

**In vivo functional screens reveal KEAP1 loss as a driver of chemoresistance in
small cell lung cancer**

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Abstract

In vivo functional screens reveal KEAP1 loss as a driver of chemoresistance in small cell lung cancer

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Among the most chemosensitive of all cancer types, small cell lung cancer (SCLC) exhibits dismal clinical outcomes owing to rapid transition to chemoresistance. Elucidating the genetic underpinnings of chemoresistance has been challenging owing to limitations with cellular models. Patient derived xenograft (PDX) models mimic patient responses to chemotherapy, raising potential to use such models for high throughput identification of chemoresistance driver genes. We apply cDNA overexpression, CRISPR knockout screens, and CRISPR activation screens to chemosensitive PDX models of SCLC. cDNA overexpression screens highlight *MYC*, *MYCN* and *MYCL* overexpression as promoting survival in the context of chemotherapy treatment. CRISPR deletion screens identify *KEAP1* loss as driving chemoresistance. Deletion of

KEAP1 switched a chemosensitive PDX model of SCLC to become chemoresistant and resulted in sensitivity to inhibition of glutamine metabolism. Data from the IMpower133 clinical trial revealed ~6% of extensive stage SCLC patients exhibit *KEAP1* genetic alterations, with activation of a KEAP1/NRF2 transcriptional signature associated with reduced SCLC patient survival in the chemotherapy arm. While roles for the KEAP1/NRF2 pathway have been previously overlooked in SCLC, our genetic screens revealed KEAP1 loss as a driver of chemoresistance and we demonstrate functional importance for this pathway in human SCLC. Finally, a CRISPR activation screen revealed multiple new candidate drivers of resistance to chemotherapy in SCLC.

A version of chapters 1, 2, and 4 is currently in preparation as a journal article entitled:
In vivo functional screens reveal KEAP1 loss as a driver of chemoresistance in small
cell lung cancer

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Chapter 1: Introduction

Overview of small cell lung cancer

Lung cancer is one of the most commonly diagnosed forms of cancer and is responsible for close to 20% of cancer deaths in the US and worldwide.¹ It is broadly classified into non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC). NSCLC accounts for approximately 85% of lung cancer cases and includes lung adenocarcinoma (most common), squamous cell carcinoma, and large cell carcinoma. SCLC is a highly aggressive and lethal malignancy that accounts for approximately 15% of the lung cancer cases that occur each year and an estimated 250,000 deaths.² Characterized by rapid growth and early metastasis, SCLC has the worst prognosis among lung cancer subtypes with a five-year survival rate of less than 6%.³ SCLC presents significant challenges in clinical management and treatment. Despite considerable advancements in understanding and treating other types of lung cancer, SCLC remains a formidable adversary due to its unique biological and molecular characteristics.

Epidemiology and Clinical Presentation

SCLC is almost exclusively associated with a history of smoking, with over 95% of cases occurring in individuals who have used tobacco products.⁴ Typical symptoms include cough, dyspnea, chest pain, and weight loss. These symptoms overlap with other more common conditions, contributing to a difficulty in diagnosing SCLC early.⁵ The staging of SCLC is traditionally divided into limited-stage (LS-SCLC) and extensive-

stage (ES-SCLC), with the latter being associated with a poorer prognosis. The differentiating factor between these stages is how widespread the cancer is; LS-SCLC is present in a defined area whereas ES-SCLC has spread throughout multiple areas. Most patients (60-70%) are diagnosed with ES-SCLC and exhibit metastatic disease at the time of diagnosis.⁶ Common metastatic sites include liver, bones, brain, and adrenal glands.⁷

Molecular Landscape of SCLC

The molecular landscape of SCLC is complex and distinct from non-small cell lung cancer (NSCLC). Genomic studies have revealed a high mutation burden in SCLC, driven largely by tobacco-induced DNA damage.^{8,9} There is near-universal inactivation of the tumor suppressor genes *RB1* (encoding the retinoblastoma protein) and *TP53* (encoding p53), each mutated in roughly 90% of SCLC cases.¹⁰⁻¹² Inactivation of these two genes disrupts cell cycle and apoptosis regulation, contributing to unchecked cellular proliferation and tumorigenesis. SCLC is known to have a high mitotic index.¹³

A majority of SCLC tumors have neuroendocrine features including expression of markers such as chromogranin A, synaptophysin, and insulinoma-associated 1 (INSM1).³ Past work indicates that pulmonary neuroendocrine cells (PNECs) are a possible cell of origin for SCLC.^{14,15} Neuroendocrine cells are cells that bridge the nervous and endocrine systems via signaling. They respond to environmental stimuli and neuronal signals, and respond by secreting hormones and sometimes

neurotransmitters.¹⁶ PNECs are a rare cell type that constitute approximately 0.01% of the total lung cell population.¹⁶ These cells are involved in oxygen sensing including hypoxia response, nicotine response via expression of nicotinic acetylcholine receptors (nAChRs), response to other environmental stimuli, development of the fetal lungs, and regeneration of the airway epithelial cell population following injury.¹⁶⁻¹⁸ Activation of nAChRs has been linked to increased proliferation and hyperplasia.^{16,19} PNECs release neuropeptides and neurotransmitters, and they have secretory vesicles that can contain the neurotransmitter serotonin as well as hormones such as gastrin-releasing peptide, calcitonin, and endothelin.^{16-18,20}

There is ongoing work in the field to define the subtypes of SCLC, with one common categorization based on transcription factor expression: ASCL1, NEUROD1, YAP1, and POU2F3.³ ASCL1, a master regulator of neuronal differentiation, is expressed in approximately 75% of SCLC and has been shown to be required for tumor initiation in mouse models of SCLC.^{2,21,22} NEUROD1 is expressed in 15% of SCLC.² In addition to regulation of neuronal function, ASCL1 and NEUROD1 are involved in transcriptional regulation of oncogenes including *MYCL1* for ASCL1 and *MYC* for NEUROD1.²¹ MYC family members including *MYC*, *MYCN*, and *MYCL1* are commonly amplified in SCLC, contributing to aggressive tumor growth.^{10,12,23} *MYCL1* is commonly upregulated in ASCL1-expressing SCLC whereas *MYC* is commonly upregulated in NEUROD1-expressing SCLC. Additionally, Notch inactivation is present in most SCLC cases. Commonly observed drivers of this are inactivating mutations present in ~25% of cases and expression of Notch inhibitors such as *DLL3*, which is regulated by ASCL1.¹⁰

Inactivating mutations of tumor suppressor gene *PTEN*²⁴ and amplification of the oncogene *SOX2*³ are also frequent.

Additional common alterations include alterations in genes that encode proteins involved in epigenetic regulation as well as epigenetic silencing and overexpression. Histone modifier *CREBBP* is mutated in roughly 9% of SCLC and previous work from our lab has indicated it acts as a tumor suppressor gene in SCLC.^{10-12,25,26} Mutations in *CREBBP* are mutually exclusive with mutations in another histone modifier *EP300* that also occur in a subset of SCLC.²⁷ Another commonly mutated epigenetic regulator (in 8% of tumors) is *KMT2D*, which encodes lysine methyltransferase 2D.²⁷ There is evidence of epigenetic silencing of *REST*, *SLFN11*, and *NEUROD1* in some cases of SCLC.² Transcriptional regulator enhancer of zeste homologue 2 (*EZH2*)²⁸ and lysine demethylase 1A (*LSD1*)²⁹ are often overexpressed in SCLC.

Current therapeutic approaches and the challenge of chemoresistance

The primary treatment modalities for SCLC include chemotherapy, radiation therapy, and, more recently, immunotherapy. The standard of care is platinum doublet chemotherapy consisting of cisplatin or carboplatin administered in combination with etoposide and immune checkpoint blockade (ICB).³⁰ Approximately two-thirds of patients exhibit a strong response to initial chemotherapy, but relapse typically occurs within months. The addition of ICB to the standard of care in 2019 only modestly improved treatment responses.^{31,32} More recently in 2024, the first bispecific T-cell engager (BiTE) therapeutic, tarlatamab, got approved for ES-SCLC that has relapsed

following attempted treatment.³³ There is still ample need for new therapeutic strategies to overcome chemoresistance and improve outcomes.

Patient derived xenograft models of SCLC

One challenge in therapeutics development for SCLC is our poor understanding of the genes and pathways that confer chemoresistance in SCLC, in part owing to limitations with the model systems available. SCLC is generally not surgically resected owing in part to the disease generally already being metastatic at the time of diagnosis.³⁴ Study of SCLC cell lines has provided few major insights into mechanisms of chemoresistance, in part because SCLC cell lines generally fail to recapitulate patient tumor response to treatment. Indeed, comparison of cell lines derived from chemo-naïve SCLC patients vs. chemotherapy treated patients showed no difference in sensitivity to a panel of chemotherapeutic agents.³⁵ One study did find evidence of frequent WNT pathway alterations in SCLC and demonstrated that activating WNT signaling in cell lines induced chemoresistance.³⁶ Genetically engineered mouse models of SCLC harboring *Rb/p53* mutation exhibit cytostatic responses rather than the striking chemosensitivity that is observed in most SCLC patients upon initial treatment.³⁷

In contrast, patient derived xenograft (PDX) models of SCLC do recapitulate the chemotherapy response of the patients from which they were derived.^{34,38-42} Moreover, PDX models better maintain gene expression fidelity from the original patient compared

to cell lines.^{34,38,39,41,42} Together, these factors indicate that PDX models may be the ideal system for studying chemotherapy response in SCLC.

By treating chemosensitive PDX models with cycles of chemotherapy and then comparing parental models to more chemoresistant variants, the Rudin lab demonstrated that epigenetic suppression of *SLFN11* expression promotes SCLC chemoresistance.⁴³ Recent work from our lab used in vivo lentiviral perturbation studies to demonstrate that *MYCN* or *MYCL* overexpression switches chemosensitive PDX models of SCLC to become resistant to cisplatin-etoposide,³⁷ a finding corroborated by recent analyses of patient samples and serially derived PDX models.³⁸

CRISPR screens in cancer

CRISPR screening has emerged as a transformative tool in cancer research. The CRISPR-Cas9 system enables targeted modification of the genome⁴⁴⁻⁴⁷, allowing researchers to systematically interrogate the function of individual genes in cancer biology. Leveraging this technology allows for high-throughput genetic screens to identify genes essential for cancer cell survival, proliferation, and metastasis, as well as those involved in drug resistance.⁴⁸⁻⁵⁰ In the context of cancer, CRISPR-Cas9 screening involves creating a library of single-guide RNAs (sgRNAs) designed to target and induce loss-of-function mutations in specific genes across the genome.^{51,52} These libraries are introduced into cancer cells, and subsequent phenotypic changes are analyzed to determine the impact of gene disruptions.⁵³ Furthermore, CRISPR-Cas9 screening has advanced our understanding of synthetic lethality in cancer. Synthetic

lethal mutations are mutations in two genes that cause cell death when present in combination but not independently. By conducting combinatorial screens, researchers can identify gene pairs that, when simultaneously disrupted, result in cell death, thereby highlighting potential targets for combination therapies.⁵⁴

CRISPR activation to overexpress genes of interest

First developed in 2013, CRISPR activation (CRISPRa) leverages a nuclease-dead version of Cas9 (dCas9) fused to one or more transcription activation domains to drive increased gene expression^{55,56}. A sgRNA directs the dCas9-transcriptional activator complex to the promoter region of a gene of interest to increase transcription of that gene without making any cuts to the DNA. One of the earliest iterations of CRISPRa involved a fusion of dCas9 to the omega subunit of RNA polymerase, which resulted in a 2.8-fold increase in gene expression at best.⁵⁶ The true first-generation CRISPRa system, published around the same time as the dCas9-RNA polymerase omega system, consists of dCas9 fused to VP64.⁵⁷ The VP64 transcriptional activator consists of four copies of VP16, a transcription factor found in herpes simplex virus that can potently induce transcription.⁵⁸

The invention of second-generation CRISPRa systems has paved the way for more efficient activation than was possible with the first-generation dCas9-VP64 approach.^{59,60} One commonly used CRISPRa system consists of dCas9 fused to three activation domains: VP64, p65, and Rta (dCas9-VPR), each of which has a distinct

mechanism of promoting transcription.^{59,60} Chavez *et al* were able to achieve overexpression up to multiple thousand fold (gauged by relative RNA expression) with the dCas9-VPR system⁵⁹.

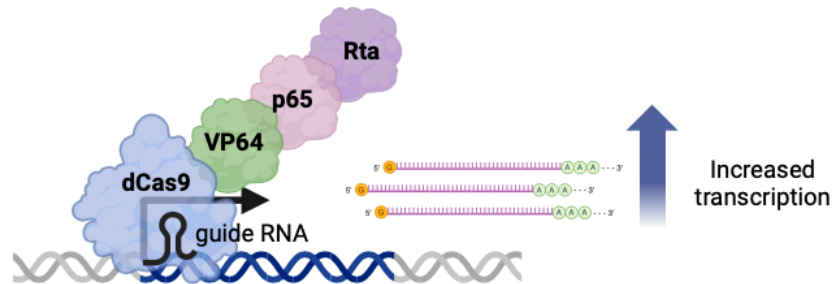


Figure 1.1: Schematic depicting how dCas9-VPR drives increased gene expression.

CRISPRa technology presents some advantages for performing screens relative to traditional ORF overexpression screens. First, making a new library for CRISPRa is cheaper and more practical than generating an ORF library. Second, CRISPRa may better capture the diversity of splice variants produced by a gene. Finally, CRISPRa allows for overexpression of a gene from its native promoter.⁵⁵ There are also fewer issues with maintaining even representation in the library with a CRISPRa library compared to an ORF library as all of the gRNAs are roughly the same size (around 20 nucleotides). Only a small number of CRISPRa screens designed to investigate chemoresistance have been published to date, few of which are *in vivo*, and none of which have been done in SCLC.^{61,62}

The present study

Continued research into the genetic alterations driving SCLC is essential for the development of more effective therapies. By deepening our understanding of the

molecular landscape of SCLC, we can work to improve therapeutic approaches and ultimately improve patient outcomes. Here, we sought to leverage the fidelity of PDX models of SCLC to test, in a multiplexed manner, hundreds to thousands of perturbations for ability to make chemosensitive PDX models chemoresistant. cDNA overexpression and CRISPR knockout functional screens confirmed known pathways and revealed novel pathways underlying SCLC chemoresistance, including roles for *KEAP1*. To evaluate clinical importance, we queried genomic data from patients in the chemotherapy arm of the IMpower133 clinical trial³¹ revealing that the *KEAP1/NFE2L2* pathway is genetically altered in SCLC and pathway activation correlates with impaired response to chemotherapy in SCLC patients.

Chapter 2: Results

In vivo cDNA screening in a chemosensitive SCLC PDX model identifies MYC family members as drivers of tumor cell growth and chemoresistance

Our prior work using single gene lentiviral perturbation of chemosensitive SCLC PDX models in vivo demonstrated that *MYCN* or *MYCL* overexpression could switch these models to become chemoresistant.³⁷ To determine whether we could query many genes in a multiplexed manner for ability to promote in vivo tumor growth under chemotherapeutic pressure, we modified a barcoded ORF library⁶³ to add *MYCN* and *MYCL* and conducted an in vivo screen (Figure 2.1A). Using a chemosensitive SCLC PDX model (SC151) that was previously only propagated in vivo, we briefly explanted tumors ex vivo for lentiviral transduction, minimizing the time the cells were in culture (< 18 hours) before implanting 1 million cells/flank into a cohort of immunocompromised NOD scid gamma (NSG) mice. To establish a population zero (P0) reference point, we maintained a subset of the cells in culture for 72 hours following lentivirus exposure prior to collection. In the P0 population, 353 cDNAs passed library representation filters. Once flank tumors reached 300 – 350 mm³, the mice were treated with either saline or 2-3 weekly cycles of cisplatin-etoposide (cis-eto) chemotherapy, which led to ablation of tumors followed by regrowth, with tumor collection an average of 58 days following the end of cis-eto treatment. Tumors from the saline treated group (n=13) and those that returned following cis-eto chemotherapy (n=45) had genomic DNA extracted and sequencing libraries prepared.

We performed edgeR⁶⁴ analysis to identify cDNAs enriched (relative to the P0 reference point) in either the saline treated or cis-eto treated groups. Plotting the average Log₂ fold change (Log₂FC) vs. -Log₁₀ false discovery rate (-Log₁₀FDR) for each ORF in the saline and cis-eto treatment groups reveals *MYC*, *MYCN*, and *MYCL* as top hits in both treatment arms (Figure 2.1B, also see Table 1, which shows analysis and results for the cDNA screen). Waterfall plots depicting cDNA representation in individual tumors show strong and consistent enrichment of *MYC*, *MYCN*, and *MYCL* cDNAs across individual tumors in both treatment groups (Figure 2.1C). Other hits identified were also enriched in both treatment arms, including *CCND1*, encoding CYCLIN D1 and *TMEM241* encoding Transmembrane Protein 241. As our previous work demonstrated that lentiviral single gene overexpression of *MYCN* or *MYCL* in chemosensitive PDX models results in a switch to chemoresistance,³⁷ a finding supported by recent independent studies,³⁸ these data now show that in vivo multiplexed positive selection screens in this system reflect a powerful approach to identify drivers of chemoresistance in a multiplexed manner.

Figure 2.1

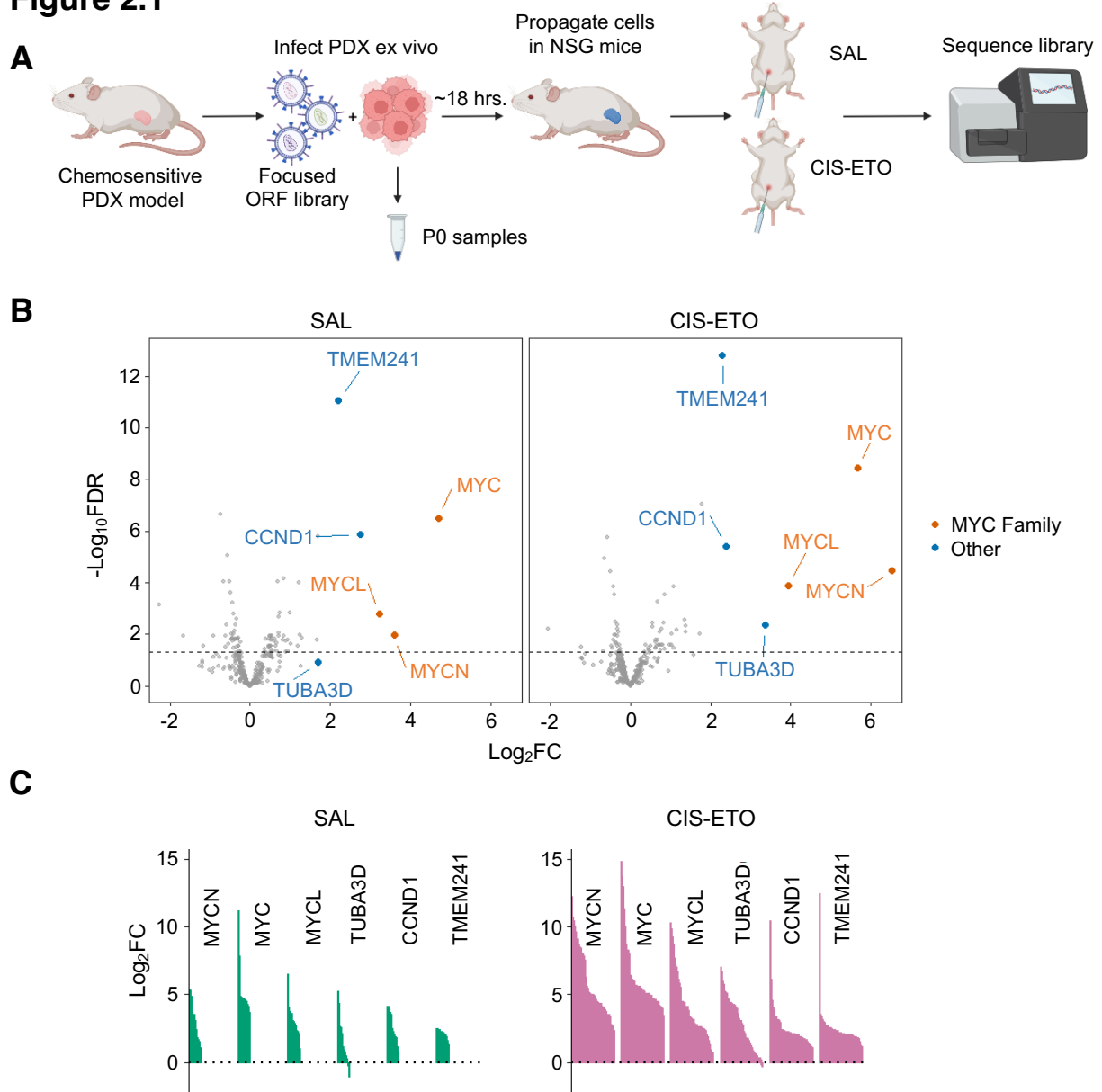


Figure 2.1: In vivo cDNA screening in a chemosensitive SCLC PDX model identifies drivers of chemoresistance

(a) Schematic of in vivo cDNA screen design in the SCLC PDX model SC151.

(b) cDNA-level volcano plots of edgeR analysis results showing average Log₂ fold change (Log₂FC) enrichment vs P0 and -Log₁₀FDR for each cDNA across tumors for the saline (n=13) and cis-eto (n=45) treatment arms. Each dot depicts one cDNA. MYC

family members are displayed in orange, while additional top hits are displayed in blue ($\text{Log}_2\text{FC} > 2$ and $\text{FDR} < 0.05$ in the cis-eto vs. P0 comparison).

(c) Waterfall plots depicting top 6 hits ($\text{Log}_2\text{FC} > 2$ and $\text{FDR} < 0.05$ in the cis-eto vs P0 comparison) at the individual tumor level for both the saline and cis-eto vs. P0. Each vertical bar depicts one tumor.

In vivo CRISPR-Cas9 deletion screens identify drivers of chemoresistance in SCLC PDX models

SCLC is dominated by inactivation of tumor suppressor genes rather than activation of oncogenes.^{10,12,27} With demonstration that in vivo cDNA overexpression screens in SCLC PDX models are feasible, we next performed a CRISPR/Cas9 deletion screen. Moving to the CRISPR approach allowed us to rapidly generate libraries targeting genes relevant to SCLC. We generated a focused library, targeting 400 high priority genes with 6 gRNAs/gene and included 120 non-targeting gRNAs as controls for a total of 2520 gRNAs (see Table 2, which shows the focused library composition). We mined genomic data from SCLC to identify genes in regions of deletion or that exhibited truncating mutations.^{10,12,36} The focused library also targeted genes such as SLFN11 and WNT pathway members, previously implicated in SCLC chemoresistance,^{36,43} as well as additional genes of interest that emerged from a pilot genome scale screen. To generate the SCLC focused library, sgRNA sequences from the Brunello Human CRISPR Knockout Pooled Library were cloned into the lentiCRISPRv2 backbone.⁶⁵

We propagated the chemosensitive ASCL1-expressing PDX model FHSC14⁶⁶ in vivo, explanted tumors into cell culture for addition of lentivirus containing the focused library and ~18 hours later, injected transduced cells subcutaneously into the flanks of NSG mice at 1×10^6 cells/flank (Figure 2.2A). We also maintained a subset of cells ex vivo for 72 hours before genomic DNA isolation to establish a P0 reference population of initial gRNA representation. We screened the FHSC14 model with this focused gRNA library just as described for the cDNA screen above and collected 27 saline and 48 cis-eto treated return tumors for sequencing, with the kinetics of tumor response to cis-eto and later regrowth off therapy shown in Figure 2.2B.

A challenge with in vivo screens is bottlenecking results in only a subset of implanted cells contributing to the tumor, substantially reducing library representation.^{67,68} We developed a strategy to randomly assign independent tumors into pooled sets and computationally pool read counts, normalizing per tumor read depth to increase library representation in the pooled tumor sets. While individual tumors in the saline group had a median of <50% of all gRNAs present, library representation was improved by computational pooling, with 6 tumors/pool increasing library representation to >95% (Figure 2.2C). Applying the MAGeCK algorithm⁶⁹ to the computationally pooled tumors (6 tumors/pool), in the saline condition (with n=4 pools analyzed) there were 3 genes for which at least 3 of their corresponding sgRNAs were enriched relative to P0 (Figure 2.2D and 2.2E). These genes included *MBOAT4*, *OTOP3*, as well as *CREBBP*, which as mentioned in Chapter 1 is mutated in ~9% of SCLC^{10-12,26} and acts as a tumor suppressor in genetically engineered mouse models of SCLC²⁵. *CREBBP* emerging as

a top hit in the saline group provides confidence that the screen is working as expected given its known role as a tumor suppressor gene.

In the cis-eto condition (with n=8 pools analyzed), 6 genes had at least 3 of their corresponding sgRNAs enriched relative to P0 (Figure 2.2D and E). 5 out of 6 of the most highly enriched sgRNA-targeted genes in our screen were members of the SAGA (Spt-Ada-Gcn5 acetyltransferase) complex, including *USP22*, *TAF5L*, *TADA2B*, *TAF6L*, and *TADA1*. Also included amongst these 6 genes with highly enriched sgRNAs was *KEAP1*, a master regulator of the NRF2 oxidative stress response pathway (also see Table 3, which shows *KEAP1* specific results of the knockout screen). Previous in vivo work demonstrated that *KEAP1* deletion can drive NSCLC tumorigenesis and therapeutic resistance by stabilizing NRF2, increasing proliferation, and helping to resist oxidative stress,^{70,71} but there has been limited study of the KEAP1/NFR2 pathway in SCLC, with thus far little functional evidence for pathway importance in this cancer type.

Figure 2.2

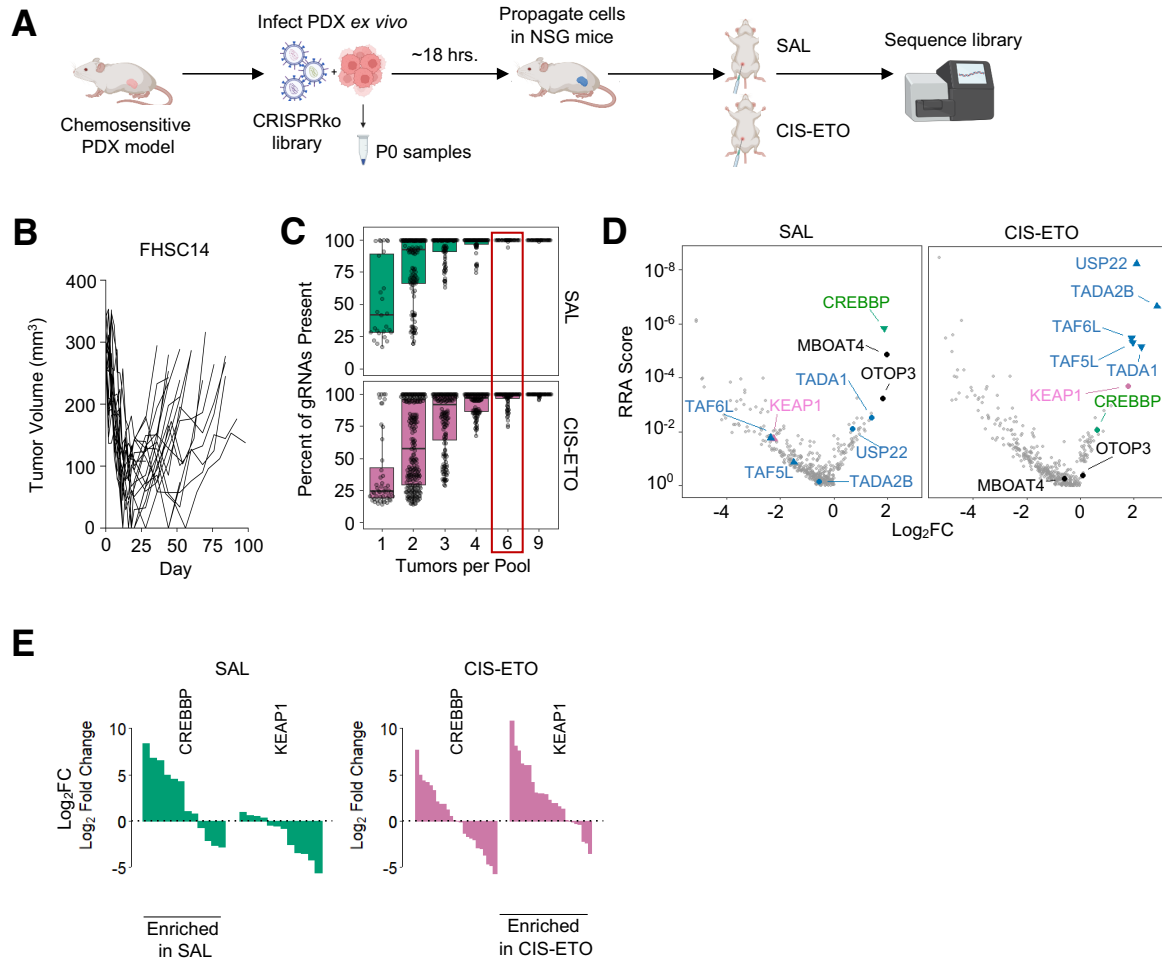


Figure 2.2: In vivo CRISPR-Cas9 deletion screens identify drivers of chemoresistance in SCLC PDX models (screen done by Scott Best)

(a) Schematic of in vivo focused gRNA screen design in SCLC PDX models.

(b) FHSC14 tumor volume kinetics over the course of the in vivo focused gRNA screen.

Mice were treated for 2-3 weekly cycles of cis-eto. Tumor volume over time for the largest of two tumors implanted in each mouse illustrates kinetics of tumor regression and return.

(c) Computational pooling of FHSC14 tumors and percentage of focused library sgRNAs present per pool. Each point depicts one pool of tumors generated by randomly selecting the number of tumors specified on the x-axis for pooling. For each number of tumors per pool, tumors were randomly pooled 10 times to generate the distributions shown. Six tumors per pool was selected for subsequent analyses based on the high sgRNA coverage achieved in the saline group. The boxes indicate the 25th percentile (bottom edge), median (thick horizontal line), and 75th percentile (top edge) of the individual points. The vertical lines ("whiskers") attached to the boxes extend to the minimum or maximum values or up to 1.5 times the inter-quartile range from the box edges.

(d) Gene-level volcano plots of MAGeCK analyses results of FHSC14 tumors screened with the focused sgRNA library. The gene-level \log_2FC was calculated as the median of the sgRNA-level \log_2FC values. SAGA complex member gene names are displayed in blue. FDR < 0.05 for genes with right-side up triangles, FDR 0.05-0.20 for genes with upside down triangles, and FDR > 0.2 for genes with solid filled circles.

(e) Waterfall plots depicting \log_2FC enrichment vs P0 of sgRNAs targeting CREBBP and KEAP1, showing the top 3 sgRNAs per gene for all FHSC14 tumor pools. Each vertical bar depicts one sgRNA from one pooled tumor.

***KEAP1* loss leads to chemoresistance in SCLC PDX model**

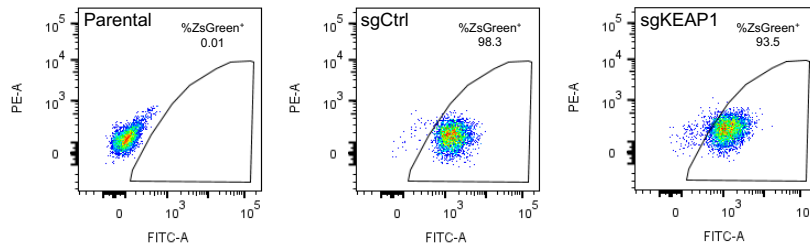
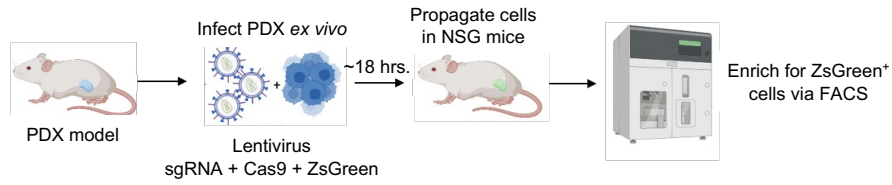
To validate hits from our loss-of-function genetic screens in vivo we generated isogenic PDX models with CRISPR-Cas9 single gene deletions. We focused on *KEAP1*, given its known roles in chemotherapy response in NSCLC but lack of study in SCLC. In normal

conditions, KEAP1 binds to the CUL3-RBX1 ubiquitin ligase complex and the transcription factor NRF2, leading to proteasomal degradation of NRF2. Interaction of reactive oxygen species or other molecular stressors with KEAP1 sensor cysteine residues triggers release of NRF2, allowing its accumulation and enabling transcription of genes that promote stress responses.⁷²⁻⁷⁴ We cloned the top enriched sgRNA from the FHSC14 CRISPR deletion screen as well as a non-targeting control sgRNA into lentiCRISPRv2-ZsGreen (see Table 4, which shows the gRNA sequences used). Dissociated FHSC14 tumors were transduced in vitro with lentivirus containing these vectors for up to 18 hours and re-engrafted in NSG mice for expansion in vivo (Figure 2.3A). Successfully transduced cells from returning tumors were enriched by fluorescence-activated cell sorting (FACS) based on ZsGreen expression and were immediately re-injected into NSG mice (Figures 2.3A). With two rounds of propagation in vivo and sorting, we developed transduced models (>90% ZsGreen positive, see Figure 2.3A) and used Western blotting to successfully confirm KEAP1 protein knockout upon expression of the *KEAP1*-targeting sgRNA (sgKEAP1) (Figure 2.3B). We also confirmed expected increased protein levels of both NRF2 and a canonical target, NQO1, in sgKEAP1 tumors (Figure 2.3B). To test the impact of *KEAP1* deletion on response to chemotherapy, we set up parallel cohorts of NSG mice with subcutaneous right flank injections of sgCtrl or sgKEAP1 FHSC14 tumors. Once tumors reached ~150 mm³, we treated mice with three weekly cycles of saline or cis-eto and measured tumor volume over 21 days. While sgCtrl tumors slightly regressed in response to cis-eto, sgKEAP1 tumors grew at comparable rates to the saline-treated group, exhibiting almost complete resistance to chemotherapy (Figure 2.3C). To assess the impact of

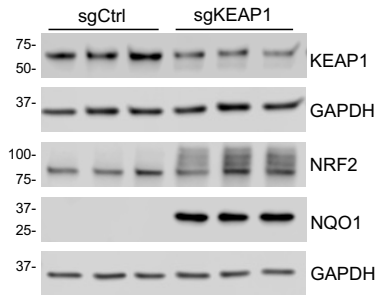
KEAP1 deletion on the short-term response to cis-eto, in a parallel experiment, we collected tumors from each isogenic model for molecular analyses 48 hours after the start of treatment. We performed immunohistochemistry (IHC) on fixed tumor samples from this experiment. sgCtrl tumors exhibited decreased mitotic cells (as assessed by Ser-10 phospho-histone H3, pH3) and increased apoptosis (as assessed by Cleaved Caspase 3, CC3) in response to cis-eto (interaction $p < 0.0001$ for both comparisons, Figure 2.3D). However, no changes in pH3 or CC3 positivity were observed with 48 hour cis-eto treatment in the sgKEAP1 PDX model.

Figure 2.3

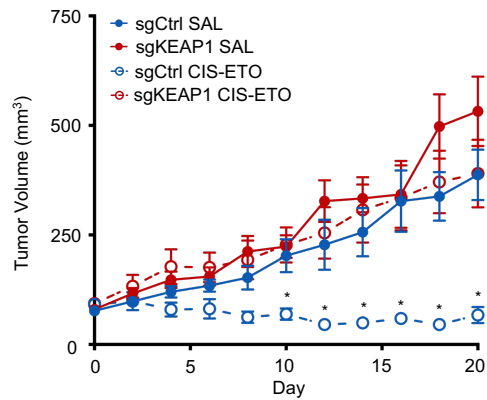
A



B



C



D

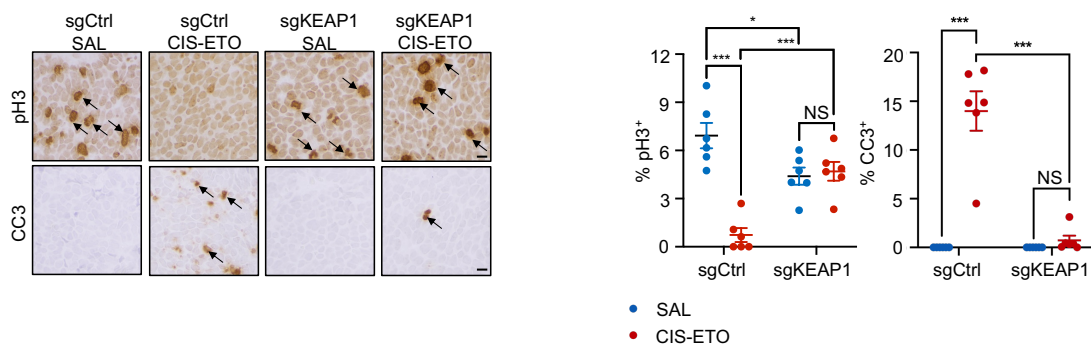


Figure 2.3: Isogenic PDX model reveals KEAP1 loss as a driver of chemoresistance in SCLC

(a) Schematic of isogenic PDX model generation and flow cytometry with lentiviral sgRNA expression showing purity of the resulting models.

(b) Western blot confirming KEAP1 deletion with sgKEAP1 expression as well as corresponding NRF2 and NQO1 increase.

(c) Tumor volume growth curves of non-targeting sgRNA versus KEAP1-targeting sgRNA-expressing FHSC14 PDX models over 21 days of treatment with saline or three weekly cycles of cis-eto. Data are means \pm SEM; n=7 animals per treatment group.

(d) Immunohistochemistry analyses and representative images for pH3 and CC3 to assess proliferation and cell death, respectively, in sgCtrl versus sgKEAP1 FHSC14 PDX models at a 48-hour timepoint after treatment with either saline or cis-eto. Scale bar, 10 μ m. Statistical analyses in **c** and **d** were performed by 2-way ANOVA with Tukey's multiple comparisons test. *p < 0.05, **p < 0.01, ***p < 0.001.

Glutamine metabolism represents a targetable vulnerability for *KEAP1*-deleted SCLC

To analyze changes in gene expression with *KEAP1* deletion, we extracted RNA from snap-frozen tumor tissue from the 48-hour experiment and performed RNA-seq.

Querying the molecular signatures database (MSigDB) using Gene Set Enrichment Analysis (GSEA)⁷⁵⁻⁷⁷ we identified the top 6 Hallmark gene pathways positively enriched with *KEAP1* deletion (Figure 2.4A). The reactive oxygen species pathway was the most enriched, consistent with the KEAP1-NRF2 pathway's role in coordinating the antioxidant response⁷²⁻⁷⁴ with consistent upregulation of key genes *NQO1*, *TXNRD1*, and *GCLC* (Figure 2.4B). Genes in several additional metabolic pathways, including hypoxia and glycolysis, were also enriched. For the pathways shown, including reactive oxygen species, we observed a general increase in expression for both saline and cis-

eto treated sgKEAP1 tumors relative to the sgCtrl tumors, with fewer differences between the two treatment conditions within the same genotype.

To further explore the gene expression changes with *KEAP1* deletion, we applied log fold change and FDR cutoffs to the edgeR differential expression analysis and ran Enrichr^{78,79} on the resulting gene sets. Several of the top positively enriched KEGG pathways with *KEAP1* deletion are related to metabolism, including glutathione metabolism (Figure 2.4C). Given the enrichment of metabolic pathways with *KEAP1* deletion, we performed metabolomic analysis using liquid chromatography mass spectrometry analyses on untreated tumors which revealed an increase in reduced glutathione (GSH) in sgKEAP1 relative to sgCtrl tumors, as expected (Figure 2.4D). Glutamate levels relative to the control were lower in sgKEAP1 consistent with prior reports of increased glutamate usage to support cystine uptake through the cystine/glutamate antiporter xCT and for increased synthesis of glutathione resulting in a higher dependence on glutamine catabolism for *KEAP1*-mutant tumor models.^{80,81,70,82} Given this reported dependency, we tested whether sgKEAP1 SCLC is sensitive to inhibition of glutaminase, the enzyme that hydrolyzes glutamine to glutamate using the glutaminase inhibitor telaglenastat also known as CB-839.^{70,80}

We propagated parallel cohorts of sgKEAP1 and sgCtrl tumors in NSG mice and treated with vehicle or CB-839 twice daily via oral gavage once tumors reached 200-250 mm³ (Figure 2.4E). Tumors were measured daily for 1 week prior to collection. While FHSC14 sgCtrl treated with CB-839 increased in tumor volume similar to the sgCtrl and

sgKEAP1 vehicle-treated tumors, sgKEAP1 tumors treated with CB-839 exhibited partial tumor regression. Therefore, glutamine metabolism represents a targetable vulnerability for *KEAP1*-deleted SCLC.

Figure 2.4

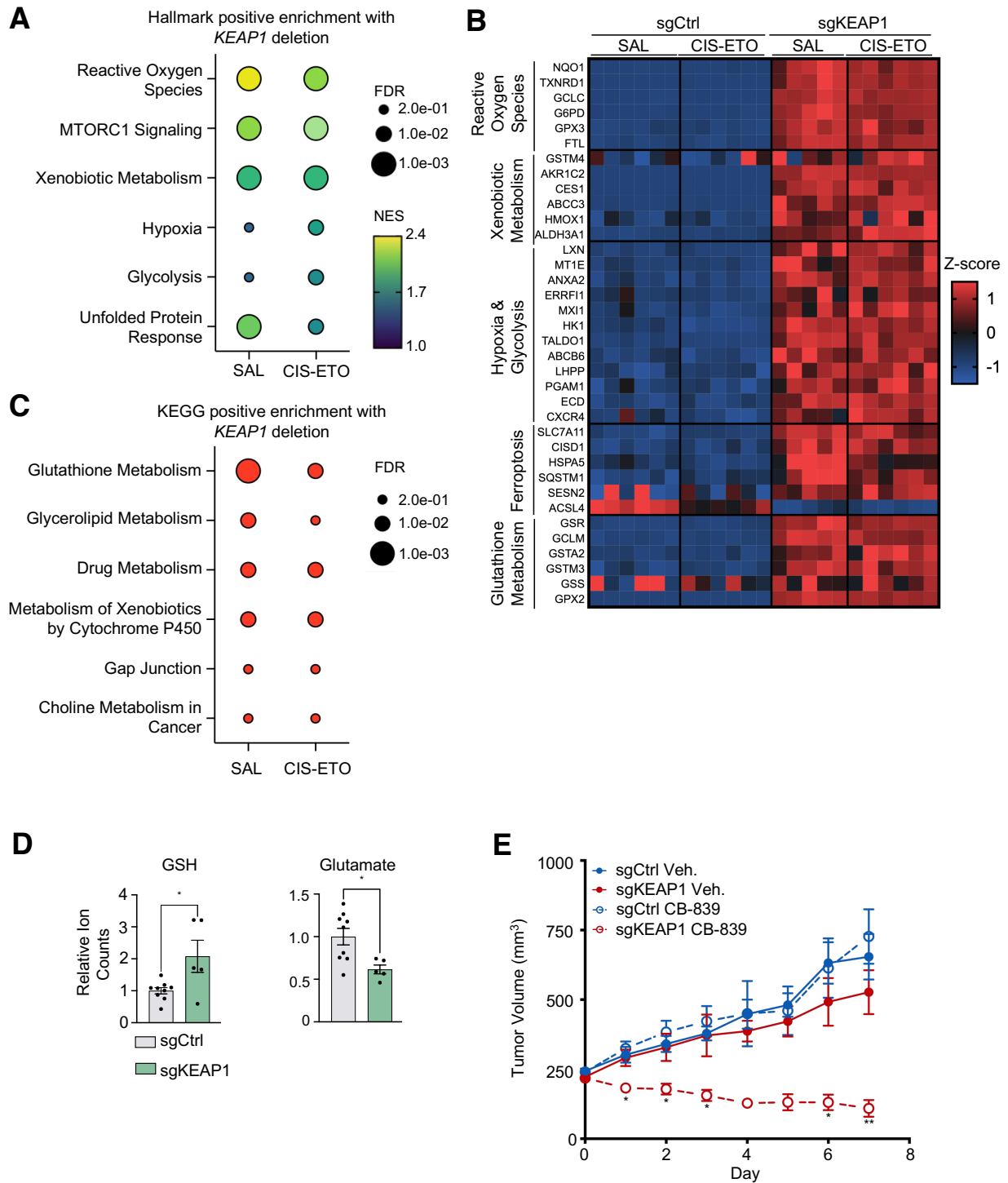


Figure 2.4: Glutamine metabolism represents a targetable vulnerability for *KEAP1*-deleted SCLC

(a) Top 6 molecular signatures database (MSigDB) Hallmark pathways that are upregulated in sgKEAP1 FHSC14 tumors relative to sgCtrl tumors, based on gene set enrichment analysis of RNA-seq data after treatment for 48 hours with saline or cis-eto. Point size is scaled to FDR and point color is scaled to normalized enrichment score (NES).

(b) Heatmap showing select gene enrichment for the indicated MSigDB pathways in sgKEAP1 vs sgCtrl FHSC14 tumors treated for 48 hours with saline or cis-eto.

(c) Top six KEGG pathways positively enriched in sgKEAP1 relative to sgCtrl tumors, based on Enrichr analysis of RNA-seq data after treatment for 48 hours with saline or cis-eto. The input list of genes was defined based on applying a cutoff of log fold change > 2 and FDR of < 0.05 to the edgeR data.

(d) Bar charts showing relative ion counts (normalized to sgCtrl) for reduced glutathione (GSH) and glutamate for FHSC14 sgCtrl and sgKEAP1.

(e) Tumor volume growth curves of non-targeting sgRNA versus KEAP1-targeting sgRNA-expressing FHSC14 PDX models over a 1-week treatment period with vehicle or twice daily with 200 mg/kg of CB-839. Data are means \pm SEM; n=5 animals total per treatment group. Statistical analysis in **e** was performed by 2-way ANOVA with Tukey's multiple comparisons test. Statistical analysis in **d** was performed by unpaired t-test. *p < 0.05, **p < 0.01, ***p < 0.001.

Evaluating whether sgKEAP1 tumors are sensitive to glycolysis inhibition

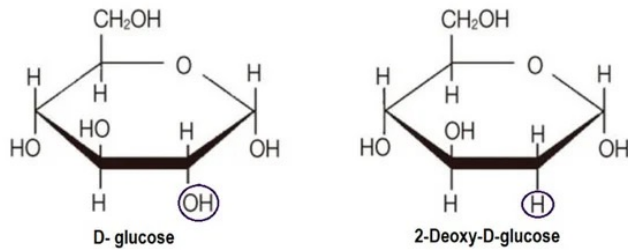
Given the enrichment of the glycolysis Hallmark pathway with *KEAP1* loss, we were interested in evaluating whether sgKEAP1 FHSC14 tumors would be vulnerable to

inhibition of glycolysis. 2-deoxy-d-glucose (2-DG) is a glycolysis inhibitor that has a hydrogen instead of the 2-OH that regular glucose has (Figure 2.5A). The similarity of its structure to glucose enables 2-DG to compete with glucose for use by enzymes in the glycolysis pathway; however, 2-DG cannot be metabolized by these enzymes, so glycolysis is inhibited.^{83,84} This ultimately leads to apoptotic cell death. Cancer cells have increased rate of glycolysis, a phenomenon known as the Warburg effect, making them more vulnerable to inhibition of glycolysis.^{83,84}

We tested whether 2-DG, alone or combined with cis-eto, would induce tumor regression in sgKEAP1 FHSC14 tumors. To do so, we performed a 3-week treatment experiment comparing tumor kinetics for sgCtrl vs. sgKEAP1 FHSC14 tumors treated with saline, cis-eto, 2-DG, or 2-DG + cis-eto (Figure 2.5B). The impact of *KEAP1* loss on driving chemoresistance validated again in this independent experiment. Additionally, neither sgCtrl nor sgKEAP1 tumors responded to 2-DG alone. However, sgKEAP1 tumors treated with both 2-DG and cis-eto did respond somewhat, albeit with a lesser degree of tumor volume decrease compared to the sgCtrl tumors treated with 2-DG and cis-eto. The effect was not as striking as the impact of CB-839 treatment however, so glutaminase inhibition remains a more promising therapeutic vulnerability.

Figure 2.5

A



B

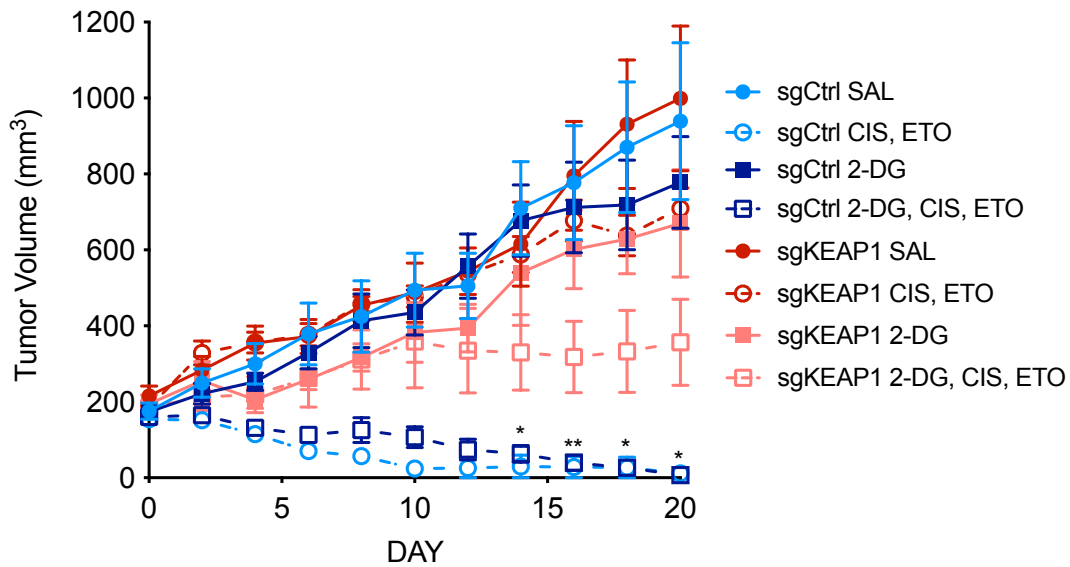


Figure 2.5: Evaluating whether sgKEAP1 tumors are sensitive to glycolysis inhibition

(a) Structure of 2-deoxy-d-glucose compared to that of the typical d-glucose. 2-deoxy-d-glucose is missing the 2-OH group and instead just has a hydrogen at that position.

(b) Tumor volume growth curves of non-targeting sgRNA versus KEAP1-targeting sgRNA-expressing FHSC14 PDX models over a 3-week treatment period with saline, cis-eto, 2-DG, or 2-DG plus cis-eto. Cycles of 2-DG were administered via intraperitoneal injection at 500 mg/kg as follows: every other day on days 1, 3, and 5 of a week, followed by 2 days off. Data are means \pm SEM; n=7 animals per sgKEAP1 treatment group and sgCtrl saline, n=6 animals for sgCtrl cis-eto, and n=5 for sgCtrl 2-

DG as well as sgCtrl 2-DG + cis-eto. Statistical analysis in **b** was performed by 2-way ANOVA with Tukey's multiple comparisons test. * $p < 0.05$, ** $p < 0.01$.

KEAP1/NRF2 pathway signal is associated with patient outcomes

With validation that deletion of *KEAP1* promotes resistance to SCLC chemotherapy we sought to determine clinical relevance. The IMpower133 trial, with chemotherapy alone and chemotherapy plus PD-L1 inhibitor atezolizumab arms, included both RNA-seq and exome analyses of pre-treatment samples for most patients. Whole exome sequencing (WES) analysis on 191 patients revealed expected high frequency of mutations in RB1 and TP53, and demonstrated *KEAP1* deep deletions and predicted pathogenic mutations in 6% of samples (Figure 2.6A). We also observed a case of *NFE2L2* high level amplification. We queried the IMpower133 RNA-seq data for activation of an 11 gene KEAP1/NRF2 pathway signature (see Materials and Methods). Transcriptome data from the IMpower133 trial data depict a subset of patients with robust KEAP1/NRF2 signature score (Figure 2.6B). NRF2 signature activation was more evident in ASCL1-high samples while we did not observe clear activation of this signature in the NEUROD1-high samples and saw a modest enrichment in non-neuroendocrine samples. Overlaying DNA alteration status and KEAP1/NRF2 expression signature revealed *KEAP1/NFE2L2* genetic alterations in many of the samples that exhibited strong transcriptional activation of KEAP1/NRF2 target genes (Figure 2.6B). Finally, we asked whether the KEAP1/NRF2 signature correlated with patient survival in the chemotherapy arm. Stratifying patients by lower (<Median) vs. higher (>Median) KEAP1/NRF2 pathway signature revealed shorter progression free

survival (PFS) with higher KEAP1/NRF2 signature expression (HR=1.41, 95% CI [1.00-1.99], p=0.049) and similarly shorter overall survival (OS) (HR=1.44, 95% CI [0.99-2.09], p=0.056) (Figures 2.6C and D). These data indicate that *KEAP1* mutations are present in a significant subset of SCLC patients and increased activity of the KEAP1/NRF2 pathway associates with worse clinical outcomes for SCLC patients treated with chemotherapy.

Figure 2.6

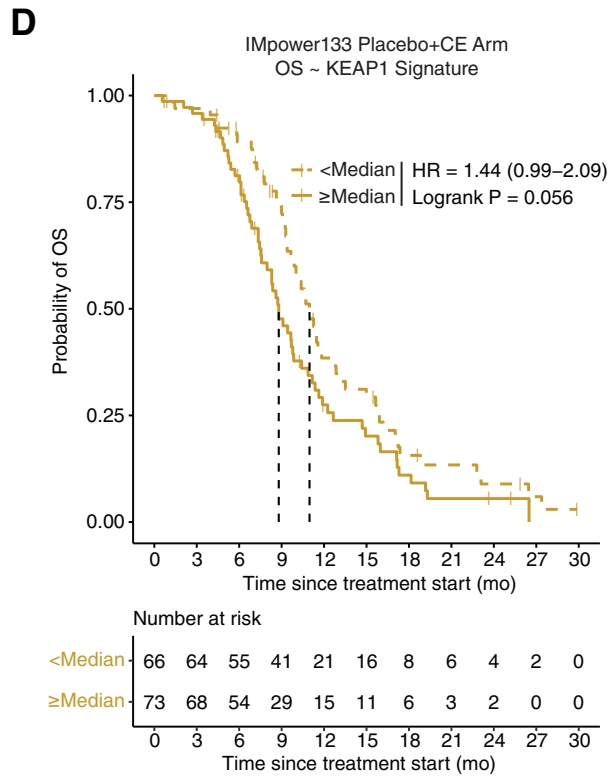
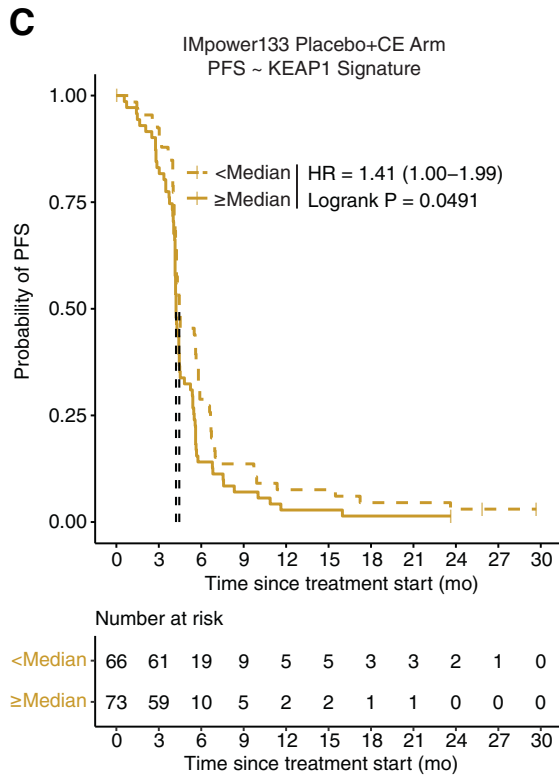
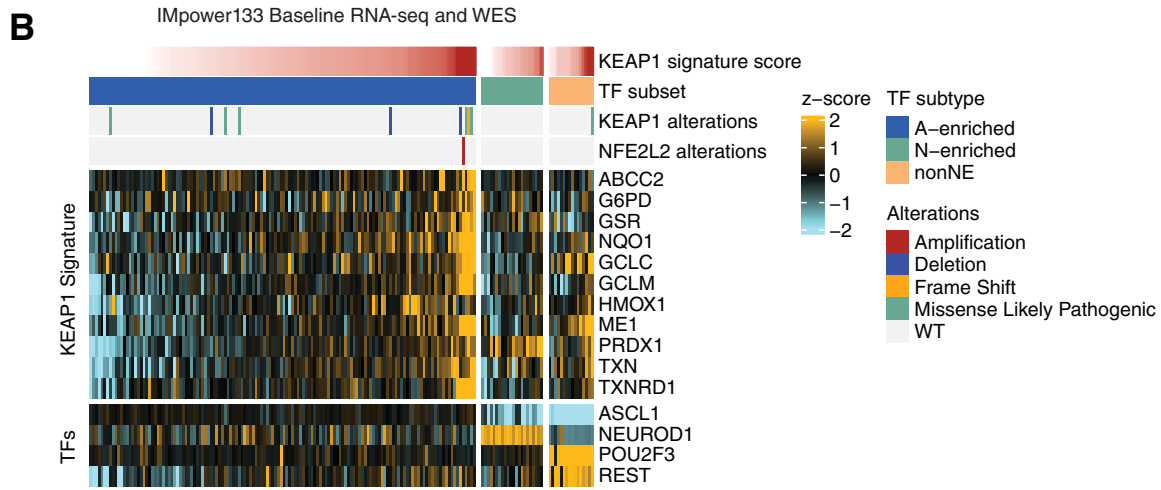
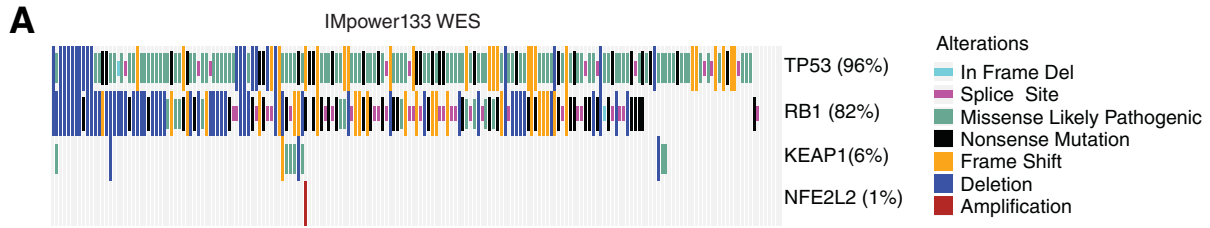


Figure 2.6: KEAP1/NRF2 pathway is altered in a subset of SCLC patients and associated with SCLC clinical response to chemotherapy treatment (Collaboration with Genentech)

(a) Whole exome sequencing (WES) alteration data for patient tumors at baseline in the IMpower-133 trial. Mutations for TP53, RB1, KEAP1, and NFE2L2 are shown. Each vertical bar corresponds to one patient tumor.

(b) KEAP1 signature score and WES alteration data for patient tumors at baseline in the IMpower-133 trial organized by transcription factor (TF) subset. Each vertical bar corresponds to one patient tumor. Gene expression data for transcription factor subsets and genes comprising the KEAP1/NRF2 signature shown.

(c) Progression Free Survival (PFS) curves stratified by median KEAP1/NRF2 pathway signature score. Dashed curve indicates less than the median KEAP1/NRF2 pathway signature, solid curve indicates greater than the median KEAP1/NRF2 pathway signature.

(d) Overall Survival (OS) curves stratified by KEAP1/NRF2 pathway signal. Dashed curve indicates less than the median KEAP1/NRF2 pathway signature, solid curve indicates greater than the median KEAP1/NRF2 pathway signature. Vertical dashed lines indicate median OS in each group.

Chapter 3: Focused CRISPR activation screen to identify novel drivers of chemoresistance in SCLC

In vivo focused CRISPR activation screen to identify drivers of chemoresistance

The library we used for the focused cDNA screen in Chapter 2 was originally designed to probe drivers of breast cancer; thus, not all of the genes were SCLC-relevant.⁶³ We wanted to perform a screen for novel drivers of chemoresistance in SCLC from a gain-of-function perspective with a library that is relevant to SCLC. To do so, we leveraged a CRISPRa platform. CRISPRa libraries are cheaper and easier to produce compared to cDNA libraries, the technology is more novel compared to the traditional approach of cDNA screening, and this method allows for overexpression of genes from their native promoter. This last point helps to avoid supraphysiological gene expression that can occur with cDNA-based overexpression and allows for the overexpression of multiple splice isoforms of a given gene compared to just one.⁸⁵

We developed a focused CRISPRa library targeting 399 genes with 6 gRNAs/gene along with 120 non-targeting control gRNAs using gRNA sequences from the Calabrese CRISPRa genome-scale library.⁵² The genes were selected from eight different studies of SCLC tumor genetics (see Table 5 for a list of genes and gRNA sequences).^{10-12,36,42,86-88} Our selection criteria was evidence of amplification or overexpression in SCLC. This captured genes with functionality across a wide range of biological pathways including DNA damage response, proliferation, cell cycle, and apoptosis. Importantly, similar to the cDNA library, the focused CRISPRa library included MYC

family members *MYC*, *MYCN*, and *MYCL*. Our collaborators in the Paddison Lab helped clone the library into a lentiviral vector for use in the screen.

At present, CRISPRa requires at least 2 vectors to work. One vector carries dCas9 fused to the transcriptional activators, in this case dCas9 VPR, and another vector carries the gRNA of interest. Thus, the first step required to perform the CRISPRa screen was to generate a PDX model that stably expressed dCas9 VPR. Similar to the single-gene lentiviral perturbation done for sgCtrl and sgKEAP1 FHSC14 tumors, we transduced NCI109B with the dCas9 VPR vector and used successive cycles of FACS and tumor propagation to enrich for mCherry positive cells with the dCas9 VPR vector (Figure 3.1A). This model can then be transduced with high-titer lentivirus containing the library.

The setup for this screen was very similar to that for the other screens described herein and is shown in Figure 3.1B. We produced high-titer lentivirus bearing the focused CRISPRa library and dissociated the chemosensitive NEUROD1-high NCI109B dCas9 VPR PDX model into a single cell suspension *ex vivo*. Then, we transduced these cells with the library lentivirus for 18 hours *ex vivo* prior to propagating cells at 1 million cells per flank into a cohort of NSG mice; a subset of the cells were maintained in cell culture to serve as P0 samples for assessing initial guide representation. Once tumors reached roughly 250-350 mm³, mice were treated with saline and collected or with 2 weekly cycles cis-eto chemotherapy to induce tumor regression via IP injection. Cis-eto treated return tumors were collected as they grew back over a period of 3 months. From this

screen, 51 cis-eto treated return tumors, 18 saline treated tumors, and 3 P0 samples were collected. We extracted genomic DNA, performed library preparation, and submitted the library for sequencing.

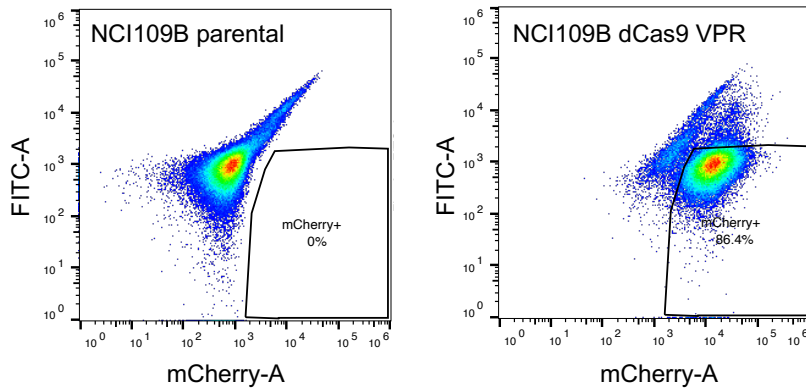
We performed edgeR⁶⁴ analysis to identify CRISPRa gRNAs enriched (relative to the P0 reference point) in the saline treated and cis-eto treated groups (see Table 6, which shows results of this analysis for the CRISPRa focused screen). The results of plotting the average Log₂ fold change (Log₂FC) vs. -Log₁₀ adjusted p-value for each gRNA in the saline and cis-eto treatment groups are shown in Figure 3.1C. Two *MYCN* guides are top hits in both the saline and cis-eto groups, which is expected considering the role of *MYCN* as a driver of tumor growth and chemoresistance in SCLC.³⁷ *MYCN* emerging as a top screen hit is a promising sign that the screen is working as expected. Other top hits in the cis-eto group labeled on the volcano plots included *REST*, *PAX9*, *BMP8A*, *PPP2R1A*, and *YES1*. *BMP8A* has not been well studied in SCLC, but a recent paper on clear cell renal carcinoma demonstrated that *BMP8A* promotes phosphorylation of *NRF2*, mitigating *NRF2* degradation and promoting chemoresistance.⁸⁹ Currently, there are active efforts in the MacPherson Lab following up on this screen to investigate the roles of *BMP8A*, *REST*, *PPP2R1A*, and *YES1* in driving chemoresistance.

One interesting phenomenon that differs from the CRISPR knockout screen results is that a relatively small number of genes in both cis-eto and saline treatment groups had 2 or more gRNAs enriched relative to the P0. Considering the criteria of log fold change > 0.5 and FDR < 0.2, only 27 genes had 2 or more gRNAs that met these parameters in

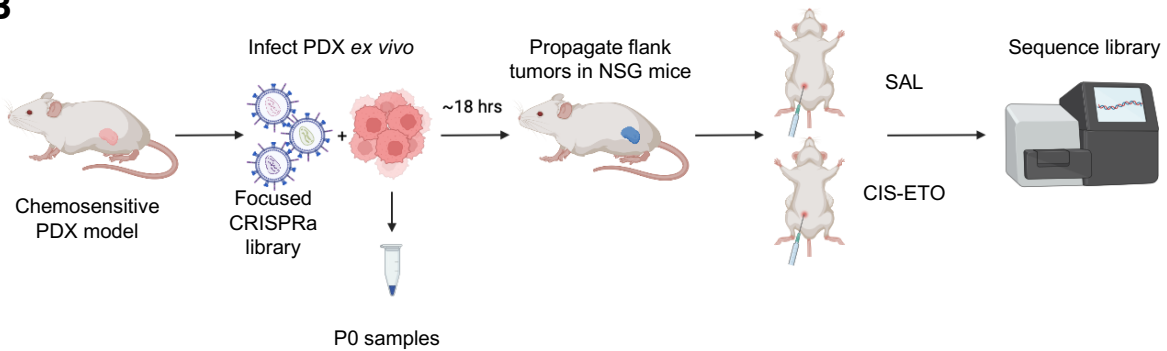
the cis-eto group and only 24 genes qualified in the saline group. *MYCN* meets those criteria for both groups. It is possible that this reflects a lower success rate of guides working in CRISPRa compared to CRISPR knockout.

Figure 3.1

A



B



C

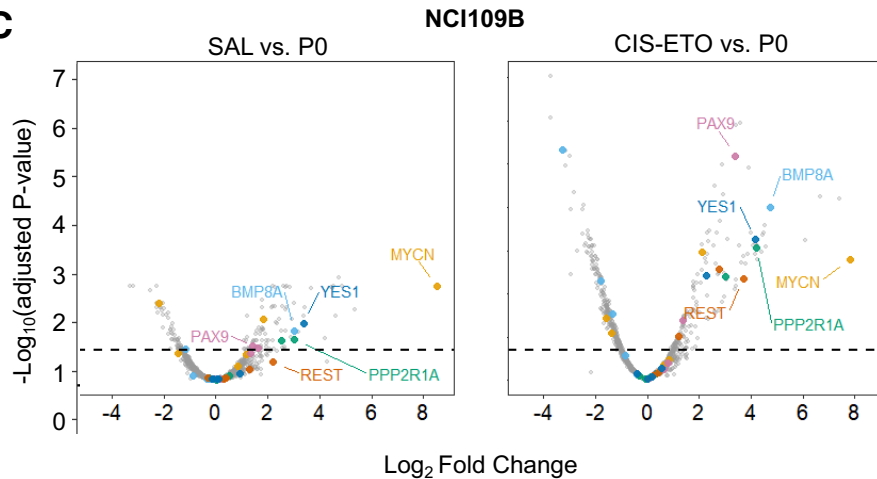


Figure 3.1: In vivo focused CRISPR activation screen to identify drivers of chemoresistance

(a) FACS plots for NCI109B parental and NCI109B dCas9 VPR showing mCherry positive cells in the dCas9 VPR model.

(b) Schematic depicting the workflow of the CRISPR activation screen.

(c) Volcano plots showing gRNA level results of the focused CRISPR activation screen in NCI109B comparing Log_2 fold change to $-\text{Log}_{10}$ adjusted p-value. Computational pooling was done with 12 samples per pool for cis-eto and 6 samples per pool for SAL, and TMM normalization was done using the control guides. Left, comparison SAL vs. P0; right, comparison cis-eto vs. P0. Each dot represents one gRNA. 6 genes are highlighted in different colors, each of which met the criteria of 2+ enriched guides (FDR < 0.2) or a guide with Log_2 fold change > 4 in the cis-eto vs. P0; only the top performing guide is labeled for each gene.

Chapter 4: Discussion

To elucidate the functional genomic landscape of chemotherapy response and resistance in SCLC, we developed a novel screening platform focused on PDX models. Validating our approach, cDNA overexpression screen revealed top hits known to confer chemoresistance in SCLC, such as *MYCN*, *MYCL* and *MYC*.^{23,37,38} We focused our loss of function studies on *KEAP1*, revealing this gene as a novel driver of resistance to cis-eto chemotherapy in SCLC. Mining patient data from the IMpower133 trial³¹ revealed a previously unappreciated role for KEAP1/NRF2 pathway transcriptional activation and genetic disruption in human SCLC, with relevance for clinical impact on chemotherapy response.

Our functional screens and subsequent hit validation focused on genetic perturbation of PDX models that recapitulate the chemosensitivity of SCLC patients. Deletion of *KEAP1* switched the FHSC14 SCLC PDX model to become chemoresistant. We observed activation of canonical NRF2 targets and transcriptional alteration of redox metabolism in the *KEAP1*-deleted model. In NSCLC, the KEAP1/NRF2 pathway is well appreciated as being functionally important, with inactivating mutations in *KEAP1* and activating mutations in *NFE2L2* prevalent.^{90,91} Also, *KEAP1* loss has a known role in conferring chemoresistance in NSCLC.^{70,71} However, initial genomic analyses of SCLC, which focused on earlier stage resected tumors, did not highlight roles for mutational alteration in *KEAP1*.^{10,12} The first hint of KEAP1/NRF2 pathway roles in SCLC came with recent observations that ~3% of a large, real-world cohort of 3600 SCLC samples subject to targeted sequencing (largely from blood ctDNA analyses) harbored *KEAP1* mutations,

but the functional importance was unknown⁹². By analyzing exome data from IMpower133 patients, we identified functional mutations/deep deletions in *KEAP1* in 6% of the samples. We also identified a subset of SCLC with clear activation of a *KEAP1/NRF2* gene expression signature. This subset appeared in ASCL1-positive SCLC but was not prevalent in NEUROD1-expressing SCLC patients. Moreover, strong transcriptional activation of the pathway was often coupled with presence of genetic alterations in *KEAP1* supporting functional importance of the observed mutations. *KEAP1/NRF2* alteration in SCLC may be underappreciated as many genomic analyses of SCLC focused on earlier stage cases that underwent surgical resection.^{10,12} Notably, the genomic analyses presented here were of IMpower133 patient samples collected prior to treatment, and, based on our functional studies, we predict higher rates of *KEAP1/NRF2* pathway mutation and/or transcriptional activation in SCLC tumors that have become chemoresistant. Critically, activation of a *KEAP1/NRF2* gene signature was associated with shorter PFS and OS in the chemotherapy arm of IMpower133, highlighting the clinical relevance of our genetic observations. With evidence of *KEAP1* having an important role in a subset of SCLC, further study is warranted of the functional role of this pathway, the prevalence of alterations in post-relapse patients, and potential avenues of targeted treatment for *KEAP1*-mutant SCLC patients.

One potential approach for targeted treatment of SCLC patients with *KEAP1* loss is glutaminase inhibition, as we showed here that a *KEAP1*-mutant SCLC PDX model is sensitive to glutaminase inhibition with CB-839. Glutaminase inhibition blocks the conversion of glutamine to glutamate, further compounding the glutamate deficit in

KEAP1-mutant SCLC.^{80,82} CB-839 has been shown to be well-tolerated by patients in Phase I and Phase II clinical trials in other cancer types (see NCT03163667 in renal cell carcinoma, NCT03057600 in triple negative breast cancer, and NCT03428217 in metastatic renal cell carcinoma). One study, NCT03163667, did show that CB-839 improved clinical outcomes as measured by progression free survival for renal cell carcinoma patients.⁹³ However, another study of CB-839 in renal cell carcinoma patients failed to find improved clinical outcomes,⁹⁴ and two studies of CB-839 in NSCLC have been terminated due to lack of efficacy (NCT02771626 and NCT04265534). The latter of these studies, NCT04265534, combined CB-839 with standard of care chemotherapy specifically for a *KEAP1/NFE2L2*-mutant patient population of NSCLC. Additional studies of CB-839, including in *KEAP1*-mutant patient populations, are still ongoing (see NCT03872427 and NCT04250545). Given the striking effect on tumor growth with CB-839 alone over just a week of treatment in the *KEAP1*-mutant PDX model, it would be interesting combine this with cis-eto chemotherapy in the same model to assess whether there is a more striking or durable response over time. Furthermore, there could still be a rationale for testing CB-839 in combination with standard of care for SCLC patients given these promising in vivo data.

While the data presented here do not confirm a particular mechanism for chemoresistance driven by *KEAP1* loss, there are some possibilities based on biology observed here and in the literature. First, it is possible that chemoresistance is induced by the increase in GSH in sg*KEAP1* tumors (see Figure 2.4D). Although cisplatin primarily targets DNA, it also binds to GSH. This binding of cisplatin and GSH

is irreversible and results in cisplatin inactivation.⁹⁵⁻⁹⁷ Increased GSH levels are a common trait of cisplatin resistant cell lines as well.^{98,99} Thus, it is feasible that the increased GSH level observed in sgKEAP1 tumors at least contributes to chemoresistance via promoting increased sequestration of cisplatin.

In addition to a direct interaction between GSH and cisplatin, general increased activity of the antioxidant response pathway could be a contributing factor to the chemoresistance observed in sgKEAP1 tumors. Resistance to oxidative stress is a known mode of chemoresistance driven by *KEAP1* loss in NSCLC.⁷¹ A study in NSCLC demonstrated that increased NRF2 levels resulted in increased glutathione, thioredoxin (another antioxidant), and drug efflux to drive chemoresistance.¹⁰⁰ Knockdown of NRF2 in that study resulted in increased ROS and resensitization to chemotherapy.¹⁰⁰

Reactive oxygen species (ROS), including hydroxyl radicals, hydrogen peroxide, and superoxide anions, can be induced by cisplatin treatment.^{95,101} ROS-mediated damage to cells can impact proteins (protein carbonyl content), lipids (peroxidation), and the DNA (thymidine glycol) and ultimately induce apoptosis.¹⁰² Future work could investigate whether any of these markers of ROS-mediated damage are present with cisplatin treatment in sgCtrl tumors and reduced in sgKEAP1 tumors.

As mentioned earlier, *KEAP1* loss is linked to driving chemoresistance in NSCLC in part through stabilization of NRF2 and through increased proliferation.⁷⁰ While we actually observed reduced proliferation at baseline in sgKEAP1 vs. sgCtrl saline treated tumors, we did observe maintained proliferation in the context of cis-eto chemotherapy

treatment for the sgKEAP1 tumors (Figure 2.3D). Another possibility for the mechanism of chemoresistance is that *KEAP1* loss is inhibiting apoptosis, as we see reduced induction of apoptosis as measured by CC3 in the sgKEAP1 tumors treated with cis-eto compared to the sgCtrl tumors (Figure 2.3D). In the literature, previous work has shown that NRF2 induces expression of an antiapoptotic protein called Bcl-xL via an antioxidant response element in the promoter for Bcl-xL.¹⁰³

Based on the literature as well as on the upregulation of NRF2 and its targets with *KEAP1* loss observed here, it is feasible that chemoresistance from *KEAP1* loss is driven by its role as a negative regulator of NRF2. Knockdown of NRF2 in cells with defective KEAP1 has been shown to activate ROS stress and damage as well as re-sensitization to cisplatin in the literature.^{100,104} Further evidence of NRF2 being the primary target of KEAP1 regulation is found in a study of *Keap1* and *Nfe2l2* double knockout mice, wherein *Keap1* single knockout mice died postnatally with excessive upregulation of cytoprotective genes but adding *Nfe2l2* knockout reversed this phenotype and enabled mouse survival.¹⁰⁵ Nevertheless, to confirm that *KEAP1* loss is driving chemoresistance via NRF2 activity in our model system, future experiments could include genetic knockout or knockdown of *NFE2L2*. If chemosensitivity is restored with reduced NRF2 levels, that would provide convincing evidence that the mechanism of resistance is linked to NRF2 activity. Another option for this would be treatment with a pharmacological inhibitor of NRF2, such as brusatol which has previously been shown to specifically target NRF2 via enhanced ubiquitination and degradation.^{106,107} A

previous in vivo experiment in NSCLC A549 xenografts demonstrated that brusatol treatment sensitized the tumors to cisplatin.¹⁰⁶

The CRISPRa screens performed in this study mark 1) the first use of CRISPRa in PDX models and 2) the first use of CRISPRa to screen for drivers of chemoresistance in SCLC to the best of our knowledge. There are some key drawbacks compared to cDNA-based overexpression, such as the known risk of silencing of CRISPRa complexes over time, the risk of off-target effects, and inconsistency in how well CRISPRa works across different cell lines.^{108,109} Improving the efficacy and consistency of CRISPRa overexpression is an area of active research in the field, with one intriguing approach involving addition of histone acetyltransferase p300 to dCas9 VPR (dCas9 VPRP).¹¹⁰ The aforementioned pitfalls aside, our focused CRISPRa screen identified several novel candidate drivers of chemoresistance in SCLC for which there are ongoing efforts in the MacPherson Lab to validate.

Clinical outcomes for SCLC remain dismal as chemoresistance is a persistent challenge. Our work identified new drivers of resistance to chemotherapy as well as new candidate drivers of chemoresistance with previously unappreciated roles in SCLC, and we provide evidence of clinical relevance for impact of KEAP1 pathway alterations on response to chemotherapy in patients. Despite limited progress over recent decades in understanding factors that contribute to SCLC chemoresistance, high throughput study of chemosensitive PDX models now enables systematic interrogation of genes

that modulate this process, providing critical information for future efforts to target relapsed SCLC in the clinic.

Chapter 5: Materials and Methods

Mice

We obtained male or female immunodeficient NOD scid gamma mice (NSG, JAX strain 005557) from Translational Research Model Services at Fred Hutch. Mice were housed in group settings of no more than 5 mice per cage in a temperature controlled, pathogen free environment with a standard 12-hour light/dark cycle. All procedures performed in this study were approved by the Institutional Animal Care and Use Committee at Fred Hutch (protocol #50783).

Patient Derived Xenograft (PDX) models

PDX models used in the study include FHSC14⁶⁶, NCI109B (NCI Patient-Derived Models Repository, distribution lot 594431-109-B), and SC151 (Jackson Labs, model TM00269). Only adult mice ~12 weeks of age received xenografts. Mice were monitored weekly while awaiting tumor growth and multiple times per week when tumors were present.

Cell lines

293TN producer cells (LV900A-1, System Bioscience) were used for production of lentivirus in this study. We grew the cells in D10 medium: 500 mL DMEM, FBS at 10% w/v, Pen-Strep/L-glut mix at 1% w/v, 100 mM sodium pyruvate at 1% w/v, and 7.5% sodium bicarbonate at 1% w/v. This media was changed to virus production media (VPM) at 16 hours post-transfection: 500 mL DMEM, 100 mM sodium pyruvate at 1% w/v, 7.5% sodium bicarbonate at 1% w/v, 0.5M sodium butyrate at 1% w/v, FBS at 2%

w/v, and 2 ug/mL insulin human recombinant zinc. The cells were cultured in a humidified incubator at 37°C, 95% air, and 5% CO₂.

Focused knockout library generation

The SCLC sgRNA library was designed to target 400 genes mutated/deleted in SCLC or implicated in chemotherapy response or found enriched in a pilot genome scale screen. For each gene, six sgRNA sequences were generated using GUIDES (Graphical User Interface for DNA Editing Screens).¹¹¹ 120 non-targeting sgRNAs were sourced as controls from the GeCKO v2.0 library⁵¹ for a total of 2520 sgRNAs (Table 2). The SCLC sgRNA library was synthesized (Twist Biosciences, San Francisco, CA) and cloned into lentiCRISPRv2 (Addgene #52961). Oligo pools were amplified using Phusion High-Fidelity DNA Polymerase (NEB) combined with 1 ng of pooled oligo template, primers ArrayF and ArrayR (ArrayF primer: TAACTTGAAAGTATTTTCGATTTCTTGGCTTTATATATCTTGTGGAAAGGACGAAACA CCG and ArrayR primer: ACTTTTTCAAGTTGATAACGGACTAGCCTTATTTAACTTGCTATTTCT AGCTCTAAAC), an annealing temperature of 59°C, an extension time of 20 s, and 25 cycles. Following PCR amplification, a 140 bp amplicon was gel-purified and cloned into BsmBI (NEB; R0580) digested lentiCRISPRv2 using Gibson Assembly (NEB; E2611S). Each Gibson reaction was carried out at 50°C for 60 min. 5 µl of the reaction was used to transform 25 µl of Endura electrocompetent cells (Lucigen; 60242–2) according to the manufacturer's protocol using a Gene Pulser (BioRad). To ensure adequate representation, sufficient parallel transformations were performed and plated onto

carbenicillin containing LB agarose 245 mm x 245 mm plates (Thermo Fisher) at 300-times the total number of oligos of each library pool. After overnight growth at 37°C, colonies were scraped off, pelleted, and used for plasmid DNA preps using the Endotoxin-Free Nucleobond Plasmid Midiprep kit (Takara Bio; 740422.10). ~400 clones were sequenced validated as an initial quality control measure.

Focused CRISPRa library generation and screen model

Guide RNA sequences for the genes of interest were gathered from the previously published Calabrese genome-scale CRISPRa library.⁵² Collaborators in the Paddison Lab performed the cloning of this library into lentiGuide-Hygro-eGFP (Addgene #99375) following the previously described protocol (same as for focused CRISPR knockout library).^{51,112} The NCI109B dCas9 VPR model used Addgene #102245, a previously unpublished dCas9 VPR mCherry vector from the lab of Jacob Corn.

Library Propagation

We followed the protocol provided by the Zhang Lab for pooled library propagation for both our CRISPRko library and our cDNA library.^{51,113} Briefly, each library was diluted to 50 ng/uL in nuclease-free water and electroporated into electrocompetent Lucigen Endura cells (VWR, 71003-038) according to manufacturer's guidelines. The transformations were then plated on 24.5 cm² bioassay plates with ampicillin. After 14 hours of incubation at 32°C, the amplified libraries were harvested from transformed bacteria using the PureLink HiPure Plasmid Maxiprep Kit (Invitrogen, K210007).

Lentiviral production and concentration

We produced concentrated lentivirus following a protocol modified from the Deisseroth Lab.¹¹⁴ 293TN producer cells were plated on poly-L-lysine coated (Millipore Sigma, P4832-50ML) 500 cm² plates (Corning, 431111). Cells were co-transfected once approximately 65 – 75% confluent with the lentiviral vector of interest, psPAX2 (Addgene #12260), and pMD2.G (Addgene #12259) at a 2:2:1 ratio via calcium chloride. Media was changed to VPM (see recipe above under “Cell lines”) at 16 hours post-transfection. Viral supernatants were collected 64 hours post-transfection, filtered through 0.45 µm Millipore low-protein binding filter units (Millipore Sigma, S2HVVU02RE), then concentrated 70-fold in Millipore Centricon 70 Plus cartridges (Fisher, UFC710008) by centrifuging at 3300 x g for 45 minutes. Concentrated viral supernatant was recovered by inverting the upper filter cartridge from the Centricon and placing it on an included collection cup, then centrifuging at 1000 x g for 2 minutes.

Chemotherapy treatments

For treatment experiments, tumors were measured daily or every other day. Saline treatments were performed via intraperitoneal injection once per week, while cisplatin-etoposide treatments were administered intraperitoneally on weekly cycles as follows: 5 mg/kg cisplatin (Millipore Sigma, 479306) and 10 mg/kg etoposide (Millipore Sigma, E1383) day 0, followed by 2 more days of etoposide, then 4 days off until the next cycle. CB-839 (MedChemExpress, HY-12248) was administered twice daily via oral gavage at a dose of 200 mg/kg. At the end of experiments, tumor tissue was collected for molecular and histopathological analyses.

CRISPR knockout, CRISPR activation, and cDNA screening in vivo

Tumor processing and transduction with library

PDX tumors were dissociated into single cell suspensions and transduced with concentrated lentivirus carrying the screening library of interest in the presence of 4 µg/mL polybrene for no more than 18 hours ex vivo. A subset of the cells were left in culture for 72 hours to serve as an initial timepoint (P0), while the majority of the cells were spun down to remove virus and injected subcutaneously at ~1 (cDNA and CRISPRa screen) or 4 (CRISPRko screen) million cells per flank in NSG mice. Once tumors reached a model-dependent threshold size, mice were treated with saline or 2-3 cycles of cis-eto to ablate tumors. Tumors treated with saline and tumors that returned following cis-eto treatment were collected and snap frozen on dry ice. Genomic DNA extraction was performed as previously described.¹¹⁵

cDNA screen library preparation

For all PCR reactions, we used Phusion Flash High Fidelity Master Mix (ThermoFisher Scientific, F548L). To prepare libraries from genomic DNA (gDNA) for sequencing, a two-step protocol was performed. The first PCR step (30 cycles) amplified the cDNA barcodes while preserving library complexity and added an additional barcode to identify individual samples. Following gel extraction of the 110 base pair (bp) PCR product with a PureLink quick gel extraction kit (Invitrogen, K210012), individually barcoded samples were combined into pools such that no barcodes were repeated within a pool. The second PCR step followed manufacturer's instructions for the NEBNext Ultra II RNA Library Prep Kit (New England Biolabs, E7770L) end prep of

cDNA library, with each pool of samples getting a secondary barcode. This second step also added Illumina sequencing adapters. Individual samples were identified by a unique combination of sample and pool barcode. Samples were pooled and submitted at 2 nM for sequencing.

CRISPRko and CRISPRa screen library preparation

Genomic DNA libraries were prepared for sequencing in a two-step protocol as described previously.¹¹³ For all PCR reactions, we used Phusion Flash High Fidelity Master Mix. For the first PCR step (16 cycles), a total of 8 µg genomic DNA per sample (8 x 100 µL reactions with 1 µg gDNA per reaction) was amplified and pooled to preserve library complexity. A second PCR step (16 cycles) was performed on 10 µL of the previous pooled PCR product to add Illumina sequencing adapters and barcodes to identify individual samples. Following gel extraction of the 230 bp PCR product, individual samples were quantified, pooled, and submitted at 2 nM for sequencing.

Sequencing

The cDNA screen library consisted of single end reads of 50 bp and the CRISPRko and CRISPRa screen libraries consisted of single end reads of 57 bp. Libraries were loaded at 11.5 pM and sequenced on an Illumina HiSeq2500 using a high output flow cell.

Generating single-gene perturbed PDX models

We collected PDX tumors from NSG mice and dissociated them into single-cell suspensions in 1 mg/mL collagenase (Millipore Sigma, C5138) prior to infecting the

cells with concentrated lentivirus carrying a lentiCRISPRv2-ZsGreen vector with KEAP1-targeting or control non targeting sgRNA .Transduced cells were collected after no more than 18 hours ex vivo, mixed with Matrigel at a 1:1 ratio and injected subcutaneously into the flanks of NSG mice. Once tumors formed, we again dissociated them and used FACS to isolate ZsGreen⁺ (lentiCRISPRv2) cells successfully transduced with the vectors of interest. Typically, 2-3 rounds of sorting followed by reimplantation were needed to generate models that were nearly completely composed of transduced cells.

Western Blot Analysis

Protein extracts were prepared via homogenization of snap-frozen tumor tissue with the AgileGrinder™ Tissue Grinder (Thomas Scientific-ACTGene, ACT-AG3080) in ice-cold 1X RIPA cell lysis buffer (Cell Signaling, 9806S) with protease and phosphatase inhibitor cocktail (ThermoFisher, 78444). Homogenized tumor samples in lysis buffer were then rotated for 60 minutes at 4°C followed by centrifugation at max speed for 20 minutes at 4°C. We quantified protein extracts with the Pierce BCA Protein Assay Kit (ThermoFisher, 23227) and loaded ~10 µg of samples in 1X Laemmli sample buffer + beta-mercaptomethanol on 4-20% Mini-PROTEAN TGX Precast Protein Gels (BioRad, 4561096). We used 0.45 µm nitrocellulose membranes (GE Healthcare Life Sciences, 10600002) for the protein transfer and imaged membranes with a LI-COR Odyssey Fc. We used GAPDH (Santa Cruz, sc-32233) for protein loading normalization.

Immunohistochemistry

PDX tumor tissue fragments were fixed in 10% neutral-buffered formalin for 72 hours and transferred to 70% ethanol prior to processing to paraffin blocks sectioned at 4 μ M thickness. Paraffin sections were dewaxed in xylene and re-hydrated by passage through a series of ethanol to water. Antigen masking was performed in citrate buffer (10 mM Citric Acid, 0.05% Tween-20, pH 6.0 in Tris-buffered saline solution) pre-heated in a steamer for 20 minutes. Endogenous peroxidases were blocked with 3.5% H₂O₂. Tissue sections were blocked in 5% goat serum and then incubated overnight in primary antibody within humidified chamber at 4 °C. Primary antibodies used were anti-phospho Ser10 histone H3 (Millipore, Cat #06-570), anti-cleaved caspase-3 (Cell Signaling, Cat#9661). Sections were then incubated in biotinylated goat anti-rabbit IgG secondary antibody (Vector Laboratories, BP-9100-50) for 1 hour. Biotin-peroxide complexes were formed using the VectaStain ABC kit (Vector Laboratories, PK-4000) according to the manufacturer's protocol. Development was performed using the DAB Substrate Kit Peroxidase (Vector Laboratories, SK-4100) according to the manufacturer's protocol. Slides were imaged with a Nikon Ni-UI microscope and manually quantified at 400X magnification with 2-3 fields per section.

RNA-seq

RNA was isolated and purified from snap-frozen PDX tumor tissue by mechanical disruption in TRIzol reagent according to the manufacturer's protocol. mRNA was poly(A) enriched using the NEBNext Poly (A) mRNA Magnetic Isolation Module (New England Biolabs, E7490) kit. Indexed libraries were generated using the NEBNext Ultra

II RNA Library Prep Kit for Illumina (New England BioLabs, E7770) according to the manufacturer's protocol. Single-end sequencing (50 bp) was performed on an Illumina NextSeq P3. STAR v2.7.7a¹¹⁶ with 2-pass mapping was used to align single-end reads to human genome assembly hg38 and Gencode gene annotation v38 and mouse genome assembly mm10 and Gencode gene annotation vM23. R package Xenofilter¹¹⁷ was used to remove reads of mouse origin with parameters recommended by authors. FastQC 0.11.9, RNA-SeQC 2.3.4, RSeQC 4.0.0 were used to check various QC metrics including insert fragment size, read quality, read duplication rates, rRNA rates, gene body coverage and read distribution in different genomic regions. FeatureCounts in Subread 2.0.0 was used to quantify gene-level expression by counting reads in an unstranded fashion. Bioconductor package edgeR 3.34.1⁶⁴ was used to detect differential gene expression between sample groups. Genes with low expression were excluded using edgeR function filterByExpr with min.count = 10 and min.total.count = 15. The filtered expression matrix was normalized by TMM Method¹¹⁸ and subject to significance testing using GLM LRT method and paired donor as blocking factor (if applicable). Genes were deemed differentially expressed if Benjamini-Hochberg adjusted p-values were less than 0.05. STAR v2.7.1a and Gencode gene annotation v31 were used. Gene-set enrichment analysis (GSEA, version 4.2.3 software) was performed by querying the Hallmark gene set in the molecular signatures database MSigDB.⁷⁵ Commonly upregulated and downregulated genes in sgKEAP1 vs sgCtrl FHSC14 model were analyzed using the Enrichr^{78,79} website application querying the MSigDB Hallmark gene set.⁷⁵

Metabolomics

Lung tumors frozen in liquid N₂ were pulverized to powder and extracted with 1000 μ L of ice cold 80% HPLC-grade methanol (80:20 methanol:water) (Sigma Aldrich, 646377; 270733). Each tube was vortexed briefly then kept at -20 °C for 30 minutes. Samples were then vortexed at 4 °C for 5 minutes and then centrifuged at 17,000 g for 5 minutes at 4 °C. Supernatant volumes equivalent to 8 mg of extracted tissue was transferred to a fresh microcentrifuge tube and dried on a Centrivap vacuum concentrator (Labonco, 10269602) at 4 °C overnight. The next day, samples were resuspended in 40 μ L 80% methanol containing an isotopically-labeled canonical amino acid mix standard (Cambridge Isotopes, MSK-CAA-1). Samples were then vortexed for 5 minutes at 4 °C and centrifuged at 17,000 g for 5 minutes at 4 °C, and the top 20 μ L of supernatant was transferred to an LC-MS vial (Thermo Scientific, 03-452-259) ran for LC-MS analysis.

Metabolite quantitation of resolubilized tumor extracts was performed using a Q Exactive HF-X Hybrid Quadrupole-Orbitrap Mass Spectrometer equipped with an Ion Max API source and H-ESI II probe, coupled to a Vanquish Flex Binary UHPLC system (Thermo Scientific). Mass calibrations were completed at least every 5 days in positive and negative polarity modes using LTQ Velos ESI Calibration Solution (Pierce).

