Identification and Mechanistic Investigation of Recurrent Functional Genomic and Transcriptional Alterations in Advanced Prostate Cancer

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Abstract

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Novel functionally altered transcripts may be recurrent in prostate cancer (PCa) and may underlie lethal and advanced disease and the neuroendocrine small cell carcinoma (SCC) phenotype. We conducted an RNASeq survey of the LuCaP series of 24 PCa xenograft tumors from 19 men, and validated observations on metastatic tumors and PCa cell lines. Key findings include discovery and validation of 40 novel fusion transcripts including one recurrent chimera, many SCC-specific and castration resistance (CR) -specific novel splice isoforms, new observations on SCC-specific and TMPRSS2-ERG specific differential expression, the allele-specific expression of certain recurrent non-synonymous somatic single nucleotide variants (nsSNVs) previously discovered via exome sequencing of the same tumors, rgw ubiquitous A-to-I RNA editing of base excision repair (BER) gene NEIL1 as well as CDK13, a kinase involved in RNA splicing, and the SCC expression of a previously unannotated long noncoding RNA (lncRNA) at Chr6p22.2. Mechanistic investigation of the novel lncRNA indicates expression is regulated by derepression by master neuroendocrine regulator RE1-silencing transcription factor (REST), and may regulate some genes of axonogenesis and angiogenesis. Taken together these variant transcripts offer insight into aggressive metastatic PCa, both broadly and with regard to castration-resistant and neuroendocrine disease.

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LIST OF ABBREVIATIONS

ADT: androgen deprivation therapy

AR: androgen receptor

AS: alternate splicing

BPH: benign prostatic hyperplasia

CNV: copy number variation

CR: castration resistant

CRPC: castration resistant prostate cancer

CS: castration sensitive

DHT: dihydroxy testosterone

DRE: digital rectal exam

FISH: fluorescent in situ hybridization

lncRNA: long noncoding RNA

NCI: National Cancer Institute

NEPC: neuroendocrine prostate cancer

nsSNV: non-synonymous single nucleotide variant

PCa: prostate cancer

PCR: polymerase chain reaction

PSA: prostate specific antigen

RP: radical prostatectomy

RPKM: reads per kilobase per million aligned reads

RT-PCR: real-time PCR

SCC: small cell carcinoma

SCLC: small cell lung carcinoma

SNV: single nucleotide variant

XRT: external beam radiation therapy

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Dedication

To my friends Ruthy F. Dumpit and Kenneth B. Herrington,

to my parents Drs. Beverly J. White and Lon R. White,

and with fondness to my friend Mr. Dennis Coleman.

Chapter 1: Introduction

The opportunity for carcinogenesis arises as cells in a conducive environment accumulate genetic insults such that key pathways governing cellular identity, proliferation and migration are compromised. The idea that the key genomic and transcriptomic distribution of somatic alterations driving prostate cancer (PCa) initiation, progression and metastasis may be somewhat recurrent across individuals rather than completely stochastic is based on the observation that spontaneous PCa takes on recurring cellular phenotypes and predictable responses to therapies, by the fact that alterations in key pathways may offer a proliferative or metastatic advantage, and by the notion that there likely are key loci in the otherwise robust human genome that are particularly vulnerable to alteration in the milieu of the aging prostate epithelium. Until recently only a handful of recurrent cytogenetic anomalies (e.g., *TMPRSS2-ETS* gene family rearrangements), certain somatic functional mutations in previously suspect genes (*AR, PTEN, p53, RAS*, etc.) and recurrent copy number alterations have been discovered in subsets of PCa primary and metastatic disease, but these discoveries do not fully account for the necessary dysregulation or the phenotypes observed. With the advent of high throughput sequencing technologies, the catalog of singular and recurrently altered genes and transcripts in PCa has expanded, shedding light on mechanisms of PCa and enabling the investigation of phenotypic subsets of disease. The expression of newly discovered recurrent somatic alterations, rearrangement transcripts, novel splice isoforms, non-coding RNAs and other transcriptional phenomena are being evaluated mechanistically to understand their contributions to cancer cell proliferation and metastasis.

The objective of this work is to further explore the assertion that advanced PCa is driven by recurrent functional alterations in the transcripts of key regulatory genes and pathways, and that transcriptional alterations restricted to certain PCa subtypes may contribute to their development of castration resistance, chemotherapy resistance and renewed metastatic capability. To this end, this thesis project has involved sequencing of the exome (the known protein-encoding portion of the Human genome) and the transcriptome (the full complement of mRNAs) of the LuCaP series of 24 advanced PCa xenograft tumors. The exome sequencing effort was led by Akash Kumar and Dr. Jay Shendure of the Shendure lab at the University of Washington, who performed the analysis and further investigations. The LuCaP tumor series was developed by Drs. Robert Vessella, Colm Morriessey and colleagues at the University of Washington. The contribution of this doctoral student to investigation of the exome was limited to preparation of LuCaP samples for high throughput sequencing as well as validation of genomic variants discovered by the analysis of Mr. Kumar and Dr. Shendure; In addition, the student surveyed key variants in a panel of metastatic samples obtained from the PCa rapid autopsy program at the University of Washington. This exome sequencing effort will not be addressed in this thesis beyond its introduction and as a foundation for analyses of the transcriptome. The primary contribution of the doctoral student was the high-throughput sequencing and analysis of the whole transcriptome data derived from RNA (RNAseq) captured from the identical set of LuCaP tumors, the discovery and validation of novel gene rearrangement transcripts, of splice variants restricted to key PCa phenotypes, an assessment of RNA editing in LuCaPs, assessments of the degree of expression of somatic mutations, and the performance of mechanistic investigations of key variant transcripts of interest; the outcomes of these efforts are described in Chapters 2-4 of this thesis.

Significance

Prostate cancer (PCa) is the second leading cancer-related cause of death among men. In addition to the personal suffering and loss of quality of life, PCa imposes an enormous socioeconomic burden. In 2008 approximately 258,000 deaths worldwide were attributable to PCa, and roughly 899,000 new cases were reported (1,2). It is estimated that in the United States in 2012 alone, 241,740 new cases of PCa were diagnosed, and approximately 28,170 men died of this disease (3). The NCI estimates that, in 2010, the national expenditure for PCa care amounted to $11.85 billion, and projects this to rise to $16.34 billion in 2020 (4). One in six American men will be diagnosed with PCa in their lifetime (5).

More than 80% of and perhaps as many as 95% of prostate cancers are initially dependent on intact androgen receptor (AR) signaling (6), and androgen deprivation therapy (ADT) therapy initially results in tumor regression. However, cases treated with ADT generally progress to become castration resistant. For men whose PCa has progressed and who have developed advanced castration-resistant PCa (CRPC), abiraterone as a first-line treatment offers a survival benefit of an additional five months, but tumors inevitably develop resistance to this as well (7). Second-line treatments such as MDV3100 and cabazitaxel may provide additional benefit after chemotherapy, but CRPC presently proves uniformly lethal. Castration resistance most likely occurs because one or more PCa cells at some point acquire additional DNA damage or epigenetic alteration conferring a proliferative advantage despite androgen blockade; perhaps the AR signaling pathway is short-circuited, or an alternative pathway is exploited. The work described here is an effort to discover recurrently functionally altered genes via unbiased high-throughput screening of the transcriptome and to explore the role of such variation in the progression to lethal PCa. If genes found to be recurrently functionally altered in CRPC turn out to directly influence cell survival, proliferation or migration, then therapies targeting these key genes and their pathways may enhance the survival of men with otherwise incurable PCa.

Prostate Adenocarcinoma and Neuroendocrine Prostate Cancer (NEPC)

Approximately 95% of prostate malignancies are acinar adenocarcinomas, occuring in the epithelia of this glandular tissue, and can arise independently at multiple primary foci. Adenocarcinoma is marked histologically by small, crowded glands with enlarged nuclei occasionally displaying prominent nucleoli or mitotic figures (8). The two traditional screening methods for PCa are digital rectal exam (DRE): transrectal palpation to evaluate size, shape, firmness and texture of the walnut-shaped gland, and the prostate specific antigen (PSA) test, which assays serum level of PSA or KLK3, a protein secreted by the prostate. The PSA test is sensitive in that the majority of adenocarcinomas are detectable by elevated serum PSA, but it is not highly specific; an elevated PSA often points to a non-malignant enlargement of the gland termed benign prostatic hyperplasia (BPH), or other conditions. If not treated at an early stage, adenocarcinoma will typically spread to lymphatic tissue and bone, and less frequently to other soft tissues such as adjacent organs, lung or liver. Although testosterone and dihydrotestosterone (DHT)-mediated induction of transcription via the androgen receptor (AR) is critical to normal prostate development (9), AR signaling is also critical for the development and progression of prostate adenocarcinoma (10). As described previously, although adenocarcinoma typically responds initially to chemical or surgical castration and adjuvant chemotherapies blockading AR signaling, the inevitable progression to CRPC is marked by an effective evasion of androgen blockade. A subset of these CRPC tumors exhibits a neuroendocrine-like differentiation phenotype.

Neuroendocrine or small-cell carcinoma (NEPC or SCC) is a rare but highly aggressive form of prostate cancer. The prognosis with NEPC diagnosis is grim, with a short survival time (typically < 18 months) with no effective treatment. Less than 1% of prostate cancers are primary NEPC originating from normal neuroendocrine cells, and these frequently present histologically as an admixture with common adenocarcinoma, most typically low-grade (11). The majority of NEPCs present late as advanced metastatic disease, typically discovered first in viscera or other soft tissue locations and much less frequently in bone than adenocarcinoma. NEPCs are generally AR-negative and not sensitive to hormone therapy; in fact, PCa progression subsequent to androgen deprivation therapy may occur as a result of neuroendocrine differentiation of adenocarcinoma. NEPC is not reliably associated with elevated serum PSA but may be detected by suspicious DRE or report of urinary obstruction, and may be suspected upon detection of aforementioned atypical metastases or diagnosis of any of a variety of syndromes attributable to aberrant endocrine secretions. Evaluation of metastases with a panel of histologic immunohistochemical markers such as synaptophysin and neuron specific enolase (NSE) or serum chromogranin A (CGA) may suggest a neuroendocrine tumor, though not necessarily of prostate origin. Attributibility of metastatic sites to a primary prostate small cell tumor may be supported by evidence in the metastasis of NCAM (CD55) or CD44 expression, or prostate-specific markers such as *ETS* family genomic rearrangements present in roughly half of NEPCs, or histologic detection of similar neuroendocrine differentiation in the prostate itself. Since neuroendocrine differentiation is one route by which adenocarcinoma commonly achieves castration resistance and progression to lethality, factors regulating and associated with the expression of neuroendocrine phenotype genes are of great interest. Reduced expression of RE-1 silencing transcription factor (REST), which is thought to be a master repressor of neuronal differentiation, is associated with upregulation of neuroendocrine phenotype genes in NEPCs (12) and may therefore be crucial to lethal progression in a significant proportion of cases. The contribution of REST and individual targets of REST repression to the proliferative and metastatic potential of NEPCs has not been delineated. Though primary NEPCs are rare, the greater frequency of the neuroendocrine phenotype among CRPC patients, the aggressive nature of NEPCs and the unvarying lethality underscore the importance of careful evaluation of the neuroendocrine phenotype for mechanistic insights and a search for potentially drugable targets.

Risk Factors for Prostate Cancer Development

Aging is the strongest identified risk factor for PCa. Diagnosis of PCa is infrequent among men less than 50 years of age in the U.S. (13), but a third to a half of all men in their 70s will have developed histologically detectable primary PCa (14,15). A first-degree family history of PCa, race/ethnicity and country of origin are also clearly associated with elevated risk (13).

PCa is influenced by both heritable factors and environmental exposures. Approximately 42% of PCa risk may be attributable to genetic factors (16). Although large genome-wide single nucleotide polymorphism (SNP) association studies have revealed over 70 susceptibility loci with weak to modest effect sizes (per allele ORs ~1.1-1.3) (17), these account in aggregate for only approximately 30% of heritable risk. A recently developed panel composed of five SNPs, when considered in addition to PCa family history was confirmed to reflect a population attributable risk percent (PAR%) of up to 45% (18) among Caucasian men. While provocative, this panel failed to improve upon current methods for predicting individual PCa risk and shed little light on as-yet unaccounted-for genetic factors underlying PCa etiology as the combined alleles occurred only rarely in the study population (19).

Substantial effort has been made to investigate the contribution of lifestyle factors to the risk of PCa development. Although two NIH-AARP healthy eating indices were associated with modestly lower risk of PCa, few specific dietary factors have been identified (20). Consumption of fish and ω-3 fatty acids (20), legumes or cruciferous vegetables (21, 22) or red wine (23), regular aspirin or to a lesser degree other non-steroidal anti-inflammatory drug (NSAID) use (24) and diabetes mellitus (25) have been associated with reduced PCa risk in some but not all studies. The evidence supporting putative PCa risk factors such as obesity (26), smoking habits (27), sexual factors (28, 29), and red meat consumption (30) is also mixed.

With the exception of clinical features of tumor aggressiveness and mode of primary therapy, factors influencing prognosis both in general and after curative intent treatment, including radical prostatectomy (RP), brachytherapy or external beam therapy (XRT), are poorly understood. Nevertheless, many genetic and environmental factors have been considered. Several studies indicate that smoking is associated with higher PCa-specific mortality (31), despite varying methodologies for defining the exposure. Obesity is associated with aggressive PCa (Gleason 8-10 disease) and PCa-specific mortality (32), biochemical recurrence after RP (33-35) and external beam radiation therapy or XRT (36,37), but probably not brachytherapy (38). The underlying connection between obesity and patient outcomes is complicated, however, by the relationship between obesity, other types of inflammation and the use of androgen deprivation therapy (ADT). Vitamin D insufficiency also may be associated with outcomes due to factors influencing bioavailability (e.g., diet, UV exposure as a function of latitude, and seasonality of diagnosis) (39). Although genome-wide association studies have thus far not yielded any germline polymorphisms with with PCa specific mortality (PCSM) with genome-wide significance, several studies targeting individual genes or pathways have revealed polymorphisms of key genes tied to PCSM. One recent study examining SNPs from 196 genes of interest linked polymorphism of *LEPR*, *RNASEL*, *IL4*, *CRY1* and *ARVCF* to PCSM (40). Germline polymorphism of TLR pathway genes *MIC-1* and *TLR9* (41,42), common variation in sex horomone uptake factor *megalin* (43), androgen synthesis gene *CYP17* (44) and vitamin D synthesis gene *CYP24A1* (45) are also associated with PSCM, *BRCA1* and *BRCA2* mutations may be also be associated with more aggressive disease at diagnosis and poorer outcomes (46).

These and other findings suggest inherited polymorphisms influencing steroidogenesis, lipid metabolism, AR signaling and other key pathways may play a role in PCa outcome.

Primary therapy may be associated with the likelihood of PCa recurrence, though this is partly because the selection of a medical strategy is often based on clinical characteristics directly related to prognosis. Recent efforts to develop diagnostic and prognostic markers for PCa have renewed interest in molecules associated with the neuroendocrine phenotype, and genetic polymorphisms modulating the activity of neuroendocrine-related effectors may account for some susceptibility to NEPC or PCa progression displaying a neuroendocrine phenotype.

Prevalence and Roles of Somatic Mutations and Transcript Alterations in PCa

Evidence is emerging to support the assertion that recurrent functional genomic and transcriptional alterations arise in the course of PCa, but with a few important exceptions (e.g., *p53, PTEN*) the recurrent alterations detected thus far have had little overlap with those found in other cancers.

Recurrent protein-altering point mutations and copy number alterations

The occurrence of somatic mutations that alter the amino acid sequence of proteins is very low in PCa relative to other cancers, however a handful of selected genes including *AR, PTEN, RB1, AKT1, ATBF1, p53, RAS, CHD1, ZFHX3, APC, PIK3CA, SPOP, FOXA1* and *MLL2* have been shown in multiple cohorts to recurrently harbor point mutations at low frequency (47-50). In 2010 Taylor and colleagues (48) sequenced 157 genes in 181 primary PCa tumors, 37 PCa metastases, 7 PCa cell lines and 7 PCa xenografts, and included copy number alteration (CNA) analysis. Although the sequenced genes were selected for their tendency to harbor somatic point mutations in other types of cancer, none were found to be mutated in the PCa sample set. However the genomic regions containing *TP53, PTEN* and *RB1* were commonly found to have reduced copy number, and the genomic regions containing *AR* and *NCOA2* were recurrently amplified. The failure of this study to detect PCa point mutations in the usual suspects was unexpected, but the candidates represented <1% of all annotated genes and a more agnostic search was warranted. By mid-2012 the advent of high-throughput deep sequencing had facilitated the completion of three PCa whole-exome sequencing studies. Our collaboration led by Kumar et al. (49) sequenced the exome of a series of 24 xenografted advanced PCa tumors referred to collectively as LuCaPs, which are the subject of this thesis; the findings are described in the next section of this chapter. Grasso and colleagues (49) sequenced the exomes of 50 lethal CRPCs and 11 treatment-naïve high-grade primary tumors and performed CGH analysis. In addition to confirming a half-dozen recurrently mutated genes and a tendency for oncogene activation and tumor suppressor deactivation, their integrated analysis suggested enrichment for mutations or CNAs in genes in several functional categories such as androgen regulation, DNA damage response, chromatin architecture, WNT signaling and spindle formation. Lastly, an exome survey of 112 treatment naïve primaries by Barbieri and colleagues (51) overlapped and extended the small list of recurrently mutated genes, citing 12 such genes with statistical confidence and several likely candidates that did not reach statistical significance. Barbieri et al. made the interesting observation that mutations in *SPOP*, *FOXA1* and *MED12* were strategically restricted to key residues in functionally critical portions of these proteins. In collaboration with multiple groups including our own, Barbieri et al. collected sequencing data on 300 primary adenocarcinomas, 36 benign prostates and 41 metastases and found that *SPOP* mutations occured at one of 8 amino acid positions composing the substrate binding cleft in about 14% of patients with adenocarcinoma regardless of stage, and furthermore resolved that the presence of *SPOP* mutations and *TMPRSS2-ETS* family rearrangements are mutually exclusive. Further work has revealed that these recurrent mutations abrogate SPOP's ability to promote ubiquitination and degradation of AR coactivator SRC-3, an oncogenic regulator of metabolism, survival, proliferation and metastasis (51). Development and progression of PCa therefore appear to occur in part by virtue of the expression of a number of infrequent but recurrent non-synonymous point mutations.

Recurrent expression of gene rearrangement transcripts

Roughly half of clinically localized stage prostate cancers bear an interstitial chromosomal deletion between the *TMPRSS2* and *ERG* genes on chromosome 21 (53), and other PCas exhibit expression of a variety of chimeric transcripts composed of 5 prime partners such as *TMPRSS2* or nearby *SLC45A3* or *NDRG1* spliced to 3 prime partners such as *ETV1* or *ERG* as a result of other rearrangements. TMPRSS2 is a prostate specific serine protease that is normally androgen responsive. AR binding of the *TMPRSS2* promoter can therefore result in overexpression of the ERG transcription factor or other *ETS* family members not normally influenced by AR, thereby inducing a rearrangement-specific potentially oncogenic expression pattern. There is also evidence, however, that rearrangement transcript expression may persist in androgen depleted conditions and CRPC. The high prevalence of these PCa-specific rearrangements makes them attractive candidates as biomarkers, however their presence does not appear to be significantly associated with outcomes. ERG is a transcription factor and may interact with AR in gene regulation, and while upregulation of ERG-regulated genes is observed in rearrangement-positive tumors it is uncertain whether ERG is truly a driver of progression. Recently a new method to identify the genomic coordinates of the rearrangement was applied and it was asserted that lesions may be attributable to improper function of non-homologous end joining DNA repair mechanisms (53).

In addition to *TMPRSS2-ETS* family rearrangements, several studies have reported a large number of gene rearrangements that occur at very low frequency or are private to individual tumors (55-58). It is unclear what role, if any, these rearrangements may play in the onset or outcome of PCa in these individuals, nor is it clear whether these rearrangements share any commonality.

RNA editing in PCa

RNA editing is a process by which individual nucleotides in an RNA molecule are covalently altered and subsequently interpreted as a different nucleotide. The majority of transcript editing is performed by the adenosine deaminase (ADAR) family of enzymes and consists of conversion of adenosines (A) to inosines (I), which preferentially base pair with cytosines and therefore are interpreted by translational machinery as guanines (59). RNA editing may impact RNA function in several ways. A-to-I edits are highly prevalent in brain, causing non-synonymous changes or premature stop codons and thus significant functional consequences in the translated form of several proteins such as glutamate receptors (60). Pre-mRNAs may have their splice sites or splice site enhancers altered thus changing the inclusion of entire exons and translation of the transcript. Additionally, RNA editing may alter the secondary structure of an RNA molecule and interfere with translational processes such as miRNA recognition, specific binding of proteins, or altered signals influencing nuclear retention. With the exception of an examination of *AR* transcripts (61), and despite the demonstration that A-to-I edits can accurately be detected in RNA-seq datasets (62,63), there have been no reports describing the presence, extent or disturbance of RNA editing in PCa.

Alternate splicing (AS) in PCa

Alternate splicing is a process by which pre-mRNAs are edited to include or exclude individual exons or retain introns in an altered pattern and may result in a variety of functionally distinct transcripts. Several studies have evaluated a variety of normal tissues and cancers to determine the degree to which AS occurs and whether there are AS events specific to cancer (64,65). These studies have shown a large degree of "noisy" splicing events in normal tissue as well as a large number of AS events in cancer not seen elsewhere, but it remains unclear whether any or many aberrant splice isoforms play any role in cancer onset or progression as validation of individual splice isoforms and attribution of any phenotype to specific splice isoforms is an enormous challenge.

Cancer-specific alternative splicing tends to be rare and enriched for premature stop codons, especially among oncogene and tumor suppressor transcripts relative to those of other genes (66). The presence of a large number of AS events, such as exon skipping in *AMACR* and *KLK3* (PSA) intron retention (67), have been reported in PCa but their consequences are unknown.

LuCaP Xenografts: Surgically Acquired Models of Advanced Metastatic PCa

The LuCaP series of xenografts are living tumors obtained from metastatic sites from men with advanced PCa. Propagation of LuCaPs xenografts requires passage in a mouse host (68). As with *in vitro* cell culture, *in vivo* propagation has permitted expansion of each line which, in turn, has facilitated their widespread use as experimental models in the PCa research community (69). The pool of available LuCaP xenografts includes four with a neuroendocrine phenotype: two single tumors obtained from different individuals and one pair of tumors from the same patient. In addition there are three sets of LuCaP tumors that were derived from different metastases obtained from the same individual yet display differing degrees of androgen sensitivity (68). LuCaPs are therefore unique and valuable in their ability to shed light on the acquisition of castration resistance in CRPC, including cancers that overcome androgen blockade via development of a NEPC phenotype.

Growth and passage of human tumors in a mouse model has advantages and drawbacks. While not human, the use of a mouse host allows for treatments such as castration and experimental drug administration, and provides a more physiologically relevant environment than a culture dish. While growth in the mouse allows for vascularization and other interactions with host stromal tissue, this presents a challenge when acquiring and analyzing DNA and RNA from the tumor because contamination with host tissue is unavoidable. When small quantities are needed, laser capture microscopy allows for the selective acquisition of material guided by histologic staining, thus reducing contamination. Methods such as exome sequencing and RNASeq, which require larger unamplified quantities of tumor DNA or RNA, however must rely on bulk tumors with accompanying histology ensuring a low overall proportion of contamination, and computational tools to screen out non-human sequences must be applied.

Conclusions

Advanced PCa inevitably attains lethal castration resistance through poorly understood mechanisms. Identification of the genomic and transcriptional fingerprints of aggressive tumors may shed light on these mechanisms. The LuCaP series of advanced PCa xenograft tumors includes representatives of important PCa subtypes and offers a widely used system for study of mechanisms of PCa progression. The work presented in this thesis is a companion study to that of Kumar et al (49) in that the 24 LuCaP tumors used to perform both studies were halved and dedicated to the two lines of inquiry. Kumar et al.'s analysis found 20 novel protein-altering point DNA mutations present in between 2 and 5 of 16 LuCaPs, and revealed a subset of three "hypermutated" LuCaPs with approximately 2,500 – 4,000 novel single nucleotide variants (SNVs), whereas the remainder averaged roughly 400 such SNVs. That analysis also revealed several novel non-synonymous variants found in one of three castration resistant xenografts but absent from their castration sensitive counterparts, raising the possibility of their roles as drivers of each tumor's unique path to attainment of castration resistance. Transcriptome sequencing of the LuCaP series provided an opportunity to confirm and extend the findings of exome sequencing, and may reveal expression patterns and variant RNAs associated with PCa phenotypes as well as disease aggressiveness, progression and patient outcome.

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Chapter 2: RNAseq of LuCaP prostate cancers reveals recurrent expression of novel functional variants

SUMMARY

Novel functionally altered transcripts may be recurrent in prostate cancer (PCa) and may underlie disease development, progression to castration-resistant prostate cancer (CRPC) and the neuroendocrine phenotype. We conducted an RNAseq survey of the LuCaP series of 24 PCa xenograft tumors from 19 patients, and validated observations in the original tumor RNA as well as on a panel of 40 metastatic tumors and two dozen commonly studied PCa cell lines. Key findings include the discovery and validation of 40 novel fusion transcripts including one recurrent chimera, a large number of neuroendocrine-specific and CRPC-specific novel splice isoforms, new observations on neuroendocrine-specific and *TMPRSS2-ERG* specific differential expression, the allele-specific expression of certain recurrent non-synonymous somatic single nucleotide variants (nsSNVs) previously discovered via exome sequencing of the same tumors, the neuroendocrine expression of a previously unannotated long noncoding RNA (lncRNA) at chromosome 6p22.2, and ubiquitous A-to-I RNA editing of base excision repair (BER) gene *NEIL1* as well as *CDK13*, which encodes a kinase involved in RNA splicing. These variant transcripts offer insight into aggressive metastatic PCa, both broadly and with regard to castration-resistant and neuroendocrine disease.

INTRODUCTION

The diversity of of genomic aberrations and their roles in advanced prostate cancer (PCa) have not been well characterized. High-throughput sequencing has provided an exome-level perspective on recurrent somatic functional point mutations in PCa (1-4), but the allele-specific expression of such lesions has not been equally well resolved, nor has the full spectrum or role of recurrently altered transcripts in the development of aggressive disease phenomena such as attainment of castration resistance and the neuroendocrine phenotype been adequately investigated.

Transcriptomics has begun to enhance our understanding of the contributions of key genes to PCa by discerning recurrent mRNA variation above and beyond abundance and highlighting features not represented on microarray platforms. RNAseq analysis has expanded the catalog of gene rearrangements recurrently found in prostate cancer beyond the *ETS* family (5-7), revealing an abundance of low-prevalence and private chimeras; given their rate of discovery many more will arise. Although many alternative splice isoforms specific to PCa have been revealed (7-8), the full extent and the degree to which these are noisy artifacts or recurrent and functionally relevant is unclear. Those splice isoforms that are recurrently present in subcategories of PCa may occur for reasons other than chance and may merit closer examination. In this context, RNAseq approaches were recently used to identify 121 long noncoding RNAs (lncRNAs) associated with PCa (9), many of which were completely novel. Little is known about their function, and the catalog of PCa-specific lncRNAs is likely to expand. In addition, RNAseq offers a window on RNA editing, but beyond edits to the androgen receptor (*AR*) mRNA (10) and selected genes profiled in glioblastoma (11) little is known about the abundance or perturbation of RNA editing in cancer. As the difficulty and cost of RNAseq falls the opportunity to search for markers and functionally relevant transcripts associated with clinical strata of PCa among these types of variants has grown.

Here we report the results of assessing the transcriptomes of the LuCaP series of advanced prostate cancers using RNAseq methodology. The LuCaP series consists of two dozen primary and metastatic prostatic carcinomas obtained by surgical resection or rapid autopsy and propagated by serial xenografting into immunocompromised mice. The LuCaP lines have been used extensively to study the in vivo response of aggressive PCa to a variety of treatments (12). The LuCaP series includes four tumors displaying the rare and aggressive neuroendocrine phenotype and three pairs of castration-resistant/castration-sensitive xenografts. *TMPRSS2-ERG* rearrangement positive and negative tumors are both well represented. LuCaPs therefore provide a unique opportunity to uncover transcript variation relevant to the phenotypes of neuroendocrine prostate cancer, castration-resistance and *TMPRSS2-ERG* rearrangement in late-stage aggressive disease.

We previously performed whole exome sequencing of LuCaP tumors and reported a number of recurrent novel nonsynonymous single nucleotide variations (nsSNVs) and described the phenomenon of genomic hypermutation in 3 tumors (1). A tendency for castration resistant tumors to carry somatic alterations in the WNT signaling pathway relative to castration sensitive tumors from the same individuals was also detected. The comprehensive analysis of LuCaP transcriptomes described here includes variant allele specificity of expression of recurrent nsSNVs, differential expression of genes for neuroendocrine vs. adenocarcinoma tumors and for *TMPRSS2-ERG* rearrangement positive vs. negative tumors, detection of novel rearrangement transcripts, presence of novel splice isoforms in CPRC and NEPC tumors, the presence of recurrent RNA edits, and a novel lncRNA associated with NEPC. These findings may serve as markers and may also have functional relevance to advanced disease.

RESULTS

Transcriptome Sequencing

In order to identify the recurrent expression of novel functional RNA variants that may drive or serve as markers of prostate cancer and its subtypes we performed whole transcriptome sequencing of 24 well-characterized LuCaP prostate xenograft tumors from 19 individuals. Previously we applied a method to identify somatic genomic variation in the exomes of these same xenografts in which the potential for inclusion of reads derived from mouse xenograft host is minimized (1), and here we adapted this strategy for the analysis of the corresponding transcriptome. Transcriptome sequencing yielded between 8.49 and 84.7 million reads (183 to 6822 MB of sequence) aligning preferentially to the human genome (hg19, NCBI build 37) (**Table 1**), corresponding to a median expression of 0.57 to 1.76 reads per kb of transcript per million mapped reads (RPKM). Reads aligning preferentially to mouse varied between 3.7% and 22.9% and were proportional to the fraction of the tumor estimated to be supporting murine stromal tissue by histology. Genes found to be among the top 500 most abundant (by RPKM) in one or more LuCaP are reported in Table S1.

Differential Gene Expression

Gene expression was estimated from unsupervised clustering of RPKM of the top 1,000 most variable loci. Cluster analysis revealed a distinct expression motif across tumors corresponding to a neuroendocrine phenotype (Figure 1). The CPRC phenotype observed across two pairs and one trio of castration-sensitive and castration-resistant xenografts derived from the same tumor was not revealed by unsupervised clustering, as expression of each CRPC sample was most similar to that of the castration sensitive tumor of origin. RPKMs correlated with prior expression microarray results for the corresponding LuCaPs (Spearman ρ=0.80; data not shown).

Differential expression analysis was performed using RPKM as a surrogate for expression to examine the contrast between neuroendocrine and adenocarcinoma. LuCaPs 49, 93 and 145.1 and 145.2 have been histologically characterized as NEPC. A total of 1,361 genes were found to be significantly differentially expressed in NEPC (FDR < 0.01, Table S2). Enrichment analysis indicated that upregulation of KEGG pathway genes for neuroactive ligand-receptor interactions, MAP kinase signaling, calcium signaling, cell adhesion molecules, axon guidance and ECM-receptor interaction was prevalent among neuroendocrine LuCaPs (Figure 2).

The contrast in expression of *TMPRSS2-ERG* rearrangement positive vs. negative LuCaPs was similarly examined. NEPC LuCaPs were excluded from this analysis because their substantially different expression would skew the results. 188 genes were significantly differentially expressed in *ERG*-rearrangement positive vs. negative tumors with FDR < 0.01 (**Table S3**). *GREM1* and *GREM2* were not expressed in rearrangement-negative LuCaPs but were uniformly upregulated in rearrangement-positive tumors. Focal amplification of *GREM1*, which encodes a secreted BMP antagonist and VEGFR agonist, has been shown in other cancers, and although BMP signaling deactivation has been described in rearrangement-positive PCa, *GREM1* and *2* have not previously been implicated. WNT signaling components *WNT11* and *FZD10* were significantly upregulated, consistent with prior observations of ERG-induced activation of WNT signaling in rearrangement-positive PCa. Five GO categories for signal transduction and four related to sequence-specific DNA binding transcription activity were significantly overrepresented in genes differentially expressed in rearrangement-positive vs. negative tumors.

Interestingly, differential expression analysis also revealed an unannotated long noncoding RNA (lncRNA) encoded at 6p22.2 that was expressed strictly in NEPC tumors 49, 93, 145.1 and 145.2 (figure 2). This transcript is approximately 650nt in length, spans 4 exons and has no substantial coding potential. Validation sequencing confirmed expression of the lncRNA in these tumors, as well as all 4 NEPC samples in a panel of 40 metastatic tumors. The transcript was also found in the neuroendocrine PCa cell line NCI-H660 and 4 of 9 small cell lung carcinoma (SCLC) cell lines (NCI-H209, DMS79, DMS153 and NCI-H748) but not in Merkel cell carcinoma cell line MKL-1. This lncRNA is currently undergoing functional evaluation.

Expression of Somatic nsSNVs

In our previous work we discovered numerous previously unidentified somatic nonsynonymous single nucleotide variants via exome sequencing of DNA from LuCaP tumors. Most tumors were found to carry between 89 and 326 somatic nsSNVs, but LuCaPs 58, 73 and 147 presented with genomic hypermutation, harboring 2,393, 1,681 and 1,452 such variants respectively. Here we evaluate the extent of expression of these point mutations.

The proportion of expressed nsSNVs did not differ significantly between hypermutated and non-hypermutated LuCaPs (Figure 5). Approximately 58% of genes with a nsSNV identified by exome sequencing had insufficient total read depth (<8) at the nsSNV locus in the corresponding transcriptome to confidently infer expression of the alternate allele. From 63% to 80% of transcribed nsSNVs showed evidence of variant allele expression at a threshold read depth of ≥ 4 and at ≥ 10% of total transcript abundance. Of the 25 nsSNV alleles predicted with greatest confidence to be recurrent in 3 or more individuals by exome and confirmatory Sanger sequencing, 10 were found to be recurrently expressed in LuCaPs from 2 or more individuals (**Table 2**). There were no genes differentially expressed, or recurrently and exclusively mutated in NEPC or in castration-resistant LuCaPs.

In our previous analysis of interesting somatic nsSNVs in DNA from these LuCaP tumors we detected an enrichment of variants in genes of the WNT signaling pathway in CR tumors 23.1v, 35v and 96v when compared to their CS counterparts (23.1, 35 and 96); however these genes were not detected at sufficient read depth in RNAseq data to suggest expression. But with regard to the entire cohort of LuCaP tumors, 16 of the 152 WNT pathway genes as delineated by KEGG were found to express a nsSNV in 1 or more LuCaPs at a level of ≥ 10% of total transcript abundance.

RNA Edits

Candidate somatic nsSNVs in the transcriptomes of 2 or more LuCaPs for which the matching variant was absent from the exome were evaluated further as potential recurrent RNA edits. Candidates located near splice sites which could reasonably be attributed to alignment error were discarded, and candidates from sequences with low uniqueness and therefore potentially attributable to other gene family members or pseudogenes were similarly ruled out.

Two A-to-I mRNA edits previously described in the literature were ubiquitous across the LuCaPs in our screen. We detected A/G heterozygosity in *NEIL1* mRNA corresponding to chromosome 15 hg19 position 75646086 in all LuCaPs, and validated that this observation was present in cDNA but absent from gDNA by Sanger sequencing. This polymorphism results in amino acid substitution of Arginine for Lysine in NEIL1 residue 242. The impact of this edit on NEIL1 base excision and repair (BER) biochemistry has been studied *in vitro* and a role in carcinogenesis proposed, but to our knowledge no survey of abundance, tissue specificity or disease association has been reported. We sequenced a commercial panel of thirteen normal tissue cDNAs and found the edit was also present in all samples, though often excessive amplification was required as *NEIL1* was very weakly expressed. Further sequencing of 26 PCa cell lines and our panel of 48 cDNAs from PCa metastases indicated the edit was similarly ubiquitous, though total expression was not always abundant and the degree of mRNA editing varied similarly to that of the normal panel. We also detected A/G heterozygosity in gene *CDK13* at Chr. 7 hg19 position 39990548 in all LuCaPs, resulting in substitution Q103R. CDK13 is a kinase involved in potentiating RNA splicing. This modification was also ubiquitous in PCa cell lines, metastases and normal human tissues where expression was detectable. These results do not suggest a pattern of perturbation of mRNA editing of these genes relative to normal tissues.

Rearrangement Transcripts

In light of multiple findings of gene rearrangements in PCa, such as highly prevalent *TMPRSS2-ETS* family rearrangements and other less frequent but recurrent structural events, we searched for known and novel non-*ETS* family chimeric transcripts in our LuCaP tumors. Although single-end (SE) reads do not offer the redundancy of coverage associated with the longer genomic interval of paired-end (PE) reads, we had sufficient coverage depth to align a large number of junction-spanning reads and thus perform *de novo* discovery and experimental Sanger sequencing validation of several chimeric transcripts of interest (**Table 3**). Rearrangements previously discovered in PCa and found in LuCaPs included read-through chimera *WDR55-DND1*, *C19orf25-APC2* and *ZNF649-ZNF577*. We confirmed 40 novel candidate rearrangement transcripts, one of which was recurrent. Rearrangement transcript *STK39-COL5A2* was detected in LuCaPs 105 and 141, and was present 4 of 40 of the PCa metastases tested (Figure 4). The resulting mRNA truncates the *STK39* transcript at exon 14 of 18 and fuses it to the intron between exons 6 and 7 of *COL5A2*, appending an 8 amino acid open reading frame and a stop codon. *STK39* encodes the protein SPAK, an AR-regulated kinase that potentiates Na+K+Cl- cotransporters and is tied to aldosterone levels in the adrenal cortex and renal physiology. It is unknown what role, if any, SPAK plays in the prostate epithelium. Expression of fused gene partners was examined by IGV and by comparing RPKMs to determine whether rearrangement might be associated with altered expression such as observed with AR-regulated TMPRSS2 driving increased expression of potentially oncogenic ERG. In the case of *STK39-COL5A2*, neither individual gene appears to be differentially expressed in either LuCaP 105 or 141 compared to other LuCaPs despite the rearrangement event. Of the remaining 39 candidates, 13 showed 4-fold or greater change in expression as measured by gene-wide RPKM of either or both partners compared to the mean RPKMs of the remaining LuCaPs. *RERG*, fused to *ATF71P* and substantially elevated in LuCAP 141, encodes an ER-regulated tumor suppressor implicated in breast cancer. The chimera consists of exons 1-8 of 15 of *ATF71P* fused to exons 3-5 of *RERG* with no disruption of the reading frame. The *APC-CAMK4* chimera in LuCaP 77 is a fusion of the end of *APC* exon 8 to *CAMK4* exon 3, with no disruption of the open reading frame. *SKIL*, or SKI-Like oncogene, is involved in SMAD/TGFb signaling and is upregulated when the end of exon 6 of partner *SLC2A2* is fused to the 3'UTR of *SKIL* in LuCaP77. The resulting transcript includes a frameshift and premature stop codon in *SKIL*, but it is unclear whether the remainder of the 3'UTR and coding portion of the *SKIL* transcript are subject to translational activity. Rearrangements involving the vicinity of *PVT1* / *miR-204* / *MYC* in 8q24 fused to other genes have been reported in multiple myeloma and other cancers. *PVT1* is a lncRNA encoded at Chr. 8q24, and inherited polymorphisms have been shown to be associated with PCa risk (14). LuCaP35 and 35V show downregulation of *PVT1* but substantial expression in an intergenic region adjacent to *miR-204*. The remaining 9 overexpressed rearrangement transcripts all involve frameshifts, most with premature stop codons: The 3'UTR of *THRAP3* is fused to the start of exon 2 of *HSD17B3*, which encodes a protein that catalyzes conversion of androstenedione to testosterone, and *HSD17B3* mRNA is substantially more abundant; however, the fusion results in a frameshift and a novel ORF and thus activation of HSD17B3 is not expected. Expression of *ARHGAP18*, which encodes a RhoGTPase that enhances cell migration, is upregulated in LuCaP35 and 35V, most likely driven by rearrangement partner *MRPS2*, but the rearrangement transcript involves a frameshift altering the amino acid sequence early in exon 2 of 15. One rearrangement resulted in a fusion joining the first four exons and a short intronic stretch of *SPOP* to a large intronic region in *SRGAP3*, resulting in a truncated open reading frame lacking most of the gene. Read depth, however, is not significantly altered, suggesting this change would not cause a significant functional impact.

Novel Splice Isoforms

By aligning the LuCaP transcriptomes with the reference human genome, we identified numerous transcript variants that have not been previous reported. Of these, we found that more than 1,800 were recurrent, occurring in 4 or more LuCaPs lines. A subset is exclusively or particularly enriched in subsets of tumors such as NEPC (**Table 4**) or CRPC variants (**Table 5**). For example, multiple alternative splice arrangements of the intron between exons 1 and 2 of *SEC11C* are prevalent in NEPC LuCaPs and may result in the inclusion of cryptic exons. SEC11C is thought to participate in the removal of signal peptides from newly translated proteins entering the ER lumen. *GRP* or *Bombesin*, which encodes a protein shown to stimulate proliferation in SCLC, exhibits a handful of altered acceptor and donor sites joining exons 2 and 3 and is highly expressed in all four NEPC LuCaPs. *UTRN* encodes the tumor suppressor Utrophin and splicing errors and deletions have been reported in multiple tumors, though not specifically tumors with neuroendocrine characteristics. The observation of NEPC exclusivity of these isoforms may be more a reflection of the general lack of expression of this gene in adenocarcinoma LuCaPs than an absence of the isoform.

DISCUSSION

RNAseq of the LuCaP panel of 24 prostate cancers identified several novel recurrent and NEPC-specific transcript alterations and expanded our understanding of the expression of somatic genetic variants. In our search for differentially expressed genes that may have been overlooked by prior microarray studies we discovered the expression of a novel lncRNA restricted to four NEPC LuCaPs from 3 individuals. Subsequent sequencing confirmed the presence and of this lncRNA at 6p22.2 in all 4 NEPC metastases in a panel of 40 PCa tumors and in the neuroendocrine PCa cell line NCI-H660. To evaluate whether this was a prostate cancer-specific NEPC transcript we examined the Merkel cell carcinoma cell line MKL-1, 9 small cell lung cancer (SCLC) cell lines and 4 primary SCLCs, and a panel of 13 normal tissue cDNAs. The lncRNA was found in 4 of the 9 SCLC cell lines (NCI-H209, DMS79, DMS153 and NCI-H748) but not in the Merkel cell carcinoma cell line MKL1 or normal tissue cDNAs, indicating this lncRNA may be a marker of prostate NEPC and a subset of other neuroendocrine tumors. The predicted secondary structure of the transcript is complex and includes multiple stem-loop structures. The transcript does not include sequence homology to any known human microRNAs but could conceivably be a novel microRNA precursor; alternatively, the structure may support selective protein binding. By virtue of these possibilities and the specificity of expression we are currently investigating what functional role, if any, this transcript may play in neuroendocrine disease.

We sought to determine the degree to which recurrent non-synonymous somatic point mutations we previously detected in LuCaPs by exome sequencing were expressed relative to the germline allele, thus shedding some light on the likelihood of their functional relevance to advanced PCa. We also wished to know whether we could detect such variants in the transcriptome but absent from the exome, indicating possible post-transcriptional mRNA edits. Of the 25 genes found to recurrently harbor somatic nsSNVs in LuCaPs from 3 or more individuals, 15 were not expressed in any LuCaP bearing the mutation. The remaining 10, however, showed some degree of expression, and the variant allele was consistently represented at a moderate proportion of total read depth, suggesting the altered form of the protein may well be present. Functional assessment of many of these recurrent changes may be warranted.

Previous studies have expanded the list of rearrangement transcripts observed in PCa well beyond the highly prevalent TMPRSS2-ETS family rearrangements to include several low-frequency recurrent and numerous unique chimeras. In our examination of the 24 LuCaP tumors we observed previously reported low-frequency chimera *WDR55-DND1*, *C19orf25-APC2* and *ZNF649-ZNF577*, and validated 40 novel chimeras. Novel rearrangement transcripts included the recurrent chimera *STK39-COL5A2* in LuCaPs 105 and 141, but the remaining chimeras were private to single LuCaPs. These findings expand the known repertoire of chimeric transcripts in PCa. It is unclear what impact, if any, the recurrently truncated *STK39* mRNA might have if translated in the context of advanced PCa, as little is understood about the role of this gene in normal prostate physiology.

Private rearrangements included a mixture of readthrough chimera such as *ATF71P-RERG* and *APC-CAMK4* which also displayed elevated expression relative to the wildtype genes, but the majority of rearrangements consisted of a frameshift and nearly immediate stop codon, most likely resulting in loss of function of both the donor and acceptor transcripts.

Our search for novel splice isoforms turned up a vast number of alternative splicing arrangements. It seems unlikely that isoforms ubiquitously expressed in our tumors are necessarily pathologic, but many are small variations in the exon-intron boundaries resulting in frameshift mutations, small deletions or non-synonymous changes at splice acceptor or donor sites. Some alternative splicing events found exclusively in NEPC tumors may be involved in the development of this aggressive form of PCa and merit mechanistic examination.

While a tantalizing possibility, we found no evidence to indicate RNA editing was functionally altered or dysregulated in LuCaP PCa tumors relative to normal tissues. There were no genomic or transcriptomic alterations of adenosine deaminases *ADAR1* or *ADAR2*,which encode the only enzymes known to catalyze A-to-I alterations. Only the previously reported RNA edits in *NEIL1* and *CDK13* mRNAs were found to be recurrent in these tumors, and there was no indication the variant form of either was any more or less prevalent than in normal tissues including prostate. With regard to NEIL1 base excision repair function, there was no indication of a nucleotide imbalance in somatic mutations as might be expected if repair of specific lesion types were chronically compromised. *CDK13* expression was similarly not aberrant with respect to normal tissue samples, and although novel splice variants were observed there was no indication that normal splicing was compromised. Taken together these findings suggest that RNA editing of coding genes does not play a significant role in advanced PCa.

METHODS AND MATERIALS

RNAseq of Prostate Cancer Xenografts

The LuCaP series of 24 xenografts were derived from prostate cancer metastases and primary tumors of 19 patients enrolled in the rapid autopsy program of the University of Washington Department of Urology (15). Total RNA was isolated from frozen tissue using the Qiagen RNEasy kit with DNAse treatment. H&E slides cut from the same block were reviewed by pathologist to ensure xenograft composition of at least 80% tumor. Dynabeads mRNA purification kit was used to purify mRNA from 10 ug of starting total RNA. mRNA was then fragmented at 70C for 5 minutes, reverse transcribed using SuperScript III RT Kit, and converted to cDNA. cDNA end repair and the addition of a single [A] base were performed prior to Illumina adaptor ligation, PCR amplification and gel size selection for 200-225bp inserts. Massively parallel sequencing generated 76bp single end (SE) reads for 9 samples using the Genome Analyzer II (Illumina), and 15 samples with 100bp reads were sequenced on HiSeq (Illumina) as reagents were upgraded during the study. Five GAII runs with low abundance of alignments were duplicated on HiSeq. Reads were aligned to the human genome (hg19) and mouse genome (mm9) obtained from UCSC using Bowtie v. 2.0.0, then indexed and converted to BAM file format using SAMtools. All reads that aligned preferentially to the mouse genome were excluded from human alignments and removed from further study.

Detection and Allele-specific Expression of Ssomatic nsSNVs and Recurrent RNA Edits

SAMtools was used to identify candidate SNVs in the aligned LuCaP transcriptomes. Because normal tissue was unavailable, we ignored the expression of likely common germline polymorphisms by excluding loci found to be variable in dbSNP or in the approximately 2,000 exomes available via the 1,000 Genomes Project. Only loci with one candidate alternative allele at sites expected to otherwise be homozygous were considered. Only base calls with a Phred-like SNP quality ≥ 30 and an RMS mapping quality of ≥ 30 were included. A position was considered to be expressed if total transcriptome coverage depth was eight reads or better, and the variant allele was considered expressed if it was present at a depth of 4 or more qualifying reads and at least 10% (e.g., 4+ reads out of 8, 10+ reads out of 100, etc.). As with exome variant calling, evaluation of nsSNV expression excluded positions within the first or last 4 nucleotides of the read, and alignment artifacts at splice sites were screened. For each candidate genomic nsSNV discovered by prior exome sequencing, the corresponding results in the same LuCaP were examined at the same locus for evidence of expression of the variant allele.

To discern possible RNA edits from expressed somatic genomic SNVs we subtracted candidates with matching variant reads in the corresponding aligned exome and considered the remaining variants. Conservative criteria were used to minimize the inclusion of false positive RNA edits. Variant reads within 4 nucleotides of either end of aligned reads were excluded to reduce the likelihood of alignment error. Reads at loci with a mappability index <1 were discarded where the alignment could plausibly be attributed to another locus, such as another gene family member or a pseudogene. The remaining candidates were manually screened using IGV to rule out inaccurate alignment at or near splice junctions. After applying these filters two candidate RNA edits were detected in the transcriptomes of 2 or more individuals.

Differential Gene Expression by PCa Phenotype

Categorical comparison of gene expression in LuCaPs segregating into two clinically relevant categories of PCa was performed. Ensembl Hg19 gene models (~52k) were used as the basis for a union gene structure, and this was augmented by a list of additional loci of interest such as known lncRNA-encoding genes. Reads aligned over all union gene models were summed and normalized by library size and by gene model length. To simplify the analysis, candidates for differential expression were limited to those genes for which reads were present in 2 or more LuCaP transcriptomes. A generalized linear model which included estimated variability of read depth was used to determine fold change (FC) estimates and p values, and false discovery rate (FDR) adjustments were made. Differential expression was analyzed comparing four small cell carcinomas (49, 93, 145.1 and 145.2) to the remaining adenocarcinomas in the LuCaP series. Differential expression analysis between TMPRSS2-ERG rearrangement positive vs. negative LuCaPs was also performed (LuCaPs 23.1, 23.12, 23.1V, 35, 35V, 86.2, 92, 93, 145.1 and 145.2 are are known by FISH and RT-PCR to be rearrangement positive; 145.1 and 145.2 were excluded from the analysis as their expression pattern is dominated by their neuroendocrine phenotype. The remaining LuCaPs are rearrangement negative and were included, except for neuroendocrine LuCaP 49). Since three of the castration resistant LuCaP samples (23.1 V, 35V and 96V) were experimentally derived from castration sensitive LuCaPs (23.1, 35 and 96), differential expression associated with castration sensitivity was restricted to these samples.

Novel Splice Isoform Identification

Junction-spanning reads were resolved using Tophat v. 1.1.0. The 6 outermost nucleotides were excluded from each end of each read and a minimum anchor length of 8 nucleotides on each side of the junction was required; this permitted up to 56 nt on one side for our 76 nt reads and up to 80 nt for 100 nt reads. A maximum intron length of 100kb was applied and a minimum isoform fraction of 15% was used.

