Interplay of cell proliferation and tissue remodelling in colorectal cancer

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Abstract

Human cancers can be classified based on gene expression signatures quantifying the degree of cell proliferation and a feature we term tissue remodelling. Yet, specific factors regulating the gene expression programs of cell proliferation and tissue remodelling are not well understood. In this work, I address this question using colorectal cancer as a case study.

In an initial evaluation of clinical outcome prediction in the case study cohort, our classification based on cell proliferation and tissue remodelling signatures delivers a better patient stratification than a recently reported consensus molecular subtyping (CMS). Although the CMS scheme predicts a worse prognosis for patients with a mesenchymal signature (a feature that strongly overlaps with tissue remodelling), it cannot differentiate the remaining patients based on clinical outcome. I show that cell proliferation is the missing factor, which is associated with good prognosis.

In the analyses of specific factors driving the tissue remodelling programme, I identify transcription factor KLF4 and microRNA mir-22 as putative regulators. Concordant with KLF4 role in immune cell regulation, KLF4 activity scores are significantly higher in colorectal tumours with predicted myeloid cells infiltration, suggesting its association with myeloid cell infiltration and poor prognosis in colorectal cancer. However, mir-22 is not associated with immune cell infiltration, suggesting it may be expressed in the tumour stroma as well.

Lastly, I propose a network that may be regulated by IRF8, SPI1, KLF4 and mir-22 in monocyte differentiation and in colorectal cancer. The correlation analysis suggests a negative feedback loop, whereby mir-22 may repress *Irf8* gene to control the rate of IRF8 transcription.

Taken together, I have identified specific regulators driving remodelling processes and their association with immune cell infiltration. In the future, it will be beneficial to conduct further studies to understand the mechanisms driving myeloid cell infiltration in colorectal cancer, particularly to propose treatments for patients exhibiting poor prognosis.

Table of Contents

List of Tables

List of Figures

Publications arising from this work

Halim, S., Markert, E.K. & Vazquez, A. 2018, 'Analysis of cell proliferation and tissue remodelling uncovers a KLF4 activity score associated with poor prognosis in colorectal cancer', *Br J Cancer*, vol. 119, no. 7, pp. 855-63.

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Author's Declaration

I declare that this thesis presented for the degree of Doctor of Philosophy has been composed entirely by myself and solely the result of my own work except where indicated by referencing. None of the work has been previously submitted for another degree at any other institution.

Silvia Halim

Abbreviations

APC	adenomatous polyposis coli
BH	Benjamini-Hochberg
cDC	conventional dendritic cell
ChIP-seq	chromatin immunoprecipitation sequencing
CI	confidence interval
CIMP	CpG island methylator phenotype
CMS	consensus molecular subtypes
CRCSC	colorectal cancer subtyping consortium
EGF	epidermal growth factor
EMT	epithelial-mesenchymal transition
FDR	false discovery rate
GEO	gene expression omnibus
GO	gene ontology
GSEA	gene set enrichment analysis
GTP	guanosine triphosphate
GTPase	guanosine triphosphate hydrolase
IBD	inflammatory bowel disease
ICSBP	interferon consensus sequence binding protein
IHC	immunohistochemistry
IRF8	interferon regulatory factor-8
KLF4	kruppel-like factor 4
MMS	mesenchymal metabolic signature
MSI	microsatellite instability
MSS	microsatellite stable
miRNA	microRNA
MMR	DNA mismatch repair
mRNA	messenger RNA
NK	natural killer cells
OxPhos	oxidative phosphorylation
P	cell proliferation gene signature
PCNA	proliferating cell nuclear antigen
pDC	plasmacytoid dendritic cell
pM	distant metastasis staging

pN	regional lymph nodes staging
pT	primary tumour staging
R	tissue remodelling gene signature
RISC	RNA-induced silencing complex
RMA	robust multi-array average
RNA-seq	RNA sequencing
RSEM	RNA-Seq by Expectation Maximization
TCGA	the cancer genome atlas
TCGACRC	TCGA colorectal cancer
TF	transcription factor
TGFβ	transforming growth factor beta
TIAM1	T-cell lymphoma invasion and metastasis 1
TNM	tumour, node and metastasis
tRNA	transfer RNA
TTRUST	Transcriptional Regulatory Relationships Unravelled by Sentence-based Text-mining

1 Introduction

1.1 Molecular classifications of cancer

Cancer patients had been previously classified based on tissue morphology as well as clinical and pathological features (Finak et al. 2006) (Onitilo et al. 2009) (Feeley et al. 2014). After the sequencing of the human genome (Lander et al. 2001) (Venter et al. 2001), gene expression arrays were developed allowing researchers to investigate molecular features at the genome scale. In a pioneering work, Sorlie et al. performed an unbiased clustering analysis of gene expression profiles of 82 samples including 78 breast tumours and four normal tissues (Sorlie et al. 2001). They uncovered five major subtypes: normal-like, luminal A, luminal B, ERBB2+ and basal-like. Later on, Wang et al. recapitulated this analysis in a much larger cohort of 892 breast cancer patients (Wang et al. 2012). These studies lead to two key conclusions. First, that gene expression profiles can be used to identify disease subgroups with significantly different prognosis. Second, that some molecular features specific to each subgroup can guide the development of stratified medicine.

1.2 Gene signatures of cell proliferation and tissue remodelling

Cell proliferation and tissue remodelling have been associated with metabolic changes that are required for the transformation of normal to cancerous cells and the high metabolic demands of cancer cells. A number of oncogenic and tumour suppressor pathway alterations have been reported to sustain metabolism required for cell proliferation and migration. MYC promotes proliferation by coordinating nutrients for cell division and DNA replication through its targets (Stine et al. 2015) and its deregulation has been implicated in cancer. P53 is a tumour suppressor with a pro-apoptotic function and over half of human cancers carry mutations in p53 gene (Ozaki and Nakagawara 2011). On the other hand, transforming growth factor beta (TGFß) regulates cell invasion, immune system and modification of cellular microenvironment, which are hijacked by cancer cells (Massague 2008). However, an understanding of a preferential mode of increased cell proliferation or increased tissue remodelling required for cancer development is still lacking.

Several studies have reported the association of gene signatures of cell proliferation and tissue remodelling with prognosis. Poor prognosis in breast cancer has been shown to be highly correlated with cell proliferation (Venet et al. 2011) (van Diest et al. 2004) (Aleskandarany et al. 2012). Venet et al. constructed a meta-PCNA (proliferating cell nuclear antigen) gene signature that comprised of 1% of the genes that were most positively correlated with PCNA expression and also included other known proliferation markers, such as MKI67, TOP2A and MCM2 (Venet et al. 2011). They used 47 published signatures, compared the correlations with the meta-PCNA and found that majority of the genes that were associated with outcome in breast cancer were highly correlated with meta-PCNA (Venet et al. 2011). Their findings show that 58% of the breast cancer transcriptome is highly correlated with meta-PCNA and a signature does not necessarily need to be enriched with known proliferation genes to carry a strong proliferation signal (Venet et al. 2011).

Shaul et at. studied metabolic gene expression profiles of human cancer cell lines and developed a mesenchymal metabolic signature (MMS) to investigate the aggressiveness of cancer cells (Shaul et al. 2014). They classified the cell lines into five groups based on tissue origin, i.e. melanoma cell lines, hematopoietic system cancers, neuroendocrine or neuroectodermal cancers, epithelial cancer cell lines and mesenchymal (from mixed lineage) (Shaul et al. 2014). The mesenchymal subtype has an increased expression of mesenchymal markers, such as vimentin, SNAI1/2, CDH2, TWIST1 and ZEB1 but a lower expression of CLDN1 and E-cadherin (Shaul et al. 2014). In a separate study, Aruga et al. investigated the relationships of clinicopathological features of lung squamous cell carcinoma with E-cadherin and vimentin (Aruga et al. 2018). They demonstrated epithelial-mesenchymal transition (EMT) phenotype to be a significant predictor of poor prognosis in lung squamous cell carcinoma (Aruga et al. 2018).

The association of gene signatures with prognosis has also been investigated in the context of colorectal cancer. Anjomshoaa et al. developed a colon-specific gene proliferation signature (Anjomshoaa et al. 2008). They demonstrated that lower expression of gene proliferation signature was associated with increased

risk of recurrence and shorter disease-free survival in colorectal cancer, in contrary with previous reports in other cancer types (Anjomshoaa et al. 2008). In an independent study, Loboda et al. reported a signature of EMT was associated with poor prognosis in colorectal cancer (Loboda et al. 2011). These two studies are consistent with a previous report that showed metastatic colorectal tumours yielded a lower proliferative index than primary non-metastatic tumours (Ganepola et al. 2010). Collectively, these studies on colorectal cancer patient stratifications highlight that a down-regulation of cell proliferation signature and a signature of EMT (tissue remodelling) are associated with poor prognosis. This observation is opposed to breast cancer patient stratifications, which demonstrate cell proliferation is associated with poor prognosis (Venet et al. 2011) (van Diest et al. 2004) (Aleskandarany et al. 2012).

To investigate the selective mode of cell proliferation or tissue remodelling in different cancer types, a previous study in our laboratory had unified these two approaches. Using gene ontology (GO) terms, Market et al. developed cell proliferation and tissue remodelling gene signatures from literature reporting genes implicated in these two sets of processes. To define the cell proliferation signature, they included processes involved in or associated with cell cycle, namely G_1/S transition, DNA replication, telomere organisation, DNA packaging, chromosome segregation, G_2/M transition and cell division (Markert et al. 2012). For the tissue remodelling signature, they considered processes involving a change relative to the microenvironment or an interaction with the microenvironment. These include cell junction organisation, cell adhesion, cell migration, angiogenesis, cytokine production, inflammatory response and response to wounding (Markert et al. 2012). Cell proliferation was found to have a positive correlation with glycolysis, oxidative phosphorylation (OxPhos), and serine or glycine metabolism, whereas tissue remodelling was negatively correlated with OxPhos (Markert et al. 2012).

In the same study, it was showed that tumour samples, including breast and colorectal cancer, could be classified based on the quantification of cell proliferation and tissue remodelling gene signatures (Markert et al. 2012). The majority of the tumour samples exhibit a significant up-regulation of either of these two gene signatures, highlighting the partially independent relationship of

cell proliferation and tissue remodelling (Markert et al. 2012). In this study, the prognostic values of these gene signatures were also demonstrated in different cancer types. Using patient survival data, cell proliferation was found to be indicative of poor prognosis in lung, prostate, breast and brain cancer, while tissue remodelling was found to be associated with poor prognosis in colorectal and ovarian cancer (Markert et al. 2012). In other words, patients with a proliferation signature manifest worst outcome in most cancer types being studied, while colorectal and ovarian tumours with a remodelling signature exhibit worse survival than those with a proliferation signature. Taken together, cell proliferation and tissue remodelling gene signatures serve as a universal scheme for patient stratification and this study highlights the dichotomy of cell proliferation and tissue remodelling programmes in different cancer types. However, at this point, we still do not know specific transcriptional regulations that drive the preferential mode of cell proliferation and tissue remodelling in cancer development and progression.

1.3 Consensus molecular subtyping of colorectal cancer

Recently, several groups of researchers formed a colorectal cancer subtyping consortium (CRCSC) and made use of gene expression profiles of a large colorectal cancer cohort from different published studies. They performed an unsupervised clustering to stratify colorectal tumours based on gene expression profiles. Their unsupervised approach resulted in a classification of colorectal patients into four subtypes, namely, CMS1, CMS2, CMS3 and CMS4, where CMS stands for consensus molecular subtypes (Guinney et al. 2015). They showed that CMS4 is the subtype that is indicative of worst prognosis and enriched for a gene signature of mesenchymal (Guinney et al. 2015).

1.4 Regulation of cell proliferation and tissue remodelling

As elaborated in section 1.2, several reports unanimously showed that a signature of EMT or tissue remodelling was indicative of worst prognosis, while cell proliferation was associated with good prognosis in colorectal cancer (Anjomshoaa et al. 2008) (Loboda et al. 2011) (Markert et al. 2012) (Guinney et al. 2015). However, the mechanisms driving increased tissue remodelling or

increased cell proliferation in different cancer types are still not well understood.

Cells respond to changes in the environment by receiving and processing signals from outside the cells. Receptors of the cells bind to ligands that in turn activate intracellular signalling pathways. Intracellular signals are released inside the cells to activate pathways that regulate gene expression in response to the external stimuli. The biogenesis of gene expression is regulated by regulatory elements, such as transcription factors (TFs) and microRNAs (miRNAs). They control the dependencies of cell proliferation and tissue remodelling in the cells, as depicted in Figure 1-1. These regulatory mechanisms are hijacked in cancer cells, resulting in constitutively active growth and/or tissue remodelling signals that drive tumourigenesis. Therefore, the cell proliferation and tissue remodelling programmes can be regulated at multiple levels.

Transcriptional regulation controls the gene expression program to maintain specific cell states. This regulation determines the number of RNA copies to be transcribed and when the gene transcription should happen. Transcription factors regulate gene transcription by binding enhancer elements and recruiting RNA polymerase II and cofactors to their target genes to initiate the transcription (Lee and Young 2013). Transcription factor MYC activates transcriptional programs promoting cell growth and proliferation but represses cell growth arrest (Dang 2013). The deregulation of its proto-oncogene *MYC* has been implicated in cancer, which causes the withdrawal of normal cell cycle into a G_1-like state (Dang 2013). On the other hand, transcription factors Goosecoid, Snail, Twist and TGFß can induce EMT program that promotes cancer cell invasiveness and migration and exhibits stem cell properties (Taube et al. 2010). Collectively, these studies show that there are some transcription factors that specifically promote either the cell proliferation or tissue remodelling transcriptional programme.

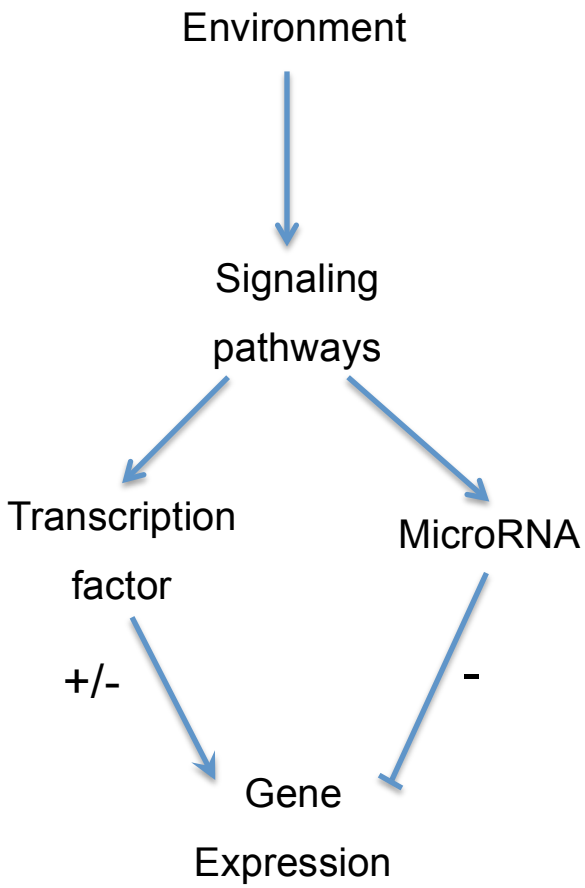

Figure 1-1. A model of regulatory of gene expression program

Another potential layer of regulation is codon bias. Gingold et al. studied the differential regulation of the tRNAs and codon usage of the genes involved in proliferation and differentiation (Gingold et al. 2014). The genes that are involved in proliferation preferentially use codons ending with A or T nucleotide, while differentiation genes tend to use codons ending with G or C nucleotide (Gingold et al. 2014). In the study, they also confirmed the clear separation between genes involved in proliferation and differentiation processes as well as the promoters and histone modifications within proximity of the tRNAs involved in these processes (Gingold et al. 2014). Their findings suggested that proliferation genes that were induced in cancer had distinct codon usage from differentiation genes that were repressed in cancer (Gingold et al. 2014). Additionally, they reported that the proliferative status of a cell (differentiated, senescent and arrested) was reflected in the tRNA pool, while the tissue origin was contained in mRNA expression and there was a correlation between changes at the tRNA availability and changes in gene expression (Gingold et al. 2014).

This study emphasises that the selective mode of proliferation and differentiation (remodelling) is also present in the tRNA pool and codon usage of genes.

Finally, microRNAs and other non-coding RNAs are involved in the post-transcriptional regulation of gene expression. In particular, microRNAs regulate gene transcription through RNA-induced silencing complex (RISC) where they assemble into the complex and activate the complex to the target gene (Macfarlane and Murphy 2010). The complementarity between microRNA and its target gene determines the silencing mechanism that is used, i.e. cleavage of target gene leading to its degradation or inhibition of its translation (Macfarlane and Murphy 2010). MicroRNAs play an important role in various metabolic and cellular pathways, including cell proliferation, differentiation and survival, and their dysregulation has been implicated in cancer (Macfarlane and Murphy 2010). The let-7 family of microRNAs regulate cell proliferation, while the microRNAs from the mir-15 and mir-16 family act as tumour suppressors through their pro-apoptotic function and mir-21 suppresses genes that promote invasion and metastasis (Macfarlane and Murphy 2010). Taken together, this observation highlights that there are some microRNAs that specifically promote either the cell proliferation or tissue remodelling programme.

When analysing gene expression profiles from human tumours we should also bear in mind that, in addition to the tumour cells, there may be other compartments of cells that have not been genetically altered. That includes the fibroblasts and blood vessels making up the tumour stroma and infiltrating immune cells as well. Various immune cell types from the lymphoid and myeloid lineages may be present in a tumour, including B cells, effector T cells, naive and memory lymphocytes, natural killer (NK) cells, macrophages, mast cells and dendritic cells (Fridman et al. 2012). Lymphocyte infiltration has been associated with an antitumour response and better prognosis (Angell and Galon 2013) (James et al. 2017). Pollard described that macrophages recruited at the invasive front of breast tumours enhanced cancer cell migration and invasion by secreting chemotactic and chemokinetic factors, such as epidermal growth factor (EGF) (Pollard 2008). Collectively, these reports suggest that infiltration

of different immune cells plays different roles in malignancy, which is then reflected in patient outcome.

1.5 The biology and development of colorectal cancer

Colorectal cancer is the third-most common cancer and it is preceded by a polypoid precursor (Kuipers et al. 2015). Inflammatory bowel disease (IBD) is associated with an increased risk of colorectal cancer and the risk increases with the duration of IBD (Jess et al. 2012). A positive family history is also associated with an increased risk of colorectal cancer, whereby the two most common hereditary colorectal cancer syndromes are Lynch and familial adenomatous polyposis syndromes (Kuipers et al. 2015). A mutation of the DNA mismatch-repair genes (MLH1, MSH2, MSH6, PMS2 and EPCAM) gives rise to Lynch syndrome (Kuipers et al. 2015). On the other hand, familial adenomatous polyposis syndrome is caused by a mutation in adenomatous polyposis coli (APC) gene, which controls the WNT signalling pathway activity (Vasen et al. 2015).

The genetic mutations and epigenetic alterations in the colon result in the polyp, which is the transformation of normal colonic epithelium into colon adenocarcinoma (Grady and Carethers 2008). The loss of genomic stability can be observed in early neoplastic lesions of the colon and majority of them are aberrant crypt foci, adenomas and serrated polyps (Kuipers et al. 2015). Most colorectal cancer cells originate from a stem cell or stem-like cell that can be found in the base of the colonic crypts (Zeki et al. 2011). Mutations in the tumour suppressor genes or the oncogenes in these multipotent stem cells give rise to cancer stem cell formation, which is important for tumour initiation and maintenance (Kuipers et al. 2015).

Most of the colorectal tumours originate from a polyp that arises from an aberrant crypt and develop into an early adenoma then further evolve into an advanced adenoma and finally a colorectal cancer (Kuipers et al. 2015). They arise via the tumour suppressor or serrated neoplasia molecular pathway (Goldstein 2006). Conventional tubular and tubulovillous adenomatous polyps are widely recognised premalignant precursor lesions arising from the tumour suppressor (chromosomal instability) pathway and biallelic inactivation of APC

(Goldstein 2006) (Grady and Pritchard 2014). In contrast, serrated polyps arise from the serrated neoplasia (mutator) pathway, which originate from the accumulation of insertion or deletion mutations in the genome and result in genomic instability and microsatellite unstable-high (MSI-H) adenocarcinomas (Goldstein 2006).

The molecular and histological events that the serrated polyps go through are distinct from tubular adenomas and these polyps can be categorised into three categories, namely hyperplastic polyps, sessile serrated polyps (SSP) and traditional serrated adenomas (TSA) (Kuipers et al. 2015). A fraction of hyperplastic polyps advance into serrated adenomas (SSP or TSA) and a subset of the serrated adenomas advance into colorectal cancer (Grady and Pritchard 2014). Serrated polyps that grow in the right colon, including the transverse colon, ascending colon and caecum, generally demonstrate microsatellite instability (MSI) and CpG island methylator phenotype (CIMP) (Kuipers et al. 2015). On the other hand, the polyps that grow in the left colon, including the sigmoid colon, descending colon and rectum, are generally microsatellite stable (MSS) but carry KRAS mutations and some of these polyps have an attenuated CIMP (Kuipers et al. 2015).

The most frequent mutations in colorectal cancer are APC, ARID1A, BRAF, CTNNB1, FAM123B, KRAS, PIK3CA, SMAD4, SOX9, TGFBR2, TP53 and ERBB2 that perturbs the key signalling pathways, namely WNT-ß-catenin, EGFR-MAPK, TGFß and PI3K pathways, or alters genes involved in proliferation and DNA repair (Kuipers et al. 2015). APC mutations can be observed in up to 70% of sporadic colorectal cancer (Grady and Pritchard 2014) and as mentioned previously, it leads to the familial adenomatous polyposis syndrome (Vasen et al. 2015). The mutations occur at the earliest stages of neoplasia and are associated with the conventional tubular adenoma pathway and chromosomal instability tumours (Grady and Pritchard 2014). The mutations in APC gene result in disrupted APC protein, which leads to an increase of WNT signalling by nuclear ß-catenin stabilisation then an increase of the gene transcription of WNT targets (Grady and Pritchard 2014). An activating ß-catenin (CTNNB1) mutation inhibits its degradation that is mediated by APC (Samowitz et al. 1999). The beta-catenin mutation occurs in colorectal neoplasia but it happens more frequently in small

adenomas than in large adenomas and invasive cancers, suggesting CTNNB1-mutant adenomas often do not advance into carcinoma (Samowitz et al. 1999).

KRAS is a proto-oncogene in the RAS family and it is frequently mutated in human cancer, including colorectal cancer. KRAS protein acts downstream of EGFR signalling via BRAF to activate MAPK signalling pathway and sustain cell growth and survival (Grady and Pritchard 2014). Mutations of codon 12 or 13 of KRAS can be observed in around 40% of colorectal tumours and it results in constitutive signalling by deregulating guanosine triphosphate hydrolase (GTPase)-activating proteins in KRAS-bound guanosine triphosphate (GTP) hydrolysis (Downward 2003). Although KRAS mutations take place after APC mutations in the progression from adenoma into carcinoma, it is considered as an early event in the tumourigenesis (Grady and Pritchard 2014). Using primary and metastatic colorectal tumours, Artale et al. demonstrated that acquired KRAS mutations were maintained throughout carcinogenesis, suggesting that KRAS mutations are not required for metastasis (Artale et al. 2008).

Mutations in BRAF gene can be observed in around 10% to 15% of colorectal cancer and BRAF protein is a direct downstream effector of KRAS in the EGFR/RAS/RAF/MAPK signalling pathway (Grady and Pritchard 2014). Most of the BRAF mutations are a single base substitution of glutame for valine residue at codon 600 (V600E, sometimes also known as V599E) (Rajagopalan et al. 2002). Mutations of KRAS and BRAF genes occur at a similar stage of tumour initiation and an activating mutation of either KRAS or BRAF is sufficient to promote tumourigenesis (Rajagopalan et al. 2002). The frequency of BRAF mutations is higher in MSI than in MSS tumours (Lubomierski et al. 2005) and sessile serrated adenomas frequently carry BRAF mutations (Kambara et al. 2004). BRAF mutations are highly associated with CIMP tumours and the serrated neoplasia (mutator) pathway (Grady and Pritchard 2014).

TGFß signalling is a tumour suppressor pathway in the colon and its deregulation can be observed in the majority of colorectal tumours (Grady and Pritchard 2014). Inactivating mutations occur in the receptor genes TGFBR2 and TGFBR1, post-receptor signalling pathway genes SMAD2 and SMAD4 as well as a TGFBR2 family member ACVR2 (Deacu et al. 2004). Functionally significant mutations of

TGFBR2 have been reported in up to 30% of colorectal tumours and are linked with the malignant transformation into late adenomas (Grady and Pritchard 2014). Mutations in TGFBR2 are more common in MSI than in MSS tumours (Grady et al. 1999). SMAD4 is located in the long arm of chromosome 18, which is commonly deleted in colorectal cancer and is correlated with adenoma formation and the progression of adenoma into carcinoma, suggesting that SMAD4 is a tumour suppressor gene (Takaku et al. 1998). Additionally, loss of SMAD4 protein expression was observed in 50% of colorectal tumours and both chromosome 18q deletion and inactivation of SMAD4 protein are associated with lymph node metastasis (Tanaka et al. 2008).

Mutations of PI3K pathway genes occur in up to 40% of colorectal tumours (Grady and Pritchard 2014). The most frequently mutated gene in this pathway is PIK3CA and such mutations were reported in up to 32% of colorectal cancer (Samuels et al. 2004). PIK3CA mutation is linked with adenoma to carcinoma progression and it is usually observed late in tumourigenesis (Samuels et al. 2004). PTEN mutation can also be observed in this pathway and it is a tumour suppressor gene that inhibits PI3K signalling in up to 9% chromosomal instable tumours and 30% MSI tumours (Danielsen et al. 2008). Additionally, PTEN protein expression is lost in around 30% of colorectal tumours (Yu et al. 2014).

Apart from the four key signalling pathways discussed above, another widely studied molecular characteristic of colorectal cancer is microsatellite instability (MSI). It is a hypermutability phenotype of short repetitive sequences that is caused by impaired DNA mismatch repair (MMR) (Cortes-Ciriano et al. 2017). In sporadic cases, MSI arises from inactivation of MMR genes, such as MLH1, MSH2, MSH3, MSH6 and PMS2 (Cortes-Ciriano et al. 2017). It is associated with an increased risk of colorectal cancer for those with Lynch syndrome and majority of Lynch syndrome patients develop MSI colorectal cancer (Grady and Pritchard 2014). Majority of sporadic MSI tumours (80%) have hypermethylation of MLH1 promoter (Poynter et al. 2008). MSI also arises from the MSH2 inactivation or silencing of the MMR genes by miRNAs (Cortes-Ciriano et al. 2017). MSI tumours that frequently have BRAF V600E mutations are linked with the serrated neoplasia molecular pathway, whereas colorectal tumours with the Lynch syndrome (mutations in the MMR genes) do not carry BRAF mutation (Wang et al.

2003). MSI occurs in 15% of sporadic colorectal cancer (Vilar and Gruber 2010) and it is detected by the presence of 30% of unstable loci using a panel of two mononucleotide and three dinucleotide markers (Boland et al. 1998). Colorectal cancer patients with MSI tumours have been reported to have a better survival than those with MSS tumours (Popat et al. 2005). MSI leads to frameshift mutations and neoantigens that may be detected by the host immune system and the higher frequency of neoantigens in MSI may contribute to better prognosis (Xiao and Freeman 2015). Additionally, MSI colorectal tumours have a reduced rate of recurrence in early stages as compared to advanced stages of the disease (Halpern et al. 2017).

The pathogenesis of colorectal cancer is also determined by its anatomical location and the molecular characteristics and histology are different between the distal (left side) and proximal (right side) colon (Baran et al. 2018). As mentioned above, colorectal tumours in the right side commonly demonstrate MSI, which is characterised by the mutations in MMR genes. These tumours usually show a flat morphology (Nawa et al. 2008). On the other hand, the left-sided tumours are characterised by MSS pathway-related mutations, such as APC, KRAS, PIK3CA and p53, and demonstrate a polypoid-like morphology (Baran et al. 2018). Tumours arising in the right colon demonstrate sessile serrated adenomas, while tumours in the left colon manifest tubulovillous adenocarcinomas (Baran et al. 2018) and the tumours arising from these adenomas have distinct molecular characteristics, as elaborated above. Because of their morphology, the left-sided tumours are easier to detect with colonoscopy than the right-sided tumours in early stages of carcinogenesis (Nawa et al. 2008). Additionally, left-sided colorectal tumours tend to metastasise into liver and lung, while the right-sided colorectal cancer patients tend to have peritoneal carcinomatosis (Benedix et al. 2010).

1.6 Aim of thesis

In my doctoral research, I study specific regulators driving the preferential mode of cell proliferation and tissue remodelling in cancer, with a specific focus on colorectal cancer. Breast cancer has been widely studied as a canonical example where cell proliferation is the major prognostic factor. We would like to study a cancer type where tissue remodelling is a predictor of worse prognosis. Therefore, the choice of colorectal cancer is mainly motivated by the fact that it is a canonical example where 1) cell proliferation is not a marker of poor prognosis and 2) tissue remodeling is associated with poor prognosis. Additionally, a large meta-cohort of colorectal cancer patient samples, reporting gene expression profiles for 2,423 patients, is publicly available. Working with a large size cohort busts the statistical power in deriving at sensible conclusions.

First, I investigate the prognostic value of a colorectal cancer classification based on gene expression signatures quantifying the degree of cell proliferation and tissue remodelling using the datasets in the CRCSC cohort. Then I evaluate the performance of colorectal cancer classifications based on a recently reported unsupervised CMS approach and our gene signatures of cell proliferation and tissue remodelling.

Afterwards, I study the transcriptional regulation of gene expression program that drives the selective mode of cell proliferation and tissue remodelling. I aim to uncover transcription factors and microRNAs that sustain either the cell proliferation or tissue remodelling transcriptional programme in different cancer types. Then I focus on specific transcription factors and microRNAs that promote the tissue remodelling programme, which lead to worse prognosis in colorectal cancer.

Additionally, I assess the association between immune cell infiltration and these specific transcription factors and microRNAs to understand the causal relationship of poor prognosis in colorectal cancer. These findings will broaden our understanding of regulatory networks and the interaction of tumour cells with the microenvironment, beneficial for predicting putative targets for cancer therapies.

1.7 Chapter briefings

Chapter 2 lists the datasets utilised in this thesis and describes the methods that are generic or utilised repeatedly in different chapters. On the other hand, methods that are specific to a chapter are detailed in the chapter itself.

Chapter 3 presents the comparison of unsupervised and reductionist supervised clustering approaches of colorectal cancer patients based on the CMS scheme and our gene signatures of proliferation and remodelling (PR), respectively. In this chapter, I provide a mapping of sample group membership between both classifications and compare the performance of survival analyses based on both approaches. Additionally, I also investigate the interdependence of PR signatures as prognostic factors. Lastly, because of the interdependence of PR signatures, I determine if R signature alone can be applied for patient classification.

In chapter 4, I identify specific transcription factors that sustain the transcriptional programmes of cell proliferation and tissue remodelling. Then I focus on transcription factors that sustain the tissue remodelling programme because tissue remodelling is indicative of worse prognosis in colorectal cancer. From the list of these transcription factors, I decide to do a further study on KLF4 and find that KLF4 may be driving tissue remodelling via myeloid cell infiltration. I also analyse the prognostic value of KLF4 transcription activity and the enrichment of KLF4 activity score with clinical variables.

Chapter 5 evaluates specific microRNAs that promote the cell proliferation and tissue remodelling programmes. Similarly, I focus on microRNAs that sustain the tissue remodelling programme and decide to do a further study on mir-22. I find that mir-22 is not associated with immune cell infiltration.

Finally, in chapter 6, I study the regulatory of monocyte differentiation and myeloid cell infiltration in colorectal cancer that may be driven by KLF4 and mir-22 and other regulators and conclude with various discussions.

Please note that most of the results presented in chapters 3 and 4 have been published in the work titled “Analysis of cell proliferation and tissue remodelling

uncovers a KLF4 activity score associated with poor prognosis in colorectal cancer" in British Journal of Cancer.

2 Materials and Methods

2.1 Publicly available datasets

Throughout my doctoral research, I utilise various datasets from publicly available data, i.e. The Cancer Genome Atlas (TCGA), Gene Expression Omnibus (GEO) and Synapse, which hosts datasets originally used by the CRCSC consortium.

2.1.1 The Cancer Genome Atlas

Preliminary results presented in this thesis are based on the analyses of three datasets from TCGA with matching gene and microRNA (miRNA) expression of tumour samples. First, I use these datasets to assess the regulation of the cell proliferation and tissue remodelling programmes in different cancer types, focusing on mRNA and miRNA expression.

Initially, we selected TCGA breast, lung, ovarian, and colorectal cancer datasets. This selection provides a good balance for the study, following a previous work in our laboratory that showed proliferation to be prognostic in breast and lung cancers, while remodelling was prognostic in colorectal and ovarian cancers (Markert et al. 2012). Later on, I could analyse only the breast, ovarian, and colorectal cancer datasets because the lung cancer dataset has only six samples with matching mRNA and miRNA expression, which are insufficient for deriving at sensible biological conclusions. On the other hand, the number of samples is 132, 184 and 472 in colorectal, breast and ovarian cancer datasets, respectively. These samples were quantified on an Agilent microarray platform and they had been previously quantile-normalised and mean-centred upon download.

I then use the gene expression profiles from these datasets to infer transcription factor activities and establish the relationship between transcription activities and the gene signatures of cell proliferation or tissue remodelling.

2.1.2 Colorectal Cancer Subtyping Consortium

The findings reported in the colorectal cancer case study are mainly based on the analyses performed on the datasets that were originally utilised by the CRCSC consortium. I retrieve normalised gene expression datasets of colorectal cancer samples from Synapse with a Synapse ID syn2634742. The data hosted under this Synapse ID consists of TCGA colorectal cancer dataset and ten GEO datasets with accession numbers: GSE13067, GSE13294, GSE14333, GSE17536, GSE20916, GSE2109, GSE23878, GSE33113, GSE37892 and GSE39582. I exclude overlapping samples in GSE14333 and GSE17536 from GSE14333. The GEO datasets were generated on an Affymetrix microarray platform, while the TCGA dataset was generated on an RNA-seq platform.

Altogether, there are 2,434 samples in these datasets, including 2,207 samples with clinical information. Additionally, 129 out of 132 samples in TCGA colorectal cancer dataset mentioned in section 2.1.1 also appear in this cohort.

This data is used to execute and compare classification approaches (in chapter 3) and perform the analysis of gene expression program regulated by TFs and miRNAs in the case study in chapters 4 and 5, respectively.

2.1.3 Gene Expression Omnibus

I retrieve different datasets from GEO for various validation work. The data is typically retrieved in raw formats from the GEO website and normalised as described in section 2.2.2.

Following is the list of the GEO datasets together with the accession numbers and aim of the validation:

1). Human immune cell transcriptome data (GSE3982):
   - to establish if TF activity inference model is valid in the context of pure immune cell populations in human

2). Human immune cell subsets transcriptome data (GSE28492):
   - the miRNA dataset is utilised to determine if mir-22 expression is higher in phagocytes (myeloid cells) than in lymphoid cells in the context of pure immune cell populations

- the mRNA dataset is applied into TF inference model to examine the correlation of mir-22 expression with IRF8, KLF4 and SPI1 activity scores in pairwise comparisons

2.2 Methods

2.2.1 Gene signatures of cell proliferation and tissue remodelling

Gene signatures of cell proliferation (P) and tissue remodelling (R) are obtained from a previous study in our laboratory, ref. (Markert et al. 2012). As elaborated in the introduction, cell proliferation gene signature includes processes involved in or associated with cell cycle. On the other hand, tissue remodelling gene signature includes processes that involve a change relative to the microenvironment. The gene signatures are comprised of GO term signatures from literature reporting genes implicated in corresponding processes. These processes together with their GO terms are as tabulated in Table 2-1. The list of genes for both P and R signatures can be found in Appendix.

Table 2-1. Processes in gene signatures of cell proliferation and tissue remodelling

Gene signature	Process	GO term
Cell Proliferation	G_1/S transition	GO:000082
	DNA replication	GO:0006260
	Telomere organisation	GO:0032200
	DNA packaging	GO:0006323
	Chromosome segregation	GO:0007059
	G_2/M transition	GO:0000086
	Cell division	GO:0051301
Tissue Remodelling	Cell junction organisation	GO:0034330
	Cell adhesion	GO:0007155
	Cell migration	GO:0016477
	Angiogenesis	GO:0001525
	Cytokine production	GO:0001816
	Inflammatory response	GO:0006954
	Response to wounding	GO:0009611

2.2.2 Normalisation of gene expression data

As mentioned in section 2.1.2, the gene expression datasets from the CRCSC cohort had been previously normalised. The GEO datasets had been previously normalised using robust multi-array average (RMA) method. The TCGA dataset was previously normalised using RNA-Seq by Expectation Maximization (RSEM) method and log-transformed. For details on data normalisation and outlier sample detection as well as other pre-processing steps, please refer to the original research article (ref. (Guinney et al. 2015)).

For each GEO dataset in the cohort, I include only probes with gene annotation for subsequent analyses. Then I select the most variable probe (a probe with largest interquartile range) for each gene. In contrast, the TCGA dataset comes with gene annotation and there is already one probe per gene. Subsequently, for each GEO and TCGA datasets in the cohort, I perform mean-centering for each gene by subtracting the expression values of all samples from the mean expression value across all samples.

The GEO datasets used for validation work, as listed in section 2.1.3, are raw data upon retrieval. I quantile-normalise the gene expression data using 'preprocessCore' bioconductor package and log2 transform it. Next, I perform the same steps above after normalisation, i.e. including only probes with gene annotation, selecting the most variable probe and mean-centring the expression values.

Conversely, the TCGA datasets used for preliminary analyses, as mentioned in section 2.1.1, had been quantile-normalised and mean-centred. Therefore, no further pre-processing step is necessary for these datasets.

2.2.3 Gene Set Enrichment Analysis

I analyse enrichment of the gene signatures using gene set enrichment analysis (GSEA) (Subramanian et al. 2005). The inputs are a gene set (also referred to as a gene signature) and an array of expression values of genes across genome (all genes in the gene list) for a given sample. The output is the enrichment score of

a gene signature and it informs the extent of the correlation of the gene signature with expression values of all genes in the gene list for the corresponding sample.

Specifically, given *m* genes in a gene signature *L*, I initially create a reference score vector by going through *n* genes in the dataset then assigning a score $h_g = \begin{matrix} 1/m & g \in L \\ -1/(n-m) & otherwise \end{matrix}$ for each gene *g*. This reference score vector is reused for all samples in the gene expression data. Before calculating the enrichment score, I sort the reference score vector based on the order of the sorted expression values (from highest to lowest) for a given sample. Next, I calculate a running enrichment score E_k for a sample *k* by summing the sorted reference score vector $E_{ik} = \sum_{j=1}^{i} h_{gjk}$. After going through all h_g in the sorted reference score vector, the enrichment of a gene signature *L* within the tail of low and high values in a sample is represented by $E_{k-} = \min_i E_{ik}$ and $E_{k+} = \max_i E_{ik}$, respectively.

Subsequently, I adopt a permutation test as a non-parametric estimate of the statistical significance of the enrichment scores. I generate 100,000 permutations (n_p) of the reference score vector and calculate the corresponding enrichment scores E_{l-} and E_{l+} at both tails where l=1,…,n_p. Then I correct the statistical significance of E_{k-} and E_{k+} based on a less bias estimate $p_{k-} = (1 + \sum_{l|El- \le Ek-} 1)/(1+n_p)$ and $p_{k+} = (1 + \sum_{l|El+ \ge Ek+} 1)/(1+n_p)$ (North et al. 2002). Lastly, I report E_{k+} as the enrichment score if $p_{k+} < p_{k-}$ or E_{k-} if $p_{k-} < p_{k+}$.

2.2.4 Correlation of gene expression with PR signatures

For a given gene in the gene expression data, I correlate the expression values across all samples with the enrichment scores of all samples with P gene signature using Spearman's rank correlation coefficient. The enrichment scores are calculated following the steps in section 2.2.3. Similarly, I also correlate the expression values with the enrichment scores of all samples with R gene

signature. Then I compare these two sets of results to examine and visualise the relationship between cell proliferation and tissue remodelling at gene expression level.

2.2.5 Survival analysis

I perform two types of survival analyses, i.e. univariate and multivariate survival analyses. In both types of analyses, I fit cox proportional hazards regression model.

2.2.5.1 Univariate survival analysis

I perform univariate survival analysis to assess the performance of a classification scheme in distinguishing different subtypes. I carry out the analysis using overall survival or relapse-free survival information and sample group membership based on the respective classifications. I report p-value from log-rank test as the significance of the classification in predicting an event occurring, i.e. death or relapse in overall survival or relapse-free survival data, respectively. P-value < 0.05 is reported as a significant result in all cases.

2.2.5.2 Multivariate survival analysis

Using multivariate survival analysis, I determine if a covariate is able to predict an event occurring independently of other covariates, i.e. clinical variables in this case. Specifically, I analyse if P and R enrichment scores are independent prognostic factors after considering other clinical variables. The covariates included in the analysis are P and R enrichment scores, stage, age and gender.

I carry out the analysis using overall survival or relapse-free survival information together with the covariates. I report p-value from Wald test as the significance of each covariate (P or R enrichment scores, stage, age or gender) in predicting an event occurring, i.e. death or relapse. P-value < 0.05 is reported as a significant result in all cases.

2.2.6 Multiple testing correction

To address multiple testing problem, I correct the statistical significance following Benjamini-Hochberg (BH) procedure, controlling false discovery rate (FDR) at 0.05. I report the raw p-value together with a Boolean value indicating if it is significant after the correction.

2.2.7 Estimation of immune cell types abundance

I perform this analysis on the CRCSC cohort. First, I combine all GEO gene expression datasets in the CRCSC cohort and estimate the composition of immune cell types in all samples using CIBERSORT (Newman et al. 2015). For running 'CIBERSORT' function, I utilise LM22 signature genes file provided by CIBERSORT as 'sig_matrix' variable and the combined gene expression data as the mixture file. I run the function with 1,000 permutations and quantile normalisation. Next, I also perform the same analysis on the TCGA dataset in the CRCSC cohort then combine the results from CIBERSORT function for both GEO and TCGA datasets. I conduct the analysis this way because the GEO and TCGA datasets do not have the same number of probes or genes in each platform. If I merge all the datasets before running CIBERSORT, some genes that are not in common in these platforms will not be included and potentially important information may be lost in this case.

2.2.8 Permutation test

To determine the statistical significance of a correlation score, I permute Pearson correlation coefficient scores of 2 vectors of ranks for 100,000 times using two-tailed tests to assign p-values at lower and upper tails. The length of the vector equals to the number of samples or genes or transcription factors or miRNAs being tested. Then I calculate the p-value based on a less bias estimate, as described in section 2.2.3. Subsequently, I correct the p-value for multiple testing problem as elaborated in section 2.2.6.

2.2.9 Statistical significance test of TF or miRNA

For a given TF (or miRNA), I correlate the activity scores (or the expression values) across all samples with the samples' PR enrichment scores, as calculated in section 2.2.3, using Spearman's rank correlation coefficient. To establish if a TF (or miRNA) is significantly correlated with a gene signature, I determine the statistical significance of the correlation following the method in section 2.2.8.

I categorise a TF (or miRNA) to be significantly correlated with P signature (P+) if the correlation of its activity score (or expression value) with P enrichment score > 0 and p-value of the correlation remains significant after BH correction. Otherwise, I denote the TF (or miRNA) as not significantly correlated with P signature (P-). Similarly, I categorise a TF (or miRNA) to be significantly correlated with R signature (R+) if the correlation of its activity score (or expression value) with R enrichment score > 0 and p-value of the correlation remains significant after BH correction. Otherwise, I denote the TF (or miRNA) as R-.

2.2.10 Statistical significance test of target genes enrichment

This analysis is similar to the analysis in section 2.2.9. From the enrichment analysis of TF (or miRNA) targets, there is an enrichment score of P or R signature in the target genes of every TF (or miRNA). To determine if the target genes of a particular TF (or miRNA) are significantly enriched for a given gene signature, I estimate the statistical significance of the enrichment score following the method in section 2.2.8.

I categorise the target genes of a TF (or miRNA) to be significantly enriched for P signature (P+) if they have P enrichment score > 0 and a p-value being significant after BH correction. Otherwise, I denote the target genes as not significantly enriched for P signature (P-). Similarly, I categorise the target genes of a TF (or miRNA) to be significantly enriched for R signature (R+) if they have R enrichment score > 0 and a p-value being significant after BH correction. Otherwise, I denote the target genes as not significantly enriched for R signature (R-).

3 Colorectal cancer classifications based on CMS versus PR schemes

3.1 Background

Here I study the prognostic values of cell proliferation and tissue remodelling gene signatures in the context of a colorectal cancer classification. In a recent report, the CRCSC consortium stratified colorectal cancer patients based on gene classifiers without using a prior biological knowledge. They demonstrated that the subtype that indicated worst prognosis (CMS4 subtype) was enriched for a signature of mesenchymal. Yet, cell proliferation gene signature was not studied in their approach and it might affect the ability of their approach to classify colorectal cancer patients beyond the CMS4 or the mesenchymal subtype. This motivates me to re-analyse this cohort of patients using our gene signatures of cell proliferation and tissue remodelling then compare the performance of both approaches in stratifying patients.

Then I evaluate if there are overlaps of sample group membership between both approaches. Next, I assess if both PR signatures are independent prognostic factors or one of these gene signatures alone can be adopted for patient classifications.

3.2 Methods

3.2.1 Sample classification based on PR gene signatures

I classify patient samples based on the enrichment of the cell proliferation and tissue remodelling gene signatures. The calculation of the enrichment scores and their statistical significance is as elaborated in section 2.2.3. If a sample has a significant up-regulation of cell proliferation signature (enrichment score for P signature > 0 with p-value < 0.05), I classify it as P+ and P- if otherwise. For reporting the significance of the enrichment score, I choose the smaller p-value from the two-tailed tests. Similarly, if a sample has a significant up-regulation of tissue remodelling signature (enrichment score for R signature > 0 with p-value < 0.05), I classify it as R+ and R- if otherwise. By construction, this classification

results in four subtypes, namely P+/R+, P+/R-, P-/R+, and P-/R-, as presented in the following.

3.2.2 Similarity of sample group membership between CMS and PR

After excluding samples that were not assigned to a specific CMS group in the original analysis (ref. (Guinney et al. 2015)), I quantify the similarity of CMS and PR sample group memberships using a hypergeometric distribution (one-tailed version of Fisher's exact test). I perform pairwise comparisons on all PR and CMS groups. The variables for the test are defined as follows. The population size (N) of the model is the number of samples classified into CMS groups. The number of success cases in the population (K) is the number of samples classified into PR groups. Subsequently, the number of draws (n) is the number of samples that belong to a particular CMS group. Then, the number of observed successes (k) is the number of samples that belong to both a particular CMS group and a particular PR group. I calculate the significance of the similarity of the sample group memberships using a cumulative hypergeometric distribution function where p-value is $P(X \geq k)$ or the probability of getting the number of observed successes or more.

3.2.3 Percentage of expressed genome with PR gene signatures

Spearman's rank correlation coefficient of the expression values of all samples with the enrichment scores with a gene signature is calculated as described in section 2.2.4. I determine the statistical significance of the correlation following the method in section 2.2.8.

A gene is defined to be up-regulated for a given signature if its expression value has a positive correlation with the enrichment score of the signature and this correlation remains significant after BH correction. I specify the percentage of expressed genome with a gene signature to be the percentage of genes having a significant up-regulation of the signature but having a negative correlation with the other signature across genome.

3.2.4 Sample classification using four quartiles of R enrichment score

The R enrichment score and the statistical significance based on a less bias estimate are obtained from the calculation in section 2.2.3. I classify the samples into four groups based on four quartiles of R enrichment score. I label the samples in first quartile as R--, second quartile as R-, third quartile as R+ and lastly, the samples in fourth quartile as R++.

3.3 Comparison of CMS versus PR classifications

To assess the advantages and disadvantages of both classifications, I carry out a side-by-side comparison of the unsupervised versus supervised classifications, as illustrated in Figure 3-1. CMS classification represents the unsupervised clustering approach. The input of this scheme does not make use of prior biological knowledge, and hence it is unbiased and unsupervised. Contrarily, the PR classification represents the supervised clustering approach. This scheme is developed based on our observation that the hallmarks of cancer can be arranged into two groups of processes that promote cell proliferation or tissue remodelling (Figure 3-2, ref. (Markert et al. 2012)). It is supervised as it is based on prior biological knowledge and it may be biased towards previous knowledge. Very often, it is assumed that unsupervised approaches outperform supervised methods based on prior knowledge. However, this assumption does not hold true in general and it should be assessed in a case-by-case bases.

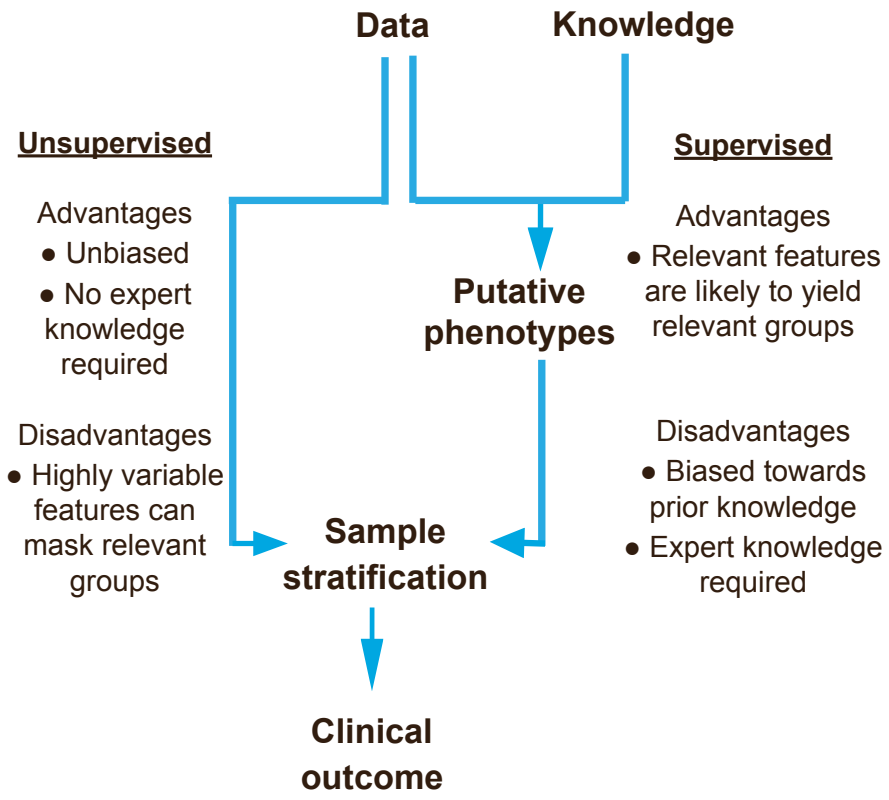

Figure 3-1. Flow diagrams of patient stratification based on the unsupervised and supervised clustering methods

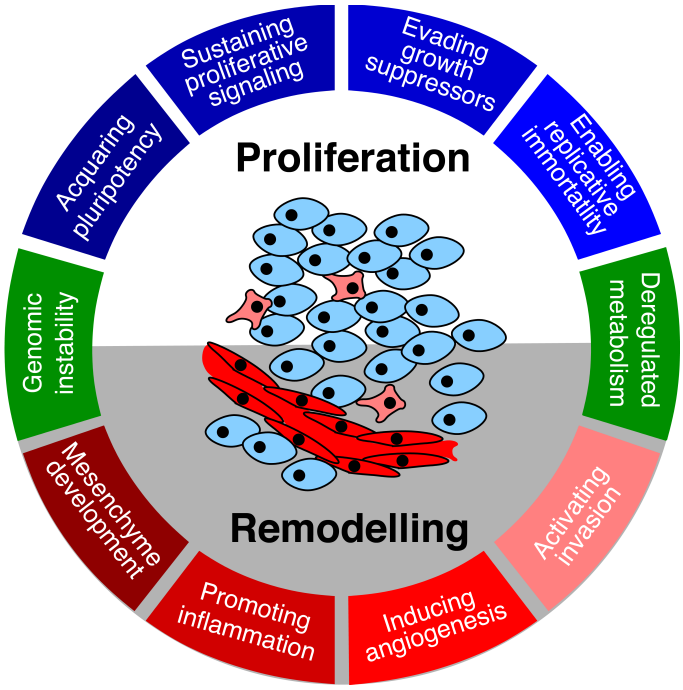

Figure 3-2. The hallmarks of cancer drive two major features of cancer, cell proliferation and tissue remodelling

To investigate the performance of the CMS and PR classification schemes with regard to prognosis, I perform a meta-analysis of a cohort of colorectal cancer patients recently reported by the CRCSC consortium. This cohort consists of gene expression profiles and survival information from different published studies. The samples had been previously classified based on the CMS scheme into four subtypes, namely, CMS1, CMS2, CMS3 and CMS4. I reclassify the same cohort of patients based on our PR scheme. I quantify the degree of cell proliferation and tissue remodelling in each sample, as described in section 3.2.1 and stratify all samples into four subtypes, namely P+/R+, P+/R-, P-/R+, and P-/R-. The assignment of each sample into the PR groups can be found in Appendix.

3.3.1 Mapping between CMS and PR sample group memberships

To compare the sample group memberships and determine the overlaps between both classifications, I analyse the similarity of the sample group memberships in both the CMS and PR schemes, as detailed in section 3.2.2. Even though both classifications are performed separately, the resulting subtypes show some overlaps, as can be seen in Figure 3-3. CMS2 subtype maps to a great extent to our P+/R- subtype (p-value = 2.3×10^{-48}, one-tailed Fisher's exact test), whereas CMS4 subtype maps to a great extent to our P-/R+ subtype (p-value = 8.9×10^{-144}, one-tailed Fisher's exact test). The full list of overlap sizes between both classifications together with their statistical significances is presented in Table 3-1.

Table 3-1. Number of overlaps between subtypes in CMS and PR schemes

	P+/R+ (371)		P+/R- (716)		P-/R- (398)		P-/R+ (490)	
	Overlap	P-value	Overlap	P-value	Overlap	P-value	Overlap	P-value
CMS1 (336)	**151**	**3.70E-35**	134	0.07	21	1	30	1
CMS2 (823)	78	1	**452**	**2.30E-48**	217	5.10E-09	76	1
CMS3 (282)	14	1	108	0.24	**134**	**7.10E-30**	26	1
CMS4 (534)	128	2.60E-04	22	1	26	1	**358**	**8.90E-144**

The number in brackets next to the subtype label is the number of samples that belong to that subtype. The number in the cells in bold indicates the most significant mapping of a PR subtype with a CMS subtype in the pairwise comparisons.

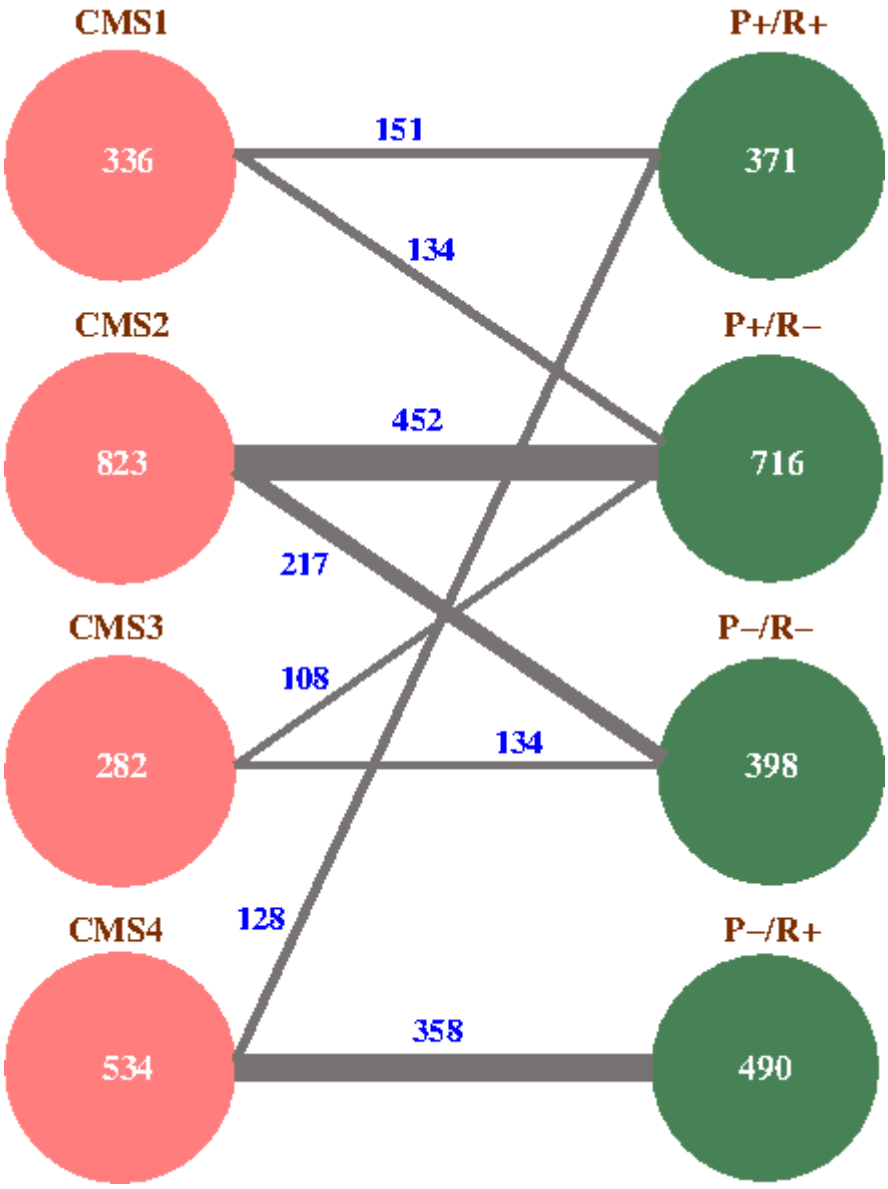

Figure 3-3. Mapping between CMS and PR groups. The grey lines connecting the circles show the most and second most overlaps among subtypes in both classifications.

The overlaps between the CMS and PR classifications can be elucidated by the high correlation between some genes and our gene signatures of cell proliferation and tissue remodelling. A high proportion of the expressed genome (34.25%) is significantly correlated with tissue remodelling enrichment score (p-value < 0.05, permutation test for Spearman's rank correlation coefficient). Likewise, there is 35.56% of the expressed genome that is significantly correlated with cell proliferation enrichment score (p-value < 0.05, permutation test for Spearman's rank correlation coefficient). Consequently, any unsupervised clustering approach would reflect this strong signal. The calculation for the correlation of the proportion of expressed genome with the gene signatures can be found in section 3.2.3.

Because the CMS classification is unsupervised, it does not include any information about proliferation or remodelling when assigning samples to different CMS subtypes. Therefore, one may ask how such classification ends up being correlated with our classification based on the gene signatures of proliferation and remodelling. As described in the introduction, there is a previous report indicating that a large proportion of the expressed genome is correlated with cell proliferation (Venet et al. 2011). To test this hypothesis in the context of the CRCSC cohort, I quantify the correlation between expression of a gene G and enrichment score of P or R signature across all samples, denoted by Spearman's rank correlation coefficients $S(G,P)$ or $S(G,R)$, respectively. There is a significant negative correlation between $S(G,P)$ and $S(G,R)$ across genes (S = -0.70, p-value = 1×10^{-5}, permutation test), as illustrated in Figure 3-4. In other words, there are a large number of genes whose expression are highly and positively correlated with P enrichment score but negatively correlated with R enrichment score. Likewise, there are a large number of genes whose expression are highly and positively correlated with R enrichment score but negatively correlated with P enrichment score. Taken together, this data demonstrates that how the partial overlap between the CMS and PR classifications is rooted can be explained by the fact that large proportions of the expressed genome are correlated with cell proliferation or tissue remodelling in colorectal cancer samples.

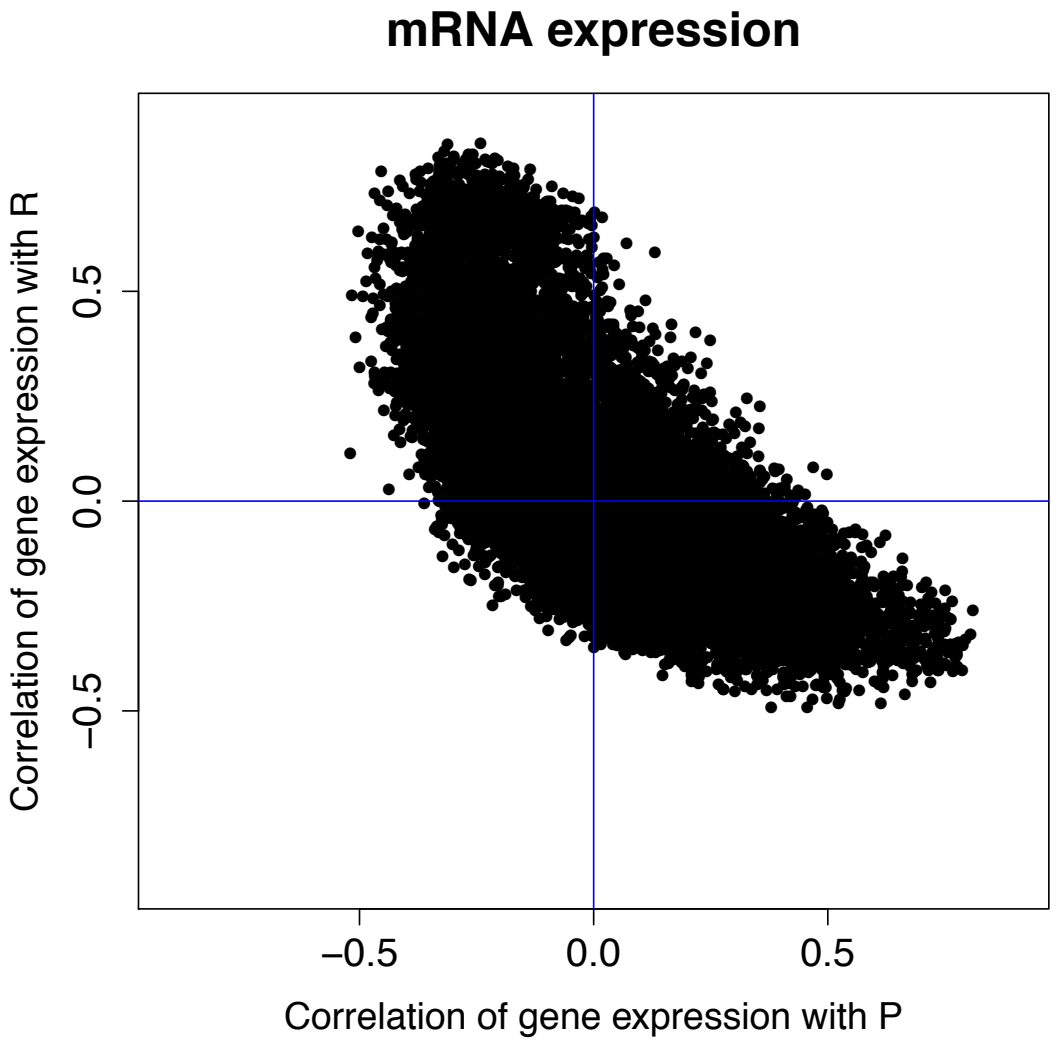

Figure 3-4. Scatter plot of Spearman's rank correlation coefficients between gene expression and tissue remodelling signature (Y-axis) as a function of Spearman's rank correlation between gene expression and cell proliferation signature (X-axis) in the CRCSC cohort. Each dot represents a gene and the correlation is calculated across all patients.

3.4 Performance of CMS and PR survival analysis

Now I proceed to evaluate the performance of the CMS and PR classifications with regard to outcome prognosis of colorectal cancer patients. The datasets brought together by the CRCSC consortium come with survival information. In this section, I compare the performance of both CMS and PR schemes in stratifying the patients' overall and relapse-free survival. The method for this type of survival analysis is as described in section 2.2.5.1.

In terms of predicting patient outcome, both approaches yield statistical significance in splitting survival curves (Figure 3-5). The CMS4 subtype in the unsupervised approach and the P-/R+ subtype in the supervised approach, which are associated with tissue remodelling, exhibit worst prognosis compared to the remaining groups in the respective schemes. However, the unsupervised approach cannot distinguish the remaining patients based on survival. In other words, the CMS scheme predicts a poor prognosis for patients with tissue remodelling, or mesenchymal features, but it is not able to set apart the rest of patients with respect to survival. On the other hand, in the PR classification, both of its two features are associated with clinical outcome. Apart from distinguishing the remodelling group (P-/R+), it yields the P+/R- group that exhibits significantly better prognosis than the P-/R- group. This observation indicates that the cell proliferation and tissue remodelling gene signatures are both relevant for patient stratification.

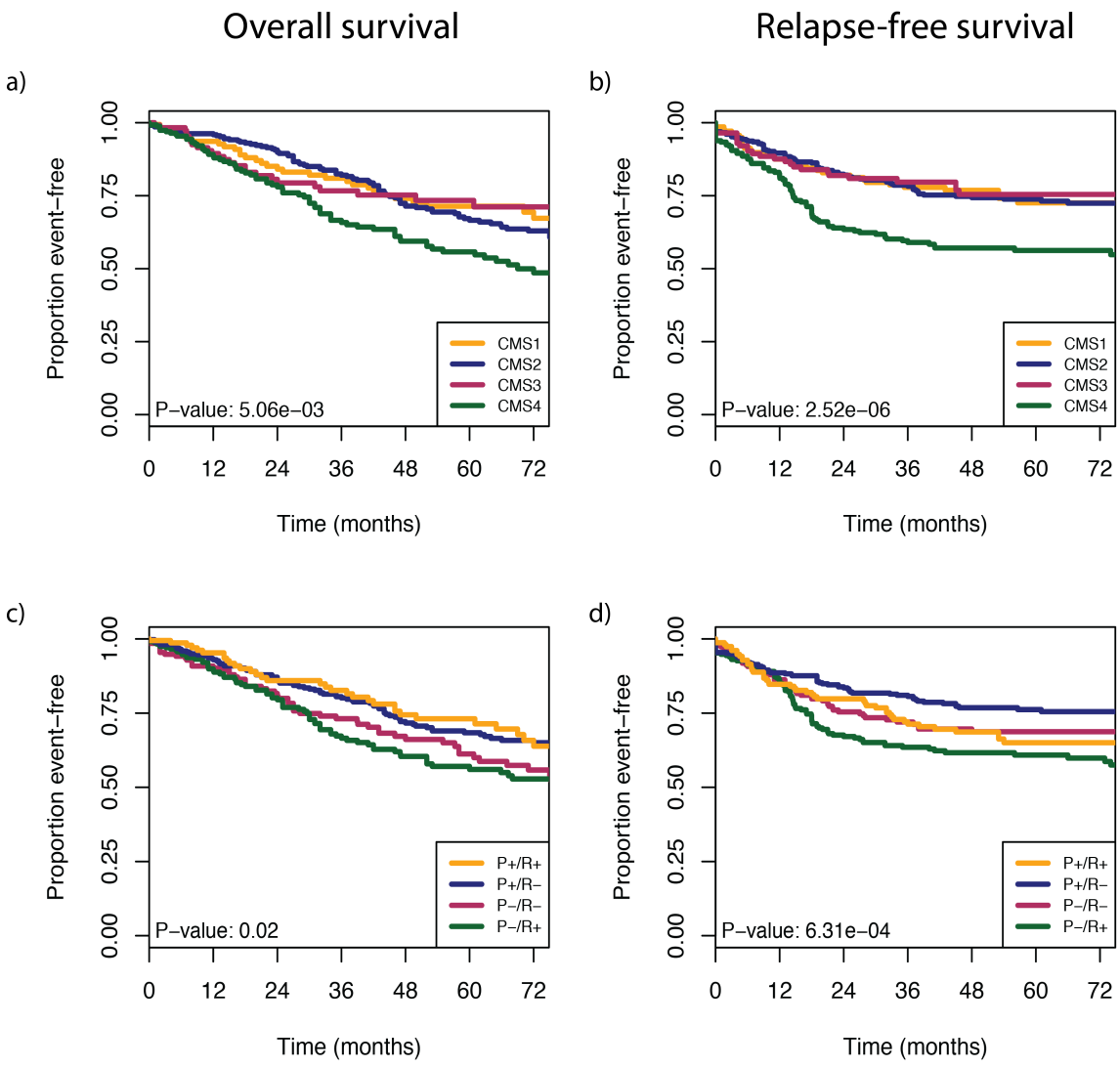

Figure 3-5. Kaplan-Meier plots of colorectal cancer subtypes survival based on the CMS and PR classification schemes. P-values indicate the statistical significance based on log-rank test. (**a**, **b**) CMS classification based on (**a**) overall survival and (**b**) relapse-free survival. (**c**, **d**) PR classification based on (**c**) overall survival and (**d**) relapse-free survival.

Because the CMS scheme differentiates only patients with tissue remodelling (CMS4 subtype), I evaluate if our cell proliferation signature can further split the CMS4 subtype. To this end, I take the CMS4 samples only and split them into patients with a significant up-regulation of the cell proliferation signature (CMS4/P+) and the remaining (CMS4/P-). The CMS4/P+ group has a significantly better overall survival (Figure 3-6a, p-value = 0.01, log-rank test) and a trend of better relapse-free survival than the CMS4/P- group (Figure 3-6b, p-value = 0.14, log-rank test). This observation indicates that CMS classification is not exhaustive. The results also highlight that the cell proliferation signature serves as an additional prognostic factor, indicative of good prognosis in colorectal cancer, besides the tissue remodelling signature.

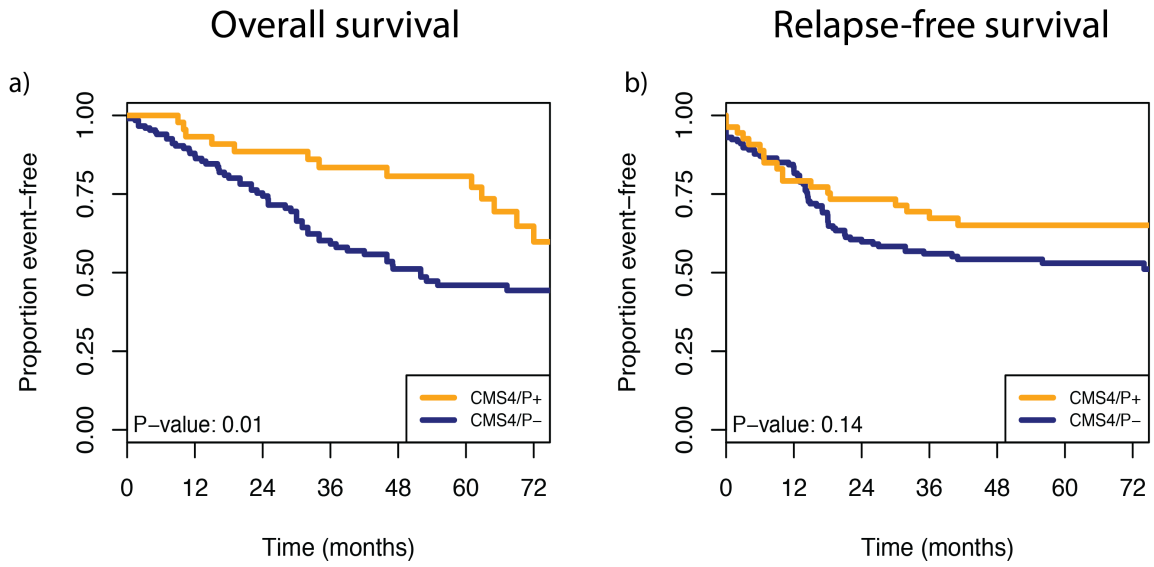

Figure 3-6. Kaplan-Meier plots of CMS4 patients further stratified by P signature based on (**a**) overall survival and (**b**) relapse-free survival. P-values indicate the statistical significance based on log-rank test.

3.5 The interdependence of PR signatures as prognostic factors

As cell proliferation is associated with good prognosis in colorectal cancer, we ask if the treatments might work better at targeting proliferating cells and patients with increased cell proliferation responded better to treatments. However, the information about which patients received treatment and the type of treatments given is not reported. Yet, we would like to evaluate if PR signatures can serve as an unbiased prognostic tool for patients who received treatments versus those who did not. Consequently, I cannot include treatment options as a covariate in the multivariate survival analysis. Nonetheless, age and stage are reported, which are two clinical variables commonly used for making treatment decisions.

Here I establish whether P and R enrichment scores are independent prognostic factors when considering other clinical variables. This is achieved through a multivariate survival analysis, as outlined in section 2.2.5.2. I determine whether P and R enrichment scores are able to predict an event (death or relapse) occurring, independently of the clinical variables age, stage and gender.

As expected, stage manifests a significant association with an increased risk of both death and relapse (Table 3-2). As can be observed from Table 3-2a, enrichment score of R exhibits a significant association with increased risk of relapse (hazard ratio = 4.60, 95% confidence interval (CI) = 1.14-18.52, p-value = 0.03, Wald test). In contrast, P enrichment score is significantly associated with reduced risk of death (hazard ratio = 0.32, 95% CI = 0.10-0.99, p-value = 0.05, Wald test).

Without considering R enrichment score in the analysis, P enrichment score exhibits a significant association with reduced risk of both death and relapse (Table 3-2b). Similarly, when P enrichment score is not considered, R enrichment score is significantly associated with increased risk of both death and relapse (Table 3-2c).

These results suggest that P and R enrichment scores are not independent prognostic factors. Indeed, there is a strong negative correlation between P and R enrichment scores (Spearman's rank correlation coefficients = -0.44, p-value = 1×10^{-5}, permutation test). However, when being considered at the same time, both P and R enrichment scores are able to predict patient outcome, independently of other clinical variables.

Table 3-2. Multivariate survival analysis considering clinical variables and enrichment scores of (**a**) P and R, (**b**) P only and (**c**) R only

Variable		Overall survival			Recurrence-free survival		
		Hazard ratio	95% Confidence interval	P-value	Hazard ratio	95% Confidence interval	P-value
(a)	P & R						
	P scores	0.32	0.10-0.99	0.05	0.41	0.13-1.26	0.12
	R scores	1.32	0.37-4.70	0.67	4.60	1.14-18.52	0.03
	Stage	1.98	1.67-2.34	2.6E-15	2.86	2.35-3.49	<2e-16
	Age	1.03	1.02-1.04	4.6E-09	1.00	0.99-1.01	0.56
	Gender	1.26	0.99-1.61	0.07	1.36	1.05-1.77	0.02
(b)	P						
	P scores	0.28	0.11-0.76	1.2E-02	0.23	0.08-0.62	3.8E-03
	Stage	1.98	1.67-2.34	2.1E-15	2.87	2.36-3.49	< 2e-16
	Age	1.03	1.02-1.04	4.8E-09	1.00	0.99-1.01	0.58
	Gender	1.26	0.98-1.60	0.07	1.34	1.03-1.74	0.03
(c)	R						
	R scores	2.46	0.81-7.45	1.1E-01	7.76	2.27-26.50	1.1E-03
	Stage	2.00	1.69-2.37	7.8E-16	2.90	2.38-3.54	< 2e-16
	Age	1.03	1.02-1.04	8.4E-09	1.00	0.99-1.01	0.63
	Gender	1.28	1.00-1.63	0.05	1.38	1.06-1.79	0.02

Multivariate survival analysis considering clinical variables stage, age and gender together with enrichment scores of (**a**) P and R, (**b**) P only and (**c**) R only.

3.6 Survival analysis using R enrichment score

In section 3.3.1, I demonstrate that there is a significant negative correlation between cell proliferation and tissue remodelling across genes. Then in section 3.5, I show that P and R enrichment scores are strongly inversely correlated. These observations raise the possibility that a finer gradation of one of the signatures (e.g. R) could substitute the PR scheme. To test this possibility, here I investigate if R enrichment score alone can serve as an independent prognostic factor, especially because tissue remodelling is associated with worse prognosis in colorectal cancer.

To do this, I stratify the colorectal tumours in the CRCSC cohort into four groups based on four quartiles of the R enrichment score (see section 3.2.4), instead of the four groups determined by P and R signatures. Then I perform a univariate survival analysis as before (see method in section 2.2.5.1).

This classification also yields statistical significance in splitting survival curves, where the R++ group exhibits worst overall and relapse-free survival (Figure 3-7). With regard to relapse-free survival, which is a more accurate measure of the disease impact on survival, the R+ group comes as the second worst prognosis. This suggests that indeed we could substitute the PR classification for one with a finer gradation of R. However, we believe that having a positive marker (P+) is more informative from the point of view of treatment choice than a negative one (R- or R--). Furthermore, we should keep in mind that the PR classification can be deployed to other cancer types (Markert et al. 2012). Therefore, taken together, this evidence indicates that the PR classification is a more universal scheme.

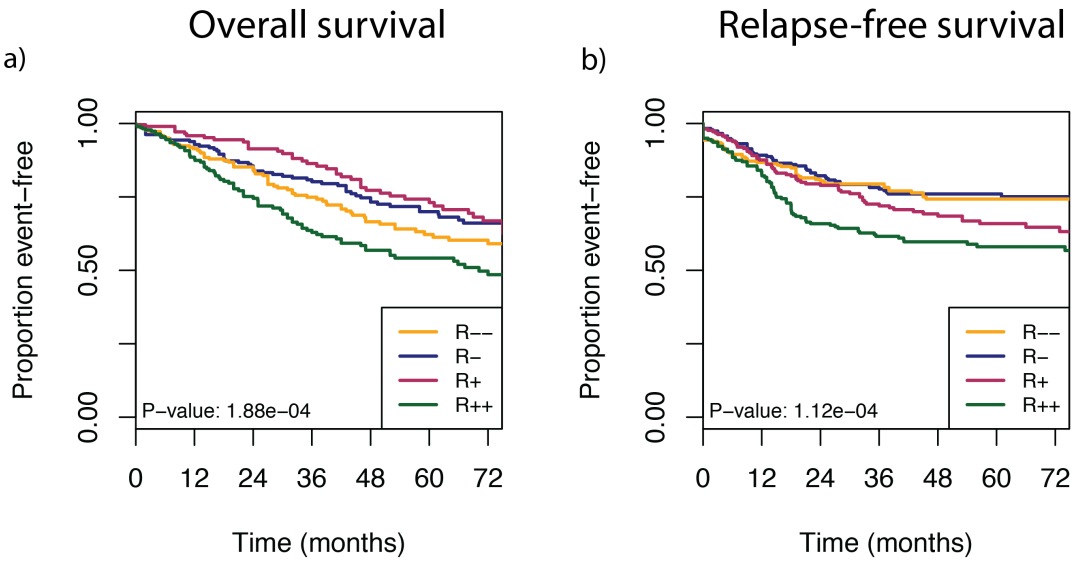

Figure 3-7. Kaplan-Meier plots of colorectal cancer subtypes survival using R enrichment score based on (**a**) overall survival and (**b**) relapse-free survival. P-values indicate the statistical significance based on log-rank test.

3.7 Conclusions

The CMS2 group in the unsupervised scheme maps significantly to the P+/R- group in our supervised scheme, while the CMS4 group maps significantly to our P-/R+ group. The overlaps can be explained by the fact that large proportions of the expressed genome are correlated with cell proliferation or tissue remodelling in colorectal tumours. Although the CMS4 subtype is indicative of worst prognosis, the unsupervised scheme cannot distinguish the remaining patients based on survival. On the other hand, our PR classification demonstrates that cell proliferation is associated with good prognosis, in addition to the current knowledge that tissue remodelling is indicative of worse prognosis in colorectal cancer. Both the cell proliferation and tissue remodelling gene signatures are relevant for patient stratification.

Enrichment scores of PR can predict an event (death or relapse) occurring, independently of the clinical variables but they are interdependent. A classification with a finer gradation of R can substitute the PR classification. However, having a positive marker (P+) is more informative than a negative one (R- or R--) from the point of view of treatment decisions.

4 Putative transcription factors driving PR programmes

4.1 Background

As noted previously, the expression of 35.56% and 34.25% of the genes is correlated with the P and R signatures, respectively. This suggests that there are gene regulation programs driving the P and R signatures.

Transcription factors (TFs) regulate gene expression by binding to specific region of their target genes and controlling the transcription of DNA into mRNA. They function by allowing RNA polymerase to access a gene or preventing it from accessing a gene, resulting in gene activation or repression, respectively. Their activities control cell growth, cell types maintenance and transition among them.

In chapter 3, I elaborate that tissue remodelling is associated with worse prognosis, whereas cell proliferation is associated with good prognosis in colorectal cancer. Yet, we do not have an understanding about specific regulators that drive increased tissue remodelling or increased cell proliferation in this disease. Here I address this question by investigating specific transcription factors that drive the transcriptional programmes of cell proliferation and tissue remodelling.

4.2 Methods

4.2.1 Identification of TF targets

To identify target genes of human TFs, I retrieve Transcriptional Regulatory Relationships Unravelled by Sentence-based Text-mining (TTRUST) database (Han et al. 2015). At the time of download, the latest version of the database was version 1. It consists of annotations of 748 human TFs with 2,374 unique target genes and 8,015 transcriptional regulatory relationships. TTRUST is a manually curated database with experimentally validated interactions and it provides information on the mode of regulation, i.e. activating or repressing.

The database contains unknown interactions but I include only activating and repressing interactions for the analysis.

4.2.2 Inference model of TF activity

I infer TF activity scores using linear least squares model $G_{ik} = \Sigma_j T_{ij} A_{jk}$ where G_{ik} is expression of gene i in sample k, A_{jk} is activity of TF j in sample k and T_{ij} is the transcription regulation derived from TRRUST database (section 4.2.1). In the model, T_{ij} reflects the interactions between TFs and their target genes where it is 1, 0 or -1 if TF j activates, does not regulate or represses gene i, respectively. I fit in gene expression matrix G and the transcription regulation matrix T constructed from TRRUST database as two inputs for the model. I obtain inferred TF activity matrix A by solving linear equation system in the least squares sense. I retain only TFs with standard deviation of activity scores across all samples not equal to zero for further analyses.

To measure significance, I adopt a permutation test as a non-parametric estimate for the statistical significance of observed activity score X_{j0} of TF j being high in a given sample. For the colorectal cancer samples in the CRCSC cohort, I generate 100 permutations of gene expression values of the 2,423 samples in the cohort. Then I infer the corresponding TF activity scores for these permuted gene expression values, obtaining X_{jk} reference scores for activity of each TF j where k = 1, …, n=242,300. I correct the statistical significance of X_{j0} being high based on a less bias estimate $p_{j-} = (1 + \sum_{X_{jk} \le X_{j0}} 1) / (1 + n)$ and $p_{j+} = (1 + \sum_{X_{jk} \ge X_{j0}} 1) / (1 + n)$ (North et al. 2002). I report p_{j+} as the statistical significance if $p_{j+} < p_{j-}$ or p_{j-} if $p_{j-} < p_{j+}$. Lastly, I specify a sample having a significant high TF j activity score if $X_{j0} > 0$, $p_j < 0.05$ and remains significant after BH correction, while not significant if otherwise.

4.2.3 Enrichment analysis of TF targets

This analysis is similar to the GSEA method in section 2.2.3 but the two inputs are different in this case. I swap the expression values and the gene signature in the original method with Spearman's rank correlation of expression values with P or R enrichment score and target genes of a TF as the two inputs, respectively.

Because TFs generally activate or repress target genes, I include only interactions that agree with a particular signature in the analysis. In other words, for testing the enrichment of P signature in the target genes, I consider only interactions that promote P or repress R. These include interactions with TFs activating target genes that are significantly and positively correlated with P and interactions with TFs repressing target genes that are significantly and positively correlated with R. In contrast, for testing the enrichment of R signature in the target genes, I consider only interactions that promote R or repress P.

To ensure there is no bias introduced by TFs having few target genes, I include only TFs that have at least five target genes for the analysis. Then I create the reference score vector and calculate the enrichment score together with its statistical significance following the GSEA method in section 2.2.3.

4.2.4 Sample classification into PK subtypes

For this analysis, I classify patient samples based on P enrichment score and the level of KLF4 (kruppel-like factor 4) activity. The sample classification into P+ or P- is as explained in section 3.2.1. I retrieve putative KLF4 activity from the TF activity scores, as detailed in section 4.2.2. If a sample has a significant and positive KLF4 activity score, I classify it into K+ and K- if otherwise.

4.2.5 Fisher's exact test of KLF4 activity score with clinical variables

To quantify the enrichment of KLF4 activity score with biomarkers and clinical variables, I adopt a hypergeometric distribution, which is one-tailed version of Fisher's exact test. I perform the test for pairwise comparisons on high and low

levels of KLF4 activity versus all biomarkers and clinical variables. I characterise patients with a significant (p-value < 0.05) and positive KLF4 activity score to have high KLF4 activity. Similarly, I characterise patients with a significant and negative KLF4 activity score to have low KLF4 activity. For each test, I include only patients with available information on the corresponding biomarker or clinical variable.

The variables for the statistical test are defined as follows. The population size (N) is the number of patients that have information on the corresponding biomarker or clinical variable. Next, the number of success cases in the population (K) is the number of patients with the corresponding level (high or low) of KLF4 activity being tested. Then, the number of draws (n) is the number of patients with the biomarker or clinical variable equals to the value or range being tested. Lastly, the number of observed successes (k) is the number of patients with the corresponding level of KLF4 activity and the biomarker or clinical variable being equal to the value or range being tested. I calculate the significance of the enrichment using a cumulative hypergeometric distribution function where p-value is $P(X \geq k)$ or the probability of getting the number of observed successes or more.

4.2.6 Processing of human immune cell dataset (GSE3982)

I retrieve gene expression data files of the human immune cells from GEO with accession number GSE3982. Before combining the expression values from all data files into a single matrix, I correct the order of the probes so that it is the same across all files. After getting the combined expression value matrix, I quantile-normalise the expression values, annotate the probes with their gene names and mean-centre the expression values following the method in section 2.2.2.

I infer KLF4 activity using the TF activity inference model described above. Then I assign the samples into different groups, as tabulated in Table 4-1, for pairwise comparisons of KLF4 activity score in phagocytes (myeloid cells) versus other groups.

Table 4-1. List of samples in human immune cell transcriptome (GSE3982)

Sample ID	Immune cell	Condition	Group
GSM90660	Eosinophils	control	Granu_BME
GSM92194	Eosinophils	control	Granu_BME
GSM90661	Eosinophils	PMA stimulated	Granu_BME_sti
GSM90662	Mast cells	control	Granu_BME
GSM90842	Mast cells	control	Granu_BME
GSM90663	Mast cells	IgE stimulated	Granu_BME_sti
GSM90665	Mast cells	IgE stimulated	Granu_BME_sti
GSM90664	Dendritic cells	LPS stimulated	Phago_sti
GSM90837	Dendritic cells	LPS stimulated	Phago_sti
GSM90666	Dendritic cells	control	Phago
GSM90836	Dendritic cells	control	Phago
GSM90838	Macrophages	control	Phago
GSM90839	Macrophages	control	Phago
GSM90840	Macrophages	LPS stimulated	Phago_sti
GSM90841	Macrophages	LPS stimulated	Phago_sti
GSM90843	Neutrophils	control	Phago
GSM90844	Neutrophils	control	Phago
GSM90847	Neutrophils	LPS stimulated	Phago_sti
GSM90845	B cells	control	Lym
GSM90846	B cells	control	Lym
GSM90848	Basophils	control	Granu_BME
GSM90853	Basophils	control	Granu_BME
GSM90849	T cells	control	Lym
GSM90850	T cells	control	Lym
GSM90854	T cells	control	Lym
GSM90855	T cells	control	Lym
GSM90851	NK cells	control	Lym
GSM90852	NK cells	control	Lym
GSM90856	Th1 cells	control	Lym
GSM90857	Th1 cells	control	Lym
GSM90858	Th2 cells	control	Lym
GSM90859	Th2 cells	control	Lym

‘Granu’ indicates granulocytes.
‘BME’ indicates basophils, mast cells and eosinophils.
‘sti’ indicates stimulated.
‘Phago’ indicates phagocytes.
‘Lym’ indicates lymphoid cells.

4.2.7 Estimation of immune cell types in PK subtypes

I infer the composition of each immune cell type for all colorectal cancer samples in the CRCSC cohort using CIBERSORT (Newman et al. 2015), as elaborated in section 2.2.7. Then I correlate KLF4 activity score with the estimated composition of a particular immune cell type across all samples using Spearman's rank correlation coefficient. This is performed for all immune cell types estimated by CIBERSORT. Subsequently, I estimate the statistical significance of the correlations based on a less bias estimate (permutation test in section 2.2.8) to identify immune cell types that are significantly correlated with KLF4 activity score.

To assess the abundance of different immune cells in each PK subtypes, I group all samples that belong to a particular PK subtype together. Next, I visualise the inferred compositions of the immune cells of interest in the PK subtypes to examine if the level of KLF4 activity score can predict the extent of immune cell infiltration.

4.3 Correlation of R signature with other related signatures

The gene signatures of cell proliferation and tissue remodelling can be driven by multiple factors. The former can reflect an enrichment of epithelial cells at the expense of stromal cells. On the other hand, the latter can be the consequence of various processes, such as mesenchyme development, response to wounding and immune cell infiltration.

Here I investigate the correlation of the R enrichment score with enrichment scores of other reported gene signatures associated with tissue remodelling processes, particularly because tissue remodelling is indicative of worse prognosis in colorectal cancer. As shown in Table 4-2, a previously reported gene signature of "Response to wounding" has the highest correlation with the R enrichment score (S = 0.95). The R enrichment score is also highly correlated with gene signatures of "Stromal tissue" (S = 0.90), "Immune cell infiltration" (S = 0.74), "Mesenchyme development" (S = 0.72) and "Epithelial mesenchymal transition" (S = 0.65). The statistical significances for these correlations are all 1×10^{-5} and performed using permutation test (section 2.2.8). These associations suggest that the signal of tissue remodelling could reflect different biological processes, including high stromal cell content, immune cell infiltration and EMT. The lists of genes in these signatures can be found in Appendix.

Table 4-2. Correlation of enrichment scores of R and tissue remodelling-associated gene signatures

Signature	*S*	P-value	Number of genes	Source
Response to wounding	0.95	1.0E-05	1023	GO:0009611
Stromal tissue	0.90	1.0E-05	141	Ref. (Yoshihara et al. 2013)
Immune cell infiltration	0.74	1.0E-05	141	Ref. (Yoshihara et al. 2013)
Mesenchyme development	0.72	1.0E-05	130	GO:0060485
Epithelial mesenchymal transition	0.65	1.0E-05	9	GO:0001837

S denotes Spearman's rank correlation coefficients between enrichment scores of R and the signature.
GO denotes a Gene Ontology gene set.

4.4 Identification of TFs driving PR

The colorectal cancer samples in the CRCSC cohort do not come with TF activity data (proteomics, ChIP-seq or similar). As we do not have access to these samples, I develop a linear regression inference model to predict TF activity, as detailed in section 4.2.2. This model takes gene expression profiles and annotations of TF targets together with their mode of regulation, either activation or repression, as the inputs. A representation of the method is as illustrated in Figure 4-1. The output is a putative transcriptional activity score for each TF annotated in TRRUST database, referred to as TF activity scores throughout this thesis.

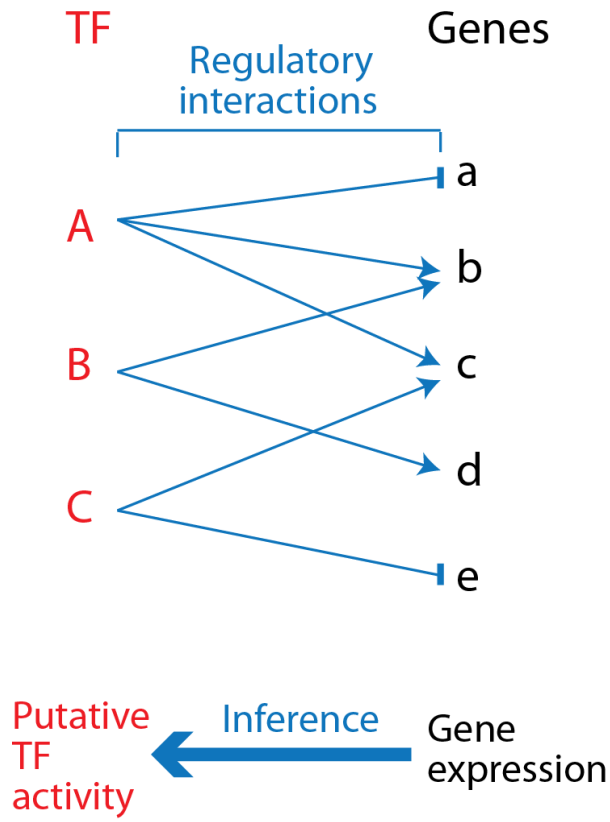

Figure 4-1. Schematic diagram of gene regulation and transcription factor activity inference

I fit the gene expression profiles from the CRCSC cohort into the TF inference model and obtain the inferred TF activity for every annotated TF on each sample in the cohort, as outlined in Figure 4-2. Then I focus on associations between the TF activity scores and the PR gene signatures. For each transcription factor, I

calculate the Spearman's rank correlation coefficient between the TF activity score and the P and R enrichment scores across all samples. The correlation is done following the method in section 2.2.4 but substituting gene expression with TF activity score. These correlation coefficients are represented by S(TF,P) and S(TF,R), respectively. S(TF,P) takes values between -1 and 1, whereby a value close to 1 indicating that the TF manifests a high activity score in samples with a high degree of cell proliferation, while a value close to -1 indicating that the TF manifests a low activity score in samples with a high degree of cell proliferation. Same interpretation for S(TF,R) but with respect to the tissue remodelling gene signature.

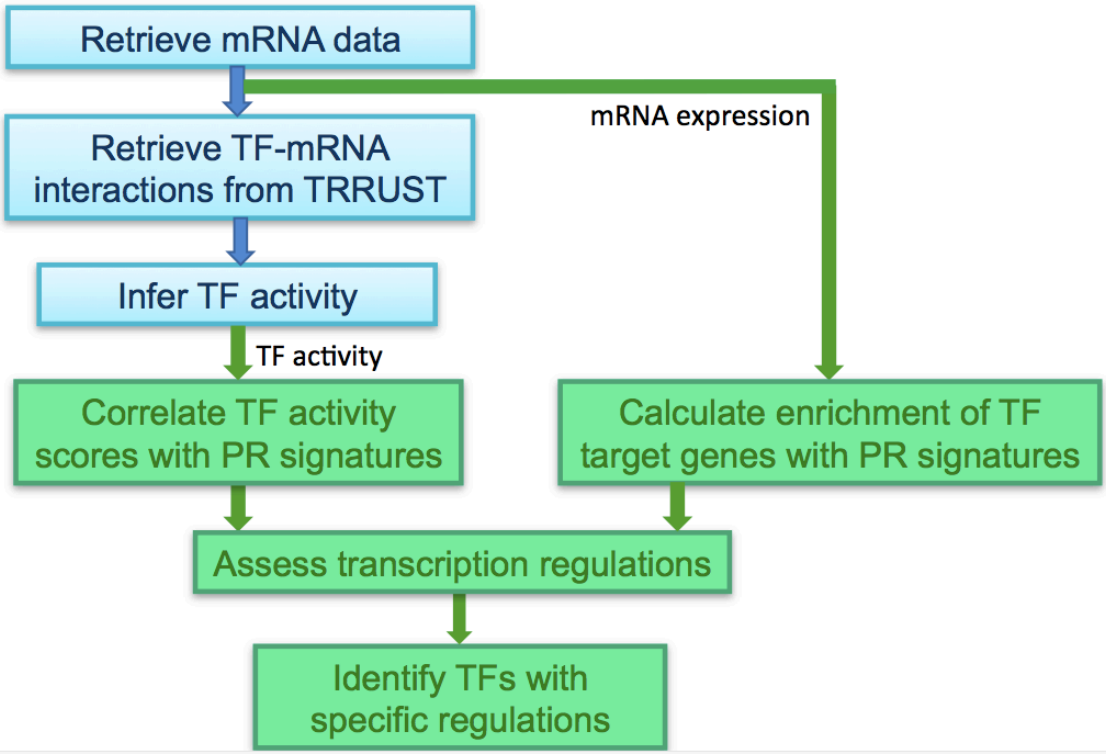

Figure 4-2. Workflow of TF activity inference analysis and identification of TF regulation. Blue boxes indicate the pre-processing steps, while green boxes indicate the processing steps.

As can be observed in Figure 4-3, the TFs exhibiting high S(TF,P) have high but negative S(TF,R), and vice versa. Based on the Spearman's rank correlation coefficient between S(TF,P) and S(TF,R), there is indeed a significant negative correlation between the tendency of TFs to have activity associated with the proliferation or remodelling programmes (S = -0.56, p-value = 1×10^{-5}, permutation test). This suggests that the biases of PR in gene expression are driven by biases in the transcriptional programmes. We highlight that this negative correlation is highly significant, which implies that it cannot be deduced from the negative correlation reported for gene expression (Figure 3-4) alone. There is some information in the TF targets annotations that contributes to the emergence of the negative correlation in Figure 4-3.

