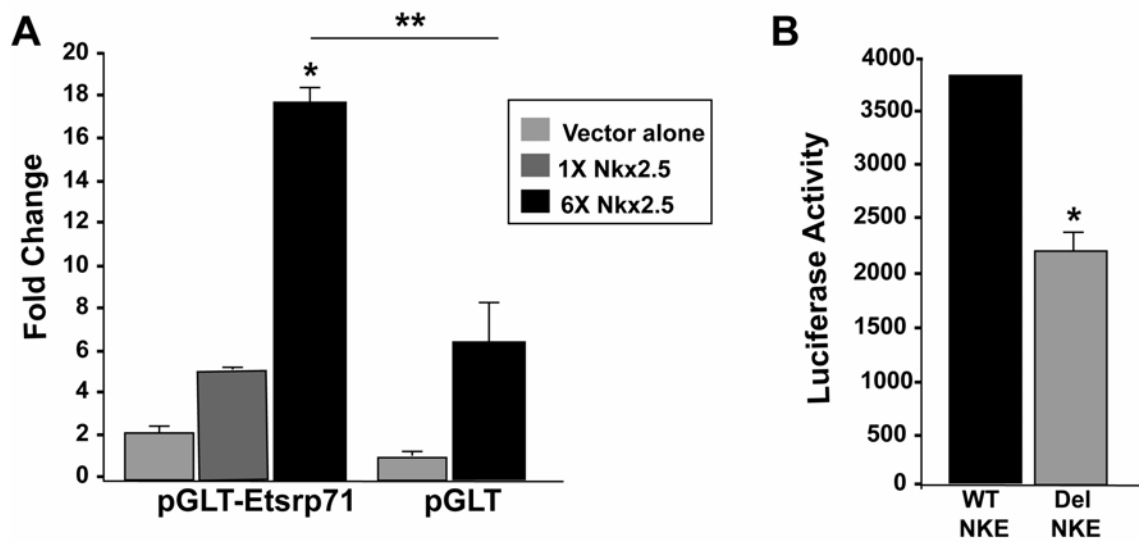


Figure 15. The *Etsrp71* upstream enhancer exhibits transactivation in response to *Nkx2.5* that is sensitive to the deletion of NKEs. A) COS-1 cells were transfected with the 1.5 kB *Etsrp71* enhancer and varying levels of *Nkx2.5* expression construct. Luciferase values were normalized to β -galactosidase activity. Asterisks indicate significant fold change. B) Mutagenesis of NKEs in the *Etsrp71* enhancer diminished transactivation by *Nkx2.5*. COS-1 cells were transfected with *Etsrp71* enhancer constructs containing either wild type or mutated NKEs, shown is data from mutagenesis of the 9615 NKE (see methods).

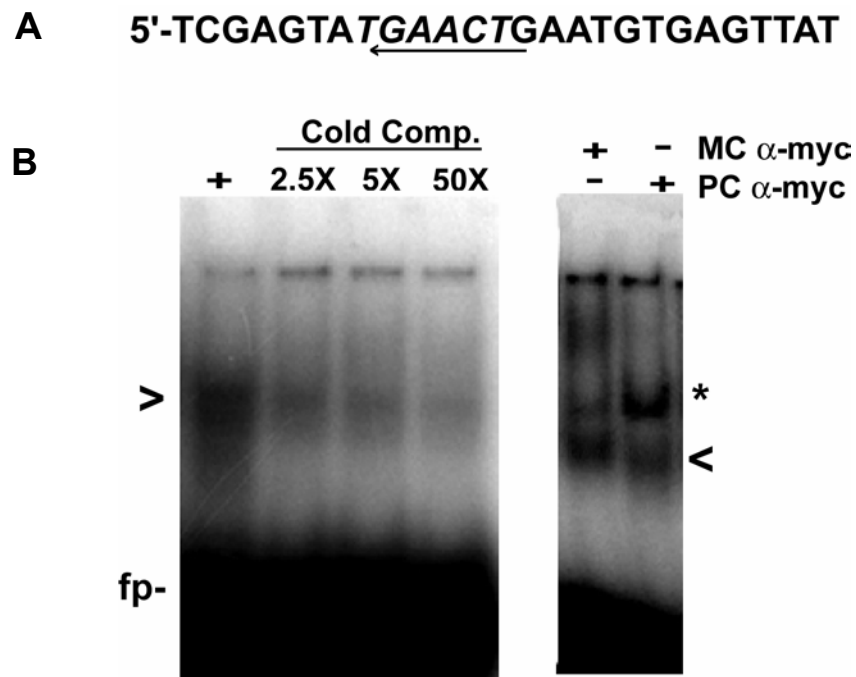


Figure 16. EMSA demonstrates Nkx2.5 binding to NKEs in the *Etsrp71* enhancer. A). Sequence of the 8911 NKE (underlined). B) Labeled oligonucleotides containing NKE sequences were incubated with nuclear extracts made from COS-1 cells overexpressing *Nkx2.5*-myc and the indicated amounts of cold competitor DNA. The arrowhead indicates the shifted complex. fp, free probe. Specificity of the Nkx2.5 interaction was shown by supershift with monoclonal and polyclonal α -myc antibody (asterisk).

NKEs demonstrated specific binding, further supporting a role for *Nkx2.5* in transcriptional activation of *Etsrp71*.

The *VCAM* enhancers tested, however, did not respond to *Nkx2.5* in transactivation assays (data not shown). Overexpression analysis did demonstrate that *VCAM* transcripts are induced by *Nkx2.5* in C2C12 cells (Figure 17). Furthermore, *Nkx2.5* did bind to selected NKEs identified in the *VCAM* 1 kB intronic conserved region. The sequences required for *Nkx2.5* regulation of this transcript may involve a combination of this proximal intronic region with distal modifying regions.

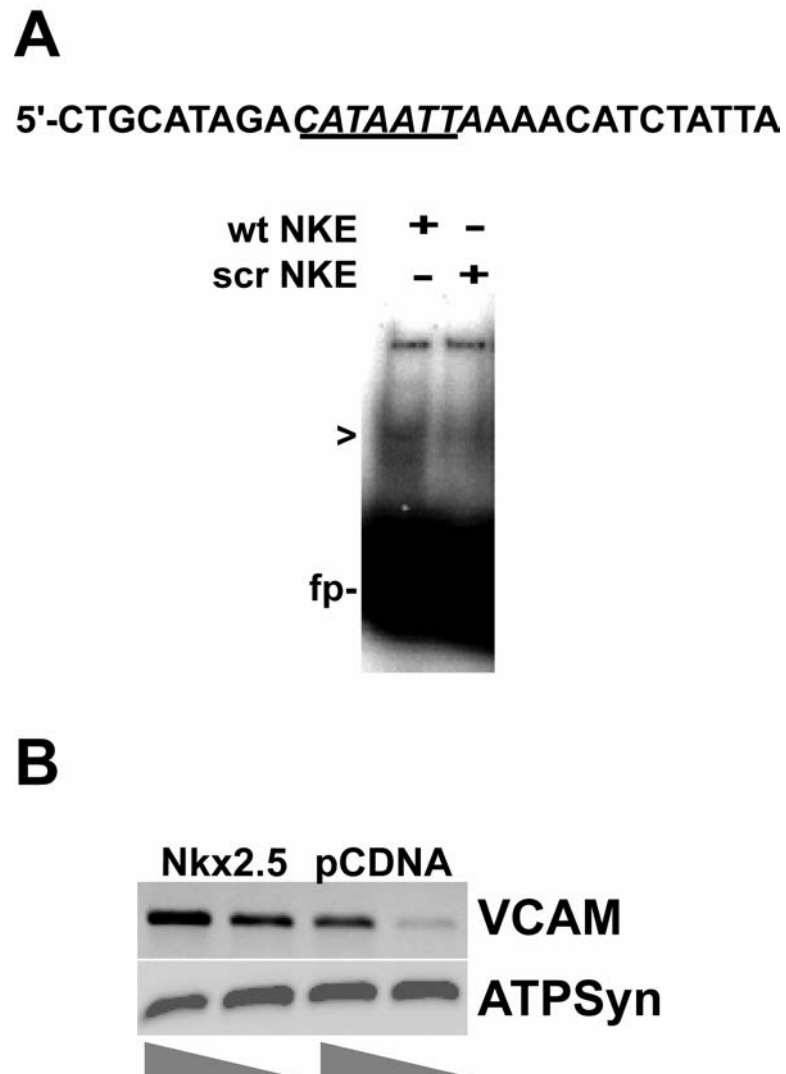


Figure 17. *VCAM* is a putative target of *Nkx2.5* regulation. A) A conserved region between exons 2 and 3 of the *VCAM* genomic locus contains an NKE (underlined) that bind to *Nkx2.5* *in vitro*. B) Overexpression of *Nkx2.5* in C2C12 myoblasts induced the expression of *VCAM-1*. pCDNA was used as a control.

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Discussion

This analysis of the *Nkx2.5* null cardiac transcriptome presents for the first time a comprehensive and cardiac-specific catalog of the transcriptional response to *Nkx2.5* loss of function. In addition to providing new insight into the *Nkx2.5* null phenotype, these data allow for the identification of putative transcriptional targets of *Nkx2.5*, including *etsrp71* and *VCAM*.

The *Nkx2.5* Null Transcriptome and the *Nkx2.5* Null Phenotype

Overall, relatively few transcripts were depleted in the *Nkx2.5* null at early stages of development, and of these, only six were depleted at all three early stages. I expected that a greater amount of transcript depletion would precede morphological manifestation of the null phenotype. The small number of disrupted transcripts may reflect the discrepancy between the early function of *tinman* in fly cardiogenesis and the relatively late function of murine *Nkx2.5*. One explanation is genetic redundancy. The *NK* family member *Nkx2.6* is expressed in the developing mouse heart, with expression in caudal cardiac progenitors at E8.0, the sinus venosus at E8.5, and outflow tract at E9.5 (Biben et al., 1998). *Nkx2.6* is also expressed in the foregut endoderm and pharyngeal pouches. Our data do not show increased expression of any known *NK* family members in the *Nkx2.5* null (Appendix 4). However, *Nkx2.5/Nkx2.6* double null animals show reduced expression of *ANF* in the atria as well as the ventricles (Tanaka et al., 2001), suggesting that *Nkx2.6*, though not expressed atrially, may be contributing to the *Nkx2.5* transcriptional pathway in this tissue. Other *NK* family

genes may similarly compensate for the *Nkx2.5* null state through inductive pathways, perhaps originating from the pharyngeal endoderm, a common site of expression of *Nkx2.5*, *Nkx2.3*, and *Nkx2.6* (Lints et al., 1990; Pabst et al., 1997; Biben et al., 1998).

Another explanation for the late effects of the *Nkx2.5* null state on cardiac development, and one that also addresses the relatively small number of dysregulated transcripts identified at early developmental stages in the current study, is related to the multifactor model of cardiac development mentioned in Chapter 3. In this model, cardiac-specific transcription factors complex with more broadly expressed factors and elements of the general transcriptional machinery to form multiprotein complexes that regulate cardiac gene expression. This transcriptional complex as a whole may be resistant to single factor perturbations early in development and exhibit greater sensitivity later, when there is less overlap between the expression domains of the relevant factors. Data from several knockout models supports the idea that functional redundancy among cooperating factors is at play during early cardiogenesis. *Nkx2.5* and *Hand2* (*dHAND*) nulls each exhibit lethality during cardiac morphogenesis but correctly form a primitive ventricle (Lyons et al., 1995; Srivastava et al., 1997; Tanaka et al., 1999). *Nkx2.5/dHAND* double null embryos, however, exhibit almost complete loss of the ventricular lineage, and fail to form a ventricle (Yamagashi et al., 2001).

The Roles of Downstream *Nkx2.5* Targets in Cardiac Development

Two candidate factors for *Nkx2.5* regulation that I selected for further study are *VCAM* and *etsrp71*, based on published data regarding their roles in cardiac development.

VCAM was initially a promising target for study since it has been previously studied in the heart, though not known to be downstream of *Nkx2.5*. *VCAM* null mice are embryonic lethal around E11.5; they fail to develop an epicardium, exhibit a thin compact ventricular layer, and die due to hemodynamic insufficiency (Kwee et al., 1995). Array data demonstrated that *VCAM* is downstream of *Nkx2.5* in the developing heart. Overexpression analyses also support this finding. However, a direct effect of *Nkx2.5* on putative VCAM enhancer regions was not identified. Transgenic analysis will be needed to examine larger regions of the VCAM enhancer for *Nkx2.5* responsiveness.

I had interest in *Etsrp71* because it showed strong conservation with *pointed*, a *Drosophila* ETS-domain factor that acts downstream of the GATA factor *pannier* to specify the pericyte lineage in the dorsal vessel (Alvarez et al., 2003). Previous studies of the ETS family members *Ets1* and *Ets2* in the developing chick heart have implicated these factors in epicardial migration and coronary vessel remodeling (Lie-Venema et al., 2003), but cardiac effects in the murine *Ets1* and *Ets2* knockouts have not been reported (Remy et al., 2000). This study demonstrated early cardiac expression of *etsrp71*, by RT-PCR, array, and *in situ* hybridization, and identified regions of the *etsrp71* promoter that may serve as direct interaction sites for *Nkx2.5*. Further studies will focus on identifying the role of *etsrp71* in cardiac development.

Application of Microarray Technologies to the Study of Null Phenotypes

While this study allowed me to collect a large amount of data on transcriptional changes in the *Nkx2.5* null heart, follow-up of putative direct downstream targets was complicated by several factors related to the biology of *Nkx2.5*. For example, despite the large number of published studies that utilize transcriptional activation assays to demonstrate *Nkx2.5* activity on enhancer fragments, I found interpretation of these data complicated by the high and dose-dependent activity of *Nkx2.5* on empty reporter vectors. This effect may be less problematic for studies of stronger activators, but for a relatively weak activator like *Nkx2.5*, it tended to obscure analysis. Overexpression analyses also yielded mixed results, perhaps indicating cell-type dependent effects that also may impact promoter studies in culture. The limited agreement of transcript depletion patterns between cardiac stages also highlights the context dependence of transcript dysregulation. A recent study of expression levels of the well-characterized *Nkx2.5* targets *ANF* and *BNP* in the developing heart showed that these genes were dependent on *Nkx2.5* levels at E8.0, independent of *Nkx2.5* levels midgestationally, and again dependent on *Nkx2.5* levels in the adult heart (Jay et al., 2005). *Nkx2.5* also negatively regulates its own expression in cardiac regions (Schwartz and Olson, 1999; this study), which impacts dosage effects as well. In summary, transcriptional analysis can be a powerful tool for analyzing null phenotypes, but robust secondary screens, such as chromatin immunoprecipitation, overexpression analyses, or transactivation assays in a low background system, are needed to distinguish direct from indirect effects.

CHAPTER FIVE

An *Nkx2.5*-Dependent Pathway is Upstream Left-Right Asymmetric Gene Expression in the Cardiac Crescent.

Background

The mammalian heart originates as a bilaterally symmetric region of specified precursors termed the cardiac crescent at mouse embryonic day E7.75 (reviewed in Harvey, 2002). Cells of the cardiac crescent fuse at the midline to form the early heart tube, which is patterned along the anterior-posterior axis so that atrial precursors are initially caudal and ventricular precursors rostral. The heart then loops, breaking left-right symmetry and bringing the atria to a cranial position while the ventricles become oriented caudal to the atria. When looping is complete, the heart consists of four chambers with distinct molecular and morphological identities that reflect patterning along the body axes.

Though the left-right axis is the last to develop in the embryo, it is the first to be morphologically evident (at looping) in the heart. Embryonic left-right axis determination initiates with the appearance of the node, a ciliated organ located at the distal tip of the pre-gastrulation embryo. Morphogen flow directed by nodal ciliary motion triggers a signaling cascade in the left lateral plate mesoderm (Nonaka et al., 2002) that culminates in expression of the TGF β factors *nodal*, *lefty-1* and *lefty-2* on the left side of the embryo (Collington et al., 1996; Lowe et al., 1996). Nodal signaling, dependent on its co-ligand *cripto/cryptic* (Yan et al., 2002) and a *SMAD/FAST* pathway (Chang et al., 2000; Saijoh et al., 2000) triggers the

asymmetric expression of *paired-related transcription factor 2c* (*Pitx2c*), a key determinant of laterality in many mesodermal tissues (Ryan et al., 1998; Yoshioka et al., 1998; Logan et al., 1998; Piedra et al., 1998).

The relationship between left-right orientation and cardiac development has been explored in several morphological studies. The left and right sides of the cardiac crescent contribute to the left and right regions of the newly formed heart tube, respectively (Stalsberg, 1969). Subsequently, the left side of the linear heart tube contributes cells to the left atria and to ventral regions of the primitive ventricle while the right side of the linear heart tube is traced to the right atria and dorsal regions of the ventricles (Campione et al., 2001; Meilhac et al., 2004). As looping progresses, ventromedial regions of the early heart tube will contribute to the outer curvature of the four-chambered heart while more dorsal and lateral regions contribute to structures along the inner curvature (De la Cruz and Markwald, 1999; reviewed in Moorman and Christoffels, 2004). Labeling studies conducted in amphibians have also revealed a greater contribution to the “primary loop” of the heart from the left side of the heart-forming field (Stalsberg, 1969, describing the work of Wilens, 1955). Together, these studies indicate that the left-right orientation of the cardiac crescent (E7.75) is maintained in the linear heart tube (E8.0), becomes transformed into dorsoventral polarity in the ventricles of early looping heart (E8.5), and ultimately corresponds to distinct myocyte populations at the outer and inner curvatures of the looping heart (E9.5-E11.5).

Molecular markers that correspond to these morphological events have been described for later stages of looping. *Pitx2c* expression marks the left linear heart tube, then the ventral region of the looping heart (Campione et al., 2001). Genes that exhibit dorsoventral expression gradients in the ventricular region of the early looping heart at E8.5-E9.5, including *connexin 43* (*Cx43*), *Iroquois 5* (*Irx5*), *atrial natriuretic factor* (*ANF*), *small muscle protein x-linked* (*chisel*), and *CBP/p300 interacting transcription factor 1* (*Cited 1*), are markers for the outer curvature of the heart at E10-E12 (Zeller et al., 1987; Dunwoodie et al., 1998; Christoffels et al., 2000a, 2000b; Palmer et al., 2001). However, this type of transcriptional patterning has not been characterized in the cardiac crescent. I hypothesized that left-right asymmetric gene expression patterns would be present in the cardiac crescent and distinguish between these future ventricular lineages.

In order to investigate this question, I performed transcriptional analysis on cardiac cells from the left and right regions of the cardiac crescent. I found that transcripts encoding cardiac structural proteins and selected cardiac transcription factors, including the homeobox protein *Nkx2.5*, are enriched in the left region of the cardiac crescent with respect to the right. To further investigate the significance of this early transcriptional program to cardiac development, I analyzed the same transcriptional program in the *Nkx2.5* mutant mouse, which displays an early and lethal defect in ventricular morphogenesis (Lyons et al, 1995). I found that *Nkx2.5* mutant embryos show no enrichment of the left-sided cardiac program and exhibit perturbations in the expression patterns of the left-right regulator *Pitx2c* and the factors *cripto* and *nodal*. This work demonstrates a novel transcriptional program in the left

and right regions of the cardiac crescent and reveals a new role for *Nkx2.5* in conveying LR patterning information in the early developing heart.

Results

Isolation of Cells From the Left and Right Sides of the Cardiac Crescent

The *Nkx2.5-EYFP* transgenic mouse line utilizes a 6.65 kB enhancer from the *Nkx2.5* genomic region to direct the expression of EYFP in cardiac lineages during early development (described in Chapter 3). Transgenic embryos exhibit fluorescence throughout the cardiac crescent at E7.75 (Figure 18). Embryos were bisected, and cell populations from the left and right sides of the crescent collected by FACS. Cell counts showed that the number of cells collected from the left (mean =1723; n =4) and right (mean=1746; n = 4) sides of the crescent were comparable.

The Left Region of the Cardiac Crescent is Enriched For a Cardiac Structural Transcriptional Program.

RNA isolated from cell populations from the left and right sides of three wild type crescents was amplified for analysis. Two samples were used for GeneChip analysis and two used for semi-quantitative RT-PCR. Fifty-eight features, representing 47 annotated genes and 5 ESTs (6 redundant features) exhibited two-fold or greater enrichment in the left side of the crescent with respect to the right in both samples arrayed (Table 6). This data set includes two genes that are key mediators of the left-right asymmetry pathway, *Pitx2c* and *tdgf-1* (*teratoma-derived growth factor 1*, also called *cripto*). Both of these transcripts are expressed in the left lateral plate mesoderm and left cardiac crescent at E7.75 (Dono et al., 1993; Gage and Camper, 1997) and serve as positive controls for our array analysis. I also

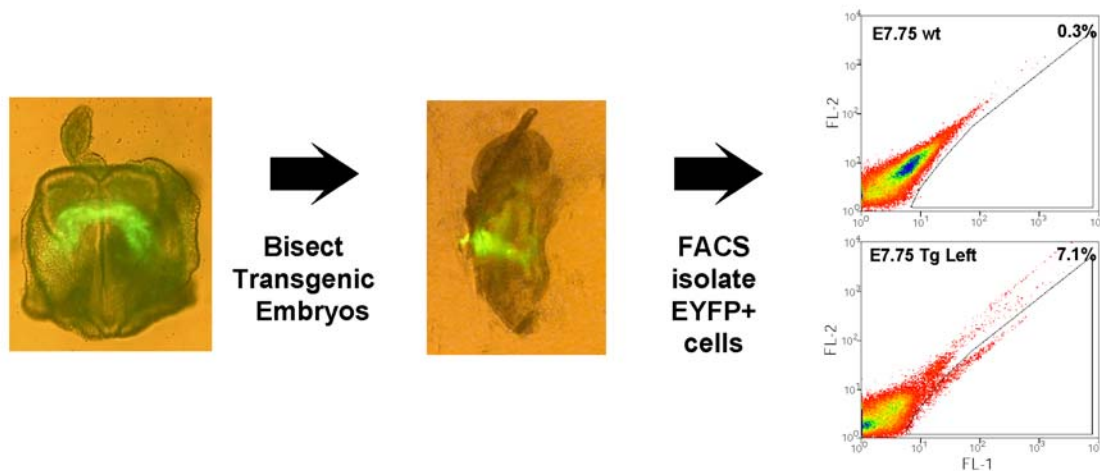


Figure 18. Strategy used to isolate cells from the left and right sides of the cardiac crescent. E7.75 *Nkx2.5*-EYFP transgenic embryos were bisected and FACS used to isolate cardiac cell populations. On the far right are fluorescence profiles for the left side of a transgenic embryo and a wild type littermate. The percentage of live-gated EYFP+ cells is shown on the top right of each profile. The numbers of EYFP+ cells recovered from the heart were comparable (see text), serving as confirmation that bisection of embryos was successful.

expected left-sided enrichment for the TGF β family member *Nodal*, a factor that acts upstream of *Pitx2c* and coordinately with *cripto/cryptic* in specifying left-sided identity. *Nodal* was significantly enriched in one replicate (8.00 fold enrichment, p value = .0095) but was filtered out of the final data set because the second replicate showed a low p-value for the fold change observed (2.00 fold enrichment, p-value = .0092). *Lefty-1* and *Lefty-2*, two additional left-side determinants are not featured on the Affymetrix array.

Left-enriched genes included a number of cardiac sarcomeric transcripts (*Acta1*, *Myla*, *Mylc*, *Mylpc*, *Myh7*, *Myhca*, *Tpm1*, *Tncc*, *Tnni1*, *Tnnt2*). Other cardiac transcripts enriched on the left include the transcription factor *Smarcd3*, the heat-shock proteins *Cryab* and *Hsp2*, and an enzyme involved in synthesis of the cardiac jelly, *Has2*. Twenty-one features, representing 20 annotated genes (1 redundant feature) were enriched on the right with respect to the left. *Zic3* has been previously described as enriched on the right (Nagai et al., 1997) and serves as a positive control for this data set. In contrast to left-enriched transcripts, of which about half are cardiac markers, right-enriched transcripts represent multiple lineages (Table 7). Semi-quantitative RT-PCR was used to confirm array results (Figure 19) on independent samples.

Left-Right Expression Patterns are Perturbed in the *Nkx2.5* Null Animal

I next chose to examine this transcriptional program in an *Nkx2.5* mutant model. I had interest in *Nkx2.5* for several reasons. First, I searched the array data for candidate transcription factors exhibiting left-right asymmetry that might be responsible for directing the left sided program. *Nkx2.5* was left-enriched but excluded from Table 6 due to a low

Category	Symbol	Name	Left-sided Fold Enrichment		Cellular process and/or component
			A	B	
Cardiac-Sarcomeric	Acta1	actin, alpha 1, skeletal muscle	4.59	3.25	motor activity, thin filament
	Ankrd1	ankyrin repeat domain protein1	3.73	2.14	cell signalling, titin-associated
	Krt2-8	keratin complex 2, basic, gene 8	2.00	1.87	adhesion, sarcolemmal associated
	Ldb3	LIM domain binding 3	4.59	2.00	signal transduction, Z-band associated
	Mybpc3	myosin binding protein 3	3.48	2.46	motor activity, thick filament
	Myh6	myosin heavy chain 6	3.03	3.03	motor activity, thick filament
	Myl4	myosin light chain 4	2.64	2.46	motor activity, thick filament
	Myl 3	myosin light chain 3	3.73	4.00	motor activity, thick filament
	Myl2	myosin light chain 2	3.03	1.87	motor activity, thick filament
	Myh7	myosin, heavy polypeptide 7	5.66	8.00	motor activity, thick filament
	Tpm1	tropomyosin 1, alpha	2.83	3.03	motor activity; thin filament
	Tncc	troponin C, cardiac/slow skeletal	3.48	3.25	motor activity; thin filament
	Tnni1	troponin I, skeletal, slow 1	3.73	2.14	motor activity; thin filament
	Tnnt2	troponin T2, cardiac	4.29	4.00	motor activity; thin filament
Cardiac-Other	Akap2	A kinase anchor protein 2	2.00	1.87	cytoskeletal
	Apeg1	aortic preferentially expressed gene 1	3.48	2.00	putative kinase
	Atp1a1	ATPase, Na ⁺ /K ⁺ transporting, alpha 1	2.46	1.87	cardiac automaticity; t tubule-associated
	Has2	hyaluronan synthase 2	2.00	2.46	synthesis of cardiac jelly
	Cryab	crystallin, alpha B	4.00	2.30	stress response
	Hspb2	heat shock protein 2	1.87	1.87	stress response
	Pitx2	paired-like homeodomain transcription factor 2	4.59	11.31	transcription
	Smarcd3	SWI/SNF related d3	3.03	1.87	transcription
	Tdgf1	teratocarcinoma-derived growth factor	24.25	2.83	signal transduction, ligand
Additional transcripts	Vcam1	vascular cell adhesion molecule 1	3.25	2.00	adhesion
	Apoe	apolipoprotein E	2.30	6.06	lipid metabolism
	Car4	carbonic anhydrase 4	2.30	2.30	CO2 metabolism
	Cdh1	cadherin 1	2.46	4.00	cell adhesion; membrane associated
	Cldn6	claudin 6	2.46	2.30	cell adhesion; tight-junctions
	Cyba	cytochrome b-245, alpha polypeptide	2.00	2.30	oxygen metabolism; mitochondrial
	Dia1	diaphorase 1 (NADH)	2.00	2.83	actin regulation
	Dri2	dead ringer homolog 2 (Drosophila)	2.00	1.87	putative transcription factor
	Foxa1	forkhead box A1	5.28	2.83	transcription
	fus	fusion derived from liposarcoma	1.87	4.00	putative transcription factor
	Gucy1b3	guanylate cyclase 1, soluble, beta 3	3.48	2.30	metabolism; putatively NO binding
	Ing4	inhibitor of growth family, member 4	1.87	2.83	putative transcription factor
	Krt1-18	keratin complex 1, acidic, gene 18	2.14	2.83	component of intermediate filaments
	Lrpap1	LDL receptor-related protein associated protein 1	1.87	2.64	cholesterol transport
	Mageh1	melanoma antigen family H, 1	1.87	2.30	putative adhesion protein
	Mical	microtubule associated 1	1.87	2.00	cytoskeletal
	Prnp	prion protein	4.00	2.00	putative adhesion protein
	Rian	RNA imprinted and accumulated in nucleus	3.03	2.46	putative ncRNA
	Ripk4	receptor interacting serine threonine kinase 4	2.64	2.30	signal transduction
	Snrpd3	small nuclear ribonucleoprotein D3	2.00	3.25	RNA processing
	Spink3	serine protease inhibitor, Kazal type 3	2.00	4.59	stress response
	Tacstd1	tumor-associated calcium signal transducer 1	2.30	10.56	function unknown
	Thbs4	thrombospondin 4	4.92	2.30	adhesion
	Tmem46	transmembrane protein 46	5.28	2.30	putative adhesion protein

Table 6. The transcriptome of the left side of the cardiac crescent is enriched for cardiac transcripts, including many sarcomeric proteins. Displayed are transcripts exhibiting a signal strength equal to or greater than 100, and a fold change of 1.87 or greater. A and B represent two independent samples. Cellular process and component were defined through database searches of Entrez Gene, Mouse Genome Informatics, and Pubmed.

Symbol	Name	Right-sided Fold Enrichment		Cellular process and tissue specificity
		A	B	
Aldh2	aldehyde dehydrogenase 2, mitochondrial	2.00	1.87	stress-response, specificity unknown
Amd1	S-adenosylmethionine decarboxylase 1	2.30	2.30	cell growth, ubiquitous
Bbx	bobby sox homolog	3.25	2.00	putative transcription factor
Calm3	calmodulin 3	2.30	1.87	signal transduction, ubiquitous
Enc1	ectodermal-neural cortex 1	2.00	2.00	cytoskeleton, neuronal
Fli1	Friend leukemia integration 1	2.14	2.00	transcription, hematolymphatic and vascular
Hmgb1	high mobility group box 1	4.00	2.30	chromatin associated, specificity unknown
Hoxa1	homeo box A1	2.14	2.14	transcription, multiple lineages
Hoxb1	homeo box B1	4.59	2.14	transcription, multiple lineages
Kdr	kinase insert domain protein receptor	2.46	2.00	signal transduction, multiple lineages
Klf7	Kruppel-like factor 7	2.30	3.03	transcription, ubiquitous
Mef2a	myocyte enhancer factor 2A	2.30	2.00	transcription, multiple lineages
Mrpl45	mitochondrial ribosomal protein L45	2.00	2.00	protein processing, ubiquitous
Ncoa6ip	nuclear receptor coactivator 6 interacting protein	4.92	2.00	cell growth, specificity unknown
Notch1	Notch gene homolog 1	2.00	2.46	signal transduction, multiple lineages
Rdx	radixin	4.29	1.87	cell adhesion, multiple lineages
Styx	phosphoserine/threonine/tyrosine interaction protein	2.46	2.46	RNA processing, specificity unknown
Tgfb2	transforming growth factor, beta 2	2.00	2.14	signal transduction, multiple lineages
Tnfaip1	tumor necrosis factor, alpha-induced protein 1	1.87	1.87	putative channel
Zic3	zinc finger protein of the cerebellum 3	2.14	2.64	multiple lineages

Table 7. Transcripts significantly enriched on the right side of the cardiac crescent with respect to the left. Displayed are transcripts exhibiting a signal strength equal to or greater than 100, and a fold change of 1.87 or greater. A and B represent two independent samples. Right-enriched transcripts represent markers of several lineages. Cellular process and tissue specificity were defined through database searches of Entrez Gene, Mouse Genome Informatics, and Pubmed.

confidence bound value (91.3%; criterion for Table 6 was 95%). In addition, several of the genes asymmetrically expressed (*acta1*, *ankrd1*, *myl3*) are known to be downstream of *Nkx2.5* (Lyons et al., 1995; Tanaka et al., 1999; Chen and Schwartz, 1998). Lastly, *Nkx2.5* loss of function mice show impaired ventricular morphogenesis, primarily affecting chamber myocardium (Lyons et al., 1995; Tanaka et al., 1999). I crossed the *Nkx2.5*-EYFP transgenic mouse into an *Nkx2.5* loss of function mouse line (Lyons et al., 1995). Once again, I obtained crescent stage embryos from timed pregnancies, bisected the embryos, and utilized FACS to isolate the appropriate cell populations. The fluorescence profile of null transgenic embryos was essentially identical to those of wild type transgenic (data not shown). EYFP-cells collected in parallel with the cardiac cells were used for genotyping. No significant differences were observed in the number of EYFP+ cells recovered from *Nkx2.5* null cardiac crescents (mean = 1689, N=6), compared to wild type crescents (mean = 1734, N=8).

The transcriptome of the *Nkx2.5* null crescent presented many contrasts to the wild type pattern (Figure 20). *Nkx2.5* nulls exhibited a complete loss of left-sided enrichment for the left-sided markers *nodal*, *pitx2c*, and *cripto*. Loss of enrichment of *pitx2* and *nodal* was due to approximately five-fold diminished signal strength in the *Nkx2.5* null crescent samples. *Cripto*, on the other hand, was expressed at higher levels on both the left and the right in the *Nkx2.5* null background. Similarly, the cardiac transcripts enriched on the left side of the crescent in the wild type state were no longer enriched in *Nkx2.5* null crescents. These transcripts were expressed at high levels on both sides of the crescent. In contrast, many right-enriched transcripts retain the patterns they exhibited in the wild type.

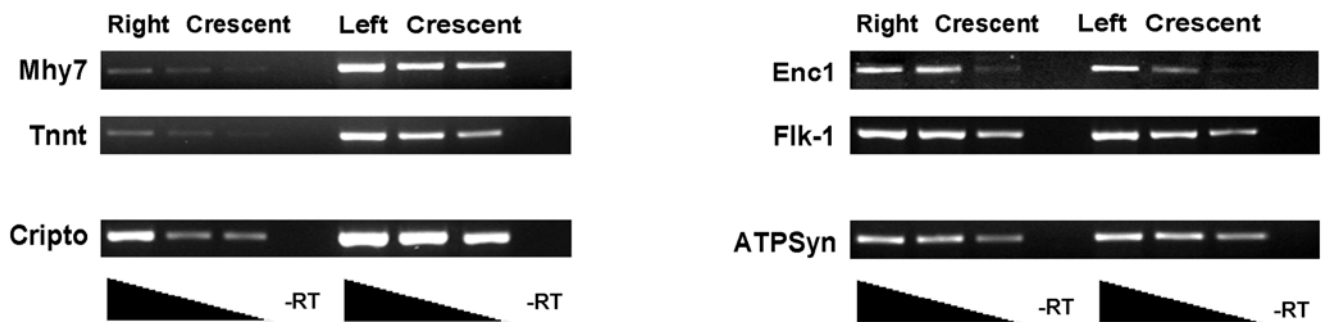


Figure 19. Confirmation of transcripts enriched in the left and right sides of the cardiac crescent. The left-sided enrichment of *Mhy7*, *Tpm2*, and *Tdgfl*, and the right-sided enrichment of *Bbx1* and *flk-1* was confirmed by semi-quantitative RT-PCR with the performed on independently collected set of samples. *ATPSynthase* was used as a loading control.

	Left vs. Right Fold Change			
	WT		Nkx2.5 null	
	A	B	A	B
Acta1	4.59	3.25	-1.32	-1.52
Akap2	2.00	1.87	-1.74	nsc
Ankrd1	3.73	2.14	1.07	-1.07
Apeg1	3.48	2.00	nsc	-1.52
Atp1a1	2.46	1.87	nsc	nsc
Cryab	4.00	2.30	-1.52	-1.23
Has2	2.00	2.46	-1.74	-1.32
Hspb2	1.87	1.87	-1.52	-1.32
Krt2-8	2.00	1.87	-1.41	-1.74
Ldb3	4.59	2.00	nsc	-1.41
Mybpc3	3.48	2.46	-1.52	-1.32
Myh6	3.03	3.03	-1.52	-1.15
Myh7	5.66	8.00	nsc	nsc
Myl 3	3.73	4.00	-1.41	-1.41
Myl2	3.03	1.87	nsc	-1.23
Myl4	2.64	2.46	-1.41	-1.32
Pitx2	4.59	11.31	-1.87	-2.64
Smarcd3	3.03	1.87	-1.74	-1.52
Tdgf1	24.25	2.83	-1.52	-1.15
Tncc	3.48	3.25	-1.41	-1.52
Tnni1	3.73	2.14	-1.52	-1.41
Tnnt2	4.29	4.00	-1.52	-1.32
Tpm1	2.83	3.03	-1.41	-1.52
Vcam1	3.25	2.00	nsc	nsc
Aldh2	-2.00	-1.87	-2.62	nsc
Bbx	-3.25	-2.00	nsc	-2.64
Enc1	-2.00	-2.00	nsc	-3.03
Fli1	-2.14	-2.00	-2.3	-2.83
Hmgb1	-4.00	-2.30	-1.62	nsc
Hoxa1	-2.14	-2.14	-2.46	nsc
Kdr	-2.46	-2.00	nsc	-2.46
Mef2a	-2.30	-2.00	3.03	-3.25
Ncoa6ip	-4.92	-2.00	nsc	-2.46
Notch1	-2.00	-2.46	nsc	-2.46

Figure 20. Comparison of fold change values between the wild type and *Nkx2.5* mutant crescents for selected transcripts enriched in the wild type state. All fold change values are expressed as left signal/right signal. Color bars represent significant fold change ≥ 1.87 ; nsc, no significant change (p-value for change is outside of a 95% confidence bound)

Discussion

This study characterizes for the first time the transcriptional program of the left and right regions of the cardiac crescent. The differences in these transcriptomes reflect differences in patterning predicted to impact the development of distinct myocardial lineages. In addition, this work examines the role of the homeodomain transcription factor *Nkx2.5* in conveying LR patterning information in the cardiac crescent. These results show that *Nkx2.5* is required for proper patterning of left-right asymmetry in the cardiac crescent and indicate that dysregulation of transcriptional identity in the cardiac crescent correlates with developmental defects.

The Transcriptional Identity of the Left Cardiac Crescent Anticipates Cell Fate.

Direct labeling studies have demonstrated continuity between the left side of the cardiac crescent, the left linear heart tube, the ventral early looping heart tube, then the outer curvature of the looping heart (Stalsberg, 1969; Campione et al., 2001; Meilhac et al. 2004). Outer curvature myocardium exhibits distinct morphological and physiological properties as it gives rise to chamber myocardium. The region undergoes extensive outgrowth during looping (“ballooning”), forms trabeculae, organizes gap junctions and mature sarcomeres, and develops fast conduction velocity and conductivity (Moorman and Christoffels, 2003). This study revealed the enrichment of transcripts that encode proteins of the sarcoplasmic reticulum in the left side of the crescent. This transcriptional program may represent a

mechanism for the rapid development of sarcomeric structure in this lineage of future chamber cardiomyocytes.

The sarcomere of the cardiomyocyte, in contrast to that of skeletal muscle, must organize over a short time frame. Specified cardiac precursors are identifiable at E7.75. Rhythmic contractions initiate in the linear heart tube at about E8.25-E8.5. Detailed studies of developing chick cardiomyocytes show diffuse staining for myosin and accumulation of unorganized actin filaments prior to the onset of beating (Ehler et al., 1999). Once rhythmic contractions begin, organized sarcomeric structure is present, detectable by immunohistochemistry and characteristic calcium transients (Ehler et al., 1999; Moorman et al., 2000). One mechanism of sarcomere assembly involves early accumulation of sarcomeric proteins followed by rapid organization at titin and actinin-positive assembly structures just before the heart begins to beat. Our study suggests that accumulation of sarcomeric transcripts may precede protein accumulation in this model.

Additional left-enriched transcripts identified in this study include genes involved in stress-response (*Cryab*, *Hspb2*, *Car2*, *Spink3*), and cell adhesion (*Cdh1*, *Cldn6*, *Thbs4*, *Vcam*). Both processes are predicted to play roles in further stages of cardiogenesis. Reactive oxygen species have complex but critical effects on cardiac differentiation (Morel and Barouki, 1999; Sauer et al., 2000; Puceat et al., 2003), while differential adhesion is a basic mechanism of cell migration. Another possible interpretation involves a hypothetical mechanism to couple early AP axis patterning in the embryo to left-right asymmetry

(Majumder and Overbeek, 1999). In this “axis conversion” model, directional cell surface interactions between epithelial cells already polarized along the AP axis would result in intracellular specification of the left-right axis in neighboring cells.

The Transcriptional Program of The Right Side of the Crescent

The left side of the crescent is enriched in transcripts that are known or predicted to have functions critical to future chamber myocardium. This constitutes a molecular continuity that complements previously described morphological continuity between these regions. The right side of the crescent, in contrast, is not enriched for a specific gene program. Right cardiac crescent is predicted to contribute to inner curvature myocardium, which has a primary myocardium phenotype during looping. The right crescent displays fewer enriched transcripts than the left, and of those, only one, *Mef2A*, is enriched at cardiac or muscle lineages at any point during development (Edmonson et al., 1994). One possible explanation is that initiation of an inner curvature-specific program does not occur until after the crescent stage. Another factor that may impact the right sided transcriptional program is that regions of the outflow tract and right ventricle, specifically dorsal regions in direct apposition to pharyngeal endoderm, receive contributions of cardiac precursors from a secondary heart field not included in the cardiac crescent (Kelly et al., 2001; Mjaatvedt et al., 2001, Waldo et al., 2001). Analysis of these cells may be useful in identifying a transcriptional program for inner curvature myocardium.

Nkx2.5 is Required for Early LR Patterning of the Cardiac Crescent

Nkx2.5 came to our attention as a candidate factor for regulation of LR asymmetric pathways for several reasons. Our array data showed left crescent enrichment of *Nkx2.5*, and several of the genes enriched on the left side of the crescent are known *Nkx2.5* downstream targets. The phenotype of *Nkx2.5* null animals also indicated that investigating left-right patterning may elucidate novel aspects of *Nkx2.5* activity. Murine embryos homozygous for either a truncated (Lyons et al., 1995) or complete null allele (Tanaka et al., 1999) of *Nkx2.5* exhibit lethality at E10.5 and are severely growth retarded. Both nulls exhibit deficient ventricular trabeculation, poor distinction between future left and right ventricles (no interventricular ring) and failure to form endocardial cushions. It was also noted that cell adhesion characteristics of the chamber myocardium – specifically, appear affected in nulls (Lyons et al., 1995). The expression levels of several cardiac proteins normally expressed in the developing ventricles, such as *MLC2V*, *HAND1*, and *ANF*, are greatly reduced in *Nkx2.5* nulls. The transcription factor *eHAND* is also downstream of *Nkx2.5* in the left ventricle (Biben and Harvey, 1997). All of these genes are highly enriched in the chamber myocardium at about E10-E12.

Our data show that *Nkx2.5* null crescents completely lack the left-enriched transcriptional program present in wild type crescents. Since this program was enriched in genes predicted to function in ventricular chamber myocardium, and it is the chamber lineage that appears to be defective in *Nkx2.5* nulls, the disruption of this program in the nulls supports a functional role for early LR asymmetry in patterning future myocardial lineages.

The absence of left-sided enrichment for the sarcomere program may serve as a general early indicator that chamber morphogenesis will be dysmorphic. Examination of this transcriptional program in other null models that display defective chamber myocardium will be needed to fully determine the applicability of our observations.

Points of Intersection between the *Nkx2.5* Transcriptional Network and the LR

Asymmetric Pathway

There are several known interactions that may impact the role of *Nkx2.5* in LR asymmetry. *Nkx2.5* is known to interact with *Pitx2c*. *Nkx2.5* binding sites in an asymmetric enhancer element (ASE) of *Pitx2c* are required for maintenance of expression in the left atrium at E10 (Shiratori et al, 2001). *Nkx2.5* and *Pitx2c* act synergistically on the *ANF* and *PLOD1* (*procollagen lysyl hydroxylase*) promoters *in vitro*, an interaction that is mediated by binding at *Nkx2.5*-response elements and *Pitx2c* binding sites (Ganga et al., 2000). Our results indicate that *Nkx2.5* is needed for maintenance of asymmetric expression of *Pitx2c* even earlier in the cardiac crescent. The shifts in the left crescent transcriptional program I observed, however, are unlikely to be due solely to *Pitx2c* dysregulation. The *Pitx2* mutant exhibits relatively late cardiac defects, including malrotation, a single atrium, incomplete ventricular septation, and valve dysplasia (Gage et al., 1999; Kitamura et al., 1999; Lin et al., 1999; Liu et al, 1999). In addition, the *Pitx2* null state primarily affects processes related to secondary heart field migration (Liu et al., 2002), and chamber myocardium appears to differentiate normally.

Cripto is another candidate for *Nkx2.5* interaction (Childs et al., 2005). The *cripto-1* null animal is embryonic lethal early in development, with defects in gastrulation and axis formation. Null embryos lack early cardiac marker gene expression, suggesting a cardiac specification defect. *Cripto*-null ES cells also fail to give rise to cardiomyocyte lineages. In my studies of the *Nkx2.5* null transcriptome (Chapter 4) – *cripto* is initially depleted in *Nkx2.5* null hearts but is enriched at later stages (Appendix 4). Future work will be directed towards examining the mechanism through which *Nkx2.5* interacts with *cripto*, and potentially other members of the LR pathway, to enhance a left-sided chamber program.

CHAPTER SIX

Concluding Statements

Transcriptome-wide analysis has the potential to elucidate key aspects of cardiac development. The heart, as the first organ to develop in the mammal, is a technically challenging but clinically relevant target for study. In these studies, I applied a robust transcriptional analysis strategy to examine the molecular regulation of early cardiac development. I examined the transcriptional program of the heart under three frameworks - that of the normal developing heart, in a dysmorphic *Nkx2.5* null state, and in relation to embryonic patterning. These individual studies yielded unique but overlapping results.

A transcriptional survey of cardiac cells from three landmark stages of early cardiogenesis - the cardiac crescent, the linear heart tube, and the looped heart - allowed for the identification of a shared genetic program among early cardiac cell populations. This set of genes contained novel cardiac transcripts that can serve as markers of this population. In addition, transcriptional shifts between crescent stage progenitors and the looped heart indicated shared identity between cardiac mesoderm and hematopoietic/vascular populations. The significance of this shared identity to questions of cardiac specification and lineage transdifferentiation is an area that invites further study. Similarly, a study of the *Nkx2.5* transcriptome identified several novel candidates for *Nkx2.5* regulation, including *VCAM*, a cell adhesion gene that has an essential cardiac function, and *etsrp71*, a transcription factor whose role in the heart at this time is unclear. Continued studies will examine the role of

etsrp71 in cardiac development and, potentially, examine the factors that were perturbed by *Nkx2.5* at only one developmental stage. These factors may provide a unique means of elucidating the dynamic role of *Nkx2.5* in the developing heart.

Nkx2.5 pathways also are related to patterning of the cardiac crescent. Left-right asymmetry is morphologically evident early during cardiac development, though the function of patterning along this axis is unclear. Few studies have addressed cardiac-specific aspects of left-right asymmetric patterning at the earliest stage of heart development, the cardiac crescent stage. In this study, I examined the transcriptional program of the left and right sides of the cardiac crescent and identified a distinct chamber myocardial program enriched in the left side of the cardiac crescent. This program was completely disrupted in embryos lacking *Nkx2.5*, as were expression patterns for known components of the left-right signaling pathway, including *Pitx2c* and *cripto*. These results characterize for the first time asymmetries in gene expression along the left-right axis in the cardiac crescent and demonstrate a novel role of *Nkx2.5* in this pathway. Further work, to be continued in the Garry lab, will focus on the interactions between *Nkx2.5* and members of the left-right asymmetry pathway that mediate this effect.

It is my hope that the data generated in this study will be of interest to other researchers as a method for selecting interesting genes for study and as a global snapshot of a cell population that can be compared at a transcriptome level to developmentally and therapeutically interesting candidate cells.

APPENDIX A **Transcripts Enriched in Cardiac Progenitors Compared to Non-Cardiac Age-Matched Embryonic Cells (Affymetrix Mgu74v2 Genechip Data)**

				Fold Change compared to EYFP- age-matched cells		
Class	Unigene Number	Symbol	Gene Name	E7.75	E8.5	E9.5
Antigens	Mm.30246	Cd151	CD151 antigen	1.41	2.00	2.46
	Mm.29798	Cd34	CD34 antigen	-1.74	12.13	8.00
	Mm.8457	Cd59a	CD59a antigen	2.30	2.30	1.07
	Mm.2956	Cd9	CD9 antigen	1.52	1.41	2.64
	Mm.116916	Grasp	GRP1 (general receptor for phosphoinositides 1)-associated	-1.52	1.87	1.23
	Mm.219676	Ly6e	lymphocyte antigen 6 complex, locus E	1.15	1.52	1.87
	Mm.22575	Maged 2	melanoma antigen, family D, 2	-1.15	2.83	2.00
	Mm.26702	Tmem2	transmembrane protein 2	-1.87	3.73	1.52
Apoptosis-Related	Mm.153797	Bcl2	B-cell leukemia/lymphoma 2 (Bcl2), mRNA	1.15	1.87	-1.52
	Mm.149115	Birc4	baculoviral IAP repeat-containing 4	1.87	-1.41	1.00
	Mm.8552	Birc5	baculoviral IAP repeat-containing 5	14.93	-2.30	-2.46
	Mm.35687	Casp7	caspase 7	1.32	2.30	2.64
	Mm.10736	Casp8	caspase 8	-1.07	2.64	2.46
	Mm.196344	Clu	clusterin	1.32	2.46	1.32
	Mm.46856	Pawr	PRKC, apoptosis, WT1, regulator	1.00	1.87	2.00
	Mm.3117	Tdag	T-cell death associated gene	2.00	-1.15	-1.15
	Mm.29351	Tiaf1	TGF-beta1-induced anti-apoptotic factor 1	1.52	3.48	-3.73
	Mm.10331	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	-1.23	1.52	2.00
	Mm.220978	Zac1	zinc finger protein regulator of apoptosis and cell cycle arrest	1.41	2.64	2.30
Cell Cycle	Mm.29189	Ak1	adenylate kinase 1	-4.59	5.28	5.66
	Mm.34246	Calm1	calmodulin 1	1.07	2.00	1.00
	Mm.18041	Calm2	calmodulin 2	-1.74	1.87	-1.23
	Mm.168789	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	1.15	4.59	1.74
	Mm.22701	Gas1	growth arrest specific 1	-1.74	-1.52	1.87
	Mm.4394	Kit	kit oncogene	1.32	2.00	-1.15
	Mm.2444	Myc	Myelocytomatosis oncogene	2.00	-1.74	-1.15
	Mm.1237	Pmp22	peripheral myelin protein, 22 kDa	2.30	1.87	7.46
	Mm.100144	S100a6	S100 calcium binding protein A6 (calcyclin)	-1.87	1.87	1.32
	Mm.10141	Xnp	X-linked nuclear protein	7.46	6.96	7.46

Cell Matrix and Cell Adhesion	Mm.2877	Alcam	activated leukocyte cell adhesion molecule	-11.31	2.46	2.30
	Mm.24138	AW121933	expressed sequence AW121933	1.00	2.00	3.48
	Mm.2608	Bgn	biglycan	1.00	16.00	5.66
	Mm.218571	Cd2ap	CD2-associated protein	1.23	2.83	3.48
	Mm.22768	Cldn5	claudin 5	1.52	24.25	36.76
	Mm.86421	Cldn6	claudin 6	-2.00	2.64	1.32
	Mm.4911	Cntn1	contactin 1	1.32	3.25	-1.87
	Mm.41332	Col14a1	procollagen, type XIV, alpha 1	-1.15	4.59	1.32
	Mm.4352	Col15a1	procollagen, type XV	1.32	3.03	2.46
	Mm.196000	Col18a1	procollagen, type XVIII, alpha 1	1.15	4.29	3.03
	Mm.22621	Col1a1	procollagen, type I, alpha 1	-1.15	-1.07	3.03
	Mm.4482	Col1a2	procollagen, type I, alpha 2	-2.83	-1.15	1.87
	Mm.738	Col4a1	procollagen, type IV, alpha 1	1.07	2.14	4.92
	Mm.181021	Col4a2	procollagen, type IV, alpha 2	1.52	2.64	3.03
	Mm.10299	Col5a2	procollagen, type V, alpha 2	2.30	1.62	2.30
	Mm.20904	Crtap	cartilage associated protein	1.15	1.23	3.03
	Mm.42207	Crtl1	cartilage link protein 1	5.66	9.19	21.11
	Mm.41716	Edil3	EGF-like repeats and discordin I-like domains 3	9.85	18.38	2.00
	Mm.41751	Esam-pending	endothelial cell-selective adhesion molecule	2.30	6.06	2.64
	Mm.735	Fbn1	fibrillin 1	1.62	2.30	4.92
	Mm.193099	Fn1	fibronectin 1	1.07	1.41	1.87
	Mm.28518	Fn14-pending	type I transmembrane protein Fn14	1.00	1.41	2.00
	Mm.34118	Gjb2	Gap junction membrane channel protein beta 2	1.32	2.64	2.46
	Mm.394	Icam2	intercellular adhesion molecule 2	-1.07	51.98	22.63
	Mm.25232	Itga6	integrin alpha 6	-1.41	2.64	2.00
	Mm.4712	Itgb1	integrin beta 1 (fibronectin receptor beta)	1.15	1.32	2.83
	Mm.6424	Itgb5	integrin beta 5	1.00	1.00	1.87
	Mm.167842	Itgp	integrin-associated protein	1.62	2.64	1.52
	Mm.20903	Jcam1	junction cell adhesion molecule1	-2.30	2.00	2.83
	Mm.2399	Lama4	laminin, alpha 4	1.32	2.83	4.59
	Mm.148395	Lamb1-1	laminin B1 subunit 1	1.07	1.15	3.48
	Mm.68887	Lamb2	Laminin, beta 2	3.03	2.46	1.41
	Mm.1249	Lamc1	laminin, gamma 1	1.74	-1.41	2.30
	Mm.39103	Mcam	melanoma cell adhesion molecule	1.15	5.66	8.57
	Mm.7386	Mfap2	microfibrillar-associated protein 2	-1.07	-1.23	1.87
	Mm.19945	Mmp14	Matrix metalloproteinase 14 (membrane-inserted)	-1.62	1.62	2.46
	Mm.20348	Nid2	nidogen 2	-1.23	2.00	3.48
	Mm.27448	Nrp	neuropilin	2.14	2.83	4.00
	Mm.143763	Parva	parvin, alpha	1.15	2.14	2.30
	Mm.11964	Pcdh7	protocadherin 7	-1.15	2.14	-1.41
	Mm.34346	Phlda3	pleckstrin homology-like domain, family A, member 3	-1.32	1.23	6.50
	Mm.3057	Reln	reelin	3.25	-1.62	-6.96
	Mm.35439	Sparc	secreted acidic cysteine rich glycoprotein	1.62	4.29	2.30

	Mm.8245	Timp	tissue inhibitor of metalloproteinase	1.23	1.23	1.87
	Mm.4871	Timp3	Tissue inhibitor of metalloproteinase 3	-1.15	2.83	4.59
	Mm.980	Tnc	tenascin C	1.00	2.00	9.19
	Mm.1021	Vcam1	vascular cell adhesion molecule 1	-1.32	5.28	2.30
	Mm.1021	Vcam1	vascular cell adhesion molecule 1	2.14	4.29	-1.74
Cell Surface Receptors	Mm.689	Acvr1	activin A receptor, type 1	1.15	3.03	1.52
	Mm.4839	Acvr1	activin A receptor, type II-like 1	1.00	2.64	2.14
	Mm.2857	Admr	adrenomedullin receptor	3.03	18.38	6.50
	Mm.3425	Agpt2	angiopoietin 2	1.62	3.25	16.00
	Mm.29368	Agtr1	angiotensin receptor-like 1	1.41	4.29	5.66
	Mm.75467	Calcrl	calcitonin receptor-like	-1.07	3.48	3.48
	Mm.30700	Clec2-pending	C-type lectin-like receptor 2	1.62	25.99	39.40
	Mm.220174	Cubn	cubilin (intrinsic factor-cobalamin receptor)	4.00	3.25	-1.15
	Mm.2653	Epor	Erythropoietin receptor	4.59	-2.30	-4.29
	Mm.24816	F2r	coagulation factor II (thrombin) receptor	1.15	1.41	1.87
	Mm.12948	F2rl3	coagulation factor II (thrombin) receptor-like 3	2.64	27.86	7.46
	Mm.2938	Igf2r	insulin-like growth factor 2 receptor	1.41	2.46	3.73
	Mm.193451	Il11ra2	interleukin 11 receptor, alpha chain 2	2.30	2.30	2.83
	Mm.7800	Itpr5	Inositol 1,4,5-triphosphate receptor 5	-1.74	2.64	1.62
	Mm.285	Kdr	kinase insert domain protein receptor	2.30	8.57	8.57
	Mm.4756	Lepr	leptin receptor	1.07	2.14	1.62
	Mm.28465	Lrp10	low-density lipoprotein receptor-related protein 10	1.15	2.30	2.00
	Mm.2019	Mrc1	mannose receptor, C type 1	-1.15	103.97	2.00
	Mm.31255	Notch1	Notch gene homolog 1, (Drosophila)	-1.74	2.64	-1.15
	Mm.2924	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	-1.23	-2.00	2.00
	Mm.4146	Pdgfrb	platelet derived growth factor receptor, beta polypeptide	-1.15	-1.23	3.25
	Mm.3243	Procr	protein C receptor, endothelial	-1.23	4.92	2.00
	Mm.945	Ptpre	protein tyrosine phosphatase, receptor type, E	2.83	12.13	2.14
	Mm.37213	Ptprb	Protein tyrosine phosphatase, receptor type, B	1.07	13.93	12.13
	Mm.4345	Tie1	tyrosine kinase receptor 1	8.00	97.01	222.86
Chromatin Regulators	Mm.28148	Cbx3	chromobox homolog 3 (Drosophila HP1 gamma)	2.00	1.00	3.48
	Mm.8556	Cbx4	chromobox homolog 4 (Drosophila Pc class)	1.15	1.87	1.00
	Mm.193557	H4	H4 histone family, member A	-1.07	-1.15	2.00
	Mm.38474	Hmg20b	high mobility group 20 B	-1.41	1.15	4.29
	Mm.21772	Smardc2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, d2	-1.74	1.00	1.87
	Mm.140672	Smardc3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, d3	2.30	8.57	4.00
	Mm.22478	Smardc1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, f1	1.87	1.87	-4.00
Intracellular Signaling	Mm.20193	Adcy4	adenylate cyclase 4	-1.52	5.28	3.48
	Mm.157091	Adcy6	adenylate cyclase 6	1.23	2.30	1.00
	Mm.27481	Akap12	A kinase (PRKA) anchor protein (gravin) 12	1.23	3.25	10.56
	Mm.757	Arha2	aplysia ras-related homolog A2	-1.52	1.15	2.00
	Mm.262	Arhc	aplysia ras-related homolog 9 (RhoC)	-1.32	1.41	2.14
	Mm.2241	Arhgdib	rho, GDP dissociation inhibitor (GDI) beta	1.15	2.64	3.48

	Mm.3181	Arhgef1	Rho guanine nucleotide exchange factor (GEF) 1	2.30	1.52	2.30
	Mm.219644	Arhn	aplysia ras-related homolog N (RhoN)	4.29	1.87	1.32
	Mm.31695	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	1.23	3.25	8.00
	Mm.17554	C2pa-pending	C2 membrane binding, PDZ protein/protein interaction, ATP/GTP binding domains	3.73	5.66	4.92
	Mm.1231	Cyr61	cysteine rich protein 61	1.41	2.83	2.00
	Mm.34248	Dab2	disabled homolog 2 (Drosophila)	1.62	2.64	3.73
	Mm.203949	Dok4	downstream of tyrosine kinase 4	1.52	2.46	2.64
	Mm.3464	Flt1	FMS-like tyrosine kinase 1	2.46	24.25	5.66
	Mm.68712	Fzd4	frizzled homolog 4 (Drosophila)	1.07	1.52	3.73
	Mm.9336	Gnb4	guanine nucleotide binding protein, beta 4	1.23	1.87	-6.06
	Mm.27995	Gpr97	G protein-coupled receptor 97	-1.23	3.48	4.92
	Mm.34576	lerepo1 - pending	immediate early response, erythropoietin 1	1.07	2.83	1.41
	Mm.29254	Igfbp3	insulin-like growth factor binding protein 3	-2.00	12.13	14.93
	Mm.218877	Igfbp5	insulin-like growth factor binding protein 5	-2.14	3.73	1.74
	Mm.56685	Iqgap1	IQ motif containing GTPase activating protein 1	-1.41	1.74	1.87
	Mm.28598	Jak1	Janus kinase 1	1.07	2.14	2.30
	Mm.4181	Jak3	Janus kinase 3	1.07	1.23	1.87
	Mm.1834	Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	-1.15	3.25	9.19
	Mm.24022	Map4k5	mitogen-activated protein kinase kinase kinase kinase 5	1.23	1.87	2.64
	Mm.18856	Mapk6	mitogen-activated protein kinase 6	2.46	-1.23	-2.14
	Mm.29857	Nrgn	neurogranin (protein kinase C substrate, RC3)	1.32	1.52	2.14
	Mm.89850	Nrk	Nik related kinase	-6.96	1.87	12.13
	Mm.4390	Numb	numb gene homolog (Drosophila)	1.07	2.14	-2.64
	Mm.23978	Pacs1n2	protein kinase C and casein kinase substrate in neurons 2	1.00	1.41	1.87
	Mm.5241	Pcsk3	proprotein convertase subtilisin/kexin type 3	1.00	1.32	2.46
	Mm.25594	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	2.64	-1.87	-2.00
	Mm.21852	Ptk9l	protein tyrosine kinase 9-like (A6-related protein)	-1.07	2.14	2.00
	Mm.153891	Ptp4a3	protein tyrosine phosphatase 4a3	9.19	-1.41	-2.30
	Mm.2404	Ptpn16	protein tyrosine phosphatase, non-receptor type 16	-1.07	1.87	-1.52
	Mm.1387	Rab11a	RAB11a, member RAS oncogene family	1.32	2.14	2.00
	Mm.21759	Rab12	RAB12, member RAS oncogene family	1.23	1.87	1.87
	Mm.34867	Rab27a	RAB27A, member RAS oncogene family	-1.41	6.50	3.48
	Mm.27832	Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	1.15	3.73	3.48
	Mm.218611	Ramp2	receptor (calcitonin) activity modifying protein 2	4.00	13.93	13.00
	Mm.18517	Rasa3	RAS p21 protein activator 3	1.32	3.03	2.00
	Mm.3903	Rasd1	RAS, dexamethasone-induced 1	-1.87	4.00	12.13
	Mm.20884	Rasgrp 2	RAS, guanyl releasing protein 2	1.87	4.92	4.59
	Mm.4485	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	-2.64	13.93	5.28
	Mm.20156	Rgs19i p1	regulator of G-protein signaling 19 interacting protein 1	1.00	1.15	2.00
	Mm.28262	Rgs2	regulator of G-protein signaling 2	-1.52	2.30	1.87
	Mm.46612	Ripk3	receptor-interacting serine-threonine kinase 3	1.87	2.83	3.48
	Mm.32033	Rps6ka 2	ribosomal protein S6 kinase, 90kD, polypeptide 2	1.23	1.87	1.52