Chimeric Transcript Identification and Validation

We searched for candidate chimeric transcripts by requiring each end of single end reads to map uniquely to separate chromosomes or to different genes over 1MB apart on the same chromosome. As with splice isoform mapping, we excluded the 6 outermost nucleotides and required a minimum anchor length of 8 nucleotides. Only alignments with two or fewer combined mismatches for both segments were considered. Candidate rearrangements with at least three unique supporting reads (i.e., after exclusion of clonal reads) spanning the fusion boundary were screened against a database of known chimera (16). Of the approximately 50 novel candidates remaining, 8 were culled on manual examination due to a degree of complexity of predicted splicing that made them prohibitive or impossible to validate. RT-PCR and Sanger sequencing was performed using cDNA synthesized independently of RNAseq library construction, using a different block of tissue but derived from the corresponding xenograft. Where possible, PCR primers were selected beyond the aligned reads but within the same exons or next most proximal exons; the depth of other aligned reads was manually examined in IGV in order to ensure maximum likelihood of amplifying the splice isoform corresponding to the chimeric rather than intact gene

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Table 1. Next-generation sequencing of prostate cancer xenografts

Sample	Tissue	Histology	Read length	Total reads (M)	Reads mapped hg19 (M)	% mapped	Nucleotides mapped (MB)
LuCaP 23.1	Lymph node	Adenocarcinoma	80	17.5	13	74.3	1016
LuCaP 23.12	Liver	Adenocarcinoma	100	64.6	22.4	34.7	1925
LuCaP 23.1 AI	23.1 derived	Adenocarcinoma	100	83.2	68.0	81.7	5336
LuCaP 35	Inguinal lymph node	Adenocarcinoma	100	21.2	12.5	59.0	974
LuCaP 35V	35 derived	Adenocarcinoma	80	20.1	17.3	86.1	1352
LuCaP 49	Omental fat met	small cell carcinoma	80	21.1	15.4	73.0	1198
LuCaP 58	Lymph node	Adenocarcinoma	100	29.7	21.7	73.1	1968
LuCaP 70	Liver met	Adenocarcinoma	100	74.3	65.3	87.9	5035
LuCaP 73	Prostate	Adenocarcinoma	100	76.2	68.3	89.6	5891
LuCaP 77	Femur met	Adenocarcinoma	100	65.2	60.8	93.3	5257
LuCaP 78	Peritoneal met	Adenocarcinoma	100	79.5	68.2	85.8	6234
LuCaP 81	R. Pelvic met	Adenocarcinoma	100			#DIV/0!	
LuCaP 86.2	Bladder met	Adenocarcinoma	80	79.3	61.5	77.6	480
LuCaP 92	Peritoneal met	Adenocarcinoma	100	7.41	5.23	70.6	408
LuCaP 93	Prostate (TURP)	Small Cell Carcinoma	100	4.47	2.35	52.6	183
LuCaP 96	Prostate (TURP)	Adenocarcinoma	80	21	15.1	71.9	1177
LuCaP 96 AI	96 derived	Adenocarcinoma	80	21	16.7	79.5	1306
LuCaP 105	Rib mets R5,L5	Adenocarcinoma	100	28.7	15.5	54.0	1397
LuCaP 115	Lymph node	Adenocarcinoma	100			#DIV/0!	
LuCaP 136	Ascites fluid	Adenocarcinoma	100	7.81	5.02	64.3	1602
LuCaP 141	Prostate (TURP)	Adenocarcinoma	100	84.7	70.7	83.5	6822
LuCaP 145.1	Liver met	Small Cell Carcinoma	80	9.76	5.39	55.2	421
LuCaP 145.2	Lymph node	Small Cell Carcinoma	80	8.49	7.22	85.0	563
LuCaP 147	Liver met	Adenocarcinoma	100	84.6	72.7	85.9	5707

Table 2. Expression of most frequently recurrent somatic-nsSNVs

Gene	Gene Name	LuCaP	Chr	hg19	Mutation	Allele Fraction[1]	RPKM
BDH1	3-hydroxybutyrate dehydrogenase, type 1	LuCaP73	chr3	197239230	VAL190ILE	0.393	25.7
		LuCaP23.1AI	chr3	197241170	THR176MET	0.184	6.7
		LuCaP147	chr3	197241273	VAL142ILE	0.469	28.5
		LuCaP115	chr3	197259330	HIS74TYR	0.208	26.8
		LuCaP147	chr3	197260367	ALA50VAL	0.516	28.5
DLK2	delta-like 2 homolog	LuCaP70	chr6	43418317	ARG371HIS	1	0.6
		LuCaP145.2	chr6	43418346	SER361ARG	0.6	4.2
		LuCaP96V	chr6	43418589	HIS280GLN	--	0.2
KDM4B	Lysine-specific demethylase 4B	LuCaP73	Chr19	5082391	ALA265VAL	0.505	19.3
		LuCap105	Chr19	5131171	ARG534TRP	0.174	36.3
		LuCaP35V	Chr19	5131435	ALA555VAL	0.636	19.1
		LuCaP73	Chr19	5138011	ALA827VAL	0.603	19.3
		LuCaP86.2	Chr19	5150454	SER1036CYS	--	27
MGAT4B	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme B	LuCaP105	chr5	179225392	ALA504THR	0.448	50.3
		LuCaP23.1AI	chr5	179228435	ARG168CYS	0.52	51.3
		LuCaP136	chr5	179228580	VAL150MET	1	134.5
PDZRN3	PDZ domain containing RING finger 3	LuCaP23.1AI	chr3	73433538	ARG727CYS	0.99	13.9
		LuCaP105	chr3	73434009	GLY570SER	0.1	16.1
		LuCaP73	chr3	73438996	ARG463CYS	0.581	32.9
		LuCaP92	chr3	73453480	ILE331LEU	0.5	14.2
RNF220	ring finger protein 220	LuCaP73	chr1	44878128	PHE120LEU	--	27
		LuCaP115	chr1	45079864	ASP218TYR	--	34
		LuCaP73	chr1	45101801	ARG365TRP	0.271	27
SDF4	stromal cell derived factor 4	LuCaP105	chr1	1153924	ASP276ASN	0.485	182.3
		LuCaP73	chr1		GLY76SER		61.4
		LuCaP115	chr1	1164150	ALA9SER	1	96.3
TFG	TRK-fused gene	LuCaP23.1AI	Chr3	100447687	ASN134HIS	0.516	74.5
		LuCaP141	Chr3	100467124	GLN318stop	0.625	93.9
		LuCaP147	Chr3	100467129	TYR319stop	0.464	52.9
TP53	tumor protein p53	LuCaP73	chr17	7577021	ARG306GLN	0.553	19.6
		LuCaP136	chr17	7577100	ARG280STOP	1	3.3
		LuCaP23.1AI	chr17	7577568	CYS238TYR	1	27.9
		LuCaP92	chr17		GLU198STOP	--	3.8
		LuCaP73	chr17	7578407	ARG175CYS	0.675	19.6
		LuCaP70	chr17	7578443	TYR163HIS	1	45.2
		LuCaP77	chr17	7577106	PRO278SER	1	31.4
UBR4	E3 ubiquitin-protein ligase	LuCaP147	chr1	19420592	MET4596ILE	0.747	8
		LuCaP58	chr1	19426976	TYR4372CYS	0.097	21.7
		LuCaP58	chr1	19436652	MET4015VAL	0.143	21.7
		LuCaP73	chr1	19479812	ARG2272HIS	0.143	10.9
		LuCaP136	chr1	19480389	SER2168TYR	--	6.7
		LuCaP23.1AI	chr1	19482797	GLU2014LYS	0.467	7.8
		LuCaP35V	chr1	19484389	LEU1894ILE	--	10.6

		LuCaP73	chr1	19486690	ALA1831VAL	0.318	10.9
		LuCaP58	chr1		ARG901CYS	--	21.7
		LuCaP93	chr1		LEU865VAL	0.5	12.1
		LuCaP58	chr1	19504160	LEU811PRO	0.333	21.7

1. “—“ indicates zero total read depth.

Table 3. Novel rearrangement transcript expression in LuCaP prostate cancers (excluding TMPRSS2-ERG)

LuCaPs	Rearrangement	hg19 Coordinates	L RPKM	R RPKM	L Mean RPKM	R Mean RPKM
23.12	*ADAM7 - ZMAT4*	chr8 :24339820 - chr8 :40500221	44.4	0.9	4.2	2.4
23.12	*ADAM7 - ZMAT4*	chr8 :24342871 - chr8 :40500222	44.4	0.9	4.2	2.4
141	*AFTPH - C2orf3*	chr2 :64751743 - chr2 :75921554	23.3	**12.3**	20.7	5.7
86.2	*AGPAT3 - DPY19L3*	chr21 :45391368 - chr19 :32968425	28.2	**26.1**	22	5.8
96, 96V	*ALG5 - HDLBP*	chr13 :37568800 - chr2 :242175101	7.8, 11.8	52.0, 50.2	22.1	123.5
77	*APC - CAMK4*	chr5 :112128223 - chr5 :110710545	2.3	**0.3**	2.8	3.1
73	*ARHGAP5 - SNX6*	chr14 :32586490 - chr14 :35055512	7.2	19.9	8.4	16.8
23.1, 23.12, 23.1v	*ARHGAP6 - COL4A5*	chrX :11272666 - chrX :107935978	2.7, 1.2, 2.3	5.2, 5.5, 6.0	7.1	4.1
23.1, 23.12, 23.1v	*ARHGAP6 - COL4A5*	chrX :11272667 - chrX :107939526	2.7, 1.2, 2.3	5.2, 5.5, 6.0	7.1	4.1
141	*ATF7IP - RERG*	chr12 :14610228 - chr12 :15274052	7.1	**12.6**	9	1.9
73	*C2orf34 - FBXO11*	chr2 :44995035 - chr2 :48035466	4.5	7.6	3	16.6
115	*CD58 - SDF2*	chr1 :117078584 - chr17 :26982498	2.8	41.6	3.4	35.2
81	*CUL1 - TPK1*	chr7 :148427375 - chr7 :144245693	22.3	**18**	26.8	1.6
92	*FOXP1 - ULK4*	chr3 :71247352 - chr3 :41439754	19.9	1.2	17.3	1.3
73	*GSK3B - FOXO3*	chr3 :119624603 - chr6 :108960693	10	16.1	15.2	19.7
49	*GXYLT2 - FOXP1*	chr3 :72940774 - chr3 :71154483	1.3	9.3	0.53	17.3
77	*MID2 - ENSG00000229269*	chrX :107097931 - chrX :140056186	6.2	N/A	3.8	N/A
35, 35V	*MRPS28 - ARHGAP18*	chr8 :80915233 - chr6 :129963162	68.7, 64.8	**28.5, 26.8**	46.2	5.9
141	*NIPSNAP3A - DHX32*	chr9 :107516978 - chr10 :127541691	13.4	15.7	15.6	11.2
35, 35V	*NKAIN3 - PVT1*	chr8 :63214961 - chr8 :128806979	0.54, 0.32	**0.071, 0.0**	0.037	5.9
70	*PIK3R4 - ACAD11*	chr3 :130422565 - chr3 :132338387	7.3	**0.14**	9	0.58
77	*PPAP2A - MTRR*	chr5 :54763696 - chr5 :7870882	153.2	7.1	140.5	8.9
77	*PPAP2A - MTRR*	chr5 :54737737 - chr5 :7871033	153.2	7.1	140.5	8.9
73	*PSPC1 - CRYL1*	chr13 :20346381 - chr13 :21047212	18	43.3	13.5	28.5
77	*PTPN4 - LYPD1*	chr2 :120567566 - chr2 :133402673	1	**0**	1.4	1.1
81	*RALGAPA2 - PRKRIR*	chr20 :20483994 - chr11 :76063837	8.7	20.1	10.6	22.3
77	*RBM47 - NRXN3*	chr4 :40516535 - chr14 :79432364	44.8	0.92	30.9	0.79
105	*RCOR1 - PGCP*	chr14 :103059660 - chr8 :98155246	7.2	5.4	12.2	8.9
77	*SLC2A2 - SKIL*	chr3 :170723731 - chr3 :170077486	0.3	**154.7**	0.014	12.6
115	*SORBS1 - LIFR*	chr10 :97274430 - chr5 :38523520	0.8	6.7	1.8	14
115	*SORBS1 - LIFR*	chr10 :97278592 - chr5 :38523520	0.8	6.7	1.8	14
77	*SPOP - SRGAP3*	chr17 :47714115 - chr3 :9212027	13.1	1.7	19	2.5
105	*STK39 - COL5A2*	chr2 :168821171 - chr2 :189960561	28.9	0.1	34.5	0.36
141			62.7	0.61		
70	*SUPT6H - GABRA4*	chr17 :27009868 - chr4 :46930455	32.6	**4.4**	29.5	1
86.2	*TBL1XR1 - HNF1A*	chr3 :176816252 - chr12 :121426636	**0.91**	**37.4**	27.2	6.9
81	*THRAP3 - HSD17B3*	chr1 :36725082 - chr9 :99060745	39.1	**3.9**	37.7	82.9
35V	*TJP1 - ZFP106*	chr15 :30164929 - chr15 :42731749	21	28.3	11.9	8.6
70	*TNIP1 - CTNNA1*	chr5 :150436329 - chr5 :138221897	19.9	138.2	29.1	116.5
70	*TNS3 - CDR2*	chr7 :47481600 - chr16 :22376334	11.2	26	8.7	13.4
93	*WASF1 - UBE2D4*	chr6 :110448796 - chr7 :43992494	7.6	5.6	4.7	5.3

Table 4. Neuroendocrine-specific novel splice junctions

Symbol	Junction	NEPC LuCaPs
SEC11C	chr18:56813824-56815296	3
	chr18:56813824-56814214	3
	chr18:56813824-56815410	3
	chr18:56813829-56815296	3
GRP (Bombesin)	chr18:56892966-56897642	3
	chr18:56892947-56897642	3
	chr18:56892947-56897656	3
RYR2	chr1:237900238-237905595	3
UTRN	chr6:145044289-145046540	3
--	chr6:58196172-58204985	3
ISLR2	chr15:74420648-74423547	3
ASXL3	chr18:31325710-31328517	3
NAV2	chr11:19799063-19854029	3
LOC100507003	chr19:49928746-49929666	3
BX118339 (EST)	chr6:21502742-21521481	3

Table 5. CRPC specific novel splice junctions

Symbol	Junction	CRPC LuCaPs
AK294518; RP11-90J7.3	chr10:80288571-80302309	3
	chr10:80184447-80225750	2
--	chr4:78555874-78557942	3
--	chrX:66139789-66140320	3
CT45A3; CT45A2; CT45A4	chrX:134874222-134887226	2
	chrX:134856962-134887226	2
CT45A5; CT45A4	chrX:134932989-134945989	2
CT45A5; CT45A4; CT45A6	chrX:134932989-134963240	2
	chrX:134950252-134963240	2
CT45A1; CT45A3; CT45A2; CT45A4	chrX:134856962-134869957	2
--	chr4:188298319-188301341	2
UBB; UBC	chr12:125396412-125397286	2
TARP; TCRG	chr7:38289173-38289258	2
--	chrX:151804441-151808119	2
LGALS3BP	chr17:76973296-76973485	2
--	chr6:110872770-110875310	2
SPNS1	chr16:28985785-28986421	2
CGN	chr1:151505054-151506450	2
LMO1	chr11:8252051-8256101	2
IDH2	chr15:90641257-90645507	2

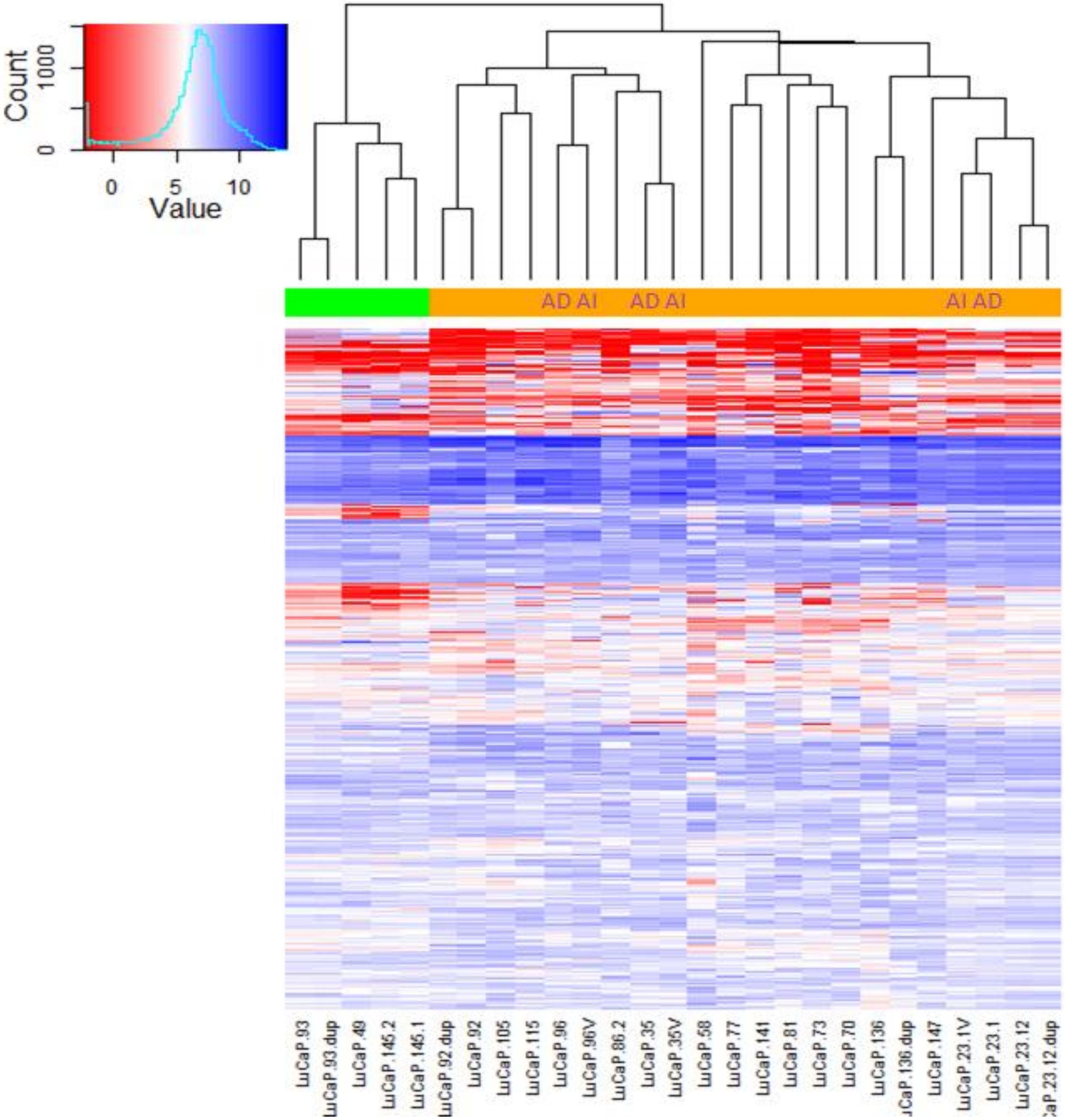

Figure 1: Unsupervised clustering of expression of top 1,000 most variable transcripts. Expression was estimated from read depth adjusted by transcript length and total reads (RPKM). CR tumor expression was most similar to that of the AD tumor of origin (purple). Neuroendocrine and adenocarcinoma tumors segregated on expression similarity (green and orange, respectively).

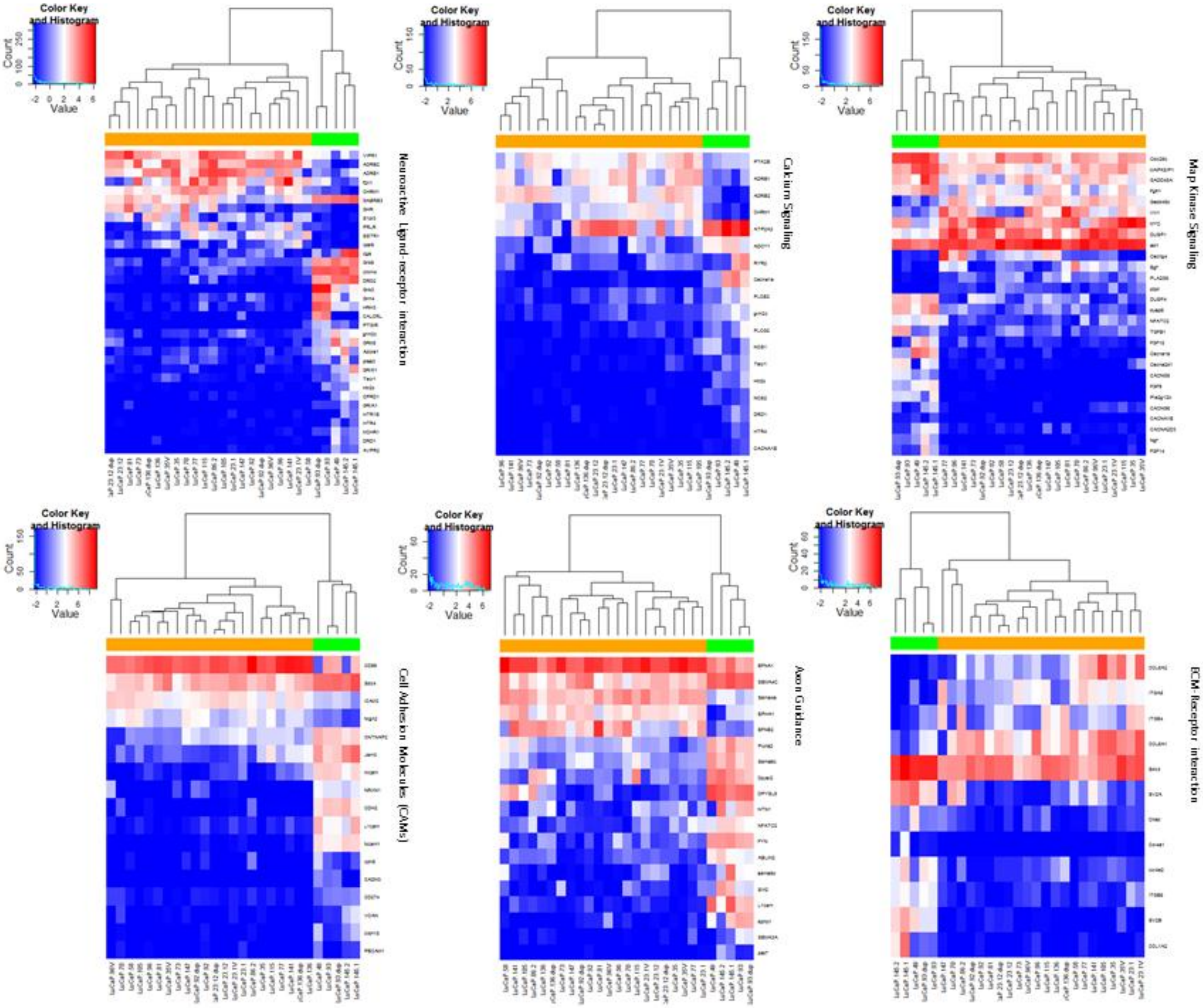

Figure 2: Differentially expressed genes in NE LuCaPs vs. Adenocarcinoma, by significantly enriched KEGG pathway.

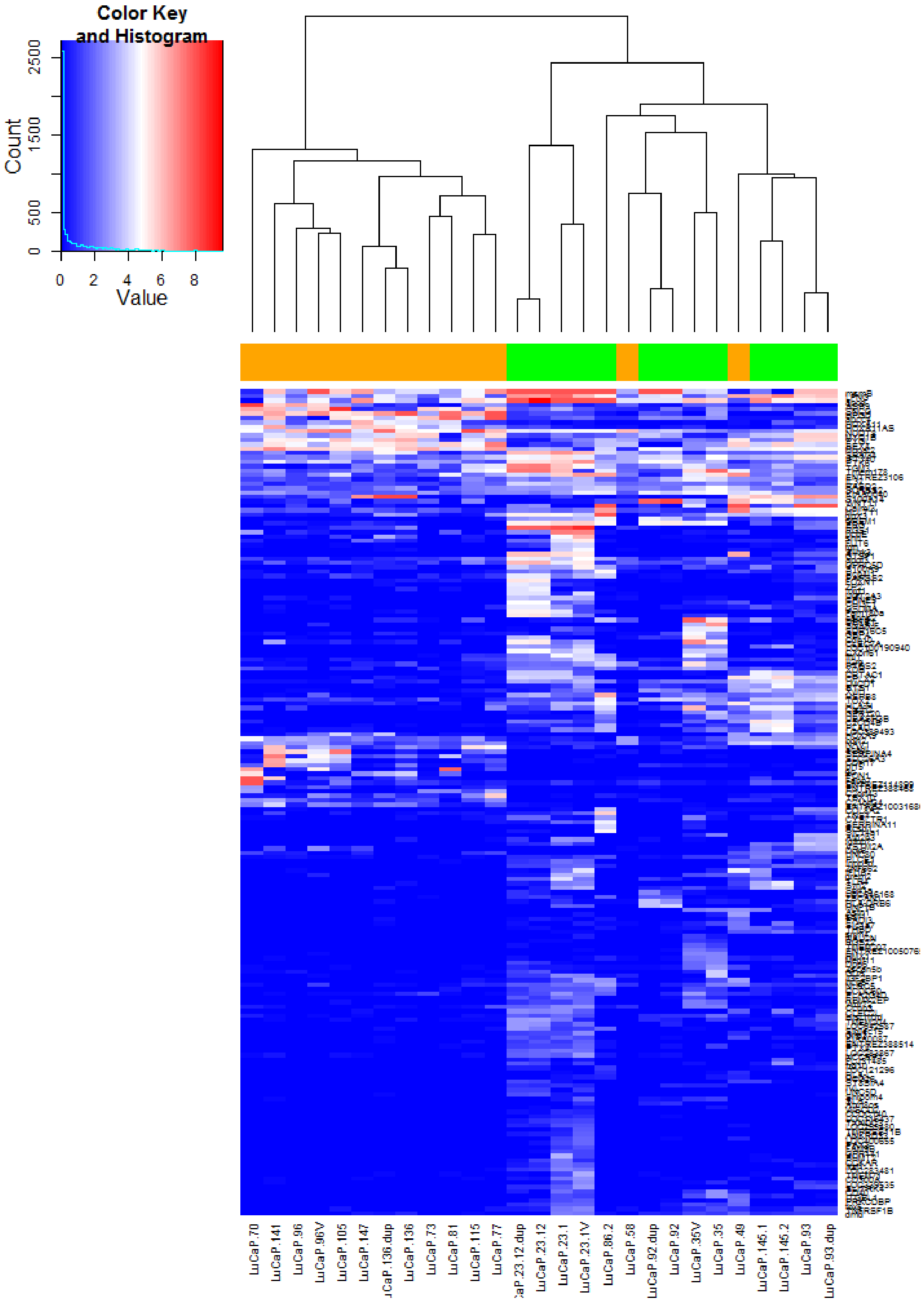

Figure 3. Differentially expressed genes in *TMPRSS2-ERG* rearrangement (+) vs. (-) LuCaPs.

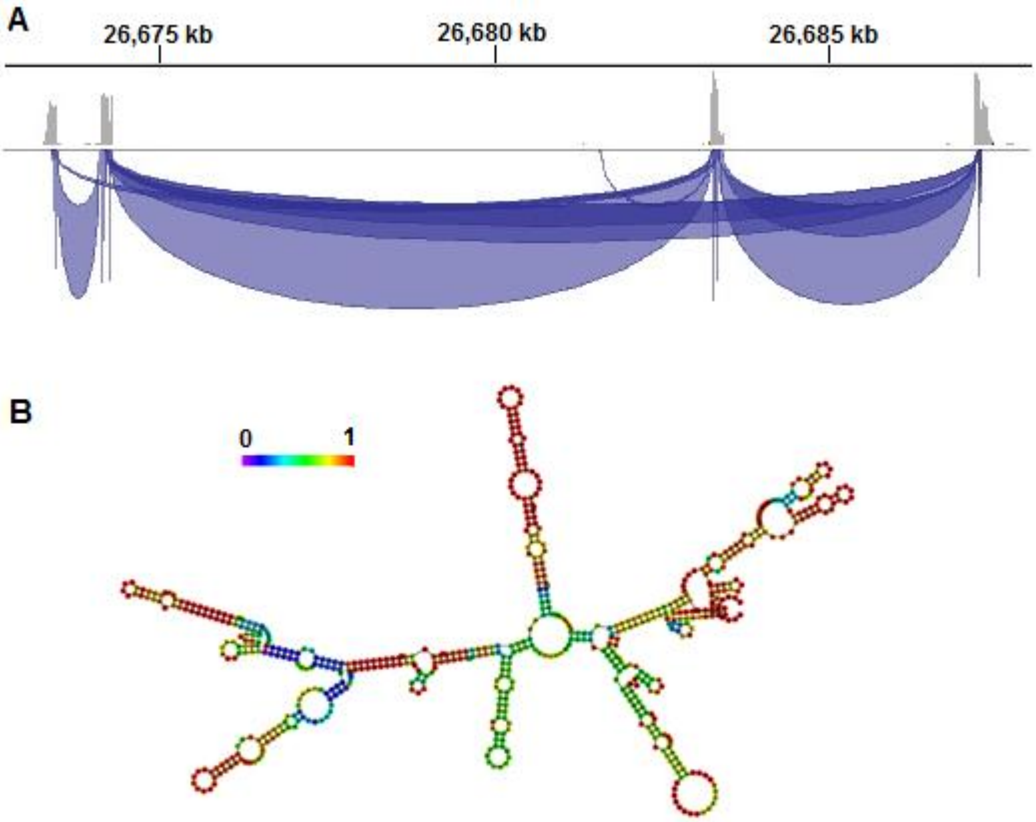

Figure 4: Neuroendocrine-specific lncRNA at chr6 p22.2. A) The lncRNA consists of approximately 655 nt encoded across 4 exons spanning a genomic region of approximately 15kb. RNAseq read depth is depicted in grey, exon junction spanning reads in blue. B) Predicted secondary structure of the full lncRNA sequence colored by confidence.

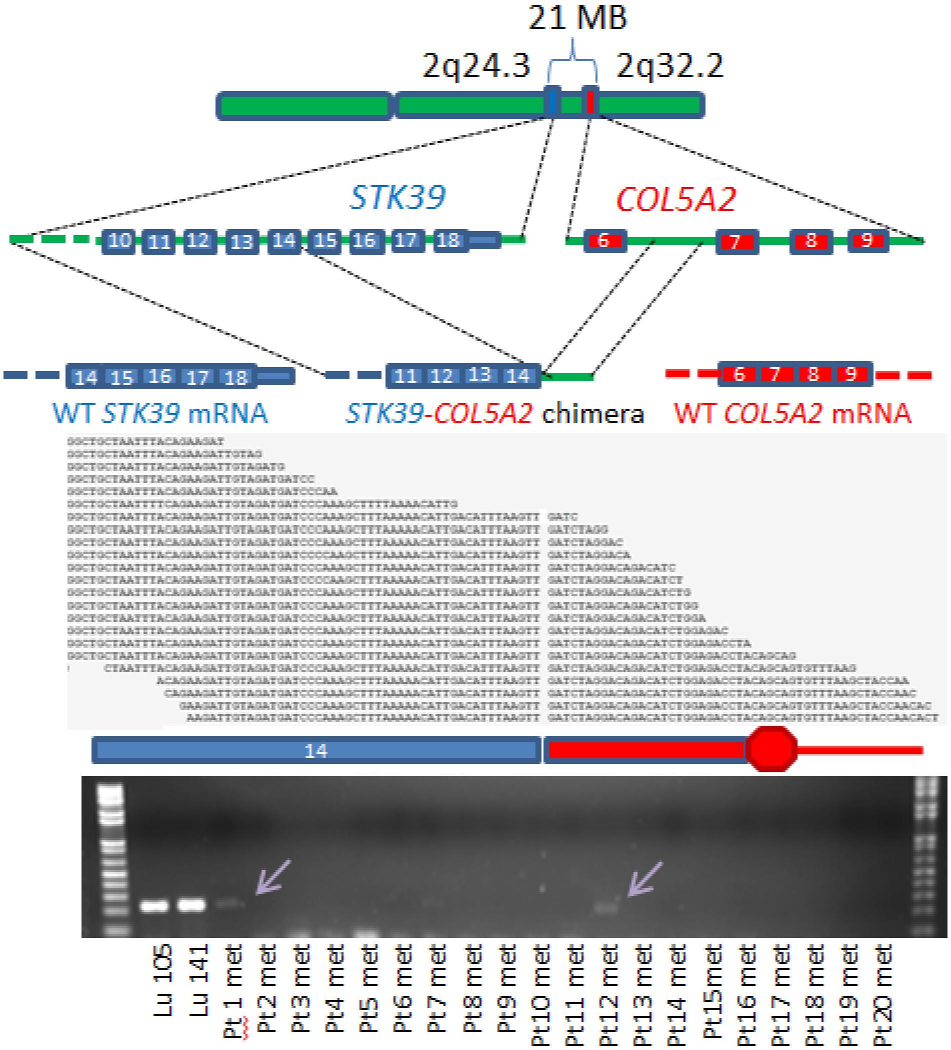

Figure 5: *STK39-COL5A2* rearrangement transcript. Genes *STK39* and *COL5A2* are encoded 21 MB apart on the q arm of chromosome 2. The chimeric transcript consists of the *STK39* transcript truncated at the end of exon 13 fused to a short portion of an intron in *COL5A2*. The intronic sequence appends an ORF with 8 amino acids before a stop codon is reached. RT-PCR confirms the chimera is present in LuCaPs 105 and 141. A survey revealed metastases from 4/40 patients expressed the chimeric transcript.

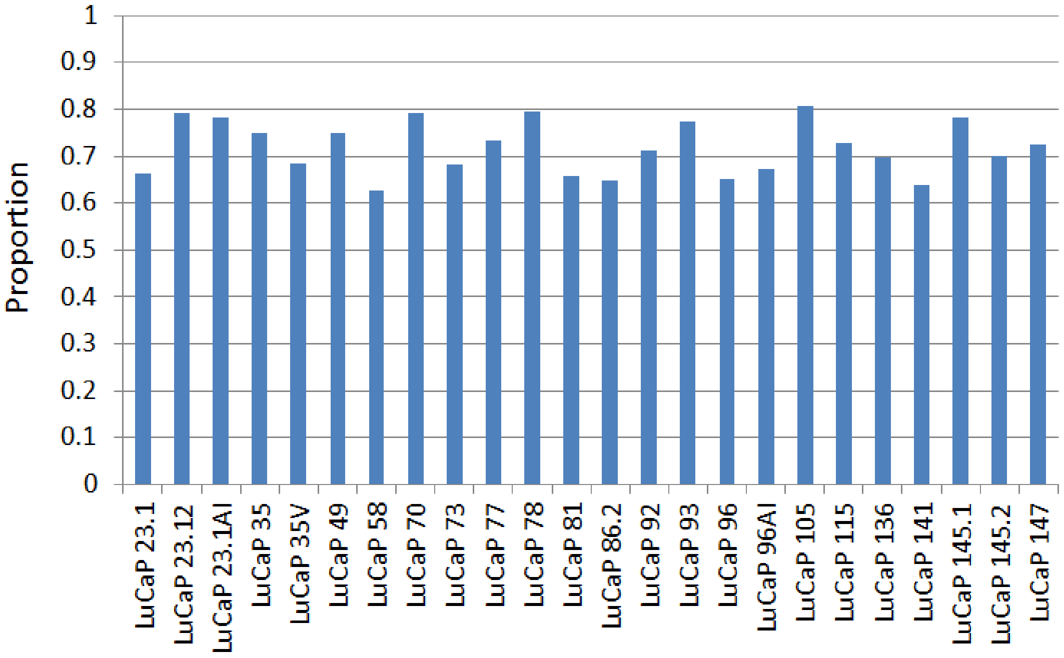

Figure 6: Proportion of expressed genes harboring somatic nsSNVs which display variant allele expression fraction ≥ 10%, by LuCaP

Chapter 3: lncRNA6p22.2: A Novel Neuroendocrine Prostate Cancer Specific Long Noncoding RNA

SUMMARY

RNAseq analyses of 24 LuCaP tumors identified several long noncoding RNAs differentially expressed in prostate neuroendocrine tumors versus adenocarcinomas, including a novel lncRNA at chromosome 6p22.2. We report here our efforts to characterize the extent of expression, regulation and function of this lncRNA.

A survey of PCa metastases, human cancer cell lines and a normal tissue panel confirmed this lncRNA is restricted to neuroendocrine tumors. Overexpression of the lncRNA in prostate adenocarcinoma cell lines resulted in a visible phenotype of spindle-like membrane projections and numerous cytoplasmic lipid droplets; in addition, once trypsinized as is done for standard passage cells are no longer capable of re-adhering but remain in suspension. Transcript profiles of cells engineered to express lncRNA 6p22.2 identified the differential expression of approximately 110 genes, including 14 consistent with significant differential expression in neuroendocrine LuCaPs relative to PCa LuCaPs. No changes in genes commonly expressed in neuroendocrine cells such as *NSE*, *CHRGA* or *SYNA* were observed.

The promoter region of the lncRNA contains a binding motif for REST, a master repressor of neuroendocrine expression. Differential expression analysis of RNAseq data indicates *REST* expression is significantly reduced and REST target genes significantly upregulated in neuroendocrine LuCaPs relative to prostate adenocarcinoma. Knockdown of REST resulted in upregulation of the lncRNA and NE markers in 2 of 3 PCa cell lines. Taken together these findings suggest lncRNA at Chr6p22.2 may function as a downstream effector of REST by regulating a subset of neuroendocrine-associated genes, but additional investigation is warranted

to evaluate whether it may, for example, serve as a scaffold for chromatin modifying complexes or guide transcription factors to promoters of genes of lipid metabolism or cytoskeletal formation.

INTRODUCTION

With the advent of high throughput transcriptome sequencing it is apparent that much of the genome beyond protein-coding genes is transcribed. Non-protein-coding RNAs act as basic cellular machinery, guide gene regulation and perform a spectrum of other unique functions. Ribosomal RNAs and tRNAs are core components of the translational machinery for all known life, and small regulatory RNAs (miRNAs and siRNAs) play critical roles in post-transcriptional gene regulation. RNAs of length greater than 200 nt possessing no significant open reading frame are termed long noncoding RNAs (lncRNAs); intergenic lncRNAs may be referred to as lincRNAs. We are beginning to understand the diverse and important roles lncRNAs play in cellular differentiation, development and cancer, but the functions and roles of only a small number of lncRNAs have been characterized. It has been shown, for example, that lncRNA *XIST*, a 17kb transcript, is involved in X chromosome inactivation (1) by specific binding of histone H2A and silencing proteins. *HOTAIR* (2) is a 2.2kb transcript with expression associated with aggressiveness and metastasis in breast cancer. *HOTAIR* specifically binds Polycomb Repressive Complex 2 and histone demethylase LSD1 and is necessary for epigenetic regulation of the *HOXD* locus. *PCA3* is a 3.7kb transcript being intensively investigated as a specific marker of prostate cancer (3), though what role it may play in PCa development or progression is not adequately resolved.

In Chapter 2 we reported the results of RNAseq analyses of the LuCaP series of primary and metastatic prostate cancers. The LuCaP series includes four tumors from three individuals (49, 93, 145.1 and 145.2) displaying the rare and aggressive neuroendocrine phenotype. Differential expression analysis of the transcriptomes of these tumors versus LuCaP prostate adenocarcinomas revealed 1,366 differentially expressed genes, including 29 known lncRNAs (**Table 1**) as well as one unannotated lncRNA encoded at 6p22.2. This novel transcript was expressed strictly in these four neuroendocrine tumors. Of these 29 differentially expressed lncRNAs, 17 are essentially completely uncharacterized in the literature. Of the remaining 12, 7 are significantly upregulated *(Miat*, *HOXD-AS1*, *H19, PTCSC3*, *NRON*, *TRAF31P2-AS1* and *NAG7*), and 5 are downregulated (*TP53TG1*, *NEAT1, HOTTIP*, *SNHG4, PCAT1*) in NEPC relative to adenocarcinoma LuCaPs. *Miat* is a nuclear localized neuron-specific transcript of unknown function in normal brain tissue (4), *NRON* is a cofactor of NFAT neuronal transcriptional regulation (5), and *NAG7* is an estrogen respressor and enhances adhesion and migration (6). The fact that the characterized lncRNAs upregulated in neuroendocrine LuCaPs seem to have neurooncogenic relevance suggests that much remains to be learned about the role of these and the as-yet uncharacterized molecules in neuroendocrine PCa.

Differential expression analysis of LuCaP RNAseq data also showed reduced expression of repressor element 1 (RE-1) – silencing transcription factor (REST), a master regulator of neural gene expression and cell fate (7). The majority of known REST target genes were upregulated in neuroendocrine LuCaPs relative to prostate adenocarcinoma (**Table 2**), presumably as a result of loss of repression associated with lower REST expression. Examination of the genomic context of the novel lncRNA at Chr6p22.2 revealed a REST binding motif approximately 1 kb from the transcription start site (**Figure 1 A**), and expression of the novel lncRNA in neuroendocrine

LuCaPs but not elsewhere was consistent with REST regulated genes. We therefore hypothesize that the lncRNA is subject to transcriptional regulation by REST. The lncRNA is encoded adjacent to a series of transfer RNA (tRNA) genes coding multiple copies each of Methionine, Isoleucine and Alanine tRNA genes, and two Alanine genes are located between exons of the lncRNA. The lncRNA is flanked downstream approximately 15kb away by *ZNF322*, which encodes a transcription factor involved in MAPK signaling, and upstream beyond the series of tRNAs the pseudogene *GUSBP4*. Neither *ZNF322* nor *GUSBP4* is differentially expressed in NEPC LuCaPs compared to PCa.

Since the functions of noncoding RNAs are frequently related to their folded structure the Vienna RNAfold algorithm was applied with default settings to predict the minimum free energy secondary structure and base-pairing probabilities of the RNA molecule (8). The predicted structure is highly complex and includes several hairpins with moderate to high base pairing probabilities (**Figure 1 B**). None of the hairpin structures has any sequence homology to any known family of human miRNAs. The full-length transcript is approximately 650nt in length, spans 4 exons and has no substantial coding potential (largest open reading frame would code for 9 amino acids). The fact that this novel transcript was consistently expressed in just neuroendocrine LuCaPs led us to investigate the role of this long noncoding RNA in the neuroendocrine phenotype.

RESULTS

Assessment of lncRNA 6p22 expression in prostate cancer

RT-PCR and validation sequencing confirmed the expression of the lncRNA in all four neuroendocrine LuCaP tumors and absence of expression in the remainder. In the panel of metastatic tumors from 40 individuals, the lncRNA was only detected in the 4 tumors determined to be NEPC by pathological review of the histology. The transcript was also expressed in the neuroendocrine PCa cell line NCI-H660 and in 4 of 9 small cell lung carcinoma (SCLC) cell lines (NCI-H209, DMS79, DMS153 and NCI-H748). The lncRNA was not detected in the Merkel Cell Carcinoma cell line MKL-1, nor was it observed in the panel of normal tissue cDNAs. These results suggest the lncRNA may be expressed in all neuroendocrine PCa and some, but not all, non-prostate neuroendocrine tumors.

lncRNA 6p22 influences the transcriptional program of prostate cancer cells

To evaluate the functional consequences of lncRNA6p22 expression in prostate cancer, we transfected 22Rv1 and BPH-1 PCa cell lines with an inducible lncRNA6p22-RFP vector. We collected total RNA and protein after 1d, 2d, 3d, 4d, 8d, 12d and 16d of induction. Using RT-PCR, we confirmed lncRNA6p22 expression (**Figure 2**). We next evaluated the expression of several known neuroendocrine markers including synaptophysin, chromogranin A and neuron-specific enolase. Transcripts encoding these proteins were not altered by lncRNA6p22 expression (**Figure 2**). We next sought to determine if lncRNA6p22 influenced the expression of other genes. We quantitated cellular transcripts by microarray hybridization and identified 110 differentially expressed genes, 14 of which were also altered in neuroendocrine LuCaPs 49, 93, 145.1 and 145.2 relative to adenocarcinomas. Of these, thirteen were upregulated in neuroendocrine tumors relative to adenocarcinomas. These genes were associated with axonogenesis *(Slitrk6, AVIL* and *ODZ4*), angiogenesis (*OSMR, Ang* and *Rnase4*) or are otherwise implicated in carcinogenesis (*CXCL1, Ceacam6, dusp6, Fst, SYK* and *NGPTL4*).

lncRNA 6p22 is regulated by the REST transcriptional repressor

The RE1-silencing transcription factor (REST) is a master negative regulator of neurogenesis and is know to repress neuronal genes in non-neuronal tissues including prostate cancer cells (7). To determine if REST could function as a negative regulator of lncRNA6p22, we evaluated the promoter region upstreatm of the lncRNA6p22 transcriptional start site and identified a consensus REST binding site (**Figure 1**). We next transfected 22Rv1, LNCaP and BPH-1 PCa cell lines with lentivirus pGIPZ-shREST to knockd-down REST or shRNA controls. We confirmed the expression of these constructs by RT-PCR at 2d and subsequent timepoints. Following REST knock-down, transcripts encoding lncRNA6p22 and the neuroendocrine markers neuron-specific enolase, chromogranin A, and synaptophysin were upregulated in BPH-1 and LNCaP (**Figure 3A**). No effect was observed in cell line 22Rv1 (**Figure 3A**). Slight reduction of REST was detected by western blot (**Figure 3B**). These results indicate that lncRNA 6p22.2 is subject to transcriptional repression by REST.

DISCUSSION

At present long noncoding RNAs are rapidly being discovered with expression patterns specific to tissue, development or disease state. The expression of the lncRNA at Chr. 6p22.2 was shown here to be absent from normal tissues but present in neuroendocrine prostate cancers and some neuroendocrine tumors originating from other tissues. The neuroendocrine specificity of expression of this lncRNA was shown to be subject to transcriptional repression by REST, a master transcriptional regulator of neural gene expression and cell fate in the prostate epithelial LNCaP and BPH-1 cell lines. Overexpression of this lncRNA resulted in differential expression of 110 genes, 13 of which were consistent with differential expression patterns in neuroendocrine

LuCaPs relative to adenocarcinoma LuCaPs, but not common neuroendocrine markers chromogranin A, synaptophysin or neuron specific enolase. It remains unknown whether this lncRNA is relevant to neurologic development or other disease states, but our data suggest it may regulate a subset of genes associated with neuroendocrine PCa, including those modulating axonogenesis (*Slitrk6*, *AVIL* and *ODZ4*), angiogenesis (*OSMR*, *Ang* and *Rnase4*) as well as proliferation, differentiation and anchoring (*CXCL1*, *Ceacam6*, *dusp6*, *Fst*, *SYK* and *NGPTL4*). Tha majority of lncRNAs displaying elevated expression in neuroendocrine LuCaPs are basically completely uncharacterized in the literature. Several lncRNAs that have been investigated were found to be significantly upregulated, however *(Miat*, *HOXD-AS1*, *H19*, *PTCSC3*, *NRON*, *TRAF31P2-AS1* and *NAG7*), and 5 are downregulated (*TP53TG1*, *NEAT1*, *HOTTIP*, *SNHG4*, *PCAT1*) in NEPC relative to adenocarcinoma LuCaPs. *Miat* is known to be a neuron-specific transcript but its function is unresolved (4); it may play a role in any number of cellular functions, from development to gene regulation. *NRON*, a neuronal transcription cofactor (5) may be necessary to neuroendocrine expression in NEPC, and warrants further examination. *NAG7*, an estrogen respressor, has been shown to enhance adhesion and migration and has clear relevance to NEPC (6). These noncoding RNAs as well as those implicated but as yet completely uncharacterized represent an enormous opportunity to resolve the mechanisms of aggressive NEPC proliferation and may even serve as specific markers, perhaps even at an early enough stage to intervene prior to metastasis of this rare but lethal form of PCa.

METHODS AND MATERIALS

Samples, survey and validation

Total RNA was obtained from the LuCaP series of tumors and a variety of other samples. A panel of 24 human PCa cell lines obtained from the American Type Culture Collection (Mannassas VA, USA), nine small cell lung carcinoma (SCLC) cell lines generously provided by Dr. David MacPherson (Seattle, WA USA), Merkel cell carcinoma cell line MKL-1 kindly provided by Dr. Paul Nghiem (Seattle, WA USA), a commercially available panel of normal Human cDNAs (Clontech, Mountain View, CA USA), and a series of block-embedded flash frozen human PCa metastases from 49 individuals obtained from the University of Washington rapid autopsy program were sampled.

cDNA was reverse transcribed from total RNA using a 50/50 mix of oligo-dT and random primers. PCR was performed using primers designed at the outer edges of the first and last exon as predicted by RNAseq alignments. RNAseq alignments suggested a small degree of leaky splicing resulting in four isoforms, with a majority of junction-spanning reads consistent with a four-exon gene model but a minority skipping one or both middle exons. As expected, multiple bands were observed upon standard PCR of cDNAs from LuCaPs expressing the lncRNA by RNAseq. Individual bands were cut, gel purified and Sanger sequenced. Sanger sequencing of all isoforms indicated the inclusion of both exons 2 and 3 was restricted to the dominant four-exon isoform. For this reason RT-PCR was performed on the full panel of cDNAs using primers in exons 2 and 3 by standard methods, and Sanger sequencing was used to confirm expression where detected by RT-PCR in the sample panel.

Cell line overexpression

The full-length lncRNA 6p22.2 was PCR amplified from LuCaP 49 cDNA, gel purified, cloned into TopoTA cloning vectors (Life Technologies, Carlsbad CA USA), cultured and individual clones verified by restriction digest and Sanger sequencing. The insert was cut, gel purified and transferred into inducible pTRIPZ lentiviral vector, cultured, and the plasmid was isolated and again sequence validated. This plasmid, designated pTRIPZ-lncRNA-Fwd, was then packaged into lentivirus and produced in 293FT media. Targeted cells (22rv1, BPH1 and LNCaP) were transfected for 48hr and subjected to 1ug/ml puromycin selection until a test well of cells exceeded 90% RFP-positive subsequent to 48hr of doxycycline induction. Experimental wells were then cultured in triplicate in RPMI-1640 supplemented with 10% FBS and with either 1 ug/ml doxycycline or without doxycycline (negative control) to 24h, 48h, 72h, 4d, 8d, 12d and 16d timepoints. RNA and protein were harvested in triplicate at each timepoint. The lncRNA construct expression relative to RPL13A was assessed by RT-PCR. RT-PCR indicated maximal induced lncRNA expression was essentially reached by 2d (**Figure 2**).

Expression profiling

Total RNA was obtained from BPH1 and 22Rv1 cells engineered to express lncRNA 6p22.2 lines at timepoints of 1d, 2d, 3d, 4d, 8d, 12 and 16d after doxycycline (DOX) induction. cDNA was reverse transcribed from total RNA by standard methods using a 50/50 mix of oligo-dT and random primers. RT-PCR was performed to quantitate expression of the lncRNA and neuroendocrine markers neuron-specific enolase, synaptophysin and chromogranin A in the timecourse. Total RNA from the 4d timepoint with and without DOX induction were labeled for hybridization to custom 4x44k Agilent microarrays (Agilent Technologies, Santa Clara CA, USA) in duplicate.

Regulation by REST master neuroendocrine regulator

Five GIPZ lentiviral shRNA clones designed to knock down the expression of REST and a non-silencing clone were obtained from Thermo Scientific / Open Biosystems via the RNAi Core Facility at the Fred Hutchinson Cancer Research Center. All plasmids were verified by

Sanger sequencing. The five REST shRNA plasmids were pooled and co-packaged into lentivirus and produced in 293FT media. Targeted cells (22rv1, BPH1 and LNCaP) were then transfected for 48hr and subjected to 1ug/ml puromycin selection. When cells exceeded 90% GFP-positive, total RNA and protein were harvested in triplicate. RNA was reverse transcribed and lncRNA and other gene expression were assessed by RT-PCR. REST knockdown was assessed by western blot.

