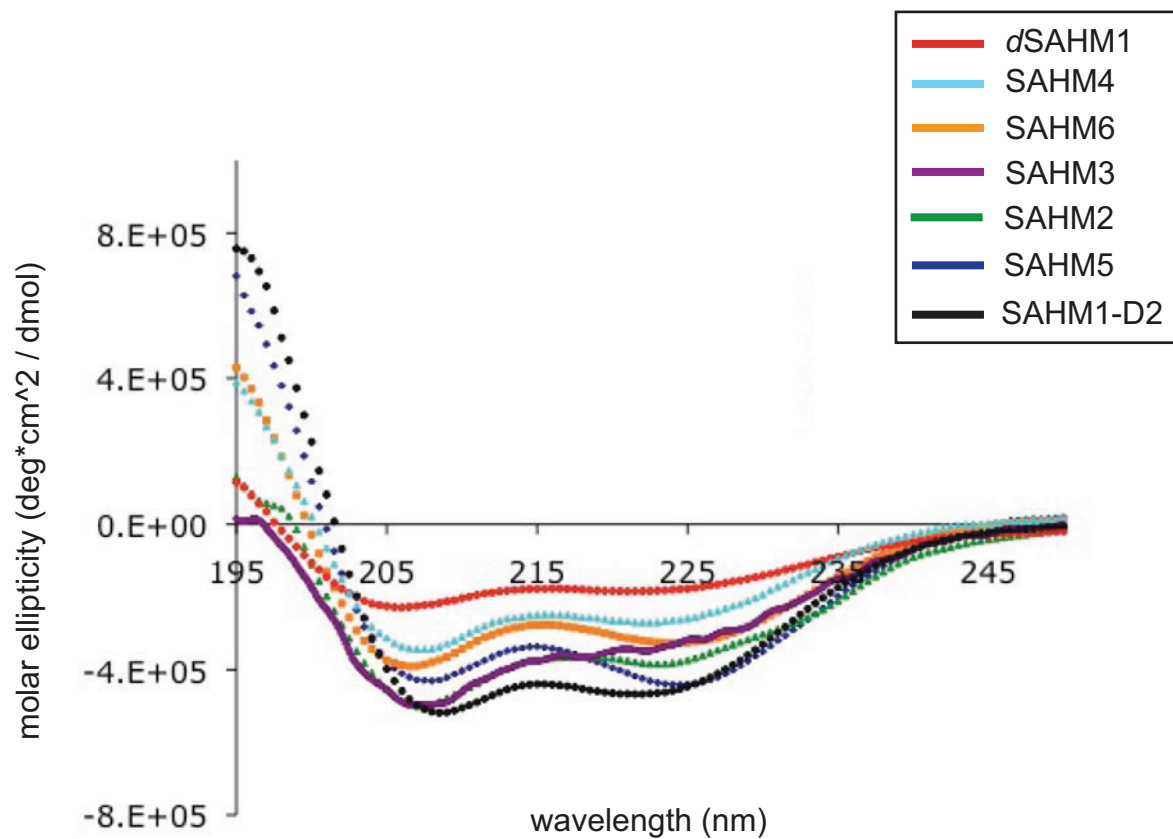


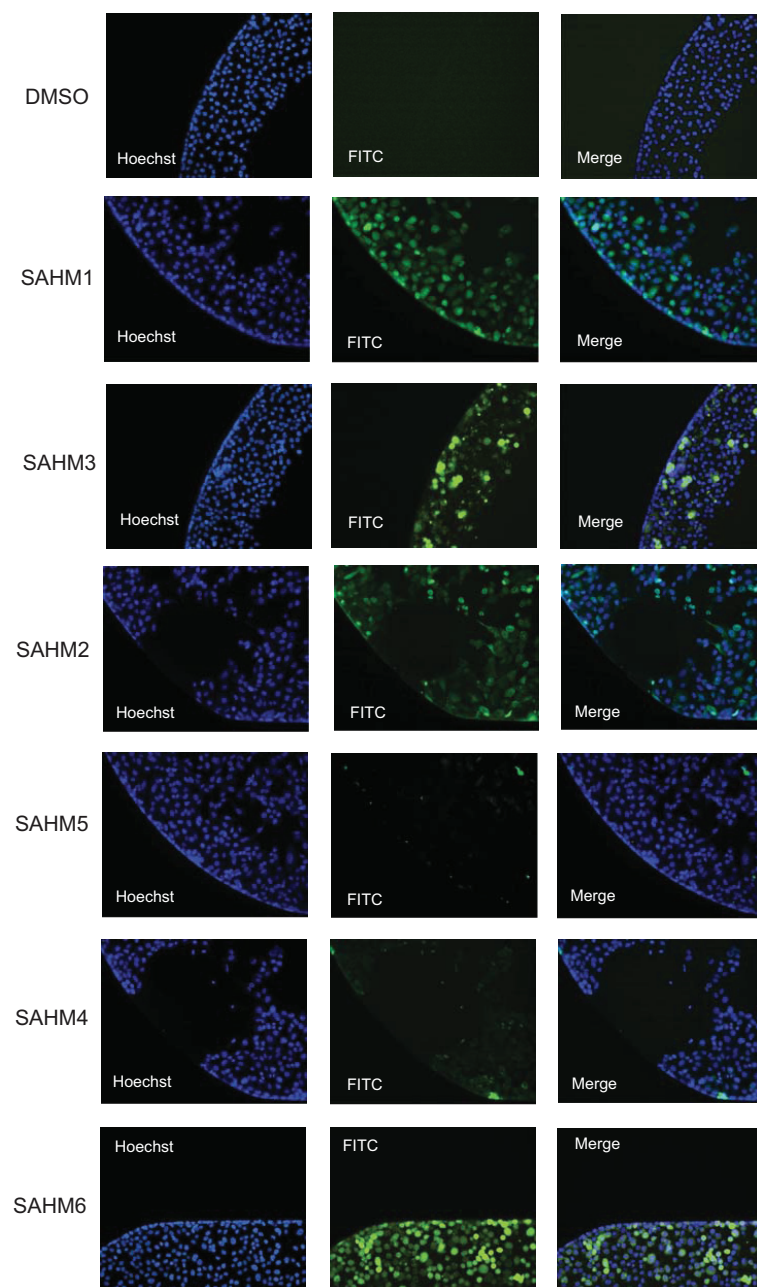
SUPPLEMENTARY INFORMATION

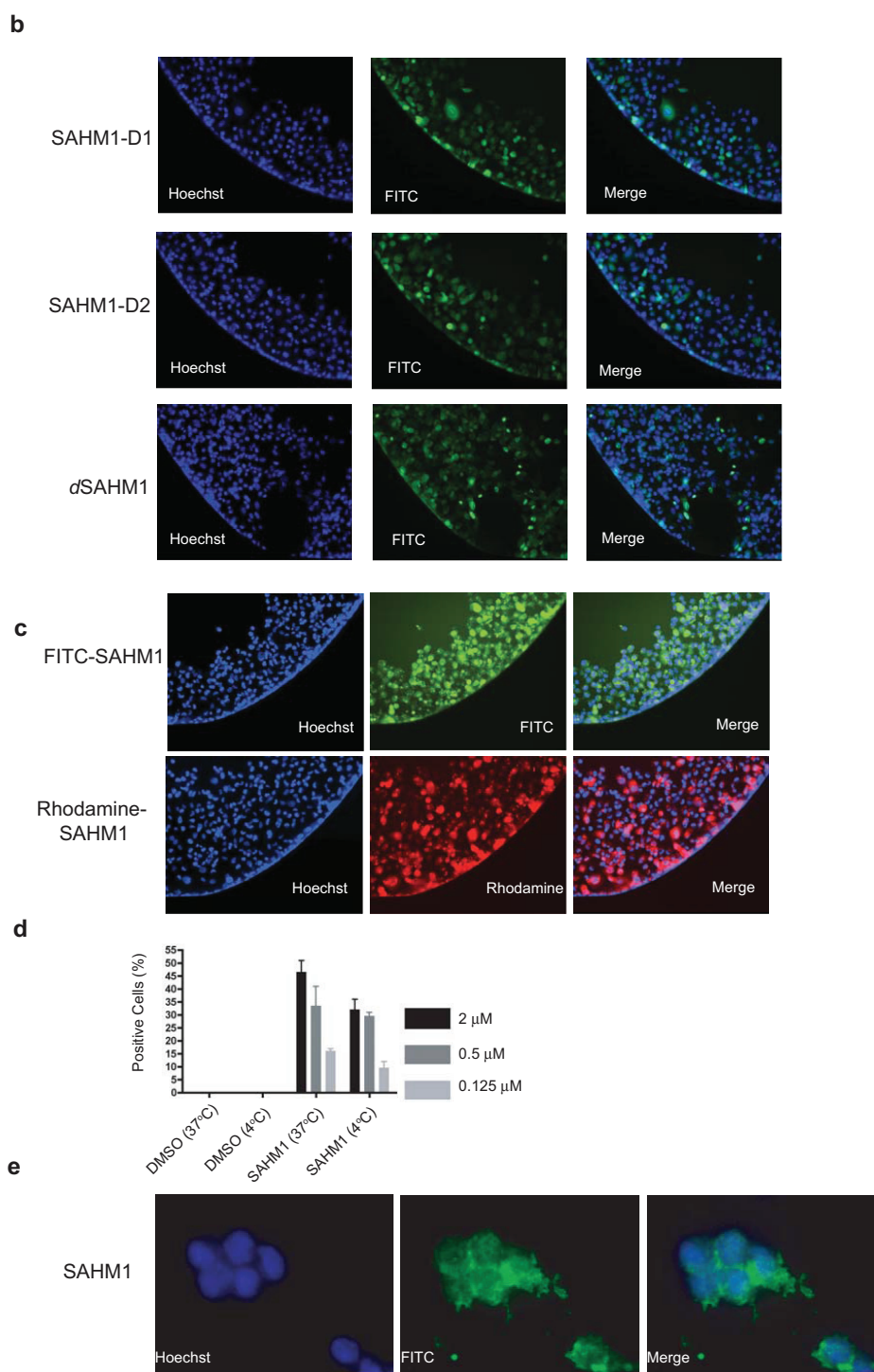


Supplementary Figure 1. CD spectra of SAHM peptides. Circular dichroism spectroscopy (CD) of additional MAML1 derived peptides and SAHM1 mutant peptides. Molar ellipticity at 222 nm was used to determine percent helicity at room temperature.