Metabolites were chromatographically separated by injecting 1 μ L into a SeQuant ZIC-pHILIC Polymeric column (2.1x150 mm 5 mM, EMD Millipore). The flow rate was set to 150 mL/min, with autosampler temperature set to 10 °C, and column temperature set to 30 °C. Mobile Phase A consisted of 20 mM ammonium carbonate and 0.1% (v/v) ammonium hydroxide, and Mobile Phase B consisted of 100% acetonitrile. The sample was gradient eluted (%B) from the column as follows: 0–20 min.: linear gradient from

85% to 20 % B; 20–24 min.: hold at 20% B; 24–24.5 min.: linear gradient from 20% to 85% B; 24.5 min.-end: hold at 85% B until equilibrated with ten column volumes. Mobile Phase was directed into the ion source with the following parameters: sheath gas = 45, auxiliary gas = 15, sweep gas = 2, spray voltage = 2.9 kV in the negative mode or 3.5 kV in the positive mode, capillary temperature = 300 °C, RF level = 40%, auxiliary gas heater temperature = 325 °C. Mass detection was conducted with a 240,000 mass resolution in full scan mode, with an AGC target of 3,000,000 and maximum injection time of 250 msec. Metabolites were detected over a mass range of 70–1050 m/z. Quantitation of metabolites was performed using Tracefinder 4.1 (Thermo Scientific) referencing an in-house metabolite standards library using ≤ 5 ppm mass error.

IMpower133 analyses

RNA-seq data and whole exome sequencing data from IMpower133 samples were processed as previously described.¹¹⁹ In brief, RNA-seq reads were aligned to the human reference genome (NCBI Build 38) and adjusted for gene length using transcript-per-million (TPM) normalization and subsequently log₂-transformed. Sample-level gene signature scores were calculated as the mean cohort-wide z-score for all the genes in the signature. For Kaplan-Meier analyses, samples were dichotomized by the cohort-wide median using KEAP1/NRF2 11-gene (*G6PD*, *ABCC2*, *TXNRD1*, *GSR*, *PRDX1*, *TXN*, *HMOX1*, *ME1*, *GCLC*, *NQO1*, *GCLM*) signature score. KEAP1 and NFE2L2 mutations were called from whole-exome libraries from tumor DNA and matched germline DNA as previously described.¹¹⁹ Variants were called by three variant callers (Mutect2, LoFreq, and Strelka)¹²⁰⁻¹²² and nonsynonymous variants were only

reported if identified by 2 out of 3 variant callers. AlphaMissense annotation for hg38 genome was used to assess potential pathogenicity of the missense alterations.¹²³

Statistical Analysis

cDNA Screen Analysis

Differential abundance analysis between the cis-eto, saline, and P0 groups was performed using edgeR version 3.36.0 based on the quasi-likelihood negative binomial regression pipeline.¹²⁴ cDNA counts were normalized using the trimmed mean of M values (TMM) method.¹¹⁸ Estimate of dispersion and regression parameters were weighted according to a robust-regression algorithm to minimize the influence of potential outliers.¹²⁵ Multiple testing was accounted for using the Benjamini-Hochberg (BH) procedure to control the false discovery rate (FDR).¹²⁶

CRISPRko and CRISPRa Screen Analyses

Differential abundance analysis between the cis-eto, saline, and P0 groups in the focused CRISPRko and CRISPRa screens used MAGeCK version 0.5.9.⁶⁹ Samples were pooled to increase gRNA coverage, defined as the proportion of gRNAs present. In the SCLC focused library screens, individual samples were computationally pooled after read alignment. Samples were randomly assigned to pools and the samples from each pool were treated as technical replicates and combined using the mageck count command. To help select the number of samples per pool, 10 random assignments were generated for each pool size and the relationship between gRNA coverage versus pool size was visualized using boxplots. Pool size was selected based on the saline

group where gRNA coverage was at least 90% across all cases and predominantly >99%. After pooling, gRNA counts were median-normalized by MAGeCK. The gRNA-level differences were summarized and ranked at the gene-level using robust rank aggregation (RRA) score generated by the MAGeCK pipeline and the median log₂ fold change. Gene- and gRNA-level p-values were adjusted for multiple testing using the BH FDR procedure. edgeR was also used in analysis of the CRISPRa screen and was the basis for the volcano plots shown.¹²⁴

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Appendix: Tables

Table 1: SC151 cDNA screen analysis and results

Gene	CIS-ETO vs. P0			SAL vs. P0		
	Log2(FC)	Unadj. p	Adj. p	Log2(FC)	Unadj. p	Adj. p
MYCN	6.52	6.9E-07	3.5E-05	3.58	8.7E-04	1.1E-02
MYC	5.66	1.9E-11	3.4E-09	4.69	2.7E-09	3.1E-07
MYCL	3.93	3.2E-06	1.3E-04	3.22	7.8E-05	1.6E-03
TUBA3D	3.37	2.4E-04	4.4E-03	1.69	4.4E-02	1.2E-01
CCND1	2.39	5.6E-08	3.9E-06	2.73	1.6E-08	1.4E-06
TMEM241	2.30	4.3E-16	1.5E-13	2.19	2.4E-14	8.5E-12
TRIP13	1.79	7.7E-10	9.1E-08	1.70	2.2E-08	1.6E-06
ZBP2	1.73	8.2E-04	9.5E-03	1.66	2.3E-03	1.6E-02
CAPN1	1.59	1.4E-02	6.3E-02	1.27	7.0E-02	1.7E-01
SDHA	1.38	2.7E-04	4.5E-03	1.29	1.5E-03	1.4E-02
CEACAM3	1.38	6.1E-04	7.8E-03	1.18	5.0E-03	2.7E-02
TMEM231	1.35	1.2E-04	2.8E-03	1.24	8.5E-04	1.1E-02
PPP1R1B	1.16	5.0E-04	6.8E-03	1.02	4.3E-03	2.5E-02
RNASE4	1.09	4.4E-06	1.5E-04	1.21	3.1E-06	1.0E-04
PPL	1.08	5.3E-03	3.4E-02	0.73	7.9E-02	1.8E-01
CACNA2D4	1.04	8.3E-04	9.5E-03	0.76	2.0E-02	7.0E-02
ACP5	1.03	3.2E-03	2.6E-02	0.75	4.5E-02	1.2E-01
HMGCLL1	0.99	3.0E-03	2.5E-02	0.93	9.9E-03	4.4E-02
NAB1	0.96	1.4E-01	2.7E-01	-0.35	5.0E-01	6.9E-01
HRas_G12V	0.87	1.1E-05	2.9E-04	0.71	6.0E-04	8.8E-03
SLFN5	0.86	6.4E-03	3.8E-02	0.88	1.1E-02	4.7E-02
NINJ2	0.84	1.8E-04	3.6E-03	1.00	6.9E-05	1.5E-03
POU5F1B	0.80	3.4E-03	2.6E-02	0.71	1.8E-02	6.5E-02
HOXB2	0.79	4.5E-04	6.4E-03	0.53	2.5E-02	7.7E-02
PRMT8	0.78	3.5E-03	2.6E-02	0.44	1.2E-01	2.5E-01
C2orf88	0.75	7.7E-03	4.2E-02	0.95	2.5E-03	1.7E-02
PMS1	0.74	6.2E-04	7.8E-03	0.64	5.3E-03	2.7E-02
KLF5	0.73	3.0E-03	2.5E-02	0.58	2.9E-02	8.7E-02
ZNF221	0.72	3.5E-03	2.6E-02	0.82	2.6E-03	1.7E-02
MFSD2A	0.71	1.9E-02	8.0E-02	0.46	1.6E-01	3.0E-01
SLC9B1	0.69	3.1E-02	1.1E-01	0.18	6.0E-01	7.6E-01
TCEA2	0.69	2.2E-05	5.5E-04	0.46	6.5E-03	3.1E-02
KCNA5	0.69	3.6E-02	1.2E-01	0.23	5.1E-01	6.9E-01
HPV16_E6	0.67	1.6E-03	1.6E-02	0.60	1.1E-02	4.6E-02
TCEAL7	0.66	4.2E-03	2.9E-02	0.85	1.0E-03	1.2E-02
ADIPOR2	0.64	1.8E-03	1.7E-02	0.66	3.7E-03	2.2E-02
IFNGR2	0.64	5.8E-03	3.5E-02	0.66	9.9E-03	4.4E-02
GRB7	0.63	2.0E-03	1.9E-02	0.51	2.0E-02	7.0E-02
ZER1	0.63	5.8E-03	3.5E-02	0.21	3.9E-01	5.7E-01
HSD17B11	0.61	2.1E-02	8.2E-02	0.89	3.0E-03	1.8E-02
FEN1	0.56	3.3E-04	5.3E-03	0.47	5.2E-03	2.7E-02
Lrrc14b	0.56	1.7E-04	3.6E-03	0.83	1.4E-06	6.8E-05
PPFIA1	0.55	7.7E-02	1.8E-01	0.17	6.2E-01	7.7E-01
ANG	0.51	6.7E-02	1.7E-01	0.13	6.7E-01	8.0E-01
BCL2L1	0.51	3.9E-03	2.8E-02	0.51	7.9E-03	3.6E-02
ZC2HC1C	0.49	1.0E-02	5.2E-02	0.73	9.1E-04	1.1E-02
EYA2	0.48	7.1E-03	4.1E-02	0.49	1.4E-02	5.5E-02
EDDM3B	0.47	7.4E-03	4.1E-02	0.58	2.9E-03	1.8E-02
RNASE7	0.45	5.1E-03	3.3E-02	0.71	1.1E-04	2.1E-03
SLC6A19	0.45	2.0E-02	8.0E-02	0.25	2.3E-01	4.0E-01
RNASE1	0.42	3.0E-02	1.1E-01	0.50	2.1E-02	7.0E-02
CEP70	0.40	4.2E-02	1.3E-01	0.15	5.0E-01	6.9E-01
WNK1	0.38	3.2E-03	2.6E-02	0.37	7.9E-03	3.6E-02
KCNMB3	0.38	1.2E-02	5.6E-02	0.51	2.7E-03	1.7E-02
OS9	0.37	4.5E-02	1.3E-01	0.53	1.3E-02	5.3E-02
KCNA1	0.36	4.5E-02	1.3E-01	0.50	1.4E-02	5.5E-02
PARP11	0.35	1.5E-02	6.7E-02	0.55	9.9E-04	1.2E-02
INTU	0.35	9.0E-03	4.8E-02	0.49	1.2E-03	1.2E-02
SERPINA10	0.33	3.9E-02	1.2E-01	0.52	5.5E-03	2.7E-02
SOX2	0.32	4.8E-01	6.3E-01	0.70	1.4E-01	2.7E-01
PNMT	0.31	1.1E-01	2.3E-01	0.29	1.8E-01	3.3E-01
GABRA5	0.30	3.6E-02	1.2E-01	0.54	1.2E-03	1.2E-02
RNASE6	0.30	4.5E-02	1.3E-01	0.49	5.2E-03	2.7E-02
GPR119	0.29	4.9E-02	1.4E-01	0.54	1.9E-03	1.5E-02
CD180	0.29	4.3E-02	1.3E-01	0.37	2.2E-02	7.2E-02
MRPL47	0.28	6.9E-02	1.7E-01	0.11	5.1E-01	6.9E-01
STMN3	0.28	2.0E-02	8.0E-02	0.31	2.0E-02	7.0E-02

C12orf5	0.28	3.6E-02	1.2E-01	0.21	1.5E-01	2.8E-01
SLITRK6	0.28	2.2E-01	3.6E-01	-0.24	3.4E-01	5.3E-01
MFSD6	0.27	2.4E-02	9.0E-02	0.07	6.2E-01	7.7E-01
ERC1	0.27	1.1E-01	2.4E-01	0.61	2.2E-03	1.6E-02
FAM111B	0.27	6.9E-02	1.7E-01	0.42	1.4E-02	5.5E-02
TGIF1	0.26	3.1E-02	1.1E-01	0.15	2.7E-01	4.5E-01
ZNF462	0.25	8.5E-02	1.9E-01	0.41	1.5E-02	5.8E-02
TXNDC11	0.25	5.1E-02	1.4E-01	0.46	2.0E-03	1.5E-02
RFX7	0.25	3.6E-01	5.2E-01	0.26	3.8E-01	5.6E-01
MFN1	0.24	6.0E-02	1.6E-01	0.28	5.3E-02	1.4E-01
STK10	0.24	7.0E-01	8.0E-01	0.32	6.4E-01	7.8E-01
NYNRIN	0.23	1.3E-01	2.7E-01	0.32	6.5E-02	1.6E-01
AKT2	0.23	8.3E-02	1.9E-01	0.50	1.2E-03	1.2E-02
HIBCH	0.22	1.5E-01	2.8E-01	0.51	5.1E-03	2.7E-02
HNRNPC	0.22	1.3E-01	2.7E-01	0.10	5.2E-01	7.0E-01
GNB4	0.22	1.7E-01	3.2E-01	0.30	9.5E-02	2.1E-01
PNLIP	0.22	1.4E-01	2.8E-01	0.73	6.5E-05	1.5E-03
ANO2	0.21	6.9E-01	7.9E-01	0.43	4.5E-01	6.4E-01
TRMT2A	0.21	1.0E-01	2.2E-01	0.16	2.6E-01	4.4E-01
GCLC	0.21	7.2E-02	1.8E-01	0.68	2.0E-06	8.8E-05
FBXL13	0.21	1.6E-01	3.0E-01	0.19	2.7E-01	4.5E-01
RAD21	0.21	1.9E-01	3.3E-01	0.15	4.1E-01	6.0E-01
DDX1	0.20	2.6E-01	4.1E-01	-0.05	8.1E-01	8.8E-01
SNX18	0.20	6.4E-02	1.7E-01	0.39	2.0E-03	1.5E-02
LRRC1	0.20	2.0E-01	3.4E-01	-0.03	8.5E-01	9.0E-01
REEP1	0.19	2.4E-01	3.9E-01	0.29	1.2E-01	2.4E-01
GFP	0.19	1.9E-01	3.3E-01	0.14	3.8E-01	5.6E-01
RHNO1	0.19	2.9E-01	4.4E-01	0.34	8.5E-02	1.9E-01
FGF23	0.19	2.3E-01	3.7E-01	-0.09	6.0E-01	7.6E-01
ORMDL1	0.18	5.0E-01	6.5E-01	0.31	3.0E-01	4.8E-01
COPZ1	0.17	1.4E-01	2.8E-01	0.05	7.1E-01	8.1E-01
STARD3	0.16	5.7E-01	6.9E-01	0.50	1.1E-01	2.4E-01
GDPD1	0.15	1.2E-01	2.6E-01	0.03	8.1E-01	8.8E-01
ZNF547	0.15	6.2E-01	7.4E-01	-0.63	8.6E-02	1.9E-01
ATP1B3	0.15	2.6E-01	4.1E-01	0.04	8.0E-01	8.8E-01
TLK2	0.15	1.9E-01	3.3E-01	-0.03	8.3E-01	8.8E-01
LRRC7	0.15	2.5E-01	4.0E-01	0.23	1.1E-01	2.4E-01
FKBP4	0.14	1.3E-01	2.6E-01	0.20	5.1E-02	1.3E-01
DYRK4	0.14	3.6E-01	5.2E-01	0.26	1.3E-01	2.7E-01
ABLIM1	0.13	3.2E-01	4.9E-01	0.06	6.8E-01	8.1E-01
PIK3CA_A1035V	0.13	4.0E-01	5.7E-01	0.41	2.1E-02	7.0E-02
HCRT2	0.12	3.6E-01	5.3E-01	0.14	3.7E-01	5.6E-01
PDS5B	0.12	3.5E-01	5.2E-01	0.37	1.2E-02	4.9E-02
TMEM132B	0.11	2.6E-01	4.1E-01	0.08	4.8E-01	6.6E-01
FAM131A	0.11	3.1E-01	4.8E-01	0.08	5.2E-01	7.0E-01
EPS8	0.11	5.1E-01	6.5E-01	0.33	8.7E-02	1.9E-01
RGS7	0.10	5.1E-01	6.5E-01	0.10	5.8E-01	7.5E-01
HOXB6	0.10	3.2E-01	4.9E-01	0.24	4.9E-02	1.3E-01
LRTM2	0.10	4.2E-01	5.9E-01	0.25	8.6E-02	1.9E-01
ZNF639	0.10	5.6E-01	6.9E-01	0.10	6.0E-01	7.6E-01
TAP63	0.09	3.4E-01	5.1E-01	-0.03	7.7E-01	8.5E-01
SRC	0.09	3.4E-01	5.1E-01	0.05	6.1E-01	7.6E-01
TCAP	0.09	5.0E-01	6.5E-01	0.03	8.2E-01	8.8E-01
CCDC127	0.08	5.3E-01	6.7E-01	0.37	1.1E-02	4.7E-02
STAT1	0.07	6.7E-01	7.9E-01	-0.27	1.5E-01	2.8E-01
KIF5B	0.06	6.7E-01	7.8E-01	0.21	2.1E-01	3.7E-01
SOX5	0.06	5.4E-01	6.8E-01	0.04	7.0E-01	8.1E-01
ZMAT3	0.06	7.3E-01	8.2E-01	0.01	9.6E-01	9.8E-01
ABCC8	0.06	7.0E-01	8.0E-01	-0.03	8.3E-01	8.8E-01
ETV6	0.05	5.4E-01	6.8E-01	-0.12	2.2E-01	3.8E-01
PRKAA1	0.05	6.8E-01	7.9E-01	0.00	9.9E-01	1.0E+00
ERCC6L2	0.05	7.6E-01	8.4E-01	0.26	1.9E-01	3.5E-01
TPPP2	0.05	5.8E-01	7.0E-01	0.19	7.2E-02	1.7E-01
DCUN1D1	0.05	7.5E-01	8.4E-01	-0.04	8.3E-01	8.8E-01
NTF3	0.05	6.9E-01	7.9E-01	0.04	7.6E-01	8.5E-01
MID2	0.05	5.7E-01	6.9E-01	0.15	1.3E-01	2.5E-01
OLAH	0.04	8.3E-01	8.8E-01	0.54	2.1E-02	7.0E-02
PLEKHA3	0.04	6.7E-01	7.9E-01	0.01	9.4E-01	9.7E-01
FLOT2	0.04	7.1E-01	8.0E-01	-0.01	9.3E-01	9.7E-01
CATSPER2	0.03	8.3E-01	8.8E-01	0.26	1.5E-01	2.8E-01
HPV16_E5	0.03	7.5E-01	8.4E-01	0.05	5.9E-01	7.6E-01
PSCA	0.03	8.0E-01	8.6E-01	-0.03	7.7E-01	8.5E-01

CERS3	0.03	7.8E-01	8.4E-01	-0.11	2.7E-01	4.5E-01
RASSF9	0.02	8.8E-01	9.1E-01	-0.22	2.0E-01	3.6E-01
PEG10	0.02	8.9E-01	9.2E-01	0.09	6.5E-01	7.8E-01
SLC6A12	0.02	8.0E-01	8.6E-01	0.12	2.5E-01	4.3E-01
ABCB4	0.02	8.3E-01	8.8E-01	0.07	5.4E-01	7.2E-01
GNL1	0.02	8.6E-01	9.0E-01	0.15	1.6E-01	3.1E-01
CCDC8	0.02	8.9E-01	9.2E-01	-0.24	5.1E-02	1.3E-01
MAST2	0.01	9.7E-01	9.8E-01	-0.21	3.3E-01	5.1E-01
BCL6	0.01	9.6E-01	9.7E-01	-0.03	8.5E-01	9.0E-01
PLCB4	0.00	9.9E-01	9.9E-01	0.02	8.0E-01	8.8E-01
PIK3CA_H1047R	0.00	1.0E+00	1.0E+00	-0.04	7.0E-01	8.1E-01
OR5H6	0.00	9.7E-01	9.8E-01	0.15	3.1E-01	4.9E-01
NDUFA9	-0.01	9.4E-01	9.6E-01	0.00	9.9E-01	1.0E+00
PLEKHG2	-0.01	9.4E-01	9.6E-01	-0.05	6.8E-01	8.1E-01
BRD9	-0.01	9.2E-01	9.4E-01	0.08	4.1E-01	5.9E-01
SPICE1	-0.01	9.2E-01	9.4E-01	-0.04	7.5E-01	8.4E-01
SEMA3E	-0.01	9.4E-01	9.6E-01	0.09	6.6E-01	7.9E-01
UBE3A	-0.02	8.8E-01	9.1E-01	0.04	8.1E-01	8.8E-01
ASAP1	-0.02	8.5E-01	8.9E-01	-0.10	4.5E-01	6.3E-01
VPS33B	-0.02	9.2E-01	9.4E-01	-0.33	2.0E-01	3.6E-01
SLC12A7	-0.02	8.8E-01	9.2E-01	-0.09	6.3E-01	7.7E-01
KLHL31	-0.02	7.6E-01	8.4E-01	-0.12	1.8E-01	3.3E-01
METTL17	-0.03	8.3E-01	8.8E-01	0.08	5.8E-01	7.5E-01
GLS	-0.03	7.7E-01	8.4E-01	-0.06	6.1E-01	7.6E-01
FBXL14	-0.03	8.3E-01	8.8E-01	0.02	8.8E-01	9.2E-01
ITFG2	-0.03	8.2E-01	8.8E-01	-0.07	6.9E-01	8.1E-01
HFM1	-0.03	7.8E-01	8.4E-01	0.02	8.6E-01	9.0E-01
RAD51AP1	-0.03	7.6E-01	8.4E-01	0.09	5.0E-01	6.9E-01
GPR133	-0.04	7.1E-01	8.0E-01	0.04	7.0E-01	8.1E-01
ABTB2	-0.04	7.7E-01	8.4E-01	-0.01	9.6E-01	9.8E-01
NFE2L2	-0.04	6.9E-01	7.9E-01	0.18	1.2E-01	2.5E-01
KIAA0513	-0.04	7.8E-01	8.4E-01	0.15	3.6E-01	5.6E-01
FOXM1	-0.04	7.2E-01	8.0E-01	0.05	7.1E-01	8.1E-01
KIRREL	-0.04	7.6E-01	8.4E-01	0.07	7.0E-01	8.1E-01
STEAP4	-0.05	8.3E-01	8.8E-01	-0.37	1.4E-01	2.7E-01
XRN1	-0.05	7.1E-01	8.0E-01	0.08	6.3E-01	7.7E-01
SLC9A3	-0.05	6.0E-01	7.2E-01	-0.12	3.1E-01	4.9E-01
SYT16	-0.05	6.8E-01	7.9E-01	-0.12	4.2E-01	6.0E-01
FXR1	-0.05	5.7E-01	6.9E-01	-0.07	5.1E-01	6.9E-01
AKT3	-0.06	4.7E-01	6.2E-01	-0.11	2.3E-01	4.0E-01
WDR63	-0.06	5.2E-01	6.6E-01	-0.15	1.4E-01	2.7E-01
TPPP	-0.06	5.6E-01	6.9E-01	0.04	7.3E-01	8.3E-01
KRT24	-0.06	5.9E-01	7.1E-01	-0.06	6.8E-01	8.1E-01
NDRG2	-0.06	5.4E-01	6.7E-01	-0.05	6.5E-01	7.8E-01
ZNF536	-0.07	6.8E-01	7.9E-01	-0.07	7.1E-01	8.1E-01
DNAJC19	-0.07	5.7E-01	6.9E-01	-0.11	4.2E-01	6.0E-01
LETM2	-0.07	4.6E-01	6.2E-01	0.08	4.3E-01	6.1E-01
YAP1	-0.07	4.5E-01	6.1E-01	-0.01	9.4E-01	9.7E-01
MOCOS	-0.08	4.9E-01	6.4E-01	0.07	6.0E-01	7.6E-01
ZNF460	-0.08	4.5E-01	6.1E-01	-0.08	5.0E-01	6.9E-01
CPXCR1	-0.09	4.4E-01	6.1E-01	-0.01	9.3E-01	9.7E-01
ARFGAP1	-0.09	4.8E-01	6.3E-01	-0.04	7.9E-01	8.7E-01
PIK3CA_E545K	-0.09	4.6E-01	6.2E-01	-0.11	4.2E-01	6.0E-01
NID2	-0.09	4.7E-01	6.2E-01	-0.35	1.8E-02	6.5E-02
EGFR	-0.09	3.9E-01	5.6E-01	-0.10	4.3E-01	6.1E-01
DNAAF2	-0.09	2.8E-01	4.3E-01	-0.15	1.4E-01	2.7E-01
VPS4A	-0.09	4.5E-01	6.1E-01	0.05	7.4E-01	8.3E-01
N4BP1	-0.09	5.0E-01	6.4E-01	-0.05	7.3E-01	8.2E-01
PDCD6	-0.10	3.3E-01	4.9E-01	-0.15	1.7E-01	3.1E-01
MYL12A	-0.10	4.4E-01	6.0E-01	-0.13	3.6E-01	5.5E-01
CPNE2	-0.10	5.1E-01	6.5E-01	-0.03	8.8E-01	9.2E-01
WIP1	-0.10	3.3E-01	4.9E-01	-0.12	2.8E-01	4.6E-01
LAMP3	-0.10	4.2E-01	5.9E-01	-0.15	2.9E-01	4.7E-01
AP1G2	-0.10	5.6E-01	6.9E-01	-0.11	5.7E-01	7.5E-01
KLHL23	-0.10	3.9E-01	5.6E-01	-0.21	1.2E-01	2.5E-01
ADORA1	-0.11	2.5E-01	4.0E-01	0.00	1.0E+00	1.0E+00
SCAMP3	-0.11	3.1E-01	4.7E-01	-0.06	6.4E-01	7.8E-01
SYNE2	-0.11	1.9E-01	3.3E-01	-0.16	8.5E-02	1.9E-01
ERBB2	-0.11	2.5E-01	4.0E-01	-0.04	6.9E-01	8.1E-01
NKD2	-0.11	4.3E-01	6.0E-01	-0.26	1.2E-01	2.5E-01
OXGR1	-0.12	3.7E-01	5.4E-01	-0.02	9.1E-01	9.5E-01
CLK1	-0.12	3.6E-01	5.2E-01	0.01	9.6E-01	9.8E-01

RNASE2	-0.12	1.5E-01	2.9E-01	-0.19	5.0E-02	1.3E-01
ZNF667	-0.12	4.3E-01	6.0E-01	-0.36	4.6E-02	1.3E-01
POU4F1	-0.12	2.2E-01	3.7E-01	0.03	7.7E-01	8.5E-01
NRIP2	-0.12	2.5E-01	4.0E-01	-0.15	2.2E-01	3.9E-01
NDUFB5	-0.12	1.9E-01	3.4E-01	-0.11	3.2E-01	4.9E-01
TERT	-0.13	1.9E-01	3.3E-01	-0.20	7.4E-02	1.8E-01
LGMN	-0.13	5.1E-01	6.5E-01	0.13	5.6E-01	7.4E-01
WNT2	-0.13	7.5E-02	1.8E-01	-0.24	3.4E-03	2.0E-02
PPFIA2	-0.13	2.1E-01	3.6E-01	-0.33	6.1E-03	3.0E-02
HPV16_E7	-0.13	3.1E-01	4.8E-01	-0.06	6.9E-01	8.1E-01
HPV16_E2	-0.13	1.1E-01	2.3E-01	-0.02	8.2E-01	8.8E-01
MED12L	-0.14	3.2E-01	4.8E-01	-0.24	7.9E-02	1.8E-01
SCN4A	-0.14	2.1E-01	3.5E-01	-0.18	1.4E-01	2.8E-01
MARK3	-0.14	1.7E-01	3.2E-01	-0.03	8.2E-01	8.8E-01
CNKSR1	-0.14	1.8E-01	3.3E-01	-0.28	2.2E-02	7.1E-02
TLR1	-0.14	1.4E-01	2.7E-01	-0.25	2.2E-02	7.1E-02
ZC3H18	-0.14	5.5E-01	6.8E-01	-0.24	3.7E-01	5.6E-01
SLC39A2	-0.14	1.5E-01	2.9E-01	-0.01	9.6E-01	9.8E-01
TTC14	-0.14	9.9E-02	2.2E-01	-0.09	3.6E-01	5.5E-01
GABRA3	-0.15	1.3E-01	2.7E-01	-0.22	4.8E-02	1.3E-01
MAPK9	-0.15	1.1E-01	2.4E-01	-0.09	3.7E-01	5.6E-01
MB21D2	-0.15	2.0E-01	3.4E-01	-0.10	4.5E-01	6.3E-01
NRG4	-0.15	8.9E-02	2.0E-01	0.00	9.8E-01	9.9E-01
FDXR	-0.15	7.1E-02	1.8E-01	-0.19	4.8E-02	1.3E-01
AGBL2	-0.15	4.9E-01	6.4E-01	-0.12	6.3E-01	7.8E-01
CACNA1C	-0.16	2.3E-01	3.7E-01	-0.27	7.8E-02	1.8E-01
IKZF3	-0.16	4.5E-02	1.3E-01	-0.11	2.3E-01	4.0E-01
MCCC2	-0.16	3.6E-02	1.2E-01	-0.22	1.4E-02	5.5E-02
VPS35	-0.16	6.4E-01	7.6E-01	-2.27	2.8E-05	7.0E-04
DLGAP1	-0.17	1.5E-01	2.8E-01	-0.29	3.0E-02	8.9E-02
CADPS2	-0.17	4.9E-02	1.4E-01	-0.31	2.1E-03	1.6E-02
FOXA1	-0.17	1.8E-01	3.3E-01	-0.15	3.1E-01	4.9E-01
MLIP	-0.17	2.4E-01	3.9E-01	-0.05	7.6E-01	8.5E-01
ZNF785	-0.17	1.9E-01	3.3E-01	0.19	2.0E-01	3.7E-01
TTL6	-0.17	5.9E-02	1.6E-01	-0.20	5.8E-02	1.5E-01
CCND2	-0.17	8.6E-02	2.0E-01	-0.25	3.4E-02	9.9E-02
TUBGCP6	-0.17	2.5E-01	4.0E-01	-0.23	1.7E-01	3.1E-01
CCDC136	-0.18	3.8E-02	1.2E-01	-0.22	2.4E-02	7.7E-02
OPN3	-0.18	2.7E-02	9.7E-02	-0.11	2.3E-01	4.0E-01
WIPF2	-0.18	4.5E-01	6.1E-01	-0.34	2.1E-01	3.7E-01
RPP40	-0.18	1.5E-02	6.5E-02	-0.33	1.4E-04	2.5E-03
SLC6A3	-0.19	1.6E-01	2.9E-01	0.09	5.6E-01	7.3E-01
HRas_WT	-0.19	1.3E-01	2.6E-01	-0.35	1.3E-02	5.1E-02
PGAP3	-0.19	5.6E-02	1.5E-01	-0.13	2.7E-01	4.5E-01
BRAF_V600E	-0.19	2.1E-01	3.5E-01	0.08	6.3E-01	7.8E-01
BMP5	-0.19	2.0E-01	3.4E-01	-0.26	1.2E-01	2.5E-01
ATP11B	-0.19	8.8E-02	2.0E-01	-0.05	7.1E-01	8.1E-01
HEXIM2	-0.19	1.2E-01	2.4E-01	-0.34	1.6E-02	5.9E-02
SNX8	-0.19	6.4E-02	1.7E-01	-0.13	2.8E-01	4.6E-01
RBL1	-0.20	7.7E-02	1.8E-01	-0.07	5.9E-01	7.6E-01
CIART	-0.20	4.0E-01	5.7E-01	0.22	4.0E-01	5.9E-01
NCSTN	-0.20	6.5E-02	1.7E-01	-0.27	3.0E-02	8.9E-02
EYA4	-0.20	7.5E-02	1.8E-01	0.09	5.1E-01	6.9E-01
LINC00966	-0.20	2.0E-02	8.0E-02	-0.32	1.7E-03	1.4E-02
KCNMB2	-0.20	1.0E-02	5.2E-02	-0.29	1.5E-03	1.4E-02
KCNA6	-0.20	1.5E-02	6.6E-02	-0.24	1.2E-02	5.0E-02
ZNF219	-0.21	2.3E-02	8.7E-02	-0.29	5.0E-03	2.7E-02
NR1H4	-0.21	1.1E-01	2.4E-01	-0.09	5.4E-01	7.1E-01
WDR52	-0.21	4.4E-02	1.3E-01	-0.11	3.8E-01	5.6E-01
MCCC1	-0.22	1.3E-01	2.6E-01	-0.17	3.0E-01	4.8E-01
TINAG	-0.22	3.8E-01	5.5E-01	-0.12	6.5E-01	7.8E-01
CLPTM1L	-0.22	3.0E-02	1.1E-01	-0.28	1.7E-02	6.1E-02
HNRNPA3	-0.22	1.3E-02	6.2E-02	-0.28	5.3E-03	2.7E-02
ARHGEF40	-0.22	6.6E-02	1.7E-01	-0.11	4.1E-01	6.0E-01
MSTN	-0.22	7.2E-02	1.8E-01	-0.15	2.9E-01	4.8E-01
CFHR4	-0.22	4.0E-02	1.3E-01	-0.25	4.4E-02	1.2E-01
OR11L1	-0.22	4.7E-01	6.2E-01	-0.24	4.6E-01	6.4E-01
USH1C	-0.23	4.9E-01	6.4E-01	0.02	9.6E-01	9.8E-01
NPHP3	-0.23	4.8E-01	6.3E-01	-0.90	2.5E-02	7.7E-02
SLC52A2	-0.23	6.6E-03	3.9E-02	-0.36	2.8E-04	4.5E-03
PLEKHG4B	-0.23	6.4E-02	1.7E-01	-0.45	1.8E-03	1.4E-02
AFF2	-0.24	4.0E-01	5.7E-01	-0.24	4.6E-01	6.4E-01

RNASE3	-0.24	3.3E-02	1.1E-01	-0.27	3.6E-02	1.0E-01
SLC30A8	-0.24	7.8E-02	1.8E-01	-0.23	1.5E-01	2.8E-01
DCP1B	-0.24	1.3E-01	2.6E-01	-0.09	6.4E-01	7.8E-01
OSGEPL1	-0.25	3.3E-01	4.9E-01	-0.48	1.0E-01	2.2E-01
HDX	-0.25	4.8E-02	1.4E-01	-0.27	6.3E-02	1.6E-01
HPV16_E1	-0.25	1.1E-02	5.4E-02	-0.35	2.2E-03	1.6E-02
B4GALNT3	-0.25	6.1E-02	1.6E-01	-0.21	1.9E-01	3.5E-01
ACTL6A	-0.26	5.6E-02	1.5E-01	-0.26	8.3E-02	1.9E-01
CD44	-0.27	3.7E-03	2.7E-02	-0.33	1.9E-03	1.5E-02
OPA3	-0.27	8.7E-02	2.0E-01	-0.37	3.8E-02	1.1E-01
KLF3	-0.27	7.7E-02	1.8E-01	-0.07	7.0E-01	8.1E-01
STAT2	-0.27	7.4E-02	1.8E-01	-0.40	2.1E-02	7.0E-02
FRMD7	-0.28	7.3E-03	4.1E-02	-0.26	2.3E-02	7.4E-02
EXOC3	-0.28	3.5E-02	1.2E-01	-0.15	3.1E-01	4.9E-01
Kcna4	-0.28	8.7E-03	4.7E-02	-0.42	6.9E-04	9.4E-03
STAT4	-0.28	6.1E-01	7.3E-01	-1.19	8.2E-02	1.9E-01
AQP4	-0.28	2.8E-02	9.9E-02	-0.17	2.5E-01	4.2E-01
CACNG6	-0.29	1.1E-02	5.3E-02	-0.45	6.8E-04	9.4E-03
COL5A2	-0.29	1.8E-02	7.5E-02	-0.44	1.7E-03	1.4E-02
ENPP4	-0.29	6.8E-04	8.3E-03	-0.25	9.9E-03	4.4E-02
AGPS	-0.30	2.0E-02	8.0E-02	-0.44	2.9E-03	1.8E-02
HDAC10	-0.30	2.3E-02	8.7E-02	-0.36	1.9E-02	6.7E-02
RAF1	-0.30	1.4E-02	6.2E-02	-0.16	2.6E-01	4.4E-01
FGF6	-0.30	2.6E-02	9.6E-02	-0.42	7.0E-03	3.3E-02
NBPF15	-0.31	4.3E-03	2.9E-02	-0.28	2.0E-02	7.0E-02
PBX2P1	-0.31	4.0E-02	1.3E-01	-0.37	3.0E-02	8.9E-02
ANKRD17	-0.32	6.3E-01	7.4E-01	-0.94	1.5E-01	2.8E-01
CNST	-0.32	1.3E-02	6.0E-02	-0.23	1.0E-01	2.2E-01
ACACB	-0.32	1.1E-01	2.4E-01	-0.38	9.7E-02	2.1E-01
CCDC97	-0.32	4.1E-04	6.2E-03	-0.42	8.2E-05	1.6E-03
MET	-0.32	2.5E-04	4.4E-03	-0.44	2.2E-05	6.1E-04
ZCCHC11	-0.33	1.1E-03	1.1E-02	-0.23	4.8E-02	1.3E-01
FADD	-0.33	2.5E-03	2.2E-02	-0.24	5.1E-02	1.3E-01
CLIP4	-0.34	1.1E-01	2.4E-01	-0.45	6.8E-02	1.7E-01
LPIN2	-0.35	1.0E-02	5.2E-02	-0.59	2.5E-04	4.2E-03
RNASE8	-0.36	2.6E-03	2.3E-02	-0.34	1.2E-02	5.1E-02
USP13	-0.36	1.5E-04	3.3E-03	-0.50	8.3E-06	2.4E-04
RNFT1	-0.37	1.4E-01	2.7E-01	-0.49	8.5E-02	1.9E-01
PEX5L	-0.38	9.5E-04	1.0E-02	-0.40	2.5E-03	1.7E-02
UMODL1	-0.38	2.7E-01	4.3E-01	-0.67	1.0E-01	2.2E-01
VPS16	-0.39	9.9E-04	1.1E-02	-0.43	1.6E-03	1.4E-02
MAPK8IP2	-0.39	5.6E-02	1.5E-01	-0.13	5.7E-01	7.5E-01
DZIP3	-0.40	9.9E-06	2.9E-04	-0.56	1.5E-07	9.0E-06
CES1P1	-0.40	1.6E-03	1.6E-02	-0.15	3.1E-01	4.9E-01
MYO1B	-0.41	2.1E-01	3.5E-01	0.21	5.4E-01	7.2E-01
SOCS5	-0.43	4.6E-06	1.5E-04	-0.51	2.5E-06	8.8E-05
TEAD4	-0.43	1.3E-01	2.7E-01	-0.76	2.5E-02	7.7E-02
POLR3A	-0.45	5.7E-03	3.5E-02	-0.53	4.2E-03	2.5E-02
BTK	-0.45	5.8E-02	1.6E-01	-0.59	2.9E-02	8.7E-02
GEN1	-0.46	3.9E-03	2.8E-02	-0.60	1.1E-03	1.2E-02
NFIB	-0.47	4.8E-02	1.4E-01	-0.92	1.2E-03	1.2E-02
PRKCE	-0.47	2.1E-01	3.5E-01	-0.47	2.6E-01	4.4E-01
MED11	-0.48	1.4E-02	6.2E-02	-0.61	6.3E-03	3.0E-02
GALNT8	-0.48	8.6E-07	3.8E-05	-0.38	5.0E-04	7.6E-03
FSTL1	-0.48	1.5E-01	2.8E-01	-1.17	5.4E-03	2.7E-02
ZNF563	-0.50	9.6E-02	2.1E-01	-0.84	1.6E-02	5.9E-02
NRD1	-0.52	1.2E-01	2.5E-01	0.05	9.0E-01	9.4E-01
ACBD5	-0.54	1.8E-01	3.2E-01	-0.79	7.4E-02	1.8E-01
NFATC3	-0.58	1.9E-08	1.7E-06	-0.73	1.3E-09	2.3E-07
MYL12B	-0.65	1.9E-07	1.1E-05	-0.67	2.5E-06	8.8E-05
RAD52	-0.66	7.9E-03	4.3E-02	-0.51	6.8E-02	1.7E-01
FGFR1	-0.71	3.4E-02	1.2E-01	0.17	6.1E-01	7.6E-01
PXDN	-0.91	5.6E-02	1.5E-01	-0.91	9.2E-02	2.0E-01
ZBTB32	-1.13	1.3E-02	6.0E-02	0.01	9.7E-01	9.9E-01
C12orf4	-1.14	4.3E-02	1.3E-01	-0.47	3.7E-01	5.6E-01
TARBP1	-1.19	2.3E-02	8.7E-02	-1.02	1.2E-01	2.4E-01
TRPM6	-1.20	1.9E-02	8.0E-02	-1.20	3.9E-02	1.1E-01
CD226	-1.22	1.9E-02	8.0E-02	-1.20	4.7E-02	1.3E-01
NFIL3	-1.23	4.7E-03	3.1E-02	-1.67	1.1E-03	1.2E-02
MEFV	-2.03	4.4E-04	6.4E-03	-1.25	7.2E-02	1.7E-01

Table 2: SCLC focused CRISPR knockout library composition

Gene	Sequence	Gene	Sequence	Gene	Sequence	Gene	Sequence
AKT3	TTATAATCAGATGTCCTCAG	EPHA5	TGTTATGAACTGAATACAG	MAP2K4	TGGATAAGGAAATCGGCCTG	RPL22L1	AAGGTCCAAATTAACCTCC
AKT3	ATTTCACTGTAGATATCCAG	EPHA5	ATACAGTTCAAATGGACCGTG	MAP2K4	CAACTAACACAAGTCGTGAA	RPL22L1	CGGAGAAGGTTTAAAGTCAA
AKT3	TGGACTCATGTGACAAATGAG	EPHA5	ATCAGTAGGTAAATGGCTGAG	MAP2K4	TCTCAAGAATTAATCAAGCTG	RPL22L1	GGAGACAATTTCTACGGGAGA
AKT3	ACTGCATGGCAATGAGGAGG	EPHA5	TCAGAATGGGAGAACAATCA	MAP2K4	GACCCAAGCCGACATCAAGCA	RPL22L1	CTACTCTACCCAGTAGAAGA
AKT3	TAGAAAATTTGAGGAAATG	EPHA5	CTGGGGGCTACAGATCAGT	MAP2K4	CTTCCAGAGAATAATTGGA	RPL22L1	CTACTTCTACTGGATGAGTA
AKT3	TCTCTATAACAGTAGTCCAC	EPHA5	ATACCAAGTATGCCAAGTGA	MAP2K4	TTACGAAGGATGAATCCAAA	RPL22L1	AATGGGAAAATCCGAAAATCT
ALDH3A1	CCAGTCCCGGGTGTGCACAG	EPHA7	TGGTTTCAGATTAATATGG	MAP2K7	CATTCTGGGCAAGATGACAG	RPTOR	TCATGAGCTCAGGAGCCGTG
ALDH3A1	TTAGTGGCCGGCACTCCAG	EPHA7	AATCCACATTAGCTGTGTA	MAP2K7	GCACGATGTAGGGGCACTGC	RPTOR	AACAACATCAAGTACTACGA
ALDH3A1	CGTGTGCGTGCCAGCCTCGG	EPHA7	TTATGCGTTTACCAGCAACCC	MAP2K7	CGAGGCTCCATACCTCGGCC	RPTOR	CGTCTCTGAGCTCATGAGG
ALDH3A1	TTGCATCTCTGCGCCCTTCGG	EPHA7	TCCATTAATAATCTGAAACC	MAP2K7	AATGCGGGGCTCCGGGAACA	RPTOR	TTCCACCGGCTCACTCATCG
ALDH3A1	GATGTGGACGATGACATCGT	EPHA7	CCTTTGTTCAGTGTGGAGAA	MAP2K7	CATCCTCATGGACCTGGATG	RPTOR	ATGCGATAGCTCCGGCTGG
ALDH3A1	ACTGGGGTCCAGCTCCGCTG	EPHA7	AATGTTGGATTTGTGCCAAA	MAP2K7	CCGGATGTCATAGTCCGGCT	RPTOR	GGCCACCCAGATGAGTGA
ALDOA	CATTGGACCAGAGAACACCG	EPHB1	GCTGAGCCAGTATCCACCG	MAP3K1	TGGCTTTGCAAAACCAACA	RUNX1	CTCTTGCCGCAAAACCTGG
ALDOA	CAAGTTATCAAAATCAAAGG	EPHB1	AGGCAAGAGGGAATCTACG	MAP3K1	TGTTTTCTGCATTCATGG	RUNX1	GAGTGGTTCCAGGAGGCACG
ALDOA	CCCAATGACAGGGTTCCAG	EPHB1	GATCTGAGGTGCTATCCTGG	MAP3K1	GTAAATTTGCTCTCTCACCG	RUNX1	GGAGCTTGTCTTTCCGAG
ALDOA	AGGTGGCTCCAGGTAGTAG	EPHB1	TGTGATGATGCACGCTCCAG	MAP3K1	TAAGAGCTCAACAGTATGGA	RUNX1	AGCTGCGGCGACAGCCATG
ALDOA	CCCAATTTCTCCCTCCAGG	EPHB1	CGCTGCGGAGTTCTGAGTG	MAP3K1	TGGCTGAAAGGTCAACAGAT	RUNX1	TGCCATCTGGAACATCCCCT
ALDOA	TGACAGCGGGGGCCACTGTG	EPHB1	CATACCACAAGCTGGATCA	MAP3K1	TGATGTTGGATGATTCAGA	RUNX1	GGTCAATTAATCTTGCAACC
ALK	TGGTCTCTGAGTCTATCGAG	ERBB3	TGATCCAGCAGAGAACCCAG	MAP3K11	CTACGCCATAGGCCACAGCA	S100G	GAGTACTAAAAGTGTCTCTG
ALK	TGTCCATTTCCACAAGATGA	ERBB3	ATCATGTAGAGCAACCCCGG	MAP3K11	AGTCGCCCTAGAGAGGTTGG	S100G	AGTCTCTGAAAGGATCTGAG
ALK	ACCACCCACTCTCAATGCG	ERBB3	AAAGTCAATGAGGCAAGAG	MAP3K11	ACCGGGGAGGTGCCATACCG	S100G	TGATCTGAGACCGATTGTCAA
ALK	GAGGCCGTGTGACTTCGCC	ERBB3	AGCTGCAATTAAGACTTTTG	MAP3K11	GCCCGCCGCACTATTGTG	S100G	GTCTTGAAAGGATGATGAG
ALK	AGGGTCCCTGAGCTCCACTG	ERBB3	GTCCACAGCAGCTTCAAGT	MAP3K11	CATCCAGCCGATAGGTGCCG	S100G	TTTCAAGAGCTGCAACAAGT
ALK	AACNTTGAAGATGGCTTCTG	ERBB3	GGCCGGTATCAGAAAGTCC	MAP3K11	AGGCACTAATGCCACGGTA	S100G	ATACTTTTCTACTAATAT
ALOX12B	ACACCCGCAAGCTGTCACTG	ERBB4	CTGTGCTTGAGGATTAAGCA	MAP3K13	ACGGAAGAAAATGAAATTCAG	SCML1	GTCTTCTGCGAGATCCCTG
ALOX12B	TGGGAAGTGTGGCAGTCCAGG	ERBB4	ATTGTGCTCAGTGTGAAAGG	MAP3K13	TATAGGCTGAGTCACTCCCT	SCML1	ATTAAGTCTCAGAGAATATCTG
ALOX12B	GTCCATGAAGGTCTCCAGAG	ERBB4	CAGGCACTGGAACCTGTAGAG	MAP3K13	CATCCAGACTCAATATGCA	SCML1	TAAGCACCCTCAACCTGGT
ALOX12B	ATATCGATCAGCTCAGGCA	ERBB4	TGATGAATTTCAATGACAG	MAP3K13	GTCTGACTCCAGATTTGTG	SCML1	ACAAAGGCCAATATGCAAG
ALOX12B	TTACCCGAGTAGCCACGCCG	ERBB4	TGGCAGCAGCTCACTGACCTA	MAP3K13	TATCATCCATCCCAATGCCA	SCML1	GATCCACTGACTCGGAGTG
ALOX12B	GCGATGACAGCTTGCCGGTG	ERBB4	GGTGGTGGATTGTAGACAA	MAP3K13	GGGTGTGCTTTGTAGTTCC	SCML1	GCCACTGGTCTCCACGGCT
AMER1	GGCCTGTGAGAAACTCAGAG	ERCC4	TGAAGTCCGCGCAAGATAGC	MAX	GGTGTAGAGGCTGTTGTCTG	SEMA6C	AGGCATCAATCTCTCCAGG
AMER1	CTCGGGGTAGACAATCCCTG	ERCC4	AAAGCCGCTTTCTTGTTGG	MAX	GGTAGCTTGAATGAAGGTTG	SEMA6C	AGGTGAGACATCAACGGG
AMER1	GCAGTCCAAGTATCCGAGG	ERCC4	TTTCGCCAAAACAACAACG	MAX	ATGCACTGGAAGCAAAACCT	SEMA6C	GGACAGCCCAACAGCCAGA
AMER1	AAGCTGAGTAACTCCCGCG	ERCC4	AGACTATCACTCTGGAG	MAX	TCCGTCAGCTGGAGAAAGCG	SEMA6C	TGATGCTGCACCTCATCA
AMER1	TAAAGCCAGTCATCCAGG	ERCC4	AGAAAGCAACCCAAAGTGG	MAX	AACGAGGAAAGCTCCCGGA	SEMA6C	CTGCTAGTGAAGTGAATG
AMER1	TCCCGGTGGGAAATCTGAG	ERCC4	TGTGAGGAAACTGTATCTG	MAX	GACTCAGTCCCACTCACTCA	SEMA6C	CCTACTGACCCAGATGCTG
ANKRD11	CCACCCCTTATGACCCCGG	ESR1	GGGATACGAAAGACCGAAG	MBOAT4	GAAAGCAGAAGGTCCACCTG	SNP2	TATCTAAATTAAGTCTTGG
ANKRD11	CGGCTCTCAGCCACTACGG	ESR1	GACCACTTGATAAAAACAGG	MBOAT4	GTGCAGACTAGGTCAGCA	SNP2	TTTTACATGAAATCTTGG
ANKRD11	ATCTTGGTAGCCTGCACTG	ESR1	CAAGCCAGTCACTCTGTTG	MBOAT4	AGCAGGGGTGAAGACGAGCA	SNP2	TTCAAAATGGCAATTAACCTG
ANKRD11	GGGGAAGCTGCCCTCAGCC	ESR1	GGAAGTGGACCTGATCTG	MBOAT4	CAAAAGGAAATGCAAGCCCC	SNP2	AGACATTAAGAACTATCA
ANKRD11	AAGACCCAAACTGAGCCG	ESR1	CGGGGCTCAGCATAACCA	MBOAT4	TCCATATCGTTTTACCAGG	SNP2	GCAGTGAACAGTAGCCAAA
ANKRD11	TTAAGAAGGAGCTGTCCAC	ESR1	GCTCCGTAATGCTCAAGAG	MBOAT4	ATAATTGAAGAGGAGTGCA	SNP2	GTGATCTGAACTTTTACAG
ANKS1A	TTGGCAATGTTGTCCAGCCG	ESRP2	GTAGTTCAGTGAAGTGTAG	MCM2	GAGTTCATGATCCGCACTG	SETD2	CGAGTGTCTTCCAGTTGGG
ANKS1A	ATGCTGATCAAAAGTTCTGG	ESRP2	AGACATCTGAGCTTCTGG	MCM2	GGACAGAACCCAGCATCCAG	SETD2	CTCGGGCTTCCCAAGTAGG
ANKS1A	GATCCGCAAAATTTCTGTG	ESRP2	TCAA11TGT11TTCAGCCCG	MCM2	CGTGACGAGCCGTCGAGGG	SETD2	CCGGAACCTGACGTGAAAG
ANKS1A	TGACACATGACCAATAGTGG	ESRP2	GATGAAGGAGCCTCAGCTGG	MCM2	GATGACTACTAGCCTTCCA	SETD2	CACTTGTCTACCTCCCAAC
ANKS1A	GTATGTGTGGACAGATGAG	ESRP2	TGGTGTAGTGTGTTGGTGG	MCM2	CTAGGACTCCATGATCCGCA	SETD2	CTCAGTCCAGCTTCTCTACT
ANKS1A	CTTTGGCAGGGGCTGCTGGG	ESRP2	GCTCAGGATGTCTCAATGG	MCM2	ACAGAGCATCTCCATTCGA	SETD2	TAGTAATAAATTTCCCTCT
APC	CCGGCTCACATGATCTGAC	ETV1	TACAGGTTTCAGAAAGCTGG	MDC1	ACAGGAACCTTGAAGCTGG	SFB1	AAAACGTACACAGATCTG
APC	AGGATGGGAGAATCAACA	ETV1	GGGAAGACCCACATACCA	MDC1	GTGGTCAGAGCAAAACACTG	SFB1	ATAACCAATGTTGTGACTG
APC	CAGCTTGATAGTCAAAATG	ETV1	GTATGCCTGCGATGAGGG	MDC1	GTACCACATTTATCTCCGG	SFB1	AGACCTGTACACAGACGA
APC	GCTACTAGAATCAAAAACAC	ETV1	GCTGAAGTATCTCTCGCGT	MDC1	AACCGGCATAGCTCTTACTG	SFB1	ATAACTGCCTGAATTACATG
APC	ATGCTGTGACAAAATTCCTA	ETV1	GGTTCCTGTTTAATCATGAG	MDC1	AGGAGATTGGAATTCAGGG	SFB1	CAGACAGACGCTGATGCAG
APC	AAAGCGTATGTAGTCCCTTA	ETV1	AACATCCCCTTCCCCACACA	MDC1	TAAAGAAGAAACCAGCCCTG	SFB1	AATATGATGTCAAGAGAG
APMAP	CTCGTGGCAGAAACCAACA	ETV3	ATGCTGGAAGGCAAGGAGG	MDM2	AATTGCTCTCCTTCTAGATG	SFN	TATTTAGGCAAGGAAAGCA
APMAP	TTACAGTCTACAGGATGGG	ETV3	GAAAGCCGCTGTAGCATCG	MDM2	AACAGGTTGACCTTTGAAAG	SFN	AGCCCGGCTACAGCTCACGG
APMAP	AAGTTTTATGGACAGCTG	ETV3	GTTGGAAGGCAAGGAGGAG	MDM2	GTACATCTGTAGTGAGAGC	SFN	TGATCTGCACCCCTCAGCG
APMAP	TGGCAAAAACCACTGGCC	ETV3	TTCATCAACTCTCGTCAAG	MDM2	GTCTTGTCTCTCTTCACTA	SFN	GGCCAAGACCCACTTTGAGC
APMAP	GAATGATCTACAGTCACTG	ETV3	TAAATTTAATCTCAACAAGC	MDM2	CAGAGCCAGGCTTTTATCAA	SFN	AGTAGCTATAAAGAACGTTG
APMAP	GTGATGGAGGCAACAGATGA	ETV3	TTTTCCCTTGTTTTTATAGA	MDM2	CTTCTGAAGCTCTTGTACA	SFN	AGACAACCTGACACTGTTGA
AQP9	GATTAATGAGGATATCATGG	FAH	CAAATGTATGGGCTCTGCA	MDM4	AACAGATACAGAAAACATGG	SFRP5	TGGAGCACTACTGCTCATG
AQP9	AGAAAATTTGGAGCCCCAG	FAH	GAGGTTGTGTCAAAATGTTG	MDM4	TATGGCAGTGATATCAGAGC	SFRP5	CGGTGGCTACAGGCTGCTG
AQP9	GCCACTGTTCAAGTCCGAGG	FAH	ACTTGATATGTTAGCCCGC	MDM4	AAGTTTCTAAAACCAACA	SFRP5	AAGCCGTAGCCGCTCATAG
AQP9	GCGTCCCGAGAGATAGATA	FAH	CGTCAAGGCAGATACAGCC	MDM4	GGGAAAATGATGACCTGG	SFRP5	TAGCCACCTGTGCGTAGAG
AQP9	GACGTTGACGCCCCAGCA	FAH	CTTAAATTTGACCTTGCTA	MDM4	TGTGAGAAAAGACCAGAGA	SFRP5	GAGATGGAGCAGCTGCTGG
AQP9	CAGCTTAAAGACACAGC	FAH	AACATGGAGCCGAAGTTTC	MDM4	GAACAACAAGTGAAGAAGT	SFRP5	CACTGTGCTCCTCACCAC
AR	ACATCCGGACITGTGCATG	FAM90A1	GCTCAAGTCAAAAACCTGG	MED12	TTGCTGCTGCGGATACACG	SFXN2	CCATTGCAGCTCATGTCCAG
AR	GCATCCAAACTTTGAGAG	FAM90A1	CAGATAATCAAGATTCGG	MED12	CTACCCGCCACCTGCAACAG	SFXN2	CCTCATCTCATGTTGCCAG
AR	ACAGCCAGTGTCTCCGAATG	FAM90A1	GTTTCTGGAAAATATGTGG	MED12	GCATTGGTAAAGCGCACAGGA	SFXN2	CCTGTCAGGATCATGTAGAA
AR	ACTTGGAAATGACTCACTGA	FAM90A1	ACCTGGACTTCTGCGCGTG	MED12	CACCTGCAACAGCGGCCAG	SFXN2	TGCTGGCAGTATCATGTA
AR	GGTCTGCACGGTGAAGTGTG	FAM90A1	GGAAGGAAAACCTGAAACCA	MED12	GAGCGGATGGGTCACACGC	SFXN2	GGGGAGAGCCGATTTCTGT
AR	GCATATTGATAAATTCGGA	FAM90A1	TTTGGCAGCGCTTCTGTGG	MED12	GAGTGGATGTTGAGAAAGGG	SFXN2	GGGAAAAGCCCAACGCCAC
ARAF	CATGGCCAGCTCATCGAAGC	FANCA	TATGAAGTGCAGCTACAGG	MED16	GATCATCAACCTCAAGACGG	SHC2	AAAAGTGTCTTGCCCAAGGA
ARAF	TGTGTGATGATGGCAATCC	FANCA	CTGCCCAGAGGACGAGAGA	MED16	AGCCAAAGATCGACCCACTG	SHC2	TGGTGCAGCTGTCTGCACA
ARAF	GGCCGACACACAGTGTGACA	FANCA	CTGCCTTCTGCTGCTCTG	MED16	CACTCCTCGGGAATTCAGTG	SHC2	CGCCGGATGAGCCGCCCCG
ARAF	TTGGCACCCTGTTTCGAGGG	FANCA	CCATCTCAGATGTGCAACAG	MED16	TTCCCAAGCATGCCCAGCG	SHC2	GGCCGTTGGCAGGACGGAG
ARAF	ATGCCACCCTCCGCAAGCA	FANCA	TGCAGAAAGTACAAGAGGG	MED16	GCTGCTCGGATTCGGAGG	SHC2	GAGGACATAGCTGCCGGGTT
ARAF	GTGAGGTGCAAGCTGCTGAAG	FANCA	TCCGCAAGCAGGCTTCAGG	MED16	CAAGGTGCAGCCTCCGAGG	SHC2	TGCTACTGCCGGCAAGGCA
ARID1A	TGGCTTCAACAGCCAGCCAG	FAS	AAGTGGAAAATAACTGCAAC	MED23	CTACTTACAGACCCAGCCCTG	SHQ1	AGTCATTCAGTATGTACAG
ARID1A	CATATGCCCCTCTGCAAGG	FAS	AGATGTAGATTTGTTGATGA	MED23	GTTTTCTTGGAGAAATGGC	SHQ1	CATCTTCAGACTGCTGTG
ARID1A	GAATGGAGACTTGTAGGAG	FAS	GTTTGGTTTAACTGTCACT	MED23	ATGGCTTATGAATGCACAG	SHQ1	TATCTTATAGTGTCCCTG
ARID1A	GAGTAACTTATCATCCCCA	FAS	GACTGCTGCTGCCCCAAGA	MED23	GTATGAGGAGATGCACAGA	SHQ1	TTTACATGATATGACAGA
ARID1A	GGCAACTCACTTCCACCCA	FAS	GTAGACTGCAAAAAGGTT	MED23	AATTTAAATGGGTGCTACAC	SHQ1	TATGAAAACCCGTACTCAGTA
ARID1A	CTGCCAGGAGACCAGACTTG	FAS	GTACTCCTTCCCTCTGCG	MED23	GTAAGAAATGGTCCAACAAGA	SHQ1	ACTGTAGCAGACTTGCAGC
ARID1B	GATGCTTACTGAGCCAGG	FAT1	CTCGACTCAAAATTTGACTG	MED24	TGTGGGAGGATAGGAAGT	SKOR1	GGAAATCCTATCCAGCAAA
ARID1B	GTACCATCATCTCGTGTGT	FAT1	AGTACGTCAGCTGACTCG	MED24	GAGGGAAACTGTGATCTGG	SKOR1	ATTTCCGCTCCAGCTTCTG
ARID1B	CCCAACAAAGGCCCTTTGG	FAT1	AGCCGTGCGTGTCTCAGAG	MED24	GTAGGGCATTTGCTCCACC	SKOR1	TGTCAGAGGAACCTATTGG
ARID1B	GATGCCCTATGAGCCAAACA	FAT1	CATGGAAGAGTCCCTCAAGT	MED24	GGGCATTTGTGCCACCCTGG	SKOR1	CCGGCATGATTTGGAAAGC
ARID1B	GATAAATCATGAGGACCCAG	FAT1	CGCCCTCTGTGAGAACAGCA	MED24	ACTGCACGAAGTGGGTGGG	SKOR1	GGGCTTACCTTGGATGTAC
ARID1B	CAGGTATAGACTTGCTCCGG	FAT1	ACATCCCTGCAGCAGGAACA	MED24	GGAAGTGGAGGACACCAACA	SKOR1	CCTCGTTTCCAAATCATGG
ARID2	CATGCACCACTGAACATGG	FBXW7	AAAGTGCATACACCCAGAG	MET	ATGATGGTAGGACCCAGCC	SLC25A33	CGTTACGTTTACCAGACCA
ARID2	GTGCTGACCTTATGGCTCTG	FBXW7	ACATTAGTGGGCATACAGG	MET	AGTTTCCCAATTTCTGACCG	SLC25A33	GGTAAACCTACAGAGACAC
ARID2	ACTTGTGACAGCTGTTGAGG	FBXW7	CAGATCGGCACACTAAAAGT	MET	TTTGGTCTTCAAGTAGCCAA	SLC25A33	CACTAGAATCATTAAGACA
ARID2	AGCATCCGGATGATTCACAA	FBXW7	GGCACCAGCTGCTTAAACAG	MET	AAGTGAAGGCTCCGCTGG	SLC25A33	TTGGAATTTCCAGCAACG
ARID2	GGAATAAAACAAGATGACG	FBXW7	AATATAAAACAACCTTAAG	MET	GGATGAAAATTCACAGTCA	SLC25A33	CTGAAGAGTCCAGGTTGCA
ARID2	GACAGAACCTTCAATGTCTT	FBXW7	CCATCAAAAATGATAAACAC	MET	AAAGTTTTGCCACAGAGACT	SLC25A33	TTCAGAAAGCTGAAAGACT
ARID5B	ATAATGTCTGCGGGTACAG	FGFR1	CCAGATGGAAGATCTCCAC	METTL14	CAGAGAAAATAAATGATCG	SLC2A5	GCTGCTCTCCAACTCACC
ARID5B	AGATGAACAAGCTTCTTTG	FGFR1	CAACATGTCAACGCCACTT	METTL14	CAGTCTTTTGTATCCCTAG	SLC2A5	GAGGCAATGCTCTAGCT
ARID5B	CATATTTATGATGAATCTG	FGFR1	ACTGTGCTTAGGCAACCCG	METTL14	GACTAAGACTTTAGATCCAA	SLC2A5	AATGATAGCTCAAAATGG
ARID5B	CATAAATATGTTCCACAGA	FGFR1	ACCCAACGGTGTGACCAACG	METTL14	ACTGTAAAGCTGACACAGA	SLC2A5	TGACAGCCAGCAGCATGTG
ARID5B	TAATAAATCTTCAATATG	FGFR1	CCCATACCCGGTGTGCTG	METTL14	CTGTAATTTCTTCTAAAG	SLC2A5	CCCCCACCAGGAGGAGA
ARID5B	TTATAAAGTGCACCAAGA	FGFR1	AAGTTCCTCAGCAGGCAC	METTL14	TATCTCTCAAATAGATGA	SLC2A5	TGTGGGAGCTGGTGTGG
ARNT2	GCAAACTTTACGCAACCCG	FGFR3	TGGAGCTGCGCTAAGGACA	METTL3	GAGTTGATGAGGTAAGGCG	SLC30A9	ACAGAAGCACTGTTTAGG
ARNT2	GTAGGCATTTCCACTTGCG	FGFR3	CAGGCTGTGTTGACGTTG	METTL3	CTGTGACTTAGGAACCAAGG	SLC30A9	TGCCAACCCAAAGAACCT

ARNT2	ACCCAGCAGATCTACTCCA	FGFR3	CGACACCTGGAACGGCCGCG	MITTL3	ATGTTAAGGCCAGATCAGAG	SLC30A9	TCCAGCCAGAAACAGTACAA
ARNT2	GAATTCGATACATCAAGCCAG	FGFR3	TCGGAAGGAGTAGTCAGCCG	MITTL3	TCATGTGAATATCCAGCG	SLC30A9	AGAAGTAGGCCAGATCAAGA
ARNT2	GGAAATGTGAAGCTGCTGGT	FGFR3	CTGGGAGATGCTCAAGCTGG	MITTL3	CCACCCCTGGGATATTCACA	SLC30A9	TTTACATATCCAGCTAGCTG
ARNT2	ATTCTGGAATGTGAAGCTGG	FGFR3	CCTGTGACCTACCAAGTGGC	MITTL3	ATACCCGTACTACAGGATGA	SLC30A9	TCAAAATGTGATATATTTGG
ARPC5L	ATTCTGCATGTCCAAACCCGG	FGFR4	GCAGAGGACCAAGGACTGGGA	MGA	CACACACTCCCAATGAGCGG	SLC35F1	TCGAAGCGAGAACTCAAGCG
ARPC5L	GCAGCCGAGTGTACTCCAG	FGFR4	GCAGGCTCTCCGAGCACTGG	MGA	GGACACACTGCCCAATGAG	SLC35F1	AAAGCGAGAAGCAGCCGCTGG
ARPC5L	GTTCACGGGAGAGTTCGCG	FGFR4	GCATGCAGTATCTGAGTCC	MGA	ACAAGSTTGGCAGAGTGTG	SLC35F1	TCACATCTCCCAATGCAAG
ARPC5L	AGGCCCGGACCCGAGCGAGG	FGFR4	CTCCCGTATCTGGCATCC	MGA	TCAGTTGCCGTGAGTCTG	SLC35F1	TCATAATGATCCGGGACAG
ARPC5L	GTCCACCCGGCGAGCGCCG	FGFR4	GTATCTGGGATCCCCTGGG	MGA	AGAATTAGCAAAACAGCAGGA	SLC35F1	GGCCACCATGCCCATCTGGG
ARPC5L	GGGCATTCCTGAGCAGCTTG	FGFR4	GCTGCGGAGGACATCGGA	MGA	ACACTGCCAATGAGCGCGG	SLC35F1	GAGGACAGCCCAAGATGGGCA
ASXL1	GAATCAGTCCGTATACAGCG	FHL3	GTAGGGATCTCATCCC	MGAT5	TGTTGACCTCAACAATCAGG	SLC46A2	ACTGATTCAGGATCCAGAGTG
ASXL1	TAGCCTGCCTCAGGAACCTG	FHL3	ACAAAAGGACCGGGAGCCAG	MGAT5	AGGTCAACAGTCCACATG	SLC46A2	TCTCTTCCAAAAGGCCAAG
ASXL1	ATAGCATTGAGGCATCGGAG	FHL3	CATGACAGCTCCCACAA	MGAT5	ACGCTGAAGTTTTATCGGG	SLC46A2	CGTAGGACGCCTCAGCCAG
ASXL1	GAGGAGGGCTGAAATCAAAG	FHL3	GGATGAAGATCCCTACTGG	MGAT5	GTCCCTTGTGATAGGCAAG	SLC46A2	GATGAGAGGCACAACGATGA
ASXL1	TAAAGAGTTTTTACCAGTG	FHL3	AGCAGCCCTCGGGAATGG	MGAT5	GCTTGACCTGTAGGCGCGT	SLC46A2	TTTGGACATAGCTGATCGGA
ASXL1	ATGCTACATCCAAATCAAG	FHL3	TGACATCCGTTACTCAGCG	MGAT5	GTGGCCACATCACTTGCCCA	SLC46A2	TGAGTTGGACATAGCTGAT
ATM	TTCATGCTCCGATCAAAGAG	FLCN	TCACGCCATTCCTACCCAG	MID1	CTCCGTGATGAGTTCAAGG	SLFN11	GACCTGATCAGGACAGCAG
ATM	CTCACCAGAGATATTTGGA	FLCN	TGACAAGTGTACACACTG	MID1	CACGCTGAACATCATCCG	SLFN11	GTATATCGCAAATATCCG
ATM	GAACCTGTCTCAGGAGTAGGA	FLCN	GATGCCCAACAGCGCTCAAG	MID1	ATGACACCATCACTGTGAT	SLFN11	TGTCACTGTAGTCTACTAG
ATM	AGTTTCCGTACTCTTGCA	FLCN	GTGGCTGACGTTTAAATGG	MID1	TGACCCATTCCTCAATAATG	SLFN11	GTCCCTGATTTGCAAAAC
ATM	TATTTGGTTTGAAGAAGGAT	FLCN	GGAAGGGCCGAGGTTGATG	MID1	TGCGCCGATTAATGCGAAG	SLFN11	TTGACCTGACTCTTGGAGA
ATM	GGAACTGATGAGAATCTCT	FLCN	GGCTCCGACCAAGGCTGG	MID1	ATGTTTATGATAGTGGC	SLFN11	ATTCACAAATTTGAGTGTG
ATP6V1G3	ACGGCCAGGCAAGCAGTAG	FLT1	TCTAGACTCAGCCACAACA	MITF	CAACTTCCGATATAGTCCA	SLPI	AGATGTTCTGCACACTGG
ATP6V1G3	AAAGGCTTAAAGCAACCCA	FLT1	AGTTGAGGATACCATATG	MITF	AAACCATCTAAAGCATCCG	SLPI	GGGGTTAAGCATCAACAT
ATP6V1G3	GGGATGAGCAAGCAAGG	FLT1	TAACTTGAGAAAATGCCGA	MITF	ATTGATCTTATGGAACCA	SLPI	GGGTGACTTGAAGTGTGCA
ATP6V1G3	TCAGGCCAGAAAAGCGGCCA	FLT1	ACGTTACTTGGATTTTACTG	MITF	AAGTACCTAGTCTTTAATG	SLPI	ACTTCAAGTCAAGGCTGCA
ATP6V1G3	TTTCTTAAACAGGAAGAGC	FLT1	CGGGTCTGGAAACGATGACA	MITF	GGCCAAGAGAGGCGAGAAAA	SLPI	GCCTCAGCTACTTGGCACTC
ATP6V1G3	TATCTCTGCAATCTGTGAT	FLT1	AGGATTTGTCTGCTGCCAG	MITF	GTCCACGGATGCTTTTAAAG	SLPI	CTGGAGACTGCCGACTCACT
ATR	GAGCATGTGAAGTACAAATG	FLT3	GGTCATATGGAATATTAATG	MMP14	GGGATCCCTGAGTCTCCAG	SLX4	GTCGCACTATCTACAGCT
ATR	TGACATCTCAGCAGTGGAA	FLT3	GCCTTCAAACAGCGTTCCG	MMP14	CCATCAACACTGCCTCACAG	SLX4	ATAGTCAGGAAAGCTCGGG
ATR	AATGGTACTGTGGGAACAG	FLT3	TTTGCATATCAATGTTGCCA	MMP14	CGAGCATCAATCTGTCCGT	SLX4	GTGGGTTGACGTGAGCAAC
ATR	CTGACCTTGGTGCATACAG	FLT3	AAACGAAGTCAAATTGAGGA	MMP14	TAGGCACTGTGTTGGAACCC	SLX4	TCTGAACTGGACATCACTC
ATR	AACCCTTGTAAATATGAG	FLT3	GAAGTCAAATTAGGAAAGGA	MMP14	GATGGATACCCAAATGCCAT	SLX4	GTTCACAGCGGACAGCGGG
ATR	AAAAGGCCCTGTGTTCCAT	FLT3	ATATCAAGTTGCCAAAGGAA	MMP14	GCCTCTTCTGGATGCCCAA	SLX4	GAGTGTATCCAGTTCAGGA
ATRX	CAAACTGCTGACAGCAGTG	FLT4	TATCTGTCAAACCTCTCGG	MMP26	ATATATACTGCTTTCAGTG	SMAD3	CAAAAATAGCCGTTTCCAG
ATRX	TGAGAGTTTGAACCTGACGG	FLT4	AGCAGGCATCGCAAGAAG	MMP26	TGTGTCTCTGGGTAAGGAG	SMAD3	CTCGAGCCTCCTAAGTGTG
ATRX	AGTGAGGATTAACCTCTTG	FLT4	CTGAGCTCTGAGAGTCCGG	MMP26	TCTCCGCAAGGATGCAAG	SMAD3	GTCCGCTACTACATCATCG
ATRX	GGGGTAAATTTGCTCCAGT	FLT4	ACACGAGTCTGAGCATGAG	MMP26	GAGTGCCCACTCTTACCC	SMAD3	GCTCTACTACTCGGAGGG
ATRX	GCTGAAATTAATCTTCTGCA	FLT4	CTGGTGGTCGGAGACCCCA	MMP26	GAATGGAGATGCAGACATCA	SMAD3	GTAGGAGATGCAGCAGGA
ATRX	AGTGGATGTGTAAGCCCA	FLT4	ACCTGCATCTCGGAGCTGG	MMP26	GGGATGCGTTTATATCATG	SMAD3	GTTTGGAGCTGGCCGAG
ATXN7	TGTCGGTGAAGAACTACTG	FOXF2	CACTCCGCTGAAGCCCGG	MRM1	GGAGATGAGGCCTCCAG	SMARCA4	CAGTGAGCTGAGCTCAGCG
ATXN7	AATGCCAGTAGCAGTACCAG	FOXF2	AAATCTTTCTGTCACACAC	MRM1	GGGGGCTGCCAAGCACAG	SMARCA4	GAGAGCGCTGCAAGACGA
ATXN7	GTTCACGTTGAGGGTAGGG	FOXF2	ATAATGAGGCCCTAGTCT	MRM1	GGGCTAGCTTATCCCAGG	SMARCA4	CGAGCTATCCGCAAGCCCG
ATXN7	CAAACTGTTTCTCTACCC	FOXF2	TCGTTCCGCGCCGCGCGG	MRM1	TGAGTCTTGAACGTCTCTG	SMARCA4	CGTTGAGGCTGGGTACTTG
ATXN7	CACATTCCITAAACCAGCCG	FOXF2	GAGTAGGATGATGTGGTAA	MRM1	TTCAAGGACTCAAGTCCAGG	SMARCA4	CATCCAGTGCCTCCGCGAA
ATXN7	CCGAGGAAAACAAACAAACC	FOXF2	AGAAGGGGAAGCCGCTGCG	MRM1	TGTGTAATCTGGAAGTGA	SMARCA4	TCTCATAGGCTTGTAGGCTG
ATXN7L3	CACAGCAGACAGATGAGCAG	FOXH1	CTTGGCGAAGCATGGTGTG	MRPL14	CAGATTCGACTCCAACAACG	SMC1A	GAGATTCGTAAGAAACTCCG
ATXN7L3	CAGATGGGGAAGAACCGGG	FOXH1	GATCATGGCAAGTAGTGTG	MRPL14	TATAGACATGGATGCAAGG	SMC1A	CATCATCGGACAGGAAGG
ATXN7L3	TCTCCAGATGGGGAAGCAAG	FOXH1	GGCCAGCTTCAAGTGGCGG	MRPL14	GTGTTGGAGTCAAGTCCG	SMC1A	GAGATCATAGTAGGACCA
ATXN7L3	AGAACTGCTGGGAATGGTG	FOXH1	GGAAGCATCGTGGGAGGAA	MRPL14	GCTAGCAGCTCTGCTTACAC	SMC1A	ATAGACTCCATGAGGCTCT
ATXN7L3	CCGAGAAAATAAATCGTA	FOXH1	ATCGTGTGGAGAAAGGTGT	MRPL14	CACCTGCTTACAGAGGTTGA	SMC1A	TGACGATTCGCAAGAAAGT
ATXN7L3	ATGAGCAGGGCAGAACGTA	FOXH1	CAAGCCCGCTCAACCTACT	MRPL14	TGGCTTTTCTTACTGGGCTC	SMC1A	AGTCTCTGGAACTGTCTG
AURKB	CAAGTCCGAGATAGAGACTG	FOXJ1	TTGACGCCCAGTACCGGAG	MSH2	GTAGCAGAAGTGTCCATTG	SMG9	CGGACAAAAGCTGGCGGAG
AURKB	ACAATGAGAAGTGTAGTCTG	FOXJ1	AGCGTGGCACTACGAGTAGG	MSH2	CATAGTTAAGGTTCTCTCAG	SMG9	TGGGAAAGGTTGACTCATG
AURKB	TCTCTATCTGGGACTTGAAG	FOXJ1	GCCGATGACCCTCAGTACG	MSH2	AGAGGACTTCTACTACGA	SMG9	GCTGCATTTCAAGTAAGTG
AURKB	GGGGCCATGACCAATGAGA	FOXJ1	TACCGAGGCGCCACTGAG	MSH2	TCTAACCCAAATCCACTGT	SMG9	ACTTCTGCTCCGGAAGTG
AURKB	CCATTTCCTGGCCGCTCA	FOXJ1	GCCAGGTTGGATCTGGTGG	MSH2	AACGTTGGATGATGACTCA	SMG9	TCCGAGGACAGAAGCTCCT
AURKB	GATGCTCTAATGACTGCCA	FOXJ1	CCCTGTCGGCTACTACAAG	MSH2	GACTGCATCTTAGCCGAGT	SMG9	CCGATGAGCTGCTGAGCTG
BAP1	CAGCAGATGAGAGTACAGCA	FOXO1	GGTGACAGCAACAGCTCGG	MSH6	TGACATCTAATAGGCTGTG	SMYD3	GGTCCGATCCCATGAAAGCA
BAP1	AAGCAGCTGGAGATGTGGG	FOXO1	GGTGGCGCAACAGGATGACA	MSH6	TCCTTTAAGCTCAAGAAGG	SMYD3	ATCACAATCAAAGAGTCA
BAP1	CTGCTAGTCTTGTGGACAG	FOXO1	GGTATGTGAGCTGTGACGG	MSH6	AGAAATCTTGGGCAACAT	SMYD3	GGTCAAGTCAAGTGTCTGAA
BAP1	ATATGCGATTTGCAATGCC	FOXO1	TAAAGGTGACAGCAACAGCT	MSH6	TGTTGATGATGATGATGAC	SMYD3	GGCAAACTCAGGCTACTGA
BAP1	GATTGGCAATGCCCGGAGT	FOXO1	CGGGACGAGTCTGCTTCCG	MSH6	TACTGCAAACTTTGATGGGA	SMYD3	CAGCATATCCAGATGACAGGA
BAP1	CAATGCCCGGAGTGTGCCCA	FOXO1	CACGAATGAACTTGTGTGT	MSH6	ACGTCCTGCTGAAGTGTC	SMYD3	CACCTGTACAGGATATCC
BAX	GGGGGAGTCTGTGTCACCG	FOXP1	TCCGACGCAACGCGCCACG	MST1R	CGAGTCAATCAAGTCAAGG	SPEN	CCCCACTAAGGCTGCCGAG
BAX	CTCGGAAAGAACCTCTCCG	FOXP1	TGCTTACTTCCGACGCAAG	MST1R	TAAAGGTCAAAAGGGTCAATG	SPEN	TCCCAACATCTTCTGGTCA
BAX	GGACAGACACTCCCAGGGG	FOXP1	TGCATTTAGAGGTGTGAGT	MST1R	GTCCAAAAGGGTCAATGTTG	SPEN	GCCCTGTGGCCGAGCAGG
BAX	TTCTTGGTGGAGCAGCTCG	FOXP1	TCCAGCTGCCCGGCTTGGCT	MST1R	ACATGGGGCAAGCCTCCAGG	SPEN	CTCTGGCCAGCTTATGGT
BAX	AGCCAGTCTTCAAGCCGAT	FOXP1	TGATGTTTTTAAAGAAGGA	MST1R	TGAGAGCCAGCATATCCGG	SPEN	GCAACAAAGCTCTGGCCCAT
BAX	CAAGCCATCGGGGACAGCA	FOXP1	ATTAAGATGATATGTAA	MST1R	GGACGAGTCAATCACAGTCA	SPEN	TCTGGCTCAACATCCTCT
BBC3	ACCTCAACCGCAGATCAAG	FRAT1	GCCCAAGTCTCCGCAACG	MTOR	ATGAATAGATTTCTGGCACTG	SRSF4	CAATTACTGCTCACCACAA
BBC3	TCCCGGGGAGGAGACAGG	FRAT1	TCCGCAATGAAGGCTCCGA	MTOR	AGACGGTTGGTGAACGAG	SRSF4	TGTTGGAGAATTTGTCAAGT
BBC3	GCCGCTGCTACTGTGCTG	FRAT1	TCATCAAGGAGCCGTGCGA	MTOR	GCACAAGCATCCGCAACG	SRSF4	GATGCTTGTATAGACTGAA
BBC3	CAGCTCCCGGAGCCGCTAG	FRAT1	CCATCAAGTCCGCTGAGG	MTOR	ATGACAGCTCACTTCCGT	SRSF4	AGAGCTTGGAAAAGTTGGA
BBC3	CATGGCCCGGACGCGCAGG	FRAT1	TCATGACCAGGCGGCGGAG	MTOR	CTTCTCATGATGACACTT	SRSF4	CTGAATGGCAAGACTCTTG
BBC3	TGCGGGGAGCCGAGCCAGG	FRAT1	TGCGAAGGCTTCAATCGCGA	MTOR	CGCACTGCCAGAGGTTTCA	SRSF4	ATTTTGTCAAATCCGCTGAG
BBS4	AGAGCTTGATAGAGCCAG	FTSJ3	AGAAGCCGTGGTGAACAG	MUC1	GGGTGGTAGGAGATACAGAG	SSR4	TGAGGTTGATTTCTTGACG
BBS4	CCTGAAACGAGCCAACACT	FTSJ3	GATGCTTCTGTTTACCA	MUC1	GCTCTACTTGTGGACAA	SSR4	TAACTTCAAGTGGCCCTGG
BBS4	ATCAAAGGGTCCGAAGTAA	FTSJ3	GTTGCTGTTTGGTAAAGG	MUC1	CTGTGATTGGAGGAGGTGAG	SSR4	CGCCACCGCAGCCACTTGT
BBS4	ATACAGAAATCTTCAAGTAG	FTSJ3	TGCACGTCCCAACAAGAAG	MUC1	TGAAGCTGTCTCCAGCTG	SSR4	ATGGCCGGAGTGCACTCT
BBS4	CAGAAGGCAATTTGAACATCT	FTSJ3	CATCTCAGAACGAGAGAAG	MUC1	CAAGGCAATGAGATAGACAA	SSR4	GATGGCTCTCTCGGCGCC
BBS4	CAAGATCTTCAAATGCTTC	FTSJ3	AACCCTGCTCATCTGACTT	MUC1	GATGCTCAGGTTATATCGAG	SSR4	AGCGGAGAGGCTGGACAG
BCAR1	CAAAGCCGCTATGACAATG	FZD1	GTGTAAGTCAAGTTCGCG	NBN	TCTGATCTTCAATGATGTTG	STAG2	TTAGTGGAAATCAGCAGCGG
BCAR1	TGGGAGTACGAGAACAGCG	FZD1	CAGGAAGAACTGTAGCTAG	NBN	AAACTTCCACACATCTTGG	STAG2	GATTCACCAATGACTGACA
BCAR1	CATGGACACAGCAGCTGAG	FZD1	GTGGACGGGATGTGCTGAG	NBN	TGGGAAGAAAGTGAACATCA	STAG2	GAAITTCGGTAAGACATAG
BCAR1	GGCACATCATAGATGTCTG	FZD1	CTTGTGGGGCTTAAACAG	NBN	AACTCAAGGAAGACTCACTA	STAG2	GCCCCAAGGATACCGGCTG
BCAR1	GTTGGAGTTTCCCGCAGCG	FZD1	GCAAGCCCTCAACTCTGG	NBN	AGAGTGGCTAAGGCAAGGAA	STAG2	ATAATGTTGAGGTTGATG
BCAR1	CCGAAAGGGTGCATCATAG	FZD1	ACTTGTCACTACCACTACT	NBN	TCTACTTCAAGAAATCAGT	STAG2	TGATGATAGTACAGAGTGT
BCL2L11	AGGTGAGCAATGTCAGCTG	FZD3	AGTAAAAAAGTAAAAAATG	NCOR1	ATCCCTCTCAAGTGTACAG	STAT5B	CCGAATGGAGAAGTCTGCTG
BCL2L11	TGTGGCTCTGTCTAGAGG	FZD3	GGGGCTCTGGGAAACAAG	NCOR1	ATCAGAGTCACTCCAGCAG	STAT5B	TATAGAGTCTCCAGCGGT
BCL2L11	AGTCTGAGTGTGACCGAGA	FZD3	TCATGCATCAACATCTGAT	NCOR1	AAGGCTACTTAGAACGGAA	STAT5B	GGGCTGGGTAGGACCGGAA
BCL2L11	TATGGTCTGCCAAGAGTG	FZD3	ATTCAGATTCACCATAGG	NCOR1	TCTTGGAAATGAGAAGTAG	STAT5B	GCACCTGAGATGCCGGGG
BCL2L11	AGTTTAACTGTACTATGTA	FZD3	GAACAATCCAGATTCACTC	NCOR1	ACCATAGGAGAGCCGAGGG	STAT5B	GTACTGGCGCTGCCCGCC
BCL2L11	TGCAGGTTTCAAGCTGCCTA	FZD3	CTTTGAACTTAATCTTGT	NCOR1	CTTTGATCTCACACTGTG	STAT5B	GCTCATGTTATAGTGAAG
BCOR	GGGGTGGAGCCACTGACAG	FZD7	GAGAAGCAATGAGGCGTCG	NDUFV3	TGAGTCTAGTCCAGTCCAG	STIP1	GGTCTTGGAGGAGAAGACAA
BCOR	ATTCAGCAAGATATCGCGG	FZD7	GGAGTGTGCTACCCGCGG	NDUFV3	GTTCCCTGTGAGAATAACCA	STIP1	CTTCAAAGGAAAAAGTCA
BCOR	TATAAAGCATCAAGTATCTG	FZD7	GTCGGGCTGACTCTCATGG	NDUFV3	GGATCAGTAATGTCACACTG	STIP1	CACCACTCCGAGGTTCCAG
BCOR	TCTACTGTAGTACGTAGCCA	FZD7	GATAGTGTGGCTTTGACGG	NDUFV3	AAGCAAGTCTCGAAACACC	STIP1	AGACTTGTCTTATAAGAAAG
BCOR	TATGGTGTAGTACCCCACT	FZD7	TGTACTTAAAGGAGGAGG	NDUFV3	GCCCGCTGTTGTGCTGGCGCA	STIP1	GTACTTITTTCTTTGAAAG
BCOR	CACCAATAGAGGAGGATGAT	FZD7	ACATGGAGCATAAAGAAAG	NDUFV3	GGAATCAGGGAAGGAGTGA	STIP1	AAACCCCGACTGCCTTTGG
BLM	CAAACTGGAATAATGTTG	GAB4	AACACAGCTCAAGAAAGG	NEGR1	GGAAGGCTCTGTTTCCGAG	SUMO1	GGGGCAAAACCTTCAACTG
BLM	TGCAAGCTCTTGAAGGTA	GAB4	CACCTGTAACACTCACTAG	NEGR1	CAACAAAGTAAAGGTGAGCT	SUMO1	ACCTTCAACTGAGGACTGG
BLM	AGTGTCTCAGAGGAGGAGA	GAB4	ACTCAGAGAGACTGGAGG	NEGR1	GGGAGGTTAAGTGGTTCAG	SUMO1	GTGTTCCAAAGTAITCTACT
BLM	TCAATTTGAAGCAAACTCT	GAB4	TGCATAGAAAGCTGTGAG	NEGR1	CATCTCATCTGATCTGCG	SUMO1	TATATAAATCAAGAGTCA
BLM	TATACAGAAATACTCTGAA	GAB4	CAGAGCTCAGCCGCGCG	NEGR1	AGTGGCTGATAGAGTGTGA	SUMO1	AGAACCTGAGTGAATTCAT
BLM	GAGATGGTAAAAATGCTG	GAB4	CTGTGTCTTCTAGTGTGG	NEGR1	TGTACCATCAAGGCTGG	SUMO1	TTCACTCAGTTCTCTTGG
BRAF	GAACAGCTACAGGGAAG	GATA3	CGAGGAGGCTCACCAGGG	NELFB	TCCTGCACATCACCAGCAG	TADA1	AGATGATGATGTTCCAGG