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Table 1. **Annotated lncRNAs differentially expressed in neuroendocrine versus prostate adenocarcinoma (FDR < 0.01) n=29**

SYMBOL	-logFC	logCPM	P-Value	FDR	Length (nt)	Gene Name
Miat	6.86	2.92	3.06E-19	7.95E-17	10193	myocardial infarction associated transcript (non-protein coding)
ENTREZ100507377	7.42	-0.24	4.40E-13	4.99E-11	750	NR_038300
ENTREZ100506305	6.92	1.10	1.42E-11	1.13E-09	1576	NR_038904
ENTREZ100422737	6.72	-1.83	2.59E-10	1.66E-08	1387	NR_033557
HOXD-AS1	4.88	3.17	2.60E-09	1.41E-07	3819	HOXD-AS1 HOXD cluster antisense RNA 1
C8orf56	5.21	-2.57	1.14E-07	4.56E-06	496	chromosome 8 open reading frame 56 / NR_027071
H19	6.84	8.24	1.26E-07	5.01E-06	2322	H19, imprinted maternally expressed transcript (non-protein coding) / NR_002196.1
LOC100133612	4.15	0.14	1.69E-07	6.48E-06	1965	similar to hCG1815312 / NR_024455
LOC100130298	5.04	-1.66	2.64E-07	9.79E-06	528	similar to hCG1816373 / NR_034003
PTCSC3	5.86	-3.68	3.43E-07	1.24E-05	1152	papillary thyroid carcinoma susceptibility candidate 3 (non-protein coding) / NR_049735
ENTREZ100506394	3.32	-0.65	3.73E-06	1.08E-04	1942	LOC100506394
LINC00565	4.44	-1.38	5.66E-06	1.54E-04	2494	long intergenic non-protein coding RNA 565 / NR_047495
LINC00511	3.86	-0.22	1.60E-05	3.77E-04	2265	long intergenic non-protein coding RNA 511 /NR_033876
LOC100126784	4.66	-2.15	2.00E-05	4.56E-04	3753	uncharacterized LOC100126784, non-coding RNA /NR_015384
TP53TG1	-3.17	5.24	2.11E-05	4.79E-04	751	TP53 target 1 (non-protein coding) / NR_015381.1
ENTREZ100506776	-8.36	3.45	2.47E-05	5.45E-04	3516	NR_040085
LOC100130776	3.94	-0.01	3.36E-05	7.14E-04	1567	hypothetical LOC100130776 non-coding RNA / NR_027032
Neat1	-2.61	9.76	3.37E-05	7.14E-04	3756	non-protein coding RNA 84 / NR_028272.1
ENTREZ100506190	-2.40	5.20	5.76E-05	1.13E-03	2123	uncharacterized LOC100506190, non-coding RNA / NR_038955
NRON	4.47	-3.43	1.17E-04	2.03E-03	2730	non-protein coding RNA, repressor of NFAT / NR_045006.1
HOTTIP	-13.13	2.84	1.73E-04	2.83E-03	3772	HOTTIP HOXA distal transcript antisense RNA / NR_037843.2
TRAF31P2-AS1	2.34	2.13	2.23E-04	3.49E-03	4943	TRAF31P2 antisense RNA 1 / NR_034108
SNHG4	-4.30	3.39	4.45E-04	6.28E-03	1100	small nucleolar RNA host gene 4 (non-protein coding) / NR_003141
PCAT1	-6.33	4.79	6.33E-04	8.30E-03	1992	prostate cancer associated transript 1 (non-protein coding) / NR_045262
LOC285548	4.59	-2.86	6.40E-04	8.37E-03	1749	hypothetical LOC285548 / NR_015450.1
LOC100128338	-2.55	6.26	6.42E-04	8.38E-03	2743	hypothetical LOC100128338 / NR_033849
ENTREZ100506795	-10.04	0.32	7.98E-04	9.95E-03	2860	uncharacterized LOC100506795, non-coding RNA / NR_038426
LINC00294	1.81	3.79	8.02E-04	9.98E-03	3322	long intergenic non-protein coding RNA 294 / NR_015451
LINC00312 / NAG7	2.69	-1.53	8.04E-04	9.99E-03	2903	LINC00312 LOH3CR2A loss of heterozygosity, 3, chromosomal region 2, gene A

Table 2.

REST-regulated gene expression in neuroendocrine vs adenocarcinoma LuCaPs

Symbol		NE RPKM (Mean)	Adeno RPKM (Mean)	Log2FC
AURKA		30.78	13.40	1.20
REST		1.79	5.94	-1.73
REST regulated genes	*Ascl1*	444.60	0.54	9.68
	Cacna1a	28.73	0.06	9.02
	CHGB	67.65	0.65	6.70
	ELAVL3	10.51	0.24	5.45
	Six2	65.86	2.44	4.75
	Cabp7	8.90	0.35	4.68
	Scgn	94.08	4.13	4.51
	CPLX2	30.60	1.98	3.95
	Syt1	26.87	2.23	3.59
	Syp	51.81	4.32	3.58
	MYCN	0.76	0.16	2.23
	gpr173	5.19	1.22	2.09
	NOVA1	2.96	0.86	1.78
	KCNA4	0.17	0.06	1.55
	SHANK2	4.50	3.07	0.55
	SYNGR4	7.80	5.55	0.49
	RLN2	2.46	1.84	0.42
	LINGO4	0.33	0.79	-1.27
	CUX2	0.26	7.46	-4.82

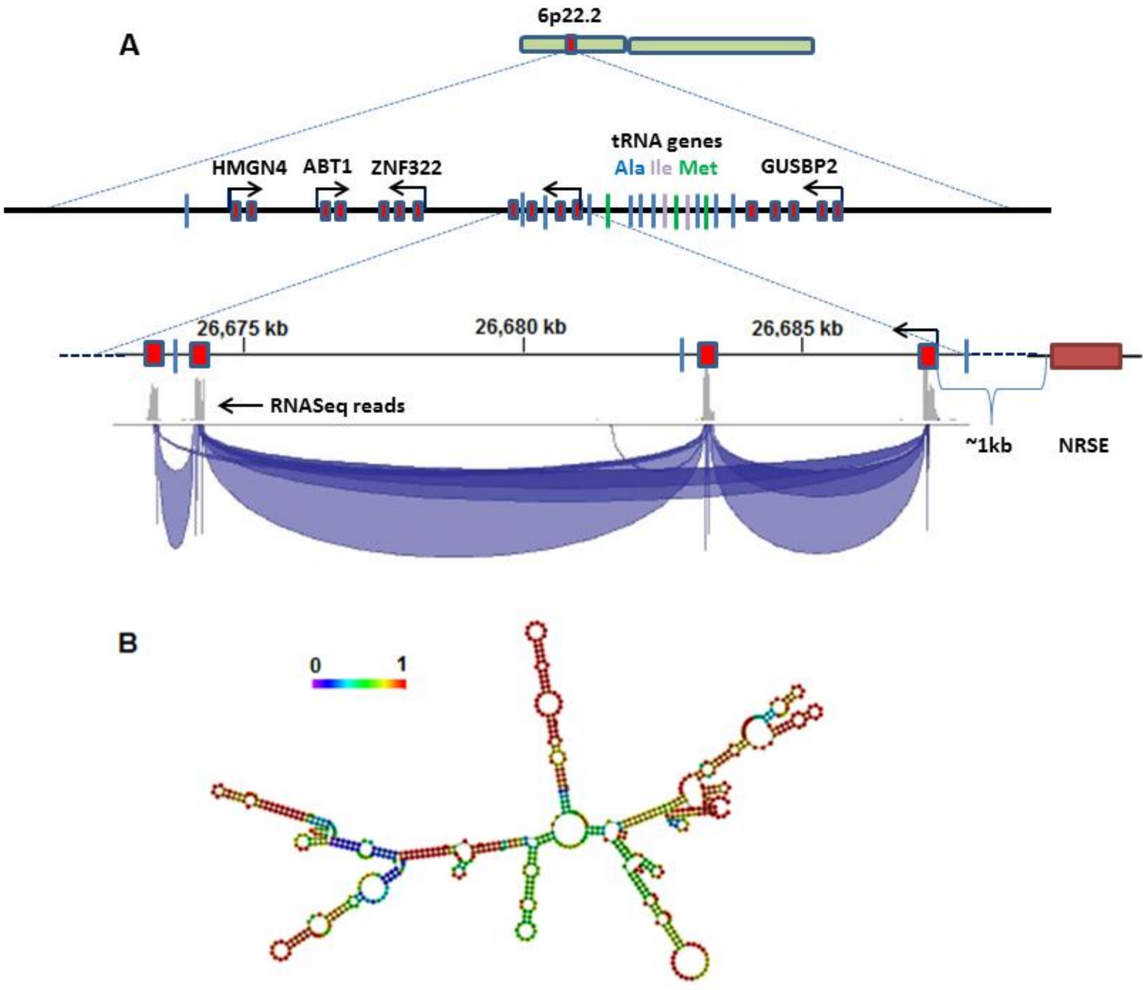

Figure 1. Genomic context of novel neuroendocrine-specific LncRNA. A) Genomic context. The lncRNA is encoded on a 15kb region of the minus strand of chromosome 6 and consists of approximately 655 nt encoded across 4 exons. The gene overlaps the edge of a field of ~20 tRNA genes encoding Alanine, Isoleucine and Methionine transfer RNAs. The nearest protein coding gene is *ZNF322*, approximately 15 kb away. A binding site for REST (NRSE) is located ~1 kb from the transcription start site. RNAseq read depth is depicted in grey, exon junction spanning reads in blue. B) Predicted secondary structure of the full lncRNA sequence colored by confidence.

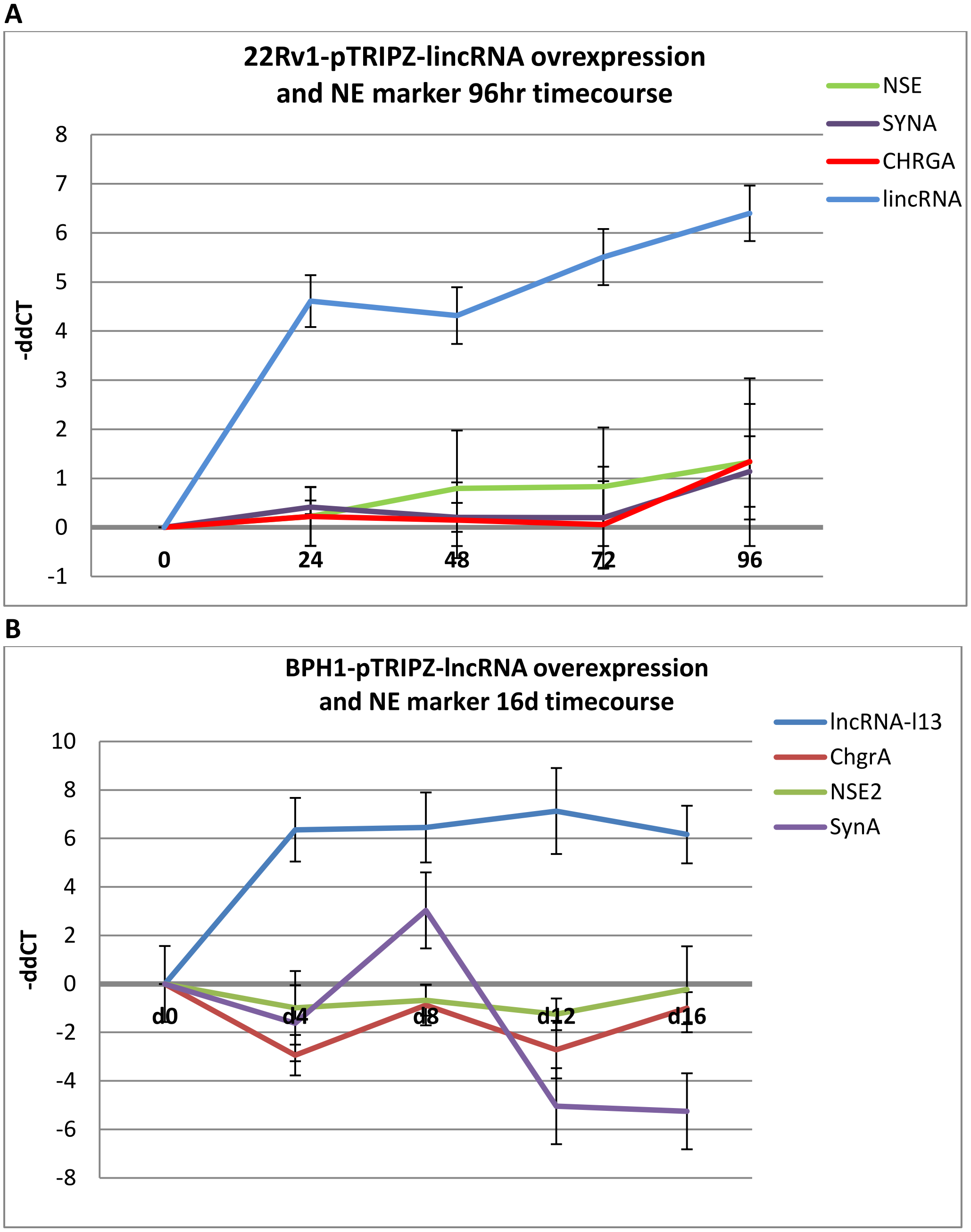

Figure 2. RT-PCR of lncRNA and neuroendocrine markers in A) 22Rv1 and B) BPH-1 with pTRIPZ-lncRNA overexpression over timecourse. Expression of lncRNA plateaus rapidly. Little to no reduction in expression of neuroendocrine markers *ChrgA* and *NSE* is observed. *SYN* expression is variable.

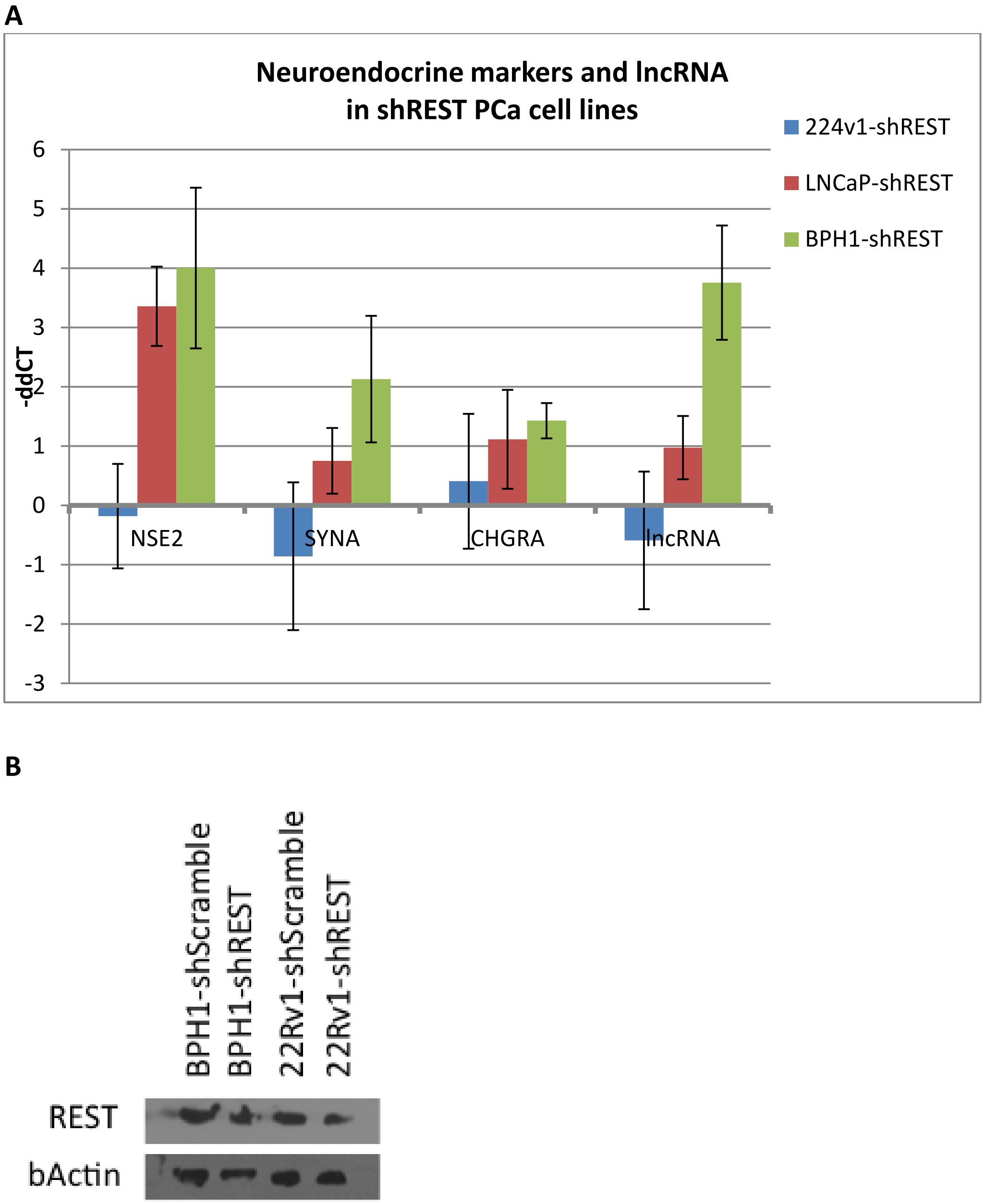

Figure 3. Knockdown of REST relieves repression of lncRNA 6p22.2 and neuroendocrine markers. A) RT-PCR of lncRNA 6p22.2 and REST-regulated neuroendocrine markers in PCa cell lines 22Rv1, LNCaP and BPH-1 with pooled shREST knockdown. B) REST knockdown by western.

Chapter 4: Conclusions and Perspectives

Cancer is a disease rooted the inherited genome and acquired somatic mutations. Until the advent of second-generation sequencing the task of comprehensively interrogating the genome for cancer-associated loci at the nucleotide level was infeasible due to sheer enormity (~$3x10^9$ bases in the haploid human genome, with sequencing of large patient cohorts desired). The challenge of scaling up was answered in part by the pragmatic and clever focus on the exome, or protein-coding portion of the genome. Today exome sequencing to screen for single nucleotide variants (SNVs) associated with the development, progression, resistance to treatment, and outcomes of specific cancers and their subtypes is becoming feasible in increasingly larger cohorts Most exciting is the finding that many somatically acquired variations in key genes are found recurrently across patients, often in ways which similarly compromise or enhance the function of the gene, and surprisingly even occasionally occur at precisely the same nucleotide. In prostate cancer however, our work and that of our collaborators has shown that individual genes with recurrently altered primary sequence tend to be compromised in only about 20% of patients at most, suggesting that PCa can develop and elude treatment by a number of pathways. Cytogenetic anomalies such as small or large genomic deletions, duplications or genomic rearrangements play an important role, as haploinsufficiency or complete elimination of tumor suppressor genes or the amplification of driver genes such as *AR* can occur. In addition, chromosomal rearrangements can result in the fusion of two genes such that the resulting gene product either eliminates or enhances gene activity, occasionally to the advantage of cancer cellular proliferation, migration or identity. Prior to our own work other studies had identified a substantial number of such chimeras present at very low frequency in PCa. Our finding that just one chimera among 40 novel rearrangement transcripts discovered in 15 of 19 patients sequenced proved recurrent suggests that most such events are private to the patient. Taken together, recurrent functionally altered SNVs, deletions, amplifications and rearrangements form only a partial explanation of the etiology and progression of PCa, and no two tumors share the same array of genomic lesions.

The accumulation of genetic mutations in somatic tissues is mainly relevant to the extent that it influences the activity or abundance of gene products, so the quantity and sequence of the complement of transcribed RNA molecules, though transient in nature and only a snapshot of the cellular processes underway, can be a good indication of the relevance of individual genetic mutations and can delineate the cellular and tissue-level trends in metabolic activity and cellular identity. While microarray technologies may accurately quantitate abundance at the exon level, RNAseq can be informative of expression and function at single nucleotide resolution. Interpreting RNAseq data as expression must be done cautiously, however. One critical caveat is that software aligning RNAseq reads to the genome must apply filters to ensure accurate alignment; a maximum threshold number of positions with base calls not concurring with the reference sequence or known SNPs is necessary, and thresholds of acceptable confidence in read quality must be set. Any true but unanticipated polymorphism correctly increases this dissenting count, making a read reflecting a true mutation less likely to be properly aligned, and thereby potentially resulting in a false negative. It may also be impossible to correctly align short polymorphic reads where gene families or other sequences with high homology or nearly identical sequence are present in the genome; a guess between two equally statistically likely alignments can result in a false positive that can only be corrected by manual inspection.

With these caveats in mind we examined the expression of SNVs that we previously reported from exome sequencing of the same tumors. Our findings indicate most recurrent non-synonymous SNVs are not particularly silenced or amplified, but are instead expressed on par with the wildtype allele. Non-synonymous SNVs in RNA were detected by first comparing the sequence to the reference genome and a large database of known SNPs, then by comparison to corresponding exome results, thus permitting discernment of mRNA editing from genomic nsSNV expression. Since genomic sequence was only available for coding regions and not the remainder of the genome, this approach was unable to detect potential editing of Alu repeats in noncoding RNAs reported as commonplace. With regard to coding regions however, we detected and validated ubiquitous RNA editing of genes *NEIL1* and *CDK13* consistent with prior characterization in all LuCaPs, PCa metastases and cell lines as well as normal tissue samples. There was no indication of a bias towards increased or decreased editing of these genes in tumor relative to normal samples, suggesting RNA editing of these genes is not highly relevant to advanced PCa. It remains undetermined whether editing of Alu repeats in noncoding genes not profiled by exome probes is altered in LuCaPs. It seems unlikely however that aberrant activity of ADARs would be restricted to noncoding Alu sequences without altering coding gene editing.

Splice isoform expression normally displays consistent patterns of tissue and cell type specificity. Recent work however has revealed an imbalance in the proportion of various alternative splice isoforms of a large number of genes when comparing tumor and normal transcriptomes. Variant splicing frequently results in frameshifts and premature stop codons, but has also been shown in some tumors to skip exons encoding domains necessary for tumor suppressor activity while retaining the reading frame of the remaining protein. In our data a bewildering array of novel splice junctions were present, and some were found to be recurrent in tumors with PCa phenotypes of neuroendocrine or castration resistance. It is unclear whether the restriction of such splice isoforms to tumor subsets is deterministic and relevant to carcinogenesis and progression or simply a matter of chance. Mechanistic investigations of individual variant transcripts observed in experimental models may demonstrate the capacity to recapitulate conditions consistent with the evolutionary history of an individual tumor (i.e., enhance proliferation, mobility or changes in cellular identity), but it can be difficult to attribute cause and effect where multiple permutations of alternative splicing are present. In addition to the mechanistic evaluation of individual candidates, the search for conditions that predispose a cell to oncogenic deregulation of splicing will prove invaluable. At present it is unclear what factors driving phenotypes such as neuroendocrine differentiation may facilitate the particular complement of alternately spliced transcripts we observed.

The discovery of a novel lncRNA at 6p22.2 is exciting, due largely to its apparent specificity of expression. Subsequent testing of a larger panel of samples confirmed that this transcript is indeed present in all neuroendocrine prostate tumors surveyed and absent from adenocarcinomas; the transcript was also detected in a subset of non-prostate tumors with small-cell or neuroendocrine characteristics, suggesting it might prove relevant to other malignancies. It was not surprising that our experimental observations indicate this lncRNA is upregulated by loss of REST, a master repressor of neurologic expression, as there was a REST binding motif nearby. Prior work has in fact shown that loss of REST in PCa cell lines results in upregulation of several genes associated with neuroendocrine differentiation. Some noncoding RNAs are involved in guiding transcription complexes, so we also investigated whether overexpression of this lncRNA without repressing REST altered the expression of neuron-specific enolase, chromogranin A, or synaptophysin or other markers of a neuroendocrine phenotype. Although classical markers were not altered, a number of genes associated with neurologic activity and with functionality relevant to cancer were activated (metabolism, anchorage-independent growth, mobility, angiogenesis and invasion). Fourteen of these were also significantly differentially expressed in our LuCaP transcriptomes, and thirteen of these in the same direction. While this overlap might be the result of chance, it might be the case that this lncRNA is acting as a downstream effector of the REST transcriptional program.

Further investigation of the role of this lncRNA in neuroendocrine cancer is warranted. Several failed attempts were made to knock down the transcript in neuroendocrine cell lines using shRNA constructs. shRNAs were designed manually as high-quality commercial reagents are not available for unannotated sequences. It is unclear whether failure was the result of poorly chosen portions of the message to target, or because the complex secondary structure of the message precludes base pairing with the intended inhibitory RNA molecule. Still, additional efforts might succeed in knocking down the transcript and examining the cells for a number of outcomes. Transcriptional regulation or indeed any function of this message would rely on specific interaction with proteins, so an RNA immunoprecipitation (RNA-IP) assay would be warranted. In this assay the RNA would be synthesized and labeled for streptavidin-biotin pulldown, then incubated with protein lysates. The resulting pulldown could either be probed for individual candidate proteins via western, or submitted in bulk for mass spectrometry analysis. Given the broad range of functions that noncoding RNAs are known to play, the more agnostic approach of mass-spectometry may be warranted for identifying this lncRNA’s binding partners. Depending on what binding partners were observed and what roles for the lncRNA were subsequently hypothesized, it might be valuable to examine the subcellular localization of the lncRNA via RNA fluorescent in situ hybridization (RNA-FISH). This would require the use of either in vitro tissue culture or fresh or flash-frozen tissue, as RNA degradation can be extremely rapid. Observation of the lncRNA in subcellular compartments (punctate cytoplasmic foci, nuclear, nucleolar, etc.) would shed light on the role of this transcript, and immunofluorescent colocalization with other key proteins could be tested. One key caveat, however, is that FISH relies on base pair recognition between probe and target, and secondary structure of noncoding RNAs might prohibit specific binding unless denaturing were adequate. Once specific activities were identified, functional testing of the lncRNA could be performed by synthesizing constructs missing one or more hairpins and testing for loss of function. More subtle tests involving individual bases would permit the probing of the importance of the secondary structure to activity.

It is becoming clear as the roles of individual noncoding RNAs are being revealed that these enigmatic molecules may play a large part in a variety of cellular activities and disease processes. The development of high-throughput approaches to investigating their activities is warranted. A synthesized library of all known noncoding RNAs could be used for several purposes, including parallel protein pulldown assays in which an individual protein or unaltered protein lysate are assayed for binding affinity, for RNA-FISH probe synthesis, or for capture and high throughput of barcoded DNA or other RNA fragments by virtue of specific base pairing.

As the cost of high throughput sequencing drops and the technologies are refined, the opportunity to apply genome-wide and transcriptome-wide interrogation of disease tissue will grow. Our experience with examining parallel datasets of LuCaPs including exome, transcriptome, expression microarray, CGH and individual RT-PCR and Sanger sequencing suggests that most PCa tumors will not be readily binned into causal pathways involving just one, two or three genes recurrently compromised in the same way, but rather will reflect a large number of relevant genes compromised to differing degrees in different ways in any of numerous key pathways. These pathways might be found to be compromised in distinct combinations – the activity of tumor suppressor genes may be reduced via non-synonymous mutation, copy number loss and reduced expression, splicing that compromises activity, transcript repression via altered miRNA activity, negative regulation via interactions with as-yet uncharacterized noncoding RNAs, etc. Similarly, oncogenes may be activated via genomic amplification, a rare rearrangement event that drives increased expression, splicing that removes a negative regulatory motif, transcriptional activation via noncoding RNAs, etc. In essence, it is likely that every tumor is a "one-off" having successfully navigated a unique route through selective pressures involving perhaps similar environmental exposures, but largely a reflection of the individual's underlying genetic and epigenetic makeup and the vagaries of chance. Prostate cancer is therefore a prime candidate for the development of methodologies to improve approaches for personalized medicine.

Table S1.

Composite list of transcripts among the top 500 most abundant in one or more LuCaPs

SYMBOL	LuCaP Ct	RPKM (MEAN)	RPKM (MAX)	Gene Name
RPL41	22	4901	12071	ribosomal protein L41
rps2	22	3408	7289	ribosomal protein S2 pseudogene 8; ribosomal protein S2 pseudogene 11; ribosomal protein S2 pseudogene 5; ribosomal protein S2 pseudogene 12; ribosomal protein S2 pseudogene 51; ribosomal protein S2 pseudogene 17; ribosomal protein S2 pseudogene 55; ribos
RpL30	22	3330	11110	ribosomal protein L30
GAPDH	22	3160	14006	glyceraldehyde-3-phosphate dehydrogenase-like 6; hypothetical protein LOC100133042; glyceraldehyde-3-phosphate dehydrogenase
rpl8	22	3157	7279	ribosomal protein L8; ribosomal protein L8 pseudogene 2
Pla2g2a	8	2820	7648	phospholipase A2, group IIA (platelets, synovial fluid)
rplp1	22	2767	7734	ribosomal protein, large, P1
EEF1A1	22	2742	6820	eukaryotic translation elongation factor 1 alpha-like 7; eukaryotic translation elongation factor 1 alpha-like 3; similar to eukaryotic translation elongation factor 1 alpha 1; eukaryotic translation elongation factor 1 alpha 1
RPL7	22	2493	7661	ribosomal protein L7 pseudogene 26; ribosomal protein L7 pseudogene 16; ribosomal protein L7; ribosomal protein L7 pseudogene 32; ribosomal protein L7 pseudogene 23; ribosomal protein L7 pseudogene 24; ribosomal protein L7 pseudogene 20
CTSE	1	2429	2429	cathepsin E
AMTN	2	2393	3463	amelotin
Entrez6175	22	2366	5674	
rps11	22	2342	4532	ribosomal protein S11 pseudogene 5; ribosomal protein S11
NPY	5	2331	7103	neuropeptide Y
RPL37A	22	2310	6055	ribosomal protein L37a
RPS6	22	2186	5396	ribosomal protein S6 pseudogene 25; ribosomal protein S6; ribosomal protein S6 pseudogene 1
LOC653881	22	2151	3899	ribosomal protein L3; similar to 60S ribosomal protein L3 (L4)
rps8	22	2093	5647	ribosomal protein S8; ribosomal protein S8 pseudogene 8; ribosomal protein S8 pseudogene 10
CST1	4	2091	7110	cystatin SN
KLK3	19	2049	5485	kallikrein-related peptidase 3
Rpl7a	22	2046	5082	ribosomal protein L7a pseudogene 70; ribosomal protein L7a; ribosomal protein L7a pseudogene 30; ribosomal protein L7a pseudogene 66; ribosomal protein L7a pseudogene 27; ribosomal protein L7a pseudogene 11; ribosomal protein L7a pseudogene 62
RpL18A	22	1994	4335	ribosomal protein L18a pseudogene 6; ribosomal protein L18a
rps21	22	1869	7031	ribosomal protein S21
ACTB	22	1845	6246	actin, beta
Entrez6143	22	1827	4403	
GNB2L1	22	1785	4530	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
rps27	22	1763	3122	ribosomal protein S27 pseudogene 29; ribosomal protein S27 pseudogene 9; ribosomal protein S27 pseudogene 23; ribosomal protein S27 pseudogene 13; ribosomal protein S27; ribosomal protein S27 pseudogene 21; ribosomal protein S27 pseudogene 7; ribosomal pr
ACTG1	22	1763	4136	actin, gamma 1
rps12	22	1718	4679	ribosomal protein S12; ribosomal protein S12 pseudogene 4; ribosomal protein S12 pseudogene 11; ribosomal protein S12 pseudogene 9
RPS28	22	1671	3914	ribosomal protein S28 pseudogene 6; ribosomal protein S28 pseudogene 9; ribosomal protein S28
RPL39	22	1626	3555	ribosomal protein L39 pseudogene 10; ribosomal protein L39 pseudogene 20; ribosomal protein L39 pseudogene 27; ribosomal protein L39; ribosomal protein L39 pseudogene 13; ribosomal protein L39 pseudogene 32

msmB	6	1615	4490	microseminoprotein, beta-
PABPC1	22	1584	5918	poly(A) binding protein, cytoplasmic pseudogene 5; poly(A) binding protein, cytoplasmic 1
Rps5	22	1573	3660	ribosomal protein S5
rpl23	22	1572	3612	ribosomal protein L23 pseudogene 6; ribosomal protein L23
EEF1G	22	1517	3312	eukaryotic translation elongation factor 1 gamma
TMSB4X	21	1496	3076	thymosin-like 2 (pseudogene); thymosin-like 1 (pseudogene); thymosin beta 4, X-linked
Nnat	2	1491	2053	neuronatin
Entrez3921	22	1479	3169	
rpl12	22	1450	3118	ribosomal protein L12 pseudogene 2; ribosomal protein L12 pseudogene 32; ribosomal protein L12 pseudogene 35; ribosomal protein L12 pseudogene 19; ribosomal protein L12 pseudogene 6; ribosomal protein L12; ribosomal protein L12 pseudogene 14
rps16	22	1432	3503	ribosomal protein S16 pseudogene 1; ribosomal protein S16 pseudogene 10; ribosomal protein S16
rpl29	22	1419	3862	ribosomal protein L29 pseudogene 9; ribosomal protein L29 pseudogene 12; ribosomal protein L29 pseudogene 11; ribosomal protein L29; ribosomal protein L29 pseudogene 26
rpl4	22	1404	6012	ribosomal protein L4; ribosomal protein L4 pseudogene 5; ribosomal protein L4 pseudogene 4
Rpl27	22	1391	4536	ribosomal protein L27
rps15	22	1385	4395	ribosomal protein S15 pseudogene 5; ribosomal protein S15
LOC285741	22	1384	4680	similar to tumor protein, translationally-controlled 1; tumor protein, translationally-controlled 1
rps14	22	1377	3013	ribosomal protein S14
Rplp2	22	1370	4176	ribosomal protein, large, P2 pseudogene 3; ribosomal protein, large, P2
Eef2	22	1366	3157	eukaryotic translation elongation factor 2
rpl35	22	1354	4854	ribosomal protein L35; ribosomal protein L35 pseudogene 1; ribosomal protein L35 pseudogene 2
Entrez100507537	1	1342	1342	
UBC	22	1289	2977	ubiquitin C
Entrez5757	22	1262	3678	
Cdipt	1	1227	1227	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)
rps4x	22	1218	2159	ribosomal protein S4X pseudogene 6; ribosomal protein S4X pseudogene 13; ribosomal protein S4, X-linked
rpl36	22	1210	3188	ribosomal protein L36; ribosomal protein L36 pseudogene 14
rps9	22	1196	2663	ribosomal protein S9; ribosomal protein S9 pseudogene 4
rpl11	22	1193	2253	ribosomal protein L11
H19	3	1178	2883	H19, imprinted maternally expressed transcript (non-protein coding)
RpL35A	22	1164	4167	ribosomal protein L35a
RPL18	22	1137	2242	ribosomal protein L18
Entrez2495	22	1132	2257	
rpl24	21	1114	2603	ribosomal protein L24; ribosomal protein L24 pseudogene 6
RPS15A	22	1114	2079	ribosomal protein S15a pseudogene 17; ribosomal protein S15a pseudogene 19; ribosomal protein S15a pseudogene 12; ribosomal protein S15a pseudogene 24; ribosomal protein S15a pseudogene 11; ribosomal protein S15a
rpl5	22	1104	1943	ribosomal protein L5 pseudogene 34; ribosomal protein L5 pseudogene 1; ribosomal protein L5
RPS25	22	1093	2111	ribosomal protein S25 pseudogene 8; ribosomal protein S25
RPL38	22	1087	2148	ribosomal protein L38
UBB	21	1086	4194	ubiquitin B
RPL10A	22	1079	1901	ribosomal protein L10a pseudogene 6; ribosomal protein L10a; ribosomal protein L10a pseudogene 9
rps19	22	1072	2980	ribosomal protein S19 pseudogene 3; ribosomal protein S19
rps13	21	1058	2473	ribosomal protein S13 pseudogene 8; ribosomal protein S13; ribosomal protein S13 pseudogene 2
LOC399942	22	1058	3656	hypothetical gene supported by AF081484; NM_006082; tubulin, alpha 1b

rps7	22	1049	2179	ribosomal protein S7; ribosomal protein S7 pseudogene 11; ribosomal protein S7 pseudogene 4; ribosomal protein S7 pseudogene 10
Entrez100861532	22	1046	3128	
CALR	22	1038	2181	calreticulin
TMSB10	21	1030	1928	thymosin beta 10
RDH12	1	1023	1023	retinol dehydrogenase 12 (all-trans/9-cis/11-cis)
RPL26	22	1022	2777	ribosomal protein L26 pseudogene 33; ribosomal protein L26; ribosomal protein L26 pseudogene 16; ribosomal protein L26 pseudogene 19; ribosomal protein L26 pseudogene 6
SMR3A	1	1018	1018	submaxillary gland androgen regulated protein 3A
Agr2	9	1004	2162	anterior gradient homolog 2 (Xenopus laevis)
LOC342918	2	985	1220	similar to mCG134545
Rpl23a	22	970	1924	ribosomal protein L23a pseudogene 63; ribosomal protein L23a pseudogene 75; ribosomal protein L23a pseudogene 37; ribosomal protein L23a pseudogene 65; ribosomal protein L23a pseudogene 43; ribosomal protein L23a pseudogene 44; ribosomal protein L23a
sec11c	7	963	4033	SEC11 homolog C (S. cerevisiae)
rpl6	22	947	1875	ribosomal protein L6 pseudogene 27; ribosomal protein L6 pseudogene 19; ribosomal protein L6; ribosomal protein L6 pseudogene 10
SPINK1	1	895	895	serine peptidase inhibitor, Kazal type 1
FTL	22	884	1616	similar to ferritin, light polypeptide; ferritin, light polypeptide
ndrg1	21	869	2286	N-myc downstream regulated 1
CKB	19	843	3526	creatine kinase, brain
IFI27	6	831	1798	interferon, alpha-inducible protein 27
Entrez388524	22	825	1508	
Hspb1	20	822	3350	heat shock 27kDa protein-like 2 pseudogene; heat shock 27kDa protein 1
rpl14	22	820	1857	ribosomal protein L14
nupr1	18	809	2172	nuclear protein, transcriptional regulator, 1
TARP	16	807	2551	TCR gamma alternate reading frame protein; T cell receptor gamma variable 9; T cell receptor gamma constant 1
rpl9	22	806	1986	ribosomal protein L9; ribosomal protein L9 pseudogene 25
acpP	9	798	2702	acid phosphatase, prostate
KLK2	15	794	1540	kallikrein-related peptidase 2
HSPA8	22	792	2014	heat shock 70kDa protein 8
SLC25A6	22	777	1644	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 6
SELENBP1	2	763	1325	selenium binding protein 1
ALDOA	22	757	1849	aldolase A, fructose-bisphosphate
myl6	22	754	1816	myosin, light chain 6, alkali, smooth muscle and non-muscle
HSP90AB1	22	754	1668	heat shock protein 90kDa alpha (cytosolic), class B member 1
rpl10	22	753	1558	ribosomal protein L10; ribosomal protein L10 pseudogene 15; ribosomal protein L10 pseudogene 6; ribosomal protein L10 pseudogene 16; ribosomal protein L10 pseudogene 9
IFI6	7	749	1430	interferon, alpha-inducible protein 6
Fau	22	730	1271	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed
rps18	22	722	1561	ribosomal protein S18 pseudogene 12; ribosomal protein S18 pseudogene 5; ribosomal protein S18
Ppdpf	19	716	2218	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)
rps20	22	712	1795	ribosomal protein S20
rps3	22	707	2045	ribosomal protein S3 pseudogene 3; ribosomal protein S3
CST4	2	700	1216	cystatin S
Entrez114899	1	687	687	
CEACAM5	3	685	886	carcinoembryonic antigen-related cell adhesion molecule 5
CFL1	22	684	2374	cofilin 1 (non-muscle)
Spon2	7	680	2081	spondin 2, extracellular matrix protein

Cel	1	675	675	carboxyl ester lipase (bile salt-stimulated lipase)
Cox7c	20	674	1340	cytochrome c oxidase subunit VIIc
CRABP1	1	667	667	cellular retinoic acid binding protein 1
Entrez563	7	662	1730	
CRISP3	5	645	2455	cysteine-rich secretory protein 3
LOC100130107	21	633	2016	ribosomal protein S3A pseudogene 5; ribosomal protein S3a pseudogene 47; ribosomal protein S3a pseudogene 49; ribosomal protein S3A; hypothetical LOC100131699; hypothetical LOC100130107
Entrez6161	22	631	1460	
p4hb	22	611	1189	prolyl 4-hydroxylase, beta polypeptide
HSP90AA1	22	611	1553	heat shock protein 90kDa alpha (cytosolic), class A member 2; heat shock protein 90kDa alpha (cytosolic), class A member 1
LOC439953	22	610	1170	similar to TRIMCyp; peptidylprolyl isomerase A (cyclophilin A); peptidylprolyl isomerase A (cyclophilin A)-like 3
apod	5	604	1259	apolipoprotein D
igfbp2	12	604	1376	insulin-like growth factor binding protein 2, 36kDa
Calml3	3	604	981	calmodulin-like 3
CSRP2	2	601	776	cysteine and glycine-rich protein 2
FSTL1	2	596	698	follistatin-like 1
GRP	3	595	1127	gastrin-releasing peptide
COX8A	22	592	1455	cytochrome c oxidase subunit 8A (ubiquitous)
RPL37	22	592	1914	ribosomal protein L37
Entrez563	5	592	1707	
Cox6a1	22	581	961	cytochrome c oxidase subunit VIa polypeptide 1
RPS26	22	577	1032	ribosomal protein S26 pseudogene 38; ribosomal protein S26 pseudogene 39; ribosomal protein S26 pseudogene 35; ribosomal protein S26 pseudogene 31; ribosomal protein S26 pseudogene 20; ribosomal protein S26 pseudogene 54; ribosomal protein S26 pseudogene
cotl1	5	575	829	coactosin-like 1 (Dictyostelium)
TMEM219	2	569	1004	transmembrane protein 219
gpX3	1	569	569	glutathione peroxidase 3 (plasma)
ISG15	6	566	983	ISG15 ubiquitin-like modifier
TUBA1C	22	566	1901	tubulin, alpha 1c
RN5-8S1	13	560	1464	5.8S ribosomal RNA
LOC100131044	21	557	1498	nucleophosmin 1 (nucleolar phosphoprotein B23, numatrin) pseudogene 21; hypothetical LOC100131044; similar to nucleophosmin 1; nucleophosmin (nucleolar phosphoprotein B23, numatrin)
SNAR-C3	1	540	540	small ILF3/NF90-associated RNA C3
Ceacam6	1	538	538	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
SNAR-C4	1	538	538	small ILF3/NF90-associated RNA C4
PSCA	3	537	752	prostate stem cell antigen
B2M	20	537	2475	beta-2-microglobulin
Tmeff2	9	526	1412	transmembrane protein with EGF-like and two follistatin-like domains 2
CALML5	1	521	521	calmodulin-like 5
MALAT1	18	521	1474	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding)
ATP5B	22	520	1038	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide
vstm2l	4	519	771	V-set and transmembrane domain containing 2 like
rpl31	22	509	1209	ribosomal protein L31 pseudogene 49; ribosomal protein L31 pseudogene 17; ribosomal protein L31
eno1	22	509	913	enolase 1, (alpha)
krt8	21	508	1594	keratin 8 pseudogene 9; similar to keratin 8; keratin 8
TPI1	22	504	1237	TPI1 pseudogene; triosephosphate isomerase 1
Ndufa13	22	501	1141	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 13

C10orf116	7	494	954	chromosome 10 open reading frame 116
EEF1A2	8	490	974	eukaryotic translation elongation factor 1 alpha 2
RAMP1	6	490	1031	receptor (G protein-coupled) activity modifying protein 1
PTMS	22	485	1538	parathymosin
BST2	7	483	918	NPC-A-7; bone marrow stromal cell antigen 2
KLK4	15	481	1349	kallikrein-related peptidase 4
vgll3	1	480	480	vestigial like 3 (Drosophila)
Hsp90b1	21	476	1157	heat shock protein 90kDa beta (Grp94), member 1
MT2A	12	475	1094	metallothionein 2A
KRT19	14	471	1010	keratin 19
KRT18	22	470	1280	keratin 18; keratin 18 pseudogene 26; keratin 18 pseudogene 19
celP	1	470	470	carboxyl ester lipase pseudogene
Fabp7	1	467	467	fatty acid binding protein 7, brain
LdhA	21	466	974	lactate dehydrogenase A
RPS24	21	462	1089	ribosomal protein S24
Dhrs2	4	461	906	dehydrogenase/reductase (SDR family) member 2
MAGEH1	2	459	708	melanoma antigen family H, 1
PTN	2	458	724	pleiotrophin
VCX3A	1	457	457	variable charge, X-linked 3A
VCX3B	1	454	454	variable charge, X-linked 3B
Gdf15	13	452	1115	growth differentiation factor 15
RPL13AP20	18	448	1121	ribosomal protein L13a pseudogene 20; ribosomal protein L13a pseudogene 22; ribosomal protein L13a pseudogene 25
PSAP	21	448	1624	prosaposin
Ascl1	4	445	540	achaete-scute complex homolog 1 (Drosophila)
Slpi	2	444	737	secretory leukocyte peptidase inhibitor
YWHAZ	20	443	1043	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide
Rpl34	20	442	953	ribosomal protein L34
Pcsk1n	4	438	638	proprotein convertase subtilisin/kexin type 1 inhibitor
Ube2e3	1	435	435	ubiquitin-conjugating enzyme E2E 3 (UBC4/5 homolog, yeast)
LOC652797	22	432	780	similar to Pyruvate kinase, isozymes M1/M2 (Pyruvate kinase muscle isozyme) (Cytosolic thyroid hormone-binding protein) (CTHBP) (THBP1); pyruvate kinase, muscle
Chchd2	22	430	720	coiled-coil-helix-coiled-coil-helix domain containing 2; similar to coiled-coil-helix-coiled-coil-helix domain containing 2
C19orf48	18	430	1243	chromosome 19 open reading frame 48
RGS2	4	430	870	regulator of G-protein signaling 2, 24kDa
ybx1	22	427	1005	Y box binding protein 1
NDUFB9	22	423	1405	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9, 22kDa
LRRC4B	2	422	470	leucine rich repeat containing 4B
Krt7	1	422	422	keratin 7
COX6C	17	420	1267	cytochrome c oxidase subunit VIc
Cd24	17	420	1182	CD24 molecule; CD24 molecule-like 4
SLC45A3	9	420	980	solute carrier family 45, member 3
APP	8	417	885	amyloid beta (A4) precursor protein
oaz1	22	416	792	ornithine decarboxylase antizyme 1
CLDN3	15	414	826	claudin 3
TUBA1A	13	414	1488	tubulin, alpha 1a
sez6l2	2	407	695	seizure related 6 homolog (mouse)-like 2
NDUFA4L2	2	406	442	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2
Hist1h2ac	1	405	405	histone cluster 1, H2ac
SNCG	1	405	405	synuclein, gamma (breast cancer-specific protein 1)

CHGA	2	403	550	chromogranin A (parathyroid secretory protein 1)
SLC4A4	1	402	402	solute carrier family 4, sodium bicarbonate cotransporter, member 4
PEBP1	22	401	879	phosphatidylethanolamine binding protein 1
MME	1	400	400	membrane metallo-endopeptidase
arg2	3	398	706	arginase, type II
Entrez23521	16	398	720	
RPS27A	20	397	697	ribosomal protein S27a pseudogene 12; ribosomal protein S27a; ribosomal protein S27a pseudogene 11; ribosomal protein S27a pseudogene 16
gp2	3	392	723	glycoprotein 2 (zymogen granule membrane)
TAGLN2	19	387	961	transgelin 2
CST2	1	386	386	cystatin SA
SNAR-H	1	385	385	small ILF3/NF90-associated RNA H
TIMP1	3	384	581	TIMP metallopeptidase inhibitor 1
Mdk	13	384	744	midkine (neurite growth-promoting factor 2)
Pla2g16	1	384	384	phospholipase A2, group XVI
Entrez7388	22	383	862	
HSPD1	19	382	917	heat shock 60kDa protein 1 (chaperonin) pseudogene 5; heat shock 60kDa protein 1 (chaperonin) pseudogene 6; heat shock 60kDa protein 1 (chaperonin) pseudogene 1; heat shock 60kDa protein 1 (chaperonin) pseudogene 4; heat shock 60kDa protein 1 (chaperonin)
GSTP1	11	381	715	glutathione S-transferase pi 1
RPS4Y1	16	379	754	ribosomal protein S4, Y-linked 1
ACSL1	1	377	377	acyl-CoA synthetase long-chain family member 1
crip1	6	377	623	cysteine-rich protein 1 (intestinal)
COX4I1	21	377	1433	cytochrome c oxidase subunit IV isoform 1
Arf1	22	376	811	ADP-ribosylation factor 1
srprb	2	376	551	signal recognition particle receptor, B subunit
Kctd13	1	376	376	potassium channel tetramerisation domain containing 13
MT1X	7	373	808	metallothionein 1X
Lrrc26	5	372	556	leucine rich repeat containing 26
NKX3-1	18	371	748	NK3 homeobox 1
Tff3	5	370	1190	trefoil factor 3 (intestinal)
RPL15	20	368	936	ribosomal protein L15 pseudogene 22; ribosomal protein L15 pseudogene 18; ribosomal protein L15 pseudogene 17; ribosomal protein L15 pseudogene 3; ribosomal protein L15 pseudogene 7; ribosomal protein L15
COX6B1	22	367	844	cytochrome c oxidase subunit Vib polypeptide 1 (ubiquitous)
Cst3	20	366	1096	cystatin C
TUBB2C	22	364	641	tubulin, beta 2C
Entrez100873969	1	364	364	
PGK1	18	361	1002	phosphoglycerate kinase 1
GLO1	8	359	908	glyoxalase I
FASN	12	357	872	fatty acid synthase
LOC440917	22	356	687	similar to 14-3-3 protein epsilon (14-3-3E) (Mitochondrial import stimulation factor L subunit) (MSF L); tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide
SLC25A5	21	354	682	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5; solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5 pseudogene 8
C8orf55	1	352	352	chromosome 8 open reading frame 55
COX5B	22	352	515	cytochrome c oxidase subunit Vb
GAS5	19	350	767	growth arrest-specific 5 (non-protein coding)
fn1	4	350	850	fibronectin 1
Entrez3303	9	350	758	
CCDC72	20	348	944	coiled-coil domain containing 72; hypothetical LOC729973; hypothetical LOC728416