Supplementary Figure 2

a





Supplementary Figure 2. SAHMs penetrate cells and access cytosolic and nuclear compartments.

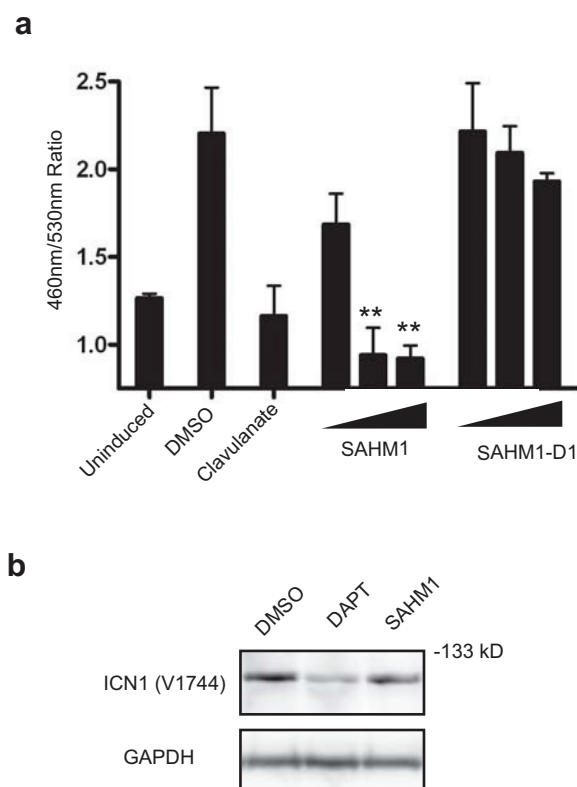
a) Analysis of FITC-SAHM peptide (5 μ M) intracellular access in U2OS cells by epifluorescent microscopy. After incubation for 12 hr, washed cells were imaged on Hoescht and FITC channels at 20X. **b)**

Epifluorescence microscopy of the mutated peptides SAHM1-D1, SAHM1-D2 and dSAHM1, imaged as in **(a)**. **c)** Intracellular penetration by rhodamine-labelled SAHM1, and FITC-SAHM1 imaged after 24 hr incubation. **d)**

Temperature dependent uptake of FITC-SAHM1 after four-hour incubation at

37°C or 4°C. **e)** Confocal microscopy of FITC-SAHM1 treated KOPT-K1 cells (12

hr).



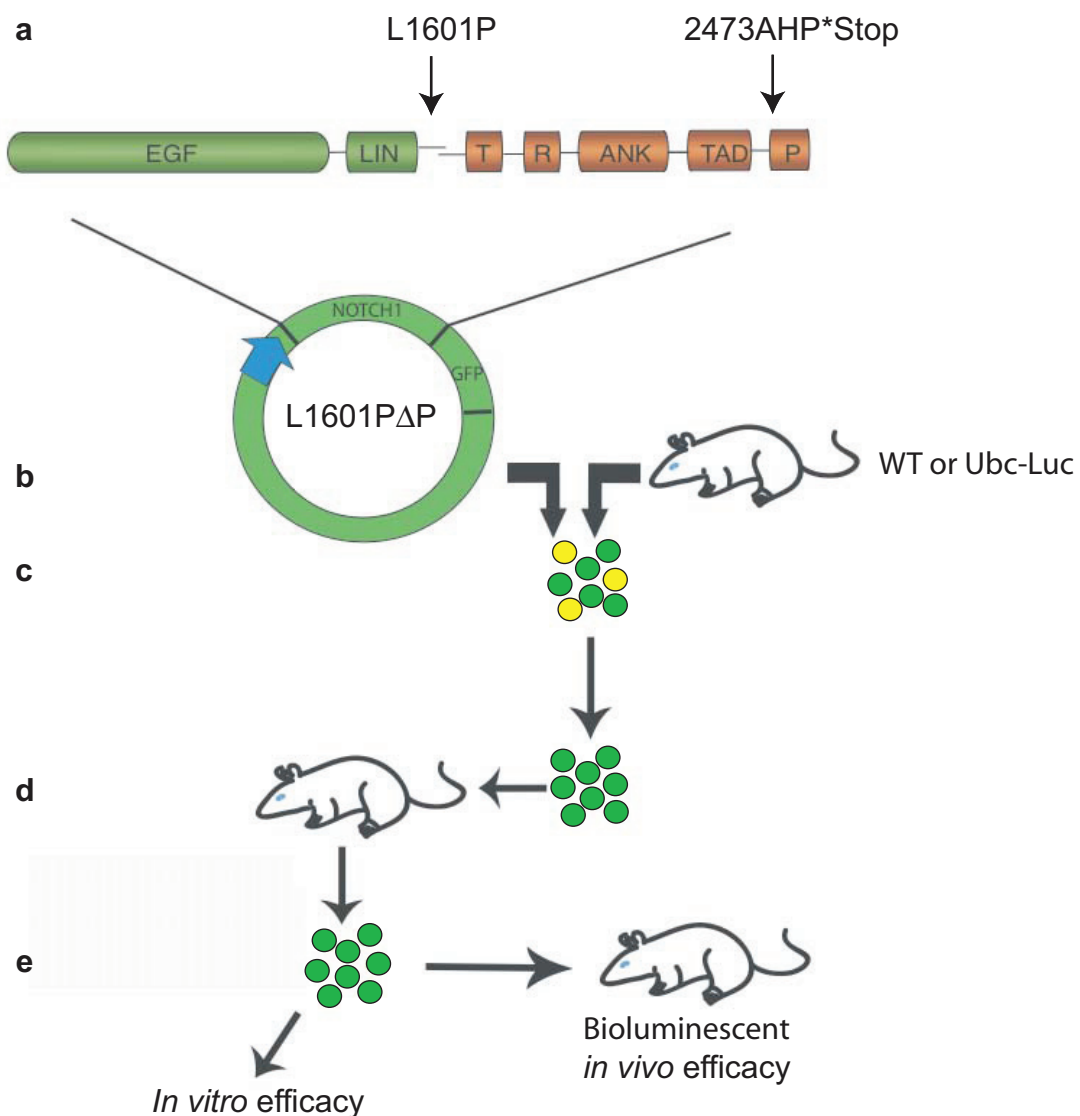
Supplementary Figure 3. Effects of SAHM peptides on NOTCH

transactivation. a) Suppression of the transactivation activity of ICN1 in HeLa cells by SAHM1, as assessed using a CSL-dependent β -lactamase reporter gene. Both SAHM1 and SAHM1-D1 peptides were dosed at 0.625, 2.5 and 10 μ M, from left to right. Clavulanate (0.625 μ M) was used as a positive β -lactamase inhibitor control. **b)** Effect of vehicle (DMSO), DAPT (1 μ M) or SAHM1 (10 μ M) on ICN1 protein levels in KOPT-K1 cells. Cells were treated for 24 hr prior to preparation of lysates, which were probed on Western blots with antibodies specific for ICN1 and GAPDH. All graphical representations represent mean \pm s.d. (n=3).

