# NPM-ALK

John K. Everett

2019-05-16

This analysis examines the effect of NPM-ALK transgenes delivered to CD4 T-cells by means of a lentiviral vector. Four NPM-ALK transgenes were studied: a naturally occurring NPM-ALK fusion (WT), a NPM-ALK triple mutant (TrpM), NPM-ALK with no kinase activity (KD), and a singly substituted transgene (Y664F). Wild type NPM-ALK is known to transform T-cells where Y664F has been shown to transform cells more efficiently. WT and Y664 transformation is dependent upon an active kinase domain. The triple mutant (Y567F, Y644F, Y646F) is of particular interest because it begins to transform T-cells at early time points similar to WT though these cells loose their CD30 marking and begin to die after three weeks similar to KD clones (Figure 1).

Figure 1. Cell sorting experiments.
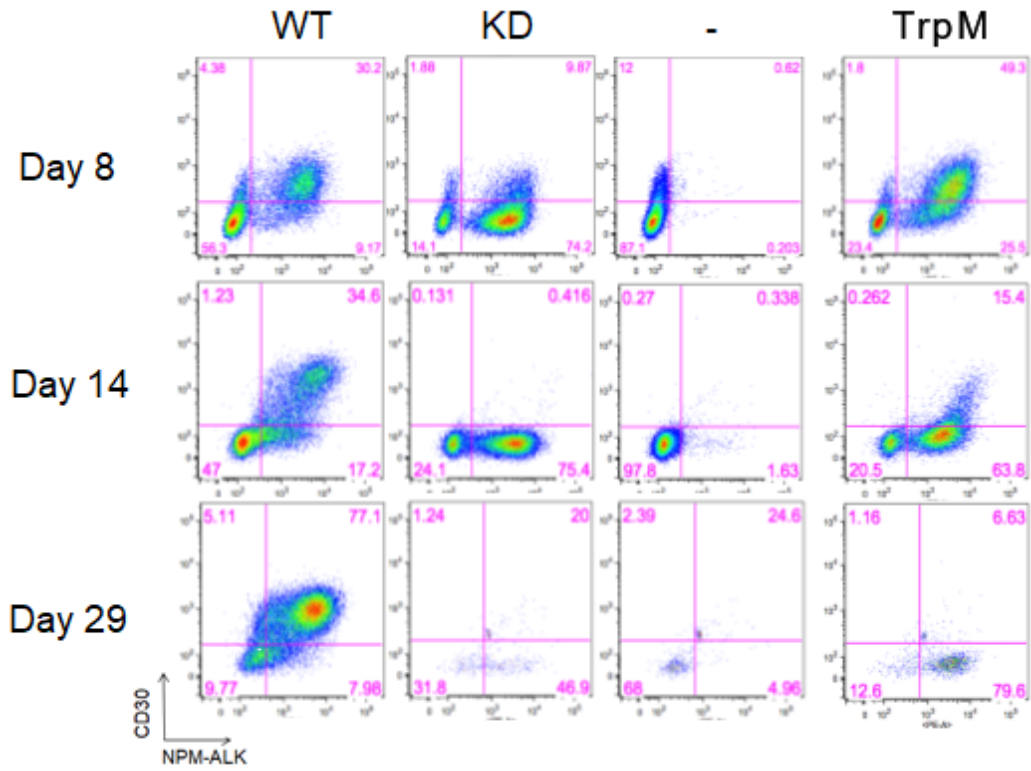
RNAseq analyses were performed in order to identify changes in the transcriptome of clones (WT, Y664F, and KD) at different time points. While KD clones possesed transcriptomes rather similar to uninfected cells, WT and Y664F clones possesed transcriptomes distinct from KD. In the PCA analysis (Figure 2), WT and Y664F clones moved downward in the plot over time where the Y664F clones move downard faster which may explain in part why they transform cells more effectively.

Figure 2. RNAseq of WT, Y664F, KD, and uninfected cells at different time points. Different donors are denoted with numbers.
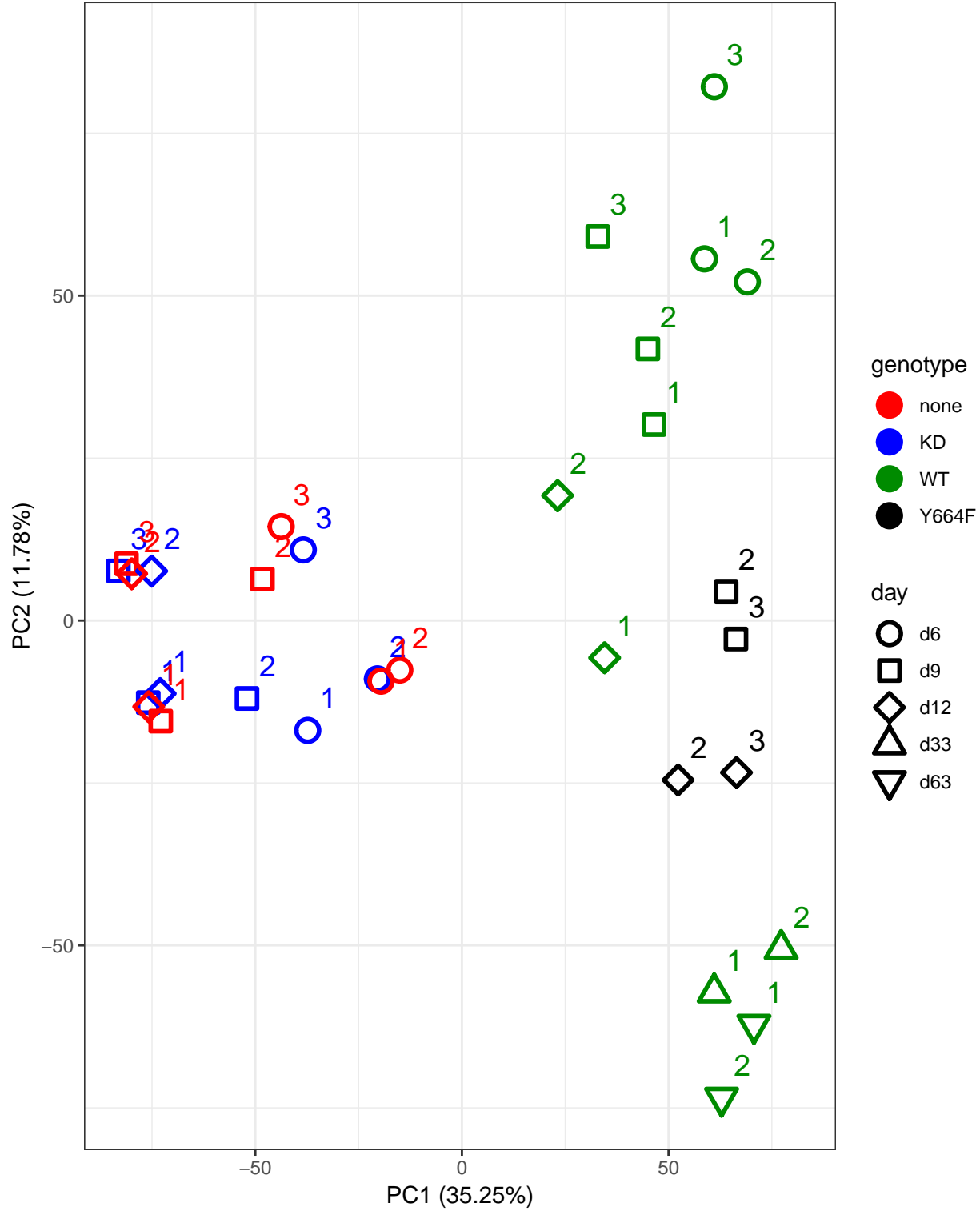
Comparing WT clone transcription levels (days 9, 12, 33, and 63) to day 6 reveals a number of genes with transcription levels that significantly change over time (Figure 3).

Figure 3. RNAseq of WT clones compared to the earliest WT clone. Genes are ordered from the most significant transcription change (top) to less significant changes (bottom). Genes shown are the more significant genes which can easily be visualized in a single figure.
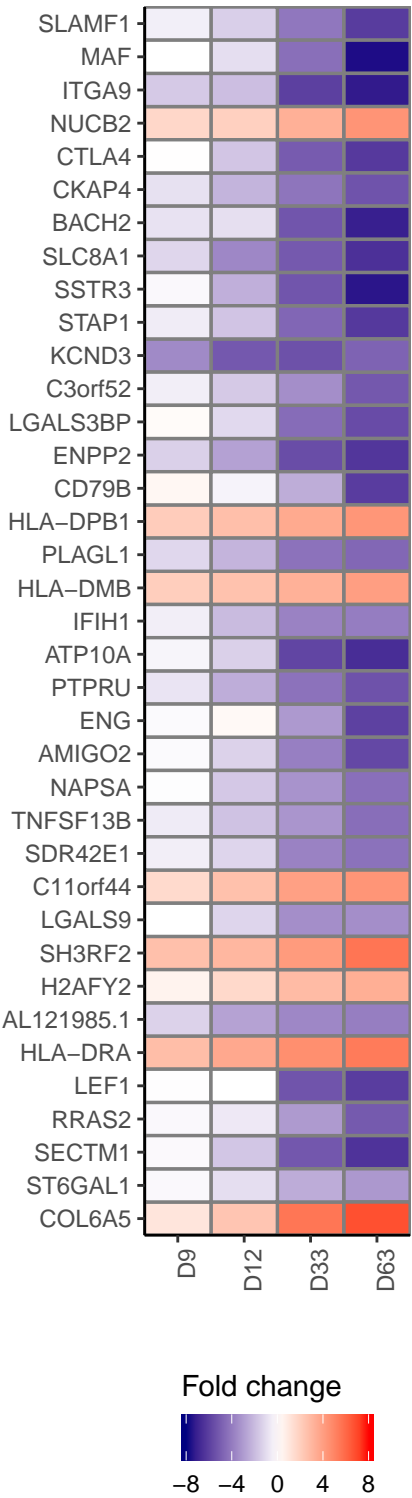
Comparing Y664F clone transcription levels to WT clones at the same time point reveals significant changes in the transcription of select genes (Figure 4). The most significant change in transcription atop of Figure 4, MYD88, may be of interest.

Figure 4. RNAseq of Y664F clone compared to WT clones at the same time points. Genes are ordered from the most significant transcription change (top) to less significant changes (bottom). Genes shown are the more significant genes which can easily be visualized in a single figure.
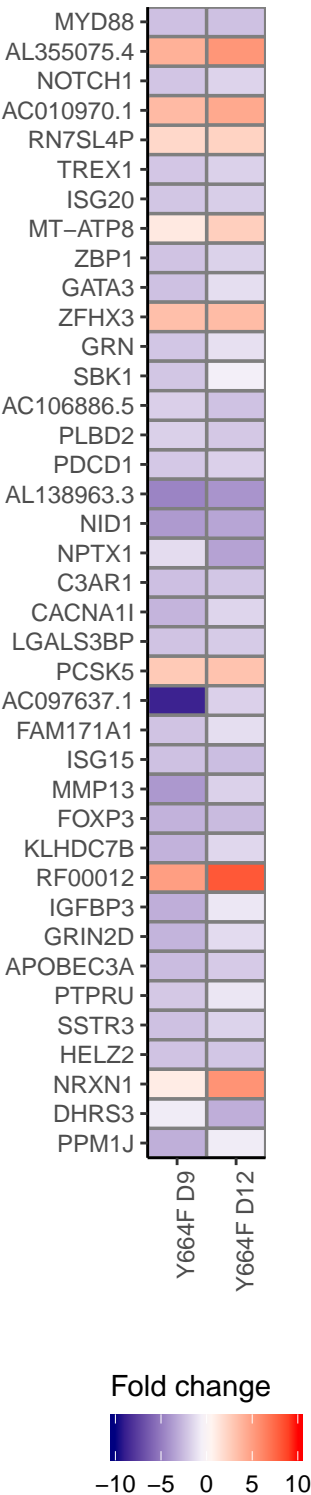
A second RNAseq analysis was performed in order to identify changes in the transcriptome of WT, TrpM, and KD at different time points. Time points of day 6 and day 9 were selected as time points of interest because they mark the beginning of cellular transformation and the beginning of CD30 loss in TrpM clones. Figure 5 shows a RNAseq PCA analysis which clearly separates clones and time points with the TrpM clones plotted between WT and KD samples which is reflective of TrpM's inability to fully transform cells.

Figure 5. PCA analysis of RNAseq experiment of WT, TrpM and KD clones.
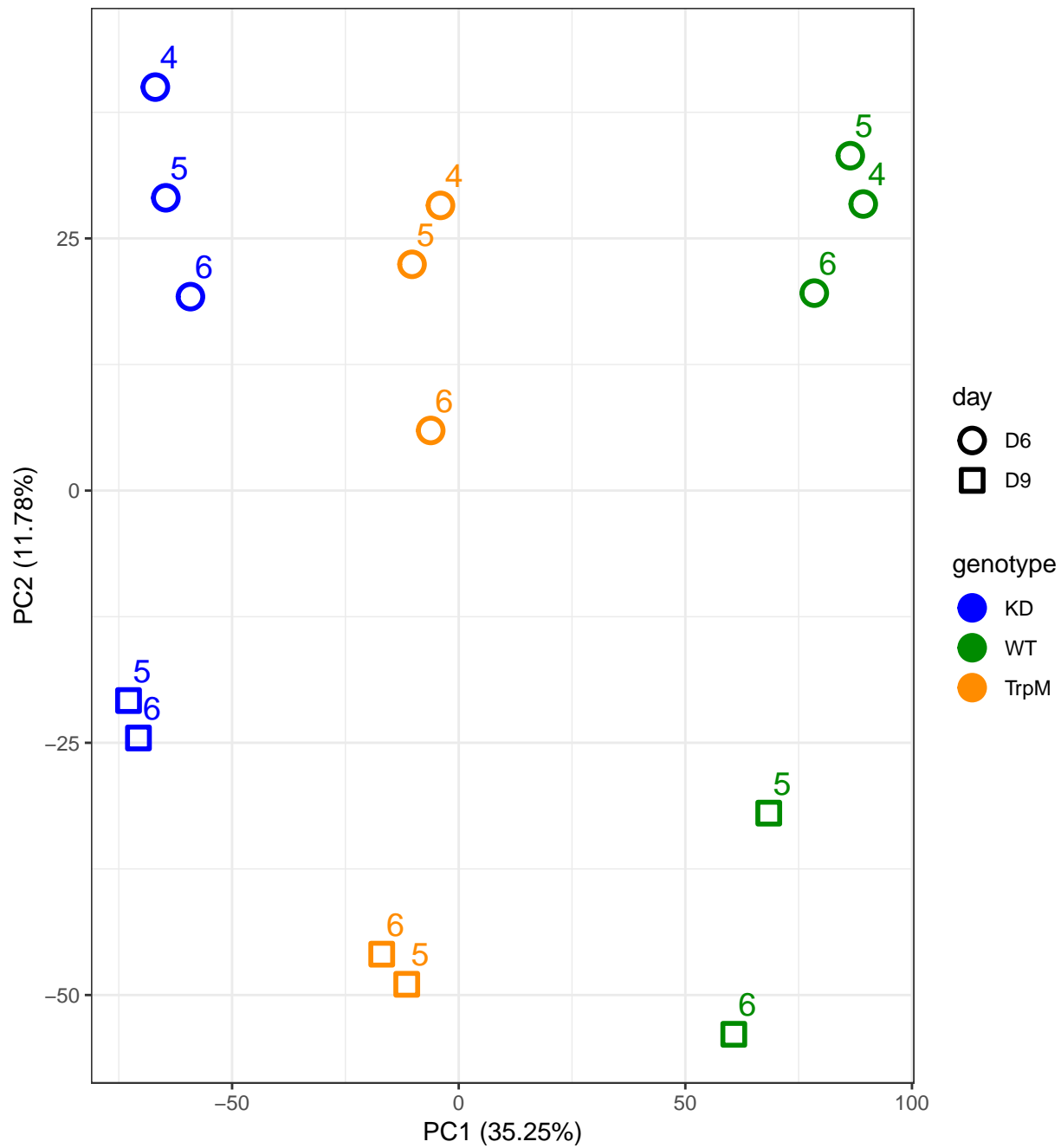
WT and TrpM genes with the most significantly different changes in transcription compared to KD clones is shown in Figure 6.

Figure 6. RNAseq analyses of WT and TrpM clones compared to KD clones. Genes are ordered from the most significant change (top left) to less significant changes (bottom right) where the second heatmap on the right is a continuation of the heatmap on the left.
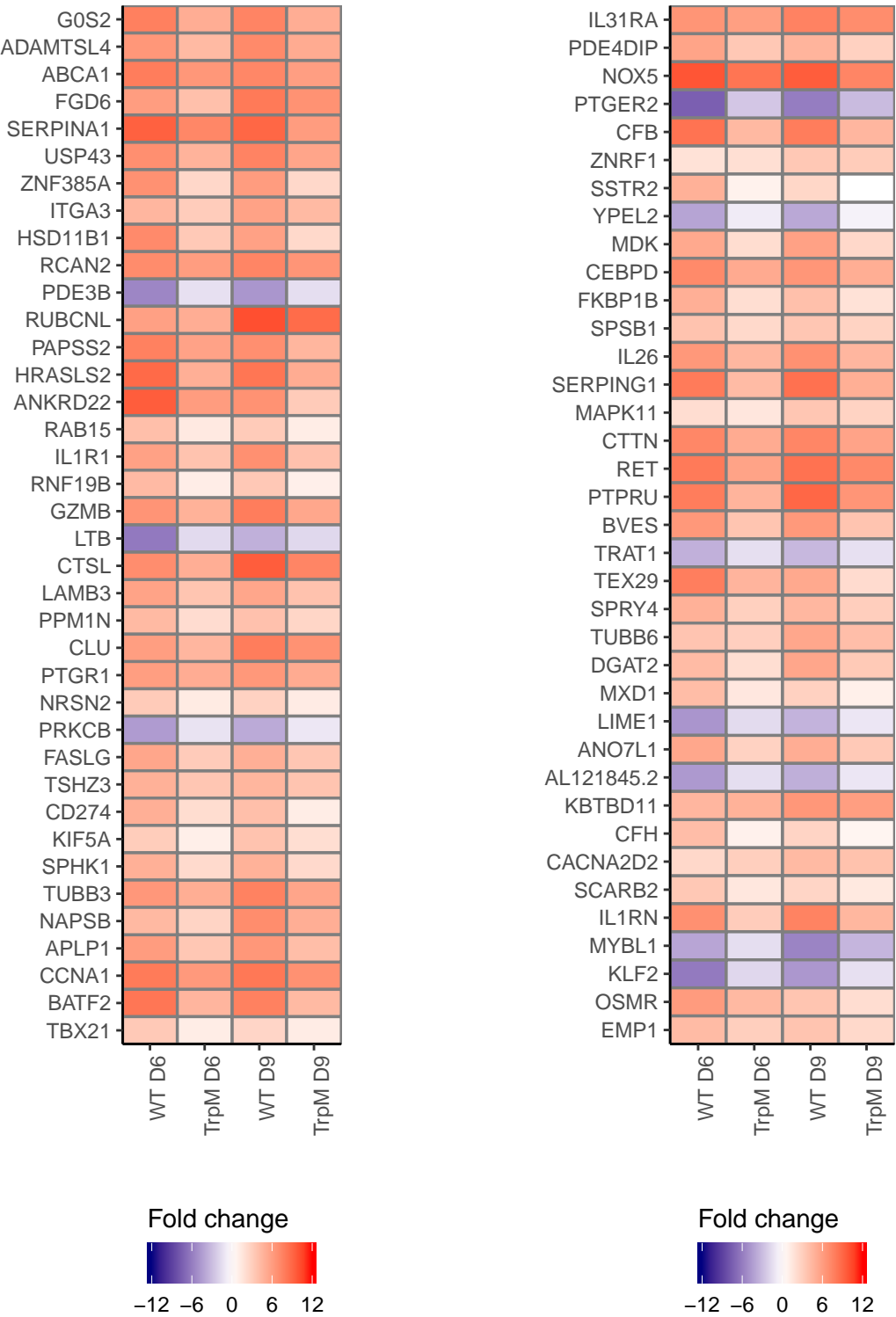
Comparing TrpM clones to WT clones reveals a number of genes with significantly different transcription levels most of which are lower in the TrpM clones (Figure 7).