	Mm.29467	Rrad	Ras-related associated with diabetes	-2.14	7.46	3.48
	Mm.257	Rras	Harvey rat sarcoma oncogene, subgroup R	-2.46	2.46	3.03
	Mm.905	Rsu1	Ras suppressor protein 1	1.15	2.00	1.41
	Mm.2214	Sep	septin 4	8.57	2.30	3.25
	Mm.28405	Sgk	serum/glucocorticoid regulated kinase	-1.15	3.25	3.03
	Mm.22240	Sh3bgrl3	SH3 domain binding glutamic acid-rich protein-like 3	1.41	1.87	2.64
	Mm.40285	Sh3d1B	SH3 domain protein 1B	2.46	1.15	1.23
	Mm.1773	Sh3d2b	SH3 domain protein 2B	1.23	1.07	2.83
	Mm.10701	Siat8d	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D	1.00	2.30	1.41
	Mm.3072	Sipa1	signal-induced proliferation associated gene 1	-3.73	8.57	4.00
	Mm.380	Snk	Serum-inducible kinase	1.15	3.73	2.14
	Mm.27467	Tc10l-pending	TC10-like Rho GTPase	1.74	8.00	5.28
	Mm.14313	Tek	endothelial-specific receptor tyrosine kinase	3.03	8.57	3.48
	Mm.33653	Wnt2	wingless-related MMTV integration site 2	1.32	2.46	2.30
	Mm.2438	Wnt6	wingless-related MMTV integration site 6	-1.41	-1.52	3.25
Ligands	Mm.7486	Bmp2	bone morphogenetic protein 2	3.73	2.64	6.50
	Mm.6813	Bmp4	bone morphogenetic protein 4	1.00	1.41	2.64
	Mm.157069	Dlk1	delta-like 1 homolog (Drosophila)	-1.07	1.23	1.87
	Mm.24573	Gab1	growth factor receptor bound protein 2-associated protein 1	1.87	1.23	-1.62
	Mm.2770	Igf1	insulin-like growth factor 1	-1.07	42.22	6.96
	Mm.3862	Igf2	Insulin-like growth factor 2	2.00	1.52	4.29
	Mm.4952	Irs1	insulin receptor substrate 1	1.87	-1.07	-1.07
	Mm.4235	Kitl	kit ligand (steel)	1.23	1.23	2.46
	Mm.2740	Nppb	Natriuretic peptide precursor type B	4.29	8.57	13.93
	Mm.18213	Tgfb2	transforming growth factor, beta 2	2.30	2.64	2.46
Metabolism	Mm.23368	Acate2-pending	acyl-Coenzyme A thioesterase 2, mitochondrial	1.07	2.30	2.64
	Mm.196075	Acate3-pending	acyl-Coenzyme A thioesterase 3, mitochondrial	1.32	2.14	-1.15
	Mm.3440	Adss1	adenylosuccinate synthetase 1, muscle	-1.07	1.87	-1.32
	Mm.80	Afp	alpha fetoprotein	1.32	2.46	1.07
	Mm.6988	Alad	aminolevulinate, delta-, dehydratase	2.14	-2.46	-2.64
	Mm.140509	Alas2	aminolevulinic acid synthase 2, erythroid	4.29	-8.00	-14.93
	Mm.19844	Alox5ap	arachidonate 5-lipoxygenase activating protein	1.23	2.64	-1.32
	Mm.26743	Apoa1	Apolipoprotein A-I	1.41	3.48	4.59
	Mm.4533	Apoa4	apolipoprotein A-IV	2.64	3.73	-1.23
	Mm.28394	Apoc2	Apolipoprotein CII	1.62	3.25	1.00
	Mm.2161	Apom	apolipoprotein M	6.96	4.59	3.48
	Mm.620	As2	arylsulfatase A	-1.15	1.87	2.46
	Mm.38010	Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	1.15	-1.62	4.59
	Mm.182377	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 4	-1.15	2.00	-1.32
	Mm.156583	Cals1	carbonic anhydrase-like sequence 1	2.83	2.64	5.66
	Mm.1186	Car2	carbonic anhydrase 2	3.48	-2.83	-7.46
	Mm.1641	Car4	Carbonic anhydrase 4	1.74	3.03	1.52
	Mm.29996	Cdo1	cysteine dioxygenase 1, cytosolic	1.00	3.03	4.59
	Mm.16831	Ckb	creatine kinase, brain	-1.52	2.00	-3.25

	Mm.43824	Cox6a2	cytochrome c oxidase, subunit VI a, polypeptide 2	1.00	6.96	18.38
	Mm.35820	Cpo	coproporphyrinogen oxidase	1.87	-2.83	-3.73
	Mm.6587	Cpp2	1-Cys peroxiredoxin protein 2 gene	2.14	-1.23	-1.23
	Mm.1457	Ddah2	dimethylarginine dimethylaminohydrolase 2	1.52	1.87	1.15
	Mm.5731	Ddt	D-dopachrome tautomerase	1.15	1.74	2.00
	Mm.22001	Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	1.00	1.15	1.87
	Mm.14543	Edn1	endothelin 1	8.00	1.87	2.14
	Mm.29492	Elov1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.23	1.41	2.14
	Mm.22220	Fabp3	fatty acid binding protein 3, muscle and heart	-1.32	-1.41	1.87
	Mm.30263	Fac15	fatty acid Coenzyme A ligase, long chain 5	1.32	1.62	1.87
	Mm.24402	Gfpt2	glutamine fructose-6-phosphate transaminase 2	-1.07	5.28	1.62
	Mm.1548	Ggta1	glycoprotein galactosyltransferase alpha 1, 3	2.46	2.30	5.66
	Mm.7156	Gpx3	glutathione peroxidase 3	1.32	1.74	16.00
	Mm.2746	Gstt1	glutathione S-transferase, theta 1	-1.32	3.25	2.30
	Mm.6375	Gyg1	glycogenin 1	2.30	3.48	5.66
	Mm.5148	Has2	hyaluronan synthase 2	2.14	1.74	1.23
	Mm.196718	Hbb	Hemoglobin beta, pseudogene	5.66	-1.41	-1.52
	Mm.141758	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	6.96	-3.03	-5.28
	Mm.35830	Hbb-y	Hemoglobin Y, beta-like embryonic chain	3.48	-2.14	-1.74
	Mm.1710	Hmbs	Hydroxymethylbilane synthase	2.30	-3.25	-3.25
	Mm.6994	Hsd17b 10	hydroxysteroid (17-beta) dehydrogenase 10	1.07	-1.15	2.00
	Mm.1187	Hsd17b 11	hydroxysteroid 17-beta dehydrogenase 11	-1.52	2.64	2.64
	Mm.486	Lamp2	lysosomal membrane glycoprotein 2	1.52	1.87	1.15
	Mm.4554	Laptm5	lysosomal-associated protein transmembrane 5	1.62	4.92	3.73
	Mm.1721	Lipe	lipase, hormone sensitive	-1.87	8.57	-3.03
	Mm.117294	Man1a	mannosidase 1, alpha	-1.15	4.92	-1.87
	Mm.4389	Man1b	mannosidase 1, beta	1.00	-1.07	2.00
	Mm.2433	Man2a 1	mannosidase 2, alpha 1	-1.07	1.87	1.62
	Mm.148155	Mod1	malic enzyme, supernatant	-1.32	2.00	6.06
	Mm.31748	Nox4	NADPH oxidase 4	3.25	3.25	6.96
	Mm.41722	Nt5c	5' nucleotidase, deoxy (pyrimidine), cytosolic type C	-1.15	1.41	1.87
	Mm.21199	Obph1-pending	oxysterol binding protein homolog 1	-1.32	2.30	1.41
	Mm.108076	Pfcp	phosphofructokinase, platelet	1.87	3.48	2.30
	Mm.219627	Pgam2	phosphoglycerate mutase 2	3.73	27.86	9.85
	Mm.155620	Pla2g6	phospholipase A2, group VI	2.30	-1.07	3.03
	Mm.29124	Ppab2b	phosphatidic acid phosphatase type 2B	-2.14	1.87	2.00
	Mm.2598	Ppap2a	phosphatidic acid phosphatase 2a	1.15	1.87	1.32
	Mm.28873	Ppap2c	phosphatidic acid phosphatase type 2c	-1.15	2.14	2.14
	Mm.30929	Prdx1	peroxiredoxin 1	-1.15	1.23	2.00
	Mm.28456	Prodh	proline dehydrogenase	2.14	1.00	2.14
	Mm.27454	Prps1	phosphoribosyl pyrophosphate synthetase 1	3.03	-1.87	-1.15
	Mm.2008	Pter	phosphotriesterase related	-1.41	-1.23	2.46
	Mm.2792	Ptgs1	prostaglandin-endoperoxide synthase 1	-3.25	24.25	3.03
	Mm.2450	Rbp1	Retinol binding protein 1, cellular	-3.25	-1.87	2.00
	Mm.2605	Rbp4	retinol binding protein 4, plasma	3.03	4.59	7.46

	Mm.2734	Sat	spermidine/spermine N1-acetyl transferase	-1.15	3.73	7.46
	Mm.18443	Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	4.59	2.64	2.83
	Mm.17804	Slc31a2	solute carrier family 31, member 2	-1.15	2.46	1.32
	Mm.142455	Slc7a7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	1.00	3.03	3.03
	Mm.67837	Spph1-pending	sphingosine-1-phosphate phosphatase 1	1.07	3.25	2.83
	Mm.10	Srm	Spermidine synthase	2.14	-1.32	1.41
	Mm.21545	Tdo2	tryptophan 2,3-dioxygenase	2.64	5.28	1.00
	Mm.24178	Tgut-pending	tRNA-guanine transglycosylase	1.87	-1.41	1.07
	Mm.2108	Ttr	Transthyretin	4.92	4.29	-1.87
	Mm.3533	Txn2-pending	thioredoxin, mitochondrial	1.87	-1.41	1.23
	Mm.44552	Txnrd1	thioredoxin reductase 1	-2.30	1.00	4.00
	Mm.4610	Upp	uridine phosphorylase	-7.46	11.31	4.92
	Mm.27154	Vnn1	vanin 1	6.50	2.00	3.25
Protein	Mm.116721	Cab140	calcium binding protein, 140 kDa	1.15	1.23	1.87
Folding	Mm.2442	Cai	calcium binding protein, intestinal	-1.32	1.62	2.00
	Mm.3894	Fkbp10	FK506 binding protein 10 (65 kDa)	1.00	1.23	2.00
	Mm.24720	Fkbp7	FK506 binding protein 7 (23 kDa)	3.73	2.30	1.23
	Mm.88777	Fts	fused toes	-1.32	1.87	-1.41
	Mm.709	Grp58	glucose regulated protein, 58 kDa	1.52	1.32	2.14
	Mm.1980	Hspb2	heat shock 27kD protein 2	1.23	6.06	5.28
	Mm.2412	Ppib	peptidylprolyl isomerase B	1.00	1.52	2.30
	Mm.4587	Ppic	peptidylprolyl isomerase C	1.62	2.83	4.29
	Mm.218627	Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	1.07	1.00	1.87
	Mm.2044	Serpinf1	serine (or cysteine) proteinase inhibitor, clade F, member 1	-1.23	1.62	3.03
	Mm.22708	Serpinh1	serine (or cysteine) proteinase inhibitor, clade H (heat shock protein 47), member 1	1.52	1.62	3.03
	Mm.14722	Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta	1.15	6.06	1.07
Protein	Mm.89940	Adam19	a disintegrin and metalloproteinase domain 19 (meltrin beta)	1.52	2.14	1.62
Processing	Mm.22239	Ap1m2	adaptor protein complex AP-1, mu 2 subunit	-1.52	1.87	-4.59
	Mm.6958	Capn2	calpain 2	-1.07	2.83	1.07
	Mm.30290	Capn6	calpain 6	2.00	2.46	5.28
	Mm.6534	Capns1	calpain, small subunit 1	1.41	1.41	2.46
	Mm.29473	Copz1	coatamer protein complex, subunit zeta 1	2.00	-1.41	1.23
	Mm.22144	Copz2	coatamer protein complex, subunit zeta 2	-1.23	1.52	2.00
	Mm.2277	Ctsh	cathepsin H	4.00	6.06	1.74
	Mm.930	Ctsl	cathepsin L	1.00	1.87	-1.15
	Mm.1193	Enpep	glutamyl aminopeptidase	10.56	2.14	-1.87
	Mm.38929	Esm1	endothelial cell-specific molecule 1	3.25	4.29	12.13
	Mm.2578	F10	coagulation factor X	3.48	-1.32	-1.23
	Mm.5193	Klk8	kallikrein 8	1.07	2.00	6.06
	Mm.18808	Pcolce	procollagen C-proteinase enhancer protein	1.74	1.74	2.30
	Mm.7046	Ppgb	protective protein for beta-galactosidase	1.15	1.32	2.00
	Mm.203928	Stx3	syntaxin 3	-2.14	2.30	8.57

	Mm.24867	Stx4a	syntaxin 4A (placental)	-1.32	2.64	1.41
	Mm.2368	Timm17a	translocator of inner mitochondrial membrane 17 kDa, a	1.23	-1.15	1.87
	Mm.42184	Vamp5	vesicle-associated membrane protein 5	1.00	21.11	11.31
	Mm.28356	Vps29	vacuolar protein sorting 29 (S. pombe)	1.07	1.23	1.87
Protein	Mm.6700	Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	1.15	1.15	1.87
Synthesis	Mm.9653	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	2.83	2.30	-2.83
	Mm.28494	Mrpl11	mitochondrial ribosomal protein L11	-1.07	-1.15	1.87
	Mm.25293	Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.23	1.07	1.87
	Mm.142380	Rpl27a	ribosomal protein L27a	1.87	-1.23	-1.23
	Mm.14244	Rpl9	ribosomal protein L9	1.23	2.14	1.15
	Mm.147693	Rps3	ribosomal protein S3	1.07	1.07	2.14
RNA	Mm.27822	Apobec2	apolipoprotein B editing complex 2	13.00	36.76	1.52
Processing	Mm.22722	Raly	HnRNP-associated with lethal yellow	1.07	1.00	2.64
	Mm.27230	Rbms1	RNA binding motif, single stranded interacting protein 1	-1.32	1.32	2.00
	Mm.42247	Rbms2	RNA binding motif, single stranded interacting protein 2	1.15	1.62	2.30
	Mm.175173	Rnase4	ribonuclease, RNase A family 4	4.92	13.00	2.30
Structural	Mm.214950	Acta1	Actin, alpha 1, skeletal muscle	3.48	48.50	16.00
	Mm.16537	Acta2	actin, alpha 2, smooth muscle, aorta	1.52	4.59	27.86
	Mm.686	Actc1	actin, alpha, cardiac	1.62	68.59	32.00
	Mm.3526	Ank3	ankyrin 3, epithelial	-1.87	1.87	1.32
	Mm.142814	Arpc4	actin related protein 2/3 complex, subunit 4 (20 kDa)	1.23	1.15	1.87
	Mm.197387	Bicd2	bicaudal D homolog 2 (Drosophila)	-1.52	1.52	3.48
	Mm.12829	Casq1	calsequestrin 1	1.52	7.46	9.19
	Mm.18962	Catna1	catenin alpha 1	1.00	2.30	1.23
	Mm.178	Cryab	crystallin, alpha B	1.07	3.03	4.29
	Mm.196484	Csrp	cysteine rich protein	1.15	3.03	25.99
	Mm.16080	Dnm	dynamain	-1.07	1.00	2.14
	Mm.28919	Dstn	desmin	1.07	1.74	1.87
	Mm.182607	Epln-pending	epithelial protein lost in neoplasm	1.52	3.03	8.57
	Mm.22479	Krt1-18	Keratin complex 1, acidic, gene 18	1.32	2.46	6.06
	Mm.1012	Krt1-19	Keratin complex 1, acidic, gene 19	-1.87	1.15	11.31
	Mm.6800	Krt2-8	Keratin complex 2, basic, gene 8	1.87	2.30	16.00
	Mm.218	Mns1	meiosis-specific nuclear structural protein 1	2.46	-1.23	1.07
	Mm.28687	Msn	moesin	1.52	1.41	1.87
	Mm.10728	Mybpc3	myosin binding protein C, cardiac	-1.07	51.98	13.00
	Mm.221164	Myhca	myosin heavy chain, cardiac muscle, adult	-1.15	59.71	21.11
	Mm.155714	Myhcb	myosin heavy chain, cardiac muscle, fetal	1.00	181.02	97.01
	Mm.43	Myla	myosin light chain, alkali, cardiac atria	6.06	45.25	32.00
	Mm.7353	Mylc	Myosin light chain, alkali, cardiac ventricles	2.00	78.79	222.86
	Mm.46514	Mylc2a	myosin light chain, regulatory A	13.93	73.52	64.00
	Mm.1000	Mylf	Myosin light chain, alkali, fast skeletal muscle	1.87	1.87	2.46
	Mm.1529	Mylpc	myosin light chain, phosphorylatable, cardiac ventricles	-1.32	128.00	181.02
	Mm.3390	Myo1b	myosin Ib	1.07	1.87	-1.23
	Mm.1403	Myo7a	myosin VIIa	1.87	3.25	2.64

	Mm.4103	Myom1	myomesin 1	-1.23	13.93	3.03
	Mm.86483	Spry1	sprouty homolog 1 (Drosophila)	1.87	-1.41	-1.52
	Mm.89982	Spry2	sprouty homolog 2 (Drosophila)	-1.62	1.32	2.00
	Mm.4053	Tln	Talin	1.74	2.00	2.64
	Mm.712	Tncc	troponin C, cardiac/slow skeletal	12.13	137.19	10.56
	Mm.36900	Tnni1	troponin I, skeletal, slow 1	2.30	13.00	17.15
	Mm.604	Tnni3	troponin I, cardiac	1.41	3.25	4.92
	Mm.711	Tnnt1	troponin T1, skeletal, slow	-2.46	6.50	8.00
	Mm.632	Tnnt2	Troponin T2, cardiac	3.48	42.22	8.57
	Mm.121878	Tpm1	tropomyosin 1, alpha	1.52	1.74	2.00
	Mm.89866	Tuba7	tubulin alpha 7	1.87	-1.07	1.23
	Mm.1703	Tubb5	tubulin, beta 5	1.15	1.87	1.32
	Mm.4010	Vil	villin	-1.32	3.03	1.07
Transcriptional Regulation	Mm.10279	Alrp	ankyrin-like repeat protein	4.29	48.50	17.15
	Mm.2706	Atf3	activating transcription factor 3	1.87	12.13	2.30
	Mm.6110	Bnc	basonuclin	1.41	1.32	2.64
	Mm.89727	Bop	CD8beta opposite strand	-1.07	24.25	17.15
	Mm.32257	BSAC	Mus musculus transcription factor myocardin mRNA, complete cds	3.25	9.85	2.64
	Mm.12429	Cbfa2t3h	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 homolog (human)	2.64	1.41	1.52
	Mm.4639	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	1.32	3.48	13.93
	Mm.45029	Cerd4-pending	cerebellum D4	1.23	1.62	2.64
	Mm.196627	Copeb	core promoter element binding protein	-2.64	2.30	3.48
	Mm.24621	Ctrr1-pending	Tcfcp2-related transcriptional repressor 1	-2.14	2.46	-1.07
	Mm.9474	Dermo1	dermis expressed 1	-1.23	2.14	2.64
	Mm.3896	Dlx2	distal-less homeobox 2	2.46	-5.28	2.46
	Mm.14115	Ets1	E26 avian leukemia oncogene 1, 5' domain	2.64	2.00	2.83
	Mm.22365	Ets2	E26 avian leukemia oncogene 2, 3' domain	1.32	2.14	2.83
	Mm.4829	Etsrp71	ets related protein 71	3.48	2.30	3.25
	Mm.6799	Fhl2	four and a half LIM domains 2	1.00	2.00	1.52
	Mm.119781	Fli1	Friend leukemia integration 1	27.86	13.93	7.46
	Mm.5043	Fos	FBJ osteosarcoma oncogene	1.00	4.00	1.32
	Mm.1344	Gata1	GATA binding protein 1	6.96	-3.48	-2.00
	Mm.1391	Gata2	GATA binding protein 2	1.62	2.64	1.23
	Mm.1428	Gata4	GATA binding protein 4	2.83	3.48	9.85
	Mm.4746	Hand1	heart and neural crest derivatives expressed transcript 1	-2.00	-1.23	3.03
	Mm.33797	Hdac7a	histone deacetylase 7A	1.15	2.00	1.62
	Mm.33896	Hhex	Hematopoietically expressed homeobox	2.14	6.06	2.00
	Mm.4694	Hoxa9	homeo box A9	-1.74	-5.66	2.46
	Mm.26544	Hoxd9	homeo box D9	-1.41	-1.62	7.46
	Mm.444	Idb1	inhibitor of DNA binding 1	-1.07	2.46	2.30
	Mm.42242	Isl1	ISL1 transcription factor, LIM/homeodomain, (islet-1)	1.41	3.73	-3.48
	Mm.482	Jun	Jun oncogene	-1.62	9.85	1.23
	Mm.4847	Klf1	Kruppel-like factor 1 (erythroid)	3.73	-5.28	-3.25
	Mm.29466	Klf7	Kruppel-like factor 7 (ubiquitous)	1.32	1.32	1.87
	Mm.29466	Klf7	Kruppel-like factor 7 (ubiquitous)	-1.32	4.00	1.74

	Mm.29466	Klf7	Kruppel-like factor 7 (ubiquitous)	1.07	5.28	-1.15
	Mm.29466	Klf7	Kruppel-like factor 7 (ubiquitous)	1.41	12.13	7.46
	Mm.25785	Ldb2	LIM domain binding 2	-1.32	3.03	2.46
	Mm.29266	Lmo2	LIM only 2	5.28	1.32	1.87
	Mm.29266	Lmo2	LIM only 2	3.48	1.15	-1.23
	Mm.4925	Lyl1	lymphoblastic leukemia	4.29	1.52	1.41
	Mm.4925	Lyl1	lymphoblastic leukemia	6.50	1.41	1.32
	Mm.27935	Madh6	MAD homolog 6 (Drosophila)	1.52	1.52	3.48
	Mm.3931	Max	Max protein	-1.07	1.23	2.46
	Mm.87279	Mef2a	myocyte enhancer factor 2A	1.52	2.64	2.00
	Mm.24001	Mef2c	myocyte enhancer factor 2C	3.48	2.14	8.57
	Mm.870	Msx1	homeo box, msh-like 1	-2.14	-2.00	3.03
	Mm.1763	Msx2	homeo box, msh-like 2	-1.41	-1.52	13.93
	Mm.1202	Myb	Myeloblastosis oncogene	3.48	3.25	-2.00
	Mm.25903	Nab1	Ngfi-A binding protein 1	-1.23	2.00	3.48
	Mm.6549	Nab2	Ngfi-A binding protein 2	1.07	1.41	2.46
	Mm.10085	Nfatc1	nuclear factor of activated T-cells, cytoplasmic 1	2.46	2.30	3.48
	Mm.3420	Nfkb1	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	1.15	1.87	1.52
	Mm.7507	Nkx2-6	NK2 transcription factor related, locus 6 (Drosophila)	1.07	119.43	16.00
	Mm.28308	Nkx6-2	NK6 transcription factor related, locus 2 (Drosophila)	-1.52	2.00	5.28
	Mm.7331	Pbx3	pre B-cell leukemia transcription factor 3	-1.74	1.07	2.30
	Mm.6923	Pem	placentae and embryos oncofetal gene	-2.46	2.46	1.41
	Mm.3616	Polg	polymerase, gamma	2.30	1.87	3.25
	Mm.3869	Prrx1	paired related homeobox 1	-2.00	-2.30	3.03
	Mm.1802	Prrx2	paired related homeobox 2	1.62	1.52	5.28
	Mm.34570	Rpo1-3	RNA polymerase 1-3 (16 kDa subunit)	2.00	1.00	1.00
	Mm.2186	Rpo2-3	RNA polymerase II 3	1.32	1.23	3.25
	Mm.4081	Runx1	runt related transcription factor 1	6.50	2.14	1.52
	Mm.5039	Six2	sine oculis-related homeobox 2 homolog (Drosophila)	1.23	1.52	3.73
	Mm.4272	Slugh	slug, chicken homolog	2.46	1.15	1.52
	Mm.5080	Sox17	SRY-box containing gene 17	2.14	3.03	5.66
	Mm.2878	Sox18	SRY-box containing gene 18	48.50	22.63	12.13
	Mm.42162	Sox7	SRY-box containing gene 7	2.00	4.29	1.74
	Mm.3102	Tal1	T-cell acute lymphocytic leukemia 1	25.99	-1.15	-1.74
	Mm.103636	Tbx5	T-box 5	-1.15	3.03	3.73
	Mm.4292	Tieg	TGFB inducible early growth response	1.23	3.73	1.41
	Mm.222	Trp53	transformation related protein 53	1.15	-1.52	2.00
	Mm.3280	Twist	Twist gene homolog, (Drosophila)	1.32	-1.15	2.64
	Mm.22718	Xbp1	X-box binding protein 1	2.00	1.52	1.32
	Mm.1161	Zfp185	zinc finger protein 185	2.64	-1.07	2.83
	Mm.3105	Zfp1	zinc finger protein, multitype 1	2.46	-1.87	-1.07
	Mm.156616	Zrfp1-pending	Zinc ring finger protein 1	1.00	2.14	1.87
Transporters	Mm.369	Abca1	ATP-binding cassette, sub-family A (ABC1), member 1	1.00	2.00	6.96
	Mm.3918	Abca4	ATP-binding cassette, sub-family A (ABC1), member 4	1.07	1.87	4.92
	Mm.143731	Abcb10	ATP-binding cassette, sub-family B (MDR/TAP), member 10	2.83	-2.46	-4.00

	Mm.42255	Atp2a2	ATPase, Ca ⁺⁺ transporting, cardiac muscle, slow twitch 2	-1.07	3.48	1.62
	Mm.10288	Atp9a	ATPase, class II, type 9A	-1.62	2.00	1.23
	Mm.100236	Cacna2d2	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.23	2.46	1.52
	Mm.448	Cyba	cytochrome b-245, alpha polypeptide	1.74	2.64	1.87
	Mm.976	Fmo1	flavin containing monooxygenase 1	1.00	12.13	2.64
	Mm.1870	Fxyd5	FXD domain-containing ion transport regulator 5	1.41	4.92	3.48
	Mm.2726	Itpr1	Inositol 1,4,5-triphosphate receptor 1	1.00	1.87	-1.32
	Mm.27861	P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	-1.15	2.83	3.03
	Mm.4190	Slc12a4	solute carrier family 12, member 4	1.52	1.74	1.87
	Mm.16228	Slc25a4	solute carrier family 25 (adenine nucleotide translocator), member 4	1.15	1.52	1.87
	Mm.29744	Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	2.14	-1.52	1.00
	Mm.21002	Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	-1.07	-1.15	2.00
	Mm.4580	Slc4a2	solute carrier family 4 (anion exchanger), member 2	1.32	2.14	3.25
	Mm.4211	Slc8a1	solute carrier family 8 (sodium/calcium exchanger), member 1	-1.62	17.15	5.66
	Mm.20948	Tcn2	transcobalamin 2	-1.23	2.64	1.41
	Mm.195498	Tm4sf7	transmembrane 4 superfamily member 7	1.62	2.00	3.48
	Mm.83615	Trp2	transient receptor protein 2	-1.07	5.28	8.57
	Mm.7444	Viaat	vesicular inhibitory amino acid transporter	4.92	8.57	3.73
	Mm.88850	Zrt1	zinc-iron transporter-like	1.23	1.32	1.87

APPENDIX B

Annotated Transcripts Expressed in Cardiac Crescent Stage (E7.75) Cardiac Progenitors (Affymetrix Mgu74v2 Genechip Data)

Gene Symbol	Gene Name	Detection Call		
		E7.75 A	E7.75 B	E7.75 C
Sep15-(p)	15-kDa selenoprotein	P	P	P
Sep15-(p)	15-kDa selenoprotein	P	P	P
Agpat3	1-acylglycerol-3-phosphate O-acyltransferase 3	A	P	P
Bpgm	2,3-bisphosphoglycerate mutase	P	P	P
Decr1	2,4-dienoyl CoA reductase 1, mitochondrial	P	A	P
Poh1-(p)	26S proteasome-associated pad1 homolog	P	P	P
Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	P	P	P
Hmgcl	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	P	A	P
Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	P	P	P
Ywhag	3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	P	P	P
Oxct	3-oxoacid CoA transferase	P	P	P
Papss1	3'-phosphoadenosine 5'-phosphosulfate synthase 1	P	A	P
Nipsnap1	4-nitrophenylphosphatase domain and non-neuronal SNAP25-like protein homolog 1 (C. elegans)	P	P	P
Htr4	5 hydroxytryptamine (serotonin) receptor 4	P	P	A
Azi2	5-azacytidine induced gene 2	P	A	P
Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	A	P	P
Pgl3	6-phosphogluconolactonase	P	P	P
Pts	6-pyruvoyl-tetrahydropterin synthase	P	P	P
Pcbd	6-pyruvoyl-tetrahydropterin synthase/dimerization cofactor of hepatocyte nuclear factor 1 alpha	P	P	P
Adam10	a disintegrin and metalloprotease domain 10	P	P	P
Adam19	a disintegrin and metalloproteinase domain 19 (meltrin beta)	P	M	P
Adam9	a disintegrin and metalloproteinase domain 9 (meltrin gamma)	P	P	P
Akap12	A kinase (PRKA) anchor protein (gravin) 12	P	A	P
Akap1	A kinase (PRKA) anchor protein 1	P	A	P
Akap8	A kinase (PRKA) anchor protein 8	P	P	P
Akap8	A kinase (PRKA) anchor protein 8	P	P	P
Aim1	absent in melanoma 1	P	P	P
Ash1-(p)	absent, small, or homeotic discs 1 (Drosophila)	P	P	P
Acaa1	acetyl-Coenzyme A acyltransferase 1	P	P	P
Acadm	acetyl-Coenzyme A dehydrogenase, medium chain	P	P	P
Acas2l	acetyl-Coenzyme A synthetase 2 (AMP forming)-like	P	A	P
Gba	acid beta glucosidase	P	P	P
Acp1	acid phosphatase 1, soluble	P	P	P
Acp1	acid phosphatase 1, soluble	A	P	P
Acp1	acid phosphatase 1, soluble	A	P	P
Acp2	acid phosphatase 2, lysosomal	P	P	P
Acp6	acid phosphatase 6, lysophosphatidic	P	P	P
Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	P	P	P
Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	P	A	P
Anp32b	acidic nuclear phosphoprotein 32 family, member B	P	P	P
Arbp	acidic ribosomal phosphoprotein PO	P	P	P
Aco2	aconitase 2, mitochondrial	P	P	P
Arpc1a	actin related protein 2/3 complex, subunit 1A	P	P	P
Arpc2	actin related protein 2/3 complex, subunit 2	P	P	P
Arpc3	actin related protein 2/3 complex, subunit 3	P	P	P
Arpc4	actin related protein 2/3 complex, subunit 4	P	P	P
Arpc5	actin related protein 2/3 complex, subunit 5	P	P	P

Acta2	actin, alpha 2, smooth muscle, aorta	P	P	P
Actc1	actin, alpha, cardiac	P	P	P
Actc1	actin, alpha, cardiac	P	P	P
Actb	actin, beta, cytoplasmic	P	P	P
Actb	actin, beta, cytoplasmic	P	P	P
Actg2	actin, gamma 2, smooth muscle, enteric	P	P	P
Actg	actin, gamma, cytoplasmic	P	P	P
Actn4	actinin alpha 4	P	P	P
Actn1	actinin, alpha 1	P	P	P
Actn1	actinin, alpha 1	P	P	P
Atf1	activating transcription factor 1	P	P	P
Atf2	activating transcription factor 2	P	P	P
Atf3	activating transcription factor 3	P	P	P
Atf4	activating transcription factor 4	P	P	P
Abt1	activator of basal transcription	P	P	P
Acvr2b	activin receptor IIB	P	P	P
Acate2-(p)	acyl-Coenzyme A thioesterase 2, mitochondrial	P	P	P
Acate3-(p)	acyl-Coenzyme A thioesterase 3, mitochondrial	P	P	P
Acyp2	acylphosphatase 2, muscle type	M	P	P
Ap1g1	adaptor protein complex AP-1, gamma 1 subunit	P	P	P
Ap1s1	adaptor protein complex AP-1, sigma 1	P	P	P
Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	P	P	P
Ap2m1	adaptor protein complex AP-2, mu1	P	P	P
Ap2m1	adaptor protein complex AP-2, mu1	P	P	P
Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	P	P	P
Ap1m1	adaptor-related protein complex AP-1, mu subunit 1	P	P	P
Ap3b1	adaptor-related protein complex AP-3, beta 1 subunit	P	P	P
Ap3d	adaptor-related protein complex AP-3, delta subunit	P	P	P
Ap3m1	adaptor-related protein complex AP-3, mu 1 subunit	P	P	P
Ap3s1	adaptor-related protein complex AP-3, sigma 1 subunit	P	P	P
Ap4s1	adaptor-related protein complex AP-4, sigma 1	P	P	P
Adora2a	adenosine A2a receptor	P	P	P
Adarb1	adenosine deaminase, RNA-specific, B1	P	P	P
Adcy6	adenylate cyclase 6	P	A	P
Ak2	adenylate kinase 2	P	P	P
Ak4	adenylate kinase 4	P	P	P
Ak4	adenylate kinase 4	P	P	P
Adsl	adenylosuccinate lyase	P	P	P
Adss1	adenylosuccinate synthetase 1, muscle	P	A	P
Adss2	adenylosuccinate synthetase 2, non muscle	P	P	P
Adss2	adenylosuccinate synthetase 2, non muscle	P	P	P
Adrm1	adhesion regulating molecule 1	M	P	P
Adfp	adipose differentiation related protein	P	P	P
Adprh	ADP-ribosylarginine hydrolase	P	P	P
Arf1	ADP-ribosylation factor 1	P	P	P
Arf4	ADP-ribosylation factor 4	P	P	P
Arf5	ADP-ribosylation factor 5	P	P	M
Arf6	ADP-ribosylation factor 6	P	P	P
Arfrp1	ADP-ribosylation factor related protein 1	P	P	P
Arl3	ADP-ribosylation-like 3	P	M	P
Arl6	ADP-ribosylation-like 6	P	P	P
Arl6ip	ADP-ribosylation-like factor 6 interacting protein	P	P	P
Arl6ip2	ADP-ribosylation-like factor 6 interacting protein 2	P	P	P
Arl6ip4	ADP-ribosylation-like factor 6 interacting protein 4	P	P	P
Adprt1	ADP-ribosyltransferase (NAD+; poly (ADP-ribose) polymerase) 1	P	P	P
Adprt2	ADP-ribosyltransferase (NAD+; poly(ADP-ribose) polymerase)-like 2	P	P	P
Admr	adrenomedullin receptor	P	A	P
Aebp2	AE binding protein 2	P	P	P
Afg3l1	AFG3(ATPase family gene 3)-like 1 (yeast)	P	P	P
Afar	aflatoxin B1 aldehyde reductase	P	M	P
Agp	agouti related protein	P	M	P
Aars	alanyl-tRNA synthetase	P	P	P

Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	P	P	P
Adh5	alcohol dehydrogenase 5 (class III), chi polypeptide	P	P	P
Aldh2	aldehyde dehydrogenase 2, mitochondrial	P	P	P
Aldh2	aldehyde dehydrogenase 2, mitochondrial	P	P	P
Aldh9a1	aldehyde dehydrogenase 9, subfamily A1	P	P	P
Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	P	A	P
Aldh3a2	aldehyde dehydrogenase family 3, subfamily A2	A	P	P
Aldh7a1	aldehyde dehydrogenase family 7, member A1	P	P	P
Aldh7a1	aldehyde dehydrogenase family 7, member A1	P	P	P
Akr1a4	aldo-keto reductase family 1, member A4 (aldehyde reductase)	P	P	P
Akr1b8	aldo-keto reductase family 1, member B8	P	P	P
Aldo1	aldolase 1, A isoform	P	P	P
Aldo1	aldolase 1, A isoform	P	P	P
Afp	alpha fetoprotein	P	P	A
G2an	alpha glucosidase 2, alpha neutral subunit	P	P	P
Spna2	alpha-spectrin 2, brain	P	P	P
Aass	aminoadipate-semialdehyde synthase	P	P	M
Alad	aminolevulinate, delta-, dehydratase	P	P	P
Alas1	aminolevulinic acid synthase 1	P	P	P
Alas2	aminolevulinic acid synthase 2, erythroid	A	P	P
App	amyloid beta (A4) precursor protein	P	P	P
Apba3	amyloid beta (A4) precursor protein-binding, family A, member 3	P	P	P
Apbb1	amyloid beta (A4) precursor protein-binding, family B, member 1	P	A	P
Aplp2	amyloid beta (A4) precursor-like protein 2	P	P	P
Appbp1	amyloid beta precursor protein binding protein 1	P	P	P
Anapc11	anaphase promoting complex subunit 11 homolog (yeast)	P	P	P
Anapc5	anaphase-promoting complex subunit 5	P	P	P
Alk	anaplastic lymphoma kinase	P	P	P
Aup1	ancient ubiquitous protein	P	P	P
Aamp	angio-associated migratory protein	P	P	P
Amotl2	angiomotin like 2	P	P	P
Angptl2	angiotensin-like 2	P	A	P
Agtrap	angiotensin II, type I receptor-associated protein	P	M	P
Ank1	ankyrin 1, erythroid	P	M	P
Ank3	ankyrin 3, epithelial	P	A	P
Asb3	ankyrin repeat and SOCS box-containing protein 3	P	P	P
Ankhzn	ankyrin repeat hooked to zinc finger motif	P	P	P
Anxa11	annexin A11	P	P	P
Anxa2	annexin A2	P	P	P
Anxa3	annexin A3	P	P	P
Anxa4	annexin A4	A	P	P
Anxa5	annexin A5	P	P	P
Anxa6	annexin A6	P	P	M
Mki67	antigen identified by monoclonal antibody Ki 67	P	P	P
Mox2	antigen identified by monoclonal antibody MRC OX-2	P	A	P
Kin	antigenic determinant of rec-A protein	P	P	P
Aop2-(p)	anti-oxidant protein 2	P	P	P
Aop2-(p)	anti-oxidant protein 2	P	P	P
Apoa1	apolipoprotein A-I	P	P	A
Apoa1bp	apolipoprotein A-I binding protein	P	P	P
Apoa1bp	apolipoprotein A-I binding protein	P	P	P
Apoa4	apolipoprotein A-IV	P	P	A
Apobec1	apolipoprotein B editing complex 1	A	P	P
Apoc2	apolipoprotein C-II	P	P	P
ApoE	apolipoprotein E	P	P	P
Apom	apolipoprotein M	P	P	A
Api5	apoptosis inhibitor 5	P	P	P
Acinus	apoptotic chromatin condensation inducer in the nucleus	P	P	P
Apaf1	apoptotic protease activating factor 1	P	P	P
Apex1	apurinic/apyrimidinic endonuclease 1	P	P	P
Aqr	aquarius	P	P	P
Arcn1	archain 1	P	P	P

Arcn1	archain 1	P	P	P
Arg1	arginase 1, liver	P	P	P
Armet	arginine-rich, mutated in early stage tumors	P	P	P
Asl	argininosuccinate lyase	A	P	P
Rnpep	arginyl aminopeptidase (aminopeptidase B)	P	A	P
Arih2	ariadne homolog 2 (Drosophila)	P	P	P
Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	P	P	P
Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein homolog 1 (Drosophila)	M	P	P
Actr10	ARP10 actin-related protein 10 homolog (S. cerevisiae)	P	P	P
Actr2	ARP2 actin-related protein 2 homolog (yeast)	P	P	P
Actr3	ARP3 actin-related protein 3 homolog (yeast)	P	P	P
Asna1	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	A	P	P
Ars2-(p)	arsenate resistance protein 2	P	P	P
Aip	aryl-hydrocarbon receptor-interacting protein	P	P	P
Aip	aryl-hydrocarbon receptor-interacting protein	P	P	P
Asns	asparagine synthetase	P	P	P
Asns	asparagine synthetase	A	P	P
Nars	asparaginyl-tRNA synthetase	P	P	P
Awp1-(p)	associated with Prkcl1	P	P	P
Atm	ataxia telangiectasia mutated homolog (human)	P	M	P
Apacd-(p)	ATP binding protein associated with cell differentiation	P	P	P
Acly	ATP citrate lyase	P	P	P
Atp5g1	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 1	P	P	P
Atp5g2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit c (subunit 9), isoform 2	P	P	P
Atp5j	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F	P	P	P
Atp5j2	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit f, isoform 2	M	P	P
Atp5l	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit g	P	P	P
Atp5a1	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit, isoform 1	P	P	P
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	P	P	P
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	P	P	P
Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	P	P	P
Atp5o	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	P	P	P
Atpi	ATPase inhibitor	P	P	P
Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	P	M	P
Atp2a3	ATPase, Ca++ transporting, ubiquitous	A	P	P
Atp7a	ATPase, Cu++ transporting, alpha polypeptide	P	P	A
Atp6ip1	ATPase, H+ transporting, lysosomal interacting protein 1	P	P	P
Atp6v0a1	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	P	P	P
Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2	P	P	P
Atp6v0a2	ATPase, H+ transporting, lysosomal V0 subunit a isoform 2	P	P	A
Atp6v0e	ATPase, H+ transporting, V0 subunit	P	P	P
Atp6v0b	ATPase, H+ transporting, V0 subunit B	P	P	P
Atp6v0c	ATPase, H+ transporting, V0 subunit C	P	P	P
Atp6v0d1	ATPase, H+ transporting, V0 subunit D isoform 1	P	P	P
Atp6v1a1	ATPase, H+ transporting, V1 subunit A, isoform 1	P	P	P
Atp6v1a1	ATPase, H+ transporting, V1 subunit A, isoform 1	P	P	P
Atp6v1b2	ATPase, H+ transporting, V1 subunit B, isoform 2	P	P	P
Atp6v1d	ATPase, H+ transporting, V1 subunit D	P	P	P
Atp6v1e1	ATPase, H+ transporting, V1 subunit E isoform 1	P	P	P
Atp6v1g1	ATPase, H+ transporting, V1 subunit G isoform 1	P	P	P
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	P	P	P
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	A	P	P
Atp1b3	ATPase, Na+/K+ transporting, beta 3 polypeptide	P	P	P
Abcb4	ATP-binding cassette, sub-family B (MDR/TAP), member 4	A	P	P
Abcb7	ATP-binding cassette, sub-family B (MDR/TAP), member 7	P	P	P
Abcd3	ATP-binding cassette, sub-family D (ALD), member 3	P	P	P
Abcd4	ATP-binding cassette, sub-family D (ALD), member 4	M	P	P
Abce1	ATP-binding cassette, sub-family E (OABP), member 1	P	P	P
Abcg1	ATP-binding cassette, sub-family G (WHITE), member 1	P	P	P
Abcg2	ATP-binding cassette, sub-family G (WHITE), member 2	P	P	P
Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	P	P	P
Auh	AU RNA binding protein/enoyl-coenzyme A hydratase	P	P	P

Amfr	autocrine motility factor receptor	P	P	P
Apg12l	autophagy 12-like (S. cerevisiae)	P	P	P
Apg5l	autophagy 5-like (S. cerevisiae)	P	P	P
Axin	axin	P	P	P
Axot	axotrophin	P	P	P
Bmi1	B lymphoma Mo-MLV insertion region 1	P	P	P
Birc3	baculoviral IAP repeat-containing 3	P	M	P
Birc5	baculoviral IAP repeat-containing 5	P	P	P
Birc6	baculoviral IAP repeat-containing 6	P	P	P
Bzw1	basic leucine zipper and W2 domains 1	P	P	P
Bzw2	basic leucine zipper and W2 domains 2	P	P	P
Bsg	basigin	P	P	P
Bcl6b	B-cell CLL/lymphoma 6, member B	P	A	P
Bcl10	B-cell leukemia/lymphoma 10	P	P	P
Bcap29	B-cell receptor-associated protein 29	P	P	P
Bcap31	B-cell receptor-associated protein 31	P	P	P
Bcap37	B-cell receptor-associated protein 37	P	P	P
Bcap37	B-cell receptor-associated protein 37	M	P	P
Btg1	B-cell translocation gene 1, anti-proliferative	P	P	P
Btg2	B-cell translocation gene 2, anti-proliferative	P	P	P
Btg3	B-cell translocation gene 3	P	P	P
Bnip2	BCL2/adenovirus E1B 19 kDa-interacting protein 1, NIP2	P	P	P
Bnip3	BCL2/adenovirus E1B 19 kDa-interacting protein 1, NIP3	P	P	P
Bnip3l	BCL2/adenovirus E1B 19 kDa-interacting protein 3-like	P	P	P
Bak1	BCL2-antagonist/killer 1	A	P	P
Bag1	Bcl2-associated athanogene 1	P	P	P
Bag2	Bcl2-associated athanogene 2	P	P	P
Bag2	Bcl2-associated athanogene 2	P	P	P
Bag3	Bcl2-associated athanogene 3	P	P	P
Bag3	Bcl2-associated athanogene 3	P	P	P
Bax	Bcl2-associated X protein	P	P	P
Bcl2l	Bcl2-like	P	P	P
Bcl2l11	BCL2-like 11 (apoptosis facilitator)	P	P	P
Bcl2l13	BCL2-like 13 (apoptosis facilitator)	P	P	P
Bcl2l2	Bcl2-like 2	P	P	P
Bok	Bcl-2-related ovarian killer protein	P	A	P
Bad	Bcl-associated death promoter	P	P	P
Becn1	beclin 1 (coiled-coil, myosin-like BCL2-interacting protein)	P	P	P
Bzrp	benzodiazepine receptor, peripheral	P	P	P
Bet3-(p)	Bet3 homolog (S. cerevisiae)	P	P	P
B3Gat3	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	P	P	P
B2m	beta-2 microglobulin	P	P	P
Gus	beta-glucuronidase	P	P	P
Bid	BH3 interacting domain death agonist	P	P	P
Bgn	biglycan	P	P	P
Blvra	biliverdin reductase A	P	P	P
Bing4	BING4 protein	P	P	P
Blmh	bleomycin hydrolase	P	P	P
Blmh	bleomycin hydrolase	A	P	P
Bop1	block of proliferation 1	P	P	P
Bet1l	blocked early in transport 1 homolog (S. cerevisiae)-like	A	P	P
Blm	Bloom syndrome homolog (human)	P	P	P
Bike-(p)	Bmp2-inducible kinase	P	M	P
Bmp4	bone morphogenetic protein 4	P	P	P
Bmp4	Bone morphogenetic protein 4	A	P	P
Bmpr1a	bone morphogenetic protein receptor, type 1A	P	P	P
T	brachyury	A	P	P
Basp1	brain abundant, membrane attached signal protein 1	P	P	P
Basp1	brain abundant, membrane attached signal protein 1	P	P	P
Pygb	brain glycogen phosphorylase	P	P	P
Brp17	brain protein 17	P	P	P
Bri3	brain protein I3	P	P	P

Bcat1	branched chain aminotransferase 1, cytosolic	P	P	P
Bckdhh	branched chain ketoacid dehydrogenase E1, beta polypeptide	P	P	P
Bckdk	branched chain ketoacid dehydrogenase kinase	P	P	P
Brap	BRCA1 associated protein	P	P	P
Bcrp1-(p)	breakpoint cluster region protein 1	P	P	P
Brca1	breast cancer 1	P	P	P
Brca2	breast cancer 2	P	P	P
Bcas2	breast carcinoma amplified sequence 2	P	P	P
---	Brf2 gene, 3' UTR	P	P	P
Baf53a-(p)	BRG1/brm-associated factor 53A	P	P	P
Bin1	bridging integrator 1	P	P	P
Bin1	bridging integrator 1	P	A	P
Baz1b	bromodomain adjacent to zinc finger domain, 1B	P	P	P
Baz2a	bromodomain adjacent to zinc finger domain, 2A	P	P	P
Brd2	bromodomain containing 2	P	P	P
Brd4	bromodomain containing 4	P	P	P
Brd4	bromodomain containing 4	P	P	A
Brd7	bromodomain containing 7	P	P	P
Brd7	bromodomain containing 7	A	P	P
Brd8	bromodomain containing 8	P	P	P
Btbd1	BTB (POZ) domain containing 1	P	P	P
Btbd1	BTB (POZ) domain containing 1	M	P	P
Banp	Btg3 associated nuclear protein	P	P	P
Bub1	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	P	P	P
Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	P	P	P
Bysl	bystin-like	P	P	P
Cdh1	cadherin 1	P	P	P
Cdh11	cadherin 11	P	A	P
Cdh2	cadherin 2	P	P	P
Cdh5	cadherin 5	P	P	P
Calb3	calbindin-D9K	P	P	A
Crcp	calcitonin gene-related peptide-receptor component protein	P	P	P
Cib1	calcium and integrin binding 1 (calmyrin)	M	P	P
Cab39	calcium binding protein	P	P	P
Chp-(p)	calcium binding protein P22	P	M	P
Cai	calcium binding protein, intestinal	P	P	P
Cam1	calcium modulating ligand	P	P	P
Cask	calcium/calmodulin-dependent serine protein kinase	P	P	P
Cacybp	calcyclin binding protein	P	P	P
Calm1	calmodulin 1	P	P	P
Calm2	calmodulin 2	P	P	P
Calm3	calmodulin 3	P	P	P
Calm3	calmodulin 3	P	P	P
Calmbp1	calmodulin binding protein 1	M	P	P
Canx	calnexin	P	P	P
Canx	calnexin	P	A	P
Capn10	calpain 10	A	P	P
Capn2	calpain 2	P	P	P
Capn5	calpain 5	P	A	P
Capn6	calpain 6	P	P	P
Capn6	calpain 6	P	P	P
Capn7	calpain 7	P	P	P
Capns1	calpain, small subunit 1	P	A	P
Cnn2	calponin 2	P	P	P
Cnn3	calponin 3, acidic	P	P	P
Calu	calumenin	P	P	P
Creb1	cAMP responsive element binding protein-like 1	P	P	P
Creml	cAMP responsive element modulator	P	A	P
Capza2	capping protein (actin filament) muscle Z-line, alpha 2	P	P	P
Capzb	capping protein (actin filament) muscle Z-line, beta	P	P	P
Cappa1	capping protein alpha 1	P	P	P
Car14	carbonic anhydrase 14	P	P	P

Car2	carbonic anhydrase 2	P	P	P
Car4	carbonic anhydrase 4	P	P	P
Car4	carbonic anhydrase 4	P	P	P
Cals1	carbonic anhydrase-like sequence 1	P	A	P
Cbr1	carbonyl reductase 1	P	A	P
Cpe	carboxypeptidase E	P	P	P
Cpe	carboxypeptidase E	P	P	P
Flana-(p)	carcinoma related gene	P	P	P
Ctf1	cardiotrophin 1	P	A	P
Cdv1	carnitine deficiency-associated gene expressed in ventricle 1	P	P	P
Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	P	P	P
Cpt2	carnitine palmitoyltransferase 2	P	P	P
Crtap	cartilage associated protein	P	P	P
Csnk1a1	casein kinase 1, alpha 1	P	P	P
Csnk1d	casein kinase 1, delta	P	P	P
Csnk1d	casein kinase 1, delta	P	P	P
Csnk1e	casein kinase 1, epsilon	P	P	P
Csnk2a1-rs4	casein kinase II, alpha 1 related sequence 4	P	P	P
Csnk2a1-rs4	casein kinase II, alpha 1 related sequence 4	P	P	P
Csnk2a1-rs4	casein kinase II, alpha 1 related sequence 4	P	P	P
Csnk2a2	casein kinase II, alpha 2, polypeptide	P	P	P
Csnk2a2	casein kinase II, alpha 2, polypeptide	P	P	P
Csnk2b	casein kinase II, beta subunit	P	P	P
Clpp	caseinolytic protease, ATP-dependent, proteolytic subunit homolog (E. coli)	P	P	P
Casp2	caspase 2	P	P	P
Casp2	caspase 2	P	P	P
Casp3	caspase 3, apoptosis related cysteine protease	P	P	P
Casp6	caspase 6	P	P	P
Casp7	caspase 7	P	P	P
Casp8ap2	caspase 8 associated protein 2	P	P	P
Casp9	caspase 9	P	P	P
Casp9	caspase 9	A	P	P
Cat	catalase	P	P	P
Comt	catechol-O-methyltransferase	P	P	P
Catna1	catenin alpha 1	P	P	P
Catnb	catenin beta	P	P	P
Catns	catenin src	P	P	P
Catns	catenin src	P	P	P
Ctsb	cathepsin B	P	P	P
Ctsc	cathepsin C	P	P	P
Ctsd	cathepsin D	P	P	P
Ctsh	cathepsin H	P	P	P
Ctsl	cathepsin L	P	P	P
Ctsz	cathepsin Z	P	P	P
catp	cation-transporting atpase	P	P	P
Cited2	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	P	P	P
Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	P	P	P
Cebpg	CCAAT/enhancer binding protein (C/EBP), gamma	P	P	A
Cebpa-rs1	CCAAT/enhancer binding protein alpha (C/EBP), related sequence 1	P	P	P
Cebpa-rs1	CCAAT/enhancer binding protein alpha (C/EBP), related sequence 1	A	P	P
Ctcf	CCCTC-binding factor	P	P	P
Cbpin	CCNDBP1 interactor	P	P	P
Ccrn4l	CCR4 carbon catabolite repression 4-like (S. cerevisiae)	P	P	P
Cnot2	CCR4-NOT transcription complex, subunit 2	P	P	P
Cnot4	CCR4-NOT transcription complex, subunit 4	A	P	P
Cnot8	CCR4-NOT transcription complex, subunit 8	P	P	P
Cd81	CD 81 antigen	P	P	P
Cd14	CD14 antigen	M	P	P
Cd151	CD151 antigen	P	P	P
Cd151	CD151 antigen	P	P	P
Cd164	CD164 antigen	P	P	P
Cd24a	CD24a antigen	P	P	P

Siva-(p)	Cd27 binding protein (Hindu God of destruction)	P	P	P
Cd2ap	CD2-associated protein	P	P	P
Clast3-(p)	CD40 ligand-activated specific transcript 3	P	P	P
Cd47	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	P	P	P
Cd59a	CD59a antigen	P	P	P
Cd63	Cd63 antigen	P	P	P
Cd8b	CD8 antigen, beta chain	P	M	P
Cd9	CD9 antigen	P	P	P
Clk4	CDC like kinase 4	P	P	P
Cdc16	CDC16 cell division cycle 16 homolog (S. cerevisiae)	P	P	P
Cks1	CDC28 protein kinase 1	P	P	P
Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	P	M	P
Clk	CDC-like kinase	P	P	P
Clk2	CDC-like kinase 2	P	P	P
Clk3	CDC-like kinase 3	P	P	P
Cdkap1	CDK2 (cyclin-dependent kinase 2)-associated protein 1	P	P	P
---	CDK2 gene intron V containing the alternatively spliced exon Ve	P	P	P
Cds2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	P	A	P
Cpr2-(p)	cell cycle progression 2 protein	P	P	P
Cdc2l2	cell division cycle 2 homolog (S. pombe)-like 2	P	P	P
Cdc2l2	cell division cycle 2 homolog (S. pombe)-like 2	P	P	P
Cdc2a	cell division cycle 2 homolog A (S. pombe)	P	P	P
Cdc20	cell division cycle 20 homolog (S. cerevisiae)	P	P	P
Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)	P	P	P
Cdc25c	cell division cycle 25 homolog C (S. cerevisiae)	P	P	P
Cdc25c	cell division cycle 25 homolog C (S. cerevisiae)	P	P	P
Cdc37	cell division cycle 37 homolog (S. cerevisiae)	P	P	P
Cdc42	cell division cycle 42 homolog (S. cerevisiae)	P	P	P
Cdc45l	cell division cycle 45 homolog (S. cerevisiae)-like	P	P	P
Cdc5l	cell division cycle 5-like (S. pombe)	P	P	P
Cdc6	cell division cycle 6 homolog (S. cerevisiae)	P	P	P
Cdc7l1	cell division cycle 71 homolog (S. cerevisiae)-like 1	P	P	P
Mel	cell line NK14 derived transforming oncogene	P	P	P
Cnbp	cellular nucleic acid binding protein	P	P	P
Cnbp	cellular nucleic acid binding protein	P	P	P
Crabp1	cellular retinoic acid binding protein I	P	P	P
Crabp2	cellular retinoic acid binding protein II	P	P	P
Centg3	centaurin, gamma 3	P	P	P
Cetn2	centrin 2	P	P	P
Cetn3	centrin 3	P	P	P
Cetn3	centrin 3	P	P	P
Cenpa	centromere autoantigen A	P	P	P
Cer1	cerberus 1 homolog (Xenopus laevis)	A	P	P
Cdr2	cerebellar degeneration-related 2	P	P	P
Cpd1-(p)	cerebellar postnatal development protein 1	P	P	P
Cln2	ceroid-lipofuscinosis, neuronal 2	P	P	P
Gkap42-(p)	cGMP-dependent protein kinase anchoring protein	P	P	P
Cct2	chaperonin subunit 2 (beta)	P	P	P
Cct3	chaperonin subunit 3 (gamma)	P	P	P
Cct3	chaperonin subunit 3 (gamma)	P	P	P
Cct4	chaperonin subunit 4 (delta)	P	P	P
Cct5	chaperonin subunit 5 (epsilon)	P	P	P
Cct5	chaperonin subunit 5 (epsilon)	P	P	P
Cct6a	chaperonin subunit 6a (zeta)	P	P	P
Cct7	chaperonin subunit 7 (eta)	P	P	P
Cct8	chaperonin subunit 8 (theta)	P	P	P
Criz1	charged amino acid rich leucine zipper 1	P	P	P
Chek1	checkpoint kinase 1 homolog (S. pombe)	P	P	P
Ccl27	chemokine (C-C motif) ligand 27	P	A	P
Cxcl12	chemokine (C-X-C motif) ligand 12	P	A	P
Chek2	CHK2 checkpoint homolog (S. pombe)	P	P	P
Clcn3	chloride channel 3	P	P	P

Clcn3	chloride channel 3	P	P	P
Clcn4-2	chloride channel 4-2	A	P	P
Clcn7	chloride channel 7	P	P	P
---	chloride channel regulator Icln (Icln) pseudogene	P	P	P
Clns1a	chloride channel, nucleotide-sensitive, 1A	P	P	P
Clc1	chloride intracellular channel 1	P	P	P
Clc4	chloride intracellular channel 4 (mitochondrial)	P	P	P
Clc4	chloride intracellular channel 4 (mitochondrial)	P	P	P
Clc4	chloride intracellular channel 4 (mitochondrial)	P	P	P
Cckbr	cholecystokinin B receptor	P	P	P
Cspg2	chondroitin sulfate proteoglycan 2	P	P	P
Cspg6	chondroitin sulfate proteoglycan 6	P	P	P
Chrac1	chromatin accessibility complex 1	P	P	P
Chaf1a	chromatin assembly factor 1, subunit A (p150)	P	A	P
Cbx2	chromobox homolog 2 (Drosophila Pc class)	P	M	P
Cbx3	chromobox homolog 3 (Drosophila HP1 gamma)	P	P	P
Cbx5	chromobox homolog 5 (Drosophila HP1a)	P	P	P
Cbx5	chromobox homolog 5 (Drosophila HP1a)	P	P	P
Chd1	chromodomain helicase DNA binding protein 1	P	P	P
Chd4	chromodomain helicase DNA binding protein 4	P	P	P
Cse1l	chromosome segregation 1-like (S. cerevisiae)	P	P	P
Clock	circadian locomotor output cycles kaput	P	P	P
Cs	citrate synthase	P	P	P
Cltc	clathrin, heavy polypeptide (Hc)	P	P	P
Clta	clathrin, light polypeptide (Lca)	P	P	P
Cltb	clathrin, light polypeptide (Lcb)	P	P	P
Cldn3	claudin 3	P	A	P
Cldn6	claudin 6	P	P	M
Cpsf2	cleavage and polyadenylation specific factor 2	P	P	P
Cpsf2	cleavage and polyadenylation specific factor 2	A	P	P
Cpsf4	cleavage and polyadenylation specific factor 4	P	P	P
Cpsf5	cleavage and polyadenylation specific factor 5	P	P	P
Cpsf3	cleavage and polyadenylation specificity factor 3	P	P	P
Cstf2t-(p)	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	P	P	P
Clptm1	cleft lip and palate associated transmembrane protein 1	P	P	P
Clu	clusterin	P	P	P
Carm1-(p)	coactivator-associated arginine methyltransferase 1	P	P	P
F2r	coagulation factor II (thrombin) receptor	P	P	P
F2r1	coagulation factor II (thrombin) receptor-like 1	A	P	P
F10	coagulation factor X	P	P	P
F13a	coagulation factor XIII, alpha subunit	P	P	P
Rnp24-(p)	coated vesicle membrane protein	P	P	P
Rnp24-(p)	coated vesicle membrane protein	P	P	P
Copa	coatamer protein complex subunit alpha	P	P	P
Copb1	coatamer protein complex, subunit beta 1	P	P	P
Copb2	coatamer protein complex, subunit beta 2 (beta prime)	P	P	P
Copb2	coatamer protein complex, subunit beta 2 (beta prime)	P	P	P
Cope	coatamer protein complex, subunit epsilon	P	P	P
Copg1	coatamer protein complex, subunit gamma 1	P	P	P
Copg1	coatamer protein complex, subunit gamma 1	P	P	P
Copz1	coatamer protein complex, subunit zeta 1	P	P	P
Copz2	coatamer protein complex, subunit zeta 2	P	P	A
Crsp3	cofactor required for Sp1 transcriptional activation, subunit 3	P	P	P
Cfl1	cofilin 1, non-muscle	P	P	P
Cfl2	cofilin 2, muscle	P	P	P
Coil	coilin	A	P	P
Cirbp	cold inducible RNA binding protein	P	P	P
Csda	cold shock domain protein A	P	P	P
Crmp1	collapsin response mediator protein 1	P	A	P
Csf1r	colony stimulating factor 1 receptor	A	P	P
C1qr1	complement component 1, q subcomponent, receptor 1	P	P	A
Crry	complement receptor related protein	P	P	P

Crry	complement receptor related protein	A	P	P
Cplx2	complexin 2	A	P	P
Cog8	component of oligomeric golgi complex 8	P	P	P
Cog8	component of oligomeric golgi complex 8	P	M	P
Ctgf	connective tissue growth factor	P	A	P
Chuk	conserved helix-loop-helix ubiquitous kinase	P	P	P
Cop1-(p)	constitutive photomorphogenic protein 1 (Arabidopsis)	P	P	P
Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (A. thaliana)	P	P	P
Cops2	COP9 (constitutive photomorphogenic) homolog, subunit 2 (A. thaliana)	A	P	P
Cops3	COP9 (constitutive photomorphogenic) homolog, subunit 3 (A. thaliana)	P	P	P
Cops4	COP9 (constitutive photomorphogenic) homolog, subunit 4 (A. thaliana)	P	P	P
Cops5	COP9 (constitutive photomorphogenic) homolog, subunit 5 (A. thaliana)	P	P	P
Cops6	COP9 (constitutive photomorphogenic) homolog, subunit 6 (A. thaliana)	P	P	P
Cops7a	COP9 (constitutive photomorphogenic) homolog, subunit 7a (A. thaliana)	P	P	P
Cops7b	COP9 (constitutive photomorphogenic) homolog, subunit 7b (A. thaliana)	P	P	P
Cpo	coproporphyrinogen oxidase	P	P	P
Cbfb	core binding factor beta	P	P	P
Cbfb	core binding factor beta	P	P	P
Copeb	core promoter element binding protein	P	P	P
Cbfa2t3h	core-binding factor, runt domain, alpha2; translocated to, 3 homolog E676	P	P	P
Cnih	cornichon homolog (Drosophila)	P	P	P
Coro1b	coronin, actin binding protein 1B	P	P	P
Coro1c	coronin, actin binding protein 1C	P	P	P
Cttn	cortactin	P	P	P
Cgbp-(p)	CpG binding protein	P	P	P
Cfdp	craniofacial development protein 1	P	P	P
Ckb	creatine kinase, brain	P	P	P
Cri1	CREBBP/EP300 inhibitory protein 1	P	P	P
Crnk1	Crm, crooked neck-like 1 (Drosophila)	P	P	P
Cry1	cryptochrome 1 (photolyase-like)	P	P	P
Cryab	crystallin, alpha B	A	P	P
Crygs	crystallin, gamma S	P	P	P
Cryl1	crystallin, lamda 1	P	M	P
Csk	c-src tyrosine kinase	P	A	P
Ctbp1	C-terminal binding protein 1	P	P	P
Ctbp2	C-terminal binding protein 2	P	P	P
Ctbp2	C-terminal binding protein 2	P	P	P
Cubn	cubilin (intrinsic factor-cobalamin receptor)	P	P	P
Cul1	cullin 1	P	P	P
Cul2	cullin 2	P	P	P
Cul3	cullin 3	P	P	P
Cul4a	cullin 4A	P	P	P
Arpp19-(p)	cyclic AMP phosphoprotein	P	P	P
Arpp19-(p)	cyclic AMP phosphoprotein	P	A	P
Ccna2	cyclin A2	P	P	P
Ccnb1	cyclin B1	P	P	P
Ccnb2	cyclin B2	P	P	P
Ccnd1	cyclin D1	P	P	P
Ccnd2	cyclin D2	P	P	P
Ccnd3	cyclin D3	P	P	P
Ccne2	cyclin E2	P	P	P
Ccne2	cyclin E2	A	P	P
Ccnf	cyclin F	P	P	P
Ccng1	cyclin G1	P	P	P
Ccng2	cyclin G2	P	P	P
Ccni	cyclin I	P	P	P
Ccni	cyclin I	P	P	P
Ccnt1	cyclin T1	A	P	P
Cdk4	cyclin-dependent kinase 4	P	P	P
Cdk4	cyclin-dependent kinase 4	P	P	P
Cdk7	cyclin-dependent kinase 7 (homolog of Xenopus MO15 cdk-activating kinase)	P	P	P
Cdk9	cyclin-dependent kinase 9 (CDC2-related kinase)	P	P	P

Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	P	P	P
Cstb	cystatin B	P	P	P
Cst3	cystatin C	P	P	P
Cst3	cystatin C	P	P	P
Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	P	P	P
Chordc1	cysteine and histidine-rich domain (CHORD)-containing, zinc-binding protein 1	P	P	P
Csrp1	cysteine rich protein 1	P	P	P
Csrp1	cysteine rich protein 1	P	A	P
Crip2	cysteine rich protein 2	P	P	P
Cyr61	cysteine rich protein 61	P	A	P
Csad	cysteine sulfinic acid decarboxylase	P	P	A
Csrp2	cysteine-rich protein 2	P	P	P
Cars	cysteinyl-tRNA synthetase	P	P	P
Cftr	cystic fibrosis transmembrane conductance regulator homolog	P	A	P
Ctps	cytidine 5'-triphosphate synthase	P	P	P
Ctps2	cytidine 5'-triphosphate synthase 2	P	P	P
Cmas	cytidine monophospho-N-acetylneuraminic acid synthetase	P	P	P
Cyba	cytochrome b-245, alpha polypeptide	P	P	P
Cyba	cytochrome b-245, alpha polypeptide	P	P	P
Cyb5	cytochrome b-5	P	P	P
Cox7a2l	cytochrome c oxidase subunit VIIa polypeptide 2-like	P	P	P
Cox7b	cytochrome c oxidase subunit VIIb	P	P	P
Cox4a	cytochrome c oxidase, subunit IVa	P	P	P
Cox5b	cytochrome c oxidase, subunit Vb	P	P	P
Cox6a1	cytochrome c oxidase, subunit VI a, polypeptide 1	P	P	P
Cox6c	cytochrome c oxidase, subunit VIc	P	P	P
Cox7a2	cytochrome c oxidase, subunit VIIa 2	P	P	P
Cox7c	cytochrome c oxidase, subunit VIIc	P	P	P
Cox7c	cytochrome c oxidase, subunit VIIc	P	P	P
Cycs	cytochrome c, somatic	P	P	P
Cyc1	cytochrome c-1	P	P	P
Cyp26a1	cytochrome P450, 26, retinoic acid A1	P	P	P
Crlf3	cytokine receptor-like factor 3	P	P	P
Ckap2	cytoskeleton associated protein 2	P	P	P
Cte1	cytosolic acyl-CoA thioesterase 1	P	P	P
Tia1	cytotoxic granule-associated RNA binding protein 1	P	P	P
Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta	P	P	A
Ddb1	damage specific DNA binding protein 1	P	P	P
Ddb1	damage specific DNA binding protein 1	P	P	P
Dazap1	DAZ associated protein 1	P	P	P
Dazap2	DAZ associated protein 2	P	P	P
Ddt	D-dopachrome tautomerase	P	P	P
Dx+D766d6	D-E-A-D (aspartate-glutamate-alanine-aspartate) box polypeptide 6	P	P	P
Dri1	dead ringer homolog 1 (Drosophila)	P	P	P
Dri2	dead ringer homolog 2 (Drosophila)	P	P	P
Ddx1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	P	P	P
Ddx1	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 1	P	P	P
Ddx24	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 13 (RNA helicase A)	P	P	P
Ddx15	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 15 (RNA helicase A)	P	P	P
Ddx16	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 16	P	P	P
Ddx19	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19	P	P	P
Ddx21	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (RNA helicase II/Gu)	P	P	P
Ddx3	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3	P	P	P
Ddx5	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 5	P	P	P
Ddx50	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 50	P	P	P
Ddx6	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6	P	P	P
Ddx9	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9	P	P	P
Dap3	death associated protein 3	P	P	P
Dad1	defender against cell death 1	P	P	P
Dad1	defender against cell death 1	P	P	P
Degs	degenerative spermatocyte homolog (Drosophila)	P	P	P
Dhrsx	dehydrogenase/reductase (SDR family) X chromosome	P	P	P

Dp1	deleted in polyposis 1	P	P	P
Dp1	deleted in polyposis 1	P	P	P
Dp111	deleted in polyposis 1-like 1	A	P	P
Dlk1	delta-like 1 homolog (Drosophila)	P	P	P
Coq7	demethyl-Q 7	P	P	P
Dck	deoxycytidine kinase	P	P	P
Dck	deoxycytidine kinase	P	P	P
Dguok	deoxyguanosine kinase	P	P	P
Dguok	deoxyguanosine kinase	P	P	P
Dtymk	deoxythymidylate kinase	P	P	P
Dtymk	deoxythymidylate kinase	P	P	P
Dsc2	desmocollin 2	P	P	P
Dsg2	desmoglein 2	P	P	P
Dstn	destrin	P	P	P
Ddef1	development and differentiation enhancing	P	A	P
Ddef1	development and differentiation enhancing	P	A	P
Drg1	developmentally regulated GTP binding protein 1	P	P	P
Dgat1	diacylglycerol O-acyltransferase 1	P	P	P
Diap3	diaphanous homolog 3 (Drosophila)	P	P	M
Dia1	diaphorase 1 (NADH)	P	M	P
Dbi	diazepam binding inhibitor	P	P	P
Deb1	differentially expressed in B16F10 1	P	P	P
Def8	differentially expressed in FDCP 8	P	P	P
Dgcr2	DiGeorge syndrome critical region gene 2	P	P	P
Dgcr2	DiGeorge syndrome critical region gene 2	P	P	P
Dgcr6	DiGeorge syndrome critical region gene 6	A	P	P
Dbt	dihydrolipoamide branched chain transacylase E2	P	P	P
Dld	dihydrolipoamide dehydrogenase	P	P	P
Dlat	dihydrolipoamide S-acetyltransferase E741	P	P	P
Dhodh	dihydroorotate dehydrogenase	P	P	P
Dpysl2	dihydropyrimidinase-like 2	P	P	P
Ddah2	dimethylarginine dimethylaminohydrolase 2	P	P	P
Dpp7	dipeptidylpeptidase 7	P	P	P
Dtr	diphtheria toxin receptor	P	P	P
Dab2	disabled homolog 2 (Drosophila)	P	P	P
Dab2	disabled homolog 2 (Drosophila)	P	P	P
Ddr1	discoidin domain receptor family, member 1	P	A	P
Dlgh1	discs, large homolog 1 (Drosophila)	P	P	P
Dvl1	dishevelled, dsh homolog 1 (Drosophila)	P	P	P
Dclre1a	DNA cross-link repair 1A, PSO2 homolog (S. cerevisiae)	P	A	P
Dffa	DNA fragmentation factor, alpha subunit	P	P	P
Dffa	DNA fragmentation factor, alpha subunit	P	P	P
Dnmt1	DNA methyltransferase (cytosine-5) 1	P	P	P
Dmtap1	DNA methyltransferase 1-associated protein 1	P	P	P
Dnmt2	DNA methyltransferase 2	P	P	P
Dnmt3a	DNA methyltransferase 3A	P	P	P
Prim1	DNA primase, p49 subunit	P	P	P
Prim2	DNA primase, p58 subunit	P	P	P
Dnaja1	DnaJ (Hsp40) homolog, subfamily A, member 1	P	P	P
Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	P	P	P
Dnaja3	DnaJ (Hsp40) homolog, subfamily A, member 3	P	P	P
Dnaja1	DnaJ (Hsp40) homolog, subfamily B, member 1	P	P	P
Dnaja11	DnaJ (Hsp40) homolog, subfamily B, member 11	P	P	P
Dnaja3	DnaJ (Hsp40) homolog, subfamily B, member 3	P	P	P
Dnaja6	DnaJ (Hsp40) homolog, subfamily B, member 6	P	P	P
Dnaja6	DnaJ (Hsp40) homolog, subfamily B, member 6	P	P	P
Dnaja9	DnaJ (Hsp40) homolog, subfamily B, member 9	A	P	P
Dnaja1	DnaJ (Hsp40) homolog, subfamily C, member 1	P	P	P
Dnaja2	DnaJ (Hsp40) homolog, subfamily C, member 2	P	P	P
Dnaja3	DnaJ (Hsp40) homolog, subfamily C, member 3	P	P	P
Dnaja3	DnaJ (Hsp40) homolog, subfamily C, member 3	P	P	A
Dnaja3	DnaJ (Hsp40) homolog, subfamily C, member 3	P	P	A

Dnajc5	DnaJ (Hsp40) homolog, subfamily C, member 5	P	M	P
Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	P	P	P
Dpm1	dolichol-phosphate (beta-D) mannosyltransferase 1	P	P	P
Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	P	P	P
Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	P	P	P
Ddost	dolichyl-di-phosphooligosaccharide-protein glycotransferase	P	P	P
Dpagt1	dolichyl-phosphate acetylglucosaminophosphotransferase 1 E781	P	P	P
Dom3z	DOM-3 homolog Z (C. elegans)	A	P	P
Ddc	dopa decarboxylase	P	P	P
Doc2a	double C2, alpha	P	P	P
Dscr3	Down syndrome critical region gene 3	P	P	P
Dscr3	Down syndrome critical region gene 3	P	P	P
Dscr1	Down syndrome critical region homolog 1 (human)	P	P	P
Dscr2	Down syndrome critical region homolog 2 (human)	P	P	P
Dr1	down-regulator of transcription 1	P	P	P
Donson	downstream neighbor of SON	P	P	P
Drap1	Dr1 associated protein 1 (negative cofactor 2 alpha)	P	P	P
Dbn1	drebrin 1	P	A	P
Dbnl	drebrin-like	P	P	P
Dusp1	dual specificity phosphatase 1	P	P	P
Dusp12	dual specificity phosphatase 12	P	P	P
Dusp19	dual specificity phosphatase 19	P	P	P
Dusp2	dual specificity phosphatase 2	P	P	P
Dusp6	dual specificity phosphatase 6	P	P	P
Dusp9	dual specificity phosphatase 9	P	P	P
Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	P	P	P
Dyrk1a	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	P	P	P
Dctn3	dynactin 3	P	P	P
Dctn5	dynactin 5	P	P	P
Dctn6	dynactin 6	P	P	P
Dnm1l	dynamitin 1-like	P	P	P
Dnalc4	dynein, axonemal, light chain 4	P	A	P
Dnchc1	dynein, cytoplasmic, heavy chain 1	P	P	P
Dncic1	dynein, cytoplasmic, intermediate chain 1	M	P	P
Dncic2	dynein, cytoplasmic, intermediate chain 2	P	P	P
Dnclc1	dynein, cytoplasmic, light chain 1	P	P	P
Dncl2a	dynein, cytoplasmic, light chain 2A	P	P	P
Dncl2a	dynein, cytoplasmic, light chain 2A	P	P	P
Dag1	dystroglycan 1	P	P	P
Dag1	dystroglycan 1	P	A	P
Ets2	E26 avian leukemia oncogene 2, 3' domain	P	P	P
Ets2	E26 avian leukemia oncogene 2, 3' domain	P	P	P
E2f5	E2F transcription factor 5	P	P	P
E4f1	E4F transcription factor 1	P	A	P
Edr1	early development regulator 1 (homolog of polyhomeotic 1)	P	P	P
Ebna1bp2	EBNA1 binding protein 2	P	P	P
Evi5	ecotropic viral integration site 5	P	P	P
Ect2	ect2 oncogene	P	P	P
Epcs3	Epcs3 gene	P	P	P
Egln2	EGL nine homolog 2 (C. elegans)	P	P	P
Elac2	elaC homolog 2 (E. coli)	P	P	P
Elac2	elaC homolog 2 (E. coli)	P	A	P
Elavl1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	P	P	P
Etfa	electron transferring flavoprotein, alpha polypeptide	P	P	P
Eil	eleven-nineteen lysine-rich leukemia gene	P	P	P
Elk1	ELK1, member of ETS oncogene family	P	P	M
Eil2	ELL-related RNA polymerase II, elongation factor	M	P	P
Eil2	ELL-related RNA polymerase II, elongation factor	A	P	P
Elp3	elongation protein 3 homolog (S. cerevisiae)	P	P	P
Emb	embigin	P	P	P
Efs	embryonal Fyn-associated substrate	P	P	P
Eed	embryonic ectoderm development	P	P	P

---	embryonic H3 histone	P	P	P
Emd	emerin	P	P	P
Emu2-(p)	Emu2 gene	P	P	P
Enah	enabled homolog (Drosophila)	P	P	P
Evl	Ena-vasodilator stimulated phosphoprotein	P	P	P
Evl	Ena-vasodilator stimulated phosphoprotein	P	M	P
Eng	endoglin	P	P	P
Emcn-(p)	endomucin	P	M	P
Endog	endonuclease G	P	A	P
Ermelin-(p)	endoplasmic reticulum membrane protein	P	P	P
Erp29	endoplasmic reticulum protein 29	P	P	P
Edg3	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	P	P	P
Edf1	endothelial differentiation-related factor 1	P	P	P
Eppb9	endothelial precursor protein B9	P	P	P
Eg1-(p)	endothelial-derived gene	P	P	P
Tek	endothelial-specific receptor tyrosine kinase	P	P	P
Epc1	enhancer of polycomb homolog 1, (Drosophila)	P	P	P
Erh	enhancer of rudimentary homolog (Drosophila)	P	P	P
Ezh1	enhancer of zeste homolog 1 (Drosophila)	P	P	P
Ezh2	enhancer of zeste homolog 2 (Drosophila)	P	P	P
Etl1	enhancer trap locus 1	P	P	P
Etl1	enhancer trap locus 1	P	P	P
Eno1	enolase 1, alpha non-neuron	P	P	P
Eno3	enolase 3, beta muscle	P	P	P
Ech1	enoyl coenzyme A hydratase 1, peroxisomal	P	P	P
Echs1	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	P	A	P
Epha8	Eph receptor A8	P	P	P
Ephb4	Eph receptor B4	P	P	P
Efna3	ephrin A3	P	P	P
Efnb1	ephrin B1	P	P	A
Efnb2	ephrin B2	P	P	P
Efnb3	ephrin B3	P	P	P
Efnb3	ephrin B3	P	P	P
Eps8	epidermal growth factor receptor pathway substrate 8	A	P	P
Emp1	epithelial membrane protein 1	P	P	A
Emp3	epithelial membrane protein 3	P	P	P
Epn1	epsin 1	P	P	P
Eral1	Era (G-protein)-like 1 (E. coli)	P	P	P
Ero1l	ERO1-like (S. cerevisiae)	P	P	P
Epb4.1	erythrocyte protein band 4.1	P	P	P
Epb7.2	erythrocyte protein band 7.2	A	P	P
edr	erythroid differentiation regulator	P	P	P
Epor	erythropoietin receptor	A	P	P
Erf	Est2 repressor factor	P	A	P
Es10	esterase 10	P	P	P
Esrra	estrogen related receptor, alpha	P	P	P
Etold2	ethanol decreased 2	P	P	P
EIG180	ethanol induced gene product EIG180	P	P	P
Ei24	etoposide induced 2.4 mRNA	P	P	P
Etsrp71	ets related protein 71	P	P	P
Etv1	ets variant gene 1	P	A	P
Etv4	ets variant gene 4 (E1A enhancer binding protein, E1AF)	A	P	P
Eef1a1	eukaryotic translation elongation factor 1 alpha 1	P	P	P
Eef1b2	eukaryotic translation elongation factor 1 beta 2	P	P	P
Eef1d	eukaryotic translation elongation factor 1 delta E1159	P	P	P
Eef2	eukaryotic translation elongation factor 2	P	P	P
Eif1a	eukaryotic translation initiation factor 1A	P	P	P
Eif1a	eukaryotic translation initiation factor 1A	P	P	P
Eif2ak3	eukaryotic translation initiation factor 2 alpha kinase 3	P	P	P
Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	P	P	P
Eif2s2	eukaryotic translation initiation factor 2, subunit 2 (beta)	A	P	P
Eif2a	eukaryotic translation initiation factor 2A	P	P	P

Eif2b	eukaryotic translation initiation factor 2B	P	P	P
Eif2b1	eukaryotic translation initiation factor 2B, subunit 1 (alpha, 26kDa)	P	P	P
Eif2c2	eukaryotic translation initiation factor 2C, 2	P	P	P
Eif3	eukaryotic translation initiation factor 3	P	P	P
Eif3s4	eukaryotic translation initiation factor 3, subunit 4 (delta)	P	P	P
Eif3s6	eukaryotic translation initiation factor 3, subunit 6	P	P	P
Eif3s6ip	eukaryotic translation initiation factor 3, subunit 6 interacting protein	P	P	P
Eif3s7	eukaryotic translation initiation factor 3, subunit 7 (zeta)	P	P	P
Eif3s8	eukaryotic translation initiation factor 3, subunit 8	P	P	P
Eif4g2	eukaryotic translation initiation factor 4, gamma 2	P	P	P
Eif4a1	eukaryotic translation initiation factor 4A1	P	P	P
Eif4a2	eukaryotic translation initiation factor 4A2	P	P	P
Eif4a2	eukaryotic translation initiation factor 4A2	P	A	P
Eif4ebp1	eukaryotic translation initiation factor 4E binding protein 1	P	P	P
Ewsh	Ewing sarcoma homolog	P	P	P
Ercc2	excision repair cross-complementing rodent repair deficiency, complementation group 2	P	P	P
Ercc2	excision repair cross-complementing rodent repair deficiency, complementation group 2	P	P	A
Ercc3	excision repair cross-complementing rodent repair deficiency, complementation group 3	P	P	P
Ercc5	excision repair cross-complementing rodent repair deficiency, complementation group 5	M	P	P
Exo70	exocyst component protein homolog (S. cerevisiae)	P	P	P
Exo1	exonuclease 1	P	P	P
Ext1	exostoses (multiple) 1	P	P	P
Ext2	exostoses (multiple) 2	P	P	P
Xpo1	exportin 1, CRM1 homolog (yeast)	P	P	P
Nme1	expressed in non-metastatic cells 1, protein (NM23A) (nucleoside diphosphate kinase)	P	P	P
Nme2	expressed in non-metastatic cells 2, protein (NM23B) (nucleoside diphosphate kinase)	P	P	P
Nme3	expressed in non-metastatic cells 3	P	P	P
Nme3	expressed in non-metastatic cells 3	P	P	P
Nme4	expressed in non-metastatic cells 4, protein (NM23-M4)(nucleoside diphosphate kinase)	P	P	P
Nme6	expressed in non-metastatic cells 6, protein (nucleoside diphosphate kinase)	P	P	P
F11r	F11 receptor	P	P	P
Atp5k-ps1	F1F0 ATP synthase E subunit pseudogene	P	P	P
Fdft1	farnesyl diphosphate farnesyl transferase 1	P	P	P
Fdps	farnesyl diphosphate synthetase	P	P	P
Fdps	farnesyl diphosphate synthetase	P	P	P
Fnta	farnesyltransferase, CAAX box, alpha	P	P	P
Daxx	Fas death domain-associated protein	P	P	P
Fastk	Fas-activated serine/threonine kinase	P	P	P
Faf1	Fas-associated factor 1	P	P	P
Faf1	Fas-associated factor 1	P	P	P
Fscn1	fascin homolog 1, actin bundling protein (Strongylocentrotus purpuratus)	P	P	P
Fto	fatso	P	P	P
Fabp3	fatty acid binding protein 3, muscle and heart	P	A	P
Fabp5	fatty acid binding protein 5, epidermal	P	P	P
Facl2	fatty acid Coenzyme A ligase, long chain 2	A	P	P
Facl5	fatty acid Coenzyme A ligase, long chain 5	P	P	P
Fasn	fatty acid synthase	P	P	P
Fos	FBJ osteosarcoma oncogene	P	P	P
Fosb	FBJ osteosarcoma oncogene B	A	P	P
Fbxw1b	F-box and WD-40 domain protein 1B	P	P	P
Fbxw2	F-box and WD-40 domain protein 2	P	P	P
Fbxw4	F-box and WD-40 domain protein 4	P	P	P
Fbxw5	F-box and WD-40 domain protein 5	P	P	P
Fbxo3	F-box only protein 3	P	P	P
Fbxo3	F-box only protein 3	P	P	P
Fbxo6b	F-box only protein 6b	M	P	P
Fbxo8	F-box only protein 8	P	A	P
Fcgr1	Fc receptor, IgG, high affinity I	P	A	P
Fem1a	feminization 1 homolog a (C. elegans)	P	P	P
Fdx1	ferredoxin 1	P	P	P
Fth	ferritin heavy chain	P	P	P
Ftl1	ferritin light chain 1	P	P	P

Ftl1	ferritin light chain 1	P	P	P
Fech	ferrochelatase	P	A	P
Fbl	fibrillarin	P	P	P
Fbn1	fibrillin 1	P	A	P
Fbn2	fibrillin 2	P	P	P
Fibp	fibroblast growth factor (acidic) intracellular binding protein	P	P	P
Fgf3	fibroblast growth factor 3	A	P	P
Fin14	fibroblast growth factor inducible 14	A	P	P
Fin15	fibroblast growth factor inducible 15	A	P	P
Fin16	fibroblast growth factor inducible 16	P	P	P
Fgfr1	fibroblast growth factor receptor 1	A	P	P
Fgfr2	fibroblast growth factor receptor 2	P	P	P
Fgfr2	fibroblast growth factor receptor 2	P	M	P
Fn1	fibronectin 1	P	P	P
Fbln1	fibulin 1	P	P	P
Fbln1	fibulin 1	P	P	P
Figl1	figlet-like 1	P	P	P
Fkbp10	FK506 binding protein 10	A	P	P
Frap1	FK506 binding protein 12-rapamycin associated protein 1	P	P	P
Frap1	FK506 binding protein 12-rapamycin associated protein 1	P	P	P
Fkbp1a	FK506 binding protein 1a	P	P	P
Fkbp2	FK506 binding protein 2	P	P	P
Fkbp3	FK506 binding protein 3	P	P	P
Fkbp4	FK506 binding protein 4	P	P	P
Fkbp4	FK506 binding protein 4	P	P	P
Fkbp5	FK506 binding protein 5	P	P	P
Fkbp7	FK506 binding protein 7	P	P	P
Fkbp9	FK506 binding protein 9	P	P	P
Fen1	flap structure specific endonuclease 1	P	P	P
Fmo1	flavin containing monooxygenase 1	P	P	A
Fliih	flightless I homolog (Drosophila)	P	P	P
Fliih	flightless I homolog (Drosophila)	P	P	P
Fliih	flightless I homolog (Drosophila)	P	P	P
Fln29-(p)	FLN29 gene product	P	P	P
Flot1	flotillin 1	P	P	A
Flt1	FMS-like tyrosine kinase 1	P	P	P
Flt3	FMS-like tyrosine kinase 3	P	P	A
Fst	follicle-stimulating hormone	A	P	P
Fstl	follicle-stimulating hormone-like	P	A	P
Fpgs	folylpolyglutamate synthetase	P	P	P
Foxa1	forkhead box A1	A	P	P
Foxc2	forkhead box C2	P	P	P
Foxc2	forkhead box C2	A	P	P
Fnbp4	formin binding protein 4	P	P	P
Fhl1	four and a half LIM domains 1	P	P	P
Fhl1	four and a half LIM domains 1	P	P	P
Fhl2	four and a half LIM domains 2	P	P	P
Fxc1	fractured callus expressed transcript 1	P	P	P
Fxr1h	fragile X mental retardation gene 1, autosomal homolog	P	P	P
Fmr1	fragile X mental retardation syndrome 1 homolog	P	P	P
Frda	Friedreich ataxia	P	P	P
Fzd2	frizzled homolog 2 (Drosophila)	P	P	P
Fzd3	frizzled homolog 3 (Drosophila)	P	P	P
Fzd4	frizzled homolog 4 (Drosophila)	P	P	M
Frg1	FSDH region gene 1	P	P	P
Fut8	fucosyltransferase 8	P	P	P
Fh1	fumarate hydratase 1	P	P	P
Furin	furin (paired basic amino acid cleaving enzyme)	P	P	P
Fts	fused toes	P	P	P
Fts	fused toes	P	P	P
Fxyd6	FXD domain-containing ion transport regulator 6	P	P	P
Fyn	Fyn proto-oncogene	P	P	P

Gfm	G elongation factor	P	P	P
Gbl-(p)	G protein beta subunit-like	P	A	P
Gng3lg	G protein gamma 3 linked gene	M	P	P
Gps1	G protein pathway suppressor 1	P	P	P
Gprk6	G protein-coupled receptor kinase 6	P	M	P
Gtse1	G two S phase expressed protein 1	P	A	P
Gspt1	G1 to phase transition 1	P	P	P
G7e-(p)	G7e protein	P	P	P
Gabpa	GA repeat binding protein, alpha	P	P	P
Gabpb1	GA repeat binding protein, beta 1	P	P	P
Gabarapl2	GABA(A) receptor-associated protein like 2	P	P	P
Galk1	galactokinase 1	P	P	P
Gal	galanin	P	P	P
GalR3	galanin receptor type 3	P	P	A
Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	P	P	P
Gabt3	gamma-aminobutyric acid (GABA-A) transporter 3	P	A	P
Gabarap	gamma-aminobutyric acid receptor associated protein	P	P	P
Gdap10	ganglioside-induced differentiation-associated-protein 10	P	P	P
Gdap3	ganglioside-induced differentiation-associated-protein 3	P	P	P
Gja1	gap junction membrane channel protein alpha 1	P	P	P
Gja1	gap junction membrane channel protein alpha 1	P	P	P
Gjb2	gap junction membrane channel protein beta 2	P	P	P
Gjb3	gap junction membrane channel protein beta 3	M	P	P
Gbx2	gastrulation brain homeobox 2	A	P	P
Gata1	GATA binding protein 1	A	P	P
Gata1	GATA binding protein 1	A	P	P
Gata3	GATA binding protein 3	P	P	P
Gata6	GATA binding protein 6	P	A	P
Gmnn	geminin	P	P	P
Grcc10	gene rich cluster, C10 gene	P	P	P
Grcc2f	gene rich cluster, C2f gene	P	P	P
Grcc3f	gene rich cluster, C3f gene	P	P	P
Grcc8	gene rich cluster, C8 gene	P	P	P
Gtl3	gene trap locus 3	P	P	P
Gtl6	gene trap locus 6	P	M	P
Gtpat12	gene trap PAT 12	P	P	P
Gtrosa26asSor	gene trap ROSA 26 antisense, Philippe Soriano	P	P	P
Gcn5l1	general control of amino acid synthesis-like 1 (yeast)	P	P	P
Gtf2e2	general transcription factor II E, polypeptide 2 (beta subunit)	P	P	P
Gtf2h1	general transcription factor II H, polypeptide 1	P	P	P
Gtf2h4	general transcription factor II H, polypeptide 4	P	P	P
Gtf2l	general transcription factor II I	P	P	P
Gtf3a	general transcription factor III A	P	P	P
Grim19-(p)	genes associated with retinoid-IFN-induced mortality 19	P	P	P
Gsg2	germ cell-specific gene 2	A	P	P
---	germinal center kinase-like kinase-like	P	P	P
Gbas	glioblastoma amplified sequence	P	P	P
Gltscr2	glioma tumor suppressor candidate region gene 2	P	P	P
Gbif-(p)	globin inducing factor, fetal	M	P	P
Gnpi	glucosamine-6-phosphate deaminase	A	P	P
Gnpnat1	glucosamine-phosphate N-acetyltransferase 1	P	P	P
Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	P	P	P
Gpi1	glucose phosphate isomerase 1	P	P	P
Gpi1	glucose phosphate isomerase 1	P	P	P
Grp58	glucose regulated protein	P	P	P
G6pdx	glucose-6-phosphate dehydrogenase X-linked	P	P	P
Gcs1	glucosidase 1	P	P	P
Gaa	glucosidase, alpha, acid	P	P	P
Glud	glutamate dehydrogenase	P	P	P
Grin1a	glutamate receptor, ionotropic, N-methyl D-aspartate-like 1A	P	P	P
Glul	glutamate-ammonia ligase (glutamine synthase)	P	P	P

Glul	glutamate-ammonia ligase (glutamine synthase)	A	P	P
Gclm	glutamate-cysteine ligase , modifier subunit	P	P	P
Gclc	glutamate-cysteine ligase, catalytic subunit	P	A	P
Enpep	glutamyl aminopeptidase	P	A	P
Eprs	glutamyl-prolyl-tRNA synthetase	P	P	P
Glrx1	glutaredoxin 1 (thioltransferase)	P	P	P
Gcdh	glutaryl-Coenzyme A dehydrogenase	P	P	P
Gpx1	glutathione peroxidase 1	P	P	P
Gpx2	glutathione peroxidase 2	P	A	P
Gpx3	glutathione peroxidase 3	P	P	P
Gpx4	glutathione peroxidase 4	P	P	P
Gsr	glutathione reductase 1	P	P	P
Gsto1	glutathione S-transferase omega 1	P	P	P
Gsta4	glutathione S-transferase, alpha 4	P	P	P
Gstm1	glutathione S-transferase, mu 1	P	P	P
Gstm1	glutathione S-transferase, mu 1	P	P	P
Gstm2	glutathione S-transferase, mu 2	P	P	A
Gstm5	glutathione S-transferase, mu 5	P	P	P
Gstm5	glutathione S-transferase, mu 5	P	P	P
Gstp2	glutathione S-transferase, pi 2	P	P	P
Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	P	P	P
Gapd	glyceraldehyde-3-phosphate dehydrogenase	P	P	P
Gapd	glyceraldehyde-3-phosphate dehydrogenase	P	P	P
Gpd2	glycerol phosphate dehydrogenase 1, mitochondrial	P	P	P
Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	P	P	P
Gnpat	glyceronephosphate O-acyltransferase	P	P	P
Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	P	P	P
Gys3	glycogen synthase 3, brain	P	P	P
Gyg1	glycogenin 1	P	P	P
Gyg1	glycogenin 1	P	P	P
GltP-(p)	glycolipid transfer protein	P	P	P
GltP-(p)	glycolipid transfer protein	A	P	P
Gypa	glycophorin A	P	P	P
Gp38	glycoprotein 38	P	P	P
Ggta1	glycoprotein galactosyltransferase alpha 1, 3	P	P	P
Grhpr	glyoxylate reductase/hydroxypyruvate reductase	P	P	P
Gpc1	glypican 1	P	M	P
Gpc3	glypican 3	P	P	P
Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	P	P	P
Gga2	golgi associated, gamma adaptin ear containing, ARF binding protein 2	P	P	P
Golga3	golgi autoantigen, golgin subfamily a, 3	P	A	P
Golga4	golgi autoantigen, golgin subfamily a, 4	P	P	P
Golga5	golgi autoantigen, golgin subfamily a, 5	P	P	P
Golph3	golgi phosphoprotein 3	P	P	P
Gorasp2	golgi reassembly stacking protein 2	P	P	P
Gosr2	golgi SNAP receptor complex member 2	P	P	P
Gosr2	golgi SNAP receptor complex member 2	P	P	P
Gpaa1	GPI anchor attachment protein 1	P	A	P
Gpaa1	GPI anchor attachment protein 1	P	A	P
Gpiap1	GPI-anchored membrane protein 1	P	P	P
Gpiap1	GPI-anchored membrane protein 1	P	A	P
Gpr50	G-protein-coupled receptor 50	P	P	P
Grn	granulin	P	P	P
Gadd45a	growth arrest and DNA-damage-inducible 45 alpha	P	A	P
Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	P	P	P
Gas1	growth arrest specific 1	P	P	P
Gas2	growth arrest specific 2	P	P	P
Gas5	growth arrest specific 5	P	P	P
Gas8	growth arrest specific 8	P	P	P
Gap43	growth associated protein 43	P	P	P
Gfi1b	growth factor independent 1B	A	P	P
Grb10	growth factor receptor bound protein 10	P	P	A

Gab1	growth factor receptor bound protein 2-associated protein 1	P	P	P
Grb7	growth factor receptor bound protein 7	M	P	P
Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	P	P	P
Gh	growth hormone	P	P	P
Ghitm	growth hormone inducible transmembrane protein	P	P	P
Ghitm	growth hormone inducible transmembrane protein	P	P	P
Grpel1	GrpE-like 1, mitochondrial	P	P	P
Grpel2	GrpE-like 2, mitochondrial	P	M	P
Gtpbp1	GTP binding protein 1	P	P	P
Gtpbp1	GTP binding protein 1	P	A	P
Gtpbp4-(p)	GTP binding protein 4	P	P	P
Gamt	guanidinoacetate methyltransferase	P	P	P
Gng10	guanine nucleotide binding protein (G protein), gamma 10	P	P	P
Gng5	guanine nucleotide binding protein (G protein), gamma 5 subunit	P	P	P
Gna11	guanine nucleotide binding protein, alpha 11	P	P	P
Gna12	guanine nucleotide binding protein, alpha 12	P	P	P
Gna13	guanine nucleotide binding protein, alpha 13	P	P	P
Gnai1	guanine nucleotide binding protein, alpha inhibiting 1	A	P	P
Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	P	P	P
Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	P	P	P
Gnai2	guanine nucleotide binding protein, alpha inhibiting 2	P	P	P
Gnai3	guanine nucleotide binding protein, alpha inhibiting 3	P	P	P
Gnao	guanine nucleotide binding protein, alpha o	P	P	P
Gnb1	guanine nucleotide binding protein, beta 1	P	P	P
Gnb1	guanine nucleotide binding protein, beta 1	P	P	P
Gnb1	guanine nucleotide binding protein, beta 1	P	P	P
Gnb2	guanine nucleotide binding protein, beta 2	P	P	P
Gnb2-rs1	guanine nucleotide binding protein, beta 2, related sequence 1	P	P	P
Gna-rs1	guanine nucleotide binding protein, related sequence 1	P	P	P
Gdi1	guanosine diphosphate (GDP) dissociation inhibitor 1	P	A	P
Gdi3	guanosine diphosphate (GDP) dissociation inhibitor 3	P	P	P
Guk1	guanylate kinase 1	P	P	P
Hmga2	h+E1270igh mobility group protein I, isoform C	P	P	P
H1f0	H1 histone family, member 0	P	P	P
H19	H19 fetal liver mRNA	P	P	P
Hlx	H2.0-like homeo box gene	P	P	A
H2afx	H2A histone family, member X	P	P	P
H2afy	H2A histone family, member Y	P	P	P
H2afy	H2A histone family, member Y	P	P	P
H2afz	H2A histone family, member Z	P	P	P
H2-Ke2	H2-K region expressed gene 2	P	P	P
H2-Ke4	H2-K region expressed gene 4	P	P	P
H3f3a	H3 histone, family 3A	P	P	P
H3f3b	H3 histone, family 3B	P	P	P
Hes1	hairy and enhancer of split 1, (Drosophila)	P	P	P
Hes2	Hairy and enhancer of split 2 (Drosophila)	P	P	P
Hras1	Harvey rat sarcoma virus oncogene	P	P	P
Hbs1l	Hbs1-like (S. cerevisiae)	P	P	P
Hand1	heart and neural crest derivatives expressed transcript 1	P	P	P
Hspa5	heat shock 70kD protein 5 (glucose-regulated protein)	P	P	P
Hsf1	heat shock factor 1	A	P	P
Hsp30-(p)	heat shock protein	P	P	P
Hsp30-(p)	heat shock protein	P	P	P
Hsp105	heat shock protein	P	P	P
Hspe1	heat shock protein 1 (chaperonin 10)	P	P	P
Hspd1	heat shock protein 1 (chaperonin)	P	P	P
Hspcb	heat shock protein 1, beta	P	P	P
Hspa1b	heat shock protein 1B	P	P	P
Hspb2	heat shock protein 2	P	P	M
Hspa4	heat shock protein 4	P	P	P
Hsp70-4	heat shock protein 4	P	P	P
Hspa4	heat shock protein 4	P	P	P

Hspa4	heat shock protein 4	P	P	P
Hspa4	heat shock protein 4	P	P	P
Hspa8	heat shock protein 8	P	P	P
Hsp86-1	heat shock protein, 1	P	P	P
Hspa9a	heat shock protein, A	P	P	P
Hrsp12	heat-responsive protein 12	P	P	P
Herc2	hect domain and RCC1-like domain (RLD) 2	P	P	P
Helb	helicase (DNA) B	P	P	P
Helb	helicase (DNA) B	P	A	P
Hells	helicase, lymphoid specific	P	P	P
Hn1	hematological and neurological expressed sequence 1	P	P	P
Hhex	hematopoietically expressed homeobox	P	P	P
Hebp1	heme binding protein 1	P	P	A
Hmox1	heme oxygenase (decycling) 1	P	P	P
Hmox2	heme oxygenase (decycling) 2	P	A	P
Hba-a1	hemoglobin alpha, adult chain 1	P	P	P
Hba-a1	hemoglobin alpha, adult chain 1	P	P	P
Hbb-bh3	hemoglobin beta, pseudogene bh3	P	A	P
Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	P	P	P
Hbb-y	hemoglobin Y, beta-like embryonic chain	P	P	P
Hbb-y	hemoglobin Y, beta-like embryonic chain	P	A	P
Hbb-b1	hemoglobin, beta adult major chain	A	P	P
Hs2st1	heparan sulfate 2-O-sulfotransferase 1	P	P	P
Hdgf	hepatoma-derived growth factor	P	P	P
Hdgf	hepatoma-derived growth factor	P	P	P
Hdgfrp2	hepatoma-derived growth factor, related protein 2	P	P	P
Heph	hephaestin	P	P	P
Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	P	P	A
Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	P	A	P
Hp1bp3	heterochromatin protein 1, binding protein 3	P	M	P
Hnrpab	heterogeneous nuclear ribonucleoprotein A/B	P	P	P
Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	P	P	P
Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	P	P	P
Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	P	P	P
Hnrpa2b1	heterogeneous nuclear ribonucleoprotein A2/B1	P	P	P
Hnrpc	heterogeneous nuclear ribonucleoprotein C	P	P	P
Hnrpd	heterogeneous nuclear ribonucleoprotein D	P	P	P
Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	P	P	P
Hnrpdl	heterogeneous nuclear ribonucleoprotein D-like	P	P	P
Hnrph1	heterogeneous nuclear ribonucleoprotein H1	P	P	P
Hnrph2	heterogeneous nuclear ribonucleoprotein H2	P	P	P
Hnrpk	heterogeneous nuclear ribonucleoprotein K	P	P	P
Hnrpl	heterogeneous nuclear ribonucleoprotein L	A	P	P
Hrmt1l2	heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)	P	P	P
Hk1	hexokinase 1	P	P	P
Hk2	hexokinase 2	P	P	P
Hexa	hexosaminidase A	P	P	P
Hgs	HGF-regulated tyrosine kinase substrate	P	P	P
Hmgb1	high mobility group box 1	P	P	P
Hmgb2	high mobility group box 2	P	P	P
Hmgb3	high mobility group box 3	P	P	P
Hmgn1	high mobility group nucleosomal binding domain 1	P	P	P
Hmgn2	high mobility group nucleosomal binding domain 2	P	P	P
Hiat1	hippocampus abundant gene transcript 1	P	P	P
Hint	histidine triad nucleotide binding protein	P	P	P
Hars	histidyl-tRNA synthetase	P	P	P
H13	histocompatibility 13	P	P	P
H2-Eb1	histocompatibility 2, class II antigen E beta	P	P	P
H2-D1	histocompatibility 2, D region locus 1	P	P	P
H2-K	histocompatibility 2, K region	P	P	P
H2-M2	Histocompatibility 2, M region locus 2	P	P	P
H2-T17	histocompatibility 2, T region locus 17	P	A	P

H47	histocompatibility 47	P	P	P
Hist1h2bc	histone 1, H2bc	A	P	P
Hist1h3f	histone 1, H3f	P	P	P
Hist1h3f	histone 1, H3f	P	P	P
Hdac1	histone deacetylase 1	P	P	P
Hdac2	histone deacetylase 2	P	P	P
Hdac3	histone deacetylase 3	P	A	P
Hdac5	histone deacetylase 5	P	P	P
Hdac6	histone deacetylase 6	P	P	P
Hdac7a	histone deacetylase 7A	P	P	P
Hist1h2ab	histone H2A.1	P	P	P
---	histone H2a.2-615 and histone H3.2-615 genes	P	P	P
Hrb	HIV-1 Rev binding protein	P	P	P
Hrb	HIV-1 Rev binding protein	P	P	P
Bat4	HLA-B associated transcript 4	P	P	P
Bat4	HLA-B associated transcript 4	P	P	P
Bat8	HLA-B associated transcript 8	P	P	P
Bat1a	HLA-B-associated transcript 1A	P	P	P
Bat3	HLA-B-associated transcript 3	P	P	M
Raly	hnRNP-associated with lethal yellow	P	P	P
Hccs	holocytochrome c synthetase	P	P	P
Hoxa1	homeo box A1	P	P	P
Hoxa5	homeo box A5	P	A	P
Hoxb1	homeo box B1	P	P	P
Hoxb3	homeo box B3	P	P	P
Hoxb6	homeo box B6	A	P	P
Msx1	homeo box, msh-like 1	P	P	P
Hop-(p)	homeodomain only protein	P	P	P
Homer2	homer homolog 2 (Drosophila)	P	P	P
Herpud1	homocysteine-inducible, ER+E1519 stress-inducible, ubiquitin-like domain member 1	A	P	P
Hcfc1	host cell factor C1	P	P	P
Hkp1	house-keeping protein 1	P	A	P
Ha1r-(p)	Hoxa1 regulated gene	P	P	P
Htf9c	Hpal1 tiny fragments locus 9c	P	A	P
Hs1bp1	HS1 binding protein	P	P	P
Hs1bp3-(p)	HS1 binding protein 3	P	P	P
Hip2	huntingtin interacting protein 2	P	P	P
Hus1	Hus1 homolog (S. pombe)	P	P	P
Has2	hyaluronan synthase 2	P	A	P
Hagh	hydroxyacyl glutathione hydrolase	A	P	P
Hadh2	hydroxyacyl-Coenzyme A dehydrogenase type II	P	P	P
Hmbs	hydroxymethylbilane synthase	P	P	P
Hsd17b11	hydroxysteroid (17-beta) dehydrogenase 11	P	P	M
Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	P	P	P
Hsd17b4	hydroxysteroid (17-beta) dehydrogenase 4	P	P	P
Hprt	hypoxanthine guanine phosphoribosyl transferase	P	P	P
Hig1-(p)	hypoxia induced gene 1	P	P	P
Hif1a	hypoxia inducible factor 1, alpha subunit	P	P	P
Hif1a	hypoxia inducible factor 1, alpha subunit	P	P	P
lpp	IAP promoted placental gene	P	P	P
ler5	ler5 gene	P	P	P
---	Ig Vheavy-PCG-4 gene	P	P	P
Ik	IK cytokine	P	P	P
Itk	IL2-inducible T-cell kinase	P	P	P
Ict1	immature colon carcinoma transcript 1	P	P	P
ler2	immediate early response 2	P	P	P
Ierepo4-(p)	immediate early response, erythropoietin 4	P	P	P
Igbp1	immunoglobulin (CD79A) binding protein 1	P	P	P
Igbp1	immunoglobulin (CD79A) binding protein 1	P	P	P
Igk-V8	immunoglobulin kappa chain variable 8 (V8)	P	M	P
Igsf4	immunoglobulin superfamily, member 4	P	P	P
Igsf4	immunoglobulin superfamily, member 4	A	P	P

Igsf8	immunoglobulin superfamily, member 8	P	P	P
Imp4a-(p)	importin 4a	P	P	P
Imp4a-(p)	importin 4a	P	P	P
Xist	inactive X specific transcripts	P	P	P
Idb1	inhibitor of DNA binding 1	P	P	P
Idb2	inhibitor of DNA binding 2	P	P	P
Idb3	inhibitor of DNA binding 3	P	P	P
Ing1	inhibitor of growth family, member 1	P	P	P
Ing4	inhibitor of growth family, member 4	P	P	P
Incenp	inner centromere protein	P	P	P
Immt	inner membrane protein, mitochondrial	P	P	P
Impdh2	inosine 5'-phosphate dehydrogenase 2	P	P	P
Itpa	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	P	P	P
Impa1	inositol (myo)-1(or 4)-monophosphatase 1	P	P	P
Itpr1	inositol 1,4,5-triphosphate receptor 1	P	A	P
Ihpk1	inositol hexaphosphate kinase 1	P	P	P
Inpp1	inositol polyphosphate phosphatase-like 1	P	A	P
Inpp5b	inositol polyphosphate-5-phosphatase	P	P	P
Ide	insulin degrading enzyme	A	P	P
Ins1	insulin I	P	P	P
Igf2	insulin-like growth factor 2	P	P	P
Igf2r	insulin-like growth factor 2 receptor	P	P	P
Igf2bp1	insulin-like growth factor 2, binding protein 1	P	P	P
Igfbp2	insulin-like growth factor binding protein 2	P	P	P
Igfbp3	insulin-like growth factor binding protein 3	P	P	A
Igfbp4	insulin-like growth factor binding protein 4	P	P	A
Igfbp4	insulin-like growth factor binding protein 4	P	M	P
Igfbp5	insulin-like growth factor binding protein 5	P	P	P
Igf1r	insulin-like growth factor I receptor	P	P	P
Itm2a	integral membrane protein 2A	P	P	P
Itm2b	integral membrane protein 2B	P	P	P
Itm2c	integral membrane protein 2C	P	P	P
Itga6	integrin alpha 6	P	A	P
Itgb1	integrin beta 1 (fibronectin receptor beta)	P	P	P
Itgb1	integrin beta 1 (fibronectin receptor beta)	P	P	P
Itgb1bp1	integrin beta 1 binding protein 1	P	P	P
Itgb2l	integrin beta 2-like	A	P	P
Itgb4bp	integrin beta 4 binding protein	P	P	P
Itgb5	integrin beta 5	P	P	A
Itgb5	integrin beta 5	P	A	P
Ilk	integrin linked kinase	P	P	P
Icam1	intercellular adhesion molecule	P	P	P
Icam1	intercellular adhesion molecule	P	A	P
Ifnar1	interferon (alpha and beta) receptor 1	P	A	P
Ifnar2	interferon (alpha and beta) receptor 2	A	P	P
Ifrg15-(p)	interferon alpha responsive gene	P	P	P
Ifi30	interferon gamma inducible protein 30	P	P	A
Ifitm3l	interferon induced transmembrane protein 3-like	P	A	P
Irf3	interferon regulatory factor 3	P	P	P
Ifrd1	interferon-related developmental regulator 1	P	P	P
Ifrd2	interferon-related developmental regulator 2	P	P	P
Itm1	integral membrane protein 1	P	P	P
Il10rb	interleukin 10 receptor, beta	P	M	P
Il11ra2	interleukin 11 receptor, alpha chain 2	P	P	P
Il16	interleukin 16	P	A	P
Il25	interleukin 25	P	P	P
Ilf3	interleukin enhancer binding factor 3	P	P	P
Irak1	interleukin-1 receptor-associated kinase 1	P	P	P
Itsn	intersectin (SH3 domain protein 1A)	P	P	P
Iap	intracisternal A particles	P	P	P
Gag	intracisternal A-particle gag gene	P	P	P
Iqgap1	IQ motif containing GTPase activating protein 1	P	P	P

lrx3	Iroquois related homeobox 3 (Drosophila)	P	P	P
ldh1	isocitrate dehydrogenase 1 (NADP+), soluble	P	A	P
ldh2	isocitrate dehydrogenase 2 (NADP+), mitochondrial	P	P	P
ldh3a	isocitrate dehydrogenase 3 (NAD+) alpha	P	P	M
ldh3g	isocitrate dehydrogenase 3 (NAD+), gamma	P	P	P
Itch	itchy	P	P	P
Jmj	jumonji	P	P	P
Jtb	jumping translocation breakpoint	P	P	P
Jund1	Jun proto-oncogene related gene d1	P	P	P
Jcam3	junction cell adhesion molecule 3	P	P	P
Kpna1	karyopherin (importin) alpha 1	P	P	P
Kpna2	karyopherin (importin) alpha 2	P	P	P
Kpna3	karyopherin (importin) alpha 3	P	P	P
Kpnb1	karyopherin (importin) beta 1	P	P	P
Kpnb3	karyopherin (importin) beta 3	P	P	P
Kpnb3	karyopherin (importin) beta 3	P	P	P
Klhdc2	kelch domain containing 2	P	P	P
Krt1-18	keratin complex 1, acidic, gene 18	P	P	P
Krt1-19	keratin complex 1, acidic, gene 19	P	P	A
Krt2-8	keratin complex 2, basic, gene 8	P	P	P
Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1	P	P	P
Kdt1	kidney cell line derived transcript 1	P	P	P
Kdr	kinase insert domain protein receptor	P	P	P
Kip2-(p)	kinase interacting protein 2	P	P	A
Ktn1	kinectin 1	P	P	P
Ktn1	kinectin 1	A	P	P
Kns2	kinesin 2 60/70kDa	P	M	P
Kif11	kinesin family member 11	P	P	P
Kif20a	kinesin family member 20A	P	P	P
Kif20a	kinesin family member 20A	P	P	P
Kif20a	kinesin family member 20A	P	P	P
Kif22-ps	kinesin family member 22, pseudogene	P	P	P
Kif23	kinesin family member 23	P	P	P
Kif2a	kinesin family member 2A	P	P	P
Kif2c	kinesin family member 2C	P	P	P
Kif4	kinesin family member 4	P	P	P
Kif5b	kinesin family member 5B	A	P	P
Kifap3	kinesin-associated protein 3	P	P	P
Kras2	Kirsten rat sarcoma oncogene 2, expressed	P	P	P
Kitl	kit ligand	P	P	P
Kit	kit oncogene	P	P	P
Klf1	Kruppel-like factor 1 (erythroid)	A	P	P
Klf13	Kruppel-like factor 13	A	P	P
Klf3	Kruppel-like factor 3 (basic)	P	P	P
Klf9	Kruppel-like factor 9	A	P	P
Lmyc1	I+E1450ung carcinoma myc related oncogene	P	A	P
Hadhs	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain	P	P	P
Ldh1	lactate dehydrogenase 1, A chain	P	P	P
Ldh2	lactate dehydrogenase 2, B chain	P	P	P
Lmna	lamin A	P	P	P
Lbr	lamin B receptor	P	P	P
Lmnb1	lamin B1	A	P	P
Lmnb2	lamin B2	P	A	P
Lamb1-1	laminin B1 subunit 1	P	P	P
Lamb1-1	laminin B1 subunit 1	P	P	P
Lamr1	laminin receptor 1 (ribosomal protein SA)	P	P	P
Lama1	laminin, alpha 1	P	A	P
Lamc1	laminin, gamma 1	P	A	P
Lanc1	LanC (bacterial lantibiotic synthetase component C)-like	P	P	P
Lss	lanosterol synthase	P	P	P
Lxn	latexin	P	P	P
Lgals1	lectin, galactose binding, soluble 1	P	P	P

Lgals2	lectin, galactose-binding, soluble 2	P	P	A
Lgmn	legumain	P	P	P
Llg1h	lethal giant larvae homolog	P	P	P
LOC217325	lethal giant larvae-like protein 2	P	P	P
Lrpb7	leucine rich protein, B7 gene	P	P	P
Lrrfp1	leucine rich repeat (in FLII) interacting protein 1	P	P	P
Lrrn1	leucine rich repeat protein 1, neuronal	A	P	P
Lta4h	leukotriene A4 hydrolase	P	P	P
Lig1	ligase I, DNA, ATP-dependent	P	P	P
Lig3	ligase III, DNA, ATP-dependent	P	P	P
Lig3	ligase III, DNA, ATP-dependent	P	A	P
Lgtn	ligatin	M	P	P
Large	like-glycosyltransferase	P	A	P
Lims1	LIM and senescent cell antigen-like domains 1	P	P	P
Lasp1	LIM and SH3 protein 1	P	P	P
Lmo2	LIM only 2	P	P	P
Lmo2	LIM only 2	A	P	P
Lmo4	LIM only 4	P	P	P
Lias	lipoic acid synthetase	P	P	P
Lpl	lipoprotein lipase	P	P	P
Lisch7-(p)	liver-specific bHLH-Zip transcription factor	P	P	P
Lce-(p)	long chain fatty acyl elongase	P	P	P
Lce-(p)	long chain fatty acyl elongase	P	P	P
Ldlr	low density lipoprotein receptor	P	P	P
Lrp1	low density lipoprotein receptor-related protein 1	P	P	P
Lrp2	low density lipoprotein receptor-related protein 2	P	P	P
Lrpap1	low density lipoprotein receptor-related protein associated protein 1	P	P	P
Lrp10	low-density lipoprotein receptor-related protein 10	P	P	P
Litaf	LPS-induced TN factor	P	P	P
Lrba	LPS-responsive beige-like anchor	P	A	P
Luc7l	Luc7 homolog (S. cerevisiae)-like	P	P	P
Lt1	lurcher transcript 1	P	A	P
Lyl1	lymphoblastic leukemia	P	P	P
Ly6c	lymphocyte antigen 6 complex, locus C	P	P	P
Ly6e	lymphocyte antigen 6 complex, locus E	P	P	P
Ly75	lymphocyte antigen 75	P	P	P
Lypla1	lysophospholipase 1	P	P	P
Lypla1	lysophospholipase 1	P	P	P
Lypla2	lysophospholipase 2	P	P	P
Lysal1	lysosomal apyrase-like 1	P	P	P
Lamp1	lysosomal membrane glycoprotein 1	P	P	P
Lamp2	lysosomal membrane glycoprotein 2	P	P	P
Lamp2	lysosomal membrane glycoprotein 2	P	P	P
Laptm4a	lysosomal-associated protein transmembrane 4A	P	P	P
Laptm4b	lysosomal-associated protein transmembrane 4B	P	P	P
Maea	macrophage erythroblast attacher	P	P	P
Madh1	MAD homolog 1 (Drosophila)	P	P	P
Madh1	MAD homolog 1 (Drosophila)	P	P	P
Madh2	MAD homolog 2 (Drosophila)	P	P	P
Madh4	MAD homolog 4 (Drosophila)	P	P	P
Madh6	MAD homolog 6 (Drosophila)	P	P	P
Madh7	MAD homolog 7 (Drosophila)	M	P	P
Mad2l1	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	P	P	P
Mago	mago-nashi homolog, proliferation-associated (Drosophila)	P	P	P
Mkrn1	makorin, ring finger protein, 1	P	P	P
Mkrn1	makorin, ring finger protein, 1	A	P	P
Mor1	malate dehydrogenase, mitochondrial	P	P	P
Mor2	malate dehydrogenase, soluble	M	P	P
Mea1	male enhanced antigen 1	P	P	P
Mea1	male enhanced antigen 1	P	P	P
Mfng	manic fringe homolog (Drosophila)	P	A	P
M6pr	mannose-6-phosphate receptor, cation dependent	P	P	P

Man2a1	mannosidase 2, alpha 1	P	P	P
Mgat1	mannoside acetylglucosaminyltransferase 1	P	P	A
Mapkapk2	MAP kinase-activated protein kinase 2	P	P	P
Mapkapk5	MAP kinase-activated protein kinase 5	P	P	P
Mknk2	MAP kinase-interacting serine/threonine kinase 2	P	P	P
Mark2	MAP/microtubule affinity-regulating kinase 2	P	P	P
Mark3	MAP/microtubule affinity-regulating kinase 3	P	P	P
Mlp	MARCKS-like protein	P	P	P
Mas1	MAS1 oncogene	P	P	M
Maid	maternal inhibition of differentiation	P	P	P
Meg3	maternally expressed gene 3	P	A	P
Matr3	matrin 3	P	P	P
Matr3	matrin 3	P	P	P
Matr3	matrin 3	P	P	P
Mglap	matrix gamma-carboxyglutamate (gla) protein	P	P	P
Mmp11	matrix metalloproteinase 11	P	A	P
Mmp14	matrix metalloproteinase 14 (membrane-inserted)	P	P	P
Mtcp1	mature T-cell proliferation 1	P	P	P
Mtcp1	mature T-cell proliferation 1	A	P	P
Mad4	Max dimerization protein 4	P	P	P
Mxi1	Max interacting protein 1	P	P	P
Max	Max protein	P	P	P
Mbtd1	mbt domain containing 1	P	P	P
mCAC	mCAC gene	P	P	P
Mkl1	megakaryoblastic leukemia (translocation) 1 homolog (human)	P	P	A
Mns1	meiosis-specific nuclear structural protein 1	P	P	P
Mcpr	meiotic check point regulator	P	P	P
Mre11a	meiotic recombination 11 homolog A (S. cerevisiae)	P	P	P
Mc5r	melanocortin 5 receptor	P	P	P
Myg1-(p)	melanocyte proliferating gene 1	P	M	P
Maged1	melanoma antigen, family D, 1	P	P	P
Maged2	melanoma antigen, family D, 2	P	P	P
Mpp1	membrane protein, palmitoylated	P	P	P
Mbtps1	membrane-bound transcription factor protease, site 1	P	P	P
Ms4a1	membrane-spanning 4-domains, subfamily A, member 1	P	A	P
Mnat1	menage a trois 1	P	P	P
Mgea5	meningioma expressed antigen 5 (hyaluronidase)	P	P	P
Mesdc2	mesoderm development candidate 2	P	P	P
Mest	mesoderm specific transcript	P	P	P
Mtf2	metal response element binding transcription factor 2	P	P	P
Mt1	metallothionein 1	P	P	P
Mt2	metallothionein 2	P	P	P
Mt1a	metallothionein-I activator	P	P	P
Mta1l1	metastasis associated 1-like 1	P	P	P
Mtx1	metaxin 1	P	P	P
Mtx2	metaxin 2	P	P	P
Mat2a	methionine adenosyltransferase II, alpha	P	P	P
Metap1	methionyl aminopeptidase 1	P	P	P
Mbd1	methyl-CpG binding domain protein 1	A	P	P
Mbd3	methyl-CpG binding domain protein 3	P	P	P
Mbd4	methyl-CpG binding domain protein 4	P	P	A
Mccc1	methylcrotonoyl-Coenzyme A carboxylase 1 (alpha)	P	P	P
Mthfd2	methylenetetrahydrofolate dehydrogenase methenyltetrahydrofolate cyclohydrolase	P	P	P
Mettl3	methyltransferase-like 3	P	P	M
Mgst3	microsomal glutathione S-transferase 3	P	P	M
Mcrs1	microspherule protein 1	P	P	P
Map1lc3	microtubule-associated protein 1 light chain 3	P	P	P
Map1lc3	microtubule-associated protein 1 light chain 3	P	P	P
Mtap4	microtubule-associated protein 4	P	P	P
Mtap7	microtubule-associated protein 7	A	P	P
Mapre1	microtubule-associated protein, RP/EB family, member 1	P	P	P
Mdk	midkine	P	P	P

Midn	midnolin	P	P	P
Mfge8	milk fat globule-EGF factor 8 protein	P	P	P
Mcmd	mini chromosome maintenance deficient (S. cerevisiae)	P	P	P
Mcmd	mini chromosome maintenance deficient (S. cerevisiae)	P	P	P
Mcmd2	mini chromosome maintenance deficient 2 (S. cerevisiae)	P	P	P
Mcmd4	mini chromosome maintenance deficient 4 homolog (S. cerevisiae)	P	P	P
Mcmd5	mini chromosome maintenance deficient 5 (S. cerevisiae)	P	P	P
Mcmd7	mini chromosome maintenance deficient 7 (S. cerevisiae)	P	P	P
Mcm3ap	minichromosome maintenance deficient (S. cerevisiae) 3-associated protein	P	P	P
Mrps7	mitochondrial ribosomal protein S7	P	P	P
Mtch1-(p)	mitochondrial carrier homolog 1	P	P	P
Mtch2-(p)	mitochondrial carrier homolog 2	P	P	P
Mrpl11	mitochondrial ribosomal protein L11	M	P	P
Mrpl12	mitochondrial ribosomal protein L12	P	P	P
Mrpl13	mitochondrial ribosomal protein L13	P	P	P
Mrpl15	mitochondrial ribosomal protein L15	P	P	P
Mrpl16	mitochondrial ribosomal protein L16	P	P	P
Mrpl17	mitochondrial ribosomal protein L17	P	P	P
Mrpl2	mitochondrial ribosomal protein L2	P	P	P
Mrpl20	mitochondrial ribosomal protein L20	P	P	P
Mrpl23	mitochondrial ribosomal protein L23	P	P	P
Mrpl27	mitochondrial ribosomal protein L27	P	P	P
Mrpl28	mitochondrial ribosomal protein L28	P	P	P
Mrpl3	mitochondrial ribosomal protein L3	P	P	P
Mrpl30	mitochondrial ribosomal protein L30	P	P	P
Mrpl33	mitochondrial ribosomal protein L33	P	P	P
Mrpl34	mitochondrial ribosomal protein L34	P	P	P
Mrpl36	mitochondrial ribosomal protein L36	P	P	P
Mrpl37	mitochondrial ribosomal protein L37	P	P	P
Mrpl38	mitochondrial ribosomal protein L38	P	P	P
Mrpl39	mitochondrial ribosomal protein L39	P	P	P
Mrpl4	mitochondrial ribosomal protein L4	P	P	P
Mrpl40	mitochondrial ribosomal protein L40	P	P	P
Mrpl43	mitochondrial ribosomal protein L43	P	P	P
Mrpl44	mitochondrial ribosomal protein L44	P	P	P
Mrpl45	mitochondrial ribosomal protein L45	P	P	P
Mrpl45	mitochondrial ribosomal protein L45	P	P	P
Mrpl51	mitochondrial ribosomal protein L51	P	P	P
Mrpl52	mitochondrial ribosomal protein L52	P	P	P
Mrpl53	mitochondrial ribosomal protein L53	P	P	P
Mrpl55	mitochondrial ribosomal protein L55	P	A	P
Mrpl9	mitochondrial ribosomal protein L9	P	P	P
Mrps10	mitochondrial ribosomal protein S10	P	P	P
Mrps11	mitochondrial ribosomal protein S11	P	P	P
Mrps12	mitochondrial ribosomal protein S12	P	P	P
Mrps14	mitochondrial ribosomal protein S14	P	P	P
Mrps15	mitochondrial ribosomal protein S15	P	P	P
Mrps17	mitochondrial ribosomal protein S17	P	P	P
Mrps18a	mitochondrial ribosomal protein S18A	P	P	P
Mrps18a	mitochondrial ribosomal protein S18A	P	P	P
Mrps2	mitochondrial ribosomal protein S2	P	P	P
Mrps21	mitochondrial ribosomal protein S21	P	P	P
Mrps22	mitochondrial ribosomal protein S22	P	P	P
Mrps24	mitochondrial ribosomal protein S24	P	P	P
Mrps25	mitochondrial ribosomal protein S25	P	P	P
Mrps25	mitochondrial ribosomal protein S25	P	P	P
Mrps31	mitochondrial ribosomal protein S31	P	P	P
Mrps5	mitochondrial ribosomal protein S5	P	P	P
Mapbpip-(p)	mitogen activated protein binding protein interacting protein	P	P	P
Mapk1	mitogen activated protein kinase 1	P	P	P
Mapk1	mitogen activated protein kinase 1	P	P	P
Mapk14	mitogen activated protein kinase 14	P	P	P

Mapk3	mitogen activated protein kinase 3	P	P	P
Mapk8	mitogen activated protein kinase 8	P	P	P
Map2k1	mitogen activated protein kinase kinase 1	P	P	P
Map2k2	mitogen activated protein kinase kinase 2	P	P	P
Map2k3	mitogen activated protein kinase kinase 3	P	P	P
Map2k5	mitogen activated protein kinase kinase 5	P	P	P
Map3k1	mitogen activated protein kinase kinase kinase 1	P	P	P
Map3k1	mitogen activated protein kinase kinase kinase 1	P	A	P
Map3k3	mitogen activated protein kinase kinase kinase 3	P	P	P
Map3k4	mitogen activated protein kinase kinase kinase 4	P	P	P
Map3k7	mitogen activated protein kinase kinase kinase 7	P	P	P
Map4k1	mitogen activated protein kinase kinase kinase kinase 1	P	A	P
Mapk12	mitogen-activated protein kinase 12	P	P	P
Mapk6	mitogen-activated protein kinase 6	P	P	P
Map2k1ip1	mitogen-activated protein kinase kinase 1 interacting protein 1	P	P	P
Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	P	A	P
Mki67ip	Mki67 (FHA domain) interacting nucleolar phosphoprotein	P	P	P
Mms19l	MMS19 (MET18 <i>S. cerevisiae</i>)-like	P	P	P
Msn	moesin	P	P	P
Mail-(p)	molecule possessing ankyrin-repeats induced by lipopolysaccharide	A	P	P
Mocs2	molybdenum cofactor synthesis 2	P	P	P
Maoa	monoamine oxidase A	P	P	P
Mmrp19-(p)	monocyte macrophage 19	P	P	P
Mrgx-(p)	MORF-related gene X	P	P	P
Mrgx-(p)	MORF-related gene X	P	P	P
---	Mouse Ig germline H-chain gene V-region	P	P	P
Mrps18b	Mrps18b	P	P	P
Miz1	Msx-interacting-zinc finger	P	P	P
Minpp1	multiple inositol polyphosphate histidine phosphatase 1	P	P	P
Mpdz	multiple PDZ domain protein	P	P	P
Mpdz	multiple PDZ domain protein	P	P	P
Mbnl	muscleblind-like (Drosophila)	P	M	P
Mlh1	mutL homolog 1 (E. coli)	P	P	P
Msh2	mutS homolog 2 (E. coli)	P	P	P
Msh2	mutS homolog 2 (E. coli)	P	P	P
Mybbp1a	MYB binding protein (P160) 1a	P	P	P
Mybbp1a	MYB binding protein (P160) 1a	A	P	P
P42pop-(p)	Myb protein P42POP	P	P	P
Mina	myc induced nuclear antigen	P	P	P
Myef2	myelin basic protein expression factor 2, repressor	P	P	P
Myb	myeloblastosis oncogene	A	P	P
Mybl2	myeloblastosis oncogene-like 2	P	P	P
Myc	myelocytomatosis oncogene	P	P	P
Mcl1	myeloid cell leukemia sequence 1	P	P	P
Meis1	myeloid ecotropic viral integration site 1	P	A	P
Mllt3	myeloid/lymphoid or mixed lineage-leukemia translocation to 3 homolog E1969	P	P	P
Mll	myeloid/lymphoid or mixed-lineage leukemia	P	P	P
Myadm	myeloid-associated differentiation marker	P	P	P
Mdfi	MyoD family inhibitor	A	P	P
Myh9	myosin heavy chain IX	P	P	P
Myh9	myosin heavy chain IX	P	P	P
Myo1b	myosin IB	P	P	P
Myo1h	myosin IH	P	P	P
Myla	myosin light chain, alkali, cardiac atria	P	P	P
Myla	myosin light chain, alkali, cardiac atria	P	P	A
Mylf	myosin light chain, alkali, fast skeletal muscle	P	P	P
Mylic2a	myosin light chain, regulatory A	P	P	P
Myo10	myosin X	P	P	A
Mtpn	myotrophin	P	P	P
Marcks	myristoylated alanine rich protein kinase C substrate	P	P	P
Npl	N-acetylneuraminate pyruvate lyase	P	P	A
Nans	N-acetylneuraminic acid synthase (sialic acid synthase)	P	P	P

