Supplementary Figure legends

Supplementary Fig. 1: Expression of putative CTA in HL cells (HG_U133A analysis). Putative HL-associated CTA were identified by using MAFilter software (http://steingrube-home.de/software_MAFilter.html) as described in the text. The following GEO data sets have been used: GSE26325, GSE2361. Presented is a cluster analysis with the identified probe sets (log2 transformed and median centered signal intensities, absolute Manhattan distance, complete linkage clustering). Cluster analysis was performed with Genesis.

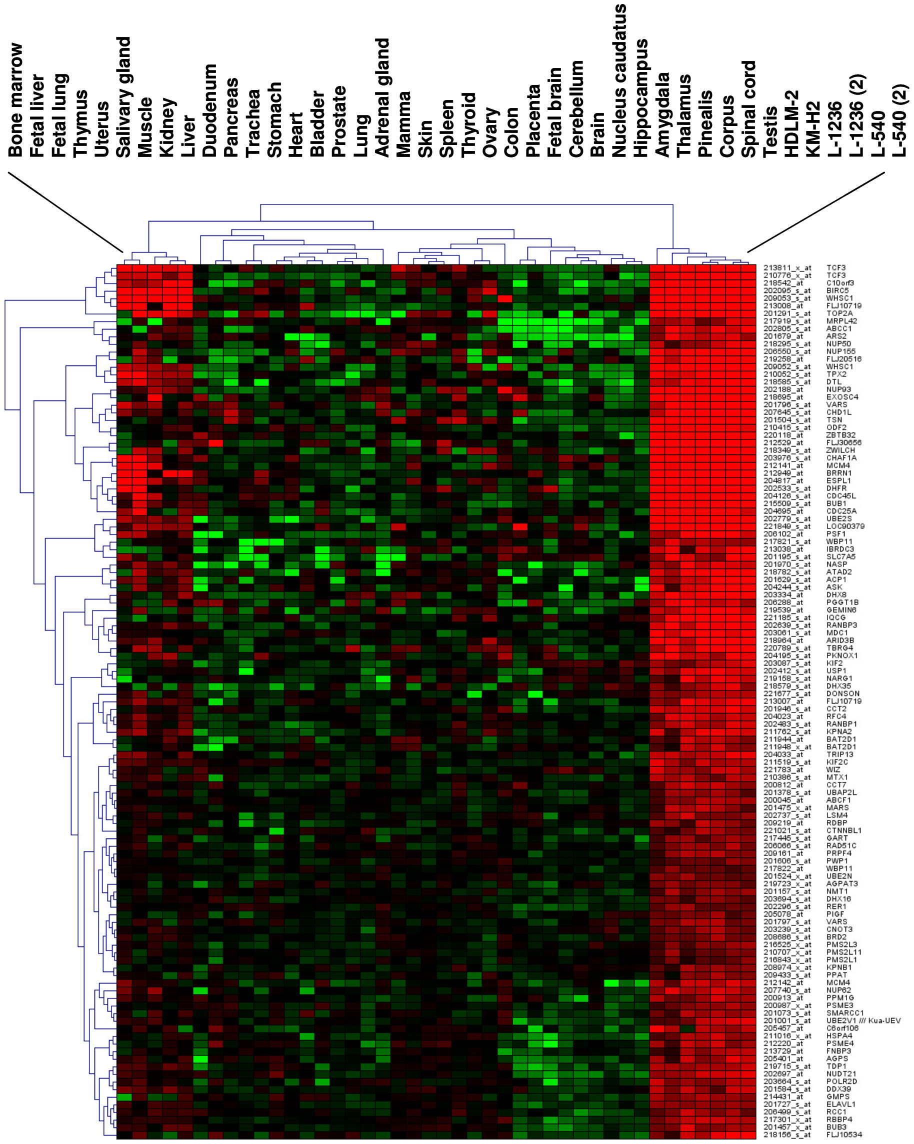
Supplementary Fig. 2: Expression of ZBTB32 in HL cells. Quantitative RT-PCR was used for quantification of ZBTB32 transcripts in HL cell lines and other samples. PBMC were separated into the indicated cell lineages. No signal was obtained for SK-N-MC cells after 40 cycles of PCR. For the calculation of relative expression values, ACTB was used as housekeeping control and expression in testis (not shown) was set as 1.

Supplementary Fig. 3: Expression of PRAME in HL cells. Quantitative RT-PCR was used for quantification of PRAME transcripts in HL cells. L-540 cells were cultured for the indicated time in the presence or in the absence of 5µM 5'-azacytidine. For calculation of relative expression values, glyceraldehyde-3-phosphate dehydrogenase was used as housekeeping control and expression in untreated L-540 cells on day zero was set as 1. Presented are means and standard deviation from three independent experiments. Asterisk indicate statistical significance ($p<0.05$).

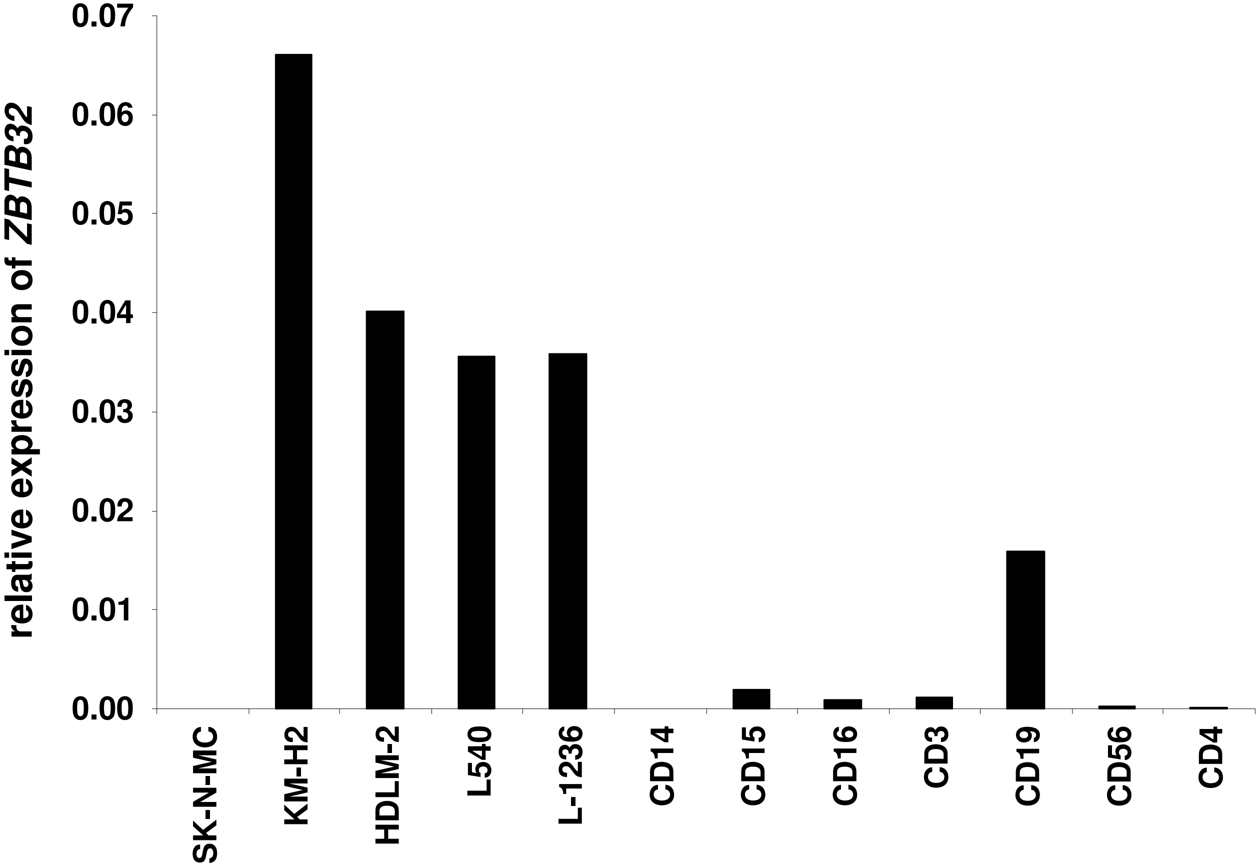
Supplementary Fig. 4: Sequence of PRAME protein from HL cell lines. Presented are amino acid sequences of PRAME from HL cell lines. The position of known HLA-A2 binding peptides from PRAME is indicated by solid black lines. The position of a known HLA-B62 binding peptide is indicated by a solid blue line. The position of a known HLA-A24 binding peptide from PRAME is indicated by a dashed line. The X at position 47 of HDLM-2 denotes heterozygosity (L/M; single nucleotide polymorphism rs41310248). Data visualization was performed with GeneDoc http://www.psc.edu/biomed/genedoc).