Figure 7. RNAseq analyses of TrpM clones compared to WT clones. Genes are ordered from the most significant change (top) to less significant changes (bottom). Genes shown are the more significant genes which can easily be visualized in a single figure.

In order to better understand which pathways are altered in WT clones compared to KD clones, gene with significantly changed transcription levels in WT clones were used for KEGG pathway enrichment analyses (Table 1).

The top two KEGG pathways from Table 1 are illustrated below where log2 fold gene transcription changes compared to KD are color coded. The top 10 KEGG pathways identified in Table 1 are illustrated in supplemental Figure S1.
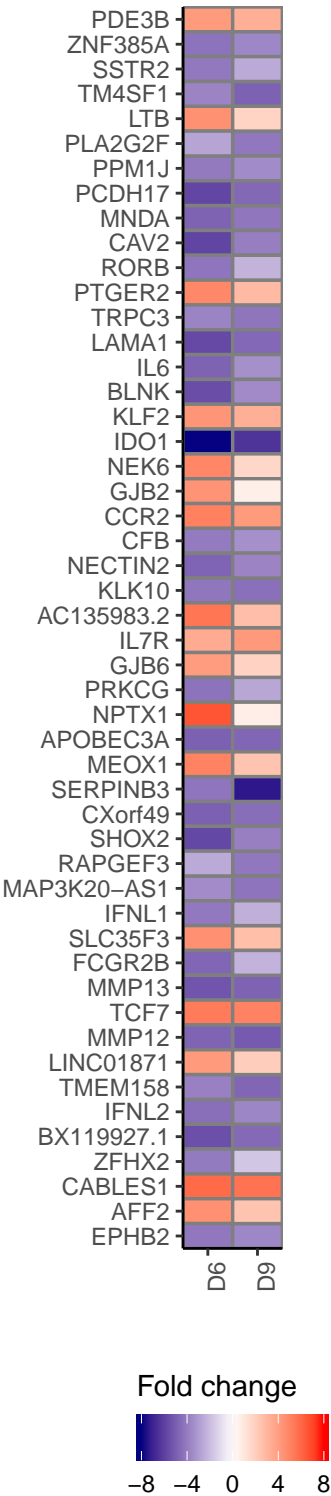
Table 1. Enriched pathways from the day 9 WT vs KD RNAseq comparison. Genes with increased transcription are shown with uppercase names while genes with decreased transcription are shown with lowercase names. Full table is provided in Table S1.

proteins	hits	pvalue_fdr	term_description	genes
260	51	1.55e-30	Cytokine-cytokine receptor interaction	CCL22, CCR1, ccr2, ccr8, cd27, CD40, cd40lg, CSF1R, CSF3R, CXCL11, CXCL13, cxcr1, cxcr3, cxcr4, CXCR6, FASLG, flt3lg, FLT4, IFNG, IFNGR1, IFNK, IL10, il13, IL13RA1, IL15, IL15RA, IL1R1, IL1R2, IL1RAP, IL22RA2, IL23R, IL26, IL28A, IL6, IL6R, il7r, LIFR, ltb, LTBR, NGFR, OSMR, PDGFA, PDGFRB, TNFRSF10C, TNFRSF21, TNFRSF8, TNFSF10, TNFSF13B, tnfsf14, tnfsf8, VEGFC
154	28	1.56e-15	Jak-STAT signaling pathway	ccnd2, cish, CSF3R, IFNG, IFNGR1, IFNK, IL10, il13, IL13RA1, IL15, IL15RA, IL22RA2, IL23R, IL26, IL28A, IL6, IL6R, il7r, LIFR, myc, OSMR, pik3r5, socs2, SOCS3, sos1, SPRED1, SPRED3, SPRY4
219	31	3.06e-14	Ras signaling pathway	CSF1R, EFNA1, ETS2, FASLG, fgfr1, FLT4, GAB1, GNB4, HTR7, MRAS, NGFR, PDGFA, PDGFRB, pik3r5, PLA2G16, PLA2G2C, PLA2G2F, PLCG2, prkacb, prkcb, PRKCG, prkx, rasa3, RASAL2, RASGRF1, rasgrp4, rras2, SHC2, SHC4, sos1, VEGFC
320	35	8.92e-13	Pathways in cancer	axin2, bcl2, CCNA1, CDKN1A, COL4A2, CSF1R, CSF3R, DAPK2, FASLG, fgfr1, flt3lg, IL6, ITGA3, itga6, LAMA1, LAMB3, LAMC1, lef1, myc, NFKBIA, PDGFA, PDGFRB, pik3r5, PLCG2, prkcb, PRKCG, RET, sos1, SPI1, tcf7, TGFA, VEGFC, WNT11, WNT7B, WNT8B
1160	70	2.92e-12	Metabolic pathways	ACSL1, acsl6, AK7, ALPL, AMACR, AOX1, ass1, ATP6V0A1, ATP6V0A4, atp6v1e2, B3GNT3, B4GALNT1, bdh1, CDS1, CMPK2, COX6B2, cpox, CYP27B1, CYP2E1, CYP2J2, DGAT2, DGKG, dhrs3, DHRS9, dpyd, DSE, FUT7, GALM, GALNT10, GALNT2, GBGT1, GCNT1, GCNT3, GCNT4, GGT5, GK, GLDC, hadh, HAL, HDC, HK3, HSD11B1, hsd17b8, HSD3B7, IL4I1, IMPA2, inpp4b, LPIN3, man1c1, mgat5, NAGS, nt5m, PAPSS2, PGD, PGS1, PLA2G16, PLA2G2C, PLA2G2F, PLCG2, PNLIPRP3, PPAP2C, pycr1, PYGL, rdh10, SAT1, SPHK1, SPR, ST3GAL4, TST, TYMP
250	30	4.19e-12	HTLV-I infection	atm, ccnd2, CD40, CDKN1A, ETS2, FOSL1, IL15, IL15RA, IL1R1, IL1R2, IL6, LTBR, map3k1, MRAS, mybl1, myc, NFKBIA, NRP1, PDGFA, PDGFRB, pik3r5, ppp3ca, prkacb, prkx, rras2, SLC25A4, SPI1, WNT11, WNT7B, WNT8B
104	20	6.85e-12	Amoebiasis	COL1A1, COL4A2, GNAL, gnaq, IFNG, IL10, IL1R1, IL1R2, IL6, LAMA1, LAMB3, LAMC1, pik3r5, prkacb, prkcb, PRKCG, prkx, SERPINB4, serpinb6, TLR2
336	34	1.04e-11	PI3K-Akt signaling pathway	bcl2, ccnd2, CDKN1A, COL1A1, COL4A2, CSF1R, CSF3R, EFNA1, FASLG, fgfr1, FLT4, GNB4, IL6, IL6R, il7r, ITGA3, itga4, itga6, ITGA9, LAMA1, LAMB3, LAMC1, myc, NGFR, OSMR, PDGFA, PDGFRB, PIK3AP1, pik3r5, PPP2R2B, sos1, TLR2, TNR, VEGFC
218	27	2.3e-11	Proteoglycans in cancer	CAV2, CDKN1A, CTSL1, CTTN, FASLG, fgfr1, GAB1, hbegf, MAPK11, MAPK12, MRAS, myc, pdcd4, pik3r5, PLAUR, PLCG2, prkacb, prkcb, PRKCG, prkx, rras2, sos1, TLR2, TWIST1, WNT11, WNT7B, WNT8B
178	24	6.21e-11	Chemokine signaling pathway	arrb1, CCL22, CCR1, ccr2, ccr8, CXCL11, CXCL13, cxcr1, cxcr3, cxcr4, CXCR6, GNB4, HCK, LYN, NCF1, NFKBIA, PARD3, pik3r5, prkacb, prkcb, prkx, SHC2, SHC4, sos1
164	23	7.06e-11	Transcriptional misregulation in cancer	atm, BCL2A1, CCNA1, ccnd2, CD40, CDK14, CDKN1A, CEBPB, CSF1R, ETV1, ETV5, ETV7, GZMB, IL1R2, IL6, klf3, myc, NGFR, PAX5, PDGFA, SIX1, SMAD1, SPI1
123	20	1.06e-10	Osteoclast differentiation	camk4, CSF1R, FOSL1, FOSL2, IFNG, IFNGR1, IL1R1, JUNB, LILRB4, MAPK11, MAPK12, NCF1, NFKBIA, OSCAR, pik3r5, PLCG2, ppp3ca, SOCS3, SPI1, TEC

Table 1 (continued).

proteins	hits	pvalue_fdr	term_description	genes
202	25	1.15e-10	Focal adhesion	bcl2, CAV2, ccnd2, COL1A1, COL4A2, FLT4, ITGA3, itga4, itga6, ITGA9, LAMA1, LAMB3, LAMC1, MYL9, PDGFA, PDGFRB, pik3r5, prkcb, PRKCG, RASGRF1, SHC2, SHC4, sos1, TNR, VEGFC
88	17	2.08e-10	NF-kappa B signaling pathway	atm, bcl2, BCL2A1, CD40, cd40lg, DDX58, IL1R1, ltb, LTBR, LYN, malt1, NFKBIA, PLCG2, prkcb, TNFSF13B, tnfsf14, TRIM25
115	19	2.17e-10	Neurotrophin signaling pathway	bcl2, camk4, FASLG, GAB1, IRAK2, map3k1, MAPK11, MAPK12, matk, NFKBIA, NGFR, pik3r5, PLCG2, rps6ka2, SH2B2, sh2b3, SHC2, SHC4, sos1
251	27	3.67e-10	MAPK signaling pathway	arrb1, CACNA2D2, dusp10, FASLG, fgfr1, GADD45A, IL1R1, IL1R2, map3k1, MAP3K6, MAPK11, MAPK12, MRAS, myc, PDGFA, PDGFRB, ppp3ca, prkacb, prkcb, PRKCG, prkx, RASGRF1, rasgrp4, rps6ka2, rras2, sos1, STK3
123	18	4.98e-09	Axon guidance	ablim1, ABLIM3, cxcr4, EFNA1, epha4, EPHB2, FES, NRP1, NTN4, NTNG2, PLXNB1, PLXNB3, ppp3ca, RND1, SEMA4A, SEMA4B, SEMA6A, SEMA7A
123	18	4.98e-09	Natural killer cell mediated cytotoxicity	FASLG, FCER1G, GZMB, IFNG, IFNGR1, KIR2DL4, ncr3, pik3r5, PLCG2, ppp3ca, prkcb, PRKCG, RAET1E, SHC2, SHC4, sos1, TNFRSF10C, TNFSF10
85	15	9.6e-09	Hematopoietic cell lineage	cd55, CD59, CD8B, CD9, CSF1R, CSF3R, flt3lg, IL1R1, IL1R2, IL6, IL6R, il7r, ITGA3, itga4, itga6
146	19	1.13e-08	Hippo signaling pathway	axin2, ccnd2, ID1, LATS2, lef1, myc, PARD3, PPP2R2B, SMAD1, smad7, SOX2, STK3, tcf7, TEAD3, WNT11, WNT7B, WNT8B, WWTR1, YAP1
103	16	1.67e-08	HIF-1 signaling pathway	bcl2, CDKN1A, EDN1, HK3, HMOX1, IFNG, IFNGR1, IL6, IL6R, LTBR, PFKFB3, pik3r5, PLCG2, prkcb, PRKCG, TF
204	22	1.84e-08	Rap1 signaling pathway	CSF1R, DOCK4, DRD2, EFNA1, fgfr1, FLT4, gnao1, gnaq, ID1, MAPK11, MAPK12, MRAS, NGFR, PARD3, PDGFA, PDGFRB, pik3r5, prkcb, PRKCG, RAPGEF3, SIPA1L2, VEGFC
33	10	2.07e-08	African trypanosomiasis	APOL1, F2RL1, FASLG, gnaq, hba1, IFNG, IL10, IL6, prkcb, PRKCG
44	11	2.97e-08	Intestinal immune network for IgA production	CD40, cd40lg, cxcr4, icoslg, IL10, IL15, IL15RA, IL6, itga4, LTBR, TNFSF13B
94	15	3.13e-08	Inflammatory mediator regulation of TRP channels	CYP2J2, F2RL1, gnaq, HRH1, IL1R1, IL1RAP, MAPK11, MAPK12, pik3r5, PLCG2, prkacb, prkcb, PRKCG, prkx, ptger2
143	18	4.14e-08	MicroRNAs in cancer	atm, bcl2, ccnd2, CDKN1A, CYP1B1, HMOX1, irs2, myc, pdcd4, PDGFA, PDGFRB, PLCG2, prkcb, PRKCG, SHC4, sos1, TNR, ZEB2
112	16	4.56e-08	Toxoplasmosis	bcl2, CD40, cd40lg, gnao1, IFNG, IFNGR1, IL10, itga6, LAMA1, LAMB3, LAMC1, MAPK11, MAPK12, NFKBIA, pik3r5, TLR2
166	19	7.09e-08	Influenza A	DDX58, FASLG, FURIN, IFIH1, IFNG, IFNGR1, IL6, MAPK11, MAPK12, MX1, NFKBIA, pik3r5, prkcb, RSAD2, SOCS3, TLR3, TNFRSF10C, TNFSF10, TRIM25
170	19	1.02e-07	Tuberculosis	ATP6V0A1, ATP6V0A4, bcl2, CEBPB, CYP27B1, FCER1G, IFNG, IFNGR1, IL10, IL6, IRAK2, ITGAX, lsp1, malt1, MAPK11, MAPK12, ppp3ca, SPHK1, TLR2
174	19	1.44e-07	Calcium signaling pathway	camk4, GNAL, gnaq, GRIN2D, HRH1, HTR7, PDGFRB, PHKA1, PLCG2, ppp3ca, prkacb, prkcb, PRKCG, prkx, RYR2, SLC25A4, SLC8A1, SLC8A2, SPHK1

Viral integration site analysis of cultures transfected with both WT and Y664F transgenes show that cultures become oligoclonal over time. The relative clonal abundances of provided samples, arranged by earliest time point, are shown in Figure 8 where the relative abundances of the most abundant 50 clones are shown as stacked colored bars while less abundant clones are relegated to single gray low abundance bars.

Figure 8. Clonal relative abundance plots.
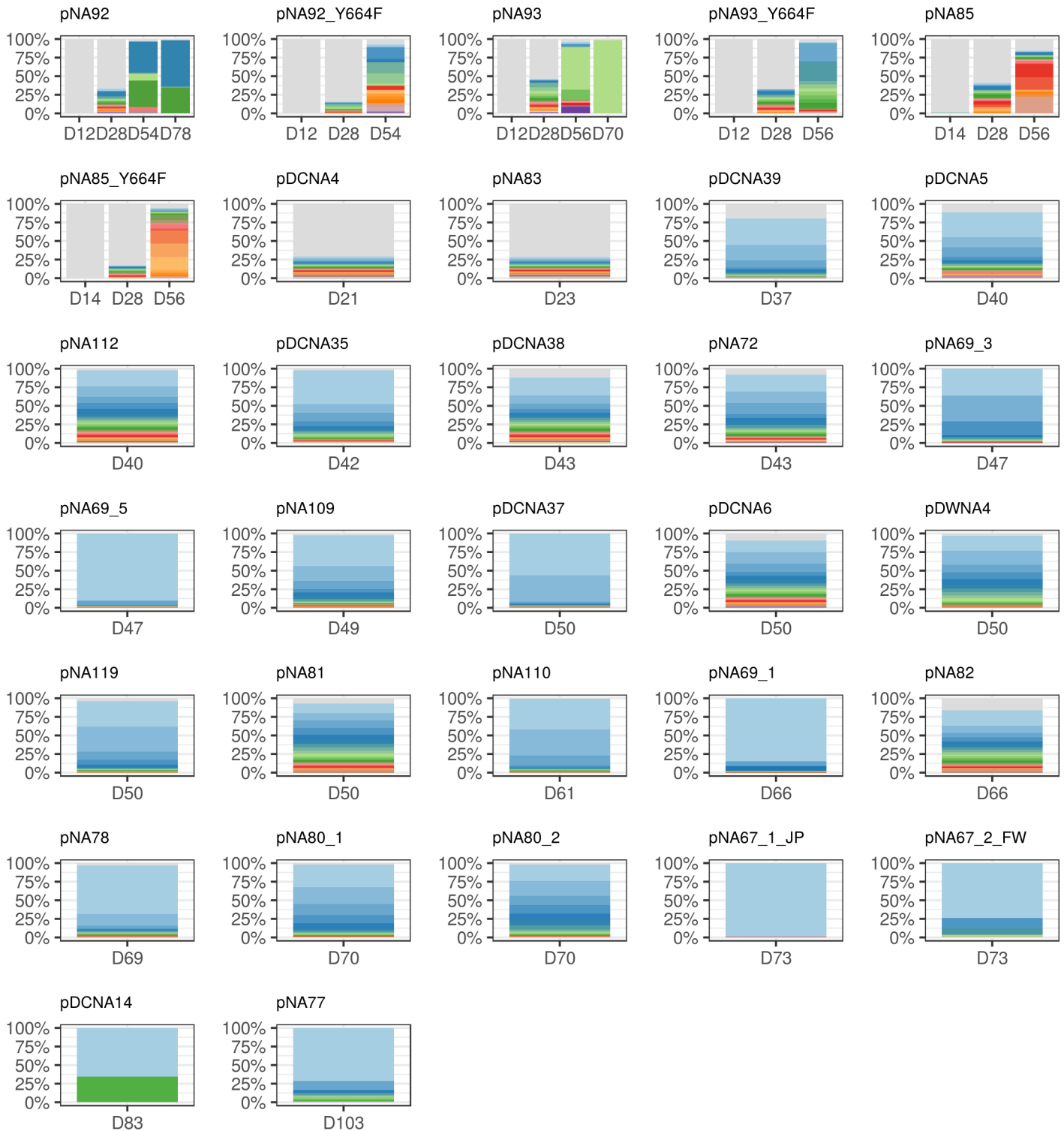
Integration profiles of cultures from three donors transfected with both WT and Y664F transgene were tracked over multiple time points and the rate at which they become oligoclonal is depicted in Figure 9.