Afterwards, I focus on the TF targets and assess whether these targets go along with the P and R gene signatures. I identify target genes of TFs using TRRUST (see section 4.2.1). The expression of each of these target genes may or may not be correlated with the P gene signature. If the expression of a target gene is indeed positively correlated with P then it scores as a positive and the enrichment of these positives within the target list of a TF is used as putative evidence that this TF may regulate the cell proliferation programme. Similarly, if the expression of a target gene is indeed positively correlated with R then it scores as a positive and the enrichment of these positives within the target list of a TF is used as putative evidence that this TF may regulate the tissue remodelling programme (see section 4.2.3 for technical details). Subsequently, I assess regulatory relationships between the activity score of a TF and the expression of its targets, aiming to identify TFs whose activity scores are associated with PR enrichment scores and their targets are enriched for the PR signatures as well (Figure 4-2). This analysis can result in different patterns of regulations, depending on following factors:

- the association between the TF activity scores and the PR enrichment scores
- the mode of regulation of the TFs have on the target genes (activation or repression), and
- the enrichment of the TF target genes with the P and R signatures (calculated based on the method in section 4.2.3).

The significance of the association of TF activity score with the P or R enrichment score is as calculated in section 2.2.9. The calculation for the significance of the enrichment of target genes with the gene signature is as described in section 2.2.10.

From the biological point of view, transcription regulations that sustain one specific transcriptional programme are of more interest. This includes TFs having activity score significantly correlated with the P enrichment score and targeting genes significantly enriched for the P signature (P -> P) and TFs having the corresponding relationship with the R signature (R -> R). Following these particular patterns of regulations, I identify PROX1, RUNX3, SOX2 and TP53 as the TFs associated with the cell proliferation programme in colorectal cancer (Table 4-3 and Appendix, P -> P). Similarly, I identify CEBPB, CLOCK, CREB1, ERG, ESR1, ETS2, ETV4, FOXO3, GATA3, JUN, KLF4, NFE2L2, NR5A2, PML, PPARD, RELA, SNAI2, SPI1 and STAT1 as the TFs that promote the tissue remodelling programme (Table 4-3 and Appendix, R -> R). The master list of TFs together with their correlation of activity scores with the P and R enrichment scores and the enrichment scores of their targets with the PR signatures can be found in Appendix.

In TRRUST database, BRCA1 is listed as a transcription factor and the results from the TF inference model indicate that BRCA1 also has a regulation pattern that is associated with tissue remodelling programme. BRCA1 can interact with RNA polymerase II holoenzyme components and its ectopic expression can induce transcription from various promoters (Monteiro 2000). The C terminus of BRCA1 can activate transcription when fused to a GAL4 DNA-binding domain and a number of its interacting proteins have various roles in transcription (Monteiro 2000). However, there is no evidence of sequence-specific binding to DNA by BRCA1 (Monteiro 2000). Therefore, I do not report BRCA1 as one of the TFs promoting the tissue remodelling programme.

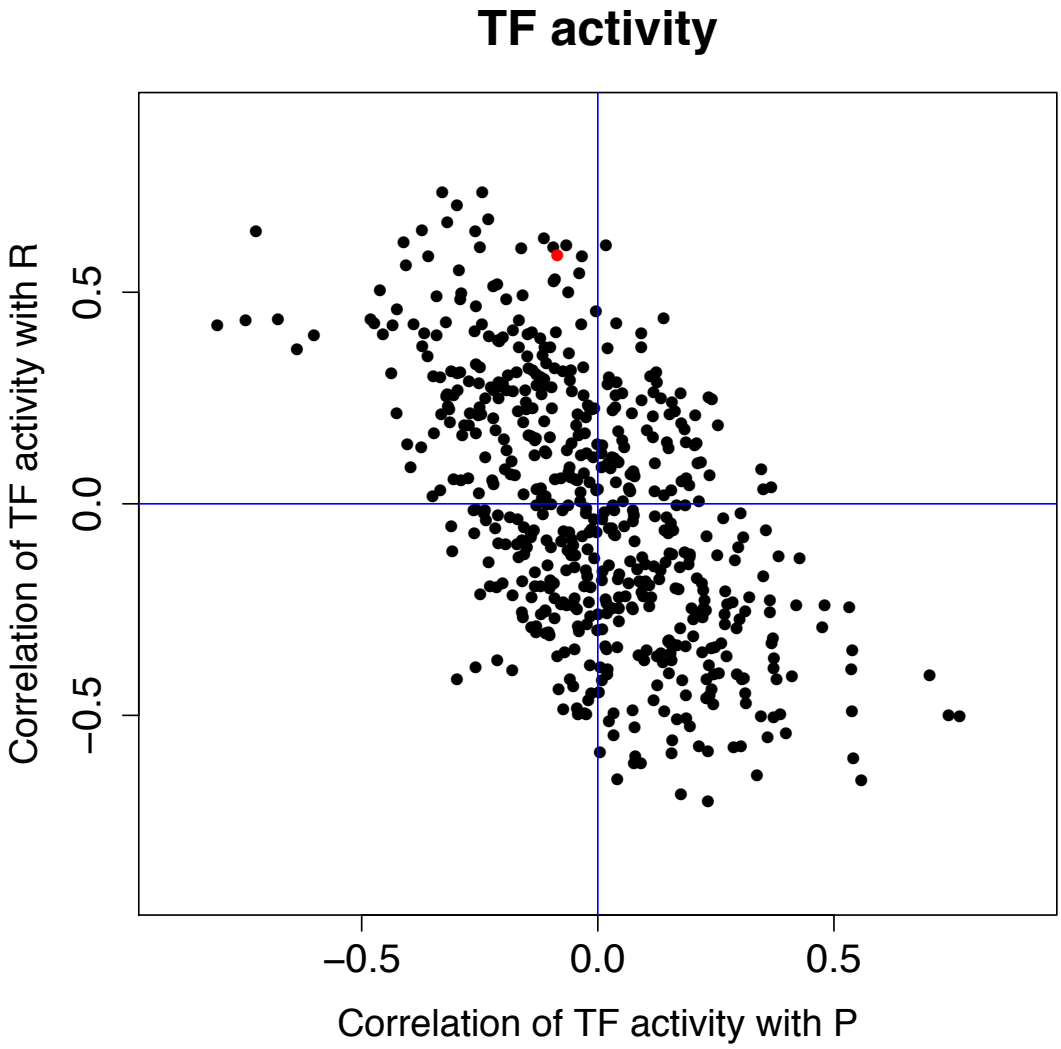

Figure 4-3. Scatter plot of Spearman's rank correlation coefficients between TF activity scores and tissue remodelling signature (Y-axis) as a function of Spearman's rank correlation between TF activity scores and cell proliferation signature (X-axis) in CRCSC cohort. Each symbol represents a transcription factor and the correlation is calculated across all patients. The transcription factor in red is KLF4.

I note that my findings are in agreement with literature reports. Some of these TFs that I find to be sustaining the tissue remodelling programme are associated with stroma or EMT or immune cell infiltration. Pitarresi et al. showed that gene expression of *Ets2* was higher in stromal fibroblasts in pancreatic ductal adenocarcinoma tissues and transcription factor ETS2 established an immune-suppressive microenvironment during the tumour initiation (Pitarresi et al. 2016). In a different study, Wallace et al. reported that *Ets2* in fibroblasts functioned by promoting tumour growth and angiogenesis (Wallace et al. 2013). In lung fibrosis, overexpression of SNAI2 (also known as SLUG) was demonstrated to be able to induce EMT, even without TGFβ1 treatment (Jayachandran et al. 2009). KLF4 was reported to be an important regulator of monocyte/macrophage differentiation (Feinberg et al. 2007). *PU.1* gene was shown to be expressed in hematopoietic tissues, specifically in B lymphoid and monocytic lineages and transcription factor SPI1 (also known as PU.1) was reported to regulate the development of B cell and myeloid lineage at the level of progenitors (Scott et al. 1994). STAT1 has been known to regulate the immune system, protect from pathogen infections (Meissl et al. 2017) and transduce the activities of various cytokines, such as type I-III interferons and various interleukins (Najjar and Fagard 2010) (Boisson-Dupuis et al. 2012).

Table 4-3. List of putative transcription factors sustaining transcriptional programmes of (**a**) cell proliferation (P -> P) and (**b**) tissue remodelling (R -> R) in CRCSC cohort

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -> P												
PROX1	0.53	1.0E-05	Y	-0.24	1.0E-05	Y	0.17	1.0E-05	Y	0	0.50	N
RUNX3	0.18	1.0E-05	Y	-0.11	2.8E-03	Y	0.12	2.2E-03	Y	-0.13	1.2E-03	Y
SOX2	0.19	1.0E-05	Y	0.06	0.08	N	0.08	0.02	Y	0.00	0.46	N
TP53	0.09	0.02	Y	-0.36	1.0E-05	Y	0.25	1.0E-05	Y	0.00	0.49	N
(b) R -> R												
CEBPB	-0.02	0.29	N	0.12	1.9E-03	Y	-0.08	0.02	Y	0.44	1.0E-05	Y
CLOCK	-0.26	1.0E-05	Y	0.17	2.0E-05	Y	0	0.50	N	0.39	1.0E-05	Y
CREB1	-0.32	1.0E-05	Y	0.25	1.0E-05	Y	0.08	0.03	N	0.55	1.0E-05	Y
ERG	-0.03	0.24	N	0.26	1.0E-05	Y	0	0.50	N	0.90	1.0E-05	Y
ESR1	-0.40	1.0E-05	Y	0.14	3.0E-04	Y	0.04	0.16	N	0.34	1.0E-05	Y
ETS2	-0.22	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0.76	1.0E-05	Y
ETV4	-0.41	1.0E-05	Y	0.62	1.0E-05	Y	0	0.50	N	0.66	1.0E-05	Y
FOXO3	-0.29	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0.27	1.0E-05	Y
GATA3	-0.03	0.24	N	0.32	1.0E-05	Y	-0.21	1.0E-05	Y	0.48	1.0E-05	Y
JUN	-0.20	1.0E-05	Y	0.15	8.0E-05	Y	-0.20	1.0E-05	Y	0.47	1.0E-05	Y
KLF4	-0.09	0.02	Y	0.59	1.0E-05	Y	-0.29	1.0E-05	Y	0.18	1.0E-05	Y
NFE2L2	-0.06	0.09	N	0.32	1.0E-05	Y	0	0.50	N	0.24	1.0E-05	Y
NR5A2	-0.33	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0.29	1.0E-05	Y
PML	-0.07	0.06	N	0.61	1.0E-05	Y	0	0.50	N	0.30	1.0E-05	Y
PPARD	-0.14	4.9E-04	Y	0.23	1.0E-05	Y	0	0.50	N	0.62	1.0E-05	Y
RELA	-0.11	3.1E-03	Y	0.29	1.0E-05	Y	-0.01	0.41	N	0.43	1.0E-05	Y
SNAI2	-0.09	0.02	Y	0.41	1.0E-05	Y	-0.37	1.0E-05	Y	0.54	1.0E-05	Y
SPI1	-0.03	0.21	N	0.42	1.0E-05	Y	0	0.50	N	0.51	1.0E-05	Y
STAT1	-0.06	0.07	N	0.36	1.0E-05	Y	-0.36	1.0E-05	Y	0.55	1.0E-05	Y

S(TF,P) and *S*(TF,R) indicate the correlation of TF activity scores with P and R enrichment scores, respectively.
ES_P and ES_R indicate the enrichment scores of target genes with P and R gene signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

4.4.1 Preliminary analyses using TCGA datasets

To address the relevance of the candidate TFs in a wider context, I perform similar analysis in cohorts of colorectal cancer and other cancer types from TCGA. I make use of TCGA colorectal, breast, ovarian, and lung cancer gene expression datasets, as mentioned in section 2.1.1. However, I can study only the colorectal, breast, ovarian cancer datasets due to insufficient samples in the lung cancer dataset. As mentioned before, the number of samples is 132, 184 and 472 in colorectal, breast and ovarian cancer datasets, respectively, and 129 out of 132 samples in TCGA colorectal cancer (TCGACRC) dataset also appear in the CRCSC cohort.

Using the inference model, I predict the TF activity score for every TF annotated on each sample in every TCGA gene expression dataset. I analyse these datasets following the methodology in Figure 4-2. As can be seen in Figure 4-4, there is a clear negative correlation between *S*(TF,P) and *S*(TF,R) across TFs in all three datasets, in agreement with the finding using the CRCSC cohort.

Next, I identify transcription factors that promote a specific transcriptional programme of cell proliferation or tissue remodelling, as listed in Table 4-4, Table 4-5 and Table 4-6. These results demonstrate that KLF4 is one of the TFs that has a consistent pattern across all three datasets, as highlighted in bold in these three tables. Additionally, for KLF4, it exhibits a significant and positive *S*(TF,R) but significant and negative *S*(TF,P) and its target genes have a significant and positive R enrichment score but their P enrichment score is significant and negative. This finding partly leads me to conduct a further study on KLF4, as elaborated in section 4.5.

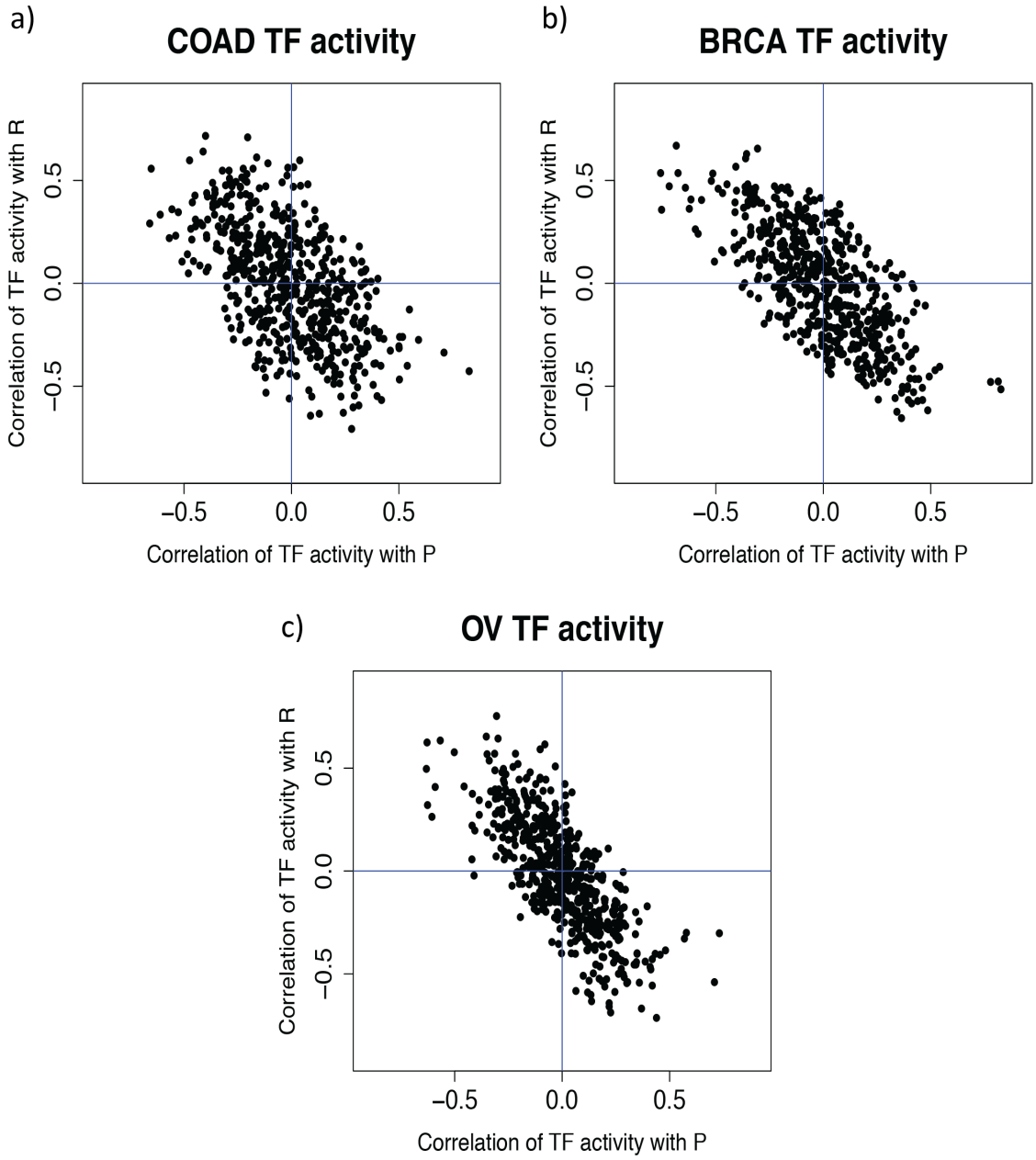

Figure 4-4. Scatter plot of Spearman's rank correlation coefficients between TF activity scores and tissue remodelling signature (Y-axis) as a function of Spearman's rank correlation between TF activity scores and cell proliferation signature (X-axis) in TCGA (**a**) colorectal, (**b**) breast and (**c**) ovarian cancer datasets. Each symbol represents a transcription factor and the correlation is calculated across all patients.

Table 4-4. List of putative transcription factors sustaining transcriptional programmes of (**a**) cell proliferation (P -> P) and (**b**) tissue remodelling (R -> R) in TCGA colorectal cancer dataset

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -> P												
GATA4	0.15	1.1E-04	Y	0	0.50	N	0.17	3.0E-05	Y	1.1E-03	0.49	N
ATF3	0.21	1.0E-05	Y	0	0.50	N	0.29	1.0E-05	Y	-0.20	1.0E-05	Y
SOX2	0.32	1.0E-05	Y	-0.28	1.0E-05	Y	0.15	8.0E-05	Y	-0.19	1.0E-05	Y
NR1H4	0.51	1.0E-05	Y	4.8E-03	0.45	N	0.20	1.0E-05	Y	-0.23	1.0E-05	Y
(b) R -> R												
KLF4	**-0.45**	**1.0E-05**	**Y**	**0.16**	**8.0E-05**	**Y**	**-0.26**	**1.0E-05**	**Y**	**0.23**	**1.0E-05**	**Y**
GATA3	-0.06	0.08	N	0.31	1.0E-05	Y	-0.04	0.16	N	0.31	1.0E-05	Y
PPARG	-0.06	0.09	N	0.15	2.0E-04	Y	-0.31	1.0E-05	Y	0.39	1.0E-05	Y
CDX2	0	0.50	N	0.08	0.03	Y	-0.14	4.9E-04	Y	0.09	0.01	Y
CLOCK	0	0.50	N	0.08	0.04	Y	-0.36	1.0E-05	Y	0.44	1.0E-05	Y
ERG	0	0.50	N	0.76	1.0E-05	Y	-0.28	1.0E-05	Y	0.47	1.0E-05	Y
ETS2	0	0.50	N	0.55	1.0E-05	Y	-0.33	1.0E-05	Y	0.25	1.0E-05	Y
ETV4	0	0.50	N	0.52	1.0E-05	Y	-0.37	1.0E-05	Y	0.39	1.0E-05	Y
FOXO3	0	0.50	N	0.18	3.0E-05	Y	-0.42	1.0E-05	Y	0.29	1.0E-05	Y
MITF	0	0.50	N	0.45	1.0E-05	Y	-0.03	0.23	N	0.13	9.8E-04	Y
RUNX1	0	0.50	N	0.07	0.04	Y	-0.14	4.9E-04	Y	0.28	1.0E-05	Y
STAT6	0	0.50	N	0.26	1.0E-05	Y	-0.24	1.0E-05	Y	0.10	8.8E-03	Y

S(TF,P) and *S*(TF,R) indicate the correlation of TF activity scores with P and R enrichment scores, respectively.
ES_P and ES_R indicate the enrichment scores of target genes with P and R gene signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

Table 4-5. List of putative transcription factors sustaining transcriptional programmes of (**a**) cell proliferation (P -> P) and (**b**) tissue remodelling (R -> R) in TCGA breast cancer dataset

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -> P												
FLI1	0.45	1.0E-05	Y	0	0.50	N	0.38	1.0E-05	Y	-0.30	1.0E-05	Y
MYCN	0.34	1.0E-05	Y	0.05	0.14	N	0.30	1.0E-05	Y	-0.11	4.0E-03	Y
PGR	0.24	1.0E-05	Y	0	0.50	N	0.44	1.0E-05	Y	-0.46	1.0E-05	Y
RUNX3	0.12	1.6E-03	Y	0.04	0.17	N	0.09	0.02	Y	-0.17	6.0E-05	Y
(b) R -> R												
GATA3	0.03	0.24	N	0.32	1.0E-05	Y	0.06	0.07	N	0.29	1.0E-05	Y
APEX1	0	0.50	N	0.26	1.0E-05	Y	-0.23	1.0E-05	Y	0.42	1.0E-05	Y
ERG	0	0.50	N	0.55	1.0E-05	Y	0.04	0.18	N	0.34	1.0E-05	Y
ETS1	0	0.50	N	0.39	1.0E-05	Y	-0.17	3.0E-05	Y	0.15	8.0E-05	Y
ETS2	0	0.50	N	0.51	1.0E-05	Y	-0.30	1.0E-05	Y	0.39	1.0E-05	Y
ETV4	0	0.50	N	0.65	1.0E-05	Y	-0.39	1.0E-05	Y	0.19	2.0E-05	Y
KLF10	0	0.50	N	0.21	1.0E-05	Y	-0.51	1.0E-05	Y	0.10	6.0E-03	Y
MITF	0	0.50	N	0.63	1.0E-05	Y	-0.08	0.03	Y	0.18	2.0E-05	Y
PML	0	0.50	N	0.34	1.0E-05	Y	-0.17	3.0E-05	Y	0.08	0.04	Y
KLF4	**-0.11**	**3.9E-03**	**Y**	**0.15**	**1.3E-04**	**Y**	**-0.34**	**1.0E-05**	**Y**	**0.25**	**1.0E-05**	**Y**
NR1I2	-0.13	7.7E-04	Y	0.36	1.0E-05	Y	-0.02	0.36	N	0.20	1.0E-05	Y
PPARA	-0.65	1.0E-05	Y	0.32	1.0E-05	Y	-0.45	1.0E-05	Y	0.48	1.0E-05	Y

S(TF,P) and *S*(TF,R) indicate the correlation of TF activity scores with P and R enrichment scores, respectively.
ES_P and ES_R indicate the enrichment scores of target genes with P and R gene signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

Table 4-6. List of putative transcription factors sustaining transcriptional programmes of (**a**) cell proliferation (P -> P) and (**b**) tissue remodelling (R -> R) in TCGA ovarian cancer dataset

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -> P												
NR5A1	0.50	1.0E-05	Y	0	0.50	N	0.10	9.3E-03	Y	-0.12	1.6E-03	Y
SOX2	0.37	1.0E-05	Y	0.06	0.06	N	0.29	1.0E-05	Y	-0.18	2.0E-05	Y
TCF4	0.28	1.0E-05	Y	0	0.50	N	0.13	9.5E-04	Y	-0.27	1.0E-05	Y
(b) R -> R												
ERG	0.04	0.18	N	0.35	1.0E-05	Y	-0.31	1.0E-05	Y	0.35	1.0E-05	Y
ATF1	0	0.50	N	0.35	1.0E-05	Y	-0.02	0.32	N	0.13	1.3E-03	Y
ATF2	0	0.50	N	0.43	1.0E-05	Y	-0.03	0.21	N	0.27	1.0E-05	Y
ETS2	0	0.50	N	0.73	1.0E-05	Y	-0.15	1.7E-04	Y	0.14	3.0E-04	Y
ETV4	0	0.50	N	0.43	1.0E-05	Y	-0.15	1.9E-04	Y	0.12	1.8E-03	Y
FOXO3	0	0.50	N	0.22	1.0E-05	Y	-0.28	1.0E-05	Y	0.48	1.0E-05	Y
HNF4A	0	0.50	N	0.36	1.0E-05	Y	-0.46	1.0E-05	Y	0.41	1.0E-05	Y
IRF1	0	0.50	N	0.21	1.0E-05	Y	-0.39	1.0E-05	Y	0.34	1.0E-05	Y
JUND	0	0.50	N	0.14	2.9E-04	Y	-0.11	3.5E-03	Y	0.10	0.01	Y
MITF	0	0.50	N	0.58	1.0E-05	Y	-0.13	1.1E-03	Y	0.15	8.0E-05	Y
NR1H4	0	0.50	N	0.33	1.0E-05	Y	0.03	0.26	N	0.16	7.0E-05	Y
REL	0	0.50	N	0.63	1.0E-05	Y	-0.10	7.2E-03	Y	0.59	1.0E-05	Y
RUNX1	0	0.50	N	0.27	1.0E-05	Y	-0.08	0.03	Y	0.22	1.0E-05	Y
RUNX2	0	0.50	N	0.67	1.0E-05	Y	-0.17	4.0E-05	Y	0.22	1.0E-05	Y
SMAD4	0	0.50	N	0.54	1.0E-05	Y	-0.08	0.03	Y	0.22	1.0E-05	Y
CEBPB	-0.05	0.12	N	0.43	1.0E-05	Y	-0.03	0.27	N	0.14	5.3E-04	Y
NFKB1	-0.16	9.0E-05	Y	0.50	1.0E-05	Y	-0.16	1.0E-04	Y	0.19	2.0E-05	Y
GATA3	-0.19	1.0E-05	Y	0.33	1.0E-05	Y	-0.08	0.03	Y	0.30	1.0E-05	Y
SPI1	-0.27	1.0E-05	Y	0.66	1.0E-05	Y	0.02	0.32	N	0.32	1.0E-05	Y
PPARG	-0.30	1.0E-05	Y	0.35	1.0E-05	Y	0.04	0.18	N	0.17	3.0E-05	Y
KLF4	**-0.34**	**1.0E-05**	**Y**	**0.19**	**2.0E-05**	**Y**	**-0.10**	**9.8E-03**	**Y**	**0.25**	**1.0E-05**	**Y**
NR1I2	-0.46	1.0E-05	Y	0.47	1.0E-05	Y	-0.08	0.02	Y	0.24	1.0E-05	Y

S(TF,P) and *S*(TF,R) indicate the correlation of TF activity scores with P and R enrichment score, respectively.
ES_P and ES_R indicate the enrichment score of target genes with P and R signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

Then I quantify the similarity of these lists of TFs in Table 4-3 with Table 4-4, Table 4-5 and Table 4-6 (pairwise comparisons) using one-tailed version of Fisher's exact test. In this case, the population size (N) is the number of combined TFs in both datasets being considered. The number of success cases in the population (K) is the number TFs in Table 4-3. The number of draws (n) is the number of TFs in the other list being considered (Table 4-4 or Table 4-5 or Table 4-6). Lastly, the number of observed successes (k) is the number of samples that belong to both tables. I calculate the significance of the similarity of both lists following the method in section 3.2.2.

From the results, I note that the significance of Table 4-3 with Table 4-4, Table 4-5 and Table 4-6 is 1.6×10^{-9}, 5.4×10^{-8} and 1.1×10^{-7}, respectively. In other words, the similarity of the lists of TFs associated with the cell proliferation or tissue remodelling programme in the CRCSC cohort and the TCGACRC dataset is the most significant one. Although the number of samples in the TCGACRC dataset is only about 5% of the CRCSC cohort, this observation highlights the consistency of the TF inference model in identifying TFs associated with these transcriptional programmes in colorectal cancer from different sources. Another interesting observation from these results is the similarities of these lists of TFs in the CRCSC cohort and TCGA breast and ovarian cancer datasets are also significant. Taken together, these findings demonstrate the reliability of the TF inference model in distinguishing TFs that promote a specific transcriptional programme across different cancer types.

4.5 Further study on KLF4

I identify KLF4 as a putative TF promoting tissue remodelling programme in section 4.4. Specifically, in the CRCSC cohort the activity score of KLF4 is significantly and positively associated with R enrichment score (S = 0.59, p-value = 1×10^{-5}, permutation test). Additionally, KLF4 targets are enriched for genes with expression significantly and positively associated with the R signature (ES = 0.18, p-value = 1×10^{-5}, GSEA method).

KLF4 has been linked with pluripotency (Okita et al. 2007) and reported to be regulating differentiation of monocytes into myeloid cells (Feinberg et al. 2007). Here I interrogate the role of KLF4 in regulating the tissue remodelling programme as well as assess if the KLF4 activity score can substitute the tissue remodelling signature in predicting survival. The findings will hopefully advance our knowledge of tissue remodelling processes in colorectal cancer.

4.5.1 Prognostic value of the KLF4 activity score

As there is a strong association between the KLF4 activity score and the R enrichment score in CRCSC cohort, here I evaluate if the KLF4 activity score can substitute the tissue remodelling signature in predicting patient outcome. The scope of this analysis is to determine how the KLF4 activity score performs as a prognostic variable, substituting the R signature.

I classify a sample into K+ if it has a significant and positive KLF4 activity score and K- if otherwise. The K status alone does not have a prognostic value either based on overall or relapse-free survival (Figure 4-5). Therefore, I consider adding cell proliferation signature and classify all samples into four PK subtypes (details in section 4.2.4), namely P+/K+, P+/K-, P-/K+, and P-/K-. The assignment of each sample into the PK groups can be found in Appendix. As illustrated in Figure 4-6, this PK classification yields a significant splitting of different subtypes based on both overall and relapse-free survival. This shows that the KLF4 activity score can substitute the tissue remodelling signature in patient stratification.

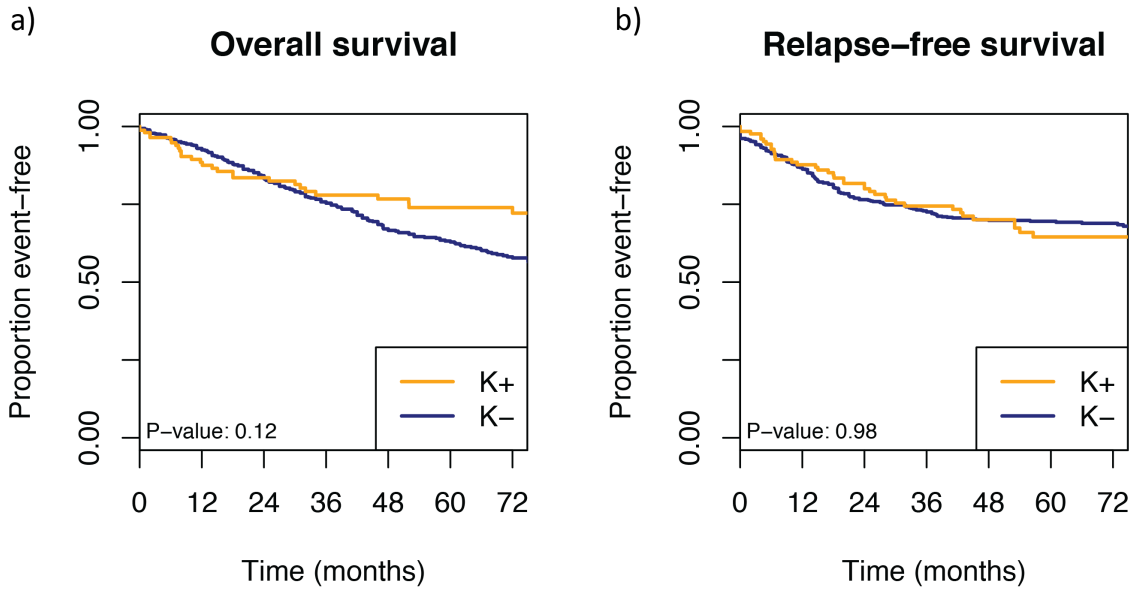

Figure 4-5. Kaplan-Meier plots of colorectal cancer subtypes stratified based on KLF4 activity score using (**a**) overall survival and (**b**) relapse-free survival. P-values indicate statistical significance based on log-rank test.

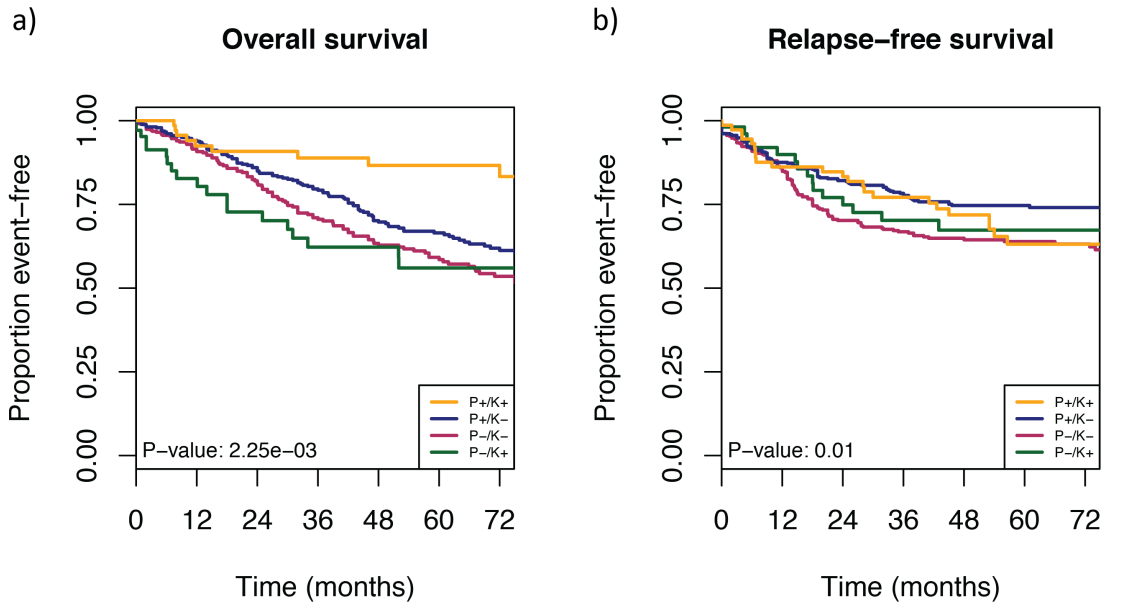

Figure 4-6. Kaplan-Meier plots of colorectal cancer subtypes stratified by cell proliferation signature and KLF4 activity score based on (**a**) overall survival and (**b**) relapse-free survival. P-values indicate statistical significance based on log-rank test.

4.5.2 Enrichment of the KLF4 activity score with clinical variables

I perform enrichment tests of the KLF4 activity score with all available biomarkers and clinical variables in the CRCSC cohort to examine the association of the KLF4 activity score with these covariates (one-tailed Fisher's exact test in section 4.2.5). As tabulated in Table 4-7 and Table 4-8, high level of KLF4 activity is significantly enriched for patients with:

- BRAF mutation,
- CIMP high,
- MSI,
- disease stage 1,
- pT (primary tumour) stage 2, and
- TNM (tumour, node and metastasis) stage I.

On the contrary, low level of KLF4 activity is significantly associated with patients having:

- MSS,
- pT stage 3, and
- TNM stage IIA.

Andersen et al. demonstrated that KLF4 transcription factor was down-regulated and significantly associated with recurrent stage II MSS colorectal tumours (Andersen et al. 2009). This report is in agreement with my finding that suggests a significant association between low KLF4 activity and MSS.

Patel et al. also evaluated if KLF4 protein expression is associated with clinical covariates in colorectal cancer. They found that there are decreasing odds of KLF4 protein expression in higher stages of the disease relative to stage 1 (Patel et al. 2010). My findings also suggest low KLF4 activity is significantly enriched for higher pT and TNM stages, whereas high KLF4 activity is significantly enriched for lower pT, TNM and disease stages. They reported gender to be associated with KLF4 protein expression where there are a higher proportion of men with KLF4-positive than women (Patel et al. 2010). However, my results suggest low KLF4 activity is enriched for male patients but I also note that its p-value of 0.05 is in the margin of being significant.

One should be careful in making claims about the results in Table 4-7 and Table 4-8, particularly because in some cases a lot of patients have missing information about the covariates. For example, there are only 87 patients with disease stage information though in total there are 2,207 patients listed in the clinical variable table provided by the CRCSC consortium. Further study needs to be conducted before the level of KLF4 activity score can be used to predict the extent of the clinical covariates.

Table 4-7. Enrichment of KLF4 activity score with biomarkers and clinical variables

Clinical variable	Number of patients	Value	KLF4 level	P-value
KRAS mutation	1,001	no	high	0.09
		no	low	0.21
		yes	high	0.94
		yes	low	0.84
BRAF mutation	968	no	high	1
		no	low	0.09
		yes	high	4.2E-05
		yes	low	0.95
CIMP	1,062	High	high	2.2E-06
		High	low	0.85
		Low	high	0.98
		Low	low	0.67
		Neg	high	0.99
		Neg	low	0.18
MSI or MSS	1,397	MSI	high	5.6E-07
		MSI	low	0.99
		MSS	high	1
		MSS	low	0.01
Age	1,402	> 60	high	0.06
		> 60	low	0.34
		<= 60	high	0.95
		<= 60	low	0.72
Gender	1,978	female	high	0.28
		female	low	0.96
		male	high	0.76
		male	low	0.05

Significant p-values are highlighted in red.

Table 4-8. Enrichment of KLF4 activity score with various disease stages

Clinical variable	Number of patients	Value	KLF4 level	P-value
Grade	87	1	high	1
		1	low	1
		2	high	0.80
		2	low	0.12
		3	high	0.42
		3	low	0.97
Stage	1,838	1	high	2.3E-03
		1	low	0.69
		2	high	0.98
		2	low	0.89
		3	high	0.41
		3	low	0.18
		4	high	0.88
		4	low	0.22
pT	1,204	1	high	0.47
		1	low	0.99
		2	high	0.05
		2	low	1.00
		3	high	0.93
		3	low	0.02
		4	high	0.55
		4	low	0.48
pN	1,199	0	high	0.34
		0	low	0.68
		1	high	0.64
		1	low	0.37
		2	high	0.59
		2	low	0.46
		3	high	1
		3	low	1
pM	1,145	0	high	0.15
		0	low	0.86
		1	high	0.91
		1	low	0.20
TNM	1,191	I	high	0.02
		I	low	1.00
		IIA	high	0.83
		IIA	low	0.03
		IIB/IIC	high	0.34
		IIB/IIC	low	0.86
		IIIA	high	0.89
		IIIA	low	0.86
		IIIB	high	0.12
		IIIB	low	0.82
		IIIC	high	0.92
		IIIC	low	0.20
		IV	high	0.90
		IV	low	0.22

Significant p-values are highlighted in red.

4.5.3 KLF4 targets driving the KLF4 transcriptional activity score

To observe how KLF4 target genes drive KLF4 transcriptional activity in the inference model, first I examine the genes annotated as KLF4 targets based on TRRUST database. About half of the target genes manifest a significant association between their expression and the KLF4 activity scores (Figure 4-7 and Table 4-9). Among those with a positive association, their correlation score is still far from a perfect correlation. These indicate that not all KLF4 targets contribute to the putative KLF4 transcriptional activity and there is no single target gene that can replace other target genes in deriving at the KLF4 activity score. This phenomenon is expected because a TF can regulate multiple target genes and a gene may be regulated by several TFs, as depicted in Figure 4-1. In other words, the KLF4 activity score is an aggregate signal considering the concomitant expression of multiple targets.

The three most highly correlated genes in this analysis are IL1B, IL6 and CCNB1. To study their individual impact, I split the patients in the CRCSC cohort into three groups based on the level of the KLF4 activity score. If a sample has a significant and positive KLF4 activity score, I categorise it into ‘high’ group. Conversely, if a sample has a significant and negative KLF4 activity score, I categorise it into ‘low’ group. Otherwise, I denote it as ‘middle’. As shown in Figure 4-8, these three genes exhibit an increasing average expression from patient groups having low to high KLF4 activity score. This confirms the positive correlation between the expression of these genes and the KLF4 activity score.

As can be seen in Figure 4-7 and Table 4-9, the two KLF4 target genes having highest correlation with the KLF4 activity score are IL1B and IL6 genes, which encode for cytokines that are secreted by immune cells. This observation leads us to hypothesise that KLF4 activity may be related to immune cells infiltrating the tumour. Additionally, KLF4 has been shown to be regulating myelopoiesis (Feinberg et al. 2007), further supporting the idea that the tissue remodelling gene signature may be partly associated with immune cell infiltration via the contribution of KLF4.

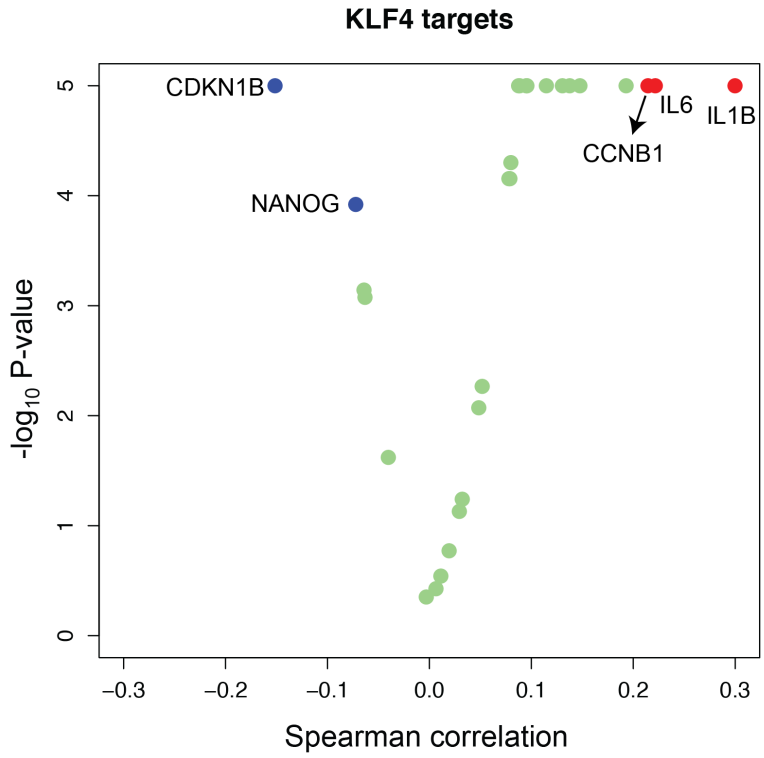

Figure 4-7. Volcano plot of statistical significance versus Spearman's rank correlation between expression of annotated KLF4 target genes and KLF4 activity score. Each point is a KLF4 target derived from TRRUST. Annotated genes from left to right in the figure are CDKN1B, NANOG, CCNB1, IL6 and IL1B.

Table 4-9. Correlation of KLF4 activity score with expression of its target genes

KLF4 target	Correlation with KLF4 activity score	P-value	BH
IL1B	0.30	1.0E-05	Y
IL6	0.22	1.0E-05	Y
CCNB1	0.21	1.0E-05	Y
BIRC5	0.19	1.0E-05	Y
GDF15	0.15	1.0E-05	Y
MMP2	0.14	1.0E-05	Y
ODC1	0.13	1.0E-05	Y
KRT19	0.11	1.0E-05	Y
TP53	0.10	1.0E-05	Y
THBD	0.10	1.0E-05	Y
CCND1	0.09	1.0E-05	Y
IFITM3	0.09	1.0E-05	Y
CDH5	0.08	5.0E-05	Y
LAMA3	0.08	7.0E-05	Y
HSPA8	0.08	7.0E-05	Y
ALPI	0.05	5.4E-03	N
BDKRB2	0.05	8.4E-03	N
VDR	0.03	0.06	N
CDKN1A	0.03	0.07	N
RARA	0.02	0.17	N
CDKN1C	0.01	0.29	N
GPA33	0.01	0.37	N
HDC	0.00	0.44	N
ATF3	-0.04	0.02	N
LXN	-0.06	8.4E-04	Y
CDH1	-0.06	7.2E-04	Y
NANOG	-0.07	1.2E-04	Y
CDKN1B	-0.15	1.0E-05	Y

BH indicates the Boolean value whether the p-value remains significant after BH correction.

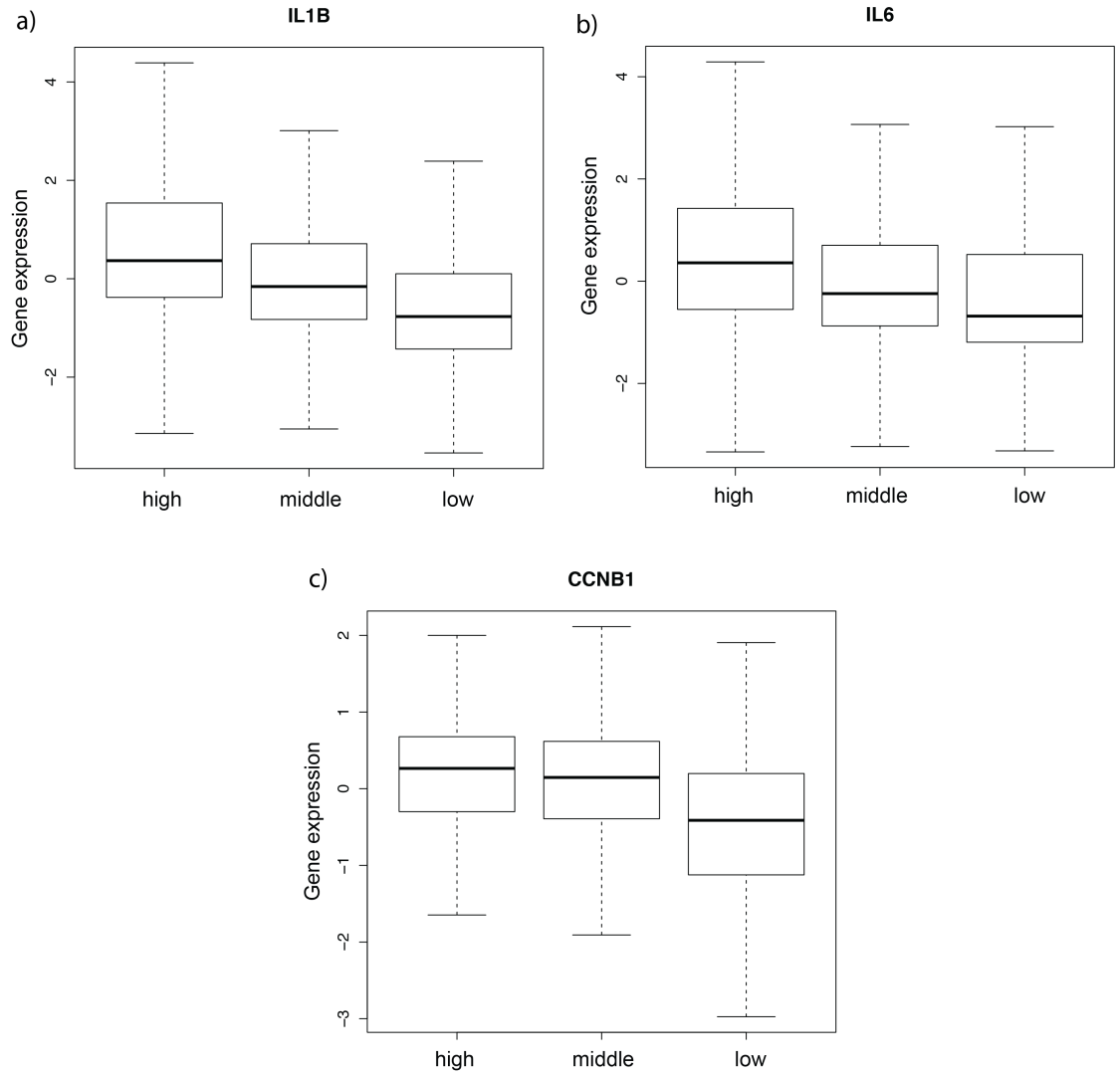

Figure 4-8. Box plots of expression of top three KLF4 targets having positive correlation with KLF4 activity score: (**a**) IL1B, (**b**) IL6 and (**c**) CCNB1. Expression values are grouped into patient groups having high to middle to low KLF4 activity score.

4.5.4 Validation of KLF4 activity in immune cells

Because KLF4 activity is obtained from the TF activity inference model, there is a need to validate its robustness in a controlled scenario. As mentioned previously, KLF4 has been reported to be regulating myeloid differentiation (Feinberg et al. 2007). In line with this knowledge, I establish if the inference model is valid in pure immune cell populations then compare the level of inferred KLF4 activity in myeloid versus lymphoid cells.

To this end, I retrieve a publicly available human immune cell transcriptome dataset, quantifying genome-wide gene expression in immune cell types (ref. (Jeffrey et al. 2006), GEO accession number GSE3982). I pre-process this dataset and group the samples into different groups of immune cell types, as described in section 4.2.6.

I apply the TF activity inference method using gene expression profiles from this dataset as the input and compute the KLF4 activity score for every sample. As can be observed in Figure 4-9, the inferred KLF4 activity is significantly higher in phagocytes (myeloid cells) versus lymphoid cells (p-value = 2.8×10^{-3}, one tailed t-test). This observation of a high KLF4 activity score in the myeloid cells serves as both a confirmation that KLF4 regulates myelopoiesis and a validation of my TF activity inference model in a controlled scenario.

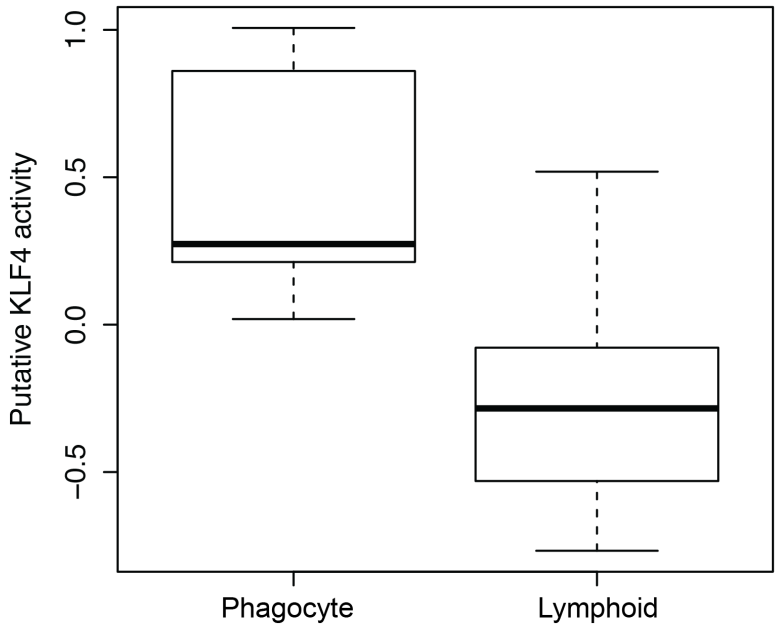

Figure 4-9. Box plot of KLF4 activity scores across phagocytes (myeloid) versus lymphoid cells in human immune cell transcriptome dataset (GSE3982).

4.5.4.1 Activity scores of TFs promoting R programme in immune cells

Here I evaluate other TFs that also promote the tissue remodelling programme and compare their activity scores in myeloid versus lymphoid cells using the same immune cell dataset as before (GSE3982). Among the TFs that sustain tissue remodelling (Table 4-3, R -> R), KLF4 is the TF with the strongest statistical significance for high activity score in myeloid as compared to lymphoid cells (Table 4-10).

Table 4-10. Statistical significance of activity scores of TFs that promote R programme in myeloid versus lymphoid cells

	P-value from t-test (myeloid vs lymphoid)		
TF	Higher in myeloid	Higher in lymphoid	Two-tailed
KLF4	2.76E-03	1	5.52E-03
CEBPB	2.83E-03	1	5.65E-03
STAT1	5.99E-03	0.99	0.01
ETS2	0.02	0.98	0.03
ESR1	0.04	0.96	0.08
CLOCK	0.11	0.89	0.22
FOXO3	0.15	0.85	0.29
ETV4	0.17	0.83	0.34
NR5A2	0.17	0.83	0.33
ERG	0.19	0.81	0.38
RELA	0.31	0.69	0.62
NFE2L2	0.32	0.68	0.64
JUN	0.37	0.63	0.73
CREB1	0.41	0.59	0.82
PML	0.86	0.14	0.27
SPI1	0.88	0.12	0.24
PPARD	0.89	0.11	0.23
GATA3	0.99	0.01	0.03
SNAI2	1	6.54E-05	1.31E-04

Higher in myeloid' is performed using one-tailed t-test, assuming the activity score is higher in myeloid than in lymphoid.

Higher in lymphoid' is performed using one-tailed t-test, assuming the activity score is higher in lymphoid than in myeloid.

Two-tailed' is performed using two-tailed t-test without the assumption of the activity score being higher in either cell types.

4.5.5 Enrichment of myeloid versus lymphoid cells in PK subtypes

We hypothesise that tissue remodelling processes are in part associated with immune cells infiltrating colorectal tumours. In this section, I investigate the association of the KLF4 activity score with immune cell infiltration. First, I estimate the composition of different immune cell types in the CRCSC cohort using a computational inference method CIBERSORT (Newman et al. 2015), as detailed in section 2.2.7. This method infers the composition of immune cell types in a mixed sample population using gene expression profiles as input. Then I correlate the KLF4 activity score with the estimated composition of immune cell types and assess the abundance of the immune cell types in the PK subtypes, as outlined in section 4.2.7.

The results demonstrate that there is a significant positive correlation between the KLF4 activity score and the estimated fraction of various myeloid cell types: macrophages (M0, M1), neutrophils and dendritic cells (resting, activated) (Figure 4-10 and Table 4-11). On the other hand, there is a significant negative association or no association between the KLF4 activity score and majority of lymphoid cell types: B cells and T cells (Figure 4-10 and Table 4-11). In other words, the level of the KLF4 activity score can be used to predict the extent of myeloid or lymphoid cell infiltration.

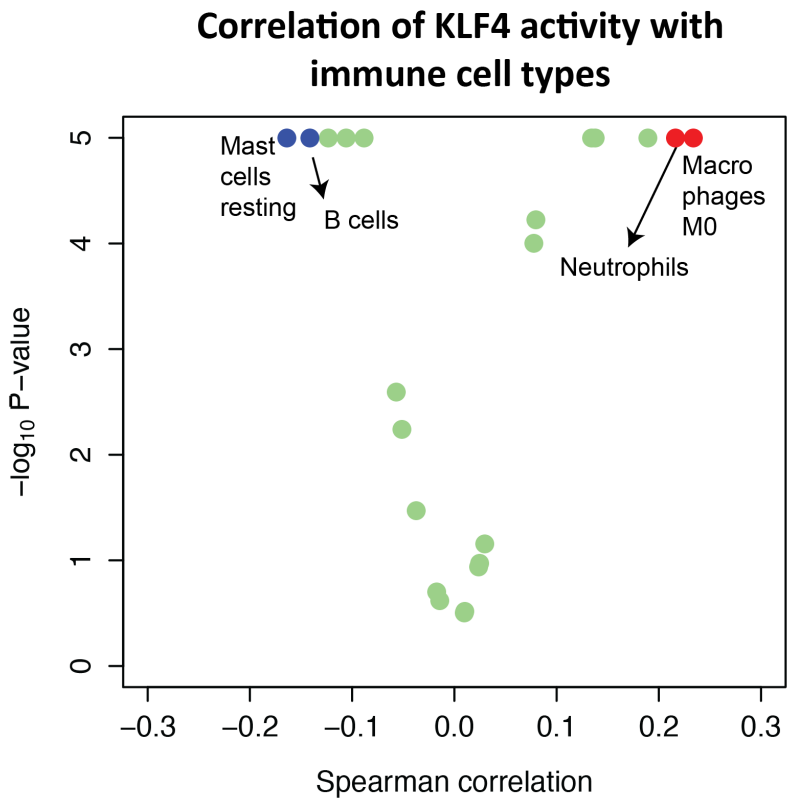

Figure 4-10. Volcano plot of statistical significance versus Spearman's rank correlation between estimated fractions of immune cells and KLF4 activity score in CRCSC cohort. Each point represents an immune cell type. Annotated immune cell types from left to right in the figure are mast cells (resting), B-cells (naive), neutrophils and macrophages (M0).

Subsequently, I visualise the tail distribution of the estimated fractions of myeloid and lymphoid cells in the PK subtypes to determine if the KLF4 activity score is related to immune cell infiltration. The distribution of neutrophils enrichment for patients in K+ subtypes yields a longer tail than for K- patients, independently of the P status (Figure 4-11a, p-value = 3.23×10^{-11}, two-sided Kolmogorov-Smirnov test). Similarly, the distribution of macrophages M0 enrichment for K+ patients also yields a longer tail than for K- patients (Figure 4-11b, p-value = 5.22×10^{-15}, two-sided Kolmogorov-Smirnov test). Indeed, macrophages M0 and neutrophils are the two myeloid cell types with the highest positive correlation with the KLF4 activity score. In contrast, I observe an opposite pattern for B cells. The distribution of B cells (naive) enrichment for K- patients exhibits a longer tail than for K+ patients (Figure 4-11c, p-value = 1.04×10^{-4}, two-sided Kolmogorov-Smirnov test). These findings suggest the odds

of having a high KLF4 activity score increase with having a higher fraction of myeloid cells in a tumour sample. In other words, the results suggest that KLF4 activity score is associated with myeloid cell infiltration.

Table 4-11. Correlation of KLF4 activity score with estimated composition of immune cell types

Immune cell type	Correlation with KLF4 activity score	P-value	BH
Macrophages M0	0.23	1.0E-05	Y
Neutrophils	0.22	1.0E-05	Y
Mast cells activated	0.19	1.0E-05	Y
Dendritic cells activated	0.14	1.0E-05	Y
NK cells resting	0.13	1.0E-05	Y
Macrophages M1	0.08	6.0E-05	Y
Dendritic cells resting	0.08	1.0E-04	Y
T cells CD4 memory activated	0.03	0.07	N
B cells memory	0.03	0.11	N
T cells follicular helper	0.02	0.12	N
T cells CD4 naive	0.01	0.31	N
T cells regulatory (Tregs)	0.01	0.32	N
T cells CD8	-0.01	0.24	N
NK cells activated	-0.02	0.20	N
Monocytes	-0.04	0.03	N
Eosinophils	-0.05	0.01	Y
Plasma cells	-0.06	2.6E-03	Y
T cells gamma delta	-0.09	1.0E-05	Y
Macrophages M2	-0.11	1.0E-05	Y
T cells CD4 memory resting	-0.12	1.0E-05	Y
B cells naive	-0.14	1.0E-05	Y
Mast cells resting	-0.16	1.0E-05	Y

BH indicates the Boolean value whether the p-value remains significant after BH correction.

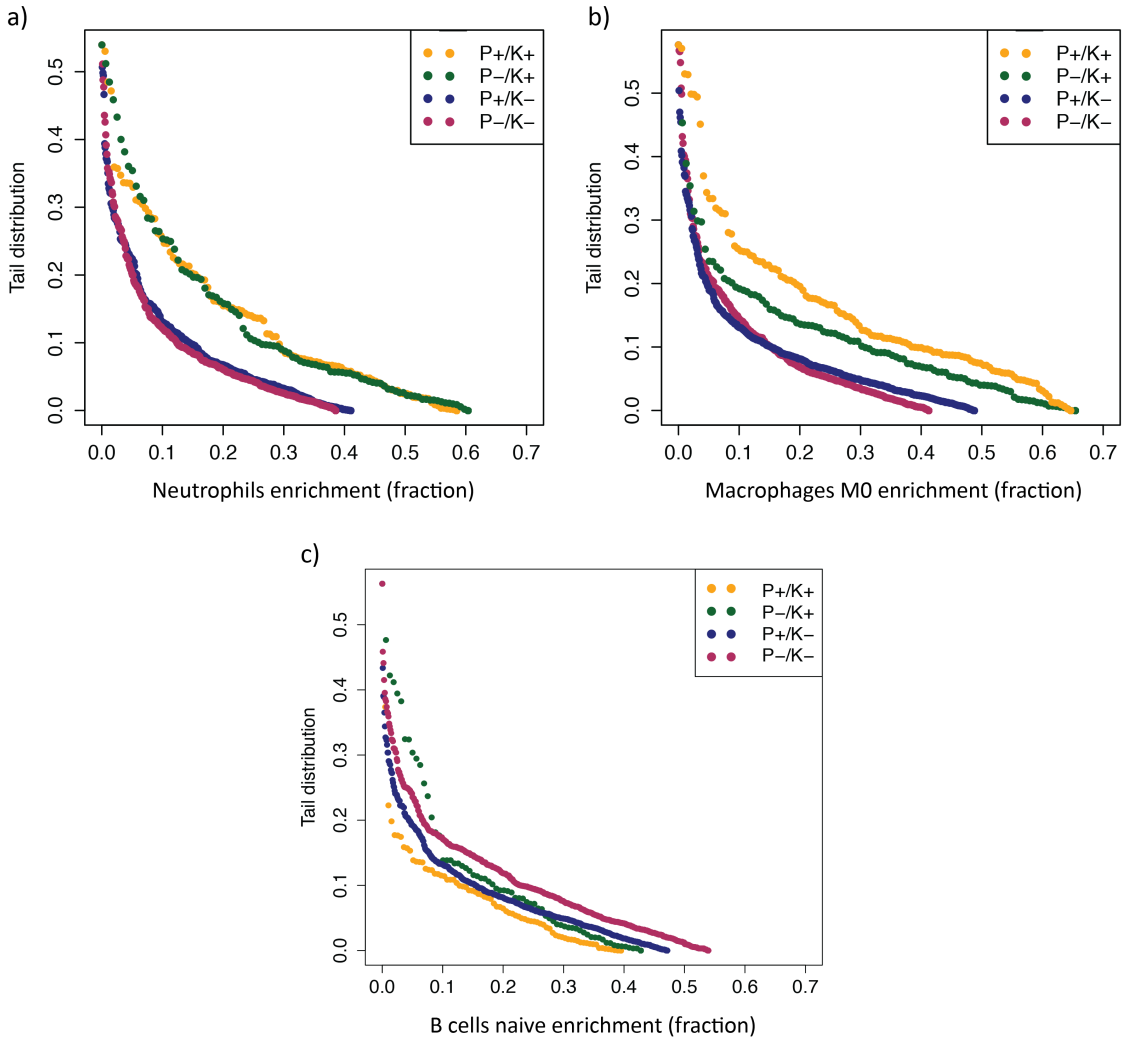

Figure 4-11. Tail distribution of the enrichment of (**a**) neutrophils, (**b**) macrophages M0 and (**c**) B cells (naive) across colorectal tumours in CRCSC cohort grouped according to their PK subtype.

4.6 Conclusions

Tissue remodelling signal could reflect various biological processes, such as high stromal cell content, immune cell infiltration and EMT. PROX1, RUNX3, SOX2 and TP53 are the putative TF regulators associated with the cell proliferation programme in the CRCSC cohort. Similarly, CEBPB, CLOCK, CREB1, ERG, ESR1, ETS2, ETV4, FOXO3, GATA3, JUN, KLF4, NFE2L2, NR5A2, PML, PPARD, RELA, SNAI2, SPI1 and STAT1 are the putative TF regulators promoting the tissue remodelling programme.

The activity score of KLF4 can be used to substitute the tissue remodelling signature in stratifying patients. There is an association between high level of KLF4 activity and low stages of colorectal cancer. However, we should interpret the results with care, particularly because a lot of patients have missing information for some clinical variables.

KLF4 activity score is significantly higher in phagocytes (myeloid cells) relative to lymphoid cells. Among the putative TF regulators that sustain tissue remodelling, KLF4 is the TF with the most statistical significance of high activity score in myeloid versus lymphoid cells. Additionally, KLF4 activity score is associated with myeloid cell infiltration in colorectal cancer.

5 MicroRNAs driving PR programmes

5.1 Background

MicroRNAs (miRNAs) add another layer of regulation that could contribute to the dichotomy between the gene expression programs of cell proliferation and tissue remodelling. MiRNAs constitute 1% to 5% of RNAs encoded in the human genome and they regulate around 30% of protein-coding genes (Macfarlane and Murphy 2010). Their expression is controlled by transcription factors or other miRNA in response to various internal and external stimuli (Kulshreshtha et al. 2007) (Davis and Ross 2008). Multiple miRNAs may work together to regulate a gene and a miRNA may control the expression of a number of target genes. MiRNAs function at the post-transcriptional level by assembling into the RNA-induced silencing complex and activating the complex (Macfarlane and Murphy 2010) to repress or silence the genes. They bind to target genes through sequence complementarity to degrade the mRNAs or inhibit their translation. MiRNAs regulate various cellular and metabolic pathways, particularly those regulating cell proliferation, differentiation and survival, and their dysregulation is associated with cancer as they can function as tumour suppressors or oncogenes (Macfarlane and Murphy 2010).

As previously mentioned, I aim to uncover specific regulators that drive increased tissue remodelling or increased cell proliferation in colorectal cancer. In this chapter, I interrogate specific miRNAs that drive the cell proliferation and tissue remodelling programmes.

5.2 Methods

5.2.1 Processing of miRNA expression data

We retrieve quantile-normalised and mean-centred miRNA expression datasets from TCGA. There is one probe for each miRNA in the expression data. I retain only miRNAs with standard deviation of expression values not equal to zero for further analyses. Some miRNAs are expressed at low levels and they are not included for subsequent analyses. To avoid any bias incurred by these miRNAs, I

then sort the expression data based on the average expression values and keep the top 95% miRNAs for further analyses.

5.2.2 Identification of miRNA targets

I retrieve miRWalk database (Dweep et al. 2011) to identify target genes of human miRNAs. The validated target module of miRWalk consists of 13,650 publications documented on 3,081 experimentally validated miRNA-target interactions (Dweep and Gretz 2015). There are some differences in the annotations of miRNAs in miRWalk database and in TCGA datasets. Most miRNAs in miRWalk are annotated as their mature IDs, ending with 5p and 3p. On the other hand, some miRNAs in the TCGA dataset are annotated as their stem-loop IDs without the 5p or 3p ending. If a miRNA in the TCGA dataset is annotated with its stem-loop ID, I assign the target genes of this miRNA in its mature form to be its target genes.

5.2.3 Enrichment analysis of miRNA targets

This analysis is similar to the analysis in section 4.2.3 where I swap the two inputs of the GSEA method. In this case, the inputs are Spearman's rank correlation of expression values with the P or R enrichment score and target genes of a miRNA, instead of expression values and gene signature in the original GSEA method. In contrast to enrichment analysis of TF targets, I include all interactions from miRWalk for this analysis.

To ensure there is no bias introduced by miRNAs having a small number of target genes, I include only miRNAs that have at least ten target genes for further analyses. I then create the reference score vector and calculate the enrichment score together with its statistical significance following the GSEA method in section 2.2.3.

5.2.4 Processing of human immune cell subsets (GSE28492)

I retrieve miRNA expression data files of the human immune cell subsets from GEO with an accession number GSE28492. I ensure that the order of the miRNA probes is the same across all data files before combining the miRNA expression values from all files into a single matrix. After obtaining the combined expression matrix, I annotate the probes with their miRNA IDs, quantile-normalise and mean-centre the expression values following the steps in section 2.2.2. Then I assign the samples into their immune cell groups, as tabulated in Table 5-1 and Table 5-2, for comparing mir-22 expression values in phagocytes (myeloid cells) versus lymphoid cells.

5.2.5 Sample classification into Pmir22 subtypes

I classify patient samples based on the P enrichment score and the level of mir-22 expression values. The sample classification into P+ or P- is obtained from the results in section 3.2.1.

Then I adopt a permutation test as a non-parametric estimate for the statistical significance of observed expression value Y_{j0} of miRNA j being high in a given sample. For the colorectal tumours in the TCGA dataset, I generate 1,000 permutations of miRNA expression values of the 132 samples in the cohort. Subsequently, I obtain corresponding mir-22 expression values from these permuted miRNA expression values, resulting in Y_{jk} reference scores for mir-22 expression where k = 1, …, n=132,000. I correct the statistical significance of Y_{j0} being high based on a less bias estimate $p_{j-} = (1 + \sum_{Y_{jk} \le Y_{j0}} 1) / (1 + n)$ and $p_{j+} = (1 + \sum_{Y_{jk} \ge Y_{j0}} 1) / (1 + n)$ (North et al. 2002). I report p_{j+} as the statistical significance if $p_{j+} < p_{j-}$ or p_{j-} if $p_{j-} < p_{j+}$. Finally, if a sample has a significant and positive mir-22 expression value, I denote it as mir22+ and mir22- if otherwise.

Table 5-1. List of samples in human immune cell subsets (GSE28492) from Roche platform

Sample ID	Immune cell	Group
GSM703871	Monocytes	Phago
GSM703872	Monocytes	Phago
GSM703873	Monocytes	Phago
GSM703874	Monocytes	Phago
GSM703875	Monocytes	Phago
GSM703876	Monocytes	Phago
GSM703877	Monocytes	Phago
GSM703878	Monocytes	Phago
GSM703879	Monocytes	Phago
GSM703880	B cells	Lym
GSM703881	B cells	Lym
GSM703882	B cells	Lym
GSM703883	B cells	Lym
GSM703884	B cells	Lym
GSM703885	CD4+ T cells	Lym
GSM703886	CD4+ T cells	Lym
GSM703887	CD4+ T cells	Lym
GSM703888	CD4+ T cells	Lym
GSM703889	NK cells	Lym
GSM703890	NK cells	Lym
GSM703891	NK cells	Lym
GSM703892	NK cells	Lym
GSM703893	NK cells	Lym
GSM703894	CD8+ T cells	Lym
GSM703895	CD8+ T cells	Lym
GSM703896	CD8+ T cells	Lym
GSM703897	CD8+ T cells	Lym
GSM703898	CD8+ T cells	Lym
GSM703899	Eosinophils	Granu
GSM703900	Eosinophils	Granu
GSM703901	Eosinophils	Granu
GSM703902	Eosinophils	Granu
GSM703903	mDC	Phago
GSM703904	mDC	Phago
GSM703905	Neutrophils	Phago
GSM703906	Neutrophils	Phago
GSM703907	Neutrophils	Phago
GSM703908	Neutrophils	Phago
GSM703909	pDC	Lym
GSM703910	pDC	Lym
GSM703911	pDC	Lym
GSM703912	pDC	Lym
GSM703913	pDC	Lym

'Phago' indicates phagocytes.
'Lym' indicates lymphoid cells.
'Granu' indicates granulocytes.

Table 5-2. List of samples in human immune cell subsets (GSE28492) from HUG platform

Sample ID	Immune cell	Group
GSM704631	CD4+ T cells	Lym
GSM704633	CD4+ T cells	Lym
GSM704635	CD4+ T cells	Lym
GSM704636	CD4+ T cells	Lym
GSM704638	CD4+ T cells	Lym
GSM704640	CD8+ T cells	Lym
GSM704643	CD8+ T cells	Lym
GSM704645	CD8+ T cells	Lym
GSM704647	CD8+ T cells	Lym
GSM704649	CD8+ T cells	Lym
GSM704650	Monocytes	Phago
GSM704652	Monocytes	Phago
GSM704654	Monocytes	Phago
GSM704656	Monocytes	Phago
GSM704658	Monocytes	Phago
GSM704660	NK cells	Lym
GSM704661	NK cells	Lym
GSM704663	NK cells	Lym
GSM704665	NK cells	Lym
GSM704667	NK cells	Lym
GSM704668	B cells	Lym
GSM704670	B cells	Lym
GSM704672	B cells	Lym
GSM704674	B cells	Lym
GSM704676	B cells	Lym
GSM704677	Eosinophils	Granu
GSM704679	Eosinophils	Granu
GSM704681	Eosinophils	Granu
GSM704683	Neutrophils	Phago
GSM704685	Neutrophils	Phago
GSM704686	Neutrophils	Phago
GSM704688	Neutrophils	Phago
GSM704690	Neutrophils	Phago

Phago' indicates phagocytes.
'Lym' indicates lymphoid cells.
'Granu' indicates granulocytes.

5.3 Identification of miRNAs driving PR

To investigate candidate miRNAs driving the cell proliferation and tissue remodelling programmes in a wider context, I analyse the correlation of miRNA expression and the enrichment of miRNA targets with the PR signatures. The methodology is as outlined in Figure 5-1. I perform the analyses using gene and miRNA expression of the TCGA colorectal, breast and ovarian cancer datasets, as previously mentioned in section 4.4.1. As mentioned before, the number of samples is 132, 184 and 472 in colorectal, breast and ovarian cancer datasets, respectively.

First, I select samples with matching gene and miRNA expression then pre-process the miRNA expression datasets following the steps in section 5.2.1. Next, I focus on associations between miRNA expression values and the PR gene signatures for each dataset. For each miRNA, I calculate the Spearman's rank correlation coefficient between the miRNA expression values and the P and R enrichment scores across all samples. The correlation is done following the method in section 2.2.4 but substituting gene expression with miRNA expression. These correlation coefficients are represented by $S(M,P)$ and $S(M,R)$, respectively. $S(M,P)$ takes values between -1 and 1, whereby a value close to 1 indicating that the miRNA exhibits high expression in samples with a high degree of cell proliferation and a value close to -1 indicating that the miRNA exhibits low expression in samples with a high degree of cell proliferation. Same interpretation for $S(M,R)$ but with respect to the tissue remodelling gene signature.

Similar to the pattern observed for TFs, the miRNAs yielding high $S(M,P)$ have high but negative $S(M,R)$, and vice versa (Figure 5-2). Based on the Spearman's rank correlation coefficient between $S(M,P)$ and $S(M,R)$, there is a clear negative correlation between the tendency of miRNAs to be expressed together with the proliferation or remodelling programmes. In the colorectal cancer dataset, the correlation score is -0.31, while it is -0.50 and -0.37 in the breast and ovarian cancer datasets, respectively (p-value = 1×10^{-5} in all cases, permutation test). This suggests that the expression biases associated with the P and R programmes are also manifested at the level of miRNA expression.

Subsequently, I focus my attention on the miRNA targets and assess whether these targets themselves go along with the P and R gene expression signatures. I identify target genes of miRNAs using miRWalk (section 5.2.2). The expression of each of these target genes may or may not be correlated with the P gene signature. If the expression of a target gene is indeed positively correlated with P then it scores as a positive and the enrichment of these positives within the target list of a miRNA is used as a putative evidence that this miRNA may be involved in the regulation of cell proliferation programme. Similarly, if the expression of a target gene is indeed positively correlated with R then it scores as a positive and the enrichment of these positives within the target list of a miRNA is used as a putative evidence that this miRNA may be involved in the regulation of tissue remodelling programme (see section 5.2.3 for more technical details). Following the same rationale as before, I assess regulatory relationships between the expression of a miRNA and its targets, aiming to identify miRNAs whose expression values are associated with PR enrichment scores and their targets are enriched for the PR signatures as well (Figure 5-1). This analysis also results in different patterns of regulations, depending on:

- the association between the miRNA expression values and the PR enrichment scores, and
- the enrichment of the miRNA target genes with the P and R signatures.

The significance of the association of miRNA expression value with the P or R enrichment score is as calculated in section 2.2.9. The calculation for the significance of the enrichment of target genes with the gene signature is as described in section 2.2.10.

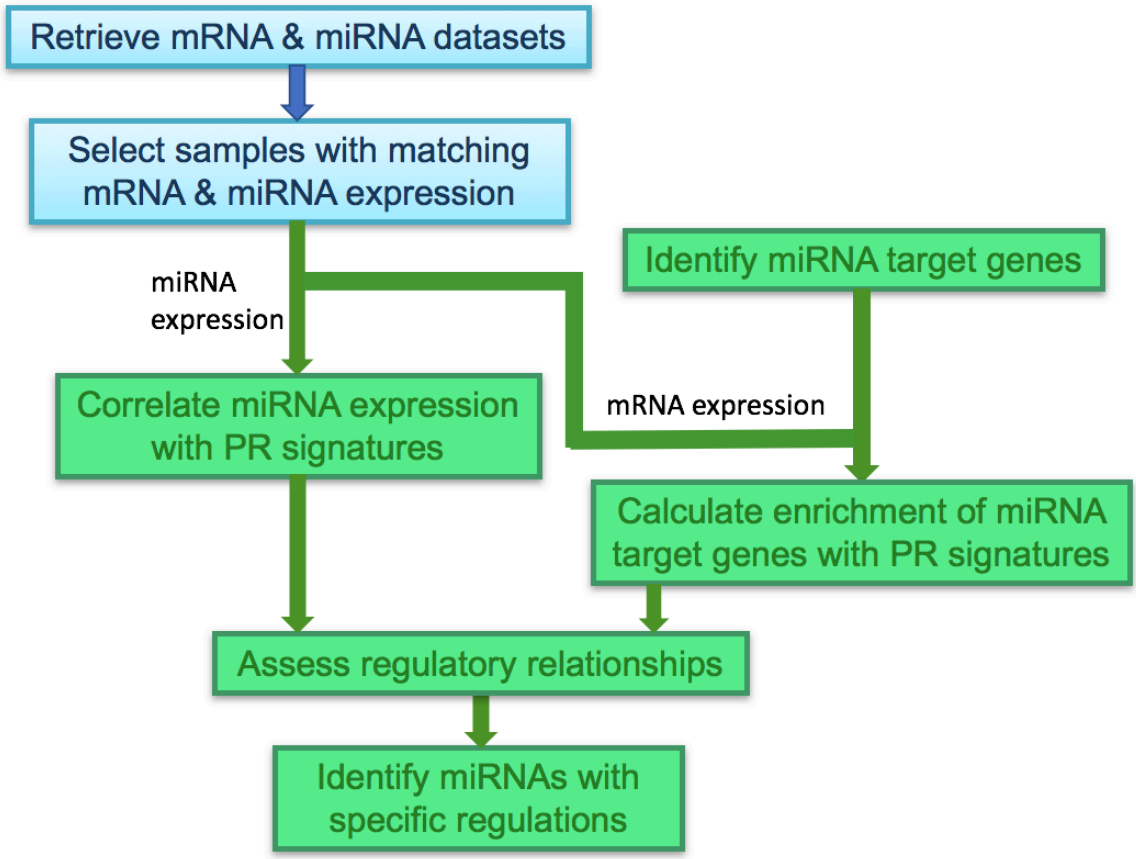

Figure 5-1. Workflow of identification of miRNA regulatory relationships. Blue boxes indicate the pre-processing steps, while green boxes indicate the processing steps.

Given that miRNAs function by suppressing gene expression, I focus my attention on miRNAs whose expression is significantly correlated with one programme but target genes whose expression is correlated with the other programme. This includes miRNAs having expression values significantly correlated with the P gene signature and having a significant enrichment score for the R signature among its target genes (P -| R). Similarly, it includes miRNAs having expression values significantly correlated with the R gene signature and having a significant enrichment score for the P signature among its target genes (R -| P). Following these patterns of regulations, I identify mir-19a as the only miRNA that satisfies the pattern of a putative miRNA associated with the cell proliferation programme across all three datasets (Table 5-3, Table 5-4, Table 5-5 and Appendix, P -| R). Similarly, I identify mir-193a, mir-22 and mir-23b as miRNAs that satisfy the pattern of putative miRNA regulators promoting the tissue remodelling programme across all three datasets (Table 5-3, Table 5-4, Table 5-

5 and Appendix, R -| P). These are as highlighted in bold in Table 5-3, Table 5-4 and Table 5-5. The master list of miRNAs together with their correlation of expression values with the P and R enrichment scores and the enrichment scores of their targets with the PR signatures can be found in Appendix.

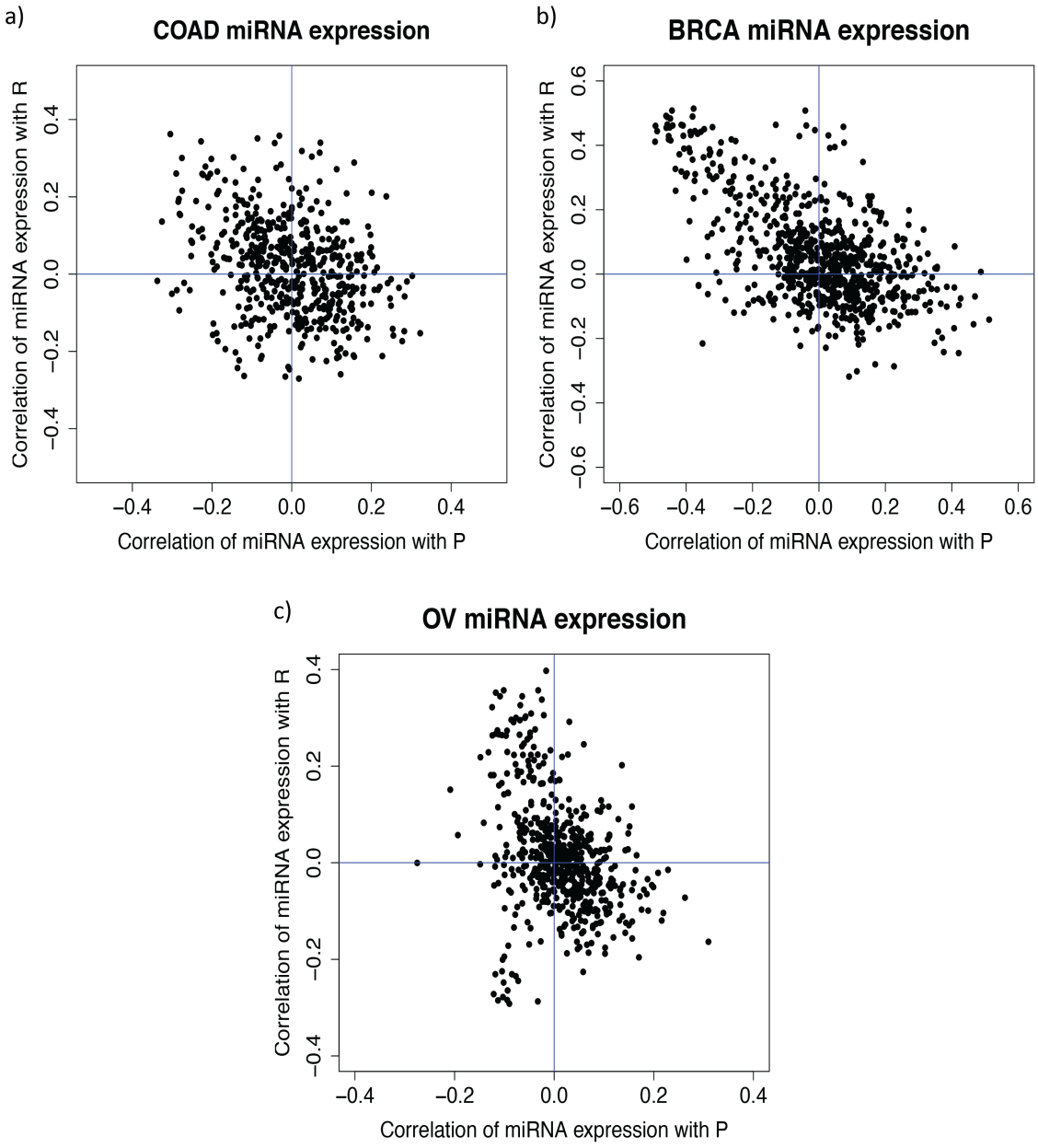

Figure 5-2. Scatter plot of Spearman's rank correlation coefficients between miRNA expression values and tissue remodelling signature (Y-axis) as a function of Spearman's rank correlation between miRNA expression values and cell proliferation signature (X-axis) in TCGA (**a**) colorectal, (**b**) breast and (**c**) ovarian cancer datasets. Each symbol represents a miRNA and the correlation is calculated across all patients.

Table 5-3. List of putative miRNAs sustaining programmes of (**a**) cell proliferation (P -| R) and (**b**) tissue remodelling (R -| P) in TCGA colorectal cancer dataset

miRNA	*S*(M,P)	P-value	BH	*S*(M,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -| R												
mir-625	0.17	4.0E-05	Y	0.04	0.15	N	-0.06	0.08	N	0.11	6.1E-03	Y
mir-302a	0.15	3.0E-04	Y	-0.09	0.02	Y	-0.27	1.0E-05	Y	0.34	1.0E-05	Y
mir-19a	**0.12**	**2.5E-03**	**Y**	**-0.09**	**0.02**	**Y**	**-0.03**	**0.27**	**N**	**0.33**	**1.0E-05**	**Y**
mir-141	0.09	0.01	Y	-0.07	0.04	Y	0.03	0.23	N	0.13	1.5E-03	Y
mir-346	0.09	0.02	Y	-0.09	0.01	Y	0.02	0.35	N	0.20	1.0E-05	Y
mir-33a	0.08	0.02	Y	-0.06	0.08	N	3.2E-03	0.47	N	0.10	9.3E-03	Y
(b) R -| P												
mir-212	0.07	0.05	N	0.34	1.0E-05	Y	0.30	1.0E-05	Y	-0.14	6.1E-04	Y
mir-615	0.07	0.05	N	0.24	1.0E-05	Y	0.24	1.0E-05	Y	-0.04	0.18	N
mir-155	0.05	0.12	N	0.30	1.0E-05	Y	0.18	3.0E-05	Y	0.02	0.34	N
mir-326	0.05	0.12	N	0.17	6.0E-05	Y	0.13	9.3E-04	Y	3.0E-03	0.47	N
mir-31	0.03	0.28	N	0.32	1.0E-05	Y	0.10	8.5E-03	Y	0.04	0.16	N
mir-330	7.6E-05	0.50	N	0.22	1.0E-05	Y	0.26	1.0E-05	Y	-0.03	0.21	N
mir-221	3.9E-05	0.50	N	0.17	6.0E-05	Y	0.15	3.4E-04	Y	0.02	0.28	N
mir-340	-3.1E-03	0.47	N	0.10	0.01	Y	0.18	4.0E-05	Y	-0.03	0.22	N
mir-935	-0.01	0.39	N	0.09	0.02	Y	0.27	1.0E-05	Y	-0.10	6.7E-03	Y
mir-1260	-0.03	0.27	N	0.09	0.02	Y	0.22	1.0E-05	Y	-0.09	0.01	Y
mir-15a	-0.03	0.27	N	0.12	2.8E-03	Y	0.11	7.0E-03	Y	0.07	0.05	N
mir-193b	-0.03	0.25	N	0.09	0.02	Y	0.31	1.0E-05	Y	-0.09	0.01	Y
mir-34c	-0.03	0.24	N	0.36	1.0E-05	Y	0.36	1.0E-05	Y	-0.12	2.4E-03	Y
let-7i	-0.04	0.18	N	0.28	1.0E-05	Y	0.28	1.0E-05	Y	0.02	0.35	N
mir-342	-0.05	0.11	N	0.16	1.0E-04	Y	0.26	1.0E-05	Y	-0.14	6.1E-04	Y
mir-126	-0.06	0.10	N	0.12	3.1E-03	Y	0.21	1.0E-05	Y	-0.04	0.18	N
mir-149	-0.07	0.05	N	0.11	5.2E-03	Y	0.25	1.0E-05	Y	-0.08	0.03	Y
mir-328	-0.08	0.04	Y	0.14	5.9E-04	Y	0.37	1.0E-05	Y	-0.10	9.5E-03	Y
mir-214	-0.08	0.03	Y	0.20	1.0E-05	Y	0.11	4.9E-03	Y	-0.03	0.28	N
mir-181b-1	-0.08	0.03	Y	0.09	0.01	Y	0.22	1.0E-05	Y	-0.11	5.6E-03	Y
mir-10b	-0.09	0.02	Y	0.14	5.7E-04	Y	0.22	1.0E-05	Y	9.2E-03	0.42	N
mir-34b	-0.09	0.01	Y	0.13	1.1E-03	Y	0.33	1.0E-05	Y	-0.08	0.04	Y
mir-708	-0.12	2.1E-03	Y	0.27	1.0E-05	Y	0.21	1.0E-05	Y	0.02	0.32	N
mir-199a-2	-0.12	1.6E-03	Y	0.19	1.0E-05	Y	0.15	2.0E-04	Y	0.03	0.21	N
mir-199a-1	-0.13	6.7E-04	Y	0.19	1.0E-05	Y	0.15	2.0E-04	Y	0.03	0.21	N
mir-125a	-0.14	3.7E-04	Y	0.15	1.9E-04	Y	0.18	4.0E-05	Y	-0.02	0.36	N
let-7e	-0.15	2.1E-04	Y	0.09	0.02	Y	0.22	1.0E-05	Y	0.01	0.37	N
mir-193a	**-0.17**	**4.0E-05**	**Y**	**0.11**	**5.8E-03**	**Y**	**0.10**	**9.3E-03**	**Y**	**-0.13**	**7.7E-04**	**Y**
mir-497	-0.18	2.0E-05	Y	0.10	8.5E-03	Y	0.36	1.0E-05	Y	0.07	0.06	N
mir-21	-0.18	1.0E-05	Y	0.22	1.0E-05	Y	0.15	2.0E-04	Y	0.02	0.34	N
mir-125b-1	-0.20	1.0E-05	Y	0.30	1.0E-05	Y	0.14	4.4E-04	Y	-0.02	0.32	N
mir-22	**-0.20**	**1.0E-05**	**Y**	**0.26**	**1.0E-05**	**Y**	**0.18**	**4.0E-05**	**Y**	**5.1E-03**	**0.45**	**N**
let-7b	-0.21	1.0E-05	Y	0.17	4.0E-05	Y	0.23	1.0E-05	Y	-0.06	0.08	N
mir-125b-2	-0.22	1.0E-05	Y	0.26	1.0E-05	Y	0.32	1.0E-05	Y	-0.11	6.4E-03	Y
mir-23b	**-0.23**	**1.0E-05**	**Y**	**0.12**	**3.2E-03**	**Y**	**0.19**	**1.0E-05**	**Y**	**0.02**	**0.28**	**N**
mir-30e	-0.23	1.0E-05	Y	0.11	4.9E-03	Y	0.20	1.0E-05	Y	-0.07	0.04	Y
let-7a-1	-0.25	1.0E-05	Y	0.08	0.03	Y	0.20	1.0E-05	Y	-0.03	0.25	N
let-7a-2	-0.25	1.0E-05	Y	0.09	0.02	Y	0.20	1.0E-05	Y	-0.03	0.25	N
mir-99a	-0.28	1.0E-05	Y	0.22	1.0E-05	Y	0.15	3.6E-04	Y	2.3E-03	0.48	N
mir-218-2	-0.28	1.0E-05	Y	0.30	1.0E-05	Y	0.14	5.1E-04	Y	-0.06	0.08	N
mir-9-1	-0.28	1.0E-05	Y	0.15	2.0E-04	Y	0.16	1.0E-04	Y	4.6E-03	0.46	N
mir-9-2	-0.28	1.0E-05	Y	0.16	1.9E-04	Y	0.16	1.0E-04	Y	4.6E-03	0.46	N
mir-101-1	-0.28	1.0E-05	Y	0.19	1.0E-05	Y	0.17	4.0E-05	Y	-0.02	0.34	N
mir-30a	-0.28	1.0E-05	Y	0.19	1.0E-05	Y	0.20	1.0E-05	Y	0.01	0.38	N
let-7c	-0.29	1.0E-05	Y	0.26	1.0E-05	Y	0.21	1.0E-05	Y	-0.10	7.3E-03	Y
mir-100	-0.30	1.0E-05	Y	0.36	1.0E-05	Y	0.14	3.8E-04	Y	-0.05	0.13	N
mir-1-2	-0.33	1.0E-05	Y	0.14	6.6E-04	Y	0.15	3.4E-04	Y	0.03	0.22	N

S(M,P) and *S*(M,R) indicate the correlation of miRNA expression values with P and R enrichment score, respectively.
ES_P and ES_R indicate the enrichment score of target genes with P and R signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

Table 5-4. List of putative miRNAs sustaining programmes of (**a**) cell proliferation (P -| R) and (**b**) tissue remodelling (R -| P) in TCGA breast cancer dataset

miRNA	*S*(M,P)	P-value	BH	*S*(M,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -| R												
mir-429	0.09	4.4E-03	Y	-0.10	2.0E-03	Y	-0.13	3.0E-04	Y	0.39	1.0E-05	Y
mir-200c	0.11	6.4E-04	Y	-0.30	1.0E-05	Y	-0.14	6.0E-05	Y	0.28	1.0E-05	Y
mir-141	0.09	5.9E-03	Y	-0.32	1.0E-05	Y	0.04	0.11	N	0.24	1.0E-05	Y
mir-20b	0.07	0.03	Y	-0.03	0.20	N	-0.16	3.0E-05	Y	0.19	1.0E-05	Y
mir-19a	**0.32**	**1.0E-05**	**Y**	**-0.05**	**0.08**	**N**	**-0.22**	**1.0E-05**	**Y**	**0.15**	**1.0E-05**	**Y**
mir-19b-2	0.14	5.0E-05	Y	-0.13	2.8E-04	Y	-0.04	0.14	N	0.12	3.1E-04	Y
mir-33a	0.30	1.0E-05	Y	-0.05	0.07	N	-5.6E-03	0.44	N	0.11	7.1E-04	Y
mir-128-1	0.14	9.0E-05	Y	0.06	0.05	N	0.04	0.16	N	0.11	1.2E-03	Y
mir-130b	0.36	1.0E-05	Y	0.02	2.6E-01	N	-2.8E-03	0.47	N	0.08	0.01	Y
(b) R -| P												
mir-195	-0.39	1.0E-05	Y	0.16	1.0E-05	Y	0.18	1.0E-05	Y	0.06	0.05	N
mir-376a-2	-0.24	1.0E-05	Y	0.24	1.0E-05	Y	0.11	1.2E-03	Y	0.06	0.06	N
mir-376a-1	-0.31	1.0E-05	Y	0.30	1.0E-05	Y	0.11	1.2E-03	Y	0.06	0.06	N
mir-190	-0.26	1.0E-05	Y	0.08	0.02	Y	0.14	5.0E-05	Y	0.05	0.07	N
mir-23a	-0.10	3.2E-03	Y	0.22	1.0E-05	Y	0.15	1.0E-05	Y	0.04	0.14	N
mir-28	-0.16	2.0E-05	Y	0.24	1.0E-05	Y	0.17	1.0E-05	Y	0.04	0.14	N
mir-10b	-0.43	1.0E-05	Y	0.26	1.0E-05	Y	0.11	1.6E-03	Y	0.03	0.24	N
mir-1-2	-0.25	1.0E-05	Y	0.24	1.0E-05	Y	0.10	3.3E-03	Y	0.02	0.30	N
mir-1-1	-0.03	0.23	N	0.09	7.5E-03	Y	0.10	3.3E-03	Y	0.02	0.30	N
mir-101-2	-0.19	1.0E-05	Y	0.10	3.0E-03	Y	0.12	3.4E-04	Y	0.02	0.30	N
mir-101-1	-0.34	1.0E-05	Y	0.12	5.6E-04	Y	0.12	3.4E-04	Y	0.02	0.30	N
mir-652	-0.02	0.26	N	0.11	1.4E-03	Y	0.21	1.0E-05	Y	0.02	0.33	N
mir-155	0.03	0.18	N	0.39	1.0E-05	Y	0.13	2.4E-04	Y	2.8E-03	0.47	N
mir-21	-0.14	1.5E-04	Y	0.20	1.0E-05	Y	0.13	1.9E-04	Y	-9.9E-03	0.39	N
mir-23b	**-0.16**	**1.0E-05**	**Y**	**0.17**	**1.0E-05**	**Y**	**0.13**	**1.0E-04**	**Y**	**-0.01**	**0.39**	**N**
mir-708	-0.27	1.0E-05	Y	0.25	1.0E-05	Y	0.23	1.0E-05	Y	-0.02	0.31	N
mir-424	-0.17	1.0E-05	Y	0.28	1.0E-05	Y	0.22	1.0E-05	Y	-0.02	0.30	N
mir-874	-0.24	1.0E-05	Y	0.06	0.04	Y	0.49	1.0E-05	Y	-0.02	0.29	N
mir-100	-0.45	1.0E-05	Y	0.42	1.0E-05	Y	0.13	1.3E-04	Y	-0.03	0.24	N
mir-34a	-0.20	1.0E-05	Y	0.11	9.3E-04	Y	0.21	1.0E-05	Y	-0.03	0.20	N
mir-598	-0.17	1.0E-05	Y	0.22	1.0E-05	Y	0.33	1.0E-05	Y	-0.03	0.18	N
mir-605	-0.13	1.6E-04	Y	0.16	1.0E-05	Y	0.18	1.0E-05	Y	-0.04	0.17	N
mir-26a-1	-0.24	1.0E-05	Y	0.15	1.0E-05	Y	0.13	1.9E-04	Y	-0.04	0.13	N
mir-30e	-0.17	1.0E-05	Y	0.23	1.0E-05	Y	0.12	2.9E-04	Y	-0.04	0.12	N
mir-125b-1	-0.49	1.0E-05	Y	0.41	1.0E-05	Y	0.11	1.0E-03	Y	-0.04	0.11	N
mir-126	-0.19	1.0E-05	Y	0.25	1.0E-05	Y	0.13	1.7E-04	Y	-0.05	0.07	N
mir-22	**-0.33**	**1.0E-05**	**Y**	**0.39**	**1.0E-05**	**Y**	**0.13**	**1.0E-04**	**Y**	**-0.05**	**0.07**	**N**
mir-32	0.06	0.06	N	0.08	0.01	Y	0.14	9.0E-05	Y	-0.07	0.02	Y
mir-222	-0.10	3.6E-03	Y	0.31	1.0E-05	Y	0.17	1.0E-05	Y	-0.08	0.01	Y
mir-215	7.2E-03	0.42	N	0.23	1.0E-05	Y	0.21	1.0E-05	Y	-0.09	5.9E-03	Y
mir-361	-0.16	3.0E-05	Y	0.18	1.0E-05	Y	0.22	1.0E-05	Y	-0.11	1.1E-03	Y
mir-99a	-0.49	1.0E-05	Y	0.44	1.0E-05	Y	0.14	6.0E-05	Y	-0.11	9.6E-04	Y
mir-196b	-0.25	1.0E-05	Y	0.35	1.0E-05	Y	0.14	6.0E-05	Y	-0.11	8.4E-04	Y
let-7c	-0.49	1.0E-05	Y	0.46	1.0E-05	Y	0.15	1.0E-05	Y	-0.13	3.0E-04	Y
mir-503	-0.09	7.4E-03	Y	0.24	1.0E-05	Y	0.25	1.0E-05	Y	-0.17	1.0E-05	Y
mir-193a	**-0.13**	**1.9E-04**	**Y**	**0.08**	**0.01**	**Y**	**0.13**	**1.4E-04**	**Y**	**-0.17**	**1.0E-05**	**Y**
mir-432	-0.46	1.0E-05	Y	0.46	1.0E-05	Y	0.39	1.0E-05	Y	-0.25	1.0E-05	Y

S(M,P) and *S*(M,R) indicate the correlation of miRNA expression values with P and R enrichment score, respectively.
ES_P and ES_R indicate the enrichment score of target genes with P and R signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

Table 5-5. List of putative miRNAs sustaining programmes of (**a**) cell proliferation (P -| R) and (**b**) tissue remodelling (R -| P) in TCGA ovarian cancer dataset

miRNA	*S*(M,P)	P-value	BH	*S*(M,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
(a) P -| R												
mir-130a	0.14	2.5E-04	Y	-0.15	2.6E-04	Y	-0.07	0.04	N	0.39	1.0E-05	Y
mir-19a	**0.14**	**1.7E-04**	**Y**	**-0.12**	**1.0E-03**	**Y**	**-0.12**	**1.2E-03**	**Y**	**0.32**	**1.0E-05**	**Y**
mir-200a	0.09	0.02	Y	-0.15	2.0E-04	Y	0.06	0.06	N	0.32	1.0E-05	Y
mir-138-2	0.08	0.02	Y	-0.03	0.20	N	0.07	0.04	N	0.19	1.0E-05	Y
mir-18b	0.18	1.0E-05	Y	-0.06	0.09	N	0.06	0.06	N	0.16	1.0E-05	Y
mir-625	0.11	5.3E-03	Y	-0.11	4.3E-03	Y	-0.16	3.0E-05	Y	0.15	6.0E-05	Y
mir-335	0.09	0.01	Y	-0.12	1.0E-03	Y	-0.15	1.1E-04	Y	0.15	1.1E-04	Y
mir-548b	0.09	0.02	Y	-0.04	0.14	N	-0.03	0.23	N	0.10	8.3E-03	Y
(b) R -| P												
mir-340	0.02	0.31	N	0.08	0.03	Y	0.16	1.0E-05	Y	0.07	0.05	N
mir-125a	-0.11	3.3E-03	Y	0.07	0.04	Y	0.10	8.3E-03	Y	0.05	0.10	N
mir-221	-0.11	3.0E-03	Y	0.16	1.0E-05	Y	0.20	1.0E-05	Y	0.05	0.14	N
mir-181a-1	-0.04	0.15	N	0.17	1.0E-05	Y	0.09	0.02	Y	0.04	0.16	N
mir-222	-0.13	8.1E-04	Y	0.18	1.0E-05	Y	0.22	1.0E-05	Y	0.04	0.18	N
mir-22	**-0.02**	**0.27**	**N**	**0.34**	**1.0E-05**	**Y**	**0.19**	**1.0E-05**	**Y**	**0.03**	**0.25**	**N**
mir-23b	**-0.03**	**0.25**	**N**	**0.08**	**0.02**	**Y**	**0.13**	**7.3E-04**	**Y**	**0.02**	**0.29**	**N**
mir-34a	-0.07	0.04	Y	0.18	1.0E-05	Y	0.23	1.0E-05	Y	0.02	0.32	N
mir-455	-0.05	0.10	N	0.21	1.0E-05	Y	0.14	4.4E-04	Y	0.02	0.35	N
mir-181b-2	0.04	0.14	N	0.11	4.8E-03	Y	0.15	5.0E-05	Y	-4.1E-03	0.46	N
let-7i	-0.06	0.08	N	0.11	4.3E-03	Y	0.41	1.0E-05	Y	-7.2E-03	0.43	N
mir-342	-0.02	0.29	N	0.16	1.0E-05	Y	0.18	1.0E-05	Y	-0.01	0.37	N
let-7e	-5.1E-03	0.45	N	0.14	3.2E-04	Y	0.20	1.0E-05	Y	-0.02	0.34	N
let-7a-2	-0.10	6.4E-03	Y	0.14	2.9E-04	Y	0.15	1.2E-04	Y	-0.03	0.26	N
let-7a-1	-0.09	0.01	Y	0.15	1.7E-04	Y	0.15	1.2E-04	Y	-0.03	0.26	N
mir-605	-0.05	0.13	N	0.31	1.0E-05	Y	0.15	1.1E-04	Y	-0.03	0.21	N
mir-193b	-0.07	0.05	N	0.08	0.03	Y	0.25	1.0E-05	Y	-0.04	0.15	N
let-7b	-0.15	1.8E-04	Y	0.22	1.0E-05	Y	0.18	1.0E-05	Y	-0.04	0.14	N
mir-193a	**-0.11**	**4.5E-03**	**Y**	**0.17**	**1.0E-05**	**Y**	**0.10**	**7.5E-03**	**Y**	**-0.05**	**0.09**	**N**
mir-326	0.01	0.36	N	0.12	2.5E-03	Y	0.15	1.5E-04	Y	-0.06	0.07	N
mir-212	0.06	0.07	N	0.25	1.0E-05	Y	0.20	1.0E-05	Y	-0.12	1.2E-03	Y

S(M,P) and *S*(M,R) indicate the correlation of miRNA expression values with P and R enrichment score, respectively.
ES_P and ES_R indicate the enrichment score of target genes with P and R signatures, respectively.
BH indicates the Boolean value whether the p-value remains significant after BH correction.