Supplementary Fig. 5: Characterization of T cells after DC stimulation *in vitro*. PBMC ($5x10^6$) were primed with DC ($1x10^6$) that had been transfected with total RNA from cell line HDLM-2. Cells were analyzed by flow cytometry using antibodies with specificity for the indicated surface molecules.

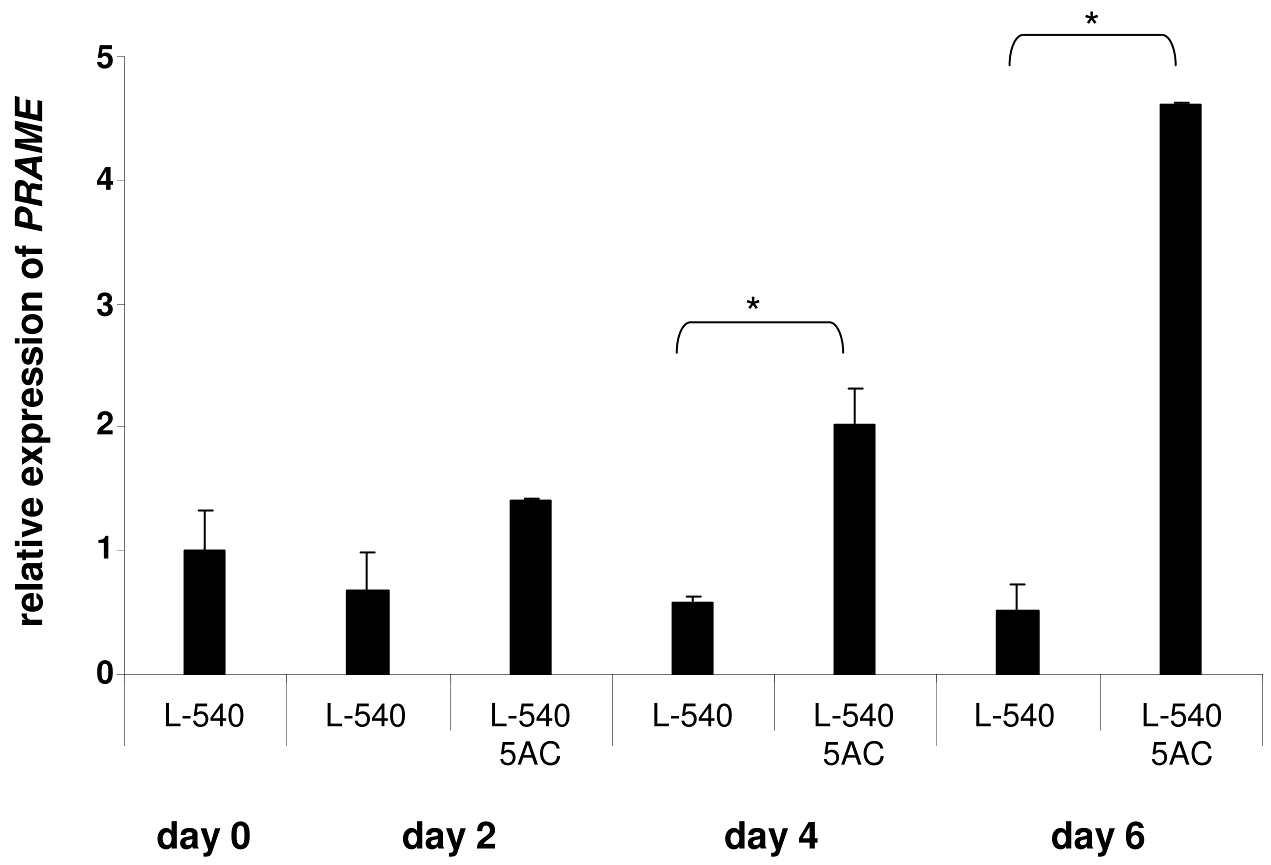
Supplementary Fig. 6: Specificity of PRAME stimulated PBMC. HLA-A2-positive PBMC were primed with T2 cells that had been pulsed with 100µg/ml of PRAME-derived peptide SLY or LIPI-derived peptide SLS, respectively. Both peptides have similar HLA-A2 stabilization activity (n-fold increase in HLA-A2 mean fluorescence intensity of T2 cells pulsed with PRAME peptide: 1.428; LIPI peptide: 1.433). Reactivity of stimulated cells with peptide-pulsed T2 cells was assessed by lactate dehydrogenase assay. For this end, target cells had been pulsed with PRAME derived peptides or peptides derived from the irrelevant antigen LIPI. Presented are means from three experiments after background subtraction. ** denotes statistical significance ($p<0.005$).



