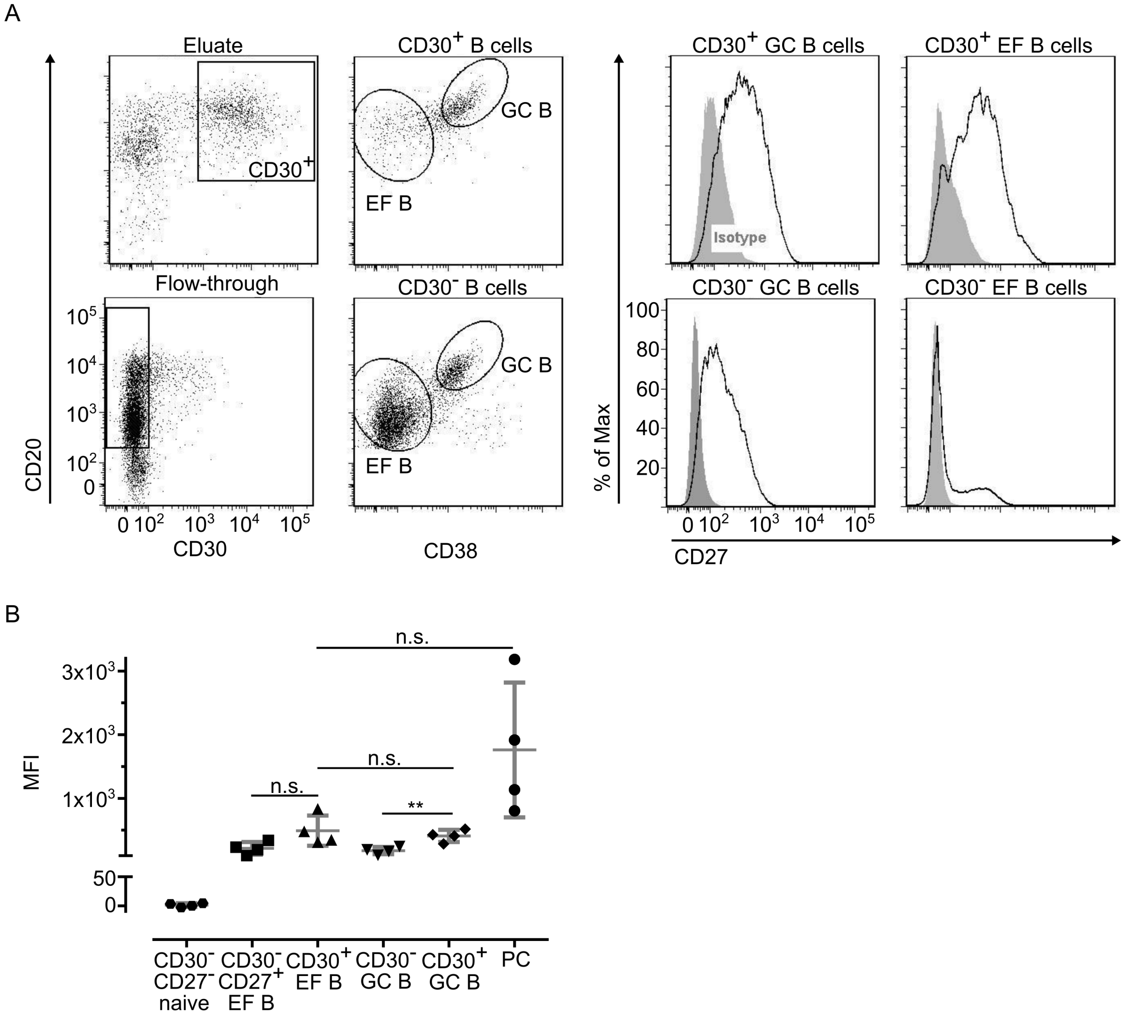
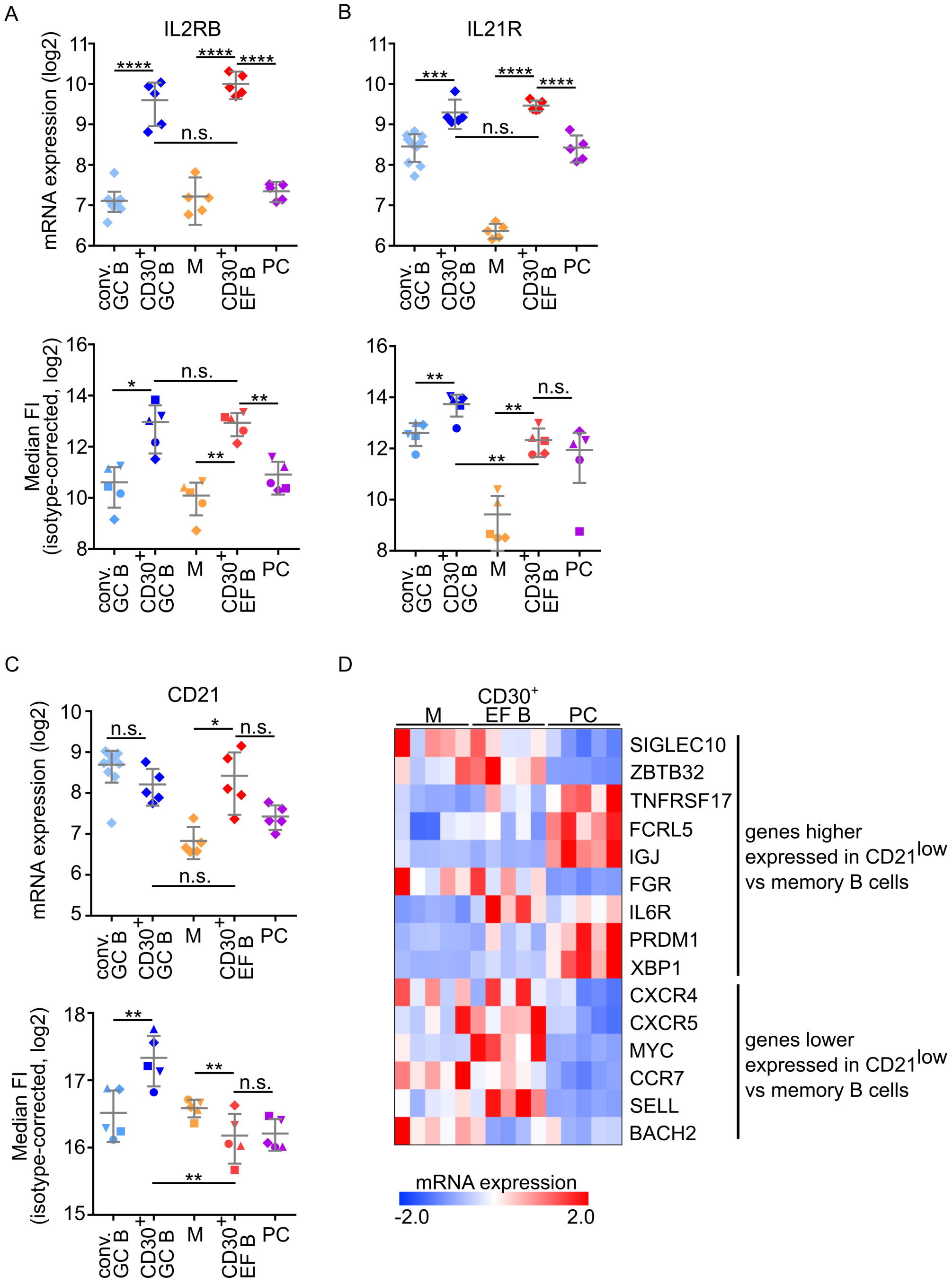
Supplemental Figure 1



Supplemental Figure 1. CD27 expression by CD30$^+$ B cells.

Tonsillar mononuclear cells were depleted of CD3$^+$ T cells and enriched for CD30$^+$ B cells by consecutive MACS isolation steps. The flow-through of the CD30-MACS enrichment was used to analyze CD30$^-$ B cells. Isolated B cells were stained for CD20, CD30, CD38, and CD27 or isotype control. Dot plots in panel A depict the gating strategy, and histograms show the staining patterns for CD27 and isotype control of the four subsets. In B, the mean fluorescence intensities (MFI) for CD27 of the four B cell subsets, as well as naive and plasma cells, are given for four tonsils analyzed. Graphs indicate mean ± SD. The MFI of the CD27 staining have been corrected for the respective values of the isotype control staining. As CD30$^-$ non-GC B cells include CD27$^-$ naïve B cells and CD27$^+$ memory B cells, they show a biphasic CD27 expression. n.s., not significant; ** $p<0.01$ (unpaired t test).

Supplemental Figure 2

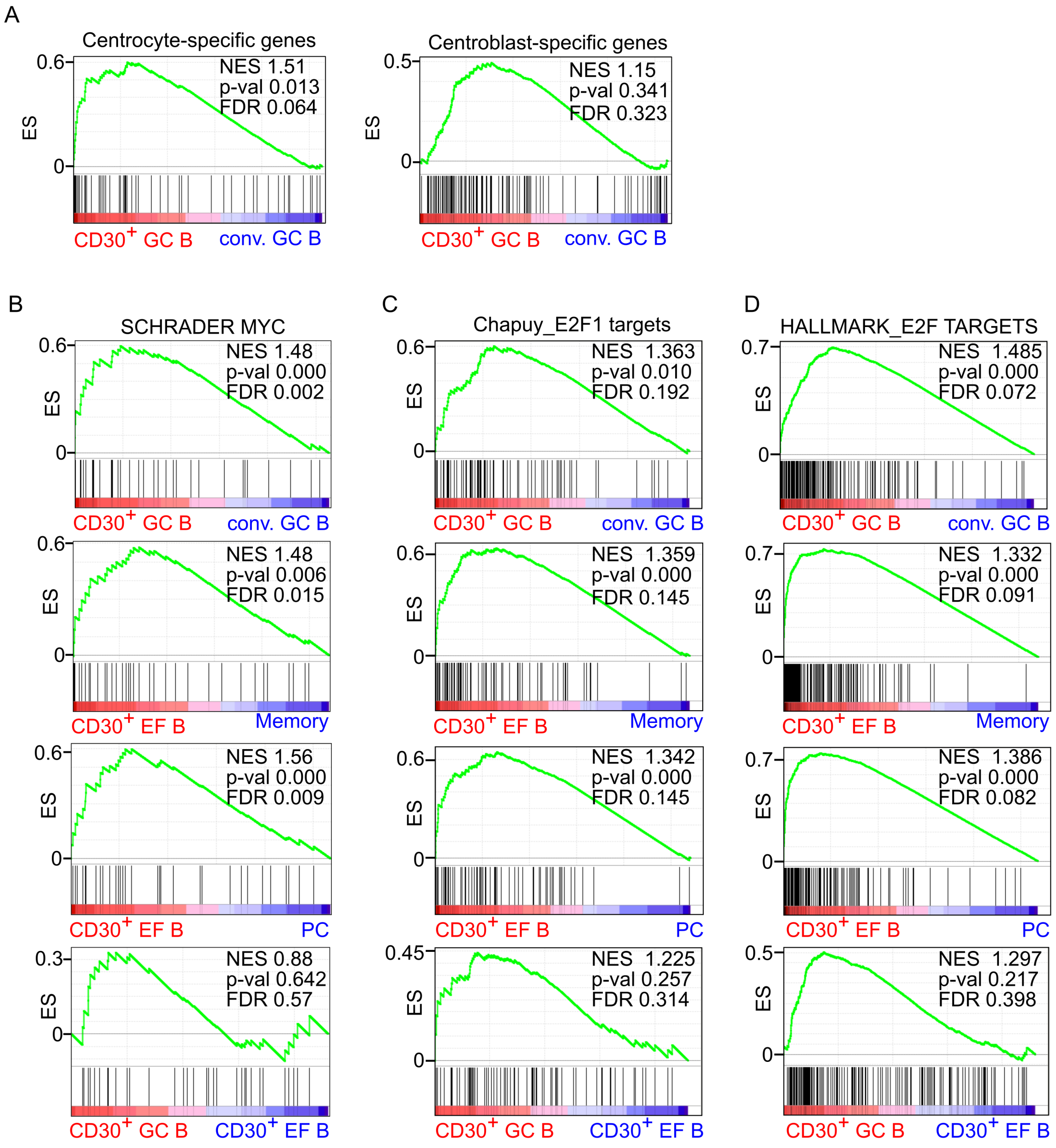


Supplemental Figure 2. Interleukin receptor expression by CD30^{+} B cells and relatedness of CD30^{+} EF B cells to CD21^{low} B cells.

mRNA and surface protein expression of IL2RB (A), IL21R (B) and CD21 (C) are shown for indicated B cell subsets of five tonsils (conventional (conv.) CD30^{-} GC (germinal center) B cells (CD20^{high}CD38^{+}), CD30^{+} GC B cells, CD30^{-} memory and CD30^{+} EF (extra follicular) B cells (CD20^{+}CD38$^{-/low}$CD27^{+}), and plasma cells (PC) (CD20^{+}CD38^{high}). mRNA data originate from Affymetrix genechip analyses (Tiacci et al., Blood, 2012; 120:4609-4620) and were analyzed using an unpaired t test. For the flow cytometric analysis, median fluorescence intensity (FI) is shown, and data were analyzed using a paired t test.

Graphs indicate mean ± SD. * $p<0.05$; ** $p<0.01$; *** $p<0.001$; **** $p<0.0001$ n.s., not significant. Heat map in D shows the expression of genes differentially expressed between CD21^{low} and memory B cells reported by Lau et al. (Sci Immunol, 2017; 2:eaai8153) in CD30^{+} EF, memory B cells and PC. Note that a number of genes that are upregulated in CD21^{low} B cells in comparison to memory B cells are expressed at lower levels or at a similar level in CD30^{+} EF B cells compared with memory B cells (e.g. SIGLEC10, FCRL5, IGJ), and vice versa, several genes with reduced expression in CD21^{low} B cells showed increased expression in CD30^{+} EF B cells, compared with memory B cells (CXCR5, MYC, SELL).

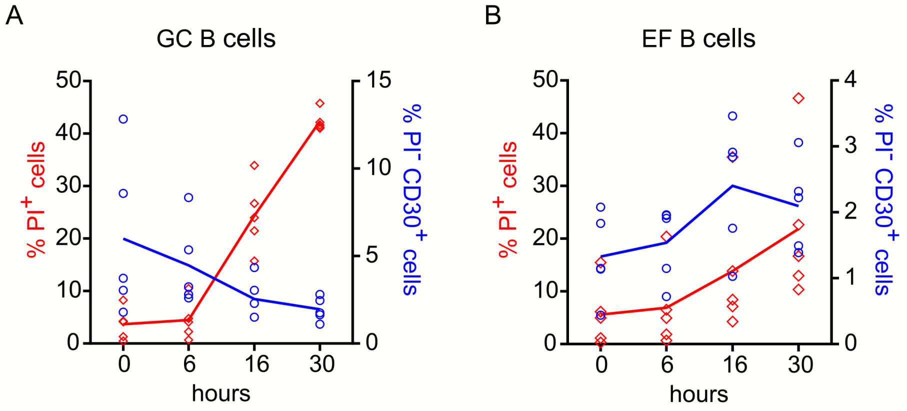
Supplemental Figure 3



Supplemental Figure 3. Enrichment of centrocyte-specific genes in CD30$^+$ versus conventional GC B cells cells, and MYC and E2F1 signatures in CD30$^+$ B cells.

(A) GSEA enrichment plots of centrocyte- and centroblast-specific gene sets (Victora et al., Blood, 2012; 120:2240-2248) are shown for the comparison of CD30$^+$ GC B cells with conventional (conv.) GC B cells. Enrichment plots for experimentally derived MYC (B) (Schrader et al., Int J Cancer 2012; 131:E348-E361) and E2F1 target genes (C) (Chapuy et al., Cancer Cell 2013; 24:777-790) as well as the (D) E2F1 hallmark gene set (hallmark; MSigDB v5) for comparisons of CD30$^+$ B cells with conventional B cell subsets are shown. NES, normalized enrichment score; FDR, false discovery rate.

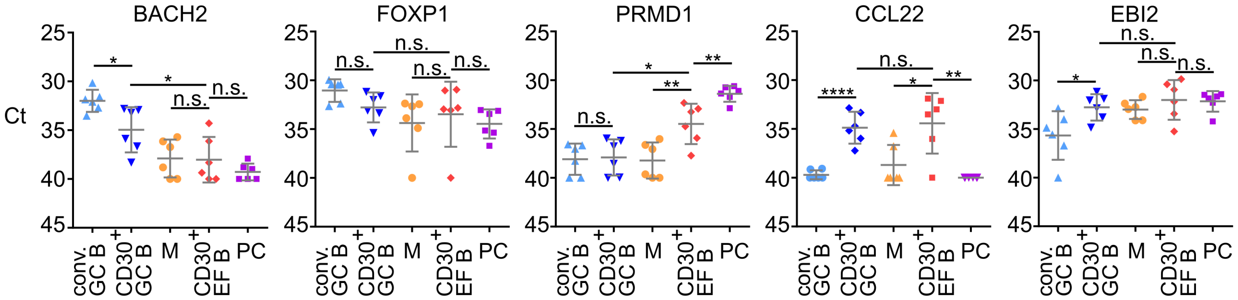
Supplemental Figure 4



Supplemental Figure 4. Survival capacity of CD30$^+$ B cells in vitro.

Isolated GC B cells (CD20^{high}CD38$^+$) (A) and EF memory B cells (CD20$^+$CD38$^{-/low}$CD27$^+$) were maintained ex vivo and analyzed for proportions of propidium iodide (PI)$^+$ cells, as well as PI$^-$CD30$^+$ surviving cells at indicated time points. Trend lines of mean values are shown. Each dot represents a measurement from an independent tonsil (n=5). The decrease of CD30$^+$ B cells among surviving (PI$^-$) GC B cells over time indicates a slightly increased cell death of these cells (and/or perhaps a downregulation of CD30 on the cells), whereas the increase in the proportion of CD30$^+$ B cells among non-GC B cells over time indicates increased survival of these cells in comparison to conventional memory B cells.

Supplemental Figure 5



Supplemental Figure 5. Validation of differential expression of selected genes between CD30$^+$ and conventional B cell subsets.

RT-qPCR analysis of selected genes of sorted memory B cells (M), plasma cells (PC), conventional GC B cells (conv. GC B), CD30$^+$ GC B cells, and CD30$^+$ EF B cells. Cycle threshold (Ct) values are shown. Graphs indicate mean ± SD. *p<0.05; **p<0.01; ***p<0.001; ****p<0.0001 (unpaired t test); n.s., not significant. Cells from six tonsils were analyzed.

Supplemental Table 1. Frequency of $CD30^+$ B cells among human tonsillar mononuclear cells.

Tonsil	Donor age	% B cells ($CD20^+$)	% GC B cells ($CD20^{hi}/CD38^+$)	% $CD30^+$ B cells	% GC B cells among $CD30^+$ B cells^
1	23	42.8	3.3	0.18	18.1
2	7	66.6	35.6	1.7	85.8
3	4	75	40.5	0.5	31
4	16	36.5	26.2	0.9	46.9
5	11	62.7	34.9	1.5	76
6	5	79.5	34	0.7	80.3
7	21	66.4	30	1.3	79.5
8	5	72	38.2	1.3	78.5
9	26	42.1	6.5	0.4	27.9
10	3	75	20	0.5	48.8
11	2	77.7	29.9	0.4	56.9
12	5	66.2	24.5	0.1	58.5
13	23	72.8	38.5	0.5	78.3
14	18	61.8	15.8	0.4	52.3
19	4	78.8	47.3	0.7	78.6
20	14	62.4	6.1	0.5	55.4
21	16	78.7	23.6	0.6	41.2
Mean	11.9	65.7	26.8	0.7	58.5
Max	26	79.5	47.3	1.7	85.8
Min	2	36.5	3.3	0.1	18.1

^Assessed in tonsillar mononuclear cells before or, when available, after MACS enrichment of $CD30^+$ B cells.

Supplemental Table 2. Phenotypic characterization of CD30^{+} B cells

Cell type	Donor	IgM^{+} %[a]	IgM^{+} IgD$^{-/low}$ % [a]	IgD-only %	IgG^{+} %	IgA^{+} %	IgG^{+} or IgA^{+} %	IgE^{+} %[b]
CD30^{+} GC B cells	1	n.a.	n.a.	n.a.	63	16	79	n.a.
	2	n.a.	n.a.	n.a.	61	21	82	n.a.
	3	5	n.a.	n.a.	59	3	62	n.a.
	4	19	n.a.	n.a.	43	27	70	n.a.
	5	9	n.a.	n.a.	48	35	83	n.a.
	6	4	n.a.	n.a.	66	4	70	n.a.
	7	4	3	2	39	48	87	0
	8	14	9	7	54	16	70	0
	9	8	6	12	46	27	73	0
	10	10	7	10	n.a.	n.a.	n.a.	n.a.
	Average	9	6	8	53	22	75	0
	(Range)	(4-19)	(3-9)	(2-12)	(39-66)	(3-48)	(62-87)	
CD30^{+} EF B cells	1	n.a.	n.a.	n.a.	46	19	65	n.a.
	2	n.a.	n.a.	n.a.	52	33	85	n.a.
	3	4	n.a.	n.a.	58	9	67	n.a.
	4	37	n.a.	n.a.	26	19	45	n.a.
	5	21	n.a.	n.a.	42	23	65	n.a.
	6	9	n.a.	n.a.	69	6	75	n.a.
	7	8	5	2	50	38	88	0
	8	54	43	19	17	9	26	0
	9	8	7	3	49	39	88	0
	10	36	29	25	n.a.	n.a.	n.a.	n.a.
	Average	22	21	12	45	22	67	0
	(Range)	(4-54)	(5-43)	(2-25)	(17-69)	(6-39)	(26-88)	
CD30^{-} GC B cells	1	n.a.	n.a.	n.a.	59	20	79	n.a.
	2	n.a.	n.a.	n.a.	52	24	76	n.a.
	3	16	n.a.	n.a.	49	0	49	n.a.
	4	33	n.a.	n.a.	41	15	56	n.a.
	5	18	n.a.	n.a.	54	19	73	n.a.
	6	8	n.a.	n.a.	51	2	53	n.a.
	7	9	4	19	36	43	79	0
	8	19	12	3	56	13	69	0
	9	24	8	9	38	21	59	0
	10	25	12	14	n.a.	n.a.	n.a.	n.a.
	Average	19	9	11	48	17	66	0
	(Range)	(8-33)	(4-12)	(3-19)	(36-59)	(0-43)	(49-79)	

a) For donors 1-6, the fraction of IgM^{+}CD30^{+} B cells was determined by four color staining for the markers CD20, CD30, CD38 and IgM; for donors 7-10 a CD30, CD38, IgM and IgD four color staining was performed on isolated B cells, so that also IgM^{+}IgD$^{-/low}$ and IgD-only B cells could be analyzed. The percentage of cells positive for the markers investigated is given.

b) For IgE staining, 0% means that not significantly more positive events compared to isotype control were detected.

n.a.: not analyzed

Supplemental Table 3. Supervised comparison of CD30$^+$ GC B cells versus CD30$^+$ extrafollicular (EF) B cells

Probeset ID	Fold change CD30+ GC/ CD30+ EF B cells	Gene Title	Gene Symbol
		Higher expression in CD30+ GC B cells	
218692_at	4.9	Golgi-localized protein	GOLSYN
204141_at	4.5	tubulin. beta 2A	TUBB2A
225637_at	4.4	differentially expressed in FDCP 8 homolog (mouse)	DEF8
205692_s_at	4.1	CD38 molecule	CD38
1560397_s_at	4.0	kelch-like 6 (Drosophila)	KLHL6
210258_at	3.7	regulator of G-protein signaling 13	RGS13
213906_at	3.5	v-myb myeloblastosis viral oncogene homolog (avian)-like 1	MYBL1
229656_s_at	3.4	echinoderm microtubule associated protein like 6	EML6
212458_at	3.4	sprouty-related. EVH1 domain containing 2	SPRED2
242334_at	3.3	NLR family. pyrin domain containing 4	NLRP4
1560396_at	3.3	kelch-like 6 (Drosophila)	KLHL6
219304_s_at	3.3	platelet derived growth factor D	PDGFD
218862_at	3.3	ankyrin repeat and SOCS box-containing 13	ASB13
204891_s_at	3.2	lymphocyte-specific protein tyrosine kinase	LCK
201678_s_at	3.2	chromosome 3 open reading frame 37	C3orf37
203140_at	3.2	B-cell CLL/lymphoma 6	BCL6
227684_at	3.2	sphingosine-1-phosphate receptor 2	S1PR2
1559618_at	3.1	hypothetical protein LOC100129447	LO..
204430_s_at	3.0	solute carrier family 2 (facilitated glucose/fructose transporter). member 5	SLC2A5
205383_s_at	3.0	zinc finger and BTB domain containing 20	ZBTB20
		Higher expression in extrafollicular CD30+ B cells	
225368_at	-3.0	homeodomain interacting protein kinase 2	HIPK2
205419_at	-3.0	G protein-coupled receptor 183	GPR183
218935_at	-3.0	EH-domain containing 3	EHD3
202156_s_at	-3.0	CUG triplet repeat. RNA binding protein 2	CUGBP2
201722_s_at	-3.0	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1
202887_s_at	-3.1	DNA-damage-inducible transcript 4	DDIT4
212956_at	-3.1	TBC1 domain family. member 9 (with GRAM domain)	TBC1D9
218699_at	-3.1	RAB7. member RAS oncogene family-like 1	RAB7L1
224404_s_at	-3.1	Fc receptor-like 5	FCRL5
207691_x_at	-3.1	ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1
226841_at	-3.1	macrophage expressed 1	MPEG1
242268_at	-3.2	CUG triplet repeat. RNA binding protein 2	CUGBP2
207861_at	-3.3	chemokine (C-C motif) ligand 22	CCL22
212509_s_at	-3.3	matrix-remodelling associated 7	MXRA7
209685_s_at	-3.3	protein kinase C. beta	PRKCB
204014_at	-3.4	dual specificity phosphatase 4	DUSP4
226811_at	-3.4	family with sequence similarity 46. member C	FAM46C
226905_at	-3.4	family with sequence similarity 101. member B	FAM101B
219836_at	-3.6	zinc finger. BED-type containing 2	ZBED2
201724_s_at	-3.6	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 1 (GalNAc-T1)	GALNT1
209374_s_at	-3.6	immunoglobulin heavy constant mu	IGHM
221530_s_at	-3.7	basic helix-loop-helix family. member e41	BHLHE41
204489_s_at	-3.8	CD44 molecule (Indian blood group)	CD44
213241_at	-3.8	plexin C1	PLXNC1
212063_at	-3.8	CD44 molecule (Indian blood group)	CD44
224406_s_at	-3.9	Fc receptor-like 5	FCRL5
204563_at	-3.9	selectin L	SELL

225331_at	-4.3	coiled-coil domain containing 50	CCDC50
230245_s_at	-4.3	hypothetical LOC283663	LOC..
203915_at	-4.3	chemokine (C-X-C motif) ligand 9	CXCL9
202727_s_at	-4.4	interferon gamma receptor 1	IFNGR1
219667_s_at	-4.4	B-cell scaffold protein with ankyrin repeats 1	BANK1
201426_s_at	-4.8	vimentin	VIM
1558662_s_at	-4.9	B-cell scaffold protein with ankyrin repeats 1	BANK1
209473_at	-5.2	ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1
217762_s_at	-5.3	RAB31. member RAS oncogene family	RAB31
208683_at	-5.8	calpain 2. (m/II) large subunit	CAPN2
204533_at	-5.8	chemokine (C-X-C motif) ligand 10	CXCL10
217764_s_at	-6.7	RAB31. member RAS oncogene family	RAB31
202157_s_at	-8.6	CUG triplet repeat. RNA binding protein 2	CUGBP2
219014_at	-11.7	placenta-specific 8	PLAC8

Significantly differentially expressed genes with an at least 3-fold difference in average expression levels are listed ($p<0.05$, false discovery rate (FDR)<0.05).