BRAF	GGCAGGAAGACTCTAACGAT	GATA3	CCACCACAACCACACTCTGG	NELFB	GGAAGGACATGAGCATCGGG	TADA1	AACCGGTGAAGATGGCCAGG
BRAF	TCTGATGGCGAGATACAG	GATA3	GGGCAACCTCGACCACACTG	NELFB	AGTGTAGTCATCCACCAGGA	TADA1	GGGTTTTCCAGGTTTTGCTG
BRAF	CTCCAGATCTCAGTAAAGTA	GATA3	CTCCAGAGGTGTGTTTTGG	NELFB	TGGGAGAGGATGTGCGCCAA	TADA1	TGACCTCAGTTGTGTCAAGA
BRAF	CCTTACTAGATCTGGAGAC	GATA3	ACTGTGGCGCAGATGTGCA	NELFB	TGAAAGTGTATGTCATCCAC	TADA1	TACTACCTGTTTTGCTCT
BRAF	CTGTCTCCAGATCTAGTA	GATA3	TCCCGCCACATGGGGTCCG	NELFB	GCCAAAGGCCAAGTCCCAA	TADA1	AAACGTTTTCCGTTTACGAGA
BRC2A	GTACAAATGGGACTAACGG	GLI1	CCGTATGTATGTAAGCTCCG	NELL1	CAATGGGAAGCCAAAGGACG	TADA2B	GAGTCCGGGAAGCCAAAGC
BRC2A	TTGTCCCAAGCAACTCCAG	GLI1	GACGCCACTCGCTGACACA	NELL1	AGAGCAGCTTCTTACCGCA	TADA2B	TGCTTCCCGACTCCCAAG
BRC2A	AGAAGGCATTCAGCCACA	GLI1	CCAGGAGCTTACATACATA	NELL1	ACCGCATGCGAGATGGACAA	TADA2B	GGCCGGCTGCACACTCGCG
BRC2A	CATCTGGCTGAGACAGGTG	GLI1	TCTGGTCAGCTTCTGCTGA	NELL1	CCAGATACCAACCTTCCGCC	TADA2B	TCCGAAGGCTGAACCTGTCTGA
BRC2A	TGCTAGCAAATGATCXAAG	GLI1	TCGTAGGATCTGTATAGCGT	NELL1	ATTGATTCCTGGGGAAAGT	TADA2B	GCGACATGCTCCAGCGCCCT
BRC2A	CTGAAGTGAAGGGGCTCCG	GLI1	CGAGGGCTGAGTATGACTTC	NELL1	ATAAATTTGATTCCTGGGGGA	TADA2B	CGTAATGCTCCATGACTCT
BRD9	CTCTGGACCAGATCCAGG	GOT1	ACAGGCGTGGAGGACAACA	NF1	ACCAGTGGCCACTGTAACAG	TAFL5	AAACGTCCGAAGAGGACAG
BRD9	CGCCTGTGATCTGGTCCAG	GOT1	AATGTCTTTAAACCAGCAG	NF1	TGCTGTGATCAAACACTATCTG	TAFL5	AAGTACAGTTTGGACACTG
BRD9	GAGCTGTCTACTAGCCCTA	GOT1	TACTGGGATGCGAGAAGAG	NF1	GAGTTCCTCCAGCTTTACAG	TAFL5	ATTCCTAGATAAACAAGTACG
BRD9	GAAGCACAGGCGGAGCGCGG	GOT1	GACAGGTAATGTGAAGACAA	NF1	TCCACTGTTACAGTGGCCAG	TAFL5	GGTAGACAAAAGAGGATAG
BRD9	AGTATTTGGCGACTTGAAGT	GOT1	AGGACAACAATGGAGAACCT	NF1	ATGTGGGTGCTGTTGTGATG	TAFL5	AGTGTCTGCAGCCCTTGCC
BRD9	CCCTGTCCACGCTCCCGAG	GOT1	GATCATTCAGGAAGCCCTGG	NF1	GACTTTGGGAAAACACACAC	TAFL5	AGGGGTCTGCAGACTATGT
C2CD4A	AGTACTGTCGGGAACCGGG	GP6	ACGGTGACCAGCCGACCAG	NFE2L2	CACATCCAGCTCAGAAACCAG	TAFL6	GCTCCTAAGTCCAGGACAGAG
C2CD4A	GAGCACATTTGGCAGCCGGG	GP6	TAACCTACAGTGTGACAGT	NFE2L2	TAATTCGGGATATACGTAGG	TAFL6	GTTGGCTCCAGGACACTAGT
C2CD4A	GAAGGCATCGAGACCAGAG	GP6	GGAGAAAGCTGTAGCATCGGT	NFE2L2	TATTTGACTTCACTGACCGA	TAFL6	GAGTCCAGTGTCTCACTAGG
C2CD4A	AGTCTGCTATCCGGAAAGCG	GP6	TACCCTGCTCTCACAGAA	NFE2L2	GGACATTAAGCAAAGTTTGGG	TAFL6	AAGAAAGTCCAGGCCCAACA
C2CD4A	CAGGTGGCGAGTACAGCG	GP6	GAGTATCACCGCTGACTCAA	NFE2L2	CATTAACTTCGGGATATACTG	TAFL6	TGAATGACCCTGACTGCTG
C2CD4A	GTGCGCAAAATGCTCAACT	GP6	CCAGAGGCTTCCGTTCTGGT	NFE2L2	TAGGAGGGTAAAGATAAAG	TAFL6	ATACAGGATATGCTGATAG
CACNA1H	GCTGTCCGCTGTCCACCG	GPX3	ATAGCTCCTCTTGTCAAG	NKX3-1	GGTCTTCTGCCCCCGCGC	TBX3	TGCTAITGSCITCTACAATG
CACNA1H	GCTGGCGGAGTCTCCGCTG	GPX3	TATAGGACAAGCTCCACC	NKX3-1	GATCACCTGAGTGTGGGAGA	TBX3	AAAGGAGATGTACATCCAC
CACNA1H	TACTTGTGACTTCTGTCTG	GPX3	CCCGAATGACCAGACCACC	NKX3-1	TCCTGCGGAGCGCCGCCAG	TBX3	CCGACCCCGAAATGCCAAAG
CACNA1H	GGCCATGCCAAGTGTCTGA	GPX3	AGCCCTACCAATTTGATGGG	NKX3-1	GTCTGCTGCGCTGTCTGTTG	TBX3	CATCCTACTTCCCAAGTATG
CACNA1H	TACGGAGTGTCTGTCTCTA	GPX3	GGCCACTGATGAGCCCTGA	NKX3-1	CCCAACTAGGTGATGCACTG	TBX3	AGGGAGTTCGAAGTGATCAT
CACNA1H	TACGGGATGTCCGCGCCTCG	GPX3	AGAGCTGCTACCAATTCGCTG	NKX3-1	CCAACCTGATCACCTGAGTG	TBX3	TTCGGCCATTTCAAAGTGTCC
CACNG8	GAGATCAATCATTTCCCGG	GRHL1	CGGCGCACCTTGTGAGAAG	NME6	AGTGTCCGAGCAGCCGACTG	TCF25	CGGCTTCTGATCTCAGAG
CACNG8	CTTGGACTGTAGAGCCGCGG	GRHL1	AAGTCACTCTTGTGCCGTA	NME6	CAGTGAGGCCGAAACTCCCA	TCF25	AAACCCCTGACACTGCGC
CACNG8	CCCGCGCTCAAAAGTCCAG	GRHL1	CGCTGTGAGAGGGAAGAGC	NME6	AGGATGCCATCCAGCTCCTG	TCF25	GAGTAGATTGTTCCGAAG
CACNG8	TCTCTTGGACTTGTAGCAG	GRHL1	GATATCCATTCGCTTGTGAG	NME6	TTTTTTTATCAGAGGCTG	TCF25	TAGGAGTAGATTGTGTCCGA
CACNG8	CGTGAAGTAACTCATTTCC	GRHL1	ATGAGTCCCGGCTCGAAGT	NME6	CATGCTCGGTAAACCTC	TCF25	TGATCTCAGAGAGGATCACA
CACNG8	TGCTGTAGTCCGCTCCTC	GRHL1	GTCTTAAAAGGEGGCCGTA	NME6	GGGTTTTTCTATCAGAGG	TCF25	CAGAGAGGCATACACTAGGC
CADM1	CGATACCCAGAAAGACTG	GRIN2A	CACGTTGCTCAGAGCAGCAG	NOP10	TCATCTGGGGAGAACCGGAGC	TCF7	TGTGACTCTGCAATGACTCT
CADM1	CTATGTTTGAAGCTTCAAG	GRIN2A	GATGAGGCTAGGGCCACTGG	NOP10	CTCGATCTCCCTGCTCTGTTG	TCF7	CTGCATCTCCAGCTATACCTG
CADM1	AGCCAGCCAGCATGATCAGG	GRIN2A	AACTGGAAGTAGTATGAGCT	NOP10	CCAGTATTACCTCAACGAGC	TCF7	ATGAGTCCGCGCCCAAGGAG
CADM1	TTTGAACCCACTGATAGTGT	GRIN2A	GCTCACTGTTTCCAAAGCG	NOP10	CTGGGGAGAACCCGAGCAGGA	TCF7	GTACAGCATTAAGGCACTTGT
CADM1	GTGGTGTAACTTCTCTGCG	GRIN2A	GCGGGCGCTTATCTCATCTG	NOP10	CACCATCAAGAACGCTTCA	TCF7	GAGAGTCTAGGGGTCTGCAG
CADM1	ATGCTGGTGAATCTTCTCTG	GRIN2A	GGCAGATCCAGTGAACCCAC	NOP10	CCTGCTGTTGAGGTAATAC	TCF7	GAGCTCCCATGCTCTCCTG
CAMK2D	AGTGTGTGAAGAACCCAGA	GSG1L	TGTGGGCGACCTTCCACG	NOTCH1	GTCTTCAGGAGCACAATCTG	TER1	CCCCAGGACAGGCTCACCG
CAMK2D	GAGTCAAATACAACAATTTG	GSG1L	CTTGTGTAGGAGTTTGGG	NOTCH1	ATCAGAGCCTGATAGCGGG	TER1	TGACCCAGGAGTGGCACCT
CAMK2D	CTGATCGAAGTATCAACAA	GSG1L	GGGAGGATATCTCTGTGG	NOTCH1	GGCATTCCACATTTTCAAGG	TER1	TTGACAAAGTAACTGACTCAG
CAMK2D	TGCTTCCATGATGACAGCAG	GSG1L	CCCATCTCTGGGACTCGGG	NOTCH1	CCTGGAGAGCGGCAACAGCG	TER1	GAAGCTGCCTTCCACCTG
CAMK2D	GCTTTTGGTAAATTTAGTGA	GSG1L	CGCCACATGATGTACACGC	NOTCH1	CTCGGGCTGTGAGTGTGATG	TER1	GGAGTGGCAGTAGTGGACA
CAMK2D	TGTTTCTTCAACAACACTCT	GSG1L	GAGAGGAGCGGGAGCCGAGG	NOTCH1	ATGAAATCGGAGATGACCGCC	TER1	ATCGTCCAGGCCCCAGACAG
CAMSP3	TCCACCCTCAGAACCAAGC	GSK3B	GAATGTGCACAAGCTTCCAG	NOTCH2	AGAATGATCAACTGCCCAAG	TE11	CAATCACAGGCTTGCCAGG
CAMSP3	ACGTTGGGCTCTTCAACCCG	GSK3B	CCGACCCGAACTCCACCCG	NOTCH2	CCAAGCCGATGTGTAATGAC	TE11	GAGGAAATAACCCCAAGGAG
CAMSP3	AGCAGTGTGATAGGGCAATG	GSK3B	TGTGTATATCTCCAGACAGA	NOTCH2	CACTGATCTACATCCGCT	TE11	GAGCTCTGTGTATCGCCGCT
CAMSP3	CTATACACTGCTGCTCGCTG	GSK3B	TGGAAATGATCATTTGGTG	NOTCH2	GCGACGTCTGCTCAATAATG	TE11	TCATGTTTGAATGTCCCTG
CAMSP3	GTTGGCCTCGTGTGGCCACG	GSK3B	TATACAGACACTAAAGTGAT	NOTCH2	GTTCCTGCTGATCTCTCGTG	TE11	GATCAAAATGGGCGCACTG
CAMSP3	GCTGTGTTCTGAGGTGGGG	GSK3B	GCTCCCTTGTGGAGTTCCG	NOTCH2	TGGGGCCACCCGAGACATGC	TE11	GCTTAAAGAGGTTGACACA
CARM1	CAACCTGACTGACCAGGACTG	GSTM5	GTGTGTATTCGAGGAGCAAG	NOTCH3	GTGTGCTGTGACATCCGCG	TE12	GGCCTGAGGTCCAGGACTG
CARM1	AGGGGTTTTAGACTCCAGG	GSTM5	TGTGAAAAGAGTACACGC	NOTCH3	CTCAACGGCACTGATCCTG	TE12	AGAATTTGGAGAAAACCTG
CARM1	GGTGAAGAGTAACACTGTA	GSTM5	CTTACGTCAAAGCACTCAT	NOTCH3	AGCCCTGCGAGCATCAGGT	TE12	TTTAAACAAGTCTTCAAGG
CARM1	AGCACCACACACTCAGCAG	GSTM5	GAACTCTCAAGTTTGA	NOTCH3	CCGCTGCTGATCGACCCAG	TE12	CAGGAGSAGAAAACCCGAG
CARM1	CTCCACTACACATCTCCCT	GSTM5	CAAAATACCCCTTATGTCA	NOTCH3	CCGATGGCAGATGGCTCAA	TE12	GAGTGCACAACATGCAAGA
CARM1	CTGGTACTCCCGGCAAGG	GSTM5	CCACGATCTCGCTTCTCC	NOTCH3	ACCAAATCCCGAGGACACTC	TE12	ATATGTTCCGGTCAATAAGAG
CASP14	GTGAGCCATGAGTACCACA	HAGH	TCGGGACTGAAAGGTGACGG	NOTCH4	CCGGGTGTCAGGGCCACAG	TFAP2B	CATGCTGCTCAACCCGCGG
CASP14	CACAGCTGTGATAGGGCAGG	HAGH	GATGTGATAAGCTCTGCTGG	NOTCH4	GGTGTGGATTTGTCCCGTGG	TFAP2B	GGGTTGGTGTATGCTCCGCT
CASP14	GACCCGGTGAACAGTATGA	HAGH	GAAATTTATGAAGGGAGCTG	NOTCH4	TGCAGCCCAAGCAGACGTTG	TFAP2B	TTCCGAAGTAAAGTAACTG
CASP14	AGGTGGAGTGTAGATTGTA	HAGH	AACAAATGCTTCCGAAAGT	NOTCH4	TGAGGGTGACAGCCAGCGC	TFAP2B	CGCCAGGAGATGACTTATG
CASP14	AGGGACCCCGGTGAAACATG	HAGH	ATGTTCTCGAAGTGTGGCA	NOTCH4	GACATCCCAACCTAGCCCT	TFAP2B	TCTCCGGCCCTTACCCCCGG
CASP14	TGTTACTACTTGCTCCAGG	HAGH	CCCGAGGCCAGCCACAACA	NOTCH4	CCACTGCAGTTTTGCTGCTA	TFAP2B	GCACAGCACGCTCCCGCGG
CASP3	TGTGGCATGTAGACAGCAG	HEATR1	CTCGGAAAGTTGACACAACA	NPM1	GCAGAGGCAATGAATACGA	TFAP4	AGATGCGCAACAGCAAGCAG
CASP3	CGTGGTACAGAACTGCACTG	HEATR1	AGCGGTTTACGTCAGACTGA	NPM1	GACTCCAATTAAGATAACAC	TFAP4	GCCTCTCCGCTGTGTGAG
CASP3	GCGCTGTCAATAAATCCAG	HEATR1	CATTTACTGCTTAGTAGCCA	NPM1	CAAGTTAGGGCTGGTGCAA	TFAP4	ACCCTATCCCCACACAGA
CASP3	AGTTTCTGAATGTTTCCGCT	HEATR1	TAAAATGCTGGGATACAAA	NPM1	CAAGGATTAACCTTTAAGG	TFAP4	AGCCGATACATCTTCTCC
CASP3	AAAATAACAAATGTTTTAG	HEATR1	TCTGGAGGAAGTTGAAAAA	NPM1	GCACAAAAGTCAAAACAGAA	TFAP4	AGATGTACTCGCTGTCTG
CASP3	GAAACTTGAATATGAACTG	HEATR1	TCTTCTTAATATAAACTG	NPM1	GACTTTTTGTGCTTTTTGGC	TFAP4	CTGCGCTGTCTGTGGAGAA
CASP6	AGTACAAATGGACCAGG	HECW1	GGATCAGATGACCCTGCTG	NOO1	TGCTACTGCTCACTCAGAG	TGFB1	GCTGATGTTGACTCTCCCA
CASP6	ACTTACCACTGCCAAGAG	HECW1	GCTTCTCATAGAAATGAG	NOO1	GAATGACATTTCACTCCCGC	TGFB1	CGGAAAGAACTGCTGGCTG
CASP6	CAAAGCAATCCGCTCTGCG	HECW1	CCACCGAGCCAGAACCCAG	NOO1	TTTGAAGAAGAGGATGG	TGFB1	GTTAAAAGTGGAGCAGCAC
CASP6	GTCTTCTGAGCCATGCGCA	HECW1	TGACCTGGAATTTTTGAGT	NOO1	CATGGGCACTGCGCAGCAG	TGFB1	CAGGGATAACACTCAGCAAG
CASP6	AAAAGTACAAAATGGAACCC	HECW1	CCAGAGTTCGACGTGGATGA	NOO1	GGACTTCAAACCACTGACG	TGFB1	GGGTTCACTACCGCCCGCC
CASP6	AAATGTGATTTGCTTGCACA	HECW1	CCGGGCTGGGAGATCAAAA	NOO1	CTGGAATATCACAAGTCTGT	TGFB1	GCTGAGGCTCAAGTTAAGG
CASP7	TCTCCGATACAAGATCCCG	HESX1	CATGTCCCAAACTCCAG	NSD1	TCAGATGTAGACAGCTTGGC	TGFB2	CACATGGGTTGATCAGCTG
CASP7	GAACCGTGGAAATAGGCCAAG	HESX1	AGCTCAAAAATGAACTAG	NSD1	CCCAAACCCGCTGTAATGTG	TGFB2	CAGAGCCATGGGATAGCAT
CASP7	GAAGCACTGGAAGAGCCGCT	HESX1	TCTTCTTAATATCGATACC	NSD1	TGCCAAAAGGAAACTATGCT	TGFB2	GGGAAAAGCCAAAGTCCAC
CASP7	AGACAATCACGTCAAAACCC	HESX1	TTTTGAGTAAAGCAAGTCT	NSD1	TTAGTCAAAGGCGCTACA	TGFB2	ATGAGGTTGATCACTGTGG
CASP7	TCACCTGGACTTGTATATG	HESX1	TAAAAGCAATCTTGGTCT	NSD1	ATCATTTGATGCTGGTCCCAA	TGFB2	CCGCTTTGGAACCCAAATGG
CASP7	TCATGTGCTTAAAGAGTATG	HESX1	TTTTAGGTAACCTGCTATCC	NSD1	ACATTTAGGTTGTGATTTGA	TGFB2	CCCCTGTGTCAAAGGATGTA
CBFB	GAGAGACAGATTGTTTCTG	HEXA	TATACGGTTCAGTACCAGG	NTRK1	TGGTACCAGCTCCTCAACA	TJP1	GGCATATTTAACCAGAACTGG
CBFB	GGAGTCTGTGTTACTGGAA	HEXA	GAGGAAAGAAAGGCTTCCGTTG	NTRK1	GCCACTAGACAGTTTCCGTTG	TJP1	CCTCAAGGACCACTCCCGA
CBFB	AAGTGCAGATCTCTCGGCT	HEXA	CACAGCAAGGATGTAAGG	NTRK1	TCCGCAAGGACTTCCAGCGTG	TJP1	TGGGACCAACATCAACAAA
CBFB	GTCTCATCCGGGAGAAATGG	HEXA	CTGTCCTCCAGGACAAAGTG	NTRK1	TCTAGTGGCCAGGAGCTG	TJP1	CTGACTCCTTGTGATGTTG
CBFB	CGATTTCCAGAGCGGCCCTG	HEXA	AGGAGGCTCTTAATAACGCA	NTRK1	CGCAGCCACTGCTGACCCA	TJP1	CTTCTTCTTTACTTAAAGG
CBFB	AGCACACAGCCCTTTGAAG	HEXA	ACTGGATCTCACTGTCCAA	NTRK1	CTTACGATCAGGATGCTCT	TJP1	TTGGTGTGTGGTCCCACA
CBL	GCAGCATGAGTCTCAAAG	HGF	TAATGTCCAGACTCCCG	NTRK3	GCTGTGAAATGTGACGAGTG	TL2	GCTGTGTTGAGCAACCGGGA
CBL	AGATATCTGAGAGAGTCTCG	HGF	GGGATCATCAGACACCAC	NTRK3	AATGTGACGAGTGGAGCAA	TL2	GCTGGTATTCTCCGCTTG
CBL	ATCCAGAGACAACCCAGCA	HGF	CTATGAGTGGCTATTACGAG	NTRK3	TCATGGCATCAACTTGACGC	TL2	ATATTTCCGATTTGAGCACT
CBL	GATTACTAAAGCAGATCTG	HGF	AAATGACCCAGCATCATCG	NTRK3	CTATCCAGTCCACATCAGGA	TL2	GGAGCGTGTGTTTTGAGCAC
CBL	AGATGAGGGCAGTGTGGTT	HGF	TTTACGGCAAGAATTTGCTG	NTRK3	AACCGTGTATCACTTGCAG	TL2	GGAGAAAGCAACTTGCCCT
CBL	TCTCCCTGAAAGACTGCACT	HGF	CCCTTCAATAGCATGTCAAG	NTRK3	TGGATCACCCTTCTCGATG	TL2	CCGATTCGGGCACTCGGCT
CBX3	ACGTGTAGTGAATGGGAAAG	HHP1L2	GTGGGAGTCACTGCACTGG	OPN4	TGTGGCCTCAAAGAGCGCTG	TL3	CCCATGATGGCCAAACTG
CBX3	ATTTGTCACAGACAGCAG	HHP1L2	CTATGGGATCAGAACTAG	OPN4	AGGGCAATGGCCGAGTCCCTG	TL3	TCTCCAAGGACCAACAGCT
CBX3	CAATTTCCCACTGCTGCTG	HHP1L2	ACTGAGGATTTAGTCTATCG	OPN4	AGATGATGATAAGCAGAGG	TL3	TGCAATGACATCTCCCAACT
CBX3	TCTTTCAGACTCAAGCCCTC	HHP1L2	GGGCAGGCTACATGGCAGG	OPN4	CCTTTGGTGTGGCTCCAGG	TL3	GGAAAGTGTACTGACTGGAAG
CBX3	CTAGATAGCCGCTGTAGTGA	HHP1L2	AAACTTTGGCTGGAGAGCAA	OPN4	TGCGAGTTTACTATGCTTCTG	TL3	TTTCCAGCCCAATTTCCAG
CBX3	GGAAATTTCTCTGAAGTGA	HHP1L2	TGACTGACTTCCCACTGCA	OPN4	CTGGCTCCCTACTCCGCTG	TL3	ATGGGACTGCTACTGAGCTG
CCDC170	CGAGAAAATAGGCCAGCTGG	HIST1H3A	CTCCTGCAAGAGCATCACAG	OTC	TGATCACTAGTTTCCAG	TMEM50A	GTATCGAATGGAGCAAGTCCG
CCDC170	GTTTGCAACTCTCAACACCA	HIST1H3A	TTTACGAAATAGCAGTTGAG	OTC	TCTGGGAAACACTAGTGATCG	TMEM50A	CTTCACTGTAACACTCACT
CCDC170	ACTGGATACCACAGAACTAG	HIST1H3A	CTGCCACTAAGCAAACTGT	OTC	GTGAAAATATGCTCAGTCA	TMEM50A	AACCCTCATACATGACCTG
CCDC170	AGCTGAAATGGAGACTTACA	HIST1H3A	CAAAGCCGACAGCAAACTG	OTC	GAACTATAGCTTCTGTGAA	TMEM50A	CGAGTGTATGTTACAGCT
CCDC170	CTGAACTGCTCTCAAAG	HIST1H3A	TAACTACTTTCACAGGCC	OTC	AAGGCGTCCAGGCTTCCA	TMEM50A	GTGTTGAAATTTCTCATGG
CCDC170	GGCCAGAAAATGATAGAAG	HIST1H3A	CCTGGCAATCTCCGGCAC	OTC	ACAATCAGATTGGACACCC	TMEM50A	AGATGCAATCAGAGTCCAA

CCDC34	ACCAGAGATGATGACTTGTG	HIST1H4L	CATCTCAGGCCATTATACG	OTOP3	GCTCTACCAAGATCCCACG	TNFRSF14	CCCTCCGGACGTCACCACGG
CCDC34	AAGCCGCTGACACATTGGG	HIST1H4L	CGCCAAAGGCCATACAGGTTG	OTOP3	TCCTTGGTAGGAGCCAGCGT	TNFRSF14	TGAGGTTATGTCTCTCCCA
CCDC34	ACACCCCTCCAGTGGTCAAG	HIST1H4L	CCGCTGCCAGCGTCGGATGG	OTOP3	CTGAAATGGGTGTCCTGGG	TNFRSF14	AGCTCTGCCGTCTCCGAAG
CCDC34	CCCTTATATAATCAATTCGG	HIST1H4L	CTCCACCGCCGTCGACGGGT	OTOP3	GGCTCACATCTGAGCCCACT	TNFRSF14	TCTGCTCTCCTCTTGAACG
CCDC34	GTAATTTGCACAGATTCCTA	HIST1H4L	TAAACGCTCCACGCGCTGCC	OTOP3	CTGCCCTCAACATCTCCGAG	TNFRSF14	ACTACCAGGTCTGTCTAGCT
CCDC34	TAGCTCTTGCAGCTGGACG	HIST1H4L	CGSAGTCTTAAAGTGTTTT	OTOP3	AGCCCACTCGGAAGATGTG	TNFRSF14	TGGTACTGCTCCTCTCCG
CCND2	GTAAGTGCACGCTCTCCG	HMOX1	TATCACCTCTGCTGACTG	PALB2	TGCTTGGCTTACAAAGAGG	TOP3B	CCAGCCAACTATGTCCAGG
CCND2	CCAGTTCGATCATCGACCG	HMOX1	CAGAGAAATGCTGAGTTCA	PALB2	CCCTAAGACGACTCTCAGG	TOP3B	AAAGTTCCTAGGTTAGTGG
CCND2	ATGTCGCTCAATGAAGTCTG	HMOX1	CATGCCCCAGGATTTGTCAG	PALB2	CTGTGCTTGGCTGACAAAG	TOP3B	ACGCCATCGACGCGCTAGG
CCND2	TGAAGTCTGAGCATCTGCTG	HMOX1	TTTGTCTAGAGGCTGAAGG	PALB2	TTACGGAACAGGAACCTGA	TOP3B	GGAAAGAAAAGGCCAAGCAG
CCND2	CTTCGAGTTGCAGTACCTGA	HMOX1	CCATCGACGGTATGTGAAG	PALB2	ACCGGCTCTTCCCAAACA	TOP3B	CTGCCAGCCGAATATGTGA
CCND2	CATGAGGAGTGACAGCTGCC	HMOX1	GTACCCAGGTAGCGGGTGT	PALB2	AGTGGGAAAACCTTTATACC	TOP3B	CAGGAGCATGCCCAGGTTGG
CDC34	CCACTCTGTACATCACCG	HNF1A	GCAGAAAGACCCTAGCAAAG	PARP1	GATGTCCACCGAGGCCAAGG	TP53	GCAGTCAAGCACATCAGCG
CDC34	TTTCCACTTCTGTACATCA	HNF1A	GCAGAAAGTACCCTCAAGCAG	PARP1	CTACAAGTGCAGCTTCTGG	TP53	CAAGCATCCAGGACCATGA
CDC34	CATCTTGGTCAGGAACCGAA	HNF1A	AGACACGCACTCCGTGAG	PARP1	TTTATAACCGAAGATTTGCT	TP53	TGGGAGAGACCGGGCCAGC
CDC34	TCAGGAGGGAGTACACACT	HNF1A	GGAGGAGCGAGAGACGCTAG	PARP1	ACATATCAGCAAGTACCCA	TP53	CCTCGCTTAGTGCTCCTGG
CDC34	CCGGTGGACGACCCTCCAGG	HNF1A	GGAGCGAGGAGACCATGTGG	PARP1	CTGTCTGCATTTGTTCAGGAG	TP53	TATCTGAGCAGCCGTCTAGG
CDC34	TATCTCCTCCTCCACCCCG	HNF1A	GAAGTACCCTCAAGCAGCGG	PARP1	GCGCATGCTCTGGAGAAAG	TP53	GGTGGAGTCTCCCTTCTTGG
CDCP1	GGTTCGCACTGTACCAACGG	HS2ST1	TGGGGGCACTATAATCTCG	PBRM1	AAACGGAAAATCAACATGAG	TP73	GCTGGAAAGTCAACCTCAAAG
CDCP1	CAAAAAGCAAGCTTACTCTG	HS2ST1	CATGAGAAAAGTTTGTGCG	PBRM1	TCCATTCTGTCCCACCAGG	TP73	CATGAGTCTTAAAGCTAGG
CDCP1	CGGCCGAATGCAGTGCACCG	HS2ST1	AGTGGGGAGTTCCTCTCTG	PBRM1	CGTGTGCTCTCATTTGAG	TP73	CAGTGAAGTCTTCTCAAGG
CDCP1	TCTAAGTGCAGCCACGAG	HS2ST1	CATGGCTTTCGAGAAAAGA	PBRM1	TTTCAAGTGGCTTGCAGGAG	TP73	TGGGCGCTCAAGGACCGCG
CDCP1	CACCGTCAAGCCCTGCCTGG	HS2ST1	CACCGCAGCAGCTGCAACT	PBRM1	TCAGAGCTTCTCTCTCTCG	TP73	GMAAAGTCCACTCAAAGTGG
CDCP1	ACTTTCTTAAAGGCGGAG	HS2ST1	CCGGTGGGCTGCTCTCT	PBRM1	CGAAAGAGTACTTGGGGTGT	TP73	TGAAAGTCCCTCAGGACGCTG
CDH1	GTGAAGGGAGATGTTAGGG	HTR1F	AGTAAATGGTGGAAACAATG	PDCD1	GCGTACTTCCCATGAGGG	TRADD	GCGCTGCGAAAATCTGAAGT
CDH1	TCAAATGATTTTGTAGCTG	HTR1F	TCCAAATGTTGAGTAAATGG	PDCD1	CGGCCAGTCCAAACCCCTGG	TRADD	TCGCGAGAGAGGGCAACCGG
CDH1	ACACACGTCGACTCCTAAGG	HTR1F	TCGCTGCAATTTGTGACC	PDCD1	CTGTCTCACACAATGCCCAA	TRADD	AAATCTGAAAGTGGCGCTCG
CDH1	TTCAGCCGAGAACAACAACA	HTR1F	TGGTCCCTCAGAAATAGAGG	PDCD1	GCAGTGTGTGACACGGGAAG	TRADD	CTCTCTCCGGCCTCACCGG
CDH1	CAACCCCTAGTGTCCTCCG	HTR1F	ACCACAGCAACAAGCAAGT	PDCD1	GCAGCCAGACTAGCAGCACT	TRADD	TTCGCGGGCGGACCGCCCTG
CDH1	CAGGGCGGGAGAGTACCGG	HTR1F	CCTCTATTCTGGAGCAACA	PDCD1	AGCCGGCCAGTCCAAACCC	TRADD	GCATCTAGCTGGGCTCCGCT
CDK6	AAACCTCCAGAGTACCAGG	HTR6	GCAGCAACTCAGTGGAAAG	PDGFR4	TCGCCGAGACAGGAGTACC	TRAF2	TGCTCGCTATCTACTCAA
CDK6	ATGATGTTTTCAGCTCTCCG	HTR6	GTTGACGTGTTGCCGACGG	PDGFR4	CCGAGACAGGAGTACCCTGG	TRAF2	CGTATCTACTGTAAGGCGGCA
CDK6	GTCCAGACTACGCCACCCTGG	HTR6	GCAGAGGATGACGAGGTTAG	PDGFR4	TTCAGCCAGGATATCTGGG	TRAF2	CAGGAAGCCGACGGAAGCTG
CDK6	GTAACAGATATCGAGTAACT	HTR6	CAGGACCCCAAGCAGGAGGG	PDGFR4	ATTAAGAGTGTAGCGTGCTA	TRAF2	CGCCGAAGTGCAGGCTGCTG
CDK6	TGGAACTTTTACGAATTAAG	HTR6	TCAAAGAGAACTGCCCAAG	PDGFR4	CAGTGAATCACCACCATGAG	TRAF2	GGGAAAGTGGGGCGGTGTTG
CDK6	ACTCCAGAGACTCCACGGGG	HTR6	GGCCCAAAAGGAGGGCAACC	PDGFR4	AACATTTTGTGAGAGGTTG	TRAF2	AAGCCGCGGAAAGTGTCAAAG
CDK8	AATATTTACTGTCGACAGT	HUS1B	CTGGTGAAGAACAACCTCAG	PDGFRB	AGGAACGTGCTCATCTGTGA	TREX2	TGCCAGGCTGTAAGCCTGGG
CDK8	ATACTTATGAAAGGTCGAGT	HUS1B	ACAGCAAAATACATCTCAGA	PDGFRB	GACTCGAATTACATCTCCAA	TREX2	AATCATTAATCAAGCCATTG
CDK8	CTCTTATCAGCACTGACAGT	HUS1B	CCTGAGTATAGAGCAGGAGG	PDGFRB	GCTAAGTACATGGAAGCTCG	TREX2	GGCTGGCTTATGATGCGCGC
CDK8	GTTTTCATATACTTGTATA	HUS1B	GCACCTGAGTATAGAGACGG	PDGFRB	ACTCCTGTATCAAAAGTTGCT	TREX2	AGGCCAGGACTGTCCGGCGG
CDK8	GGACAGAAATCTCAATGTAA	HUS1B	GCGCCCGCTTCCCTCAGG	PDGFRB	TGAGCAGTCTCCTAGCCCG	TREX2	CCTTTGATGGCGCTGGTG
CDK8	AAGTGAATGCTTTACTATC	HUS1B	GGCGGAGACCTGTCCGGG	PDGFRB	AGGTGCATGTAGCTTACGAC	TREX2	CAAGCCATTTGGGCGCACA
CDKN1A	AATGGCGGGTGCATCCAGG	HYOU1	ACTGAGCTTGGAGTTAGG	PIGG	GCCTCGGAGATGTCCACGG	TRMT11	ATGATCTAAACCTCTCTGG
CDKN1A	GCGGGTGATCTTCTCCAAG	HYOU1	CAACACAGGCTTCTGTGG	PIGG	TCTCAACAACATTTGCCACCG	TRMT11	CTCCTCTCAACCTAAAACG
CDKN1A	TGTCACCGAGACCCACTGG	HYOU1	GGCTGGGAAGATGCAACTG	PIGG	GTCTAAGCCAGCAAGGCTG	TRMT11	AAAAGAAAGGCTTCCAGGA
CDKN1A	CAGGCGAACTGACCCTCCG	HYOU1	TATGAACTTCTCAAGCTGT	PIGG	TGCCCGTGAACAGATGCCA	TRMT11	TTACAGAAAGGAGATACAA
CDKN1A	ATTTCTACACCTCAAACCG	HYOU1	GTTCCTGTCTTCCAGGTTG	PIGG	TCATTAGAGTGTGAATCAAG	TRMT11	AACCTAAGGAACAAGGAACA
CDKN1A	AGATCCAGCCGGGTTGGAG	HYOU1	GGAAAAGCTTCCCAACGCT	PIGG	GCAGCTTCCCAACAGCGGATG	TRMT11	CATCTCAAGCAAGGACATCA
CDKN1B	GGGCAAGTACGAGTGCCAG	ICAM4	CGTACCGCAGGTGTCCCGG	PIK3C2G	TTTGTTCGACAGCCCTCAGAG	TRRAP	AAGAGGGGTTGTCTCCAGC
CDKN1B	TTTACGTTTACGCTCTCTG	ICAM4	TCCAAAATCACGCTGTGGG	PIK3C2G	ATCCCAGTGAAGTTCTGAGG	TRRAP	CCTCTTGGAGGTGTCCGGG
CDKN1B	CAAGTACGAGTGGCAAGAG	ICAM4	TTTTTCCTCGCCAGGTCAGC	PIK3C2G	ACTTAGCTTTTCTCTCTG	TRRAP	GCTGCTTTGATGATCCCAAC
CDKN1B	CCCTAGAGGCAAGTACGAG	ICAM4	GTGCGGGGCTGGAATTTCTG	PIK3C2G	CATATCCAGTGAAGTTCCT	TRRAP	TGCTACTGTGAACCTCTTGG
CDKN1B	TCGACAGGTTCCCAAAATGC	ICAM4	AGGTACGAGGCGGATGCCGG	PIK3C2G	ATGCAAACTGCTTCAAGT	TRRAP	GCACCAGTCCCAATGTCCA
CDKN1B	ACAGAAAGAATAATTTCCAG	ICAM4	TTCTCGGCTTIAAGACGG	PIK3C2G	AAATCTGTITTCAAAATGTG	TRRAP	TTCCCCAGAGTGCCTGCTG
CDKN2A	CATCAGCAGGAGGCGCAGG	IFNA7	ACATGAATTCAGATCCAG	PIK3C3	GTITACAGTCAAGTCTGCT	TSC2	AGGTTCACTGATGTCAGG
CDKN2A	ACCAGACAAACCTCACTCG	IFNA7	TGAAATGGATTCCGACAG	PIK3C3	GCCAATGGGATTAAGTCTG	TSC2	TGCTCAACTGATCCGCTG
CDKN2A	ACGACCGAATGATACCAGT	IFNA7	TTCTTACTGATGGCTGTC	PIK3C3	CTTACGACAGGAAGTACTG	TSC2	GCTGGCGCTTCTTGCGGAC
CDKN2A	TTTTCTGGTTCACATCCCG	IFNA7	AGACCCACAGCCCTGGTAA	PIK3C3	ACCTCAGCACTAATCCCATT	TSC2	CCAGCCGGGTCAGCATCCG
CDKN2A	CCATGCCCGCATAGATGCCG	IFNA7	AGAATACACTCTTATCTAA	PIK3C3	GCTGTTACGGAAAGAAATCT	TSC2	GCAAGGCTTGAAGTCTCTAC
CDKN2A	GGTACCCTCGCATCTCCGGA	IFNA7	TTTTCAACAACTGAAAATA	PIK3C3	CTGGTGGCTAACACCTTATA	TSC2	CCAGCTGTGCTCACCCCGC
CDKN2B	CAGAGTACCCTGCACCTGCG	IGF1R	AGATGAAGCTGAAACAGAG	PIK3CA	AGACCCACAGCACTACATCAG	TSRHR	CGATTTGGAGGATAGTACG
CDKN2B	TCCACTAGTCCCGCGCCCG	IGF1R	GGCCATTAACAACTGAAGCG	PIK3CA	ATGCAAAATCAGTGCAAAAG	TSRHR	TCCTGATGGCACTGCCAGGG
CDKN2B	GGTACCTGCACAGTCCGCG	IGF1R	TCATCTGGAAGTGAACGCA	PIK3CA	ACAATAAAACAGTTAGCCAG	TSRHR	ACTCCGCACTGCCCATTGG
CDKN2B	GTTCGAGCCCACTCCCGCG	IGF1R	TTGCTGGGTGGTGTGCCA	PIK3CA	TGAGCCACTGATGTAGTGT	TSRHR	ATTGACAAAGATGCTTTGG
CDKN2B	ACGGAGTCAACCGTTTGGG	IGF1R	TCACAGAGACTTGTCTGCC	PIK3CA	GAACAATAGACTCCEAAAGG	TSRHR	AGATAGAATAATGCTACTG
CDKN2B	CCCTGCCACTCTCCACCAGG	IGF1R	CCTTGTGCCTCCGAAATGCA	PIK3CA	TGCTCACAATGATTAACAAT	TSRHR	ACGAAGAATTAATCCGGCCG
CDKN2C	CAAAGAGCCCACTCCCGGG	IGFBP1	AGTCGTAGAGGATTTCGAG	PIK3CG	CAAAAATTCAGCAAAAGCACG	UGT2B28	ATTTTGTCCAAAGGATGATG
CDKN2C	GAAGTGTCTAGGTCCTCCG	IGFBP1	AGAGAGTTTAGCCAAAGCCAG	PIK3CG	GTCCCTATTCCAAGAACAA	UGT2B28	TCAGGTTGATCCCAAAAACA
CDKN2C	ACAAAATGAGTAAGTGTCTG	IGFBP1	ACTGACTGATGGCGTCCCAA	PIK3CG	AAATGCAACCAATTTGCCGAG	UGT2B28	GATCAGAGCTTTGGTGAATA
CDKN2C	GACGCCAACTCTGTCCGGCA	IGFBP1	CGAGCCTACTAGTACTGCA	PIK3CG	TTGAAATGCAACCAATGTCG	UGT2B28	CAAGGGAGAGCAGCTGTAGAC
CDKN2C	GGAACTACACCCACCGGAG	IGFBP1	CAGTACCTATGATGGCTCGA	PIK3CG	GTAAATTTGGCAATTTGTCG	UGT2B28	TTTTCCCATTTGTCTAAATA
CDKN2C	TGGCAGCAAGTGCAGGCG	IGFBP1	TCTGTAGAGTTCATCTCCG	PIK3CG	AGATTTGTTTTCCTGTGCG	UGT2B28	TGGTAGGCACTTAATTTGTT
CDKN2D	ATGACGTAGACTTGTACC	IKZF1	GGCAGCGGTGATGCAAGG	PIK3R1	AACAGTCCGACCCCAAGAG	USP22	CAGGGGAAGAACCATACAG
CDKN2D	GGGTGCCAGATCCAGT	IKZF1	CAGTGGCGGCTCCTCCCG	PIK3R1	AAAGCTGAAACCTGTTGCG	USP22	AGCCCAAGATCAAGTCCAG
CDKN2D	GGACACCTCGAAGTCTAG	IKZF1	ATCAGAGAGTCTCTGCTG	PIK3R1	ATAGAAAAGTITAAACGTGA	USP22	TGTTAACCATCAAGGACCT
CDKN2D	CGTGGAGTGCACCAAGTCC	IKZF1	AGGCATAGAGCTTACTGTT	PIK3R1	GGCAAAGAAGTTGAAGCGAG	USP22	CAGTATGTGTCTCTCCTCCC
CDKN2D	AGGTCGCGCCCTCTGCAG	IKZF1	GCAGAAAGCTTGCAGAAAT	PIK3R1	AGCCCTGTTTACTGCTGCTC	USP22	ATTCACAGACAGCAGCAGG
CDKN2D	CGCCGAGCCGCTGAGTGGG	IKZF1	CCGAGAGGGCAACTGGCTC	PIK3R1	GAGATGGCACTTTTCTGTC	USP22	GCACCCCTGCACTTGTATCT
CELF5	CCGCTGTCCAAACTCCTGG	IL7R	TACGAGCTTTACTCCAGC	PLS3	AGAGTTCATCCAGTTACGGA	VWC2L	GCACACCAATTCATGAGGAG
CELF5	AGCTCGATGCATAAACCCT	IL7R	CAAGTCGTTTCTGGAGAAAG	PLS3	GCATAGAGATGTTTACGTCG	VWC2L	TGTAATAAAGTGAACACAA
CELF5	GAGGAGAAATGATATGGCCA	IL7R	TGTTTTCACTCTTTCTCTGG	PLS3	CCAACCAAGGAGAAATTAAGC	VWC2L	AAAAAATCTCTGTAATATCA
CELF5	GAAGGACAGTGCAGTGTCT	IL7R	AAAGCAAGATATAGTGTGA	PLS3	TTTTATACAGCTGGCTTGG	VWC2L	AACACAGTAACTCATTTG
CELF5	TGCTGGGCTCCGGAGAGGCG	IL7R	CTGAGTGTCTCTATCCGGA	PLS3	AACTATGACCTTGTGAAGAG	VWC2L	CGGGAAAAATACAATAATCT
CELF5	GATGGGCGTGTGGCCCGGG	IL7R	CTTCCGATAGACGACACTC	PLS3	GCATCTCTGTAATTTCTCC	VWC2L	CATTTTCTGTGTCATAGAC
CHD8	ACCACATCTCCAGTTCAGTC	INHBA	GGCAAACGTGATGATCTCCG	PMS1	CACTACAATAAGAAGACTG	WDR27	CTGCTGAGCCCTGACTAGCG
CHD8	GCCGCGCTGAAGTGGAGAG	INHBA	AGTGGTGTATGACTTGTGAG	PMS1	GCAGATGACCAAGATACAG	WDR27	GATCAGAGTGAAGGTCGGT
CHD8	ATCTCCAGTTCAGGCCGGG	INHBA	CTGTCTCCAGCAGCAGTCCAG	PMS1	AAACCTTCGCTGTAAAGAG	WDR27	AATTTCCGATACAGTGGAG
CHD8	AGAAITGAAGCTTGGGAA	INHBA	GTAGTTGGCATATAGCCAG	PMS1	GGATTTCATGAGAAAAGT	WDR27	TGGCCGATCTGTGTGAGG
CHD8	CTAGAGTTAGCTGTGATCA	INHBA	TGAACATATGAGCAGACTC	PMS1	GTGGAACAGTATGAGTGAAG	WDR27	TGCCAAGGAGGAAGATGAC
CHD8	CAGACAGCAACTCTGTACAA	INHBA	AGATAGAGATGACATGTGA	PMS1	AGAGAAGGCTACTAAAGACT	WDR27	AATCTCCCGCAAGAGAGGG
CHRM4	CACAGAGCTGCCACCACG	INPP4A	TTTACAAGAGTATCAACG	POGK	GTACGAATCTGCTGAGGG	WDR45	GGAAGGAGTACATAGATG
CHRM4	GGCTTCTTGGTGTCTGCG	INPP4A	TCAAAGTGGAGATTTGGTG	POGK	GTACCGCCCTATTGTTAGT	WDR45	ACTACTCACCCGCCCCACA
CHRM4	TTATACCCAGCGGGCAGCG	INPP4A	GTTTAAAGGAATTTGGCTG	POGK	CAGAGCCGGAAGTGAAGGA	WDR45	CTTGAAGATTTGCGACCGA
CHRM4	ATTGCGGAGCTCCTCCGGG	INPP4A	TGCCCGGGGAGATCCAGAG	POGK	AGTCTCAGAAITCTGACGAG	WDR45	GCCTTAGTGGGAGCAGCG
CHRM4	CACAAACTGCCAGAACAAG	INPP4A	TGAACCGGACCCCAATAAG	POGK	AGCCCGCCTATTGTATGAGG	WDR45	GATCTGGGACGAGCCCGG
CHRM4	GATGAGAAGTTCATGACCG	INPP4A	TAAAGACCGTACAGCCTAT	POGK	CAAAAATTCCTTCTCTCAT	WDR45	GGCCCAAGAAAGCATGCTG
CLDN1	CATCACTTCATCAACACCG	INPP4B	AGATGAGACCGATTACACA	POLD1	GTTGGAGTCTTAAGTACACAG	WDR49	CCGCTACAAGAGTGTGCTG
CLDN1	AGATTGCTATCACTCCAGG	INPP4B	CGATGAAATTGGAAATGTAG	POLD1	GTGACCTGACACCCAGTCCG	WDR49	TGTTGGGCAAGTGGAGCTG
CLDN1	ATGAGGATGGCTGTACTTTG	INPP4B	CTTAAAATCGGAATAGCCAA	POLD1	TGACCGAGTGGCCAGCAGG	WDR49	GGTAACTCAGGTTGAAGAAC
CLDN1	TCTATTGCCATACCACTGCT	INPP4B	AGCTGTACCGCAAGTCTCTGA	POLD1	CGGCATTGAGCCTGTAGAG	WDR49	GTTATTTCTTCTTAAAGATG
CLDN1	CTAATTTAGTATGCCACAGCA	INPP4B	ATGTCCAGGACTGCTTTGGCT	POLD1	CAGTAGGACAGTGACCCAGT	WDR49	ATTTTCTTTAGCAACCTC
CLDN1	TTAGTGTCCACAGCATGCTA	INPP4B	GAAAGCTGCTAGTGGAGAAC	POLD1	CAGGGAACACTGCCCTCTG	WDR49	TTTTTACGCTGTGAAGAA
CLDN11	GGATGACACAGCCACCCAG	IQGAP2	CTTTTCCATCTCAACACCA	POLE	CTGTACAAGAAGGCGGCTG	WDR70	GGCCGAGTGGCAACCACCG
CLDN11	GATGCCAAAGCTCAGGATGG	IQGAP2	GATGAAAAGAGGAAACCCAA	POLE	AAGCGATGGCATCTTCCACA	WDR70	TGTTCCGAAAGCCCCCAAA
CLDN11	GGAGTAGCCAAAGCTCACGA	IQGAP2	GAAAGTATCTATATCTAGC	POLE	CACCGCCTCTTGTATACAG	WDR70	TTAGCCCTTAGGCTTCCC
CLDN11	CCGGTGTGGCTAAGTACAG	IQGAP2	TCAAATTAACAGTATGAAA	POLE	ATGATCCATCTAACTATGG	WDR70	ACTGGTACATCTATCAAAG
CLDN11	GTCAGCAGCATAAATGGC	IQGAP2	GTCTAACAAGTCTTATGT	POLE	AGAAATGTGAGAAATGGA	WDR70	GGGCTCACGGAACATAGCA

Table with 4 columns: ID (e.g., CLDN11, CPN1), Sequence (e.g., GATGGCCAGGACCCGGTG), Gene (e.g., IQGAP2), and RefSeq (e.g., TAAGCTTCAAAAGCTGAAT). Includes multiple rows for each gene, showing various isoforms and subtypes. The table ends with ID DDX2 and RefSeq ACAGGTGTGCCAAAGTCGG.

DDR2	TCGGTGACAAAATTAAGAG	KLK5	CAACCAGCTACTGCGGGG	PTRPS	CGACCATGCTGATGAGG	NTC 111	TCCGCTGGTTAATACGCT
DDR2	AGGAGATAAAGATCATGTCT	KLK5	ACAGGGAGTAGTGCGCGAGA	PTRPS	GTCCAGTTCACAGACTGCG	NTC 112	CTATCTCGAGTGGTAATCGC
DLCL1	CCAAGCAGGTCATCTCCAG	KMT2A	GAGATGGTGTAGTATGCG	PTRPT	GATGAGCACTACAGCAACTG	NTC 113	AATCGACTGGAACCTTGGTG
DLCL1	TGCCGATCTGATCCACAG	KMT2A	GCTCCATCCAGACTGCAAG	PTRPT	CAGCAACTGTGGTTAATAGT	NTC 114	CCCGGTGACATAACCGAAC
DLCL1	TGAGCGAAGGCCCTCTCTG	KMT2A	TTCTCTTACAGAAAAGACC	PTRPT	ACTCTCCAACTATAAGCTG	NTC 115	ACCTCTCGACTAAGCCACTG
DLCL1	TAAGTCAACTCTGCACATCT	KMT2A	TSAGAAACAACTGCATCA	PTRPT	ATCGCACCACCAGGGCAGG	NTC 116	CDCGAGCACTAACCTAGTC
DLCL1	TTAACCCCTCACACCACAC	KMT2A	ACTGAGAAAACCCCAAGAA	PTRPT	GTCTCCAGGTTGAACCCAT	NTC 117	GTCCACCCTGAGCACTAG
DLCL1	GACTCCAAAGCTCAGAGG	KMT2A	GTCATTGACAGATAAAGTC	PTRPT	CCTCACAGGAGGAGTGGG	NTC 118	CTCAACCAGCCGATAGTCA
DLEU7	CCGAAGTCGATCCACACG	KMT2B	GCAAAAGGGGACCTTCTGG	RAB8B	AGACAAGTGTCAAAAGAAAG	NTC 119	CTGATTCGACTCTCAACGG
DLEU7	TGGGAGGTCGGCCGCGCG	KMT2B	GAAGACGTCCAAAGAAAGCTG	RAB8B	CAGGATCATCTTTCGACAT	NTC 12	CGATCCCGAGACTTCGAGCC
DLEU7	GACTTCGAGACTGGTCAGCG	KMT2B	GGTAACGGAACTTATAGTGC	RAB8B	CATTCTTTCGACATCGGAG	NTC 120	GAATCGACCGACACTAATGT
DLEU7	TCTGCAGAGCCACCAITGG	KMT2B	ACTTATAGTCTGGCAACGCG	RAB8B	CCAATTTTAAATTTGTCAA	NTC 13	ACTTCAGITTCGGGTAGTCA
DLEU7	TCCATCAGCCACCAATGG	KMT2B	GTGCTGGCAACGCTGGGCT	RAB8B	AGTACGGCTCGGTGATTGT	NTC 14	GTGCGATGTCCTTCAAGCT
DLEU7	GGTAGTGCCAGGCCGTGAGG	KMT2B	GTAGACACCACAGCTTCT	RAB8B	TGACTATGGGATTAATTTCT	NTC 15	CGCCTAATTCGCGATCAAT
DLX3	TAGCTGGAGTAGCTGCTAG	KMT2C	TGCGGAACATGTACACACCA	RAC2	CTTGCCTGCCACATCAAT	NTC 16	CGTGGCCCGAACCCGTATAG
DLX3	GGGCGCTTACTGCACCAGT	KMT2C	TCACATGGCTGTTATCCATG	RAC2	TCTGTGGATAGGAGAGCGG	NTC 17	ACCTCGCAATCGTAACCGA
DLX3	ATACGCCCCGATTTGCCGGT	KMT2C	AGACCGTGCCAGATAACAT	RAC2	GGCGCGGACGTTCTCATAAG	NTC 18	AAACCGTACGACAGCGTGTG
DLX3	TGGCGGATGAGAGGCTCCGT	KMT2C	ATTGACCGGCTGCACAGG	RAC2	CCGGATGCGCTCGTCAACA	NTC 19	ACATAGTACGACCGTGTG
DLX3	GCGCGAAGCAGAGGTGCGCA	KMT2C	AATCCAACTGTGATCTGGCA	RAC2	CATAAAGAGGCTGGCTGACG	NTC 20	GATGCGGCTTCAGTCGCGG
DLX3	AGTAGACTCTACCGGCTT	KMT2C	TTTTTCTACTACATGCCCAC	RAC2	AGGGCACAGCAGCGGCCGGA	NTC 21	ATAATCGCCAGTTCGAGTCA
DNMT1	AGGTGCATCTAGGCCCATG	KMT2D	ATTGATGTACTGTTGACCGG	RAD50	GGCGAATTAATACTACCAGG	NTC 22	CGCCGGGTCAGCAATTACG
DNMT1	ATGCTCTGACATTTCCAGG	KMT2D	GGACCTAGAAAAGCACAAA	RAD50	CTGTGGGCAAGTACTATCG	NTC 23	CTGCGCATATGCCGCTGGC
DNMT1	ACGGCTGGCCAGACTGAGG	KMT2D	CCTGGGCTCTATGCAGGCA	RAD50	GAACGTTCTGCTCAACTG	NTC 24	CGGGCTATACACCATTCA
DNMT1	GAGGCTGACTTCCAGACCA	KMT2D	TGATTCACCTATGCGAAGCA	RAD50	ATAAAATATACGTCACCTG	NTC 25	CGGGCTTCCAGACTTTGA
DNMT1	AAGCTTGATCTCCAGACCA	KMT2D	CACCATACTCCGGAACGAGG	RAD50	ATTTGTTGTTGGCTATCCA	NTC 26	GGGGAGTGGGAAAATGTA
DNMT1	TATGGAAGGCTCGAGTGGGA	KMT2D	GTTTTGACGCTCTCCACCG	RAD50	AGCCTCACTCATCTCCGCG	NTC 27	TCCGCACTCGGACAGCACG
DNMT3A	AAGTGAGGCATTCGACTAG	KNSTRN	ACTGAGTGAACAAAAATCAG	RASA1	GAGATGATAATGAAACATCCG	NTC 28	AGCTCATTCGCGCGGTTG
DNMT3A	CTCCAGCTATCATTACAG	KNSTRN	AACGCAAAACAGAGGATG	RASA1	GAACATCCGTGGATTCAAGA	NTC 29	ATCGTATCATCAGCTAAGCC
DNMT3A	GAGCAGGTTGACAGTGGAG	KNSTRN	TCTGATTTTTGTCTACTACG	RASA1	ATCCGTGGATTCAGGATGGC	NTC 30	TGATCGAGTCTGCTTCGCG
DNMT3A	CTCCTGACAGGGTTCAGCA	KNSTRN	AGAACTCCACTACTGATCACA	RASA1	GAACATACTTTCAGAGCTTG	NTC 31	CTCGAGACTTCCTCCGCGAC
DNMT3A	TCTAGAAGCAGGAATAATGC	KNSTRN	AGACTCCACTGATCAGTACG	RASA1	TGCAAGAACACTGATATTAG	NTC 32	CCTGATATTAAATCCGTGAC
DNMT3A	GGAGTGGGCCCCATTCGACT	KNSTRN	GCTGTAGAAACTTTTGAAG	RASA1	ATCAGTGTTCTTCGAGCAAT	NTC 33	TGAACGGCTGTTCTCTGCA
DNMT3B	GAATTAAGCTCACGCCCCAAGG	KRT27	CATCTTCTTCACTATCAGG	RB1	TAAGGGTCTCGAGGAATGTG	NTC 34	CGACGCTAGTAAGCTAGAG
DNMT3B	GGCGTAGATAATTGAGGAG	KRT27	AAAGTCTTCCGGGCTGAGG	RB1	AAATGAGGATTTGGTGACA	NTC 35	CATTGTGAGCGGGCGGTTG
DNMT3B	GCTGAGTACTCACGCCCCA	KRT27	TCTAAATCCAAAGGCTATGG	RB1	GGAACTCGTAAGGGTGAAC	NTC 36	CCGGTATTGAAACCCGCCAC
DNMT3B	CGTCGCTTGAAGTGTG	KRT27	TGTTCTAAATCAAAAAGCTA	RB1	TTTATAAAACAGTGAAGAG	NTC 37	AGACACGTCACGGCTCAAAA
DNMT3B	AAAGATTGGGCCATAAAGTG	KRT27	ATAGCCCTTTGATTTAAGCA	RB1	GAAGAGGAGGTAGATTTCAA	NTC 38	TTTACAGCTATCGCGGCTAG
DNMT3B	TGTTGGAACCGTGAAGCACG	KRT27	TCATCTCTGATAAGCTCACT	RB1	GTCCAATTTCAAGCAGAAAC	NTC 39	TTCCAGACTTTCAGCCTGG
DNMT3B	GGAGACACAGTCAGCCAGG	KRT33B	GAATCAGTATGAGGCTCCGG	RBL1	TGATATAAAAGCCACAAAG	NTC 40	GGTTAGACACTAGCCCGCG
DOK3	ACCAGTCCCATCTACCACAA	KRT33B	GCCGACGGGACTGCTCCCTG	RBL1	TAAGAAAGACTCTTTGGAG	NTC 41	CCTCCGTCTAACGCCGACG
DOK3	GGCCAAACAGACTCCCTGG	KRT33B	CAGGAATCAGTATGAGGCC	RBL1	TGTCCAAATCTTCAACA	NTC 42	TTATCGCTATGCTGAGCT
DOK3	GCACACAGGTTCTCATAG	KRT33B	CAGGGCTCATACTGATTCC	RBL1	ATGTTTCAAATGAGTTACGA	NTC 43	TAGCCTTTGGTTTAGCGTCC
DOK3	CGTGGTGGTCAGGAGACTG	KRT33B	CCTCCTGAGGCACTCCATC	RBL1	GTCCCTGATTAATGAAAGAC	NTC 44	CGCGCCCAACCGCTCATCCG
DOK3	CAGTAGTTGGCTTCAGCTGG	KRT33B	CAACAGCTCGCGGAGATT	RBL1	TCTTCGTAATAATGTTGTA	NTC 45	AGCTCCGATTCGCTTCTCT
DOT1L	CCTCCCGAAGGCTCTCCAG	KRTAP25-1	CAGCCGAAAAATAAAGCT	RBL2	TGGCAGAGAGTCCCGAAGG	NTC 46	AACTAGCCCGGAGCAGCTTG
DOT1L	GCTGTGAAAATCAGGTCCG	KRTAP25-1	CTAAGAAGCAATGTTTTG	RBL2	TGCTACTGTTGGCAGCTGTG	NTC 47	CGCAAGGCTCGTAACTCC
DOT1L	GACAAGACCCCACTGCTGAG	KRTAP25-1	CCCAAAAATCAGAAAAGC	RBL2	GTTGGCCAGAGATCCCGCA	NTC 48	CTCTGACGCCATCGTCTCA
DOT1L	CTCCCACTACCTCAGACAG	KRTAP25-1	ATTGACAGCAATAAGAGACA	RBL2	GTAGGGCGAGTGGGTTG	NTC 49	TTCGCTGATACCGGCTGTTA
DOT1L	CCATTTTCAAGGTTTTCCGG	KRTAP25-1	TTGAAACTGCTGTCAGTGA	RBL2	TTGGCAGCTGTGAGGGGAGT	NTC 50	ATAGCCGCGCTCAACTTCT
DOT1L	CCCGCGTCTCAAGAGGAGG	KRTAP25-1	CAAAAATCAGAAAAGGCTGT	RBL2	TGTTATAGGACTCAGCCCG	NTC 51	GCTGCTCGGATTTAAAAAT
DUP4	ACAGAAATCTGGGATCTCCG	LAMA1	TTTTCCATCAGACAGCAGG	RBPJ	CATTGCTCAGGAAACAAGG	NTC 52	TATGCTCAGCACTCCGGAAT
DUP4	AACTAGACAGATGCCCCCA	LAMA1	ACACACCAGTCTACTCAG	RBPJ	AGATACTTCGATGAGAAG	NTC 53	TATCGCTTCGAGTTCCG
DUP4	CAGCATTGGTACAGCTGCC	LAMA1	GAGGAGCCGATTCGCGAG	RBPJ	AGGCTCTTACCAAGAGCAG	NTC 54	GATCCATACCCGCTACCTTT
DUP4	GGAAAGAAAGTTCACCTCAA	LAMA1	TAACAGCAAAAACGCTGGA	RBPJ	CTACTCCAAATTAAGAGTG	NTC 55	TAAGATCCCGGGTGGCAAC
DUP4	CGAGTGCATACCTGCTCCG	LAMA1	CAGGAGGACGCCTTCTGCG	RBPJ	GTAGCAATGCTTGAACCTAC	NTC 56	GTAGACTCTGAGGCTTAC
DUP4	AAAGTGGTTGGGCACTCCG	LAMA1	ATTGACTAGAGCTTGGGA	RBPJ	CCAATTTACGAGTGTGGTT	NTC 57	TCCGGBACATGAGCCTTAA
DVL2	GGGAGAGTGAATAGGCCCTG	LATS2	GGAGTAGTGCCAAAAGGG	RET	GAGGCCAGCAACTCGAGCG	NTC 58	AGCCAGATAGCGGATCA
DVL2	TTGTTGGCCAGGCAATGAG	LATS2	TCCAACCTACTCGCAAGG	RET	ACATCTGTTAGCTGAGGG	NTC 59	GTTCGTTGTAACAGAGAA
DVL2	GGCCAAACATGGAGTACCC	LATS2	GAGTGTCCACCTTCAAGCA	RET	ATCTGGGATTCCTCOTGAG	NTC 60	GACCCCGGACTAATTTTCA
DVL2	CCCTGGCTCAAATGCCCCCT	LATS2	GACTGGCAGGAGGATCAG	RET	AAGAGGATTCCTACGTGAA	NTC 61	ACGTCCATCCTGTCCGCTAC
DVL2	CGGACTTCCAGTCCAGACT	LATS2	CGAGGTTCCAGTAAATGGA	RET	TCGGATTCAGTAAATGGA	NTC 62	GTAGCATTTCCGCGCTCCCTA
DVL2	GCCATGCGCAGCTCCAGATG	LATS2	ACACTCAACTTGTGACTGG	RET	ACCTTCTGAAGACCCGGCCAC	NTC 63	TGTTTCCGTAAGCGTGATTA
EGFR	AACCAACAATTTCCAGTCC	LCE1D	CTTAGGGGGAATTTAGGG	RHOQ	CGTGTCTAGAGTCTTAGG	NTC 64	CTTGGCTTAGCAGCAGCTT
EGFR	TCTATCAATGCAAGCCACGG	LCE1D	GCTGCAGGAGCCCCAGAGT	RHOQ	CCTCCTAGGACTCTATGACA	NTC 65	CGCTAGGCTCCGGAATGGCG
EGFR	GAATGCAAGAGTGGCCGTTG	LCE1D	AGCTCTGGGCTGCGACCG	RHOQ	GAGGTAAGCTGCTGCCCCCA	NTC 66	AGGTACTTAATGTCGGTGA
EGFR	ATTTTCTCAATGCAAGGCA	LCE1D	TGACTGTTGAGGCAAGCCT	RHOQ	CTTCTTATATGCTTCTCGG	NTC 67	AAAGGCGCCGAATGGGAG
EGFR	AGAATTCAGATGATCACTCA	LCE1D	ACATTTAGCCGGGGGCACT	RHOQ	GGTAAGATAAAGGCCCTCAGA	NTC 68	ACTGCGGAGCCGCAATGTA
EGFR	ATGATCAACTCAGGAACTT	LCE1D	GCGCCGCTGGCTCAACTC	RHOQ	TGTAAGAGGAGTGGGTCAT	NTC 69	CGTGCAGTCTGCAACTCCA
EIF1AY	AAGAGAGTGGTGTATAAG	LHDD	GGTCAACCTGTAGCCGCG	RICTOR	AGCAGTATGAGAAGAACCTGG	NTC 70	TCCGAGAGTGGGATCGG
EIF1AY	ACATCAGACATATAATTGG	LHDD	GACACTGGGGAAGCAGCACG	RICTOR	ACAACTGGAGCAGACTG	NTC 71	ATCTGTCTAATTCGGATCG
EIF1AY	AATGTGGGAAATGGAGCAT	LHDD	GATGGGCACACACATCCG	RICTOR	GGACACCATGGACCGCACTG	NTC 72	TCCGCGGTAATGCTTGAAG
EIF1AY	TGGAAAGCATTTGTTTGA	LHDD	CCCTGCGGCTGAGGCGCACG	RICTOR	AGAGACAGATGTTAGACTG	NTC 73	CGAATTAATCCGCGGCCAA
EIF1AY	ACATTAATGGTGTGGCTA	LHDD	CTCCACTGATGACTTATCC	RICTOR	ATACCACCATGATGATCG	NTC 74	CGCGTGTGTGGATAGCCG
EIF1AY	TTCTCAATTTCCCTGTGA	LHDD	ATGGAATCCAGGAAGAGTG	RICTOR	TCTGTATGAACCTCCGACA	NTC 75	TACCCTCGGATACCGACTG
ELANE	GAGCCATAACCTCTCCGCG	LGAL9	GCAGGACAGTGCTGACAGG	RIPK1	GTTTCGTCTGCCTGTCTCTG	NTC 76	CCGTGGACTATGGCGGGTC
ELANE	GAAGTTGGGCGAATCAGGG	LGAL9	TGGGTACAGCCCTCCAGAA	RIPK1	GTGTGGGAGTACCTTCAAG	NTC 77	GTACGGGGGATCATCCACA
ELANE	TGGGAGCCCATAACCTCCTG	LGAL9	ACTTGCTCCTCAGACCCCG	RIPK1	ACAGCAGCCGAGCAGAAAT	NTC 78	AAGAGTAGTAGAGCCCGCG
ELANE	GCAGGAGCTCAACGTGACGG	LGAL9	AAAACGGGGGTTGAGGTGGA	RIPK1	GCAAAACAGGACTCTCCAC	NTC 79	AAGAGCAATCGATTTCTGTG
ELANE	GTTTTGCAAGATGCGCTGCA	LGAL9	TCCAAGTCCATCCTCCTCTG	RIPK1	TACAATATATGGAGATTGG	NTC 80	CGGCTCGTTCTACGACTGA
ELANE	CTGCGGGAGGCCACTCTCT	LGAL9	TCTCATCAAAACGGGGTTC	RIPK1	TAGCTTGGTACTTAGCAGC	NTC 81	TCCAGCCGAGCTTACTCGT
ENY2	AGAGCTAAATTAATGAAAT	LMO7	CAGGGACTCGATGATGCTG	RNASEB	TCAATCAATAGTACACAGAA	NTC 82	GGAGTGGTCCCGTACGCAAC
ENY2	CGTACTGTTGATGACTGG	LMO7	AGTCTGGGCTCAGCTCTGG	RNASEB	CCTGAACACACTTACATAG	NTC 83	CAAGACTTATCTGTCGAGCG
ENY2	GTGGCTGAAATCACTCCAAA	LMO7	GTTGCTGTGAGTGTGACTC	RNASEB	GTACTTATGATGATGCTCA	NTC 84	ACGTGTTTAGCAGCCGGCT
ENY2	ACAGTCTACTGTTGATGACT	LMO7	AGTCGTGAGCATAGTTGG	RNASEB	ACAACITTTCAAGTGAC	NTC 85	TTTACGGCTACGGGCGGG
ENY2	ATAATTAAGTGGGCTGGA	LMO7	GCAAATTAACAAGAAGCACC	RNASEB	TGTCAGGAGACATGGGCGCC	NTC 86	CAATCCGGGACTGTTTAAAT
ENY2	TGGCTGGAAGGATCACTTTA	LMO7	TGCAATAACATTTGCGCAA	RNASEB	CTCCACACAGGGGTGACCC	NTC 87	TACCCCTATGGCGTTTCTA
EP300	TGATGCTTCTGACAAAACCG	LYN	CTATAACCAAGTACCAAGG	RNF138	ATCTGGCTAGGATCTCCCA	NTC 88	TACCCAGGGAATTCGACTG
EP300	GAATACCCCTGAGTCCAGG	LYN	AGGAAATGGCATACATCGAG	RNF138	CACAGGGGCACTTAAAGT	NTC 89	CTTTGGCTAGCTTACGATC
EP300	AGATAGATTAAACAGTCAA	LYN	TTCTGGAAGAGCGGATGAA	RNF138	AGTTTCTGTTTATCAGATG	NTC 90	GAAACCGCTCAAGTGTGTA
EP300	AAAGAAATGGCTTAATTCG	LYN	CTACGCTGGTCCAGCAGG	RNF138	CAGATCTCTCAAGATTCAGT	NTC 91	CGCAGTATGATACACTTAA
EP300	AAGGTGCCAAGCTGCTGATA	LYN	TTACTATAACAAGTACCA	RNF138	GTGATCCAGTAACCGCTGTC	NTC 92	CGAACCCTGAGGACCGCT
EP300	AATGCTTCTCCAGAACT	LYN	TTGTAATGAGGAGTTCCAA	RNF138	CAAGGAAGAGACACAAAT	NTC 93	CTCGGGGCTAAATACTACT
EPH3A	TAAGCAAGTCACTGTTGTG	MAP2K1	AACATCTAGTCACTCCCG	ROS1	TGAGGTTGGCTGATGACG	NTC 94	AGGCGACCCGGTTGATACGC
EPH3A	CCAGTTCGAAATGATTTGGG	MAP2K1	CACAGAGCTTGATCTCCCA	ROS1	AGAGAATCTGCTCAAACTG	NTC 95	CAGGGCTAACTTGTGATTA
EPH3A	TGTTCTGACAGCACACTGCA	MAP2K1	TAAAAGGCTGACATACTG	ROS1	TCTCAATCTTCACTACTCG	NTC 96	CCGCGAGATTAACGTTAAT
EPH3A	TTCAAATAAGAGATTTCTAG	MAP2K1	TGGCGAGATCAGTACTGCA	ROS1	TGAGGTCGACTAATAGAGG	NTC 97	ATCTCGGGTCACTCGGAT
EPH3A	ACACTGCAGGAAATTTCTCA	MAP2K1	TTTGCTGCTTTACAGTCCA	ROS1	TGAAAGACTATAACAGTCCA	NTC 98	CCGGCCGGGCGAGTGGAA
EPH3A	TATGATGTCACAGAAATA	MAP2K1	ACGGGAGTTGACTGAGTGT	ROS1	TATAGTCTTCCAGGAAACA	NTC 99	GCAAACCCGAGTGCACGCT

Table 3: FHSC14 CRISPR knockout screen KEAP1 results

Gene	CIS-ETO vs. P0								
	Median Log2(FC)	Max Log2(FC)	Pos. RRA	Pos. Unadj. P	Pos. Adj. P	Neg. RRA	Neg. Unadj. P	Neg. Adj. P	Guides Enriched
KEAP1	1.8	2.4	2.0E-04	2.2E-02	1.0E+00	8.8E-01	5.2E-01	5.8E-01	3
	SAL vs. P0								
	Median Log2(FC)	Max Log2(FC)	Pos. RRA	Pos. Unadj. P	Pos. Adj. P	Neg. RRA	Neg. Unadj. P	Neg. Adj. P	Guides Enriched
	-2.2	0.5	5.3E-01	8.8E-01	1.0E+00	1.8E-02	3.5E-04	2.7E-03	0

Gene	Guide ID	CIS-ETO vs. P0						Guide Enriched
		Guide Log2(FC)	Pos. Unadj. P	Pos. Adj. P	Neg. Unadj. P	Neg. Adj. P		
KEAP1	EGSC_1146	2.4	4.6E-93	5.6E-92	1.0E+00	1.0E+00	Y	
KEAP1	EGSC_1144	2.2	5.4E-82	6.3E-81	1.0E+00	1.0E+00	Y	
KEAP1	EGSC_1143	2.2	2.6E-65	2.8E-64	1.0E+00	1.0E+00	Y	
KEAP1	EGSC_1141	1.4	4.0E-19	2.9E-18	1.0E+00	1.0E+00	N	
KEAP1	EGSC_1142	0.3	1.7E-01	5.1E-01	8.3E-01	1.0E+00	N	
KEAP1	EGSC_1145	-1.9	1.0E+00	1.0E+00	1.1E-04	1.1E-02	N	
Gene	Guide ID	SAL vs. P0						Guide Enriched
		Guide Log2(FC)	Pos. Unadj. P	Pos. Adj. P	Neg. Unadj. P	Neg. Adj. P		
KEAP1	EGSC_1146	-1.1	9.9E-01	1.0E+00	6.5E-03	2.6E-01	N	
KEAP1	EGSC_1144	-3.4	1.0E+00	1.0E+00	1.5E-06	3.3E-04	N	
KEAP1	EGSC_1143	0.3	1.2E-01	3.6E-01	8.8E-01	1.0E+00	N	
KEAP1	EGSC_1141	0.5	1.3E-02	4.6E-02	9.9E-01	1.0E+00	N	
KEAP1	EGSC_1142	-4.5	1.0E+00	1.0E+00	3.8E-06	6.9E-04	N	
KEAP1	EGSC_1145	-6.6	1.0E+00	1.0E+00	1.4E-07	4.8E-05	N	

Table 4: sgRNA sequences used in this study

Name	sgRNA sequence (5'->3')
CRISPR Ctrl-sg1 FWD	CACCGGAGACGGTTGTAAATGAGCA
CRISPR Ctrl-sg1 REV	AAACTGCTCATTTACAACCGTCTCC
CRISPR KEAP1-sg1 FWD	CACCGCTGTCGGAAGTAGCCGCCCG
CRISPR KEAP1-sg1 REV	AAACGACAGCCTTCATCGGCGGGCC

Table 5: SCLC focused CRISPR activation library composition

Gene	Guide ID	Guide Sequence	Gene	Guide ID	Guide Sequence
CONTROL	NT1	AAAACAGGACGATGTGCGGC	LRCH3	LRCH3-1	CCTTGAAAAGCGCATCATGT
CONTROL	NT2	AAAACATCGACCGAAAGCGT	LRCH3	LRCH3-2	TCCCCTGATGGGCAGCACCG
CONTROL	NT3	AAAATAGCAGTAAACTCAAC	LRCH3	LRCH3-3	TGAAAAGCGCATCATGTGGG
CONTROL	NT4	AAACCTAGCCCCAATACTTA	LRCH3	LRCH3-4	AAAGCGCATCATGTGGCGG
CONTROL	NT5	AAACGAGATCGAGAAAGGTA	LRCH3	LRCH3-5	CACCACGGTGGCTGCCATCA
CONTROL	NT6	AAACGGTACGACAGCGTGTG	LRCH3	LRCH3-6	CCCTTGAAAAGCGCATCATG
CONTROL	NT7	AAAGAAAGGAAATAGTAGC	LRRC15	LRRC15-1	GACATGCGAGCTGCACTG
CONTROL	NT8	AAAGATATAGCAAATTATGG	LRRC15	LRRC15-2	GTACCCTGTAGTGTACGCC
CONTROL	NT9	AAAGCGACGTAGGCATACTT	LRRC15	LRRC15-3	TGTCCCGGGCTGACACTACA
CONTROL	NT10	AAATAATATGCATCTCTCGA	LRRC15	LRRC15-4	AGTGTGACGCCGGGACATGC
CONTROL	NT11	AAATACAAGCTATAGCGATA	LRRC15	LRRC15-5	GTGCAGTGCCTGCATGTCCC
CONTROL	NT12	AAATGCACAGATCGGTGATC	LRRC15	LRRC15-6	TGTACCCTGTAGTGTACGCC
CONTROL	NT13	AAATTGGCTTTCGTTCTGTGC	NRROS	NRROS-1	AGCACAGGCTCACTCAGACC
CONTROL	NT14	AACATCTCGTTAGGGGTATC	NRROS	NRROS-2	CGGCCTTTAGAGGGGAAGCG
CONTROL	NT15	AACGCGAGTCCGGTGGCTAG	NRROS	NRROS-3	TCTTAGAGGGAAGCGCGCG
CONTROL	NT16	AACTACAAGTAAAAGTATCG	NRROS	NRROS-4	CTCAGACCCGGCCTCTTAGA
CONTROL	NT17	AACTAGAATAGCGGGCTTG	NRROS	NRROS-5	GCGCCGCTTCCCTCTAAG
CONTROL	NT18	AAGAATTAGGCACGGTACT	NRROS	NRROS-6	GCGCTTCCCTCTAAGAGGCC
CONTROL	NT19	AAGAGCGAATCGATTTCGTG	LRRFIP1	LRRFIP1-1	GCCCCCTGCGCGCTCCGCCTGTT
CONTROL	NT20	AATATTTGGCTCGGCTGCGC	LRRFIP1	LRRFIP1-2	GCCTGGGTGGGGCGGAGCCGGTGT
CONTROL	NT21	AATCGACTCGAACTTCGTGT	LRRFIP1	LRRFIP1-3	GTGGGGCGGAGCCGGTGGGGGTGT
CONTROL	NT22	AATCGCAGGTATCCCAAGAGC	LRRFIP1	LRRFIP1-4	GGTGGGGAAAGGGCGTAAACGTT
CONTROL	NT23	AATGCGAGTGTATCCGCGAGT	LRRFIP1	LRRFIP1-5	GGAGGGACCCTCCGAGGGCGAGGTT
CONTROL	NT24	AATTTAAGCTTCGTAAGTGG	LRRFIP1	LRRFIP1-6	GAGCGCGCAGGGGGCGGGGAGTT
CONTROL	NT25	AATTTATCGTCAACATTAAT	LSG1	LSG1-1	AGTTCAAGCTCAAACCTTGAG
CONTROL	NT26	ACAAAAAAGTACGGTGATTA	LSG1	LSG1-2	GTTCAAGCTCAAACCTTGAGA
CONTROL	NT27	ACAAAATGCCGTGCGTCAAT	LSG1	LSG1-3	TTCAGCTCAAACCTTGAGAG
CONTROL	NT28	ACAAAGATCGCATGGCATAAC	LSG1	LSG1-4	CTCGCTTATCGTCACTTCCG
CONTROL	NT29	ACAGCCCTCAGAGCCCGAA	LSG1	LSG1-5	GGGATCGAAGTGTGAATCC
CONTROL	NT30	ACAGCGCTCTCGTGTACTAT	LSG1	LSG1-6	TCACTTATATTCTATAATAC
CONTROL	NT31	ACAGGTTCTTATTCATTGAC	LYN	LYN-1	AAACACCCAAACCTTGGGCA
CONTROL	NT32	ACATAGTCGACGGCTCGATT	LYN	LYN-2	CAAAACCCAAACCTTGGGC
CONTROL	NT33	ACCCATGAGTTAAGTTTTCT	LYN	LYN-3	GCCTCAAAGCCCTGCGCGA
CONTROL	NT34	ACCCGATAATAGCTACTGGT	LYN	LYN-4	ACACCAACCCAAACCTTGGC
CONTROL	NT35	ACCCTCCGAATCGTAACGGA	LYN	LYN-5	GACCGTTTGGTCCCTGCCA
CONTROL	NT36	ACCTATAATCGACCACATTT	LYN	LYN-6	TTTGGTGTGGCCGTGCGCGA
CONTROL	NT37	ACCTATTGTCCCTCAAGCT	MACF1	MACF1-1	CCTGGGGCCGAGACTCGCC
CONTROL	NT38	ACGATCGGTAATGGTCTGTT	MACF1	MACF1-2	GAGGACTCGCGGGGACCCGG
CONTROL	NT39	ACGCATGCTTCCCAAAGCGT	MACF1	MACF1-3	GGCCTGGCGCTCCTGACAGG
CONTROL	NT40	ACGGGGTGAAAACCATGTCTG	MACF1	MACF1-4	CCTGTCAGGAGCGCCAGGCC
CONTROL	NT41	ACGGTACATGCGCATGAGTC	MACF1	MACF1-5	GCCGAGGACTCGCCGGGACC
CONTROL	NT42	ACGTCCATACTGTCGCTAC	MACF1	MACF1-6	GCCTGGGGCCGAGGACTCGC
CONTROL	NT43	ACGTTGAGTACGACCAGCT	MAGEF1	MAGEF1-1	GGAAAAGGAGGGGCTGCGCG
CONTROL	NT44	ACTACTGGCTATCCCGCCCA	MAGEF1	MAGEF1-2	GGCACACCCCAACCCAGAA
CONTROL	NT45	ACTAGATCATGATCAGCGA	MAGEF1	MAGEF1-3	GGGCACCCCAACCCAGAGA
CONTROL	NT46	ACTAGCCTGTTCCGAGTAG	MAGEF1	MAGEF1-4	ATTTCCACTTATAGCAGCCT
CONTROL	NT47	ACTATCATGACCCAAATG	MAGEF1	MAGEF1-5	TGCTATAAGTGGAAATGCC
CONTROL	NT48	ACTATTTAATATTGGTAAGT	MAGEF1	MAGEF1-6	TGTGCCCAAGTGTCTATAAG
CONTROL	NT49	ACTCAGCCATTTTATTAGAA	MALT1	MALT1-1	CGCAGCCGACCGCAGCAGT
CONTROL	NT50	ACTGAGTGGGTAAACAGCAT	MALT1	MALT1-2	GCCCCGCCCTCGAGGCCCA
CONTROL	NT51	ACTGCGGAGCGCCCAATATC	MALT1	MALT1-3	GGTGCCTACTGCGTGCCTG
CONTROL	NT52	ACTGCTGCTGACATCTTTA	MALT1	MALT1-4	ACCTTGGCTCGAGGGGCG
CONTROL	NT53	ACTTACGGCACTCGCATGCC	MALT1	MALT1-5	GCGGGACCTTGGCCCTCGAG
CONTROL	NT54	AGAACTGAACTATCTCTACT	MALT1	MALT1-6	GGCGGACCTTGGGCCTCGA
CONTROL	NT55	AGAACCAGACGCCAGCGGT	MANSC4	MANSC4-1	CTGGAGTTTAGACAGTCTC
CONTROL	NT56	AGAAGAAAAAATGTCTACG	MANSC4	MANSC4-2	GAACGTGAGAGGTGTTGTTA
CONTROL	NT57	AGAATGCCATCTAGTTAGTA	MANSC4	MANSC4-3	GACTCTCCAGAAAAGCTGCA
CONTROL	NT58	AGACAGTCAACCGTCAAAA	MANSC4	MANSC4-4	AAAAATCAATGTGCAAGAG
CONTROL	NT59	AGACTCGTATTGTCAATTA	MANSC4	MANSC4-5	CAGCAATCAATGTTTACC
CONTROL	NT60	AGCACGTAATGTCCGTGGAT	MANSC4	MANSC4-6	TCCAGACAGAAAGCTGAACAC
CONTROL	NT61	AGCGATTACGTTATAGATG	MAP2K1	MAP2K1-1	GATGACGCGGAAATACGTCA
CONTROL	NT62	AGCTGGACTCTGTAGAAATC	MAP2K1	MAP2K1-2	TGCCTCGCAGACAACCAATG
CONTROL	NT63	AGCTTTCGAAATTGAGTGTG	MAP2K1	MAP2K1-3	TGTCTGCGAGGCAATAGGGG
CONTROL	NT64	AGGGCACCCGGTTCATACGC	MAP2K1	MAP2K1-4	ATGACGCGGAAATACGTCA
CONTROL	NT65	AGGGTCAGTCTGTCCITTTT	MAP2K1	MAP2K1-5	CAAATGGGGGCAAGCCCTCG
CONTROL	NT66	AGGTCAAGCCGACCTCGAAC	MAP2K1	MAP2K1-6	GCCTCGCAGACAACCAATGG
CONTROL	NT67	AGGTGCGCCGAACATACGGT	MAP3K1	MAP3K1-1	CCCACCTTGCCTGAGGC
CONTROL	NT68	AGGTTGAATACCCCTACTA	MAP3K1	MAP3K1-2	CTGCGCAACTGCGTGAGCG
CONTROL	NT69	AGTATTGTGTGTCTGCTCAAC	MAP3K1	MAP3K1-3	GGCCTGGACTGACCGAGCGG
CONTROL	NT70	AGTCATAACTGAGTGAATCG	MAP3K1	MAP3K1-4	AGTCAGGCGAGGCGCCCGG
CONTROL	NT71	AGTGTTTGAAAAAGGCGCG	MAP3K1	MAP3K1-5	GACCCAGTGCAGCCCGCCGT
CONTROL	NT72	AGTCCAGAAATATTGCG	MAP3K1	MAP3K1-6	GGCGCACTGGGTCCGGCCTG
CONTROL	NT73	AGTTCTGTTGATAGATGCC	MAP3K13	MAP3K13-1	AGGTGAATCAAGACAGGT
CONTROL	NT74	AGTTGAATGGACCTCGACTA	MAP3K13	MAP3K13-2	AGTGAGTCACTAGCCGAGT
CONTROL	NT75	ATAATCCGGAACCGCTCGAC	MAP3K13	MAP3K13-3	TAGCCAGCTCGGGCGCTCAG
CONTROL	NT76	ATACCAGATGCGTCCGCTTG	MAP3K13	MAP3K13-4	GTCCCGCTGAGCGCCGACT
CONTROL	NT77	ATACGAGCGCTTTTCTTTG	MAP3K13	MAP3K13-5	TCGGGCGCTCAGCGGACTG
CONTROL	NT78	ATACGCATGATTGCAAGAGG	MAP3K13	MAP3K13-6	TGCCAGGTGAATCAAGAC

CONTROL	NT79	ATAGCAGGACGAGGTTCTT	MAP3K14	MAP3K14-1	AGGCAAGTTACAGCCTCCG
CONTROL	NT80	ATAGCCGCCGCTCATTACTT	MAP3K14	MAP3K14-2	GCGGTGCGGCCAAAGAAAGG
CONTROL	NT81	ATAGCTAAAGTTGATGTGTA	MAP3K14	MAP3K14-3	GGCAAAGTTACAGCCTCCGG
CONTROL	NT82	ATAGTAACGTCAGGGAGTAA	MAP3K14	MAP3K14-4	AAGAAAGTAGCGCGCAAGCG
CONTROL	NT83	ATATAAACTGTCGGGTAAA	MAP3K14	MAP3K14-5	CGCCTTCTCGCCGCCCCCGG
CONTROL	NT84	ATATTTCCGGCAGTTGCGAGCA	MAP3K14	MAP3K14-6	CGGGGCCACGCCTCCCCCGG
CONTROL	NT85	ATATTTTATGACATAAAAAAT	MAP6D1	MAP6D1-1	ACGCCACCCCTCGTGCCGGG
CONTROL	NT86	ATCAAAGTGTCTGACTTATT	MAP6D1	MAP6D1-2	GACGCCACCCCTCGTGCCGG
CONTROL	NT87	ATCAAGTCAGGTTATGCGGG	MAP6D1	MAP6D1-3	GCCCAGCGTCCCGCCCCCGG
CONTROL	NT88	ATCACGTGATCGGATGGTTC	MAP6D1	MAP6D1-4	AGCACCGCCCGCCCGCACGA
CONTROL	NT89	ATCAGCCCATTTCTGCGCAC	MAP6D1	MAP6D1-5	CGGGACGCCACCCCTCGTGC
CONTROL	NT90	ATCAGGCCTTGTCGGTATT	MAP6D1	MAP6D1-6	GGACGCCACCCCTCGTGCCG
CONTROL	NT91	ATCCAGATCACCCACGGCTCA	MAPK1	MAPK1-1	GATTGGTTCCTCGCGGCTGG
CONTROL	NT92	ATCCATGTGGTTACAATATT	MAPK1	MAPK1-2	GCATGCGGATTTGGTCTCTCG
CONTROL	NT93	ATCCTAGGTACAAAAGGACG	MAPK1	MAPK1-3	GGGACAGAAAGTGTGCATG
CONTROL	NT94	ATCGGTACCTCTTCACATAT	MAPK1	MAPK1-4	CAAGAAGTGTGCATGCGGAT
CONTROL	NT95	ATCGTATCATCAGCTAGCGC	MAPK1	MAPK1-5	CGGCCCGCCCGCAGCCGCG
CONTROL	NT96	ATCGTTGCTGACAGGATCTA	MAPK1	MAPK1-6	GCCGCTTCCGCCCGCCCGCG
CONTROL	NT97	ATCGTTTCCGCTTAAACGGCG	MAPK3	MAPK3-1	GACAGCTCCAGGCCACGCG
CONTROL	NT98	ATCTCGGGTGCAGTCCGGAT	MAPK3	MAPK3-2	GCGGGTACGTCGACAGCTCC
CONTROL	NT99	ATCTCTATACTGTACTCGC	MAPK3	MAPK3-3	GTGACAGCTCCAGGCCACG
CONTROL	NT100	ATCTGAGCGTTTTCCGGCCG	MAPK3	MAPK3-4	CCCTTGCCCGGCCCGCGT
CONTROL	NT101	ATCTGTCTAATTCGGATCG	MAPK3	MAPK3-5	GCCCTTGCCCGGCCCGCGG
CONTROL	NT102	ATCTTCAGGGTAACTACGAA	MAPK3	MAPK3-6	GCCTGGCGCGCGGCCCTCG
CONTROL	NT103	ATCTTCTCGACAAAATGCG	MASP1	MASP1-1	AAAAGCCAGAGGAGAGAGG
CONTROL	NT104	ATGACATTGCGCGTCTACGG	MASP1	MASP1-2	AGGAGAGAGAAAAGCCAGA
CONTROL	NT105	ATGATATCTGACATCCAGCG	MASP1	MASP1-3	AGGGGAAGCGCTGACCTGAA
CONTROL	NT106	ATGCAAGACAGCTCCAGCAG	MASP1	MASP1-4	AGAGGGGATGCTTGCAGGC
CONTROL	NT107	ATGCCTTAGACTTAACTCG	MASP1	MASP1-5	AGGGGATCTGTTGACGGCAG
CONTROL	NT108	ATGCGAAACGACATTTATTA	MASP1	MASP1-6	GATCTGTTGACAGCAGGGGA
CONTROL	NT109	ATGCGCAGCTCCAGAATTTT	MAX	MAX-1	GGGACAAGAAGTACAAGTCT
CONTROL	NT110	ATGCGCTTAAATCGCCGTTT	MAX	MAX-2	GTTCTTGTCCCTCTAACAGA
CONTROL	NT111	ATGTCTAGACCTAATCGTTT	MAX	MAX-3	TACCCGGGCGCTGTGTTAGA
CONTROL	NT112	ATGTTATTACAGACCGGTGT	MAX	MAX-4	GTCCCTCTAACAGACGGCCC
CONTROL	NT113	ATTAACGACACCTTATTCT	MAX	MAX-5	TCCAGAAAACTACAAATCC
CONTROL	NT114	ATTAGCACGGCGACCTTCTA	MAX	MAX-6	TGTCCCTCTAACAGACGGCC
CONTROL	NT115	ATTAGCCGTTGCCATCAAA	MB21D2	MB21D2-1	AGGCTTTGGCCCGGCTCGT
CONTROL	NT116	ATTAGGCCTTTTCTTAAGT	MB21D2	MB21D2-2	CACGCCAGAGCGCACGGAG
CONTROL	NT117	ATTGCGCAATCCTTAGGATA	MB21D2	MB21D2-3	GCCCAGAGCGCACGGAGCGG
CONTROL	NT118	ATTGCTCTGTGCATCAATC	MB21D2	MB21D2-4	ACGAGCCGGGGCAAAGCCT
CONTROL	NT119	ATTTAGTAGACATTGGGTCT	MB21D2	MB21D2-5	AGGCTCCAGGCTTTGGCCC
CONTROL	NT120	ATTTATAAACACAGGGTCCG	MB21D2	MB21D2-6	GCCCGGCTCGTGGGCGGGT
ABCC5	ABCC5-1	AAAGCATTCCAAGGCTGAA	MCCC1	MCCC1-1	ACCAATCAAAGACCAGAGCC
ABCC5	ABCC5-2	AGCCCTGGGCACTCGGAAGG	MCCC1	MCCC1-2	GCCACACCCACGAGCAGC
ABCC5	ABCC5-3	CAAAGCATTCCAAGGCTGA	MCCC1	MCCC1-3	GTCTGGCCACGTGCTCGTGG
ABCC5	ABCC5-4	CAGGGCTGCGGACGCGGGA	MCCC1	MCCC1-4	CAATCGTGCCTACTGAAGCC
ABCC5	ABCC5-5	CGCAGCCCTGGGCACTCGGA	MCCC1	MCCC1-5	CCGGCTTCACTAGCAGCAT
ABCC5	ABCC5-6	GTCCTCCTTCCGAGTCCCA	MCCC1	MCCC1-6	CGGCTTCACTAGCAGCAT
ABCF3	ABCF3-1	CTTGCAAGGCGCATGTGTAG	MCF2L2	MCF2L2-1	GGCCAGCCCTTCTCTCCG
ABCF3	ABCF3-2	GCGGTGACGCGAGGAAGGAG	MCF2L2	MCF2L2-2	GGGTGTCTGCGGAGGAGCCG
ABCF3	ABCF3-3	GTFAGCGGTGACGCGAGAA	MCF2L2	MCF2L2-3	TCCTCCGACGACCCGCGG
ABCF3	ABCF3-4	AGTGCGCAGAGCCGGTGGG	MCF2L2	MCF2L2-4	GAGGAGCCGCGGAGAGAAGG
ABCF3	ABCF3-5	CGCATGTGTAGCGGTGACGC	MCF2L2	MCF2L2-5	GGAGAGCCGCGGAGAGAAG
ABCF3	ABCF3-6	GGAGCGGAGTGGCAGAGCC	MCF2L2	MCF2L2-6	TCTTCCGCGCGGGTGTCTG
ACAP2	ACAP2-1	CCACGAACCTGCGGCCAAG	MCL1	MCL1-1	AAAAAGTATTTCCATAAAAG
ACAP2	ACAP2-2	CCAGCCAGCCAGAACCTGG	MCL1	MCL1-2	AAGGGCGGCGAGCTCCGGA
ACAP2	ACAP2-3	GCATCCGGCAGCACCCTGG	MCL1	MCL1-3	CCATAAAAAGGGGAAAGGGG
ACAP2	ACAP2-4	CCGCCAGGTTCTGCTGGTGC	MCL1	MCL1-4	AGCTTCCGAGGGTGTGCGCA
ACAP2	ACAP2-5	GTTGCCCGGGCGCCCGCAGG	MCL1	MCL1-5	AGGTGCCGTGCGCAACCCTC
ACAP2	ACAP2-6	TTGGCCGCCAGGTTCTGTGC	MCL1	MCL1-6	GTATTTCCATAAAAAGGGGAA
ACVR1	ACVR1-1	CCAGCTGGGCTTGCCCGCGG	MDC1	MDC1-1	ACCTGGTCCGACCCGTTAC
ACVR1	ACVR1-2	GTCTCCCGCCGCCCCCGG	MDC1	MDC1-2	AGTAACGGTTCGCGACCCAGG
ACVR1	ACVR1-3	TCGGGCTGGGAGCAGACCCG	MDC1	MDC1-3	CACACGCAGTCCCTCCACT
ACVR1	ACVR1-4	ACCAGCTGGGCTTGCCCGCG	MDC1	MDC1-4	AGTTTAGGATGAAGACACA
ACVR1	ACVR1-5	CGGGCTGGGAGCAGCAGCCG	MDC1	MDC1-5	CACCTATTTGAACCTAAGG
ACVR1	ACVR1-6	TGGTCCGCCCGCCCGCCCG	MDC1	MDC1-6	GAGGTGGGGACCAAGATGG
ADAMTS12	ADAMTS12-1	CTGACAGTGTCCGCTTTCCG	MDM2	MDM2-1	CCCCACTCCATCATCCCCGG
ADAMTS12	ADAMTS12-2	GACAGTGTCCGCTTTCCGCG	MDM2	MDM2-2	GAGTGGGCTGGTTCGCCCGG
ADAMTS12	ADAMTS12-3	TGGAATGGGCCAGAGCGGGA	MDM2	MDM2-3	GGACCAATTGGCGGAAGCG
ADAMTS12	ADAMTS12-4	ATTCACACCCCGCCGAAAG	MDM2	MDM2-4	CCATCATCCCGGAGGTTGGT
ADAMTS12	ADAMTS12-5	CCCTCCCTCCTCCTAAAG	MDM2	MDM2-5	CTCCGGGATGATGGAGTGG
ADAMTS12	ADAMTS12-6	CGGGAGGGCGCAGCCACCC	MDM2	MDM2-6	GCTTCCGCCAATTGGTCCG
ADIPOQ	ADIPOQ-1	AGTGAGGGCCAGAGGCCGGT	MDM4	MDM4-1	ACCATAGATGAGCAATGGG
ADIPOQ	ADIPOQ-2	GCCAAGTCACTGAGGGCCAG	MDM4	MDM4-2	ATAGAGTAGATCCTAGTCCG
ADIPOQ	ADIPOQ-3	TCCCATTTGGCCAACTCAGTG	MDM4	MDM4-3	GGAAACCATAGATGGAGCAA
ADIPOQ	ADIPOQ-4	CAGGCTGTGGGCAACTGCCA	MDM4	MDM4-4	CTAGTCCGGGGAGAGAGTCCG
ADIPOQ	ADIPOQ-5	CAGTGAGGGCCAGAGCCCGG	MDM4	MDM4-5	GAAACCATAGATGGAGCAAT
ADIPOQ	ADIPOQ-6	CCCATTGGCCAACTCAGTGA	MDM4	MDM4-6	GGAGGACTAGAGAGCTAGAA
AGO2	AGO2-1	CGCGAGCGGCTCCCGCCG	MEF2B	MEF2B-1	CATACAGGGCGTACCCTGG
AGO2	AGO2-2	GGCGGGAGCGGCTCGCGGG	MEF2B	MEF2B-2	GACGGGCTTATTTGCATACA
AGO2	AGO2-3	GGGAGGCGAGGCCGGCGG	MEF2B	MEF2B-3	TCCCAGGCCATGAACCTCC