Figure 9. Clonality of transfected cultures over time.
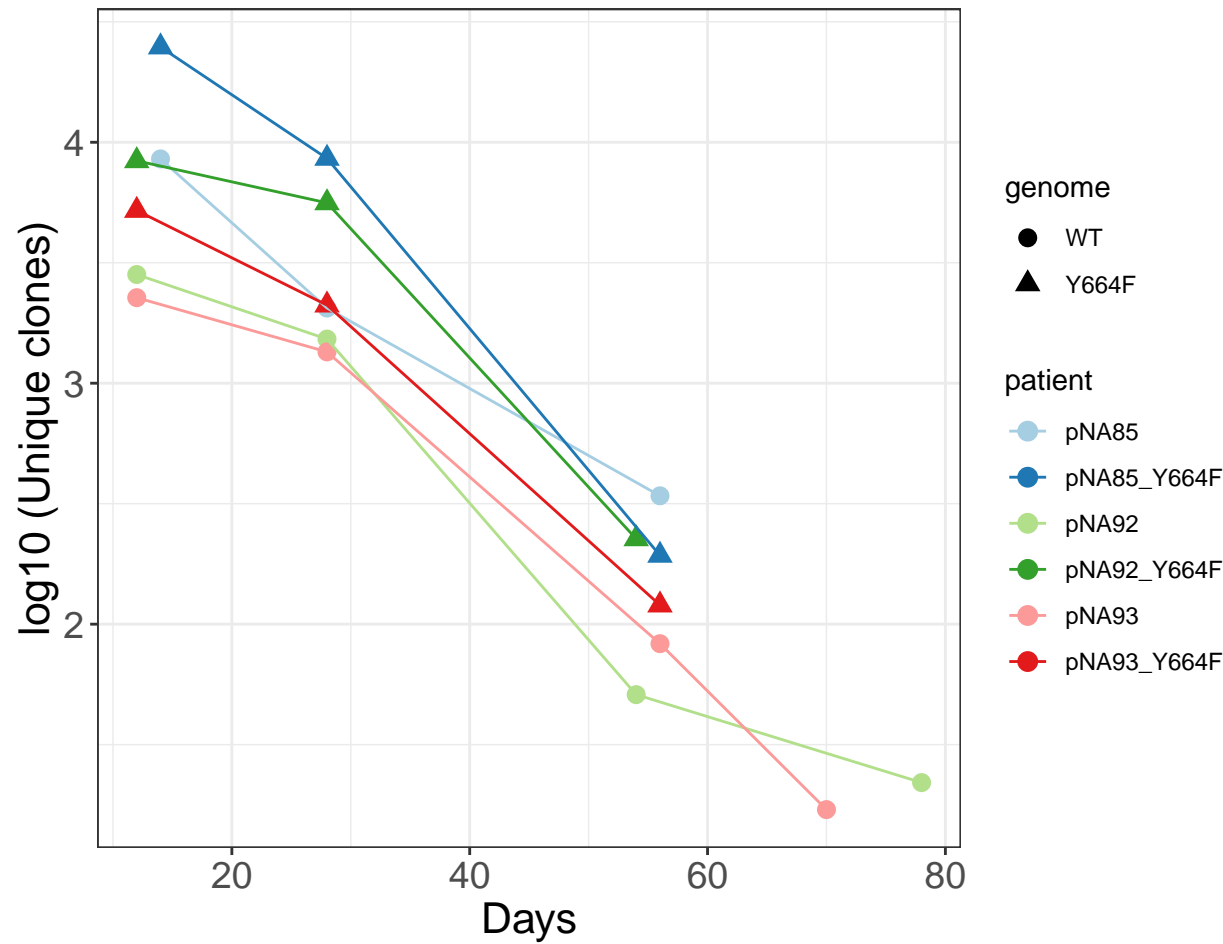
Some 753 clones (1.56% of all clones) in the longitudinal data set reached a maxim abundance of ≥ 25 cells at one or more time points (Figure 10). Four types of clonal abundance trajectories were observed:

1. Clones which were only observed at the earliest time points (98.44% of all clones).
2. Clones which reached a maximal abundance ≥ 25 cells by day 28 and then declined (Figure 10, top pane).
3. Clones which slowly increased in abundance and exceeded 25 cells (Figure 10, bottom pane, bottom cluster).
4. Clones which rapidly increased in abundance beyond 25 cells (Figure 10, bottom pane, top cluster).

The genes nearest to integration sites in clones from each clonal trajectory type do not substantially overlap with the enriched KEGG pathways genes found the WT vs KD day 9 RNAseq contrast (Table 1) nor do they strongly cluster to a discrete number of KEGG pathways (Table S2). The nearest genes for clones from each trajectory type are provided in Table S3.

Table 2. Clonal abundance trajectories clone counts.

Class	Clones	WT / Y664F
Type 2	706	184 / 522
Type 3	32	2 / 30
Type 4	15	6 / 9

Instances of clones with abundances ≥ 25 cells with integrations found near the same gene across multiple trial subjects are reported in Table 3.

Figure 10. Clonal abundance trajectories. Top pane: clones which exceeded abundances of 25 cells and then declined in later time points. Bottom pane: Subset of clones that exceeded abundances of 25 cells and reached their highest abundance at their final time point. Data points not connected with lines originate from clones which were not analyzed or detected at earlier time points presumably due to their low abundance.
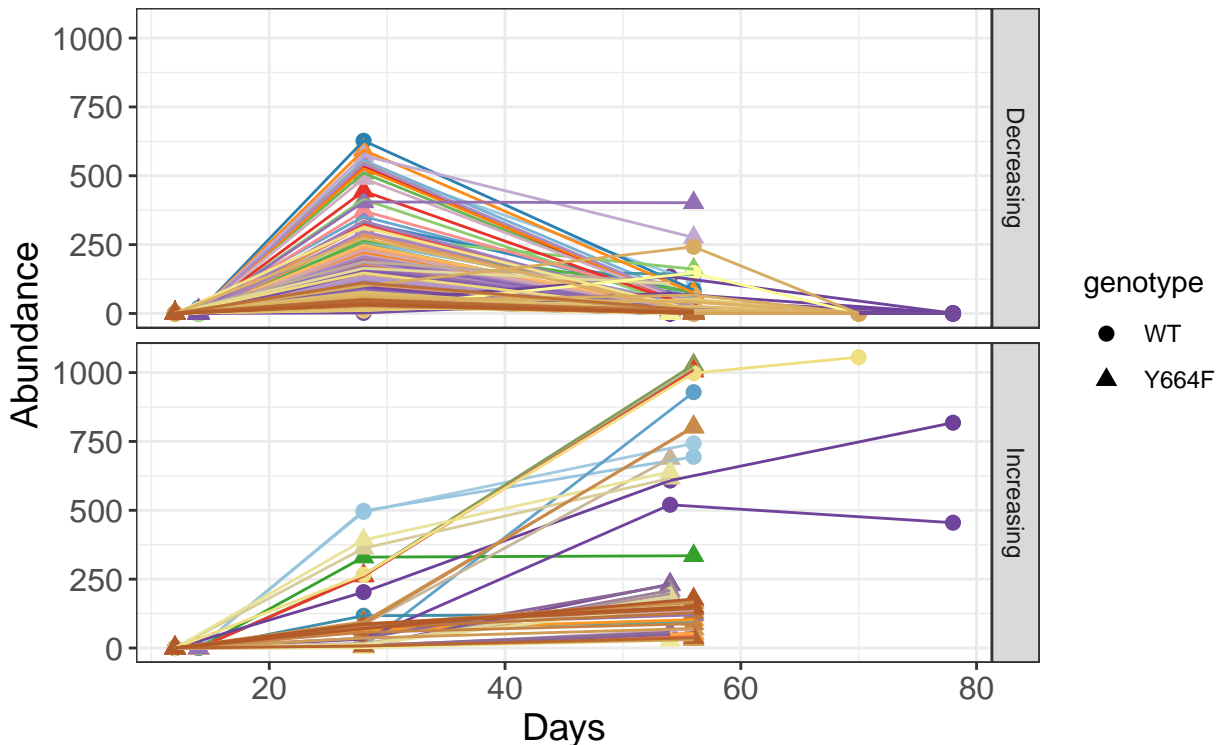
Table 3. Tally of trial subjects with three or more abundant clones near the same gene.

nearestFeature	WT.subjects	Y664F.subjects	WT.maxAbundance	Y664F.maxAbundance
ARID1A	4	3	95	801
AHR	4	0	818	NA
DIAPH2	3	1	101	49
DIP2A	3	1	61	86
SMARCE1	4	0	1056	NA
ACTR3	2	1	442	188
ADK	3	0	909	NA
CBLB	2	1	199	43
CCNL2	2	1	50	84
CUL3	2	1	318	43
GNB1	3	0	70	NA
HNRNPC	2	1	117	28
KNTC1	3	0	473	NA
MAP3K7	1	2	213	151
NSD1	2	1	60	55
PACS1	2	1	53	251
PIBF1	1	2	160	57
PRR12	1	2	33	197
RC3H2	3	0	82	NA
VPS13D	3	0	574	NA
VTI1A	2	1	139	25
YTHDF3	3	0	158	NA

Considering only donors with longitudinal trials and both WT and Y664F transgenes (pNA92, pNA93, pNA85), plotting nearest gene integration frequencies between early and later time points (Figure 11) show that ARID1A is placed more starkly above the diagonal in the Y664F trials than WT trials suggesting that it confers more of a survival advantage to clones with the Y664F transgene. Table 4 below shows the number of unique clones with integrations within ARID1A and their maximum abundance while Figure 12 shows the integration positions within ARID1A's transcription unit. Fisher's exact tests do not find a significant difference between the proportions of clones with maximal abundances < 25 and ≥ 25 cells which suggests that integration within ARID1A and higher clonal abundances are not dependent on the transgene though there is a trend toward higher abundances with the Y664F transgene.

Table 4. Unique clones with integrations within ARID1A separated by transgene and maximum observed abundance.

	Abund < 25	Abund $>= 25$
WT	24	1
Y664F	55	7

Figure 12. Schematic of ARID1A where exons are shown as gray bars and clones are shown by data points denoting both their integration position and maximum abundance.
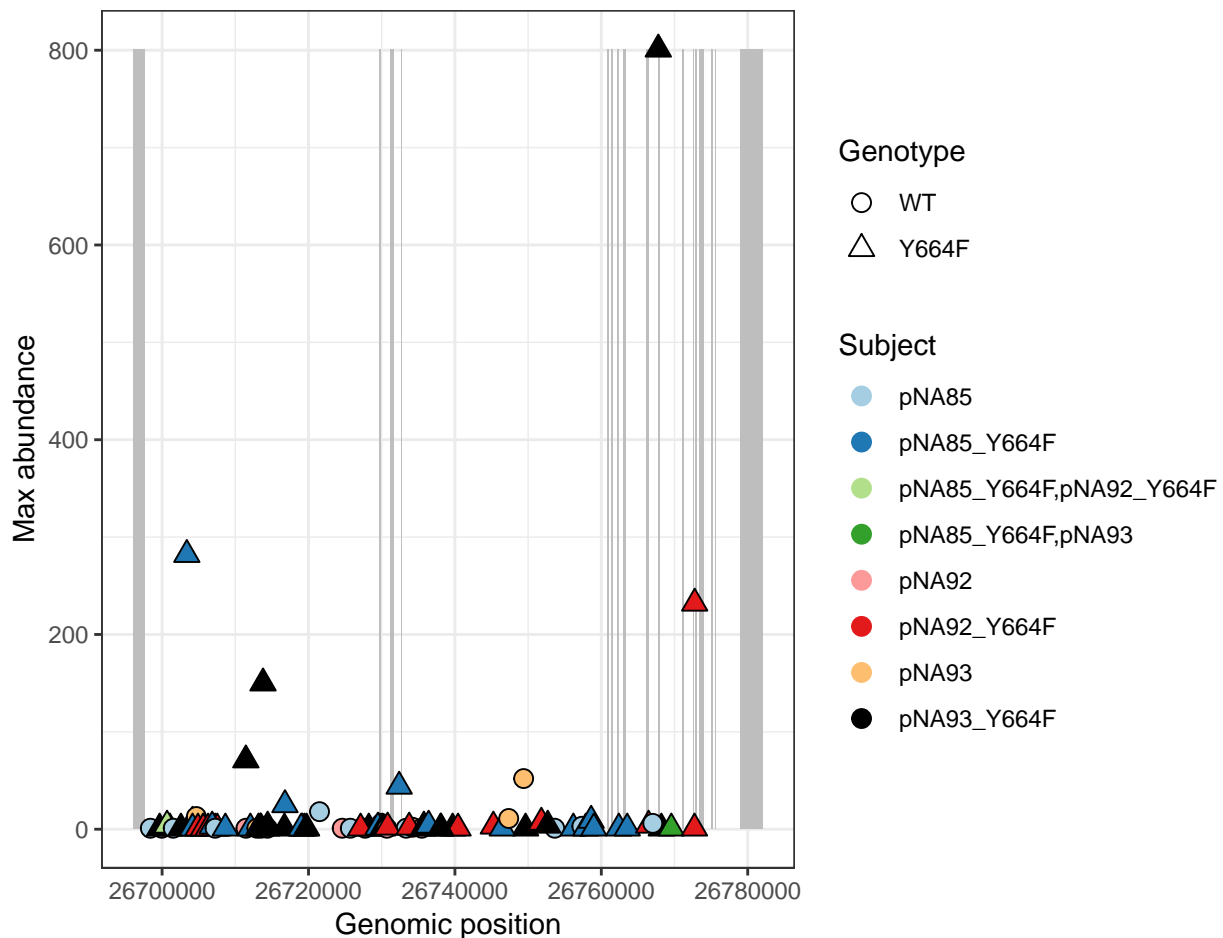
Figure 11a. Bivariate nearest gene frequency plot for clones with the Y664F transgene.
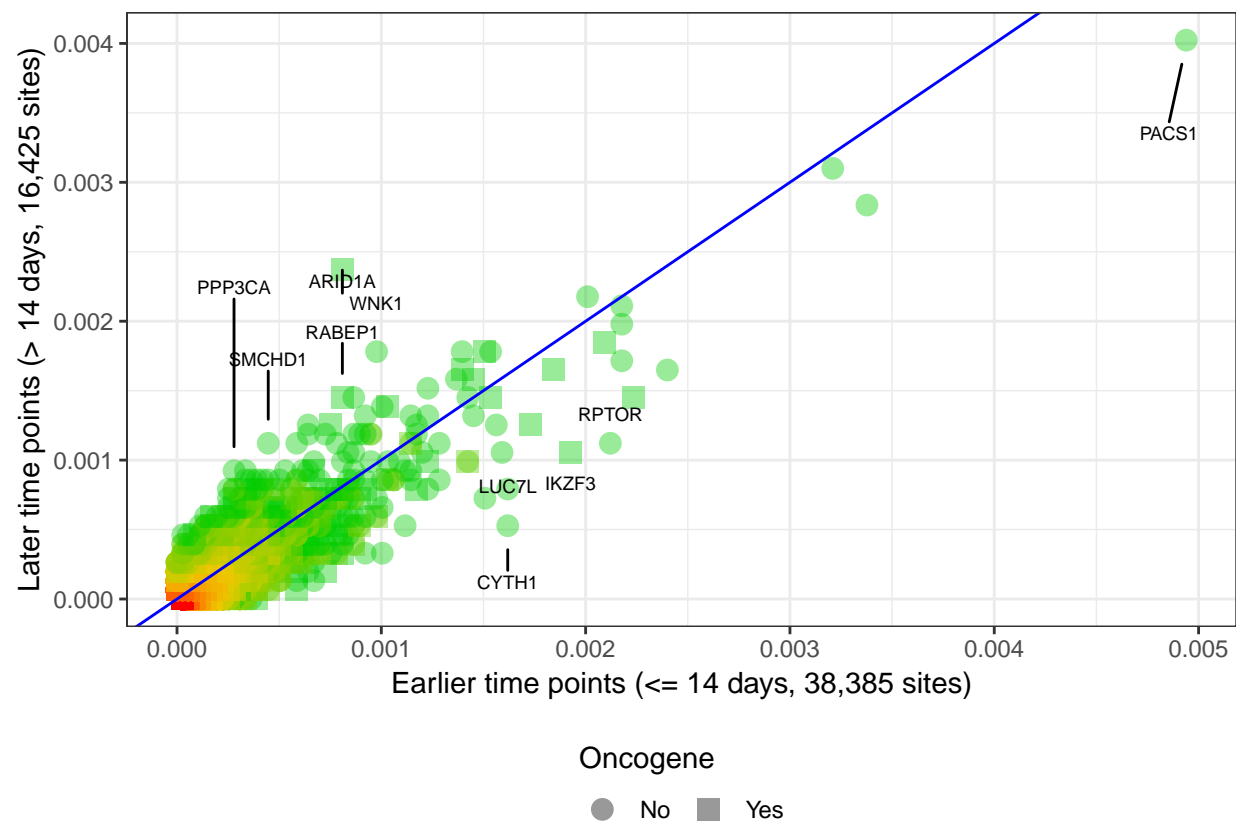
Figure 11b. Bivariate nearest gene frequency plot for clones with the WT transgene.
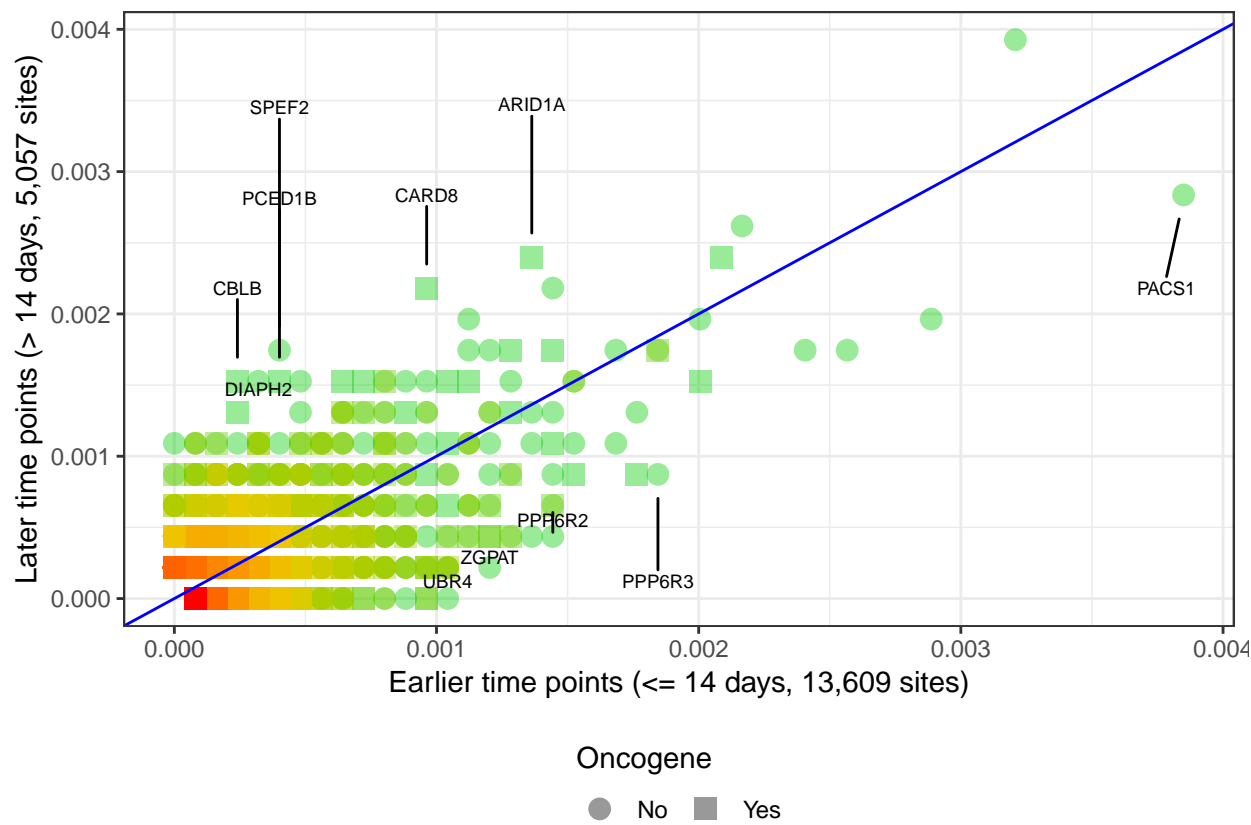
Supplemental