5.4 Further study on mir-22

As emphasized in previous sections, our primary focus is on the identification of putative regulatory mechanisms of tissue remodelling in the context of colorectal cancer. To this end, in section 5.3, I identify mir-22, mir-193a and mir-23b as putative miRNAs promoting the tissue remodelling programme. I perform a literature search about previous investigations of these miRNAs, paying particular attention to their association with the work on the context of tissue remodelling and immune cells. I then decide to focus my attention on mir-22 because there is some evidence on the regulation of immune cells differentiation by mir-22 and myeloid cell infiltration was found to be associated with tissue remodelling in colorectal cancer.

Mir-22 has been previously reported to be regulating monocyte/macrophage differentiation and its expression was shown to be decreased in acute myeloid leukaemia (Shen et al. 2016). On a different study, it has been demonstrated that mir-22 expression enhances conventional dendritic cell (cDC) development but inhibits plasmacytoid dendritic cell (pDC) generation in murine (Li et al. 2012). In line with these reports, we hypothesise that mir-22 may be regulating the immune cells of the myeloid lineage. Here I evaluate if there is also a higher mir-22 expression in myeloid as compared to lymphoid cells. Additionally, I investigate whether mir-22 is associated with immune cell infiltration in colorectal cancer.

5.4.1 Observation of mir-22 expression in human immune cell subsets

Previously I validate that KLF4 activity score is significantly higher in phagocytes (myeloid cells, myeloblast lineage) versus lymphoid cells in section 4.5.2. Here I establish if there is also a similar pattern of mir-22 expression in the immune cells. To facilitate this, I retrieve a different publicly available human immune cell transcriptome dataset, quantifying both genome-wide gene and miRNA expression in immune cell subsets (ref. (Allantaz et al. 2012), GEO accession number GSE28492). I pre-process the miRNA expression data (generated on Roche and HUG platforms) and assign the samples into different groups of immune cell types, as detailed in section 5.2.4.

As can be observed in Figure 5-3, the expression of mir-22 is significantly higher in phagocytes versus lymphoid cells (p-value = 2.54×10^{-5}, one tailed t-test). This observation of a high mir-22 expression in myeloid cells further supports our hypothesis that mir-22 may be regulating the immune cells in the myeloid lineage.

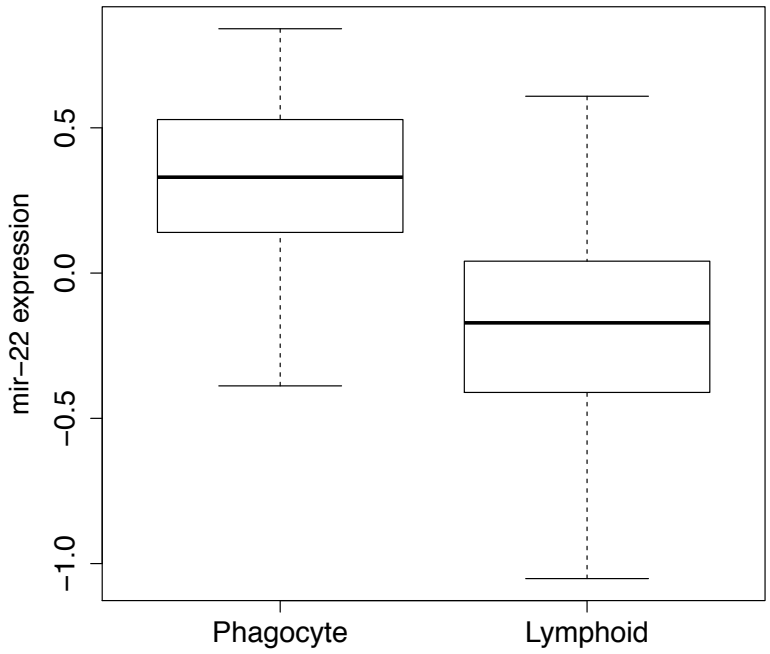

Figure 5-3. Box plot of mir-22 expression values in phagocytes (myeloid cells) versus lymphoid cells in human immune cell subsets (GSE28492).

5.4.2 Enrichment of myeloid versus lymphoid cells in Pmir22 subtypes

Previously I elaborate that tissue remodelling processes are associated with KLF4 activity score via myeloid cell infiltration. Here I evaluate if there is also an association between mir-22 expression value with immune cell infiltration, specifically the immune cells in the myeloid lineage.

Using TCGACRC miRNA expression data, I correlate mir-22 expression value with the estimated fraction of immune cell types of these colorectal tumours. As mentioned before, 129 out of 132 samples in this dataset also appear in the

CRCSC cohort so I can reuse the inferred composition of the immune cell types previously obtained using CIBERSORT in section 4.5.4.

In Figure 5-4, it can be observed that there is a significant positive correlation between mir-22 expression value and the inferred neutrophils fraction (Table 5-6). On the other hand, there is a significant negative association between mir-22 expression value and the estimated composition of T cells CD4 memory (activated) (Figure 5-4 and Table 5-6). In other words, the level of mir-22 expression value is associated with inferred fraction of neutrophils, despite the low number of samples in this dataset. I note, however, that there is no significant association between the expression of mir-22 and other myeloid subtypes (e.g. macrophages) that were found significantly associated with KLF4 activity score.

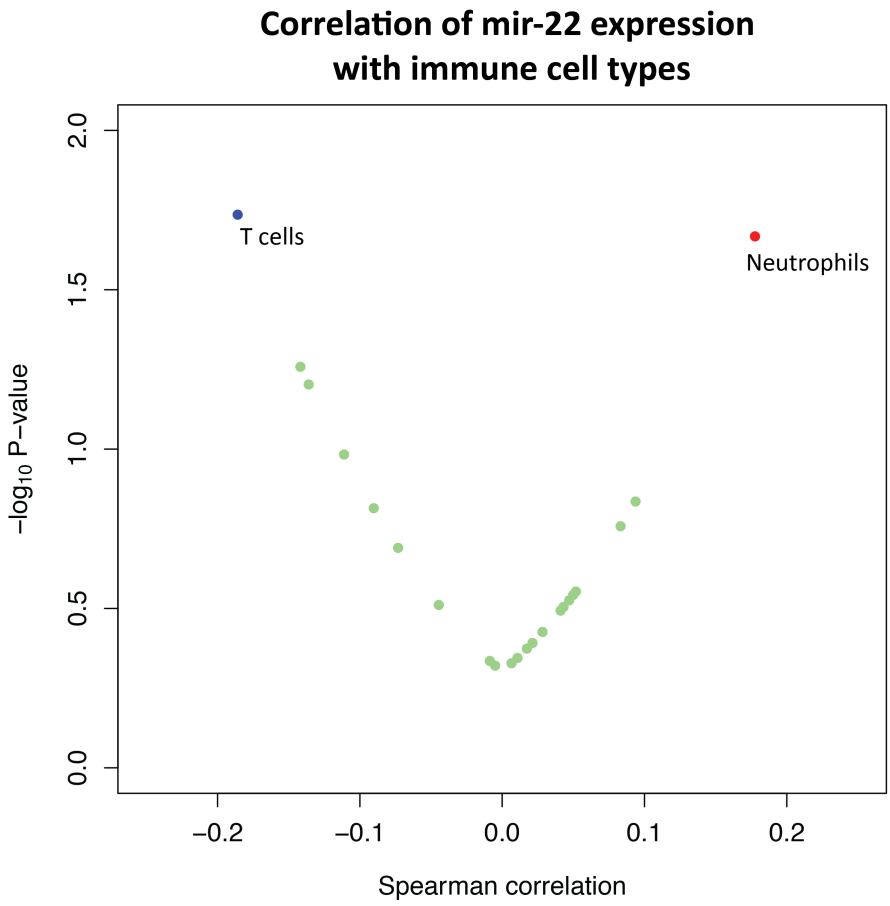

Figure 5-4. Volcano plot of statistical significance versus Spearman's rank correlation between estimated fractions of immune cells and mir-22 expression values in TCGACRC dataset. Each point represents an immune cell type. Annotated immune cell types from left to right in the figure are T cells CD4 memory (activated) and neutrophils.

Table 5-6. Correlation of mir-22 expression value with estimated fraction of immune cell types

Immune cell type	Correlation with mir-22 expression value	P-value	BH
Neutrophils	0.18	2.1E-02	Y
NK cells activated	0.09	1.5E-01	N
Eosinophils	0.08	1.7E-01	N
Macrophages M2	0.05	2.8E-01	N
T cells follicular helper	0.05	2.9E-01	N
T cells CD8	0.05	3.0E-01	N
T cells regulatory (Tregs)	0.04	3.1E-01	N
Macrophages M1	0.04	3.2E-01	N
Macrophages M0	0.03	3.8E-01	N
Dendritic cells resting	0.02	4.1E-01	N
Monocytes	0.02	4.2E-01	N
B cells naive	0.01	4.5E-01	N
B cells memory	0.01	4.7E-01	N
T cells CD4 naive	-0.01	4.8E-01	N
Mast cells resting	-0.01	4.6E-01	N
Mast cells activated	-0.04	3.1E-01	N
Dendritic cells activated	-0.07	2.0E-01	N
T cells CD4 memory resting	-0.09	1.5E-01	N
NK cells resting	-0.11	1.0E-01	N
T cells gamma delta	-0.14	6.3E-02	N
Plasma cells	-0.14	5.5E-02	N
T cells CD4 memory activated	-0.19	1.8E-02	Y

BH indicates the Boolean value whether the p-value remains significant after BH correction.

Next, I classify the samples into Pmir22 subtypes following the steps in section 5.2.5. The assignment of the samples into the Pmir22 groups can be found in Appendix. Then I assess the abundance of the immune cell types in the Pmir22 subtypes following the method in section 4.2.7 but substituting the PK subtypes with the Pmir22 subtypes.

Afterwards, I visualise the tail distribution of the estimated fractions of myeloid and lymphoid cells in the Pmir22 subtypes to determine if mir-22 expression value is related to immune cell infiltration. As illustrated in Figure 5-5, there is no clear separation of the tail distribution of macrophages M0, neutrophils, B

cells (naive) and T cells CD4 memory (activated) enrichment between mir22+ and mir22- patient groups. Also, the two-sided Kolmogorov-Smirnov test does not yield statistical significance for the comparison of estimated fraction of all four immune cell types in mir22+ and mir22- patient groups. These findings suggest the level of mir-22 expression is not a predictor of the composition of myeloid or lymphoid cells in a tumour sample. In other words, the results suggest that mir-22 expression value is not associated with immune cell infiltration and mir-22 may have other functions in other compartments of the tumours as well.

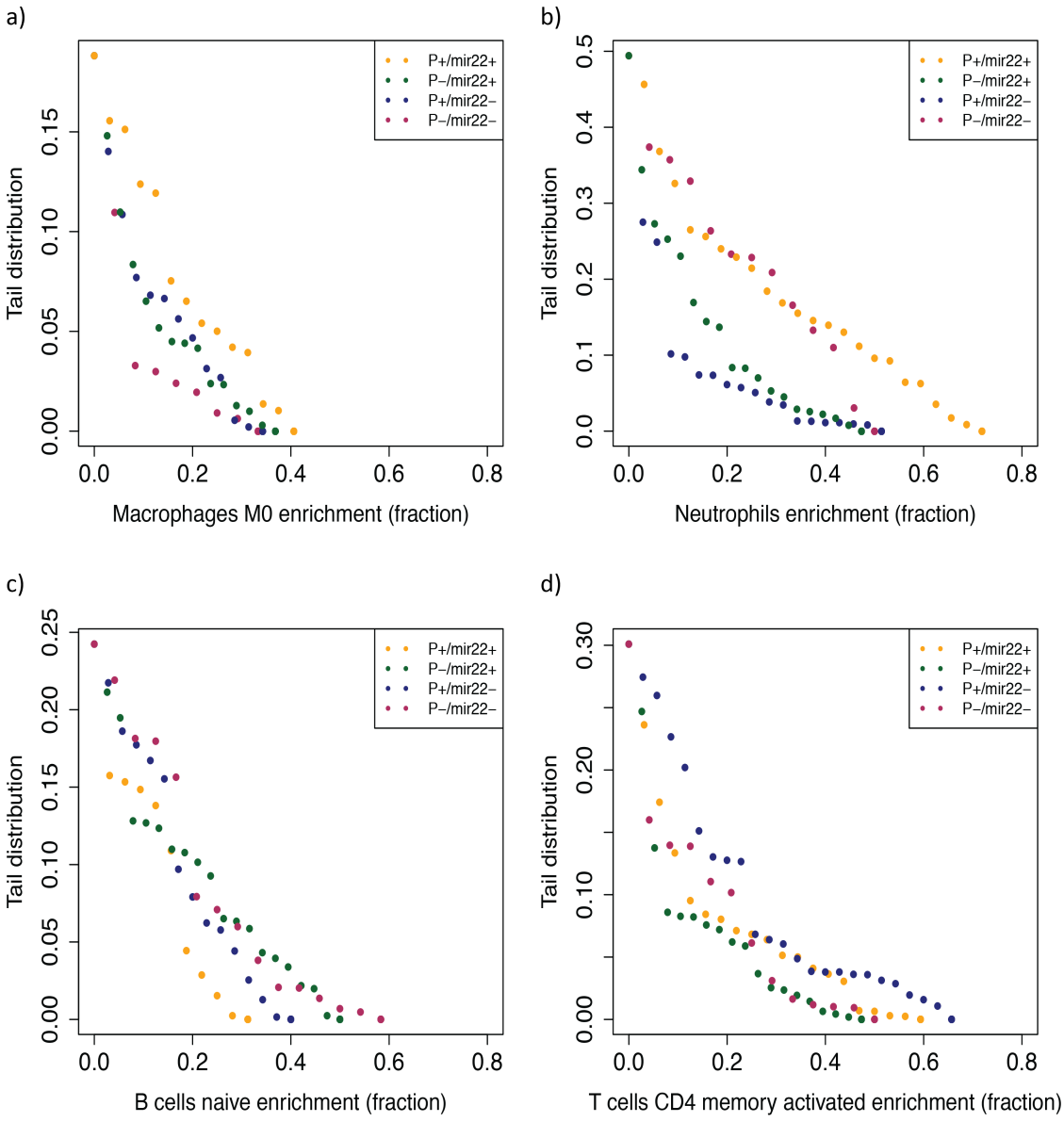

Figure 5-5. Tail distribution of the enrichment of (**a**) macrophages M0, (**b**) neutrophils, (**c**) B cells (naive) and (**d**) T cells CD4 memory (activated) across TCGACRC grouped according to their Pmir22 subtype.

5.5 Conclusions

Mir-19a is the putative miRNA regulator associated with the cell proliferation programme in all three datasets (TCGA colorectal, breast and ovarian cancer) analysed. Similarly, mir-193a, mir-22 and mir-23b are the putative miRNA regulators sustaining the tissue remodelling programme in the same datasets. Expression value of mir-22 is significantly higher in myeloid cells from the myeloblast lineage relative to other immune cell types. However, mir-22 expression value has a weak association with immune cell composition in colorectal cancer. This observation suggests that mir-22 may be expressed in the tumour stroma, which may explain why it is less correlated with the presence of the myeloid cells in the tumour samples.

6 Outlook

6.1 Putative regulatory network of infiltrating myeloid cells

The observations made in this work suggest that a component of what we define by tissue remodelling based on gene expression signatures may be actually driven by immune cell infiltration. To shed further light in this direction, I make a final effort to put these observations together and draw a working model of a core regulatory network of myeloid cell infiltration of colorectal tumours.

As mentioned previously, mir-22 has been shown to be a regulator of monocyte/macrophage differentiation in human (Shen et al. 2016) and cDC development in mouse (Li et al. 2012). Similarly, KLF4 has also been reported to regulate the differentiation of monocytes into myeloid cells (Feinberg et al. 2007). Additionally, I have previously demonstrated that there is a higher KLF4 activity score and mir-22 expression value in myeloid versus lymphoid cells. In line with this knowledge, I aim to delineate the network that is potentially regulated by both KLF4 and mir-22 in the context of monocyte/macrophage differentiation and in infiltrating myeloid cells in colorectal cancer. The findings will hopefully broaden our knowledge of tissue remodelling processes, motivate future work and enable us to propose further studies for targeting the network that may be regulated by both KLF4 and mir-22 in colorectal cancer.

An earlier work by Tamura et al. established that interferon regulatory factor-8 (IRF8), also known as interferon consensus sequence binding protein (ICSBP), directed the differentiation of myeloid progenitor cells into macrophages (Tamura et al. 2000). In the same study, they showed that IRF8 formed heterodimeric complexes with PU.1 (also known as SPI1) in the cells of the monocyte or macrophage lineage in mouse (Tamura et al. 2000). In a different study, Feinberg et al. reported that a suppression of KLF4 resulted in a significant decrease in PU.1 and differentiation markers of monocytes and *Klf4* gene was a downstream target of PU.1 (Feinberg et al. 2007). They also showed that KLF4 could induce the differentiation of monocytes into macrophages independently of PU.1 (Feinberg et al. 2007). Later on, Kurotaki et al. demonstrated that IRF8 functioned primarily as a transcriptional activator of

monocyte differentiation and IRF8 bound to distal H3K4me1 regions together with PU.1 (Kurotaki et al. 2013). They also elaborated that KLF4 acted downstream of IRF8 in inducing differentiation of monocytes/ macrophages and showed that IRF8 directly targeted *Klf4* gene (Kurotaki et al. 2013). Li et al. then demonstrated that mir-22 enhanced development of cDC but inhibited generation of pDC and mir-22 negatively regulated *Irf8* gene by repressing its transcription (Li et al. 2012). More recently, Shen et al. reported that PU.1 transcriptionally regulated mir-22 and mir-22 was a regulator in monocyte/macrophage differentiation (Shen et al. 2016). Collectively, I propose a network regulated by IRF8, SPI1, KLF4 and mir-22 in the context of monocyte differentiation based on these regulations, as illustrated in Figure 6-1.

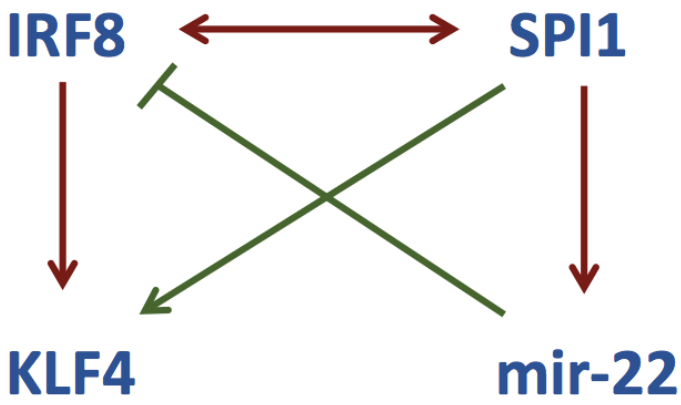

Figure 6-1. A network potentially regulated by IRF8, SPI1, KLF4 and mir-22 in the context of monocyte/macrophage differentiation. Maroon arrows denote the interaction involves the transcription factors, whereas green lines denote the regulation happens at the gene transcription.

Three out of the four nodes depicted in Figure 6-1 are identified as being associated with tissue remodelling in the previous chapters. In addition to the previously discussed KLF4 and mir-22, SPI1 was also identified as a TF whose activity score is positively correlated with tissue remodelling (Table 4-3). The next obvious question is whether the interactions between them are also supported by the genomics datasets characterising pure immune cell populations and the colorectal tumour samples.

To interrogate the associations between the IRF8, SPI1 and KLF4 activity scores and mir-22 expression, I analyse gene expression profiles of isolated human immune cells (GSE28492). First, I infer TF activity scores of IRF8, SPI1 and KLF4 using gene expression profiles in this dataset following the steps in section 4.2.2. Then I utilise mir-22 expression values from the samples in common between miRNA expression (obtained in section 5.2.4) and TF activity score matrices for correlating IRF8, KLF4, SPI1 and mir-22 in pairwise comparisons. To interrogate their associations in the context of colorectal tumour samples, I repeat the same analysis using the TCGACRC dataset to evaluate if this network is relevant in colorectal tumours. TF activity scores of IRF8, KLF4 and SPI1 are as obtained in section 4.2.2, while mir-22 expression is obtained from section 5.2.1.

There is a significant and positive correlation between IRF8 and KLF4 activity scores in both immune cells and colorectal tumours (Table 6-1 and Table 6-2). The correlation between mir-22 expression value and IRF8 activity score is significant in GSE28492 dataset and it is positive in the TCGACRC dataset. The co-expression of the IRF8 activity score and the expression of its annotated negative regulator mir-22 suggests that there is a negative feedback loop, whereby mir-22 represses *Irf8* gene to control the rate of IRF8 transcription. Future experimental work should interrogate whether this negative feedback is actually active in the context of myeloid cells infiltrating the colorectal tumour tissue.

SPI1 activity score has no variance in the pure immune cells dataset, so I limit my analysis to the colorectal tumour samples dataset. There is a significant correlation between SPI1 and KLF4 activity scores (Table 6-2, S = 0.40, p-value = 1×10^{-5}, permutation test), while there is no significant correlation between IRF8 and SPI1 in the colorectal tumour samples (Table 6-2, S = 0.12, p-value = 0.10, permutation test). The correlation between SPI1 activity score and mir-22 expression value is very small and not significant (Table 6-2, S = 4.3×10^{-3}, p-value = 0.48, permutation test). To represent the signals observed in our data, I propose the putative network of infiltrating myeloid cells in colorectal tumours, as presented in Figure 6-2. The arrow between KLF4 and SPI1 in Figure 6-2 is to reflect the positive correlation of KLF4 and SPI1 transcriptional activity scores

and the fact that KLF4 can induce differentiation markers in PU.1-null myeloid cells to a similar level as the induction by PU.1 alone (Feinberg et al. 2007).

Taken together, this evidence supports the association between IRF8 and KLF4 in the context of monocyte differentiation (Figure 6-1) and colorectal tumour samples (Figure 6-2). Furthermore, given that SPI1 and KLF4 activity scores are correlated but SPI1 and IRF8 activity score are not, this evidence suggests that SPI1 acts independently of IRF8. For mir-22, I find no evidence of its regulation by SPI1. I note that my analysis is not sufficient to pinpoint that mir-22 is regulated by SPI1. There could be other factors regulating mir-22 that are relevant and active in the colorectal tumour samples, for instance, in the stroma or tumour cells.

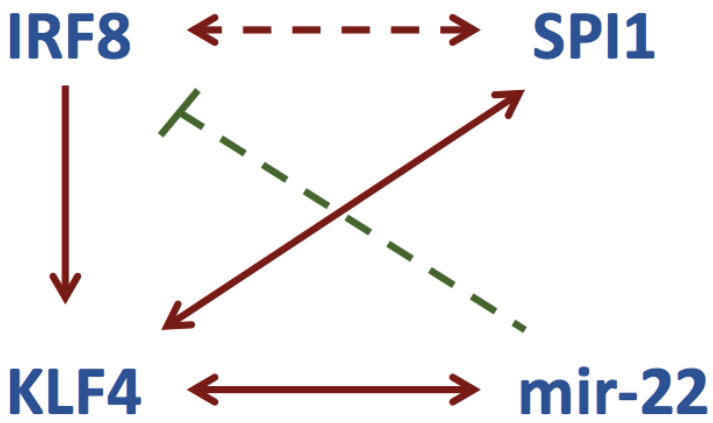

Figure 6-2. A network potentially regulated by IRF8, SPI1, KLF4 and mir-22 in colorectal cancer. Maroon arrows denote the interaction involves the transcription factors, whereas green line denotes the suppression happens at the gene transcription. Dotted arrows reflect insignificant correlation between the nodes in our data.

Table 6-1. Correlation of IRF8 and KLF4 activity scores and mir-22 expression values in pairwise comparisons in human immune cell subsets (GSE28492)

P-value / Cor	IRF8	KLF4	mir-22
IRF8		3.7E-03	1.6E-03
KLF4	0.31		6.0E-05
mir-22	0.34	0.43	

Lower triangle indicates correlation score based on Spearman's rank coefficients.
Upper triangle indicates statistical significance of the correlation.

Table 6-2. Correlation of IRF8, KLF4 and SPI1 activity scores and mir-22 expression values in pairwise comparisons in TCGACRC dataset

P-value / Cor	IRF8	KLF4	SPI1	mir-22
IRF8		9.9E-04	0.10	0.07
KLF4	0.27		1.0E-05	1.2E-03
SPI1	0.12	0.40		0.48
mir-22	0.13	0.27	4.3E-03	

Lower triangle indicates correlation score based on Spearman's rank coefficients.
Upper triangle indicates statistical significance of the correlation.

6.2 Discussion

I have utilised a colorectal cancer case study. I have assessed the advantages and disadvantages of both unsupervised and supervised clustering approaches of patient classifications. Specifically, I have compared the performance of colorectal cancer patient stratification based on a recently reported unsupervised CMS clustering approach (ref. (Guinney et al. 2015)) versus a supervised clustering method using PR signatures (ref. (Markert et al. 2012)). Both classifications exhibit statistical significance in splitting overall and relapse-free survival curves. The CMS4 and P-/R+ subtypes yield worst prognosis as compared to the remaining subtypes in the unsupervised and supervised approaches, respectively. Yet, the unsupervised scheme cannot separate the remaining patients in the other three subtypes based on survival. In contrast, both cell proliferation and tissue remodelling in the supervised scheme predict clinical outcome. Our approach distinguishes P+/R- group that yields significantly better survival than P-/R- group. This observation shows that patient stratification based on the PR scheme highlights that cell proliferation is a relevant prognostic factor, in addition to tissue remodelling. They are both indicative of good and poor prognosis in colorectal cancer, respectively.

At the moment, we have no clear explanation of why colorectal cancer patients with an up-regulation of cell proliferation signature have good prognosis. We speculate that the treatments received by these patients are designed to target proliferating cancer cells. Consequently, patients harbouring tumours with increased cell proliferation respond better to therapy. Another reasoning is because increased tissue remodelling is the characteristic of colorectal tumours causally linked to poor prognosis. As there is a negative correlation between cell proliferation and tissue remodelling, it gives rise to the association of cell proliferation with good prognosis. However, we should note that increased cell proliferation is an indicator of worse prognosis in other cancer types, such as breast (van Diest et al. 2004) and prostate cancer (Markert et al. 2011). As mentioned in the introduction, a previous work in our laboratory had elaborated the dichotomy of cell prognosis and tissue remodelling in patient outcome when considering different cancer types. In breast, brain, prostate and lung cancer, increased cell proliferation indicates poor prognosis. In contrast, increased

tissue remodelling is indicative of poor prognosis in colorectal and ovarian cancer.

Subsequently, I study specific transcription factors that drive the transcriptional programmes of cell proliferation and tissue remodelling. Specifically, I aim to understand specific TFs that drive increased tissue remodelling, which is linked to poor prognosis in colorectal cancer. Among the TFs with activity score that is significantly associated with the tissue remodelling enrichment score, I choose KLF4 for a further study on the tissue remodelling transcriptional programme. I focus on KLF4 because it has been reported to be a regulator of myelopoiesis (Feinberg et al. 2007) and one of the reprogramming factors required in induced pluripotent stem cells (Okita et al. 2007). Both features can potentially contribute to poor clinical outcome and malignancy linked with tissue remodelling. Using an immune cell dataset, I have validated that KLF4 activity score is significantly higher in myeloid as compared to lymphoid cells, which agrees with its documented role in myelopoiesis (Feinberg et al. 2007). Additionally, I observe that KLF4 activity score is positively correlated with predicted infiltration of myeloid cells in colorectal tumours. Collectively, these findings suggest that myeloid cell infiltration gives rise to tissue remodelling processes in colorectal cancer and KLF4 sustains myelopoiesis in these infiltrating immune cells.

When assessing the enrichment of KLF4 activity score with the biomarkers, I do not observe a significant correlation between the level of KLF4 activity and KRAS mutation although KRAS is highly mutated in colorectal cancer. An explanation for this observation is because KRAS mutations occur in an early stage of tumour initiation (Grady and Pritchard 2014) (Rajagopalan et al. 2002), whereas the samples in our data are already in the carcinoma stage. On the other hand, SMAD4 deletion occurs when the tumour progresses from adenoma into carcinoma (Takaku et al. 1998) and PIK3CA mutation is generally observed late in tumourigenesis (Samuels et al. 2004). If the information on SMAD4 deletion and PIK3CA mutation is available, it will be interesting to assess if the level of KLF4 activity is significantly correlated with these biomarkers.

I have uncovered specific microRNAs that regulate the cell proliferation and tissue remodelling programmes in the next part of my work. Among the miRNAs whose expression value is significantly correlated with tissue remodelling enrichment score, I select mir-22 for a further study. This is because mir-22 has been shown to be promoting differentiation of monocytes into macrophages (Shen et al. 2016). This leads me to hypothesise that there may be a network regulated by both KLF4 and mir-22 in monocyte differentiation. Using a different immune cell dataset, I have demonstrated that there is also a significantly higher mir-22 expression in myeloid versus lymphoid cells. However, I establish that mir-22 expression level does not predict the extent of the predicted infiltration from any immune cells in colorectal tumours. The results suggest that mir-22 signalling may also be present in other tumour compartments.

My findings are consistent with the literature, whereby mir-22 has been reported to attenuate EMT and colon cancer metastasis by targeting T-cell lymphoma invasion and metastasis 1 (TIAM1) (Li et al. 2013). This further confirms the significant correlation between mir-22 expression and our tissue remodelling signature. Mir-22 has also been documented to regulate various cellular processes in cancer by accelerating senescence, inhibiting energy supply, blocking angiogenesis and promoting apoptosis in some cancer types (Wang et al. 2017). Furthermore, mir-22 exhibits dual effects in various cancer types by inhibiting proliferation, invasion and metastasis in some cancer types but promoting proliferation, migration and invasion in other cancer types (Wang et al. 2017). Collectively, these reports demonstrate that mir-22 play various roles in cancer, in agreement with my observation that mir-22 is less correlated with the myeloid cells and its signalling may be present in the tumour stroma. Future work should investigate the role of mir-22 in colorectal cancer, particularly to uncover its role in regulating various cellular processes in colorectal cancer.

In the last part of my work, I propose a network that may be regulated by IRF8, SPI1, KLF4 and mir-22 in the context of monocyte differentiation then assess its relevance in colorectal cancer dataset. KLF4 has been reported to act downstream of IRF8 in monocyte/macrophage differentiation (Kurotaki et al. 2013), while IRF8 directs this differentiation (Tamura et al. 2000) and targets *Klf4* gene (Kurotaki et al. 2013). IRF8 has been demonstrated to form

heterodimeric complexes with SPI1 in the monocyte or macrophage lineage (Tamura et al. 2000). Additionally, SPI1 has been shown to transcriptionally regulate mir-22, which regulates monocyte/macrophage differentiation (Shen et al. 2016) and suppresses *Irf8* gene (Li et al. 2012). In the correlation analysis of IRF8, KLF4, SPI1 and mir-22, I have shown that IRF8 is positively correlated with KLF4, which agrees with their reported function in monocyte differentiation (Kurotaki et al. 2013). On the other hand, there is a positive correlation between IRF8 and mir-22, indicating a negative feedback loop between them. The significant and positive correlation between mir-22 and KLF4 supports my findings that both mir-22 and KLF4 are indeed in part associated with tissue remodelling processes. My results also demonstrate there is no regulation of mir-22 by SPI1 but SPI1 has a positive correlation with IRF8 and a significant and positive correlation with KLF4. These suggest that SPI1 may not be involved in regulating myeloid cells beyond their maturation and as shown in a previous report, its primary role is in the regulation of myeloid and lymphoid lineage commitment (Scott et al. 1994). Future work should be carried out to establish if SPI1 regulates KLF4 in colorectal tumours with infiltrating myeloid cells or the regulation happens only in differentiating monocytes.

Having identified these specific regulators driving tissue remodelling, there is a need to conduct further studies to understand the molecular pathways and specific factors driving the enrichment of myeloid cell infiltration in colorectal cancer. These studies will help identify therapies for colorectal cancer patients exhibiting poor prognosis, characterised by increased tissue remodelling. TGFß drives tissue remodelling and plays an important role in the tumour microenvironment (Pickup et al. 2013). The role of TGFß signalling in the exclusion of T cells has also been reported in genetically engineered colorectal cancer metastasis (Tauriello et al. 2018). Yet, it is not known how T cell exclusion affects myeloid cell abundance in colorectal tumours characterised by a high degree of tissue remodelling.

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Appendix

Master list of TFs in CRCSC cohort together the correlation scores of their activity scores with PR signatures and enrichment scores of target genes with PR signatures

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
LHX3	-0.33	1.0E-05	Y	0.74	1.0E-05	Y	0	0.50	N	0	0.50	N
NFYB	-0.24	1.0E-05	Y	0.74	1.0E-05	Y	0	0.50	N	0	0.50	N
RBL2	-0.30	1.0E-05	Y	0.70	1.0E-05	Y	0	0.50	N	0	0.50	N
MAFF	-0.23	1.0E-05	Y	0.67	1.0E-05	Y	0	0.50	N	0	0.50	N
SATB2	-0.32	1.0E-05	Y	0.67	1.0E-05	Y	0	0.50	N	0	0.50	N
MAZ	-0.37	1.0E-05	Y	0.65	1.0E-05	Y	0	0.50	N	0	0.50	N
MBD1	-0.26	1.0E-05	Y	0.64	1.0E-05	Y	0	0.50	N	0	0.50	N
SREBF1	-0.72	1.0E-05	Y	0.64	1.0E-05	Y	-0.03	0.22	N	0	0.50	N
RARG	-0.11	3.0E-03	Y	0.63	1.0E-05	Y	0	0.50	N	0	0.50	N
ETV4	-0.41	1.0E-05	Y	0.62	1.0E-05	Y	0	0.50	N	0.66	1.0E-05	Y
CTCFL	0.02	0.34	N	0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
PML	-0.07	0.06	N	0.61	1.0E-05	Y	0	0.50	N	0.30	1.0E-05	Y
EHMT2	-0.25	1.0E-05	Y	0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
DDB2	-0.09	0.01	Y	0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF4	-0.09	0.02	Y	0.59	1.0E-05	Y	-0.29	1.0E-05	Y	0.18	1.0E-05	Y
ENO1	-0.03	0.22	N	0.59	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC9	-0.36	1.0E-05	Y	0.59	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N
TBP	-0.41	1.0E-05	Y	0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
MEN1	-0.29	1.0E-05	Y	0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
HIPK2	-0.04	0.18	N	0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRG	-0.09	0.02	Y	0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
AHR	-0.09	0.01	Y	0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF5	-0.21	1.0E-05	Y	0.52	1.0E-05	Y	0.80	1.0E-05	Y	0.65	1.0E-05	Y
CDX1	-0.22	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
HEY2	-0.46	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXB13	-0.06	0.07	N	0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC1	-0.29	1.0E-05	Y	0.50	1.0E-05	Y	-0.40	1.0E-05	Y	-0.05	0.12	N
SOX10	-0.16	6.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
TRIB3	-0.34	1.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXO3	-0.29	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0.27	1.0E-05	Y
ARNT	-0.19	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
PTTG1	-0.26	1.0E-05	Y	0.47	1.0E-05	Y	0.23	1.0E-05	Y	0.50	1.0E-05	Y
CRTC1	-0.42	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
NANOG	-3.6E-	0.47	N	0.46	1.0E-05	Y	0.04	0.18	N	0	0.50	N
BTG2	0.14	3.8E-04	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
HNF4G	-0.48	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
TCF19	-0.68	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F6	-0.75	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
GCM2	-0.17	5.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM4	-0.32	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
KAT6A	-0.47	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
SPEN	0.04	0.17	N	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA2	-0.24	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
SPI1	-0.03	0.21	N	0.42	1.0E-05	Y	0	0.50	N	0.51	1.0E-05	Y
GFI1	-0.39	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F1	-0.81	1.0E-05	Y	0.42	1.0E-05	Y	0.55	1.0E-05	Y	0.07	0.05	N
CRABP2	-0.43	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
EGR3	-0.18	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL1	-0.26	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
SNAI2	-0.09	0.02	Y	0.41	1.0E-05	Y	-0.37	1.0E-05	Y	0.54	1.0E-05	Y
SKI	-0.14	4.2E-04	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRA	-0.37	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
SHOX	0.09	0.01	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIL3	-0.15	1.8E-04	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N

DNMT1	-0.45	1.0E-05	Y	0.40	1.0E-05	Y	0.03	0.26	N	0	0.50	N
LMO4	-0.34	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM2	-0.60	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
DACH1	-0.23	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
EPAS1	-0.20	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF5	-0.12	1.6E-03	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
SPIB	-0.21	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL2	-0.21	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
SMAD3	-0.37	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
NOTCH3	-0.17	5.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
MDM4	-0.11	3.3E-03	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
NR3C1	-0.10	8.4E-03	Y	0.37	1.0E-05	Y	0.26	1.0E-05	Y	0.23	1.0E-05	Y
RBPJ	0.09	0.01	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
FOSL1	0.02	0.31	N	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
TP73	-0.64	1.0E-05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT1	-0.06	0.07	N	0.36	1.0E-05	Y	-0.36	1.0E-05	Y	0.55	1.0E-05	Y
HEY1	-0.12	2.4E-03	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
PURA	-0.15	1.8E-04	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
TEF	-0.36	1.0E-05	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF4	-0.11	4.5E-03	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
TP63	-0.26	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA3	-0.03	0.24	N	0.32	1.0E-05	Y	-0.21	1.0E-05	Y	0.48	1.0E-05	Y
CEBPZ	-0.25	1.0E-05	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXC9	-0.09	0.01	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
TBX3	-0.15	2.1E-04	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
NFE2L2	-0.06	0.09	N	0.32	1.0E-05	Y	0	0.50	N	0.24	1.0E-05	Y
ONECUT1	-0.14	4.7E-04	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
ARNTL2	-0.07	0.04	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF1	-0.31	1.0E-05	Y	0.31	1.0E-05	Y	-0.39	1.0E-05	Y	-	0.46	N
NFRKB	-0.17	2.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
TAF1	0.12	1.4E-03	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
PKNOX1	-0.29	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX11	-0.44	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
MYF6	-0.30	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS4	-0.13	9.4E-04	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
TP53BP1	-0.19	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
THRB	-0.35	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
MECP2	0.11	3.8E-03	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
PLAG1	-0.33	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
SIM2	0.02	0.28	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
MYF5	-0.12	1.9E-03	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
RELA	-0.11	3.1E-03	Y	0.29	1.0E-05	Y	-9.5E-	0.41	N	0.43	1.0E-05	Y
NFE2L1	-0.06	0.08	N	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
KDM2A	-0.27	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
RREB1	-0.21	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
SIRT1	0.13	1.3E-03	Y	0.29	1.0E-05	Y	-0.08	0.02	Y	-0.15	1.2E-04	Y
MLXIPL	0.04	0.17	N	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA1	-0.20	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
RELB	-0.25	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
BCL11B	0.02	0.31	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
FUS	-0.13	9.6E-04	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
SKIL	-0.20	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA1	-0.12	2.7E-03	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIC	-0.23	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
APEX1	-0.10	9.8E-03	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
POU1F1	-0.19	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
ETS2	-0.22	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0.76	1.0E-05	Y
SMARCA4	-0.30	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
MED23	-0.15	1.2E-04	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
RFX1	-0.18	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
TOB1	-0.05	0.10	N	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC5	0.12	2.2E-03	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
HCFC1	0.05	0.11	N	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
ANKRD1	0.18	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
TBX21	-0.12	2.0E-03	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N

LHX2	-0.32	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
SMAD4	-0.30	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
ERG	-0.03	0.24	N	0.26	1.0E-05	Y	0	0.50	N	0.90	1.0E-05	Y
ELF4	0.04	0.18	N	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB1	-0.32	1.0E-05	Y	0.25	1.0E-05	Y	0.08	0.03	N	0.55	1.0E-05	Y
IRF8	0.23	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
RBMX	0.13	6.0E-04	Y	0.25	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N
KLF12	-0.21	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
ING4	-0.24	1.0E-05	Y	0.25	1.0E-05	Y	-0.16	7.0E-05	Y	0	0.50	N
PRDM1	0.24	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOR2	0.09	0.01	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA4	0.16	5.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXN1	-0.15	1.3E-04	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID3A	-0.02	0.32	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
TEAD1	-0.32	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2C2	0.04	0.19	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
LHX4	-0.25	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
NAB2	-0.10	0.01	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARD	-0.14	4.9E-04	Y	0.23	1.0E-05	Y	0	0.50	N	0.62	1.0E-05	Y
SP1	-0.02	0.35	N	0.22	1.0E-05	Y	0.27	1.0E-05	Y	0.39	1.0E-05	Y
HDAC11	-0.01	0.43	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
PBX2	-0.15	1.3E-04	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
PDX1	-0.01	0.39	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ETV2	-0.31	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ILF2	0.03	0.22	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
IFI16	0.16	2.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
LRRFIP1	-0.17	4.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F3	-0.27	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
APBB1	-0.43	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2A	0.07	0.04	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
EN1	-0.25	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
DDIT3	-0.04	0.16	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIB	0.15	8.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
NR5A2	-0.33	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0.29	1.0E-05	Y
ELF1	0.21	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
LDB1	-0.25	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
TLX1	0.12	2.4E-03	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
E4F1	-0.02	0.28	N	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX3	-0.22	1.0E-05	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
HHEX	-0.11	3.1E-03	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
SP2	-0.16	6.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F7	-0.31	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
EIF2AK2	0.18	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP2B	-0.05	0.14	N	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF8	-0.28	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXF1	-0.27	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF2	0.25	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0.73	1.0E-05	Y
HIC1	0.18	1.0E-05	Y	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID1B	-0.22	1.0E-05	Y	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
PHOX2A	0.10	6.3E-03	Y	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
PARP1	0.04	0.15	N	0.17	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N
TCF4	-0.35	1.0E-05	Y	0.17	2.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N
TAF4	-0.03	0.26	N	0.17	2.0E-05	Y	0	0.50	N	0	0.50	N
CLOCK	-0.26	1.0E-05	Y	0.17	2.0E-05	Y	0	0.50	N	0.39	1.0E-05	Y
NRF1	-0.04	0.17	N	0.16	2.0E-05	Y	0	0.50	N	0	0.50	N
NR1H2	-0.15	2.1E-04	Y	0.16	4.0E-05	Y	0	0.50	N	0	0.50	N
TCF7L2	-0.29	1.0E-05	Y	0.16	4.0E-05	Y	0	0.50	N	0	0.50	N
NPM1	-0.14	3.3E-04	Y	0.16	4.0E-05	Y	0	0.50	N	0	0.50	N
HOXA5	-0.10	8.1E-03	Y	0.16	5.0E-05	Y	0	0.50	N	0	0.50	N
MSX2	0.12	2.4E-03	Y	0.16	5.0E-05	Y	0	0.50	N	0	0.50	N
GATA4	-0.13	9.3E-04	Y	0.16	5.0E-05	Y	-0.15	1.3E-04	Y	0	0.50	N
JUN	-0.20	1.0E-05	Y	0.15	8.0E-05	Y	-0.20	1.0E-05	Y	0.47	1.0E-05	Y
ERCC2	0.05	0.11	N	0.15	1.2E-04	Y	0	0.50	N	0	0.50	N
REST	-0.13	8.1E-04	Y	0.15	1.3E-04	Y	-0.59	1.0E-05	Y	-0.06	0.06	N
TFDP1	0.19	1.0E-05	Y	0.15	2.1E-04	Y	0.95	1.0E-05	Y	0	0.50	N

ETV5	0.15	2.1E-04	Y	0.15	2.1E-04	Y	0	0.50	N	0	0.50	N
DLX3	-0.06	0.09	N	0.14	2.4E-04	Y	0	0.50	N	0	0.50	N
EAPP	0.21	1.0E-05	Y	0.14	2.5E-04	Y	0	0.50	N	0	0.50	N
HIRA	-6.1E-	0.50	N	0.14	2.7E-04	Y	0	0.50	N	0	0.50	N
ESR1	-0.40	1.0E-05	Y	0.14	3.0E-04	Y	0.04	0.16	N	0.34	1.0E-05	Y
PRDM14	0.21	1.0E-05	Y	0.14	4.0E-04	Y	0	0.50	N	0	0.50	N
NR2F2	0.01	0.40	N	0.14	4.0E-04	Y	0	0.50	N	0	0.50	N
FOXP2	-0.37	1.0E-05	Y	0.13	6.2E-04	Y	0	0.50	N	0	0.50	N
AES	0.06	0.09	N	0.13	6.4E-04	Y	0	0.50	N	0	0.50	N
KLF3	0.15	1.2E-04	Y	0.13	6.7E-04	Y	0	0.50	N	0	0.50	N
MYOD1	-0.07	0.06	N	0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
IRF9	-0.19	1.0E-05	Y	0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
GBX2	-0.11	3.5E-03	Y	0.12	1.6E-03	Y	0	0.50	N	0	0.50	N
CEBPB	-0.02	0.29	N	0.12	1.9E-03	Y	-0.08	0.02	Y	0.44	1.0E-05	Y
BCL3	-0.11	4.7E-03	Y	0.12	2.1E-03	Y	0	0.50	N	0	0.50	N
CRX	0.01	0.42	N	0.12	2.1E-03	Y	0	0.50	N	0	0.50	N
FOXO1	-0.13	7.9E-04	Y	0.12	2.7E-03	Y	0	0.50	N	0	0.50	N
MTF1	-0.04	0.20	N	0.11	2.8E-03	Y	0	0.50	N	0	0.50	N
GTF2I	-0.24	1.0E-05	Y	0.11	3.8E-03	Y	0	0.50	N	0	0.50	N
BCL6	-0.01	0.41	N	0.11	4.0E-03	Y	-0.26	1.0E-05	Y	0	0.50	N
ETV3	0.03	0.23	N	0.11	4.4E-03	Y	0	0.50	N	0	0.50	N
HDAC10	0.03	0.20	N	0.11	5.2E-03	Y	0	0.50	N	0	0.50	N
SATB1	0.04	0.16	N	0.10	7.9E-03	Y	0	0.50	N	0	0.50	N
FOSB	-0.18	1.0E-05	Y	0.10	8.1E-03	Y	0	0.50	N	0	0.50	N
HDGF	0.04	0.14	N	0.10	8.6E-03	Y	0	0.50	N	0	0.50	N
NFYC	0.22	1.0E-05	Y	0.10	8.9E-03	Y	0	0.50	N	0	0.50	N
ELK3	0.02	0.30	N	0.10	0.01	Y	0	0.50	N	0	0.50	N
CDX2	0.03	0.24	N	0.10	0.01	Y	0	0.50	N	-	0.47	N
PHOX2B	0.21	1.0E-05	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
GTF3A	0.12	1.8E-03	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
PAX2	-0.40	1.0E-05	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
OTX2	-0.06	0.08	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
STAT5B	0.01	0.42	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
RFWD2	0.03	0.25	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
SF1	0.35	1.0E-05	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
HEXIM1	-0.20	1.0E-05	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
LYL1	0.08	0.04	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
E2F4	-0.06	0.07	N	0.08	0.04	N	0	0.50	N	-0.87	1.0E-05	Y
NPAS2	0.08	0.03	Y	0.07	0.04	N	0	0.50	N	0	0.50	N
GLI3	-0.03	0.25	N	0.07	0.05	N	0	0.50	N	0	0.50	N
NR2F6	-0.18	1.0E-05	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
AIP	0.07	0.05	N	0.07	0.05	N	0	0.50	N	0	0.50	N
RUNX2	0.24	1.0E-05	Y	0.07	0.05	N	0	0.50	N	0.66	1.0E-05	Y
PPARGC1	-0.18	2.0E-05	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
SUGP1	0.08	0.03	Y	0.07	0.06	N	0	0.50	N	0	0.50	N
SRCAP	-0.06	0.09	N	0.06	0.07	N	0	0.50	N	0	0.50	N
SP3	-0.08	0.03	Y	0.06	0.07	N	-0.03	0.22	N	0.32	1.0E-05	Y
STAT3	-0.27	1.0E-05	Y	0.06	0.07	N	0.10	6.3E-03	Y	0.52	1.0E-05	Y
SOX2	0.19	1.0E-05	Y	0.06	0.08	N	0.08	0.02	Y	-	0.46	N
ETV6	-0.31	1.0E-05	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
SIRT2	-0.05	0.13	N	0.06	0.08	N	0	0.50	N	0	0.50	N
L3MBTL1	-0.09	0.02	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
HAX1	-0.04	0.15	N	0.06	0.09	N	0	0.50	N	0	0.50	N
HNF4A	-0.29	1.0E-05	Y	0.06	0.09	N	0.13	1.1E-03	Y	-0.02	0.29	N
HOXC10	-0.22	1.0E-05	Y	0.05	0.10	N	0	0.50	N	0	0.50	N
IKZF1	0.18	1.0E-05	Y	0.05	0.10	N	0	0.50	N	0	0.50	N
GCM1	-0.02	0.34	N	0.05	0.11	N	0	0.50	N	0	0.50	N
ATF3	0.04	0.18	N	0.05	0.11	N	0.32	1.0E-05	Y	0	0.50	N
GATA6	-0.22	1.0E-05	Y	0.05	0.13	N	0	0.50	N	0	0.50	N
IRF7	0.19	1.0E-05	Y	0.04	0.15	N	0	0.50	N	0	0.50	N
KDM4C	0.37	1.0E-05	Y	0.04	0.18	N	0	0.50	N	0	0.50	N
IRF5	-0.12	1.9E-03	Y	0.04	0.19	N	0	0.50	N	0	0.50	N
MEIS1	0.07	0.06	N	0.04	0.19	N	0	0.50	N	0	0.50	N
NR4A2	0.35	1.0E-05	Y	0.04	0.20	N	0	0.50	N	0	0.50	N
KAT2B	2.7E-04	0.50	N	0.03	0.20	N	0	0.50	N	0	0.50	N

HOXB1	-0.13	9.6E-04	Y	0.03	0.20	N	0	0.50	N	0	0.50	N
OTX1	-0.33	1.0E-05	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
ING2	0.07	0.05	N	0.03	0.22	N	0	0.50	N	0	0.50	N
TFDP3	-3.0E-	0.47	N	0.03	0.22	N	0	0.50	N	0	0.50	N
MCM6	0.16	5.0E-05	Y	0.03	0.23	N	0	0.50	N	0	0.50	N
NR4A3	0.12	1.9E-03	Y	0.03	0.24	N	0	0.50	N	0	0.50	N
SMAD7	0.07	0.05	N	0.03	0.24	N	0	0.50	N	0	0.50	N
LMO3	-0.04	0.20	N	0.03	0.26	N	0	0.50	N	0	0.50	N
PITX2	-0.25	1.0E-05	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
POU2F1	-0.16	6.0E-05	Y	0.02	0.30	N	0	0.50	N	0.53	1.0E-05	Y
IRF2	0.14	3.5E-04	Y	0.02	0.31	N	0	0.50	N	0	0.50	N
NR2F1	-0.35	1.0E-05	Y	0.02	0.33	N	0	0.50	N	0	0.50	N
SALL4	-0.11	4.2E-03	Y	0.02	0.34	N	0	0.50	N	0	0.50	N
FOXQ1	-0.12	2.2E-03	Y	0.01	0.38	N	0	0.50	N	0	0.50	N
NCOA3	-0.04	0.19	N	6.0E-03	0.44	N	0	0.50	N	0	0.50	N
PCGF2	0.05	0.10	N	5.6E-03	0.44	N	0	0.50	N	0	0.50	N
BTAF1	0.21	1.0E-05	Y	5.1E-03	0.45	N	0	0.50	N	0	0.50	N
RARA	-0.10	9.7E-03	Y	-1.2E-	0.50	N	0	0.50	N	0.33	1.0E-05	Y
NR1I3	-0.11	5.0E-03	Y	-2.0E-	0.48	N	0	0.50	N	0	0.50	N
MAFB	0.03	0.22	N	-2.6E-	0.48	N	0	0.50	N	0	0.50	N
CTNNB1	-0.06	0.07	N	-3.3E-	0.47	N	0	0.50	N	0	0.50	N
ID1	0.17	2.0E-05	Y	-3.4E-	0.47	N	0	0.50	N	0	0.50	N
HLF	-0.13	9.4E-04	Y	-3.5E-	0.47	N	0	0.50	N	0	0.50	N
NR1H4	0.19	1.0E-05	Y	-3.9E-	0.46	N	0.28	1.0E-05	Y	0.37	1.0E-05	Y
NFYA	0.03	0.24	N	-0.01	0.41	N	0	0.50	N	0.45	1.0E-05	Y
EGR2	-0.02	0.28	N	-0.01	0.40	N	0	0.50	N	0	0.50	N
NR5A1	-0.26	1.0E-05	Y	-0.01	0.39	N	0	0.50	N	0.27	1.0E-05	Y
POU4F2	-0.24	1.0E-05	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
MSX1	0.04	0.20	N	-0.01	0.37	N	0	0.50	N	0	0.50	N
BTF3	0.07	0.04	Y	-0.02	0.36	N	-0.32	1.0E-05	Y	0	0.50	N
E2F8	-0.07	0.04	Y	-0.02	0.35	N	0	0.50	N	0	0.50	N
GFI1B	-0.26	1.0E-05	Y	-0.02	0.35	N	0	0.50	N	0	0.50	N
JDP2	0.01	0.37	N	-0.02	0.32	N	0	0.50	N	0	0.50	N
MAX	0.30	1.0E-05	Y	-0.02	0.31	N	0	0.50	N	0	0.50	N
RFX5	-0.02	0.28	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
SERTAD1	-0.24	1.0E-05	Y	-0.02	0.29	N	0	0.50	N	0	0.50	N
NR4A1	-0.12	2.6E-03	Y	-0.02	0.28	N	0	0.50	N	0	0.50	N
SMURF2	-0.21	1.0E-05	Y	-0.03	0.27	N	0	0.50	N	0	0.50	N
MYOG	0.08	0.03	Y	-0.03	0.26	N	0	0.50	N	0	0.50	N
POLR1A	0.12	1.8E-03	Y	-0.03	0.25	N	0	0.50	N	0	0.50	N
KLF13	0.15	2.2E-04	Y	-0.03	0.23	N	0	0.50	N	0	0.50	N
THRA	-0.19	1.0E-05	Y	-0.03	0.22	N	0	0.50	N	0	0.50	N
TEAD4	0.27	1.0E-05	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
STAT5A	-0.01	0.43	N	-0.04	0.20	N	0	0.50	N	0	0.50	N
NRL	0.01	0.41	N	-0.04	0.20	N	0	0.50	N	0	0.50	N
GABPA	-0.17	4.0E-05	Y	-0.04	0.19	N	0	0.50	N	0	0.50	N
TGIF1	-0.24	1.0E-05	Y	-0.04	0.18	N	0	0.50	N	0	0.50	N
RB1	0.07	0.04	Y	-0.04	0.16	N	-8.5E-	0.42	N	-0.58	1.0E-05	Y
ECD	0.16	5.0E-05	Y	-0.05	0.14	N	0	0.50	N	0	0.50	N
PAWR	0.06	0.09	N	-0.05	0.11	N	0	0.50	N	0	0.50	N
CITED2	-0.31	1.0E-05	Y	-0.05	0.10	N	0	0.50	N	0	0.50	N
HNF1A	-0.16	7.0E-05	Y	-0.06	0.10	N	0	0.50	N	0	0.50	N
SPIC	0.03	0.23	N	-0.06	0.09	N	0	0.50	N	0	0.50	N
TBPL1	0.02	0.28	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
SP4	-0.22	1.0E-05	Y	-0.06	0.08	N	0	0.50	N	0	0.50	N
NKX3-1	-0.01	0.38	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
GLI1	0.36	1.0E-05	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
PLAGL1	0.14	3.0E-04	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
PPARG	0.16	4.0E-05	Y	-0.06	0.07	N	-0.16	6.0E-05	Y	0.31	1.0E-05	Y
POU4F1	-0.14	6.5E-04	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
SOX4	-0.07	0.04	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
FOS	-0.06	0.08	N	-0.07	0.06	N	-0.04	0.15	N	0.48	1.0E-05	Y
DBP	-0.02	0.34	N	-0.07	0.06	N	0	0.50	N	0	0.50	N
SOX9	-2.0E-	0.48	N	-0.07	0.06	N	-0.13	6.6E-04	Y	0.25	1.0E-05	Y
TRERF1	-0.26	1.0E-05	Y	-0.07	0.05	N	-0.45	1.0E-05	Y	0	0.50	N

TBX5	-0.14	3.7E-04	Y	-0.07	0.05	N	0	0.50	N	0	0.50	N
SIX1	0.15	1.3E-04	Y	-0.07	0.05	N	0	0.50	N	0	0.50	N
HIF1A	-0.14	3.3E-04	Y	-0.07	0.05	N	0.28	1.0E-05	Y	0.50	1.0E-05	Y
AR	0.03	0.21	N	-0.07	0.04	N	-0.26	1.0E-05	Y	0.24	1.0E-05	Y
HLTF	0.04	0.19	N	-0.08	0.04	N	0	0.50	N	0	0.50	N
PITX1	0.23	1.0E-05	Y	-0.08	0.04	Y	-0.32	1.0E-05	Y	0	0.50	N
NHLH2	-0.03	0.22	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
CBX8	0.31	1.0E-05	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
SRY	-0.14	3.2E-04	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
ELL	-0.06	0.09	N	-0.08	0.02	Y	0	0.50	N	0	0.50	N
SOX17	-0.11	4.9E-03	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
MXI1	-0.16	6.0E-05	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
DEK	0.08	0.03	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
RXRA	-0.08	0.03	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
ID2	-0.21	1.0E-05	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
FOSL2	-0.17	2.0E-05	Y	-0.10	0.01	Y	0	0.50	N	0	0.50	N
STAT6	-0.19	1.0E-05	Y	-0.10	0.01	Y	0	0.50	N	0.59	1.0E-05	Y
RUNX1	-0.05	0.11	N	-0.10	9.2E-03	Y	0	0.50	N	0.25	1.0E-05	Y
ID4	-0.15	1.8E-04	Y	-0.10	7.1E-03	Y	0	0.50	N	0	0.50	N
RFX3	0.30	1.0E-05	Y	-0.10	6.6E-03	Y	0	0.50	N	0	0.50	N
NFATC2	-0.10	9.0E-03	Y	-0.10	6.6E-03	Y	0	0.50	N	0	0.50	N
JUND	-0.02	0.31	N	-0.11	5.4E-03	Y	0	0.50	N	0	0.50	N
NCOR1	-0.06	0.06	N	-0.11	4.3E-03	Y	0	0.50	N	0	0.50	N
NFIA	-0.31	1.0E-05	Y	-0.11	3.3E-03	Y	0	0.50	N	0	0.50	N
RUNX3	0.18	1.0E-05	Y	-0.11	2.8E-03	Y	0.12	2.2E-03	Y	-0.13	1.2E-03	Y
ATF1	0.15	8.0E-05	Y	-0.12	2.7E-03	Y	0	0.50	N	0.77	1.0E-05	Y
ISL1	0.20	1.0E-05	Y	-0.12	2.2E-03	Y	0	0.50	N	0	0.50	N
NFATC1	0.16	5.0E-05	Y	-0.12	2.0E-03	Y	0	0.50	N	0	0.50	N
MAF	-0.16	9.0E-05	Y	-0.12	2.0E-03	Y	0	0.50	N	0	0.50	N
CEBPA	-0.05	0.13	N	-0.12	1.8E-03	Y	0	0.50	N	0.25	1.0E-05	Y
ESR2	-0.06	0.09	N	-0.12	1.8E-03	Y	0	0.50	N	0	0.50	N
JUNB	0.25	1.0E-05	Y	-0.12	1.6E-03	Y	0	0.50	N	0	0.50	N
NFATC3	0.38	1.0E-05	Y	-0.12	1.5E-03	Y	0	0.50	N	0	0.50	N
ASCL1	-0.17	4.0E-05	Y	-0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
DLX5	0.09	0.01	Y	-0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
ATF4	0.19	1.0E-05	Y	-0.13	1.1E-03	Y	0.43	1.0E-05	Y	0.45	1.0E-05	Y
PIAS1	0.43	1.0E-05	Y	-0.13	1.0E-03	Y	0	0.50	N	0	0.50	N
NR1I2	-0.01	0.44	N	-0.13	9.8E-04	Y	0	0.50	N	0.38	1.0E-05	Y
FOXH1	0.29	1.0E-05	Y	-0.13	6.8E-04	Y	0	0.50	N	0	0.50	N
ATF6	0.07	0.05	N	-0.14	5.7E-04	Y	0	0.50	N	0	0.50	N
ARNTL	0.14	2.5E-04	Y	-0.14	4.9E-04	Y	0	0.50	N	0	0.50	N
CUX1	-0.23	1.0E-05	Y	-0.14	4.7E-04	Y	0	0.50	N	0	0.50	N
PITX3	0.10	7.9E-03	Y	-0.14	2.7E-04	Y	0	0.50	N	0	0.50	N
IRF3	0.19	1.0E-05	Y	-0.14	2.6E-04	Y	0	0.50	N	0	0.50	N
GZF1	-0.11	5.8E-03	Y	-0.15	2.2E-04	Y	0	0.50	N	0	0.50	N
FOXE1	0.02	0.28	N	-0.15	2.2E-04	Y	0	0.50	N	0	0.50	N
STAT4	0.12	2.1E-03	Y	-0.15	1.8E-04	Y	0	0.50	N	0	0.50	N
HAND2	-0.05	0.12	N	-0.15	1.8E-04	Y	0	0.50	N	0	0.50	N
CBX7	0.17	1.0E-05	Y	-0.15	1.7E-04	Y	0	0.50	N	0	0.50	N
MXD1	0.08	0.02	Y	-0.15	1.2E-04	Y	0	0.50	N	0	0.50	N
FOXM1	-0.02	0.28	N	-0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
RUVBL1	-0.07	0.06	N	-0.16	6.0E-05	Y	0	0.50	N	0	0.50	N
FOXO4	0.13	6.2E-04	Y	-0.16	6.0E-05	Y	0	0.50	N	0	0.50	N
HMGA2	0.01	0.40	N	-0.16	6.0E-05	Y	0	0.50	N	0	0.50	N
REL	-0.13	8.1E-04	Y	-0.16	6.0E-05	Y	0	0.50	N	0.45	1.0E-05	Y
PBX1	0.05	0.14	N	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
HOXA9	-0.02	0.30	N	-0.17	2.0E-05	Y	0	0.50	N	0	0.50	N
MLLT10	0.35	1.0E-05	Y	-0.17	2.0E-05	Y	0	0.50	N	0	0.50	N
MAML1	0.21	1.0E-05	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
MTA2	0.13	7.5E-04	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
PGR	0.04	0.15	N	-0.18	2.0E-05	Y	-0.11	4.2E-03	Y	0.60	1.0E-05	Y
EGR1	0.01	0.41	N	-0.18	1.0E-05	Y	0.30	1.0E-05	Y	0.44	1.0E-05	Y
FOXA2	-0.10	8.3E-03	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
PLAGL2	0.09	0.02	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS2	-0.16	6.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N

EP300	0.10	7.4E-03	Y	-0.18	1.0E-05	Y	0.33	1.0E-05	Y	0.17	1.0E-05	Y
SNAI1	-0.20	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
HR	0.07	0.06	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
ILF3	-0.09	0.01	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
MITF	0.09	0.01	Y	-0.19	1.0E-05	Y	0	0.50	N	0.73	1.0E-05	Y
NR0B2	0.22	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXF2	0.11	4.3E-03	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
TCF12	-0.13	8.1E-04	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
EHF	-0.03	0.25	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
MBD2	-0.12	1.8E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
NELFCD	-0.23	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
NPAS1	-0.21	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
NEUROD	-0.02	0.36	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX6	-0.10	7.7E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
MYOCD	0.17	2.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKBIB	0.17	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
DR1	0.22	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
EVX1	0.27	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
ATM	0.09	0.01	Y	-0.21	1.0E-05	Y	0.31	1.0E-05	Y	0.34	1.0E-05	Y
HMGA1	-0.25	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
PA2G4	-0.18	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KAT5	0.06	0.08	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
NUPR1	0.10	0.01	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
BCL11A	-0.14	3.9E-04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF15	0.32	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
RBBP7	0.11	3.2E-03	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
RARB	0.05	0.14	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ABL1	-0.05	0.12	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF2	-0.09	0.02	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ATRX	0.02	0.34	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
RBL1	0.36	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
IKBKB	0.23	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX4	0.29	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
HMGB2	-0.07	0.04	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
MKL1	-0.02	0.33	N	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF2	0.02	0.32	N	-0.23	1.0E-05	Y	0	0.50	N	0.29	1.0E-05	Y
FOXD3	0.27	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MSC	-0.08	0.03	Y	-0.24	1.0E-05	Y	0	0.50	N	-0.15	1.4E-04	Y
PAX8	0.48	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
GLI2	0.42	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0.63	1.0E-05	Y
SPDEF	-0.07	0.06	N	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
SUPT3H	-0.05	0.12	N	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
ATOH1	0.11	4.2E-03	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
PROX1	0.53	1.0E-05	Y	-0.24	1.0E-05	Y	0.17	1.0E-05	Y	0	0.50	N
BACH1	0.07	0.04	N	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
SETBP1	0.03	0.22	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
BHLHE41	0.22	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
FHL2	0.20	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA3	0.05	0.14	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXC1	0.07	0.04	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
SALL3	-0.04	0.15	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS3	0.23	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NELFB	-0.11	3.7E-03	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXA1	-0.11	4.0E-03	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2AF1	0.31	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC4	0.22	1.0E-05	Y	-0.26	1.0E-05	Y	-0.06	0.09	N	0	0.50	N
HOXC13	-0.16	6.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID1A	0.36	1.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
ERF	0.02	0.32	N	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA6	-0.12	1.9E-03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF6	0.27	1.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF9	2.1E-04	0.50	N	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP1	-0.02	0.36	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
ETS1	0.22	1.0E-05	Y	-0.27	1.0E-05	Y	-0.08	0.03	N	0.57	1.0E-05	Y
CREM	-0.16	6.0E-05	Y	-0.27	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N

CREB5	-0.09	0.01	Y	-0.27	1.0E-05	Y	-0.01	0.37	N	0	0.50	N
MED1	0.30	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
HOPX	0.20	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
PER1	0.04	0.14	N	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXG1	-0.02	0.30	N	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
PTMA	0.27	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCA1	-0.04	0.16	N	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
LEF1	-0.13	9.6E-04	Y	-0.29	1.0E-05	Y	-0.17	4.0E-05	Y	0.50	1.0E-05	Y
NRIP1	0.48	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2E3	-0.14	3.4E-04	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPG	0.29	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
CTCF	0.17	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	-0.04	0.17	N
TBX2	0.01	0.41	N	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ELK1	-8.0E-	0.49	N	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPD	-0.04	0.17	N	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF1	-0.10	6.6E-03	Y	-0.30	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N
CHD4	-0.13	9.1E-04	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ONECUT2	-0.11	4.2E-03	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
POU5F1	-0.10	7.6E-03	Y	-0.31	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N
AATF	0.20	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX5	0.37	1.0E-05	Y	-0.32	1.0E-05	Y	-0.03	0.23	N	0.49	1.0E-05	Y
SND1	0.15	1.2E-04	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF4	0.15	1.3E-04	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA7	0.26	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
CTBP1	0.15	8.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
SFPQ	0.37	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
ELK4	0.16	4.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX3	0.17	2.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT2	0.19	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
RAD51	0.02	0.35	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
MLLT3	0.04	0.16	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
LMX1B	0.25	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
EZH2	0.24	1.0E-05	Y	-0.34	1.0E-05	Y	-0.21	1.0E-05	Y	0.18	1.0E-05	Y
NFIX	-0.05	0.12	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
MYCN	0.02	0.33	N	-0.34	1.0E-05	Y	0.35	1.0E-05	Y	0.28	1.0E-05	Y
HES1	0.10	6.5E-03	Y	-0.35	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N
NR1H3	0.54	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKB2	-0.07	0.05	N	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA1	0.22	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
NR3C2	0.13	6.0E-04	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
SREBF2	0.15	7.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
TP53	0.09	0.02	Y	-0.36	1.0E-05	Y	0.25	1.0E-05	Y	-	0.49	N
NKX2-5	0.27	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
RORA	0.13	1.3E-03	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
DEAF1	-0.09	0.02	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
NF1	0.37	1.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX6	0.16	5.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPE	0.10	9.3E-03	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
MYB	-0.21	1.0E-05	Y	-0.37	1.0E-05	Y	0.28	1.0E-05	Y	0.73	1.0E-05	Y
TFAP2C	0.14	4.2E-04	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
CIITA	-0.02	0.35	N	-0.38	1.0E-05	Y	0	0.50	N	0.60	1.0E-05	Y
HSF2	0.24	1.0E-05	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
KHDRBS1	-0.26	1.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
HINFP	0.01	0.45	N	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF3	0.37	1.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3L	0.54	1.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
BARD1	0.02	0.31	N	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXC6	-0.18	1.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
MAFA	0.15	1.2E-04	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
NEUROG	0.26	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
PHB2	0.02	0.31	N	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
LMO2	0.25	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
HBP1	0.29	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
SP7	0.70	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
NFAT5	0.41	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N

LIMD1	0.31	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2F2	0.38	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
BRD7	0.31	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF11	-0.30	1.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX2-1	-0.06	0.08	N	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
RNF14	0.23	1.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
CREBBP	0.01	0.42	N	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
MYBL2	0.18	1.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCB1	0.13	1.2E-03	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
CDCA7L	-0.05	0.11	N	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3L1	0.24	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
HES6	-0.08	0.02	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
SRF	2.8E-03	0.47	N	-0.44	1.0E-05	Y	0	0.50	N	0.82	1.0E-05	Y
NFKBIA	-0.01	0.37	N	-0.45	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N
NR0B1	0.31	1.0E-05	Y	-0.45	1.0E-05	Y	-0.54	1.0E-05	Y	0	0.50	N
CREB3	0.19	1.0E-05	Y	-0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
SSB	0.24	1.0E-05	Y	-0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
FLI1	0.23	1.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0.42	1.0E-05	Y
PER2	0.12	2.2E-03	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF10	-0.02	0.32	N	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
MZF1	0.31	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
MYC	0.24	1.0E-05	Y	-0.47	1.0E-05	Y	0.39	1.0E-05	Y	0.35	1.0E-05	Y
EWSR1	-0.04	0.15	N	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXD9	-0.07	0.04	Y	-0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3A	0.07	0.04	Y	-0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
APC	0.14	3.2E-04	Y	-0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXB7	0.54	1.0E-05	Y	-0.49	1.0E-05	Y	0	0.50	N	0.57	1.0E-05	Y
KLF16	-0.03	0.26	N	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
KCNIP3	0.03	0.21	N	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
CBX6	-0.02	0.29	N	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKB1	-0.04	0.16	N	-0.50	1.0E-05	Y	-3.3E-	0.50	N	0.46	1.0E-05	Y
TFAP4	0.39	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2D	0.74	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC2	0.35	1.0E-05	Y	-0.50	1.0E-05	Y	-0.08	0.03	N	-0.45	1.0E-05	Y
TFCP2	0.77	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
SIN3A	0.37	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC3	0.19	1.0E-05	Y	-0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX2-2	0.17	2.0E-05	Y	-0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARA	0.02	0.28	N	-0.52	1.0E-05	Y	-0.22	1.0E-05	Y	0.59	1.0E-05	Y
COPS5	0.20	1.0E-05	Y	-0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
HTATIP2	0.08	0.03	Y	-0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
DLX4	0.40	1.0E-05	Y	-0.54	1.0E-05	Y	0	0.50	N	0	0.50	N
TAL1	0.03	0.21	N	-0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA1	0.36	1.0E-05	Y	-0.55	1.0E-05	Y	0	0.50	N	0.54	1.0E-05	Y
NR1D1	0.16	5.0E-05	Y	-0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP3	0.21	1.0E-05	Y	-0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
SLC2A4R	0.30	1.0E-05	Y	-0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
TCFL5	0.29	1.0E-05	Y	-0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA10	0.23	1.0E-05	Y	-0.59	1.0E-05	Y	0	0.50	N	0.13	1.2E-03	Y
GATA2	4.6E-03	0.45	N	-0.59	1.0E-05	Y	0	0.50	N	0	0.50	N
ING1	0.16	5.0E-05	Y	-0.59	1.0E-05	Y	0	0.50	N	0	0.50	N
RB1CC1	0.08	0.03	Y	-0.60	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2C	0.54	1.0E-05	Y	-0.60	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA11	0.09	0.01	Y	-0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
TNFAIP3	0.08	0.03	Y	-0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP2A	0.34	1.0E-05	Y	-0.64	1.0E-05	Y	-0.20	1.0E-05	Y	0.64	1.0E-05	Y
TCF3	0.04	0.16	N	-0.65	1.0E-05	Y	0	0.50	N	-0.23	1.0E-05	Y
HDAC7	0.56	1.0E-05	Y	-0.65	1.0E-05	Y	-0.67	1.0E-05	Y	0	0.50	N
SRSF1	0.18	1.0E-05	Y	-0.69	1.0E-05	Y	0	0.50	N	0	0.50	N
POU3F2	0.23	1.0E-05	Y	-0.70	1.0E-05	Y	0	0.50	N	0	0.50	N

Master list of TFs in TCGA colorectal cancer dataset together the correlation scores of their activity scores with PR signatures and enrichment scores of target genes with PR signatures

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
SERTAD1	-0.40	1.0E-05	Y	0.72	1.0E-05	Y	0	0.50	N	0	0.50	N
POLR1A	-0.20	1.0E-05	Y	0.71	1.0E-05	Y	0	0.50	N	0	0.50	N
LIMD1	-0.41	1.0E-05	Y	0.64	1.0E-05	Y	0	0.50	N	0	0.50	N
CDX1	-0.16	9.0E-05	Y	0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
KCNIP3	-0.47	1.0E-05	Y	0.60	1.0E-05	Y	0	0.50	N	0	0.50	N
BTG2	0.04	0.18	N	0.60	1.0E-05	Y	0	0.50	N	0	0.50	N
BTAF1	-0.11	4.4E-03	Y	0.58	1.0E-05	Y	0	0.50	N	0	0.50	N
ENO1	0.01	0.40	N	0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
CTCFL	-0.02	0.34	N	0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
AHR	-0.22	1.0E-05	Y	0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
MYOD1	-0.65	1.0E-05	Y	0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
TBP	-0.18	2.0E-05	Y	0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
NFYC	-0.29	1.0E-05	Y	0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF9	-0.32	1.0E-05	Y	0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
SKI	-0.21	1.0E-05	Y	0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRG	-0.02	0.31	N	0.52	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL1	-0.23	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
MAX	-0.29	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF6	-0.22	1.0E-05	Y	0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM2	-0.29	1.0E-05	Y	0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC1	-0.26	1.0E-05	Y	0.49	1.0E-05	Y	-0.40	1.0E-05	Y	-0.20	1.0E-05	Y
CEBPB	-0.21	1.0E-05	Y	0.49	1.0E-05	Y	0.13	1.5E-03	Y	0.08	0.02	Y
SPIB	-0.04	0.15	N	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
MBD2	-0.37	1.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
RB1	0.08	0.03	Y	0.48	1.0E-05	Y	-0.35	1.0E-05	Y	-0.49	1.0E-05	Y
PRDM1	-0.31	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXB13	0.04	0.16	N	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
ERG	-0.28	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0.76	1.0E-05	Y
SOX11	-0.12	2.0E-03	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
IFI16	-0.24	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
SND1	-0.24	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
CRABP2	-0.15	1.9E-04	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCB1	-0.36	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
CLOCK	-0.36	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0.08	0.04	Y
KDM4C	-0.39	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID3A	-0.21	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT2	-0.28	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARGC1A	-0.24	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM6	-0.45	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
SPIC	-0.19	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF5	-0.39	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
TRIB3	-0.30	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXM1	-0.36	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOR1	-0.30	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
SLC2A4RG	-0.17	6.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
TBX21	-0.33	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPZ	-0.46	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA4	-0.19	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
TP53BP1	-0.17	3.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
ETV4	-0.37	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0.52	1.0E-05	Y
PPARG	-0.31	1.0E-05	Y	0.39	1.0E-05	Y	-0.06	0.09	N	0.15	2.0E-04	Y
EAPP	0.06	0.07	N	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
SKIL	-0.20	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
EGR3	-0.35	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1H3	-0.35	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA2	-0.08	0.03	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA3	-0.28	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
DDB2	-0.01	0.38	N	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
MKL1	-0.37	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N

RBMX	-0.20	1.0E-05	Y	0.37	1.0E-05	Y	-0.68	1.0E-05	Y	0	0.50	N
POU2AF1	-0.56	1.0E-05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
SIX1	-0.15	2.7E-04	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
TP63	-0.07	0.05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
SFPQ	0.11	4.7E-03	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
TP73	-0.53	1.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
HIPK2	8.2E-03	0.42	N	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
EHMT2	-0.03	0.21	N	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
ARNTL	-0.07	0.04	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
SREBF2	-0.61	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIX	-0.08	0.02	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC9	-0.36	1.0E-05	Y	0.33	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N
PITX1	-0.07	0.04	Y	0.33	1.0E-05	Y	-0.70	1.0E-05	Y	0	0.50	N
HDAC10	-0.19	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
NR0B1	-0.05	0.12	N	0.33	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N
CREB1	-0.28	1.0E-05	Y	0.32	1.0E-05	Y	0.26	1.0E-05	Y	0.37	1.0E-05	Y
HOXC9	-0.01	0.38	N	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
CRTC1	-0.32	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
TLX1	-0.21	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
RFX5	0.11	3.8E-03	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF1	-0.39	1.0E-05	Y	0.31	1.0E-05	Y	-0.11	3.7E-03	Y	0.05	0.12	N
APBB1	-0.45	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA3	-0.04	0.16	N	0.31	1.0E-05	Y	-0.06	0.08	N	0.31	1.0E-05	Y
PLAG1	-0.29	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF4	-0.23	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
DLX3	0.01	0.37	N	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXO3	-0.42	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0.18	3.0E-05	Y
E2F6	-0.66	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF8	0.08	0.03	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
HNF4A	-0.26	1.0E-05	Y	0.29	1.0E-05	Y	0.03	0.20	N	-0.11	5.2E-03	Y
AES	0.02	0.35	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
RUNX1	-0.14	4.9E-04	Y	0.28	1.0E-05	Y	0	0.50	N	0.07	0.04	Y
LRRFIP1	-0.25	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIC	-0.41	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
TEF	-0.45	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL2	-0.30	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
HCFC1	0.16	8.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
ASCL1	-0.34	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
REL	0.14	3.9E-04	Y	0.27	1.0E-05	Y	0	0.50	N	0.42	1.0E-05	Y
STAT5B	-0.21	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
GLI1	-0.01	0.37	N	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
ESR1	-0.47	1.0E-05	Y	0.26	1.0E-05	Y	0.21	1.0E-05	Y	0.05	0.13	N
DDIT3	0.01	0.37	N	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
ETS2	-0.33	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0.55	1.0E-05	Y
TBX5	-0.32	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
LHX2	-0.27	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2F2	-0.31	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2D	-0.14	3.3E-04	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
HEY1	-0.26	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MDM4	-0.10	6.9E-03	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MED1	0.15	9.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
SP2	-0.21	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
TRERF1	-0.40	1.0E-05	Y	0.23	1.0E-05	Y	-0.66	1.0E-05	Y	0	0.50	N
STAT4	1.5E-03	0.49	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF1	0.13	7.9E-04	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
APC	-0.19	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT5A	-0.02	0.34	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
ID4	-0.54	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF4	-0.26	1.0E-05	Y	0.23	1.0E-05	Y	-0.45	1.0E-05	Y	0.16	8.0E-05	Y
ARNTL2	-0.23	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2E3	-0.08	0.03	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
HNF4G	-0.15	2.1E-04	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
CRX	-0.26	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2F2	-0.08	0.04	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
RARB	-0.24	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N

PAWR	0.14	2.9E-04	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF5	-0.11	3.3E-03	Y	0.22	1.0E-05	Y	0.88	1.0E-05	Y	0.44	1.0E-05	Y
E2F1	-0.57	1.0E-05	Y	0.22	1.0E-05	Y	0.62	1.0E-05	Y	-0.09	0.02	Y
PER1	-0.14	6.0E-04	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
POU5F1	-0.39	1.0E-05	Y	0.22	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N
EPAS1	0.02	0.32	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF15	-0.27	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
PURA	0.02	0.31	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
TFDP1	0.18	2.0E-05	Y	0.21	1.0E-05	Y	0.92	1.0E-05	Y	0	0.50	N
ATF2	0.24	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0.51	1.0E-05	Y
EIF2AK2	-0.22	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
MSX1	0.13	1.1E-03	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRA	-0.46	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
REST	-0.06	0.07	N	0.21	1.0E-05	Y	-0.50	1.0E-05	Y	-0.09	0.02	Y
NHLH2	0.11	4.2E-03	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
RELB	0.04	0.17	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
SMAD7	-0.15	1.9E-04	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
TAF4	-0.12	1.8E-03	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS1	-0.25	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
KAT5	-0.03	0.20	N	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
NFIL3	-0.15	2.8E-04	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
ELK3	0.10	7.7E-03	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
PHOX2B	0.08	0.04	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
NCOA3	-0.06	0.08	N	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
NRF1	-0.35	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
MEF2C	-0.20	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
NRIP1	0.11	5.2E-03	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
KLF13	-0.07	0.04	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
ARNT	-1.1E-03	0.49	N	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
SREBF1	-0.04	0.18	N	0.19	2.0E-05	Y	0.04	0.14	N	0	0.50	N
POU1F1	-0.16	9.0E-05	Y	0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
MTA2	0.03	0.25	N	0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
PIAS2	0.32	1.0E-05	Y	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
RUNX3	-0.13	1.2E-03	Y	0.18	3.0E-05	Y	-0.34	1.0E-05	Y	-0.03	0.26	N
NFIB	0.04	0.19	N	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
TOB1	-1.5E-03	0.49	N	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
NELFB	-0.21	1.0E-05	Y	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
RFX3	-0.11	3.0E-03	Y	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
RFX1	-0.11	4.5E-03	Y	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
APEX1	-0.35	1.0E-05	Y	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
HOPX	0.17	3.0E-05	Y	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
KHDRBS1	0.12	2.3E-03	Y	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
DNMT1	-0.34	1.0E-05	Y	0.16	6.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N
MED23	-0.15	2.7E-04	Y	0.16	6.0E-05	Y	0	0.50	N	0	0.50	N
GFI1	-0.28	1.0E-05	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
PROX1	-0.16	1.0E-04	Y	0.16	8.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N
LMX1B	-0.11	4.0E-03	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
FOXP2	-0.33	1.0E-05	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
MTA1	-0.05	0.12	N	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
MAF	-0.28	1.0E-05	Y	0.15	1.0E-04	Y	0	0.50	N	0	0.50	N
SATB2	0.11	5.3E-03	Y	0.15	1.3E-04	Y	0	0.50	N	0	0.50	N
FOSL1	-0.20	1.0E-05	Y	0.15	1.3E-04	Y	0	0.50	N	0	0.50	N
NPAS1	0.18	3.0E-05	Y	0.15	1.7E-04	Y	0	0.50	N	0	0.50	N
NCOA1	-0.14	3.7E-04	Y	0.15	2.0E-04	Y	0	0.50	N	0	0.50	N
DACH1	-0.23	1.0E-05	Y	0.14	2.9E-04	Y	0	0.50	N	0	0.50	N
LMO3	0.05	0.11	N	0.14	3.2E-04	Y	0	0.50	N	0	0.50	N
IRF2	-0.16	9.0E-05	Y	0.14	3.2E-04	Y	0	0.50	N	0	0.50	N
BCL6	-0.19	1.0E-05	Y	0.14	3.7E-04	Y	-0.33	1.0E-05	Y	0	0.50	N
TEAD1	-6.0E-03	0.44	N	0.14	3.9E-04	Y	0	0.50	N	0	0.50	N
SOX17	-0.48	1.0E-05	Y	0.14	3.9E-04	Y	0	0.50	N	0	0.50	N
RAD51	-0.06	0.07	N	0.14	5.2E-04	Y	0	0.50	N	0	0.50	N
MITF	-0.03	0.23	N	0.13	9.8E-04	Y	0	0.50	N	0.45	1.0E-05	Y
BACH1	-0.10	8.3E-03	Y	0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
HDAC5	0.16	8.0E-05	Y	0.12	1.7E-03	Y	0	0.50	N	0	0.50	N
MZF1	-0.27	1.0E-05	Y	0.12	1.8E-03	Y	0	0.50	N	0	0.50	N

FOSB	-0.28	1.0E-05	Y	0.12	2.0E-03	Y	0	0.50	N	0	0.50	N
SIN3A	0.23	1.0E-05	Y	0.12	2.5E-03	Y	0	0.50	N	0	0.50	N
TFAP2B	-0.19	1.0E-05	Y	0.12	2.7E-03	Y	0	0.50	N	0	0.50	N
AIP	-0.20	1.0E-05	Y	0.11	3.1E-03	Y	0	0.50	N	0	0.50	N
CBX8	0.29	1.0E-05	Y	0.11	3.4E-03	Y	0	0.50	N	0	0.50	N
LHX4	-0.05	0.12	N	0.11	3.4E-03	Y	0	0.50	N	0	0.50	N
L3MBTL1	-0.24	1.0E-05	Y	0.11	3.6E-03	Y	0	0.50	N	0	0.50	N
PAX4	-0.46	1.0E-05	Y	0.11	4.6E-03	Y	0	0.50	N	0	0.50	N
NR4A3	0.33	1.0E-05	Y	0.11	5.7E-03	Y	0	0.50	N	0	0.50	N
SMAD4	-0.51	1.0E-05	Y	0.10	6.0E-03	Y	0	0.50	N	0	0.50	N
ERCC2	0.20	2.0E-05	Y	0.10	6.0E-03	Y	0	0.50	N	0	0.50	N
ETV2	-0.27	1.0E-05	Y	0.10	6.7E-03	Y	0	0.50	N	0	0.50	N
JDP2	-0.22	1.0E-05	Y	0.10	7.6E-03	Y	0	0.50	N	0	0.50	N
E2F7	-0.02	0.36	N	0.10	8.6E-03	Y	0	0.50	N	0	0.50	N
STAT6	-0.24	1.0E-05	Y	0.10	8.8E-03	Y	0	0.50	N	0.26	1.0E-05	Y
GTF3A	-0.25	1.0E-05	Y	0.10	8.9E-03	Y	0	0.50	N	0	0.50	N
RBPJ	0.08	0.04	Y	0.10	9.2E-03	Y	0	0.50	N	0	0.50	N
SIM2	0.29	1.0E-05	Y	0.10	9.5E-03	Y	0	0.50	N	0	0.50	N
STAT3	0.08	0.04	Y	0.10	9.8E-03	Y	0.23	1.0E-05	Y	0.35	1.0E-05	Y
FOXH1	0.14	3.2E-04	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
FOXF1	-0.24	1.0E-05	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
TCF7L2	0.04	0.18	N	0.10	0.01	Y	0	0.50	N	0	0.50	N
NFKB1	-0.26	1.0E-05	Y	0.10	0.01	Y	0.12	2.6E-03	Y	0.36	1.0E-05	Y
DBP	-0.05	0.10	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
CDX2	-0.14	4.9E-04	Y	0.09	0.01	Y	0	0.50	N	0.08	0.03	Y
MYCN	-0.07	0.04	Y	0.09	0.02	Y	0.40	1.0E-05	Y	0.12	1.8E-03	Y
JUNB	-0.43	1.0E-05	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
DLX5	-0.02	0.31	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
SOX6	-0.09	0.02	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
MXI1	0.15	1.3E-04	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
ARID1A	0.09	0.01	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
ISL1	-0.22	1.0E-05	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
SRCAP	-0.05	0.10	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
RNF14	-9.0E-03	0.42	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
HOXB1	0.15	1.4E-04	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
HNF1A	-0.39	1.0E-05	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
FOXN1	-0.09	0.02	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
ETV3	-0.05	0.12	N	0.08	0.04	Y	0	0.50	N	0	0.50	N
FHL2	-0.17	3.0E-05	Y	0.07	0.04	Y	0	0.50	N	0	0.50	N
ETV6	-0.28	1.0E-05	Y	0.07	0.04	Y	0	0.50	N	0	0.50	N
THRA	-0.26	1.0E-05	Y	0.07	0.05	Y	0	0.50	N	0	0.50	N
BCL3	-0.09	0.02	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
SP3	-0.08	0.02	Y	0.07	0.05	N	0.12	2.3E-03	Y	0.03	0.20	N
ARID1B	-0.25	1.0E-05	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
PBX1	0.35	1.0E-05	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
HDGF	-0.04	0.18	N	0.07	0.06	N	0	0.50	N	0	0.50	N
CTNNB1	-0.12	1.9E-03	Y	0.07	0.06	N	0	0.50	N	0	0.50	N
NR2F6	0.16	8.0E-05	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
HOXC10	-0.23	1.0E-05	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
PAX2	-0.09	0.02	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
ESR2	0.04	0.16	N	0.06	0.07	N	0	0.50	N	0	0.50	N
E2F3	-0.20	1.0E-05	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
THRB	-0.12	2.6E-03	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
CITED2	-0.40	1.0E-05	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
SIRT2	0.24	1.0E-05	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
MECP2	0.34	1.0E-05	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
PLAGL1	-0.27	1.0E-05	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
NR5A2	-0.14	5.9E-04	Y	0.05	0.10	N	0	0.50	N	-0.03	0.25	N
SUPT3H	-0.05	0.10	N	0.05	0.10	N	0	0.50	N	0	0.50	N
PRDM14	0.33	1.0E-05	Y	0.05	0.11	N	0	0.50	N	0	0.50	N
RFWD2	0.02	0.36	N	0.05	0.11	N	0	0.50	N	0	0.50	N
FOXQ1	-0.05	0.13	N	0.05	0.12	N	0	0.50	N	0	0.50	N
TCF19	-0.48	1.0E-05	Y	0.05	0.13	N	0	0.50	N	0	0.50	N
GTF2I	-0.05	0.10	N	0.05	0.13	N	0	0.50	N	0	0.50	N
MAFA	0.19	2.0E-05	Y	0.05	0.14	N	0	0.50	N	0	0.50	N