CT45A1	1	347	347	cancer/testis antigen family 45, member A1
Ar	3	347	457	androgen receptor
Entrez805	19	346	644	
Eif3e	18	346	1221	eukaryotic translation initiation factor 3, subunit E
ifitm3	6	345	687	interferon induced transmembrane protein 3 (1-8U)
Steap2	1	345	345	six transmembrane epithelial antigen of the prostate 2
Cox7b	20	340	701	cytochrome c oxidase subunit VIIb
DEGS1	4	340	760	degenerative spermatocyte homolog 1, lipid desaturase (Drosophila)
Spint2	21	340	666	serine peptidase inhibitor, Kunitz type, 2
GPR172A	1	339	339	G protein-coupled receptor 172A
tubb2b	4	339	649	tubulin, beta 2B
HMGN2	21	338	852	hypothetical LOC729505; similar to hCG2040565; high-mobility group nucleosomal binding domain 2; similar to high-mobility group nucleosomal binding domain 2
clu	4	337	443	clusterin
esd	2	336	421	esterase D/formylglutathione hydrolase
EDF1	22	335	754	endothelial differentiation-related factor 1
rpl28	16	335	958	ribosomal protein L28
PIGR	3	335	562	polymeric immunoglobulin receptor
CD81	19	333	1001	CD81 molecule
Insm1	3	333	557	insulinoma-associated 1
rdh11	9	333	698	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)
TSPAN1	9	332	668	tetraspanin 1
DHRS7	9	331	692	dehydrogenase/reductase (SDR family) member 7
epcam	18	330	594	epithelial cell adhesion molecule
MT1G	8	330	655	metallothionein 1G
ASB9	1	329	329	ankyrin repeat and SOCS box-containing 9
LCP1	6	328	673	lymphocyte cytosolic protein 1 (L-plastin)
pfn1	22	328	819	profilin 1
ORM2	1	328	328	orosomucoid 2
Hes6	4	326	675	hairy and enhancer of split 6 (Drosophila)
Eef1b2	20	326	708	eukaryotic translation elongation factor 1 beta 2; eukaryotic translation elongation factor 1 beta 2-like
Entrez3304	9	326	677	
FLJ38028	5	325	497	hypothetical gene supported by AK095347
MYBPC1	4	324	823	myosin binding protein C, slow type
DBI	12	322	955	diazepam binding inhibitor (GABA receptor modulator, acyl-Coenzyme A binding protein)
PPAP2A	8	322	889	phosphatidic acid phosphatase type 2A
aplp2	19	322	1139	amyloid beta (A4) precursor-like protein 2
Uchl1	4	321	443	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)
Neat1	14	320	728	non-protein coding RNA 84
GATA2	1	319	319	GATA binding protein 2
ncl	21	319	706	nucleolin
tmbim6	21	318	511	transmembrane BAX inhibitor motif containing 6
RPL36AL	19	317	937	ribosomal protein L36a-like
Camk2n1	8	316	804	calcium/calmodulin-dependent protein kinase II inhibitor 1
PRDX2	21	315	540	peroxiredoxin 2
MARCKSL1	21	315	687	MARCKS-like 1
CRYAB	2	315	427	crystallin, alpha B
DCXR	18	314	551	dicarbonyl/L-xylulose reductase
ERLEC1	1	314	314	chromosome 2 open reading frame 30
PRAC	14	313	687	prostate cancer susceptibility candidate

RPS29	20	313	621	ribosomal protein S29 pseudogene 11; ribosomal protein S29 pseudogene 16; ribosomal protein S29 pseudogene 17; ribosomal protein S29 pseudogene 3; ribosomal protein S29 pseudogene 9; ribosomal protein S29
Eif1	21	313	531	similar to eukaryotic translation initiation factor 1; eukaryotic translation initiation factor 1
tmem8a	1	313	313	transmembrane protein 8A
H1fx	13	312	636	H1 histone family, member X
RGS1	3	312	424	regulator of G-protein signaling 1
IGFBP5	1	310	310	insulin-like growth factor binding protein 5
Tmprss2	13	310	710	transmembrane protease, serine 2
PDIA3	20	309	785	protein disulfide isomerase family A, member 3
scube2	2	309	419	signal peptide, CUB domain, EGF-like 2
CD9	19	308	501	CD9 molecule
MVP	1	306	306	major vault protein
Entrez10016	1	303	303	
eIF3h	19	303	570	eukaryotic translation initiation factor 3, subunit H
scd	9	302	1049	stearoyl-CoA desaturase (delta-9-desaturase)
EEF1D	17	302	650	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)
cyc1	21	300	764	cytochrome c-1
Xbp1	16	300	752	X-box binding protein 1
CLDN4	17	299	528	claudin 4
Ran	22	299	503	RAN, member RAS oncogene family
Tspan8	7	299	811	tetraspanin 8
CAPS	1	298	298	calcyphosine
WNT11	1	297	297	wingless-type MMTV integration site family, member 11
WNK4	1	297	297	WNK lysine deficient protein kinase 4
SNORD104	3	296	355	small nucleolar RNA, C/D box 104
ZNF444	1	296	296	zinc finger protein 444
scgn	1	296	296	secretagogin, EF-hand calcium binding protein
Gtf3c6	4	295	487	general transcription factor IIIC, polypeptide 6, alpha 35kDa
FOLH1	7	295	532	folate hydrolase (prostate-specific membrane antigen) 1
MS4A8B	2	294	422	membrane-spanning 4-domains, subfamily A, member 8B
ppyr1	1	293	293	pancreatic polypeptide receptor 1
ATP2A3	3	293	378	ATPase, Ca++ transporting, ubiquitous
PSMB4	22	293	518	proteasome (prosome, macropain) subunit, beta type, 4
SEPW1	10	292	734	selenoprotein W, 1
S100A11	20	291	709	S100 calcium binding protein A11; S100 calcium binding protein A11 pseudogene
FAM128A	11	291	696	family with sequence similarity 128, member A
NDUFA1	18	290	738	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1, 7.5kDa
ST14	10	290	426	suppression of tumorigenicity 14 (colon carcinoma)
LOC100130794	19	288	586	similar to NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase); NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase)
Pdia4	13	288	640	protein disulfide isomerase family A, member 4
ywhaq	20	288	509	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide
HNRNPA2B1	21	288	634	heterogeneous nuclear ribonucleoprotein A2/B1
RPL13	15	287	678	ribosomal protein L13 pseudogene 12; ribosomal protein L13
Entrez1984	20	287	612	
NME4	15	286	423	non-metastatic cells 4, protein expressed in
HINT1	20	286	687	histidine triad nucleotide binding protein 1
H1f0	15	285	475	H1 histone family, member 0
MAZ	22	285	708	MYC-associated zinc finger protein (purine-binding transcription factor)

itm2b	6	284	578	integral membrane protein 2B
SOD1	22	284	438	superoxide dismutase 1, soluble
AMD1	5	284	367	adenosylmethionine decarboxylase 1
SNRPB	19	284	465	small nuclear ribonucleoprotein polypeptides B and B1
sec61g	13	284	486	Sec61 gamma subunit
NDUFS6	17	284	678	NADH dehydrogenase (ubiquinone) Fe-S protein 6, 13kDa (NADH-coenzyme Q reductase)
ERGIC1	17	283	488	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
PHGDH	6	282	555	phosphoglycerate dehydrogenase
SYNGR2	17	281	612	synaptogyrin 2
ddit4	9	281	601	DNA-damage-inducible transcript 4
S100P	7	281	387	S100 calcium binding protein P
Pnma5	4	281	464	paraneoplastic antigen like 5
Canx	16	280	562	calnexin
Dpysl3	3	280	501	dihydropyrimidinase-like 3
ALDH1A3	1	279	279	aldehyde dehydrogenase 1 family, member A3
SRPR	1	279	279	signal recognition particle receptor (docking protein)
ANXA2P2	1	279	279	annexin A2 pseudogene 2
odam	1	278	278	odontogenic, ameloblast asssociated
Ergic3	20	278	1609	ERGIC and golgi 3
SHFM1	21	278	535	split hand/foot malformation (ectrodactyly) type 1
HPGD	2	278	382	hydroxyprostaglandin dehydrogenase 15-(NAD)
mdh2	21	278	528	malate dehydrogenase 2, NAD (mitochondrial)
Sat1	15	278	696	spermidine/spermine N1-acetyltransferase 1
Fabp5	7	277	702	fatty acid binding protein 5-like 2; fatty acid binding protein 5 (psoriasis-associated); fatty acid binding protein 5-like 8; fatty acid binding protein 5-like 7; fatty acid binding protein 5-like 9
S100A10	5	277	474	S100 calcium binding protein A10
RPN1	19	276	912	ribophorin I
Ndufb7	15	275	412	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 7, 18kDa
gnb2	19	275	447	guanine nucleotide binding protein (G protein), beta polypeptide 2
GOLM1	13	274	437	golgi membrane protein 1
CHPF	1	274	274	chondroitin polymerizing factor
DHCR24	13	274	623	24-dehydrocholesterol reductase
FKBP1A	4	273	349	FK506 binding protein 1A, 12kDa
SPDEF	14	273	819	SAM pointed domain containing ets transcription factor
WFDC2	4	273	316	WAP four-disulfide core domain 2
H2AFZ	20	272	561	H2A histone family, member Z
STEAP1	8	272	782	six transmembrane epithelial antigen of the prostate 1
RAD21	6	271	432	RAD21 homolog (S. pombe)
HSPA5	19	271	558	hypothetical gene supported by AF216292; NM_005347; heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
Gnas	22	270	798	GNAS complex locus
UBL5	22	270	551	ubiquitin-like 5
metrn	2	270	335	meteorin, glial cell differentiation regulator
EIF4G2	16	270	659	eukaryotic translation initiation factor 4 gamma, 2
bsg	16	268	765	basigin (Ok blood group)
NPTX1	1	267	267	neuronal pentraxin I
emp1	1	267	267	epithelial membrane protein 1
Entrez100463486	7	267	786	
LOC391358	22	267	593	tRNA methyltransferase 11-2 homolog (S. cerevisiae); similar to CG12975
Ssr4	17	267	768	signal sequence receptor, delta (translocon-associated protein delta)
BCYRN1	4	266	383	brain cytoplasmic RNA 1 (non-protein coding)

HSPE1	3	266	376	heat shock 10kDa protein 1 (chaperonin 10)
Aprt	13	266	534	adenine phosphoribosyltransferase
Tubb2a	5	266	545	tubulin, beta 2A
Entrez100462981	14	266	790	
TM4SF1	4	266	458	transmembrane 4 L six family member 1
NCRNA00188	11	265	401	chromosome 17 open reading frame 45
capns1	22	264	530	calpain, small subunit 1
grina	17	264	787	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)
ppp1r14b	20	263	456	protein phosphatase 1, regulatory (inhibitor) subunit 14B
LGALS3BP	7	263	452	lectin, galactoside-binding, soluble, 3 binding protein
CHPT1	3	261	406	choline phosphotransferase 1
FLNB	1	261	261	filamin B, beta (actin binding protein 278)
Entrez689	15	261	555	
Impdh2	11	261	481	IMP (inosine monophosphate) dehydrogenase 2
VCX	1	260	260	variable charge, X-linked
Akr1c1	1	259	259	aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase)
aes	19	259	633	amino-terminal enhancer of split
CD99	12	259	689	CD99 molecule
HOXB13	12	259	448	homeobox B13
GPX4	16	259	626	glutathione peroxidase 4 (phospholipid hydroperoxidase)
Cyp27a1	1	258	258	cytochrome P450, family 27, subfamily A, polypeptide 1
Idh3g	1	257	257	isocitrate dehydrogenase 3 (NAD+) gamma
ssr2	20	256	460	signal sequence receptor, beta (translocon-associated protein beta)
HIST1H2BK	7	254	428	histone cluster 1, H2bk
RUVBL2	3	254	353	RuvB-like 2 (E. coli)
NDUFB10	19	254	675	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10, 22kDa
Entrez4493	9	254	388	
Cbr1	1	254	254	carbonyl reductase 1
uba52	20	254	652	ubiquitin A-52 residue ribosomal protein fusion product 1
Gbas	1	254	254	glioblastoma amplified sequence
Pcbd1	6	254	432	pterin-4 alpha-carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha
nonO	19	254	391	non-POU domain containing, octamer-binding
srp9	11	253	378	signal recognition particle 9-like 1; signal recognition particle 9kDa
Fam162a	13	253	407	family with sequence similarity 162, member A
ZG16B	1	253	253	zymogen granule protein 16 homolog B (rat)
nme3	2	253	267	non-metastatic cells 3, protein expressed in
PSMA7	22	252	548	proteasome (prosome, macropain) subunit, alpha type, 7
Rhoa	16	252	505	ras homolog gene family, member A
TXN	16	251	450	thioredoxin
ODC1	15	251	614	ornithine decarboxylase 1
Phpt1	2	251	259	phosphohistidine phosphatase 1
Golph3	5	251	421	golgi phosphoprotein 3 (coat-protein)
SLC25A3	18	251	504	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3
Tomm7	17	250	467	translocase of outer mitochondrial membrane 7 homolog (yeast)
IDH2	19	250	405	isocitrate dehydrogenase 2 (NADP+), mitochondrial
FADS2	12	249	526	fatty acid desaturase 2
C12orf57	11	249	391	chromosome 12 open reading frame 57
BCAM	9	249	390	basal cell adhesion molecule (Lutheran blood group)
TPH1	1	249	249	tryptophan hydroxylase 1

Laptm4b	6	248	492	lysosomal protein transmembrane 4 beta
PFDN5	21	248	411	prefoldin subunit 5
aldoc	1	247	247	aldolase C, fructose-bisphosphate
atp5h	18	247	385	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d
MAL2	5	247	473	mal, T-cell differentiation protein 2
Ggct	9	247	732	gamma-glutamyl cyclotransferase
akr1c3	3	247	335	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
HERPUD1	9	246	454	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1
gpaa1	8	246	618	glycosylphosphatidylinositol anchor attachment protein 1 homolog (yeast)
BNIP3	6	245	376	BCL2/adenovirus E1B 19kDa interacting protein 3
Fkbp10	3	245	446	FK506 binding protein 10, 65 kDa
Entrez29997	13	244	370	
CKS2	6	244	529	CDC28 protein kinase regulatory subunit 2
Asna1	1	243	243	arsA arsenite transporter, ATP-binding, homolog 1 (bacterial)
HOXB9	1	243	243	homeobox B9
Hnrnpk	21	242	376	heterogeneous nuclear ribonucleoprotein K; similar to heterogeneous nuclear ribonucleoprotein K
PRDX1	18	242	648	peroxiredoxin 1
KIAA0114	10	242	395	KIAA0114
Ube2s	11	242	373	ubiquitin-conjugating enzyme E2S
S100A6	4	241	305	S100 calcium binding protein A6
FDFT1	3	241	344	farnesyl-diphosphate farnesyltransferase 1
NANS	10	241	416	N-acetylneuraminic acid synthase
Prdx4	14	241	373	peroxiredoxin 4
TRIM28	17	241	372	tripartite motif-containing 28
LOC642590	10	240	388	spermine synthase; similar to spermine synthase
Egr1	1	240	240	early growth response 1
SDHA	5	240	469	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)
NEFH	2	239	266	neurofilament, heavy polypeptide
Atp5i	21	239	429	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit E
KLK1	3	238	305	kallikrein 1
LOC119358	22	238	378	small nuclear ribonucleoprotein D2 polypeptide 16.5kDa; similar to hCG2040270
prkcsh	19	238	386	protein kinase C substrate 80K-H
MYL12B	15	237	512	myosin, light chain 12B, regulatory
cope	17	237	381	coatomer protein complex, subunit epsilon
EIF4A2	11	237	315	similar to eukaryotic translation initiation factor 4A2; eukaryotic translation initiation factor 4A, isoform 2
ncapd3	1	237	237	non-SMC condensin II complex, subunit D3
FBL	14	237	574	fibrillarin
UCP2	6	237	301	uncoupling protein 2 (mitochondrial, proton carrier)
IDH1	9	237	429	isocitrate dehydrogenase 1 (NADP+), soluble
PDIA3P	1	237	237	protein disulfide isomerase family A, member 3 pseudogene
Entrez302	9	237	612	
arf5	19	237	499	ADP-ribosylation factor 5
Adamts1	1	236	236	ADAM metallopeptidase with thrombospondin type 1 motif, 1
grn	9	236	516	granulin
rpl22	19	235	438	ribosomal protein L22 pseudogene 11; ribosomal protein L22
LGALS1	4	235	292	lectin, galactoside-binding, soluble, 1
BLVRB	3	235	248	biliverdin reductase B (flavin reductase (NADPH))
tdo2	2	235	316	tryptophan 2,3-dioxygenase

tmed9	21	235	372	transmembrane emp24 protein transport domain containing 9
Atp5a1	15	235	393	ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle
Naca	16	235	339	nascent polypeptide-associated complex alpha subunit
TGFB2	1	234	234	transforming growth factor, beta 2
ldhb	8	234	413	lactate dehydrogenase B
LAS1L	1	234	234	LAS1-like (S. cerevisiae)
NSMCE2	1	233	233	non-SMC element 2, MMS21 homolog (S. cerevisiae)
mRpL41	11	233	355	mitochondrial ribosomal protein L41
RHOB	4	233	459	ras homolog gene family, member B
ANXA1	5	233	292	annexin A1
PPP1R16A	1	233	233	protein phosphatase 1, regulatory (inhibitor) subunit 16A
pfn2	5	233	289	profilin 2
EIF3L	13	233	338	eukaryotic translation initiation factor 3, subunit L
mfsd3	1	233	233	major facilitator superfamily domain containing 3
fxyd3	9	232	513	FXYD domain containing ion transport regulator 3
CPE	7	232	463	carboxypeptidase E
TCF25	1	232	232	transcription factor 25 (basic helix-loop-helix)
MICAL2	1	232	232	microtubule associated monoxygenase, calponin and LIM domain containing 2
RAB1B	22	232	554	RAB1B, member RAS oncogene family
LOC388564	2	232	275	hypothetical protein LOC388564
Alcam	2	231	329	hypothetical protein LOC100133690; activated leukocyte cell adhesion molecule
ST6GAL1	2	231	282	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1
Basp1	3	231	242	brain abundant, membrane attached signal protein 1
GPNMB	4	231	353	glycoprotein (transmembrane) nmb
ATP5G2	20	231	349	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)
CTSZ	6	230	376	cathepsin Z
Fgfrl1	2	230	295	fibroblast growth factor receptor-like 1
Hmg20b	6	230	363	high-mobility group 20B
ATP6V0C	16	230	407	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
Pld3	2	230	301	phospholipase D family, member 3
PARK7	20	229	432	Parkinson disease (autosomal recessive, early onset) 7
BZW2	1	229	229	basic leucine zipper and W2 domains 2
Fam128b	2	229	280	family with sequence similarity 128, member B
COX5A	17	229	330	cytochrome c oxidase subunit Va
Mbip	1	228	228	MAP3K12 binding inhibitory protein 1
PGRMC1	1	228	228	progesterone receptor membrane component 1
Prdx5	21	228	512	peroxiredoxin 5
pgam1	19	228	397	phosphoglycerate mutase 1 (brain)
pfkp	2	228	295	phosphofructokinase, platelet
Spock1	2	228	230	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1
DNAJB1	10	228	501	DnaJ (Hsp40) homolog, subfamily B, member 1
Uqcrc1	18	227	472	ubiquinol-cytochrome c reductase core protein I
PEG10	3	227	343	paternally expressed 10
NUCB1	7	227	415	nucleobindin 1
Ctag2	2	227	263	cancer/testis antigen 2
JUND	7	227	331	jun D proto-oncogene
Sharpin	1	226	226	SHANK-associated RH domain interactor
kcnj8	1	226	226	potassium inwardly-rectifying channel, subfamily J, member 8
	2	225	243	
sdc1	5	225	407	syndecan 1

Hist1h1c	6	225	426	histone cluster 1, H1c
atp5o	18	225	334	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit
HMGB2	8	225	484	high-mobility group box 2
ARHGDIA	13	225	341	Rho GDP dissociation inhibitor (GDI) alpha
nsmce1	3	225	365	non-SMC element 1 homolog (S. cerevisiae)
FKBP8	18	225	364	FK506 binding protein 8, 38kDa
ZNF664	1	224	224	zinc finger protein 664
HSD17B6	1	224	224	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse)
ilf2	9	224	373	interleukin enhancer binding factor 2, 45kDa
Entrez6613	18	223	493	
SHISA2	2	223	228	shisa homolog 2 (Xenopus laevis)
gc	1	223	223	group-specific component (vitamin D binding protein)
HSPA9	10	223	303	heat shock 70kDa protein 9 (mortalin)
TSPAN13	4	223	320	tetraspanin 13
GABARAP	17	223	503	GABA(A) receptor-associated protein
NUDT8	2	222	281	nudix (nucleoside diphosphate linked moiety X)-type motif 8
Fam3b	4	222	371	family with sequence similarity 3, member B
Entrez653162	13	222	393	
mccc2	6	222	421	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
PPP1R1B	7	222	315	protein phosphatase 1, regulatory (inhibitor) subunit 1B
C7orf50	3	221	353	chromosome 7 open reading frame 50
PUF60	10	221	512	poly-U binding splicing factor 60KDa
LOC100129773	1	221	221	hypothetical LOC100129773; ralA binding protein 1
CBX3	7	221	514	similar to chromobox homolog 3; chromobox homolog 3 (HP1 gamma homolog, Drosophila)
Ly6e	9	221	333	lymphocyte antigen 6 complex, locus E
CDK2AP2	1	221	221	cyclin-dependent kinase 2 associated protein 2
CTSD	12	221	391	cathepsin D
ITM2C	4	221	255	integral membrane protein 2C
SEC61A1	14	221	387	Sec61 alpha 1 subunit (S. cerevisiae)
por	1	220	220	P450 (cytochrome) oxidoreductase
Cps1	1	220	220	carbamoyl-phosphate synthetase 1, mitochondrial
CYP1B1	3	220	299	cytochrome P450, family 1, subfamily B, polypeptide 1
Ppap2c	4	220	302	phosphatidic acid phosphatase type 2C
LOC100131294	1	220	220	RAB13, member RAS oncogene family; similar to hCG24991
SNHG5	7	220	347	small nucleolar RNA host gene 5 (non-protein coding)
c11orf10	18	220	365	chromosome 11 open reading frame 10
LOC646817	16	220	487	SET nuclear oncogene; similar to SET translocation
PMEPA1	8	220	432	prostate transmembrane protein, androgen induced 1
MIPEP	4	220	316	mitochondrial intermediate peptidase
PPP2R1A	14	220	397	protein phosphatase 2 (formerly 2A), regulatory subunit A, alpha isoform
CXCL17	1	219	219	chemokine (C-X-C motif) ligand 17
MRPS26	8	219	337	mitochondrial ribosomal protein S26
Ifitm1	1	219	219	interferon induced transmembrane protein 1 (9-27)
rps23	17	218	403	ribosomal protein S23
RPS19BP1	2	218	287	ribosomal protein S19 binding protein 1
SNHG8	10	217	426	small nucleolar RNA host gene 8 (non-protein coding)
APOA1BP	7	217	387	apolipoprotein A-I binding protein
TM9SF3	3	217	272	transmembrane 9 superfamily member 3
dynll1	20	217	462	dynein, light chain, LC8-type 1
Dnaja1	14	217	336	DnaJ (Hsp40) homolog, subfamily A, member 1

Entrez3021	15	217	367	
ATP5G1	14	216	360	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C1 (subunit 9)
arl6ip1	15	216	368	ADP-ribosylation factor-like 6 interacting protein 1
HMGN1	16	216	496	high-mobility group nucleosome binding domain 1
etfB	4	216	329	electron-transfer-flavoprotein, beta polypeptide
OR51E2	3	216	298	olfactory receptor, family 51, subfamily E, member 2
COX7A2	14	216	309	cytochrome c oxidase subunit VIIa polypeptide 2 (liver)
SLC25A39	18	216	344	solute carrier family 25, member 39
NDUFA3	16	215	327	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 3, 9kDa
SNRNP70	5	215	290	small nuclear ribonucleoprotein 70kDa (U1)
PCBP2	18	215	609	poly(rC) binding protein 2
ARF4	2	215	280	ADP-ribosylation factor 4
lbh	3	215	278	limb bud and heart development homolog (mouse)
HDLBP	9	215	356	high density lipoprotein binding protein
ARPC3	12	215	312	similar to actin related protein 2/3 complex subunit 3; hypothetical LOC729841; actin related protein 2/3 complex, subunit 3, 21kDa
MUC1	1	215	215	mucin 1, cell surface associated
sorD	8	214	456	sorbitol dehydrogenase
DSTN	17	214	428	destrin (actin depolymerizing factor)
eif4h	17	214	298	eukaryotic translation initiation factor 4H
Adrm1	5	214	253	adhesion regulating molecule 1
SEC61B	18	213	443	Sec61 beta subunit
Atp1b1	5	213	318	ATPase, Na+/K+ transporting, beta 1 polypeptide
PKDCC	1	212	212	protein kinase-like protein SgK493
maf1	7	212	334	MAF1 homolog (S. cerevisiae)
GNB1	15	212	714	guanine nucleotide binding protein (G protein), beta polypeptide 1
WDR13	1	212	212	WD repeat domain 13
DEFB1	1	212	212	defensin, beta 1
ABHD2	3	212	299	abhydrolase domain containing 2
ROMO1	14	211	368	reactive oxygen species modulator 1
HIGD2A	9	211	313	HIG1 hypoxia inducible domain family, member 2A
Ptges3	15	210	374	prostaglandin E synthase 3 (cytosolic)
NDUFB1	10	210	348	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa
cxcr7	1	210	210	chemokine (C-X-C motif) receptor 7
Nrip3	1	210	210	nuclear receptor interacting protein 3
psmb1	13	210	557	proteasome (prosome, macropain) subunit, beta type, 1
AP2M1	19	210	346	adaptor-related protein complex 2, mu 1 subunit
Hnrnpab	16	210	431	heterogeneous nuclear ribonucleoprotein A/B
Sox4	5	210	327	SRY (sex determining region Y)-box 4
VPS28	11	210	421	vacuolar protein sorting 28 homolog (S. cerevisiae)
S100A14	2	210	300	S100 calcium binding protein A14
ALOX15B	3	210	273	arachidonate 15-lipoxygenase, type B
Wbscr22	1	210	210	Williams Beuren syndrome chromosome region 22
SDF2L1	5	210	252	stromal cell-derived factor 2-like 1
STMN1	2	210	281	stathmin 1
USMG5	2	210	273	up-regulated during skeletal muscle growth 5 homolog (mouse)
gadd45gip1	4	209	231	growth arrest and DNA-damage-inducible, gamma interacting protein 1
dsp	3	209	265	desmoplakin
EIF4EBP1	4	209	320	eukaryotic translation initiation factor 4E binding protein 1
rac1	12	209	410	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
Atp5d	9	209	299	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit

ADM	2	209	265	adrenomedullin
MFAP2	1	208	208	microfibrillar-associated protein 2
tspO	3	208	261	translocator protein (18kDa)
TMEM66	9	208	329	transmembrane protein 66
SEMA3C	2	208	287	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3C
Ndufs8	15	208	365	NADH dehydrogenase (ubiquinone) Fe-S protein 8, 23kDa (NADH-coenzyme Q reductase)
PABPC3	2	207	263	poly(A) binding protein, cytoplasmic 3
mrpl13	1	207	207	mitochondrial ribosomal protein L13
HMGB1	12	207	364	high-mobility group box 1; high-mobility group box 1-like 10
CT45A3	1	207	207	cancer/testis antigen family 45, member A3
MAL	1	207	207	mal, T-cell differentiation protein
Atp6v0b	14	207	388	ATPase, H+ transporting, lysosomal 21kDa, V0 subunit b
stip1	11	207	267	stress-induced-phosphoprotein 1
LOC100133673	1	207	207	tubulin, gamma 1; similar to Tubulin, gamma 1
NXPH4	4	207	270	neurexophilin 4
Itm2a	4	207	342	integral membrane protein 2A
DDOST	14	207	653	dolichyl-diphosphooligosaccharide-protein glycosyltransferase
PPP4C	5	206	353	protein phosphatase 4 (formerly X), catalytic subunit
crabp2	4	206	307	cellular retinoic acid binding protein 2
eif3d	5	206	301	eukaryotic translation initiation factor 3, subunit D
Fam50a	1	206	206	family with sequence similarity 50, member A
Cant1	5	206	244	calcium activated nucleotidase 1
STARD3NL	2	206	230	STARD3 N-terminal like
Tppp3	1	206	206	tubulin polymerization-promoting protein family member 3
CCDC74A	1	206	206	coiled-coil domain containing 74A
Snhg6	11	206	435	small nucleolar RNA host gene 6 (non-protein coding)
Atp5c1	12	206	362	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1
DECR1	1	205	205	2,4-dienoyl CoA reductase 1, mitochondrial
GPI	15	205	315	glucose phosphate isomerase
POLR2L	12	205	349	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa
VDAC1	14	205	499	voltage-dependent anion channel 1; similar to voltage-dependent anion channel 1
OST4	16	205	415	dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 4
Vcp	11	205	394	valosin-containing protein
KLHDC3	1	205	205	kelch domain containing 3
NPDC1	9	204	311	neural proliferation, differentiation and control, 1
Echs1	12	204	263	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial
LAPTM4A	4	204	274	lysosomal protein transmembrane 4 alpha
pcnA	5	204	287	proliferating cell nuclear antigen
HINT2	3	204	250	histidine triad nucleotide binding protein 2
manf	13	204	471	mesencephalic astrocyte-derived neurotrophic factor
slc9a3r2	1	204	204	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2
ATF4	18	204	388	activating transcription factor 4 (tax-responsive enhancer element B67); activating transcription factor 4C
CHKA	1	203	203	choline kinase alpha
ANPEP	3	203	250	alanyl (membrane) aminopeptidase
cldn7	2	203	261	claudin 7
Prdx6	14	203	419	peroxiredoxin 6
tmem54	5	203	282	transmembrane protein 54
DYNLRB1	19	203	432	dynein, light chain, roadblock-type 1
MAGED2	6	203	403	melanoma antigen family D, 2

dpp7	5	202	263	dipeptidyl-peptidase 7
Entrez541465	2	202	273	
Uqcr11	5	202	236	ubiquinol-cytochrome c reductase, 6.4kDa subunit
FRZB	1	202	202	frizzled-related protein
CCDC124	5	202	261	coiled-coil domain containing 124
HEBP2	6	202	278	heme binding protein 2
ATP6V0E1	9	202	337	ATPase, H+ transporting, lysosomal 9kDa, V0 subunit e1
c16orf13	5	202	278	chromosome 16 open reading frame 13
lamp1	8	202	306	lysosomal-associated membrane protein 1
PFKL	5	201	268	phosphofructokinase, liver
rabac1	4	201	286	Rab acceptor 1 (prenylated)
RHBDD2	2	201	264	rhomboid domain containing 2
LOC647302	2	201	204	LSM3 homolog, U6 small nuclear RNA associated (S. cerevisiae); similar to Lsm3 protein
Cstb	5	201	284	cystatin B (stefin B)
hyou1	4	201	269	hypoxia up-regulated 1
MAOA	2	201	235	monoamine oxidase A
Tmed2	16	201	330	transmembrane emp24 domain trafficking protein 2
Vamp8	2	201	244	vesicle-associated membrane protein 8 (endobrevin)
ID2	3	201	274	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
Ndufv2	13	201	327	NADH dehydrogenase (ubiquinone) flavoprotein 2, 24kDa
hdgf	11	200	313	hepatoma-derived growth factor (high-mobility group protein 1-like)
Tax1bp1	1	200	200	Tax1 (human T-cell leukemia virus type I) binding protein 1
TACSTD2	6	200	227	tumor-associated calcium signal transducer 2
EIF4B	16	200	372	similar to eukaryotic translation initiation factor 4H; eukaryotic translation initiation factor 4B
ARPC1B	4	200	248	actin related protein 2/3 complex, subunit 1B, 41kDa; similar to Actin-related protein 2/3 complex subunit 1B (ARP2/3 complex 41 kDa subunit) (p41-ARC)
CDH1	5	200	281	cadherin 1, type 1, E-cadherin (epithelial)
AKR1A1	5	200	370	aldo-keto reductase family 1, member A1 (aldehyde reductase)
Exosc4	4	199	345	exosome component 4
KDELR1	11	199	418	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1
Fam83h	1	199	199	family with sequence similarity 83, member H
LOC100128775	4	198	365	neural precursor cell expressed, developmentally down-regulated 8; similar to neural precursor cell expressed, developmentally down-regulated gene 8
PSMD4	8	198	449	proteasome (prosome, macropain) 26S subunit, non-ATPase, 4
c16orf42	1	198	198	chromosome 16 open reading frame 42
CRELD2	4	198	253	cysteine-rich with EGF-like domains 2
TOP2A	3	198	326	topoisomerase (DNA) II alpha 170kDa
Stoml2	8	198	287	stomatin (EPB72)-like 2
lsm7	10	198	382	LSM7 homolog, U6 small nuclear RNA associated (S. cerevisiae)
serp1	6	198	353	stress-associated endoplasmic reticulum protein 1
ATP6AP1	12	197	299	ATPase, H+ transporting, lysosomal accessory protein 1
DAPL1	1	197	197	death associated protein-like 1
arpc1a	4	197	291	actin related protein 2/3 complex, subunit 1A, 41kDa
RRBP1	4	197	292	ribosome binding protein 1 homolog 180kDa (dog)
ARL6IP5	2	197	241	ADP-ribosylation-like factor 6 interacting protein 5
Entrez808	19	197	360	
NAMPT	1	197	197	nicotinamide phosphoribosyltransferase
TPD52	10	197	335	tumor protein D52
hadhb	4	196	240	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit
cdc37	9	196	305	cell division cycle 37 homolog (S. cerevisiae)

KRTCAP2	19	196	316	keratinocyte associated protein 2
FIS1	13	195	324	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)
Entrez100132406	13	195	426	
Entrez10381	2	195	208	
c19orf10	17	195	310	chromosome 19 open reading frame 10
HNRNPL	18	195	303	similar to heterogeneous nuclear ribonucleoprotein L-like; heterogeneous nuclear ribonucleoprotein L
DAD1	17	195	267	defender against cell death 1
TSTA3	5	195	306	tissue specific transplantation antigen P35B
Sfrs5	1	195	195	splicing factor, arginine/serine-rich 5
UGDH	2	195	238	UDP-glucose dehydrogenase
sqlE	3	195	231	squalene epoxidase
Wdr6	1	195	195	WD repeat domain 6
ggt1	2	194	236	gamma-glutamyltransferase light chain 3; gamma-glutamyltransferase 4 pseudogene; gamma-glutamyltransferase 2; gamma-glutamyltransferase 1; gamma-glutamyltransferase light chain 5 pseudogene
Pigt	2	194	209	phosphatidylinositol glycan anchor biosynthesis, class T
CopG	9	194	476	coatomer protein complex, subunit gamma
Mrpl24	4	194	291	mitochondrial ribosomal protein L24
abcc4	1	194	194	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
SIVA1	8	194	336	SIVA1, apoptosis-inducing factor
Tufm	13	194	299	Tu translation elongation factor, mitochondrial
KDELR2	6	194	297	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2
SEPT2	3	193	244	septin 2
NUMA1	7	193	307	nuclear mitotic apparatus protein 1
CD63	19	193	316	CD63 molecule
PSMB3	17	193	409	proteasome (prosome, macropain) subunit, beta type, 3
ppiB	12	193	270	peptidylprolyl isomerase B (cyclophilin B)
ATP5J2	11	193	274	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2
Cct3	14	193	313	chaperonin containing TCP1, subunit 3 (gamma)
ptp4a3	1	193	193	protein tyrosine phosphatase type IVA, member 3
glud1	1	193	193	glutamate dehydrogenase 1
RAG1AP1	1	193	193	recombination activating gene 1 activating protein 1
EIF3K	15	192	348	eukaryotic translation initiation factor 3, subunit K
HMGCS2	2	191	220	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
cd151	11	191	346	CD151 molecule (Raph blood group)
SMR3B	1	191	191	submaxillary gland androgen regulated protein 3B
hsf1	2	191	236	heat shock transcription factor 1
SCGB1D2	1	191	191	secretoglobin, family 1D, member 2
UQCRQ	9	191	275	ubiquinol-cytochrome c reductase, complex III subunit VII, 9.5kDa
FOLH1B	1	190	190	folate hydrolase 1B
NUBP2	2	190	194	nucleotide binding protein 2 (MinD homolog, E. coli)
C7orf68	2	190	201	chromosome 7 open reading frame 68
bhlhe40	1	190	190	basic helix-loop-helix family, member e40
DUS1L	7	190	243	dihydrouridine synthase 1-like (S. cerevisiae)
eIF6	3	190	281	eukaryotic translation initiation factor 6
ANAPC5	1	190	190	anaphase promoting complex subunit 5
PPA1	8	190	241	pyrophosphatase (inorganic) 1
PSME2	8	190	315	proteasome (prosome, macropain) activator subunit 2 (PA28 beta)
NHP2	12	189	267	NHP2 ribonucleoprotein homolog (yeast)
BCAP31	11	189	336	B-cell receptor-associated protein 31
TCEAL4	2	189	203	transcription elongation factor A (SII)-like 4

PRMT1	11	189	566	protein arginine methyltransferase 1
ech1	12	189	295	enoyl Coenzyme A hydratase 1, peroxisomal
Rpn2	15	189	422	ribophorin II
GANAB	14	189	267	glucosidase, alpha; neutral AB
PLP2	5	189	249	proteolipid protein 2 (colonic epithelium-enriched)
SFN	4	189	261	stratifin
Entrez653635	1	189	189	
psmA2	5	189	236	proteasome (prosome, macropain) subunit, alpha type, 2
ATP6V1F	12	189	351	ATPase, H+ transporting, lysosomal 14kDa, V1 subunit F
C17orf89	2	188	197	chromosome 17 open reading frame 89
stard10	3	188	222	StAR-related lipid transfer (START) domain containing 10
EBP	4	188	243	emopamil binding protein (sterol isomerase)
Ndufv1	12	188	253	NADH dehydrogenase (ubiquinone) flavoprotein 1, 51kDa
chchd10	8	188	253	coiled-coil-helix-coiled-coil-helix domain containing 10
REG4	1	188	188	regenerating islet-derived family, member 4
Klk11	5	188	267	kallikrein-related peptidase 11
AHSA1	6	188	251	AHA1, activator of heat shock 90kDa protein ATPase homolog 1 (yeast)
taldo1	11	188	245	transaldolase 1
rab5c	1	188	188	RAB5C, member RAS oncogene family
gmpr	4	188	277	guanosine monophosphate reductase
SERGEF	3	188	219	secretion regulating guanine nucleotide exchange factor
SPCS1	3	188	293	signal peptidase complex subunit 1 homolog (S. cerevisiae)
Tmem147	5	188	360	transmembrane protein 147
ERH	13	187	299	enhancer of rudimentary homolog (Drosophila)
LOC442308	1	187	187	tubulin, beta; similar to tubulin, beta 5; tubulin, beta pseudogene 2; tubulin, beta pseudogene 1
Pttg1ip	1	187	187	pituitary tumor-transforming 1 interacting protein
C1orf43	16	187	289	chromosome 1 open reading frame 43
GPX1	11	187	307	glutathione peroxidase 1
fam195a	2	187	187	chromosome 16 open reading frame 14
AQP3	4	187	244	aquaporin 3 (Gill blood group)
SIGMAR1	4	187	317	sigma non-opioid intracellular receptor 1
SLC2A12	1	187	187	solute carrier family 2 (facilitated glucose transporter), member 12
AP2S1	15	187	303	adaptor-related protein complex 2, sigma 1 subunit
SLC39A6	3	187	201	solute carrier family 39 (zinc transporter), member 6
anp32b	14	187	342	similar to Acidic leucine-rich nuclear phosphoprotein 32 family member B (PHAPI2 protein) (Silver-stainable protein SSP29) (Acidic protein rich in leucines); acidic (leucine-rich) nuclear phosphoprotein 32 family, member B
QARS	4	187	213	glutaminyl-tRNA synthetase
STRA13	14	187	277	stimulated by retinoic acid 13 homolog (mouse)
RPL27A	16	187	292	ribosomal protein L27a
ahcY	10	187	276	adenosylhomocysteinase
POLR2K	5	187	263	polymerase (RNA) II (DNA directed) polypeptide K, 7.0kDa
RHOC	7	186	280	ras homolog gene family, member C
KLK12	2	186	192	kallikrein-related peptidase 12
Entrez100132406	14	186	363	
TIMM10	2	186	230	translocase of inner mitochondrial membrane 10 homolog (yeast)
C21orf33	1	186	186	chromosome 21 open reading frame 33
CCNI	18	186	298	cyclin I
rrs1	1	186	186	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)
LRP10	1	186	186	low density lipoprotein receptor-related protein 10
C7orf59	15	185	333	chromosome 7 open reading frame 59

SNHG9	2	185	232	small nucleolar RNA host gene 9 (non-protein coding)
Psma4	7	185	296	proteasome (prosome, macropain) subunit, alpha type, 4
NOP58	1	185	185	NOP58 ribonucleoprotein homolog (yeast)
Entrez801	3	185	246	
Phb	9	185	357	prohibitin
GUSB	1	185	185	glucuronidase, beta
SKP1	3	185	236	S-phase kinase-associated protein 1
Irak1	7	185	284	interleukin-1 receptor-associated kinase 1
WDR34	7	184	235	WD repeat domain 34
Mlec	6	184	290	malectin
LOC653889	2	184	227	similar to U5 snRNP-associated 102 kDa protein (U5-102 kDa protein); PRP6 pre-mRNA processing factor 6 homolog (S. cerevisiae)
C19orf63	6	184	233	chromosome 19 open reading frame 63
Pkib	1	184	184	protein kinase (cAMP-dependent, catalytic) inhibitor beta
LOC642132	1	184	184	roundabout, axon guidance receptor, homolog 1 (Drosophila); similar to roundabout 1 isoform b
MYL12A	10	183	387	myosin, light chain 12A, regulatory, non-sarcomeric
c14orf143	1	183	183	chromosome 14 open reading frame 143
CYCS	1	183	183	cytochrome c, somatic
FLNA	2	183	190	filamin A, alpha (actin binding protein 280)
H2afj	1	183	183	H2A histone family, member J
Eif3f	16	183	250	eukaryotic translation initiation factor 3, subunit F; similar to hCG2040283
ANGPTL4	4	183	303	angiopoietin-like 4
Ifitm2	2	183	199	interferon induced transmembrane protein 2 (1-8D)
TRAM1	3	183	215	translocation associated membrane protein 1
LOC100130003	11	183	369	hypothetical protein LOC100132425; similar to small nuclear ribonucleoprotein polypeptide G; small nuclear ribonucleoprotein polypeptide G; small nuclear ribonucleoprotein G-like protein
FOS	2	183	214	v-fos FBJ murine osteosarcoma viral oncogene homolog
TRIB1	1	183	183	tribbles homolog 1 (Drosophila)
LOC652460	1	182	182	similar to Plectin 1 (PLTN) (PCN) (Hemidesmosomal protein 1) (HD1); plectin 1, intermediate filament binding protein 500kDa
CHMP2A	10	182	214	chromatin modifying protein 2A
Trap1	4	182	260	TNF receptor-associated protein 1
sqstm1	8	182	234	sequestosome 1
Mrfap1	11	182	296	Mof4 family associated protein 1
LUC7L3	1	182	182	cisplatin resistance-associated overexpressed protein
DCTN3	2	182	187	dynactin 3 (p22)
ptprf	3	182	256	protein tyrosine phosphatase, receptor type, F
AURKAIP1	3	182	224	aurora kinase A interacting protein 1
SCNN1A	4	182	189	sodium channel, nonvoltage-gated 1 alpha
Cct7	18	181	251	chaperonin containing TCP1, subunit 7 (eta)
SNAR-G1	2	181	199	small ILF3/NF90-associated RNA G1
Ppm1g	2	181	205	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform
LOC643668	3	181	212	proteasome (prosome, macropain) 26S subunit, ATPase, 1; similar to protease (prosome, macropain) 26S subunit, ATPase 1
PDLIM5	4	181	239	PDZ and LIM domain 5
PDZK1IP1	1	181	181	PDZK1 interacting protein 1
ATP1A1	12	181	258	ATPase, Na+/K+ transporting, alpha 1 polypeptide
ERP29	8	181	314	endoplasmic reticulum protein 29
Tmem178	2	180	195	transmembrane protein 178
PSMB6	5	180	220	proteasome (prosome, macropain) subunit, beta type, 6
ppapdc1b	1	180	180	phosphatidic acid phosphatase type 2 domain containing 1B

TRPM4	1	180	180	transient receptor potential cation channel, subfamily M, member 4
MLF2	11	180	241	myeloid leukemia factor 2
EWSR1	2	180	186	similar to Ewing sarcoma breakpoint region 1; Ewing sarcoma breakpoint region 1
ZYX	1	180	180	zyxin
ADI1	9	180	280	acireductone dioxygenase 1
mRpL12	10	180	281	mitochondrial ribosomal protein L12
Entrez7381	1	180	180	
c19orf43	16	180	234	chromosome 19 open reading frame 43
BOP1	2	180	232	block of proliferation 1
cdc20	2	180	229	cell division cycle 20 homolog (S. cerevisiae)
pdia6	9	180	234	protein disulfide isomerase family A, member 6
C9orf142	1	180	180	chromosome 9 open reading frame 142
CTNNB1	7	180	298	catenin (cadherin-associated protein), beta 1, 88kDa
Fbp1	1	180	180	fructose-1,6-bisphosphatase 1
LOC100129085	1	179	179	selenoprotein K; similar to HSPC297
epn1	3	179	186	epsin 1
C14orf156	4	179	213	chromosome 14 open reading frame 156
dnajb11	2	179	180	DnaJ (Hsp40) homolog, subfamily B, member 11
tspan15	1	179	179	tetraspanin 15
C11orf92	2	179	209	chromosome 11 open reading frame 92
c11orf59	2	179	213	chromosome 11 open reading frame 59
Uqcrc2	6	179	232	ubiquinol-cytochrome c reductase core protein II
PQBP1	3	178	194	polyglutamine binding protein 1
ccng1	4	178	221	cyclin G1
cct6a	8	178	271	chaperonin containing TCP1, subunit 6A (zeta 1)
Psma6	9	178	250	proteasome (prosome, macropain) subunit, alpha type, 6
Atp1b3	1	178	178	ATPase, Na+/K+ transporting, beta 3 polypeptide
Hnrnph1	9	178	331	heterogeneous nuclear ribonucleoprotein H1 (H)
RPS26P11	7	178	290	ribosomal protein S26 pseudogene 11
mcm2	2	177	197	minichromosome maintenance complex component 2
LFNG	2	177	206	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
CCT8	10	177	275	similar to chaperonin containing TCP1, subunit 8 (theta); chaperonin containing TCP1, subunit 8 (theta)
YIF1A	2	177	212	Yip1 interacting factor homolog A (S. cerevisiae)
Rnf187	2	177	177	ring finger protein 187
CDKN1C	1	177	177	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
gnl3	3	177	201	guanine nucleotide binding protein-like 3 (nucleolar)
Dek	3	177	190	DEK oncogene
c1qbp	2	177	195	complement component 1, q subcomponent binding protein
SSNA1	4	176	192	Sjogren syndrome nuclear autoantigen 1
ssb	1	176	176	Sjogren syndrome antigen B (autoantigen La)
tbca	7	176	205	tubulin folding cofactor A
ATP2C1	2	176	234	ATPase, Ca++ transporting, type 2C, member 1
IMP4	1	176	176	IMP4, U3 small nucleolar ribonucleoprotein, homolog (yeast)
LOC652147	1	176	176	similar to U5 snRNP-specific protein, 200 kDa; small nuclear ribonucleoprotein 200kDa (U5)
ddx39	1	176	176	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39
MGP	1	176	176	matrix Gla protein
fkbp4	5	176	204	FK506 binding protein 4, 59kDa
Hnrnpc	18	176	285	heterogeneous nuclear ribonucleoprotein C (C1/C2)
Entrez7341	5	176	252	

c19orf6	2	176	225	chromosome 19 open reading frame 6
HSPH1	1	175	175	heat shock 105kDa/110kDa protein 1
Adam15	3	175	222	ADAM metallopeptidase domain 15
Lman2	6	175	241	lectin, mannose-binding 2
BTBD2	1	175	175	BTB (POZ) domain containing 2
EZR	7	175	278	hypothetical protein LOC100129652; ezrin
eif2s3	4	175	247	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa
CCND1	6	175	304	cyclin D1
Pcbp1	12	175	246	poly(rC) binding protein 1
psmd3	9	175	290	proteasome (prosome, macropain) 26S subunit, non-ATPase, 3
Esrp1	2	175	216	epithelial splicing regulatory protein 1
ACLY	5	175	210	ATP citrate lyase
TNFSF10	1	175	175	tumor necrosis factor (ligand) superfamily, member 10
RBBP7	6	175	251	retinoblastoma binding protein 7
GDI2	8	175	233	GDP dissociation inhibitor 2
CORO1B	4	174	282	coronin, actin binding protein, 1B
Entrez100616408	3	174	235	
EIF3I	14	174	312	eukaryotic translation initiation factor 3, subunit I
TXN2	1	174	174	thioredoxin 2
AAMP	4	174	200	angio-associated, migratory cell protein
eif3g	12	174	291	eukaryotic translation initiation factor 3, subunit G
hnrnpm	15	174	288	heterogeneous nuclear ribonucleoprotein M
tmem59	8	174	292	transmembrane protein 59
ephX1	5	174	206	epoxide hydrolase 1, microsomal (xenobiotic)
foxa1	16	173	237	forkhead box A1
lrig1	2	173	206	leucine-rich repeats and immunoglobulin-like domains 1
SURF1	1	173	173	surfeit 1
c3orf10	16	173	318	chromosome 3 open reading frame 10
c14orf166	6	173	190	chromosome 14 open reading frame 166
Psmg2	1	173	173	proteasome (prosome, macropain) assembly chaperone 2
VEGFA	4	173	266	vascular endothelial growth factor A
NDUFA12	1	173	173	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 12
GUK1	10	173	280	guanylate kinase 1
homer2	3	173	201	homer homolog 2 (Drosophila)
TMED3	7	173	304	transmembrane emp24 protein transport domain containing 3
cox17	9	173	261	COX17 cytochrome c oxidase assembly homolog (S. cerevisiae)
PSME1	7	173	211	proteasome (prosome, macropain) activator subunit 1 (PA28 alpha)
SRP14	13	173	277	signal recognition particle 14kDa (homologous Alu RNA binding protein) pseudogene 1; signal recognition particle 14kDa (homologous Alu RNA binding protein)
Ctbp1	1	173	173	C-terminal binding protein 1
ifi30	4	172	236	interferon, gamma-inducible protein 30
CSDE1	12	172	230	cold shock domain containing E1, RNA-binding
MTCH1	10	172	248	mitochondrial carrier homolog 1 (C. elegans)
RBM3	1	172	172	RNA binding motif (RNP1, RRM) protein 3
CIB1	4	172	176	calcium and integrin binding 1 (calmyrin)
Entrez100132247	1	172	172	
NPIP	1	172	172	nuclear pore complex interacting protein
Pycr1	12	172	256	pyrroline-5-carboxylate reductase 1
plk2	1	172	172	polo-like kinase 2 (Drosophila)
Golim4	1	172	172	golgi integral membrane protein 4
C6orf108	2	171	180	chromosome 6 open reading frame 108