Supplemental Table 4. GSEAs of CD30$^+$ and conventional B cells using the motif-based collection (c3tft; MSigDBv4).

CD30$^+$ GC B cells vs CD30$^+$ extrafollicular (EF) B cells ($p < 0.01$, FDR < 0.1)

Enriched in CD30$^+$ GC B cells

None

Enriched in CD30$^+$ EF B cells

Factor	Gene set	NES	p-value	FDR
NFKB	V$NFKAPPAB_01	-1.72	0	0.022
	GGGNNTTTCC_V$NFKB_Q6_01	-1.57	0	0.056
	V$NFKAPPAB65_01	-1.56	0.008	0.058
IRF	V$IRF2_01	-1.75	0	0.035
	V$IRF_Q6	-1.64	0	0.067
	STTTCRNTTT_V$IRF_Q6	-1.65	0	0.069
	V$IRF7_01	-1.52	0	0.075
	V$ICSBP_Q6	-1.5	0	0.08
AP1	V$AP1_Q4	-1.58	0	0.055
	V$AP1_Q2	-1.62	0	0.075
MEF2	V$MEF2_Q6_01	-1.55	0	0.057
	V$MEF2_03	-1.53	0.006	0.072
	V$HMEF2_Q6	-1.59	0.004	0.058
	V$AMEF2_Q6	-1.54	0.006	0.063
AML	V$AML1_Q6	-1.59	0	0.058
	V$AML1_01	-1.59	0	0.062
STAT5B	TTCYNRGAA_V$STAT5B_01	-1.58	0	0.054
ETS	V$ETS_Q4	-1.51	0.004	0.076
CEBPDELTA	V$CEBPDELTA_Q6	-1.49	0	0.08
FOXO1	V$FOXO1_01	-1.48	0	0.092
GR	V$GR_Q6	-1.73	0	0.022
SRY	V$SRY_01	-1.57	0	0.057
IK2	V$IK2_01	-1.56	0	0.057
ISRE	V$ISRE_01	-1.62	0	0.059
PIT1	V$PIT1_Q6	-1.58	0	0.059
P300	V$P300_01	-1.57	0	0.059
OLF1	V$OLF1_01	-1.56	0	0.059
AP2	V$AP2_Q6	-1.56	0	0.061
DR3	V$DR3_Q4	-1.65	0	0.062
FREAC4	V$FREAC4_01	-1.62	0	0.069
FREAC2	RTAAACA_V$FREAC2_01	-1.5	0	0.081
TCF1P	V$TCF1P_Q6	-1.53	0	0.071
CORE BINDING FACTOR	V$COREBINDINGFACTOR_Q6	-1.53	0	0.072
FAC1	V$FAC1_01	-1.52	0	0.075
HNF3	V$HNF3_Q6	-1.52	0	0.075
GATA	GATAAGR_V$GATA_C	-1.51	0	0.075
MSX1	V$MSX1_01	-1.49	0.004	0.085
RORA2	V$RORA2_01	-1.47	0	0.095

CD30$^+$ GC B cells vs conventional GC B cells ($p < 0.01$, FDR < 0.3)

Enriched in CD30$^+$ GC B cells

Factor	Gene set	NES	p-value	FDR
E2F	V$E2F_Q4_01	1.41	0	0.242
	V$E2F_01	1.43	0	0.261
	V$E2F_Q6	1.46	0.002	0.274
	V$E2F_Q4	1.46	0.002	0.281
	V$E2F_Q3_01	1.42	0.006	0.259
E2F1	V$E2F1_Q4_01	1.42	0	0.261
	V$E2F1_Q4	1.44	0	0.281
	SGCGSSAAA_V$E2F1DP2_01	1.44	0.002	0.271

E4F1	GTGACGY_V$E4F1_Q6	1.35	0.004	0.256
MYC/MAX	CACGTG_V$MYC_Q2	1.46	0	0.297
	V$MAX_01	1.43	0	0.265
ERR1	V$ERR1_Q2	1.4	0.002	0.256
	TGACCTY_V$ERR1_Q2	1.42	0.002	0.259
HNF4	V$HNF4_01	1.42	0.002	0.256
	V$HNF4ALPHA_Q6	1.43	0.004	0.277
GABP	MGGAAGTG_V$GABP_B	1.36	0	0.257
	V$GABP_B	1.37	0.002	0.254
CETS1P54	V$CETS1P54_01	1.46	0	0.284
GRE	V$GRE_C	1.44	0.009	0.277
HSF	TTCNRGNNNNTTC_V$HSF_Q6	1.43	0.006	0.271
ATF3	TGACGTCA_V$ATF3_Q6	1.4	0.002	0.255
NFY	GATTGGY_V$NFY_Q6_01	1.38	0.006	0.255
USF	V$USF_Q6	1.37	0	0.256
SP1	GGGCGGR_V$SP1_Q6	1.37	0	0.26
ELK1	SCGGAAGY_V$ELK1_02	1.37	0	0.26
NRF1	RCGCANGCGY_V$NRF1_Q6	1.36	0	0.259
XBP1	V$XBP1_01	1.36	0.006	0.251
STAT1	V$STAT1_02	1.35	0.006	0.255
Enriched in conventional GC B cells				
None				
CD30$^+$ extrafollicular (EF) B cells vs memory B cells (p < 0.01, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
Factor	**Gene set**	**NES**	**p-value**	**FDR**
E2F	V$E2F_Q6	1.51	0	0.08
	V$E2F_Q4	1.53	0	0.086
	V$E2F_Q4_01	1.49	0	0.089
	V$E2F_02	1.53	0	0.093
	V$E2F_Q3_01	1.48	0	0.093
	V$E2F_Q2	1.54	0	0.095
	V$E2F_Q6_01	1.56	0	0.096
	V$E2F_Q3	1.55	0	0.098
E2F1	V$E2F1_Q3	1.58	0	0.087
	V$E2F1_Q6	1.49	0	0.088
	V$E2F1_Q3_01	1.6	0	0.09
	V$E2F1_Q4_01	1.48	0	0.094
	V$E2F1DP1_01	1.53	0	0.089
	V$E2F1DP1RB_01	1.58	0	0.087
	SGCGSSAAA_V$E2F1DP2_01	1.51	0	0.081
	V$E2F1DP2_01	1.53	0	0.09
E2F4	V$E2F4DP1_01	1.53	0	0.086
	V$E2F4DP2_01	1.53	0	0.087
E4F1	GTGACGY_V$E4F1_Q6	1.51	0	0.081
	V$E4F1_Q6	1.54	0	0.097
MYC/MAX	V$MYCMAX_02	1.64	0	0.093
	V$MYC_Q2	1.63	0	0.095
	CACGTG_V$MYC_Q2	1.56	0	0.095
	V$MYCMAX_B	1.55	0	0.095
	V$MAX_01	1.45	0	0.097
N MYC	V$NMYC_01	1.59	0	0.084
AP1/ATF/CREB	V$CREB_01	1.51	0	0.081
	V$AP1_Q4	1.5	0.006	0.085
	TGACGTCA_V$ATF3_Q6	1.5	0	0.086
	V$CREB_Q2	1.48	0.004	0.092
	V$ATF4_Q2	1.53	0	0.093
	V$CREBP1CJUN_01	1.47	0	0.093
	V$ATF_B	1.47	0.004	0.093

NFY	V$NFY_01	1.53	0.002	0.092
	GATTGGY_V$NFY_Q6_01	1.53	0	0.095
	V$NFY_C	1.51	0.004	0.08
YY1	V$YY1_01	1.52	0	0.081
	V$YY1_Q6	1.47	0	0.093
USF	V$USF_C	1.71	0	0.058
	V$USF2_Q6	1.64	0	0.099
	V$USF_Q6_01	1.45	0	0.099
ERR	TGACCTY_V$ERR1_Q2	1.71	0	0.066
	V$ERR1_Q2	1.73	0	0.072
MAFG	V$TCF11MAFG_01	1.73	0	0.061
	TGANNYRGCA_V$TCF11MAFG_01	1.51	0	0.081
SF1	TGACCTTG_V$SF1_Q6	1.8	0	0.073
	V$SF1_Q6	1.59	0.004	0.085
SP1	GGGCGGR_V$SP1_Q6	1.51	0	0.078
	V$SP1_Q6	1.48	0	0.094
HIF1	V$HIF1_Q5	1.59	0	0.084
	V$HIF1_Q3	1.6	0	0.094
HSF	RGAANNTTC_V$HSF1_01	1.5	0	0.086
	TTCNRGNNNNTTC_V$HSF_Q6	1.54	0	0.092
	V$HSF1_01	1.47	0.004	0.092
	V$HSF2_01	1.55	0	0.098
NFAT	V$NFAT_Q4_01	1.53	0	0.085
	TGGAAA_V$NFAT_Q4_01	1.47	0	0.092
HNF4	V$HNF4ALPHA_Q6	1.53	0	0.093
	V$HNF4_01	1.54	0.004	0.093
NRF2	V$NRF2_Q4	1.73	0	0.084
COUP	V$COUP_01	1.71	0	0.053
STAT6	V$STAT6_01	1.65	0	0.099
EFC	V$EFC_Q6	1.61	0	0.096
PPARG	V$PPARG_01	1.59	0	0.081
ER	V$ER_Q6_02	1.58	0	0.088
ZF5	V$ZF5_B	1.57	0	0.094
ALPHACP1	V$ALPHACP1_01	1.54	0.002	0.095
LEF1	V$LEF1_Q2	1.54	0	0.096
SOX9	CATTGTYY_V$SOX9_B1	1.54	0	0.096
GABP	MGGAAGTG_V$GABP_B	1.52	0	0.084
GRE	V$GRE_C	1.49	0.008	0.088
NFE2	V$NFE2_01	1.48	0	0.09
CEBPB	TTGCWCAAY_V$CEBPB_02	1.48	0.008	0.092
PAX3	CGTSACG_V$PAX3_B	1.44	0.008	0.099
Enriched in memory B cells				
None				
CD30$^+$ extrafollicular (EF) B cells vs plasma cells ($p < 0.01$, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
Factor	**Gene set**	**NES**	**p-value**	**FDR**
E2F	V$E2F_01	1.82	0	0.073
	V$E2F_Q3	1.63	0	0.051
	V$E2F_03	1.6	0	0.059
	V$E2F_Q6_01	1.56	0	0.079
	V$E2F_Q3_01	1.55	0	0.08
	V$E2F_Q2	1.54	0	0.082
	V$E2F_Q6	1.53	0	0.082
	V$E2F_Q4	1.53	0	0.082
	V$E2F_Q4_01	1.52	0	0.083
	V$E2F_02	1.5	0	0.093
E2F1	V$E2F1_Q3	1.62	0	0.053
	V$E2F1DP1RB_01	1.55	0	0.085

	V$E2F1_Q4_01	1.54	0	0.083
	V$E2F1_Q6	1.49	0	0.091
	V$E2F1_Q6_01	1.49	0	0.091
	SGCGSSAAA_V$E2F1DP2_01	1.52	0	0.084
	V$E2F1_Q4	1.51	0	0.086
	V$E2F1DP2_01	1.5	0	0.09
	V$E2F1DP1_01	1.5	0	0.091
E2F4	V$E2F4DP2_01	1.5	0	0.088
	V$E2F4DP1_01	1.5	0	0.09
MYC	V$MYCMAX_02	1.68	0	0.052
	V$MYCMAX_01	1.63	0	0.049
	V$MYCMAX_B	1.59	0	0.069
	V$MYC_Q2	1.58	0	0.066
	CACGTG_V$MYC_Q2	1.5	0	0.091
N MYC	V$NMYC_01	1.58	0	0.065
SF1	TGACCTTG_V$SF1_Q6	1.76	0	0.062
	V$SF1_Q6	1.57	0.002	0.076
HIF1	V$HIF1_Q3	1.71	0	0.057
	V$HIF1_Q5	1.65	0	0.043
DR1/COUP	V$DR1_Q3	1.72	0	0.075
	V$COUP_01	1.7	0	0.052
	V$COUP_DR1_Q6	1.6	0	0.06
USF	V$USF_C	1.69	0	0.055
	V$USF2_Q6	1.52	0	0.086
	V$USF_01	1.47	0	0.092
PPAR	V$PPAR_DR1_Q2	1.68	0	0.056
	V$PPARG_01	1.65	0	0.045
ERR1	TGACCTY_V$ERR1_Q2	1.67	0	0.045
	V$ERR1_Q2	1.67	0	0.052
PAX6	V$PAX6_01	1.67	0	0.054
SP1	V$SP1_Q4_01	1.66	0	0.044
	V$SP1_Q6	1.65	0	0.045
	GGGCGGR_V$SP1_Q6	1.48	0	0.09
HSF	TTCNRGNNNNTTC_V$HSF_Q6	1.62	0	0.051
	V$HSF1_01	1.49	0	0.09
	V$HSF2_01	1.49	0	0.092
NFY	V$NFY_C	1.52	0	0.084
	V$NFY_Q6_01	1.48	0	0.091
	GATTGGY_V$NFY_Q6_01	1.46	0.008	0.099
NERF	V$NERF_Q2	1.59	0	0.065
CEBPB	TTGCWCAAY_V$CEBPB_02	1.56	0	0.078
HNF4ALPHA	V$HNF4ALPHA_Q6	1.54	0	0.082
GATA1	V$GATA1_01	1.54	0.006	0.083
ARNT	V$ARNT_01	1.53	0	0.083
SREBP1	V$SREBP1_02	1.53	0	0.084
SOX9	CATTGTYY_V$SOX9_B1	1.53	0	0.085
NRF2	V$NRF2_Q4	1.48	0.006	0.089
TEF1	V$TEF1_Q6	1.48	0.006	0.092
NRF1	V$NRF1_Q6	1.47	0	0.092
ER	V$ER_Q6_02	1.47	0.006	0.092
TCF11MAFG	V$TCF11MAFG_01	1.46	0	0.094
Enriched in plasma cells				
None				

GSEAs of CD30$^+$ and conventional B cells using canonical pathway collection (c2cp; MSigDBv4).

CD30$^+$ GC B cells vs CD30$^+$ extrafollicular (EF) B cells ($p < 0.01$, FDR < 0.1)				
Enriched in CD30$^+$ GC B cells				
None				
Enriched in CD30$^+$ EF B cells				
	Gene set	**NES**	**p-value**	**FDR**
G-protein coupled receptor	REACTOME_GPCR_LIGAND_BINDING	-2	0	0.009
	REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	-1.82	0	0.041
	REACTOME_SIGNALING_BY_GPCR	-1.78	0	0.042
	ST_GA13_PATHWAY	-1.73	0	0.06
	REACTOME_GPCR_DOWNSTREAM_SIGNALING	-1.71	0	0.071
NFKB / MAPK	PID_CD40_PATHWAY	-1.77	0	0.04
	ST_JNK_MAPK_PATHWAY	-1.69	0.008	0.078
	REACTOME_ERKS_ARE_INACTIVATED	-1.67	0	0.082
	BIOCARTA_TNFR2_PATHWAY	-1.66	0.006	0.078
	REACTOME_ERK_MAPK_TARGETS	-1.65	0	0.078
	REACTOME_NFKB_AND_MAP_KINASES_ACTIVATION_MEDIATED_BY_TLR4_SIGNALING_REPERTOIRE	-1.65	0	0.079
	ST_ERK1_ERK2_MAPK_PATHWAY	-1.64	0	0.083
	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	-1.63	0	0.084
	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	-1.64	0	0.083
	REACTOME_TRAF6_MEDIATED_INDUCTION_OF_NFKB_AND_MAP_KINASES_UPON_TLR7_8_OR_9_ACTIVATION	-1.61	0	0.095
TLR	BIOCARTA_STRESS_PATHWAY	-1.62	0.008	0.092
	KEGG_TOLL_LIKE_RECEPTOR_SIGNALING_PATHWAY	-1.78	0	0.041
	REACTOME_ACTIVATED_TLR4_SIGNALLING	-1.69	0	0.078
	REACTOME_TRIF_MEDIATED_TLR3_SIGNALING	-1.64	0	0.085
	REACTOME_TOLL_RECEPTOR_CASCADES	-1.63	0	0.084
	REACTOME_MYD88_MAL_CASCADE_INITIATED_ON_PLASMA_MEMBRANE	-1.63	0	0.086
Akt	REACTOME_AKT_PHOSPHORYLATES_TARGETS_IN_THE_CYTOSOL	-1.9	0	0.022
	BIOCARTA_GLEEVEC_PATHWAY	-1.69	0	0.075
	REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	-1.64	0.006	0.083
Pattern recognition	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	-1.82	0.008	0.039
	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	-1.72	0	0.061
Chemokine	KEGG_CHEMOKINE_SIGNALING_PATHWAY	-1.74	0	0.049
Cytokine	KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACTION	-1.64	0	0.084
	SA_MMP_CYTOKINE_CONNECTION	-1.61	0	0.097
Interferon	REACTOME_INTERFERON_SIGNALING	-1.63	0	0.085
innate immune system	REACTOME_INNATE_IMMUNE_SYSTEM	-1.66	0	0.083
Rho signaling	PID_RHOA_PATHWAY	-1.65	0.008	0.079
GPI biosynthesis	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	-1.63	0.008	0.086
ECM	KEGG_ECM_RECEPTOR_INTERACTION	-1.75	0	0.045
NCAM1	REACTOME_NCAM1_INTERACTIONS	-1.66	0.004	0.081
ARF6	PID_ARF6_TRAFFICKINGPATHWAY	-1.65	0	0.078
CXCR3	PID_CXCR3PATHWAY	-1.61	0	0.096
peptide ligand binding	REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTORS	-1.77	0	0.038
apoptosis	KEGG_APOPTOSIS	-1.68	0	0.078
post-translational	REACTOME_O_LINKED_GLYCOSYLATION_OF_MUCINS	-1.9	0	0.028
	REACTOME_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	-1.62	0	0.093
glycan	REACTOME_GLYCOSAMINOGLYCAN_METABOLISM	-1.89	0	0.021
	REACTOME_HS_GAG_DEGRADATION	-1.67	0	0.08
	KEGG_O_GLYCAN_BIOSYNTHESIS	-1.68	0	0.073
transport	REACTOME_METAL_ION_SLC_TRANSPORTERS	-1.63	0	0.084
	REACTOME_ZINC_TRANSPORTERS	-1.62	0	0.089
	REACTOME_TRANSPORT_OF_INORGANIC_CATIONS_ANIONS_AND_AMINO_ACIDS_OLIGOPEPTIDES	-1.61	0.008	0.096
miscellaneous	REACTOME_CLASS_A1_RHODOPSIN_LIKE_RECEPTORS	-1.93	0	0.02
	REACTOME_STRIATED_MUSCLE_CONTRACTION	-1.81	0	0.039
	KEGG_AMYOTROPHIC_LATERAL_SCLEROSIS_ALS	-1.69	0	0.079

	KEGG_DILATED_CARDIOMYOPATHY	-1.7	0	0.08
	REACTOME_KERATAN_SULFATE_KERATIN_METABOLISM	-1.66	0	0.08
CD30$^+$ GC B cells vs conventional GC B cells (p < 0.01, FDR < 0.3)				
Enriched in CD30$^+$ GC B cells				
	Gene set	**NES**	**p-value**	**FDR**
	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	1.97	0	0.092
DNA repair	REACTOME_REPAIR_SYNTHESIS_FOR_GAP_FILLING_BY_DNA_POL_IN_TC_NER	1.4	0.004	0.288
	REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	1.4	0.006	0.29
	REACTOME_DNA_REPAIR	1.38	0.002	0.283
antigen processing	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	1.4	0	0.29
	REACTOME_CLASS_I_MHC_MEDIATED_ANTIGEN_PROCESSING_PRESENTATION	1.38	0	0.282
cell cycle / replication	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	1.4	0	0.293
	REACTOME_AUTODEGRADATION_OF_CDH1_BY_CDH1_APC_C	1.39	0.008	0.284
	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_MITOTIC_PROTEINS	1.37	0.008	0.28
	BIOCARTA_RACCYCD_PATHWAY	1.37	0	0.282
	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	1.37	0.002	0.288
	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	1.36	0.004	0.284
	PID_P53DOWNSTREAMPATHWAY	1.41	0.002	0.297
transcription	REACTOME_TRANSCRIPTION	1.38	0	0.281
	REACTOME_RNA_POL_II_PRE_TRANSCRIPTION_EVENTS	1.35	0.008	0.29
	REACTOME_RNA_POL_II_TRANSCRIPTION	1.34	0.006	0.296
metabolism	KEGG_PYRIMIDINE_METABOLISM	1.41	0.006	0.296
	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	1.38	0.008	0.281
tRNA acylation	REACTOME_TRNA_AMINOACYLATION	1.39	0.006	0.282
Enriched in conventional GC B cells				
None				
CD30$^+$ extrafollicular (EF) B cells vs memory B cells (p < 0.01, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
	Gene set	**NES**	**p-value**	**FDR**
P53	BIOCARTA_P53_PATHWAY	2.02	0	0.02
MTA3	BIOCARTA_MTA3_PATHWAY	1.8	0.006	0.092
ATF2	PID_ATF2_PATHWAY	1.79	0	0.085
metabolism	KEGG_TRYPTOPHAN_METABOLISM	2.08	0	0.015
	KEGG_GLYCEROLIPID_METABOLISM	1.9	0	0.05
	KEGG_ARGININE_AND_PROLINE_METABOLISM	1.91	0	0.053
	REACTOME_GLUCOSE_METABOLISM	1.78	0	0.086
glycolysis	KEGG_GLYCOLYSIS_GLUCONEOGENESIS	1.95	0	0.042
SLC transport	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	1.78	0	0.081
kinesins	REACTOME_KINESINS	1.8	0	0.088
muscle contraction	KEGG_CARDIAC_MUSCLE_CONTRACTION	1.79	0	0.082
Enriched in memory B cells				
None				
CD30$^+$ extrafollicular (EF) B cells vs plasma cells (p < 0.01, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
	Gene set	**NES**	**p-value**	**FDR**
ATF2	PID_ATF2_PATHWAY	2.1	0	0.02
BICARBONATE_RECLAMATION	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	1.97	0	0.067
METABOLISM	KEGG_TRYPTOPHAN_METABOLISM	1.89	0	0.085
S1P_S1P1_PATHWAY	PID_S1P_S1P1_PATHWAY	1.91	0	0.086
Enriched in plasma cells				
None				

GSEAs of CD30$^+$ and conventional B cells using hallmark gene sets (h.all.v5; MSigDBv5).