ILF3	-0.22	1.0E-05	Y	0.04	0.17	N	0	0.50	N	0	0.50	N
LMO2	-0.30	1.0E-05	Y	0.04	0.17	N	0	0.50	N	0	0.50	N
PCGF2	0.14	2.9E-04	Y	0.04	0.18	N	0	0.50	N	0	0.50	N
OTX2	-0.30	1.0E-05	Y	0.04	0.19	N	0	0.50	N	0	0.50	N
NPM1	0.13	1.3E-03	Y	0.04	0.19	N	0	0.50	N	0	0.50	N
MLLT10	-0.08	0.02	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
MYOCD	0.05	0.11	N	0.03	0.24	N	0	0.50	N	0	0.50	N
SMARCA1	0.02	0.30	N	0.03	0.24	N	0	0.50	N	0	0.50	N
HEY2	-0.19	1.0E-05	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
CBX7	0.23	1.0E-05	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
GFI1B	-0.18	1.0E-05	Y	0.02	0.29	N	0	0.50	N	0	0.50	N
SETBP1	-0.09	0.02	Y	0.02	0.30	N	0	0.50	N	0	0.50	N
NFYB	-0.13	1.1E-03	Y	0.02	0.30	N	0	0.50	N	0	0.50	N
PITX2	0.40	1.0E-05	Y	0.02	0.31	N	0	0.50	N	0	0.50	N
E4F1	-0.02	0.28	N	0.02	0.31	N	0	0.50	N	0	0.50	N
NELFCD	0.20	2.0E-05	Y	0.02	0.32	N	0	0.50	N	0	0.50	N
GCM2	-0.03	0.24	N	0.02	0.32	N	0	0.50	N	0	0.50	N
SF1	-0.04	0.20	N	0.02	0.33	N	0	0.50	N	0	0.50	N
RB1CC1	-0.14	5.8E-04	Y	0.02	0.34	N	0	0.50	N	0	0.50	N
CEBPA	-0.26	1.0E-05	Y	0.01	0.37	N	0	0.50	N	-0.10	0.01	Y
SOX10	-0.03	0.21	N	0.01	0.38	N	0	0.50	N	0	0.50	N
DEK	-0.15	2.5E-04	Y	0.01	0.40	N	0	0.50	N	0	0.50	N
FOXD3	0.37	1.0E-05	Y	6.9E-03	0.43	N	0	0.50	N	0	0.50	N
ILF2	0.12	2.5E-03	Y	6.3E-03	0.44	N	0	0.50	N	0	0.50	N
KLF2	0.35	1.0E-05	Y	5.7E-03	0.45	N	0	0.50	N	0.18	3.0E-05	Y
TAF1	0.24	1.0E-05	Y	4.3E-03	0.46	N	0	0.50	N	0	0.50	N
RUNX2	-0.13	1.1E-03	Y	2.6E-03	0.48	N	0	0.50	N	0.60	1.0E-05	Y
CTBP1	-0.10	8.9E-03	Y	2.1E-03	0.48	N	0	0.50	N	0	0.50	N
GATA4	0.17	3.0E-05	Y	1.1E-03	0.49	N	0.15	1.1E-04	Y	0	0.50	N
SPI1	0.08	0.02	Y	5.1E-04	0.50	N	0	0.50	N	0.53	1.0E-05	Y
SATB1	-0.17	5.0E-05	Y	2.4E-05	0.50	N	0	0.50	N	0	0.50	N
PKNOX1	0.03	0.27	N	-5.4E-04	0.49	N	0	0.50	N	0	0.50	N
SOX3	0.34	1.0E-05	Y	-1.7E-03	0.48	N	0	0.50	N	0	0.50	N
GCM1	-0.05	0.13	N	-2.8E-03	0.47	N	0	0.50	N	0	0.50	N
NFIA	0.28	1.0E-05	Y	-4.5E-03	0.46	N	0	0.50	N	0	0.50	N
MAFB	0.02	0.30	N	-6.6E-03	0.44	N	0	0.50	N	0	0.50	N
HDAC4	0.08	0.02	Y	-7.5E-03	0.43	N	-0.33	1.0E-05	Y	0	0.50	N
HDAC11	0.26	1.0E-05	Y	-8.1E-03	0.42	N	0	0.50	N	0	0.50	N
TFDP3	-7.6E-03	0.43	N	-0.01	0.40	N	0	0.50	N	0	0.50	N
NR1I2	0.32	1.0E-05	Y	-0.01	0.37	N	0	0.50	N	0.26	1.0E-05	Y
NR1D1	0.11	3.5E-03	Y	-0.02	0.34	N	0	0.50	N	0	0.50	N
ATRX	-0.05	0.10	N	-0.02	0.33	N	0	0.50	N	0	0.50	N
PITX3	-0.30	1.0E-05	Y	-0.02	0.31	N	0	0.50	N	0	0.50	N
SSB	-0.03	0.27	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
ECD	0.14	2.6E-04	Y	-0.03	0.27	N	0	0.50	N	0	0.50	N
HES1	0.08	0.02	Y	-0.03	0.26	N	-0.37	1.0E-05	Y	0	0.50	N
CUX1	-0.20	1.0E-05	Y	-0.03	0.25	N	0	0.50	N	0	0.50	N
POU4F2	-0.09	0.01	Y	-0.03	0.25	N	0	0.50	N	0	0.50	N
EN1	0.21	1.0E-05	Y	-0.03	0.24	N	0	0.50	N	0	0.50	N
GBX2	-0.02	0.28	N	-0.03	0.23	N	0	0.50	N	0	0.50	N
HIC1	0.02	0.36	N	-0.03	0.22	N	0	0.50	N	0	0.50	N
HSF4	0.17	3.0E-05	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
ANKRD1	0.12	2.9E-03	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
MLXIPL	0.25	1.0E-05	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
NFATC3	0.28	1.0E-05	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
MYF5	0.02	0.28	N	-0.04	0.19	N	0	0.50	N	0	0.50	N
ATM	0.15	8.0E-05	Y	-0.04	0.19	N	-0.02	0.33	N	0.23	1.0E-05	Y
RUVBL1	0.39	1.0E-05	Y	-0.04	0.18	N	0	0.50	N	0	0.50	N
HOXD9	-0.03	0.21	N	-0.04	0.15	N	0	0.50	N	0	0.50	N
ATF1	0.08	0.03	Y	-0.04	0.15	N	0	0.50	N	0.58	1.0E-05	Y
NR1I3	0.23	1.0E-05	Y	-0.05	0.14	N	0	0.50	N	0	0.50	N
RBL2	0.23	1.0E-05	Y	-0.05	0.14	N	0	0.50	N	0	0.50	N
JUND	0.29	1.0E-05	Y	-0.05	0.13	N	0	0.50	N	0	0.50	N
SHOX	0.01	0.40	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
FOXO4	0.17	6.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N

SALL3	-0.20	1.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
HAX1	-0.11	3.6E-03	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
SP1	0.29	1.0E-05	Y	-0.05	0.10	N	0.32	1.0E-05	Y	0.32	1.0E-05	Y
KLF16	0.02	0.29	N	-0.05	0.10	N	0	0.50	N	0	0.50	N
HOXA5	-0.03	0.21	N	-0.05	0.10	N	0	0.50	N	0	0.50	N
LEF1	0.09	0.01	Y	-0.06	0.09	N	-0.10	7.0E-03	Y	0.07	0.04	N
EGR2	-0.02	0.29	N	-0.06	0.09	N	0	0.50	N	0	0.50	N
NR3C2	0.29	1.0E-05	Y	-0.06	0.09	N	0	0.50	N	0	0.50	N
TEAD4	0.35	1.0E-05	Y	-0.06	0.08	N	0	0.50	N	0	0.50	N
BCL11B	-8.5E-04	0.49	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
ELL	-0.28	1.0E-05	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
RELA	-0.26	1.0E-05	Y	-0.06	0.07	N	0.10	8.1E-03	Y	0.33	1.0E-05	Y
FUS	-0.03	0.27	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
NFATC2	0.30	1.0E-05	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
AR	0.20	2.0E-05	Y	-0.07	0.06	N	-0.23	1.0E-05	Y	0.28	1.0E-05	Y
ELK4	-0.06	0.08	N	-0.07	0.05	N	0	0.50	N	0	0.50	N
GLI2	0.36	1.0E-05	Y	-0.07	0.05	N	0	0.50	N	0.10	7.7E-03	Y
TBX2	-0.08	0.03	Y	-0.07	0.05	Y	0	0.50	N	0	0.50	N
NPAS2	-0.03	0.26	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
GLI3	0.07	0.05	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
NFAT5	0.22	1.0E-05	Y	-0.07	0.04	Y	0	0.50	N	0	0.50	N
PLAGL2	0.27	1.0E-05	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
TCF4	-0.17	4.0E-05	Y	-0.08	0.02	Y	0.14	3.2E-04	Y	0	0.50	N
HHEX	0.17	3.0E-05	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
SNAI2	0.04	0.15	N	-0.08	0.02	Y	-0.18	1.0E-05	Y	0.46	1.0E-05	Y
CTCF	-0.10	5.9E-03	Y	-0.08	0.02	Y	0	0.50	N	-0.48	1.0E-05	Y
HOXC13	-0.25	1.0E-05	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
ETS1	0.05	0.12	N	-0.09	0.02	Y	0.17	6.0E-05	Y	0.34	1.0E-05	Y
NR3C1	0.16	7.0E-05	Y	-0.09	0.02	Y	-0.06	0.09	N	-0.06	0.09	N
NKX2-1	-0.05	0.14	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
SNAI1	-0.04	0.16	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
NAB2	0.14	5.6E-04	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
MBD1	0.27	1.0E-05	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
NR5A1	0.10	1.0E-02	Y	-0.09	0.01	Y	0	0.50	N	0.07	0.04	N
GATA6	-0.25	1.0E-05	Y	-0.10	9.8E-03	Y	0	0.50	N	0	0.50	N
NFYA	0.12	2.6E-03	Y	-0.10	9.7E-03	Y	0	0.50	N	0.36	1.0E-05	Y
PML	0.17	6.0E-05	Y	-0.10	8.7E-03	Y	0	0.50	N	0.32	1.0E-05	Y
ING4	0.15	2.1E-04	Y	-0.10	7.2E-03	Y	0.08	0.02	N	0	0.50	N
IRF3	0.09	0.02	Y	-0.11	5.0E-03	Y	0	0.50	N	0	0.50	N
NFE2L2	0.36	1.0E-05	Y	-0.11	3.7E-03	Y	0	0.50	N	0.14	2.6E-04	Y
NCOR2	-7.7E-03	0.43	N	-0.11	3.1E-03	Y	0	0.50	N	0	0.50	N
HDAC2	0.31	1.0E-05	Y	-0.11	3.0E-03	Y	-0.51	1.0E-05	Y	-0.57	1.0E-05	Y
ELF3	0.19	2.0E-05	Y	-0.11	3.0E-03	Y	0	0.50	N	0	0.50	N
ATF4	-0.11	4.4E-03	Y	-0.12	1.7E-03	Y	0.58	1.0E-05	Y	0.42	1.0E-05	Y
PAX3	-0.31	1.0E-05	Y	-0.12	1.7E-03	Y	0	0.50	N	0	0.50	N
HMGA1	-0.15	2.7E-04	Y	-0.12	1.6E-03	Y	0	0.50	N	0	0.50	N
MYOG	-0.06	0.08	N	-0.12	1.6E-03	Y	0	0.50	N	0	0.50	N
PAX6	0.55	1.0E-05	Y	-0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
PPARA	-0.20	1.0E-05	Y	-0.13	1.1E-03	Y	-0.45	1.0E-05	Y	0.09	0.01	Y
MCM4	-0.10	8.3E-03	Y	-0.13	9.9E-04	Y	0	0.50	N	0	0.50	N
NF1	-0.02	0.33	N	-0.13	9.4E-04	Y	0	0.50	N	0	0.50	N
NR4A2	0.06	0.07	N	-0.13	9.2E-04	Y	0	0.50	N	0	0.50	N
EP300	0.04	0.19	N	-0.13	7.6E-04	Y	0.33	1.0E-05	Y	0.16	8.0E-05	Y
TBX3	0.25	1.0E-05	Y	-0.14	5.8E-04	Y	0	0.50	N	0	0.50	N
HLF	-0.17	6.0E-05	Y	-0.14	5.1E-04	Y	0	0.50	N	0	0.50	N
MAZ	-0.12	1.5E-03	Y	-0.14	5.0E-04	Y	0	0.50	N	0	0.50	N
MTF1	0.16	8.0E-05	Y	-0.14	4.9E-04	Y	0	0.50	N	0	0.50	N
FOXF2	0.22	1.0E-05	Y	-0.14	4.6E-04	Y	0	0.50	N	0	0.50	N
ONECUT2	0.14	2.5E-04	Y	-0.14	4.3E-04	Y	0	0.50	N	0	0.50	N
IKZF1	0.19	2.0E-05	Y	-0.14	4.0E-04	Y	0	0.50	N	0	0.50	N
FOXA2	-0.03	0.27	N	-0.14	3.7E-04	Y	0	0.50	N	0	0.50	N
TCF12	-0.17	5.0E-05	Y	-0.14	3.4E-04	Y	0	0.50	N	0	0.50	N
SMARCA4	-0.19	1.0E-05	Y	-0.14	3.3E-04	Y	0	0.50	N	0	0.50	N
SUGP1	0.14	3.9E-04	Y	-0.14	3.2E-04	Y	0	0.50	N	0	0.50	N
FOSL2	0.17	6.0E-05	Y	-0.14	3.1E-04	Y	0	0.50	N	0	0.50	N

PAX5	0.20	2.0E-05	Y	-0.15	2.7E-04	Y	-0.07	0.04	N	0.20	2.0E-05	Y
DR1	0.05	0.10	N	-0.15	2.5E-04	Y	0	0.50	N	0	0.50	N
ELF2	-0.15	2.8E-04	Y	-0.15	1.6E-04	Y	0	0.50	N	0	0.50	N
NUPR1	0.17	6.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
PIAS3	-0.24	1.0E-05	Y	-0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
FOXE1	-0.01	0.39	N	-0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
FOS	-0.17	4.0E-05	Y	-0.17	6.0E-05	Y	-0.14	4.9E-04	Y	0.28	1.0E-05	Y
KDM2A	0.11	5.2E-03	Y	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
FOXC1	0.15	8.0E-05	Y	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
SMAD3	0.29	1.0E-05	Y	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
NRL	0.34	1.0E-05	Y	-0.17	4.0E-05	Y	0	0.50	N	0	0.50	N
KLF10	-0.30	1.0E-05	Y	-0.17	4.0E-05	Y	0	0.50	N	0	0.50	N
TBPL1	-2.4E-04	0.50	N	-0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
SP7	0.09	0.01	Y	-0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
HR	0.21	1.0E-05	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
SOX9	0.23	1.0E-05	Y	-0.18	2.0E-05	Y	0.18	2.0E-05	Y	0.10	7.3E-03	Y
HIF1A	-0.08	0.03	Y	-0.18	2.0E-05	Y	0.34	1.0E-05	Y	0.29	1.0E-05	Y
NOTCH3	0.15	2.0E-04	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
PPARD	-0.12	2.0E-03	Y	-0.18	1.0E-05	Y	0	0.50	N	0.06	0.09	N
TFAP2C	-0.10	6.3E-03	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
CREBBP	-0.18	1.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2C2	0.17	5.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
EVX1	0.32	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF4	0.29	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX2	0.15	8.0E-05	Y	-0.19	1.0E-05	Y	0.32	1.0E-05	Y	-0.28	1.0E-05	Y
E2F4	-0.14	5.3E-04	Y	-0.19	1.0E-05	Y	0	0.50	N	-0.66	1.0E-05	Y
MYC	0.08	0.02	Y	-0.19	1.0E-05	Y	0.46	1.0E-05	Y	0.28	1.0E-05	Y
IRF8	0.10	7.1E-03	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
OTX1	0.15	2.0E-04	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPE	-0.11	4.3E-03	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
IKBKB	0.34	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2A	0.13	7.5E-04	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF3	0.29	1.0E-05	Y	-0.20	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N
ETV5	0.02	0.33	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
BCL11A	-0.23	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
RBL1	-0.02	0.30	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA9	-0.03	0.26	N	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
NR4A1	-0.15	2.7E-04	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
SPEN	-0.04	0.16	N	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
PER2	-0.12	2.1E-03	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF7	0.32	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF12	-0.28	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
RARG	9.9E-03	0.41	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
POU3F2	0.09	0.01	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HBP1	0.39	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ING2	0.20	2.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF6	0.14	5.0E-04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
NEUROG3	0.15	1.3E-04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HLTF	-0.24	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
FLI1	0.15	2.0E-04	Y	-0.23	1.0E-05	Y	0	0.50	N	0.38	1.0E-05	Y
ID2	0.21	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1H4	0.20	1.0E-05	Y	-0.23	1.0E-05	Y	0.51	1.0E-05	Y	4.8E-03	0.45	N
NR2F1	0.35	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
BTF3	0.41	1.0E-05	Y	-0.24	1.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N
ATOH1	0.39	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
PDX1	-0.08	0.03	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
PTTG1	0.40	1.0E-05	Y	-0.24	1.0E-05	Y	0.14	2.9E-04	Y	0.50	1.0E-05	Y
MAFF	0.19	2.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MYBL2	0.21	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
HINFP	0.02	0.28	N	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF9	0.24	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
HEXIM1	-0.07	0.05	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NFE2L1	0.11	3.7E-03	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
PA2G4	0.01	0.40	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
HAND2	0.02	0.30	N	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N

HOXB7	0.50	1.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0.21	1.0E-05	Y
KLF3	0.13	1.3E-03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPG	0.52	1.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
RXRA	0.17	3.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
MYB	0.08	0.03	Y	-0.26	1.0E-05	Y	0.24	1.0E-05	Y	0.49	1.0E-05	Y
NR1H2	-0.13	9.5E-04	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
HMGB2	0.14	2.7E-04	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX3-1	0.41	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC3	0.17	3.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
MAML1	0.25	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F8	0.05	0.11	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
DLX4	0.30	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
GABPA	-0.02	0.31	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
MEIS1	0.43	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
ABL1	-0.05	0.10	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF11	-0.27	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3L	0.59	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
CDCA7L	-0.20	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
PARP1	-0.06	0.08	N	-0.28	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N
CEBPD	0.04	0.19	N	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
HIRA	0.30	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
ONECUT1	0.06	0.08	N	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXA1	0.10	9.4E-03	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
NEUROD1	-0.21	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
TGIF1	-0.10	5.8E-03	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF5	-0.15	2.5E-04	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
BARD1	-0.05	0.10	N	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
SIRT1	0.35	1.0E-05	Y	-0.29	1.0E-05	Y	-0.19	1.0E-05	Y	-0.43	1.0E-05	Y
EGR1	0.19	2.0E-05	Y	-0.30	1.0E-05	Y	0.14	4.5E-04	Y	0.26	1.0E-05	Y
JUN	0.11	3.5E-03	Y	-0.30	1.0E-05	Y	0.03	0.22	N	0.30	1.0E-05	Y
PTMA	0.50	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
TAL1	0.19	2.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
SALL4	0.24	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
ID1	0.36	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
SRSF1	0.04	0.16	N	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX8	0.28	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
KAT2B	-4.9E-03	0.45	N	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
SPDEF	0.50	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
LMO4	0.32	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
BHLHE41	0.34	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA1	0.09	0.01	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
SRF	0.26	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0.71	1.0E-05	Y
PHOX2A	-0.07	0.05	N	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
SP4	0.08	0.02	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3	0.13	1.5E-03	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
BRD7	0.46	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
ERF	0.07	0.04	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF2	0.19	2.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
MSC	0.12	1.9E-03	Y	-0.33	1.0E-05	Y	0	0.50	N	0.16	8.0E-05	Y
MSX2	0.13	1.3E-03	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
NFATC1	0.13	7.9E-04	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP4	0.34	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
TFCP2	0.71	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
NANOG	0.22	1.0E-05	Y	-0.34	1.0E-05	Y	0.05	0.13	N	0	0.50	N
POU2F1	0.33	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0.33	1.0E-05	Y
FOXO1	-8.3E-04	0.49	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
SMURF2	-0.04	0.16	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
ELK1	-0.15	1.1E-04	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3L1	0.13	6.4E-04	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
DEAF1	0.12	2.1E-03	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
MXD1	0.31	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
HMGA2	0.09	0.02	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
PBX2	0.18	2.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
RARA	7.8E-04	0.49	N	-0.36	1.0E-05	Y	0	0.50	N	0.28	1.0E-05	Y
NKX2-5	-0.03	0.24	N	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N

NKX2-2	-0.16	1.0E-04	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
EWSR1	-0.13	1.3E-03	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
CREM	0.17	6.0E-05	Y	-0.38	1.0E-05	Y	-0.62	1.0E-05	Y	0	0.50	N
EHF	-0.04	0.15	N	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP1	-0.10	7.4E-03	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXG1	0.02	0.30	N	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
MLLT3	0.25	1.0E-05	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS4	0.18	3.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
EZH2	0.39	1.0E-05	Y	-0.39	1.0E-05	Y	-0.29	1.0E-05	Y	-0.02	0.29	N
ING1	0.38	1.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
NR0B2	0.32	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB5	0.16	8.0E-05	Y	-0.40	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N
HDAC7	0.54	1.0E-05	Y	-0.40	1.0E-05	Y	-0.73	1.0E-05	Y	0	0.50	N
AATF	0.19	2.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
MYF6	0.42	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
HES6	0.29	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXC6	-0.17	4.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
GZF1	0.12	2.5E-03	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKBIB	-0.17	6.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
TP53	0.21	1.0E-05	Y	-0.41	1.0E-05	Y	-5.0E-	0.49	N	-0.07	0.05	N
DNMT3A	-0.13	8.9E-04	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
PGR	0.14	3.0E-04	Y	-0.42	1.0E-05	Y	-0.05	0.12	N	0.31	1.0E-05	Y
HOXA10	0.29	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	-0.35	1.0E-05	Y
TCF3	-0.05	0.12	N	-0.43	1.0E-05	Y	0	0.50	N	-0.43	1.0E-05	Y
MEN1	0.83	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
HTATIP2	0.20	2.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA6	0.34	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKB2	-7.3E-03	0.43	N	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
LYL1	0.23	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
RBBP7	-0.07	0.05	N	-0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
CHD4	0.02	0.28	N	-0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT1	0.20	2.0E-05	Y	-0.46	1.0E-05	Y	-0.22	1.0E-05	Y	0.44	1.0E-05	Y
LDB1	-0.12	1.7E-03	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
PHB2	0.28	1.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX4	0.50	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
KAT6A	0.17	6.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
NFRKB	0.29	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF1	0.22	1.0E-05	Y	-0.49	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N
CIITA	0.20	2.0E-05	Y	-0.49	1.0E-05	Y	0	0.50	N	0.53	1.0E-05	Y
RORA	0.38	1.0E-05	Y	-0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP2A	0.31	1.0E-05	Y	-0.51	1.0E-05	Y	-0.15	1.6E-04	Y	0.49	1.0E-05	Y
LHX3	0.08	0.03	Y	-0.52	1.0E-05	Y	0	0.50	N	0	0.50	N
TNFAIP3	-0.12	2.3E-03	Y	-0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
RREB1	0.29	1.0E-05	Y	-0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
COPS5	0.40	1.0E-05	Y	-0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA11	0.09	0.01	Y	-0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP3	0.23	1.0E-05	Y	-0.55	1.0E-05	Y	0	0.50	N	0	0.50	N
CBX6	-0.01	0.40	N	-0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA1	0.42	1.0E-05	Y	-0.57	1.0E-05	Y	0	0.50	N	0.37	1.0E-05	Y
HOXA7	0.31	1.0E-05	Y	-0.59	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKBIA	0.29	1.0E-05	Y	-0.60	1.0E-05	Y	-0.67	1.0E-05	Y	0	0.50	N
TCFL5	0.24	1.0E-05	Y	-0.63	1.0E-05	Y	0	0.50	N	0	0.50	N
POU4F1	0.13	1.0E-03	Y	-0.63	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA2	0.09	0.02	Y	-0.64	1.0E-05	Y	0	0.50	N	0	0.50	N
SRY	0.28	1.0E-05	Y	-0.71	1.0E-05	Y	0	0.50	N	0	0.50	N

Master list of TFs in TCGA breast cancer dataset together the correlation scores of their activity scores with PR signatures and enrichment scores of target genes with PR signatures

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
SREBF2	-0.68	1.0E-05	Y	0.67	1.0E-05	Y	0.10	8.5E-03	Y	0	0.50	N
DDB2	-0.31	1.0E-05	Y	0.66	1.0E-05	Y	0	0.50	N	0	0.50	N
SIRT2	-0.36	1.0E-05	Y	0.63	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2D	-0.36	1.0E-05	Y	0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
LIMD1	-0.41	1.0E-05	Y	0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F6	-0.76	1.0E-05	Y	0.54	1.0E-05	Y	0	0.50	N	0	0.50	N
TBP	-0.68	1.0E-05	Y	0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXM1	-0.51	1.0E-05	Y	0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
GFI1	-0.52	1.0E-05	Y	0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
CTCFL	-0.35	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARA	-0.45	1.0E-05	Y	0.48	1.0E-05	Y	-0.65	1.0E-05	Y	0.32	1.0E-05	Y
TCF19	-0.72	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
SKI	-0.23	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM2	-0.36	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
CDX1	-0.17	6.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
HEY2	-0.31	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM6	-0.64	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP2B	-0.19	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
CRTC1	-0.49	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
RNF14	-0.33	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA4	-0.34	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
MBD2	-0.34	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
POLR1A	-0.17	3.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXO3	-0.21	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0.04	0.19	N
NR2F2	-0.40	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
ELK3	-0.07	0.06	N	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
SETBP1	-0.32	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
TP63	-0.34	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF8	-0.15	1.0E-04	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT1	-0.47	1.0E-05	Y	0.44	1.0E-05	Y	-0.05	0.13	N	0	0.50	N
HDAC9	-0.34	1.0E-05	Y	0.43	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N
STAT5B	-0.32	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
APEX1	-0.23	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0.26	1.0E-05	Y
NFYC	-0.01	0.39	N	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
CTCF	-0.08	0.03	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX11	-0.33	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
ENO1	-0.22	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
TRIB3	-0.31	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRA	-0.62	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
SERTAD1	-0.34	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
SPIB	-0.04	0.15	N	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
SMAD4	-0.57	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL1	-0.04	0.18	N	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF5	-0.33	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
SIX1	-0.06	0.07	N	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
PER1	-0.35	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
DACH1	-0.41	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
ARNTL2	-0.29	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
ETS2	-0.30	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0.51	1.0E-05	Y
PIAS1	-0.32	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
AHR	-0.20	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
RBMX	0.08	0.04	Y	0.38	1.0E-05	Y	-0.62	1.0E-05	Y	0	0.50	N
HDAC1	-0.20	1.0E-05	Y	0.38	1.0E-05	Y	-0.45	1.0E-05	Y	-0.15	2.1E-04	Y
EIF2AK2	-0.12	2.7E-03	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX4	-0.18	2.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
PURA	-0.35	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARGC1	-0.37	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
EGR3	-0.08	0.03	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N

AES	-0.26	1.0E-05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
PLAGL1	-0.62	1.0E-05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
SLC2A4R	-0.12	2.1E-03	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
MAF	-0.09	0.02	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F1	-0.75	1.0E-05	Y	0.36	1.0E-05	Y	0.61	1.0E-05	Y	0.12	1.8E-03	Y
ESRRG	-0.12	2.5E-03	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
HIPK2	0.06	0.08	N	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
JUNB	-0.41	1.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPZ	-0.17	4.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
ERG	0.04	0.18	N	0.34	1.0E-05	Y	0	0.50	N	0.55	1.0E-05	Y
THRB	0.01	0.38	N	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF9	0.08	0.03	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
NR0B1	-0.10	7.0E-03	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
MKL1	-0.17	3.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
ETV3	-0.16	1.0E-04	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF4	-0.20	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1H3	-0.10	8.6E-03	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXN1	-0.36	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXC9	0.05	0.10	N	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
REST	-0.07	0.04	Y	0.32	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N
POU5F1	-0.36	1.0E-05	Y	0.32	1.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N
NFYB	-0.12	1.4E-03	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
TFDP1	-0.14	4.9E-04	Y	0.32	1.0E-05	Y	0.94	1.0E-05	Y	0	0.50	N
STAT2	-0.04	0.16	N	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIB	-0.09	0.01	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
AIP	-0.03	0.21	N	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
FUS	-0.20	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
BTG2	-0.06	0.08	N	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA3	-0.24	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
MED1	-0.07	0.04	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT5A	-0.05	0.12	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXB13	-0.18	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ARNT	0.04	0.17	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA1	-0.28	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
SF1	0.03	0.25	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA3	0.06	0.07	N	0.29	1.0E-05	Y	0.03	0.24	N	0.32	1.0E-05	Y
HEY1	-0.13	9.7E-04	Y	0.29	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N
MED23	-0.19	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
L3MBTL1	-3.2E-03	0.47	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
GTF3A	-0.28	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
SPIC	-0.05	0.10	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
MAX	-0.25	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
TEF	-0.04	0.14	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCB1	0.13	1.3E-03	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
MZF1	-0.16	9.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB1	-0.05	0.14	N	0.27	1.0E-05	Y	0.10	6.0E-03	Y	0.34	1.0E-05	Y
HNF1A	-0.34	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2AF1	-0.25	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
TP73	-0.59	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
CITED2	-0.28	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
FOSL1	-0.30	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
SALL3	-0.13	9.3E-04	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA2	0.07	0.05	N	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
RARB	-0.12	1.4E-03	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID1B	-0.06	0.08	N	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA3	-0.21	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
MBD1	-0.22	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NFYA	-0.03	0.23	N	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF4	-0.34	1.0E-05	Y	0.25	1.0E-05	Y	-0.11	3.9E-03	Y	0.15	1.3E-04	Y
TCF7L2	-0.14	4.9E-04	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
APBB1	-0.41	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
PKNOX1	-0.26	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F3	-0.27	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
ERCC2	-0.10	0.01	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA2	0.09	0.02	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N

SOX17	-0.58	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC5	-0.34	1.0E-05	Y	0.24	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N
NR2C2	0.12	2.5E-03	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
JUN	-0.24	1.0E-05	Y	0.23	1.0E-05	Y	0.22	1.0E-05	Y	0.45	1.0E-05	Y
NFIX	-0.29	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
TLX1	0.16	7.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOR1	-0.14	4.5E-04	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXC10	0.11	4.7E-03	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF6	-0.09	0.01	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
NELFCD	-0.12	1.4E-03	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
RAD51	-0.11	5.2E-03	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF15	-0.02	0.34	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F8	5.4E-03	0.45	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID3A	-0.37	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIA	-0.19	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
PLAG1	-0.09	0.01	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1I2	-0.02	0.36	N	0.20	1.0E-05	Y	-0.13	7.7E-04	Y	0.36	1.0E-05	Y
HOPX	0.11	4.6E-03	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
MTA1	-0.09	0.02	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
SOX10	0.17	6.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
GCM2	0.06	0.09	N	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
SREBF1	-0.13	9.0E-04	Y	0.20	2.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N
APC	-0.12	1.5E-03	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
RB1CC1	-0.25	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
SMAD7	-0.19	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
IFI16	-0.20	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
SIN3A	-0.09	0.01	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
GATA4	-0.24	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
TBPL1	-0.18	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
ETV4	-0.39	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0.65	1.0E-05	Y
PCGF2	0.08	0.03	Y	0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
MITF	-0.08	0.03	Y	0.18	2.0E-05	Y	0	0.50	N	0.63	1.0E-05	Y
PDX1	-0.14	2.8E-04	Y	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
JUND	0.08	0.02	Y	0.17	3.0E-05	Y	-0.17	3.0E-05	Y	0.40	1.0E-05	Y
HNF4G	-0.42	1.0E-05	Y	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
TGIF1	-0.20	1.0E-05	Y	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
CRX	0.06	0.08	N	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
NPM1	0.21	1.0E-05	Y	0.17	5.0E-05	Y	0	0.50	N	0	0.50	N
PPARG	0.13	1.2E-03	Y	0.17	6.0E-05	Y	-0.20	1.0E-05	Y	0.27	1.0E-05	Y
NR4A1	6.6E-03	0.44	N	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
EZH2	0.14	3.7E-04	Y	0.17	6.0E-05	Y	-0.26	1.0E-05	Y	0.10	7.2E-03	Y
ID4	-0.41	1.0E-05	Y	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
HCFC1	-0.13	1.2E-03	Y	0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
EN1	0.07	0.05	N	0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
PITX1	0.07	0.05	N	0.16	8.0E-05	Y	-0.71	1.0E-05	Y	0	0.50	N
PITX3	-0.47	1.0E-05	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
BCL3	-0.27	1.0E-05	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
ETS1	-0.17	3.0E-05	Y	0.15	8.0E-05	Y	0	0.50	N	0.39	1.0E-05	Y
KLF8	-0.11	5.2E-03	Y	0.15	8.0E-05	Y	0	0.50	N	0	0.50	N
E2F7	-0.10	7.2E-03	Y	0.15	1.0E-04	Y	0	0.50	N	0	0.50	N
FOXF1	-0.12	1.4E-03	Y	0.15	1.1E-04	Y	0	0.50	N	0	0.50	N
TFAP2C	-0.46	1.0E-05	Y	0.15	1.8E-04	Y	0	0.50	N	0	0.50	N
JDP2	0.02	0.32	N	0.15	2.1E-04	Y	0	0.50	N	0	0.50	N
SMARCA1	-0.33	1.0E-05	Y	0.15	2.4E-04	Y	0	0.50	N	0	0.50	N
TOB1	0.09	0.01	Y	0.14	3.8E-04	Y	0	0.50	N	0	0.50	N
ELF2	-0.07	0.05	N	0.14	3.8E-04	Y	0	0.50	N	0	0.50	N
RFX5	0.20	2.0E-05	Y	0.14	3.8E-04	Y	0	0.50	N	0	0.50	N
NFE2L2	-0.03	0.22	N	0.14	4.2E-04	Y	0	0.50	N	0	0.50	N
NPAS2	-0.24	1.0E-05	Y	0.14	4.5E-04	Y	0	0.50	N	0	0.50	N
TRERF1	-0.35	1.0E-05	Y	0.14	4.5E-04	Y	0	0.50	N	0	0.50	N
DLX3	-0.08	0.03	Y	0.14	4.9E-04	Y	0	0.50	N	0	0.50	N
FOXC1	-0.06	0.08	N	0.14	4.9E-04	Y	0	0.50	N	0	0.50	N
SND1	-0.17	6.0E-05	Y	0.14	6.0E-04	Y	0	0.50	N	0	0.50	N
ESR1	-0.27	1.0E-05	Y	0.13	6.4E-04	Y	0.34	1.0E-05	Y	0.18	3.0E-05	Y
TEAD1	-0.19	1.0E-05	Y	0.13	6.5E-04	Y	0	0.50	N	0	0.50	N

HOXC6	-0.12	1.7E-03	Y	0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
GCM1	-0.02	0.32	N	0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
SIM2	0.02	0.28	N	0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
LHX2	-0.06	0.06	N	0.12	1.6E-03	Y	0	0.50	N	0	0.50	N
RFX1	-0.33	1.0E-05	Y	0.12	2.1E-03	Y	0	0.50	N	0	0.50	N
ETV2	-0.15	1.6E-04	Y	0.12	2.1E-03	Y	0	0.50	N	0	0.50	N
NEUROD	-0.27	1.0E-05	Y	0.12	2.2E-03	Y	0	0.50	N	0	0.50	N
GTF2I	-0.24	1.0E-05	Y	0.12	2.4E-03	Y	0	0.50	N	0	0.50	N
PRDM1	-0.30	1.0E-05	Y	0.12	2.5E-03	Y	0	0.50	N	0	0.50	N
KAT2B	-0.37	1.0E-05	Y	0.12	2.5E-03	Y	0	0.50	N	0	0.50	N
KAT5	-0.09	0.02	Y	0.12	2.6E-03	Y	0	0.50	N	0	0.50	N
BCL11B	0.03	0.23	N	0.11	3.0E-03	Y	0	0.50	N	0	0.50	N
ELK1	-0.24	1.0E-05	Y	0.11	3.2E-03	Y	0	0.50	N	0	0.50	N
LMO2	-0.27	1.0E-05	Y	0.11	3.3E-03	Y	0	0.50	N	0	0.50	N
PAX8	-6.3E-03	0.44	N	0.11	3.8E-03	Y	0	0.50	N	0	0.50	N
ESR2	0.04	0.19	N	0.11	5.5E-03	Y	0	0.50	N	0	0.50	N
KLF10	-0.51	1.0E-05	Y	0.10	6.0E-03	Y	0	0.50	N	0.21	1.0E-05	Y
HOXA5	0.04	0.19	N	0.10	6.2E-03	Y	0	0.50	N	0	0.50	N
SP7	-0.03	0.26	N	0.10	6.5E-03	Y	0	0.50	N	0	0.50	N
MECP2	-0.09	0.01	Y	0.10	7.4E-03	Y	0	0.50	N	0	0.50	N
GFI1B	0.08	0.03	Y	0.10	7.7E-03	Y	0	0.50	N	0	0.50	N
DLX5	-2.4E-03	0.48	N	0.10	8.6E-03	Y	0	0.50	N	0	0.50	N
HHEX	0.31	1.0E-05	Y	0.10	9.8E-03	Y	0	0.50	N	0	0.50	N
RBPJ	-0.40	1.0E-05	Y	0.10	1.0E-02	Y	0	0.50	N	0	0.50	N
FOSB	-0.22	1.0E-05	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
HR	-0.03	0.24	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
GBX2	-0.16	1.0E-04	Y	0.09	0.01	Y	0	0.50	N	0	0.50	N
REL	0.22	1.0E-05	Y	0.09	0.01	Y	0	0.50	N	0.53	1.0E-05	Y
RB1	-0.05	0.13	N	0.09	0.02	Y	-0.16	9.0E-05	Y	-0.67	1.0E-05	Y
PHB2	-0.30	1.0E-05	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
ELK4	0.02	0.28	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
HOXB1	-0.19	1.0E-05	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
SPI1	0.11	5.3E-03	Y	0.08	0.02	Y	-0.24	1.0E-05	Y	0.40	1.0E-05	Y
HDAC11	-0.12	1.6E-03	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
BRD7	-3.5E-03	0.47	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
HAX1	-0.01	0.39	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
HMGA1	-0.09	0.02	Y	0.08	0.03	Y	0	0.50	N	0.05	0.12	N
HOXC13	-0.22	1.0E-05	Y	0.08	0.04	Y	0	0.50	N	0	0.50	N
PML	-0.17	3.0E-05	Y	0.08	0.04	Y	0	0.50	N	0.34	1.0E-05	Y
ANKRD1	0.02	0.33	N	0.07	0.04	N	0	0.50	N	0	0.50	N
BTAF1	0.25	1.0E-05	Y	0.07	0.04	N	0	0.50	N	0	0.50	N
SATB2	-0.04	0.19	N	0.07	0.04	N	0	0.50	N	0	0.50	N
POU1F1	0.15	2.3E-04	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
KHDRBS1	0.29	1.0E-05	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
NFE2L1	0.03	0.27	N	0.07	0.06	N	0	0.50	N	0	0.50	N
NFIL3	-0.06	0.08	N	0.07	0.06	N	0	0.50	N	0	0.50	N
CEBPB	0.09	0.02	Y	0.07	0.06	N	0.32	1.0E-05	Y	0.33	1.0E-05	Y
RXRA	-0.14	3.2E-04	Y	0.06	0.06	N	0	0.50	N	0	0.50	N
ONECUT2	-0.18	2.0E-05	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
EP300	0.05	0.12	N	0.06	0.08	N	0.37	1.0E-05	Y	0.11	5.2E-03	Y
EHMT2	-0.02	0.29	N	0.06	0.08	N	0	0.50	N	0	0.50	N
TBX5	0.04	0.19	N	0.06	0.09	N	0	0.50	N	0	0.50	N
NAB2	0.02	0.28	N	0.06	0.09	N	0	0.50	N	0	0.50	N
SUGP1	-0.11	5.5E-03	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
PAX2	-0.14	3.3E-04	Y	0.05	0.09	N	0	0.50	N	0	0.50	N
NFKB1	-0.20	1.0E-05	Y	0.05	0.10	N	-0.04	0.15	N	0.43	1.0E-05	Y
TBX21	0.01	0.40	N	0.05	0.10	N	0	0.50	N	0	0.50	N
RFX3	0.15	8.0E-05	Y	0.05	0.12	N	0	0.50	N	0	0.50	N
ABL1	-0.05	0.12	N	0.04	0.14	N	0	0.50	N	0.42	1.0E-05	Y
MSX1	-0.07	0.04	N	0.04	0.15	N	0	0.50	N	0	0.50	N
KLF13	0.37	1.0E-05	Y	0.04	0.15	N	0	0.50	N	0	0.50	N
SSB	-0.14	5.9E-04	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
CDX2	0.06	0.09	N	0.04	0.16	N	0.15	2.0E-04	Y	0.29	1.0E-05	Y
LMO3	0.18	2.0E-05	Y	0.04	0.17	N	0	0.50	N	0	0.50	N
PA2G4	0.06	0.08	N	0.04	0.19	N	0	0.50	N	0	0.50	N

PAX5	0.32	1.0E-05	Y	0.04	0.19	N	0	0.50	N	0.43	1.0E-05	Y
RUNX2	-0.30	1.0E-05	Y	0.04	0.20	N	0	0.50	N	0.60	1.0E-05	Y
FOXL2	-0.15	2.8E-04	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
KLF12	-0.30	1.0E-05	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
PIAS3	0.12	1.8E-03	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
GATA6	-0.03	0.21	N	0.03	0.23	N	0	0.50	N	0	0.50	N
FOXO1	0.19	2.0E-05	Y	0.03	0.23	N	-0.33	1.0E-05	Y	0.39	1.0E-05	Y
KDM4C	-0.15	1.0E-04	Y	0.03	0.24	N	0	0.50	N	0	0.50	N
MDM4	-0.25	1.0E-05	Y	0.03	0.24	N	0	0.50	N	0	0.50	N
DR1	0.34	1.0E-05	Y	0.03	0.26	N	0	0.50	N	0	0.50	N
NR5A2	0.11	5.0E-03	Y	0.03	0.27	N	0	0.50	N	0	0.50	N
MYOD1	-0.27	1.0E-05	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
STAT6	-0.07	0.04	Y	0.02	0.29	N	0	0.50	N	0.38	1.0E-05	Y
CREBBP	0.08	0.03	Y	0.02	0.32	N	0	0.50	N	0.34	1.0E-05	Y
ING4	-0.11	4.0E-03	Y	0.02	0.32	N	0	0.50	N	0	0.50	N
NR1H4	0.19	2.0E-05	Y	0.02	0.34	N	0.28	1.0E-05	Y	0.36	1.0E-05	Y
RELA	-0.31	1.0E-05	Y	0.02	0.35	N	0.02	0.28	N	0.42	1.0E-05	Y
PAX3	-0.18	1.0E-05	Y	0.02	0.35	N	0	0.50	N	0	0.50	N
IRF1	-0.19	1.0E-05	Y	0.02	0.36	N	0	0.50	N	-0.12	1.5E-03	Y
SUPT3H	0.23	1.0E-05	Y	0.01	0.37	N	0	0.50	N	0	0.50	N
TAF4	-0.09	0.02	Y	0.01	0.40	N	0	0.50	N	0	0.50	N
ELL	-0.09	0.01	Y	0.01	0.40	N	0	0.50	N	0	0.50	N
ISL1	-0.09	0.01	Y	9.9E-03	0.41	N	0	0.50	N	0	0.50	N
EWSR1	7.3E-03	0.43	N	9.8E-03	0.41	N	0	0.50	N	0	0.50	N
IRF3	2.0E-03	0.48	N	4.7E-03	0.46	N	0	0.50	N	0	0.50	N
HES1	0.02	0.36	N	2.5E-03	0.48	N	0	0.50	N	0	0.50	N
KCNIP3	-0.37	1.0E-05	Y	1.7E-03	0.48	N	0	0.50	N	0	0.50	N
HNF4A	-0.20	1.0E-05	Y	-8.6E-	0.49	N	0.48	1.0E-05	Y	0	0.50	N
SP3	-0.19	1.0E-05	Y	-2.1E-	0.48	N	0.26	1.0E-05	Y	0.24	1.0E-05	Y
ATF2	0.41	1.0E-05	Y	-4.2E-	0.46	N	0	0.50	N	0.47	1.0E-05	Y
MYB	0.11	5.3E-03	Y	-6.1E-	0.44	N	0	0.50	N	0.55	1.0E-05	Y
CRABP2	-0.13	8.4E-04	Y	-6.7E-	0.44	N	0	0.50	N	0	0.50	N
SKIL	-0.13	1.2E-03	Y	-7.0E-	0.43	N	0	0.50	N	0	0.50	N
NEUROG	0.04	0.16	N	-7.6E-	0.43	N	0	0.50	N	0	0.50	N
ECD	-0.20	1.0E-05	Y	-7.7E-	0.43	N	0	0.50	N	0	0.50	N
HINFP	0.13	7.4E-04	Y	-8.6E-	0.42	N	0	0.50	N	0	0.50	N
NRF1	-0.07	0.06	N	-8.9E-	0.42	N	0	0.50	N	0	0.50	N
TCF4	0.05	0.14	N	-9.3E-	0.41	N	0.30	1.0E-05	Y	0	0.50	N
ARNTL	0.14	6.0E-04	Y	-0.01	0.38	N	0	0.50	N	0.08	0.04	N
EGR2	0.23	1.0E-05	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
FOXP1	0.25	1.0E-05	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
THRA	0.09	0.02	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
FOXO4	0.34	1.0E-05	Y	-0.02	0.34	N	0	0.50	N	0	0.50	N
MYF5	0.13	8.4E-04	Y	-0.02	0.33	N	0	0.50	N	0	0.50	N
TAF1	-0.23	1.0E-05	Y	-0.02	0.32	N	0	0.50	N	0	0.50	N
RFWD2	-0.38	1.0E-05	Y	-0.02	0.32	N	0	0.50	N	0	0.50	N
PIAS4	0.15	1.0E-04	Y	-0.02	0.31	N	0	0.50	N	0	0.50	N
HDAC10	0.22	1.0E-05	Y	-0.02	0.31	N	0	0.50	N	0	0.50	N
TBX2	0.42	1.0E-05	Y	-0.02	0.30	N	0	0.50	N	0	0.50	N
KLF5	0.35	1.0E-05	Y	-0.03	0.27	N	0	0.50	N	0	0.50	N
TBX3	0.25	1.0E-05	Y	-0.03	0.27	N	0	0.50	N	0	0.50	N
MEF2A	7.0E-03	0.43	N	-0.03	0.26	N	0	0.50	N	0	0.50	N
HMGB2	-0.08	0.03	Y	-0.03	0.25	N	0	0.50	N	0	0.50	N
NFIC	-0.20	1.0E-05	Y	-0.03	0.25	N	0	0.50	N	0.26	1.0E-05	Y
RELB	-0.20	1.0E-05	Y	-0.03	0.25	N	0	0.50	N	0	0.50	N
MYOG	-0.05	0.12	N	-0.03	0.25	N	0	0.50	N	0	0.50	N
FOXE1	-0.11	4.0E-03	Y	-0.03	0.24	N	0	0.50	N	0	0.50	N
IKZF1	0.10	6.7E-03	Y	-0.03	0.24	N	0	0.50	N	0	0.50	N
MXI1	0.12	1.9E-03	Y	-0.03	0.23	N	0	0.50	N	0	0.50	N
POU4F2	0.03	0.25	N	-0.03	0.22	N	0	0.50	N	0	0.50	N
NF1	0.09	0.02	Y	-0.03	0.22	N	0	0.50	N	0	0.50	N
PAWR	0.01	0.37	N	-0.03	0.22	N	0	0.50	N	0	0.50	N
FHL2	-0.07	0.05	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
BCL11A	-0.03	0.20	N	-0.04	0.19	N	0	0.50	N	0	0.50	N
NR4A2	-0.17	3.0E-05	Y	-0.04	0.17	N	0	0.50	N	0	0.50	N

GZF1	0.02	0.28	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
ILF3	0.16	8.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
MCM4	-0.34	1.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
PHOX2B	-0.08	0.02	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
SP2	0.24	1.0E-05	Y	-0.06	0.09	N	0	0.50	N	0	0.50	N
FOXA2	-0.21	1.0E-05	Y	-0.06	0.08	N	0	0.50	N	0	0.50	N
ELF1	-0.19	1.0E-05	Y	-0.06	0.08	N	0	0.50	N	0	0.50	N
SRSF1	-0.16	1.0E-04	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
PITX2	-0.01	0.38	N	-0.06	0.06	N	0	0.50	N	0	0.50	N
ETV5	0.29	1.0E-05	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
AR	-0.03	0.25	N	-0.07	0.05	N	-0.11	4.8E-03	Y	0.07	0.05	N
ID2	-0.30	1.0E-05	Y	-0.07	0.04	N	0	0.50	N	0	0.50	N
RUNX1	0.01	0.40	N	-0.07	0.04	Y	0	0.50	N	0.31	1.0E-05	Y
NR1D1	-0.20	1.0E-05	Y	-0.08	0.04	Y	0	0.50	N	0	0.50	N
NRIP1	0.06	0.08	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
NELFB	0.07	0.06	N	-0.08	0.02	Y	0	0.50	N	0	0.50	N
CLOCK	-0.14	3.0E-04	Y	-0.08	0.02	Y	0	0.50	N	0.08	0.04	N
FOXF2	-0.15	1.0E-04	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
ASCL1	-0.03	0.22	N	-0.08	0.02	Y	0	0.50	N	0	0.50	N
ILF2	0.07	0.04	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
NUPR1	0.23	1.0E-05	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
ETV6	-0.14	3.2E-04	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
FOS	0.05	0.10	N	-0.09	0.01	Y	-0.09	0.01	Y	0.29	1.0E-05	Y
NFATC1	0.44	1.0E-05	Y	-0.10	0.01	Y	0	0.50	N	0	0.50	N
CDCA7L	-0.16	1.0E-04	Y	-0.10	9.5E-03	Y	0	0.50	N	0	0.50	N
MYOCD	-0.04	0.17	N	-0.10	6.3E-03	Y	0	0.50	N	0	0.50	N
TP53BP1	-0.04	0.18	N	-0.10	5.9E-03	Y	0	0.50	N	0	0.50	N
SNAI2	-0.05	0.12	N	-0.11	5.7E-03	Y	-0.72	1.0E-05	Y	0.11	3.4E-03	Y
SOX2	0.10	8.5E-03	Y	-0.11	5.4E-03	Y	0	0.50	N	0.07	0.05	N
RBL1	-0.11	5.2E-03	Y	-0.11	4.9E-03	Y	0	0.50	N	0	0.50	N
NR4A3	0.47	1.0E-05	Y	-0.11	4.9E-03	Y	0	0.50	N	0	0.50	N
NFATC3	-0.07	0.04	Y	-0.11	4.7E-03	Y	0	0.50	N	0	0.50	N
LHX4	0.02	0.34	N	-0.11	4.5E-03	Y	0	0.50	N	0	0.50	N
FOXG1	0.11	3.2E-03	Y	-0.11	4.4E-03	Y	0	0.50	N	0	0.50	N
MYCN	0.30	1.0E-05	Y	-0.11	4.0E-03	Y	0.34	1.0E-05	Y	0.05	0.14	N
SNAI1	0.06	0.09	N	-0.11	3.9E-03	Y	0	0.50	N	0	0.50	N
NR5A1	0.04	0.16	N	-0.11	3.8E-03	Y	0.13	9.5E-04	Y	0	0.50	N
KLF9	0.13	1.2E-03	Y	-0.11	3.5E-03	Y	0	0.50	N	0	0.50	N
NR3C2	0.08	0.03	Y	-0.11	2.9E-03	Y	0	0.50	N	0	0.50	N
MEF2C	0.21	1.0E-05	Y	-0.12	2.7E-03	Y	0	0.50	N	0	0.50	N
NANOG	0.07	0.05	N	-0.12	2.4E-03	Y	0	0.50	N	-0.21	1.0E-05	Y
SFPQ	0.15	9.0E-05	Y	-0.12	2.1E-03	Y	0	0.50	N	0	0.50	N
ATM	0.29	1.0E-05	Y	-0.13	1.3E-03	Y	0	0.50	N	-0.02	0.29	N
RBL2	-0.14	5.5E-04	Y	-0.13	8.4E-04	Y	0	0.50	N	0	0.50	N
ONECUT1	0.02	0.36	N	-0.13	7.9E-04	Y	0	0.50	N	0	0.50	N
IRF7	0.24	1.0E-05	Y	-0.13	7.2E-04	Y	0	0.50	N	0	0.50	N
FOXD3	0.19	2.0E-05	Y	-0.14	5.8E-04	Y	0	0.50	N	0	0.50	N
LEF1	0.06	0.06	N	-0.14	5.4E-04	Y	0	0.50	N	0.30	1.0E-05	Y
MLXIPL	-0.03	0.22	N	-0.14	4.9E-04	Y	0	0.50	N	0	0.50	N
LMX1B	0.42	1.0E-05	Y	-0.14	4.3E-04	Y	0	0.50	N	0	0.50	N
ING2	0.27	1.0E-05	Y	-0.15	2.7E-04	Y	0	0.50	N	0	0.50	N
CTBP1	-0.25	1.0E-05	Y	-0.15	2.7E-04	Y	0	0.50	N	0	0.50	N
MAZ	0.31	1.0E-05	Y	-0.15	1.6E-04	Y	0	0.50	N	0	0.50	N
HSF2	0.14	3.8E-04	Y	-0.15	1.1E-04	Y	0	0.50	N	0	0.50	N
IRF4	0.12	1.6E-03	Y	-0.15	1.0E-04	Y	0	0.50	N	0	0.50	N
NR1I3	0.30	1.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
CEBPD	-0.15	2.4E-04	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
DBP	-0.17	6.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
GABPA	-0.21	1.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
MAFF	0.29	1.0E-05	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
MLLT10	0.09	0.02	Y	-0.16	9.0E-05	Y	0	0.50	N	0	0.50	N
ATOH1	0.03	0.26	N	-0.16	9.0E-05	Y	0	0.50	N	0	0.50	N
DEK	-0.05	0.12	N	-0.16	9.0E-05	Y	0	0.50	N	0	0.50	N
POU2F1	0.15	8.0E-05	Y	-0.16	9.0E-05	Y	0	0.50	N	0.71	1.0E-05	Y
NFRKB	-0.20	1.0E-05	Y	-0.16	8.0E-05	Y	0	0.50	N	0	0.50	N

SRCAP	0.16	8.0E-05	Y	-0.16	6.0E-05	Y	0	0.50	N	0	0.50	N
RUNX3	0.09	0.02	Y	-0.17	6.0E-05	Y	0.12	1.6E-03	Y	0.04	0.17	N
MTF1	0.24	1.0E-05	Y	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
POU3F2	0.28	1.0E-05	Y	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
RORA	0.30	1.0E-05	Y	-0.17	6.0E-05	Y	0	0.50	N	0	0.50	N
HOXB7	-0.25	1.0E-05	Y	-0.17	5.0E-05	Y	0	0.50	N	0	0.50	N
HDAC4	0.35	1.0E-05	Y	-0.17	3.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N
KAT6A	0.11	3.5E-03	Y	-0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
PARP1	-0.17	3.0E-05	Y	-0.17	3.0E-05	Y	-0.39	1.0E-05	Y	0.26	1.0E-05	Y
IRF2	0.26	1.0E-05	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
HLF	0.09	0.02	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
SMURF2	0.21	1.0E-05	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
NOTCH3	-0.17	3.0E-05	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
STAT3	0.28	1.0E-05	Y	-0.18	1.0E-05	Y	0.17	5.0E-05	Y	0.39	1.0E-05	Y
HTATIP2	0.39	1.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
EAPP	0.21	1.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
HBP1	0.24	1.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
SPEN	-0.02	0.28	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID1A	0.27	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
DDIT3	0.16	8.0E-05	Y	-0.19	1.0E-05	Y	0.03	0.22	N	0	0.50	N
NKX2-2	3.3E-03	0.47	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX9	-0.01	0.38	N	-0.19	1.0E-05	Y	0	0.50	N	-0.18	1.0E-05	Y
RUVBL1	0.27	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
MAML1	-0.07	0.05	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA1	0.26	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2F2	0.29	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF1	0.11	3.4E-03	Y	-0.19	1.0E-05	Y	0	0.50	N	0.40	1.0E-05	Y
NFATC2	0.32	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3	-0.17	3.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
NRL	0.24	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
CHD4	-0.27	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
MYBL2	0.12	2.3E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
SATB1	0.01	0.40	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
HEXIM1	0.10	8.7E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
SALL4	0.17	3.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP2	-0.06	0.09	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
PRDM14	-0.02	0.30	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF3	0.25	1.0E-05	Y	-0.20	1.0E-05	Y	-0.12	1.8E-03	Y	0	0.50	N
HOXA11	-0.04	0.20	N	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
GLI1	0.29	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
MAFB	0.03	0.21	N	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
MAFA	0.07	0.05	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2E3	0.23	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF4	0.01	0.40	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF4	0.05	0.12	N	-0.22	1.0E-05	Y	0.44	1.0E-05	Y	0.52	1.0E-05	Y
SHOX	0.08	0.03	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT4	0.16	8.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
FOSL2	-0.07	0.05	N	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT1	0.20	2.0E-05	Y	-0.23	1.0E-05	Y	-0.05	0.13	N	0.41	1.0E-05	Y
NCOR2	-0.10	5.8E-03	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
PLAGL2	0.14	3.9E-04	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
RARA	0.06	0.06	N	-0.24	1.0E-05	Y	0.17	6.0E-05	Y	0.19	2.0E-05	Y
SOX6	0.36	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
ATRX	-0.08	0.03	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MSC	0.14	4.8E-04	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
GLI2	-0.14	5.0E-04	Y	-0.25	1.0E-05	Y	0	0.50	N	0.42	1.0E-05	Y
CEBPE	0.25	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
TCFL5	0.14	3.7E-04	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
HLTF	0.10	9.2E-03	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
HAND2	-0.07	0.04	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXH1	0.26	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
E4F1	-0.09	0.02	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
TNFAIP3	0.21	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
BACH1	0.17	6.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
TAL1	-7.0E-03	0.43	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N

SP1	0.36	1.0E-05	Y	-0.25	1.0E-05	Y	0.33	1.0E-05	Y	0.36	1.0E-05	Y
CREM	0.03	0.27	N	-0.26	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N
OTX1	0.08	0.03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
HIF1A	-0.17	4.0E-05	Y	-0.26	1.0E-05	Y	0.08	0.04	Y	0.42	1.0E-05	Y
TCF12	8.9E-03	0.42	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
EVX1	0.22	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF1	-4.9E-03	0.45	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXA1	0.03	0.25	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2F6	0.24	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF2	0.31	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0.24	1.0E-05	Y
OTX2	-8.3E-03	0.42	N	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
CBX8	0.07	0.06	N	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
CBX7	0.18	2.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
PROX1	0.19	2.0E-05	Y	-0.28	1.0E-05	Y	0.03	0.24	N	0	0.50	N
LRRFIP1	0.05	0.13	N	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKBIA	-0.10	5.8E-03	Y	-0.28	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N
TFAP4	0.19	2.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
LDB1	0.06	0.06	N	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF3	0.14	4.9E-04	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
MXD1	0.16	8.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
NPAS1	0.24	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
TEAD4	0.25	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ID1	0.23	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ING1	0.16	6.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
BCL6	-7.3E-03	0.43	N	-0.30	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N
FLI1	0.38	1.0E-05	Y	-0.30	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N
KLF16	7.8E-03	0.43	N	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
MSX2	-0.05	0.14	N	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
HDGF	0.16	7.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
NHLH2	0.24	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF6	0.32	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
NR3C1	0.03	0.21	N	-0.32	1.0E-05	Y	0	0.50	N	-0.06	0.09	N
CUX1	0.15	1.7E-04	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX3-1	0.43	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXD9	0.13	1.1E-03	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
PER2	0.08	0.03	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF5	0.07	0.04	N	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
EHF	0.06	0.06	N	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXQ1	0.30	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
BARD1	-0.08	0.03	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
PTTG1	0.26	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0.54	1.0E-05	Y
PBX1	0.41	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
EGR1	0.07	0.05	N	-0.34	1.0E-05	Y	0.22	1.0E-05	Y	0.34	1.0E-05	Y
HOXA7	0.02	0.35	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
HMGA2	0.27	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF11	0.09	0.01	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCA4	-0.03	0.25	N	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
DEAF1	0.08	0.02	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
SMAD3	0.41	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	-3.1E-	0.47	N
CEBPG	0.26	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC3	0.25	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
MYF6	0.19	2.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
HIRA	0.34	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
KDM2A	0.40	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
MLLT3	0.27	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKBIB	0.33	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3A	0.26	1.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
RARG	0.28	1.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPA	0.19	2.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0.42	1.0E-05	Y
PTMA	0.29	1.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
EPAS1	0.17	6.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0.65	1.0E-05	Y
CREB5	0.27	1.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
ERF	0.01	0.37	N	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
HIC1	0.29	1.0E-05	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
TCF3	0.04	0.17	N	-0.37	1.0E-05	Y	0	0.50	N	-0.31	1.0E-05	Y

NFKB2	0.25	1.0E-05	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F4	0.36	1.0E-05	Y	-0.38	1.0E-05	Y	0	0.50	N	-0.96	1.0E-05	Y
BHLHE41	0.11	3.2E-03	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA6	0.20	2.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
SRY	0.15	8.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
MYC	0.03	0.26	N	-0.40	1.0E-05	Y	0.53	1.0E-05	Y	0.19	2.0E-05	Y
NR2F1	0.04	0.17	N	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
RBBP7	0.31	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
CIITA	0.25	1.0E-05	Y	-0.40	1.0E-05	Y	-0.40	1.0E-05	Y	0.43	1.0E-05	Y
GLI3	0.21	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
SPDEF	0.54	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3L1	0.19	2.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
BTF3	0.42	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS2	0.16	8.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
PHOX2A	0.21	1.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
RREB1	0.18	2.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
MEIS1	0.29	1.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
TP53	0.02	0.29	N	-0.42	1.0E-05	Y	0.08	0.04	Y	-0.22	1.0E-05	Y
SIRT1	0.52	1.0E-05	Y	-0.42	1.0E-05	Y	-0.27	1.0E-05	Y	0.04	0.19	N
POU4F1	0.33	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
SRF	0.26	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0.71	1.0E-05	Y
PPARD	0.26	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0.22	1.0E-05	Y
LYL1	0.28	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
SP4	0.04	0.20	N	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
CTNNB1	0.22	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX4	0.19	2.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
IKBKB	0.49	1.0E-05	Y	-0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX2-1	0.16	7.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA2	0.40	1.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
COPS5	0.26	1.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
PGR	0.44	1.0E-05	Y	-0.46	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N
PBX2	0.18	3.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
LHX3	0.17	3.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF3	0.43	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
TFCP2	0.81	1.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3L	0.78	1.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
DLX4	0.30	1.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA9	0.19	2.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
HES6	0.23	1.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
LMO4	0.20	2.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
CBX6	0.39	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX3	0.37	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
NR0B2	0.46	1.0E-05	Y	-0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
AATF	0.39	1.0E-05	Y	-0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
MEN1	0.83	1.0E-05	Y	-0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP2A	0.42	1.0E-05	Y	-0.53	1.0E-05	Y	0.08	0.02	Y	0.23	1.0E-05	Y
NFAT5	0.36	1.0E-05	Y	-0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
TFDP3	0.33	1.0E-05	Y	-0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX2-5	0.26	1.0E-05	Y	-0.57	1.0E-05	Y	-0.49	1.0E-05	Y	0	0.50	N
HDAC2	0.46	1.0E-05	Y	-0.57	1.0E-05	Y	-0.69	1.0E-05	Y	-0.56	1.0E-05	Y
HDAC7	0.40	1.0E-05	Y	-0.57	1.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N
GATA1	0.44	1.0E-05	Y	-0.57	1.0E-05	Y	0.27	1.0E-05	Y	0.25	1.0E-05	Y
PAX6	0.41	1.0E-05	Y	-0.58	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA10	0.49	1.0E-05	Y	-0.62	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP3	0.34	1.0E-05	Y	-0.62	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1H2	0.36	1.0E-05	Y	-0.66	1.0E-05	Y	0	0.50	N	0	0.50	N

Master list of TFs in TCGA ovarian cancer dataset together the correlation scores of their activity scores with PR signatures and enrichment scores of target genes with PR signatures

TF	*S*(TF,P)	P-value	BH	*S*(TF,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
E2F4	0.27	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	-0.76	1.0E-05	Y
SREBF2	-0.63	1.0E-05	Y	0.63	1.0E-05	Y	0	0.50	N	-0.52	1.0E-05	Y
RB1	0.07	0.05	N	0.16	8.0E-05	Y	0	0.50	N	-0.43	1.0E-05	Y
BCL6	0.15	2.4E-04	Y	-0.25	1.0E-05	Y	-0.49	1.0E-05	Y	-0.35	1.0E-05	Y
NANOG	0.06	0.07	N	-0.34	1.0E-05	Y	0.03	0.21	N	-0.32	1.0E-05	Y
SOX9	0.06	0.06	N	-0.21	1.0E-05	Y	0.39	1.0E-05	Y	-0.30	1.0E-05	Y
HDAC2	0.05	0.14	N	-0.20	1.0E-05	Y	0	0.50	N	-0.30	1.0E-05	Y
SIRT1	0.43	1.0E-05	Y	-0.40	1.0E-05	Y	-0.47	1.0E-05	Y	-0.23	1.0E-05	Y
HOXB7	0.10	0.01	Y	-0.31	1.0E-05	Y	0	0.50	N	0.21	1.0E-05	Y
LEF1	0.11	3.3E-03	Y	-0.08	0.03	Y	0	0.50	N	0.21	1.0E-05	Y
KLF10	-0.41	1.0E-05	Y	-0.02	0.30	N	0	0.50	N	0.21	1.0E-05	Y
PAX5	0.11	3.4E-03	Y	-0.03	0.22	N	-0.16	8.0E-05	Y	0.21	1.0E-05	Y
IRF1	-0.39	1.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0.21	1.0E-05	Y
PPARA	-0.15	2.7E-04	Y	0.05	0.12	N	-0.49	1.0E-05	Y	0.22	1.0E-05	Y
AR	-0.16	9.0E-05	Y	0.03	0.26	N	-0.13	1.0E-03	Y	0.22	1.0E-05	Y
FOXO3	-0.28	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0.22	1.0E-05	Y
MSC	-0.01	0.40	N	-0.28	1.0E-05	Y	0	0.50	N	0.26	1.0E-05	Y
APEX1	-0.03	0.26	N	-0.04	0.16	N	0	0.50	N	0.26	1.0E-05	Y
RUNX1	-0.08	0.03	Y	0.22	1.0E-05	Y	0	0.50	N	0.27	1.0E-05	Y
PML	-0.13	8.5E-04	Y	-0.12	1.8E-03	Y	0	0.50	N	0.27	1.0E-05	Y
CREB1	-0.18	1.0E-05	Y	0.06	0.07	N	0.07	0.05	N	0.28	1.0E-05	Y
NFE2L2	0.09	0.02	Y	-0.03	0.21	N	0	0.50	N	0.29	1.0E-05	Y
SP3	-0.13	1.0E-03	Y	0.34	1.0E-05	Y	0.51	1.0E-05	Y	0.29	1.0E-05	Y
ABL1	0.09	0.02	Y	-0.02	0.33	N	0	0.50	N	0.30	1.0E-05	Y
HMGA1	0.10	7.4E-03	Y	-0.15	2.8E-04	Y	0	0.50	N	0.31	1.0E-05	Y
FOS	0.11	4.6E-03	Y	-0.24	1.0E-05	Y	-0.36	1.0E-05	Y	0.32	1.0E-05	Y
MYC	0.04	0.16	N	-0.40	1.0E-05	Y	0.33	1.0E-05	Y	0.33	1.0E-05	Y
NR1H4	0.03	0.26	N	0.16	7.0E-05	Y	0	0.50	N	0.33	1.0E-05	Y
EGR1	0.28	1.0E-05	Y	-0.44	1.0E-05	Y	0.12	2.9E-03	Y	0.33	1.0E-05	Y
GATA3	-0.08	0.03	Y	0.30	1.0E-05	Y	-0.19	1.0E-05	Y	0.33	1.0E-05	Y
ATF1	-0.02	0.32	N	0.13	1.3E-03	Y	0	0.50	N	0.35	1.0E-05	Y
PPARG	0.04	0.18	N	0.17	3.0E-05	Y	-0.30	1.0E-05	Y	0.35	1.0E-05	Y
ERG	-0.31	1.0E-05	Y	0.35	1.0E-05	Y	0.04	0.18	N	0.35	1.0E-05	Y
HNF4A	-0.46	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0.36	1.0E-05	Y
HIF1A	-0.04	0.20	N	-0.13	1.3E-03	Y	0.21	1.0E-05	Y	0.36	1.0E-05	Y
CIITA	0.20	2.0E-05	Y	-0.56	1.0E-05	Y	0	0.50	N	0.38	1.0E-05	Y
GATA1	0.35	1.0E-05	Y	-0.40	1.0E-05	Y	0.24	1.0E-05	Y	0.39	1.0E-05	Y
MTA1	-0.09	0.01	Y	0.04	0.20	N	0	0.50	N	0.40	1.0E-05	Y
JUN	0.12	2.6E-03	Y	0.10	0.01	Y	-0.13	9.2E-04	Y	0.41	1.0E-05	Y
SP1	0.10	7.6E-03	Y	-0.32	1.0E-05	Y	0.41	1.0E-05	Y	0.41	1.0E-05	Y
STAT6	-0.01	0.37	N	-0.06	0.09	N	0	0.50	N	0.42	1.0E-05	Y
RARA	-0.06	0.09	N	-0.09	0.02	Y	0	0.50	N	0.42	1.0E-05	Y
CTNNB1	-0.10	0.01	Y	-0.08	0.03	Y	0	0.50	N	0.42	1.0E-05	Y
SNAI2	-0.14	5.8E-04	Y	-0.02	0.32	N	-0.39	1.0E-05	Y	0.42	1.0E-05	Y
ETV4	-0.15	1.9E-04	Y	0.12	1.8E-03	Y	0	0.50	N	0.43	1.0E-05	Y
CEBPB	-0.03	0.27	N	0.14	5.3E-04	Y	-0.05	0.12	N	0.43	1.0E-05	Y
ATF2	-0.03	0.21	N	0.27	1.0E-05	Y	0	0.50	N	0.43	1.0E-05	Y
NR3C2	0.26	1.0E-05	Y	-0.07	0.04	Y	0	0.50	N	0.43	1.0E-05	Y
TFAP2A	0.22	1.0E-05	Y	-0.36	1.0E-05	Y	-0.11	3.2E-03	Y	0.43	1.0E-05	Y
ETS1	-0.15	1.0E-04	Y	0.18	3.0E-05	Y	0.30	1.0E-05	Y	0.43	1.0E-05	Y
ATM	0.10	0.01	Y	-0.08	0.02	Y	0	0.50	N	0.44	1.0E-05	Y
SMAD3	0.25	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0.45	1.0E-05	Y
STAT3	0.27	1.0E-05	Y	-0.28	1.0E-05	Y	-0.20	1.0E-05	Y	0.46	1.0E-05	Y
NR1I2	-0.08	0.02	Y	0.24	1.0E-05	Y	-0.46	1.0E-05	Y	0.47	1.0E-05	Y
CDX2	-0.25	1.0E-05	Y	0.23	1.0E-05	Y	0.15	2.0E-04	Y	0.50	1.0E-05	Y
EP300	0.02	0.33	N	-0.17	5.0E-05	Y	0.34	1.0E-05	Y	0.50	1.0E-05	Y
NFKB1	-0.16	1.0E-04	Y	0.19	2.0E-05	Y	-0.16	9.0E-05	Y	0.50	1.0E-05	Y
RELA	0.17	3.0E-05	Y	-0.52	1.0E-05	Y	-0.20	1.0E-05	Y	0.51	1.0E-05	Y
MYB	0.08	0.04	Y	-0.13	6.7E-04	Y	-0.40	1.0E-05	Y	0.53	1.0E-05	Y

PTTG1	0.41	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N	0.53	1.0E-05	Y
SMAD4	-0.08	0.03	Y	0.22	1.0E-05	Y	0	0.50	N	0.54	1.0E-05	Y
POU2F1	-0.03	0.26	N	0.06	0.07	N	0.21	1.0E-05	Y	0.55	1.0E-05	Y
CEBPA	0.28	1.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0.55	1.0E-05	Y
STAT1	0.11	5.2E-03	Y	-0.18	1.0E-05	Y	-0.17	4.0E-05	Y	0.57	1.0E-05	Y
MITF	-0.13	1.1E-03	Y	0.15	8.0E-05	Y	0	0.50	N	0.58	1.0E-05	Y
KLF5	0.10	8.3E-03	Y	0.01	0.37	N	0	0.50	N	0.62	1.0E-05	Y
REL	-0.10	7.2E-03	Y	0.59	1.0E-05	Y	0	0.50	N	0.63	1.0E-05	Y
SRF	0.04	0.15	N	-0.17	6.0E-05	Y	0.50	1.0E-05	Y	0.63	1.0E-05	Y
SPI1	0.02	0.32	N	0.32	1.0E-05	Y	-0.27	1.0E-05	Y	0.66	1.0E-05	Y
ATF4	0.14	5.9E-04	Y	-0.04	0.18	N	0.50	1.0E-05	Y	0.66	1.0E-05	Y
RXRA	0.25	1.0E-05	Y	-0.15	2.8E-04	Y	0	0.50	N	0.67	1.0E-05	Y
RUNX2	-0.17	4.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0.67	1.0E-05	Y
ETS2	-0.15	1.7E-04	Y	0.14	3.0E-04	Y	0	0.50	N	0.73	1.0E-05	Y
EPAS1	0.05	0.10	N	-0.09	0.01	Y	0	0.50	N	0.95	1.0E-05	Y
KLF4	-0.10	9.8E-03	Y	0.25	1.0E-05	Y	-0.34	1.0E-05	Y	0.19	2.0E-05	Y
MYCN	0.03	0.24	N	-0.04	0.17	N	0.43	1.0E-05	Y	0.20	2.0E-05	Y
NR3C1	0.25	1.0E-05	Y	-0.32	1.0E-05	Y	-0.02	0.36	N	-0.16	7.0E-05	Y
JUND	-0.11	3.5E-03	Y	0.10	0.01	Y	0	0.50	N	0.14	2.9E-04	Y
TP53	0.15	1.3E-04	Y	-0.30	1.0E-05	Y	0.02	0.31	N	-0.12	1.3E-03	Y
KLF2	0.11	3.3E-03	Y	-0.28	1.0E-05	Y	0	0.50	N	0.12	1.7E-03	Y
EZH2	0.27	1.0E-05	Y	-0.07	0.04	Y	-0.28	1.0E-05	Y	-0.11	4.4E-03	Y
NFYA	0.02	0.28	N	0.04	0.19	N	0	0.50	N	0.11	5.0E-03	Y
E2F1	-0.63	1.0E-05	Y	0.32	1.0E-05	Y	0.61	1.0E-05	Y	0.09	0.01	N
ESR1	-0.25	1.0E-05	Y	0.09	0.02	Y	0.29	1.0E-05	Y	0.09	0.02	N
HOXA10	0.05	0.14	N	-0.25	1.0E-05	Y	0	0.50	N	-0.08	0.02	N
CREM	-0.03	0.20	N	-0.23	1.0E-05	Y	-0.58	1.0E-05	Y	-0.07	0.05	N
SOX2	0.29	1.0E-05	Y	-0.18	2.0E-05	Y	0.37	1.0E-05	Y	0.06	0.06	N
HDAC4	0.04	0.19	N	0.20	2.0E-05	Y	-0.28	1.0E-05	Y	0.06	0.08	N
RUNX3	-0.24	1.0E-05	Y	0.38	1.0E-05	Y	-0.02	0.36	N	0.04	0.19	N
HDAC1	-0.22	1.0E-05	Y	0.36	1.0E-05	Y	-0.67	1.0E-05	Y	4.1E-	0.46	N
TRERF1	-0.12	2.0E-03	Y	-0.05	0.10	N	-0.85	1.0E-05	Y	0	0.50	N
NFKBIA	-2.1E-03	0.48	N	-0.21	1.0E-05	Y	-0.70	1.0E-05	Y	0	0.50	N
PITX1	0.02	0.32	N	0.24	1.0E-05	Y	-0.51	1.0E-05	Y	0	0.50	N
GATA2	0.30	1.0E-05	Y	-0.54	1.0E-05	Y	-0.47	1.0E-05	Y	0	0.50	N
RBMX	-0.21	1.0E-05	Y	0.34	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N
CREB5	0.34	1.0E-05	Y	-0.46	1.0E-05	Y	-0.35	1.0E-05	Y	0	0.50	N
HDAC9	-0.25	1.0E-05	Y	0.33	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N
REST	-0.11	3.4E-03	Y	0.23	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N
HEY1	-0.16	1.0E-04	Y	0.15	2.0E-04	Y	-0.26	1.0E-05	Y	0	0.50	N
SREBF1	0.08	0.02	Y	-3.4E-	0.47	N	-0.23	1.0E-05	Y	0	0.50	N
DNMT1	-0.20	1.0E-05	Y	0.22	1.0E-05	Y	-0.23	1.0E-05	Y	0	0.50	N
HNF1A	-0.32	1.0E-05	Y	0.16	7.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N
TCF4	0.13	9.5E-04	Y	-0.27	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N
NR5A1	0.10	9.3E-03	Y	-0.12	1.6E-03	Y	0.50	1.0E-05	Y	0	0.50	N
TFDP1	-0.10	0.01	Y	0.16	8.0E-05	Y	0.95	1.0E-05	Y	0	0.50	N
PROX1	-0.04	0.16	N	0.24	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N
ATF3	0.19	2.0E-05	Y	-0.37	1.0E-05	Y	-0.11	3.9E-03	Y	0	0.50	N
ING4	-0.02	0.29	N	-0.08	0.02	Y	-0.11	4.7E-03	Y	0	0.50	N
POU5F1	-0.42	1.0E-05	Y	0.06	0.09	N	-0.08	0.03	Y	0	0.50	N
DDIT3	0.15	9.0E-05	Y	0.08	0.03	Y	-0.04	0.16	N	0	0.50	N
PGR	0.14	6.0E-04	Y	-0.23	1.0E-05	Y	0.04	0.16	N	0	0.50	N
POU4F1	0.44	1.0E-05	Y	-0.71	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA11	0.23	1.0E-05	Y	-0.69	1.0E-05	Y	0	0.50	N	0	0.50	N
CBX6	0.37	1.0E-05	Y	-0.67	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF1	0.22	1.0E-05	Y	-0.66	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPE	0.22	1.0E-05	Y	-0.64	1.0E-05	Y	0	0.50	N	0	0.50	N
RBBP7	0.14	5.3E-04	Y	-0.63	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1H2	0.13	6.7E-04	Y	-0.60	1.0E-05	Y	0	0.50	N	0	0.50	N
TCF3	0.12	2.3E-03	Y	-0.59	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARD	0.25	1.0E-05	Y	-0.59	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF11	0.06	0.06	N	-0.58	1.0E-05	Y	0	0.50	N	0	0.50	N
DLX4	0.42	1.0E-05	Y	-0.56	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX4	0.30	1.0E-05	Y	-0.54	1.0E-05	Y	0	0.50	N	0	0.50	N
SRY	0.36	1.0E-05	Y	-0.54	1.0E-05	Y	0	0.50	N	0	0.50	N

MEN1	0.71	1.0E-05	Y	-0.54	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX2-2	0.19	2.0E-05	Y	-0.54	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXC6	0.13	1.4E-03	Y	-0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
PHOX2A	0.21	1.0E-05	Y	-0.53	1.0E-05	Y	0	0.50	N	0	0.50	N
TFDP3	0.29	1.0E-05	Y	-0.52	1.0E-05	Y	0	0.50	N	0	0.50	N
TNFAIP3	0.10	9.7E-03	Y	-0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
MXD1	0.29	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3A	0.26	1.0E-05	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
TAL1	0.15	2.5E-04	Y	-0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3L1	0.41	1.0E-05	Y	-0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP3	0.18	3.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
EWSR1	0.16	8.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
RORA	0.33	1.0E-05	Y	-0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
ERF	0.24	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
LYL1	0.35	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
LHX3	0.29	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA6	0.39	1.0E-05	Y	-0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX6	0.42	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXA1	0.26	1.0E-05	Y	-0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
AATF	0.25	1.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
DEAF1	0.19	2.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKB2	0.19	2.0E-05	Y	-0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
ING1	0.25	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
NR0B2	0.46	1.0E-05	Y	-0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2F2	0.35	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
BCL11A	0.06	0.07	N	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
TFAP4	0.23	1.0E-05	Y	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
LDB1	-2.4E-03	0.48	N	-0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
COPS5	0.48	1.0E-05	Y	-0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
BARD1	0.12	2.6E-03	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA7	0.12	2.9E-03	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
NFKBIB	0.15	9.0E-05	Y	-0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
NFAT5	0.14	5.2E-04	Y	-0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
MYF5	0.15	8.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXP1	0.18	2.0E-05	Y	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
SATB1	-0.02	0.35	N	-0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
TCF12	0.04	0.17	N	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF5	0.12	2.2E-03	Y	-0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2A	-0.05	0.13	N	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
HLTF	0.11	3.5E-03	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
MSX2	0.26	1.0E-05	Y	-0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
KDM2A	0.27	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
LMO4	0.26	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
SPDEF	0.57	1.0E-05	Y	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
OTX1	0.07	0.04	N	-0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
MDM4	0.08	0.03	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
NKX2-5	0.26	1.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
PBX2	0.17	3.0E-05	Y	-0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF2	0.16	8.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
IKBKB	0.34	1.0E-05	Y	-0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
GATA6	0.05	0.13	N	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXA9	0.18	3.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
TFCP2	0.73	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
PER2	0.24	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
DNMT3L	0.58	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC7	0.25	1.0E-05	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
NR1I3	0.14	2.9E-04	Y	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
TBPL1	0.05	0.14	N	-0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF3	0.14	4.5E-04	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
TCFL5	0.15	2.1E-04	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
BHLHE41	0.25	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
MYF6	0.22	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXD3	0.08	0.03	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
CREBBP	0.21	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX3	0.22	1.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N

HIRA	0.12	2.4E-03	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPG	0.17	5.0E-05	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
ELK1	0.07	0.06	N	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
FLI1	0.30	1.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
KAT6A	0.16	8.0E-05	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
SSB	0.18	2.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF3	0.16	8.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXA2	0.08	0.03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF6	0.22	1.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
GFI1B	0.15	9.0E-05	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
FOSL2	0.12	2.5E-03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
NEUROD	0.06	0.06	N	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
PTMA	0.29	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NR2E3	0.24	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
HEXIM1	0.16	8.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOR2	0.05	0.14	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
SPEN	0.01	0.40	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF13	0.26	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
MXI1	0.13	1.5E-03	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NFE2L1	0.21	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
MAFF	0.36	1.0E-05	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
HNF4G	0.13	9.8E-04	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
HES1	0.08	0.02	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
MYBL2	0.17	3.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
GZF1	0.27	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
NFRKB	-0.02	0.31	N	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF2	0.09	0.01	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
CREB3	0.09	0.02	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF12	-0.19	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
DEK	0.08	0.04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HAND2	0.08	0.04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
E4F1	0.09	0.02	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
L3MBTL1	0.06	0.06	N	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HBP1	0.27	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ESR2	0.13	8.5E-04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXB1	0.17	6.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
ING2	0.24	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
SP4	0.24	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
MLXIPL	0.24	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
ID1	0.34	1.0E-05	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXC1	0.15	2.0E-04	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
HINFP	-0.02	0.30	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
ATOH1	0.11	4.3E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
SRSF1	-0.08	0.03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
SMURF2	-0.12	2.6E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXQ1	0.07	0.04	N	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
RREB1	0.24	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
HSF4	-0.08	0.03	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
MAFB	0.06	0.07	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCA4	0.06	0.09	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
IKZF1	0.17	3.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
RBL2	0.05	0.11	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
NPAS2	0.01	0.39	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
HR	0.02	0.32	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
ATRX	0.06	0.08	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
CHD4	-0.09	0.02	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
CUX1	-0.09	0.01	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
NF1	0.25	1.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
ERCC2	0.19	2.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
CITED2	-0.13	1.1E-03	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
BTF3	0.28	1.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
CDX1	-0.27	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
RARB	-0.30	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
CLOCK	-0.23	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
TAF1	-0.05	0.10	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N

FOXO4	-0.04	0.19	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
BCL3	-0.24	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
CEBPZ	-0.30	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
RB1CC1	-0.14	6.1E-04	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXF1	-0.12	2.3E-03	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
TBX21	-0.17	4.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ILF2	-0.08	0.03	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
AES	-0.02	0.31	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
ID2	-0.20	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
KCNIP3	-0.42	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
POU2AF1	-0.27	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
EN1	-0.17	3.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
PHOX2B	-0.05	0.11	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
POU4F2	-0.32	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
ILF3	-0.18	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
SPIC	-0.11	5.2E-03	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
ELK3	-0.06	0.08	N	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIL3	-0.19	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA4	-0.21	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
IFI16	-0.23	1.0E-05	Y	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF6	-0.10	9.1E-03	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
CRX	-0.22	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F7	-0.19	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
SFPQ	-0.12	1.4E-03	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
SATB2	-0.04	0.14	N	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
TP73	-0.61	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXG1	-0.08	0.03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
EAPP	-0.09	0.01	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
APC	-0.20	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM6	-0.39	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
TEF	-0.28	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
HAX1	-0.31	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
CRTC1	-0.17	6.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
HIPK2	0.01	0.37	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
IRF9	-0.21	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
SIX1	-0.30	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
SKIL	-0.24	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
MAX	-0.28	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC5	-0.03	0.25	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOA3	-0.22	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
PITX2	7.6E-03	0.43	N	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA2	-0.24	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF8	-0.16	9.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
SPIB	-0.09	0.02	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
SMARCB1	-0.10	0.01	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
GFI1	-0.34	1.0E-05	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
PER1	-0.11	4.8E-03	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
MED1	-0.03	0.22	N	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
HDAC10	-0.21	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
MEF2D	-0.25	1.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT2	-0.16	8.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
NCOR1	-0.14	2.8E-04	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL2	-0.11	3.6E-03	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
SOX11	-0.30	1.0E-05	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
PAX4	-0.17	5.0E-05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
ATF5	-0.28	1.0E-05	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
ARNT	0.02	0.35	N	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
NFYB	-0.17	3.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIX	-0.30	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXM1	-0.42	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
FOSL1	-0.18	2.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
ARNTL2	-0.14	6.0E-04	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
KDM4C	-0.23	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
NFIA	0.05	0.14	N	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
SKI	-0.32	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N

HEY2	-0.33	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
SND1	-0.26	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
KHDRBS1	-0.09	0.02	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
ELF4	-0.18	2.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
RFX1	-0.05	0.10	N	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
POLR1A	-0.29	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
PPARGC1	-0.31	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
AIP	-0.26	1.0E-05	Y	0.40	1.0E-05	Y	0	0.50	N	0	0.50	N
TCF19	-0.59	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
NFYC	0.01	0.38	N	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
ARID3A	-0.12	1.6E-03	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
DLX3	-0.27	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
MTA3	-0.27	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
HCFC1	-0.08	0.03	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
PIAS1	-0.20	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
AHR	-0.10	6.9E-03	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
FOXL1	-0.17	6.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
BTAF1	-0.16	8.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
SIRT2	-0.10	7.0E-03	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
SERTAD1	-0.26	1.0E-05	Y	0.47	1.0E-05	Y	0	0.50	N	0	0.50	N
LIMD1	-0.27	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
MECP2	-0.15	2.3E-04	Y	0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
MAF	-0.31	1.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
STAT5A	-0.27	1.0E-05	Y	0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
E2F6	-0.63	1.0E-05	Y	0.50	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRG	-0.23	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
BTG2	-0.03	0.22	N	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
LRRFIP1	-0.21	1.0E-05	Y	0.52	1.0E-05	Y	0	0.50	N	0	0.50	N
MBD2	-0.35	1.0E-05	Y	0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
HOXB13	-0.31	1.0E-05	Y	0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
MKL1	-0.22	1.0E-05	Y	0.57	1.0E-05	Y	0	0.50	N	0	0.50	N
TBP	-0.50	1.0E-05	Y	0.58	1.0E-05	Y	0	0.50	N	0	0.50	N
DDB2	-0.08	0.03	Y	0.61	1.0E-05	Y	0	0.50	N	0	0.50	N
ESRRA	-0.57	1.0E-05	Y	0.63	1.0E-05	Y	0	0.50	N	0	0.50	N
CTCFL	-0.30	1.0E-05	Y	0.64	1.0E-05	Y	0	0.50	N	0	0.50	N
MCM2	-0.35	1.0E-05	Y	0.65	1.0E-05	Y	0	0.50	N	0	0.50	N
ENO1	-0.30	1.0E-05	Y	0.75	1.0E-05	Y	0	0.50	N	0	0.50	N
KLF16	0.20	2.0E-05	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
PRDM1	-0.18	2.0E-05	Y	0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
TP53BP1	-0.22	1.0E-05	Y	0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
SF1	-0.05	0.10	N	0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
ID4	-0.35	1.0E-05	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
FOXF2	-0.09	0.02	Y	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
NCOA1	0.01	0.37	N	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
ELK4	-0.05	0.13	N	0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
PITX3	-0.41	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
THRB	-0.03	0.21	N	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
NR0B1	-0.09	0.02	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
JUNB	-0.26	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
TOB1	-0.22	1.0E-05	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
GTF3A	-0.13	9.9E-04	Y	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
ASCL1	-0.05	0.12	N	0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
HTATIP2	0.40	1.0E-05	Y	-0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
MED23	0.04	0.18	N	0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
STAT5B	-0.08	0.02	Y	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
GLI1	0.08	0.03	Y	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
HIC1	0.24	1.0E-05	Y	-0.17	5.0E-05	Y	0	0.50	N	0	0.50	N
RFX3	0.13	1.1E-03	Y	-0.17	5.0E-05	Y	0	0.50	N	0	0.50	N
SOX10	-0.17	5.0E-05	Y	0.16	6.0E-05	Y	0	0.50	N	0	0.50	N
HDAC3	0.03	0.25	N	-0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
SLC2A4R	-0.28	1.0E-05	Y	0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
NR1H3	-9.0E-03	0.42	N	0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
TAF4	-0.11	4.7E-03	Y	0.16	7.0E-05	Y	0	0.50	N	0	0.50	N
ETV6	-0.08	0.03	Y	-0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
GBX2	-0.22	1.0E-05	Y	0.15	8.0E-05	Y	0	0.50	N	0	0.50	N

SMARCA1	0.02	0.29	N	0.15	8.0E-05	Y	0	0.50	N	0	0.50	N
PAX3	-0.11	3.6E-03	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
MSX1	0.04	0.16	N	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
FUS	-0.03	0.26	N	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
EGR3	-0.18	1.0E-05	Y	0.16	8.0E-05	Y	0	0.50	N	0	0.50	N
PKNOX1	5.4E-03	0.45	N	-0.16	9.0E-05	Y	0	0.50	N	0	0.50	N
PA2G4	0.11	3.6E-03	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
KAT2B	-0.10	8.7E-03	Y	-0.16	1.0E-04	Y	0	0.50	N	0	0.50	N
MLLT3	0.26	1.0E-05	Y	-0.15	1.0E-04	Y	0	0.50	N	0	0.50	N
SALL4	0.07	0.04	Y	-0.15	1.0E-04	Y	0	0.50	N	0	0.50	N
NR4A2	-0.06	0.09	N	-0.15	1.0E-04	Y	0	0.50	N	0	0.50	N
MAML1	-0.12	2.2E-03	Y	-0.15	1.1E-04	Y	0	0.50	N	0	0.50	N
MYOG	-0.14	3.7E-04	Y	-0.15	1.3E-04	Y	0	0.50	N	0	0.50	N
FOXN1	-0.02	0.31	N	0.15	1.3E-04	Y	0	0.50	N	0	0.50	N
TP63	-0.16	1.0E-04	Y	0.15	1.3E-04	Y	0	0.50	N	0	0.50	N
NRIP1	-0.25	1.0E-05	Y	0.15	1.4E-04	Y	0	0.50	N	0	0.50	N
ISL1	0.08	0.03	Y	-0.15	1.6E-04	Y	0	0.50	N	0	0.50	N
NAB2	-0.03	0.22	N	-0.15	1.7E-04	Y	0	0.50	N	0	0.50	N
NEUROG	-0.12	1.5E-03	Y	-0.15	1.7E-04	Y	0	0.50	N	0	0.50	N
NKX3-1	0.20	2.0E-05	Y	-0.15	1.9E-04	Y	0	0.50	N	0	0.50	N
SP7	-0.01	0.37	N	-0.15	2.3E-04	Y	0	0.50	N	0	0.50	N
NFIC	-0.18	1.0E-05	Y	0.15	2.3E-04	Y	0	0.50	N	0	0.50	N
HES6	0.02	0.34	N	-0.15	2.8E-04	Y	0	0.50	N	0	0.50	N
ONECUT2	0.07	0.04	N	-0.14	2.9E-04	Y	0	0.50	N	0	0.50	N
NRL	0.15	8.0E-05	Y	-0.14	3.3E-04	Y	0	0.50	N	0	0.50	N
JDP2	0.11	3.7E-03	Y	-0.14	3.9E-04	Y	0	0.50	N	0	0.50	N
POU3F2	-0.07	0.05	N	0.14	4.2E-04	Y	0	0.50	N	0	0.50	N
MEIS1	0.20	2.0E-05	Y	-0.14	5.2E-04	Y	0	0.50	N	0	0.50	N
PAX2	0.20	2.0E-05	Y	-0.14	5.4E-04	Y	0	0.50	N	0	0.50	N
CRABP2	-0.09	0.01	Y	-0.13	7.2E-04	Y	0	0.50	N	0	0.50	N
NR4A1	-0.03	0.26	N	-0.13	1.0E-03	Y	0	0.50	N	0	0.50	N
RBL1	-0.05	0.11	N	-0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
SOX17	-0.17	4.0E-05	Y	-0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
HOXC10	0.03	0.26	N	0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
BACH1	1.8E-03	0.48	N	-0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
PURA	-0.22	1.0E-05	Y	0.13	1.5E-03	Y	0	0.50	N	0	0.50	N
RARG	-0.06	0.07	N	-0.12	1.8E-03	Y	0	0.50	N	0	0.50	N
SIM2	0.06	0.07	N	0.12	2.0E-03	Y	0	0.50	N	0	0.50	N
PBX1	0.15	9.0E-05	Y	-0.12	2.0E-03	Y	0	0.50	N	0	0.50	N
CBX7	-0.04	0.19	N	0.12	2.6E-03	Y	0	0.50	N	0	0.50	N
MCM4	-0.10	6.9E-03	Y	-0.12	2.6E-03	Y	0	0.50	N	0	0.50	N
POU1F1	-0.07	0.05	N	0.12	2.6E-03	Y	0	0.50	N	0	0.50	N
DLX5	-1.7E-03	0.48	N	-0.12	2.7E-03	Y	0	0.50	N	0	0.50	N
EGR2	-0.08	0.03	Y	-0.12	2.8E-03	Y	0	0.50	N	0	0.50	N
HOXC9	0.02	0.33	N	0.12	2.9E-03	Y	0	0.50	N	0	0.50	N
BCL11B	-0.13	7.6E-04	Y	0.12	3.0E-03	Y	0	0.50	N	0	0.50	N
NPAS1	-0.01	0.40	N	-0.11	3.4E-03	Y	0	0.50	N	0	0.50	N
SHOX	0.10	9.0E-03	Y	-0.11	3.4E-03	Y	0	0.50	N	0	0.50	N
PLAG1	-0.04	0.14	N	0.11	3.4E-03	Y	0	0.50	N	0	0.50	N
FOXO1	0.13	7.3E-04	Y	-0.11	3.6E-03	Y	0	0.50	N	0	0.50	N
RNF14	-0.28	1.0E-05	Y	0.11	3.8E-03	Y	0	0.50	N	0	0.50	N
NR4A3	0.21	1.0E-05	Y	0.11	4.2E-03	Y	0	0.50	N	0	0.50	N
NFATC2	0.12	1.6E-03	Y	-0.11	4.3E-03	Y	0	0.50	N	0	0.50	N
ARNTL	0.04	0.15	N	0.11	4.6E-03	Y	0	0.50	N	0	0.50	N
EHMT2	0.12	2.1E-03	Y	-0.11	4.7E-03	Y	0	0.50	N	0	0.50	N
IRF7	0.07	0.06	N	0.11	4.7E-03	Y	0	0.50	N	0	0.50	N
HMGB2	-0.11	5.6E-03	Y	-0.10	6.7E-03	Y	0	0.50	N	0	0.50	N
FHL2	0.16	8.0E-05	Y	-0.10	7.0E-03	Y	0	0.50	N	0	0.50	N
PAWR	-0.11	4.4E-03	Y	0.10	7.6E-03	Y	0	0.50	N	0	0.50	N
NFATC1	0.14	2.9E-04	Y	-0.10	8.6E-03	Y	0	0.50	N	0	0.50	N
PIAS4	-0.05	0.12	N	-0.10	8.6E-03	Y	0	0.50	N	0	0.50	N
SNAI1	0.06	0.09	N	-0.10	8.9E-03	Y	0	0.50	N	0	0.50	N
IRF4	0.03	0.21	N	-0.10	1.0E-02	Y	0	0.50	N	0	0.50	N
NFIB	-0.03	0.21	N	0.10	0.01	Y	0	0.50	N	0	0.50	N
MLLT10	0.02	0.31	N	0.10	0.01	Y	0	0.50	N	0	0.50	N