Figure S1a. KEGG pathway: 04060 Cytokine-cytokine receptor interaction
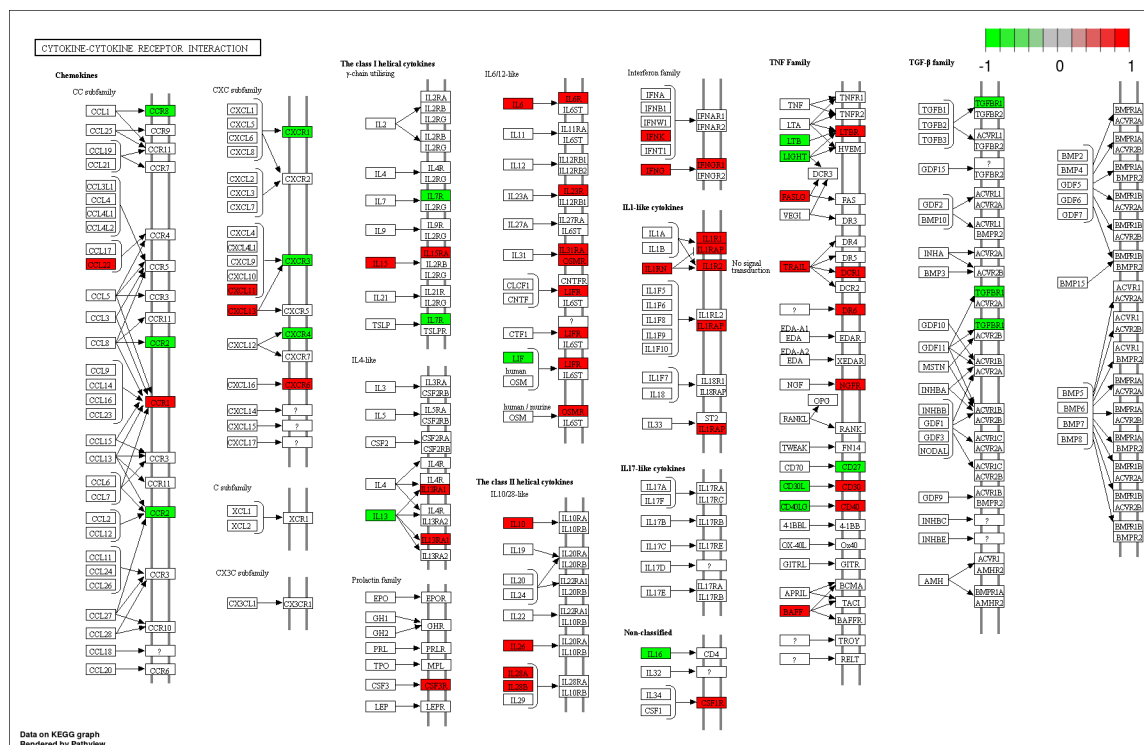
Figure S1b. KEGG pathway: 04630 Jak-STAT signaling pathway
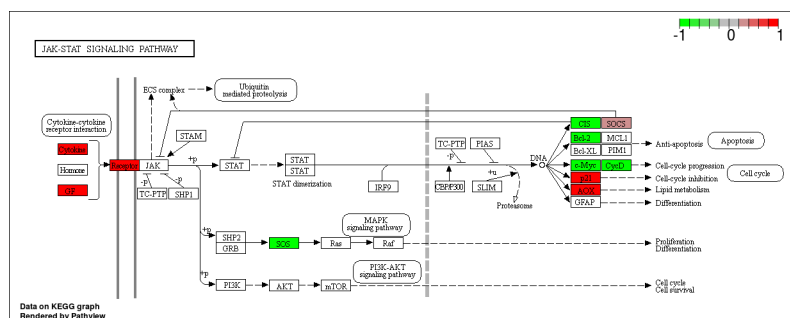
Figure S1c. KEGG pathway: 04014 Ras signaling pathway
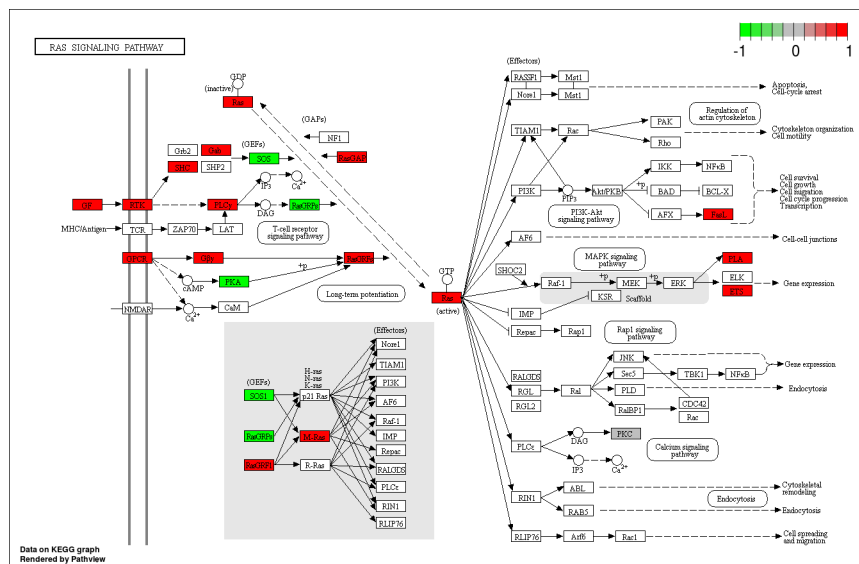
Figure S1d. KEGG pathway: 05200 Pathways in cancer

Figure S1e. KEGG pathway: 01100 Metabolic pathways

Figure S1f. KEGG pathway: 05166 HTLV-I infection

Human T-lymphotropic virus-I CD4+ T cell

GLUT1

gp46
gp21
HSPG

Virus entry

MAPK signaling pathway

-1 0 1

Increased S-phase progression

CycD2

DNA

TRRAP
TIP60

p30II

Virus latency

Reduced virion production

Inhibition of nuclear export

Tax mRNA
Rex mRNA

(Target cell) (Donor cell)

Virological synapse

LFA1
CD4
ICAM1
p8

ICAM1
Env
LFA1
TLN
Gag

RAS   MEK1/2   ERK1/2

Microtubule organizing center (MTOC) relocation

RNA transport

RanBP2
Ran
CRM1

Rex

MHC-I

p8

Gag/Pro/Pol mRNA
Env mRNA

Nuclear export

Virion production

ER
CRT
CNX

p12

Ca²⁺

CN   —P   NFAT   DNA   IL-2   T cell activation

Interference with MHC1 antigen presentation

Antigen processing and presentation

IL2R   Jak1/3   +P   STAT5

MHC-I
β2M

Proteasomal degradation

Genetic alterations in adult T-cell leukemia
Tumor suppressors: p16, p53

FPPS   Ras

Tax1BP2
RanBP1

p13II

Tax

ROS

IkB

FP12

Ca²⁺

Apoptosis

Apoptosis

Inl3INK4a
p14INK4a

Cdk4
CycD   +P   Rb

Mad1

Mad2
BubR1
Bub3

APC/C
Cdc20

+u
Securin   Esp1   Aneuploidy

CycB2

Tax

p21/waf1   Cyc/A/E
Cdk2   +P   E2F   DNA   G1/S progression

Cell cycle

Cell cycle

Attenuation of DNA-damage induced G2 arrest

ATM/ATR   Chk1/2   +P   p53

p53 signaling pathway

PI3K   PIP3   Akt

Protein translation
Cell survival
Cell proliferation

PTEN

PI3K-Akt signaling pathway

HBZ

TNF signaling pathway

MEKK1   DLG-1   SEK1   JNK   +P   AP1   DNA   MMP7   Matrix proteolytic degradation

TNFα   TNFR

IL1R
TCR
CD3

MEKK3

IKKα
IKKβ
IKKγ

+P
RelA   DNA

IL2   IL2R   Proliferation

GPS2   Tax   IKKγ   NF-kappa B signaling pathway   NFκB

IL13   IL-15   Inflammation

IL10R
CD40
BAFFR

NIK   IKKα   NFκB

IL-6
GM-CSF
TNFβ
BcnL   XIAP   Anti-apoptotic effect

TTP   TNFα overexpression

TNFα mRNA   TGF-β signaling pathway

TGFβ   TGFBR   +P   Smad2/3
Smad4   DNA

NFY   DNA   MHC-II

SRF   TBP   DNA   c-Fos   Egr-1   Cellular transformation

HTLV-I proteins

Structural proteins   Non-structural proteins

Gag   p12I   Rex
Pro   p13II   Tax
Pol   p30II   HBZ
Env   p21III

AC   cAMP   PKA   +P

TCF   Fra1   Egr-2

CREB   TORC   CycD1   Cell cycle progression

HBZ   Viral transcription

MSX2   Tax   p300
P/CAF

E47   DNA   βpol   Lck
Bax   p55INK4a

c-myc   DNA   TERT

Data on KEGG graph
Rendered by Pathview

Figure S1g. KEGG pathway: 05146 Amoebiasis

Figure S1h. KEGG pathway: 04151 PI3K-Akt signaling pathway

Figure S1i. KEGG pathway: 05205 Proteoglycans in cancer

Figure S1j. KEGG pathway: 04062 Chemokine signaling pathway

Table S1. Enriched pathways from the day 9 WT vs KD RNAseq comparison.

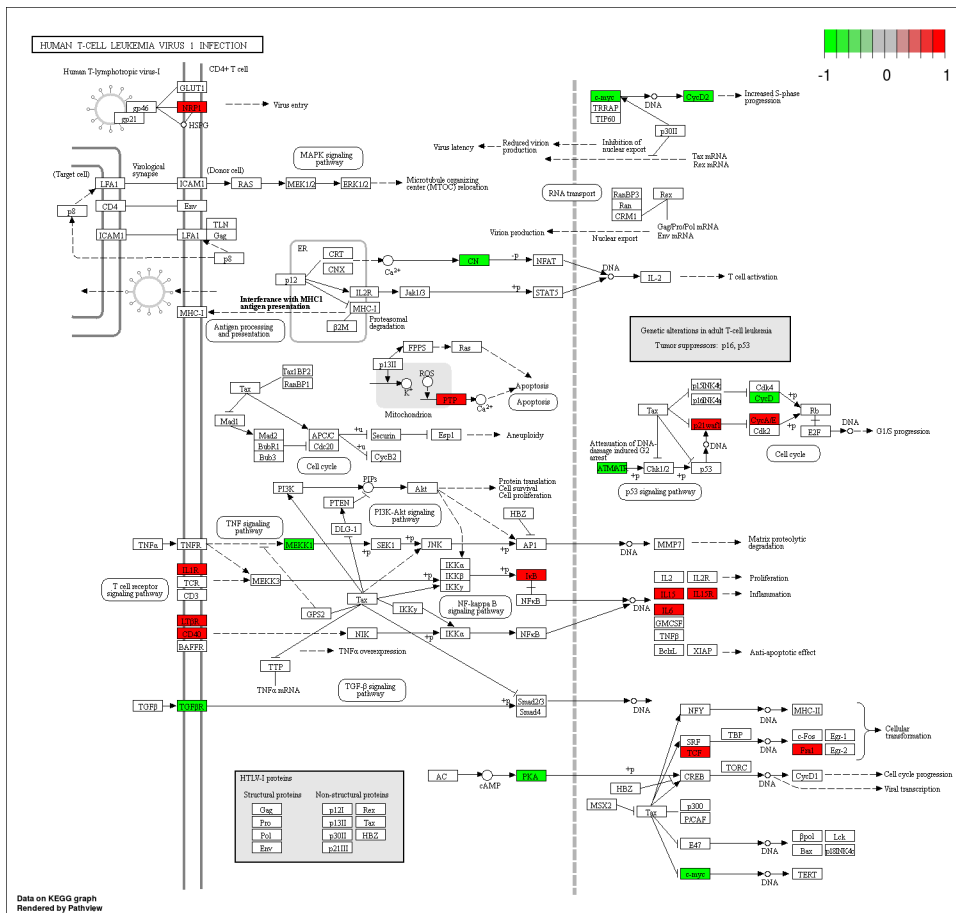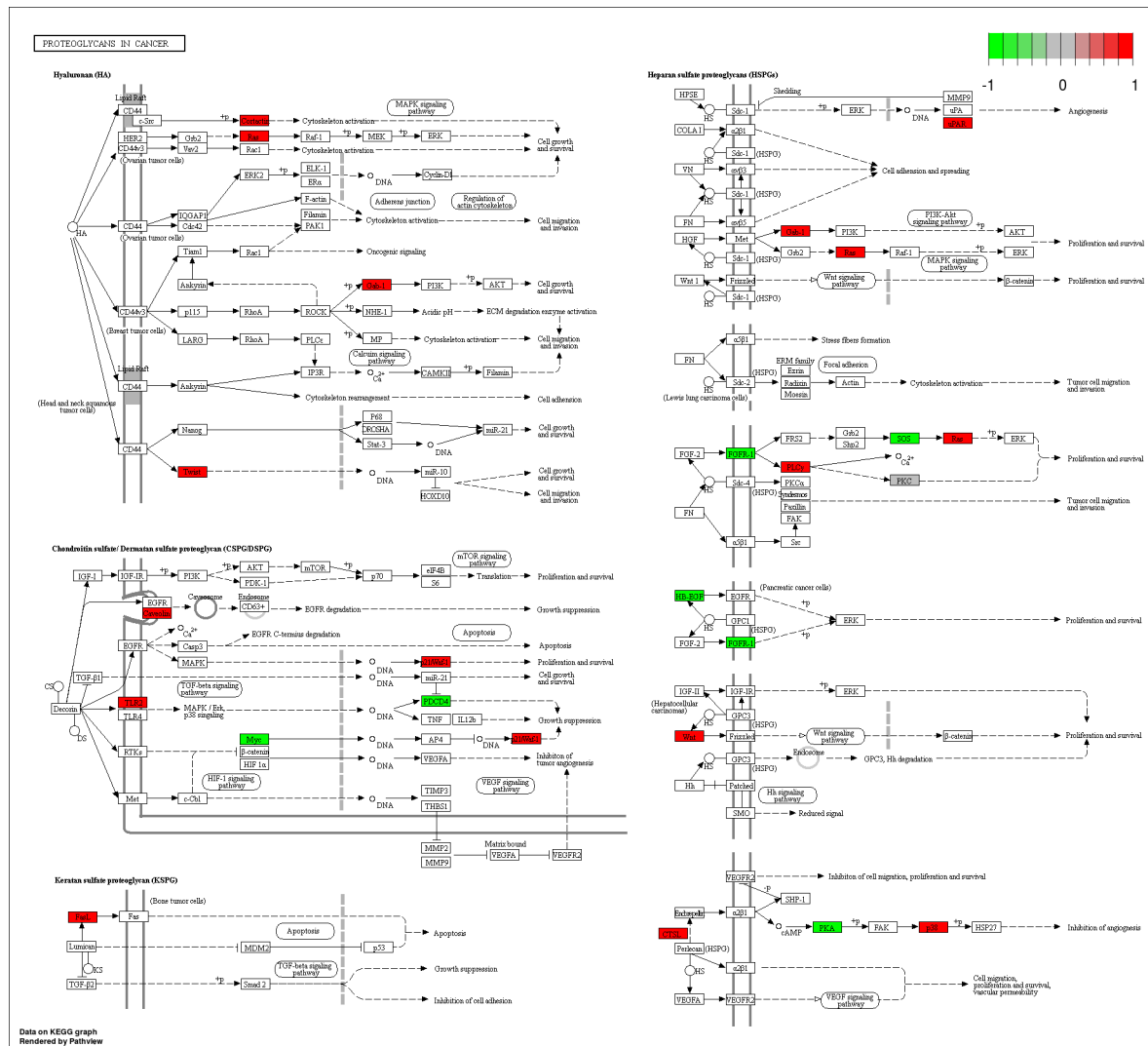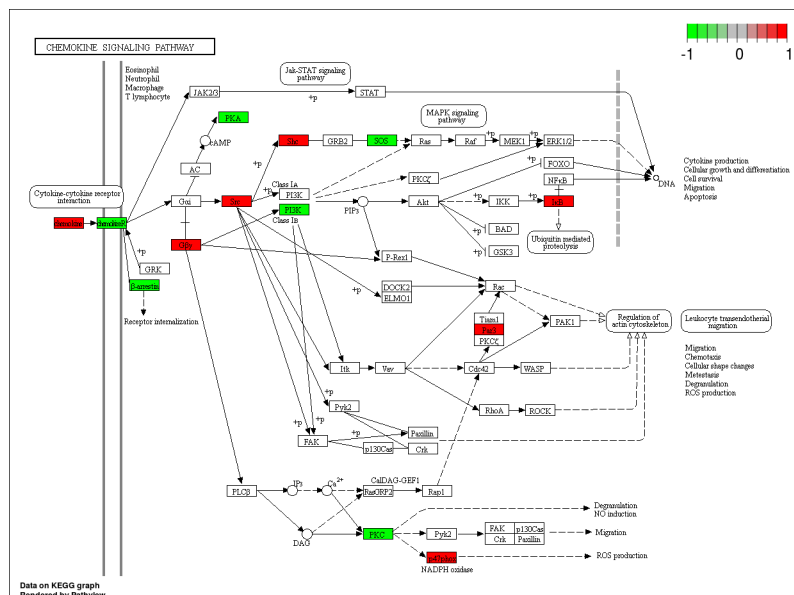| proteins	hits	pvalue__fdr	term__description	genes
260	51	1.55e-30	Cytokine-cytokine receptor interaction	CCL22, CCR1, ccr2, ccr8, cd27, CD40, cd40lg, CSF1R, CSF3R, CXCL11, CXCL13, cxcr1, cxcr3, cxcr4, CXCR6, FASLG, flt3lg, FLT4, IFNG, IFNGR1, IFNK, IL10, il13, IL13RA1, IL15, IL15RA, IL1R1, IL1R2, IL1RAP, IL22RA2, IL23R, IL26, IL28A, IL6, IL6R, il7r, LIFR, ltb, LTBR, NGFR, OSMR, PDGFA, PDGFRB, TNFRSF10C, TNFRSF21, TNFRSF8, TNFSF10, TNFSF13B, tnfsf14, tnfsf8, VEGFC
154	28	1.56e-15	Jak-STAT signaling pathway	ccnd2, cish, CSF3R, IFNG, IFNGR1, IFNK, IL10, il13, IL13RA1, IL15, IL15RA, IL22RA2, IL23R, IL26, IL28A, IL6, IL6R, il7r, LIFR, myc, OSMR, pik3r5, socs2, SOCS3, sos1, SPRED1, SPRED3, SPRY4
219	31	3.06e-14	Ras signaling pathway	CSF1R, EFNA1, ETS2, FASLG, fgfr1, FLT4, GAB1, GNB4, HTR7, MRAS, NGFR, PDGFA, PDGFRB, pik3r5, PLA2G16, PLA2G2C, PLA2G2F, PLCG2, prkacb, prkcb, PRKCG, prkx, rasa3, RASAL2, RASGRF1, rasgrp4, rras2, SHC2, SHC4, sos1, VEGFC
320	35	8.92e-13	Pathways in cancer	axin2, bcl2, CCNA1, CDKN1A, COL4A2, CSF1R, CSF3R, DAPK2, FASLG, fgfr1, flt3lg, IL6, ITGA3, itga6, LAMA1, LAMB3, LAMC1, lef1, myc, NFKBIA, PDGFA, PDGFRB, pik3r5, PLCG2, prkcb, PRKCG, RET, sos1, SPI1, tcf7, TGFA, VEGFC, WNT11, WNT7B, WNT8B
1160	70	2.92e-12	Metabolic pathways	ACSL1, acsl6, AK7, ALPL, AMACR, AOX1, ass1, ATP6V0A1, ATP6V0A4, atp6v1e2, B3GNT3, B4GALNT1, bdh1, CDS1, CMPK2, COX6B2, cpox, CYP27B1, CYP2E1, CYP2J2, DGAT2, DGKG, dhrs3, DHRS9, dpyd, DSE, FUT7, GALM, GALNT10, GALNT2, GBGT1, GCNT1, GCNT3, GCNT4, GGT5, GK, GLDC, hadh, HAL, HDC, HK3, HSD11B1, hsd17b8, HSD3B7, IL4I1, IMPA2, inpp4b, LPIN3, man1c1, mgat5, NAGS, nt5m, PAPSS2, PGD, PGS1, PLA2G16, PLA2G2C, PLA2G2F, PLCG2, PNLIPRP3, PPAP2C, pycr1, PYGL, rdh10, SAT1, SPHK1, SPR, ST3GAL4, TST, TYMP
250	30	4.19e-12	HTLV-I infection	atm, ccnd2, CD40, CDKN1A, ETS2, FOSL1, IL15, IL15RA, IL1R1, IL1R2, IL6, LTBR, map3k1, MRAS, mybl1, myc, NFKBIA, NRP1, PDGFA, PDGFRB, pik3r5, ppp3ca, prkacb, prkx, rras2, SLC25A4, SPI1, WNT11, WNT7B, WNT8B
104	20	6.85e-12	Amoebiasis	COL1A1, COL4A2, GNAL, gnaq, IFNG, IL10, IL1R1, IL1R2, IL6, LAMA1, LAMB3, LAMC1, pik3r5, prkacb, prkcb, PRKCG, prkx, SERPINB4, serpinb6, TLR2
336	34	1.04e-11	PI3K-Akt signaling pathway	bcl2, ccnd2, CDKN1A, COL1A1, COL4A2, CSF1R, CSF3R, EFNA1, FASLG, fgfr1, FLT4, GNB4, IL6, IL6R, il7r, ITGA3, itga4, itga6, ITGA9, LAMA1, LAMB3, LAMC1, myc, NGFR, OSMR, PDGFA, PDGFRB, PIK3AP1, pik3r5, PPP2R2B, sos1, TLR2, TNR, VEGFC
218	27	2.3e-11	Proteoglycans in cancer	CAV2, CDKN1A, CTSL1, CTTN, FASLG, fgfr1, GAB1, hbegf, MAPK11, MAPK12, MRAS, myc, pdcd4, pik3r5, PLAUR, PLCG2, prkacb, prkcb, PRKCG, prkx, rras2, sos1, TLR2, TWIST1, WNT11, WNT7B, WNT8B
178	24	6.21e-11	Chemokine signaling pathway	arrb1, CCL22, CCR1, ccr2, ccr8, CXCL11, CXCL13, cxcr1, cxcr3, cxcr4, CXCR6, GNB4, HCK, LYN, NCF1, NFKBIA, PARD3, pik3r5, prkacb, prkcb, prkx, SHC2, SHC4, sos1
164	23	7.06e-11	Transcriptional misregulation in cancer	atm, BCL2A1, CCNA1, ccnd2, CD40, CDK14, CDKN1A, CEBPB, CSF1R, ETV1, ETV5, ETV7, GZMB, IL1R2, IL6, klf3, myc, NGFR, PAX5, PDGFA, SIX1, SMAD1, SPI1
123	20	1.06e-10	Osteoclast differentiation	camk4, CSF1R, FOSL1, FOSL2, IFNG, IFNGR1, IL1R1, JUNB, LILRB4, MAPK11, MAPK12, NCF1, NFKBIA, OSCAR, pik3r5, PLCG2, ppp3ca, SOCS3, SPI1, TEC
202	25	1.15e-10	Focal adhesion	bcl2, CAV2, ccnd2, COL1A1, COL4A2, FLT4, ITGA3, itga4, itga6, ITGA9, LAMA1, LAMB3, LAMC1, MYL9, PDGFA, PDGFRB, pik3r5, prkcb, PRKCG, RASGRF1, SHC2, SHC4, sos1, TNR, VEGFC
88	17	2.08e-10	NF-kappa B signaling pathway	atm, bcl2, BCL2A1, CD40, cd40lg, DDX58, IL1R1, ltb, LTBR, LYN, malt1, NFKBIA, PLCG2, prkcb, TNFSF13B, tnfsf14, TRIM25
115	19	2.17e-10	Neurotrophin signaling pathway	bcl2, camk4, FASLG, GAB1, IRAK2, map3k1, MAPK11, MAPK12, matk, NFKBIA, NGFR, pik3r5, PLCG2, rps6ka2, SH2B2, sh2b3, SHC2, SHC4, sos1
251	27	3.67e-10	MAPK signaling pathway	arrb1, CACNA2D2, dusp10, FASLG, fgfr1, GADD45A, IL1R1, IL1R2, map3k1, MAP3K6, MAPK11, MAPK12, MRAS, myc, PDGFA, PDGFRB, ppp3ca, prkacb, prkcb, PRKCG, prkx, RASGRF1, rasgrp4, rps6ka2, rras2, sos1, STK3
123	18	4.98e-09	Axon guidance	ablim1, ABLIM3, cxcr4, EFNA1, epha4, EPHB2, FES, NRP1, NTN4, NTNG2, PLXNB1, PLXNB3, ppp3ca, RND1, SEMA4A, SEMA4B, SEMA6A, SEMA7A
123	18	4.98e-09	Natural killer cell mediated cytotoxicity	FASLG, FCER1G, GZMB, IFNG, IFNGR1, KIR2DL4, ncr3, pik3r5, PLCG2, ppp3ca, prkcb, PRKCG, RAET1E, SHC2, SHC4, sos1, TNFRSF10C, TNFSF10
85	15	9.6e-09	Hematopoietic cell lineage	cd55, CD59, CD8B, CD9, CSF1R, CSF3R, flt3lg, IL1R1, IL1R2, IL6, IL6R, il7r, ITGA3, itga4, itga6
146	19	1.13e-08	Hippo signaling pathway	axin2, ccnd2, ID1, LATS2, lef1, myc, PARD3, PPP2R2B, SMAD1, smad7, SOX2, STK3, tcf7, TEAD3, WNT11, WNT7B, WNT8B, WWTR1, YAP1
103	16	1.67e-08	HIF-1 signaling pathway	bcl2, CDKN1A, EDN1, HK3, HMOX1, IFNG, IFNGR1, IL6, IL6R, LTBR, PFKFB3, pik3r5, PLCG2, prkcb, PRKCG, TF
204	22	1.84e-08	Rap1 signaling pathway	CSF1R, DOCK4, DRD2, EFNA1, fgfr1, FLT4, gnao1, gnaq, ID1, MAPK11, MAPK12, MRAS, NGFR, PARD3, PDGFA, PDGFRB, pik3r5, prkcb, PRKCG, RAPGEF3, SIPA1L2, VEGFC