a

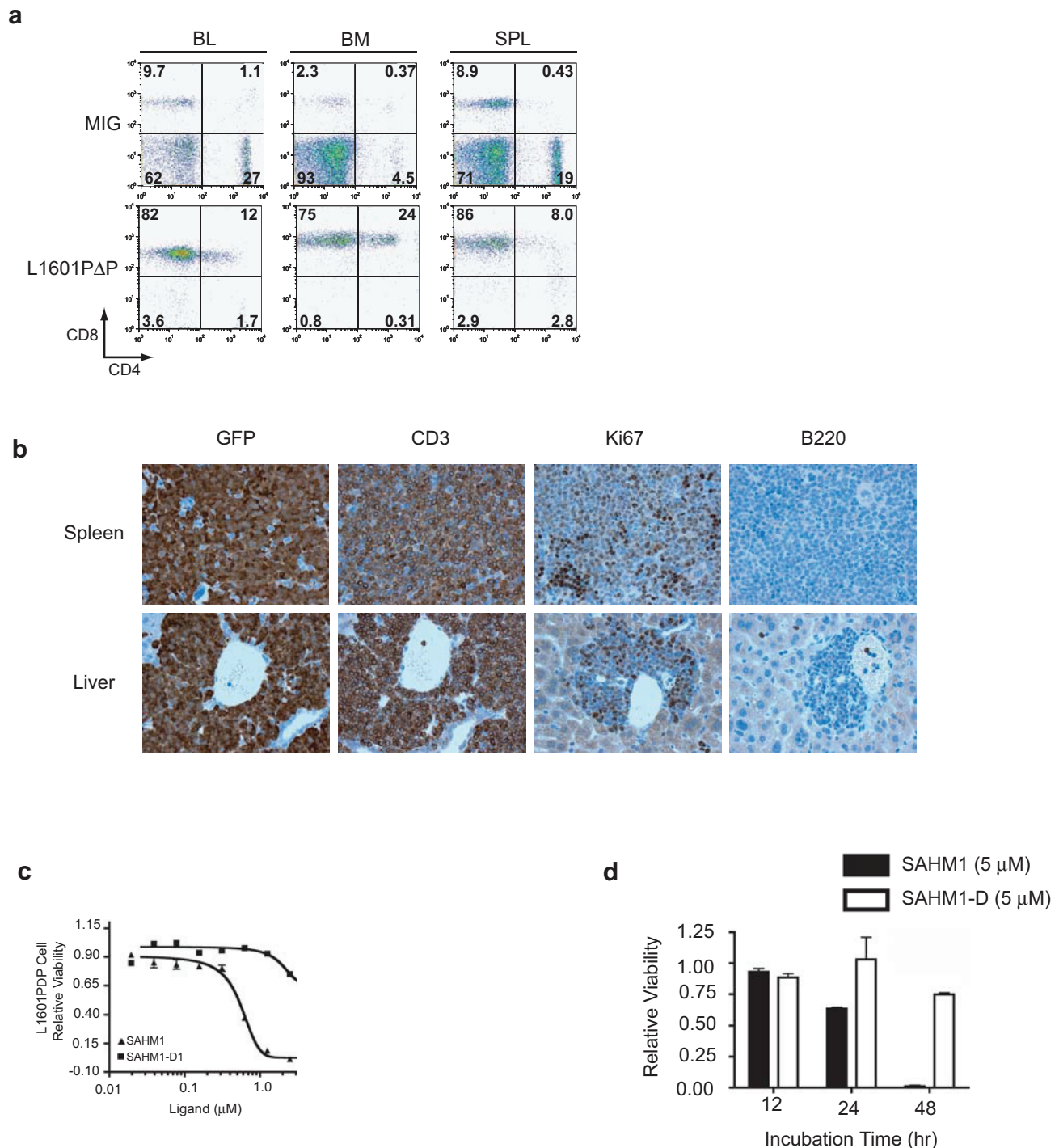
PROBE	GENE SYMBOL	PROBE	GENE SYMBOL
216557_x_at	IGHA1 /// IGHG1 ///	207515_s_at	POLR1C
228071_at	GIMAP7	219777_at	GIMAP6
219361_s_at	ISG20L1	214427_at	NOL1
218270_at	MRPL24	202613_at	CTPS
218597_s_at	ZCD1	203701_s_at	TRMT1
221712_s_at	WDR74	223018_at	NOB1
1564906_at	MATR3	222288_at	PPP4R2
218512_at	WDR12	203023_at	HSPC111
218866_s_at	POLR3K	201675_at	AKAP1
223413_s_at	LYAR	204133_at	RNU3IP2
201802_at	SLC29A1	222632_s_at	LZTFL1
224714_at	MKI67IP	218199_s_at	NOL6
203219_s_at	APRT	212456_at	KIAA0664
219006_at	C6ORF66	222875_at	DHX33
208799_at	PSMB5	227093_at	USP36
218105_s_at	MRPL4	218016_s_at	POLR3E
220865_s_at	PDSS1	218670_at	PUS1
209760_at	KIAA0922	203238_s_at	NOTCH3
204514_at	DPH2	203119_at	CCDC86
226410_at	LOC348180	218594_at	HEATR1
211949_s_at	NOLC1	210463_x_at	TRMT1
215792_s_at	DNAJC11	217884_at	NAT10
218238_at	GTPBP4	224632_at	GPATC4
217838_s_at	EVL	221649_s_at	PPAN
200895_s_at	FKBP4	217850_at	GNL3
219083_at	SHQ1	220688_s_at	C10RF33
202138_x_at	JTV1	203612_at	BYSL
201489_at	PPIF	209100_at	IFRD2
225866_at	BXDC1	210448_s_at	P2RX5
201574_at	ETF1	211576_s_at	SLC19A1
232154_at	LOC199800	224634_at	GPATC4
216397_s_at	BOP1 /// LOC653119	209336_at	PWP2H
224596_at	SLC44A1	202431_s_at	MYC
214011_s_at	HSPC111	203737_s_at	PPRC1
209971_x_at	JTV1	218984_at	PUS7
201478_s_at	DKC1	225943_at	NLN
218758_s_at	D21S2056E	203394_s_at	HES1
63009_at	SHQ1	202934_at	HK2
209567_at	RRS1	227336_at	DTX1
225682_s_at	POLR3H	227347_x_at	HES4

Supplementary Figure 4: GSEA analysis of SAHM gene expression profile and pathway specificity. a) Probe identifiers and gene names for the GSI-NOTCH gene set used in GSEA.



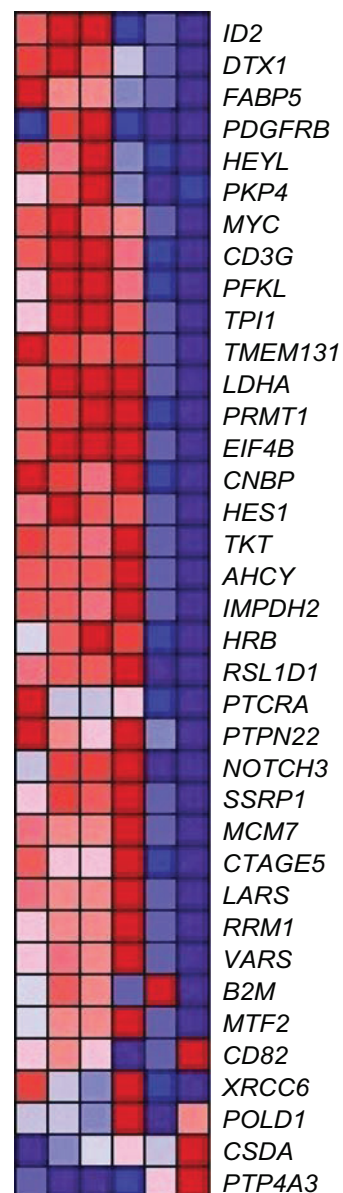
Supplementary Figure 5: Generation of the L1601PΔP & Luc: L1601PΔP models of NOTCH1 activation-dependent T-ALL.

a) Schematic of the retroviral construct expressing a constitutively active *NOTCH1* allele bearing dual mutations initially identified in human T-ALL. EGF, EGF-like repeats; LIN, LIN-12 repeats; T, transmembrane domain; R, RAM domain; ANK, ankyrin repeat domain; TAD, transactivation domain; P, PEST regulatory domain. The relative locations of extracellular and PEST domain mutations are indicated. **b)** Bone marrow harvested from 5-fluorouracil treated adult wild-type or Ubc-Luc C57BL/6-Tyr^{C/C} mice was transduced with L1601PΔP vector. **c)** Isolated GFP+ cells were transplanted into primary recipient mice and followed for signs of morbidity, organomegaly and progressively increasing bioluminescence. **d-e)** Primary cells were collected from leukemic recipient animals and used for *in vitro* and *in vivo* studies.

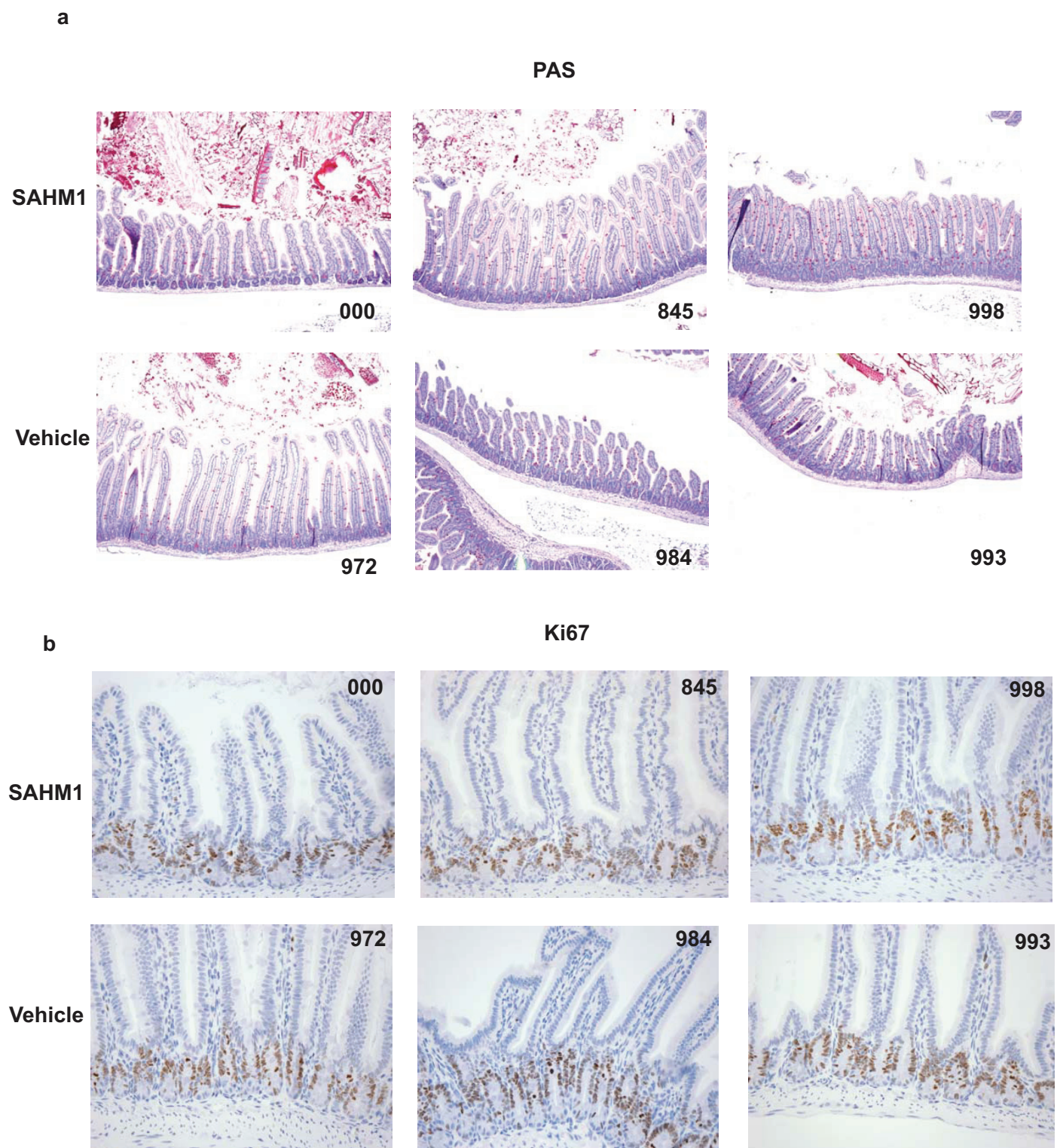


Supplementary Figure 6. Analysis of primary leukemic animals from the L1601PΔP T-ALL model. **a)** Flow cytometric analysis of tissues derived from primary leukemic L1601PΔP (donor) mice. **b)** Immunohistochemical staining of spleen and liver from primary leukemic (donor) mice. Both tissues are heavily infiltrated by GFP+/CD3+ blasts that are negative for the B cell marker B220. A high fraction of cells are also positive for Ki67, a cell cycle marker. **c)** Effects of SAHMs on primary murine T-ALL cells *in vitro*. Cell viability was measured using Cell Titer-Glo. **d)** Kinetic study of SAHM1 or SAHM1-D1 (5 μM) treatment in sorted (FACS) primary leukaemia cells (GFP+CD3+) for 12, 24 or 48 hours. No impairment in viability is observed at 12 hours, establishing the duration of *ex vivo* SAHM1 exposure in studies of leukaemia initiation in secondary recipients.