MYOCD	0.03	0.23	N	-0.10	0.01	Y	0	0.50	N	0	0.50	N
NR2F2	-0.27	1.0E-05	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
HLF	-0.08	0.03	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
EIF2AK2	0.02	0.31	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
SIN3A	-3.1E-03	0.47	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
ELF1	0.15	1.3E-04	Y	0.09	0.01	Y	0	0.50	N	0	0.50	N
PIAS2	0.29	1.0E-05	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
HOXD9	-0.09	0.01	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
HMGA2	9.2E-03	0.41	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
NRF1	-0.25	1.0E-05	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
FOXH1	0.27	1.0E-05	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
TBX3	-0.05	0.11	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
IRF8	0.13	1.3E-03	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
NR1D1	7.5E-03	0.43	N	-0.08	0.02	Y	0	0.50	N	0	0.50	N
TEAD4	-0.06	0.07	N	-0.08	0.02	Y	0	0.50	N	0	0.50	N
PRDM14	0.17	5.0E-05	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
FOXE1	0.13	1.1E-03	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
HOXA1	-0.06	0.07	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
TLX1	0.11	4.8E-03	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
GLI2	1.3E-03	0.49	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
ELF2	-0.10	7.0E-03	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
PLAGL2	0.09	0.02	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
NFATC3	0.04	0.16	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
SOX6	-0.09	0.01	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
LHX4	0.10	7.4E-03	Y	-0.08	0.04	Y	0	0.50	N	0	0.50	N
OTX2	-0.07	0.04	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
SP2	-0.24	1.0E-05	Y	0.08	0.04	Y	0	0.50	N	0	0.50	N
ONECUT1	0.04	0.15	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
PCGF2	0.10	9.7E-03	Y	0.07	0.04	Y	0	0.50	N	0	0.50	N
RAD51	0.03	0.21	N	0.07	0.04	Y	0	0.50	N	0	0.50	N
TBX2	-0.02	0.32	N	0.07	0.04	Y	0	0.50	N	0	0.50	N
EHF	0.08	0.03	Y	-0.07	0.04	Y	0	0.50	N	0	0.50	N
PLAGL1	-0.31	1.0E-05	Y	0.07	0.04	Y	0	0.50	N	0	0.50	N
TFAP2C	-0.23	1.0E-05	Y	-0.07	0.04	Y	0	0.50	N	0	0.50	N
MEF2C	0.13	9.8E-04	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
ECD	-0.08	0.04	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
THRA	0.02	0.30	N	-0.07	0.05	N	0	0.50	N	0	0.50	N
TCF7L2	-3.9E-03	0.46	N	0.07	0.05	N	0	0.50	N	0	0.50	N
HOPX	-0.06	0.07	N	0.07	0.05	N	0	0.50	N	0	0.50	N
MTF1	0.03	0.25	N	-0.06	0.06	N	0	0.50	N	0	0.50	N
PHB2	-0.15	1.0E-04	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
PIAS3	-0.20	1.0E-05	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
MYOD1	-0.22	1.0E-05	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
SMAD7	-0.18	1.0E-05	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
GLI3	0.06	0.07	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
RFX5	0.25	1.0E-05	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
NR2F1	-0.06	0.06	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
ELL	-0.07	0.05	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
GCM2	0.02	0.32	N	0.06	0.08	N	0	0.50	N	0	0.50	N
DACH1	-0.10	9.7E-03	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
HHEX	0.16	8.0E-05	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
MZF1	-0.27	1.0E-05	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
E2F8	8.2E-03	0.42	N	0.05	0.10	N	0	0.50	N	0	0.50	N
TFAP2B	0.03	0.20	N	0.05	0.10	N	0	0.50	N	0	0.50	N
KAT5	0.01	0.37	N	-0.05	0.10	N	0	0.50	N	0	0.50	N
ETV3	0.02	0.35	N	-0.05	0.13	N	0	0.50	N	0	0.50	N
IRF3	-0.12	1.7E-03	Y	-0.05	0.13	N	0	0.50	N	0	0.50	N
NUPR1	0.19	2.0E-05	Y	-0.04	0.14	N	0	0.50	N	0	0.50	N
ETV2	-0.08	0.02	Y	-0.04	0.15	N	0	0.50	N	0	0.50	N
MAFA	6.3E-03	0.44	N	0.04	0.15	N	0	0.50	N	0	0.50	N
NKX2-1	0.07	0.05	N	-0.04	0.15	N	0	0.50	N	0	0.50	N
CTBP1	-0.08	0.03	Y	-0.04	0.15	N	0	0.50	N	0	0.50	N
SRCAP	0.13	1.1E-03	Y	-0.04	0.17	N	0	0.50	N	0	0.50	N
TBX5	0.02	0.28	N	-0.04	0.18	N	0	0.50	N	0	0.50	N
BRD7	0.18	2.0E-05	Y	-0.04	0.18	N	0	0.50	N	0	0.50	N

NELFCD	-0.12	2.0E-03	Y	0.04	0.18	N	0	0.50	N	0	0.50	N
PAX8	-0.03	0.26	N	-0.04	0.19	N	0	0.50	N	0	0.50	N
NR5A2	-0.01	0.37	N	0.04	0.19	N	0	0.50	N	0	0.50	N
SUPT3H	-0.14	4.9E-04	Y	-0.04	0.19	N	0	0.50	N	0	0.50	N
LMO2	-0.13	8.4E-04	Y	-0.04	0.20	N	0	0.50	N	0	0.50	N
RFWD2	-0.09	0.02	Y	0.04	0.20	N	0	0.50	N	0	0.50	N
NELFB	0.05	0.13	N	0.03	0.21	N	0	0.50	N	0	0.50	N
NPM1	0.05	0.12	N	0.03	0.21	N	0	0.50	N	0	0.50	N
DBP	-0.03	0.25	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
SALL3	-0.07	0.05	N	0.03	0.21	N	0	0.50	N	0	0.50	N
NOTCH3	-0.04	0.19	N	0.03	0.21	N	0	0.50	N	0	0.50	N
PDX1	1.5E-05	0.50	N	0.03	0.22	N	0	0.50	N	0	0.50	N
CBX8	0.12	2.7E-03	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
MAZ	0.10	9.3E-03	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
LHX2	-0.20	1.0E-05	Y	-0.03	0.23	N	0	0.50	N	0	0.50	N
NR2F6	-0.06	0.07	N	0.03	0.23	N	0	0.50	N	0	0.50	N
KLF15	-0.02	0.31	N	-0.03	0.25	N	0	0.50	N	0	0.50	N
EVX1	0.19	2.0E-05	Y	-0.03	0.25	N	0	0.50	N	0	0.50	N
NR2C2	-0.05	0.13	N	-0.03	0.27	N	0	0.50	N	0	0.50	N
ARID1B	-0.09	0.01	Y	0.03	0.27	N	0	0.50	N	0	0.50	N
ETV5	-0.02	0.30	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
RELB	-0.04	0.18	N	0.02	0.28	N	0	0.50	N	0	0.50	N
GATA4	-0.05	0.13	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
CTCF	0.07	0.06	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
NHLH2	0.17	6.0E-05	Y	-0.02	0.29	N	0	0.50	N	0	0.50	N
KLF9	-4.5E-04	0.50	N	-0.02	0.29	N	0	0.50	N	0	0.50	N
PARP1	-0.05	0.12	N	-0.02	0.29	N	0	0.50	N	0	0.50	N
LMX1B	0.19	2.0E-05	Y	-0.02	0.29	N	0	0.50	N	0	0.50	N
GCM1	0.14	4.9E-04	Y	0.02	0.29	N	0	0.50	N	0	0.50	N
FOXP2	-0.19	1.0E-05	Y	-0.02	0.30	N	0	0.50	N	0	0.50	N
HDAC11	0.04	0.17	N	0.02	0.30	N	0	0.50	N	0	0.50	N
SETBP1	-0.14	4.5E-04	Y	0.02	0.31	N	0	0.50	N	0	0.50	N
E2F3	-0.05	0.11	N	-0.02	0.32	N	0	0.50	N	0	0.50	N
TRIB3	7.5E-03	0.43	N	0.02	0.32	N	0	0.50	N	0	0.50	N
DR1	0.10	0.01	Y	0.02	0.32	N	0	0.50	N	0	0.50	N
RBPJ	-0.15	1.0E-04	Y	0.02	0.32	N	0	0.50	N	0	0.50	N
TEAD1	0.06	0.08	N	-0.02	0.33	N	0	0.50	N	0	0.50	N
HDGF	-3.9E-03	0.46	N	0.02	0.35	N	0	0.50	N	0	0.50	N
CEBPD	-0.11	3.2E-03	Y	0.02	0.35	N	0	0.50	N	0	0.50	N
HOXA5	0.07	0.05	N	-0.02	0.36	N	0	0.50	N	0	0.50	N
TGIF1	0.03	0.23	N	-0.01	0.36	N	0	0.50	N	0	0.50	N
CDCA7L	-0.18	1.0E-05	Y	0.01	0.37	N	0	0.50	N	0	0.50	N
FOSB	-0.08	0.03	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
MBD1	-0.10	8.3E-03	Y	0.01	0.39	N	0	0.50	N	0	0.50	N
HOXC13	-0.13	1.2E-03	Y	8.7E-03	0.42	N	0	0.50	N	0	0.50	N
NCOA2	-0.20	1.0E-05	Y	-8.6E-	0.42	N	0	0.50	N	0	0.50	N
APBB1	-0.21	1.0E-05	Y	-8.3E-	0.42	N	0	0.50	N	0	0.50	N
ARID1A	-0.08	0.03	Y	-7.1E-	0.43	N	0	0.50	N	0	0.50	N
SUGP1	-0.14	6.0E-04	Y	5.3E-03	0.45	N	0	0.50	N	0	0.50	N
GTF2I	-0.21	1.0E-05	Y	-4.8E-	0.45	N	0	0.50	N	0	0.50	N
GABPA	-0.02	0.32	N	-4.8E-	0.45	N	0	0.50	N	0	0.50	N
RUVBL1	0.28	1.0E-05	Y	-4.5E-	0.46	N	0	0.50	N	0	0.50	N
LMO3	0.13	6.3E-04	Y	2.6E-03	0.48	N	0	0.50	N	0	0.50	N
STAT4	0.02	0.29	N	2.4E-03	0.48	N	0	0.50	N	0	0.50	N
ANKRD1	0.07	0.04	N	5.8E-05	0.50	N	0	0.50	N	0	0.50	N

Master list of miRNAs in TCGA colorectal cancer dataset together the correlation scores of their expression values with PR signatures and enrichment scores of target genes with PR signatures

miRNA	*S*(M,P)	P-value	BH	*S*(M,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
mir-1914	0.25	1.0E-05	Y	-0.08	0.03	Y	0.29	1.0E-05	Y	-0.29	1.0E-05	Y
mir-1307	0.25	1.0E-05	Y	-0.14	3.7E-04	Y	0.31	1.0E-05	Y	-0.28	1.0E-05	Y
mir-449a	0.12	3.0E-03	Y	-0.08	0.04	Y	0.41	1.0E-05	Y	-0.27	1.0E-05	Y
mir-766	0.20	1.0E-05	Y	0.10	9.1E-03	Y	0.30	1.0E-05	Y	-0.23	1.0E-05	Y
mir-1303	-0.13	1.4E-03	Y	0.06	0.09	N	0.29	1.0E-05	Y	-0.22	1.0E-05	Y
mir-191	0.12	2.1E-03	Y	-0.19	1.0E-05	Y	0.24	1.0E-05	Y	-0.20	1.0E-05	Y
mir-671	0.21	1.0E-05	Y	0.02	0.35	N	0.21	1.0E-05	Y	-0.19	1.0E-05	Y
mir-605	4.2E-03	0.46	N	-0.08	0.04	Y	0.20	1.0E-05	Y	-0.18	1.0E-05	Y
mir-29a	-0.10	0.01	Y	-0.04	0.17	N	0.04	0.18	N	0.18	1.0E-05	Y
mir-150	-0.14	3.9E-04	Y	0.17	4.0E-05	Y	-0.13	1.2E-03	Y	0.19	1.0E-05	Y
mir-346	0.09	0.02	Y	-0.09	0.01	Y	0.02	0.35	N	0.20	1.0E-05	Y
mir-133b	-0.21	1.0E-05	Y	0.25	1.0E-05	Y	-0.09	0.02	Y	0.21	1.0E-05	Y
mir-133a-1	-0.24	1.0E-05	Y	0.19	1.0E-05	Y	-5.3E-	0.45	N	0.21	1.0E-05	Y
mir-133a-2	-0.19	1.0E-05	Y	0.27	1.0E-05	Y	-5.3E-	0.45	N	0.21	1.0E-05	Y
mir-203	-0.13	1.3E-03	Y	-0.13	7.2E-04	Y	0.18	4.0E-05	Y	0.22	1.0E-05	Y
mir-181c	-0.30	1.0E-05	Y	-0.05	0.12	N	-0.17	2.0E-05	Y	0.22	1.0E-05	Y
mir-204	-0.11	3.8E-03	Y	-0.04	0.19	N	0.02	0.30	N	0.24	1.0E-05	Y
mir-302d	0.08	0.04	Y	0.09	0.02	Y	-0.07	0.04	N	0.25	1.0E-05	Y
mir-20b	-0.14	3.5E-04	Y	0.20	1.0E-05	Y	0.03	0.21	N	0.25	1.0E-05	Y
mir-874	-0.19	1.0E-05	Y	0.02	0.32	N	0.43	1.0E-05	Y	0.26	1.0E-05	Y
mir-146a	0.07	0.06	N	0.06	0.09	N	0.06	0.07	N	0.28	1.0E-05	Y
mir-200c	-0.01	0.39	N	-0.11	6.0E-03	Y	0.08	0.03	Y	0.29	1.0E-05	Y
mir-130a	-0.13	1.3E-03	Y	0.13	9.1E-04	Y	-0.16	5.0E-05	Y	0.30	1.0E-05	Y
mir-200a	0.02	0.33	N	-0.11	3.8E-03	Y	-0.09	0.02	Y	0.32	1.0E-05	Y
mir-146b	-0.04	0.16	N	0.34	1.0E-05	Y	-0.02	0.36	N	0.33	1.0E-05	Y
mir-451	0.03	0.27	N	-0.04	0.18	N	-0.10	8.8E-03	Y	0.33	1.0E-05	Y
mir-19a	0.12	2.5E-03	Y	-0.09	0.02	Y	-0.03	0.27	N	0.33	1.0E-05	Y
mir-302a	0.15	3.0E-04	Y	-0.09	0.02	Y	-0.27	1.0E-05	Y	0.34	1.0E-05	Y
mir-224	-0.14	5.4E-04	Y	-0.24	1.0E-05	Y	-0.03	0.24	N	0.37	1.0E-05	Y
mir-200b	-0.10	9.1E-03	Y	-0.12	2.2E-03	Y	0.09	0.02	Y	0.38	1.0E-05	Y
mir-429	0.04	0.20	N	-0.12	1.5E-03	Y	-0.06	0.09	N	0.39	1.0E-05	Y
mir-143	-0.23	1.0E-05	Y	0.34	1.0E-05	Y	0.11	6.7E-03	Y	0.40	1.0E-05	Y
mir-338	-0.13	6.1E-04	Y	0.12	2.0E-03	Y	-0.40	1.0E-05	Y	0.56	1.0E-05	Y
mir-501	0.07	0.05	N	-0.14	3.5E-04	Y	0.56	1.0E-05	Y	-0.18	2.0E-05	Y
mir-30c-2	-0.06	0.10	N	-0.09	0.02	Y	0.29	1.0E-05	Y	-0.17	3.0E-05	Y
mir-137	-7.2E-03	0.43	N	0.25	1.0E-05	Y	0.17	6.0E-05	Y	0.18	3.0E-05	Y
mir-223	0.16	1.9E-04	Y	0.29	1.0E-05	Y	0.15	1.9E-04	Y	0.18	4.0E-05	Y
mir-140	-0.12	2.6E-03	Y	0.18	3.0E-05	Y	0.08	0.04	Y	0.17	6.0E-05	Y
mir-205	0.04	0.17	N	0.05	0.11	N	0.06	0.09	N	0.16	1.5E-04	Y
mir-432	-0.08	0.03	Y	0.06	0.07	N	0.33	1.0E-05	Y	0.15	1.9E-04	Y
mir-138-1	-0.06	0.07	N	0.09	0.02	Y	-0.13	1.1E-03	Y	0.16	1.9E-04	Y
mir-138-2	-0.05	0.11	N	0.05	0.13	N	-0.13	1.1E-03	Y	0.16	1.9E-04	Y
mir-532	-0.13	7.5E-04	Y	-0.22	1.0E-05	Y	0.31	1.0E-05	Y	-0.15	2.2E-04	Y
mir-503	0.05	0.15	N	0.07	0.06	N	0.25	1.0E-05	Y	-0.15	2.6E-04	Y
mir-190	-0.07	0.05	N	0.08	0.04	Y	0.34	1.0E-05	Y	0.15	2.7E-04	Y
mir-425	0.07	0.04	Y	-0.13	1.2E-03	Y	0.24	1.0E-05	Y	-0.14	3.9E-04	Y
mir-18b	0.03	0.27	N	0.06	0.09	N	0.21	1.0E-05	Y	0.14	4.2E-04	Y
mir-335	0.02	0.34	N	-0.27	1.0E-05	Y	-0.14	3.5E-04	Y	0.14	5.1E-04	Y
mir-28	-0.20	1.0E-05	Y	0.05	0.11	N	0.24	1.0E-05	Y	0.14	5.4E-04	Y
mir-342	-0.05	0.11	N	0.16	1.0E-04	Y	0.26	1.0E-05	Y	-0.14	6.1E-04	Y
mir-212	0.07	0.05	N	0.34	1.0E-05	Y	0.30	1.0E-05	Y	-0.14	6.1E-04	Y
mir-193a	-0.17	4.0E-05	Y	0.11	5.8E-03	Y	0.10	9.3E-03	Y	-0.13	7.7E-04	Y
mir-941-1	0.09	0.02	Y	-5.7E-03	0.45	N	0.19	1.0E-05	Y	0.13	8.2E-04	Y
mir-145	-0.17	5.0E-05	Y	0.24	1.0E-05	Y	0.06	0.08	N	0.13	1.2E-03	Y
mir-217	-0.29	1.0E-05	Y	-0.04	0.17	N	-9.4E-	0.41	N	0.13	1.4E-03	Y
mir-141	0.09	0.01	Y	-0.07	0.04	Y	0.03	0.23	N	0.13	1.5E-03	Y
mir-365-2	-0.08	0.04	Y	0.04	0.17	N	0.18	2.0E-05	Y	0.13	1.7E-03	Y
mir-365-1	-0.12	2.8E-03	Y	-4.9E-03	0.45	N	0.18	2.0E-05	Y	0.13	1.7E-03	Y
mir-34c	-0.03	0.24	N	0.36	1.0E-05	Y	0.36	1.0E-05	Y	-0.12	2.4E-03	Y

mir-1180	0.21	1.0E-05	Y	5.4E-03	0.45	N	0.21	1.0E-05	Y	-0.12	3.0E-03	Y
mir-124-3	-0.02	0.31	N	0.18	3.0E-05	Y	0.02	0.33	N	0.12	3.1E-03	Y
mir-124-2	-0.09	0.02	Y	-0.06	0.08	N	0.02	0.34	N	0.12	3.3E-03	Y
mir-124-1	-0.06	0.09	N	-5.1E-03	0.45	N	0.02	0.34	N	0.12	3.3E-03	Y
mir-99b	-0.14	3.9E-04	Y	0.11	5.3E-03	Y	0.17	4.0E-05	Y	0.11	3.8E-03	Y
mir-130b	0.17	4.0E-05	Y	-0.13	9.4E-04	Y	0.09	0.02	Y	0.11	4.1E-03	Y
mir-376a-2	-0.05	0.14	N	-0.02	0.32	N	0.32	1.0E-05	Y	-0.11	4.5E-03	Y
mir-376a-1	-0.09	0.02	Y	0.02	0.33	N	0.32	1.0E-05	Y	-0.11	4.5E-03	Y
mir-19b-2	0.05	0.13	N	-0.09	0.02	Y	0.06	0.09	N	0.11	5.2E-03	Y
mir-142	-0.08	0.02	Y	0.24	1.0E-05	Y	0.02	0.31	N	0.11	5.5E-03	Y
mir-181b-1	-0.08	0.03	Y	0.09	0.01	Y	0.22	1.0E-05	Y	-0.11	5.6E-03	Y
mir-181b-2	-4.2E-03	0.46	N	0.05	0.13	N	0.22	1.0E-05	Y	-0.11	5.6E-03	Y
mir-625	0.17	4.0E-05	Y	0.04	0.15	N	-0.06	0.08	N	0.11	6.1E-03	Y
mir-125b-2	-0.22	1.0E-05	Y	0.26	1.0E-05	Y	0.32	1.0E-05	Y	-0.11	6.4E-03	Y
mir-362	-0.08	0.04	Y	-0.21	1.0E-05	Y	0.45	1.0E-05	Y	-0.10	6.6E-03	Y
mir-935	-0.01	0.39	N	0.09	0.02	Y	0.27	1.0E-05	Y	-0.10	6.7E-03	Y
mir-107	-0.07	0.05	N	0.07	0.06	N	0.19	1.0E-05	Y	0.11	6.7E-03	Y
mir-148a	-0.19	1.0E-05	Y	-0.17	2.0E-05	Y	0.15	3.1E-04	Y	0.10	7.2E-03	Y
let-7c	-0.29	1.0E-05	Y	0.26	1.0E-05	Y	0.21	1.0E-05	Y	-0.10	7.3E-03	Y
mir-33a	0.08	0.02	Y	-0.06	0.08	N	3.2E-03	0.47	N	0.10	9.3E-03	Y
mir-328	-0.08	0.04	Y	0.14	5.9E-04	Y	0.37	1.0E-05	Y	-0.10	9.5E-03	Y
mir-454	0.11	4.3E-03	Y	-0.05	0.11	N	0.24	1.0E-05	Y	-0.10	9.7E-03	Y
mir-211	-0.01	0.38	N	-0.06	0.08	N	0.26	1.0E-05	Y	0.10	0.01	Y
mir-1260	-0.03	0.27	N	0.09	0.02	Y	0.22	1.0E-05	Y	-0.09	0.01	Y
mir-106a	0.15	2.4E-04	Y	-0.09	0.02	Y	0.19	1.0E-05	Y	0.10	0.01	Y
mir-29c	-0.22	1.0E-05	Y	0.26	1.0E-05	Y	0.09	0.02	Y	0.09	0.01	Y
mir-29b-1	-0.08	0.03	Y	0.04	0.16	N	0.13	1.2E-03	Y	0.09	0.01	Y
mir-193b	-0.03	0.25	N	0.09	0.02	Y	0.31	1.0E-05	Y	-0.09	0.01	Y
let-7d	0.11	3.9E-03	Y	-0.11	5.1E-03	Y	0.20	1.0E-05	Y	-0.09	0.02	Y
mir-195	-0.20	1.0E-05	Y	0.03	0.23	N	0.26	1.0E-05	Y	0.09	0.02	Y
mir-148b	0.03	0.28	N	-0.13	6.2E-04	Y	-0.04	0.16	N	0.09	0.02	Y
let-7g	-0.04	0.18	N	-0.08	0.03	Y	0.27	1.0E-05	Y	0.09	0.02	Y
mir-378	0.12	2.8E-03	Y	-0.21	1.0E-05	Y	0.19	1.0E-05	Y	-0.08	0.03	Y
mir-769	0.09	0.02	Y	-0.22	1.0E-05	Y	0.25	1.0E-05	Y	-0.08	0.03	Y
mir-149	-0.07	0.05	N	0.11	5.2E-03	Y	0.25	1.0E-05	Y	-0.08	0.03	Y
mir-30d	-0.26	1.0E-05	Y	-0.04	0.17	N	0.16	1.3E-04	Y	0.08	0.03	Y
mir-215	-0.09	0.02	Y	-8.3E-03	0.42	N	0.22	1.0E-05	Y	-0.08	0.03	Y
mir-1296	0.10	8.8E-03	Y	-0.07	0.05	N	0.22	1.0E-05	Y	-0.08	0.03	Y
mir-548b	-0.08	0.03	Y	0.03	0.22	N	-0.15	2.6E-04	Y	-0.08	0.03	Y
mir-34b	-0.09	0.01	Y	0.13	1.1E-03	Y	0.33	1.0E-05	Y	-0.08	0.04	Y
mir-194-1	-0.20	1.0E-05	Y	-0.16	1.5E-04	Y	-0.03	0.22	N	0.08	0.04	Y
mir-194-2	-0.19	1.0E-05	Y	-0.15	1.9E-04	Y	-0.03	0.22	N	0.08	0.04	Y
mir-30e	-0.23	1.0E-05	Y	0.11	4.9E-03	Y	0.20	1.0E-05	Y	-0.07	0.04	Y
mir-652	-0.06	0.10	N	-0.01	0.38	N	0.20	1.0E-05	Y	-0.07	0.04	N
mir-15a	-0.03	0.27	N	0.12	2.8E-03	Y	0.11	7.0E-03	Y	0.07	0.05	N
mir-181d	-0.28	1.0E-05	Y	-0.09	0.01	Y	0.24	1.0E-05	Y	0.07	0.06	N
mir-375	-0.09	0.02	Y	-0.11	3.6E-03	Y	0.09	0.02	Y	0.07	0.06	N
mir-196b	-0.11	6.0E-03	Y	-0.17	5.0E-05	Y	0.28	1.0E-05	Y	-0.07	0.06	N
mir-497	-0.18	2.0E-05	Y	0.10	8.5E-03	Y	0.36	1.0E-05	Y	0.07	0.06	N
mir-940	0.20	1.0E-05	Y	0.07	0.05	N	0.29	1.0E-05	Y	-0.07	0.06	N
mir-598	8.6E-04	0.49	N	-0.02	0.33	N	0.50	1.0E-05	Y	-0.07	0.06	N
mir-132	-0.09	0.02	Y	0.35	1.0E-05	Y	0.03	0.24	N	0.06	0.07	N
let-7b	-0.21	1.0E-05	Y	0.17	4.0E-05	Y	0.23	1.0E-05	Y	-0.06	0.08	N
mir-30b	-0.01	0.37	N	-0.07	0.04	Y	0.18	1.0E-05	Y	-0.06	0.08	N
mir-185	0.07	0.05	N	0.02	0.29	N	0.22	1.0E-05	Y	0.06	0.08	N
mir-218-2	-0.28	1.0E-05	Y	0.30	1.0E-05	Y	0.14	5.1E-04	Y	-0.06	0.08	N
mir-192	-0.02	0.35	N	-0.27	1.0E-05	Y	0.21	1.0E-05	Y	-0.06	0.08	N
mir-361	-0.13	1.2E-03	Y	-0.02	0.33	N	0.27	1.0E-05	Y	-0.06	0.09	N
mir-128-1	0.08	0.03	Y	-0.08	0.03	Y	0.04	0.18	N	0.06	0.09	N
mir-23a	-0.08	0.03	Y	0.02	0.30	N	0.17	9.0E-05	Y	0.06	0.09	N
mir-455	0.04	0.20	N	0.06	0.07	N	0.18	2.0E-05	Y	0.06	0.09	N
mir-301a	0.13	9.4E-04	Y	-0.05	0.15	N	0.22	1.0E-05	Y	0.06	0.09	N
mir-331	0.10	9.5E-03	Y	0.11	4.3E-03	Y	0.23	1.0E-05	Y	-0.06	0.09	N
mir-151	-0.07	0.05	N	-0.04	0.19	N	0.26	1.0E-05	Y	-0.06	0.09	N
mir-374a	-0.13	1.1E-03	Y	-0.03	0.21	N	0.17	9.0E-05	Y	-0.05	0.11	N

mir-103-1	-0.10	0.01	Y	0.05	0.11	N	0.13	1.4E-03	Y	0.05	0.11	N
mir-103-2	0.15	2.4E-04	Y	-2.2E-03	0.48	N	0.13	1.4E-03	Y	0.05	0.11	N
mir-296	0.03	0.22	N	-0.16	1.3E-04	Y	0.10	7.7E-03	Y	0.05	0.12	N
mir-26b	-0.04	0.17	N	0.04	0.16	N	0.01	0.37	N	0.05	0.13	N
mir-96	-0.08	0.03	Y	0.06	0.07	N	0.19	1.0E-05	Y	0.05	0.13	N
mir-100	-0.30	1.0E-05	Y	0.36	1.0E-05	Y	0.14	3.8E-04	Y	-0.05	0.13	N
mir-320a	0.05	0.11	N	0.03	0.23	N	0.19	1.0E-05	Y	-0.05	0.13	N
mir-590	0.13	1.2E-03	Y	-0.12	2.4E-03	Y	0.25	1.0E-05	Y	-0.05	0.15	N
mir-186	0.03	0.23	N	-0.09	0.02	Y	0.18	4.0E-05	Y	-0.04	0.15	N
mir-92a-1	-0.05	0.11	N	-0.15	2.6E-04	Y	0.38	1.0E-05	Y	-0.04	0.15	N
mir-92a-2	-6.8E-03	0.44	N	-0.15	2.6E-04	Y	0.20	1.0E-05	Y	-0.04	0.16	N
mir-98	-0.07	0.06	N	-0.02	0.33	N	0.14	3.6E-04	Y	-0.04	0.16	N
mir-31	0.03	0.28	N	0.32	1.0E-05	Y	0.10	8.5E-03	Y	0.04	0.16	N
mir-32	0.12	2.5E-03	Y	-5.5E-03	0.45	N	0.19	1.0E-05	Y	-0.04	0.17	N
mir-182	-0.12	2.0E-03	Y	0.04	0.17	N	0.09	0.01	Y	0.04	0.17	N
mir-615	0.07	0.05	N	0.24	1.0E-05	Y	0.24	1.0E-05	Y	-0.04	0.18	N
mir-126	-0.06	0.10	N	0.12	3.1E-03	Y	0.21	1.0E-05	Y	-0.04	0.18	N
mir-760	0.21	1.0E-05	Y	-0.04	0.17	N	0.25	1.0E-05	Y	-0.04	0.18	N
mir-10a	-0.07	0.07	N	0.02	0.31	N	0.18	4.0E-05	Y	-0.04	0.19	N
mir-1229	0.11	3.8E-03	Y	-6.1E-03	0.44	N	0.28	1.0E-05	Y	-0.04	0.19	N
mir-15b	0.18	1.0E-05	Y	0.02	0.34	N	0.20	1.0E-05	Y	-0.04	0.20	N
mir-484	0.16	1.0E-04	Y	0.04	0.19	N	0.21	1.0E-05	Y	-0.04	0.20	N
mir-122	0.02	0.30	N	-0.12	1.7E-03	Y	0.13	8.7E-04	Y	0.04	0.20	N
mir-504	-0.19	1.0E-05	Y	0.01	0.39	N	0.16	1.4E-04	Y	-0.04	0.21	N
mir-330	7.6E-05	0.50	N	0.22	1.0E-05	Y	0.26	1.0E-05	Y	-0.03	0.21	N
mir-199a-2	-0.12	1.6E-03	Y	0.19	1.0E-05	Y	0.15	2.0E-04	Y	0.03	0.21	N
mir-199a-1	-0.13	6.7E-04	Y	0.19	1.0E-05	Y	0.15	2.0E-04	Y	0.03	0.21	N
mir-340	-3.1E-03	0.47	N	0.10	0.01	Y	0.18	4.0E-05	Y	-0.03	0.22	N
mir-324	0.10	8.8E-03	Y	0.07	0.06	N	0.19	1.0E-05	Y	-0.03	0.22	N
mir-1-2	-0.33	1.0E-05	Y	0.14	6.6E-04	Y	0.15	3.4E-04	Y	0.03	0.22	N
mir-1-1	-0.05	0.12	N	0.07	0.05	N	0.15	3.4E-04	Y	0.03	0.22	N
mir-92b	0.24	1.0E-05	Y	0.20	1.0E-05	Y	0.19	1.0E-05	Y	-0.03	0.23	N
mir-1226	0.14	4.2E-04	Y	-0.16	7.0E-05	Y	0.20	1.0E-05	Y	-0.03	0.23	N
mir-373	-0.06	0.07	N	-0.06	0.08	N	0.18	3.0E-05	Y	-0.03	0.23	N
mir-34a	8.0E-04	0.49	N	0.04	0.19	N	0.24	1.0E-05	Y	-0.03	0.23	N
let-7a-2	-0.25	1.0E-05	Y	0.09	0.02	Y	0.20	1.0E-05	Y	-0.03	0.25	N
let-7a-1	-0.25	1.0E-05	Y	0.08	0.03	Y	0.20	1.0E-05	Y	-0.03	0.25	N
mir-210	0.12	3.7E-03	Y	0.04	0.15	N	0.18	4.0E-05	Y	0.03	0.27	N
mir-505	0.12	2.1E-03	Y	-5.5E-03	0.45	N	0.27	1.0E-05	Y	-0.03	0.27	N
mir-214	-0.08	0.03	Y	0.20	1.0E-05	Y	0.11	4.9E-03	Y	-0.03	0.28	N
mir-221	3.9E-05	0.50	N	0.17	6.0E-05	Y	0.15	3.4E-04	Y	0.02	0.28	N
mir-374b	0.02	0.35	N	-0.13	6.5E-04	Y	0.08	0.02	Y	0.02	0.28	N
mir-23b	-0.23	1.0E-05	Y	0.12	3.2E-03	Y	0.19	1.0E-05	Y	0.02	0.28	N
mir-345	0.12	3.5E-03	Y	-0.06	0.10	N	0.21	1.0E-05	Y	-0.02	0.28	N
mir-339	0.06	0.10	N	-0.04	0.21	N	0.18	3.0E-05	Y	-0.02	0.28	N
mir-17	0.11	4.4E-03	Y	-0.11	4.2E-03	Y	0.14	3.9E-04	Y	0.02	0.28	N
mir-423	0.09	0.02	Y	-0.14	3.9E-04	Y	0.19	1.0E-05	Y	-0.02	0.31	N
mir-26a-1	0.10	7.9E-03	Y	-0.14	3.9E-04	Y	0.19	1.0E-05	Y	0.02	0.31	N
mir-27b	-0.11	4.3E-03	Y	0.05	0.13	N	0.13	9.6E-04	Y	-0.02	0.31	N
mir-1301	0.12	2.4E-03	Y	0.02	0.29	N	0.24	1.0E-05	Y	0.02	0.32	N
mir-708	-0.12	2.1E-03	Y	0.27	1.0E-05	Y	0.21	1.0E-05	Y	0.02	0.32	N
mir-93	0.08	0.02	Y	-0.12	3.2E-03	Y	0.18	4.0E-05	Y	0.02	0.32	N
mir-125b-1	-0.20	1.0E-05	Y	0.30	1.0E-05	Y	0.14	4.4E-04	Y	-0.02	0.32	N
mir-421	0.19	1.0E-05	Y	-0.17	5.0E-05	Y	0.19	1.0E-05	Y	0.02	0.33	N
mir-27a	-3.7E-03	0.46	N	0.06	0.09	N	0.13	1.4E-03	Y	0.02	0.33	N
mir-744	0.15	1.9E-04	Y	-0.11	3.7E-03	Y	0.17	6.0E-05	Y	-0.02	0.33	N
mir-155	0.05	0.12	N	0.30	1.0E-05	Y	0.18	3.0E-05	Y	0.02	0.34	N
mir-101-1	-0.28	1.0E-05	Y	0.19	1.0E-05	Y	0.17	4.0E-05	Y	-0.02	0.34	N
mir-101-2	-0.10	7.2E-03	Y	-0.05	0.15	N	0.17	4.0E-05	Y	-0.02	0.34	N
mir-21	-0.18	1.0E-05	Y	0.22	1.0E-05	Y	0.15	2.0E-04	Y	0.02	0.34	N
let-7i	-0.04	0.18	N	0.28	1.0E-05	Y	0.28	1.0E-05	Y	0.02	0.35	N
mir-320b-2	0.10	8.5E-03	Y	0.05	0.14	N	0.14	4.2E-04	Y	-0.02	0.35	N
mir-125a	-0.14	3.7E-04	Y	0.15	1.9E-04	Y	0.18	4.0E-05	Y	-0.02	0.36	N
mir-18a	0.25	1.0E-05	Y	-0.06	0.07	N	0.20	1.0E-05	Y	0.02	0.36	N
mir-25	0.08	0.03	Y	-0.09	0.02	Y	0.22	1.0E-05	Y	0.01	0.37	N

let-7e	-0.15	2.1E-04	Y	0.09	0.02	Y	0.22	1.0E-05	Y	0.01	0.37	N
mir-424	0.13	1.5E-03	Y	0.07	0.05	N	0.24	1.0E-05	Y	0.01	0.38	N
mir-30a	-0.28	1.0E-05	Y	0.19	1.0E-05	Y	0.20	1.0E-05	Y	0.01	0.38	N
mir-20a	0.03	0.21	N	-0.09	0.02	Y	0.13	8.1E-04	Y	-0.01	0.40	N
mir-181a-1	-0.12	1.7E-03	Y	0.13	9.0E-04	Y	0.06	0.09	N	-9.4E-03	0.41	N
mir-10b	-0.09	0.02	Y	0.14	5.7E-04	Y	0.22	1.0E-05	Y	9.2E-03	0.42	N
mir-196a-1	0.05	0.11	N	-0.22	1.0E-05	Y	0.17	4.0E-05	Y	-8.9E-03	0.42	N
mir-196a-2	0.06	0.09	N	-0.12	1.7E-03	Y	0.17	4.0E-05	Y	-8.9E-03	0.42	N
mir-183	0.01	0.37	N	-0.07	0.06	N	0.22	1.0E-05	Y	9.0E-03	0.42	N
mir-877	0.22	1.0E-05	Y	-0.03	0.22	N	0.20	1.0E-05	Y	-7.9E-03	0.43	N
mir-7-3	0.20	1.0E-05	Y	0.05	0.14	N	0.13	1.3E-03	Y	-5.0E-03	0.45	N
mir-7-2	0.30	1.0E-05	Y	-4.3E-03	0.46	N	0.13	1.3E-03	Y	-5.0E-03	0.45	N
mir-22	-0.20	1.0E-05	Y	0.26	1.0E-05	Y	0.18	4.0E-05	Y	5.1E-03	0.45	N
mir-197	0.15	3.2E-04	Y	-0.05	0.11	N	0.22	1.0E-05	Y	-4.6E-03	0.46	N
mir-9-2	-0.28	1.0E-05	Y	0.16	1.9E-04	Y	0.16	1.0E-04	Y	4.6E-03	0.46	N
mir-9-1	-0.28	1.0E-05	Y	0.15	2.0E-04	Y	0.16	1.0E-04	Y	4.6E-03	0.46	N
mir-106b	0.22	1.0E-05	Y	-0.04	0.17	N	0.13	9.0E-04	Y	4.1E-03	0.46	N
mir-326	0.05	0.12	N	0.17	6.0E-05	Y	0.13	9.3E-04	Y	3.0E-03	0.47	N
mir-222	0.09	0.02	Y	0.18	1.0E-05	Y	0.22	1.0E-05	Y	-2.5E-03	0.47	N
mir-99a	-0.28	1.0E-05	Y	0.22	1.0E-05	Y	0.15	3.6E-04	Y	2.3E-03	0.48	N
mir-592	-0.12	2.4E-03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-506	0.12	2.0E-03	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-578	-5.9E-03	0.44	N	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-509-1	-9.1E-03	0.41	N	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-549	-0.08	0.04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-527	0.11	4.2E-03	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1246	0.16	1.9E-04	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-611	0.23	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1291	0.15	1.9E-04	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-548f-1	0.13	7.3E-04	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-452	-0.14	3.6E-04	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-2110	0.11	4.0E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-552	-0.17	5.0E-05	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-208b	0.02	0.30	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-509-2	-0.08	0.02	Y	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-33b	0.06	0.07	N	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-525	0.03	0.28	N	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-873	-0.10	8.0E-03	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-187	-0.19	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-551a	0.14	6.1E-04	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1293	0.20	1.0E-05	Y	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-654	0.02	0.33	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-379	-0.10	0.01	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1245	0.04	0.20	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-363	-0.14	3.6E-04	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-511-1	0.11	4.3E-03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-490	-0.22	1.0E-05	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-656	-0.03	0.26	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-628	-0.15	2.6E-04	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-511-2	0.07	0.05	N	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-513c	0.03	0.27	N	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-188	0.11	6.8E-03	Y	-0.18	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-942	0.28	1.0E-05	Y	-0.17	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-520b	0.02	0.32	N	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-199b	-0.11	4.4E-03	Y	0.18	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-410	-0.09	0.02	Y	0.17	4.0E-05	Y	0	0.50	N	0	0.50	N
mir-377	4.4E-05	0.50	N	0.17	4.0E-05	Y	0	0.50	N	0	0.50	N
mir-184	-0.08	0.03	Y	-0.17	5.0E-05	Y	0	0.50	N	0	0.50	N
mir-892a	0.06	0.07	N	-0.16	5.0E-05	Y	0	0.50	N	0	0.50	N
mir-937	0.05	0.14	N	0.17	9.0E-05	Y	0	0.50	N	0	0.50	N
mir-152	-0.17	5.0E-05	Y	0.17	1.0E-04	Y	0	0.50	N	0	0.50	N
mir-622	0.26	1.0E-05	Y	-0.16	1.3E-04	Y	0	0.50	N	0	0.50	N
mir-1289-1	-0.06	0.08	N	-0.16	1.5E-04	Y	0	0.50	N	0	0.50	N
mir-1305	0.07	0.04	N	0.16	1.7E-04	Y	0	0.50	N	0	0.50	N
mir-512-1	-2.5E-03	0.48	N	0.16	1.7E-04	Y	0	0.50	N	0	0.50	N

mir-1251	-7.1E-03	0.43	N	0.16	1.8E-04	Y	0	0.50	N	0	0.50	N
mir-573	0.32	1.0E-05	Y	-0.15	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-485	-0.02	0.33	N	0.15	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-758	-0.11	4.4E-03	Y	0.16	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-154	-0.09	0.02	Y	0.16	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-1281	0.11	4.9E-03	Y	-0.15	2.5E-04	Y	0	0.50	N	0	0.50	N
mir-1292	0.28	1.0E-05	Y	-0.15	2.6E-04	Y	0	0.50	N	0	0.50	N
mir-617	0.13	1.2E-03	Y	-0.15	2.6E-04	Y	0	0.50	N	0	0.50	N
mir-644	0.13	1.2E-03	Y	-0.15	2.6E-04	Y	0	0.50	N	0	0.50	N
mir-612	0.04	0.19	N	-0.14	3.2E-04	Y	0	0.50	N	0	0.50	N
mir-627	0.02	0.35	N	-0.14	3.6E-04	Y	0	0.50	N	0	0.50	N
mir-518a-1	0.14	6.2E-04	Y	-0.14	3.6E-04	Y	0	0.50	N	0	0.50	N
mir-662	-8.1E-03	0.42	N	0.14	3.6E-04	Y	0	0.50	N	0	0.50	N
mir-519a-1	-1.5E-03	0.48	N	0.15	3.6E-04	Y	0	0.50	N	0	0.50	N
mir-411	-0.10	9.0E-03	Y	0.15	3.6E-04	Y	0	0.50	N	0	0.50	N
mir-1539	0.17	1.0E-04	Y	-0.14	3.9E-04	Y	0	0.50	N	0	0.50	N
mir-1179	0.05	0.13	N	-0.14	3.9E-04	Y	0	0.50	N	0	0.50	N
mir-219-2	-0.03	0.23	N	0.14	4.2E-04	Y	0	0.50	N	0	0.50	N
mir-139	-0.16	5.0E-05	Y	0.14	4.9E-04	Y	0	0.50	N	0	0.50	N
mir-1234	0.19	1.0E-05	Y	-0.14	5.0E-04	Y	0	0.50	N	0	0.50	N
mir-1287	-0.08	0.03	Y	0.14	5.1E-04	Y	0	0.50	N	0	0.50	N
mir-127	-0.11	5.0E-03	Y	0.14	5.1E-04	Y	0	0.50	N	0	0.50	N
mir-495	0.03	0.24	N	0.14	5.5E-04	Y	0	0.50	N	0	0.50	N
mir-499	-0.05	0.10	N	-0.14	5.6E-04	Y	0	0.50	N	0	0.50	N
mir-509-3	-0.14	3.0E-04	Y	-0.14	5.8E-04	Y	0	0.50	N	0	0.50	N
mir-206	-0.04	0.15	N	-0.13	6.1E-04	Y	0	0.50	N	0	0.50	N
mir-526b	0.13	1.5E-03	Y	0.14	6.3E-04	Y	0	0.50	N	0	0.50	N
mir-655	0.04	0.20	N	0.14	6.6E-04	Y	0	0.50	N	0	0.50	N
mir-660	-0.10	7.7E-03	Y	-0.13	7.1E-04	Y	0	0.50	N	0	0.50	N
mir-1537	0.14	5.7E-04	Y	0.14	7.3E-04	Y	0	0.50	N	0	0.50	N
mir-409	-0.05	0.14	N	0.13	8.2E-04	Y	0	0.50	N	0	0.50	N
mir-889	-0.06	0.08	N	0.13	8.3E-04	Y	0	0.50	N	0	0.50	N
mir-1285-1	9.6E-03	0.41	N	-0.13	8.7E-04	Y	0	0.50	N	0	0.50	N
mir-574	0.02	0.30	N	0.13	8.7E-04	Y	0	0.50	N	0	0.50	N
mir-320d-2	-0.02	0.32	N	0.13	9.4E-04	Y	0	0.50	N	0	0.50	N
mir-572	-0.12	3.3E-03	Y	-0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
mir-508	-0.20	1.0E-05	Y	-0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
mir-198	0.02	0.28	N	0.13	1.1E-03	Y	0	0.50	N	0	0.50	N
mir-577	0.15	2.3E-04	Y	-0.13	1.2E-03	Y	0	0.50	N	0	0.50	N
mir-216b	-0.06	0.09	N	0.12	1.8E-03	Y	0	0.50	N	0	0.50	N
mir-581	0.17	9.0E-05	Y	-0.12	1.8E-03	Y	0	0.50	N	0	0.50	N
mir-1258	-0.25	1.0E-05	Y	0.12	1.9E-03	Y	0	0.50	N	0	0.50	N
mir-582	0.19	1.0E-05	Y	0.12	1.9E-03	Y	0	0.50	N	0	0.50	N
mir-1231	0.07	0.05	N	-0.12	2.0E-03	Y	0	0.50	N	0	0.50	N
mir-559	0.01	0.36	N	-0.12	2.2E-03	Y	0	0.50	N	0	0.50	N
mir-496	-0.02	0.31	N	0.12	2.2E-03	Y	0	0.50	N	0	0.50	N
mir-487b	-0.04	0.20	N	0.12	2.3E-03	Y	0	0.50	N	0	0.50	N
mir-522	0.06	0.08	N	0.12	2.3E-03	Y	0	0.50	N	0	0.50	N
mir-1271	-0.10	0.01	Y	0.12	2.3E-03	Y	0	0.50	N	0	0.50	N
mir-512-2	-0.02	0.34	N	0.12	2.4E-03	Y	0	0.50	N	0	0.50	N
mir-523	0.11	5.1E-03	Y	-0.12	2.6E-03	Y	0	0.50	N	0	0.50	N
mir-639	0.07	0.05	N	-0.12	2.8E-03	Y	0	0.50	N	0	0.50	N
mir-936	-0.08	0.03	Y	-0.12	2.9E-03	Y	0	0.50	N	0	0.50	N
mir-337	-0.05	0.11	N	0.12	2.9E-03	Y	0	0.50	N	0	0.50	N
mir-518c	-0.09	0.02	Y	0.12	2.9E-03	Y	0	0.50	N	0	0.50	N
mir-675	0.09	0.02	Y	0.12	2.9E-03	Y	0	0.50	N	0	0.50	N
mir-1247	-0.07	0.05	N	-0.12	3.0E-03	Y	0	0.50	N	0	0.50	N
mir-516a-1	0.11	6.4E-03	Y	0.12	3.0E-03	Y	0	0.50	N	0	0.50	N
mir-520d	0.07	0.04	N	-0.12	3.1E-03	Y	0	0.50	N	0	0.50	N
mir-299	0.04	0.19	N	0.12	3.1E-03	Y	0	0.50	N	0	0.50	N
mir-1207	0.03	0.22	N	-0.12	3.2E-03	Y	0	0.50	N	0	0.50	N
mir-1915	0.03	0.22	N	-0.12	3.2E-03	Y	0	0.50	N	0	0.50	N
mir-635	0.03	0.22	N	-0.12	3.2E-03	Y	0	0.50	N	0	0.50	N
mir-888	0.03	0.22	N	-0.12	3.2E-03	Y	0	0.50	N	0	0.50	N
mir-545	0.01	0.38	N	-0.12	3.2E-03	Y	0	0.50	N	0	0.50	N

mir-136	-0.08	0.04	Y	0.11	3.8E-03	Y	0	0.50	N	0	0.50	N
mir-542	-0.11	5.5E-03	Y	0.11	3.9E-03	Y	0	0.50	N	0	0.50	N
mir-488	-0.08	0.04	Y	0.11	4.1E-03	Y	0	0.50	N	0	0.50	N
mir-135b	-0.12	2.1E-03	Y	-0.11	4.3E-03	Y	0	0.50	N	0	0.50	N
mir-892b	0.09	0.02	Y	-0.11	4.4E-03	Y	0	0.50	N	0	0.50	N
mir-875	-0.01	0.39	N	-0.11	4.5E-03	Y	0	0.50	N	0	0.50	N
mir-519a-2	0.06	0.07	N	0.11	4.7E-03	Y	0	0.50	N	0	0.50	N
mir-887	-0.09	0.02	Y	0.11	4.8E-03	Y	0	0.50	N	0	0.50	N
mir-623	0.04	0.18	N	0.11	5.4E-03	Y	0	0.50	N	0	0.50	N
mir-576	0.10	0.01	Y	-0.11	6.2E-03	Y	0	0.50	N	0	0.50	N
mir-494	0.03	0.25	N	0.10	7.7E-03	Y	0	0.50	N	0	0.50	N
mir-516a-2	-0.11	3.7E-03	Y	0.10	7.8E-03	Y	0	0.50	N	0	0.50	N
mir-1283-2	0.03	0.27	N	0.10	8.5E-03	Y	0	0.50	N	0	0.50	N
mir-95	0.01	0.39	N	-0.10	9.1E-03	Y	0	0.50	N	0	0.50	N
mir-520c	-0.11	3.5E-03	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-591	0.13	1.0E-03	Y	-0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-933	-0.10	0.01	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-502	2.0E-03	0.48	N	-0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-526a-1	-0.07	0.06	N	0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-147	-0.05	0.13	N	-0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-134	0.04	0.18	N	0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-491	0.04	0.21	N	-0.10	0.01	Y	0	0.50	N	0	0.50	N
let-7f-2	-0.22	1.0E-05	Y	0.10	0.01	Y	0	0.50	N	0	0.50	N
mir-516b-2	-0.11	4.0E-03	Y	0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-521-2	-0.07	0.05	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-517a	-0.02	0.33	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-517b	-0.02	0.33	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-19b-1	0.15	2.2E-04	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-614	0.11	3.9E-03	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-302c	0.08	0.04	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-367	0.08	0.04	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-520f	0.09	0.02	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-586	0.10	0.01	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-1249	-0.01	0.40	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-514-3	-0.11	4.0E-03	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-584	0.07	0.05	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-613	0.15	2.4E-04	Y	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-607	-0.01	0.37	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-548f-4	-0.03	0.28	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-513a-2	-0.11	6.3E-03	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-1468	-0.04	0.20	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-632	0.09	0.01	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-381	-0.02	0.35	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-1269	-0.13	6.7E-04	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-493	-0.07	0.06	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
let-7a-3	-0.25	1.0E-05	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-219-1	0.05	0.11	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-1238	0.13	1.2E-03	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-1280	0.11	6.6E-03	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-767	-0.19	1.0E-05	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-658	-0.02	0.35	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-521-1	0	0.50	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-329-2	0.18	3.0E-05	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-26a-2	-0.14	4.7E-04	Y	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-938	0.05	0.13	N	0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-603	-0.08	0.04	Y	-0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-580	0.10	9.8E-03	Y	-0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-636	0.11	5.2E-03	Y	0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-621	0.15	2.4E-04	Y	-0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-492	0.20	1.0E-05	Y	-0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-556	0.02	0.36	N	-0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-431	-0.10	9.0E-03	Y	0.08	0.04	Y	0	0.50	N	0	0.50	N
mir-190b	-0.08	0.04	Y	0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-1911	-0.01	0.41	N	-0.07	0.04	N	0	0.50	N	0	0.50	N
mir-891a	-0.03	0.27	N	0.07	0.04	N	0	0.50	N	0	0.50	N

mir-1825	0.06	0.08	N	-0.07	0.04	N	0	0.50	N	0	0.50	N
mir-1185-2	-0.15	2.5E-04	Y	0.07	0.04	N	0	0.50	N	0	0.50	N
mir-1282	-0.02	0.30	N	-0.07	0.04	N	0	0.50	N	0	0.50	N
mir-1178	0.01	0.38	N	-0.07	0.04	N	0	0.50	N	0	0.50	N
mir-382	-0.02	0.33	N	0.07	0.04	N	0	0.50	N	0	0.50	N
mir-610	6.5E-03	0.44	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-518f	0.12	2.2E-03	Y	-0.07	0.05	N	0	0.50	N	0	0.50	N
mir-548d-1	0.11	4.5E-03	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-543	-0.04	0.20	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-657	0	0.50	N	-0.07	0.05	N	0	0.50	N	0	0.50	N
mir-1909	0.07	0.06	N	-0.07	0.05	N	0	0.50	N	0	0.50	N
mir-520g	-0.09	0.02	Y	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-370	-0.05	0.11	N	0.07	0.06	N	0	0.50	N	0	0.50	N
mir-489	-0.19	1.0E-05	Y	0.07	0.06	N	0	0.50	N	0	0.50	N
mir-135a-2	-1.3E-03	0.49	N	-0.07	0.06	N	0	0.50	N	0	0.50	N
mir-570	-4.7E-03	0.45	N	-0.07	0.06	N	0	0.50	N	0	0.50	N
mir-202	-9.8E-03	0.41	N	0.07	0.06	N	0	0.50	N	0	0.50	N
mir-450a-1	0.05	0.12	N	0.07	0.06	N	0	0.50	N	0	0.50	N
mir-519e	-0.11	5.9E-03	Y	-0.07	0.07	N	0	0.50	N	0	0.50	N
mir-450b	-0.03	0.25	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1913	0.07	0.05	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1908	0.07	0.05	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1248	0.10	0.01	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-604	0.09	0.02	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-561	5.5E-03	0.45	N	0.06	0.08	N	0	0.50	N	0	0.50	N
mir-144	-0.05	0.12	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
mir-376b	0.08	0.04	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
mir-1277	-0.10	6.7E-03	Y	0.06	0.08	N	0	0.50	N	0	0.50	N
mir-1267	-0.07	0.05	N	0.06	0.08	N	0	0.50	N	0	0.50	N
mir-412	-0.03	0.24	N	-0.06	0.09	N	0	0.50	N	0	0.50	N
mir-548n	0.02	0.29	N	-0.06	0.09	N	0	0.50	N	0	0.50	N
mir-7-1	0.28	1.0E-05	Y	-0.06	0.09	N	0	0.50	N	0	0.50	N
mir-320d-1	-0.02	0.29	N	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-9-3	-5.2E-03	0.45	N	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-668	0.08	0.04	Y	-0.06	0.09	N	0	0.50	N	0	0.50	N
mir-422a	-0.08	0.03	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-922	-0.08	0.03	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-618	0.20	1.0E-05	Y	0.06	0.10	N	0	0.50	N	0	0.50	N
mir-1976	-0.02	0.34	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-147b	0.10	8.7E-03	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-631	0.12	2.0E-03	Y	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-1181	-0.03	0.27	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-579	0.17	4.0E-05	Y	0.05	0.12	N	0	0.50	N	0	0.50	N
mir-513b	0.12	2.1E-03	Y	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-641	0.11	6.4E-03	Y	0.05	0.12	N	0	0.50	N	0	0.50	N
mir-449b	0.08	0.03	Y	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-1290	0.06	0.09	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-1224	0.02	0.32	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-302b	0.16	1.0E-04	Y	0.05	0.12	N	0	0.50	N	0	0.50	N
mir-651	-0.06	0.07	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-616	0.12	3.0E-03	Y	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-1284	0.18	4.0E-05	Y	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-486	-0.06	0.10	N	0.05	0.13	N	0	0.50	N	0	0.50	N
mir-153-2	-0.17	2.0E-05	Y	-0.05	0.14	N	0	0.50	N	0	0.50	N
mir-520e	0.12	2.4E-03	Y	0.05	0.14	N	0	0.50	N	0	0.50	N
mir-1228	0.14	5.1E-04	Y	0.05	0.14	N	0	0.50	N	0	0.50	N
mir-664	-0.25	1.0E-05	Y	0.05	0.14	N	0	0.50	N	0	0.50	N
mir-1252	0.04	0.19	N	0.05	0.14	N	0	0.50	N	0	0.50	N
mir-1286	0.15	1.9E-04	Y	-0.05	0.15	N	0	0.50	N	0	0.50	N
mir-606	-0.11	3.7E-03	Y	0.04	0.15	N	0	0.50	N	0	0.50	N
mir-514-2	-0.09	0.02	Y	0.04	0.15	N	0	0.50	N	0	0.50	N
mir-599	0.06	0.08	N	-0.04	0.15	N	0	0.50	N	0	0.50	N
mir-1827	-0.04	0.16	N	-0.04	0.15	N	0	0.50	N	0	0.50	N
mir-24-1	-0.17	4.0E-05	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-128-2	0.06	0.08	N	-0.04	0.16	N	0	0.50	N	0	0.50	N

mir-630	0.05	0.13	N	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-29b-2	-0.10	9.8E-03	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-323	0.08	0.03	Y	0.04	0.17	N	0	0.50	N	0	0.50	N
mir-600	0.10	8.5E-03	Y	0.04	0.17	N	0	0.50	N	0	0.50	N
mir-135a-1	-0.16	7.0E-05	Y	0.04	0.17	N	0	0.50	N	0	0.50	N
mir-519d	-0.03	0.22	N	0.04	0.17	N	0	0.50	N	0	0.50	N
mir-510	0.09	0.02	Y	-0.04	0.18	N	0	0.50	N	0	0.50	N
mir-329-1	0.05	0.11	N	0.04	0.18	N	0	0.50	N	0	0.50	N
mir-934	-0.16	1.5E-04	Y	0.04	0.18	N	0	0.50	N	0	0.50	N
mir-487a	0.02	0.28	N	0.04	0.18	N	0	0.50	N	0	0.50	N
mir-891b	0.08	0.03	Y	-0.04	0.18	N	0	0.50	N	0	0.50	N
mir-885	-8.6E-03	0.42	N	-0.04	0.19	N	0	0.50	N	0	0.50	N
mir-1912	0.07	0.06	N	-0.04	0.19	N	0	0.50	N	0	0.50	N
mir-663	0.16	1.1E-04	Y	-0.04	0.20	N	0	0.50	N	0	0.50	N
mir-181a-2	-0.13	6.3E-04	Y	-0.04	0.20	N	0	0.50	N	0	0.50	N
mir-876	-0.07	0.04	N	0.04	0.20	N	0	0.50	N	0	0.50	N
mir-1255a	0.17	4.0E-05	Y	0.04	0.20	N	0	0.50	N	0	0.50	N
mir-1266	0.27	1.0E-05	Y	-0.04	0.20	N	0	0.50	N	0	0.50	N
mir-208a	7.3E-03	0.43	N	-0.04	0.21	N	0	0.50	N	0	0.50	N
mir-1302-3	0.02	0.36	N	0.04	0.21	N	0	0.50	N	0	0.50	N
mir-376c	0.04	0.16	N	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-519c	0.13	1.6E-03	Y	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-551b	-0.08	0.03	Y	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-564	0.02	0.36	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-518a-2	-4.4E-03	0.46	N	-0.03	0.22	N	0	0.50	N	0	0.50	N
mir-301b	0.18	3.0E-05	Y	-0.03	0.22	N	0	0.50	N	0	0.50	N
mir-1182	0.15	2.0E-04	Y	-0.03	0.22	N	0	0.50	N	0	0.50	N
mir-588	0.14	5.1E-04	Y	-0.03	0.23	N	0	0.50	N	0	0.50	N
mir-548e	0.08	0.03	Y	0.03	0.23	N	0	0.50	N	0	0.50	N
mir-483	0.13	9.6E-04	Y	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-602	-0.02	0.32	N	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-585	-0.02	0.31	N	0.03	0.24	N	0	0.50	N	0	0.50	N
mir-939	0.12	2.5E-03	Y	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-105-1	-0.04	0.17	N	0.03	0.24	N	0	0.50	N	0	0.50	N
mir-1225	0.05	0.13	N	0.03	0.24	N	0	0.50	N	0	0.50	N
mir-589	0.04	0.17	N	0.03	0.25	N	0	0.50	N	0	0.50	N
mir-369	-0.04	0.15	N	0.03	0.25	N	0	0.50	N	0	0.50	N
mir-518e	-0.06	0.08	N	0.03	0.25	N	0	0.50	N	0	0.50	N
mir-597	9.4E-04	0.49	N	-0.03	0.25	N	0	0.50	N	0	0.50	N
mir-539	-0.08	0.04	Y	-0.03	0.26	N	0	0.50	N	0	0.50	N
mir-643	0.08	0.03	Y	-0.03	0.26	N	0	0.50	N	0	0.50	N
mir-520h	-0.02	0.32	N	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-650	-0.04	0.19	N	-0.03	0.26	N	0	0.50	N	0	0.50	N
mir-1274b	0.12	2.2E-03	Y	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-1256	1.4E-03	0.49	N	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1274a	0.13	1.3E-03	Y	-0.03	0.27	N	0	0.50	N	0	0.50	N
mir-448	1.6E-03	0.49	N	-0.03	0.27	N	0	0.50	N	0	0.50	N
mir-515-1	-0.10	9.1E-03	Y	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1306	0.15	2.7E-04	Y	0.03	0.28	N	0	0.50	N	0	0.50	N
mir-659	0.03	0.26	N	-0.03	0.28	N	0	0.50	N	0	0.50	N
mir-1185-1	0.13	1.6E-03	Y	-0.03	0.28	N	0	0.50	N	0	0.50	N
mir-24-2	-0.02	0.34	N	0.02	0.28	N	0	0.50	N	0	0.50	N
mir-665	-0.13	8.1E-04	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
mir-802	0.06	0.09	N	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-1298	0.03	0.22	N	0.02	0.29	N	0	0.50	N	0	0.50	N
mir-1257	0.24	1.0E-05	Y	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-1265	-0.13	1.5E-03	Y	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-371	7.6E-03	0.43	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-1236	0.02	0.33	N	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-653	-0.27	1.0E-05	Y	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-548j	-0.06	0.07	N	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-637	-0.05	0.12	N	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-1288	0.05	0.11	N	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-1243	0.05	0.11	N	0.02	0.32	N	0	0.50	N	0	0.50	N
let-7f-1	0.06	0.10	N	0.02	0.32	N	0	0.50	N	0	0.50	N

mir-1283-1	-0.02	0.31	N	0.02	0.32	N	0	0.50	N	0	0.50	N
mir-16-2	0.29	1.0E-05	Y	-0.02	0.33	N	0	0.50	N	0	0.50	N
mir-433	-0.02	0.36	N	-0.02	0.33	N	0	0.50	N	0	0.50	N
mir-1538	-0.01	0.37	N	0.02	0.33	N	0	0.50	N	0	0.50	N
mir-216a	-0.34	1.0E-05	Y	-0.02	0.34	N	0	0.50	N	0	0.50	N
mir-1322	-0.03	0.22	N	-0.02	0.34	N	0	0.50	N	0	0.50	N
mir-548a-3	0.01	0.38	N	-0.02	0.35	N	0	0.50	N	0	0.50	N
mir-544	-0.11	3.8E-03	Y	-0.01	0.36	N	0	0.50	N	0	0.50	N
mir-555	0.08	0.04	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
mir-647	0.15	3.4E-04	Y	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-498	0.14	4.2E-04	Y	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-596	0.05	0.11	N	-0.01	0.37	N	0	0.50	N	0	0.50	N
mir-1323	0.06	0.09	N	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-513a-1	-0.03	0.27	N	-0.01	0.38	N	0	0.50	N	0	0.50	N
mir-629	0.05	0.12	N	0.01	0.38	N	0	0.50	N	0	0.50	N
mir-524	0.25	1.0E-05	Y	-0.01	0.38	N	0	0.50	N	0	0.50	N
mir-1278	-0.01	0.37	N	0.01	0.39	N	0	0.50	N	0	0.50	N
mir-1262	-0.09	0.02	Y	-0.01	0.40	N	0	0.50	N	0	0.50	N
mir-519b	-0.05	0.13	N	0.01	0.41	N	0	0.50	N	0	0.50	N
mir-516b-1	0.10	0.01	Y	7.1E-03	0.44	N	0	0.50	N	0	0.50	N
mir-624	0.01	0.39	N	7.1E-03	0.44	N	0	0.50	N	0	0.50	N
mir-30c-1	0.14	4.2E-04	Y	-6.8E-03	0.44	N	0	0.50	N	0	0.50	N
mir-1910	0.16	1.0E-04	Y	6.6E-03	0.44	N	0	0.50	N	0	0.50	N
mir-595	0.09	0.02	Y	-5.7E-03	0.45	N	0	0.50	N	0	0.50	N
mir-507	0.01	0.38	N	6.0E-03	0.45	N	0	0.50	N	0	0.50	N
mir-548k	0.02	0.34	N	-4.8E-03	0.45	N	0	0.50	N	0	0.50	N
mir-770	0.10	0.01	Y	-4.3E-03	0.46	N	0	0.50	N	0	0.50	N
mir-16-1	0.08	0.03	Y	4.3E-03	0.46	N	0	0.50	N	0	0.50	N
mir-548d-2	0.18	3.0E-05	Y	-3.5E-03	0.47	N	0	0.50	N	0	0.50	N
mir-515-2	-0.11	4.4E-03	Y	-3.4E-03	0.47	N	0	0.50	N	0	0.50	N
mir-105-2	-0.09	0.02	Y	3.1E-03	0.47	N	0	0.50	N	0	0.50	N
mir-450a-2	0.11	6.8E-03	Y	-2.8E-03	0.47	N	0	0.50	N	0	0.50	N
mir-153-1	-0.15	1.9E-04	Y	-1.9E-03	0.48	N	0	0.50	N	0	0.50	N
mir-517c	0.03	0.24	N	1.2E-03	0.49	N	0	0.50	N	0	0.50	N

Master list of miRNAs in TCGA breast cancer dataset together the correlation scores of their expression values with PR signatures and enrichment scores of target genes with PR signatures

miRNA	*S*(M,P)	P-value	BH	*S*(M,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
mir-501	0.27	1.0E-05	Y	0.20	1.0E-05	Y	0.54	1.0E-05	Y	-0.37	1.0E-05	Y
mir-1914	0.23	1.0E-05	Y	-0.07	0.03	Y	0.38	1.0E-05	Y	-0.27	1.0E-05	Y
mir-92a-1	0.11	7.0E-04	Y	-0.18	1.0E-05	Y	0.32	1.0E-05	Y	-0.25	1.0E-05	Y
mir-432	-0.46	1.0E-05	Y	0.46	1.0E-05	Y	0.39	1.0E-05	Y	-0.25	1.0E-05	Y
mir-497	-0.32	1.0E-05	Y	0.13	2.2E-04	Y	0.04	0.15	N	-0.23	1.0E-05	Y
mir-362	0.20	1.0E-05	Y	0.05	0.07	N	0.44	1.0E-05	Y	-0.22	1.0E-05	Y
mir-671	0.13	1.5E-04	Y	-0.09	4.5E-03	Y	0.11	1.4E-03	Y	-0.21	1.0E-05	Y
mir-500a	0.16	1.0E-05	Y	0.24	1.0E-05	Y	0.31	1.0E-05	Y	-0.17	1.0E-05	Y
mir-193a	-0.13	1.9E-04	Y	0.08	0.01	Y	0.13	1.4E-04	Y	-0.17	1.0E-05	Y
mir-548b	0.33	1.0E-05	Y	-0.03	0.21	N	-0.09	6.2E-03	Y	-0.17	1.0E-05	Y
mir-328	0.06	0.05	N	5.9E-03	0.44	N	0.20	1.0E-05	Y	-0.17	1.0E-05	Y
mir-503	-0.09	7.4E-03	Y	0.24	1.0E-05	Y	0.25	1.0E-05	Y	-0.17	1.0E-05	Y
mir-19a	0.32	1.0E-05	Y	-0.05	0.08	N	-0.22	1.0E-05	Y	0.15	1.0E-05	Y
mir-372	-0.19	1.0E-05	Y	0.19	1.0E-05	Y	-0.37	1.0E-05	Y	0.16	1.0E-05	Y
mir-335	-0.02	0.28	N	0.15	2.0E-05	Y	-0.14	9.0E-05	Y	0.16	1.0E-05	Y
mir-1307	0.47	1.0E-05	Y	-0.16	3.0E-05	Y	0.26	1.0E-05	Y	0.17	1.0E-05	Y
mir-124-2	0.01	0.36	N	-0.07	0.03	Y	-0.06	0.06	N	0.18	1.0E-05	Y
mir-124-1	0.03	0.21	N	-0.03	0.24	N	-0.06	0.06	N	0.18	1.0E-05	Y
mir-124-3	0.04	0.12	N	-0.08	0.02	Y	-0.06	0.06	N	0.18	1.0E-05	Y
mir-20b	0.07	0.03	Y	-0.03	0.20	N	-0.16	3.0E-05	Y	0.19	1.0E-05	Y
mir-133b	-0.11	1.3E-03	Y	0.24	1.0E-05	Y	-0.12	4.1E-04	Y	0.19	1.0E-05	Y
mir-205	-0.25	1.0E-05	Y	0.01	0.34	N	-0.06	0.05	N	0.21	1.0E-05	Y
mir-203	0.02	0.25	N	-0.03	0.22	N	0.04	0.11	N	0.21	1.0E-05	Y
mir-29b-1	-0.15	3.0E-05	Y	-0.06	0.05	N	0.06	0.05	N	0.21	1.0E-05	Y
mir-302a	0.01	0.36	N	-0.08	0.01	Y	-0.34	1.0E-05	Y	0.22	1.0E-05	Y
mir-199a-1	-0.46	1.0E-05	Y	0.46	1.0E-05	Y	-0.18	1.0E-05	Y	0.22	1.0E-05	Y
mir-199a-2	-0.44	1.0E-05	Y	0.46	1.0E-05	Y	-0.18	1.0E-05	Y	0.22	1.0E-05	Y
mir-224	0.13	1.3E-04	Y	0.35	1.0E-05	Y	-0.02	0.27	N	0.24	1.0E-05	Y
mir-141	0.09	5.9E-03	Y	-0.32	1.0E-05	Y	0.04	0.11	N	0.24	1.0E-05	Y
mir-200b	-0.02	0.28	N	-0.18	1.0E-05	Y	-0.03	0.20	N	0.26	1.0E-05	Y
mir-150	-0.04	0.13	N	0.51	1.0E-05	Y	-0.19	1.0E-05	Y	0.26	1.0E-05	Y
mir-204	-0.30	1.0E-05	Y	0.37	1.0E-05	Y	-0.08	9.9E-03	Y	0.27	1.0E-05	Y
mir-200c	0.11	6.4E-04	Y	-0.30	1.0E-05	Y	-0.14	6.0E-05	Y	0.28	1.0E-05	Y
mir-133a-2	-0.07	0.03	Y	0.19	1.0E-05	Y	-0.11	1.4E-03	Y	0.29	1.0E-05	Y
mir-133a-1	-0.27	1.0E-05	Y	0.26	1.0E-05	Y	-0.11	1.4E-03	Y	0.29	1.0E-05	Y
mir-146a	0.05	0.09	N	0.40	1.0E-05	Y	0.04	0.13	N	0.30	1.0E-05	Y
mir-200a	-3.8E-03	0.46	N	-0.06	0.05	N	-0.05	0.10	N	0.31	1.0E-05	Y
mir-137	0.06	0.04	Y	0.14	9.0E-05	Y	0.19	1.0E-05	Y	0.34	1.0E-05	Y
mir-146b	-0.01	0.37	N	0.45	1.0E-05	Y	-0.24	1.0E-05	Y	0.35	1.0E-05	Y
mir-130a	-0.13	2.3E-04	Y	0.21	1.0E-05	Y	-0.34	1.0E-05	Y	0.36	1.0E-05	Y
mir-429	0.09	4.4E-03	Y	-0.10	2.0E-03	Y	-0.13	3.0E-04	Y	0.39	1.0E-05	Y
mir-338	-0.09	4.6E-03	Y	-1.1E-04	0.50	N	-0.39	1.0E-05	Y	0.39	1.0E-05	Y
mir-935	-6.9E-03	0.42	N	-0.01	0.38	N	0.18	1.0E-05	Y	-0.16	2.0E-05	Y
mir-365-1	-0.15	3.0E-05	Y	-0.08	0.01	Y	0.16	1.0E-05	Y	-0.16	3.0E-05	Y
mir-365-2	-0.15	3.0E-05	Y	-0.07	0.03	Y	0.16	1.0E-05	Y	-0.16	3.0E-05	Y
mir-191	-0.06	0.06	N	-0.22	1.0E-05	Y	0.26	1.0E-05	Y	-0.15	3.0E-05	Y
mir-30c-2	-0.30	1.0E-05	Y	-0.02	0.26	N	0.28	1.0E-05	Y	-0.14	5.0E-05	Y
mir-346	-0.08	9.4E-03	Y	0.12	4.0E-04	Y	-0.03	0.21	N	0.14	7.0E-05	Y
mir-148b	-0.17	1.0E-05	Y	-0.09	7.0E-03	Y	-0.02	0.33	N	0.14	9.0E-05	Y
mir-425	0.02	0.26	N	-6.2E-03	0.43	N	0.17	1.0E-05	Y	-0.14	1.5E-04	Y
mir-3200	0.42	1.0E-05	Y	-0.10	3.9E-03	Y	0.22	1.0E-05	Y	-0.13	1.6E-04	Y
mir-1260b	0.13	1.4E-04	Y	-0.20	1.0E-05	Y	0.18	1.0E-05	Y	-0.13	1.9E-04	Y
mir-217	-0.21	1.0E-05	Y	0.14	7.0E-05	Y	-0.20	1.0E-05	Y	-0.13	2.3E-04	Y
let-7i	-0.14	1.0E-04	Y	0.35	1.0E-05	Y	0.15	3.0E-05	Y	0.13	2.4E-04	Y
mir-766	0.08	0.02	Y	0.24	1.0E-05	Y	0.24	1.0E-05	Y	-0.13	2.5E-04	Y
mir-145	-0.35	1.0E-05	Y	0.36	1.0E-05	Y	0.08	0.02	Y	0.12	2.9E-04	Y
let-7c	-0.49	1.0E-05	Y	0.46	1.0E-05	Y	0.15	1.0E-05	Y	-0.13	3.0E-04	Y
mir-19b-2	0.14	5.0E-05	Y	-0.13	2.8E-04	Y	-0.04	0.14	N	0.12	3.1E-04	Y
mir-339	-0.03	0.23	N	-0.04	0.17	N	0.11	1.1E-03	Y	-0.12	3.9E-04	Y

mir-34b	-0.27	1.0E-05	Y	0.20	1.0E-05	Y	0.03	0.21	N	0.12	4.0E-04	Y
mir-99b	0.11	1.6E-03	Y	-0.04	0.14	N	0.16	1.0E-05	Y	-0.12	4.1E-04	Y
mir-1229	0.33	1.0E-05	Y	-0.11	8.9E-04	Y	0.18	1.0E-05	Y	-0.12	5.9E-04	Y
mir-194-2	-0.08	0.02	Y	8.7E-03	0.41	N	-0.30	1.0E-05	Y	0.11	6.8E-04	Y
mir-194-1	-0.08	0.01	Y	-4.7E-03	0.45	N	-0.30	1.0E-05	Y	0.11	6.8E-04	Y
mir-33a	0.30	1.0E-05	Y	-0.05	0.07	N	-5.6E-	0.44	N	0.11	7.1E-04	Y
mir-196b	-0.25	1.0E-05	Y	0.35	1.0E-05	Y	0.14	6.0E-05	Y	-0.11	8.4E-04	Y
mir-99a	-0.49	1.0E-05	Y	0.44	1.0E-05	Y	0.14	6.0E-05	Y	-0.11	9.6E-04	Y
mir-361	-0.16	3.0E-05	Y	0.18	1.0E-05	Y	0.22	1.0E-05	Y	-0.11	1.1E-03	Y
mir-128-1	0.14	9.0E-05	Y	0.06	0.05	N	0.04	0.16	N	0.11	1.2E-03	Y
mir-940	0.29	1.0E-05	Y	-0.07	0.02	Y	0.19	1.0E-05	Y	0.11	1.3E-03	Y
mir-193b	4.0E-03	0.46	N	-0.07	0.03	Y	0.26	1.0E-05	Y	-0.11	1.4E-03	Y
mir-301a	0.51	1.0E-05	Y	-0.14	6.0E-05	Y	0.13	2.4E-04	Y	0.11	1.6E-03	Y
mir-92b	-0.02	0.28	N	-2.4E-03	0.47	N	0.16	1.0E-05	Y	-0.11	1.8E-03	Y
mir-223	-0.13	2.1E-04	Y	0.46	1.0E-05	Y	-0.13	2.5E-04	Y	0.10	1.9E-03	Y
mir-449a	-0.31	1.0E-05	Y	5.3E-03	0.44	N	0.25	1.0E-05	Y	-0.10	1.9E-03	Y
mir-760	0.17	1.0E-05	Y	-0.28	1.0E-05	Y	0.15	3.0E-05	Y	-0.10	2.0E-03	Y
mir-211	-0.22	1.0E-05	Y	0.18	1.0E-05	Y	-0.06	0.05	N	0.10	2.4E-03	Y
mir-25	0.21	1.0E-05	Y	0.02	0.29	N	0.13	1.0E-04	Y	-0.09	4.9E-03	Y
mir-423	0.07	0.03	Y	-0.14	1.5E-04	Y	0.13	1.7E-04	Y	-0.09	5.0E-03	Y
mir-484	0.10	3.0E-03	Y	-0.13	1.9E-04	Y	0.15	4.0E-05	Y	-0.09	5.1E-03	Y
mir-98	0.11	1.0E-03	Y	-0.02	0.30	N	0.13	1.7E-04	Y	0.09	5.1E-03	Y
mir-197	0.24	1.0E-05	Y	0.11	1.6E-03	Y	0.10	1.8E-03	Y	-0.09	5.8E-03	Y
mir-215	7.2E-03	0.42	N	0.23	1.0E-05	Y	0.21	1.0E-05	Y	-0.09	5.9E-03	Y
mir-1226	0.30	1.0E-05	Y	-0.07	0.02	Y	0.11	1.3E-03	Y	-0.09	6.1E-03	Y
mir-769	0.12	4.2E-04	Y	-0.08	0.01	Y	0.15	1.0E-05	Y	-0.09	6.4E-03	Y
let-7b	-0.40	1.0E-05	Y	0.05	0.11	N	0.16	1.0E-05	Y	-0.09	7.3E-03	Y
mir-625	-0.18	1.0E-05	Y	0.06	0.05	N	-0.12	4.1E-04	Y	-0.09	8.2E-03	Y
mir-505	0.27	1.0E-05	Y	0.15	1.0E-05	Y	0.23	1.0E-05	Y	-0.09	8.8E-03	Y
mir-132	-0.15	3.0E-05	Y	0.15	3.0E-05	Y	0.02	0.29	N	0.09	9.1E-03	Y
mir-615	0.16	1.0E-05	Y	-0.14	7.0E-05	Y	0.19	1.0E-05	Y	-0.09	9.2E-03	Y
mir-532	0.15	1.0E-05	Y	0.22	1.0E-05	Y	0.18	1.0E-05	Y	-0.09	9.2E-03	Y
mir-96	0.02	0.28	N	-0.23	1.0E-05	Y	0.13	1.1E-04	Y	-0.08	0.01	Y
mir-222	-0.10	3.6E-03	Y	0.31	1.0E-05	Y	0.17	1.0E-05	Y	-0.08	0.01	Y
mir-130b	0.36	1.0E-05	Y	0.02	0.26	N	-2.8E-	0.47	N	0.08	0.01	Y
mir-320c-1	-0.06	0.06	N	-0.07	0.04	Y	0.25	1.0E-05	Y	0.08	0.01	Y
mir-320c-2	-0.09	9.2E-03	Y	-0.03	0.19	N	0.25	1.0E-05	Y	0.08	0.01	Y
mir-181b-2	0.07	0.03	Y	0.08	0.01	Y	0.14	7.0E-05	Y	-0.08	0.01	Y
mir-181b-1	-0.01	0.37	N	0.06	0.05	N	0.14	7.0E-05	Y	-0.08	0.01	Y
mir-331	0.06	0.05	N	-0.06	0.05	N	0.10	2.8E-03	Y	-0.08	0.01	Y
mir-296	-0.24	1.0E-05	Y	0.14	5.0E-05	Y	0.07	0.03	N	-0.08	0.01	Y
mir-324	0.19	1.0E-05	Y	-0.07	0.02	Y	0.13	1.4E-04	Y	-0.08	0.01	Y
mir-877	0.41	1.0E-05	Y	-0.04	0.12	N	0.17	1.0E-05	Y	-0.08	0.02	Y
mir-142	0.08	0.02	Y	0.41	1.0E-05	Y	-0.05	0.06	N	0.08	0.02	Y
mir-373	0.08	0.02	Y	0.09	4.1E-03	Y	0.11	6.2E-04	Y	-0.07	0.02	Y
mir-92a-2	0.16	1.0E-05	Y	-0.07	0.03	Y	0.14	1.0E-04	Y	-0.07	0.02	Y
mir-186	0.16	1.0E-05	Y	0.04	0.13	N	0.13	2.2E-04	Y	-0.07	0.02	Y
mir-32	0.06	0.06	N	0.08	0.01	Y	0.14	9.0E-05	Y	-0.07	0.02	Y
mir-138-2	0.06	0.04	Y	0.25	1.0E-05	Y	-0.07	0.03	N	0.07	0.02	Y
mir-138-1	-0.07	0.02	Y	0.25	1.0E-05	Y	-0.07	0.03	N	0.07	0.02	Y
mir-31	-0.22	1.0E-05	Y	0.36	1.0E-05	Y	0.12	2.9E-04	Y	0.07	0.02	Y
mir-1296	0.05	0.07	N	0.03	0.20	N	0.15	2.0E-05	Y	-0.07	0.03	Y
mir-192	0.12	6.1E-04	Y	-0.06	0.04	Y	0.16	1.0E-05	Y	-0.07	0.03	Y
mir-26b	-0.28	1.0E-05	Y	0.07	0.03	Y	0.03	0.24	N	0.07	0.03	Y
mir-345	0.18	1.0E-05	Y	-0.01	0.35	N	0.17	1.0E-05	Y	-0.07	0.03	Y
mir-18a	0.49	1.0E-05	Y	7.0E-03	0.43	N	0.09	4.7E-03	Y	-0.07	0.03	Y
mir-210	0.37	1.0E-05	Y	-0.20	1.0E-05	Y	0.08	0.01	Y	-0.07	0.03	Y
mir-106a	0.19	1.0E-05	Y	0.01	0.34	N	0.16	1.0E-05	Y	0.07	0.03	Y
let-7e	-0.14	1.3E-04	Y	-0.09	4.4E-03	Y	0.11	1.5E-03	Y	-0.07	0.03	N
mir-181d	-0.21	1.0E-05	Y	-0.09	4.7E-03	Y	0.16	1.0E-05	Y	-0.06	0.04	N
mir-151	0.08	0.01	Y	-0.04	0.13	N	0.15	5.0E-05	Y	-0.06	0.04	N
mir-1301	0.38	1.0E-05	Y	-0.10	2.6E-03	Y	0.17	1.0E-05	Y	-0.06	0.05	N
mir-20a	0.29	1.0E-05	Y	-0.12	6.2E-04	Y	0.11	8.0E-04	Y	-0.06	0.05	N
mir-183	0.11	8.2E-04	Y	-0.14	5.0E-05	Y	0.13	1.7E-04	Y	-0.06	0.05	N
mir-149	-0.07	0.03	Y	-0.17	1.0E-05	Y	0.15	1.0E-05	Y	-0.06	0.05	N

mir-454	0.38	1.0E-05	Y	-0.24	1.0E-05	Y	0.15	3.0E-05	Y	-0.06	0.05	N
mir-195	-0.39	1.0E-05	Y	0.16	1.0E-05	Y	0.18	1.0E-05	Y	0.06	0.05	N
mir-10a	-0.34	1.0E-05	Y	0.06	0.06	N	0.09	6.9E-03	Y	-0.06	0.05	N
mir-376a-2	-0.24	1.0E-05	Y	0.24	1.0E-05	Y	0.11	1.2E-03	Y	0.06	0.06	N
mir-376a-1	-0.31	1.0E-05	Y	0.30	1.0E-05	Y	0.11	1.2E-03	Y	0.06	0.06	N
mir-106b	0.30	1.0E-05	Y	0.05	0.09	N	0.12	5.3E-04	Y	-0.06	0.06	N
mir-744	0.07	0.02	Y	-0.12	5.7E-04	Y	0.10	3.1E-03	Y	-0.06	0.06	N
mir-22	-0.33	1.0E-05	Y	0.39	1.0E-05	Y	0.13	1.0E-04	Y	-0.05	0.07	N
mir-125a	-0.20	1.0E-05	Y	-0.08	0.01	Y	0.15	3.0E-05	Y	-0.05	0.07	N
mir-126	-0.19	1.0E-05	Y	0.25	1.0E-05	Y	0.13	1.7E-04	Y	-0.05	0.07	N
mir-190	-0.26	1.0E-05	Y	0.08	0.02	Y	0.14	5.0E-05	Y	0.05	0.07	N
mir-18b	0.27	1.0E-05	Y	0.05	0.08	N	0.06	0.05	N	-0.05	0.07	N
mir-342	-0.28	1.0E-05	Y	-0.08	0.01	Y	0.12	2.6E-04	Y	-0.05	0.10	N
let-7d	0.13	1.7E-04	Y	0.09	6.0E-03	Y	0.16	1.0E-05	Y	-0.05	0.10	N
mir-941-1	0.15	4.0E-05	Y	-0.14	1.3E-04	Y	0.27	1.0E-05	Y	0.05	0.10	N
mir-93	0.41	1.0E-05	Y	-0.17	1.0E-05	Y	0.11	1.6E-03	Y	-0.05	0.11	N
mir-504	0.03	0.22	N	0.13	1.4E-04	Y	-0.11	1.4E-03	Y	0.04	0.11	N
mir-125b-1	-0.49	1.0E-05	Y	0.41	1.0E-05	Y	0.11	1.0E-03	Y	-0.04	0.11	N
mir-185	0.10	3.8E-03	Y	0.06	0.06	N	0.09	5.4E-03	Y	-0.04	0.11	N
mir-30e	-0.17	1.0E-05	Y	0.23	1.0E-05	Y	0.12	2.9E-04	Y	-0.04	0.12	N
mir-26a-1	-0.24	1.0E-05	Y	0.15	1.0E-05	Y	0.13	1.9E-04	Y	-0.04	0.13	N
mir-326	3.7E-03	0.46	N	0.23	1.0E-05	Y	0.08	0.02	N	-0.04	0.13	N
let-7a-1	-0.36	1.0E-05	Y	-0.04	0.16	N	0.12	4.0E-04	Y	-0.04	0.13	N
let-7a-2	-0.36	1.0E-05	Y	-0.03	0.18	N	0.12	4.0E-04	Y	-0.04	0.13	N
mir-196a-2	0.12	5.7E-04	Y	-0.20	1.0E-05	Y	0.15	4.0E-05	Y	-0.04	0.13	N
mir-196a-1	0.05	0.09	N	-0.15	3.0E-05	Y	0.15	4.0E-05	Y	-0.04	0.13	N
mir-23a	-0.10	3.2E-03	Y	0.22	1.0E-05	Y	0.15	1.0E-05	Y	0.04	0.14	N
mir-28	-0.16	2.0E-05	Y	0.24	1.0E-05	Y	0.17	1.0E-05	Y	0.04	0.14	N
mir-103-2	0.24	1.0E-05	Y	0.04	0.13	N	0.10	3.2E-03	Y	0.04	0.15	N
mir-455	0.09	4.3E-03	Y	0.22	1.0E-05	Y	0.15	1.0E-05	Y	-0.04	0.16	N
mir-605	-0.13	1.6E-04	Y	0.16	1.0E-05	Y	0.18	1.0E-05	Y	-0.04	0.17	N
mir-330	0.12	5.4E-04	Y	0.03	0.24	N	0.14	5.0E-05	Y	0.03	0.17	N
mir-7-3	0.28	1.0E-05	Y	-0.12	6.0E-04	Y	0.09	5.0E-03	Y	-0.03	0.17	N
mir-7-2	0.14	5.0E-05	Y	-0.12	6.1E-04	Y	0.09	5.0E-03	Y	-0.03	0.17	N
mir-598	-0.17	1.0E-05	Y	0.22	1.0E-05	Y	0.33	1.0E-05	Y	-0.03	0.18	N
let-7g	-0.15	3.0E-05	Y	0.05	0.08	N	0.04	0.16	N	0.03	0.19	N
mir-15a	0.02	0.31	N	-0.02	0.26	N	0.06	0.06	N	-0.03	0.20	N
mir-34a	-0.20	1.0E-05	Y	0.11	9.3E-04	Y	0.21	1.0E-05	Y	-0.03	0.20	N
mir-302d	-0.05	0.06	N	-0.07	0.02	Y	-0.28	1.0E-05	Y	0.03	0.20	N
mir-218-2	-0.38	1.0E-05	Y	0.36	1.0E-05	Y	-0.06	0.04	N	-0.03	0.22	N
mir-374b	-0.06	0.06	N	0.16	1.0E-05	Y	-0.10	3.0E-03	Y	0.03	0.23	N
mir-10b	-0.43	1.0E-05	Y	0.26	1.0E-05	Y	0.11	1.6E-03	Y	0.03	0.24	N
mir-100	-0.45	1.0E-05	Y	0.42	1.0E-05	Y	0.13	1.3E-04	Y	-0.03	0.24	N
mir-122	0.11	1.2E-03	Y	-0.02	0.31	N	0.10	3.6E-03	Y	-0.02	0.28	N
mir-30b	-0.13	1.8E-04	Y	-0.08	0.02	Y	0.11	6.2E-04	Y	0.02	0.29	N
mir-874	-0.24	1.0E-05	Y	0.06	0.04	Y	0.49	1.0E-05	Y	-0.02	0.29	N
mir-1-2	-0.25	1.0E-05	Y	0.24	1.0E-05	Y	0.10	3.3E-03	Y	0.02	0.30	N
mir-1-1	-0.03	0.23	N	0.09	7.5E-03	Y	0.10	3.3E-03	Y	0.02	0.30	N
mir-424	-0.17	1.0E-05	Y	0.28	1.0E-05	Y	0.22	1.0E-05	Y	-0.02	0.30	N
mir-101-1	-0.34	1.0E-05	Y	0.12	5.6E-04	Y	0.12	3.4E-04	Y	0.02	0.30	N
mir-101-2	-0.19	1.0E-05	Y	0.10	3.0E-03	Y	0.12	3.4E-04	Y	0.02	0.30	N
mir-708	-0.27	1.0E-05	Y	0.25	1.0E-05	Y	0.23	1.0E-05	Y	-0.02	0.31	N
mir-652	-0.02	0.26	N	0.11	1.4E-03	Y	0.21	1.0E-05	Y	0.02	0.33	N
mir-421	0.23	1.0E-05	Y	0.12	5.3E-04	Y	0.13	1.9E-04	Y	-0.02	0.33	N
mir-9-1	0.35	1.0E-05	Y	0.02	0.30	N	0.11	8.0E-04	Y	-0.01	0.35	N
mir-9-2	0.36	1.0E-05	Y	0.02	0.31	N	0.11	8.0E-04	Y	-0.01	0.35	N
mir-1303	0.08	0.01	Y	-0.10	2.3E-03	Y	0.13	2.2E-04	Y	0.01	0.35	N
mir-3176	0.36	1.0E-05	Y	-0.05	0.09	N	0.36	1.0E-05	Y	-0.01	0.35	N
mir-1227	0.12	5.4E-04	Y	0.07	0.02	Y	0.39	1.0E-05	Y	-0.01	0.36	N
mir-17	0.37	1.0E-05	Y	-0.09	5.6E-03	Y	0.08	0.01	Y	0.01	0.38	N
mir-23b	-0.16	1.0E-05	Y	0.17	1.0E-05	Y	0.13	1.0E-04	Y	-0.01	0.39	N
mir-21	-0.14	1.5E-04	Y	0.20	1.0E-05	Y	0.13	1.9E-04	Y	-9.9E-03	0.39	N
mir-590	0.27	1.0E-05	Y	0.05	0.06	N	0.18	1.0E-05	Y	-9.3E-03	0.40	N
mir-214	-0.45	1.0E-05	Y	0.42	1.0E-05	Y	-0.05	0.09	N	8.6E-03	0.41	N
mir-148a	-0.24	1.0E-05	Y	0.11	9.6E-04	Y	0.07	0.02	N	-8.0E-03	0.41	N

mir-155	0.03	0.18	N	0.39	1.0E-05	Y	0.13	2.4E-04	Y	2.8E-03	0.47	N
mir-182	-0.14	1.3E-04	Y	-0.14	7.0E-05	Y	-2.4E-	0.47	N	2.6E-03	0.47	N
mir-374a	-0.13	1.9E-04	Y	0.24	1.0E-05	Y	0.05	0.10	N	-6.1E-04	0.49	N
mir-1252	0.23	1.0E-05	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1254	0.42	1.0E-05	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-33b	0.12	4.0E-04	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-190b	-0.35	1.0E-05	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3127	0.35	1.0E-05	Y	-0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-499	0.05	0.08	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-219-2	0.03	0.21	N	-0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3180-4	0.13	1.7E-04	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3619	0.36	1.0E-05	Y	-0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-641	0.18	1.0E-05	Y	-0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1224	0.07	0.02	Y	-0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-592	-4.2E-03	0.45	N	-0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1251	-2.0E-03	0.48	N	-0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-670	0.11	6.4E-04	Y	-0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3132	0.21	1.0E-05	Y	-0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-520b	0.06	0.05	N	0.15	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-24-1	-0.13	2.5E-04	Y	0.15	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-548s	0.14	7.0E-05	Y	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1323	9.8E-03	0.40	N	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3150b	0.20	1.0E-05	Y	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-202	-0.32	1.0E-05	Y	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-516a-1	0.11	1.3E-03	Y	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-520a	-0.06	0.05	N	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-551a	0.03	0.20	N	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-585	-0.22	1.0E-05	Y	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1537	0.11	1.3E-03	Y	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-892a	0.06	0.05	N	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-545	0.18	1.0E-05	Y	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1468	0.02	0.29	N	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3926-2	-0.31	1.0E-05	Y	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3910-2	-0.10	2.5E-03	Y	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-582	-0.11	1.2E-03	Y	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-519a-1	0.19	1.0E-05	Y	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-23c	-0.10	2.1E-03	Y	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-574	-0.25	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-599	-0.06	0.05	N	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3647	0.19	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-378c	0.17	1.0E-05	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-934	0.17	1.0E-05	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-502	0.14	9.0E-05	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-206	0.02	0.29	N	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1262	-0.21	1.0E-05	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3690	-0.10	3.1E-03	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3199-1	-0.03	0.17	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
let-7f-1	-0.05	0.08	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-518c	-0.03	0.20	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-518b	-0.03	0.21	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1185-1	-0.24	1.0E-05	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-548j	-0.10	3.6E-03	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-660	0.02	0.26	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-500b	0.15	1.0E-05	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-628	-0.12	3.9E-04	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3605	-0.01	0.36	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-2116	0.09	5.5E-03	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-656	-0.38	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-2355	5.2E-03	0.45	N	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-24-2	-0.04	0.11	N	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-135b	0.15	3.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-891a	0.07	0.02	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-488	-0.21	1.0E-05	Y	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-526b	-0.03	0.20	N	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-329-1	-0.34	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N

mir-376b	-0.28	1.0E-05	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1271	-0.13	1.9E-04	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-450a-2	-0.26	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3193	-0.10	2.5E-03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-944	-0.20	1.0E-05	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1185-2	-0.07	0.03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-383	-0.14	1.0E-04	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3922	0.02	0.32	N	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1976	-0.09	5.0E-03	Y	0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1247	-0.27	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-450b	-0.26	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-483	-0.38	1.0E-05	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1228	-0.13	2.3E-04	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-494	-0.32	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-517b	-9.5E-03	0.40	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-517a	-9.5E-03	0.40	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-412	-0.21	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1249	-0.21	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-380	-0.26	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3926-1	-0.40	1.0E-05	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-329-2	-0.33	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-152	-0.37	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-218-1	-0.40	1.0E-05	Y	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-655	-0.41	1.0E-05	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-675	-0.30	1.0E-05	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-450a-1	-0.29	1.0E-05	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-433	-0.34	1.0E-05	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-493	-0.43	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-3129	-0.16	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-376c	-0.30	1.0E-05	Y	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-542	-0.32	1.0E-05	Y	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-551b	-0.20	1.0E-05	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-323b	-0.25	1.0E-05	Y	0.35	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-543	-0.33	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-377	-0.42	1.0E-05	Y	0.37	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-139	-0.33	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-541	-0.30	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-665	-0.39	1.0E-05	Y	0.38	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-495	-0.41	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-487b	-0.39	1.0E-05	Y	0.39	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1245	-0.29	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1258	-0.25	1.0E-05	Y	0.41	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-323	-0.26	1.0E-05	Y	0.42	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-511-2	-0.06	0.05	N	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-337	-0.45	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-411	-0.41	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-584	0.03	0.22	N	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-369	-0.39	1.0E-05	Y	0.43	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-889	-0.37	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-485	-0.37	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-431	-0.39	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-136	-0.36	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-539	-0.37	1.0E-05	Y	0.44	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-299	-0.35	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-382	-0.46	1.0E-05	Y	0.45	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-409	-0.45	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-487a	-0.32	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-452	0.07	0.02	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-154	-0.41	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-511-1	-0.04	0.15	N	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-199b	-0.41	1.0E-05	Y	0.46	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-379	-0.45	1.0E-05	Y	0.48	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-370	-0.46	1.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-381	-0.38	1.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-127	-0.46	1.0E-05	Y	0.49	1.0E-05	Y	0	0.50	N	0	0.50	N

