Supplementary Materials

Details of quality control

Having discarded samples from participants 21, 23, and 35 due to insufficient RNA, we normalized the CEL files of the remaining 140 chipable samples with the RMA method using the APT software in three runs, one per RNA source. The quality control parameters of these samples are shown in Supplementary Table 13.

Since participant 45 did not yield sufficient RNA in its LCL sample, its PAX and PBMC samples were discarded. PBMC samples of participants 2 and 8 and PAX samples of participants 43 and 44 were found mislabeled by the inspection of Y chromosome probesets. These four samples were discarded. LCL sample of participant 18 was identical to that of participant 17, and LCL sample of participant 42 was identical to that of participant 43. Only LCL sample from participant 18 could be restored. We select only participants with samples having all probeset RLE mean of at most 0.75. This step removed samples from participants 37, 38, 40, 41, 46, and 47. We renormalized the 105 CEL files altogether from the remaining 35 patients.

Details of postnormalization

There is an apparent systematic bias in gene expression values between PAX results and either PBMC or LCL (Supplementary Figure 1, left panel), which is manifested in a skew in RMA-normalized gene expression mean values across 35 samples for LCL *vs.* PAX. RMA normalization alone failed to normalize gene expression quantiles between LCL and PAX samples. This skew also appears in PBMC *vs.* PAX. This is likely arising from the differences in labeling protocol.

In order to address this bias, we examined further data normalization (“postnormalization”) with the S10 procedure(2) and quantile post-normalization (QPN). S10 is a variance-stabilizing and quantile-normalizing transform, while QPN is only a quantile-normalization transform. We will choose the transform that minimizing variance across participants.

Using QPN, we computed the mean value of each probeset per RNA source, yielding three sets of mean values. We chose PBMC as the reference distribution because its mean values correlate well with those of LCL and PAX (Spearman’s correlation = 0.8973 and 0.8565, respectively). Such selection is aimed to minimize drastic quantile correction. After the mean value of each gene for LCL and PAX was quantile-normalized against that of PBMC, its individual expression values were shifted by the difference between the original and normalized mean values.

For S10, we computed the anti-log of the RMA expression values, calculated the normal quantiles, then computed mean and standard deviations across samples, then fit a spline to the standard deviation as a function of the mean. A variance-stabilizing transform function is computed from this smooth function, and then applied to the data. Finally, the log base 2 was computed on the normalized data.

After postnormalization, the QPN-transformed mean densities were identical to that of PBMC, while those S10-transformed were shown in Supplementary Figure 2. QPN mean differences between any two RNA sources are better correlated than those of S10 with those of the original. Some S10 mean differences lie slightly away from the line of identity. Both corrections yielded slightly deflated values for differences in mean values (Supplementary Table 14). The deflation induced by QPN method is minimal compared to that of by S10.

Using two-way ANOVA with RNA source and participant as fixed factors, we determined to use S10 because S10 minimizes variance across participants while normalizing the quantiles. We also found that the deflation rate to be of no concern since we declared significance based on fold change.

Bibliography

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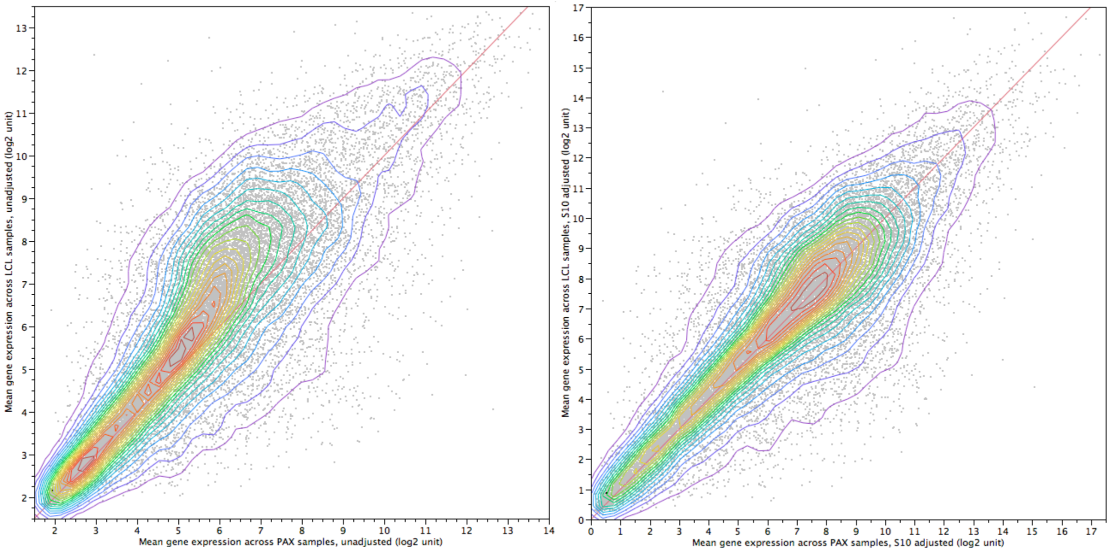
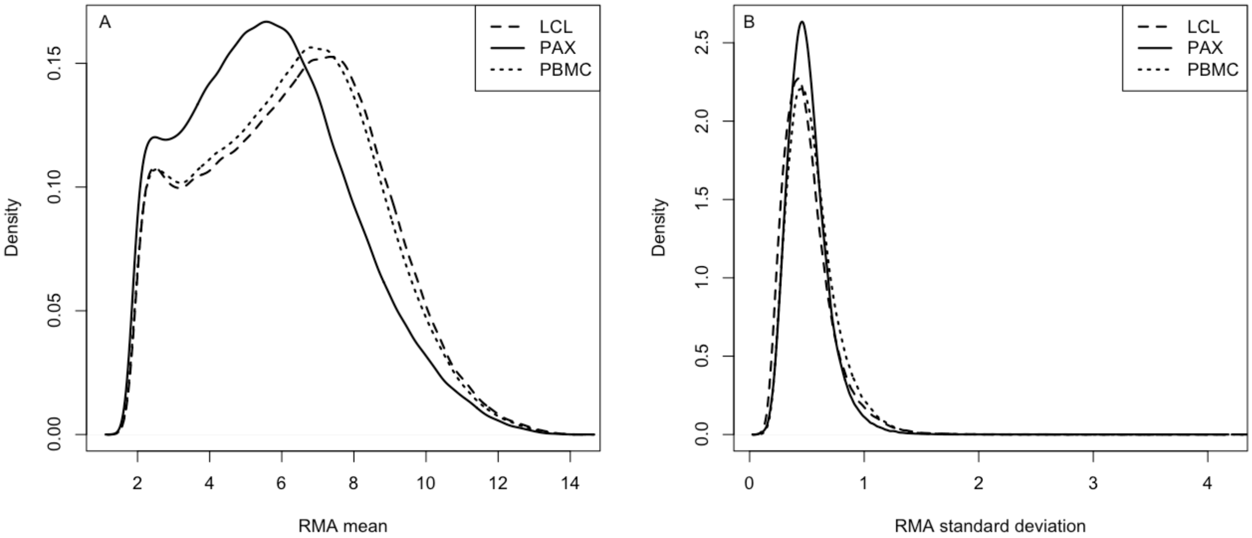
Figure Legends:



Supplementary Figure 1. Comparison of RMA-normalized gene expression mean values across 35 samples for LCL *vs.* PAX, before (left panel) and after (right panel) S10 postnormalization. RMA normalization alone failed to normalize gene expression quantiles between LCL and PAX samples. This skew also appears in PBMC *vs.* PAX. Diagonal lines are identity lines.



Supplementary Figure 2. (A) Mean and (B) standard deviation densities taken over samples (n=35) across the probesets (n=287,329) of the three RNA sources after S10 correction at an exon-probeset level on $\log_2$ RMA scale.

Supplementary Table 1. Partial list of exons highly expressed in PAX.

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PAX[b]	PAX / LCL[c]	PAX / PBMC[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
1	2648705	MME	3	membrane metallo-endopeptidase	13.5	914	605	605	15	29
3	3646486	UBN1	16	ubinuclein 1	13.9	705	507	507	4	27
4	4009851	ALAS2	X	aminolevulinate, delta-, synthase 2	16	1076	487	487	12	16
5	2787959	GYPB	4	glycophorin B (MNS blood group)	13.6	383	401	383	2	9
6	3629207	OAZ2	15	ornithine decarboxylase antizyme 2	17.6	642	380	380	2	11
7	3037101	RSPH10B2	7	radial spoke head 10 homolog B (Chlamydomonas)	12.5	445	336	336	1	8
8	2527593	CXCR2	2	chemokine (C-X-C motif) receptor 2	15	5360	321	321	7	10
10	3838227	SNRNP70	19	small nuclear ribonucleoprotein 70kDa (U1)	14.8	314	390	314	2	14
11	3890137	C20orf108	20	chromosome 20 open reading frame 108	11.5	481	307	307	1	10
12	3771677	ST6GALNAC2	17	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 2	12.6	599	284	284	2	15
13	3756593	KRT23	17	keratin 23 (histone deacetylase inducible)	12.1	437	282	282	3	13
14	3990530	SASH3	X	SAM and SH3 domain containing 3	13.2	643	267	267	2	13
15	3864505	ZNF428	19	zinc finger protein 428	12.9	394	264	264	4	11
16	3457164	CD63	12	CD63 molecule	16.8	363	257	257	6	10
17	3304013	MGEA5	10	meningioma expressed antigen 5 (hyaluronidase)	11.5	320	252	252	6	26
18	3475785	GPR109A	12	G protein-coupled receptor 109A	12.3	481	222	222	6	11
19	3873715	STK35	20	serine/threonine kinase 35	12.6	305	218	218	1	6
21	3334570	CCDC88B	11	coiled-coil domain containing 88B	12	379	213	213	1	41
22	3724534	MYL4	17	myosin, light chain 4, alkali; atrial, embryonic	12.4	384	202	202	3	13
23	3766416	SMARCD2	17	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 2	13.6	277	199	199	1	21
24	3292635	RUFY2	10	RUN and FYVE domain containing 2	11.7	193	259	193	1	24
25	3453838	TUBA1A	12	tubulin, alpha 1a	13.9	938	193	193	2	11
26	3823333	CYP4F3	19	cytochrome P450, family 4, subfamily F, polypeptide 3	11.3	244	188	188	7	17
27	3360408	HBB	11	hemoglobin, beta	17.6	8261	186	186	9	9
28	4007645	OTUD5	X	OTU domain containing 5	11.5	254	185	185	1	19
31	3359532	CARS	11	cysteinyl-tRNA synthetase	14.1	205	175	175	4	27
32	2682274	PROK2	3	prokineticin 2	13.2	1302	175	175	2	5
33	3192641	EEF1A1	9	eukaryotic translation elongation factor 1 alpha 1 pseudogene 9	16.4	173	187	173	1	43
36	3360450	HBG1	11	hemoglobin, gamma A	13.3	1658	166	166	5	9
37	3836037	SFRS16	19	splicing factor, arginine/serine-rich 16	10.9	206	162	162	1	29
38	3846784	UBXN6	19	UBX domain protein 6	10.6	202	162	162	2	17
39	2845979	LPCAT1	5	lysophosphatidylcholine acyltransferase 1	10.1	160	170	160	2	22
40	3090013	SLC25A37	8	solute carrier family 25, member 37	15.7	194	152	152	15	17
42	3676181	HAGH	16	hydroxyacylglutathione hydrolase	15.1	408	150	150	2	14
43	3823330	CYP4F2	19	cytochrome P450, family 4, subfamily F, polypeptide 3	14.8	156	149	149	2	21
45	2599904	C2orf24	2	chromosome 2 open reading frame 24	14.1	226	145	145	4	16
46	3901667	C20orf3	20	chromosome 20 open reading frame 3	12.3	180	143	143	3	16
47	3302230	FRAT2	10	frequently rearranged in advanced T-cell lymphomas 2	11.3	539	140	140	1	4
48	3937171	C22orf25	22	chromosome 22 open reading frame 25	12.3	336	137	137	2	14
49	2907174	HCRP1	6	hepatocellular carcinoma-related HCRP1	10.4	156	136	136	1	3
50	3416506	HNRNPA1	12	heterogeneous nuclear ribonucleoprotein A1	10.5	160	135	135	3	18
51	2831969	IK	5	IK cytokine, down-regulator of HLA II	13.8	149	134	134	10	21
52	3772662	TIMP2	17	TIMP metallopeptidase inhibitor 2	11.9	806	132	132	2	9
53	2927889	CCDC28A	6	coiled-coil domain containing 28A	13.1	282	132	132	8	11
55	3874280	ITPA	20	inosine triphosphatase (nucleoside triphosphate pyrophosphatase)	10.1	131	164	131	3	14