Vehicle SAHM1



Supplementary Figure 7. GSEA analysis of *in vivo* gene expression profile in SAHM1 treated mice. a) The rank-ordered GSI/dnMAML1 gene-set curated from a published study in murine T6E cells, which is a T-ALL cell line dependent on mutant NOTCH1. This gene set was queried against the gene expression profile generated from SAHM1 (30mg/kg, bid, n=3) and vehicle treated mice (n=3) as discussed in Methods and presented in figure 5.



Supplementary Figure 8. Effects of SAHM1 on gastrointestinal tract of treated mice. Gastrointestinal tracts from mice treated with SAHM1 (30mg/kg, bid, n = 3) or vehicle alone (n = 3) for five days were harvested and stained for **a)** PAS and **b)** Ki67 to assess proliferative changes and goblet cells. No apparent changes were present.

Cell Line	<i>NOTCH1</i> HD	<i>NOTCH1</i> PEST	<i>FBXW7</i>	<i>PTEN</i>
KOPT-K1	L1601P	2515 RVP*STOP	WT	WT
HPB-ALL	L1575P	Insertion 2442: EGRGRCSHWAPAAWRCTL FCPRRAPPCPRRCHPRWSP*STOP	WT	WT
DND-41	L1594P	Insertion 2444: CCSHWAPAAWRCTLFCPRR APPCPRRCHPRWSHP*STOP	WT	WT
TALL-1	WT	WT	WT	WT
CUTTL1	t(7;9): <i>TCRB- NOTCH1</i> fusion transcript	WT	WT	WT
SUTP1	t(7;9): <i>TCRB- NOTCH1</i> fusion transcript	WT	WT	WT
MOLT-4	L1601P	2515 RVP*STOP	WT	MUT
JURKAT	WT	WT	R505C	MUT
K-562 (BCR-Abl driven)	-	-	-	-

Supplementary Table 1. Genetic annotation of human T-ALL cell lines.

Mutational status of *NOTCH1*, *FBXW7* and *PTEN* in human T-ALL cell lines, curated from published reports. Notch mutational status imperfectly correlates with sensitivity to GSI. For example, T-ALL1 is a human cell line with wild-type *NOTCH1* widely reported as GSI-sensitive^{14,15,41,43}. At present, the mechanism of GSI-sensitivity is not known.

Supplemental Table 2

NAME	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val
GSI-NOTCH	74	-0.846375	-3.1334748	0	0	0
V\$MYCMAX_01	220	-0.465162	-2.0055006	0	0.001106901	0.002
V\$HIF1_Q3	193	-0.459135	-1.9349917	0	0.001827828	0.005
V\$MAX_01	223	-0.42508	-1.8283559	0	0.011064745	0.04
V\$NMYC_01	224	-0.423833	-1.8250479	0	0.009269679	0.042
GGAANCGBAANY_UNKNOWN	92	-0.473854	-1.813707	0	0.008432279	0.045
V\$PAX5_02	15	-0.680415	-1.7850482	0.00506757	0.011392025	0.071
TCCCRNNRTGC_UNKNOWN	152	-0.411702	-1.6770186	0.00143885	0.039689474	0.255
V\$AP1_Q4	239	-0.383013	-1.6707138	0	0.038405724	0.274
V\$MYCMAX_02	226	-0.384965	-1.6554859	0	0.042554364	0.32
SGCGSSAAA_V\$E2F1DP2_01	141	-0.404592	-1.6551933	0	0.038781524	0.321
MCAATNNNNNGCG_UNKNOWN	73	-0.44842	-1.6533995	0.00455235	0.036001686	0.325
V\$E2F1DP1_01	195	-0.384104	-1.6457547	0	0.037119344	0.356
V\$E2F_02	195	-0.386431	-1.6451302	0	0.03485097	0.359
V\$AHR_Q5	184	-0.385866	-1.640435	0	0.033744745	0.367
V\$E2F1DP2_01	195	-0.384104	-1.636795	0	0.03331251	0.38
V\$MYC_Q2	152	-0.396799	-1.6366893	0	0.031352952	0.38
V\$GABP_B	193	-0.381874	-1.6337395	0	0.0309882	0.395
V\$E2F4DP2_01	195	-0.384104	-1.6318874	0	0.030039176	0.401
V\$E2F4DP1_01	200	-0.38167	-1.6299274	0.00133511	0.029510718	0.411
V\$E2F1_Q6_01	202	-0.379753	-1.6223896	0	0.03092572	0.442
V\$USF_C	234	-0.370987	-1.6193031	0	0.030699233	0.455
V\$HIF1_Q5	201	-0.378179	-1.6186676	0	0.029600894	0.459
V\$PU1_Q6	196	-0.381613	-1.6108115	0	0.03130702	0.495
V\$MYCMAX_B	227	-0.372174	-1.6095405	0	0.03035857	0.5
V\$USF_01	221	-0.371717	-1.6075568	0	0.029943569	0.505
STTTTCRNTTT_V\$IRF_Q6	159	-0.381142	-1.5860609	0.00276625	0.036952764	0.586
V\$E2F_01	59	-0.440857	-1.5797954	0.01624815	0.038634833	0.614
V\$USF_Q6	212	-0.365567	-1.5753105	0	0.039243575	0.64
V\$USF2_Q6	204	-0.366774	-1.5724796	0	0.039125167	0.655
V\$ETF_Q6	88	-0.410365	-1.5700983	0.010279	0.0387674	0.667
V\$E2F1_Q6	191	-0.366111	-1.555231	0.00262812	0.045647103	0.744
V\$ZF5_B	204	-0.359398	-1.5518134	0	0.0460451	0.766
KCCGNSWTTT_UNKNOWN	90	-0.402721	-1.5508087	0	0.04504086	0.767
AACYNNNNNTTCCS_UNKNOWN	74	-0.412865	-1.5506848	0.00887574	0.04375398	0.767
TGANNYRGCA_V\$TCF11MAFG_01	249	-0.353931	-1.5477366	0.00125471	0.044130098	0.781
V\$ELK1_Q2	194	-0.366118	-1.5391612	0.00137931	0.047196355	0.813
GKCGCNNNNNNNTGAYG_UNKNOWN	47	-0.449685	-1.5345855	0.02204724	0.04839654	0.83
YGCGYRCGC_UNKNOWN	251	-0.350144	-1.5340669	0.00128041	0.04732332	0.83
ACAWNRRNSRCGG_UNKNOWN	56	-0.430335	-1.5204555	0.01843318	0.05395835	0.873
RRCCGTTA_UNKNOWN	66	-0.41425	-1.5178387	0.01834862	0.054144185	0.879
V\$STAT6_Q2	212	-0.349625	-1.5086721	0.00530504	0.0586709	0.907
V\$NRF2_Q1	200	-0.354235	-1.5065964	0.00397351	0.058138598	0.91
V\$YY1_Q6	189	-0.35545	-1.5044674	0.00791557	0.05801557	0.913
V\$ARNT_Q1	224	-0.348598	-1.5022506	0.00131406	0.058445793	0.917
V\$AHRARNT_Q1	118	-0.376041	-1.5013615	0.01057402	0.05793296	0.92
V\$MYCMAX_Q3	217	-0.351657	-1.4983815	0.00269906	0.05856729	0.924
KTGGYRSGAA_UNKNOWN	60	-0.41921	-1.497364	0.01935484	0.05811114	0.925
V\$ELK1_Q1	204	-0.347153	-1.4915819	0.01054019	0.0613514	0.946
V\$E2F_Q3	194	-0.347754	-1.4752431	0.00777202	0.072630934	0.966
ACTAYRNNNCCCR_UNKNOWN	337	-0.32999	-1.4751631	0	0.07122808	0.966
CTCNANGTGNY_UNKNOWN	75	-0.396048	-1.4666252	0.01538462	0.07742269	0.976
GCCATNTTG_V\$YY1_Q6	344	-0.326583	-1.4653096	0	0.076981746	0.977
V\$NFMUE1_Q6	200	-0.343373	-1.4552855	0.00390117	0.08422096	0.981
V\$E2F1_Q3	195	-0.342598	-1.4536194	0.01104972	0.08432257	0.983
CCGNMNNNTNACG_UNKNOWN	63	-0.40189	-1.4535406	0.03148426	0.08287463	0.983
YGTCTTGR_UNKNOWN	80	-0.379444	-1.4518101	0.03759398	0.08307271	0.983
V\$E2F_Q4_Q1	191	-0.341929	-1.4406415	0.00396301	0.092896104	0.991
V\$USF_Q6_Q1	199	-0.337029	-1.4404073	0.00517464	0.09148593	0.991
V\$SRF_Q1	48	-0.413747	-1.440305	0.03358779	0.09008743	0.991
V\$AP1_Q2	237	-0.327919	-1.4368657	0.00398936	0.09255326	0.993