S100a16	1	171	171	S100 calcium binding protein A16
PRSS8	3	171	190	protease, serine, 8
u2af1	6	171	213	U2 small nuclear RNA auxiliary factor 1
TSTD1	4	171	284	thiosulfate sulfurtransferase KAT, putative
Ptbp1	5	171	188	polypyrimidine tract binding protein 1
BZW1	3	171	210	basic leucine zipper and W2 domains 1 pseudogene 1; basic leucine zipper and W2 domains 1 like 1; basic leucine zipper and W2 domains 1
dynlt1	8	171	217	dynein, light chain, Tctex-type 1
Apex1	11	171	214	APEX nuclease (multifunctional DNA repair enzyme) 1
Tecr	10	171	241	glycoprotein, synaptic 2
RHOT2	2	170	180	ras homolog gene family, member T2
ASS1	3	170	206	argininosuccinate synthetase 1
CDKN1A	1	170	170	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
PTOV1	5	170	224	prostate tumor overexpressed 1
LOC100133770	1	170	170	hypothetical protein LOC100133770; vacuolar protein sorting 35 homolog (S. cerevisiae)
slc25a1	3	170	238	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
HMGA1	2	170	198	hypothetical LOC100130009; high mobility group AT-hook 1
ddt	1	170	170	D-dopachrome tautomerase
SF3B14	3	170	201	splicing factor 3B, 14 kDa subunit
NGFRAP1	7	170	260	nerve growth factor receptor (TNFRSF16) associated protein 1
FKBP9L	1	170	170	FK506 binding protein 9-like
cct5	5	170	200	chaperonin containing TCP1, subunit 5 (epsilon)
LOC613037	1	170	170	nuclear pore complex interacting protein pseudogene
Rexo2	6	169	211	REX2, RNA exonuclease 2 homolog (S. cerevisiae)
TIMM17B	1	169	169	translocase of inner mitochondrial membrane 17 homolog B (yeast)
PKN1	6	169	215	protein kinase N1
grhpr	5	169	184	glyoxylate reductase/hydroxypyruvate reductase
sdcbp	5	169	228	syndecan binding protein (syntenin)
nucb2	2	169	179	nucleobindin 2
NDUFAB1	12	169	302	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1, 8kDa
HSD17B10	11	169	274	hydroxysteroid (17-beta) dehydrogenase 10
cyb5a	6	169	209	cytochrome b5 type A (microsomal)
mrpl51	16	169	229	mitochondrial ribosomal protein L51
ociad2	3	169	190	OCIA domain containing 2
tm7sf2	5	169	201	transmembrane 7 superfamily member 2
HADHA	5	169	253	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha subunit
RAB7A	10	169	239	RAB7A, member RAS oncogene family
nfix	5	169	195	nuclear factor I/X (CCAAT-binding transcription factor)
POLR2G	3	168	231	polymerase (RNA) II (DNA directed) polypeptide G
SLC2A4RG	1	168	168	SLC2A4 regulator
Tceb2	15	168	257	transcription elongation factor B (SIII), polypeptide 2 (18kDa, elongin B)
scyl1	1	168	168	SCY1-like 1 (S. cerevisiae)
PHB2	15	168	279	prohibitin 2
DDB1	1	168	168	damage-specific DNA binding protein 1, 127kDa
U2AF2	3	168	185	U2 small nuclear RNA auxiliary factor 2
ORM1	1	168	168	orosomucoid 1
AP1M2	3	168	207	adaptor-related protein complex 1, mu 2 subunit
Ndufb5	1	168	168	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5, 16kDa
SHISA5	2	168	188	shisa homolog 5 (Xenopus laevis)
HN1	5	167	229	hematological and neurological expressed 1

NDUFB2	9	167	244	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 2, 8kDa
Ndufa7	1	167	167	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7, 14.5kDa
actn4	7	167	222	actinin, alpha 4
SLC16A3	1	167	167	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)
HNRNPD	6	167	227	heterogeneous nuclear ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa)
ARL6IP4	9	167	228	ADP-ribosylation-like factor 6 interacting protein 4
MAGED1	6	167	236	melanoma antigen family D, 1
SELM	1	167	167	selenoprotein M
GGTLC2	1	167	167	gamma-glutamyltransferase light chain 2
Ehf	6	167	250	ets homologous factor
TCP1	6	166	193	hypothetical gene supported by BC000665; t-complex 1
TMEM205	8	166	231	transmembrane protein 205
Tmem9	6	166	265	transmembrane protein 9
NUTF2	2	166	197	nuclear transport factor 2
NAAA	1	166	166	N-acylethanolamine acid amidase
H2AFY	7	166	253	H2A histone family, member Y
Ndufb8	9	166	209	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 8, 19kDa
Nucks1	6	166	298	nuclear casein kinase and cyclin-dependent kinase substrate 1
LOC389901	17	166	235	X-ray repair complementing defective repair in Chinese hamster cells 6; similar to ATP-dependent DNA helicase II, 70 kDa subunit
hsbp1	1	166	166	heat shock factor binding protein 1
SDF4	4	166	201	stromal cell derived factor 4
SND1	10	166	236	staphylococcal nuclease and tudor domain containing 1
TMEM123	4	166	224	transmembrane protein 123
PRR13	4	166	236	proline rich 13
lsr	7	166	268	lipolysis stimulated lipoprotein receptor
Ptdss1	1	166	166	phosphatidylserine synthase 1
Uba1	9	166	230	ubiquitin-like modifier activating enzyme 1
Mrpl3	3	166	170	mitochondrial ribosomal protein L3
FBXW5	3	165	181	F-box and WD repeat domain containing 5
anapc11	6	165	217	anaphase promoting complex subunit 11
akt1	8	165	209	v-akt murine thymoma viral oncogene homolog 1
NDUFB3	2	165	197	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 3, 12kDa
SCAP	2	165	193	SREBF chaperone
VKORC1	3	165	192	vitamin K epoxide reductase complex, subunit 1
npc2	4	165	189	Niemann-Pick disease, type C2
PDCD5	2	165	168	programmed cell death 5
Gsn	2	165	171	gelsolin (amyloidosis, Finnish type)
EIF3M	3	165	185	eukaryotic translation initiation factor 3, subunit M
SNRNP25	1	165	165	small nuclear ribonucleoprotein 25kDa (U11/U12)
HNRNPF	8	165	307	heterogeneous nuclear ribonucleoprotein F
CDKN2C	3	165	180	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
Anxa7	2	165	203	annexin A7
Chmp2b	1	165	165	chromatin modifying protein 2B
PRIMA1	1	165	165	proline rich membrane anchor 1
Trpv6	3	165	219	transient receptor potential cation channel, subfamily V, member 6
DDRGK1	4	165	182	DDRGK domain containing 1
CRIP2	4	165	210	cysteine-rich protein 2
acad8	1	164	164	acyl-Coenzyme A dehydrogenase family, member 8
PSMD8	8	164	291	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8

sub1	2	164	173	SUB1 homolog (S. cerevisiae)
Bri3	1	164	164	brain protein I3; brain protein I3 pseudogene 1
dci	7	164	223	dodecenoyl-Coenzyme A delta isomerase (3,2 trans-enoyl-Coenzyme A isomerase)
SMC4	1	164	164	structural maintenance of chromosomes 4
RPL22L1	1	164	164	ribosomal protein L22-like 1
EIF3B	7	164	188	eukaryotic translation initiation factor 3, subunit B
CREB3L4	2	164	177	cAMP responsive element binding protein 3-like 4
HNRNPA1L2	7	164	212	heterogeneous nuclear ribonucleoprotein A1-like 2
CAP1	1	164	164	CAP, adenylate cyclase-associated protein 1 (yeast)
Got2	2	163	165	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)
NDUFS4	2	163	168	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18kDa (NADH-coenzyme Q reductase)
CYB561	7	163	192	cytochrome b-561
H2afx	6	163	198	H2A histone family, member X
JUP	11	163	215	junction plakoglobin
atp5l	14	163	236	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G
ZNF395	1	163	163	zinc finger protein 395
hmp19	1	163	163	HMP19 protein
Atp5j	1	163	163	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F6
XRCC5	6	163	225	X-ray repair complementing defective repair in Chinese hamster cells 5 (double-strand-break rejoining)
HOXB2	2	163	206	homeobox B2
LASS4	4	163	195	LAG1 homolog, ceramide synthase 4
MYC	4	163	225	v-myc myelocytomatosis viral oncogene homolog (avian)
c20orf108	2	163	180	chromosome 20 open reading frame 108
PKD1P1	1	163	163	polycystic kidney disease 1 (autosomal dominant) pseudogene 1
tmed10	4	163	206	transmembrane emp24-like trafficking protein 10 (yeast)
FAM127A	1	163	163	family with sequence similarity 127, member A
HOXB8	1	163	163	homeobox B8
KPNA2	5	162	211	karyopherin alpha 2 (RAG cohort 1, importin alpha 1); karyopherin alpha-2 subunit like
C14orf2	10	162	203	chromosome 14 open reading frame 2
FAM173A	1	162	162	family with sequence similarity 173, member A
Sdc4	2	162	206	syndecan 4
SAFB2	2	162	164	scaffold attachment factor B2
VGF	1	162	162	VGF nerve growth factor inducible
Dynll2	10	162	194	dynein, light chain, LC8-type 2
LOC100129272	7	162	202	similar to translocase of outer mitochondrial membrane 20 homolog; similar to mitochondrial outer membrane protein 19; translocase of outer mitochondrial membrane 20 homolog (yeast)
LGALS3	1	162	162	lectin, galactoside-binding, soluble, 3
CMTM6	1	162	162	CKLF-like MARVEL transmembrane domain containing 6
C9orf16	3	162	196	chromosome 9 open reading frame 16
Ppp1ca	10	162	258	protein phosphatase 1, catalytic subunit, alpha isoform
NDUFA5	1	162	162	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5, 13kDa
GJB1	3	162	203	gap junction protein, beta 1, 32kDa
Entrez9066	2	162	183	
Elovl5	3	161	173	ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)
Rnf181	1	161	161	ring finger protein 181
Wbp5	1	161	161	WW domain binding protein 5
Fam129b	5	161	209	family with sequence similarity 129, member B
Il1r1	1	161	161	interleukin 1 receptor, type I
anxa11	2	161	169	annexin A11

INPPL1	1	161	161	inositol polyphosphate phosphatase-like 1
Ccdc56	2	161	162	coiled-coil domain containing 56
FASTK	1	161	161	Fas-activated serine/threonine kinase
SRM	6	161	179	spermidine synthase
Ndufa4	5	161	188	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa
napA	2	161	184	N-ethylmaleimide-sensitive factor attachment protein, alpha
Fkbp2	4	161	211	FK506 binding protein 2, 13kDa
Entrez23117	1	161	161	
etfA	2	161	167	electron-transfer-flavoprotein, alpha polypeptide
MORF4	2	161	201	mortality factor 4; mortality factor 4 like 1
uqcrfs1	3	160	192	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide-like 1; ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1
taf15	10	160	288	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa
GHITM	4	160	183	growth hormone inducible transmembrane protein
PSMC5	5	160	219	proteasome (prosome, macropain) 26S subunit, ATPase, 5
Ptprn2	1	160	160	protein tyrosine phosphatase, receptor type, N polypeptide 2
psmc3	7	160	195	proteasome (prosome, macropain) 26S subunit, ATPase, 3
SSR3	1	160	160	signal sequence receptor, gamma (translocon-associated protein gamma)
SF3B2	6	160	228	splicing factor 3b, subunit 2, 145kDa
CNBP	6	160	226	CCHC-type zinc finger, nucleic acid binding protein
CLTA	12	160	185	clathrin, light chain (Lca)
Dhrs3	1	160	160	dehydrogenase/reductase (SDR family) member 3
c17orf28	1	159	159	chromosome 17 open reading frame 28
atox1	2	159	166	ATX1 antioxidant protein 1 homolog (yeast)
ssrp1	6	159	202	structure specific recognition protein 1
TPM1	1	159	159	tropomyosin 1 (alpha)
PIH1D1	1	159	159	PIH1 domain containing 1
GLB1L2	2	159	178	galactosidase, beta 1-like 2
PPIF	3	159	174	peptidylprolyl isomerase F
prdx3	7	159	194	peroxiredoxin 3
C3orf57	1	159	159	chromosome 3 open reading frame 57
MRPS34	8	159	235	mitochondrial ribosomal protein S34
STUB1	1	159	159	STIP1 homology and U-box containing protein 1
ADRBK1	2	159	160	adrenergic, beta, receptor kinase 1
Entrez100616318	1	159	159	
ier2	1	159	159	immediate early response 2
Entrez25832	3	159	174	
TOMM6	8	159	206	translocase of outer mitochondrial membrane 6 homolog (yeast)
C11orf75	1	159	159	hypothetical LOC728675; chromosome 11 open reading frame 75
CDK5RAP3	1	159	159	CDK5 regulatory subunit associated protein 3
CAPN1	1	159	159	calpain 1, (mu/I) large subunit
OS9	7	159	234	osteosarcoma amplified 9, endoplasmic reticulum associated protein
eno2	1	158	158	enolase 2 (gamma, neuronal)
Tmem176a	1	158	158	transmembrane protein 176A
SERPINA4	1	158	158	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4
CD164	7	158	207	CD164 molecule, sialomucin
sfpq	4	158	199	splicing factor proline/glutamine-rich (polypyrimidine tract binding protein associated)
SF3B5	10	158	206	splicing factor 3b, subunit 5, 10kDa
C15orf24	1	158	158	chromosome 15 open reading frame 24
HMGB3	1	158	158	similar to high mobility group box 3; high-mobility group box 3
emd	1	158	158	emerin

SNRPF	6	158	194	small nuclear ribonucleoprotein polypeptide F
TCEA1	2	158	159	transcription elongation factor A (SII), 1 pseudogene 2; transcription elongation factor A (SII), 1
arpc2	3	158	176	actin related protein 2/3 complex, subunit 2, 34kDa
HNRNPUL1	4	158	185	heterogeneous nuclear ribonucleoprotein U-like 1
Mdh1	1	158	158	malate dehydrogenase 1, NAD (soluble)
PIM3	1	158	158	pim-3 oncogene
Paip2	1	157	157	poly(A) binding protein interacting protein 2
TMEM106C	4	157	195	transmembrane protein 106C
Cd46	3	157	195	CD46 molecule, complement regulatory protein
thoc4	4	157	221	THO complex 4
CD276	2	157	167	CD276 molecule
C2orf28	1	157	157	chromosome 2 open reading frame 28
mgst1	2	157	182	microsomal glutathione S-transferase 1
SAP18	1	157	157	Sin3A-associated protein, 18kDa
hsd17b4	3	157	163	hydroxysteroid (17-beta) dehydrogenase 4
ANXA5	11	157	204	annexin A5
scg2	3	157	202	secretogranin II (chromogranin C)
SURF4	8	157	199	surfeit 4
Entrez408050	3	157	179	
DBNL	1	157	157	drebrin-like
PSMD2	10	157	190	proteasome (prosome, macropain) 26S subunit, non-ATPase, 2
SC4MOL	1	157	157	sterol-C4-methyl oxidase-like
Trappc5	7	157	213	trafficking protein particle complex 5
CSRP1	3	157	203	cysteine and glycine-rich protein 1
prpf19	5	157	258	PRP19/PSO4 pre-mRNA processing factor 19 homolog (S. cerevisiae)
RAB11B	4	157	180	RAB11B, member RAS oncogene family
stt3a	4	157	210	STT3, subunit of the oligosaccharyltransferase complex, homolog A (S. cerevisiae)
LOC389842	6	157	194	similar to RAN binding protein 1; RAN binding protein 1
Ttyh3	1	157	157	tweety homolog 3 (Drosophila)
Entrez23420	3	157	181	
SLC9A3R1	4	156	186	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1
DAP	3	156	163	death-associated protein
Entrez514	2	156	171	
BANF1	10	156	270	similar to barrier-to-autointegration factor; barrier to autointegration factor 1
NDUFS7	4	156	189	NADH dehydrogenase (ubiquinone) Fe-S protein 7, 20kDa (NADH-coenzyme Q reductase)
podxl2	4	156	197	podocalyxin-like 2
C19orf56	1	156	156	chromosome 19 open reading frame 56
LOC645181	2	156	185	PDGFA associated protein 1; similar to PDGFA associated protein 1
Hnrnpa3	1	156	156	heterogeneous nuclear ribonucleoprotein A3
HK1	1	156	156	hexokinase 1
Entrez283820	4	156	182	
prcp	1	156	156	prolylcarboxypeptidase (angiotensinase C)
Nop10	1	156	156	NOP10 ribonucleoprotein homolog (yeast)
Lpar3	1	156	156	lysophosphatidic acid receptor 3
PSMB5	8	156	194	proteasome (prosome, macropain) subunit, beta type, 5
AZIN1	4	155	172	antizyme inhibitor 1
Pold2	6	155	196	polymerase (DNA directed), delta 2, regulatory subunit 50kDa
VDAC3	5	155	177	voltage-dependent anion channel 3
tkt	9	155	215	transketolase
Entrez84293	2	155	157	

CHMP4B	10	155	201	chromatin modifying protein 4B
CTSB	1	155	155	cathepsin B
ATF5	2	155	171	activating transcription factor 5
Gars	1	155	155	glycyl-tRNA synthetase
Morf4l2	8	155	212	mortality factor 4 like 2
GAA	2	155	174	glucosidase, alpha; acid
Ndufa2	3	155	195	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa
TXNIP	4	154	192	thioredoxin interacting protein
NDRG3	1	154	154	NDRG family member 3
ACSL3	1	154	154	acyl-CoA synthetase long-chain family member 3
snx3	1	154	154	sorting nexin 3
RCN1	2	154	167	reticulocalbin 1, EF-hand calcium binding domain
C19orf53	2	154	169	chromosome 19 open reading frame 53
prss23	2	154	155	protease, serine, 23
DPP4	1	154	154	dipeptidyl-peptidase 4
Entrez9751	1	154	154	
CLPTM1	1	154	154	cleft lip and palate associated transmembrane protein 1
Uqcr10	6	154	178	ubiquinol-cytochrome c reductase complex (7.2 kD)
C20orf199	7	154	196	chromosome 20 open reading frame 199
Hist3h2a	3	154	168	histone cluster 3, H2a
LOC344328	1	154	154	similar to heat shock 70kD protein binding protein; suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
scrib	3	154	215	scribbled homolog (Drosophila)
KPNB1	2	154	155	karyopherin (importin) beta 1
Jtb	1	154	154	jumping translocation breakpoint
Timm13	2	153	174	translocase of inner mitochondrial membrane 13 homolog (yeast)
gnai2	2	153	156	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2
GPS1	1	153	153	G protein pathway suppressor 1
wdr45l	2	153	162	WDR45-like
Spint1	5	153	178	serine peptidase inhibitor, Kunitz type 1
RALY	1	153	153	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse))
MRPL36	2	153	154	mitochondrial ribosomal protein L36
SLC26A3	1	153	153	solute carrier family 26, member 3
naprt1	1	153	153	nicotinate phosphoribosyltransferase domain containing 1
SH3BGRL3	1	153	153	SH3 domain binding glutamic acid-rich protein like 3
HSD11B2	1	153	153	hydroxysteroid (11-beta) dehydrogenase 2
PFDN2	4	153	189	prefoldin subunit 2
copb2	4	153	204	coatomer protein complex, subunit beta 2 (beta prime)
NAP1L1	4	153	185	nucleosome assembly protein 1-like 1
TMEM87A	1	153	153	transmembrane protein 87A
PPP2CB	2	152	172	protein phosphatase 2 (formerly 2A), catalytic subunit, beta isoform
actn1	1	152	152	actinin, alpha 1
YWHAB	4	152	184	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide
SLC1A5	1	152	152	solute carrier family 1 (neutral amino acid transporter), member 5
Cd320	2	152	180	CD320 molecule
ACADVL	4	152	169	acyl-Coenzyme A dehydrogenase, very long chain
arhgdib	1	152	152	Rho GDP dissociation inhibitor (GDI) beta
MLLT11	1	152	152	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11
SMARCA4	2	152	179	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4

Eif4a3	4	152	208	eukaryotic translation initiation factor 4A, isoform 3
elf3	5	152	201	E74-like factor 3 (ets domain transcription factor, epithelial-specific)
GTF3A	3	152	165	general transcription factor IIIA
SYPL1	1	151	151	synaptophysin-like 1
PCA3	1	151	151	prostate cancer antigen 3 (non-protein coding)
hes1	2	151	165	hairy and enhancer of split 1, (Drosophila)
EVL	3	151	182	Enah/Vasp-like
farsa	1	151	151	phenylalanyl-tRNA synthetase, alpha subunit
Magea3	1	151	151	melanoma antigen family A, 3
rab25	1	151	151	RAB25, member RAS oncogene family
Tmem134	1	151	151	transmembrane protein 134
Tmed4	3	151	176	transmembrane emp24 protein transport domain containing 4
PLOD1	1	151	151	procollagen-lysine 1, 2-oxoglutarate 5-dioxygenase 1
degs2	1	151	151	degenerative spermatocyte homolog 2, lipid desaturase (Drosophila)
Sh3glb2	1	151	151	SH3-domain GRB2-like endophilin B2
sec13	1	151	151	SEC13 homolog (S. cerevisiae)
ufc1	2	151	156	ubiquitin-fold modifier conjugating enzyme 1
Furin	2	151	166	furin (paired basic amino acid cleaving enzyme)
dpf2	1	151	151	D4, zinc and double PHD fingers family 2
PPT1	1	150	150	palmitoyl-protein thioesterase 1
HNRNPR	1	150	150	heterogeneous nuclear ribonucleoprotein R
Entrez9232	4	150	176	
Rassf3	2	150	164	Ras association (RalGDS/AF-6) domain family member 3
PGC	1	150	150	progastricsin (pepsinogen C)
SERPINH1	1	150	150	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)
EI24	6	150	211	etoposide induced 2.4 mRNA
Eif4g1	9	150	186	eukaryotic translation initiation factor 4 gamma, 1
COL2A1	1	150	150	collagen, type II, alpha 1
ITFG3	1	150	150	integrin alpha FG-GAP repeat containing 3
Itgb1	3	150	180	integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)
pygb	6	150	184	phosphorylase, glycogen; brain
Mrpl55	1	150	150	mitochondrial ribosomal protein L55
MYH9	7	149	199	myosin, heavy chain 9, non-muscle
BRP44	6	149	187	brain protein 44
TSPYL2	1	149	149	TSPY-like 2
TPM4	4	149	165	tropomyosin 4
MRPL23	3	149	168	mitochondrial ribosomal protein L23
paics	1	149	149	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase
Entrez9232	1	149	149	
HPN	2	149	150	hepsin
Entrez1831	1	149	149	
PPP2CA	1	149	149	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform
PDLIM1	1	149	149	PDZ and LIM domain 1
UBE2E1	1	149	149	ubiquitin-conjugating enzyme E2E 1 (UBC4/5 homolog, yeast)
NCOA4	1	149	149	nuclear receptor coactivator 4
supt5h	1	149	149	suppressor of Ty 5 homolog (S. cerevisiae)
Entrez9040	1	149	149	
Ctnna1	11	149	191	catenin (cadherin-associated protein), alpha 1, 102kDa
NGRN	1	149	149	neugrin, neurite outgrowth associated

cttn	1	149	149	cortactin
cks1b	2	148	157	CDC28 protein kinase regulatory subunit 1B
Zfat	1	148	148	zinc finger and AT hook domain containing
tk1	3	148	158	thymidine kinase 1, soluble
DDX5	7	148	174	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5
bchE	2	148	152	butyrylcholinesterase
DUSP1	1	148	148	dual specificity phosphatase 1
RAD23A	5	148	180	RAD23 homolog A (S. cerevisiae)
EIF1AY	1	148	148	eukaryotic translation initiation factor 1A, Y-linked
Muc13	2	148	173	mucin 13, cell surface associated
Entrez6612	2	148	149	
WNT5A	1	148	148	wingless-type MMTV integration site family, member 5A
CCK	1	148	148	cholecystokinin
TGM3	1	148	148	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
Eif2ak1	1	147	147	eukaryotic translation initiation factor 2-alpha kinase 1
Tex264	1	147	147	testis expressed 264
aph1a	7	147	185	anterior pharynx defective 1 homolog A (C. elegans)
ZC3H15	1	147	147	zinc finger CCCH-type containing 15
RAB11FIP3	1	147	147	RAB11 family interacting protein 3 (class II)
gstk1	1	147	147	glutathione S-transferase kappa 1
CCT2	3	147	158	chaperonin containing TCP1, subunit 2 (beta)
NAA10	1	147	147	ARD1 homolog A, N-acetyltransferase (S. cerevisiae)
ACAT1	1	147	147	acetyl-Coenzyme A acetyltransferase 1
C9orf86	2	147	148	chromosome 9 open reading frame 86
Ppp1cc	4	146	176	protein phosphatase 1, catalytic subunit, gamma isoform
GSTO1	1	146	146	glutathione S-transferase omega 1
PLEKHJ1	1	146	146	pleckstrin homology domain containing, family J member 1
NMRAL1	1	146	146	NmrA-like family domain containing 1
ctsf	2	146	167	cathepsin F
vdac2	5	146	169	voltage-dependent anion channel 2
NFIB	1	146	146	nuclear factor I/B
Entrez5500	2	146	164	
FLJ20021	1	146	146	hypothetical LOC90024
CTXN1	1	146	146	cortexin 1
GTF2F1	1	146	146	general transcription factor IIF, polypeptide 1, 74kDa
c20orf30	1	146	146	hypothetical LOC642975; chromosome 20 open reading frame 30
c17orf37	4	146	186	chromosome 17 open reading frame 37
TCEA3	2	146	152	transcription elongation factor A (SII), 3
Spg21	1	146	146	spastic paraplegia 21 (autosomal recessive, Mast syndrome)
dpm3	2	146	149	dolichyl-phosphate mannosyltransferase polypeptide 3
LOC100288778	1	145	145	similar to WAS protein family homolog 1
NDUFB11	9	145	180	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 11, 17.3kDa
SFRS9	5	145	171	splicing factor, arginine/serine-rich 9
CS	4	145	167	citrate synthase
akt2	1	145	145	v-akt murine thymoma viral oncogene homolog 2
gtf3c5	1	145	145	general transcription factor IIIC, polypeptide 5, 63kDa
TP53TG1	1	145	145	TP53 target 1 (non-protein coding)
AP2B1	1	145	145	adaptor-related protein complex 2, beta 1 subunit
COL9A2	2	145	161	collagen, type IX, alpha 2
clpP	2	145	156	ClpP caseinolytic peptidase, ATP-dependent, proteolytic subunit homolog (E. coli)

SF3A2	1	145	145	splicing factor 3a, subunit 2, 66kDa
Ap3d1	1	145	145	adaptor-related protein complex 3, delta 1 subunit
ACSM1	2	145	149	acyl-CoA synthetase medium-chain family member 1
Mlph	2	144	147	melanophilin
RTN1	1	144	144	reticulon 1
Impa2	2	144	167	inositol(myo)-1(or 4)-monophosphatase 2
smarcd2	1	144	144	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2
POLR2H	2	144	167	polymerase (RNA) II (DNA directed) polypeptide H
PECI	2	144	153	peroxisomal D3,D2-enoyl-CoA isomerase
C6orf173	1	144	144	chromosome 6 open reading frame 173
LOC100132658	1	144	144	hypothetical gene supported by NM_014886; TGF beta-inducible nuclear protein 1; similar to TGF beta-inducible nuclear protein 1
COX7B2	1	144	144	cytochrome c oxidase subunit VIIb2
NENF	3	144	163	neuron derived neurotrophic factor
ATP5F1	2	143	152	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1
anxa3	1	143	143	annexin A3
pam	2	143	161	peptidylglycine alpha-amidating monooxygenase
taf10	3	143	152	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30kDa
DDX17	1	143	143	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17
tomm40	1	143	143	translocase of outer mitochondrial membrane 40 homolog (yeast)
COMMD4	1	143	143	COMM domain containing 4
C6orf115	1	143	143	chromosome 6 open reading frame 115
mx1	1	143	143	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)
CNIH4	1	143	143	cornichon homolog 4 (Drosophila)
Entrez1159	2	143	148	
USP22	4	143	192	ubiquitin specific peptidase 22
RNASEH2A	2	143	157	ribonuclease H2, subunit A
MEA1	1	143	143	male-enhanced antigen 1
Hnrnpu	4	143	160	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)
snrpd3	1	143	143	small nuclear ribonucleoprotein D3 polypeptide 18kDa
vat1	2	143	152	vesicle amine transport protein 1 homolog (T. californica)
Tars	1	143	143	threonyl-tRNA synthetase
serbp1	1	142	142	SERPINE1 mRNA binding protein 1
LOC100131801	7	142	184	similar to hCG2036585
gsr	2	142	148	glutathione reductase
CAPZB	1	142	142	capping protein (actin filament) muscle Z-line, beta
gng5	1	142	142	guanine nucleotide binding protein (G protein), gamma 5
nkx2-1	2	142	154	NK2 homeobox 1
NR2F6	2	142	154	nuclear receptor subfamily 2, group F, member 6
MON1B	1	142	142	MON1 homolog B (yeast)
ACTL8	1	142	142	actin-like 8
UAP1	4	142	164	UDP-N-acteylglucosamine pyrophosphorylase 1
mael	1	142	142	maelstrom homolog (Drosophila)
tp53i11	1	142	142	tumor protein p53 inducible protein 11
TRIB2	1	142	142	tribbles homolog 2 (Drosophila)
SSBP1	2	142	146	single-stranded DNA binding protein 1
BACE2	1	142	142	beta-site APP-cleaving enzyme 2
FDPS	1	142	142	farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltranstransferase, geranyltranstransferase)
CLSTN1	2	141	143	calsyntenin 1
parp1	4	141	156	poly (ADP-ribose) polymerase 1

btg1	1	141	141	B-cell translocation gene 1, anti-proliferative
GDI1	5	141	152	GDP dissociation inhibitor 1
c11orf2	2	141	151	chromosome 11 open reading frame2
TRAPPC2L	2	141	151	trafficking protein particle complex 2-like
Entrez548596	2	141	144	
CYBA	2	141	146	cytochrome b-245, alpha polypeptide
sf3b1	2	141	143	splicing factor 3b, subunit 1, 155kDa
GIPC1	3	141	163	GIPC PDZ domain containing family, member 1
Cops6	4	140	153	COP9 constitutive photomorphogenic homolog subunit 6 (Arabidopsis)
FAM96B	2	140	148	family with sequence similarity 96, member B
safb	1	140	140	scaffold attachment factor B
Psma3	3	140	148	proteasome (prosome, macropain) subunit, alpha type, 3
ARPC5	2	140	159	actin related protein 2/3 complex, subunit 5, 16kDa
YWHAH	1	140	140	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide
C17orf93	1	140	140	chromosome 17 open reading frame 93
Entrez154043	2	140	152	
CLNS1A	2	140	152	chloride channel, nucleotide-sensitive, 1A
ppp3ca	2	140	140	protein phosphatase 3 (formerly 2B), catalytic subunit, alpha isoform
SFRS3	2	140	149	splicing factor, arginine/serine-rich 3
Tmem79	1	140	140	transmembrane protein 79
YKT6	1	140	140	YKT6 v-SNARE homolog (S. cerevisiae)
PIGS	1	140	140	phosphatidylinositol glycan anchor biosynthesis, class S
TMBIM1	1	139	139	transmembrane BAX inhibitor motif containing 1
MESP1	1	139	139	mesoderm posterior 1 homolog (mouse)
Aup1	1	139	139	ancient ubiquitous protein 1
Entrez100505641	1	139	139	
EFNA1	1	139	139	ephrin-A1
SEC63	1	139	139	SEC63 homolog (S. cerevisiae)
LSM4	3	139	146	LSM4 homolog, U6 small nuclear RNA associated (S. cerevisiae)
LOC643167	1	139	139	similar to RNA binding motif protein 39; RNA binding motif protein 39
Magea6	1	139	139	melanoma antigen family A, 6
DRAP1	3	139	158	DR1-associated protein 1 (negative cofactor 2 alpha)
EID1	1	138	138	EP300 interacting inhibitor of differentiation 1
LOC643446	4	138	151	similar to ribonucleic acid binding protein S1; RNA binding protein S1, serine-rich domain
POLR2J	3	138	151	polymerase (RNA) II (DNA directed) polypeptide J, 13.3kDa
csnk1a1	2	138	142	casein kinase 1, alpha 1
MRPL14	1	138	138	mitochondrial ribosomal protein L14
RNASET2	1	138	138	ribonuclease T2
LOC100132308	1	138	138	solute carrier family 29 (nucleoside transporters), member 4; similar to solute carrier family 29 (nucleoside transporters), member 4
Six2	1	138	138	SIX homeobox 2
GADD45A	1	138	138	growth arrest and DNA-damage-inducible, alpha
Tmem111	1	138	138	transmembrane protein 111
CAPN2	3	138	139	calpain 2, (m/II) large subunit
cct4	4	138	150	chaperonin containing TCP1, subunit 4 (delta)
Ubxn1	1	138	138	UBX domain protein 1
lass2	1	138	138	LAG1 homolog, ceramide synthase 2
IMPDH1	1	138	138	IMP (inosine monophosphate) dehydrogenase 1
BEX1	2	137	154	brain expressed, X-linked 1
SEPHS2	2	137	138	selenophosphate synthetase 2

SFTPA2	1	137	137	surfactant protein A2; surfactant protein A2B
Cdc25b	1	137	137	cell division cycle 25 homolog B (S. pombe)
mcl1	1	137	137	myeloid cell leukemia sequence 1 (BCL2-related)
Cirbp	5	137	175	cold inducible RNA binding protein
rasd1	1	137	137	RAS, dexamethasone-induced 1
C12orf44	1	137	137	chromosome 12 open reading frame 44
nudC	1	137	137	nuclear distribution gene C homolog (A. nidulans)
MRPS21	1	137	137	mitochondrial ribosomal protein S21
psmd7	1	137	137	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7
ZNF207	1	137	137	zinc finger protein 207
ENDOD1	1	137	137	endonuclease domain containing 1
TP53INP1	1	137	137	tumor protein p53 inducible nuclear protein 1
MCM7	1	136	136	minichromosome maintenance complex component 7
RTN3	2	136	144	reticulon 3
Cox7a2l	3	136	142	cytochrome c oxidase subunit VIIa polypeptide 2 like
Spsb3	1	136	136	splA/ryanodine receptor domain and SOCS box containing 3
sumf2	2	136	154	sulfatase modifying factor 2
ssu72	4	136	144	SSU72 RNA polymerase II CTD phosphatase homolog (S. cerevisiae)
UBA2	1	136	136	ubiquitin-like modifier activating enzyme 2
MAOB	1	136	136	monoamine oxidase B
HIF1A	1	136	136	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
ebpl	1	136	136	emopamil binding protein-like
LOC100129585	1	136	136	similar to RNA binding motif protein, X-linked; similar to hCG2011544; RNA binding motif protein, X-linked
PDXDC1	3	136	137	pyridoxal-dependent decarboxylase domain containing 1
Nop56	1	136	136	NOP56 ribonucleoprotein homolog (yeast)
FH	1	136	136	fumarate hydratase
Cdk4	3	135	145	cyclin-dependent kinase 4
atp6v0d1	1	135	135	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d1
Cdk2ap1	1	135	135	cyclin-dependent kinase 2 associated protein 1
CRMP1	1	135	135	collapsin response mediator protein 1
Actr2	2	135	141	ARP2 actin-related protein 2 homolog (yeast)
NFE2L1	1	135	135	nuclear factor (erythroid-derived 2)-like 1
copz1	1	135	135	coatomer protein complex, subunit zeta 1
ATP2A2	2	135	154	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2
TMEM176B	1	135	135	transmembrane protein 176B
isoc2	1	135	135	isochorismatase domain containing 2
SHMT2	3	135	141	serine hydroxymethyltransferase 2 (mitochondrial)
PRKCD	1	135	135	protein kinase C, delta
Ckap4	1	135	135	cytoskeleton-associated protein 4
CLPTM1L	2	135	136	CLPTM1-like
LOC402175	3	135	143	hypothetical gene supported by AF044957; NM_004547; NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 4, 15kDa
Lpcat3	2	135	144	lysophosphatidylcholine acyltransferase 3
SMARCC1	1	135	135	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1
LOC647979	2	134	141	hypothetical LOC647979
HNRNPA0	2	134	135	heterogeneous nuclear ribonucleoprotein A0
fus	2	134	147	fusion (involved in t(12;16) in malignant liposarcoma)
CDKN2A	1	134	134	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
CAB39L	1	134	134	calcium binding protein 39-like
Igfbpl1	1	134	134	insulin-like growth factor binding protein-like 1

Eif5b	1	134	134	eukaryotic translation initiation factor 5B
ATP6V1G1	2	134	141	ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1
COPB1	1	134	134	coatomer protein complex, subunit beta 1
PDCD4	2	134	138	programmed cell death 4 (neoplastic transformation inhibitor)
Cenpb	2	133	150	centromere protein B, 80kDa
YWHAG	3	133	147	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide
KIF1A	1	133	133	kinesin family member 1A
Scoc	1	133	133	short coiled-coil protein
DDX3X	1	133	133	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, X-linked
mRpS33	2	133	137	mitochondrial ribosomal protein S33
plxnb2	1	132	132	plexin B2
SURF2	1	132	132	surfeit 2
SdhB	1	132	132	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)
ELOF1	2	132	137	elongation factor 1 homolog (S. cerevisiae)
Zdhhc12	1	132	132	zinc finger, DHHC-type containing 12
Uts2d	1	132	132	urotensin 2 domain containing
FKBP3	2	132	145	FK506 binding protein 3, 25kDa
Jam3	1	132	132	junctional adhesion molecule 3
wdr1	3	132	137	WD repeat domain 1
tomm5	2	132	149	translocase of outer mitochondrial membrane 5 homolog (yeast)
hbxip	1	132	132	hepatitis B virus x interacting protein
REPIN1	2	132	136	replication initiator 1
CDKN3	1	131	131	cyclin-dependent kinase inhibitor 3
SIM2	2	131	132	single-minded homolog 2 (Drosophila)
SPATA20	1	131	131	spermatogenesis associated 20
CLEC7A	1	131	131	C-type lectin domain family 7, member A
SAE1	1	131	131	SUMO1 activating enzyme subunit 1
SYT4	1	131	131	synaptotagmin IV
lpcat1	2	131	139	lysophosphatidylcholine acyltransferase 1
KIAA1522	1	131	131	KIAA1522
calca	1	131	131	calcitonin-related polypeptide alpha
RNPEPL1	1	130	130	arginyl aminopeptidase (aminopeptidase B)-like 1
Alkbh7	1	130	130	alkB, alkylation repair homolog 7 (E. coli)
glrx5	2	130	140	glutaredoxin 5
STAP2	2	130	131	signal transducing adaptor family member 2
ASRGL1	2	130	130	asparaginase like 1
strap	2	130	138	serine/threonine kinase receptor associated protein
TFDP1	1	129	129	transcription factor Dp-1
SLC36A4	1	129	129	solute carrier family 36 (proton/amino acid symporter), member 4
Mapre1	1	129	129	microtubule-associated protein, RP/EB family, member 1
rheb	1	129	129	Ras homolog enriched in brain
Crat	1	128	128	carnitine acetyltransferase
Pcsk2	1	128	128	proprotein convertase subtilisin/kexin type 2
rbm38	2	128	131	RNA binding motif protein 38
H2AFV	1	128	128	H2A histone family, member V
MCM4	1	128	128	minichromosome maintenance complex component 4
DCTPP1	1	128	128	dCTP pyrophosphatase 1
Entrez154043	1	128	128	
C4orf48	1	128	128	chromosome 4 open reading frame 48
HLA-A	1	128	128	major histocompatibility complex, class I, A

LARP1	1	128	128	La ribonucleoprotein domain family, member 1
PGD	1	128	128	phosphogluconate dehydrogenase
GLUL	1	127	127	glutamate-ammonia ligase (glutamine synthetase)
FARSB	1	127	127	phenylalanyl-tRNA synthetase, beta subunit
ilf3	1	127	127	interleukin enhancer binding factor 3, 90kDa
ptp4a1	1	127	127	protein tyrosine phosphatase type IVA, member 1
Rrm1	1	127	127	ribonucleotide reductase M1
Rgs10	2	127	129	regulator of G-protein signaling 10
CCDC85B	1	127	127	coiled-coil domain containing 85B
SNHG1	1	127	127	small nucleolar RNA host gene 1 (non-protein coding)
SUPT16H	1	127	127	suppressor of Ty 16 homolog (S. cerevisiae); suppressor of Ty 16 homolog (S. cerevisiae) pseudogene
TBCB	1	127	127	tubulin folding cofactor B
BTG2	1	126	126	BTG family, member 2
KIAA0196	1	126	126	KIAA0196
C6orf62	1	126	126	chromosome 6 open reading frame 62
Cdc42	1	126	126	cell division cycle 42 (GTP binding protein, 25kDa); cell division cycle 42 pseudogene 2
rars	1	126	126	arginyl-tRNA synthetase
thoc7	1	126	126	THO complex 7 homolog (Drosophila)
INSIG1	1	126	126	insulin induced gene 1
Dazap2	1	125	125	DAZ associated protein 2
PCNP	1	125	125	PEST proteolytic signal containing nuclear protein
WBP2	1	125	125	WW domain binding protein 2
LOC652798	1	125	125	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome); similar to plakophilin 1 isoform 1a
Sertad3	1	125	125	SERTA domain containing 3
Bub3	1	125	125	budding uninhibited by benzimidazoles 3 homolog (yeast)
RAD23B	2	125	131	RAD23 homolog B (S. cerevisiae)
Jun	2	125	126	jun oncogene
Tob1	1	125	125	transducer of ERBB2, 1
PSMD13	1	124	124	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13
Galnt7	1	124	124	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)
aldh1a1	1	124	124	aldehyde dehydrogenase 1 family, member A1
ndufs3	1	124	124	NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reductase)
ddc	2	124	129	dopa decarboxylase (aromatic L-amino acid decarboxylase)
nthl1	1	124	124	nth endonuclease III-like 1 (E. coli)
C20orf3	3	124	127	chromosome 20 open reading frame 3
Tpx2	1	123	123	TPX2, microtubule-associated, homolog (Xenopus laevis)
STARD7	1	123	123	StAR-related lipid transfer (START) domain containing 7
RPL23P8	1	123	123	ribosomal protein L23 pseudogene 8
FLJ26850	1	122	122	FLJ26850 protein
MGLL	1	122	122	monoglyceride lipase
SFTA3	2	122	125	surfactant associated 3
Smarce1	1	119	119	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1
Sept9	1	119	119	septin 9
MBD3	1	119	119	methyl-CpG binding domain protein 3
TBL1XR1	1	119	119	transducin (beta)-like 1 X-linked receptor 1
SEC11A	1	118	118	SEC11 homolog A (S. cerevisiae)
PSIP1	1	118	118	PC4 and SFRS1 interacting protein 1
Khdrbs1	1	117	117	KH domain containing, RNA binding, signal transduction associated 1

ISLR	1	116	116	immunoglobulin superfamily containing leucine-rich repeat
NET1	1	116	116	neuroepithelial cell transforming 1
MAGEF1	1	116	116	melanoma antigen family F, 1
cpd	1	116	116	carboxypeptidase D
MYBL2	1	115	115	v-myb myeloblastosis viral oncogene homolog (avian)-like 2
CORO1C	1	115	115	coronin, actin binding protein, 1C
actl6a	1	115	115	actin-like 6A
Yipf3	1	114	114	Yip1 domain family, member 3
cebpd	1	113	113	CCAAT/enhancer binding protein (C/EBP), delta

Table S2.

Differential Expression (DE) in neuroendocrine vs adenocarcinoma LuCaPs (n=24)
FDR < 0.01: n=1,361 genes

SYMBOL	logFC	logCPM	PValue	FDR	Gene Name
PCSK1	10.97	5.34	2.19E-63	3.69E-59	proprotein convertase subtilisin/kexin type 1
Grik3	10.97	4.37	1.89E-50	1.59E-46	glutamate receptor, ionotropic, kainate 3
CHRNB2	8.96	4.11	9.23E-50	5.20E-46	cholinergic receptor, nicotinic, beta 2 (neuronal)
ADCYAP1	12.35	3.76	3.15E-45	1.33E-41	adenylate cyclase activating polypeptide 1 (pituitary)
Ncam1	9.45	4.57	2.63E-44	8.89E-41	neural cell adhesion molecule 1
SLC6A5	12.75	3.92	8.54E-41	2.40E-37	solute carrier family 6 (neurotransmitter transporter, glycine), member 5
Pcsk2	11.51	5.07	3.89E-38	9.38E-35	proprotein convertase subtilisin/kexin type 2
SEZ6	8.28	5.04	2.13E-37	4.49E-34	seizure related 6 homolog (mouse)
SFTA3	10.09	4.13	7.45E-37	1.40E-33	surfactant associated 3
Cacna1a	9.18	5.19	3.23E-36	5.46E-33	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit
HOXD11	11.27	2.78	1.21E-33	1.86E-30	homeobox D11
SLC35D3	11.31	3.16	1.86E-32	2.62E-29	solute carrier family 35, member D3
NR0B2	10.28	2.62	5.71E-32	7.41E-29	nuclear receptor subfamily 0, group B, member 2
FGF9	10.67	2.11	4.15E-31	5.01E-28	fibroblast growth factor 9 (glia-activating factor)
GRP	12.05	5.81	2.36E-29	2.65E-26	gastrin-releasing peptide
L1cam	7.11	4.15	2.57E-29	2.71E-26	L1 cell adhesion molecule
adcy5	6.36	4.94	3.87E-29	3.84E-26	adenylate cyclase 5
islr2	9.23	3.33	4.90E-29	4.59E-26	immunoglobulin superfamily containing leucine-rich repeat 2
Kcnb2	14.30	1.86	5.47E-29	4.87E-26	potassium voltage-gated channel, Shab-related subfamily, member 2
SNAP25	10.31	2.63	7.99E-29	6.75E-26	synaptosomal-associated protein, 25kDa
HOXD10	10.39	2.38	2.00E-28	1.61E-25	homeobox D10
SEZ6L	11.97	3.68	4.99E-28	3.83E-25	seizure related 6 homolog (mouse)-like
CA10	10.51	2.80	2.63E-27	1.93E-24	carbonic anhydrase X
Ascl1	9.09	7.31	4.70E-27	3.31E-24	achaete-scute complex homolog 1 (Drosophila)
DLL3	7.18	4.33	9.78E-26	6.61E-23	delta-like 3 (Drosophila)
NEUROG3	9.67	2.09	1.30E-25	8.44E-23	neurogenin 3
KCNA1	11.97	3.06	4.00E-25	2.50E-22	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)
SLCO3A1	7.99	3.00	5.20E-25	3.14E-22	solute carrier organic anion transporter family, member 3A1
scg2	8.18	5.48	7.01E-25	4.08E-22	secretogranin II (chromogranin C)
TAGLN3	9.25	2.62	1.60E-24	9.02E-22	transgelin 3
FRZB	8.39	4.19	1.88E-24	1.03E-21	frizzled-related protein
ASXL3	9.41	2.62	1.98E-24	1.04E-21	additional sex combs like 3 (Drosophila)
PTPRN	7.61	3.72	2.36E-24	1.21E-21	protein tyrosine phosphatase, receptor type, N
CHRNA9	9.85	1.57	4.82E-24	2.40E-21	cholinergic receptor, nicotinic, alpha 9
PDE5A	7.17	4.40	6.52E-24	3.15E-21	phosphodiesterase 5A, cGMP-specific
SLC6A20	7.22	3.34	6.99E-24	3.28E-21	solute carrier family 6 (proline IMINO transporter), member 20
Serpinf1	5.42	3.52	7.89E-24	3.60E-21	serpin peptidase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1
Kbtbd12	8.14	1.98	1.06E-23	4.73E-21	kelch domain containing 6
BTBD17	9.25	1.63	1.22E-23	5.29E-21	BTB (POZ) domain containing 17
ISLR	11.50	3.21	1.31E-23	5.52E-21	immunoglobulin superfamily containing leucine-rich repeat
FAM163B	10.43	1.17	1.43E-23	5.88E-21	family with sequence similarity 163, member B
Tmem176a	9.47	3.54	2.09E-23	8.42E-21	transmembrane protein 176A
PEX5L	6.57	2.80	1.10E-22	4.33E-20	peroxisomal biogenesis factor 5-like
SFRP5	9.08	3.11	1.61E-22	6.19E-20	secreted frizzled-related protein 5
CHST1	6.47	4.69	4.24E-22	1.59E-19	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1
rgs7	8.48	1.37	6.48E-22	2.38E-19	regulator of G-protein signaling 7
ACTL6B	8.98	1.49	6.91E-22	2.48E-19	actin-like 6B
C1orf127	7.61	3.47	7.67E-22	2.70E-19	chromosome 1 open reading frame 127
LOC283731	9.54	2.00	9.46E-22	3.26E-19	hypothetical protein LOC283731

fli1	10.43	0.76	1.63E-21	5.51E-19	Friend leukemia virus integration 1
TMEM176B	8.17	4.06	4.08E-21	1.35E-18	transmembrane protein 176B
CTHRC1	6.16	2.86	5.41E-21	1.76E-18	collagen triple helix repeat containing 1
KLHL14	9.68	3.21	8.54E-21	2.72E-18	kelch-like 14 (Drosophila)
ADAMTS18	8.62	1.11	1.27E-20	3.98E-18	ADAM metallopeptidase with thrombospondin type 1 motif, 18
CEACAM5	8.02	8.09	1.50E-20	4.60E-18	carcinoembryonic antigen-related cell adhesion molecule 5
SCN3A	7.55	4.96	5.64E-20	1.70E-17	sodium channel, voltage-gated, type III, alpha subunit
AJAP1	8.85	1.03	6.99E-20	2.07E-17	adherens junctions associated protein 1
COL1A2	7.50	3.38	1.28E-19	3.71E-17	collagen, type I, alpha 2
SLC26A9	8.37	1.84	1.31E-19	3.74E-17	solute carrier family 26, member 9
Ceacam6	5.29	5.63	1.63E-19	4.58E-17	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen)
LMO3	6.70	4.44	2.05E-19	5.60E-17	LIM domain only 3 (rhombotin-like 2)
CRMP1	5.92	5.40	2.06E-19	5.60E-17	collapsin response mediator protein 1
hmp19	9.89	4.21	2.15E-19	5.77E-17	HMP19 protein
KCNH7	7.97	1.51	2.41E-19	6.36E-17	potassium voltage-gated channel, subfamily H (eag-related), member 7
Miat	6.86	2.92	3.06E-19	7.95E-17	myocardial infarction associated transcript (non-protein coding)
GPC3	4.93	4.67	3.28E-19	8.41E-17	glypican 3
mmp16	8.06	2.18	3.47E-19	8.75E-17	matrix metallopeptidase 16 (membrane-inserted)
RUNDC3A	5.29	4.03	7.33E-19	1.82E-16	RUN domain containing 3A
STK32B	11.18	1.03	9.82E-19	2.40E-16	serine/threonine kinase 32B
csf3r	8.54	1.92	1.74E-18	4.19E-16	colony stimulating factor 3 receptor (granulocyte)
Fam181a	7.89	0.15	1.92E-18	4.56E-16	family with sequence similarity 181, member A
CRABP1	6.78	4.43	4.38E-18	1.03E-15	cellular retinoic acid binding protein 1
cspg4	5.72	2.99	8.18E-18	1.89E-15	chondroitin sulfate proteoglycan 4
HAPLN1	10.97	1.08	8.84E-18	2.02E-15	hyaluronan and proteoglycan link protein 1
DCX	8.22	1.12	9.69E-18	2.18E-15	doublecortin
NDST4	8.78	0.68	1.13E-17	2.50E-15	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
B3GNT8	7.31	1.92	1.73E-17	3.79E-15	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 8
npas4	9.34	-0.41	2.58E-17	5.59E-15	neuronal PAS domain protein 4
cldn18	8.20	0.51	2.80E-17	5.99E-15	claudin 18
sec11c	4.25	7.88	3.60E-17	7.51E-15	SEC11 homolog C (S. cerevisiae)
IGFBP5	5.42	6.94	3.59E-17	7.51E-15	insulin-like growth factor binding protein 5
col19a1	7.36	1.04	5.50E-17	1.13E-14	collagen, type XIX, alpha 1
SV2B	7.99	4.29	1.11E-16	2.26E-14	synaptic vesicle glycoprotein 2B; hypothetical protein LOC100128403
JAKMIP2	6.56	1.94	1.95E-16	3.93E-14	Janus kinase and microtubule interacting protein 2
Kcnk16	9.63	0.34	2.02E-16	4.01E-14	potassium channel, subfamily K, member 16
Pla2g12b	8.20	-0.81	2.87E-16	5.63E-14	phospholipase A2, group XIIB
vstm2b	11.96	1.22	3.44E-16	6.69E-14	V-set and transmembrane domain containing 2B
nkx2-1	7.20	5.42	4.84E-16	9.29E-14	NK2 homeobox 1
Kcnj6	6.98	0.47	4.95E-16	9.40E-14	potassium inwardly-rectifying channel, subfamily J, member 6
Zdhhc22	8.00	1.76	5.33E-16	9.89E-14	zinc finger, DHHC-type containing 22
LCN10	7.53	0.98	5.29E-16	9.89E-14	lipocalin 10
chrm4	6.90	2.35	7.10E-16	1.30E-13	cholinergic receptor, muscarinic 4
ralyl	7.22	2.48	7.30E-16	1.33E-13	RALY RNA binding protein-like
Slitrk6	6.27	4.93	1.38E-15	2.48E-13	SLIT and NTRK-like family, member 6
CDH2	7.77	3.95	1.45E-15	2.59E-13	cadherin 2, type 1, N-cadherin (neuronal)
NUAK1	3.42	4.95	1.49E-15	2.62E-13	NUAK family, SNF1-like kinase, 1
NRSN1	7.87	0.36	1.63E-15	2.84E-13	neurensin 1
INSRR	7.49	-0.39	1.82E-15	3.13E-13	insulin receptor-related receptor
POMC	8.29	2.77	2.26E-15	3.85E-13	proopiomelanocortin
slc34a2	6.42	2.34	2.35E-15	3.97E-13	solute carrier family 34 (sodium phosphate), member 2
Foxb1	8.56	0.46	2.82E-15	4.72E-13	forkhead box B1
ENTREZ100507003	8.61	1.06	2.93E-15	4.86E-13	
mafA	6.18	2.54	4.44E-15	7.29E-13	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)
GPR6	8.79	-0.23	4.62E-15	7.50E-13	G protein-coupled receptor 6