(continued)

proteins	hits	pvalue_fdr	term_description	genes
33	10	2.07e-08	African trypanosomiasis	APOL1, F2RL1, FASLG, gnaq, hba1, IFNG, IL10, IL6, prkcb, PRKCG
44	11	2.97e-08	Intestinal immune network for IgA production	CD40, cd40lg, cxcr4, icoslg, IL10, IL15, IL15RA, IL6, itga4, LTBR, TNFSF13B
94	15	3.13e-08	Inflammatory mediator regulation of TRP channels	CYP2J2, F2RL1, gnaq, HRH1, IL1R1, IL1RAP, MAPK11, MAPK12, pik3r5, PLCG2, prkacb, prkcb, PRKCG, prkx, ptger2
143	18	4.14e-08	MicroRNAs in cancer	atm, bcl2, ccnd2, CDKN1A, CYP1B1, HMOX1, irs2, myc, pdcd4, PDGFA, PDGFRB, PLCG2, prkcb, PRKCG, SHC4, sos1, TNR, ZEB2
112	16	4.56e-08	Toxoplasmosis	bcl2, CD40, cd40lg, gnao1, IFNG, IFNGR1, IL10, itga6, LAMA1, LAMB3, LAMC1, MAPK11, MAPK12, NFKBIA, pik3r5, TLR2
166	19	7.09e-08	Influenza A	DDX58, FASLG, FURIN, IFIH1, IFNG, IFNGR1, IL6, MAPK11, MAPK12, MX1, NFKBIA, pik3r5, prkcb, RSAD2, SOCS3, TLR3, TNFRSF10C, TNFSF10, TRIM25
170	19	1.02e-07	Tuberculosis	ATP6V0A1, ATP6V0A4, bcl2, CEBPB, CYP27B1, FCER1G, IFNG, IFNGR1, IL10, IL6, IRAK2, ITGAX, lsp1, malt1, MAPK11, MAPK12, ppp3ca, SPHK1, TLR2
174	19	1.44e-07	Calcium signaling pathway	camk4, GNAL, gnaq, GRIN2D, HRH1, HTR7, PDGFRB, PHKA1, PLCG2, ppp3ca, prkacb, prkcb, PRKCG, prkx, RYR2, SLC25A4, SLC8A1, SLC8A2, SPHK1
96	14	2.79e-07	Chagas disease (American trypanosomiasis)	FASLG, GNAL, gnao1, gnaq, IFNG, IFNGR1, IL10, IL6, MAPK11, MAPK12, NFKBIA, pik3r5, PPP2R2B, TLR2
68	12	2.91e-07	Complement and coagulation cascades	C1R, C2, C3AR1, cd55, CD59, CFB, CFH, F5, PLAUR, PROS1, SERPINA1, SERPING1
84	13	3.91e-07	Apoptosis	atm, bcl2, FASLG, IL1R1, IL1RAP, IRAK2, NFKBIA, pik3r5, ppp3ca, prkacb, prkx, TNFRSF10C, TNFSF10
136	16	6.04e-07	Cell adhesion molecules (CAMs)	CD274, CD276, CD40, cd40lg, CD8B, CLDN1, CLDN14, icoslg, itga4, itga6, ITGA9, NCAM2, NFASC, NLGN2, NTNG2, PVR
120	15	6.64e-07	FoxO signaling pathway	atm, ccnd2, CDKN1A, FASLG, GADD45A, IL10, IL6, il7r, irs2, klf2, MAPK11, MAPK12, pik3r5, sos1, TNFSF10
61	11	7.62e-07	Glioma	CDKN1A, PDGFA, PDGFRB, pik3r5, PLCG2, prkcb, PRKCG, SHC2, SHC4, sos1, TGFA
106	14	8.39e-07	TNF signaling pathway	BCL3, CEBPB, EDN1, IL15, IL6, JUNB, MAPK11, MAPK12, MLKL, MMP14, NFKBIA, pik3r5, SOCS3, VEGFC
107	14	9.2e-07	Cholinergic synapse	bcl2, camk4, CHRNA6, gnao1, gnaq, GNB4, kcnq1, KCNQ4, kcnq5, pik3r5, prkacb, prkcb, PRKCG, prkx
96	13	1.67e-06	Melanogenesis	EDN1, gnao1, gnaq, lef1, MC1R, prkacb, prkcb, PRKCG, prkx, tcf7, WNT11, WNT7B, WNT8B
189	18	2.03e-06	Epstein-Barr virus infection	bcl2, CCNA1, CD40, CDKN1A, DDX58, IFNG, IL10, LYN, MAPK11, MAPK12, myc, NFKBIA, pik3r5, PLCG2, prkacb, prkx, ptma, SPI1
98	13	2.03e-06	T cell receptor signaling pathway	cd40lg, CD8B, grap2, IFNG, IL10, malt1, MAPK11, MAPK12, NFKBIA, pik3r5, ppp3ca, sos1, TEC
83	12	2.12e-06	ErbB signaling pathway	CDKN1A, GAB1, hbegf, myc, pik3r5, PLCG2, prkcb, PRKCG, SHC2, SHC4, sos1, TGFA
83	12	2.12e-06	Gap junction	DRD2, gnaq, PDGFA, PDGFRB, prkacb, prkcb, PRKCG, prkx, sos1, TUBB2A, TUBB3, TUBB6
69	11	2.31e-06	RIG-I-like receptor signaling pathway	DDX58, IFIH1, IFNK, ISG15, map3k1, MAPK11, MAPK12, NFKBIA, rnf125, TBKBP1, TRIM25
192	18	2.33e-06	Endocytosis	arrb1, CAV2, CHMP4C, CSF1R, cxcr1, cxcr4, EHD3, EHD4, IQSEC2, ldlrap1, NEDD4L, PARD3, PSD3, RAB11FIP5, RAB31, RET, smad7, zfyve9
135	15	2.41e-06	Wnt signaling pathway	axin2, ccnd2, FOSL1, lef1, myc, ppp3ca, PRICKLE1, prkcb, PRKCG, prkx, tcf7, WNT11, WNT7B, WNT8B
139	15	3.44e-06	Hepatitis B	bcl2, CCNA1, CDKN1A, DDX58, FASLG, IFIH1, IL6, map3k1, myc, NFKBIA, pik3r5, prkcb, PRKCG, TLR2, TLR3
73	11	3.81e-06	Arrhythmogenic right ventricular cardiomyopathy (ARVC)	CACNA2D2, DSP, ITGA3, itga4, itga6, ITGA9, lef1, LMNA, RYR2, SLC8A1, tcf7
124	14	4.5e-06	Dopaminergic synapse	DRD2, GNAL, gnao1, gnaq, GNB4, KIF5A, MAPK11, MAPK12, PPP2R2B, ppp3ca, prkacb, prkcb, PRKCG, prkx
49	9	6.78e-06	Mineral absorption	HMOX1, MT1E, MT1F, MT1G, MT1H, MT1M, SLC8A1, STEAP1, TF
129	14	6.88e-06	Measles	ccnd2, DDX58, FASLG, IFIH1, IFNG, IFNGR1, il13, IL6, MX1, NFKBIA, pik3r5, TLR2, TNFRSF10C, TNFSF10
63	10	6.88e-06	Long-term potentiation	camk4, gnaq, GRIN2D, ppp3ca, prkacb, prkcb, PRKCG, prkx, RAPGEF3, rps6ka2
113	13	8.24e-06	Leukocyte transendothelial migration	CLDN1, CLDN14, cxcr4, itga4, MAPK11, MAPK12, MYL9, NCF1, pik3r5, PLCG2, prkcb, PRKCG, RAPGEF3
132	14	8.61e-06	Insulin signaling pathway	HK3, irs2, pde3b, PHKA1, pik3r5, prkacb, prkx, PYGL, SH2B2, SHC2, SHC4, socs2, SOCS3, sos1

proteins	hits	pvalue_fdr	term_description	genes
65	10	8.61e-06	Epithelial cell signaling in Helicobacter pylori infection	ATP6V0A1, ATP6V0A4, atp6v1e2, cxcr1, hbegf, LYN, MAPK11, MAPK12, NFKBIA, PLCG2
51	9	8.61e-06	Vibrio cholerae infection	ATP6V0A1, ATP6V0A4, atp6v1e2, kcnq1, PLCG2, prkacb, prkcb, PRKCG, prkx
84	11	1.34e-05	Protein digestion and absorption	COL1A1, COL4A2, COL7A1, COL9A2, KCNE3, KCNN4, kcnq1, slc16a10, SLC7A8, SLC8A1, SLC8A2
69	10	1.43e-05	Prolactin signaling pathway	ccnd2, cish, MAPK11, MAPK12, pik3r5, SHC2, SHC4, socs2, SOCS3, sos1
69	10	1.43e-05	Leishmaniasis	IFNG, IFNGR1, IL10, itga4, MAPK11, MAPK12, NCF1, NFKBIA, prkcb, TLR2
85	11	1.43e-05	Prostate cancer	bcl2, CDKN1A, fgfr1, lef1, NFKBIA, PDGFA, PDGFRB, pik3r5, sos1, tcf7, TGFA
141	14	1.69e-05	Adrenergic signaling in cardiomyocytes	bcl2, CACNA2D2, gnaq, kcnq1, MAPK11, MAPK12, pik3r5, PPP2R2B, prkacb, prkx, RAPGEF3, RYR2, SLC8A1, TNNI3
87	11	1.75e-05	Fc gamma R-mediated phagocytosis	GSN, HCK, LYN, MYO10, NCF1, pik3r5, PLCG2, PPAP2C, prkcb, PRKCG, SPHK1
88	11	1.92e-05	Dilated cardiomyopathy	CACNA2D2, ITGA3, itga4, itga6, ITGA9, LMNA, prkacb, prkx, RYR2, SLC8A1, TNNI3
127	13	2.54e-05	Tight junction	CGN, CLDN1, CLDN14, CTTN, epb41, MRAS, MYH11, MYL9, PARD3, PPP2R2B, prkcb, PRKCG, rras2
59	9	2.61e-05	VEGF signaling pathway	MAPK11, MAPK12, pik3r5, PLCG2, ppp3ca, prkcb, PRKCG, SHC2, SPHK1
128	13	2.68e-05	Hepatitis C	CDKN1A, CLDN1, CLDN14, DDX58, IFIT1, MAPK11, MAPK12, NFKBIA, pik3r5, PPP2R2B, SOCS3, sos1, TLR3
46	8	3.03e-05	Malaria	CD40, cd40lg, hba1, IFNG, IL10, IL6, klrb1, TLR2
62	9	3.79e-05	Inflammatory bowel disease (IBD)	foxp3, IFNG, IFNGR1, IL10, il13, IL23R, IL6, TBX21, TLR2
174	15	3.89e-05	Herpes simplex infection	cfp, DDX58, FASLG, GTF2IRD1, IFIH1, IFIT1, IFNG, IFNGR1, IL15, IL6, NFKBIA, SOCS3, TLR2, TLR3, tnfsf14
82	10	5.83e-05	Hypertrophic cardiomyopathy (HCM)	CACNA2D2, IL6, ITGA3, itga4, itga6, ITGA9, LMNA, RYR2, SLC8A1, TNNI3
66	9	6.12e-05	Fc epsilon RI signaling pathway	FCER1G, il13, LYN, MAPK11, MAPK12, pik3r5, PLCG2, prkcb, sos1
84	10	7.03e-05	Small cell lung cancer	bcl2, COL4A2, ITGA3, itga6, LAMA1, LAMB3, LAMC1, myc, NFKBIA, pik3r5
85	10	7.59e-05	ECM-receptor interaction	COL1A1, COL4A2, ITGA3, itga4, itga6, ITGA9, LAMA1, LAMB3, LAMC1, TNR
85	10	7.59e-05	Rheumatoid arthritis	ATP6V0A1, ATP6V0A4, atp6v1e2, CTSL1, IFNG, IL15, IL6, ltb, TLR2, TNFSF13B
69	9	8.35e-05	B cell receptor signaling pathway	LYN, malt1, NFKBIA, PIK3AP1, pik3r5, PLCG2, ppp3ca, prkcb, sos1
87	10	9.08e-05	GnRH signaling pathway	gnaq, hbegf, map3k1, MAPK11, MAPK12, MMP14, prkacb, prkcb, prkx, sos1
70	9	9.15e-05	Gastric acid secretion	CA2, gnaq, KCNJ10, kcnq1, prkacb, prkcb, PRKCG, prkx, SSTR2
90	10	0.000119	Pancreatic secretion	CA2, gnaq, kcnq1, PLA2G2C, PLA2G2F, prkcb, PRKCG, RAB27B, RYR2, slc4a4
91	10	0.000129	Glycerophospholipid metabolism	CDS1, DGKG, gpd1l, lpgat1, LPIN3, PGS1, PLA2G16, PLA2G2C, PLA2G2F, PPAP2C
152	13	0.00014	Oxytocin signaling pathway	CACNA2D2, camk4, CDKN1A, gnao1, gnaq, MYL9, pik3r5, ppp3ca, prkacb, prkcb, PRKCG, prkx, RYR2
31	6	0.000186	Mucin type O-Glycan biosynthesis	B4GALT5, GALNT10, GALNT2, GCNT1, GCNT3, GCNT4
137	12	0.00021	Alcoholism	camk4, DRD2, gnao1, GNB4, GRIN2D, GRIN3B, HIST1H2AC, HIST1H2BD, HIST1H2BJ, SHC2, SHC4, sos1
181	14	0.00021	Viral carcinogenesis	CCNA1, ccnd2, ccr8, CDKN1A, GSN, HIST1H2BD, HIST1H2BJ, LTBR, LYN, NFKBIA, pik3r5, PMAIP1, prkacb, prkx
46	7	0.00022	Endocrine and other factor-regulated calcium reabsorption	gnaq, KLK1, prkacb, prkcb, PRKCG, prkx, SLC8A1
208	15	0.000253	Regulation of actin cytoskeleton	fgfr1, GSN, ITGA3, itga4, itga6, ITGA9, ITGAX, MRAS, MYL9, NCKAP1, PDGFA, PDGFRB, pik3r5, rras2, sos1
34	6	0.000302	Allograft rejection	CD40, cd40lg, FASLG, GZMB, IFNG, IL10
65	8	0.000309	Amphetamine addiction	camk4, GRIN2D, GRIN3B, ppp3ca, prkacb, prkcb, PRKCG, prkx
66	8	0.000341	p53 signaling pathway	atm, ccnd2, CDKN1A, GADD45A, PERP, PMAIP1, sesn3, TP53I3
50	7	0.000358	Amyotrophic lateral sclerosis (ALS)	bcl2, GRIN2D, MAPK11, MAPK12, NEFM, ppp3ca, PRPH