V\$ZF5_01	196	-0.336744	-1.4358346	0.01209677	0.09213992	0.994
V\$EGR_Q6	230	-0.328971	-1.4354475	0.00782269	0.091004595	0.994
V\$SP1_Q4_01	208	-0.33251	-1.4332408	0.00900901	0.091779076	0.994
V\$ELF1_Q6	195	-0.340333	-1.4303921	0.00925926	0.093245514	0.994
V\$ETS1_B	212	-0.332021	-1.4294254	0.0091623	0.09279926	0.996
V\$AP1_Q6	220	-0.328669	-1.4293357	0.01041667	0.09147818	0.996
V\$PEA3_Q6	198	-0.33393	-1.426731	0.01061008	0.09316525	0.998
V\$AP1FJ_Q2	240	-0.32958	-1.4261028	0.00777202	0.092298985	0.998
WWTAAGGC_UNKNOWN	124	-0.355822	-1.4257383	0.02586207	0.09139442	0.998
V\$SP1_Q6_01	190	-0.334917	-1.4254208	0.00662252	0.09028937	0.998
V\$E2F_Q6	192	-0.333851	-1.4208217	0.01069519	0.09420662	0.998
V\$HNF4_01_B	210	-0.332195	-1.4195863	0.00655308	0.0941269	0.998
CGGAARNGGCNG_UNKNOWN	39	-0.431889	-1.4149487	0.0601626	0.097995654	0.999
V\$E2F_Q4	194	-0.333696	-1.4137579	0.0135318	0.09782387	0.999
V\$AP2_Q3	213	-0.328188	-1.402819	0.00780234	0.10858628	0.999
V\$PAX4_01	221	-0.323428	-1.4026189	0.00762389	0.10738702	0.999
V\$E2F1DP1RB_01	191	-0.330201	-1.4024242	0.01062417	0.10621905	0.999
V\$DR1_Q3	203	-0.327628	-1.4016556	0.01058201	0.105627164	0.999
V\$TEL2_Q6	181	-0.335269	-1.3999805	0.01604278	0.1059651	0.999
V\$HNF4_DR1_Q3	214	-0.32134	-1.3987306	0.00903226	0.10578115	1
GCGNNANTTCC_UNKNOWN	98	-0.356648	-1.3969787	0.03448276	0.106241964	1
V\$LFA1_Q6	207	-0.328002	-1.3940724	0.01174935	0.108693734	1
V\$CMYB_01	200	-0.326078	-1.3923022	0.00909091	0.10938369	1
CAGNYGKNAAN_UNKNOWN	59	-0.39041	-1.3908838	0.05247377	0.10990368	1
TMTCGCGANR_UNKNOWN	111	-0.351593	-1.389675	0.02124646	0.109694675	1
TTCYRGAA_UNKNOWN	256	-0.314163	-1.3878443	0.00770218	0.11055498	1
TNCATNTCCYR_UNKNOWN	101	-0.357059	-1.3842447	0.03851852	0.11357373	1
GCTNWTGK_UNKNOWN	252	-0.316036	-1.3829402	0.00376412	0.11391955	1
V\$PPAR_DR1_Q2	214	-0.319056	-1.3776807	0.01456954	0.11903341	1
V\$E2F_Q6_01	191	-0.321567	-1.3758668	0.02300406	0.119736485	1
V\$PPARG_01	38	-0.419125	-1.3741385	0.07914764	0.120632745	1
V\$STAT1_01	54	-0.38974	-1.3706933	0.07763975	0.124155946	1
V\$XPB1_01	116	-0.342906	-1.3693836	0.03429355	0.124341704	1
V\$ATF4_Q2	208	-0.319577	-1.3689097	0.01236264	0.123578146	1
V\$NRF2_Q4	216	-0.316891	-1.367806	0.01699347	0.12360512	1
V\$E2F1_Q4_01	184	-0.327054	-1.3675861	0.01583114	0.12268653	1
V\$STAT1_02	201	-0.321306	-1.3651437	0.0185923	0.12427513	1
V\$PAX4_03	226	-0.314403	-1.3646072	0.01164295	0.12363862	1
V\$NRF1_Q6	198	-0.320746	-1.3642207	0.01886793	0.1228531	1
V\$NFE2_01	228	-0.314357	-1.3634562	0.0139417	0.122600205	1
V\$HNF4_01	219	-0.316886	-1.3626075	0.01237964	0.12235247	1
V\$STAT_01	215	-0.316323	-1.3605535	0.02533333	0.123995736	1
YGACNNYACAR_UNKNOWN	79	-0.36341	-1.3585131	0.05823864	0.12571198	1
V\$E2F_Q3	180	-0.322517	-1.3583636	0.03238867	0.12468991	1
V\$NERF_Q2	202	-0.320299	-1.3572872	0.01978892	0.124808684	1
V\$ATF_01	220	-0.309546	-1.3566707	0.01643489	0.12458347	1
V\$SP1_01	206	-0.316821	-1.3536702	0.01839685	0.12737526	1
TGASTMAGC_V\$NFE2_01	171	-0.325235	-1.352652	0.03351206	0.12743075	1
V\$AREB6_04	216	-0.317082	-1.3522449	0.02021563	0.12671171	1
V\$COUP_DR1_Q6	199	-0.318955	-1.3518867	0.01864181	0.12604715	1
V\$ATF6_01	99	-0.346228	-1.3503369	0.05988024	0.12704362	1
V\$SP1_Q2_01	210	-0.31705	-1.3494184	0.02005348	0.12704669	1
V\$CHOP_01	202	-0.312523	-1.3360827	0.02203857	0.14443153	1
V\$STAT3_01	21	-0.465608	-1.3329073	0.13207547	0.14779325	1
V\$STAT1_03	205	-0.306527	-1.3285682	0.02734375	0.1532541	1
AACWWCAANK_UNKNOWN	110	-0.336711	-1.3278906	0.05807366	0.15293744	1
V\$CREB_Q2	213	-0.304496	-1.3274455	0.02384106	0.15223567	1
KMCATNNWGA_UNKNOWN	73	-0.354726	-1.3258634	0.07110439	0.15321198	1
V\$USF_02	225	-0.306839	-1.323693	0.03631647	0.15518682	1
V\$E2F_Q3_01	188	-0.311845	-1.320356	0.0331565	0.1594396	1
WCAANNNYCAG_UNKNOWN	200	-0.306316	-1.3156942	0.03355705	0.1656129	1
V\$CREB_02	208	-0.305926	-1.3099557	0.03178808	0.17347085	1
GGCKCATGS_UNKNOWN	52	-0.375183	-1.3083518	0.11520737	0.1751147	1
V\$PXR_Q2	222	-0.301923	-1.3042154	0.02486911	0.18112238	1
GCGNKCCATNK_UNKNOWN	94	-0.339108	-1.3033785	0.07819549	0.18107131	1

V\$ARNT_02	208	-0.303188	-1.2922053	0.04302477	0.19922498	1
V\$TGIF_01	190	-0.305351	-1.2908591	0.04617414	0.20026325	1
V\$TATA_01	224	-0.299162	-1.2897108	0.05345502	0.20076631	1
V\$HNF4_Q6	213	-0.300066	-1.2884092	0.04113111	0.20148428	1
V\$SOX9_B1	198	-0.299881	-1.2854477	0.04666667	0.20516245	1
V\$SRF_C	187	-0.303764	-1.2790625	0.0646438	0.21600312	1
V\$MAZ_Q6	150	-0.307867	-1.2735022	0.07	0.22578734	1
V\$ETS_Q4	200	-0.296655	-1.2720021	0.04842932	0.2271866	1
YTTCCNNNGGAMR_UNKNOWN	36	-0.399176	-1.2712717	0.14772727	0.22684057	1
RGAGGAARY_V\$PU1_Q6	410	-0.275483	-1.2696722	0.02696079	0.22839169	1
CGTSACG_V\$PAX3_B	114	-0.317643	-1.2679584	0.08643815	0.2300422	1
V\$SREBP_Q3	201	-0.295237	-1.2679361	0.05733333	0.22839881	1
GTTNYNNNGGTNA_UNKNOWN	68	-0.346653	-1.265151	0.11377245	0.23211029	1
RNCTGNYNRNCTGNY_UNKNOWN	61	-0.355264	-1.2627324	0.11544462	0.23552467	1
V\$CREBP1CJUN_01	215	-0.291292	-1.2615381	0.05269923	0.23646465	1
V\$SP3_Q3	203	-0.295189	-1.2587173	0.06684857	0.24090566	1
V\$BACH2_01	232	-0.291876	-1.2553977	0.06169666	0.24668783	1
YRTCANNRCGC_UNKNOWN	50	-0.363755	-1.2536844	0.14331724	0.24856639	1
V\$COUP_01	218	-0.288535	-1.2517781	0.06468305	0.25128898	1
V\$AP2_Q6_01	215	-0.288754	-1.2510163	0.08016305	0.25132385	1
V\$FXR_IR1_Q6	100	-0.318954	-1.2501707	0.1038961	0.25145793	1
ACTWSNACTNY_UNKNOWN	73	-0.340481	-1.2472546	0.13394216	0.2561748	1
GTGGGTGK_UNKNOWN	245	-0.286134	-1.2468671	0.05822785	0.25539485	1
V\$GCM_Q2	196	-0.292918	-1.2468034	0.06905711	0.25382936	1
V\$E2F_Q2	132	-0.307838	-1.2436256	0.08251748	0.25933644	1
V\$ICSBP_Q6	209	-0.289435	-1.2426231	0.072	0.25981545	1
V\$CREB_01	215	-0.28749	-1.240451	0.07105943	0.26336452	1
V\$IRF2_01	105	-0.316236	-1.2377642	0.12089552	0.26734734	1
V\$MZF1_02	195	-0.290323	-1.2371988	0.07662338	0.2670056	1
TGACGTCA_V\$ATF3_Q6	190	-0.291008	-1.2345243	0.06629834	0.2719174	1
V\$AP1_C	245	-0.28142	-1.2296448	0.06623377	0.28154048	1
YTCCCRNNAGGY_UNKNOWN	60	-0.345175	-1.2290574	0.14728682	0.2811707	1
V\$CETS1P54_01	206	-0.286992	-1.2282337	0.07984293	0.28132096	1
V\$SMAD_Q6	215	-0.284602	-1.2262139	0.08168643	0.28403303	1
V\$CREB_Q4	209	-0.287596	-1.2256857	0.09043928	0.2835709	1
V\$LMO2COM_01	205	-0.285337	-1.2256325	0.08481532	0.28196022	1
TGACCTTG_V\$SF1_Q6	210	-0.285034	-1.2248856	0.08255659	0.2819899	1
V\$HSF_Q6	160	-0.295066	-1.2240885	0.09861111	0.282154	1
V\$AP1_Q6_01	219	-0.283833	-1.2220508	0.09736842	0.2852732	1
V\$E2F1_Q4	199	-0.286043	-1.220342	0.0923277	0.28753537	1
V\$PAX3_01	16	-0.458374	-1.2203149	0.20973155	0.28589842	1
V\$SPZ1_01	206	-0.283189	-1.2158176	0.10131579	0.29495767	1
V\$VDR_Q6	207	-0.283362	-1.2148778	0.09299363	0.2954499	1
CCCNNGGGAR_V\$OLF1_01	268	-0.274613	-1.2145617	0.08035714	0.29459113	1
V\$CREB_Q2_01	184	-0.289081	-1.214161	0.10225764	0.29396138	1
V\$YY1_02	196	-0.286771	-1.2099556	0.09917355	0.30269626	1
V\$E4BP4_01	178	-0.284854	-1.2097756	0.1188251	0.30139422	1
V\$SF1_Q6	206	-0.2833	-1.2080448	0.10416666	0.3038719	1
YRCCAKNNGNCGC_UNKNOWN	58	-0.339793	-1.2074555	0.1770335	0.3036728	1
GCCNNMSMYNTTG_UNKNOWN	58	-0.341706	-1.206096	0.17289719	0.30533102	1
V\$NGFIC_01	208	-0.280537	-1.2054536	0.10121457	0.30521166	1
V\$IRF_Q6	194	-0.283856	-1.2000425	0.1171875	0.31707937	1
V\$AP2_Q6	215	-0.27688	-1.1999769	0.10303831	0.31550574	1
V\$ER_Q6_01	223	-0.276968	-1.1991795	0.11182519	0.3155869	1
V\$SREBP1_Q6	213	-0.277074	-1.1990277	0.10939511	0.3142548	1
V\$AHRARNT_02	15	-0.44909	-1.1975245	0.25127333	0.31633478	1
GATGKMRGCG_UNKNOWN	53	-0.346597	-1.1949217	0.1952	0.3214155	1
TGTYNNNNNRGCARM_UNKNOWN	59	-0.328046	-1.193669	0.17546584	0.3229151	1
V\$HEN1_02	157	-0.288455	-1.19255	0.13399154	0.3240815	1
V\$E4F1_Q6	227	-0.275471	-1.1847558	0.11914324	0.34306952	1
RGAANNTTC_V\$HSF1_01	361	-0.261109	-1.1837367	0.10278114	0.3438885	1
V\$SP1_Q6	203	-0.276417	-1.1770704	0.12433155	0.36097425	1
V\$MMEF2_Q6	234	-0.272075	-1.1762358	0.1183355	0.36134884	1
YAATNRNNNNYNTT_UNKNOWN	91	-0.30802	-1.1730983	0.18063584	0.3683257	1
GCGSCMNTTT_UNKNOWN	56	-0.333953	-1.1728667	0.215478	0.3670974	1