Ard1	N-acetyltransferase ARD1 homolog (<i>S. cerevisiae</i>)	P	P	P
Asah1	N-acylsphingosine amidohydrolase 1	P	M	P
Nsdhl	NAD(P) dependent steroid dehydrogenase-like	P	P	P
Nsdhl	NAD(P) dependent steroid dehydrogenase-like	P	P	P
Ndufa2	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	P	P	P
Ndufa4	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	P	P	P
Ndufa6	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	P	P	P
Ndufa7	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7 (B14.5a)	P	P	P
Ndufaf1	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 1	P	P	P
Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	P	P	P
Ndufb9	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	P	P	P
Ndufc1	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1	P	P	P
Ndufs2	NADH dehydrogenase (ubiquinone) Fe-S protein 2	P	P	P
Ndufs3	NADH dehydrogenase (ubiquinone) Fe-S protein 3	P	P	P
Ndufs5	NADH dehydrogenase (ubiquinone) Fe-S protein 5	P	P	P
Ndufv1	NADH dehydrogenase (ubiquinone) flavoprotein 1	P	P	P
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	P	P	P
Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	A	P	P
Ncb5or	NADPH cytochrome B5 oxidoreductase	P	P	P
Naca	nascent polypeptide-associated complex alpha polypeptide	P	P	P
Nppb	natriuretic peptide precursor type B	P	P	P
Nckap1	NCK-associated protein 1	P	P	P
Nd1-(p)	Nd1	P	P	P
Ndn	necdin	P	P	P
Ndn	necdin	P	P	P
Ndfip1	Nedd4 family interacting protein 1	P	P	P
Ndfip2	Nedd4 family interacting protein 2	P	P	P
Noc4	neighbor of Cox4	P	P	P
Noc4	neighbor of Cox4	P	P	P
Nlk	nemo like kinase	P	P	P
Nphp1	nephronophthisis 1 (juvenile) homolog (human)	P	A	P
Nes	nestin	P	P	P
Napa	N-ethylmaleimide sensitive fusion protein attachment protein alpha	P	P	P
Ngrn-(p)	neugrin	P	P	P
Ncam1	neural cell adhesion molecule 1	P	P	P
Nedd1	neural precursor cell expressed, developmentally down-regulated gene 1	P	P	P
Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	P	A	P
Nedd8	neural precursor cell expressed, developmentally down-regulated gene 8	P	P	P
Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	P	A	P
Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	P	P	P
Nedd4	neural precursor cell expressed, developmentally down-regulated gene 4	P	A	P
Sdnf-(p)	neural stem cell derived neuronal survival protein	P	P	P
Nssr	neural-salient serine/arginine-rich	P	P	P
Nssr	neural-salient serine/arginine-rich	P	P	P
Nmyc1	neuroblastoma myc-related oncogene 1	P	P	P
Nras	neuroblastoma ras oncogene	P	P	P
Ncdn-(p)	neurochondrin	P	P	P
Net1	neuroepithelial cell transforming gene 1	P	P	P
Nf2	neurofibromatosis 2	P	P	P
Nav1	neuron navigator 1	P	P	P
Npy6r	neuropeptide Y receptor Y6	P	A	P
Nrp	neuropilin	P	P	P
Nrtin	neurturin	A	P	P
Nsmaf	neutral sphingomyelinase (N-SMase) activation associated factor	P	P	P
Nbr1	next to the Brca1	P	P	P
Nab1	Ngfi-A binding protein 1	P	P	P
Nbn	nibrin	P	P	P
Nnt	nicotinamide nucleotide transhydrogenase	P	P	P
Nid2	nidogen 2	P	P	P
Npc1	Niemann Pick type C1	P	P	P
Npc2	Niemann Pick type C2	P	P	P
Nek2	NIMA (never in mitosis gene a)-related expressed kinase 2	P	P	P

Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	P	P	P
Nisch	nischarin	P	P	P
Nit1	nitrilase 1	M	P	P
Nfs1	nitrogen fixation gene 1 (S. cerevisiae)	P	P	P
Nkx6-2	NK6 transcription factor related, locus 2 (Drosophila)	P	A	P
Narg1	NMDA receptor-regulated gene 1	P	P	P
Narg1	NMDA receptor-regulated gene 1	P	P	P
Narg1	NMDA receptor-regulated gene 1	P	P	P
Ndr1	N-myc downstream regulated 1	A	P	P
Nmt1	N-myristoyltransferase 1	P	P	P
Nmt1	N-myristoyltransferase 1	P	P	P
Nono	non-POU-domain-containing, octamer binding protein	P	P	P
Nono	non-POU-domain-containing, octamer binding protein	P	P	P
Notch3	Notch gene homolog 3, (Drosophila)	P	P	P
Nnp1	novel nuclear protein 1	P	P	P
Nsap1-(p)	NS1-associated protein 1	P	P	P
Nsap1l-(p)	NS1-associated protein 1-like	P	P	P
Nxt1	NTF2-related export protein 1	P	P	P
Nasp	nuclear autoantigenic sperm protein (histone-binding)	P	P	P
Ncbp2	nuclear cap binding protein subunit 2	P	P	P
Nude-(p)	nuclear distribution gene E homolog (Aspergillus)	P	P	P
Nudel-(p)	nuclear distribution gene E-like	P	P	P
Nudel-(p)	nuclear distribution gene E-like	P	P	P
C1d-(p)	nuclear DNA binding protein	P	P	P
Nfatc2ip	nuclear factor of activated T-cells, cytoplasmic 2 interacting protein	P	P	P
Nfkb1	nuclear factor of kappa light chain gene enhancer in B-cells 1, p105	P	A	P
Nfkb1a	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	A	P	P
Nfe2	nuclear factor, erythroid derived 2	A	P	P
Nfe2l1	nuclear factor, erythroid derived 2, -like 1	P	P	P
Nfil3	nuclear factor, interleukin 3, regulated	P	A	P
Nufip1	nuclear fragile X mental retardation protein interacting protein	P	P	P
Pom121	nuclear pore membrane protein 121	P	P	P
Np15	nuclear protein 15.6	P	P	P
Np220	nuclear protein 220	P	P	P
Np95	nuclear protein 95	P	P	P
Nrbp	nuclear receptor binding protein	P	P	P
Ncoa3	nuclear receptor coactivator 3	A	P	P
Ncoa4	nuclear receptor coactivator 4	P	P	P
Ncoa6	nuclear receptor coactivator 6	P	P	P
Ncoa6ip	nuclear receptor coactivator 6 interacting protein	P	P	P
Ncor1	nuclear receptor co-repressor 1	P	P	P
Ncor2	nuclear receptor co-repressor 2	P	P	P
Nrip1	nuclear receptor interacting protein 1	P	P	P
Nr1i3	nuclear receptor subfamily 1, group I, member 3	P	P	P
Nr2f6	nuclear receptor subfamily 2, group F, member 6	P	P	P
Nxf1	nuclear RNA export factor 1 homolog (S. cerevisiae)	P	P	P
Nfya	nuclear transcription factor-Y alpha	P	P	P
Nfyb	nuclear transcription factor-Y beta	P	P	P
Nfyc	nuclear transcription factor-Y gamma	P	P	P
Nutf2	nuclear transport factor 2	P	P	P
Nfe2l2	nuclear, factor, erythroid derived 2, like 2	P	P	P
Nsep1	nuclease sensitive element binding protein 1	P	P	P
Nucb	nucleobindin	P	P	P
Nucb2	nucleobindin 2	P	P	A
Nol1	nucleolar protein 1	P	P	P
Nol5	nucleolar protein 5	P	P	P
Nola1	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	P	P	P
Ncl	nucleolin	P	P	P
Ncl	nucleolin	P	P	P
Npm1	nucleophosmin 1	P	P	P
Npm3	nucleoplasmin 3	P	M	P
Nup62	nucleoporin 62	P	P	P

Nup88	nucleoporin 88kDa	P	P	P
Nup50	nucleoprotein 50	P	P	P
Nap111	nucleosome assembly protein 1-like 1	P	P	P
Nap111	nucleosome assembly protein 1-like 1	P	P	P
Nsbp1	nucleosome binding protein 1	P	P	P
Nubp1	nucleotide binding protein 1	P	P	P
Nudt1	nudix (nucleoside diphosphate linked moiety X)-type motif 1	P	P	P
Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	P	P	P
Nudt3	nudix (nucleotide diphosphate linked moiety X)-type motif 3	P	P	P
Numb	numb gene homolog (Drosophila)	P	P	P
Nyren18-(p)	NY-REN-18 antigen	A	P	P
Odz3	odd Oz/ten-m homolog 3 (Drosophila)	P	A	P
Olf158	olfactory receptor 158	P	P	P
Olf171	olfactory receptor 171	P	P	P
ORF11	open reading frame 11	P	P	P
Ogfr	opioid growth factor receptor	P	P	P
Oprs1	opioid receptor, sigma 1	P	P	P
Orc1l	origin recognition complex, subunit 1-like (S. cerevisiae)	P	P	P
Orc2l	origin recognition complex, subunit 2-like (S. cerevisiae)	P	M	P
Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	P	P	P
Orc3l	origin recognition complex, subunit 3-like (S. cerevisiae)	P	P	P
Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	P	P	P
Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	M	P	P
Orc5l	origin recognition complex, subunit 5-like (S. cerevisiae)	P	P	P
Orc6l	origin recognition complex, subunit 6-like (S. cerevisiae)	P	P	P
Ormdl2	ORM1-like 2 (S. cerevisiae)	P	P	P
Ormdl3	ORM1-like 3 (S. cerevisiae)	P	P	P
Oat	ornithine aminotransferase	P	P	P
Oaz1	ornithine decarboxylase antizyme	P	P	P
Oaz1	ornithine decarboxylase antizyme	P	P	P
Oaz2	ornithine decarboxylase antizyme 2	P	P	P
Oazin	ornithine decarboxylase antizyme inhibitor	P	P	P
Odc	ornithine decarboxylase, structural	P	P	P
Odf2	outer dense fiber of sperm tails 2	P	P	P
Ovcov1	ovarian cancer overexpressed 1	P	P	P
Ovcov1	ovarian cancer overexpressed 1	P	P	P
Ogdh	oxoglutarate dehydrogenase (lipoamide)	P	P	P
Osbpl1a	oxysterol binding protein-like 1A	P	M	P
Osbpl5	oxysterol binding protein-like 5	P	P	A
Pcaf	p300/CBP-associated factor	P	A	P
Por	P450 (cytochrome) oxidoreductase	P	A	P
Prrx2	paired related homeobox 2	P	A	P
Pitx2	paired-like homeodomain transcription factor 2	P	P	M
Palad	paladin	P	P	P
Phemx	pan hematopoietic expression	A	P	P
Pcee-(p)	Paneth cell enhanced expression	P	P	P
Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	P	P	P
Pon2	paraoxonase 2	P	P	P
Pthr1	parathyroid hormone receptor 1	P	P	P
Peg3	paternally expressed 3	P	P	P
Pxn	paxillin	P	P	P
Pctk1	PCTAIRE-motif protein kinase 1	P	P	P
Pctk3	PCTAIRE-motif protein kinase 3	P	A	P
Pdlim1	PDZ and LIM domain 1 (elfin)	P	P	P
Pdlim1	PDZ and LIM domain 1 (elfin)	P	P	P
Peli1	pellino 1	P	P	P
Pelo	pelota homolog (Drosophila)	P	P	P
Pep4	peptidase 4	P	P	P
Ppil2	peptidylprolyl isomerase (cyclophilin)-like 2	P	P	P
Ppia	peptidylprolyl isomerase A	P	P	P
Ppib	peptidylprolyl isomerase B	P	P	P
Ppic	peptidylprolyl isomerase C	P	P	P

Ppid	peptidylprolyl isomerase D (cyclophilin D)	P	P	P
Pcnt2	pericentrin 2	P	P	P
Pcnt2	pericentrin 2	P	P	P
Per3	period homolog 3 (Drosophila)	P	P	P
Pmp22	peripheral myelin protein, 22 kDa	P	P	P
Ppl	periplakin	P	P	P
Prdx1	peroxiredoxin 1	P	P	P
Prdx1	peroxiredoxin 1	P	P	P
Prdx2	peroxiredoxin 2	P	P	P
Prdx2	peroxiredoxin 2	P	P	P
Prdx3	peroxiredoxin 3	P	P	P
Prdx4	peroxiredoxin 4	P	P	P
Pex11b	peroxisomal biogenesis factor 11b	P	P	P
Pex14	peroxisomal biogenesis factor 14	P	P	P
Pex14	peroxisomal biogenesis factor 14	P	P	P
Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	P	P	P
Pxf	peroxisomal farnesylated protein	P	P	P
Pxmp3	peroxisomal membrane protein 3, 35 kDa	P	P	P
Pso	peroxisomal sarcosine oxidase	A	P	P
Pex7	peroxisome biogenesis factor 7	P	P	P
Pparbp	peroxisome proliferator activated receptor binding protein	P	P	P
Ppnr-(p)	per-pentamer repeat gene	P	P	A
Pes1	pescadillo homolog 1, containing BRCT domain (zebrafish)	P	P	P
Pftk1	PFTAIRE protein kinase 1	P	P	P
Phf5a	PHD finger protein 5A	P	P	P
Phf7	PHD finger protein 7	P	P	P
Farsl	phenylalanine-tRNA synthetase-like	P	P	P
Ebp	phenylalkylamine Ca2+ antagonist (emopamil) binding protein	P	P	P
Pten	phosphatase and tensin homolog	P	P	P
Pcyt11a	phosphate cytidyltransferase 1, choline, alpha isoform	P	P	P
Ppap2a	phosphatidic acid phosphatase 2a	P	P	A
Pbp	phosphatidylethanolamine binding protein	P	P	P
Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	P	P	P
Pi4k2a-(p)	phosphatidylinositol 4-kinase type 2 alpha	P	M	P
Picalm	phosphatidylinositol binding clathrin assembly protein	P	P	P
Picalm	phosphatidylinositol binding clathrin assembly protein	P	P	P
Piga	phosphatidylinositol glycan, class A	P	P	P
Piga	phosphatidylinositol glycan, class A	P	P	P
Pigf	phosphatidylinositol glycan, class F	P	P	P
Pigq	phosphatidylinositol glycan, class Q	P	P	P
Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	P	P	P
Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	P	P	P
Ptdsr	phosphatidylserine receptor	P	P	P
Ptdss1	phosphatidylserine synthase 1	P	P	P
Ptdss1	phosphatidylserine synthase 1	P	P	P
Ptdss2	phosphatidylserine synthase 2	P	P	P
Pde6d	phosphodiesterase 6D, cGMP-specific, rod, delta	P	A	P
Pde7a	phosphodiesterase 7A	P	P	P
Pfkl	phosphofructokinase, liver, B-type	P	P	P
Pfkm	phosphofructokinase, muscle	P	P	P
Pfkp	phosphofructokinase, platelet	P	P	P
Pfkp	phosphofructokinase, platelet	P	P	P
Pgk1	phosphoglycerate kinase 1	P	P	P
Pgam1	phosphoglycerate mutase 1	P	P	P
Plaa	phospholipase A2, activating protein	P	P	P
Plscr1	phospholipid scramblase 1	P	P	P
Pmm1	phosphomannomutase 1	A	P	P
Prps1	phosphoribosyl pyrophosphate synthetase 1	P	P	P
Prpsap2	phosphoribosyl pyrophosphate synthetase-associated protein 2	P	P	P
Gart	phosphoribosylglycinamide formyltransferase	P	P	P
Psat-(p)	phosphoserine aminotransferase	P	P	P
Styx	phosphoserine/threonine/tyrosine interaction protein	P	P	P

Pitpnb	phosphatidylinositol transfer protein, beta	P	P	P
BC003940	phosphotyrosyl phosphatase activator	P	P	P
Phyh	phytanoyl-CoA hydroxylase	P	P	P
Pnn	pinin	P	P	P
Pttg1	pituitary tumor-transforming 1	P	P	P
Pl6-(p)	PL6 protein	P	P	A
Pem	placentae and embryos oncofetal gene	P	P	P
Plac1	placental specific protein 1	P	P	P
Plac8	placenta-specific 8	P	P	P
Plat	plasminogen activator, tissue	P	A	P
Pdgfra	platelet derived growth factor receptor, alpha polypeptide	P	P	P
Pdgfa	platelet derived growth factor, alpha	P	P	P
Pafah1b3	platelet-activating factor acetylhydrolase, isoform 1b, alpha1 subunit	P	P	P
Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	P	P	P
Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	P	P	P
Pafah1b2	platelet-activating factor acetylhydrolase, isoform 1b, alpha2 subunit	P	P	P
Pafah1b1	platelet-activating factor acetylhydrolase, isoform 1b, beta1 subunit	P	P	P
Plekha2	pleckstrin homology domain containing, family B (evectins) member 2	P	A	P
Pscd2	pleckstrin homology, Sec7 and coiled/coiled domains 2	P	M	P
Phlda1	pleckstrin homology-like domain, family A, member 1	A	P	P
Plrg1	pleiotropic regulator 1, PRL1 homolog (Arabidopsis)	P	P	P
Plxnb2	plexin B2	P	P	P
Plxnb2	plexin B2	P	P	P
Pm5-(p)	pM5 protein	P	P	P
Pvrl2	poliovirus receptor-related 2	P	P	P
Pvrl2	poliovirus receptor-related 2	A	P	P
Pvrl3	poliovirus receptor-related 3	P	P	P
Plk	polo-like kinase homolog, (Drosophila)	P	P	P
Plk	polo-like kinase homolog, (Drosophila)	P	P	P
Plk-ps1	Polo-like kinase, pseudogene 1	P	P	P
Plk-ps1	Polo-like kinase, pseudogene 1	P	A	P
Papola	poly (A) polymerase alpha	P	P	P
Parg	poly (ADP-ribose) glycohydrolase	A	P	P
Pabpc1	poly A binding protein, cytoplasmic 1	P	P	P
Pabpc4	poly(A) binding protein, cytoplasmic 4 (inducible form)	P	P	P
Pabpn1	poly(A) binding protein, nuclear I	P	P	P
Parn	poly(A)-specific ribonuclease (deadenylation nuclease)	P	P	P
Pcbp1	poly(rC) binding protein 1	P	P	P
Pcbp2	poly(rC) binding protein 2	P	P	P
Pkd1	polycystic kidney disease 1 homolog	P	A	P
Pkd2	polycystic kidney disease 2	P	P	P
Pqbp1	polyglutamine binding protein 1	P	P	P
Phc2	polyhomeotic-like 2 (Drosophila)	P	P	P
Pola1	polymerase (DNA directed), alpha 1	P	P	P
Pola2	polymerase (DNA directed), alpha 2	P	P	P
Polb	polymerase (DNA directed), beta	P	P	P
Pold1	polymerase (DNA directed), delta 1, catalytic subunit (125kDa)	P	P	P
Pold2	polymerase (DNA directed), delta 2, regulatory subunit (50 kDa)	M	P	P
Pole2	polymerase (DNA directed), epsilon 2 (p59 subunit)	P	P	P
Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	P	P	P
Pole3	polymerase (DNA directed), epsilon 3 (p17 subunit)	M	P	P
Polg	polymerase (DNA directed), gamma	P	P	P
Polg2	polymerase (DNA directed), gamma 2, accessory subunit	M	P	P
Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	P	P	P
Pole4	polymerase (DNA-directed), epsilon 4 (p12 subunit)	P	A	P
Polr2a	polymerase (RNA) II (DNA directed) polypeptide A	P	P	P
Polr2c	polymerase (RNA) II (DNA directed) polypeptide C	P	P	P
Polr2e	polymerase (RNA) II (DNA directed) polypeptide E (25kDa)	P	P	P
Polr2g	polymerase (RNA) II (DNA directed) polypeptide G	P	P	P
Polr2h	polymerase (RNA) II (DNA directed) polypeptide H	P	P	P
Polr2i	polymerase (RNA) II (DNA directed) polypeptide I	P	P	P
Ptfr	polymerase I and transcript release factor	A	P	P

Pnkp	polynucleotide kinase 3'-phosphatase	P	A	P
Pms2	postmeiotic segregation increased 2 (S. cerevisiae)	P	P	P
Cript-(p)	postsynaptic protein Cript	P	P	P
Kcnk1	potassium channel, subfamily K, member 1	A	P	P
Kcnk2	potassium channel, subfamily K, member 2	P	P	A
Pou2f1	POU domain, class 2, transcription factor 1	P	P	P
Pou2f1	POU domain, class 2, transcription factor 1	P	P	P
Pou5f1	POU domain, class 5, transcription factor 1	A	P	P
Prdm1	PR domain containing 1, with ZNF domain	P	A	P
Pja1	praja1, RING-H2 motif containing	P	P	P
Pja1	praja1, RING-H2 motif containing	P	P	P
Pbx1	pre B-cell leukemia transcription factor 1	P	P	P
Pbx2	pre B-cell leukemia transcription factor 2	P	A	P
Pbx3	pre B-cell leukemia transcription factor 3	P	P	P
Pbx3	pre B-cell leukemia transcription factor 3	P	P	P
Pbx3	pre B-cell leukemia transcription factor 3	A	P	P
Pbef-(p)	pre-B-cell colony-enhancing factor	P	P	P
Pfdn2	prefoldin 2	P	P	P
Pfdn5	prefoldin 5	P	P	P
Psg17	pregnancy specific glycoprotein 17	M	P	P
Prpf8	pre-mRNA processing factor 8	P	P	P
Ykt6-(p)	prenylated SNARE protein	P	A	P
Penk1	preproenkephalin 1	P	P	P
Psen1	presenilin 1	P	P	P
4833416109Rik	presenilin-like protein 4	P	P	P
Pmp	prion protein	P	P	P
Pawr	PRKC, apoptosis, WT1, regulator	P	P	P
Col1a1	procollagen, type I, alpha 1	M	P	P
Col4a1	procollagen, type IV, alpha 1	P	P	P
Col4a2	procollagen, type IV, alpha 2	P	P	P
Col9a2	procollagen, type IX, alpha 2	P	P	P
Col9a3	procollagen, type IX, alpha 3	P	A	P
Col5a1	procollagen, type V, alpha 1	P	P	P
Col5a2	procollagen, type V, alpha 2	P	P	P
Col13a1	procollagen, type XIII, alpha 1	P	A	P
Col18a1	procollagen, type XVIII, alpha 1	P	P	P
Col18a1	procollagen, type XVIII, alpha 1	P	P	P
Col18a1	procollagen, type XVIII, alpha 1	P	P	P
Plod3	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	P	P	P
P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase, alpha 1 polypeptide	P	P	P
P4ha2	procollagen-proline, 2-oxoglutarate 4-dioxygenase+E2104, alpha II polypeptide	P	A	P
Pfn2	profilin 2	P	A	P
Pgrmc1	progesterone receptor membrane component 1	P	P	P
Pdcd2	programmed cell death 2	P	P	P
Pdcd4	programmed cell death 4	P	P	P
Pdcd5	programmed cell death 5	P	P	P
Pdcd6	programmed cell death 6	P	P	P
Pdcd6ip	programmed cell death 6 interacting protein	P	P	P
Pdcd6ip	programmed cell death 6 interacting protein	P	P	P
Pdcd8	programmed cell death 8	P	P	P
Pdcd7	programmed cell death protein 7	P	P	P
ank	progressive ankylosis	P	P	P
Pcna	proliferating cell nuclear antigen	P	P	P
Pa2g4	proliferation-associated 2G4, 38kD	P	P	P
Prep	prolyl endopeptidase	P	A	P
Proml1	prominin-like 1	P	P	P
Proml1	prominin-like 1	P	P	P
Pml	promyelocytic leukemia	P	M	P
Pccb	propionyl Coenzyme A carboxylase, beta polypeptide	P	P	P
Pcsk5	proprotein convertase subtilisin/kexin type 5	P	P	M
Psap	prosaposin	P	P	P

Psap	prosaposin	P	M	P
Ptges2	prostaglandin E synthase 2	P	P	P
Ptgis	prostaglandin I2 (prostacyclin) synthase	P	P	P
Ptov1	prostate tumor over expressed gene 1	P	P	P
Ptov1	prostate tumor over expressed gene 1	P	P	P
Psmc1	protease (prosome, macropain) 26S subunit, ATPase 1	P	P	P
Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	P	P	P
Psmc1	Protease (prosome, macropain) 28 subunit, alpha+E2085	P	P	P
Prss11	protease, serine, 11 (Igf binding)	A	P	P
Prss19	protease, serine, 19 (neuropsin)	P	P	P
Prss25	protease, serine, 25	P	P	P
Prss25	protease, serine, 25	P	P	P
Psmc3	proteaseome (prosome, macropain) 28 subunit, 3	P	P	P
Psmc2	proteasome (prosome, macropain) 26S subunit, ATPase 2	P	P	P
Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	P	P	P
Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	P	P	P
Psmc3	proteasome (prosome, macropain) 26S subunit, ATPase 3	P	P	P
Psmc1	proteasome (prosome, macropain) 26S subunit, non-ATPase, 1	P	P	P
Psmc11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	P	P	P
Psmc11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	P	P	P
Psmc12	proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	P	P	P
Psmc13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	P	P	P
Psmc3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3	P	P	P
Psmc4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	P	P	P
Psmc5	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	P	P	P
Psmc7	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	P	P	P
Psmc8	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	P	P	P
Psmc9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	P	P	P
Psmc2	proteasome (prosome, macropain) 28 subunit, beta	P	P	P
Psmc1	proteasome (prosome, macropain) subunit, alpha type 1	P	P	P
Psmc2	proteasome (prosome, macropain) subunit, alpha type 2	P	P	P
Psmc3	proteasome (prosome, macropain) subunit, alpha type 3	P	P	P
Psmc4	proteasome (prosome, macropain) subunit, alpha type 4	P	P	P
Psmc5	proteasome (prosome, macropain) subunit, alpha type 5	P	P	P
Psmc6	proteasome (prosome, macropain) subunit, alpha type 6	P	P	P
Psmc7	proteasome (prosome, macropain) subunit, alpha type 7	P	P	P
Psmc1	proteasome (prosome, macropain) subunit, beta type 1	P	P	P
Psmc2	proteasome (prosome, macropain) subunit, beta type 2	P	P	P
Psmc3	proteasome (prosome, macropain) subunit, beta type 3	P	P	P
Psmc4	proteasome (prosome, macropain) subunit, beta type 4	P	P	P
Psmc5	proteasome (prosome, macropain) subunit, beta type 5	P	P	P
Psmc5	proteasome (prosome, macropain) subunit, beta type 5	P	P	P
Psmc5	proteasome (prosome, macropain) subunit, beta type 5	A	P	P
Psmc6	proteasome (prosome, macropain) subunit, beta type 6	P	P	P
Psmc7	proteasome (prosome, macropain) subunit, beta type 7	P	P	P
Psmc1	proteasome beta-subunit C5	P	P	P
Ppqb	protective protein for beta-galactosidase	P	P	P
Pin1	protein (peptidyl-prolyl cis/trans isomerase) NIMA-interacting 1	P	P	P
Procr	protein C receptor, endothelial	P	P	P
Pdir-(p)	protein disulfide isomerase-related	P	M	P
P5-(p)	protein disulfide isomerase-related protein	P	P	P
P5-(p)	protein disulfide isomerase-related protein	P	P	P
Pias3	protein inhibitor of activated STAT 3	P	A	P
Prkcs	protein kinase C substrate 80K-H	P	P	P
Prkca	protein kinase C, alpha	M	P	P
Prkcd	protein kinase C, delta	P	P	P
Prkcd	protein kinase C, delta	P	P	P
Pkig	protein kinase inhibitor, gamma	P	P	P
Prkab1	protein kinase, AMP-activated, beta 1 non-catalytic subunit	P	P	P
Prkar1a	protein kinase, cAMP dependent regulatory, type I, alpha	P	P	P
Prkacb	protein kinase, cAMP dependent, catalytic, beta	P	P	P
Prkdc	protein kinase, DNA activated, catalytic polypeptide	M	P	P

Ppp3r1	protein phosphatase 3, regulatory subunit B, alpha isoform (calcineurin B, type I)	P	P	P
Ppp1cb	protein phosphatase 1, catalytic subunit, beta isoform	P	P	P
Ppp1cc	protein phosphatase 1, catalytic subunit, gamma isoform	P	P	P
Ppp1r14b	protein phosphatase 1, regulatory (inhibitor) subunit 14B	P	P	P
Ppp1r7	protein phosphatase 1, regulatory (inhibitor) subunit 7	P	P	P
Ppm1a	protein phosphatase 1A, magnesium dependent, alpha isoform	P	P	P
Ppm1b	protein phosphatase 1B, magnesium dependent, beta isoform	P	P	P
Ppm1g	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	P	P	P
Ppp2r1a	protein phosphatase 2 (formerly 2A), regulatory subunit A (PR 65), alpha isoform	P	P	P
Ppp2r5d	protein phosphatase 2, regulatory subunit B (B56), delta isoform	P	A	P
Ppp2r5C	protein phosphatase 2A B'alpha3 regulatory subunit mRNA	P	P	P
Ppp2ca	protein phosphatase 2a, catalytic subunit, alpha isoform	P	P	P
Ppp2cb	protein phosphatase 2a, catalytic subunit, beta isoform	P	P	P
Ppp2r4	protein phosphatase 2A, regulatory subunit B (PR 53)	P	P	P
Ppp3ca	protein phosphatase 3, catalytic subunit, alpha isoform	P	P	P
Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	A	P	P
Ppp4c	protein phosphatase 4, catalytic subunit	P	P	P
Ppp5c	protein phosphatase 5, catalytic subunit	P	A	P
Prc1	protein regulator of cytokinesis 1-like	P	P	P
Ptp4a1	protein tyrosine phosphatase 4a1	P	P	P
Ptp4a2	protein tyrosine phosphatase 4a2	P	P	P
Ptp4a3	protein tyrosine phosphatase 4a3	A	P	P
Ptpn1	protein tyrosine phosphatase, non-receptor type 1	P	P	P
Ptpn13	protein tyrosine phosphatase, non-receptor type 13	P	P	P
Ptpn14	protein tyrosine phosphatase, non-receptor type 14	P	P	P
Ptpn2	protein tyrosine phosphatase, non-receptor type 2	P	P	P
Ptpn9	protein tyrosine phosphatase, non-receptor type 9	P	P	P
Ptpnj	protein tyrosine phosphatase, receptor type, J	P	A	P
Ptpnk	protein tyrosine phosphatase, receptor type, K	P	P	P
Ptpnr	protein tyrosine phosphatase, receptor type, R	P	P	A
Ptpns	protein tyrosine phosphatase, receptor type, S	P	A	P
Pkrir	P58 repressor+E2239	P	P	P
Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	P	P	P
Pcmt1	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	P	P	P
Tpst1	protein-tyrosine sulfotransferase 1	P	P	P
Plp2	proteolipid protein 2	P	P	P
Ptma	prothymosin alpha	P	P	P
Pim1	proviral integration site 1	P	P	P
PRUNEM1	PRUNEM1	P	P	P
Hba-ps3	pseudogene for alpha-globin	P	A	P
---	PTD008 protein	P	P	P
Ptk2	PTK2 protein tyrosine kinase 2	P	P	P
Ptk2b	PTK2 protein tyrosine kinase 2 beta	P	M	P
Ptk9l	PTK9 protein tyrosine kinase 9-like (A6-related protein)	P	P	M
Pum2	pumilio 2 (Drosophila)	P	P	P
Pura	purine rich element binding protein A	P	P	P
Pnp	purine-nucleoside phosphorylase	P	P	P
P2rx4	purinergic receptor P2X, ligand-gated ion channel 4	P	P	M
P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	P	P	P
Psa	puromycin-sensitive aminopeptidase	P	P	P
Phf	putative homeodomain transcription factor	P	A	P
Mrs3/4-(p)	putative mitochondrial solute carrier	P	M	P
Punc	putative neuronal cell adhesion molecule	P	P	P
Pdhd	pyruvate dehydrogenase (lipoamide) beta	P	P	P
Pdha1	pyruvate dehydrogenase E1 alpha 1	P	P	P
Pdk3	pyruvate dehydrogenase kinase, isoenzyme 3	P	P	P
Pkm2	pyruvate kinase, muscle	P	P	P
Pkm2	pyruvate kinase, muscle	P	P	P
qk	quaking	P	P	P
qk	quaking	P	P	P
Qdpr	quinoid dihydropteridine reductase	P	P	P
Rabac1	Rab acceptor 1 (prenylated)	P	P	P

Rabggtb	RAB geranylgeranyl transferase, b subunit	P	P	P
Rab1	RAB1, member RAS oncogene family	P	P	P
Rab10	RAB10, member RAS oncogene family	P	P	P
Rab10	RAB10, member RAS oncogene family	P	P	P
Rab11a	RAB11a, member RAS oncogene family	P	P	P
Rab11a	RAB11a, member RAS oncogene family	P	P	P
Rab11b	RAB11B, member RAS oncogene family	P	P	P
Rab12	RAB12, member RAS oncogene family	P	P	P
Rab14	RAB14, member RAS oncogene family	P	P	P
Rab14	RAB14, member RAS oncogene family	P	P	M
Rab18	RAB18, member RAS oncogene family	P	P	P
Rab2	RAB2, member RAS oncogene family	P	P	P
Rab21	RAB21, member RAS oncogene family	P	P	P
Rab24	RAB24, member RAS oncogene family	P	P	P
Rab33b	RAB33B, member of RAS oncogene family	P	M	P
Rab34	RAB34, member of RAS oncogene family	P	P	P
Rab4a	RAB4A, member RAS oncogene family	P	P	P
Rab5a	RAB5A, member RAS oncogene family	P	P	P
Rab5c	RAB5C, member RAS oncogene family	A	P	P
Rab6ip1	Rab6 interacting protein 1	P	P	P
Rab6	RAB6, member RAS oncogene family	P	P	P
Rab6	RAB6, member RAS oncogene family	P	A	P
Rab7	RAB7, member RAS oncogene family	P	P	P
Rab9	RAB9, member RAS oncogene family	P	P	P
Rab5ep-(p)	rabaptin 5	P	P	P
Rab5ep-(p)	rabaptin 5	P	P	P
Rab5ep-(p)	rabaptin 5	P	A	P
Racgap1	Rac GTPase-activating protein 1	P	P	P
Rad17	RAD17 homolog (S. pombe)	P	P	P
Rad21	RAD21 homolog (S. pombe)	P	P	P
Rad23b	RAD23b homolog (S. cerevisiae)	P	P	P
Rad23b	RAD23b homolog (S. cerevisiae)	P	P	P
Rad50	RAD50 homolog (S. cerevisiae)	P	P	P
Rad51ap1	RAD51 associated protein 1	P	P	P
Rad51	RAD51 homolog (S. cerevisiae)	P	P	P
Rfng	radical fringe gene homolog, (Drosophila)	P	P	P
Rdx	radixin	P	P	P
Rae1	RAE1 RNA export 1 homolog (S. pombe)	P	P	P
Rae1	RAE1 RNA export 1 homolog (S. pombe)	M	P	P
Ralgds	ral guanine nucleotide dissociation stimulator	P	P	P
Rgl2	ral guanine nucleotide dissociation stimulator,-like 2	P	P	P
Ralbp1	ralA binding protein 1	P	P	P
Ranbp1	RAN binding protein 1	P	P	P
Ranbp16	RAN binding protein 16	P	P	P
Ranbp16	RAN binding protein 16	P	P	P
Ranbp9	RAN binding protein 9	P	P	P
Rangap1	RAN GTPase activating protein 1	P	P	P
Ran	RAN, member RAS oncogene family	P	P	P
Rin2	Ras and Rab interactor 2	P	P	P
Rassf1	Ras association (RalGDS/AF-6) domain family 1	P	P	P
Rassf5	Ras association (RalGDS/AF-6) domain family 5	P	A	P
Arha2	ras homolog gene family, member A2	P	P	P
Arha2	ras homolog gene family, member A2	P	P	P
Arhb	ras homolog gene family, member AB	P	P	P
Arhu	ras homolog gene family, member U	P	P	P
Arhu	ras homolog gene family, member U	P	A	P
Rasa3	RAS p21 protein activator 3	P	P	P
Rsu1	Ras suppressor protein 1	P	P	P
Rasd1	RAS, dexamethasone-induced 1	P	A	P
G3bp2-(p)	Ras-GTPase-activating protein (GAP<120>) SH3-domain binding protein 2	P	P	P
G3bp-(p)	Ras-GTPase-activating protein SH3-domain binding protein	P	P	P
Tc10-(p)	ras-like protein	P	P	P

Rit1	Ras-like without CAAX 1	P	P	P
Rasl2-9	RAS-like, family 2, locus 9	P	P	P
Rac1	RAS-related C3 botulinum substrate 1	P	P	P
Rdbp	RD RNA binding protein	P	P	P
Rdbp	RD RNA-binding protein	P	P	P
Rest	RE1-silencing transcription factor	P	P	P
Ramp2	receptor (calcitonin) activity modifying protein 2	P	P	P
Ror2	receptor tyrosine kinase-like orphan receptor 2	P	P	P
Ryk	receptor-like tyrosine kinase	P	P	P
Rga	recombination activating gene 1 gene activation	P	A	P
Rbpsuh	recombining binding protein suppressor of hairless (Drosophila)	P	A	P
Rex3	reduced expression 3	P	P	P
Rex3	reduced expression 3	P	P	P
Reln	reelin	A	P	P
Reg3a	regenerating islet-derived 3 alpha	P	A	P
Rrr-(p)	regulator for ribosome resistance homolog (S. cerevisiae)	P	P	P
Rgs16	regulator of G-protein signaling 16	P	A	P
Rgs19	regulator of G-protein signaling 19	P	P	P
Rgs19	regulator of G-protein signaling 19	P	P	P
Rgs19ip1	regulator of G-protein signaling 19 interacting protein 1	P	P	P
Rgs2	regulator of G-protein signaling 2	P	A	P
Rgs3	regulator of G-protein signaling 3	P	P	A
Rgs10	regulator of G-protein signalling 10	P	P	P
Rgs10	regulator of G-protein signalling 10	P	P	P
Rfxank	regulatory factor X-associated ankyrin-containing protein	A	P	P
Renbp	renin binding protein	P	P	P
Rfc2	replication factor C (activator 1) 2 (40kD)	P	P	P
Rfc3	replication factor C (activator 1) 3 (38 kDa)	P	P	P
Rfc5	replication factor C (activator 1) 5 (36.5 kDa)	P	P	P
Recc1	replication factor C, 140 kDa	P	P	P
Rpa1	replication protein A1 (70 kDa)	P	P	P
Rpa2	replication protein A2	P	A	P
Req	requiem	P	P	P
Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	P	M	P
Rcn	reticulocalbin	P	P	P
Rcn2	reticulocalbin 2	P	P	P
Rtn3	reticulon 3	P	P	P
Rtn3	reticulon 3	P	P	P
Rtn3	reticulon 3	P	A	P
Rtn4	reticulon 4	P	P	P
Rp9h	retinitis pigmentosa 9 homolog (human)	P	P	P
Rpgr	retinitis pigmentosa GTPase regulator	P	M	P
Rbbp4	retinoblastoma binding protein 4	P	P	P
Rbbp6	retinoblastoma binding protein 6	P	P	P
Rbbp7	retinoblastoma binding protein 7	P	P	P
Rbbp9	retinoblastoma binding protein 9	P	P	P
Rbl1	retinoblastoma-like 1 (p107)	P	A	P
Raet1c	retinoic acid early transcript gamma	P	P	P
Rxrip110	retinoid X receptor interacting protein 110	A	P	P
Risc-(p)	retinoid-inducible serine carboxypeptidase	P	P	P
Rbp1	retinol binding protein 1, cellular	P	P	P
Rbp4	retinol binding protein 4, plasma	P	P	P
Rdh11	retinol dehydrogenase 11	P	P	P
Ris2	retroviral integration site 2	P	P	P
Ris2	retroviral integration site 2	P	P	P
Rev3l	REV3-like, catalytic subunit of DNA polymerase zeta RAD54 like E2419	P	P	P
Reck	reversion-inducing-cysteine-rich protein with kazal motifs	P	M	P
Arhgdia	Rho GDP dissociation inhibitor (GDI) alpha	P	P	P
Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	P	P	P
Rhoip3-(p)	Rho interacting protein 3	P	P	P
Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	P	P	A
Rock1	Rho-associated coiled-coil forming kinase 1	P	A	P

Rock1	Rho-associated coiled-coil forming kinase 1	A	P	P
Rock2	Rho-associated coiled-coil forming kinase 2	P	P	P
Rnaseh1	ribonuclease H1	A	P	P
Rnasep2-(p)	ribonuclease P2	P	P	P
Rnh1	ribonuclease/angiogenin inhibitor 1	P	A	P
Rnps1	ribonucleic acid binding protein S1	P	P	P
Rrm1	ribonucleotide reductase M1	P	P	P
Rrm2	ribonucleotide reductase M2	P	P	P
Rpn1	ribophorin I	P	P	P
Rpn1	ribophorin I	P	P	P
Rpn2	ribophorin II	P	P	P
Rpn2	ribophorin II	P	P	P
Rpia	ribose 5-phosphate isomerase A	P	P	P
Rpl10	ribosomal protein 10	P	P	P
Rpl10	ribosomal protein 10	P	P	P
Rpl10a	ribosomal protein L10A	P	P	P
Rpl10a	ribosomal protein L10A	P	P	P
Rpl13	ribosomal protein L13	P	P	P
Rpl13a	ribosomal protein L13a	P	P	P
Rpl18	ribosomal protein L18	P	P	P
Rpl19	ribosomal protein L19	P	P	P
Rpl21	ribosomal protein L21	P	P	P
Rpl22	ribosomal protein L22	P	A	P
Rpl24	ribosomal protein L24	P	P	P
Rpl26	ribosomal protein L26	P	P	P
Rpl27a	ribosomal protein L27a	P	P	P
Rpl27a	ribosomal protein L27a	P	P	P
Rpl28	ribosomal protein L28	P	P	P
Rpl3	ribosomal protein L3	P	P	P
Rpl3	ribosomal protein L3	P	P	P
Rpl30	ribosomal protein L30	P	P	P
Rpl36	ribosomal protein L36	P	P	P
Rpl37a	ribosomal protein L37a	P	P	P
Rpl41	ribosomal protein L41	P	P	P
Rpl44	ribosomal protein L44	P	P	P
Rpl44	ribosomal protein L44	P	P	P
Rpl5	ribosomal protein L5	P	P	P
Rpl6	ribosomal protein L6	P	P	P
Rpl7	ribosomal protein L7	P	P	P
Rpl7	ribosomal protein L7	P	P	P
Rpl7a	ribosomal protein L7a	P	P	P
Rpl8	ribosomal protein L8	P	P	P
Rps11	ribosomal protein S11	P	P	P
Rps12	ribosomal protein S12	P	P	P
Rps16	ribosomal protein S16	P	P	P
Rps17	ribosomal protein S17	P	P	P
Rps18	ribosomal protein S18	P	P	P
Rps19	ribosomal protein S19	P	P	P
Rps2	ribosomal protein S2	P	P	P
Rps23	ribosomal protein S23	P	P	P
Rps25	ribosomal protein S25	P	P	P
Rps26	ribosomal protein S26	P	P	P
Rps27	ribosomal protein S27	P	P	P
Rps27	ribosomal protein S27	M	P	P
Rps27a	ribosomal protein S27a	P	P	P
Rps28	ribosomal protein S28	P	P	P
Rps3	ribosomal protein S3	P	P	P
Rps3a	ribosomal protein S3a	P	P	P
Rps4x	ribosomal protein S4, X-linked	P	P	P
Rps5	ribosomal protein S5	P	P	P
Rps6	ribosomal protein S6	P	P	P
Rps6ka1	ribosomal protein S6 kinase polypeptide 1	P	P	P

Rps6ka2	ribosomal protein S6 kinase, 90kD, polypeptide 2	P	P	P
RpS7	ribosomal protein S7	P	P	P
Rps8	ribosomal protein S8	P	P	P
Rplp1	ribosomal protein, large, P1	P	P	P
Rplp1	ribosomal protein, large, P1	P	P	P
Rnf19	ring finger protein (C3HC4 type) 19	P	P	P
Rnf10	ring finger protein 10	P	P	P
Rnf11	ring finger protein 11	P	P	P
Rnf13	ring finger protein 13	P	M	P
Rnf14	ring finger protein 14	P	P	P
Rnf2	ring finger protein 2	P	P	P
Rnf34	ring finger protein 34	P	P	P
Rnf4	ring finger protein 4	P	P	P
Rnf44	ring finger protein 44	P	P	P
Rnf5	ring finger protein 5	P	P	P
Rnf7	ring finger protein 7	P	P	P
Rnf8	ring finger protein 8	P	P	P
Rbx1	ring-box 1	P	P	P
Rbx1	ring-box 1	P	P	P
Refbp1	RNA and export factor binding protein 1	P	P	P
Rbm8	RNA binding motif protein	P	P	P
Rbm10	RNA binding motif protein 10	P	P	P
Rbm14	RNA binding motif protein 14	P	P	P
Rbm3	RNA binding motif protein 3	P	P	P
Rbmx	RNA binding motif protein, X chromosome	P	P	P
Rbmx	RNA binding motif protein, X chromosome	P	P	P
Rbmxt	RNA binding motif protein, X chromosome retrogene	P	P	P
Rbms1	RNA binding motif, single stranded interacting protein 1	P	P	P
Rbms2	RNA binding motif, single stranded interacting protein 2	P	P	P
Rbpms	RNA binding protein gene with multiple splicing	P	P	P
Rbpms	RNA binding protein gene with multiple splicing	P	P	P
Dj1-(p)	RNA binding protein regulatory subunit	P	P	P
Rnac-(p)	RNA cyclase homolog	P	P	P
Rnglt	RNA guanylyltransferase and 5'-phosphatase	P	A	P
Rpo1-1	RNA polymerase 1-1 (40 kDa subunit)	P	P	P
Rpo1-1	RNA polymerase 1-1 (40 kDa subunit)	P	P	P
Rpo1-2	RNA polymerase 1-2 (128 kDa subunit)	P	P	P
Rpo1-3	RNA polymerase 1-3 (16 kDa subunit)	P	P	P
Rpo1-4	RNA polymerase 1-4 (194 kDa subunit)	P	P	P
Paf53-(p)	RNA polymerase I associated factor, 53 kD	P	P	P
Rnpc1	RNA-binding region (RNP1, RRM) containing 1	P	P	P
Rnpc2	RNA-binding region (RNP1, RRM) containing 2	P	P	P
Rttn	rotatin	P	P	P
Rmp-(p)	RPB5-mediating protein	P	P	P
Rmp-(p)	RPB5-mediating protein	M	P	P
Runx1	runt related transcription factor 1	A	P	P
Ruvbl1	RuvB-like protein 1	P	P	P
Ruvbl2	RuvB-like protein 2	P	P	P
Rw1-(p)	RW1 protein	P	P	P
Ryr3	ryanodine receptor 3	P	A	P
S100a1	S100 calcium binding protein A1	P	P	A
S100a10	S100 calcium binding protein A10 (calpactin)	P	P	P
S100a11	S100 calcium binding protein A11 (calizzarin)	P	P	P
S100a13	S100 calcium binding protein A13	P	P	A
S100a13	S100 calcium binding protein A13	P	P	A
S100a14	S100 calcium binding protein A14	P	P	P
S100a6	S100 calcium binding protein A6 (calcyclin)	P	P	P
Sah	SA rat hypertension-associated homolog	P	P	P
Sacm1l	SAC1 (supressor of actin mutations 1, homolog)-like (S. cerevisiae)	P	P	P
Sacm2l	SAC2 (supressor of actin mutations 2, homolog)-like (S. cerevisiae)	P	P	P
Ahcy	S-adenosylhomocysteine hydrolase	P	P	P
Ahcy	S-adenosylhomocysteine hydrolase	P	P	P

Ahcy	S-adenosylhomocysteine hydrolase	P	P	P
Amd1	S-adenosylmethionine decarboxylase 1	P	P	P
Amd3	S-adenosylmethionine decarboxylase 3	P	P	P
Amd3	S-adenosylmethionine decarboxylase 3	P	P	A
Sall3	sal-like 3 (Drosophila)	P	P	P
Samhd1	SAM domain and HD domain, 1	P	P	P
Sara	SAR1a gene homolog (S. cerevisiae)	P	P	P
Sgcb	sarcoglycan, beta (43kD dystrophin-associated glycoprotein)	P	M	P
Sgce	sarcoglycan, epsilon	P	P	P
Simap	sarcolemma associated protein	P	P	P
Skz1-(p)	SCAN-KRAB-zinc finger gene 1	P	P	P
Scarb1	scavenger receptor class B, member 1	P	P	P
Schip1	schwannomin interacting protein 1	P	P	P
Scotin-(p)	scotin gene	P	P	P
Sec13r	SEC13 related gene (S. cerevisiae)	P	P	P
Sec22l1	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)	P	P	P
Sec23a	SEC23A (S. cerevisiae)	P	P	P
Sec23b	SEC23B (S. cerevisiae)	P	P	P
Sec61a	SEC61, alpha subunit (S. cerevisiae)	P	P	P
Sec61a	SEC61, alpha subunit (S. cerevisiae)	P	P	P
Sec61a2-(p)	SEC61, alpha subunit 2 (S. cerevisiae)	P	P	P
Sec61g	SEC61, gamma subunit (S. cerevisiae)	P	P	P
Sparc	secreted acidic cysteine rich glycoprotein	P	P	P
Sparc	secreted acidic cysteine rich glycoprotein	P	M	P
Sfrp2	secreted frizzled-related sequence protein 2	P	A	P
Sct	secretin	P	P	M
Scamp1	secretory carrier membrane protein 1	P	P	P
Scamp2	secretory carrier membrane protein 2	P	P	P
Scamp3	secretory carrier membrane protein 3	P	P	P
Slpi	secretory leukocyte protease inhibitor	P	P	P
Sel1h	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	P	P	P
Selel	selectin, endothelial cell, ligand	P	P	P
Selel	selectin, endothelial cell, ligand	P	P	P
Shyc	selective hybridizing clone	P	P	P
Sps2	selenophosphate synthetase 2	P	P	P
Sema4f	sema domain, lg domain, TM domain, and short cytoplasmic domain	P	P	P
Sema4b	sema domain, lg domain, TM domain and short cytoplasmic domain, 4B	P	P	P
Sept2	septin 2	P	P	P
Sept4	septin 4	P	A	P
Sept7	septin 7	P	P	P
Sept9	septin 9	P	P	P
Sqstm1	sequestosome 1	P	P	P
Serpinb6	serine (or cysteine) proteinase inhibitor, clade B, member 6	P	P	P
Serpine2	serine (or cysteine) proteinase inhibitor, clade E, member 2	P	A	P
Serpinh1	serine (or cysteine) proteinase inhibitor, clade H, member 1	P	P	P
Shmt1	serine hydroxymethyl transferase 1 (soluble)	P	P	P
Sptlc1	serine palmitoyltransferase, long chain base subunit 1	P	P	P
Sptlc2	serine palmitoyltransferase, long chain base subunit 2	P	P	P
Spint1	serine protease inhibitor, Kunitz type 1	P	A	P
Srr	serine racemase	P	P	P
Srrm1	serine/arginine repetitive matrix 1	P	P	P
Srpk2	serine/arginine-rich protein specific kinase 2	P	P	P
Stk11	serine/threonine kinase 11+E1180	P	M	P
Stk16	serine/threonine kinase 16	P	P	P
Stk18	serine/threonine kinase 18	P	P	P
Stk2	serine/threonine kinase 2	P	P	P
Stk39	serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	P	A	P
Stk6	serine/threonine kinase 6	P	P	P
Strap	serine/threonine kinase receptor associated protein	P	P	P
Scr59-(p)	serine-rich spermatocytes and round spermatid protein, 59kDa	P	P	P
Sdbcag84	serologically defined breast cancer antigen 84	P	P	P
Sgk	serum/glucocorticoid regulated kinase	P	P	P

Snk	serum-inducible kinase	P	M	P
Setdb1	SET domain, bifurcated 1	P	P	P
Setdb1	SET domain, bifurcated 1	A	P	P
Set	SET translocation	P	P	P
Set	SET translocation	P	P	P
Siah1a	seven in absentia 1A	A	P	P
Siah1b	seven in absentia 1B	M	P	P
Siah2	seven in absentia 2	P	P	P
Sh3d3	SH3 domain protein 3	P	P	A
Sh3bgr1	SH3-binding domain glutamic acid-rich protein like	P	P	P
Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	P	P	P
Shkbp1	Sh3kbp1 binding protein 1	P	P	P
Scoc	short coiled coil protein	A	P	P
shrm	shroom	P	P	P
Siat1	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	P	P	P
Siat10	sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	P	A	P
Siat8c	sialyltransferase 8 (alpha-2, 8-sialyltransferase) C	A	P	P
Siat8d	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D	P	P	P
Siat9	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	P	P	A
Sfxn1	sideroflexin 1	P	P	P
Spc18-(p)	signal peptidase complex (18kD)	P	P	P
Srp14	signal recognition particle 14 kDa (homologous Alu RNA binding protein)	P	P	P
Srp9	signal recognition particle 9 kDa	P	P	P
Ssr1	signal sequence receptor, alpha	P	P	P
Ssr2	signal sequence receptor, beta	P	P	P
Stat3	signal transducer and activator of transcription 3	P	P	P
Stat3	signal transducer and activator of transcription 3	P	P	A
Stat5a	signal transducer and activator of transcription 5A	A	P	P
Statip1	signal transducer and activator of transcription interacting protein 1	P	P	P
Stam	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	P	P	P
Siig41	silica-induced gene 41	P	P	P
Sap30	sin3 associated polypeptide, 30kD	P	P	P
Six4	sine oculis-related homeobox 4 homolog (Drosophila)	P	P	P
Six4	sine oculis-related homeobox 4 homolog (Drosophila)	P	A	P
Ssbp2	single-stranded DNA binding protein 2	P	P	P
Ssa2	Sjogren syndrome antigen A2	P	P	P
Ssb	Sjogren syndrome antigen B	P	P	P
Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	P	P	P
Skiip	SKI interacting protein	M	P	P
Ski	Sloan-Kettering viral oncogene homolog	P	P	P
Smap-(p)	small acidic protein	P	P	P
Smfn	small fragment nuclease	P	P	P
Sgt	small glutamine-rich tetratricopeptide repeat (TPR)-containing	P	P	P
Gtr2	small GTPase, homolog (S. cerevisiae)	P	P	P
Scye1	small inducible cytokine subfamily E, member 1	P	P	P
Snrpb	small nuclear ribonucleoprotein B	P	P	P
Snrpd1	small nuclear ribonucleoprotein D1	P	P	P
Snrpd2	small nuclear ribonucleoprotein D2	P	P	P
Snrpe	small nuclear ribonucleoprotein E	P	P	P
Snrpa	small nuclear ribonucleoprotein polypeptide A	A	P	P
Snrpa1	small nuclear ribonucleoprotein polypeptide A'	P	P	P
Snrpg	small nuclear ribonucleoprotein polypeptide G	P	P	P
Spr2a	small proline-rich protein 2A	M	P	P
Spec1-(p)	small protein effector 1 of Cdc42	P	P	P
Smo	smoothened homolog (Drosophila)	P	P	P
Smt3h1	SMT3 (suppressor of mif two, 3) homolog 1 (S. cerevisiae)	P	P	P
Smt3ip1-(p)	smt3-specific isopeptidase 1	P	P	P
Snai2	snail homolog 2 (Drosophila)	P	P	P
Snrk	SNF related kinase	P	A	P
Scn1b	sodium channel, voltage-gated, type I, beta polypeptide	P	P	P
Slc1a7	solute carrier family 1, member 7	P	M	P
Slc11a2	solute carrier family 11+E2572, member 2	P	P	P

Slc11a2	solute carrier family 11, member 2	P	P	P
Slc12a2	solute carrier family 12, member 2	P	P	P
Slc12a4	solute carrier family 12, member 4	P	A	P
Slc12a7	solute carrier family 12, member 7	P	P	P
Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	P	P	P
Slc16a2	solute carrier family 16 (monocarboxylic acid transporters), member 2	P	P	P
Slc19a1	solute carrier family 19 (sodium/hydrogen exchanger), member 1	A	P	P
Slc2a1	solute carrier family 2 (facilitated glucose transporter), member 1	P	P	P
Slc2a2	solute carrier family 2 (facilitated glucose transporter), member 2	P	P	A
Slc2a3	solute carrier family 2 (facilitated glucose transporter), member 3	P	P	P
Slc20a1	solute carrier family 20, member 1	P	P	P
Slc25a4	solute carrier family 25, member 4	P	P	P
Slc25a5	solute carrier family 25, member 5	P	P	P
Slc25a1	solute carrier family 25, member 1	P	P	P
Slc25a1	solute carrier family 25, member 1	P	P	P
Slc25a15	solute carrier family 25, member 15	P	P	P
Slc25a11	solute carrier family 25, member 11	P	P	P
Slc25a17	solute carrier family 25, member 17	P	P	P
Slc29a1	solute carrier family 29 (nucleoside transporters), member 1	P	P	P
Slc3a2	solute carrier family 3, member 2	P	P	P
Slc30a1	solute carrier family 30 (zinc transporter), member 1	P	P	P
Slc30a3	solute carrier family 30 (zinc transporter), member 3	P	A	P
Slc30a5	solute carrier family 30 (zinc transporter), member 5	P	P	P
Slc30a5	solute carrier family 30 (zinc transporter), member 5	P	P	P
Slc31a1	solute carrier family 31, member 1	P	P	P
Slc31a1	solute carrier family 31, member 1	P	P	P
Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member 1	P	P	P
Slc38a4	solute carrier family 38, member 4	P	P	P
Slc4a1ap	solute carrier family 4 (anion exchanger), member 1, adaptor protein	P	A	P
Slc4a2	solute carrier family 4 (anion exchanger), member 2	P	P	P
Slc6a6	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	P	P	P
Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	P	P	P
Son	Son cell proliferation protein	P	P	P
Sorbs1	sorbin and SH3 domain containing 1	P	P	P
Snx1	sorting nexin 1	P	P	P
Snx12	sorting nexin 12	P	A	P
Snx12	sorting nexin 12	A	P	P
Snx2	sorting nexin 2	P	P	P
Snx3	sorting nexin 3	P	P	P
Snx4	sorting nexin 4	P	P	P
Snx5	sorting nexin 5	P	P	P
Snx9	sorting nexin 9	P	P	P
Solt	SoxLZ/Sox6 leucine zipper binding protein in testis	P	P	P
Spg4	spastic paraplegia 4 homolog (human)	P	P	P
Spg4	spastic paraplegia 4 homolog (human)	A	P	P
Satb1	special AT-rich sequence binding protein 1	P	P	P
Spop	speckle-type POZ protein	P	P	P
Ssfa1	sperm specific antigen 1	P	P	P
Spnr	spermatid perinuclear RNA binding protein	P	P	P
Spaf	spermatogenesis associated factor	P	P	P
Srm	spermidine synthase	P	P	P
---	spermidine synthase pseudogene	P	P	P
Sat	spermidine/spermine N1-acetyl transferase	P	P	P
Sms	spermine synthase	P	P	P
Sms	spermine synthase	P	P	P
Smpd1	sphingomyelin phosphodiesterase 1, acid lysosomal	P	A	P
Sgpl1	sphingosine phosphate lyase 1	P	P	P
Spin	spindlin	P	P	P
Spin	spindlin	P	P	P
Sca10	spinocerebellar ataxia 10 homolog (human)	P	P	P
Sca10	spinocerebellar ataxia 10 homolog (human)	P	P	P
Sca2	spinocerebellar ataxia 2 homolog (human)	P	P	P

Sca2	spinocerebellar ataxia 2 homolog (human)	P	P	P
Syk	spleen tyrosine kinase	P	A	P
Sf3a2	splicing factor 3a, subunit 2, 66kD	P	P	P
Sf3b1	splicing factor 3b, subunit 1, 155 kDa	P	P	P
Sf3b1	splicing factor 3b, subunit 1, 155 kDa	P	P	P
Sfpq	splicing factor proline/glutamine rich	P	P	P
Sfpq	splicing factor proline/glutamine rich E2649	P	P	P
Sfrs9	splicing factor, arginine/serine rich 9 (25 kDa)	P	P	P
Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	P	P	P
Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	A	P	P
Sfrs10	splicing factor, arginine/serine-rich 10	P	P	P
Sfrs2	splicing factor, arginine/serine-rich 2 (SC-35)	P	P	P
Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	P	P	P
Sfrs3	splicing factor, arginine/serine-rich 3 (SRp20)	P	P	P
Sfrs4	splicing factor, arginine/serine-rich 4 (SRp75)	P	P	P
Sfrs4	splicing factor, arginine/serine-rich 4 (SRp75)	P	P	P
Sfrs5	splicing factor, arginine/serine-rich 5 (SRp40, HRS)	P	P	P
Shfdg1	split hand/foot deleted gene 1	P	P	P
Spry4	sprouty homolog 4 (Drosophila)	P	P	P
Spred2	sprouty protein with EVH-1 domain 2, related sequence	P	P	P
Sqle	squalene epoxidase	P	P	P
Sart1	squamous cell carcinoma antigen recognized by T-cells 1	P	A	P
Sart3	squamous cell carcinoma antigen recognized by T-cells 3	P	P	P
Sart3	squamous cell carcinoma antigen recognized by T-cells 3	P	P	P
Srcasm	Src activating and signaling molecule	P	P	P
Scap2	src family associated phosphoprotein 2	P	P	P
Shc1	src homology 2 domain-containing transforming protein C1	P	P	P
Sox10	SRY-box containing gene 10	P	P	P
Sox11	SRY-box containing gene 11	P	P	P
Sox17	SRY-box containing gene 17	P	P	P
Sox18	SRY-box containing gene 18	P	P	P
Sox18	SRY-box containing gene 18	P	A	P
Sox2	SRY-box containing gene 2	P	P	P
Sox3	SRY-box containing gene 3	P	P	P
Sox4	SRY-box containing gene 4	P	P	P
Sox4	SRY-box containing gene 4	P	P	P
Sox7	SRY-box containing gene 7	P	P	P
Stab1	stabilin 1	P	P	P
Snd1-(p)	staphylococcal nuclease domain containing 1	P	P	P
Stard3	START domain containing 3	P	P	P
Stmn1	stathmin 1	P	P	P
Scd1	stearoyl-Coenzyme A desaturase 1	P	P	P
Scd1	stearoyl-Coenzyme A desaturase 1	P	P	P
Scd1	stearoyl-Coenzyme A desaturase 1	P	P	P
Scd2	stearoyl-Coenzyme A desaturase 2	P	P	P
Scd2	stearoyl-Coenzyme A desaturase 2	P	P	P
Slbp	stem-loop binding protein	P	P	P
Slu7-(p)	step II splicing factor SLU7	P	P	P
Sra1	steroid receptor RNA activator 1	P	P	P
Scp2	sterol carrier protein 2, liver	P	P	P
Scp2	sterol carrier protein 2, liver	P	P	P
Sreb1	sterol regulatory element binding factor 1	P	P	P
Sc4mol	sterol-C4-methyl oxidase-like	P	P	P
Stub1	STIP1 homology and U-Box containing protein 1	P	P	P
Stoml2	stomatin (Epb7.2)-like 2	P	P	P
Stip1	stress-induced phosphoprotein 1	P	P	P
Strn3	striatin, calmodulin binding protein 3	P	P	P
Stag1	stromal antigen 1	P	M	P
Stag2	stromal antigen 2	P	P	P
Stag2	stromal antigen 2	P	P	P
Sdfr1	stromal cell derived factor receptor 1	P	P	P
Sdfr2	stromal cell derived factor receptor 2	P	P	P