mir-134	-0.44	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-496	-0.38	1.0E-05	Y	0.51	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-506	0.06	0.06	N	-0.16	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-939	0.24	1.0E-05	Y	-0.16	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-1250	0.15	1.0E-05	Y	-0.15	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-718	0.23	1.0E-05	Y	-0.15	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-663b	-0.10	3.3E-03	Y	0.15	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-1287	0.01	0.39	N	0.15	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-3165	0.09	4.7E-03	Y	-0.14	5.0E-05	Y	0	0.50	N	0	0.50	N
mir-3135	-0.01	0.39	N	0.14	6.0E-05	Y	0	0.50	N	0	0.50	N
mir-653	-0.29	1.0E-05	Y	0.14	7.0E-05	Y	0	0.50	N	0	0.50	N
mir-1193	-0.06	0.06	N	0.14	7.0E-05	Y	0	0.50	N	0	0.50	N
mir-516b-1	0.05	0.08	N	0.14	7.0E-05	Y	0	0.50	N	0	0.50	N
mir-922	-0.06	0.04	Y	0.14	7.0E-05	Y	0	0.50	N	0	0.50	N
mir-3140	0.15	1.0E-05	Y	0.14	8.0E-05	Y	0	0.50	N	0	0.50	N
mir-3120	-0.05	0.10	N	0.14	8.0E-05	Y	0	0.50	N	0	0.50	N
mir-577	0.32	1.0E-05	Y	0.14	8.0E-05	Y	0	0.50	N	0	0.50	N
mir-187	0.05	0.07	N	0.14	9.0E-05	Y	0	0.50	N	0	0.50	N
mir-581	-0.02	0.31	N	0.13	1.0E-04	Y	0	0.50	N	0	0.50	N
mir-448	0.02	0.33	N	0.14	1.0E-04	Y	0	0.50	N	0	0.50	N
mir-3921	-0.09	5.6E-03	Y	0.13	1.1E-04	Y	0	0.50	N	0	0.50	N
mir-1266	0.08	0.01	Y	-0.14	1.3E-04	Y	0	0.50	N	0	0.50	N
mir-3150	0.11	1.6E-03	Y	-0.14	1.5E-04	Y	0	0.50	N	0	0.50	N
mir-3156-1	-0.03	0.20	N	-0.13	1.7E-04	Y	0	0.50	N	0	0.50	N
mir-3653	-0.08	0.02	Y	0.13	1.7E-04	Y	0	0.50	N	0	0.50	N
mir-518e	0.07	0.03	Y	0.13	1.7E-04	Y	0	0.50	N	0	0.50	N
mir-873	0.05	0.10	N	0.13	1.7E-04	Y	0	0.50	N	0	0.50	N
mir-3622b	0.05	0.08	N	-0.13	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-509-2	0.04	0.15	N	0.13	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-936	-0.11	1.1E-03	Y	0.13	1.9E-04	Y	0	0.50	N	0	0.50	N
mir-548a-1	-0.04	0.16	N	0.13	2.2E-04	Y	0	0.50	N	0	0.50	N
mir-3180-5	-0.04	0.16	N	0.13	2.2E-04	Y	0	0.50	N	0	0.50	N
mir-523	-0.16	2.0E-05	Y	0.13	2.2E-04	Y	0	0.50	N	0	0.50	N
mir-597	0.25	1.0E-05	Y	-0.13	2.3E-04	Y	0	0.50	N	0	0.50	N
mir-548q	-0.12	4.6E-04	Y	0.13	2.4E-04	Y	0	0.50	N	0	0.50	N
mir-3156-2	-0.09	5.2E-03	Y	-0.13	2.5E-04	Y	0	0.50	N	0	0.50	N
mir-770	-0.04	0.15	N	0.12	2.6E-04	Y	0	0.50	N	0	0.50	N
mir-466	-0.06	0.06	N	0.12	2.7E-04	Y	0	0.50	N	0	0.50	N
mir-216a	-0.08	0.01	Y	0.12	2.7E-04	Y	0	0.50	N	0	0.50	N
mir-3147	-0.09	7.0E-03	Y	0.12	2.9E-04	Y	0	0.50	N	0	0.50	N
mir-517c	-0.10	2.2E-03	Y	0.12	2.9E-04	Y	0	0.50	N	0	0.50	N
mir-9-3	0.16	1.0E-05	Y	-0.13	3.0E-04	Y	0	0.50	N	0	0.50	N
mir-1267	0.13	1.7E-04	Y	-0.12	3.4E-04	Y	0	0.50	N	0	0.50	N
mir-618	0.02	0.28	N	-0.12	3.4E-04	Y	0	0.50	N	0	0.50	N
mir-3128	-0.12	5.2E-04	Y	0.12	3.4E-04	Y	0	0.50	N	0	0.50	N
mir-3199-2	-0.09	7.4E-03	Y	0.12	3.4E-04	Y	0	0.50	N	0	0.50	N
mir-561	6.3E-03	0.43	N	0.12	3.5E-04	Y	0	0.50	N	0	0.50	N
mir-3160-2	-0.10	2.5E-03	Y	0.12	3.6E-04	Y	0	0.50	N	0	0.50	N
mir-3178	-0.06	0.05	N	-0.12	4.1E-04	Y	0	0.50	N	0	0.50	N
mir-1265	-0.04	0.14	N	0.12	4.4E-04	Y	0	0.50	N	0	0.50	N
mir-3656	-0.03	0.22	N	-0.12	4.9E-04	Y	0	0.50	N	0	0.50	N
mir-135a-2	-0.23	1.0E-05	Y	-0.12	5.0E-04	Y	0	0.50	N	0	0.50	N
mir-548o	8.0E-03	0.42	N	0.12	5.0E-04	Y	0	0.50	N	0	0.50	N
mir-135a-1	-0.26	1.0E-05	Y	-0.12	5.3E-04	Y	0	0.50	N	0	0.50	N
mir-3942	0.27	1.0E-05	Y	-0.12	5.5E-04	Y	0	0.50	N	0	0.50	N
mir-559	0.10	2.9E-03	Y	0.12	5.6E-04	Y	0	0.50	N	0	0.50	N
mir-1292	0.27	1.0E-05	Y	-0.12	5.7E-04	Y	0	0.50	N	0	0.50	N
mir-663	0.15	1.0E-05	Y	-0.12	6.3E-04	Y	0	0.50	N	0	0.50	N
mir-4254	-0.04	0.15	N	-0.12	6.5E-04	Y	0	0.50	N	0	0.50	N
mir-3610	0.23	1.0E-05	Y	-0.12	6.6E-04	Y	0	0.50	N	0	0.50	N
mir-548a-3	0.15	3.0E-05	Y	0.11	6.9E-04	Y	0	0.50	N	0	0.50	N
mir-3622a	0.07	0.02	Y	0.11	7.1E-04	Y	0	0.50	N	0	0.50	N
mir-548t	-0.05	0.09	N	-0.12	7.2E-04	Y	0	0.50	N	0	0.50	N
mir-1246	0.22	1.0E-05	Y	-0.12	7.7E-04	Y	0	0.50	N	0	0.50	N
mir-573	0.16	1.0E-05	Y	-0.11	8.6E-04	Y	0	0.50	N	0	0.50	N

mir-520e	0.08	0.02	Y	0.11	8.7E-04	Y	0	0.50	N	0	0.50	N
mir-556	0.07	0.02	Y	-0.11	9.7E-04	Y	0	0.50	N	0	0.50	N
mir-325	0.11	9.8E-04	Y	-0.11	9.9E-04	Y	0	0.50	N	0	0.50	N
mir-3614	0.25	1.0E-05	Y	0.11	9.9E-04	Y	0	0.50	N	0	0.50	N
mir-3941	-0.05	0.08	N	0.11	1.1E-03	Y	0	0.50	N	0	0.50	N
mir-1277	0.20	1.0E-05	Y	-0.11	1.1E-03	Y	0	0.50	N	0	0.50	N
mir-3661	-0.06	0.04	N	0.11	1.3E-03	Y	0	0.50	N	0	0.50	N
mir-1913	0.15	3.0E-05	Y	0.11	1.4E-03	Y	0	0.50	N	0	0.50	N
mir-1908	0.12	3.0E-04	Y	-0.11	1.4E-03	Y	0	0.50	N	0	0.50	N
mir-219-1	0.09	4.7E-03	Y	-0.11	1.4E-03	Y	0	0.50	N	0	0.50	N
mir-3682	0.26	1.0E-05	Y	0.11	1.4E-03	Y	0	0.50	N	0	0.50	N
mir-3126	-0.05	0.07	N	0.11	1.5E-03	Y	0	0.50	N	0	0.50	N
mir-3157	0.16	1.0E-05	Y	0.11	1.5E-03	Y	0	0.50	N	0	0.50	N
mir-514-2	-0.12	4.4E-04	Y	0.11	1.6E-03	Y	0	0.50	N	0	0.50	N
mir-548n	-0.09	7.5E-03	Y	0.10	1.8E-03	Y	0	0.50	N	0	0.50	N
mir-512-2	0.09	5.4E-03	Y	0.10	1.9E-03	Y	0	0.50	N	0	0.50	N
mir-519a-2	0.14	8.0E-05	Y	0.10	1.9E-03	Y	0	0.50	N	0	0.50	N
mir-1264	-0.02	0.28	N	-0.11	1.9E-03	Y	0	0.50	N	0	0.50	N
mir-374c	-0.01	0.37	N	0.10	2.0E-03	Y	0	0.50	N	0	0.50	N
mir-371	-0.06	0.06	N	0.10	2.0E-03	Y	0	0.50	N	0	0.50	N
mir-548f-4	0.15	1.0E-05	Y	-0.10	2.1E-03	Y	0	0.50	N	0	0.50	N
mir-3144	0.06	0.06	N	-0.10	2.1E-03	Y	0	0.50	N	0	0.50	N
mir-3685	0.10	4.0E-03	Y	-0.10	2.1E-03	Y	0	0.50	N	0	0.50	N
mir-1263	0.10	4.0E-03	Y	-0.10	2.1E-03	Y	0	0.50	N	0	0.50	N
mir-1243	-0.08	9.7E-03	Y	0.10	2.1E-03	Y	0	0.50	N	0	0.50	N
mir-513c	-0.02	0.25	N	0.10	2.2E-03	Y	0	0.50	N	0	0.50	N
mir-30c-1	-0.07	0.02	Y	0.10	2.3E-03	Y	0	0.50	N	0	0.50	N
mir-491	-0.24	1.0E-05	Y	0.10	2.4E-03	Y	0	0.50	N	0	0.50	N
mir-3130-2	0.05	0.07	N	0.10	2.6E-03	Y	0	0.50	N	0	0.50	N
mir-1276	0.26	1.0E-05	Y	-0.10	2.6E-03	Y	0	0.50	N	0	0.50	N
mir-1184-1	0.11	1.7E-03	Y	-0.10	2.6E-03	Y	0	0.50	N	0	0.50	N
mir-1294	-0.11	8.8E-04	Y	0.10	2.7E-03	Y	0	0.50	N	0	0.50	N
mir-876	0.08	0.02	Y	0.10	2.7E-03	Y	0	0.50	N	0	0.50	N
mir-2113	0.17	1.0E-05	Y	-0.10	2.8E-03	Y	0	0.50	N	0	0.50	N
mir-629	0.08	0.01	Y	-0.10	2.9E-03	Y	0	0.50	N	0	0.50	N
mir-3188	0.07	0.02	Y	-0.10	3.0E-03	Y	0	0.50	N	0	0.50	N
mir-3934	0.19	1.0E-05	Y	0.10	3.1E-03	Y	0	0.50	N	0	0.50	N
mir-2278	0.03	0.19	N	-0.10	3.3E-03	Y	0	0.50	N	0	0.50	N
mir-3688	0.09	4.1E-03	Y	0.10	3.3E-03	Y	0	0.50	N	0	0.50	N
mir-933	0.16	1.0E-05	Y	-0.10	3.3E-03	Y	0	0.50	N	0	0.50	N
mir-3191	7.7E-03	0.42	N	0.10	3.3E-03	Y	0	0.50	N	0	0.50	N
mir-3121	-0.05	0.08	N	-0.10	3.4E-03	Y	0	0.50	N	0	0.50	N
mir-3663	0.13	1.4E-04	Y	-0.10	3.6E-03	Y	0	0.50	N	0	0.50	N
mir-3179-1	-0.04	0.15	N	0.10	3.7E-03	Y	0	0.50	N	0	0.50	N
mir-1274b	0.19	1.0E-05	Y	0.10	3.7E-03	Y	0	0.50	N	0	0.50	N
mir-1280	1.3E-03	0.49	N	-0.10	3.8E-03	Y	0	0.50	N	0	0.50	N
mir-3141	5.9E-03	0.44	N	-0.10	4.0E-03	Y	0	0.50	N	0	0.50	N
mir-548d-2	0.32	1.0E-05	Y	-0.10	4.0E-03	Y	0	0.50	N	0	0.50	N
mir-188	0.30	1.0E-05	Y	0.10	4.0E-03	Y	0	0.50	N	0	0.50	N
mir-550b-2	0.07	0.03	Y	0.09	4.3E-03	Y	0	0.50	N	0	0.50	N
mir-492	-0.03	0.22	N	-0.09	4.4E-03	Y	0	0.50	N	0	0.50	N
mir-648	-0.12	4.9E-04	Y	0.09	4.4E-03	Y	0	0.50	N	0	0.50	N
mir-563	-0.12	4.9E-04	Y	0.09	4.4E-03	Y	0	0.50	N	0	0.50	N
mir-4265	-0.12	4.9E-04	Y	0.09	4.4E-03	Y	0	0.50	N	0	0.50	N
mir-4279	0.01	0.34	N	-0.09	4.6E-03	Y	0	0.50	N	0	0.50	N
mir-3117	-0.02	0.26	N	0.09	4.7E-03	Y	0	0.50	N	0	0.50	N
mir-3679	0.15	2.0E-05	Y	0.09	5.0E-03	Y	0	0.50	N	0	0.50	N
mir-3167	-0.03	0.18	N	-0.09	5.6E-03	Y	0	0.50	N	0	0.50	N
mir-3153	0.05	0.09	N	-0.09	5.8E-03	Y	0	0.50	N	0	0.50	N
mir-3202-1	0.14	8.0E-05	Y	0.09	5.8E-03	Y	0	0.50	N	0	0.50	N
mir-147b	0.10	3.1E-03	Y	0.09	5.9E-03	Y	0	0.50	N	0	0.50	N
mir-520h	-0.07	0.04	Y	0.09	6.0E-03	Y	0	0.50	N	0	0.50	N
mir-549	0.02	0.26	N	0.09	6.3E-03	Y	0	0.50	N	0	0.50	N
mir-1302-3	0.04	0.15	N	0.09	6.4E-03	Y	0	0.50	N	0	0.50	N
mir-642b	0.05	0.09	N	-0.09	6.4E-03	Y	0	0.50	N	0	0.50	N

mir-617	0.04	0.13	N	-0.09	6.7E-03	Y	0	0.50	N	0	0.50	N
mir-508	-0.06	0.04	N	-0.09	6.7E-03	Y	0	0.50	N	0	0.50	N
mir-512-1	0.19	1.0E-05	Y	0.09	7.4E-03	Y	0	0.50	N	0	0.50	N
mir-3687	0.25	1.0E-05	Y	0.09	7.4E-03	Y	0	0.50	N	0	0.50	N
mir-1269	0.33	1.0E-05	Y	-0.09	7.7E-03	Y	0	0.50	N	0	0.50	N
mir-1298	0.04	0.16	N	0.09	7.9E-03	Y	0	0.50	N	0	0.50	N
mir-892b	0.06	0.05	N	0.09	7.9E-03	Y	0	0.50	N	0	0.50	N
mir-570	0.10	1.7E-03	Y	-0.09	8.3E-03	Y	0	0.50	N	0	0.50	N
mir-942	0.41	1.0E-05	Y	0.09	8.4E-03	Y	0	0.50	N	0	0.50	N
mir-3606	-0.06	0.05	N	0.09	9.0E-03	Y	0	0.50	N	0	0.50	N
mir-647	0.07	0.03	Y	0.09	9.0E-03	Y	0	0.50	N	0	0.50	N
mir-659	-0.10	2.9E-03	Y	0.09	9.1E-03	Y	0	0.50	N	0	0.50	N
mir-3913-2	-0.04	0.16	N	0.09	9.2E-03	Y	0	0.50	N	0	0.50	N
mir-3116-2	0.11	7.2E-04	Y	-0.09	9.2E-03	Y	0	0.50	N	0	0.50	N
mir-1225	0.19	1.0E-05	Y	-0.08	9.3E-03	Y	0	0.50	N	0	0.50	N
mir-516b-2	0.01	0.37	N	0.09	9.4E-03	Y	0	0.50	N	0	0.50	N
mir-3675	-0.07	0.03	Y	0.08	1.0E-02	Y	0	0.50	N	0	0.50	N
mir-3678	-0.07	0.02	Y	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1469	0.02	0.28	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-363	-0.13	2.5E-04	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-4322	-0.10	3.0E-03	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-128-2	0.10	2.5E-03	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-3148	0.04	0.12	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-645	0.01	0.36	N	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-3667	0.04	0.15	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1304	0.26	1.0E-05	Y	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-518a-1	0.08	0.01	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-519d	-5.1E-03	0.44	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-2114	-0.17	1.0E-05	Y	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-198	-0.05	0.08	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1273c	-0.07	0.03	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1204	-0.07	0.03	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-3936	0.03	0.23	N	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1179	-0.03	0.22	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1231	0.04	0.12	N	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-3658	0.04	0.15	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-3689b	0.09	5.5E-03	Y	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1293	0.11	1.1E-03	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-4310	-0.07	0.02	Y	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-887	-5.9E-04	0.49	N	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-320d-1	-0.04	0.16	N	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-3692	0.10	1.9E-03	Y	0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-1291	0.02	0.27	N	-0.08	0.01	Y	0	0.50	N	0	0.50	N
mir-2117	0.02	0.33	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-676	-0.09	8.8E-03	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-3192	0.19	1.0E-05	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-580	0.12	3.2E-04	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-3650	0.04	0.16	N	-0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-29b-2	-0.18	1.0E-05	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-516a-2	0.12	3.2E-04	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-3618	0.12	2.6E-04	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-885	0.03	0.21	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-1915	0.22	1.0E-05	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-3677	0.43	1.0E-05	Y	-0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-643	0.15	3.0E-05	Y	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3607	-0.17	1.0E-05	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3612	-0.16	1.0E-05	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3197	0.08	0.01	Y	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3174	0.11	1.1E-03	Y	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-550a-2	0.10	3.7E-03	Y	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3652	0.25	1.0E-05	Y	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3179-3	0.05	0.09	N	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3664	0.22	1.0E-05	Y	-0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-153-2	-0.18	1.0E-05	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-668	-0.07	0.03	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N

mir-3154	-0.09	4.9E-03	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-1197	-0.16	1.0E-05	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-767	0.22	1.0E-05	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-378b	0.12	2.6E-04	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-544	-0.09	8.9E-03	Y	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-548y	-0.03	0.21	N	0.07	0.02	Y	0	0.50	N	0	0.50	N
mir-3616	0.10	3.0E-03	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3918	-0.02	0.28	N	0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3655	0.06	0.05	N	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3648	0.22	1.0E-05	Y	0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-301b	0.47	1.0E-05	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-2276	0.16	1.0E-05	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-16-2	0.27	1.0E-05	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-548d-1	0.21	1.0E-05	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3166	-0.10	2.6E-03	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-1234	0.02	0.32	N	0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3122	-0.07	0.04	Y	0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-498	-0.03	0.21	N	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3151	0.21	1.0E-05	Y	-0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-3171	-0.06	0.04	Y	0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-1278	0.06	0.04	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-3198	0.22	1.0E-05	Y	-0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-7-1	-7.2E-03	0.42	N	-0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-1283-1	0.13	1.4E-04	Y	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-521-1	0.05	0.06	N	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-105-2	0.33	1.0E-05	Y	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-1284	-0.06	0.04	N	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-548e	-5.6E-03	0.44	N	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-3681	-0.02	0.27	N	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-2110	0.02	0.27	N	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-3195	0.07	0.02	Y	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-1270-1	0.06	0.05	N	-0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-572	0.10	2.2E-03	Y	-0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-3914-1	-0.08	0.01	Y	0.06	0.04	Y	0	0.50	N	0	0.50	N
mir-507	0.02	0.27	N	0.06	0.04	N	0	0.50	N	0	0.50	N
mir-658	0.09	5.0E-03	Y	-0.06	0.04	N	0	0.50	N	0	0.50	N
mir-664	-0.33	1.0E-05	Y	-0.06	0.04	N	0	0.50	N	0	0.50	N
mir-3139	0.03	0.20	N	0.06	0.04	N	0	0.50	N	0	0.50	N
mir-208a	0.05	0.09	N	0.06	0.05	N	0	0.50	N	0	0.50	N
mir-564	-0.06	0.06	N	0.06	0.05	N	0	0.50	N	0	0.50	N
mir-3654	-7.4E-03	0.42	N	0.06	0.05	N	0	0.50	N	0	0.50	N
mir-544b	0.04	0.13	N	-0.06	0.05	N	0	0.50	N	0	0.50	N
mir-3115	0.21	1.0E-05	Y	-0.06	0.05	N	0	0.50	N	0	0.50	N
mir-1538	0.07	0.03	Y	0.06	0.05	N	0	0.50	N	0	0.50	N
mir-567	0.05	0.10	N	-0.06	0.05	N	0	0.50	N	0	0.50	N
mir-208b	0.08	0.01	Y	-0.06	0.05	N	0	0.50	N	0	0.50	N
mir-1281	-0.05	0.09	N	0.06	0.05	N	0	0.50	N	0	0.50	N
mir-527	0.12	4.0E-04	Y	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-548f-1	0.25	1.0E-05	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-642a	-8.1E-03	0.41	N	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-3684	0.16	1.0E-05	Y	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-510	-0.06	0.06	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-4320	-0.06	0.06	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-607	-0.04	0.12	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-3149	0.11	7.0E-04	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-3186	0.10	1.7E-03	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-3925	0.18	1.0E-05	Y	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-3935	0.08	0.02	Y	0.05	0.06	N	0	0.50	N	0	0.50	N
mir-875	0.02	0.28	N	0.05	0.07	N	0	0.50	N	0	0.50	N
mir-1286	0.17	1.0E-05	Y	-0.05	0.07	N	0	0.50	N	0	0.50	N
mir-3662	0.23	1.0E-05	Y	-0.05	0.07	N	0	0.50	N	0	0.50	N
mir-1283-2	0.12	5.4E-04	Y	0.05	0.07	N	0	0.50	N	0	0.50	N
mir-1297	0.05	0.10	N	-0.05	0.07	N	0	0.50	N	0	0.50	N
mir-3613	0.11	9.8E-04	Y	0.05	0.07	N	0	0.50	N	0	0.50	N
mir-520f	0.07	0.03	Y	0.05	0.07	N	0	0.50	N	0	0.50	N

mir-2115	-0.12	5.5E-04	Y	0.05	0.07	N	0	0.50	N	0	0.50	N
mir-651	0.10	2.3E-03	Y	0.05	0.07	N	0	0.50	N	0	0.50	N
mir-520g	-0.02	0.25	N	0.05	0.08	N	0	0.50	N	0	0.50	N
mir-519c	0.05	0.07	N	0.05	0.08	N	0	0.50	N	0	0.50	N
mir-3152	-0.07	0.03	Y	0.05	0.08	N	0	0.50	N	0	0.50	N
mir-515-2	-0.10	4.0E-03	Y	0.05	0.08	N	0	0.50	N	0	0.50	N
mir-548k	0.16	1.0E-05	Y	-0.05	0.08	N	0	0.50	N	0	0.50	N
mir-526a-1	0.09	7.1E-03	Y	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-4257	0.09	7.1E-03	Y	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-3657	0.09	6.7E-03	Y	0.05	0.09	N	0	0.50	N	0	0.50	N
mir-4315-1	0.10	3.6E-03	Y	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-3175	0.05	0.10	N	0.05	0.09	N	0	0.50	N	0	0.50	N
mir-2861	-4.9E-03	0.44	N	0.05	0.09	N	0	0.50	N	0	0.50	N
mir-3202-2	-0.09	8.7E-03	Y	0.05	0.09	N	0	0.50	N	0	0.50	N
mir-4328	-0.05	0.10	N	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-1244-2	0.03	0.21	N	-0.05	0.10	N	0	0.50	N	0	0.50	N
mir-105-1	0.27	1.0E-05	Y	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-3189	0.14	8.0E-05	Y	-0.05	0.10	N	0	0.50	N	0	0.50	N
mir-623	6.3E-03	0.43	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-3155	0.15	1.0E-05	Y	-0.05	0.10	N	0	0.50	N	0	0.50	N
mir-3194	0.07	0.03	Y	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-603	0.10	2.4E-03	Y	-0.05	0.10	N	0	0.50	N	0	0.50	N
mir-3944	0.13	1.7E-04	Y	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-1305	0.10	3.8E-03	Y	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-4326	0.34	1.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-1910	0.23	1.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-525	-0.05	0.07	N	0.04	0.11	N	0	0.50	N	0	0.50	N
mir-518f	0.04	0.14	N	0.04	0.11	N	0	0.50	N	0	0.50	N
mir-3913-1	-0.21	1.0E-05	Y	-0.04	0.11	N	0	0.50	N	0	0.50	N
mir-938	-4.2E-03	0.45	N	0.04	0.11	N	0	0.50	N	0	0.50	N
mir-16-1	0.08	0.02	Y	0.04	0.12	N	0	0.50	N	0	0.50	N
mir-490	-0.03	0.18	N	-0.04	0.12	N	0	0.50	N	0	0.50	N
mir-1290	0.17	1.0E-05	Y	-0.04	0.12	N	0	0.50	N	0	0.50	N
mir-3943	-0.09	6.1E-03	Y	-0.04	0.12	N	0	0.50	N	0	0.50	N
mir-3929	0.11	1.5E-03	Y	-0.04	0.12	N	0	0.50	N	0	0.50	N
mir-3180-2	0.01	0.39	N	0.04	0.12	N	0	0.50	N	0	0.50	N
mir-3143	0.24	1.0E-05	Y	-0.04	0.12	N	0	0.50	N	0	0.50	N
mir-3916	-0.07	0.03	Y	0.04	0.13	N	0	0.50	N	0	0.50	N
mir-489	-0.25	1.0E-05	Y	0.04	0.13	N	0	0.50	N	0	0.50	N
mir-3185	-0.02	0.26	N	0.04	0.13	N	0	0.50	N	0	0.50	N
mir-1322	0.11	1.6E-03	Y	-0.04	0.13	N	0	0.50	N	0	0.50	N
mir-4306	9.9E-03	0.40	N	0.04	0.13	N	0	0.50	N	0	0.50	N
mir-3184	-0.12	4.4E-04	Y	-0.04	0.13	N	0	0.50	N	0	0.50	N
mir-513a-2	0.04	0.12	N	-0.04	0.13	N	0	0.50	N	0	0.50	N
mir-520d	0.09	4.9E-03	Y	-0.04	0.13	N	0	0.50	N	0	0.50	N
mir-3065	-0.08	0.02	Y	-0.04	0.14	N	0	0.50	N	0	0.50	N
mir-518a-2	0.08	9.6E-03	Y	0.04	0.14	N	0	0.50	N	0	0.50	N
mir-937	0.39	1.0E-05	Y	-0.04	0.14	N	0	0.50	N	0	0.50	N
mir-1248	0.12	4.8E-04	Y	-0.04	0.15	N	0	0.50	N	0	0.50	N
mir-602	0.04	0.15	N	0.04	0.15	N	0	0.50	N	0	0.50	N
mir-1178	0.03	0.17	N	0.04	0.15	N	0	0.50	N	0	0.50	N
mir-1238	0.02	0.30	N	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-1306	0.24	1.0E-05	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-578	-0.11	9.6E-04	Y	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-3945	0.10	1.9E-03	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-548x	-0.07	0.03	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-3159	0.08	9.9E-03	Y	0.04	0.16	N	0	0.50	N	0	0.50	N
let-7a-3	-0.36	1.0E-05	Y	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-621	0.13	1.4E-04	Y	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-3937	0.08	0.01	Y	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-3183	0.11	9.1E-04	Y	0.03	0.17	N	0	0.50	N	0	0.50	N
mir-891b	0.08	0.02	Y	0.03	0.17	N	0	0.50	N	0	0.50	N
mir-3074	0.17	1.0E-05	Y	-0.03	0.17	N	0	0.50	N	0	0.50	N
mir-1285-1	0.10	1.9E-03	Y	0.03	0.17	N	0	0.50	N	0	0.50	N
mir-3611	0.05	0.09	N	-0.03	0.18	N	0	0.50	N	0	0.50	N

mir-513a-1	0.02	0.26	N	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-4289	0.03	0.23	N	0.03	0.18	N	0	0.50	N	0	0.50	N
mir-95	-0.05	0.07	N	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-614	0.03	0.24	N	0.03	0.18	N	0	0.50	N	0	0.50	N
mir-1255a	-0.03	0.21	N	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-3146	0.13	1.8E-04	Y	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-1256	0.05	0.08	N	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-449b	-0.19	1.0E-05	Y	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-3915	0.01	0.37	N	0.03	0.18	N	0	0.50	N	0	0.50	N
mir-802	0.15	4.0E-05	Y	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-612	0.06	0.04	Y	-0.03	0.18	N	0	0.50	N	0	0.50	N
mir-1911	6.9E-03	0.43	N	-0.03	0.19	N	0	0.50	N	0	0.50	N
mir-320e	0.01	0.36	N	-0.03	0.19	N	0	0.50	N	0	0.50	N
mir-3177	0.09	6.3E-03	Y	0.03	0.19	N	0	0.50	N	0	0.50	N
mir-3919	-0.12	6.0E-04	Y	0.03	0.19	N	0	0.50	N	0	0.50	N
let-7f-2	-0.25	1.0E-05	Y	0.03	0.19	N	0	0.50	N	0	0.50	N
mir-3660	0.10	3.6E-03	Y	-0.03	0.20	N	0	0.50	N	0	0.50	N
mir-662	0.14	5.0E-05	Y	0.03	0.20	N	0	0.50	N	0	0.50	N
mir-3158-2	0.12	3.1E-04	Y	-0.03	0.20	N	0	0.50	N	0	0.50	N
mir-3909	0.26	1.0E-05	Y	0.03	0.20	N	0	0.50	N	0	0.50	N
mir-3646	-0.09	8.0E-03	Y	0.03	0.20	N	0	0.50	N	0	0.50	N
mir-1825	-0.01	0.37	N	-0.03	0.20	N	0	0.50	N	0	0.50	N
mir-509-3	0.15	4.0E-05	Y	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-888	-0.06	0.05	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-554	0.01	0.36	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-3680	0.19	1.0E-05	Y	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-3938	0.13	1.7E-04	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-524	4.2E-03	0.46	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-548l	0.09	6.8E-03	Y	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-522	0.17	1.0E-05	Y	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-3164	0.16	1.0E-05	Y	0.03	0.22	N	0	0.50	N	0	0.50	N
mir-610	0.10	2.6E-03	Y	-0.03	0.22	N	0	0.50	N	0	0.50	N
mir-513b	0.06	0.05	N	-0.03	0.23	N	0	0.50	N	0	0.50	N
mir-3136	0.20	1.0E-05	Y	0.03	0.23	N	0	0.50	N	0	0.50	N
mir-509-1	0.06	0.04	Y	0.03	0.23	N	0	0.50	N	0	0.50	N
mir-3124	0.16	1.0E-05	Y	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-3137	0.18	1.0E-05	Y	0.03	0.24	N	0	0.50	N	0	0.50	N
mir-514-3	-0.08	0.01	Y	0.03	0.24	N	0	0.50	N	0	0.50	N
mir-622	0.05	0.08	N	0.02	0.25	N	0	0.50	N	0	0.50	N
mir-631	0.02	0.33	N	0.02	0.25	N	0	0.50	N	0	0.50	N
mir-1236	0.24	1.0E-05	Y	0.02	0.25	N	0	0.50	N	0	0.50	N
mir-3920	-0.07	0.03	Y	0.02	0.25	N	0	0.50	N	0	0.50	N
mir-3617	0.06	0.05	N	-0.02	0.25	N	0	0.50	N	0	0.50	N
mir-3158-1	0.05	0.10	N	0.02	0.25	N	0	0.50	N	0	0.50	N
mir-3173	0.09	6.4E-03	Y	0.02	0.26	N	0	0.50	N	0	0.50	N
mir-1912	-0.14	6.0E-05	Y	0.02	0.27	N	0	0.50	N	0	0.50	N
mir-3912	-0.02	0.34	N	-0.02	0.27	N	0	0.50	N	0	0.50	N
mir-3125	0.10	2.9E-03	Y	-0.02	0.27	N	0	0.50	N	0	0.50	N
mir-639	0.08	0.02	Y	-0.02	0.27	N	0	0.50	N	0	0.50	N
mir-3145	0.21	1.0E-05	Y	0.02	0.27	N	0	0.50	N	0	0.50	N
mir-3651	0.14	9.0E-05	Y	-0.02	0.27	N	0	0.50	N	0	0.50	N
mir-609	-0.12	3.4E-04	Y	0.02	0.27	N	0	0.50	N	0	0.50	N
mir-596	-0.08	0.01	Y	-0.02	0.28	N	0	0.50	N	0	0.50	N
mir-449c	-0.19	1.0E-05	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
mir-3907	0.04	0.14	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
mir-550a-1	0.21	1.0E-05	Y	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-3156-3	-0.09	5.4E-03	Y	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-514b	8.5E-03	0.41	N	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-216b	0.04	0.16	N	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-765	0.07	0.02	Y	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-3923	0.04	0.16	N	0.02	0.29	N	0	0.50	N	0	0.50	N
mir-3131	0.08	0.01	Y	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-630	-0.09	5.8E-03	Y	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-3939	0.13	1.7E-04	Y	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-588	0.29	1.0E-05	Y	0.02	0.31	N	0	0.50	N	0	0.50	N

mir-720	0.02	0.25	N	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-550b-1	9.2E-03	0.40	N	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-595	0.07	0.02	Y	-0.02	0.32	N	0	0.50	N	0	0.50	N
mir-3927	0.05	0.08	N	0.02	0.32	N	0	0.50	N	0	0.50	N
mir-3659	-0.04	0.15	N	-0.02	0.32	N	0	0.50	N	0	0.50	N
mir-514-1	-0.10	2.2E-03	Y	0.02	0.33	N	0	0.50	N	0	0.50	N
mir-3168	-1.3E-03	0.48	N	0.02	0.33	N	0	0.50	N	0	0.50	N
mir-2277	0.29	1.0E-05	Y	0.01	0.34	N	0	0.50	N	0	0.50	N
mir-3162	-0.03	0.24	N	-0.01	0.35	N	0	0.50	N	0	0.50	N
mir-1289-1	-0.02	0.30	N	0.01	0.36	N	0	0.50	N	0	0.50	N
mir-583	-0.01	0.34	N	0.01	0.36	N	0	0.50	N	0	0.50	N
mir-1257	0.05	0.09	N	-0.01	0.36	N	0	0.50	N	0	0.50	N
mir-4286	-0.04	0.15	N	-0.01	0.36	N	0	0.50	N	0	0.50	N
mir-4284	0.08	0.01	Y	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-3187	0.21	1.0E-05	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
mir-422a	0.06	0.05	N	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-19b-1	0.17	1.0E-05	Y	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-552	0.10	1.8E-03	Y	-0.01	0.38	N	0	0.50	N	0	0.50	N
mir-3161	0.01	0.38	N	0.01	0.38	N	0	0.50	N	0	0.50	N
mir-650	0.12	5.9E-04	Y	-0.01	0.38	N	0	0.50	N	0	0.50	N
mir-515-1	-0.02	0.26	N	0.01	0.38	N	0	0.50	N	0	0.50	N
mir-153-1	-0.10	2.0E-03	Y	-0.01	0.39	N	0	0.50	N	0	0.50	N
mir-1181	0.02	0.33	N	-9.8E-03	0.39	N	0	0.50	N	0	0.50	N
mir-579	0.34	1.0E-05	Y	-9.5E-03	0.40	N	0	0.50	N	0	0.50	N
mir-520c	-8.6E-03	0.40	N	9.7E-03	0.40	N	0	0.50	N	0	0.50	N
mir-519b	0.10	2.3E-03	Y	9.1E-03	0.40	N	0	0.50	N	0	0.50	N
mir-616	0.27	1.0E-05	Y	-8.6E-03	0.40	N	0	0.50	N	0	0.50	N
mir-3138	0.06	0.04	Y	-8.1E-03	0.41	N	0	0.50	N	0	0.50	N
mir-593	0.01	0.34	N	-7.9E-03	0.41	N	0	0.50	N	0	0.50	N
mir-3190	-0.06	0.05	N	-7.7E-03	0.41	N	0	0.50	N	0	0.50	N
mir-632	-0.08	0.02	Y	-7.6E-03	0.41	N	0	0.50	N	0	0.50	N
mir-1909	0.22	1.0E-05	Y	-7.5E-03	0.42	N	0	0.50	N	0	0.50	N
mir-1275	-0.09	6.5E-03	Y	-7.4E-03	0.42	N	0	0.50	N	0	0.50	N
mir-3163	-0.06	0.05	N	-7.0E-03	0.42	N	0	0.50	N	0	0.50	N
mir-1270-2	1.9E-03	0.48	N	-6.8E-03	0.42	N	0	0.50	N	0	0.50	N
mir-1539	0.17	1.0E-05	Y	7.2E-03	0.42	N	0	0.50	N	0	0.50	N
mir-3940	0.25	1.0E-05	Y	-6.5E-03	0.43	N	0	0.50	N	0	0.50	N
mir-606	-0.08	0.02	Y	-6.3E-03	0.43	N	0	0.50	N	0	0.50	N
mir-3621	-0.08	0.02	Y	-6.3E-03	0.43	N	0	0.50	N	0	0.50	N
mir-586	-0.05	0.07	N	6.3E-03	0.43	N	0	0.50	N	0	0.50	N
mir-600	-0.06	0.04	Y	-5.6E-03	0.44	N	0	0.50	N	0	0.50	N
mir-3928	0.22	1.0E-05	Y	-5.2E-03	0.44	N	0	0.50	N	0	0.50	N
mir-1237	0.26	1.0E-05	Y	5.6E-03	0.44	N	0	0.50	N	0	0.50	N
mir-320d-2	-0.05	0.09	N	5.4E-03	0.44	N	0	0.50	N	0	0.50	N
mir-657	-0.09	8.9E-03	Y	4.9E-03	0.45	N	0	0.50	N	0	0.50	N
mir-3181	-0.07	0.03	Y	-4.2E-03	0.45	N	0	0.50	N	0	0.50	N
mir-548v	-0.01	0.39	N	-4.2E-03	0.45	N	0	0.50	N	0	0.50	N
mir-3911	0.19	1.0E-05	Y	4.3E-03	0.46	N	0	0.50	N	0	0.50	N
mir-611	0.11	1.5E-03	Y	-3.8E-03	0.46	N	0	0.50	N	0	0.50	N
mir-3170	0.06	0.06	N	-3.7E-03	0.46	N	0	0.50	N	0	0.50	N
mir-1288	0.01	0.39	N	-3.7E-03	0.46	N	0	0.50	N	0	0.50	N
mir-519e	0.03	0.20	N	-3.5E-03	0.46	N	0	0.50	N	0	0.50	N
mir-576	0.28	1.0E-05	Y	-3.5E-03	0.46	N	0	0.50	N	0	0.50	N
mir-555	0.13	1.9E-04	Y	-3.4E-03	0.46	N	0	0.50	N	0	0.50	N
mir-636	0.32	1.0E-05	Y	3.5E-03	0.46	N	0	0.50	N	0	0.50	N
mir-3179-2	0.06	0.05	N	3.5E-03	0.47	N	0	0.50	N	0	0.50	N
mir-3620	0.23	1.0E-05	Y	-2.2E-03	0.47	N	0	0.50	N	0	0.50	N
mir-3609	0.04	0.13	N	2.6E-03	0.48	N	0	0.50	N	0	0.50	N
mir-943	0.22	1.0E-05	Y	2.5E-03	0.48	N	0	0.50	N	0	0.50	N
mir-521-2	0.16	1.0E-05	Y	-1.8E-03	0.48	N	0	0.50	N	0	0.50	N
mir-3691	0.15	1.0E-05	Y	-1.6E-03	0.48	N	0	0.50	N	0	0.50	N
mir-627	-0.04	0.17	N	1.7E-03	0.48	N	0	0.50	N	0	0.50	N
mir-604	-0.04	0.11	N	-7.0E-04	0.49	N	0	0.50	N	0	0.50	N
mir-3160-1	-0.12	4.1E-04	Y	1.2E-04	0.50	N	0	0.50	N	0	0.50	N

Master list of miRNAs in TCGA ovarian cancer dataset together the correlation scores of their expression values with PR signatures and enrichment scores of target genes with PR signature

miRNA	*S*(M,P)	P-value	BH	*S*(M,R)	P-value	BH	ES_P	P-value	BH	ES_R	P-value	BH
mir-376a-2	0.02	0.29	N	-0.02	0.28	N	0.45	1.0E-05	Y	-0.42	1.0E-05	Y
mir-376a-1	0.08	0.02	Y	-0.01	0.37	N	0.45	1.0E-05	Y	-0.42	1.0E-05	Y
mir-501	0.09	0.01	Y	2.2E-03	0.48	N	0.45	1.0E-05	Y	-0.26	1.0E-05	Y
mir-598	-0.10	7.7E-03	Y	0.01	0.39	N	0.45	1.0E-05	Y	-0.21	1.0E-05	Y
mir-1303	0.07	0.05	N	-0.02	0.28	N	0.08	0.02	Y	0.16	1.0E-05	Y
mir-18b	0.18	1.0E-05	Y	-0.06	0.09	N	0.06	0.06	N	0.16	1.0E-05	Y
mir-194-2	-0.02	0.32	N	-0.05	0.11	N	0.14	2.0E-04	Y	0.16	1.0E-05	Y
mir-194-1	-0.02	0.31	N	-0.05	0.12	N	0.14	2.0E-04	Y	0.16	1.0E-05	Y
mir-1307	0.09	0.02	Y	-1.3E-03	0.49	N	0.34	1.0E-05	Y	0.17	1.0E-05	Y
mir-132	-0.04	0.16	N	0.21	1.0E-05	Y	0.01	0.40	N	0.18	1.0E-05	Y
mir-140	-0.05	0.11	N	0.18	1.0E-05	Y	6.9E-03	0.44	N	0.18	1.0E-05	Y
mir-19b-2	0.03	0.23	N	-0.06	0.07	N	0.08	0.03	N	0.18	1.0E-05	Y
mir-130b	0.21	1.0E-05	Y	-0.02	0.31	N	0.09	0.01	Y	0.19	1.0E-05	Y
mir-138-1	-0.02	0.32	N	0.08	0.02	Y	0.07	0.04	N	0.19	1.0E-05	Y
mir-138-2	0.08	0.02	Y	-0.03	0.20	N	0.07	0.04	N	0.19	1.0E-05	Y
mir-124-2	-0.05	0.13	N	0.08	0.02	Y	-1.4E-	0.49	N	0.19	1.0E-05	Y
mir-124-1	-0.07	0.05	N	0.05	0.11	N	-1.4E-	0.49	N	0.19	1.0E-05	Y
mir-124-3	-7.2E-03	0.43	N	0.02	0.29	N	-4.1E-	0.46	N	0.19	1.0E-05	Y
mir-181c	-0.03	0.23	N	-0.09	0.01	Y	0.16	1.0E-05	Y	0.20	1.0E-05	Y
mir-941-1	0.05	0.11	N	0.06	0.09	N	0.18	1.0E-05	Y	0.21	1.0E-05	Y
mir-143	-5.8E-03	0.44	N	0.17	1.0E-05	Y	0.13	8.7E-04	Y	0.21	1.0E-05	Y
mir-29a	-0.19	2.0E-05	Y	0.06	0.08	N	0.09	0.02	Y	0.21	1.0E-05	Y
mir-224	-0.02	0.32	N	0.22	1.0E-05	Y	0.19	1.0E-05	Y	0.22	1.0E-05	Y
mir-374b	0.06	0.06	N	-0.02	0.34	N	0.04	0.15	N	0.22	1.0E-05	Y
mir-211	-0.02	0.30	N	-0.07	0.05	N	0.10	9.9E-03	Y	0.23	1.0E-05	Y
mir-33a	0.15	7.0E-05	Y	0.08	0.03	Y	0.04	0.14	N	0.23	1.0E-05	Y
mir-137	-0.02	0.28	N	0.07	0.03	Y	0.11	4.8E-03	Y	0.23	1.0E-05	Y
mir-146a	-0.04	0.16	N	0.24	1.0E-05	Y	0.02	0.33	N	0.26	1.0E-05	Y
mir-200b	-0.02	0.28	N	-0.08	0.03	Y	0.05	0.13	N	0.27	1.0E-05	Y
mir-133a-2	-0.03	0.25	N	0.16	1.0E-05	Y	-0.10	8.2E-03	Y	0.28	1.0E-05	Y
mir-133a-1	-0.06	0.08	N	0.30	1.0E-05	Y	-0.10	8.2E-03	Y	0.28	1.0E-05	Y
mir-141	0.05	0.13	N	-0.16	3.0E-05	Y	0.08	0.03	N	0.29	1.0E-05	Y
mir-146b	-0.06	0.06	N	0.01	0.41	N	-0.03	0.22	N	0.29	1.0E-05	Y
mir-199a-2	-0.11	3.6E-03	Y	0.34	1.0E-05	Y	-0.19	2.0E-05	Y	0.29	1.0E-05	Y
mir-199a-1	-0.12	1.7E-03	Y	0.35	1.0E-05	Y	-0.19	2.0E-05	Y	0.29	1.0E-05	Y
mir-205	-5.4E-03	0.45	N	0.04	0.18	N	-0.09	0.01	Y	0.30	1.0E-05	Y
mir-203	-0.07	0.04	Y	0.08	0.02	Y	0.12	1.9E-03	Y	0.31	1.0E-05	Y
mir-200a	0.09	0.02	Y	-0.15	2.0E-04	Y	0.06	0.06	N	0.32	1.0E-05	Y
mir-200c	-0.08	0.03	Y	-0.13	5.2E-04	Y	0.08	0.03	N	0.32	1.0E-05	Y
mir-19a	0.14	1.7E-04	Y	-0.12	1.0E-03	Y	-0.12	1.2E-03	Y	0.32	1.0E-05	Y
mir-150	-0.02	0.35	N	0.40	1.0E-05	Y	2.2E-03	0.48	N	0.37	1.0E-05	Y
mir-429	0.06	0.06	N	-0.10	9.3E-03	Y	-0.09	0.02	Y	0.37	1.0E-05	Y
mir-130a	0.14	2.5E-04	Y	-0.15	2.6E-04	Y	-0.07	0.04	N	0.39	1.0E-05	Y
mir-372	0.03	0.26	N	-0.10	5.3E-03	Y	-0.18	2.0E-05	Y	0.53	1.0E-05	Y
mir-766	0.14	5.0E-04	Y	0.20	1.0E-05	Y	0.18	1.0E-05	Y	-0.19	2.0E-05	Y
mir-625	0.11	5.3E-03	Y	-0.11	4.3E-03	Y	-0.16	3.0E-05	Y	0.15	6.0E-05	Y
mir-1227	0.04	0.18	N	-0.06	0.08	N	0.31	1.0E-05	Y	-0.15	1.1E-04	Y
mir-335	0.09	0.01	Y	-0.12	1.0E-03	Y	-0.15	1.1E-04	Y	0.15	1.1E-04	Y
mir-671	0.11	2.8E-03	Y	-0.01	0.38	N	0.16	1.0E-05	Y	-0.15	1.3E-04	Y
mir-103-2	0.19	1.0E-05	Y	-0.06	0.06	N	0.14	4.3E-04	Y	0.14	1.7E-04	Y
mir-103-1	0.01	0.36	N	-0.03	0.26	N	0.14	4.3E-04	Y	0.14	1.7E-04	Y
mir-214	-0.10	5.6E-03	Y	0.44	1.0E-05	Y	0.10	6.0E-03	Y	0.14	1.7E-04	Y
let-7g	-0.06	0.06	N	0.03	0.27	N	0.23	1.0E-05	Y	0.14	3.4E-04	Y
mir-374a	-0.02	0.33	N	0.07	0.05	N	0.11	4.6E-03	Y	0.14	3.6E-04	Y
mir-217	0.03	0.26	N	0.22	1.0E-05	Y	0.10	7.3E-03	Y	0.13	6.6E-04	Y
mir-98	0.02	0.33	N	2.6E-04	0.50	N	0.11	4.0E-03	Y	0.13	7.5E-04	Y
mir-29b-1	-0.11	2.2E-03	Y	6.9E-03	0.44	N	0.12	2.7E-03	Y	0.13	7.9E-04	Y
mir-92a-1	-0.02	0.34	N	-0.07	0.05	N	0.22	1.0E-05	Y	-0.13	8.1E-04	Y
mir-30d	-0.11	2.7E-03	Y	-0.04	0.15	N	0.06	0.06	N	0.13	8.5E-04	Y

mir-345	0.22	1.0E-05	Y	-0.12	1.4E-03	Y	0.24	1.0E-05	Y	0.13	8.9E-04	Y
mir-301a	0.16	1.0E-05	Y	-0.16	8.0E-05	Y	0.22	1.0E-05	Y	0.13	1.1E-03	Y
mir-212	0.06	0.07	N	0.25	1.0E-05	Y	0.20	1.0E-05	Y	-0.12	1.2E-03	Y
mir-375	-0.03	0.25	N	-0.16	3.0E-05	Y	0.12	1.3E-03	Y	0.13	1.2E-03	Y
mir-142	0.03	0.23	N	0.29	1.0E-05	Y	0.07	0.05	N	0.12	1.4E-03	Y
mir-346	-0.05	0.13	N	0.13	1.2E-03	Y	-0.11	4.0E-03	Y	0.12	1.5E-03	Y
mir-29c	-0.10	8.9E-03	Y	0.04	0.19	N	0.22	1.0E-05	Y	0.12	1.5E-03	Y
mir-532	0.04	0.19	N	-0.03	0.21	N	0.26	1.0E-05	Y	-0.12	1.5E-03	Y
mir-190	0.05	0.14	N	7.7E-03	0.43	N	0.04	0.14	N	0.12	1.6E-03	Y
mir-223	-0.09	0.02	Y	0.30	1.0E-05	Y	0.01	0.40	N	0.12	1.8E-03	Y
mir-195	-0.11	2.5E-03	Y	0.12	2.7E-03	Y	0.08	0.03	N	0.12	1.9E-03	Y
mir-96	0.01	0.36	N	-0.15	1.6E-04	Y	0.15	7.0E-05	Y	0.12	2.2E-03	Y
mir-708	-0.03	0.21	N	0.05	0.12	N	0.28	1.0E-05	Y	-0.11	2.4E-03	Y
mir-155	0.01	0.40	N	0.17	1.0E-05	Y	0.15	2.0E-05	Y	0.12	2.5E-03	Y
mir-1914	0.19	1.0E-05	Y	-0.03	0.20	N	0.23	1.0E-05	Y	-0.11	2.8E-03	Y
mir-145	-0.12	1.0E-03	Y	0.26	1.0E-05	Y	0.10	9.5E-03	Y	0.11	2.8E-03	Y
mir-30a	-0.04	0.19	N	-0.05	0.09	N	0.18	1.0E-05	Y	0.11	2.8E-03	Y
mir-590	0.12	2.2E-03	Y	-0.04	0.18	N	0.15	4.0E-05	Y	0.11	3.1E-03	Y
mir-365-2	-0.06	0.06	N	0.06	0.06	N	-0.03	0.20	N	0.11	4.6E-03	Y
mir-365-1	-0.07	0.05	N	0.05	0.10	N	-0.03	0.20	N	0.11	4.6E-03	Y
mir-362	0.08	0.03	Y	-0.10	6.9E-03	Y	0.54	1.0E-05	Y	0.11	5.4E-03	Y
mir-302a	-0.04	0.18	N	0.01	0.41	N	0.09	0.01	Y	0.10	5.5E-03	Y
mir-320c-2	-0.06	0.06	N	-0.08	0.02	Y	0.19	1.0E-05	Y	0.10	5.8E-03	Y
mir-320c-1	-0.12	1.5E-03	Y	0.01	0.37	N	0.19	1.0E-05	Y	0.10	5.8E-03	Y
mir-21	-0.04	0.17	N	0.28	1.0E-05	Y	0.17	1.0E-05	Y	0.10	6.2E-03	Y
mir-10b	0.08	0.02	Y	-0.13	8.9E-04	Y	0.13	7.7E-04	Y	0.10	6.8E-03	Y
mir-373	0.10	6.0E-03	Y	-0.08	0.03	Y	0.17	1.0E-05	Y	0.10	7.1E-03	Y
mir-34b	-0.05	0.10	N	-0.12	1.1E-03	Y	0.12	1.4E-03	Y	0.10	7.2E-03	Y
mir-548b	0.09	0.02	Y	-0.04	0.14	N	-0.03	0.23	N	0.10	8.3E-03	Y
mir-148b	-5.5E-03	0.45	N	-0.10	5.1E-03	Y	0.04	0.15	N	0.10	8.8E-03	Y
mir-133b	-0.02	0.30	N	0.12	1.7E-03	Y	-0.17	3.0E-05	Y	0.09	0.01	Y
mir-148a	-0.09	0.02	Y	-0.01	0.37	N	0.22	1.0E-05	Y	0.09	0.01	Y
mir-128-1	0.09	0.01	Y	-0.06	0.06	N	0.10	7.7E-03	Y	0.09	0.01	Y
mir-424	0.02	0.34	N	0.01	0.38	N	0.27	1.0E-05	Y	0.09	0.01	Y
mir-1-2	3.4E-03	0.47	N	0.10	5.9E-03	Y	0.15	1.4E-04	Y	0.09	0.01	Y
mir-1-1	0.02	0.33	N	0.02	0.35	N	0.15	1.4E-04	Y	0.09	0.01	Y
mir-497	-0.02	0.33	N	0.04	0.16	N	0.18	1.0E-05	Y	-0.09	0.01	Y
mir-27b	-0.02	0.35	N	0.07	0.04	Y	0.18	1.0E-05	Y	0.09	0.02	Y
mir-330	0.06	0.07	N	0.05	0.14	N	0.06	0.07	N	0.09	0.02	Y
mir-183	0.07	0.03	Y	-0.17	3.0E-05	Y	0.18	1.0E-05	Y	0.08	0.02	Y
mir-1180	0.09	0.01	Y	-0.12	1.1E-03	Y	0.13	7.1E-04	Y	-0.08	0.03	Y
mir-23a	-0.06	0.06	N	0.08	0.03	Y	0.24	1.0E-05	Y	0.08	0.03	Y
mir-339	0.11	3.2E-03	Y	-0.04	0.15	N	0.24	1.0E-05	Y	-0.08	0.03	Y
mir-500	0.05	0.14	N	0.03	0.20	N	0.35	1.0E-05	Y	0.08	0.03	Y
mir-1296	0.12	1.6E-03	Y	-6.3E-03	0.44	N	0.32	1.0E-05	Y	-0.08	0.03	Y
mir-328	-0.05	0.12	N	-0.14	5.0E-04	Y	0.18	1.0E-05	Y	-0.07	0.04	Y
mir-1260	-0.03	0.25	N	-5.9E-03	0.44	N	0.26	1.0E-05	Y	-0.07	0.04	N
mir-26b	-0.01	0.38	N	-0.08	0.02	Y	0.05	0.10	N	0.07	0.04	N
mir-17	0.07	0.05	N	-0.08	0.02	Y	0.10	7.9E-03	Y	0.07	0.05	N
mir-101-2	-0.09	0.01	Y	-0.06	0.08	N	0.22	1.0E-05	Y	0.07	0.05	N
mir-101-1	-0.12	1.5E-03	Y	-7.5E-03	0.43	N	0.22	1.0E-05	Y	0.07	0.05	N
mir-340	0.02	0.31	N	0.08	0.03	Y	0.16	1.0E-05	Y	0.07	0.05	N
mir-26a-1	0.14	4.4E-04	Y	-0.11	3.1E-03	Y	0.14	4.4E-04	Y	0.06	0.06	N
mir-122	0.04	0.19	N	-0.09	0.01	Y	0.16	1.0E-05	Y	0.06	0.06	N
mir-30b	-0.02	0.35	N	-0.07	0.04	Y	0.18	1.0E-05	Y	0.06	0.06	N
mir-449a	-0.09	0.01	Y	-0.17	3.0E-05	Y	0.22	1.0E-05	Y	-0.06	0.07	N
mir-326	0.01	0.36	N	0.12	2.5E-03	Y	0.15	1.5E-04	Y	-0.06	0.07	N
mir-106b	0.13	7.4E-04	Y	-0.06	0.08	N	0.14	3.6E-04	Y	0.06	0.08	N
mir-760	0.13	7.0E-04	Y	-0.09	0.02	Y	0.20	1.0E-05	Y	-0.06	0.08	N
mir-454	0.19	1.0E-05	Y	-0.10	7.3E-03	Y	0.25	1.0E-05	Y	0.06	0.09	N
mir-197	0.08	0.02	Y	0.02	0.28	N	0.18	1.0E-05	Y	-0.06	0.09	N
mir-191	0.05	0.13	N	-0.18	2.0E-05	Y	0.24	1.0E-05	Y	-0.06	0.09	N
mir-93	0.10	6.6E-03	Y	-0.09	0.01	Y	0.13	6.0E-04	Y	0.06	0.09	N
mir-193a	-0.11	4.5E-03	Y	0.17	1.0E-05	Y	0.10	7.5E-03	Y	-0.05	0.09	N
mir-503	0.09	0.01	Y	0.02	0.29	N	0.25	1.0E-05	Y	-0.05	0.10	N

mir-99b	0.09	0.02	Y	-0.02	0.35	N	0.22	1.0E-05	Y	-0.05	0.10	N
mir-125a	-0.11	3.3E-03	Y	0.07	0.04	Y	0.10	8.3E-03	Y	0.05	0.10	N
mir-215	-0.05	0.12	N	0.01	0.40	N	0.24	1.0E-05	Y	0.05	0.13	N
mir-935	0.03	0.27	N	-0.07	0.05	N	0.22	1.0E-05	Y	-0.05	0.13	N
mir-221	-0.11	3.0E-03	Y	0.16	1.0E-05	Y	0.20	1.0E-05	Y	0.05	0.14	N
mir-182	0.07	0.06	N	-0.17	3.0E-05	Y	0.18	1.0E-05	Y	0.04	0.14	N
let-7b	-0.15	1.8E-04	Y	0.22	1.0E-05	Y	0.18	1.0E-05	Y	-0.04	0.14	N
mir-9-1	0.10	6.5E-03	Y	-0.19	2.0E-05	Y	0.13	5.4E-04	Y	0.04	0.14	N
mir-9-2	0.10	6.3E-03	Y	-0.18	2.0E-05	Y	0.13	5.4E-04	Y	0.04	0.14	N
mir-30c-2	-0.04	0.19	N	-0.07	0.05	N	0.13	7.6E-04	Y	0.04	0.15	N
mir-874	0.05	0.13	N	-0.02	0.33	N	0.39	1.0E-05	Y	-0.04	0.15	N
mir-151	0.04	0.18	N	0.06	0.08	N	0.20	1.0E-05	Y	0.04	0.15	N
mir-193b	-0.07	0.05	N	0.08	0.03	Y	0.25	1.0E-05	Y	-0.04	0.15	N
mir-185	0.09	0.02	Y	0.11	4.4E-03	Y	0.23	1.0E-05	Y	0.04	0.15	N
mir-361	3.3E-03	0.47	N	-6.4E-03	0.44	N	0.20	1.0E-05	Y	-0.04	0.15	N
mir-181a-1	-0.04	0.15	N	0.17	1.0E-05	Y	0.09	0.02	Y	0.04	0.16	N
mir-615	0.03	0.21	N	-7.0E-03	0.43	N	0.20	1.0E-05	Y	-0.04	0.16	N
mir-324	0.11	3.0E-03	Y	-0.05	0.10	N	0.18	1.0E-05	Y	-0.04	0.16	N
mir-421	0.15	1.0E-04	Y	0.03	0.25	N	0.13	8.9E-04	Y	-0.04	0.17	N
mir-92b	0.04	0.19	N	-0.12	1.3E-03	Y	0.20	1.0E-05	Y	-0.04	0.17	N
mir-27a	-4.1E-03	0.46	N	0.07	0.04	N	0.14	5.0E-04	Y	0.04	0.18	N
mir-192	0.05	0.10	N	-0.10	7.1E-03	Y	0.21	1.0E-05	Y	0.04	0.18	N
mir-222	-0.13	8.1E-04	Y	0.18	1.0E-05	Y	0.22	1.0E-05	Y	0.04	0.18	N
let-7d	3.9E-03	0.46	N	0.05	0.10	N	0.18	1.0E-05	Y	-0.04	0.18	N
mir-605	-0.05	0.13	N	0.31	1.0E-05	Y	0.15	1.1E-04	Y	-0.03	0.21	N
mir-1226	0.06	0.06	N	-0.08	0.03	Y	0.18	1.0E-05	Y	0.03	0.21	N
mir-425	0.09	0.02	Y	-0.10	7.3E-03	Y	0.28	1.0E-05	Y	-0.03	0.22	N
mir-331	0.14	4.3E-04	Y	-0.04	0.14	N	0.13	7.9E-04	Y	-0.03	0.23	N
mir-7-3	0.08	0.02	Y	-0.05	0.12	N	0.09	0.01	Y	0.03	0.23	N
mir-7-2	-0.02	0.30	N	-0.03	0.27	N	0.09	0.01	Y	0.03	0.23	N
mir-210	0.13	5.4E-04	Y	-0.07	0.05	N	0.22	1.0E-05	Y	0.03	0.23	N
mir-10a	-0.06	0.07	N	0.04	0.15	N	0.14	3.4E-04	Y	0.03	0.24	N
mir-504	-0.06	0.08	N	0.02	0.30	N	0.03	0.23	N	0.03	0.25	N
mir-22	-0.02	0.27	N	0.34	1.0E-05	Y	0.19	1.0E-05	Y	0.03	0.25	N
mir-32	0.31	1.0E-05	Y	-0.16	3.0E-05	Y	0.17	1.0E-05	Y	-0.03	0.26	N
mir-92a-2	0.05	0.11	N	-0.11	3.9E-03	Y	0.14	2.5E-04	Y	-0.03	0.26	N
mir-30e	0.01	0.40	N	-0.14	4.0E-04	Y	0.19	1.0E-05	Y	-0.03	0.26	N
mir-940	0.20	1.0E-05	Y	-0.05	0.13	N	0.03	0.22	N	0.03	0.26	N
let-7a-1	-0.09	0.01	Y	0.15	1.7E-04	Y	0.15	1.2E-04	Y	-0.03	0.26	N
let-7a-2	-0.10	6.4E-03	Y	0.14	2.9E-04	Y	0.15	1.2E-04	Y	-0.03	0.26	N
mir-18a	0.22	1.0E-05	Y	-0.10	5.0E-03	Y	0.17	1.0E-05	Y	0.02	0.28	N
mir-196a-2	0.06	0.06	N	0.04	0.15	N	0.21	1.0E-05	Y	-0.02	0.29	N
mir-196a-1	0.09	0.01	Y	0.03	0.26	N	0.21	1.0E-05	Y	-0.02	0.29	N
let-7c	-0.05	0.12	N	-0.03	0.22	N	0.15	7.0E-05	Y	-0.02	0.29	N
mir-23b	-0.03	0.25	N	0.08	0.02	Y	0.13	7.3E-04	Y	0.02	0.29	N
mir-320a	-3.3E-03	0.47	N	-0.04	0.16	N	0.18	1.0E-05	Y	-0.02	0.30	N
mir-1229	-0.03	0.25	N	0.02	0.34	N	0.30	1.0E-05	Y	-0.02	0.30	N
mir-34a	-0.07	0.04	Y	0.18	1.0E-05	Y	0.23	1.0E-05	Y	0.02	0.32	N
mir-186	0.04	0.19	N	-0.06	0.08	N	0.16	1.0E-05	Y	-0.02	0.33	N
let-7e	-5.1E-03	0.45	N	0.14	3.2E-04	Y	0.20	1.0E-05	Y	-0.02	0.34	N
mir-455	-0.05	0.10	N	0.21	1.0E-05	Y	0.14	4.4E-04	Y	0.02	0.35	N
mir-126	0.11	3.5E-03	Y	0.03	0.24	N	0.22	1.0E-05	Y	0.02	0.35	N
mir-181d	-0.03	0.24	N	-0.02	0.27	N	0.29	1.0E-05	Y	0.02	0.36	N
mir-15b	0.16	1.0E-05	Y	-0.02	0.35	N	0.20	1.0E-05	Y	-0.01	0.36	N
mir-25	0.12	2.0E-03	Y	-0.15	8.0E-05	Y	0.16	1.0E-05	Y	0.02	0.36	N
mir-342	-0.02	0.29	N	0.16	1.0E-05	Y	0.18	1.0E-05	Y	-0.01	0.37	N
mir-877	0.10	7.8E-03	Y	0.03	0.26	N	0.21	1.0E-05	Y	-0.01	0.38	N
mir-744	-0.04	0.15	N	0.06	0.07	N	0.12	1.7E-03	Y	-0.01	0.38	N
mir-423	-0.04	0.15	N	0.05	0.12	N	0.14	4.4E-04	Y	0.01	0.38	N
mir-99a	-0.02	0.31	N	-0.08	0.03	Y	0.17	1.0E-05	Y	0.01	0.39	N
mir-28	0.04	0.19	N	0.03	0.21	N	0.21	1.0E-05	Y	0.01	0.39	N
mir-378	-2.0E-03	0.48	N	0.01	0.39	N	0.15	1.0E-04	Y	-0.01	0.40	N
mir-125b-1	-0.10	7.0E-03	Y	-0.02	0.27	N	0.13	1.2E-03	Y	0.01	0.40	N
mir-320b-2	8.8E-03	0.42	N	-0.05	0.12	N	0.15	2.0E-05	Y	-8.7E-03	0.41	N
mir-320b-1	0.03	0.26	N	-9.0E-03	0.41	N	0.15	2.0E-05	Y	-8.7E-03	0.41	N

let-7i	-0.06	0.08	N	0.11	4.3E-03	Y	0.41	1.0E-05	Y	-7.2E-03	0.43	N
mir-196b	0.09	0.01	Y	0.13	8.5E-04	Y	0.11	5.2E-03	Y	-6.1E-03	0.44	N
mir-1301	0.15	7.0E-05	Y	-0.13	7.2E-04	Y	0.24	1.0E-05	Y	5.9E-03	0.45	N
mir-769	0.18	1.0E-05	Y	-0.10	8.6E-03	Y	0.16	1.0E-05	Y	5.8E-03	0.45	N
mir-181b-2	0.04	0.14	N	0.11	4.8E-03	Y	0.15	5.0E-05	Y	-4.1E-03	0.46	N
mir-181b-1	0.03	0.23	N	0.04	0.18	N	0.15	5.0E-05	Y	-4.1E-03	0.46	N
mir-505	0.06	0.07	N	-0.06	0.07	N	0.17	1.0E-05	Y	-2.8E-03	0.47	N
mir-100	-0.07	0.04	N	0.06	0.06	N	0.19	1.0E-05	Y	2.5E-03	0.48	N
mir-296	0.07	0.05	N	-0.19	2.0E-05	Y	0.12	1.9E-03	Y	2.4E-03	0.48	N
mir-125b-2	1.1E-03	0.49	N	-0.04	0.18	N	0.17	1.0E-05	Y	-1.7E-03	0.48	N
mir-149	-0.08	0.02	Y	-0.03	0.27	N	0.18	1.0E-05	Y	1.6E-03	0.49	N
mir-484	0.05	0.11	N	-0.05	0.09	N	0.17	1.0E-05	Y	1.2E-03	0.49	N
mir-652	0.01	0.38	N	-0.02	0.35	N	0.18	1.0E-05	Y	4.4E-04	0.50	N
mir-509-1	-0.09	0.01	Y	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-514-1	-0.03	0.21	N	-0.29	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-508	-0.11	2.5E-03	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-509-3	-0.09	0.01	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-509-2	-0.10	5.3E-03	Y	-0.28	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-513c	-0.12	1.2E-03	Y	-0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-513a-2	-0.09	0.01	Y	-0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-506	-0.10	6.0E-03	Y	-0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-514-2	-0.07	0.04	Y	-0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-507	-0.08	0.03	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-514-3	-0.09	0.02	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-513a-1	-0.12	1.6E-03	Y	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-135a-1	0.06	0.08	N	-0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-513b	-0.10	4.9E-03	Y	-0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-510	-0.10	5.1E-03	Y	-0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-486	-0.03	0.27	N	0.16	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-543	-0.06	0.07	N	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1197	2.1E-03	0.48	N	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-412	-7.1E-03	0.43	N	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-511-2	0.01	0.40	N	0.17	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-139	-0.04	0.16	N	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-574	-0.12	1.2E-03	Y	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-431	-0.09	9.9E-03	Y	0.18	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-511-1	-2.4E-03	0.47	N	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-323	-0.07	0.05	N	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-494	-0.05	0.12	N	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-329-1	-0.07	0.04	Y	0.19	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-618	-0.03	0.23	N	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-136	-0.05	0.11	N	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-410	-0.08	0.03	Y	0.20	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-379	-0.02	0.30	N	0.21	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-541	0.02	0.35	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-329-2	-0.05	0.13	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1976	-0.08	0.03	Y	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-369	-0.06	0.06	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-539	-0.03	0.21	N	0.22	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-433	-0.13	5.5E-04	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-487b	-0.09	0.01	Y	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-411	-7.3E-03	0.43	N	0.23	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-381	-0.06	0.06	N	0.24	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-154	-0.06	0.07	N	0.25	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1249	-0.05	0.09	N	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-496	-0.05	0.12	N	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-654	-0.10	8.6E-03	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1295	-0.10	4.7E-03	Y	0.26	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-337	-0.07	0.04	N	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-127	-0.11	3.1E-03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-377	-0.12	1.7E-03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-758	-0.05	0.12	N	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-370	-0.09	0.01	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1294	-0.11	2.4E-03	Y	0.27	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-134	-0.08	0.02	Y	0.29	1.0E-05	Y	0	0.50	N	0	0.50	N

mir-487a	-0.07	0.05	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-382	-0.08	0.03	Y	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-299	-0.06	0.08	N	0.30	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1228	-0.02	0.31	N	0.31	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-485	-0.12	1.0E-03	Y	0.32	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-199b	-0.07	0.05	N	0.33	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-409	-0.06	0.06	N	0.34	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1245	-0.03	0.22	N	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-1247	-0.10	6.1E-03	Y	0.36	1.0E-05	Y	0	0.50	N	0	0.50	N
mir-577	0.17	1.0E-05	Y	-0.20	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-202	-0.10	6.7E-03	Y	-0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-488	0.03	0.27	N	-0.19	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-1251	0.05	0.11	N	-0.17	2.0E-05	Y	0	0.50	N	0	0.50	N
mir-449b	-0.05	0.11	N	-0.17	3.0E-05	Y	0	0.50	N	0	0.50	N
mir-1248	-0.21	1.0E-05	Y	0.15	6.0E-05	Y	0	0.50	N	0	0.50	N
let-7a-3	-0.09	0.01	Y	0.14	1.7E-04	Y	0	0.50	N	0	0.50	N
mir-490	0.01	0.37	N	-0.15	2.5E-04	Y	0	0.50	N	0	0.50	N
mir-129-1	0.06	0.09	N	-0.15	2.5E-04	Y	0	0.50	N	0	0.50	N
mir-1266	0.06	0.08	N	-0.14	3.4E-04	Y	0	0.50	N	0	0.50	N
mir-1911	0.04	0.17	N	-0.13	5.1E-04	Y	0	0.50	N	0	0.50	N
mir-1298	0.08	0.03	Y	-0.13	5.1E-04	Y	0	0.50	N	0	0.50	N
mir-129-2	0.05	0.13	N	-0.13	5.5E-04	Y	0	0.50	N	0	0.50	N
mir-1269	0.02	0.32	N	-0.13	5.5E-04	Y	0	0.50	N	0	0.50	N
mir-1915	0.08	0.03	Y	-0.13	6.6E-04	Y	0	0.50	N	0	0.50	N
mir-889	0.03	0.24	N	0.13	7.7E-04	Y	0	0.50	N	0	0.50	N
mir-187	0.02	0.29	N	-0.13	7.8E-04	Y	0	0.50	N	0	0.50	N
mir-483	2.7E-03	0.48	N	0.13	8.3E-04	Y	0	0.50	N	0	0.50	N
let-7f-1	-0.02	0.31	N	0.13	1.0E-03	Y	0	0.50	N	0	0.50	N
mir-448	0.06	0.07	N	-0.12	1.2E-03	Y	0	0.50	N	0	0.50	N
mir-933	0.16	1.0E-05	Y	-0.12	1.2E-03	Y	0	0.50	N	0	0.50	N
mir-641	0.13	7.9E-04	Y	-0.12	1.4E-03	Y	0	0.50	N	0	0.50	N
mir-219-1	0.05	0.10	N	-0.12	1.4E-03	Y	0	0.50	N	0	0.50	N
mir-665	-0.05	0.13	N	0.12	1.8E-03	Y	0	0.50	N	0	0.50	N
mir-639	0.04	0.17	N	-0.12	2.1E-03	Y	0	0.50	N	0	0.50	N
mir-24-1	0.11	4.0E-03	Y	0.12	2.5E-03	Y	0	0.50	N	0	0.50	N
mir-588	0.16	1.0E-05	Y	0.12	2.5E-03	Y	0	0.50	N	0	0.50	N
mir-33b	0.10	9.0E-03	Y	0.12	2.5E-03	Y	0	0.50	N	0	0.50	N
mir-765	-0.01	0.40	N	0.12	2.6E-03	Y	0	0.50	N	0	0.50	N
mir-545	0.06	0.08	N	0.11	2.8E-03	Y	0	0.50	N	0	0.50	N
mir-720	0.09	0.02	Y	-0.11	3.3E-03	Y	0	0.50	N	0	0.50	N
mir-320d-2	-0.08	0.03	Y	-0.11	3.9E-03	Y	0	0.50	N	0	0.50	N
mir-609	0.04	0.20	N	-0.11	4.0E-03	Y	0	0.50	N	0	0.50	N
mir-873	0.03	0.24	N	0.11	4.2E-03	Y	0	0.50	N	0	0.50	N
mir-190b	-8.5E-03	0.42	N	-0.10	4.9E-03	Y	0	0.50	N	0	0.50	N
mir-453	0.09	0.01	Y	0.11	5.0E-03	Y	0	0.50	N	0	0.50	N
mir-578	0.07	0.05	N	-0.10	5.1E-03	Y	0	0.50	N	0	0.50	N
mir-616	0.11	3.6E-03	Y	-0.10	5.6E-03	Y	0	0.50	N	0	0.50	N
mir-647	0.11	5.4E-03	Y	-0.10	6.3E-03	Y	0	0.50	N	0	0.50	N
mir-1262	0.06	0.07	N	-0.10	6.4E-03	Y	0	0.50	N	0	0.50	N
mir-599	-0.08	0.03	Y	0.10	7.1E-03	Y	0	0.50	N	0	0.50	N
mir-612	0.06	0.07	N	0.10	7.5E-03	Y	0	0.50	N	0	0.50	N
mir-589	0.06	0.06	N	0.10	8.6E-03	Y	0	0.50	N	0	0.50	N
mir-371	0.01	0.40	N	-0.10	8.7E-03	Y	0	0.50	N	0	0.50	N
mir-655	0.03	0.21	N	0.10	8.9E-03	Y	0	0.50	N	0	0.50	N
mir-105-2	0.08	0.02	Y	-0.10	9.0E-03	Y	0	0.50	N	0	0.50	N
mir-29b-2	-0.10	7.2E-03	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-651	0.07	0.04	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-668	-0.07	0.04	Y	0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-518b	-0.03	0.20	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
let-7f-2	-0.04	0.17	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-885	-0.07	0.04	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-629	0.05	0.09	N	0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-1912	0.02	0.34	N	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-1246	0.13	9.2E-04	Y	0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-642	-0.01	0.37	N	0.09	0.01	Y	0	0.50	N	0	0.50	N

mir-1292	8.4E-03	0.42	N	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-1276	0.11	3.2E-03	Y	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-548d-2	-1.0E-03	0.49	N	-0.09	0.01	Y	0	0.50	N	0	0.50	N
mir-2110	-0.06	0.08	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-675	4.0E-03	0.46	N	0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-499	0.06	0.08	N	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-636	0.11	3.3E-03	Y	-0.09	0.02	Y	0	0.50	N	0	0.50	N
mir-517b	-0.02	0.35	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-650	-0.02	0.32	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-934	-0.14	3.5E-04	Y	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-1825	0.03	0.27	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-638	0.03	0.22	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-517a	-0.02	0.31	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-549	-0.03	0.22	N	0.08	0.02	Y	0	0.50	N	0	0.50	N
mir-188	0.07	0.04	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-1286	-0.02	0.33	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-600	0.02	0.28	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-1287	0.10	0.01	Y	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-657	-5.3E-03	0.45	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-614	-0.07	0.05	N	0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-30c-1	0.04	0.18	N	-0.08	0.03	Y	0	0.50	N	0	0.50	N
mir-216a	3.1E-03	0.47	N	0.07	0.03	Y	0	0.50	N	0	0.50	N
mir-147	-0.03	0.27	N	0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-548k	-0.04	0.19	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-1178	4.5E-03	0.46	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-19b-1	0.05	0.12	N	-0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-7-1	0.26	1.0E-05	Y	-0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-520d	0.02	0.35	N	0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-571	-0.06	0.08	N	0.07	0.04	Y	0	0.50	N	0	0.50	N
mir-552	0.05	0.13	N	0.07	0.04	N	0	0.50	N	0	0.50	N
mir-2113	0.05	0.10	N	-0.07	0.04	N	0	0.50	N	0	0.50	N
mir-301b	0.17	1.0E-05	Y	-0.07	0.04	N	0	0.50	N	0	0.50	N
mir-1255a	0.04	0.18	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-1183	-0.06	0.09	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-587	-0.06	0.09	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-1234	-9.5E-03	0.41	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-559	0.04	0.17	N	-0.07	0.05	N	0	0.50	N	0	0.50	N
mir-1185-2	0.03	0.21	N	0.07	0.05	N	0	0.50	N	0	0.50	N
mir-572	0.04	0.20	N	-0.07	0.05	N	0	0.50	N	0	0.50	N
mir-1185-1	0.05	0.11	N	0.07	0.06	N	0	0.50	N	0	0.50	N
mir-645	0.05	0.13	N	-0.07	0.06	N	0	0.50	N	0	0.50	N
mir-921	0.05	0.13	N	-0.07	0.06	N	0	0.50	N	0	0.50	N
mir-888	0.05	0.09	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-519d	4.8E-03	0.46	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-298	-0.01	0.39	N	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-1253	0.08	0.03	Y	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-1910	0.07	0.05	N	-0.06	0.06	N	0	0.50	N	0	0.50	N
mir-519b	6.1E-03	0.44	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-1538	-0.01	0.38	N	0.06	0.06	N	0	0.50	N	0	0.50	N
mir-579	0.10	8.5E-03	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1826	0.01	0.40	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-554	-0.06	0.07	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1271	-0.01	0.39	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1323	-0.04	0.14	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-661	-0.09	0.02	Y	-0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1908	0.15	1.0E-04	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-648	-0.03	0.20	N	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-626	1.7E-04	0.50	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1257	0.04	0.17	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
mir-450a-1	0.02	0.29	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
mir-582	0.07	0.05	N	-0.06	0.07	N	0	0.50	N	0	0.50	N
mir-607	0.07	0.04	Y	0.06	0.07	N	0	0.50	N	0	0.50	N
mir-1283-1	0.02	0.33	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
mir-649	-9.6E-03	0.40	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
mir-922	0.11	3.5E-03	Y	0.06	0.08	N	0	0.50	N	0	0.50	N

mir-561	0.06	0.09	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
mir-1979	0.04	0.17	N	-0.06	0.08	N	0	0.50	N	0	0.50	N
mir-942	0.16	1.0E-05	Y	-0.06	0.08	N	0	0.50	N	0	0.50	N
mir-548j	-0.03	0.23	N	0.06	0.08	N	0	0.50	N	0	0.50	N
mir-320d-1	-0.06	0.08	N	-0.06	0.09	N	0	0.50	N	0	0.50	N
mir-632	0.07	0.05	N	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-592	-1.7E-03	0.48	N	-0.06	0.09	N	0	0.50	N	0	0.50	N
mir-24-2	-0.01	0.36	N	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-380	0.11	3.7E-03	Y	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-770	0.02	0.33	N	0.06	0.09	N	0	0.50	N	0	0.50	N
mir-573	0.04	0.18	N	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-498	7.6E-03	0.43	N	0.05	0.09	N	0	0.50	N	0	0.50	N
mir-1263	0.07	0.04	Y	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-548e	0.02	0.33	N	-0.05	0.09	N	0	0.50	N	0	0.50	N
mir-1304	0.04	0.16	N	0.05	0.09	N	0	0.50	N	0	0.50	N
mir-886	0.02	0.32	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-1290	0.13	6.5E-04	Y	-0.05	0.10	N	0	0.50	N	0	0.50	N
mir-516b-2	-0.03	0.25	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-1293	0.05	0.10	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-526b	0.04	0.19	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-575	-6.8E-03	0.43	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-520g	-0.02	0.30	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-662	-0.02	0.31	N	0.05	0.10	N	0	0.50	N	0	0.50	N
mir-551a	0.20	1.0E-05	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-450b	-0.02	0.29	N	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-518d	0.04	0.14	N	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-544	0.08	0.02	Y	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-1909	4.9E-03	0.45	N	0.05	0.11	N	0	0.50	N	0	0.50	N
mir-526a-1	0.04	0.16	N	-0.05	0.11	N	0	0.50	N	0	0.50	N
mir-875	0.07	0.04	Y	0.05	0.12	N	0	0.50	N	0	0.50	N
mir-1270	-0.02	0.28	N	0.05	0.12	N	0	0.50	N	0	0.50	N
mir-1265	0.11	4.7E-03	Y	0.05	0.12	N	0	0.50	N	0	0.50	N
mir-1289-1	0.12	1.6E-03	Y	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-596	-0.06	0.06	N	-0.05	0.12	N	0	0.50	N	0	0.50	N
mir-383	-0.12	1.3E-03	Y	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-548i-2	0.04	0.15	N	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-938	0.11	4.0E-03	Y	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-1225	0.05	0.13	N	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-198	0.07	0.05	N	0.05	0.13	N	0	0.50	N	0	0.50	N
mir-105-1	0.04	0.14	N	-0.05	0.13	N	0	0.50	N	0	0.50	N
mir-550-2	0.05	0.09	N	-0.04	0.14	N	0	0.50	N	0	0.50	N
mir-944	0.06	0.07	N	0.05	0.14	N	0	0.50	N	0	0.50	N
mir-450a-2	0.04	0.15	N	0.04	0.14	N	0	0.50	N	0	0.50	N
mir-181a-2	0.09	0.02	Y	-0.04	0.14	N	0	0.50	N	0	0.50	N
mir-128-2	0.08	0.03	Y	-0.04	0.14	N	0	0.50	N	0	0.50	N
mir-520c	0.02	0.33	N	-0.04	0.15	N	0	0.50	N	0	0.50	N
mir-603	0.09	0.01	Y	-0.04	0.15	N	0	0.50	N	0	0.50	N
mir-1238	8.4E-03	0.42	N	0.04	0.15	N	0	0.50	N	0	0.50	N
mir-16-1	0.16	1.0E-05	Y	-0.04	0.15	N	0	0.50	N	0	0.50	N
mir-376c	0.05	0.12	N	0.04	0.16	N	0	0.50	N	0	0.50	N
mir-1272	-0.04	0.14	N	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-564	5.6E-03	0.45	N	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-519c	-0.03	0.25	N	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-1244	0.07	0.04	Y	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-640	0.09	0.02	Y	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-637	0.04	0.17	N	-0.04	0.16	N	0	0.50	N	0	0.50	N
mir-1264	0.01	0.39	N	-0.04	0.17	N	0	0.50	N	0	0.50	N
mir-548a-3	0.02	0.34	N	-0.04	0.17	N	0	0.50	N	0	0.50	N
mir-520e	1.3E-03	0.49	N	-0.04	0.17	N	0	0.50	N	0	0.50	N
mir-1539	3.0E-03	0.47	N	-0.04	0.17	N	0	0.50	N	0	0.50	N
mir-602	0.08	0.02	Y	-0.04	0.17	N	0	0.50	N	0	0.50	N
mir-1204	0.07	0.05	N	-0.04	0.18	N	0	0.50	N	0	0.50	N
mir-1268	-0.01	0.40	N	0.04	0.18	N	0	0.50	N	0	0.50	N
mir-422a	-0.02	0.30	N	-0.04	0.18	N	0	0.50	N	0	0.50	N
mir-1224	9.2E-03	0.42	N	0.04	0.18	N	0	0.50	N	0	0.50	N

mir-208a	0.06	0.09	N	-0.04	0.18	N	0	0.50	N	0	0.50	N
mir-216b	0.02	0.32	N	0.04	0.19	N	0	0.50	N	0	0.50	N
mir-1236	0.02	0.29	N	-0.04	0.19	N	0	0.50	N	0	0.50	N
mir-147b	0.05	0.09	N	0.04	0.20	N	0	0.50	N	0	0.50	N
mir-516b-1	0.02	0.34	N	0.04	0.20	N	0	0.50	N	0	0.50	N
mir-595	0.02	0.32	N	-0.03	0.20	N	0	0.50	N	0	0.50	N
mir-622	0.03	0.21	N	-0.03	0.20	N	0	0.50	N	0	0.50	N
mir-1470	0.06	0.06	N	0.04	0.20	N	0	0.50	N	0	0.50	N
mir-520h	-0.02	0.34	N	0.03	0.20	N	0	0.50	N	0	0.50	N
mir-9-3	-0.01	0.37	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-220b	0.02	0.36	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-519a-1	-7.5E-04	0.49	N	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-1284	0.11	2.8E-03	Y	-0.03	0.21	N	0	0.50	N	0	0.50	N
mir-939	5.8E-03	0.45	N	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-1205	-0.03	0.26	N	0.03	0.21	N	0	0.50	N	0	0.50	N
mir-1250	0.09	0.01	Y	-0.03	0.22	N	0	0.50	N	0	0.50	N
mir-489	0.05	0.12	N	0.03	0.22	N	0	0.50	N	0	0.50	N
mir-555	-0.02	0.35	N	0.03	0.22	N	0	0.50	N	0	0.50	N
mir-1181	0.07	0.05	N	0.03	0.23	N	0	0.50	N	0	0.50	N
mir-517c	-4.2E-03	0.46	N	0.03	0.23	N	0	0.50	N	0	0.50	N
mir-220a	0.06	0.09	N	-0.03	0.23	N	0	0.50	N	0	0.50	N
mir-524	0.02	0.33	N	-0.03	0.23	N	0	0.50	N	0	0.50	N
mir-1237	-0.02	0.28	N	0.03	0.23	N	0	0.50	N	0	0.50	N
mir-1978	-0.03	0.22	N	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-604	-0.03	0.25	N	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-1254	0.07	0.05	N	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-1208	-0.03	0.21	N	-0.03	0.24	N	0	0.50	N	0	0.50	N
mir-518c	0.01	0.39	N	0.03	0.25	N	0	0.50	N	0	0.50	N
mir-1231	0.02	0.31	N	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-492	-0.06	0.06	N	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-597	1.5E-03	0.49	N	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-1977	0.09	0.02	Y	-0.03	0.26	N	0	0.50	N	0	0.50	N
mir-548l	0.03	0.21	N	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-1289-2	-0.02	0.33	N	0.03	0.26	N	0	0.50	N	0	0.50	N
mir-659	-0.04	0.14	N	-0.03	0.27	N	0	0.50	N	0	0.50	N
mir-518a-2	0.04	0.16	N	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1282	-0.01	0.38	N	-0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1322	-3.4E-03	0.46	N	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-556	0.07	0.04	Y	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1258	0.10	6.3E-03	Y	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1306	0.14	2.5E-04	Y	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-890	7.9E-03	0.43	N	0.03	0.27	N	0	0.50	N	0	0.50	N
mir-1302-3	0.05	0.11	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
mir-1243	0.04	0.18	N	-0.02	0.28	N	0	0.50	N	0	0.50	N
mir-611	6.4E-03	0.44	N	0.02	0.28	N	0	0.50	N	0	0.50	N
mir-521-1	0.07	0.04	Y	0.02	0.28	N	0	0.50	N	0	0.50	N
mir-943	0.03	0.27	N	0.02	0.29	N	0	0.50	N	0	0.50	N
mir-548f-1	-0.04	0.14	N	0.02	0.29	N	0	0.50	N	0	0.50	N
mir-658	0.02	0.33	N	-0.02	0.29	N	0	0.50	N	0	0.50	N
mir-1913	0.02	0.32	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-153-1	-4.1E-03	0.46	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-1278	-0.04	0.19	N	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-1267	-0.06	0.06	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-591	4.1E-03	0.46	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-522	0.02	0.32	N	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-26a-2	-0.09	0.01	Y	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-767	0.03	0.21	N	-0.02	0.30	N	0	0.50	N	0	0.50	N
mir-663b	-0.01	0.37	N	0.02	0.30	N	0	0.50	N	0	0.50	N
mir-1974	0.07	0.05	N	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-2052	0.08	0.03	Y	-0.02	0.31	N	0	0.50	N	0	0.50	N
mir-376b	0.06	0.09	N	0.02	0.31	N	0	0.50	N	0	0.50	N
mir-581	0.03	0.24	N	0.02	0.31	N	0	0.50	N	0	0.50	N
mir-644	0.02	0.31	N	-0.02	0.32	N	0	0.50	N	0	0.50	N
mir-624	-0.04	0.16	N	-0.02	0.33	N	0	0.50	N	0	0.50	N
mir-219-2	0.03	0.27	N	0.02	0.33	N	0	0.50	N	0	0.50	N

mir-515-1	0.04	0.15	N	-0.02	0.33	N	0	0.50	N	0	0.50	N
mir-570	0.08	0.03	Y	0.02	0.33	N	0	0.50	N	0	0.50	N
mir-1288	0.06	0.08	N	-0.02	0.33	N	0	0.50	N	0	0.50	N
mir-1256	0.05	0.13	N	0.02	0.34	N	0	0.50	N	0	0.50	N
mir-586	-0.07	0.05	N	0.02	0.34	N	0	0.50	N	0	0.50	N
mir-892b	-0.01	0.40	N	-0.02	0.34	N	0	0.50	N	0	0.50	N
mir-1283-2	0.03	0.25	N	-0.02	0.35	N	0	0.50	N	0	0.50	N
mir-518e	0.01	0.38	N	0.02	0.35	N	0	0.50	N	0	0.50	N
mir-512-1	-0.01	0.40	N	0.02	0.35	N	0	0.50	N	0	0.50	N
mir-516a-2	-2.1E-03	0.48	N	-0.02	0.35	N	0	0.50	N	0	0.50	N
mir-16-2	0.17	1.0E-05	Y	0.02	0.35	N	0	0.50	N	0	0.50	N
mir-1972	-0.04	0.18	N	-0.02	0.35	N	0	0.50	N	0	0.50	N
mir-548o	2.0E-03	0.48	N	0.02	0.36	N	0	0.50	N	0	0.50	N
mir-520a	0.08	0.03	Y	0.02	0.36	N	0	0.50	N	0	0.50	N
mir-542	0.04	0.20	N	0.02	0.36	N	0	0.50	N	0	0.50	N
mir-1299	-0.07	0.04	N	-0.01	0.36	N	0	0.50	N	0	0.50	N
mir-628	0.03	0.26	N	0.02	0.36	N	0	0.50	N	0	0.50	N
mir-663	0.23	1.0E-05	Y	-0.01	0.36	N	0	0.50	N	0	0.50	N
mir-1184	9.5E-03	0.41	N	0.01	0.36	N	0	0.50	N	0	0.50	N
mir-491	0.06	0.08	N	-0.01	0.36	N	0	0.50	N	0	0.50	N
mir-653	-4.5E-03	0.45	N	0.01	0.36	N	0	0.50	N	0	0.50	N
mir-1280	0.02	0.31	N	0.01	0.37	N	0	0.50	N	0	0.50	N
mir-551b	0.08	0.02	Y	-0.01	0.37	N	0	0.50	N	0	0.50	N
mir-518a-1	0.06	0.06	N	-0.01	0.37	N	0	0.50	N	0	0.50	N
mir-520b	-0.04	0.17	N	-0.01	0.38	N	0	0.50	N	0	0.50	N
mir-512-2	0.02	0.33	N	0.01	0.39	N	0	0.50	N	0	0.50	N
mir-153-2	-0.03	0.21	N	0.01	0.39	N	0	0.50	N	0	0.50	N
mir-891b	0.05	0.09	N	-0.01	0.39	N	0	0.50	N	0	0.50	N
mir-920	-0.03	0.24	N	-0.01	0.39	N	0	0.50	N	0	0.50	N
mir-623	-0.03	0.26	N	0.01	0.39	N	0	0.50	N	0	0.50	N
mir-519e	4.7E-03	0.46	N	-0.01	0.39	N	0	0.50	N	0	0.50	N
mir-1274b	0.10	5.8E-03	Y	0.01	0.39	N	0	0.50	N	0	0.50	N
mir-527	4.1E-04	0.50	N	-0.01	0.40	N	0	0.50	N	0	0.50	N
mir-876	0.02	0.33	N	0.01	0.40	N	0	0.50	N	0	0.50	N
mir-1259	-0.03	0.23	N	0.01	0.40	N	0	0.50	N	0	0.50	N
mir-580	0.04	0.18	N	0.01	0.40	N	0	0.50	N	0	0.50	N
mir-1203	0.03	0.23	N	-9.9E-03	0.40	N	0	0.50	N	0	0.50	N
mir-593	8.3E-03	0.42	N	0.01	0.41	N	0	0.50	N	0	0.50	N
mir-516a-1	-0.02	0.33	N	-9.5E-03	0.41	N	0	0.50	N	0	0.50	N
mir-1285-1	-0.01	0.38	N	-9.3E-03	0.41	N	0	0.50	N	0	0.50	N
mir-1469	-0.08	0.02	Y	9.9E-03	0.41	N	0	0.50	N	0	0.50	N
mir-563	-0.02	0.31	N	-8.6E-03	0.41	N	0	0.50	N	0	0.50	N
mir-1277	0.10	7.6E-03	Y	9.0E-03	0.42	N	0	0.50	N	0	0.50	N
mir-518f	5.7E-03	0.45	N	8.3E-03	0.42	N	0	0.50	N	0	0.50	N
mir-520f	-0.02	0.30	N	-7.7E-03	0.42	N	0	0.50	N	0	0.50	N
mir-937	0.05	0.10	N	8.2E-03	0.42	N	0	0.50	N	0	0.50	N
mir-936	-0.06	0.07	N	-7.6E-03	0.42	N	0	0.50	N	0	0.50	N
mir-521-2	-0.03	0.26	N	8.0E-03	0.43	N	0	0.50	N	0	0.50	N
mir-656	0.02	0.36	N	7.7E-03	0.43	N	0	0.50	N	0	0.50	N
mir-1297	0.04	0.19	N	-6.9E-03	0.43	N	0	0.50	N	0	0.50	N
mir-610	0.03	0.23	N	7.5E-03	0.43	N	0	0.50	N	0	0.50	N
mir-892a	0.06	0.08	N	-6.7E-03	0.43	N	0	0.50	N	0	0.50	N
mir-1182	-0.02	0.33	N	-6.6E-03	0.43	N	0	0.50	N	0	0.50	N
mir-630	0.02	0.34	N	-5.9E-03	0.44	N	0	0.50	N	0	0.50	N
mir-635	-0.06	0.08	N	-5.6E-03	0.44	N	0	0.50	N	0	0.50	N
mir-576	0.04	0.14	N	-5.3E-03	0.45	N	0	0.50	N	0	0.50	N
mir-523	-0.02	0.32	N	-5.2E-03	0.45	N	0	0.50	N	0	0.50	N
mir-525	0.01	0.39	N	5.3E-03	0.45	N	0	0.50	N	0	0.50	N
mir-135b	-0.10	6.2E-03	Y	-4.6E-03	0.45	N	0	0.50	N	0	0.50	N
mir-1281	1.0E-03	0.49	N	5.0E-03	0.45	N	0	0.50	N	0	0.50	N
mir-1291	0.04	0.16	N	-4.2E-03	0.46	N	0	0.50	N	0	0.50	N
mir-558	-0.02	0.34	N	-3.9E-03	0.46	N	0	0.50	N	0	0.50	N
mir-553	-0.02	0.34	N	-3.9E-03	0.46	N	0	0.50	N	0	0.50	N
mir-515-2	0.03	0.27	N	3.7E-03	0.47	N	0	0.50	N	0	0.50	N
mir-1275	-0.15	1.8E-04	Y	-3.2E-03	0.47	N	0	0.50	N	0	0.50	N

mir-526a-2	0.05	0.10	N	3.3E-03	0.47	N	0	0.50	N	0	0.50	N
mir-302c	-9.0E-03	0.41	N	3.2E-03	0.47	N	0	0.50	N	0	0.50	N
mir-627	-0.02	0.30	N	-2.8E-03	0.47	N	0	0.50	N	0	0.50	N
mir-643	2.4E-03	0.48	N	3.1E-03	0.47	N	0	0.50	N	0	0.50	N
mir-660	0.02	0.31	N	-2.3E-03	0.48	N	0	0.50	N	0	0.50	N
mir-631	0.02	0.29	N	2.3E-03	0.48	N	0	0.50	N	0	0.50	N
mir-1305	-0.02	0.33	N	2.2E-03	0.48	N	0	0.50	N	0	0.50	N
mir-1201	3.1E-03	0.47	N	-1.6E-03	0.48	N	0	0.50	N	0	0.50	N
mir-606	-0.02	0.30	N	1.9E-03	0.48	N	0	0.50	N	0	0.50	N
mir-548d-1	8.7E-03	0.42	N	1.8E-03	0.48	N	0	0.50	N	0	0.50	N
mir-1179	0.02	0.29	N	1.1E-03	0.49	N	0	0.50	N	0	0.50	N
mir-519a-2	0.03	0.25	N	8.4E-04	0.49	N	0	0.50	N	0	0.50	N
mir-502	0.02	0.29	N	-4.7E-04	0.49	N	0	0.50	N	0	0.50	N
mir-621	1.0E-03	0.49	N	6.6E-04	0.50	N	0	0.50	N	0	0.50	N
mir-664	-0.27	1.0E-05	Y	-2.2E-04	0.50	N	0	0.50	N	0	0.50	N