proteins	hits	pvalue_fdr	term_description	genes
87	9	0.000439	Morphine addiction	arrb1, gnao1, GNB4, pde3b, pde7b, prkacb, prkcb, PRKCG, prkx
69	8	0.000453	Pertussis	C1R, C2, IL10, IL6, IRF8, MAPK11, MAPK12, SERPING1
109	10	0.000508	Glutamatergic synapse	gnao1, gnaq, GNB4, GRIN2D, GRIN3B, ppp3ca, prkacb, prkcb, PRKCG, prkx
109	10	0.000508	Serotonergic synapse	CYP2J2, gnao1, gnaq, GNB4, HTR7, prkacb, prkcb, PRKCG, prkx, RAPGEF3
90	9	0.000546	Circadian entrainment	gnao1, gnaq, GNB4, GRIN2D, prkacb, prkcb, PRKCG, prkx, RYR2
55	7	0.000618	Acute myeloid leukemia	CCNA1, lef1, myc, pik3r5, sos1, SPI1, tcf7
26	5	0.000679	Collecting duct acid secretion	ATP6V0A1, ATP6V0A4, atp6v1e2, CA2, slc12a7
93	9	0.000679	Estrogen signaling pathway	gnao1, gnaq, hbegf, pik3r5, prkacb, prkx, SHC2, SHC4, sos1
94	9	0.000728	Systemic lupus erythematosus	C1R, C2, CD40, cd40lg, HIST1H2AC, HIST1H2BD, HIST1H2BJ, IFNG, IL10
115	10	0.000732	Vascular smooth muscle contraction	CALD1, gnaq, MYH11, MYL9, PLA2G2C, PLA2G2F, prkacb, prkcb, PRKCG, prkx
115	10	0.000732	Thyroid hormone signaling pathway	myc, pik3r5, PLCG2, prkacb, prkcb, PRKCG, prkx, RCAN2, slc16a10, tbc1d4
96	9	0.000828	Retrograde endocannabinoid signaling	gnao1, gnaq, GNB4, MAPK11, MAPK12, prkacb, prkcb, PRKCG, prkx
77	8	0.000868	TGF-beta signaling pathway	CHRD, E2F5, ID1, IFNG, myc, SMAD1, smad7, zfyve9
28	5	0.000905	Linoleic acid metabolism	CYP2E1, CYP2J2, PLA2G16, PLA2G2C, PLA2G2F
28	5	0.000905	Asthma	CD40, cd40lg, FCER1G, IL10, il13
78	8	0.000921	Phosphatidylinositol signaling system	CDS1, DGKG, IMPA2, inpp4b, pik3r5, PLCG2, prkcb, PRKCG
79	8	0.000996	Progesterone-mediated oocyte maturation	CCNA1, MAPK11, MAPK12, pde3b, pik3r5, prkacb, prkx, rps6ka2
269	16	0.00107	Neuroactive ligand-receptor interaction	C3AR1, CHRNA6, CHRNE, DRD2, F2RL1, GRIN2D, GRIN3B, HRH1, HTR7, MC1R, p2ry10, PARD3, ptger2, SSTR2, SSTR3, vipr1
101	9	0.00113	Toll-like receptor signaling pathway	CD40, CXCL11, IL6, MAPK11, MAPK12, NFKBIA, pik3r5, TLR2, TLR3
81	8	0.00115	Insulin secretion	gnaq, KCNN4, prkacb, prkcb, PRKCG, prkx, RYR2, TRPM4
126	10	0.00138	Platelet activation	COL1A1, FCER1G, gnaq, LYN, MAPK11, MAPK12, pik3r5, PLCG2, prkacb, prkx
68	7	0.00196	PPAR signaling pathway	ACSL1, acsl6, CPT1C, FABP5, GK, PLTP, SLC27A2
50	6	0.002	Hedgehog signaling pathway	GAS1, prkacb, prkx, WNT11, WNT7B, WNT8B
50	6	0.002	Endometrial cancer	axin2, lef1, myc, pik3r5, sos1, tcf7
157	11	0.00206	cGMP-PKG signaling pathway	CNGA1, gnaq, GTF2IRD1, irs2, MYL9, pde3b, pik3r5, ppp3ca, SLC25A4, SLC8A1, SLC8A2
69	7	0.00207	Chronic myeloid leukemia	CDKN1A, myc, NFKBIA, pik3r5, SHC2, SHC4, sos1
51	6	0.00217	Staphylococcus aureus infection	C1R, C2, C3AR1, CFB, CFH, IL10
70	7	0.00222	Thyroid hormone synthesis	gnaq, gsr, prkacb, prkcb, PRKCG, prkx, SLC26A4
36	5	0.00264	Prion diseases	IL6, LAMC1, NCAM2, prkacb, prkx
54	6	0.00283	Glycerolipid metabolism	DGAT2, DGKG, GK, LPIN3, PNLIPRP3, PPAP2C
54	6	0.00283	Non-small cell lung cancer	pik3r5, PLCG2, prkcb, PRKCG, sos1, TGFA
22	4	0.00287	Dorso-ventral axis formation	ETS2, ETV7, sos1, SPIRE1
55	6	0.00307	Basal cell carcinoma	axin2, lef1, tcf7, WNT11, WNT7B, WNT8B
142	10	0.00309	Phagosome	ATP6V0A1, ATP6V0A4, atp6v1e2, C1R, CTSL1, NCF1, TLR2, TUBB2A, TUBB3, TUBB6
120	9	0.00338	Lysosome	ATP6V0A1, ATP6V0A4, CD68, CTSL1, gnptab, LAMP3, NAPSA, NPC1, SCARB2
121	9	0.00353	Cell cycle	atm, CCNA1, ccnd2, cdc14a, CDC14B, CDKN1A, E2F5, GADD45A, myc
39	5	0.00353	Fat digestion and absorption	ABCA1, DGAT2, PLA2G2C, PLA2G2F, PPAP2C
57	6	0.00353	Arginine and proline metabolism	ass1, CARNS1, NAGS, pycr1, SAT1, SMOX

(continued)

proteins	hits	pvalue_fdr	term_description	genes
57	6	0.00353	Colorectal cancer	axin2, bcl2, lef1, myc, pik3r5, tcf7
61	6	0.00496	Arachidonic acid metabolism	CYP2E1, CYP2J2, GGT5, PLA2G16, PLA2G2C, PLA2G2F
82	7	0.005	Salivary secretion	CST3, gnaq, KCNN4, prkacb, prkcb, PRKCG, prkx
26	4	0.005	Glycosphingolipid biosynthesis - lacto and neolacto series	B3GNT3, FUT7, GBGT1, ST3GAL4
26	4	0.005	Butanoate metabolism	bdh1, hadh, L2HGDH, OXCT2
27	4	0.00572	Thyroid cancer	lef1, myc, RET, tcf7
45	5	0.00637	Type II diabetes mellitus	HK3, irs2, pik3r5, socs2, SOCS3
67	6	0.00761	Adipocytokine signaling pathway	ACSL1, acsl6, CPT1C, irs2, NFKBIA, SOCS3
68	6	0.00813	Bile secretion	AQP9, CA2, NCEH1, prkacb, prkx, slc4a4
49	5	0.00897	Cocaine addiction	DRD2, GRIN2D, GRIN3B, prkacb, prkx
49	5	0.00897	Autoimmune thyroid disease	CD40, cd40lg, FASLG, GZMB, IL10
17	3	0.0112	Nitrogen metabolism	CA12, CA2, ca6
73	6	0.0112	Bacterial invasion of epithelial cells	CAV2, CTTN, GAB1, pik3r5, SHC2, SHC4
52	5	0.0113	Pathogenic Escherichia coli infection	CLDN1, CTTN, TUBB2A, TUBB3, TUBB6
35	4	0.0139	Primary immunodeficiency	CD40, cd40lg, CD8B, il7r
78	6	0.015	Peroxisome	abcd2, ACSL1, acsl6, AMACR, DECR2, SLC27A2
36	4	0.015	Aldosterone-regulated sodium reabsorption	NEDD4L, pik3r5, prkcb, PRKCG
36	4	0.015	Graft-versus-host disease	FASLG, GZMB, IFNG, IL6
37	4	0.0164	Bladder cancer	CDKN1A, DAPK2, myc, TYMP
58	5	0.0171	Long-term depression	gnao1, gnaq, LYN, prkcb, PRKCG
59	5	0.0183	mTOR signaling pathway	CAB39L, pik3r5, prkcb, PRKCG, rps6ka2
83	6	0.0192	GABAergic synapse	gnao1, GNB4, prkacb, prkcb, PRKCG, prkx
39	4	0.0192	Tryptophan metabolism	AOX1, CYP1B1, hadh, IL4I1
61	5	0.0205	Cytosolic DNA-sensing pathway	AIM2, DDX58, IL6, NFKBIA, ZBP1
40	4	0.0207	Ether lipid metabolism	PLA2G16, PLA2G2C, PLA2G2F, PPAP2C
23	3	0.024	Fatty acid elongation	ELOVL3, ELOVL7, hadh
43	4	0.0262	Fatty acid degradation	ACSL1, acsl6, CPT1C, hadh
24	3	0.0267	alpha-Linolenic acid metabolism	PLA2G16, PLA2G2C, PLA2G2F
9	2	0.0268	Synthesis and degradation of ketone bodies	bdh1, OXCT2
66	5	0.0271	Antigen processing and presentation	CD8B, CTSL1, IFI30, IFNG, KIR2DL4
44	4	0.0276	Valine, leucine and isoleucine degradation	AOX1, hadh, IL4I1, OXCT2
119	7	0.0298	AMPK signaling pathway	CAB39L, CCNA1, CPT1C, irs2, PFKFB3, pik3r5, PPP2R2B
147	8	0.03	Non-alcoholic fatty liver disease (NAFLD)	COX6B2, CYP2E1, FASLG, IL6, IL6R, irs2, pik3r5, SOCS3
69	5	0.0314	Melanoma	CDKN1A, fgfr1, PDGFA, PDGFRB, pik3r5
10	2	0.0317	Sulfur metabolism	PAPSS2, TST
27	3	0.0347	Histidine metabolism	CARNS1, HAL, HDC
27	3	0.0347	Nicotinate and nicotinamide metabolism	AOX1, NAMPTL, nt5m

proteins	hits	pvalue_fdr	term_description	genes
48	4	0.0353	Fatty acid metabolism	ACSL1, acsl6, CPT1C, hadh
49	4	0.0375	Glutathione metabolism	GGT5, gsr, GSTT2B, PGD
50	4	0.0398	Ovarian steroidogenesis	CYP1B1, CYP2J2, prkacb, prkx
29	3	0.0409	beta-Alanine metabolism	CARNS1, dpyd, SMOX
75	5	0.0412	Cardiac muscle contraction	CACNA2D2, COX6B2, RYR2, SLC8A1, TNNI3
53	4	0.0469	Steroid hormone biosynthesis	CYP1B1, CYP2E1, HSD11B1, hsd17b8
53	4	0.0469	Legionellosis	eef1a1, IL6, NFKBIA, TLR2

Table S2a. Type 2 clone enriched KEGG pathways.

proteins	hits	pvalue_fdr	term_description
143	13	1.11e-07	MicroRNAs in cancer
134	12	3.09e-07	Ubiquitin mediated proteolysis
115	11	4.74e-07	Neurotrophin signaling pathway
202	13	1.85e-06	Focal adhesion
336	15	1.59e-05	PI3K-Akt signaling pathway
139	10	1.67e-05	Hepatitis B
56	7	1.67e-05	NOD-like receptor signaling pathway
57	7	1.67e-05	Shigellosis
181	11	1.67e-05	Viral carcinogenesis
192	11	2.69e-05	Endocytosis
208	11	5.33e-05	Regulation of actin cytoskeleton
320	13	0.000106	Pathways in cancer
52	6	0.000106	Pathogenic Escherichia coli infection
151	9	0.000125	RNA transport
115	8	0.000125	Thyroid hormone signaling pathway
85	7	0.000141	Prostate cancer
120	8	0.00015	FoxO signaling pathway
70	6	0.00043	Adherens junction
73	6	0.000517	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
189	9	0.000539	Epstein-Barr virus infection
50	5	0.000777	Lysine degradation
250	10	0.000777	HTLV-I infection
51	5	0.000777	Fanconi anemia pathway
251	10	0.000777	MAPK signaling pathway
83	6	0.000807	ErbB signaling pathway
84	6	0.000807	Small cell lung cancer
162	8	0.000807	Protein processing in endoplasmic reticulum
164	8	0.000848	Transcriptional misregulation in cancer
218	9	0.0011	Proteoglycans in cancer
59	5	0.00122	mTOR signaling pathway
132	7	0.00122	Insulin signaling pathway
63	5	0.00153	Long-term potentiation
98	6	0.00153	T cell receptor signaling pathway
142	7	0.00175	Phagosome
1160	23	0.00175	Metabolic pathways
69	5	0.00213	Chronic myeloid leukemia
204	8	0.00281	Rap1 signaling pathway
119	6	0.00375	AMPK signaling pathway
121	6	0.00399	Cell cycle
123	6	0.00424	Axon guidance
50	4	0.00502	Endometrial cancer
129	6	0.00515	Measles
87	5	0.00515	GnRH signaling pathway
88	5	0.0053	NF-kappa B signaling pathway
135	6	0.00609	Wnt signaling pathway
55	4	0.0064	Acute myeloid leukemia
29	3	0.00901	Circadian rhythm
61	4	0.00901	Glioma
64	4	0.0105	Renal cell carcinoma
32	3	0.0113	SNARE interactions in vesicular transport
66	4	0.0113	p53 signaling pathway
112	5	0.0129	Toxoplasmosis
113	5	0.0131	Leukocyte transendothelial migration
163	6	0.0131	Purine metabolism
73	4	0.0151	Bacterial invasion of epithelial cells

proteins	hits	pvalue_fdr	term_description
170	6	0.0155	Tuberculosis
39	3	0.0176	Regulation of autophagy
127	5	0.0197	Tight junction
83	4	0.0217	Gap junction
43	3	0.0217	Aminoacyl-tRNA biosynthesis
43	3	0.0217	Proteasome
84	4	0.022	Apoptosis
44	3	0.0222	Basal transcription factors
85	4	0.0222	ECM-receptor interaction
47	3	0.0261	Notch signaling pathway
49	3	0.0288	Mineral absorption
93	4	0.0289	Estrogen signaling pathway
54	3	0.0363	Non-small cell lung cancer
154	5	0.0363	Jak-STAT signaling pathway
105	4	0.0417	Oocyte meiosis
106	4	0.0425	TNF signaling pathway

Table S2b. Class 3 clone enriched KEGG pathways.

proteins	hits	pvalue_fdr	term_description
142	3	0.00347	Phagosome
120	2	0.0453	Lysosome
162	2	0.0453	Protein processing in endoplasmic reticulum
163	2	0.0453	Purine metabolism

Table S2c. Class 4 clones enriched KEGG pathways.

proteins	hits	pvalue_fdr	term_description
189	2	0.0075	Epstein-Barr virus infection
35	1	0.0305	Primary immunodeficiency
43	1	0.0305	Proteasome
66	1	0.0305	Antigen processing and presentation
71	1	0.0305	RNA degradation
85	1	0.0305	Hematopoietic cell lineage
98	1	0.0305	T cell receptor signaling pathway
136	1	0.0369	Cell adhesion molecules (CAMs)
192	1	0.0461	Endocytosis

Table S3a. Class 4 clones.

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr17-40636995	1056	SMARCE1	0	FALSE
chr12+6798669	1028	CD4	0	FALSE
chr13+28237187	1013	PAN3	0	FALSE
chr19+15410659	1005	AKAP8L	0	FALSE
chr14-31134696	929	HECTD1	0	FALSE
chr7+17293342	818	* anti-AHR	0	FALSE
chr10+100153865	804	ERLIN1	0	FALSE
chr1-26767786	801	ARID1A	0	TRUE
chr1-151432952	743	POGZ	0	FALSE
chr10-118040403	694	RAB11FIP2	0	FALSE
chr22-39133906	688	CBX7	0	FALSE
chr7+50229821	640	* AC020743.2	0	FALSE
chr5+137960267	616	FAM13B	0	FALSE
chr2+29127458	520	CLIP4	0	FALSE
chr11+244890	335	PSMD13	0	FALSE

Table S3b. Class 3 clones.

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr1-26772756	232	ARID1A	0	TRUE
chr11+88380500	229	CTSC	-42712	FALSE
chr16+53751175	209	FTO	0	FALSE
chr19-49613201	197	PRR12	0	FALSE
chr6-664023	186	EXOC2	0	FALSE
chr5-119383116	183	TNFAIP8	0	FALSE
chr9+89395778	178	SEMA4D	0	TRUE
chr2+71142723	175	MPHOSPH10	0	FALSE
chr12+123723972	173	ATP6V0A2	0	FALSE
chr1+27790582	165	STX12	0	FALSE
chr7+121359607	152	FAM3C	0	FALSE
chr6+90427063	151	MAP3K7	86508	TRUE
chr1-26713787	150	ARID1A	0	TRUE
chr5-179729487	143	CANX	0	FALSE
chr7-140145601	137	KDM7A	0	FALSE
chr19+9648087	128	ZNF562	0	FALSE
chr20-7991743	123	TMX4	0	FALSE
chr9+26913605	120	PLAA	0	FALSE
chr4-173365250	103	* AC097534.2	0	FALSE
chr3-60393473	95	FHIT	0	TRUE
chr16+14147619	88	MKL2	0	FALSE
chr1-26711441	71	ARID1A	0	TRUE
chr7-8011852	68	GLCCI1	0	FALSE
chr13-72883130	57	PIBF1	0	FALSE
chr2-58127212	54	VRK2	0	FALSE
chr3-94008956	52	ARL13B	0	FALSE
chr11-45957006	49	PHF21A	0	FALSE
chr2-224542227	43	CUL3	0	FALSE
chr3+48927526	37	ARIH2	0	FALSE
chr4-56446698	33	PAICS	0	FALSE
chr1-155541420	30	ASH1L	0	FALSE
chr8+100404494	28	* AP003472.1	0	FALSE

Table S3c. Class 2 clones.