RNF182	6.63	3.16	5.40E-15	8.69E-13	ring finger protein 182
KCNK2	9.69	0.72	5.66E-15	9.02E-13	potassium channel, subfamily K, member 2
CALB2	7.23	1.19	6.31E-15	9.96E-13	calbindin 2
SLC7A14	9.44	1.55	7.79E-15	1.22E-12	solute carrier family 7 (cationic amino acid transporter, y+ system), member 14
TPH1	8.45	4.20	1.08E-14	1.68E-12	tryptophan hydroxylase 1
LYPD1	6.53	1.65	1.10E-14	1.69E-12	LY6/PLAUR domain containing 1
Grik5	5.04	3.19	1.21E-14	1.84E-12	glutamate receptor, ionotropic, kainate 5
Nell1	8.96	3.56	1.25E-14	1.89E-12	NEL-like 1 (chicken)
BAALC	6.91	4.03	1.29E-14	1.92E-12	brain and acute leukemia, cytoplasmic
PGM2L1	3.90	5.47	1.34E-14	1.99E-12	phosphoglucomutase 2-like 1
TRIM67	5.90	1.05	1.36E-14	2.00E-12	tripartite motif-containing 67
fxyd6	5.94	4.23	1.42E-14	2.07E-12	FXYD domain containing ion transport regulator 6
JSRP1	7.11	2.26	1.56E-14	2.26E-12	junctional sarcoplasmic reticulum protein 1
FAM123C	7.05	3.12	1.59E-14	2.27E-12	family with sequence similarity 123C
Insm1	7.25	6.69	1.91E-14	2.71E-12	insulinoma-associated 1
KCNH8	6.50	2.89	2.14E-14	3.01E-12	potassium voltage-gated channel, subfamily H (eag-related), member 8
DRD2	6.40	2.92	2.26E-14	3.16E-12	dopamine receptor D2
AP3B2	5.89	2.89	2.38E-14	3.29E-12	adaptor-related protein complex 3, beta 2 subunit
pam	5.17	6.47	2.65E-14	3.64E-12	peptidylglycine alpha-amidating monooxygenase
Kirrel2	10.18	2.12	3.84E-14	5.22E-12	kin of IRRE like 2 (Drosophila)
Rftn1	5.63	2.40	4.16E-14	5.62E-12	raftlin, lipid raft linker 1
Arhgef2	3.53	5.66	4.34E-14	5.82E-12	Rho/Rac guanine nucleotide exchange factor (GEF) 2
ELAVL3	7.58	2.85	4.49E-14	5.97E-12	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)
SCG3	6.09	4.25	4.59E-14	6.06E-12	secretogranin III
sftpb	7.00	0.50	5.45E-14	7.13E-12	surfactant protein B
hoxb5	6.45	4.37	6.29E-14	8.17E-12	homeobox B5
GFRA4	8.02	-0.31	6.35E-14	8.18E-12	GDNF family receptor alpha 4
PLAC8	6.37	1.69	7.36E-14	9.42E-12	placenta-specific 8
Col22a1	7.76	3.92	7.61E-14	9.66E-12	collagen, type XXII, alpha 1
CCDC129	8.18	-0.86	8.10E-14	1.02E-11	coiled-coil domain containing 129
NPTX1	6.58	6.59	8.55E-14	1.07E-11	neuronal pentraxin I
VAT1L	9.96	-0.93	1.05E-13	1.31E-11	vesicle amine transport protein 1 homolog (T. californica)-like
COL21A1	6.25	1.55	1.31E-13	1.62E-11	collagen, type XXI, alpha 1
Ngf	7.92	-0.96	1.85E-13	2.27E-11	nerve growth factor (beta polypeptide)
Sgip1	6.95	0.05	1.90E-13	2.31E-11	SH3-domain GRB2-like (endophilin) interacting protein 1
GNG2	7.27	1.65	1.92E-13	2.32E-11	guanine nucleotide binding protein (G protein), gamma 2
Ceacam3	9.10	-0.66	2.05E-13	2.46E-11	carcinoembryonic antigen-related cell adhesion molecule 3
Hes6	4.43	6.43	2.13E-13	2.53E-11	hairy and enhancer of split 6 (Drosophila)
BAI3	8.53	0.81	2.22E-13	2.63E-11	brain-specific angiogenesis inhibitor 3
DES	7.67	0.30	2.24E-13	2.63E-11	desmin
CACNG5	8.56	-2.13	2.98E-13	3.47E-11	calcium channel, voltage-dependent, gamma subunit 5
ADAMTSL2	6.75	3.50	3.24E-13	3.75E-11	similar to ADAMTS-like 2; ADAMTS-like 2
NPHS1	8.30	1.26	3.68E-13	4.23E-11	nephrosis 1, congenital, Finnish type (nephrin)
PGLYRP4	7.84	0.26	4.09E-13	4.66E-11	peptidoglycan recognition protein 4
ENTREZ100507377	7.42	-0.24	4.40E-13	4.99E-11	
Kcnc1	5.82	2.49	4.58E-13	5.16E-11	potassium voltage-gated channel, Shaw-related subfamily, member 1
EFR3B	4.78	4.76	4.62E-13	5.17E-11	EFR3 homolog B (S. cerevisiae)
ADAM23	6.07	2.49	5.69E-13	6.32E-11	ADAM metallopeptidase domain 23
Col4a1	7.11	0.34	5.82E-13	6.42E-11	collagen, type IV, alpha 1
HOXB8	5.79	4.60	6.15E-13	6.74E-11	homeobox B8
RPRM	6.27	2.37	6.37E-13	6.95E-11	reprimo, TP53 dependent G2 arrest mediator candidate
ampH	5.78	0.93	6.60E-13	7.13E-11	amphiphysin
C18orf34	7.93	-1.03	6.63E-13	7.13E-11	chromosome 18 open reading frame 34
Rab3c	8.45	-1.81	6.70E-13	7.16E-11	RAB3C, member RAS oncogene family
REV3L	2.97	5.37	7.36E-13	7.82E-11	REV3-like, catalytic subunit of DNA polymerase zeta (yeast)
RHOJ	7.13	-1.48	7.53E-13	7.95E-11	ras homolog gene family, member J

ENTREZ10407	8.21	1.92	7.66E-13	8.03E-11	
Kcnk10	6.18	0.51	8.43E-13	8.79E-11	potassium channel, subfamily K, member 10
KCNK9	6.61	0.24	8.80E-13	9.12E-11	potassium channel, subfamily K, member 9
BEX1	4.87	3.89	8.93E-13	9.20E-11	brain expressed, X-linked 1
nr5a1	7.80	1.10	9.06E-13	9.28E-11	nuclear receptor subfamily 5, group A, member 1
RETNLB	6.44	-0.87	9.52E-13	9.69E-11	resistin like beta
TMEM163	6.36	1.89	1.10E-12	1.10E-10	transmembrane protein 163
C12orf39	7.23	1.23	1.10E-12	1.10E-10	chromosome 12 open reading frame 39
SIT1	8.45	-1.93	1.09E-12	1.10E-10	signaling threshold regulating transmembrane adaptor 1
pak7	7.36	-1.11	1.35E-12	1.34E-10	p21 protein (Cdc42/Rac)-activated kinase 7
HMSD	7.88	-0.94	1.37E-12	1.35E-10	histocompatibility (minor) serpin domain containing
GLT8D2	4.53	0.85	1.38E-12	1.35E-10	glycosyltransferase 8 domain containing 2
GRM8	7.38	2.28	1.48E-12	1.44E-10	glutamate receptor, metabotropic 8
tubb2b	3.38	7.37	1.49E-12	1.44E-10	tubulin, beta 2B
HMX2	7.94	-0.51	1.50E-12	1.44E-10	H6 family homeobox 2
FCGBP	4.28	4.18	1.79E-12	1.71E-10	Fc fragment of IgG binding protein; similar to IgGFc-binding protein precursor (FcgammaBP) (Fcgamma-binding protein antigen)
FGF14	6.93	0.88	2.05E-12	1.95E-10	fibroblast growth factor 14
phyhipl	6.76	2.66	2.28E-12	2.16E-10	phytanoyl-CoA 2-hydroxylase interacting protein-like
CADM3	11.38	-1.46	2.44E-12	2.30E-10	cell adhesion molecule 3
cotl1	3.68	7.90	2.53E-12	2.37E-10	coactosin-like 1 (Dictyostelium)
MYT1L	6.47	-0.77	2.64E-12	2.46E-10	myelin transcription factor 1-like
SPDEF	-7.55	8.60	2.93E-12	2.72E-10	SAM pointed domain containing ets transcription factor
KIF26A	5.58	5.21	3.20E-12	2.93E-10	kinesin family member 26A
HS3ST6	7.06	0.44	3.20E-12	2.93E-10	heparan sulfate (glucosamine) 3-O-sulfotransferase 6
lpgat1	3.16	6.71	3.30E-12	3.01E-10	lysophosphatidylglycerol acyltransferase 1
cxcr7	4.65	4.32	3.42E-12	3.11E-10	chemokine (C-X-C motif) receptor 7
Lrtm2	5.94	2.71	3.49E-12	3.15E-10	leucine-rich repeats and transmembrane domains 2
ddc	5.76	5.26	3.71E-12	3.33E-10	dopa decarboxylase (aromatic L-amino acid decarboxylase)
LOC404266	5.80	2.35	3.80E-12	3.39E-10	hypothetical LOC404266
FAM70B	6.40	-0.03	4.33E-12	3.85E-10	family with sequence similarity 70, member B
SLC36A4	4.27	5.02	4.40E-12	3.89E-10	solute carrier family 36 (proton/amino acid symporter), member 4
psd	4.76	3.02	5.33E-12	4.68E-10	pleckstrin and Sec7 domain containing
SCGB1D1	10.04	-1.45	5.39E-12	4.72E-10	secretoglobin, family 1D, member 1
PLUNC	10.47	-2.01	6.10E-12	5.31E-10	palate, lung and nasal epithelium associated
NHS	5.03	2.89	6.23E-12	5.40E-10	Nance-Horan syndrome (congenital cataracts and dental anomalies)
NRP2	5.20	1.48	6.96E-12	5.99E-10	neuropilin 2
LOXHD1	5.70	-0.93	7.01E-12	6.01E-10	lipoxygenase homology domains 1
C13orf36	7.17	-0.44	7.46E-12	6.37E-10	chromosome 13 open reading frame 36
ADAM33	5.97	2.72	7.66E-12	6.50E-10	ADAM metallopeptidase domain 33
HMX3	10.31	-0.33	7.72E-12	6.52E-10	H6 family homeobox 3
EML1	-6.45	5.03	8.17E-12	6.87E-10	echinoderm microtubule associated protein like 1
MYBPHL	8.75	-0.56	9.24E-12	7.73E-10	myosin binding protein H-like
Jakmip1	6.63	1.63	9.40E-12	7.82E-10	Janus kinase and microtubule interacting protein 1
Sorcs2	4.94	1.61	1.02E-11	8.48E-10	sortilin-related VPS10 domain containing receptor 2
Itln1	7.27	0.81	1.06E-11	8.70E-10	intelectin 1 (galactofuranose binding)
FGF18	5.75	1.57	1.15E-11	9.43E-10	fibroblast growth factor 18
celf3	5.09	2.76	1.19E-11	9.69E-10	trinucleotide repeat containing 4
IRF8	6.50	0.74	1.29E-11	1.05E-09	interferon regulatory factor 8
LEMD1	6.20	-1.64	1.33E-11	1.07E-09	LEM domain containing 1
gck	6.01	1.40	1.33E-11	1.07E-09	glucokinase (hexokinase 4)
Grm4	5.34	2.26	1.39E-11	1.11E-09	glutamate receptor, metabotropic 4
KIRREL3	6.05	0.72	1.39E-11	1.11E-09	kin of IRRE like 3 (Drosophila)
ENTREZ100506305	6.92	1.10	1.42E-11	1.13E-09	
ina	6.25	5.03	1.50E-11	1.19E-09	internexin neuronal intermediate filament protein, alpha
PEG10	4.46	7.62	1.53E-11	1.20E-09	paternally expressed 10

LCN15	6.54	1.10	1.67E-11	1.31E-09	lipocalin 15
pth2	9.15	-1.27	1.70E-11	1.32E-09	parathyroid hormone 2
gfra1	6.54	2.63	1.71E-11	1.33E-09	GDNF family receptor alpha 1
dusp6	3.51	3.45	1.85E-11	1.43E-09	dual specificity phosphatase 6
DLL4	5.06	1.60	1.90E-11	1.46E-09	delta-like 4 (Drosophila)
KIF19	6.42	4.31	2.20E-11	1.68E-09	kinesin family member 19
PROM1	6.38	1.37	2.23E-11	1.70E-09	prominin 1
phyhd1	5.89	1.77	2.41E-11	1.83E-09	phytanoyl-CoA dioxygenase domain containing 1
ENTREZ5644	9.79	-2.07	2.44E-11	1.84E-09	
Dscaml1	5.47	1.83	2.77E-11	2.08E-09	Down syndrome cell adhesion molecule like 1
UGT3A1	5.31	3.08	2.80E-11	2.10E-09	UDP glycosyltransferase 3 family, polypeptide A1
KIAA1644	6.19	2.73	2.82E-11	2.10E-09	KIAA1644
PRMT8	7.57	0.63	2.85E-11	2.11E-09	protein arginine methyltransferase 8
DNAJC6	4.06	3.82	2.87E-11	2.12E-09	DnaJ (Hsp40) homolog, subfamily C, member 6
CCDC88A	4.44	4.68	3.13E-11	2.30E-09	coiled-coil domain containing 88A
CBLN2	5.59	2.81	3.25E-11	2.38E-09	cerebellin 2 precursor
SERGEF	2.92	5.70	3.56E-11	2.59E-09	secretion regulating guanine nucleotide exchange factor
Otof	6.75	0.67	4.08E-11	2.96E-09	otoferlin
Fam5b	5.84	-0.47	4.81E-11	3.47E-09	family with sequence similarity 5, member B
srrm4	5.96	1.44	5.55E-11	3.99E-09	KIAA1853
Fam26e	7.15	-0.87	6.02E-11	4.31E-09	family with sequence similarity 26, member E
nppb	6.90	-1.73	7.32E-11	5.21E-09	natriuretic peptide precursor B
DLGAP3	5.52	2.94	7.34E-11	5.21E-09	discs, large (Drosophila) homolog-associated protein 3
SGCZ	7.61	-1.91	8.43E-11	5.96E-09	sarcoglycan zeta
Jam3	4.29	5.55	9.25E-11	6.51E-09	junctional adhesion molecule 3
FCRL5	6.79	0.55	9.88E-11	6.90E-09	Fc receptor-like 5
CDKN1C	3.59	4.78	9.86E-11	6.90E-09	cyclin-dependent kinase inhibitor 1C (p57, Kip2)
LRP4	4.56	5.13	1.04E-10	7.23E-09	low density lipoprotein receptor-related protein 4
HOXB9	4.67	4.99	1.06E-10	7.33E-09	homeobox B9
GRIK1	4.80	1.14	1.11E-10	7.64E-09	glutamate receptor, ionotropic, kainate 1
cga	6.50	1.24	1.16E-10	7.98E-09	glycoprotein hormones, alpha polypeptide
CHGB	6.42	4.73	1.17E-10	7.98E-09	chromogranin B (secretogranin 1)
TMIE	5.35	0.71	1.25E-10	8.51E-09	transmembrane inner ear
KIAA1409	4.32	1.52	1.32E-10	8.94E-09	KIAA1409
calca	8.23	2.93	1.36E-10	9.20E-09	calcitonin-related polypeptide alpha
CHGA	6.03	6.07	1.46E-10	9.84E-09	chromogranin A (parathyroid secretory protein 1)
AVIL	4.44	3.32	1.55E-10	1.03E-08	advillin
Htr2b	6.07	-1.51	1.54E-10	1.03E-08	5-hydroxytryptamine (serotonin) receptor 2B
FLJ42280	6.60	-1.49	1.83E-10	1.22E-08	hypothetical LOC401388
HOXB2	4.93	5.10	1.94E-10	1.29E-08	homeobox B2
NKX3-1	-6.79	10.01	1.98E-10	1.30E-08	NK3 homeobox 1
TNNI2	8.20	-2.36	2.01E-10	1.32E-08	troponin I type 2 (skeletal, fast)
nrcam	5.35	4.48	2.07E-10	1.36E-08	neuronal cell adhesion molecule
HOXD13	5.85	2.30	2.09E-10	1.36E-08	homeobox D13
SHISA2	4.53	5.81	2.13E-10	1.39E-08	shisa homolog 2 (Xenopus laevis)
VIT	5.08	0.11	2.23E-10	1.44E-08	vitrin
FMNL3	3.77	2.90	2.40E-10	1.55E-08	formin-like 3
IGSF10	6.51	2.21	2.56E-10	1.64E-08	immunoglobulin superfamily, member 10
ENTREZ100422737	6.72	-1.83	2.59E-10	1.66E-08	
Myh6	6.51	-0.36	2.61E-10	1.66E-08	myosin, heavy chain 6, cardiac muscle, alpha
Rnf183	5.70	2.74	2.67E-10	1.70E-08	ring finger protein 183
ZG16B	-5.75	5.75	2.82E-10	1.78E-08	zymogen granule protein 16 homolog B (rat)
lpin1	2.31	5.65	2.91E-10	1.84E-08	lipin 1
MCHR1	6.10	-1.39	3.01E-10	1.89E-08	melanin-concentrating hormone receptor 1
ENTREZ3481	7.37	1.79	3.25E-10	2.03E-08	
Syt11	5.68	4.63	3.27E-10	2.04E-08	synaptotagmin XI

S100A2	4.46	0.82	3.33E-10	2.07E-08	S100 calcium binding protein A2
SCD5	3.08	4.74	3.59E-10	2.22E-08	stearoyl-CoA desaturase 5
PCDH8	6.67	0.39	3.80E-10	2.35E-08	protocadherin 8
C1orf116	-4.14	8.36	4.17E-10	2.56E-08	chromosome 1 open reading frame 116
Ptprh	5.15	2.92	4.54E-10	2.78E-08	protein tyrosine phosphatase, receptor type, H
CCDC33	5.11	0.14	4.62E-10	2.82E-08	coiled-coil domain containing 33
CALHM1	7.13	-0.63	5.15E-10	3.13E-08	calcium homeostasis modulator 1
ism2	3.69	1.41	5.57E-10	3.37E-08	isthmin 2 homolog (zebrafish)
NAV2	5.13	5.26	5.68E-10	3.43E-08	neuron navigator 2
RASL11B	3.82	1.44	5.77E-10	3.47E-08	RAS-like, family 11, member B
LOC201477	6.41	-1.16	5.81E-10	3.48E-08	hypothetical protein LOC201477
TRIM9	4.93	3.11	5.94E-10	3.54E-08	tripartite motif-containing 9
Slc18a3	9.13	-0.63	6.03E-10	3.59E-08	solute carrier family 18 (vesicular acetylcholine), member 3
HOXB3	3.62	3.79	6.16E-10	3.65E-08	homeobox B3
MUC4	3.67	2.70	7.06E-10	4.17E-08	mucin 4, cell surface associated
ENTREZ387104	6.87	2.21	8.34E-10	4.91E-08	
OPRD1	6.24	-1.48	8.78E-10	5.15E-08	opioid receptor, delta 1
HRH3	5.06	1.66	9.47E-10	5.53E-08	histamine receptor H3
KLK4	-6.19	8.84	1.00E-09	5.85E-08	kallikrein-related peptidase 4
PCDH9	5.26	3.04	1.02E-09	5.93E-08	protocadherin 9
VCAN	4.77	2.42	1.03E-09	5.95E-08	versican
WFDC2	6.58	4.59	1.09E-09	6.29E-08	WAP four-disulfide core domain 2
ELAVL4	6.07	0.76	1.11E-09	6.38E-08	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 4 (Hu antigen D)
ENTREZ3039	5.25	1.65	1.15E-09	6.60E-08	
C10orf47	-9.17	4.11	1.21E-09	6.88E-08	chromosome 10 open reading frame 47
CHST11	5.48	2.27	1.35E-09	7.63E-08	carbohydrate (chondroitin 4) sulfotransferase 11
Tox	5.88	4.06	1.34E-09	7.63E-08	thymocyte selection-associated high mobility group box
NEUROD4	7.88	-1.53	1.38E-09	7.82E-08	neurogenic differentiation 4
C11orf16	5.35	-0.64	1.40E-09	7.87E-08	chromosome 11 open reading frame 16
CD244	6.72	-1.21	1.40E-09	7.88E-08	CD244 molecule, natural killer cell receptor 2B4
Igfn1	5.79	-1.59	1.51E-09	8.47E-08	immunoglobulin-like and fibronectin type III domain containing 1
PIPOX	4.95	0.81	1.84E-09	1.03E-07	pipecolic acid oxidase
ckm	4.73	-0.33	1.95E-09	1.08E-07	creatine kinase, muscle
POU3F1	5.21	-0.99	2.00E-09	1.11E-07	POU class 3 homeobox 1
GPR44	5.98	1.08	2.09E-09	1.15E-07	G protein-coupled receptor 44
LOC100128239	5.87	-0.20	2.11E-09	1.16E-07	hypothetical LOC100128239
ENTREZ3040	5.26	1.53	2.18E-09	1.20E-07	
pAG1	-6.53	5.60	2.24E-09	1.23E-07	phosphoprotein associated with glycosphingolipid microdomains 1
Mbip	2.17	4.77	2.36E-09	1.29E-07	MAP3K12 binding inhibitory protein 1
DBH	6.58	1.16	2.38E-09	1.29E-07	dopamine beta-hydroxylase (dopamine beta-monooxygenase)
LOC401022	4.88	3.17	2.60E-09	1.41E-07	hypothetical LOC401022
IL19	6.61	-2.46	2.70E-09	1.46E-07	interleukin 19
Tceal7	8.40	0.51	2.83E-09	1.52E-07	transcription elongation factor A (SII)-like 7
SGK269	3.19	2.92	3.06E-09	1.64E-07	NKF3 kinase family member
SLC7A8	-7.05	6.84	3.13E-09	1.67E-07	solute carrier family 7 (cationic amino acid transporter, y+ system), member 8
TLR1	5.82	-0.07	3.22E-09	1.72E-07	toll-like receptor 1
Dhrs3	-4.36	6.39	3.30E-09	1.75E-07	dehydrogenase/reductase (SDR family) member 3
C1orf94	7.14	-1.76	3.34E-09	1.77E-07	chromosome 1 open reading frame 94
ADRB2	-7.41	4.60	3.52E-09	1.86E-07	adrenergic, beta-2-, receptor, surface
DRD1	6.62	-0.90	3.72E-09	1.96E-07	dopamine receptor D1
socs3	4.24	1.43	3.91E-09	2.05E-07	suppressor of cytokine signaling 3
Sulf1	4.52	1.55	4.34E-09	2.27E-07	sulfatase 1
PAX5	5.62	3.16	4.36E-09	2.27E-07	paired box 5
Xkr7	7.66	1.56	4.94E-09	2.56E-07	XK, Kell blood group complex subunit-related family, member 7
Pvalb	8.20	0.44	4.95E-09	2.56E-07	parvalbumin
Lrrn4	5.52	-0.30	5.04E-09	2.60E-07	leucine rich repeat neuronal 4

Kifc3	4.48	3.34	5.39E-09	2.78E-07	kinesin family member C3
KBTBD10	4.72	1.73	5.48E-09	2.81E-07	kelch repeat and BTB (POZ) domain containing 10
RB1	-8.15	4.13	5.78E-09	2.96E-07	retinoblastoma 1
Pcsk6	-7.52	4.62	6.00E-09	3.06E-07	proprotein convertase subtilisin/kexin type 6
Tmprss2	-6.85	9.52	6.24E-09	3.18E-07	transmembrane protease, serine 2
syn1	5.13	2.39	6.70E-09	3.40E-07	synapsin I
NCOA7	2.68	4.23	6.98E-09	3.53E-07	nuclear receptor coactivator 7
NEUROG2	7.02	-0.74	7.17E-09	3.62E-07	neurogenin 2
TMEM169	5.22	0.77	7.21E-09	3.62E-07	transmembrane protein 169
nkain4	5.40	-1.91	7.66E-09	3.84E-07	Na+/K+ transporting ATPase interacting 4
Egr4	7.04	0.11	7.95E-09	3.97E-07	early growth response 4
ERGIC1	-3.46	9.57	8.32E-09	4.15E-07	endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1
ETV5	4.82	3.71	8.35E-09	4.15E-07	ets variant 5
GNAO1	6.46	4.08	8.41E-09	4.15E-07	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O
MGC87042	-14.18	3.92	8.40E-09	4.15E-07	similar to Six transmembrane epithelial antigen of prostate
frmd3	5.47	3.07	8.54E-09	4.19E-07	FERM domain containing 3
tfcp2l1	3.08	6.19	8.52E-09	4.19E-07	transcription factor CP2-like 1
t	5.91	0.78	8.82E-09	4.32E-07	T, brachyury homolog (mouse)
Syt5	5.78	1.08	9.27E-09	4.52E-07	synaptotagmin V
HOXB6	4.55	4.08	9.94E-09	4.82E-07	homeobox B6
IQSEC3	5.83	0.01	9.94E-09	4.82E-07	IQ motif and Sec7 domain 3; similar to IQ motif and Sec7 domain-containing protein 3; similar to IQ motif and SEC7 domain-containing protein 3; similar to IQ motif and Sec7 domain 3
Pglyrp3	9.21	-3.11	1.00E-08	4.85E-07	peptidoglycan recognition protein 3
Six2	6.08	4.62	1.02E-08	4.92E-07	SIX homeobox 2
RIMKLA	3.00	5.95	1.03E-08	4.96E-07	ribosomal modification protein rimK-like family member A
ZEB1	6.17	-1.10	1.09E-08	5.25E-07	zinc finger E-box binding homeobox 1
Cabp7	4.66	2.18	1.10E-08	5.26E-07	calcium binding protein 7
PTHLH	4.36	-1.16	1.13E-08	5.37E-07	parathyroid hormone-like hormone
MYBPH	7.24	-2.64	1.16E-08	5.54E-07	myosin binding protein H
C10orf10	4.13	2.44	1.22E-08	5.77E-07	chromosome 10 open reading frame 10
Fst	6.10	-1.19	1.26E-08	5.97E-07	follistatin
STRA6	5.83	2.81	1.35E-08	6.35E-07	stimulated by retinoic acid gene 6 homolog (mouse)
Syp	3.54	4.70	1.45E-08	6.82E-07	synaptophysin
Steap2	-8.00	8.53	1.48E-08	6.92E-07	six transmembrane epithelial antigen of the prostate 2
Clic6	5.12	-1.13	1.49E-08	6.95E-07	chloride intracellular channel 6
PLS1	2.87	4.69	1.52E-08	7.09E-07	plastin 1 (I isoform)
Trpv6	-7.88	7.56	1.55E-08	7.23E-07	transient receptor potential cation channel, subfamily V, member 6
dlgap1	5.11	5.22	1.59E-08	7.38E-07	discs, large (Drosophila) homolog-associated protein 1
KCNT2	7.45	-3.02	1.61E-08	7.47E-07	potassium channel, subfamily T, member 2
CDKN2C	2.98	6.30	1.65E-08	7.61E-07	cyclin-dependent kinase inhibitor 2C (p18, inhibits CDK4)
ABO	9.50	-3.27	1.67E-08	7.67E-07	ABO blood group (transferase A, alpha 1-3-N-acetylgalactosaminyltransferase; transferase B, alpha 1-3-galactosyltransferase)
Gramd1b	5.48	1.29	1.68E-08	7.70E-07	GRAM domain containing 1B
ephb1	5.54	2.43	1.69E-08	7.72E-07	EPH receptor B1
CACNA1E	4.97	-0.87	1.69E-08	7.72E-07	calcium channel, voltage-dependent, R type, alpha 1E subunit
pou3f2	6.29	0.93	1.73E-08	7.85E-07	POU class 3 homeobox 2
Cpt1c	4.57	3.13	1.75E-08	7.93E-07	carnitine palmitoyltransferase 1C
Nedd9	-5.69	5.64	1.79E-08	8.10E-07	neural precursor cell expressed, developmentally down-regulated 9
Ar	-7.11	9.71	1.84E-08	8.32E-07	androgen receptor
YAP1	-7.30	6.38	1.85E-08	8.35E-07	Yes-associated protein 1, 65kDa
LOC284395	5.55	-1.26	1.91E-08	8.58E-07	hypothetical protein LOC284395
SNCAIP	6.20	3.90	1.97E-08	8.81E-07	synuclein, alpha interacting protein
Fam119a	1.88	6.67	2.18E-08	9.73E-07	family with sequence similarity 119, member A
March4	5.09	3.41	2.30E-08	1.02E-06	membrane-associated ring finger (C3HC4) 4
KLK3	-7.86	12.02	2.73E-08	1.21E-06	kallikrein-related peptidase 3

Adora1	4.47	1.24	2.77E-08	1.23E-06	adenosine A1 receptor
OIT3	5.27	-1.61	3.08E-08	1.36E-06	oncoprotein induced transcript 3
Tctex1d1	8.74	-3.65	3.37E-08	1.49E-06	Tctex1 domain containing 1
Mycl1	3.80	5.85	3.57E-08	1.57E-06	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)
DOK2	6.51	-2.15	3.56E-08	1.57E-06	docking protein 2, 56kDa
ZBTB16	-6.74	5.12	3.83E-08	1.68E-06	zinc finger and BTB domain containing 16
MIER1	1.96	5.58	3.89E-08	1.70E-06	mesoderm induction early response 1 homolog (Xenopus laevis)
LOC100287466	6.41	-2.10	3.96E-08	1.73E-06	similar to Paraneoplastic antigen-like protein 6A
Trem1	5.10	-1.78	4.17E-08	1.81E-06	triggering receptor expressed on myeloid cells 1
Slc43a3	3.66	3.33	4.29E-08	1.86E-06	solute carrier family 43, member 3
SCG5	5.50	3.19	4.35E-08	1.88E-06	secretogranin V (7B2 protein)
ENTREZ100132916	5.16	-3.00	4.60E-08	1.98E-06	
rassf6	4.05	4.59	5.11E-08	2.20E-06	Ras association (RalGDS/AF-6) domain family member 6
RUNX1T1	4.81	2.32	5.17E-08	2.22E-06	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)
C6orf223	5.37	1.69	5.19E-08	2.22E-06	chromosome 6 open reading frame 223
Golga7b	3.94	4.36	5.25E-08	2.24E-06	golgi autoantigen, golgin subfamily a, 7B
PDLIM1	2.53	5.45	5.30E-08	2.26E-06	PDZ and LIM domain 1
ank2	5.08	5.38	5.50E-08	2.33E-06	ankyrin 2, neuronal
STARD9	3.55	1.64	5.61E-08	2.37E-06	StAR-related lipid transfer (START) domain containing 9
Sestd1	2.23	5.22	5.73E-08	2.42E-06	SEC14 and spectrin domains 1
ABLIM2	3.92	2.59	5.74E-08	2.42E-06	actin binding LIM protein family, member 2
INHBE	4.64	0.21	5.94E-08	2.50E-06	inhibin, beta E
Blk	6.26	-1.44	6.11E-08	2.56E-06	B lymphoid tyrosine kinase
fmo3	5.67	0.73	6.21E-08	2.60E-06	flavin containing monooxygenase 3
CDK5R2	6.64	2.88	6.83E-08	2.85E-06	cyclin-dependent kinase 5, regulatory subunit 2 (p39)
RIMBP2	6.47	2.13	6.92E-08	2.88E-06	RIMS binding protein 2
TMEM181	2.24	6.07	7.02E-08	2.91E-06	transmembrane protein 181
KCNE1	3.83	0.87	7.13E-08	2.95E-06	potassium voltage-gated channel, Isk-related family, member 1
COL6A2	-9.07	5.75	8.10E-08	3.35E-06	collagen, type VI, alpha 2
NCKAP1L	4.72	-0.70	8.19E-08	3.37E-06	NCK-associated protein 1-like
Eya1	4.58	0.76	8.36E-08	3.43E-06	eyes absent homolog 1 (Drosophila)
Pcyt1b	4.70	1.60	8.86E-08	3.63E-06	phosphate cytidylyltransferase 1, choline, beta
KDR	5.54	1.67	9.57E-08	3.91E-06	kinase insert domain receptor (a type III receptor tyrosine kinase)
rasd1	3.30	4.77	9.63E-08	3.93E-06	RAS, dexamethasone-induced 1
TCEAL2	6.12	0.52	9.77E-08	3.98E-06	transcription elongation factor A (SII)-like 2
PPAP2A	-5.09	8.04	9.82E-08	3.98E-06	phosphatidic acid phosphatase type 2A
GDAP1L1	5.69	-0.90	9.83E-08	3.98E-06	ganglioside-induced differentiation-associated protein 1-like 1
TEAD1	2.22	6.12	1.04E-07	4.21E-06	TEA domain family member 1 (SV40 transcriptional enhancer factor)
Slc25a37	-3.59	5.61	1.06E-07	4.27E-06	solute carrier family 25, member 37
KLK12	5.07	4.73	1.08E-07	4.35E-06	kallikrein-related peptidase 12
prsS12	4.19	-0.53	1.10E-07	4.41E-06	protease, serine, 12 (neurotrypsin, motopsin)
Art1	5.75	-1.56	1.12E-07	4.48E-06	ADP-ribosyltransferase 1
C8orf56	5.21	-2.57	1.14E-07	4.56E-06	chromosome 8 open reading frame 56
MEX3B	2.56	3.69	1.18E-07	4.71E-06	mex-3 homolog B (C. elegans)
AVPR2	6.13	-2.29	1.26E-07	4.99E-06	arginine vasopressin receptor 2
H19	6.84	8.24	1.26E-07	5.01E-06	H19, imprinted maternally expressed transcript (non-protein coding)
Rabgap1l	2.40	5.09	1.27E-07	5.03E-06	RAB GTPase activating protein 1-like
BSND	5.22	-2.66	1.29E-07	5.11E-06	Bartter syndrome, infantile, with sensorineural deafness (Barttin)
CCND1	-7.11	8.48	1.34E-07	5.26E-06	cyclin D1
gas6	2.69	4.34	1.37E-07	5.40E-06	similar to growth arrest-specific 6; growth arrest-specific 6
tgfbi	5.44	3.81	1.42E-07	5.55E-06	transforming growth factor, beta-induced, 68kDa
SLC45A3	-7.38	9.42	1.45E-07	5.66E-06	solute carrier family 45, member 3
SCHIP1	8.85	-3.69	1.46E-07	5.68E-06	schwannomin interacting protein 1
ID2	3.70	5.73	1.55E-07	6.04E-06	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
C19orf30	5.38	-2.33	1.61E-07	6.24E-06	chromosome 19 open reading frame 30

HPN	-3.81	6.65	1.64E-07	6.35E-06	hepsin
Fam176a	5.81	2.16	1.65E-07	6.37E-06	family with sequence similarity 176, member A
MAGEA11	6.44	1.13	1.67E-07	6.44E-06	melanoma antigen family A, 11
Igfbpl1	4.08	4.92	1.68E-07	6.45E-06	insulin-like growth factor binding protein-like 1
LOC100133612	4.15	0.14	1.69E-07	6.48E-06	similar to hCG1815312
KITLG	2.35	4.34	1.83E-07	7.01E-06	KIT ligand
SLC13A2	5.66	0.84	1.83E-07	7.01E-06	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 2
KCNK17	5.10	2.19	1.86E-07	7.10E-06	potassium channel, subfamily K, member 17
SOX2	5.45	4.79	1.90E-07	7.22E-06	SRY (sex determining region Y)-box 2
Trpm5	5.15	1.15	1.95E-07	7.40E-06	transient receptor potential cation channel, subfamily M, member 5
HTR4	5.67	-2.32	1.96E-07	7.43E-06	5-hydroxytryptamine (serotonin) receptor 4
TCF12	2.10	6.30	2.10E-07	7.93E-06	transcription factor 12
Mcoln3	6.07	2.58	2.23E-07	8.39E-06	mucolipin 3
HHATL	4.88	-3.19	2.28E-07	8.57E-06	hedgehog acyltransferase-like
MAL	6.04	3.46	2.34E-07	8.80E-06	mal, T-cell differentiation protein
STK32A	5.27	0.71	2.41E-07	9.02E-06	serine/threonine kinase 32A
STEAP1	-8.60	7.37	2.46E-07	9.18E-06	six transmembrane epithelial antigen of the prostate 1
lgi2	2.64	2.90	2.50E-07	9.31E-06	leucine-rich repeat LGI family, member 2
LOC728978	5.99	-1.69	2.56E-07	9.54E-06	hCG1818231
PCP4	6.30	1.46	2.57E-07	9.55E-06	Purkinje cell protein 4
LOC100130298	5.04	-1.66	2.64E-07	9.79E-06	similar to hCG1816373
KLK2	-7.53	10.72	2.65E-07	9.81E-06	kallikrein-related peptidase 2
RYR2	3.85	5.89	2.72E-07	1.00E-05	ryanodine receptor 2 (cardiac)
tnfrsf11b	5.49	0.10	2.92E-07	1.08E-05	tumor necrosis factor receptor superfamily, member 11b
sept11	1.78	6.59	2.97E-07	1.09E-05	septin 11
CXXC4	4.62	3.82	2.97E-07	1.09E-05	CXXC finger 4
STXBP1	2.49	5.45	2.97E-07	1.09E-05	syntaxin binding protein 1
HMGCS2	-7.67	7.00	3.11E-07	1.13E-05	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2 (mitochondrial)
fxyd3	-4.27	8.31	3.11E-07	1.13E-05	FXYD domain containing ion transport regulator 3
SYNPO	4.19	1.45	3.36E-07	1.22E-05	synaptopodin
ENTREZ100886964	5.86	-3.68	3.43E-07	1.24E-05	
OLFML2A	5.11	1.00	3.44E-07	1.24E-05	olfactomedin-like 2A
CRYL1	-3.37	5.57	3.53E-07	1.27E-05	crystallin, lambda 1
GNAT1	4.47	-3.15	3.56E-07	1.28E-05	guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1
PLLP	3.37	2.25	3.56E-07	1.28E-05	plasma membrane proteolipid (plasmolipin)
Prosapip1	2.50	5.59	3.78E-07	1.35E-05	ProSAPiP1 protein
C3orf59	4.68	-0.22	3.78E-07	1.35E-05	chromosome 3 open reading frame 59
FLRT1	2.45	2.84	3.84E-07	1.37E-05	fibronectin leucine rich transmembrane protein 1
TARP	-9.09	9.26	4.01E-07	1.43E-05	TCR gamma alternate reading frame protein; T cell receptor gamma variable 9; T cell receptor gamma constant 1
FYN	4.38	3.75	4.23E-07	1.50E-05	FYN oncogene related to SRC, FGR, YES
ILDR2	5.36	3.34	4.28E-07	1.52E-05	immunoglobulin-like domain containing receptor 2
Rab39	4.78	2.19	4.36E-07	1.54E-05	RAB39, member RAS oncogene family
ZBTB8B	5.34	1.31	4.46E-07	1.58E-05	zinc finger and BTB domain containing 8B
MAPRE2	2.97	4.27	4.64E-07	1.64E-05	microtubule-associated protein, RP/EB family, member 2
CACNA2D3	3.72	1.01	4.70E-07	1.65E-05	calcium channel, voltage-dependent, alpha 2/delta subunit 3
MANEAL	3.34	5.71	4.72E-07	1.66E-05	mannosidase, endo-alpha-like
Kcnh4	4.31	-0.86	4.73E-07	1.66E-05	potassium voltage-gated channel, subfamily H (eag-related), member 4
LRRC14B	4.22	0.57	4.83E-07	1.69E-05	leucine-rich repeat-containing protein 14-like
SELV	6.22	-1.57	4.90E-07	1.71E-05	selenoprotein V
ENTREZ729786	4.17	-1.58	4.95E-07	1.72E-05	
Galnt6	3.16	3.70	4.98E-07	1.73E-05	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)
Dpysl3	3.84	8.20	5.00E-07	1.73E-05	dihydropyrimidinase-like 3
STEAP4	-8.09	6.08	5.03E-07	1.74E-05	STEAP family member 4

PLCG2	3.76	1.10	5.27E-07	1.82E-05	phospholipase C, gamma 2 (phosphatidylinositol-specific)
ABP1	4.92	4.67	5.30E-07	1.83E-05	amiloride binding protein 1 (amine oxidase (copper-containing))
SLC24A3	4.10	2.03	5.43E-07	1.87E-05	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
ST18	4.66	4.20	5.48E-07	1.88E-05	suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)
Tet1	3.06	3.71	5.54E-07	1.90E-05	tet oncogene 1
TMEM22	4.44	2.55	5.85E-07	2.00E-05	transmembrane protein 22
grin2c	3.78	1.64	5.89E-07	2.01E-05	glutamate receptor, ionotropic, N-methyl D-aspartate 2C
Hes3	8.50	-4.23	6.16E-07	2.09E-05	hairy and enhancer of split 3 (Drosophila)
ZNF488	5.13	1.37	6.15E-07	2.09E-05	zinc finger protein 488
Smo	-5.69	5.96	6.16E-07	2.09E-05	smoothened homolog (Drosophila)
EFNB2	-5.12	5.93	6.76E-07	2.29E-05	ephrin-B2
C16orf89	3.40	0.42	6.79E-07	2.29E-05	chromosome 16 open reading frame 89
Tmeff2	-10.90	8.75	6.97E-07	2.35E-05	transmembrane protein with EGF-like and two follistatin-like domains 2
CD99	-4.86	8.93	7.27E-07	2.45E-05	CD99 molecule
FOXA2	6.67	4.35	7.56E-07	2.54E-05	forkhead box A2
BMP3	3.32	0.02	7.67E-07	2.57E-05	bone morphogenetic protein 3
Gdap1	2.09	5.24	8.21E-07	2.75E-05	ganglioside-induced differentiation-associated protein 1
H2afj	-6.17	7.64	8.28E-07	2.76E-05	H2A histone family, member J
ZDHHC13	2.19	4.50	8.77E-07	2.92E-05	zinc finger, DHHC-type containing 13
PROX1	5.71	4.83	8.76E-07	2.92E-05	prospero homeobox 1
C2orf72	-7.78	5.59	9.14E-07	3.03E-05	chromosome 2 open reading frame 72
CHRNA2	-8.19	6.09	9.75E-07	3.23E-05	cholinergic receptor, nicotinic, alpha 2 (neuronal)
Nlgn2	-3.46	5.09	9.86E-07	3.26E-05	neuroligin 2
Bmp8a	2.89	4.14	1.00E-06	3.31E-05	bone morphogenetic protein 8a
TMEM151A	4.62	0.39	1.02E-06	3.36E-05	transmembrane protein 151A
nfix	-3.82	8.91	1.04E-06	3.43E-05	nuclear factor I/X (CCAAT-binding transcription factor)
TSPAN12	2.96	3.85	1.05E-06	3.43E-05	tetraspanin 12
TSPAN33	-5.07	5.53	1.05E-06	3.45E-05	tetraspanin 33
cdkal1	1.88	4.23	1.15E-06	3.75E-05	CDK5 regulatory subunit associated protein 1-like 1
TRPV3	3.97	-1.37	1.20E-06	3.92E-05	transient receptor potential cation channel, subfamily V, member 3
CHRM1	-5.29	4.10	1.20E-06	3.92E-05	cholinergic receptor, muscarinic 1
Acsl4	3.44	3.71	1.24E-06	4.04E-05	acyl-CoA synthetase long-chain family member 4
Kif1c	-2.81	7.65	1.29E-06	4.19E-05	kinesin family member 1C
TMEM100	3.69	0.11	1.29E-06	4.19E-05	transmembrane protein 100
gcat	-3.96	4.95	1.30E-06	4.20E-05	glycine C-acetyltransferase (2-amino-3-ketobutyrate coenzyme A ligase)
SCNN1A	2.91	7.30	1.32E-06	4.25E-05	sodium channel, nonvoltage-gated 1 alpha
GDF11	2.59	4.21	1.37E-06	4.41E-05	growth differentiation factor 11
Sema4a	-2.96	5.71	1.39E-06	4.45E-05	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A
ZNF620	2.46	3.14	1.40E-06	4.48E-05	zinc finger protein 620
Sema6c	2.85	3.98	1.46E-06	4.67E-05	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C
RTBDN	5.62	1.44	1.50E-06	4.80E-05	retbindin
PLEKHH1	-2.80	6.26	1.59E-06	5.06E-05	pleckstrin homology domain containing, family H (with MyTH4 domain) member 1
HPSE	3.68	2.16	1.59E-06	5.06E-05	heparanase
SLC44A4	-4.51	8.20	1.70E-06	5.40E-05	solute carrier family 44, member 4
Agr2	-7.30	8.76	1.72E-06	5.45E-05	anterior gradient homolog 2 (Xenopus laevis)
Lhx2	4.62	1.99	1.76E-06	5.55E-05	LIM homeobox 2
col4a2	3.68	3.05	1.80E-06	5.67E-05	collagen, type IV, alpha 2
SVOP	4.73	0.22	1.84E-06	5.79E-05	SV2 related protein homolog (rat)
CUX2	-6.04	5.48	1.86E-06	5.85E-05	cut-like homeobox 2
CNTNAP2	2.41	6.21	1.86E-06	5.85E-05	contactin associated protein-like 2
DCXR	-2.64	7.83	1.87E-06	5.87E-05	dicarbonyl/L-xylulose reductase
Ephx2	-4.52	5.64	1.89E-06	5.91E-05	epoxide hydrolase 2, cytoplasmic
STEAP3	1.87	5.76	1.94E-06	6.06E-05	STEAP family member 3
STAP1	6.08	2.49	1.95E-06	6.06E-05	signal transducing adaptor family member 1

TRPM4	-3.43	8.02	1.97E-06	6.13E-05	transient receptor potential cation channel, subfamily M, member 4
ENTREZ8577	5.08	-1.38	1.98E-06	6.14E-05	
HEPACAM2	4.13	3.26	2.07E-06	6.42E-05	HEPACAM family member 2
SFTPA2	-5.53	6.08	2.12E-06	6.55E-05	surfactant protein A2; surfactant protein A2B
LOC643201	5.20	0.93	2.12E-06	6.55E-05	hypothetical protein LOC643201
Plekhn1	-12.35	2.82	2.20E-06	6.76E-05	pleckstrin homology domain containing, family N member 1
c4orf32	-6.03	4.59	2.20E-06	6.76E-05	chromosome 4 open reading frame 32
ATP4B	5.09	-2.10	2.21E-06	6.79E-05	ATPase, H+/K+ exchanging, beta polypeptide
Cgref1	-5.99	5.17	2.27E-06	6.95E-05	cell growth regulator with EF-hand domain 1
id4	3.98	3.37	2.32E-06	7.10E-05	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
RHBDL3	4.10	2.38	2.48E-06	7.57E-05	rhomboid, veinlet-like 3 (Drosophila)
KCNH1	4.81	-0.12	2.53E-06	7.73E-05	potassium voltage-gated channel, subfamily H (eag-related), member 1
Tubb2a	2.42	7.25	2.65E-06	8.06E-05	tubulin, beta 2A
Gsn	2.79	6.48	2.73E-06	8.28E-05	gelsolin (amyloidosis, Finnish type)
Pgbd5	4.19	4.37	2.73E-06	8.29E-05	piggyBac transposable element derived 5
BCAS1	-6.63	6.18	2.75E-06	8.33E-05	breast carcinoma amplified sequence 1
GLIPR2	-5.37	4.73	2.82E-06	8.53E-05	GLI pathogenesis-related 2
FKBP11	-3.92	4.97	2.88E-06	8.67E-05	FK506 binding protein 11, 19 kDa
ENTREZ653423	5.96	-3.59	2.89E-06	8.69E-05	
PITPNC1	2.20	4.03	2.92E-06	8.78E-05	phosphatidylinositol transfer protein, cytoplasmic 1
MYBPC1	-7.81	8.49	3.06E-06	9.15E-05	myosin binding protein C, slow type
tgm2	-5.38	6.14	3.06E-06	9.15E-05	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)
cmip	2.11	6.03	3.12E-06	9.32E-05	c-Maf-inducing protein
IFT57	-3.10	6.82	3.15E-06	9.39E-05	intraflagellar transport 57 homolog (Chlamydomonas)
tp53bp2	1.65	5.98	3.17E-06	9.44E-05	tumor protein p53 binding protein, 2
BLVRB	-4.19	6.66	3.26E-06	9.69E-05	biliverdin reductase B (flavin reductase (NADPH))
ARHGAP30	4.37	2.90	3.28E-06	9.74E-05	Rho GTPase activating protein 30
MS4A8B	3.61	5.57	3.34E-06	9.89E-05	membrane-spanning 4-domains, subfamily A, member 8B
RAB24	-2.54	5.65	3.34E-06	9.89E-05	RAB24, member RAS oncogene family
emp1	-9.52	5.88	3.36E-06	9.93E-05	epithelial membrane protein 1
Slit2	3.66	2.92	3.38E-06	9.96E-05	slit homolog 2 (Drosophila)
BCL2	3.29	4.48	3.41E-06	1.00E-04	B-cell CLL/lymphoma 2
LOC441869	4.52	3.43	3.43E-06	1.01E-04	hypothetical protein LOC441869
DZIP1	3.27	4.34	3.47E-06	1.02E-04	DAZ interacting protein 1
Lats2	-6.26	4.29	3.50E-06	1.02E-04	LATS, large tumor suppressor, homolog 2 (Drosophila)
Mlph	-3.74	7.68	3.50E-06	1.02E-04	melanophilin
C2CD4B	4.99	2.22	3.52E-06	1.03E-04	family with sequence similarity 148, member B
SLCO2A1	-7.03	4.04	3.57E-06	1.04E-04	solute carrier organic anion transporter family, member 2A1
tdrd6	-7.57	2.66	3.63E-06	1.05E-04	tudor domain containing 6
PLEKHH2	3.81	3.50	3.68E-06	1.07E-04	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2
ENTREZ100506394	3.32	-0.65	3.73E-06	1.08E-04	
CNGA4	3.53	0.53	3.77E-06	1.09E-04	cyclic nucleotide gated channel alpha 4
Cnrip1	6.29	0.78	3.92E-06	1.13E-04	cannabinoid receptor interacting protein 1
Adamts1	-10.70	6.54	3.98E-06	1.15E-04	ADAM metallopeptidase with thrombospondin type 1 motif, 1
THBD	5.88	0.46	4.05E-06	1.17E-04	thrombomodulin
Cttnbp2	3.57	2.38	4.09E-06	1.17E-04	cortactin binding protein 2
Tmem233	4.34	-2.99	4.09E-06	1.17E-04	similar to mCG53783
Ube2ql1	6.59	1.81	4.10E-06	1.17E-04	probable ubiquitin-conjugating enzyme E2 FLJ25076
Sptb	3.06	4.31	4.14E-06	1.18E-04	spectrin, beta, erythrocytic
Syt13	4.07	5.78	4.15E-06	1.18E-04	synaptotagmin XIII
clspn	1.95	5.30	4.40E-06	1.25E-04	claspin homolog (Xenopus laevis)
CADPS	4.81	2.96	4.40E-06	1.25E-04	Ca++-dependent secretion activator
CEACAM7	5.48	-1.81	4.41E-06	1.25E-04	carcinoembryonic antigen-related cell adhesion molecule 7
SLC2A10	-4.61	5.28	4.42E-06	1.25E-04	solute carrier family 2 (facilitated glucose transporter), member 10