CD30$^+$ GC B cells vs CD30$^+$ extrafollicular (EF) B cells ($p < 0.01$, FDR < 0.1)

Enriched in CD30$^+$ GC B cells

None

Enriched in CD30$^+$ EF B cells

	Gene set	NES	p-value	FDR
STAT	HALLMARK_IL6_JAK_STAT3_SIGNALING	-1.74	0	0.018
	HALLMARK_IL2_STAT5_SIGNALING	-1.65	0	0.025
IFN	HALLMARK_INTERFERON_ALPHA_RESPONSE	-1.71	0	0.02
	HALLMARK_INTERFERON_GAMMA_RESPONSE	-1.58	0.004	0.031
inflammation	HALLMARK_INFLAMMATORY_RESPONSE	-1.69	0	0.02
EMT	HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	-1.72	0	0.018
RAS	HALLMARK_KRAS_SIGNALING_UP	-1.62	0	0.025
	HALLMARK_ALLOGRAFT_REJECTION	-1.61	0	0.027
NFKB	HALLMARK_TNFA_SIGNALING_VIA_NFKB	-1.57	0	0.032
	HALLMARK_ESTROGEN_RESPONSE_LATE	-1.54	0	0.039
apoptosis	HALLMARK_APOPTOSIS	-1.54	0	0.039
	HALLMARK_HEME_METABOLISM	-1.63	0	0.023
	HALLMARK_MYOGENESIS	-1.55	0	0.036

CD30$^+$ GC B cells vs conventional GC B cells ($p < 0.01$, FDR < 0.1)

Enriched in CD30$^+$ GC B cells

	Gene set	NES	p-value	FDR
cell cycle	HALLMARK_G2M_CHECKPOINT	1.45	0.002	0.064
proliferation	HALLMARK_E2F_TARGETS	1.49	0	0.073
DNA repair	HALLMARK_DNA_REPAIR	1.43	0	0.076
	HALLMARK_UV_RESPONSE_UP	1.56	0	0.083
MYC MYC	HALLMARK_MYC_TARGETS_V1	1.5	0	0.079
	HALLMARK_MYC_TARGETS_V2	1.49	0.004	0.079
	HALLMARK_OXIDATIVE_PHOSPHORYLATION	1.47	0	0.067
	HALLMARK_XENOBIOTIC_METABOLISM	1.71	0	0.078
	HALLMARK_GLYCOLYSIS	1.58	0	0.088
	HALLMARK_ADIPOGENESIS	1.47	0	0.063
	HALLMARK_FATTY_ACID_METABOLISM	1.5	0	0.09
mTORC1	HALLMARK_MTORC1_SIGNALING	1.51	0	0.092

Enriched in conventional GC B cells

None

CD30$^+$ extrafollicular (EF) B cells vs memory B cells ($p < 0.01$, FDR < 0.1)

Enriched in CD30$^+$ EF B cells

	Gene set	NES	p-value	FDR
cell cycle	HALLMARK_G2M_CHECKPOINT	1.46	0	0.055
mitotic spindle	HALLMARK_MITOTIC_SPINDLE	1.5	0.006	0.053
DNA repair	HALLMARK_UV_RESPONSE_UP	1.55	0	0.044
	HALLMARK_DNA_REPAIR	1.39	0	0.066
E2F	HALLMARK_E2F_TARGETS	1.33	0	0.091
MYC	HALLMARK_MYC_TARGETS_V1	1.43	0	0.058
	HALLMARK_CHOLESTEROL_HOMEOSTASIS	1.78	0	0.032
	HALLMARK_ESTROGEN_RESPONSE_LATE	1.77	0	0.019
	HALLMARK_XENOBIOTIC_METABOLISM	1.72	0	0.019
	HALLMARK_GLYCOLYSIS	1.68	0	0.02
	HALLMARK_PANCREAS_BETA_CELLS	1.67	0	0.02
	HALLMARK_ADIPOGENESIS	1.63	0	0.022

	HALLMARK_ANDROGEN_RESPONSE	1.47	0	0.056
	HALLMARK_PEROXISOME	1.46	0	0.051
mTORC1	HALLMARK_MTORC1_SIGNALING	1.46	0	0.049
ROS	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	1.42	0	0.055
	HALLMARK_FATTY_ACID_METABOLISM	1.41	0	0.056
	HALLMARK_OXIDATIVE_PHOSPHORYLATION	1.31	0	0.097
Enriched in memory B cells				
None				
CD30$^+$ extrafollicular (EF) B cells vs plasma cells ($p < 0.01$, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
	Gene set	**NES**	**p-value**	**FDR**
DNA damage/repair	HALLMARK_UV_RESPONSE_UP	1.6	0	0.032
cell cycle	HALLMARK_G2M_CHECKPOINT	1.45	0	0.064
spindle	HALLMARK_MITOTIC_SPINDLE	1.46	0	0.068
E2F	HALLMARK_E2F_TARGETS	1.39	0	0.083
	HALLMARK_GLYCOLYSIS	1.7	0	0.018
	HALLMARK_ESTROGEN_RESPONSE_LATE	1.76	0	0.021
metabolism	HALLMARK_XENOBIOTIC_METABOLISM	1.66	0	0.024
	HALLMARK_ADIPOGENESIS	1.55	0	0.057
STAT	HALLMARK_IL2_STAT5_SIGNALING	1.44	0.004	0.06
ROS	HALLMARK_REACTIVE_OXIGEN_SPECIES_PATHWAY	1.5	0	0.068
	HALLMARK_CHOLESTEROL_HOMEOSTASIS	1.48	0.006	0.069
metabolism	HALLMARK_FATTY_ACID_METABOLISM	1.47	0	0.071
	HALLMARK_PEROXISOME	1.51	0	0.072
mTORC1	HALLMARK_MTORC1_SIGNALING	1.48	0	0.077
Enriched in plasma cells				
None				

NES, normalized enrichment score; FDR, false discovery rate

GSEA of CD30$^+$ extrafollicular B cells versus memory B and plasma cells using a customized collection of experimentally validated JAK/STAT gene sets.

CD30$^+$ extrafollicular (EF) B cells vs memory B cells ($p < 0.01$, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
	Gene set	**NES**	**p-value**	**FDR**
JAK/STAT	BAUS_HL_SHSTAT6_2FC_DN	1.71	0	0.013
	NGO_ABCDLBCL_JAKSIG48	1.59	0	0.036
	BAKER_HEMATOPOIESIS_STAT3_TARGETS	1.56	0	0.036
	LAM_ABC_STAT3IDFF_TOP125	1.43	0	0.072
Enriched in memory B cells				
None				
CD30$^+$ EF B cells vs plasma cells ($p < 0.01$, FDR < 0.1)				
Enriched in CD30$^+$ EF B cells				
	Gene set	**NES**	**p-value**	**FDR**
JAK/STAT	NGO_ABCDLBCL_JAKSIG48	1.79	0	0.005
	BAUS_HL_SHSTAT6_2FC_DN	1.62	0	0.024
	BAKER_HEMATOPOIESIS_STAT3_TARGETS	1.59	0.008	0.023
	HALLMARK_IL2_STAT5_SIGNALING	1.44	0.004	0.036
	LAM_ABC_STAT3IDFF_TOP125	1.42	0	0.039
	STAT3HIGH_ABC_DLBCL_SUBGROUP	1.42	0	0.032
Enriched in plasma cells				
None				

Supplemental Table 5. Genes differentially expressed between conventional GC B cells and CD30$^+$ GC B cells

Higher expression in conventional GC B cells than in CD30$^+$ GC B cells

Probeset ID	FC GC B cells vs CD30+ GC B cells	Gene title	Gene symbol
231093_at	4.9	Fc receptor-like 3	FCRL3
219841_at	4.3	activation-induced cytidine deaminase	AICDA
224838_at	4.2	forkhead box P1	FOXP1
221234_s_at	4.0	BTB and CNC homology 1. basic leucine zipper transcription factor 2	BACH2
219396_s_at	3.9	nei endonuclease VIII-like 1 (E. coli)	NEIL1
225912_at	3.7	tumor protein p53 inducible nuclear protein 1	TP53INP1
209771_x_at	3.7	CD24 molecule	CD24
204446_s_at	3.7	arachidonate 5-lipoxygenase	ALOX5
216379_x_at	3.6	CD24 molecule	CD24
217783_s_at	3.3	yippee-like 5 (Drosophila)	YPEL5
224499_s_at	3.3	activation-induced cytidine deaminase	AICDA
206169_x_at	3.3	zinc finger CCCH-type containing 7B	ZC3H7B
243968_x_at	3.2	Fc receptor-like 1	FCRL1
217853_at	3.1	tensin 3	TNS3
229723_at	3.0	T-cell activation RhoGTPase activating protein	TAGAP
201721_s_at	3.0	lysosomal protein transmembrane 5	LAPTM5

Higher expression in CD30$^+$ GC B cells than conventional GC B cells

Probeset ID	FC GC B cells vs CD30+ GC B cells	Gene title	Gene symbol
202854_at	-3.0	hypoxanthine phosphoribosyltransferase 1	HPRT1
218993_at	-3.0	RNA methyltransferase like 1	RNMTL1
212432_at	-3.0	GrpE-like 1. mitochondrial (E. coli)	GRPEL1
223151_at	-3.0	DCN1. defective in cullin neddylation 1. domain containing 5 (S. cerevisiae)	DCUN1D5
217848_s_at	-3.0	pyrophosphatase (inorganic) 1	PPA1
1555889_a_at	-3.0	cartilage associated protein	CRTAP
208955_at	-3.0	deoxyuridine triphosphatase	DUT
218882_s_at	-3.0	WD repeat domain 3	WDR3
201323_at	-3.0	EBNA1 binding protein 2	EBNA1BP2
220865_s_at	-3.0	prenyl (decaprenyl) diphosphate synthase. subunit 1	PDSS1
203219_s_at	-3.0	adenine phosphoribosyltransferase	APRT
209317_at	-3.0	polymerase (RNA) I polypeptide C. 30kDa	POLR1C
225541_at	-3.0	ribosomal protein L22-like 1	RPL22L1
201938_at	-3.0	cyclin-dependent kinase 2 associated protein 1	CDK2AP1
222163_s_at	-3.0	spermatogenesis associated 5-like 1	SPATA5L1
209971_x_at	-3.0	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	AIMP2
202431_s_at	-3.0	v-myc myelocytomatosis viral oncogene homolog (avian)	MYC
213129_s_at	-3.0	glycine cleavage system protein H (aminomethyl carrier)	GCSH
218594_at	-3.0	HEAT repeat containing 1	HEATR1
235117_at	-3.0	ChaC. cation transport regulator homolog 2 (E. coli)	CHAC2
211615_s_at	-3.0	leucine-rich PPR-motif containing	LRPPRC
203119_at	-3.0	coiled-coil domain containing 86	CCDC86
223032_x_at	-3.0	PRELI domain containing 1	PRELID1
200987_x_at	-3.0	proteasome (prosome. macropain) activator subunit 3 (PA28 gamma; Ki)	PSME3
200039_s_at	-3.0	proteasome (prosome. macropain) subunit. beta type. 2	PSMB2
201391_at	-3.0	TNF receptor-associated protein 1	TRAP1
215438_x_at	-3.0	G1 to S phase transition 1	GSPT1

202309_at	-3.0	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1. methenyltetrahydrofolate cyclohydrolase. formyltetrahydrofolate synthetase	MTHFD1
208972_s_at	-3.0	ATP synthase. H+ transporting. mitochondrial F0 complex. subunit C1 (subunit 9)	ATP5G1
217809_at	-3.1	basic leucine zipper and W2 domains 2	BZW2
200843_s_at	-3.1	glutamyl-prolyl-tRNA synthetase	EPRS
200877_at	-3.1	chaperonin containing TCP1. subunit 4 (delta)	CCT4
200064_at	-3.1	heat shock protein 90kDa alpha (cytosolic). class B member 1	HSP90AB1
201573_s_at	-3.1	eukaryotic translation termination factor 1	ETF1
219162_s_at	-3.1	mitochondrial ribosomal protein L11	MRPL11
213523_at	-3.1	cyclin E1	CCNE1
212110_at	-3.1	solute carrier family 39 (zinc transporter). member 14	SLC39A14
201530_x_at	-3.1	eukaryotic translation initiation factor 4A. isoform 1	EIF4A1
1558152_at	-3.1	hypothetical LOC100131262	LOC100131262
223306_at	-3.1	emopamil binding protein-like	EBPL
218512_at	-3.1	WD repeat domain 12	WDR12
201066_at	-3.1	cytochrome c-1	CYC1
208787_at	-3.1	mitochondrial ribosomal protein L3	MRPL3
201489_at	-3.1	peptidylprolyl isomerase F	PPIF
218188_s_at	-3.1	translocase of inner mitochondrial membrane 13 homolog (yeast)	TIMM13
224932_at	-3.2	coiled-coil-helix-coiled-coil-helix domain containing 10	CHCHD10
204143_s_at	-3.2	enolase superfamily member 1	ENOSF1
204033_at	-3.2	thyroid hormone receptor interactor 13	TRIP13
203622_s_at	-3.2	partner of NOB1 homolog (S. cerevisiae)	PNO1
211969_at	-3.2	heat shock protein 90kDa alpha (cytosolic). class A member 1	HSP90AA1
225036_at	-3.2	translocase of outer mitochondrial membrane 5 homolog (yeast)	TOMM5
203405_at	-3.2	proteasome (prosome. macropain) assembly chaperone 1	PSMG1
201516_at	-3.2	spermidine synthase	SRM
202715_at	-3.2	carbamoyl-phosphate synthetase 2. aspartate transcarbamylase. and dihydroorotase	CAD
201274_at	-3.2	proteasome (prosome. macropain) subunit. alpha type. 5	PSMA5
218213_s_at	-3.2	chromosome 11 open reading frame 10	C11orf10
220651_s_at	-3.2	minichromosome maintenance complex component 10	MCM10
221923_s_at	-3.2	nucleophosmin (nucleolar phosphoprotein B23. numatrin)	NPM1
218558_s_at	-3.2	mitochondrial ribosomal protein L39	MRPL39
211787_s_at	-3.2	eukaryotic translation initiation factor 4A. isoform 1	EIF4A1
217963_s_at	-3.2	nerve growth factor receptor (TNFRSF16) associated protein 1	NGFRAP1
203234_at	-3.3	uridine phosphorylase 1	UPP1
201479_at	-3.3	dyskeratosis congenita 1. dyskerin	DKC1
213302_at	-3.3	phosphoribosylformylglycinamidine synthase	PFAS
224523_s_at	-3.3	chromosome 3 open reading frame 26	C3orf26
234000_s_at	-3.3	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
205909_at	-3.3	polymerase (DNA directed). epsilon 2 (p59 subunit)	POLE2
223413_s_at	-3.3	Ly1 antibody reactive homolog (mouse)	LYAR
218984_at	-3.3	pseudouridylate synthase 7 homolog (S. cerevisiae)	PUS7
208921_s_at	-3.3	sorcin	SRI
227517_s_at	-3.4	growth arrest-specific 5 (non-protein coding)	GAS5
221434_s_at	-3.4	chromosome 14 open reading frame 156	C14orf156
228238_at	-3.4	growth arrest-specific 5 (non-protein coding)	GAS5
200842_s_at	-3.4	glutamyl-prolyl-tRNA synthetase	EPRS
201892_s_at	-3.4	IMP (inosine monophosphate) dehydrogenase 2	IMPDH2
201112_s_at	-3.4	CSE1 chromosome segregation 1-like (yeast)	CSE1L
201013_s_at	-3.4	phosphoribosylaminoimidazole carboxylase. phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
211576_s_at	-3.4	solute carrier family 19 (folate transporter). member 1	SLC19A1

201695_s_at	-3.4	nucleoside phosphorylase	NP
222404_x_at	-3.4	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
210338_s_at	-3.5	heat shock 70kDa protein 8	HSPA8
230656_s_at	-3.5	cirrhosis. autosomal recessive 1A (cirhin)	CIRH1A
212282_at	-3.6	transmembrane protein 97	TMEM97
202246_s_at	-3.6	cyclin-dependent kinase 4	CDK4
209104_s_at	-3.6	NHP2 ribonucleoprotein homolog (yeast)	NHP2
210027_s_at	-3.6	APEX nuclease (multifunctional DNA repair enzyme) 1	APEX1
209302_at	-3.6	polymerase (RNA) II (DNA directed) polypeptide H	POLR2H
212372_at	-3.7	myosin. heavy chain 10. non-muscle	MYH10
208864_s_at	-3.7	thioredoxin	TXN
201144_s_at	-3.8	eukaryotic translation initiation factor 2. subunit 1 alpha. 35kDa	EIF2S1
220358_at	-3.8	basic leucine zipper transcription factor. ATF-like 3	BATF3
224232_s_at	-3.9	PRELI domain containing 1	PRELID1
202345_s_at	-3.9	fatty acid binding protein 5 (psoriasis-associated)	FABP5
201923_at	-3.9	peroxiredoxin 4	PRDX4
224903_at	-3.9	cirrhosis. autosomal recessive 1A (cirhin)	CIRH1A
217871_s_at	-3.9	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF
219117_s_at	-4.0	FK506 binding protein 11. 19 kDa	FKBP11
208910_s_at	-4.1	complement component 1. q subcomponent binding protein	C1QBP
212281_s_at	-4.1	transmembrane protein 97	TMEM97
211968_s_at	-4.1	heat shock protein 90kDa alpha (cytosolic). class A member 1	HSP90AA1
200691_s_at	-4.2	heat shock 70kDa protein 9 (mortalin)	HSPA9
241937_s_at	-4.3	WD repeat domain 4	WDR4
202483_s_at	-4.5	RAN binding protein 1	RANBP1
224870_at	-4.5	KIAA0114	KIAA0114
207861_at	-4.8	chemokine (C-C motif) ligand 22	CCL22
205291_at	-5.2	interleukin 2 receptor. beta	IL2RB
201014_s_at	-5.3	phosphoribosylaminoimidazole carboxylase. phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS

Significantly differentially expressed genes with an at least 3-fold difference in average expression levels are listed.

Supplemental Table 6. Supervised comparison of CD30$^+$ extrafollicular (EF) B cells versus memory B cells

Probesets with higher expression in CD30$^+$ EF B cells

Affymetrix ID	fold up-regulation	Gene name	Gene symbol
209773_s_at	27.2	ribonucleotide reductase M2	RRM2
201890_at	21.6	ribonucleotide reductase M2	RRM2
204026_s_at	17.3	ZW10 interactor	ZWINT
221521_s_at	17.2	GINS complex subunit 2 (Psf2 homolog)	GINS2
224428_s_at	15.7	cell division cycle associated 7	CDCA7
207861_at	15.5	chemokine (C-C motif) ligand 22	CCL22
201930_at	14.2	minichromosome maintenance complex component 6	MCM6
202107_s_at	13.4	minichromosome maintenance complex component 2	MCM2
214710_s_at	13.4	cyclin B1	CCNB1
218039_at	12.3	nucleolar and spindle associated protein 1	NUSAP1
201202_at	12.1	proliferating cell nuclear antigen	PCNA
201739_at	11.9	serum/glucocorticoid regulated kinase 1	SGK1
202503_s_at	11.7	KIAA0101	KIAA0101
201761_at	11.0	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	MTHFD2
201277_s_at	10.9	heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
202589_at	10.0	thymidylate synthetase	TYMS
203358_s_at	9.9	enhancer of zeste homolog 2 (Drosophila)	EZH2
212281_s_at	9.9	transmembrane protein 97	TMEM97
202705_at	9.8	cyclin B2	CCNB2
201013_s_at	9.5	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
241937_s_at	9.5	WD repeat domain 4	WDR4
221923_s_at	9.5	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	NPM1
207165_at	9.4	hyaluronan-mediated motility receptor (RHAMM)	HMMR
213523_at	9.1	cyclin E1	CCNE1
204170_s_at	8.9	CDC28 protein kinase regulatory subunit 2	CKS2
200650_s_at	8.9	lactate dehydrogenase A	LDHA
211969_at	8.7	heat shock protein 90kDa alpha (cytosolic), class A member 1	HSP90AA1
212295_s_at	8.7	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	SLC7A1
223307_at	8.7	cell division cycle associated 3	CDCA3
226905_at	8.7	family with sequence similarity 101, member B	FAM101B
221658_s_at	8.6	interleukin 21 receptor	IL21R
205436_s_at	8.6	H2A histone family, member X	H2AFX
218350_s_at	8.5	geminin, DNA replication inhibitor	GMNN
206052_s_at	8.4	stem-loop binding protein	SLBP
212296_at	8.3	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	PSMD14
206102_at	8.3	GINS complex subunit 1 (Psf1 homolog)	GINS1
217848_s_at	8.0	pyrophosphatase (inorganic) 1	PPA1
208805_at	7.9	proteasome (prosome, macropain) subunit, alpha type, 6	PSMA6
201477_s_at	7.9	ribonucleotide reductase M1	RRM1
201619_at	7.9	peroxiredoxin 3	PRDX3
222404_x_at	7.9	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
234000_s_at	7.8	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
201112_s_at	7.8	CSE1 chromosome segregation 1-like (yeast)	CSE1L
219517_at	7.7	elongation factor RNA polymerase II-like 3 /// serine incorporator 4	ELL3 /// SERINC4
203213_at	7.7	cyclin-dependent kinase 1	CDK1
201672_s_at	7.7	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	USP14
218213_s_at	7.7	chromosome 11 open reading frame 10	C11orf10
213911_s_at	7.6	H2A histone family, member Z	H2AFZ
208079_s_at	7.5	aurora kinase A	AURKA

207332_s_at	7.5	transferrin receptor (p90, CD71)	TFRC
225036_at	7.4	translocase of outer mitochondrial membrane 5 homolog (yeast)	TOMM5
204825_at	7.4	maternal embryonic leucine zipper kinase	MELK
201014_s_at	7.4	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
220358_at	7.3	basic leucine zipper transcription factor, ATF-like 3	BATF3
202345_s_at	7.3	fatty acid binding protein 5 (psoriasis-associated)	FABP5
222606_at	7.2	Zwilch, kinetochore associated, homolog (Drosophila)	ZWILCH
203764_at	7.2	discs, large (Drosophila) homolog-associated protein 5	DLGAP5
212330_at	7.2	transcription factor Dp-1	TFDP1
AFFX-HUMGAPDH/M33197_M_at	7.2	glyceraldehyde-3-phosphate dehydrogenase	GAPDH
218493_at	7.2	small nuclear ribonucleoprotein 25kDa (U11/U12)	SNRNP25
213088_s_at	7.1	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9
219990_at	7.1	E2F transcription factor 8	E2F8
202911_at	7.1	mutS homolog 6 (E. coli)	MSH6
203344_s_at	7.1	retinoblastoma binding protein 8	RBBP8
201144_s_at	7.1	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	EIF2S1
225687_at	7.1	family with sequence similarity 83, member D	FAM83D
212646_at	7.0	raftlin, lipid raft linker 1	RFTN1
205291_at	7.0	interleukin 2 receptor, beta	IL2RB
202854_at	7.0	hypoxanthine phosphoribosyltransferase 1	HPRT1
215171_s_at	7.0	translocase of inner mitochondrial membrane 17 homolog A (yeast)	TIMM17A
200877_at	7.0	chaperonin containing TCP1, subunit 4 (delta)	CCT4
226517_at	7.0	branched chain amino-acid transaminase 1, cytosolic	BCAT1
213453_x_at	6.9	glyceraldehyde-3-phosphate dehydrogenase	GAPDH
220651_s_at	6.9	minichromosome maintenance complex component 10	MCM10
218883_s_at	6.9	MLF1 interacting protein	MLF1IP
203755_at	6.8	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	BUB1B
204962_s_at	6.8	centromere protein A	CENPA
202483_s_at	6.8	RAN binding protein 1	RANBP1
38158_at	6.8	extra spindle pole bodies homolog 1 (S. cerevisiae)	ESPL1
225535_s_at	6.8	translocase of inner mitochondrial membrane 23 homolog (yeast)-like /// translocase of inner mitochondrial membrane 23 homolog (yeast)	LOC10431 /// TIMM23
210766_s_at	6.8	CSE1 chromosome segregation 1-like (yeast)	CSE1L
205909_at	6.7	polymerase (DNA directed), epsilon 2 (p59 subunit)	POLE2
227517_s_at	6.7	growth arrest-specific 5 (non-protein coding)	GAS5
222231_s_at	6.7	leucine rich repeat containing 59	LRRC59
208639_x_at	6.7	protein disulfide isomerase family A, member 6	PDIA6
201274_at	6.7	proteasome (prosome, macropain) subunit, alpha type, 5	PSMA5
208691_at	6.7	transferrin receptor (p90, CD71)	TFRC
212124_at	6.7	zinc finger, MIZ-type containing 1	ZMIZ1
222077_s_at	6.6	Rac GTPase activating protein 1	RACGAP1
200978_at	6.6	malate dehydrogenase 1, NAD (soluble)	MDH1
208836_at	6.6	ATPase, Na+/K+ transporting, beta 3 polypeptide	ATP1B3
207668_x_at	6.6	protein disulfide isomerase family A, member 6	PDIA6
201479_at	6.6	dyskeratosis congenita 1, dyskerin	DKC1
200691_s_at	6.5	heat shock 70kDa protein 9 (mortalin)	HSPA9
218558_s_at	6.5	mitochondrial ribosomal protein L39	MRPL39
205024_s_at	6.5	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51
219836_at	6.5	zinc finger, BED-type containing 2	ZBED2
209053_s_at	6.5	Wolf-Hirschhorn syndrome candidate 1	WHSC1
209408_at	6.5	kinesin family member 2C	KIF2C
206074_s_at	6.5	high mobility group AT-hook 1	HMGA1
201457_x_at	6.4	budding uninhibited by benzimidazoles 3 homolog (yeast)	BUB3
208002_s_at	6.4	acyl-CoA thioesterase 7	ACOT7
208696_at	6.4	chaperonin containing TCP1, subunit 5 (epsilon)	CCT5
203362_s_at	6.4	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1

200068_s_at	6.3	calnexin	CANX
209251_x_at	6.3	tubulin, alpha 1c	TUBA1C
208910_s_at	6.3	complement component 1, q subcomponent binding protein	C1QBP
201111_at	6.3	CSE1 chromosome segregation 1-like (yeast)	CSE1L
201664_at	6.3	structural maintenance of chromosomes 4	SMC4
208808_s_at	6.3	high-mobility group box 2	HMGB2
212282_at	6.3	transmembrane protein 97	TMEM97
201489_at	6.3	peptidylprolyl isomerase F	PPIF
211765_x_at	6.3	peptidylprolyl isomerase A (cyclophilin A)	PPIA
201068_s_at	6.3	proteasome (prosome, macropain) 26S subunit, ATPase, 2	PSMC2
200822_x_at	6.3	triosephosphate isomerase 1	TPI1
208693_s_at	6.2	glycyl-tRNA synthetase	GARS
218662_s_at	6.2	non-SMC condensin I complex, subunit G	NCAPG
203145_at	6.2	sperm associated antigen 5	SPAG5
200039_s_at	6.2	proteasome (prosome, macropain) subunit, beta type, 2	PSMB2
202144_s_at	6.2	adenylosuccinate lyase	ADSL
200807_s_at	6.2	heat shock 60kDa protein 1 (chaperonin)	HSPD1
225655_at	6.2	ubiquitin-like with PHD and ring finger domains 1	UHRF1
224903_at	6.1	cirrhosis, autosomal recessive 1A (cirhin)	CIRH1A
224232_s_at	6.1	PRELI domain containing 1	PRELID1
208638_at	6.1	protein disulfide isomerase family A, member 6	PDIA6
225153_at	6.1	G elongation factor, mitochondrial 1	GFM1
204533_at	6.1	chemokine (C-X-C motif) ligand 10	CXCL10
200030_s_at	6.1	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	SLC25A3
201293_x_at	6.1	peptidylprolyl isomerase A (cyclophilin A)	PPIA
219918_s_at	6.1	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	ASPM
208787_at	6.1	mitochondrial ribosomal protein L3	MRPL3
223151_at	6.0	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	DCUN1D5
218984_at	6.0	pseudouridylate synthase 7 homolog (S. cerevisiae)	PUS7
209610_s_at	6.0	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	SLC1A4
39729_at	6.0	peroxiredoxin 2	PRDX2
208955_at	6.0	deoxyuridine triphosphatase	DUT
209104_s_at	6.0	NHP2 ribonucleoprotein homolog (yeast)	NHP2
218585_s_at	6.0	denticleless homolog (Drosophila)	DTL
223100_s_at	6.0	nudix (nucleoside diphosphate linked moiety X)-type motif 5	NUDT5
218768_at	5.9	nucleoporin 107kDa	NUP107
201892_s_at	5.9	IMP (inosine 5'-monophosphate) dehydrogenase 2	IMPDH2
214214_s_at	5.9	complement component 1, q subcomponent binding protein	C1QBP
204033_at	5.9	thyroid hormone receptor interactor 13	TRIP13
201589_at	5.9	structural maintenance of chromosomes 1A	SMC1A
208864_s_at	5.9	thioredoxin	TXN
201938_at	5.9	cyclin-dependent kinase 2 associated protein 1	CDK2AP1
209397_at	5.9	malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2
211750_x_at	5.9	tubulin, alpha 1c	TUBA1C
218188_s_at	5.9	translocase of inner mitochondrial membrane 13 homolog (yeast)	TIMM13
212661_x_at	5.9	peptidylprolyl isomerase A (cyclophilin A)	PPIA
202727_s_at	5.9	interferon gamma receptor 1	IFNGR1
200783_s_at	5.9	stathmin 1	STMN1
218542_at	5.9	centrosomal protein 55kDa	CEP55
202824_s_at	5.8	transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C)	TCEB1
209317_at	5.8	polymerase (RNA) I polypeptide C, 30kDa	POLR1C
202244_at	5.8	proteasome (prosome, macropain) subunit, beta type, 4	PSMB4
208921_s_at	5.8	sorcin	SRI
202095_s_at	5.8	baculoviral IAP repeat-containing 5	BIRC5
213092_x_at	5.8	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9