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr2-25556775	627	DTNB	0	FALSE
chr4+106288473	593	TBCK	0	FALSE
chr8-6481555	573	MCPH1	0	TRUE
chr11+83167655	556	PCF11	0	FALSE
chr14-50504264	547	MAP4K5	0	FALSE
chr9-19095678	543	HAUS6	0	FALSE
chr1+180999423	535	STX6	0	FALSE
chr19-13124733	534	NACC1	0	FALSE
chr5-123407807	526	CEP120	0	FALSE
chr10+113876212	510	NHLRC2	0	FALSE
chr7-65388315	490	ZNF92	0	FALSE
chr19+10111211	444	PPAN,PPAN-P2RY11	0	FALSE
chr1+160582436	414	CD84	-2919	FALSE
chr9+7067305	405	KDM4C	0	TRUE
chr15+96894570	372	SPATA8	108954	FALSE
chr13-29818426	352	UBL3	0	TRUE
chr9+131688880	335	RAPGEF1	0	TRUE
chr17+12057361	330	MAP2K4	0	TRUE
chr17+4206976	323	ANKFY1	0	FALSE
chr1+155677040	321	YY1AP1	0	FALSE
chr12-120875751	318	SPPL3	0	TRUE
chr6-169706115	315	C6orf120,PHF10	0	FALSE
chr15+93003376	313	CHD2	0	TRUE
chr9-37867813	297	DCAF10	143	FALSE
chr11-107533164	292	ALKBH8	0	FALSE
chr6-73437663	290	CGAS	0	FALSE
chr5+37614750	286	WDR70	0	FALSE
chr1+26703377	282	ARID1A	0	TRUE
chr8-144784896	273	ZNF34	0	FALSE
chr11-105015840	265	CASP5	0	FALSE
chr11-34961888	259	PDHX	0	FALSE
chr11-66122073	251	PACS1	0	FALSE
chr13+111237167	249	ARHGEF7	0	FALSE
chr22+31533214	248	SFI1	0	FALSE
chr12+110145934	242	IFT81	0	FALSE
chr8+116693657	242	EIF3H	0	FALSE
chrX-48723402	240	SUV39H1	14385	FALSE
chr2+97766483	239	TMEM131	0	FALSE
chr14+104817801	238	LINC00638	-3398	FALSE
chr7-135617511	230	NUP205	0	FALSE
chr12+65208910	227	LEMD3	0	FALSE
chr1+113792074	225	RSBN1	0	FALSE
chr13+94576285	223	TGDS	0	FALSE
chr2+111134217	223	BCL2L11	0	TRUE
chr5-41812345	218	OXCT1	0	FALSE
chr4-173390431	216	SCRG1	0	FALSE
chr1-11017781	213	TARDBP	0	FALSE
chr7-105058647	212	KMT2E	0	FALSE
chr6-33699832	211	UQCC2	0	FALSE
chr7-111484560	211	IMMP2L	0	FALSE
chr17+63009173	210	TANC2	-362	FALSE
chr5+111488721	208	CAMK4	0	FALSE
chr7-38901332	208	VPS41	0	FALSE
chr9-5361612	206	PLGRKT	0	FALSE
chr11+90224755	204	CHORDC1	-1390	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr2+196785066	204	GTF3C3	0	FALSE
chr4-36136537	203	ARAP2	0	TRUE
chr21+15738024	202	USP25	0	FALSE
chr16+69579666	201	NFAT5	0	TRUE
chr3+105688148	199	CBLB	0	TRUE
chr5-171927932	199	FBXW11	0	FALSE
chrX-110017103	194	TMEM164	0	FALSE
chr22-21614243	191	UBE2L3	0	FALSE
chr1-70237527	188	SRSF11	0	FALSE
chr2+113917927	188	ACTR3	0	FALSE
chr9-130773011	185	ABL1	0	TRUE
chr1-42314207	184	FOXJ3	0	FALSE
chr5-58976258	180	PDE4D	0	TRUE
chr15-94242906	174	MCTP2	-55293	FALSE
chr4+672630	172	ATP5ME	0	FALSE
chr5+35909280	171	CAPSL	0	FALSE
chr9+5661422	170	RIC1	0	FALSE
chr7-100096743	164	MCM7	0	FALSE
chr21+29041930	161	USP16	0	FALSE
chrX-139835635	160	ATP11C	0	FALSE
chr15-90710978	159	CRTC3-AS1	0	FALSE
chr6+111325984	158	REV3L	0	FALSE
chr10+102138624	157	PPRC1	0	FALSE
chr12+6992436	157	EMG1,LPCAT3	0	FALSE
chr17-8204032	157	AURKB	697	FALSE
chr11+95844989	156	MTMR2	0	FALSE
chrX+154010642	155	IRAK1	0	FALSE
chr10+43158621	153	CSGALNACT2	0	FALSE
chr1-150090353	150	VPS45	0	FALSE
chr5+146257032	148	RBM27	0	FALSE
chrX+41154874	148	USP9X	0	FALSE
chr2-15449586	147	NBAS	0	FALSE
chr18-42007623	147	PIK3C3	0	FALSE
chr1+108806672	147	STXBP3	0	FALSE
chr11-66103928	146	PACS1	0	FALSE
chr19+47171312	145	SAE1	0	FALSE
chr16-89810967	144	FANCA	0	TRUE
chr22+50512528	144	NCAPH2	0	FALSE
chr18+79978412	143	TXNL4A	0	FALSE
chr1-41705000	143	HIVEP3	0	TRUE
chr12-132702732	141	PXMP2	0	FALSE
chr12-123336433	140	SBNO1	0	TRUE
chr3-185621362	140	SENP2	0	FALSE
chr16-688406	139	WDR24	0	FALSE
chr11-87276414	138	TMEM135	0	FALSE
chr12+71920998	138	TBC1D15	0	FALSE
chr4+186196333	137	CYP4V2	0	FALSE
chr9-111365651	134	ECPAS	0	FALSE
chr8+140766184	134	PTK2	0	FALSE
chr7-156735863	131	LMBR1	0	FALSE
chr21-45125852	130	ADARB1	0	FALSE
chr3+20155242	130	KAT2B	837	FALSE
chr4+168232819	130	DDX60	0	FALSE
chr13+52666940	129	SUGT1	0	FALSE
chr19+49791582	129	AP2A1	0	FALSE
chr3-105739471	128	CBLB	0	TRUE
chr5+169916820	128	DOCK2,FAM196B	0	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr16+697859	127	FBXL16	0	FALSE
chr2+44172322	126	PPM1B	0	FALSE
chr14+34537250	126	EAPP	0	FALSE
chr8-29445939	126	DUSP4	-95188	FALSE
chr9-124372473	125	PSMB7	0	FALSE
chr17+63234629	122	TANC2	0	FALSE
chr16+30068700	121	ALDOA	0	FALSE
chrY-13306528	121	UTY	0	FALSE
chr1-218296886	121	RRP15	0	FALSE
chrX-46616459	119	SLC9A7	0	FALSE
chr17+77978416	119	TNRC6C	-25819	FALSE
chr17-51002645	118	SPAG9	0	FALSE
chr11+16746960	117	C11orf58	0	FALSE
chr12-56106716	117	PA2G4	0	FALSE
chr8+86485122	116	RMDN1	0	FALSE
chr19+55596779	115	FIZ1	0	FALSE
chr21+46467575	115	DIP2A,DIP2A-IT1	0	FALSE
chr4-108151568	115	LEF1	0	TRUE
chr8-144394444	115	CPSF1	0	FALSE
chr9+132331433	115	SETX	0	FALSE
chr17-49737776	114	FAM117A	0	TRUE
chr1-42315075	113	FOXJ3	0	FALSE
chr18+39795276	113	MIR924HG	-43280	FALSE
chr10-112443730	113	ZDHHC6	0	FALSE
chr7-92806708	112	CDK6	0	TRUE
chr20-41064884	112	TOP1	0	TRUE
chr4+99905015	112	DNAJB14	0	FALSE
chr8-144204962	112	MROH1	0	FALSE
chr18+70024780	111	RTTN	0	FALSE
chr2+62795313	111	EHBP1	0	FALSE
chr8+53824240	111	ATP6V1H	0	FALSE
chr3-183475583	111	KLHL6	11943	FALSE
chr1-23751640	110	ELOA	0	FALSE
chr17+81608349	110	NPLOC4	0	FALSE
chr4+88980143	110	FAM13A	0	FALSE
chr1-169885649	110	SCYL3	0	FALSE
chr1+45854518	108	MAST2	0	FALSE
chr19+10660276	108	ILF3	0	FALSE
chr7-114981050	108	MDFIC	0	FALSE
chr16-89453764	107	ANKRD11,LOC101927817	0	FALSE
chr12-2882041	107	RHNO1	0	FALSE
chr21+15762247	106	USP25	0	FALSE
chr11-65283070	104	POLA2	0	FALSE
chr19+14587638	102	CLEC17A	0	FALSE
chr19+49608368	102	PRR12	0	FALSE
chr4+150268007	102	LRBA	0	TRUE
chr10-32932684	101	ITGB1	0	FALSE
chr2-168489303	101	CERS6	0	FALSE
chrX-96938264	101	DIAPH2	0	FALSE
chr3-49976866	100	RBM6	0	FALSE
chr15-90783154	99	BLM	0	TRUE
chr21-17798937	99	C21orf91	0	FALSE
chr11-3748220	98	NUP98	0	TRUE
chr14-31569282	98	NUBPL	0	FALSE
chr3-48901934	97	SLC25A20	-2940	FALSE
chr1-28086734	96	EYA3	0	FALSE
chr12+89621284	94	ATP2B1	0	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr13+45469281	94	COG3	0	FALSE
chr17+2334266	93	TSR1	0	FALSE
chr22+37651125	93	SH3BP1,LOC101927051	0	FALSE
chr6+142200530	93	VTA1	0	FALSE
chr11+118236608	92	MPZL3	0	FALSE
chr4-141229851	92	ZNF330	0	FALSE
chr12-57498438	92	MARS	0	TRUE
chr12+96305498	92	CDK17	0	FALSE
chr17+44443996	92	GPATCH8	0	FALSE
chr18-13120331	92	CEP192	0	FALSE
chr18+5998462	92	L3MBTL4	0	FALSE
chr19+21174810	92	ZNF431	0	FALSE
chr4+67782032	92	GNRHR	-25945	FALSE
chr4+163531326	91	MARCH1	0	FALSE
chr5-121975249	91	SRFBP1	0	FALSE
chr13+28951157	90	MTUS2	-73452	FALSE
chr9+74755305	90	TRPM6	0	FALSE
chr4+131123500	89	SNHG27	-641336	FALSE
chr12-53477930	89	PCBP2	0	FALSE
chr5+111509968	89	STARD4	0	FALSE
chr6+77470177	89	HTR1B	-6154	FALSE
chr9+136829208	89	RABL6	0	FALSE
chr10-28373933	87	LOC105376468	59073	FALSE
chr11+228263	87	SIRT3	0	FALSE
chr22+30113959	87	HORMAD2	0	FALSE
chr12+69509257	86	FRS2	0	FALSE
chr16-53688145	86	RPGRIP1L	0	FALSE
chr2-239175216	86	HDAC4	0	TRUE
chr21-46524417	86	DIP2A	0	FALSE
chr14-49741783	85	KLHDC1	0	FALSE
chr6-99562841	85	CCNC	0	TRUE
chr9+132274230	85	SETX	0	FALSE
chr1+1392006	84	CCNL2	0	FALSE
chr22+38721633	84	GTPBP1	0	FALSE
chr8+28167116	84	ELP3	0	FALSE
chr15-75445253	83	SIN3A	0	FALSE
chrUn_KI270442v1+326635	83	None.found	Inf	FALSE
chr5-87069109	82	MIR4280	45768	FALSE
chr9-122847455	81	RC3H2	0	FALSE
chr12-56272420	80	CS	0	FALSE
chr19+19799565	80	ZNF56,ZNF506	0	FALSE
chr9-95897086	79	ERCC6L2	0	FALSE
chr14-61717204	78	HIF1A,LOC105370526	0	FALSE
chr14-75747222	78	TTLL5	0	FALSE
chr16-115383	78	NPRL3	0	FALSE
chr2-148032390	78	MBD5	0	FALSE
chr3+56764690	78	ARHGEF3	0	FALSE
chr6+35651099	78	FKBP5	0	FALSE
chr5-6608532	77	NSUN2	0	FALSE
chr1-147267465	76	CHD1L	0	FALSE
chr17+62600831	75	TLK2	0	FALSE
chr16+2885995	75	FLYWCH2	0	FALSE
chr6+43591307	75	POLH	0	TRUE
chr19-10625164	75	SLC44A2	0	FALSE
chr11-117244761	74	RNF214	0	FALSE
chr2+27596761	74	ZNF512	0	FALSE
chr17-82480228	74	NARF	0	FALSE

(continued)

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr7-100549061	74	AGFG2	0	FALSE
chr3-119448204	73	TMEM39A	0	FALSE
chr6+46139757	73	ENPP4	0	FALSE
chr20-35067184	73	TRPC4AP	0	FALSE
chr19-18085165	73	IL12RB1	0	FALSE
chr22-45322301	72	FAM118A	0	FALSE
chr6-106298672	72	ATG5	0	FALSE
chr7-24952152	71	OSBPL3	0	TRUE
chr10-118317652	71	FAM204A	0	FALSE
chr10+110087766	71	ADD3	0	TRUE
chr15-77005490	70	PSTPIP1	0	FALSE
chr3-20113076	70	KAT2B	0	FALSE
chrX-49057586	70	CCDC120	0	FALSE
chr1-1851512	70	GNB1	0	FALSE
chr18-14890951	69	ANKRD30B	38212	FALSE
chr14-60293506	69	PPM1A	0	FALSE
chr6+100802811	69	ASCC3	0	FALSE
chr8-123267001	69	ZHX1-C8orf76,ZHX1	0	FALSE
chr15+90188802	68	SEMA4B	0	TRUE
chr13-42484205	68	LINC02341	0	FALSE
chr17+82525562	68	FOXK2	0	FALSE
chr19-17417047	68	MVB12A	0	FALSE
chr22+40195723	68	TNRC6B	0	FALSE
chr6+125786485	68	NCOA7	0	FALSE
chr12-66374985	67	GRIP1	0	FALSE
chr10-60278691	67	ANK3	0	FALSE
chr7+37314619	67	ELMO1	0	TRUE
chr8+100298539	67	RNF19A	0	FALSE
chr8+112688563	67	CSMD3	0	TRUE
chr5-61529690	66	ZSWIM6	0	FALSE
chr12-56141120	66	ESYT1	0	FALSE
chr19-21147740	66	ZNF431	0	FALSE
chr6+70537452	66	FAM135A	0	FALSE
chr15+85612466	65	AKAP13	0	TRUE
chr16+22017992	65	MOSMO	0	FALSE
chr6+163428613	65	QKI	0	FALSE
chr13-25260689	65	MTMR6	0	FALSE
chr7+123709715	64	WASL	0	FALSE
chr1-111137734	63	DRAM2	0	FALSE
chr21-36865313	63	HLCS	0	FALSE
chr14-55065052	63	MAPK1IP1L	0	FALSE
chr2-9613836	63	YWHAQ	0	FALSE
chrX+46843453	63	RP2	0	FALSE
chr14-100354392	63	WARS	0	FALSE
chr11-9413400	62	IPO7	0	FALSE
chr9+21319348	62	KLHL9	10321	FALSE
chr10+46258405	61	ANTXRLP1	0	FALSE
chr22+37536993	61	CARD10	-17789	FALSE
chr5+57177291	61	GPBP1	0	FALSE
chr6-42439811	61	TRERF1	0	FALSE
chr21-17788639	61	C21orf91-OT1	0	FALSE
chr12-45860338	60	ARID2	0	TRUE
chr20+59026948	60	TUBB1	293	FALSE
chr8-89791015	60	RIPK2	0	FALSE
chr7+65399541	59	ZNF92	0	FALSE
chr15+90540633	59	CRTC3	0	TRUE
chr4+1106529	59	RNF212	0	FALSE

(continued)