Kcnh3	4.24	3.18	4.61E-06	1.31E-04	potassium voltage-gated channel, subfamily H (eag-related), member 3
PLA2G7	-6.87	5.20	4.63E-06	1.31E-04	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)
PGF	2.69	1.43	4.74E-06	1.34E-04	placental growth factor
OLFM3	4.73	-1.94	4.75E-06	1.34E-04	olfactomedin 3
ITGB6	3.32	1.23	4.87E-06	1.37E-04	integrin, beta 6
flj41603	-2.83	7.12	4.88E-06	1.37E-04	FLJ41603 protein
GFI1	4.74	2.43	5.00E-06	1.40E-04	growth factor independent 1 transcription repressor
CAMK2N2	3.46	3.70	5.04E-06	1.41E-04	calcium/calmodulin-dependent protein kinase II inhibitor 2
samd4a	-7.25	4.07	5.04E-06	1.41E-04	sterile alpha motif domain containing 4A
CTSS	3.17	3.34	5.07E-06	1.41E-04	cathepsin S
DLX6	3.96	0.64	5.08E-06	1.41E-04	distal-less homeobox 6
HOXD9	5.60	2.33	5.15E-06	1.43E-04	homeobox D9
CDKN2A	4.03	5.45	5.17E-06	1.43E-04	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
fam20a	3.68	-0.48	5.23E-06	1.45E-04	family with sequence similarity 20, member A
KRT83	4.61	1.41	5.27E-06	1.46E-04	keratin 83
Hs3st1	3.53	3.49	5.30E-06	1.46E-04	heparan sulfate (glucosamine) 3-O-sulfotransferase 1
KLF9	-2.96	5.49	5.32E-06	1.47E-04	Kruppel-like factor 9
ENPP2	4.22	1.94	5.34E-06	1.47E-04	ectonucleotide pyrophosphatase/phosphodiesterase 2
Arhgef7	1.69	6.29	5.39E-06	1.48E-04	Rho guanine nucleotide exchange factor (GEF) 7
TLE2	2.52	5.48	5.39E-06	1.48E-04	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila)
RLTPR	4.30	2.75	5.53E-06	1.51E-04	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing
acpP	-7.55	10.39	5.65E-06	1.54E-04	acid phosphatase, prostate
ENTREZ100861555	4.44	-1.38	5.66E-06	1.54E-04	
C1QTNF6	-6.12	4.47	5.76E-06	1.57E-04	C1q and tumor necrosis factor related protein 6
rbp2	3.19	-0.77	5.85E-06	1.59E-04	retinol binding protein 2, cellular
scgn	5.52	4.75	5.88E-06	1.60E-04	secretagogin, EF-hand calcium binding protein
Gadd45b	-3.67	3.96	5.93E-06	1.61E-04	growth arrest and DNA-damage-inducible, beta
TMEM61	3.66	3.33	5.97E-06	1.62E-04	transmembrane protein 61
Egf	-8.17	4.42	6.05E-06	1.64E-04	epidermal growth factor (beta-urogastrone)
Gpr142	3.85	-2.58	6.15E-06	1.65E-04	G protein-coupled receptor 142
RIMS2	4.43	3.94	6.15E-06	1.65E-04	regulating synaptic membrane exocytosis 2
PPAPDC3	5.71	-1.56	6.15E-06	1.65E-04	phosphatidic acid phosphatase type 2 domain containing 3
Apbb2	1.93	4.70	6.19E-06	1.66E-04	amyloid beta (A4) precursor protein-binding, family B, member 2
FLRT2	4.01	-1.65	6.23E-06	1.67E-04	fibronectin leucine rich transmembrane protein 2
PTPN14	-5.19	5.07	6.24E-06	1.67E-04	protein tyrosine phosphatase, non-receptor type 14
Ccdc136	-5.97	4.17	6.25E-06	1.67E-04	coiled-coil domain containing 136
Crat	-3.17	7.57	6.33E-06	1.69E-04	carnitine acetyltransferase
srl	3.49	-1.01	6.35E-06	1.69E-04	sarcalumenin
il6r	-4.61	5.28	6.60E-06	1.76E-04	interleukin 6 receptor
HTR3A	4.54	1.08	6.76E-06	1.80E-04	5-hydroxytryptamine (serotonin) receptor 3A
PMEPA1	-3.39	9.30	6.91E-06	1.83E-04	prostate transmembrane protein, androgen induced 1
PPP1R14D	3.38	0.14	6.95E-06	1.84E-04	protein phosphatase 1, regulatory (inhibitor) subunit 14D
ENTREZ100132979	3.86	-1.40	7.08E-06	1.87E-04	
ST6GALNAC4	3.37	3.28	7.28E-06	1.92E-04	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
ATP2C2	-4.85	5.78	7.34E-06	1.93E-04	ATPase, Ca++ transporting, type 2C, member 2
mccc2	-3.87	8.47	7.39E-06	1.94E-04	methylcrotonoyl-Coenzyme A carboxylase 2 (beta)
ANP32E	2.12	6.02	7.39E-06	1.94E-04	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
CALCRL	2.75	1.39	7.43E-06	1.95E-04	calcitonin receptor-like
HCN4	4.41	1.69	7.47E-06	1.96E-04	hyperpolarization activated cyclic nucleotide-gated potassium channel 4
MARK1	2.73	4.56	7.52E-06	1.97E-04	MAP/microtubule affinity-regulating kinase 1
Frmd5	3.45	0.51	7.54E-06	1.97E-04	FERM domain containing 5
Celf4	3.36	1.99	7.61E-06	1.98E-04	bruno-like 4, RNA binding protein (Drosophila)
FAH	-3.96	4.37	8.30E-06	2.16E-04	fumarylacetoacetate hydrolase (fumarylacetoacetase)
aldh1a1	4.65	4.37	8.29E-06	2.16E-04	aldehyde dehydrogenase 1 family, member A1

hoxd3	3.87	0.44	8.37E-06	2.17E-04	homeobox D3
HOXB13	-4.44	9.01	8.50E-06	2.20E-04	homeobox B13
DUSP1	-3.10	6.53	8.52E-06	2.20E-04	dual specificity phosphatase 1
LGR5	4.73	1.83	8.54E-06	2.20E-04	leucine-rich repeat-containing G protein-coupled receptor 5
Ankrd35	5.16	0.10	8.61E-06	2.22E-04	ankyrin repeat domain 35
tmcc3	-5.08	5.04	8.71E-06	2.24E-04	transmembrane and coiled-coil domain family 3
TSPAN7	3.20	1.84	8.90E-06	2.29E-04	tetraspanin 7
Ogdhl	3.38	3.56	8.93E-06	2.29E-04	oxoglutarate dehydrogenase-like
C1orf95	4.95	2.87	9.01E-06	2.31E-04	chromosome 1 open reading frame 95
MAPK8IP1	2.18	6.26	9.06E-06	2.32E-04	mitogen-activated protein kinase 8 interacting protein 1
dsp	2.15	9.19	9.13E-06	2.33E-04	desmoplakin
C11orf41	5.51	2.87	9.38E-06	2.39E-04	chromosome 11 open reading frame 41
Gpr114	4.47	-2.43	9.58E-06	2.44E-04	G protein-coupled receptor 114
CIT	1.61	5.83	9.67E-06	2.46E-04	citron (rho-interacting, serine/threonine kinase 21)
BMPER	3.99	-1.29	9.99E-06	2.54E-04	BMP binding endothelial regulator
LOC151162	1.49	6.64	1.05E-05	2.65E-04	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase; hypothetical LOC151162
MRAP2	4.01	1.40	1.05E-05	2.65E-04	melanocortin 2 receptor accessory protein 2
ARHGAP9	3.18	-1.78	1.05E-05	2.65E-04	Rho GTPase activating protein 9
PSIP1	1.78	6.56	1.05E-05	2.65E-04	PC4 and SFRS1 interacting protein 1
saal1	1.99	4.63	1.06E-05	2.67E-04	serum amyloid A-like 1
TSPAN11	4.34	2.50	1.06E-05	2.67E-04	tetraspanin 11
CEP170	2.03	4.87	1.06E-05	2.67E-04	centrosomal protein 170kDa
Syt1	3.43	5.00	1.08E-05	2.71E-04	synaptotagmin I
gpr37l1	3.50	-0.71	1.08E-05	2.71E-04	G protein-coupled receptor 37 like 1
GAB2	2.51	4.75	1.08E-05	2.71E-04	GRB2-associated binding protein 2
COL6A1	-4.90	6.39	1.09E-05	2.71E-04	collagen, type VI, alpha 1
PIRT	5.19	-1.61	1.10E-05	2.74E-04	phosphoinositide-interacting regulator of transient receptor potential channels
FLJ10357	2.69	4.83	1.10E-05	2.75E-04	hypothetical protein FLJ10357
SIM2	-3.38	7.43	1.16E-05	2.89E-04	single-minded homolog 2 (Drosophila)
ENTREZ57491	3.46	1.68	1.17E-05	2.90E-04	
shox2	3.65	1.02	1.19E-05	2.96E-04	short stature homeobox 2
TPD52L1	-4.84	5.18	1.22E-05	3.01E-04	tumor protein D52-like 1
Tmcc2	3.50	2.30	1.23E-05	3.05E-04	transmembrane and coiled-coil domain family 2
CWH43	-6.88	5.32	1.24E-05	3.05E-04	hypothetical protein FLJ21511
MGP	-7.85	4.63	1.28E-05	3.15E-04	matrix Gla protein
PYY2	2.45	1.29	1.31E-05	3.22E-04	peptide YY, 2 (seminalplasmin)
hgd	-8.58	5.75	1.31E-05	3.22E-04	homogentisate 1,2-dioxygenase (homogentisate oxidase)
zcchc24	-3.58	4.93	1.32E-05	3.24E-04	zinc finger, CCHC domain containing 24
EPS8L1	-5.15	4.43	1.34E-05	3.28E-04	EPS8-like 1
PLAU	4.88	2.66	1.36E-05	3.34E-04	plasminogen activator, urokinase
ERC2	4.01	0.30	1.37E-05	3.35E-04	ELKS/RAB6-interacting/CAST family member 2
Ang	-6.63	4.09	1.37E-05	3.35E-04	angiogenin, ribonuclease, RNase A family, 5
CENPF	1.78	7.23	1.38E-05	3.35E-04	centromere protein F, 350/400ka (mitosin)
CIB1	-2.67	6.69	1.39E-05	3.39E-04	calcium and integrin binding 1 (calmyrin)
HTR1E	4.95	-2.91	1.40E-05	3.40E-04	5-hydroxytryptamine (serotonin) receptor 1E
gyg2	-5.74	4.36	1.40E-05	3.40E-04	glycogenin 2
abcc4	-8.37	7.88	1.41E-05	3.40E-04	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
CHIA	4.77	-2.65	1.40E-05	3.40E-04	chitinase, acidic
CSGALNACT1	-5.47	4.36	1.40E-05	3.40E-04	chondroitin sulfate N-acetylgalactosaminyltransferase 1
FAM83A	2.53	1.88	1.43E-05	3.44E-04	family with sequence similarity 83, member A
UGT2B15	-10.29	6.20	1.43E-05	3.45E-04	UDP glucuronosyltransferase 2 family, polypeptide B15
Magea4	5.45	1.39	1.45E-05	3.49E-04	melanoma antigen family A, 4
GRIA1	4.78	-0.92	1.46E-05	3.51E-04	glutamate receptor, ionotropic, AMPA 1
ENTREZ154043	2.20	6.07	1.48E-05	3.55E-04	
OSBPL3	2.22	4.18	1.48E-05	3.55E-04	oxysterol binding protein-like 3

DUSP4	2.72	4.83	1.49E-05	3.57E-04	dual specificity phosphatase 4
Plxna2	2.44	5.56	1.50E-05	3.58E-04	plexin A2
MUC16	3.56	3.21	1.51E-05	3.60E-04	mucin 16, cell surface associated
SLC6A11	-6.20	3.88	1.51E-05	3.61E-04	solute carrier family 6 (neurotransmitter transporter, GABA), member 11
KCNMB2	3.64	1.42	1.52E-05	3.62E-04	potassium large conductance calcium-activated channel, subfamily M, beta member 2
Prame	-4.35	5.25	1.54E-05	3.66E-04	preferentially expressed antigen in melanoma
TMEM35	5.03	0.75	1.58E-05	3.74E-04	transmembrane protein 35
NRXN1	5.08	3.86	1.59E-05	3.76E-04	neurexin 1
CA8	3.31	3.38	1.60E-05	3.77E-04	carbonic anhydrase VIII
FLJ26484	3.86	-0.22	1.60E-05	3.77E-04	hypothetical gene supported by AK129994
PLA2G4F	-3.37	4.65	1.61E-05	3.80E-04	phospholipase A2, group IVF
IVNS1ABP	1.33	6.22	1.64E-05	3.87E-04	influenza virus NS1A binding protein
March11	6.77	0.82	1.68E-05	3.95E-04	membrane-associated ring finger (C3HC4) 11
NME4	-2.75	7.80	1.69E-05	3.96E-04	non-metastatic cells 4, protein expressed in
Tacr1	4.30	0.29	1.69E-05	3.96E-04	tachykinin receptor 1
CMAH	4.50	1.44	1.69E-05	3.96E-04	cytidine monophosphate-N-acetylneuraminic acid hydroxylase (CMP-N-acetylneuraminate monooxygenase) pseudogene
SCN9A	3.32	2.01	1.69E-05	3.96E-04	sodium channel, voltage-gated, type IX, alpha subunit
Camk1d	3.74	3.72	1.69E-05	3.96E-04	calcium/calmodulin-dependent protein kinase ID
PIWIL1	5.72	-1.58	1.73E-05	4.03E-04	piwi-like 1 (Drosophila)
Npc1l1	4.36	2.83	1.73E-05	4.04E-04	NPC1 (Niemann-Pick disease, type C1, gene)-like 1
PCLO	2.27	4.70	1.79E-05	4.15E-04	piccolo (presynaptic cytomatrix protein)
C1orf173	4.36	2.14	1.80E-05	4.18E-04	chromosome 1 open reading frame 173
cyr61	-4.55	4.01	1.82E-05	4.23E-04	cysteine-rich, angiogenic inducer, 61
FAM38A	-4.95	7.86	1.83E-05	4.24E-04	family with sequence similarity 38, member A
CROT	-3.94	5.83	1.85E-05	4.28E-04	carnitine O-octanoyltransferase
DSCR6	2.48	4.20	1.86E-05	4.29E-04	Down syndrome critical region gene 6
C6orf112	3.28	-2.30	1.86E-05	4.29E-04	chromosome 6 open reading frame 112
glud1	-2.90	7.89	1.87E-05	4.31E-04	glutamate dehydrogenase 1
FSD1L	2.67	2.97	1.91E-05	4.40E-04	fibronectin type III and SPRY domain containing 1-like
ST6GAL2	3.65	3.11	1.92E-05	4.40E-04	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2
C3orf57	-9.04	5.26	1.93E-05	4.43E-04	chromosome 3 open reading frame 57
PLEKHO1	2.38	4.54	1.94E-05	4.46E-04	pleckstrin homology domain containing, family O member 1
ppapdc1b	-3.44	6.84	1.98E-05	4.53E-04	phosphatidic acid phosphatase type 2 domain containing 1B
S1pr3	-8.44	3.47	1.99E-05	4.55E-04	sphingosine-1-phosphate receptor 3
LOC100126784	4.66	-2.15	2.00E-05	4.56E-04	hypothetical LOC100126784
ahnak	-2.85	9.31	2.01E-05	4.58E-04	AHNAK nucleoprotein
ank1	3.11	4.13	2.02E-05	4.61E-04	ankyrin 1, erythrocytic
homer2	-3.17	7.34	2.07E-05	4.70E-04	homer homolog 2 (Drosophila)
Fam162a	-2.55	7.29	2.08E-05	4.72E-04	family with sequence similarity 162, member A
TP53TG1	-3.17	5.24	2.11E-05	4.79E-04	TP53 target 1 (non-protein coding)
NOS2	3.63	-1.88	2.11E-05	4.79E-04	nitric oxide synthase 2, inducible
BAIAP2	-3.99	7.07	2.13E-05	4.81E-04	BAI1-associated protein 2
ggt1	-4.20	6.94	2.13E-05	4.82E-04	gamma-glutamyltransferase light chain 3; gamma-glutamyltransferase 4 pseudogene; gamma-glutamyltransferase 2; gamma-glutamyltransferase 1; gamma-glutamyltransferase light chain 5 pseudogene
SMAD9	2.72	4.67	2.15E-05	4.85E-04	SMAD family member 9
C1orf54	3.65	0.01	2.18E-05	4.90E-04	chromosome 1 open reading frame 54
IGFBP6	3.76	-0.79	2.18E-05	4.90E-04	insulin-like growth factor binding protein 6
ATP2A3	3.10	8.07	2.23E-05	5.02E-04	ATPase, Ca++ transporting, ubiquitous
prkcq	4.48	-0.08	2.25E-05	5.04E-04	protein kinase C, theta
IL17REL	4.20	1.50	2.25E-05	5.04E-04	interleukin 17 receptor E-like
KIF26B	5.45	1.44	2.25E-05	5.04E-04	kinesin family member 26B
ADCY1	3.51	5.25	2.26E-05	5.06E-04	adenylate cyclase 1 (brain)
FSTL1	-7.51	8.52	2.27E-05	5.06E-04	follistatin-like 1
Fam102b	1.89	4.81	2.28E-05	5.07E-04	family with sequence similarity 102, member B

Cacna2d1	4.76	1.58	2.30E-05	5.12E-04	calcium channel, voltage-dependent, alpha 2/delta subunit 1
C7orf63	-6.94	5.64	2.33E-05	5.19E-04	chromosome 7 open reading frame 63
PPP1R1B	-3.72	7.90	2.34E-05	5.20E-04	protein phosphatase 1, regulatory (inhibitor) subunit 1B
chchd10	-2.59	6.37	2.37E-05	5.26E-04	coiled-coil-helix-coiled-coil-helix domain containing 10
NOP16	-2.35	5.50	2.43E-05	5.39E-04	NOP16 nucleolar protein homolog (yeast)
TTLL12	-2.22	7.23	2.44E-05	5.40E-04	tubulin tyrosine ligase-like family, member 12
ENTREZ100506776	-8.36	3.45	2.47E-05	5.45E-04	
lpcat1	1.95	7.15	2.48E-05	5.47E-04	lysophosphatidylcholine acyltransferase 1
CCL28	3.19	2.23	2.55E-05	5.61E-04	chemokine (C-C motif) ligand 28
IMPDH1	-2.76	7.55	2.55E-05	5.61E-04	IMP (inosine monophosphate) dehydrogenase 1
HAS3	2.49	2.42	2.55E-05	5.61E-04	hyaluronan synthase 3
GRTP1	-4.72	3.96	2.59E-05	5.68E-04	growth hormone regulated TBC protein 1
DBC1	5.06	0.59	2.63E-05	5.75E-04	deleted in bladder cancer 1
KLKP1	-5.19	3.16	2.63E-05	5.76E-04	kallikrein pseudogene 1
Tmem150c	1.86	4.46	2.72E-05	5.94E-04	hypothetical LOC441027
Adarb1	-2.96	5.04	2.82E-05	6.14E-04	adenosine deaminase, RNA-specific, B1 (RED1 homolog rat)
ACCN2	-4.12	4.41	2.88E-05	6.28E-04	amiloride-sensitive cation channel 2, neuronal
DDIT4L	-8.28	4.53	2.91E-05	6.33E-04	DNA-damage-inducible transcript 4-like
ST6GALNAC1	-5.88	4.83	2.93E-05	6.37E-04	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
FASN	-2.54	10.94	2.94E-05	6.38E-04	fatty acid synthase
SMC2	1.90	6.58	2.95E-05	6.40E-04	structural maintenance of chromosomes 2
ZACN	3.38	-2.00	2.97E-05	6.44E-04	zinc activated ligand-gated ion channel
LOC440297	-2.90	6.61	2.98E-05	6.45E-04	chondroitin sulfate proteoglycan 4 pseudogene
Klf12	3.67	3.21	2.99E-05	6.46E-04	Kruppel-like factor 12
ldlrap1	-3.66	5.51	2.99E-05	6.46E-04	low density lipoprotein receptor adaptor protein 1
SERINC5	-3.45	8.32	3.01E-05	6.48E-04	serine incorporator 5
chrna1	3.58	-1.52	3.05E-05	6.56E-04	cholinergic receptor, nicotinic, alpha 1 (muscle)
zp3	-3.15	5.26	3.12E-05	6.69E-04	zona pellucida glycoprotein 3 (sperm receptor)
HOXB4	3.58	2.51	3.24E-05	6.95E-04	homeobox B4
Cdc25b	2.30	6.94	3.24E-05	6.95E-04	cell division cycle 25 homolog B (S. pombe)
acsm3	-5.14	5.05	3.26E-05	6.98E-04	acyl-CoA synthetase medium-chain family member 3
DBNDD2	3.71	-0.97	3.29E-05	7.02E-04	dysbindin (dystrobrevin binding protein 1) domain containing 2
SSTR1	-7.75	3.05	3.31E-05	7.06E-04	somatostatin receptor 1
sall1	5.65	0.69	3.32E-05	7.08E-04	sal-like 1 (Drosophila)
SLC6A8	-2.87	7.73	3.37E-05	7.14E-04	solute carrier family 6 (neurotransmitter transporter, creatine), member 8
LOC100130776	3.94	-0.01	3.36E-05	7.14E-04	hypothetical LOC100130776
MLLT11	4.43	4.84	3.36E-05	7.14E-04	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11
Neat1	-2.61	9.76	3.37E-05	7.14E-04	non-protein coding RNA 84
B4galt5	1.45	6.39	3.36E-05	7.14E-04	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5
NPAS2	-4.22	4.72	3.46E-05	7.32E-04	neuronal PAS domain protein 2
PRTFDC1	3.32	2.45	3.58E-05	7.56E-04	phosphoribosyl transferase domain containing 1
RECQL	2.03	4.44	3.59E-05	7.58E-04	RecQ protein-like (DNA helicase Q1-like)
KCNK3	4.43	5.77	3.63E-05	7.65E-04	potassium channel, subfamily K, member 3
CBFA2T2	1.99	7.13	3.63E-05	7.65E-04	core-binding factor, runt domain, alpha subunit 2; translocated to, 2
ZNF660	3.75	-0.61	3.65E-05	7.68E-04	zinc finger protein 660
PTGIR	5.35	-2.37	3.68E-05	7.74E-04	prostaglandin I2 (prostacyclin) receptor (IP)
NLRP11	6.00	-0.35	3.71E-05	7.78E-04	NLR family, pyrin domain containing 11
SGCB	2.57	4.83	3.71E-05	7.78E-04	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)
RCAN1	2.22	4.50	3.73E-05	7.82E-04	regulator of calcineurin 1
REEP6	-4.71	5.18	3.74E-05	7.83E-04	receptor accessory protein 6
EMILIN1	3.68	1.47	3.83E-05	8.00E-04	elastin microfibril interfacer 1
Coro1a	3.37	2.45	3.85E-05	8.02E-04	coronin, actin binding protein, 1A
B4galnt2	3.39	-0.04	3.87E-05	8.06E-04	beta-1,4-N-acetyl-galactosaminyl transferase 2
LOC440905	-5.67	5.71	3.89E-05	8.07E-04	hypothetical LOC440905

Fmn2	4.06	2.46	3.88E-05	8.07E-04	formin 2
FAM190B	2.22	5.96	3.90E-05	8.09E-04	KIAA1128
PGAP1	2.29	3.94	3.91E-05	8.10E-04	post-GPI attachment to proteins 1
CDHR1	4.87	3.19	3.91E-05	8.10E-04	protocadherin 21
Agtrap	-2.20	6.09	3.96E-05	8.18E-04	angiotensin II receptor-associated protein
KCTD11	-3.41	4.30	3.99E-05	8.23E-04	potassium channel tetramerisation domain containing 11
Colec12	-6.12	6.36	3.99E-05	8.23E-04	collectin sub-family member 12
Slc23a1	-6.42	3.09	4.01E-05	8.25E-04	solute carrier family 23 (nucleobase transporters), member 1
HOXD1	5.09	0.12	4.07E-05	8.37E-04	homeobox D1
C8orf47	3.63	2.66	4.11E-05	8.44E-04	chromosome 8 open reading frame 47
GPNMB	-7.69	7.22	4.14E-05	8.50E-04	glycoprotein (transmembrane) nmb
DPYSL5	3.78	5.43	4.17E-05	8.54E-04	dihydropyrimidinase-like 5
CCR10	3.94	1.34	4.22E-05	8.63E-04	chemokine (C-C motif) receptor 10
Cpa2	4.72	-2.87	4.23E-05	8.65E-04	carboxypeptidase A2 (pancreatic)
Sft2d1	-2.71	4.85	4.24E-05	8.67E-04	SFT2 domain containing 1
NAP1L2	-4.59	4.09	4.27E-05	8.70E-04	nucleosome assembly protein 1-like 2
KIF1A	3.27	7.40	4.27E-05	8.70E-04	kinesin family member 1A
ENTREZ100507421	2.63	5.18	4.29E-05	8.73E-04	
PSCA	-8.11	6.89	4.38E-05	8.90E-04	prostate stem cell antigen
PECAM1	4.83	-1.20	4.39E-05	8.92E-04	platelet/endothelial cell adhesion molecule
Fgfrl1	-6.03	7.18	4.41E-05	8.94E-04	fibroblast growth factor receptor-like 1
ANGPTL4	-4.98	6.23	4.41E-05	8.94E-04	angiopoietin-like 4
xkr5	5.32	0.39	4.44E-05	8.99E-04	XK, Kell blood group complex subunit-related family, member 5
Tm6sf1	2.22	1.40	4.47E-05	9.04E-04	transmembrane 6 superfamily member 1
six1	2.30	5.25	4.49E-05	9.04E-04	SIX homeobox 1
VIPR1	-3.79	5.51	4.49E-05	9.04E-04	vasoactive intestinal peptide receptor 1
BSN	2.73	4.27	4.49E-05	9.04E-04	bassoon (presynaptic cytomatrix protein)
ZMAT4	3.14	2.06	4.50E-05	9.06E-04	zinc finger, matrin type 4
GOLGA8E	3.54	-1.05	4.55E-05	9.14E-04	golgi autoantigen, golgin subfamily a, 8E
CYB561	-2.06	8.55	4.58E-05	9.19E-04	cytochrome b-561
SYT4	4.36	5.32	4.71E-05	9.44E-04	synaptotagmin IV
PNKD	-2.16	6.88	4.89E-05	9.79E-04	paroxysmal nonkinesigenic dyskinesia
ARHGAP6	-6.39	5.63	4.91E-05	9.81E-04	Rho GTPase activating protein 6
GUCY2D	-11.32	1.33	4.98E-05	9.95E-04	guanylate cyclase 2D, membrane (retina-specific)
FAM115C	-5.51	3.66	5.07E-05	1.01E-03	family with sequence similarity 115, member C; family with sequence similarity 115, member D (pseudogene)
Sh2d3c	4.51	-1.35	5.13E-05	1.02E-03	SH2 domain containing 3C
Il1r1	-5.28	6.77	5.14E-05	1.02E-03	interleukin 1 receptor, type I
POU2AF1	2.58	-0.35	5.15E-05	1.02E-03	POU class 2 associating factor 1
KIAA1211	3.24	3.87	5.31E-05	1.05E-03	KIAA1211
RADIL	-12.07	2.30	5.32E-05	1.05E-03	Ras association and DIL domains
C1orf38	3.79	1.63	5.38E-05	1.06E-03	chromosome 1 open reading frame 38
iyd	-6.06	2.21	5.41E-05	1.07E-03	iodotyrosine deiodinase
SATB2	4.04	2.71	5.43E-05	1.07E-03	SATB homeobox 2
LOC728392	4.60	1.41	5.52E-05	1.09E-03	hypothetical protein LOC728392
Rgs10	-4.40	5.62	5.59E-05	1.10E-03	regulator of G-protein signaling 10
MPPED2	-7.23	3.68	5.60E-05	1.10E-03	metallophosphoesterase domain containing 2
ALK	3.84	-1.60	5.62E-05	1.10E-03	anaplastic lymphoma receptor tyrosine kinase
CYP39A1	-5.81	3.71	5.64E-05	1.11E-03	cytochrome P450, family 39, subfamily A, polypeptide 1
dnajc12	3.21	3.92	5.68E-05	1.11E-03	DnaJ (Hsp40) homolog, subfamily C, member 12
PLCL2	2.91	3.11	5.70E-05	1.12E-03	phospholipase C-like 2
PDE9A	-3.56	6.60	5.75E-05	1.12E-03	phosphodiesterase 9A
ENTREZ100506190	-2.40	5.20	5.76E-05	1.13E-03	
ivd	-2.16	6.91	5.89E-05	1.15E-03	isovaleryl Coenzyme A dehydrogenase
igsf3	1.71	5.82	5.94E-05	1.16E-03	immunoglobulin superfamily, member 3
Syt8	5.26	-1.77	5.99E-05	1.17E-03	synaptotagmin VIII

Bmf	1.49	4.99	6.05E-05	1.18E-03	Bcl2 modifying factor
Casp8ap2	1.93	4.71	6.10E-05	1.19E-03	caspase 8 associated protein 2
Slc35f2	-4.48	5.57	6.24E-05	1.21E-03	solute carrier family 35, member F2
Rbp1	4.34	3.87	6.25E-05	1.21E-03	retinol binding protein 1, cellular
KCNN2	-6.76	4.06	6.37E-05	1.23E-03	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2
PART1	-4.03	5.16	6.38E-05	1.24E-03	prostate androgen-regulated transcript 1
nupr1	-2.82	9.29	6.41E-05	1.24E-03	nuclear protein, transcriptional regulator, 1
Tmem88b	4.21	-2.02	6.41E-05	1.24E-03	Transmembrane protein 88B
AK3L1	-2.73	7.34	6.46E-05	1.25E-03	adenylate kinase 3-like 2; adenylate kinase 3-like 1
ASPM	2.03	5.88	6.50E-05	1.25E-03	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)
rdh11	-3.21	8.98	6.72E-05	1.29E-03	retinol dehydrogenase 11 (all-trans/9-cis/11-cis)
CREB3L4	-2.49	7.20	6.75E-05	1.30E-03	cAMP responsive element binding protein 3-like 4
HNF4G	-12.68	2.57	6.76E-05	1.30E-03	hepatocyte nuclear factor 4, gamma
ITGA5	-3.99	4.46	6.80E-05	1.30E-03	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
slc25a1	-2.00	7.41	6.83E-05	1.31E-03	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1
IKZF3	3.17	3.42	6.84E-05	1.31E-03	IKAROS family zinc finger 3 (Aiolos)
BCAN	4.37	0.04	6.94E-05	1.33E-03	brevican
RAPGEF5	1.86	4.31	6.96E-05	1.33E-03	Rap guanine nucleotide exchange factor (GEF) 5
STRA13	-1.76	6.98	6.99E-05	1.33E-03	stimulated by retinoic acid 13 homolog (mouse)
CELSR2	2.18	5.73	7.02E-05	1.34E-03	cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila)
ELL2	-3.39	6.43	7.05E-05	1.34E-03	elongation factor, RNA polymerase II, 2
C12orf42	4.46	-1.73	7.09E-05	1.35E-03	chromosome 12 open reading frame 42
DNASE2B	-6.67	2.05	7.09E-05	1.35E-03	deoxyribonuclease II beta
STOX2	2.70	0.53	7.16E-05	1.36E-03	storkhead box 2
ADAMTS14	3.05	-0.34	7.18E-05	1.36E-03	ADAM metallopeptidase with thrombospondin type 1 motif, 14
SV2A	3.42	4.85	7.19E-05	1.36E-03	synaptic vesicle glycoprotein 2A
TOP2A	1.63	8.21	7.20E-05	1.36E-03	topoisomerase (DNA) II alpha 170kDa
CAND2	2.84	3.11	7.23E-05	1.36E-03	cullin-associated and neddylation-dissociated 2 (putative)
Tex101	4.84	-0.61	7.33E-05	1.38E-03	testis expressed 101
AIM1	-3.27	7.20	7.35E-05	1.38E-03	absent in melanoma 1
FKBP5	-4.62	8.50	7.41E-05	1.39E-03	FK506 binding protein 5
Bmpr1b	-7.00	6.38	7.47E-05	1.40E-03	bone morphogenetic protein receptor, type IB
ENO3	2.45	3.15	7.50E-05	1.41E-03	enolase 3 (beta, muscle)
Atp1b1	1.82	7.21	7.55E-05	1.42E-03	ATPase, Na+/K+ transporting, beta 1 polypeptide
TCERG1L	4.01	3.30	7.58E-05	1.42E-03	transcription elongation regulator 1-like
SYNGR2	-2.18	8.64	7.59E-05	1.42E-03	synaptogyrin 2
ETS1	3.46	3.42	7.61E-05	1.42E-03	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
f2rl1	-5.57	5.08	7.64E-05	1.43E-03	coagulation factor II (thrombin) receptor-like 1
IL12RB2	2.43	-0.34	7.70E-05	1.44E-03	interleukin 12 receptor, beta 2
RAB11FIP5	-2.02	5.50	7.76E-05	1.45E-03	RAB11 family interacting protein 5 (class I)
b3gnt7	3.51	2.93	7.80E-05	1.45E-03	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 7
Tmem171	4.06	1.49	7.86E-05	1.46E-03	transmembrane protein 171
ATP13A3	1.86	7.38	7.89E-05	1.46E-03	ATPase type 13A3
ARL6IP6	2.02	4.24	7.89E-05	1.46E-03	ADP-ribosylation-like factor 6 interacting protein 6
ANXA1	-5.87	6.63	7.95E-05	1.47E-03	annexin A1
Fam3d	-7.42	4.22	8.04E-05	1.49E-03	family with sequence similarity 3, member D
Odz3	3.57	2.16	8.07E-05	1.49E-03	odz, odd Oz/ten-m homolog 3 (Drosophila)
TPH2	5.06	-2.54	8.06E-05	1.49E-03	tryptophan hydroxylase 2
Gli3	-7.95	3.03	8.08E-05	1.49E-03	GLI family zinc finger 3
CD81	-2.34	8.92	8.15E-05	1.50E-03	CD81 molecule
TUBA1A	2.31	9.44	8.36E-05	1.54E-03	tubulin, alpha 1a
KIAA1614	3.23	0.11	8.36E-05	1.54E-03	KIAA1614
Loxl4	2.53	2.53	8.47E-05	1.55E-03	lysyl oxidase-like 4
st8sia5	3.50	0.00	8.49E-05	1.56E-03	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5
klf11	1.61	5.15	8.49E-05	1.56E-03	Kruppel-like factor 11

tbx3	-4.05	7.32	8.51E-05	1.56E-03	T-box 3
Upk3a	-6.80	4.59	8.90E-05	1.63E-03	uroplakin 3A
ACSM1	-4.84	5.75	8.92E-05	1.63E-03	acyl-CoA synthetase medium-chain family member 1
MCM6	1.51	6.41	8.95E-05	1.63E-03	minichromosome maintenance complex component 6
ACTL8	3.75	3.36	8.96E-05	1.63E-03	actin-like 8
EMX1	4.11	0.02	8.99E-05	1.64E-03	empty spiracles homeobox 1
NQO2	-3.06	4.81	9.01E-05	1.64E-03	NAD(P)H dehydrogenase, quinone 2
C6orf81	-10.98	1.07	9.01E-05	1.64E-03	chromosome 6 open reading frame 81
ASMTL	-2.06	6.74	9.08E-05	1.64E-03	acetylserotonin O-methyltransferase-like
ADAMTS5	3.88	-0.82	9.07E-05	1.64E-03	ADAM metallopeptidase with thrombospondin type 1 motif, 5
Nol4	3.83	3.78	9.09E-05	1.65E-03	nucleolar protein 4
gsr	-2.15	7.58	9.16E-05	1.66E-03	glutathione reductase
CNTNAP5	2.38	-0.35	9.18E-05	1.66E-03	contactin associated protein-like 5
LOC727849	-3.00	6.95	9.22E-05	1.66E-03	similar to cis-Golgi matrix protein GM130
CD164L2	-11.92	1.50	9.35E-05	1.69E-03	CD164 sialomucin-like 2
pitpnm2	2.36	4.21	9.41E-05	1.69E-03	phosphatidylinositol transfer protein, membrane-associated 2
NOS1	3.64	1.83	9.47E-05	1.70E-03	nitric oxide synthase 1 (neuronal)
MIPEP	-4.57	7.32	9.67E-05	1.74E-03	mitochondrial intermediate peptidase
GDNF	3.46	-0.01	9.86E-05	1.77E-03	glial cell derived neurotrophic factor
Krt40	3.43	-0.37	9.87E-05	1.77E-03	keratin 40
ITSN1	1.61	5.26	9.96E-05	1.78E-03	intersectin 1 (SH3 domain protein)
GRAP2	4.29	-0.41	9.97E-05	1.78E-03	GRB2-related adaptor protein 2
ZNF702P	-6.01	2.88	1.01E-04	1.80E-03	zinc finger protein 702 pseudogene
TLE6	2.63	1.90	1.02E-04	1.82E-03	transducin-like enhancer of split 6 (E(sp1) homolog, Drosophila)
REN	3.56	-1.70	1.03E-04	1.84E-03	renin
TMPRSS3	4.16	4.46	1.03E-04	1.84E-03	transmembrane protease, serine 3
CD274	2.69	-0.13	1.04E-04	1.85E-03	CD274 molecule
Fabp5	-4.93	6.42	1.04E-04	1.85E-03	fatty acid binding protein 5-like 2; fatty acid binding protein 5 (psoriasis-associated); fatty acid binding protein 5-like 8; fatty acid binding protein 5-like 7; fatty acid binding protein 5-like 9
KATNAL1	2.17	3.54	1.04E-04	1.85E-03	katanin p60 subunit A-like 1
Tmem145	2.99	2.98	1.04E-04	1.85E-03	transmembrane protein 145
RAB26	-2.65	4.52	1.05E-04	1.86E-03	RAB26, member RAS oncogene family
A2ML1	-8.90	4.17	1.05E-04	1.87E-03	alpha-2-macroglobulin-like 1
FAM20C	-4.77	4.59	1.06E-04	1.88E-03	family with sequence similarity 20, member C
HSPA12A	-7.22	2.21	1.07E-04	1.89E-03	heat shock 70kDa protein 12A
CA14	2.69	0.03	1.08E-04	1.90E-03	carbonic anhydrase XIV
LOC652798	-6.16	7.60	1.08E-04	1.91E-03	plakophilin 1 (ectodermal dysplasia/skin fragility syndrome); similar to plakophilin 1 isoform 1a
STAT5A	2.05	4.90	1.10E-04	1.94E-03	signal transducer and activator of transcription 5A
ENTREZ85014	-2.11	7.04	1.10E-04	1.94E-03	
EEF1A2	-6.79	8.62	1.10E-04	1.94E-03	eukaryotic translation elongation factor 1 alpha 2
Scgb2a1	2.20	2.42	1.11E-04	1.95E-03	secretoglobin, family 2A, member 1
HEY1	2.68	2.76	1.12E-04	1.97E-03	hairy/enhancer-of-split related with YRPW motif 1
Fam125b	1.94	5.03	1.12E-04	1.97E-03	family with sequence similarity 125, member B
SMOX	-3.90	5.59	1.13E-04	1.98E-03	spermine oxidase
ADRB1	-3.75	5.04	1.14E-04	1.99E-03	adrenergic, beta-1-, receptor
PLA2G5	-11.18	1.07	1.15E-04	2.00E-03	phospholipase A2, group V
B3gnt3	-8.12	5.22	1.15E-04	2.01E-03	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3
GGTLC2	-4.31	4.55	1.16E-04	2.01E-03	gamma-glutamyltransferase light chain 2
C5orf4	3.52	2.68	1.16E-04	2.02E-03	chromosome 5 open reading frame 4
GNB2L1	-2.11	11.14	1.16E-04	2.02E-03	guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
NRON	4.47	-3.43	1.17E-04	2.03E-03	likely ortholog of mouse noncoding repressor of NFAT
S100P	-7.65	5.99	1.20E-04	2.09E-03	S100 calcium binding protein P
ENTREZ113457	-4.66	3.34	1.21E-04	2.09E-03	
LOC729683	2.97	1.31	1.22E-04	2.11E-03	hypothetical protein LOC729683
POU4F1	3.32	0.88	1.23E-04	2.13E-03	POU class 4 homeobox 1

Plxnd1	2.83	5.45	1.24E-04	2.14E-03	plexin D1
PDZK1IP1	-4.59	5.15	1.24E-04	2.15E-03	PDZK1 interacting protein 1
KCNH5	5.17	-0.07	1.25E-04	2.15E-03	potassium voltage-gated channel, subfamily H (eag-related), member 5
Orai3	-2.77	4.57	1.26E-04	2.17E-03	ORAI calcium release-activated calcium modulator 3
LOC100129269	2.83	-0.37	1.29E-04	2.23E-03	hypothetical protein LOC100129269
GLYATL1	-6.06	4.78	1.31E-04	2.25E-03	glycine-N-acyltransferase-like 1
NDN	-7.63	3.76	1.31E-04	2.25E-03	necdin homolog (mouse)
GATA2	-3.12	7.71	1.32E-04	2.27E-03	GATA binding protein 2
WNT9A	3.75	1.69	1.33E-04	2.28E-03	wingless-type MMTV integration site family, member 9A
ENTREZ134701	5.77	-1.85	1.33E-04	2.28E-03	
Ranbp3l	-5.66	2.89	1.33E-04	2.28E-03	RAN binding protein 3-like
PLCB2	2.54	2.28	1.36E-04	2.32E-03	phospholipase C, beta 2
MGC29506	-5.37	1.61	1.36E-04	2.32E-03	hypothetical protein MGC29506
PLP2	3.21	5.83	1.36E-04	2.33E-03	proteolipid protein 2 (colonic epithelium-enriched)
IDH1	-2.97	8.36	1.38E-04	2.35E-03	isocitrate dehydrogenase 1 (NADP+), soluble
pppde2	-2.31	5.68	1.38E-04	2.35E-03	PPPDE peptidase domain containing 2
plekha1	1.57	4.75	1.39E-04	2.37E-03	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1
loxl2	2.95	2.85	1.39E-04	2.37E-03	lysyl oxidase-like 2
TRIT1	1.98	5.00	1.40E-04	2.38E-03	tRNA isopentenyltransferase 1
LOC100287428	4.11	1.98	1.41E-04	2.39E-03	similar to Paraneoplastic antigen-like protein 6A
WNK4	-6.14	6.40	1.44E-04	2.44E-03	WNK lysine deficient protein kinase 4
ALDH1A3	-6.47	7.23	1.44E-04	2.44E-03	aldehyde dehydrogenase 1 family, member A3
AMTN	-18.58	7.81	1.44E-04	2.44E-03	amelotin
C14orf162	3.80	-1.00	1.45E-04	2.45E-03	chromosome 14 open reading frame 162
PDLIM5	-3.99	9.44	1.45E-04	2.45E-03	PDZ and LIM domain 5
KNTC1	1.32	5.52	1.46E-04	2.47E-03	kinetochore associated 1
GHR	-8.12	4.58	1.46E-04	2.47E-03	growth hormone receptor
ptprz1	2.89	-0.51	1.47E-04	2.48E-03	protein tyrosine phosphatase, receptor-type, Z polypeptide 1
TXNRD2	-2.03	6.09	1.48E-04	2.49E-03	thioredoxin reductase 2
Lpcat3	-2.81	6.97	1.50E-04	2.51E-03	lysophosphatidylcholine acyltransferase 3
mfsd2a	3.17	2.43	1.51E-04	2.52E-03	major facilitator superfamily domain containing 2
Chad	3.45	0.31	1.51E-04	2.53E-03	chondroadherin
TMEM74	3.48	-0.43	1.51E-04	2.53E-03	transmembrane protein 74
PTPRG	2.56	3.40	1.51E-04	2.53E-03	protein tyrosine phosphatase, receptor type, G
SETBP1	1.93	4.09	1.53E-04	2.56E-03	SET binding protein 1
NANS	-1.98	7.61	1.53E-04	2.56E-03	N-acetylneuraminic acid synthase
SH3TC2	-10.79	0.73	1.54E-04	2.57E-03	SH3 domain and tetratricopeptide repeats 2
PARP4	1.30	6.22	1.55E-04	2.58E-03	poly (ADP-ribose) polymerase family, member 4
SCRT1	3.12	-0.47	1.57E-04	2.61E-03	scratch homolog 1, zinc finger protein (Drosophila)
ptprr	-11.18	1.16	1.58E-04	2.62E-03	protein tyrosine phosphatase, receptor type, R
sema5b	3.60	3.45	1.58E-04	2.63E-03	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B
CTSL1	-2.20	6.21	1.59E-04	2.63E-03	cathepsin L1
nox5	-11.22	1.09	1.59E-04	2.64E-03	NADPH oxidase, EF-hand calcium binding domain 5
LRRC8C	3.22	2.04	1.59E-04	2.64E-03	leucine rich repeat containing 8 family, member C
TMCO4	-2.43	5.49	1.60E-04	2.65E-03	transmembrane and coiled-coil domains 4
EMID2	-8.20	3.48	1.63E-04	2.69E-03	EMI domain containing 2
COMT	-1.66	6.43	1.64E-04	2.71E-03	catechol-O-methyltransferase
PECI	-2.64	6.36	1.64E-04	2.71E-03	peroxisomal D3,D2-enoyl-CoA isomerase
ca12	-6.48	4.79	1.66E-04	2.73E-03	carbonic anhydrase XII
sytl3	1.73	3.35	1.69E-04	2.78E-03	synaptotagmin-like 3
CYP4F11	-3.97	3.65	1.69E-04	2.78E-03	cytochrome P450, family 4, subfamily F, polypeptide 11
TGFB1	1.96	1.63	1.71E-04	2.81E-03	transforming growth factor, beta 1
DNAJB13	2.90	0.33	1.71E-04	2.81E-03	DnaJ (Hsp40) related, subfamily B, member 13
ENTREZ100316868	-13.13	2.84	1.73E-04	2.83E-03	

Mrgprx3	3.01	0.32	1.73E-04	2.84E-03	MAS-related GPR, member X3
SIAE	-2.87	4.69	1.74E-04	2.85E-03	sialic acid acetylesterase
SIDT2	-2.34	6.21	1.75E-04	2.86E-03	SID1 transmembrane family, member 2
Mgat5b	2.99	4.13	1.76E-04	2.87E-03	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B
DUSP26	4.17	0.32	1.77E-04	2.89E-03	dual specificity phosphatase 26 (putative)
RPS4Y1	-4.68	8.11	1.82E-04	2.96E-03	ribosomal protein S4, Y-linked 1
GABRB3	1.63	5.50	1.84E-04	3.00E-03	gamma-aminobutyric acid (GABA) A receptor, beta 3
Espn	3.19	4.08	1.86E-04	3.02E-03	espin
Rnf144b	-2.42	5.20	1.87E-04	3.04E-03	ring finger protein 144B
RAB3D	-1.90	7.97	1.87E-04	3.04E-03	RAB3D, member RAS oncogene family
CPLX2	4.22	4.84	1.88E-04	3.06E-03	complexin 2
SCN7A	4.17	-2.81	1.89E-04	3.07E-03	sodium channel, voltage-gated, type VII, alpha
prss3	3.35	-1.16	1.90E-04	3.07E-03	protease, serine, 3
PF4V1	4.88	-3.28	1.90E-04	3.08E-03	platelet factor 4 variant 1
CHRNA3	1.73	1.35	1.92E-04	3.10E-03	cholinergic receptor, nicotinic, alpha 3
MYC	-3.93	7.11	1.92E-04	3.11E-03	v-myc myelocytomatosis viral oncogene homolog (avian)
cyp46a1	-10.40	0.69	1.94E-04	3.13E-03	cytochrome P450, family 46, subfamily A, polypeptide 1
KCNK5	2.16	3.98	1.95E-04	3.14E-03	potassium channel, subfamily K, member 5
HIF3A	2.69	1.18	1.96E-04	3.16E-03	hypoxia inducible factor 3, alpha subunit
MOGAT2	-6.44	1.86	1.99E-04	3.19E-03	monoacylglycerol O-acyltransferase 2
ZNF655	5.94	1.18	1.99E-04	3.20E-03	zinc finger protein 655
Olr1	3.14	-1.96	1.99E-04	3.20E-03	oxidized low density lipoprotein (lectin-like) receptor 1
AKAP12	-3.82	7.05	2.00E-04	3.20E-03	A kinase (PRKA) anchor protein 12
Olfml2b	4.81	-0.61	2.03E-04	3.25E-03	olfactomedin-like 2B
FBLN7	3.39	4.49	2.03E-04	3.25E-03	fibulin 7
DPP4	-7.23	5.83	2.04E-04	3.26E-03	dipeptidyl-peptidase 4
SYDE2	2.69	2.56	2.04E-04	3.26E-03	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)
ANTXR2	-3.67	4.87	2.05E-04	3.28E-03	anthrax toxin receptor 2
Igfals	4.20	0.42	2.05E-04	3.28E-03	insulin-like growth factor binding protein, acid labile subunit
ZNF350	-2.83	5.45	2.06E-04	3.28E-03	zinc finger protein 350
CREB3L1	-3.77	6.57	2.07E-04	3.29E-03	cAMP responsive element binding protein 3-like 1
add2	4.03	4.38	2.09E-04	3.33E-03	adducin 2 (beta)
Baz2b	1.62	5.61	2.10E-04	3.34E-03	bromodomain adjacent to zinc finger domain, 2B
fbxo27	-4.21	3.67	2.12E-04	3.36E-03	F-box protein 27
KIAA1199	2.66	2.27	2.13E-04	3.38E-03	KIAA1199
UGT2B17	-9.09	4.17	2.14E-04	3.39E-03	UDP glucuronosyltransferase 2 family, polypeptide B17
Myo7b	3.34	1.22	2.14E-04	3.39E-03	myosin VIIB
PGBD1	2.01	3.05	2.16E-04	3.41E-03	piggyBac transposable element derived 1
Aprt	-2.31	7.24	2.16E-04	3.41E-03	adenine phosphoribosyltransferase
ICAM3	-2.19	4.81	2.17E-04	3.42E-03	intercellular adhesion molecule 3
LOC375295	4.26	0.14	2.17E-04	3.43E-03	hypothetical protein LOC375295
CSRNP3	3.64	1.78	2.18E-04	3.43E-03	cysteine-serine-rich nuclear protein 3
REST	-3.62	5.40	2.20E-04	3.46E-03	RE1-silencing transcription factor
MAOB	-10.67	5.19	2.20E-04	3.46E-03	monoamine oxidase B
DDR2	3.72	0.84	2.21E-04	3.47E-03	discoidin domain receptor tyrosine kinase 2
Arhgap25	4.30	0.95	2.22E-04	3.48E-03	Rho GTPase activating protein 25
SLCO2B1	3.77	-2.12	2.22E-04	3.48E-03	solute carrier organic anion transporter family, member 2B1
LOC643749	2.34	2.13	2.23E-04	3.49E-03	hypothetical LOC643749
GLDN	3.34	-0.70	2.23E-04	3.49E-03	gliomedin
Abca12	3.06	1.71	2.23E-04	3.49E-03	ATP-binding cassette, sub-family A (ABC1), member 12
NLRP2	-8.64	5.32	2.25E-04	3.51E-03	NLR family, pyrin domain containing 2
MCAM	3.34	4.07	2.26E-04	3.53E-03	melanoma cell adhesion molecule
CAB39L	-3.76	6.98	2.27E-04	3.55E-03	calcium binding protein 39-like
CSMD2	4.48	1.83	2.31E-04	3.60E-03	CUB and Sushi multiple domains 2
GAB3	3.67	-1.03	2.34E-04	3.65E-03	GRB2-associated binding protein 3