AGO2	AGO2-4	AGGGGAGGCGAGGCCGGCGG	MEF2B	MEF2B-4	AGGCCCATGAACTCCCGGGT
AGO2	AGO2-5	GCGCGCTCGCGGGGGAGCG	MEF2B	MEF2B-5	CACGCCATCGCCGCTCCA
AGO2	AGO2-6	GGGAGGGGAGGCGAGCCCGG	MEF2B	MEF2B-6	TTGCATACAGGGCGTCAACC
AHSG	AHSG-1	CAAACAGGTTAGGACATCGC	MTF1	MTF1-1	GCCAACCAGAGGCCAGGG
AHSG	AHSG-2	CCTGGAAAAGCAAACAGGTT	MTF1	MTF1-2	TGACAACTGAGCCAAACAG
AHSG	AHSG-3	TCAGCCCTGGAAAAGCAAAC	MTF1	MTF1-3	TTGGCGAGCGGGCACCAG
AHSG	AHSG-4	ATACAGGATGATTTCTGCTT	MTF1	MTF1-4	AATTGGCGAGCGGGCACC
AHSG	AHSG-5	CCTGCCGGAAGAAATGCATA	MTF1	MTF1-5	GGTTGGCTCAGGTTGTCAGG
AHSG	AHSG-6	GCATCTCCCCACAGCAGCA	MTF1	MTF1-6	TGAGCCAACCAGAGGCGCCA
AK3	AK3-1	CGTCCGCCTCTCGGCTACCC	MFN1	MFN1-1	CCCTTAAGGAAAATGGCGCC
AK3	AK3-2	GCGCGGGGTAGCCGAGAGG	MFN1	MFN1-2	GCAGAAGCAAGGTTTGTG
AK3	AK3-3	GGTGCGCCGGGTAGCCGAG	MFN1	MFN1-3	TTCTTAAGGGCAGAAGGCA
AK3	AK3-4	CCGCTGTTGCGTCCGCCCTC	MFN1	MFN1-4	CATAGATCGCTTCCGGCCA
AK3	AK3-5	CGCGGCTTGC CGCGCTTGG	MFN1	MFN1-5	CTCTGTTCTGTTGGCTCC
AK3	AK3-6	GCGCGGCTTGC CGCGCTGGG	MFN1	MFN1-6	GCCGGAAGCGCATGTGCC
AKT1	AKT1-1	CCCGGGCGTCCCACCAGCG	MFSD2A	MFSD2A-1	CCTGCCCGGCTCGCCCGG
AKT1	AKT1-2	CGTCCCCACCGCGCGCCGG	MFSD2A	MFSD2A-2	CTCGGTGGCACAGAGCCCG
AKT1	AKT1-3	TCGGGAGCTGCCCTCAGCC	MFSD2A	MFSD2A-3	GCTTGGAGAAGCTGGCTCG
AKT1	AKT1-4	CGCCCTCGCGCGCGCCGCG	MFSD2A	MFSD2A-4	AGGCGGGCGACGGGATTGG
AKT1	AKT1-5	GAGCGCGCTCGGGGAGCGCG	MFSD2A	MFSD2A-5	CGGGCCAGGGGATTGGCTGG
AKT1	AKT1-6	TCGCCCGCGCGCGCGGTG	MFSD2A	MFSD2A-6	GGGGCTTGGAGAAGCTGGCT
AKT2	AKT2-1	AGAGCGAGAGCGCAAGAGCA	MIPOL1	MIPOL1-1	CAGACGATCCGGCGGAGGAG
AKT2	AKT2-2	CTTCTGTTTGTGGCGCGAG	MIPOL1	MIPOL1-2	GATCCGGCGGAGGAGCGGG
AKT2	AKT2-3	TTCTGTTTGTGGCGCGAGA	MIPOL1	MIPOL1-3	GCCGCTTGCCTTCCCTCG
AKT2	AKT2-4	GAGAGCGAGAGCGCAAGAGC	MIPOL1	MIPOL1-4	GACGATCCGGCGGAGGAGCG
AKT2	AKT2-5	GGGCGGTATTTCCGTCCAGA	MIPOL1	MIPOL1-5	GAGCGCAAGCGCGGAGCACC
AKT2	AKT2-6	TGTACGTCACCTCTCTGTTT	MIPOL1	MIPOL1-6	GGCGGCGCTGGGGCTACG
AKT3	AKT3-1	AGGAGCGGAGACTTACAT	MPL	MPL-1	CCAGACCAGTGGGGCCAG
AKT3	AKT3-2	CGGAGACTTACATGGGAAT	MPL	MPL-2	CCTGGCCCTGGCCCCAGTG
AKT3	AKT3-3	GAGGAGGCGGAGACTTACA	MPL	MPL-3	GGCCCATCCAGACCACACTG
AKT3	AKT3-4	GAGGAGAGGCGCGCGCGCG	MPL	MPL-4	CAGGACAGGGACAGGACGT
AKT3	AKT3-5	GGAGGGAGGAGAGGGCGCG	MPL	MPL-5	GGTCTGGATGGGCCCCAGAG
AKT3	AKT3-6	TCTACATGGGAATCGGATAT	MPL	MPL-6	GTGGTCTGGATGGGCCCCAG
ALG1L2	ALG1L2-1	CGAGATGAATGCTGGGAGAG	MRPS35	MRPS35-1	CAGAGCCGAGTCAAATGTGC
ALG1L2	ALG1L2-2	CTAACTTATCCTTAAAGCCCA	MRPS35	MRPS35-2	TGGAGAAAGAGGAAACACGT
ALG1L2	ALG1L2-3	TACGTCACGAGATGAATGCT	MRPS35	MRPS35-3	TTTCTCTTTCTCCAGCCTA
ALG1L2	ALG1L2-4	AAGAAGAGCTGGTATGGCCC	MRPS35	MRPS35-4	ATCTTCTGCACATTTGACT
ALG1L2	ALG1L2-5	CATTTGTCAACAAGAAAGAGC	MRPS35	MRPS35-5	CCGCCCTAGGCTGGAGAAAG
ALG1L2	ALG1L2-6	GTACGTCACGAGATGAATGC	MRPS35	MRPS35-6	GTTTCTCTTTTCTCCAGCCT
ALG3	ALG3-1	GTAATGAAGACTGGCTACT	MTOR	MTOR-1	CAGGACCCGGCTTCTCCAGG
ALG3	ALG3-2	TGGAGCGTGGAGTGTCATCAG	MTOR	MTOR-2	GTTCAAATAGACAACCCAGC
ALG3	ALG3-3	TTAGTGGAGTAAATGAAGAC	MTOR	MTOR-3	TTCACTGCCACTGGCCGCG
ALG3	ALG3-4	CCAGGCTGGGTATAAAGCTG	MTOR	MTOR-4	AGAAGAGAAGCTTCCAGACC
ALG3	ALG3-5	CTCCACGCTCCATAGGAGCA	MTOR	MTOR-5	CCCCCCCCCTGGAGAAGCC
ALG3	ALG3-6	TGAAGACTGGCTACTCGGAT	MTOR	MTOR-6	TCAGGACCCGGCTTCTCCAG
ANKRD10	ANKRD10-1	AGAGGACGCCTTGTGCAAGCC	MUC20	MUC20-1	CACTCCAGAGCCCTACTAG
ANKRD10	ANKRD10-2	GACCCTGCCCGGCTGCACA	MUC20	MUC20-2	GATCACCTGGTCCACACACT
ANKRD10	ANKRD10-3	TCCAGGCCCGGACCCCTGCC	MUC20	MUC20-3	GCATCTCACAAAGGACACTG
ANKRD10	ANKRD10-4	CAGAGGACGCCTTGTGCAAGC	MUC20	MUC20-4	CCTGCTTCTCAAACCAGGG
ANKRD10	ANKRD10-5	CGCCTTGTGCAAGCCGGGACG	MUC20	MUC20-5	GAGCCACCCCTCATGGGCAA
ANKRD10	ANKRD10-6	GGCTGCACAAGGCGCTCCTCT	MUC20	MUC20-6	TCCCAGCAGAAGAAAGAAAG
AP2M1	AP2M1-1	AGCGCTTCAAATGCAAGCA	MUC4	MUC4-1	AAGCAGAGCAACGGGTGTAT
AP2M1	AP2M1-2	GCTTCAAATGCAAGCAAGG	MUC4	MUC4-2	CTGATGAGAAGCAGAGCAAC
AP2M1	AP2M1-3	TTGCAAGCAAGGAGCCCGCG	MUC4	MUC4-3	GCTGATGAGAAGCAGAGCAA
AP2M1	AP2M1-4	AGGCGGGGGCGGTTTCTCGA	MUC4	MUC4-4	CCCCACCCACTACCCACC
AP2M1	AP2M1-5	CTTGCAATTTGAAGCGCTCT	MUC4	MUC4-5	TCTTCTCTGGTGGGGTAGTG
AP2M1	AP2M1-6	GGCGGTTTCTCGAAGGCAGT	MUC4	MUC4-6	TTTCTTCTGGTGGGGTAG
APOBEC1	APOBEC1-1	CTGAGCTGTCTGTACAACA	MUTYH	MUTYH-1	ATGTAGTCTGGAGCTATAA
APOBEC1	APOBEC1-2	GAGCTGTCTGTACAACAGG	MUTYH	MUTYH-2	CCTGGAGCGTTGGGAGCATG
APOBEC1	APOBEC1-3	TCATCCTCTGCCCAAGCAGG	MUTYH	MUTYH-3	TGGGGCTGATGGAGGCATGG
APOBEC1	APOBEC1-4	ATGACTCATTCCGACTCTG	MUTYH	MUTYH-4	CGTTGGGAGCATGGGGCTGA
APOBEC1	APOBEC1-5	GAGTCATCCTCTGCCCAAGC	MUTYH	MUTYH-5	GCATGGCGGGAGATGTAGTC
APOBEC1	APOBEC1-6	TCCCATAACTGCCTGAGATG	MUTYH	MUTYH-6	GGGGCTGATGGAGGCATGGC
APOD	APOD-1	CAACCCTCCTGACTGGATGG	MYB	MYB-1	GCAGGGGCGCCAGATTTGGC
APOD	APOD-2	CCCTCCTGACTGGATGGGGG	MYB	MYB-2	GGGCGCCAGATTTGGCGGGA
APOD	APOD-3	CCGCCCCATCCAGTCAAGGA	MYB	MYB-3	TGCCATCAAACAAGAGCTT
APOD	APOD-4	CTGTATCGAAACCAAAGAT	MYB	MYB-4	ACTCCCCCTCCGCCAAATC
APOD	APOD-5	GCCGCCCCATCCAGTCAAGG	MYB	MYB-5	GGGGCGCCAGATTTGGCGGG
APOD	APOD-6	TCTGTATCGAAACCAAAGA	MYB	MYB-6	TGCAGGGGCGCCAGATTTGG
ARAF	ARAF-1	GAACACGACTCATTCCCTG	MYC	MYC-1	CCCCGAGCTGTGCTGCTCG
ARAF	ARAF-2	GTCTGTTCGGATTAGGAG	MYC	MYC-2	CTCCTGCCTCAGAAAGGCA
ARAF	ARAF-3	TGACCCTGACCCAATAAGGG	MYC	MYC-3	GAGAAGCCCTGCCCTTCTCG
ARAF	ARAF-4	AGTCGTGTTCCGGATTAGGA	MYC	MYC-4	CCTGCCCTTCTCGAGGACGG
ARAF	ARAF-5	GGTCAGGGTCACTGTGTA	MYC	MYC-5	CTCCCCTCCTGCCTCGAGAA
ARAF	ARAF-6	GTCTGTCAAGGCCAAGACCAA	MYC	MYC-6	CTGCCCTTCTCGAGGACGGA
ARHGEF7	ARHGEF7-1	CGAAGACGTCGCCGCGGGG	MYCL	MYCL-1	CCTCCTCGCTCGCGCACGG
ARHGEF7	ARHGEF7-2	GGACGCTTTCGGATAGCGTC	MYCL	MYCL-2	CGACGAGATATAAGGCAGTC
ARHGEF7	ARHGEF7-3	TCCTCAGACC CGCCCGCGC	MYCL	MYCL-3	GGACGCTATCGGATCCGCG
ARHGEF7	ARHGEF7-4	CTATCCGAAGACGTCGCCGCG	MYCL	MYCL-4	CGCCCTCCTCGCTCGCGCA
ARHGEF7	ARHGEF7-5	GGGACGCTTTCGGATAGCGT	MYCL	MYCL-5	CGCCGATCCCGAGAGCGTCC
ARHGEF7	ARHGEF7-6	TATCCGAAGACGTCGCCGCG	MYCL	MYCL-6	GACGCTCTCGGATCGGGCG

ARID2	ARID2-1	AAATCGGAGCGAAACTAGAA	MYCN	MYCN-1	CCTGATTCCATAAAAAATCA
ARID2	ARID2-2	CTAAAAAAGTTTAAAGAAAT	MYCN	MYCN-2	CTGATTTCATAAAAATCAG
ARID2	ARID2-3	GAGCAGGAGGCCAGGGGGAG	MYCN	MYCN-3	TTTATGGAATCAGGAGGGG
ARID2	ARID2-4	CGGAGCGAAACTAGAAGGGC	MYCN	MYCN-4	ATTTCCATAAAAAATCAGGGG
ARID2	ARID2-5	CGGATCCCGCGCAAGCCGCG	MYCN	MYCN-5	TCCTGATTTCATAAAAATC
ARID2	ARID2-6	CTAGAAGGGCAGGCGACTGC	MYCN	MYCN-6	TTATGGAATCAGGAGGGGCG
ASCL1	ASCL1-1	AGCCGCTCGCTGCAGCAGCG	MYLK2	MYLK2-1	AGGAGAGGATCTCTTACACC
ASCL1	ASCL1-2	CTCCCGCTGCTGCAGCGAG	MYLK2	MYLK2-2	CTGGGGCCCAAGAGTGACAGG
ASCL1	ASCL1-3	GGAGGGGAGTTTGGGGAGT	MYLK2	MYLK2-3	GAGAGGATCTCTTACACCAG
ASCL1	ASCL1-4	GCAGCCGCTCGCTGCAGCAG	MYLK2	MYLK2-4	AATGCCGTGTCTCTGAAAT
ASCL1	ASCL1-5	GCTGCAGCAGCGGGAGTGG	MYLK2	MYLK2-5	CACTCTTGGCCCCAGTTCAG
ASCL1	ASCL1-6	GGAGGAAGAGGTAAGAGGAG	MYLK2	MYLK2-6	GGGCCAAGAGTGACAGGTGG
ASCL2	ASCL2-1	CCAGGGTCTCAGCCAATCGT	MYO16	MYO16-1	AGCCACATCTGTCTGCACGG
ASCL2	ASCL2-2	GCGTACGCGCTTCCCTAATG	MYO16	MYO16-2	TGCAGCCACTTCTGTCTGCA
ASCL2	ASCL2-3	TGCGCGATTGGCCAAACGGG	MYO16	MYO16-3	TTGAAAAGCCATTAACAGGC
ASCL2	ASCL2-4	CCAAACGGGTGGCCACGAT	MYO16	MYO16-4	AAGCCATTAACAGGCAGGAC
ASCL2	ASCL2-5	CCCCTTGGCCAAATCGCGCA	MYO16	MYO16-5	AGCCATTAACAGGCAGGACC
ASCL2	ASCL2-6	GCCAGGGTCTCAGCCAATCG	MYO16	MYO16-6	CACCTCCGTGCAGCAAGATG
ASXL1	ASXL1-1	CCTGGGAGTCGTAGTCCCAA	KAT6A	KAT6A-1	GCGAGGGAACGGCGGCTGG
ASXL1	ASXL1-2	GCGGCCATATTTCTCCGGAG	KAT6A	KAT6A-2	GCTGGAAGAGCCTGGGCGGG
ASXL1	ASXL1-3	TGTGGTCCACGCGCTTACCG	KAT6A	KAT6A-3	GGAGCTGGAAGAGCCTGGGC
ASXL1	ASXL1-4	ATATGGCCGCGTGAAGCGCG	KAT6A	KAT6A-4	CTCTTCCAGCTCCCTCCCC
ASXL1	ASXL1-5	GCCATATTCTCCGGAGCGG	KAT6A	KAT6A-5	GGGAACGGCGGCTGGGGGA
ASXL1	ASXL1-6	GGGGAGGCCAGAGAGCCCGT	KAT6A	KAT6A-6	GGGAGCTGGAAGAGCCTGGG
ATOH1	ATOH1-1	GAAGACACGCGACCGGCGCG	NAALADL2	NAALADL2-1	CAAGCGGTGACGCTCGCGG
ATOH1	ATOH1-2	GTGTCTTCTCAGCCAATGGA	NAALADL2	NAALADL2-2	CCAGCCGTTCTTGCCAAAG
ATOH1	ATOH1-3	TGGCTGAGAAGACACGCGAC	NAALADL2	NAALADL2-3	GTCAGCCGCTTGGCAAGGAA
ATOH1	ATOH1-4	ACACGCGACCGCGCGAGGA	NAALADL2	NAALADL2-4	CGAGCCTCAGCCGCTTGGCA
ATOH1	ATOH1-5	CACGCGACCGGCGCGAGGAG	NAALADL2	NAALADL2-5	CGGAAACCCTCGCCCCGAG
ATOH1	ATOH1-6	GACACGCGACCGGCGCGAGG	NAALADL2	NAALADL2-6	TGCCAAGCGGCTGACGCTCG
ATP11B	ATP11B-1	ACGTGACGAAAGGGGGTCCG	NADK2	NADK2-1	ACGTACCAGCGGCTTGACGA
ATP11B	ATP11B-2	CCCCCTTTCGTACGTCGCGG	NADK2	NADK2-2	GGAAACGGGAGACCCACGC
ATP11B	ATP11B-3	GCCCCCGGACGCTGACGAAAG	NADK2	NADK2-3	GGGAAACGGGAGACCCACGC
ATP11B	ATP11B-4	ACCCCTTTCGTACGTCGCG	NADK2	NADK2-4	GCCACCTTTCGTCCGCGTG
ATP11B	ATP11B-5	CCCCCGGACGTGACGAAAGG	NADK2	NADK2-5	TACCCAGGCGTTGACGAAAG
ATP11B	ATP11B-6	CCGCCCCCGGACGCTGACGAA	NADK2	NADK2-6	TGACGAAGGCGGGGAAAGCG
ATP13A3	ATP13A3-1	GGGTGGCAAAGGCGATGGGT	NANOG	NANOG-1	TAGGGGTGTGCCCGCCAGG
ATP13A3	ATP13A3-2	TCGAGGGTGGCAAAGGCGAT	NANOG	NANOG-2	TCACAAGGGTGGTTCAGTAG
ATP13A3	ATP13A3-3	TGCCCGTTCGAGGGTGGCAA	NANOG	NANOG-3	TTAGACCCACCCTCTCTGGC
ATP13A3	ATP13A3-4	AGGGTGGCAAAGGCGATGGG	NANOG	NANOG-4	ATTCACAAGGGTGGGTGAGT
ATP13A3	ATP13A3-5	TGCGCTTTCGCCACCCTCGAA	NANOG	NANOG-5	GTGTGCCCGCCAGGAGGGGT
ATP13A3	ATP13A3-6	TTCGAGGGTGGCAAAGGCGA	NANOG	NANOG-6	TTCACAAGGGTGGGTGAGTA
ATP13A4	ATP13A4-1	ACGAGTCCGCTCTGTCTAGG	NANOGB	NANOGB-1	ACCCAGTGGCAATTCACAAA
ATP13A4	ATP13A4-2	GATTTGCAGTCAGAAGTCTG	NANOGB	NANOGB-2	CCACAATATGAGCACCCAG
ATP13A4	ATP13A4-3	GTCAGAAGTCTGAGGCTGGC	NANOGB	NANOGB-3	TGGCTCAAAAATAGATGTCT
ATP13A4	ATP13A4-4	CAGCAATTCCTCCTAGCAGA	NANOGB	NANOGB-4	AAATGCTTCCAAAATACAG
ATP13A4	ATP13A4-5	CCAGCAATTCCTCCTAGCAG	NANOGB	NANOGB-5	CCAATGGGTGCTCATATTTG
ATP13A4	ATP13A4-6	CTGAGAGAATGCAATTAAGCA	NANOGB	NANOGB-6	GCCCACTGACATCCAAAAGA
ATP13A5	ATP13A5-1	AACTTGTGATTGCTCTTCCC	NBN	NBN-1	CGCCACCTGGTGGTTGGAAA
ATP13A5	ATP13A5-2	CTTGCCATTTAGACTAACAA	NBN	NBN-2	CTAAGGTGTGCTGTAATGTA
ATP13A5	ATP13A5-3	CTTTGTAGTCTAATAGGCA	NBN	NBN-3	TTGAAATGTGCTGCGTTAAA
ATP13A5	ATP13A5-4	GAAAGAGAGAAAATCTTCTC	NBN	NBN-4	ATGAGGCGGGAGTGCGACTT
ATP13A5	ATP13A5-5	GAGAAATGTCAAATCCCTT	NBN	NBN-5	GGCGCTTGCCCGCCACTGG
ATP13A5	ATP13A5-6	TCCAAGTTCACAGAAGCCCA	NBN	NBN-6	TCCGACTCCCGCTCATCCA
ATR	ATR-1	CGGCGCCCGACGGAGCCGTG	NCBP2	NCBP2-1	CATTGACCCCAATCCGAGGG
ATR	ATR-2	GGCCAGTAGCGGCTTCCGGG	NCBP2	NCBP2-2	CGTGTGCTCATCAAGCTGCG
ATR	ATR-3	GTCCTATGCAGAAAAGACGC	NCBP2	NCBP2-3	GTCGTCATCAAGCTGCGCG
ATR	ATR-4	AAGACGCTGGGCTGGCAAG	NCBP2	NCBP2-4	ATCTCATTTGAAACCAATCCG
ATR	ATR-5	CGCCGACGGAGCCGTGTGG	NCBP2	NCBP2-5	GCGCGGGGCATAGACGTCC
ATR	ATR-6	TCCTATGCAGAAAAGACGCT	NCBP2	NCBP2-6	GGGGGCATAGACGTCCGGGT
AURKA	AURKA-1	GCGCCCTTAAACGCGACTCA	NCOA3	NCOA3-1	CCCCACCTGGGCTTCCGCGG
AURKA	AURKA-2	TTAAACGCGACTCAAGGCGT	NCOA3	NCOA3-2	CGTCGCCACGCCCTCCGCGG
AURKA	AURKA-3	TTTGTGTCAACCAATCACA	NCOA3	NCOA3-3	GACCCCAACCTGGCTTCCG
AURKA	AURKA-4	GGAGCAAGTGCCTGCGCG	NCOA3	NCOA3-4	CGCCGCGGAAGCCAGGGTGG
AURKA	AURKA-5	TAAACGCGACTCAAGGCGTC	NCOA3	NCOA3-5	CCTGGCGACGTGGGCTCGTG
AURKA	AURKA-6	TAAGGGCGCACCCGCGCG	NCOA3	NCOA3-6	GGTTCAGCGACCCCAACCC
AXL	AXL-1	ATCAGGGGTTAACTCAAGAG	NCOR1	NCOR1-1	AAGCTCCGCGGAGGTAGGAG
AXL	AXL-2	GGGTTAACTCAAGAGGAGG	NCOR1	NCOR1-2	GCCGAGGTAGGAGAGGGGCC
AXL	AXL-3	TTAACCCCTGATTGTCCAGG	NCOR1	NCOR1-3	GGGCGCTCTCTACCTCGG
AXL	AXL-4	AGGGGCCACCTGGACAATCA	NCOR1	NCOR1-4	CCGGGAAGCTCCGCGAGGT
AXL	AXL-5	CCCTTTCCTCCGCCCAACCA	NCOR1	NCOR1-5	GGGAGACCAACTCCCTCCGC
AXL	AXL-6	GAGTTAACCCCTGATTGTCC	NCOR1	NCOR1-6	TAGGAGAGGGCGCCGCGCAG
B3GNT5	B3GNT5-1	ACCTTACCTACGCGCCGGG	NECAP1	NECAP1-1	CGGGGAGCCATTTGAAACC
B3GNT5	B3GNT5-2	CATCACCTTACCTACGCGC	NECAP1	NECAP1-2	GAACTCACTTGAATCTCGG
B3GNT5	B3GNT5-3	GCCGTGACGCGGAGAGTGGC	NECAP1	NECAP1-3	GGCTCCCGCTGACCCGAAA
B3GNT5	B3GNT5-4	CCTTACCTACGCGCCGGGA	NECAP1	NECAP1-4	ATCGTTTCCAGGTTTCAATA
B3GNT5	B3GNT5-5	GGGCGGTGACGCGGAGAGTG	NECAP1	NECAP1-5	ATTGAAACCTGGAACGATG
B3GNT5	B3GNT5-6	TCACCTACGCGCCGGAGGG	NECAP1	NECAP1-6	CTGGAACGATGAGGGTGC
BBC3	BBC3-1	AAGTCTGACTTGTCCGCGG	NEUROD1	NEUROD1-1	AGAACGGGGAGCGCACAGCC
BBC3	BBC3-2	GGGGCGTAGCGTACGCGG	NEUROD1	NEUROD1-2	AGGCGTGGGGAGAAGTGGG
BBC3	BBC3-3	TGCAAGTCTGACTTGTCCG	NEUROD1	NEUROD1-3	CACAGCCTGGACGCGTGCC

BBC3	BBC3-4	ACGGCCCCGCCGCCGCCG	NEUROD1	NEUROD1-4	CCGCTAGCTGAGGGGCTAGC
BBC3	BBC3-5	CCTGACTTGTCCGCGCGGG	NEUROD1	NEUROD1-5	TGACGCCTGCCACGCGTCC
BBC3	BBC3-6	CTGACTTGTCCGCGCGGG	NEUROD1	NEUROD1-6	TGGACGCGTCCGCCAGGCGTC
BCL2	BCL2-1	AGAGAATGAAGTAAGAGGAC	NFE2L2	NFE2L2-1	AAAATCCCCACCCCGCGCG
BCL2	BCL2-2	GTTACGCACAGGAAACCGGT	NFE2L2	NFE2L2-2	TTCTTGCCTCAGCCCCGCG
BCL2	BCL2-3	TTACGCACAGGAAACCGGT	NFE2L2	NFE2L2-3	TTTCGGGAAGCTCAGCCGCG
BCL2	BCL2-4	CATTCTCTGCACAGCCGAC	NFE2L2	NFE2L2-4	CGAAATCCCCACCCCGCGC
BCL2	BCL2-5	TGACGTTACGCACAGGAAAC	NFE2L2	NFE2L2-5	CGGGCCCTTCTTCCCCCGC
BCL2	BCL2-6	TGTGCAGAGAATGAAGTAAG	NFE2L2	NFE2L2-6	TCCTTCCCCCGCGCGCGCG
BCL2L1	BCL2L1-1	AATCCATACCAGCCACTCC	NFKB1	NFKB1-1	GGACACAGCGCGCACGCGAG
BCL2L1	BCL2L1-2	AGCCAGGAGTACTCTCCGG	NFKB1	NFKB1-2	GGGGAAGCCCGCACTTCTAG
BCL2L1	BCL2L1-3	TACTCTGGCTCCCAGTAGG	NFKB1	NFKB1-3	GTGCGGGCTTCCCCACCCC
BCL2L1	BCL2L1-4	AAATCCATACCAGCCACTCC	NFKB1	NFKB1-4	ACACACGCGCGCACGAGCGG
BCL2L1	BCL2L1-5	GGGAGCCAGGAGTACTCTCC	NFKB1	NFKB1-5	CACAGCGCCCCCTAGAAGTGC
BCL2L1	BCL2L1-6	TCCTGGCTCCAGTAGGAGG	NFKB1	NFKB1-6	GCACAGCGCCCCCTAGAAGTG
BCL2L2-PABPN1	BCL2L2-PABPN1-1	AGGGCCACTACTCAGGAAGA	NFKBIA	NFKBIA-1	CTGGCTTCGTCTCTCTGCTAG
BCL2L2-PABPN1	BCL2L2-PABPN1-2	GATGCGTCCAGAGAGAGGG	NFKBIA	NFKBIA-2	TCAGACCAGAAAAGAGAAC
BCL2L2-PABPN1	BCL2L2-PABPN1-3	GCCACTACTCAGGAAGAGG	NFKBIA	NFKBIA-3	TGGCTTCGTCTCTCTGCTAGG
BCL2L2-PABPN1	BCL2L2-PABPN1-4	AAGGGCCACTACTCAGGAAG	NFKBIA	NFKBIA-4	AACTGGCTTCGTCTCTGCT
BCL2L2-PABPN1	BCL2L2-PABPN1-5	AGAGATGCGTCCAGAGAGAG	NFKBIA	NFKBIA-5	ACTGGCTTCGTCTCTGCTA
BCL2L2-PABPN1	BCL2L2-PABPN1-6	CCACTACTCAGGAAGAGGGA	NFKBIA	NFKBIA-6	TGAACCCAGCTCAGGGTTT
BCL6	BCL6-1	AAAAAATCTTGTGGCTTTGA	NHLH1	NHLH1-1	CCCCGCCCCAGCTCCCAG
BCL6	BCL6-2	CGGCCAGTGAATAATCTTG	NHLH1	NHLH1-2	GCCAGGCAGCCATTGGCAGA
BCL6	BCL6-3	GAAAAAATCTTGTGGCTTTG	NHLH1	NHLH1-3	GGCTGTTAATATTGATGAG
BCL6	BCL6-4	CCTCCCTCCAGCAGTACGAG	NHLH1	NHLH1-4	CTCATCAATATTAACAGCC
BCL6	BCL6-5	CGGACTTACCACTGCTTACG	NHLH1	NHLH1-5	CTGTTAATATTGATGAGGG
BCL6	BCL6-6	CTTGTGGCTTTGAGGGCTTT	NHLH1	NHLH1-6	GCTGTTAATATTGATGAGG
BCOR	BCOR-1	AGGGGAGCGCGTGTGGGA	NKX2-1	NKX2-1-1	GATCCGGGACAGCCCTCCGG
BCOR	BCOR-2	GAGGCGGCTGTTGGGAGGGA	NKX2-1	NKX2-1-2	GGGGATCGACTGCCTCCCG
BCOR	BCOR-3	GGGCGGGCGGGAGGGAGGAC	NKX2-1	NKX2-1-3	GTAGGGGATCGACTGCCTCC
BCOR	BCOR-4	CCGAGCGCTGCGCTGCGGG	NKX2-1	NKX2-1-4	AGAGAATCCGAGCGGGCGGA
BCOR	BCOR-5	GCCCGAGCGCTGCGCCTGCG	NKX2-1	NKX2-1-5	GAGAATCCGAGCGGGCGGAG
BCOR	BCOR-6	GGGGAGGGGAGGCGGCTGTT	NKX2-1	NKX2-1-6	GGGGATCCGGGACAGCCCTCC
BDH1	BDH1-1	ATCAGGGCACCTGGGCGGG	NKX2-8	NKX2-8-1	AGTTACCTCCAGAGGCTGC
BDH1	BDH1-2	CACCGGGAGCCTAGCGATCA	NKX2-8	NKX2-8-2	GGAGGTAACCTGGGCGCCAA
BDH1	BDH1-3	TGATCGCTAGGCTCCCGGTG	NKX2-8	NKX2-8-3	GGCGCCAGTTACCTCCAG
BDH1	BDH1-4	CAGCCGGGACCCAGCCGCGG	NKX2-8	NKX2-8-4	GCGCAAGGGGCGGGTGC
BDH1	BDH1-5	CCCAAGGTGCCCTGATCGCT	NKX2-8	NKX2-8-5	GGGAGGTAACCTGGGCGCCAA
BDH1	BDH1-6	TGCCCTGATCGTAGGCTCC	NKX2-8	NKX2-8-6	GTAACCTGGGCGCAAGGGGC
BMP8A	BMP8A-1	CCGCCGCCCGGGGCTCCAG	NSD3	NSD3-1	AGCCCCAGCGTCCCGAACCA
BMP8A	BMP8A-2	CGCCCGCTAGGAGCCCGGG	NSD3	NSD3-2	CTCCGGGAGGAAAGCGGAGT
BMP8A	BMP8A-3	GCAACACCTGCCCGCCCGG	NSD3	NSD3-3	GAGGAAGCGGCGAGTCCGGC
BMP8A	BMP8A-4	CCCGGGGCTCCAGCGGGCG	NSD3	NSD3-4	CAGGGACTGCATTTCGCCGC
BMP8A	BMP8A-5	CCGGGCGGCGGAGGCTGTT	NSD3	NSD3-5	GAGCCCCAGCTCCCGAAC
BMP8A	BMP8A-6	CGGGGCGAGGTTGCGGGT	NSD3	NSD3-6	TCGGGACGCTGGGCGCCGG
BMP8B	BMP8B-1	AGCGGGGCGGACGCTGCGA	NT5C1A	NT5C1A-1	AGGCGAGTCCCGGCGAGGGA
BMP8B	BMP8B-2	CAGGCGTGGCCCCGCTCCC	NT5C1A	NT5C1A-2	GAGGGAGGCGAGTCCCGGCG
BMP8B	BMP8B-3	CCCGGGCCCCCTCGCAGCG	NT5C1A	NT5C1A-3	TCCCGCGAGGGAAGGGGGC
BMP8B	BMP8B-4	CGGGGGCCACGCTGCGAGG	NT5C1A	NT5C1A-4	ACCTCCCCCGCCCGGCGGG
BMP8B	BMP8B-5	GAGCGGGGGCCACGCTGCG	NT5C1A	NT5C1A-5	AGGGAGGCGAGTCCCGGCGA
BMP8B	BMP8B-6	GCGGGGGCCACGCTGCGAG	NT5C1A	NT5C1A-6	GGAGGCTGTGCGTGTGACT
BRF2	BRF2-1	AGTGGCGCGCAGCCTCCAG	NTRK1	NTRK1-1	GCGGGTGGAGAAGAGGGGCA
BRF2	BRF2-2	GTAGAAACGTGAGCTAGGAG	NTRK1	NTRK1-2	GGGCGTCAGAGAGTAGGAAG
BRF2	BRF2-3	GTTTCTACCCGAGCCCGGG	NTRK1	NTRK1-3	GTCAGAGAGTAGGAAGCGGG
BRF2	BRF2-4	ACTTCCGGTCTGTGCCCTCCG	NTRK1	NTRK1-4	ACGCTGGGGCCCTAACAG
BRF2	BRF2-5	AGGCGGTTCCCTCCGCTGGG	NTRK1	NTRK1-5	GTAGGAAGCGGGTGGAGAAG
BRF2	BRF2-6	CACGTTTCTACCCGAGCCCG	NTRK1	NTRK1-6	TCTGCCCTCCCTGTTAG
BTK	BTK-1	AGAGGTCCTCAAGCAAATGAA	OPA1	OPA1-1	ACAGTGCCTCGGGAACCGGAC
BTK	BTK-2	GGTCCAAGCAAATGAAGGG	OPA1	OPA1-2	CCAAATCGGAAGCAAGAGGG
BTK	BTK-3	GTGGAATAGGGACGGGACGA	OPA1	OPA1-3	GCGCATGCGCTGGTCTCCG
BTK	BTK-4	AAGGCGGGGACAGTTGAGG	OPA1	OPA1-4	AGAGGGCGGGGCCCGTGAAG
BTK	BTK-5	CAGAGGTCCTCAAGCAAATGA	OPA1	OPA1-5	CAAATCGGAAGCAAGAGGGC
BTK	BTK-6	GTCCCAAGCAAATGAAGGGG	OPA1	OPA1-6	TGCGCACAGTCCGTCGGGAA
C1QTNF3	C1QTNF3-1	AATCGTTCTTGTGTTGGTG	OSTN	OSTN-1	AAGAGATCGAAGAGAGGCTT
C1QTNF3	C1QTNF3-2	ACACAAATCGTTCTTGTCTTG	OSTN	OSTN-2	AGGCTTGGGAAAATGTTTCCAG
C1QTNF3	C1QTNF3-3	ATCGTTCTTGTGTTGGTGT	OSTN	OSTN-3	GAGAGAAGAGATCGAAGAG
C1QTNF3	C1QTNF3-4	ACTTCAACAGAAACGTGCCA	OSTN	OSTN-4	AATAGATAGACTAAATATGG
C1QTNF3	C1QTNF3-5	TGAATGGGGGCTGTTCTGCC	OSTN	OSTN-5	AATGATGTAAGAGAAAGCAA
C1QTNF3	C1QTNF3-6	TGACAGCAGCCCTCCTCCC	OSTN	OSTN-6	ATAGATAGACTAAATATGGA
CALR	CALR-1	CTAACATAGTGAACCGACGA	OXCT2	OXCT2-1	ACTCGGGGGCCCCAGGCCA
CALR	CALR-2	GAAGGTCCTCAATGAAAGAA	OXCT2	OXCT2-2	CCTAGGCTGTGCCCTTCTCG
CALR	CALR-3	GGCATAGACCAATGACAAAG	OXCT2	OXCT2-3	GACACGGAGGACTGACTCGG
CALR	CALR-4	AGACCAATGACAAAGTGGA	OXCT2	OXCT2-4	AGGCTCCGCGAGAAGGGCAC
CALR	CALR-5	CAATGAAAAAGACGGCCAT	OXCT2	OXCT2-5	GAGGTCAGGCTCCGCGAGAA
CALR	CALR-6	GACCAATGACAAAGTGGCAG	OXCT2	OXCT2-6	TGAGGTCAGGCTCCGCGAGA
CAMK2N2	CAMK2N2-1	CGGCGGCGGTGGCGGGGACC	PABPC4	PABPC4-1	CCTCGGGCCCCCGGGCCGAG
CAMK2N2	CAMK2N2-2	CGGCGGCGGTGGCGGGGACC	PABPC4	PABPC4-2	CGGCGGCGGTGCTCTCGCG
CAMK2N2	CAMK2N2-3	CGGTGGCGGGGACCGGGCGG	PABPC4	PABPC4-3	GGGCGGCGGACGACTGCGCCC
CAMK2N2	CAMK2N2-4	CCGACTGCGGCAGAGCACGG	PABPC4	PABPC4-4	CACGCGAGAGCGACCCGCGG
CAMK2N2	CAMK2N2-5	GGCGGCTGGGCGGGCGGG	PABPC4	PABPC4-5	GCGGCCACGCGAGAGCGACC
CAMK2N2	CAMK2N2-6	TGACGATGAGCGCCGACTG	PABPC4	PABPC4-6	GTGCCCGCCCACTCGGCCCG

CAP1	CAP1-1	AAGAGGGGCGGAGTCACGAG	PAK2	PAK2-1	AGACGAGCGCCACCTCCCAT
CAP1	CAP1-2	GAGGGGCGGAGTCACGAGCG	PAK2	PAK2-2	CGCGCGGGCCTGCCATGGG
CAP1	CAP1-3	GGGCGGAGTACGAGCGGGG	PAK2	PAK2-3	GAAGCCGGAGTCCCCGGGG
CAP1	CAP1-4	CGGGCGTGGCGAAGAGGGG	PAK2	PAK2-4	CCATGGGCGAGCCCGCGCGG
CAP1	CAP1-5	GAGACTTCCTGCCAGTCGC	PAK2	PAK2-5	CCCGGGGAGCTCCGGCTTCG
CAP1	CAP1-6	TGAGACTTCCTGCCAGTCGC	PAK2	PAK2-6	GTCTCCGCCCGGGGAGCTC
CAPSL	CAPSL-1	AATACTAAGAGAGTGACC	PALB2	PALB2-1	CAGCGCGCTCTCTTTAGG
CAPSL	CAPSL-2	CTCTTACCTGTCTTCTCAG	PALB2	PALB2-2	AGTGGAGCGAGGGCCGCTAA
CAPSL	CAPSL-3	GAATCTGCAGCAGTGATCCC	PALB2	PALB2-3	GCTCCACTGCTCGGCCGTAGTT
CAPSL	CAPSL-4	ACTCTCTAGTATTAATTTGG	PALB2	PALB2-4	GCGGCCTCGTCCACTGCTGTT
CAPSL	CAPSL-5	TAGTATTAATTGGAGACCT	PALB2	PALB2-5	GGAAGAGGAGGATACATATCGTT
CAPSL	CAPSL-6	TCCAATTAATACTAAGAGAG	PALB2	PALB2-6	GCCTCAAAGGGACGACAGGGTGT
CARM1	CARM1-1	GAGCTAGCGAGCGAACGAGA	PARL	PARL-1	AGCCAGTCGTCGGGGCACCG
CARM1	CARM1-2	CGAACGAGAGGGCACCCCG	PARL	PARL-2	CAGTCTAGAGCGCCCCCGCG
CARM1	CARM1-3	GTAGCCGGTCCCGCCACG	PARL	PARL-3	GCAGTGGGAGGGAAGCGGT
CARM1	CARM1-4	CGAACGAGAGGGCACCCCGT	PARL	PARL-4	ACGGTGCCTCGGACGACTGGC
CARM1	CARM1-5	GAACGAGAGGGCACCCCGT	PARL	PARL-5	AGGGCGCCAGCCAGTCGTC
CARM1	CARM1-6	GGAGCTAGCGAGCGAACGAG	PARL	PARL-6	GGGGAGCGGTGGGACAGAA
CARS2	CARS2-1	ACTCGAGCCAGGCCAAAGGG	PARP1	PARP1-1	GCGGCCGCGAGAGCTCCACC
CARS2	CARS2-2	CCAAAGGGGAGCGCTACTCTG	PARP1	PARP1-2	GCTCAGCCAAAGCCCGCCT
CARS2	CARS2-3	GGCCTGGCTCGAGTCGCCG	PARP1	PARP1-3	TTTCCGGGCGCTGCGGGG
CARS2	CARS2-4	GCGACTCGAGCCAGGCCAAA	PARP1	PARP1-4	GCCCGGAAACTCCGCCCC
CARS2	CARS2-5	GGTAGCGCCTCCTTTGGCC	PARP1	PARP1-5	GCCTGCCGGGTGGAGCTCTG
CARS2	CARS2-6	TGAGGACTGCTTCCGGGAGT	PARP1	PARP1-6	TCTCGGCGCGCTGCCCTGG
CCDC39	CCDC39-1	CGTGATTCAGGCTTAAGGG	PAX5	PAX5-1	AAGGTGCGGCTGGAAGACCC
CCDC39	CCDC39-2	GGCCGTGATTCAGGCTTAA	PAX5	PAX5-2	TAGCCAGCGCACCTACGGGA
CCDC39	CCDC39-3	TATCACTGATACAGAAATGGC	PAX5	PAX5-3	TTCCGGTCTGCCCTTCCCGT
CCDC39	CCDC39-4	ATGGCCACAGGATGAGGGCG	PAX5	PAX5-4	GCCAGCTCACCTACGGGAAG
CCDC39	CCDC39-5	CAACTACTGATACAGAA	PAX5	PAX5-5	GCGCTAGCCAGCGCACCTAC
CCDC39	CCDC39-6	CCTGCCAGCCCTATCTCTG	PAX5	PAX5-6	GTCTTAATGAAAGGTGCGGC
CCDC50	CCDC50-1	GCAGCTCCCCCTCCCCAGC	PAX9	PAX9-1	GCATGCTGATTGTTGCGGGT
CCDC50	CCDC50-2	TCGCCAGCCACTCGCAATTG	PAX9	PAX9-2	GGACACGCCCTAAAAGGGGC
CCDC50	CCDC50-3	TCTGTAACCCGCAATTTGCGAG	PAX9	PAX9-3	GGGACACGCCCTAAAAGGGG
CCDC50	CCDC50-4	AAGGCGGGCGGGCCGGCTGG	PAX9	PAX9-4	AAGCTGCATGGTATTGGTG
CCDC50	CCDC50-5	AGACAGAAAGCGGGCCGGGC	PAX9	PAX9-5	AGGGCAAGCTGCATGGTGAT
CCDC50	CCDC50-6	TAACCGCAATTTGCGAGTGGC	PAX9	PAX9-6	CTGGGGACACGCCCTAAAAG
CCDC91	CCDC91-1	AGACCACGCTCAAGCTGGGG	PCYT1A	PCYT1A-1	AGTCTGGTGGATTGACAG
CCDC91	CCDC91-2	CAAAGACCACGCTCAAGCTG	PCYT1A	PCYT1A-2	GGTCGATTGACAGAGGTAG
CCDC91	CCDC91-3	CTGCCACCCAGCTTGAGCG	PCYT1A	PCYT1A-3	TGGTGGATTGACAGAGGTA
CCDC91	CCDC91-4	ACGCTCAAGCTGGGGTGGCA	PCYT1A	PCYT1A-4	AACTACTGTTCAGGAGTCCG
CCDC91	CCDC91-5	CACGCGCTCAGTGGGCC	PCYT1A	PCYT1A-5	GGAGGCGGAACCTACTGTGTC
CCDC91	CCDC91-6	CCAAAGACCAGCTCAAGCT	PCYT1A	PCYT1A-6	TTGACAGAGGTAGGGGAAGT
CCND1	CCND1-1	AGCCCGCGCAGAGAATGGGAG	PDCD1LG2	PDCD1LG2-1	GCTCTTGGCTTAGCTATGTT
CCND1	CCND1-2	GCCCGGCAGAGAATGGGAGC	PDCD1LG2	PDCD1LG2-2	TTAGCAGTTTGTGTGAAT
CCND1	CCND1-3	GTAAAGCAAAGATCAAAGCC	PDCD1LG2	PDCD1LG2-3	TTTGGCTTTGGCTTAGCTA
CCND1	CCND1-4	AGAGAATGGGAGCGGGAGGG	PDCD1LG2	PDCD1LG2-4	CAAACCTTCCAAATAAGCC
CCND1	CCND1-5	GATCAAAGCCCGCAGAGAA	PDCD1LG2	PDCD1LG2-5	CTGAGGAACCTGACGAAAGCC
CCND1	CCND1-6	TCCCGCTCCCATTCTCTGCC	PDCD1LG2	PDCD1LG2-6	CTTAGCTATGTTTGGTGT
CCND2	CCND2-1	AATAACGAGAGGGGAAAAGG	PDGFRA	PDGFRA-1	GTTGCGCGTTTTGAAGTAGTT
CCND2	CCND2-2	GTTCTCCTTAATAACGAGAG	PDGFRA	PDGFRA-2	GAAATGTCCCTTCAAACTGTT
CCND2	CCND2-3	TGTTCTCCTTAATAACGAGA	PDGFRA	PDGFRA-3	GTTGGTGTCTGACGGGAAAGTT
CCND2	CCND2-4	CTGTTCTCCTTAATAACGAG	PDGFRA	PDGFRA-4	GGGGGAGGTGTTGGTGTCTGCGTT
CCND2	CCND2-5	CTTAATAACGAGAGGGGAAA	PDGFRA	PDGFRA-5	GCGGGGAGAGCAGACCATGTT
CCND2	CCND2-6	GAGGACCGGGAGGGGAGGAA	PDGFRA	PDGFRA-6	GTTCAAACGCGCAACCGCTGTT
CCND3	CCND3-1	GCGCCCGGACGGAAAGGGT	PEX5L	PEX5L-1	CACAGGAAGTATTGCCCTG
CCND3	CCND3-2	GGACGTGCAACGCTCCGAG	PEX5L	PEX5L-2	CTGTGGGAGGAGAAGCCACA
CCND3	CCND3-3	TGGGACGTGCAACGCTCCG	PEX5L	PEX5L-3	GGAGCTGAGGATTTCCACTG
CCND3	CCND3-4	CAGCCAACCTTTCCGTCGG	PEX5L	PEX5L-4	GCCTAACCTTACTGCCTCAG
CCND3	CCND3-5	TCGCAACGCTCCGAGGGCG	PEX5L	PEX5L-5	GTCTTGCCACTGAAGGTGGG
CCND3	CCND3-6	TGTAGCAACCGTGAATGCT	PEX5L	PEX5L-6	GTTGGCAAGACACTGGAGCTG
CCNE1	CCNE1-1	CCAGCCCTCAGCGCCCGCG	PIGX	PIGX-1	CCCGGCGAGCGTGGCCTAG
CCNE1	CCNE1-2	GACGGGCTCTGGTCCCGCG	PIGX	PIGX-2	CTGTGCTGTGAAACCGCT
CCNE1	CCNE1-3	GGTCCCGCGCGCCGCTGAG	PIGX	PIGX-3	GGTTTCCACAGCGACAGGCC
CCNE1	CCNE1-4	AGGGGCTGGGAGCCGGCGG	PIGX	PIGX-4	CGGTTCCACAGCGACAGGC
CCNE1	CCNE1-5	GACGGGCGGGACGGCTCT	PIGX	PIGX-5	CTAGCGTTCACACAGCGAC
CCNE1	CCNE1-6	GCCCTCGACCGCCCGCGCG	PIGX	PIGX-6	TTCTTGTCTCGCCACCCG
FAM58A	FAM58A-1	CCGCCCCGCCCCGCCCTCA	PIGZ	PIGZ-1	CAGCTCGCTCCGGGACCCCG
FAM58A	FAM58A-2	CCTTGGGCGAGGGCCCTGAG	PIGZ	PIGZ-2	CCCCAGGACCTCCCCAGCG
FAM58A	FAM58A-3	GCGCGCTCACCTTGGGCGA	PIGZ	PIGZ-3	CGCGGTCCCGGAGCGAGCTG
FAM58A	FAM58A-4	CCCTTGGGCGAGGGCCCTGA	PIGZ	PIGZ-4	CCAGCTCGCTCCGGGACCG
FAM58A	FAM58A-5	CGCGGCTCACCTTGGGCGG	PIGZ	PIGZ-5	CCCAGCTCGTCCGGGACCG
FAM58A	FAM58A-6	GCGGAGGGCCCTGAGGGGCG	PIGZ	PIGZ-6	TCCCGCCCGCCTGGCCCG
CD274	CD274-1	CTGACCTTCGGTGAATTCGG	PIK3C3	PIK3C3-1	CGGAGCGAGTTCGACCGCG
CD274	CD274-2	GCTTCCGCGGATTTACCGA	PIK3C3	PIK3C3-2	GCCCGGAGCGATTTCCGACG
CD274	CD274-3	GGTCAGGAAATCCACGCGC	PIK3C3	PIK3C3-3	GCGGAAGGGTGTTCGCGG
CD274	CD274-4	AAATCCAGTTTGGCGGGCGT	PIK3C3	PIK3C3-4	CCTTGTGCACATGCGCGGAA
CD274	CD274-5	GCGAGCAAATCCAGTTTGCC	PIK3C3	PIK3C3-5	GGCGGGGAGTTCCGCCGCT
CD274	CD274-6	TTCTGACCTTCGGTGAAT	PIK3C3	PIK3C3-6	GGCGCGCTGTGCACATGCG
CD79A	CD79A-1	AGCAAAGGGCCAGTAGCGA	PIK3CA	PIK3CA-1	AAGTTTATTCTGGAACAAA
CD79A	CD79A-2	CTCACAGCCTGAAGCATACC	PIK3CA	PIK3CA-2	GGAAAAAAAACAGGGGCGA
CD79A	CD79A-3	GCCTGAAGCATACCCGCGAG	PIK3CA	PIK3CA-3	GTTTGTACACGATGTGAG

CD79A	CD79A-4	AAGCAAAGGGGCCAGTAGCG	PIK3CA	PIK3CA-4	CGAACTCTTCCCACCCCT
CD79A	CD79A-5	AGCCTGAAGCATAACCCGGCA	PIK3CA	PIK3CA-5	GAGACCAATAAAGTTTATTC
CD79A	CD79A-6	CCCCAGGCCAAACAAGAAA	PIK3CA	PIK3CA-6	GTTTCCAGAATAAACCTTAT
CDC37L1	CDC37L1-1	CGAAGAGCTCAAGAAAACG	PIK3CB	PIK3CB-1	CGGGCAATCCCGGGCCCG
CDC37L1	CDC37L1-2	GATCCACCCACTACACGCAA	PIK3CB	PIK3CB-2	CGGGCCCGGGGATTGGCCCG
CDC37L1	CDC37L1-3	GGCCCTTTGCGTGTAGTGGG	PIK3CB	PIK3CB-3	GCCAATCCCGGGCCCGCGG
CDC37L1	CDC37L1-4	ATCCACCCACTACACGCAA	PIK3CB	PIK3CB-4	ATTGGCCCGAGGGCGGGCA
CDC37L1	CDC37L1-5	CCACTACACGCAAAGGGCCC	PIK3CB	PIK3CB-5	GCCCGGGATTGGCCGAGGG
CDC37L1	CDC37L1-6	CCGGGCCCTTTGCGTGTAGT	PIK3CB	PIK3CB-6	GGGGCCCGGGATTGGCCGA
CDK4	CDK4-1	ACCGCCACCCATGCGCTGAG	PIK3R3	PIK3R3-1	AGAATCCCGGTACATCGAGG
CDK4	CDK4-2	AGAGGCGCGCGAAACTGGG	PIK3R3	PIK3R3-2	GAATCCCGGTACATCGAGGC
CDK4	CDK4-3	TGACCGCCACCCATGCGCTG	PIK3R3	PIK3R3-3	GACAGAATCCCGGTACATCG
CDK4	CDK4-4	GAGGCGCGCGGAAACTGGGA	PIK3R3	PIK3R3-4	CCCGGTACATCGAGGGCGGA
CDK4	CDK4-5	GCCACCCATGCGCTGAGGG	PIK3R3	PIK3R3-5	GCGGTTGGGTGGCGCTCAG
CDK4	CDK4-6	TCCGCCCTCAGCGCATGGG	PIK3R3	PIK3R3-6	TACATCGAGCGGGACGGCG
CDKAL1	CDKAL1-1	ATTGCTGAAAGCGCTAGTTC	PIM1	PIM1-1	ACCCCTCTCTCCCTCGGC
CDKAL1	CDKAL1-2	TAAGCATTTCTAGGAACCC	PIM1	PIM1-2	CCCCACCCCTCTCTCCCT
CDKAL1	CDKAL1-3	TATTTGCGCATGCTACGCGA	PIM1	PIM1-3	GGCCGGCCGAGGGAGGAGAG
CDKAL1	CDKAL1-4	AATAACAACCTGAGTCTC	PIM1	PIM1-4	GCTGCCGGCCGGCCGAGGG
CDKAL1	CDKAL1-5	TCTAGGAACCCGAGGACTCA	PIM1	PIM1-5	GGAGGCCAAGCCGGGGAGCA
CDKAL1	CDKAL1-6	TTGCGCATGCTCAGCGACGG	PIM1	PIM1-6	GGCCGGCCGAGGGAGGAGA
CEBPA	CEBPA-1	CATGGGGCGGCGAACCCAGCG	PMAIP1	PMAIP1-1	CCATAACGCCGTCTGCGGGG
CEBPA	CEBPA-2	CCGAGGCGGCCCTCTGTCCCC	PMAIP1	PMAIP1-2	CTCCCAATAACGCCGTCTGCG
CEBPA	CEBPA-3	GCCTGCTGGGTCTAGCGCG	PMAIP1	PMAIP1-3	GGCGTTATGGGAGCGGACGC
CEBPA	CEBPA-4	CCTCTGTCCCGGGTTCGCG	PMAIP1	PMAIP1-4	ATAACGCCGTCTGCGGGCG
CEBPA	CEBPA-5	CGGCCTCTGTCCCGGGCTG	PMAIP1	PMAIP1-5	CGCAGACGGCGTTATGGGAG
CEBPA	CEBPA-6	GCTGGTCTAGCGCGCGCG	PMAIP1	PMAIP1-6	TGGGAGCGGACGGGGACGC
CEP19	CEP19-1	ACGCCGCGCGGAAACCTTG	POLR2H	POLR2H-1	CCCGAAAGATTGCTCCGAG
CEP19	CEP19-2	GGCCCCAAGGGTCCCGCG	POLR2H	POLR2H-2	GGAAGTTAAGTAGCCCGGAG
CEP19	CEP19-3	TGCAGGCAGCTGGGAACCCG	POLR2H	POLR2H-3	TCGGAAACAATCTTTCCGGA
CEP19	CEP19-4	AAGGGTCCCGCGCGCGGTG	POLR2H	POLR2H-4	CCGGACAGCCCTCCCGCTCG
CEP19	CEP19-5	CGCCGCGCGGAAACCTTGG	POLR2H	POLR2H-5	GAAGTTAAGTAGCCCGGAGC
CEP19	CEP19-6	GTGCGCGCGCTAGCGCCCG	POLR2H	POLR2H-6	GTTAAGTAGCCCGGAGCGGG
CHIC2	CHIC2-1	AGACTTCCCGGGCCAACGGG	POU2F3	POU2F3-1	AAAGGAACAGAAGAAAGAA
CHIC2	CHIC2-2	GACTTCCCGGGCCAACGGG	POU2F3	POU2F3-2	AGAGATAGGGGTTTGCCTGG
CHIC2	CHIC2-3	TGGGCGAGCGGACTGGCTGG	POU2F3	POU2F3-3	AGGGAAAAAGAACCCAGGAC
CHIC2	CHIC2-4	CGGGCGGGCGCGCGCACGTG	POU2F3	POU2F3-4	GGCAGCAAAATTTCTGTCC
CHIC2	CHIC2-5	TCCCGGGCCAACGGCCGGG	POU2F3	POU2F3-5	GGTTTGCCTGGAGTTAGAA
CHIC2	CHIC2-6	TGCGTGGGCGGTGGGCGAG	POU2F3	POU2F3-6	TCTGTTCTTTCTAACCTCC
CHRD	CHRD-1	AGTGCCGCGAGGGGCTGCTC	POU5F1B	POU5F1B-1	CAGATCGGCCACTGACACAA
CHRD	CHRD-2	CAGTGCCGCGAGGGGCTGCT	POU5F1B	POU5F1B-2	CCTACACTGGAATTTTCAGT
CHRD	CHRD-3	GCCGCCGACGAGCCCTCG	POU5F1B	POU5F1B-3	TAATGTGTCCATTGTGTGAG
CHRD	CHRD-4	AGCCCTCGCGGACTGCCCC	POU5F1B	POU5F1B-4	AAATGTGACTGAATGTGTT
CHRD	CHRD-5	CCGGGGCGGGTGGGCGGGA	POU5F1B	POU5F1B-5	GTATGACACACAGCCATA
CHRD	CHRD-6	CGGGCGGGGGCGGTGGCGG	POU5F1B	POU5F1B-6	TCAACATTTAATGATGCTTC
CIC	CIC-1	CCCGCCCGCGGACTCCGCG	PDP1	PDP1-1	ATTGCTGCGCAGTGACGAG
CIC	CIC-2	CCCGCCGACTCCCGGAGGG	PDP1	PDP1-2	GCAGTGACGAGTGGGAGGG
CIC	CIC-3	CCGGAATCCGCGAGGGAGGA	PDP1	PDP1-3	TTGGCTGCGCAGTGACGAGT
CIC	CIC-4	CCTCCCTCGCGGAGTCCGCG	PDP1	PDP1-4	CTGCGCAGCCAATCGGCAGG
CIC	CIC-5	TCACGGGGCGCGCGGCACGG	PDP1	PDP1-5	CTGCGCAGTGACGAGTGGGA
CIC	CIC-6	TCCTCCCTCGCGGAGTCCGCG	PDP1	PDP1-6	GCTGCGCAGTGACGAGTGGG
CLCN2	CLCN2-1	CAGCCAGGCTGGGGTCCGCG	PPF1B1	PPF1B1-1	CAGCCAAAGAGAGTACGAG
CLCN2	CLCN2-2	CTGGGCGGTCCCTCCGGAT	PPF1B1	PPF1B1-2	GCTGATTCCTGCAGGGAGGG
CLCN2	CLCN2-3	GCCTCTCGGGAGGCCCCGCG	PPF1B1	PPF1B1-3	TTTGGCTGATTCCTGCAGGG
CLCN2	CLCN2-4	GCCAGGCTGGGGTCCGCGCG	PPF1B1	PPF1B1-4	AAAGAGAGTGCAGTGGGG
CLCN2	CLCN2-5	GCCCGCCGGCCATCCGGAG	PPF1B1	PPF1B1-5	AGCCAAAGAGAGTACGAGT
CLCN2	CLCN2-6	GTCCCTCCGAGTGGGCCGG	PPF1B1	PPF1B1-6	GTTCCCGGCTCCAATCAGC
CLDN1	CLDN1-1	GCCCCCTGGCGTTCAGGG	PPIE	PPIE-1	CCAACCCGACTCCCGCTACC
CLDN1	CLDN1-2	GCCGCCCTGAAACCGCCAGG	PPIE	PPIE-2	GCGCCTGTGAGGTGCGCAG
CLDN1	CLDN1-3	TTTCAGGGCGGCTCACCGAG	PPIE	PPIE-3	TGCCGTTGGACCAACCGGA
CLDN1	CLDN1-4	AGCCGCCCTGAAACCGCCAG	PPIE	PPIE-4	ACAAGCGGCTGAGGTGATCC
CLDN1	CLDN1-5	GAGCCGCCCTGAAACCGCCA	PPIE	PPIE-5	GACCCCGCCACCCCTCGCGT
CLDN1	CLDN1-6	GCGCCCGGTTGGGGAACGG	PPIE	PPIE-6	GATGCACTGGGCGCCTGTG
CLDN16	CLDN16-1	ACCACCACTAGCCACAGTT	PPP1R2	PPP1R2-1	CCGCCCTCCGTCGCCGCC
CLDN16	CLDN16-2	GACCACTAGCCACAGT	PPP1R2	PPP1R2-2	CGCCCCCGCGGCGCTGGG
CLDN16	CLDN16-3	TCAGAAGGCAGTCAAGTCA	PPP1R2	PPP1R2-3	CGCCTCCAGCGCCGCGGG
CLDN16	CLDN16-4	GCTGAGTGTGTTCCGGTGG	PPP1R2	PPP1R2-4	CCGCTCCGAGCGCCGCGG
CLDN16	CLDN16-5	GGGCTGAGTGTGTTCCGGT	PPP1R2	PPP1R2-5	GCGGGCGGAGCAGCCGGGG
CLDN16	CLDN16-6	GTGTTCCGGTGGGGGAGAG	PPP1R2	PPP1R2-6	TCCCGCTCCAGCGCCGCG
CLEC4C	CLEC4C-1	ATCTCTCTTTGCAAGAT	PPP2R1A	PPP2R1A-1	AATGGCAAAATCGGAAGTGGG
CLEC4C	CLEC4C-2	GTAGGCGAAGAAGACTAA	PPP2R1A	PPP2R1A-2	AGAAAGCGGAGCTTAGCCCT
CLEC4C	CLEC4C-3	TTCTTCGCTACTCTTGCAA	PPP2R1A	PPP2R1A-3	GAGCTTAGCCCTGGGTAGCG
CLEC4C	CLEC4C-4	AGTAGGCGAAGAAGGACTA	PPP2R1A	PPP2R1A-4	AGTTTACAGGGGCTGCTCCA
CLEC4C	CLEC4C-5	CGAAGAAGGATCTAAGGCT	PPP2R1A	PPP2R1A-5	ATGGCAAAATCGGAAGTGGG
CLEC4C	CLEC4C-6	CTCCAAAGATGTTACTTTCC	PPP2R1A	PPP2R1A-6	TGGGGGAACTTCAACAAGTC
COL4A1	COL4A1-1	AAGGGGAGGACCCTGCGCG	PPT1	PPT1-1	ATGCCAGCCTGATGGGCGT
COL4A1	COL4A1-2	CCTGCGGCGCGGGTAAGAGG	PPT1	PPT1-2	CGCAACTGCGCATCCCGAA
COL4A1	COL4A1-3	CGGCGCGGTAAGAGGCGG	PPT1	PPT1-3	CTGTCCGCTGAAAGCTCCA
COL4A1	COL4A1-4	CGCACTGCAGCCACTCCC	PPT1	PPT1-4	CGCGCTGAAAGCTCCAGGGT
COL4A1	COL4A1-5	CGGGCGGCGCCTCAAAGGGG	PPT1	PPT1-5	GCGCTGAAAGCTCCAGGGTA
COL4A1	COL4A1-6	GCGGCGGGTAAGAGGCGG	PPT1	PPT1-6	GGCCGAGCCCATCAGGCT

COL4A2	COL4A2-1	AAGCGGAGACCTGAGCGCGG	PRDM1	PRDM1-1	CGAAGAGAGGAAGCTCTCGG
COL4A2	COL4A2-2	CCGGGTGCGCGGCTCCAAG	PRDM1	PRDM1-2	CGGCTGTGCTAGCAATCTGG
COL4A2	COL4A2-3	TCCAAGCGGAGACCTGAGCG	PRDM1	PRDM1-3	TGAAATACACATGCCAAGAG
COL4A2	COL4A2-4	ACGCACCGTCCCAGGCTCGG	PRDM1	PRDM1-4	ATCGAAGAGAGGAAGCTCT
COL4A2	COL4A2-5	GGGGCAGCGCCAAACAATTG	PRDM1	PRDM1-5	GCAATCTGGGGGAAAGCCCT
COL4A2	COL4A2-6	TGGCGCTGCCCTCCCGCC	PRDM1	PRDM1-6	GCGGCTGTGCTAGCAATCTG
COL9A2	COL9A2-1	CTGTACCTGAGAGGACCGG	PRDM14	PRDM14-1	ACAGAGGGCGAGTTCGAGAGT
COL9A2	COL9A2-2	GGAGGCTGGACCGCGGGG	PRDM14	PRDM14-2	AGACGACGCGGGGATCTGCG
COL9A2	COL9A2-3	GTCACCTGAGAGGACCGGCG	PRDM14	PRDM14-3	GACGACGCGGGGATCTGCGT
COL9A2	COL9A2-4	CTCCCTCCCGGCAACCCCGC	PRDM14	PRDM14-4	AGTCGGCAATGGCTCGGCT
COL9A2	COL9A2-5	GCATCCAGCTCCGCCCGCT	PRDM14	PRDM14-5	GCGAGTCGAGAGTCGGCCAA
COL9A2	COL9A2-6	TGTACCTGAGAGGACCGGC	PRDM14	PRDM14-6	GGGCGGGGAGAAGACGACGC
CPN2	CPN2-1	AATCTTCAGAGGCTTTGCCA	PREX2	PREX2-1	ACAGAAGACTTTACATGCTG
CPN2	CPN2-2	AGCGTCCCAGAATGTACCA	PREX2	PREX2-2	AGACTTTACATGCTGGGAG
CPN2	CPN2-3	GGTGACATTTGGGACGCTG	PREX2	PREX2-3	TGCCGCTCCGCGCAACTCCG
CPN2	CPN2-4	ATGTCACCAGGGTCACAGGA	PREX2	PREX2-4	AGACAGAAGACTTTACATGC
CPN2	CPN2-5	CAGAATGTACCAGGGTTCAC	PREX2	PREX2-5	CTTCTGTCTCTCTCCGAGT
CPN2	CPN2-6	GACGGGAGAGGCGTTGCCA	PREX2	PREX2-6	TTACATGCTGGGGAGAGGCT
CRKL	CRKL-1	ACGTAACGGGAGGGCCCGG	PRKCI	PRKCI-1	CTCCAAAGGCCACATTCGG
CRKL	CRKL-2	GCCCCACCTGATCGTCGGA	PRKCI	PRKCI-2	GATGGTTAGCCCGGATTTG
CRKL	CRKL-3	GCGCTGTGTGACGTAACGGG	PRKCI	PRKCI-3	GCAACCATCCAGCCAGCTCA
CRKL	CRKL-4	CGCTGTGTGACGTAACGGGA	PRKCI	PRKCI-4	AAAGGCCACATTCGGGGT
CRKL	CRKL-5	GAGCACCGTCCGCGACGTCA	PRKCI	PRKCI-5	CCCGCCCTACCCCGGAATGT
CRKL	CRKL-6	GCTGCGCTGTGTGACGTAAC	PRKCI	PRKCI-6	GCTCAAGGAGCCTCAATACC
CRLF2	CRLF2-1	AAAAAGTCAGAAAGGAAACT	PRKD1	PRKD1-1	ACTGGGAGGCCACCACCCGG
CRLF2	CRLF2-2	AAAAGTCAGAAAGGAAACT	PRKD1	PRKD1-2	CGACTCCCGCGCCCGCGGG
CRLF2	CRLF2-3	CTAGGGAAATGATTACAGGC	PRKD1	PRKD1-3	CGGGCACCTCGCGCCACTG
CRLF2	CRLF2-4	CACACACACACAATCAATCC	PRKD1	PRKD1-4	CAGCGCCGCGCAGTGGCCGA
CRLF2	CRLF2-5	CACTCATGACTCATAAGCAG	PRKD1	PRKD1-5	CGCAGGAGCAGCGGCCGAG
CRLF2	CRLF2-6	GAAACTAGGGAAATGATTAC	PRKD1	PRKD1-6	CGCGGAGTCGAGGAGGAG
CROCC	CROCC-1	AAGCAGAGGCAAGGAGCCAA	PSMD10	PSMD10-1	CTCCAGACCGCGCCGCGCA
CROCC	CROCC-2	GAGCAGGATGTGGGCTGAGG	PSMD10	PSMD10-2	TCCCGTCGCGCGGCGCTCT
CROCC	CROCC-3	GCGCCCCATGTGACCACCG	PSMD10	PSMD10-3	TGCAGTTGAGAGCAGTTCC
CROCC	CROCC-4	CAGATTAAGCTTAAATCCGG	PSMD10	PSMD10-4	TTCCGTCGCGCGGCGCTC
CROCC	CROCC-5	CCACCGCGGTGTCACATGG	PSMD10	PSMD10-5	TTGCAGTTTGAAGAGCAGTTC
CROCC	CROCC-6	CCCCCATGTGACCACCGCGG	PSMD10	PSMD10-6	GGCAACTTGACTACGGAGGAGT
CRYGS	CRYGS-1	ACAGTGACATTTATATGGGC	PSMD2	PSMD2-1	CGCGCACCCACCCACCCCT
CRYGS	CRYGS-2	AGTCATTTAGACGCTATTGA	PSMD2	PSMD2-2	CTCAGCGCGGGGGTGGGT
CRYGS	CRYGS-3	CCTTTAATGCTTACCAAGCA	PSMD2	PSMD2-3	GCCTGCGACCGGAAACGCCG
CRYGS	CRYGS-4	AGGCACAGTGACATTTATAT	PSMD2	PSMD2-4	AGGCGGCTCTGGAGGAGGA
CRYGS	CRYGS-5	ATTTGCTTAGTCATGAAT	PSMD2	PSMD2-5	CCGCCTGCGCGGGAACGC
CRYGS	CRYGS-6	GTCTGTAATGCAGCCCTGCT	PSMD2	PSMD2-6	CCGGCGTTTCCGGTCCGAGG
CSF3R	CSF3R-1	CTCACAGGCTCCTTCTGGG	PTHLH	PTHLH-1	ATTCTCTCAATATATACCC
CSF3R	CSF3R-2	GCAGCCCTTCTCCAGGA	PTHLH	PTHLH-2	CATCCTCTGCTATTATATGA
CSF3R	CSF3R-3	TCCCAGGAAGGAGCCTGTGA	PTHLH	PTHLH-3	GGAGATTACTAGTATTGTT
CSF3R	CSF3R-4	CTGTGCCCTCGAAGGCGCAA	PTHLH	PTHLH-4	AGGCAAAAAGTCAGGGTCT
CSF3R	CSF3R-5	GCCCTCGAAGGCGCAAGGGA	PTHLH	PTHLH-5	CAGGCAAAAAGTCAGGGTCC
CSF3R	CSF3R-6	TGCCCTCGAAGGCGCAAGGG	PTHLH	PTHLH-6	CCAAAACAGGCAAAAAGTCA
CTBP2	CTBP2-1	CCAATGACACAACCCACAT	PTPRD	PTPRD-1	CGGAAGCCGCGGGCTCAGAA
CTBP2	CTBP2-2	GTAGTGAGGAGTATCTGAAG	PTPRD	PTPRD-2	GCGGGCTCAGAAGGGCCAA
CTBP2	CTBP2-3	TAGTGAGGAGTATCTGAAGG	PTPRD	PTPRD-3	TCTTGCCCTTCTGAGCCCG
CTBP2	CTBP2-4	CTACAAATCGGCTCTCTCGG	PTPRD	PTPRD-4	AGAAACCGCCGCGGAAGCCG
CTBP2	CTBP2-5	GAGAGAGCCGATTTGTAGTG	PTPRD	PTPRD-5	GAAACCGCCGCGGAAGCCG
CTBP2	CTBP2-6	TGTAGTGAGGAGTATCTGAA	PTPRD	PTPRD-6	TTCTGAGCCCGCGGCTCCG
CTNND2	CTNND2-1	GCCAGCGGGGAGCCCGCGG	PTPRS	PTPRS-1	CCATTGGCCGGGGCGGCTG
CTNND2	CTNND2-2	GGAGCTGGAGTAGTAGAGCG	PTPRS	PTPRS-2	CGGCCCTGCCCGGACCCGG
CTNND2	CTNND2-3	TTGGTGGGCGAACCCCGCTG	PTPRS	PTPRS-3	GCGCCCTCCATTGGCCGGG
CTNND2	CTNND2-4	AGCGGGGAGCCCGCGCGG	PTPRS	PTPRS-4	CGCGTCACTGCGCAGCCGCG
CTNND2	CTNND2-5	CCGCTGGCCGCGCCCGAGG	PTPRS	PTPRS-5	CGGCTGCGCAGTGACCGCA
CTNND2	CTNND2-6	CTGCCCGCGCCCGCGCGG	PTPRS	PTPRS-6	GGCTGCGCAGTGACCGCAC
DCUN1D1	DCUN1D1-1	GGAGGACGCCCGGACCTCG	PTPRT	PTPRT-1	CAGGCGCGGCGTGCAGCTG
DCUN1D1	DCUN1D1-2	GGCAGCCCGGACCTCGGGG	PTPRT	PTPRT-2	GCCGAGGCGGAGCGCCCGG
DCUN1D1	DCUN1D1-3	TCCGTCCTCCGCTCCCGG	PTPRT	PTPRT-3	TGAGGGTGTGTGCACGCGG
DCUN1D1	DCUN1D1-4	ACCTCGGGGAGGCGGAGGGA	PTPRT	PTPRT-4	ACGGCCGAGGCGGAGCGCC
DCUN1D1	DCUN1D1-5	CCGGACCTCGGGAGGCGGA	PTPRT	PTPRT-5	AGGCGCGGCGTGCAGCTGA
DCUN1D1	DCUN1D1-6	CTCCGCTCCCGGAGGTCGG	PTPRT	PTPRT-6	AGGCGGAGCGCCCGGGCGG
DDR2	DDR2-1	ATTTGGTTTCAATTAGGAAG	PYDC2	PYDC2-1	AAATGTGAGAACCAGAGCAT
DDR2	DDR2-2	CATTTGGTTTCAATTAGGAA	PYDC2	PYDC2-2	GAGAACCATGAGCATAGGGCC
DDR2	DDR2-3	TTTGGTTTCAATTAGGAAGG	PYDC2	PYDC2-3	GCGTATCGCGTATCTAATGA
DDR2	DDR2-4	AAACGAAAAACAGCTTGAT	PYDC2	PYDC2-4	AGAGTCTTTTATATAGTCTA
DDR2	DDR2-5	ACATTTGGTTTCAATTAGGA	PYDC2	PYDC2-5	CAGAGCATAGGCGCAGGCGT
DDR2	DDR2-6	GTTTCAATTAGGAAGGGGGT	PYDC2	PYDC2-6	TCTTTATATAGTCTAGGGAC
DDX1	DDX1-1	AGGCGCGCTCCAGAAGCCCT	RAB20	RAB20-1	CGAAACGCGGAGTCCAGCA
DDX1	DDX1-2	CCAGAAGCCCTAGGTCCCG	RAB20	RAB20-2	CGGATGCTTGCAGAAACGGG
DDX1	DDX1-3	GGTCCAGAGGTCGCTCAG	RAB20	RAB20-3	GAAACGGGCGGTCAGCGAG
DDX1	DDX1-4	AACGGTTCGATGGAAGGAA	RAB20	RAB20-4	CCCGGGCCCTTACCAGCCG
DDX1	DDX1-5	ATGGAAGGAAAGGCGCCGC	RAB20	RAB20-5	GGGCGGAGGAGGATAGGGCG
DDX1	DDX1-6	GGGAGAACGGTTCGATGGA	RAB20	RAB20-6	TGGCGGAGGAGGATAGGGCG
DGKG	DGKG-1	CCCGCCCGCCACACACAC	RAD21	RAD21-1	CCAGGAGTCCGGCTCCCGCA
DGKG	DGKG-2	CGCGCGCGCGGCTGTGTG	RAD21	RAD21-2	CCGGCTCCCGGACGGCAGAG
DGKG	DGKG-3	GGCGCGCGGCTACACACA	RAD21	RAD21-3	TCCCGACGGCAGAGCGCGG

DGKG	DGKG-4	CGCGCGGTTGTGTGGCGG	RAD21	RAD21-4	GTCGGGGAGCCGGACTCCTG
DGKG	DGKG-5	GCGCGCGGTTGTGTGGCG	RAD21	RAD21-5	TCCCGCGGCTCTGCCGTCG
DGKG	DGKG-6	GCGCGCGCGGTTGTGTGG	RAD21	RAD21-6	TCCTGGGGGGGGAGGGCGGA
DICER1	DICER1-1	AGCCAGTGGGATTCTCCAAG	RAD51B	RAD51B-1	AGAGCCCAAGTTGGCTCCG
DICER1	DICER1-2	AGCCGCTGGAGAATCCAC	RAD51B	RAD51B-2	CTACAATTCCAGCAAGCCG
DICER1	DICER1-3	GGGGCGGTGCGGGAGCCAGT	RAD51B	RAD51B-3	TGGCTACTGTATCCAATCAG
DICER1	DICER1-4	ACGGGGCGAGCGGAGCGTGG	RAD51B	RAD51B-4	AGGCCGGCAGAGGCCAGGT
DICER1	DICER1-5	CACGGGGCGAGCGGAGCGTG	RAD51B	RAD51B-5	GCAAGCCGCGAGGCCAACCT
DICER1	DICER1-6	GGCAACGGCGCACAGCCGCT	RAD51B	RAD51B-6	TACTGTATCCAATCAGAGGC
DIS3	DIS3-1	CCACTCTCGCCCAATCCCGG	RAD52	RAD52-1	AAAAAACACAGACCAGAGA
DIS3	DIS3-2	GAAAATGCCGAGATAAACAT	RAD52	RAD52-2	AACCCAGCCAGCCGCGGGA
DIS3	DIS3-3	TTGGCTCTGACGGCCGCG	RAD52	RAD52-3	ACCCAGCCAGCGCCGGAG
DIS3	DIS3-4	ATGCCGAGATAAACATTGGT	RAD52	RAD52-4	CCCAGCCAGCGCCGGAGG
DIS3	DIS3-5	GTCCAGAAGGAAGCCCGCTGTT	RAD52	RAD52-5	TCCGAACCCAGCCAGCCG
DIS3	DIS3-6	GCCGCGGAAGTCAACTCTCCGTT	RAD52	RAD52-6	TCCGCGCTGGCGTGGGTT
DLG1	DLG1-1	ACTTAACAATCAGCCTGGAG	RAD54L	RAD54L-1	AGTTCCGCGCTCGCGACCCA
DLG1	DLG1-2	AGTGAAGGCAATGCAGAT	RAD54L	RAD54L-2	GAATAGTGCTCGCCCAATG
DLG1	DLG1-3	GAGTAACTTAACAATCAGCC	RAD54L	RAD54L-3	TCGCGACCCAAGGAAGAGGC
DLG1	DLG1-4	AACAATCAGCCTGGAGTGA	RAD54L	RAD54L-4	CTCGGACCCAAGGAAGAGG
DLG1	DLG1-5	CGGGCCCTGGGAGGGGAGA	RAD54L	RAD54L-5	CTGCGCCCAATGAGGAGTCT
DLG1	DLG1-6	TCTGCATTGCCTTCCATCC	RAD54L	RAD54L-6	GCGCTCGCGACCGAAGGAAG
DNAJB11	DNAJB11-1	AGTACACTTCACCTCCGAGG	RANBP3L	RANBP3L-1	CTAGGATGATTAGCATAAAG
DNAJB11	DNAJB11-2	CGCAGTACACTTCACCTCCG	RANBP3L	RANBP3L-2	GAGGCAAGCAAGACGGGCAT
DNAJB11	DNAJB11-3	GGTTGCCCGTGGCCCTCGG	RANBP3L	RANBP3L-3	GATGATTAGCATAAAGAGGC
DNAJB11	DNAJB11-4	ACTTCACCTCCGAGCGGCA	RANBP3L	RANBP3L-4	CATAAAGAGGCGAGGCAAGAC
DNAJB11	DNAJB11-5	GGCGGCACGGGCAACCAGTT	RANBP3L	RANBP3L-5	GTTACTGTAACATAAAGGGA
DNAJB11	DNAJB11-6	GTGAAGTGTACTGCGCTGAT	RANBP3L	RANBP3L-6	TAAGGGACTCTGAAGGAGG
DNAJC19	DNAJC19-1	AAGGAAAGTCGCTAAGCAG	RBM10	RBM10-1	CAGCGCTTGCCAACTCAGAGG
DNAJC19	DNAJC19-2	CGCTCAAGCAGTGGACAGAG	RBM10	RBM10-2	CAGGGCTGTCCCTAGCGGG
DNAJC19	DNAJC19-3	TGTCGTAAGGGGAGCGGG	RBM10	RBM10-3	GATTGGTACCAGCCCGCTAG
DNAJC19	DNAJC19-4	AGAGCGGAGAAAGCAGCTTC	RBM10	RBM10-4	ACTAGGCGAGGCTTCGCAAG
DNAJC19	DNAJC19-5	CGGAGAAAGCGACTTCGGGT	RBM10	RBM10-5	CACTAGGGGAGCGTTCGCAA
DNAJC19	DNAJC19-6	CGGGTTGGTTGAAGGTTGGG	RBM10	RBM10-6	GGCCAGCGCTTGCCAATCAG
DNMT3B	DNMT3B-1	CGCCGGGCGGGGATCTGAG	RCL1	RCL1-1	GATCCGCGCGGGCCAAATAG
DNMT3B	DNMT3B-2	GAGGGAAATTTGAAATCGCT	RCL1	RCL1-2	GGCGCGGGCCAATAGCGGCG
DNMT3B	DNMT3B-3	GGCGGGGATCTGAGTGGCTG	RCL1	RCL1-3	TGGCCGCGCCGATCAGGG
DNMT3B	DNMT3B-4	AGCCACTCAGATCCCCGCC	RCL1	RCL1-4	ACGCCGCTATTGGCCCGCGC
DNMT3B	DNMT3B-5	CCGTTCCCCCGCGCCGGG	RCL1	RCL1-5	GCCTCCCGCCAGCCGGGG
DNMT3B	DNMT3B-6	GAACGGGGGGGCGGGGACGA	RCL1	RCL1-6	GGCACCGCCCTGATCCGGCG
DPPA3	DPPA3-1	ATCCCTTAATCTCTAATCA	RECQL4	RECQL4-1	GAGGCGTCAACGTCATCGCG
DPPA3	DPPA3-2	GGGTGTAGTTTAGACTCATA	RECQL4	RECQL4-2	GGGAGGCGTCAACGTCATCG
DPPA3	DPPA3-3	TCCCTTAATCTCTAATCAT	RECQL4	RECQL4-3	TCGGACAAGCAGCCAATGGG
DPPA3	DPPA3-4	TAAGGGATCCAAATGATTA	RECQL4	RECQL4-4	TCCCTTGGGCTGCTTGCCG
DPPA3	DPPA3-5	TCCCATGATTAGAGGATTA	RECQL4	RECQL4-5	GGTCCCCCGCCCTTGAGCCGTT
DPPA3	DPPA3-6	TGGGTGTAGTTTAGACTCAT	RECQL4	RECQL4-6	GGCCCGCGGTGGCACTCCCGTT
RNASE3	RNASE3-1	CTGCATGGCCAGACCCACCA	REP15	REP15-1	ACAAAACATCTGTCTATCT
RNASE3	RNASE3-2	TAAATAAAGCTTCCCTTGGT	REP15	REP15-2	CTTTAACTTAATAAACCCAGC
RNASE3	RNASE3-3	TAAATAAAGCTTCCCTTGG	REP15	REP15-3	TGTGTTCATACAGTTCCTGC
RNASE3	RNASE3-4	AAAGCTTCCCTTGGTGGGTC	REP15	REP15-4	AGTTCTCTCTGTTTGTGAGT
RNASE3	RNASE3-5	GCCGGTGGGATCTGGACTCT	REP15	REP15-5	TATATGCTTAACTACACCCG
RNASE3	RNASE3-6	TGTTTAAATAAAGCTTCCCT	REP15	REP15-6	TCTAACTTCAAGCTTCCCTC
DVL3	DVL3-1	ACGCGGCGCCTCTCCGCGG	REST	REST-1	CTCCTTGTCTGGTAGAGGGG
DVL3	DVL3-2	GCGACGCGCGCCCTCTCCG	REST	REST-2	GAGGGGCGGGGCGCGCTAG
DVL3	DVL3-3	TGGCAGGTTTCCGCGCCAC	REST	REST-3	GCCTCTTGTCTGGTAGAG
DVL3	DVL3-4	CGGCGTCCGCGGAGTGGCA	REST	REST-4	CCCTCCGAGCCGCGCGCGG
DVL3	DVL3-5	GGCGCGGCGTCCGCGGAGA	REST	REST-5	CCTTGTCTGGTAGAGGGCG
DVL3	DVL3-6	GGGTTTCCCGCCCACTGGCC	REST	REST-6	TCGGAGGGGCGGTGTCTCGC
E2F3	E2F3-1	CCCCGCCCTCAACCCCGCG	RET	RET-1	CAGTGTCTGCTCTGGCTCG
E2F3	E2F3-2	GCTGTGGGAACGGTCTCCG	RET	RET-2	TCCCGCACCCACCCGCTC
E2F3	E2F3-3	TGATTGGGACTGAAGTAAGG	RET	RET-3	TGCTTGGCTGCGCGGGGTG
E2F3	E2F3-4	GGACTGAAGTAAGGAGGTAG	RET	RET-4	AGGCGGGGCGGAGCGGGGT
E2F3	E2F3-5	GTAAGGAGGTAGCGGCCAA	RET	RET-5	CGCGCAGCCAGAGCAAGCAC
E2F3	E2F3-6	GTAGCGGCCCAATGGGCTGT	RET	RET-6	CGGTCCAGGGGTGGGCCAGG
ECE2	ECE2-1	AGTTGCTCAACACAAACACG	RFC4	RFC4-1	GCCTAAATAAACCCGTATAC
ECE2	ECE2-2	CTTCGAAGAATCCTCCGGCT	RFC4	RFC4-2	GTTCTGCCTGAAAGTCCGCG
ECE2	ECE2-3	GAAGAGCGCTTAGTAAGGA	RFC4	RFC4-3	TAGGCAAGGTATGAGCCAGC
ECE2	ECE2-4	CTTCGAAGAGCGCTTAGTAA	RFC4	RFC4-4	CTGGGGCGCGCTGCTTGGCG
ECE2	ECE2-5	GCGCTCTCGAAGAATCCTAC	RFC4	RFC4-5	TCCAGTCTGCTGCTGAAAGTC
ECE2	ECE2-6	TCTTCGAAGAATCCTCCGGC	RFC4	RFC4-6	TGGGGCGCGCTGCTTGGCGGA
EHHADH	EHHADH-1	ACAAGCGTCTGTAGAGCGCC	RHPN2	RHPN2-1	GGCCCTTACAGCCCGGCTG
EHHADH	EHHADH-2	AGCGTCTGTAGAGCGCGGG	RHPN2	RHPN2-2	GGCGGGGCTAGAAAGGGCCG
EHHADH	EHHADH-3	GACAAGCGTCTGTAGAGCGC	RHPN2	RHPN2-3	TCCACTCCACCCCGTCCCG
EHHADH	EHHADH-4	CGTCTGTAGAGCGCGGGTG	RHPN2	RHPN2-4	AGGCGGGGCTAGAAGGGCCG
EHHADH	EHHADH-5	CGCTCTGTAGAGCGCGGGT	RHPN2	RHPN2-5	CCAGTGTCTGCGCTCAGCGG
EHHADH	EHHADH-6	TCCTCTCCGAGACCCACCC	RHPN2	RHPN2-6	GAAGGCGCGCGGACGGGGT
EIF2B5	EIF2B5-1	GCGATGGACTAATTAACGAA	RICTOR	RICTOR-1	ACTCCTTGACACCTTGGGT
EIF2B5	EIF2B5-2	TCTTCCCGGGAGCCACAG	RICTOR	RICTOR-2	GGGAGCACTGAGCCGACCCA
EIF2B5	EIF2B5-3	TGGACTAATTAACGAAGGA	RICTOR	RICTOR-3	TCAGTCTCCCTCAGCGCTG
EIF2B5	EIF2B5-4	ATCCAGCACTTGAATGCGA	RICTOR	RICTOR-4	AGGCTCGGCCAGCGCTGA
EIF2B5	EIF2B5-5	GATCAACCTCAGACCCTGT	RICTOR	RICTOR-5	CACCTCCCCCGCCCTCGG
EIF2B5	EIF2B5-6	TGCGATGGACTAATTAACGA	RICTOR	RICTOR-6	CCGCGCGCTGCGCGCGAG

EIF4A2	EIF4A2-1	GCTACAAAATTGTGATCCTG	RIT1	RIT1-1	ACCAGAGGACCTTCAGCGGT
EIF4A2	EIF4A2-2	GGATAAAATCCTAAGCAAGT	RIT1	RIT1-2	GACCAGAGGACCTTCAGCGG
EIF4A2	EIF4A2-3	TGATCCTGGGGTTCGTTACCT	RIT1	RIT1-3	GGTGACCAGGAGGACCTTCAG
EIF4A2	EIF4A2-4	AGCTACAAAATTGTGATCCT	RIT1	RIT1-4	ACCCACCGCTGAAGGTCTCTC
EIF4A2	EIF4A2-5	CAGCTACAAAATTGTGATCC	RIT1	RIT1-5	AGTCCCTAAAACCCAGTTTC
EIF4A2	EIF4A2-6	TTATCCGAGGTAACGACCCC	RIT1	RIT1-6	GTTCCGGGACCACCCGCTGA
EIF4G1	EIF4G1-1	GCGGCGCAGATCGCCCGCG	RLF	RLF-1	CGGACTCCGGTGCTCTCAG
EIF4G1	EIF4G1-2	GGCAAATCCCATGTCTCGG	RLF	RLF-2	GACGCACTCCTTAGCGACGC
EIF4G1	EIF4G1-3	GGGGGCAAATCCCATGTGCT	RLF	RLF-3	TGACGCACTCCTTAGCGACGC
EIF4G1	EIF4G1-4	ATCTGCGCCGCGGAGCACAT	RLF	RLF-4	AGCACCCGGAGTCCGAGTGA
EIF4G1	EIF4G1-5	GATCTGCGCCGCGGAGCACACA	RLF	RLF-5	GTCCGAGTGACGGAATCAGG
EIF4G1	EIF4G1-6	GCTCGGCGGCGCAGATCGCC	RLF	RLF-6	TGTCAGGACTGGCGATGCGT
ELF3	ELF3-1	ACACCAGCTCAGGTTACTGCG	RLN1	RLN1-1	AAGGGCCAAGGACAGAGGAA
ELF3	ELF3-2	ACCAGCTCAGGTTACTGCGAG	RLN1	RLN1-2	ACAAAACCTGTAAGAGGGCCA
ELF3	ELF3-3	CACCAGCTCAGGTTACTGCA	RLN1	RLN1-3	ATGGGCAAAATGAAGGAAGGG
ELF3	ELF3-4	AGGAGCCAGTCTAAAGGCC	RLN1	RLN1-4	AAGGAGAAAATTTCTGTGGAG
ELF3	ELF3-5	GCTGGTGTCTCATTGGATGG	RLN1	RLN1-5	AGAGGCAGAACAGAGCTGA
ELF3	ELF3-6	TGAGCTGGTGTCTATTGGA	RLN1	RLN1-6	CGAAAAACAAAACCTGAAAA
ELOC	ELOC-1	CATAGGCTGGCCTACTATAG	RLN2	RLN2-1	ACACAACTGTAAAAGGGCCA
ELOC	ELOC-2	CGCTACGCCCTACTCCAGA	RLN2	RLN2-2	AGAAGAACACAACCTGTAATA
ELOC	ELOC-3	TGTCGCTCACTTCGGTCTGG	RLN2	RLN2-3	GTAAGAGGGCCAGGACAGAGA
ELOC	ELOC-4	CTCACTTCGGTCTGGAGGTA	RLN2	RLN2-4	AAGGGCCAAGGACAGAGGGA
ELOC	ELOC-5	GTGTGTGCTCACTTCGGTCT	RLN2	RLN2-5	AGGGAGACCAAGAGCTGAGG
ELOC	ELOC-6	TACTATAGGGGAAAGAGATA	RLN2	RLN2-6	TTTGCCCACTCCCTCTGTCT
EPHB1	EPHB1-1	CTAACAAATGCCAGTGAAGG	RNF168	RNF168-1	GACCCCGGAAGTCCCGCCCG
EPHB1	EPHB1-2	GCGCGAGCACCTCCTTACAC	RNF168	RNF168-2	GCGGGGCTGCGACGCCAGGG
EPHB1	EPHB1-3	GCTCGCGCCTGATTGGCCGG	RNF168	RNF168-3	TAGCGGGGCTGCGACGCCA
EPHB1	EPHB1-4	AAACTAACAAATGCCAGTGA	RNF168	RNF168-4	CCCTCCCTCCAGCCCGAGA
EPHB1	EPHB1-5	TCAAACCTGCAAAATCCCC	RNF168	RNF168-5	CGGGGCTGCGACGCCAGGGC
EPHB1	EPHB1-6	TGCTCGCGCCTGATTGGCCG	RNF168	RNF168-6	GGCGGGCGCCGCGAGACCC
EPHB3	EPHB3-1	ACTCCAGCTAGTGTCTCG	RPTOR	RPTOR-1	AAACGGAATTAAGTAACCG
EPHB3	EPHB3-2	CGCTGAGGCCCGCCCTAG	RPTOR	RPTOR-2	GAACAAATGGCGATTAACCTG
EPHB3	EPHB3-3	GGCCGAACCAAGCGGGCCTGG	RPTOR	RPTOR-3	TTATGGTAACCGAGGTAACG
EPHB3	EPHB3-4	AGTGGTGGCCAGCCGCTAG	RPTOR	RPTOR-4	AATTATGGTAACCGAGGTAAC
EPHB3	EPHB3-5	GCTCTCGAGGCCGAACCAGC	RPTOR	RPTOR-5	AGTCCCGGACCCCGTTACCT
EPHB3	EPHB3-6	GGGCTGGCGGTCTGTGAGT	RPTOR	RPTOR-6	GGTAACCGAGGTAACCGGGT
ERC1	ERC1-1	AGCGTGACGCGCGCCCGCG	RRAGC	RRAGC-1	CTCTCGATAGCAGCTCGGG
ERC1	ERC1-2	CGCCGCTCAGCTCCCGGG	RRAGC	RRAGC-2	GCTGCTACTCGAGAGCAGCA
ERC1	ERC1-3	CTCCGGGAGCGTGACCGGG	RRAGC	RRAGC-3	GGTGATTCCGGCACGTGACG
ERC1	ERC1-4	AGCCTCCCGGAGCGTGACG	RRAGC	RRAGC-4	CAGGTGATCCCGCACGTGTA
ERC1	ERC1-5	CGGGAGGCTGAGGAAAGGG	RRAGC	RRAGC-5	CTACTCGAGAGCAGCAGGGT
ERC1	ERC1-6	TCACGCTCCCGGAGGCTGA	RRAGC	RRAGC-6	CTCGAGAGCAGCAGGGTAGG
ERCC2	ERCC2-1	ACCTGCCCGTCAATCCGCTA	RTEL1	RTEL1-1	AAAAACCGCGTGTAGGCCCTGG
ERCC2	ERCC2-2	CAATGGTCTCGTAATATAGG	RTEL1	RTEL1-2	AAGTGAGGTTCACTGGCCAG
ERCC2	ERCC2-3	TTGACGGGCAGGTTAGCCAA	RTEL1	RTEL1-3	GAACGCGCAAAACCGCGTGT
ERCC2	ERCC2-4	AACCTGCCCGTCAATCCGCT	RTEL1	RTEL1-4	GCCTGTGGCGGATGGAAGTG
ERCC2	ERCC2-5	CACCTATATTACGAGACCAT	RTEL1	RTEL1-5	CGGATGGAAGTGGAGTTTAC
ERCC2	ERCC2-6	CCCGATTGGCTCGCCCTAG	RTEL1	RTEL1-6	TCGGTCTCCAGGCCCTACA
ERCC4	ERCC4-1	CAGCCAGCCGAACGTAGCCG	RTP1	RTP1-1	ATTGCAGAGGCAGAGTTTGT
ERCC4	ERCC4-2	CGAAGAGAGCCGAGTCCGAG	RTP1	RTP1-2	GCCTGAACTAGATTTGCAG
ERCC4	ERCC4-3	GCCGACTCCTAGTGGAGAGT	RTP1	RTP1-3	GGAGGAGGAGTCTCTGAAG
ERCC4	ERCC4-4	AGTTCCGGCTACTCTCCACT	RTP1	RTP1-4	GCCTCTGCAATCTCAGTTCA
ERCC4	ERCC4-5	ATCTCAGTCTCAGCTCTCCT	RTP1	RTP1-5	GTCTCTGAAGAGGTGTTTCA
ERCC4	ERCC4-6	CAGCTCTCCTCGGCTACGTT	RTP1	RTP1-6	TGCCTCTGCAATCTCAGTTCA
ERCC5	ERCC5-1	GCCCTGCGCTCGTATTAGA	RTP2	RTP2-1	AGCGGTTTGTCTAGGCACA
ERCC5	ERCC5-2	GTCTAATACGACGCGCAGGG	RTP2	RTP2-2	GCTAGGCACATGGTAAGTGA
ERCC5	ERCC5-3	TCCGTCTAATACGACGCGCA	RTP2	RTP2-3	TGGCCAGTACACAGGTTCAAG
ERCC5	ERCC5-4	CCTGCGTGGCCCTTGCAACC	RTP2	RTP2-4	ATCTCGCTTGGCCAGCACAC
ERCC5	ERCC5-5	GCGCCGCTAATGGAAGACCG	RTP2	RTP2-5	CAGGTCAAGCGGTTTGTGCT
ERCC5	ERCC5-6	TTCCGTCTAATACGACGCGC	RTP2	RTP2-6	TGGCCAAAGCAGATCAGATC
ERF	ERF-1	GCACCTACACACAGCTCGT	RTP4	RTP4-1	ACTCAGACAGTCTAAATGA
ERF	ERF-2	GGGCGGGCGCAGTGTCTCCA	RTP4	RTP4-2	GAGACAAAACAGTTTCAAGTTT
ERF	ERF-3	GTGTCTCCATGGCGACGCGG	RTP4	RTP4-3	TCTTTATCTCTCTCAGCA
ERF	ERF-4	ACGTCACCGCCGCTCGCCA	RTP4	RTP4-4	ACAGTTTCAAGTTTCTGTTT
ERF	ERF-5	GAGCGTGTGTGTGAGTGCGC	RTP4	RTP4-5	GCAAAACTGTGTTAGTTAAT
ERF	ERF-6	GTGTGTGAGTGCAGCGGGAG	RTP4	RTP4-6	TCAGTTTCTGTTTCTGTGTA
ERMP1	ERMP1-1	GAAGCTGGGTCTTGGCGCGG	RUNX1T1	RUNX1T1-1	AGAGAGGAGGGCCATCAGAG
ERMP1	ERMP1-2	GAGCGGACGGAACCTGACAGA	RUNX1T1	RUNX1T1-2	CAGAGAGGAGGGCCATCAGX
ERMP1	ERMP1-3	TGAGCGGACGGAACCTGCAG	RUNX1T1	RUNX1T1-3	GCCTGCCAGGCAGAGACAGA
ERMP1	ERMP1-4	AAAGAAGCTGGTCTTGGCG	RUNX1T1	RUNX1T1-4	GCAGAGGAGGAGGCCATCAG
ERMP1	ERMP1-5	AGCGCCTCCTAGTGAGCGGA	RUNX1T1	RUNX1T1-5	GGGCGGCTCAGCGGAGGCGA
ERMP1	ERMP1-6	CCGCAGCGCCTCCTAGTGAG	RUNX1T1	RUNX1T1-6	TGCCGCCCCAGCCCTCTGA
ETV1	ETV1-1	ATTTCCGGGCTGCAATCAGG	SCAF11	SCAF11-1	GCGAGCGAGTAAGCAGAATG
ETV1	ETV1-2	GATGGATCGTGCCTCCAT	SCAF11	SCAF11-2	GCGCGCTAAGGTGACGACGG
ETV1	ETV1-3	GGCGAGGGAGACCCCGGGGA	SCAF11	SCAF11-3	TCGGCCGCTAAGGTGACGGA
ETV1	ETV1-4	CGGCTTGCTGCCCTTCCCG	SCAF11	SCAF11-4	ACCTTAGCGCGCCGACAGCG
ETV1	ETV1-5	GCGAGGGAGACCCCGGGAA	SCAF11	SCAF11-5	CCTTAGCGCGCCGACAGCGA
ETV1	ETV1-6	GGCTTGCTGCCCTTCCCGC	SCAF11	SCAF11-6	CTCCTCCCTCCCTCCGCTGT
ETV5	ETV5-1	AAGAGGTGATGGACAGCCG	SDHA	SDHA-1	AGCCCCGCTCGACTCCGGCG
ETV5	ETV5-2	CAAGAGGTGATGGACAGCCG	SDHA	SDHA-2	CACCACGCCGAGTCCGAGCG
ETV5	ETV5-3	TTGGCCAGAGGCCGTTCCCG	SDHA	SDHA-3	CCGGAGCGGGTACTGAGTGG