213655_at	5.8	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	YWHAE
223032_x_at	5.8	PRELI domain containing 1	PRELID1
200750_s_at	5.8	RAN, member RAS oncogene family	RAN
213007_at	5.8	Fanconi anemia, complementation group I	FANCI
200996_at	5.8	ARP3 actin-related protein 3 homolog (yeast)	ACTR3
225340_s_at	5.7	cell cycle associated protein 1	CAPRIN1
218009_s_at	5.7	protein regulator of cytokinesis 1	PRC1
217809_at	5.7	basic leucine zipper and W2 domains 2	BZW2
211075_s_at	5.7	CD47 molecule	CD47
200873_s_at	5.7	chaperonin containing TCP1, subunit 8 (theta)	CCT8
202567_at	5.7	small nuclear ribonucleoprotein D3 polypeptide 18kDa	SNRPD3
211755_s_at	5.7	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit B1	ATP5F1
218477_at	5.7	transmembrane protein 14A	TMEM14A
205644_s_at	5.6	small nuclear ribonucleoprotein polypeptide G	SNRPG
229437_at	5.6	MIR155 host gene (non-protein coding)	MIR155HG
200876_s_at	5.6	proteasome (prosome, macropain) subunit, beta type, 1	PSMB1
204092_s_at	5.6	aurora kinase A	AURKA
212264_s_at	5.6	wings apart-like homolog (Drosophila)	WAPAL
218622_at	5.6	nucleoporin 37kDa	NUP37
213011_s_at	5.6	triosephosphate isomerase 1	TPI1
219841_at	5.6	activation-induced cytidine deaminase	AICDA
200723_s_at	5.6	cell cycle associated protein 1	CAPRIN1
1553984_s_at	5.6	deoxythymidylate kinase (thymidylate kinase)	DTYMK
218357_s_at	5.6	translocase of inner mitochondrial membrane 8 homolog B (yeast)	TIMM8B
217871_s_at	5.6	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	MIF
201584_s_at	5.5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	DDX39
203209_at	5.5	replication factor C (activator 1) 5, 36.5kDa	RFC5
203290_at	5.5	major histocompatibility complex, class II, DQ alpha 1	HLA-DQA1
201322_at	5.5	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	ATP5B
208909_at	5.5	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	UQCRFS1
212639_x_at	5.5	tubulin, alpha 1b	TUBA1B
206790_s_at	5.5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	NDUFB1
200853_at	5.5	H2A histone family, member Z	H2AFZ
201947_s_at	5.5	chaperonin containing TCP1, subunit 2 (beta)	CCT2
201030_x_at	5.5	lactate dehydrogenase B	LDHB
202097_at	5.5	nucleoporin 153kDa	NUP153
227141_at	5.5	tRNA-yW synthesizing protein 3 homolog (S. cerevisiae)	TYW3
203554_x_at	5.5	pituitary tumor-transforming 1	PTTG1
217907_at	5.5	mitochondrial ribosomal protein L18	MRPL18
211762_s_at	5.4	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	KPNA2
208901_s_at	5.4	topoisomerase (DNA) I	TOP1
225413_at	5.4	up-regulated during skeletal muscle growth 5 homolog (mouse)	USMG5
224867_at	5.4	chromosome 1 open reading frame 151	C1orf151
204146_at	5.4	RAD51 associated protein 1	RAD51AP1
215691_x_at	5.4	heat shock protein family B (small), member 11	HSPB11
209473_at	5.4	ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1
215227_x_at	5.4	acid phosphatase 1, soluble	ACP1
202520_s_at	5.4	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	MLH1
200611_s_at	5.4	WD repeat domain 1	WDR1
213646_x_at	5.4	tubulin, alpha 1b	TUBA1B
219449_s_at	5.4	transmembrane protein 70	TMEM70
212581_x_at	5.4	glyceraldehyde-3-phosphate dehydrogenase	GAPDH
203406_at	5.4	microfibrillar-associated protein 1	MFAP1
208821_at	5.4	small nuclear ribonucleoprotein polypeptides B and B1	SNRPB
213302_at	5.3	phosphoribosylformylglycinamidine synthase	PFAS
217834_s_at	5.3	synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP

202961_s_at	5.3	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit F2	ATP5J2
205394_at	5.3	CHK1 checkpoint homolog (S. pombe)	CHEK1
201569_s_at	5.3	sorting and assembly machinery component 50 homolog (S. cerevisiae)	SAMM50
207168_s_at	5.3	H2A histone family, member Y	H2AFY
211787_s_at	5.3	eukaryotic translation initiation factor 4A1	EIF4A1
201472_at	5.3	von Hippel-Lindau binding protein 1	VBP1
225541_at	5.3	ribosomal protein L22-like 1	RPL22L1
211933_s_at	5.3	heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	HNRNPA3 /// HNRNPA3P1
218594_at	5.3	HEAT repeat containing 1	HEATR1
1559946_s_at	5.3	RuvB-like 2 (E. coli)	RUVBL2
220990_s_at	5.3	microRNA 21 /// transmembrane protein 49	MIR21 /// TMEM49
204639_at	5.3	adenosine deaminase	ADA
202870_s_at	5.3	cell division cycle 20 homolog (S. cerevisiae)	CDC20
201231_s_at	5.3	enolase 1, (alpha)	ENO1
218992_at	5.3	chromosome 9 open reading frame 46	C9orf46
200792_at	5.3	X-ray repair complementing defective repair in Chinese hamster cells 6	XRCC6
223556_at	5.3	helicase, lymphoid-specific	HELLS
219306_at	5.3	kinesin family member 15	KIF15
202413_s_at	5.2	ubiquitin specific peptidase 1	USP1
201066_at	5.2	cytochrome c-1	CYC1
212110_at	5.2	solute carrier family 39 (zinc transporter), member 14	SLC39A14
211968_s_at	5.2	heat shock protein 90kDa alpha (cytosolic), class A member 1	HSP90AA1
208778_s_at	5.2	t-complex 1	TCP1
224654_at	5.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	DDX21
226242_at	5.2	chromosome 1 open reading frame 131	C1orf131
218882_s_at	5.2	WD repeat domain 3	WDR3
203721_s_at	5.2	UTP18, small subunit (SSU) processome component, homolog (yeast)	UTP18
201528_at	5.2	replication protein A1, 70kDa	RPA1
211378_x_at	5.2	peptidylprolyl isomerase A (cyclophilin A)	PPIA
201196_s_at	5.2	adenosylmethionine decarboxylase 1	AMD1
201241_at	5.2	DEAD (Asp-Glu-Ala-Asp) box polypeptide 1	DDX1
201114_x_at	5.2	proteasome (prosome, macropain) subunit, alpha type, 7	PSMA7
201090_x_at	5.2	tubulin, alpha 1b	TUBA1B
222464_s_at	5.2	chromosome 10 open reading frame 119	C10orf119
225849_s_at	5.1	SFT2 domain containing 1	SFT2D1
204493_at	5.1	BH3 interacting domain death agonist	BID
214141_x_at	5.1	splicing factor, arginine/serine-rich 7, 35kDa	SFRS7
212021_s_at	5.1	antigen identified by monoclonal antibody Ki-67	MKI67
224523_s_at	5.1	chromosome 3 open reading frame 26	C3orf26
200790_at	5.1	ornithine decarboxylase 1	ODC1
225520_at	5.1	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	MTHFD1L
223334_at	5.1	transmembrane protein 126A	TMEM126A
208640_at	5.0	ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)	RAC1
204767_s_at	5.0	flap structure-specific endonuclease 1	FEN1
227211_at	5.0	PHD finger protein 19	PHF19
211954_s_at	5.0	importin 5	IPO5
208103_s_at	5.0	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	ANP32E
223413_s_at	5.0	Ly1 antibody reactive homolog (mouse)	LYAR
200818_at	5.0	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	ATP5O
201459_at	5.0	RuvB-like 2 (E. coli)	RUVBL2
202428_x_at	5.0	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein)	DBI
200708_at	5.0	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2)	GOT2

209971_x_at	5.0	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	AIMP2
211072_x_at	5.0	tubulin, alpha 1b	TUBA1B
210250_x_at	5.0	adenylosuccinate lyase	ADSL
219148_at	5.0	PDZ binding kinase	PBK
226296_s_at	5.0	mitochondrial ribosomal protein S15	MRPS15
200843_s_at	5.0	glutamyl-prolyl-tRNA synthetase	EPRS
217958_at	5.0	trafficking protein particle complex 4	TRAPPC4
204744_s_at	5.0	isoleucyl-tRNA synthetase	IARS
209025_s_at	5.0	synaptotagmin binding, cytoplasmic RNA interacting protein	SYNCRIP
209482_at	5.0	processing of precursor 7, ribonuclease P/MRP subunit (S. cerevisiae)	POP7
230326_s_at	5.0	chromosome 11 open reading frame 73	C11orf73
204240_s_at	5.0	structural maintenance of chromosomes 2	SMC2
202243_s_at	5.0	proteasome (prosome, macropain) subunit, beta type, 4	PSMB4
213129_s_at	5.0	glycine cleavage system protein H (aminomethyl carrier) /// glycine cleavage system protein H pseudogene	GCSH /// LOC100329108
201323_at	5.0	EBNA1 binding protein 2	EBNA1BP2
224610_at	5.0	small nucleolar RNA host gene 1 (non-protein coding)	SNHG1

Probesets with higher expression in memory B cells

Affymetrix ID	fold up-regulation	Gene name	Gene symbol
204446_s_at	-11.3	arachidonate 5-lipoxygenase	ALOX5
214414_x_at	-9.0	hemoglobin. alpha 1 /// hemoglobin. alpha 2	HBA1 /// HBA2
206169_x_at	-6.2	zinc finger CCCH-type containing 7B	ZC3H7B
230245_s_at	-5.0	hypothetical LOC283663	LOC283663
201010_s_at	-4.8	thioredoxin interacting protein	TXNIP
214715_x_at	-4.7	zinc finger protein 160	ZNF160
211696_x_at	-4.5	hemoglobin. beta	HBB
214594_x_at	-4.5	ATPase. aminophospholipid transporter. class I. type 8B. member 1	ATP8B1
206792_x_at	-4.5	phosphodiesterase 4C. cAMP-specific (phosphodiesterase E1 dunce homolog. Drosophila)	PDE4C
234762_x_at	-4.2	Neurolysin (metallopeptidase M3 family)	NLN
232215_x_at	-4.2	proline rich 11	PRR11
223697_x_at	-4.1	chromosome 9 open reading frame 64	C9orf64
220796_x_at	-4.1	solute carrier family 35. member E1	SLC35E1
224667_x_at	-3.8	anaphase promoting complex subunit 16	ANAPC16
234981_x_at	-3.8	carboxymethylenebutenolidase homolog (Pseudomonas)	CMBL
236715_x_at	-3.8	uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA
220071_x_at	-3.7	HAUS augmin-like complex. subunit 2	HAUS2
215404_x_at	-3.7	fibroblast growth factor receptor 1	FGFR1
237475_x_at	-3.7	coiled-coil domain containing 152	CCDC152
230983_at	-3.6	family with sequence similarity 129. member C	FAM129C
215179_x_at	-3.6	Placental growth factor	PGF
221601_s_at	-3.6	Fas apoptotic inhibitory molecule 3	FAIM3
215600_x_at	-3.6	F-box and WD repeat domain containing 12	FBXW12
205370_x_at	-3.5	dihydrolipoamide branched chain transacylase E2	DBT
215208_x_at	-3.5	Ribosomal protein L35a	RPL35A
208137_x_at	-3.5	zinc finger protein 611	ZNF611
233056_x_at	-3.5	discs. large (Drosophila) homolog-associated protein 4	DLGAP4
233775_x_at	-3.4	Hypothetical protein LOC100289333	LOC100289333
212827_at	-3.4	immunoglobulin heavy constant mu	IGHM
226062_x_at	-3.4	family with sequence similarity 63. member A	FAM63A
239748_x_at	-3.4	OCIA domain containing 1	OCIAD1
242578_x_at	-3.3	Solute carrier family 22 (extraneuronal monoamine transporter).	SLC22A3

		member 3	
219392_x_at	-3.3	proline rich 11	PRR11
1566480_x_at	-3.3	Chromosome 17 open reading frame 104	C17orf104
222252_x_at	-3.3	ubiquilin 4	UBQLN4
215978_x_at	-3.3	zinc finger protein 721	ZNF721
217807_s_at	-3.3	glioma tumor suppressor candidate region gene 2	GLTSCR2
222557_at	-3.3	stathmin-like 3	STMN3
215588_x_at	-3.2	RIO kinase 3 (yeast)	RIOK3
242608_x_at	-3.2	Family with sequence similarity 161. member B	FAM161B
209771_x_at	-3.1	CD24 molecule	CD24
208763_s_at	-3.1	TSC22 domain family. member 3	TSC22D3
231886_at	-3.1	similar to hCG1739109	LOC100134822
216379_x_at	-3.1	CD24 molecule	CD24
201041_s_at	-3.0	dual specificity phosphatase 1	DUSP1
218155_x_at	-3.0	TSR1. 20S rRNA accumulation. homolog (S. cerevisiae)	TSR1

Supplemental Table 7. Supervised comparison of CD30$^+$ extrafollicular (EF) B cells versus plasma cells

Probesets with higher expression in CD30$^+$ EF B cells

Affymetrix ID	FC_CD30_EF B/PC cells	Gene Name	Gene Symbol
209773_s_at	15.1	ribonucleotide reductase M2	RRM2
207861_at	14.1	chemokine (C-C motif) ligand 22	CCL22
221521_s_at	13.9	GINS complex subunit 2 (Psf2 homolog)	GINS2
202107_s_at	13.1	minichromosome maintenance complex component 2	MCM2
224428_s_at	12.9	cell division cycle associated 7	CDCA7
201890_at	11.7	ribonucleotide reductase M2	RRM2
204026_s_at	10.7	ZW10 interactor	ZWINT
202503_s_at	10.3	KIAA0101	KIAA0101
201930_at	10.2	minichromosome maintenance complex component 6	MCM6
200934_at	9.4	DEK oncogene	DEK
214710_s_at	9.4	cyclin B1	CCNB1
201202_at	9.3	proliferating cell nuclear antigen	PCNA
212281_s_at	9.2	transmembrane protein 97	TMEM97
219014_at	9.1	placenta-specific 8	PLAC8
202589_at	8.9	thymidylate synthetase	TYMS
213523_at	8.2	cyclin E1	CCNE1
206102_at	8.1	GINS complex subunit 1 (Psf1 homolog)	GINS1
211969_at	8.1	heat shock protein 90kDa alpha (cytosolic), class A member 1	HSP90AA1
201277_s_at	8.1	heterogeneous nuclear ribonucleoprotein A/B	HNRNPAB
218493_at	8.0	small nuclear ribonucleoprotein 25kDa (U11/U12)	SNRNP25
202854_at	7.8	hypoxanthine phosphoribosyltransferase 1	HPRT1
201112_s_at	7.6	CSE1 chromosome segregation 1-like (yeast)	CSE1L
214097_at	7.6	ribosomal protein S21	RPS21
203290_at	7.6	major histocompatibility complex, class II, DQ alpha 1	HLA-DQA1
203358_s_at	7.4	enhancer of zeste homolog 2 (Drosophila)	EZH2
217809_at	7.4	basic leucine zipper and W2 domains 2	BZW2
211765_x_at	7.4	peptidylprolyl isomerase A (cyclophilin A)	PPIA
218558_s_at	7.4	mitochondrial ribosomal protein L39	MRPL39
218039_at	7.2	nucleolar and spindle associated protein 1	NUSAP1
202345_s_at	7.2	fatty acid binding protein 5 (psoriasis-associated)	FABP5
205909_at	7.2	polymerase (DNA directed), epsilon 2 (p59 subunit)	POLE2
216237_s_at	7.2	minichromosome maintenance complex component 5	MCM5
228056_s_at	7.2	napsin B aspartic peptidase pseudogene	NAPSB
241937_s_at	7.2	WD repeat domain 4	WDR4
208691_at	7.1	transferrin receptor (p90, CD71)	TFRC
220358_at	7.1	basic leucine zipper transcription factor, ATF-like 3	BATF3
201293_x_at	7.0	peptidylprolyl isomerase A (cyclophilin A)	PPIA
209104_s_at	7.0	NHP2 ribonucleoprotein homolog (yeast)	NHP2
202705_at	7.0	cyclin B2	CCNB2
207332_s_at	7.0	transferrin receptor (p90, CD71)	TFRC
208696_at	6.9	chaperonin containing TCP1, subunit 5 (epsilon)	CCT5
204825_at	6.9	maternal embryonic leucine zipper kinase	MELK
226517_at	6.8	branched chain amino-acid transaminase 1, cytosolic	BCAT1
212661_x_at	6.8	peptidylprolyl isomerase A (cyclophilin A)	PPIA
222606_at	6.7	Zwilch, kinetochore associated, homolog (Drosophila)	ZWILCH
221923_s_at	6.7	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	NPM1
218883_s_at	6.6	MLF1 interacting protein	MLF1IP
220651_s_at	6.5	minichromosome maintenance complex component 10	MCM10
201892_s_at	6.5	IMP (inosine 5'-monophosphate) dehydrogenase 2	IMPDH2
208002_s_at	6.5	acyl-CoA thioesterase 7	ACOT7
218768_at	6.4	nucleoporin 107kDa	NUP107

210766_s_at	6.4	CSE1 chromosome segregation 1-like (yeast)	CSE1L
201477_s_at	6.4	ribonucleotide reductase M1	RRM1
242560_at	6.4	Fanconi anemia, complementation group D2	FANCD2
202727_s_at	6.3	interferon gamma receptor 1	IFNGR1
219990_at	6.3	E2F transcription factor 8	E2F8
201013_s_at	6.3	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
207165_at	6.3	hyaluronan-mediated motility receptor (RHAMM)	HMMR
212330_at	6.3	transcription factor Dp-1	TFDP1
205291_at	6.3	interleukin 2 receptor, beta	IL2RB
225687_at	6.2	family with sequence similarity 83, member D	FAM83D
224903_at	6.2	cirrhosis, autosomal recessive 1A (cirhin)	CIRH1A
208955_at	6.2	deoxyuridine triphosphatase	DUT
226905_at	6.2	family with sequence similarity 101, member B	FAM101B
212282_at	6.2	transmembrane protein 97	TMEM97
208910_s_at	6.2	complement component 1, q subcomponent binding protein	C1QBP
208821_at	6.2	small nuclear ribonucleoprotein polypeptides B and B1	SNRPB
201014_s_at	6.2	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
200877_at	6.2	chaperonin containing TCP1, subunit 4 (delta)	CCT4
206052_s_at	6.1	stem-loop binding protein	SLBP
203764_at	6.1	discs, large (Drosophila) homolog-associated protein 5	DLGAP5
227517_s_at	6.1	growth arrest-specific 5 (non-protein coding)	GAS5
208808_s_at	6.1	high-mobility group box 2	HMGB2
208775_at	6.1	exportin 1 (CRM1 homolog, yeast)	XPO1
38158_at	6.1	extra spindle pole bodies homolog 1 (S. cerevisiae)	ESPL1
204962_s_at	6.0	centromere protein A	CENPA
230110_at	6.0	mucolipin 2	MCOLN2
234000_s_at	6.0	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
222404_x_at	6.0	protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
205436_s_at	5.9	H2A histone family, member X	H2AFX
229437_at	5.9	MIR155 host gene (non-protein coding)	MIR155HG
213088_s_at	5.8	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9
218585_s_at	5.8	denticleless homolog (Drosophila)	DTL
200691_s_at	5.8	heat shock 70kDa protein 9 (mortalin)	HSPA9
218350_s_at	5.8	geminin, DNA replication inhibitor	GMNN
202483_s_at	5.8	RAN binding protein 1	RANBP1
201111_at	5.8	CSE1 chromosome segregation 1-like (yeast)	CSE1L
203362_s_at	5.8	MAD2 mitotic arrest deficient-like 1 (yeast)	MAD2L1
204023_at	5.8	replication factor C (activator 1) 4, 37kDa	RFC4
218984_at	5.8	pseudouridylate synthase 7 homolog (S. cerevisiae)	PUS7
223413_s_at	5.7	Ly1 antibody reactive homolog (mouse)	LYAR
201144_s_at	5.7	eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa	EIF2S1
223307_at	5.7	cell division cycle associated 3	CDCA3
218662_s_at	5.7	non-SMC condensin I complex, subunit G	NCAPG
229353_s_at	5.7	nuclear casein kinase and cyclin-dependent kinase substrate 1	NUCKS1
217388_s_at	5.7	kynureninase (L-kynurenine hydrolase)	KYNU
204533_at	5.7	chemokine (C-X-C motif) ligand 10	CXCL10
219306_at	5.7	kinesin family member 15	KIF15
222077_s_at	5.7	Rac GTPase activating protein 1	RACGAP1
202911_at	5.7	mutS homolog 6 (E. coli)	MSH6
211075_s_at	5.7	CD47 molecule	CD47
218542_at	5.7	centrosomal protein 55kDa	CEP55
201584_s_at	5.7	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39	DDX39
214141_x_at	5.6	splicing factor, arginine/serine-rich 7, 35kDa	SFRS7
204033_at	5.6	thyroid hormone receptor interactor 13	TRIP13
215001_s_at	5.6	glutamate-ammonia ligase	GLUL
201479_at	5.6	dyskeratosis congenita 1, dyskerin	DKC1
228055_at	5.6	napsin B aspartic peptidase pseudogene	NAPSB

218069_at	5.6	dCTP pyrophosphatase 1	DCTPP1
211378_x_at	5.6	peptidylprolyl isomerase A (cyclophilin A)	PPIA
208079_s_at	5.6	aurora kinase A	AURKA
225340_s_at	5.6	cell cycle associated protein 1	CAPRIN1
200750_s_at	5.5	RAN, member RAS oncogene family	RAN
225204_at	5.5	PTC7 protein phosphatase homolog (S. cerevisiae)	PPTC7
211576_s_at	5.5	solute carrier family 19 (folate transporter), member 1	SLC19A1
202567_at	5.5	small nuclear ribonucleoprotein D3 polypeptide 18kDa	SNRPD3
211968_s_at	5.5	heat shock protein 90kDa alpha (cytosolic), class A member 1	HSP90AA1
211615_s_at	5.5	leucine-rich PPR-motif containing	LRPPRC
204198_s_at	5.5	runt-related transcription factor 3	RUNX3
203213_at	5.5	cyclin-dependent kinase 1	CDK1
205229_s_at	5.5	coagulation factor C homolog, cochlin (Limulus polyphemus)	COCH
203145_at	5.4	sperm associated antigen 5	SPAG5
219918_s_at	5.4	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	ASPM
213092_x_at	5.4	DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9
1553551_s_at	5.4	similar to NADH dehydrogenase subunit 2	LOC100131754
209083_at	5.4	coronin, actin binding protein, 1A	CORO1A
1553984_s_at	5.4	deoxythymidylate kinase (thymidylate kinase)	DTYMK
225655_at	5.4	ubiquitin-like with PHD and ring finger domains 1	UHRF1
208864_s_at	5.4	thioredoxin	TXN
204146_at	5.3	RAD51 associated protein 1	RAD51AP1
224232_s_at	5.3	PRELI domain containing 1	PRELID1
217848_s_at	5.3	pyrophosphatase (inorganic) 1	PPA1
214214_s_at	5.3	complement component 1, q subcomponent binding protein	C1QBP
218882_s_at	5.3	WD repeat domain 3	WDR3
37012_at	5.3	capping protein (actin filament) muscle Z-line, beta	CAPZB
202413_s_at	5.3	ubiquitin specific peptidase 1	USP1
201051_at	5.3	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	ANP32A
218992_at	5.3	chromosome 9 open reading frame 46	C9orf46
202626_s_at	5.2	v-yes-1 Yamaguchi sarcoma viral related oncogene homolog	LYN
209317_at	5.2	polymerase (RNA) I polypeptide C, 30kDa	POLR1C
218477_at	5.2	transmembrane protein 14A	TMEM14A
202097_at	5.2	nucleoporin 153kDa	NUP153
203316_s_at	5.2	small nuclear ribonucleoprotein polypeptide E	SNRPE
210338_s_at	5.2	heat shock 70kDa protein 8	HSPA8
200783_s_at	5.2	stathmin 1	STMN1
203209_at	5.2	replication factor C (activator 1) 5, 36.5kDa	RFC5
209408_at	5.2	kinesin family member 2C	KIF2C
211978_x_at	5.2	peptidylprolyl isomerase A (cyclophilin A)	PPIA
213302_at	5.1	phosphoribosylformylglycinamidine synthase	PFAS
238480_at	5.1	tetratricopeptide repeat domain 39C	TTC39C
226242_at	5.1	chromosome 1 open reading frame 131	C1orf131
201528_at	5.1	replication protein A1, 70kDa	RPA1
213007_at	5.1	Fanconi anemia, complementation group I	FANCI
202144_s_at	5.1	adenylosuccinate lyase	ADSL
202095_s_at	5.1	baculoviral IAP repeat-containing 5	BIRC5
205024_s_at	5.1	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	RAD51
1558662_s_at	5.1	B-cell scaffold protein with ankyrin repeats 1	BANK1
230656_s_at	5.1	cirrhosis, autosomal recessive 1A (cirhin)	CIRH1A
209053_s_at	5.1	Wolf-Hirschhorn syndrome candidate 1	WHSC1
225285_at	5.1	branched chain amino-acid transaminase 1, cytosolic	BCAT1
202870_s_at	5.1	cell division cycle 20 homolog (S. cerevisiae)	CDC20
212296_at	5.0	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	PSMD14
206790_s_at	5.0	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	NDUFB1
203695_s_at	5.0	deafness, autosomal dominant 5	DFNA5
203721_s_at	5.0	UTP18, small subunit (SSU) processome component, homolog (yeast)	UTP18
204866_at	5.0	PHD finger protein 16	PHF16