V\$E2F1_Q3_01	208	-0.274217	-1.1671201	0.15314136	0.3816793	1
TGCTGAY_UNKNOWN	455	-0.255391	-1.1664044	0.08232445	0.38173133	1
V\$MZF1_01	204	-0.271473	-1.1659796	0.14686248	0.38094485	1
V\$NFAT_Q4_01	218	-0.269644	-1.164009	0.16688742	0.38479018	1
V\$CREB_Q3	204	-0.271148	-1.1629292	0.14557824	0.38607877	1
V\$CACCCBINDINGFACTOR_Q6	227	-0.271345	-1.1627377	0.16154873	0.38476664	1
V\$PR_01	120	-0.289081	-1.1600512	0.18813314	0.39100552	1
V\$RFX1_01	203	-0.270012	-1.1545279	0.16842106	0.4055444	1
V\$STAT3_Q2	122	-0.291955	-1.1533629	0.19765739	0.4068542	1
V\$AREB6_Q3	197	-0.271098	-1.1502323	0.17173052	0.41438282	1
V\$PAX3_B	77	-0.307133	-1.148934	0.22288261	0.41632634	1
V\$HNF4ALPHA_Q6	219	-0.265958	-1.1418309	0.19505852	0.4360818	1
V\$ER_Q6	227	-0.266575	-1.1415839	0.16775033	0.43478656	1
V\$NFY_01	207	-0.266912	-1.1392747	0.19319728	0.43986043	1
V\$LEF1_Q2	173	-0.270599	-1.1379014	0.19015048	0.44225582	1
V\$SREBP1_01	144	-0.276023	-1.1377014	0.19662921	0.4407001	1
TGCGCANK_UNKNOWN	435	-0.247917	-1.1341286	0.15658364	0.45022014	1
TGGNNNNNNKCCAR_UNKNOWN	350	-0.25252	-1.1327997	0.16730037	0.45213866	1
V\$HTF_01	58	-0.318882	-1.1325674	0.25609756	0.4507304	1
RACCACAR_V\$AML_Q6	213	-0.262755	-1.1314658	0.18915343	0.4522425	1
SYATTGTG_UNKNOWN	188	-0.264852	-1.1283143	0.20476858	0.4604334	1
V\$AR_Q3	47	-0.331448	-1.1278067	0.26564884	0.45985165	1
V\$MAZR_01	189	-0.268021	-1.126178	0.20603675	0.4627701	1
V\$AP1_Q4_01	225	-0.25563	-1.1208776	0.21073298	0.47794068	1
V\$LEF1_Q6	226	-0.260625	-1.117513	0.22976501	0.4866212	1
V\$TFIIA_Q6	212	-0.259312	-1.1173313	0.24057217	0.4849089	1
TTCYNRGAA_V\$STAT5B_01	272	-0.252876	-1.1161169	0.21778351	0.4867588	1
V\$MYOGENIN_Q6	211	-0.259601	-1.1123285	0.24898511	0.49721432	1
GTCNYYATGR_UNKNOWN	91	-0.289545	-1.1115562	0.27219796	0.49760178	1
CRGAARNNNNCGA_UNKNOWN	38	-0.335778	-1.1102667	0.28548896	0.49986416	1
V\$HEN1_01	165	-0.265629	-1.1082169	0.2465181	0.504769	1
TCANNTGAY_V\$SREBP1_01	392	-0.241108	-1.106247	0.19976498	0.50885814	1
V\$HMX1_01	38	-0.33436	-1.1009536	0.3176661	0.52451783	1
V\$NFKB_C	231	-0.255401	-1.098669	0.24577373	0.5300469	1
WCTCNATGGY_UNKNOWN	61	-0.305973	-1.0982162	0.3131783	0.52921146	1
V\$IRF7_01	212	-0.255168	-1.0971407	0.25695366	0.53057283	1
V\$PAX_Q6	218	-0.254178	-1.0963117	0.25751635	0.531004	1
V\$TTF1_Q6	215	-0.256631	-1.0953783	0.2621871	0.5321351	1
V\$CEBPB_Q2	221	-0.253048	-1.0891366	0.27792206	0.5519305	1
V\$NFY_Q6_01	213	-0.251152	-1.0871633	0.28165373	0.5563186	1
V\$ETS2_B	226	-0.254097	-1.0849112	0.28795812	0.5618426	1
RACTNNRRTTNC_UNKNOWN	104	-0.272789	-1.0823777	0.29760227	0.5683926	1
V\$CDPCR3_01	42	-0.321513	-1.0820774	0.35117057	0.56713015	1
V\$E47_Q2	200	-0.254642	-1.0786494	0.2948886	0.576616	1
CCTNTMAGA_UNKNOWN	104	-0.271058	-1.07803	0.3069307	0.57648885	1
V\$MYOD_Q6	202	-0.252503	-1.0768441	0.29287598	0.5783471	1
V\$MTF1_Q4	222	-0.251665	-1.0731064	0.2996159	0.5893229	1
CATTGTYT_V\$SOX9_B1	303	-0.242259	-1.0713751	0.2914573	0.59325916	1
V\$EGR1_01	216	-0.24661	-1.0704826	0.28074867	0.5937368	1
V\$E2A_Q2	202	-0.248358	-1.0684294	0.29737207	0.5988252	1
V\$PAX8_B	86	-0.280808	-1.0682276	0.32544377	0.59705466	1
V\$CEBPA_01	199	-0.250207	-1.0662074	0.29419526	0.6019033	1
V\$TFIIQ_Q6	175	-0.252512	-1.0647123	0.3263434	0.605123	1
V\$AP1_01	233	-0.244849	-1.0598332	0.33117723	0.61991626	1
V\$HLF_01	213	-0.245514	-1.0578157	0.33110815	0.62470484	1
V\$CP2_01	217	-0.246686	-1.0571336	0.33022636	0.62462664	1
V\$AR_01	121	-0.264385	-1.0553734	0.3598862	0.62829643	1
V\$T3R_Q6	217	-0.245675	-1.0543779	0.33678755	0.62947476	1
V\$CREL_01	222	-0.244018	-1.0542824	0.34214002	0.6273018	1
V\$CEBPB_01	215	-0.244709	-1.0540376	0.32774192	0.62570095	1
V\$DR3_Q4	113	-0.264084	-1.0524191	0.35561877	0.629439	1
V\$IRF1_01	207	-0.243319	-1.0498049	0.34954008	0.6362813	1
V\$MYOD_01	207	-0.244668	-1.044919	0.34912044	0.65130234	1
V\$ISRE_01	194	-0.248918	-1.0440774	0.3810179	0.65175736	1
V\$MYB_Q6	208	-0.2432	-1.0440447	0.3727034	0.64930415	1