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PAX[b]	PAX / LCL[c]	PAX / PBMC[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
57	3815869	DAZAP1	19	DAZ associated protein 1	11.1	177	129	129	2	19
59	4026670	BCAP31	X	B-cell receptor-associated protein 31	14.6	372	129	129	1	12
60	3506942	GTF3A	13	mitochondrial translational initiation factor 3	13.3	248	128	128	5	20
61	3499679	ERCC5	13	excision repair cross-complementing rodent repair deficiency, complementation group 5	9.8	226	127	127	4	26
62	2324119	PINK1	1	PTEN induced putative kinase 1	13.3	190	127	127	5	17
65	2396422	MASP2	1	mannan-binding lectin serine peptidase 2	11.8	155	122	122	2	15
66	2764199	SEL1L3	4	sel-1 suppressor of lin-12-like 3 (C. elegans)	13.3	193	121	121	1	35
67	3190551	GLE1	9	GLE1 RNA export mediator homolog (yeast)	12.1	121	121	121	1	25
69	3870450	VSTM1	19	V-set and transmembrane domain containing 1	11.7	386	117	117	1	11
70	3475800	GPR109B	12	G protein-coupled receptor 109B	13.8	171	117	117	1	4
71	3203491	BAG1	9	BCL2-associated athanogene	14.5	116	149	116	11	15
74	3218538	ABCA1	9	ATP-binding cassette, sub-family A (ABC1), member 1	10.7	289	114	114	7	62
75	2435006	SELENBP1	1	selenium binding protein 1	12.3	202	114	114	6	16
76	3882710	CHMP4B	20	chromatin modifying protein 4B	10.1	192	111	111	1	14
77	3479359	GOLGA3	12	golgin A3	11.8	110	116	110	1	38
79	2603071	SP110	2	SP110 nuclear body protein	12.6	109	114	109	3	24
80	3959632	EIF3D	22	eukaryotic translation initiation factor 3, subunit D	13.4	107	115	107	2	17
81	3337099	RPS6KB2	11	ribosomal protein S6 kinase, 70kDa, polypeptide 2	12.7	141	106	106	2	18
83	3850446	CDKN2D	19	cyclin-dependent kinase inhibitor 2D (p19, inhibits CDK4)	13.6	520	105	105	1	4
85	3717038	RPL41	17	ribosomal protein L41	18.4	150	104	104	3	11
87	3180029	PHF2	9	PHD finger protein 2	11.4	252	104	104	2	34
88	2317451	TPRG1L	1	tumor protein p63 regulated 1-like	10	202	104	104	2	10
89	3645314	SRRM2	16	serine/arginine repetitive matrix 2	8.5	103	123	103	3	43
90	2354006	FAM46C	1	family with sequence similarity 46, member C	11.7	103	129	103	3	7
92	4045599	S100A4	1	S100 calcium binding protein A4	16.7	2203	102	102	3	8
93	2583056	BAZ2B	2	bromodomain adjacent to zinc finger domain, 2B	10.3	154	101	101	25	50
94	3214453	NFIL3	9	nuclear factor, interleukin 3 regulated	11	261	101	101	3	5
95	2714308	PCGF3	4	polycomb group ring finger 3	11.2	122	101	101	1	24
96	2622431	RBM6	3	RNA binding motif protein 6	10.2	100	102	100	5	31
97	3758159	BECN1	17	beclin 1, autophagy related	12.9	146	99	99	1	13
98	2639118	PARP14	3	poly (ADP-ribose) polymerase family, member 14	13.7	99	109	99	4	28
99	3942887	LIMK2	22	LIM domain kinase 2	13.9	236	98	98	3	29
100	2329021	RBBP4	1	retinoblastoma binding protein 4	13.2	98	107	98	2	20
102	2564827	LOC150759	2	ankyrin repeat domain 36B	8.4	156	98	98	6	9
103	3608050	NGRN	15	tubulin tyrosine ligase-like family, member 13	12.9	132	97	97	4	14
104	3780318	RNMT	18	RNA (guanine-7-) methyltransferase	12.4	97	157	97	1	18
105	3122766	DEFA3	8	defensin, alpha 3, neutrophil-specific	14.9	1042	97	97	9	12
108	3725022	CDK5RAP3	17	CDK5 regulatory subunit associated protein 3	12	109	97	97	5	20
111	2892200	WRNIP1	6	Werner helicase interacting protein 1	11.9	186	95	95	2	20
112	3375864	MTA2	11	metastasis associated 1 family, member 2	12	95	122	95	2	23
113	3248912	NRBF2	10	nuclear receptor binding factor 2	12.1	166	94	94	2	10
114	2522813	STRADB	2	STE20-related kinase adaptor beta	13.3	94	98	94	7	17
115	3243750	BMS1	10	BMS1 homolog, ribosome assembly protein (yeast)	14	94	131	94	2	31
116	2599318	CXCR1	2	chemokine (C-X-C motif) receptor 2 pseudogene 1	11.1	189	93	93	8	8
117	3449370	CAPRIN2	12	caprin family member 2	9.9	106	93	93	6	34

Rank [a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PAX[b]	PAX / LCL[c]	PAX / PBMC[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
118	2440951	FCGR3A	1	Fc fragment of IgG, low affinity IIIa, receptor (CD16a)	10	314	93	93	2	15
120	3941955	EWSR1	22	Ewing sarcoma breakpoint region 1	14.3	93	135	93	4	24
121	2694398	RPN1	3	ribophorin I	13.4	93	110	93	2	14
123	2485476	AFTPH	2	aftiphilin	11.7	102	91	91	1	17
125	2349435	AMY1A	1	amylase, alpha 2B (pancreatic)	12.1	323	91	91	11	71
126	3959415	APOL2	22	apolipoprotein L, 2	10.5	90	101	90	1	12
128	3458579	ARHGAP9	12	Rho GTPase activating protein 9	10.2	90	94	90	3	23
129	3642682	HBA1	16	hemoglobin, alpha 1	18	644	89	89	13	14
130	2981913	EZR	6	ezrin	13.2	89	97	89	2	25
134	3712054	UBB	17	ubiquitin B	17	88	126	88	2	7
135	3966626	SFRS17A	X	splicing factor, arginine/serine-rich 17A	10.8	94	87	87	2	28
136	3920876	KCNJ15	21	potassium inwardly-rectifying channel, subfamily J, member 15	11.8	356	87	87	7	10
137	3842302	ZNF581	19	zinc finger protein 581	11.4	114	86	86	1	10
138	3643270	RHOT2	16	ras homolog gene family, member T2	9.9	126	86	86	3	25
139	2622534	RBM5	3	RNA binding motif protein 5	14.1	131	85	85	9	29
142	2488234	ZNF638	2	zinc finger protein 638	8.9	85	91	85	9	43
144	2999835	YKT6	7	YKT6 v-SNARE homolog (S. cerevisiae)	10.2	120	85	85	1	13
147	3221546	CDC26	9	cell division cycle 26 homolog (S. cerevisiae)	11.8	84	99	84	3	9
148	2584267	KCNH7	2	potassium voltage-gated channel, subfamily H (eag-related), member 7	10.5	106	84	84	1	23
149	3795684	THOC1	18	THO complex 1	9.7	83	86	83	2	23
150	2451595	CHI3L1	1	chitinase 3-like 1 (cartilage glycoprotein-39)	10.7	83	88	83	4	14
151	3855012	ELL	19	elongation factor RNA polymerase II	11.4	83	136	83	2	20
152	2334302	UROD	1	uroporphyrinogen decarboxylase	10.3	82	88	82	2	12
154	3392841	BUD13	11	BUD13 homolog (S. cerevisiae)	11.9	82	103	82	3	17
155	2363796	HSPA6	1	heat shock 70kDa protein 6 (HSP70B')	12	179	82	82	4	8
157	2347752	TMEM56	1	transmembrane protein 56	10.3	82	80	80	5	7
158	2528383	ANKZF1	2	ankyrin repeat and zinc finger domain containing 1	10.5	80	82	80	2	21
159	3862662	BLVRB	19	biliverdin reductase B (flavin reductase (NADPH))	11.6	139	79	79	1	7
160	3669110	TERF2IP	16	telomeric repeat binding factor 2, interacting protein	14.8	85	79	79	1	9
162	3091041	BNIP3L	8	BCL2/adenovirus E1B 19kDa interacting protein 3-like	12	148	79	79	2	15
163	2939215	TUBB2A	6	tubulin, beta 2A	11.5	78	418	78	1	9
165	2709783	BCL6	3	B-cell CLL/lymphoma 6	12	379	78	78	2	16
166	3261523	NOLC1	10	nucleolar and coiled-body phosphoprotein 1	9.3	78	84	78	1	23
168	3824220	DDA1	19	DET1 and DDB1 associated 1	16.4	77	96	77	1	8
171	3385181	PICALM	11	phosphatidylinositol binding clathrin assembly protein	9.3	109	76	76	1	2
172	3428710	CHPT1	12	choline phosphotransferase 1	8.7	88	76	76	3	17
173	3896079	SLC23A2	20	solute carrier family 23 (nucleobase transporters), member 2	9.3	113	76	76	1	31
174	2888116	THOC3	5	THO complex 3	13	76	87	76	2	14
175	3548051	PRO1768	14	PRO1768	10.9	80	76	76	2	3
177	2577706	ZRANB3	2	zinc finger, RAN-binding domain containing 3	11.2	75	76	75	1	19
178	3907653	NCOA5	20	nuclear receptor coactivator 5	9.6	121	75	75	1	18
181	2393671	KIAA0495	1	KIAA0495	13.7	89	74	74	2	17
182	2974636	VNN2	6	vanin 2	11.1	190	74	74	6	17
183	3434796	P2RX4	12	purinergic receptor P2X, ligand-gated ion channel, 4	8.7	120	74	74	1	15
184	3457753	STAT2	12	signal transducer and activator of transcription 2, 113kDa	10.6	74	75	74	1	26

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185	3770564	ATP5H	17	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit d	10.2	85	73	73	2	7
187	2406785	CSF3R	1	colony stimulating factor 3 receptor (granulocyte)	13.2	613	72	72	2	28
188	2350304	PRPF38B	1	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	11.9	72	83	72	6	17
189	3453775	LMBR1L	12	limb region 1 homolog (mouse)-like	10.5	113	72	72	2	26
193	2814456	SMN1	5	survival of motor neuron 1, telomeric	10.9	71	76	71	3	31
194	3227071	PTGES	9	prostaglandin E synthase	11.4	85	71	71	1	9
195	3730970	PSMC5	17	proteasome (prosome, macropain) 26S subunit, ATPase, 5	14.7	71	83	71	6	13
196	3456667	NFE2	12	nuclear factor (erythroid-derived 2), 45kDa	12.4	559	70	70	2	6
197	3226370	CIZ1	9	CDKN1A interacting zinc finger protein 1	10.3	77	70	70	2	32
198	3633554	IMP3	15	IMP3, U3 small nucleolar ribonucleoprotein, homolog (yeast)	12.6	70	82	70	2	4
199	3525703	ANKRD10	13	ankyrin repeat domain 10	11	70	119	70	4	20
200	3434464	RNF10	12	ring finger protein 10	11.3	90	70	70	5	26
201	3360419	HBD	11	hemoglobin, delta	9.9	144	70	70	5	7
202	2907832	CUL9	6	cullin 9	8.5	71	70	70	2	51
203	3901697	ACSS1	20	acyl-CoA synthetase short-chain family member 1	12.4	96	70	70	2	23
204	3444253	CSDA	12	cold shock domain protein A	9.8	72	69	69	3	7
206	3399624	THYN1	11	thymocyte nuclear protein 1	12.7	93	69	69	1	1
207	3735829	SEC14L1	17	SEC14-like 1 (S. cerevisiae)	15.1	69	96	69	6	29
212	3945932	ATF4	22	activating transcription factor 4 (tax-responsive enhancer element B67)	14.1	68	76	68	3	13
213	3235445	SEC61A2	10	Sec61 alpha 2 subunit (S. cerevisiae)	11.6	70	68	68	7	17
215	3874475	CDC25B	20	cell division cycle 25 homolog B (S. pombe)	12.9	370	67	67	3	27
216	3057522	TMEM120A	7	transmembrane protein 120A	13.1	76	67	67	1	17
217	3654987	LAT	16	linker for activation of T cells	13.2	322	67	67	1	17
218	3621043	EPB42	15	erythrocyte membrane protein band 4.2	12.1	135	67	67	4	17
220	2701295	TMEM14E	3	transmembrane protein 14E	9	84	66	66	2	3
222	3642087	CHSY1	15	chondroitin sulfate synthase 1	9.9	70	66	66	1	14
223	3142985	CA1	8	carbonic anhydrase I	11	362	66	66	8	13
225	3489676	KCNRG	13	potassium channel regulator	9.6	101	65	65	3	4
226	2603972	KCNJ13	2	potassium inwardly-rectifying channel, subfamily J, member 13	10.7	74	65	65	2	8
228	3718815	TAF15	17	TAF15 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 68kDa	15.7	65	96	65	9	26
229	3966226	RABL2A	22	RAB, member of RAS oncogene family-like 2B	12.1	143	65	65	2	23
232	3938243	SDF2L1	22	stromal cell-derived factor 2-like 1	14.2	64	129	64	1	4
233	2328504	KHDRBS1	1	KH domain containing, RNA binding, signal transduction associated 1	12.4	72	64	64	1	18
234	3779400	IMPA2	18	inositol(myo)-1(or 4)-monophosphatase 2	12.2	128	64	64	1	14
235	2402433	PAQR7	1	progestin and adipoQ receptor family member VII	10.8	94	64	64	1	6
236	2496938	IL1R2	2	interleukin 1 receptor, type II	9	91	63	63	8	14
237	3930240	RCAN1	21	regulator of calcineurin 1	9.9	83	63	63	1	14
238	2477460	QPCT	2	glutaminyl-peptide cyclotransferase	10.2	254	63	63	5	12
239	3212260	KIF27	9	kinesin family member 27	10.8	63	73	63	7	26
240	2406678	STK40	1	serine/threonine kinase 40	10.6	135	63	63	1	19
241	2503639	TSN	2	translin	10.2	81	63	63	2	14
242	3890257	C20orf43	20	chromosome 20 open reading frame 43	12.1	89	63	63	5	14
243	2638072	ADPRH	3	ADP-ribosylarginine hydrolase	12.5	63	96	63	1	11
244	2458290	LBR	1	lamin B receptor	11.4	63	75	63	1	18
245	2475647	YPEL5	2	yippee-like 5 (Drosophila)	12.2	306	63	63	1	6