208956_x_at	5.0	deoxyuridine triphosphatase	DUT
219258_at	5.0	TIMELESS interacting protein	TIPIN
203344_s_at	5.0	retinoblastoma binding protein 8	RBBP8
227607_at	5.0	STAM binding protein-like 1	STAMBPL1
208758_at	5.0	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	ATIC
200790_at	5.0	ornithine decarboxylase 1	ODC1
208683_at	5.0	calpain 2, (m/II) large subunit	CAPN2
204249_s_at	5.0	LIM domain only 2 (rhombotin-like 1)	LMO2
201947_s_at	5.0	chaperonin containing TCP1, subunit 2 (beta)	CCT2
225153_at	5.0	G elongation factor, mitochondrial 1	GFM1
225535_s_at	5.0	translocase of inner mitochondrial membrane 23 homolog (yeast)-like /// translocase of inner mitochondrial membrane 23 homolog (yeast)	LOC10431 /// TIMM23
217779_s_at	5.0	proline-rich nuclear receptor coactivator 2	PNRC2
208921_s_at	5.0	sorcin	SRI

Probesets with higher expression in plasma cells

Affymetrix ID	FC_CD30_EF B/PC cells	Gene Name	Gene Symbol
211430_s_at	-29.4	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant gamma 2 (G2m marker) /// immunoglobulin heavy constant mu /// immunoglobulin heavy variable 4-31 /// hypothetical protein LOC100290146 /// 004867 // serine-type endopeptidase inhibitor activ	IGH@ /// IGHG1 /// IGHG2 /// IGHM /// IGHV4-31 ///
205692_s_at	-13.3	CD38 molecule	CD38
213674_x_at	-10.2	immunoglobulin heavy constant delta	IGHD
209374_s_at	-9.6	immunoglobulin heavy constant mu	IGHM
215176_x_at	-9.0	immunoglobulin kappa locus /// immunoglobulin kappa constant /// similar to hCG26659	IGK@ /// IGKC /// LOC100291464
214836_x_at	-9.0	immunoglobulin kappa locus /// immunoglobulin kappa constant	IGK@ /// IGKC
212592_at	-8.8	immunoglobulin J polypeptide, linker protein for immunoglobulin alpha and mu polypeptides	IGJ
229656_s_at	-8.7	echinoderm microtubule associated protein like 6	EML6
214669_x_at	-8.6	Immunoglobulin kappa constant	IGKC
221651_x_at	-8.2	immunoglobulin kappa locus /// immunoglobulin kappa constant	IGK@ /// IGKC
230777_s_at	-8.2	PR domain containing 15	PRDM15
209138_x_at	-8.0	Immunoglobulin lambda locus	IGL@
202842_s_at	-8.0	DnaJ (Hsp40) homolog, subfamily B, member 9	DNAJB9
224795_x_at	-7.8	immunoglobulin kappa locus /// immunoglobulin kappa constant	IGK@ /// IGKC
214677_x_at	-7.8	cyclosporin A transporter 1 /// immunoglobulin lambda variable 1-44	CYAT1 /// IGLV1-44
221671_x_at	-7.6	immunoglobulin kappa locus /// immunoglobulin kappa constant	IGK@ /// IGKC
229721_x_at	-7.4	Der1-like domain family, member 3	DERL3
221286_s_at	-7.1	plasma cell-induced ER protein 1	MGC29506
215946_x_at	-6.8	immunoglobulin lambda-like polypeptide 3	IGLL3
210387_at	-6.7	histone cluster 1, H2bg	HIST1H2BG
215121_x_at	-6.4	cyclosporin A transporter 1 /// immunoglobulin lambda variable 1-44	CYAT1 /// IGLV1-44
215379_x_at	-6.3	immunoglobulin lambda variable 1-44	IGLV1-44
1556183_at	-6.0	hypothetical LOC645784	FLJ40330
231931_at	-5.9	PR domain containing 15	PRDM15
213502_x_at	-5.8	glucuronidase, beta/immunoglobulin lambda-like polypeptide 1 pseudogene	LOC91316
219505_at	-5.7	cat eye syndrome chromosome region, candidate 1	CECR1
217148_x_at	-5.6	similar to Ig lambda chain	LOC100293440
217022_s_at	-5.6	immunoglobulin heavy locus /// immunoglobulin heavy constant alpha 1 /// immunoglobulin heavy constant alpha 2 (A2m marker) /// hypothetical LOC100126583	IGH@ /// IGHA1 /// IGHA2 /// LOC100126583
200999_s_at	-5.5	cytoskeleton-associated protein 4	CKAP4
225912_at	-5.5	tumor protein p53 inducible nuclear protein 1	TP53INP1
1569040_s_at	-5.4	hypothetical LOC645784	FLJ40330
229147_at	-4.9	Ras association (RalGDS/AF-6) domain family member 6	RASSF6
234764_x_at	-4.7	Immunoglobulin lambda variable 1-44	IGLV1-44

206700_s_at	-4.5	lysine (K)-specific demethylase 5D	KDM5D
200670_at	-4.4	X-box binding protein 1	XBP1
225706_at	-4.3	glucocorticoid induced transcript 1	GLCCI1
242029_at	-4.3	Fibronectin type III domain containing 3B	FNDC3B
206169_x_at	-4.3	zinc finger CCCH-type containing 7B	ZC3H7B
226811_at	-4.2	family with sequence similarity 46, member C	FAM46C
212311_at	-4.1	sel-1 suppressor of lin-12-like 3 (C. elegans)	SEL1L3
203066_at	-4.1	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	CHST15
396_f_at	-4.1	erythropoietin receptor	EPOR
216560_x_at	-4.0	Immunoglobulin lambda locus	IGL@
201004_at	-4.0	signal sequence receptor, delta (translocon-associated protein delta)	SSR4
201678_s_at	-3.9	chromosome 3 open reading frame 37	C3orf37
214715_x_at	-3.8	zinc finger protein 160	ZNF160
212345_s_at	-3.8	cAMP responsive element binding protein 3-like 2	CREB3L2
202083_s_at	-3.8	SEC14-like 1 (S. cerevisiae)	SEC14L1
207761_s_at	-3.6	methyltransferase like 7A	METTL7A
210401_at	-3.6	purinergic receptor P2X, ligand-gated ion channel, 1	P2RX1
223565_at	-3.6	plasma cell-induced ER protein 1	MGC29506
206792_x_at	-3.6	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	PDE4C
221004_s_at	-3.6	integral membrane protein 2C	ITM2C
208658_at	-3.6	protein disulfide isomerase family A, member 4	PDIA4
225032_at	-3.5	fibronectin type III domain containing 3B	FNDC3B
217260_x_at	-3.5	Immunoglobulin heavy constant gamma 1 (G1m marker) /// Similar to hCG1812074	IGHG1 /// LOC100293559
211936_at	-3.5	heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)	HSPA5
233463_at	-3.5	Ras association (RalGDS/AF-6) domain family member 6	RASSF6
211458_s_at	-3.4	GABA(A) receptor-associated protein like 1 /// GABA(A) receptors associated protein like 3 (pseudogene)	GABARAPL1 /// GABARAPL3
216576_x_at	-3.4	immunoglobulin kappa locus /// immunoglobulin kappa constant /// similar to Ig kappa chain V-I region HK102 precursor /// similar to Ig kappa chain V-I region HK102 precursor	IGK@ /// IGKC /// LOC652493 /// LOC652694
226150_at	-3.3	phosphatidic acid phosphatase type 2 domain containing 1B	PPAPDC1B
232215_x_at	-3.3	proline rich 11	PRR11
200998_s_at	-3.3	cytoskeleton-associated protein 4	CKAP4
211048_s_at	-3.3	protein disulfide isomerase family A, member 4	PDIA4
223697_x_at	-3.3	chromosome 9 open reading frame 64	C9orf64
204698_at	-3.3	interferon stimulated exonuclease gene 20kDa	ISG20
220796_x_at	-3.2	solute carrier family 35, member E1	SLC35E1
224667_x_at	-3.2	anaphase promoting complex subunit 16	ANAPC16
216207_x_at	-3.2	Immunoglobulin kappa variable 1D-13	IGKV1D-13
234762_x_at	-3.2	Neurolysin (metallopeptidase M3 family)	NLN
219117_s_at	-3.2	FK506 binding protein 11, 19 kDa	FKBP11
221253_s_at	-3.2	muted homolog (mouse) /// thioredoxin domain containing 5 (endoplasmic reticulum)	MUTED /// TXNDC5
204254_s_at	-3.1	vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR
202636_at	-3.1	ring finger protein 103	RNF103
204255_s_at	-3.1	vitamin D (1,25- dihydroxyvitamin D3) receptor	VDR
216984_x_at	-3.1	immunoglobulin lambda variable 2-23 /// similar to Ig lambda chain	IGLV2-23 // LOC100293440
231886_at	-3.1	similar to hCG1739109	LOC100134822
219229_at	-3.1	solute carrier organic anion transporter family, member 3A1	SLCO3A1
33304_at	-3.1	interferon stimulated exonuclease gene 20kDa	ISG20
210258_at	-3.0	regulator of G-protein signaling 13	RGS13
234981_x_at	-3.0	carboxymethylenebutenolidase homolog (Pseudomonas)	CMBL
216401_x_at	-3.0	similar to Ig kappa chain V-I region HK102 precursor	LOC652493
220071_x_at	-3.0	HAUS augmin-like complex, subunit 2	HAUS2
236715_x_at	-3.0	uveal autoantigen with coiled-coil domains and ankyrin repeats	UACA
208982_at	-3.0	platelet/endothelial cell adhesion molecule	PECAM1
222838_at	-3.0	SLAM family member 7	SLAMF7

Supplemental Table 8. Genes differentially expressed between CD30$^+$ extrafollicular (EF) B cells and HRS cells

Probesets with higher expression in HRS cells

Affymetrix ID	Fold change	Gene Title	Gene Symbol
203936_s_at	16.0	matrix metallopeptidase 9 (gelatinase B, 92kDa gelatinase, 92kDa type IV collagenase)	MMP9
213975_s_at	14.0	lysozyme (renal amyloidosis)	LYZ
209924_at	12.9	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	CCL18
32128_at	10.3	chemokine (C-C motif) ligand 18 (pulmonary and activation-regulated)	CCL18
207900_at	9.4	chemokine (C-C motif) ligand 17	CCL17
209392_at	9.0	ectonucleotide pyrophosphatase/phosphodiesterase 2	ENPP2
1556499_s_at	7.3	collagen, type I, alpha 1	COL1A1
213553_x_at	7.3	apolipoprotein C-I	APOC1
204971_at	7.1	cystatin A (stefin A)	CSTA
201631_s_at	6.9	immediate early response 3	IER3
204416_x_at	6.9	apolipoprotein C-I	APOC1
204580_at	6.8	matrix metallopeptidase 12 (macrophage elastase)	MMP12
202237_at	6.4	nicotinamide N-methyltransferase	NNMT
211748_x_at	6.3	prostaglandin D2 synthase 21kDa (brain)	PTGDS
214079_at	5.9	dehydrogenase/reductase (SDR family) member 2	DHRS2
213539_at	5.8	CD3d molecule, delta (CD3-TCR complex)	CD3D
1552316_a_at	5.7	GTPase, IMAP family member 1	GIMAP1
200839_s_at	5.5	cathepsin B	CTSB
201141_at	5.4	glycoprotein (transmembrane) nmb	GPNMB
202252_at	5.3	RAB13, member RAS oncogene family	RAB13
219386_s_at	5.1	SLAM family member 8	SLAMF8
209395_at	4.9	chitinase 3-like 1 (cartilage glycoprotein-39)	CHI3L1
203973_s_at	4.6	CCAAT/enhancer binding protein (C/EBP), delta	CEBPD
200665_s_at	4.5	secreted protein, acidic, cysteine-rich (osteonectin)	SPARC
212187_x_at	4.4	prostaglandin D2 synthase 21kDa (brain)	PTGDS
201163_s_at	4.4	insulin-like growth factor binding protein 7	IGFBP7
218805_at	4.4	GTPase, IMAP family member 5	GIMAP5
209278_s_at	4.4	tissue factor pathway inhibitor 2	TFPI2
213275_x_at	4.3	cathepsin B	CTSB
202953_at	4.3	complement component 1, q subcomponent, B chain	C1QB
200871_s_at	4.2	prosaposin	PSAP
205403_at	4.1	interleukin 1 receptor, type II	IL1R2
205114_s_at	4.0	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3	CCL3 /// CCL3L1 /// CCL3L3
201059_at	3.9	cortactin	CTTN
221185_s_at	3.8	IQ motif containing G	IQCG
211005_at	3.8	linker for activation of T cells /// spinster homolog 1 (Drosophila)	LAT /// SPNS1
212788_x_at	3.7	ferritin, light polypeptide	FTL
214211_at	3.7	ferritin, heavy polypeptide 1	FTH1
206134_at	3.7	ADAM-like, decysin 1	ADAMDEC1
204655_at	3.7	chemokine (C-C motif) ligand 5	CCL5
205479_s_at	3.6	plasminogen activator, urokinase	PLAU
206169_x_at	3.6	zinc finger CCCH-type containing 7B	ZC3H7B
214023_x_at	3.6	tubulin, beta 2B	TUBB2B
221943_x_at	3.5	Ribosomal protein L38	RPL38
210164_at	3.5	granzyme B (granzyme 2, cytotoxic T-lymphocyte-associated serine esterase 1)	GZMB
218559_s_at	3.4	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	MAFB
1405_i_at	3.4	chemokine (C-C motif) ligand 5	CCL5
203979_at	3.4	cytochrome P450, family 27, subfamily A, polypeptide 1	CYP27A1
212884_x_at	3.4	apolipoprotein E	APOE
213193_x_at	3.3	T cell receptor beta constant 1	TRBC1

214041_x_at	3.3	Ribosomal protein L37a	RPL37A
214428_x_at	3.2	complement component 4A (Rodgers blood group) /// complement component 4B (Chido blood group) /// similar to Complement component 4A (Rodgers blood group)	C4A /// C4B /// LOC100292046
216442_x_at	3.2	fibronectin 1	FN1
215076_s_at	3.2	collagen, type III, alpha 1	COL3A1
210495_x_at	3.1	fibronectin 1	FN1
214715_x_at	3.1	zinc finger protein 160	ZNF160
202087_s_at	3.1	cathepsin L1	CTSL1
217767_at	3.1	complement component 3	C3
211719_x_at	3.1	fibronectin 1	FN1
206363_at	3.1	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	MAF
202284_s_at	3.1	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	CDKN1A
226218_at	3.1	interleukin 7 receptor	IL7R
214395_x_at	3.1	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	EEF1D
209803_s_at	3.0	pleckstrin homology-like domain, family A, member 2	PHLDA2
201162_at	3.0	insulin-like growth factor binding protein 7	IGFBP7
201506_at	3.0	transforming growth factor, beta-induced, 68kDa	TGFBI
202450_s_at	3.0	cathepsin K	CTSK
206792_x_at	3.0	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila)	PDE4C
213931_at	3.0	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein /// inhibitor of DNA binding 2B, dominant negative helix-loop-helix protein (pseudogene)	ID2 /// ID2B
222670_s_at	3.0	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	MAFB
209568_s_at	3.0	ral guanine nucleotide dissociation stimulator-like 1	RGL1
208450_at	3.0	lectin, galactoside-binding, soluble, 2	LGALS2
213869_x_at	3.0	Thy-1 cell surface antigen	THY1

Probesets with higher expresion in CD30$^+$ EF B cells

Affymetrix ID	Fold change	FC DLBCL/ CD30 EF B cells	FC FL/ CD30+ EF B cells	Gene Title	Gene Symbol
228592_at	-17.6			membrane-spanning 4-domains, subfamily A, member 1	MS4A1
209199_s_at	-13.2			myocyte enhancer factor 2C	MEF2C
210356_x_at	-12.1			membrane-spanning 4-domains, subfamily A, member 1	MS4A1
228518_at	-11.8			immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu	IGH@ /// IGHG1 /// IGHM
205267_at	-11.7			POU class 2 associating factor 1	POU2AF1
219563_at	-11.4			chromosome 14 open reading frame 139	C14orf139
224428_s_at	-10.5			cell division cycle associated 7	CDCA7
217418_x_at	-10.1			membrane-spanning 4-domains, subfamily A, member 1	MS4A1
212124_at	-9.9			zinc finger, MIZ-type containing 1	ZMIZ1
207655_s_at	-8.6			B-cell linker	BLNK
202413_s_at	-8.4			ubiquitin specific peptidase 1	USP1
218237_s_at	-8.4			solute carrier family 38, member 1	SLC38A1
201112_s_at	-8.3	-6.7	6.6	CSE1 chromosome segregation 1-like (yeast)	CSE1L
219014_at	-8.1			placenta-specific 8	PLAC8
206052_s_at	-8.1			stem-loop binding protein	SLBP
209473_at	-7.9			ectonucleoside triphosphate diphosphohydrolase 1	ENTPD1
212330_at	-7.8			transcription factor Dp-1	TFDP1
219517_at	-7.7			elongation factor RNA polymerase II-like 3 /// serine incorporator 4	ELL3 /// SERINC4
218039_at	-7.7	-4.0	-4.6	nucleolar and spindle associated protein 1	NUSAP1
201084_s_at	-7.6			BCL2-associated transcription factor 1	BCLAF1
200774_at	-7.5			family with sequence similarity 120A	FAM120A
214710_s_at	-7.2			cyclin B1	CCNB1
227346_at	-7.1			IKAROS family zinc finger 1 (Ikaros)	IKZF1
209397_at	-7.0			malic enzyme 2, NAD(+)-dependent, mitochondrial	ME2

202107_s_at	-7.0			minichromosome maintenance complex component 2	MCM2
212295_s_at	-6.8			solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	SLC7A1
208766_s_at	-6.8			heterogeneous nuclear ribonucleoprotein R	HNRNPR
202370_s_at	-6.7			core-binding factor, beta subunit	CBFB
223059_s_at	-6.7			family with sequence similarity 107, member B	FAM107B
201371_s_at	-6.7			cullin 3	CUL3
200723_s_at	-6.6			cell cycle associated protein 1	CAPRIN1
201013_s_at	-6.6			phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
226068_at	-6.4			spleen tyrosine kinase	SYK
217779_s_at	-6.4			proline-rich nuclear receptor coactivator 2	PNRC2
202911_at	-6.4			mutS homolog 6 (E. coli)	MSH6
225626_at	-6.3			phosphoprotein associated with glycosphingolipid microdomains 1	PAG1
201589_at	-6.3	-4.1	-4.1	structural maintenance of chromosomes 1A	SMC1A
202097_at	-6.2			nucleoporin 153kDa	NUP153
201014_s_at	-6.2			phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	PAICS
202157_s_at	-6.2			CUG triplet repeat, RNA binding protein 2	CUGBP2
207165_at	-6.2			hyaluronan-mediated motility receptor (RHAMM)	HMMR
201773_at	-6.2			activity-dependent neuroprotector homeobox	ADNP
224588_at	-6.2			X (inactive)-specific transcript (non-protein coding)	XIST
200934_at	-6.1			DEK oncogene	DEK
201528_at	-6.1			replication protein A1, 70kDa	RPA1
201811_x_at	-6.1			SH3-domain binding protein 5 (BTK-associated)	SH3BP5
201457_x_at	-6.1	-3.7	-4.8	budding uninhibited by benzimidazoles 3 homolog (yeast)	BUB3
203721_s_at	-6.1			UTP18, small subunit (SSU) processome component, homolog (yeast)	UTP18
224579_at	-6.1			solute carrier family 38, member 1	SLC38A1
201273_s_at	-6.0			signal recognition particle 9kDa	SRP9
200754_x_at	-6.0			splicing factor, arginine/serine-rich 2	SFRS2
226459_at	-6.0			phosphoinositide-3-kinase adaptor protein 1	PIK3AP1
225310_at	-6.0	-4.2	-4.2	RNA binding motif protein, X-linked	RBMX
201857_at	-6.0			zinc finger RNA binding protein	ZFR
212250_at	-6.0			metadherin	MTDH
201672_s_at	-6.0			ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	USP14
225343_at	-5.9			transmembrane emp24 protein transport domain containing 8	TMED8
202900_s_at	-5.9			nucleoporin 88kDa	NUP88
209773_s_at	-5.9			ribonucleotide reductase M2	RRM2
212296_at	-5.9			proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	PSMD14
203344_s_at	-5.9			retinoblastoma binding protein 8	RBBP8
202520_s_at	-5.9			mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	MLH1
218768_at	-5.9	-4.7	-7.0	nucleoporin 107kDa	NUP107
218350_s_at	-5.9			geminin, DNA replication inhibitor	GMNN
200726_at	-5.9			protein phosphatase 1, catalytic subunit, gamma isoform	PPP1CC
201385_at	-5.9			DEAH (Asp-Glu-Ala-His) box polypeptide 15	DHX15
205909_at	-5.9			polymerase (DNA directed), epsilon 2 (p59 subunit)	POLE2
227517_s_at	-5.9			growth arrest-specific 5 (non-protein coding)	GAS5
210338_s_at	-5.9			heat shock 70kDa protein 8	HSPA8
221476_s_at	-5.9			ribosomal protein L15	RPL15
205229_s_at	-5.8			coagulation factor C homolog, cochlin (Limulus polyphemus)	COCH
222404_x_at	-5.8			protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
200691_s_at	-5.8			heat shock 70kDa protein 9 (mortalin)	HSPA9
201959_s_at	-5.7			MYC binding protein 2	MYCBP2
234000_s_at	-5.7			protein tyrosine phosphatase-like A domain containing 1	PTPLAD1
207186_s_at	-5.7			bromodomain PHD finger transcription factor	BPTF
204744_s_at	-5.7			isoleucyl-tRNA synthetase	IARS
208778_s_at	-5.7			t-complex 1	TCP1
209685_s_at	-5.7			protein kinase C, beta	PRKCB
219990_at	-5.7			E2F transcription factor 8	E2F8

212129_at	-5.7			non imprinted in Prader-Willi/Angelman syndrome 2	NIPA2
212414_s_at	-5.7	-3.1	-2.0	glyoxylate reductase 1 homolog (Arabidopsis) /// septin 6	GLYR1 /// SEPT6
225153_at	-5.7			G elongation factor, mitochondrial 1	GFM1
231896_s_at	-5.7			density-regulated protein	DENR
202396_at	-5.7			transcription elongation regulator 1	TCERG1
207540_s_at	-5.7			spleen tyrosine kinase	SYK
223716_s_at	-5.7			zinc finger, RAN-binding domain containing 2	ZRANB2
224731_at	-5.6			high-mobility group box 1	HMGB1
200790_at	-5.6			ornithine decarboxylase 1	ODC1
235372_at	-5.6			Fc receptor-like A	FCRLA
222435_s_at	-5.6			ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	UBE2J1
213088_s_at	-5.6			DnaJ (Hsp40) homolog, subfamily C, member 9	DNAJC9
223553_s_at	-5.6			docking protein 3	DOK3
212281_s_at	-5.6			transmembrane protein 97	TMEM97
212539_at	-5.6			chromodomain helicase DNA binding protein 1-like	CHD1L
223013_at	-5.6			transducin (beta)-like 1 X-linked receptor 1	TBL1XR1
217764_s_at	-5.6			RAB31, member RAS oncogene family	RAB31
200843_s_at	-5.6			glutamyl-prolyl-tRNA synthetase	EPRS
208775_at	-5.5			exportin 1 (CRM1 homolog, yeast)	XPO1
200626_s_at	-5.5			matrin 3	MATR3
224654_at	-5.5			DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	DDX21
225340_s_at	-5.5			cell cycle associated protein 1	CAPRIN1
201036_s_at	-5.5			hydroxyacyl-Coenzyme A dehydrogenase	HADH
217724_at	-5.5			SERPINE1 mRNA binding protein 1	SERBP1
226905_at	-5.5			family with sequence similarity 101, member B	FAM101B
200996_at	-5.5			ARP3 actin-related protein 3 homolog (yeast)	ACTR3
202633_at	-5.5	-4.2	-4.6	topoisomerase (DNA) II binding protein 1	TOPBP1
201664_at	-5.4			structural maintenance of chromosomes 4	SMC4
218558_s_at	-5.4			mitochondrial ribosomal protein L39	MRPL39
214141_x_at	-5.4			splicing factor, arginine/serine-rich 7, 35kDa	SFRS7
200027_at	-5.4			asparaginyl-tRNA synthetase	NARS
201202_at	-5.4			proliferating cell nuclear antigen	PCNA
210766_s_at	-5.4			CSE1 chromosome segregation 1-like (yeast)	CSE1L
200989_at	-5.4			hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	HIF1A
201479_at	-5.4			dyskeratosis congenita 1, dyskerin	DKC1
201996_s_at	-5.4			spen homolog, transcriptional regulator (Drosophila)	SPEN
217873_at	-5.4			calcium binding protein 39	CAB39
208788_at	-5.4			ELOVL family member 5, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	ELOVL5
218935_at	-5.4			EH-domain containing 3	EHD3
224738_x_at	-5.3			ribosomal protein L7-like 1	RPL7L1
225297_at	-5.3	-3.0	-3.7	HAUS augmin-like complex, subunit 1	HAUS1
209307_at	-5.3			SWAP switching B-cell complex 70kDa subunit	SWAP70
206102_at	-5.3			GINS complex subunit 1 (Psf1 homolog)	GINS1
209141_at	-5.3			ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	UBE2G1
224903_at	-5.3			cirrhosis, autosomal recessive 1A (cirhin)	CIRH1A
241937_s_at	-5.3			WD repeat domain 4	WDR4
201180_s_at	-5.3			guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3	GNAI3
201960_s_at	-5.3			MYC binding protein 2	MYCBP2
201739_at	-5.3			serum/glucocorticoid regulated kinase 1	SGK1
226032_at	-5.3			caspase 2, apoptosis-related cysteine peptidase	CASP2
200893_at	-5.3			transformer 2 beta homolog (Drosophila)	TRA2B
208638_at	-5.3			protein disulfide isomerase family A, member 6	PDIA6
201930_at	-5.3			minichromosome maintenance complex component 6	MCM6
201071_x_at	-5.3			splicing factor 3b, subunit 1, 155kDa	SF3B1
211758_x_at	-5.2			thioredoxin domain containing 9	TXNDC9
222606_at	-5.2	-4.2	-5.0	Zwilch, kinetochore associated, homolog (Drosophila)	ZWILCH