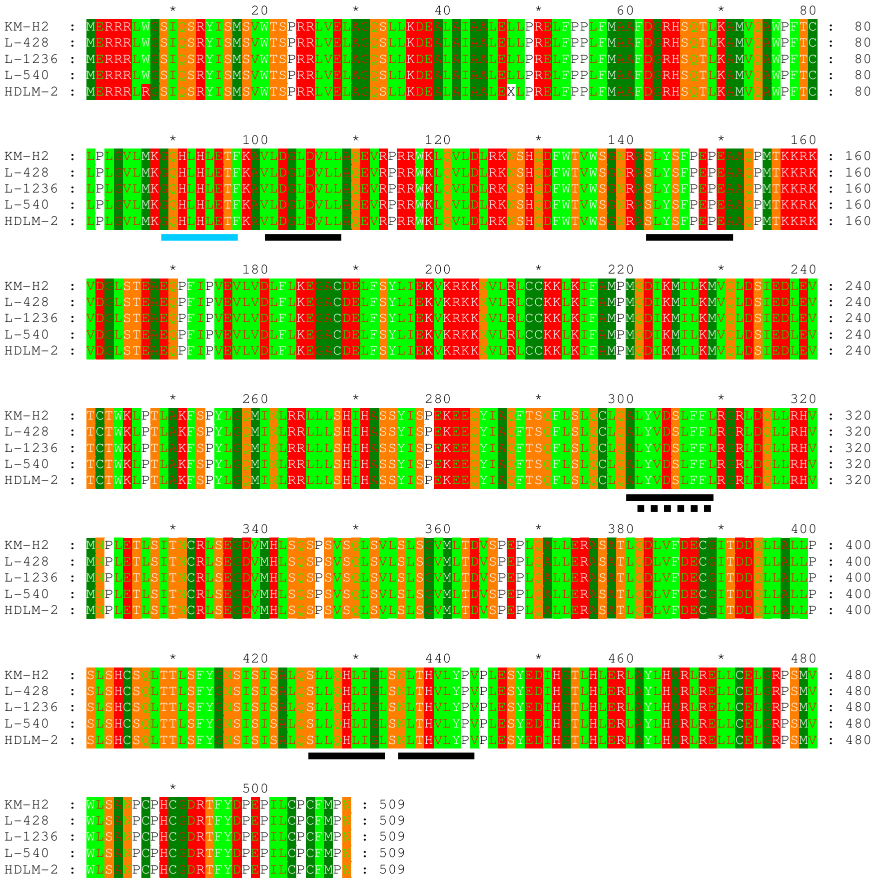
Supplementary Figure 1



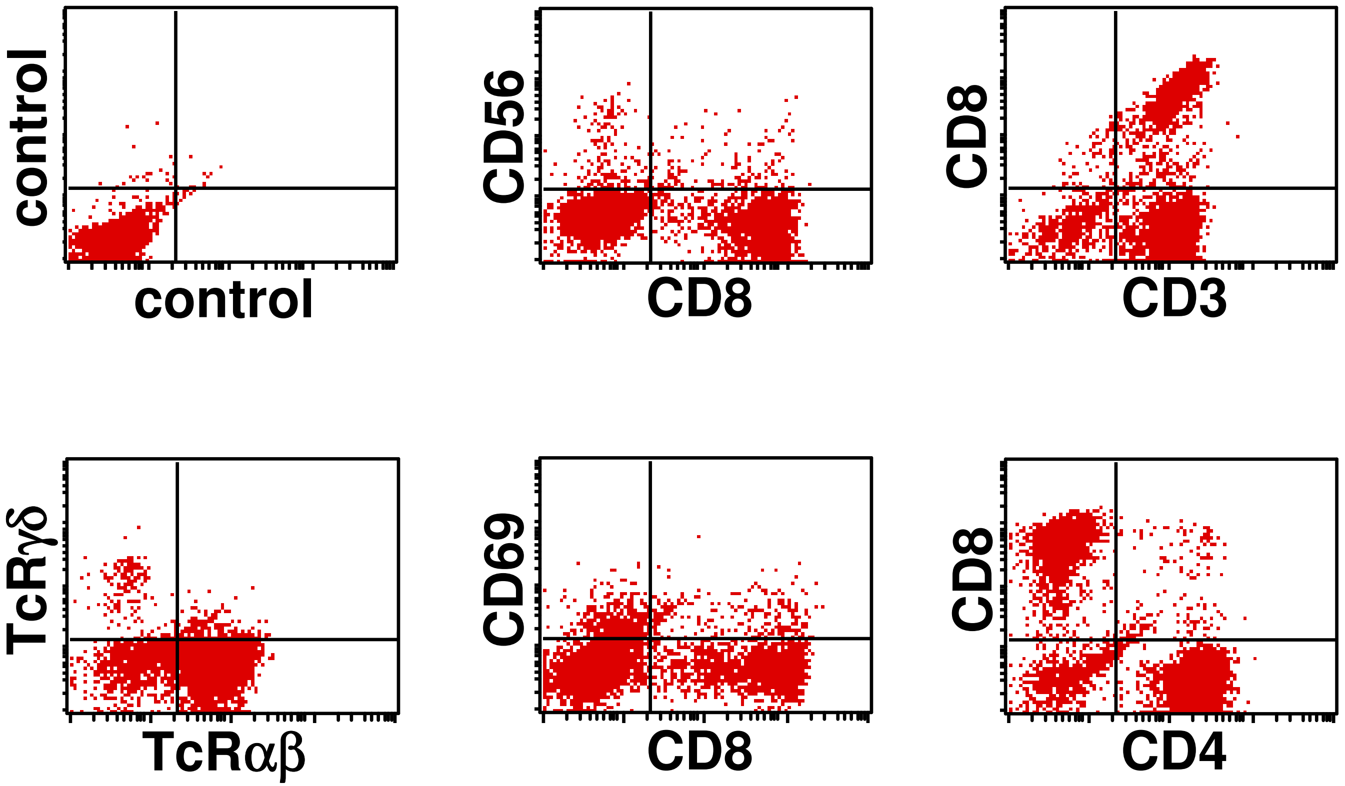
Supplementary Figure 2



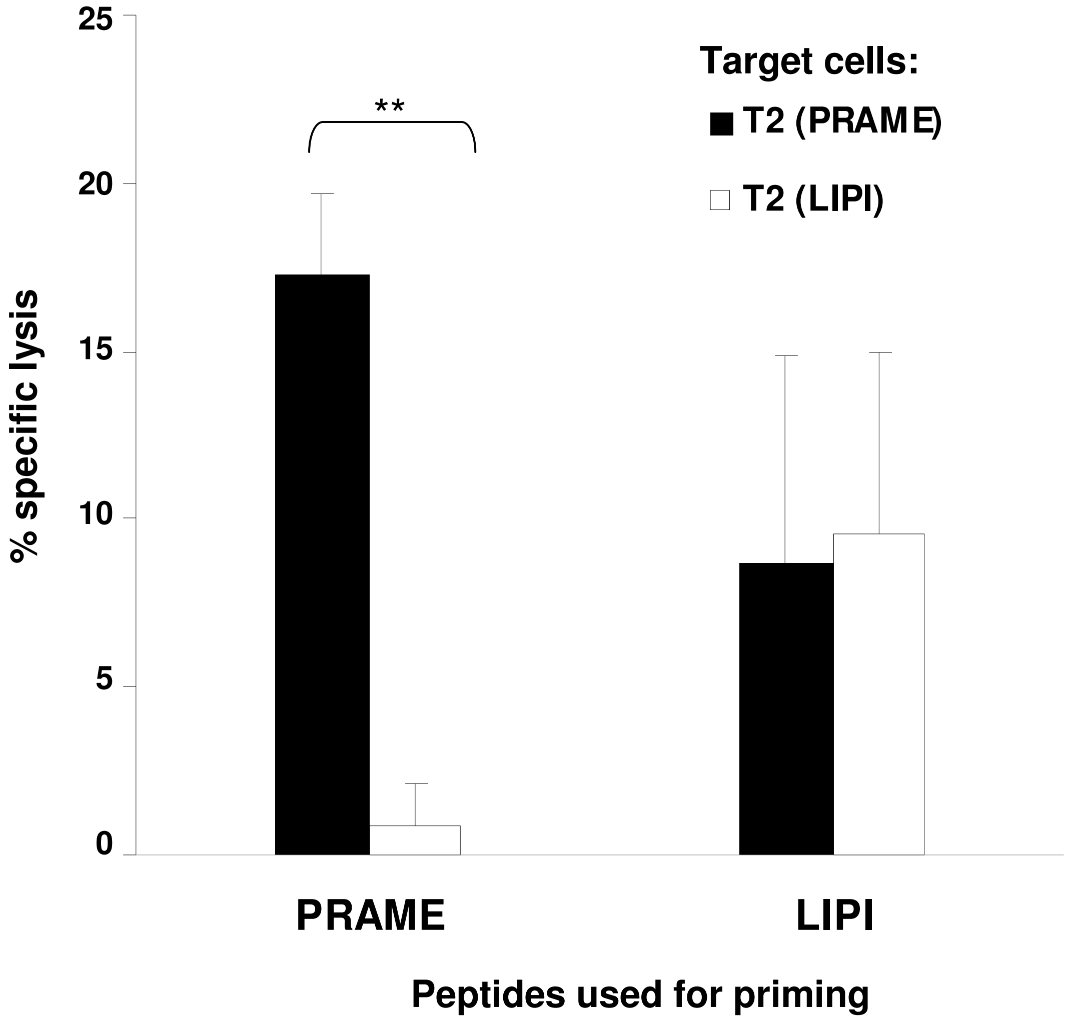
Supplementary Figure 3



Supplementary Figure 4



Supplementary Figure 5



Supplementary Figure 6

Supplementary Table 1. Detection of HL-reactivity in primed PBMC by interferon-gamma-ELISPOT. DC were transfected with total RNA (50µg/mL) or mRNA (10µg/mL; isolated with µMACS mRNA isolation kit, Miltenyi, Bergisch-Gladbach, Germany; donor 6) from HL cell lines and used as antigen presenting cells for PBMC from the same donors. On day 7, primed PBMC were re-stimulated with RNA transfected DC. Six days after re-stimulation, the reactivity of stimulated cells against indicated cell lines was assessed by interferon gamma ELISPOT. Different sarcoma cells, autologous PBMC (autol. PBMC) or allogeneic PBMC (allo. PBMC) served as controls. Presented are mean spot numbers per well from triplicates or quadruplicates (donor 6) from 9 independent experiments. -: not done. If not otherwise stated, 5x10^4 responder PBMC were used.

		Stimulatory cells used in ELISPOT assay										
Donor number	**Transfected RNA**	**HDLM-2**	**KM-H2**	**L-1236**	**L-428**	**L-540**	**L-540+5AC**	**autol. PBMC**	**allo. PBMC**	**SK-N-MC**	**A673**	**TE-671**
1(Exp.1)	HDLM-2 (1x10^5 PBMC)	190	-	-	-	-	-	60	0	-	-	45
1(Exp.1)	HDLM-2	249	-	-	-	-	-	0	10	-	-	6
1(Exp.2)	HDLM-2 (1x10^5 PBMC)	208	130	14	-	0	-	17	-	-	-	16
1(Exp.2)	HDLM-2	42	37	0	-	0	-	0	-	-	-	0
2(Exp.3)	HDLM-2	40	9	166	-	19	-	-	-	-	-	-
2(Exp.3)	KM-H2	0	43	130	-	67	-	-	-	-	-	-
2(Exp.3)	L-1236	3	11	127	-	49	-	-	-	-	-	-
2(Exp.3)	L-540	0	44	162	-	14	-	-	-	-	-	-
3(Exp.4)	HDLM-2	9	80	142	-	0	-	-	-	0	0	-
3(Exp.4)	KM-H2	33	16	111	-	12	-	-	-	73	0	-
3(Exp.4)	L-1236	32	0	173	-	19	-	-	-	38	0	-
3(Exp.4)	L-540	18	0	103	-	9	-	-	-	55	0	-
4(Exp.5)	HDLM-2	33	19	65	-	0	-	-	-	-	-	-
4(Exp.5)	KM-H2	34	35	82	-	0	-	-	-	-	-	-
4(Exp.5)	L-1236	26	28	70	-	0	-	-	-	-	-	-
4(Exp.5)	L-540	19	20	55	-	0	-	-	-	-	-	-