ETV5	ETV5-4	ACAGGGTAAACAAGAGTGTA	SDHA	SDHA-4	CGCCCCGAGCGGGTACTGAG
ETV5	ETV5-5	GCCTTGTTCCATTGGCCAG	SDHA	SDHA-5	GCACCATGCCACGCCCGGAG
ETV5	ETV5-6	GTGATGGACAGCCCGCGGAA	SDHA	SDHA-6	GCCTGAAACGCCAGACCCGAGTT
FAM131A	FAM131A-1	AGGTGGCAGTCGGCTTGGG	SDHB	SDHB-1	CCGCGTACGAGCAACCAAGT
FAM131A	FAM131A-2	TCGCCCGCCCTGCCCTCAGG	SDHB	SDHB-2	CGCCCCACCTACATCCACTG
FAM131A	FAM131A-3	TGGACCGGGTTCGAAAATGC	SDHB	SDHB-3	CGTACGAGCAACCAAGTGGG
FAM131A	FAM131A-4	CAGAGCCGACTGCCACCTGA	SDHB	SDHB-4	CCCATTGGTTGCTCGTACG
FAM131A	FAM131A-5	CCCTGCCTTCAGGTGGCCAGT	SDHB	SDHB-5	CGCGGCTAGTGGTCCCTCAG
FAM131A	FAM131A-6	CCGACTGCCACTGAAGGCA	SDHB	SDHB-6	GCCGCGTACGAGCAACCAAG
FAM43A	FAM43A-1	ACCAGGAATCCGCCCGGAGT	SDHC	SDHC-1	AAACAACCAGCAAAACCAGCT
FAM43A	FAM43A-2	CTCGACCAATGGCTGTCACG	SDHC	SDHC-2	ACCAGCTAGGCAGAGCTGAG
FAM43A	FAM43A-3	TAAGAAACCAGGAATCCGCC	SDHC	SDHC-3	AGAGTCTCTTTAAAGGCTC
FAM43A	FAM43A-4	AGGGACCCGCGTACAGCCAT	SDHC	SDHC-4	GCTCTGCCTAGCTGGTTTGC
FAM43A	FAM43A-5	CGCGTGACAGCCATTGGTCTG	SDHC	SDHC-5	GTGACGAGAGTCTCTTTAAA
FAM43A	FAM43A-6	CTCCCGCTCCCTCGACCAA	SDHC	SDHC-6	TCCGCTCAGCTCTGCCTAGC
FAM90A1	FAM90A1-1	CCACGTGGCAGCGGAGAGAGA	SEN2	SEN2-1	AATGGAAGCTTCCGGTCCGGG
FAM90A1	FAM90A1-2	GAGAAAAGCAGACACTGCCA	SEN2	SEN2-2	GGAGGAGGTGACGCTCAGGAG
FAM90A1	FAM90A1-3	TCCTCGGCCCTCCAGCCAGG	SEN2	SEN2-3	TGAGAAATGGAGCTTCCGGT
FAM90A1	FAM90A1-4	CCAAGACTCCCCCTAGGA	SEN2	SEN2-4	ATGGAGCTTCCGGTCCGGC
FAM90A1	FAM90A1-5	CCCAAGACTCCCCCTAGG	SEN2	SEN2-5	CGCGCTGCGCAGATTGAGAA
FAM90A1	FAM90A1-6	GTCTTGGGCCTGGGCCACG	SEN2	SEN2-6	GGAGGTGACTGAGGATGGG
FANCG	FANCG-1	CTGGGTTCCCGCTTCCACCG	SEN5	SEN5-1	CCGCCCGCCTCCGACCCG
FANCG	FANCG-2	GGAGCTGATGACCCGACCG	SEN5	SEN5-2	CGGGGCTAAGGACCGCGTGA
FANCG	FANCG-3	GTCGTAGTACCCACCCGGG	SEN5	SEN5-3	GGAGGCCGGGCTAAGGACG
FANCG	FANCG-4	ACCTCGCAGTCGCCCTCGG	SEN5	SEN5-4	CTAAGGACCGGCTGACGGGC
FANCG	FANCG-5	GGAGCTGTTCCGCCCGGGT	SEN5	SEN5-5	GGGGCGGGAGCGCCGGAAGC
FANCG	FANCG-6	TCCACCGAGGGCCGACTCGG	SEN5	SEN5-6	GGGGCTAAGGACCGGGTAC
FBX045	FBX045-1	CTAGTGATAACCTCACCCGC	SESN2	SESN2-1	ATCAGAGTCTGTTTCCCGG
FBX045	FBX045-2	GAGGTTACTACTAGGCGCCG	SESN2	SESN2-2	GCGGAGCCCGTACTCCAGG
FBX045	FBX045-3	GTTACTACTAGGCGCCGAGG	SESN2	SESN2-3	GCGGGGACACAAAAGCCCGG
FBX045	FBX045-4	CGCGGGGTGAGGTTATCACT	SESN2	SESN2-4	AGAGGTTCTGTTTCCCGGGG
FBX045	FBX045-5	TATCACTAGGCGCCGAGGAG	SESN2	SESN2-5	CCGGCGGTCCAGCCAATCAG
FBX045	FBX045-6	TTACTACTAGGCGCCGAGGA	SESN2	SESN2-6	GGCGGAGCCCGTACTCCAG
FETUB	FETUB-1	GCTATCCAAAGTACTGACTT	SKP2	SKP2-1	GCTGTCTGGCGAGATCGGAGTT
FETUB	FETUB-2	GGTGGATATGAGGTTGCTCA	SKP2	SKP2-2	GCTGTGGCGCCCGGCTTCCGTT
FETUB	FETUB-3	GTGGATATGAGGTTGCTCAA	SKP2	SKP2-3	GACTGGGAAATGTCAGCCGCGTT
FETUB	FETUB-4	AATTCATTTGATGTACAGG	SKP2	SKP2-4	GGTCCGCCACGGGGTAGGCGTT
FETUB	FETUB-5	GGGTCTAAGGTTAGAATCAT	SKP2	SKP2-5	GCGCTCACGCGGTTCCGCTGTT
FETUB	FETUB-6	TGAGGTTGCTCAAGGGTCTA	SKP2	SKP2-6	GACAGCGTCTGGACGGGACCGTT
FGF10	FGF10-1	CTAGGCTGCTGGGAACGCCA	SLC1A1	SLC1A1-1	CCTACCACGCCTGCTCCCTA
FGF10	FGF10-2	GGGAACGCCAGGGAGAGGGA	SLC1A1	SLC1A1-2	GCAGGCCGGGAAGGAGGGT
FGF10	FGF10-3	GGTGGGACATCTGAAACCTT	SLC1A1	SLC1A1-3	GTGCGTGCGTGGGACGCCCG
FGF10	FGF10-4	GGAGGGGGTCAACCCGGCGT	SLC1A1	SLC1A1-4	ACGCACCCACCCCTCCTTCCC
FGF10	FGF10-5	GGTTTCAGATGTCACCCCG	SLC1A1	SLC1A1-5	AGCGGACGGCCCGGGAAGGA
FGF10	FGF10-6	TGGGAACGCCAGGGAGAGGG	SLC1A1	SLC1A1-6	TGGGACCGCCCGGGTCCCTA
FGF12	FGF12-1	CTCCTCAGCTGGGATAACTG	SLC2A14	SLC2A14-1	CTAAGAGTTACTTCTGTTT
FGF12	FGF12-2	GAGGACCGTATTGGGGAGG	SLC2A14	SLC2A14-2	GACCCAGGAGCAGAGTGACG
FGF12	FGF12-3	GATAACTGAGGACCGTATTG	SLC2A14	SLC2A14-3	TAAGAGTTACTTCTGTTT
FGF12	FGF12-4	ACTGAGGACCGTATTGGGGA	SLC2A14	SLC2A14-4	CTGGAGAAGAGTCAAGATGG
FGF12	FGF12-5	GGGAGGCGGTGAAAAGGGGA	SLC2A14	SLC2A14-5	GAAAGTCTGTTGAAACCCAGG
FGF12	FGF12-6	GATTGGGGAGGGAGGCCGAA	SLC2A14	SLC2A14-6	TTACTTCTGTTTGGGAAAT
FGF19	FGF19-1	AATCCCGATAAGAAATGCTC	SLC2A3	SLC2A3-1	AGATCACAAAGATTGCTTCAG
FGF19	FGF19-2	CAATCCCGATAAGAAATGCT	SLC2A3	SLC2A3-2	ATCACAAAGATTGCTTCAGGG
FGF19	FGF19-3	GCCGGAGGCGGGGTGAGT	SLC2A3	SLC2A3-3	GATCACAAAGATTGCTTCAGG
FGF19	FGF19-4	ACACCCGAGCATTCTTCTATC	SLC2A3	SLC2A3-4	ACAAGATTGCTTCAGGGGGG
FGF19	FGF19-5	ACCCACTCACACCCCGCCTC	SLC2A3	SLC2A3-5	GAAGCAATCTGTGATCTCT
FGF19	FGF19-6	TGGGGCTGGGGCCGAGGGCG	SLC2A3	SLC2A3-6	GAGATCACAAAGATTGCTTCA
FGF3	FGF3-1	CCCGAACCCCGAGCCCGCG	SMAD2	SMAD2-1	GGGCGGGTATGGAAGACGGGA
FGF3	FGF3-2	GCGGAGCCGCGCTCGACGG	SMAD2	SMAD2-2	GTGCTCGCCCTAACGGG
FGF3	FGF3-3	TGGCGCGAGTGTATGCAGA	SMAD2	SMAD2-3	TCTTCCATACCCGCCCCGCG
FGF3	FGF3-4	GCTCGACGCGGTCGCGTGG	SMAD2	SMAD2-4	CACGCCGCGGAAAGCCGCG
FGF3	FGF3-5	GGAGCGGAGCCGCGGCTCGA	SMAD2	SMAD2-5	CAGCCGCCCCGTTAGGGCGCG
FGF3	FGF3-6	GGCCCGAACCCCGAGCCCGC	SMAD2	SMAD2-6	CGCGGGCGGGTATGGAAGA
FGF4	FGF4-1	CCCCGGCCCTGATTGGCAGG	SMAD4	SMAD4-1	GCCTCCGCTCCGAGTGACG
FGF4	FGF4-2	CGCCTGCCAATCAGGGCCGG	SMAD4	SMAD4-2	TCCCGTCACTCGGAGCGGG
FGF4	FGF4-3	GGCGCCAGGAGAACCGCAA	SMAD4	SMAD4-3	TCCCGTCCGAGTGACGGGG
FGF4	FGF4-4	CCTGGGCGCCCGGGCCGCTG	SMAD4	SMAD4-4	ACCCCTCCGCTCACTCGGAG
FGF4	FGF4-5	CGCAGGCCCGCTGCAATCA	SMAD4	SMAD4-5	CCCGTCCGAGTGACGGGGA
FGF4	FGF4-6	CGCGTCTCTGGGCGCCCG	SMAD4	SMAD4-6	GAGCGACCCCTCCCGTCACT
FGFR1	FGFR1-1	CCAGCCCGCGCCCAAAAGGA	SMAP2	SMAP2-1	AACCAATCCGTGGAGAAGCG
FGFR1	FGFR1-2	GCCCGGCTGGGGAACATA	SMAP2	SMAP2-2	AGGAAGAGCCCAAGTCCGCG
FGFR1	FGFR1-3	GCCTTGATGTTCCCGAGCCG	SMAP2	SMAP2-3	TCCACGGATTGGTTCCCGAG
FGFR1	FGFR1-4	GGAAGAGAAGGGCAGAGCCG	SMAP2	SMAP2-4	ACGGATTGGTTCCCGAGAGG
FGFR1	FGFR1-5	GGCCCGCTCCCGTCTTTG	SMAP2	SMAP2-5	GCCTCTGGGAAACCAATCCG
FGFR1	FGFR1-6	GGGGAACATAAAGGCCACG	SMAP2	SMAP2-6	GGAACCAATCCGTGGAGAAG
FGFR3	FGFR3-1	ATGCCCGCTCCGCCCGAG	SMARCB1	SMARCB1-1	CCTCTACACCAGACTTGGG
FGFR3	FGFR3-2	GGATGCCCGCTCCGCCCGG	SMARCB1	SMARCB1-2	GGAGAAAGAGAAATAGTCCG
FGFR3	FGFR3-3	GGTCCCGCGCTCCGCCCGG	SMARCB1	SMARCB1-3	GTGGTGTAGAGGACTTCTCA
FGFR3	FGFR3-4	CAGGGCACGCCCTCGGGG	SMARCB1	SMARCB1-4	AAGTCTCTACACCAGACT
FGFR3	FGFR3-5	GGCGGAGCGGGGATCCGAG	SMARCB1	SMARCB1-5	AGTCTCTACACCAGACT
FGFR3	FGFR3-6	TGCCCGCTCCGCCCGAGG	SMARCB1	SMARCB1-6	CCAGGCTGCCTCCCAAGTCCG

FH	FH-1	AATGACCAGTAAAGAATGAG	SMYD3	SMYD3-1	ATGCGCAGATGGAGTCTGGA
FH	FH-2	ATGACCAGTAAAGAATGAGG	SMYD3	SMYD3-2	CATGCGCAGATGGAGTCTGG
FH	FH-3	CAGCCTCACACCCGACAGGTG	SMYD3	SMYD3-3	GAGTGTGTGGGACCTGAAGG
FH	FH-4	ACAGCCTCACACCCGACAGGT	SMYD3	SMYD3-4	CCATGGGCACGAGCCGACCG
FH	FH-5	CCAGTAAAGAATGAGGGGGC	SMYD3	SMYD3-5	GCAGATGGAGTCTGGAGGGA
FH	FH-6	GAATGACCAGTAAAGAATGA	SMYD3	SMYD3-6	TGGTCGTAAGGCTCCGCGTG
FLCN	FLCN-1	GCGGTGCAGGACGCGCTCGGAGTT	SOCS1	SOCS1-1	AGAAACCAAAAGTGGAGCTG
FLCN	FLCN-2	GTAGGACTCGGACTGTGTTCCGTT	SOCS1	SOCS1-2	GTCCTCGCCGACGCCACCG
FLCN	FLCN-3	GGGGCACCGGAATAGGGGCGGGT	SOCS1	SOCS1-3	TTTGGTTTCTCTTTCCGCGG
FLCN	FLCN-4	GAGGGGGGCACCCGAATAGGTT	SOCS1	SOCS1-4	AGGGCCGAAGCCGCTCCTCGC
FLCN	FLCN-5	GAACITCCCAGAGGGGGCAGGTT	SOCS1	SOCS1-5	GCGGAAAGAGAAACCAAAAG
FLCN	FLCN-6	GTTTTCCCCAGCATCCCCAGCGTT	SOCS1	SOCS1-6	TTCCGCGGTGGCGTCCGCGG
NAXD	NAXD-1	CCAACCTCGCTCAATCACACC	SOX17	SOX17-1	GCGTCGTTAGGCCACGCCCC
NAXD	NAXD-2	CCGGGTGTGATTGACGAGT	SOX17	SOX17-2	GGGACGTGGGACTCGGACCA
NAXD	NAXD-3	CTTGTCAATCACTAGAACC	SOX17	SOX17-3	TTAGGCCACGCCACGCGCG
NAXD	NAXD-4	GACAAGCGCGACGCCAACCC	SOX17	SOX17-4	GTGGGGTTGGACTGGGACGT
NAXD	NAXD-5	GCGCGACGCCAACCCGCGCC	SOX17	SOX17-5	TGGGACTCGGACCCAGCGCT
NAXD	NAXD-6	TCCGCGCGGCTGTCGGCAGT	SOX17	SOX17-6	TTGGACTGGGACGTGGGACT
FLYWCH1	FLYWCH1-1	GCGTAAAGGGGCTGGGGTAGGGTT	SOX2	SOX2-1	CAAAACCCGGCAGCGAGGCT
FLYWCH1	FLYWCH1-2	GACGCTCTTGGCGTAAAGGTT	SOX2	SOX2-2	GCCCCCTTTCATGCAAAACC
FLYWCH1	FLYWCH1-3	GGAGCTGAACAGCGCTCTGTT	SOX2	SOX2-3	TCATGCAAAACCCGCGACCG
FLYWCH1	FLYWCH1-4	GTCCAGGGGCGGAGCTAGGATGTT	SOX2	SOX2-4	CCCCGGCTCCCCGCGCGGGC
FLYWCH1	FLYWCH1-5	GCCATCCCCAGATTGGACGGGTT	SOX2	SOX2-5	CTCGAGCCAGCCTCGCTGC
FLYWCH1	FLYWCH1-6	GGCGGGCCATCCCGAGATGTT	SOX2	SOX2-6	GGCCTCCCCCGCGCGCGCGG
FOXA1	FOXA1-1	CCCCAGGTGCACCTGCAAGG	SOX4	SOX4-1	CAAGCCAATGGGAAGCCCGG
FOXA1	FOXA1-2	GCTCGCACCTACAAAGCCCG	SOX4	SOX4-2	CCAAGCCAATGGGAAGCCCG
FOXA1	FOXA1-3	GTGCGAGCGTCTTTGTGCGG	SOX4	SOX4-3	TTGGAGCTTCTCATTGCACG
FOXA1	FOXA1-4	CTTTGTGCGCGGCAACAATG	SOX4	SOX4-4	GCATCGGCTTCCAAGCCAAT
FOXA1	FOXA1-5	TAGGTGCGAGCGTCTTTGTG	SOX4	SOX4-5	TCATGCCAAACCCCTCCCC
FOXA1	FOXA1-6	TCCGCGGACAAATGGGGAG	SOX4	SOX4-6	TGCATCGGGTTCCAAGCCAA
FOXL2	FOXL2-1	CTTCGCCCCCTATAGCGGGG	SPATA6L	SPATA6L-1	CGTGGGCAACAGCGACCGTGA
FOXL2	FOXL2-2	GAGATGAACTCGCCCGTGC	SPATA6L	SPATA6L-2	GTGGGCAACAGCGACCGTGA
FOXL2	FOXL2-3	GCGCCTTCGCCCCATAGCG	SPATA6L	SPATA6L-3	TCCGCTTAGCACGCCAGACA
FOXL2	FOXL2-4	AGGCCGTCAGGCTGTGCG	SPATA6L	SPATA6L-4	CCAGACAGGCGCAGTCTCTC
FOXL2	FOXL2-5	GGCGTTTACAAAAAGTGA	SPATA6L	SPATA6L-5	GCCCTGTGGCGGTGCTAGA
FOXL2	FOXL2-6	TGTAACCGCCCCGACAGCC	SPATA6L	SPATA6L-6	GGGCCAGTCTCTCCGGCTGG
FUBP1	FUBP1-1	AAAATCTCGCGATGTTCCG	SPEN	SPEN-1	ACGGGCGGACGCGACTACGA
FUBP1	FUBP1-2	ATGTTCCGAGGCAACGCGC	SPEN	SPEN-2	GGAGCTGGCGCTGTGGCAGC
FUBP1	FUBP1-3	CCCACACCAGCGGTTGCCT	SPEN	SPEN-3	GGCAGCGACTACGACGGAGC
FUBP1	FUBP1-4	CAACGCGCTGGTGTGGGTTA	SPEN	SPEN-4	GAGCGGGAGGAGGGGCGGAGC
FUBP1	FUBP1-5	CCGAGGCAACGCGCTGGTGT	SPEN	SPEN-5	GCGCGCAGTGGGAAGCGTCT
FUBP1	FUBP1-6	TCCGAGGCAACGCGCTGGTG	SPEN	SPEN-6	GGCAGCCGACGCTTCCAC
FXR1	FXR1-1	GCGGCACGTTGAGACCCAG	SPOP	SPOP-1	AGGAGAAGGGGATAATGGGG
FXR1	FXR1-2	GGATCCCACCTGGAGAGTCG	SPOP	SPOP-2	CCGCCAGACCCACCCCGCG
FXR1	FXR1-3	TCCCACCTGAGAGTCGGGG	SPOP	SPOP-3	GTAATGGGGAGGAGGGCCGCG
FXR1	FXR1-4	AGGGATCCCACCTGGAGAGT	SPOP	SPOP-4	AATGGGGAGGAGGCCCGCGG
FXR1	FXR1-5	GGCGGCACGTTGAGACCCCA	SPOP	SPOP-5	AGGGAACCCAGGGAGGGGA
FXR1	FXR1-6	GTTGAGACCCCGGGGTGAA	SPOP	SPOP-6	TGGGGTCTGGCGGACTCGCGC
FYTTD1	FYTTD1-1	ACACTCGCGGGCGACCAGAG	SRC	SRC-1	GAGCGCGGAGCTGGGAGGA
FYTTD1	FYTTD1-2	ATGCCTCGTCCGACTCTGCG	SRC	SRC-2	GAGGAGCGCGGAGCTGGG
FYTTD1	FYTTD1-3	GCGCCGTGACTCGCTCTAG	SRC	SRC-3	GGGCCGCGGAGCGCCGGG
FYTTD1	FYTTD1-4	GCTAGGAGCGAGTACGCGG	SRC	SRC-4	AGCGCGGAGCTGGGAGGAG
FYTTD1	FYTTD1-5	GGGCCGCTAGGAGCGAGTCA	SRC	SRC-5	AGGGAGGGAGCGCGGAGCT
FYTTD1	FYTTD1-6	TGCCTCGTCCGATCTGCGA	SRC	SRC-6	GAGGGAGGGAGCGCGGAGC
GATA2	GATA2-1	GCCAGGCGGCTGGACCTGGT	SRSF2	SRSF2-1	GCGGCAAGGTCGTTACGAAG
GATA2	GATA2-2	GGGTACCCTCCTGCCCCCTG	SRSF2	SRSF2-2	GGCAGGTCGTTACGAAGCG
GATA2	GATA2-3	TAGGCCGGGTGCAGAGCCCC	SRSF2	SRSF2-3	GGCGCGGTGGGCCAATCAGA
GATA2	GATA2-4	CAGGGGGCAGGAGGATACCC	SRSF2	SRSF2-4	CGGAAATGAAACCTTCTGAT
GATA2	GATA2-5	CCAGCCGCTGGCCGGCCAA	SRSF2	SRSF2-5	GGTCGTTACGAAGCGGGGCG
GATA2	GATA2-6	GCGGCCCTTGGCCGGCCAG	SRSF2	SRSF2-6	GTTACGAAGCGGGGCGGCT
GATA6	GATA6-1	AACAACAGCGCTCGCGGAA	SST	SST-1	AAAATCAATCACAGAAGACA
GATA6	GATA6-2	AAGGGTGCCAGGCTGTGGGT	SST	SST-2	AAATCAATCACAGAAGACAG
GATA6	GATA6-3	GTGAGTCCAATCAGGAGCCC	SST	SST-3	TCAATCACAGAAGACAGGGG
GATA6	GATA6-4	AAACAACAGCGCTCGCGGA	SST	SST-4	CTAATGGTGCCTAAAAGGGC
GATA6	GATA6-5	AGGGCTCGGTGAGTCCAATC	SST	SST-5	GAGGCTAATGGTGCCTAAAA
GATA6	GATA6-6	GCCGAAGGGTGCAGGCTGT	SST	SST-6	GGAGGTGACAAGATCTAAAG
GDF3	GDF3-1	AAAGGCCATTGGATGTGAAG	ST6GAL1	ST6GAL1-1	CCCACCTCACCTCCTCGCCAC
GDF3	GDF3-2	AAGGCCATTGGATGTGAAGA	ST6GAL1	ST6GAL1-2	CGCCGCCCAACCCGCGCTGG
GDF3	GDF3-3	AATCCCTCTTACATCCAA	ST6GAL1	ST6GAL1-3	GCGACCTCCAGCCGCTTTG
GDF3	GDF3-4	ATAAATTCTACAACATGTT	ST6GAL1	ST6GAL1-4	GCCTGGAGGTCGCTAGCGAG
GDF3	GDF3-5	TTCACATCCAATGGCCTTTG	ST6GAL1	ST6GAL1-5	GTGTGGCCGTTGCGGAGAGG
GDF3	GDF3-6	TTCTCTTGCTCTACTCTTCC	ST6GAL1	ST6GAL1-6	TTGGGGCGCGGTGTGGCCGG
GLIS3	GLIS3-1	CACTAGGCTGGCCAATTCGA	STK40	STK40-1	GCCCCAATCCGAAAGCCGTTG
GLIS3	GLIS3-2	GTGTGTGTGAATGCGTCAAG	STK40	STK40-2	GCGCCCAATCCGAAAGCCG
GLIS3	GLIS3-3	TGTGTGTGAATGCGTCAAGA	STK40	STK40-3	GGCGGAAAGCTTACGGCAAG
GLIS3	GLIS3-4	AAGAGTGGGGGCGGGCTCGC	STK40	STK40-4	GGCGCCATCTTGACGATGGG
GLIS3	GLIS3-5	CACAAGCTCGGCTTCCGAAT	STK40	STK40-5	TCTTCCGCCATCTGCTCAAGA
GLIS3	GLIS3-6	GGGCGGCTCGGCGCTACT	STK40	STK40-6	TGGGGCGGCTTGGAGAT
GMNC	GMNC-1	AATCACAGAGCGGCGCTCGC	TARS	TARS-1	CGAGCAGCCAATGGATAACG
GMNC	GMNC-2	CCGCTCTGTGATTTGGTGAG	TARS	TARS-2	GAGCAGCCAATGGATAACGG
GMNC	GMNC-3	CCTCTACCAATCACAGAG	TARS	TARS-3	TCCACTGGCTTAGAGGAGGG

GMNC	GMNC-4	CGGGAGCTCTGGGCGTACC	TARS	TARS-4	AGCCATGGATAACGGGGGA
GMNC	GMNC-5	TGACTCCTGGCTCACGTAC	TARS	TARS-5	CCCTCCTCCTCTAAGCCAG
GMNC	GMNC-6	TTCTAATCTGCGGGAGCTCC	TARS	TARS-6	CGCGACCTGATTTCCTAGAA
GNAS	GNAS-1	AAAGCGCCGCGCGGGCGGG	TAZ	TAZ-1	CAGGAAGCGGGAGCCCCACG
GNAS	GNAS-2	GCCAAAAGCGCCGCGGGGG	TAZ	TAZ-2	GGCCACTTCCCGCCGCCCCG
GNAS	GNAS-3	GCGCGCGGAGGGGGTGGGA	TAZ	TAZ-3	GGGAAGTGGCCGTACCCCCG
GNAS	GNAS-4	AAAAGCGCCGCGGGCGGG	TAZ	TAZ-4	AGACAAAAGCGGAGCGCAGG
GNAS	GNAS-5	CAAAAAGCGCCGCGGGGG	TAZ	TAZ-5	CAGCGAGGCCAGCCCCGGG
GNAS	GNAS-6	CCAAAAGCGCCGCGGGGG	TAZ	TAZ-6	GGAAGTGGCCGTACCCCCGT
GNB4	GNB4-1	GCCGGGACGCGCAGACCT	TBCCD1	TBCCD1-1	AATCTGCCGTCTAGCAACG
GNB4	GNB4-2	GGCGGAGGCGGAGGCACG	TBCCD1	TBCCD1-2	CCCCACCACCGAGACCTGG
GNB4	GNB4-3	GGCTGGAGGCGGAGGCGCG	TBCCD1	TBCCD1-3	CGGGTCCGCCAGGTCTCGG
GNB4	GNB4-4	CGTCCCCGGCAGTCCCCCG	TBCCD1	TBCCD1-4	CGTCTGAGAAAATCTAGGCT
GNB4	GNB4-5	GTCCCCGGCAGTCCCCGCC	TBCCD1	TBCCD1-5	GTCTGAGAAAATCTAGGCTG
GNB4	GNB4-6	TCCGAGGTCTGCGCGTCC	TBCCD1	TBCCD1-6	GTTGCTAGAGCGCGCAGATTG
GP5	GP5-1	GATCATGAGGCGCTGCAAGGA	TCF4	TCF4-1	AAGTTCAGCAAGAAATGGG
GP5	GP5-2	TCTGGCTCTGAGGACGCGG	TCF4	TCF4-2	ACTTGCATTTCCGTGCGCT
GP5	GP5-3	TGTGGCTGTCGGAGATCATG	TCF4	TCF4-3	TCAGCAAGAAATGGGTGG
GP5	GP5-4	CTGCAGAGCCAGAGCTTACG	TCF4	TCF4-4	AGTTCAGCAAGAAATGGGT
GP5	GP5-5	CTGCTCTTCCGAAATGGGCC	TCF4	TCF4-5	GGGAAACACGCGGAGGCCGA
GP5	GP5-6	GCACATCTGCTCTTGGGAA	TCF4	TCF4-6	TTACGCAAGAAATGGGTGG
ADGRA2	ADGRA2-1	CCCTAGCGCCGACCGACACG	TCTEX1D2	TCTEX1D2-1	CAGCAGCCGGTGCAGGCGG
ADGRA2	ADGRA2-2	CTAGACCCTCTGCCGAGTGG	TCTEX1D2	TCTEX1D2-2	CCCTGCCCGCGCTGCGCAC
ADGRA2	ADGRA2-3	GGCCTAGACCCTCTGCCGAG	TCTEX1D2	TCTEX1D2-3	CCGCCAGCAGCCGGTGC
ADGRA2	ADGRA2-4	CCTAGACCCTCTGCCGAGTGG	TCTEX1D2	TCTEX1D2-4	GCGGCTGATAGTGCCTGAGG
ADGRA2	ADGRA2-5	CGCAGGCTCCTGCAACCAGC	TCTEX1D2	TCTEX1D2-5	GGCGCGCTGATTACTGCCTG
ADGRA2	ADGRA2-6	GTTGGTGCAGGCGGGCGCG	TCTEX1D2	TCTEX1D2-6	TATTTCTCCGACTCGCGG
GRIN2A	GRIN2A-1	CCCAGCAGCGAAGGGCCCGG	TEK	TEK-1	AAAGGCATTTGGTATCAGCA
GRIN2A	GRIN2A-2	GAAGTGGGAGCCGAACGCC	TEK	TEK-2	GATGAATTGCGAGATGGATA
GRIN2A	GRIN2A-3	GGGGAGCCGAACGGCCGCG	TEK	TEK-3	TTTGGTATCAGCAGGCTGG
GRIN2A	GRIN2A-4	CCGCGGTCCCGCCGAGAG	TEK	TEK-4	GCATTTGGTATCAGCAGGCG
GRIN2A	GRIN2A-5	GGAGCTGGCCAGCAGCGAA	TEK	TEK-5	TAAAGGCATTTGGTATCAGC
GRIN2A	GRIN2A-6	GTCCCCGGCCGAGAGAGGCG	TEK	TEK-6	TGATGAATTGCGAGATGGAT
GSX2	GSX2-1	ACTCGGCGAGCCTATCCCG	TERT	TERT-1	CCAGCTCCGCCTCCTCCGG
GSX2	GSX2-2	GAGTCACAACAGAAGCCCGG	TERT	TERT-2	GGCGGAGCTGGAAGGTGAAG
GSX2	GSX2-3	TCACAACAGAAGCCGCGAGG	TERT	TERT-3	GGCTGGGCGGGGACCCGGG
GSX2	GSX2-4	ACAACAGAAGCCGCGAGGAG	TERT	TERT-4	GAGGCGGAGCTGGAAGGTGA
GSX2	GSX2-5	ACCGCTCGGCTCAGGCTCCT	TERT	TERT-5	GCTGGGCGGGGACCCGGGA
GSX2	GSX2-6	GACTCGGCGAGCCTATCCCG	TERT	TERT-6	GGGACGGGCGGGGTCCCGG
H3F3B	H3F3B-1	CCACCAATAGAAAAAGTCTG	TFRC	TFRC-1	GGTGCTGTGACAGATCGCCC
H3F3B	H3F3B-2	GCTGACATGCCCGACACAA	TFRC	TFRC-2	GTGCTGTGACAGATCGCCCG
H3F3B	H3F3B-3	GTCGGGGGATGTCAGCGCGT	TFRC	TFRC-3	TGCTGTGACAGATCGCCCG
H3F3B	H3F3B-4	AAGCAGCGCTTTGTGTCCGG	TFRC	TFRC-4	AGGTGCTGTGACAGATCGCC
H3F3B	H3F3B-5	CATGGAACAGTGCCGAAGCA	TFRC	TFRC-5	CTCGGAGCCTACGTGCTCC
H3F3B	H3F3B-6	GAAGCAGCGCTTTGTGTCCG	TFRC	TFRC-6	CTGAGGCACGTACGCTCGCG
H3F3C	H3F3C-1	ATGGGCTTTGAAAGATGGAA	THPO	THPO-1	AAGAGAAGCGCTCACTTCCG
H3F3C	H3F3C-2	CAAAAACGAAACCCGAA	THPO	THPO-2	AGAGAAGCGCTCACTTCCCG
H3F3C	H3F3C-3	CCATTCTTCAAAGCAATTT	THPO	THPO-3	GAGCCACGATGAGTGGTGA
H3F3C	H3F3C-4	GAGGAGGGCGCAGAGCGGTT	THPO	THPO-4	AAGTGACGCTTCTCTTCCC
H3F3C	H3F3C-5	GATGCAGATAAAAAGAGAGGA	THPO	THPO-5	CAGACACTGGTGAAGGCCCC
H3F3C	H3F3C-6	GGATGCAGATAAAAAGAGAGG	THPO	THPO-6	GTGGGTGGAGGATGGACCC
HES1	HES1-1	AGTAACTTTCAGCCAATGGG	TM4SF19	TM4SF19-1	AATCACATGAAAATGAGCAG
HES1	HES1-2	CATTGGCTGAAAGTTACTGT	TM4SF19	TM4SF19-2	CATCAGGACAGGGCTCTCCG
HES1	HES1-3	CCATTGGCTGAAAGTTACTGT	TM4SF19	TM4SF19-3	CATGAAAATGAGCAGAGGCT
HES1	HES1-4	CAATGGGAGGAGGAGACACG	TM4SF19	TM4SF19-4	GAGGGTGGGTATCAGGACA
HES1	HES1-5	GAGACACGCGGACCCGCTCG	TM4SF19	TM4SF19-5	GCGCCTTCAATGACGGCTG
HES1	HES1-6	GGGGGGGCGGCTCCACGAG	TM4SF19	TM4SF19-6	TTGAAGCGCTTCCGCTCCC
HES6	HES6-1	ATTGGCTGACGCGCCCTCG	TMCO2	TMCO2-1	AATCTTACTCAAAAACCAACC
HES6	HES6-2	GCGCGCTTTGTCCGGCCAG	TMCO2	TMCO2-2	AATGAACTGAAAACCCAGGC
HES6	HES6-3	GTCCGGCCAGCGGCTCTGG	TMCO2	TMCO2-3	TATGAATGAACTGAAAACCC
HES6	HES6-4	AGGCGCGCTGACGCCAATCG	TMCO2	TMCO2-4	ACTCAAAACCAACCAGGCAC
HES6	HES6-5	GCCCGGGGCGGCGGACCCG	TMCO2	TMCO2-5	AGATTCAATGGTTGGGTGAG
HES6	HES6-6	GCTGCAGCGCGCTCGCGGT	TMCO2	TMCO2-6	TGAAAACCCAGGCCGGTCC
HEYL	HEYL-1	CCGCCCGGCCCCGCTCGG	TMEM207	TMEM207-1	CTAGTAAGTTCTGAGAAGA
HEYL	HEYL-2	GCCGCCACCGCCCTTCCCA	TMEM207	TMEM207-2	TATAAGTTATGCTTCTTACC
HEYL	HEYL-3	GCGGCGCAGGAAAGGGCCCT	TMEM207	TMEM207-3	TTATTAATGCATGTCTGGT
HEYL	HEYL-4	GAAAGGGCCCTGGGAAAGGG	TMEM207	TMEM207-4	ACCAGACATGCATTAATAA
HEYL	HEYL-5	GGGCGGTGGCGGCGCCCG	TMEM207	TMEM207-5	ACTCGTAAAGTGACCTAG
HEYL	HEYL-6	TGCGGCGCAGGAAAGGGCC	TMEM207	TMEM207-6	GCCATTATTAATGCATGTCC
HOXB13	HOXB13-1	AGAAGCTAATAAAATCTCTAA	TMEM41A	TMEM41A-1	AGAGGGCGGAGTCAGAATCG
HOXB13	HOXB13-2	AGAGAGAGAGAGAATAAGC	TMEM41A	TMEM41A-2	GAGGGCGGAGTCAGAATCG
HOXB13	HOXB13-3	GAGAGAGAGAGAGAATAAGC	TMEM41A	TMEM41A-3	GTCTCCACCGAAGGACAGAG
HOXB13	HOXB13-4	GCCAAATCAGCGCGCTGCC	TMEM41A	TMEM41A-4	CCACCGAAGGACAGGAGGG
HOXB13	HOXB13-5	GCTGATTGGCTGCGGCTGG	TMEM41A	TMEM41A-5	CCGCCCTCTCTGCTTCCG
HOXB13	HOXB13-6	TTTATTAGCTTCTCTCCCC	TMEM41A	TMEM41A-6	TTTCCCGGAGTCTCCACCGA
HPCAL4	HPCAL4-1	CTGGAGCGGAGTGGCAGCGG	TMEM44	TMEM44-1	CCGGCCAGGATGTTGGAGGT
HPCAL4	HPCAL4-2	GGCTATTGGCTCCTCTGGAG	TMEM44	TMEM44-2	CTGCGCGGCGCACAAGACTG
HPCAL4	HPCAL4-3	TTGGCTCCTCTGGAGCGGAG	TMEM44	TMEM44-3	GGAGGTGGGTGACCCGGAAG
HPCAL4	HPCAL4-4	CGCCTGCCACTCCGCTCCAG	TMEM44	TMEM44-4	CGCTCCGGCCAGGATGTTGG
HPCAL4	HPCAL4-5	GGTTTCAGGTGGGGACCGGG	TMEM44	TMEM44-5	GCCCCCGCCGACCTTCTCG
HPCAL4	HPCAL4-6	TGGCAGCGGGGTTTACGTT	TMEM44	TMEM44-6	GTGGGTGACCCGGAAGAGGT

HRASLS	HRASLS-1	AGAAGGTGCAGTTCGCCGGC	TMPRSS11E	MPRSS11E-	AAGTCTGGCTGGTGTAGTG
HRASLS	HRASLS-2	AGGTGCAGTTCGCCGGGG	TMPRSS11E	MPRSS11E-	CCAGCCAAGACTTGTGAGAC
HRASLS	HRASLS-3	GAGAAGGTGCAGTTCGCCGG	TMPRSS11E	MPRSS11E-	TATATGTGACTAGCAGGACA
HRASLS	HRASLS-4	CGCTCCGGCTAGACCTCGCT	TMPRSS11E	MPRSS11E-	AGAACCAGTCTGACAAGTCT
HRASLS	HRASLS-5	GCAGTTCGCCGGGGCGGG	TMPRSS11E	MPRSS11E-	CCAGTCTGACAAAGCTTTGGC
HRASLS	HRASLS-6	GGTCTGCGTCCGGGGCGGAGA	TMPRSS11E	MPRSS11E-	GGGGACTATATGTGACTAGC
HRG	HRG-1	ACAAGCTGTAATGATTAGT	TNK2	TNK2-1	GAGACACAGCCCCAAACAC
HRG	HRG-2	AGGGTGTTCACCTTGACCCT	TNK2	TNK2-2	GCCACTCTGAGTCACCCCTG
HRG	HRG-3	TTGATGGTTATTTGAACCCA	TNK2	TNK2-3	TCCCAGGGGTGACTCAGAG
HRG	HRG-4	AAATGATTAGTGGGTCTGCG	TNK2	TNK2-4	AGGCCACTCTGAGTCACCCC
HRG	HRG-5	AACAAGCTGTAATGATTAG	TNK2	TNK2-5	GGCCACTCTGAGTCACCCCT
HRG	HRG-6	AATCATTACAGCTTGTGA	TNK2	TNK2-6	TGTGCCTGCCAGTGTCCCCA
ID1	ID1-1	GGAGGCTGGACCTAGGAGCG	TOP1	TOP1-1	CCGTCTGGCGAACAGCGAGG
ID1	ID1-2	GTTCAAAGCAGCCAAATGGG	TOP1	TOP1-2	GCGGAGCGCGCAGGTCGGG
ID1	ID1-3	TCTAGTCCCTGCTCGCAGTG	TOP1	TOP1-3	GGTCCGTCTGGCGAACAGCG
ID1	ID1-4	ACGAGCAGGAGGCTGGACCT	TOP1	TOP1-4	AAATCACAGCGGAGCGCGCA
ID1	ID1-5	GCAGCCAATGGCGGCATGG	TOP1	TOP1-5	GGGGCTTGCATGCAAAGAC
ID1	ID1-6	GCAGGCACTAGACGAGCAGG	TOP1	TOP1-6	TCCGTCTGGCGAACAGCGAG
IGF2BP2	IGF2BP2-1	CAGCCTGGCTCCCCCACC	TP63	TP63-1	ACTACTTAATGAGATGGGAG
IGF2BP2	IGF2BP2-2	CCTCCGCTCTGCCCCCGGG	TP63	TP63-2	GAGGCCCTCACTCCATTGGAG
IGF2BP2	IGF2BP2-3	GGCCGGCCCGGCGCCCGGG	TP63	TP63-3	TCCTCCACTCGAGTCACAGTG
IGF2BP2	IGF2BP2-4	CTGGCTCCCCCACC	TP63	TP63-4	CCAATCCATCAACTTCCACC
IGF2BP2	IGF2BP2-5	GGCCCGCCCGGGGGCAGAGG	TP63	TP63-5	GCCTCACTCCATTGGAGTGG
IGF2BP2	IGF2BP2-6	TCCCCCACC	TP63	TP63-6	TTCTAACTTAATGAGAT
IL1RAP	IL1RAP-1	CGGGTGGAGCCTGAGCCGTG	TPRG1	TPRG1-1	AACTGACTGAGAAAAGACAT
IL1RAP	IL1RAP-2	CGGTGGATCGCGAGCCAAGG	TPRG1	TPRG1-2	TCAGTCAGTTATTGCTTCTG
IL1RAP	IL1RAP-3	TTCCAGGAGCTGCGGCCGCG	TPRG1	TPRG1-3	TGTGGAAACTGTTATTGTCA
IL1RAP	IL1RAP-4	CGCCGGTGGATCGCGAGCCA	TPRG1	TPRG1-4	AAAGAGAGGAGGTATCAAAG
IL1RAP	IL1RAP-5	TCGCGAGCCAAGGCGCGGG	TPRG1	TPRG1-5	AGTAACAGAACAGTTCAGGT
IL1RAP	IL1RAP-6	TGGATCGCGAGCCAAGCGGG	TPRG1	TPRG1-6	CAGTAACAGAACAGTTCAGG
IL7R	IL7R-1	AGAAGCAAGTTCAGAAAC	TPX2	TPX2-1	CAATACCGGAGTTCAGAAAG
IL7R	IL7R-2	GCTGCTGTAAGCAGAGGTCA	TPX2	TPX2-2	CAGCAATACCGGAAGTCAGA
IL7R	IL7R-3	TGTAAGCACAGTAAGTGTGG	TPX2	TPX2-3	TCTGACTTCCGGTATTGCTG
IL7R	IL7R-4	ACTTATCTAACACAGACAA	TPX2	TPX2-4	AATGCACCAATCAGAGCGCC
IL7R	IL7R-5	ATGTAAGCACAGTAAGTGTG	TPX2	TPX2-5	AGCAATCCAGGCTCCCGAT
IL7R	IL7R-6	GGCTGCGAGGGAATATCCAGG	TPX2	TPX2-6	GAATGCACCAATCAGAGCGC
ING1	ING1-1	CCTCACCGTCCCAGGCCCTG	TRA2B	TRA2B-1	AGAAAGCGCGCTTTCTGGG
ING1	ING1-2	CTCACCGTCCCAGGCCCTGG	TRA2B	TRA2B-2	GCGCGCTTTCTGGGAGGGG
ING1	ING1-3	GCAGCCCCCAGGCCCTGGGA	TRA2B	TRA2B-3	TGGAGAGGAAAGGCAGAGCG
ING1	ING1-4	CCAGGGCCTGGAGCGGTGAG	TRA2B	TRA2B-4	AGAGGAAAGGCAGAGCGGAG
ING1	ING1-5	CCCCAGGCCCTGGAGCGGTG	TRA2B	TRA2B-5	GAAAGCGCGCTTTCTGGGA
ING1	ING1-6	GACGGTGAGGGCGTGAATG	TRA2B	TRA2B-6	GGGACGCGCTGCAGCTGGAG
INSL4	INSL4-1	GGAGAAAGTTCCTTGTAGGT	TRIT1	TRIT1-1	GCGAGGTTGCTTAGGGAGGA
INSL4	INSL4-2	GGAGACTAAATAAGAACTGA	TRIT1	TRIT1-2	TGACTGCAGTCACTCGCCT
INSL4	INSL4-3	GGGAGACTAAATAAGAACTG	TRIT1	TRIT1-3	TGTAGCGAGGTTGCTTAGGG
INSL4	INSL4-4	AAAGTTCCTTGTAGGTGGGT	TRIT1	TRIT1-4	AAAAAGACGGCGGGTAGTTG
INSL4	INSL4-5	AGGGATATGAGAGTGTGGT	TRIT1	TRIT1-5	CTTTGTAGCGAGGTTGCTTA
INSL4	INSL4-6	GGGAGAAAGTTCCTTGTAGG	TRIT1	TRIT1-6	GTTGCTTAGGGAGGGAGGAG
INSL6	INSL6-1	CTGCGGAATTCCGAGCGCT	TSHR	TSHR-1	CAGCCTCCTCCACAGTGGTG
INSL6	INSL6-2	GCGGAATCCGAGCGCGTGG	TSHR	TSHR-2	GGGCTGTGACCTCACCCTG
INSL6	INSL6-3	GGCGTCCGAGAACTCAA	TSHR	TSHR-3	TTCTCCAGCTCCTCCACAG
INSL6	INSL6-4	ACTGCGGAATCCGAGCGCG	TSHR	TSHR-4	CTGTGACCTCACCCTGTGG
INSL6	INSL6-5	AGGCTTCCCGCCAGCTCAG	TSHR	TSHR-5	CTTAAGTGTCTCCGCTTCCCT
INSL6	INSL6-6	GTCGCCAGAACTCAAGGGA	TSHR	TSHR-6	GTTTGGTCAAGGTTGCCTA
INSM1	INSM1-1	AGCTCCTCAGCCTGGCAGGG	TTC14	TTC14-1	CGTCCGTTTCCGAGATCG
INSM1	INSM1-2	CGCAGCTCCTCAGCCTGGCA	TTC14	TTC14-2	TTACACCCGGAAGTGTCTG
INSM1	INSM1-3	GCTCCTCAGCCTGGCAGGGT	TTC14	TTC14-3	TTCTGGGCTGCCCCACGG
INSM1	INSM1-4	AAAAGGGGGCGGGACTCGG	TTC14	TTC14-4	CGCGAAACCGGAGCGACTA
INSM1	INSM1-5	GCGATGGGGCGGCAAAAGG	TTC14	TTC14-5	CGGCCTTCCGTAGTCTCGCT
INSM1	INSM1-6	GCGTCCGAGCTCCTCAGCC	TTC14	TTC14-6	GGGTCGCCCCCAGGGCGCG
IQCG	IQCG-1	AATGTAAGTTCGGGAACAA	TXNRD1	TXNRD1-1	GCAATTAGCATAGGTTGCCA
IQCG	IQCG-2	GGCTGCAAAATGTAAGTACTT	TXNRD1	TXNRD1-2	TAGGTTGCCAGGGCTGCACG
IQCG	IQCG-3	TTGACGCTACCAAGATGAA	TXNRD1	TXNRD1-3	TTAGGAGCTCTCAGCTTACG
IQCG	IQCG-4	AAATGTAAGTTCGGGAACAA	TXNRD1	TXNRD1-4	ATCCACTCCTCGTGCAGCCC
IQCG	IQCG-5	CTACCAAGATGAAAGGACTT	TXNRD1	TXNRD1-5	GCTTACGAGGCAATTAGCAT
IQCG	IQCG-6	TACTACTTGGGAACAAGGGA	TXNRD1	TXNRD1-6	TGCCAGGGCTGCACGAGGAG
IRF4	IRF4-1	ACTTTGCAAGCCGAGCGCC	UBXN7	UBXN7-1	CCCGCCCTCCCGTCCCAG
IRF4	IRF4-2	CCTCCTCCCGACTCCAACCCC	UBXN7	UBXN7-2	GCAGACCGTGGGACGGGA
IRF4	IRF4-3	CGGGGGTTGGACTGGGGAGA	UBXN7	UBXN7-3	TGCGCTGCGCAGACCGCTG
IRF4	IRF4-4	GGGGCCGGGGTTGGACTG	UBXN7	UBXN7-4	CCGTCCCAGCGGTCTGCGC
IRF4	IRF4-5	GTCCAACCCCGGCCACCTAC	UBXN7	UBXN7-5	GAGCAGCAACCCGAGAGCT
IRF4	IRF4-6	TGCAAGCCGAGAGCCGGGGC	UBXN7	UBXN7-6	TGGGAGCGCGGGGCCGGT
IRS2	IRS2-1	CGAGCGCGCCGTCCGTGGG	UGT2B15	UGT2B15-1	AACACACTAAAATAAATATG
IRS2	IRS2-2	GCGCGCTCGGCAATCGCGG	UGT2B15	UGT2B15-2	ATAACTACTAACAGTCTGAAT
IRS2	IRS2-3	GGCGCAATGCGAGGCGAGCG	UGT2B15	UGT2B15-3	GTCTGAATAGTGTGCATGCCA
IRS2	IRS2-4	GCCAATGCGAGGCGAGCGGG	UGT2B15	UGT2B15-4	ACAGGTTACTTACATATTCT
IRS2	IRS2-5	GCGCCGCGCCCCCAGCGGA	UGT2B15	UGT2B15-5	ATAAAAATAATTACATAAGAC
IRS2	IRS2-6	GGGGCGCGCCGCAATCGG	UGT2B15	UGT2B15-6	ATTTCATACCTTATATCTG
IRX2	IRX2-1	ATATGCAGATGAGCGCGTGA	UGT2B17	UGT2B17-1	ACAGGTTACTTACGTATTCT
IRX2	IRX2-2	GCGCTCATCTGCATATTCCG	UGT2B17	UGT2B17-2	ATACTGTTAAGAACAGTGGC
IRX2	IRX2-3	ACGCGCTCATCTGCATATTC	UGT2B17	UGT2B17-3	TAAGAACAGTGGCAGGTGAG

IRX2	IRX2-4	AGGCTGCAGCGGGCGGAGCA	UGT2B17	UGT2B17-4	TATAATACTGTTAAGAACAG
IRX2	IRX2-5	GGCTGCGCCACAAAAGCCTGCGTT	UGT2B17	UGT2B17-5	SACCTCATATTTATTTTAGTGTGTGT
IRX2	IRX2-6	GGGCCGGAGCTGCTAGAGAGGGTT	UGT2B17	UGT2B17-6	GACAGGTTACTACGTATTTCTGTT
JAG2	JAG2-1	CAGGCTTTAAAGGAGGTGGA	UGT3A1	UGT3A1-1	GGTGAGGGCAGATTATCCA
JAG2	JAG2-2	GGCGCCCGAGGCTTTAAAGG	UGT3A1	UGT3A1-2	TCAAACCTACCTAGGATCAGT
JAG2	JAG2-3	TCCACCGCCTTTAAAGCCTG	UGT3A1	UGT3A1-3	TGAAGTCAGTAGGAGGGGGT
JAG2	JAG2-4	GCCCCAGGCTTTAAAGCGCG	UGT3A1	UGT3A1-4	AACTACCTGAAGTCAGTAGG
JAG2	JAG2-5	GGCGCCCGCGGACCCGCC	UGT3A1	UGT3A1-5	CTACCTGAAGTCAGTAGGAG
JAG2	JAG2-6	TTTAAAGCCTGGGGCGCCC	UGT3A1	UGT3A1-6	GTGATTACGCAGGCAGAGAA
JAK2	JAK2-1	AGTTGTCTCCACCCTCTCCG	UGT3A2	UGT3A2-1	GATTATCCAATGGAGCACGA
JAK2	JAK2-2	GCGGCGTTGAGAAGACGGTG	UGT3A2	UGT3A2-2	GCTGGTAGTTTGGTAGAGCG
JAK2	JAK2-3	TGAGTTCCAAGCTAGCAGGG	UGT3A2	UGT3A2-3	TATCCAATGGAGCACGAGGG
JAK2	JAK2-4	ACACCGTCTTCTCAACGCCG	UGT3A2	UGT3A2-4	ACTAACCCAGCTCAGTAGGA
JAK2	JAK2-5	AGACGGTGTGGCCCGGAGA	UGT3A2	UGT3A2-5	CCAACTACCAGCAGTCAGT
JAK2	JAK2-6	GGCGAAGCCAGTGTCCGCCG	UGT3A2	UGT3A2-6	CTACCAGCAGTCAGTAGGAG
KCNMB2	KCNMB2-1	AGGGCGATGTCGGTCTGGGA	URI1	URI1-1	CATCAAGCGCACTCCCCTGG
KCNMB2	KCNMB2-2	GATCCAGTGCAGGCGCATGT	URI1	URI1-2	GCATCAAGCGCACTCCCCTG
KCNMB2	KCNMB2-3	TGGAATCTGATCCAGTGCA	URI1	URI1-3	TGCGCTTGATGCGAACCCGCG
KCNMB2	KCNMB2-4	AGACCAGCATCGCCCTGCAC	URI1	URI1-4	AACCGCGTGGCTGGGGCTGG
KCNMB2	KCNMB2-5	GTGCGAGGCGATGTCGGTCT	URI1	URI1-5	CACCGCCAGCCCGCAGCCAGC
KCNMB2	KCNMB2-6	TTGGAATCTGATCCAGTGCA	URI1	URI1-6	CGCGCAGCCCGCAGCCAG
KCNMB3	KCNMB3-1	ACGAACCTTTGTTATCTTTCA	USP13	USP13-1	GAGCGCCAGCCGACGCGTGC
KCNMB3	KCNMB3-2	ATTCTCCTTTGAATTCACACA	USP13	USP13-2	GCCCCCTCCCAGCCAGCGTGC
KCNMB3	KCNMB3-3	GATCTCTACAGACTTGCATG	USP13	USP13-3	CGCCAGCCGCGAGCGTGC
KCNMB3	KCNMB3-4	GAATTAACAGCGCTCTGAAC	USP13	USP13-4	CAGCCGCGAGCGTGC
KCNMB3	KCNMB3-5	TCTTTCCATGTGGAATTCAA	USP13	USP13-5	CCAGCCGCGAGCGTGC
KCNMB3	KCNMB3-6	TGCATGAGGCAACATTTCTT	USP13	USP13-6	CTGGAGAGGGGCGCTGC
KDM5A	KDM5A-1	AGGATTCGGTTTCTGCGAGG	UTS2B	UTS2B-1	CAGATTTGTTATGGAGTCAA
KDM5A	KDM5A-2	CTTACCAAGGGCGAGCTGCG	UTS2B	UTS2B-2	GGGTATGAGATGTATTGATT
KDM5A	KDM5A-3	GGCGGAGGGATTTGACAGCA	UTS2B	UTS2B-3	TTTGTATGGAGTCAATGGC
KDM5A	KDM5A-4	CAAAATCCCTCCGCCCTGCG	UTS2B	UTS2B-4	CGGGTATGAGATGTATTGAT
KDM5A	KDM5A-5	GACTCCACGCAGCTCGCCCT	UTS2B	UTS2B-5	GAGAAGTGACAGATTTGTTA
KDM5A	KDM5A-6	GGCGAGCTGCGTGGAGTCGT	UTS2B	UTS2B-6	TTGAATGTGTGGGCATGCAT
KDR	KDR-1	CCCCTCACCGGGTACC	VPS8	VPS8-1	AGGGGCGTGGTGAAGAGCGG
KDR	KDR-2	GGAGGAGGGGCTCTCCCGTG	VPS8	VPS8-2	ATCTCTGGCCCTTTAAATAG
KDR	KDR-3	GGGAGATGTAATGGGCTTG	VPS8	VPS8-3	GCACCTGCTCCCGCTCTGGG
KDR	KDR-4	CCGCGGGTACC	VPS8	VPS8-4	AGAGGCGCGGACCCCGCAGG
KDR	KDR-5	GAGATCGCCGCGGTCACCC	VPS8	VPS8-5	TAAATAGGGGCGTGGTGAAG
KDR	KDR-6	GGGAGCTGGAGATCGCCGCC	VPS8	VPS8-6	TGGCCCTTTAAATAGGGGCG
KIT	KIT-1	CGGGTCTCGTCTTCTCCCGG	VWA5B2	VWA5B2-1	CGTAACTATTAAACCTCCG
KIT	KIT-2	GCCGGGAAGAAGCGAGACCC	VWA5B2	VWA5B2-2	GTGACCGCCCGCAGCCCGG
KIT	KIT-3	GGGAAGAAGCGAGACCCGGG	VWA5B2	VWA5B2-3	TGTGACCGCCCGCAGCCCGG
KIT	KIT-4	GCGAGACCCGGCGGGCGCG	VWA5B2	VWA5B2-4	GTCCCGCCCGCTCCCGCG
KIT	KIT-5	GGAAGAAGCGAGACCCGGG	VWA5B2	VWA5B2-5	TCCCGCCCGCTCCCGCG
KIT	KIT-6	GGGGCGTGGCGCGCGCAG	VWA5B2	VWA5B2-6	TTAATGATTAAACCGCGCTT
KLHL42	KLHL42-1	CGCTCGCCCGGCTCTCCGG	WDR53	WDR53-1	CAGCCAAACAGTCACATCCG
KLHL42	KLHL42-2	TCCCGGGGCGGCTCCCGG	WDR53	WDR53-2	CAGTCACATCCGGGGCGGAG
KLHL42	KLHL42-3	TCCCGCGCCCGCTCTCCCG	WDR53	WDR53-3	GGGTTGAGGGACAGAAAGCAA
KLHL42	KLHL42-4	AGGGCAGGGCGCGCCTCG	WDR53	WDR53-4	AGAGGAACCGGACAGGAGCT
KLHL42	KLHL42-5	CCGGGAGGAGCGGCGAGGTG	WDR53	WDR53-5	AGCTCGTTCGGGTTCTCT
KLHL42	KLHL42-6	CGGGCCCGCTCCCGGAGG	WDR53	WDR53-6	GCAGCCAAACAGTCACATCC
KLHL24	KLHL24-1	ACATCTCCCAGGGTTCCCGG	WNK1	WNK1-1	ATAAGTCCCAGGGTGCCTCG
KLHL24	KLHL24-2	ACCCGACACCCACCCACCGG	WNK1	WNK1-2	CCCGTAAACTATAAGTCCCA
KLHL24	KLHL24-3	ATGTAGTTCACGTTCCCGG	WNK1	WNK1-3	CGCCAGGCGTGTAGCCCGG
KLHL24	KLHL24-4	ALCGTGAACATACATCTCCA	WNK1	WNK1-4	ACCCGTAACATATAAGTCCC
KLHL24	KLHL24-5	CCCACGGCGGAGCCCAAGG	WNK1	WNK1-5	GGGACTTATAGTTACGGGT
KLHL24	KLHL24-6	GGTGGGCGTCTCCGCCCCG	WNK1	WNK1-6	TTATAGTTACGGGTTGGCG
KLHL6	KLHL6-1	AGAAGAAGAATAAGAGTTGC	WNT5B	WNT5B-1	CGGGCCGCGACACCCCTCCG
KLHL6	KLHL6-2	GGTTAGAAATTACTTAGAAT	WNT5B	WNT5B-2	GGGCCGCGACACCCCTCCGA
KLHL6	KLHL6-3	TCTTTCTGTGAGTAATCACA	WNT5B	WNT5B-3	TCGGGTCGCGAGCCGCTGGG
KLHL6	KLHL6-4	CACCTACAGTGGACTCTGAG	WNT5B	WNT5B-4	GAGCCCTGGGAGGGTGTCCG
KLHL6	KLHL6-5	TTCTTTCTGTGAGTAATCAC	WNT5B	WNT5B-5	GCCTGGGAGGAGCCCTCGGG
KLHL6	KLHL6-6	TTGCTGGCATTGTAGTAAC	WNT5B	WNT5B-6	TGGTGGGCGAGGAGCGAGCCG
KMT2B	KMT2B-1	CTCCCGTGGTGCCTGCGCG	WWTR1	WWTR1-1	ATGACCTCCTAGTCCCTAGC
KMT2B	KMT2B-2	CTGGTTGTTGTCGTCGCGCG	WWTR1	WWTR1-2	CTGGCCGCTAGGGACTAGG
KMT2B	KMT2B-3	GACAACAACCAGCGCCGCGG	WWTR1	WWTR1-3	GAGCGGGGCTGCGCGGCTA
KMT2B	KMT2B-4	ACAACAACCAGCGCCGCGG	WWTR1	WWTR1-4	AGGAAGAGGAGGGGCGGAGCG
KMT2B	KMT2B-5	CGGCCCGCGCTCCCGCGG	WWTR1	WWTR1-5	AGGGCGGAGCGGGGCTGGC
KMT2B	KMT2B-6	GCCCCGCCCGGCTCTCCCG	WWTR1	WWTR1-6	GGGCTGGCCGCTAGGGACT
KNG1	KNG1-1	CAGCTAGAACATGCAACAC	XXYL1	XXYL1-1	CCTTGGACAACCTAGGACCCAG
KNG1	KNG1-2	GCTAGAACATGCAACACTG	XXYL1	XXYL1-2	GGTTCCAAGGGTATTAGAGG
KNG1	KNG1-3	GCTAGTTGCCTGTTCCCAA	XXYL1	XXYL1-3	GTTCCAAGGGTATTAGAGGA
KNG1	KNG1-4	AAAGGTTAAATGGCTCTGCT	XXYL1	XXYL1-4	AACCCCTCCTCTAATACCCT
KNG1	KNG1-5	CATAAAGTTGTATAATCACC	XXYL1	XXYL1-5	CGTGGGCTCCTAGGTTCCAA
KNG1	KNG1-6	CCATTTAACCTTTGGGAACA	XXYL1	XXYL1-6	TTCCAAGGGTATTAGAGGAG
KRAS	KRAS-1	CTTCAGACGGCGTACGAGA	YAP1	YAP1-1	AGGAAGGAAGAGCCGAGAGG
KRAS	KRAS-2	GTCTGAAGAAGAATCGAGCG	YAP1	YAP1-2	CAGAGGAAGGAAGAGCCGAG
KRAS	KRAS-3	TCTTCAGACGGCGTACGAG	YAP1	YAP1-3	GCGGGCGGGCGCGCAGAGGA
KRAS	KRAS-4	GACGGCGTACGAGAGGGAG	YAP1	YAP1-4	CGGTGCGGGCGGGCGCGCAG
KRAS	KRAS-5	GCGCTCGATTCTTTCAGA	YAP1	YAP1-5	CTGCGCGCCCGCCGACCCG
KRAS	KRAS-6	GGGAGCGGCTGAGGGCGGTG	YAP1	YAP1-6	GCGGCCGCGGGCAGCGCA

LAMP3	LAMP3-1	CCTACCCCTACGGAGCAGGG	YEATS2	YEATS2-1	AGGGCACTTCCTGGGCAGTG
LAMP3	LAMP3-2	CGCCCCCTCCCTGCTCCGTAG	YEATS2	YEATS2-2	GTGGGCGTCGATTCTTGCAA
LAMP3	LAMP3-3	CTGCTCCGTAGGGGTAGGAG	YEATS2	YEATS2-3	TGCCCAGGAAGTGCCCTCGC
LAMP3	LAMP3-4	CCCAGAGGCCCGGGCCCGG	YEATS2	YEATS2-4	AATCGACGCCACACTGCCC
LAMP3	LAMP3-5	CCGGCCCCCTCCTACCCCTA	YEATS2	YEATS2-5	CTGCCCAGGAAGTGCCCTCG
LAMP3	LAMP3-6	CCTCCTACCCCTACGGAGCA	YEATS2	YEATS2-6	GGGCACTTCCTGGGCAGTGT
P3H2	P3H2-1	AGGAGGAGCGTGTGAGCTGT	YES1	YES1-1	CCGCCCCCGCTAGAAGTCAG
P3H2	P3H2-2	CCTGGCCAGCCGCTCTTAAA	YES1	YES1-2	CGCCCCCGCTAGAAGTCAGG
P3H2	P3H2-3	TGTGGGCGTCCCTTTAAGAG	YES1	YES1-3	CGCCCCCTGACTTCTAGCGG
P3H2	P3H2-4	GCCTGGCCAGCCGCTCTTAA	YES1	YES1-4	CCCCGCCCTGACTTCTAG
P3H2	P3H2-5	GGCGTCCCTTTAAGAGCGGC	YES1	YES1-5	CCCCCGCTAGAAGTCAGGGG
P3H2	P3H2-6	TGAGAGGGCGGAGGCCGTGCC	YES1	YES1-6	CCGCCCCCTGACTTCTAGCG
LHX1	LHX1-1	AGCGCCCGCTGACGTCACTG	YTHDC1	YTHDC1-1	AGGTACCAGTGGGCTGAGGG
LHX1	LHX1-2	CAGGCCGCACTGACGTCACTG	YTHDC1	YTHDC1-2	GAACGTCACAGTGCAGGAG
LHX1	LHX1-3	GCAGGCCGCACTGACGTCACTG	YTHDC1	YTHDC1-3	GGGAACGTCACAGTGCAGG
LHX1	LHX1-4	CGTCAGCGGGCGCTGCATTA	YTHDC1	YTHDC1-4	CCAGTGGGCTGAGGGCGGCA
LHX1	LHX1-5	GGATGCAGAAATGGTTTACAG	YTHDC1	YTHDC1-5	CGTCACAGTGCAGGAGGGG
LHX1	LHX1-6	TGGTTTACAGAGGGACCCGC	YTHDC1	YTHDC1-6	GGAACGTCACAGTGCAGGAGA
LHX3	LHX3-1	AAGGCGCTCAGAGTCCGCAG	ZDHHC19	ZDHHC19-1	CACCCGAGGCAGCTAGAGCA
LHX3	LHX3-2	ACTCTGAGCGCCTTTGCGCC	ZDHHC19	ZDHHC19-2	CGGTTCCCCAGCACATGTCCG
LHX3	LHX3-3	GAGACCAGCCCGGGCCACTG	ZDHHC19	ZDHHC19-3	TTGGAAGTGCCTGTCAACCG
LHX3	LHX3-4	CACCCGAGGTCCCGGCCCAA	ZDHHC19	ZDHHC19-4	AGCCCTGCTCTAGCTGCCTC
LHX3	LHX3-5	CGCCTTTGCCCGGGGACCTG	ZDHHC19	ZDHHC19-5	CTGTTGGAAGTGCCTGTCC
LHX3	LHX3-6	GGGCGGCCTTGGGCAACCCG	ZDHHC19	ZDHHC19-6	TTCCCCAGCACATGTCCGGG
LIPH	LIPH-1	ATAGTTTTCATTCTTCGTGGG	ZMAT3	ZMAT3-1	AGCGGTGGCAGCGGTAGCAG
LIPH	LIPH-2	GTCAAAGATCCTGAAAGGGT	ZMAT3	ZMAT3-2	GACCACGCGCGCCCGCCG
LIPH	LIPH-3	GTTCCCTAGGACTGACTGC	ZMAT3	ZMAT3-3	GGCGGCTCCCGCATCCCCGG
LIPH	LIPH-4	AGAATAGTTTCATTCTTCGT	ZMAT3	ZMAT3-4	ATCCCCGGCGGGCGGCGCT
LIPH	LIPH-5	CAGAATAGTTTCATTCTTCG	ZMAT3	ZMAT3-5	GCGGCTCCCGCATCCCCGGC
LIPH	LIPH-6	TCAAAGATCCTGAAAGGGTT	ZMAT3	ZMAT3-6	GCTCCCGCATCCCCGGCGGG
LMBRD2	LMBRD2-1	CGTCGGACTACGAAGCGGGA	ZMPSTE24	ZMPSTE24-1	GACTAGGAGAGTCTGCAAG
LMBRD2	LMBRD2-2	GAAGGCGGGTAAAGCTGCAA	ZMPSTE24	ZMPSTE24-2	GGACTAGGAGAGTCTGCAA
LMBRD2	LMBRD2-3	GAGCCCGTCGGACTACGAAG	ZMPSTE24	ZMPSTE24-3	GGGACTAGGAGAGTCTGCA
LMBRD2	LMBRD2-4	GCGGGTAAAGCTGCAAGGGA	ZMPSTE24	ZMPSTE24-4	AGCGCGCAGAGGGAGGGATG
LMBRD2	LMBRD2-5	GGAAAGTAAGGGCGAGCCCGT	ZMPSTE24	ZMPSTE24-5	GCAGCGCGCAGAGGGAGGGA
LMBRD2	LMBRD2-6	GTTGTGGGTATCTCGAAGGC	ZMPSTE24	ZMPSTE24-6	GGGGGCGGGTATCGGCGTAG
LMLN	LMLN-1	AAGTTCGCCCGCAGAAGATGA	ZNF703	ZNF703-1	AGGCCGGCTCCATCGGTGGG
LMLN	LMLN-2	ATCGCCGCCCTCATCTTCTG	ZNF703	ZNF703-2	CAGTCTCGCCGGGACCCCG
LMLN	LMLN-3	TTCGCCGCAGAAGATGAGGG	ZNF703	ZNF703-3	TCCCCGCCACCGATGGAGC
LMLN	LMLN-4	GGGTAGACGGAGGGCCAGC	ZNF703	ZNF703-4	CTGAGCCGGCTCCATCGGT
LMLN	LMLN-5	TAGACGGAGGGCCAGCCGG	ZNF703	ZNF703-5	GTCCCGCGCAGAGCTGCGAT
LMLN	LMLN-6	TTCTGCGGCGAACTTCTAGC	ZNF703	ZNF703-6	TCCCCGCGAGAGTCTGCGATT
LPP	LPP-1	CCTCCCTTGGTCTCCCGTG			
LPP	LPP-2	GCACCGCACGGGAGACCAAG			
LPP	LPP-3	TTACATGGACAAAATGCGTGC			
LPP	LPP-4	CGCACGGGAGACCAAGGGGA			
LPP	LPP-5	GCGCTGGAGGCTGACGTCA			
LPP	LPP-6	GGCACCGCACGGGAGACCAA			

Table 6: Focused CRISPR activation screen results (EdgeR)

Gene	Guide ID	CIS-ETO vs. P0					SAL vs. P0					CIS-ETO vs. SAL				
		Log2(FC)	Unadj. p	Adj. p	FDR <0.05	FDR <0.2	Log2(FC)	Unadj. p	Adj. p	FDR <0.05	FDR <0.2	Log2(FC)	Unadj. p	Adj. p	FDR <0.05	FDR <0.2
ABCC5	ABCC5-1	-0.33	0.3871	0.6089	0	0	0.22	0.6132	0.8945	0	0	-0.55	0.1300	0.6144	0	0
ABCC5	ABCC5-2	-0.86	0.0241	0.0891	0	1	-0.84	0.0641	0.4118	0	0	-0.02	0.8646	0.8872	0	0
ABCC5	ABCC5-3	-0.05	0.8514	0.8984	0	0	0.01	0.9719	0.9723	0	0	-0.06	0.8344	0.8862	0	0
ABCC5	ABCC5-4	-0.72	0.0660	0.1833	0	1	-0.32	0.4630	0.8506	0	0	-0.40	0.2629	0.7677	0	0
ABCC5	ABCC5-5	-0.24	0.5646	0.7556	0	0	-0.03	0.9055	0.9454	0	0	-0.20	0.5236	0.8862	0	0
ABCC5	ABCC5-6	-0.81	0.0279	0.0978	0	1	-0.88	0.0516	0.3663	0	0	0.07	0.8162	0.8862	0	0
ABCF3	ABCF3-1	0.50	0.2382	0.4451	0	0	0.59	0.2655	0.7214	0	0	-0.09	0.8188	0.8862	0	0
ABCF3	ABCF3-2	0.89	0.0484	0.1473	0	1	1.00	0.0473	0.3532	0	0	-0.11	0.4946	0.8862	0	0
ABCF3	ABCF3-3	-0.62	0.0886	0.2264	0	0	-0.14	0.8000	0.9227	0	0	-0.48	0.1861	0.6947	0	0
ABCF3	ABCF3-4	-0.22	0.5850	0.7712	0	0	-0.21	0.5820	0.8818	0	0	-0.01	0.7596	0.8862	0	0
ABCF3	ABCF3-5	0.35	0.4501	0.6713	0	0	0.24	0.6323	0.8955	0	0	0.11	0.8403	0.8862	0	0
ABCF3	ABCF3-6	-0.18	0.6565	0.8264	0	0	0.24	0.8063	0.9227	0	0	-0.42	0.3389	0.8301	0	0
ACAP2	ACAP2-1	0.02	0.8599	0.8984	0	0	-0.01	0.9488	0.9556	0	0	0.03	0.8528	0.8872	0	0
ACAP2	ACAP2-2	0.26	0.5462	0.7424	0	0	0.57	0.2239	0.6846	0	0	-0.31	0.3510	0.8319	0	0
ACAP2	ACAP2-3	-0.18	0.6382	0.8117	0	0	-0.11	0.8052	0.9227	0	0	-0.07	0.7623	0.8862	0	0
ACAP2	ACAP2-4	-0.18	0.6266	0.8044	0	0	-0.04	0.9284	0.9485	0	0	-0.14	0.7212	0.8862	0	0
ACAP2	ACAP2-5	-2.08	0.0000	0.0000	1	1	-0.82	0.1852	0.6431	0	0	-1.25	0.0077	0.1569	0	1
ACAP2	ACAP2-6	0.13	0.7478	0.8764	0	0	-0.13	0.8282	0.9287	0	0	0.26	0.6401	0.8862	0	0
ACVR1	ACVR1-1	-0.15	0.6970	0.8495	0	0	0.31	0.3709	0.7836	0	0	-0.46	0.1873	0.6947	0	0
ACVR1	ACVR1-2	-1.74	0.0000	0.0001	1	1	-1.16	0.0191	0.2389	0	0	-0.57	0.1774	0.6836	0	0
ACVR1	ACVR1-3	-0.12	0.7322	0.8683	0	0	-0.04	0.9183	0.9476	0	0	-0.08	0.7524	0.8862	0	0
ACVR1	ACVR1-4	-0.20	0.6421	0.8140	0	0	-0.12	0.7840	0.9227	0	0	-0.08	0.7597	0.8862	0	0
ACVR1	ACVR1-5	0.18	0.6423	0.8140	0	0	0.51	0.2981	0.7387	0	0	-0.33	0.3662	0.8358	0	0
ACVR1	ACVR1-6	-0.90	0.0187	0.0737	0	1	-0.61	0.1880	0.6438	0	0	-0.29	0.5154	0.8862	0	0
ADAMTS12	ADAMTS12-1	0.10	0.7510	0.8766	0	0	0.40	0.3819	0.7922	0	0	-0.30	0.4356	0.8764	0	0
ADAMTS12	ADAMTS12-2	-0.06	0.8345	0.8984	0	0	-0.05	0.9220	0.9485	0	0	-0.01	0.7388	0.8862	0	0
ADAMTS12	ADAMTS12-3	-0.72	0.0520	0.1551	0	1	-0.16	0.7190	0.9151	0	0	-0.56	0.1367	0.6223	0	0
ADAMTS12	ADAMTS12-4	0.52	0.1548	0.3320	0	0	0.56	0.1947	0.6525	0	0	-0.04	0.5813	0.8862	0	0
ADAMTS12	ADAMTS12-5	-1.29	0.0005	0.0040	1	1	0.52	0.6021	0.8878	0	0	-1.81	0.0000	0.0036	1	1
ADAMTS12	ADAMTS12-6	-0.73	0.0773	0.2063	0	0	-0.28	0.5931	0.8878	0	0	-0.45	0.2215	0.7398	0	0
ADGRA2	ADGRA2-1	-0.11	0.8556	0.8984	0	0	0.47	0.3511	0.7807	0	0	-0.58	0.2055	0.7202	0	0
ADGRA2	ADGRA2-2	-1.16	0.0020	0.0127	1	1	-0.94	0.0395	0.3329	0	0	-0.22	0.5660	0.8862	0	0
ADGRA2	ADGRA2-3	-0.87	0.0219	0.0831	0	1	-0.30	0.4857	0.8506	0	0	-0.57	0.1127	0.5872	0	0
ADGRA2	ADGRA2-4	-0.25	0.5414	0.7397	0	0	-0.02	0.9112	0.9468	0	0	-0.23	0.5053	0.8862	0	0
ADGRA2	ADGRA2-5	0.22	0.6019	0.7837	0	0	0.55	0.2283	0.6900	0	0	-0.32	0.3564	0.8319	0	0
ADGRA2	ADGRA2-6	-0.38	0.3830	0.6064	0	0	-0.27	0.6032	0.8878	0	0	-0.12	0.8172	0.8862	0	0
ADIPOQ	ADIPOQ-1	3.12	0.0000	0.0000	1	1	0.60	0.2319	0.6934	0	0	2.52	0.0000	0.0012	1	1
ADIPOQ	ADIPOQ-2	-0.30	0.4465	0.6677	0	0	0.08	0.7950	0.9227	0	0	-0.38	0.3574	0.8319	0	0
ADIPOQ	ADIPOQ-3	0.71	0.0799	0.2112	0	0	1.22	0.0127	0.1963	0	1	-0.52	0.1085	0.5833	0	0
ADIPOQ	ADIPOQ-4	-0.01	0.8685	0.8986	0	0	0.15	0.7157	0.9151	0	0	-0.16	0.6691	0.8862	0	0
ADIPOQ	ADIPOQ-5	0.88	0.0180	0.0719	0	1	0.47	0.3258	0.7599	0	0	0.40	0.2902	0.7917	0	0
ADIPOQ	ADIPOQ-6	3.97	0.0000	0.0000	1	1	2.28	0.0065	0.1363	0	1	1.69	0.0266	0.3091	0	0
AGO2	AGO2-1	-0.89	0.0166	0.0677	0	1	0.45	0.2969	0.7378	0	0	-1.34	0.0001	0.0076	1	1
AGO2	AGO2-2	0.26	0.5339	0.7359	0	0	0.35	0.4204	0.8313	0	0	-0.09	0.6122	0.8862	0	0
AGO2	AGO2-3	-0.18	0.6705	0.8365	0	0	-0.35	0.4268	0.8341	0	0	0.17	0.6930	0.8862	0	0
AGO2	AGO2-4	1.26	0.0262	0.0933	0	1	0.98	0.1293	0.5497	0	0	0.27	0.6816	0.8862	0	0
AGO2	AGO2-5	-0.65	0.0853	0.2209	0	0	-0.39	0.3945	0.8003	0	0	-0.26	0.4845	0.8862	0	0
AGO2	AGO2-6	-0.72	0.0543	0.1596	0	1	-0.39	0.3663	0.7821	0	0	-0.34	0.4322	0.8764	0	0
AHSG	AHSG-1	0.05	0.7506	0.8766	0	0	-0.23	0.6181	0.8955	0	0	0.28	0.4658	0.8862	0	0
AHSG	AHSG-2	0.62	0.0906	0.2301	0	0	1.27	0.0056	0.1336	0	1	-0.65	0.0901	0.5302	0	0
AHSG	AHSG-3	-0.08	0.8510	0.8984	0	0	-0.33	0.4876	0.8506	0	0	0.25	0.6030	0.8862	0	0
AHSG	AHSG-4	-1.17	0.0055	0.0281	1	1	-0.88	0.1031	0.5120	0	0	-0.29	0.4950	0.8862	0	0
AHSG	AHSG-5	-0.84	0.0252	0.0913	0	1	-0.19	0.7068	0.9141	0	0	-0.66	0.0820	0.5091	0	0
AHSG	AHSG-6	0.21	0.5731	0.7608	0	0	0.51	0.2319	0.6934	0	0	-0.30	0.3887	0.8491	0	0
AK3	AK3-1	-0.20	0.6286	0.8053	0	0	-0.21	0.6468	0.9022	0	0	0.01	0.8370	0.8862	0	0
AK3	AK3-2	-0.97	0.0112	0.0491	1	1	-0.49	0.2934	0.7378	0	0	-0.48	0.1973	0.7094	0	0
AK3	AK3-3	-1.04	0.0041	0.0224	1	1	-0.87	0.0539	0.3774	0	0	-0.17	0.5525	0.8862	0	0
AK3	AK3-4	-0.63	0.0865	0.2224	0	1	-0.41	0.3592	0.7812	0	0	-0.23	0.5382	0.8862	0	0
AK3	AK3-5	-1.54	0.0000	0.0003	1	1	-0.95	0.0323	0.3118	0	0	-0.59	0.1333	0.6151	0	0
AK3	AK3-6	-0.54	0.1443	0.3167	0	0	-0.40	0.3756	0.7854	0	0	-0.14	0.6593	0.8862	0	0
AKT1	AKT1-1	-0.46	0.2534	0.4635	0	0	1.09	0.0043	0.1110	0	1	-1.55	0.0000	0.0008	1	1
AKT1	AKT1-2	-0.67	0.0731	0.1976	0	1	-0.33	0.4523	0.8506	0	0	-0.33	0.4041	0.8598	0	0
AKT1	AKT1-3	-1.02	0.0075	0.0358	1	1	-0.59	0.1713	0.6276	0	0	-0.43	0.2474	0.7554	0	0
AKT1	AKT1-4	-2.14	0.0000	0.0000	1	1	-1.63	0.0007	0.0329	1	1	-0.52	0.1602	0.6624	0	0
AKT1	AKT1-5	-0.95	0.0185	0.0732	0	1	-0.60	0.2397	0.7006	0	0	-0.35	0.3746	0.8412	0	0
AKT1	AKT1-6	-1.37	0.0002	0.0016	1	1	-0.82	0.0678	0.4219	0	0	-0.56	0.1596	0.6623	0	0
AKT2	AKT2-1	0.52	0.2195	0.4221	0	0	0.95	0.0666	0.4184	0	0	0.43	0.3312	0.8258	0	0
AKT2	AKT2-2	0.11	0.7945	0.8960	0	0	-0.12	0.7746	0.9227	0	0	-0.24	0.5262	0.8862	0	0
AKT2	AKT2-3	-0.35	0.3470	0.5714	0	0	-0.06	0.8792	0.9417	0	0	-0.29	0.4566	0.8862	0	0
AKT2	AKT2-4	0.29	0.4558	0.6761	0	0	0.61	0.2426	0.7028	0	0	-0.32	0.4326	0.8764	0	0
AKT2	AKT2-5	-1.28	0.0021	0.0129	1	1	-0.02	0.6713	0.9075	0	0	-1.26	0.0103	0.1874	0	1
AKT2	AKT2-6	0.17	0.6773	0.8388	0	0	0.19	0.6929	0.9092	0	0	-0.02	0.8628	0.8872	0	0
AKT3	AKT3-1	-0.95	0.0094	0.0424	1	1	-0.50	0.2843	0.7355	0	0	-0.45	0.1949	0.7060	0	0
AKT3	AKT3-2	-0.84	0.0287	0.0997	0	1	-0.60	0.2078	0.6677	0	0	-0.23	0.5161	0.8862	0	0
AKT3	AKT3-3	-0.80	0.0321	0.1077	0	1	-0.53	0.2529	0.7043	0	0	-0.27	0.5114	0.8862	0	0
AKT3	AKT3-4	-1.10	0.0025	0.0149	1	1	-0.49	0.2477	0.7043	0	0	-0.61	0.1171	0.5930	0	0
AKT3	AKT3-5	0.18	0.5283	0.7324	0	0	-0.21	0.6250	0.8955	0	0	0.39	0.3107	0.8077	0	0
AKT3	AKT3-6	0.00	0.8616	0.8984	0	0	-0.12	0.8162	0.9243	0	0	0.12	0.8385	0.8862	0	0
ALG1L2	ALG1L2-1	-0.23	0.5736	0.7608	0	0	0.03	0.9033	0.9442	0	0	-0.26	0.5235	0.8862	0	0
ALG1L2	ALG1L2-2	0.10	0.80													