YYCATCAWW_UNKNOWN	160	-0.252349	-1.0439423	0.35309973	0.64716	1
ARGGGTTAA_UNKNOWN	107	-0.266251	-1.0402977	0.3810219	0.65774226	1
V\$NKX62_Q2	197	-0.245822	-1.0397087	0.36437246	0.6574888	1
V\$OLF1_Q1	226	-0.239956	-1.0385921	0.36903226	0.6589575	1
V\$AP2ALPHA_Q1	201	-0.242515	-1.0372158	0.36340207	0.6613056	1
V\$NKX25_Q1	109	-0.262105	-1.0368458	0.38864627	0.66015816	1
V\$MAF_Q6	225	-0.241047	-1.0358804	0.36617842	0.6610602	1
V\$SOX5_Q1	219	-0.239173	-1.0355005	0.37209302	0.6600091	1
V\$AP2REP_Q1	146	-0.250545	-1.0338734	0.35944057	0.6636111	1
V\$AML_Q6	217	-0.242695	-1.0309372	0.37967914	0.67184895	1
V\$SRF_Q5_Q1	199	-0.241949	-1.0305691	0.39005235	0.67068475	1
WTTGKCTG_UNKNOWN	429	-0.232753	-1.0298104	0.38210398	0.6710245	1
TAANNYSGCG_UNKNOWN	64	-0.287063	-1.0282524	0.41252005	0.6741717	1
RYAAAKNNNNNNNTTGW_UNKNOWN	74	-0.277102	-1.0272521	0.42065868	0.6752837	1
V\$COREBINDINGFACTOR_Q6	220	-0.237475	-1.0246178	0.4	0.68202484	1
V\$DR4_Q2	211	-0.237539	-1.0229993	0.40832248	0.685572	1
V\$SRF_Q6	218	-0.236643	-1.0197679	0.41192052	0.6948517	1
V\$BACH1_Q1	225	-0.234085	-1.0189584	0.4213264	0.6952216	1
GTTRYCATRR_UNKNOWN	133	-0.252653	-1.0179372	0.4119318	0.69664943	1
V\$STAT5A_Q1	211	-0.23691	-1.01639	0.41153845	0.6996776	1
V\$ZIC2_Q1	207	-0.235876	-1.0161893	0.4268617	0.69792175	1
V\$STAT6_Q1	218	-0.23547	-1.0127856	0.4365285	0.7075428	1
V\$CP2_Q2	199	-0.237743	-1.011378	0.43386245	0.7101147	1
V\$FOXO4_Q1	201	-0.236848	-1.0100409	0.44113666	0.71237123	1
V\$SRY_Q2	212	-0.233546	-1.0094737	0.4224806	0.71194243	1
V\$E12_Q6	199	-0.2372	-1.0085809	0.43678162	0.7126142	1
WGTTNNNNNAAA_UNKNOWN	466	-0.217984	-1.0062473	0.43550295	0.7183216	1
V\$YY1_Q1	210	-0.234372	-1.0037863	0.44987145	0.724732	1
ATGGYGGA_UNKNOWN	79	-0.266818	-1.0002711	0.45870206	0.7349637	1
V\$P300_Q1	201	-0.234538	-0.99610263	0.44702843	0.74777126	1
V\$AR_Q2	101	-0.256148	-0.99194926	0.46814814	0.76009464	1
V\$ER_Q6_Q2	213	-0.230593	-0.99134064	0.48687664	0.7597649	1
V\$SMAD3_Q6	196	-0.23563	-0.9894759	0.47925034	0.76424813	1
V\$TEF1_Q6	178	-0.235167	-0.9853324	0.48724833	0.7771921	1
RYTAAWNNNTGAY_UNKNOWN	58	-0.274785	-0.98372704	0.49846625	0.78026944	1
V\$CREBP1_Q1	143	-0.239596	-0.9828547	0.49788433	0.7807154	1
V\$NFKB_Q6	217	-0.226992	-0.98078835	0.49800798	0.7854151	1
V\$PPARA_Q2	104	-0.251617	-0.98013437	0.49710983	0.78517807	1
V\$SRY_Q1	169	-0.234578	-0.9798824	0.5159575	0.7835038	1
V\$SMAD4_Q6	204	-0.230873	-0.97895676	0.5047106	0.7841558	1
V\$CEBP_C	171	-0.232262	-0.9763328	0.5033289	0.7907677	1
ACCTGTTG_UNKNOWN	127	-0.245033	-0.97428674	0.516129	0.7956259	1
RRAGTTGT_UNKNOWN	212	-0.226346	-0.9727394	0.51660025	0.79839456	1
CCAWWNAAGG_V\$SRF_Q4	76	-0.261266	-0.96963733	0.49459043	0.80728203	1
V\$CREBP1_Q2	201	-0.227344	-0.9694854	0.53350854	0.80510706	1
V\$OSF2_Q6	222	-0.224882	-0.96707237	0.5387648	0.8108521	1
V\$TBP_Q1	201	-0.226211	-0.96618396	0.5509934	0.8114685	1
V\$MYOD_Q6_Q1	199	-0.226377	-0.96556854	0.54304636	0.810974	1
V\$PAX8_Q1	29	-0.312243	-0.9629618	0.51480263	0.81736916	1
V\$SRF_Q4	201	-0.224379	-0.95980847	0.5536424	0.8259001	1
V\$VDR_Q3	194	-0.223601	-0.95940614	0.5648649	0.82458425	1
V\$GR_Q1	169	-0.228367	-0.9590257	0.5506849	0.82329714	1
RYCACNNRNNRNCAG_UNKNOWN	59	-0.26748	-0.9580224	0.52194357	0.8240381	1
V\$AP4_Q1	219	-0.219993	-0.95761836	0.5530504	0.8229928	1
V\$LBP1_Q6	179	-0.228134	-0.9574761	0.55186725	0.82079774	1
V\$HAND1E47_Q1	224	-0.221877	-0.9564224	0.57198954	0.8218703	1
TGAYRTCA_V\$ATF3_Q6	444	-0.208306	-0.95564884	0.6011765	0.8220794	1
V\$STAT5B_Q1	211	-0.223562	-0.9553857	0.57563585	0.8204764	1
V\$CREB_Q4_Q1	171	-0.226778	-0.95458055	0.56875837	0.8207502	1
V\$P53_Q2	213	-0.219903	-0.9504752	0.59395534	0.83230627	1
V\$ATF_B	158	-0.228845	-0.94790155	0.5635135	0.83854705	1
TTGCWCAAY_V\$CEBPB_Q2	56	-0.26917	-0.9470659	0.5421133	0.8388174	1
V\$NFY_Q6	212	-0.220003	-0.94537455	0.6026667	0.84229594	1
V\$FOXO3_Q1	199	-0.219614	-0.94424176	0.5964912	0.84363514	1
V\$ZIC1_Q1	218	-0.220987	-0.9432094	0.62027025	0.8444764	1

GGAMTNNNNNTCCY_UNKNOWN	96	-0.239763	-0.94299203	0.54232424	0.8426266	1
V\$AP2GAMMA_01	207	-0.219834	-0.94248325	0.60686016	0.84170127	1
TTCNRGNNTTC_V\$HSF_Q6	125	-0.235121	-0.9412346	0.57954544	0.8434613	1
V\$HSF1_01	218	-0.219177	-0.94020647	0.6051613	0.8443664	1
V\$HEB_Q6	222	-0.217064	-0.9368511	0.6475943	0.8532238	1
V\$CEBP_Q3	205	-0.218008	-0.9355038	0.61738	0.8550053	1
V\$CACBINDINGPROTEIN_Q6	198	-0.220421	-0.9339569	0.63502675	0.8577542	1
V\$ERR1_Q2	221	-0.217469	-0.93273294	0.6231691	0.8593525	1
V\$TAL1ALPHA47_01	211	-0.215777	-0.9271164	0.64257556	0.87540174	1
V\$PAX2_02	214	-0.216499	-0.92594653	0.6323155	0.87672013	1
V\$GFI1_01	223	-0.212974	-0.92592627	0.65929776	0.8741645	1
V\$ATF1_Q6	191	-0.21643	-0.9235589	0.6586667	0.8792025	1
V\$TAXCREB_01	119	-0.227989	-0.922692	0.6396011	0.87939197	1
V\$AML1_01	207	-0.215321	-0.92197055	0.64470285	0.8791895	1
V\$EGR2_01	165	-0.220371	-0.920079	0.6586667	0.88274074	1
V\$GR_Q6	221	-0.215366	-0.9183374	0.6864516	0.88584286	1
YGCANTGCR_UNKNOWN	107	-0.234532	-0.9174677	0.60926193	0.8860671	1
V\$HSF2_01	202	-0.212543	-0.91740113	0.67824966	0.88364136	1
V\$EFC_Q6	225	-0.212075	-0.915461	0.66753244	0.88738066	1
V\$FOXO4_02	214	-0.211853	-0.9148324	0.6626984	0.8868118	1
V\$AML1_Q6	207	-0.215321	-0.91386694	0.6515354	0.8873734	1
V\$MIF1_01	140	-0.221585	-0.91220284	0.6510989	0.890085	1
V\$TCF11MAFG_01	174	-0.21923	-0.9115531	0.66050196	0.8894926	1
V\$STAT4_01	218	-0.210311	-0.9104576	0.6939314	0.8905731	1
V\$CEBP_Q2	191	-0.214084	-0.90930146	0.68929505	0.89147466	1
V\$HNF3ALPHA_Q6	183	-0.214834	-0.9072031	0.696011	0.89529777	1
CCAATNNSNNGCG_UNKNOWN	52	-0.260893	-0.90635145	0.62362206	0.8953056	1
V\$FAC1_01	179	-0.216061	-0.9048754	0.6975477	0.89739615	1
TAAYNRNNTCC_UNKNOWN	146	-0.21927	-0.901167	0.6924138	0.9066092	1
V\$FOX_Q2	185	-0.212608	-0.90052694	0.69529086	0.9062085	1
YNGTTNNATT_UNKNOWN	292	-0.20184	-0.89942414	0.7533742	0.90694183	1
V\$FREAC3_01	207	-0.210714	-0.89928406	0.7435567	0.9047491	1
V\$PTF1BETA_Q6	195	-0.211319	-0.89624643	0.73230374	0.91152006	1
CAAWNWWNNNGGC_UNKNOWN	66	-0.242798	-0.8935208	0.6559633	0.9169907	1
V\$PBX1_02	114	-0.220316	-0.8857467	0.70679885	0.937512	1
V\$HNF3B_01	185	-0.207744	-0.88282263	0.73761714	0.94325763	1
V\$IPF1_Q4	211	-0.204759	-0.87761354	0.77326345	0.9555579	1
CCNNNNNNAAGWT_UNKNOWN	83	-0.231429	-0.87614214	0.69473684	0.957084	1
TTANWNANTGGM_UNKNOWN	48	-0.253063	-0.8761215	0.6807818	0.95447004	1
V\$E47_01	211	-0.203156	-0.8680921	0.791612	0.9744583	1
RYTGCNRRGNAAC_V\$MIF1_01	67	-0.239045	-0.86684453	0.71610844	0.97519016	1
V\$EV11_06	21	-0.301442	-0.85762835	0.6502636	0.9977648	1
V\$RP58_01	186	-0.20338	-0.8570627	0.79591835	0.99649286	1
V\$NFY_C	207	-0.200848	-0.8557819	0.8214748	0.99722594	1
V\$STAT_Q6	209	-0.198919	-0.8535738	0.8069948	1	1
V\$GATA1_01	203	-0.199808	-0.85194814	0.82626	1	1
CTAWWWATA_V\$RSRFC4_Q2	301	-0.191885	-0.8511773	0.8569652	1	1
V\$NF1_Q6_01	229	-0.195311	-0.8467041	0.83825415	1	1
V\$STAT5A_03	217	-0.196547	-0.8458868	0.87614083	1	1
V\$NF1_Q6	234	-0.195919	-0.8453984	0.8470437	1	1
SNACANNYSYAGA_UNKNOWN	63	-0.231503	-0.8430189	0.72981364	1	1
MYAATNNNNNNGGC_UNKNOWN	103	-0.214518	-0.8413597	0.7877493	1	1
RYTGCNWTGGR_UNKNOWN	93	-0.21812	-0.84058857	0.76217765	1	1
V\$PBX1_01	210	-0.196729	-0.8404123	0.86092716	1	1
V\$TITF1_Q3	198	-0.195038	-0.8308733	0.8733509	1	1
TTAYRTAA_V\$E4BP4_01	212	-0.19412	-0.8308214	0.88676673	1	1
V\$AP3_Q6	215	-0.192048	-0.83001465	0.8651102	1	1
V\$EGR3_01	65	-0.228159	-0.8292527	0.7841945	1	1
V\$ALPHACP1_01	213	-0.193743	-0.82872534	0.8635135	1	1
V\$CDPCR3HD_01	202	-0.194973	-0.82842517	0.87435234	1	1
V\$ATF3_Q6	207	-0.19297	-0.82820344	0.89320385	1	1
V\$GATA4_Q3	200	-0.193647	-0.82743406	0.87024903	1	1
AAGWWRNYYGC_UNKNOWN	96	-0.216509	-0.82469255	0.7971223	1	1
V\$GATA1_05	231	-0.190597	-0.8243985	0.87533873	1	1
V\$HFH1_01	205	-0.192582	-0.8205376	0.88962764	1	1