5(Exp.6)	L-1236	70	87	104	-	14	-	-	-	124	90	-
6(Exp.7)	L-1236 (2.5x10^4 PBMC)	24	10	106	-	13	-	-	-	-	-	-
7(Exp.8)	HDLM-2	61	83	22	82	439	185	0	-	1	3	25
8(Exp.9)	HDLM-2	41	58	6	-	131	61	0	-	1	1	0

Supplementary Table 2. Putative HL-associated CTA (HG_U133A data base). Putative HL-associated CTA were identiefied in Affymetrix HG_U133A microarray data sets by using MAFilter (http://steingrube-home.de/software_MAFilter.html) as decribed in the text. Presented are probe set IDs of putative CTA, corresponding gene symbols, signal intensities in testis, HL cell lines and normal tissues (NBA) and the quotients of the variances in the merged groups and the variance in normal tissues (see the main text of the manuscript for details).

Probe Set ID	Gene Symbol	Signal intensity testis	Mean signal intensity HL lines	Mean signal intensity NBA	variance (NBA+testis) / variance (NBA)	variance (NBA+HL) / variance (NBA)
200045_at	ABCF1	2267	4920.3	1222.3	1.6	36.5
200812_at	CCT7	2646	6059.0	1390.6	1.1	10.9
200913_at	PPM1G	2032	1688.5	438.1	3.1	8.4
200987_x_at	PSME3	1184	2324.0	675.7	1.1	9.5
201001_s_at	UBE2V1 /// Ku	828	2061.5	418.8	1.1	17.8
201073_s_at	SMARCC1	851	1209.2	344.7	1.4	7.1
201157_s_at	NMT1	1329	2451.2	695.5	1.4	16.9
201195_s_at	SLC7A5	2032	4434.3	655.8	1.2	10.9
201291_s_at	TOP2A	760	1884.3	52.4	3.4	98.6
201378_s_at	UBAP2L	999	1822.7	540.0	1.2	8.5
201457_x_at	BUB3	2874	4425.2	1146.7	1.3	8.3
201475_x_at	MARS	2385	6101.3	1498.7	1.2	29.4
201504_s_at	TSN	736	988.5	73.0	3.7	29.6
201524_x_at	UBE2N	5287	4447.8	1653.2	3.5	8.9
201584_s_at	DDX39	4366	3640.0	982.2	2.6	7.0
201606_s_at	PWP1	1223	2065.8	775.3	1.1	8.5
201629_s_at	ACP1	1058	1723.3	250.3	1.6	11.9
201679_at	ARS2	249	474.8	70.7	1.3	8.4
201727_s_at	ELAVL1	1586	1559.8	450.1	2.4	7.3
201796_s_at	VARS	322	714.5	97.6	1.2	8.3
201797_s_at	VARS	847	1048.8	304.8	2.0	11.2
201946_s_at	CCT2	4226	4299.8	717.2	4.9	20.8
201970_s_at	NASP	1340	1892.5	315.8	1.4	6.3
202095_s_at	BIRC5	736	1352.8	126.5	1.2	5.6
202188_at	NUP93	678	1372.5	111.4	1.7	17.5
202296_s_at	RER1	3451	4496.7	1608.4	1.4	6.1