APOD	APOD-1	-0.64	0.1159	0.2756	0	0	-0.38	0.4711	0.8506	0	0	-0.26	0.5070	0.8862	0	0
APOD	APOD-2	0.85	0.0304	0.1033	0	1	0.51	0.2705	0.7275	0	0	0.34	0.4242	0.8764	0	0
APOD	APOD-3	-0.51	0.1911	0.3852	0	0	0.22	0.6272	0.8955	0	0	-0.72	0.1006	0.5549	0	0
APOD	APOD-4	0.10	0.8571	0.8984	0	0	0.46	0.3041	0.7468	0	0	-0.36	0.2698	0.7751	0	0
APOD	APOD-5	0.27	0.4959	0.7070	0	0	0.21	0.6331	0.8955	0	0	0.06	0.8122	0.8862	0	0
APOD	APOD-6	-0.34	0.5349	0.7361	0	0	-0.33	0.4896	0.8506	0	0	0.00	0.6737	0.8862	0	0
ARAF	ARAF-1	0.42	0.2799	0.4935	0	0	0.50	0.2301	0.6921	0	0	-0.08	0.6664	0.8862	0	0
ARAF	ARAF-2	-1.22	0.0009	0.0065	1	1	-0.81	0.0711	0.4296	0	0	-0.40	0.2745	0.7786	0	0
ARAF	ARAF-3	-0.61	0.1072	0.2599	0	0	-0.51	0.2420	0.7028	0	0	-0.10	0.7033	0.8862	0	0
ARAF	ARAF-4	-0.12	0.7659	0.8837	0	0	0.57	0.2315	0.6934	0	0	-0.69	0.0932	0.5403	0	0
ARAF	ARAF-5	-0.29	0.4509	0.6713	0	0	0.02	0.8670	0.9417	0	0	-0.31	0.4269	0.8764	0	0
ARAF	ARAF-6	0.40	0.2987	0.5134	0	0	0.80	0.0743	0.4414	0	0	-0.40	0.2864	0.7898	0	0
ARHGEF7	ARHGEF7-1	-0.20	0.5887	0.7739	0	0	-0.37	0.3942	0.8003	0	0	0.17	0.6967	0.8862	0	0
ARHGEF7	ARHGEF7-2	-1.22	0.0009	0.0065	1	1	-0.89	0.0465	0.3510	0	0	-0.33	0.3904	0.8491	0	0
ARHGEF7	ARHGEF7-3	0.17	0.6788	0.8394	0	0	0.39	0.4301	0.8343	0	0	-0.22	0.6264	0.8862	0	0
ARHGEF7	ARHGEF7-4	-1.30	0.0004	0.0034	1	1	-0.92	0.0441	0.3428	0	0	-0.38	0.3407	0.8301	0	0
ARHGEF7	ARHGEF7-5	-0.43	0.2746	0.4894	0	0	-0.03	0.9406	0.9531	0	0	-0.40	0.2931	0.7919	0	0
ARHGEF7	ARHGEF7-6	0.27	0.4701	0.6871	0	0	0.41	0.3124	0.7516	0	0	-0.14	0.6105	0.8862	0	0
ARID2	ARID2-1	0.08	0.8926	0.9051	0	0	-0.02	0.9110	0.9468	0	0	0.10	0.8375	0.8862	0	0
ARID2	ARID2-2	-3.86	0.0000	0.0000	1	1	-3.22	0.0004	0.0249	1	1	-0.64	0.4091	0.8649	0	0
ARID2	ARID2-3	-0.73	0.0454	0.1403	0	1	-0.50	0.2809	0.7355	0	0	-0.23	0.5528	0.8862	0	0
ARID2	ARID2-4	-1.58	0.0000	0.0003	1	1	-0.90	0.0612	0.4034	0	0	-0.69	0.0623	0.4576	0	0
ARID2	ARID2-5	-0.05	0.8422	0.8984	0	0	-0.10	0.8115	0.9227	0	0	0.05	0.8134	0.8862	0	0
ARID2	ARID2-6	0.22	0.5580	0.7513	0	0	0.28	0.5403	0.8699	0	0	-0.06	0.7728	0.8862	0	0
ASCL1	ASCL1-1	-0.18	0.6733	0.8378	0	0	0.02	0.7753	0.9227	0	0	-0.20	0.5794	0.8862	0	0
ASCL1	ASCL1-2	-0.58	0.1380	0.3078	0	0	0.10	0.7519	0.9184	0	0	-0.68	0.0917	0.5355	0	0
ASCL1	ASCL1-3	-0.90	0.0247	0.0905	0	1	-0.68	0.1640	0.6182	0	0	-0.21	0.5572	0.8862	0	0
ASCL1	ASCL1-4	-0.41	0.2760	0.4905	0	0	-0.38	0.3878	0.7961	0	0	-0.03	0.7251	0.8862	0	0
ASCL1	ASCL1-5	0.36	0.3438	0.5680	0	0	0.04	0.8429	0.9334	0	0	0.33	0.4229	0.8764	0	0
ASCL1	ASCL1-6	-1.10	0.0040	0.0217	1	1	-0.64	0.1663	0.6208	0	0	-0.46	0.2816	0.7870	0	0
ASCL2	ASCL2-1	-0.31	0.4029	0.6252	0	0	-0.22	0.6419	0.9022	0	0	-0.09	0.6895	0.8862	0	0
ASCL2	ASCL2-2	-0.07	0.8930	0.9051	0	0	-0.17	0.6912	0.9092	0	0	0.10	0.8619	0.8872	0	0
ASCL2	ASCL2-3	0.07	0.8448	0.8984	0	0	-0.12	0.8334	0.9306	0	0	0.19	0.6492	0.8862	0	0
ASCL2	ASCL2-4	0.83	0.0447	0.1386	0	1	1.15	0.0207	0.2484	0	0	-0.31	0.4939	0.8862	0	0
ASCL2	ASCL2-5	-0.19	0.6896	0.8448	0	0	0.07	0.7478	0.9177	0	0	-0.26	0.3740	0.8408	0	0
ASCL2	ASCL2-6	0.02	0.8353	0.8984	0	0	0.17	0.6989	0.9133	0	0	-0.15	0.6772	0.8862	0	0
ASXL1	ASXL1-1	-0.53	0.1448	0.3169	0	0	-0.37	0.4264	0.8341	0	0	-0.16	0.6694	0.8862	0	0
ASXL1	ASXL1-2	-0.65	0.0967	0.2404	0	0	-0.31	0.4856	0.8506	0	0	-0.34	0.3830	0.8463	0	0
ASXL1	ASXL1-3	0.16	0.7307	0.8681	0	0	0.25	0.6462	0.9022	0	0	-0.09	0.8060	0.8862	0	0
ASXL1	ASXL1-4	0.25	0.5370	0.7367	0	0	0.01	0.9493	0.9557	0	0	0.24	0.5794	0.8862	0	0
ASXL1	ASXL1-5	0.20	0.6208	0.8016	0	0	0.32	0.4712	0.8506	0	0	-0.12	0.7184	0.8862	0	0
ASXL1	ASXL1-6	-0.76	0.0471	0.1447	0	1	-0.56	0.2190	0.6837	0	0	-0.20	0.5786	0.8862	0	0
ATOH1	ATOH1-1	-0.18	0.6796	0.8400	0	0	-0.28	0.5123	0.8594	0	0	0.10	0.8112	0.8862	0	0
ATOH1	ATOH1-2	-1.15	0.0048	0.0252	1	1	-0.85	0.0834	0.4665	0	0	-0.30	0.5115	0.8862	0	0
ATOH1	ATOH1-3	-0.09	0.7941	0.8960	0	0	-0.17	0.7164	0.9151	0	0	0.08	0.8930	0.8992	0	0
ATOH1	ATOH1-4	-0.08	0.8580	0.8984	0	0	0.29	0.5174	0.8619	0	0	-0.37	0.3522	0.8319	0	0
ATOH1	ATOH1-5	-0.55	0.1503	0.3259	0	0	-0.28	0.5448	0.8702	0	0	-0.27	0.4919	0.8862	0	0
ATOH1	ATOH1-6	0.31	0.4637	0.6810	0	0	0.22	0.5934	0.8878	0	0	0.09	0.8067	0.8862	0	0
ATP11B	ATP11B-1	-0.03	0.9102	0.9144	0	0	0.32	0.6043	0.8878	0	0	-0.35	0.4714	0.8862	0	0
ATP11B	ATP11B-2	2.28	0.0013	0.0089	1	1	0.46	0.5425	0.8699	0	0	1.82	0.0072	0.1498	0	1
ATP11B	ATP11B-3	-0.96	0.0093	0.0420	1	1	-0.59	0.1839	0.6431	0	0	-0.37	0.2978	0.7965	0	0
ATP11B	ATP11B-4	2.36	0.0009	0.0065	1	1	1.34	0.0916	0.4894	0	0	1.03	0.1305	0.6144	0	0
ATP11B	ATP11B-5	-0.56	0.1414	0.3132	0	0	-0.40	0.3841	0.7927	0	0	-0.15	0.6929	0.8862	0	0
ATP11B	ATP11B-6	0.11	0.8260	0.8984	0	0	0.08	0.7997	0.9227	0	0	0.03	0.7681	0.8862	0	0
ATP13A3	ATP13A3-1	-0.33	0.4104	0.6339	0	0	-0.06	0.9356	0.9508	0	0	-0.27	0.4566	0.8862	0	0
ATP13A3	ATP13A3-2	0.25	0.5312	0.7342	0	0	0.61	0.1761	0.6347	0	0	-0.36	0.3479	0.8319	0	0
ATP13A3	ATP13A3-3	0.28	0.5058	0.7157	0	0	0.84	0.0666	0.4184	0	0	-0.56	0.1255	0.6068	0	0
ATP13A3	ATP13A3-4	-0.44	0.2659	0.4785	0	0	-0.39	0.3836	0.7926	0	0	-0.05	0.7375	0.8862	0	0
ATP13A3	ATP13A3-5	-0.03	0.8921	0.9051	0	0	0.22	0.6343	0.8957	0	0	-0.25	0.4373	0.8769	0	0
ATP13A3	ATP13A3-6	0.56	0.1922	0.3853	0	0	0.57	0.2612	0.7140	0	0	-0.01	0.8542	0.8872	0	0
ATP13A4	ATP13A4-1	-0.83	0.0299	0.1021	0	1	-0.21	0.6036	0.8878	0	0	-0.61	0.1057	0.5739	0	0
ATP13A4	ATP13A4-2	-0.26	0.5353	0.7361	0	0	-0.11	0.8355	0.9312	0	0	-0.16	0.7542	0.8862	0	0
ATP13A4	ATP13A4-3	3.91	0.0000	0.0000	1	1	1.08	0.1693	0.6245	0	0	2.83	0.0002	0.0117	1	1
ATP13A4	ATP13A4-4	-0.57	0.1646	0.3465	0	0	-0.38	0.4318	0.8356	0	0	-0.19	0.6348	0.8862	0	0
ATP13A4	ATP13A4-5	-1.76	0.0000	0.0002	1	1	-1.07	0.0400	0.3416	0	0	-0.69	0.0890	0.5257	0	0
ATP13A4	ATP13A4-6	-0.24	0.5598	0.7525	0	0	-0.60	0.1859	0.6431	0	0	0.36	0.3897	0.8491	0	0
ATP13A5	ATP13A5-1	0.08	0.7538	0.8779	0	0	2.50	0.0000	0.0013	1	1	-2.42	0.0000	0.0000	1	1
ATP13A5	ATP13A5-2	-1.40	0.0006	0.0047	1	1	-0.56	0.2938	0.7378	0	0	-0.84	0.0378	0.3695	0	0
ATP13A5	ATP13A5-3	-0.97	0.0170	0.0686	0	1	-0.58	0.2230	0.6846	0	0	-0.39	0.3944	0.8528	0	0
ATP13A5	ATP13A5-4	1.09	0.0130	0.0553	0	1	1.09	0.0294	0.3017	0	0	0.00	0.8423	0.8867	0	0
ATP13A5	ATP13A5-5	-0.42	0.3648	0.5865	0	0	-0.48	0.3752	0.7854	0	0	0.05	0.8908	0.8986	0	0
ATP13A5	ATP13A5-6	-0.84	0.0412	0.1298	0	1	-0.46	0.3157	0.7516	0	0	-0.38	0.3973	0.8578	0	0
ATR	ATR-1	-0.57	0.1514	0.3275	0	0	0.05	0.7696	0.9227	0	0	-0.62	0.1651	0.6679	0	0
ATR	ATR-2	-2.50	0.0000	0.0000	1	1	-1.65	0.0028	0.0856	0	1	-0.85	0.0371	0.3673	0	0
ATR	ATR-3	0.52	0.1660	0.3483	0	0	0.65	0.1373	0.5697	0	0	-0.13	0.7277	0.8862	0	0
ATR	ATR-4	0.11	0.6136	0.7949	0	0	0.49	0.3232	0.7592	0	0	-0.38	0.3512	0.8319	0	0
ATR	ATR-5	0.06	0.8171	0.8984	0	0	0.29	0.5084	0.8575	0	0	-0.22	0.5569	0.8862	0	0
ATR	ATR-6	-1.27	0.0011	0.0078	1	1	-0.96	0.0394	0.3329	0	0	-0.31	0.4750	0.8862	0	0
AURKA	AURKA-1	-1.01	0.0049	0.0257	1	1	-0.60	0.1919	0.6492	0	0	-0.41	0.2923	0.7918	0	0
AURKA	AURKA-2	-0.11	0.7836	0.8938	0	0	-0.13	0.7618	0.9206	0	0	0.02	0.8329	0.8862	0	0
AURKA	AURKA-3	0.29	0.4648	0.6820	0	0	0.31	0.4544								

BCL2L1	BCL2L1-6	-0.05	0.8861	0.9035	0	0	0.41	0.3583	0.7812	0	0	-0.46	0.1820	0.6875	0	0
BCL2L2-PAB	BCL2L2-PAB	0.03	0.8083	0.8984	0	0	0.52	0.1967	0.6546	0	0	-0.48	0.1259	0.6068	0	0
BCL2L2-PAB	BCL2L2-PAB	-0.36	0.3306	0.5523	0	0	-0.35	0.4288	0.8343	0	0	-0.01	0.8349	0.8862	0	0
BCL2L2-PAB	BCL2L2-PAB	-0.25	0.5578	0.7513	0	0	-0.29	0.5031	0.8547	0	0	0.03	0.6969	0.8862	0	0
BCL2L2-PAB	BCL2L2-PAB	-0.30	0.4545	0.6750	0	0	0.48	0.3235	0.7592	0	0	-0.78	0.0440	0.3999	0	0
BCL2L2-PAB	BCL2L2-PAB	-0.10	0.7674	0.8841	0	0	0.20	0.6885	0.9092	0	0	-0.29	0.4656	0.8862	0	0
BCL2L2-PAB	BCL2L2-PAB	0.10	0.7858	0.8938	0	0	0.06	0.9013	0.9426	0	0	0.04	0.7820	0.8862	0	0
BCL6	BCL6-1	-1.75	0.0001	0.0011	1	1	-0.99	0.0969	0.4995	0	0	-0.76	0.1172	0.5930	0	0
BCL6	BCL6-2	-0.45	0.2862	0.5011	0	0	0.09	0.6481	0.9026	0	0	-0.54	0.1553	0.6518	0	0
BCL6	BCL6-3	-2.19	0.0000	0.0000	1	1	-1.08	0.0606	0.4028	0	0	-1.11	0.0144	0.2317	0	0
BCL6	BCL6-4	-0.17	0.7146	0.8614	0	0	0.19	0.6820	0.9091	0	0	-0.36	0.3610	0.8319	0	0
BCL6	BCL6-5	-0.12	0.7758	0.8900	0	0	1.42	0.0033	0.0943	0	1	-1.54	0.0000	0.0036	1	1
BCL6	BCL6-6	-0.43	0.2536	0.4635	0	0	0.13	0.6741	0.9091	0	0	-0.56	0.1426	0.6362	0	0
BCOR	BCOR-1	-0.50	0.1723	0.3555	0	0	-0.06	0.8210	0.9265	0	0	-0.44	0.1158	0.5913	0	0
BCOR	BCOR-2	-1.36	0.0003	0.0028	1	1	-1.16	0.0135	0.2012	0	0	-0.20	0.5854	0.8862	0	0
BCOR	BCOR-3	-2.68	0.0606	0.1732	0	1	-0.88	0.6501	0.9036	0	0	-1.80	0.1859	0.6947	0	0
BCOR	BCOR-4	0.61	0.1261	0.2907	0	0	1.78	0.0004	0.0249	1	1	-1.17	0.0020	0.0644	0	1
BCOR	BCOR-5	-0.44	0.2980	0.5126	0	0	-0.29	0.5490	0.8713	0	0	-0.15	0.7483	0.8862	0	0
BCOR	BCOR-6	-0.37	0.3365	0.5596	0	0	-0.21	0.6628	0.9070	0	0	-0.16	0.6438	0.8862	0	0
BDH1	BDH1-1	-0.45	0.2659	0.4785	0	0	-0.59	0.1861	0.6431	0	0	0.14	0.7684	0.8862	0	0
BDH1	BDH1-2	-0.18	0.6370	0.8116	0	0	-0.24	0.5510	0.8729	0	0	0.06	0.8636	0.8872	0	0
BDH1	BDH1-3	-0.26	0.4833	0.7012	0	0	-0.34	0.4393	0.8427	0	0	0.08	0.8200	0.8862	0	0
BDH1	BDH1-4	-0.84	0.0263	0.0934	0	1	-0.55	0.2069	0.6676	0	0	-0.28	0.4964	0.8862	0	0
BDH1	BDH1-5	-0.12	0.7849	0.8938	0	0	0.15	0.7469	0.9177	0	0	-0.28	0.5548	0.8862	0	0
BDH1	BDH1-6	-0.01	0.9024	0.9022	0	0	-0.06	0.8966	0.9419	0	0	0.05	0.8894	0.8980	0	0
BMP8A	BMP8A-1	4.57	0.0000	0.0000	1	1	2.70	0.0013	0.0454	1	1	1.87	0.0147	0.2319	0	0
BMP8A	BMP8A-2	-0.55	0.1916	0.3852	0	0	-0.23	0.5555	0.8733	0	0	-0.31	0.5795	0.8862	0	0
BMP8A	BMP8A-3	-1.08	0.0022	0.0137	1	1	-0.30	0.6159	0.8955	0	0	-0.78	0.0441	0.3999	0	0
BMP8A	BMP8A-4	-3.46	0.0000	0.0000	1	1	-0.73	0.4873	0.8506	0	0	-2.73	0.0000	0.0000	1	1
BMP8A	BMP8A-5	-1.98	0.0000	0.0000	1	1	-0.34	0.6171	0.8955	0	0	-1.64	0.0002	0.0088	1	1
BMP8A	BMP8A-6	-1.59	0.0000	0.0002	1	1	-1.19	0.0079	0.1544	0	1	-0.40	0.2885	0.7917	0	0
BMP8B	BMP8B-1	-0.19	0.6361	0.8108	0	0	-0.15	0.7394	0.9167	0	0	-0.05	0.7940	0.8862	0	0
BMP8B	BMP8B-2	-1.10	0.0030	0.0171	1	1	-0.82	0.0674	0.4219	0	0	-0.28	0.5640	0.8862	0	0
BMP8B	BMP8B-3	-1.68	0.0000	0.0002	1	1	-1.35	0.0089	0.1667	0	1	-0.33	0.3414	0.8301	0	0
BMP8B	BMP8B-4	-1.10	0.0022	0.0138	1	1	-0.91	0.0431	0.3416	0	0	-0.18	0.5877	0.8862	0	0
BMP8B	BMP8B-5	-0.77	0.0382	0.1228	0	1	-0.63	0.1538	0.6025	0	0	-0.14	0.7122	0.8862	0	0
BMP8B	BMP8B-6	-1.25	0.0007	0.0053	1	1	-0.71	0.1099	0.5280	0	0	-0.53	0.1518	0.6504	0	0
BRF2	BRF2-1	0.23	0.5847	0.7712	0	0	0.57	0.1572	0.6087	0	0	-0.34	0.2511	0.7554	0	0
BRF2	BRF2-2	-0.67	0.0698	0.1917	0	1	-0.58	0.2076	0.6677	0	0	-0.09	0.8019	0.8862	0	0
BRF2	BRF2-3	-1.26	0.0019	0.0121	1	1	-0.73	0.1344	0.5626	0	0	-0.53	0.1658	0.6679	0	0
BRF2	BRF2-4	0.17	0.6646	0.8317	0	0	0.59	0.2016	0.6638	0	0	-0.42	0.3021	0.7981	0	0
BRF2	BRF2-5	-0.07	0.8987	0.9082	0	0	-0.11	0.8142	0.9238	0	0	0.05	0.7719	0.8862	0	0
BRF2	BRF2-6	0.21	0.5452	0.7416	0	0	0.62	0.1933	0.6518	0	0	-0.41	0.3494	0.8319	0	0
BTK	BTK-1	-0.78	0.0471	0.1447	0	1	-0.51	0.2723	0.7299	0	0	-0.27	0.4127	0.8690	0	0
BTK	BTK-2	-0.03	0.8838	0.9034	0	0	0.03	0.9150	0.9471	0	0	-0.07	0.7622	0.8862	0	0
BTK	BTK-3	0.68	0.0898	0.2287	0	0	0.16	0.7677	0.9227	0	0	0.52	0.2520	0.7554	0	0
BTK	BTK-4	0.34	0.3707	0.5925	0	0	-0.49	0.3042	0.7468	0	0	0.83	0.0615	0.4569	0	0
BTK	BTK-5	-0.03	0.8674	0.8986	0	0	-0.21	0.6876	0.9092	0	0	0.18	0.7372	0.8862	0	0
BTK	BTK-6	0.10	0.7847	0.8938	0	0	0.11	0.7841	0.9227	0	0	-0.01	0.8488	0.8869	0	0
C1QTNF3	C1QTNF3-1	0.44	0.2819	0.4956	0	0	0.64	0.1047	0.5145	0	0	-0.20	0.2234	0.7398	0	0
C1QTNF3	C1QTNF3-2	1.54	0.0003	0.0028	1	1	0.44	0.4658	0.8506	0	0	1.10	0.0208	0.2807	0	0
C1QTNF3	C1QTNF3-3	0.41	0.3595	0.5835	0	0	0.95	0.0829	0.4665	0	0	-0.54	0.2515	0.7554	0	0
C1QTNF3	C1QTNF3-4	0.02	0.8503	0.8984	0	0	0.48	0.2960	0.7378	0	0	-0.45	0.2346	0.7479	0	0
C1QTNF3	C1QTNF3-5	0.89	0.0878	0.2250	0	0	2.94	0.0000	0.0027	1	1	-2.05	0.0000	0.0023	1	1
C1QTNF3	C1QTNF3-6	0.31	0.4619	0.6799	0	0	0.86	0.1080	0.5236	0	0	-0.55	0.1877	0.6947	0	0
CALR	CALR-1	-0.03	0.9213	0.9236	0	0	-0.17	0.6947	0.9092	0	0	0.14	0.8019	0.8862	0	0
CALR	CALR-2	-0.36	0.4060	0.6295	0	0	0.31	0.5171	0.8619	0	0	-0.67	0.0670	0.4675	0	0
CALR	CALR-3	-0.61	0.1148	0.2741	0	0	0.01	0.9231	0.9485	0	0	-0.62	0.0840	0.5114	0	0
CALR	CALR-4	2.51	0.0001	0.0014	1	1	1.27	0.0818	0.4657	0	0	1.23	0.0587	0.4525	0	0
CALR	CALR-5	-0.06	0.8850	0.9035	0	0	-0.21	0.6555	0.9051	0	0	-0.15	0.7380	0.8862	0	0
CALR	CALR-6	-0.93	0.0097	0.0434	1	1	-0.58	0.2178	0.6829	0	0	0.35	0.3529	0.8319	0	0
CAMK2N2	CAMK2N2-1	-1.11	0.0026	0.0153	1	1	-0.68	0.1174	0.5346	0	0	-0.43	0.2428	0.7554	0	0
CAMK2N2	CAMK2N2-2	-0.54	0.1411	0.3130	0	0	-0.58	0.1845	0.6431	0	0	0.04	0.7287	0.8862	0	0
CAMK2N2	CAMK2N2-3	-0.73	0.0475	0.1449	0	1	-0.42	0.3253	0.7599	0	0	-0.31	0.3864	0.8477	0	0
CAMK2N2	CAMK2N2-4	-0.18	0.6970	0.8495	0	0	0.58	0.2761	0.7316	0	0	-0.75	0.0766	0.4939	0	0
CAMK2N2	CAMK2N2-5	-0.81	0.0375	0.1210	0	1	-0.86	0.0603	0.4018	0	0	0.05	0.7321	0.8862	0	0
CAMK2N2	CAMK2N2-6	0.16	0.6950	0.8489	0	0	0.30	0.4882	0.8506	0	0	-0.14	0.7177	0.8862	0	0
CAP1	CAP1-1	-0.47	0.2095	0.4097	0	0	-0.21	0.6359	0.8965	0	0	-0.26	0.4465	0.8819	0	0
CAP1	CAP1-2	-0.21	0.5702	0.7596	0	0	0.14	0.7058	0.9141	0	0	-0.36	0.2993	0.7965	0	0
CAP1	CAP1-3	-0.70	0.0557	0.1622	0	1	-0.49	0.2752	0.7313	0	0	-0.20	0.6838	0.8862	0	0
CAP1	CAP1-4	-0.52	0.1946	0.3891	0	0	0.42	0.5343	0.8699	0	0	-0.94	0.0233	0.2913	0	0
CAP1	CAP1-5	0.66	0.1220	0.2844	0	0	0.48	0.3506	0.7807	0	0	0.17	0.6936	0.8862	0	0
CAP1	CAP1-6	0.00	0.8555	0.8984	0	0	0.33	0.4386	0.8419	0	0	-0.33	0.3546	0.8319	0	0
CAPSL	CAPSL-1	-0.13	0.7275	0.8665	0	0	0.09	0.7251	0.9151	0	0	-0.22	0.4461	0.8819	0	0
CAPSL	CAPSL-2	0.49	0.1985	0.3956	0	0	0.46	0.2875	0.7360	0	0	0.04	0.8698	0.8891	0	0
CAPSL	CAPSL-3	0.14	0.6854	0.8436	0	0	0.29	0.5156	0.8614	0	0	-0.15	0.7078	0.8862	0	0
CAPSL	CAPSL-4	-0.20	0.6716	0.8371	0	0	-0.13	0.8416	0.9334	0	0	-0.07	0.6958	0.8862	0	0
CAPSL	CAPSL-5	0.16	0.6899	0.8448	0	0	0.50	0.2777	0.7330	0	0	-0.34	0.4407	0.8801	0	0
CAPSL	CAPSL-6	-1.22	0.0086	0.0396	1	1	-0.69	0.2582	0.7123	0	0	-0.53	0.2715	0.7761	0	0
CARM1	CARM1-1	-0.10	0.7555	0.8782	0	0	-0.15	0.7251	0.9151	0	0	0.04	0.7999	0.8862	0	0
CARM1	CARM1-2	0.03	0.8668	0.8986	0	0	0.01	0.9407	0.9531	0	0	0.02	0.8329	0.8862	0	0
CARM1	CARM1-3	-0.37	0.3219	0.5415												

CCND1	CCND1-5	-1.36	0.0012	0.0085	1	1	-0.49	0.3785	0.7880	0	0	-0.87	0.0502	0.4190	0	0
CCND1	CCND1-6	0.19	0.6223	0.8024	0	0	-0.07	0.8701	0.9417	0	0	0.26	0.5707	0.8862	0	0
CCND2	CCND2-1	-0.46	0.2252	0.4298	0	0	-0.31	0.5009	0.8538	0	0	-0.15	0.6137	0.8862	0	0
CCND2	CCND2-2	-1.17	0.0040	0.0220	1	1	-0.62	0.2167	0.6829	0	0	-0.56	0.1687	0.6693	0	0
CCND2	CCND2-3	-0.23	0.6217	0.8023	0	0	-0.37	0.3973	0.8046	0	0	0.14	0.7548	0.8862	0	0
CCND2	CCND2-4	-0.21	0.6462	0.8168	0	0	-0.15	0.7278	0.9151	0	0	-0.06	0.7360	0.8862	0	0
CCND2	CCND2-5	-0.73	0.0753	0.2022	0	0	-0.61	0.2367	0.6979	0	0	-0.12	0.7503	0.8862	0	0
CCND2	CCND2-6	-0.27	0.5162	0.7230	0	0	-0.08	0.7473	0.9177	0	0	-0.18	0.5969	0.8862	0	0
CCND3	CCND3-1	-1.04	0.0050	0.0260	1	1	-0.38	0.4487	0.8486	0	0	-0.65	0.1232	0.6063	0	0
CCND3	CCND3-2	0.08	0.8020	0.8966	0	0	1.46	0.0012	0.0436	1	1	-1.38	0.0001	0.0074	1	1
CCND3	CCND3-3	0.19	0.6520	0.8219	0	0	0.14	0.7923	0.9227	0	0	0.06	0.8365	0.8862	0	0
CCND3	CCND3-4	-0.29	0.4949	0.7069	0	0	-0.20	0.6336	0.8955	0	0	-0.09	0.7419	0.8862	0	0
CCND3	CCND3-5	-1.38	0.0001	0.0015	1	1	-1.02	0.0237	0.2691	0	0	-0.36	0.3522	0.8319	0	0
CCND3	CCND3-6	-0.32	0.4098	0.6333	0	0	-0.14	0.7713	0.9227	0	0	-0.18	0.6395	0.8862	0	0
CCNE1	CCNE1-1	-1.24	0.0009	0.0066	1	1	-0.78	0.0821	0.4657	0	0	-0.46	0.2447	0.7554	0	0
CCNE1	CCNE1-2	0.26	0.5006	0.7121	0	0	0.39	0.3652	0.7821	0	0	-0.13	0.6794	0.8862	0	0
CCNE1	CCNE1-3	-2.31	0.0000	0.0000	1	1	-1.46	0.0024	0.0764	0	1	-0.85	0.0314	0.3374	0	0
CCNE1	CCNE1-4	-1.11	0.0029	0.0167	1	1	-0.76	0.0980	0.5004	0	0	-0.35	0.3546	0.8319	0	0
CCNE1	CCNE1-5	-0.62	0.1167	0.2764	0	0	0.30	0.4954	0.8506	0	0	-0.91	0.0333	0.3463	0	0
CCNE1	CCNE1-6	-0.79	0.0392	0.1249	0	0	-0.25	0.6065	0.8891	0	0	-0.54	0.1592	0.6623	0	0
CD274	CD274-1	-0.95	0.0131	0.0556	0	1	-0.47	0.3044	0.7468	0	0	-0.48	0.2282	0.7411	0	0
CD274	CD274-2	-1.71	0.0000	0.0005	1	1	-0.30	0.5219	0.8648	0	0	-1.40	0.0027	0.0801	0	1
CD274	CD274-3	-0.55	0.1250	0.2889	0	0	-0.16	0.7848	0.9227	0	0	-0.39	0.2689	0.7747	0	0
CD274	CD274-4	-0.80	0.0394	0.1253	0	1	0.21	0.5269	0.8656	0	0	-1.01	0.0062	0.1367	0	1
CD274	CD274-5	-0.02	0.8728	0.8989	0	0	0.34	0.4345	0.8370	0	0	-0.36	0.3288	0.8252	0	0
CD274	CD274-6	-0.25	0.5626	0.7549	0	0	-0.13	0.7809	0.9227	0	0	-0.12	0.7546	0.8862	0	0
CD79A	CD79A-1	-0.90	0.0180	0.0719	0	1	-0.56	0.1988	0.6565	0	0	-0.34	0.4106	0.8666	0	0
CD79A	CD79A-2	-0.15	0.6999	0.8517	0	0	0.40	0.4429	0.8449	0	0	-0.56	0.1675	0.6693	0	0
CD79A	CD79A-3	-0.16	0.6845	0.8433	0	0	-0.24	0.5480	0.8713	0	0	0.08	0.8191	0.8862	0	0
CD79A	CD79A-4	0.50	0.1912	0.3852	0	0	1.75	0.0003	0.0216	1	1	-1.25	0.0019	0.0632	0	1
CD79A	CD79A-5	0.45	0.2224	0.4256	0	0	1.12	0.0194	0.2416	0	0	-0.66	0.0677	0.4684	0	0
CD79A	CD79A-6	-0.79	0.0339	0.1123	0	1	-0.21	0.6863	0.9092	0	0	-0.58	0.0976	0.5522	0	0
CDC37L1	CDC37L1-1	-0.35	0.3539	0.5773	0	0	-0.24	0.6703	0.9075	0	0	-0.11	0.6214	0.8862	0	0
CDC37L1	CDC37L1-2	0.18	0.6734	0.8378	0	0	0.61	0.1866	0.6431	0	0	-0.43	0.2423	0.7554	0	0
CDC37L1	CDC37L1-3	-0.83	0.0242	0.0893	0	1	-0.39	0.3753	0.7854	0	0	-0.44	0.2432	0.7554	0	0
CDC37L1	CDC37L1-4	-0.02	0.8576	0.8984	0	0	-0.05	0.9239	0.9485	0	0	0.02	0.8538	0.8872	0	0
CDC37L1	CDC37L1-5	0.20	0.6258	0.8043	0	0	0.03	0.9261	0.9485	0	0	0.17	0.7385	0.8862	0	0
CDC37L1	CDC37L1-6	1.94	0.0000	0.0006	1	1	-0.03	0.8979	0.9420	0	0	1.97	0.0000	0.0027	1	1
CDK4	CDK4-1	0.42	0.4182	0.6401	0	0	0.57	0.3488	0.7803	0	0	-0.15	0.7568	0.8862	0	0
CDK4	CDK4-2	-1.04	0.0045	0.0239	1	1	-0.60	0.1872	0.6438	0	0	-0.44	0.2498	0.7554	0	0
CDK4	CDK4-3	-0.17	0.7036	0.8549	0	0	-0.12	0.8267	0.9287	0	0	-0.05	0.8167	0.8862	0	0
CDK4	CDK4-4	-1.05	0.0036	0.0203	1	1	-0.89	0.0487	0.3586	0	0	-0.16	0.5823	0.8862	0	0
CDK4	CDK4-5	0.14	0.7570	0.8789	0	0	0.48	0.3413	0.7741	0	0	-0.33	0.3538	0.8319	0	0
CDK4	CDK4-6	-0.04	0.8553	0.8984	0	0	0.70	0.1653	0.6182	0	0	-0.74	0.0781	0.4972	0	0
CDKAL1	CDKAL1-1	-0.43	0.2688	0.4820	0	0	0.06	0.8681	0.9417	0	0	-0.50	0.1811	0.6871	0	0
CDKAL1	CDKAL1-2	-0.55	0.1646	0.3465	0	0	-0.49	0.3099	0.7508	0	0	-0.06	0.7050	0.8862	0	0
CDKAL1	CDKAL1-3	1.02	0.0310	0.1051	0	1	2.00	0.0009	0.0385	1	1	-0.97	0.0466	0.4091	0	0
CDKAL1	CDKAL1-4	0.23	0.5521	0.7464	0	0	0.23	0.5425	0.8699	0	0	0.00	0.7378	0.8862	0	0
CDKAL1	CDKAL1-5	-0.29	0.5390	0.7383	0	0	0.75	0.0760	0.4465	0	0	-1.04	0.0012	0.0409	1	1
CDKAL1	CDKAL1-6	3.90	0.0000	0.0001	1	1	1.12	0.1944	0.6525	0	0	2.78	0.0006	0.0243	1	1
CEBPA	CEBPA-1	-0.82	0.0285	0.0996	0	1	-0.39	0.3672	0.7821	0	0	-0.43	0.2624	0.7671	0	0
CEBPA	CEBPA-2	-1.36	0.0003	0.0029	1	1	-1.19	0.0096	0.1705	0	1	-0.17	0.5891	0.8862	0	0
CEBPA	CEBPA-3	-0.49	0.2132	0.4140	0	0	-0.33	0.4421	0.8442	0	0	-0.17	0.6302	0.8862	0	0
CEBPA	CEBPA-4	-1.36	0.0002	0.0017	1	1	-0.85	0.0709	0.4296	0	0	-0.51	0.1871	0.6947	0	0
CEBPA	CEBPA-5	1.44	0.0012	0.0083	1	1	1.18	0.0351	0.3197	0	0	0.26	0.2561	0.7586	0	0
CEBPA	CEBPA-6	-0.91	0.0157	0.0646	0	1	-0.26	0.5611	0.8762	0	0	-0.65	0.0833	0.5113	0	0
CEP19	CEP19-1	-0.46	0.2324	0.4399	0	0	0.16	0.7083	0.9141	0	0	-0.63	0.1451	0.6406	0	0
CEP19	CEP19-2	-2.30	0.0000	0.0000	1	1	-1.48	0.0090	0.1678	0	1	-0.82	0.0641	0.4666	0	0
CEP19	CEP19-3	0.72	0.2365	0.4433	0	0	1.32	0.0627	0.4079	0	0	-0.60	0.2824	0.7870	0	0
CEP19	CEP19-4	-0.72	0.0561	0.1631	0	1	-0.52	0.2498	0.7043	0	0	-0.21	0.6060	0.8862	0	0
CEP19	CEP19-5	-1.11	0.0020	0.0124	1	1	-0.19	0.6567	0.9051	0	0	-0.92	0.0159	0.2422	0	0
CEP19	CEP19-6	-2.06	0.0000	0.0000	1	1	-1.10	0.0306	0.3066	0	0	-0.96	0.0206	0.2807	0	0
CHIC2	CHIC2-1	-0.63	0.1109	0.2669	0	0	-0.09	0.8332	0.9306	0	0	-0.54	0.2149	0.7289	0	0
CHIC2	CHIC2-2	-1.43	0.0001	0.0013	1	1	-0.52	0.2952	0.7378	0	0	-0.91	0.0247	0.2989	0	0
CHIC2	CHIC2-3	-0.34	0.4621	0.6799	0	0	0.14	0.7973	0.9227	0	0	0.20	0.6805	0.8862	0	0
CHIC2	CHIC2-4	-0.61	0.1166	0.2764	0	0	-0.51	0.2531	0.7043	0	0	-0.10	0.7035	0.8862	0	0
CHIC2	CHIC2-5	-1.59	0.0001	0.0007	1	1	-1.58	0.0028	0.0856	0	1	-0.01	0.8373	0.8862	0	0
CHIC2	CHIC2-6	0.70	0.2757	0.4904	0	0	1.46	0.0704	0.4296	0	0	-0.76	0.2661	0.7718	0	0
CHRD	CHRD-1	-0.56	0.1337	0.3014	0	0	-0.13	0.7593	0.9201	0	0	-0.43	0.3006	0.7965	0	0
CHRD	CHRD-2	-0.16	0.6923	0.8464	0	0	0.19	0.6783	0.9091	0	0	-0.36	0.3605	0.8319	0	0
CHRD	CHRD-3	-0.21	0.5511	0.7454	0	0	0.22	0.6247	0.8955	0	0	-0.01	0.7626	0.8862	0	0
CHRD	CHRD-4	-0.33	0.3943	0.6169	0	0	-0.50	0.2929	0.7378	0	0	0.17	0.6675	0.8862	0	0
CHRD	CHRD-5	-2.29	0.0000	0.0000	1	1	-1.83	0.0008	0.0335	1	1	-0.45	0.3292	0.8252	0	0
CHRD	CHRD-6	-1.64	0.0000	0.0002	1	1	-0.47	0.4138	0.8235	0	0	-1.17	0.0038	0.0968	0	1
CIC	CIC-1	-0.68	0.0776	0.2069	0	0	-0.40	0.3560	0.7812	0	0	-0.28	0.4526	0.8860	0	0
CIC	CIC-2	-0.37	0.3519	0.5754	0	0	0.14	0.7082	0.9141	0	0	-0.51	0.1260	0.6068	0	0
CIC	CIC-3	-1.35	0.0004	0.0034	1	1	-0.92	0.0436	0.3428	0	0	-0.42	0.2968	0.7965	0	0
CIC	CIC-4	-0.78	0.0312	0.1055	0	1	-0.17	0.6801	0.9091	0	0	-0.61	0.1107	0.5872	0	0
CIC	CIC-5	-0.45	0.2782	0.4929	0	0	-0.01	0.8829	0.9417	0	0	-0.44	0.2924	0.7918	0	0
CIC	CIC-6	-1.07	0.0046	0.0245	1	1	-0.46	0.3260	0.7599	0	0	-0.61	0.1215	0.6048	0	0
CLCN2	CLCN2-1	-0.33	0.3808	0.6041	0	0	-0.11	0.8063	0.9227	0	0	-0.22	0.5904	0.8862	0	0

COL4A2	COL4A2-4	1.31	0.0018	0.0115	1	1	0.57	0.3073	0.7493	0	0	0.74	0.1391	0.6308	0	0
COL4A2	COL4A2-5	-0.12	0.7417	0.8744	0	0	0.41	0.3257	0.7599	0	0	-0.53	0.1312	0.6144	0	0
COL4A2	COL4A2-6	0.04	0.8365	0.8984	0	0	3.73	0.0000	0.0020	1	1	-3.69	0.0000	0.0000	1	1
COL9A2	COL9A2-1	0.05	0.8345	0.8984	0	0	-0.08	0.8862	0.9417	0	0	0.12	0.7997	0.8862	0	0
COL9A2	COL9A2-2	-1.39	0.0002	0.0018	1	1	-1.24	0.0064	0.1363	0	1	-0.16	0.7095	0.8862	0	0
COL9A2	COL9A2-3	-1.14	0.0036	0.0203	1	1	-1.09	0.0221	0.2578	0	0	-0.05	0.7083	0.8862	0	0
COL9A2	COL9A2-4	0.10	0.7494	0.8764	0	0	0.06	0.8667	0.9417	0	0	0.05	0.7836	0.8862	0	0
COL9A2	COL9A2-5	-0.49	0.1908	0.3852	0	0	-0.21	0.6350	0.8957	0	0	-0.29	0.3601	0.8319	0	0
COL9A2	COL9A2-6	0.45	0.2347	0.4424	0	0	0.71	0.1523	0.6019	0	0	-0.26	0.5448	0.8862	0	0
CONTROL1	NT1	-0.49	0.1955	0.4116	0	0	-0.28	0.5103	0.8128	0	0	-0.20	0.5844	0.8639	0	0
CONTROL1	NT10	-0.98	0.0193	0.0963	0	1	-1.06	0.0351	0.4494	0	0	0.08	0.8090	0.8639	0	0
CONTROL1	NT100	-0.20	0.5912	0.7821	0	0	-0.21	0.6360	0.8367	0	0	0.01	0.8509	0.8653	0	0
CONTROL1	NT101	-0.09	0.8466	0.8644	0	0	0.06	0.8565	0.9083	0	0	-0.14	0.6812	0.8639	0	0
CONTROL1	NT102	-2.46	0.0000	0.0000	1	1	-1.27	0.0141	0.2649	0	0	-1.19	0.0037	0.1114	0	1
CONTROL1	NT103	0.12	0.6062	0.7821	0	0	-0.12	0.7828	0.8891	0	0	0.23	0.4371	0.8639	0	0
CONTROL1	NT104	0.20	0.6014	0.7821	0	0	0.17	0.6898	0.8623	0	0	0.03	0.7573	0.8639	0	0
CONTROL1	NT105	-0.48	0.2125	0.4179	0	0	-0.41	0.3681	0.8128	0	0	-0.07	0.6952	0.8639	0	0
CONTROL1	NT106	-0.03	0.8353	0.8644	0	0	-0.12	0.7780	0.8891	0	0	0.09	0.8374	0.8639	0	0
CONTROL1	NT107	0.33	0.3993	0.6204	0	0	0.37	0.4185	0.8128	0	0	-0.05	0.7633	0.8639	0	0
CONTROL1	NT108	-0.78	0.0700	0.1954	0	1	-0.90	0.0681	0.4494	0	0	0.12	0.6239	0.8639	0	0
CONTROL1	NT109	-2.68	0.0000	0.0000	1	1	-1.02	0.0786	0.4494	0	0	-1.66	0.0002	0.0249	1	1
CONTROL1	NT11	0.02	0.8196	0.8644	0	0	-0.47	0.3383	0.7987	0	0	0.49	0.2576	0.7359	0	0
CONTROL1	NT110	-0.47	0.1877	0.4022	0	0	-0.46	0.2656	0.7774	0	0	-0.01	0.8100	0.8639	0	0
CONTROL1	NT111	-1.55	0.0002	0.0040	1	1	-0.77	0.1547	0.6585	0	0	-0.78	0.0549	0.3833	0	0
CONTROL1	NT112	-0.63	0.1166	0.2916	0	0	-0.55	0.2514	0.7764	0	0	-0.08	0.7714	0.8639	0	0
CONTROL1	NT113	-0.66	0.1117	0.2851	0	0	0.37	0.5347	0.8128	0	0	-1.03	0.0203	0.2436	0	0
CONTROL1	NT114	-0.76	0.0469	0.1406	0	1	-0.34	0.4417	0.8128	0	0	-0.42	0.2420	0.7359	0	0
CONTROL1	NT115	-1.11	0.0034	0.0311	1	1	-0.41	0.3782	0.8128	0	0	-0.70	0.0733	0.4189	0	0
CONTROL1	NT116	-1.32	0.0022	0.0240	1	1	-1.86	0.0012	0.0901	0	1	0.54	0.2703	0.7542	0	0
CONTROL1	NT117	-1.10	0.0034	0.0311	1	1	0.23	0.6829	0.8623	0	0	-1.33	0.0008	0.0486	1	1
CONTROL1	NT118	-0.82	0.0245	0.1089	0	1	-0.04	0.8193	0.9083	0	0	-0.78	0.0575	0.3833	0	0
CONTROL1	NT119	-0.82	0.0322	0.1247	0	1	-0.14	0.7499	0.8891	0	0	-0.69	0.0872	0.4418	0	0
CONTROL1	NT12	-0.13	0.7659	0.8644	0	0	0.08	0.8487	0.9083	0	0	-0.21	0.5656	0.8639	0	0
CONTROL1	NT120	0.20	0.6053	0.7821	0	0	-0.05	0.8523	0.9083	0	0	0.25	0.5367	0.8639	0	0
CONTROL1	NT13	-0.57	0.1291	0.3021	0	0	-0.46	0.2994	0.7811	0	0	-0.11	0.7437	0.8639	0	0
CONTROL1	NT14	-0.48	0.2153	0.4179	0	0	-0.27	0.5622	0.8128	0	0	-0.20	0.5421	0.8639	0	0
CONTROL1	NT15	-1.00	0.0057	0.0393	1	1	-0.27	0.5590	0.8128	0	0	-0.74	0.0421	0.3477	0	0
CONTROL1	NT16	0.35	0.3707	0.6011	0	0	1.13	0.0064	0.1628	0	1	-0.77	0.0184	0.2436	0	0
CONTROL1	NT17	-0.11	0.7846	0.8644	0	0	-0.10	0.8029	0.9004	0	0	-0.01	0.7448	0.8639	0	0
CONTROL1	NT18	-0.06	0.7667	0.8644	0	0	-0.07	0.8930	0.9207	0	0	0.01	0.8250	0.8639	0	0
CONTROL1	NT19	-0.85	0.0207	0.0992	0	1	-0.14	0.7553	0.8891	0	0	-0.71	0.0609	0.3843	0	0
CONTROL2	NT2	0.48	0.2151	0.4179	0	0	0.44	0.3180	0.7949	0	0	0.03	0.8611	0.8683	0	0
CONTROL2	NT20	1.00	0.0186	0.0963	0	1	0.87	0.0691	0.4494	0	0	0.12	0.6466	0.8639	0	0
CONTROL2	NT21	-0.63	0.0903	0.2408	0	0	-0.43	0.3623	0.8128	0	0	-0.20	0.5427	0.8639	0	0
CONTROL2	NT22	-0.17	0.6364	0.8039	0	0	0.81	0.0636	0.4494	0	0	-0.99	0.0101	0.1739	0	1
CONTROL2	NT23	-0.18	0.6031	0.7821	0	0	0.13	0.5407	0.8128	0	0	-0.32	0.3182	0.8256	0	0
CONTROL2	NT24	-0.80	0.0437	0.1406	0	1	-0.52	0.2799	0.7811	0	0	-0.29	0.5311	0.8639	0	0
CONTROL2	NT25	-0.24	0.5609	0.7725	0	0	-0.63	0.2204	0.7764	0	0	0.39	0.4054	0.8639	0	0
CONTROL2	NT26	0.93	0.0254	0.1090	0	1	0.82	0.0734	0.4494	0	0	0.11	0.8104	0.8639	0	0
CONTROL2	NT27	-0.46	0.2159	0.4179	0	0	-0.52	0.2538	0.7764	0	0	0.06	0.7739	0.8639	0	0
CONTROL2	NT28	0.33	0.4114	0.6250	0	0	0.39	0.4096	0.8128	0	0	-0.06	0.8179	0.8639	0	0
CONTROL2	NT29	-0.52	0.1501	0.3274	0	0	0.24	0.5995	0.8269	0	0	-0.76	0.0435	0.3477	0	0
CONTROL3	NT3	-0.62	0.1237	0.2970	0	0	-0.36	0.4748	0.8128	0	0	-0.26	0.5135	0.8639	0	0
CONTROL3	NT30	-0.01	0.8132	0.8644	0	0	-0.13	0.7742	0.8891	0	0	0.11	0.6725	0.8639	0	0
CONTROL3	NT31	-0.88	0.0303	0.1247	0	1	-0.81	0.1150	0.5519	0	0	-0.07	0.7511	0.8639	0	0
CONTROL3	NT32	-1.01	0.0064	0.0405	1	1	-0.62	0.1608	0.6585	0	0	-0.39	0.3234	0.8256	0	0
CONTROL3	NT33	-1.11	0.0053	0.0393	1	1	-0.48	0.3336	0.7987	0	0	-0.63	0.0983	0.4434	0	0
CONTROL3	NT34	-0.46	0.2325	0.4428	0	0	0.19	0.6977	0.8632	0	0	-0.65	0.1035	0.4434	0	0
CONTROL3	NT35	-0.54	0.1437	0.3194	0	0	-0.31	0.4832	0.8128	0	0	-0.23	0.5406	0.8639	0	0
CONTROL3	NT36	0.46	0.2451	0.4438	0	0	0.30	0.4851	0.8128	0	0	0.16	0.7307	0.8639	0	0
CONTROL3	NT37	-0.84	0.0231	0.1067	0	1	-0.44	0.3394	0.7987	0	0	-0.40	0.2567	0.7359	0	0
CONTROL3	NT38	-0.25	0.5033	0.7190	0	0	-0.30	0.5000	0.8128	0	0	0.06	0.8718	0.8718	0	0
CONTROL3	NT39	-0.12	0.8303	0.8644	0	0	1.08	0.1000	0.5002	0	0	-1.21	0.0228	0.2484	0	0
CONTROL4	NT4	-0.24	0.6171	0.7878	0	0	-0.01	0.7665	0.8891	0	0	-0.23	0.6361	0.8639	0	0
CONTROL4	NT40	0.78	0.0417	0.1406	0	1	1.41	0.0068	0.1628	0	1	-0.63	0.1950	0.6875	0	0
CONTROL4	NT41	0.31	0.4762	0.6993	0	0	1.19	0.6859	0.8623	0	0	0.12	0.8252	0.8639	0	0
CONTROL4	NT42	3.34	0.0000	0.0005	1	1	0.23	0.0023	0.0901	0	1	0.72	0.2965	0.7996	0	0
CONTROL4	NT43	-0.43	0.3091	0.5375	0	0	0.13	0.6415	0.8367	0	0	-0.57	0.1667	0.6629	0	0
CONTROL4	NT44	-0.55	0.1362	0.3083	0	0	-0.56	0.2290	0.7764	0	0	0.01	0.8423	0.8639	0	0
CONTROL4	NT45	0.08	0.8493	0.8644	0	0	0.01	0.9207	0.9207	0	0	0.07	0.7784	0.8639	0	0
CONTROL4	NT46	-0.27	0.4837	0.6993	0	0	0.06	0.8987	0.9207	0	0	-0.33	0.3568	0.8639	0	0
CONTROL4	NT47	-0.99	0.0098	0.0562	0	1	-0.29	0.5266	0.8128	0	0	-0.70	0.0887	0.4418	0	0
CONTROL4	NT48	-1.44	0.1237	0.2970	0	0	1.65	0.1541	0.6585	0	0	-3.10	0.0026	0.1045	0	1
CONTROL4	NT49	-0.56	0.2140	0.4179	0	0	-0.35	0.5422	0.8128	0	0	-0.21	0.5806	0.8639	0	0
CONTROL5	NT5	-0.18	0.6764	0.8455	0	0	-0.62	0.1646	0.6585	0	0	0.44	0.2536	0.7359	0	0
CONTROL5	NT50	1.95	0.0007	0.0090	1	1	1.25	0.0582	0.4494	0	0	0.70	0.2301	0.7359	0	0
CONTROL5	NT51	-1.26	0.0007	0.0090	1	1	-0.91	0.0466	0.4494	0	0	-0.35	0.3667	0.8639	0	0
CONTROL5	NT52	-0.57	0.1309	0.3021	0	0	-0.28	0.5327	0.8128	0	0	-0.29	0.4357	0.8639	0	0
CONTROL5	NT53	-0.10	0.8272	0.8644	0	0	0.97	0.0278	0.4163	0	0	-1.06	0.0052	0.1248	0	1
CONTROL5	NT54	-0.77	0.0573	0.1638	0	1	-0.40	0.4151	0.8128	0	0	-0.37	0.3682	0.8639	0	0
CONTROL5	NT55	0.05	0.8219	0.8644	0	0	0.22	0.6094	0.8310	0	0	-0.17	0.4289	0.8639	0	0
CONTROL5	NT56	-0.91	0.0419	0.1406	0	1	-0.61	0.2988	0.7811	0	0	-0.30	0.4168	0.8639	0	0
CONTROL5	NT57	-0.46	0.2478	0.4438	0	0	-0.46	0.2941	0.7811	0	0	0.00	0.6479	0.8639	0	0
CONTROL5																

CONTROL8	NT85	-1.40	0.0041	0.0352	1	1	-0.50	0.4231	0.8128	0	0	-0.90	0.0856	0.4418	0	0
CONTROL8	NT86	-1.02	0.0112	0.0613	0	1	-0.31	0.5355	0.8128	0	0	-0.72	0.0694	0.4164	0	0
CONTROL8	NT87	-0.34	0.3991	0.6204	0	0	-0.51	0.2476	0.7764	0	0	0.17	0.7133	0.8639	0	0
CONTROL8	NT88	-0.12	0.7566	0.8644	0	0	-0.08	0.8629	0.9083	0	0	-0.04	0.8108	0.8639	0	0
CONTROL8	NT89	-0.06	0.8199	0.8644	0	0	-0.09	0.8519	0.9083	0	0	0.03	0.8423	0.8639	0	0
CONTROL9	NT9	0.79	0.0417	0.1406	0	1	0.91	0.0574	0.4494	0	0	-0.12	0.6834	0.8639	0	0
CONTROL9	NT90	0.11	0.7755	0.8644	0	0	0.49	0.3137	0.7949	0	0	-0.38	0.3895	0.8639	0	0
CONTROL9	NT91	-0.23	0.5487	0.7656	0	0	-0.13	0.7689	0.8891	0	0	-0.10	0.7755	0.8639	0	0
CONTROL9	NT92	-1.47	0.0002	0.0040	1	1	-0.63	0.2147	0.7764	0	0	-0.83	0.0413	0.3477	0	0
CONTROL9	NT93	-1.34	0.0004	0.0057	1	1	-0.92	0.0503	0.4494	0	0	-0.42	0.2515	0.7359	0	0
CONTROL9	NT94	-0.11	0.8219	0.8644	0	0	0.62	0.2451	0.7764	0	0	-0.73	0.0921	0.4418	0	0
CONTROL9	NT95	0.12	0.7749	0.8644	0	0	-0.14	0.7832	0.8891	0	0	0.26	0.6157	0.8639	0	0
CONTROL9	NT96	0.07	0.8567	0.8644	0	0	0.75	0.0784	0.4494	0	0	-0.68	0.0521	0.3833	0	0
CONTROL9	NT97	-0.77	0.0450	0.1406	0	1	-0.53	0.2588	0.7764	0	0	-0.24	0.5765	0.8639	0	0
CONTROL9	NT98	0.70	0.0734	0.2001	0	0	0.78	0.0947	0.4940	0	0	-0.08	0.6872	0.8639	0	0
CONTROL9	NT99	-0.03	0.8572	0.8644	0	0	0.16	0.6803	0.8623	0	0	-0.19	0.5429	0.8639	0	0
CPN2	CPN2-1	-0.38	0.3401	0.5636	0	0	-0.56	0.3088	0.7506	0	0	0.18	0.7434	0.8862	0	0
CPN2	CPN2-2	-0.80	0.0429	0.1341	0	1	-0.39	0.3912	0.7998	0	0	-0.41	0.3204	0.8205	0	0
CPN2	CPN2-3	-1.16	0.0015	0.0098	1	1	-0.44	0.3252	0.7599	0	0	-0.72	0.0445	0.3999	0	0
CPN2	CPN2-4	-0.31	0.3829	0.6064	0	0	0.12	0.8416	0.9334	0	0	-0.43	0.2458	0.7554	0	0
CPN2	CPN2-5	0.38	0.3533	0.5773	0	0	0.76	0.1296	0.5501	0	0	-0.38	0.3249	0.8243	0	0
CPN2	CPN2-6	0.34	0.4368	0.6580	0	0	1.07	0.0403	0.3345	0	0	-0.73	0.0871	0.5187	0	0
CRKL	CRKL-1	-0.70	0.0654	0.1821	0	1	0.14	0.7026	0.9141	0	0	-0.84	0.0357	0.3575	0	0
CRKL	CRKL-2	0.38	0.4128	0.6347	0	0	0.30	0.5726	0.8789	0	0	0.09	0.8576	0.8872	0	0
CRKL	CRKL-3	1.55	0.0205	0.0790	0	1	1.97	0.0063	0.1363	0	1	-0.42	0.3627	0.8319	0	0
CRKL	CRKL-4	1.63	0.0192	0.0751	0	1	0.57	0.4509	0.8506	0	0	1.05	0.1174	0.5930	0	0
CRKL	CRKL-5	-0.31	0.4269	0.6481	0	0	-0.23	0.6242	0.8955	0	0	-0.08	0.7489	0.8862	0	0
CRKL	CRKL-6	0.00	0.8970	0.9078	0	0	-0.11	0.7779	0.9227	0	0	0.11	0.8264	0.8862	0	0
CRLF2	CRLF2-1	-1.78	0.0000	0.0005	1	1	-1.13	0.0447	0.3428	0	0	-0.66	0.1652	0.6679	0	0
CRLF2	CRLF2-2	-1.10	0.0086	0.0396	1	1	-0.37	0.4842	0.8506	0	0	-0.73	0.0937	0.5403	0	0
CRLF2	CRLF2-3	-0.99	0.0286	0.0996	0	1	-0.96	0.0964	0.4995	0	0	-0.03	0.7203	0.8862	0	0
CRLF2	CRLF2-4	0.68	0.0861	0.2217	0	0	0.54	0.2422	0.7028	0	0	0.14	0.7769	0.8862	0	0
CRLF2	CRLF2-5	-0.17	0.6590	0.8283	0	0	-0.08	0.8579	0.9386	0	0	-0.09	0.7556	0.8862	0	0
CRLF2	CRLF2-6	-1.68	0.0000	0.0006	1	1	-0.52	0.3146	0.7516	0	0	-1.16	0.0072	0.1498	0	1
CROCC	CROCC-1	0.27	0.4921	0.7060	0	0	0.57	0.2059	0.6676	0	0	-0.30	0.3622	0.8319	0	0
CROCC	CROCC-2	0.05	0.8244	0.8984	0	0	0.66	0.1232	0.5405	0	0	-0.61	0.0798	0.5068	0	0
CROCC	CROCC-3	-0.59	0.1055	0.2566	0	0	0.16	0.6937	0.9092	0	0	-0.75	0.0473	0.4091	0	0
CROCC	CROCC-4	-0.38	0.3611	0.5847	0	0	-0.29	0.5645	0.8770	0	0	-0.09	0.7967	0.8862	0	0
CROCC	CROCC-5	-1.68	0.0000	0.0001	1	1	-1.33	0.0047	0.1175	0	1	-0.35	0.3767	0.8421	0	0
CROCC	CROCC-6	-0.02	0.8494	0.8984	0	0	0.48	0.2745	0.7313	0	0	-0.50	0.1965	0.7082	0	0
CRYGS	CRYGS-1	-1.95	0.0000	0.0000	1	1	-1.02	0.0426	0.3408	0	0	-0.94	0.0227	0.2909	0	0
CRYGS	CRYGS-2	-0.19	0.6655	0.8324	0	0	-0.20	0.6566	0.9051	0	0	0.01	0.8203	0.8862	0	0
CRYGS	CRYGS-3	0.43	0.2453	0.4546	0	0	0.23	0.5991	0.8878	0	0	0.21	0.6165	0.8862	0	0
CRYGS	CRYGS-4	0.11	0.7587	0.8791	0	0	-0.03	0.8894	0.9418	0	0	0.14	0.7740	0.8862	0	0
CRYGS	CRYGS-5	2.70	0.0000	0.0000	1	1	1.57	0.0093	0.1692	0	1	1.13	0.0371	0.3673	0	0
CRYGS	CRYGS-6	0.04	0.8671	0.8986	0	0	0.24	0.5806	0.8818	0	0	-0.20	0.5551	0.8862	0	0
CSF3R	CSF3R-1	-0.07	0.8925	0.9051	0	0	-0.21	0.6278	0.8955	0	0	0.13	0.7550	0.8862	0	0
CSF3R	CSF3R-2	-0.23	0.5666	0.7569	0	0	0.14	0.7666	0.9227	0	0	-0.36	0.2768	0.7796	0	0
CSF3R	CSF3R-3	-0.18	0.7091	0.8589	0	0	0.03	0.9232	0.9485	0	0	-0.21	0.6610	0.8862	0	0
CSF3R	CSF3R-4	0.26	0.5617	0.7542	0	0	0.30	0.5283	0.8663	0	0	-0.04	0.8268	0.8862	0	0
CSF3R	CSF3R-5	-0.85	0.0191	0.0750	0	1	-0.67	0.1510	0.6006	0	0	-0.17	0.6021	0.8862	0	0
CSF3R	CSF3R-6	0.17	0.6597	0.8283	0	0	0.69	0.1877	0.6438	0	0	-0.52	0.2475	0.7554	0	0
CTBP2	CTBP2-1	0.15	0.7126	0.8594	0	0	0.21	0.6249	0.8955	0	0	-0.06	0.7659	0.8862	0	0
CTBP2	CTBP2-2	-0.78	0.0434	0.1353	0	1	-0.67	0.1672	0.6218	0	0	-0.11	0.6261	0.8862	0	0
CTBP2	CTBP2-3	-0.10	0.7523	0.8774	0	0	0.03	0.8881	0.9417	0	0	-0.13	0.6370	0.8862	0	0
CTBP2	CTBP2-4	-0.63	0.1038	0.2538	0	0	-0.88	0.0586	0.3966	0	0	0.24	0.5494	0.8862	0	0
CTBP2	CTBP2-5	-0.67	0.0928	0.2333	0	0	-0.44	0.3447	0.7771	0	0	-0.23	0.5720	0.8862	0	0
CTBP2	CTBP2-6	0.68	0.0794	0.2104	0	0	0.48	0.2919	0.7378	0	0	0.20	0.6816	0.8862	0	0
CTNND2	CTNND2-1	-1.48	0.0002	0.0018	1	1	-0.81	0.1028	0.5120	0	0	-0.68	0.0943	0.5416	0	0
CTNND2	CTNND2-2	-0.13	0.7179	0.8617	0	0	-0.17	0.7118	0.9142	0	0	0.04	0.7909	0.8862	0	0
CTNND2	CTNND2-3	-0.21	0.5997	0.7824	0	0	0.41	0.3933	0.8002	0	0	-0.61	0.1132	0.5872	0	0
CTNND2	CTNND2-4	-1.67	0.0004	0.0034	1	1	-1.20	0.0498	0.3626	0	0	-0.47	0.3295	0.8252	0	0
CTNND2	CTNND2-5	-1.02	0.0053	0.0270	1	1	-0.96	0.0374	0.3276	0	0	-0.06	0.7785	0.8862	0	0
CTNND2	CTNND2-6	-2.00	0.0000	0.0001	1	1	-1.45	0.0114	0.1889	0	1	-0.55	0.1660	0.6679	0	0
DCUN1D1	DCUN1D1-1	-0.74	0.0461	0.1423	0	1	-0.29	0.4782	0.8506	0	0	-0.45	0.2064	0.7216	0	0
DCUN1D1	DCUN1D1-2	-2.01	0.0000	0.0000	1	1	-0.46	0.5597	0.8762	0	0	-1.54	0.0001	0.0086	1	1
DCUN1D1	DCUN1D1-3	1.31	0.0370	0.1204	0	1	1.50	0.0470	0.3525	0	0	-0.19	0.4969	0.8862	0	0
DCUN1D1	DCUN1D1-4	-0.52	0.1585	0.3379	0	0	-0.06	0.8912	0.9418	0	0	-0.46	0.2400	0.7542	0	0
DCUN1D1	DCUN1D1-5	-1.32	0.0009	0.0066	1	1	-0.69	0.1649	0.6182	0	0	-0.63	0.1205	0.6010	0	0
DCUN1D1	DCUN1D1-6	-1.00	0.0088	0.0406	1	1	-0.94	0.0354	0.3197	0	0	-0.07	0.6669	0.8862	0	0
DDR2	DDR2-1	0.41	0.3053	0.5206	0	0	-0.02	0.8881	0.9417	0	0	0.43	0.3039	0.7991	0	0
DDR2	DDR2-2	-0.60	0.1985	0.3956	0	0	-0.53	0.3531	0.7812	0	0	-0.06	0.8316	0.8862	0	0
DDR2	DDR2-3	-0.56	0.1615	0.3419	0	0	-0.55	0.2671	0.7223	0	0	-0.01	0.8512	0.8871	0	0
DDR2	DDR2-4	-0.72	0.0833	0.2182	0	0	-0.73	0.1277	0.5470	0	0	0.00	0.7919	0.8862	0	0
DDR2	DDR2-5	1.14	0.0045	0.0239	1	1	0.22	0.6546	0.9051	0	0	0.92	0.0254	0.3050	0	0
DDR2	DDR2-6	-0.19	0.6518	0.8219	0	0	0.09	0.8475	0.9336	0	0	-0.28	0.5172	0.8862	0	0
DDX1	DDX1-1	-1.42	0.0001	0.0013	1	1	-1.00	0.0279	0.2939	0	0	-0.42	0.2473	0.7554	0	0
DDX1	DDX1-2	-1.83	0.0000	0.0000	1	1	-0.83	0.1040	0.5136	0	0	-1.00	0.0110	0.1961	0	1
DDX1	DDX1-3	-0.12	0.8258	0.8984	0	0	-0.33	0.4894	0.8506	0	0	0.20	0.5832	0.8862	0	0
DDX1	DDX1-4	-0.53	0.1666	0.3484	0	0	-0.37	0.4096	0.8190	0	0	-0.16	0.6146	0.8862	0	0
DDX1	DDX1-5	1.02	0.0107	0.0473	1	1	0.58	0.1831	0.6427	0	0	0.44	0.4660	0.8862	0	0
DDX1	DDX1-6	2.77	0.0001	0.0010	1	1	2.17	0.0037	0.1040							

DNAJC19	DNAJC19-2	-0.01	0.8728	0.8989	0	0	0.17	0.6779	0.9091	0	0	-0.19	0.5837	0.8862	0	0
DNAJC19	DNAJC19-3	0.03	0.8545	0.8984	0	0	0.01	0.9408	0.9531	0	0	0.03	0.8238	0.8862	0	0
DNAJC19	DNAJC19-4	-0.90	0.0151	0.0623	0	1	-0.11	0.7838	0.9227	0	0	-0.79	0.0373	0.3673	0	0
DNAJC19	DNAJC19-5	0.10	0.7744	0.8888	0	0	-0.19	0.6753	0.9091	0	0	0.29	0.4147	0.8701	0	0
DNAJC19	DNAJC19-6	-1.70	0.0000	0.0001	1	1	-0.74	0.1630	0.6174	0	0	-0.95	0.0408	0.3907	0	0
DNMT3B	DNMT3B-1	-1.44	0.0004	0.0031	1	1	-1.31	0.0097	0.1705	0	1	-0.14	0.7092	0.8862	0	0
DNMT3B	DNMT3B-2	-0.39	0.3996	0.6212	0	0	-0.29	0.5731	0.8790	0	0	-0.09	0.8152	0.8862	0	0
DNMT3B	DNMT3B-3	-0.28	0.4634	0.6810	0	0	-0.08	0.8370	0.9322	0	0	-0.20	0.5666	0.8862	0	0
DNMT3B	DNMT3B-4	0.00	0.8673	0.8986	0	0	-0.01	0.9286	0.9485	0	0	0.00	0.8139	0.8862	0	0
DNMT3B	DNMT3B-5	-0.81	0.0239	0.0887	0	1	-0.30	0.5090	0.8576	0	0	-0.50	0.1611	0.6648	0	0
DNMT3B	DNMT3B-6	-0.37	0.3407	0.5636	0	0	-0.17	0.7273	0.9151	0	0	-0.20	0.6277	0.8862	0	0
DPPA3	DPPA3-1	-0.93	0.0411	0.1295	0	1	-1.07	0.0559	0.3834	0	0	0.14	0.7611	0.8862	0	0
DPPA3	DPPA3-2	-2.29	0.0000	0.0000	1	1	-1.36	0.0205	0.2482	0	0	-0.93	0.0320	0.3400	0	0
DPPA3	DPPA3-3	-0.11	0.7206	0.8626	0	0	0.15	0.7357	0.9167	0	0	-0.27	0.4051	0.8601	0	0
DPPA3	DPPA3-4	0.80	0.0501	0.1515	0	1	0.42	0.4594	0.8506	0	0	0.38	0.3867	0.8477	0	0
DPPA3	DPPA3-5	0.27	0.4909	0.7054	0	0	0.03	0.8678	0.9417	0	0	0.24	0.5934	0.8862	0	0
DPPA3	DPPA3-6	0.39	0.3159	0.5341	0	0	0.49	0.2922	0.7378	0	0	-0.10	0.8177	0.8862	0	0
DVL3	DVL3-1	-1.43	0.0001	0.0010	1	1	-1.13	0.0128	0.1963	0	1	-0.30	0.3719	0.8401	0	0
DVL3	DVL3-2	-2.35	0.0000	0.0000	1	1	-1.41	0.0079	0.1544	0	1	-0.94	0.0271	0.3091	0	0
DVL3	DVL3-3	-0.68	0.0610	0.1736	0	1	-0.20	0.6321	0.8955	0	0	-0.48	0.2222	0.7398	0	0
DVL3	DVL3-4	-0.37	0.3477	0.5721	0	0	0.35	0.4946	0.8506	0	0	-0.71	0.0538	0.4282	0	0
DVL3	DVL3-5	-1.60	0.0000	0.0003	1	1	-1.17	0.0158	0.2156	0	0	-0.44	0.2563	0.7586	0	0
DVL3	DVL3-6	-2.21	0.0000	0.0000	1	1	-1.20	0.0183	0.2311	0	0	-1.01	0.0127	0.2167	0	0
E2F3	E2F3-1	0.06	0.8204	0.8984	0	0	-0.17	0.6929	0.9092	0	0	0.23	0.6171	0.8862	0	0
E2F3	E2F3-2	-0.65	0.0823	0.2157	0	0	-0.33	0.4544	0.8506	0	0	-0.32	0.4218	0.8764	0	0
E2F3	E2F3-3	0.20	0.5880	0.7739	0	0	0.26	0.5299	0.8682	0	0	-0.06	0.7693	0.8862	0	0
E2F3	E2F3-4	-0.60	0.1265	0.2912	0	0	-0.36	0.4157	0.8251	0	0	-0.24	0.5915	0.8862	0	0
E2F3	E2F3-5	0.08	0.8379	0.8984	0	0	0.11	0.6492	0.9031	0	0	-0.03	0.5207	0.8862	0	0
E2F3	E2F3-6	0.05	0.8571	0.8984	0	0	0.31	0.5254	0.8653	0	0	-0.26	0.4030	0.8598	0	0
ECE2	ECE2-1	-0.27	0.4725	0.6889	0	0	-0.19	0.6704	0.9075	0	0	-0.08	0.7465	0.8862	0	0
ECE2	ECE2-2	-0.45	0.2865	0.5011	0	0	-0.62	0.1875	0.6438	0	0	0.17	0.7043	0.8862	0	0
ECE2	ECE2-3	-0.86	0.0335	0.1113	0	1	-0.64	0.2159	0.6828	0	0	-0.22	0.5560	0.8862	0	0
ECE2	ECE2-4	-0.13	0.6875	0.8445	0	0	0.26	0.5219	0.8648	0	0	-0.39	0.2322	0.7476	0	0
ECE2	ECE2-5	0.75	0.0545	0.1597	0	1	0.56	0.2371	0.6981	0	0	0.19	0.6738	0.8862	0	0
ECE2	ECE2-6	0.36	0.3767	0.6000	0	0	0.05	0.8938	0.9418	0	0	0.31	0.4410	0.8801	0	0
EHHADH	EHHADH-1	-0.21	0.5671	0.7569	0	0	0.20	0.6608	0.9070	0	0	0.01	0.8290	0.8862	0	0
EHHADH	EHHADH-2	1.46	0.0004	0.0032	1	1	-0.59	0.2424	0.7028	0	0	-0.88	0.0224	0.2900	0	0
EHHADH	EHHADH-3	0.53	0.1765	0.3634	0	0	0.52	0.2529	0.7043	0	0	0.01	0.7556	0.8862	0	0
EHHADH	EHHADH-4	-0.48	0.2169	0.4194	0	0	-0.33	0.4776	0.8506	0	0	-0.15	0.6819	0.8862	0	0
EHHADH	EHHADH-5	-0.38	0.4377	0.6590	0	0	-0.36	0.5171	0.8619	0	0	-0.02	0.8505	0.8871	0	0
EHHADH	EHHADH-6	-0.92	0.0141	0.0590	0	1	-0.70	0.1159	0.5346	0	0	-0.22	0.5946	0.8862	0	0
EIF2B5	EIF2B5-1	-0.84	0.0363	0.1186	0	1	0.37	0.4795	0.8506	0	0	-1.22	0.0030	0.0848	0	1
EIF2B5	EIF2B5-2	-0.50	0.1814	0.3703	0	0	-0.33	0.4778	0.8506	0	0	-0.17	0.6216	0.8862	0	0
EIF2B5	EIF2B5-3	0.90	0.0185	0.0732	0	1	0.63	0.1480	0.5954	0	0	0.27	0.5105	0.8862	0	0
EIF2B5	EIF2B5-4	0.74	0.0474	0.1448	0	1	0.49	0.3270	0.7608	0	0	0.25	0.5793	0.8862	0	0
EIF2B5	EIF2B5-5	0.02	0.8475	0.8984	0	0	-0.15	0.8329	0.9306	0	0	0.17	0.7619	0.8862	0	0
EIF2B5	EIF2B5-6	-1.31	0.0004	0.0035	1	1	-0.83	0.0757	0.4465	0	0	-0.48	0.1888	0.6966	0	0
EIF4A2	EIF4A2-1	-0.49	0.2269	0.4316	0	0	-0.35	0.4827	0.8506	0	0	-0.15	0.7110	0.8862	0	0
EIF4A2	EIF4A2-2	-0.33	0.4724	0.6889	0	0	0.05	0.7299	0.9159	0	0	-0.38	0.4388	0.8790	0	0
EIF4A2	EIF4A2-3	-0.11	0.7623	0.8819	0	0	0.09	0.7925	0.9227	0	0	-0.20	0.5049	0.8862	0	0
EIF4A2	EIF4A2-4	-0.78	0.0631	0.1779	0	1	-0.04	0.6316	0.8955	0	0	-0.74	0.0917	0.5355	0	0
EIF4A2	EIF4A2-5	0.26	0.4940	0.7067	0	0	0.32	0.4521	0.8506	0	0	-0.06	0.8021	0.8862	0	0
EIF4A2	EIF4A2-6	-0.04	0.8427	0.8984	0	0	-0.06	0.8854	0.9417	0	0	0.02	0.8948	0.8992	0	0
EIF4G1	EIF4G1-1	-1.33	0.0004	0.0033	1	1	-0.95	0.0509	0.3663	0	0	-0.38	0.2775	0.7796	0	0
EIF4G1	EIF4G1-2	-0.11	0.7418	0.8744	0	0	-0.26	0.5656	0.8776	0	0	0.15	0.7413	0.8862	0	0
EIF4G1	EIF4G1-3	-0.87	0.0230	0.0866	0	1	-0.56	0.2374	0.6981	0	0	-0.32	0.3661	0.8358	0	0
EIF4G1	EIF4G1-4	-0.13	0.7456	0.8763	0	0	0.00	0.9698	0.9710	0	0	-0.13	0.7238	0.8862	0	0
EIF4G1	EIF4G1-5	-0.30	0.4246	0.6466	0	0	0.35	0.4954	0.8506	0	0	-0.65	0.0759	0.4939	0	0
EIF4G1	EIF4G1-6	-0.04	0.8920	0.9051	0	0	0.02	0.9455	0.9542	0	0	-0.07	0.8386	0.8862	0	0
ELF3	ELF3-1	-0.50	0.1943	0.3889	0	0	-0.13	0.7574	0.9198	0	0	-0.36	0.3031	0.7991	0	0
ELF3	ELF3-2	1.25	0.0054	0.0272	1	1	0.66	0.2354	0.6967	0	0	0.58	0.2597	0.7640	0	0
ELF3	ELF3-3	-0.14	0.7078	0.8584	0	0	0.25	0.5601	0.8762	0	0	-0.39	0.2759	0.7795	0	0
ELF3	ELF3-4	-0.08	0.8756	0.8989	0	0	-0.20	0.6766	0.9091	0	0	0.12	0.7770	0.8862	0	0
ELF3	ELF3-5	0.46	0.2505	0.4607	0	0	0.05	0.8948	0.9418	0	0	0.42	0.2886	0.7917	0	0
ELF3	ELF3-6	-0.58	0.1191	0.2799	0	0	-0.30	0.4940	0.8506	0	0	-0.28	0.5176	0.8862	0	0
ELOC	ELOC-1	-0.90	0.0157	0.0645	0	1	-0.65	0.1706	0.6276	0	0	-0.25	0.4668	0.8862	0	0
ELOC	ELOC-2	0.08	0.8460	0.8984	0	0	0.06	0.8934	0.9418	0	0	0.02	0.8356	0.8862	0	0
ELOC	ELOC-3	-0.15	0.7337	0.8684	0	0	0.08	0.8555	0.9369	0	0	-0.23	0.5217	0.8862	0	0
ELOC	ELOC-4	-0.08	0.8127	0.8984	0	0	0.30	0.5220	0.8648	0	0	-0.39	0.2370	0.7500	0	0
ELOC	ELOC-5	-0.52	0.1992	0.3961	0	0	-0.15	0.7616	0.9206	0	0	-0.37	0.3459	0.8319	0	0
ELOC	ELOC-6	-0.09	0.8616	0.8984	0	0	-0.50	0.2858	0.7356	0	0	0.40	0.3587	0.8319	0	0
EPHB1	EPHB1-1	0.63	0.0879	0.2250	0	0	0.43	0.3479	0.7795	0	0	0.20	0.5433	0.8862	0	0
EPHB1	EPHB1-2	-0.82	0.0248	0.0905	0	1	-0.26	0.5488	0.8713	0	0	-0.56	0.1549	0.6518	0	0
EPHB1	EPHB1-3	1.81	0.0024	0.0148	1	1	2.84	0.0001	0.0129	1	1	-1.03	0.0777	0.4971	0	0
EPHB1	EPHB1-4	-0.44	0.2594	0.4714	0	0	-0.48	0.2748	0.7313	0	0	0.04	0.7960	0.8862	0	0
EPHB1	EPHB1-5	0.35	0.3673	0.5890	0	0	0.96	0.0836	0.4665	0	0	-0.61	0.1978	0.7099	0	0
EPHB1	EPHB1-6	-0.31	0.4505	0.6713	0	0	0.15	0.6607	0.9070	0	0	-0.46	0.2727	0.7761	0	0
EPHB3	EPHB3-1	-0.18	0.6459	0.8168	0	0	0.11	0.7901	0.9227	0	0	-0.29	0.4973	0.8862	0	0
EPHB3	EPHB3-2	-0.13	0.7846	0.8938	0	0	0.03	0.9128	0.9468	0	0	-0.16	0.6501	0.8862	0	0
EPHB3	EPHB3-3	-0.10	0.7923	0.8960	0	0	-0.06	0.8161	0.9243	0	0	-0.03	0.7444	0.8862	0	0
EPHB3	EPHB3-4	-1.59	0.0000	0.0002	1	1	-0.99	0.0349	0.3197	0	0	-0.60	0.0852	0.5139	0	0
EPHB3	EPHB3-5	0.72	0.0718	0.1950	0	1	0.60	0.1901	0.6466	0	0	0.				

ERMP1	ERMP1-1	-0.71	0.0653	0.1821	0	1	-0.15	0.7398	0.9167	0	0	-0.56	0.1544	0.6518	0	0
ERMP1	ERMP1-2	-0.45	0.2158	0.4176	0	0	-0.33	0.4670	0.8506	0	0	-0.12	0.7207	0.8862	0	0
ERMP1	ERMP1-3	0.21	0.6259	0.8043	0	0	0.07	0.8653	0.9417	0	0	0.14	0.8098	0.8862	0	0
ERMP1	ERMP1-4	0.15	0.7185	0.8617	0	0	0.24	0.5187	0.8636	0	0	-0.09	0.7125	0.8862	0	0
ERMP1	ERMP1-5	-0.60	0.0993	0.2456	0	0	-0.48	0.2658	0.7214	0	0	-0.12	0.7754	0.8862	0	0
ERMP1	ERMP1-6	-0.42	0.3009	0.5156	0	0	-0.01	0.8481	0.9336	0	0	-0.40	0.2899	0.7917	0	0
ETV1	ETV1-1	-0.91	0.0148	0.0613	0	1	-0.86	0.0541	0.3774	0	0	-0.05	0.7648	0.8862	0	0
ETV1	ETV1-2	-0.34	0.4068	0.6303	0	0	0.24	0.6459	0.9022	0	0	-0.57	0.1495	0.6471	0	0
ETV1	ETV1-3	-1.02	0.0080	0.0375	1	1	-0.60	0.1969	0.6546	0	0	-0.42	0.2543	0.7571	0	0
ETV1	ETV1-4	-0.26	0.5292	0.7328	0	0	-0.04	0.9356	0.9508	0	0	-0.22	0.5315	0.8862	0	0
ETV1	ETV1-5	-0.55	0.1479	0.3222	0	0	-0.24	0.5823	0.8818	0	0	-0.31	0.4253	0.8764	0	0
ETV1	ETV1-6	-1.20	0.0010	0.0074	1	1	-0.57	0.2205	0.6841	0	0	-0.63	0.0753	0.4939	0	0
ETV5	ETV5-1	0.13	0.7327	0.8683	0	0	0.38	0.3868	0.7961	0	0	-0.24	0.5548	0.8862	0	0
ETV5	ETV5-2	-0.10	0.7999	0.8966	0	0	0.35	0.5399	0.8699	0	0	-0.45	0.3297	0.8252	0	0
ETV5	ETV5-3	0.19	0.6680	0.8343	0	0	0.44	0.3337	0.7659	0	0	-0.25	0.4205	0.8761	0	0
ETV5	ETV5-4	-0.41	0.3129	0.5308	0	0	0.01	0.9189	0.9476	0	0	-0.42	0.2472	0.7554	0	0
ETV5	ETV5-5	0.19	0.6395	0.8122	0	0	0.21	0.6244	0.8955	0	0	-0.02	0.8534	0.8872	0	0
ETV5	ETV5-6	-0.57	0.1374	0.3072	0	0	-0.34	0.5242	0.8653	0	0	-0.23	0.5237	0.8862	0	0
FAM131A	FAM131A-1	-0.37	0.3570	0.5806	0	0	-0.32	0.4778	0.8506	0	0	-0.05	0.8145	0.8862	0	0
FAM131A	FAM131A-2	0.86	0.0847	0.2200	0	0	0.79	0.1537	0.6025	0	0	0.07	0.8469	0.8869	0	0
FAM131A	FAM131A-3	-0.97	0.0078	0.0368	1	1	-0.63	0.1763	0.6347	0	0	-0.34	0.3386	0.8301	0	0
FAM131A	FAM131A-4	0.80	0.0870	0.2234	0	0	1.46	0.0061	0.1357	0	1	-0.65	0.1110	0.5872	0	0
FAM131A	FAM131A-5	-1.01	0.0057	0.0289	1	1	-0.59	0.1867	0.6431	0	0	-0.42	0.2858	0.7897	0	0
FAM131A	FAM131A-6	0.50	0.1997	0.3967	0	0	0.37	0.4078	0.8164	0	0	0.13	0.7635	0.8862	0	0
FAM43A	FAM43A-1	-1.96	0.0000	0.0000	1	1	-1.72	0.0010	0.0389	1	1	-0.24	0.5849	0.8862	0	0
FAM43A	FAM43A-2	0.26	0.5257	0.7306	0	0	0.18	0.6817	0.9091	0	0	0.09	0.8882	0.8972	0	0
FAM43A	FAM43A-3	-0.77	0.0389	0.1244	0	1	-0.40	0.3895	0.7982	0	0	-0.37	0.3384	0.8301	0	0
FAM43A	FAM43A-4	0.88	0.0353	0.1165	0	1	0.95	0.0492	0.3589	0	0	-0.07	0.5789	0.8862	0	0
FAM43A	FAM43A-5	0.34	0.4946	0.7069	0	0	1.24	0.0419	0.3846	0	0	-0.90	0.0573	0.4450	0	0
FAM43A	FAM43A-6	-0.50	0.2079	0.4074	0	0	0.33	0.4292	0.8343	0	0	-0.83	0.0295	0.3256	0	0
FAM58A	FAM58A-1	0.08	0.8134	0.8984	0	0	0.15	0.7355	0.9167	0	0	-0.06	0.8111	0.8862	0	0
FAM58A	FAM58A-2	0.14	0.6886	0.8445	0	0	0.55	0.2716	0.7288	0	0	-0.41	0.3608	0.8319	0	0
FAM58A	FAM58A-3	-0.11	0.7765	0.8900	0	0	-0.04	0.9473	0.9556	0	0	-0.07	0.7915	0.8862	0	0
FAM58A	FAM58A-4	0.18	0.6754	0.8388	0	0	0.35	0.4409	0.8437	0	0	-0.17	0.6165	0.8862	0	0
FAM58A	FAM58A-5	-0.93	0.0126	0.0542	0	1	-0.69	0.1245	0.5405	0	0	-0.25	0.5406	0.8862	0	0
FAM58A	FAM58A-6	-0.69	0.0946	0.2363	0	0	-0.78	0.0933	0.4941	0	0	0.09	0.6962	0.8862	0	0
FAM90A1	FAM90A1-1	0.26	0.5169	0.7233	0	0	0.28	0.5541	0.8733	0	0	-0.02	0.7941	0.8862	0	0
FAM90A1	FAM90A1-2	-0.35	0.3820	0.6057	0	0	0.03	0.8237	0.9283	0	0	-0.38	0.2299	0.7457	0	0
FAM90A1	FAM90A1-3	-0.53	0.1842	0.3750	0	0	-0.10	0.7804	0.9227	0	0	-0.43	0.3034	0.7991	0	0
FAM90A1	FAM90A1-4	-0.71	0.6599	0.8283	0	0	-0.28	0.5841	0.8823	0	0	0.07	0.7155	0.8862	0	0
FAM90A1	FAM90A1-5	0.28	0.0445	0.1384	0	1	0.40	0.3628	0.7812	0	0	0.38	0.3607	0.8319	0	0
FAM90A1	FAM90A1-6	-0.65	0.0894	0.2281	0	0	-0.28	0.5402	0.8699	0	0	-0.37	0.3361	0.8301	0	0
FANCG	FANCG-1	-1.02	0.0034	0.0192	1	1	-0.35	0.4480	0.8486	0	0	-0.67	0.0588	0.4525	0	0
FANCG	FANCG-2	0.01	0.8356	0.8984	0	0	-0.06	0.8088	0.9227	0	0	0.06	0.7740	0.8862	0	0
FANCG	FANCG-3	-0.36	0.3986	0.6205	0	0	0.24	0.5424	0.8699	0	0	-0.60	0.1087	0.5833	0	0
FANCG	FANCG-4	-1.34	0.0002	0.0019	1	1	-0.31	0.4907	0.8506	0	0	-1.03	0.0093	0.1777	0	1
FANCG	FANCG-5	-1.52	0.0004	0.0035	1	1	-0.69	0.2852	0.7355	0	0	-0.83	0.0749	0.4939	0	0
FANCG	FANCG-6	-0.63	0.1121	0.2690	0	0	-0.03	0.8483	0.9336	0	0	-0.60	0.1563	0.6541	0	0
FBXO45	FBXO45-1	0.09	0.7602	0.8805	0	0	-0.08	0.8695	0.9417	0	0	0.17	0.6392	0.8862	0	0
FBXO45	FBXO45-2	-1.11	0.0071	0.0342	1	1	-0.80	0.1247	0.5405	0	0	-0.31	0.4146	0.8701	0	0
FBXO45	FBXO45-3	-0.62	0.1053	0.2565	0	0	0.05	0.6948	0.9092	0	0	-0.66	0.0999	0.5522	0	0
FBXO45	FBXO45-4	-0.49	0.2176	0.4201	0	0	-0.35	0.4339	0.8370	0	0	-0.14	0.7333	0.8862	0	0
FBXO45	FBXO45-5	0.05	0.8802	0.9005	0	0	0.19	0.6423	0.9022	0	0	-0.14	0.6524	0.8862	0	0
FBXO45	FBXO45-6	-0.50	0.1786	0.3664	0	0	-0.35	0.4298	0.8343	0	0	-0.15	0.6244	0.8862	0	0
FETUB	FETUB-1	0.59	0.1328	0.3006	0	0	-0.07	0.8185	0.9252	0	0	0.66	0.1525	0.6505	0	0
FETUB	FETUB-2	-0.17	0.6297	0.8054	0	0	-0.44	0.3626	0.7812	0	0	0.27	0.5590	0.8862	0	0
FETUB	FETUB-3	-0.22	0.5795	0.7665	0	0	-0.09	0.8628	0.9406	0	0	-0.14	0.6821	0.8862	0	0
FETUB	FETUB-4	-0.53	0.2144	0.4152	0	0	0.19	0.5915	0.8876	0	0	-0.72	0.0424	0.3988	0	0
FETUB	FETUB-5	-0.34	0.4157	0.6375	0	0	-0.16	0.7509	0.9184	0	0	-0.18	0.5219	0.8862	0	0
FETUB	FETUB-6	-0.93	0.0088	0.0404	1	1	-0.65	0.1448	0.5865	0	0	-0.28	0.4524	0.8860	0	0
FGF10	FGF10-1	-1.09	0.0039	0.0214	1	1	-1.05	0.0177	0.2292	0	0	-0.04	0.7756	0.8862	0	0
FGF10	FGF10-2	-0.81	0.0335	0.1113	0	1	-0.07	0.7930	0.9227	0	0	-0.73	0.0658	0.4673	0	0
FGF10	FGF10-3	-0.80	0.0447	0.1386	0	1	-0.22	0.6889	0.9092	0	0	-0.58	0.2278	0.7410	0	0
FGF10	FGF10-4	-1.70	0.0001	0.0007	1	1	-1.19	0.0308	0.3066	0	0	-0.51	0.1965	0.7082	0	0
FGF10	FGF10-5	-1.79	0.0000	0.0000	1	1	-1.23	0.0100	0.1751	0	1	-0.57	0.1689	0.6693	0	0
FGF10	FGF10-6	0.35	0.3636	0.5861	0	0	0.64	0.1550	0.6036	0	0	-0.29	0.3930	0.8522	0	0
FGF12	FGF12-1	-0.48	0.1904	0.3850	0	0	-0.35	0.4294	0.8343	0	0	-0.13	0.6917	0.8862	0	0
FGF12	FGF12-2	-0.68	0.0607	0.1732	0	1	0.14	0.7398	0.9167	0	0	-0.81	0.0212	0.2807	0	0
FGF12	FGF12-3	-0.66	0.0856	0.2210	0	0	-0.75	0.1109	0.5280	0	0	0.09	0.8721	0.8903	0	0
FGF12	FGF12-4	0.30	0.4390	0.6597	0	0	0.33	0.4264	0.8341	0	0	-0.03	0.8086	0.8862	0	0
FGF12	FGF12-5	-0.52	0.1739	0.3585	0	0	-0.35	0.3931	0.8002	0	0	-0.17	0.6494	0.8862	0	0
FGF12	FGF12-6	-1.31	0.0003	0.0028	1	1	-1.13	0.0135	0.2012	0	0	-0.18	0.5864	0.8862	0	0
FGF19	FGF19-1	-0.62	0.1428	0.3147	0	0	0.06	0.7496	0.9184	0	0	-0.68	0.1107	0.5872	0	0
FGF19	FGF19-2	4.33	0.0000	0.0000	1	1	2.52	0.0029	0.0859	0	1	1.82	0.0218	0.2863	0	0
FGF19	FGF19-3	-0.60	0.0990	0.2452	0	0	0.13	0.7405	0.9168	0	0	-0.74	0.0928	0.5395	0	0
FGF19	FGF19-4	0.12	0.7259	0.8658	0	0	0.35	0.4556	0.8506	0	0	-0.22	0.6157	0.8862	0	0
FGF19	FGF19-5	0.93	0.0528	0.1566	0	1	1.40	0.0176	0.2287	0	0	-0.47	0.3557	0.8319	0	0
FGF19	FGF19-6	0.10	0.7794	0.8928	0	0	0.57	0.2068	0.6676	0	0	-0.47	0.1640	0.6676	0	0
FGF3	FGF3-1	-1.07	0.0031	0.0180	1	1	-0.57	0.2194	0.6841	0	0	-0.50	0.1512	0.6504	0	0
FGF3	FGF3-2	0.32	0.3952	0.6174	0	0	0.43	0.3463	0.7772	0	0	-0.11	0.6215	0.8862	0	0
FGF3	FGF3-3	0.07	0.8329	0.8984	0	0	0.35	0.34								