Syt12	-5.81	2.29	2.35E-04	3.65E-03	synaptotagmin XII
F5	-4.03	5.23	2.39E-04	3.71E-03	coagulation factor V (proaccelerin, labile factor)
SLC37A2	-4.88	2.95	2.39E-04	3.71E-03	solute carrier family 37 (glycerol-3-phosphate transporter), member 2
Zmynd15	-10.72	0.68	2.41E-04	3.74E-03	zinc finger, MYND-type containing 15
adam19	3.17	2.09	2.42E-04	3.75E-03	ADAM metallopeptidase domain 19 (meltrin beta)
akr1c3	-7.72	6.44	2.44E-04	3.78E-03	aldo-keto reductase family 1, member C3 (3-alpha hydroxysteroid dehydrogenase, type II)
ARID5B	-2.64	6.38	2.45E-04	3.79E-03	AT rich interactive domain 5B (MRF1-like)
SEMA4C	1.79	5.79	2.47E-04	3.82E-03	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C
GREB1L	-4.86	3.19	2.49E-04	3.84E-03	KIAA1772
sox1	4.28	-0.88	2.49E-04	3.84E-03	SRY (sex determining region Y)-box 1
klf15	-2.91	3.65	2.50E-04	3.86E-03	Kruppel-like factor 15
Pnma3	2.66	2.95	2.51E-04	3.87E-03	paraneoplastic antigen MA3
HOXA13	-6.23	4.35	2.53E-04	3.90E-03	homeobox A13
WNT6	5.17	-2.42	2.55E-04	3.91E-03	wingless-type MMTV integration site family, member 6
FOLH1	-6.19	8.56	2.55E-04	3.91E-03	folate hydrolase (prostate-specific membrane antigen) 1
Tgif2	-3.79	4.57	2.55E-04	3.91E-03	TGFB-induced factor homeobox 2
SLC38A8	3.82	-2.86	2.56E-04	3.93E-03	solute carrier family 38, member 8
abhd11	-1.71	6.53	2.57E-04	3.93E-03	abhydrolase domain containing 11
napB	2.10	3.81	2.57E-04	3.93E-03	N-ethylmaleimide-sensitive factor attachment protein, beta
C10orf116	-5.79	6.81	2.59E-04	3.96E-03	chromosome 10 open reading frame 116
SLC30A4	-4.18	6.31	2.60E-04	3.97E-03	solute carrier family 30 (zinc transporter), member 4
Akr7a3	2.82	1.93	2.61E-04	3.98E-03	aldo-keto reductase family 7, member A3 (aflatoxin aldehyde reductase)
Acaa1	-2.08	6.79	2.61E-04	3.98E-03	acetyl-Coenzyme A acyltransferase 1
OSGIN1	-4.57	2.82	2.61E-04	3.98E-03	oxidative stress induced growth inhibitor 1
phf19	2.00	5.79	2.62E-04	3.98E-03	PHD finger protein 19
GADD45A	2.15	4.47	2.63E-04	4.00E-03	growth arrest and DNA-damage-inducible, alpha
KDELR3	-4.54	4.36	2.64E-04	4.00E-03	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3
PHF21B	4.33	1.38	2.64E-04	4.01E-03	PHD finger protein 21B
DONSON	1.56	4.88	2.65E-04	4.02E-03	downstream neighbor of SON
ANGPT2	3.92	2.22	2.67E-04	4.04E-03	angiopoietin 2
GVIN1	3.44	-2.65	2.67E-04	4.04E-03	GTPase, very large interferon inducible 1
PRLR	-6.95	4.76	2.71E-04	4.09E-03	prolactin receptor
ATP8A2	2.77	3.13	2.73E-04	4.13E-03	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2
SELM	-3.32	4.71	2.73E-04	4.13E-03	selenoprotein M
IRS1	-4.89	4.67	2.75E-04	4.15E-03	insulin receptor substrate 1
Rab2b	1.36	4.75	2.75E-04	4.15E-03	RAB2B, member RAS oncogene family
BLVRA	-1.91	5.56	2.75E-04	4.15E-03	biliverdin reductase A
ORM1	-13.97	3.71	2.78E-04	4.18E-03	orosomucoid 1
L3mbtl4	4.48	0.83	2.79E-04	4.19E-03	l(3)mbt-like 4 (Drosophila)
TUBGCP3	1.46	5.37	2.79E-04	4.19E-03	tubulin, gamma complex associated protein 3
LOC388152	-2.65	6.26	2.81E-04	4.21E-03	hypothetical LOC388152
SLC15A3	3.31	0.94	2.83E-04	4.23E-03	solute carrier family 15, member 3
Cacng4	-7.68	5.04	2.83E-04	4.23E-03	calcium channel, voltage-dependent, gamma subunit 4
P704P	-6.12	4.03	2.84E-04	4.25E-03	prostate-specific P704P
POTEF	-4.71	3.84	2.87E-04	4.28E-03	POTE ankyrin domain family, member F
GPR12	3.79	-2.78	2.89E-04	4.32E-03	G protein-coupled receptor 12
RGS16	2.57	3.94	2.90E-04	4.33E-03	regulator of G-protein signaling 16
HPGD	-8.53	7.62	2.91E-04	4.33E-03	hydroxyprostaglandin dehydrogenase 15-(NAD)
CFHR3	3.74	-0.36	2.92E-04	4.35E-03	complement factor H-related 3
CHL1	4.39	1.32	2.93E-04	4.36E-03	cell adhesion molecule with homology to L1CAM (close homolog of L1)
tbc1d9b	-1.65	8.00	2.96E-04	4.40E-03	TBC1 domain family, member 9B (with GRAM domain)
KIF14	1.70	4.52	2.97E-04	4.41E-03	kinesin family member 14
TCP11L1	2.13	3.73	2.98E-04	4.43E-03	t-complex 11 (mouse)-like 1
CD83	2.29	2.79	3.00E-04	4.45E-03	CD83 molecule

SLC6A17	4.19	2.58	3.04E-04	4.50E-03	solute carrier family 6, member 17
Ppm1k	-2.71	5.12	3.04E-04	4.50E-03	protein phosphatase 1K (PP2C domain containing)
LOC80054	-5.40	2.84	3.06E-04	4.52E-03	hypothetical LOC80054
Klf4	-2.64	5.11	3.07E-04	4.53E-03	Kruppel-like factor 4 (gut)
UGT8	1.78	4.25	3.08E-04	4.55E-03	UDP glycosyltransferase 8
DAAM2	2.18	1.40	3.12E-04	4.60E-03	dishevelled associated activator of morphogenesis 2
KIT	3.19	5.24	3.16E-04	4.66E-03	similar to Mast/stem cell growth factor receptor precursor (SCFR) (Proto-oncogene tyrosine-protein kinase Kit) (c-kit) (CD117 antigen); v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog
C10orf81	-5.16	3.54	3.17E-04	4.67E-03	chromosome 10 open reading frame 81
Smpd3	3.53	5.20	3.18E-04	4.68E-03	sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II)
LHFP	3.50	3.24	3.19E-04	4.69E-03	lipoma HMGIC fusion partner
cdh5	5.75	0.49	3.20E-04	4.70E-03	cadherin 5, type 2 (vascular endothelium)
PNPLA4	-2.08	5.02	3.25E-04	4.77E-03	patatin-like phospholipase domain containing 4
rpl11	-1.69	9.62	3.26E-04	4.79E-03	ribosomal protein L11
Xylt1	3.12	4.12	3.27E-04	4.79E-03	xylosyltransferase I
CXCL16	-3.60	4.67	3.29E-04	4.80E-03	chemokine (C-X-C motif) ligand 16
ARNTL2	3.54	2.95	3.29E-04	4.80E-03	aryl hydrocarbon receptor nuclear translocator-like 2
SLC26A3	-10.30	4.76	3.29E-04	4.80E-03	solute carrier family 26, member 3
STAP2	-1.81	6.66	3.30E-04	4.82E-03	signal transducing adaptor family member 2
LOC442421	3.42	0.56	3.31E-04	4.82E-03	hypothetical LOC442421
FAM46C	-3.37	5.35	3.32E-04	4.84E-03	family with sequence similarity 46, member C
PHLDB1	1.86	5.61	3.35E-04	4.88E-03	pleckstrin homology-like domain, family B, member 1
ccdc73	3.42	0.41	3.37E-04	4.91E-03	coiled-coil domain containing 73
S100A6	3.33	5.34	3.46E-04	5.02E-03	S100 calcium binding protein A6
Adamts15	2.45	1.61	3.46E-04	5.02E-03	ADAM metallopeptidase with thrombospondin type 1 motif, 15
DLX5	2.23	1.77	3.48E-04	5.05E-03	distal-less homeobox 5
PCBP3	4.41	3.15	3.52E-04	5.10E-03	poly(rC) binding protein 3
lpar6	-11.81	1.67	3.53E-04	5.11E-03	purinergic receptor P2Y, G-protein coupled, 5
WWTR1	-3.31	4.59	3.53E-04	5.11E-03	WW domain containing transcription regulator 1
Xpnpep3	-2.07	5.10	3.57E-04	5.17E-03	X-prolyl aminopeptidase (aminopeptidase P) 3, putative
ACVR2B	1.23	4.89	3.59E-04	5.18E-03	activin A receptor, type IIB
AQP3	-2.77	7.03	3.70E-04	5.33E-03	aquaporin 3 (Gill blood group)
C19orf48	-2.54	9.22	3.70E-04	5.33E-03	chromosome 19 open reading frame 48
ALOX15	-4.13	4.45	3.73E-04	5.38E-03	arachidonate 15-lipoxygenase
Rnase4	-5.96	5.80	3.76E-04	5.41E-03	ribonuclease, RNase A family, 4
fbxo25	-2.39	6.13	3.77E-04	5.43E-03	F-box protein 25
myoz1	2.38	-0.36	3.87E-04	5.56E-03	myozenin 1
LOC653881	-1.84	11.56	3.89E-04	5.59E-03	ribosomal protein L3; similar to 60S ribosomal protein L3 (L4)
Slc4a11	2.25	4.37	3.96E-04	5.67E-03	solute carrier family 4, sodium borate transporter, member 11
NAB1	1.66	5.10	3.96E-04	5.67E-03	NGFI-A binding protein 1 (EGR1 binding protein 1)
BEND4	-7.97	4.29	3.96E-04	5.67E-03	BEN domain containing 4
GUCY1A3	-4.91	7.38	3.97E-04	5.68E-03	guanylate cyclase 1, soluble, alpha 3
TMTC1	2.88	3.75	4.04E-04	5.77E-03	transmembrane and tetratricopeptide repeat containing 1
SEPW1	1.64	7.19	4.04E-04	5.77E-03	selenoprotein W, 1
gng7	-7.04	3.01	4.05E-04	5.78E-03	guanine nucleotide binding protein (G protein), gamma 7
MFAP3L	-5.79	2.79	4.07E-04	5.81E-03	microfibrillar-associated protein 3-like
ODZ4	3.23	3.17	4.10E-04	5.85E-03	odz, odd Oz/ten-m homolog 4 (Drosophila)
mcm2	1.53	7.54	4.16E-04	5.92E-03	minichromosome maintenance complex component 2
FRAS1	1.71	5.52	4.21E-04	6.00E-03	Fraser syndrome 1
TRIB1	-2.09	7.87	4.29E-04	6.10E-03	tribbles homolog 1 (Drosophila)
TNS1	1.95	5.37	4.30E-04	6.11E-03	tensin 1
MAOA	-3.57	8.03	4.33E-04	6.15E-03	monoamine oxidase A
nupl1	1.22	5.84	4.36E-04	6.18E-03	nucleoporin like 1
Bean	3.43	1.91	4.37E-04	6.19E-03	brain expressed, associated with Nedd4
arhgap18	-3.10	4.47	4.37E-04	6.19E-03	Rho GTPase activating protein 18

NEK5	1.65	3.53	4.39E-04	6.21E-03	NIMA (never in mitosis gene a)-related kinase 5
TPK1	-7.34	2.06	4.43E-04	6.26E-03	thiamin pyrophosphokinase 1
MPZL2	-2.98	5.32	4.44E-04	6.27E-03	myelin protein zero-like 2
SNHG4	-4.30	3.39	4.45E-04	6.28E-03	small nucleolar RNA host gene 4 (non-protein coding)
CYP4F8	-12.67	3.84	4.45E-04	6.28E-03	cytochrome P450, family 4, subfamily F, polypeptide 8
CORO2B	5.11	0.00	4.48E-04	6.30E-03	coronin, actin binding protein, 2B
Col9a3	-3.98	3.22	4.49E-04	6.32E-03	collagen, type IX, alpha 3
GPR176	2.91	4.22	4.49E-04	6.32E-03	G protein-coupled receptor 176
PBX3	1.52	5.48	4.50E-04	6.32E-03	pre-B-cell leukemia homeobox 3
Itm2a	-11.47	6.54	4.53E-04	6.36E-03	integral membrane protein 2A
dera	1.52	4.52	4.55E-04	6.38E-03	2-deoxyribose-5-phosphate aldolase homolog (C. elegans)
SCN3B	3.98	0.91	4.62E-04	6.47E-03	sodium channel, voltage-gated, type III, beta
OSMR	-6.63	3.07	4.64E-04	6.49E-03	oncostatin M receptor
fbxo44	-2.38	4.40	4.64E-04	6.49E-03	F-box protein 44
CACNG6	3.29	-0.93	4.66E-04	6.52E-03	calcium channel, voltage-dependent, gamma subunit 6
ZBTB42	-1.83	6.01	4.72E-04	6.59E-03	zinc finger and BTB domain containing 42
atp1a3	3.37	3.59	4.74E-04	6.61E-03	ATPase, Na+/K+ transporting, alpha 3 polypeptide
SPARC	3.14	-0.87	4.76E-04	6.63E-03	secreted protein, acidic, cysteine-rich (osteonectin)
Gnpnat1	-2.28	6.65	4.78E-04	6.67E-03	glucosamine-phosphate N-acetyltransferase 1
Hmgxb3	-1.64	6.95	4.81E-04	6.69E-03	HMG box domain containing 3
Prr16	-7.08	3.54	4.81E-04	6.69E-03	proline rich 16
rpl12	-1.74	10.01	4.81E-04	6.69E-03	ribosomal protein L12 pseudogene 2; ribosomal protein L12 pseudogene 32; ribosomal protein L12 pseudogene 35; ribosomal protein L12 pseudogene 19; ribosomal protein L12 pseudogene 6; ribosomal protein L12; ribosomal protein L12 pseudogene 14
SH3PXD2A	1.66	5.87	4.83E-04	6.70E-03	SH3 and PX domains 2A
LEPREL1	-6.76	5.09	4.84E-04	6.72E-03	leprecan-like 1
Herc3	-3.03	6.04	4.87E-04	6.76E-03	hect domain and RLD 3
ARHGAP28	-5.82	5.16	4.89E-04	6.77E-03	Rho GTPase activating protein 28
hal	2.03	0.03	4.89E-04	6.77E-03	histidine ammonia-lyase
SP4	1.90	3.79	4.91E-04	6.79E-03	Sp4 transcription factor
DNAH10	1.05	3.29	4.92E-04	6.80E-03	dynein, axonemal, heavy chain 10
Pde4a	-4.51	2.55	4.93E-04	6.81E-03	phosphodiesterase 4A, cAMP-specific (phosphodiesterase E2 dunce homolog, Drosophila)
foxa1	-2.00	8.95	4.94E-04	6.82E-03	forkhead box A1
BTG3	1.97	4.74	4.99E-04	6.88E-03	BTG family, member 3
TMEM179	3.62	0.56	5.04E-04	6.95E-03	transmembrane protein 179
Srcrb4d	3.03	1.42	5.08E-04	6.99E-03	scavenger receptor cysteine rich domain containing, group B (4 domains)
Znf467	-2.93	4.36	5.09E-04	7.00E-03	zinc finger protein 467
SLC1A6	5.20	2.28	5.14E-04	7.05E-03	solute carrier family 1 (high affinity aspartate/glutamate transporter), member 6
Dpysl2	3.05	4.96	5.13E-04	7.05E-03	dihydropyrimidinase-like 2
mtss1	1.64	6.26	5.16E-04	7.08E-03	metastasis suppressor 1
NAV1	1.70	5.90	5.18E-04	7.10E-03	neuron navigator 1
WIPF1	2.33	1.96	5.20E-04	7.13E-03	WAS/WASL interacting protein family, member 1
CA5A	5.58	-3.06	5.21E-04	7.13E-03	carbonic anhydrase VA, mitochondrial
ANO7	-5.27	3.55	5.23E-04	7.15E-03	anoctamin 7
PTK2B	-2.04	5.78	5.23E-04	7.15E-03	PTK2B protein tyrosine kinase 2 beta
Sobp	2.74	3.99	5.27E-04	7.19E-03	sine oculis binding protein homolog (Drosophila)
Acy3	-7.26	2.73	5.27E-04	7.19E-03	aspartoacylase (aminocyclase) 3
DNASE1	-2.09	4.93	5.28E-04	7.19E-03	deoxyribonuclease I
PTPRB	-6.79	4.25	5.28E-04	7.20E-03	protein tyrosine phosphatase, receptor type, B
slc25a24	1.88	4.60	5.32E-04	7.24E-03	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24
GLUD2	-2.46	5.13	5.33E-04	7.24E-03	glutamate dehydrogenase 2
Krt14	-11.76	2.40	5.34E-04	7.26E-03	keratin 14
ACADSB	-2.61	6.15	5.36E-04	7.26E-03	acyl-Coenzyme A dehydrogenase, short/branched chain
TMEM108	4.00	2.34	5.36E-04	7.26E-03	transmembrane protein 108
CXCL1	3.46	0.04	5.35E-04	7.26E-03	chemokine (C-X-C motif) ligand 1 (melanoma growth stimulating activity, alpha)

SLC27A1	-2.78	4.76	5.45E-04	7.39E-03	solute carrier family 27 (fatty acid transporter), member 1
LOC728666	-1.63	6.23	5.56E-04	7.51E-03	PRELI domain containing 1; similar to Px19-like protein (25 kDa protein of relevant evolutionary and lymphoid interest) (PRELI)
Rilpl2	-3.46	3.68	5.56E-04	7.51E-03	Rab interacting lysosomal protein-like 2
SALL2	1.65	5.11	5.56E-04	7.51E-03	sal-like 2 (Drosophila)
ankrd29	-13.08	2.71	5.56E-04	7.51E-03	ankyrin repeat domain 29
EBF4	-4.02	4.38	5.58E-04	7.53E-03	early B-cell factor 4
akt1	-1.70	8.63	5.63E-04	7.59E-03	v-akt murine thymoma viral oncogene homolog 1
gmpr	-2.64	6.94	5.66E-04	7.62E-03	guanosine monophosphate reductase
EPHA1	-3.70	4.68	5.67E-04	7.62E-03	EPH receptor A1
c2cd4c	3.38	1.19	5.69E-04	7.65E-03	family with sequence similarity 148, member C; hypothetical protein LOC100133882
NUDT8	-3.63	5.52	5.70E-04	7.66E-03	nudix (nucleoside diphosphate linked moiety X)-type motif 8
LOC340037	-9.34	-0.40	5.73E-04	7.69E-03	hypothetical protein LOC340037
rps14	-1.57	10.18	5.75E-04	7.71E-03	ribosomal protein S14
QSER1	2.21	5.33	5.76E-04	7.72E-03	glutamine and serine rich 1
FAHD2B	-2.18	4.38	5.77E-04	7.73E-03	fumarylacetoacetate hydrolase domain containing 2B
ACSL1	-2.40	8.10	5.78E-04	7.73E-03	acyl-CoA synthetase long-chain family member 1
Rhebl1	2.31	0.64	5.79E-04	7.74E-03	Ras homolog enriched in brain like 1
PKDCC	-5.28	6.04	5.79E-04	7.74E-03	protein kinase-like protein SgK493
AFF3	-4.54	5.20	5.81E-04	7.76E-03	AF4/FMR2 family, member 3
UBD	3.30	0.85	5.86E-04	7.82E-03	ubiquitin D
KRT19	-3.38	8.87	5.92E-04	7.88E-03	keratin 19
IQSEC2	-2.56	5.15	5.92E-04	7.88E-03	IQ motif and Sec7 domain 2
LRRC55	3.47	-1.72	5.92E-04	7.88E-03	leucine rich repeat containing 55
SEMA3A	2.10	0.01	6.00E-04	7.97E-03	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A
AKAP7	-3.24	3.24	5.99E-04	7.97E-03	A kinase (PRKA) anchor protein 7
Sdc4	1.53	7.12	6.01E-04	7.98E-03	syndecan 4
Notch2	-2.59	7.69	6.05E-04	8.03E-03	Notch homolog 2 (Drosophila)
cpd	1.54	8.06	6.09E-04	8.07E-03	carboxypeptidase D
Lyl1	3.54	-1.21	6.09E-04	8.07E-03	lymphoblastic leukemia derived sequence 1
cdc42ep1	-4.17	5.11	6.10E-04	8.08E-03	CDC42 effector protein (Rho GTPase binding) 1
rbm38	3.03	6.37	6.12E-04	8.09E-03	RNA binding motif protein 38
EPM2A	2.06	2.65	6.13E-04	8.10E-03	epilepsy, progressive myoclonus type 2A, Lafora disease (laforin)
Dmkn	2.74	3.69	6.17E-04	8.15E-03	dermokine
CDC14B	-4.14	4.49	6.24E-04	8.23E-03	CDC14 cell division cycle 14 homolog B (S. cerevisiae)
LOC100287482	-3.95	3.24	6.28E-04	8.28E-03	similar to hCG2038584
Fam100b	1.62	5.90	6.28E-04	8.28E-03	family with sequence similarity 100, member B
NMRAL1	-1.59	6.61	6.31E-04	8.29E-03	NmrA-like family domain containing 1
NFATC2	2.19	3.85	6.31E-04	8.29E-03	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 2
CLIP3	3.12	2.48	6.30E-04	8.29E-03	CAP-GLY domain containing linker protein 3
C10orf114	3.00	-0.06	6.31E-04	8.29E-03	chromosome 10 open reading frame 114
ATP10A	-6.76	3.58	6.32E-04	8.29E-03	ATPase, class V, type 10A
ENTREZ100750225	-6.33	4.79	6.33E-04	8.30E-03	
tbx2	-5.04	3.64	6.34E-04	8.30E-03	T-box 2
MAST1	2.72	2.76	6.37E-04	8.35E-03	microtubule associated serine/threonine kinase 1
SLC12A2	-2.96	7.27	6.40E-04	8.37E-03	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
LOC285548	4.59	-2.86	6.40E-04	8.37E-03	hypothetical LOC285548
LOC100128338	-2.55	6.26	6.42E-04	8.38E-03	hypothetical LOC100128338
COL18A1	-3.05	6.09	6.42E-04	8.38E-03	collagen, type XVIII, alpha 1
FIS1	-1.60	6.94	6.47E-04	8.43E-03	fission 1 (mitochondrial outer membrane) homolog (S. cerevisiae)
TUB	-4.63	4.70	6.51E-04	8.48E-03	tubby homolog (mouse)
PRKAB1	1.59	4.93	6.53E-04	8.51E-03	protein kinase, AMP-activated, beta 1 non-catalytic subunit
fam198b	-4.88	5.42	6.54E-04	8.51E-03	chromosome 4 open reading frame 18
entpd3	1.76	2.52	6.62E-04	8.61E-03	ectonucleoside triphosphate diphosphohydrolase 3
FOLH1B	-5.92	6.54	6.62E-04	8.61E-03	folate hydrolase 1B

cybrd1	-5.38	3.15	6.64E-04	8.62E-03	cytochrome b reductase 1
Fgfr1	1.53	5.96	6.66E-04	8.64E-03	fibroblast growth factor receptor 1
AGPS	1.82	4.79	6.67E-04	8.65E-03	alkylglycerone phosphate synthase
MGC16703	3.16	-2.06	6.74E-04	8.72E-03	tubulin, alpha pseudogene
LOC219731	3.18	-0.35	6.73E-04	8.72E-03	hypothetical protein LOC219731
Dhrs2	-6.97	7.18	6.75E-04	8.73E-03	dehydrogenase/reductase (SDR family) member 2
TBR1	3.07	-2.11	6.77E-04	8.75E-03	T-box, brain, 1
EFNA1	-1.79	6.61	6.79E-04	8.76E-03	ephrin-A1
Ccdc23	1.87	2.94	6.79E-04	8.76E-03	coiled-coil domain containing 23
Glt1d1	3.85	-2.58	6.81E-04	8.78E-03	glycosyltransferase 1 domain containing 1
tapt1	1.69	4.76	6.84E-04	8.81E-03	transmembrane anterior posterior transformation 1
ITGB4	-4.74	4.86	6.85E-04	8.81E-03	integrin, beta 4
CT45A1	-9.71	5.29	6.85E-04	8.81E-03	cancer/testis antigen family 45, member A1
ENTREZ441520	-9.72	5.19	6.89E-04	8.86E-03	
CELF5	-6.40	2.00	6.92E-04	8.89E-03	bruno-like 5, RNA binding protein (Drosophila)
syt3	-8.59	4.73	6.93E-04	8.90E-03	synaptotagmin III
slc22a5	-2.18	5.05	6.97E-04	8.94E-03	solute carrier family 22 (organic cation/carnitine transporter), member 5
PDCD4	-2.43	7.87	7.09E-04	9.07E-03	programmed cell death 4 (neoplastic transformation inhibitor)
ENTREZ100507050	4.29	0.73	7.08E-04	9.07E-03	
calY	4.68	0.68	7.10E-04	9.08E-03	calcyon neuron-specific vesicular protein
Tff3	3.29	6.78	7.12E-04	9.10E-03	trefoil factor 3 (intestinal)
CEBPA	-4.27	5.60	7.14E-04	9.12E-03	CCAAT/enhancer binding protein (C/EBP), alpha
KCNS3	1.91	4.12	7.15E-04	9.13E-03	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 3
LOC154761	-4.85	2.70	7.17E-04	9.15E-03	hypothetical LOC154761
hibadh	-1.87	6.20	7.24E-04	9.23E-03	3-hydroxyisobutyrate dehydrogenase
SYK	2.12	5.59	7.26E-04	9.24E-03	spleen tyrosine kinase
ASB9	-7.22	5.65	7.35E-04	9.36E-03	ankyrin repeat and SOCS box-containing 9
DNM1	3.83	4.25	7.42E-04	9.43E-03	dynamin 1
NEB	2.01	3.25	7.43E-04	9.44E-03	nebulin
ANO9	2.08	3.93	7.44E-04	9.44E-03	anoctamin 9
slc9a7	-2.49	6.26	7.49E-04	9.51E-03	solute carrier family 9 (sodium/hydrogen exchanger), member 7
POLR3H	-1.90	5.82	7.54E-04	9.56E-03	polymerase (RNA) III (DNA directed) polypeptide H (22.9kD)
MAP6	2.46	3.76	7.56E-04	9.58E-03	microtubule-associated protein 6
Adam15	-1.65	8.46	7.58E-04	9.59E-03	ADAM metallopeptidase domain 15
NTN1	2.75	3.93	7.58E-04	9.59E-03	netrin 1
ENTREZ541465	-9.72	5.18	7.67E-04	9.70E-03	
rasal1	1.77	3.76	7.73E-04	9.76E-03	RAS protein activator like 1 (GAP1 like)
Ltbp1	-3.93	5.31	7.76E-04	9.79E-03	latent transforming growth factor beta binding protein 1
C3orf14	-5.63	4.15	7.78E-04	9.81E-03	chromosome 3 open reading frame 14
Fam167a	3.57	3.38	7.79E-04	9.81E-03	family with sequence similarity 167, member A
LMO2	2.72	1.71	7.78E-04	9.81E-03	LIM domain only 2 (rhombotin-like 1)
dhrs1	-1.87	4.60	7.83E-04	9.84E-03	dehydrogenase/reductase (SDR family) member 1
C1QTNF9	-5.88	2.84	7.83E-04	9.84E-03	C1q and tumor necrosis factor related protein 9
MUC1	1.84	5.94	7.82E-04	9.84E-03	mucin 1, cell surface associated
Bmp8b	3.01	3.65	7.83E-04	9.84E-03	bone morphogenetic protein 8b
UNC13A	2.49	4.50	7.84E-04	9.84E-03	unc-13 homolog A (C. elegans)
KCNQ3	5.56	2.76	7.85E-04	9.84E-03	potassium voltage-gated channel, KQT-like subfamily, member 3
FAT3	3.52	0.70	7.86E-04	9.85E-03	FAT tumor suppressor homolog 3 (Drosophila)
Pacsin3	-2.91	6.08	7.92E-04	9.92E-03	protein kinase C and casein kinase substrate in neurons 3
ENTREZ100507436	-6.52	2.92	7.93E-04	9.92E-03	
etfB	-1.64	7.08	7.94E-04	9.92E-03	electron-transfer-flavoprotein, beta polypeptide
BEND7	1.95	2.61	7.94E-04	9.92E-03	BEN domain containing 7
LOC342918	-9.05	6.19	7.98E-04	9.95E-03	similar to mCG134545
ENTREZ100506795	-10.04	0.32	7.98E-04	9.95E-03	
stk33	2.12	2.23	8.00E-04	9.98E-03	serine/threonine kinase 33
LOC283267	1.81	3.79	8.02E-04	9.98E-03	hypothetical LOC283267

LOC286002	-11.64	1.28	8.03E-04	9.98E-03	hypothetical protein LOC286002
Fahd2a	-1.96	4.79	8.02E-04	9.98E-03	fumarylacetoacetate hydrolase domain containing 2A
LOH3CR2A	2.69	-1.53	8.04E-04	9.99E-03	loss of heterozygosity, 3, chromosomal region 2, gene A
CDC7	1.90	4.56	8.05E-04	9.99E-03	cell division cycle 7 homolog (S. cerevisiae)
Syn2	3.16	3.04	8.06E-04	1.00E-02	synapsin II

Table S3.

Differential Expression (DE) in TMPRSS2-ERG rearrangement (+) vs. (-) LuCaPs (n=20)
FDR < 0.01: n=188 genes

Symbol	logFC	logCPM	PValue	FDR	Gene Name
ERG	7.15	6.13	2.32E-17	3.76E-13	v-ets erythroblastosis virus E26 oncogene homolog (avian)
LOC100190940	9.16	2.46	1.23E-15	9.96E-12	hypothetical LOC100190940
GREM1	7.18	3.75	3.08E-14	1.66E-10	gremlin 1, cysteine knot superfamily, homolog (Xenopus laevis)
CXorf61	10.09	1.20	3.83E-13	1.55E-09	chromosome X open reading frame 61
UBASH3B	8.61	2.08	1.20E-12	3.88E-09	ubiquitin associated and SH3 domain containing, B
tbx5	7.05	1.17	3.21E-12	8.68E-09	T-box 5
capns2	9.89	1.42	4.76E-12	1.10E-08	calpain, small subunit 2
ITGBL1	8.24	1.64	2.37E-11	4.80E-08	integrin, beta-like 1 (with EGF-like repeat domains)
ikzf1	9.38	1.11	4.24E-11	7.65E-08	IKAROS family zinc finger 1 (Ikaros)
GPR120	7.68	1.95	7.69E-11	1.25E-07	G protein-coupled receptor 120
Sprr1a	7.65	-0.24	9.08E-11	1.34E-07	small proline-rich protein 1A
TLR4	8.14	2.81	3.59E-10	4.85E-07	toll-like receptor 4
IVL	7.01	-0.99	4.21E-10	5.25E-07	involucrin
Dpp6	7.82	1.02	4.79E-10	5.55E-07	dipeptidyl-peptidase 6
GTSF1	10.07	2.51	7.54E-10	8.15E-07	gametocyte specific factor 1
ETS1	6.21	1.76	8.81E-10	8.93E-07	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)
SDR16C5	8.47	2.84	1.05E-09	9.99E-07	short chain dehydrogenase/reductase family 16C, member 5
gpX3	5.87	5.68	1.42E-09	1.28E-06	glutathione peroxidase 3 (plasma)
LOC255480	7.33	0.04	2.94E-09	2.51E-06	hypothetical protein LOC255480
RBMY2EP	6.49	-1.45	4.00E-09	2.98E-06	RNA binding motif protein, Y-linked, family 2, member E pseudogene
Gria3	7.52	1.53	3.97E-09	2.98E-06	glutamate receptor, ionotrophic, AMPA 3
CHI3L1	8.30	1.64	4.04E-09	2.98E-06	chitinase 3-like 1 (cartilage glycoprotein-39)
HOXA11AS	-5.45	4.55	4.24E-09	2.99E-06	HOXA11 antisense RNA (non-protein coding)
fzd10	7.99	-0.59	4.93E-09	3.33E-06	frizzled homolog 10 (Drosophila)
Cdh10	7.20	3.31	7.29E-09	4.73E-06	cadherin 10, type 2 (T2-cadherin)
LMCD1	3.61	1.94	8.55E-09	5.33E-06	LIM and cysteine-rich domains 1
fhl1	6.08	4.18	9.21E-09	5.53E-06	four and a half LIM domains 1
HPGD	-5.94	7.81	9.76E-09	5.65E-06	hydroxyprostaglandin dehydrogenase 15-(NAD)
HOXA11	-6.24	4.52	1.26E-08	6.83E-06	homeobox A11
LOC642587	7.30	-0.75	1.26E-08	6.83E-06	NPC-A-5
FLJ31485	6.45	-1.51	1.60E-08	8.37E-06	hypothetical protein LOC440119
Slc14a1	7.44	2.09	1.83E-08	9.27E-06	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
ZNF662	6.17	1.26	2.14E-08	1.05E-05	zinc finger protein 662
SLITRK4	7.77	2.35	2.21E-08	1.05E-05	SLIT and NTRK-like family, member 4
GBP4	4.46	3.57	2.73E-08	1.26E-05	guanylate binding protein 4
LOC283867	8.73	0.00	2.94E-08	1.33E-05	hypothetical LOC283867
CD40	6.97	-0.20	3.80E-08	1.67E-05	CD40 molecule, TNF receptor superfamily member 5
PLAU	4.35	0.71	5.00E-08	2.13E-05	plasminogen activator, urokinase
Gc	-13.60	5.54	5.34E-08	2.22E-05	group-specific component (vitamin D binding protein)
Rgn	6.39	1.82	5.69E-08	2.31E-05	regucalcin (senescence marker protein-30)
IFI16	7.98	2.03	7.05E-08	2.79E-05	interferon, gamma-inducible protein 16
PTX4	4.53	-0.42	1.04E-07	4.03E-05	chromosome 16 open reading frame 38
HNF1B	7.15	1.68	1.12E-07	4.13E-05	HNF1 homeobox B
ENTREZ100507651	6.81	-0.49	1.10E-07	4.13E-05	
ZP2	6.86	0.85	1.16E-07	4.17E-05	zona pellucida glycoprotein 2 (sperm receptor)
SLC26A3	-8.42	5.05	1.22E-07	4.30E-05	solute carrier family 26, member 3
Calml3	8.95	5.77	1.28E-07	4.32E-05	calmodulin-like 3
NAV1	-2.64	5.34	1.25E-07	4.32E-05	neuron navigator 1
PAX3	7.07	0.35	1.42E-07	4.70E-05	paired box 3
UNC5D	7.21	0.21	1.56E-07	5.07E-05	unc-5 homolog D (C. elegans)

CPLX2	5.96	3.20	1.68E-07	5.35E-05	complexin 2
CCKAR	7.21	-1.12	1.73E-07	5.40E-05	cholecystokinin A receptor
WSCD2	6.06	-1.62	2.19E-07	6.71E-05	WSC domain containing 2
Megf11	4.64	1.44	2.66E-07	7.94E-05	multiple EGF-like-domains 11
Astn1	6.97	1.73	2.69E-07	7.94E-05	astrotactin 1
Fam180a	7.46	2.08	2.97E-07	8.59E-05	family with sequence similarity 180, member A
LOC646168	5.78	-1.63	3.31E-07	9.42E-05	hypothetical protein LOC646168
Apod	3.90	7.50	4.37E-07	1.22E-04	apolipoprotein D
BHMT2	6.79	0.47	4.64E-07	1.28E-04	betaine-homocysteine methyltransferase 2
RGS1	7.43	6.09	5.01E-07	1.35E-04	regulator of G-protein signaling 1
msmB	4.25	7.98	5.93E-07	1.58E-04	microseminoprotein, beta-
UGT2A3	7.49	3.59	6.46E-07	1.69E-04	UDP glucuronosyltransferase 2 family, polypeptide A3
TMEM207	7.26	-1.75	6.64E-07	1.70E-04	transmembrane protein 207
TMPRSS11B	7.58	-0.56	6.71E-07	1.70E-04	transmembrane protease, serine 11B
ST8SIA4	5.54	-0.81	7.34E-07	1.83E-04	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
HSPB8	5.39	3.17	8.07E-07	1.98E-04	heat shock 22kDa protein 8
Slitrk3	6.75	3.11	9.67E-07	2.34E-04	SLIT and NTRK-like family, member 3
CRTAC1	5.85	1.99	1.01E-06	2.40E-04	cartilage acidic protein 1
Fabp7	-12.88	4.85	1.05E-06	2.46E-04	fatty acid binding protein 7, brain
NALCN	6.23	-0.06	1.19E-06	2.76E-04	sodium leak channel, non-selective
KIAA0040	2.00	5.37	1.29E-06	2.95E-04	KIAA0040
LOC116437	6.14	-1.33	1.55E-06	3.49E-04	hypothetical LOC116437
Zscan5b	4.15	-0.32	1.79E-06	3.98E-04	zinc finger and SCAN domain containing 5B
TXNDC3	5.94	-0.81	2.09E-06	4.58E-04	thioredoxin domain containing 3 (spermatozoa)
CCDC60	5.49	0.51	2.17E-06	4.67E-04	coiled-coil domain containing 60
bdh2	-3.57	3.70	2.19E-06	4.67E-04	3-hydroxybutyrate dehydrogenase, type 2
Slc1a7	5.25	-1.16	2.25E-06	4.74E-04	solute carrier family 1 (glutamate transporter), member 7
Wdr72	5.58	2.46	2.29E-06	4.75E-04	WD repeat domain 72
hcp5	5.19	2.94	2.37E-06	4.86E-04	HLA complex P5
ZSCAN1	4.84	-0.67	2.42E-06	4.87E-04	zinc finger and SCAN domain containing 1
Tmem178	3.45	5.70	2.43E-06	4.87E-04	transmembrane protein 178
ENTREZ100316868	-5.18	3.02	2.57E-06	5.08E-04	
SERPINA11	5.96	0.46	2.92E-06	5.59E-04	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 11
Atp2b3	5.79	0.57	2.91E-06	5.59E-04	ATPase, Ca++ transporting, plasma membrane 3
PRKCDBP	5.23	-1.33	2.94E-06	5.59E-04	protein kinase C, delta binding protein
il2rg	3.83	2.00	2.96E-06	5.59E-04	interleukin 2 receptor, gamma (severe combined immunodeficiency)
S100A9	5.50	1.05	3.57E-06	6.66E-04	S100 calcium binding protein A9
LFNG	2.83	6.38	3.66E-06	6.74E-04	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
GPRC5D	3.68	3.05	4.25E-06	7.74E-04	G protein-coupled receptor, family C, group 5, member D
Atxn8os	5.75	-1.66	4.65E-06	8.38E-04	ATXN8 opposite strand (non-protein coding)
HLA-H	3.43	5.40	4.90E-06	8.58E-04	major histocompatibility complex, class I, H (pseudogene)
LOC400655	5.79	-0.10	4.96E-06	8.58E-04	hypothetical gene supported by BC013370; BC034583
CPNE5	5.25	2.48	4.98E-06	8.58E-04	copine V
FOXN1	5.09	2.26	4.93E-06	8.58E-04	forkhead box N1
BEX4	-3.37	5.05	5.42E-06	9.17E-04	brain expressed, X-linked 4
SLA	4.61	0.38	5.43E-06	9.17E-04	Src-like-adaptor
LOC389493	4.75	-0.77	5.51E-06	9.21E-04	hypothetical protein LOC389493
WNT11	5.13	5.08	5.60E-06	9.27E-04	wingless-type MMTV integration site family, member 11
IGF2BP1	5.26	3.50	5.72E-06	9.37E-04	insulin-like growth factor 2 mRNA binding protein 1
CLEC2L	5.32	-0.29	5.82E-06	9.44E-04	C-type lectin domain family 2, member L
Rcsd1	5.91	0.49	6.81E-06	1.08E-03	RCSD domain containing 1
HCG26	4.78	-0.57	6.81E-06	1.08E-03	HLA complex group 26
ENTREZ3106	2.71	7.56	7.06E-06	1.11E-03	
VSTM2A	6.34	-1.45	7.33E-06	1.14E-03	V-set and transmembrane domain containing 2A
KIAA0087	4.26	0.64	7.57E-06	1.17E-03	KIAA0087

LOC339535	5.71	-0.20	7.89E-06	1.21E-03	hypothetical LOC339535
LOC283481	5.78	-0.59	8.38E-06	1.27E-03	hypothetical protein LOC283481
CDH17	-8.39	4.81	9.00E-06	1.35E-03	cadherin 17, LI cadherin (liver-intestine)
Shroom4	4.83	0.26	9.28E-06	1.38E-03	shroom family member 4
TNS4	4.51	3.25	9.43E-06	1.38E-03	tensin 4
ANKRD33	5.19	-0.58	9.46E-06	1.38E-03	ankyrin repeat domain 33
GPR141	6.28	-1.82	9.89E-06	1.43E-03	G protein-coupled receptor 141
TMEM71	6.02	0.75	1.14E-05	1.62E-03	transmembrane protein 71
RGS22	3.97	-0.93	1.14E-05	1.62E-03	regulator of G-protein signaling 22
DEFB1	6.42	2.71	1.15E-05	1.62E-03	defensin, beta 1
Hist1h1d	3.59	-0.88	1.17E-05	1.63E-03	histone cluster 1, H1d
Siglec15	5.01	-0.59	1.19E-05	1.65E-03	sialic acid binding Ig-like lectin 15
Dmd	4.03	3.39	1.26E-05	1.74E-03	dystrophin
CCDC140	5.40	-2.07	1.30E-05	1.78E-03	coiled-coil domain containing 140
COL8A2	4.55	0.79	1.34E-05	1.81E-03	collagen, type VIII, alpha 2
HLA-DRB6	4.78	-0.60	1.36E-05	1.82E-03	major histocompatibility complex, class II, DR beta 6 (pseudogene)
Pcp4l1	4.70	1.25	1.40E-05	1.86E-03	Purkinje cell protein 4 like 1
bchE	5.30	5.30	1.41E-05	1.86E-03	butyrylcholinesterase
CLEC7A	5.19	5.03	1.43E-05	1.86E-03	C-type lectin domain family 7, member A
SNAR-F	7.43	-0.95	1.50E-05	1.95E-03	small ILF3/NF90-associated RNA F
UNC80	-7.01	2.25	1.61E-05	2.07E-03	chromosome 2 open reading frame 21
THBD	4.46	-1.68	1.64E-05	2.10E-03	thrombomodulin
Xylt1	3.61	2.95	1.68E-05	2.13E-03	xylosyltransferase I
PLA2G4D	3.41	2.10	1.90E-05	2.39E-03	phospholipase A2, group IVD (cytosolic)
C2CD4B	4.33	-0.22	1.91E-05	2.39E-03	family with sequence similarity 148, member B
apol3	2.72	4.27	2.25E-05	2.72E-03	apolipoprotein L, 3
GSDMA	4.92	1.58	2.20E-05	2.72E-03	gasdermin A
ENTREZ114899	-7.29	7.16	2.25E-05	2.72E-03	
HOXA9	-6.94	1.20	2.24E-05	2.72E-03	homeobox A9
ENTREZ388514	4.29	-0.01	2.33E-05	2.80E-03	
CD300A	4.96	0.33	2.54E-05	3.03E-03	CD300a molecule
ASB9	-5.12	5.94	2.57E-05	3.04E-03	ankyrin repeat and SOCS box-containing 9
srrm4	3.86	-1.34	3.10E-05	3.65E-03	KIAA1853
HLA-L	3.21	0.56	3.22E-05	3.75E-03	major histocompatibility complex, class I, L (pseudogene)
abcc4	-4.53	8.16	3.48E-05	4.00E-03	ATP-binding cassette, sub-family C (CFTR/MRP), member 4
PADI3	3.85	-2.19	3.48E-05	4.00E-03	peptidyl arginine deiminase, type III
GDA	4.76	2.15	3.72E-05	4.25E-03	guanine deaminase
Dok6	-8.29	2.27	3.93E-05	4.46E-03	docking protein 6
SNCG	-4.19	5.15	4.11E-05	4.63E-03	synuclein, gamma (breast cancer-specific protein 1)
PLCE1	2.50	1.80	4.16E-05	4.66E-03	phospholipase C, epsilon 1
NCCRP1	4.00	0.73	4.23E-05	4.69E-03	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)
IL32	2.64	2.53	4.75E-05	5.24E-03	interleukin 32
FAM9B	5.13	-1.52	4.81E-05	5.27E-03	family with sequence similarity 9, member B
Clstn2	4.24	4.76	4.93E-05	5.37E-03	calsyntenin 2
TMEM204	3.88	0.27	4.97E-05	5.38E-03	transmembrane protein 204
HMX1	6.35	-0.34	5.12E-05	5.50E-03	H6 family homeobox 1
TGM3	3.04	5.54	5.34E-05	5.70E-03	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase)
SERPINA4	-8.65	4.70	5.40E-05	5.73E-03	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 4
grem2	5.61	2.27	5.65E-05	5.91E-03	gremlin 2, cysteine knot superfamily, homolog (Xenopus laevis)
TBX10	-5.85	2.71	5.64E-05	5.91E-03	T-box 10
C2orf43	-7.32	2.32	5.74E-05	5.96E-03	chromosome 2 open reading frame 43
MLLT11	2.95	3.59	6.13E-05	6.33E-03	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11
sall1	5.20	-1.45	6.39E-05	6.56E-03	sal-like 1 (Drosophila)

Inpp5d	4.30	0.99	6.56E-05	6.69E-03	inositol polyphosphate-5-phosphatase, 145kDa
IFT140	1.79	5.81	6.72E-05	6.77E-03	intraflagellar transport 140 homolog (Chlamydomonas)
CYSLTR1	3.88	-0.13	6.71E-05	6.77E-03	cysteinyl leukotriene receptor 1
MYO1B	-2.89	6.00	6.94E-05	6.82E-03	myosin IB
PTGS2	3.63	4.31	6.93E-05	6.82E-03	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)
XDH	2.65	3.51	6.94E-05	6.82E-03	xanthine dehydrogenase
C21orf34	-5.30	2.69	6.93E-05	6.82E-03	chromosome 21 open reading frame 34
PYGL	-2.81	5.61	7.04E-05	6.88E-03	phosphorylase, glycogen, liver
PTK6	2.12	5.60	7.37E-05	7.16E-03	PTK6 protein tyrosine kinase 6
Acadl	-4.11	4.48	7.44E-05	7.18E-03	acyl-Coenzyme A dehydrogenase, long chain
PON1	-7.30	2.63	7.60E-05	7.25E-03	paraoxonase 1
Syn2	5.04	1.62	7.58E-05	7.25E-03	synapsin II
RASD2	2.01	3.50	7.67E-05	7.27E-03	RASD family, member 2
S100A14	-6.74	4.50	7.91E-05	7.45E-03	S100 calcium binding protein A14
NLRC5	2.81	3.02	7.96E-05	7.46E-03	NLR family, CARD domain containing 5
FUT6	4.40	3.37	9.02E-05	8.41E-03	fucosyltransferase 6 (alpha (1,3) fucosyltransferase)
SORBS2	1.80	5.79	9.19E-05	8.46E-03	sorbin and SH3 domain containing 2
ENTREZ388468	-7.19	0.81	9.15E-05	8.46E-03	
PAPSS2	3.46	3.32	9.29E-05	8.51E-03	3'-phosphoadenosine 5'-phosphosulfate synthase 2
igfbp7	4.30	-0.02	9.52E-05	8.67E-03	insulin-like growth factor binding protein 7
SPAG4	2.89	4.60	9.80E-05	8.88E-03	sperm associated antigen 4
NUDT8	-2.34	5.50	9.86E-05	8.88E-03	nudix (nucleoside diphosphate linked moiety X)-type motif 8
tprg1	4.72	2.06	1.03E-04	9.20E-03	tumor protein p63 regulated 1
Shh	5.30	3.18	1.04E-04	9.26E-03	sonic hedgehog homolog (Drosophila)
TOX2	2.95	3.27	1.05E-04	9.33E-03	TOX high mobility group box family member 2
pi15	-5.52	5.42	1.08E-04	9.48E-03	peptidase inhibitor 15
TNFRSF1B	3.94	1.40	1.11E-04	9.73E-03	tumor necrosis factor receptor superfamily, member 1B
Ccnb3	3.06	2.69	1.12E-04	9.78E-03	cyclin B3
Mboat2	-2.38	7.22	1.14E-04	9.81E-03	membrane bound O-acyltransferase domain containing 2
LOC121296	4.48	-1.17	1.14E-04	9.81E-03	transmembrane protein 132B; hypothetical LOC121296