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PAX[b]	PAX / LCL[c]	PAX / PBMC[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
246	3759039	SLC4A1	17	solute carrier family 4, anion exchanger, member 1 (erythrocyte membrane protein band 3, Diego blood group)	11.3	110	63	63	4	22
250	4052393	SNRNP35	12	small nuclear ribonucleoprotein 35kDa (U11/U12)	8.9	61	71	61	2	8
252	3335950	SF3B2	11	splicing factor 3b, subunit 2, 145kDa	14.9	61	84	61	4	26
253	3830492	FFAR2	19	free fatty acid receptor 2	10.6	85	61	61	1	2
254	2403302	RPA2	1	replication protein A2, 32kDa	12.1	79	61	61	5	13
255	3664842	CMTM2	16	CKLF-like MARVEL transmembrane domain containing 2	9.8	66	60	60	3	6
256	2739266	GAR1	4	GAR1 ribonucleoprotein homolog (yeast)	10.1	60	149	60	2	13
259	3721690	STAT5A	17	signal transducer and activator of transcription 5A	13	81	60	60	1	27
260	3041520	TRA2A	7	transformer 2 alpha homolog (Drosophila)	9.6	75	60	60	2	16
263	3531194	COCH	14	coagulation factor C homolog, cochlin (Limulus polyphemus)	11.2	59	240	59	2	20
265	4007735	TFE3	X	transcription factor binding to IGHM enhancer 3	12.8	78	59	59	1	20
266	4044638	SLC35E2	1	similar to solute carrier family 35, member E2	9.3	94	59	59	1	25
268	3701626	GAFA2	16	FGF-2 activity-associated protein 2	9.5	71	58	58	1	3
270	3065248	RASA4	7	RAS p21 protein activator 4	13.4	220	58	58	2	50
271	3904945	BLCAP	20	bladder cancer associated protein	12.4	71	58	58	1	7
273	2910526	FBXO9	6	F-box protein 9	9.8	110	58	58	6	23
274	3944146	HMOX1	22	heme oxygenase (decycling) 1	11.4	123	58	58	1	6
277	2358686	C1orf56	1	chromosome 1 open reading frame 56	8.6	83	58	58	2	13
278	3861980	PAF1	19	Paf1, RNA polymerase II associated factor, homolog (S. cerevisiae)	12.5	58	91	58	2	18
279	2531461	SP100	2	SP100 nuclear antigen	9.9	65	57	57	1	41
281	2896978	FAM8A1	6	family with sequence similarity 8, member A1	8.3	96	57	57	2	16
282	3377046	SF1	11	splicing factor 1	12.9	81	57	57	3	35
283	3591693	C15orf63	15	chromosome 15 open reading frame 63	12.8	56	119	56	3	15
284	3551338	CCNK	14	cyclin K	8.6	56	57	56	2	17
285	3609192	CHD2	15	chromodomain helicase DNA binding protein 2	13.7	62	56	56	24	48
286	3293727	C10orf54	10	chromosome 10 open reading frame 54	13.8	537	56	56	2	15
287	2988871	C7orf28A	7	chromosome 7 open reading frame 28A	13.8	102	56	56	6	40
288	2320070	TARDBP	1	TAR DNA binding protein	14.7	58	56	56	8	23
289	3992544	HTATSF1	X	HIV-1 Tat specific factor 1	9.6	82	56	56	4	16
290	3063771	C7orf43	7	chromosome 7 open reading frame 43	10.7	95	56	56	1	18
291	3679505	TMEM186	16	transmembrane protein 186	12.8	60	56	56	2	6
293	2375339	OCR1	1	ovarian cancer-related protein 1	9.7	99	56	56	2	3
294	3535132	ATP5S	14	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit s (factor B)	11	63	56	56	2	14
295	3833780	SNRPA	19	small nuclear ribonucleoprotein polypeptide A	11.6	56	74	56	1	10
296	3923568	C21orf33	21	chromosome 21 open reading frame 33	12.3	74	55	55	1	11
297	2362345	MNDA	1	myeloid cell nuclear differentiation antigen	9.6	135	55	55	3	9
298	2854349	FYB	5	FYN binding protein	11.2	407	55	55	1	18
299	3446870	LDHB	12	lactate dehydrogenase B	12.5	55	100	55	2	12
301	3567190	DHRS7	14	dehydrogenase/reductase (SDR family) member 7	8.5	61	55	55	8	13
302	3966058	CHKB-CPT1B	22	choline kinase-like, carnitine palmitoyltransferase 1B (muscle) transcription unit	10.9	64	55	55	2	42
307	3645625	MMP25	16	matrix metallopeptidase 25	11	67	54	54	1	15
308	3502594	LAMP1	13	lysosomal-associated membrane protein 1	15.7	114	54	54	2	14
310	3664807	CKLF	16	chemokine-like factor	8.3	124	54	54	4	9
311	3952704	C22orf39	22	chromosome 22 open reading frame 39	10.8	65	54	54	1	5
314	2327726	EPB41	1	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	7.7	99	54	54	5	27

[a] rank of the top probeset of the gene, according to minimum fold change.

[b] Mean of the top probeset of the gene in RMA units, $\log_2$ scale.
[c] Fold change ratio of gene expression between PAX and LCL or between PAX and PBMC for the top probeset of the gene
[d] Minimum fold change of the top probeset of the gene
[e] Number of exons of the gene with ≥ 8 minimum fold change
[f] Total number of exons of the gene in the annotation

Supplementary Table 2. Partial list of exons highly expressed in LCL.

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean LCL[b]	LCL / PAX[c]	LCL / PBMC[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
1	3662688	CCL22	16	chemokine (C-C motif) ligand 22	12.8	290	399	290	6	8
3	3595983	CCNB2	15	cyclin B2	11.2	354	125	125	7	12
4	3756211	TOP2A	17	topoisomerase (DNA) II alpha 170kDa	11.2	191	118	118	36	42
5	3090706	CDCA2	8	cell division cycle associated 2	10.6	401	115	115	8	29
6	3197994	GLDC	9	glycine dehydrogenase (decarboxylating)	10.6	184	109	109	10	31
7	3040576	MACC1	7	metastasis associated in colon cancer 1	10.7	153	105	105	12	14
8	3629117	KIAA0101	15	KIAA0101	10.4	618	104	104	7	8
9	3881451	TPX2	20	TPX2, microtubule-associated, homolog (Xenopus laevis)	9.9	192	101	101	20	28
10	3589740	BUB1B	15	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	9.2	98	116	98	17	29
11	3260610	SCD	10	stearoyl-CoA desaturase (delta-9-desaturase)	10.9	307	93	93	12	13
13	3703116	GINS2	16	GINS complex subunit 2 (Psf2 homolog)	10.8	297	92	92	6	8
14	3775853	TYMS	18	thymidylate synthetase	12.8	585	92	92	8	13
15	3653079	PLK1	16	polo-like kinase 1 (Drosophila)	10.8	298	92	92	10	13
16	3744282	AURKB	17	aurora kinase B	10.7	91	124	91	5	13
17	2378944	DTL	1	denticleless homolog (Drosophila)	9.5	103	89	89	15	16
19	2784122	CCNA2	4	cyclin A2	12.1	140	88	88	6	10
21	2333158	CDC20	1	cell division cycle 20 homolog (S. cerevisiae)	11.7	160	86	86	11	15
22	2372794	RGS1	1	regulator of G-protein signaling 1	10.1	231	85	85	5	8
23	3565694	DLGAP5	14	discs, large (Drosophila) homolog-associated protein 5	11.6	168	85	85	19	23
24	2436878	KCNN3	1	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	11.1	92	84	84	11	19
31	3258464	CEP55	10	centrosomal protein 55kDa	10.5	125	79	79	8	15
32	2720268	NCAPG	4	non-SMC condensin I complex, subunit G	9.5	87	78	78	13	23
36	3754015	CCL3	17	chemokine (C-C motif) ligand 3	12	141	76	76	5	8
42	3781576	CABLES1	18	Cdk5 and Abl enzyme substrate 1	11.3	186	72	72	4	12
44	3129171	PBK	8	PDZ binding kinase	10.8	78	71	71	2	14
45	3817385	EBI3	19	Epstein-Barr virus induced 3	11.1	71	88	71	4	8
52	3440634	FOXM1	12	forkhead box M1	9.2	95	68	68	6	19
53	2494497	NCAPH	2	non-SMC condensin I complex, subunit H	10.8	261	68	68	19	26
54	4004051	DMD	X	dystrophin	11.1	178	67	67	6	108
56	2330776	CDCA8	1	cell division cycle associated 8	9.5	111	66	66	8	13
61	3886251	MYBL2	20	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	9.2	172	65	65	14	19
65	2570670	BUB1	2	budding uninhibited by benzimidazoles 1 homolog (yeast)	9.3	156	64	64	24	31
66	3331910	FAM111B	11	family with sequence similarity 111, member B	11.5	137	64	64	6	9
68	4040935	CCL3L1	17	chemokine (C-C motif) ligand 3-like 1	11.9	132	63	63	4	13
72	3168519	MELK	9	maternal embryonic leucine zipper kinase	10.8	64	62	62	7	23
75	2638090	PLA1A	3	phospholipase A1 member A	8.6	61	66	61	6	15
78	3248308	CDK1	10	cyclin-dependent kinase 1	8.2	60	65	60	5	10
79	2914786	TTK	6	TTK protein kinase	9.5	130	60	60	10	24
81	2830655	KIF20A	5	kinesin family member 20A	9	71	59	59	9	19
84	2707895	LAMP3	3	lysosomal-associated membrane protein 3	13.5	100	59	59	6	10
86	3648405	TNFRSF17	16	tumor necrosis factor receptor superfamily, member 17	10	151	59	59	5	7
89	3013269	PEG10	7	paternally expressed 10	12	171	58	58	12	21
92	2693027	SLC12A8	3	solute carrier family 12 (potassium/chloride transporters), member 8	10.4	57	82	57	6	21
94	2946371	HIST1H3G	6	histone cluster 1, H3g	14	323	57	57	2	2
102	3910788	AURKA	20	aurora kinase A	10.6	98	56	56	7	16
104	3868683	KLK1	19	kallikrein 1	12	71	55	55	4	10

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean LCL[b]	LCL / PAX[c]	LCL / PBMC[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
107	3312511	MKI67	10	antigen identified by monoclonal antibody Ki-67	12.2	91	55	55	24	31
109	2690916	CD80	3	CD80 molecule	10.6	120	54	54	9	14
110	3887059	UBE2C	20	ubiquitin-conjugating enzyme E2C	10.5	77	54	54	3	15
111	3919324	CLIC6	21	chloride intracellular channel 6	9.4	100	54	54	5	11
115	2469276	RRM2	2	ribonucleotide reductase M2	11.1	58	53	53	10	14
117	2988748	FSCN1	7	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	9.6	100	53	53	9	14
119	2620262	KIF15	3	kinesin family member 15	9.4	89	52	52	18	36
122	2947074	HIST1H1B	6	histone cluster 1, H1b	12	340	52	52	2	3
123	2813424	CCNB1	5	cyclin B1	8	68	52	52	6	15
126	2434082	HIST2H3A	1	histone cluster 2, H3a	14.9	1033	51	51	2	4
135	3354810	CHEK1	11	CHK1 checkpoint homolog (S. pombe)	10.9	51	49	49	12	17
136	3258181	KIF11	10	kinesin family member 11	8.5	63	48	48	19	26
138	3750824	SPAG5	17	sperm associated antigen 5	11.5	77	48	48	16	31
140	3595004	TEX9	15	testis expressed 9	9.2	57	48	48	5	12
144	2417534	DEPDC1	1	DEP domain containing 1	8.9	65	47	47	4	18
149	2334100	KIF2C	1	kinesin family member 2C	10.6	55	47	47	11	27
151	3536340	CDKN3	14	cyclin-dependent kinase inhibitor 3	8.1	79	46	46	7	13
155	2449571	ASPM	1	asp (abnormal spindle) homolog, microcephaly associated (Drosophila)	8.3	47	46	46	24	46
159	2742961	HSPA4L	4	heat shock 70kDa protein 4-like	9	63	46	46	7	21
161	2798922	TRIP13	5	thyroid hormone receptor interactor 13	9.9	91	46	46	11	21
167	3590392	NUSAP1	15	nucleolar and spindle associated protein 1	10.2	78	45	45	14	17
170	3041818	DFNA5	7	deafness, autosomal dominant 5	9.7	44	68	44	6	15
177	3962177	CENPM	22	centromere protein M	8.4	44	47	44	1	9
180	3847996	CD70	19	CD70 molecule	11.8	44	48	44	3	8
182	2946217	HIST1H3B	6	histone cluster 1, H3b	14.2	588	43	43	1	2
187	2379919	CENPF	1	centromere protein F, 350/400ka (mitosin)	9.2	46	42	42	16	34
189	3581925	IGHM	14	ADAM metallopeptidase domain 6 (pseudogene)	15.9	69	42	42	7	31
192	3980604	KIF4A	X	kinesin family member 4A	10.5	65	42	42	4	34
199	2899104	HIST1H3C	6	histone cluster 1, H3c	14.2	2389	41	41	1	1
201	3754805	HNF1B	17	HNF1 homeobox B	9.2	41	42	41	5	19
206	2902414	LTA	6	lymphotoxin alpha (TNF superfamily, member 1)	12.5	225	41	41	3	5
208	3140232	MSC	8	musculin	9.8	177	41	41	4	10
216	3463134	E2F7	12	E2F transcription factor 7	9.6	40	44	40	8	22
218	2529435	SGPP2	2	sphingosine-1-phosphate phosphotase 2	10.4	161	40	40	7	10
219	3061827	SGCE	7	sarcoglycan, epsilon	10.3	63	39	39	5	18
228	3689885	SHCBP1	16	SHC SH2-domain binding protein 1	10.8	45	39	39	11	16
229	3590024	CASC5	15	cancer susceptibility candidate 5	9.1	58	39	39	18	47
230	3129733	DUSP4	8	dual specificity phosphatase 4	9.5	39	47	39	3	12
231	3390865	POU2AF1	11	POU class 2 associating factor 1	12.2	165	39	39	5	10
232	2798651	AHRR	5	aryl-hydrocarbon receptor repressor	8.5	41	39	39	1	19
235	3377427	CDCA5	11	cell division cycle associated 5	9.7	58	39	39	4	10
246	2947097	HIST1H3J	6	histone cluster 1, H3j	11.2	363	38	38	3	3
248	3632918	SEMA7A	15	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	10.6	56	38	38	11	15
249	2900060	HIST1H2BM	6	histone cluster 1, H2bm	11.8	321	38	38	2	2
252	3936920	CDC45	22	cell division cycle 45 homolog (S. cerevisiae)	9.9	99	38	38	7	20
253	3880836	GINS1	20	GINS complex subunit 1 (Psf1 homolog)	9.4	49	38	38	5	10
258	3516038	DIAPH3	13	diaphanous homolog 3 (Drosophila)	9.3	77	38	38	9	23
273	3409163	ARNTL2	12	aryl hydrocarbon receptor nuclear translocator-like 2	8	57	36	36	9	26
274	3365778	E2F8	11	E2F transcription factor 8	8.8	62	36	36	8	18
280	2334663	RAD54L	1	RAD54-like (S. cerevisiae)	9.7	120	36	36	3	21

Probeset Det. Tot.