FLCN	FLCN-6	0.81	0.0853	0.2209	0	0	2.44	0.0000	0.0004	1	1	-1.63	0.0000	0.0003	1	1
FLYWCH1	FLYWCH1-1	-1.43	0.0027	0.0156	1	1	-1.40	0.0229	0.2638	0	0	-0.03	0.8077	0.8862	0	0
FLYWCH1	FLYWCH1-2	-0.05	0.9149	0.9180	0	0	-0.06	0.8879	0.9417	0	0	0.01	0.8942	0.8992	0	0
FLYWCH1	FLYWCH1-3	-0.79	0.1041	0.2543	0	0	-0.65	0.2812	0.7355	0	0	-0.14	0.7240	0.8862	0	0
FLYWCH1	FLYWCH1-4	-0.39	0.4502	0.6713	0	0	0.61	0.3105	0.7509	0	0	-1.00	0.0447	0.3999	0	0
FLYWCH1	FLYWCH1-5	0.10	0.7916	0.8960	0	0	0.32	0.5622	0.8762	0	0	-0.22	0.6496	0.8862	0	0
FLYWCH1	FLYWCH1-6	-0.86	0.0811	0.2134	0	0	-0.31	0.7289	0.9151	0	0	-0.55	0.2726	0.7761	0	0
FOXA1	FOXA1-1	-0.56	0.1355	0.3041	0	0	0.00	0.7848	0.9227	0	0	-0.57	0.1258	0.6068	0	0
FOXA1	FOXA1-2	0.35	0.3492	0.5738	0	0	0.93	0.0452	0.3444	0	0	-0.58	0.1663	0.6679	0	0
FOXA1	FOXA1-3	-0.89	0.0127	0.0546	0	1	-0.48	0.3680	0.7821	0	0	-0.41	0.1720	0.6729	0	0
FOXA1	FOXA1-4	-1.30	0.0005	0.0040	1	1	-0.60	0.1717	0.6276	0	0	-0.70	0.0652	0.4670	0	0
FOXA1	FOXA1-5	0.83	0.0494	0.1499	0	1	0.76	0.1115	0.5295	0	0	0.06	0.7575	0.8862	0	0
FOXA1	FOXA1-6	-0.05	0.8580	0.8984	0	0	-0.40	0.3743	0.7854	0	0	0.36	0.3433	0.8314	0	0
FOXL2	FOXL2-1	-1.92	0.0000	0.0000	1	1	-1.18	0.0277	0.2933	0	0	-0.73	0.0443	0.3999	0	0
FOXL2	FOXL2-2	-0.81	0.0205	0.0790	0	1	-0.72	0.1138	0.5340	0	0	-0.09	0.7643	0.8862	0	0
FOXL2	FOXL2-3	-0.22	0.5669	0.7569	0	0	-0.11	0.8001	0.9227	0	0	-0.11	0.6857	0.8862	0	0
FOXL2	FOXL2-4	-0.83	0.0262	0.0933	0	1	-0.26	0.6618	0.9070	0	0	-0.57	0.1044	0.5708	0	0
FOXL2	FOXL2-5	-1.84	0.0000	0.0005	1	1	-0.99	0.1162	0.5346	0	0	-0.85	0.1170	0.5930	0	0
FOXL2	FOXL2-6	-0.09	0.8035	0.8967	0	0	0.01	0.8446	0.9334	0	0	-0.09	0.6311	0.8862	0	0
FUBP1	FUBP1-1	0.12	0.7224	0.8640	0	0	0.14	0.7245	0.9151	0	0	-0.02	0.7546	0.8862	0	0
FUBP1	FUBP1-2	1.27	0.0216	0.0823	0	1	0.24	0.6864	0.9092	0	0	1.03	0.0538	0.4282	0	0
FUBP1	FUBP1-3	-0.25	0.5584	0.7515	0	0	-0.26	0.5790	0.8818	0	0	0.00	0.8288	0.8862	0	0
FUBP1	FUBP1-4	-0.37	0.3217	0.5415	0	0	-0.30	0.4769	0.8506	0	0	-0.07	0.7919	0.8862	0	0
FUBP1	FUBP1-5	0.15	0.7237	0.8646	0	0	-0.07	0.8804	0.9417	0	0	-0.09	0.7475	0.8862	0	0
FUBP1	FUBP1-6	1.28	0.0543	0.1596	0	1	1.33	0.0731	0.4377	0	0	-0.05	0.8203	0.8862	0	0
FXR1	FXR1-1	0.20	0.6471	0.8175	0	0	0.27	0.5870	0.8849	0	0	-0.07	0.8443	0.8862	0	0
FXR1	FXR1-2	-0.69	0.0550	0.1609	0	1	-0.75	0.1012	0.5089	0	0	0.06	0.8628	0.8872	0	0
FXR1	FXR1-3	0.37	0.3575	0.5810	0	0	1.12	0.0298	0.3036	0	0	-0.75	0.0730	0.4869	0	0
FXR1	FXR1-4	1.25	0.0034	0.0193	1	1	0.94	0.0592	0.3984	0	0	0.31	0.5160	0.8862	0	0
FXR1	FXR1-5	4.42	0.0000	0.0000	1	1	1.57	0.0646	0.4126	0	0	2.85	0.0004	0.0201	1	1
FXR1	FXR1-6	-0.39	0.3314	0.5532	0	0	-0.26	0.5742	0.8791	0	0	-0.13	0.7663	0.8862	0	0
FYTTD1	FYTTD1-1	-0.16	0.7047	0.8554	0	0	-0.09	0.8457	0.9334	0	0	-0.07	0.8692	0.8889	0	0
FYTTD1	FYTTD1-2	-0.55	0.1696	0.3524	0	0	-0.11	0.8554	0.9369	0	0	-0.44	0.2218	0.7398	0	0
FYTTD1	FYTTD1-3	-0.26	0.4872	0.7031	0	0	-0.08	0.8501	0.9336	0	0	-0.18	0.5157	0.8862	0	0
FYTTD1	FYTTD1-4	0.30	0.4909	0.7054	0	0	0.22	0.6212	0.8955	0	0	0.08	0.8646	0.8872	0	0
FYTTD1	FYTTD1-5	-1.18	0.0014	0.0096	1	1	-0.55	0.3291	0.7622	0	0	-0.63	0.2015	0.7138	0	0
FYTTD1	FYTTD1-6	-0.52	0.1767	0.3634	0	0	-0.32	0.5007	0.8538	0	0	-0.21	0.6523	0.8862	0	0
GATA2	GATA2-1	-1.37	0.0003	0.0024	1	1	-0.55	0.2339	0.6957	0	0	-0.82	0.0408	0.3907	0	0
GATA2	GATA2-2	-0.89	0.0180	0.0719	0	1	-0.54	0.2298	0.6920	0	0	-0.35	0.3755	0.8416	0	0
GATA2	GATA2-3	-1.53	0.0001	0.0007	1	1	-0.96	0.1080	0.5236	0	0	-0.58	0.1360	0.6201	0	0
GATA2	GATA2-4	0.40	0.3406	0.5636	0	0	0.98	0.0589	0.3972	0	0	-0.58	0.1688	0.6693	0	0
GATA2	GATA2-5	-0.59	0.1130	0.2704	0	0	-0.33	0.4692	0.8506	0	0	-0.26	0.4193	0.8759	0	0
GATA2	GATA2-6	-3.98	0.0000	0.0000	1	1	-2.20	0.0008	0.0335	1	1	-1.78	0.0001	0.0062	1	1
GATA6	GATA6-1	-0.39	0.3116	0.5295	0	0	-0.49	0.2769	0.7316	0	0	0.10	0.7634	0.8862	0	0
GATA6	GATA6-2	-1.07	0.0059	0.0296	1	1	-0.59	0.2447	0.7028	0	0	-0.47	0.2183	0.7373	0	0
GATA6	GATA6-3	-0.45	0.2106	0.4110	0	0	-0.39	0.4027	0.8096	0	0	-0.07	0.7490	0.8862	0	0
GATA6	GATA6-4	-0.29	0.4407	0.6614	0	0	-0.51	0.2515	0.7043	0	0	0.22	0.6126	0.8862	0	0
GATA6	GATA6-5	-0.69	0.0753	0.2022	0	0	-0.62	0.2065	0.6676	0	0	-0.07	0.7926	0.8862	0	0
GATA6	GATA6-6	0.39	0.3300	0.5516	0	0	0.21	0.6557	0.9051	0	0	0.18	0.6148	0.8862	0	0
GDF3	GDF3-1	0.44	0.2486	0.4594	0	0	0.52	0.2460	0.7029	0	0	-0.08	0.8415	0.8862	0	0
GDF3	GDF3-2	-0.22	0.5416	0.7397	0	0	-0.21	0.5974	0.8878	0	0	-0.01	0.7313	0.8862	0	0
GDF3	GDF3-3	-0.02	0.8771	0.8989	0	0	-0.18	0.6882	0.9092	0	0	0.16	0.6731	0.8862	0	0
GDF3	GDF3-4	-3.27	0.0000	0.0000	1	1	0.05	0.6675	0.9075	0	0	-3.32	0.0000	0.0000	1	1
GDF3	GDF3-5	0.31	0.4187	0.6401	0	0	0.35	0.4515	0.8506	0	0	-0.04	0.7314	0.8862	0	0
GDF3	GDF3-6	-0.37	0.3504	0.5740	0	0	-0.02	0.8542	0.9364	0	0	-0.34	0.3613	0.8319	0	0
GLIS3	GLIS3-1	-0.80	0.0262	0.0933	0	1	-0.19	0.7033	0.9141	0	0	-0.61	0.1479	0.6427	0	0
GLIS3	GLIS3-2	0.41	0.3257	0.5465	0	0	0.47	0.3300	0.7622	0	0	-0.07	0.8068	0.8862	0	0
GLIS3	GLIS3-3	-0.32	0.3836	0.6070	0	0	-0.03	0.9254	0.9485	0	0	-0.29	0.4411	0.8801	0	0
GLIS3	GLIS3-4	-0.23	0.5467	0.7424	0	0	0.45	0.2854	0.7355	0	0	-0.68	0.0779	0.4971	0	0
GLIS3	GLIS3-5	-0.41	0.2632	0.4761	0	0	-0.19	0.6816	0.9091	0	0	-0.21	0.5994	0.8862	0	0
GLIS3	GLIS3-6	-0.50	0.2354	0.4424	0	0	0.08	0.7253	0.9151	0	0	-0.58	0.1303	0.6144	0	0
GMNC	GMNC-1	0.04	0.8331	0.8984	0	0	-0.14	0.7433	0.9170	0	0	0.18	0.7027	0.8862	0	0
GMNC	GMNC-2	-0.71	0.0535	0.1574	0	1	-0.29	0.5685	0.8784	0	0	-0.41	0.3096	0.8058	0	0
GMNC	GMNC-3	-0.06	0.8731	0.8989	0	0	0.13	0.7145	0.9151	0	0	-0.19	0.6368	0.8862	0	0
GMNC	GMNC-4	-0.19	0.6224	0.8024	0	0	0.17	0.6017	0.8878	0	0	-0.36	0.3637	0.8319	0	0
GMNC	GMNC-5	-0.05	0.8792	0.9005	0	0	0.49	0.3383	0.7718	0	0	-0.54	0.2094	0.7274	0	0
GMNC	GMNC-6	-0.86	0.0254	0.0918	0	1	-0.59	0.1977	0.6552	0	0	-0.27	0.5223	0.8862	0	0
GNAS	GNAS-1	-0.65	0.0857	0.2210	0	0	-0.45	0.2963	0.7378	0	0	-0.20	0.5313	0.8862	0	0
GNAS	GNAS-2	-0.60	0.1345	0.3022	0	0	0.00	0.9320	0.9502	0	0	-0.61	0.1099	0.5872	0	0
GNAS	GNAS-3	-0.71	0.0589	0.1695	0	1	-0.10	0.8024	0.9227	0	0	-0.61	0.0996	0.5522	0	0
GNAS	GNAS-4	-1.01	0.0078	0.0366	1	1	-0.48	0.2932	0.7378	0	0	-0.53	0.2210	0.7398	0	0
GNAS	GNAS-5	-0.71	0.0699	0.1918	0	1	-0.32	0.5743	0.8791	0	0	-0.39	0.2252	0.7405	0	0
GNAS	GNAS-6	0.45	0.2597	0.4714	0	0	0.17	0.6705	0.9075	0	0	0.28	0.5367	0.8862	0	0
GNB4	GNB4-1	0.28	0.5021	0.7126	0	0	0.00	0.8972	0.9420	0	0	0.29	0.5080	0.8862	0	0
GNB4	GNB4-2	-0.84	0.0329	0.1095	0	1	-0.68	0.1430	0.5821	0	0	-0.16	0.6512	0.8862	0	0
GNB4	GNB4-3	0.10	0.7813	0.8938	0	0	0.30	0.4992	0.8536	0	0	-0.20	0.5833	0.8862	0	0
GNB4	GNB4-4	-0.41	0.3458	0.5705	0	0	-0.24	0.6557	0.9051	0	0	-0.16	0.6411	0.8862	0	0
GNB4	GNB4-5	-0.07	0.0680	0.1878	0	1	0.23	0.7095	0.9142	0	0	-0.90	0.0272	0.3091	0	0
GNB4	GNB4-6	-0.65	0.8738	0.8989	0	0	0.14	0.7345	0.9167	0	0	-0.19	0.5972	0.8862	0	0
GP5	GP5-1	-0.64	0.0877	0.2250	0	0	-0.17	0.7475	0.9177	0	0	-0.47	0.2016	0.7138	0	0
GP5	GP5-2	0.22	0.5947	0.7778	0	0	0.13	0.7383	0.9167	0	0	0.09	0.8196	0.8862	0	0
GP5	GP5-3	-0.07	0.8613	0.8984	0	0	0									

HES1	HES1-5	-0.16	0.7234	0.8646	0	0	-0.07	0.8769	0.9417	0	0	-0.09	0.8050	0.8862	0	0
HES1	HES1-6	-1.18	0.0012	0.0083	1	1	-0.89	0.0595	0.3989	0	0	-0.29	0.2927	0.7918	0	0
HES6	HES6-1	-0.49	0.1915	0.3852	0	0	0.24	0.5717	0.8785	0	0	-0.73	0.0332	0.3463	0	0
HES6	HES6-2	-1.44	0.0001	0.0008	1	1	-0.96	0.0303	0.3058	0	0	-0.47	0.2206	0.7398	0	0
HES6	HES6-3	-1.07	0.0027	0.0157	1	1	-0.73	0.1109	0.5280	0	0	-0.34	0.3144	0.8135	0	0
HES6	HES6-4	-0.45	0.2382	0.4451	0	0	-0.07	0.7944	0.9227	0	0	-0.38	0.3254	0.8243	0	0
HES6	HES6-5	-1.18	0.0012	0.0082	1	1	-0.74	0.0972	0.4995	0	0	-0.44	0.2278	0.7410	0	0
HES6	HES6-6	-0.31	0.4116	0.6347	0	0	-0.26	0.5612	0.8762	0	0	-0.05	0.8317	0.8862	0	0
HEYL	HEYL-1	-1.41	0.0001	0.0010	1	1	-0.56	0.3224	0.7592	0	0	-0.85	0.0493	0.4157	0	0
HEYL	HEYL-2	-0.34	0.4022	0.6244	0	0	-0.13	0.8094	0.9227	0	0	-0.21	0.5569	0.8862	0	0
HEYL	HEYL-3	-0.04	0.8512	0.8984	0	0	0.03	0.9316	0.9502	0	0	-0.07	0.7576	0.8862	0	0
HEYL	HEYL-4	-1.78	0.0000	0.0002	1	1	-1.09	0.0344	0.3197	0	0	-0.70	0.1078	0.5828	0	0
HEYL	HEYL-5	-1.67	0.0001	0.0010	1	1	-1.31	0.0144	0.2049	0	0	-0.36	0.4209	0.8761	0	0
HEYL	HEYL-6	0.14	0.7404	0.8744	0	0	1.10	0.0354	0.3197	0	0	-0.97	0.0286	0.3197	0	0
HOXB13	HOXB13-1	-0.76	0.1219	0.2844	0	0	-0.52	0.4919	0.8506	0	0	-0.24	0.4438	0.8807	0	0
HOXB13	HOXB13-2	-2.55	0.0000	0.0000	1	1	-2.04	0.0003	0.0223	1	1	-0.51	0.2505	0.7554	0	0
HOXB13	HOXB13-3	-1.90	0.0000	0.0001	1	1	-0.70	0.1858	0.6431	0	0	-1.20	0.0047	0.1109	0	1
HOXB13	HOXB13-4	0.49	0.2981	0.5126	0	0	0.20	0.8035	0.9227	0	0	0.29	0.4944	0.8862	0	0
HOXB13	HOXB13-5	0.12	0.7697	0.8851	0	0	0.02	0.7244	0.9151	0	0	0.10	0.7354	0.8862	0	0
HOXB13	HOXB13-6	-1.37	0.0004	0.0035	1	1	-1.33	0.0058	0.1356	0	1	-0.04	0.7979	0.8862	0	0
HPCAL4	HPCAL4-1	-1.20	0.0011	0.0076	1	1	-1.06	0.0216	0.2565	0	0	-0.14	0.6625	0.8862	0	0
HPCAL4	HPCAL4-2	-1.42	0.0008	0.0058	1	1	-1.00	0.0600	0.4013	0	0	-0.42	0.3247	0.8243	0	0
HPCAL4	HPCAL4-3	-0.41	0.2752	0.4899	0	0	-0.12	0.7655	0.9227	0	0	-0.29	0.4462	0.8819	0	0
HPCAL4	HPCAL4-4	0.87	0.1602	0.3406	0	0	2.02	0.0038	0.1044	0	1	-1.15	0.0280	0.3147	0	0
HPCAL4	HPCAL4-5	-0.89	0.0250	0.0908	0	1	-0.58	0.2139	0.6782	0	0	-0.31	0.4287	0.8764	0	0
HPCAL4	HPCAL4-6	3.58	0.0000	0.0001	1	1	2.75	0.0012	0.0454	1	1	0.83	0.2322	0.7476	0	0
HRASL5	HRASL5-1	-1.55	0.0000	0.0006	1	1	-0.83	0.0758	0.4465	0	0	-0.71	0.0668	0.4675	0	0
HRASL5	HRASL5-2	0.05	0.8011	0.8966	0	0	0.00	0.9266	0.9485	0	0	0.05	0.8191	0.8862	0	0
HRASL5	HRASL5-3	-0.61	0.1206	0.2823	0	0	-0.51	0.3407	0.7741	0	0	-0.10	0.6626	0.8862	0	0
HRASL5	HRASL5-4	-0.34	0.3496	0.5738	0	0	-0.21	0.6462	0.9022	0	0	-0.14	0.6984	0.8862	0	0
HRASL5	HRASL5-5	-1.18	0.0022	0.0133	1	1	-1.06	0.0310	0.3066	0	0	-0.12	0.6605	0.8862	0	0
HRASL5	HRASL5-6	-0.83	0.0273	0.0962	0	1	-0.52	0.2883	0.7360	0	0	-0.31	0.4749	0.8862	0	0
HRG	HRG-1	-0.78	0.0653	0.1821	0	1	-0.91	0.0752	0.4454	0	0	0.13	0.8298	0.8862	0	0
HRG	HRG-2	0.29	0.4215	0.6431	0	0	1.22	0.0119	0.1940	0	1	-0.93	0.0260	0.3068	0	0
HRG	HRG-3	-0.48	0.2202	0.4223	0	0	-0.01	0.7954	0.9227	0	0	-0.47	0.2698	0.7751	0	0
HRG	HRG-4	-0.66	0.0910	0.2308	0	0	-0.67	0.1439	0.5848	0	0	0.01	0.8320	0.8862	0	0
HRG	HRG-5	-0.17	0.7121	0.8594	0	0	-0.02	0.6312	0.8955	0	0	-0.16	0.5237	0.8862	0	0
HRG	HRG-6	-0.99	0.0123	0.0535	0	1	-0.11	0.7646	0.9227	0	0	-0.88	0.0442	0.3999	0	0
ID1	ID1-1	-1.41	0.0001	0.0013	1	1	-0.92	0.0446	0.3428	0	0	-0.49	0.1928	0.7025	0	0
ID1	ID1-2	-1.29	0.0011	0.0080	1	1	-1.04	0.0345	0.3197	0	0	-0.25	0.5460	0.8862	0	0
ID1	ID1-3	0.11	0.7951	0.8960	0	0	0.31	0.5377	0.8699	0	0	-0.20	0.6021	0.8862	0	0
ID1	ID1-4	0.30	0.4382	0.6590	0	0	0.58	0.2215	0.6841	0	0	-0.28	0.4819	0.8862	0	0
ID1	ID1-5	-0.38	0.3502	0.5740	0	0	-0.03	0.8433	0.9334	0	0	-0.35	0.3853	0.8468	0	0
ID1	ID1-6	0.09	0.8082	0.8984	0	0	0.24	0.6045	0.8878	0	0	-0.15	0.7876	0.8862	0	0
IGF2BP2	IGF2BP2-1	-0.16	0.6722	0.8373	0	0	-0.12	0.7917	0.9227	0	0	-0.04	0.7515	0.8862	0	0
IGF2BP2	IGF2BP2-2	0.17	0.6539	0.8239	0	0	0.54	0.2825	0.7355	0	0	-0.36	0.3601	0.8319	0	0
IGF2BP2	IGF2BP2-3	-3.02	0.0000	0.0000	1	1	-2.00	0.0032	0.0937	0	1	-1.02	0.0271	0.3091	0	0
IGF2BP2	IGF2BP2-4	-2.17	0.0000	0.0000	1	1	-0.98	0.0742	0.4414	0	0	-1.19	0.0073	0.1509	0	1
IGF2BP2	IGF2BP2-5	-1.84	0.0000	0.0001	1	1	-0.84	0.1422	0.5810	0	0	-1.00	0.0133	0.2219	0	0
IGF2BP2	IGF2BP2-6	-0.01	0.8671	0.8986	0	0	0.58	0.1474	0.5940	0	0	-0.59	0.0800	0.5068	0	0
IL1RAP	IL1RAP-1	-0.43	0.2749	0.4897	0	0	0.13	0.7365	0.9167	0	0	-0.56	0.1418	0.6362	0	0
IL1RAP	IL1RAP-2	0.05	0.9059	0.9112	0	0	0.88	0.1339	0.5623	0	0	-0.93	0.0601	0.4538	0	0
IL1RAP	IL1RAP-3	-0.15	0.7112	0.8591	0	0	0.02	0.9240	0.9485	0	0	0.13	0.8143	0.8862	0	0
IL1RAP	IL1RAP-4	-0.02	0.8709	0.8989	0	0	0.43	0.5039	0.8547	0	0	-0.45	0.3236	0.8243	0	0
IL1RAP	IL1RAP-5	0.32	0.4093	0.6329	0	0	0.28	0.5433	0.8702	0	0	0.05	0.8508	0.8871	0	0
IL1RAP	IL1RAP-6	-0.30	0.4528	0.6733	0	0	-0.17	0.6923	0.9092	0	0	-0.13	0.6874	0.8862	0	0
IL7R	IL7R-1	0.19	0.6283	0.8053	0	0	0.17	0.7069	0.9141	0	0	0.03	0.7280	0.8862	0	0
IL7R	IL7R-2	-0.42	0.2896	0.5039	0	0	-0.16	0.7385	0.9167	0	0	-0.27	0.5293	0.8862	0	0
IL7R	IL7R-3	-0.46	0.2415	0.4489	0	0	-0.56	0.2095	0.6694	0	0	0.09	0.9035	0.9054	0	0
IL7R	IL7R-4	1.13	0.0037	0.0208	1	1	0.65	0.1508	0.6006	0	0	0.48	0.1657	0.6679	0	0
IL7R	IL7R-5	1.01	0.0170	0.0686	0	1	1.04	0.0286	0.3002	0	0	-0.03	0.7553	0.8862	0	0
IL7R	IL7R-6	-0.99	0.0091	0.0414	1	1	-0.25	0.5998	0.8878	0	0	-0.74	0.0472	0.4091	0	0
ING1	ING1-1	0.11	0.8220	0.8984	0	0	0.56	0.2542	0.7043	0	0	-0.45	0.2608	0.7659	0	0
ING1	ING1-2	-0.39	0.2929	0.5081	0	0	-0.10	0.8117	0.9227	0	0	-0.28	0.4610	0.8862	0	0
ING1	ING1-3	-2.22	0.0000	0.0000	1	1	-1.89	0.0004	0.0247	1	1	-0.33	0.4201	0.8761	0	0
ING1	ING1-4	-0.82	0.0320	0.1077	0	1	-0.57	0.2220	0.6841	0	0	-0.26	0.5033	0.8862	0	0
ING1	ING1-5	-0.96	0.0295	0.1011	0	1	-0.77	0.1404	0.5770	0	0	-0.19	0.6200	0.8862	0	0
ING1	ING1-6	-0.63	0.1024	0.2509	0	0	-0.40	0.3750	0.7854	0	0	-0.23	0.4954	0.8862	0	0
INSL4	INSL4-1	-0.63	0.1457	0.3183	0	0	0.03	0.7885	0.9227	0	0	-0.67	0.1051	0.5721	0	0
INSL4	INSL4-2	-1.37	0.0015	0.0097	1	1	-0.73	0.1746	0.6318	0	0	-0.64	0.1123	0.5872	0	0
INSL4	INSL4-3	-0.88	0.0443	0.1378	0	0	-0.17	0.7288	0.9151	0	0	-0.71	0.1308	0.6144	0	0
INSL4	INSL4-4	-0.97	0.0164	0.0669	0	1	-0.84	0.1665	0.6208	0	0	-0.13	0.6404	0.8862	0	0
INSL4	INSL4-5	-0.12	0.7580	0.8791	0	0	0.30	0.4831	0.8506	0	0	-0.42	0.2254	0.7405	0	0
INSL4	INSL4-6	0.21	0.5914	0.7757	0	0	0.03	0.8117	0.9227	0	0	0.18	0.7034	0.8862	0	0
INSL6	INSL6-1	-1.07	0.0083	0.0387	1	1	-0.95	0.0608	0.4031	0	0	-0.12	0.4884	0.8862	0	0
INSL6	INSL6-2	-0.21	0.5813	0.7676	0	0	0.11	0.8107	0.9227	0	0	-0.32	0.4114	0.8671	0	0
INSL6	INSL6-3	0.11	0.8247	0.8984	0	0	0.40	0.3693	0.7821	0	0	-0.29	0.4043	0.8598	0	0
INSL6	INSL6-4	0.15	0.7225	0.8640	0	0	-0.07	0.7256	0.9151	0	0	0.22	0.6427	0.8862	0	0
INSL6	INSL6-5	-0.91	0.0118	0.0514	0	1	-0.67	0.1302	0.5516	0	0	-0.24	0.4501	0.8851	0	0
INSL6	INSL6-6	0.31	0.4170	0.6387	0	0	0.32	0.3888	0.7977	0	0	0.00	0.7363	0.8862	0	0
INSM1	INSM1-1	-0.71	0.0568	0.1650	0	1	-0.50	0.2324	0.6934	0	0	-0.21	0.6484	0.8862	0	0
INSM1	INSM1-2	0.60	0.1660	0.3483	0	0										

JAG2	JAG2-4	-1.69	0.0000	0.0004	1	1	-1.04	0.0387	0.3308	0	0	-0.66	0.1474	0.6427	0	0
JAG2	JAG2-5	-2.97	0.0000	0.0000	1	1	-1.03	0.0889	0.4788	0	0	-1.94	0.0000	0.0012	1	1
JAG2	JAG2-6	-1.13	0.0060	0.0300	1	1	-0.68	0.1678	0.6218	0	0	-0.46	0.2505	0.7554	0	0
JAK2	JAK2-1	-1.60	0.0019	0.0118	1	1	1.41	0.0158	0.2156	0	0	0.19	0.5172	0.8862	0	0
JAK2	JAK2-2	-1.52	0.0000	0.0005	1	1	-1.11	0.0315	0.3106	0	0	-0.41	0.3071	0.8034	0	0
JAK2	JAK2-3	0.09	0.8095	0.8984	0	0	0.03	0.8949	0.9418	0	0	0.05	0.7984	0.8862	0	0
JAK2	JAK2-4	-0.13	0.7451	0.8763	0	0	0.09	0.8168	0.9245	0	0	-0.22	0.5387	0.8862	0	0
JAK2	JAK2-5	-0.55	0.1518	0.3278	0	0	-0.61	0.1553	0.6036	0	0	0.06	0.6944	0.8862	0	0
JAK2	JAK2-6	-1.26	0.0043	0.0233	1	1	-0.64	0.2450	0.7028	0	0	-0.63	0.1508	0.6504	0	0
KAT6A	KAT6A-1	-0.03	0.8434	0.8984	0	0	-0.12	0.7586	0.9200	0	0	0.10	0.8845	0.8953	0	0
KAT6A	KAT6A-2	-0.53	0.1846	0.3756	0	0	-0.12	0.8438	0.9334	0	0	-0.41	0.3450	0.8314	0	0
KAT6A	KAT6A-3	-0.51	0.2036	0.4015	0	0	-0.42	0.3744	0.7854	0	0	-0.09	0.8094	0.8862	0	0
KAT6A	KAT6A-4	-0.28	0.4596	0.6792	0	0	-0.28	0.5444	0.8702	0	0	0.00	0.8897	0.8980	0	0
KAT6A	KAT6A-5	0.50	0.1920	0.3853	0	0	1.01	0.0514	0.3663	0	0	-0.51	0.1823	0.6875	0	0
KAT6A	KAT6A-6	-0.99	0.0107	0.0473	1	1	-0.14	0.8076	0.9227	0	0	-0.86	0.0454	0.4025	0	0
KCNMB2	KCNMB2-1	0.06	0.8540	0.8984	0	0	0.29	0.4944	0.8506	0	0	-0.23	0.5067	0.8862	0	0
KCNMB2	KCNMB2-2	-0.53	0.1373	0.3072	0	0	-0.46	0.3059	0.7473	0	0	-0.07	0.7862	0.8862	0	0
KCNMB2	KCNMB2-3	-0.02	0.8729	0.8989	0	0	0.00	0.8444	0.9334	0	0	-0.02	0.6837	0.8862	0	0
KCNMB2	KCNMB2-4	1.03	0.0839	0.2192	0	0	1.13	0.1020	0.5100	0	0	-0.10	0.7245	0.8862	0	0
KCNMB2	KCNMB2-5	0.12	0.7690	0.8847	0	0	0.17	0.7012	0.9141	0	0	-0.06	0.8072	0.8862	0	0
KCNMB2	KCNMB2-6	0.08	0.8307	0.8984	0	0	0.41	0.3058	0.7473	0	0	-0.33	0.2879	0.7917	0	0
KCNMB3	KCNMB3-1	0.54	0.1705	0.3537	0	0	0.97	0.0243	0.2708	0	0	-0.43	0.2611	0.7659	0	0
KCNMB3	KCNMB3-2	-1.07	0.0123	0.0535	0	1	-0.65	0.1890	0.6454	0	0	-0.42	0.3222	0.8233	0	0
KCNMB3	KCNMB3-3	-0.61	0.1193	0.2800	0	0	-0.28	0.5714	0.8785	0	0	-0.34	0.3547	0.8319	0	0
KCNMB3	KCNMB3-4	-0.40	0.3623	0.5852	0	0	1.71	0.0046	0.1161	0	1	-2.11	0.0000	0.0008	1	1
KCNMB3	KCNMB3-5	-0.79	0.0417	0.1308	0	1	-0.52	0.2880	0.7360	0	0	-0.27	0.4705	0.8862	0	0
KCNMB3	KCNMB3-6	0.14	0.7540	0.8779	0	0	0.11	0.7720	0.9227	0	0	0.03	0.8443	0.8867	0	0
KDM5A	KDM5A-1	0.02	0.8611	0.8984	0	0	0.48	0.2920	0.7378	0	0	-0.46	0.2721	0.7761	0	0
KDM5A	KDM5A-2	0.24	0.6051	0.7867	0	0	0.68	0.1693	0.6245	0	0	-0.44	0.2247	0.7405	0	0
KDM5A	KDM5A-3	-0.56	0.1453	0.3177	0	0	0.02	0.8100	0.9227	0	0	-0.57	0.1602	0.6624	0	0
KDM5A	KDM5A-4	0.10	0.8006	0.8966	0	0	4.01	0.0000	0.0020	1	1	-3.91	0.0000	0.0000	1	1
KDM5A	KDM5A-5	0.06	0.8303	0.8984	0	0	1.30	0.0256	0.2809	0	0	-1.24	0.0097	0.1809	0	1
KDM5A	KDM5A-6	0.19	0.6176	0.7991	0	0	-0.17	0.7199	0.9151	0	0	0.36	0.3898	0.8491	0	0
KDR	KDR-1	-0.58	0.2249	0.4297	0	0	-0.27	0.6335	0.8955	0	0	-0.31	0.4921	0.8862	0	0
KDR	KDR-2	-1.10	0.0077	0.0364	1	1	-0.91	0.0726	0.4364	0	0	-0.20	0.6253	0.8862	0	0
KDR	KDR-3	-1.92	0.0000	0.0000	1	1	-0.77	0.1228	0.5405	0	0	-1.15	0.0042	0.1049	0	1
KDR	KDR-4	-1.05	0.0081	0.0379	1	1	-0.16	0.8079	0.9227	0	0	-0.89	0.0473	0.4091	0	0
KDR	KDR-5	-0.08	0.8021	0.8966	0	0	-0.12	0.7534	0.9188	0	0	0.20	0.6039	0.8862	0	0
KDR	KDR-6	0.08	0.8957	0.9070	0	0	-0.03	0.7658	0.9227	0	0	-0.05	0.6986	0.8862	0	0
KIT	KIT-1	0.26	0.5495	0.7443	0	0	0.66	0.1248	0.5405	0	0	-0.40	0.2425	0.7554	0	0
KIT	KIT-2	-0.50	0.1788	0.3665	0	0	-0.31	0.4845	0.8506	0	0	-0.18	0.6651	0.8862	0	0
KIT	KIT-3	-0.74	0.0619	0.1757	0	1	-0.54	0.2635	0.7185	0	0	-0.20	0.5796	0.8862	0	0
KIT	KIT-4	-0.33	0.4000	0.6214	0	0	-0.15	0.7533	0.9188	0	0	-0.18	0.5467	0.8862	0	0
KIT	KIT-5	-2.03	0.0000	0.0000	1	1	-1.40	0.0104	0.1790	0	1	-0.63	0.1251	0.6068	0	0
KIT	KIT-6	-0.70	0.0627	0.1772	0	1	-0.13	0.7948	0.9227	0	0	-0.57	0.0922	0.5369	0	0
KLHL24	KLHL24-1	-0.18	0.6454	0.8166	0	0	2.21	0.0004	0.0249	1	1	-2.38	0.0000	0.0002	1	1
KLHL24	KLHL24-2	-0.91	0.0155	0.0642	0	1	-0.22	0.5978	0.8878	0	0	-0.69	0.0553	0.4342	0	0
KLHL24	KLHL24-3	-0.08	0.8505	0.8984	0	0	-0.11	0.8461	0.9334	0	0	0.03	0.7472	0.8862	0	0
KLHL24	KLHL24-4	-0.13	0.7481	0.8764	0	0	-0.06	0.8739	0.9417	0	0	-0.07	0.8178	0.8862	0	0
KLHL24	KLHL24-5	-2.49	0.0000	0.0000	1	1	-1.65	0.0014	0.0508	0	1	-0.83	0.0357	0.3575	0	0
KLHL24	KLHL24-6	-0.79	0.0323	0.1080	0	1	-0.60	0.1920	0.6492	0	0	-0.19	0.5659	0.8862	0	0
KLHL42	KLHL42-1	-0.67	0.0586	0.1690	0	1	-0.54	0.2430	0.7028	0	0	-0.13	0.6827	0.8862	0	0
KLHL42	KLHL42-2	-1.21	0.0010	0.0070	1	1	-0.71	0.1129	0.5322	0	0	-0.50	0.1967	0.7082	0	0
KLHL42	KLHL42-3	-1.16	0.0018	0.0117	1	1	-0.46	0.3590	0.7812	0	0	-0.69	0.0691	0.4709	0	0
KLHL42	KLHL42-4	-1.04	0.0039	0.0216	1	1	-0.80	0.0701	0.4296	0	0	-0.24	0.5268	0.8862	0	0
KLHL42	KLHL42-5	-0.47	0.2128	0.4138	0	0	-0.29	0.4955	0.8506	0	0	-0.18	0.6097	0.8862	0	0
KLHL42	KLHL42-6	-2.36	0.0000	0.0000	1	1	-1.58	0.0043	0.1116	0	1	-0.78	0.0837	0.5114	0	0
KLHL6	KLHL6-1	-0.56	0.1464	0.3194	0	0	-0.24	0.6196	0.8955	0	0	-0.32	0.3689	0.8381	0	0
KLHL6	KLHL6-2	-0.70	0.1332	0.3009	0	0	-2.20	0.0007	0.0319	1	1	1.49	0.0146	0.2319	0	0
KLHL6	KLHL6-3	-0.44	0.2556	0.4668	0	0	-0.62	0.2744	0.7313	0	0	0.18	0.7340	0.8862	0	0
KLHL6	KLHL6-4	0.24	0.5192	0.7256	0	0	0.12	0.7516	0.9184	0	0	0.12	0.5383	0.8862	0	0
KLHL6	KLHL6-5	-0.82	0.0309	0.1048	0	1	-0.58	0.2118	0.6753	0	0	-0.24	0.5494	0.8862	0	0
KLHL6	KLHL6-6	-0.16	0.7086	0.8589	0	0	0.09	0.8280	0.9287	0	0	-0.25	0.4980	0.8862	0	0
KMT2B	KMT2B-1	0.34	0.4820	0.6998	0	0	1.05	0.0986	0.5010	0	0	-0.71	0.1744	0.6790	0	0
KMT2B	KMT2B-2	0.11	0.7658	0.8837	0	0	0.03	0.8917	0.9418	0	0	0.09	0.8840	0.8953	0	0
KMT2B	KMT2B-3	-0.39	0.2979	0.5126	0	0	0.08	0.8485	0.9336	0	0	-0.47	0.1712	0.6718	0	0
KMT2B	KMT2B-4	0.23	0.5560	0.7503	0	0	0.32	0.4717	0.8506	0	0	-0.08	0.7275	0.8862	0	0
KMT2B	KMT2B-5	1.23	0.0024	0.0149	1	1	1.15	0.7432	0.9170	0	0	1.09	0.0164	0.2485	0	0
KMT2B	KMT2B-6	-2.30	0.0000	0.0000	1	1	-1.27	0.0164	0.2207	0	0	-1.03	0.0132	0.2219	0	0
KNG1	KNG1-1	0.79	0.0473	0.1448	0	1	0.41	0.3583	0.7812	0	0	0.38	0.3396	0.8301	0	0
KNG1	KNG1-2	0.50	0.2484	0.4594	0	0	2.09	0.0000	0.0027	1	1	-1.59	0.0000	0.0005	1	1
KNG1	KNG1-3	0.30	0.3631	0.5858	0	0	0.31	0.4896	0.8506	0	0	-0.01	0.8096	0.8862	0	0
KNG1	KNG1-4	0.63	0.0958	0.2383	0	0	0.36	0.4068	0.8157	0	0	0.27	0.5140	0.8862	0	0
KNG1	KNG1-5	-0.53	0.2350	0.4424	0	0	-0.35	0.5039	0.8547	0	0	-0.18	0.6856	0.8862	0	0
KNG1	KNG1-6	0.23	0.5393	0.7383	0	0	0.30	0.5256	0.8653	0	0	-0.06	0.8925	0.8992	0	0
KRAS	KRAS-1	-0.70	0.0521	0.1552	0	1	-0.36	0.4473	0.8479	0	0	-0.34	0.3097	0.8058	0	0
KRAS	KRAS-2	0.59	0.0999	0.2463	0	0	0.23	0.5810	0.8818	0	0	0.37	0.3170	0.8149	0	0
KRAS	KRAS-3	-0.92	0.0134	0.0562	0	1	-0.58	0.2198	0.6841	0	0	-0.35	0.4005	0.8592	0	0
KRAS	KRAS-4	-0.15	0.7547	0.8782	0	0	0.42	0.3580	0.7812	0	0	-0.56	0.1416	0.6362	0	0
KRAS	KRAS-5	0.15	0.7094	0.8589	0	0	0.21	0.6155	0.8955	0	0	-0.06	0.7314	0.8862	0	0
KRAS	KRAS-6	-0.15	0.6973	0.8495	0	0	-0.20	0.6333	0.8955	0	0	0.05	0.8482	0.8862	0	0
LAMP3	LAMP3-1	-0.83	0.0192	0.0751	0	1	-0.84	0.0548	0.3774	0	0	0.01				

LMLN	LMLN-3	-0.28	0.5764	0.7637	0	0	0.40	0.5810	0.8818	0	0	-0.68	0.2556	0.7586	0	0
LMLN	LMLN-4	3.19	0.0000	0.0004	1	1	1.30	0.0805	0.4602	0	0	1.88	0.0063	0.1370	0	1
LMLN	LMLN-5	0.52	0.1865	0.3787	0	0	0.00	0.8355	0.9312	0	0	0.52	0.2119	0.7289	0	0
LMLN	LMLN-6	0.56	0.1388	0.3085	0	0	0.77	0.0802	0.4602	0	0	-0.21	0.4982	0.8862	0	0
LPP	LPP-1	-0.18	0.6739	0.8378	0	0	0.05	0.7252	0.9151	0	0	-0.23	0.7083	0.8862	0	0
LPP	LPP-2	-0.27	0.4860	0.7031	0	0	0.20	0.6260	0.8955	0	0	-0.47	0.1805	0.6871	0	0
LPP	LPP-3	0.62	0.1159	0.2756	0	0	0.62	0.1775	0.6354	0	0	0.00	0.7178	0.8862	0	0
LPP	LPP-4	-0.73	0.0509	0.1529	0	1	-0.59	0.1949	0.6525	0	0	-0.15	0.6617	0.8862	0	0
LPP	LPP-5	-0.79	0.0401	0.1272	0	1	-0.50	0.2524	0.7043	0	0	-0.29	0.5258	0.8862	0	0
LPP	LPP-6	-0.98	0.0094	0.0425	1	1	-0.58	0.2055	0.6676	0	0	-0.39	0.3253	0.8243	0	0
LRCH3	LRCH3-1	1.18	0.0039	0.0213	1	1	1.19	0.0125	0.1961	0	1	-0.02	0.8203	0.8862	0	0
LRCH3	LRCH3-2	-0.19	0.6376	0.8117	0	0	-0.30	0.5406	0.8699	0	0	0.11	0.7891	0.8862	0	0
LRCH3	LRCH3-3	-0.25	0.5118	0.7199	0	0	-0.03	0.9312	0.9502	0	0	-0.23	0.5751	0.8862	0	0
LRCH3	LRCH3-4	-0.15	0.7195	0.8617	0	0	0.33	0.4266	0.8341	0	0	-0.48	0.1676	0.6693	0	0
LRCH3	LRCH3-5	-0.26	0.4860	0.7031	0	0	-0.21	0.6312	0.8955	0	0	-0.05	0.7892	0.8862	0	0
LRCH3	LRCH3-6	-0.10	0.7886	0.8952	0	0	0.01	0.9545	0.9585	0	0	-0.11	0.7275	0.8862	0	0
LRRC15	LRRC15-1	0.18	0.6063	0.7868	0	0	0.08	0.8626	0.9406	0	0	0.11	0.7765	0.8862	0	0
LRRC15	LRRC15-2	-0.04	0.8716	0.8989	0	0	0.78	0.1897	0.6462	0	0	-0.82	0.0941	0.5415	0	0
LRRC15	LRRC15-3	-0.52	0.1829	0.3727	0	0	-0.34	0.4664	0.8506	0	0	-0.19	0.5883	0.8862	0	0
LRRC15	LRRC15-4	-0.15	0.6995	0.8517	0	0	-0.19	0.6598	0.9070	0	0	0.05	0.8634	0.8872	0	0
LRRC15	LRRC15-5	-0.16	0.7109	0.8591	0	0	0.07	0.8009	0.9227	0	0	-0.23	0.5682	0.8862	0	0
LRRC15	LRRC15-6	0.50	0.2119	0.4125	0	0	0.36	0.4243	0.8341	0	0	0.15	0.7856	0.8862	0	0
LRRFIP1	LRRFIP1-1	0.93	0.0358	0.1176	0	1	1.30	0.0220	0.2578	0	0	-0.38	0.3838	0.8463	0	0
LRRFIP1	LRRFIP1-2	3.41	0.0000	0.0000	1	1	2.73	0.0000	0.0045	1	1	0.69	0.2522	0.7554	0	0
LRRFIP1	LRRFIP1-3	0.07	0.8644	0.8986	0	0	0.52	0.3751	0.7854	0	0	-0.45	0.3483	0.8319	0	0
LRRFIP1	LRRFIP1-4	-0.29	0.5535	0.7478	0	0	-0.04	0.8184	0.9252	0	0	-0.25	0.5754	0.8862	0	0
LRRFIP1	LRRFIP1-5	-0.68	0.2410	0.4489	0	0	-0.38	0.5648	0.8770	0	0	-0.30	0.6383	0.8862	0	0
LRRFIP1	LRRFIP1-6	-0.46	0.3536	0.5773	0	0	0.04	0.8104	0.9227	0	0	-0.50	0.3279	0.8250	0	0
LSG1	LSG1-1	-0.22	0.5580	0.7513	0	0	0.12	0.7607	0.9202	0	0	-0.34	0.3361	0.8301	0	0
LSG1	LSG1-2	-0.76	0.0585	0.1690	0	1	-0.45	0.3617	0.7812	0	0	-0.31	0.4627	0.8862	0	0
LSG1	LSG1-3	0.28	0.4749	0.6915	0	0	0.33	0.4596	0.8506	0	0	-0.05	0.5847	0.8862	0	0
LSG1	LSG1-4	0.86	0.0652	0.1821	0	1	1.19	0.0272	0.2924	0	0	-0.33	0.3763	0.8421	0	0
LSG1	LSG1-5	-0.51	0.1667	0.3484	0	0	-0.30	0.5077	0.8580	0	0	-0.21	0.5672	0.8862	0	0
LSG1	LSG1-6	-1.95	0.0000	0.0004	1	1	-0.72	0.2248	0.6866	0	0	-1.23	0.0094	0.1780	0	1
LYN	LYN-1	-1.34	0.0004	0.0035	1	1	-1.13	0.0195	0.2423	0	0	-0.22	0.5700	0.8862	0	0
LYN	LYN-2	-0.20	0.6265	0.8044	0	0	-0.28	0.5449	0.8702	0	0	0.07	0.7532	0.8862	0	0
LYN	LYN-3	-1.27	0.0006	0.0050	1	1	-0.28	0.6854	0.9092	0	0	-0.99	0.0052	0.1191	0	1
LYN	LYN-4	-0.57	0.1382	0.3078	0	0	-0.21	0.6643	0.9073	0	0	-0.36	0.3637	0.8319	0	0
LYN	LYN-5	-1.25	0.0007	0.0056	1	1	-0.90	0.0475	0.3532	0	0	-0.35	0.2764	0.7795	0	0
LYN	LYN-6	-0.36	0.3697	0.5916	0	0	-0.37	0.4360	0.8384	0	0	0.01	0.8403	0.8862	0	0
MACF1	MACF1-1	-0.37	0.3854	0.6083	0	0	1.61	0.0002	0.0200	1	1	-1.98	0.0000	0.0000	1	1
MACF1	MACF1-2	-1.39	0.0004	0.0037	1	1	-0.79	0.0854	0.4723	0	0	-0.59	0.1422	0.6362	0	0
MACF1	MACF1-3	-2.16	0.0000	0.0000	1	1	-1.04	0.0309	0.3066	0	0	-1.12	0.0043	0.1058	0	1
MACF1	MACF1-4	0.09	0.7820	0.8938	0	0	1.36	0.0040	0.1057	0	1	-1.27	0.0007	0.0266	1	1
MACF1	MACF1-5	0.20	0.5883	0.7739	0	0	0.50	0.2512	0.7043	0	0	-0.20	0.4346	0.8764	0	0
MACF1	MACF1-6	-0.79	0.0386	0.1238	0	1	-1.02	0.0275	0.2924	0	0	0.23	0.5042	0.8862	0	0
MAGEF1	MAGEF1-1	-0.42	0.2675	0.4804	0	0	-0.08	0.8786	0.9417	0	0	-0.34	0.2784	0.7803	0	0
MAGEF1	MAGEF1-2	-1.85	0.0000	0.0002	1	1	-1.31	0.0123	0.1940	0	1	-0.55	0.1412	0.6362	0	0
MAGEF1	MAGEF1-3	-0.35	0.3628	0.5856	0	0	0.13	0.7009	0.9141	0	0	-0.48	0.2676	0.7718	0	0
MAGEF1	MAGEF1-4	-0.82	0.0364	0.1190	0	1	-0.30	0.5041	0.8547	0	0	-0.52	0.2065	0.7216	0	0
MAGEF1	MAGEF1-5	-0.28	0.4804	0.6987	0	0	-0.37	0.3927	0.8002	0	0	0.10	0.8384	0.8862	0	0
MAGEF1	MAGEF1-6	-0.65	0.0754	0.2022	0	0	-0.56	0.2042	0.6676	0	0	-0.10	0.8789	0.8923	0	0
MALT1	MALT1-1	-1.07	0.0036	0.0201	1	1	-0.32	0.5485	0.8713	0	0	-0.74	0.0591	0.4531	0	0
MALT1	MALT1-2	-0.72	0.0447	0.1386	0	1	-0.31	0.5197	0.8645	0	0	-0.41	0.2588	0.7631	0	0
MALT1	MALT1-3	0.43	0.3927	0.6152	0	0	1.18	0.0442	0.3428	0	0	-0.75	0.1379	0.6264	0	0
MALT1	MALT1-4	-1.49	0.0000	0.0005	1	1	-1.02	0.0240	0.2696	0	0	-0.47	0.2276	0.7410	0	0
MALT1	MALT1-5	0.17	0.6690	0.8350	0	0	0.18	0.6807	0.9091	0	0	-0.01	0.8635	0.8872	0	0
MALT1	MALT1-6	-0.51	0.1681	0.3500	0	0	-0.53	0.2273	0.6900	0	0	0.02	0.8628	0.8872	0	0
MANSC4	MANSC4-1	-0.35	0.3201	0.5397	0	0	-0.32	0.4914	0.8506	0	0	-0.03	0.8445	0.8867	0	0
MANSC4	MANSC4-2	0.67	0.7368	0.8714	0	0	-0.14	0.7166	0.9151	0	0	0.16	0.5995	0.8862	0	0
MANSC4	MANSC4-3	-0.02	0.0705	0.1927	0	1	-0.28	0.5716	0.8785	0	0	-0.39	0.2854	0.7897	0	0
MANSC4	MANSC4-4	0.54	0.1790	0.3666	0	0	0.26	0.5534	0.8733	0	0	0.28	0.5479	0.8862	0	0
MANSC4	MANSC4-5	0.54	0.1503	0.3259	0	0	0.31	0.4805	0.8506	0	0	0.22	0.5150	0.8862	0	0
MANSC4	MANSC4-6	0.15	0.6880	0.8445	0	0	0.44	0.3038	0.7468	0	0	-0.29	0.4090	0.8649	0	0
MAP2K1	MAP2K1-1	-0.04	0.9212	0.9236	0	0	0.22	0.5638	0.8770	0	0	-0.27	0.3839	0.8463	0	0
MAP2K1	MAP2K1-2	0.80	0.1441	0.3166	0	0	2.78	0.0000	0.0044	1	1	-1.98	0.0000	0.0011	1	1
MAP2K1	MAP2K1-3	-0.17	0.6717	0.8371	0	0	0.19	0.6860	0.9092	0	0	-0.37	0.3390	0.8301	0	0
MAP2K1	MAP2K1-4	2.81	0.0001	0.0015	1	1	1.15	0.2019	0.6640	0	0	1.66	0.0310	0.3360	0	0
MAP2K1	MAP2K1-5	1.85	0.0001	0.0011	1	1	1.75	0.1180	0.5348	0	0	0.09	0.0101	0.1868	0	1
MAP2K1	MAP2K1-6	0.37	0.3368	0.5596	0	0	0.37	0.4099	0.8190	0	0	0.00	0.8554	0.8872	0	0
MAP3K1	MAP3K1-1	-0.34	0.4317	0.6524	0	0	0.73	0.1214	0.5405	0	0	-1.06	0.0027	0.0801	0	1
MAP3K1	MAP3K1-2	-0.64	0.0918	0.2317	0	0	0.00	0.6542	0.9051	0	0	-0.64	0.0982	0.5522	0	0
MAP3K1	MAP3K1-3	-0.89	0.0133	0.0562	0	1	-0.72	0.1087	0.5255	0	0	-0.18	0.6411	0.8862	0	0
MAP3K1	MAP3K1-4	-1.84	0.0000	0.0000	1	1	-1.27	0.0097	0.1705	0	1	-0.57	0.1009	0.5555	0	0
MAP3K1	MAP3K1-5	-0.80	0.0372	0.1205	0	1	-0.20	0.6305	0.8955	0	0	-0.60	0.1701	0.6707	0	0
MAP3K1	MAP3K1-6	-0.89	0.0159	0.0650	0	1	-0.34	0.4011	0.8096	0	0	-0.55	0.1326	0.6151	0	0
MAP3K13	MAP3K13-1	-0.27	0.4922	0.7060	0	0	0.11	0.8029	0.9227	0	0	-0.39	0.3091	0.8058	0	0
MAP3K13	MAP3K13-2	0.43	0.2641	0.4761	0	0	0.20	0.6676	0.9075	0	0	0.24	0.5727	0.8862	0	0
MAP3K13	MAP3K13-3	1.33	0.0059	0.0296	1	1	1.23	0.0411	0.3348	0	0	0.10	0.3242	0.8243	0	0
MAP3K13	MAP3K13-4	3.62	0.0000	0.0001	1	1	0.88	0.2701	0.7273	0	0	2.74	0.0004	0.0178	1	1
MAP3K13	MAP3K13-5	0.04	0.8455	0.8984	0	0	-0.07	0.9101	0.9467	0	0	0.11	0.8508	0.8871	0	0
MAP3K13	MAP3K13-6</															

MAX	MAX-2	-0.81	0.0514	0.1539	0	1	-0.52	0.3110	0.7513	0	0	-0.28	0.4495	0.8849	0	0
MAX	MAX-3	-0.23	0.5804	0.7672	0	0	0.18	0.6471	0.9022	0	0	-0.42	0.2669	0.7718	0	0
MAX	MAX-4	-1.00	0.0066	0.0325	1	1	-0.69	0.1321	0.5559	0	0	-0.31	0.4017	0.8298	0	0
MAX	MAX-5	-2.17	0.0000	0.0000	1	1	-0.93	0.1221	0.5405	0	0	-1.24	0.0204	0.2807	0	0
MAX	MAX-6	0.58	0.1383	0.3078	0	0	0.42	0.3664	0.7821	0	0	0.16	0.7048	0.8862	0	0
MB21D2	MB21D2-1	-1.25	0.0013	0.0088	1	1	-0.82	0.0944	0.4956	0	0	-0.42	0.2764	0.7795	0	0
MB21D2	MB21D2-2	2.02	0.0027	0.0159	1	1	1.66	0.0386	0.3308	0	0	0.36	0.4108	0.8666	0	0
MB21D2	MB21D2-3	-1.12	0.0025	0.0151	1	1	-0.81	0.0766	0.4465	0	0	-0.31	0.4310	0.8764	0	0
MB21D2	MB21D2-4	-0.88	0.0173	0.0699	0	1	-0.53	0.2384	0.6994	0	0	-0.35	0.3227	0.8235	0	0
MB21D2	MB21D2-5	-0.47	0.1986	0.3956	0	0	-0.22	0.6130	0.8945	0	0	-0.25	0.5362	0.8862	0	0
MB21D2	MB21D2-6	-1.82	0.0000	0.0001	1	1	-0.41	0.4787	0.8506	0	0	-1.41	0.0006	0.0252	1	1
MCCC1	MCCC1-1	-1.40	0.0005	0.0044	1	1	-0.60	0.2237	0.6846	0	0	-0.80	0.0601	0.4538	0	0
MCCC1	MCCC1-2	0.13	0.7485	0.8764	0	0	0.75	0.2165	0.6829	0	0	-0.62	0.2247	0.7405	0	0
MCCC1	MCCC1-3	0.20	0.6354	0.8104	0	0	0.49	0.3862	0.7956	0	0	-0.29	0.5736	0.8862	0	0
MCCC1	MCCC1-4	0.27	0.5102	0.7189	0	0	0.65	0.1273	0.5470	0	0	-0.38	0.2993	0.7965	0	0
MCCC1	MCCC1-5	-0.59	0.1286	0.2947	0	0	-0.29	0.5150	0.8609	0	0	-0.29	0.4515	0.8860	0	0
MCCC1	MCCC1-6	-0.24	0.5602	0.7526	0	0	-0.32	0.4575	0.8506	0	0	0.08	0.8165	0.8862	0	0
MCF2L2	MCF2L2-1	-0.90	0.0128	0.0548	0	1	-0.31	0.4795	0.8506	0	0	-0.59	0.1151	0.5901	0	0
MCF2L2	MCF2L2-2	-1.74	0.0000	0.0002	1	1	-1.22	0.0143	0.2049	0	0	-0.52	0.2000	0.7138	0	0
MCF2L2	MCF2L2-3	-0.59	0.0970	0.2409	0	0	-0.26	0.5555	0.8733	0	0	-0.32	0.3943	0.8528	0	0
MCF2L2	MCF2L2-4	-1.51	0.0000	0.0005	1	1	-0.71	0.1549	0.6036	0	0	-0.80	0.0391	0.3798	0	0
MCF2L2	MCF2L2-5	-0.10	0.7619	0.8819	0	0	-0.51	0.2432	0.7028	0	0	0.41	0.2507	0.7554	0	0
MCF2L2	MCF2L2-6	0.25	0.5137	0.7209	0	0	0.48	0.2890	0.7360	0	0	-0.23	0.5109	0.8862	0	0
MCL1	MCL1-1	-4.03	0.0000	0.0000	1	1	-3.08	0.0001	0.0052	1	1	-0.95	0.0434	0.3999	0	0
MCL1	MCL1-2	-0.07	0.8193	0.8984	0	0	-0.09	0.7876	0.9227	0	0	0.02	0.7683	0.8862	0	0
MCL1	MCL1-3	-0.45	0.3062	0.5214	0	0	-0.23	0.6409	0.9015	0	0	-0.22	0.5987	0.8862	0	0
MCL1	MCL1-4	-0.27	0.5124	0.7203	0	0	0.17	0.6950	0.9092	0	0	-0.44	0.2598	0.7640	0	0
MCL1	MCL1-5	-0.39	0.3004	0.5155	0	0	-0.27	0.5696	0.8784	0	0	-0.13	0.7502	0.8862	0	0
MCL1	MCL1-6	1.13	0.0064	0.0314	1	1	0.46	0.3418	0.7741	0	0	0.67	0.1766	0.6836	0	0
MDC1	MDC1-1	-0.59	0.1101	0.2663	0	0	-0.45	0.3165	0.7517	0	0	-0.13	0.6940	0.8862	0	0
MDC1	MDC1-2	-1.10	0.7840	0.8938	0	0	0.06	0.8773	0.9417	0	0	0.04	0.8740	0.8910	0	0
MDC1	MDC1-3	0.34	0.3864	0.6083	0	0	0.36	0.5125	0.8594	0	0	-0.02	0.7775	0.8862	0	0
MDC1	MDC1-4	-0.32	0.3694	0.5915	0	0	-0.05	0.9119	0.9468	0	0	-0.27	0.4401	0.8801	0	0
MDC1	MDC1-5	0.61	0.1477	0.3220	0	0	1.05	0.0387	0.3308	0	0	-0.44	0.2525	0.7554	0	0
MDC1	MDC1-6	-0.72	0.0679	0.1877	0	1	-0.35	0.5010	0.8538	0	0	-0.36	0.3416	0.8301	0	0
MDM2	MDM2-1	-0.60	0.1512	0.3272	0	0	0.49	0.3088	0.7506	0	0	-1.09	0.0044	0.1073	0	1
MDM2	MDM2-2	-0.75	0.0534	0.1574	0	1	-0.18	0.7283	0.9151	0	0	-0.57	0.1521	0.6504	0	0
MDM2	MDM2-3	-1.64	0.0000	0.0002	1	1	-0.65	0.1847	0.6431	0	0	-1.00	0.0121	0.2100	0	0
MDM2	MDM2-4	-0.70	0.0698	0.1917	0	1	0.54	0.2257	0.6875	0	0	0.16	0.7335	0.8862	0	0
MDM2	MDM2-5	-0.47	0.2255	0.4298	0	0	-0.55	0.2238	0.6846	0	0	0.07	0.7598	0.8862	0	0
MDM2	MDM2-6	-1.27	0.0007	0.0055	1	1	-1.19	0.0123	0.1940	0	1	-0.09	0.8130	0.8862	0	0
MDM4	MDM4-1	0.52	0.1710	0.3538	0	0	0.56	0.2091	0.6691	0	0	-0.03	0.7940	0.8862	0	0
MDM4	MDM4-2	-1.52	0.0001	0.0015	1	1	-1.29	0.0108	0.1837	0	1	-0.24	0.5710	0.8862	0	0
MDM4	MDM4-3	-0.71	0.0786	0.2087	0	0	-0.32	0.5122	0.8594	0	0	-0.39	0.4245	0.8764	0	0
MDM4	MDM4-4	3.67	0.0000	0.0001	1	1	2.02	0.0208	0.2484	0	0	1.64	0.0291	0.3228	0	0
MDM4	MDM4-5	0.30	0.4533	0.6736	0	0	0.13	0.6883	0.9092	0	0	0.17	0.7319	0.8862	0	0
MDM4	MDM4-6	-0.26	0.4914	0.7057	0	0	-0.20	0.6799	0.9091	0	0	-0.06	0.7337	0.8862	0	0
MEF2B	MEF2B-1	0.00	0.8727	0.8989	0	0	0.62	0.2357	0.6967	0	0	-0.62	0.1632	0.6667	0	0
MEF2B	MEF2B-2	-0.58	0.1557	0.3331	0	0	-0.28	0.5321	0.8690	0	0	-0.30	0.3979	0.8582	0	0
MEF2B	MEF2B-3	2.38	0.0001	0.0014	1	1	0.67	0.2549	0.7054	0	0	1.71	0.0037	0.0956	0	1
MEF2B	MEF2B-4	0.03	0.8973	0.9078	0	0	0.08	0.8439	0.9334	0	0	-0.11	0.7724	0.8862	0	0
MEF2B	MEF2B-5	0.32	0.4815	0.6998	0	0	-0.26	0.5743	0.8791	0	0	-0.06	0.8623	0.8872	0	0
MEF2B	MEF2B-6	0.16	0.6838	0.8433	0	0	0.07	0.8782	0.9417	0	0	0.09	0.8320	0.8862	0	0
MFN1	MFN1-1	-1.05	0.0053	0.0271	1	1	-0.78	0.0875	0.4782	0	0	-0.27	0.4769	0.8862	0	0
MFN1	MFN1-2	0.34	0.3802	0.6039	0	0	0.19	0.6585	0.9060	0	0	0.15	0.7009	0.8862	0	0
MFN1	MFN1-3	-0.09	0.8179	0.8984	0	0	-0.16	0.7573	0.9198	0	0	0.07	0.7643	0.8862	0	0
MFN1	MFN1-4	-0.67	0.0685	0.1886	0	1	-0.46	0.3210	0.7581	0	0	-0.21	0.5934	0.8862	0	0
MFN1	MFN1-5	-0.57	0.1378	0.3077	0	0	-0.28	0.5279	0.8663	0	0	-0.29	0.5161	0.8862	0	0
MFN1	MFN1-6	-0.13	0.7667	0.8837	0	0	0.04	0.9004	0.9425	0	0	-0.17	0.6636	0.8862	0	0
MFSD2A	MFSD2A-1	-1.25	0.0008	0.0060	1	1	-0.28	0.5907	0.8876	0	0	-0.97	0.0211	0.2807	0	0
MFSD2A	MFSD2A-2	-0.71	0.0491	0.1493	0	1	-0.45	0.3282	0.7620	0	0	-0.26	0.4035	0.8598	0	0
MFSD2A	MFSD2A-3	0.23	0.5672	0.7569	0	0	0.20	0.6432	0.9022	0	0	0.03	0.7962	0.8862	0	0
MFSD2A	MFSD2A-4	0.08	0.7161	0.8617	0	0	0.19	0.6724	0.9079	0	0	-0.10	0.6013	0.8862	0	0
MFSD2A	MFSD2A-5	0.25	0.5419	0.7397	0	0	-0.01	0.9151	0.9471	0	0	0.26	0.6456	0.8862	0	0
MFSD2A	MFSD2A-6	-0.47	0.1908	0.3852	0	0	-0.30	0.4804	0.8506	0	0	-0.17	0.5502	0.8862	0	0
MIPOL1	MIPOL1-1	-0.89	0.0157	0.0645	0	1	-0.56	0.2066	0.6676	0	0	-0.33	0.2989	0.7965	0	0
MIPOL1	MIPOL1-2	-1.43	0.0001	0.0012	1	1	-1.18	0.0120	0.1940	0	1	-0.25	0.4353	0.8764	0	0
MIPOL1	MIPOL1-3	-0.49	0.2073	0.4068	0	0	-0.27	0.5377	0.8699	0	0	-0.22	0.6041	0.8862	0	0
MIPOL1	MIPOL1-4	-1.00	0.0073	0.0349	1	1	-0.29	0.5049	0.8554	0	0	-0.71	0.0805	0.5070	0	0
MIPOL1	MIPOL1-5	-0.61	0.1809	0.3696	0	0	0.13	0.8077	0.9227	0	0	0.48	0.3488	0.8319	0	0
MIPOL1	MIPOL1-6	0.05	0.7574	0.8789	0	0	0.05	0.7839	0.9227	0	0	-0.10	0.5781	0.8862	0	0
MPL	MPL-1	0.41	0.2737	0.4890	0	0	-0.11	0.8910	0.9418	0	0	-0.30	0.3779	0.8432	0	0
MPL	MPL-2	-1.67	0.0008	0.0061	1	1	1.80	0.0024	0.0765	0	1	-0.13	0.3622	0.8319	0	0
MPL	MPL-3	-0.26	0.5164	0.7230	0	0	0.00	0.9179	0.9476	0	0	-0.26	0.4208	0.8761	0	0
MPL	MPL-4	0.51	0.2929	0.5081	0	0	0.85	0.1308	0.5522	0	0	-0.34	0.4585	0.8862	0	0
MPL	MPL-5	-1.43	0.0004	0.0037	1	1	-1.16	0.0179	0.2295	0	0	-0.27	0.4481	0.8836	0	0
MPL	MPL-6	-0.48	0.2802	0.4935	0	0	-0.47	0.2875	0.7360	0	0	-0.01	0.6119	0.8862	0	0
MRPS35	MRPS35-1	0.05	0.8445	0.8984	0	0	0.00	0.9480	0.9556	0	0	0.06	0.8781	0.8921	0	0
MRPS35	MRPS35-2	-0.04	0.8533	0.8984	0	0	0.02	0.9415	0.9533	0	0	-0.06	0.7959	0.8862	0	0
MRPS35	MRPS35-3	-1.80	0.0000	0.0001	1	1	-0.70	0.2173	0.6829	0	0	-1.10	0.0068	0.1446	0	1
MRPS35	MRPS35-4	0.44	0.2524	0.4626	0	0	0.51	0.2835	0.7355	0	0	-0.07	0.7681	0.8862	0	0
MRPS35	MRPS35-5	-0.77	0.0461	0.												

MYB	MYB-1	-1.21	0.0015	0.0101	1	1	-0.38	0.4164	0.8259	0	0	-0.83	0.0220	0.2863	0	0
MYB	MYB-2	-2.19	0.0000	0.0000	1	1	-1.32	0.0176	0.2287	0	0	-0.87	0.0425	0.3988	0	0
MYB	MYB-3	-0.32	0.3984	0.6205	0	0	-0.22	0.6632	0.9070	0	0	-0.11	0.6286	0.8862	0	0
MYB	MYB-4	-0.12	0.7124	0.8594	0	0	0.25	0.5225	0.8651	0	0	-0.37	0.2950	0.7955	0	0
MYB	MYB-5	-2.29	0.0000	0.0000	1	1	-1.40	0.0105	0.1801	0	1	-0.89	0.0493	0.4157	0	0
MYB	MYB-6	-0.31	0.4326	0.6534	0	0	0.21	0.5890	0.8873	0	0	-0.52	0.1626	0.6661	0	0
MYC	MYC-1	-0.94	0.0118	0.0515	0	1	-0.46	0.3170	0.7520	0	0	-0.48	0.2255	0.7405	0	0
MYC	MYC-2	1.32	0.0294	0.1011	0	1	1.76	0.0159	0.2156	0	0	-0.44	0.4678	0.8862	0	0
MYC	MYC-3	-0.10	0.8140	0.8984	0	0	0.02	0.9227	0.9485	0	0	-0.11	0.6944	0.8862	0	0
MYC	MYC-4	0.10	0.7997	0.8966	0	0	0.37	0.3858	0.7955	0	0	-0.27	0.5098	0.8862	0	0
MYC	MYC-5	-0.18	0.6477	0.8178	0	0	0.33	0.4212	0.8313	0	0	-0.51	0.1730	0.6758	0	0
MYC	MYC-6	-0.32	0.4381	0.6590	0	0	-0.40	0.3877	0.7961	0	0	0.08	0.8691	0.8889	0	0
MYCL	MYCL-1	-0.11	0.8408	0.8984	0	0	-0.25	0.6345	0.8957	0	0	0.14	0.7844	0.8862	0	0
MYCL	MYCL-2	0.06	0.9241	0.9252	0	0	0.17	0.6803	0.9091	0	0	-0.22	0.5095	0.8862	0	0
MYCL	MYCL-3	-0.06	0.8539	0.8984	0	0	-0.01	0.9338	0.9505	0	0	0.08	0.8756	0.8913	0	0
MYCL	MYCL-4	-0.41	0.3338	0.5568	0	0	0.04	0.9205	0.9485	0	0	-0.46	0.2637	0.7681	0	0
MYCL	MYCL-5	0.74	0.1162	0.2757	0	0	0.99	0.0871	0.4770	0	0	-0.25	0.5973	0.8862	0	0
MYCL	MYCL-6	-0.57	0.1529	0.3295	0	0	-0.31	0.4967	0.8519	0	0	-0.26	0.4673	0.8862	0	0
MYCN	MYCN-1	0.61	0.1294	0.2953	0	0	1.82	0.0004	0.0248	1	1	-1.22	0.0010	0.0377	1	1
MYCN	MYCN-2	-1.79	0.0001	0.0013	1	1	-2.20	0.0003	0.0216	1	1	0.42	0.4432	0.8807	0	0
MYCN	MYCN-3	0.36	0.3368	0.5596	0	0	0.87	0.0514	0.3663	0	0	-0.51	0.2013	0.7138	0	0
MYCN	MYCN-4	1.82	0.0000	0.0004	1	1	1.16	0.0141	0.2044	0	0	0.66	0.2349	0.7479	0	0
MYCN	MYCN-5	-1.60	0.0008	0.0063	1	1	-1.41	0.0346	0.3197	0	0	-0.19	0.6571	0.8862	0	0
MYCN	MYCN-6	7.58	0.0000	0.0000	1	1	8.52	0.0000	0.0000	1	1	-0.94	0.2144	0.7289	0	0
MYLK2	MYLK2-1	0.25	0.4934	0.7064	0	0	0.31	0.4708	0.8506	0	0	-0.05	0.7058	0.8862	0	0
MYLK2	MYLK2-2	-1.16	0.0013	0.0088	1	1	-0.94	0.0362	0.3229	0	0	-0.22	0.5665	0.8862	0	0
MYLK2	MYLK2-3	2.50	0.0001	0.0007	1	1	3.39	0.0000	0.0013	1	1	-0.88	0.1339	0.6151	0	0
MYLK2	MYLK2-4	0.62	0.1113	0.2676	0	0	0.93	0.0409	0.3348	0	0	-0.31	0.3446	0.8314	0	0
MYLK2	MYLK2-5	0.43	0.2670	0.4801	0	0	1.55	0.0004	0.0244	1	1	-1.12	0.0005	0.0202	1	1
MYLK2	MYLK2-6	-0.53	0.1496	0.3251	0	0	-0.24	0.5625	0.8762	0	0	-0.29	0.4016	0.8598	0	0
MYO16	MYO16-1	-0.53	0.1635	0.3451	0	0	-0.08	0.8623	0.9406	0	0	-0.45	0.2499	0.7554	0	0
MYO16	MYO16-2	0.60	0.1496	0.3251	0	0	0.30	0.4778	0.8506	0	0	0.30	0.4703	0.8862	0	0
MYO16	MYO16-3	-1.36	0.0015	0.0096	1	1	-0.93	0.0921	0.4903	0	0	-0.43	0.2778	0.7796	0	0
MYO16	MYO16-4	1.17	0.0052	0.0267	1	1	0.34	0.4524	0.8506	0	0	0.83	0.0392	0.3798	0	0
MYO16	MYO16-5	-0.14	0.7096	0.8589	0	0	0.43	0.3494	0.7803	0	0	-0.57	0.1188	0.5987	0	0
MYO16	MYO16-6	-0.64	0.1048	0.2555	0	0	-0.37	0.4112	0.8210	0	0	-0.27	0.5349	0.8862	0	0
NAALADL2	NAALADL2-1	-0.97	0.0182	0.0722	0	1	-0.60	0.2285	0.6900	0	0	-0.37	0.3925	0.8519	0	0
NAALADL2	NAALADL2-2	0.83	0.1202	0.2815	0	0	1.20	0.0420	0.3386	0	0	-0.37	0.3910	0.8494	0	0
NAALADL2	NAALADL2-3	-0.76	0.0366	0.1193	0	1	-0.13	0.7813	0.9227	0	0	-0.63	0.0807	0.5073	0	0
NAALADL2	NAALADL2-4	-0.05	0.8373	0.8984	0	0	0.03	0.8655	0.9417	0	0	-0.08	0.7483	0.8862	0	0
NAALADL2	NAALADL2-5	-0.46	0.2383	0.4451	0	0	-0.46	0.3128	0.7516	0	0	0.00	0.8074	0.8862	0	0
NAALADL2	NAALADL2-6	1.59	0.0068	0.0333	1	1	0.90	0.1583	0.6087	0	0	-0.68	0.2401	0.7542	0	0
NADK2	NADK2-1	-0.24	0.5663	0.7569	0	0	-0.10	0.8450	0.9334	0	0	-0.15	0.7376	0.8862	0	0
NADK2	NADK2-2	-0.11	0.7635	0.8825	0	0	-0.16	0.7171	0.9151	0	0	0.05	0.8431	0.8867	0	0
NADK2	NADK2-3	-0.18	0.6080	0.7881	0	0	0.19	0.5972	0.8878	0	0	-0.37	0.2436	0.7554	0	0
NADK2	NADK2-4	2.55	0.0005	0.0044	1	1	2.49	0.0060	0.1357	0	1	0.06	0.2830	0.7870	0	0
NADK2	NADK2-5	-0.25	0.5131	0.7204	0	0	0.20	0.6643	0.9073	0	0	-0.45	0.2265	0.7408	0	0
NADK2	NADK2-6	0.69	0.1107	0.2666	0	0	0.55	0.3226	0.7592	0	0	0.14	0.7911	0.8862	0	0
NANOG	NANOG-1	-1.29	0.0006	0.0048	1	1	-1.03	0.0248	0.2748	0	0	-0.26	0.5160	0.8862	0	0
NANOG	NANOG-2	-0.07	0.7925	0.8960	0	0	-0.41	0.3211	0.7581	0	0	0.35	0.3888	0.8491	0	0
NANOG	NANOG-3	-1.11	0.0030	0.0175	1	1	-0.50	0.2653	0.7214	0	0	-0.61	0.1284	0.6144	0	0
NANOG	NANOG-4	-0.23	0.5364	0.7366	0	0	0.01	0.9002	0.9425	0	0	-0.23	0.5524	0.8862	0	0
NANOG	NANOG-5	-0.27	0.4291	0.6506	0	0	0.72	0.0709	0.4296	0	0	-0.98	0.0024	0.0734	0	1
NANOG	NANOG-6	0.54	0.1565	0.3343	0	0	0.45	0.3316	0.7633	0	0	0.09	0.8714	0.8900	0	0
NANOGNB	NANOGNB-1	0.87	0.0250	0.0908	0	1	1.17	0.0065	0.1363	0	1	-0.30	0.2496	0.7554	0	0
NANOGNB	NANOGNB-2	-0.32	0.4230	0.6446	0	0	0.39	0.2952	0.7378	0	0	-0.71	0.0515	0.4242	0	1
NANOGNB	NANOGNB-3	-0.51	0.2010	0.3983	0	0	-0.56	0.2228	0.6846	0	0	0.05	0.7208	0.8862	0	0
NANOGNB	NANOGNB-4	-2.72	0.0000	0.0000	1	1	-1.43	0.0178	0.2292	0	0	-1.29	0.0080	0.1592	0	1
NANOGNB	NANOGNB-5	-1.05	0.0049	0.0255	1	1	-0.03	0.5899	0.8876	0	0	-0.22	0.0058	0.1292	0	1
NANOGNB	NANOGNB-6	2.04	0.0000	0.0001	1	1	1.40	0.0062	0.1363	0	1	0.64	0.1344	0.6162	0	0
NAXD	NAXD-1	0.21	0.5995	0.7824	0	0	0.15	0.7595	0.9201	0	0	0.06	0.8098	0.8862	0	0
NAXD	NAXD-2	-0.45	0.2265	0.4313	0	0	0.11	0.7366	0.9167	0	0	-0.56	0.1316	0.6151	0	0
NAXD	NAXD-3	0.08	0.7866	0.8938	0	0	0.24	0.5033	0.8547	0	0	-0.15	0.5172	0.8862	0	0
NAXD	NAXD-4	-0.54	0.1447	0.3168	0	0	-0.30	0.5214	0.8648	0	0	-0.24	0.5161	0.8862	0	0
NAXD	NAXD-5	-0.24	0.5507	0.7452	0	0	-0.19	0.7709	0.9227	0	0	0.42	0.3813	0.8463	0	0
NAXD	NAXD-6	-0.39	0.3003	0.5155	0	0	-0.31	0.4934	0.8506	0	0	-0.08	0.7970	0.8862	0	0
NBN	NBN-1	0.05	0.8852	0.9035	0	0	0.10	0.7929	0.9227	0	0	-0.05	0.7813	0.8862	0	0
NBN	NBN-2	0.91	0.0272	0.0962	0	1	1.23	0.0096	0.1705	0	1	-0.32	0.4025	0.8598	0	0
NBN	NBN-3	-0.90	0.0257	0.0924	0	1	-0.98	0.0481	0.3565	0	0	0.08	0.8869	0.8968	0	0
NBN	NBN-4	0.73	0.0679	0.1877	0	1	-0.01	0.8965	0.9419	0	0	0.74	0.0868	0.5184	0	0
NBN	NBN-5	-1.00	0.0112	0.0491	1	1	-0.71	0.1524	0.6019	0	0	-0.29	0.3817	0.8463	0	0
NBN	NBN-6	0.24	0.5436	0.7402	0	0	0.47	0.3048	0.7468	0	0	-0.23	0.5308	0.8862	0	0
NCBP2	NCBP2-1	-0.70	0.0650	0.1821	0	1	-0.16	0.7551	0.9192	0	0	-0.54	0.1637	0.6676	0	0
NCBP2	NCBP2-2	0.83	0.1297	0.2953	0	0	0.75	0.2353	0.6967	0	0	0.08	0.8620	0.8872	0	0
NCBP2	NCBP2-3	-0.72	0.0575	0.1667	0	1	1.11	0.0263	0.2853	0	0	-1.83	0.0000	0.0011	1	1
NCBP2	NCBP2-4	-0.09	0.7818	0.8938	0	0	0.07	0.8354	0.9312	0	0	-0.16	0.6461	0.8862	0	0
NCBP2	NCBP2-5	-0.56	0.1328	0.3006	0	0	-0.31	0.4856	0.8506	0	0	-0.25	0.5165	0.8862	0	0
NCBP2	NCBP2-6	-0.49	0.2130	0.4139	0	0	-0.03	0.8955	0.9418	0	0	-0.46	0.2157	0.7296	0	0
NCOA3	NCOA3-1	-0.26	0.5183	0.7248	0	0	-0.19	0.6845	0.9092	0	0	-0.07	0.8353	0.8862	0	0
NCOA3	NCOA3-2	-0.40	0.3751	0.5978	0	0	-0.32	0.5388	0.8699	0	0	-0.08	0.8227	0.8862	0	0
NCOA3	NCOA3-3	-0.73	0.0608	0.1734	0	1	-0.49	0.2829	0.7355	0	0	-0.25	0.4867	0.8862	0	0
NCOA3	NCOA3-4	-1.66	0.0000	0.0001	1	1	-0.87	0.0549	0.3774							

NFKB1	NFKB1-6	-0.04	0.9024	0.9092	0	0	0.01	0.9100	0.9467	0	0	-0.05	0.8331	0.8862	0	0
NFKB1A	NFKB1A-1	-0.76	0.0382	0.1228	0	1	-0.47	0.2862	0.7360	0	0	-0.28	0.3723	0.8401	0	0
NFKB1A	NFKB1A-2	-1.05	0.0083	0.0385	1	1	-0.54	0.2443	0.7028	0	0	-0.51	0.2637	0.7681	0	0
NFKB1A	NFKB1A-3	-0.04	0.8470	0.8984	0	0	0.25	0.6001	0.8878	0	0	-0.29	0.4846	0.8862	0	0
NFKB1A	NFKB1A-4	0.00	0.8161	0.8984	0	0	0.15	0.7125	0.9145	0	0	-0.15	0.6642	0.8862	0	0
NFKB1A	NFKB1A-5	-0.69	0.0509	0.1529	0	1	-0.49	0.2810	0.7355	0	0	-0.20	0.5301	0.8862	0	0
NFKB1A	NFKB1A-6	-0.42	0.3190	0.5386	0	0	0.52	0.2217	0.6841	0	0	-0.94	0.0079	0.1587	0	1
NHLH1	NHLH1-1	-0.10	0.8130	0.8984	0	0	0.08	0.8424	0.9334	0	0	-0.18	0.6141	0.8862	0	0
NHLH1	NHLH1-2	0.30	0.4487	0.6702	0	0	0.32	0.4265	0.8341	0	0	-0.02	0.8572	0.8872	0	0
NHLH1	NHLH1-3	0.45	0.2255	0.4298	0	0	0.63	0.1637	0.6182	0	0	-0.18	0.5463	0.8862	0	0
NHLH1	NHLH1-4	2.42	0.0000	0.0000	1	1	2.17	0.0000	0.0037	1	1	0.25	0.5136	0.8862	0	0
NHLH1	NHLH1-5	-0.80	0.0767	0.2050	0	0	-0.67	0.2887	0.7360	0	0	-0.13	0.6090	0.8862	0	0
NHLH1	NHLH1-6	-0.78	0.0652	0.1821	0	1	-0.77	0.1906	0.6474	0	0	-0.01	0.7615	0.8862	0	0
NKX2-1	NKX2-1-1	-2.13	0.0000	0.0000	1	1	-1.73	0.0015	0.0517	0	1	-0.39	0.2976	0.7965	0	0
NKX2-1	NKX2-1-2	-0.30	0.4488	0.6702	0	0	-0.07	0.8784	0.9417	0	0	-0.23	0.5085	0.8862	0	0
NKX2-1	NKX2-1-3	-0.54	0.1659	0.3483	0	0	0.17	0.7176	0.9151	0	0	-0.70	0.0684	0.4695	0	0
NKX2-1	NKX2-1-4	-1.66	0.0000	0.0005	1	1	-0.87	0.1018	0.5100	0	0	-0.79	0.0437	0.3999	0	0
NKX2-1	NKX2-1-5	-1.97	0.0000	0.0000	1	1	-0.75	0.1103	0.5280	0	0	-1.22	0.0015	0.0497	1	1
NKX2-1	NKX2-1-6	-0.79	0.0421	0.1318	0	1	-0.76	0.1057	0.5177	0	0	-0.03	0.7237	0.8862	0	0
NKX2-8	NKX2-8-1	-0.16	0.6763	0.8388	0	0	-0.12	0.8128	0.9230	0	0	-0.04	0.7496	0.8862	0	0
NKX2-8	NKX2-8-2	-0.80	0.0388	0.1242	0	1	-0.34	0.4724	0.8506	0	0	-0.46	0.2532	0.7559	0	0
NKX2-8	NKX2-8-3	-0.03	0.8682	0.8986	0	0	-0.22	0.6119	0.8943	0	0	0.19	0.7283	0.8862	0	0
NKX2-8	NKX2-8-4	-0.28	0.4865	0.7031	0	0	-0.17	0.6836	0.9092	0	0	-0.11	0.6980	0.8862	0	0
NKX2-8	NKX2-8-5	-0.04	0.8291	0.8984	0	0	-0.03	0.8802	0.9417	0	0	-0.01	0.8205	0.8862	0	0
NKX2-8	NKX2-8-6	-0.33	0.3991	0.6208	0	0	-0.28	0.5586	0.8758	0	0	-0.04	0.8224	0.8862	0	0
NRROS	NRROS-1	-0.46	0.2179	0.4203	0	0	-0.50	0.2542	0.7043	0	0	0.04	0.8727	0.8905	0	0
NRROS	NRROS-2	-0.49	0.2498	0.4604	0	0	-0.31	0.5266	0.8656	0	0	-0.19	0.6842	0.8862	0	0
NRROS	NRROS-3	-0.02	0.8723	0.8989	0	0	-0.13	0.7928	0.9227	0	0	0.11	0.7640	0.8862	0	0
NRROS	NRROS-4	0.31	0.4649	0.6820	0	0	0.07	0.8762	0.9417	0	0	0.24	0.6308	0.8862	0	0
NRROS	NRROS-5	-0.40	0.2801	0.4935	0	0	-0.05	0.9439	0.9541	0	0	-0.35	0.3149	0.8135	0	0
NRROS	NRROS-6	-0.09	0.8634	0.8986	0	0	-0.09	0.8847	0.9417	0	0	0.00	0.8805	0.8924	0	0
NSD3	NSD3-1	0.35	0.3804	0.6039	0	0	0.40	0.4209	0.8313	0	0	-0.05	0.6234	0.8862	0	0
NSD3	NSD3-2	0.42	0.2803	0.4935	0	0	-0.29	0.7103	0.9142	0	0	0.71	0.1823	0.6875	0	0
NSD3	NSD3-3	-0.33	0.4130	0.6347	0	0	0.01	0.9447	0.9542	0	0	-0.34	0.3413	0.8301	0	0
NSD3	NSD3-4	-0.73	0.0527	0.1564	0	1	-0.45	0.3160	0.7516	0	0	-0.28	0.4346	0.8764	0	0
NSD3	NSD3-5	0.04	0.8598	0.8984	0	0	0.45	0.2606	0.7140	0	0	-0.41	0.1649	0.6679	0	0
NSD3	NSD3-6	-0.70	0.0604	0.1732	0	1	-0.61	0.1790	0.6376	0	0	-0.09	0.7052	0.8862	0	0
NT5C1A	NT5C1A-1	-0.98	0.0077	0.0364	1	1	-0.80	0.0890	0.4788	0	0	-0.19	0.5603	0.8862	0	0
NT5C1A	NT5C1A-2	-0.31	0.3953	0.6174	0	0	-0.27	0.5559	0.8733	0	0	-0.04	0.7479	0.8862	0	0
NT5C1A	NT5C1A-3	-0.46	0.2460	0.4555	0	0	-0.49	0.2920	0.7378	0	0	0.03	0.8461	0.8869	0	0
NT5C1A	NT5C1A-4	-0.03	0.8351	0.8984	0	0	-0.08	0.8625	0.9406	0	0	0.05	0.8798	0.8924	0	0
NT5C1A	NT5C1A-5	-0.51	0.2364	0.4433	0	0	-0.23	0.5814	0.8818	0	0	-0.28	0.4503	0.8851	0	0
NT5C1A	NT5C1A-6	-0.41	0.2937	0.5090	0	0	-0.40	0.3666	0.7821	0	0	-0.01	0.9030	0.9053	0	0
NTRK1	NTRK1-1	-0.26	0.5295	0.7328	0	0	0.30	0.4999	0.8538	0	0	-0.56	0.1779	0.6837	0	0
NTRK1	NTRK1-2	-0.88	0.0262	0.0933	0	1	-0.52	0.2889	0.7133	0	0	-0.35	0.3818	0.8463	0	0
NTRK1	NTRK1-3	0.60	0.0880	0.2250	0	0	0.40	0.3719	0.7850	0	0	0.21	0.4334	0.8764	0	0
NTRK1	NTRK1-4	-0.66	0.1345	0.3022	0	0	-0.06	0.8780	0.9417	0	0	-0.60	0.1615	0.6654	0	0
NTRK1	NTRK1-5	-0.88	0.0201	0.0782	0	1	-0.40	0.3695	0.7821	0	0	-0.48	0.2485	0.7554	0	0
NTRK1	NTRK1-6	0.75	0.0720	0.1956	0	1	0.06	0.6516	0.9043	0	0	0.69	0.1143	0.5901	0	0
OPA1	OPA1-1	0.23	0.6010	0.7836	0	0	0.20	0.6467	0.9022	0	0	0.03	0.7890	0.8862	0	0
OPA1	OPA1-2	-0.39	0.3080	0.5240	0	0	0.17	0.5794	0.8818	0	0	-0.56	0.1335	0.6151	0	0
OPA1	OPA1-3	0.33	0.4310	0.6520	0	0	0.29	0.5418	0.8699	0	0	0.04	0.7672	0.8862	0	0
OPA1	OPA1-4	-0.71	0.0781	0.2078	0	0	-0.41	0.3726	0.7854	0	0	-0.31	0.4373	0.8769	0	0
OPA1	OPA1-5	-0.35	0.3446	0.5690	0	0	-0.31	0.4843	0.8506	0	0	-0.04	0.8072	0.8862	0	0
OPA1	OPA1-6	0.24	0.5733	0.7608	0	0	0.50	0.4422	0.8442	0	0	-0.26	0.6204	0.8862	0	0
OSTN	OSTN-1	0.20	0.6271	0.8045	0	0	0.52	0.2847	0.7355	0	0	-0.32	0.4520	0.8860	0	0
OSTN	OSTN-2	0.19	0.6064	0.7868	0	0	0.92	0.0618	0.4045	0	0	-0.73	0.0779	0.4971	0	0
OSTN	OSTN-3	-2.05	0.0000	0.0001	1	1	-0.86	0.1642	0.6182	0	0	-1.20	0.0047	0.1109	0	1
OSTN	OSTN-4	-0.03	0.8486	0.8984	0	0	0.16	0.6333	0.8955	0	0	-0.19	0.4271	0.8764	0	0
OSTN	OSTN-5	2.65	0.0000	0.0000	1	1	1.62	0.0141	0.2044	0	0	1.03	0.0531	0.4282	0	0
OSTN	OSTN-6	0.10	0.6762	0.8388	0	0	0.89	0.0866	0.4757	0	0	-0.80	0.1091	0.5844	0	0
OXCT2	OXCT2-1	-0.62	0.1505	0.3261	0	0	0.09	0.8877	0.9417	0	0	-0.71	0.1114	0.5872	0	0
OXCT2	OXCT2-2	-0.19	0.6184	0.7998	0	0	0.60	0.1848	0.6431	0	0	-0.79	0.0238	0.2913	0	0
OXCT2	OXCT2-3	-0.63	0.0997	0.2462	0	0	-0.46	0.3095	0.7508	0	0	-0.17	0.6570	0.8862	0	0
OXCT2	OXCT2-4	0.25	0.5212	0.7268	0	0	0.22	0.6213	0.8955	0	0	0.04	0.7233	0.8862	0	0
OXCT2	OXCT2-5	-0.59	0.1436	0.3159	0	0	0.29	0.5553	0.8733	0	0	-0.88	0.0321	0.3400	0	0
OXCT2	OXCT2-6	0.29	0.4702	0.6871	0	0	0.43	0.3525	0.7807	0	0	-0.14	0.7571	0.8862	0	0
P3H2	P3H2-1	-0.26	0.5282	0.7324	0	0	-0.41	0.3698	0.7821	0	0	0.15	0.7260	0.8862	0	0
P3H2	P3H2-2	0.13	0.7641	0.8828	0	0	0.33	0.4257	0.8341	0	0	-0.21	0.5306	0.8862	0	0
P3H2	P3H2-3	-0.32	0.3980	0.6205	0	0	-0.33	0.4412	0.8437	0	0	0.01	0.8327	0.8862	0	0
P3H2	P3H2-4	-1.23	0.0014	0.0096	1	1	-0.91	0.0642	0.4118	0	0	-0.33	0.4339	0.8764	0	0
P3H2	P3H2-5	-1.80	0.0000	0.0001	1	1	-1.20	0.0152	0.2143	0	0	-0.60	0.1461	0.6406	0	0
P3H2	P3H2-6	0.06	0.7993	0.8966	0	0	1.81	0.0010	0.0389	1	1	-1.75	0.0000	0.0035	1	1
PABPC4	PABPC4-1	1.74	0.0000	0.0004	1	1	0.43	0.3662	0.7821	0	0	1.31	0.0041	0.1042	0	1
PABPC4	PABPC4-2	-0.25	0.5234	0.7285	0	0	0.07	0.9122	0.9468	0	0	-0.32	0.4434	0.8807	0	0
PABPC4	PABPC4-3	-0.30	0.4261	0.6476	0	0	0.41	0.3382	0.7718	0	0	-0.71	0.0665	0.4675	0	0
PABPC4	PABPC4-4	-0.65	0.0902	0.2296	0	0	0.06	0.8105	0.9227	0	0	-0.71	0.0649	0.4669	0	0
PABPC4	PABPC4-5	-0.27	0.4585	0.6787	0	0	-0.03	0.9559	0.9591	0	0	-0.24	0.5561	0.8862	0	0
PABPC4	PABPC4-6	-0.45	0.3657	0.5869	0	0	0.82	0.2206	0.6841	0	0	-1.27	0.0179	0.2644	0	0
PAK2	PAK2-1	0.11	0.7896	0.8959	0	0	0.29	0.5496	0.8713	0	0	-0.17	0.6280	0.8862	0	0
PAK2	PAK2-2	-1.24	0.0007	0.0055	1	1	-0.74	0.1002	0.5054	0	0	-0.50	0.1814	0.6872		