202412_s_at	USP1	809	1101.0	166.0	3.2	24.4
202483_s_at	RANBP1	2768	4815.2	979.3	1.4	10.2
202533_s_at	DHFR	161	478.8	29.6	1.2	17.0
202639_s_at	RANBP3	370	470.8	63.9	5.2	37.1
202697_at	NUDT21	1615	2603.3	458.5	1.7	14.0
202737_s_at	LSM4	1755	3301.3	927.9	1.2	9.8
202779_s_at	UBE2S	3726	10603.0	466.5	3.0	95.7
202805_s_at	ABCC1	611	1380.5	172.9	1.3	14.5
203061_s_at	MDC1	600	332.8	34.7	91.4	133.6
203087_s_at	KIF2	2172	2441.7	595.6	1.8	7.6
203239_s_at	CNOT3	458	710.3	231.7	1.3	9.1
203334_at	DHX8	221	469.8	44.2	1.8	25.0
203664_s_at	POLR2D	1764	1131.7	297.2	5.1	7.5
203694_s_at	DHX16	1518	1474.2	551.2	2.3	7.1
203976_s_at	CHAF1A	145	427.7	22.7	1.2	13.6
204023_at	RFC4	995	2318.5	437.3	1.2	12.1
204033_at	TRIP13	1504	1663.2	325.7	2.2	8.8
204126_s_at	CDC45L	242	883.7	36.2	1.6	52.3
204195_s_at	PKNOX1	423	136.3	23.8	16.1	7.6
204244_s_at	ASK	3246	908.5	117.7	46.2	18.3
204695_at	CDC25A	383	629.7	44.5	1.3	6.5
204817_at	ESPL1	1029	1542.0	193.9	1.3	5.9
205078_at	PIGF	1077	1216.0	437.0	1.7	7.0
205401_at	AGPS	1439	1531.0	337.6	2.5	12.3
205457_at	C6orf106	1403	646.8	170.8	7.8	7.1
206066_s_at	RAD51C	534	933.5	275.5	1.2	8.6
206102_at	PSF1	668	1428.0	176.5	1.2	10.9
206288_at	PGGT1B	83	132.5	24.4	1.3	6.4
206499_s_at	RCC1	676	1146.7	339.5	1.2	7.9
206550_s_at	NUP155	1827	777.0	72.0	21.5	17.5
207645_s_at	CHD1L	115	317.5	31.3	1.3	20.2
207740_s_at	NUP62	586	969.7	195.5	1.3	8.0
208686_s_at	BRD2	1433	1972.5	702.9	1.4	7.1
208974_x_at	KPNB1	3010	4314.0	1356.8	1.6	11.7
209052_s_at	WHSC1	600	1070.2	96.8	1.7	13.2
209053_s_at	WHSC1	1187	1658.5	116.8	1.6	7.6

209161_at	PRPF4	703	1713.5	457.9	1.2	25.5
209219_at	RDBP	2391	2125.2	598.6	3.7	12.4
209433_s_at	PPAT	589	908.8	306.1	1.2	7.7
210052_s_at	TPX2	1746	3182.5	342.3	1.2	5.7
210386_s_at	MTX1	2779	2211.2	563.0	3.5	8.2
210415_s_at	ODF2	6484	161.8	15.3	23129.8	66.3
210707_x_at	PMS2L11	1158	1620.7	604.3	1.5	11.2
210776_x_at	TCF3	971	3047.2	243.6	1.1	14.3
211016_x_at	HSPA4	627	1363.5	297.5	1.2	11.4
211519_s_at	KIF2C	2025	1230.2	315.2	6.6	9.0
211762_s_at	KPNA2	5980	5357.8	1079.5	2.3	6.5
211944_at	BAT2D1	418	744.5	193.3	1.1	6.8
211948_x_at	BAT2D1	800	1618.3	403.1	1.1	11.1
212141_at	MCM4	827	1431.8	94.3	2.0	19.7
212142_at	MCM4	696	763.0	151.3	2.2	9.2
212220_at	PSME4	593	593.3	146.0	2.1	7.4
212529_at	FLJ30656	510	823.2	44.5	3.4	35.0
212949_at	BRRN1	970	1052.0	89.4	2.4	9.7
213007_at	FLJ10719	609	1222.7	194.5	1.3	11.8
213008_at	FLJ10719	492	1157.7	51.0	1.7	26.1
213038_at	IBRDC3	1837	1997.8	322.9	2.3	10.2
213729_at	FNBP3	1373	3114.2	752.2	1.2	16.8
213811_x_at	TCF3	1497	3617.3	309.1	1.2	10.7
214431_at	GMPS	1729	1426.2	393.1	2.9	6.4
215509_s_at	BUB1	398	639.3	33.1	5.3	70.4
216525_x_at	PMS2L3	1122	2068.0	647.0	1.2	9.9
216843_x_at	PMS2L1	1506	2160.8	910.9	1.2	6.3
217301_x_at	RBBP4	2712	5092.3	1059.6	1.5	15.0
217445_s_at	GART	126	236.0	68.1	1.1	7.5
217821_s_at	WBP11	1228	1738.7	363.2	1.7	10.7
217822_at	WBP11	1597	1949.2	804.2	1.7	9.3
217919_s_at	MRPL42	1953	2490.8	452.7	1.6	7.0
218156_s_at	FLJ10534	577	1289.7	200.3	1.4	23.4
218295_s_at	NUP50	645	598.7	119.6	2.0	6.2
218349_s_at	ZWILCH	1386	596.5	34.3	51.5	45.7
218542_at	C10orf3	1040	2147.3	68.2	3.3	59.3

218579_s_at	DHX35	173	228.5	48.7	1.5	7.3
218585_s_at	DTL	568	1090.5	137.6	1.2	7.2
218695_at	EXOSC4	917	1008.0	105.7	2.2	8.3
218782_s_at	ATAD2	748	1013.5	123.0	2.1	12.6
218964_at	ARID3B	534	898.3	73.8	3.5	44.7
219158_s_at	NARG1	304	815.7	143.7	1.1	18.9
219258_at	FLJ20516	493	463.5	50.1	4.0	14.5
219539_at	GEMIN6	728	1078.7	139.6	2.2	16.6
219715_s_at	TDP1	1615	1532.7	350.1	2.4	6.6
219723_x_at	AGPAT3	600	698.7	228.1	1.6	6.2
220118_at	ZBTB32	891	541.0	22.9	138.1	272.4
220789_s_at	TBRG4	428	969.3	143.7	1.2	9.2
221021_s_at	CTNNBL1	555	847.5	265.2	1.2	7.4
221185_s_at	IQCG	922	3768.2	258.0	1.7	107.0
221677_s_at	DONSON	704	837.8	205.9	1.7	6.7
221783_at	WIZ	641	432.0	107.7	5.4	9.4
221849_s_at	LOC90379	410	448.2	59.7	1.8	6.1

Supplementary Table 3. Putative HL-associated CTA (HG_U133Plus2.0 data base). Putative HL-associated CTA were identiefied in Affymetrix HG_U133Plus2.0 microarray data sets by using MAFilter (http://steingrube-home.de/software_MAFilter.html) as decribed in the text. Presented are probe set IDs of putative CTA, corresponding gene symbols, signal intensities (SI) in testis, micro-dissected HL cells (cHL), HL cell lines and normal tissues (NBA) and the quotients of the variances (var) in the merged groups and the variance in normal tissues (see the main text of the manuscript for details).