222231_s_at	-5.2			leucine rich repeat containing 59	LRRC59
219918_s_at	-5.2	-4.7	-5.6	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	ASPM
213982_s_at	-5.2			RAB GTPase activating protein 1-like	RABGAP1L
203185_at	-5.2			Ras association (RalGDS/AF-6) domain family member 2	RASSF2
227646_at	-5.2			early B-cell factor 1	EBF1
226242_at	-5.2			chromosome 1 open reading frame 131	C1orf131
204613_at	-5.2			phospholipase C, gamma 2 (phosphatidylinositol-specific)	PLCG2
201619_at	-5.2			peroxiredoxin 3	PRDX3
225136_at	-5.2			pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	PLEKHA2
202727_s_at	-5.2			interferon gamma receptor 1	IFNGR1
214988_s_at	-5.2			SON DNA binding protein	SON
202266_at	-5.1			TRAF and TNF receptor associated protein	TTRAP
208881_x_at	-5.1			isopentenyl-diphosphate delta isomerase 1	IDI1
210211_s_at	-5.1			heat shock protein 90kDa alpha (cytosolic), class A member 1	HSP90AA1
202705_at	-5.1			cyclin B2	CCNB2
214363_s_at	-5.1			matrin 3	MATR3
227607_at	-5.1			STAM binding protein-like 1	STAMBPL1
209053_s_at	-5.1			Wolf-Hirschhorn syndrome candidate 1	WHSC1
217956_s_at	-5.1			enolase-phosphatase 1	ENOPH1
204146_at	-5.1			RAD51 associated protein 1	RAD51AP1
218757_s_at	-5.1			UPF3 regulator of nonsense transcripts homolog B (yeast)	UPF3B
220651_s_at	-5.1			minichromosome maintenance complex component 10	MCM10
200627_at	-5.1			prostaglandin E synthase 3 (cytosolic)	PTGES3
208152_s_at	-5.1			DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	DDX21
211945_s_at	-5.1			integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK12)	ITGB1
225687_at	-5.1	-3.7	-4.5	family with sequence similarity 83, member D	FAM83D
225763_at	-5.1			RCSD domain containing 1	RCSD1
214677_x_at	-5.1			immunoglobulin lambda locus	IGL@
212408_at	-5.1			torsin A interacting protein 1	TOR1AIP1
201051_at	-5.1			acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	ANP32A
221509_at	-5.1			density-regulated protein	DENR
201477_s_at	-5.0			ribonucleotide reductase M1	RRM1
202432_at	-5.0			protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform	PPP3CB
221654_s_at	-5.0			ubiquitin specific peptidase 3	USP3
208955_at	-5.0			deoxyuridine triphosphatase	DUT
211724_x_at	-5.0			missing oocyte, meiosis regulator, homolog (Drosophila)	MIOS
211933_s_at	-5.0			heterogeneous nuclear ribonucleoprotein A3 /// heterogeneous nuclear ribonucleoprotein A3 pseudogene 1	HNRNPA3 /// HNRNPA3P1
213682_at	-5.0			nucleoporin 50kDa	NUP50
200791_s_at	-5.0			IQ motif containing GTPase activating protein 1	IQGAP1
211954_s_at	-5.0			importin 5	IPO5
224591_at	-5.0			heterochromatin protein 1, binding protein 3	HP1BP3
211075_s_at	-5.0			CD47 molecule	CD47
236295_s_at	-5.0			NLR family, CARD domain containing 3	NLRC3
213738_s_at	-5.0			ATP synthase, H+ transporting, mitochondrial F1 complex, alpha subunit 1, cardiac muscle	ATP5A1
203513_at	-5.0			spastic paraplegia 11 (autosomal recessive)	SPG11

Genes marked in violett represent key regulators of the spindle apparatus, cytokinesis and polyploidity. Those marked in yellow represwnt additional regulators of mitosis.

Supplemental Table 9. Supervised comparsion of HRS cells versus CD30$^+$ GC B cells

Probesets with higher expression in CD30$^+$ GC B cells

FC cHL/ CD30 GC	Gene Title	Affymetrix ID	Gene Symbol
-5.0	chromosome 11 open reading frame 58	200084_at	C11orf58
-5.0	stathmin 1	200783_s_at	STMN1
-5.0	vesicle-associated membrane protein 1 (synaptobrevin 1)	213326_at	VAMP1
-5.0	translocase of inner mitochondrial membrane 23 homolog (yeast)	225535_s_at	TIMM23
-5.0	differentially expressed in FDCP 8 homolog (mouse)	225637_at	DEF8
-5.0	NLR family, CARD domain containing 3	236295_s_at	NLRC3
-5.0	G1 to S phase transition 1	215438_x_at	GSPT1
-5.0	DEAH (Asp-Glu-Ala-His) box polypeptide 15	201386_s_at	DHX15
-5.0	splicing factor 3b, subunit 1, 155kDa	201071_x_at	SF3B1
-5.0	GINS complex subunit 2 (Psf2 homolog)	221521_s_at	GINS2
-5.0	ARP3 actin-related protein 3 homolog (yeast)	200996_at	ACTR3
-5.0	YY1 transcription factor	200047_s_at	YY1
-5.0	hypoxanthine phosphoribosyltransferase 1	202854_at	HPRT1
-5.0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	224654_at	DDX21
-5.0	APEX nuclease (multifunctional DNA repair enzyme) 1	210027_s_at	APEX1
-5.0	protein tyrosine phosphatase-like A domain containing 1	234000_s_at	PTPLAD1
-5.0	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	213720_s_at	SMARCA4
-5.0	BRCA2 and CDKN1A interacting protein	227322_s_at	BCCIP
-5.0	docking protein 3	223553_s_at	DOK3
-5.0	TRAF and TNF receptor associated protein	202266_at	TTRAP
-5.0	DEAD (Asp-Glu-Ala-Asp) box polypeptide 46	202462_s_at	DDX46
-5.0	thioredoxin domain containing 9	203008_x_at	TXNDC9
-5.1	budding uninhibited by benzimidazoles 3 homolog (yeast)	201458_s_at	BUB3
-5.1	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	219918_s_at	ASPM
-5.1	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	211762_s_at	KPNA2
-5.1	tumor protein D52	201690_s_at	TPD52
-5.1	methyl-CpG binding domain protein 4	214047_s_at	MBD4
-5.1	UPF3 regulator of nonsense transcripts homolog A (yeast)	214323_s_at	UPF3A
-5.1	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	200989_at	HIF1A
-5.1	Zwilch, kinetochore associated, homolog (Drosophila)	222606_at	ZWILCH
-5.1	branched chain aminotransferase 1, cytosolic	226517_at	BCAT1
-5.1	structural maintenance of chromosomes 4	201664_at	SMC4
-5.1	cell division cycle 2, G1 to S and G2 to M	203213_at	CDC2
-5.1	suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)	208667_s_at	ST13
-5.1	PR domain containing 15	230777_s_at	PRDM15
-5.1	ADP-ribosylation factor-like 5A	218150_at	ARL5A
-5.1	chromobox homolog 3 (HP1 gamma homolog, Drosophila)	200037_s_at	CBX3
-5.2	HEAT repeat containing 1	218594_at	HEATR1
-5.2	heat shock 70kDa protein 4	208815_x_at	HSPA4
-5.2	SWAP switching B-cell complex 70kDa subunit	209306_s_at	SWAP70
-5.2	GINS complex subunit 1 (Psf1 homolog)	206102_at	GINS1
-5.2	IKAROS family zinc finger 1 (Ikaros)	227346_at	IKZF1
-5.2	minichromosome maintenance complex component 3	201555_at	MCM3
-5.2	glycyl-tRNA synthetase	208693_s_at	GARS
-5.2	activity-dependent neuroprotector homeobox	201773_at	ADNP
-5.2	protein tyrosine phosphatase-like A domain containing 1	222404_x_at	PTPLAD1
-5.2	minichromosome maintenance complex component 6	201930_at	MCM6
-5.2	Wolf-Hirschhorn syndrome candidate 1	209053_s_at	WHSC1
-5.2	leucine rich repeat containing 59	222231_s_at	LRRC59
-5.2	enolase-phosphatase 1	217956_s_at	ENOPH1

-5.2	zinc finger RNA binding protein	201857_at	ZFR
-5.3	chromosome X open reading frame 15	227520_at	CXorf15
-5.3	cirrhosis, autosomal recessive 1A (cirhin)	230656_s_at	CIRH1A
-5.3	adenosine deaminase	204639_at	ADA
-5.3	protein disulfide isomerase family A, member 6	208638_at	PDIA6
-5.3	asparaginyl-tRNA synthetase	200027_at	NARS
-5.3	matrin 3	214363_s_at	MATR3
-5.3	family with sequence similarity 72, member A ///, member B /// member C /// member D	225834_at	FAM72A /// B /// C /// D
-5.3	kelch-like 6 (Drosophila)	1560397_s_at	KLHL6
-5.3	t-complex 1	208778_s_at	TCP1
-5.3	Fanconi anemia, complementation group A	236976_at	FANCA
-5.3	methyl-CpG binding domain protein 2	202484_s_at	MBD2
-5.4	MAD2 mitotic arrest deficient-like 1 (yeast)	203362_s_at	MAD2L1
-5.4	mutL homolog 1, colon cancer, nonpolyposis type 2 (E. coli)	202520_s_at	MLH1
-5.4	PDZ binding kinase	219148_at	PBK
-5.4	ribonucleotide reductase M1	201477_s_at	RRM1
-5.4	eukaryotic translation initiation factor 3, subunit C /// eukaryotic translation initiation factor 3, subunit C-like	210949_s_at	EIF3C /// EIF3CL
-5.4	chromosome 7 open reading frame 23	204215_at	C7orf23
-5.4	CXXC finger 5	233955_x_at	CXXC5
-5.4	syntaxin 7	212632_at	STX7
-5.4	spleen tyrosine kinase	226068_at	SYK
-5.5	RAN binding protein 1	202483_s_at	RANBP1
-5.5	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	203755_at	BUB1B
-5.5	lamin B receptor	201795_at	LBR
-5.5	replication protein A1, 70kDa	201528_at	RPA1
-5.5	topoisomerase (DNA) II binding protein 1	202633_at	TOPBP1
-5.5	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	201672_s_at	USP14
-5.5	thymocyte selection-associated high mobility group box	204529_s_at	TOX
-5.5	dyskeratosis congenita 1, dyskerin	201479_at	DKC1
-5.5	heat shock protein 90kDa alpha (cytosolic), class A member 1	210211_s_at	HSP90AA1
-5.5	SH3-domain kinase binding protein 1	223082_at	SH3KBP1
-5.5	complement component 1, q subcomponent binding protein	208910_s_at	C1QBP
-5.6	transformer 2 beta homolog (Drosophila)	200893_at	TRA2B
-5.6	matrin 3	200626_s_at	MATR3
-5.6	transcription elongation regulator 1	202396_at	TCERG1
-5.6	spermatogenesis associated 5-like 1	222163_s_at	SPATA5L1
-5.6	peroxiredoxin 2	39729_at	PRDX2
-5.6	thioredoxin domain containing 9	211758_x_at	TXNDC9
-5.7	splicing factor, arginine/serine-rich 7, 35kDa	214141_x_at	SFRS7
-5.7	CSE1 chromosome segregation 1-like (yeast)	210766_s_at	CSE1L
-5.7	deoxyuridine triphosphatase	208955_at	DUT
-5.7	HAUS augmin-like complex, subunit 1	225297_at	HAUS1
-5.7	transducin (beta)-like 1 X-linked receptor 1	223013_at	TBL1XR1
-5.7	serum/glucocorticoid regulated kinase 1	201739_at	SGK1
-5.7	solute carrier family 38, member 1	218237_s_at	SLC38A1
-5.7	heterogeneous nuclear ribonucleoprotein A3 /// .. pseudogene 1	211933_s_at	HNRNPA3 /HNRNPA3P1
-5.7	prostaglandin E synthase 3 (cytosolic)	200627_at	PTGES3
-5.7	minichromosome maintenance complex component 5	216237_s_at	MCM5
-5.8	phosphoribosyl pyrophosphate synthetase-associated protein 2	203537_at	PRPSAP2
-5.8	family with sequence similarity 83, member D	225687_at	FAM83D
-5.8	cell division cycle 20 homolog (S. cerevisiae)	202870_s_at	CDC20
-5.8	dehydrogenase/reductase (SDR family) member 9	219799_s_at	DHRS9
-5.8	SERPINE1 mRNA binding protein 1	217724_at	SERBP1
-5.8	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	212295_s_at	SLC7A1
-5.8	synaptotagmin binding, cytoplasmic RNA interacting protein	209025_s_at	SYNCRIP
-5.8	glutamyl-prolyl-tRNA synthetase	200843_s_at	EPRS

-5.8	mitochondrial ribosomal protein L39	218558_s_at	MRPL39
-5.8	peroxiredoxin 3	201619_at	PRDX3
-5.8	polymerase (DNA directed), epsilon 2 (p59 subunit)	205909_at	POLE2
-5.9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	212296_at	PSMD14
-5.9	RNA binding motif protein, X-linked	225310_at	RBMX
-5.9	isoleucyl-tRNA synthetase	204744_s_at	IARS
-5.9	signal recognition particle 9kDa	201273_s_at	SRP9
-5.9	DEAH (Asp-Glu-Ala-His) box polypeptide 15	201385_at	DHX15
-5.9	syntaxin 7	212631_at	STX7
-5.9	core-binding factor, beta subunit	202370_s_at	CBFB
-5.9	growth arrest-specific 5 (non-protein coding)	227517_s_at	GAS5
-6.0	retinoblastoma binding protein 8	203344_s_at	RBBP8
-6.0	structural maintenance of chromosomes 1A	201589_at	SMC1A
-6.0	nucleoporin 107kDa	218768_at	NUP107
-6.0	PC4 and SFRS1 interacting protein 1	209337_at	PSIP1
-6.0	DnaJ (Hsp40) homolog, subfamily C, member 9	213088_s_at	DNAJC9
-6.0	high-mobility group box 1	224731_at	HMGB1
-6.1	UTP18, small subunit (SSU) processome component, homolog (yeast)	203721_s_at	UTP18
-6.1	early B-cell factor 1	227646_at	EBF1
-6.1	Fc receptor-like A	235400_at	FCRLA
-6.1	ribosomal protein L15	221476_s_at	RPL15
-6.1	LIM domain only 2 (rhombotin-like 1)	204249_s_at	LMO2
-6.1	ribonucleotide reductase M2	209773_s_at	RRM2
-6.1	PPPDE peptidase domain containing 1	212371_at	PPPDE1
-6.2	myotubularin related protein 12	225232_at	MTMR12
-6.2	cirrhosis, autosomal recessive 1A (cirhin)	224903_at	CIRH1A
-6.2	heat shock 70kDa protein 8	210338_s_at	HSPA8
-6.2	G protein-coupled receptor 160	223423_at	GPR160
-6.2	ankyrin repeat domain 13A	224810_s_at	ANKRD13A
-6.2	mutS homolog 6 (E. coli)	202911_at	MSH6
-6.2	proline-rich nuclear receptor coactivator 2	217779_s_at	PNRC2
-6.2	heat shock 70kDa protein 9 (mortalin)	200691_s_at	HSPA9
-6.2	proliferating cell nuclear antigen	201202_at	PCNA
-6.2	malic enzyme 2, NAD(+)-dependent, mitochondrial	209397_at	ME2
-6.3	nucleoporin 153kDa	202097_at	NUP153
-6.3	CDV3 homolog (mouse)	228746_s_at	CDV3
-6.3	KIAA0114	224870_at	KIAA0114
-6.3	histone deacetylase 1	201209_at	HDAC1
-6.3	methionyl aminopeptidase 2	209861_s_at	METAP2
-6.4	forty-two-three domain containing 1	224641_at	FYTTD1
-6.4	phosphoinositide-3-kinase adaptor protein 1	226459_at	PIK3AP1
-6.4	cell cycle associated protein 1	200723_s_at	CAPRIN1
-6.4	RAB GTPase activating protein 1-like	213982_s_at	RABGAP1L
-6.4	family with sequence similarity 107, member B	223059_s_at	FAM107B
-6.5	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	201013_s_at	PAICS
-6.5	hydroxyacyl-Coenzyme A dehydrogenase	201036_s_at	HADH
-6.5	ornithine decarboxylase 1	200790_at	ODC1
-6.5	spen homolog, transcriptional regulator (Drosophila)	201996_s_at	SPEN
-6.5	chromosome 10 open reading frame 18	218331_s_at	C10orf18
-6.5	cytoplasmic FMR1 interacting protein 2	215785_s_at	CYFIP2
-6.5	transcription elongation factor A (SII), 1	216241_s_at	TCEA1
-6.5	protein phosphatase 1, catalytic subunit, gamma isoform	200726_at	PPP1CC
-6.6	budding uninhibited by benzimidazoles 3 homolog (yeast)	201457_x_at	BUB3
-6.6	E2F transcription factor 8	219990_at	E2F8
-6.7	minichromosome maintenance complex component 2	202107_s_at	MCM2
-6.7	splicing factor, arginine/serine-rich 2	200754_x_at	SFRS2
-6.8	kelch-like 6 (Drosophila)	228167_at	KLHL6

-6.8	WD repeat domain 4	241937_s_at	WDR4
-6.8	nucleoporin 88kDa	202900_s_at	NUP88
-6.9	guanine nucleotide binding protein (G protein), alpha 13	224761_at	GNA13
-6.9	purinergic receptor P2X, ligand-gated ion channel, 5	210448_s_at	P2RX5
-6.9	DEK oncogene	200934_at	DEK
-6.9	family with sequence similarity 120A	200774_at	FAM120A
-7.0	heterogeneous nuclear ribonucleoprotein R	208766_s_at	HNRNPR
-7.1	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	209142_s_at	UBE2G1
-7.3	transmembrane emp24 protein transport domain containing 8	225343_at	TMED8
-7.4	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	222435_s_at	UBE2J1
-7.4	geminin, DNA replication inhibitor	218350_s_at	GMNN
-7.4	hyaluronan-mediated motility receptor (RHAMM)	207165_at	HMMR
-7.5	cyclin B2	202705_at	CCNB2
-7.8	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	201014_s_at	PAICS
-7.8	cullin 3	201371_s_at	CUL3
-7.8	transcription factor Dp-1	212330_at	TFDP1
-7.9	ubiquitin-conjugating enzyme E2G 1 (UBC7 homolog, yeast)	209141_at	UBE2G1
-8.0	chromosome 14 open reading frame 139	219563_at	C14orf139
-8.1	BCL2-associated transcription factor 1	201084_s_at	BCLAF1
-8.2	myocyte enhancer factor 2C	209199_s_at	MEF2C
-8.2	SWAP switching B-cell complex 70kDa subunit	209307_at	SWAP70
-8.3	Fc receptor-like A	235372_at	FCRLA
-8.3	phosphoprotein associated with glycosphingolipid microdomains 1	225626_at	PAG1
-8.4	B-cell linker	207655_s_at	BLNK
-8.4	stem-loop binding protein	206052_s_at	SLBP
-8.5	ubiquitin specific peptidase 1	202413_s_at	USP1
-8.5	zinc finger, MIZ-type containing 1	212124_at	ZMIZ1
-8.6	B-cell CLL/lymphoma 6	203140_at	BCL6
-9.1	cyclin B1	214710_s_at	CCNB1
-9.2	CSE1 chromosome segregation 1-like (yeast)	201112_s_at	CSE1L
-9.3	T-cell leukemia/lymphoma 1A	39318_at	TCL1A
-9.7	nucleolar and spindle associated protein 1	218039_at	NUSAP1
-10.0	sortilin-related receptor, L(DLR class) A repeats-containing	212560_at	SORL1
-10.2	membrane-spanning 4-domains, subfamily A, member 1	217418_x_at	MS4A1
-10.2	bromodomain PHD finger transcription factor	207186_s_at	BPTF
-10.2	T-cell leukemia/lymphoma 1A	209995_s_at	TCL1A
-11.0	regulator of G-protein signaling 13	210258_at	RGS13
-11.6	cell division cycle associated 7	224428_s_at	CDCA7
-12.2	POU class 2 associating factor 1	205267_at	POU2AF1
-12.4	membrane-spanning 4-domains, subfamily A, member 1	210356_x_at	MS4A1
-12.5	immunoglobulin heavy locus /// immunoglobulin heavy constant gamma 1 (G1m marker) /// immunoglobulin heavy constant mu	228518_at	IGH@ /// IGHG1 /// IGHM
-13.5	elongation factor RNA polymerase II-like 3 /// serine incorporator 4	219518_s_at	ELL3 /// SERINC4
-17.7	membrane-spanning 4-domains, subfamily A, member 1	228592_at	MS4A1
-18.7	elongation factor RNA polymerase II-like 3 /// serine incorporator 4	219517_at	ELL3 /// SERINC4

Probesets with higher expression in HRS cells

FC cHL/ CD30 GC	Gene Title	Affymetrix ID	Gene Symbol
18.3	lysozyme (renal amyloidosis)	213975_s_at	LYZ
17.3	matrix metallopeptidase 9	203936_s_at	MMP9
13.0	chemokine (C-C motif) ligand 18	209924_at	CCL18
11.6	ectonucleotide pyrophosphatase/phosphodiesterase 2	209392_at	ENPP2
10.4	chemokine (C-C motif) ligand 17	207900_at	CCL17

9.8	chemokine (C-C motif) ligand 18	32128_at	CCL18
9.1	cathepsin B	200839_s_at	CTSB
8.0	collagen, type I, alpha 1	1556499_s_at	COL1A1
7.4	cystatin A (stefin A)	204971_at	CSTA
7.4	chemokine (C-X-C motif) ligand 9	203915_at	CXCL9
7.2	matrix metallopeptidase 12	204580_at	MMP12
7.0	RAB13, member RAS oncogene family	202252_at	RAB13
6.6	apolipoprotein C-I	213553_x_at	APOC1
6.6	apolipoprotein C-I	204416_x_at	APOC1
6.2	prostaglandin D2 synthase 21kDa (brain)	211748_x_at	PTGDS
6.1	cathepsin B	213275_x_at	CTSB
6.1	nicotinamide N-methyltransferase	202237_at	NNMT
6.0	immediate early response 3	201631_s_at	IER3
5.9	CD3d molecule, delta (CD3-TCR complex)	213539_at	CD3D
5.8	dehydrogenase/reductase (SDR family) member 2	214079_at	DHRS2
5.8	GTPase, IMAP family member 1	1552316_a_at	GIMAP1
5.6	glycoprotein (transmembrane) nmb	201141_at	GPNMB
5.3	chemokine (C-C motif) ligand 5	204655_at	CCL5
5.2	SLAM family member 8	219386_s_at	SLAMF8
5.2	prosaposin	200871_s_at	PSAP
5.0	chitinase 3-like 1 (cartilage glycoprotein-39)	209395_at	CHI3L1
4.9	chemokine (C-C motif) ligand 3 /// chemokine (C-C motif) ligand 3-like 1 /// chemokine (C-C motif) ligand 3-like 3	205114_s_at	CCL3 // CCL3L1 //CCL3L3
4.8	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	202284_s_at	CDKN1A
4.7	T cell receptor beta constant 1	213193_x_at	TRBC1
4.7	tissue factor pathway inhibitor 2	209278_s_at	TFPI2
4.7	chemokine (C-X-C motif) ligand 10	204533_at	CXCL10
4.6	interleukin 1 receptor, type II	205403_at	IL1R2
4.6	serglycin	201859_at	SRGN
4.6	chemokine (C-C motif) ligand 5	1405_i_at	CCL5
4.6	prostaglandin D2 synthase 21kDa (brain)	212187_x_at	PTGDS
4.6	insulin-like growth factor binding protein 7	201163_s_at	IGFBP7
4.6	lectin, galactoside-binding, soluble, 1	201105_at	LGALS1
4.5	CCAAT/enhancer binding protein (C/EBP), delta	203973_s_at	CEBPD
4.5	linker for activation of T cells /// spinster homolog 1 (Drosophila)	211005_at	LAT /// SPNS1
4.5	secreted protein, acidic, cysteine-rich (osteonectin)	200665_s_at	SPARC
4.5	cathepsin C	225646_at	CTSC
4.5	interferon induced transmembrane protein 1 (9-27)	214022_s_at	IFITM1
4.4	complement component 1, q subcomponent, B chain	202953_at	C1QB
4.3	GTPase, IMAP family member 5	218805_at	GIMAP5
4.3	chemokine (C-C motif) ligand 22	207861_at	CCL22
4.3	family with sequence similarity 26, member F	229390_at	FAM26F
4.2	Ribosomal protein L38	221943_x_at	RPL38
4.2	signal transducer and activator of transcription 1, 91kDa	209969_s_at	STAT1
4.2	basic leucine zipper transcription factor, ATF-like 3	220358_at	**BATF3**
4.0	thymosin beta 10	217733_s_at	TMSB10
3.9	tumor necrosis factor (ligand) superfamily, member 13b	223502_s_at	TNFSF13B
3.8	Ras association (RalGDS/AF-6) domain family member 4	226436_at	RASSF4
3.8	ferritin, light polypeptide	212788_x_at	FTL
3.8	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein	213931_at	ID2 /// ID2B
3.8	suppressor of cytokine signaling 3	227697_at	SOCS3
3.7	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	218559_s_at	**MAFB**
3.7	chemokine (C-C motif) receptor 7	206337_at	CCR7
3.7	IQ motif containing G	221185_s_at	IQCG
3.7	ADAM-like, decysin 1	206134_at	ADAMDEC1