Assignment of samples into P, R and K groups in CRCSC cohort

Sample	P group	R group	K group
GSM327282	P+	R-	K-
GSM327283	P+	R-	K-
GSM327284	P-	R-	K-
GSM327285	P-	R-	K-
GSM327286	P-	R+	K-
GSM327287	P+	R-	K+
GSM327288	P+	R+	K-
GSM327289	P+	R+	K-
GSM327290	P+	R-	K-
GSM327291	P-	R+	K-
GSM327292	P+	R-	K-
GSM327293	P+	R+	K-
GSM327294	P+	R-	K-
GSM327295	P+	R-	K-
GSM327296	P+	R-	K-
GSM327297	P-	R+	K+
GSM327298	P-	R+	K-
GSM327299	P-	R-	K-
GSM327300	P-	R+	K-
GSM327301	P+	R-	K+
GSM327302	P-	R+	K-
GSM327303	P+	R+	K-
GSM327304	P+	R-	K+
GSM327305	P+	R-	K-
GSM327306	P+	R-	K-
GSM327307	P+	R-	K-
GSM327308	P+	R-	K-
GSM327309	P+	R-	K-
GSM327310	P+	R-	K+
GSM327311	P+	R-	K-
GSM327312	P-	R-	K-
GSM327313	P+	R+	K+
GSM327314	P+	R-	K-
GSM327315	P-	R+	K-
GSM327316	P+	R-	K-
GSM327317	P+	R+	K+
GSM327318	P+	R-	K-
GSM327319	P+	R-	K-
GSM327320	P+	R+	K-
GSM327321	P+	R+	K-
GSM327322	P+	R+	K-
GSM327323	P+	R-	K-
GSM327324	P+	R-	K-
GSM327325	P+	R+	K-
GSM327326	P+	R-	K-
GSM327327	P+	R+	K-
GSM327328	P+	R+	K-
GSM327329	P-	R-	K-
GSM327330	P+	R+	K-
GSM327331	P+	R+	K+
GSM327332	P+	R+	K-
GSM327333	P-	R+	K-
GSM327334	P+	R-	K-
GSM327335	P-	R-	K-
GSM327336	P-	R-	K-
GSM327337	P+	R-	K-
GSM327338	P+	R-	K-
GSM327339	P-	R+	K-
GSM327340	P-	R-	K-
GSM327341	P-	R-	K-
GSM327342	P-	R-	K-

GSM327343	P-	R-	K+
GSM327344	P-	R+	K+
GSM327345	P-	R+	K-
GSM327346	P-	R-	K-
GSM327347	P-	R+	K-
GSM327348	P-	R+	K+
GSM327349	P-	R-	K-
GSM327350	P-	R-	K-
GSM327351	P-	R+	K-
GSM327352	P-	R-	K-
GSM327353	P+	R-	K-
GSM327354	P-	R-	K-
GSM327355	P-	R-	K-
GSM335510	P+	R-	K-
GSM335511	P-	R-	K-
GSM335512	P+	R+	K-
GSM335513	P-	R+	K-
GSM335514	P+	R+	K-
GSM335515	P+	R+	K-
GSM335516	P+	R+	K-
GSM335517	P+	R-	K-
GSM335518	P+	R+	K-
GSM335519	P+	R+	K-
GSM335520	P-	R+	K-
GSM335521	P+	R+	K-
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GSM335551	P+	R+	K+
GSM335552	P-	R+	K+
GSM335553	P-	R-	K+
GSM335554	P+	R-	K-
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GSM335556	P+	R-	K-
GSM335557	P+	R-	K-
GSM335558	P+	R-	K-
GSM335559	P-	R-	K-
GSM335560	P+	R-	K-
GSM335561	P-	R-	K-

GSM335562	P+	R-	K-
GSM335563	P-	R-	K-
GSM335564	P-	R+	K-
GSM335565	P+	R+	K+
GSM335566	P+	R-	K-
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GSM335573	P+	R-	K+
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GSM335624	P-	R-	K-
GSM335625	P-	R-	K+
GSM335626	P-	R-	K-

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GSM358513	P-	R+	K+

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GSM358626	P+	R-	K-
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GSM358628	P+	R+	K+
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GSM523258	P+	R-	K-
GSM523259	P+	R-	K-

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GSM523263	P+	R-	K-
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GSM523288	P+	R-	K-
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GSM523317	P+	R+	K-
GSM523318	P+	R+	K+
GSM523319	P-	R+	K-
GSM523320	P-	R+	K-
GSM523321	P+	R+	K-
GSM523322	P+	R-	K-
GSM523323	P+	R+	K-
GSM523324	P-	R+	K-

GSM523325	P+	R+	K+
GSM523326	P+	R-	K+
GSM523327	P-	R+	K-
GSM523328	P+	R-	K-
GSM523329	P+	R-	K+
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GSM523331	P+	R+	K-
GSM523332	P-	R+	K+
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GSM523336	P+	R+	K-
GSM523337	P+	R-	K+
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GSM53073	P-	R+	K+
GSM53083	P+	R-	K+
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GSM53111	P-	R-	K-
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GSM53126	P-	R+	K-
GSM53135	P-	R-	K+
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GSM53146	P-	R+	K-
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GSM53156	P-	R-	K-
GSM53169	P+	R-	K-
GSM53178	P-	R+	K-
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GSM76524	P-	R+	K+
GSM76526	P+	R-	K-
GSM76529	P-	R-	K-
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GSM76583	P+	R-	K+
GSM76598	P-	R-	K-
GSM76605	P-	R-	K+
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GSM76617	P+	R+	K-
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GSM588862	P+	R+	K-

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GSM820084	P-	R-	K-
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GSM820087	P-	R-	K-
GSM820088	P-	R+	K-

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GSM820092	P-	R+	K-
GSM820093	P-	R-	K-
GSM820094	P-	R+	K-
GSM820095	P-	R-	K-
GSM820096	P-	R+	K+
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GSM820127	P+	R+	K+
GSM820128	P+	R-	K+
GSM820129	P-	R+	K-
GSM820130	P-	R+	K-
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GSM929498	P+	R-	K-
GSM929499	P-	R+	K+
GSM929500	P+	R-	K+
GSM929501	P-	R+	K-
GSM929502	P+	R-	K+
GSM929503	P-	R+	K-
GSM929504	P-	R+	K-
GSM929505	P-	R+	K-
GSM929506	P+	R-	K-
GSM929507	P-	R+	K-
GSM929508	P-	R+	K-
GSM929509	P-	R+	K-

GSM929510	P+	R-	K-
GSM929511	P+	R+	K+
GSM929512	P-	R-	K-
GSM929513	P-	R+	K-
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GSM929570	P+	R-	K-
GSM929571	P-	R-	K+
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GSM929573	P-	R+	K-
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GSM971976	P+	R-	K-
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GSM972037	P+	R-	K-

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GSM972099	P+	R-	K-
GSM972100	P-	R-	K-
GSM972101	P-	R-	K-
GSM972102	P-	R+	K-

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GSM972104	P-	R+	K-
GSM972105	P-	R-	K-
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GSM972164	P+	R+	K-
GSM972165	P+	R+	K-
GSM972166	P-	R-	K-
GSM972167	P+	R-	K-

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GSM972169	P+	R-	K-
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GSM972228	P-	R-	K-
GSM972229	P+	R+	K-
GSM972230	P+	R-	K+
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GSM972232	P-	R+	K-

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GSM972258	P-	R-	K-
GSM972259	P-	R-	K-
GSM972260	P-	R+	K+
GSM972261	P+	R+	K-
GSM972262	P-	R+	K-
GSM972263	P+	R+	K-
GSM972264	P+	R-	K-
GSM972265	P+	R-	K+
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GSM972278	P+	R-	K-
GSM972279	P+	R+	K+
GSM972280	P+	R+	K+
GSM972281	P+	R+	K-
GSM972282	P+	R-	K-
GSM972283	P+	R+	K+
GSM972284	P-	R-	K-
GSM972285	P-	R+	K+
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GSM972293	P-	R+	K+
GSM972294	P+	R+	K-
GSM972295	P-	R-	K-
GSM972296	P+	R-	K-
GSM972297	P-	R+	K-

GSM972298	P+	R-	K-
GSM972299	P-	R-	K-
GSM972300	P-	R-	K-
GSM972301	P-	R+	K-
GSM972302	P+	R-	K-
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GSM972325	P+	R+	K+
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GSM972327	P-	R+	K-
GSM972328	P+	R-	K-
GSM972329	P-	R+	K-
GSM972330	P-	R+	K+
GSM972331	P+	R-	K-
GSM972332	P+	R+	K+
GSM972333	P+	R-	K-
GSM972334	P+	R+	K+
GSM972335	P+	R-	K-
GSM972336	P+	R-	K-
GSM972337	P-	R+	K-
GSM972338	P-	R-	K-
GSM972339	P+	R-	K-
GSM972340	P-	R-	K-
GSM972341	P+	R-	K-
GSM972342	P-	R+	K-
GSM972343	P+	R-	K-
GSM972344	P+	R-	K-
GSM972345	P-	R+	K-
GSM972346	P+	R-	K-
GSM972347	P+	R-	K-
GSM972348	P+	R-	K-
GSM972349	P-	R+	K-
GSM972350	P+	R-	K-
GSM972351	P-	R-	K-
GSM972352	P-	R+	K-
GSM972353	P+	R+	K-
GSM972354	P+	R-	K-
GSM972355	P-	R+	K+
GSM972356	P+	R-	K-
GSM972357	P-	R+	K-
GSM972358	P+	R-	K-
GSM972359	P-	R+	K-
GSM972360	P+	R+	K-
GSM972361	P+	R+	K-
GSM972362	P+	R-	K-

GSM972363	P+	R-	K+
GSM972364	P+	R-	K-
GSM972365	P-	R+	K-
GSM972366	P-	R+	K-
GSM972367	P-	R+	K-
GSM972368	P+	R-	K-
GSM972369	P-	R+	K+
GSM972370	P-	R-	K-
GSM972371	P+	R-	K-
GSM972372	P+	R+	K-
GSM972373	P-	R-	K-
GSM972374	P-	R-	K-
GSM972375	P-	R+	K-
GSM972376	P+	R+	K-
GSM972377	P-	R+	K+
GSM972378	P-	R+	K+
GSM972379	P-	R-	K-
GSM972380	P+	R+	K+
GSM972381	P-	R-	K-
GSM972382	P+	R-	K-
GSM972383	P-	R-	K-
GSM972384	P+	R-	K-
GSM972385	P-	R+	K-
GSM972386	P+	R-	K-
GSM972387	P+	R-	K+
GSM972388	P+	R-	K+
GSM972389	P+	R-	K-
GSM972390	P-	R-	K-
GSM972391	P-	R+	K+
GSM972392	P+	R-	K-
GSM972393	P+	R+	K-
GSM972394	P-	R+	K-
GSM972395	P+	R-	K-
GSM972396	P-	R-	K-
GSM972397	P+	R-	K-
GSM972398	P+	R-	K-
GSM972399	P+	R-	K-
GSM972400	P-	R+	K-
GSM972401	P-	R+	K-
GSM972402	P-	R+	K-
GSM972403	P+	R-	K+
GSM972404	P+	R+	K-
GSM972405	P-	R+	K+
GSM972406	P+	R+	K-
GSM972407	P+	R+	K+
GSM972408	P-	R+	K-
GSM972409	P-	R+	K-
GSM972410	P-	R+	K+
GSM972411	P+	R-	K-
GSM972412	P-	R-	K-
GSM972413	P-	R+	K-
GSM972414	P+	R-	K-
GSM972415	P+	R-	K-
GSM972416	P-	R-	K+
GSM972417	P+	R-	K-
GSM972418	P-	R-	K-
GSM972419	P+	R+	K+
GSM972420	P-	R+	K+
GSM972421	P-	R+	K-
GSM972422	P-	R+	K-
GSM972423	P-	R+	K-
GSM972424	P-	R-	K+
GSM972425	P-	R+	K-
GSM972426	P-	R+	K-
GSM972427	P-	R+	K+

GSM972428	P-	R+	K-
GSM972429	P-	R-	K-
GSM972430	P+	R+	K-
GSM972431	P+	R+	K+
GSM972432	P-	R+	K-
GSM972433	P-	R+	K-
GSM972434	P+	R-	K-
GSM972435	P-	R-	K-
GSM972436	P-	R-	K-
GSM972437	P-	R+	K+
GSM972438	P-	R+	K-
GSM972439	P-	R-	K-
GSM972440	P+	R+	K-
GSM972441	P-	R+	K-
GSM972442	P+	R-	K-
GSM972443	P+	R-	K+
GSM972444	P+	R+	K-
GSM972445	P+	R-	K-
GSM972446	P+	R+	K+
GSM972447	P+	R+	K-
GSM972448	P-	R-	K-
GSM972449	P+	R+	K-
GSM972450	P+	R-	K-
GSM972451	P+	R-	K-
GSM972452	P+	R+	K+
GSM972453	P-	R-	K-
GSM972454	P+	R-	K-
GSM972455	P-	R+	K+
GSM972456	P+	R-	K-
GSM972457	P-	R-	K-
GSM972458	P+	R+	K-
GSM972459	P-	R-	K-
GSM972460	P-	R-	K-
GSM972461	P+	R-	K-
GSM972462	P+	R-	K-
GSM972463	P-	R-	K-
GSM972464	P-	R+	K-
GSM972465	P+	R-	K+
GSM972466	P+	R-	K+
GSM972467	P-	R+	K-
GSM972468	P+	R-	K-
GSM972469	P-	R-	K-
GSM972470	P+	R+	K-
GSM972471	P+	R+	K-
GSM972472	P+	R-	K-
GSM972473	P+	R+	K+
GSM972474	P+	R+	K-
GSM972475	P-	R-	K-
GSM972476	P-	R+	K-
GSM972477	P+	R-	K-
GSM972478	P-	R-	K-
GSM972479	P-	R+	K-
GSM972480	P-	R-	K-
GSM972481	P+	R+	K-
GSM972482	P-	R+	K-
GSM972483	P+	R-	K-
GSM972484	P+	R+	K+
GSM972485	P-	R-	K+
GSM972486	P-	R+	K+
GSM972487	P-	R-	K-
GSM972488	P+	R+	K-
GSM972489	P-	R+	K-
GSM972490	P+	R-	K+
GSM972491	P+	R-	K-
GSM972492	P+	R-	K-

GSM972493	P+	R+	K-
GSM972494	P-	R+	K-
GSM972495	P-	R-	K-
GSM972496	P-	R-	K-
GSM972497	P+	R-	K-
GSM972498	P+	R-	K-
GSM972499	P+	R-	K-
GSM972500	P-	R+	K+
GSM972501	P-	R+	K-
GSM972502	P-	R-	K-
GSM972503	P-	R+	K-
GSM972504	P-	R+	K+
GSM972505	P-	R+	K+
GSM972506	P-	R+	K-
GSM972507	P+	R-	K-
GSM972508	P+	R-	K-
GSM972509	P+	R-	K-
GSM972510	P-	R-	K-
GSM972511	P+	R-	K-
GSM972512	P+	R-	K-
GSM972513	P+	R-	K-
GSM972514	P+	R-	K-
GSM972515	P+	R-	K-
GSM972516	P+	R-	K-
GSM972517	P+	R+	K-
GSM972518	P-	R+	K-
GSM972519	P-	R+	K+
GSM972520	P+	R-	K-
GSM972521	P+	R+	K-
GSM972522	P-	R+	K-
TCGA-F4-6461	P-	R+	K-
TCGA-A6-6653	P+	R+	K+
TCGA-A6-A56B	P+	R-	K-
TCGA-D5-6532	P+	R-	K-
TCGA-AD-6963	P+	R-	K-
TCGA-A6-6138	P-	R+	K-
TCGA-AA-3655	P+	R+	K-
TCGA-DM-A1D7	P+	R-	K-
TCGA-AY-6386	P+	R+	K+
TCGA-DM-A280	P+	R-	K+
TCGA-AD-6965	P+	R-	K-
TCGA-A6-4105	P+	R+	K-
TCGA-AD-A5EK	P+	R-	K-
TCGA-D5-5538	P-	R+	K-
TCGA-CM-4743	P+	R-	K-
TCGA-CM-6166	P+	R-	K-
TCGA-D5-6922	P-	R+	K-
TCGA-CM-5862	P+	R-	K-
TCGA-DM-A1D9	P+	R-	K-
TCGA-AZ-6605	P-	R+	K-
TCGA-CM-6161	P+	R+	K-
TCGA-DM-A0XF	P+	R-	K-
TCGA-D5-6924	P-	R+	K-
TCGA-G4-6626	P+	R-	K-
TCGA-CM-5860	P+	R+	K-
TCGA-DM-A28G	P-	R-	K-
TCGA-AA-A01Z	P+	R-	K-
TCGA-AZ-5407	P+	R-	K-
TCGA-AA-3495	P-	R-	K-
TCGA-AD-6548	P+	R+	K+
TCGA-D5-6529	P-	R+	K-
TCGA-CM-4747	P-	R-	K-
TCGA-AA-3697	P+	R-	K+
TCGA-G4-6303	P-	R+	K-
TCGA-DM-A0X9	P+	R-	K-

TCGA-F4-6857	P-	R+	K-
TCGA-DM-A282	P-	R-	K-
TCGA-CM-6680	P-	R+	K-
TCGA-CK-4947	P+	R+	K-
TCGA-CA-5796	P-	R-	K-
TCGA-D5-6540	P+	R+	K-
TCGA-NH-A50V	P-	R+	K-
TCGA-AA-3506	P-	R+	K-
TCGA-A6-2684	P-	R+	K-
TCGA-CM-6165	P-	R+	K-
TCGA-F4-6808	P+	R-	K-
TCGA-CM-6172	P+	R-	K-
TCGA-D5-6536	P-	R+	K-
TCGA-AA-3713	P+	R+	K-
TCGA-A6-A566	P-	R+	K-
TCGA-CM-6164	P-	R-	K-
TCGA-D5-6530	P-	R-	K-
TCGA-AA-3496	P-	R+	K-
TCGA-CK-4948	P+	R+	K-
TCGA-AY-5543	P+	R-	K+
TCGA-A6-6781	P-	R+	K-
TCGA-AD-A5EJ	P+	R-	K-
TCGA-DM-A28H	P+	R-	K-
TCGA-DM-A285	P+	R-	K-
TCGA-CA-5797	P+	R+	K-
TCGA-A6-5661	P+	R-	K+
TCGA-AA-3663	P+	R-	K-
TCGA-AZ-4313	P+	R-	K-
TCGA-DM-A0XD	P+	R-	K-
TCGA-G4-6586	P+	R-	K+
TCGA-AZ-4616	P+	R-	K-
TCGA-CM-5349	P-	R+	K-
TCGA-F4-6569	P-	R+	K-
TCGA-QG-A5YW	P-	R-	K-
TCGA-AZ-4323	P-	R+	K-
TCGA-AU-3779	P-	R+	K-
TCGA-CM-6168	P-	R+	K-
TCGA-G4-6321	P-	R+	K+
TCGA-DM-A28M	P+	R-	K-
TCGA-A6-5664	P-	R+	K-
TCGA-G4-6628	P+	R+	K-
TCGA-A6-5667	P+	R-	K-
TCGA-AZ-6599	P-	R-	K-
TCGA-QG-A5YV	P+	R-	K-
TCGA-A6-5656	P-	R-	K-
TCGA-AA-3511	P-	R+	K-
TCGA-AZ-6607	P-	R+	K-
TCGA-A6-6648	P+	R-	K-
TCGA-CM-5344	P-	R+	K-
TCGA-AZ-6606	P+	R-	K+
TCGA-AA-3660	P+	R-	K-
TCGA-CM-6163	P-	R+	K-
TCGA-AD-6901	P-	R+	K-
TCGA-AZ-6600	P-	R+	K+
TCGA-A6-5660	P-	R-	K-
TCGA-D5-5539	P-	R+	K-
TCGA-F4-6703	P-	R+	K-
TCGA-AZ-4684	P-	R+	K-
TCGA-D5-6927	P+	R+	K-
TCGA-QG-A5Z2	P-	R-	K+
TCGA-CM-5861	P+	R-	K-
TCGA-AD-5900	P+	R+	K+
TCGA-CK-5914	P+	R-	K-
TCGA-D5-6533	P+	R-	K-
TCGA-DM-A1D0	P+	R-	K-

TCGA-A6-A567	P-	R-	K-
TCGA-F4-6805	P-	R+	K-
TCGA-QG-A5YX	P+	R-	K+
TCGA-G4-6322	P+	R-	K-
TCGA-F4-6809	P-	R+	K-
TCGA-AZ-6608	P+	R-	K-
TCGA-CA-5255	P-	R-	K-
TCGA-CK-6746	P+	R-	K-
TCGA-CM-6170	P-	R+	K-
TCGA-AD-6890	P+	R-	K+
TCGA-CA-5254	P-	R-	K-
TCGA-AZ-5403	P+	R-	K-
TCGA-AY-6197	P+	R-	K-
TCGA-G4-6314	P-	R+	K-
TCGA-AD-6888	P+	R-	K+
TCGA-F4-6806	P-	R+	K-
TCGA-G4-6625	P-	R+	K-
TCGA-A6-6137	P-	R+	K-
TCGA-D5-5537	P-	R-	K-
TCGA-A6-6782	P-	R+	K-
TCGA-AY-6196	P-	R+	K-
TCGA-D5-5540	P+	R-	K-
TCGA-CM-6679	P-	R+	K-
TCGA-CM-6167	P-	R+	K-
TCGA-G4-6320	P+	R-	K-
TCGA-AZ-4315	P+	R-	K-
TCGA-CM-5864	P+	R-	K-
TCGA-CK-6751	P+	R+	K-
TCGA-A6-6140	P+	R-	K-
TCGA-D5-6930	P+	R+	K+
TCGA-AA-3492	P+	R-	K+
TCGA-DM-A1DB	P+	R-	K-
TCGA-CM-6171	P+	R+	K-
TCGA-A6-6654	P-	R+	K-
TCGA-CM-6675	P+	R-	K-
TCGA-G4-6323	P-	R-	K-
TCGA-CK-5913	P+	R+	K-
TCGA-D5-6541	P-	R+	K-
TCGA-AY-A54L	P+	R-	K+
TCGA-CK-4951	P+	R+	K-
TCGA-A6-A565	P-	R+	K-
TCGA-CK-5916	P+	R+	K-
TCGA-D5-6537	P+	R-	K-
TCGA-F4-6854	P+	R+	K-
TCGA-CM-5348	P-	R+	K-
TCGA-G4-6307	P+	R-	K-
TCGA-CM-5863	P-	R+	K-
TCGA-F4-6570	P-	R+	K+
TCGA-AA-3489	P-	R+	K-
TCGA-D5-6535	P-	R+	K-
TCGA-CM-6162	P-	R+	K-
TCGA-AZ-6598	P+	R-	K-
TCGA-CM-6676	P-	R-	K-
TCGA-D5-6538	P+	R-	K-
TCGA-A6-A5ZU	P-	R+	K-
TCGA-CM-4751	P-	R+	K-
TCGA-CK-6747	P+	R-	K+
TCGA-G4-6294	P-	R-	K-
TCGA-CM-6677	P+	R-	K-
TCGA-G4-6299	P+	R+	K-
TCGA-D5-6926	P-	R+	K-
TCGA-AD-6889	P+	R-	K-
TCGA-F4-6855	P-	R+	K-
TCGA-DM-A1D6	P+	R-	K-
TCGA-DM-A1HB	P+	R-	K+

TCGA-A6-2675	P-	R+	K-
TCGA-CK-5915	P+	R-	K-
TCGA-AM-5820	P+	R-	K-
TCGA-AA-3662	P-	R+	K-
TCGA-G4-6588	P+	R+	K-
TCGA-A6-6652	P-	R-	K-
TCGA-D5-6539	P-	R+	K-
TCGA-D5-6920	P-	R+	K-
TCGA-A6-6141	P-	R+	K-
TCGA-F4-6807	P-	R+	K-
TCGA-G4-6627	P-	R+	K-
TCGA-CA-6715	P+	R-	K-
TCGA-CK-5912	P+	R-	K-
TCGA-F4-6856	P+	R-	K+
TCGA-AA-A02K	P+	R-	K-
TCGA-CM-6678	P-	R-	K-
TCGA-A6-5659	P+	R-	K-
TCGA-AD-6899	P-	R+	K-
TCGA-AA-A01P	P+	R+	K-
TCGA-CA-6719	P-	R+	K-
TCGA-AA-3509	P-	R-	K-
TCGA-AD-6964	P-	R+	K-
TCGA-CM-6169	P-	R+	K-
TCGA-A6-5665	P+	R-	K+
TCGA-CA-6717	P-	R+	K-
TCGA-A6-6651	P-	R+	K-
TCGA-G4-6297	P-	R+	K-
TCGA-DM-A1DA	P+	R-	K+
TCGA-CA-6718	P+	R+	K-
TCGA-A6-6780	P+	R-	K-
TCGA-QG-A5Z1	P-	R-	K-
TCGA-AZ-4614	P+	R-	K-
TCGA-CK-4952	P+	R-	K-
TCGA-G4-6315	P+	R-	K+
TCGA-CK-4950	P-	R+	K-
TCGA-AZ-4615	P+	R+	K-
TCGA-G4-6306	P-	R-	K+
TCGA-AM-5821	P+	R+	K-
TCGA-A6-6649	P-	R+	K-
TCGA-AD-6895	P+	R+	K-
TCGA-D5-6531	P+	R+	K-
TCGA-G4-6298	P-	R-	K-
TCGA-DM-A1D4	P+	R-	K-
TCGA-D5-5541	P+	R-	K-
TCGA-D5-6928	P-	R+	K-
TCGA-AZ-6603	P-	R+	K-
TCGA-AA-3502	P-	R-	K-
TCGA-A6-6142	P-	R+	K-
TCGA-G4-6295	P+	R-	K-
TCGA-A6-6650	P+	R-	K-
TCGA-DM-A288	P+	R-	K-
TCGA-F4-6704	P-	R+	K-
TCGA-AA-A01X	P-	R-	K-
TCGA-G4-6309	P+	R-	K-
TCGA-CK-6748	P-	R+	K-
TCGA-F4-6463	P-	R+	K-
TCGA-G4-6302	P-	R+	K-
TCGA-CA-6716	P-	R-	K-
TCGA-G4-6293	P-	R+	K+
TCGA-G4-6311	P+	R+	K-
TCGA-DM-A1D8	P+	R-	K-
TCGA-F4-6459	P-	R+	K-
TCGA-D5-6932	P-	R+	K-
TCGA-CA-5256	P+	R-	K-
TCGA-AA-3712	P+	R+	K-

TCGA-AU-6004	P-	R+	K+
TCGA-D5-6898	P-	R+	K-
TCGA-NH-A50T	P+	R-	K-
TCGA-A6-2685	P-	R+	K-
TCGA-D5-6931	P+	R+	K-
TCGA-CM-6674	P+	R+	K-
TCGA-F4-6460	P-	R+	K-
TCGA-A6-2682	P-	R+	K-
TCGA-G4-6304	P+	R-	K-
TCGA-CM-5868	P+	R-	K-
TCGA-D5-6929	P-	R+	K-
TCGA-AZ-6601	P+	R+	K-
TCGA-G4-6317	P+	R-	K-
TCGA-D5-6534	P-	R+	K-
TCGA-A6-5666	P+	R-	K-
TCGA-DM-A1HA	P+	R-	K-
TCGA-A6-5662	P-	R-	K-
TCGA-G4-6310	P-	R-	K-
TCGA-CI-6621	P+	R+	K-
TCGA-CI-6623	P+	R-	K+
TCGA-DC-5869	P+	R-	K-
TCGA-DC-6160	P+	R-	K-
TCGA-EI-6512	P+	R-	K+
TCGA-G5-6572	P-	R+	K-
TCGA-AG-3742	P+	R-	K-
TCGA-AH-6549	P+	R+	K-
TCGA-AF-2690	P-	R+	K-
TCGA-AF-5654	P+	R-	K-
TCGA-EF-5830	P-	R-	K-
TCGA-F5-6814	P+	R-	K-
TCGA-F5-6465	P-	R+	K-
TCGA-EI-6506	P-	R+	K-
TCGA-G5-6235	P-	R-	K-
TCGA-AG-3591	P-	R-	K-
TCGA-DC-6154	P-	R-	K-
TCGA-F5-6861	P+	R-	K-
TCGA-EI-6513	P+	R-	K-
TCGA-DY-A1DE	P+	R-	K-
TCGA-EI-6511	P+	R+	K-
TCGA-DC-6155	P-	R-	K-
TCGA-AH-6903	P-	R-	K-
TCGA-F5-6702	P-	R+	K-
TCGA-EI-7004	P-	R+	K-
TCGA-CI-6619	P-	R+	K-
TCGA-AG-4022	P-	R+	K-
TCGA-AH-6544	P+	R-	K-
TCGA-AF-2693	P+	R+	K-
TCGA-AG-4021	P+	R+	K-
TCGA-EI-6510	P+	R-	K-
TCGA-EF-5831	P+	R-	K-
TCGA-EI-7002	P-	R+	K-
TCGA-DT-5265	P-	R+	K-
TCGA-CI-6622	P-	R-	K-
TCGA-DY-A0XA	P+	R-	K-
TCGA-AF-6672	P-	R-	K-
TCGA-DC-5337	P+	R-	K-
TCGA-CL-4957	P+	R-	K-
TCGA-F5-6811	P-	R+	K-
TCGA-EI-6514	P-	R+	K+
TCGA-DC-6682	P+	R-	K-
TCGA-EI-6885	P-	R+	K-
TCGA-F5-6813	P+	R+	K-
TCGA-BM-6198	P-	R+	K-
TCGA-AF-6136	P+	R-	K+
TCGA-DY-A1H8	P+	R-	K-

TCGA-CL-5917	P+	R-	K-
TCGA-CI-6624	P-	R+	K+
TCGA-AG-3725	P-	R-	K-
TCGA-CI-6620	P+	R+	K-
TCGA-EI-6508	P+	R-	K-
TCGA-DC-6158	P-	R+	K-
TCGA-F5-6464	P-	R+	K-
TCGA-AH-6897	P+	R-	K-
TCGA-EI-6882	P+	R+	K-
TCGA-EI-6884	P-	R+	K-
TCGA-AG-3592	P+	R-	K-
TCGA-CL-5918	P+	R-	K-
TCGA-EI-6883	P-	R-	K-
TCGA-AF-4110	P-	R+	K-
TCGA-F5-6864	P-	R+	K-
TCGA-F5-6812	P-	R+	K-
TCGA-DY-A1DD	P-	R-	K-
TCGA-AH-6644	P-	R+	K-
TCGA-DC-4749	P+	R-	K+
TCGA-DC-6683	P-	R-	K+
TCGA-DY-A1DC	P+	R-	K-
TCGA-EI-6507	P-	R+	K-
TCGA-AF-3911	P+	R-	K-
TCGA-DC-6157	P+	R-	K-
TCGA-EI-6509	P-	R-	K-
TCGA-AH-6547	P-	R+	K-
TCGA-AF-2687	P-	R+	K-
TCGA-G5-6233	P+	R-	K-
TCGA-F5-6810	P+	R+	K-
TCGA-EI-6917	P+	R+	K-
TCGA-AH-6643	P+	R+	K-
TCGA-DC-6156	P-	R+	K-
TCGA-AG-3732	P-	R+	K+
TCGA-AF-6655	P+	R+	K-
TCGA-F5-6571	P-	R+	K-
TCGA-DY-A1DF	P-	R-	K-
TCGA-F5-6863	P-	R-	K-
TCGA-AA-A01I	P+	R-	K-
TCGA-AA-3684	P-	R+	K-
TCGA-AA-A004	P-	R+	K-
TCGA-AA-3680	P-	R-	K-
TCGA-A6-2670	P-	R+	K-
TCGA-AA-3870	P-	R+	K-
TCGA-AA-3560	P-	R-	K-
TCGA-AA-3811	P+	R+	K-
TCGA-AA-A00O	P-	R+	K-
TCGA-AA-3862	P+	R-	K-
TCGA-AA-3519	P+	R-	K-
TCGA-AA-3977	P+	R+	K-
TCGA-AA-3517	P-	R+	K-
TCGA-AA-A024	P-	R-	K-
TCGA-AA-3525	P+	R-	K-
TCGA-AA-A01D	P-	R+	K+
TCGA-AA-A01Q	P+	R-	K-
TCGA-AA-3833	P-	R+	K+
TCGA-AA-3548	P-	R-	K-
TCGA-AA-3666	P+	R-	K-
TCGA-AA-3976	P+	R-	K-
TCGA-AA-3819	P-	R-	K-
TCGA-AA-3556	P+	R-	K+
TCGA-CM-4746	P+	R-	K-
TCGA-AA-3543	P-	R+	K-
TCGA-AA-3939	P+	R-	K-
TCGA-A6-3808	P-	R+	K-
TCGA-A6-2681	P-	R+	K-

TCGA-AA-A02E	P-	R-	K-
TCGA-AA-3860	P+	R+	K-
TCGA-AA-3858	P+	R-	K-
TCGA-AA-3555	P+	R+	K-
TCGA-A6-2677	P+	R-	K-
TCGA-AA-A00R	P+	R+	K-
TCGA-AA-3856	P-	R-	K-
TCGA-AA-3531	P+	R-	K-
TCGA-AA-3973	P-	R-	K-
TCGA-CM-4750	P+	R-	K+
TCGA-A6-2680	P-	R+	K+
TCGA-AA-3875	P+	R-	K-
TCGA-AA-3850	P-	R+	K+
TCGA-AA-A00U	P+	R-	K-
TCGA-AA-3844	P+	R-	K-
TCGA-AA-3867	P-	R+	K-
TCGA-AA-3672	P-	R+	K-
TCGA-AA-3877	P+	R+	K-
TCGA-AA-3664	P+	R-	K-
TCGA-AA-3544	P-	R+	K-
TCGA-AA-A022	P-	R+	K-
TCGA-AA-A03J	P-	R+	K-
TCGA-AA-A01R	P+	R-	K-
TCGA-AA-3941	P+	R-	K+
TCGA-AA-A00F	P-	R+	K-
TCGA-AA-A03F	P-	R-	K+
TCGA-AA-3679	P+	R-	K+
TCGA-AA-3667	P-	R+	K+
TCGA-AA-3861	P-	R-	K-
TCGA-AA-3982	P-	R+	K+
TCGA-AA-A01V	P-	R-	K-
TCGA-A6-2672	P+	R+	K-
TCGA-AA-3869	P+	R+	K-
TCGA-AA-A00J	P+	R+	K-
TCGA-AA-3549	P-	R+	K+
TCGA-CM-4752	P-	R-	K-
TCGA-AA-3538	P+	R+	K-
TCGA-AA-3979	P+	R-	K-
TCGA-AA-3521	P-	R+	K-
TCGA-AA-3950	P+	R+	K-
TCGA-AA-3984	P+	R+	K-
TCGA-A6-3810	P-	R+	K-
TCGA-AA-A00N	P-	R+	K-
TCGA-AA-A00A	P+	R+	K-
TCGA-AA-3692	P-	R-	K-
TCGA-AA-3947	P+	R-	K-
TCGA-A6-2683	P-	R-	K-
TCGA-AA-A010	P+	R-	K-
TCGA-AA-3956	P-	R+	K-
TCGA-AA-3851	P-	R+	K-
TCGA-AZ-4681	P+	R-	K-
TCGA-AA-3678	P-	R-	K-
TCGA-AA-3527	P-	R+	K+
TCGA-AA-3975	P-	R+	K-
TCGA-AA-3494	P-	R-	K-
TCGA-AA-3715	P-	R+	K-
TCGA-AA-3534	P+	R+	K-
TCGA-AA-3846	P+	R-	K-
TCGA-AA-3518	P+	R-	K-
TCGA-A6-3809	P+	R+	K-
TCGA-AA-3542	P+	R-	K+
TCGA-AA-3529	P-	R-	K-
TCGA-AY-4071	P-	R+	K+
TCGA-AA-3831	P+	R-	K-
TCGA-AA-A029	P+	R-	K+

TCGA-A6-2674	P-	R+	K-
TCGA-AY-4070	P-	R+	K-
TCGA-A6-2671	P+	R+	K-
TCGA-AA-A01G	P+	R-	K-
TCGA-AA-A017	P-	R-	K-
TCGA-AA-A01F	P+	R-	K-
TCGA-AA-A00L	P+	R-	K-
TCGA-AA-3814	P-	R+	K-
TCGA-AA-3866	P+	R+	K-
TCGA-AA-3532	P+	R+	K-
TCGA-AA-A01C	P+	R-	K-
TCGA-AA-3842	P+	R-	K-
TCGA-AA-A00D	P+	R+	K-
TCGA-AA-3854	P+	R-	K-
TCGA-AA-3695	P+	R-	K-
TCGA-AA-3520	P+	R+	K-
TCGA-AA-A00K	P+	R-	K-
TCGA-AA-3972	P+	R-	K-
TCGA-AA-3864	P+	R-	K-
TCGA-AA-3968	P+	R+	K-
TCGA-AA-3516	P+	R+	K-
TCGA-A6-2678	P+	R-	K-
TCGA-CM-4748	P-	R+	K-
TCGA-AA-3952	P-	R-	K-
TCGA-AA-3855	P-	R+	K-
TCGA-AA-3971	P-	R+	K-
TCGA-AA-A01K	P-	R+	K-
TCGA-AA-3986	P-	R+	K-
TCGA-AA-A02J	P+	R-	K-
TCGA-AA-A02H	P-	R-	K-
TCGA-AA-3710	P+	R+	K-
TCGA-AA-A01S	P+	R-	K-
TCGA-AA-3524	P+	R-	K-
TCGA-AZ-4308	P-	R+	K-
TCGA-AA-A00E	P+	R+	K-
TCGA-AA-3949	P+	R+	K-
TCGA-A6-4107	P-	R+	K+
TCGA-CM-5341	P+	R-	K-
TCGA-AA-3514	P-	R+	K+
TCGA-AA-3552	P-	R+	K-
TCGA-AA-3812	P-	R+	K-
TCGA-AA-3554	P-	R+	K-
TCGA-AA-3553	P+	R+	K-
TCGA-AA-A02O	P-	R-	K-
TCGA-AA-3845	P+	R+	K-
TCGA-AA-A00W	P+	R-	K-
TCGA-AA-3696	P-	R-	K-
TCGA-AA-A00Z	P+	R-	K-
TCGA-AA-3561	P+	R-	K-
TCGA-A6-3807	P-	R+	K-
TCGA-AA-3966	P-	R+	K-
TCGA-AA-3818	P+	R-	K-
TCGA-AA-3688	P+	R-	K-
TCGA-A6-2676	P+	R+	K-
TCGA-AA-3821	P+	R-	K-
TCGA-AA-3837	P-	R+	K-
TCGA-AA-3562	P-	R-	K-
TCGA-AA-3980	P+	R-	K-
TCGA-AA-3930	P+	R-	K-
TCGA-AA-3994	P-	R+	K-
TCGA-AA-3530	P-	R-	K-
TCGA-AA-3970	P-	R-	K-
TCGA-AA-3872	P-	R+	K+
TCGA-AA-3693	P+	R-	K-
TCGA-AA-3852	P-	R+	K-

TCGA-AA-A01T	P+	R-	K-
TCGA-AA-A00Q	P-	R-	K-
TCGA-AA-A02R	P+	R+	K-
TCGA-AA-3955	P+	R-	K+
TCGA-A6-2679	P-	R+	K-
TCGA-AA-A02W	P+	R-	K-
TCGA-AA-3673	P+	R+	K-
TCGA-AA-3989	P-	R+	K-
TCGA-AA-A02F	P+	R-	K-
TCGA-AA-3522	P-	R-	K-
TCGA-AA-3841	P-	R+	K+
TCGA-AA-3488	P+	R-	K-
TCGA-AA-3815	P+	R+	K-
TCGA-AA-3681	P+	R+	K+
TCGA-AA-3848	P-	R-	K-
TCGA-AF-2691	P-	R+	K-
TCGA-AG-3611	P-	R-	K-
TCGA-AG-3593	P+	R-	K-
TCGA-AG-A015	P+	R-	K-
TCGA-AG-3881	P-	R+	K-
TCGA-AG-3605	P+	R-	K-
TCGA-AG-A00H	P-	R+	K-
TCGA-AF-3400	P-	R+	K-
TCGA-AG-3892	P+	R-	K-
TCGA-AG-A02G	P-	R-	K-
TCGA-AG-3598	P+	R-	K-
TCGA-AG-A01Y	P+	R-	K-
TCGA-AG-3882	P-	R+	K+
TCGA-AG-3726	P-	R+	K+
TCGA-AG-A023	P-	R+	K+
TCGA-AG-A01N	P+	R-	K-
TCGA-AG-A025	P+	R-	K-
TCGA-AG-A01L	P-	R-	K+
TCGA-AG-3575	P+	R+	K-
TCGA-AG-A020	P+	R-	K+
TCGA-AG-A011	P-	R-	K-
TCGA-AG-3999	P-	R-	K-
TCGA-AG-3901	P-	R+	K-
TCGA-AG-A01J	P-	R-	K-
TCGA-AG-A014	P+	R-	K-
TCGA-AG-3580	P+	R-	K-
TCGA-AG-3896	P+	R+	K-
TCGA-AG-A032	P-	R-	K-
TCGA-AG-4007	P-	R+	K+
TCGA-AG-3578	P-	R-	K-
TCGA-AG-3583	P+	R-	K-
TCGA-AG-3885	P-	R+	K+
TCGA-AG-3599	P+	R-	K+
TCGA-AG-4001	P-	R+	K-
TCGA-AG-4005	P+	R+	K-
TCGA-AG-A02N	P-	R-	K+
TCGA-AF-3913	P+	R-	K-
TCGA-AG-3727	P-	R+	K+
TCGA-AF-2692	P+	R+	K-
TCGA-AG-A02X	P+	R-	K+
TCGA-AG-4015	P+	R-	K+
TCGA-AG-3601	P-	R-	K-
TCGA-AG-3582	P+	R+	K-
TCGA-AG-4008	P-	R+	K-
TCGA-AG-3728	P-	R+	K+
TCGA-AG-3586	P+	R-	K-
TCGA-AG-3600	P+	R-	K+
TCGA-AG-A01W	P+	R-	K-
TCGA-AG-3609	P-	R+	K+
TCGA-AG-3883	P-	R+	K+

TCGA-AG-A002	P+	R-	K-
TCGA-AG-A008	P+	R-	K-
TCGA-AG-3574	P-	R-	K-
TCGA-AG-A00Y	P+	R-	K+
TCGA-AG-3587	P+	R-	K-
TCGA-AG-3894	P+	R-	K-
TCGA-AG-3612	P+	R+	K-
TCGA-AG-3909	P-	R+	K-
TCGA-AG-3890	P-	R+	K-
TCGA-AG-3602	P+	R-	K+
TCGA-AG-3878	P-	R+	K-
TCGA-AG-A036	P+	R-	K-
TCGA-AG-3584	P-	R+	K-
TCGA-AG-3608	P-	R-	K+
TCGA-AG-3893	P-	R+	K-
TCGA-AG-3898	P+	R+	K-
TCGA-AG-A026	P-	R-	K-
TCGA-AG-A016	P+	R-	K-
TCGA-AG-3887	P+	R-	K-
TCGA-AG-3581	P-	R+	K-
TCGA-AG-A00C	P-	R-	K-
TCGA-AG-3594	P+	R+	K-

Assignment of samples into P and mir22 groups in TCGACRC

Sample	P group	mir22 group
TCGA-A6-2671	P+	mir22+
TCGA-A6-2672	P+	mir22+
TCGA-A6-2674	P-	mir22+
TCGA-A6-2676	P+	mir22+
TCGA-A6-2677	P+	mir22-
TCGA-A6-2678	P+	mir22-
TCGA-A6-2679	P-	mir22+
TCGA-A6-2680	P-	mir22-
TCGA-A6-2682	P-	mir22+
TCGA-A6-2683	P-	mir22+
TCGA-A6-2684	P-	mir22+
TCGA-A6-2685	P-	mir22+
TCGA-A6-3807	P-	mir22+
TCGA-A6-3808	P-	mir22-
TCGA-A6-3809	P+	mir22-
TCGA-A6-3810	P-	mir22+
TCGA-AA-3514	P-	mir22+
TCGA-AA-3516	P+	mir22-
TCGA-AA-3517	P-	mir22+
TCGA-AA-3518	P+	mir22-
TCGA-AA-3519	P+	mir22+
TCGA-AA-3520	P+	mir22-
TCGA-AA-3521	P-	mir22-
TCGA-AA-3522	P-	mir22+
TCGA-AA-3524	P+	mir22-
TCGA-AA-3525	P+	mir22+
TCGA-AA-3527	P-	mir22-
TCGA-AA-3529	P-	mir22+
TCGA-AA-3531	P+	mir22-
TCGA-AA-3532	P+	mir22+
TCGA-AA-3534	P+	mir22-
TCGA-AA-3538	P+	mir22+
TCGA-AA-3542	P+	mir22-
TCGA-AA-3543	P-	mir22+
TCGA-AA-3548	P-	mir22-
TCGA-AA-3552	P-	mir22-
TCGA-AA-3553	P+	mir22+
TCGA-AA-3556	P+	mir22+
TCGA-AA-3560	P-	mir22-
TCGA-AA-3561	P+	mir22-
TCGA-AA-3562	P-	mir22+
TCGA-AA-3666	P+	mir22-
TCGA-AA-3667	P-	mir22-
TCGA-AA-3672	P-	mir22-
TCGA-AA-3673	P+	mir22-
TCGA-AA-3678	P-	mir22-
TCGA-AA-3679	P+	mir22-
TCGA-AA-3680	P-	mir22-
TCGA-AA-3681	P+	mir22-
TCGA-AA-3684	P-	mir22-
TCGA-AA-3688	P+	mir22-
TCGA-AA-3692	P-	mir22-
TCGA-AA-3693	P+	mir22+
TCGA-AA-3695	P+	mir22-
TCGA-AA-3696	P-	mir22-
TCGA-AA-3710	P+	mir22+
TCGA-AA-3715	P-	mir22+
TCGA-AA-3811	P+	mir22+
TCGA-AA-3812	P-	mir22+
TCGA-AA-3814	P-	mir22+
TCGA-AA-3818	P+	mir22+

TCGA-AA-3819	P-	mir22-
TCGA-AA-3821	P+	mir22+
TCGA-AA-3831	P+	mir22-
TCGA-AA-3833	P-	mir22-
TCGA-AA-3837	P-	mir22+
TCGA-AA-3842	P+	mir22-
TCGA-AA-3844	P+	mir22-
TCGA-AA-3845	P+	mir22-
TCGA-AA-3846	P+	mir22-
TCGA-AA-3848	P-	mir22-
TCGA-AA-3850	P-	mir22+
TCGA-AA-3851	P-	mir22+
TCGA-AA-3852	P-	mir22+
TCGA-AA-3854	P+	mir22-
TCGA-AA-3855	P-	mir22+
TCGA-AA-3856	P-	mir22-
TCGA-AA-3858	P+	mir22-
TCGA-AA-3861	P-	mir22-
TCGA-AA-3862	P+	mir22+
TCGA-AA-3864	P+	mir22-
TCGA-AA-3866	P+	mir22-
TCGA-AA-3867	P-	mir22+
TCGA-AA-3869	P+	mir22-
TCGA-AA-3870	P-	mir22-
TCGA-AA-3872	P-	mir22-
TCGA-AA-3875	P+	mir22+
TCGA-AA-3877	P+	mir22-
TCGA-AA-3930	P+	mir22+
TCGA-AA-3939	P+	mir22-
TCGA-AA-3947	P+	mir22+
TCGA-AA-3949	P+	mir22+
TCGA-AA-3950	P+	mir22+
TCGA-AA-3952	P-	mir22+
TCGA-AA-3956	P-	mir22-
TCGA-AA-3966	P-	mir22+
TCGA-AA-3968	P+	mir22+
TCGA-AA-3970	P-	mir22-
TCGA-AA-3971	P-	mir22+
TCGA-AA-3972	P+	mir22+
TCGA-AA-3973	P-	mir22+
TCGA-AA-3975	P-	mir22+
TCGA-AA-3976	P+	mir22-
TCGA-AA-3979	P+	mir22+
TCGA-AA-3980	P+	mir22+
TCGA-AA-3982	P-	mir22-
TCGA-AA-3984	P+	mir22+
TCGA-AA-3986	P-	mir22+
TCGA-AA-3989	P-	mir22+
TCGA-AA-3994	P-	mir22+
TCGA-AA-A00D	P+	mir22-
TCGA-AA-A00J	P+	mir22+
TCGA-AA-A00L	P+	mir22-
TCGA-AA-A00O	P-	mir22+
TCGA-AA-A00U	P+	mir22-
TCGA-AA-A00W	P+	mir22+
TCGA-AA-A010	P+	mir22-
TCGA-AA-A01D	P-	mir22+
TCGA-AA-A01F	P+	mir22+
TCGA-AA-A01G	P+	mir22+
TCGA-AA-A024	P-	mir22+
TCGA-AA-A029	P+	mir22+
TCGA-AA-A02E	P-	mir22+
TCGA-AA-A02F	P+	mir22+
TCGA-AA-A02H	P-	mir22+
TCGA-AA-A02J	P+	mir22-

TCGA-AA-A02R	P+	mir22+
TCGA-AY-4070	P-	mir22+
TCGA-AY-4071	P-	mir22+

List of genes in cell proliferation gene signature

TP73	TP53	CCND1	CDK2	DGKZ	FBXO31	RFWD3	RPS27L	TP63	PTPN6	BID	E2F1
PLK5	INO80	FGF10	EGFR	PIM1	AKT1	ADAM17	WNT9A	HUS1	NBN	HRAS	TGFB1
RB1	CDKN2B	RPL24	DLG1	USP17L2	PTEN	PRMT2	PTEN	FHL1	BRD7	BACH1	CDC45
E2F6	DHFR	TYMS	RB1	CDK1	POLA1	PCNA	CCNE1	RRM2	CCNA1	CDC6	HINFP
CDT1	NPAT	ORC1	GFI1	FBXO5	E2F4	E2F6	RB1	E2F1	ITGB1	PSMD11	PSMD12
PSMD9	CDC7	PSMD14	PPP6C	PSMA7	PSMD3	ORC5	ORC4	CDC45	PSMD10	CCNE2	DHFR
TYMS	ITGB1	RB1	CDK1	EIF4E	POLA1	UBB	UBC	BCL2	CDK4	PCNA	CCNB1
GSPT1	RPA2	PSMC3	RCC1	PSMB1	RPS6KB1	CDK2	MCM3	PSMA1	PSMA2	PSMA3	PSMA4
RPA1	PSMB8	PSMB9	PSMA5	PSMB4	PSMB6	PSMB5	WEE1	CDC25A	RRM2	MCM4	MCM5
MCM7	RPA3	PSMC2	ACVR1B	PSMB10	CDKN2A	CDKN2C	PSMC4	ID4	PSMD8	CDC34	PRIM1
PRIM2	PSMB3	PSMB2	MCM2	CDK7	PSMD7	CCNH	MNAT1	BCAT1	PSMD4	POLE2	PSMA6
PSMC1	PSMC5	PSMC6	RPS27A	UBA52	SKP1	CCNA1	CDK3	CDK6	E2F1	PPP3CA	RPA4
PSMD2	EIF4EBP1		CAMK2B	CAMK2D	POLA2	TFDP1	PSMD6	CDKN3	IQGAP3	PSMF1	CDCA5
MARK4	RBBP8	CDC6	HINFP	CDT1	PIM2	ORC3	DBF4	MCM8	ORC6	PSME3	CKS1B
PSME1	SKP2	ORC1	ORC2	MCM6	PSMD5	RHOU	MCM10	PSMB7	PSMD1	PKMYT1	FBXO5
PSME2	PSMD13	GPR132	PHF8	LATS2	CAMK2A	IQGAP3	CDKN2D	CDC25A	NFATC1	INHBA	SPDYA
CAMK2A	NFATC1	ITGB1	ACVR1	CUL1	CUL2	CUL3	CUL4A	TFDP3	USP37	CUL5	NBN
TICRR	WRNIP1	CDT1	TNKS	CCDC111	POLA1	PRIM1	PRIM2	HELB	CCDC111	ORC5L	MCM7
GMNC	POLA1	RFC3	RFC5	POLE	POLA2	LIG1	ORC5	SSBP1	ORC4	TNFAIP1	ORC2
DNAJC2	BRCA1	MCM7	POLN	POLD2	ORC2	NFIX	RFC3	NFIX	RFC4	SSBP1	NFIA
GINS4	BRCA1	POLE	ORC3	BRCA1	MCM8	MCM5	MCM4	POLN	POLE	SSBP1	POLD1
BRCA1	GINS3	FHIT	POLQ	RRM1	POLN	MCM3	POLA2	LIG1	ORC4	NFIA	POLE
MCM2	FEN1	MCM2	BLM	MCM7	POLD4	PRIM1	POLE	REV3L	NFIX	POLQ	POLD3
MCM7	BLM	RRM1	PRIM1	DNA2	NFIX	POLD2	NFIA	RFC5	NFIC	TK2	CDC7
NFIB	CHEK1	ORC5	ORC4	MCM3AP	RAD1	KIN	HUS1	POLQ	CDC45	RNASEH2A	
RAD17	RECQL4	KAT7	EGF	TK1	TYMS	IGF1	CDK1	NFIC	KRT7	CHTF8	HSMCR30
TOP1	TOP2A	PCNA	RPA2	LIG1	TYMP	PTMS	ACHE	RRM1	MCM3	RPA1	POLD1
CTGF	RBMS1	CDC25A	CDC25C	RRM2	DUT	MCM5	MCM7	PHB	RPA3	RFC2	BRCA1
IGHMBP2	FEN1	RECQL	POLD2	NASP	CENPF	PRIM1	PRIM2	MCM2	FHIT	LIG3	LIG4
NUP98	BLM	NAP1L1	POLE2	SET	SSBP1	POLE	SSRP1	RBBP4	NFIA	CHAF1A	CHAF1B
ORC1	ORC2	ATR	NAE1	TNFAIP1	POLA2	WRN	NCOA6	GINS1	NFIX	SPHAR	MED1
RBBP7	BRCA1	TBRG1	C8orf45	MCM10	LIN9	PAPD7	E4F1	RAD9B	NOL8	MCM10	RRM2B
TICRR	POLN	STRA8	PAPD5	HELB	CHTF18	ATRIP	ING5	KCTD13	UPF1	RMI2	SIRT1
CCDC111	RBM14	PEO1	WRNIP1	SIN3A	DNAJC2	RAD9A	CDC6	GINS4	GINS3	POLD4	CINP
REPIN1	CDT1	TMX1	RMI1	CLSPN	POLD4	NT5M	POLE3	MCM9	DTL	ORC3	POLK
DBF4	REV1	LRWD1	POLL	POLG2	MCM8	POLI	ING4	GINS2	POLH	SUPT16H	ORC6
MCM7	MCM2	MCM7	MCM2	MCM7	HMGA1	MCM7	MCM2	PURA	RAD51	MCM6	RAD51
PEO1	CCDC88A		PCNA	CDK2	PPP2R1A	ACVRL1	PPP2CA	ID3	CCDC88A		ESCO2
ESCO1	DSCC1	SMC3	POLD1	KIAA2022		TNKS2	CDK9	DKC1	RFC1	TERF2	RAD50
PINX1	TNKS1BP1		POT1	TERF2IP	PML	TERF1	POT1	POLD1	FEN1	DNA2	KIAA2022
C9JGY3	GMNN	D6R920	IDAS	GMNN	HCRT	HUS1	GMNN	RAD17	TGFB1	TP53	TGFB3
S100A11	NF2	TERF1	ATR	TTF1	PDS5A	ENPP7	WAPAL	MAPK15	CDC6	GTPBP4	TSPYL2
GDF2	TIPIN	TERF1	TERF2	MCM7	CDC45	MCM2	MCM7	CDC45	MCM5	MCM2	CDC45
MCM4	MCM5	CDC45	MCM5	MCM2	ORC5	ORC4	CDC45	CCNE1	MCM3	MCM4	MCM5
MCM7	CDC34	PRIM1	PRIM2	MCM2	POLE2	PURA	POLE	RPA4	ORC1	ORC2	POLA2
MCM6	LRWD1	CDC45	PCNA	RPA2	LIG1	MCM3	RPA1	POLD1	MCM4	MCM5	MCM7
RPA3	RFC4	RFC2	RFC1	FEN1	RFC5	RFC3	POLD2	PRIM1	PRIM2	MCM2	DNA2
POLA2	MCM6	GINS1	POLD3	GINS4	POLD4	MCM8	GINS2	SLBP	CACYBP	SHC1	MET
ATF1	FGF10	HRAS	INS	EPO	PLA2G1B	CSF2	MAS1	IL6	JUN	INSR	CDK1
IGF1R	GLI1	IL3	GLI2	TGFB3	AREG	PDGFRA	ATF1	KITLG	CALR	SHC1	DNA2
UCN	CTC1	CDC42	CACYBP	OBFC1	CACYBP	PDGFC	BLM	TIPIN	INO80	TK2	RRM2B
POLG	RRM2B	DNAJA3	TEFM	STRA13	BLM	FANCM	APITD1	CDK2AP1	REV3L	POLB	TOP2A
RPA2	RPA1	RFC1	POLG	TFAM	TOP2B	RPAIN	PNKP	MCMBP	BAZ1A	POLG2	MRE11A
SMC1A	STAG2	FBXW7	SMC3	POLA1	PCNA	RPA2	LIG1	RPA1	POLD1	RPA3	RFC4
RFC2	RFC1	FEN1	RFC5	RFC3	POLD2	PRIM1	PRIM2	DNA2	POLE2	POLE	POLA2
POLD3	POLD4	P10266	P63128	P63132	P63133	P63135	P63136	TERT	ERVK6	Q9QC07	Q9UQG0
ERVK6	ACD	TINF2	TERF1	TERF2	TNKS	TERF1	TERF2	ERCC4	DCLRE1B	TERF2	ACD
DCLRE1B	ZSCAN4	TINF2	OBFC1	TERF2IP	TNKS2	DKC1	RFC1	TERF2	RAD50	PINX1	TNKS1BP1
POT1	TERF2IP	MYC	PIF1	PML	TERF1	POT1	ERCC1	TERF2	TINF2	ERCC4	LIG1
RFC4	RFC2	RFC1	RFC5	RFC3	POLE2	POLE	TEP1	TERF1	TERF2	TERT	WRAP53
POT1	TERF2	TINF2	TERF2IP	TERF2	DCLRE1B	POLA1	PCNA	RPA2	LIG1	RPA1	POLD1
RPA3	RFC4	RFC2	RFC1	FEN1	RFC5	RFC3	POLD2	PRIM1	PRIM2	DNA2	POLE2
POLE	POLA2	POLD3	POLD4	DCLRE1C	POT1	PRKDC	DKC1	NBN	PARP1	POLA1	PCNA
XRCC6	XRCC5	RPA2	LIG1	RPA1	POLD1	RPA3	RFC4	RFC2	RFC1	FEN1	RFC5
RFC3	POLD2	PRIM1	PRIM2	DNA2	POLE2	PRKDC	POLE	POLA2	WRN	POLD3	PTGES3
SMG6	RAD50	ERCC4	DCLRE1C	OBFC1	DCLRE1B	POLD4	RTEL1	FBXO4	CTC1	AKAP8	SMC2

NCAPD3 PAPD7 PHF13 TTN CDCA5 NUSAP1 CHMP1A SMC4 SEP15 H1FNT TSSK6 HELLS
CENPV HELLS HMGA2 BAHD1 NCAPD2 NCAPH NCAPD2 ABCA4 NCAPD2 PRM1 PRM2 CDK1
HMGA2 HILS1 NCAPH2 H1FNT NCAPG2 AIFM2 PRM3 HAT1 PRM1 PRM2 NAA10 KAT6A
ASH1L MYST3 TSPY8 TSPY4 H2AFV NAP1L6 TSPY8 TSPY2 SET TSPY2 HIST1H2BC
SET H3F3A H2AFY NAP1L2 MCM2 H2AFV NAP1L4 H2AFV NAP1L4 H2AFJ TSPY10 MCM2
NAP1L4 H2AFY H2AFV TSPY10 TSPY3 H1F0 TSPY8 NAP1L1 NAP1L3 NAP1L5 HIST1H4A
NAP1L1 NAP1L4b TSPY8 CENPA SHPRH OIP5 HIST1H2BK H2AFY HIST1H2AB HIST1H2BJ
H1F0 H2AFZ HIST1H2AL H2BFM H2AFB1 H2AFB3 TSPY3 TSPY4 TSPY8 TSPY10 HIST1H1E
H2AFX HIST1H1B HIST1H1D HIST1H1C HIST1H2AD HIST1H1T
HIST1H2BO HMGB2 HIST1H2BB SOX9 CENPA MCM2 NAP1L1 H2BFS HIST1H2BD
HILS1 HIST1H4K HIST1H3G H3F3B SET TSPY1 HIST1H1A RBBP4 ITGB3BP
SHPRH RBBP7 HIST3H3 HIST2H2AC HIST2H2BE HIST2H2BF H2AFY2 HIST2H3PS2
SET HIST2H2BC HIST2H2BD HIST2H2AA3 CENPP H3F3C MIS18BP1 HIST2H3A
MLF1IP H2AFV CENPQ HIST3H2A H2BFWT TSPYL5 HIST2H2AB H1FOO HIST3H2BB
TSPYL6 HJURP CASC5 KAT6B H1FX CENPI KAT6A HIST1H2AC HIST1H2BH
HIST1H2BA CENPN HIST1H2AH NAP1L5 HIST1H2AA NAP1L3 HIST1H4G NAP1L4
HIST1H2BN HIST1H2AJ HIST1H2BM HIST1H2BL CENPK H2AFJ CENPO TSPYL1
TSPYL2 CENPH TSPY26P ASF1B MIS18A H2AFY2 TSPYL4 NAP1L2 RUVBL1 ASF1A NAP1L1 HMGA1
CDKN2A HMGA2 STRA8 CCNB1 SMARCA5 HIST1H1E HIST1H1D HIST1H1C
CTCF RSF1 CHAF1A CHAF1B DFFB TOP2A ACIN1 SYCP3 RBBP4 CHAF1A CHAF1B C2orf65
OIP5 SMARCA5 NPM1 CENPA HIST1H4K RBBP4 ITGB3BP RBBP7 CENPP MIS18BP1
MLF1IP CENPQ CASC5 CENPI CENPN RSF1 CENPK CENPO CENPH MIS18A RUVBL1 ESPL1
RB1 WAPAL CDCA5 HORMAD1 ZW10 CCNB1 CENPE RRS1 PSRC1 KIF18A PINX1
CCDC99 SEH1L CDCA5 CDC23 NEK2 CDC42 RACGAP1 ECT2 CENPF SPICE1 FMN2
STRA13 TOP2A MLH1 TOP2B FANCM APITD1 ERCC4 LATS1 TOP2A TOP2B MSH4 MSH5
ESPL1 STRA8 NDC80 BUB3 SGOL1 CASC5 AURKB AURKC HORMAD1 CENPE DLGAP5
CDC6 RB1 NIPBL BUB3 BUB1 BUB3 KIF2B AURKB KIF2C CENPH ABCA4 RIOK3
NDC80 BIRC5 RGS14 RAD21 BRD4 CIAO1 TOP3B PTTG1 SLC25A5 ERCC2 RCC1 PPP2R1A
BRCA1 CTCF NEK2 UBE2I ESPL1 SGOL2 SGOL1 PMF1 PHF13 SKA3 NUP43 NUP37
CASC5 SKA2 STAG1 USP9X SKA1 ARL8A SEH1L NSL1 SRPK1 CDK5RAP2 SETDB2
MMS19 CENPO METTL11A NUF2 NDEL1 CENPH DSN1 RAD21L1 FAM96A NAA60 SPC25
NEK6 INCENP ARL8B STAG3 FAM96B MAU2 BUB1 AKAP8 SMC2 NCAPD3 PAPD7 PHF13
TTN CDCA5 NUSAP1 CHMP1A SMC4 RB1 ZNF828 BRCA2 BUB3 NEK2 KIFC1 CIT
NDC80 SMC4 MAD2L1 BUB3 ZW10 ZWINT NUSAP1 NEK2 ESPL1 SMC1A DDX11 KIF25
INO80 SMC1A NIPBL POGZ GSG2 PDS5B SEH1L ZNF828 CTCF AXIN2 CCNB1 RAD51C
REC8 MRE11A SMC1A PAPD7 STAG2 FBXW7 DDX11 MCMBP NBN CDK1 CCNA2 CCNG1
HMGA2 FOXO4 TOP2A TOP2B HSPA2 FHL1 USP47 CDC45 RAD17 POLA1 CDC6 TIPIN
CDT1 RAD9A STRA8 NAE1 TICRR CLSPN CCNB2 CENPF PKIA PRKCQ CDKN2A CCNB3
BRD4 BACH1 TAF1 PLK4 CHEK1 CEP290 PPM1D BIRC5 CCP110 ENSA SSNA1 OFD1
DCTN3 CDK14 CEP152 CCNB2 PCNT FGFR1OP LATS1 TUBB4 CDK1 TUBB HSP90AA1
ABCB1 PRKACA CCNA2 TUBG1 GADD45A CDK2 PPP2R1A WEE1 CDC25A CDC25C PRKAR2B
CDKN1A CETN2 CDKN2B PAFAH1B1 CSNK1E DNM2 CDK7 CCNH MNAT1 NEK2 PLK1
TERF1 ARPP19 YWHAE DYNLL1 TUBA4A TUBB2C CCNA1 KHDRBS1 DCTN2 MELK NUMA1 PCM1
CEP78 CNTRL CEP57 CEP76 CEP192 TUBGCP3 DDX11 MARK4 TUBGCP6 TUBGCP5
CDK5RAP2 TUBGCP2 CEP250 FBXL15 CENPJ HAUS2 CEP72 ANAPC5 ANAPC4 ANAPC10
NINL DCTN1 DYNC1H1 ACTR1A SKP2 DYNC1I2 PKMYT1 AZI1 CEP63 TUBG2 NES
CSNK1D YWHAG MAPRE1 TUBA1A CLASP1 CCNY CEP70 NEDD1 TSGA14 NDE1 TUBGCP4
USH1C JMJD5 CEP164 CHEK1 SDCCAG8 SFI1 CKAP5 TPD52L1 ODF2 CEP135 TAF2
ALMS1 AKAP9 PLCB1 WNT9B POU5F1 BLM TXNIP WNT3A FZD7 HOXB4 BMI1 NOTCH1
WNT3A TGFB2 CDKN2A VANGL2 ANXA11 SPAST FGFR2 DCT VEGF MEN1 EREG FIGF
PDGFB TGFA TGFB1 IGF2 IL1A IL1B PPBP CAT PDGFA FGF1 FGF4 FGF2
TGFB3 FGF6 FGF3 FGF5 OSM VEGFA TAL1 PTN MDK FGF7 FGFR2 APC
FGF9 BTC HTR2B PGF VEGFB VEGFC FGF8 PROK1 TGFB2 YBX1 CSPP1 MACC1
NKX3-1 PDGFD MEN1 PDGFC GKN1 RGS14 CDC42 KIF23 CSPP1 PKP4 CDC6 AURKC
DAXX APC MYH10 APC DAXX APC MYH10 NUSAP1 TOP1 ERCC2 PIK3CB DPPA3
AATF STX2 TIAL1 WWTR1 RACGAP1 FMN2 CCP110 PRPF40A CETN2 CALM3 PDXP
BBS4 ASPM LEF1 IGF1R CENPV PARD3 RACGAP1 POU3F2 DIXDC1 GNB2L1 KIF18B
CABLES1 CABLES2 AURKB DSTN ARHGEF11 BIRC5 SEPT4 DAPK3 PRC1 DIAPH2 ROCK2
DCTN3 KIF20A RALA RALB SON STX2 MYH9 ARL3 PLK1 DSTN RAB11A KIF23
ROCK1 SEPT6 BECN1 ESPL1 RAB35 SEPT7 TTC19 RAB11FIP4 CNTROB PIK3C3 NEK7
AHCTF1 AURKB NOX5 SEPT5 CECR2 ROPN1B RACGAP1 KIF13A NEK6 INCENP ANLN
BIN3 KLHL9 KLHL13 SEPT3 KLHL21 VPS4A AURKC NUDC VPS24 ZFYVE26 RASA1 ASPM
SFRP2 SAC3D1 MCM5 CDC37L1 CDC7 CDK10 CDCA7L CENPH PAFAH1B1 CDC27 CDCA7
CDK4 CDK19 CDCA7 CDC20 CCNA1 PAFAH1B1 CCNB1 NCAPH NCAPD2 KIF2A CDC7
UBE2C NDC80 AURKA CETN3 ZW10 OIP5 RGS14 BUB1 BUB3 ENSA RAD21 SSSCA1
EVI5 CCNT1 BUB1B CCNT2 CLASP2 VPS4B TACC1 KATNA1 CDC123 CCNK RNF8 JTB
CDK14 HAUS5 CCNB2 ZWINT SMC2 LATS1 PTTG1 CCNE2 GNAI2 RB1 CDK1 TUBB
GNAI3 HSMCR30 CDK4 CCNB1 RCC1 LIG1 CCNA2 CCNO CCND1 CCNE1 CDK2
CCND2 CCND3 WEE1 CDC25A CDC25B CDC25C CKS2 PPP1CC CCNF CETN2 NCAPD3 CSNK1A1
CENPF LIG3 LIG4 CDK7 KNTC1 ANXA11 DYNLT3 NEK2 NEK3 NEK4 CCNG1 KIF11

HMGA2	IST1	TERF1	ARPP19	BCAR1	CKS1B	PPP1CA	PPP1CB	RAN	GNAI1	DYNLT1	UBE2I
TUBA1B	CCNA1	TXNL4A	CDK3	CDK6	CDK5	CENPE	CETN1	CDC20	CDC16	MAD2L1	CKAP5
NEDD9	SMC1A	NCAPH	SEPT2	NCAPD2	SYCP1	MAPRE2	MAPRE1	CCNG2	UBE2S	PDS5A	ERCC6L
PLK5	MAP9	CEP55	KLHL22	CDCA8	SGOL2	SGOL1	CDC2L6	CDC42	CDC16	KIAA1009	
CCNB1	PAPD7	E4F1	PPP2R2D	HAUS3	CDCA2	SPECC1L	MIS18BP1		PMF1	LLGL2	PSRC1
BORA	SYCE2	DCLRE1A	SEPT14	TUBA1A	MAEA	CHMP1B	POGZ	CLASP1	HAUS6	WAPAL	CDC16
CNTRL	CENPV	USP37	CUZD1	ZC3HC1	NCAPG2	PHF13	SKA3	SIRT2	SEPT12	CDK20	ASPM
SYCP3	SYCE1	SPICE1	STAG2	KIF2B	SPC24	CCNY	PAPD5	NUP43	NUP37	CASC5	NEDD1
CDC26	TTDN1	NEK9	PARD3B	CCNE2	PDCD6IP	SKA2	STAG1	CCNB3	SEPT1	ARHGEF2	
USP9X	SKA1	ARL8A	HAUS1	ANAPC16		CCDC99	SEH1L	CHFR	CDCA5	MASTL	SENP5
BOD1	NSL1	LMLN	CEP63	ZNF830	NEK1	KIF20B	SPAG5	SETDB2	CDCA3	KIF2C	CDC6
TSG101	HAUS7	NCAPG	TUBA1C	LZTS2	PELO	ANAPC13		HAUS8	MCMBP	FSD1	CENPO
KATNB1	TIPIN	KIFC1	CINP	SYCP2	NUSAP1	PARD6G	PARD6B	NUF2	LRRCC1	MIS12	USP44
ANAPC1	CENPH	DSN1	FAM83D	HAUS4	ZWILCH	ACTR8	SPC25	CENPJ	CHMP1A	PARD6A	SETD8
LATS2	HELLS	PDS5B	SMC4	SEPT11	ARL8B	C12orf11	HAUS2	NDE1	ANAPC11		MIS18A
SEPT10	RCC2	SPAST	SEPT9	MAD2L2	CDC23	ANAPC7	ANAPC5	ANAPC4	ANAPC2	FBXO5	INO80
TPX2	FZR1	ANAPC10		CDC14A	TIMELESS		CEP164	MAPRE3	SMC3	RUVBL1	CD2AP
USP16	MAD1L1	DYNC1LI1		MAU2	NUMB	NUMBL	CIT	JTB	RHOC	BRCA2	RHOB
KIF23	BBS4	RACGAP1		ECT2	BIN3						

List of genes in tissue remodelling gene signature

ZC3HAV1		TICAM1	CD86	ZFPM1	IL29	LEF1	APOA1	EREG	GATA6	IL18	HIF1A
F2R	SPHK1	S1PR3	SPHK1	NOD1	TLR3	CD36	NOD2	CD36	TNFRSF1A		TLR4
TLR3	RIPK2	TLR2	JAK2	SASH3	IFNG	PF4	CD14	CD36	TNFRSF1A		IL12B
FCER1G	FADD	RIPK1	IL18	TWIST1	NOD1	MAVS	TICAM1	CCL19	MYD88	CARD9	IL23A
TLR9	NOD1	IL1RL1	IL33	RARA	IL1RL1	NLRP12	TRPM4	NLRP12	IRF1	TLR4	IFNG
IRF1	RELA	REL	LTB	TNFRSF8	TLR4	TIRAP	ITK	AVPR2	ITK	TLR4	SASH3
IL4	HSPD1	TNFSF4	CD40LG	FCER1G	XCL1	CD83	TIGIT	IL20RB	IL21	NOD2	TLR9
IL17F	IFNA2	TGFB2	SMAD3	SMAD4	HIF1A	CMA1	GPAM	CD24	TLR3	IL12B	CEBPG
EBI3	CD276	ZFPM1	IL27	TNFRSF13C		IL21	TLR9	TLR8	TLR7	FCER1A	CD80
SYK	TNF	APOA1	APOA2	IL10	TNFSF4	IFNG	CSF2	IL17A	IL17RA	MYD88	IL9
CD83	NDFIP1	FOXP3	LEF1	IFNAR1	IFNAR1	IRF9	IRF3	MYD88	GSTP1	NCKAP1L	TLR4
IFNG	PRNP	TNFSF4	IL12A	IL12B	NCKAP1L	BCL10	FCER1G	NLRP3	BTK	IL33	IL4
RARA	TNFSF4	CD74	TIRAP	TLR4	BCL10	APOA2	ELANE	TLR8	TLR7	PRG3	NLRP3
TLR3	TLR9	TLR8	TLR7	TIA1	RNF128	FOXP3	ASB1	TBK1	TRIL	WNT11	TGFB1
IL15	IL2	IL18	IL23R	MYD88	IL21	NOD2	EREG	AGPAT2	SOD1	AGT	TNF
ADRA2A	LEP	HTR2B	SLC11A1	NFAM1	PELI1	C1orf190	AGPAT1	CARD11	TGFB1	TGFB3	TGFB2
IRAK3	F2RL1	AZU1	IFNA2	IFNB1	F2R	IFNAR1	WNT5A	TLR4	RIPK2	SASH3	LTA
TNF	IL1B	CD3E	IFNAR1	BCL3	ZP3	TNFSF4	KLRK1	CD40LG	WNT5A	CCR2	SLC11A1
IRF8	FZD5	IL27RA	IL29	KLRK1	IL12RB2	SMAD3	HSPB1	SMAD3	JAK2	HSPB1	SMAD3
IL18	NOD2	P2RX7	WNT5A	TRIM16	IFNG	WNT5A	NLRP12	PYDC1	NLRP3	PANX1	CCL19
NLRP1	NOD2	NLRP2	PYCARD	CARD8	SAA1	IL29	FOXP3	LEF1	IRF4	STAT5B	STAT5A
CARD11	IL1A	IL1B	CD4	CD3E	CD28	CD80	CD86	STAT5A	STAT5B	PRKCQ	IRF4
CD28	GLMN	CARD11	IL1B	IL12B	IL18	IL23R	IL23A	IL18	PTGS2	MAP3K7	SASH3
TNFSF4	XCL1	TRAF2	MALT1	TRAF6	HMOX1	HMOX1	BCL6	PCSK5	CD28	CEBPE	PCSK5
IL17F	IL6R	BPI	ARRB1	ADAM17	TLR9	NDRG2	KLRF2	LYN	MS4A2	AGT	LYN
MS4A2	LCP2	NOX5	S100A13	C3AR1	C3	IL1A	ARNT	ADORA2B		PTGS2	FLT4
IL6ST	GATA4	C3AR1	HIF1A	HPSE	NOX1	TSPO	CHRNA7	HSF1	NOD2	TLR4	CIDEA
POMC	GSTP1	RARA	ACP5	BPI	LBP	TNFAIP3	AXL	TSPO	ARRB2	HSF1	MC1R
TWIST1	ADIPOQ	SELS	CHRNA7	TWIST2	SELS	FOXP3	NOD2	IRAK3	TIRAP	TRAF3	RNF216
F2RL1	IFNG	ADAM8	AFAP1L2	MAP3K7	RIPK2	SASH3	TNFSF4	CCR2	CD83	TRAF2	MALT1
TRAF6	SLC11A1	INPP5D	NLRP12	INPP5D	GHSR	GHRL	SEMA7A	TLR4	SEMA7A	CD74	CD36
WNT5A	SLC11A1	IL4	XCL1	TLR4	DDX58	HSPD1	IRF7	IFIH1	TBK1	MAST2	NFAT5
CD4	DBH	G6PD	FABP4	TNFSF4	PTAFR	TXK	REL	ITK	NFATC2	CD226	ZCCHC11
NFATC2IP		S1PR3	FOXP3	IRAK4	CD4	BCL3	IRF4	IL4	IL12B	IL18	TNF
IFNG	IL1B	HMOX1	WNT5A	TICAM1	MYD88	WNT5A	F2R	WNT5A	CAMK4	BCL3	IL10
GHSR	GHRL	IL1RL1	NOD2	SCGB1A1	TLR4	IL33	PRNP	RARA	SCGB1A1	TNFSF4	XCL1
IL1RL1	IL20RB	GIMAP5	FOXP3	NOD2	ELANE	SIGIRR	CARD9	CHRNA7	NCKAP1L	TNFRSF1A	
TLR4	TNF	GBA	BPI	TNFRSF1A		TNFAIP3	IL10	ARRB2	ARRB1	NCKAP1L	SELS
CHRNA7	SELS	FOXP3	TLR9	KLF2	CCR7	CCL19	XCL1	FURIN	GATA6	RPS6KA5	RPS6KA4
SLC11A1	NDRG2	IL6	CCL2	CCR2	NDRG2	CIDEA	IL6	SRGN	TNFSF4	TNFRSF4	NLRP12
CX3CL1	O3FAR1	BTN2A2	FOXP3	SASH3	IL33	CD3E	RARA	ZP3	TNFSF4	GATA3	IL20RB
XCL1	FOXP3	ATP6AP2	THBS1	CX3CL1	FOXP3	ICOSLG	CD86	IRF4	IFNA2	SNAI2	IL10
GATA3	INHA	INHBA	CD276	FOXP3	IRF3	WNT5A	F2RL1	ZNF287	MAP2K3	IGF2BP3	GATA3
IL12B	MAP2K3	ZNF287	IGF2BP1	IGF2BP2	IL12B	JAK3	IL23R	FOXP3	IL23A	NOD2	THBS1
ACP5	ARRB2	JAK3	TIGIT	CMKLR1	NOD2	IL1B	TWIST1	ADIPOQ	LAG3	SFTPD	CD276
FOXP3	VSIG4	NOD2	PRNP	TNFAIP3	XCL1	IL20RB	HDAC7	KAT5	NOD2	VSIG4	PLA2G1B
CEBPB	IL17F	CARD9	INHBB	P2RX7	PANX1	PNP	GPAM	TLR4	RAC1	SMAD3	SMAD3
CREB1	SMAD3	JAK3	S100A13	P2RX7	TNFSF15	CRTAM	INS	TNF	IL1A	SAA1	CD14
FGR	MIF	IL10	HTR2B	IRF3	CLEC6A	CLEC9A	SCAMP5	GLMN	PANX1	CADM1	IL26
CLEC5A	CLEC4E	TLR4	TLR3	RIPK2	TLR2	TNF	LBP	ADORA2B		P2RY2	ADAM17
IL18	HIF1A	TLR9	TLR7	ELANE	BCL3	IL18	BCL10	IL17F	CHRNA7	GSTP1	ACP5
TNFAIP3	ARRB2	CHRNA7	GHSR	GHRL	TRIB2	NOD1	XCL1	MAVS	TLR4	TLR3	TLR5
IL1B	SERPINE1		CALCA	LBP	TIRAP	FADD	RIPK1	IL18	ADIPOQ	MAVS	AFAP1L2
TLR7	BCL10	IL19	GIMAP5	IL21	AZU1	PTGS2	CCR7	AIM2	ABCA1	F2RL1	NLRC4
NOD1	P2RX7	CD36	TLR3	CD36	NOD2	CD36	WNT5A	TLR4	MAPK13	TLR3	RIPK2
FIGF	TLR2	IL33	TNF	IL1A	IL1B	IL6	IL6R	HSPD1	CD36	LBP	TNFSF4
ADORA2B		FCER1G	WNT5A	UCN	AKIRIN2	NOD1	TICAM1	MYD88	CARD9	NOD2	TLR9
TLR7	NOD1	CALCA	IL1RL1	IL33	C5	IL4R	IL1RL1	CHIA	IL18	PAWR	TLR2
TLR9	FCER1A	SYK	SLC11A1	TLR3	CD36	NOD2	CD36	TLR4	TLR3	TLR2	HSPD1
CD36	TNFSF4	CD40	IL12B	CD40LG	CCR7	TIRAP	IRF8	IL23R	CCL19	NOD2	IL23A
PLCB1	TLR9	MAVS	IL17F	TIRAP	IL17F	CARD9	CCR7	TLR3	TLR4	POLR3A	TLR3
TLR2	POLR3D	RNF135	POLR3C	IFIH1	POLR3F	TLR9	POLR3B	TBK1	EREG	IFNG	IL1B
TIRAP	TLR1	TLR6	TLR4	TICAM1	TLR9	TLR8	TLR7	TBK1	HSPB1	SPN	TLR4
HSPB1	THBS1	SPN	LBP	AZU1	TNFRSF8	CCR2	TLR1	IL13	ELF1	SFTPD	UBASH3A
TRAF3	ELF1	ACE2	ZBTB32	HSPD1	WNT11	TRIM56	PTGS2	XCL1	UBE2L6	ATG12	DDX58
ISG15	UBB	UBC	TNFAIP3	UBA7	UBE2D3	RPS27A	UBA52	TRAF3	PIN1	IKBKE	TRIM25
IRF3	PCBP2	MAVS	NLRX1	TAX1BP1	NLRC5	RNF135	RNF125	OTUD5	ITCH	IFIH1	ATG5
CYLD	TBK1	HERC5	F2RL1	STK10	ONECUT2		BCL2	MYF5	NF1	PIK3CB	DDR1

MINK1	TSC1	ONECUT1		DDR1	ITGAL	ITGA4	L1CAM	FERMT3	OLR1	FERMT3	OLR1
ITGB2	ICAM1	ITGB1	APOA4	CALCA	ITGA5	CCL5	ITGA4	EZR	SELP	SELE	ITGAL
MSN	CD40LG	L1CAM	SYK	OLR1	ROCK1	TSTA3	CERCAM	FERMT3	CLEC4M	CD209	ADA
DPP4	FERMT3	CX3CL1	SPN	MYO1F	ADAMDEC1		DSCAM	KNG1	SPN	RASA1	ERBB3
ACVRL1	ARHGDIA	ARHGDIB	CDH13	CD164	PDE3B	ANGPT1	TGFBI	MIA3	CBLL1	DSCAML1	
RND1	SIPA1	ARHGDIG		SRCIN1	ADAM22	ITGA6	VTN	ICAM1	ADAM17	ADAM9	JUP
THBS4	CYP1B1	PODXL	CXCL13	CCL5	PIEZO1	ZAP70	JAK2	PODXL	TGFB1	WNT1	CDH1
NF2	B4GALNT2		TNR	GTPBP4	EPB41L5	LEF1	ROCK2	EPHA3	EFNA5	ROCK1	MACF1
UNCX	BMPR1B	ACAN	BMPR1B	COL2A1	MYCN	MGP	FGF4	FGF6	COL11A1	MYF5	BMP1
SOX9	PKD1	ALX1	OTOR	BARX2	TRPM7	PPAP2B	L1CAM	CXADR	PTPRU	CCL21	ASTN1
NCAM2	CDK5R1	CNTN4	NLGN2	TNR	NLGN3	NINJ2	CTNND2	TNF	IL1B	VCL	IHH
CDC42	PLEKHA7	BVES	KIFC3	CAMSAP3		CTNNA3	MYH9	NRCAM	CTNNB1	SHC1	CTNNB1
JUP	NRCAM	NRCAM	CTNNB1	ICAM1	ASTN1	THY1	PDPN	NPHP1	SRPX2	CTNND1	NPHP4
ANXA9	VNN1	NTN1	EGFR	THY1	CD2	PKHD1	BCL2	COL6A2	ICAM2	JUP	PVR
DSP	CD44	CD58	CD24	COL8A2	CTNNA2	CD34	SHC1	ICAM3	CTNNB1	MYH9	PSEN1
ITGA8	CDH11	CDH12	JAM2	DSG1	COL14A1	FOXF1	DLG1	ITGAD	SCRIB	FAT1	ICAM4
COL19A1	PVRL1	CDSN	RAPGEF1	CTNNA3	COL13A1	CBLL1	PDPN	RAPGEF1	NLGN2	DLG5	PKD1L1
GPR98	PTPRU	NRCAM	CYFIP2	PKP2	ROPN1B	SIGLEC1	CDH19	VEZT	CDH20	CD93	IGSF5
CRNN	CTNNA3	CDH9	CDH7	ICAM5	FNDC3A	ZAN	CDH10	ILK	MERTK	LAMA5	FZD7
FN1	LAMB1	LAMC1	EFNA1	EPHA1	AXL	BRCA1	EPHB3	TYRO3	MERTK	ILK	VAMP3
BVES	SRCIN1	ANTXR1	PEAK1	FZD4	C22orf28	SDC4	SDC4	KDR	SMAD3	PTPRJ	SFRP1
TSC1	EPB41L5	ITGA4	CADM1	L1CAM	CADM1	ICAM1	ITGA5	ITGA4	SELP	SELE	CDH2
VCAM1	ITGAL	L1CAM	LGALS7	CDH4	NRXN1	CXADR	CD164	REG3A	PVRL1	AMIGO2	AMIGO1
AMIGO3	AMICA1	CADM3	NLGN1	CADM1	CD209	TMEM8B	ITGBL1	CTNNB1	ITGB8	ITGBL1	C17orf57
SNED1	CTNNB1	BCL2L11	ITGB6	ITGB1	RHOA	ITGB1	ITGA6	EPDR1	RAPH1	EDA	NPNT
EPDR1	CTNNB1	ITGB1	CTNNB1	ITGB2	MUC4	BCL2L11	NPNT	CTNNB1	MUC4	ITGB6	PXN
ITGBL1	ITGB2	ITGB7	PXN	ITGB7	ITGB7	PXN	ITGB6	ITGB1BP1		BCL2L11	SGCE
PPFIA2	TECTA	ITGA10	ECM2	ITGBL1	AGT	COL3A1	VTN	ITGB3	ITGB2	ITGB1	ITGAV
ITGA2B	NID1	CD44	ITGB4	ITGA2	ITGB5	VCL	ITGB6	COL5A3	ITGA3	ITGB7	ITGB8
HOXD3	CTNNB1	PXN	THBS3	BCAM	ITGA8	ITGA1	RHOA	RAC1	PKD1	CDK5	CNTN2
PPFIA1	ITGAD	ILK	ADAM9	ADAM15	ITGA7	NID2	FREM1	COL13A1	RAPH1	ADAMTS13	
SNED1	TSC1	EDA	DEFB118	MUC4	SORBS1	JAM3	SIGLEC1	PARVG	FBLN5	ITGA11	EPDR1
COL17A1	TNN	HPSE	C22orf28	ANGPTL3		FXC1	LYVE1	CUZD1	EPB41L5	TNFRSF12A	
COL11A2	COL11A2	SSPO	LAMB4	CDHR4	CNTNAP3		TMEM8B	TSPEAR	COL27A1	HSPB11	STAB2
COL11A2	HSPB11	SIGLEC16		NLGN4Y	COL6A6	CDH8	CELSR1	ITGB2	TSPEAR	CDH2	ITGB2
COL6A5	PCDH15	SPP1	MADCAM1		ITGA10	ITGBL1	SCARB1	ITGA3	PCDHB12		PCDH8
CD34	ITGB8	CDH18	NLGN4Y	COMP	B4GALT1	NINJ2	PCDHB14		ITGBL1	THBS3	PCDHB11
VCL	C17orf57	CD34	NR2C2AP		ITGAV	SCARB1	ITGAL	ITGA3	CTNNA1	NCAM1	CD44
HAPLN2	DDR1	CDH12	DDR1	NCAM2	ITGA2B	EMB	PCDH15	SCARB1	DDR1	CTNNA2	TGFBI
COL11A2	CDHR5	PCDH15	CDH2	COL11A2	ITGB6	C9JA99	CELSR1	LMLN	PTK2B	PCDH15	TSPEAR
ITGB1	ITGA6	COL12A1	COL11A1	RHOA	ITGB1	CDH13	SPP1	NLGN3	SPP1	D6RA20	PCDH1
SPON2	PCDH1	HAPLN1	TGFBI	SPON2	SCARB2	CDH18	SPON2	CDH6	COL12A1	DDR1	VCAN
PCDH18	SPON2	CDH18	CDH10	CNTNAP3		CTNNA1	ITGB2	PTK2B	CTNNA1	ITGB2	PTK2B
CDH17	PTK2B	PCDH15	SCARB2	PCDH15	ITGA2	ACAN	COL11A2	CDH24	COL11A2	CDH17	CDHR1
DDR1	COL11A2	DDR1	ACAN	ITGA4	CD44	DDR1	CDH5	DDR1	PCDHB13		PCDH15
ITGB1	PCDH15	CDH23	ITGB1	CD36	THBS4	ITGA4	ITGA2	COL11A2	DCBLD2	COL11A2	CD36
DDR1	ITGB1	CPXM2	DDR1	CDH23	DDR1	CD36	PCDH11X		DDR1	ITGB2	CD36
ITGAV	CD36	NRP1	ACAN	CNTNAP3B		PCDH19	ITGA2	COL11A2	DCHS2	CD36	PCDH10
COL11A1	DCBLD1	FAT2	CNTNAP4		ITGA9	COL11A2	ITGB6	NRP1	CDH23	VCAN	NRP2
COMP	CNTNAP4		DCHS2	PCDHB13		COL20A1	NRP1	CD36	CD44	NCAM1	ITGB1
CD36	FAT3	ITGB1	CDON	CDHR1	CTNNA3	CNTNAP3B		CNTNAP3		PCDH7	CTNNA1
ITGA10	CDH4	CDH1	COL18A1	COL21A1	MFGE8	ITGBL1	ITGA11	CADM1	ITGB2	CNTNAP4	
CDH16	ITGA11	COL15A1	NRP2	CDH19	MADCAM1		CDH13	CDH11	NRP2	NINJ2	PCDH1
ITGA10	LAMC2	PCDHB6	CD4	PCDHB12		TYRO3	SCARB1	THBS3	MADCAM1		SCARB1
VCL	DCHS2	NELL2	MADCAM1		CDH7	CDH13	CDH5	NELL1	ITGB7	MFGE8	VCL
CDH13	FAT3	ITGA8	CDH1	CADM1	NRP1	CTNNA1	ITGB7	ITGB7	NELL2	TSPEAR	DSC2
CTNNA1	SCARB1	LMLN	ITGB6	ROBO2	NINJ2	LMLN	COL18A1	COL24A1	ARVCF	CHL1	ISLR
BAI1	PTPRT	ASTN1	NCAN	NRP1	PCDH17	CASK	PDZD2	INPPL1	SIGLEC5	NCAM2	RS1
FLRT2	ADAM12	EFS	TGFB1I1	MTSS1	CHST10	PSTPIP1	SIGLEC6	EDIL3	PCDH7	SUSD5	PCDHGA12
NRP2	DSCAM	PLXNC1	MPZL2	NPHS1	SORBS3	LPXN	CTNND1	SDC3	ADAM23	CDH16	LRRN2
CLDN11	ITGA10	WISP2	CNTN5	NFASC	CLSTN1	PCDH8	CD44	WISP1	CLDN1	ITGBL1	F8
ADA	CD4	FN1	AMBP	BGLAP	VTN	VWF	APP	ITGB3	ITGB2	ICAM1	ITGB1
ITGAV	GP1BA	LAMB1	THBS1	ITGA2B	ITGA5	RPSA	FREM3	SPP1	PTPRF	HAPLN1	LAMC1
ITGAM	COL11A1	COL6A1	COL6A3	F5	GP1BB	CCL4	CCL2	NCAM1	VCAN	ITGA4	COL11A2
SELL	CD99	NID1	GP9	B4GALT1	SELP	ACAN	ITGB4	PECAM1	SELE	FER	ATP2A2
CD36	ITGA2	ENG	ITGB5	VCL	ITGB6	CDH2	CD58	VCAM1	CD33	CD22	ITGAL
ITGAX	COL9A1	COL5A1	MAG	KITLG	EPHA1	IBSP	CD72	CD9	TNXB	CDH3	NME2
ITGA6	KAL1	OMG	PRPH2	IL32	TNC	APC	FPR2	COL5A3	ITGA3	ITGB7	ITGB8
DPP4	COL8A1	PTPRM	CTGF	EPHA2	EPHA3	CD6	L1CAM	CCR1	DSG3	CDH5	CTNNA1
CTNNB1	THBS2	THBS4	ACTN2	IGFALS	SPAM1	ITGAE	COL15A1	COL18A1	GP5	CD96	PIK3CB