RTTTNNNYTGGM_UNKNOWN	134	-0.204276	-0.8190535	0.8468085	1	1
V\$NFAT_Q6	198	-0.19295	-0.81856275	0.875	1	1
V\$ARP1_01	136	-0.201168	-0.81750524	0.8505435	1	1
V\$IK2_01	231	-0.18923	-0.81679595	0.90318304	1	1
V\$FREAC2_01	219	-0.190102	-0.81357217	0.9160207	1	1
V\$HFH3_01	167	-0.194889	-0.8105678	0.87516963	1	1
CATRRAGC_UNKNOWN	112	-0.203602	-0.8101748	0.86206895	1	1
V\$IRF1_Q6	221	-0.188359	-0.8076488	0.9080311	1	1
V\$MEIS1_01	193	-0.189989	-0.80628544	0.89544237	1	1
V\$HMG1Y_Q6	200	-0.189197	-0.8040099	0.9070385	1	1
GTTGNYNRGNAC_UNKNOWN	81	-0.212934	-0.80033016	0.85542166	1	1
V\$FOXO1_02	195	-0.187048	-0.80019647	0.9224599	1	1
V\$STAT5A_02	115	-0.20121	-0.79927707	0.87535816	1	1
V\$CIZ_01	202	-0.185228	-0.79778075	0.911958	1	1
V\$LYF1_01	223	-0.185133	-0.7976053	0.9276486	1	1
V\$POU6F1_01	202	-0.186233	-0.7968297	0.9351852	1	1
V\$RFX1_02	210	-0.185581	-0.7956163	0.9247312	1	1
V\$RREB1_01	175	-0.189708	-0.79251504	0.89136124	1	1
V\$TCF4_Q5	203	-0.185361	-0.79216343	0.92755497	1	1
V\$TAXCREB_02	22	-0.270045	-0.7884072	0.7641997	1	1
CCANNAGRKGCC_UNKNOWN	92	-0.20566	-0.78679043	0.8619677	1	1
V\$RORA1_01	212	-0.181767	-0.7806284	0.9401042	1	1
GGCNRNWCTTYS_UNKNOWN	64	-0.21691	-0.7799267	0.83753943	1	1
V\$SREBP1_02	75	-0.208007	-0.77747375	0.86158633	1	1
V\$IK1_01	224	-0.179157	-0.77448916	0.95454544	1	1
WGGAATGY_V\$TEF1_Q6	307	-0.173595	-0.7742006	0.9576923	1	1
V\$FOXJ2_02	193	-0.181948	-0.771059	0.94926566	1	1
V\$CDPCR1_01	110	-0.196415	-0.7697858	0.92395985	1	1
AGCYRWTTT_UNKNOWN	97	-0.197475	-0.7696274	0.8949704	1	1
V\$PAX5_01	131	-0.190582	-0.76940274	0.9132948	1	1
V\$TCF11_01	197	-0.17906	-0.7653505	0.9546061	1	1
SMTTTTGT_UNKNOWN	347	-0.169221	-0.76139516	0.98650306	1	1
V\$DBP_Q6	215	-0.177197	-0.76000816	0.97680414	1	1
V\$AREB6_01	224	-0.176837	-0.75606203	0.96945554	1	1
V\$NFKAPPAB_01	218	-0.176567	-0.75475913	0.96732026	1	1
V\$TATA_C	249	-0.171903	-0.7526485	0.9782609	1	1
V\$NKG25_02	218	-0.174753	-0.75038946	0.9754839	1	1
V\$AR_Q6	199	-0.172707	-0.7411241	0.98271275	1	1
YKACATTT_UNKNOWN	233	-0.170954	-0.7408624	0.9896104	1	1
V\$WHN_B	205	-0.173806	-0.7385888	0.98300654	1	1
V\$CDC5_01	225	-0.171665	-0.73800147	0.9817471	1	1
YATTNATC_UNKNOWN	315	-0.163767	-0.72273165	0.9951279	1	1
GGATTA_V\$PITX2_Q2	484	-0.156763	-0.7213298	1	1	1
V\$NFKAPPAB65_01	204	-0.167936	-0.72117937	0.9852547	1	1
V\$LXR_Q3	64	-0.201095	-0.7205029	0.92762184	1	1
V\$AREB6_02	210	-0.165724	-0.71457595	0.98793566	1	1
AAAYWAACM_V\$HFH4_01	221	-0.164219	-0.7053992	0.993395	1	1
V\$HFH4_01	177	-0.166016	-0.70512444	0.98650473	1	1
V\$AP1_Q2_01	237	-0.160114	-0.6975155	0.996119	1	1
YCATTAA_UNKNOWN	475	-0.15056	-0.6967488	1	1	1
V\$PAX4_Q4	176	-0.166152	-0.6945996	0.9896373	1	1
V\$PPARA_01	31	-0.223079	-0.6922302	0.90802675	1	1
V\$RSRFC4_Q2	190	-0.161135	-0.68727356	0.9903448	1	1
V\$GNCF_01	63	-0.191507	-0.6855531	0.95510834	1	1
V\$GATA2_01	93	-0.179924	-0.6833342	0.9776786	1	1
V\$GATA3_01	202	-0.159998	-0.6825113	1	1	1
V\$AP4_Q6_01	222	-0.157946	-0.6824374	0.99866843	1	1
V\$FOXO3_01	170	-0.159078	-0.67345446	0.99863386	1	1
RNTCANNRRNNYNATTW_UNKNOWN	55	-0.188924	-0.67084193	0.9676898	1	1
V\$RSRFC4_01	215	-0.155671	-0.6707979	0.9986807	1	1
V\$TAL1BETAE47_01	210	-0.154335	-0.6649052	0.99866664	1	1
V\$FOXJ2_01	161	-0.158919	-0.6613959	0.99728996	1	1
V\$CEBPDELTA_Q6	199	-0.155148	-0.65816283	0.99866134	1	1
V\$AP4_Q5	224	-0.152364	-0.6577048	1	1	1
V\$HNF3_Q6	164	-0.155125	-0.65333986	0.9958506	1	1

V\$ZIC3_01	217	-0.147387	-0.6324055	1	1	1
V\$RORA2_01	132	-0.155911	-0.6316755	0.99857146	1	1
V\$FREAC4_01	122	-0.15585	-0.625391	0.99559474	1	1
CTGRYYYYNATT_UNKNOWN	55	-0.175999	-0.60784626	0.9823718	0.9996495	1
ACAWYAAAG_UNKNOWN	88	-0.150415	-0.5805317	0.99854016	0.9985612	1

Supplementary Table 2. Global transcription factor gene set analysis.

Results from GSEA analysis of all available transcription factor-target (TFT) gene sets in the Molecular Signatures Database applied to the SAHM1 expression profile in KOPT-K1 and HPB-ALL cells. From left to right, columns contain the gene set name from the MSigDB, the number of genes in the gene set, the overall enrichment score (ES), the normalized enrichment score (NES), the nominal p-value (NOM p-val), the false discovery rate q-value (FDR q-val), and the family-wise error rate p-value (FWER p-val). In general, gene sets with high positive or negative NES, low FDR q-value and low FWER p-value are considered to be significantly enriched. Gene sets have been ranked by the most stringent filter of FWER p-value. By any statistical measure, however, the GSI-NOTCH gene set is the most highly correlated with the SAHM1 expression profile.