Smap1-(p)	stromal membrane-associated protein	P	P	P
Ssrp1	structure specific recognition protein 1	P	P	P
Sdha	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	P	P	P
Sucg1	succinate-CoA ligase, GDP-forming, alpha subunit	P	P	P
Suc1a2	succinate-Coenzyme A ligase, ADP-forming, beta subunit	P	P	P
Sucg2	succinate-Coenzyme A ligase, GDP-forming, beta subunit	P	P	P
Sudd	sudD, suppressor of bimD6 homolog (Aspergillus nidulans)	P	P	P
Skiv2l	superkiller viralicidic activity 2-like (S. cerevisiae)	P	P	P
Sod1	superoxide dismutase 1, soluble	P	P	P
Sod2	superoxide dismutase 2, mitochondrial	P	P	P
Svil	supervillin	P	P	P
Socs2	suppressor of cytokine signaling 2	P	P	P
Socs3	suppressor of cytokine signaling 3	P	M	P
Sui1-rs1	suppressor of initiator codon mutations, related sequence 1 (S. cerevisiae)	P	P	P
Skd3	suppressor of K+ transport defect 3	P	A	P
Skd3	suppressor of K+ transport defect 3	P	A	P
Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	P	P	P
Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	P	P	P
Supt4h2	Supt4h2 gene	P	P	P
Supt4h2	Supt4h2 gene	P	P	P
Surf3	surfeit 3	P	P	P
Surf1	surfeit gene 1	P	P	P
Surf4	surfeit gene 4	P	P	P
Surf5	surfeit gene 5	P	P	P
Surf6	surfeit gene 6	P	P	P
Smn	survival motor neuron	P	P	P
Smarca4	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, a4	P	P	P
Smarca5	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, a5	P	P	P
Smarca5	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, a5	M	P	P
Smarb1	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, b1	P	P	P
Smarrc1	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, c1	P	P	P
Smarrd2	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, d2	P	P	P
Smarrc1	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, e1	P	P	P
Smarrc1	SWI/SNF related, matrix assoc., actin dependent chromatin regulator, f1	P	P	P
Smarrc1	SWI/SNF related, matrix assoc., actin dependent chromatin regulator+E2731, f1	M	P	P
Syn1	synapsin I	P	P	P
Sybl1	synaptobrevin like 1	P	P	P
Synj2bp	synaptotagmin 2 binding protein	P	P	P
Sypl	synaptophysin-like protein	P	P	P
Snap23	synaptosomal-associated protein, 23kD	P	P	P
Snap25bp	synaptosomal-associated protein, 25 kDa, binding protein	P	P	P
Snap25bp	synaptosomal-associated protein, 25 kDa, binding protein	P	P	P
Syt14	synaptotagmin-like 4	P	A	P
Syt14	synaptotagmin-like 4	P	A	P
Sbdn	synbindin	P	P	P
Sdcbp	syndecan binding protein	P	P	P
Ss18	synovial sarcoma translocation, Chromosome 18	P	P	P
Stx12	syntaxin 12	P	P	P
Stx18	syntaxin 18	P	P	P
Stx3	syntaxin 3	P	P	P
Stx4a	syntaxin 4A (placental)	P	P	P
Stx5a	syntaxin 5A	P	P	P
Stx6	syntaxin 6	P	A	P
Stx7	syntaxin 7	P	P	P
Stxbp2	syntaxin binding protein 2	P	P	A
Stxbp3	syntaxin binding protein 3	P	P	P
Snca	synuclein, alpha	A	P	P
Tccr	T cell cytokine receptor	P	P	P
Taf10	TAF10 RNA polymerase II, TBP-associated factor, 30 kDa	P	P	P
Taf15	TAF15 RNA polymerase II, TBP-associated factor, 68 kDa	P	A	P
Taf9	TAF9 RNA polymerase II, TBP-associated factor, 32 kDa	P	P	P
Taf9	TAF9 RNA polymerase II, TBP-associated factor, 32 kDa	P	P	P

Taf9	TAF9 RNA polymerase II, TBP-associated factor, 32 kDa	P	P	P
Tln	talín	P	P	M
Tln	talín	P	A	P
Tbk1	TANK-binding kinase 1	P	P	P
Tarbp2	TAR (HIV) RNA binding protein 2	P	P	P
Tardbp	TAR DNA binding protein	P	P	P
Tbp	TATA box binding protein	A	P	P
Taf1b	TATA box binding protein-associated factor, RNA polymerase I, B	P	M	P
Taf1c	TATA box binding protein+E2829-associated factor, RNA polymerase I, C	A	P	P
Tbpl1	TATA box binding protein-like 1	P	P	P
Tbx3	T-box 3	P	P	A
Tp120a-(p)	TBP-interacting protein	A	P	P
Tal1	T-cell acute lymphocytic leukemia 1	P	P	P
Timd2	T-cell immunoglobulin and mucin domain containing 2	P	P	A
Tiam1	T-cell lymphoma invasion and metastasis 1	P	P	P
Tcrg-V2	T-cell receptor gamma, variable 2	A	P	P
Tce2	T-complex expressed gene 2	P	P	P
Tcp1	t-complex protein 1	P	P	P
Tead2	TEA domain family member 2	P	P	P
Tead4	TEA domain family member 4	P	P	P
Tebp-(p)	telomerase binding protein, p23	P	P	P
Terf1	telomeric repeat binding factor 1	P	P	P
Terf2	telomeric repeat binding factor 2	P	P	P
Terf2ip	telomeric repeat binding factor 2, interacting protein	P	A	P
Tnc	tenascin C	P	A	P
Tera-(p)	teratocarcinoma expressed, serine rich	P	P	P
Tes	testis derived transcript	P	P	P
Tex189	testis expressed gene 189	P	P	P
Tex20	testis expressed gene 20	P	P	P
Tex261	testis expressed gene 261	P	P	P
Tex292	testis expressed gene 292	P	P	P
Tspyl	testis-specific protein, Y-encoded-like	P	A	P
Ttc3	tetratricopeptide repeat domain	P	P	P
Tgif	TG interacting factor	P	P	P
Tieg	TGFB inducible early growth response	P	P	P
Tieg	TGFB inducible early growth response	P	P	P
Th1l	TH1-like homolog (Drosophila)	P	P	P
Thop1	thimet oligopeptidase 1	P	P	M
Txn1	thioredoxin 1	P	P	P
Txn2	thioredoxin 2	P	P	P
Txndc1	thioredoxin domain containing	P	P	P
Txndc4	thioredoxin domain containing 4 (endoplasmic reticulum)	P	P	P
Txnrd1	thioredoxin reductase 1	P	P	P
Txnrd2	thioredoxin reductase 2	P	P	P
Txnl	thioredoxin-like (32kD)	P	P	P
Txnl2	thioredoxin-like 2	P	P	P
Tst	thiosulfate sulfurtransferase, mitochondrial	A	P	P
Thbs1	thrombospondin 1	P	P	M
Tk1	thymidine kinase 1	P	P	P
Tk2	thymidine kinase 2, mitochondrial	P	A	P
Tyms	thymidylate synthase	P	P	P
Tyms	thymidylate synthase	P	P	P
Tdg	thymine DNA glycosylase	P	P	P
Akt1	thymoma viral proto-oncogene 1	P	P	P
Tmpo	thymopoietin	P	P	P
Tmsb10	thymosin, beta 10	P	P	P
Tmsb4x	thymosin, beta 4, X chromosome	P	P	P
G22p1	thyroid autoantigen	P	P	P
Trip13	thyroid hormone receptor interactor 13	P	P	P
Trip6	thyroid hormone receptor interactor 6	P	P	P
Trap100-(p)	thyroid hormone receptor-associated protein 100 kDa	P	P	P
Tial1	Tial1 cytotoxic granule-associated RNA binding protein-like 1	P	P	P

Tjp1	tight junction protein 1	P	P	P
Timeless	timeless homolog (Drosophila)	P	P	P
Tfpi	tissue factor pathway inhibitor	P	P	P
Timp3	tissue inhibitor of metalloproteinases-3	P	P	P
Tstap35b	tissue specific transplantation antigen P35B	P	P	P
Tstap35b	tissue specific transplantation antigen P35B	P	P	P
Tstap35b	tissue specific transplantation antigen P35B	P	P	P
Traf4	Tnf receptor associated factor 4	P	P	P
Traf4	Tnf receptor associated factor 4	P	P	P
Traf3	Tnf receptor-associated factor 3	P	P	P
Top1	topoisomerase (DNA) I	P	P	P
Top2a	topoisomerase (DNA) II alpha	P	P	P
Top2b	topoisomerase (DNA) II beta	P	P	P
Tor1b	torsin family 1, member B	P	P	P
Tor2a	torsin family 2, member A	P	A	P
Tlk2	tousled-like kinase 2 (Arabidopsis)	P	P	P
Tparl	TPA regulated locus	P	P	P
Tsbp	TPR-containing, SH2-binding phosphoprotein	P	P	P
Ttrap	Traf and Tnf receptor associated protein	P	P	P
Tank	TRAF family member-associated Nf-kappa B activator	M	P	P
Traip	TRAF-interacting protein	A	P	P
Sp1	trans-acting transcription factor 1	P	P	P
Sp3	trans-acting transcription factor 3	P	P	P
Taldo1	transaldolase 1	P	P	P
Tcn2	transcobalamin 2	P	P	M
Tcea1	transcription elongation factor A (SII) 1	P	P	P
Tcea1	transcription elongation factor A (SII) 1	P	P	P
Tcea2	transcription elongation factor A (SII), 2	A	P	P
Tceb1l	transcription elongation factor B (SIII), polypeptide 1 (15 kDa),-like	P	P	P
Tceb3	transcription elongation factor B (SIII), polypeptide 3 (110kD)	P	P	P
Tceb3	transcription elongation factor B (SIII), polypeptide 3 (110kD)	P	P	P
Tcerg1	transcription elongation regulator 1 (CA150)	P	P	P
Tcf12	transcription factor 12	P	P	P
Tcf3	transcription factor 3	P	P	P
Tcf4	transcription factor 4	P	P	P
Tcf7	transcription factor 7, T-cell specific	P	P	P
Tcf7	transcription factor 7, T-cell specific	M	P	P
Tcfcp2	transcription factor CP2	P	A	P
Tfdp1	transcription factor Dp 1	P	P	P
Tfdp1	transcription factor Dp 1	P	P	P
Tcf14	transcription factor-like 4	P	P	P
Ttf1	transcription termination factor 1	P	A	P
Sin3a	transcriptional regulator, SIN3A (yeast)	P	P	P
Sin3b	transcriptional regulator, SIN3B (yeast)	P	P	P
Tob1	transducer of ErbB-2.1	A	P	P
Tbl3	transducin (beta)-like 3	P	P	P
Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	P	P	P
Tle3	transducin-like enhancer of split 3, homolog of Drosophila E(spl)	P	P	P
Trfr	transferrin receptor	P	P	P
Trp53	transformation related protein 53	P	P	P
Trp53	transformation related protein 53	P	P	P
Trp53bp1	transformation related protein 53 binding protein 1	P	P	P
Trp63	transformation related protein 63	P	A	P
Mdm1	transformed mouse 3T3 cell double minute 1	P	A	P
Mdm2	transformed mouse 3T3 cell double minute 2	P	P	P
Mdm4	transformed mouse 3T3 cell double minute 4	P	P	P
Tgfa	transforming growth factor alpha	P	A	P
Tgfb1i4	transforming growth factor beta 1 induced transcript 4	P	P	P
Tbrg1	transforming growth factor beta regulated gene 1	P	P	P
Tgfb2	transforming growth factor, beta 2	P	A	P
Tacc3	transforming, acidic coiled-coil containing protein 3	P	P	P
Tagln	transgelin	P	P	P

Tagln2	transgelin 2	P	P	P
TgN737Rpw	transgene insert site 737, insertional mutation, polycystic kidney disease	P	P	P
TgN737Rpw	transgene insert site 737, insertional mutation, polycystic kidney disease	P	A	P
Tgm2	transglutaminase 2, C polypeptide	P	P	A
Ttgn1	trans-golgi network protein 1	P	P	P
Ttgn1	trans-golgi network protein 1	A	P	P
Trpc4ap	transient receptor potential cation channel, C4+E2919 associated protein	P	P	P
Tnp1	transition protein 1	P	P	P
Tkt	transketolase	P	P	P
Tsnax	translin-associated factor X	P	P	P
Timm10	translocase of inner mitochondrial membrane 10 homolog (yeast)	M	P	P
Timm13a	translocase of inner mitochondrial membrane 13 homolog a (yeast)	P	P	P
Timm22	translocase of inner mitochondrial membrane 22 homolog (yeast)	P	P	P
Timm23	translocase of inner mitochondrial membrane 23 homolog (yeast)	P	P	P
Timm8a	translocase of inner mitochondrial membrane 8 homolog a (yeast)	P	P	P
Timm8b	translocase of inner mitochondrial membrane 8 homolog b (yeast)	P	P	P
Timm9	translocase of inner mitochondrial membrane 9 homolog (yeast)	P	P	P
Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	P	P	P
Timm17a	translocator of inner mitochondrial membrane 17 kDa, a	P	P	P
Timm17b	translocator of inner mitochondrial membrane 17 kDa, b	P	P	P
Timm44	translocator of inner mitochondrial membrane 44	P	P	P
Tm4sf2	transmembrane 4 superfamily member 2	P	P	P
Tm4sf6	transmembrane 4 superfamily member 6	P	P	P
Tm4sf7	transmembrane 4 superfamily member 7	P	P	P
Tm9sf1	transmembrane 9 superfamily member 1	P	P	P
Tm9sf2	transmembrane 9 superfamily member 2	P	P	P
Tmprss2	transmembrane protease, serine 2	P	P	A
Tmem4	transmembrane protein 4	P	P	P
Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	P	P	P
Ttr	transthyretin	P	P	A
Tbc1d1	tre-2/USP6, BUB2, cdc16) domain family, member 1	P	P	P
Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	P	P	P
Tff1	trefoil factor 1	P	P	P
Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	P	P	P
Trfp	Trf (TATA binding protein-related factor)-proximal protein homolog (Drosophila)	P	A	P
Trif-(p)	Trif gene	P	P	P
Trif-(p)	Trif gene	P	P	P
Tnrc11	trinucleotide repeat containing 11 (THR-associated protein, 230 kDa subunit)	P	P	P
Tpi	triosephosphate isomerase	P	P	P
Trim11	tripartite motif protein 11	P	A	P
Trim21	tripartite motif protein 21	M	P	P
Trim25	tripartite motif protein 25	P	P	P
Trim27	tripartite motif protein 27	P	P	P
Trim28	tripartite motif protein 28	P	P	P
Trim41	tripartite motif-containing 41	P	A	P
Tpp2	tripeptidyl peptidase II	P	A	P
Trnt1	tRNA nucleotidyl transferase, CCA-adding, 1	P	P	P
Tro	trophinin	P	P	P
Tmod3	tropomodulin 3	P	P	P
Tpm1	tropomyosin 1, alpha	P	P	P
Tncc	troponin C, cardiac/slow skeletal	P	A	P
Tnni1	troponin I, skeletal, slow 1	P	P	P
Tnnt2	troponin T2, cardiac	P	P	P
Wars	tryptophanyl-tRNA synthetase	P	P	P
Wars	tryptophanyl-tRNA synthetase	P	P	P
Wars	tryptophanyl-tRNA synthetase	P	P	P
Ttk	Ttk protein kinase	P	P	P
Tulp4	tubby like protein 4	P	P	P
Tulp3	tubby-like protein 3	P	P	P
Tsc1	tuberous sclerosis 1	P	M	P
Tsc2	tuberous sclerosis 2	P	P	P
Tsc2	tuberous sclerosis 2	P	P	P

Tbca	tubulin cofactor a	P	P	P
Tuba1	tubulin, alpha 1	P	P	P
Tuba1	tubulin, alpha 1	P	P	P
Tuba2	tubulin, alpha 2	P	P	P
Tuba4	tubulin, alpha 4	A	P	P
Tuba6	tubulin, alpha 6	P	P	P
Tuba7	tubulin, alpha 7	P	P	P
Tubb2	tubulin, beta 2	P	P	P
Tubb3	tubulin, beta 3	P	P	P
Tubb5	tubulin, beta 5	P	P	P
Tubb5	tubulin, beta 5	P	P	P
Tubgcp3	tubulin, gamma complex associated protein 3	P	P	P
Tbce	tubulin-specific chaperone e	P	P	P
Tfip11	tuftelin interacting protein 11	P	P	P
Tde1	tumor differentially expressed 1	P	P	P
Tde1l	tumor differentially expressed 1, like	P	P	P
Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	P	P	P
Tpd52	tumor protein D52	P	P	P
Tpd52l1	tumor protein D52-like 1	P	P	P
Tpt1	tumor protein, translationally-controlled 1	P	P	P
Tra1	tumor rejection antigen gp96	P	P	P
Trap1a	tumor rejection antigen P1A	P	P	P
Tacstd1	tumor-associated calcium signal transducer 1	P	P	P
Tssc3	tumor-suppressing subchromosomal transferable fragment 3	P	P	P
Tssc4	tumor-suppressing subchromosomal transferable fragment 4	P	P	P
Twist	twist gene homolog, (Drosophila)	P	P	P
Twg-(p)	twisted gastrulation protein	P	P	P
---	type IIB intracisternal A-particle element encoding integrase and gag	P	P	P
Tyro3	TYRO3 protein tyrosine kinase 3	P	A	P
Ywhab	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase AP, beta polypeptide	P	P	P
Ywhae	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase AP, epsilon polypeptide	P	P	P
Ywhah	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase AP, eta polypeptide	P	P	P
Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase AP, theta polypeptide	P	P	P
Ywhaq	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase AP, theta polypeptide	P	P	P
Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase AP, zeta polypeptide	P	P	P
Tie1	tyrosine kinase receptor 1	P	P	P
Tnk2	tyrosine kinase, non-receptor, 2	P	M	P
Yars	tyrosyl-tRNA synthetase	P	P	P
Snrp1c	U1 small nuclear ribonucleoprotein 1C	P	P	P
U2af26	U2 auxiliary factor 26	P	M	P
U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF)	P	P	P
U2af2	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF)	P	P	P
Snrbp2	U2 small nuclear ribonucleoprotein B	P	P	P
Murr1	U2af1-rs1 region 1	P	P	P
U3-55k-(p)	U3 snoRNP-associated 55-kDa protein	P	P	P
Snrp116-(p)	U5 small nuclear ribonucleoprotein 116 kDa	P	P	P
Lsm4-(p)	U6 snRNA-associated SM-like protein 4	P	P	P
Ubqln1	ubiquilin 1	P	P	P
Ubqln2	ubiquilin 2	P	P	P
Uqcrb	ubiquinol-cytochrome c reductase binding protein	P	P	P
Uqcrc1	ubiquinol-cytochrome c reductase core protein 1	P	P	P
Uchrp	ubiquitin c-terminal hydrolase related polypeptide	P	P	P
Ubb	ubiquitin B	P	P	P
Ubc	ubiquitin C	P	P	P
Ubc	ubiquitin C	P	P	P
Ubc-rs2	ubiquitin C, related sequence 2	P	P	P
Uchl5	ubiquitin carboxyl-terminal esterase L5	P	P	P
Ubce7ip3-(p)	ubiquitin conjugating enzyme 7 interacting protein 3	P	P	P
Ubce7ip5-(p)	ubiquitin conjugating enzyme 7 interacting protein 5	P	P	P
Ufd1l	ubiquitin fusion degradation 1 like	P	P	P
Ube3a	ubiquitin protein ligase E3A	P	P	P
Usp14	ubiquitin specific protease 14	P	P	P

Usp15	ubiquitin specific protease 15	P	P	P
Usp21	ubiquitin specific protease 21	A	P	P
Usp3	ubiquitin specific protease 3	P	P	P
Usp3	ubiquitin specific protease 3	P	P	P
Usp4	ubiquitin specific protease 4 (proto-oncogene)	P	P	P
Usp8	ubiquitin specific protease 8	P	P	P
Usp9x	ubiquitin specific protease 9, X chromosome	P	P	P
Usp9x	ubiquitin specific protease 9, X chromosome	P	M	P
Ube1x	ubiquitin-activating enzyme E1, Chr X	P	P	P
Ube1c	ubiquitin-activating enzyme E1C	P	P	P
Ubap1	ubiquitin-associated protein 1	P	P	P
Ubap2	ubiquitin-associated protein 2	P	P	P
Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	P	P	P
Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	P	P	P
Ube2v2	ubiquitin-conjugating enzyme E2 variant 2	P	P	P
Ube2a	ubiquitin-conjugating enzyme E2A, RAD6 homolog (S. cerevisiae)	A	P	P
Ube2b	ubiquitin-conjugating enzyme E2B, RAD6 homolog (S. cerevisiae)	P	M	P
Ube2d2	ubiquitin-conjugating enzyme E2D 2	P	P	P
Ube2d2	ubiquitin-conjugating enzyme E2D 2	P	P	P
Ube2e1	ubiquitin-conjugating enzyme E2E 1, UBC4/5 homolog (yeast)	P	P	P
Ube2h	ubiquitin-conjugating enzyme E2H	P	A	P
Ube2i	ubiquitin-conjugating enzyme E2I	P	M	P
Ube2l3	ubiquitin-conjugating enzyme E2L 3	P	P	P
Ube2n	ubiquitin-conjugating enzyme E2N	P	P	P
Ube2r2	ubiquitin-conjugating enzyme E2R 2	P	P	P
Ubl1	ubiquitin-like 1	P	P	P
Uble1a	ubiquitin-like 1 (sentrin) activating enzyme E1A	P	P	P
Uble1b	ubiquitin-like 1 (sentrin) activating enzyme E1B	P	P	P
Ubl3	ubiquitin-like 3	P	P	P
Ubl4	ubiquitin-like 4	P	P	P
Ubl4	ubiquitin-like 4	P	P	P
Ubl5	ubiquitin-like 5	P	P	P
Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	P	P	P
Ubxdc2	UBX domain-containing 2	P	P	P
B4galt1	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	P	P	P
B4galt3	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	P	P	P
B4galt6	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	P	A	P
Ugalt2	UDP-galactose translocator 2	P	P	P
B3gnt1	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 1	P	A	P
Ugcg	UDP-glucose ceramide glucosyltransferase	P	P	P
Ugdh	UDP-glucose dehydrogenase	P	P	P
Ugp2	UDP-glucose pyrophosphorylase 2	P	P	P
Uxs1	UDP-glucuronate decarboxylase 1	A	P	P
Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	P	P	P
Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	P	A	P
Galnt3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3	P	P	P
Galnt9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 9	P	A	P
Uae1	UDP-N-acetylglucosamine-2-epimerase/N-acetylmannosamine kinase	P	P	P
Unc119h	unc119 homolog (C. elegans)	P	A	P
Unc5h3	unc5 homolog (C. elegans) 3	P	P	P
Ulk1	Unc-51 like kinase 1 (C. elegans)	P	P	P
Unc84a	unc-84 homolog A (C. elegans)	P	P	P
Usmg4	upregulated during skeletal muscle growth 4	P	M	P
Usmg5	upregulated during skeletal muscle growth 5	P	P	P
Ubp1	upstream binding protein 1	P	P	P
Ubf	upstream binding transcription factor, RNA polymerase I	P	P	P
Ureb1-(p)	upstream regulatory element binding protein 1	P	P	P
Usf1	upstream transcription factor 1	P	P	P
Ung	uracil-DNA glycosylase	P	P	P
Umpk	uridine monophosphate kinase	P	P	P
Umps	uridine monophosphate synthetase	P	P	P
Upp	uridine phosphorylase	P	P	A

Uck2-(p)	uridine-cytidine kinase 2	P	P	P
Urod	uroporphyrinogen decarboxylase	P	P	P
Uros	uroporphyrinogen III synthase	P	P	P
Abl1	v-abl Abelson murine leukemia oncogene 1	P	P	P
Vrk1	vaccinia related kinase 1	P	P	P
Vps16	vacuolar protein sorting 16 (yeast)	P	P	P
Vps26	vacuolar protein sorting 26 (yeast)	P	P	P
Vps28	vacuolar protein sorting 28 (yeast)	P	P	P
Vps29	vacuolar protein sorting 29 (S. pombe)	P	P	P
Vps35	vacuolar protein sorting 35	P	P	P
Vps41	vacuolar protein sorting 41 (yeast)	P	P	P
Vps4a	vacuolar protein sorting 4a (yeast)	P	P	P
Vps4b	vacuolar protein sorting 4b (yeast)	P	P	P
Vps54	vacuolar protein sorting 54 (yeast)	P	P	P
Vcp	valosin containing protein	P	P	P
Vars2	valyl-tRNA synthetase 2	P	P	P
Vegfb	vascular endothelial growth factor B	P	P	P
Vasp	vasodilator-stimulated phosphoprotein	P	P	P
Crkl	v-crkl sarcoma virus CT10 oncogene homolog (avian)-like	P	P	P
Vdp-(p)	vesicle docking protein	P	P	P
Vti1b	vesicle transport through interaction with t-SNAREs 1B homolog	P	P	P
Vamp2	vesicle-associated membrane protein 2	P	A	P
Vamp4	vesicle-associated membrane protein 4	P	P	P
Vamp4	vesicle-associated membrane protein 4	P	A	P
Vamp8	vesicle-associated membrane protein 8	P	P	P
Vamp8	vesicle-associated membrane protein 8	P	P	P
Vapa	vesicle-associated membrane protein, associated protein A	P	P	P
Viaat	vesicular inhibitory amino acid transporter	A	P	P
Vdu1-(p)	Vhlh-interacting deubiquitinating enzyme 1	P	P	P
Vil2	villin 2	P	P	P
Vim	vimentin	P	A	P
Vcl	vinculin	P	P	P
Vdac2	voltage-dependent anion channel 2	P	P	P
Vdac3	voltage-dependent anion channel 3	P	P	P
Vbp1	von Hippel-Lindau binding protein 1	P	P	P
Raf1	v-raf-1 leukemia viral oncogene 1	P	P	P
Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	P	P	P
Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	P	P	P
Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	P	P	P
Rela	v-rel reticuloendotheliosis viral oncogene homolog A, (avian)	P	P	P
Wdr1	WD repeat domain 1	P	P	P
Wdr13	WD repeat domain 13	P	A	P
Wdr6	WD repeat domain 6	P	P	P
Ciao1-(p)	WD40 protein Ciao1	P	P	P
Wsb1-(p)	WD-40-repeat-containing protein with a SOCS box 1	P	P	P
Wsb2-(p)	WD-40-repeat-containing protein with a SOCS box 2	P	P	P
Wee1	wee 1 homolog (S. pombe)	P	P	P
Wrip	Werner syndrome homolog (human) interacting protein	P	P	P
Wiz	widely-interspaced zinc finger motifs	P	P	P
Wig1	wild-type p53-induced gene 1	P	A	P
Wnt10a	wingless related MMTV integration site 10a	P	P	P
Wisp1	WNT1 inducible signaling pathway protein 1	P	A	P
Whsc2h	Wolf-Hirschhorn syndrome candidate 2 homolog (human)	P	P	P
Wbp1	WW domain binding protein 1	P	A	P
Wbp11	WW domain binding protein 11	P	P	P
Wbp2	WW domain binding protein 2	A	P	P
Wbp5	WW domain binding protein 5	P	P	P
Wbp5	WW domain binding protein 5	P	P	P
Wwp2-(p)	WW domain-containing protein 4	P	P	P
Wwp2-(p)	WW domain-containing protein 4	P	P	P
Xbp1	X-box binding protein 1	P	P	P
Xpr1	xenotropic and polytropic retrovirus receptor 1	P	P	P

Xpa	xeroderma pigmentosum, complementation group A	P	P	P
Xlr3b	X-linked lymphocyte-regulated 3b	A	P	P
Xpnpep1	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	P	P	P
Xrcc5	X-ray repair complementing defective repair in Chinese hamster cells 5	P	P	P
Yes	Yamaguchi sarcoma viral (v-yes) oncogene homolog	P	A	P
Lyn	Yamaguchi sarcoma viral (v-yes-1) oncogene homolog	P	P	A
Yap	yes-associated protein	P	P	P
Yme1l1	YME1-like 1 (S. cerevisiae)	P	P	P
Yme1l1	YME1-like 1 (S. cerevisiae)	P	A	P
Yspl1	yolk sac permease-like molecule 1	P	P	P
Yy1	YY1 transcription factor	P	P	P
Zap3-(p)	ZAP3 protein	P	P	P
Zfhx1a	zinc finger homeobox 1a	P	P	P
Zipro1	zinc finger proliferation 1	P	P	P
Zfp1	zinc finger protein 1	P	P	P
Zfp101	zinc finger protein 101	P	A	P
Zfp103	zinc finger protein 103	P	P	P
Zfp105	zinc finger protein 105	P	P	P
Zfp106	zinc finger protein 106	P	P	P
Zfp110	zinc finger protein 110	P	P	P
Zfp125	zinc finger protein 125	A	P	P
Zfp131	zinc finger protein 131	P	P	P
Zfp144	zinc finger protein 144	P	P	P
Zfp148	zinc finger protein 148	P	P	P
Zfp161	zinc finger protein 161	P	A	P
Zfp207	zinc finger protein 207	P	P	P
Zfp216	zinc finger protein 216	P	P	P
Zfp239	zinc finger protein 239	P	P	P
Zfp259	zinc finger protein 259	P	P	P
Zfp260	zinc finger protein 260	A	P	P
Zfp265	zinc finger protein 265	P	P	P
Zfp265	zinc finger protein 265	P	P	P
Zfp275	Zinc finger protein 275	P	P	P
Zfp289	zinc finger protein 289	P	A	P
Zfp292	zinc finger protein 292	P	P	P
Zfp292	zinc finger protein 292	P	P	A
Zfp297	zinc finger protein 297	P	P	P
Zfp297	zinc finger protein 297	A	P	P
Zfp30	zinc finger protein 30	P	P	P
Zfp326	zinc finger protein 326	P	P	P
Zfp35	zinc finger protein 35	P	P	P
Zfp36l1	zinc finger protein 36, C3H type-like 1	P	P	P
Zfp51	zinc finger protein 51	P	P	P
Zfp61	zinc finger protein 61	A	P	P
Zfp62	zinc finger protein 62	P	P	P
Zfp64	zinc finger protein 64	A	P	P
Zfp68	Zinc finger protein 68	P	P	P
Zfp68	Zinc finger protein 68	P	P	P
Zfp91	zinc finger protein 91	P	P	P
Zfp96	zinc finger protein 96	P	P	P
Zfp97	zinc finger protein 97	P	P	P
Zfp97	zinc finger protein 97	A	P	P
LOC224691	zinc finger protein BC027407	P	P	P
Zic3	zinc finger protein of the cerebellum 3	A	P	P
Pzf	zinc finger protein PZF	P	P	P
LOC170938	zinc finger protein s11-6	M	P	P
Zfx	zinc finger protein X-linked	P	P	P
Zfpm1	zinc finger protein, multitype 1	P	P	P
Zfnf1a4	zinc finger protein, subfamily 1A, 4	P	M	P
Zfr	zinc finger RNA binding protein	P	P	P
Zdhhc3	zinc finger, DHHC domain containing 3	P	M	P
Zhx1	zinc fingers and homeoboxes protein 1	P	P	P

Zrfp1-(p)	zinc ring finger protein 1	P	P	P
Zrfp1-(p)	zinc ring finger protein 1	P	P	P
Zrf2	zuotin related factor 2	P	P	P
Zw10	ZW10 homolog (Drosophila), centromere/kinetochore protein	P	P	P

APPENDIX C

Transcripts Enriched or Depleted in *Nkx2.5* Null Cardiac Cells at E8.0, E8.25, and E8.5 (Affymetrix Moe430v2 Genechip Data)

Sequence Derived From	Gene Symbol	Title	E8.0 Nkx2.5 Null Signal	E8.0 Nkx2.5 Null vs. wt Fold Change	E8.0 Nkx2.5 wt Signal	E8.25 Nkx2.5 Null Signal	E8.25 Nkx2.5 Null vs. wt Fold Change	E8.25 Nkx2.5 wt Signal	E8.5 Nkx2.5 Null Signal	E8.5 Nkx2.5 Null vs. wt Fold Change	E8.5 Nkx2.5 wt Signal
BC004589	Bpgm	2,3-bisphosphoglycerate mutase	51.9	-2.14	135.6	97.6	1.00	117.5	39.9	-1.52	87.1
BE952632	Decr2	2-4-dienoyl-Coenzyme A reductase 2, peroxisomal	140.2	1.74	89	172	3.25	41.8	132.2	1.32	98.7
NM_007856	Dhcr7	7-dehydrocholesterol reductase	153.6	1.87	89.7	134.3	-1.07	131.5	139.7	1.23	111
BB631643	EST	acetylcholinesterase-associated collagen (M.musculus)	31.2	1.87	20.3	23.5	-2.46	55.1	18.8	-1.41	33.5
AW554436	Acp1	acid phosphatase 1, soluble	38.3	-2.00	95.1	15.3	-1.15	24.9	124.3	-1.87	230.2
AF022957	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	104.3	1.07	87	90.6	-2.64	197.3	28.5	-1.07	32.6
M12233	Acta1	actin, alpha 1, skeletal muscle	307.8	1.15	285.5	256.1	-3.25	779.1	280.4	-1.15	382.7
NM_007394	Acvr1	activin A receptor, type 1	130.5	1.41	84.1	70.1	1.15	48.7	139	1.87	57.3
BQ175609	Ap2a2	adaptor protein complex AP-2, alpha 2 subunit	736.8	2.00	370.1	291	1.15	270.1	314.6	1.15	257.7
NM_007398	Ada	adenosine deaminase	55.4	-1.07	65.9	27.7	-2.30	59.9	52.2	-1.32	81.7
BC005446	Cap1	adenylyl cyclase-associated CAP protein homolog 1 (S. cerevisiae, S. pombe)	571.1	5.28	84.3	615.5	4.92	90.1	1107.4	1.87	459.9
NM_019822	Adrm1	adhesion regulating molecule 1	806.6	1.87	387.5	401.9	1.00	322.4	485.6	1.41	332.6
NM_019915	Art2b	ADP-ribosyltransferase 2b	19.2	1.23	19.6	11.7	1.07	8.8	39.6	2.83	5.9
BC024643	Alb1	albumin 1	352	-1.15	444.1	17.6	-3.03	73.7	58.5	-1.07	69.1
NM_009022	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	143.2	1.00	159.9	94.7	-1.15	86.3	163.4	1.87	76.8
BC012692	Akr1e1	aldo-keto reductase family 1, member E1	149.7	-1.87	382.9	93	-2.83	333.8	137.3	-1.41	235.6
BC024112	Aldo2	aldolase 2, B isoform	131.3	1.00	154.2	100.8	1.87	45.9	91.4	1.23	59.5
NM_007423	Afp	alpha fetoprotein	552.3	1.00	549.4	1329.1	2.14	645.9	131	-2.00	299.5
AV124668	Afp	alpha fetoprotein	158.6	-1.07	213.6	436.8	2.30	119.1	54.3	-1.87	106.8
NM_007423	Afp	alpha fetoprotein	361.3	-1.23	417.8	785.7	2.83	230.1	97.6	1.52	57.5
NM_009664	Ambn	ameloblastin	36.4	-1.15	41.7	17.5	-1.74	38.9	41.9	3.25	10.8
BC018236	Alad	aminolevulinic acid synthase 1	1945.5	4.29	401.7	1084	1.62	789.1	1101.1	2.14	510.1
AI255644	Alas1	aminolevulinic acid synthase 1	38.1	-1.52	45.6	17.5	-2.14	55.2	24.1	-1.15	24.8
M63244	Alas2	aminolevulinic acid synthase 2, erythroid	675.4	2.83	250.9	516	3.03	152.7	207.5	1.62	130.8
NM_033603	Amn	amnionless	138.9	1.23	138.9	180.2	2.00	92.6	58.9	-1.52	87.9
BQ177140	Amph	amphiphysin	364.7	1.23	301.9	387.8	1.07	377.9	357.3	-2.00	382
AA681807	Agli	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	61.7	1.00	53.2	68.5	1.41	38.2	78.4	-1.87	143.9
BB533323	Agtr1	angiotensin receptor-like 1	430.9	-1.07	455.2	326.1	-1.23	440	479.2	1.87	245
AF403044	Asb16	ankyrin repeat and SOCS box-containing 16	97.5	1.23	93.4	45.8	-1.74	83.2	120	2.64	50.4
NM_025758	Asb17	ankyrin repeat and SOCS box-containing protein 17	42.1	-1.07	40.3	25.2	6.06	2.6	20.1	1.15	15.2
NM_010730	Anxa1	annexin A1	59.4	1.15	51.6	27.6	-1.23	18.4	22.9	-2.30	179.6
BE628614	Anxa4	annexin A4	5.3	-1.74	14.7	26	2.30	7.3	4.9	-9.85	52.6
NM_007463	Apeg1	aortic preferentially expressed gene 1	114.4	-1.32	180.7	132.4	-1.15	109.2	194.5	-1.87	383.7
AI194999	Apoa1	apolipoprotein A-I	479.4	1.32	413.9	899.3	3.73	198.2	86.2	-1.74	158.1
AI527359	Apoa1	apolipoprotein A-I	668.4	1.52	532.2	1211.7	3.73	217.7	168.9	-1.32	189.6
NM_009692	Apoa1	apolipoprotein A-I	203.5	1.00	250.4	605.6	4.29	119.6	56.8	-1.74	123.1
NM_009692	Apoa1	apolipoprotein A-I	436.3	1.23	415.7	837.6	5.28	138.9	22	-10.56	163.4
AI785548	Apob	apolipoprotein B-100	182.7	1.62	133.6	151.2	3.73	39.5	70.6	1.00	64.7
NM_009695	Apoc2	apolipoprotein C-II	270.1	1.74	94.2	520.1	4.00	109.3	68.5	-1.62	125.7
NM_018816	Apom	apolipoprotein M	235.3	1.23	203	250.2	2.64	90.7	65.9	-2.00	148.6
NM_018816	Apom	apolipoprotein M	258.2	1.52	187.1	364.4	5.28	63.8	31.1	-3.03	125.6
AW228855	Acinus	apoptotic chromatin condensation inducer in the nucleus	203.8	1.15	243.7	331.1	1.07	291.3	374.7	1.87	238.1
NM_013795	Atp5l	ATP synthase, H+ transporting, mitochondrial F0	161.1	1.00	118.4	307.3	1.23	235.5	149.8	-1.87	231.2

BB303874	Atp8a1	complex, subunit g	155.9	1.52	100.1	166.9	2.00	77.5	145.4	2.00	71
NM_016920	Atp6v0a1	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	164.6	2.30	45	87.9	1.32	69.7	144	1.62	67.2
AV152334	Atp1b1	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	47.8	-1.07	56.8	93.5	1.00	110.7	89.9	-2.30	129
BM122009	ANF	Atrial natriuretic factor precursor (ANF) (Atrial natriuretic peptide) (ANP)	22.7	-4.92	177.6	28.3	-16.00	714.9	41.8	-5.66	496.7
AF110396	Btrc	beta-transducin repeat containing protein	118.1	1.87	65.9	107.8	-1.23	143.7	71.1	-1.07	66.8
BC027279	Blvrb	biliverdin reductase B (flavin reductase (NADPH))	522.1	3.25	197.8	420.5	3.73	134.2	239.9	1.23	194.3
BB094173	Bhc80-	BRAF35/HDAC2 complex	23.2	-3.03	88.6	180.1	1.87	141.2	119.7	1.00	150.6
BC003248	Brca1	breast cancer 1	139.4	1.15	134.1	55.9	1.00	58.6	129.7	2.00	67.8
BC024724	Bcaa-	breast cancer-associated antigen	40.3	2.14	23.3	23.6	-1.41	39.1	32.2	4.00	4.8
BG072367	Brd3	bromodomain containing 3	414.4	1.87	201.3	181.7	-1.15	243.7	252.8	1.32	156.6
NM_009864	Cdh1	cadherin 1	140.3	-1.23	155.2	149.3	-1.23	238.1	160.6	-2.14	295.4
NM_021415	Cacna1h	calcium channel, voltage-dependent, T type, alpha 1H subunit	10.4	1.74	4.2	15.9	-2.30	47.6	15.4	-2.00	28.2
BC019435	Cald1	caldesmon 1	97.8	-1.87	238.1	270.9	-1.15	258.5	167.7	-1.32	220.9
NM_007603	Capn6	calpain 6	115.5	1.32	76.5	127.7	-1.87	285	87.4	8.00	13.1
BG261945	Calp-	calenilin-like protein	27.7	-1.07	25.1	23.1	-1.07	17.1	41.3	1.87	23.4
NM_009813	Casq1	calsequestrin 1	227.1	1.07	282.8	122.5	-2.30	322.3	263.6	-1.32	282.6
AF448508	Creb1	cAMP responsive element binding protein 1	13.9	-1.87	29	0.7	-8.57	15	23.7	2.30	6.7
NM_009801	Car2	carbonic anhydrase 2	2721.3	1.74	1708.6	1598.3	2.46	626	1234.5	1.07	980.5
AK003671	Car3	carbonic anhydrase 3	87.9	-1.07	75.3	51.8	1.00	59.9	115.4	-2.14	187.2
NM_030703	Cpn1	carboxypeptidase N, polypeptide 1	37.5	2.46	23.8	48.7	2.30	14.1	5.3	-4.29	35.2
NM_013468	Crap	cardiac responsive adriamycin protein	447.2	-2.00	672	662.1	-1.32	846.1	476.8	-1.62	583.3
AK009959	Crap	cardiac responsive adriamycin protein	369	-2.00	807.4	966.7	-1.07	1038.4	693.6	-2.46	1605.5
BC025116	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	323.9	2.30	161.3	183.7	1.87	111.7	197.1	2.14	80.5
NM_020006	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	400	1.23	330.9	266.6	-1.23	312	318.6	2.00	167.9
BB414739	Csh1	chorionic somatomammotropin hormone 1	9.3	1.32	9.7	5	2.00	3.9	5.1	-11.31	71.3
NM_021531	Carm1-	coactivator-associated arginine methyltransferase 1	1700.4	2.30	931.2	612.3	1.15	556	930	1.41	911.8
NM_007972	F10	coagulation factor X	224.7	1.74	99.8	119.3	2.14	57.2	152.5	1.41	85.5
AI323359	Csf1r	colony stimulating factor 1 receptor	212.6	1.23	249.5	114.2	1.07	99.9	119.6	-2.00	264.9
NM_007781	Csf2rb2	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	64.3	1.32	51.1	22.4	1.00	21.4	63	2.30	26.7
NM_007757	Cpo	coproporphyrinogen oxidase	254.2	2.00	129.5	73.2	1.74	49	165.8	1.00	161.5
BG967663	Ckb	creatine kinase, brain	194.5	-1.52	236.9	183.1	-2.14	401.6	229.3	-1.87	368.4
BI076485	Cryl1	crystallin, lamda 1	727.3	3.48	201.5	1090.2	2.30	417.2	637.3	2.46	257.1
AF197159	Cubn	cubililn (intrinsic factor-cobalamin receptor)	312.9	2.00	206.7	279.4	5.28	70.7	74.4	-2.14	97.2
AF197159	Cubn	cubililn (intrinsic factor-cobalamin receptor)	195.8	2.30	100.9	154.1	3.03	52.3	43.3	1.15	39.2
BM118679	Ccnd2	cyclin D2	69.2	1.87	32.8	64.4	-1.41	77.2	62.6	-1.87	104.4
AV326194	Ccnh	cyclin H	15	-3.73	45.3	56.8	1.07	37.4	49.5	-1.62	92.2
BF124540	Csrp1	cysteine rich protein 1	46.7	-1.32	78.6	117.1	-1.87	238.3	70.8	-1.52	102.7
NM_021050	Cfr	cystic fibrosis transmembrane conductance regulator homolog	3.5	-5.28	24.5	12.9	1.07	13	8.8	-1.07	16.9
NM_031251	Ctns	cystinosis, nephropathic	40.4	-1.23	59.9	28.6	-1.15	43.9	59.3	3.25	18
NM_010000	Cyp2b9	cytochrome P450, family 2, subfamily b, polypeptide 9	90	2.83	39	37.5	-1.07	34.3	50.7	1.62	36.9
NM_019823	Cyp2d22	cytochrome P450, family 2, subfamily d, polypeptide 22	1.7	1.00	8	20.7	1.15	14.2	20.4	2.14	11.4
NM_024264	Cyp27a1	cytochrome P450, family 27, subfamily a, polypeptide 1	107.3	1.32	77.3	51.7	1.15	46.6	86.4	1.87	44.7
BB667338	Cyp7a1	cytochrome P450, family 7, subfamily a, polypeptide 1	98.1	1.15	85.3	44.7	-1.07	32.2	67.3	2.14	32.6
BG064656	Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta	110.3	-2.00	233.3	244	-1.23	289.5	225.3	-1.32	244.6
NM_007916	Ddx19	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 19	395.5	2.00	181.1	86.5	-1.07	144.9	271	1.62	232.1
BC026671	Dapk1	death associated protein kinase 1	73.4	1.15	90.5	89.1	1.00	114.3	102.1	1.87	64.3
AI642212	Dapk3	death-associated kinase 3	115.1	1.15	84.2	184	-1.15	209.1	158.9	5.66	16.3
NM_007848	Defcr-rs7	defensin related cryptdin, related sequence 7	68.9	-2.14	155.7	24.3	-2.14	56.1	33.3	-2.00	42.1
NM_010052	Dlk1	delta-like 1 homolog (Drosophila)	482	2.00	274.7	513.8	-1.32	507.3	180.6	1.00	253.2
AB015422	Dtx1	deltex 1 homolog (Drosophila)	133.1	1.52	150.8	126.9	-1.07	107.9	160.5	2.14	83.1
U65020	Dmp1	dentin matrix protein 1	53.7	1.41	32.7	7.6	-1.87	14.7	14.8	-1.41	18.8
C79957	Dsg2	desmoglein 2	277.2	1.00	268.8	321.3	1.23	309.1	348.9	-1.87	501.9
NM_010074	Dpp4	dipeptidylpeptidase 4	53.1	1.00	56.1	138.2	2.14	96.8	10.9	-7.46	68.5
BC016887	Dab2	disabled homolog 2 (Drosophila)	404.5	1.07	292.1	268.4	2.00	162.7	272	1.15	232.5
BC018472	MGC28027	dopamine responsive protein	58.1	-1.41	123.4	135.4	1.87	80.1	61.7	-1.41	77.6
BC013461	Dr1	down-regulator of transcription 1	165.7	1.00	226.1	252.8	1.07	249.8	227.1	-2.00	349.5

AF143543	Dtna	dystrobrevin alpha	63	2.46	30.1	48.6	5.28	9.4	55.1	2.30	21.4
BB131357	Dag1	dystroglycan 1	349.2	2.00	111.7	139.4	1.15	132.6	260.2	1.52	154.6
BC007150	Dag1	dystroglycan 1	396.5	2.00	225.2	138.5	-1.07	190	311.3	1.62	186.9
BC026649	E2f4	E2F transcription factor 4	168.2	1.62	105.8	97.2	1.00	87.5	142.2	2.30	47.1
NM_007913	Egr1	early growth response 1	197.4	1.23	168.8	231.9	1.87	141.1	258.7	1.32	175.8
X06746	Egr2	early growth response 2	40.7	1.15	29.7	29.5	1.52	22.7	34.4	2.30	22.3
BC005527	Enpp3	ectonucleotide pyrophosphatase/phosphodiesterase 3	19.3	-1.52	48.6	13.9	-1.87	24.5	31.3	2.14	13.4
BC020014	Ehd2	EH-domain containing 2	2.1	-9.19	31.5	44.1	1.32	30	31.2	1.23	28.3
NM_138953	Ell2	ELL-related RNA polymerase II, elongation factor	372.5	2.00	161	292	2.46	92.9	210.9	1.23	193.5
AB034693	Emcn-pending	endomucin	80.4	-2.00	151.6	124.7	-1.32	186.4	95.9	-1.07	100.9
AK009464	Enh-pending	enigma homolog (R. norvegicus)	165.4	1.32	139.3	303	1.32	274.6	224.4	-2.14	717
NM_010110	Efnb1	ephrin B1	163.5	1.15	109.1	70.4	-1.23	89.8	99.5	2.00	71.2
BC015076	Eva	epithelial V-like antigen	30.8	1.41	23	18.2	-1.15	28.2	25.7	-1.87	35.2
NM_013848	Ermap	erythroblast membrane-associated protein	236.3	2.14	103	108.4	1.87	35	74.4	-1.15	78.5
NM_133245	Eraf	erythroid associated factor	2827.3	2.30	1458.2	2002.1	3.03	665	929.9	-1.15	1132.6
AJ007909	edr	erythroid differentiation regulator	1297.9	2.30	554.6	3433	2.83	1364.1	1906.4	1.52	1020.1
BE686792	edr	erythroid differentiation regulator	173.6	3.48	50.6	652.2	2.30	115.5	184.2	-1.23	79.4
NM_007959	Etsrp71	ets related protein 71	374.4	-1.87	847.7	473.4	-2.14	1199.9	497.2	-1.41	591.8
NM_026114	Eif2s1	eukaryotic translation initiation factor 2, subunit 1 alpha	3	-9.85	85.4	67.8	1.23	52.8	1.9	1.15	4.6
AV124537	Elkd1	extra cellular link domain-containing 1	301.1	1.52	135.5	390.3	3.03	192.9	272.2	1.15	231.1
AK004726	Elkd1	extra cellular link domain-containing 1	254.7	1.41	276.5	373.7	4.29	105.7	283.1	1.23	313.8
BG072083	Fancg	Fanconi anemia, complementation group G	196	1.32	151.5	83.4	-1.23	72.9	135.5	1.87	110.8
BG063077	Fntb	farnesyltransferase, CAAX box, beta	138.5	1.87	67.1	61.3	1.87	32	112.1	2.14	54.5
NM_017399	Fabp1	fatty acid binding protein 1, liver	71.2	1.87	37.9	27.9	1.32	19.4	42.5	2.00	19.2
NM_013909	Fbxl6	F-box and leucine-rich repeat protein 6	119.2	1.23	113.1	125.7	-1.07	153.2	101	2.00	53.4
BM211336	Fech	ferrochelatase	171.7	1.87	99	108.2	1.23	87.4	89.2	1.15	85.9
BM211336	Fech	ferrochelatase	1349.9	2.14	718	721.1	1.62	432.6	743.2	1.62	498.1
NM_007998	Fech	ferrochelatase	202.6	1.52	144.1	160.2	2.00	118.5	146.6	1.00	147.3
BM234360	Fn1	fibronectin 1	81	-1.87	169.7	314.6	-1.15	328.3	238.7	1.00	208.4
AI325255	Fkbp10	FK506 binding protein 10	215.9	1.74	157.4	101.6	1.00	98.5	155.1	1.87	109
BC025939	Fthfd	formyltetrahydrofolate dehydrogenase	49.7	-2.14	117.9	13.3	-3.73	56.3	59.2	1.32	48.3
NM_008032	Fmr2	fragile X mental retardation 2 homolog	94.8	1.62	67.6	47.1	-1.07	56	75.3	2.00	34.3
NM_020510	Fzd2	frizzled homolog 2 (Drosophila)	551.9	1.07	630.6	679.7	1.07	615	655.8	1.87	302.4
NM_011046	Furin	furin (paired basic amino acid cleaving enzyme)	398.6	1.87	208.3	163.7	1.00	154.5	285.6	1.23	209.6
BC026975	Gpr85	G protein-coupled receptor 85	16.9	-1.23	23.2	25.2	1.62	8.7	50.7	2.83	11.3
BC020004	Gprc5b	G protein-coupled receptor, family C, group 5, member B	50.2	1.62	42.5	32.9	-2.30	58.9	40.7	1.32	35.7
BC026822	Gsbs-pending	G substrate	65	-1.15	55.7	22	-2.14	45.9	80.2	-1.07	70.8
BF168119	Galc	galactosylceramidase	15.2	-3.03	46.8	3.1	-6.50	48	35.3	1.15	43.8
AF216832	Gja4	gap junction membrane channel protein alpha 4	178.2	1.15	182.4	147.7	-2.00	263.6	254.4	1.32	141.7
AV025667	Gsn	gelsolin	65.7	1.74	46.6	28.2	2.14	18.2	57.8	-1.41	104.7
AF303106	Gtrgeo22	gene trap ROSA b-geo 22	174.4	1.07	163.9	206.8	-1.23	236.3	181	2.14	85.3
NM_008063	G6pt1	glucose-6-phosphatase, transport protein 1	184.9	2.46	82.7	226.1	1.15	155.7	194.2	1.52	105.3
NM_008077	Gad1	glutamic acid decarboxylase 1	4.6	-3.25	14.8	24.5	2.14	14.6	35.1	1.32	26.2
NM_008161	Gpx3	glutathione peroxidase 3	1283.1	1.87	749.3	632.4	1.00	656.1	736.5	1.62	469.1
NM_010369	Gypa	glycophorin A	97.1	3.03	29.9	96.9	3.03	14.7	43.4	1.00	42
NM_134118	Gpsn2	glycoprotein, synaptic 2	1247	1.32	811.8	1032.2	1.00	1136.6	1169.2	1.87	577.4
AK007410	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	170.8	-1.74	296.5	430.2	-2.00	734.6	180.6	-1.15	174.4
NM_008114	Gfi1b	growth factor independent 1B	141.7	1.62	89.2	76.5	3.25	13.9	99.2	-1.15	93.5
BI901126	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	227.9	-1.87	382.8	229.7	-1.52	365.9	237.6	-1.41	299.8
BQ176391	Gfer	growth factor, erv1 (S. cerevisiae)-like (augmenter of liver regeneration)	329.5	2.14	141.5	215.1	2.14	147.6	293.4	1.41	212.5
BB698398	Gch	GTP cyclohydrolase 1	31.2	2.14	11.5	18.5	-1.41	31.7	19.9	1.32	24.3
BF472806	Gucy1b3	guanylate cyclase 1, soluble, beta 3	67.1	1.00	91.7	59.6	2.00	54.8	62.3	1.00	77.6
BB561515	Hes5	hair and enhancer of split 5 (Drosophila)	36.7	-1.15	38.7	11.8	-1.23	10.1	19.9	3.73	2.1
BM124741	Hspb7	heat shock protein family, member 7 (cardiovascular)	134.8	1.00	133.4	61.3	-2.14	124.6	149.3	1.23	106.3
AF117613	Hebp1	heme binding protein 1	521.4	1.74	234.4	538.6	2.00	180.3	155.3	1.32	135.8
NM_053149	Hemgn	hemogen	218.6	2.14	157.4	217.5	2.64	62.1	109.5	1.32	54.6
AK011116	Hba-a1	hemoglobin alpha, adult chain 1	9537.9	1.87	4657	8635.5	2.14	3909.9	1837.2	-2.00	3779.2
AK011116	Hba-a1	hemoglobin alpha, adult chain 1	4558	2.00	2519.3	4675	2.46	1821.9	1375	-2.00	2576

NM_008218	Hba-a1	hemoglobin alpha, adult chain 1	5	149.2	1.62	72.9	2	297.8	2.30	103.3	9	324.7	-2.00	737.7	1
M26898	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	1	6021.	1.74	4693	2	8290.	2.14	3240.	7	2227.	-1.52	3582.	3
NM_008221	Hbb-y	hemoglobin Y, beta-like embryonic chain	9	2857.	1.74	1736.9	4	2928.	3.25	822.7	6	318.1	-1.52	551.1	8
NM_008219	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	1	1065.	1.62	7052.8	9	9489.	1.87	5010.	2	4653.	-1.15	5227.	8
BC027434	Hbb-b1	hemoglobin, beta adult major chain	1	1144	1.62	587.7	9	910.6	4.00	186.4	6	354.9	1.74	207	8
BF580781	Hnf4	hepatic nuclear factor 4	1	26.1	1.87	13.5	9	13.7	13.00	1.1	22.7	1.32	15.9	8	207
AF450241	Havcr2	hepatitis A virus cellular receptor 2	1	35.4	-1.74	49	9	20.5	2.00	14.2	6	51.2	2.14	21	8
C80147	Hdgf	hepatoma-derived growth factor	1	432.5	2.64	113.7	9	49.7	1.32	39.9	6	93.8	-1.07	116.6	8
BB291880	Hdgfrp3	hepatoma-derived growth factor, related protein 3	1	28.1	-2.00	99.2	9	173.5	3.03	61.7	6	60.6	-1.74	129.3	8
BB713410	Hk1	hexokinase 1	1	573	2.64	237.3	9	217.3	1.07	184.3	6	342.4	1.32	264.2	8
AV225808	Hexb	hexosaminidase B	1	41.5	1.07	36.4	9	83.5	-1.32	54.6	6	25.1	-3.03	84.5	8
AK017926	Rtp801-	HIF-1 responsive RTP801	1	338.3	1.87	199.9	9	737.4	1.87	433.1	6	316	2.30	149.3	8
AV127023	Hmgb1	high mobility group box 1	1	875.2	-1.87	1988.4	9	4871.	1.00	4673.	6	3374.	-1.23	3789.	8
BB051552	Hrh1	histamine receptor H 1	1	53.6	1.07	64.7	9	18.8	-1.41	30.7	6	48.3	2.14	18.9	8
NM_010386	H2-DMa	histocompatibility 2, class II, locus DMA	1	31.7	1.87	34.5	9	35.1	1.23	30.4	6	51.9	2.14	21.6	8
NM_023422	Hist1h2bc	histone 1, H2bc	1	39.5	1.23	23.1	9	92	1.00	92.6	6	54.6	-2.30	134.5	8
NM_020027	Bat2	HLA-B associated transcript 2	1	538.3	1.87	304.9	9	204.3	1.07	307.4	6	282.9	1.32	240.5	8
AK002670	Hoxa10	homeo box A10	1	31.7	-1.62	68.6	9	12.3	-3.03	55.4	6	25.5	-1.23	51.5	8
NM_010450	Hoxa11	homeo box A11	1	111.1	-1.15	135.9	9	40.7	-1.87	170.9	6	73.6	1.07	84.1	8
AA987181	Hoxa9	homeo box A9	1	113.5	-2.00	160	9	52.2	-6.96	310	6	88.3	-1.41	119.2	8
AA265122	Hoxd8	homeo box D8	1	48.1	1.87	50.5	9	23.6	-2.14	55.9	6	10.8	1.23	13.5	8
NM_010434	Hipk3	homeodomain interacting protein kinase 3	1	73.4	1.52	39.9	9	33	-1.23	38	6	70.8	2.00	39.8	8
AW541327	Hs1bp3-	HS1 binding protein 3	1	228.5	2.14	125	9	97.5	-1.15	116	6	133.7	1.15	97.3	8
BC014739	Ik	IK cytokine	1	377.7	-2.00	1226.6	9	836.5	-1.07	1233.	6	966.9	-1.15	1072	8
NM_133662	Ier3	immediate early response 3	1	179.3	2.00	82.4	9	299	1.74	142.3	6	137.5	1.15	107	8
BC008237	Igh-4	immunoglobulin heavy chain 4 (serum IgG1)	1	116.3	1.00	111.8	9	56	1.07	36.5	6	154.9	5.28	12.7	8
BB499476	Igf2bp1	insulin-like growth factor 2, binding protein 1	1	161.4	-1.07	202.1	9	634	1.23	460.2	6	541.3	2.30	238.6	8
BF225802	Igfbp5	insulin-like growth factor binding protein 5	1	2790.	1.87	1371.1	9	1844.	1.32	1180	6	3165.	1.62	1789.	8
NM_008397	Itga6	integrin alpha 6	1	561.8	1.87	290.1	9	579.6	2.14	252	6	1044.	2.14	517.5	8
BM935811	Itga6	integrin alpha 6	1	990.3	2.30	432.8	9	916	1.62	516.8	6	1065.	1.74	608.6	8
AI481797	Ifi205	interferon activated gene 205	1	3.1	-6.50	20.7	9	7.7	1.00	7.7	6	12.1	3.73	2.5	8
AK017358	Itm1	integral membrane protein 1	1	16.8	-2.64	35.3	9	27.2	1.74	21.3	6	24	-3.25	56.3	8
NM_021283	Il4	interleukin 4	1	52.9	1.15	52.8	9	37.8	-1.15	27.1	6	47.7	2.83	23	8
NM_008471	Krt1-19	keratin complex 1, acidic, gene 19	1	201.4	-1.15	249.3	9	263	1.00	249.5	6	151.5	-2.30	356.4	8
BB827235	Kif11	kinesin family member 11	1	69.1	1.32	51.8	9	57.3	-1.32	73.7	6	74.2	2.30	40.7	8
BF099632	Kif5b	kinesin family member 5B	1	141.8	6.96	12.5	9	80.3	-1.62	177.7	6	112	-1.52	149.5	8
NM_013598	Kitl	kit ligand	1	572.2	1.52	350.7	9	473.9	1.23	353.4	6	578.1	1.87	300.8	8
NM_010635	Klf1	Kruppel-like factor 1 (erythroid)	1	979.1	3.25	340.6	9	444.5	2.46	168.7	6	381.5	1.62	250	8
NM_025622	Lgals2	lectin, galactose-binding, soluble 2	1	147.3	1.07	120.2	9	182.1	1.87	74.6	6	64.9	1.00	68.1	8
BB131619	Lnx1	ligand of numb-protein X 1	1	168.4	1.15	125.5	9	119.7	1.32	98.9	6	173.3	2.14	81.3	8
AK014526	Lpin1	lipin 1	1	25.5	-1.52	51	9	22.8	-2.46	51.8	6	49.1	1.32	39.4	8
X14607	Lcn2	lipocalin 2	1	67.6	1.00	78.5	9	0.7	-3.25	4.5	6	1.6	1.32	2.4	8
NM_008509	Lpl	lipoprotein lipase	1	314.8	-1.87	687.5	9	549.2	-1.15	672.7	6	609.7	-1.52	944	8
AK005374	Qpc-	low molecular mass ubiquinone-binding protein	1	139.4	-1.07	110.8	9	47.4	-1.87	103.3	6	144.8	1.41	75	8
NM_023463	Ly6g6c	lymphocyte antigen 6 complex, locus G6C	1	61.3	1.23	42.3	9	27.4	-1.87	50.1	6	54.9	1.41	58.8	8
NM_013825	Ly75	lymphocyte antigen 75	1	51.4	-1.32	83.6	9	61.8	2.00	43.3	6	71.1	1.15	116	8
AI596237	Lip1	lysosomal acid lipase 1	1	105.5	-1.07	109.5	9	35.6	-1.74	75.2	6	128.8	1.87	77.9	8
BB218107	Laptn5	lysosomal-associated protein transmembrane 5	1	36.7	-1.62	82.8	9	33.8	1.87	21	6	59.6	-1.52	100.8	8
NM_011839	Mab21l2	mab-21-like 2 (C. elegans)	1	276.8	1.74	178.1	9	83.9	-1.32	103.1	6	132.5	2.64	68.9	8
NM_008540	Madh4	MAD homolog 4 (Drosophila)	1	1396.	1.23	1153.7	9	330.6	-2.00	887.1	6	1557.	2.14	619.2	8
AF010133	Madh6	MAD homolog 6 (Drosophila)	1	446.6	1.74	240.5	9	361.1	1.23	297.1	6	451.4	2.14	213.3	8
NM_008607	Mmp13	matrix metalloproteinase 13	1	12.6	1.32	4.5	9	0.3	-25.99	7.3	6	14.4	13.93	0.5	8
AF311316	Mageb3	melanoma antigen, family B, 3	1	39.8	-1.15	58.1	9	34.8	1.00	29	6	58.1	2.00	26	8
NM_013602	Mt1	metallothionein 1	1	354.2	1.62	218	9	212.3	2.30	112.3	6	415.7	1.23	293.6	8
BC009155	Mgst1	microsomal glutathione S-transferase 1	1	126.1	-1.41	182.5	9	103.7	-2.00	180.9	6	178.7	-1.52	195.3	8
NM_025569	Mgst3	microsomal glutathione S-transferase 3	1	517.3	1.32	284	9	345.9	2.14	186.5	6	178	-1.07	203.4	8
AW553649	Mttp	microsomal triglyceride transfer protein	1	120.4	1.23	80.4	9	85.8	2.14	75	6	54.1	-2.00	85.5	8