MCAM CXCL12 CD151 CD97 PXN CX3CR1 CXCR3 THBS3 COMP ENTPD1 BCAM RAB13
CCL11 CCR3 CCR8 APLP1 BMX PRKX EFNB2 EPHB4 EPHA4 SLURP1 MFAP4 MLLT4
LAMB2 CDH4 CDH6 CDH8 CDH11 CDH15 ITGA1 LGALS4 BCAR1 NRXN1 NRXN2 IL2
RHOA RND3 ARF6 RHOB RAC1 CXADR SIRPA CNTNAP1 CLDN10 OLR1 RELN
ADAM17 SRPX TNFAIP6 MUC5AC DGCR2 HSPG2 EFNB1 MYBPC1 COL4A3 CNTN2 COL7A1 APBA1
DSC2 DST ROM1 CD164 TYRO3 COL16A1 DPT PCDH1 DDR1 LGALS3BP MFGE8
DSC1 SPOCK1 CD47 SIGLEC14 TROAP TRO CNTN1 CDH17 AIMP1 ARHGAP5
MMRN1 MYBPH PTK7 PTPRS ITGB3BP MSLN ADAM15 LSAMP MADCAM1 SEMA5A CDH18
TPBG ITGA7 ALCAM LAMB3 LAMC2 ITGA9 PKP1 BYSL COL4A6 SCARB2 NID2 DSG2
DGCR6 SCARF1 LY6D SELPLG EMR1 FLOT2 F8B PTK2B MYBPC2 HES1 NEDD9 FAT1
HABP2 DSC3 SSPN MYBPC3 GPNMB OPCML COL19A1 HEPACAM POSTN PGM5 PVRL1
PTPRK CDSN TRIP6 CD226 ZYX IGFBP7 MOG DDR2 AOC3 COL24A1 THBS3 COL28A1
opn CDON SVEP1 FBLN7 SDK2 IGSF11 FREM1 CD34 NRP1 COL11A2 FREM2 HAPLN2
CERCAM HES5 TLN1 THEMIS2 PCDH9 DKFZp686I11137 RGMB EMB KIRREL2 MPZL3 OLFM4
AMTN NPNT FAT4 PCDHJ DCHS2 CDHR3 MAEA NEGR1 SDK1 COL11A2 AMIGO2 DSG4
CUZD1 HAPLN4 FERMT3 CD44 VCAN PPFIBP1 AMIGO1 AMIGO3 NR2C2AP AMICA1 AEBP1
EGFL6 CNTN4 CDH26 IZUMO1 COL27A1 NLGN4X CADM3 CTNNA1 NLGN1 AGGF1 CPXM2 PCDH20
DCBLD1 CHST4 BVES COL22A1 NLGN4Y CADM4 PCDH19 CD99L2 SPACA4 FAT3 SCARB1 TSPEAR
FBLIM1 STAB2 MUC16 CNTNAP5 PVRL2 PTPRU TNR SYMPK NELL1 HAS1 SEMA4D
NEO1 NINJ1 LPP FERMT2 PERP VMP1 SCARF2 BCAN ITGAL JUB RADIL CDHR1
DCHS1 hucep-12 MEGF10 MSLNL LMLN CDH19 SIGLEC10 CNTNAP3B PVRL4
COL21A1 DCBLD2 SIGLEC12 BTBD9 PCDH15 MAGI1 SIGLEC11 ERBB2IP HAPLN3 CPXM1
PCDHB17 PCDHB18 CSF3R MUC4 AMELX NELL2 PKP4 CGREF1 FEZ1 COL12A1
CIB1 ADAM2 OMD FERMT1 CLSTN3 LRFN3 SPON2 BOC JAM3 EMILIN2 CADM1 CDHR2
CNTNAP3 PCDH11X PCDH11Y CNTNAP4 HAPLN2 PCDHAC1 CDH23
PNN TTYH1 CLSTN2 CDHR5 LY9 PARVG PARVB PCDH9 MUC5B SPON1 PCDH18 TMEM8A
CELSR2 NRXN3 CD209 AMBN TNFRSF12A PCDH12 SLAMF7 CASS4 PCDHB16 PARVA
STAB1 AATF CELSR1 CELSR3 FAT2 SIGLEC8 PODXL2 NLGN3 NINJ2 FLRT3 FLRT1 NTM
SIRPG COL20A1 CNTN3 PCDH10 NRXN2 CTNNAL1 FBLN5 CFDP1 CD300A CNTNAP2
EMR2 CD84 CDH1 CDH22 LEF1 TINAG AJAP1 ITGA11 NRXN1 CLEC4A PCDHB8 PCDHB10
PCDHGC3 PCDHGB4 PCDHA7 PCDHA6 PCDHA4 PCDHA12 CNTN6 CTNND2 CLCA2
GNE HPSE SIGLEC7 SSX2IP SIGLEC9 PKP3 TLN1 NRXN3 TLN2 LOXL2 HSPB11 PCDHB9
PCDHB7 PCDHB6 PCDHB5 PCDHB4 PCDHB3 PCDHB2 PCDHB15 PCDHB14 PCDHB13
PCDHB12 PCDHB11 PCDHB1 PCDHGC5 PCDHGC4 PCDHGB7 PCDHGB6
PCDHGB5 PCDHGB3 PCDHGB2 PCDHGB1 PCDHGA9 PCDHGA8
PCDHGA7 PCDHGA6 PCDHGA5 PCDHGA4 PCDHGA3 PCDHGA2
PCDHGA11 PCDHGA10 PCDHGA1 PCDHA9 PCDHA8 PCDHA5 PCDHA3 PCDHA2 PCDHA13
PCDHA11 PCDHA10 PCDHA1 PCDHAC2 LYVE1 F11R NPTN EMILIN1 LAMC3
ROBO1 MADCAM1 IL1RN ADIPOQ VTN CDHR4 CDH26 CDH8 CELSR1 CDH2 PCDH15
PCDHB12 PCDH8 CDH18 PCDHB14 PCDHB11 CDH5 CLSTN1 CDH12 PCDH15
CDH2 PIK3CB CDHR5 PCDH15 CDH2 C9JA99 CELSR1 PCDH15 CDH2 PIK3CB CDHR3 CDH13
PIK3CB D6RA20 FAT1 CDH18 CDH6 PCDH18 CDH18 CDH10 CDH17 CDH24 CDH17 CDHR1
L1CAM CDH5 CDH9 PCDHB13 PCDH15 CDHR3 PCDH15 PCDH11X PCDH19 DCHS2
PCDH10 FAT2 CDHR3 CDH23 DCHS2 L1CAM PCDHB13 FAT3 CDHR1 PCDH7 CDH4
CDH1 CDH3 CADM1 CDHR3 L1CAM CLSTN3 CDH16 CDH19 CDH13 CDH11 PCDH1 PCDHB6
PCDHB12 DCHS2 CDH7 CDH13 CDH5 CDH11 CDH13 FAT3 CDH1 CADM1 DSC2
CDHR3 PTPRT PCDH17 PCDH7 PCDHGA12 MPZL2 CDH16 CLSTN1 PCDH8 ITGB1 RET
PTPRF CEACAM1 CDH2 CDH3 PTPRM L1CAM DSG3 CDH5 PIK3CB CDH4 CDH6
CDH8 CDH11 CDH12 CDH13 CDH15 PKD1 DSG1 DSC2 PCDH1 DSC1 TRO CDH17
CDH18 DSG2 FAT1 DSC3 PVRL1 FREM2 CLSTN3 PCDH9 DKFZp686I11137 FAT4 PCDHJ
DCHS2 CDHR3 AMIGO2 DSG4 CDH24 AMIGO1 CDH26 CADM3 PCDH20 PCDH19 DSCAML1
FAT3 PVRL2 ESAM CDHR1 DCHS1 CDH19 PCDH15 PCDHB17 PCDHB18 CLSTN3
RET CADM1 CDHR2 PCDH11X PCDH11Y PCDHAC1 CDH19 CDH23 CLSTN2
CDHR5 CDH20 PCDH9 ROBO2 PCDH18 CELSR2 PCDH12 PVRL3 PCDHB16 CELSR1 CELSR3
FAT2 PCDH10 CD84 CDH1 CDH22 CDH9 CDH7 PCDHB8 PCDHB10 PCDHGC3
PCDHGB4 PCDHA7 PCDHA6 PCDHA4 PCDHA12 PCDHB9 PCDHB7 PCDHB6 PCDHB5 PCDHB4
PCDHB3 PCDHB2 PCDHB15 PCDHB14 PCDHB13 PCDHB12 PCDHB11
PCDHB1 PCDHGC5 PCDHGC4 PCDHGB7 PCDHGB6 PCDHGB5 PCDHGB3
PCDHGB2 PCDHGB1 PCDHGA9 PCDHGA8 PCDHGA7 PCDHGA6
PCDHGA5 PCDHGA4 PCDHGA3 PCDHGA2 PCDHGA11 PCDHGA10
PCDHGA1 PCDHA9 PCDHA8 PCDHA5 PCDHA3 PCDHA2 PCDHA13 PCDHA11 PCDHA10
PCDHA1 PCDHAC2 NPTN ROBO1 CDH10 THBS1 RASA1 HOXA7 NF2 BCL6 CDKN2A
ACER2 PLAU ILK CSF1 CCL21 CSF1 CD36 EPHA1 CCR7 UTRN GSK3B CDH13
CDK6 ILK SFRP1 PLEKHA2 ANGPT1 APC ANGPT1 APC RHOC VAV3 PLD2 IFNG
ERBB2 FGF1 ITGAV PRSS2 RHOC TPM1 CCL5 VAV1 VEGFA SELP ALOX12 AZU1
TGM2 APC IL12A IL12B CCR7 ADAM8 CX3CL1 NRG1 PTPRJ LDB1 CHRD VAV3
ITGAL ITGA6 KIF26B L1CAM SMAD7 FSTL3 ITGAL L1CAM CD47 KIF26B CITED2 SIRPG
LEF1 TNF SELP SELE VCAM1 LEP ROCK1 SELPLG CHST4 PODXL2 ITGA4 CYR61
DNAJB6 ITGA4 VCAM1 LEF1 PLAU EFNA1 EPHA2 EPHA8 PTK2 PTPN11 TESC CLDN2
CLDN1 CLDN5 CLDN4 CLDN3 CLDN11 CLDN7 CLDN9 CLDN14 CLDN1 CLDN15 CLDN6 CLDN8

CLDN12 CLDN17 CLDN18 CLDN20 CLDN2 CLDN10 CLDN19 CLDN22 CLDN23 CLDN16 JAM3 LAMA3
STAT5B STAT5A LAMA4 SRF LAMA2 DLL1 PPP1R12A LAMA5 CYTH3 NUAK1 CYTIP
ROCK2 ABL1 ICAM1 GSN FES IL8 SRF S1PR1 LAMA2 LAMA1 EPHA8 PPP2R1A
STAT5A ABL2 SOX9 STAT5B PRKX PPP1CB PPP2CA PTPRJ ROCK1 IL18 CYTH1 LAMA4
LAMA3 FAF1 GSN LAMA3 CYTH2 SERPINI1 CYTH4 FAF1 WNT4 EFNA5 EPHB3 WNT4
ADAM8 EPHA7 NRARP MINK1 CELSR2 LEF1 SMOC2 VIT FBLN2 PRKCE COL8A1 ITGA6
NDNF NPNT NDNF EGFLAM RELL2 COL8A1 NPNT CYR61 EDIL3 JAK2 ECM2 VTN
ITGB1 SPP1 NID1 COL8A1 ARL2 PRKCE FOXF1 VWC2 HSD17B12 ECM2 CCDC80
ABI3BP RELL2 NDNF EMILIN1 LGALS1 JUB THY1 TESK2 LAMA5 THY1 BCL2 ACTN1
ACTN2 ACTN3 PTK2B PTPRK TRIP6 JUB DLC1 TESK2 SORBS1 TAOK2 TNFSF11 CCL5
SNAI2 SERPINE1 PDE3B ACER2 GAS6 GAS6 PPARD SMAD6 SORBS3 VWF CORO1A
PRKX EPHB1 PPARD JUB CDH17 CDH2 CDH13 NRXN1 ATP2C1 DSG1 CDH17 NLGN1
JUB DCHS1 CDH23 CDHR5 PCDHB16 PCDHB10 PCDHGC3 PCDHGB4
PCDHB9 PCDHB7 PCDHB6 PCDHB5 PCDHB4 PCDHB3 PCDHB2 PCDHB14 PCDHB13 PCDHB11
ARHGAP6 THBS1 ACVRL1 MMP14 PTEN ATP5B FOXA1 WNT3A FOXA2 MAP2K1 ZNF703
SERPINE1 ITGB1 ITGA5 L1CAM ADAM9 PKD1 ANGPT2 FZD7 PLG COL1A1 WNT1
LGALS1 NOTCH1 TBCD FZD4 FXYD5 NCKAP1L CCL21 NCKAP1L ADAM9 SFRP2 FOXC2 STXBP3
PLEK GATA1 PDGFRA WNT3A STXBP1 FERMT3 VCL CLDN19 FBF1 TRPV4 GJA4 GJA5
GJC1 LIM2 DSG1 TJP1 HDAC7 PARD6B TRPV4 TLN1 TLN2 ITGA5 ITGA6 TNS1
TLN1 SIRPB1 FYB TYROBP CTNND1 SKAP2 CLDN9 CLDN14 KRT14 ITGB1 ACTN1 CDH1
SRC KRT5 JUP PVR ITGB4 CDH2 FLNA CDH3 ITGA6 PTPN6 CDH5 CTNNA1
SFTPD PRKCI LIMS1 CD151 PXN VASP MLLT4 CDH4 CDH6 CDH8 CDH11 CDH12
CDH13 CDH15 CLDN15 CLDN12 CLDN17 CLDN18 CLDN20 ACTB GRB2 ACTG1 SIRPA PTPN11
CD47 ILK CDH18 LAMB3 LAMC2 PTK2B FLNC ARHGEF6 PLEC PVRL1 RSU1
TESK1 LAMA3 LIMS2 CDH24 SFTPA2 SFTPA1 CADM3 CADM2 MPP5 CLDN22 INADL PARD3
FBLIM1 PVRL2 FERMT2 CLDN23 PVRL4 CRB3 CADM1 PARD6G PARD6B PARVB PARD6A PVRL3
PARVA SIRPG CDH9 CDH7 COL17A1 F11R CDH10 MPZ NLGN2 PARD6A CCM2 CTNND1
CLDN9 CLDN14 TGFB1 TGFB3 CDH1 JUP PVR CDH2 CDH3 CDH5 CTNNA1 NF2
HNF4A MLLT4 CDH4 CDH6 CDH8 CDH11 CDH12 CDH13 CDH15 CLDN15 CLDN12 CLDN17
CLDN18 CLDN20 ACTB TGFB2 ACTG1 CXADR SMAD3 CDH18 PVRL1 CDH24 NLGN4X CADM3
CADM2 MPP5 CLDN22 INADL PARD3 PVRL2 CLDN23 PVRL4 CRB3 CADM1 PARD6G PARD6B
PARD6A PVRL3 CDH9 CDH7 HEG1 F11R CDH10 ROCK2 EPHA3 EFNA5 ROCK1 MACF1
GJB1 GJB2 CTNNA1 GJC1 GJD3 CTNNA1 JUB THY1 TESK2 LAMA5 THY1 BCL2
ACTN1 ACTN2 ACTN3 PTK2B PTPRK TRIP6 JUB DLC1 TESK2 SORBS1 TAOK2 PLEKHA7
KIFC3 CAMSAP3 SDC4 SDC4 KDR SMAD3 PTPRJ SFRP1 TSC1 EPB41L5 KRT14
LAMC1 KRT5 ITGA6 CD151 DST LAMB3 LAMC2 LAMA3 ARHGAP6 THBS1 ACVRL1
MMP14 PTEN CTNND1 CDH1 JUP PVR DSP CDH2 CDH3 CDH5 CTNNA1 MLLT4
CDH4 CDH6 CDH8 CDH11 CDH12 CDH13 CDH15 ACTB ACTG1 CDH18 PVRL1 CDC42
CDH24 CADM3 CADM2 PVRL2 PVRL4 CADM1 PVRL3 CDH9 CDH7 CDH10 NUMBL STRN
CLDN9 CLDN14 WNT11 ITGB1 CDH1 APC ARL2 PRKCI CLDN15 CLDN12 CLDN17 CLDN18
CLDN20 DLG1 MPP7 FRMPD2 MTDH MPP5 CLDN22 INADL CLDN23 TBCD CRB3 PARD6G
PARD6B ECT2 PARD6A F11R SMAD7 VCL TBCD ZNF703 GNPAT CD9 CNTNAP1
AKT2 AKT2 CBLL1 MAPK1 ILK RRAS2 SMAD3 PLD1 AKT2 CBLL1 PTK2B APC
PIK3R1 PTK2B AKT2 PIK3R1 ERBB4 APC CSF1 ITGB1 RRAS2 RHOC ITGB1 C3AR1
SMAD3 FLT1 JAK2 PDPN MYO1F CCL24 PODXL CYR61 ADAM10 PLD2 SNAI2 CREB3
SPAG9 FGFR1OP ONECUT2 WNT11 EGFR F10 PDGFB INS COL1A1 CXCL10
FGF1 EDN1 ITGB1 INSR ITGAV LAMB1 IGF1R RHOC F7 ADRA2A VIL1 CSF1
PDGFRB FGR FURIN BMP2 TDGF1 F3 PDGFRA FER FLT1 S1PR1 EPHA1 DRD1
APC F2R MAPK1 CORO1A AKT2 IRS1 CCR2 CCL11 AIF1 F2RL1 CDH13 BCAR1
RRAS2 GNB2L1 ADAM8 CX3CL1 ADAM17 SMAD3 ROR2 MAP2K1 FOXF1 TRIM32 PLD1 ILK
PTK2B ERBB4 TRIP6 C3AR1 CXCL12 DKFZp686D0662 CBLL1 PDPN SYNE2 PTP4A1 HBEGF
WNT5B CXCL16 ZNF703 SPHK1 ONECUT1 SUN2 AIF1 CCL26 IRS2 ANGPTL3
VEGFA MESP2 MESP1 TGFBR1 PPAP2A PPAP2B TGFB1 HMGCR ITGB1 TGFBR1 CXADR FOXC1
CXCL12 CCR2 BMPER CCL5 PECAM1 SAA1 CCL2 CCL5 XCL1 ADAM8 CX3CL1 CXCL16
CKLF CCL2 GIPC1 PLEKHG5 GIPC1 TNFSF12 CALCA SCG2 S100P DPP4 S100A2
NOS3 PRSS3 PRKX CDH13 PTEN FAP CYP1B1 TRY6 GPR124 HIF1A ACVR1 NRP2
ACVR1 ACVR1 ISL1 ACVR1 LAMA5 TBX1 ZEB2 NRP2 FOXD2 FGF19 RET EDN3
KITLG EDNRB GDNF HTR2B GBX2 SOX8 ISL1 EFNB1 ACVR1 FOXD4 SEMA3F SHH
HIF1A FOXD1 FOXD4L6 FOXD4L5 FOXD4L4 NRTN SMO SEMA3C OVOL2 FOXD4L1 LEF1 FOXD3
PAX3 FOXD4L2 AXL TYRO3 MPP1 NOD2 MPP1 JAM3 NOD2 MYH10 SDCBP OPHN1
MYH10 CD2AP FUT7 RELN ARX LHX6 NRP1 HSPB1 NR4A1 EGR3 PRKD1 PRKD2
PDGFRB C3AR1 THBS1 CCL2 CCL5 CX3CL1 C3AR1 CMKLR1 RARRES2 MACF1 SLIT2 TNF
SELP SELE VCAM1 LEP ROCK1 SELPLG CHST4 PODXL2 DRD2 DRD1 CNTN2 DRD2
ARX LHX6 NR2E1 TSPO AZU1 TSPO TGFB2 NDN NR2E1 MMP9 FGF7 ADAM9
HBEGF CXCL12 TNR FOXB1 B4GALT1 CD34 ITGA6 AIMP1 PIK3R2 PODXL ANGPT2 SLC16A3
CCL25 DOK2 SLC16A8 F2 NRAS HRAS KRAS IL1B COL1A1 FN1 MMP1 PROC
APOB ATP1B1 ITGB3 ITGB2 ICAM1 ITGB1 LCK FYN CD2 ITGAV THBD PROS1
YES1 LYN COL1A2 SLC3A2 ELANE ITGA5 DBH CD48 ITGAM SRC ITGA4 SELL
ATP1B2 B4GALT1 SELP SPN PECAM1 PLCG1 CD58 ITGAL ITGAX MAG ITGA6 ITGA3
MSN PIK3R1 CD34 PTPN6 SHC1 FCER1G L1CAM MYH9 BSG PIK3CA PIK3CB SLC16A1

ATP1B3	F2RL1	JAM2	PPIA	GRB2	CXADR	SIRPA	OLR1	SLC7A9	SLC7A5	TEK	CAV1
PTPN11	SOS1	CD47	MERTK	AIMP1	PPIL2	ROCK1	SELPLG	GAS6	GRB14	GRB7	ANGPT1
AMICA1	CD177	NKX2-3	SLC7A6	INPP5D	ESAM	JAM3	CD244	GP6	TREM1	SLC7A10	SIRPG
SLC7A8	CD84	SLC7A7	SLC7A11	ANGPT4	F11R	NANOS1	FAT2	GREM1	SLIT2	S100A7	S100A14
ILK	SLIT2	SERPINE1		IGFBP3	IGFBP5	LRP1	ILK	ADIPOQ	TRIB1	ANGPT2	TGFB1
APOE	THBS1	FGF2	AGTR2	VASH1	DLL4	GDF2	ANGPT4	VEGFA	SELP	SELE	ZP3
BDKRB1	ADAM8	MADCAM1		MIA3	SLIT2	PDGFRB	HGF	HOXB9	ENG	HMGB2	AGTR1
ARRB2	EPHB1	ITGA1	BCAR1	RHOG	ARHGEF16		DOCK4	ELMO2	LEF1	ARX	SLIT1
SLIT3	SLIT2	THBS4	SIX1	SIX4	LBP	SLIT2	ROBO1	RTN4	RTN4	PDGFB	PDGFA
PDGFRB	C5	SELE	ADAM8	JAM3	JUB	LAMA3	AKT1	GAB1	LAMA4	GNA13	LAMA2
LAMA5	UNC5C	NTN1	TGFB1	LMNA	SERPINE2		EDN3	LAMA2	LAMA1	AKT2	PRKX
SST	RHOA	TMSB4X	RAC1	JAG1	CDK5	NEXN	MAP3K1	ENPP2	GNA13	LAMA4	LAMA3
AMOT	WDR44	LAMA3	MINK1	ROBO4	JUB	PARD6B	SRCIN1	RTN4	TBCCD1	ABI3	JAG2
CCL21	FIGF	CCL5	VEGFA	VEGFB	VEGFC	XCL1	TNFSF11	PDGFB	CALCA	IL6	IL6R
CCL2	FLT1	TNFRSF11A		CCR2	RPS6KB1	NRP1	VTN	IGF1	BCL2	CCL5	F3
RPS6KB1	IL6ST	P2RY2	RAPGEF4	HIST1H2BA		EFNA1	NF1	EPHA2	ACVRL1	KRIT1	SLIT2
BMP10	APOH	THBS1	NR2F2	PTPRM	ACVRL1	GDF2	SELP	ROBO4	ABHD6	ABHD6	ACAN
TIE1	THY1	SRF	ABR	SLC9A3R1		SMAD7	ALOX15B	BMP10	WNT11	PDGFB	THY1
SERPINE1		ABHD2	TPM1	RAP2A	RRAS	BCL2	BCR	SRF	DRD2	VCL	NF1
EPHA1	DRD1	DRD5	IGFBP5	NF2	TIE1	ACVRL1	NKX2-1	CX3CR1	PTEN	RAP2B	ARAP3
PTPRJ	ABR	NOG	DAG1	PTPRK	SHH	ADIPOQ	MIA3	RNF20	DRD2	PODN	SFRP1
SCAI	ARAP3	ROBO4	SFRP2	CNN2	TBX5	CITED2	ABHD6	GTPBP4	CHRD	TIE1	EGFL7
NISCH	RAP2C	CLIC4	STK24	PLCB1	AZU1	ATP5B	CCR7	CCL19	MESP1	PLXNA2	ADAM10
CXCL13	S100A7	WNT5A	CCR2	XCL1	ADAM17	MESP1	HDAC5	C5	ZAP70	WNT7A	CX3CL1
MCC	SEMA3A	DAB2IP	NUP85	NUP85	SAA1	CCL2	CCL5	AZU1	EDN2	EDNRB	SFTPD
CX3CR1	NUP85	CKLF	PPARD	KRT2	PPARD	KPG_004	FERMT1	AMOT	FOXH1	CER1	AMOT
NODAL	WNT8A	WNT5B	MIXL1	SERPINE1		S100A7	CCR2	CXCL12	PLA2G7	S100A14	CCR3
CCL11	PIP5K1A	ZFAND5	SGPL1	ARID5B	PIP5K1A	TNS1	SCHIP1	CUZD1	EPB41L5	TNFRSF12A	
OGDH	SLIT1	OGDH	LRRK2	GAS6	TOP2B	MET	NR2F2	APBB2	PTK2	PEX5	PAFAH1B1
NR4A2	FEZF1	DRGX	CHL1	NR4A2	FZD3	FYN	PTK2	FYN	PTK2	FYN	PTK2
MYH10	PSEN1	DCX	GAS6	TOP2B	APBB2	ROBO3	PEX5	PEX7	DCX	TLX3	GFRA3
KATNA1	CDKL5	NTN1	CCK	NR2F1	FGFR1	GJA1	NR2F2	ITGA3	AXL	CCKAR	MYH10
NR4A2	NKX2-1	LHX1	PSEN1	MNX1	ASCL1	CCR4	YWHAE	RELN	CDK5	CNTN2	ALKBH1
PRKG1	CDK5R1	TWIST1	NTRK3	VAX1	BARHL1	KIAA0319		NR4A2	MARK2	NAV1	MDGA1
DNER	NDNF	DYX1C1	ESR2	NRCAM	ATOH1	PEX13	ROBO3	ARX	PHOX2B	NDN	TUBB2B
BARHL1	NDEL1	NEUROG2		CELSR2	NEUROD4		DISC1	BARHL2	CELSR1	CELSR3	MARK1
SATB2	FEZF1	CXCL12	CXCL13	TBX5	FMNL1	PDGFB	EPHA8	VEGFC	ANKS1A	PDGFB	TGFB1
THBS1	PRKCA	PLCG1	AKT1	VEGFC	ANGPT1	ANGPT4	PRKDC	KIT	KITLG	PRKDC	ICAM1
ADAM8	CYR61	GATA3	TBX21	IL8	CSF3R	IFNG	IL1B	SAA1	PLA2G1B	ITGB2	EDN1
IL8	CCL2	EDN3	CXCL3	EDN2	C5AR1	CXCR2	FCER1G	SYK	XCL1	NCKAP1L	CXADR
CX3CL1	AMICA1	CKLF	CCR2	WASF2	CXCL12	LEF1	SLIT2	AGER	TGFB1	THBS1	AGER
IL33	ADA	HMOX1	ADORA1	HOXA7	CAMK1D	POU3F2	CDK5R1	DIXDC1	NDEL1	LHX6	FSCN1
RPS6KB1	NCK1	CDH2	FSCN1	CDH2	FSCN1	TNS3	NCK1	TNS3	NCK1	CTHRC1	ITGA4
NCK2	CLASP2	BCAR1	LAMB1	NCK2	ASTN1	VAV3	GSK3A	BCAR1	PODXL	ASTN1	ITGB1BP1
NRP1	LAMA5	PLXNB1	NCK2	NRD1	PROP1	PRPF40A	PAK4	FN1	ANG	ITGB1	CDK1
THBS1	LAMC1	FGFR1	PSG2	CEACAM1		JUP	PVR	NCK1	ENG	FLT1	CDH2
HOXA5	EFNA1	COL5A1	FGFR4	RPS6KB1	APC	CD24	EPHA3	IL12A	IL12B	BDKRB1	GSK3A
VAV2	EPHB3	BCAR1	PTEN	TGFB2	BTG1	TGFBR3	ENPEP	BAMBI	PTK7	FOXE3	DGKZ
CUL3	SHROOM2		TNFAIP1	SCRIB	DOCK1	HES1	FAT1	PTPRK	FSCN1	GAB4	CCDC88A
PAX3	CDC42BPA		LRRC16A	TNS3	ARC	SRGAP1	FMNL3	WWC1	PARP9	SCYL3	RASGEF1A
USP33	NANOS1	KCTD13	MYO18A	TMEM18	SH3KBP1	RHBDF1	CTHRC1	NODAL	PPP1R9B	PIP5K1A	FUT8
PEAK1	ABI2	PAK7	ZRANB1	LIMD1	VAV3	TAOK2	FAM40B	TNN	CDC42BPB		NOX1
ITGB3	AAMP	NRP1	NRP2	AGT	ITGB3	EDN1	THBS1	ANXA3	BMP4	VEGFA	ALOX12
GATA3	FLT4	KDR	AAMP	BMPR2	ANGPT1	SCARB1	PROX1	FOXC2	ANGPT4	APOA1	HSPB1
GPX1	MYH9	SOX18	VHL	ID1	PTK2B	SCARB1	PEX5	EGFR	PSEN1	EGFR	EGFR
NKX2-1	CX3CR1	PSEN1	PEX13	CCR3	CCL5	SCG2	CCL11	FOXB1	CXCL10	IL6	F7
EDN3	EDN2	XCL1	F2RL1	ADAM17	XCL1	CCL2	CCR2	MMP14	DVL2	POU4F1	FOXB1
CCL21	HMGB1	CCL5	CXCR1	CXCR2	CCR1	CCR7	CCR2	CCR5	CCR6	CXCR4	TRPM4
CCL19	SRPX2	PTGS2	HDAC7	FOXC2	HDAC9	SRF	SLIT2	ITGB1	SRF	VEGFA	NR4A1
EFNB2	EPHB4	EGR3	ROBO1	HIF1A	FGF10	CTSH	FGF10	VIL1	CTSH	PLCG1	TAC1
TACR1	SOX9	TGFB2	BMPR2	HIF1A	EPB41L5	HDAC6	NR2E1	CDK5	LRP8	NR2E1	XCL1
NCKAP1L	EDNRA	C3AR1	CCL21	CD74	EDN1	IL8	LBP	EDNRA	CCR7	THBS4	XCL1
NCKAP1L	TIRAP	C3AR1	CAMK1D	CCL19	IL23A	PF4	S100A9	IL10	CORO1A	CX3CL1	IL16
MT-RNR2	LYST	SBDS	STK10	MSN	MET	CCR7	JUB	ITGA5	COL5A1	MSX2	ACVRL1
MMP12	SCNN1B	SCNN1G	ADAM17	JUB	HBEGF	PLAU	PDGFA	ACE	HDAC5	ANXA2P2	PLCD1
SHC1	ANGPT1	POFUT1	PTK2	HIF1A	MEIS1	FGFR1	RTN4	EPAS1	SCG2	C1GALT1	
PTK2B	SCG2	UBP1	C1GALT1		UBP1	FGF10	ANGPT1	PTK2B	PTK2B	PTK2	PTK2B
PKNOX1	MAPK14	MEIS1	THY1	FGFR1	MEIS1	EREG	LAMA5	FGF10	MAP3K7	HOXA3	TBX1
FIGF	HS6ST1	FZD6	NRP2	GREM1	SRPX2	FGF18	HAND1	PLAU	EGF	TGFA	COL4A1
FN1	PDGFA	THY1	HSPB1	SERPINE1		JUN	ATP5B	GPI	ITGAV	ANXA2	MMP2

ITGA5	HMOX1	IL8	FGF6	BMP4	CCL2	SCG2	CEACAM1		HOXB3	ANPEP	VEGFA
NCL	TYMP	S1PR1	SAT1	FGFR2	PTPRB	COL8A2	COL8A1	EPHB2	SHC1	S100A7	HOXA7
FGF9	MYH9	SOX18	KDR	GJA5	ACVRL1	COL15A1	VHL	ID1	ELK3	PIK3CA	PGF
VEGFC	MEOX2	MMP14	PRKX	VAV2	EFNB2	EPHB3	EPHB4	EPHB1	PKNOX1	TBX4	PTEN
HAND2	TGFB2	ADAM8	SRPK2	JAG1	HSPG2	TEK	TNFAIP2	ENPEP	MFGE8	AIMP1	ADAM15
FZD5	AAMP	KLF5	IL18	VEZF1	PTK2B	CASP8	SHB	TGFBI	MED1	CYP1B1	DICER1
CSPG4	EPGN	CXCL17	ARHGAP22		TMPRSS6	PLXDC1	PNPLA6	ARHGAP24		PLCD3	STAB2
ROBO4	NRCAM	HOXB13	NUS1	APOLD1	MMP19	EPAS1	OVOL2	PDCD10	JAM3	NAA15	WNT5B
POFUT1	SOX17	PROK2	NRXN3	SH2D2A	TNFRSF12A		ESM1	RTN4	DLL4	C1GALT1	
ERAP1	UBP1	EGFL7	SLC12A6	ATPIF1	VAV3	DICER1	HEY1	NOX1	WASF2	NRXN1	ZC3H12A
ANGPTL6		KLF5	ECSCR	SERPINE1		FOXO6	BAI2	BAI3	TIE1	LECT1	KRIT1
BAI1	ANGPT2	BAI2	BAI3	ROCK2	LECT1	APOH	PF4	CXCL10	HRG	KLK3	COL4A2
CCL2	LIF	NPR1	NPPB	HOXA5	NF1	PTPRM	PML	THBS2	THBS4	TIE1	SERPINF1
CCR2	FASLG	CX3CR1	GTF2I	FOXO4	HHEX	CRHR2	ROCK1	AMOT	THBS2	VASH1	IL17F
TNMD	TIE1	SPINK5	STAB1	GHRL	MEG3	GDF2	ANGPT4	B4GALT1	ITGB3	GPX1	SRF
B4GALT1	CX3CL1	DKFZp686D0662		SRPX2	PTGS2	HDAC7	FOXC2	HDAC9	TNFAIP3	SRF	SLIT2
ITGB1	SRF	VEGFA	NR4A1	EFNB2	EPHB4	EGR3	ROBO1	MAPK7	CXCL13	TSPAN12	KRT1
ERBB2	IL6	FGF2	HMOX1	RNH1	EFNA1	NF1	ADORA2B		EPHA2	CTNNB1	ID1
PROK1	MAPK7	SFRP1	GPR124	HTATIP2	CYR61	BMP4	ACVRL1	NRARP	BMPER	SEMA5A	CTNNB1
EDNRA	ENG	ACVR1	GNA13	FLT1	ENG	SRF	NRP1	FOXS1	EDN1	SRF	VEGFA
ENG	FLT1	EDNRA	TGFBR2	GBX2	PPP3R1	ACVR1	NFATC3	STK4	SEMA5A	GNA13	IHH
SHH	NRARP	SFRP2	RBM15	NOTCH4	FOXC2	LEF1	GDF2	TBX20	PLXND1	PPP3R1	CXCL12
NR2E1	HMOX1	DDAH1	GATA2	VASH2	ERAP1	NOS3	CCR3	C3AR1	TNFRSF1A		ANGPT2
TNFSF12	DDAH1	C3	C5	IL1A	IL1B	SERPINE1		FGF1	FGF2	HMOX1	ANXA3
CCL5	F3	MMP9	FLT1	PLCG1	TNFRSF1A		EPHA1	GATA2	NOS3	AQP1	KDR
WNT5A	GATA4	CX3CR1	CCL11	CCR3	BTG1	RHOB	CX3CL1	RUNX1	TWIST1	C3AR1	ECM1
HIF1A	DKFZp686N2176		DKFZp686D0662		ADM2	MTDH	VASH2	HIPK1	AGGF1	GATA6	SFRP2
ANGPTL4		HIPK2	SPHK1	GDF2	UTS2R	ANGPT4	NR2E1	ANGPTL3		FOXC2	FLT1
THBS1	FLT1	FLT4	NOTCH1	CDH13	JMJD6	CCBE1	GPR124	LEF1	MYLK3	CTNNBIP1	
FCER1A	FCER1G	PIK3CG	IL6	OSM	TAC1	IL6ST	PIK3CG	ADAM8	NPY5R	OSMR	CCR7
CHRNA7	SPECC1L	CALCRL	ADORA2A		NR1H3	ADORA2A		ADORA2A		NR1H3	ADORA2A
NR1H3	CALCRL	ABR	ADA	SERPINC1		IL2RA	APOE	SAA1	GBA	ADRB2	ELANE
BCR	ACP5	TNFRSF1B		TNFAIP3	NT5E	IL10	GATA3	ZFP36	AOAH	CNR2	SERPINF1
IL2	PRKCD	FOXF1	ABR	NR1H3	CALCRL	O3FAR1	CD276	CHRNA7	NR1H3	GHSR	SELS
NDFIP1	UACA	SHARPIN	GHRL	P2RX1	F3	MGST3	ALOX5	ALOX5AP	LTC4S	MGST2	C3
MASP1	SELS	INS	ANXA1	IL4	GSTP1	ADORA1	PPARG	ANXA1	INS	DUSP10	CD28
F3	ANO6	PTGER3	IL1A	EPHA3	TRPV1	PDE5A	PDE5A	CHIA	FCER1G	ADORA2B	
LBP	LTA	TNF	CXCL13	VNN1	S100A8	S100A9	THBS1	VCAM1	CCL11	UNC13D	CD44
HMOX1	ELANE	CCL5	IL2RA	HMGB1	IL20RB	PNMA1	IL25	F12	KLKB1	TNF	IL1B
CCL5	CNR1	PTGS2	PTGER3	PLA2G4A	LBP	AGER	STAT5B	IL1RL1	STAT5A	EDNRA	TNFRSF1A
JAK2	TLR4	PDE2A	MAPK13	TLR3	TLR2	IL33	SERPINE1		ACE	PLA2G2A	FABP4
TNFRSF1A		ZP3	TGM2	TNFSF4	EDNRA	IL12B	AGTR1	IL15	WNT5A	CCR2	STAT5A
PLA2G4A	STAT5B	NLRP12	IL2	CX3CL1	IL1RL1	CD47	PLA2G7	IL18	AGER	IL21	IL23A
TLR9	TLR7	C5	SELE	ADAM8	JAM3	IL20RB	SERPINE1		ZP3	CNR1	IL4
FOXP3	PRDX2	TNF	IL1B	LYN	LYN	TLR4	SLC7A2	STAT5B	TSC2	SAA1	SAA2
SAAL1	TFRC	PLSCR1	F8	F2	ASS1	SERPINA1		SERPINA3		INS	SAA1
CRP	APCS	FN1	ORM1	AHSG	TFRC	IL6	SERPINF2		IL6R	MBL2	CEBPB
IL1RN	ORM2	SAA3P	SAA4	STAT3	CEBPA	TSC2	STAT5B	REG3A	ITIH4	ASS1	SIGIRR
REG3G	CD163	SAAL1	MRGPRX1		APOL2	IL22	B4GALT1	VNN1	APOA2	S100A8	ALOX5
B4GALT1	VCAM1	TNFSF4	TACR1	DEFB1	ACVR1	KL	IRGM	C4B-1	C4A	NCF1B	RXRA
BMP6	C3	IGFBP4	TNFRSF1A		LAT	AKT1	TP73	IL8	CCRL2	NFKBIZ	TMEM23
CD14	CD14	BMPR1B	MECOM	SCN9A	SCN9A	CD14	P2RX7	MECOM	MS4A2	MAP2K3	C4B
TNFRSF1A		OLR1	TNFRSF1A		PDPN	C4B	F8VX64	C4A	CCL24	PIK3CD	CCRL2
CCL21	CCL22	CXCL11	IKBKB	NCR3	KDM6B	CHUK	TP73	CCL25	CCL16	MEFV	IRAK2
RIPK2	LIAS	CHST1	LY75	TPST1	TLR5	CRCP	RPS6KA5	RPS6KA4	ATRN	APOL3	IL18RAP
VNN1	LY86	SERPINA1		SERPINA3		C3	C5	KNG1	FOS	TGFB1	NGF
TNF	IFNA2	IL1A	CRP	ORM1	CXCL10	KLKB1	ANXA1	CYBB	ITGB2	S100A8	IL5
IL6	S100A9	CRH	CD14	CXCL1	LTA4H	C4A	C4B	PLA2G4B	IL8	CCL3	SPP1
BMP2	CCL4	CYBA	CCL2	SCG2	MIF	NCF1	IL9	ALOX15	SELP	SELE	CCL3L1
NPPB	CEBPB	ITGB6	TNFRSF1A		RXRA	NFKB1	CXCL2	CXCL3	AZU1	TAC1	ITGAL
BMP6	IL10	GAL	IGFBP4	CXCR1	CXCR2	FPR2	TACR1	PTAFR	F2R	CD40	PTX3
AOAH	ADORA2A		CD40LG	PRDX5	BDKRB2	AXL	ADORA1	CCR1	CCR7	ADORA3	EPHX2
IL13	HRH1	CCR2	TNFRSF4	XCR1	BDKRB1	MAP2K3	PIK3CG	CD97	SLC11A1	CCL11	CCR3
CCR4	CCR5	NDST1	AIF1	F2RL1	UCN	CCL23	CCL18	HDAC4	CARD18	TIRAP	CXCR4
LYZ	RAC1	ADAM8	OLR1	KCNJ10	ELF3	CCL20	CCL8	CCL7	CXCL6	S100A12	TNFAIP6
MS4A2	MECOM	RELA	REG3A	AOX1	CXCL9	IL10RB	AIMP1	NFATC3	NFX1	NMI	NFE2L1
NFATC4	AGER	TLR1	LTB4R	GPR68	SMAD1	IL17A	CAMK4	C3AR1	AOC3	CDO1	SPHK1
C4A	DARC	THEMIS2	IL23R	GGT5	NFRKB	C4B	REG3G	TRIL	PXK	CD163	TICAM2
PDPN	EVI1	CAMK1D	TICAM1	SCUBE1	AFAP1L2	CHST4	ABCF1	NFAM1	IL27	CCL4L2	NFKBID
IL17D	BLNK	CCL17	HIST1H2BA		KLRG1	ITCH	NLRP3	IL17F	CD180	S1PR3	CCL13

MGLL	CCL19	CLEC7A	TLR10	NFKBIZ	SIGLEC1	IL22	TOLLIP	HRH4	CYP4F11	PROK2	MMP25
IL1RAP	NOX4	TLR8	STAB1	SPHK1	PLA2G2E	IL17C	IL36A	TBK1	IL17B	PARP4	HDAC9
CELA1	PLA2G2D	PLA2G4C	HDAC5	NOD1	CCL26	PLAA	CYSLTR1	TLR6	CHST2	NOX1	F11R
IKBKG	LY96	A2M	SERPING1		NOD2	PSMA1	PSMB4	IL12B	NOD2	SCGB1A1	RELA
SEMA7A	JAK2	SEMA7A	CALCA	AHSG	IL4	SCGB1A1	SELE	GGT1	TNFSF4	CMA1	AGTR1
PTGS2	BCL6	XCL1	SLC7A2	PSMA6	RELA	SETD6	PARK7	MGLL	MYD88	ACE2	NLRP1
NOD2	IL20	SBNO2	C3	FCER1G	TNFSF11	hRANKL 3		TNFRSF11A		HIF1A	TGFB1
F2R	HIF1A	MYLK3	CTNNBIP1		PIK3CG	IL6	OSM	TAC1	IL6ST	PIK3CG	ADAM8
NPY5R	OSMR	GAS6	PROC	F2RL2	TFPI	KLKB1	TFPI	KIAA1715		F2	DTNBP1
AP3B1	PROC	GAS6	F11	F2	EFEMP2	HPS5	AP3B1	THBD	PROC	F7	KIF2A
STXBP3	AP3B1	F2RL2	LEFTY2	PDE2A	PIK3R2	SH2B2	KIF3C	ATP2A1	KIF3B	ANGPT2	RAD51B
SLC16A3	ABCC4	MAFG	PDPK1	RAD51C	LAT	AKAP10	ACTN4	CALU	FIGF	KDM1A	DOK2
JAK2	MAFK	WDR1	GUCY1B2		DGKI	PDE5A	PDE9A	MFN2	KIF4A	RASGRP1	RAPGEF3
GNA14	SLC16A8	EFEMP2	SOD1	ABL1	CFD	PLAU	PLAT	SERPINA1		TIMP1	NRAS
HRAS	KRAS	PDGFB	EGF	TGFB1	IFNA1	IFNA2	IFNA10	IFNA7	IFNA21	IFNA5	IFNA14
IFNA17	IFNB1	HBD	HBE1	COL1A1	APOA1	C9	FN1	ALB	PPBP	PF4	TF
MMP1	RAF1	ALDOA	PDGFA	APOB	HRG	TP53	GNAI2	IFNA6	IFNA4	IFNA16	IGF1
ATP1B1	APP	ITGB3	ITGB2	SERPINB2		SERPINE1		PRKCG	SERPIND1		ITGB1
PRKCB	LCK	FYN	CD2	ITGAV	PROS1	PSAP	PFN1	YES1	LYN	THBS1	COL1A2
SLC3A2	ITGA2B	PLEK	ITGA5	SERPINF2		GNAI3	ANXA5	ADRA2A	CD63	CD48	SPARC
FGR	SRGN	MYB	TGFB3	PRKAR1A		CLU	IRF1	HSPA5	ITGAM	ACTN1	SRC
LAMP2	ITGA4	PRKAR2A		ANXA8	CD59	SELL	HGF	IRF2	ATP1B2	RAC2	VAV1
VEGFA	GATA1	SELP	SPN	PECAM1	PDE6A	ATP2A2	CD36	PLCG2	PRKCA	ITGA2	PRKACA
PTPN1	ADRA2B	VCL	PDE6G	ADRA2C	PLCG1	CD58	ATP2B1	RAB5A	ITGAL	ITGAX	C4BPB
MAG	FLNA	TBXA2R	CD9	PRKACG	PRKACB	PROZ	ITGA6	CFL1	ATP2B4	DGKA	GATA2
GATA3	PRKCH	CDK2	F2R	ITGA3	MAPK3	PIK3R1	MAPK1	ADORA2A		PTPN6	SHC1
NOS3	NOS1	GNA11	FCER1G	WEE1	GNA15	PRKAR1B	PRKAR2B	AKT1	L1CAM	ARRB2	SLC8A1
IFNA8	GUCY1A2		NOS2	ACTN2	BSG	PDE6B	GGCX	THPO	MPL	HNF4A	CSK
PIK3CA	PIK3CB	WAS	PTGIR	SYK	GATA4	CBX5	CRK	PLA2G4A	CAPZA2	CAPZB	P2RY1
TFPI2	PIK3CG	LMAN1	ARRB1	DGKG	VEGFB	VEGFC	ENTPD1	GNAQ	RAB27A	P2RX1	DGKE
KIF11	VAV2	DGKQ	CAPZA1	SLC16A1	ATP1B3	PDE1A	BCAR1	JAM2	SLC8A3	GNG2	ACTB
CDC42	RAP1B	RHOA	TGFB2	CALM3	TMSB4X	RHOB	RAP1A	GNB1	PPIA	GRB2	RAC1
GNAS	GNAI1	YWHAZ	ACTG1	TUBA4A	HIST1H3G		HBB	HBG1	HBG2	CXADR	SIRPA
OLR1	SLC7A9	RHOG	H3F3B	CDK5	PDE1B	CAP1	SLC7A5	ATP2B2	GUCY1A3		GUCY1B3
PRKCE	CENPE	KIF23	TEK	GNA12	CAV1	PRKCQ	PTK2	PRKCZ	PRKCD	PTPN11	KLC1
SOS1	CD47	KCNMA1	KIF5A	STX4	MERTK	LCP2	MMRN1	PRKG2	PABPC4	PPIL2	PDE3B
TRPC3	HDAC1	ITPK1	DGKZ	STIM1	PRKG1	LRP8	DOCK1	SELPLG	GNA13	GAS6	PDE3A
GRB14	GRB7	ITPR2	ITPR3	ITPR1	KIF22	ANGPT1	SHH	JMJD1C	MAPK14	KCNMB1	NFE2
ATP2B3	DGKD	KIF4B	DOCK11	HABP4	DGKK	PIK3R6	LRRC16A	HIST2H3A		RASGRP2	APBB1IP
KCNMB4	DGKH	AMICA1	HPS6	SCUBE1	ZFPM1	KIF2B	CD177	DAGLB	DOCK8	KIF18A	CABLES1
ZFPM2	SCG3	PIK3R5	TTN	RAPGEF4	SLC7A6	PIK3R3	AKAP1	HDAC2	INPP5D	KIFAP3	HPS1
GATA6	ATP2A3	ESAM	PHF21A	ORAI1	DTNBP1	DOCK6	CPB2	F2RL3	SIN3A	KIF2C	MGLL
KIFC1	GATA5	JAM3	POTEKP	DOCK9	CD244	LNP	KLC2	RACGAP1		ZFYVE20	P2RY12
EHD1	KIF9	GP6	PDE11A	TRPC7	TREM1	KCNMB3	HPS4	F13A1	SH2B1	PLSCR4	VPS45
SLC7A10	KIF15	EHD3	EHD2	HMG20B	SIRPG	SLC7A8	CD84	AK3	RCOR1	VAV3	PLDN
BRPF3	KIF26A	MAFF	SLC7A7	PROCR	SLC8A2	SLC7A11	HPS5	SH2B3	TRPC6	PDE10A	ANGPT4
TLN1	KIF3A	DAGLA	F11R	KCNMB2	MRVI1	DGKB	WNT7A	B4GALT1	ITGB3	GPX1	SRF
B4GALT1	CX3CL1	DKFZp686D0662		F9	F10	F7	TFPI	F3	MYH10	MYH10	TRIM72
MYOF	P2RX1	MGST3	ALOX5	ALOX5AP	LTC4S	MGST2	MASP1	INS	DUSP10	ANXA2P2	F2
PLG	PLAU	PLAT	HRG	KRT1	SERPINB2		SERPINE1		ANXA2	GP1BA	SERPINF2
PLAUR	TMPRSS6	SERPINE2		RPS6KB1	MET	F2RL2	NGFR	MDK	CASP3	SERPINE2	
CD81	ADM	CTSB	CD81	CTSB	CD81	MDK	FGFR1OP2		F2RL2	NRP1	KLK8
F2	TGFB1	FN1	PDGFA	VWF	WNT1	CYP1A1	GPX1	CTSB	NGFR	ABHD2	PATE4
CLU	VCAN	F3	GFAP	ITGB4	GAP43	MDK	FGF7	ACHE	RPS6KB1	TNC	F2R
PAX6	CTGF	PEBP1	CCR1	ADORA3	ADM	CCR2	CASP3	SLC1A3	SLC1A2	SOX2	CX3CR1
CD81	RAC1	CDK5	POU5F1	ID3	DST	HHEX	GRIN2A	AIMP1	GRIN2C	AGER	
DKFZp686D0662		HOXB13	KLK6	F2RL3	SMO	FGFR1OP2		PLLP	LYVE1	CD28	F3
ANO6	CHIA	FOXF1	VTN	ADRA2A	HBEGF	CXCL13	VNN1	S100A8	S100A9	THBS1	VCAM1
CCL11	WNT7A	FZD7	IGF1	UNC13D	CCL5	F2	F12	APOH	SERPINE1		THBS1
F7	CD36	F2R	PRDX2	NFE2L2	HPSE	IL2RA	HMGB1	IL20RB	PNMA1	IL25	TNF
IL1B	CCL5	CNR1	PTGS2	PTGER3	PLA2G4A	F8	F2	F9	F10	A2M	KNG1
APOH	F11	KLKB1	VWF	SERPING1		GP1BA	GP1BB	GP9	GP5	PRCP	C1QBP
AGER	STAT5B	IL1RL1	STAT5A	EDNRA	TNFRSF1A		JAK2	TLR4	PDE2A	MAPK13	TLR3
TLR2	IL33	SERPINE1		ACE	PLA2G2A	FABP4	TNFRSF1A		ZP3	TGM2	TNFSF4
EDNRA	IL12B	AGTR1	IL15	WNT5A	CCR2	STAT5A	PLA2G4A	STAT5B	NLRP12	IL2	CX3CL1
IL1RL1	CD47	PLA2G7	IL18	AGER	IL21	IL23A	TLR9	TLR7	FZD6	FGB	ENTPD1
PIK3CB	PIK3CB	PIK3CB	FGA	MERTK	GNA13	STXBP3	F2RL2	LEFTY2	PDE2A	PIK3R2	ATP2A1
PLSCR1	ABCC4	PDPK1	LAT	ACTN4	CALU	FIGF	WDR1	GUCY1B2		DGKI	PDE5A
PDE9A	RASGRP1	GNA14	SOD1	F8	F13A1	CFD	PLG	SERPINA1		A2M	TIMP1
KNG1	PDGFB	EGF	TGFB1	COL1A1	COL3A1	APOA1	FGA	FGB	FGG	SAA1	FN1

ALB	PPBP	TF	RAF1	ALDOA	PDGFA	APOB	GNAI2	IGF1	APP	ITGB3	SERPINE1
PRKCG	SERPING1		IL6	PRKCB	LCK	FYN	PROS1	PSAP	PFN1	LYN	THBS1
COL1A2	ITGA2B	PLEK	SERPINF2		GNAI3	CD63	SPARC	FGR	SRGN	TGFB3	CLU
HSPA5	F5	ACTN1	SRC	LAMP2	HGF	GP9	RAC2	VAV1	VEGFA	SELP	PECAM1
PDE6A	ATP2A2	CD36	PLCG2	PRKCA	VCL	PDE6G	ATP2B1	IL11	FLNA	TBXA2R	CFL1
ATP2B4	DGKA	PRKCH	CD40	MAPK3	PIK3R1	MAPK1	PTPN6	NOS3	NOS1	CD40LG	GNA11
FCER1G	AXL	GNA15	AKT1	ARRB2	SLC8A1	GUCY1A2		NOS2	ACTN2	PDE6B	GP5
THPO	MPL	PIK3CA	PIK3CB	PTGIR	SYK	PLA2G4A	P2RY1	PIK3CG	ARRB1	DGKG	VEGFB
VEGFC	GNAQ	P2RX1	DGKE	VAV2	DGKQ	PDE1A	SLC8A3	GNG2	RHOA	TGFB2	CALM3
TMSB4X	RHOB	GNB1	PPIA	RAC1	GNAS	GNAI1	YWHAZ	TUBA4A	CX3CL1	RHOG	PDE1B
CAP1	ATP2B2	GUCY1A3		GUCY1B3		PRKCE	GNA12	PRKCQ	PRKCZ	PRKCD	PTPN11
TYRO3	KCNMA1	STX4	MERTK	LCP2	MMRN1	PRKG2	PDE3B	TRPC3	DGKZ	STIM1	PRKG1
LRP8	GNA13	GAS6	PDE3A	ITPR2	ITPR3	ITPR1	MAPK14	KCNMB1	ATP2B3	DGKD	HABP4
DGKK	PIK3R6	FGA	BLOC1S3	ADAMTS13		RASGRP2	ENTPD1	KCNMB4	DGKH	DAGLB	SCG3
PIK3R5	TTN	PIK3R3	ATP2A3	ORAI1	F2RL3	MGLL	POTEKP	P2RY12	PDE11A	TRPC7	KCNMB3
VAV3	BRPF3	SLC8A2	TRPC6	PDE10A	TLN1	DAGLA	ENTPD2	KCNMB2	MRVI1	DGKB	GAP43
NINJ2	SERPINE1		FGF10	E5RH35	E5RJA8	E5RJP8	E5RJZ7	NINJ2	TIMP3	NINJ2	FGF10
PLG	SERPINE1		GSN	IGFBP1	CCNB1	TIMP3	NOTCH1	TM4SF4	GATM	NOTCH2	PRKCQ
ADAM15	INA	GSN	PLG	APOA5	IGSF10	MUSTN1	KLK6	NINJ1	NINJ2	SERPINA10	
NOTCH3	PGCP	SERPINE1		ZP3	IL4	FOXP3	PRDX2	CYR61	B4GALT1	WNT7A	FGF10
FZD7	B4GALT1	MMP12	KLK8	EPHA4	XYLT1	LYN	LYN	TLR4	SLC7A2	STAT5B	TSC2
SAA1	SAA2	SAAL1	TFRC	PLSCR1	F8	F2	ASS1	SERPINA1		SERPINA3	
INS	SAA1	CRP	APCS	FN1	ORM1	AHSG	TFRC	IL6	SERPINF2		IL6R
MBL2	CEBPB	IL1RN	ORM2	SAA3P	SAA4	STAT3	CEBPA	TSC2	STAT5B	REG3A	ITIH4
ASS1	SIGIRR	REG3G	CD163	SAAL1	MRGPRX1		APOL2	IL22	B4GALT1	VNN1	APOA2
S100A8	ALOX5	B4GALT1	VCAM1	TNFSF4	TACR1	DEFB1	ACVR1	KL	TNR	IRGM	C4B-1
C4A	NCF1B	RXRA	BMP6	C3	IGFBP4	TNFRSF1A		LAT	AKT1	TP73	IL8
CCRL2	NFKBIZ	TMEM23	CD14	CD14	BMPR1B	MECOM	SCN9A	SCN9A	CD14	P2RX7	MECOM
MS4A2	MAP2K3	C4B	TNFRSF1A		OLR1	TNFRSF1A		PDPN	C4B	F8VX64	C4A
CCL24	PIK3CD	CCRL2	CCL21	CCL22	CXCL11	IKBKB	NCR3	KDM6B	CHUK	TP73	CCL25
CCL16	MEFV	IRAK2	RIPK2	LIAS	CHST1	LY75	TPST1	TLR5	CRCP	RPS6KA5	RPS6KA4
ATRN	APOL3	IL18RAP	VNN1	LY86	SERPINA1		SERPINA3		C3	C5	KNG1
FOS	TGFB1	NGF	TNF	IFNA2	IL1A	CRP	ORM1	CXCL10	KLKB1	ANXA1	CYBB
ITGB2	S100A8	IL5	IL6	S100A9	CRH	CD14	CXCL1	LTA4H	C4A	C4B	PLA2G4B
IL8	CCL3	SPP1	BMP2	CCL4	CYBA	CCL2	SCG2	MIF	NCF1	IL9	ALOX15
SELP	SELE	CCL3L1	NPPB	CEBPB	ITGB6	TNFRSF1A		RXRA	NFKB1	CXCL2	CXCL3
AZU1	TAC1	ITGAL	BMP6	IL10	GAL	IGFBP4	CXCR1	CXCR2	FPR2	TACR1	PTAFR
F2R	CD40	PTX3	AOAH	ADORA2A		CD40LG	PRDX5	BDKRB2	AXL	ADORA1	CCR1
CCR7	ADORA3	EPHX2	IL13	HRH1	CCR2	TNFRSF4	XCR1	BDKRB1	MAP2K3	PIK3CG	CD97
SLC11A1	CCL11	CCR3	CCR4	CCR5	NDST1	AIF1	F2RL1	UCN	CCL23	CCL18	HDAC4
CARD18	TIRAP	CXCR4	LYZ	RAC1	ADAM8	OLR1	KCNJ10	ELF3	CCL20	CCL8	CCL7
CXCL6	S100A12	TNFAIP6	MS4A2	MECOM	RELA	REG3A	AOX1	CXCL9	IL10RB	AIMP1	NFATC3
NFX1	NMI	NFE2L1	NFATC4	AGER	TLR1	LTB4R	GPR68	SMAD1	IL17A	CAMK4	C3AR1
AOC3	CDO1	SPHK1	C4A	DARC	THEMIS2	IL23R	GGT5	NFRKB	C4B	REG3G	TRIL
PXK	CD163	TICAM2	PDPN	EVI1	CAMK1D	TICAM1	SCUBE1	AFAP1L2	CHST4	ABCF1	NFAM1
IL27	CCL4L2	NFKBID	IL17D	BLNK	CCL17	HIST1H2BA		KLRG1	ITCH	NLRP3	IL17F
CD180	S1PR3	CCL13	MGLL	CCL19	CLEC7A	TLR10	NFKBIZ	SIGLEC1	IL22	TOLLIP	HRH4
CYP4F11	PROK2	MMP25	IL1RAP	NOX4	TLR8	STAB1	SPHK1	PLA2G2E	IL17C	IL36A	TBK1
IL17B	PARP4	HDAC9	CELA1	PLA2G2D	PLA2G4C	HDAC5	NOD1	CCL26	PLAA	CYSLTR1	TLR6
CHST2	NOX1	F11R	IKBKG	LY96	A2M	SERPING1		STXBP3	PLEK	GATA1	PDGFRA
WNT3A	STXBP1	FERMT3	HIF1A	TGFB1	F2R	HIF1A	FCER1A	FCER1G	NTRK3	CCR7	CHRNA7
SPECC1L	CALCRL	ADORA2A		NR1H3	ADORA2A		ADORA2A		NR1H3	ADORA2A	
NR1H3	CALCRL	ABR	ADA	SERPINC1		IL2RA	APOE	SAA1	GBA	ADRB2	ELANE
BCR	ACP5	TNFRSF1B		TNFAIP3	NT5E	IL10	GATA3	ZFP36	AOAH	CNR2	SERPINF1
IL2	PRKCD	FOXF1	ABR	NR1H3	CALCRL	O3FAR1	CD276	CHRNA7	NR1H3	GHSR	SELS
NDFIP1	UACA	SHARPIN	GHRL	TNFAIP3	SERPINF2		F2	PLG	APOH	SERPINE1	
THBD	THBS1	SERPINF2		USF1	CPB2	F3	MYOD1	F11	F2	F11	GP1BA
F2R	F2RL1	CAV1	VKORC1	FOXA2	C3	SELS	INS	ANXA1	IL4	GSTP1	ADORA1
PPARG	ANXA1	RXRA	ISL1	JAK2	JUN	BCL2	VCAN	RXRA	CTNNA1	ISL1	C5orf13
RTN4RL1	RTN4RL2	CTNNA1	SERPINE1		PDE5A	PDE5A	PTGER3	IL1A	EPHA3	TRPV1	FCER1G
ADORA2B		LBP	LTA	TNF	CD44	HMOX1	STK24	PLG	F12	F11	KLKB1
ELANE	LBP	F12	KLKB1	MSTN	SOX15	PLAU	GPX1	ENO3	GJA1	MYF6	PAX7
MTPN	PLAUR	ANO6	IL20RB	C5	SELE	ADAM8	JAM3	F2	PDGFB	APOE	PDGFA
THBD	PDGFRA	NOS3	CNR1	MYOD1	SERPINE1		TNF	IL1B	KNG1	APOE	APOH
VTN	PROC	SERPINE1		EDN1	THBD	TSPAN8	SPP1	TSPO	SOD2	PCSK1	LYN
ERBB2	SOD2	SOD1	EPO	SOD2	ERBB2	ARG1	CDK1	LYN	FGF2	LGALS1	GIP
DRD2	ARF4	PCSK1	TSPO	MAP1B	GIPR	AIF1	MAX	ARG2	MAP2K1	SHH	NTRK3
LTC4S	DRD2	TXN2	UCK2	AIF1	PPARA	PDGFRA	SMAD1	SDC2	SDC2	SERPINB2	
GRHL3	POU2F3	SPARC	WNT5B	PPARA	WNT5B	SPARC	WNT5B	PPARD	EREG	TGFA	INS
IL1A	IL1B	PDGFA	ERBB2	ITGB3	S100A8	ADRB2	DCN	MMP3	ADRB1	FGF2	TPM1

DSP	PDGFRA	ENG	SDC1	NF1	FGF7	ERBB3	DRD5	LOX	SDC2	MSX2	TGFBR1
WNT5A	P2RY2	ELK3	SLC11A1	TGFB2	SMAD3	PPARD	FMOD	PPARA	MAP3K1	ITGA9	SMAD1
KGFLP2	KGFLP1	TIMP1	MIA3	FUT10	SDC2	C6orf89	ARHGEF19		GRHL3	SCARB1	DCBLD2
CNN2	KLF6	SPRR3	POU2F3	MACF1	VIL1	PLAU	VIL1	CNTF	SCARF1	NDEL1	NOD2
PSMA1	PSMB4	IL12B	NOD2	SCGB1A1	RELA	SEMA7A	JAK2	SEMA7A	CALCA	AHSG	IL4
SCGB1A1	SELE	GGT1	TNFSF4	CMA1	AGTR1	PTGS2	BCL6	XCL1	SLC7A2	PSMA6	RELA
SETD6	PARK7	MGLL	MYD88	ACE2	NLRP1	NOD2	IL20	SBNO2	TSPO	TNC	APOE
TNC	TSPO	MAP1B	CHST3	C3	FCER1G	PDPN	TLR4	PLEK	SELP	PDPN	JUB
ITGA5	COL5A1	MSX2	ACVRL1	MMP12	SCNN1B	SCNN1G	ADAM17	JUB	HBEGF	FOXC2	TNFSF11
hRANKL 3		TNFRSF11A		OMG							

List of genes in EMT signature (GO:0001837)

S100A4 BMP2 TRIM28 TGFB3 HGF BMP7 TGFB1 CTNNB1 TGFB2

List of genes in mesenchyme development signature (GO:0060485)

EOMES RTN4 WNT2 BMP2 TGFB2 TGFBR3 ADAM15 RTN4 WNT16 HES1 GREM1 EPHA3
BCL2 BMP7 BMPR1A TBX20 BMP2 SOX9 ISL1 LRP6 MYC HIF1A SNAI1 HGF
BMP7 S100A4 CTNNB1 TGFBR1 WNT5A SOX9 GSK3B HMGA2 WNT4 PPP3R1 TGFBR3 FOXF2
TRIM28 HIF1A HNRNPAB LEF1 AMELX PPP3R1 BMP7 SMAD4 OSR1 SMAD4 WT1
BASP1 PAX2 SIX1 OSR1 SIX4 LRP6 WNT8A HIF1A ACVR1 NRP2 ACVR1 ACVR1
ISL1 ACVR1 LAMA5 TBX1 ZEB2 NRP2 FOXD2 FGF19 RET EDN3 KITLG EDNRB
GDNF HTR2B GBX2 SOX8 ISL1 EFNB1 ACVR1 FOXD4 SEMA3F SHH HIF1A FOXD1
FOXD4L6 FOXD4L5 FOXD4L4 NRTN SMO SEMA3C OVOL2 FOXD4L1 LEF1 FOXD3 PAX3 FOXD4L2
EFNA1 NKX2-1 FOXA1 PPP2CA DAB2IP SFRP1 SFRP2 TBX5 FOXA2 OSR1 TBX5 BMP4
ERBB3 GATA4 FOXF1 CRELD1 TBX5 FOXS1 FOXC1 SFRP1 FOXC2 WNT8A HEYL MSX2
HEYL HEY1 BMP7 FGFR1 FGFR1 WNT11 HOXA5 FGFR2 FGF9 CTNNB1 WNT7B PTK7
SHH EFNA1 BMP7 SHH HAND2 EDNRA ALDH1A2 CYP26A1 SNAI2 ALDH1A2
EDN1 EDNRA SOX11 SOX9 HAND2 NRG1 FOXC1 CYP26A1 CYP26C1 RDH10 FOXC2 LRP6
HTR2B MEF2C FRZB WNT10A TGFB1I1 COL1A1 BMP2 NOTCH1 SMAD3 BAMBI SMAD4 TWIST1
SMAD2 BCL9L SMAD4 WWTR1 ZNF703 EPB41L5 LEF1 AXIN2 FGFR2 FOXF1 NKX2-5 FGFR1
ISL1 FGFR1 BMP2 BMP7 FGFR2 TGFBR1 ISL1 PLAUR FOXC1 NOG TCF21 WNT4
PAX2 OSR1

List of genes in immune cell infiltration signature (Yoshihara et al. 2013)

LCP2 LSP1 FYB PLEK HCK IL10RA LILRB1 NCKAP1L LAIR1 NCF2 CYBB PTPRC
IL7R LAPTM5 CD53 EVI2B SLA ITGB2 GIMAP4 MYO1F HCLS1 MNDA IL2RG CD48
AOAH CCL5 LTB GMFG GIMAP6 GZMK LST1 GPR65 LILRB2 WIPF1 CD37 BIN2
FCER1G IKZF1 TYROBP FGL2 FLI1 IRF8 ARHGAP15 SH2B3 TNFRSF1B DOCK2
CD2 ARHGEF6 CORO1A LY96 LYZ ITGAL TNFAIP3 RNASE6 TGFB1 PSTPIP1 CST7
RGS1 FGR SELL MICAL1 TRAF3IP3 ITGA4 MAFB ARHGDIB IL4R RHOH HLA-DPA1
NKG7 NCF4 LPXN ITK SELPLG HLA-DPB1 CD3D CD300A IL2RB ADCY7 PTGER4
SRGN CD247 CCR7 MSN ALOX5AP PTGER2 RAC2 GBP2 VAV1 CLEC2B P2RY14 NFKBIA
S100A9 IFI30 MFSD1 RASSF2 TPP1 RHOG CLEC4A GZMB PVRIG S100A8 CASP1 BCL2A1
HLA-E KLRB1 GNLY RAB27A IL18RAP TPST2 EMP3 GMIP LCK IL32 PTPRCAP
LGALS9 CCDC69 SAMHD1 TAP1 GBP1 CTSS GZMH ADAM8 GLRX PRF1 CD69 HLA-B
HLA-DMA CD74 KLRK1 PTPRE HLA-DRA VNN2 TCIRG1 RABGAP1L CSTA ZAP70
HLA-F HLA-G CD52 CD302 CD27

List of genes in stromal tissue signature (Yoshihara et al. 2013)

DCN PAPPA SFRP4 THBS2 LY86 CXCL14 FOXF1 COL10A1 ACTG2 APBB1IP SH2D1A SULF1
MSR1 C3AR1 FAP PTGIS ITGBL1 BGN CXCL12 ECM2 FCGR2A MS4A4A WISP1 COL1A2
MS4A6A EDNRA VCAM1 GPR124 SCUBE2 AIF1 HEPH LUM PTGER3 RUNX1T1 CDH5
PIK3R5 RAMP3 LDB2 COX7A1 EDIL3 DDR2 FCGR2B LPPR4 COL15A1 AOC3 ITIH3 FMO1
PRKG1 PLXDC1 VSIG4 COL6A3 SGCD COL3A1 F13A1 OLFML1 IGSF6 COMP HGF GIMAP5
ABCA6 ITGAM MAF ITM2A CLEC7A ASPN LRRC15 ERG CD86 TRAT1 COL8A2 TCF21
CD93 CD163 GREM1 LMOD1 TLR2 ZEB2 C1QB KCNJ8 KDR CD33 RASGRP3 TNFSF4
CCR1 CSF1R BTK MFAP5 MXRA5 ISLR ARHGAP28 ZFPM2 TLR7 ADAM12 OLFML2B
ENPP2 CILP SIGLEC1 SPON2 PLXNC1 ADAMTS5 SAMSN1 CH25H COL14A1 EMCN RGS4
PCDH12 RARRES2 CD248 PDGFRB C1QA COL5A3 IGF1 SP140 TFEC TNN ATP8B4 ZNF423
FRZB SERPING1 ENPEP CD14 DIO2 FPR1 IL18R1 HDC TXNDC3 PDE2A RSAD2
ITIH5 FASLG MMP3 NOX4 WNT2 LRRC32 CXCL9 ODZ4 FBLN2 EGFL6 IL1B SPON1
CD200

List of genes in response to wounding signature (GO:0009611)

MYLK3 CTNNBIP1 PIK3CG IL6 OSM TAC1 IL6ST PIK3CG ADAM8 NPY5R OSMR
GAS6 PROC F2RL2 TFPI KLKB1 TFPI KIAA1715 F2 DTNBP1 AP3B1 PROC
GAS6 F11 F2 EFEMP2 HPS5 AP3B1 THBD PROC F7 KIF2A STXBP3 AP3B1
F2RL2 LEFTY2 PDE2A PIK3R2 SH2B2 KIF3C ATP2A1 KIF3B ANGPT2 RAD51B SLC16A3 ABCC4
MAFG PDPK1 RAD51C LAT AKAP10 ACTN4 CALU FIGF KDM1A DOK2 JAK2 MAFK

WDR1 GUCY1B2 DGKI PDE5A PDE9A MFN2 KIF4A RASGRP1 RAPGEF3 GNA14 SLC16A8
EFEMP2 SOD1 ABL1 CFD PLAU PLAT SERPINA1 TIMP1 NRAS HRAS KRAS
PDGFB EGF TGFB1 IFNA1 IFNA2 IFNA10 IFNA7 IFNA21 IFNA5 IFNA14 IFNA17 IFNB1
HBD HBE1 COL1A1 APOA1 C9 FN1 ALB PPBP PF4 TF MMP1 RAF1
ALDOA PDGFA APOB HRG TP53 GNAI2 IFNA6 IFNA4 IFNA16 IGF1 ATP1B1 APP
ITGB3 ITGB2 SERPINB2 SERPINE1 PRKCG SERPIND1 ITGB1 PRKCB LCK
FYN CD2 ITGAV PROS1 PSAP PFN1 YES1 LYN THBS1 COL1A2 SLC3A2 ITGA2B
PLEK ITGA5 SERPINF2 GNAI3 ANXA5 ADRA2A CD63 CD48 SPARC FGR SRGN
MYB TGFB3 PRKAR1A CLU IRF1 HSPA5 ITGAM ACTN1 SRC LAMP2 ITGA4
PRKAR2A ANXA8 CD59 SELL HGF IRF2 ATP1B2 RAC2 VAV1 VEGFA GATA1
SELP SPN PECAM1 PDE6A ATP2A2 CD36 PLCG2 PRKCA ITGA2 PRKACA PTPN1 ADRA2B
VCL PDE6G ADRA2C PLCG1 CD58 ATP2B1 RAB5A ITGAL ITGAX C4BPB MAG FLNA
TBXA2R CD9 PRKACG PRKACB PROZ ITGA6 CFL1 ATP2B4 DGKA GATA2 GATA3 PRKCH
CDK2 F2R ITGA3 MAPK3 PIK3R1 MAPK1 ADORA2A PTPN6 SHC1 NOS3 NOS1
GNA11 FCER1G WEE1 GNA15 PRKAR1B PRKAR2B AKT1 L1CAM ARRB2 SLC8A1 IFNA8 GUCY1A2
NOS2 ACTN2 BSG PDE6B GGCX THPO MPL HNF4A CSK PIK3CA PIK3CB WAS
PTGIR SYK GATA4 CBX5 CRK PLA2G4A CAPZA2 CAPZB P2RY1 TFPI2 PIK3CG LMAN1
ARRB1 DGKG VEGFB VEGFC ENTPD1 GNAQ RAB27A P2RX1 DGKE KIF11 VAV2 DGKQ
CAPZA1 SLC16A1 ATP1B3 PDE1A BCAR1 JAM2 SLC8A3 GNG2 ACTB CDC42 RAP1B RHOA
TGFB2 CALM3 TMSB4X RHOB RAP1A GNB1 PPIA GRB2 RAC1 GNAS GNAI1 YWHAZ
ACTG1 TUBA4A HIST1H3G HBB HBG1 HBG2 CXADR SIRPA OLR1 SLC7A9 RHOG
H3F3B CDK5 PDE1B CAP1 SLC7A5 ATP2B2 GUCY1A3 GUCY1B3 PRKCE CENPE
KIF23 TEK GNA12 CAV1 PRKCQ PTK2 PRKCZ PRKCD PTPN11 KLC1 SOS1 CD47
KCNMA1 KIF5A STX4 MERTK LCP2 MMRN1 PRKG2 PABPC4 PPIL2 PDE3B TRPC3 HDAC1
ITPK1 DGKZ STIM1 PRKG1 LRP8 DOCK1 SELPLG GNA13 GAS6 PDE3A GRB14 GRB7
ITPR2 ITPR3 ITPR1 KIF22 ANGPT1 SHH JMJD1C MAPK14 KCNMB1 NFE2 ATP2B3 DGKD
KIF4B DOCK11 HABP4 DGKK PIK3R6 LRRC16A HIST2H3A RASGRP2 APBB1IP KCNMB4 DGKH
AMICA1 HPS6 SCUBE1 ZFPM1 KIF2B CD177 DAGLB DOCK8 KIF18A CABLES1 ZFPM2 SCG3
PIK3R5 TTN RAPGEF4 SLC7A6 PIK3R3 AKAP1 HDAC2 INPP5D KIFAP3 HPS1 GATA6 ATP2A3
ESAM PHF21A ORAI1 DTNBP1 DOCK6 CPB2 F2RL3 SIN3A KIF2C MGLL KIFC1 GATA5
JAM3 POTEKP DOCK9 CD244 LNP KLC2 RACGAP1 ZFYVE20 P2RY12 EHD1 KIF9
GP6 PDE11A TRPC7 TREM1 KCNMB3 HPS4 F13A1 SH2B1 PLSCR4 VPS45 SLC7A10 KIF15
EHD3 EHD2 HMG20B SIRPG SLC7A8 CD84 AK3 RCOR1 VAV3 PLDN BRPF3 KIF26A
MAFF SLC7A7 PROCR SLC8A2 SLC7A11 HPS5 SH2B3 TRPC6 PDE10A ANGPT4 TLN1 KIF3A
DAGLA F11R KCNMB2 MRVI1 DGKB WNT7A B4GALT1 ITGB3 GPX1 SRF B4GALT1 CX3CL1
DKFZp686D0662 F9 F10 F7 TFPI F3 MYH10 MYH10 TRIM72 MYOF P2RX1
MGST3 ALOX5 ALOX5AP LTC4S MGST2 MASP1 INS DUSP10 ANXA2P2 F2 PLG PLAU
PLAT HRG KRT1 SERPINB2 SERPINE1 ANXA2 GP1BA SERPINF2 PLAUR
TMPRSS6 SERPINE2 RPS6KB1 MET F2RL2 NGFR MDK CASP3 SERPINE2 CD81
ADM CTSB CD81 CTSB CD81 MDK FGFR1OP2 F2RL2 NRP1 KLK8 F2
TGFB1 FN1 PDGFA VWF WNT1 CYP1A1 GPX1 CTSB NGFR ABHD2 PATE4 CLU
VCAN F3 GFAP ITGB4 GAP43 MDK FGF7 ACHE RPS6KB1 TNC F2R PAX6
CTGF PEBP1 CCR1 ADORA3 ADM CCR2 CASP3 SLC1A3 SLC1A2 SOX2 CX3CR1 CD81
RAC1 CDK5 POU5F1 ID3 DST HHEX GRIN2A AIMP1 GRIN2C AGER DKFZp686D0662
HOXB13 KLK6 F2RL3 SMO FGFR1OP2 PLLP LYVE1 CD28 F3 ANO6 CHIA
FOXF1 VTN ADRA2A HBEGF CXCL13 VNN1 S100A8 S100A9 THBS1 VCAM1 CCL11 WNT7A
FZD7 IGF1 UNC13D CCL5 F2 F12 APOH SERPINE1 THBS1 F7 CD36
F2R PRDX2 NFE2L2 HPSE IL2RA HMGB1 IL20RB PNMA1 IL25 TNF IL1B CCL5
CNR1 PTGS2 PTGER3 PLA2G4A F8 F2 F9 F10 A2M KNG1 APOH F11
KLKB1 VWF SERPING1 GP1BA GP1BB GP9 GP5 PRCP C1QBP AGER STAT5B
IL1RL1 STAT5A EDNRA TNFRSF1A JAK2 TLR4 PDE2A MAPK13 TLR3 TLR2 IL33
SERPINE1 ACE PLA2G2A FABP4 TNFRSF1A ZP3 TGM2 TNFSF4 EDNRA IL12B
AGTR1 IL15 WNT5A CCR2 STAT5A PLA2G4A STAT5B NLRP12 IL2 CX3CL1 IL1RL1 CD47
PLA2G7 IL18 AGER IL21 IL23A TLR9 TLR7 FZD6 FGB ENTPD1 PIK3CB PIK3CB
PIK3CB FGA MERTK GNA13 STXBP3 F2RL2 LEFTY2 PDE2A PIK3R2 ATP2A1 PLSCR1 ABCC4
PDPK1 LAT ACTN4 CALU FIGF WDR1 GUCY1B2 DGKI PDE5A PDE9A RASGRP1
GNA14 SOD1 F8 F13A1 CFD PLG SERPINA1 A2M TIMP1 KNG1 PDGFB
EGF TGFB1 COL1A1 COL3A1 APOA1 FGA FGB FGG SAA1 FN1 ALB PPBP
TF RAF1 ALDOA PDGFA APOB GNAI2 IGF1 APP ITGB3 SERPINE1 PRKCG
SERPING1 IL6 PRKCB LCK FYN PROS1 PSAP PFN1 LYN THBS1 COL1A2
ITGA2B PLEK SERPINF2 GNAI3 CD63 SPARC FGR SRGN TGFB3 CLU HSPA5
F5 ACTN1 SRC LAMP2 HGF GP9 RAC2 VAV1 VEGFA SELP PECAM1 PDE6A
ATP2A2 CD36 PLCG2 PRKCA VCL PDE6G ATP2B1 IL11 FLNA TBXA2R CFL1 ATP2B4
DGKA PRKCH CD40 MAPK3 PIK3R1 MAPK1 PTPN6 NOS3 NOS1 CD40LG GNA11 FCER1G
AXL GNA15 AKT1 ARRB2 SLC8A1 GUCY1A2 NOS2 ACTN2 PDE6B GP5 THPO
MPL PIK3CA PIK3CB PTGIR SYK PLA2G4A P2RY1 PIK3CG ARRB1 DGKG VEGFB VEGFC
GNAQ P2RX1 DGKE VAV2 DGKQ PDE1A SLC8A3 GNG2 RHOA TGFB2 CALM3 TMSB4X
RHOB GNB1 PPIA RAC1 GNAS GNAI1 YWHAZ TUBA4A CX3CL1 RHOG PDE1B CAP1
ATP2B2 GUCY1A3 GUCY1B3 PRKCE GNA12 PRKCQ PRKCZ PRKCD PTPN11 TYRO3
KCNMA1 STX4 MERTK LCP2 MMRN1 PRKG2 PDE3B TRPC3 DGKZ STIM1 PRKG1 LRP8

GNA13 GAS6 PDE3A ITPR2 ITPR3 ITPR1 MAPK14 KCNMB1 ATP2B3 DGKD HABP4 DGKK
PIK3R6 FGA BLOC1S3 ADAMTS13 RASGRP2 ENTPD1 KCNMB4 DGKH DAGLB SCG3 PIK3R5
TTN PIK3R3 ATP2A3 ORAI1 F2RL3 MGLL POTEKP P2RY12 PDE11A TRPC7 KCNMB3 VAV3
BRPF3 SLC8A2 TRPC6 PDE10A TLN1 DAGLA ENTPD2 KCNMB2 MRVI1 DGKB GAP43 NINJ2
SERPINE1 FGF10 E5RH35 E5RJA8 E5RJP8 E5RJZ7 NINJ2 TIMP3 NINJ2 FGF10 PLG
SERPINE1 GSN IGFBP1 CCNB1 TIMP3 NOTCH1 TM4SF4 GATM NOTCH2 PRKCQ ADAM15
INA GSN PLG APOA5 IGSF10 MUSTN1 KLK6 NINJ1 NINJ2 SERPINA10 NOTCH3
PGCP SERPINE1 ZP3 IL4 FOXP3 PRDX2 CYR61 B4GALT1 WNT7A FGF10 FZD7
B4GALT1 MMP12 KLK8 EPHA4 XYLT1 LYN LYN TLR4 SLC7A2 STAT5B TSC2 SAA1
SAA2 SAAL1 TFRC PLSCR1 F8 F2 ASS1 SERPINA1 SERPINA3 INS
SAA1 CRP APCS FN1 ORM1 AHSG TFRC IL6 SERPINF2 IL6R MBL2
CEBPB IL1RN ORM2 SAA3P SAA4 STAT3 CEBPA TSC2 STAT5B REG3A ITIH4 ASS1
SIGIRR REG3G CD163 SAAL1 MRGPRX1 APOL2 IL22 B4GALT1 VNN1 APOA2 S100A8
ALOX5 B4GALT1 VCAM1 TNFSF4 TACR1 DEFB1 ACVR1 KL TNR IRGM C4B-1 C4A
NCF1B RXRA BMP6 C3 IGFBP4 TNFRSF1A LAT AKT1 TP73 IL8 CCRL2
NFKBIZ TMEM23 CD14 CD14 BMPR1B MECOM SCN9A SCN9A CD14 P2RX7 MECOM MS4A2
MAP2K3 C4B TNFRSF1A OLR1 TNFRSF1A PDPN C4B F8VX64 C4A CCL24
PIK3CD CCRL2 CCL21 CCL22 CXCL11 IKBKB NCR3 KDM6B CHUK TP73 CCL25 CCL16
MEFV IRAK2 RIPK2 LIAS CHST1 LY75 TPST1 TLR5 CRCP RPS6KA5 RPS6KA4 ATRN
APOL3 IL18RAP VNN1 LY86 SERPINA1 SERPINA3 C3 C5 KNG1 FOS
TGFB1 NGF TNF IFNA2 IL1A CRP ORM1 CXCL10 KLKB1 ANXA1 CYBB ITGB2
S100A8 IL5 IL6 S100A9 CRH CD14 CXCL1 LTA4H C4A C4B PLA2G4B IL8
CCL3 SPP1 BMP2 CCL4 CYBA CCL2 SCG2 MIF NCF1 IL9 ALOX15 SELP
SELE CCL3L1 NPPB CEBPB ITGB6 TNFRSF1A RXRA NFKB1 CXCL2 CXCL3 AZU1
TAC1 ITGAL BMP6 IL10 GAL IGFBP4 CXCR1 CXCR2 FPR2 TACR1 PTAFR F2R
CD40 PTX3 AOAH ADORA2A CD40LG PRDX5 BDKRB2 AXL ADORA1 CCR1 CCR7
ADORA3 EPHX2 IL13 HRH1 CCR2 TNFRSF4 XCR1 BDKRB1 MAP2K3 PIK3CG CD97 SLC11A1
CCL11 CCR3 CCR4 CCR5 NDST1 AIF1 F2RL1 UCN CCL23 CCL18 HDAC4 CARD18
TIRAP CXCR4 LYZ RAC1 ADAM8 OLR1 KCNJ10 ELF3 CCL20 CCL8 CCL7 CXCL6
S100A12 TNFAIP6 MS4A2 MECOM RELA REG3A AOX1 CXCL9 IL10RB AIMP1 NFATC3 NFX1
NMI NFE2L1 NFATC4 AGER TLR1 LTB4R GPR68 SMAD1 IL17A CAMK4 C3AR1 AOC3
CDO1 SPHK1 C4A DARC THEMIS2 IL23R GGT5 NFRKB C4B REG3G TRIL PXK
CD163 TICAM2 PDPN EVI1 CAMK1D TICAM1 SCUBE1 AFAP1L2 CHST4 ABCF1 NFAM1 IL27
CCL4L2 NFKBID IL17D BLNK CCL17 HIST1H2BA KLRG1 ITCH NLRP3 IL17F CD180
S1PR3 CCL13 MGLL CCL19 CLEC7A TLR10 NFKBIZ SIGLEC1 IL22 TOLLIP HRH4 CYP4F11
PROK2 MMP25 IL1RAP NOX4 TLR8 STAB1 SPHK1 PLA2G2E IL17C IL36A TBK1 IL17B
PARP4 HDAC9 CELA1 PLA2G2D PLA2G4C HDAC5 NOD1 CCL26 PLAA CYSLTR1 TLR6 CHST2
NOX1 F11R IKBKG LY96 A2M SERPING1 STXBP3 PLEK GATA1 PDGFRA WNT3A
STXBP1 FERMT3 HIF1A TGFB1 F2R HIF1A FCER1A FCER1G NTRK3 CCR7 CHRNA7 SPECC1L
CALCRL ADORA2A NR1H3 ADORA2A ADORA2A NR1H3 ADORA2A NR1H3
CALCRL ABR ADA SERPINC1 IL2RA APOE SAA1 GBA ADRB2 ELANE BCR
ACP5 TNFRSF1B TNFAIP3 NT5E IL10 GATA3 ZFP36 AOAH CNR2 SERPINF1
IL2 PRKCD FOXF1 ABR NR1H3 CALCRL O3FAR1 CD276 CHRNA7 NR1H3 GHSR SELS
NDFIP1 UACA SHARPIN GHRL TNFAIP3 SERPINF2 F2 PLG APOH SERPINE1
THBD THBS1 SERPINF2 USF1 CPB2 F3 MYOD1 F11 F2 F11 GP1BA
F2R F2RL1 CAV1 VKORC1 FOXA2 C3 SELS INS ANXA1 IL4 GSTP1 ADORA1
PPARG ANXA1 RXRA ISL1 JAK2 JUN BCL2 VCAN RXRA CTNNA1 ISL1 C5orf13
RTN4RL1 RTN4RL2 CTNNA1 SERPINE1 PDE5A PDE5A PTGER3 IL1A EPHA3 TRPV1 FCER1G
ADORA2B LBP LTA TNF CD44 HMOX1 STK24 PLG F12 F11 KLKB1
ELANE LBP F12 KLKB1 MSTN SOX15 PLAU GPX1 ENO3 GJA1 MYF6 PAX7
MTPN PLAUR ANO6 IL20RB C5 SELE ADAM8 JAM3 F2 PDGFB APOE PDGFA
THBD PDGFRA NOS3 CNR1 MYOD1 SERPINE1 TNF IL1B KNG1 APOE APOH
VTN PROC SERPINE1 EDN1 THBD TSPAN8 SPP1 TSPO SOD2 PCSK1 LYN
ERBB2 SOD2 SOD1 EPO SOD2 ERBB2 ARG1 CDK1 LYN FGF2 LGALS1 GIP
DRD2 ARF4 PCSK1 TSPO MAP1B GIPR AIF1 MAX ARG2 MAP2K1 SHH NTRK3
LTC4S DRD2 TXN2 UCK2 AIF1 PPARA PDGFRA SMAD1 SDC2 SDC2 SERPINB2
GRHL3 POU2F3 SPARC WNT5B PPARA WNT5B SPARC WNT5B PPARD EREG TGFA INS
IL1A IL1B PDGFA ERBB2 ITGB3 S100A8 ADRB2 DCN MMP3 ADRB1 FGF2 TPM1
DSP PDGFRA ENG SDC1 NF1 FGF7 ERBB3 DRD5 LOX SDC2 MSX2 TGFBR1
WNT5A P2RY2 ELK3 SLC11A1 TGFB2 SMAD3 PPARD FMOD PPARA MAP3K1 ITGA9 SMAD1
KGFLP2 KGFLP1 TIMP1 MIA3 FUT10 SDC2 C6orf89 ARHGEF19 GRHL3 SCARB1 DCBLD2
CNN2 KLF6 SPRR3 POU2F3 MACF1 VIL1 PLAU VIL1 CNTF SCARF1 NDEL1 NOD2
PSMA1 PSMB4 IL12B NOD2 SCGB1A1 RELA SEMA7A JAK2 SEMA7A CALCA AHSG IL4
SCGB1A1 SELE GGT1 TNFSF4 CMA1 AGTR1 PTGS2 BCL6 XCL1 SLC7A2 PSMA6 RELA
SETD6 PARK7 MGLL MYD88 ACE2 NLRP1 NOD2 IL20 SBNO2 TSPO TNC APOE
TNC TSPO MAP1B CHST3 C3 FCER1G PDPN TLR4 PLEK SELP PDPN JUB
ITGA5 COL5A1 MSX2 ACVRL1 MMP12 SCNN1B SCNN1G ADAM17 JUB HBEGF FOXC2 TNFSF11
hRANKL 3 TNFRSF11A OMG

Source codes for inferring TF activity

```
library(stats)

# load TRRUST database
TRRUST = read.table("trrust_rawdata.txt", sep="\t")
colnames(TRRUST) = c("TF", "Target", "Type", "PMID")
# indices for unknown interactions
unknown_idx = which(TRRUST$Type == "Unknown")
# get all known interactions (activation and repression)
TRRUST_known = TRRUST[-unknown_idx,]
TRRUST_toUse = TRRUST_known

# One of the inputs for the inference model is gene expression.
# Firstly, filter out the genes with no hit in TRRUST_toUse.
# 'exp' is gene expression values where each row is a gene
# and each column is a sample.
# second column of 'TRRUST_toUse' table ('Target') is target gene.
exp = exp[which(!is.na(match(rownames(exp), unique(TRRUST_toUse$Target)))),]

# get unique TFs in TRRUST_toUse
uniqTF =  as.vector(unique(TRRUST_toUse$TF))

# Another input for the inference model is hit matrix.
# build the hit matrix (T matrix in main text).
# pre-define the matrix with zeroes (no interaction).
hit_mat = matrix(data = 0, nrow = nrow(exp), ncol = length(uniqTF))
rownames(hit_mat) = rownames(exp)
colnames(hit_mat) = uniqTF

# exclude duplicated interactions
TRRUST_noDup = cbind(as.vector(TRRUST_toUse$TF),
                     as.vector(TRRUST_toUse$Target),
                     as.vector(TRRUST_toUse$Type))
TRRUST_noDup = unique(TRRUST_noDup)

# assign 1 or -1 in each iteration if the interaction is activating
# or repressing, respectively.
for (t in 1:length(uniqTF)) {
  cur_TF = uniqTF[t]
  # get the index of current TF in the hit matrix
  TF_idx = which(colnames(hit_mat) == cur_TF)

  # get indices of activating interactions for TF in this iteration
  act_idx = intersect(which(TRRUST_noDup[,1] %in% cur_TF),
                      which(TRRUST_noDup[,3] == "Activation"))
  # if there is at least 1 activating interaction
  if (length(act_idx) > 0) {
    # get the target genes from the database
    act_TG = unique(as.vector(TRRUST_noDup[act_idx,2]))
    # get indices of these target genes in the hit matrix
    actTG_idx = which(rownames(hit_mat) %in% act_TG)
    hit_mat[actTG_idx,TF_idx] = 1 # activating = 1
  }

  # get indices of repressing interactions for TF in this iteration
  repr_idx = intersect(which(TRRUST_noDup[,1] %in% cur_TF),
                       which(TRRUST_noDup[,3] == "Repression"))
  # if there is at least 1 repressing interaction
  if (length(repr_idx) > 0) {
    repr_TG = unique(as.vector(TRRUST_noDup[repr_idx,2]))
    reprTG_idx = which(rownames(hit_mat) %in% repr_TG)
    hit_mat[reprTG_idx,TF_idx] = -1 # repressing = -1
```

```
  }
}

# use lsfit to solve the linear least squares model
TF_lsfit = lsfit(hit_mat, exp)
# access the least squares estimates of the coefficients in the model
# to retrieve TF activity scores
TF_act = TF_lsfit$coefficients
# remove the intercept (first row)
TF_act = TF_act[-1,]
colnames(TF_act) = colnames(exp)

# exclude TFs with standard deviation of activity scores = 0
sd0_rows = NULL
# collect indices of rows with SD = 0 in each iteration
for (r in 1:nrow(TF_act)){
  if(sd(as.numeric(TF_act[r,])) == 0) {
    sd0_rows = c(sd0_rows, r)
  }
}
# 'TF_act' below is the output of the inference model
TF_act = TF_act[-sd0_rows,]
```

Source codes for Benjamini-Hochberg correction

```
# function definition of BH procedure with controlling FDR
# based on http://www.biostathandbook.com/multiplecomparisons.html
BH_FDR_p.adjust <- function(pvalues, Q) {
  # order of p-values
  rank <- order(pvalues)
  # order of rank for returning later
  rev_rank <- order(rank)
  pvalues_ranked <- pvalues[rank]
  # calculate BH critical value
  crit_values <- as.numeric(as.numeric(rank/length(pvalues))*Q)
  max_idx <- max(which(pvalues_ranked < crit_values))

  sigFlag = NULL
  sigFlag[1:max_idx] = "Y"
  sigFlag[max_idx+1:length(pvalues)] = "N"

  return(sigFlag[rev_rank])
}
```

Source codes of GSEA method

```
library(gdata)
library(Biostrings)
library(marray)
library(gtools)

# load cell proliferation signature
Psig = system("more /work/halim/signatures/Proliferation_sig.txt",
        intern = TRUE)
Psig = unlist(strsplit(Psig, "\\\t"))
Psig = unique(Psig[-c(1,2)])

# load tissue remodelling signature
Rsig = system("more /work/halim/signatures/Remodeling_sig.txt",
        intern = TRUE)
Rsig = unlist(strsplit(Rsig, "\\\t"))
Rsig = unique(Rsig[-c(1,2)])

# read in gene expression data
geneExp = read.delim("coad.exp_agilent_g4502a.dt_matrix.mRNA_siRNA.txt")

# signature to use
sig = Psig # when P signature is in use
#sig = Rsig # when R signature is in use

# to build matrix S
# below are indices of genes that appear in the signature
sig_idx = which(!is.na(match(geneExp$Gene, sig)))
# below are indices of genes that don't appear in the signature
nonSig_idx = which(is.na(match(geneExp$Gene, sig)))

# hg score
A = 1/length(sig_idx) # 1/m if gEL
B = 1/(nrow(geneExp) - length(sig_idx)) # -(1/(n-m)) otherwise
matrixS = matrix(data = 0, nrow = nrow(geneExp), ncol = 1)
matrixS[sig_idx] = A
matrixS[nonSig_idx] = -B

# function from the Reduce documentation that cumulatively adds
cadd <- function(x) Reduce("+", x, accumulate = TRUE)

# function definition of 'callPerm'. It calls 'permute' function and
# calculates cumulative score matrix for current iteration then
# returns its maximum and minimum values
callPerm <- function(permNumber, matrixS) {
  permS = permute(matrixS)
  permX = cadd((permS))
  permX_max = max(permX)
  permX_min = min(permX)

  return(c(permX_max, permX_min))
}

# number of permutations
permNumber = 100000

# call 'callPerm' function as many times as assigned to 'permNumber'
# with parallelization
res = mclapply(1:permNumber,callPerm,matrixS, mc.cores =
            getOption("mc.cores", 28L))

# to unlist the returned max (permX_max) and min (permX_min) values
```

```
results = unlist(res)
# create indices to grab all permX_max
odd_indices<-seq(1,2*permNumber,2)
# create indices to grab all permX_min
even_indices<-seq(2,2*permNumber,2)
allPermX_max = results[odd_indices]
allPermX_min = results[even_indices]

# initialise variables
Xmax = NULL
Xmin = NULL
Pmax = NULL
Pmin = NULL
Xbest = NULL
# correction to a less bias p-value estimate, i.e. p = (r+1)/(n+1)
# go through expression (expr) values for every sample.
# start from 3 as the first 2 columns in geneExp are gene names
for (c in 3:ncol(geneExp)) {
  exp = as.matrix(geneExp[,c])
  # sort expr values
  sortExp = exp[order(exp, decreasing = TRUE)]
  # sort reference score matrix based on the order of expr values
  sortS = matrixS[order(exp, decreasing = TRUE)]

  # round cumulative score matrix to 6 decimal places
  matrixX = round(cadd(sortS), digits = 6)
  # enrichment score at the upper tail
  Xmax = c(Xmax,max(matrixX))
  # enrichment score at the lower tail
  Xmin = c(Xmin,min(matrixX))

  # use 'c-2' as we start from 'c=3'
  Cmax = length(which(as.numeric(allPermX_max) >= as.numeric(Xmax[c-2])))
  Cmin = length(which(as.numeric(allPermX_min) <= as.numeric(Xmin[c-2])))

  Pmax = c(Pmax,(Cmax+1)/(permNumber+1)) # p-value for Xmax
  Pmin = c(Pmin,(Cmin+1)/(permNumber+1)) # p-value for Xmin

  # to decide the enrichment score to report based on p-value at both tails
  if (as.numeric(Pmax[c-2]) < as.numeric(Pmin[c-2])) {
    Xbest = c(Xbest, Xmax[c-2])
  } else if (as.numeric(Pmax[c-2]) == as.numeric(Pmin[c-2])) {
    # when Pmax=Pmin, Xbest = Xmax+Xmin
    Xbest = c(Xbest, Xmax[c-2]+Xmin[c-2])
  } else {
    Xbest = c(Xbest, Xmin[c-2])
  }

}
# Xbest is the enrichment score to report
Xbest_P = Xbest # when P signature is in use
#Xbest_R = Xbest # when R signature is in use
```