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr10-67903278	58	SIRT1	0	TRUE
chr11-62818775	58	STX5	0	FALSE
chr13-97294202	58	MBNL2	0	FALSE
chr19-58548836	58	TRIM28	0	FALSE
chr16-53846128	57	FTO	0	FALSE
chr9+2153204	57	SMARCA2	0	FALSE
chr12+47197286	56	PCED1B	0	TRUE
chr13+77017322	56	FBXL3	0	FALSE
chr17-80786660	56	RPTOR	0	FALSE
chr10-50357649	56	SGMS1	0	TRUE
chr9+123864718	56	DENND1A	0	FALSE
chr1-156182432	56	SEMA4A	4680	FALSE
chr2+37312666	55	PRKD3	0	FALSE
chr5+177156727	55	NSD1	0	TRUE
chrX-139716193	55	MCF2	-7970	TRUE
chr14+68849175	55	ACTN1	24946	FALSE
chr11-58608502	54	ZFP91,ZFP91-CNTF	0	FALSE
chr17-62053549	54	MED13	0	FALSE
chr17+60625325	54	PPM1D	0	TRUE
chr3-47024529	54	SETD2	0	TRUE
chr6+28383183	54	ZSCAN12	0	FALSE
chr16+603963	54	RAB40C	0	FALSE
chr11+66187781	53	PACS1	0	FALSE
chr1+11224732	53	MTOR	0	TRUE
chr14-38032143	53	LINC00517	-130018	FALSE
chr19-49603812	53	PRR12	0	FALSE
chr22-40303931	53	TNRC6B	0	FALSE
chr5+109860656	53	MAN2A1	0	FALSE
chr16+48253992	52	LONP2	0	FALSE
chr16+88579042	52	ZC3H18	0	FALSE
chr17+39340299	52	FBXL20	0	FALSE
chr17+82522460	52	FOXK2	0	FALSE
chr11-108286842	52	ATM	0	TRUE
chr11+85995211	52	PICALM	0	TRUE
chr16-70774244	52	VAC14	0	TRUE
chr19+3763450	52	MRPL54	0	FALSE
chr4-163686426	52	MARCH1	0	FALSE
chr9+136467444	52	SEC16A	0	FALSE
chr9-105543321	52	FSD1L	0	FALSE
chr1-26749386	52	ARID1A	0	TRUE
chr10-7783616	52	KIN	0	FALSE
chr12-29338594	51	ERGIC2	2050	FALSE
chr21+35090633	51	RUNX1	-41334	TRUE
chr7-43615893	51	STK17A,COA1	0	FALSE
chr12-6505481	51	NCAPD2	0	TRUE
chr6+156165452	50	SNORD28B	-213296	FALSE
chr1-179900985	50	TOR1AIP1	0	FALSE
chr12+120002128	50	BICDL1	0	FALSE
chr19_GL383575v2_alt-107136	50	ZNF100	0	FALSE
chr6-162353205	50	PRKN	0	FALSE
chr5-144156190	50	YIPF5	1967	FALSE
chr5+56874461	50	MAP3K1	0	TRUE
chr3-48923545	50	ARIH2	0	FALSE
chr2+27693924	49	SLC4A1AP	0	FALSE
chr1+111154000	49	CEPT1	0	FALSE
chr10+87870731	49	PTEN	0	TRUE
chr2-17682027	49	SMC6	0	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr22+37885739	49	EIF3L	0	FALSE
chr3-52614164	49	PBRM1	0	TRUE
chr5+21406901	49	GUSBP1	-52577	FALSE
chr7-73471130	49	BAZ1B	0	FALSE
chr9-128597730	49	SPTAN1	0	TRUE
chrX+96857303	49	DIAPH2	0	FALSE
chr2-10661042	49	NOL10	0	FALSE
chrX+154067005	49	MECP2	0	FALSE
chr22+38312445	49	CSNK1E,LOC400927-CSNK1E	0	FALSE
chr10-73775294	48	FUT11	0	FALSE
chr12-2859368	48	ITFG2,FOXM1	0	FALSE
chr16-30719788	48	SRCAP	0	FALSE
chr2+223915487	48	WDFY1	0	FALSE
chr8+63175704	48	YTHDF3	0	FALSE
chr10+117289252	48	PDZD8	0	FALSE
chr2-53915465	48	PSME4	0	FALSE
chr12+28445185	47	CCDC91	0	FALSE
chr9-128608679	47	SPTAN1	0	TRUE
chr10-49845591	47	PARG	0	FALSE
chr17+81269187	47	SLC38A10	0	FALSE
chr2-53098914	47	MIR4431	-396298	FALSE
chr4-112646229	47	LARP7	0	FALSE
chr4-128283342	47	PGRMC2	0	FALSE
chrX-154048170	47	MECP2	0	FALSE
chrX+20222313	47	RPS6KA3	0	FALSE
chr18-31908293	47	TRAPPC8	0	FALSE
chr17+80323771	46	RNF213	0	TRUE
chr1-156772946	46	PRCC	0	TRUE
chr10-23325454	46	C10orf67	0	FALSE
chr19+49379520	46	LOC101928295	0	FALSE
chr2+203266986	46	CYP20A1	0	FALSE
chr4-88015117	46	PKD2	0	FALSE
chr7-33022775	46	NT5C3A	0	FALSE
chr10+102920779	46	CNNM2	0	FALSE
chr12+42329456	45	PPHLN1	0	FALSE
chr9-132291804	45	SETX	0	FALSE
chr1-161789726	45	ATF6	0	FALSE
chr1-171526758	45	PRRC2C	0	FALSE
chr10-67838227	45	DNAJC12	-47	FALSE
chr16+4713469	45	ANKS3	0	FALSE
chr17+39848885	45	IKZF3	0	TRUE
chr6+90437293	45	MAP3K7	76278	TRUE
chr8-144486975	45	PPP1R16A	0	FALSE
chr17+59805984	45	VMP1	0	FALSE
chr2+158659339	44	PKP4,PKP4-AS1	0	FALSE
chr2+55576601	44	PPP4R3B	0	FALSE
chr1-26732384	44	ARID1A	0	TRUE
chr15+82961638	44	HOMER2	-8913	FALSE
chr2-188043016	44	LINC01090	0	FALSE
chr2+177510617	44	AGPS	0	FALSE
chr3+15120069	44	RBSN	-20911	FALSE
chr4+141330042	44	LINC02432	0	FALSE
chr5-177215679	44	NSD1	0	TRUE
chr8+70377418	44	NCOA2	0	TRUE
chr9+93503108	44	FAM120A	0	FALSE
chr14+51243475	44	TMX1	0	FALSE
chr3+197822588	44	LRCH3	0	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr12+82429924	43	METTL25	0	FALSE
chr13+32744113	43	PDS5B	0	TRUE
chr16+88797469	43	CDT1	-6307	TRUE
chr22+45736267	43	ATXN10	0	FALSE
chr16+67220781	43	LRRC29	0	FALSE
chr3+105839299	43	CBLB	0	TRUE
chr6-76061886	43	IMPG1	0	FALSE
chr8+57763879	43	LOC286178	13681	FALSE
chr9-129949719	43	FNBP1	0	TRUE
chr11+118772568	43	DDX6	0	TRUE
chr10+227042	42	ZMYND11	0	FALSE
chr16-2916262	42	FLYWCH1	0	FALSE
chr17-39340303	42	FBXL20	0	FALSE
chr17-40635814	42	SMARCE1	0	FALSE
chr1+155196229	42	THBS3	0	TRUE
chr11+6691630	42	MRPL17	-8228	FALSE
chr14-81215409	42	GTF2A1	0	TRUE
chr16-57179533	42	FAM192A	0	FALSE
chr18+29330026	42	MIR302F	-968882	FALSE
chr20+45423101	42	PIGT	0	FALSE
chr5+50728431	42	PARP8	0	FALSE
chr9-128975185	42	NUP188	0	FALSE
chr7+35848779	42	SEPT7	0	FALSE
chr17-44041061	42	LSM12	0	FALSE
chr14+97719191	41	LINC02312	30071	FALSE
chr15+36607521	41	C15orf41	0	FALSE
chr2-24726623	41	NCOA1	0	TRUE
chr8+67240914	41	ARFGEF1	0	FALSE
chr9-100056278	41	ERP44	0	FALSE
chr22+47478444	41	LINC01644	0	FALSE
chr4-123034189	41	SPATA5	0	FALSE
chr3-133642628	41	TOPBP1	0	FALSE
chr12+30719488	40	CAPRIN2	0	FALSE
chr22+40156529	40	TNRC6B	0	FALSE
chr4+106332796	40	AIMP1	0	FALSE
chr7+106265182	40	NAMPT	0	FALSE
chr9+35046015	40	C9orf131	23	FALSE
chr6-147314411	40	STXBP5	0	FALSE
chr18-62157049	40	PIGN	0	FALSE
chr4+123034185	40	SPATA5	0	FALSE
chr12+92050876	40	LINC01619	0	FALSE
chr1+9930242	39	LZIC	0	FALSE
chr10+72142469	39	ASCC1	0	FALSE
chr10+88892498	39	STAMBPL1	0	FALSE
chr11+64751377	39	PYGM	0	FALSE
chr12+122497734	39	ZCCHC8	0	FALSE
chr13+102663488	39	TPP2	0	FALSE
chr14+70993068	39	PCNX1	0	FALSE
chr16+67794245	39	RANBP10	0	FALSE
chr17-6617983	39	KIAA0753	0	FALSE
chr19-57885086	39	ZNF814	0	FALSE
chr3+71056594	39	FOXP1	0	TRUE
chr4+119215938	39	USP53	0	FALSE
chr9-131255012	39	FAM78A	3064	FALSE
chr2-175985332	39	LNPK	0	FALSE
chr8-17995707	39	PCM1	0	TRUE
chr10+895012	38	LARP4B	0	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr21-14518207	38	SAMSN1	0	FALSE
chr3-134183047	38	RYK	0	FALSE
chr10-27083551	38	ANKRD26	0	FALSE
chr11-119065149	38	VPS11	-2601	FALSE
chr11+102362239	38	BIRC2	0	TRUE
chr17+35544477	38	SLFN14	3646	FALSE
chr19+48252099	38	CARD8	0	TRUE
chr5-177346555	38	LMAN2	0	FALSE
chrX-136776933	38	ARHGEF6	0	FALSE
chr5+53081818	38	ITGA2	0	FALSE
chr5-65767000	38	NLN	0	FALSE
chr3-48625177	38	SLC26A6	544	FALSE
chr11-65105082	37	VPS51	0	FALSE
chr11+65972830	37	SART1	0	FALSE
chr12+53454558	37	PCBP2	0	FALSE
chr18+46227189	37	C18orf25	0	FALSE
chr21+25757089	37	GABPA	0	FALSE
chr3-9804232	37	ARPC4,ARPC4-TTLL3	0	FALSE
chr6+4054262	37	PRPF4B	0	TRUE
chr16-734461	37	NARFL	0	FALSE
chr5+141606351	36	DIAPH1	0	FALSE
chr8-143445404	36	ZC3H3	0	FALSE
chr13-77083945	36	MYCBP2,MYCBP2-AS1	0	FALSE
chr16+57008276	36	NLRC5	0	FALSE
chr16+624951	36	RAB40C	0	FALSE
chr2-2897505	36	LINC01250	0	FALSE
chr3+149165702	36	HPS3,CP	0	FALSE
chr2+112649259	36	SLC20A1	0	FALSE
chr5+98888341	36	CHD1	0	FALSE
chr16+21641974	35	METTL9,IGSF6	0	FALSE
chr4+466683	35	ABCA11P,ZNF721	0	FALSE
chr14+45118211	35	FKBP3	0	FALSE
chr16+30462312	35	ITGAL	-10348	FALSE
chr17+43076101	35	BRCA1	0	TRUE
chr17+82071106	35	DUS1L	-5284	FALSE
chr22+29997669	35	MTMR3	0	TRUE
chr3-158670394	35	GFM1,LXN	0	FALSE
chr3-3148073	35	TRNT1	0	FALSE
chr3-98544543	35	GPR15	9863	FALSE
chr5+131439136	35	RAPGEF6	0	FALSE
chrX-79359839	35	ITM2A	543	FALSE
chr19+5642438	35	SAFB	0	FALSE
chr6-157179804	35	ARID1B	0	TRUE
chr1-89193923	35	GBP4	0	FALSE
chr18-11359375	35	LINC01928	-95101	FALSE
chr12+74909488	35	KCNC2	130588	FALSE
chr9-3490057	35	RFX3	0	FALSE
chr4-67488433	35	CENPC	0	FALSE
chr11-64337811	34	CCDC88B	-2405	FALSE
chr17+7699978	34	WRAP53	0	TRUE
chr1-202920778	34	KLHL12	0	FALSE
chr11+106028970	34	MSANTD4	-6682	FALSE
chr13-84327670	34	LINC00333	0	FALSE
chr16-29999351	34	INO80E	0	FALSE
chr17-82101883	34	CCDC57	0	FALSE
chr19-35161713	34	FXYD5	0	TRUE
chr2+183174582	34	NUP35	12897	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr3-130690688	34	PIK3R4	0	FALSE
chr9-34997200	34	DNAJB5	0	FALSE
chr17-74754429	33	SLC9A3R1	0	TRUE
chr17+80786656	33	RPTOR	0	FALSE
chr19-49609856	33	PRR12	0	FALSE
chr13+73001811	33	PIBF1	0	FALSE
chr15-85629566	33	AKAP13	0	TRUE
chr18+31910360	33	TRAPPC8	0	FALSE
chr19+58551371	33	CHMP2A	193	FALSE
chr2-144238649	33	GTDC1	0	FALSE
chr2-27403865	33	PPM1G	0	FALSE
chr2+27910000	33	BABAM2	0	FALSE
chr2+58060743	33	VRK2	0	FALSE
chr20-34775056	33	NCOA6	0	TRUE
chr6-70750029	33	SMAP1	0	TRUE
chr9+128956391	33	NUP188	0	FALSE
chrX+7299607	33	STS	0	FALSE
chr1-1868080	33	GNB1	0	FALSE
chr10-6514719	33	PRKCQ	0	FALSE
chr19+17408853	33	BISPR,MVB12A	0	FALSE
chr1-155677858	33	YY1AP1	0	FALSE
chr5+92099148	33	ARRDC3-AS1	678432	FALSE
chr16+14149373	32	MKL2	0	FALSE
chr21+31702673	32	SCAF4	0	FALSE
chr8+112293266	32	CSMD3	0	TRUE
chr10+68912484	32	DDX50	0	FALSE
chr12+29355144	32	ERGIC2	0	FALSE
chr17+48173973	32	SKAP1	0	FALSE
chr3-4591700	32	ITPR1	0	FALSE
chrX+155178404	32	VBP1	-18601	FALSE
chr14-45110549	32	PRPF39	0	FALSE
chr5-83064799	32	TMEM167A	0	FALSE
chr14+71353552	31	SIPA1L1	0	FALSE
chr4+76122971	31	NUP54	0	FALSE
chr10-100945936	31	SLF2	0	FALSE
chr13-77115378	31	MYCBP2	0	FALSE
chr16-47518337	31	PHKB	0	FALSE
chr20+59025225	31	TUBB1	0	FALSE
chr3+108566676	31	CIP2A	0	FALSE
chr8-78543862	31	PKIA,PKIA-AS1	0	FALSE
chrX+111688295	31	ALG13	0	FALSE
chr18-33660210	31	ASXL3	0	FALSE
chr11+118041220	31	SMIM35	0	FALSE
chr20+49918656	31	LOC105372653	0	FALSE
chr4+99902696	31	DNAJB14	0	FALSE
chr16+2588396	31	PDPK1	0	FALSE
chr19-4962446	31	UHRF1	291	FALSE
chr10-74538177	30	ADK	0	FALSE
chr19+52678045	30	ZNF83	0	FALSE
chr3+97916270	30	CRYBG3	0	FALSE
chr17-2287695	30	SMG6	0	TRUE
chr17-82525566	30	FOXK2	0	FALSE
chr19-2063947	30	MOB3A	7087	FALSE
chr19-48238326	30	CARD8	0	TRUE
chr19-968483	30	ARID3A	0	FALSE
chr2-237986521	30	UBE2F,UBE2F-SCLY	0	FALSE
chr2+61256888	30	USP34	0	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr21-44790633	30	UBE2G2	0	FALSE
chr3+115142273	30	ZBTB20	0	FALSE
chr7-132877618	30	CHCHD3	0	FALSE
chr7+116226599	30	TES	0	FALSE
chr7+44882778	30	PURB	0	FALSE
chr12-123193685	30	MPHOSPH9	0	FALSE
chr16+62636306	30	CDH8	-599470	FALSE
chr3+132674828	30	NPHP3-ACAD11,UBA5	0	FALSE
chr11+66082843	29	PACS1	0	FALSE
chr18-29052008	29	CDH2	-874561	FALSE
chr2+191137694	29	STAT4	0	FALSE
chr3+190596158	29	IL1RAP	0	FALSE
chr4-73215198	29	ANKRD17	0	FALSE
chr4+55964914	29	CEP135	0	FALSE
chr5+108776850	29	FER	0	FALSE
chr6+57113492	29	ZNF451	0	FALSE
chr13-71201736	29	LINC00348	33318	FALSE
chr13-74010867	29	KLF12	0	FALSE
chr17-76330567	29	PRPSAP1	0	FALSE
chr17+39807080	29	IKZF3	0	TRUE
chr2-182730221	29	DNAJC10	0	FALSE
chr2-37253905	29	NDUFAF7,PRKD3	0	FALSE
chr3-9450728	29	SETD5	0	FALSE
chr5+52868468	29	ITGA1	0	FALSE
chr6-24973060	29	RIPOR2	0	FALSE
chr7+43603728	29	STK17A	0	FALSE
chr2-95953327	29	ANKRD36C	0	FALSE
chr6-45005146	29	SUPT3H	0	FALSE
chr10-21638524	29	MLLT10	0	TRUE
chr1-107941416	28	VAV3	0	TRUE
chr15+73177025	28	NEO1	0	FALSE
chr19-58282535	28	ZNF8,ZNF8-ERVK3-1	0	FALSE
chr7-102828490	28	FAM185A,FBXL13	0	FALSE
chr1+31921816	28	PTP4A2	0	FALSE
chr1+33022088	28	AK2	0	FALSE
chr10-31339332	28	ZEB1	0	FALSE
chr13+45280618	28	GTF2F2	0	FALSE
chr14-85996416	28	LINC02328	0	FALSE
chr16-2441015	28	CCNF	0	TRUE
chr16+68120042	28	NFATC3	0	TRUE
chr17-43076105	28	BRCA1	0	TRUE
chr18-9597876	28	PPP4R1	0	FALSE
chr2-26226896	28	HADHA	0	FALSE
chr2+231760675	28	PDE6D	0	FALSE
chr22-41167290	28	EP300	0	TRUE
chr3+120755589	28	GTF2E1	0	FALSE
chr3+171270529	28	TNIK	0	FALSE
chr4-112147515	28	FAM241A	0	FALSE
chr5+44817309	28	MRPS30	1794	FALSE
chr6-36536766	28	STK38	0	FALSE
chr21+46503411	28	DIP2A	0	FALSE
chr1+220145272	28	IARS2	0	FALSE
chr1+93215050	28	CCDC18	0	FALSE
chr10-124941075	28	ZRANB1	-1046	FALSE
chr14+21241845	28	HNRNPC	0	FALSE
chr14+71380059	28	SIPA1L1	0	FALSE
chr18+29525022	28	MIR302F	-773886	FALSE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr4+158894920	28	FNIP2,C4orf45	0	FALSE
chr18+24448925	28	IMPACT	0	FALSE
chr18+55022409	28	CCDC68	-62900	FALSE
chrX+97347736	28	DIAPH2	0	FALSE
chr12-45948351	27	SCAF11	0	FALSE
chr16-21641978	27	METTL9,IGSF6	0	FALSE
chr17-64585860	27	SMURF2	0	FALSE
chr4+141222991	27	ZNF330	0	FALSE
chr1-1649083	27	CDK11B	0	TRUE
chr11-11935460	27	USP47	0	FALSE
chr16+2758883	27	SRRM2	0	FALSE
chr17+44437012	27	GPATCH8	0	FALSE
chr18-2601064	27	NDC80	0	FALSE
chr2-152697661	27	PRPF40A	0	FALSE
chr2-181066398	27	UBE2E3	2970	FALSE
chr3-105696817	27	CBLB	0	TRUE
chr3-5177149	27	ARL8B	0	FALSE
chr4-44703882	27	GNPDA2	0	FALSE
chr4-47729158	27	CORIN	0	FALSE
chr4-930886	27	GAK	0	TRUE
chr5+138018842	27	FAM13B	0	FALSE
chr5+18735794	27	CDH18	735500	FALSE
chr6-70669985	27	SMAP1	0	TRUE
chr9-137242536	27	TUBB4B	0	FALSE
chr4-106328852	27	AIMP1	0	FALSE
chr13+60450852	27	TDRD3	0	FALSE
chr17+64110718	27	ERN1	0	FALSE
chr19+51392542	27	C19orf84	-1967	FALSE
chr9+93457785	27	FAM120A	0	FALSE
chr8-129872956	27	FAM49B	0	FALSE
chr8+144235463	27	MROH1	0	FALSE
chr1+29044126	26	EPB41	0	FALSE
chr20-32395231	26	ASXL1	0	TRUE
chr21-46507149	26	DIP2A	0	FALSE
chr10-27123579	26	YME1L1	0	FALSE
chr11-36920876	26	C11orf74	261584	FALSE
chr12+56274992	26	CS	0	FALSE
chr13+42481904	26	LINC02341	0	FALSE
chr14-96558325	26	PAPOLA	0	FALSE
chr19+45044509	26	CLASRP	0	FALSE
chr2-196148509	26	STK17B	0	FALSE
chr2-68757180	26	ARHGAP25	0	TRUE
chr22+39095200	26	APOBEC3H	-2022	FALSE
chr3+125286968	26	ZNF148	0	FALSE
chr4+2881224	26	ADD1	0	FALSE
chr4+77741651	26	CNOT6L	0	FALSE
chr5+113527516	26	YTHDC2	0	FALSE
chr6-95608725	26	MANEA	0	FALSE
chr8+130229002	26	ASAP1	0	FALSE
chr9-6432817	26	UHRF2	0	TRUE
chr1-44927010	26	EIF2B3	0	FALSE
chr12-47123818	26	PCED1B	0	TRUE
chr7-72691405	26	TYW1B	0	FALSE
chr10-63376483	25	JMJD1C	0	FALSE
chr11-96065813	25	MAML2	0	TRUE
chr5+383967	25	AHRR	0	FALSE
chr1-111690342	25	RAP1A	0	TRUE

posid	estAbund	nearestFeature	nearestFeatureDist	oncogene
chr1-26716784	25	ARID1A	0	TRUE
chr10+112498190	25	VTI1A	0	TRUE
chr10+124762290	25	EEF1AKMT2	0	FALSE
chr11-247107	25	PSMD13	0	FALSE
chr11+462392	25	PTDSS2	0	FALSE
chr12+50243451	25	LIMA1	0	FALSE
chr14-27366762	25	LOC728755	0	FALSE
chr15+61940601	25	VPS13C	0	FALSE
chr15+76808095	25	SCAPER	0	FALSE
chr16+88794580	25	CDT1	-9196	TRUE
chr17-75392814	25	GRB2	0	TRUE
chr18+31863497	25	TRAPPC8	0	FALSE
chr18+67312147	25	DSEL	194433	FALSE
chr2-207571576	25	CREB1	0	TRUE
chr3-119231000	25	B4GALT4,B4GALT4-AS1	0	FALSE
chr4-55953621	25	CEP135	0	FALSE
chr4-80501222	25	CFAP299	0	FALSE
chr5-111462565	25	CAMK4	0	FALSE
chr17-7605558	25	FXR2	0	FALSE
chr19-4415361	25	CHAF1A	0	FALSE
chr2+119912255	25	PTPN4	0	FALSE
chr4+100166130	25	DDIT4L	19738	FALSE
chr8+109272781	25	NUDCD1	0	FALSE
chr11+101946968	25	CEP126	0	FALSE