NM_008566	Mcmd5	mini chromosome maintenance deficient 5 (S. cerevisiae)	900.7	1.15	957.9	856.2	-1.07	905.6	827.2	1.87	526.7
NM_026331	Mscp-pending	mitochondrial solute carrier protein	474.5	1.15	379.9	353.8	1.87	204	261	1.23	257.7
NM_031260	Mov10l1	Moloney leukemia virus 10-like 1	68.3	-1.07	109.3	17.9	-3.25	87.1	97.9	1.07	78.9
NM_010783	Mdf1	MyoD family inhibitor	94	1.32	31.9	26.3	-4.92	73.7	12.4	1.87	9.3
C80049	Myh9	myosin heavy chain IX	945.8	1.15	781.5	2428.2	1.00	2349.2	930.4	-2.00	1855.3
NM_010861	Mylpc	myosin light chain, phosphorylatable, cardiac ventricles	101.4	-4.00	498.4	175.8	-10.56	1294.4	179	-11.31	1451.6
BC022734	Npl	N-acetylneuraminate pyruvate lyase	276.3	1.23	291.5	379.7	2.30	163.1	229.1	-1.41	385.4
NM_008726	Nppb	natriuretic peptide precursor type B	42.7	-5.66	230.3	68.3	-3.03	334.3	83.6	-5.66	595.8
BB317504	Nktr	natural killer tumor recognition sequence	60.4	2.30	18.8	122.5	-1.32	118.7	139.6	1.87	51.7
BB769209	Npc1	Niemann Pick type C1	102.4	1.62	48.5	124.3	-1.23	173.8	89.5	1.87	60.4
NM_008700	Nkx2-5	NK2 transcription factor related, locus 5 (Drosophila)	921.8	4.00	306.5	621.2	2.46	322	677.9	3.03	297
NM_013864	Ndr2	N-myc downstream regulated 2	96	1.62	81.4	68.7	-1.23	57.1	93.8	1.87	50.5
AI837704	Ndr4	N-myc downstream regulated 4	63.6	1.00	58.2	40	-1.87	58	44.8	-1.62	91
BG920261	Nsap1-pending	NS1-associated protein 1	10.3	-2.00	51.1	98.3	1.32	71.7	35.3	-2.14	60.3
AV231288	Sgsh	N-sulfoglucosamine sulfohydrolase (sulfamidase)	70.1	1.52	33.3	73.8	1.00	56.8	111.2	1.87	52.9
L09600	Nfe2	nuclear factor, erythroid derived 2	120.6	2.64	90.2	77	2.00	35.9	98.3	1.52	67.1
NM_009473	Nr1h2	nuclear receptor subfamily 1, group H, member 2	208.1	1.32	112.2	92.3	-1.07	79	126.8	1.87	77
AU066920	Nr2c2	nuclear receptor subfamily 2, group C, member 2	113.1	1.23	136.9	92.5	-1.32	128.1	125.9	2.00	61.2
NM_016710	Nsbp1	nucleosome binding protein 1	172.2	-1.41	294.8	327.7	1.32	214.8	232.8	-1.87	602
AB025413	Odz4	odd Oz/ten-m homolog 4 (Drosophila)	401	2.30	149.5	252.6	1.23	176.6	559.9	3.73	135.2
AF226605	Oprs1	opioid receptor, sigma 1	101.6	1.23	104.6	55.7	-1.87	101.1	84.6	2.46	33.1
NM_021551	Boct-pending	organic cation transporter	274.1	1.41	139.3	186.2	-1.07	210.6	311.3	1.87	109.8
AV016566	Pa26-pending	p53 regulated PA26 nuclear protein	44.9	1.00	62.6	45.5	1.32	34.7	63.6	-2.00	109.2
U54499	Pitx1	paired-like homeodomain transcription factor 1	67.1	1.15	65.2	46.7	-1.87	90.3	54.1	1.15	52.6
AF175771	Phemx	pan hematopoietic expression	80.2	7.46	6.9	46.3	13.93	5.1	62.2	1.62	34.7
BC015297	Palm	paralemmin	109.2	1.74	62.5	51.6	-1.23	52.5	56.6	3.03	21.5
AK011360	RIKEN cDNA 2610009E16 gene	parathymosin (Zinc-Binding11.5 kDa protein), full insert sequence.	624.4	1.87	364.9	204.2	-1.32	369.9	454.7	1.62	255.2
BC010821	Pyy	peptide YY	399.2	1.23	321.6	487.7	2.14	331.5	416.6	1.32	634.8
AV333851	Ppib	peptidylprolyl isomerase B	147.2	1.87	104.9	42.2	-1.15	51	72.4	1.32	59.8
NM_023662	Pcm1	pericentriolar material 1	3.7	-3.03	13.9	22.6	1.00	14.6	14	-3.25	35.1
AF224264	LOC233908	pigpen	261.7	-1.62	420.8	2372.8	1.23	2263.8	484.7	2.83	161.9
NM_021879	p	pink-eyed dilution	111.1	1.62	70.9	34.3	-1.32	45.7	91.9	2.00	24.6
AF069051	Pttg1	pituitary tumor-transforming 1	387	-1.07	437	464.7	1.87	306.7	801.8	1.00	890.5
NM_008955	Psx1	placenta specific homeobox 1	33.7	-1.32	36	26	1.00	22.1	17.5	-3.73	113.6
AF250838	Plac1	placental specific protein 1	291.8	-1.74	475.9	359.3	-2.64	964.6	293.6	-2.00	482.2
NM_032398	Plvap	plasmalemma vesicle associated protein	824.4	2.46	241.5	262.7	-1.15	251.4	395.9	1.62	230.1
M57683	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	73.6	-1.15	85.2	80.7	-1.07	84.5	128.7	2.30	39.1
AW537708	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	482.2	1.41	352.4	549.6	1.32	449.3	686.9	2.46	335.2
BB425239	Phip	pleckstrin homology domain interacting protein	184.6	-1.87	433.6	728.7	1.15	700.3	455.7	-1.23	546.4
AW123286	Plec1	plectin 1 mRNA, 3'UTR	669.4	2.30	274.8	220.7	-1.07	200.4	439.5	1.15	316.7
AW537289	Plagl2	pleiomorphic adenoma gene-like 2	159.5	3.25	43	95.4	1.32	62	126.6	2.00	55.5
BF453369	Pop3	popeye 3	505.8	-1.87	832	1017.9	1.87	580.7	844.9	-1.62	1322.8
BG865910	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	261.4	2.46	101.4	71.3	5.28	9.5	142.5	1.52	81
NM_010603	Kcnj12	potassium inwardly-rectifying channel, subfamily J, member 12	51	2.00	17.8	19.8	-1.23	24.1	87.7	2.46	29.8
L27453	Pbx1	pre B-cell leukemia transcription factor 1	397.3	1.62	141.6	252.2	1.23	193.7	339.9	2.30	138.4
NM_020031	Pfnd5	prefoldin 5	291.4	-1.32	221.3	345.7	1.23	350.8	179	-2.30	410.6
BC021405	Prnpip1	prion protein interacting protein 1	259.1	1.62	155.1	169.1	-1.15	228.5	215.2	2.00	115
AF352788	Pcolce2	procollagen C-endopeptidase enhancer 2	43.7	-2.00	93.7	68.5	-1.41	101.8	76.8	1.00	80
BF227507	Col1a2	procollagen, type I, alpha 2	1340.3	2.00	718.2	705.1	1.23	568.4	821.5	1.32	597.1
NM_031163	Col2a1	procollagen, type II, alpha 1	205.6	1.00	268.4	133.6	-2.00	275.7	208.3	-1.32	214.7
BG074456	Col9a3	procollagen, type IX, alpha 3	0.5	-5.28	5.9	6.5	1.41	5.6	0.7	-4.92	21.9
BI455189	Col6a2	procollagen, type VI, alpha 2	284.4	1.41	174.9	139.8	1.32	60.3	339.1	2.14	159.9
X75557	Pif2	proliferin 2	42.2	5.28	19.5	5.5	-16.00	50.7	45.8	-27.86	1467.8
NM_011874	Psmc4	proteasome (prosome, macropain) 26S subunit, ATPase, 4	440.1	-2.00	585.1	506.8	-1.15	776	862.9	-1.74	963.3
NM_025959	Psmc6	proteasome (prosome, macropain) 26S subunit,	8.5	-4.92	50.9	39.6	-1.07	56.5	68.3	1.00	74.7

BB337160	Slc21a11	solute carrier family 21 (organic anion transporter), member 11	16.4	1.07	19.8	27.7	-2.83	47.8	51.1	-2.00	131.3
NM_007885	Slc26a2	solute carrier family 26 (sulfate transporter), member 2	67.6	6.96	10.7	39.1	-2.14	93.3	65.2	1.62	34.1
NM_011895	Slc35a1	solute carrier family 35 (CMP-sialic acid transporter), member 1	57.9	-2.46	155.2	184.1	1.15	214	118.3	1.07	116.6
C86506	Slc35a5	solute carrier family 35, member A5	33.8	-1.52	64.2	111.8	2.64	38.4	89.8	-1.41	152.2
NM_011403	Slc4a1	solute carrier family 4 (anion exchanger), member 1	351.3	2.00	175.8	105.6	1.41	48.2	128.5	1.32	106
BB448377	Slc4a1	solute carrier family 4 (anion exchanger), member 1	572.9	2.83	158	183.9	2.46	72	144.9	-1.07	166.5
BG066200	Slc9a3r1	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 1	580.2	2.00	294.5	253.7	-1.23	294.1	371	1.52	260.5
BC025911	Snx6	sorting nexin 6	4.2	-18.38	159	2.8	-1.23	2.2	366.5	1.87	243.4
BB740660	Spna1	spectrin alpha 1	115	1.62	51.6	86.7	2.30	17.6	70.9	1.87	24.9
BC025823	LOC216892	spinster-like protein	588.5	2.14	303.4	184.3	1.74	114	373.8	1.52	196.6
BM941586	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	321.4	3.03	85.3	45	-1.15	48.8	76.2	-1.07	79.5
BG072739	Sox11	SRY-box containing gene 11	83	-1.23	86.8	305.4	1.15	220.8	190.5	1.87	92.1
BC010581	Stmn1	stathmin 1	120.8	-1.87	219.4	295.4	1.07	260.8	104.7	-1.74	258.3
NM_023057	Zak-pending	sterile-alpha motif and leucine zipper containing kinase AZK	72.5	1.52	45.8	26.5	1.15	10	57.9	2.14	19.9
BC007132	Supt5h	suppressor of Ty 5 homolog (S. cerevisiae)	852.6	2.46	397.9	407.9	1.32	321.7	581.8	1.07	497.8
AK019882	Swap70	SWAP complex protein	106.6	-1.07	155.4	94.4	-1.87	247.2	72.5	-1.32	99.3
NM_025891	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	840.2	1.62	478	458.3	1.23	409.7	849.7	2.83	292.5
AI324124	Snca	synuclein, alpha	286	1.87	172.4	253.4	4.29	43.9	156.2	1.07	210.8
NM_009221	Snca	synuclein, alpha	449.7	3.03	213.4	156.2	4.59	43.1	204.2	1.32	117.9
NM_011602	Tln	talin	372.3	1.87	122.3	112.9	-1.07	131.1	201.4	1.74	117.9
NM_011538	Tbx6	T-box 6	93.8	1.87	53.5	32.3	1.15	34	53.5	2.46	18.8
AK014409	Tctex1	t-complex testis expressed 1	20	-5.66	129	89.6	-2.46	235.9	35.5	-2.64	112.9
NM_011607	Tnc	tenascin C	322.8	2.83	118.9	132	2.00	86.5	320.7	4.00	68.6
AV294613	Tdgf1	teratocarcinoma-derived growth factor (cripto)	66.3	-1.87	111.3	288	1.87	151.7	94.9	-2.46	277.3
NM_021344	Tesc-pending	tescalcin	8.3	-1.15	16.4	3.2	-21.11	56.9	6.4	-1.07	10.5
NM_031383	Tex17	testis expressed gene 17	281.9	1.87	188	362	2.30	207.4	466.4	2.14	183.2
AB000682	Tex21-pending	testis expressed gene 21	3.6	-2.14	11.9	2.8	1.41	1.5	19.9	7.46	2.2
NM_027910	Peas-pending	testis intracellular mediator protein	2636.6	2.00	1771.5	1047	1.07	938.1	2154.2	1.62	1482.3
BB229004	Peas-pending	testis intracellular mediator protein	1691.7	2.14	939.9	601	-1.07	632.8	1598.8	1.62	837.5
NM_011582	Thbs4	thrombospondin 4	678.8	2.14	303.9	797.2	2.00	367.7	884	1.52	612.9
AF004833	Tfpi	tissue factor pathway inhibitor	506.8	-1.62	833.1	855.5	1.15	916.7	501.6	-2.00	1058.8
BB550860	Tcfap2c	transcription factor AP-2, gamma	35.1	1.62	33.4	18.7	2.46	4.4	23.2	-3.48	83.7
NM_011641	Trp63	transformation related protein 63	40.4	1.32	30.2	9.9	-2.46	26.8	50.8	-2.14	33.3
BB533460	Tgfb1	transforming growth factor, beta induced	63.4	-2.00	117.7	102.8	-1.23	102.6	68.7	-1.62	151.8
BB532080	Tgfb1	transforming growth factor, beta induced	186.3	1.15	231.3	57.4	-1.87	157	178.4	-1.07	90.7
AW551139	Tmem4	transmembrane protein 4	43.7	-1.15	30.8	36.4	1.07	28.5	59.3	2.64	17.5
AV152953	Ttr	transthyretin	1681.4	1.32	921.3	3123.3	2.14	1219.8	716	-1.74	1107.7
BC024702	Ttr	transthyretin	910	1.52	529.8	1251.3	2.46	569.9	305.9	1.00	342.2
BC003712	Trif-pending	Trif gene	10.6	-4.00	42.2	71	1.52	34.6	67.8	-1.07	70.1
NM_011280	Trim10	tripartite motif protein 10	351.3	2.00	240.1	215.9	2.00	102.9	174.3	1.62	120
BB033733	Trim16	tripartite motif protein 16	44.5	-1.23	37.1	31.5	1.15	33.4	72.4	2.83	24
NM_021883	Tmod1	tropomodulin 1	207.2	1.23	187.3	196.4	1.23	153.9	161.8	-2.14	372.6
NM_011618	Tnnt1	troponin T1, skeletal, slow	90.6	-1.15	121.2	84.6	-2.14	114.7	121.8	-1.23	123.5
BC018390	Tdo2	tryptophan 2,3-dioxygenase	65.6	-1.41	79.6	93.5	2.00	43.1	11.5	-2.00	18.2
AK004541	Wars	tryptophanyl-tRNA synthetase	274.3	1.23	232	208.7	1.15	191.9	281.9	2.14	144.9
BM118009	Tuba4	tubulin, alpha 4	91.8	1.87	61.5	46.1	-1.15	55.4	86.8	1.41	74.7
NM_010177	Tnfsf6	tumor necrosis factor (ligand) superfamily, member 6	52	1.07	41.2	7.7	-6.06	33.8	35.6	1.15	27.9
NM_011611	Tnfrsf5	tumor necrosis factor receptor superfamily, member 5	54.4	-1.41	128.7	57.2	-2.00	108.1	113.8	1.32	109.7
NM_009434	Tssc3	tumor-suppressing subchromosomal transferable fragment 3	1044.2	-1.74	1781.4	1390.6	-1.87	2524.8	1283.2	-1.32	1409.4
NM_007855	Twist2	twist homolog 2 (Drosophila)	194.8	1.32	109.6	70.2	-2.00	203.2	144.8	1.32	89.1
BI904914	Tpcn1	two pore channel 1	262.4	1.41	198.7	149.4	1.87	79.2	148.5	1.00	181.4
NM_018798	Ubqln2	ubiquilin 2	56.5	-1.07	66.1	45	-2.00	71.6	46.2	1.07	29.5
AK012427	Ubc	ubiquitin C	523.7	2.46	240.8	107.1	-1.15	89.5	100.7	-1.87	188.3
BC021792	Ubc-rs2	ubiquitin C, related sequence 2	579.3	1.23	646.4	412.7	1.07	435.5	483.2	2.14	221.8
AV313813	Uchl5	ubiquitin carboxyl-terminal esterase L5	31	-1.15	35.1	43.3	1.87	17.2	50.3	-1.07	76.9
BC019372	Ube2v1	ubiquitin-conjugating enzyme E2 variant 1	1301.4	2.00	520.8	303.8	1.15	326.1	687.6	1.62	378.8

AV328064	B3galt6	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	1.9	-4.00	13.3	4.5	-1.52	5.8	20.1	-2.14	54.4
AV370025	Ugp2	UDP-glucose pyrophosphorylase 2	10.2	-7.46	105.6	99.5	1.15	117.1	99.1	1.15	104.9
BB487752	Galnt2	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2	17.8	-8.00	107.6	130.1	-1.23	168	122.5	1.87	69.4
BI654068	Vps35	vacuolar protein sorting 35	66.4	-1.15	82.7	63.8	-1.07	71.3	111.6	2.64	39.8
NM_011693	Vcam1	vascular cell adhesion molecule 1	124.2	-2.83	377.4	158.5	-2.64	310.7	179.1	-2.64	410.2
NM_009506	Vegfc	vascular endothelial growth factor C	116.8	1.32	80.1	86.3	-1.15	117.3	187.1	1.87	85.8
BC027080	ErbB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian)	185.9	1.07	169.4	83.4	1.00	80.7	175	2.30	82.2
NM_013703	Vldlr	very low density lipoprotein receptor	49.2	1.32	38.1	54.2	2.00	23.7	39.1	1.15	48.2
BB552111	Vamp3	vesicle-associated membrane protein 3	1077.5	-3.25	3359.6	1972.6	-1.32	2979.6	2763	1.07	2514.4
NM_009509	Vil	villin	8.2	-3.48	39	47.3	2.83	13.3	12.1	-2.14	36
AK005091	Vsn1	visinin-like 1	137.9	2.83	72.7	164.7	2.14	75	193	2.64	63.5
NM_053236	V1rc6	vomer nasal 1 receptor, C6	12.7	-1.23	8.1	5.9	1.15	4.8	17.1	9.85	1.5
NM_009491	V2r16	vomer nasal 2, receptor, 16	17.2	-2.14	38.7	8.9	-1.07	15.1	37	1.87	19.3
BC026373	Wnt2	wingless-related MMTV integration site 2	719.1	1.00	801.6	784.4	1.23	615.1	988	2.30	486.4
BB067079	Wnt5a	wingless-related MMTV integration site 5A	94.4	1.00	90.9	71.7	-1.07	106	117.2	-1.87	196.1
NM_021365	Xlr4	X-linked lymphocyte-regulated 4	65.6	2.30	34.4	91	2.64	23.7	24.4	-2.46	59.6
BC025538	Xrcc4	X-ray repair complementing defective repair in Chinese hamster cells 4	24	-1.15	28	73.5	1.07	51	36.6	-2.00	91.9
NM_021559	Zfp191	zinc finger protein 191	192	-1.32	284.4	220.7	2.46	84.4	198.1	-1.52	337.6
AY028963	Zfp288	zinc finger protein 288	5.4	-1.23	3.7	56.9	4.00	10.2	31.4	1.15	37
NM_030743	Zfp313	zinc finger protein 313	80.6	1.15	68.8	86.8	-1.62	122	92.4	2.14	53.3
BC004747	Zfp386	zinc finger protein 386 (Kruppel-like)	67	-2.46	181.5	360.6	1.52	245.7	289.9	-1.23	352
NM_011765	Zfp97	zinc finger protein 97	30	-1.62	47.6	38	-2.00	92	41.5	1.07	51.6
NM_133358	LOC170938	zinc finger protein s11-6	72.2	1.15	73.7	74.5	-1.07	76	60.2	-2.14	124
BC028506	Zfx	zinc finger protein X-linked	30.2	1.41	21.9	19.6	-2.46	34.1	25.4	1.41	24.6
AA014267	Zfp1	zinc finger protein, multitype 1	802.5	2.83	229.1	169.7	1.52	151.9	288.6	1.62	179.3
NM_133967	Zdhc7	zinc finger, DHHC domain containing 7	413.8	1.32	330.8	220	-1.07	264.3	384.6	1.87	199.2

APPENDIX D

Transcripts Enriched or Depleted in the Left and Right Halves of The Wild Type and *Nkx2.5* Null Cardiac Crescent (Affymetrix Moe430v2 Genechip Data)

Appendix 4a. Transcripts enriched or depleted in the wildtype cardiac crescent.			Sample A			Sample B		
Sequence Derived From	Gene Symbol	Gene Name	Right Crescent Signal	Right Crescent vs. Left Crescent Fold Change	Left Crescent Signal	Right Crescent Signal	Right Crescent vs. Left Crescent Fold Change	Left Crescent Signal
L21027	Phgdh	3-phosphoglycerate dehydrogenase	323.8	-1.52	522.3	121.4	-2.30	286.8
NM_011062	Pdpk1	3-phosphoinositide dependent protein kinase-1	336.8	3.25	129	60.2	-1.07	90.8
C88269	Xrn2	5'-3' exoribonuclease 2	307.9	2.00	156.1	405.6	-1.07	405.5
BC018418	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	62.9	2.30	34	95.4	1.41	67.9
BC003735	Akap2	A kinase (PRKA) anchor protein 2	190.4	-2.00	438.1	255	-1.87	462.1
NM_138679	Ash1-pending	absent, small, or homeotic discs 1 (Drosophila)	111.5	1.87	70.4	120.7	-1.00	111.7
NM_130864	Acaa1	acetyl-Coenzyme A acyltransferase 1	129.7	-1.32	215	102.6	-2.00	201.3
NM_008094	Gba	acid beta glucosidase	48.5	-2.46	188.5	12.8	1.41	11.6
NM_021330	Acp1	acid phosphatase 1, soluble	659.9	1.87	405	724.9	-1.07	822.2
NM_021330	Acp1	acid phosphatase 1, soluble	624.6	2.30	242.9	468.7	-1.00	341.4
M12233	Acta1	actin, alpha 1, skeletal muscle	119	-4.59	579.7	48	-3.25	208.5
NM_007392	Acta2	actin, alpha 2, smooth muscle, aorta	3270.6	-1.74	4648.9	3957.7	-1.87	5736.4
NM_007393	Actb	actin, beta, cytoplasmic	273.8	-1.15	268.3	288.9	2.14	159.4
NM_033268	Actn2	actinin alpha 2	80.1	-3.48	273.1	28.8	-3.25	113.6
AK019491	Add3	adducin 3 (gamma)	207	-1.87	410.3	455.7	1.41	309.4
BQ176297	Adcy7	adenylate cyclase 7	39	1.87	16.1	19.7	1.74	7.7
NM_021515	Ak1	adenylate kinase 1	138.1	-1.87	299.5	135.5	-1.74	231.4
AV261931	Cap2	adenylyl cyclase-associated protein 2	213.7	-2.83	673.8	400.5	-1.52	599.9
AB035383	Arl6ip4	ADP-ribosylation-like factor 6 interacting protein 4	1216	1.07	1133.1	517.7	-2.00	1113.5
NM_007412	Admr	adrenomedullin receptor	229.2	-1.15	293.1	198.1	2.00	61.9
A1462635	Aldh2	aldehyde dehydrogenase 2, mitochondrial	289.8	2.00	131.3	869.9	1.87	353.9
NM_009022	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	114.1	2.00	84.3	170.1	1.23	160.9
NM_007423	Afp	alpha fetoprotein	427.1	-1.62	711.7	0.9	-274.37	315.9
NM_007423	Afp	alpha fetoprotein	141.2	-1.23	172	55.9	-2.64	151.5
AV124668	Afp	alpha fetoprotein	175.5	1.00	175.1	1	-103.97	105.5
BM230515	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	72.7	2.64	33.7	107.3	1.52	98.4
BM225096	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	256.2	4.29	57.9	138.6	-1.07	165.7
BQ177140	Amph	amphiphysin	191.5	-3.73	521.6	533.7	-1.74	686.5
AA681807	Agl	amylo-1,6-glucosidase, 4-alpha-glucanotransferase	56	-2.00	104.8	39.7	1.07	36
BF468097	Aamp	angio-associated migratory protein	601	-1.41	766.2	282.2	-2.14	680.2
BC021657	Ank3	ankyrin 3, epithelial	79.9	-2.30	256.8	103.6	-2.00	179
BB628935	Ank3	ankyrin 3, epithelial	203.5	-2.00	270.8	122.6	-1.52	244.6
AF302127	Ankrd3	ankyrin repeat domain 3	67.3	-2.64	128.3	60.3	-2.30	125.7
NM_007463	Apeg1	aortic preferentially expressed gene 1	95.1	-3.48	361.3	88.4	-2.00	208.6
AI527359	Apoa1	apolipoprotein A-I	388.9	-1.62	752.1	31.6	-1.87	191.7
NM_009694	Apobec2	apolipoprotein B editing complex 2	102.5	-3.03	372.7	146.8	-1.74	254.1
AK019319	Apoe	apolipoprotein E	425.6	-2.30	1218.8	168.2	-6.06	1031
AK020468	Aqr	aquarius	55.7	2.00	28.2	89.4	1.52	61.1
BB554189	Alox12	arachidonate 12-lipoxygenase	26.5	5.66	4.2	13.6	-1.87	29.9
AI851258	Arap3-pending	ARF-GAP, RHO-GAP, ankyrin repeat and plekstrin homology domains-containing protein 3	86.4	-1.07	133.9	129.4	2.64	43

NM_007482	Arg1	arginase 1, liver	142.7	2.00	69.6	549	1.41	402.9
NM_016847	Avpr1a	arginine vasopressin receptor 1A	35.9	2.14	16.8	38.6	1.41	45.5
BG228102	Actr1b	ARP1 actin-related protein 1 homolog B (yeast)	96.3	-1.87	158.5	49	-2.14	129.6
NM_009709	Arnt	aryl hydrocarbon receptor nuclear translocator	53.6	2.14	38.3	142.6	1.41	106.6
AV312905	Asf1a	ASF1 anti-silencing function 1 homolog A (S. cerevisiae)	45.1	2.30	19.5	33	1.23	22.1
NM_016878	Dnpep	aspartyl aminopeptidase	422.5	-1.87	874.5	400.8	-1.74	868.2
AA245637	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	478.9	-2.14	1393	436.1	-1.23	557.6
NM_009722	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	1489.5	-1.87	3172	2148.6	-1.23	2849.8
NM_007508	Atp6v1a1	ATPase, H+ transporting, V1 subunit A, isoform 1	587.2	2.14	269.9	602.4	1.23	361.9
NM_029121	Atp6v1e2	ATPase, H+ transporting, V1 subunit E-like 2 isoform 2	60.5	1.87	25.4	41.8	-1.07	53.3
NM_138652	Atp12a	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	28.6	5.66	3.6	36	1.07	31
BC025618	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	463	-2.46	1210.3	474.1	-1.87	873
BC025618	Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	305.3	-2.14	647.8	174.2	-1.32	201
BC027319	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	282.5	-1.23	392.6	132.5	-2.30	357.9
AU045006	Bce1-pending	B lymphocyte gene 1	145.2	-1.52	181.6	120.9	-2.00	158.1
BM932775	Bzw2	basic leucine zipper and W2 domains 2	1613.6	2.00	542	857.3	1.32	612.5
AW322026	Btg1	B-cell translocation gene 1, anti-proliferative	320.6	-1.62	599	336.5	-2.00	712.3
NM_016778	Bok	Bcl-2-related ovarian killer protein	102.7	-2.30	316.4	153.7	-1.07	221.4
AV231340	Btc	betacellulin, epidermal growth factor family member	123.2	2.14	60	158.3	1.32	126.9
NM_024285	Bves	blood vessel epicardial substance	92.2	-2.83	304	110	-2.64	381.7
AF153440	Bambi	BMP and activin membrane-bound inhibitor, homolog (Xenopus laevis)	277	-2.00	778.4	793.9	-1.62	1229.2
BC024449	Bbx	bobby sox homolog (Drosophila)	365.1	3.25	118.9	296.8	2.00	102.7
NM_007554	Bmp4	bone morphogenetic protein 4	429.8	1.87	216.7	330.8	1.62	204.1
NM_007557	Bmp7	bone morphogenetic protein 7	72.2	-1.87	123	146.2	-1.41	110.5
AV233519	Bmpr1a	bone morphogenetic protein receptor, type 1A	88.8	-2.14	218.2	253.7	1.07	159.3
NM_009309	T	brachyury	143.2	2.83	43.9	115.9	1.74	81.3
NM_019999	Brp17	brain protein 17	40.1	-2.14	74.8	33.5	1.41	26.1
AA940256	Bcas2	breast carcinoma amplified sequence 2	135	-1.15	127.4	75.6	-1.87	112.9
NM_011714	Baz1b	bromodomain adjacent to zinc finger domain, 1B	60.6	2.30	25.9	48.1	1.23	38
BM950003	Hspc121-pending	butyrate-induced transcript 1	115.4	2.14	54.7	119.4	1.41	83.4
NM_007701	Chx10	C. elegans ceh-10 homeo domain containing homolog	73	1.87	37	252.2	1.52	87.9
NM_009864	Cdh1	cadherin 1	88.4	-2.46	223.6	92.3	-4.00	236.2
AW543698	Cdh5	cadherin 5	218	-1.23	223.4	291.5	2.14	149.4
BB048682	Cacna1d	calcium channel, voltage-dependent, L type, alpha 1D subunit	33.2	-3.03	191.7	50.8	-1.62	125.2
AV047570	Calm3	calmodulin 3	124.7	2.30	25.4	313.5	1.87	210.6
AI747133	Capn6	calpain 6	430.7	-2.00	735	856.5	-1.23	1009.6
NM_009922	Cnn1	calponin 1	30.3	-10.56	296.6	76.8	-1.15	84.9
BG065300	Clstn1	calsyntenin 1	109.2	-1.87	214.1	135.7	-1.32	203.5
NM_020501	T2r5	candidate taste receptor T2R5 gene	50.6	2.00	24.1	36.2	1.52	30
AK010166	Car13	carbonic anhydrase 13	49.1	1.87	37.6	79.3	1.32	42.4
NM_007607	Car4	carbonic anhydrase 4	195.5	-2.30	465.1	323.9	-2.30	455.7
NM_007607	Car4	carbonic anhydrase 4	477.8	-2.00	693	590.3	-1.41	724.3
NM_007754	Cpd	carboxypeptidase D	235.2	1.74	156.6	266.2	1.87	137.8
AK009959	Crap	cardiac responsive adriamycin protein	411.3	-3.73	1507.8	721.1	-2.14	1982.3
NM_013468	Crap	cardiac responsive adriamycin protein	301.2	-3.25	753.3	573.9	-2.14	944.5
NM_007786	Csnk	casein kappa	163.6	3.03	52.8	204.7	2.00	94.4
BB283759	Csnk2a1-rs4	casein kinase II, alpha 1 related sequence 4	343.9	1.15	300.4	499.9	-1.87	905
NM_009975	Csnk2b	casein kinase II, beta subunit	776.7	-1.23	1183.2	1168	1.87	554.7
NM_138315	Mical-pending	CasL interacting molecule	115.2	-1.87	142.9	50.7	-2.00	133.8
BI134907	Catnb	catenin beta	45.7	-2.00	62.7	60.1	-1.62	75.1
NM_009822	Cbfa2t1h	CBFA2T1 identified gene homolog (human)	51.6	-2.00	111.6	28.8	-4.59	86.6
X79989	Cbfa2t1h	CBFA2T1 identified gene homolog (human)	64.2	-1.23	61.6	54.3	-2.30	121.3
NM_009882	Cebpa-rs1	CCAAT/enhancer binding protein alpha (C/EBP), related sequence 1	829	1.87	528.8	500.8	1.32	356.3
BB836888	Ctcf	CCCTC-binding factor	957.5	1.87	510.8	473.3	-1.00	429
BB560574	Cd24a	CD24a antigen	889.2	-1.41	1288.3	687.2	-2.00	1359
NM_013929	Siva-pending	Cd27 binding protein (Hindu God of destruction)	421.6	1.00	362.5	69.5	-4.59	362.3
NM_133654	Cd34	CD34 antigen	284.4	-1.15	318.8	232.1	2.00	110.6
BF147656	Cdc5l	cell division cycle 5-like (S. pombe)	432.3	1.87	211.5	507.4	1.62	329.1
NM_011804	Creg	cellular repressor of E1A-stimulated genes	679.3	1.87	379.9	307.8	1.41	213.6

AK008801	Cgi94-pending	CGI-94 protein	100.4	-1.15	172.2	177.2	2.00	73.6
AL024092	Cct3	chaperonin subunit 3 (gamma)	618.7	-1.23	768.1	290.3	-1.87	511.8
AV216906	Cct4	chaperonin subunit 4 (delta)	296.5	2.00	115.7	471.9	1.41	275.3
NM_007638	Cct7	chaperonin subunit 7 (eta)	2301.3	-1.15	2585	700.5	-2.83	1627
BG867337	Ccl28	chemokine (C-C motif) ligand 28	23	2.46	9.9	33.4	1.07	40.1
NM_009835	Ccr6	chemokine (C-C motif) receptor 6	112	1.87	55.4	153.8	1.32	106.9
BC015254	Cmkor1	chemokine orphan receptor 1	76.7	-1.23	83.5	58.1	-1.87	100.1
BI692925	Cspg2	chondroitin sulfate proteoglycan 2	409.1	-1.87	969	1300.8	-1.00	1408.1
NM_021350	Chml	choroideremia-like	65.4	4.92	14.7	82	1.52	40
BB702347	Hcapg-pending	chromosome condensation protein G	297.2	3.25	65.1	251.6	1.15	310.2
BC005718	Cldn6	claudin 6	338.6	-2.46	596.3	116.8	-2.30	353
BC008104	Cldn7	claudin 7	93.5	-1.74	230.3	62.5	-2.30	144.6
BB160417	Cotl1	coactosin-like 1 (Dictyostelium)	208	-2.30	508.8	80.9	1.32	49.2
BC011068	Cotl1	coactosin-like 1 (Dictyostelium)	99.6	-2.14	250.9	247.2	1.32	203.8
AV109541	Copb2	coatamer protein complex, subunit beta 2 (beta prime)	324.1	-1.23	679.2	227	-2.46	726.3
BB316578	Copg2as2	coatamer protein complex, subunit gamma 2, antisense 2	43.4	2.46	19.8	37.9	5.66	6.6
NM_007687	Cfl1	cofilin 1, non-muscle	814.5	-1.15	654.2	151.3	2.14	35.6
NM_032006	Mcola-pending	collagenase-like A	40.5	2.46	18.9	61.4	2.14	37.3
NM_010740	C1qr1	complement component 1, q subcomponent, receptor 1	273.1	1.15	314.2	118.9	2.64	47.2
BC018243	Chuk	conserved helix-loop-helix ubiquitous kinase	96.3	2.14	56.7	60.5	1.32	65.6
BG800611	Copeb	core promoter element binding protein	77.8	2.30	33.9	136.2	1.62	65.1
BG967663	Ckb	creatine kinase, brain	200	-2.83	533.9	130.5	-1.87	238.4
NM_025613	Cri1	CREBBP/EP300 inhibitory protein 1	140.6	-2.14	289.6	99	1.87	35.2
BF303057	Cry2	cryptochrome 2 (photolyase-like)	11.2	-3.73	41.4	11.1	-1.07	13.9
AV016515	Cryab	crystallin, alpha B	177.2	-4.00	859.5	393.3	-2.30	723
NM_009964	Cryab	crystallin, alpha B	55.8	-3.25	425.6	88.3	-1.62	183.6
BG976607	Cryl1	crystallin, lamda 1	891.6	2.46	437.6	203.3	1.23	199.3
BI076485	Cryl1	crystallin, lamda 1	419.2	3.03	114.4	307.9	1.52	195.3
NM_020008	Clecsf12	C-type (calcium dependent, carbohydrate recognition domain) lectin, superfamily member 12	85.3	2.14	40.7	92.9	1.32	96
AF197159	Cubn	cubilin (intrinsic factor-cobalamin receptor)	252.8	-1.32	344.8	7.7	-13.00	114.5
AF090696	Cugbp2	CUG triplet repeat, RNA binding protein 2	82.6	-1.23	129.3	31.5	-2.64	118.9
BM118679	Ccnd2	cyclin D2	31.7	-1.23	26.8	34.8	-4.29	116.9
BM250672	Ccnl	cyclin L1	1558.5	1.87	826.4	975.2	1.62	614.5
BM216130	Ccnt2	cyclin T2	126.5	-1.23	157.2	164.8	-1.87	232.6
NM_009876	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	939.7	-2.83	2576.9	1141.3	-1.41	2245.4
NM_033037	Cdo1	cysteine dioxygenase 1, cytosolic	50.4	-2.00	136.8	89.1	-1.62	113.2
NM_010516	Cyr61	cysteine rich protein 61	102.1	-2.00	202.7	203.3	-1.32	258.2
BM202770	Cyr61	cysteine rich protein 61	67	-1.87	130.9	75.7	-1.41	134.9
NM_013808	Csrp3	cysteine-rich protein 3	346	-2.14	809.3	625.4	-1.41	853.4
BB499142	Ctps2	cytidine 5'-triphosphate synthase 2	59.3	1.87	24.1	80.9	1.52	67
AK018713	Cyba	cytochrome b-245, alpha polypeptide	262.8	-2.00	496.6	157.8	-2.30	433
AF037370	Cox7a1	cytochrome c oxidase, subunit VIIa 1	35	-2.30	59.8	52.7	-1.52	92.4
NM_007796	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	286.2	1.00	407.6	312	2.14	175.7
NM_007796	Ctla2a	cytotoxic T lymphocyte-associated protein 2 alpha	440	1.07	426.3	473	2.30	172.4
BG064656	Ctla2b	cytotoxic T lymphocyte-associated protein 2 beta	458.5	1.15	396.3	360	2.00	172.8
NM_021532	Dact1	dapper homolog 1, antagonist of beta-catenin (xenopus)	271.5	-1.87	437.8	646.5	-1.32	683.7
BM247863	Dri2	dead ringer homolog 2 (Drosophila)	183.3	-2.00	561.4	53	-1.87	108.2
BB488020	Ddx10	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 10 (RNA helicase)	196.4	2.14	85.3	188.9	1.07	219.4
BB458655	Ddx26	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 26	400.9	-1.87	753.1	1043.1	-1.00	1100.3
BC011321	Ddx27	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 27	201.1	1.07	214.3	39.4	-2.00	115.2
BC021452	Ddx6	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 6	376.2	2.46	142.6	321.9	1.07	339.8
U91922	Ddx9	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9	1090.9	1.07	1157.8	1018.2	-2.00	1902.9
U91922	Ddx9	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 9	132.8	1.23	91.2	58.1	-2.30	119.4
AA738859	Des	desmin	164.9	-2.00	190.3	51.2	2.00	16.5
Y15910	Diap2	diaphanous homolog 2 (Drosophila)	64.1	1.87	27.1	48.7	1.52	25.9
NM_029787	Dia1	diaphorase 1 (NADH)	272.6	-2.00	559.3	96.3	-2.83	298
NM_016765	Ddah2	dimethylarginine dimethylaminohydrolase 2	856.8	-1.41	1527.7	517.4	-1.87	1408.3
BB234940	Ddr1	discoidin domain receptor family, member 1	76	-2.14	96.9	49.8	-2.00	82.9
AF438610	Dmap1	DNA methyltransferase 1-associated protein 1	271	-1.23	337.7	159.9	-2.46	389.1

AF071068	Ddc	dopa decarboxylase	177.9	-2.14	340.1	291.3	-1.62	507.1
NM_024438	Dusp19	dual specificity phosphatase 19	162.9	1.00	168.2	101.5	-1.87	199.4
AV295798	Dusp9	dual specificity phosphatase 9	66.4	-2.64	196.7	138.1	-1.41	288.5
AV295798	Dusp9	dual specificity phosphatase 9	175.7	-1.87	333.3	319.9	-1.15	334.7
BB150886	Dst	dystonin	28.7	-2.83	100.8	18.3	-4.59	72.1
BB151715	Ets1	E26 avian leukemia oncogene 1, 5' domain	369	1.15	328.3	319.7	2.46	152.2
BB151715	Ets1	E26 avian leukemia oncogene 1, 5' domain	414	1.41	330.3	760.6	2.83	291.5
BC010588	Ets1	E26 avian leukemia oncogene 1, 5' domain	121.4	1.87	76.3	100.5	1.23	73.8
BC027739	Elf2	E74-like factor 2	607.3	2.46	205	422	1.32	289.3
AK007491	Ebna1bp2	EBNA1 binding protein 2	1542.3	1.23	1178.9	486.4	-1.87	1071.7
NM_010161	Evi2	ecotropic viral integration site 2	39.3	2.00	19.1	46	1.15	37.8
BM120053	Enc1	ectodermal-neural cortex 1	694.3	2.00	266.5	1619.8	2.00	624.5
BC005686	Elk3	ELK3, member of ETS oncogene family	287.7	1.23	259	206	2.30	113
NM_010112	Efs	embryonal Fyn-associated substrate	151.2	-1.87	191.8	345.6	1.07	246.9
AW553781	Evl	Ena-vasodilator stimulated phosphoprotein	130.2	-1.87	211.3	119.1	-1.62	212.8
AF361882	Esam-pending	endothelial cell-selective adhesion molecule	706.3	1.00	569.7	845.7	1.87	457.8
NM_013690	Tek	endothelial-specific receptor tyrosine kinase	326.7	-1.23	409.1	495	1.87	269.2
AK009464	Enh-pending	enigma homolog (R. norvegicus)	231	-2.30	349.8	208.3	-1.62	326.3
BC002020	Enh-pending	enigma homolog (R. norvegicus)	222.7	-2.00	621.1	375	-1.23	403.7
NM_007933	Eno3	enolase 3, beta muscle	460.9	-2.00	797.4	487.4	-1.62	604.3
NM_007937	Epha5	Eph receptor A5	40	2.00	21	82.9	-1.00	98
BC015076	Eva	epithelial V-like antigen	16.8	-2.64	64	17.3	-1.87	23.1
BE686792	edr	erythroid differentiation regulator	49	1.15	39.1	50.1	-3.48	160.9
NM_007959	Etsrp71	ets related protein 71	1239.1	3.73	361.9	750.2	1.52	422.4
AF218539	Etv3	ets variant gene 3	241.4	2.14	75.6	127.3	1.07	150.1
BB835796	Elf3	eukaryotic translation initiation factor 3	225.9	4.59	48.8	86.9	1.41	36.9
NM_007968	Ewsh	Ewing sarcoma homolog	68.7	-2.14	150	13.7	-18.38	212.4
AK004726	Xlkd1	extra cellular link domain-containing 1	333.7	-1.87	505.6	23	-1.41	27.3
NM_011810	Faim	Fas apoptotic inhibitory molecule	254.5	1.15	198.8	124.1	-1.87	218.8
AV026617	Fos	FBJ osteosarcoma oncogene	131.5	-2.14	278.1	377.5	1.23	328.6
AF441120	Fbxo32	F-box only protein 32	73.3	-5.28	364.6	173.6	-1.52	283.9
BB097480	Farp1	FERMRhoGEF (Arhgef) and pleckstrin domain protein 1 (chondrocyte-derived)	179.1	-2.14	295.1	168.8	1.23	169.4
AY049085	Fev-pending	Fev protein	153.1	1.87	88.3	240.2	1.52	151
NM_007993	Fbn1	fibrillin 1	75.3	-1.87	171.1	157.7	-1.15	162.2
NM_010181	Fbn2	fibrillin 2	550.9	1.07	587.1	389.4	2.46	157.6
U18673	Fgf8	fibroblast growth factor 8	3.2	-10.56	33.6	6.5	-10.56	60
AF321301	Fgfr1	fibroblast growth factor receptor-like 1	56.2	-2.46	118.7	80.2	-1.23	166.7
NM_021716	Fign	fidgetin	92.5	2.14	50.9	90.8	-1.00	77.7
NM_008020	Fkbp2	FK506 binding protein 2	512.1	1.23	396.5	211.3	-2.46	442.4
BC003447	Fkbp4	FK506 binding protein 4	1009.5	-1.15	1188.5	532.6	-2.46	1532.9
BB456860	Fkbp4	FK506 binding protein 4	123.5	1.87	77	130.6	1.41	73.1
NM_010222	Fkbp7	FK506 binding protein 7	136.8	-1.07	117.2	141	2.00	110.9
NM_022009	Flii	flightless I homolog (Drosophila)	250.3	-2.14	434.8	168	-1.32	231
D88690	Flt1	FMS-like tyrosine kinase 1	320.6	2.14	186	341.9	1.74	205.8
NM_010228	Flt1	FMS-like tyrosine kinase 1	266.7	2.14	166.4	286	3.03	100.3
NM_008046	Fst	follicle-stimulating hormone receptor	159.5	2.00	70	176.6	-1.32	289.5
NM_008259	Foxa1	forkhead box A1	31.5	-5.28	170.1	73.3	-2.83	125.2
NM_019739	Foxo1	forkhead box O1	153.5	2.00	65.3	120.3	1.62	87.6
BG064340	Fnbp3	formin binding protein 3	271.2	1.87	164.8	175.4	1.15	167.6
U41739	Fhl1	four and a half LIM domains 1	1131.2	-2.14	2339.2	1601	-1.74	2562.6
NM_008026	Fli1	Friend leukemia integration 1	260.1	2.14	117.3	258.7	2.00	104.5
NM_011356	Frzb	frizzled-related protein	19.4	-14.93	218.3	134.8	-1.52	320.8
NM_016905	Galk1	galactokinase 1	1211.6	-1.07	1213.7	305	-2.00	855
BF150771	Ggtb3	galactosyltransferase 3 beta 1, 4	250.7	2.14	73.2	176.6	1.32	100.2
NM_010253	Gal	galanin	78.2	-2.00	216.2	101.2	-1.52	95.6
NM_010268	Gdap10	ganglioside-induced differentiation-associated-protein 10	342.7	1.15	338.4	239.1	2.00	117.8
AF216832	Gja4	gap junction membrane channel protein alpha 4	228.3	1.15	222.1	280.4	1.87	134.4
BB447551	Gata5	GATA binding protein 5	126.6	-2.64	294.2	258.2	-1.32	288.8
AV352659	Grcc8	gene rich cluster, C8 gene	66.7	1.87	28.5	124.8	1.32	92.5
BE688673	Gtf2h1	general transcription factor II H, polypeptide 1	580.1	2.00	332.3	390.4	-1.07	325.3
AY030292	Gtf2i	general transcription factor II I	1261	-1.23	1681.4	869.8	-1.87	2303.2

BF165548	LOC225028	germinal center kinase-like kinase-like	137.3	-2.00	322.5	243.7	-1.52	279.6
NM_022024	Gmfg	glia maturation factor, gamma	218.2	1.00	183.3	210.6	3.48	70.3
BC017637	Gltscr2	glioma tumor suppressor candidate region gene 2	278.8	-1.52	414.7	9.7	-17.15	260.7
AF201288	Gilz	glucocorticoid-induced leucine zipper	85.9	-1.87	125.1	60.1	-1.07	115.5
BF319868	Grp58	glucose regulated protein	257.3	-2.14	515.5	212	1.23	174.7
NM_008129	Gclm	glutamate-cysteine ligase, modifier subunit	647.8	2.30	278	127.2	-1.00	128.5
NM_007934	Enpep	glutamyl aminopeptidase	27.2	-1.87	66.4	106.3	-1.00	102.4
BM238943	Eprs	glutamyl-prolyl-tRNA synthetase	420.4	1.87	251.6	555.9	1.07	379.4
BM238943	Eprs	glutamyl-prolyl-tRNA synthetase	1200.1	2.30	568.7	644	1.23	579
NM_008161	Gpx3	glutathione peroxidase 3	298.1	-2.64	1070.4	283.6	-1.07	303.1
NM_008182	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	47.7	2.14	23	44.3	1.07	40.3
BC012254	Gstt1	glutathione S-transferase, theta 1	115	-2.00	221.4	193.8	-1.23	275.9
NM_010274	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	969.8	1.87	588	395.1	1.74	213.5
NM_013847	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	315	1.00	317.6	29.4	-8.57	253
NM_008195	Gys3	glycogen synthase 3, brain	58.1	-2.46	144.3	27.4	1.15	24.1
NM_013755	Gyg1	glycogenin 1	230.8	-2.64	872.5	186.5	-1.74	480.3
NM_010369	Gypa	glycophorin A	150.1	1.87	93.6	3.2	1.23	2.6
AW107802	Gpc3	glypican 3	197.3	-2.00	300.8	686.1	-1.23	815.6
BI965035	Gocap1	golgi complex associated protein 1	87.2	-1.62	128.4	70.5	-3.73	361.6
AK007410	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	292.7	1.00	350.5	111.8	-2.46	413.7
NM_025278	Gng12	guanine nucleotide binding protein (G protein), gamma 12	218.5	1.87	119.2	193.5	-1.00	149.1
BF472806	Gucylb3	guanylate cyclase 1, soluble, beta 3	22.6	-3.48	64.1	66.7	-2.30	120.6
BC022974	H2-Ke2	H2-K region expressed gene 2	2472	1.07	1923.9	783.1	-2.00	1507
NM_008202	H2-Ke4	H2-K region expressed gene 4	236.5	-1.32	366.5	210.6	-1.87	394.3
NM_013904	Hey2	hairy/enhancer-of-split related with YRPW motif 2	28.5	-2.14	61.5	45.8	-1.52	77.3
NM_008284	Hras1	Harvey rat sarcoma virus oncogene 1	521.8	-1.23	641.1	241.9	-2.00	528
AY044451	Hak-pending	heart alpha-kinase	109.8	-2.64	283	116.3	-1.07	171.6
U03561	Hspb1	heat shock protein 1	192.6	-2.83	526.1	78.8	-2.14	166.4
C77384	Hspca	heat shock protein 1, alpha	6401.6	1.87	3160.2	5187.6	-1.15	6114.1
BI154147	Hspcb	heat shock protein 1, beta	3975	1.52	2572.1	1774.6	-2.00	3223.3
AK012780	Hspb2	heat shock protein 2	152.5	-1.87	283.2	114.1	-1.87	240.9
BM124741	Hspb7	heat shock protein family, member 7 (cardiovascular)	87.1	-2.00	219.6	89.2	-1.32	129.8
NM_053149	Hemgn	hemogen	146.1	1.87	77.2	23.2	1.15	23.9
NM_018805	Hs3st3b	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B	135.9	2.00	77.7	146.7	1.23	126
AK007802	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	617.4	-1.32	782.8	588.8	-1.87	968.1
BE685966	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	673.6	-1.23	800.5	581.3	-1.87	1137.3
BF320908	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	501.6	-1.15	594.8	632.2	-2.14	1037.2
AK007802	Hnrpa1	heterogeneous nuclear ribonucleoprotein A1	898.5	1.00	1011.7	908.8	-2.14	1640.4
NM_016690	Hnrpd1	heterogeneous nuclear ribonucleoprotein D-like	1712.5	1.23	1596.6	1115	-1.87	2283.3
BF228203	Hnrpu	heterogeneous nuclear ribonucleoprotein U	602.4	1.15	552	931	-2.30	1867.8
AV225808	Hexb	hexosaminidase B	25	-1.87	80	32.7	-1.23	24.8
C77256	Hdlbp	high density lipoprotein (HDL) binding protein	81.4	2.14	45.2	81.1	1.41	72.7
NM_010440	Hmg20b	high mobility group 20 B	27.8	-2.14	65.5	24.9	-1.07	42.3
AI648759	Hmgb1	high mobility group box 1	5339.2	3.25	1936.5	5512.9	1.87	2913.4
BF166000	Hmgb1	high mobility group box 1	415.6	4.00	96.7	132.8	-1.00	133.9
AV127023	Hmgb1	high mobility group box 1	4924.1	4.00	1278.2	5680.2	2.30	1834.3
BC020088	Hars	histidyl-tRNA synthetase	911.2	1.15	857	334	-2.64	872.6
M29881	H2-Q7	histocompatibility 2, Q region locus 7	54.6	2.46	27.9	60	1.15	32.6
W91024	Hist1h2ae	histone 1, H2ae	3444	1.07	3299.8	1104.1	-2.83	3474.3
NM_008229	Hdac2	histone deacetylase 2	350.1	-1.32	469.6	284.8	-1.87	519.5
AW556220	Bat1a	HLA-B-associated transcript 1A	24.8	2.30	9.5	6.9	-4.00	26.4
NM_023130	Raly	hnRNP-associated with lethal yellow	174.8	-2.30	570	129.6	-1.41	159.4
NM_010449	Hoxa1	homeo box A1	567.1	2.14	235.2	769.6	2.14	265.8
AA987181	Hoxa9	homeo box A9	130.4	19.70	3.8	57.4	11.31	7.1
AK017686	Hoxb1	homeo box B1	280.9	4.59	87.3	219.7	2.14	102.9
BC016893	Hoxb6	homeo box B6	71.5	2.14	36.4	60.5	1.32	46.4
X13721	Hoxb8	homeo box B8	74.4	1.07	100.4	125.3	2.30	59.7
AV003728	Hkp1	house-keeping protein 1	417.7	1.87	286.4	221.8	1.15	191.5
NM_010437	Hivep2	human immunodeficiency virus type I enhancer binding protein 2	33.3	2.14	17	43.7	1.07	45.8
NM_008216	Has2	hyaluronan synthase 2	141.8	-2.46	609.4	202.9	-2.00	513.2
U69695	Has2	hyaluronan synthase 2	304.8	-2.00	547.2	338.3	-2.46	846.8

NM_008317	Hyal1	hyaluronidase 1	78.1	1.87	45	84.6	-1.00	91.7
BC014739	Ik	IK cytokine	564.6	-1.32	678.1	208.9	-3.73	796.3
BC014739	Ik	IK cytokine	776.1	-1.15	833.2	404.6	-2.30	582.7
NM_010499	Ier2	immediate early response 2	296.6	-1.74	684.2	294.3	-2.64	708.3
BC005577	Ian1	immune associated nucleotide 1	274.2	-1.15	332	156.1	2.00	103.1
BC006026	Igj	immunoglobulin joining chain	28	7.46	3.3	35.8	1.52	19.8
U62527	Igk-V8	immunoglobulin kappa chain variable 8 (V8)	33	5.28	7.8	15.9	-1.74	43.2
AF317839	Igsf9	immunoglobulin superfamily, member 9	103.2	-2.14	147.8	137.6	-1.07	178.3
L04961	Xist	inactive X specific transcripts	46.4	10.56	2.2	1205.1	1.32	949.4
BC010404	Inhbe	inhibin beta E	69.1	2.30	33.7	82	1.07	70.3
U43884	Idb1	inhibitor of DNA binding 1	462.8	-2.30	830.8	643.1	-1.74	1039.2
AA216889	Idb2	inhibitor of DNA binding 2	76.7	2.00	36.7	103.4	1.23	94.2
W77144	Idb4	inhibitor of DNA binding 4	54.1	-2.00	89.6	82.6	-1.62	120
BB042583	Ing4	inhibitor of growth family, member 4	50.3	-1.87	113.5	46.5	-2.83	107.8
AV296697	Ikbkap	inhibitor of kappa light polypeptide enhancer in B-cells, kinase complex-associated protein	188.9	2.83	78.4	302.3	1.23	330
AK011784	Igfbp2	insulin-like growth factor binding protein 2	307.1	-1.62	509.3	80.3	-2.30	232.2
BC019836	Igfbp4	insulin-like growth factor binding protein 4	2551.6	-1.15	3129.6	1530.1	2.00	862.5
BF225802	Igfbp5	insulin-like growth factor binding protein 5	325.9	-1.87	669.1	314.2	-1.00	269.2
AA275072	Itn2a	integral membrane protein 2A	518.9	-2.14	1093	658.2	-1.41	1084
BC021786	Itn2b	integral membrane protein 2B	640.9	-1.87	1126.6	560	1.07	563.3
BM935811	Itga6	integrin alpha 6	352.9	-2.30	785.1	220.4	-1.23	276
NM_008397	Itga6	integrin alpha 6	327.5	-2.14	717.2	64.6	-1.74	131.9
BB543979	Itgb5	integrin beta 5	76.4	-2.30	195.1	164.3	-1.62	223.9
NM_008352	Il12b	interleukin 12b	55.8	3.48	15.2	57	-1.15	59.8
AI326108	Itsn	intersectin (SH3 domain protein 1A)	87.7	1.87	57.5	45.6	-1.62	72.1
BG966742	Iap	intracisternal A particles	152	2.14	78.6	111.8	-1.00	106
NM_018885	Irx4	Iroquois related homeobox 4 (Drosophila)	41.3	-3.03	122.9	93	-1.07	118.6
NM_018826	Irx5	Iroquois related homeobox 5 (Drosophila)	403.8	1.52	290.5	512.6	2.46	181.9
NM_021459	Isl1	ISL1 transcription factor, LIM/homeodomain (islet 1)	171.8	-1.87	240.6	382.9	-1.41	323.2
AI788952	Idh1	isocitrate dehydrogenase 1 (NADP+), soluble	67.3	-1.87	123.7	87.7	-1.41	80
BC004801	Idi1	isopentenyl-diphosphate delta isomerase	246.1	1.00	311.6	107.1	-2.30	210.1
NM_030887	Jundm2-pending	Jun dimerization protein 2	51	-1.87	113.8	114.4	-1.15	141.6
NM_010643	Klk24	kallikrein 24	102.5	1.87	52.2	193.4	1.52	116.4
BC010754	Klk6	kallikrein 6	2.5	-29.86	86	30.7	2.14	16
BC010754	Klk6	kallikrein 6	14.7	-4.29	96.8	48.1	-1.32	45.7
NM_010664	Krt1-18	keratin complex 1, acidic, gene 18	1405.1	-2.14	2934	1511.4	-2.83	3624.6
NM_008471	Krt1-19	keratin complex 1, acidic, gene 19	64.9	-3.03	138.6	13.8	-2.00	28.5
NM_031170	Krt2-8	keratin complex 2, basic, gene 8	1605.1	-2.00	3055.8	2117.3	-1.87	3666.9
BB292637	Khdrbs1	KH domain containing, RNA binding, signal transduction associated 1	77.1	2.83	29.5	60.7	1.62	32.5
AK014353	Khdrbs3	KH domain containing, RNA binding, signal transduction associated 3	104.3	-2.00	185.8	122.8	-1.15	145.8
AV174022	Kap	kidney androgen regulated protein	89.7	-2.14	224.6	183.4	-1.74	174.7
U13371	Kdt1	kidney cell line derived transcript 1	164.4	1.15	136.3	301.9	1.87	128.5
AI314694	Nx17-pending	kidney-specific membrane protein	21.5	-2.64	58.4	36.8	-1.62	50.5
NM_010612	Kdr	kinase insert domain protein receptor	2334.9	2.46	841	1907.1	2.00	863.1
BG068387	Kif10	kinesin family member 10	366.4	2.46	152.5	222.3	-1.00	166.3
BB827235	Kif11	kinesin family member 11	79.3	2.64	38.4	65.8	-1.15	65.8
BI328541	Kif5b	kinesin family member 5B	296.1	2.46	129.5	122.6	1.23	71.7
AI844677	Kif5c	kinesin family member 5C	40.3	2.46	15	50	2.14	31.7
AF338369	Klf7	Kruppel-like factor 7 (ubiquitous)	473.7	2.00	231.6	245.5	1.74	188.8
BB524597	Klf7	Kruppel-like factor 7 (ubiquitous)	426.5	2.30	166.2	237.8	3.03	67.3
NM_008480	Lama1	laminin, alpha 1	85.1	-2.00	172	122.5	-1.52	193
AF104414	Lats1	large tumor suppressor	43.2	2.30	15.1	38.8	1.15	43
AI787074	Lman1	lectin, mannose-binding, 1	321	1.87	306.6	651.1	1.15	635.2
NM_011175	Lgmn	legumain	168.8	-1.52	360.7	74.4	-2.14	197.8
BB705823	Luzp1	leucine zipper protein 1	257.2	1.87	158.1	383	1.62	230.8
BB479063	Ldb3	LIM domain binding 3	58.1	-4.59	304.7	67.5	-2.00	120.5
AK013416	Lmo2	LIM domain only 2	1174	1.23	950.3	752	2.30	612.5
NM_013860	Limd1	LIM domains containing 1	353.5	1.87	171.8	168.8	1.41	102.7
NM_133198	Pygl	liver glycogen phosphorylase	93.9	-2.30	186.3	100.5	-1.15	162.7

AF480860	Lce-pending	long chain fatty acyl elongase	483.5	1.74	297.8	270.2	3.03	115.5
AI790446	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	264.9	-1.87	477.1	207.5	-2.64	503.6
AV309553	Lrpap1	low density lipoprotein receptor-related protein associated protein 1	727.6	-1.41	1264.6	584	-2.30	1487.4
AV309996	Luc7l	Luc7 homolog (S. cerevisiae)-like	183.5	2.30	79.4	91.2	-1.00	130.5
BC022943	Lcp1	lymphocyte cytosolic protein 1	96.6	1.23	80.3	106.1	1.87	36.9
NM_033565	Laf4l	lymphoid nuclear protein related to AF4-like	214.2	1.87	117	197.5	1.07	164.7
AV083741	Lytic-pending	lyric	2374.5	2.30	930.3	1352.9	1.15	1343
BC008161	Mphosph6	M phase phosphoprotein 6	453.5	1.07	434.6	509.6	-1.87	1019.6
AA717142	Mkrn1	makorin, ring finger protein, 1	195.9	-1.52	394.3	100.6	-2.00	224.9
AB049755	Masp1	mannan-binding lectin serine protease 1	12.7	-13.00	199.4	29.4	-6.50	167.1
NM_008625	Mrc1	mannose receptor, C type 1	146.5	-1.87	302.1	158.1	1.15	181.7
NM_008608	Mmp14	matrix metalloproteinase 14 (membrane-inserted)	483.3	-1.15	581.2	292.8	2.14	142
NM_019791	Maged1	melanoma antigen, family D, 1	456.1	-2.14	1206	586	-1.52	876.6
BI658327	Mcmd	mini chromosome maintenance deficient (S. cerevisiae)	270.3	1.32	203.8	162.7	-2.14	299.8
BB041267	Mrpl19	mitochondrial ribosomal protein L19	292	-1.32	386	45.2	-2.14	109.3
NM_025302	Mrpl2	mitochondrial ribosomal protein L2	1079.2	1.00	1068.8	291.2	-2.46	1119.5
C79823	Mrpl45	mitochondrial ribosomal protein L45	956.9	2.00	488.8	385.2	2.00	240.9
AY028170	Mfn2	mitofusin 2	74.7	1.87	46	175.4	1.23	130.1
NM_031248	Mapbpip-pending	mitogen activated protein binding protein interacting protein	288.9	-1.32	372.8	168.6	-1.87	365.6
BB313689	Mapk10	mitogen activated protein kinase 10	20.9	-3.73	97.2	83.7	-1.07	66.6
BM213292	Map3k3	mitogen activated protein kinase kinase kinase 3	387.6	1.87	178.4	285.5	1.87	156.7
AV269411	Mmd2	monocyte to macrophage differentiation-associated 2	43.6	3.73	8.2	11	1.74	8
BF580235	---	Mouse endogenous murine mink cell focus-forming (MCF) envelope protein mRNA	93.2	1.87	52.6	66.9	-1.52	143.1
NM_019763	Mint-pending	Msx2 interacting nuclear target protein	256.8	2.14	125.7	217	2.00	111.5
L17069	Mll	myeloid/lymphoid or mixed-lineage leukemia	458.2	2.00	259.8	283.8	1.41	198.5
NM_013597	Mef2a	myocyte enhancer factor 2A	259.3	2.30	103.6	278.4	2.00	129.2
NM_010867	Myom1	myomesin 1	28.5	-3.73	85.9	34.3	-2.14	67.6
NM_008653	Mybpc3	myosin binding protein C, cardiac	334	-3.48	1058.1	347.8	-2.46	791.3
BE630294	Mybph	myosin binding protein H	3.3	-11.31	40.3	21.4	-1.15	24
M76601	Myhca	myosin heavy chain, cardiac muscle, adult	965.8	-3.03	2926.2	598.5	-3.03	1771.2
NM_010858	Myla	myosin light chain, alkali, cardiac atria	1068.5	-2.64	3418.8	1346.5	-2.46	2998.6
X67685	Mylc	myosin light chain, alkali, cardiac ventricles	549	-3.73	2008.5	301.5	-4.00	1469.5
AK002312	Mylc	myosin light chain, alkali, cardiac ventricles	280.4	-3.73	1352.8	278.7	-2.83	826.3
X67685	Mylc	myosin light chain, alkali, cardiac ventricles	461.9	-2.83	2070.8	447.9	-3.03	688.5
AK003182	Mylf	myosin light chain, alkali, fast skeletal muscle	81	-2.30	203.6	60.2	-1.23	109.2
NM_010861	Mylpc	myosin light chain, phosphorylatable, cardiac ventricles	231.5	-3.03	660.7	129.1	-1.87	311.1
NM_022879	Mylc2a	myosin light chain, regulatory A	3034.5	-1.87	5547	4405.8	-1.32	5470.2
AV297945	Myo10	myosin X	67.4	2.46	23.4	34	-1.15	50.6
NM_080728	Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	258.8	-5.66	2128.2	128.3	-8.00	1572.6
NM_080728	Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	751.3	-4.92	3125.7	542.1	-4.92	2260.1
AK007972	Myl9	myosin, light polypeptide 9, regulatory	178.8	-4.29	974.7	125.9	-1.74	330.3
NM_008538	Marcks	myristoylated alanine rich protein kinase C substrate	896.3	-1.07	879.2	1429	2.46	650.2
BB759157	Nedd4l	neural precursor cell expressed, developmentally down-regulated gene 4-like	114.6	-1.87	237.3	163.2	1.23	139.5
NM_010917	Nid1	nidogen 1	415.3	1.23	380.5	358.9	2.46	125.3
NM_008700	Nkx2-5	NK2 transcription factor related, locus 5 (Drosophila)	268	-2.46	473.5	292	-1.32	411.3
BG067031	Narg1	NMDA receptor-regulated gene 1	1282.3	2.46	491.4	1334.5	1.15	1055.2
X70514	Nodal	nodal	73.2	-2.00	194.3	79.4	-8.00	1286.9
NM_010940	Nscn1	non-selective cation channel 1	92.8	2.30	40.8	63.1	1.32	47.2
BE952133	Notch1	Notch gene homolog 1 (Drosophila)	471.7	2.00	302	167	2.46	59.1
BG920261	Nsap1-pending	NS1-associated protein 1	239.2	2.46	101.4	135.8	1.07	126.1
BG920261	Nsap1-pending	NS1-associated protein 1	134.9	3.03	45.5	50.9	1.23	49.7
BC021434	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	147.9	1.15	155.6	202.8	2.00	113.9
BB092799	Nfib	nuclear factor I/B	80.2	1.32	68.3	141.6	3.03	46.3
U28807	Nfatc3	nuclear factor of activated T-cells, cytoplasmic 3	132.9	2.30	70.6	93.8	-1.32	122.7
BM238431	Np220	nuclear protein 220	127	2.14	44.3	80.8	1.07	86.9
BM233196	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	489.1	3.03	178.6	211.8	1.62	132.9
BB829563	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	131.7	4.92	26.5	78.5	2.00	53.1
NM_008735	Nrip1	nuclear receptor interacting protein 1	585.4	2.00	237.8	181.6	1.23	166.5