Rank[a]	ID	Gene Symbol	Chr	Description	Mean LCL[b]	LCL / PAX[c]	LCL / PBMC[c]	Min FC[d]	exons[e]	no. exons[f]
284	2450368	KIF14	1	kinesin family member 14	8.2	36	45	36	12	47
287	2947045	HIST1H2AI	6	histone cluster 1, H2aj	14	489	35	35	4	4
288	3590094	RAD51	15	RAD51 homolog (RecA homolog, E. coli) (S. cerevisiae)	7.7	57	35	35	5	12
289	3622398	GATM	15	glycine amidinotransferase (L-arginine:glycine amidinotransferase)	10.4	287	35	35	8	10
295	2767023	APBB2	4	amyloid beta (A4) precursor protein-binding, family B, member 2	7.4	38	35	35	9	20
296	3848510	FCER2	19	Fc fragment of IgE, low affinity II, receptor for (CD23)	10.9	281	35	35	13	18
298	2412831	ORC1L	1	origin recognition complex, subunit 1-like (yeast)	10	61	35	35	8	25
328	3291612	EGR2	10	early growth response 2	11	32	48	32	3	8
329	3487321	TNFSF11	13	tumor necrosis factor (ligand) superfamily, member 11	9.2	47	32	32	1	12
332	2947042	HIST1H2AJ	6	histone cluster 1, H2aj	13.9	61	32	32	1	2
333	2742994	PLK4	4	polo-like kinase 4 (Drosophila)	9.4	59	32	32	10	23
339	3504622	SKA3	13	spindle and kinetochore associated complex subunit 3	8.8	51	32	32	5	15
341	2786354	SLC7A11	4	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11	9.6	35	32	32	11	16
344	2451216	UBE2T	1	ubiquitin-conjugating enzyme E2T (putative)	10.6	85	32	32	5	8
346	2780197	CENPE	4	centromere protein E, 312kDa	7.7	43	32	32	18	61
348	3720907	CDC6	17	cell division cycle 6 homolog (S. cerevisiae)	8.6	31	43	31	9	14
352	3607737	C15orf42	15	chromosome 15 open reading frame 42	10.1	43	31	31	6	14
357	3160689	SLC1A1	9	solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1	7.7	31	43	31	5	13
360	2454457	NEK2	1	NIMA (never in mitosis gene a)-related kinase 2	9.8	31	60	31	3	12
363	3788060	SKA1	18	spindle and kinetochore associated complex subunit 1	7.6	52	31	31	3	12
368	2340330	AK3L1	1	adenylate kinase 3-like 1	8.2	60	30	30	6	11
375	3599836	KIF23	15	kinesin family member 23	8.7	35	30	30	12	25
378	2891371	IRF4	6	interferon regulatory factor 4	13.8	30	30	30	11	17
381	4052899	FAM72A	1	family with sequence similarity 72, member D	9.2	51	30	30	4	6
382	3415887	ESPL1	12	extra spindle pole bodies homolog 1 (S. cerevisiae)	9.4	34	30	30	4	47
383	2476697	RASGRP3	2	RAS guanyl releasing protein 3 (calcium and DAG-regulated)	9.8	36	30	30	18	25
386	3178592	CKS2	9	CDC28 protein kinase regulatory subunit 2	9.3	30	42	30	3	6
388	3817717	UHRF1	19	ubiquitin-like with PHD and ring finger domains 1	9	71	30	30	10	19
389	3474189	CIT	12	citron (rho-interacting, serine/threonine kinase 21)	8.7	54	30	30	16	57
390	2571471	CKAP2L	2	cytoskeleton associated protein 2-like	8.3	41	30	30	6	13
391	3367357	KIF18A	11	kinesin family member 18A	7.1	74	30	30	12	20
404	3581824	IGHG1	14	ADAM metallopeptidase domain 6 (pseudogene)	12.6	267	29	29	7	39
405	3301752	BLNK	10	B-cell linker	8.5	29	31	29	7	19
406	2838674	HMMR	5	hyaluronan-mediated motility receptor (RHAMM)	7.8	29	49	29	7	20
407	3772170	TK1	17	thymidine kinase 1, soluble	10.5	78	29	29	1	11
412	3581858	IGHG3	14	ADAM metallopeptidase domain 6 (pseudogene)	12.2	498	28	28	8	15
414	3581836	IGHV4-31	14	ADAM metallopeptidase domain 6 (pseudogene)	12.9	514	28	28	17	32
415	2900094	HIST1H2AL	6	histone cluster 1, H2al	10.1	71	28	28	2	2

Rank^a	Probeset ID	Gene Symbol	Chr.	Description	Mean LCL^b	LCL / PAX^c	LCL / PBMC^c	Min FC^d	Det. exons^e	Tot. no. exons^f
420	3097163	MCM4	8	minichromosome maintenance complex component 4	7.6	46	28	28	18	29
424	2531791	ARMC9	2	armadillo repeat containing 9	7.4	36	28	28	1	26
432	2665592	SGOL1	3	shugoshin-like 1 (S. pombe)	9.3	28	37	28	4	9
433	3945552	APOBEC3B	22	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	9.2	54	28	28	4	11
436	2411233	STIL	1	SCL/TAL1 interrupting locus	11.6	34	28	28	14	33
439	3235803	MCM10	10	minichromosome maintenance complex component 10	7.6	27	30	27	10	29
444	3603443	CHRNA5	15	cholinergic receptor, nicotinic, alpha 5	8.2	33	27	27	2	13
445	2343497	IFI44L	1	interferon-induced protein 44-like	8.9	53	27	27	15	16
448	2772095	UGT2B15	4	UDP glucuronosyltransferase 2 family, polypeptide B17	7.6	30	27	27	2	16
454	3443211	AICDA	12	activation-induced cytidine deaminase	10.8	27	36	27	2	10
462	2796540	MLF1IP	4	MLF1 interacting protein	9	89	26	26	10	24
469	3258949	HELLS	10	helicase, lymphoid-specific	7.3	44	26	26	12	28
481	3428849	C12orf48	12	chromosome 12 open reading frame 48	8.7	30	25	25	7	22
484	3768800	ABCA6	17	ATP-binding cassette, sub-family A (ABC1), member 6	8.8	32	25	25	6	53
486	2691583	POLQ	3	polymerase (DNA directed), theta	7.8	26	25	25	10	57
487	3607539	FANCI	15	Fanconi anemia, complementation group I	7.3	49	25	25	25	45
490	2516056	CDCA7	2	cell division cycle associated 7	7.3	30	25	25	1	17
502	3818520	TRIP10	19	thyroid hormone receptor interactor 10	10.3	170	25	25	8	17
510	3451968	RACGAP1	12	Rac GTPase activating protein 1 pseudogene	10	67	25	25	15	24
511	2604265	HJURP	2	Holliday junction recognition protein	9.1	26	25	25	6	17
514	2317388	TP73	1	tumor protein p73	8.3	25	27	25	2	20
520	3623062	FBN1	15	fibrillin 1	8.5	38	24	24	6	69
539	2377323	CR2	1	complement component (3d/Epstein Barr virus) receptor 2	8.3	33	24	24	13	19
540	3581692	IGHG4	14	ADAM metallopeptidase domain 6 (pseudogene)	13.1	289	24	24	3	7
551	2363862	FCRLA	1	Fc receptor-like A	10.4	116	23	23	9	13
563	2371132	LAMC1	1	laminin, gamma 1 (formerly LAMB2)	7.2	33	23	23	14	36
579	2388229	EXO1	1	exonuclease 1	8.9	36	22	22	5	17
582	3626882	MYO1E	15	myosin IE	8	36	22	22	10	36
586	2607632	CHL1	3	cell adhesion molecule with homology to L1CAM (close homolog of L1)	7.3	22	30	22	3	33
588	3587478	ARHGAP11A	15	Rho GTPase activating protein 11A	9.3	25	22	22	13	21
592	2754622	SNX25	4	sorting nexin 25	9.4	27	22	22	16	27
593	3589734	PAK6	15	budding uninhibited by benzimidazoles 1 homolog beta (yeast)	9.3	22	26	22	1	14
595	2752736	NEIL3	4	nei endonuclease VIII-like 3 (E. coli)	9.3	22	28	22	2	16
608	3205295	PAX5	9	paired box 5	11	69	22	22	6	13
610	2958511	DST	6	dystonin	8	47	22	22	33	136
611	3703904	SLC7A5	16	solute carrier family 7 (cationic amino acid transporter, y+ system), member 5	8.8	69	22	22	13	21
617	2413913	DHCR24	1	24-dehydrocholesterol reductase	10.1	109	21	21	11	12
626	3105478	E2F5	8	E2F transcription factor 5, p130-binding	7.3	78	21	21	4	17
627	3144997	RAD54B	8	RAD54 homolog B (S. cerevisiae)	8.3	29	21	21	8	27
629	2725047	UCHL1	4	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	6.5	21	23	21	3	13
630	2640866	MCM2	3	minichromosome maintenance complex component 2	9.7	49	21	21	11	21
632	2474002	CENPA	2	centromere protein A	10.3	26	21	21	2	9
642	3949070	GTSE1	22	G-2 and S-phase expressed 1	9.6	35	21	21	2	21
645	3175979	PSAT1	9	phosphoserine aminotransferase 1	10.3	56	21	21	3	12

Probeset Det. Tot.

Rank[a]	ID	Gene Symbol	Chr.	Description	Mean LCL[b]	LCL / PAX[c]	LCL / PBMC[c]	Min FC[d]	exons[e]	no. exons[f]
646	2585935	SPC25	2	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae)	8.1	21	28	21	4	7
649	3884908	FAM83D	20	family with sequence similarity 83, member D	7.5	39	21	21	3	13
661	2997402	ANLN	7	anillin, actin binding protein	6.8	33	20	20	15	31
665	3776148	NDC80	18	NDC80 homolog, kinetochore complex component (S. cerevisiae)	7.8	20	26	20	9	17
667	3728988	PRR11	17	proline rich 11	7.8	20	22	20	6	13
678	2438897	FCRL5	1	Fc receptor-like 5	8.4	25	20	20	5	33
679	3577083	LGMN	14	legumain	9.1	103	20	20	13	18
681	3850666	SPC24	19	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	6	20	20	20	1	10
686	3468348	IGF1	12	insulin-like growth factor 1 (somatomedin C)	9.6	20	24	20	2	5
699	3790710	PMAIP1	18	phorbol-12-myristate-13-acetate-induced protein 1	10.1	43	20	20	5	7
702	3736304	BIRC5	17	baculoviral IAP repeat-containing 5	8.6	26	20	20	3	12
703	3204705	C9orf100	9	chromosome 9 open reading frame 100	7.2	20	31	20	2	21
705	3639048	PRC1	15	protein regulator of cytokinesis 1	9.4	20	31	20	8	20
708	3485081	RFC3	13	replication factor C (activator 1) 3, 38kDa	10.2	82	20	20	10	13
719	3765632	BRIP1	17	BRCA1 interacting protein C-terminal helicase 1	10.8	62	19	19	13	27
725	3705498	FAM57A	17	family with sequence similarity 57, member A	11.2	19	24	19	3	8
732	3868197	IL4I1	19	nucleoporin 62kDa	10.2	34	19	19	2	14
735	3721928	TUBG1	17	tubulin, gamma 1	12.6	77	19	19	9	12
746	2360454	CKS1B	1	CDC28 protein kinase regulatory subunit 1B	10.5	40	19	19	2	5
748	2673104	CDC25A	3	cell division cycle 25 homolog A (S. pombe)	7.9	19	21	19	2	18
749	2364447	NUF2	1	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae)	9.9	38	19	19	10	17
755	3442333	CDCA3	12	cell division cycle associated 3	8.9	19	20	19	1	9
768	2676189	NT5DC2	3	5'-nucleotidase domain containing 2	10.3	66	19	19	13	22
770	4041136	KPNA2	17	karyopherin alpha 2 (RAG cohort 1, importin alpha 1)	8.6	68	19	19	22	27
773	3994939	HMGB3	X	high-mobility group box 3	8.4	27	18	18	1	12
780	2712641	TFRC	3	transferrin receptor (p90, CD71)	12.8	97	18	18	12	24
787	3722784	C17orf53	17	chromosome 17 open reading frame 53	8.8	18	20	18	4	18
795	3984669	CENPI	X	centromere protein I	7.5	19	18	18	10	24
796	2931456	MTHFD1L	6	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	8.4	71	18	18	10	36
799	3705059	FANCA	16	Fanconi anemia, complementation group A	6.9	23	18	18	1	59
806	2687999	KIAA1524	3	KIAA1524	7.7	19	18	18	8	25
809	3774439	PYCR1	17	pyrroline-5-carboxylate reductase 1	9.8	18	24	18	2	16
814	2898622	GMNN	6	geminin, DNA replication inhibitor	7.5	29	18	18	6	14
819	2728210	PAICS	4	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase	9.9	20	18	18	12	17
823	2864625	DHFR	5	dihydrofolate reductase	9.9	50	18	18	5	9
824	2354696	PHGDH	1	phosphoglycerate dehydrogenase	10.3	51	18	18	6	17
828	3936563	USP18	22	ubiquitin specific peptidase 18	7.8	73	18	18	8	18
832	3333233	FEN1	11	flap structure-specific endonuclease 1	9.9	103	18	18	1	8
835	3080288	XRCC2	7	X-ray repair complementing defective repair in Chinese hamster cells 2	8.5	46	18	18	2	8
837	3818476	TNFSF9	19	tumor necrosis factor (ligand) superfamily, member 9	10.4	18	18	18	2	8
839	3828136	CCNE1	19	cyclin E1	9.3	20	17	17	5	15
846	3677319	PKMYT1	16	protein kinase, membrane associated tyrosine/threonine 1	11.6	17	18	17	2	13
847	3852569	ASF1B	19	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	11	30	17	17	5	5
863	2320697	TNFRSF8	1	tumor necrosis factor receptor superfamily, member 8	9.6	17	24	17	1	21

[a] rank of the top probeset of the gene, according to minimum fold change.

[b] Mean of the top probeset of the gene in RMA units, $\log_2$ scale.

[c] Fold change ratio of gene expression between LCL and PAX or between LCL and PBMC for the top probeset of the gene

[d] Minimum fold change of the top probeset of the gene

[e] Number of exons of the gene with ≥ 8 minimum fold change

[f] Total number of exons of the gene in the annotation

Supplementary Table 3. Partial list of exons highly expressed in PBMC.