Probe Set ID	Gene symbol	Mean SI testis	Mean SI NBA	Mean SI cHL	Mean SI HL lines	var (NBA+HL lines) / var (NBA)	var (NBA+cHL) / var (NBA)	var (NBA+testis) / var (NBA)
1553167_a_at	SLA/LP	312.5	114.0	439.4	542.5	3.1	3.5	1.1
1553709_a_at	PRPF38A	1597.6	775.9	1642.1	2488.8	3.3	1.7	1.2
1553887_at	FLJ40235	1601.1	118.1	386.9	1324.7	52.9	4.0	13.2
1555772_a_at	CDC25A	459.4	87.4	285.7	884.3	10.0	1.9	1.5
1555943_at	PGAM5	348.8	139.4	358.8	344.1	1.3	1.8	1.1
1556588_at	C15orf37	492.5	244.9	881.3	494.1	1.7	5.1	1.1
1556613_s_at	LOC203107	462.5	159.0	292.6	383.6	1.6	1.7	1.2
1559170_at	---	455.0	126.0	1080.1	477.4	2.7	13.3	1.3
1559668_s_at	---	235.3	68.7	330.2	159.1	1.5	5.5	1.2
1559946_s_at	RUVBL2	10722.1	2046.6	10905.7	10302.7	3.6	4.3	1.9
1560916_a_at	DPY19L1	1959.2	180.3	435.9	602.5	3.7	1.8	6.2
1567912_s_at	RP13-36C9.1 /// RP13-36C9.3 /// CT45-4 /// RP13-36C9.6 /// CT45-6 /// CT45-1 /// LOC653515	773.2	42.2	3065.6	13547.5	10657.9	1427.2	7.9
200055_at	TAF10	7820.1	2489.5	9606.3	7452.6	3.0	5.3	1.7
200085_s_at	TCEB2	13333.0	5201.8	22889.3	9536.4	1.5	9.4	1.4
200812_at	CCT7	4814.8	2123.0	8118.1	15598.4	16.2	4.2	1.2
200868_s_at	ZNF313	10445.9	846.1	1800.7	2227.9	4.3	2.8	26.9
200987_x_at	PSME3	1616.2	627.8	1424.5	2331.4	3.3	1.9	1.2
201077_s_at	NHP2L1	7051.9	2923.6	5365.7	10738.6	6.6	1.7	1.5
201459_at	RUVBL2	8050.9	944.3	4420.7	7002.3	5.7	2.5	3.1
201482_at	QSCN6	2981.6	919.1	2441.8	947.9	1.1	2.2	1.2
201521_s_at	NCBP2	815.9	366.2	1358.1	1427.9	3.9	3.0	1.1
201524_x_at	UBE2N	7459.1	2721.3	6470.8	10466.0	8.0	2.6	1.6

201597_at	COX7A2	28839.2	10406.8	50913.7	19291.8	1.5	13.6	1.7
201629_s_at	ACP1	1517.7	250.0	1273.1	5086.7	48.9	4.0	2.0
201937_s_at	DNPEP	1810.3	602.3	1262.8	1354.1	1.7	1.8	1.5
201947_s_at	CCT2	17224.0	4528.6	17140.4	20256.3	4.5	6.7	1.7
201999_s_at	DYNLT1	8358.8	3741.3	8978.6	7184.7	1.3	1.7	1.1
202296_s_at	RER1	4708.3	1904.5	4778.2	4394.3	1.9	2.1	1.3
202595_s_at	LEPROTL1	1849.2	748.9	1934.0	1888.1	1.9	2.1	1.2
202697_at	NUDT21	2910.3	544.6	2176.9	4835.2	11.5	2.6	1.9
202737_s_at	LSM4	3419.9	1735.1	6579.5	6780.2	7.5	9.7	1.2
202824_s_at	TCEB1	6918.3	2731.0	11079.3	11448.3	6.5	7.2	1.3
203114_at	SSSCA1	808.1	263.7	1023.7	946.7	2.6	3.1	1.3
203119_at	CCDC86	2398.6	844.5	1799.8	1770.9	2.0	2.1	1.8
203436_at	RPP30	1399.2	722.8	1400.7	4063.4	23.3	2.2	1.3
203538_at	CAMLG /// FLJ25222	5905.6	3206.1	6355.2	5176.7	1.3	1.9	1.1
203583_at	UNC50	2840.3	1726.5	2414.9	3615.1	2.0	1.7	1.1
204086_at	PRAME	2376.2	108.2	308.6	2630.7	85.8	2.7	17.4
204126_s_at	CDC45L	619.6	95.5	631.4	1746.5	6.4	1.8	1.2
204170_s_at	CKS2	8155.2	1032.8	8784.4	11872.0	3.8	2.4	1.4
204478_s_at	RABIF	1626.2	684.7	3415.9	1191.6	1.3	11.4	1.3
204571_x_at	PIN4	723.8	1635.0	2629.6	2877.9	2.4	1.8	1.1
204659_s_at	GFER	563.4	200.7	1342.3	491.6	1.2	5.0	1.1
204695_at	CDC25A	591.5	118.1	995.6	1106.4	2.5	2.1	1.1
204900_x_at	SAP30	2101.1	829.5	2134.1	4327.2	6.5	2.2	1.2
205077_s_at	PIGF	2312.8	1457.3	3481.2	4149.0	4.5	3.8	1.1
205224_at	SURF2	1296.0	124.1	838.3	494.4	1.8	3.0	2.5
205376_at	INPP4B	831.3	222.9	605.4	484.9	2.2	1.8	1.4
206218_at	MAGEB2	1806.1	164.6	383.2	4142.2	327.1	2.8	10.2
206348_s_at	PDK3	486.2	111.1	650.6	1369.3	10.3	3.9	1.2
206441_s_at	COMMD4	1956.0	604.2	1156.6	1870.3	3.6	1.8	1.8
206451_at	TBCCD1	1446.4	342.6	658.9	769.8	2.4	2.7	3.7
206506_s_at	SUPT3H	879.8	224.8	768.2	744.4	3.3	3.8	2.0
207534_at	MAGEB1	611.8	58.4	280.2	3291.0	522.1	5.9	3.3
207844_at	IL13	649.2	170.3	695.0	649.7	10.7	3.7	1.5
208424_s_at	CIAPIN1	1682.5	603.8	1737.3	2652.6	8.8	3.3	1.6
208805_at	PSMA6	14600.5	5364.3	13838.6	19362.6	3.5	2.1	1.3
208968_s_at	CIAPIN1	6332.3	1526.4	3972.8	4604.3	3.2	2.4	2.5