BB093407	Nolc1	nucleolar and coiled-body phosphoprotein 1	73	1.00	85.2	54	-2.00	133
BF118393	Ncl	nucleolin	613.3	1.15	564.4	137	-2.14	294.1
AF318184	Ncl	nucleolin	5622.3	1.32	4461.6	1677	-2.46	4081.6
AF356506	Oit3	oncoprotein induced transcript 3	61.4	-2.00	266	99	-1.15	105.7
BB830976	Orc2l	origin recognition complex, subunit 2-like (S. cerevisiae)	98.7	2.46	33.6	85.9	1.41	80.1
BC017609	Otx2	orthodenticle homolog 2 (Drosophila)	82.8	-2.00	160.7	10.2	-10.56	153.5
NM_011021	Otp	orthopedia homolog (Drosophila)	36.3	3.73	8.7	41.6	-1.41	46
AW548944	Oxr1	oxidation resistance 1	76.7	-2.00	181.2	140.1	-1.62	235.2
NM_130885	Oxr1	oxidation resistance 1	179.7	-1.87	310.8	195.1	-1.32	217.6
U80011	Pitx2	paired-like homeodomain transcription factor 2	129.1	-4.59	998.6	105.8	-11.31	1256.1
AB006320	Pitx2	paired-like homeodomain transcription factor 2	49.1	-2.00	142.9	48.3	-2.46	197.5
BC027089	Pank3	pantothenate kinase 3	69.7	2.64	24.7	30.6	1.52	18.4
AW543460	Pard3	par-3 (partitioning defective 3) homolog (C. elegans)	419.6	1.15	313.3	386.2	1.87	216.6
BE953582	Pard6b	par-6 (partitioning defective 6) homolog beta (C. elegans)	67.8	-2.46	183.4	156.5	-1.41	245.8
BC013446	Pthr1	parathyroid hormone receptor 1	50.4	-2.30	143.9	11.1	-1.74	17.6
NM_008817	Peg3	paternally expressed 3	11.8	-6.96	117.6	13.1	1.07	17.5
BC010821	Pyy	peptide YY	273.6	-2.00	477.4	407.5	-1.32	463.9
AK009460	Ppi2	peptidylprolyl isomerase (cyclophilin)-like 2	155.7	-1.32	147.8	67	-2.83	119.5
BC014688	LOC235036	peter pan	264.8	-1.52	444.3	35.7	-4.59	324.6
NM_080555	Ppap2b	phosphatidic acid phosphatase type 2B	272.5	1.52	204.9	339	2.30	140.2
AK016901	Pgs1-pending	phosphatidylglycerophosphate synthase 1	156.8	-1.32	200.1	57.7	-2.14	136.1
BI156474	Pi4k2b-pending	phosphatidylinositol 4-kinase type 2 beta	46.2	-2.00	107.2	4.2	-18.38	75.2
BB822856	Pip5k1b	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	80.3	-2.30	154.2	86.2	-2.00	220.5
AK012196	Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	473.9	1.07	408.2	559.2	2.14	191.3
AY007702	Pde7a	phosphodiesterase 7A	69.5	1.87	30.6	71.4	1.32	35.3
NM_008826	Pfkl	phosphofructokinase, liver, B-type	864.7	-1.41	1193.8	561.4	-1.87	1146.4
NM_018870	Pgam2	phosphoglycerate mutase 2	46.1	-3.73	227	17	-1.62	38.5
NM_019637	Styx	phosphoserine/threonine/tyrosine interaction protein	507	2.46	208.2	339.2	2.46	173.2
AF224264	LOC233908	pigpen	146.7	-1.87	209.4	112.9	-4.00	350.3
AF224264	LOC233908	pigpen	575.4	-1.07	548.8	167.7	-1.87	587.1
BM210473	Pem	placentae and embryos oncofetal gene	352.3	-1.15	475	120.2	-2.46	386.3
NM_011222	Pvt1	plasmacytoma variant translocation 1	206.9	2.00	92.8	106.8	1.23	110.1
NM_032398	Plvap	plasmalemma vesicle associated protein	539	1.00	612.1	156.2	3.48	39.2
AW537708	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	127.7	-2.14	289.2	851.3	1.23	676.3
NM_019932	Pf4	platelet factor 4	241.9	1.32	198.4	323.7	2.00	146.6
BC010215	Plekha2	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 2	175.4	-1.87	357.8	194.9	-1.00	199
NM_031256	Plekha3	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	97.7	2.00	58.9	164.5	1.07	123.5
NM_009344	Phlda1	pleckstrin homology-like domain, family A, member 1	592.3	-1.15	649.4	303.1	2.00	102.8
BM230222	Papola	poly (A) polymerase alpha	549.1	1.87	288.2	505.3	1.15	327.3
BC008105	Polk	polymerase (DNA directed), kappa	217.8	2.14	77.4	163.9	1.32	115.7
BB198074	Pmscl2	polymyositis/scleroderma autoantigen 2	89.7	2.00	47.6	56.1	1.32	47.6
NM_022318	Popdc2	popeye domain containing 2	118.4	-3.25	451.3	203.3	1.07	204.7
BG865910	Kcnn4	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 4	394.1	1.87	241.1	11	1.15	7.8
NM_011136	Pou2af1	POU domain, class 2, associating factor 1	29.9	2.83	19.6	26.3	1.62	33.4
BC010287	Pbx2	pre B-cell leukemia transcription factor 2	208.6	-1.87	507.5	319.5	-1.00	204.9
NM_011070	Pfdn2	prefoldin 2	653.2	1.07	635.4	586.6	-1.87	1346.3
NM_011170	Pmp	prion protein	275.6	-4.00	1221.6	689.4	-2.00	1252.6
BB398886	Pawr	PRKC, apoptosis, WT1, regulator	246.3	-2.14	626.1	260	-1.41	440.1
AF352788	Pcolce2	procollagen C-endopeptidase enhancer 2	57.5	1.07	34.2	43.9	-2.14	110.8
NM_031163	Col2a1	procollagen, type II, alpha 1	102.8	-4.92	572.2	110.2	-2.14	270.6
NM_015734	Col5a1	procollagen, type V, alpha 1	177.4	-2.46	576	337.8	-1.15	414.7
AV246911	Col5a1	procollagen, type V, alpha 1	325.7	-2.00	589.8	347.1	-1.15	586.1
NM_011072	Pfn1	profilin 1	1028.5	-1.32	1321.8	679.5	1.87	352.7
M22958	Prlr	prolactin receptor	57.8	2.14	23.3	51.9	1.07	39.8
AW536189	Pa2g4	proliferation-associated 2G4	1702.9	1.87	1155.2	1236.7	1.32	952.9
BC013068	Pcsk5	proprotein convertase subtilisin/kexin type 5	2.9	-6.50	27.2	5.1	1.23	5.5
BG073526	Ptov1	prostate tumor over expressed gene 1	850	-1.41	1327.5	359.2	-2.00	657
NM_008950	Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	979.6	-1.32	1468.4	324.8	-2.14	927.9
NM_011875	Psmd13	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	536	-1.52	820	272.5	-3.25	560.9

AB029146	Psmc4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	281.9	1.00	341.9	93.8	-4.00	294.3
NM_008951	Psmc4	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4	2105.8	1.07	1770.7	744.9	-2.14	1652.9
NM_008906	Ppgb	protective protein for beta-galactosidase	245.4	-1.87	445.5	148	-1.23	188
BM246045	Pias1	protein inhibitor of activated STAT 1	35.6	-2.30	58.7	35.2	-1.07	39.5
NM_026731	Ppp1r14a	protein phosphatase 1, regulatory (inhibitor) subunit 14A	70.9	-1.41	128.4	26.5	-6.06	144.5
NM_133485	Ppp1r14c	protein phosphatase 1, regulatory (inhibitor) subunit 14c	164.2	-2.30	385.2	307.4	-1.23	414.3
BQ176864	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	148.9	-4.00	648.6	369	-1.23	354.7
BB188812	Ptpn5	protein tyrosine phosphatase, non-receptor type 5	65.2	1.87	19.6	69.7	1.41	55
BF465974	Rab10	RAB10, member RAS oncogene family	1737.8	1.41	1130.7	1028.2	2.83	402.8
BE533418	Rab22	RAB22, member RAS oncogene family	89.2	2.83	30.1	116.7	1.87	56
NM_009000	Rab24	RAB24, member RAS oncogene family	295.7	-1.62	436.1	98.4	-2.64	249.1
NM_009000	Rab24	RAB24, member RAS oncogene family	176.8	-1.23	251.9	70.3	-2.64	189.3
BI990563	Rdx	radixin	660.9	4.29	184.8	262.5	1.87	135.2
NM_018750	Rassf5	Ras association (RalGDS/AF-6) domain family 5	154.4	-1.87	269.7	319.2	-1.15	328.7
AF309564	Arhj	ras homolog gene family, member J	529.1	1.74	279.9	726.2	2.64	203.9
BG074180	Rasa1	RAS p21 protein activator 1	436	1.23	336.9	419.4	2.00	174.9
BM242378	Rap1b	RAS related protein 1b	617.6	1.00	597.4	469.3	2.46	220.9
NM_019662	Rrad	Ras-related associated with diabetes	45.7	-2.83	164.2	173.8	1.15	167
NM_016894	Ramp1	receptor (calcitonin) activity modifying protein 1	46.3	-2.46	119.5	68.5	-1.41	99.5
AA560093	Ramp2	receptor (calcitonin) activity modifying protein 2	605.5	4.00	262.1	218.8	-1.00	260.4
BF537798	Ramp2	receptor (calcitonin) activity modifying protein 2	1093.3	4.00	218.8	782.1	1.74	221.4
AA560093	Ramp2	receptor (calcitonin) activity modifying protein 2	223.9	4.59	57.6	120.5	-1.00	147.8
BC003882	Rgs4	regulator of G-protein signaling 4	40.8	-5.28	113.8	100.8	-1.32	128.5
NM_133736	Rgs5	regulator of G-protein signaling 5	182	-2.46	569.4	284.3	-1.74	294.1
NM_133231	Rfxap	regulatory factor X-associated protein	168.8	-1.15	181.4	74.9	-2.30	193
M88489	Recc1	replication factor C	146.4	1.87	66.9	138.6	-1.00	114.9
AF038538	Rtn2	reticulon 2 (Z-band associated protein)	13.2	-10.56	96.8	10.7	1.07	16.4
NM_023879	Rpgrp1	retinitis pigmentosa GTPase regulator interacting protein 1	492.9	1.87	258.9	255	-1.00	229
BB376407	Rbbp2	retinoblastoma binding protein 2	182	3.25	44.1	106.5	1.62	50.9
BF011461	Rbbp4	retinoblastoma binding protein 4	263.3	-2.30	567.9	473.9	-1.00	516.3
NM_011269	Rhag	Rhesus blood group-associated A glycoprotein	51.4	2.46	23.7	59.2	2.30	34.8
BF228009	Rhpn2	rhophilin, Rho GTPase binding protein 2	21.7	-2.64	57.5	40.8	-1.00	30.5
BG067990	Rpl12	ribosomal protein L12	339.9	1.15	321.1	283.8	-1.87	520.8
AV162270	Rps27	ribosomal protein S27	344	-1.87	340.5	339	-1.41	444.9
NM_011299	Rps6ka2	ribosomal protein S6 kinase, polypeptide 2	281.9	-1.87	596	611.3	1.32	507.9
AI746548	Rnf10	ring finger protein 10	311.3	-1.32	476	208.9	2.00	80.4
NM_011568	Refbp1	RNA and export factor binding protein 1	370.2	-1.15	462.4	693.8	-2.46	1347.1
NM_019484	Refbp2	RNA and export factor binding protein 2	200.2	-1.32	265.9	339	-2.46	914.1
BE446879	Rbm5	RNA binding motif protein 5	91.4	2.14	43.7	73.2	-1.00	68
AK003434	Rbpms	RNA binding protein gene with multiple splicing	131.5	-2.00	320.6	140	-1.00	210.5
BG069460	Rbpms	RNA binding protein gene with multiple splicing	477.1	-1.87	923.8	193.8	1.07	240.7
AK017440	Rian	RNA imprinted and accumulated in nucleus	44.1	-3.03	177.7	130.3	-2.46	351.1
NM_019547	Rnpc1	RNA-binding region (RNP1, RRM) containing 1	151.6	-1.87	350.3	104.7	-1.00	102.7
BC020129	Robo4	roundabout homolog 4 (Drosophila)	156.1	2.00	85.1	98.9	1.74	61.8
X83933	Ryr2	ryanodine receptor 2, cardiac	138.8	-3.73	187	138.8	1.07	120.4
BM114293	Amd1	S-adenosylmethionine decarboxylase 1	416.7	2.30	199.1	663.2	2.30	215.9
NM_023380	Samsn1	SAM domain, SH3 domain and nuclear localisation signals, 1	117.9	1.15	86.2	208.8	1.87	120.9
AW540070	Sec13l-pending	sec13-like protein	89.7	1.00	77.3	113.6	2.30	94.9
NM_009149	Selel	selectin, endothelial cell, ligand	1049.6	1.41	718.3	796.9	2.30	322.9
NM_009266	Sps2	selenophosphate synthetase 2	671.5	1.62	417.5	217.7	1.87	118.1
BC001991	Sepp1	selenoprotein P, plasma, 1	1958.9	-1.07	2222.7	1052	1.87	836.1
NM_009156	Sepw1	selenoprotein W, muscle 1	167.7	-1.32	246.9	218.5	2.46	80.6
BI220012	Serpinh1	serine (or cysteine) proteinase inhibitor, clade H, member 1	864.3	-1.87	1350.8	1263.4	-1.15	1411.2
NM_009258	Spink3	serine protease inhibitor, Kazal type 3	329.4	-2.00	736.7	139.5	-4.59	709.3
AV058358	Spint2	serine protease inhibitor, Kunitz type 2	164.2	-1.62	217.7	229.4	-2.46	308.2
BG064688	Stk17b	serine/threonine kinase 17b (apoptosis-inducing)	133.1	-1.15	166.7	146.1	-1.87	235.2
AV291373	Sdccag33	serologically defined colon cancer antigen 33	93	2.64	29.2	58.8	1.32	40.7
BI662291	Srf	serum response factor	134.4	-2.14	261.2	94.9	-1.74	185
AI594243	Smyd1	SET and MYND domain containing 1	100.3	-2.46	280.3	127.7	1.15	127.9
NM_015825	Sh3bgr	SH3-binding domain glutamic acid-rich protein	374.6	-2.83	1263.8	410	-1.74	862.5

NM_009183	Siat8d	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D	160.8	2.14	83.6	179.5	3.25	53.6
BB829192	Siat9	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	162.3	1.41	145	144.3	2.00	78.4
BC005743	Sfxn1	sideroflexin 1	2291.6	2.46	901.7	735.9	1.52	465.6
NM_025357	Smpx	small muscle protein, X-linked	51.9	-2.83	188.7	83.5	-1.87	195.1
NM_026095	Snrdp3	small nuclear ribonucleoprotein D3	639.6	-2.00	1256.5	658	-3.25	2382.5
AI875533	Smc11i	SMC (structural maintenance of chromosomes 1)-like 1 (S. cerevisiae)	308.7	2.14	175.2	186.3	-1.00	226.7
BI665568	Smc4l1	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	287.2	2.83	70.5	45.6	1.41	43.3
AU022584	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	592.1	1.87	333.3	257.8	1.07	292.1
BM225266	Smc6l1	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	179.9	2.46	62.6	185.9	1.74	133.2
U20973	Slc12a1	solute carrier family 12, member 1	89	1.87	44.9	116.6	2.00	61.3
BG069505	Slc12a2	solute carrier family 12, member 2	118.2	3.03	44.1	43.9	1.15	63
NM_009196	Slc16a1	solute carrier family 16 (monocarboxylic acid transporters), member 1	1370.9	-1.32	1694.7	1002.5	-2.00	1720.8
NM_030696	Slc16a3	solute carrier family 16 (monocarboxylic acid transporters), member 3	303.3	-1.87	455.8	193.9	1.23	101.8
NM_134038	Slc16a6	solute carrier family 16 (monocarboxylic acid transporters), member 6	172.5	2.64	99.1	14.4	-2.46	26
AK003626	Slc38a4	solute carrier family 38, member 4	261.6	-1.07	243.7	283.4	-1.87	502.1
BB448377	Slc4a1	solute carrier family 4 (anion exchanger), member 1	99.2	2.14	46	3.9	-6.06	25.6
BB701473	Son	Son cell proliferation protein	2309	1.87	1394.4	1183.1	1.62	864.6
BI143942	Sdh1	sorbitol dehydrogenase 1	292.9	1.52	157	115.4	2.14	46.4
BC025911	Snx6	sorting nexin 6	2262.1	2.30	848.7	3250	1.23	2252.6
AV344473	Snag1	sorting nexin associated golgi protein 1	144.7	1.87	87.5	184.9	-1.00	177.7
BM212545	Spg7	spastic paraplegia 7 homolog (human)	15.1	-2.46	61.1	6.8	1.07	12.8
BM213516	Spnb2	spectrin beta 2	548.7	3.03	212	348.4	-1.23	436
BC026135	Sgpl1	sphingosine phosphate lyase 1	65.9	-2.46	100.6	58	1.87	20
AK015776	Sf3a3	splicing factor 3a, subunit 3, 60kDa	150.6	1.07	163.8	69.1	-2.46	249.6
AF384055	Srfcp-pending	SRF co-factor protein (cardiac and smooth muscle)	234.2	-4.29	962.2	690	-1.74	1228.9
NM_009236	Sox18	SRY-box containing gene 18	616.8	1.23	456.3	739.7	2.14	326.4
U31967	Sox2	SRY-box containing gene 2	85.4	-1.23	122.3	58.1	-3.73	134.2
NM_011446	Sox7	SRY-box containing gene 7	316.6	1.74	181.4	372.4	2.14	264.2
AA289490	Stampb	Stam binding protein	122.9	1.87	71.2	154.9	1.32	91.5
AV007850	Stmn3	stathmin-like 3	70.8	2.30	34.5	117.4	1.23	101
NM_016665	Stra13	stimulated by retinoic acid 13	254.2	1.07	163	190.3	2.46	69.6
NM_019719	Stub1	STIP1 homology and U-Box containing protein 1	858.3	-1.32	1113.5	465.6	-2.00	894.9
NM_023231	Stoml2	stomatin (Epb7.2)-like 2	1344.8	1.00	1304.5	551.5	-1.87	1061
BB032852	Sdfr2	stromal cell derived factor receptor 2	390.8	2.14	176	91.5	-1.23	103.1
BC024835	Ssrp1	structure specific recognition protein 1	835.9	1.23	706.4	724.5	-2.14	691.1
AW701251	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	953.1	1.87	497.1	280.2	1.41	186.8
BI661719	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	476	3.73	168.6	280.9	1.07	253.7
NM_025891	Smarcd3	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	260.3	-3.03	817.3	160	-1.87	421.6
BB785152	Synj2	synaptojanin 2	58.5	2.00	31.9	96.9	1.32	65.7
NM_025292	Synj2bp	synaptojanin 2 binding protein	505.2	2.30	260.5	449.8	1.62	357.5
AV296217	Stx3	syntaxin 3	494	1.87	311.1	209.3	-1.87	449.9
NM_025444	Taf13	TAF13 RNA polymerase II, TATA box binding protei (TBP)-associated factor	463.4	-1.15	486.9	660.8	-1.87	1009.7
AW554709	Cda08-pending	T-cell immunomodulatory protein	19.8	-2.14	49.8	45.5	-1.00	65.9
AK014409	Tctex1	t-complex testis expressed 1	66.5	-1.87	144.1	109.6	-2.14	184.9
AV294613	Tdgf1	teratocarcinoma-derived growth factor	11.3	-24.25	184.2	82.2	-2.83	311.1
BC010465	Tes	testis derived transcript	546.2	-1.32	748.7	430.5	-1.87	807.3
BI466259	Tes3-ps	testis derived transcript 3, pseudogene	318.8	2.14	133.1	288.6	1.23	238.4
BM207761	Tex27	testis expressed gene 27	51.3	-2.46	136	16	-19.70	102.3
M87276	Thbs1	thrombospondin 1	84.9	2.00	41.6	97.6	1.52	69.3
NM_011582	Thbs4	thrombospondin 4	129.4	-4.92	633.5	134.1	-2.30	299.1
BC025840	Ttn	titin	288.3	-4.00	1011.3	328.3	-1.52	450.9
NM_011634	Traip	TRAF-interacting protein	35.1	-2.14	76	2.7	-13.00	68.6
NM_011545	Tcf21	transcription factor 21	148.2	-2.00	289.4	326.8	1.23	260.5
NM_013685	Tcf4	transcription factor 4	449	2.00	201.9	181.3	-1.00	164.2
AV329447	Tbl1x	transducin (beta)-like 1 X-linked	47.6	1.87	41.6	43.8	-2.64	102.9
BB810450	Trfr	transferrin receptor	55.3	2.83	25.7	60	4.29	12.1

NM_009365	Tgfb1i1	transforming growth factor beta 1 induced transcript 1	573.5	-1.87	786.2	537.5	1.23	518.9
AI323791	Tgfb2	transforming growth factor, beta 2	595.1	2.00	242.1	503	2.14	172.9
BB114067	Tagln	transgelin	123.1	-4.59	798.2	142	-1.74	254.3
BB041811	Tgm2	transglutaminase 2, C polypeptide	253.9	1.00	271.8	113.1	2.00	59.3
BM119928	Tsnax	translin-associated factor X	47.7	1.15	54.5	101.2	7.46	18.5
NM_011592	Timm44	translocator of inner mitochondrial membrane 44	381.2	1.00	474.9	216.2	-1.87	320.4
AI505784	Tm4sf10	transmembrane 4 superfamily member 10	154.6	-1.87	305	162.4	1.07	166.1
NM_019634	Tm4sf2	transmembrane 4 superfamily member 2	283.3	-2.14	744.2	464.7	1.23	474
BG974366	Tm9sf2	transmembrane 9 superfamily member 2	7.7	-2.83	22	1.3	-16.00	20.5
BC024702	Ttr	transthyretin	483.5	-1.52	517.4	12.9	-21.11	519.6
AV152953	Ttr	transthyretin	1292.6	-1.15	1155	33.6	-9.85	971.1
BG141874	Ttr	transthyretin	2337.4	-1.07	2255	163	-10.56	1796.6
NM_030706	Trim2	tripartite motif protein 2	157.9	1.15	132.9	302.7	1.87	188.8
BB667078	Trim2	tripartite motif protein 2	81.2	2.14	40.1	128.8	1.32	66.5
AF241244	Tro	trophinin	165.9	-1.15	188.9	189.3	-2.00	271
AK002271	Tpm1	tropomyosin 1, alpha	1524.3	-2.83	4284.7	1628.3	-3.03	4812.6
AK003186	Tpm2	tropomyosin 2, beta	2.6	-9.85	20.1	2.5	-6.50	31.2
BC024358	Tpm2	tropomyosin 2, beta	62	-2.00	158.3	64.8	-1.74	119.7
NM_009393	Tncc	troponin C, cardiac/slow skeletal	871.2	-3.48	3333.4	821.1	-3.25	2530.4
NM_021467	Tnni1	troponin I, skeletal, slow 1	554.6	-3.73	2429.7	815.2	-2.14	2040
NM_011618	Tnnt1	troponin T1, skeletal, slow	49.5	-2.00	164.6	7	-7.46	51.9
NM_011619	Tnnt2	troponin T2, cardiac	744.3	-4.29	3308	838.3	-4.00	3394.4
L47552	Tnnt2	troponin T2, cardiac	820.9	-3.25	3421.8	1040.2	-3.03	2461.4
BF580567	Tnfrsf12a	tumor necrosis factor receptor superfamily, member 12a	293.3	-1.87	656.2	346.2	-1.23	422.5
NM_011611	Tnfrsf5	tumor necrosis factor receptor superfamily, member 5	78.4	1.15	76.4	75.6	-2.14	132.1
BC003906	Tnfaip1	tumor necrosis factor, alpha-induced protein 1 (endothelial)	612	1.87	292.5	123.5	1.87	70.8
BB233088	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	170.3	-1.15	245.9	506.2	1.87	360.7
NM_009413	Tpd52l1	tumor protein D52-like 1	48.5	-3.03	120	137.7	-1.23	158.3
BE995678	Tra1	tumor rejection antigen gp96	772.5	2.14	353.7	967.9	1.23	841.1
BC005618	Tacstd1	tumor-associated calcium signal transducer 1	119.1	-2.30	254.2	35.6	-10.56	605.4
NM_024187	U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF)	1510	1.00	1607.5	531.6	-2.64	1365.7
NM_015816	Lsm4	U6 snRNA-associated SM-like protein 4	1175.9	-1.32	1749.6	594.5	-2.30	1538.5
NM_023137	Ubd	ubiquitin D	49.1	1.87	29.6	104.6	1.23	79.7
NM_011668	Ube3a	ubiquitin protein ligase E3A	1460	1.87	787.3	507.9	1.52	269.1
BC003835	B3galt3	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 3	112	-2.00	169.7	183.5	-1.52	213.6
AA203925	Uxs1	UDP-glucuronate decarboxylase 1	47.2	-1.52	84.9	106	-2.00	262.3
AF349573	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetyl-galactosaminyltransferase 7	68.7	2.30	33.2	104.1	2.00	83.9
AI788797	Utrn	utrophin	204.3	-1.87	304.8	240.1	-1.52	325.5
NM_030559	Vps16	vacuolar protein sorting 16 (yeast)	268.5	-1.52	269	175	-2.46	506.2
BI654068	Vps35	vacuolar protein sorting 35	139.7	4.00	33.5	172.2	1.62	96.5
AI195225	Vcp	valosin containing protein	4243.8	1.07	4076	2231.9	-1.87	3144.5
NM_011693	Vcam1	vascular cell adhesion molecule 1	72.3	-3.25	187.9	123.3	-2.00	292.9
NM_133656	Crk	v-crak sarcoma virus CT10 oncogene homolog (avian)	332	2.00	200.5	256.8	-1.00	298.7
NM_053235	V1rc5	vomeroneasal 1 receptor, C5	27.3	2.83	6.7	36	1.41	38.3
AB057663	Raf1	v-raf-1 leukemia viral oncogene 1	293.2	-1.62	503.2	266.6	-1.87	569.8
NM_031392	Wdr6	WD repeat domain 6	292	-1.87	560.2	277.3	-1.07	303.6
BB067079	Wnt5a	wingless-related MMTV integration site 5A	51.7	-2.64	142.5	122	-1.52	142
BI453048	Wbp4	WW domain binding protein 4	59.6	-1.87	97.6	134	-1.07	131.3
AF138745	Tsix	X (inactive)-specific transcript, antisense	36.4	2.64	10.5	65.5	1.52	46.9
BG806300	Tsix	X (inactive)-specific transcript, antisense	362.3	3.25	103.1	2616.5	-1.07	2986.2
NM_015753	Zfhx1b	zinc finger homeobox 1b	146.9	1.87	95.7	58.8	-1.32	53.1
NM_009550	Zfp2	zinc finger protein 2	1.7	-9.19	19.3	26.9	1.41	20.9
AY028963	Zfp288	zinc finger protein 288	23.4	-2.46	65.1	10	-1.52	20.2
BB036959	Zfp361i	zinc finger protein 36, C3H type-like 1	51.9	1.87	53.7	101.2	1.23	93.1
BC021456	Zfp397	zinc finger protein 397	173.4	1.52	103.7	251.8	1.87	197.5
AK009842	Zfp99	zinc finger protein 99	74	1.87	30.3	101.7	1.87	42.2
BB361162	Zic1	zinc finger protein of the cerebellum 1	45	2.30	20.3	52.8	1.62	31.2
BB732077	Zic3	zinc finger protein of the cerebellum 3	49	2.14	20.2	100.8	2.64	44.1
AV361868	Zdhhc14	zinc finger, DHHC domain containing 14	139.8	1.52	121.2	209.7	2.00	104.4

Appendix 4a. Transcripts enriched or depleted in the Nkx2.5 null cardiac crescent.				Sample A			Sample B	
Sequence Derived From	Gene Symbol	Gene Name	Nkx2.5 null Right Crescent A Signal	Nkx2.5 null Right vs Left Crescent A Fold Change	Nkx2.5 null Left Crescent A Signal	Nkx2.5 null Right Crescent B Signal	Nkx2.5 null Right vs Left Crescent B Fold Change	Nkx2.5 null Left Crescent B Signal
BC019797.1	Dhcr24	24-dehydrocholesterol reductase	444.9	1.74	217.9	445.2	2.83	153
AV213379	Oxct	3-oxoacid CoA transferase	557	2.30	257.5	716.3	1.87	367.7
BB393498	Atic	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	352.5	2.14	151.7	406.5	2.30	167.6
BB140287	Nt5c2	5'-nucleotidase, cytosolic II	750.3	2.46	282.9	602.2	2.00	310.2
NM_031185.1	Akap12	A kinase (PRKA) anchor protein (gravin) 12	1735.4	2.14	1002	2094.5	2.46	792.3
C79026	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	769.9	2.30	328.8	594.3	2.64	270.8
BB246410	Akap9	A kinase (PRKA) anchor protein (yotiao) 9	921.1	1.87	469.9	1008.1	3.03	427.8
NM_025341.1	Abhd6	abhydrolase domain containing 6	439.3	1.62	276.3	559	3.03	185.1
AK010738.1	Ascl2	achaete-scute complex homolog-like 2 (Drosophila)	222.2	2.14	97.1	322.3	4.00	61
AA560923	Anp32a	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	2120.3	1.87	1025.3	2560.1	2.83	935.3
BC010275.1	Arpc1b	actin related protein 2/3 complex, subunit 1B	1166	1.87	674.5	1329.5	2.64	667.8
BM244229	Arpc2	actin related protein 2/3 complex, subunit 2	405.6	1.74	182.4	632.3	4.59	140.7
BG145444	Arpc4	actin related protein 2/3 complex, subunit 4	1686.2	2.14	728.1	1679.3	2.83	579.8
AV139714	Arpc4	actin related protein 2/3 complex, subunit 4	1219.1	2.14	593.3	1286.5	2.64	442.4
BC014291.1	Acvr11	activin A receptor, type II-like 1	196.1	1.62	131	225.8	3.03	99.7
BI965035	Acbd3	acyl-Coenzyme A binding domain containing 3	646	2.14	323	961.6	2.83	344.1
AK011781.1	Acbd6	acyl-Coenzyme A binding domain containing 6	446.8	2.00	250.6	470.1	2.64	178.4
BI410363	Add3	adducin 3 (gamma)	849.4	2.46	344.9	1153.2	2.30	440.8
BG695431	Arfrp1	ADP-ribosylation factor related protein 1	1401	2.46	532.2	1352	2.30	597
BC019550.1	Arl6ip6	ADP-ribosylation factor-like 6 interacting protein 6	3790.5	2.30	1873.6	3101	1.87	1813.9
BB545273	Arl8	ADP-ribosylation factor-like 8	854.3	1.74	482.7	883.5	2.64	389
BQ032239	Arl8	ADP-ribosylation factor-like 8	73.3	1.32	48.1	154.5	4.29	46.8
AV124668	Alb1	albumin 1	154.7	9.19	21.5	264.2	1.87	135.4
NM_007423.1	Alb1	albumin 1	283.9	7.46	33.7	614.8	1.62	368
NM_009022.1	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	1209.2	2.83	493.6	744.5	1.87	404.4
BM225096	Atrx	alpha thalassemia/mental retardation syndrome X-linked homolog (human)	654.8	2.83	196.2	840.2	2.46	301.2
BI454479	Appbp2	amyloid beta precursor protein (cytoplasmic tail) binding protein 2	1732.7	2.30	679.6	1520.4	2.00	763.4
NM_080857.1	Asb13	ankyrin repeat and SOCS box-containing protein 13	391.9	2.46	169.1	298.6	1.74	180.8
AW702161	Anxa3	annexin A3	957.3	1.74	461.1	1037.3	2.83	368.1
NM_013472.1	Anxa6	annexin A6	1281.3	2.64	531.1	1524.5	3.03	493.4
AI527359	Apoa1	apolipoprotein A-I	181	1.87	102.4	279.6	2.83	89.1
BG070815	Aven	apoptosis, caspase activation inhibitor	760.6	2.30	333.4	887	2.83	325.2
NM_007482.1	Arg1	arginase 1, liver	2084.6	2.83	838.3	1006.3	1.52	855
BB362210	Arih1	ariadne ubiquitin-conjugating enzyme E2 binding protein	861.5	2.64	328	870.6	2.14	386.2

		homolog 1 (Drosophila)						
BC011284.1	Arsa	arylsulfatase A	450.9	1.87	247.1	659.9	3.03	249.6
NM_138679.1	Ash1l	ash1 (absent, small, or homeotic)-like (Drosophila)	568.4	2.64	215	688.7	2.46	286.6
BB704254	Atbf1	AT motif binding factor 1	824.1	2.00	431.3	1341.8	3.03	389.3
BM225269	Atp2c1	ATPase, Ca++-sequestering	1100.8	2.83	341.4	706.8	1.62	540.9
AV340006	Atp2c1	ATPase, Ca++-sequestering	148.8	2.46	43	135.6	2.83	52.7
U03434.1	Atp7a	ATPase, Cu++ transporting, alpha polypeptide	3365	1.74	2005.7	3778.5	2.46	1507
NM_015751.1	Abce1	ATP-binding cassette, sub-family E (OABP), member 1	1991.3	2.46	786.6	1803.6	2.00	919.3
AV309591	Abcf1	ATP-binding cassette, sub-family F (GCN20), member 1	2855.7	1.74	1782.7	3539.8	2.64	1244.9
BM210947	Atox1	ATX1 (antioxidant protein 1) homolog 1 (yeast)	508.8	2.00	285.8	714.5	2.64	230.8
AV329219	Erg	avian erythroblastosis virus E-26 (v-ets) oncogene related	1005.8	2.00	449.9	958.8	2.46	431.3
BB079254	Axot	axotrophin	407.7	2.14	186.7	482.2	3.48	183.1
BB248730	Axot	axotrophin	1110.3	2.14	479.6	1077.5	2.30	442.4
M64279.1	Bmi1	B lymphoma Mo-MLV insertion region 1	457.1	2.83	189.9	412.9	2.14	147.8
AA217399	Bmi1	B lymphoma Mo-MLV insertion region 1	1323.2	2.46	540.7	980.4	1.87	559.9
BF134200	Birc4	baculoviral IAP repeat-containing 4	311.9	2.14	152.6	386.5	3.03	120.8
BB527646	Birc6	baculoviral IAP repeat-containing 6	632.7	2.30	307.3	666.6	2.64	244.8
BB702366	Baiap1	BAI1-associated protein 1	222.7	2.14	92.7	321	3.25	96.5
AV326943	Baiap1	BAI1-associated protein 1	213.2	1.62	153.9	352.8	2.83	95.7
BB082119	Bag4	BCL2-associated athanogene 4	726	1.87	371.1	1036.8	4.00	271.9
BE686465	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	1465.9	2.30	616.1	1343.1	2.64	518
BM120925	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	318.7	2.30	141.4	343.4	3.03	151
BB667581	Bcl2l11	BCL2-like 11 (apoptosis facilitator)	2882.5	2.14	1493	2894.8	2.30	1171.9
AV318805	Bcor	Bcl6 interacting corepressor	653.3	2.64	208.9	737.5	2.46	338.6
NM_010368.1	Gus	beta-glucuronidase	856.8	2.14	407.4	887.7	2.64	291.1
NM_029791.1	Bicd2	bicaudal D homolog 2 (Drosophila)	1350.4	1.41	988.1	2246.8	2.46	879.7
AA940256	Bcas2	breast carcinoma amplified sequence 2	2162.7	2.64	814.3	1883	1.74	1072.8
AV357135	Baz1a	bromodomain adjacent to zinc finger domain 1A	2218.3	1.87	1146.5	2564.4	2.30	1025.5
BG072367	Brd3	bromodomain containing 3	666.9	2.14	349.7	811.5	2.83	305.3
	Brd4	bromodomain containing 4	526.4	1.87	299.8	545.6	2.64	258.8
BC008532.1	Btbd3	BTB (POZ) domain containing 3	368	2.64	138	416.9	3.25	116.2
BC018174.1	Bach1	BTB and CNC homology 1	406.3	1.74	222.2	545.7	2.64	162.5
NM_007520.1	Banp	Btg3 associated nuclear protein	474	2.00	242.6	741.1	3.25	202
BC013339.1	Bub3	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	167.4	2.00	61.1	221.9	2.64	70.2
AW543698	Cdh5	cadherin 5	562.8	1.74	334.6	793.4	2.83	272.5
BC003714.1	Cib1	calcium and integrin binding 1 (calmyrin)	1337.2	2.14	624.8	937.2	2.46	440.1
BM233760	Cbara1	calcium binding atopy-related autoantigen 1	216.4	1.74	134.8	222.9	2.30	95.1
NM_133781.1	Cab39	calcium binding protein 39	724.3	1.74	407.5	1027	3.03	277.4
AB026997.1	Cast	calpastatin	136.9	1.74	112.6	227	3.48	83.4
AF282864.1	CRG-L1	cancer related gene-liver 1	665.7	2.64	246.6	771.8	3.03	259.7
AV218165	Cno	cappuccino	3015.2	2.64	1148.4	3289.3	2.14	1516.3
AB046929.1	Chst7	carbohydrate (N-acetylglucosamino) sulfotransferase 7	509	2.14	248.2	457.6	2.64	163.2
X61397.1	Car8	carbonic anhydrase 8	162	2.64	64.7	219.6	2.64	78.1
NM_007754.1	Cpd	carboxypeptidase D	793.8	2.30	260.2	883.9	2.83	310.1
AI845410	Cdv3	carnitine deficiency-associated gene expressed in ventricle 3	366.4	2.00	181.9	461.2	2.46	168.5
NM_013500.1	Crtl1	cartilage link protein 1	1552.3	2.46	645.5	1641.1	3.03	606.5
BB620454	Crtl1	cartilage link protein 1	1028.4	1.62	638.3	1703.5	4.59	405.5
NM_007786	Csnk	casein kappa	258.9	2.14	125.4	328.6	3.48	99.6

1								
AK019176.1	Csnk1a1	casein kinase 1, alpha 1	1013.4	2.30	404.7	1095.9	2.83	355
BM201663	Csnk1g1	casein kinase 1, gamma 1	261.4	2.46	101.5	287.9	3.03	113.7
BB283759	Csnk2a1	casein kinase II, alpha 1 polypeptide	2023.4	1.87	1044.1	3347.2	3.03	930.8
BB385581	Cbl	Casitas B-lineage lymphoma	1989.6	2.14	901	1924.7	2.64	735.6
NM_130859.1	Card10	caspase recruitment domain family, member 10	453.2	2.64	176.3	350.9	2.83	177.6
AK003595.1	Catnbp1	catenin beta interacting protein 1	865	1.87	463.8	1159.7	3.25	299.9
NM_009982.1	Ctsc	cathepsin C	1341.3	2.64	490.6	1286.5	1.74	740.1
NM_007801.1	Ctsh	cathepsin H	782.1	2.00	405.3	900.2	3.03	289.3
NM_022325.1	Ctsz	cathepsin Z	1243.3	2.14	650.2	1371.9	2.83	433.3
NM_022325.1	Ctsz	cathepsin Z	1606.9	1.87	841.7	1817.5	2.46	768.8
NM_022325.1	Ctsz	cathepsin Z	861.5	1.74	571.5	1388.7	3.03	420.5
BC025116.1	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	151.2	6.06	18.9	560.4	1.62	266.3
NM_009883.1	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	6.6	-5.28	25.8	207.7	4.00	62.4
BB831146	Cebpd	CCAAT/enhancer binding protein (C/EBP), delta	750.3	1.87	410.8	941.6	2.46	378.9
BB836888	Ctcf	CCCTC-binding factor	3550.6	2.46	1461.1	3913.1	3.03	1364.6
BB066603	Cnot4	CCR4-NOT transcription complex, subunit 4	942	2.46	375.1	960.7	2.46	341.2
AI448404	Cnot4	CCR4-NOT transcription complex, subunit 4	1549	2.30	758.1	1365.2	2.46	605.6
NM_133655.1	Cd81	CD 81 antigen	4241.3	1.87	2250	4350.9	2.46	1778.8
NM_133654.1	Cd34	CD34 antigen	949.1	2.00	459.1	1054.1	2.46	414.2
BB256012	Cd38	CD38 antigen	918	1.87	454.5	1090.6	2.46	378.8
BC005676.1	Cd44	CD44 antigen	1999.4	1.87	1012.9	2476.4	4.59	568.5
AW146109	Cd44	CD44 antigen	352.4	1.87	192.9	406.4	2.46	140.8
AK005507.1	Cd59a	CD59a antigen	724.8	1.74	414.7	564	2.64	214.3
BC016250.1	Cdc42ep1	CDC42 effector protein (Rho GTPase binding) 1	596.3	2.14	291.4	720.2	3.48	198
BB131147	Cdc42ep4	CDC42 effector protein (Rho GTPase binding) 4	1452	2.46	583.3	1219.8	1.87	684.7
NM_021454.1	Cdc42ep5	CDC42 effector protein (Rho GTPase binding) 5	274.1	2.00	120.2	997.4	3.03	302.4
BB311117	Cdipt	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	3476	2.30	1467.9	3446.4	2.30	1519
NM_007658.1	Cdc25a	cell division cycle 25 homolog A (S. cerevisiae)	2875	2.00	1472.5	3332	2.46	1335.5
BB752135	Cdc27	cell division cycle 27 homolog (S. cerevisiae)	309.7	2.46	135.9	455.6	2.83	170.8
BC023187.1	Cdc27	cell division cycle 27 homolog (S. cerevisiae)	166.6	1.52	118.3	187.2	3.03	61
BM237919	Cnbp	cellular nucleic acid binding protein	1389	2.30	648.1	1611.3	2.64	624.7
NM_011804.1	Creg	cellular repressor of E1A-stimulated genes	1386	1.74	841.5	2035.2	2.83	729.5
NM_013496.1	Crabp1	cellular retinoic acid binding protein I	2047.3	1.74	1064.2	2534.1	3.03	892.8
NM_024217.1	Cklfs3	chemokine-like factor super family 3	713.2	2.46	309.5	839.9	3.48	262.6
NM_031161.1	Cck	cholecystokinin	208	2.14	118.4	360.3	2.83	97.4
BB129366	Chk	choline kinase	692.6	2.30	239.9	525.4	2.46	214
BB201828	Chd4	chromodomain helicase DNA binding protein 4	501.6	2.30	189.7	578.7	2.83	189.1
NM_009881.1	Cdyl	chromodomain protein, Y chromosome-like	648.6	2.46	292.4	765.7	2.64	333.7
AW551470	Chc1l	chromosome condensation 1-like	1085	2.83	389.2	710.2	2.14	347.4

NM_013805.1	Cldn5	claudin 5	1798.1	1.87	955.4	1586.1	2.64	623.1
BM239527	Cpsf2	cleavage and polyadenylation specific factor 2	2346.9	2.14	1069.6	2808.9	3.03	845.7
NM_007975.1	F2r3	coagulation factor II (thrombin) receptor-like 3	176.1	2.14	62.4	248	3.03	77.1
NM_007687.1	Cfl1	cofilin 1, non-muscle	1690	2.46	696.3	1773.3	2.46	704.3
AB006714.1	Crmp1	collapsin response mediator protein 1	426.1	3.25	149.3	456.8	3.03	163.8
AV319144	C1qr1	complement component 1, q subcomponent, receptor 1	2329.2	2.00	1190.3	2131.5	2.64	876.7
AK017702.1	Crry	complement receptor related protein	307.4	1.74	195.9	314.2	2.83	149.3
AU045682	Chuk	conserved helix-loop-helix ubiquitous kinase	1097.1	2.64	439.7	931.9	1.52	626.1
NM_009824.1	Cbfa2t3h	core-binding factor, runt domain, alpha subunit 2; translocated to, 3 homolog (human)	257.7	2.00	228.9	487.1	3.25	227.6
BB740218	Coro1a	coronin, actin binding protein 1A	91.5	3.48	35.2	123.7	2.46	48.5
NM_011778.1	Coro1b	coronin, actin binding protein 1B	857.8	2.14	385.2	1021.1	2.46	419.9
BC010712.1	Cri1	CREBBP/EP300 inhibitory protein 1	1582.3	1.87	801.7	2128	2.64	845.3
AI482548	Cryl1	crystallin, lamda 1	152.4	2.30	63.8	128.4	3.25	41.1
AF197159.1	Cubn	cubilin (intrinsic factor-cobalamin receptor)	155.4	3.25	53.1	254.3	4.00	50.4
BB357590	Dmtf1	cyclin D binding myb-like transcription factor 1	251.6	2.14	117.8	476.4	4.92	97.1
BB538325	Ccnd1	cyclin D1	3569.2	3.73	1055.2	3244.2	4.92	815.9
NM_007631.1	Ccnd1	cyclin D1	1708.1	2.00	824.4	1771.1	2.83	700.9
M64403.1	Ccnd1	cyclin D1	1122.4	2.00	508.7	1085	2.46	445.2
BM118679	Ccnd2	cyclin D2	465.3	2.64	175.6	669.4	2.64	240.7
BQ175880	Ccnd2	cyclin D2	5098.8	2.46	2070.6	3333.2	1.41	2594
BM118679	Ccnd2	cyclin D2	3444.5	1.62	2132.4	3646	2.30	1519.3
AF091432.1	Ccne2	cyclin E2	1441.7	2.64	472.8	1287	2.00	648.3
AV326194	Ccnh	cyclin H	312.1	3.73	104.6	138.4	1.62	105.2
BB426893	Ccnt2	cyclin T2	843.4	3.03	233.3	1378.7	3.25	408.3
AK013634.1	Ccnt2	cyclin T2	780.8	1.87	385.8	1205.8	2.64	448
AV265508	Cdkl3	cyclin-dependent kinase-like 3	137.1	8.00	29.1	267.3	19.70	22.9
NM_007793.1	Cstb	cystatin B	7323.7	2.64	2887.6	10424.7	3.48	3065.4
AV227314	Crim1	cysteine-rich motor neuron 1	165.8	2.46	81.6	183.8	6.50	43.5
AK008793.1	Cda	cytidine deaminase	290.7	1.74	151.4	377.4	2.64	134.4
BG075820	Dach1	dachshund 1 (Drosophila)	864.9	3.03	236.1	575.8	1.52	359
AY027937.1	Ddb2	damage specific DNA binding protein 2	227.7	3.73	64	133.8	1.52	95.2
NM_025860.1	Ddx18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	2495.7	2.46	1062.2	2265.4	2.14	1180.1
NM_019553.1	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	3189.1	2.64	1359.4	3158.3	2.00	1551.7
BG243238	Ddx46	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	1741.3	2.00	798.2	2338.4	3.03	746.9
L25126.1	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	3129.9	2.00	1346	1240	2.64	1142
NM_025748.1	Deadc1	deaminase domain containing 1	557.4	1.87	319	619.5	3.03	212.4
BC006661.1	Dbr1	debranching enzyme (S. Cerevisae) homolog 1	1791.7	2.64	675.6	993.8	1.74	873.4
BF467092	Dek	DEK oncogene (DNA binding)	92.4	3.25	24.1	111.3	3.48	26.1
BB768194	Dlc1	deleted in liver cancer 1	420.8	2.14	188.8	633.9	3.03	204.8
NM_010052.1	Dlk1	delta-like 1 homolog (Drosophila)	1488.1	2.46	578.5	1403.7	3.03	502.6
NM_007832.1	Dck	deoxycytidine kinase	1662.4	2.64	502.5	1218.7	1.74	718.6
BB094429	Dgkd	diacylglycerol kinase, delta	617.3	1.74	327.8	647.3	2.46	241.8
NM_007858.1	Diap1	diaphanous homolog 1 (Drosophila)	749.7	2.14	294.6	459.3	3.25	49.6

AW554652	Diap1	diaphanous homolog 1 (Drosophila)	98.5	2.00	40.5	131.8	3.48	50.7
BB201495	Diap3	Diaphanous homolog 3	621.8	18.38	31.7	847.4	22.63	29.5
NM_020046.1	Dhodh	dihydroorotate dehydrogenase	757.8	2.64	293.3	953.2	2.30	417.2
AK010430.1	Ddah1	dimethylarginine dimethylaminohydrolase 1	1479.7	2.00	677.5	1510.7	2.46	629.7
L07264.1	Dtr	diphtheria toxin receptor	479.6	1.62	294	990.4	3.25	301.3
AK011199.1	Dph2l2	diphtheria toxin resistance protein required for diphthamide biosynthesis (Saccharomyces)-like 2	196.6	2.64	99	182.8	2.14	96.1
AK014521.1	Dcbld1	discoidin, CUB and LCCL domain containing 1	339.6	3.73	85.8	471.3	3.48	132.9
NM_025705.1	Dcbld1	discoidin, CUB and LCCL domain containing 1	311.3	1.62	206.4	338.2	2.64	137.4
NM_019794.1	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	1456.5	2.46	588.9	1106.1	2.14	561.6
BC013461.1	Dr1	down-regulator of transcription 1	2581.7	2.64	874.1	2154.3	1.87	1139.2
NM_130447.1	Dusp16	dual specificity phosphatase 16	739.5	2.14	315.5	1059.2	4.00	235.1
L11330.1	Dusp2	dual specificity phosphatase 2	392.7	2.00	393.1	533	3.03	188.4
AK012530.1	Dusp4	dual specificity phosphatase 4	1555	2.30	651.1	1052.9	2.30	507.7
BM236717	Ep400	E1A binding protein p400	1080.5	2.64	389.6	1089.1	4.00	287
BB151715	Ets1	E26 avian leukemia oncogene 1, 5' domain	2214.5	2.14	978.5	2480.8	2.30	1127.4
BC010588.1	Ets1	E26 avian leukemia oncogene 1, 5' domain	206.9	2.14	107.7	402.3	2.46	132.6
BB151715	Ets1	E26 avian leukemia oncogene 1, 5' domain	2171.3	1.87	1311.9	2868.3	2.64	1082.9
BC005486.1	Ets2	E26 avian leukemia oncogene 2, 3' domain	1423.9	3.48	422.3	2213.1	2.83	729.9
BC027739.1	Elf2	E74-like factor 2	1853.5	2.14	837.9	2028.1	2.64	723.9
NM_007897.1	Ebf1	early B-cell factor 1	426.2	2.00	223.6	580.4	3.03	169.9
BB125261	Ebf1	early B-cell factor 1	108.9	1.74	60.9	121.1	4.59	26.9
AI255184	Evi5	ecotropic viral integration site 5	3386.2	2.00	1662.1	4473.1	2.46	1822.4
BM120053	Enc1	ectodermal-neural cortex 1	1412.8	2.30	651.1	1417.4	2.64	520.7
BI076485	Enc1	ectodermal-neural cortex 1	7113.4	2.30	2707.5	6653	2.64	2443.8
BM120053	Enc1	ectodermal-neural cortex 1	4193.4	1.87	2169.4	4399.2	3.03	1447.2
BC017134.1	Elt1	EGF, latrophilin seven transmembrane domain containing 1	285.7	2.46	121.4	369.4	3.03	124.1
NM_133222.1	Elt1	EGF, latrophilin seven transmembrane domain containing 1	210.5	1.74	108.4	299.2	3.25	81
BC024610.1	Egfl7	EGF-like domain 7	2886.1	2.14	1355.1	3308.7	2.46	1288.2
BC024610.1	Egfl7	EGF-like domain 7	1111.6	2.14	508.5	1764.7	2.30	721.7
AW491662	Egfl7	EGF-like domain 7	1961.9	1.87	1015.1	2096.8	2.64	784.3
BB284358	Egln3	EGL nine homolog 3 (C. elegans)	503.5	1.87	209	1137.5	2.46	477.2
AV222756	Ehd2	EH-domain containing 2	205.4	1.87	100.2	218	2.83	90.1
AK003759.1	Elac2	elaC homolog 2 (E. coli)	700.4	2.83	222.3	814	2.14	396.7
NM_133918.1	Emilin1	elastin microfibril interface located protein 1	1085.5	2.00	670	1150.7	2.46	459.9
AV319507	Emilin3	elastin microfibril interfacer 3	615.7	2.00	312.8	518.5	2.30	192
BB284404	Elav1	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	279.7	1.87	212.4	519.7	3.25	169.5
BC005686.1	Elk3	ELK3, member of ETS oncogene family	1373.2	2.64	489.9	1505.7	2.83	524.3
BB825801	Elk3	ELK3, member of ETS oncogene family	346.3	2.46	119.4	461.7	4.00	119.3
AW544251	Elk3	ELK3, member of ETS oncogene family	914.1	2.46	348.2	848	3.03	274.3
AW146130	Elk4	ELK4, member of ETS oncogene family	575.7	2.64	239.9	697.1	2.14	305.5
BC006735.1	Elov1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	1029.4	2.14	490.1	1028.2	2.46	438.5
BB748075	Elov1	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	1233.2	1.62	697	1399.6	2.83	542.9
AF480860.1	Elov6	ELOVL family member 6, elongation of long chain fatty acids (yeast)	1589.6	2.64	802.9	1695.3	2.30	744.6
AV104666	Endog	endonuclease G	741.2	2.14	338.4	664.7	2.64	274.5
AF361882.1	Esam1	endothelial cell-specific adhesion molecule	2096.6	2.83	710.3	2540.3	2.46	917.2
NM_013690	Tek	endothelial-specific receptor tyrosine kinase	1560.9	2.14	870.8	1429.4	2.64	541.7

1								
AI551117	LOC230857	endothelin converting enzyme 1	330.3	2.00	226.5	1175.1	4.29	247.7
BF100813	Ednrb	endothelin receptor type B	1041.1	1.52	648	1242.4	2.64	502.4
NM_007970.1	Ezh1	enhancer of zeste homolog 1 (Drosophila)	279.5	2.14	128	379.5	3.03	106.1
BC002046.1	Efna1	ephrin A1	487.4	3.25	175.1	665.8	4.29	185.7
AI649374	Eps15	epidermal growth factor receptor pathway substrate 15	129.1	1.74	97	156.8	3.73	42.5
BC028256.1	Erb2ip	Erb2 interacting protein	1278.4	2.46	572.2	1309.5	2.30	556.3
BB336138	Erb2ip	Erb2 interacting protein	190.3	1.87	110.9	301.6	2.83	98.2
NM_021300.1	Ehox	ES cell derived homeobox containing gene	68.7	-1.15	80.9	260.5	3.25	79.2
AK005093.1	Ethi1	ethanol induced 1	471.9	2.64	207.4	425.4	1.41	256.3
NM_007959.1	Etsrp71	ets related protein 71	3870.5	1.87	2081.2	2637.8	2.46	1239.2
AF218539.2	Etv3	ets variant gene 3	46.3	-1.87	74.2	423.6	2.46	154
NM_025380.1	Eef1e1	eukaryotic translation elongation factor 1 epsilon 1	3476.8	2.30	1337.4	2859.2	1.87	1469.7
BB835796	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)	1508.1	2.14	695.3	1722.2	2.46	697.4
NM_010123.1	Eif3s10	eukaryotic translation initiation factor 3, subunit 10 (theta)	1097	1.87	542.4	1387.2	2.64	509.4
BF227830	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	373.1	1.74	235.3	521.7	3.03	171.8
BB458938	Eif4e	eukaryotic translation initiation factor 4E	218.7	2.14	82.6	189.4	2.46	73.3
BM120823	Eif4el3	eukaryotic translation initiation factor 4E like 3	3647.7	2.00	1927.5	5666.8	2.64	2139.5
C77379	Etf1	eukaryotic translation termination factor 1	254.4	2.64	74.3	334.6	2.46	156.8
	Etf1	eukaryotic translation termination factor 1	1925.9	2.30	839.6	1765.4	2.00	886.2
BC013717.1	Exo1	exonuclease 1	1825.2	2.46	875.5	1668	2.14	808.4
NM_012012.1	Exo1	exonuclease 1	678	2.46	307.8	877.7	3.73	241.3
BE986864	Xpo6	exportin 6	1048.2	2.30	456.8	1103	2.30	482
NM_028816.1	Xlkd1	extra cellular link domain-containing 1	709.5	2.64	283.3	1255.3	3.03	399.6
AV124537	Xlkd1	extra cellular link domain-containing 1	708.4	2.30	207.4	661.3	2.64	313.8
AK004726.1	Eya4	eyes absent 4 homolog (Drosophila)	142.8	2.46	43.3	139.6	3.25	42.5
BB476944	Fdps	farnesyl diphosphate synthetase	952.8	1.74	552.8	1246.2	2.64	436.5
BI247584	Fbxl11	F-box and leucine-rich repeat protein 11	365.1	1.74	193.4	685	2.64	244.4
BB448023	Fbxl12	F-box and leucine-rich repeat protein 12	692.3	1.87	347.5	746.1	2.64	286.3
NM_013911.1	Fbxw2	F-box and WD-40 domain protein 2	114.5	2.83	34.2	164.4	4.29	37.4
BB320947	Fbxo6b	F-box only protein 6b	667.3	2.30	235.4	585.2	2.46	245.9
NM_015797.1	Fbxo30	F-box protein 30	725.1	2.64	263	680	2.14	340.8
AW990618	Fbn1	fibrillin 1	977	2.64	350.6	865.7	1.87	488.4
NM_007993.1	Fn1	fibronectin 1	3572.2	2.00	1775.1	2266.2	2.46	875.6
BM234360	Flt1	FMS-like tyrosine kinase 1	612.4	2.14	248.3	1123.5	3.73	268.6
NM_010228.1	Flt1	FMS-like tyrosine kinase 1	937.8	1.62	426.7	975.2	2.46	356.4
D88690.1	Flt4	FMS-like tyrosine kinase 4	1615.5	2.14	689.3	2558.7	4.00	626.8
AI323512	Foxn2	forkhead box N2	142.6	1.74	80.5	180.9	2.46	71.4
AV295543	Fbnp3	formin binding protein 3	1136.4	2.00	637.2	1333	2.64	489.4
BG064340	Fjx1	four jointed box 1 (Drosophila)	628.6	1.87	303.4	543.6	2.46	207.9
NM_010218.1	Fxc1	fractured callus expressed transcript 1	2178.7	2.46	879.1	2258.1	5.28	461.4
NM_019502.1	Fxc1	fractured callus expressed transcript 1	996.9	2.14	507.4	1303.5	2.83	530.1
NM_019502.1	Fli1	Friend leukemia integration 1	1353.4	2.30	533.6	1200.1	2.83	527.7

NM_008026.1								
BB138212	Fli1	Friend leukemia integration 1	1688.7	1.87	811.5	1767.4	2.46	737.2
BB303906	Fpgt	fucose-1-phosphate guanylyltransferase	488.5	2.83	201.2	511.1	2.00	254.2
BE985138	Fus	fusion, derived from t(12;16) malignant liposarcoma (human)	1977.4	1.74	1167.6	2617.4	2.64	950.6
NM_008761.2	Fxyd5	FXD domain-containing ion transport regulator 5	508.9	1.62	339.2	566.1	2.83	258.5
AW909391	Fyn	Fyn proto-oncogene	491.1	2.14	227.5	1813.3	2.83	623.1
BM120195	Fgd5	FYVE, RhoGEF and PH domain containing 5	1319.2	1.74	801.6	1594.7	2.46	636.9
BB037474	Gpr73	G protein-coupled receptor 73	92.1	2.46	45.8	198.2	3.03	55.3
BB461269	Gprk6	G protein-coupled receptor kinase 6	2177.1	2.30	781.2	2127.5	1.87	1054
AK017943.1	Git2	G protein-coupled receptor kinase-interactor 2	243	2.64	102.9	111	3.73	44.8
AW229713	Gspt1	G1 to phase transition 1	268.5	3.25	69.5	175.5	2.14	73.9
BB162021	Gspt1	G1 to phase transition 1	427	1.74	241.2	795.7	2.46	369.6
NM_010249.1	Gabpb1	GA repeat binding protein, beta 1	450.5	1.87	266.3	537	2.83	239
NM_016905.1	Galk1	galactokinase 1	3937.3	2.00	2028	4124.8	2.30	1785.3
BC009021.1	Gla	galactosidase, alpha	557.6	2.00	277.1	599.1	2.83	195.9
AF180518.1	Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	1489.4	2.14	559.2	1725.5	3.25	425.2
AF180518.1	Gabarapl1	gamma-aminobutyric acid (GABA(A)) receptor-associated protein-like 1	452.2	2.00	158.9	270.3	2.64	95
AF216832.1	Gja4	gap junction membrane channel protein alpha 4	953.5	2.00	513	1052.6	2.30	477.7
NM_008126.1	Gjb3	gap junction membrane channel protein beta 3	614	2.14	312.6	791.9	3.25	255
NM_010291.1	Gjb5	gap junction membrane channel protein beta 5	173.7	2.83	69.7	237.2	3.03	70.7
AK004675.1	Gata2	GATA binding protein 2	451.5	3.03	133.2	410.9	2.64	179.9
BB824003	Gemin5	gem (nuclear organelle) associated protein 5	210.6	2.83	75.4	362.3	2.83	90.6
AK017246.1	Gt(ROSA)26asSor	gene trap ROSA 26 antisense, Philippe Soriano	139.5	4.29	33.2	228.3	3.48	61.9
BB385651	Gphn	gephyrin	474.3	2.30	219.7	511.9	1.74	292.6
AI604259	Ggps1	geranylgeranyl diphosphate synthase 1	1172.1	2.46	534.6	954.1	1.87	514.3
AV251087	Gle1l	GLE1 RNA export mediator-like (yeast)	383.6	2.64	153.8	361.5	2.30	141.4
BB233668	Gbif	globin inducing factor, fetal	539.6	2.46	241.2	424.4	2.00	277.6
AW413620	Gig1	glucocorticoid induced gene 1	322.9	3.48	102.8	308.7	3.03	106.9
AK015527.1	Gnpda2	glucosamine-6-phosphate deaminase 2	461.5	3.25	131.4	571.1	3.73	125.3
U09114.1	Glul	glutamate-ammonia ligase (glutamine synthase)	1024.6	2.46	366.6	981.8	2.46	388.1
BC019374.1	Gclc	glutamate-cysteine ligase, catalytic subunit	1480.3	2.14	672.8	1957.9	3.03	655.4
AK002661.1	Gstk1	glutathione S-transferase kappa 1	497.7	2.00	241.2	782.5	2.64	221.8
AV003026	Gsto1	glutathione S-transferase omega 1	4267.4	2.83	918.4	2128.9	2.14	1439.3
NM_010362.1	Gsto1	glutathione S-transferase omega 1	1485.9	2.46	599.7	1247.1	2.14	802.1
BB265744	Gstz1	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	160	4.29	31.4	120.4	2.83	42.3
BQ175968	Gpd2	glycerol phosphate dehydrogenase 2, mitochondrial	274.8	2.14	136.4	257.4	4.00	58.6
AK017959.1	Gdpd1	glycerophosphodiester phosphodiesterase domain containing 1	526.8	2.64	236.7	1367.5	3.73	287.9
NM_013847.1	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	613.8	2.14	295.8	650.4	2.46	279.5
NM_010326.1	Gp1ba	glycoprotein 1b, alpha polypeptide	252.2	3.25	70.1	129.3	2.30	109
AK008972.1	Golga1	golgi autoantigen, golgin subfamily a, 1	138.4	1.74	96.3	155.6	3.03	54.9
AK007410.1	Gadd45g	growth arrest and DNA-damage-inducible 45 gamma	2397	2.14	1074.2	2444.3	2.64	921.9
BB770972	Gas2l3	Growth arrest-specific 2 like 3	812.4	1.74	470.2	1020.8	2.46	383.6
BB622036	Gap43	growth associated protein 43	981	2.46	385.5	945.7	3.25	285.7
BC007483.1	Gab1	growth factor receptor bound protein 2-associated protein 1	1575.6	2.00	792	1771.9	2.46	724.4
BC007483.1	Gab1	growth factor receptor bound protein 2-associated protein 1	1362.8	1.87	840.9	1207.4	3.25	557.8