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PBMC[b]	PBMC / LCL[c]	PBMC / LCL[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
1	2829952	TGFBI	5	transforming growth factor, beta-induced, 68kDa	11.2	304	305	304	8	22
3	3759171	ITGA2B	17	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	12.3	211	151	151	9	36
7	2569230	ST6GAL2	2	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	8.9	84	86	84	2	11
8	4007178	CFP	X	complement factor properdin	11.5	80	103	80	5	14
9	3293445	PRF1	10	perforin 1 (pore forming protein)	13.6	153	80	80	6	9
10	2987566	LFNG	7	LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	12.4	78	117	78	4	10
11	3220416	LPAR1	9	lysophosphatidic acid receptor 1	11.6	133	75	75	4	14
14	3417947	LRP1	12	low density lipoprotein receptor-related protein 1	11.8	90	60	60	52	110
16	3293862	SPOCK2	10	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	10.3	78	58	58	8	20
17	2791423	FAM198B	4	family with sequence similarity 198, member B	9.9	388	57	57	2	6
18	3382252	ARRB1	11	arrestin, beta 1	11.6	64	56	56	8	15
19	3891345	TUBB1	20	tubulin, beta 1	13.4	630	55	55	4	8
21	3012981	GNG11	7	guanine nucleotide binding protein (G protein), gamma 11	8.6	53	73	53	2	4
22	3503851	TPTE2	13	transmembrane phosphoinositide 3-phosphatase and tensin homolog 2	11.9	117	52	52	2	19
24	3917261	C21orf7	21	chromosome 21 open reading frame 7	13.1	59	50	50	7	23
25	3589479	THBS1	15	thrombospondin 1	10.5	55	50	50	19	26
26	3178560	S1PR3	9	chromosome 9 open reading frame 47	10.6	49	76	49	3	5
30	3870780	LILRA5	19	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 5	11.0	163	48	48	5	15
33	3774917	SECTM1	17	secreted and transmembrane 1	11.0	151	47	47	1	10
37	4053021	KIR3DS1	19	killer cell immunoglobulin-like receptor, three domains, short cytoplasmic tail, 1	9.5	156	43	43	2	14
40	3957810	PIK3IP1	22	phosphoinositide-3-kinase interacting protein 1	10.3	46	41	41	1	14
41	3726720	ABCC3	17	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	9.7	41	66	41	8	47
45	3724557	ITGB3	17	integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	12.6	39	42	39	17	21
47	2441227	SH2D1B	1	SH2 domain containing 1B	8.7	153	38	38	3	7
49	3662833	GPR56	16	G protein-coupled receptor 56	10.3	64	37	37	7	18
50	2818529	VCAN	5	versican	9.4	213	37	37	6	27
51	3841808	KIR3DL1	19	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	10.3	100	37	37	4	16
52	3904525	SLA2	20	Src-like-adaptor 2	11.1	53	36	36	5	11
54	2329293	ZNF362	1	zinc finger protein 362	11.7	41	36	36	3	13
55	2620848	CCR2	3	chemokine (C-C motif) receptor 2	8.4	64	36	36	2	11
56	2701088	P2RY12	3	purinergic receptor P2Y, G-protein coupled, 12	10.6	53	35	35	1	8
57	3188121	PTGS1	9	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	11.9	35	40	35	10	17
58	3357900	SIGIRR	11	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	11.2	35	39	35	5	17
59	3512308	TSC22D1	13	TSC22 domain family, member 1	9.4	204	35	35	6	22
60	2476582	LTBP1	2	latent transforming growth factor beta binding protein 1	10.0	50	34	34	5	45
61	3770312	CD300C	17	CD300c molecule	10.1	37	34	34	1	7
62	3734434	RAB37	17	RAB37, member RAS oncogene family	12.4	34	44	34	3	18
63	3692728	CES1	16	carboxylesterase 1 (monocyte/macrophage serine esterase 1)	11.0	42	34	34	2	18
69	3774894	CD7	17	CD7 molecule	13.3	80	33	33	3	7

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PBMC[b]	PBMC / LCL[c]	PBMC / LCL[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
70	3905888	MAFB	20	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	12.1	95	33	33	1	15
72	3043683	CPVL	7	carboxypeptidase, vitellogenic-like	11.4	202	33	33	3	20
73	3402803	CD4	12	CD4 molecule	13.0	239	33	33	4	15
74	3371023	TP53I11	11	tumor protein p53 inducible protein 11	8.2	32	34	32	1	14
75	3664867	CMTM3	16	CKLF-like MARVEL transmembrane domain containing 3	9.9	32	64	32	8	15
76	2443437	SELP	1	selectin P (granule membrane protein 140kDa, antigen CD62)	9.1	48	32	32	8	21
77	3654637	SULT1A1	16	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 1	11.3	59	32	32	1	26
79	2773364	PPBP	4	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	14.2	725	32	32	5	6
82	2878441	CD14	5	CD14 molecule	11.6	236	31	31	2	4
84	3337339	ALDH3B1	11	aldehyde dehydrogenase 3 family, member B1	10.7	45	31	31	2	21
85	3445569	PLBD1	12	phospholipase B domain containing 1	11.6	30	34	30	2	16
86	2783644	PDE5A	4	phosphodiesterase 5A, cGMP-specific	8.2	87	30	30	10	28
87	3229357	FCN1	9	ficolin (collagen/fibrinogen domain containing) 1	12.3	103	30	30	2	9
88	2792220	MARCH1	4	membrane-associated ring finger (C3HC4) 1	8.4	49	30	30	1	9
89	2562946	CD8A	2	CD8a molecule	10.6	44	30	30	6	12
90	2955841	PLA2G7	6	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	8.0	86	30	30	2	14
98	3293730	C10orf54	10	chromosome 10 open reading frame 54	10.8	29	33	29	2	15
101	4053047	KIR2DS1	19	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	8.6	66	29	29	4	18
102	2362193	CD1A	1	CD1a molecule	9.4	36	29	29	1	11
107	3870670	LILRA3	19	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	11.0	34	28	28	5	16
110	3266292	SLC18A2	10	solute carrier family 18 (vesicular monoamine), member 2	7.1	37	28	28	2	16
112	3535799	PTGER2	14	prostaglandin E receptor 2 (subtype EP2), 53kDa	9.0	28	30	28	4	7
113	2591889	SLC40A1	2	solute carrier family 40 (iron-regulated transporter), member 1	11.4	161	27	27	2	17
114	2367616	FASLG	1	Fas ligand (TNF superfamily, member 6)	8.7	63	27	27	1	8
116	2761839	FGFBP2	4	fibroblast growth factor binding protein 2	10.8	36	27	27	1	4
118	3841826	KIR3DL2	19	killer cell immunoglobulin-like receptor, three domains, long cytoplasmic tail, 1	8.8	50	27	27	1	15
119	3356185	ST14	11	suppression of tumorigenicity 14 (colon carcinoma)	8.1	27	38	27	2	20
120	2475013	FOSL2	2	FOS-like antigen 2	8.6	60	27	27	1	16
124	3872280	VN1R1	19	vomeronasal 1 receptor 1	7.7	26	127	26	2	7
127	3657033	ITGAM	16	integrin, alpha M (complement component 3 receptor 3 subunit)	10.0	27	25	25	5	36
129	2421085	COL24A1	1	collagen, type XXIV, alpha 1	8.8	34	25	25	1	62
130	2333129	MPL	1	myeloproliferative leukemia virus oncogene	9.0	38	25	25	2	22
136	3327079	PRR5L	11	proline rich 5 like	9.0	49	24	24	3	15
144	2902615	C6orf25	6	chromosome 6 open reading frame 25	13.7	61	24	24	3	10
146	3841766	KIR2DL1	19	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 1	8.9	89	24	24	3	21
148	3707338	GP1BA	17	glycoprotein Ib (platelet), alpha polypeptide	10.4	179	24	24	4	10
149	2888503	HK3	5	hexokinase 3 (white cell)	9.4	50	24	24	4	24
152	3574184	STON2	14	stonin 2	8.8	38	23	23	3	17
153	3788983	RAB27B	18	RAB27B, member RAS oncogene family	10.7	392	23	23	4	8

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PBMC[b]	PBMC / LCL[c]	PBMC / LCL[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
154	3335700	CTSW	11	cathepsin W	10.0	100	23	23	4	14
155	2773353	PF4	4	platelet factor 4	13.4	47	23	23	3	5
158	2528110	CYP27A1	2	cytochrome P450, family 27, subfamily A, polypeptide 1	9.2	29	23	23	2	13
159	3237795	PLXDC2	10	plexin domain containing 2	10.7	36	23	23	2	19
162	3291191	RHOBTB1	10	Rho-related BTB domain containing 1	7.0	22	23	22	1	23
167	3333883	LGALS12	11	lectin, galactoside-binding, soluble, 12	8.2	37	22	22	2	16
169	3757199	KRT16	17	keratin 16	11.6	142	22	22	1	15
170	2694825	PLXND1	3	plexin D1	8.8	80	22	22	13	62
171	3823692	KLF2	19	Kruppel-like factor 2 (lung)	11.3	22	70	22	3	11
173	3883930	MYL9	20	myosin, light chain 9, regulatory	11.0	43	22	22	2	7
175	2953494	TREML1	6	triggering receptor expressed on myeloid cells-like 1	10.4	32	21	21	3	9
176	2881227	CSF1R	5	colony stimulating factor 1 receptor	12.4	176	21	21	18	36
177	2583266	CD302	2	lymphocyte antigen 75	10.4	21	30	21	3	9
180	2394719	TNFRSF25	1	tumor necrosis factor receptor superfamily, member 25	9.0	38	21	21	1	20
182	3841559	LILRA1	19	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1	7.8	82	21	21	6	20
184	4001344	BEND2	X	BEN domain containing 2	8.5	48	21	21	5	19
187	3924899	TPTE	21	transmembrane phosphatase with tensin homology	12.1	63	20	20	2	36
190	3404499	KLRF1	12	killer cell lectin-like receptor subfamily F, member 1	7.9	80	20	20	1	9
194	3216415	CDC14B	9	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	6.6	28	20	20	5	25
195	3555768	NDRG2	14	NDRG family member 2	10.0	112	20	20	4	24
206	3939137	GNAZ	22	guanine nucleotide binding protein (G protein), alpha z polypeptide	9.9	24	19	19	2	11
208	3654975	LAT	16	linker for activation of T cells	10.7	20	19	19	3	17
216	3332704	CD6	11	CD6 molecule	9.9	37	18	18	3	21
218	3797098	EPB41L3	18	erythrocyte membrane protein band 4.1-like 3	7.2	44	18	18	2	42
221	3839724	CD33	19	CD33 molecule	11.5	33	18	18	3	9
222	3354233	NRGN	11	neurogranin (protein kinase C substrate, RC3)	11.7	43	18	18	3	5
223	2802708	FAM105A	5	family with sequence similarity 105, member A	7.8	75	18	18	1	11
227	2692831	ITGB5	3	integrin, beta 5	9.4	18	18	18	2	21
231	2372725	RGS18	1	regulator of G-protein signaling 18	8.4	145	17	17	2	9
234	2854463	DAB2	5	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	9.0	111	17	17	9	21
235	3129086	CLU	8	clusterin	12.1	89	17	17	8	23
237	4053062	KIR2DS2	19	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 2	8.0	24	17	17	2	14
241	3708865	CD68	17	CD68 molecule	13.1	87	17	17	3	13
244	2809795	GZMK	5	granzyme K (granzyme 3; tryptase II)	8.9	109	17	17	1	7
246	3858996	CEBPA	19	CCAAT/enhancer binding protein (C/EBP), alpha	9.2	16	17	16	1	9
247	2362164	CD1D	1	CD1d molecule	8.3	38	16	16	1	11
248	3770350	CD300E	17	CD300e molecule	11.4	103	16	16	1	5
249	2615380	TGFBR2	3	transforming growth factor, beta receptor II (70/80kDa)	11.4	24	16	16	1	12
250	3111565	PKHD1L1	8	polycystic kidney and hepatic disease 1 (autosomal recessive)-like 1	8.0	32	16	16	1	94
252	3860153	TYROBP	19	TYRO protein tyrosine kinase binding protein	13.0	326	16	16	2	9
255	3442155	ACRBP	12	acrosin binding protein	10.2	131	16	16	1	17
265	3189444	FAM125B	9	family with sequence similarity 125, member B	6.5	23	16	16	1	18
269	2735788	MMRN1	4	multimerin 1	8.6	15	16	15	3	19

Rank ^{a}	Probeset ID	Gene Symbol	Chr.	Description	Mean PBMC^{b}	PBMC / LCL^{c}	PBMC / LCL^{c}	Min FC^{d}	Det. exons^{e}	Tot. no. exons^{f}
271	3223597	MEGF9	9	multiple EGF-like-domains 9	11.5	15	28	15	1	6
272	2663318	TMEM40	3	transmembrane protein 40	10.6	59	15	15	5	13
273	2834948	ABLIM3	5	actin binding LIM protein family, member 3	8.8	29	15	15	2	30
278	3332747	CD5	11	CD5 molecule	8.5	27	15	15	3	14
281	3838566	FLT3LG	19	fms-related tyrosine kinase 3 ligand	12.1	15	17	15	4	14
282	3838635	FCGRT	19	Fc fragment of IgG, receptor, transporter, alpha	10.4	22	15	15	1	13
284	3870806	LILRA4	19	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4	8.4	15	15	15	1	13
285	2468848	ASAP2	2	ArfGAP with SH3 domain, ankyrin repeat and PH domain 2	8.4	17	15	15	7	37
286	3770365	CD300LF	17	CD300 molecule-like family member f	8.7	56	15	15	1	12
288	3888617	CEBPB	20	CCAAT/enhancer binding protein (C/EBP), beta	11.0	15	19	15	4	9
291	3432433	RPH3A	12	rabphilin 3A homolog (mouse)	10.0	171	15	15	1	28
292	2434191	MTMR11	1	myotubularin related protein 11	9.7	48	15	15	4	32
294	3535755	PTGDR	14	prostaglandin D2 receptor (DP)	9.4	19	15	15	1	9
300	3902779	C20orf112	20	chromosome 20 open reading frame 112	8.7	14	21	14	1	17
301	3351286	CD3E	11	CD3e molecule, epsilon (CD3-TCR complex)	8.4	32	14	14	2	7
302	2635360	TRAT1	3	T cell receptor associated transmembrane adaptor 1	6.2	31	14	14	1	7
303	4052996	KIR2DS5	19	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	7.7	31	14	14	1	5
306	2562994	CD8B	2	CD8b molecule	8.7	29	14	14	2	16
308	3579174	BCL11B	14	B-cell CLL/lymphoma 11B (zinc finger protein)	10.2	45	14	14	4	14
310	3252086	VCL	10	vinculin	9.5	14	15	14	2	40
312	2858148	PDE4D	5	phosphodiesterase 4D, cAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila)	8.3	39	14	14	3	43
314	3356117	APLP2	11	amyloid beta (A4) precursor-like protein 2	10.8	14	19	14	1	29
315	3549772	SERPINA3	14	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3	8.6	122	14	14	1	11
319	2431124	NOTCH2	1	Notch homolog 2 (Drosophila)	9.5	42	14	14	2	41
321	3643957	TMEM204	16	transmembrane protein 204	10.2	72	14	14	2	7
325	3151974	MTSS1	8	metastasis suppressor 1	6.0	18	14	14	2	29
331	3101829	SGK3	8	serum/glucocorticoid regulated kinase family, member 3	9.2	14	19	14	2	20
339	3212023	FRMD3	9	FERM domain containing 3	6.9	14	22	14	1	24
342	3174836	ANXA1	9	annexin A1	9.6	34	14	14	4	14
344	2617314	CTDSPL	3	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	7.5	25	13	13	3	17
347	3806245	PSTPIP2	18	proline-serine-threonine phosphatase interacting protein 2	8.7	13	20	13	1	15
348	2475925	EHD3	2	EH-domain containing 3	10.1	13	18	13	3	9
350	3706503	RAP1GAP2	17	RAP1 GTPase activating protein 2	8.4	24	13	13	1	31
353	2793418	MFAP3L	4	microfibrillar-associated protein 3-like	8.2	26	13	13	4	15
354	3543163	RGS6	14	regulator of G-protein signaling 6	7.5	13	17	13	4	28
356	2650466	PPM1L	3	protein phosphatase, Mg2+/Mn2+ dependent, 1L	7.9	21	13	13	1	8
357	2460337	C1orf198	1	chromosome 1 open reading frame 198	7.9	13	13	13	1	18
361	3300672	MYOF	10	myoferlin	8.0	39	13	13	7	59
365	3992417	FHL1	X	four and a half LIM domains 1	9.1	13	17	13	3	13
370	3105616	CA2	8	carbonic anhydrase II	10.0	13	23	13	4	10
378	3445138	HEBP1	12	heme binding protein 1	8.5	13	20	13	1	8
381	2495212	ZAP70	2	zeta-chain (TCR) associated protein kinase 70kDa	9.4	24	13	13	2	18
382	3021161	C7orf58	7	chromosome 7 open reading frame 58	8.9	76	13	13	1	3
383	3018402	PRKAR2B	7	protein kinase, cAMP-dependent, regulatory, type II, beta	8.9	174	13	13	4	20