209219_at	RDBP	4971.9	1314.4	4784.3	6440.4	5.6	2.8	1.5
209273_s_at	HBLD2	2634.5	1079.0	3678.9	2804.1	2.7	5.9	1.4
209503_s_at	PSMC5	4790.8	2685.2	4500.9	5328.5	2.0	2.1	1.1
209715_at	CBX5	1583.4	656.9	2077.1	1443.1	1.5	2.6	1.2
209853_s_at	PSME3	1252.9	393.0	1099.5	1998.3	4.7	2.1	1.3
209965_s_at	RAD51L3	610.4	291.8	546.5	453.8	1.1	1.7	1.1
210386_s_at	MTX1	4331.6	1123.0	7628.0	4034.8	2.6	8.6	1.5
210437_at	MAGEA9 /// MAGEA9B	850.8	123.5	1139.0	2565.0	205.4	82.7	3.1
210652_s_at	C1orf34	953.4	282.5	1603.0	2906.3	16.4	5.8	1.2
211702_s_at	USP32	2834.6	464.1	1198.0	698.2	1.6	3.1	5.9
211982_x_at	XPO6	3117.8	1523.3	3434.9	3936.4	3.0	2.5	1.2
212527_at	D15Wsu75e	2127.0	459.2	1500.7	899.2	1.3	2.1	1.8
212691_at	NUP188	3216.9	599.7	1310.0	1434.0	2.0	1.8	3.7
213159_at	PCNX	786.5	301.8	828.7	660.8	2.3	2.9	1.3
213507_s_at	KPNB1	10080.7	4480.0	7475.4	19512.6	8.5	1.7	1.4
213951_s_at	PSMC3IP	1253.3	336.2	1013.7	946.7	2.0	2.6	1.7
214144_at	POLR2D	386.0	219.6	422.4	622.8	2.4	2.1	1.1
214264_s_at	C14orf143	4287.7	382.9	1351.1	2017.7	13.8	8.1	20.2
214412_at	H2AFB3 /// H2AFB1	848.9	47.1	796.3	1246.7	43.7	12.9	5.2
214431_at	GMPS	5653.1	802.5	2186.8	5964.8	10.1	1.7	3.6
214784_x_at	XPO6	2641.9	1591.2	3408.5	2500.9	1.4	2.2	1.1
214838_at	SFT2D2	1180.6	334.2	2717.3	674.9	1.3	11.7	1.3
215227_x_at	ACP1	3421.9	1455.0	11920.8	6989.0	4.5	16.2	1.1
217959_s_at	TRAPPC4	1957.1	968.9	1763.1	4341.2	11.6	2.1	1.3
218305_at	IPO4	2405.6	478.7	1632.3	1102.4	1.5	2.6	2.5
218339_at	MRPL22	1566.6	715.5	1719.7	2670.2	4.5	2.1	1.2
218354_at	TRAPPC2L	3074.5	1026.7	1798.8	2032.1	2.3	1.8	2.0
218435_at	DNAJC15	4689.8	1813.5	6060.5	3407.0	2.6	2.8	1.2
218447_at	C16orf61	3799.2	1784.7	5558.2	5366.3	3.5	3.8	1.2
218558_s_at	MRPL39	2896.0	1093.6	2379.0	5283.1	5.0	1.9	1.2
218580_x_at	AURKAIP1 /// LOC643556	9192.1	2923.4	9580.4	7169.5	2.2	3.9	1.8
218647_s_at	YRDC	1485.7	629.4	2003.1	3468.8	7.7	2.9	1.2
218695_at	EXOSC4	1725.6	266.4	974.0	1354.3	4.9	2.6	2.9
218830_at	RPL26L1	3763.4	1507.8	4423.0	7192.1	13.9	4.1	1.5
218860_at	NOC4L	828.3	157.9	1452.6	1094.3	2.4	4.3	1.2

219050_s_at	ZNHIT2	874.2	101.9	373.7	266.5	1.2	2.0	2.6
219060_at	C8orf32	1262.5	691.2	1841.8	3063.6	9.7	4.4	1.1
219161_s_at	CKLF	1926.7	714.1	3896.1	4005.1	7.9	8.1	1.2
219253_at	FAM11B	772.9	339.6	1052.6	1894.3	15.3	6.8	1.3
219350_s_at	DIABLO	4877.1	1760.7	3094.9	4135.5	4.1	2.2	2.4
219526_at	C14orf169	1736.6	725.0	1636.2	1902.1	4.0	2.3	1.5
219531_at	CEP72	519.5	169.2	1217.7	1252.4	17.5	20.9	1.2
219539_at	GEMIN6	1449.9	340.9	1360.4	2307.0	14.4	6.0	2.2
219785_s_at	FBXO31	6118.3	276.3	2033.7	1250.4	2.2	4.1	9.6
220118_at	ZBTB32	2259.6	137.4	3477.4	960.6	1.2	4.1	1.3
220239_at	KLHL7	2938.3	263.1	1069.0	2561.2	29.0	3.9	7.1
220445_s_at	CSAG2	49.6	22.2	441.4	859.5	175.2	50.7	1.1
220688_s_at	C1orf33	1071.3	674.1	1720.6	2572.6	7.8	2.7	1.1
220966_x_at	ARPC5L	5501.6	2428.4	5117.2	6547.4	2.2	1.8	1.2
221058_s_at	CKLF	1088.7	561.7	3031.8	2202.3	6.7	12.4	1.1
221185_s_at	IQCG	2107.5	342.0	16310.0	7940.4	87.5	809.1	2.2
221598_s_at	CRSP8	368.9	155.0	408.0	819.2	2.8	1.7	1.1
221797_at	LOC339229	723.9	278.5	1774.0	808.1	1.6	5.8	1.1
221845_s_at	CLPB	7681.7	132.4	565.9	471.7	1.9	2.3	93.8
221979_at	NDUFB6	1250.2	317.3	733.2	559.7	1.2	2.3	1.6
222530_s_at	MKKS	2265.1	912.2	2167.8	1144.7	1.6	2.5	1.3
222684_s_at	NOL10	2567.4	1038.8	2085.9	2338.8	2.3	1.9	1.5
222703_s_at	YRDC	727.3	199.5	1035.4	1698.9	9.1	3.6	1.3
222713_s_at	FANCF	906.3	294.2	714.3	721.5	1.7	1.8	1.5
222768_s_at	CGI-09	1448.1	641.7	1671.4	2746.0	9.9	4.5	1.4
222792_s_at	CCDC59	1734.3	999.0	4140.3	1967.4	1.8	7.7	1.1
223086_x_at	MRPL51	6529.9	3499.2	7310.5	9040.4	3.7	2.8	1.2
223101_s_at	ARPC5L	3153.3	1086.7	2343.1	1698.4	1.1	1.7	1.6
223368_s_at	C9orf32	2679.4	642.5	2982.9	1845.5	1.9	4.9	1.7
223407_at	C16orf48	1121.6	264.3	791.7	511.0	1.5	1.8	1.7
223413_s_at	LYAR	5903.6	611.9	1525.5	2484.9	7.1	2.3	10.8
223414_s_at	LYAR	2527.5	605.0	1953.8	1532.4	2.2	4.2	2.3
223451_s_at	CKLF	1692.8	789.1	4549.3	2448.0	4.5	15.5	1.2
223452_s_at	DKFZP564J0863	3026.8	250.9	1265.7	1293.7	3.5	4.1	5.5
223480_s_at	MRPL47	5945.2	1961.2	9061.0	11764.7	20.9	19.5	2.0
223538_at	SERF1A	8944.9	1311.1	3459.0	3198.3	3.2	3.8	8.9