3.6	ferritin, heavy polypeptide 1	200748_s_at	FTH1
3.6	microsomal glutathione S-transferase 3	201403_s_at	MGST3
3.6	granzyme B	210164_at	GZMB
3.5	plasminogen activator, urokinase	205479_s_at	PLAU
3.4	optineurin	202074_s_at	OPTN
3.4	tensin 3	217853_at	TNS3
3.4	T cell receptor beta constant 1	210915_x_at	TRBC1
3.4	apolipoprotein E	212884_x_at	APOE
3.4	tubulin, alpha 1a	209118_s_at	TUBA1A
3.3	zinc finger CCCH-type containing 7B	206169_x_at	ZC3H7B
3.3	complement component 3	217767_at	C3
3.3	Superoxide dismutase 2, mitochondrial	1566342_at	SOD2
3.2	chemokine (C-X-C motif) ligand 13	205242_at	CXCL13
3.2	ral guanine nucleotide dissociation stimulator-like 1	209568_s_at	RGL1
3.2	Niemann-Pick disease, type C2	200701_at	NPC2
3.2	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	206363_at	MAF
3.2	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	222670_s_at	MAFB
3.2	fibronectin 1	211719_x_at	FN1
3.2	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	214395_x_at	EEF1D
3.2	chromosome 4 open reading frame 48	229860_x_at	C4orf48
3.2	Family with sequence similarity 26, member F	229543_at	FAM26F
3.2	SATB homeobox 1	203408_s_at	**SATB1**
3.2	fibronectin 1	210495_x_at	FN1
3.2	metallothionein 2A	212185_x_at	MT2A
3.2	ribosomal protein L10a	229563_s_at	RPL10A
3.2	cytochrome P450, family 27, subfamily A, polypeptide 1	203979_at	CYP27A1
3.1	ISG15 ubiquitin-like modifier	205483_s_at	ISG15
3.1	lectin, galactoside-binding, soluble, 3	208949_s_at	LGALS3
3.1	glioma tumor suppressor candidate region gene 2	217807_s_at	GLTSCR2
3.1	Ribosomal protein L37a	214041_x_at	RPL37A
3.1	fibronectin 1	216442_x_at	FN1
3.1	vimentin	201426_s_at	VIM
3.1	zinc finger protein 160	214715_x_at	ZNF160
3.1	egf-like module containing, mucin-like, hormone receptor-like 1	207111_at	EMR1
3.1	lamin A/C	203411_s_at	LMNA
3.1	phosphodiesterase 4C, cAMP-specific (phosphodiesterase E1 dunce homolog)	206792_x_at	PDE4C
3.1	chromosome 6 open reading frame 145	212923_s_at	C6orf145
3.1	ferritin, heavy polypeptide 1	214211_at	FTH1
3.1	guanylate binding protein 2, interferon-inducible	202748_at	GBP2
3.1	interleukin 7 receptor	226218_at	IL7R
3.1	pleckstrin homology-like domain, family A, member 2	209803_s_at	PHLDA2
3.1	collagen, type III, alpha 1		COL3A1
3.1	CD97 molecule	202910_s_at	CD97
3.1	solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	204588_s_at	SLC7A7
3.0	cathepsin L1	202087_s_at	CTSL1
3.0	ferritin, heavy polypeptide pseudogene 1	211628_x_at	FTHP1
3.0	cathepsin B	200838_at	CTSB
3.0	collagen, type VI, alpha 1	213428_s_at	COL6A1
3.0	CD44 molecule (Indian blood group)	204489_s_at	CD44
3.0	TIMP metallopeptidase inhibitor 1	201666_at	TIMP1
3.0	selectin P ligand	209879_at	SELPLG

Supplemental Table 10. GSEAs of CD30$^+$ and HRS cells using motif-based collection (c3tft; MSigDBv4).

CD30$^+$ cells vs HRS (p < 0.01, FDR < 0.2)							
Enriched in both CD30$^+$ GC B cells							
		CD30$^+$ GC B			**CD30$^+$ EF B**		
	Gene set	**NES**	**p-value**	**FDR**	**NES**	**p-value**	**FDR**
E2F	V$E2F_03	1.73	0.00	0.02	1.72	0.00	0.05
	V$E2F_02	1.67	0.00	0.02	1.63	0.00	0.03
	V$E2F_Q6_01	1.65	0.00	0.02	1.67	0.00	0.03
	V$E2F_Q3	1.63	0.00	0.02	1.63	0.00	0.03
	V$E2F_Q6	1.63	0.00	0.02	1.62	0.00	0.03
	V$E2F_Q4	1.62	0.00	0.02	1.60	0.00	0.03
	V$E2F_01	1.61	0.00	0.02	1.63	0.00	0.03
	V$E2F_Q3_01	1.59	0.00	0.02	1.59	0.00	0.03
	V$E2F_Q4_01	1.59	0.00	0.02	1.57	0.00	0.03
	V$E2F_Q2	1.58	0.00	0.02	1.65	0.00	0.03
E2F1	V$E2F1_Q3	1.70	0.00	0.02	1.62	0.00	0.03
	V$E2F1DP2_01	1.67	0.00	0.02	1.63	0.00	0.03
	V$E2F1DP1_01	1.67	0.00	0.02	1.63	0.00	0.03
	V$E2F1DP1RB_01	1.64	0.00	0.02	1.65	0.00	0.03
	V$E2F1_Q3_01	1.63	0.00	0.02	1.67	0.00	0.04
	V$E2F1_Q4	1.63	0.00	0.02	1.65	0.00	0.03
	SGCGSSAAA_V$E2F1DP2_01	1.62	0.00	0.02	1.56	0.00	0.03
	V$E2F1_Q6	1.61	0.00	0.02	1.61	0.00	0.03
	V$E2F1_Q4_01	1.59	0.00	0.02	1.59	0.00	0.03
	V$E2F1_Q6_01	1.56	0.00	0.02	1.51	0.00	0.03
E2F4	V$E2F4DP1_01	1.68	0.00	0.02	1.63	0.00	0.03
	V$E2F4DP2_01	1.67	0.00	0.02	1.63	0.00	0.03
MYC/MAX	V$MYCMAX_01	1.78	0.00	0.03	1.65	0.00	0.03
	V$MYCMAX_02	1.70	0.00	0.02	1.64	0.00	0.03
	CACGTG_V$MYC_Q2	1.68	0.00	0.02	1.66	0.00	0.03
	V$MYCMAX_B	1.66	0.00	0.02	1.63	0.00	0.03
	V$MYC_Q2	1.61	0.00	0.02	1.51	0.01	0.03
	V$MAX_01	1.58	0.00	0.02	1.58	0.00	0.03
	V$MYCMAX_03	1.57	0.00	0.02	1.57	0.00	0.03
N MYC	V$NMYC_01	1.77	0.00	0.02	1.66	0.00	0.04
OCT1	V$OCT1_03	1.66	0.00	0.02	1.62	0.00	0.03
STAT	V$STAT5A_03	1.77	0.00	0.03	1.72	0.00	0.04
	V$STAT5A_04	1.49	0.00	0.03	1.50	0.01	0.03
	V$STAT1_02	1.49	0.00	0.03	1.53	0.00	0.03
PAX	V$PAX6_01	1.83	0.00	0.03	1.69	0.00	0.04
	V$PAX4_01	1.70	0.00	0.02	1.63	0.00	0.03
	CGTSACG_V$PAX3_B	1.60	0.00	0.02	1.63	0.00	0.03
	V$PAX5_01	1.51	0.00	0.03	1.55	0.00	0.03
USF	V$USF_C	1.77	0.00	0.02	1.69	0.00	0.04
	V$USF2_Q6	1.61	0.00	0.02	1.54	0.00	0.03
	V$USF_01	1.57	0.00	0.02	1.55	0.00	0.03
	V$USF_02	1.53	0.00	0.02	1.47	0.00	0.03
	V$USF_Q6_01	1.52	0.00	0.03	1.56	0.00	0.03
	V$USF_Q6	1.46	0.00	0.03	1.53	0.00	0.03
GATA	V$GATA1_01	1.77	0.00	0.02	1.72	0.00	0.05
	V$GATA4_Q3	1.71	0.00	0.02	1.60	0.00	0.03
NFY	GATTGGY_V$NFY_Q6_01	1.75	0.00	0.02	1.66	0.00	0.04
	V$NFY_Q6	1.68	0.00	0.02	1.59	0.00	0.03
	V$NFY_Q6_01	1.67	0.00	0.02	1.66	0.00	0.04
	V$NFY_C	1.67	0.00	0.02	1.60	0.00	0.03
MYB	V$MYB_Q5_01	1.78	0.00	0.03	1.68	0.00	0.04
	V$MYB_Q3	1.67	0.00	0.02	1.62	0.00	0.03
	V$CMYB_01	1.64	0.00	0.02	1.65	0.00	0.03

	V$MYB_Q6	1.55	0.01	0.02	1.58	0.00	0.03
ERR	V$ERR1_Q2	1.72	0.00	0.02	1.70	0.00	0.04
	TGACCTY_V$ERR1_Q2	1.66	0.00	0.02	1.67	0.00	0.04
NKX	V$NKX25_01	1.74	0.00	0.02	1.67	0.00	0.04
	V$NKX3A_01	1.59	0.00	0.02	1.58	0.00	0.03
	V$NKX61_01	1.59	0.01	0.02	1.58	0.00	0.03
EGR	V$EGR_Q6	1.69	0.00	0.02	1.69	0.00	0.04
	V$EGR1_01	1.65	0.00	0.02	1.65	0.00	0.03
	V$EGR2_01	1.62	0.00	0.02	1.52	0.01	0.03
CREB/JUN	V$CREBP1CJUN_01	1.67	0.00	0.02	1.70	0.00	0.04
	V$CREB_02	1.61	0.00	0.02	1.59	0.00	0.03
	V$CREB_Q2	1.57	0.00	0.02	1.63	0.00	0.03
	V$CREB_Q4_01	1.57	0.00	0.02	1.49	0.00	0.03
	V$CREB_Q3	1.57	0.00	0.02	1.56	0.00	0.03
	V$CREB_01	1.55	0.00	0.02	1.54	0.00	0.03
SPZ1	V$SPZ1_01	1.77	0.00	0.03	1.64	0.00	0.03
ZID	V$ZID_01	1.71	0.00	0.02	1.70	0.00	0.04
HIF	V$HIF1_Q5	1.68	0.00	0.02	1.60	0.00	0.03
	V$HIF1_Q3	1.67	0.00	0.02	1.69	0.00	0.04
NRF	V$NRF2_Q4	1.77	0.00	0.02	1.53	0.00	0.03
	V$NRF1_Q6	1.55	0.00	0.02	1.62	0.00	0.03
	RCGCANGCGY_V$NRF1_Q6	1.53	0.00	0.02	1.52	0.00	0.03
TGIF	V$TGIF_01	1.74	0.00	0.02	1.63	0.00	0.03
TCF1P/HNF1	V$TCF1P_Q6	1.72	0.00	0.02	1.63	0.00	0.03
	V$HNF1_Q6	1.57	0.01	0.02	1.62	0.00	0.03
NGFIC	V$NGFIC_01	1.73	0.00	0.02	1.62	0.00	0.03
ZF5	V$ZF5_B	1.78	0.00	0.03	1.62	0.00	0.03
	V$ZF5_01	1.63	0.00	0.02	1.62	0.00	0.03
TCF11/MAFG	TGANNYRGCA_V$TCF11MAFG_01	1.63	0.00	0.02	1.58	0.00	0.03
MAF	V$MAF_Q6	1.56	0.00	0.02	1.65	0.00	0.03
HP1	V$HP1SITEFACTOR_Q6	1.71	0.00	0.02	1.66	0.00	0.04
ATF3	TGACGTCA_V$ATF3_Q6	1.62	0.00	0.02	1.61	0.00	0.03
SP1	GGGCGGR_V$SP1_Q6	1.60	0.00	0.02	1.60	0.00	0.03
PR	V$PR_01	1.68	0.00	0.02	1.57	0.00	0.03
	V$PR_02	1.60	0.00	0.02	1.62	0.00	0.03
YY1	V$YY1_01	1.66	0.00	0.02	1.68	0.00	0.04
	V$YY1_02	1.54	0.00	0.02	1.53	0.00	0.03
	GCCATNTTG_V$YY1_Q6	1.53	0.00	0.02	1.55	0.00	0.03
	V$YY1_Q6	1.50	0.00	0.03	1.54	0.00	0.03
GR	V$GR_Q6_01	1.68	0.00	0.02	1.53	0.00	0.03
	V$GR_01	1.67	0.00	0.02	1.61	0.00	0.03
PBX1	V$PBX1_02	1.65	0.01	0.02	1.59	0.00	0.03
AREB6	V$AREB6_02	1.71	0.00	0.02	1.59	0.00	0.03
HSF	TTCNRGNNNNTTC_V$HSF_Q6	1.66	0.00	0.02	1.59	0.00	0.03
CHOP	V$CHOP_01	1.72	0.00	0.02	1.59	0.00	0.03
CEBP	V$CEBPGAMMA_Q6	1.70	0.00	0.02	1.72	0.00	0.05
WHN/FOXN	V$WHN_B	1.65	0.00	0.02	1.65	0.00	0.03
E4F1	GTGACGY_V$E4F1_Q6	1.63	0.00	0.02	1.65	0.00	0.03
ARNT	V$ARNT_01	1.61	0.00	0.02	1.58	0.00	0.03
	V$ARNT_02	1.50	0.00	0.03	1.50	0.00	0.03
LEF1	CTTTGT_V$LEF1_Q2	1.61	0.00	0.02	1.63	0.00	0.03
	CTTTGA_V$LEF1_Q2	1.60	0.00	0.02	1.63	0.00	0.03
	V$LEF1_Q2	1.60	0.00	0.02	1.63	0.00	0.03
SOX9	CATTGTYY_V$SOX9_B1	1.63	0.00	0.02	1.57	0.01	0.03
	V$SOX9_B1	1.61	0.00	0.02	1.48	0.01	0.03
HNF4	V$HNF4ALPHA_Q6	1.61	0.01	0.02	1.57	0.01	0.03
SF1	TGACCTTG_V$SF1_Q6	1.70	0.00	0.02	1.57	0.00	0.03
ETF	V$ETF_Q6	1.61	0.00	0.02	1.56	0.00	0.03
GABP	V$GABP_B	1.58	0.00	0.02	1.55	0.00	0.03
	MGGAAGTG_V$GABP_B	1.57	0.00	0.02	1.56	0.00	0.03
AR	V$AR_01	1.58	0.01	0.02	1.60	0.00	0.03

	V$AR_02	1.57	0.01	0.02	1.60	0.00	0.03
	V$AR_Q6	1.49	0.00	0.03	1.62	0.00	0.03
alpha CP1	V$ALPHACP1_01	1.74	0.00	0.02	1.57	0.00	0.03
EFC/RFX1	V$EFC_Q6	1.84	0.00	0.03	1.55	0.00	0.03
	V$RFX1_01	1.58	0.00	0.02	1.55	0.00	0.03
MEIS/HOXA	V$MEIS1BHOXA9_01	1.82	0.00	0.03	1.54	0.00	0.03
	V$HOXA4_Q2	1.60	0.01	0.02	1.55	0.01	0.03
FOXO4	TTGTTT_V$FOXO4_01	1.58	0.00	0.02	1.55	0.00	0.03
HAND1	V$HAND1E47_01	1.56	0.01	0.02	1.55	0.00	0.03
AP2	V$AP2_Q3	1.55	0.00	0.02	1.65	0.00	0.03
	V$AP2_Q6	1.54	0.01	0.02	1.59	0.00	0.03
MTF1	V$MTF1_Q4	1.54	0.01	0.02	1.58	0.00	0.03
TAL1	V$TAL1BETAE47_01	1.57	0.01	0.02	1.53	0.00	0.03
ETS	V$CETS1P54_01	1.56	0.00	0.02	1.52	0.00	0.03
	V$ETS_Q4	1.54	0.00	0.02	1.52	0.01	0.03
AFP1	V$AFP1_Q6	1.58	0.00	0.02	1.49	0.00	0.03
TEF	V$TEF_Q6	1.56	0.01	0.02	1.50	0.00	0.03
E4BP4	TTAYRTAA_V$E4BP4_01	1.52	0.01	0.02	1.50	0.00	0.03
ELK1	V$ELK1_02	1.51	0.00	0.03	1.51	0.00	0.03
	SCGGAAGY_V$ELK1_02	1.51	0.00	0.03	1.49	0.00	0.03
DR4	V$DR4_Q2	1.51	0.01	0.03	1.54	0.01	0.03
AhR	V$AHR_Q5	1.50	0.01	0.03	1.54	0.00	0.03
SREBP1	TCANNTGAY_V$SREBP1_01	1.49	0.01	0.03	1.53	0.01	0.03
	V$SREBP1_01	1.47	0.00	0.03	1.53	0.00	0.03
Motif does not match any known transcription factor	V$NFMUE1_Q6	1.49	0.00	0.03	1.50	0.00	0.03
MIF1	V$MIF1_01	1.48	0.00	0.03	1.45	0.01	0.04
TEL2	V$TEL2_Q6	1.47	0.01	0.03	1.48	0.00	0.03
XBP1	V$XBP1_01	1.46	0.01	0.03	1.41	0.01	0.05

Enriched in CD30$^+$ GC B cells only

	Gene set	**NES**	**p-value**	**FDR**
SP1	V$SP1_Q4_01	1.800	0.000	0.029
	V$SP1_Q6	1.745	0.000	0.020
	V$SP1_Q2_01	1.524	0.007	0.025
ATF	V$ATF4_Q2	1.761	0.000	0.022
	V$ATF_B	1.670	0.000	0.018
GRE	V$GRE_C	1.750	0.000	0.020
MEIS/HOXA	TGACAGNY_V$MEIS1_01	1.743	0.000	0.020
	V$HOXA3_01	1.646	0.007	0.017
	V$MEIS1_01	1.457	0.008	0.033
STAT	V$STAT6_01	1.729	0.000	0.020
	V$STAT5A_02	1.586	0.008	0.019
NCX	V$NCX_01	1.671	0.000	0.019
GFI1	TGATTTRY_V$GFI1_01	1.661	0.000	0.017
TFIIA	V$TFIIA_Q6	1.647	0.008	0.017
EVI1	V$EVI1_03	1.640	0.007	0.017
CREB	V$CREB_Q4	1.636	0.000	0.017
CIZ	V$CIZ_01	1.634	0.005	0.018
E4F1	V$E4F1_Q6	1.632	0.000	0.017
PAX2	V$PAX2_01	1.625	0.004	0.017
SF1	V$SF1_Q6	1.609	0.002	0.018
GFI1	V$GFI1_01	1.603	0.010	0.017
TITF1	V$TITF1_Q3	1.561	0.010	0.022
CDC5	V$CDC5_01	1.557	0.003	0.022
OSF2	V$OSF2_Q6	1.549	0.002	0.023
SMAD	V$SMAD_Q6	1.548	0.002	0.022
HNF4	V$HNF4_01	1.534	0.002	0.023
ETS	V$ETS1_B	1.497	0.009	0.028
ELK1	V$ELK1_01	1.494	0.002	0.028

MIF1	RYTGCNNRGNAAC_V$MIF1_01	1.459	0.006	0.033
PXR	V$PXR_Q2	1.446	0.009	0.035
NRF2	V$NRF2_01	1.411	0.009	0.044
Enriched in CD30$^+$ extrafollicular B cells only				
	Gene set	**NES**	**p-value**	**FDR**
AR	V$AR_03	1.650	0.004	0.033
PPARG	V$PPARG_01	1.577	0.006	0.026
CEBP	TTGCWCAAY_V$CEBPB_02	1.576	0.009	0.026
MYOD	V$MYOD_01	1.567	0.000	0.026
STAT6	V$STAT6_02	1.539	0.004	0.027
P300	V$P300_01	1.530	0.002	0.028
TCF11/MAFG	V$TCF11_01	1.528	0.007	0.028
	V$TCF11MAFG_01	1.439	0.005	0.041
HFH1	V$HFH1_01	1.513	0.007	0.030
CREB	V$CREB_Q2_01	1.511	0.008	0.030
	V$TAXCREB_01	1.482	0.000	0.034
IPF1	V$IPF1_Q4	1.509	0.007	0.030
HLF	V$HLF_01	1.505	0.000	0.030
SMAD4	V$SMAD4_Q6	1.500	0.005	0.031
AREB	V$AREB6_04	1.485	0.008	0.033
FOXJ2	V$FOXJ2_02	1.479	0.007	0.034
RORA	V$RORA1_01	1.476	0.005	0.034
E4BP4	V$E4BP4_01	1.472	0.000	0.035
SOX5	V$SOX5_01	1.428	0.007	0.043
NFY	V$NFY_01	1.418	0.007	0.046
Enriched in HRS cells				
None				

GSEAs of CD30$^+$ and HRS cells using canonical pathway collection (c2cp; MSigDBv4).

CD30$^+$ B cells vs HRS cells (p < 0.01, FDR < 0.2)							
Enriched in both CD30$^+$ B cell subsets		**CD30$^+$ EF B cells**			**CD30$^+$ GC B cells**		
	Gene set	**NES**	**p-value**	**FDR**	**NES**	**p-value**	**FDR**
p38/MAPK	PID_P38_MK2PATHWAY	1.834	0.000	0.145	1.861	0.000	0.094
p38	PID_P38ALPHABETADOWNSTREAMPATHWAY	1.703	0.000	0.198	1.693	0.005	0.138
	PID_MAPKTRKPATHWAY	1.763	0.000	0.154	1.655	0.000	0.164
NFAT	BIOCARTA_NFAT_PATHWAY	1.864	0.000	0.163	1.699	0.009	0.137
	PID_NFAT_3PATHWAY	1.823	0.000	0.144	1.738	0.000	0.164
WNT	KEGG_WNT_SIGNALING_PATHWAY	1.767	0.000	0.176	1.796	0.000	0.156
	PID_BETACATENIN_NUC_PATHWAY	1.616	0.000	0.193	1.942	0.000	0.070
	REACTOME_CTNNB1_PHOSPHORYLATION_CASCADE	1.678	0.002	0.168	1.746	0.000	0.174
	BIOCARTA_WNT_PATHWAY	1.541	0.007	0.177	1.618	0.002	0.157
TGF/SMAD	REACTOME_SMAD2_SMAD3_SMAD4_HETEROTRIMER_REGULATES_TRANSCRIPTION	1.759	0.000	0.138	1.663	0.000	0.161
	REACTOME_SIGNALING_BY_TGF_BETA_RECEPTOR_COMPLEX	1.690	0.000	0.190	1.665	0.000	0.162
	PID_SMAD2_3NUCLEARPATHWAY	1.656	0.005	0.174	1.648	0.002	0.166
	REACTOME_TGF_BETA_RECEPTOR_SIGNALING_ACTIVATES_SMADS	1.695	0.000	0.189	1.577	0.006	0.165
	REACTOME_TRANSCRIPTIONAL_ACTIVITY_OF_SMAD2_SMAD3_SMAD4_HETEROTRIMER	1.598	0.000	0.188	1.633	0.000	0.175
	PID_TGFBRPATHWAY	1.553	0.000	0.169	1.567	0.002	0.165
	REACTOME_DOWNREGULATION_OF_TGF_BETA_RECEPTOR_SIGNALING	1.567	0.000	0.185	1.512	0.004	0.159
RB	PID_RB_1PATHWAY	1.731	0.000	0.184	1.624	0.000	0.168
p53	KEGG_P53_SIGNALING_PATHWAY	1.606	0.000	0.182	1.708	0.000	0.132
	PID_P53REGULATIONPATHWAY	1.423	0.000	0.183	1.520	0.000	0.161
NOTCH	PID_HES_HEYPATHWAY	1.701	0.000	0.194	1.653	0.007	0.164