Rank[a]	Probeset ID	Gene Symbol	Chr.	Description	Mean PBMC[b]	PBMC / LCL[c]	PBMC / LCL[c]	Min FC[d]	Det. exons[e]	Tot. no. exons[f]
384	2940204	F13A1	6	coagulation factor XIII, A1 polypeptide	13.6	25	13	13	1	2
386	2647915	MED12L	3	mediator complex subunit 12-like	7.4	13	17	13	1	53
387	3241656	CCDC7	10	chromosome 10 open reading frame 68	9.8	25	13	13	1	23
389	3291001	ANK3	10	ankyrin 3, node of Ranvier (ankyrin G)	8.3	46	13	13	2	66
391	3854965	LRRC25	19	leucine rich repeat containing 25	9.0	18	13	13	3	16
392	2486279	MEIS1	2	Meis homeobox 1	6.3	16	13	13	5	18
393	3451890	NELL2	12	NEL-like 2 (chicken)	7.0	81	13	13	2	28
396	2667048	EOMES	3	eomesodermin homolog (Xenopus laevis)	6.1	23	12	12	2	20
397	3735094	LOC643008	17	hypothetical protein LOC643008	8.3	38	12	12	1	6
398	2829214	TCF7	5	transcription factor 7 (T-cell specific, HMG-box)	12.8	18	12	12	2	24
401	2635754	CD96	3	CD96 molecule	6.9	15	12	12	1	22
410	3338558	CTTN	11	cortactin	7.0	12	17	12	1	27
411	3031638	TMEM176A	7	transmembrane protein 176A	9.7	83	12	12	1	7
412	3062102	PDK4	7	pyruvate dehydrogenase kinase, isozyme 4	9.6	141	12	12	4	16
413	3989844	SH2D1A	X	SH2 domain containing 1A	7.5	31	12	12	1	9
416	3656058	SULT1A3	16	sulfotransferase family, cytosolic, 1A, phenol-preferring, member 3	10.4	12	17	12	2	23
417	3936068	IL17RA	22	interleukin 17 receptor A	12.4	12	23	12	3	18
418	3349364	NCAM1	11	neural cell adhesion molecule 1	8.0	23	12	12	2	20
420	3849006	PRAM1	19	PML-RARA regulated adaptor molecule 1	10.2	41	12	12	1	14
421	3832262	SPINT2	19	serine peptidase inhibitor, Kunitz type, 2	10.7	20	12	12	2	11
422	3946110	GRAP2	22	GRB2-related adaptor protein 2	6.7	31	12	12	1	12
424	3456719	ZNF385A	12	zinc finger protein 385A	9.3	12	24	12	3	19
430	3724631	C17orf57	17	chromosome 17 open reading frame 57	9.2	12	33	12	3	34
433	3482629	WASF3	13	WAS protein family, member 3	7.6	23	12	12	1	21
434	3901318	CST3	20	cystatin C	13.7	23	12	12	2	9
435	2592550	SDPR	2	serum deprivation response	9.9	12	13	12	3	7
437	3870829	LAIR1	19	leukocyte-associated immunoglobulin-like receptor 1	8.5	32	12	12	2	14
438	4052974	KIR2DL2	19	killer cell immunoglobulin-like receptor, two domains, long cytoplasmic tail, 2	8.5	58	12	12	3	5
441	2353750	CD101	1	CD101 molecule	10.4	22	12	12	1	13
445	4017409	TSC22D3	X	TSC22 domain family, member 3	11.5	12	16	12	3	15
446	3815247	CFD	19	complement factor D (adipsin)	10.9	12	16	12	1	8
454	3741775	P2RX1	17	purinergic receptor P2X, ligand-gated ion channel, 1	7.2	12	11	11	2	18
455	3069097	TFEC	7	transcription factor EC	9.9	31	11	11	1	12
465	3908374	SULF2	20	sulfatase 2	10.6	20	11	11	1	28
466	3548890	SLC24A4	14	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	7.4	26	11	11	1	21
469	2360199	AQP10	1	aquaporin 10	9.3	19	11	11	1	13
472	2320423	AGTRAP	1	angiotensin II receptor-associated protein	10.5	11	17	11	1	7
477	3995427	ZNF185	X	zinc finger protein 185 (LIM domain)	9.4	24	11	11	1	21
478	3422857	GLIPR1	12	GLI pathogenesis-related 1	13.3	12	11	11	2	8
479	2669981	CX3CR1	3	chemokine (C-X3-C motif) receptor 1	13.2	622	11	11	1	3
484	2619313	VIPR1	3	vasoactive intestinal peptide receptor 1	6.7	17	11	11	1	16
487	3870999	GP6	19	glycoprotein VI (platelet)	7.9	27	11	11	1	13
489	2739327	EGF	4	epidermal growth factor	8.2	33	11	11	1	33
490	2662349	CAMK1	3	calcium/calmodulin-dependent protein kinase I	8.9	11	13	11	2	14
491	2623936	STAB1	3	stabilin 1	10.9	18	11	11	4	79
492	3841406	LILRA2	19	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 2	12.5	84	11	11	1	12
494	3834031	CYP2S1	19	cytochrome P450, family 2, subfamily S, polypeptide 1	8.3	13	11	11	3	20
496	2442621	CD247	1	CD247 molecule	10.1	175	11	11	1	12
498	3870403	NLRP12	19	NLR family, pyrin domain containing 12	9.4	45	11	11	3	23

[a] rank of the top probeset of the gene, according to minimum fold change.
[b] Mean of the top probeset of the gene in RMA units, $\log_2$ scale.
[c] Fold change ratio of gene expression between PBMC and LCL or between PBMC and PAX for the top probeset of the gene
[d] Minimum fold change of the top probeset of the gene
[e] Number of exons of the gene with ≥ 8 minimum fold change
[f] Total number of exons of the gene in the annotation

Supplementary Table 4. Gene ontology categories for genes associated with lymphocyte counts in PAX and PBMC, as determined by GOrilla.

GO ID	GO Category	P-value	Number of significant genes	Number of genes in category
PAX				
GO:0044260	cellular macromolecule metabolic process	2.60E-10	212	3841
GO:0090304	nucleic acid metabolic process	2.95E-10	125	1911
GO:0006396	RNA processing	4.08E-10	53	552
GO:0034660	ncRNA metabolic process	2.04E-09	32	253
GO:0016070	RNA metabolic process	4.61E-09	100	1477
GO:0043170	macromolecule metabolic process	1.00E-08	227	4358
GO:0006139	nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	6.06E-08	139	2393
GO:0050863	regulation of T cell activation	1.65E-06	21	169
GO:0034641	cellular nitrogen compound metabolic process	1.68E-06	149	2761
GO:0006807	nitrogen compound metabolic process	2.05E-06	153	2863
GO:0044237	cellular metabolic process	2.17E-06	262	5514
GO:0031294	lymphocyte costimulation	2.43E-06	12	61
GO:0031295	T cell costimulation	2.43E-06	12	61
GO:0002768	immune response-regulating cell surface receptor signaling pathway	4.99E-06	15	100
GO:0008380	RNA splicing	5.09E-06	26	257
PBMC				
GO:0051251	positive regulation of lymphocyte activation	3.13E-10	13	165
GO:0050865	regulation of cell activation	3.92E-10	15	243
GO:0051249	regulation of lymphocyte activation	6.91E-10	14	213
GO:0002696	positive regulation of leukocyte activation	6.97E-10	13	176
GO:0050867	positive regulation of cell activation	9.20E-10	13	180
GO:0048583	regulation of response to stimulus	1.96E-09	35	1571
GO:0002694	regulation of leukocyte activation	2.23E-09	14	233
GO:0002429	immune response-activating cell surface receptor signaling pathway	2.53E-09	10	96
GO:0002768	immune response-regulating cell surface receptor signaling pathway	3.79E-09	10	100
GO:0050863	regulation of T cell activation	5.13E-09	12	169
GO:0050870	positive regulation of T cell activation	5.44E-09	11	135
GO:0002682	regulation of immune system process	7.69E-09	21	628
GO:0002376	immune system process	8.53E-09	25	893
GO:0050851	antigen receptor-mediated signaling pathway	2.14E-08	9	89
GO:0001775	cell activation	3.14E-08	17	441

Supplementary Table 5. Gene ontology categories for genes associated with neutrophil counts in PAX.

GO ID	GO Category	P-value	Number of significant genes	Number of genes in category
GO:0006952	defense response	3.64E-12	43	602
GO:0002376	immune system process	9.97E-09	47	893
GO:0006955	immune response	1.84E-08	34	539
GO:0050776	regulation of immune response	1.30E-07	27	397
GO:0002682	regulation of immune system process	2.37E-07	35	628
GO:0007165	signal transduction	7.48E-07	99	2920
GO:0002532	production of molecular mediator involved in inflammatory response	1.02E-06	4	5
GO:0071260	cellular response to mechanical stimulus	1.73E-06	8	40
GO:0006954	inflammatory response	2.08E-06	19	251
GO:0009607	response to biotic stimulus	2.79E-06	26	437
GO:0051716	cellular response to stimulus	5.20E-06	109	3450
GO:0045087	innate immune response	5.81E-06	17	221
GO:0050896	response to stimulus	8.65E-06	146	5053
GO:0045088	regulation of innate immune response	9.05E-06	14	160
GO:0071214	cellular response to abiotic stimulus	1.08E-05	9	66

Supplementary Table 6. Gene ontology categories for genes associated with monocyte counts in PBMC.

GO ID	GO Category	P-value	Number of significant genes	Number of genes in category
GO:0002376	immune system process	2.61E-09	26	893
GO:0006955	immune response	2.50E-08	19	539
GO:0050896	response to stimulus	1.14E-06	64	5053
GO:0007165	signal transduction	5.56E-06	43	2920
GO:0051716	cellular response to stimulus	3.27E-05	46	3450
GO:0050776	regulation of immune response	5.16E-05	12	397
GO:0006952	defense response	5.39E-05	15	602
GO:0016046	detection of fungus	5.78E-05	2	2
GO:0016064	immunoglobulin mediated immune response	6.85E-05	3	11
GO:0002682	regulation of immune system process	8.68E-05	15	628
GO:0050778	positive regulation of immune response	1.81E-04	9	262
GO:0032732	positive regulation of interleukin-1 production	1.85E-04	3	15
GO:0019724	B cell mediated immunity	1.85E-04	3	15
GO:0080134	regulation of response to stress	2.24E-04	12	464
GO:0045088	regulation of innate immune response	2.26E-04	7	160

Supplementary Table 7. The female-to-male overexpression effect of probesets targeting *XIST* gene.

Probeset ID[¶]	CL Effect[*]	PAX Effect[*]	PBMC Effect[*]
4012533	2.84	7.54	4.23
4012534	6.57	7.26	7.88
4012535	6.17	7.77	7.43
4012536	7.95	9.05	8.40
4012537	5.93	7.78	7.21
4012538	3.29	4.77	4.53
4012540	6.38	7.29	7.31
4012546	6.83	7.37	7.67
4012547	0.23	1.71	1.03
4012548	3.57	6.77	4.89
4012567	1.78	9.46	1.88
4012568	4.53	8.51	5.14
4012569	3.51	6.75	5.09
4012570	5.75	8.39	6.81
4012571	4.55	6.51	6.10
Mean	4.66	7.13	5.71
Fold change	25.25	139.99	52.19

[*] Effect is in log2 scale. Fold change is 2^{effect}.

[¶] Probesets in the Affymetrix Extended set.

Supplementary Table 8. Autosomal genes associated with sex.

Transcript cluster ID	Gene Symbol	Chr.	Description	Effect LCL*	Effect PAX*	Effect PBMC*
3631397	UACA	15	uveal autoantigen with coiled-coil domains and ankyrin repeats	0.43	0.29	0.14
2880361	JAKMIP2	5	janus kinase and microtubule interacting protein 2	0.25	0.60	0.69
3712675	RAI1	17	retinoic acid induced 1	-0.22	-0.10	0.13
3373946	TIMM10	11	translocase of inner mitochondrial membrane 10 homolog (yeast)	0.17	0.15	0.36
3725602	ABI3	17	ABI family, member 3	-0.16	0.03	0.40
2439101	FCRL1	1	Fc receptor-like 1	-0.12	-0.58	-0.81
2893109	LOC100129033	6	QIQN5815	-0.10	-0.58	0.07
3857811	C19orf12	19	chromosome 19 open reading frame 12	0.08	0.20	0.30
3223687	PHF19	9	PHD finger protein 19	0.04	0.03	0.31
3264621	TCF7L2	10	transcription factor 7-like 2 (T-cell specific, HMG-box)	-0.04	0.22	0.61
3417184	SUOX	12	sulfite oxidase	-0.04	0.06	0.35
3543935	COQ6	14	coenzyme Q6 homolog, monooxygenase (S. cerevisiae)	-0.04	-0.26	0.06
2607055	PASK	2	PAS domain containing serine/threonine kinase	0.04	-0.18	-0.21
3870990	GP6	19	glycoprotein VI (platelet)	0.04	-0.36	-0.24
3534866	MGAT2	14	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase	0.02	-0.04	0.26
3940992	ASPHD2	22	aspartate beta-hydroxylase domain containing 2	0.01	0.15	0.40

*In $\log_2$ RMA units. Positive effects are highly expressed in males.
Partial list, genes are significant in at least one RNA source, FDR≤0.2.