AU067739	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	873.6	2.14	396.5	949.6	2.30	416.6
AV015833	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	7024.1	2.14	3243.4	7910	2.30	3386.2
Y13832.1	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	1794.2	2.00	858.9	1514.9	3.03	522.5
Y13832.1	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	2100.1	2.00	1060.6	2395.2	2.83	917.1
AK018121.1	Gtl2	GTL2, imprinted maternally expressed untranslated mRNA	608.6	1.74	357	643.3	2.64	242
U10551.1	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	78.3	2.46	35.9	114.4	3.48	26.2
BB822914	Gtpbp4	GTP binding protein 4	960.5	2.46	408.7	990.1	2.83	390.4
AI987834	Gtpbp4	GTP binding protein 4	4207	2.64	1507.5	4013.2	2.00	2121.7
NM_025331.1	Gng11	guanine nucleotide binding protein (G protein), gamma 11	3200.5	1.87	1617	3090.8	2.64	1256.1
NM_013531.1	Gnb4	guanine nucleotide binding protein, beta 4	1325.1	2.14	607.9	1392.9	2.64	512.1
BB333568	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) domain and RCC1 (CHC1)-like domain (RLD) 2	170.6	2.83	67.6	258.4	3.73	56.7
BB329527	Helic1	helicase, ATP binding 1	593.3	2.46	251.7	520.2	1.87	295.1
NM_008234.2	Hells	helicase, lymphoid specific	2782.2	2.30	1057.6	2213.5	1.74	1411.4
AK014111.1	Hhex	hematopoietically expressed homeobox	1595.1	1.87	843.5	1978.4	3.03	594.5
NM_010442.1	Hmox1	heme oxygenase (decycling) 1	198.7	1.74	86.8	284.1	3.48	74.3
M26898.1	Hba-x	hemoglobin X, alpha-like embryonic chain in Hba complex	632.3	5.66	94.4	6094.8	1.32	4845.9
AV148191	Hbb-y	hemoglobin Y, beta-like embryonic chain	167.7	4.59	37.4	7102.7	1.52	4769.1
AV156860	Hbb-y	hemoglobin Y, beta-like embryonic chain	155.4	3.25	56.5	7135.8	1.41	4731.3
NM_008219.1	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	3337.6	4.92	752.8	12962.1	1.62	8108.7
AV147727	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	6146.3	4.59	1251.1	18648.2	1.74	10888.8
AV311770	Hbb-bh1	hemoglobin Z, beta-like embryonic chain	7013.3	4.59	1446	18107.7	1.62	10825
BF228203	Hnrpu	heterogeneous nuclear ribonucleoprotein U	3161.5	2.46	1267.3	4076.4	2.30	1765.5
U07631.1	Hexa	hexosaminidase A	1693.4	2.00	848.3	1683.3	2.46	696.6
C77256	Hdlbp	high density lipoprotein (HDL) binding protein	352.8	1.32	247.3	463.4	2.83	248.3
BB105328	Hmga2	high mobility group AT-hook 2	932.1	2.00	514.3	1036.6	3.03	353
BF166000	Hmgb1	high mobility group box 1	2465.9	2.00	1279	3136.8	2.46	1206.3
AW825904	Hmgb2l1	high mobility group box 2-like 1	667.6	1.74	474.3	959.1	2.64	399.2
BB451746	Hars	histidyl-tRNA synthetase	4074.1	2.30	1862.7	3879.1	2.00	1916.8
M25487.1	Hist1h2bp	histone 1, H2bp	894	2.14	429.9	1141.1	2.46	446.4
M25487.1	Hist1h2bp	histone 1, H2bp	84.9	1.41	54.9	101.2	4.00	28.3
NM_013550.1	Hist1h3a	histone 1, H3a	923.3	2.46	434.9	1548.1	2.30	635.6
BG068396	Hrb	HIV-1 Rev binding protein	298.6	2.83	115.5	378.1	2.64	154.9
BG071632	Hrb	HIV-1 Rev binding protein	730.8	2.46	262.7	586.8	1.74	377.8
NM_023130.1	Raly	hnRNP-associated with lethal yellow	1325.5	2.64	448	1326.9	3.73	490.3
AK002670.1	Hoxa10	homeo box A10	240.4	2.00	100.3	265.2	3.25	73.2
NM_010450.1	Hoxa11	homeo box A11	924	3.48	256.4	365.9	2.64	140.1
AA987181	Hoxa9	homeo box A9	622.1	3.03	254.2	829.1	2.46	301.3
BC016893.1	Hoxb6	homeo box B6	395.8	2.00	198.1	536.5	2.83	189.6
BB283726	Hoxc8	homeo box C8	180.8	2.46	74.7	212.3	3.25	47.6
AA265122	Hoxd8	homeo box D8	147	3.48	38.7	101.8	3.25	32.8
NM_010420.1	Hesx1	homeo box gene expressed in ES cells	148.3	1.74	70.9	214.8	2.64	86.4
AV298304	Homez	homeodomain leucine zipper-encoding gene	291.2	2.46	127.8	182.2	1.62	126
NM_008316.1	Hus1	Hus1 homolog (S. pombe)	1464.4	2.46	560	1343.1	1.87	762.8
AV150884	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	3312.8	2.64	1360.2	3981.8	2.00	1893.8
NM_019657.1	Hsd17b12	hydroxysteroid (17-beta) dehydrogenase 12	1256.2	2.00	524.5	2105.3	3.48	627.7
	---	Hypothetical gene supported by AK007344; AK013851;	71.2	3.03	15.6	106.3	3.25	17.6

AK013851.1		AK077867						
BC005577.1	Ian1	immune associated nucleotide 1	668.1	2.14	326.2	795.1	2.83	318.8
BF682515	A630002K24	immune associated nucleotide family member	112.8	2.14	55	170.6	2.83	60.1
NM_008376.1	Imap38	immunity-associated protein	242.2	2.00	183.6	231.9	2.46	154.2
AV301185	Incenp	inner centromere protein	661	2.14	319.3	701.1	2.64	257.5
AV311276	Ide	insulin degrading enzyme	1724.1	2.46	691.7	1570.1	2.46	741.4
BB005488	Insig1	insulin induced gene 1	803.3	2.00	418.6	817.4	3.03	271.2
AF440694.1	Igf1	insulin-like growth factor 1	779.6	1.87	372.1	862.6	3.48	306.1
NM_009951.1	Igf2bp1	insulin-like growth factor 2, binding protein 1	1093.2	2.14	475.3	1176.5	2.64	454.1
BC019836.1	Igfbp4	insulin-like growth factor binding protein 4	3296.2	1.62	1861.5	4562.6	2.83	1510.7
BB787243	Igfbp4	insulin-like growth factor binding protein 4	12044.7	2.00	5879.1	10634.5	2.64	4077.8
BC019836.1	Igfbp4	insulin-like growth factor binding protein 4	8124	1.87	4174.9	9612.6	2.64	3489.9
AA119124	Igfbp4	insulin-like growth factor binding protein 4	844.7	1.62	590.4	1064.9	2.46	427.1
BI664675	Itga3	integrin alpha 3	852.8	2.00	385.4	1164	3.25	292.1
BB284583	Itga4	integrin alpha 4	309.6	2.64	134.9	372.6	2.83	88.6
NM_010494.1	Icam2	intercellular adhesion molecule 2	997	1.87	545.2	1051.5	2.30	514.6
AW986054	Ifi35	Interferon-induced protein 35	507.2	2.00	238.4	709.8	2.83	187.1
NM_013562.1	Ifrd1	interferon-related developmental regulator 1	1586.5	2.46	615	1592.4	2.14	776.7
BC004619.1	Il11ra1	interleukin 11 receptor, alpha chain 1	335.3	3.03	129.8	396.6	2.46	185.6
AK017211.1	Il6st	interleukin 6 signal transducer	747.6	2.64	300	688.6	2.46	276.6
BI102913	Il6st	interleukin 6 signal transducer	1705.5	2.14	781.8	2318.9	2.46	923.4
AV278060	Invs	inversin	6770.5	2.46	2768.4	5725.8	1.87	3130.4
NM_016721.1	Iqgap1	IQ motif containing GTPase activating protein 1	4049.1	1.87	2165.1	4733.4	2.64	1711.7
BC004801.1	Idi1	isopentenyl-diphosphate delta isomerase	2377.3	2.46	971.4	2321.9	2.00	1184.8
BG066552	Jade1	Jade1 PHD finger protein	470.6	2.83	166.5	375.8	1.87	160.6
BQ032637	Jak1	Janus kinase 1	997.7	2.14	511.3	1403.1	2.64	515.3
BF224937	Jak1	Janus kinase 1	245.8	1.87	136.6	290.4	2.83	100.3
AJ278133.1	Kdelr2	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	1582.1	2.00	746.9	1810.6	2.83	591.2
BB428573	Klhl2	kelch-like 2, Mayven (Drosophila)	884.5	2.30	368	738.2	2.14	335.2
BM247104	KLHL6	kelch-like 6	920.3	2.00	448.3	928.4	3.03	443.1
NM_008471.1	Krt1-19	keratin complex 1, acidic, gene 19	616	2.46	290.3	715.5	2.64	270.1
BQ174458	Khsrp	KH-type splicing regulatory protein	486.6	2.30	179.1	441.1	2.46	191.8
BQ174458	Khsrp	KH-type splicing regulatory protein	334.9	1.62	211	418.7	2.46	125.7
NM_010612.1	Kdr	kinase insert domain protein receptor	4188	1.74	2319.4	5319	2.46	2134.1
BQ175168	Kist	kinase interacting with leukemia-associated gene (stathmin)	497.8	2.46	198.7	347.2	2.00	220.3
BB827235	Kif11	kinesin family member 11	435.3	2.83	132.9	387	2.83	142.1
BG066903	Kif16b	kinesin family member 16B	548.1	2.46	226	498.4	2.83	156.4
BI109632	Kif1b	kinesin family member 1B	835.3	2.00	445.1	844.3	2.30	335.2
BE199508	Kif1b	kinesin family member 1B	616.4	1.74	345.9	771.2	2.83	259.2
X65997.1	Kit	kit oncogene	1426.1	2.00	730.5	1638.4	3.03	503.4
BE851797	Klf7	Kruppel-like factor 7 (ubiquitous)	579.5	2.30	257.5	606.4	2.83	279.3
AV320422	L3mbtl3	l(3)mbt-like 3 (Drosophila)	569.8	3.48	146.2	675.4	4.92	148.8
BG970109	Lamb1-1	laminin B1 subunit 1	208.9	1.74	145	294.8	3.25	84.8
AK014742.1	Lss	lanosterol synthase	139.2	2.64	55.9	140.4	3.03	66
NM_008495.1	Lgals1	lectin, galactose binding, soluble 1	1919.3	2.14	776.2	2225.8	2.64	785
AI642438	Lgals1	lectin, galactose binding, soluble 1	6088	1.87	3591	7350.4	2.83	2361.8
AI787074	Lman1	lectin, mannose-binding, 1	1710.2	2.00	844.8	2709.5	2.64	1060.7
BB449235	Lmtk2	Lemur tyrosine kinase 2	233.5	1.87	117.8	312.7	3.03	95.6

BB705823	Luzp1	leucine zipper protein 1	2787.1	2.30	1231.8	2747.9	2.83	1024.3
BB161653	Lztf1	leucine zipper transcription factor-like 1	145.5	2.14	88.8	166.5	2.46	87.4
BB667318	Lek1	leucine, glutamic acid, lysine family 1 protein	337.8	2.00	175.8	420.6	2.46	143.9
AK013416.1	Lmo2	LIM domain only 2	2823.5	1.74	2021.5	3295.4	2.46	1293.3
NM_013860.1	Limd1	LIM domains containing 1	540.8	2.46	200.7	549.2	2.83	212.6
NM_008499.1	Lhx5	LIM homeobox protein 5	496.1	13.93	51.2	858.3	64.00	22.3
NM_008509.1	Lpl	lipoprotein lipase	916.5	2.64	375.2	1013.8	1.74	601.2
BM207920	Ldlr	low density lipoprotein receptor	1510.7	1.52	976.5	1401	2.46	570.1
BG072227	Litaf	LPS-induced TN factor	596.6	2.00	306.3	598.2	3.25	191.3
AF204156.1	Lsm2	LSM2 homolog, U6 small nuclear RNA associated (S. cerevisiae)	837.5	2.14	374.2	1143.1	2.64	464.4
AV309996	Luc7l	Luc7 homolog (S. cerevisiae)-like	1444.1	2.30	655.1	1461	2.83	515.7
NM_008535.1	Lyl1	lymphoblastic leukemia	827.8	2.00	447.4	1157.8	3.25	352.2
BE865221	Lbcd1	lymphoid blast crisis-like 1	1396.8	2.00	707.8	1752.9	3.03	609.5
BB096368	---	M.musculus mRNA for testis-specific thymosin beta-10	8718.5	1.74	4689.6	9169.7	2.46	3792.2
NM_008539.1	Madh1	MAD homolog 1 (Drosophila)	437.1	2.30	228.3	527.4	4.00	139.7
M16360.1	Mup5	major urinary protein 5	268.4	2.46	105.3	295.3	2.83	94.7
BB831435	Mak10	MAK10 homolog, amino-acid N-acetyltransferase subunit, (S. cerevisiae)	1827	2.30	787.7	2294.6	2.64	798.2
AK013287.1	Mak3p	Mak3p homolog (S. cerevisiae)	690.5	2.46	264.1	627.9	1.62	348.3
BM235734	Me2	malic enzyme 2, NAD(+)-dependent, mitochondrial	623.9	2.64	236.5	948.2	3.25	332.9
NM_008548.1	Man1a	mannosidase 1, alpha	836.4	1.74	441.5	1115.1	3.25	318.3
BB392263	Man1c1	mannosidase, alpha, class 1C, member 1	826.4	1.87	507.9	1008.2	2.46	411.1
BB414982	Mgat1l	mannoside acetylglucosaminyltransferase 1-like	1869.7	2.00	942.4	2171.4	2.64	801
AI481328	Mgat2	mannoside acetylglucosaminyltransferase 2	1216.9	3.48	407.5	2159.1	4.92	459.2
BE628819	Mgat2	mannoside acetylglucosaminyltransferase 2	918.6	1.74	460	1209.5	2.46	434.5
AK010751.1	Mark4	MAP/microtubule affinity-regulating kinase 4	855.9	2.00	477.7	996.7	3.03	344.5
NM_010769.1	Matn1	matrilin 1, cartilage matrix protein 1	97.8	1.74	46.7	115.9	4.29	30.4
BI249188	Matr3	matrin 3	859.1	2.00	406.5	1097	2.83	346.7
NM_008611.1	Mmp8	matrix metalloproteinase 8	5.6	-1.32	28.9	309.5	3.25	92.9
AK009477.1	Mga	MAX gene associated	457.8	1.87	221.5	344.4	2.64	168
AV228095	Mlr1	Mblk1-related protein-1	245.7	3.73	66.2	298.2	2.14	101.6
BE650208	Mlr1	Mblk1-related protein-1	209.8	2.83	80.2	240.3	1.52	137.3
BB230617	Mlr1	Mblk1-related protein-1	418.6	2.14	218.7	440	3.03	137.3
BF581250	Mkks	McKusick-Kaufman syndrome protein	875.3	2.14	399.6	1184.6	2.64	490.2
BB555250	Mgea5	meningioma expressed antigen 5 (hyaluronidase)	590.3	1.74	551.2	720.2	2.83	200.9
NM_013602.1	Mt1	metallothionein 1	678.4	1.87	351.1	891.6	3.03	400.8
AA796766	Mt2	metallothionein 2	4319.1	1.74	2850	6973.2	3.03	2211.6
BG076333	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methylenetetrahydrofolate cyclohydrolase	1493.4	2.83	504.4	2586.8	3.25	756.2
AV215673	Mthfd1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent), methylenetetrahydrofolate cyclohydrolase, formyltetrahydrofolate synthase	703.3	2.46	286.7	784.8	2.00	426.2
AB056100.1	Mtap	methylthioadenosine phosphorylase	492.1	1.74	223.2	994	3.73	302.8
NM_010792.1	Mettl1	methyltransferase-like 1	528.5	2.46	235.1	812.6	3.73	174.8
AV118676	Mettl1	methyltransferase-like 1	452.7	2.30	198.8	529.5	4.29	158.5
BB311034	Mapre2	microtubule-associated protein, RP/EB family, member 2	8397.9	1.74	4989	9535.7	2.83	3367.5
BQ177132	Mib1	mindbomb homolog 1 (Drosophila)	433.1	3.25	136.3	340.5	2.30	165.7
BB242439	Mib1	mindbomb homolog 1 (Drosophila)	1232.5	2.00	551.6	1487.7	2.46	592.4
AV306676	Mrpl15	mitochondrial ribosomal protein L15	984.7	2.83	292.4	1405.8	2.46	490.1
BB314055	Mrps15	mitochondrial ribosomal protein S15	2779.3	2.00	1272	2580	3.03	884.8

NM_025544.1	Mrps15	mitochondrial ribosomal protein S15	1275.8	1.87	722.9	1840.1	2.46	677.4
NM_026768.1	Mrps18a	mitochondrial ribosomal protein S18A	1679.7	2.30	707.8	1511	2.30	668.3
BB113015	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	931.2	2.14	549.3	1032.5	2.30	539
BF450398	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	210.9	1.74	120.6	301.5	2.64	118.5
BG076273	mKIAA1064	mKIAA1064 protein	825	1.74	471.4	803.8	2.64	312.4
AW536472	Mrgef	Mras regulated guanine nucleotide exchange factor	306.6	2.30	176.7	1090.4	2.83	406.6
BM230524	Mrgef	Mras regulated guanine nucleotide exchange factor	161.2	2.00	119.8	297.7	2.83	100.2
BB836564	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	1329.8	2.64	500	1094.9	2.00	516.5
BB003847	Mbnl2	muscleblind-like 2	1145	1.87	632.3	1329.1	2.64	491.2
NM_134163.1	Mbnl3	muscleblind-like 3 (Drosophila)	601.5	3.25	156.7	826.4	4.92	147.5
AI642973	Myct1	myc target 1	179.5	3.48	44.2	279.7	3.25	60.6
W34301	Myct1	myc target 1	261.3	2.14	118.1	389	3.03	114
NM_033597.1	Myb	myeloblastosis oncogene	139.5	2.46	94	258.7	1.87	121.1
BC006728.1	Myc	myelocytomatosis oncogene	1332.2	1.87	691.2	1418.8	2.64	509.2
BB496038	Mllt10	myeloid/lymphoid or mixed lineage-leukemia translocation to 10 homolog (Drosophila)	795.9	2.46	361.5	841.6	2.64	285.4
BM238921	Mll3	myeloid/lymphoid or mixed-lineage leukemia 3	997	1.74	521.3	1096.7	3.03	510.7
NM_013597.1	Mef2a	myocyte enhancer factor 2A	1595.2	3.03	574.7	1644.9	3.25	586
BG072973	Mef2a	myocyte enhancer factor 2A	548.4	2.83	241.2	748.8	3.03	260.3
AV255689	Mef2a	myocyte enhancer factor 2A	1609.2	1.74	921.7	2211.7	3.48	629.1
AV255689	Mef2a	myocyte enhancer factor 2A	1558.9	1.74	862.2	1626	2.30	765.6
BB291766	Myh10	myosin heavy chain 10, non-muscle	452	2.30	173.4	439.5	1.74	242.8
BM121854	Myh9	myosin heavy chain IX	424.4	1.62	152.4	741.7	3.03	226.2
BQ176602	Myo1c	myosin IC	2389.2	2.30	1008.9	3065.9	3.03	892.2
NM_008663.1	Myo7a	myosin VIIa	169	2.00	114.1	282	2.83	130.9
NM_019472.1	Myo10	myosin X	1149.7	2.14	424.2	1285	3.25	435.5
AI746549	Mylk	myosin, light polypeptide kinase	198.5	1.62	117.2	268.5	2.46	123.3
BB124537	Mtpn	myotrophin	3901.8	2.14	1829	3967.9	2.83	1459.1
BM215160	Mtpn	myotrophin	4662.2	2.14	1895.1	5986.8	3.48	1680.9
BB071996	Nalp6	NACHT, leucine rich repeat and PYD containing 6	273	2.30	109.6	149.6	3.03	49.8
BI652065	Ndst1	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1740.1	2.46	734.9	3008.4	4.59	651.6
BB543376	Nakap95	neighbor of A-kinase anchoring protein 95	159.7	1.62	77.7	166.1	3.25	43.6
BB535494	Nedd9	neural precursor cell expressed, developmentally down-regulated gene 9	967.3	2.64	366.5	710.6	1.87	408.8
AV144145	Nrln1	neuralin 1	172.7	3.03	71.8	105.6	1.41	47
AA986379	Nbea	neurobeachin	389.8	2.00	176.2	418.2	2.83	154.2
BB431371	Nav1	neuron navigator 1	139.5	1.87	38.6	219.6	3.25	58.8
BB752129	Nrp2	neuroligin 2	1484.1	3.25	356.2	1570.1	2.64	546.8
BQ176723	Nrp2	neuroligin 2	1117	2.30	481.1	876.8	2.64	336.9
NM_010917.1	Nid1	nidogen 1	744.9	2.30	303.5	3600.4	2.83	1193.5
AK012873.1	Nrk	Nik related kinase	1972.4	2.00	946.6	2204.8	3.03	536.4
BB025231	Nisch	nischarin	1609.1	2.00	730.4	2074.6	2.64	729.1
BB025231	Nisch	nischarin	4307.2	1.87	2177.5	4857.2	2.46	2040.3
AV309418	Ndr1	N-myc downstream regulated 1	163.9	1.52	94.4	275.3	3.03	91.6
M88489.1	Recc1	nonamer binding protein mRNA	819.4	2.14	427.1	1043.3	2.64	478.7
NM_008714.1	Notch1	Notch gene homolog 1 (Drosophila)	523.6	2.00	249.5	605.3	2.83	205.4
BE952133	Notch1	Notch gene homolog 1 (Drosophila)	944.1	2.00	492.8	662.9	2.46	312.9
NM_025980.1	Nrarp	Notch-regulated ankyrin repeat protein	1201.7	2.00	644.3	1436.5	3.73	431.9
AV297071	Nnp1	novel nuclear protein 1	675.8	1.87	319.1	915.8	2.64	384.6
BC021434.1	Ndel1	nuclear distribution gene E-like homolog 1 (A. nidulans)	493.6	2.14	200.1	531	2.83	161.4

BB488160	Nfat5	nuclear factor of activated T-cells 5	368.2	2.46	167.5	597.7	3.73	126.6
BB702754	Np95	nuclear protein 95	1121.4	2.30	459.5	1097.9	2.64	398.4
NM_025307.1	Nrbf2	nuclear receptor binding factor 2	1415	2.46	585.7	1382.9	2.14	636.4
BG070920	Ncoa2	nuclear receptor coactivator 2	1125.4	2.46	434.2	1271.9	2.14	551.4
BB829563	Ncoa6ip	nuclear receptor coactivator 6 interacting protein	442.6	1.52	194.8	444.5	2.46	225.4
NM_008735.1	Nrip1	nuclear receptor interacting protein 1	2589.2	2.14	1017.1	2869.1	3.48	749.6
BC008556.1	Nr1d2	nuclear receptor subfamily 1, group D, member 2	452.1	3.03	163.6	346.3	2.00	183.5
AU066920	Nr2c2	nuclear receptor subfamily 2, group C, member 2	367.1	2.30	166.5	495.8	2.83	195.7
AK007201.1	Nr6a1	nuclear receptor subfamily 6, group A, member 1	2187.1	2.30	935.4	1444.2	1.74	811
BG067058	Nsd1	nuclear receptor-binding SET-domain protein 1	376	2.30	126.3	309.8	2.64	105.7
BB292874	Nup153	nucleoporin 153	4036.9	2.46	1614.8	3632	2.00	1848
NM_016714.1	Nup50	nucleoporin 50	782.8	2.00	364.6	885.4	2.64	342.7
BE951220	Nup88	nucleoporin 88	440	2.30	145.2	564.4	2.83	173.3
AV035368	Nubp2	nucleotide binding protein 2	524.6	2.46	223.4	647	2.46	221
AK004444.1	Nudt9	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2065.2	2.00	942.9	1882.3	2.83	616.9
BB549310	Olfm1	olfactomedin 1	571.4	3.25	125.2	562.9	1.87	318.7
D78264.1	Olfm1	olfactomedin 1	229.8	1.62	162.3	319.2	3.48	129.2
BG065325	Ogt	O-linked N-acetylglucosamine (GlcNAc) transferase (UDP-N-acetylglucosamine:polypeptide-N-acetylglucosaminyl transferase)	397.5	1.74	242.1	572.4	2.83	207.6
AF356506.1	Oit3	oncoprotein induced transcript 3	449.6	2.46	207.7	605.3	3.48	175.1
BB210535	Orc1l	origin recognition complex, subunit 1-like (S.cerevisiae)	913.6	2.00	419.1	1058.6	2.46	466.4
BB620704	Orc4l	origin recognition complex, subunit 4-like (S. cerevisiae)	148.7	2.64	38.2	130.1	2.14	64.4
AK019971.1	Prrx2	paired related homeobox 2	2966.4	2.46	1196.1	2220.2	1.74	1140.9
U54499.1	Pitx1	paired-like homeodomain transcription factor 1	90.1	2.64	47.4	152.5	2.83	41.6
U80011.1	Pitx2	paired-like homeodomain transcription factor 2	432.8	1.87	306.9	636.7	2.64	212.2
AB006320.1	Pitx2	paired-like homeodomain transcription factor 2	79.9	1.62	92.4	155	2.83	43.9
AW107633	Phr1	pam, highwire, rpm 1	570.5	2.00	249.8	364.7	2.83	228.9
BC027089.1	Pank3	pantothenate kinase 3	447.5	1.87	130	471.4	2.83	145.7
NM_013788.1	Peg12	paternally expressed 12	345.1	2.64	129.1	264.3	2.00	96.6
BB530368	Pxn	paxillin	1435.8	2.14	610.2	1700.9	2.46	714.4
BB247595	Psip2	PC4 and SFRS1 interacting protein 2	266.9	2.46	115.3	298.7	3.03	96.4
BM243464	Pctk2	PCTAIRE-motif protein kinase 2	1536.9	2.00	815.2	1481.4	2.64	594
BB200545	Pctk2	PCTAIRE-motif protein kinase 2	208	2.00	112	210.9	2.30	91.4
AK020915.1	Peli1	pellino 1	114.3	1.41	63.3	213	3.03	67
BB337121	Peli2	pellino 2	245.7	1.74	115.3	342.7	3.03	112.5
AV209130	Ppif	peptidylprolyl isomerase F (cyclophilin F)	2017.7	2.46	681	1899.9	2.14	737.3
NM_023662.1	Pcm1	pericentriolar material 1	218	2.46	84.6	308.8	2.30	122.5
AV116958	Farsl	phenylalanine-tRNA synthetase-like	4402.1	2.46	1792.4	3751.5	1.87	2137.8
BB030030	Pten	phosphatase and tensin homolog	1026.5	2.83	379.5	1327.1	3.73	345.9
NM_009981.1	Pcyt1a	phosphate cytidylyltransferase 1, choline, alpha isoform	682.6	2.00	382.9	693.7	2.64	267.6
AK018164.1	Pik3ca	phosphatidylinositol 3-kinase, catalytic, alpha polypeptide	353.4	2.30	109.8	354.5	2.30	168.7
NM_008845.1	Pip5k2a	phosphatidylinositol-4-phosphate 5-kinase, type II, alpha	341.8	1.87	208.7	426.8	2.83	164
BG793493	Pde4b	phosphodiesterase 4B, cAMP specific	354.1	2.46	151.4	615.9	2.64	235.3
NM_008802.1	Pde7a	phosphodiesterase 7A	364	8.57	40.4	537.6	2.83	161.8
AY007702.1	Pde7a	phosphodiesterase 7A	200.4	1.62	111.3	177.6	2.83	65.3
AV304625	Pfkip	phosphofructokinase, platelet	1156.3	3.03	333.7	891.7	1.62	511.2
AV343511	Pfkip	phosphofructokinase, platelet	561.1	1.62	313.5	663.4	3.25	353.7
BM207017	Plcl2	phospholipase C-like 2	765.1	1.41	553.9	1091.1	3.25	350.1

BG064988	Ppat	phosphoribosyl pyrophosphate amidotransferase	1657.6	2.00	818.1	1790.9	2.46	716.2
BC004827.1	Psat1	phosphoserine aminotransferase 1	2912.8	2.30	1269.8	2947.3	2.14	1330.5
NM_008955.1	Psx1	placenta specific homeobox 1	413.2	3.03	140.6	325.3	2.64	149.9
BM210473	Pem	placentae and embryos oncofetal gene	2056.7	1.87	966.6	1920.7	2.64	676.2
AF250838.1	Plac1	placental specific protein 1	1151.6	1.87	649.5	1882.1	2.46	782.5
NM_011222.1	Pvt1	plasmacytoma variant translocation 1	456	2.30	204.2	429.2	3.25	127.3
NM_032398.1	Plvap	plasmalemma vesicle associated protein	802.4	1.87	476.5	1803.3	3.25	521.8
BB554124	Plekhc1	pleckstrin homology domain containing, family C (with FERM domain) member 1	419.6	1.74	258.6	485.5	2.46	191.7
BM218981	Phip	pleckstrin homology domain interacting protein	207.8	2.30	122.6	322.7	4.00	79.6
NM_009434.1	Phlda2	pleckstrin homology-like domain, family A, member 2	9115	1.62	5891.8	10745.8	2.30	3699.1
AF147785.1	Plagl1	pleiomorphic adenoma gene-like 1	8862.3	2.30	3879.2	8435.1	2.46	3392
BB476707	Plxnc1	plexin C1	190.9	2.14	100.7	427.7	3.03	117.9
BC019530.1	Plxnd1	plexin D1	681.4	2.14	395.4	1028.6	2.83	346.8
BM230222	Papola	poly (A) polymerase alpha	1480.7	1.87	820.3	1819.2	2.46	861.6
BG064799	Polg	polymerase (DNA directed), gamma	2635.1	2.46	1050.9	3365.6	3.25	1207.8
BM934958	Polg	polymerase (DNA directed), gamma	1130.7	1.87	698.9	1509.4	2.46	572.7
BB501129	Pnpt1	polynucleotide nucleotidyltransferase 1	666.8	1.87	401.9	836.1	2.64	274.1
BB115902	Kctd11	potassium channel tetramerisation domain containing 11	464	1.74	249.7	601.8	2.46	243.1
BM220945	Kctd12	potassium channel tetramerisation domain containing 12	683.3	2.46	282	595.8	3.48	279.6
NM_020574.1	Kcne3	potassium voltage-gated channel, Isk-related subfamily, gene 3	840.9	1.87	472.5	948	2.83	393.3
NM_013633.1	Pou5f1	POU domain, class 5, transcription factor 1	171.6	1.87	80.6	209.7	3.25	55.7
BM199789	Pja1	praja1, RING-H2 motif containing	1297.3	2.64	501.6	1146.2	1.62	654.5
BC024693.1	Pfdn1	prefoldin 1	4560.8	1.62	2661.5	4790.9	2.64	2019.1
BC021352.1	Plod2	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1990.4	2.14	961.4	2401.5	2.46	968.1
NM_011072.1	Pfn1	profilin 1	669.1	1.62	373.7	6071.3	3.03	2278
AV094856	Pdcd10	programmed cell death 10	523.7	2.30	254.9	642.7	2.46	247.2
BB550758	Peo1	progressive external ophthalmoplegia 1 (human)	1201.8	2.64	477.7	1017.7	1.87	552.9
AA672939	Pa2g4	proliferation-associated 2G4	3070.9	2.30	1424.1	3094.5	2.00	1614.5
AW536189	Pa2g4	proliferation-associated 2G4	4725	1.74	2673.8	6252.3	2.46	2501.4
NM_008968.1	Ptgis	prostaglandin I2 (prostacyclin) synthase	1502.4	2.00	732.5	1631.8	2.46	687.3
NM_025959.1	Psmc6	proteasome (prosome, macropain) 26S subunit, ATPase, 6	651.9	2.64	252.2	506.1	1.87	287.2
BM230572	Psmc14	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	439	2.14	237.6	532.2	3.03	182.1
BG066125	Psmc4	proteasome (prosome, macropain) subunit, alpha type 4	6735.3	2.00	3399.1	7874.9	2.46	3341.4
NM_011171.1	Procr	protein C receptor, endothelial	426.1	2.83	153.2	502	2.46	235
BM243756	Prkch	protein kinase C, eta	1212.2	2.46	519.1	1974.6	5.28	310.8
BI695530	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	765.3	2.30	365	1183.1	2.46	463.6
BB216074	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	1894.8	2.30	846.1	2349.8	2.46	888.8
BB216074	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	3890	1.74	2112.1	4046.8	2.64	1487.7
NM_029632.1	Ppp1r11	protein phosphatase 1, regulatory (inhibitor) subunit 11	518.2	1.74	260.2	787.7	2.46	327
BG064715	Ppp1r13b	protein phosphatase 1, regulatory (inhibitor) subunit 13B	843.1	3.25	208.1	801	2.46	336.7
AV281794	Ppp1r2	protein phosphatase 1, regulatory (inhibitor) subunit 2	781.2	2.00	407.6	776.2	2.83	284.3
BB535888	Ppp2r5e	protein phosphatase 2, regulatory subunit B (B56), epsilon isoform	2288.6	2.30	1031.2	2498.5	2.30	1107.7
BQ176231	Ppp3cb	protein phosphatase 3, catalytic subunit, beta isoform	1610.6	2.46	674.4	1302.5	1.74	782.8
BC027445.1	Ptp4a3	protein tyrosine phosphatase 4a3	395.1	1.74	252	389.6	2.46	150.5
AF157628.1	Ptpnb	protein tyrosine phosphatase, receptor type, B	363.6	1.74	238	637.5	2.83	212.1

BG802688	Ptprk	Protein tyrosine phosphatase, receptor type, K	393.1	1.74	257	382.1	2.64	195.7
NM_009419.1	Tpst2	protein-tyrosine sulfotransferase 2	336	2.14	183.8	629.7	3.73	172.1
AV225493	Pcdh12	protocadherin 12	467.9	2.00	241.3	701.8	3.03	228.9
BB206220	Pim3	proviral integration site 3	4949.7	2.64	1914.3	4752.2	2.14	2160.8
AI528614	Ptk2	PTK2 protein tyrosine kinase 2	1854.2	2.46	774.6	1728.5	2.00	891.2
BB314559	Pum1	pumilio 1 (Drosophila)	2732.5	2.83	963.3	3977.6	2.83	1341.3
BB823786	Pum1	pumilio 1 (Drosophila)	720	2.30	398.5	1203	2.46	529.2
AK008143.1	Pnp	purine-nucleoside phosphorylase	10	-59.71	891.2	8.4	-128.00	1064.8
NM_008771.1	P2rx1	purinergic receptor P2X, ligand-gated ion channel, 1	203.2	2.46	72.5	300.6	2.83	76.4
BB081608	R3hdm	R3H domain (binds single-stranded nucleic acids)	376	2.00	185.2	440.2	2.64	150.4
BC010722.1	Rab11a	RAB11a, member RAS oncogene family	2999.4	1.87	1508.3	4248.5	2.30	1831.7
BC003738.1	Rad51ap1	RAD51 associated protein 1	1894.8	2.46	681.7	1587.9	1.87	1087.8
BC019123.1	Rad52	RAD52 homolog (S. cerevisiae)	284.1	2.14	163.2	240.1	2.46	123.7
BB702885	Ralbp1	ralA binding protein 1	1369.6	2.00	542.3	1467.4	2.64	601.2
AW060738	Ranbp9	RAN binding protein 9	379.7	2.46	173.2	368.1	2.30	154.3
BB233502	Rap2c	RAP2C, member of RAS oncogene family	1276.7	1.87	639.4	1348.9	2.64	586.8
AK018504.1	Rassf2	Ras association (RalGDS/AF-6) domain family 2	121.4	2.14	51	142.3	3.25	41.6
BB703307	Rassf3	Ras association (RalGDS/AF-6) domain family 3	533.6	2.00	246.6	528.3	2.83	203
AF309564.1	Arhj	ras homolog gene family, member J	1794.6	2.14	881.4	2205.9	2.83	894.5
BG074180	Rasa1	RAS p21 protein activator 1	1725.9	2.30	692.7	1649.3	2.64	586
AW557564	Rest	RE1-silencing transcription factor	3372.2	2.00	1710.4	3479.9	2.46	1124.4
AF146523.1	Ramp2	receptor (calcitonin) activity modifying protein 2	5146.4	2.00	2681.6	6374.7	2.64	2507.4
NM_019955.1	Ripk3	receptor-interacting serine-threonine kinase 3	582.2	1.87	292	793.3	2.46	291.6
AF215668.1	Rgs2	regulator of G-protein signaling 2	362.9	1.74	176.1	420.7	3.03	136.1
BC026795.1	Rfc3	replication factor C (activator 1) 3	1297.2	2.46	456.7	1062	2.00	445.1
BG969810	Rsn	restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)	177.3	1.52	114.8	232.8	3.25	61.2
NM_020599.1	Rlbp1	retinaldehyde binding protein 1	81.8	2.14	52.1	157	12.13	18.1
AJ238396.1	Rpgr	retinitis pigmentosa GTPase regulator	708.1	2.64	253.4	585.4	1.87	329.4
AU040918	Rbbp4	retinoblastoma binding protein 4	1266.7	2.30	586.9	846.7	1.62	568.5
BB092954	Rbbp6	retinoblastoma binding protein 6	1301.1	2.30	538.7	1506.3	2.14	656.6
U27178.1	Rbl1	retinoblastoma-like 1 (p107)	215.4	3.03	85.7	194.8	1.87	104
AK013909.1	Rai1	retinoic acid induced 1	916.3	1.74	609	992.6	2.46	399.1
AF274866.1	Rai14	retinoic acid induced 14	3088.7	2.46	1435.2	2806.8	2.30	1069.3
BB308974	Rai14	retinoic acid induced 14	357.8	1.87	170.9	451.7	2.46	168
AK003491.1	Rtl1	retrotransposon-like 1	4862.6	2.00	2239.1	4318.7	2.64	1807.1
BB823029	Arhgap5	Rho GTPase activating protein 5	595.3	2.83	207.8	489.4	1.87	219
NM_009707.1	Arhgap6	Rho GTPase activating protein 6	122.5	2.64	54.4	108.2	1.52	37.6
NM_017402.1	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	908.3	2.14	438.3	1014	3.48	294.8
AK002516.1	Arhgdib	Rho, GDP dissociation inhibitor (GDI) beta	1024.3	2.46	358.7	994	2.64	278.5
AV047988	Rhobtb3	Rho-related BTB domain containing 3	455	1.87	213.1	598.4	3.03	172.4
BE447059	Rpl30	ribosomal protein L30	374.2	2.64	158.5	330.2	1.87	173.8
NM_026147.1	Rps20	ribosomal protein S20	159.8	2.83	57.4	123.5	1.87	109.7
BQ175276	Rps6ka3	ribosomal protein S6 kinase polypeptide 3	1519.9	2.46	560.5	1102.5	1.52	724.3
AK019964.1	Rrbp1	ribosome binding protein 1	2597	1.62	1284.7	2569.1	2.30	1149
AK004847.1	Rnf128	ring finger protein 128	217	2.46	62.3	232.1	1.62	90.4
NM_023270.1	Rnf128	ring finger protein 128	752.9	1.74	454.4	781.7	2.64	286.3

BB295604	Rnf130	ring finger protein 130	286.7	2.14	136.3	348.6	2.64	128.3
	Rnf138	ring finger protein 138	2202.1	2.46	839.8	2257.5	2.46	828.5
AK013419.1	Rnf138	ring finger protein 138	218.7	2.00	97.3	255.1	2.83	90.8
BC003712.1	Rnf138	ring finger protein 138	175.5	1.62	117.1	332.9	3.48	88
NM_019706.1	Rnf26	ring finger protein 26	1146.4	2.46	463.6	1306.8	2.83	475.6
BC004739.1	Rnmt	RNA (guanine-7-) methyltransferase	721.8	2.46	292.1	609.5	2.30	238
BM199014	Rbm14	RNA binding motif protein 14	945	2.46	356.4	1172.1	2.30	486.9
BM218282	Rbm6	RNA binding motif protein 6	1188.9	1.87	690.5	1188.4	2.46	517.5
BB031290	Rbm9	RNA binding motif protein 9	640.7	1.74	342.9	1046.1	2.64	293.4
AF229055.1	Rcl1	RNA terminal phosphate cyclase-like 1	1951.6	2.46	861.8	2245.6	2.30	967.9
BC004574.1	Rod1	ROD1 regulator of differentiation 1 (S. pombe)	1810	1.87	503.8	1673.3	3.03	810.2
BI690175	Runx1	runt related transcription factor 1	272.2	2.00	66.5	296.2	2.83	79.7
NM_009821.1	S100a10	S100 calcium binding protein A10 (calpactin)	1351	2.00	529.9	1469.4	2.46	549
NM_009112.1	Ahcy1	S-adenosylhomocysteine hydrolase-like 1	738.9	1.87	388	808.1	2.64	310.2
BB831090	Sal4	sal-like 4 (Drosophila)	1231	1.74	661.8	1083.4	2.30	461.1
BG064756	Samsn1	SAM domain, SH3 domain and nuclear localisation signals, 1	682.6	2.64	256.3	531.4	3.25	150.4
NM_023380.1	Scarb1	scavenger receptor class B, member 1	1002.2	1.52	640.7	1282.2	2.64	467.3
BB224405	Scarb1	scavenger receptor class B, member 1	575	2.30	244	649.9	2.64	250.1
BB138434	Scarf2	scavenger receptor class F, member 2	192.4	2.30	79.8	185.2	2.83	64
BB484759	Sfmbt1	Scm-like with four mbt domains 1	118.8	1.62	92.5	258.5	2.83	70.7
AV214764	Sfmbt2	Scm-like with four mbt domains 2	1133.9	1.74	673.8	1191.4	3.48	344.1
BM200222	Sparc	secreted acidic cysteine rich glycoprotein	1025	1.87	512.4	938.9	3.25	325.9
NM_009242.1	Sparc	secreted acidic cysteine rich glycoprotein	5429.1	1.87	2917.5	7142.4	2.83	2486.8
BC004638.1	Scamp2	secretory carrier membrane protein 2	592.4	2.14	324.3	665.6	2.46	240
BG965399	6-Sep	sepin 6	620.4	2.00	307.8	558	2.64	184.3
BC010489.1	Serpinh1	serine (or cysteine) proteinase inhibitor, clade H, member 1	4863.4	2.14	2050.1	5842.3	2.46	2276.8
BI220012	Shmt1	serine hydroxymethyl transferase 1 (soluble)	1045.8	2.64	384.4	1418.4	2.14	756.8
AF237702.1	Shmt1	serine hydroxymethyl transferase 1 (soluble)	1506.8	2.46	558.9	1161.2	2.00	551
BC026055.1	Shmt2	serine hydroxymethyl transferase 2 (mitochondrial)	3855.2	2.14	1798.9	3060.3	2.30	1272.1
BB758291	SrpK2	serine/arginine-rich protein specific kinase 2	433.1	2.83	161.7	423.5	2.30	208.2
BG805074	Sgk	serum/glucocorticoid regulated kinase	1591.7	1.87	796.8	2136.4	2.64	840.3
NM_011361.1	Snk	serum-inducible kinase	1917.3	1.87	1022.7	2038.9	2.46	791.6
BM234765	Sh2bp1	SH2 domain binding protein 1 (tetraicopeptide repeat containing)	283	2.30	147.4	398.5	3.25	113.3
BB294970	Sh3bgrt3	SH3 domain binding glutamic acid-rich protein-like 3	2838.6	1.87	1484	2914.3	2.30	1204.5
NM_080559.1	Shank3	SH3/ankyrin domain gene 3	588.9	2.00	336.3	619.4	2.64	250
NM_021423.1	Sh3glb1	SH3-domain GRB2-like B1 (endophilin)	499.7	1.87	257.5	800	3.03	290.5
NM_019464.1	Siat4a	sialyltransferase 4A (beta-galactoside alpha-2,3-sialyltransferase)	115.3	2.00	53.7	102.7	3.03	33.5
NM_009177.1	Siat8d	sialyltransferase 8 (alpha-2, 8-sialyltransferase) D	928.1	2.30	422.6	832.4	2.46	301.9
NM_009183.1	Stat3	signal transducer and activator of transcription 3	391.5	1.87	217.8	640.8	3.03	188.7
AK004083.1	Stam2	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	133.8	2.14	74.2	142.8	2.30	81.4
BB277125	Six4	sine oculis-related homeobox 4 homolog (Drosophila)	431.8	2.64	144.6	575.7	3.03	187.7
D50416.1	Ssbp3	single-stranded DNA binding protein 3	836.4	2.46	332.1	1046.9	3.73	288
BM204832	Sirt1	sirtuin 1 ((silent mating type information regulation 2, homolog) 1 (S. cerevisiae)	1797.6	2.64	672.2	1475.8	2.14	724.3
NM_019812.1								

BG796845	Ssb	Sjogren syndrome antigen B	396.5	2.64	143.5	477.4	3.25	121.9
BC021593.1	Sssca1	Sjogren's syndrome/scleroderma autoantigen 1 homolog (human)	3132.4	2.30	1355.9	3888.6	2.30	1648.3
BB053082	mSSH-1L	slingshot-like 1	1714.6	2.46	769.2	2542.3	2.64	920.7
AI875533	Smc11i	SMC (structural maintenance of chromosomes 1)-like 1 (S. cerevisiae)	2595.4	2.30	1201.8	2689.2	3.25	840.9
BG065168	Smc21i	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	1102.5	2.46	467.9	1488.5	3.25	492.5
AU022584	Smc61i	SMC6 structural maintenance of chromosomes 6-like 1 (yeast)	2416.5	1.41	1644.6	2910.3	2.46	1273.5
NM_133741.1	Snrk	SNF related kinase	608.4	2.14	288	627.8	2.64	244.3
BC009652.1	Scn1b	sodium channel, voltage-gated, type I, beta polypeptide	324.4	9.19	34.5	130.7	1.52	76.7
NM_009201.1	Slc1a7	solute carrier family 1, member 7	645.3	1.74	284	592.4	2.83	259
BG069726	Slc12a2	solute carrier family 12, member 2	306.9	2.00	142.4	436.4	3.03	194.3
AV287019	Slc31a1	solute carrier family 31, member 1	429.5	2.30	283.6	598.6	2.64	213.4
BI558379	Slc35a3	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	440.3	2.46	179.5	530.8	1.74	298.3
AK003377.1	Slc35b1	solute carrier family 35, member B1	44.1	2.14	31	281.7	2.64	133.9
NM_134086.1	Slc38a1	solute carrier family 38, member 1	1997.4	2.14	776.7	2198.7	2.46	974.8
AK003626.1	Slc38a4	solute carrier family 38, member 4	1639.5	1.74	878	2144.9	2.64	774.4
NM_027052.1	Slc38a4	solute carrier family 38, member 4	1436.6	1.74	791.5	2345.2	2.83	840.3
BB454531	Slc4a7	solute carrier family 4, sodium bicarbonate cotransporter, member 7	791	2.46	297.7	805.8	2.30	353.5
AV002797	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), isoform 3 regulator 2	1270.4	2.46	600.5	1121.9	3.25	326.9
AV348121	Slco4a1	solute carrier organic anion transporter family, member 4a1	173	3.48	51.9	134.8	1.87	86.6
BQ176684	Sorbs1	sorbin and SH3 domain containing 1	996.1	2.46	398.6	1227.2	2.30	578.7
BB737680	Sorbs1	sorbin and SH3 domain containing 1	6075.8	1.87	3314.3	6215.3	2.64	2427.8
BB815008	Snx16	sorting nexin 16	349	3.03	98.5	279.3	1.74	127.5
AV344473	Snag1	sorting nexin associated golgi protein 1	713.8	3.03	279.1	581.9	1.74	326.6
BF018652	Solt	SoxLZ/Sox6 leucine zipper binding protein in testis	245.1	1.87	123.8	398.6	2.64	126.4
AA688828	Spop	speckle-type POZ protein	498.2	2.14	247.1	630.2	2.64	267.3
BM213516	Spnb2	spectrin beta 2	3846.2	1.74	2084.3	4341.9	2.46	1802.4
AW912678	Ssh3bp1	spectrin SH3 domain binding protein 1	834.5	2.46	335.4	714.6	2.14	306.9
NM_021343.1	Spata5	spermatogenesis associated 5	619.7	2.64	222.3	613.1	2.46	257
NM_021343.1	Spata5	spermatogenesis associated 5	1356.7	2.46	559.1	1163.2	2.14	521.5
NM_009121.1	Sat1	spermidine/spermine N1-acetyl transferase 1	686.1	2.00	312.1	764.2	2.83	346.3
BG071956	Sms	spermine synthase	2024.9	2.30	968.5	1893.2	2.00	949.8
BC003468.1	Skp2	S-phase kinase-associated protein 2 (p45)	1070.8	2.46	555.6	1091.9	2.83	373.3
AW536901	Sca2	spinocerebellar ataxia 2 homolog (human)	941.2	2.46	394.2	935.2	3.25	274.5
NM_009125.1	Sca2	spinocerebellar ataxia 2 homolog (human)	506.7	2.14	231.1	528.2	3.25	206.1
AW544490	Sca2	spinocerebellar ataxia 2 homolog (human)	311.9	1.87	184.7	654.6	2.46	251
AK012643.1	Sf3b2	splicing factor 3b, subunit 2	871.6	1.87	509.9	1281.4	2.64	459.6
BM125059	Sfrs1	splicing factor, arginine/serine-rich 1 (ASF/SF2)	2103.1	2.46	800.5	1757.8	1.74	969.2
BB080456	Spry4	sprouty homolog 4 (Drosophila)	209.3	2.64	82.6	180.1	3.48	60.1
BB053442	Spred2	sprouty protein with EVH-1 domain 2, related sequence	445.7	1.41	283.3	594.2	3.25	189.1
NM_009270.1	Sqle	squalene epoxidase	1830.7	2.00	984.6	2422.5	3.03	742.2
BI408715	Shb	src homology 2 domain-containing transforming protein B	307.6	3.03	100.8	370.1	3.03	112.2
NM_011441.1	Sox17	SRY-box containing gene 17	451.7	2.00	198.4	535.8	2.64	189.4
AK004781.1	Sox17	SRY-box containing gene 17	1968.3	1.87	1112.6	2348.2	2.46	927.8
NM_009236.1	Sox18	SRY-box containing gene 18	2805.1	1.74	1226	2783.1	2.30	1166.9

NM_011446.1	Sox7	SRY-box containing gene 7	868.5	2.00	437.1	848.9	3.25	400.8
BG064396	Soat1	sterol O-acyltransferase 1	930.2	2.30	317.5	977.9	2.64	397.7
BB228907	Strn3	striatin, calmodulin binding protein 3	1443.9	2.14	689.9	1618.8	3.03	564.1
BM219372	Stag1	stromal antigen 1	314.9	2.14	178.3	394.6	2.46	151.3
BB530180	Sod1	superoxide dismutase 1, soluble	724.6	2.46	303.6	835.9	2.64	284.3
AW536705	Supt16h	suppressor of Ty 16 homolog (S. cerevisiae)	959.2	2.46	361	910.3	3.03	318.1
BB821035	Smn	survival motor neuron	534.8	1.52	357.8	754.2	3.03	256.3
AV024531	Swap70	SWAP complex protein	976.9	2.14	468.1	1062.2	2.46	414.5
AK019882.1	Swap70	SWAP complex protein	421	2.00	222	493.6	2.64	183.4
NM_053123.1	Smarca1	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1	1500.4	2.30	648.3	1735.8	2.14	725
AW701251	Smarca4	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	4198.3	2.00	2154.2	4328.3	2.83	1442.6
BI661719	Smarca5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	2918.5	2.14	1264.8	2537.1	2.46	1064.7
NM_031878.1	Smarcd2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	5355.3	2.30	2326.3	5707.2	2.14	2694.5
BB365629	Syap1	synapse associated protein 1	1492.2	2.83	541.7	1262.7	1.87	693.8
BC004829.1	Syngn2	synaptogyrin 2	680.2	2.00	373.3	713.7	2.83	253.7
BC004829.1	Syngn2	synaptogyrin 2	1069.1	1.87	580.6	1427.3	3.25	447.8
AI642069	Sycp3	synaptonemal complex protein 3	438.2	2.46	180.1	339	2.14	131.9
AV232599	Sypl	synaptophysin-like protein	1127.1	2.14	505.8	1222.1	2.83	382.2
BB763153	Snap23	synaptosomal-associated protein 23	343.5	2.30	231.1	335.7	1.52	222.2
BG920261	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	897.1	2.30	389.3	1242.9	2.64	455.2
BG920261	Syncrip	synaptotagmin binding, cytoplasmic RNA interacting protein	1321.7	1.87	654.3	1418.6	2.64	422.8
BM218509	Stxbp6	syntaxin binding protein 6 (amisyn)	538.1	2.83	161	324.8	1.62	176.6
AI324124	Snca	synuclein, alpha	266.7	3.73	69.7	771.5	1.52	487.6
BB427389	Taf15	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor	342.5	1.74	188.3	427.4	3.03	153.6
NM_009324.1	Tbx2	T-box 2	128.6	2.83	39.6	108.5	2.64	37.9
AA543734	Tbx3	T-box 3	351.2	2.00	167.9	424.3	2.64	180.2
AV226212	Tbx4	T-box 4	699.5	1.62	471.6	882.6	2.83	295.4
AY075134.1	Tbx4	T-box 4	396.1	2.14	125.7	326.2	3.03	84.3
NM_011527.1	Tal1	T-cell acute lymphocytic leukemia 1	854.5	1.62	546.8	1528.3	2.64	571
NM_009384.1	Tiam1	T-cell lymphoma invasion and metastasis 1	1162.6	2.00	518.1	1016.1	2.83	365.2
NM_027884.1	ns	tensin	227	2.14	105.9	216.3	3.73	38.9
AV048122	Tes3-ps	testis derived transcript 3, pseudogene	407.9	2.83	168	434.7	2.83	182
AF285576.1	Tex13	testis expressed gene 13	156.7	4.59	29.6	165.4	7.46	12.3
NM_023719.1	Txnip	thioredoxin interacting protein	533	2.46	249.4	797	2.64	292.1
AW121720	Thsd1	thrombospondin, type I, domain 1	825	2.30	406.6	921.7	2.64	304.2
BB418472	Thsd1	thrombospondin, type I, domain 1	662	2.30	302.8	639.9	2.64	248
BG072958	Thsd2	thrombospondin, type I, domain 2	225.6	2.30	110.4	321.2	2.64	145.8
NM_016715.1	Tslpr	thymic stromal-derived lymphopoietin, receptor	285.6	2.30	155.7	356.4	3.03	118.7
BG075035	Thrap3	thyroid hormone receptor associated protein 3	3861.3	2.14	1821.9	3517.9	2.83	1193.2
AF004833.1	Tfpi	tissue factor pathway inhibitor	2184.7	2.46	818.4	2518.6	3.03	896.8
AK009693.1	Tor3a	torsin family 3, member A	189.3	2.46	87.6	286.6	3.48	90
BM244995	Tlk1	tousled-like kinase 1	345.5	2.14	176.8	315.3	3.25	98.8
BM244995	Tlk1	tousled-like kinase 1	570.5	2.00	319.3	557.9	2.64	209.9
BM198864	Tlk2	tousled-like kinase 2 (Arabidopsis)	1026.9	2.30	502.3	902.4	2.83	287.4
BG143445	Tcf12	transcription factor 12	595.9	2.00	262.7	659.2	4.00	156.7
BC004617.1	Tcf19	transcription factor 19	697.1	1.52	462.5	745.7	2.46	279.7
BB550860	Tcfap2c	transcription factor AP-2, gamma	682.4	1.74	338.9	920.9	2.64	358.2

L38620.1	Sin3a	transcriptional regulator, SIN3A (yeast)	96.7	2.14	42.5	326.6	2.30	165.3
NM_011599.1	Tle1	transducin-like enhancer of split 1, homolog of Drosophila E(spl)	514.8	2.00	261.8	979.2	3.25	300.1
BB810450	Trfr	transferrin receptor	140.5	2.30	59.7	195.3	3.73	36.8
AJ297973.1	Trp53	transformation related protein 53	240.8	2.83	105.4	281.6	3.73	103.7
AW049938	Tgfb2	transforming growth factor, beta 2	581.4	2.83	314	503.7	2.00	263.9
BG793483	Tgfr2	transforming growth factor, beta receptor II	819.5	1.87	405.1	929.2	2.64	328.7
NM_013899.1	Timm13a	translocase of inner mitochondrial membrane 13 homolog a (yeast)	4026.6	2.30	1770.5	3741.7	2.14	1827.1
AF109918.1	Tomm40	translocase of outer mitochondrial membrane 40 homolog (yeast)	2848.4	2.46	1196.7	3184.5	2.83	1022.8
BC025461.1	Tm4sf3	transmembrane 4 superfamily member 3	123.1	1.41	50.5	197.7	3.25	49.8
NM_053082.1	Tm4sf7	transmembrane 4 superfamily member 7	1058.4	2.14	454.8	1267.5	2.64	486.7
BM240385	Tm6sf1	transmembrane 6 superfamily member 1	770.9	3.48	248.3	492.9	1.87	277.3
BC023123.1	Tm6sf1	transmembrane 6 superfamily member 1	604.3	2.64	222.1	598.1	2.64	229.8
BB667469	Tmc4	transmembrane channel-like gene family 4	540.7	2.46	200.1	543.5	2.14	233.6
AV096788	Tmc4	transmembrane channel-like gene family 4	579.4	1.87	280.2	790.1	2.46	325.9
BC004840.1	Tmc6	transmembrane channel-like gene family 6	387.1	1.74	243.8	512.6	3.25	141.6
BB035414	Tmem2	transmembrane protein 2	108.9	2.00	37.4	154.1	2.83	43.2
BM114154	Tmeff1	transmembrane protein with EGF-like and two follistatin-like domains 1	1542.2	2.64	589.9	1079.7	1.52	742.4
BG069441	Tnpo3	transportin 3	2100	2.00	1043.7	2171.9	2.46	853.7
BC024702.1	Ttr	transthyretin	639.4	3.73	128.6	666	2.64	312.4
BG141874	Ttr	transthyretin	1951.6	3.48	505.1	2752.1	2.30	1114.8
AA408768	Ttr	transthyretin	1107.5	3.25	280.2	1548.3	2.46	611
AV152953	Ttr	transthyretin	1829.9	1.74	1011.9	2004.1	2.64	795.2
BB136803	Trps1	trichorhinalphalangeal syndrome I (human)	35.5	1.52	29	180.4	2.30	82
BE136147	Tnrc15	trinucleotide repeat containing 15	182.6	2.46	60.1	187.4	3.25	65.1
BC005741.1	Tnrc6	trinucleotide repeat containing 6	1619.3	2.14	748.3	1584.9	2.64	548.3
BB325847	Trim24	tripartite motif protein 24	225.4	2.83	80.1	192.4	1.87	94.9
AA960166	Trim25	tripartite motif protein 25	1630.7	2.00	815.7	1934.9	2.83	729.2
D63902.1	Trim25	tripartite motif protein 25	769	1.87	443	912.6	2.83	289.7
AW536258	Tpp2	tripeptidyl peptidase II	457.1	2.00	211.5	457.1	3.03	198
BB557374	Trio	triple functional domain (PTPRF interacting)	184.2	2.14	86.9	314.5	3.48	92.9
BM225164	Trmt1	tRNA nucleotidyl transferase, CCA-adding, 1	2108.7	2.46	632	1976.5	1.87	967.3
NM_007796.1	Tpbpb	trophoblast specific protein beta	1797.2	2.14	928.2	2313	2.64	859.6
BG064656	Tpbpb	trophoblast specific protein beta	1530.1	2.14	762	1339.6	2.64	595.5
NM_007796.1	Tpbpb	trophoblast specific protein beta	1410.8	2.00	756.8	1819.9	2.46	667.9
BB224629	Tmod3	tropomodulin 3	805.2	2.14	373	712.3	2.83	302.8
BE380713	Tpm3	tropomyosin 3, gamma	705.9	1.87	340	796	3.03	266.9
NM_011620.1	Tnnt3	troponin T3, skeletal, fast	293.8	2.64	142	230.6	2.64	89.4
BB233088	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	1766.5	2.30	673.1	1805.6	2.00	951.9
BE995678	Tra1	tumor rejection antigen gp96	4124.5	2.00	2147.2	4647.7	2.46	1863.9
NM_011635.1	Trap1a	tumor rejection antigen P1A	280.2	2.30	156.6	389.2	3.48	110.6
BM239430	LOC233400	type II cAMP-dependent protein kinase anchoring protein Ht31	1293.6	2.46	513.6	1483.6	2.83	456.5
NM_011740.1	Ywhaz	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	1205.4	2.30	506.7	1455.4	3.73	399.6
BB086152	Murr2	U2af1-rs1 region 2	160.8	4.00	43	175.8	1.52	90.2
BM235696	Murr2	U2af1-rs1 region 2	469.2	1.87	216.5	394.2	3.25	139.2
AW124741	Ubn1	ubiquitin 1	1584.7	1.74	849.2	1666.1	2.46	774.8
AV313813	Uchl5	ubiquitin carboxyl-terminal esterase L5	636.4	2.46	182	455.2	2.14	217.6
BQ173927	Ubr1	ubiquitin protein ligase E3 component n-recognin 1	861.3	2.83	348.7	940.5	2.00	470.8
NM_130879.1	Usp31	ubiquitin specific protease 31	1849.7	1.87	1080.5	2231.2	2.46	856.9

C77542	Usp7	ubiquitin specific protease 7	968.2	1.87	700.7	1100.8	2.83	407.7
BB215201	Usp8	ubiquitin specific protease 8	336.5	1.62	246.6	509.9	2.46	167.7
AV132698	Ubap1	ubiquitin-associated protein 1	642.1	2.46	277.1	608.7	2.30	246.8
BB257283	Ubap1	ubiquitin-associated protein 1	485.6	2.46	177.9	614.7	2.30	227.7
BE980685	Ube2n	ubiquitin-conjugating enzyme E2N	703.1	2.46	295.2	569.6	1.87	325.5
AW536493	Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	1037.1	2.46	427.3	691.2	2.30	299.2
BB306686	Utx	ubiquitously transcribed tetratricopeptide repeat gene, X chromosome	235.4	2.00	119.2	383.1	2.64	123.5
AF349573.1	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	218.1	2.14	124.7	292.7	3.48	91.1
AV302406	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7	1028	2.14	566.7	1243.8	3.03	413
BM217066	Galnt1	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1	477.1	1.41	337.4	636.5	2.83	220.7
BB127793	Umps	uridine monophosphate synthetase	1731.6	2.30	620.9	1359.9	1.74	753.7
NM_009477.1	Upp1	uridine phosphorylase 1	1639	2.14	743.9	1788.1	2.64	621.7
BI654068	Vps35	vacuolar protein sorting 35	271.2	1.52	190	662.7	4.92	147.4
BM240052	Vps41	vacuolar protein sorting 41 (yeast)	580.9	2.14	337	915.7	3.25	274.7
BB468447	Vps54	vacuolar protein sorting 54 (yeast)	368.1	1.87	189.1	482.7	2.46	124.5
BC027242.1	Vav3	vav 3 oncogene	217.7	3.03	86.5	264.5	2.64	90.1
BC027242.1	Vav3	vav 3 oncogene	341	1.87	193.6	467.1	2.64	150
NM_133656.1	Crk	v-crk sarcoma virus CT10 oncogene homolog (avian)	1811.8	2.30	865.7	1626	2.30	757.5
AV333363	Vldlr	very low density lipoprotein receptor	2118	1.87	1199.5	2122	2.83	814.7
AK009266.1	Vamp5	vesicle-associated membrane protein 5	1013.9	2.30	441.5	929.3	2.46	371.3
BB398605	Vil	villin	631.4	2.30	277.7	493.8	2.64	219
AV147875	Vim	vimentin	7150.5	1.74	4062.1	7524	2.46	3046.8
M24849.1	Vim	vimentin	15142.1	1.74	8105.1	16581.5	2.46	7117.7
AI324330	Rala	v-ral simian leukemia viral oncogene homolog A (ras related)	3598.4	2.00	1723.3	3446.8	2.30	1433
BB465250	Ralb	v-ral simian leukemia viral oncogene homolog B (ras related)	1288.4	2.00	719.3	1549	2.46	594.9
BB500616	Wasf2	WAS protein family, member 2	590.1	2.64	218.7	548.8	3.03	170.8
BF150771	Wdfy3	WD repeat and FYVE domain containing 3	555.7	2.46	260.5	663.7	2.64	211.9
AV095579	Wdr5	WD repeat domain 5	407.8	1.74	275.9	700.1	2.83	247
BC018425.1	Wnt5a	wingless-related MMTV integration site 5A	370.3	1.52	233.7	430.7	2.46	151.3
NM_009515.1	Was	Wiskott-Aldrich syndrome homolog (human)	206.8	1.87	99.4	336.2	3.03	104.6
BF466143	Wasl	Wiskott-Aldrich syndrome-like (human)	1734.6	2.46	633.4	2364.4	3.25	669.8
AK014104.1	Wasl	Wiskott-Aldrich syndrome-like (human)	169.8	2.30	50.5	204	2.64	58.3
BQ174116	Zfx1b	zinc finger homeobox 1b	227.9	2.14	103.7	377.1	3.48	106.9
NM_015753.1	Zfx1b	zinc finger homeobox 1b	1137.9	2.14	557.3	1000.4	2.83	340.7
BE692937	Zfp148	zinc finger protein 148	478.2	2.64	163.5	448	1.87	211.6
X98096.1	Zfp148	zinc finger protein 148	2112.3	2.14	968.5	2057.9	2.83	696.7
AK009725.1	Zfp180	zinc finger protein 180	815.8	2.46	369.4	562	2.00	359
BC021397.1	Zfp259	zinc finger protein 259	1712.5	2.83	508.3	2405.1	3.03	826.2
D45210.1	Zfp260	zinc finger protein 260	1203.7	2.14	506.5	993.9	3.03	318.5
L36316.1	Zfp260	zinc finger protein 260	64.6	1.87	41.2	153.2	4.00	43.6
BM247458	Zfp277	zinc finger protein 277	583.4	2.00	315.3	747	3.03	224.2
AV323182	Zfp294	zinc finger protein 294	511.2	2.30	222.5	732.9	2.14	378.8
BM239596	Zfp294	zinc finger protein 294	387.9	1.87	198.6	527	3.48	127.5
M58566.1	Zfp361	zinc finger protein 36, C3H type-like 1	4159.3	2.00	2164.6	4880.9	2.83	1752.7
BB252481	Zfp364	zinc finger protein 364	2910.5	2.83	1051.5	2522.9	2.30	1041.5
BC004747.1	Zfp386	zinc finger protein 386 (Kruppel-like)	1188.8	2.30	515.7	1389	1.62	917.8
Z67747.1	Zfp62	zinc finger protein 62	709.1	2.46	311.7	473.8	1.32	406.3
BE824681	Zik1	zinc finger protein interacting with K protein 1	599.5	2.46	341.9	603.4	1.74	332.5
BC028506.1	Zfx	zinc finger protein X-linked	182	2.64	59.6	134.9	3.48	74.8
AA014267	Zfp1	zinc finger protein, multitype 1	781.2	2.30	353.8	1086	2.64	429

BB319935	Znfn1a2	zinc finger protein, subfamily 1A, 2 (Helios)	1058	2.46	412	1128.2	2.14	574.7
BG072040	Znrf2	zinc finger/RING finger 2	612.4	2.46	245.9	724.6	2.46	314.9

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VITAE

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