	REACTOME_NOTCH1_INTRACELLULAR_DOMAIN_REGULATES_TRANSCRIPTION	1.681	0.000	0.182	1.658	0.000	0.163
PI3K	PID_PI3KPLCTRKPATHWAY	1.516	0.005	0.183	1.625	0.000	0.174
	ST_PHOSPHOINOSITIDE_3_KINASE_PATHWAY	1.499	0.007	0.185	1.631	0.000	0.173
mTOR	BIOCARTA_IGF1MTOR_PATHWAY	1.513	0.008	0.184	1.669	0.000	0.160
	PID_MTOR_4PATHWAY	1.471	0.000	0.186	1.465	0.000	0.165
BCR	SIG_BCR_SIGNALING_PATHWAY	1.460	0.002	0.183	1.562	0.000	0.164
	REACTOME_SIGNALING_BY_THE_B_CELL_RECEPTOR_BCR	1.485	0.004	0.185	1.497	0.000	0.160
	PID_BCR_5PATHWAY	1.444	0.002	0.182	1.456	0.000	0.162
PKB	REACTOME_PKB_MEDIATED_EVENTS	1.471	0.008	0.186	1.537	0.006	0.168
PIP3	SIG_PIP3_SIGNALING_IN_CARDIAC_MYOCTES	1.435	0.005	0.182	1.521	0.003	0.163
HDAC	PID_HDAC_CLASSII_PATHWAY	1.581	0.000	0.185	1.618	0.000	0.155
cell cycle	PID_PLK1_PATHWAY	1.605	0.000	0.181	1.620	0.000	0.164
	PID_CDC42_REG_PATHWAY	1.586	0.008	0.180	1.639	0.004	0.178
	REACTOME_G1_PHASE	1.561	0.000	0.173	1.627	0.000	0.173
	KEGG_CELL_CYCLE	1.559	0.000	0.170	1.628	0.000	0.177
	BIOCARTA_G1_PATHWAY	1.517	0.004	0.183	1.510	0.002	0.159
	REACTOME_CELL_CYCLE	1.451	0.000	0.184	1.523	0.000	0.162
	REACTOME_CELL_CYCLE_MITOTIC	1.436	0.000	0.185	1.520	0.000	0.160
	REACTOME_CELL_CYCLE_CHECKPOINTS	1.373	0.002	0.186	1.461	0.000	0.163
mitosis	REACTOME_APC_CDC20_MEDIATED_DEGRADATION_OF_NEK2A	1.505	0.000	0.185	1.552	0.000	0.160
	REACTOME_MITOTIC_G1_G1_S_PHASES	1.461	0.000	0.182	1.510	0.000	0.160
	REACTOME_G1_S_SPECIFIC_TRANSCRIPTION	1.467	0.000	0.185	1.502	0.000	0.159
	REACTOME_G1_S_TRANSITION	1.435	0.000	0.184	1.480	0.000	0.162
	REACTOME_MITOTIC_M_M_G1_PHASES	1.425	0.000	0.183	1.490	0.000	0.162
	REACTOME_M_G1_TRANSITION	1.387	0.006	0.183	1.432	0.002	0.169
meiosis	KEGG_OOCYTE_MEIOSIS	1.587	0.000	0.181	1.597	0.000	0.159
	REACTOME_MEIOSIS	1.567	0.000	0.182	1.594	0.002	0.158
	REACTOME_MEIOTIC_SYNAPSIS	1.578	0.000	0.186	1.533	0.009	0.170
	REACTOME_MEIOTIC_RECOMBINATION	1.530	0.008	0.174	1.566	0.002	0.162
telomere	REACTOME_TELOMERE_MAINTENANCE	1.546	0.008	0.173	1.571	0.002	0.166
	PID_TELOMERASEPATHWAY	1.602	0.000	0.183	1.494	0.002	0.163
chromosome	REACTOME_CHROMOSOME_MAINTENANCE	1.480	0.000	0.181	1.525	0.000	0.166
DNA repair	REACTOME_DNA_REPAIR	1.428	0.000	0.182	1.459	0.000	0.160
	KEGG_BASE_EXCISION_REPAIR	1.453	0.000	0.183	1.417	0.002	0.173
	PID_FANCONI_PATHWAY	1.389	0.002	0.185	1.446	0.007	0.161
mitosis	REACTOME_MITOTIC_PROMETAPHASE	1.398	0.000	0.184	1.482	0.000	0.162
	REACTOME_G0_AND_EARLY_G1	1.454	0.000	0.184	1.418	0.000	0.173
	REACTOME_REGULATION_OF_MITOTIC_CELL_CYCLE	1.413	0.008	0.182	1.444	0.004	0.161
	REACTOME_S_PHASE	1.388	0.002	0.184	1.459	0.000	0.161
DNA synthesis	REACTOME_SYNTHESIS_OF_DNA	1.391	0.006	0.185	1.442	0.000	0.162
ATR	PID_ATR_PATHWAY	1.429	0.000	0.182	1.397	0.000	0.182
	REACTOME_ACTIVATION_OF_ATR_IN_RESPONSE_TO_REPLICATION_STRESS	1.345	0.007	0.194	1.416	0.000	0.173
cell cycle/DNA replication	REACTOME_ACTIVATION_OF_THE_PRE_REPLICATIVE_COMPLEX	1.341	0.010	0.195	1.327	0.009	0.198
DNA replication	REACTOME_DNA_REPLICATION	1.427	0.000	0.182	1.492	0.000	0.164
DNA replication	BIOCARTA_MCM_PATHWAY	1.355	0.000	0.191	1.379	0.008	0.185
p53-related/cell cycle	PID_P73PATHWAY	1.479	0.009	0.182	1.480	0.007	0.161
E2F	PID_E2F_PATHWAY	1.594	0.000	0.185	1.561	0.000	0.162
	REACTOME_E2F_MEDIATED_REGULATION_OF_DNA_REPLICATION	1.539	0.000	0.176	1.461	0.000	0.163
MYC	PID_MYC_PATHWAY	1.458	0.008	0.181	1.596	0.004	0.159
	PID_MYC_ACTIVPATHWAY	1.555	0.000	0.170	1.560	0.000	0.160
metabolism	REACTOME_SULFUR_AMINO_ACID_METABOLISM	1.817	0.000	0.134	1.449	0.007	0.160
	REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_DERIVATIVES	1.633	0.000	0.185	1.601	0.000	0.159
	KEGG_ARGININE_AND_PROLINE_METABOLISM	1.678	0.005	0.173	1.633	0.004	0.179
	REACTOME_METABOLISM_OF_POLYAMINES	1.532	0.004	0.175	1.721	0.000	0.136
	REACTOME_FATTY_ACID_TRIACYLGLYCEROL_AND_KETONE_BODY_METABOLISM	1.613	0.000	0.186	1.612	0.000	0.158
	KEGG_PURINE_METABOLISM	1.501	0.002	0.184	1.609	0.002	0.159

	REACTOME_METABOLISM_OF_NUCLEOTIDES	1.464	0.007	0.184	1.567	0.000	0.164
	REACTOME_PURINE_METABOLISM	1.438	0.002	0.185	1.525	0.000	0.165
	REACTOME_METABOLISM_OF_NON_CODING_RNA	1.415	0.006	0.183	1.424	0.000	0.170
VEGF	BIOCARTA_VEGF_PATHWAY	1.760	0.000	0.147	1.725	0.000	0.142
EGFR	REACTOME_SIGNALING_BY_EGFR_IN_CANCER	1.554	0.004	0.169	1.564	0.000	0.163
CHREBP2	BIOCARTA_CHREBP2_PATHWAY	1.884	0.000	0.177	1.728	0.000	0.145
Retinoid acid	PID_RETINOIC_ACID_PATHWAY	1.763	0.002	0.165	1.607	0.009	0.157
LKB	PID_LKB1_PATHWAY	1.667	0.000	0.166	1.685	0.000	0.145
FOXM1	PID_FOXM1PATHWAY	1.657	0.000	0.178	1.674	0.000	0.157
androgen receptor	PID_AR_NONGENOMIC_PATHWAY	1.575	0.004	0.183	1.715	0.000	0.134
	PID_AR_TF_PATHWAY	1.559	0.000	0.172	1.524	0.006	0.163
Hedgehog	PID_HEDGEHOG_GLIPATHWAY	1.561	0.000	0.172	1.490	0.002	0.163
CARM	BIOCARTA_CARM_ER_PATHWAY	1.535	0.006	0.178	1.415	0.007	0.172
eIF	BIOCARTA_EIF_PATHWAY	1.442	0.004	0.183	1.481	0.004	0.161
BARD1	PID_BARD1PATHWAY	1.348	0.007	0.193	1.471	0.000	0.161
apoptosis	REACTOME_APOPTOTIC_EXECUTION_PHASE	1.617	0.007	0.194	1.558	0.010	0.157
Virus	REACTOME_ANTIVIRAL_MECHANISM_BY_IFN_STIMULATED_GENES	1.614	0.000	0.192	1.621	0.000	0.168
	REACTOME_HIV_INFECTION	1.467	0.000	0.184	1.510	0.000	0.158
	REACTOME_HOST_INTERACTIONS_OF_HIV_FACTORS	1.489	0.000	0.183	1.544	0.000	0.166
	REACTOME_HIV_LIFE_CYCLE	1.482	0.000	0.183	1.475	0.000	0.161
	REACTOME_LATE_PHASE_OF_HIV_LIFE_CYCLE	1.483	0.000	0.184	1.468	0.000	0.163
	REACTOME_INTERACTIONS_OF_VPR_WITH_HOST_CELLULAR_PROTEINS	1.351	0.007	0.192	1.424	0.000	0.171
transcription /RNA processing	REACTOME_TRANSCRIPTION	1.459	0.002	0.182	1.509	0.000	0.157
	REACTOME_PROCESSING_OF_CAPPED_INTRON_CONTAINING_PRE_MRNA	1.401	0.000	0.183	1.365	0.000	0.189
	KEGG_RNA_DEGRADATION	1.376	0.002	0.186	1.377	0.000	0.184
	REACTOME_RNA_POL_II_TRANSCRIPTION	1.368	0.006	0.185	1.382	0.002	0.186
	REACTOME_MRNA_PROCESSING	1.398	0.000	0.184	1.351	0.000	0.192
	REACTOME_TRANSPORT_OF_MATURE_TRANSCRIPT_TO_CYTOPLASM	1.351	0.007	0.194	1.388	0.000	0.184
miscellaneous gene sets	REACTOME_CIRCADIAN_CLOCK	1.626	0.000	0.189	1.992	0.000	0.070
	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	1.655	0.000	0.171	1.755	0.000	0.188
	REACTOME_KINESINS	1.806	0.000	0.135	1.596	0.000	0.157
	REACTOME_TRIGLYCERIDE_BIOSYNTHESIS	1.572	0.008	0.184	1.728	0.000	0.154
	REACTOME_FACTORS_INVOLVED_IN_MEGAKARYOCYTE_DEVELOPMENT_AND_PLATELET_PRODUCTION	1.610	0.000	0.182	1.638	0.000	0.175
	KEGG_COLORECTAL_CANCER	1.677	0.000	0.160	1.562	0.007	0.163
	KEGG_NON_SMALL_CELL_LUNG_CANCER	1.594	0.000	0.183	1.617	0.000	0.153
	REACTOME_GAB1_SIGNALOSOME	1.624	0.006	0.188	1.541	0.009	0.165
	KEGG_GAP_JUNCTION	1.595	0.006	0.187	1.561	0.008	0.160
	REACTOME_PPARA_ACTIVATES_GENE_EXPRESSION	1.510	0.004	0.186	1.546	0.004	0.166
	REACTOME_ASSOCIATION_OF_TRIC_CCT_WITH_TARGET_PROTEINS_DURING_BIOSYNTHESIS	1.546	0.000	0.173	1.506	0.007	0.159
	KEGG_BASAL_TRANSCRIPTION_FACTORS	1.475	0.000	0.183	1.568	0.000	0.169
	REACTOME_GLUCOSE_TRANSPORT	1.468	0.002	0.186	1.534	0.000	0.170
	SIG_INSULIN_RECEPTOR_PATHWAY_IN_CARDIAC_MYOCYTES	1.457	0.004	0.181	1.542	0.004	0.166
	REACTOME_ANTIGEN_PROCESSING_UBIQUITINATION_PROTEASOME_DEGRADATION	1.419	0.008	0.183	1.455	0.002	0.161
	REACTOME_CYTOSOLIC_TRNA_AMINOACYLATION	1.396	0.008	0.184	1.463	0.002	0.163
	REACTOME_REGULATION_OF_GLUCOKINASE_BY_GLUCOKINASE_REGULATORY_PROTEIN	1.403	0.000	0.183	1.439	0.000	0.164
	REACTOME_NEP_NS2_INTERACTS_WITH_THE_CELLULAR_EXPORT_MACHINERY	1.369	0.000	0.185	1.426	0.000	0.170
	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	1.372	0.006	0.186	1.423	0.000	0.170
	REACTOME_TRANSPORT_OF_RIBONUCLEOPROTEINS_INTO_THE_HOST_NUCLEUS	1.366	0.000	0.186	1.384	0.000	0.185

CD30$^+$ extrafollicular (EF) B cells vs HRS ($p < 0.01$, FDR < 0.2)				
Enriched in CD30$^+$ EF B cells only				
	Gene set	**NES**	**p-value**	**FDR**
ERK/MAPK/p38	REACTOME_MAPK_TARGETS_NUCLEAR_EVENTS_MEDIATED_BY_MAP_KINASES	1.726	0.000	0.183
	REACTOME_ERK_MAPK_TARGETS	1.610	0.002	0.185
	REACTOME_PROLONGED_ERK_ACTIVATION_EVENTS	1.590	0.000	0.179
	REACTOME_SIGNALLING_TO_P38_VIA_RIT_AND_RIN	1.565	0.002	0.182
	REACTOME_ARMS_MEDIATED_ACTIVATION	1.555	0.002	0.172
PIP3/Akt	REACTOME_PIP3_ACTIVATES_AKT_SIGNALING	1.564	0.004	0.181
FOXO	PID_FOXOPATHWAY	1.480	0.006	0.182
BCR	REACTOME_DOWNSTREAM_SIGNALING_EVENTS_OF_B_CELL_RECEPTOR_BCR	1.494	0.006	0.183
	KEGG_B_CELL_RECEPTOR_SIGNALING_PATHWAY	1.394	0.009	0.184
signaling in B cells	BIOCARTA_CTCF_PATHWAY	1.576	0.002	0.184
	SIG_PIP3_SIGNALING_IN_B_LYMPHOCYTES	1.512	0.004	0.185
survival	BIOCARTA_BCELLSURVIVAL_PATHWAY	1.534	0.009	0.175
mitosis	REACTOME_RECRUITMENT_OF_MITOTIC_CENTROSOME_PROTEINS_AND_COMPLEXES	1.406	0.004	0.180
	BIOCARTA_AKAP95_PATHWAY	1.491	0.004	0.183
BER	REACTOME_BASE_EXCISION_REPAIR	1.446	0.006	0.183
cell cycle	REACTOME_CYCLIN_A_B1_ASSOCIATED_EVENTS_DURING_G2_M_TRANSITION	1.446	0.002	0.184
mitosis	REACTOME_LOSS_OF_NLP_FROM_MITOTIC_CENTROSOMES	1.386	0.009	0.184
NER	REACTOME_NUCLEOTIDE_EXCISION_REPAIR	1.365	0.004	0.186
DNA	REACTOME_UNWINDING_OF_DNA	1.374	0.002	0.186
centrosome	REACTOME_DEPOSITION_OF_NEW_CENPA_CONTAINING_NUCLEOSOMES_AT_THE_CENTROMERE	1.508	0.006	0.188
	BIOCARTA_AKAPCENTROSOME_PATHWAY	1.770	0.000	0.190
mitosis	REACTOME_MITOTIC_G2_G2_M_PHASES	1.351	0.002	0.192
NER	REACTOME_TRANSCRIPTION_COUPLED_NER_TC_NER	1.339	0.004	0.196
FGFR	REACTOME_SIGNALING_BY_FGFR	1.610	0.004	0.179
	REACTOME_DOWNSTREAM_SIGNALING_OF_ACTIVATED_FGFR	1.633	0.004	0.189
	REACTOME_SIGNALING_BY_FGFR_IN_DISEASE	1.635	0.002	0.190
ERBB	REACTOME_SIGNALING_BY_ERBB2	1.564	0.005	0.179
	PID_ERBB1_DOWNSTREAM_PATHWAY	1.511	0.009	0.186
TGF	BIOCARTA_TGFB_PATHWAY	1.724	0.000	0.175
SHP2	PID_SHP2_PATHWAY	1.696	0.007	0.196
GPCR	BIOCARTA_GPCR_PATHWAY	1.649	0.002	0.173
MET	BIOCARTA_MET_PATHWAY	1.645	0.004	0.174
	BIOCARTA_MPR_PATHWAY	1.593	0.004	0.178
	BIOCARTA_SPPA_PATHWAY	1.688	0.004	0.180
	PID_AR_PATHWAY	1.502	0.007	0.185
	BIOCARTA_CARM1_PATHWAY	1.597	0.004	0.187
	BIOCARTA_CCR3_PATHWAY	1.682	0.000	0.187
metabolism	REACTOME_METABOLISM_OF_LIPIDS_AND_LIPOPROTEINS	1.525	0.009	0.179
	REACTOME_METABOLISM_OF_CARBOHYDRATES	1.679	0.007	0.179
	REACTOME_PEROXISOMAL_LIPID_METABOLISM	1.411	0.008	0.182
miscellaneous	REACTOME_AMINO_ACID_TRANSPORT_ACROSS_THE_PLASMA_MEMBRANE	2.003	0.000	0.066
	REACTOME_PLATELET_SENSITIZATION_BY_LDL	1.550	0.006	0.170
	KEGG_PENTOSE_PHOSPHATE_PATHWAY	1.550	0.002	0.171
	KEGG_LYSINE_DEGRADATION	1.532	0.004	0.174
	KEGG_LONG_TERM_DEPRESSION	1.837	0.000	0.175
	REACTOME_DARPP_32_EVENTS	1.538	0.006	0.176
	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	1.562	0.002	0.177
	KEGG_GLIOMA	1.534	0.004	0.177
	REACTOME_OPIOID_SIGNALLING	1.584	0.000	0.180
	KEGG_PANCREATIC_CANCER	1.519	0.000	0.182
	KEGG_CHRONIC_MYELOID_LEUKEMIA	1.571	0.000	0.183
	REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRANSPORT	1.577	0.010	0.184
	REACTOME_NUCLEAR_EVENTS_KINASE_AND_TRANSCRIPTION_FACTOR_ACTIVATION	1.689	0.000	0.185
	REACTOME_AMINO_ACID_SYNTHESIS_AND_INTERCONVERSION_TRANSAMINATION	1.470	0.002	0.185

	KEGG_PROXIMAL_TUBULE_BICARBONATE_RECLAMATION	1.611	0.007	0.186
	KEGG_THYROID_CANCER	1.614	0.000	0.189
Enriched in HRS cells				
None				

CD30$^+$ GC B cells vs HRS ($p < 0.01$, FDR < 0.2)

Enriched in CD30$^+$ GC B cells only

	Gene set	NES	p-value	FDR
circadian	PID_CIRCADIANPATHWAY	1.878	0.000	0.090
	REACTOME_BMAL1_CLOCK_NPAS2_ACTIVATES_CIRCADIAN_EXPRESSION	1.887	0.000	0.105
	REACTOME_CIRCADIAN_REPRESSION_OF_EXPRESSION_BY_REV_ERBA	1.699	0.000	0.133
	REACTOME_RORA_ACTIVATES_CIRCADIAN_EXPRESSION	1.746	0.000	0.161
NOTCH	PID_NOTCH_PATHWAY	1.807	0.000	0.163
	REACTOME_SIGNALING_BY_NOTCH1	1.620	0.002	0.161
	REACTOME_SIGNALING_BY_NOTCH	1.567	0.002	0.162
HDAC	BIOCARTA_HDAC_PATHWAY	1.717	0.006	0.137
	PID_HDAC_CLASSI_PATHWAY	1.545	0.000	0.166
Aurora	PID_AURORA_A_PATHWAY	1.721	0.000	0.143
	PID_AURORA_B_PATHWAY	1.491	0.000	0.163
WNT	ST_WNT_CA2_CYCLIC_GMP_PATHWAY	1.703	0.006	0.137
RAS	PID_RAS_PATHWAY	1.753	0.000	0.175
mTOR	BIOCARTA_MTOR_PATHWAY	1.624	0.004	0.171
ERK	BIOCARTA_ERK5_PATHWAY	1.567	0.006	0.167
ERBB1	PID_ERBB1_INTERNALIZATION_PATHWAY	1.521	0.004	0.164
transcription/RNA processes	REACTOME_RNA_POL_I_RNA_POL_III_AND_MITOCHONDRIAL_TRANSCRIPTION	1.520	0.004	0.159
	REACTOME_TRANSPORT_OF_MATURE_MRNA_DERIVED_FROM_AN_INTRONLESS_TRANSCRIPT	1.391	0.000	0.185
BCR	BIOCARTA_BCR_PATHWAY	1.517	0.000	0.160
	ST_B_CELL_ANTIGEN_RECEPTOR	1.529	0.006	0.165
	REACTOME_ANTIGEN_ACTIVATES_B_CELL_RECEPTOR_LEADING_TO_GENERATION_OF_SECOND_MESSENGERS	1.543	0.000	0.166
cell cycle	REACTOME_APC_C_CDC20_MEDIATED_DEGRADATION_OF_CYCLIN_B	1.453	0.002	0.160
DNA PK	PID_DNAPK_PATHWAY	1.474	0.002	0.161
DNA replication	REACTOME_INHIBITION_OF_REPLICATION_INITIATION_OF_DAMAGED_DNA_BY_RB1_E2F1	1.493	0.000	0.163
	KEGG_DNA_REPLICATION	1.416	0.002	0.173
	REACTOME_DNA_STRAND_ELONGATION	1.357	0.005	0.189
mitosis	REACTOME_INHIBITION_OF_THE_PROTEOLYTIC_ACTIVITY_OF_APC_C_REQUIRED_FOR_THE_ONSET_OF_ANAPHASE_BY_MITOTIC_SPINDLE_CHECKPOINT_COMPONENTS	1.377	0.005	0.183
	REACTOME_G2_M_CHECKPOINTS	1.379	0.002	0.186
DNA repair	REACTOME_DOUBLE_STRAND_BREAK_REPAIR	1.378	0.000	0.185
	REACTOME_RESOLUTION_OF_AP_SITES_VIA_THE_MULTIPLE_NUCLEOTIDE_PATCH_REPLACEMENT_PATHWAY	1.368	0.007	0.187
ATM	PID_ATM_PATHWAY	1.364	0.000	0.189
telomeres	REACTOME_EXTENSION_OF_TELOMERES	1.343	0.002	0.194
SMAD	REACTOME_DOWNREGULATION_OF_SMAD2_3_SMAD4_TRANSCRIPTIONAL_ACTIVITY	1.463	0.006	0.164
FAS	PID_FASPATHWAY	1.456	0.005	0.162
MET	PID_MET_PATHWAY	1.572	0.000	0.167
IL4R	SIG_IL4RECEPTOR_IN_B_LYPHOCYTES	1.546	0.007	0.167
apoptosis	BIOCARTA_CASPASE_PATHWAY	1.530	0.010	0.167
metabolism	REACTOME_GLUCOSE_METABOLISM	1.608	0.000	0.157
	KEGG_GLYOXYLATE_AND_DICARBOXYLATE_METABOLISM	1.512	0.004	0.160
	KEGG_STARCH_AND_SUCROSE_METABOLISM	1.589	0.007	0.160
	KEGG_PYRIMIDINE_METABOLISM	1.448	0.000	0.160
	REACTOME_PYRUVATE_METABOLISM_AND_CITRIC_ACID_TCA_CYCLE	1.425	0.000	0.170
miscellaneous	PID_HNF3BPATHWAY	1.708	0.010	0.137
	PID_IGF1_PATHWAY	1.607	0.000	0.155
	KEGG_CITRATE_CYCLE_TCA_CYCLE	1.501	0.002	0.157
	PID_ECADHERIN_NASCENTAJ_PATHWAY	1.588	0.000	0.157

	PID_REG_GR_PATHWAY	1.559	0.002	0.157
	REACTOME_GENERIC_TRANSCRIPTION_PATHWAY	1.509	0.000	0.157
	PID_FAK_PATHWAY	1.507	0.009	0.158
	PID_ERA_GENOMIC_PATHWAY	1.489	0.007	0.160
	KEGG_TERPENOID_BACKBONE_BIOSYNTHESIS	1.490	0.006	0.161
	PID_ILK_PATHWAY	1.450	0.008	0.161
	PID_RANBP2PATHWAY	1.455	0.002	0.161
	REACTOME_PURINE_SALVAGE	1.460	0.000	0.162
	KEGG_LONG_TERM_POTENTIATION	1.524	0.004	0.163
	REACTOME_MYOGENESIS	1.732	0.007	0.164
	BIOCARTA_TFF_PATHWAY	1.580	0.000	0.165
	PID_INSULIN_GLUCOSE_PATHWAY	1.574	0.009	0.166
	BIOCARTA_ETC_PATHWAY	1.430	0.008	0.170
	REACTOME_MITOCHONDRIAL_PROTEIN_IMPORT	1.415	0.008	0.173
	KEGG_SPLICEOSOME	1.401	0.000	0.180
	BIOCARTA_PITX2_PATHWAY	1.765	0.000	0.183
	BIOCARTA_CHEMICAL_PATHWAY	1.775	0.000	0.186
Enriched in HRS cells				
None				

GSEAs of CD30$^+$ and HRS cells using hallmark gene sets (h.all.v5; MSigDBv5).

CD30$^+$ cells vs HRS (p < 0.01, FDR < 0.2)							
Enriched in both CD30$^+$ B cells							
		CD30 EF B			**CD30 GC B**		
	Gene set	**NES**	**p-value**	**FDR**	**NES**	**p-value**	**FDR**
	HALLMARK_ANDROGEN_RESPONSE	1.74	0	0.068	1.69	0	0.059
	HALLMARK_SPERMATOGENESIS	1.67	0.002	0.103	1.91	0	0.006
PI3K/AKT/mTOR	HALLMARK_PI3K_AKT_MTOR_SIGNALING	1.44	0	0.137	1.5	0.005	0.146
E2F	HALLMARK_E2F_TARGETS	1.37	0	0.138	1.45	0	0.107
	HALLMARK_UNFOLDED_PROTEIN_RESPONSE	1.45	0	0.164	1.5	0	0.125
	HALLMARK_FATTY_ACID_METABOLISM	1.51	0.004	0.177	1.49	0.004	0.115

Enriched in CD30$^+$ EF B cells only				
	Gene set	**NES**	**p-value**	**FDR**
cell cycle	HALLMARK_G2M_CHECKPOINT	1.45	0	0.137
	HALLMARK_PEROXISOME	1.49	0.007	0.164

Enriched in CD30$^+$ GC B cells only				
	Gene set	**NES**	**p-value**	**FDR**
MYC	HALLMARK_MYC_TARGETS_V1	1.48	0	0.111
mTORC1	HALLMARK_MTORC1_SIGNALING	1.5	0	0.166
mitotic spindle	HALLMARK_MITOTIC_SPINDLE	1.54	0	0.196

Enriched in HRS cells
None

NES, normalized enrichment score; FDR, false discovery rate