Supplementary Table 9. Genes that might be associated with age, having p-values < 0.05 for all three RNA sources.

Transcript Cluster ID	Gene Symbol	Description	Chr.	CL P-value	CL effects	PAX P-value	PAX effects	PBMC P-value	PBMC effects
3743906	TP53	tumor protein p53	17	0.0062	0.0104	0.0445	-0.0135	0.0236	-0.0137
3127334	REEP4	receptor accessory protein 4	8	0.0142	-0.0162	0.0054	-0.0276	0.0009	-0.0219
2673730	PRKAR2A	protein kinase, cAMP-dependent, regulatory, type II, alpha	3	0.0252	-0.0121	0.0063	-0.0199	0.0295	-0.0111
2821347	ERAP2	endoplasmic reticulum aminopeptidase 2	5	0.0471	-0.0673	0.0042	-0.0563	0.0171	-0.0719
3829313	CEBPG	CCAAT/enhancer binding protein (C/EBP), gamma	19	0.0186	-0.0118	0.0212	0.0208	0.0246	-0.0104

Supplementary Table 10. Selected genes with known associations with HDL, having p-values ≤ 0.05 for either PAX or PBMC.

Transcript Cluster ID	Gene Symbol	Description	Chr.	LCL P-value	CL effects	PAX P-value	PAX effects	PBMC P-value	PBMC effects
3682182	ABCC6(3)	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	16	0.1896	-0.0053	0.0371	-0.0100	0.5424	-0.0027
3392986	APOA1(4)	apolipoprotein A-I	11	0.1835	-0.0049	0.0013	-0.0146	0.9605	0.0002
3350655	APOC3(4)	apolipoprotein C-III	11	0.7637	-0.0013	0.3037	0.0064	0.0235	-0.0106
3375545	FADS1(4)	fatty acid desaturase 1	11	0.4475	-0.0030	0.0233	-0.0097	0.0124	-0.0087
3821015	LDLR(4)	low density lipoprotein receptor	19	0.7011	0.0011	0.0346	-0.0076	0.0008	-0.0123
3061997	PON2(1)	paraoxonase 2	7	0.5242	-0.0034	0.2844	0.0049	0.0010	0.0112

Supplementary Table 11. List of 423 exons with FDR≤0.05 for the participant effect and standard deviation across participant of at least 2 fold for this effect. The probesets are sorted by the F-score of the participant.

Probeset ID[a]	Gene symbol	Chr.	Description	F(subject)[b]	Det. exons[c]	Tot. no. exons[d]
4030178	DDX3Y	Y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	85.2	18	22
4035087	UTY	Y	ubiquitously transcribed tetratricopeptide repeat gene, Y-linked	74.4	33	52
4030146	USP9Y	Y	ubiquitin specific peptidase 9, Y-linked	73.5	34	53
4028553	RPS4Y1	Y	ribosomal protein S4, Y-linked 1	46.4	12	12
3764386	SUPT4H1	17	suppressor of Ty 4 homolog 1 (S. cerevisiae)	46.0	1	11
4048279	HLA-DRB1	6	major histocompatibility complex, class II, DR beta 1	45.9	4	8
2350995	GSTM1	1	glutathione S-transferase mu 1	44.4	3	14
3717652	ZNF207	17	zinc finger protein 207	43.7	1	24
3505812	PARP4	13	poly (ADP-ribose) polymerase family, member 4	41.3	1	43
4031141	EIF1AY	Y	eukaryotic translation initiation factor 1A, Y-linked	41.2	7	9
2825746	HSD17B4	5	hydroxysteroid (17-beta) dehydrogenase 4	38.9	1	26
4028588	ZFY	Y	zinc finger protein, Y-linked	35.4	5	10
3988474	DOCK11	X	dedicator of cytokinesis 11	34.7	1	57
3036926	ACTB	7	actin, beta	34.7	1	11
3432446	OAS1	12	2',5'-oligoadenylate synthetase 1, 40/46kDa	31.5	1	15
2367199	BAT2L2	1	HLA-B associated transcript 2-like 2	31.3	1	48
3304629	NT5C2	10	5'-nucleotidase, cytosolic II	28.6	1	22
2984580	SFT2D1	6	SFT2 domain containing 1	28.4	1	9
3462877	NAP1L1	12	nucleosome assembly protein 1-like 1	27.9	1	22
4028462	CD99	Y	CD99 molecule	25.5	1	27
4048249	HLA-DRB5	6	major histocompatibility complex, class II, DR beta 5	25.2	5	11
2727952	EXOC1	4	exocyst complex component 1	24.7	1	25
3831276	ZNF146	19	zinc finger protein 146	24.5	1	8
4025365	IDS	X	iduronate 2-sulfatase	23.7	1	20
2469139	TAF1B	2	TATA box binding protein (TBP)-associated factor, RNA polymerase I, B, 63kDa	23.5	1	17
3067144	COG5	7	component of oligomeric golgi complex 5	23.4	1	33
2366603	C1orf112	1	SCY1-like 3 (S. cerevisiae)	23.1	1	36
2903428	HLA-DPB1	6	major histocompatibility complex, class II, DP beta 1	23.1	1	8
2367974	RABGAP1L	1	RAB GTPase activating protein 1-like	21.6	1	47
2418460	CRYZ	1	crystallin, zeta (quinone reductase)	21.3	1	15
3105938	CPNE3	8	copine III	20.2	1	22
2989124	ZDHHC4	7	zinc finger, DHHC-type containing 4	19.4	1	13
2603075	SP110	2	SP110 nuclear body protein	19.4	1	24
3975522	KDM6A	X	lysine (K)-specific demethylase 6A	19.1	1	42
2821406	ERAP2	5	endoplasmic reticulum aminopeptidase 2	18.8	22	27
3004680	ZNF138	7	zinc finger protein 138	18.7	1	15
3395427	HSPA8	11	heat shock 70kDa protein 8	18.5	1	17
3238248	MLLT10	10	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10	17.7	1	38
4015713	BTK	X	Bruton agammaglobulinemia tyrosine kinase	17.5	1	24
2518349	ITGA4	2	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	17.4	1	40
3707765	MIS12	17	MIS12, MIND kinetochore complex component, homolog (S. pombe)	16.5	1	5
2816364	IQGAP2	5	IQ motif containing GTPase activating protein 2	16.5	1	45

Probeset ID[a]	Gene symbol	Chr.	Description	F(subject)[b]	Det. exons[c]	Tot. no. exons[d]
3517836	KLF12	13	Kruppel-like factor 12	16.1	1	23
2542747	LAPTM4A	2	lysosomal protein transmembrane 4 alpha	15.8	1	10
2948952	HLA-B	6	major histocompatibility complex, class I, B	15.6	1	12
2351023	GSTM5	1	glutathione S-transferase mu 5	15.5	1	11
3056088	BAZ1B	7	bromodomain adjacent to zinc finger domain, 1B	15.3	1	39
3385778	CTSC	11	cathepsin C	15.2	1	15
3932139	PSMG1	21	proteasome (prosome, macropain) assembly chaperone 1	14.9	1	11
2961826	PHIP	6	pleckstrin homology domain interacting protein	14.9	1	48
3879393	PLK1S1	20	polo-like kinase 1 substrate 1	14.4	1	19
2723770	TBC1D1	4	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1	14.4	1	32
3576822	TRIP11	14	thyroid hormone receptor interactor 11	14.3	1	30
2903265	HLA-DQA2	6	major histocompatibility complex, class II, DQ alpha 2	14.3	1	5
3996335	RPL10	X	ribosomal protein L10	14.2	1	14
3485880	EXOSC8	13	exosome component 8	14.2	1	12
3584495	SNRPN	15	small nuclear ribonucleoprotein polypeptide N	14.0	1	23
4031106	CYorf15B	Y	chromosome Y open reading frame 15B	13.6	10	18
3425122	C12orf29	12	chromosome 12 open reading frame 29	13.5	1	11
2530554	MFF	2	mitochondrial fission factor	13.2	1	14
3243742	BMS1	10	BMS1 homolog, ribosome assembly protein (yeast)	13.2	1	31
3169339	ALDH1B1	9	aldehyde dehydrogenase 1 family, member B1	13.1	1	10
2739191	CCDC109B	4	coiled-coil domain containing 109B	13.0	1	12
2571102	ANAPC1	2	anaphase promoting complex subunit 1	12.8	1	70
3046682	TRGV5	7	TCR gamma alternate reading frame protein	12.7	1	1
2446619	STX6	1	syntaxin 6	12.7	1	11
4031175	RPS4Y2	Y	ribosomal protein S4, Y-linked 2	12.7	2	7
3458101	NACA	12	nascent polypeptide-associated complex alpha subunit	12.0	1	10
2350940	GSTM4	1	glutathione S-transferase mu 4	11.9	1	12
2676049	WDR82	3	WD repeat domain 82	11.6	1	12
3907879	ELMO2	20	engulfment and cell motility 2	11.4	1	27
3759912	LRRC37A4	17	leucine rich repeat containing 37, member A4 (pseudogene)	11.3	3	18
3315556	PSMD13	11	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	11.2	1	16
2369585	SOAT1	1	sterol O-acyltransferase 1	11.2	1	21
2492088	KDM3A	2	lysine (K)-specific demethylase 3A	10.8	1	35
3003206	CCT6A	7	chaperonin containing TCP1, subunit 6A (zeta 1)	10.7	1	23
2821249	CAST	5	calpastatin	10.7	1	42
3641887	LINS1	15	lines homolog 1 (Drosophila)	10.3	1	16
3971880	EIF2S3	X	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	10.3	1	15
3850437	KRI1	19	KRI1 homolog (S. cerevisiae)	10.1	1	24
3908171	ZMYND8	20	zinc finger, MYND-type containing 8	10.0	1	33
4029193	PRKY	Y	protein kinase, Y-linked	9.7	3	16
2501343	LOC654433	2	hypothetical LOC654433	9.6	1	8
3487448	DNAJC15	13	DnaJ (Hsp40) homolog, subfamily C, member 15	9.4	1	8
3462702	KRR1	12	KRR1, small subunit (SSU) processome component, homolog (yeast)	9.2	1	17
3742635	C17orf87	17	chromosome 17 open reading frame 87	9.0	1	6
3140703	STAU2	8	staufen, RNA binding protein, homolog 2 (Drosophila)	9.0	1	29

Probeset ID[a]	Gene symbol	Chr.	Description	F(subject)[b]	Det. exons[c]	Tot. no. exons[d]
3920468	TTC3	21	tetratricopeptide repeat domain 3	8.9	1	57
2473203	NCOA1	2	nuclear receptor coactivator 1	8.8	1	34
2421854	GBP3	1	guanylate binding protein 3	8.8	3	17
3784747	ELP2	18	elongation protein 2 homolog (S. cerevisiae)	8.8	1	26
2337291	TTC4	1	tetratricopeptide repeat domain 4	8.7	1	15
3823579	RAB8A	19	RAB8A, member RAS oncogene family	8.5	1	15
2933558	TULP4	6	tubby like protein 4	8.5	1	25
2748229	KIAA0922	4	KIAA0922	8.3	1	41
2798575	SDHA	5	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	8.3	1	19
2950130	HLA-DQB2	6	major histocompatibility complex, class II, DQ beta 2	8.2	1	6
3707605	LOC100130950	17	similar to hCG1991536	8.2	1	9
3711727	ZNF286A	17	zinc finger protein 286A	8.2	1	11
3144774	RBM12B	8	RNA binding motif protein 12B	7.9	1	10
2736280	SMARCAD1	4	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	7.8	1	29
3063553	TRIM4	7	tripartite motif-containing 4	7.7	1	15
3417247	RPS26	12	ribosomal protein S26	7.5	2	7
3341092	ACER3	11	alkaline ceramidase 3	7.5	1	16
3724617	C17orf57	17	chromosome 17 open reading frame 57	7.5	1	34
2428814	PTPN22	1	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	7.4	1	26
2800489	SRD5A1	5	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1)	7.0	1	11
3114095	WDR67	8	WD repeat domain 67	7.0	1	27
2413969	USP24	1	ubiquitin specific peptidase 24	6.9	1	20
3699056	RFWD3	16	ring finger and WD repeat domain 3	6.7	1	22
3131752	RAB11FIP1	8	RAB11 family interacting protein 1 (class I)	6.6	1	27
2565924	ANKRD36B	2	ankyrin repeat domain 36B	6.3	1	17
3857177	ZNF675	19	zinc finger protein 675	6.3	1	6
3913564	DIDO1	20	death inducer-obliterator 1	6.3	1	24
3955109	GSTT1	22	glutathione S-transferase theta 1	6.2	2	8
2925529	L3MBTL3	6	l(3)mbt-like 3 (Drosophila)	6.1	1	25
3609657	MCTP2	15	multiple C2 domains, transmembrane 2	6.0	1	28
2563435	RGPD1	2	RANBP2-like and GRIP domain containing 1	6.0	1	13
3647874	ATF7IP2	16	activating transcription factor 7 interacting protein 2	6.0	1	16
2708240	PARL	3	presenilin associated, rhomboid-like	6.0	1	13
3895595	ADAM33	20	ADAM metallopeptidase domain 33	5.8	1	30
3527423	PARP2	14	poly (ADP-ribose) polymerase 2	5.7	1	21
2531333	SP140L	2	SP140 nuclear body protein-like	5.6	1	21
3363873	RRAS2	11	related RAS viral (r-ras) oncogene homolog 2	5.5	1	12
3553120	ZNF839	14	zinc finger protein 839	5.2	2	12
2670619	ULK4	3	unc-51-like kinase 4 (C. elegans)	5.0	1	28
2421965	GBP7	1	guanylate binding protein 7	5.0	1	18
3262523	GSTO1	10	glutathione S-transferase omega 1	4.9	1	10
3556431	METTL3	14	methyltransferase like 3	4.9	1	17
3922843	PDE9A	21	phosphodiesterase 9A	4.9	1	25
3843221	ZNF548	19	zinc finger protein 548	4.9	1	9
2327382	ATPIF1	1	ATPase inhibitory factor 1	4.8	1	10
3274192	PITRM1	10	pitrilysin metallopeptidase 1	4.7	1	32
3079177	TMEM176B	7	transmembrane protein 176B	4.6	5	9
2484803	COMMD1	2	copper metabolism (Murr1) domain containing 1	4.6	1	8