PAX9	PAX9-5	0.47	0.2490	0.4594	0	0	1.28	0.0172	0.2287	0	0	-0.81	0.0599	0.4538	0	0
PAX9	PAX9-6	0.06	0.8379	0.8984	0	0	0.23	0.5953	0.8878	0	0	-0.17	0.7150	0.8862	0	0
PCYT1A	PCYT1A-1	-0.59	0.1331	0.3009	0	0	0.04	0.8034	0.9227	0	0	-0.63	0.1196	0.5997	0	0
PCYT1A	PCYT1A-2	-0.40	0.2841	0.4986	0	0	-0.05	0.9126	0.9468	0	0	-0.35	0.3472	0.8319	0	0
PCYT1A	PCYT1A-3	-0.01	0.8858	0.9035	0	0	0.51	0.1752	0.6327	0	0	-0.52	0.0971	0.5511	0	0
PCYT1A	PCYT1A-4	0.48	0.2072	0.4068	0	0	0.11	0.7336	0.9167	0	0	0.37	0.3627	0.8319	0	0
PCYT1A	PCYT1A-5	-0.32	0.3793	0.6029	0	0	-0.19	0.6721	0.9079	0	0	-0.13	0.7017	0.8862	0	0
PCYT1A	PCYT1A-6	0.19	0.6247	0.8043	0	0	0.30	0.4809	0.8506	0	0	-0.12	0.6943	0.8862	0	0
PDCD1LG2	PDCD1LG2-1	-0.30	0.4282	0.6496	0	0	0.81	0.1168	0.5346	0	0	-1.11	0.0033	0.0883	0	1
PDCD1LG2	PDCD1LG2-2	-0.28	0.4590	0.6791	0	0	-0.16	0.7273	0.9151	0	0	-0.12	0.7472	0.8862	0	0
PDCD1LG2	PDCD1LG2-3	-0.39	0.3215	0.5415	0	0	-0.37	0.4297	0.8343	0	0	-0.02	0.8553	0.8872	0	0
PDCD1LG2	PDCD1LG2-4	-1.16	0.0089	0.0408	1	1	-0.32	0.5419	0.8699	0	0	-0.84	0.0697	0.4711	0	0
PDCD1LG2	PDCD1LG2-5	0.06	0.8692	0.8986	0	0	0.17	0.7476	0.9177	0	0	-0.12	0.5492	0.8862	0	0
PDCD1LG2	PDCD1LG2-6	0.08	0.8162	0.8984	0	0	0.02	0.9372	0.9516	0	0	0.06	0.8941	0.8992	0	0
PDGFRA	PDGFRA-1	-0.30	0.5054	0.7155	0	0	0.30	0.4948	0.8506	0	0	-0.06	0.1775	0.6836	0	0
PDGFRA	PDGFRA-2	-0.96	0.0495	0.1500	0	1	-1.16	0.0707	0.4296	0	0	0.20	0.7233	0.8862	0	0
PDGFRA	PDGFRA-3	-0.84	0.0795	0.2104	0	0	-0.51	0.3934	0.8002	0	0	-0.33	0.5397	0.8862	0	0
PDGFRA	PDGFRA-4	-1.50	0.0015	0.0097	1	1	-0.68	0.2506	0.7043	0	0	-0.81	0.0985	0.5522	0	0
PDGFRA	PDGFRA-5	0.10	0.8242	0.8984	0	0	0.16	0.6869	0.9092	0	0	-0.07	0.7110	0.8862	0	0
PDGFRA	PDGFRA-6	-0.58	0.2435	0.4520	0	0	-0.23	0.7352	0.9167	0	0	-0.35	0.4570	0.8862	0	0
PDP1	PDP1-1	0.68	0.1047	0.2554	0	0	0.35	0.5255	0.8653	0	0	0.33	0.4764	0.8862	0	0
PDP1	PDP1-2	0.96	0.1035	0.2533	0	0	1.60	0.0273	0.2924	0	0	-0.63	0.3094	0.8058	0	0
PDP1	PDP1-3	0.42	0.2672	0.4801	0	0	0.05	0.8957	0.9418	0	0	0.36	0.3377	0.8301	0	0
PDP1	PDP1-4	-0.24	0.5283	0.7324	0	0	0.31	0.4732	0.8506	0	0	-0.54	0.1520	0.6504	0	0
PDP1	PDP1-5	-0.21	0.6144	0.7955	0	0	-0.28	0.5086	0.8575	0	0	0.07	0.8491	0.8869	0	0
PDP1	PDP1-6	0.63	0.2001	0.3972	0	0	0.36	0.5134	0.8595	0	0	0.26	0.6185	0.8862	0	0
PEX5L	PEX5L-1	0.64	0.1071	0.2598	0	0	0.48	0.2612	0.7140	0	0	0.16	0.8127	0.8862	0	0
PEX5L	PEX5L-2	0.95	0.0338	0.1120	0	1	0.37	0.5474	0.8713	0	0	0.58	0.2000	0.7138	0	0
PEX5L	PEX5L-3	-1.13	0.0023	0.0139	1	1	-0.80	0.0706	0.4296	0	0	-0.33	0.4082	0.8649	0	0
PEX5L	PEX5L-4	0.09	0.8166	0.8984	0	0	-0.03	0.9428	0.9540	0	0	0.12	0.8124	0.8862	0	0
PEX5L	PEX5L-5	-0.55	0.1295	0.2953	0	0	-0.07	0.8919	0.9418	0	0	-0.48	0.1854	0.6947	0	0
PEX5L	PEX5L-6	-0.56	0.1255	0.2896	0	0	-0.39	0.3695	0.7821	0	0	-0.17	0.6602	0.8862	0	0
PIGX	PIGX-1	-0.51	0.1597	0.3402	0	0	0.58	0.3329	0.7656	0	0	-1.08	0.0053	0.1203	0	1
PIGX	PIGX-2	-0.49	0.2175	0.4201	0	0	-0.06	0.8570	0.9382	0	0	-0.43	0.3007	0.7965	0	0
PIGX	PIGX-3	-1.06	0.0050	0.0259	1	1	-0.66	0.1388	0.5740	0	0	-0.40	0.3308	0.8258	0	0
PIGX	PIGX-4	0.11	0.7626	0.8819	0	0	0.17	0.6632	0.9070	0	0	-0.06	0.7556	0.8862	0	0
PIGX	PIGX-5	-0.99	0.0089	0.0408	1	1	-0.20	0.6326	0.8955	0	0	-0.79	0.0340	0.3489	0	0
PIGX	PIGX-6	-0.10	0.8186	0.8984	0	0	0.39	0.3511	0.7807	0	0	-0.49	0.1309	0.6144	0	0
PIGZ	PIGZ-1	-0.67	0.0836	0.2188	0	0	-0.51	0.2852	0.7355	0	0	-0.16	0.7002	0.8862	0	0
PIGZ	PIGZ-2	-0.64	0.0809	0.2132	0	0	-0.46	0.2967	0.7378	0	0	-0.18	0.6458	0.8862	0	0
PIGZ	PIGZ-3	0.31	0.4432	0.6640	0	0	0.15	0.7418	0.9168	0	0	0.16	0.7164	0.8862	0	0
PIGZ	PIGZ-4	0.29	0.5680	0.7575	0	0	0.70	0.2670	0.7223	0	0	-0.41	0.4147	0.8701	0	0
PIGZ	PIGZ-5	-0.69	0.0703	0.1924	0	1	-0.59	0.1895	0.6461	0	0	-0.09	0.8126	0.8862	0	0
PIGZ	PIGZ-6	-0.82	0.0317	0.1068	0	1	-0.62	0.1648	0.6182	0	0	-0.20	0.6658	0.8862	0	0
PIK3C3	PIK3C3-1	-1.58	0.0000	0.0003	1	1	-0.22	0.6104	0.8927	0	0	-1.36	0.0003	0.0134	1	1
PIK3C3	PIK3C3-2	-1.37	0.0001	0.0015	1	1	-1.15	0.0110	0.1851	0	1	-0.22	0.4268	0.8764	0	0
PIK3C3	PIK3C3-3	0.01	0.9246	0.9253	0	0	1.08	0.0070	0.1430	0	1	-1.07	0.0011	0.0401	1	1
PIK3C3	PIK3C3-4	0.11	0.7493	0.8764	0	0	-0.04	0.9245	0.9485	0	0	0.15	0.7882	0.8862	0	0
PIK3C3	PIK3C3-5	0.57	0.1125	0.2697	0	0	0.82	0.1101	0.5280	0	0	-0.24	0.4034	0.8598	0	0
PIK3C3	PIK3C3-6	0.24	0.5390	0.7383	0	0	0.23	0.5999	0.8878	0	0	0.00	0.8007	0.8862	0	0
PIK3CA	PIK3CA-1	-1.96	0.0000	0.0004	1	1	-1.36	0.0296	0.3025	0	0	-0.60	0.2196	0.7398	0	0
PIK3CA	PIK3CA-2	-0.82	0.0765	0.2048	0	0	-0.34	0.5377	0.8699	0	0	-0.47	0.3176	0.8149	0	0
PIK3CA	PIK3CA-3	0.20	0.5942	0.7778	0	0	0.05	0.9153	0.9471	0	0	0.15	0.7321	0.8862	0	0
PIK3CA	PIK3CA-4	0.03	0.8751	0.8989	0	0	0.17	0.6747	0.9091	0	0	-0.14	0.6987	0.8862	0	0
PIK3CA	PIK3CA-5	-1.10	0.0208	0.0797	0	1	-0.66	0.2605	0.7140	0	0	-0.44	0.3467	0.8319	0	0
PIK3CA	PIK3CA-6	-0.57	0.3193	0.5387	0	0	-0.06	0.9222	0.9485	0	0	-0.51	0.3375	0.8301	0	0
PIK3CB	PIK3CB-1	-1.32	0.0023	0.0139	1	1	-0.86	0.1314	0.5540	0	0	-0.46	0.2822	0.7870	0	0
PIK3CB	PIK3CB-2	-0.12	0.7978	0.8966	0	0	0.35	0.4667	0.8506	0	0	-0.47	0.1916	0.7015	0	0
PIK3CB	PIK3CB-3	-0.74	0.0674	0.1869	0	1	-0.79	0.1030	0.5120	0	0	0.06	0.8665	0.8876	0	0
PIK3CB	PIK3CB-4	-0.80	0.0263	0.0934	0	1	-0.37	0.3769	0.7873	0	0	-0.43	0.2146	0.7289	0	0
PIK3CB	PIK3CB-5	-0.87	0.0292	0.1006	0	1	-0.77	0.1223	0.5405	0	0	-0.10	0.7890	0.8862	0	0
PIK3CB	PIK3CB-6	-1.43	0.0015	0.0099	1	1	-0.91	0.1109	0.5280	0	0	-0.52	0.2921	0.7918	0	0
PIK3R3	PIK3R3-1	0.12	0.7466	0.8764	0	0	0.51	0.2284	0.6900	0	0	-0.39	0.1925	0.7025	0	0
PIK3R3	PIK3R3-2	-1.19	0.0015	0.0098	1	1	-0.82	0.0779	0.4507	0	0	-0.37	0.3173	0.8149	0	0
PIK3R3	PIK3R3-3	-0.40	0.2973	0.5126	0	0	-0.31	0.4892	0.8506	0	0	-0.09	0.7252	0.8862	0	0
PIK3R3	PIK3R3-4	-0.86	0.0205	0.0790	0	1	-0.42	0.3446	0.7771	0	0	-0.44	0.2676	0.7718	0	0
PIK3R3	PIK3R3-5	-0.04	0.7766	0.8900	0	0	0.02	0.8924	0.9418	0	0	-0.05	0.7416	0.8862	0	0
PIK3R3	PIK3R3-6	0.66	0.2370	0.4439	0	0	0.96	0.1769	0.6351	0	0	-0.30	0.6190	0.8862	0	0
PIM1	PIM1-1	-0.42	0.3238	0.5443	0	0	-0.33	0.4946	0.8506	0	0	-0.09	0.7974	0.8862	0	0
PIM1	PIM1-2	-1.03	0.0054	0.0272	1	1	-0.75	0.1018	0.5100	0	0	-0.28	0.3824	0.8463	0	0
PIM1	PIM1-3	-0.02	0.8996	0.9087	0	0	1.74	0.0001	0.0052	1	1	-1.75	0.0000	0.0000	1	1
PIM1	PIM1-4	3.50	0.0000	0.0001	1	1	1.02	0.1707	0.6276	0	0	2.48	0.0005	0.0208	1	1
PIM1	PIM1-5	-0.06	0.8771	0.8989	0	0	-0.09	0.8410	0.9334	0	0	0.02	0.8670	0.8878	0	0
PIM1	PIM1-6	-1.42	0.0001	0.0010	1	1	-0.67	0.1508	0.6006	0	0	-0.75	0.0532	0.4282	0	0
PMAIP1	PMAIP1-1	-0.87	0.0204	0.0790	0	1	-0.53	0.2432	0.7028	0	0	-0.34	0.4311	0.8764	0	0
PMAIP1	PMAIP1-2	0.04	0.8165	0.8984	0	0	-0.02	0.9572	0.9600	0	0	0.06	0.8466	0.8869	0	0
PMAIP1	PMAIP1-3	-0.55	0.1678	0.3497	0	0	-0.28	0.5702	0.8784	0	0	-0.27	0.4903	0.8862	0	0
PMAIP1	PMAIP1-4	-0.72	0.0469	0.1443	0	1	0.20	0.5468	0.8713	0	0	-0.92	0.0094	0.1777	0	1
PMAIP1	PMAIP1-5	-0.70	0.0656	0.1827	0	0	-0.27	0.5547	0.8733	0	0	-0.43	0.2971	0.7965	0	0
PMAIP1	PMAIP1-6	-0.16	0.7192	0.8617	0	0	-0.05	0.8934	0.9418	0	0	-0.11	0.7560	0.8862	0	0
POLR2H	POLR2H-1	-0.67	0.0914	0.2316	0	0	-0.79	0.0973	0.4995	0	0</					

PPP1R2	PPP1R2-4	-0.84	0.0227	0.0855	0	1	0.11	0.5844	0.8823	0	0	-0.95	0.0068	0.1446	0	1
PPP1R2	PPP1R2-5	-0.82	0.0259	0.0928	0	1	-0.48	0.2522	0.7043	0	0	-0.33	0.4021	0.8598	0	0
PPP1R2	PPP1R2-6	-0.34	0.4518	0.6722	0	0	-0.23	0.6188	0.8955	0	0	-0.11	0.8229	0.8862	0	0
PPP2R1A	PPP2R1A-1	0.05	0.8898	0.9050	0	0	0.37	0.4018	0.8096	0	0	-0.33	0.4298	0.8764	0	0
PPP2R1A	PPP2R1A-2	2.88	0.0001	0.0007	1	1	2.02	0.0122	0.1940	0	1	0.86	0.1987	0.7122	0	0
PPP2R1A	PPP2R1A-3	-0.06	0.8365	0.8984	0	0	0.45	0.3154	0.7516	0	0	-0.51	0.2616	0.7666	0	0
PPP2R1A	PPP2R1A-4	-0.57	0.1292	0.2953	0	0	-0.25	0.5420	0.8699	0	0	-0.33	0.3260	0.8243	0	0
PPP2R1A	PPP2R1A-5	4.01	0.0000	0.0000	1	1	2.73	0.0018	0.0592	0	1	1.29	0.0759	0.4939	0	0
PPP2R1A	PPP2R1A-6	-0.35	0.3519	0.5754	0	0	0.03	0.9276	0.9485	0	0	-0.38	0.2670	0.7718	0	0
PPT1	PPT1-1	-0.50	0.2346	0.4424	0	0	0.10	0.8213	0.9265	0	0	-0.60	0.1325	0.6151	0	0
PPT1	PPT1-2	0.50	0.2042	0.4023	0	0	0.39	0.3606	0.7812	0	0	0.11	0.8856	0.8961	0	0
PPT1	PPT1-3	-0.79	0.0343	0.1132	0	1	-0.15	0.7846	0.9227	0	0	-0.63	0.1084	0.5833	0	0
PPT1	PPT1-4	-1.53	0.0001	0.0008	1	1	-1.36	0.0064	0.1363	0	1	-0.17	0.6238	0.8862	0	0
PPT1	PPT1-5	-0.41	0.2926	0.5081	0	0	-0.40	0.3872	0.7961	0	0	-0.01	0.6789	0.8862	0	0
PPT1	PPT1-6	-0.27	0.4712	0.6883	0	0	0.04	0.9076	0.9460	0	0	-0.32	0.4586	0.8862	0	0
PRDM1	PRDM1-1	-1.15	0.0026	0.0155	1	1	-0.77	0.1108	0.5280	0	0	-0.39	0.3397	0.8301	0	0
PRDM1	PRDM1-2	-0.31	0.4264	0.6478	0	0	-0.24	0.6024	0.8878	0	0	-0.07	0.8310	0.8862	0	0
PRDM1	PRDM1-3	-1.74	0.0000	0.0001	1	1	-1.08	0.0294	0.3017	0	0	-0.67	0.0971	0.5511	0	0
PRDM1	PRDM1-4	-0.49	0.2047	0.4023	0	0	0.85	0.0878	0.4786	0	0	-0.36	0.4279	0.8764	0	0
PRDM1	PRDM1-5	-0.54	0.1775	0.3647	0	0	-0.31	0.5263	0.8656	0	0	-0.23	0.5203	0.8862	0	0
PRDM1	PRDM1-6	-0.62	0.1085	0.2625	0	0	-0.60	0.1814	0.6418	0	0	-0.02	0.7589	0.8862	0	0
PRDM14	PRDM14-1	-0.23	0.5280	0.7324	0	0	-0.07	0.8694	0.9417	0	0	-0.16	0.6753	0.8862	0	0
PRDM14	PRDM14-2	-0.43	0.2872	0.5014	0	0	0.07	0.7924	0.9227	0	0	-0.51	0.1698	0.6707	0	0
PRDM14	PRDM14-3	-0.85	0.0343	0.1132	0	1	-0.44	0.3462	0.7772	0	0	-0.41	0.2305	0.7468	0	0
PRDM14	PRDM14-4	-0.41	0.3115	0.5295	0	0	0.71	0.1122	0.5316	0	0	-1.12	0.0028	0.0801	0	1
PRDM14	PRDM14-5	-0.01	0.8980	0.9079	0	0	-0.12	0.7834	0.9227	0	0	0.11	0.8127	0.8862	0	0
PRDM14	PRDM14-6	0.15	0.6963	0.8495	0	0	0.07	0.8769	0.9417	0	0	0.08	0.8122	0.8862	0	0
PREX2	PREX2-1	0.79	0.0377	0.1216	0	1	1.02	0.0260	0.2840	0	0	-0.24	0.3969	0.8575	0	0
PREX2	PREX2-2	-0.64	0.0840	0.2192	0	0	-0.01	0.9186	0.9476	0	0	-0.63	0.0994	0.5522	0	0
PREX2	PREX2-3	-0.04	0.8952	0.9069	0	0	-0.02	0.9532	0.9577	0	0	-0.03	0.8192	0.8862	0	0
PREX2	PREX2-4	-0.07	0.8491	0.8984	0	0	0.10	0.7187	0.9151	0	0	-0.17	0.5633	0.8862	0	0
PREX2	PREX2-5	-0.07	0.0039	0.0213	1	1	-0.55	0.2178	0.6829	0	0	-0.52	0.1773	0.6836	0	0
PREX2	PREX2-6	1.10	0.7931	0.8960	0	0	0.11	0.7738	0.9227	0	0	-0.01	0.8307	0.8862	0	0
PRKCI	PRKCI-1	-0.26	0.4877	0.7034	0	0	-0.29	0.5149	0.8609	0	0	0.03	0.8164	0.8862	0	0
PRKCI	PRKCI-2	0.39	0.3021	0.5162	0	0	0.36	0.3780	0.7877	0	0	0.03	0.8619	0.8872	0	0
PRKCI	PRKCI-3	-0.02	0.9013	0.9092	0	0	0.06	0.8486	0.9336	0	0	-0.08	0.7131	0.8862	0	0
PRKCI	PRKCI-4	-1.26	0.0026	0.0155	1	1	-1.03	0.0511	0.3663	0	0	-0.23	0.5702	0.8862	0	0
PRKCI	PRKCI-5	-0.58	0.1277	0.2928	0	0	-0.05	0.8715	0.9417	0	0	-0.53	0.1325	0.6151	0	0
PRKCI	PRKCI-6	-1.65	0.0001	0.0007	1	1	-1.17	0.0321	0.3113	0	0	-0.49	0.1808	0.6871	0	0
PRKD1	PRKD1-1	-1.07	0.0073	0.0348	1	1	-0.56	0.2215	0.6841	0	0	-0.51	0.1870	0.6947	0	0
PRKD1	PRKD1-2	-0.43	0.2505	0.4607	0	0	0.17	0.5085	0.8575	0	0	-0.60	0.1243	0.6063	0	0
PRKD1	PRKD1-3	-1.30	0.0003	0.0027	1	1	-0.90	0.0408	0.3348	0	0	-0.40	0.2926	0.7918	0	0
PRKD1	PRKD1-4	-1.19	0.0035	0.0198	1	1	-0.58	0.2234	0.6846	0	0	-0.61	0.1773	0.6836	0	0
PRKD1	PRKD1-5	0.19	0.6601	0.8283	0	0	0.19	0.6680	0.9075	0	0	0.00	0.8013	0.8862	0	0
PRKD1	PRKD1-6	-0.04	0.8916	0.9051	0	0	-0.13	0.7787	0.9227	0	0	0.09	0.8155	0.8862	0	0
PSMD10	PSMD10-1	-0.57	0.1105	0.2665	0	0	-0.29	0.4898	0.8506	0	0	-0.28	0.4770	0.8862	0	0
PSMD10	PSMD10-2	1.03	0.0414	0.1302	0	1	1.38	0.0382	0.3308	0	0	-0.35	0.5281	0.8862	0	0
PSMD10	PSMD10-3	0.59	0.1642	0.3462	0	0	0.60	0.2438	0.7028	0	0	-0.01	0.8527	0.8872	0	0
PSMD10	PSMD10-4	5.93	0.0000	0.0000	1	1	3.85	0.0006	0.0300	1	1	2.08	0.0255	0.3050	0	0
PSMD10	PSMD10-5	0.56	0.1618	0.3422	0	0	0.40	0.3596	0.7812	0	0	0.16	0.7834	0.8862	0	0
PSMD10	PSMD10-6	-0.60	0.2312	0.4382	0	0	-0.51	0.4122	0.8217	0	0	-0.09	0.8131	0.8862	0	0
PSMD2	PSMD2-1	0.09	0.8088	0.8984	0	0	0.57	0.2057	0.6676	0	0	-0.48	0.1902	0.6982	0	0
PSMD2	PSMD2-2	0.27	0.5011	0.7124	0	0	0.23	0.6216	0.8955	0	0	0.04	0.8420	0.8867	0	0
PSMD2	PSMD2-3	-1.19	0.0013	0.0089	1	1	-0.79	0.0884	0.4788	0	0	-0.40	0.2622	0.7671	0	0
PSMD2	PSMD2-4	0.04	0.8437	0.8984	0	0	0.43	0.3576	0.7812	0	0	-0.39	0.2868	0.7900	0	0
PSMD2	PSMD2-5	-0.13	0.7338	0.8684	0	0	-0.14	0.7581	0.9199	0	0	0.01	0.8736	0.8910	0	0
PSMD2	PSMD2-6	-1.51	0.0001	0.0009	1	1	-1.22	0.0092	0.1690	0	1	-0.29	0.4725	0.8862	0	0
PTHHL	PTHHL-1	-3.30	0.0000	0.0000	1	1	-1.99	0.0017	0.0566	0	1	-1.31	0.0044	0.1073	0	1
PTHHL	PTHHL-2	-1.28	0.0012	0.0084	1	1	-0.69	0.1604	0.6123	0	0	-0.59	0.1800	0.6871	0	0
PTHHL	PTHHL-3	-1.15	0.0061	0.0307	1	1	-0.85	0.1034	0.5126	0	0	-0.30	0.5071	0.8862	0	0
PTHHL	PTHHL-4	0.06	0.7962	0.8961	0	0	0.72	0.1199	0.5404	0	0	-0.66	0.0907	0.5324	0	0
PTHHL	PTHHL-5	-0.43	0.2640	0.4761	0	0	-0.38	0.3962	0.8031	0	0	-0.04	0.8081	0.8862	0	0
PTHHL	PTHHL-6	-1.02	0.0077	0.0364	1	1	-0.17	0.7237	0.9151	0	0	-0.85	0.0333	0.3463	0	0
PTPRD	PTPRD-1	-2.50	0.0000	0.0000	1	1	-1.77	0.0040	0.1057	0	1	-0.73	0.1336	0.6151	0	0
PTPRD	PTPRD-2	-0.37	0.3241	0.5444	0	0	-0.31	0.5248	0.8653	0	0	-0.06	0.7442	0.8862	0	0
PTPRD	PTPRD-3	0.28	0.4941	0.7067	0	0	0.51	0.2940	0.7378	0	0	-0.24	0.5210	0.8862	0	0
PTPRD	PTPRD-4	-2.12	0.0000	0.0000	1	1	-1.46	0.0077	0.1538	0	1	-0.67	0.1153	0.5901	0	0
PTPRD	PTPRD-5	-1.35	0.0004	0.0037	1	1	-0.76	0.1126	0.5316	0	0	-0.58	0.1521	0.6504	0	0
PTPRD	PTPRD-6	-0.87	0.0219	0.0832	0	1	-0.32	0.6730	0.9082	0	0	-0.54	0.0935	0.5403	0	0
PTPRS	PTPRS-1	-0.91	0.0133	0.0562	0	1	-0.93	0.0386	0.3308	0	0	0.02	0.7690	0.8862	0	0
PTPRS	PTPRS-2	-1.73	0.0000	0.0000	1	1	-0.51	0.3354	0.7684	0	0	-1.22	0.0030	0.0846	0	1
PTPRS	PTPRS-3	-0.87	0.0189	0.0741	0	1	-0.88	0.0575	0.3910	0	0	0.01	0.8335	0.8862	0	0
PTPRS	PTPRS-4	-0.14	0.7431	0.8751	0	0	0.27	0.4759	0.8506	0	0	-0.41	0.2032	0.7168	0	0
PTPRS	PTPRS-5	0.26	0.5048	0.7151	0	0	0.76	0.1228	0.5405	0	0	-0.49	0.2203	0.7398	0	0
PTPRS	PTPRS-6	0.13	0.7191	0.8617	0	0	0.22	0.6029	0.8878	0	0	-0.09	0.7920	0.8862	0	0
PTPRT	PTPRT-1	-0.42	0.3012	0.5157	0	0	0.30	0.5129	0.8594	0	0	-0.72	0.0767	0.4939	0	0
PTPRT	PTPRT-2	0.17	0.6307	0.8057	0	0	1.20	0.0013	0.0454	1	1	-1.03	0.0002	0.0131	1	1
PTPRT	PTPRT-3	-0.69	0.0764	0.2046	0	0	-0.25	0.6137	0.8945	0	0	-0.44	0.2717	0.7761	0	0
PTPRT	PTPRT-4	0.62	0.1551	0.3320	0	0	1.23	0.0159	0.2156	0	0	-0.61	0.1450	0.6406	0	0
PTPRT	PTPRT-5	-0.91	0.0196	0.0764	0	1	0.17	0.6475	0.9022	0	0	-1.07	0.0046	0.1102	0	1
PTPRT	PTPRT-6	-1.19	0.0013	0.0089	1	1	0.22	0.3372	0.7716	0	0	-1.40	0.0001	0.0055	1	1
PYDC2	PYDC2-															

RAD54L	RAD54L-3	1.12	0.0087	0.0401	1	1	0.08	0.7043	0.9141	0	0	1.04	0.0319	0.3400	0	0
RAD54L	RAD54L-4	-0.77	0.0372	0.1205	0	1	-0.48	0.2947	0.7378	0	0	-0.29	0.4285	0.8764	0	0
RAD54L	RAD54L-5	0.54	0.1721	0.3555	0	0	1.42	0.0030	0.0880	0	1	-0.88	0.0122	0.2100	0	0
RAD54L	RAD54L-6	0.00	0.8448	0.8984	0	0	0.23	0.6139	0.8945	0	0	-0.22	0.5671	0.8862	0	0
RANBP3L	RANBP3L-1	-0.59	0.1665	0.3484	0	0	0.50	0.2945	0.7378	0	0	-0.09	0.7478	0.8862	0	0
RANBP3L	RANBP3L-2	0.39	0.3471	0.5714	0	0	0.16	0.7128	0.9145	0	0	0.23	0.6115	0.8862	0	0
RANBP3L	RANBP3L-3	-0.29	0.4839	0.7016	0	0	-0.56	0.2492	0.7043	0	0	0.28	0.5307	0.8862	0	0
RANBP3L	RANBP3L-4	-0.82	0.0230	0.0866	0	1	-0.38	0.4028	0.8096	0	0	-0.44	0.2033	0.7168	0	0
RANBP3L	RANBP3L-5	-1.38	0.0001	0.0015	1	1	-1.13	0.0174	0.2287	0	0	-0.25	0.4167	0.8723	0	0
RANBP3L	RANBP3L-6	-0.32	0.3864	0.6083	0	0	-0.13	0.7662	0.9227	0	0	-0.19	0.5797	0.8862	0	0
RBM10	RBM10-1	-0.24	0.5439	0.7402	0	0	-0.28	0.5076	0.8575	0	0	0.04	0.6905	0.8862	0	0
RBM10	RBM10-2	-1.72	0.0001	0.0013	1	1	-1.65	0.0054	0.1313	0	1	-0.08	0.8602	0.8872	0	0
RBM10	RBM10-3	-1.13	0.0019	0.0122	1	1	-0.71	0.1212	0.5405	0	0	-0.42	0.2380	0.7508	0	0
RBM10	RBM10-4	0.01	0.8676	0.8986	0	0	0.23	0.5802	0.8818	0	0	-0.22	0.5232	0.8862	0	0
RBM10	RBM10-5	0.07	0.8373	0.8984	0	0	-0.12	0.8259	0.9287	0	0	0.19	0.6430	0.8862	0	0
RBM10	RBM10-6	-0.89	0.0145	0.0606	0	1	-0.10	0.8739	0.9417	0	0	-0.80	0.0210	0.2807	0	0
RCL1	RCL1-1	-1.39	0.0003	0.0024	1	1	0.11	0.7017	0.9141	0	0	-1.50	0.0006	0.0245	1	1
RCL1	RCL1-2	0.58	0.1179	0.2782	0	0	0.93	0.0976	0.4995	0	0	-0.35	0.5087	0.8862	0	0
RCL1	RCL1-3	-0.41	0.3017	0.5160	0	0	-0.24	0.5756	0.8797	0	0	-0.16	0.6269	0.8862	0	0
RCL1	RCL1-4	-0.14	0.7171	0.8617	0	0	0.01	0.9361	0.9508	0	0	-0.15	0.6720	0.8862	0	0
RCL1	RCL1-5	-1.43	0.0001	0.0013	1	1	-0.74	0.1175	0.5346	0	0	-0.69	0.0649	0.4669	0	0
RCL1	RCL1-6	-1.02	0.0068	0.0331	1	1	-0.61	0.1786	0.6371	0	0	-0.40	0.2730	0.7763	0	0
RECQL4	RECQL4-1	-0.05	0.9049	0.9106	0	0	0.79	0.0785	0.4529	0	0	-0.84	0.0264	0.3091	0	0
RECQL4	RECQL4-2	-0.84	0.0240	0.0888	0	1	-0.60	0.1812	0.6418	0	0	-0.24	0.6126	0.8862	0	0
RECQL4	RECQL4-3	-0.22	0.5570	0.7513	0	0	-0.34	0.4464	0.8479	0	0	0.11	0.7278	0.8862	0	0
RECQL4	RECQL4-4	0.25	0.5429	0.7397	0	0	0.14	0.7688	0.9227	0	0	0.11	0.8002	0.8862	0	0
RECQL4	RECQL4-5	-1.71	0.0002	0.0022	1	1	-0.43	0.4467	0.8479	0	0	-1.28	0.0117	0.2048	0	0
RECQL4	RECQL4-6	-0.06	0.9286	0.9290	0	0	0.69	0.2007	0.6618	0	0	-0.75	0.0998	0.5522	0	0
REP15	REP15-1	-0.97	0.0286	0.0997	0	1	-0.79	0.1537	0.6025	0	0	-0.18	0.7046	0.8862	0	0
REP15	REP15-2	-1.04	0.0170	0.0686	0	1	-0.10	0.8121	0.9227	0	0	-0.95	0.0211	0.2807	0	0
REP15	REP15-3	-0.60	0.1138	0.2722	0	0	-0.36	0.4328	0.8363	0	0	-0.24	0.5052	0.8862	0	0
REP15	REP15-4	-0.89	0.0219	0.0831	0	1	-0.81	0.0944	0.4956	0	0	-0.08	0.7862	0.8862	0	0
REP15	REP15-5	-0.73	0.0504	0.1520	0	1	-0.70	0.1124	0.5316	0	0	-0.03	0.8444	0.8867	0	0
REP15	REP15-6	0.42	0.2587	0.4706	0	0	0.33	0.4058	0.8150	0	0	0.09	0.8784	0.8921	0	0
REST	REST-1	0.14	0.7303	0.8681	0	0	0.38	0.4134	0.8233	0	0	-0.24	0.4159	0.8718	0	0
REST	REST-2	2.60	0.0001	0.0011	1	1	1.21	0.1306	0.5522	0	0	1.39	0.0414	0.3936	0	0
REST	REST-3	0.96	0.0128	0.0548	0	1	0.27	0.5803	0.8818	0	0	0.70	0.1286	0.6144	0	0
REST	REST-4	-0.06	0.8855	0.9035	0	0	-0.13	0.7485	0.9179	0	0	0.07	0.8385	0.8862	0	0
REST	REST-5	-0.25	0.5467	0.7424	0	0	-0.29	0.4971	0.8519	0	0	0.04	0.8116	0.8862	0	0
REST	REST-6	3.55	0.0000	0.0003	1	1	1.94	0.0435	0.3428	0	0	1.61	0.0469	0.4091	0	0
RET	RET-1	-0.28	0.4670	0.6838	0	0	-0.02	0.9508	0.9564	0	0	-0.27	0.4777	0.8862	0	0
RET	RET-2	-0.06	0.8885	0.9039	0	0	0.38	0.3523	0.7807	0	0	-0.44	0.2464	0.7554	0	0
RET	RET-3	-0.57	0.1437	0.3160	0	0	-0.30	0.5373	0.8699	0	0	-0.27	0.5026	0.8862	0	0
RET	RET-4	-2.15	0.0000	0.0000	1	1	-1.21	0.0205	0.2482	0	0	-0.95	0.0238	0.2913	0	0
RET	RET-5	-0.02	0.9311	0.9311	0	0	0.86	0.0880	0.4786	0	0	-0.88	0.0472	0.4091	0	0
RET	RET-6	1.17	0.0098	0.0439	1	1	0.38	0.5165	0.8619	0	0	0.79	0.1246	0.6063	0	0
RFC4	RFC4-1	1.53	0.0002	0.0017	1	1	0.50	0.3239	0.7594	0	0	1.03	0.0230	0.2913	0	0
RFC4	RFC4-2	-1.16	0.0016	0.0101	1	1	-0.72	0.1178	0.5348	0	0	-0.44	0.2072	0.7221	0	0
RFC4	RFC4-3	-0.04	0.8561	0.8984	0	0	0.39	0.3202	0.7575	0	0	-0.43	0.2331	0.7476	0	0
RFC4	RFC4-4	-0.74	0.0509	0.1529	0	1	0.22	0.4346	0.8370	0	0	-0.96	0.0136	0.2225	0	0
RFC4	RFC4-5	0.12	0.7509	0.8766	0	0	0.46	0.2843	0.7355	0	0	-0.33	0.4224	0.8764	0	0
RFC4	RFC4-6	0.60	0.1894	0.3835	0	0	-0.26	0.5818	0.8818	0	0	-0.24	0.4802	0.8862	0	0
RHPN2	RHPN2-1	-0.57	0.3683	0.5901	0	0	1.15	0.2218	0.6841	0	0	-0.48	0.4883	0.8862	0	0
RHPN2	RHPN2-2	-1.10	0.0025	0.0151	1	1	-0.85	0.0634	0.4091	0	0	-0.25	0.5052	0.8862	0	0
RHPN2	RHPN2-3	-0.27	0.4717	0.6886	0	0	0.23	0.6711	0.9075	0	0	-0.50	0.2129	0.7289	0	0
RHPN2	RHPN2-4	-0.20	0.6053	0.7867	0	0	-0.21	0.7276	0.9151	0	0	0.01	0.7566	0.8862	0	0
RHPN2	RHPN2-5	-0.22	0.5641	0.7556	0	0	-0.27	0.5109	0.8594	0	0	0.05	0.7670	0.8862	0	0
RHPN2	RHPN2-6	-1.23	0.0011	0.0077	1	1	-0.66	0.1493	0.5977	0	0	-0.57	0.0988	0.5522	0	0
RICTOR	RICTOR-1	0.66	0.0858	0.2212	0	0	1.09	0.0287	0.3002	0	0	-0.44	0.2840	0.7878	0	0
RICTOR	RICTOR-2	4.05	0.0000	0.0000	1	1	2.38	0.0069	0.1417	0	1	1.67	0.0334	0.3463	0	0
RICTOR	RICTOR-3	-1.18	0.0021	0.0129	1	1	-0.71	0.1242	0.5405	0	0	-0.47	0.2538	0.7567	0	0
RICTOR	RICTOR-4	-0.19	0.5945	0.7778	0	0	0.00	0.9559	0.9591	0	0	-0.19	0.5645	0.8862	0	0
RICTOR	RICTOR-5	0.22	0.5974	0.7803	0	0	1.57	0.0018	0.0592	0	1	-1.34	0.0004	0.0196	1	1
RICTOR	RICTOR-6	-0.85	0.0237	0.0884	0	1	-0.26	0.6311	0.8955	0	0	-0.59	0.0817	0.5091	0	0
RIT1	RIT1-1	-0.39	0.3143	0.5321	0	0	-0.23	0.6851	0.9092	0	0	-0.16	0.5608	0.8862	0	0
RIT1	RIT1-2	0.04	0.8251	0.8984	0	0	0.60	0.2039	0.6676	0	0	-0.56	0.1427	0.6362	0	0
RIT1	RIT1-3	-0.51	0.1858	0.3776	0	0	-0.36	0.4413	0.8437	0	0	-0.15	0.5638	0.8862	0	0
RIT1	RIT1-4	0.13	0.7102	0.8591	0	0	0.06	0.8795	0.9417	0	0	0.07	0.8596	0.8872	0	0
RIT1	RIT1-5	-0.49	0.1968	0.3929	0	0	-0.35	0.4295	0.8343	0	0	-0.15	0.6887	0.8862	0	0
RIT1	RIT1-6	-0.32	0.4089	0.6328	0	0	-0.17	0.7435	0.9170	0	0	-0.15	0.6958	0.8862	0	0
RLF	RLF-1	-1.38	0.0003	0.0027	1	1	-0.69	0.1953	0.6530	0	0	-0.70	0.0720	0.4843	0	0
RLF	RLF-2	-1.19	0.6553	0.8252	0	0	-0.13	0.7833	0.9227	0	0	-0.06	0.7846	0.8862	0	0
RLF	RLF-3	0.17	0.0361	0.1182	0	1	1.38	0.0337	0.3180	0	0	-0.22	0.7219	0.8862	0	0
RLF	RLF-4	-0.83	0.0281	0.0983	0	1	-0.48	0.2443	0.7028	0	0	-0.35	0.2890	0.7917	0	0
RLF	RLF-5	0.97	0.0810	0.2133	0	0	2.63	0.0000	0.0037	1	1	-1.65	0.0001	0.0068	1	1
RLF	RLF-6	0.47	0.3638	0.5861	0	0	0.35	0.5626	0.8762	0	0	0.12	0.7690	0.8862	0	0
RLN1	RLN1-1	0.22	0.5784	0.7659	0	0	0.29	0.4859	0.8506	0	0	-0.07	0.7833	0.8862	0	0
RLN1	RLN1-2	-1.21	0.0040	0.0219	1	1	-1.30	0.0135	0.2012	0	0	0.10	0.7544	0.8862	0	0
RLN1	RLN1-3	-1.29	0.0011	0.0080	1	1	-1.21	0.0119	0.1940	0	1	-0.08	0.7517	0.8862	0	0
RLN1	RLN1-4	-2.68	0.0000	0.0000	1	1	-2.29	0.0003	0.0221	1	1	-0.39	0.3529	0.8319	0	0
RLN1	RLN1-5	-0.24	0.5476	0.7432	0	0	-0.46	0.2764	0.7316	0	0	0.22	0.6022	0.8862	0	0
RLN1	RLN1-6	-1.57	0.0013	0.0087	1	1	-0.71	0.2489	0.7043	0	0	-0.86	0.0846	0.5114		

RTEL1	RTEL1-2	0.18	0.6410	0.8136	0	0	0.30	0.4740	0.8506	0	0	-0.12	0.7099	0.8862	0	0
RTEL1	RTEL1-3	-0.50	0.2098	0.4097	0	0	-0.42	0.3547	0.7812	0	0	-0.08	0.7304	0.8862	0	0
RTEL1	RTEL1-4	-0.17	0.7172	0.8617	0	0	0.83	0.1185	0.5352	0	0	-0.99	0.0291	0.3228	0	0
RTEL1	RTEL1-5	1.04	0.0410	0.1294	0	1	2.18	0.0000	0.0032	1	1	-1.13	0.0002	0.0131	1	1
RTEL1	RTEL1-6	0.00	0.9126	0.9163	0	0	-0.30	0.4734	0.8506	0	0	0.30	0.4240	0.8764	0	0
RTP1	RTP1-1	0.49	0.2034	0.4014	0	0	0.04	0.8713	0.9417	0	0	0.45	0.2905	0.7917	0	0
RTP1	RTP1-2	-0.01	0.9080	0.9125	0	0	-0.14	0.7603	0.9202	0	0	0.12	0.7707	0.8862	0	0
RTP1	RTP1-3	-0.19	0.6384	0.8117	0	0	1.77	0.0000	0.0020	1	1	-1.96	0.0000	0.0000	1	1
RTP1	RTP1-4	0.31	0.4745	0.6914	0	0	2.35	0.0009	0.0378	1	1	-2.05	0.0003	0.0134	1	1
RTP1	RTP1-5	-0.64	0.1425	0.3147	0	0	-1.07	0.0443	0.3428	0	0	0.44	0.4665	0.8862	0	0
RTP1	RTP1-6	0.70	0.0841	0.2193	0	0	0.77	0.0887	0.4788	0	0	-0.07	0.6332	0.8862	0	0
RTP2	RTP2-1	-0.09	0.8013	0.8966	0	0	0.33	0.3576	0.7812	0	0	-0.41	0.2502	0.7554	0	0
RTP2	RTP2-2	0.95	0.0249	0.0905	0	1	0.57	0.2613	0.7140	0	0	0.38	0.3804	0.8463	0	0
RTP2	RTP2-3	0.11	0.7560	0.8782	0	0	0.05	0.8996	0.9425	0	0	0.06	0.7992	0.8862	0	0
RTP2	RTP2-4	0.15	0.7178	0.8617	0	0	0.26	0.5916	0.8876	0	0	-0.11	0.7471	0.8862	0	0
RTP2	RTP2-5	0.03	0.8450	0.8984	0	0	0.32	0.4749	0.8506	0	0	-0.30	0.4053	0.8601	0	0
RTP2	RTP2-6	0.42	0.3006	0.5156	0	0	0.79	0.0984	0.5010	0	0	-0.37	0.3721	0.8401	0	0
RTP4	RTP4-1	-1.14	0.0059	0.0297	1	1	-0.38	0.4466	0.8479	0	0	-0.76	0.0616	0.4569	0	0
RTP4	RTP4-2	0.19	0.6298	0.8054	0	0	0.21	0.6173	0.8955	0	0	-0.01	0.7549	0.8862	0	0
RTP4	RTP4-3	-0.86	0.0272	0.0962	0	1	-0.34	0.4676	0.8506	0	0	-0.51	0.1949	0.7060	0	0
RTP4	RTP4-4	6.53	0.0000	0.0000	1	1	4.25	0.0001	0.0067	1	1	2.28	0.0133	0.2219	0	0
RTP4	RTP4-5	-0.53	0.2027	0.4007	0	0	-0.27	0.5964	0.8878	0	0	-0.26	0.5168	0.8862	0	0
RTP4	RTP4-6	0.00	0.8976	0.9078	0	0	0.28	0.5241	0.8653	0	0	-0.28	0.4715	0.8862	0	0
RUNX1T1	RUNX1T1-1	-0.01	0.0296	0.1013	0	1	-0.42	0.3481	0.7795	0	0	-0.38	0.2924	0.7918	0	0
RUNX1T1	RUNX1T1-2	0.13	0.7161	0.8617	0	0	-0.02	0.8958	0.9418	0	0	0.15	0.7415	0.8862	0	0
RUNX1T1	RUNX1T1-3	0.38	0.3505	0.5740	0	0	0.47	0.3424	0.7749	0	0	-0.09	0.7175	0.8862	0	0
RUNX1T1	RUNX1T1-4	-0.10	0.7954	0.8960	0	0	0.18	0.6935	0.9092	0	0	-0.27	0.5086	0.8862	0	0
RUNX1T1	RUNX1T1-5	-0.56	0.1338	0.3014	0	0	-0.48	0.2708	0.7275	0	0	-0.07	0.7465	0.8862	0	0
RUNX1T1	RUNX1T1-6	0.47	0.2910	0.5059	0	0	0.42	0.3929	0.8002	0	0	0.05	0.7451	0.8862	0	0
SCAF11	SCAF11-1	-0.36	0.3568	0.5806	0	0	-0.25	0.5668	0.8781	0	0	-0.11	0.7221	0.8862	0	0
SCAF11	SCAF11-2	0.16	0.6740	0.8378	0	0	0.57	0.2396	0.7006	0	0	-0.40	0.2998	0.7965	0	0
SCAF11	SCAF11-3	0.24	0.4464	0.6677	0	0	0.03	0.9324	0.9503	0	0	0.21	0.5154	0.8862	0	0
SCAF11	SCAF11-4	0.24	0.5213	0.7268	0	0	1.18	0.0321	0.3113	0	0	-0.93	0.0418	0.3958	0	0
SCAF11	SCAF11-5	-0.10	0.8522	0.8984	0	0	0.07	0.8395	0.9334	0	0	-0.16	0.6828	0.8862	0	0
SCAF11	SCAF11-6	0.19	0.6384	0.8117	0	0	0.63	0.2620	0.7152	0	0	-0.45	0.3614	0.8319	0	0
SDHA	SDHA-1	-0.61	0.0943	0.2358	0	0	-0.48	0.2801	0.7355	0	0	-0.14	0.6044	0.8862	0	0
SDHA	SDHA-2	-0.11	0.7805	0.8936	0	0	-0.10	0.8043	0.9227	0	0	-0.02	0.7957	0.8862	0	0
SDHA	SDHA-3	-0.98	0.0092	0.0420	1	1	-0.48	0.2869	0.7360	0	0	-0.51	0.1743	0.6790	0	0
SDHA	SDHA-4	-0.88	0.0140	0.0586	0	1	-0.34	0.4798	0.8506	0	0	-0.55	0.1131	0.5872	0	0
SDHA	SDHA-5	-0.95	0.0115	0.0503	0	1	-0.58	0.2074	0.6677	0	0	-0.37	0.3326	0.8278	0	0
SDHA	SDHA-6	-0.42	0.3704	0.5924	0	0	0.63	0.1410	0.5771	0	0	-1.05	0.0060	0.1331	0	1
SDHB	SDHB-1	-0.18	0.6415	0.8139	0	0	0.08	0.8453	0.9334	0	0	-0.26	0.5154	0.8862	0	0
SDHB	SDHB-2	0.14	0.7297	0.8678	0	0	0.37	0.5348	0.8699	0	0	-0.23	0.6970	0.8862	0	0
SDHB	SDHB-3	0.80	0.0588	0.1693	0	1	1.92	0.0006	0.0301	1	1	-1.12	0.0194	0.2770	0	0
SDHB	SDHB-4	-0.62	0.0898	0.2287	0	0	-0.37	0.4015	0.8096	0	0	-0.25	0.4356	0.8764	0	0
SDHB	SDHB-5	0.11	0.6837	0.8433	0	0	0.34	0.4412	0.8437	0	0	-0.23	0.6219	0.8862	0	0
SDHB	SDHB-6	0.39	0.3618	0.5848	0	0	1.70	0.0006	0.0299	1	1	-1.31	0.0005	0.0230	1	1
SDHC	SDHC-1	0.26	0.4934	0.7064	0	0	0.77	0.0866	0.4757	0	0	-0.51	0.1475	0.6427	0	0
SDHC	SDHC-2	0.64	0.0845	0.2200	0	0	-0.42	0.3417	0.7741	0	0	-0.22	0.6033	0.8862	0	0
SDHC	SDHC-3	-0.55	0.1919	0.3853	0	0	0.22	0.6515	0.9043	0	0	-0.77	0.0657	0.4673	0	0
SDHC	SDHC-4	0.07	0.8587	0.8984	0	0	0.07	0.8626	0.9406	0	0	0.00	0.8652	0.8875	0	0
SDHC	SDHC-5	-2.54	0.0000	0.0000	1	1	-1.47	0.0138	0.2029	0	0	-1.07	0.0326	0.3441	0	0
SDHC	SDHC-6	1.45	0.0068	0.0333	1	1	0.92	0.1366	0.5697	0	0	0.53	0.3204	0.8205	0	0
SENP2	SENP2-1	-0.83	0.0373	0.1208	0	1	-0.47	0.3282	0.7620	0	0	-0.37	0.3452	0.8314	0	0
SENP2	SENP2-2	-0.96	0.0065	0.0322	1	1	-0.03	0.8209	0.9265	0	0	-0.93	0.0131	0.2219	0	0
SENP2	SENP2-3	0.16	0.7183	0.8617	0	0	-0.25	0.5758	0.8797	0	0	0.41	0.3113	0.8082	0	0
SENP2	SENP2-4	-1.77	0.0000	0.0002	1	1	-1.36	0.0094	0.1702	0	1	-0.42	0.3414	0.8301	0	0
SENP2	SENP2-5	-0.43	0.2702	0.4841	0	0	-0.53	0.2599	0.7140	0	0	0.09	0.7379	0.8862	0	0
SENP2	SENP2-6	-0.11	0.8005	0.8966	0	0	-0.11	0.8271	0.9287	0	0	0.00	0.8594	0.8872	0	0
SENP5	SENP5-1	0.23	0.5890	0.7739	0	0	0.59	0.2256	0.6875	0	0	-0.36	0.3637	0.8319	0	0
SENP5	SENP5-2	-0.23	0.5866	0.7729	0	0	0.21	0.6211	0.8955	0	0	-0.44	0.2722	0.7761	0	0
SENP5	SENP5-3	-0.62	0.1192	0.2799	0	0	-0.08	0.7966	0.9227	0	0	-0.54	0.1680	0.6693	0	0
SENP5	SENP5-4	-1.34	0.0002	0.0019	1	1	-0.87	0.0546	0.3774	0	0	-0.48	0.2026	0.7165	0	0
SENP5	SENP5-5	-0.84	0.0248	0.0905	0	1	-1.00	0.0377	0.3279	0	0	0.15	0.7982	0.8862	0	0
SENP5	SENP5-6	-0.09	0.8477	0.8984	0	0	-0.11	0.8186	0.9252	0	0	0.02	0.8171	0.8862	0	0
SESN2	SESN2-1	-0.87	0.0239	0.0888	0	1	0.57	0.2346	0.6967	0	0	-1.44	0.0001	0.0079	1	1
SESN2	SESN2-2	-1.27	0.0007	0.0056	1	1	-0.90	0.0446	0.3428	0	0	-0.38	0.4093	0.8649	0	0
SESN2	SESN2-3	-2.38	0.0000	0.0000	1	1	-0.02	0.7542	0.9188	0	0	-2.36	0.0000	0.0000	1	1
SESN2	SESN2-4	-1.00	0.0128	0.0548	0	1	-0.04	0.7747	0.9227	0	0	-0.96	0.0205	0.2807	0	0
SESN2	SESN2-5	-0.39	0.2869	0.5014	0	0	-0.25	0.5572	0.8742	0	0	-0.14	0.7040	0.8862	0	0
SESN2	SESN2-6	-1.66	0.0001	0.0009	1	1	-0.86	0.0961	0.4992	0	0	-0.80	0.0595	0.4538	0	0
SKP2	SKP2-1	0.31	0.4219	0.6433	0	0	0.63	0.2596	0.7140	0	0	-0.32	0.5315	0.8862	0	0
SKP2	SKP2-2	-1.98	0.0000	0.0003	1	1	-1.17	0.0626	0.4079	0	0	-0.81	0.1047	0.5710	0	0
SKP2	SKP2-3	-0.47	0.3350	0.5581	0	0	-0.45	0.4728	0.8506	0	0	-0.02	0.8273	0.8862	0	0
SKP2	SKP2-4	-0.20	0.6865	0.8445	0	0	-0.04	0.9345	0.9508	0	0	-0.16	0.7264	0.8862	0	0
SKP2	SKP2-5	-0.32	0.4953	0.7069	0	0	-0.20	0.7192	0.9151	0	0	-0.12	0.7544	0.8862	0	0
SKP2	SKP2-6	0.20	0.5322	0.7347	0	0	0.05	0.9170	0.9476	0	0	0.15	0.7378	0.8862	0	0
SLC1A1	SLC1A1-1	0.28	0.5112	0.7199	0	0	0.20	0.6464	0.9022	0	0	0.08	0.8874	0.8968	0	0
SLC1A1	SLC1A1-2	-1.40	0.0002	0.0017	1	1	-1.17	0.0116	0.1914	0	1	-0.23	0.5915	0.8862	0	0
SLC1A1	SLC1A1-3	-0.76	0.0422	0.1319	0	1	-0.24	0.5975	0.8878	0	0	-0.52	0.1461	0.6406	0	0
SLC1A1	SLC1A1-4	0.26	0.5394	0.7383	0	0	0.13	0.8021	0.9227	0	0	0.14	0.7621	0.8862	0	0
SLC1A1	SLC1A1-5	0.09	0.8171	0.8984	0	0										

SMARCB1	SMARCB1-1	0.36	0.3359	0.5593	0	0	0.49	0.2961	0.7378	0	0	-0.13	0.7091	0.8862	0	0
SMARCB1	SMARCB1-2	-2.09	0.0000	0.0001	1	1	-2.06	0.0006	0.0300	1	1	-0.03	0.8213	0.8862	0	0
SMARCB1	SMARCB1-3	-0.83	0.0308	0.1047	0	0	-0.37	0.4259	0.8341	0	0	-0.45	0.2112	0.7289	0	0
SMARCB1	SMARCB1-4	-0.21	0.5749	0.7621	0	0	0.04	0.9155	0.9471	0	0	-0.25	0.4645	0.8862	0	0
SMARCB1	SMARCB1-5	0.14	0.6825	0.8426	0	0	0.41	0.2690	0.7253	0	0	-0.27	0.3790	0.8448	0	0
SMARCB1	SMARCB1-6	0.19	0.6256	0.8043	0	0	0.69	0.1516	0.6019	0	0	-0.50	0.1807	0.6871	0	0
SMYD3	SMYD3-1	-0.14	0.7173	0.8617	0	0	0.33	0.3288	0.7622	0	0	-0.47	0.1352	0.6190	0	0
SMYD3	SMYD3-2	-0.88	0.0175	0.0703	0	1	-0.38	0.4065	0.8157	0	0	-0.50	0.1706	0.6716	0	0
SMYD3	SMYD3-3	-0.58	0.1248	0.2888	0	0	-0.25	0.5671	0.8781	0	0	-0.33	0.3991	0.8592	0	0
SMYD3	SMYD3-4	-0.39	0.3937	0.6164	0	0	-0.07	0.8779	0.9417	0	0	-0.33	0.4418	0.8806	0	0
SMYD3	SMYD3-5	0.49	0.2026	0.4007	0	0	1.00	0.0231	0.2641	0	0	-0.51	0.1453	0.6406	0	0
SMYD3	SMYD3-6	-0.37	0.3656	0.5869	0	0	0.27	0.5699	0.8784	0	0	-0.65	0.0857	0.5139	0	0
SOCS1	SOCS1-1	-1.30	0.0013	0.0087	1	1	-0.22	0.6620	0.9070	0	0	-1.08	0.0055	0.1244	0	1
SOCS1	SOCS1-2	0.13	0.7250	0.8657	0	0	0.25	0.5619	0.8762	0	0	-0.12	0.6989	0.8862	0	0
SOCS1	SOCS1-3	-0.73	0.0555	0.1618	0	1	-0.16	0.7452	0.9177	0	0	-0.56	0.1154	0.5901	0	0
SOCS1	SOCS1-4	-1.39	0.0003	0.0028	1	1	-1.49	0.0024	0.0765	0	1	0.10	0.9028	0.9053	0	0
SOCS1	SOCS1-5	-2.10	0.0000	0.0001	1	1	-1.67	0.0065	0.1363	0	1	-0.43	0.4544	0.8862	0	0
SOCS1	SOCS1-6	0.18	0.5424	0.7397	0	0	0.37	0.4932	0.8506	0	0	-0.19	0.7236	0.8862	0	0
SOX17	SOX17-1	-0.10	0.7702	0.8851	0	0	0.13	0.7523	0.9184	0	0	-0.22	0.5716	0.8862	0	0
SOX17	SOX17-2	-1.14	0.0016	0.0104	1	1	-0.50	0.2642	0.7196	0	0	-0.64	0.0823	0.5091	0	0
SOX17	SOX17-3	-0.32	0.4414	0.6621	0	0	0.41	0.3780	0.7877	0	0	-0.73	0.0669	0.4675	0	0
SOX17	SOX17-4	-0.25	0.5488	0.7439	0	0	0.23	0.6201	0.8955	0	0	-0.48	0.1577	0.6578	0	0
SOX17	SOX17-5	-1.10	0.0041	0.0224	1	1	-0.94	0.0468	0.3525	0	0	-0.16	0.6646	0.8862	0	0
SOX17	SOX17-6	0.31	0.4603	0.6798	0	0	0.42	0.4252	0.8341	0	0	-0.11	0.6547	0.8862	0	0
SOX2	SOX2-1	-0.36	0.3342	0.5572	0	0	-0.02	0.9212	0.9485	0	0	-0.34	0.3025	0.7985	0	0
SOX2	SOX2-2	1.12	0.0051	0.0263	1	1	0.87	0.0657	0.4166	0	0	0.25	0.5301	0.8862	0	0
SOX2	SOX2-3	-0.24	0.5426	0.7397	0	0	-0.02	0.8924	0.9418	0	0	-0.22	0.5757	0.8862	0	0
SOX2	SOX2-4	-2.14	0.0000	0.0000	1	1	-1.12	0.0293	0.3017	0	0	-1.02	0.0091	0.1763	0	1
SOX2	SOX2-5	0.00	0.8300	0.8984	0	0	-0.08	0.8372	0.9322	0	0	0.08	0.8870	0.8968	0	0
SOX2	SOX2-6	-0.99	0.0071	0.0342	1	1	-0.48	0.3014	0.7439	0	0	-0.51	0.1527	0.6505	0	0
SOX4	SOX4-1	0.33	0.4153	0.6374	0	0	0.29	0.4712	0.8506	0	0	0.04	0.8070	0.8862	0	0
SOX4	SOX4-2	1.62	0.0005	0.0039	1	1	0.84	0.1448	0.5865	0	0	0.79	0.0757	0.4939	0	0
SOX4	SOX4-3	-0.08	0.8196	0.8984	0	0	-0.40	0.3774	0.7877	0	0	0.32	0.3752	0.8416	0	0
SOX4	SOX4-4	-1.04	0.0071	0.0343	1	1	-0.53	0.2455	0.7029	0	0	-0.52	0.1628	0.6661	0	0
SOX4	SOX4-5	0.55	0.1635	0.3451	0	0	0.63	0.1497	0.5981	0	0	-0.09	0.6003	0.8862	0	0
SOX4	SOX4-6	-0.44	0.2536	0.4635	0	0	-0.38	0.3944	0.8003	0	0	-0.05	0.7772	0.8862	0	0
SPATA6L	SPATA6L-1	0.55	0.2351	0.4424	0	0	0.38	0.4850	0.8506	0	0	0.18	0.7149	0.8862	0	0
SPATA6L	SPATA6L-2	-0.28	0.4864	0.7031	0	0	0.21	0.7099	0.9142	0	0	-0.49	0.2055	0.7202	0	0
SPATA6L	SPATA6L-3	0.33	0.4258	0.6476	0	0	0.30	0.5207	0.8648	0	0	0.03	0.8536	0.8872	0	0
SPATA6L	SPATA6L-4	1.64	0.0017	0.0110	1	1	0.84	0.1391	0.5741	0	0	0.80	0.1246	0.6063	0	0
SPATA6L	SPATA6L-5	0.19	0.6192	0.8002	0	0	0.12	0.7605	0.9202	0	0	0.07	0.8951	0.8992	0	0
SPATA6L	SPATA6L-6	-0.86	0.0207	0.0797	0	1	-0.44	0.3451	0.7772	0	0	-0.42	0.2759	0.7795	0	0
SPEN	SPEN-1	-0.64	0.1014	0.2489	0	0	-0.08	0.8082	0.9227	0	0	-0.56	0.1618	0.6655	0	0
SPEN	SPEN-2	-0.13	0.7109	0.8591	0	0	-0.07	0.8587	0.9392	0	0	-0.06	0.7562	0.8862	0	0
SPEN	SPEN-3	1.18	0.0146	0.0606	0	1	0.88	0.1171	0.5346	0	0	0.30	0.4751	0.8862	0	0
SPEN	SPEN-4	-0.44	0.2453	0.4546	0	0	-0.17	0.5316	0.8690	0	0	-0.61	0.1442	0.6403	0	0
SPEN	SPEN-5	-0.46	0.2317	0.4389	0	0	-0.55	0.2365	0.6979	0	0	0.09	0.8011	0.8862	0	0
SPEN	SPEN-6	-0.73	0.0512	0.1535	0	1	-0.44	0.3162	0.7516	0	0	-0.29	0.4306	0.8764	0	0
SPOP	SPOP-1	-0.15	0.8123	0.8984	0	0	0.08	0.8042	0.9227	0	0	-0.23	0.5618	0.8862	0	0
SPOP	SPOP-2	-0.52	0.1710	0.3538	0	0	-0.24	0.6556	0.9051	0	0	-0.28	0.3855	0.8468	0	0
SPOP	SPOP-3	0.11	0.7666	0.8837	0	0	0.32	0.3564	0.7812	0	0	-0.22	0.4756	0.8862	0	0
SPOP	SPOP-4	-0.59	0.1309	0.2975	0	0	-0.32	0.4884	0.8506	0	0	-0.27	0.4533	0.8862	0	0
SPOP	SPOP-5	1.21	0.0930	0.2335	0	0	1.16	0.2066	0.6676	0	0	0.05	0.7515	0.8862	0	0
SPOP	SPOP-6	0.46	0.2974	0.5126	0	0	0.20	0.6906	0.9092	0	0	0.26	0.6209	0.8862	0	0
SRC	SRC-1	-0.43	0.2585	0.4706	0	0	0.23	0.5932	0.8878	0	0	-0.65	0.0621	0.4576	0	0
SRC	SRC-2	-0.11	0.8448	0.8984	0	0	0.25	0.6488	0.9030	0	0	-0.36	0.3943	0.8528	0	0
SRC	SRC-3	-2.36	0.0000	0.0000	1	1	-0.88	0.1251	0.5406	0	0	-1.49	0.0010	0.0377	1	1
SRC	SRC-4	0.44	0.2861	0.5011	0	0	0.48	0.3458	0.7772	0	0	-0.04	0.7119	0.8862	0	0
SRC	SRC-5	-0.33	0.3877	0.6090	0	0	-0.15	0.7273	0.9151	0	0	-0.18	0.6445	0.8862	0	0
SRC	SRC-6	-0.22	0.5878	0.7739	0	0	0.28	0.5436	0.8702	0	0	-0.49	0.1482	0.6427	0	0
SRSF2	SRSF2-1	0.54	0.2085	0.4081	0	0	0.95	0.0503	0.3648	0	0	-0.41	0.2700	0.7751	0	0
SRSF2	SRSF2-2	1.06	0.0247	0.0905	0	1	1.32	0.0490	0.3589	0	0	-0.26	0.2114	0.7289	0	0
SRSF2	SRSF2-3	0.05	0.8634	0.8986	0	0	0.02	0.8610	0.9406	0	0	0.03	0.7268	0.8862	0	0
SRSF2	SRSF2-4	0.71	0.0738	0.1990	0	1	0.98	0.0618	0.4045	0	0	-0.27	0.5772	0.8862	0	0
SRSF2	SRSF2-5	-0.74	0.0475	0.1449	0	1	-0.40	0.4027	0.8096	0	0	-0.34	0.3731	0.8403	0	0
SRSF2	SRSF2-6	0.80	0.0777	0.2069	0	0	1.50	0.0048	0.1175	0	1	-0.70	0.0985	0.5522	0	0
SST	SST-1	-1.56	0.0003	0.0029	1	1	-1.02	0.0680	0.4219	0	0	-0.54	0.1689	0.6693	0	0
SST	SST-2	0.54	0.1674	0.3490	0	0	0.59	0.1888	0.6454	0	0	-0.05	0.8046	0.8862	0	0
SST	SST-3	-0.78	0.0466	0.1437	0	1	-0.63	0.1769	0.6351	0	0	-0.15	0.6567	0.8862	0	0
SST	SST-4	-0.60	0.1015	0.2489	0	0	-0.66	0.1284	0.5488	0	0	0.06	0.8328	0.8862	0	0
SST	SST-5	-1.80	0.0000	0.0001	1	1	-0.71	0.1580	0.6087	0	0	-1.08	0.0077	0.1569	0	1
SST	SST-6	-0.26	0.5497	0.7443	0	0	-0.22	0.6908	0.9092	0	0	-0.04	0.8912	0.8987	0	0
ST6GAL1	ST6GAL1-1	-0.08	0.8538	0.8984	0	0	0.27	0.5895	0.8876	0	0	-0.35	0.4168	0.8723	0	0
ST6GAL1	ST6GAL1-2	-0.60	0.1181	0.2784	0	0	-0.11	0.9144	0.9471	0	0	-0.49	0.1939	0.7049	0	0
ST6GAL1	ST6GAL1-3	-0.11	0.7901	0.8960	0	0	-0.05	0.9272	0.9485	0	0	-0.06	0.7791	0.8862	0	0
ST6GAL1	ST6GAL1-4	0.24	0.5645	0.7556	0	0	0.42	0.3349	0.7680	0	0	-0.18	0.5855	0.8862	0	0
ST6GAL1	ST6GAL1-5	-0.74	0.0532	0.1574	0	1	-0.47	0.2743	0.7313	0	0	-0.28	0.3614	0.8319	0	0
ST6GAL1	ST6GAL1-6	-0.35	0.3865	0.6083	0	0	-0.33	0.4789	0.8506	0	0	-0.02	0.8018	0.8862	0	0
STK40	STK40-1	-0.90	0.0181	0.0722	0	1	-0.33	0.5272	0.8656	0	0	-0.57	0.1230	0.6063	0	0
STK40	STK40-2	-0.92	0.0238	0.0886	0	1	-0.87	0.0922	0.4903	0	0	-0.04	0.8642	0.8872	0	0
STK40	STK40-3	-1.01	0.0061	0.0305	1	1	-0.58	0.2082	0.6677	0	0	-0.43	0.2330	0.7476	0	0
STK40	STK40-4	-0.93	0.0094</													

TCDEX1D2	TCDEX1D2-6	0.11	0.7524	0.8774	0	0	0.12	0.7816	0.9227	0	0	-0.01	0.9123	0.9131	0	0
TEK	TEK-1	0.53	0.1647	0.3465	0	0	0.59	0.1849	0.6431	0	0	-0.06	0.7107	0.8862	0	0
TEK	TEK-2	-0.40	0.3151	0.5330	0	0	-0.13	0.8028	0.9227	0	0	-0.26	0.4903	0.8862	0	0
TEK	TEK-3	-0.08	0.8405	0.8984	0	0	0.69	0.1493	0.5977	0	0	-0.77	0.0547	0.4309	0	0
TEK	TEK-4	-0.83	0.0267	0.0946	0	1	-0.39	0.3911	0.7998	0	0	-0.44	0.2228	0.7398	0	0
TEK	TEK-5	-0.57	0.1344	0.3022	0	0	0.03	0.8646	0.9417	0	0	-0.60	0.1152	0.5901	0	0
TEK	TEK-6	0.29	0.4401	0.6610	0	0	0.06	0.8537	0.9362	0	0	0.23	0.5480	0.8862	0	0
TERT	TERT-1	-0.04	0.8882	0.9039	0	0	0.67	0.1585	0.6087	0	0	-0.71	0.0521	0.4254	0	0
TERT	TERT-2	1.60	0.0002	0.0017	1	1	-0.12	0.8088	0.9227	0	0	1.72	0.0001	0.0049	1	1
TERT	TERT-3	-0.17	0.7314	0.8681	0	0	-0.40	0.4548	0.8506	0	0	0.23	0.6994	0.8862	0	0
TERT	TERT-4	-0.49	0.2190	0.4214	0	0	-0.10	0.7905	0.9227	0	0	-0.39	0.3150	0.8135	0	0
TERT	TERT-5	-2.58	0.0000	0.0000	1	1	-2.11	0.0004	0.0248	1	1	-0.47	0.3686	0.8381	0	0
TERT	TERT-6	-0.87	0.0230	0.0866	0	1	-0.76	0.0999	0.5054	0	0	-0.12	0.7350	0.8862	0	0
TFRC	TFRC-1	2.01	0.0001	0.0011	1	1	0.98	0.0847	0.4703	0	0	1.03	0.0493	0.4157	0	0
TFRC	TFRC-2	0.88	0.0244	0.0898	0	1	0.11	0.7561	0.9197	0	0	0.77	0.0825	0.5091	0	0
TFRC	TFRC-3	-0.23	0.5722	0.7601	0	0	0.01	0.9502	0.9562	0	0	-0.24	0.5224	0.8862	0	0
TFRC	TFRC-4	0.20	0.5812	0.7676	0	0	1.20	0.0081	0.1560	0	1	-1.00	0.0080	0.1592	0	1
TFRC	TFRC-5	0.10	0.7957	0.8960	0	0	0.18	0.7035	0.9141	0	0	-0.07	0.8187	0.8862	0	0
TFRC	TFRC-6	0.64	0.2743	0.4893	0	0	1.64	0.0080	0.1544	0	1	-1.00	0.0260	0.3068	0	0
THPO	THPO-1	-0.30	0.4509	0.6713	0	0	-0.11	0.8007	0.9227	0	0	-0.19	0.6141	0.8862	0	0
THPO	THPO-2	-0.42	0.2374	0.4443	0	0	-0.25	0.5546	0.8733	0	0	-0.17	0.6229	0.8862	0	0
THPO	THPO-3	-0.10	0.7950	0.8960	0	0	0.10	0.7962	0.9227	0	0	-0.19	0.5753	0.8862	0	0
THPO	THPO-4	-0.02	0.8517	0.8984	0	0	0.05	0.8829	0.9417	0	0	-0.07	0.8583	0.8872	0	0
THPO	THPO-5	0.13	0.7465	0.8764	0	0	0.05	0.9187	0.9476	0	0	0.08	0.7711	0.8862	0	0
THPO	THPO-6	0.20	0.6251	0.8043	0	0	0.12	0.7833	0.9227	0	0	0.08	0.9102	0.9113	0	0
TM4SF19	TM4SF19-1	-0.65	0.0814	0.2139	0	0	-0.32	0.4893	0.8506	0	0	-0.33	0.3273	0.8250	0	0
TM4SF19	TM4SF19-2	0.33	0.3876	0.6090	0	0	0.65	0.1372	0.5697	0	0	-0.32	0.3564	0.8319	0	0
TM4SF19	TM4SF19-3	2.68	0.0001	0.0015	1	1	4.66	0.0000	0.0001	1	1	-1.98	0.0012	0.0408	1	1
TM4SF19	TM4SF19-4	-0.30	0.4337	0.6538	0	0	-0.04	0.9441	0.9541	0	0	-0.26	0.4608	0.8862	0	0
TM4SF19	TM4SF19-5	2.82	0.0000	0.0002	1	1	1.88	0.0042	0.1093	0	1	0.94	0.1441	0.6403	0	0
TM4SF19	TM4SF19-6	-0.24	0.5208	0.7268	0	0	-0.23	0.6125	0.8945	0	0	-0.01	0.8455	0.8869	0	0
TMCO2	TMCO2-1	-1.51	0.0004	0.0031	1	1	-1.44	0.0135	0.2012	0	0	-0.07	0.6288	0.8862	0	0
TMCO2	TMCO2-2	-2.35	0.0000	0.0000	1	1	-2.14	0.0003	0.0221	1	1	-0.21	0.7167	0.8862	0	0
TMCO2	TMCO2-3	-0.12	0.7880	0.8950	0	0	-0.50	0.2845	0.7355	0	0	0.38	0.3675	0.8379	0	0
TMCO2	TMCO2-4	-0.07	0.8282	0.8984	0	0	0.22	0.5845	0.8823	0	0	-0.28	0.3701	0.8381	0	0
TMCO2	TMCO2-5	1.91	0.0003	0.0024	1	1	1.78	0.0074	0.1499	0	1	0.13	0.7294	0.8862	0	0
TMCO2	TMCO2-6	0.08	0.8487	0.8984	0	0	-0.25	0.6002	0.8878	0	0	0.33	0.3607	0.8319	0	0
TMEM207	TMEM207-1	0.07	0.7911	0.8960	0	0	0.17	0.7355	0.9167	0	0	-0.10	0.8663	0.8876	0	0
TMEM207	TMEM207-2	-0.22	0.5540	0.7481	0	0	-0.06	0.8761	0.9417	0	0	-0.16	0.6944	0.8862	0	0
TMEM207	TMEM207-3	-0.39	0.2794	0.4935	0	0	0.02	0.7205	0.9151	0	0	-0.41	0.2488	0.7554	0	0
TMEM207	TMEM207-4	-1.31	0.0007	0.0054	1	1	-0.88	0.0731	0.4377	0	0	-0.43	0.2773	0.7796	0	0
TMEM207	TMEM207-5	0.56	0.1294	0.2953	0	0	0.65	0.1918	0.6492	0	0	-0.10	0.7669	0.8862	0	0
TMEM207	TMEM207-6	0.27	0.4668	0.6838	0	0	0.27	0.5702	0.8784	0	0	0.00	0.7190	0.8862	0	0
TMEM41A	TMEM41A-1	-1.25	0.0007	0.0054	1	1	-0.79	0.0803	0.4602	0	0	-0.46	0.2896	0.7917	0	0
TMEM41A	TMEM41A-2	-1.05	0.0035	0.0196	1	1	-0.48	0.3671	0.7821	0	0	-0.57	0.1102	0.5872	0	0
TMEM41A	TMEM41A-3	-0.05	0.8500	0.8984	0	0	0.40	0.3664	0.7821	0	0	-0.45	0.1882	0.6953	0	0
TMEM41A	TMEM41A-4	0.70	0.0847	0.2200	0	0	0.33	0.5011	0.8538	0	0	0.37	0.3522	0.8319	0	0
TMEM41A	TMEM41A-5	-0.32	0.3861	0.6083	0	0	-0.14	0.8039	0.9227	0	0	-0.18	0.6220	0.8862	0	0
TMEM41A	TMEM41A-6	-0.96	0.0114	0.0499	1	1	-0.71	0.1132	0.5322	0	0	-0.24	0.5743	0.8862	0	0
TMEM44	TMEM44-1	-0.12	0.7840	0.8938	0	0	-0.07	0.8826	0.9417	0	0	-0.05	0.8087	0.8862	0	0
TMEM44	TMEM44-2	-0.77	0.0371	0.1205	0	1	-0.24	0.6054	0.8886	0	0	-0.53	0.1546	0.6518	0	0
TMEM44	TMEM44-3	1.12	0.0051	0.0263	1	1	0.92	0.0584	0.3962	0	0	0.20	0.6765	0.8862	0	0
TMEM44	TMEM44-4	-0.30	0.4307	0.6520	0	0	0.18	0.7374	0.9167	0	0	-0.48	0.1873	0.6947	0	0
TMEM44	TMEM44-5	-1.14	0.0025	0.0151	1	1	-0.20	0.6503	0.9036	0	0	-0.94	0.0517	0.4242	0	0
TMEM44	TMEM44-6	3.85	0.0000	0.0001	1	1	4.15	0.0000	0.0024	1	1	-0.29	0.3067	0.8034	0	0
TMPRSS11E	TMPRSS11E	-0.50	0.1546	0.3320	0	0	-0.53	0.2153	0.6817	0	0	0.03	0.8757	0.8913	0	0
TMPRSS11E	TMPRSS11E	0.52	0.1766	0.3634	0	0	0.81	0.0665	0.4184	0	0	-0.29	0.4612	0.8862	0	0
TMPRSS11E	TMPRSS11E	0.16	0.6844	0.8433	0	0	0.05	0.8773	0.9417	0	0	0.12	0.8146	0.8862	0	0
TMPRSS11E	TMPRSS11E	-0.50	0.1614	0.3419	0	0	-0.45	0.2949	0.7378	0	0	-0.05	0.7808	0.8862	0	0
TMPRSS11E	TMPRSS11E	-0.05	0.9020	0.9092	0	0	0.15	0.7262	0.9151	0	0	-0.20	0.5854	0.8862	0	0
TMPRSS11E	TMPRSS11E	-0.25	0.5130	0.7204	0	0	-0.11	0.7328	0.9167	0	0	-0.14	0.7780	0.8862	0	0
TNK2	TNK2-1	0.62	0.1382	0.3078	0	0	0.49	0.3176	0.7528	0	0	0.12	0.8146	0.8862	0	0
TNK2	TNK2-2	-0.25	0.5028	0.7126	0	0	0.22	0.5663	0.8781	0	0	-0.47	0.1908	0.6996	0	0
TNK2	TNK2-3	-1.38	0.0003	0.0026	1	1	-0.82	0.0823	0.4657	0	0	-0.56	0.1465	0.6411	0	0
TNK2	TNK2-4	0.46	0.2297	0.4357	0	0	0.60	0.1776	0.6354	0	0	-0.14	0.5985	0.8862	0	0
TNK2	TNK2-5	0.04	0.8719	0.8989	0	0	0.29	0.4582	0.8506	0	0	-0.25	0.4468	0.8819	0	0
TNK2	TNK2-6	-0.02	0.8581	0.8984	0	0	0.34	0.4904	0.8506	0	0	-0.37	0.3818	0.8463	0	0
TOP1	TOP1-1	-0.92	0.0123	0.0535	0	1	-0.59	0.1739	0.6309	0	0	-0.33	0.4841	0.8862	0	0
TOP1	TOP1-2	-0.94	0.0124	0.0538	0	1	-0.40	0.4812	0.8506	0	0	-0.54	0.1595	0.6623	0	0
TOP1	TOP1-3	-0.86	0.0105	0.0465	1	1	-0.17	0.6681	0.9075	0	0	-0.79	0.0498	0.4170	0	0
TOP1	TOP1-4	-0.96	0.0174	0.0700	0	1	-0.46	0.2933	0.7378	0	0	-0.40	0.3070	0.8034	0	0
TOP1	TOP1-5	-0.85	0.0288	0.0997	0	1	-1.13	0.0411	0.3348	0	0	0.28	0.7294	0.8862	0	0
TOP1	TOP1-6	-0.11	0.8519	0.8984	0	0	0.83	0.0944	0.4956	0	0	-0.94	0.0269	0.3091	0	0
TP63	TP63-1	-0.24	0.5628	0.7549	0	0	0.13	0.5515	0.8731	0	0	-0.37	0.2489	0.7554	0	0
TP63	TP63-2	-0.18	0.6053	0.7867	0	0	-0.18	0.6769	0.9091	0	0	0.00	0.7914	0.8862	0	0
TP63	TP63-3	-1.67	0.0000	0.0002	1	1	-1.21	0.0170	0.2280	0	0	-0.46	0.2504	0.7554	0	0
TP63	TP63-4	0.75	0.0683	0.1882	0	1	1.63	0.0007	0.0319	1	1	-0.88	0.0174	0.2582	0	0
TP63	TP63-5	0.07	0.8526	0.8984	0	0	-0.12	0.7824	0.9227	0	0	0.18	0.6401	0.8862	0	0
TP63	TP63-6	-0.23	0.5709	0.7601	0	0	-0.16	0.7248	0.9151	0	0	-0.07	0.8407	0.8862	0	0
TPRG1	TPRG1-1	0.57	0.1234	0.2868	0	0	0.36	0.3388	0.7718	0	0	0.21	0.6120	0.8862	0	0
TPRG1	TPRG1-2	0.02	0.8531	0.8984	0	0	0.14	0.7670	0.9227	0	0	-0.11	0.7581	0.8862	0	0
TPRG1	TPRG1-3	-0.97	0.0134	0.0562	0	1	-0.45	0.3510	0.7807</							

TTC14	TTC14-5	-0.45	0.2391	0.4461	0	0	-0.28	0.5366	0.8699	0	0	-0.17	0.6083	0.8862	0	0
TTC14	TTC14-6	-1.89	0.0000	0.0000	1	1	-0.96	0.0333	0.3153	0	0	-0.93	0.0159	0.2422	0	0
TXNRD1	TXNRD1-1	0.50	0.1950	0.3896	0	0	0.74	0.1146	0.5346	0	0	-0.24	0.5127	0.8862	0	0
TXNRD1	TXNRD1-2	0.48	0.3270	0.5475	0	0	0.42	0.4538	0.8506	0	0	0.06	0.8813	0.8929	0	0
TXNRD1	TXNRD1-3	-1.74	0.0000	0.0001	1	1	-0.77	0.1051	0.5155	0	0	-0.98	0.0182	0.2654	0	0
TXNRD1	TXNRD1-4	0.10	0.8283	0.8984	0	0	-0.14	0.7819	0.9227	0	0	0.23	0.6272	0.8862	0	0
TXNRD1	TXNRD1-5	0.59	0.1248	0.2888	0	0	0.86	0.0845	0.4703	0	0	-0.27	0.4990	0.8862	0	0
TXNRD1	TXNRD1-6	0.51	0.2340	0.4421	0	0	0.56	0.2431	0.7028	0	0	-0.05	0.7429	0.8862	0	0
UBXN7	UBXN7-1	-1.11	0.0047	0.0248	1	1	-0.83	0.0767	0.4465	0	0	-0.28	0.4186	0.8752	0	0
UBXN7	UBXN7-2	1.56	0.0037	0.0204	1	1	2.26	0.0005	0.0289	1	1	-0.70	0.1554	0.6518	0	0
UBXN7	UBXN7-3	0.18	0.6873	0.8445	0	0	-0.04	0.9266	0.9485	0	0	0.22	0.6415	0.8862	0	0
UBXN7	UBXN7-4	-0.29	0.4867	0.7031	0	0	0.42	0.3612	0.7812	0	0	-0.72	0.0612	0.4562	0	0
UBXN7	UBXN7-5	-0.44	0.2608	0.4731	0	0	-0.29	0.5070	0.8575	0	0	-0.15	0.6624	0.8862	0	0
UBXN7	UBXN7-6	-0.49	0.2197	0.4221	0	0	-0.35	0.4335	0.8369	0	0	-0.14	0.6896	0.8862	0	0
UGT2B15	UGT2B15-1	-1.83	0.0000	0.0005	1	1	-1.13	0.0960	0.4992	0	0	-0.70	0.1133	0.5872	0	0
UGT2B15	UGT2B15-2	-0.46	0.2586	0.4706	0	0	-0.02	0.6233	0.8955	0	0	-0.44	0.3144	0.8135	0	0
UGT2B15	UGT2B15-3	0.55	0.1604	0.3406	0	0	0.13	0.7812	0.9227	0	0	0.42	0.3276	0.8250	0	0
UGT2B15	UGT2B15-4	-1.30	0.0025	0.0151	1	1	-0.77	0.1811	0.6418	0	0	-0.53	0.1831	0.6882	0	0
UGT2B15	UGT2B15-5	-1.90	0.0000	0.0006	1	1	-1.70	0.0128	0.1963	0	1	-0.20	0.4836	0.8862	0	0
UGT2B15	UGT2B15-6	-2.31	0.0000	0.0000	1	1	-1.04	0.0942	0.4956	0	0	-1.27	0.0052	0.1191	0	1
UGT2B17	UGT2B17-1	0.37	0.3788	0.6027	0	0	0.80	0.0970	0.4995	0	0	-0.43	0.2454	0.7554	0	0
UGT2B17	UGT2B17-2	-0.97	0.0083	0.0385	1	1	-0.69	0.1365	0.5697	0	0	-0.28	0.3729	0.8403	0	0
UGT2B17	UGT2B17-3	-0.05	0.8679	0.8986	0	0	-0.03	0.9652	0.9672	0	0	-0.02	0.8054	0.8862	0	0
UGT2B17	UGT2B17-4	-0.66	0.1609	0.3413	0	0	-0.10	0.7663	0.9227	0	0	-0.55	0.3249	0.8243	0	0
UGT2B17	UGT2B17-5	-3.48	0.0000	0.0000	1	1	-1.01	0.1716	0.6276	0	0	-2.47	0.0002	0.0089	1	1
UGT2B17	UGT2B17-6	0.25	0.5288	0.7326	0	0	0.73	0.1214	0.5405	0	0	-0.48	0.1953	0.7061	0	0
UGT3A1	UGT3A1-1	-0.38	0.2945	0.5090	0	0	-0.57	0.2097	0.6694	0	0	0.18	0.6536	0.8862	0	0
UGT3A1	UGT3A1-2	0.25	0.5309	0.7342	0	0	0.46	0.2889	0.7360	0	0	-0.21	0.4916	0.8862	0	0
UGT3A1	UGT3A1-3	-0.62	0.0916	0.2317	0	0	-0.27	0.5649	0.8770	0	0	-0.35	0.3158	0.8138	0	0
UGT3A1	UGT3A1-4	-0.10	0.7997	0.9966	0	0	-0.06	0.8865	0.9417	0	0	-0.04	0.7684	0.8862	0	0
UGT3A1	UGT3A1-5	-0.09	0.8828	0.8928	0	0	0.32	0.4760	0.8506	0	0	-0.41	0.2907	0.7917	0	0
UGT3A1	UGT3A1-6	0.04	0.7310	0.8681	0	0	-0.07	0.8829	0.9417	0	0	0.11	0.6740	0.8862	0	0
UGT3A2	UGT3A2-1	-0.88	0.0197	0.0768	0	1	-0.29	0.5318	0.8690	0	0	-0.59	0.0825	0.5091	0	0
UGT3A2	UGT3A2-2	-0.46	0.2293	0.4353	0	0	-0.32	0.4781	0.8506	0	0	-0.14	0.6915	0.8862	0	0
UGT3A2	UGT3A2-3	-0.61	0.1249	0.2888	0	0	-0.45	0.3138	0.7516	0	0	-0.16	0.6939	0.8862	0	0
UGT3A2	UGT3A2-4	-0.61	0.1010	0.2483	0	0	-0.42	0.3580	0.7812	0	0	-0.19	0.6349	0.8862	0	0
UGT3A2	UGT3A2-5	-0.19	0.5922	0.7764	0	0	0.05	0.8698	0.9417	0	0	-0.25	0.5128	0.8862	0	0
UGT3A2	UGT3A2-6	-0.55	0.1368	0.3067	0	0	-0.19	0.6625	0.9070	0	0	-0.36	0.3394	0.8301	0	0
URI1	URI1-1	-0.08	0.8865	0.9035	0	0	0.44	0.3829	0.7926	0	0	-0.51	0.2428	0.7554	0	0
URI1	URI1-2	1.04	0.0225	0.0850	0	1	0.59	0.2808	0.7355	0	0	0.45	0.2984	0.7965	0	0
URI1	URI1-3	0.84	0.0951	0.2370	0	0	0.80	0.1624	0.6166	0	0	0.03	0.8945	0.8992	0	0
URI1	URI1-4	0.48	0.2732	0.4884	0	0	0.34	0.6698	0.9075	0	0	0.14	0.6418	0.8862	0	0
URI1	URI1-5	-0.37	0.3854	0.6083	0	0	-0.15	0.7159	0.9151	0	0	-0.22	0.6564	0.8862	0	0
URI1	URI1-6	0.07	0.8437	0.8984	0	0	0.47	0.3051	0.7468	0	0	-0.39	0.2572	0.7600	0	0
USP13	USP13-1	0.03	0.8771	0.8989	0	0	0.12	0.8138	0.9238	0	0	-0.09	0.8225	0.8862	0	0
USP13	USP13-2	0.08	0.7862	0.8938	0	0	0.35	0.4495	0.8489	0	0	-0.27	0.4423	0.8807	0	0
USP13	USP13-3	-1.66	0.0000	0.0001	1	1	-0.82	0.0764	0.4465	0	0	-0.83	0.0236	0.2913	0	0
USP13	USP13-4	-0.01	0.9031	0.9092	0	0	-0.11	0.8282	0.9287	0	0	0.11	0.8602	0.8872	0	0
USP13	USP13-5	-0.53	0.1605	0.3406	0	0	-0.25	0.6195	0.8955	0	0	-0.28	0.4293	0.8764	0	0
USP13	USP13-6	-0.25	0.4890	0.7040	0	0	-0.46	0.2995	0.7408	0	0	0.20	0.6560	0.8862	0	0
UTS2B	UTS2B-1	0.88	0.3582	0.5817	0	0	3.32	0.0226	0.2608	0	0	-2.44	0.0227	0.2909	0	0
UTS2B	UTS2B-2	1.61	0.0001	0.0010	1	1	0.97	0.0391	0.3329	0	0	0.64	0.2111	0.7289	0	0
UTS2B	UTS2B-3	0.24	0.5343	0.7360	0	0	0.79	0.0651	0.4145	0	0	-0.55	0.1200	0.5997	0	0
UTS2B	UTS2B-4	0.45	0.2517	0.4622	0	0	0.21	0.5907	0.8876	0	0	0.24	0.5719	0.8862	0	0
UTS2B	UTS2B-5	-0.62	0.1421	0.3142	0	0	-0.10	0.7367	0.9167	0	0	-0.53	0.2261	0.7407	0	0
UTS2B	UTS2B-6	0.51	0.2353	0.4424	0	0	0.48	0.3009	0.7435	0	0	0.03	0.8194	0.8862	0	0
VPS8	VPS8-1	-0.05	0.8755	0.8989	0	0	0.04	0.7912	0.9227	0	0	-0.09	0.7125	0.8862	0	0
VPS8	VPS8-2	-1.78	0.0001	0.0011	1	1	-1.59	0.0058	0.1356	0	1	-0.19	0.6070	0.8862	0	0
VPS8	VPS8-3	7.30	0.0000	0.0000	1	1	4.94	0.0000	0.0034	1	1	2.36	0.0151	0.2356	0	0
VPS8	VPS8-4	-0.42	0.2800	0.4935	0	0	-0.20	0.7108	0.9142	0	0	-0.22	0.5419	0.8862	0	0
VPS8	VPS8-5	-0.02	0.8847	0.9035	0	0	-0.01	0.9747	0.9747	0	0	0.01	0.9094	0.9109	0	0
VPS8	VPS8-6	-0.33	0.4125	0.6347	0	0	-0.03	0.8100	0.9227	0	0	-0.31	0.4233	0.8764	0	0
VVA5B2	VVA5B2-1	-0.91	0.0217	0.0826	0	1	-0.75	0.1403	0.5770	0	0	-0.16	0.6690	0.8862	0	0
VVA5B2	VVA5B2-2	-0.71	0.0516	0.1543	0	1	-0.02	0.7972	0.9227	0	0	-0.70	0.0694	0.4709	0	0
VVA5B2	VVA5B2-3	0.08	0.7859	0.8938	0	0	0.12	0.7771	0.9227	0	0	-0.04	0.7763	0.8862	0	0
VVA5B2	VVA5B2-4	-1.29	0.0005	0.0040	1	1	-0.87	0.0520	0.3685	0	0	-0.42	0.3019	0.7981	0	0
VVA5B2	VVA5B2-5	-0.96	0.0094	0.0424	1	1	-0.50	0.2842	0.7355	0	0	-0.47	0.2136	0.7289	0	0
VVA5B2	VVA5B2-6	-0.36	0.3403	0.5636	0	0	-0.25	0.5551	0.8733	0	0	-0.12	0.6897	0.8862	0	0
WDR53	WDR53-1	-0.02	0.9073	0.9123	0	0	0.42	0.3837	0.7926	0	0	-0.44	0.2830	0.7870	0	0
WDR53	WDR53-2	2.82	0.0001	0.0008	1	1	1.70	0.0304	0.3058	0	0	1.11	0.0960	0.5470	0	0
WDR53	WDR53-3	-0.23	0.5223	0.7278	0	0	-0.13	0.7509	0.9184	0	0	-0.10	0.7871	0.8862	0	0
WDR53	WDR53-4	-0.46	0.2046	0.4023	0	0	-0.45	0.3296	0.7622	0	0	-0.01	0.8233	0.8862	0	0
WDR53	WDR53-5	0.09	0.8077	0.8984	0	0	0.28	0.4643	0.8506	0	0	-0.19	0.6774	0.8862	0	0
WDR53	WDR53-6	0.95	0.1195	0.2802	0	0	1.64	0.0275	0.2924	0	0	-0.69	0.2707	0.7760	0	0
WNK1	WNK1-1	-0.45	0.2365	0.4433	0	0	-0.33	0.4255	0.8506	0	0	-0.13	0.7019	0.8862	0	0
WNK1	WNK1-2	-0.24	0.7039	0.8549	0	0	-0.69	0.1593	0.6103	0	0	0.45	0.2501	0.7554	0	0
WNK1	WNK1-3	-0.06	0.8545	0.8984	0	0	0.09	0.8263	0.9287	0	0	-0.15	0.6811	0.8862	0	0
WNK1	WNK1-4	-0.61	0.1268	0.2915	0	0	-0.26	0.6300	0.8955	0	0	-0.35	0.2957	0.7964	0	0
WNK1	WNK1-5	-1.93	0.0000	0.0004	1	1	-1.22	0.0805	0.4602	0	0	-0.71	0.2129	0.7289	0	0
WNK1	WNK1-6	-0.49	0.2219	0.4252	0	0	-0.55	0.2377	0.6981	0	0	0.06	0.7594	0.8862	0	0
WNT5B	WNT5B-															

YES1	YES1-4	4.04	0.0000	0.0000	1	1	2.89	0.0011	0.0426	1	1	1.15	0.0810	0.5079	0	0
YES1	YES1-5	-0.10	0.7919	0.8960	0	0	0.09	0.8395	0.9334	0	0	-0.19	0.6560	0.8862	0	0
YES1	YES1-6	0.28	0.4593	0.6791	0	0	0.09	0.8533	0.9362	0	0	0.19	0.6219	0.8862	0	0
YTHDC1	YTHDC1-1	0.09	0.8105	0.8984	0	0	-0.14	0.7701	0.9227	0	0	0.23	0.6102	0.8862	0	0
YTHDC1	YTHDC1-2	-0.20	0.6080	0.7881	0	0	-0.03	0.9512	0.9564	0	0	-0.17	0.6352	0.8862	0	0
YTHDC1	YTHDC1-3	0.38	0.3412	0.5641	0	0	0.66	0.1259	0.5420	0	0	-0.28	0.3620	0.8319	0	0
YTHDC1	YTHDC1-4	-0.13	0.7504	0.8766	0	0	-0.16	0.7112	0.9142	0	0	0.03	0.8127	0.8862	0	0
YTHDC1	YTHDC1-5	-0.09	0.8114	0.8984	0	0	0.10	0.8147	0.9239	0	0	-0.19	0.5971	0.8862	0	0
YTHDC1	YTHDC1-6	-0.19	0.6588	0.8283	0	0	0.03	0.7937	0.9227	0	0	-0.22	0.7857	0.8862	0	0
ZDHHHC19	ZDHHHC19-1	0.18	0.6663	0.8327	0	0	0.33	0.4670	0.8506	0	0	-0.15	0.7353	0.8862	0	0
ZDHHHC19	ZDHHHC19-2	1.05	0.0316	0.1067	0	1	0.67	0.2284	0.6900	0	0	0.38	0.4791	0.8862	0	0
ZDHHHC19	ZDHHHC19-3	-0.77	0.0320	0.1077	0	1	-0.02	0.8389	0.9334	0	0	-0.75	0.0622	0.4576	0	0
ZDHHHC19	ZDHHHC19-4	-0.10	0.8151	0.8984	0	0	0.36	0.3977	0.8048	0	0	-0.46	0.2012	0.7138	0	0
ZDHHHC19	ZDHHHC19-5	0.27	0.5334	0.7359	0	0	0.18	0.7052	0.9141	0	0	0.09	0.8319	0.8862	0	0
ZDHHHC19	ZDHHHC19-6	-0.33	0.3908	0.6133	0	0	0.29	0.5357	0.8699	0	0	-0.62	0.1121	0.5872	0	0
ZMAT3	ZMAT3-1	-0.92	0.0128	0.0548	0	1	-0.35	0.4168	0.8259	0	0	-0.57	0.1303	0.6144	0	0
ZMAT3	ZMAT3-2	-0.56	0.1825	0.3722	0	0	-0.20	0.7218	0.9151	0	0	-0.36	0.3736	0.8406	0	0
ZMAT3	ZMAT3-3	-1.23	0.0028	0.0161	1	1	-1.31	0.0327	0.3135	0	0	0.08	0.6373	0.8862	0	0
ZMAT3	ZMAT3-4	-0.31	0.5025	0.7126	0	0	-0.46	0.3140	0.7516	0	0	0.15	0.6127	0.8862	0	0
ZMAT3	ZMAT3-5	-0.87	0.0238	0.0887	0	1	0.15	0.7630	0.9216	0	0	-1.02	0.0235	0.2913	0	0
ZMAT3	ZMAT3-6	-1.81	0.0000	0.0001	1	1	-1.17	0.0159	0.2156	0	0	-0.64	0.0767	0.4939	0	0
ZMPSTE24	ZMPSTE24-1	-0.22	0.6017	0.7837	0	0	-0.02	0.8353	0.9312	0	0	-0.20	0.5856	0.8862	0	0
ZMPSTE24	ZMPSTE24-2	-1.05	0.0063	0.0313	1	1	0.16	0.6695	0.9075	0	0	-1.20	0.0033	0.0883	0	1
ZMPSTE24	ZMPSTE24-3	0.86	0.0402	0.1274	0	1	2.42	0.0029	0.0859	0	1	-1.56	0.0724	0.4855	0	0
ZMPSTE24	ZMPSTE24-4	-0.09	0.8582	0.8984	0	0	0.60	0.1863	0.6431	0	0	-0.70	0.0726	0.4858	0	0
ZMPSTE24	ZMPSTE24-5	-0.46	0.2420	0.4495	0	0	-0.29	0.5327	0.8694	0	0	-0.17	0.6470	0.8862	0	0
ZMPSTE24	ZMPSTE24-6	-1.09	0.0037	0.0204	1	1	-0.36	0.4470	0.8479	0	0	-0.74	0.0674	0.4682	0	0
ZNF703	ZNF703-1	-0.97	0.0099	0.0440	1	1	-0.68	0.1145	0.5346	0	0	-0.29	0.4605	0.8862	0	0
ZNF703	ZNF703-2	-0.93	0.0095	0.0427	1	1	-0.58	0.1824	0.6418	0	0	-0.35	0.3694	0.8381	0	0
ZNF703	ZNF703-3	-0.45	0.2636	0.4761	0	0	-0.42	0.3392	0.7718	0	0	-0.03	0.7594	0.8862	0	0
ZNF703	ZNF703-4	-1.48	0.0002	0.0020	1	1	-0.88	0.0835	0.4665	0	0	-0.59	0.1682	0.6693	0	0
ZNF703	ZNF703-5	-0.27	0.5102	0.7189	0	0	0.01	0.9451	0.9542	0	0	-0.27	0.4245	0.8764	0	0
ZNF703	ZNF703-6	-0.61	0.1179	0.2782	0	0	0.03	0.7070	0.9141	0	0	-0.64	0.0759	0.4939	0	0