223677_at	ATG10	579.2	259.9	434.8	429.3	1.5	1.7	1.3
223689_at	IGF2BP1	148.3	48.5	293.3	241.1	2.3	3.2	1.1
223791_at	FAM27A	595.6	72.8	527.8	238.3	1.8	5.2	2.2
223808_s_at	PTPMT1	1833.3	576.6	2360.3	1970.3	5.4	8.4	2.1
223811_s_at	C7orf20	595.5	233.0	520.0	409.9	1.2	1.7	1.2
223917_s_at	SLC39A3	4130.2	691.2	1988.2	1084.9	1.2	2.4	3.8
224301_x_at	H2AFJ	16151.5	1574.9	4972.5	2473.4	1.2	2.2	3.7
224365_s_at	TIGD7	915.7	483.4	450.0	110.2	1.2	1.7	1.1
224467_s_at	PDCD2L	943.5	447.8	1045.7	1570.4	5.3	2.6	1.3
224733_at	CMTM3	2725.1	658.7	2514.4	1845.6	2.0	3.1	1.9
224885_s_at	KRTCAP2	8298.6	3981.1	8409.4	8382.0	1.6	1.9	1.2
224903_at	CIRH1A	2757.4	1147.6	3264.6	10327.1	15.5	1.8	1.1
225075_at	PDRG1	2574.7	818.8	1667.7	1468.6	1.7	2.4	1.9
225082_at	CPSF3	3369.9	1020.2	4170.7	7191.9	4.3	2.0	1.1
225156_at	ELOF1	4086.2	1143.0	1917.2	1596.2	1.3	2.2	3.0
225441_x_at	LSMD1	3609.1	1451.0	4986.3	3054.6	1.7	3.3	1.3
225472_at	BAT4	3315.3	1149.5	5063.1	4191.5	1.9	2.4	1.1
225552_x_at	AURKAIP1 /// LOC643556	9796.4	3043.1	12397.0	9093.6	3.2	6.1	1.8
225765_at	TNPO1	1764.2	765.2	1206.5	3446.8	5.4	1.8	1.2
225802_at	TOP1MT	827.3	273.2	1052.9	940.2	1.6	2.0	1.1
225898_at	WDR54	3225.6	933.7	6003.7	6801.6	14.3	10.0	1.6
225908_at	LOC285148	4271.4	1461.5	3013.4	2860.6	7.7	3.9	2.4
226024_at	COMMD1	2981.0	1656.8	2878.6	3326.4	2.1	2.2	1.2
226089_at	RABL3 /// LOC653256	452.6	237.1	414.0	296.7	1.1	1.8	1.1
226196_s_at	C14orf179	1341.4	629.6	1946.3	1001.0	1.3	4.1	1.3
226243_at	LOC391356	2787.5	1151.6	3558.3	4381.0	6.1	3.8	1.4
226254_s_at	KIAA1430	4710.5	1794.4	3625.6	6380.9	4.3	1.8	1.3
226278_at	DKFZp313A2432	2902.0	1020.3	3127.6	2720.3	1.4	2.1	1.2
226320_at	THOC4	1723.3	557.1	1284.2	1569.6	2.4	1.8	1.3
226434_at	MGC22793	3177.8	883.7	1827.9	1838.1	1.7	1.7	2.2
226565_at	TMEM99	4904.6	602.4	2473.9	1601.9	2.7	5.5	4.7
227037_at	LOC201164	2102.6	571.8	1202.6	1017.7	1.7	2.9	2.8
227678_at	XRCC6BP1	2472.1	444.4	1091.8	2432.6	7.7	2.5	3.0
227711_at	FAM112B	10990.0	283.1	1512.4	5573.4	174.2	17.6	170.1
227901_at	LOC648987	236.3	95.2	222.4	256.0	1.6	2.4	1.2

227904_at	AZI2	650.8	237.1	486.3	938.6	5.2	2.6	1.5
227916_x_at	EXOSC3	1163.1	487.5	1299.6	3351.7	12.6	2.6	1.2
227941_at	LOC339803	1679.0	440.1	1729.1	1035.2	1.7	4.5	2.0
227972_at	TOR2A	561.4	209.7	643.2	434.7	1.2	2.1	1.1
228066_at	LOC642705	566.6	102.5	2506.1	868.1	3.5	24.6	1.3
228774_at	CEP78	1841.7	528.3	2398.0	1336.0	1.3	3.1	1.3
228899_at	CUL1	736.4	300.8	517.3	1126.9	6.7	3.2	1.3
229106_at	DYNLL2	3844.1	420.4	1594.0	786.5	1.7	4.9	9.7
229716_at	---	713.2	225.0	1453.5	135.9	1.2	7.3	1.2
230026_at	MRPL43	1336.2	439.9	1509.8	1143.0	1.4	2.3	1.2
230425_at	EPHB1	991.0	335.0	1121.0	6127.5	48.5	2.3	1.1
230860_at	---	704.8	212.1	544.8	581.4	1.9	1.8	1.4
230871_at	DHX30	2230.5	776.0	1681.4	1044.3	1.2	2.3	1.6
230924_at	TTLL6	1966.1	70.5	534.8	200.3	2.2	5.8	21.7
230966_at	IL4I1	800.8	109.6	6052.4	3537.5	87.1	135.3	1.7
231303_at	C21orf42	760.7	105.4	295.6	791.2	14.3	2.7	3.8
231730_at	SLA/LP	395.2	119.9	305.8	433.5	2.1	2.1	1.3
231769_at	FBXO6	995.9	403.0	8679.7	1655.0	5.8	193.9	1.2
232798_at	DNAJC5B	825.1	274.2	1735.8	1786.5	26.9	13.1	1.4
234016_at	LOC90499	1136.6	50.8	172.1	101.1	1.3	1.9	9.7
235088_at	LOC201725	946.6	149.6	410.6	2852.4	44.5	1.8	2.2
235700_at	RP13-36C9.1 /// RP13-36C9.3 /// CT45-4 /// RP13-36C9.6 /// CT45-6 /// CT45-1 /// LOC653515	2208.2	102.8	10692.6	17429.9	3777.3	3084.5	15.7
237065_s_at	---	909.8	169.3	424.8	286.5	2.0	2.4	2.8
237105_at	---	302.5	139.1	407.2	777.6	13.9	3.1	1.1
237344_at	FLJ45743	1676.6	88.1	327.3	169.0	1.6	4.2	15.9
240037_at	KIAA1754L	891.2	266.0	607.5	318.4	1.1	1.7	1.6
240744_at	CPA5	806.5	98.9	369.5	221.2	2.4	2.6	3.1
242069_at	CBX5	290.7	66.5	519.8	394.8	3.0	6.5	1.2
244519_at	ASXL1	824.1	350.7	3095.1	1770.7	4.8	17.7	1.1
36566_at	CTNS	1143.3	506.9	1482.3	1906.4	6.0	2.6	1.1
51146_at	GFRA1 /// PIGV	2133.2	363.3	549.9	475.9	1.1	1.7	6.0
58696_at	EXOSC4	2228.9	606.9	1814.5	2050.0	4.8	3.6	2.3
59705_at	SCLY	394.7	172.8	777.6	331.1	1.5	6.0	1.2

78383_at	NDUFB6	1153.3	432.7	768.8	475.2	1.1	2.2	1.7

Supplementary Table 4. Detection of PRAME-reactive T cells in primed PBMC. PBMC were stimulated with DC that had been transfected with total RNA from L-1236 cells or without RNA (H_2O). PRAME specific T cells were identified by pentamer staining using pentamers corresponding to PRAME peptides ALY or VLD (ALY/HLA-A2, VLD/HLA-A2). Presented are percentages of pentamer reactive cells from 4 independent donors. Each combination of L-1236 and H_2O represents a single experiment. In one experiment (donor 4), RNA from SK-N-MC sarcoma cells was used for control transfection. For donors 1 and 3 stimulation was performed in duplicates. For donor 3, cells were analyzed at 4 different time points (t1-t4). -: not done.

		Pentamer positive cells [%]	
Donor number	**Transfected RNA**	**ALY/HLA-A2-pentamer**	**VLD/HLA-A2-pentamer**
1(1)	**H_2O**	0.051	-
1(1)	**L-1236**	0.069	-
1(2)	**H_2O**	0.041	-
1(2)	**L-1236**	0.058	-
2	**H_2O**	0.035	0.034
2	**L-1236**	0.124	0.037
3(t1)	**H_2O**	0.018	0.025
3(t1;1)	**L-1236**	0.014	0.041
3(t1;2)	**L-1236**	0.011	0.036
3(t2)	**H_2O**	0.070	0.203
3(t2)	**L-1236**	0.044	0.344
3(t3)	**H_20**	0.154	0.098
3(t3)	**L-1236**	0.526	0.290
3(t4)	**H_20**	0.143	0.176
3(t4)	**L-1236**	0.707	0.360
4	**SK-N-MC**	0.428	0.196
4	**L-1236**	0.525	0.457