Probeset ID[a]	Gene symbol	Chr.	Description	F(subject)[b]	Det. exons[c]	Tot. no. exons[d]
2812137	CWC27	5	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	4.5	1	19
3429348	HSP90B1	12	heat shock protein 90kDa beta (Grp94), member 1	4.5	1	20
3207247	FLJ20444	9	hypothetical protein FLJ20444	4.5	1	8
2737340	DAPP1	4	dual adaptor of phosphotyrosine and 3-phosphoinositides	4.4	1	13
2405660	CSMD2	1	CUB and Sushi multiple domains 2	4.4	1	86
3012413	AKAP9	7	A kinase (PRKA) anchor protein (yotiao) 9	4.4	1	73
2666534	TOP2B	3	topoisomerase (DNA) II beta 180kDa	4.4	1	44
3142386	FABP4	8	fatty acid binding protein 4, adipocyte	4.3	1	6
2427222	GSTM3	1	glutathione S-transferase mu 3 (brain)	4.3	2	17
2372958	TROVE2	1	TROVE domain family, member 2	4.2	1	15
3841856	KIR3DS1	19	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 4	4.2	1	14
3811114	PIGN	18	phosphatidylinositol glycan anchor biosynthesis, class N	4.2	1	43
2583647	RBMS1	2	RNA binding motif, single stranded interacting protein 1	4.1	1	28
3018413	PRKAR2B	7	protein kinase, cAMP-dependent, regulatory, type II, beta	4.0	1	20
2366948	FMO3	1	flavin containing monooxygenase 3	3.8	1	16
3071957	KCP	7	kielin/chordin-like protein	3.8	1	28
3837782	GRIN2D	19	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	3.7	1	26
3712272	LOC162632	17	coiled-coil domain containing 144A	3.7	1	8
2811763	IPO11	5	importin 11	3.7	1	36
2997354	EEPD1	7	endonuclease/exonuclease/phosphatase family domain containing 1	3.6	1	18
3636993	NMB	15	neuromedin B	3.6	1	8
2806472	IL7R	5	interleukin 7 receptor	3.6	2	11
2739863	ALPK1	4	alpha-kinase 1	3.6	1	21
2771750	UBA6	4	ubiquitin-like modifier activating enzyme 6	3.6	2	44
2319650	UBE4B	1	ubiquitination factor E4B (UFD2 homolog, yeast)	3.6	1	43
3568684	MAX	14	MYC associated factor X	3.5	1	19
3031645	TMEM176A	7	transmembrane protein 176A	3.5	3	7
3964071	CELSR1	22	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	3.5	1	41
2780559	PPA2	4	pyrophosphatase (inorganic) 2	3.4	1	17
2880419	JAKMIP2	5	janus kinase and microtubule interacting protein 2	3.4	1	29
3540373	CHURC1	14	churchill domain containing 1	3.4	1	8
2784694	ANKRD50	4	ankyrin repeat domain 50	3.3	1	5
4053054	KIR2DS1	19	killer cell immunoglobulin-like receptor, two domains, short cytoplasmic tail, 1	3.3	2	18
2796582	ACSL1	4	acyl-CoA synthetase long-chain family member 1	3.3	1	27
3364450	SOX6	11	SRY (sex determining region Y)-box 6	3.3	1	23
3791968	SERPINB10	18	serpin peptidase inhibitor, clade B (ovalbumin), member 10	3.3	2	8
3484645	BRCA2	13	breast cancer 2, early onset	3.2	1	39
3622029	SPG11	15	spastic paraplegia 11 (autosomal recessive)	3.2	1	56
3018659	CBLL1	7	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	3.2	1	9
2343481	IFI44L	1	interferon-induced protein 44-like	3.2	2	16
3470619	SSH1	12	slingshot homolog 1 (Drosophila)	3.2	1	24
2409018	LEPRE1	1	leucine proline-enriched proteoglycan (leprecan) 1	3.2	1	31

Probeset ID[a]	Gene symbol	Chr.	Description	F(subject)[b]	Det. exons[c]	Tot. no. exons[d]
3581945	IGHA1	14	ADAM metallopeptidase domain 6 (pseudogene)	3.2	1	16
3083057	MYOM2	8	myomesin (M-protein) 2, 165kDa	3.1	4	39
3867866	PIH1D1	19	PIH1 domain containing 1	3.1	1	13
3142987	CA1	8	carbonic anhydrase I	3.1	2	13
3562789	C14orf106	14	chromosome 14 open reading frame 106	3.1	1	25
3894747	SIRPB1	20	signal-regulatory protein beta 1	3.0	1	22
2326663	ARID1A	1	AT rich interactive domain 1A (SWI-like)	3.0	1	41
2897185	RNF144B	6	ring finger protein 144B	2.9	1	19
3203108	DDX58	9	DEAD (Asp-Glu-Ala-Asp) box polypeptide 58	2.8	1	24
3357845	IFITM3	11	interferon induced transmembrane protein 3 (1-8U)	2.7	1	6
3031598	GIMAP5	7	GTPase, IMAP family member 5	2.7	1	14
3722404	NBR2	17	neighbor of BRCA1 gene 2 (non-protein coding)	2.7	1	9
2808452	NNT	5	nicotinamide nucleotide transhydrogenase	2.7	1	29
4009861	ALAS2	X	aminolevulinate, delta-, synthase 2	2.7	3	16
3998312	NLGN4X	X	neuroligin 4, X-linked	2.6	1	27
2555374	USP34	2	ubiquitin specific peptidase 34	2.6	1	90
3810462	CPLX4	18	complexin 4	2.6	1	6
3221556	CDC26	9	cell division cycle 26 homolog (S. cerevisiae)	2.6	1	9
3982481	PGK1	X	phosphoglycerate kinase 1	2.6	1	13
3906229	CHD6	20	chromodomain helicase DNA binding protein 6	2.5	1	46
3870667	LILRA3	19	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3	2.5	2	16
3297673	DYDC1	10	DPY30 domain containing 1	2.5	1	8
3242887	ANKRD30A	10	ankyrin repeat domain 30A	2.5	1	39
2915517	CYB5R4	6	cytochrome b5 reductase 4	2.5	1	19
2427041	SORT1	1	sortilin 1	2.5	1	36
2766968	APBB2	4	amyloid beta (A4) precursor protein-binding, family B, member 2	2.5	1	20
4045792	SFRS13A	1	splicing factor, arginine/serine-rich 13A	2.5	1	36
3698112	PMFBP1	16	polyamine modulated factor 1 binding protein 1	2.5	1	31
2867452	MCTP1	5	multiple C2 domains, transmembrane 1	2.5	1	35
2560208	PCGF1	2	polycomb group ring finger 1	2.5	1	12
3912772	TAF4	20	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	2.4	1	34
2340970	IL12RB2	1	interleukin 12 receptor, beta 2	2.4	1	27
3757509	DNAJC7	17	DnaJ (Hsp40) homolog, subfamily C, member 7	2.4	1	16
2555646	CCT4	2	chaperonin containing TCP1, subunit 4 (delta)	2.4	1	22
3942821	RNF185	22	ring finger protein 185	2.4	1	15
3177577	NAA35	9	N(alpha)-acetyltransferase 35, NatC auxiliary subunit	2.4	1	25
3746956	NCOR1	17	nuclear receptor co-repressor 1	2.3	1	64
3122764	DEFA3	8	defensin, alpha 3, neutrophil-specific	2.3	4	12
3760307	ARL17A	17	ADP-ribosylation factor-like 17A	2.3	2	17
3575689	FOXN3	14	forkhead box N3	2.3	1	24
2687855	IFT57	3	intraflagellar transport 57 homolog (Chlamydomonas)	2.3	1	17
3582206	IGHM	14	ADAM metallopeptidase domain 6 (pseudogene)	2.3	1	31
3667875	HP	16	haptoglobin	2.3	1	18
2871046	EPB41L4A	5	erythrocyte membrane protein band 4.1 like 4A	2.3	1	28
3421956	CNOT2	12	CCR4-NOT transcription complex, subunit 2	2.3	1	26
3449602	OVOS2	12	ovostatin 2	2.2	2	16

Probeset ID[a]	Gene symbol	Chr.	Description	F(subject)[b]	Det. exons[c]	Tot. no. exons[d]
3686388	XPO6	16	exportin 6	2.2	1	27
3466657	CCDC38	12	coiled-coil domain containing 38	2.2	1	18
2339516	ATG4C	1	ATG4 autophagy related 4 homolog C (S. cerevisiae)	2.2	1	17
2914020	SENP6	6	SUMO1/sentrin specific peptidase 6	2.2	1	29
3262456	SLK	10	STE20-like kinase (yeast)	2.2	1	27
2878681	DIAPH1	5	diaphanous homolog 1 (Drosophila)	2.2	1	33
2393717	LRRC47	1	leucine rich repeat containing 47	2.2	1	13
2400328	HP1BP3	1	heterochromatin protein 1, binding protein 3	2.2	1	18
2694003	MGLL	3	monoglyceride lipase	2.2	1	18
3558349	CTSG	14	cathepsin G	2.1	1	7
3108508	LAPTM4B	8	lysosomal protein transmembrane 4 beta	2.1	1	12
3105846	WWP1	8	WW domain containing E3 ubiquitin protein ligase 1	2.1	1	35
2857150	DHX29	5	DEAH (Asp-Glu-Ala-His) box polypeptide 29	2.1	1	31
2672153	LTF	3	lactotransferrin	2.1	1	20
2426573	SLC25A24	1	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 24	2.1	1	16
2831308	UBE2D2	5	ubiquitin-conjugating enzyme E2D 2 (UBC4/5 homolog, yeast)	2.1	1	14
3568036	PPP2R5E	14	protein phosphatase 2, regulatory subunit B', epsilon isoform	2.1	1	20
2609582	THUMPD3	3	THUMP domain containing 3	2.1	1	17
2735093	DSPP	4	dentin sialophosphoprotein	2.1	1	22
3819584	HNRNPM	19	heterogeneous nuclear ribonucleoprotein M	2.0	1	28
2951603	FKBP5	6	FK506 binding protein 5	2.0	1	19
3826614	ZNF493	19	zinc finger protein 493	2.0	1	17
3057380	HIP1	7	huntingtin interacting protein 1	2.0	1	38
3581738	LOC100290146	14	ADAM metallopeptidase domain 6 (pseudogene)	2.0	1	7

[a] ID of the probeset of the gene with the highest F statistics.

[b] F statistics of the top probeset of the gene

[c] Number of exons of the gene with ≥ 2 F statistics

[d] Total number of exons of the gene in the annotation

Supplementary Table 12. Some genes that are stable across three tissue types and across participants.

Transcript Cluster ID	Gene Symbol	Chr.	Description	Grand mean[a]	P(RNA source)[b]	P(Subject)[c]	Max. FC[d]	Subject SD[e]
2320472	CLCN6	1	chloride channel 6	8.77	0.96	0.53	1.01	0.16
2951500	TEAD3	6	TEA domain family member 3	6.23	0.93	0.23	1.02	0.15
3359881	ART5	11	ADP-ribosyltransferase 5	6.10	0.94	0.85	1.02	0.15
3770512	C17orf28	17	chromosome 17 open reading frame 28	6.79	0.94	0.43	1.02	0.16
3688362	COX6A2	16	cytochrome c oxidase subunit VIa polypeptide 2	7.79	0.95	0.23	1.02	0.22
3986412	LOC100293553	X	similar to L-myc-2 protein	4.54	0.97	0.81	1.02	0.20
3840952	ZNF331	19	zinc finger protein 331	5.84	0.97	0.92	1.02	0.21
2895650	SIRT5	6	sirtuin (silent mating type information regulation 2 homolog) 5 (S. cerevisiae)	7.06	0.92	0.73	1.02	0.15
3552344	FLJ41170	14	hypothetical LOC440200	5.18	0.98	0.27	1.02	0.40
3064204	ACTL6B	7	actin-like 6B	6.36	0.92	0.48	1.02	0.18
3994964	GPR50	X	G protein-coupled receptor 50	4.73	0.94	0.28	1.02	0.24
3839489	GPR32	19	G protein-coupled receptor 32	5.28	0.96	0.71	1.02	0.25
3554104	KIF26A	14	kinesin family member 26A	5.09	0.92	0.30	1.02	0.23
3715935	PIPOX	17	pipecolic acid oxidase	5.31	0.88	0.78	1.02	0.14
3268548	PSTK	10	phosphoseryl-tRNA kinase	5.79	0.90	0.55	1.02	0.17
3597476	RAB8B	15	RAB8B, member RAS oncogene family	10.72	0.83	0.20	1.02	0.18
2334932	CYP4B1	1	cytochrome P450, family 4, subfamily B, polypeptide 1	5.53	0.82	0.54	1.02	0.13
2951191	SPDEF	6	SAM pointed domain containing ets transcription factor	6.30	0.85	0.22	1.03	0.20
3873824	TMC2	20	transmembrane channel-like 2	4.81	0.62	0.62	1.03	0.10
3567970	GPHB5	14	glycoprotein hormone beta 5	6.53	0.92	0.55	1.03	0.26
3882413	C20orf114	20	chromosome 20 open reading frame 114	4.85	0.70	0.24	1.03	0.15
3122631	XKR5	8	XK, Kell blood group complex subunit-related family, member 5	5.36	0.80	0.22	1.03	0.18
3952703	C22orf39	22	chromosome 22 open reading frame 39	7.82	0.71	0.63	1.03	0.13
3249369	LRRTM3	10	leucine rich repeat transmembrane neuronal 3	5.32	0.86	0.67	1.03	0.17
3850331	CDC37	19	cell division cycle 37 homolog (S. cerevisiae)	9.36	0.69	0.23	1.03	0.14
2708203	MAP6D1	3	MAP6 domain containing 1	7.02	0.84	0.67	1.03	0.20
3838845	CPT1C	19	carnitine palmitoyltransferase 1C	6.07	0.80	0.26	1.03	0.19
3959203	RBM9	22	RNA binding motif protein 9	5.90	0.70	0.21	1.04	0.18
3637818	NTRK3	15	neurotrophic tyrosine kinase, receptor, type 3	4.21	0.44	0.41	1.04	0.12
3231835	C10orf110	10	chromosome 10 open reading frame 110	4.59	0.85	0.94	1.04	0.20
3509910	FAM48A	13	family with sequence similarity 48, member A	9.46	0.53	0.31	1.04	0.14

[a] Grand mean across three RNA sources > 4.0

[b,c] $p > 0.2$

[d] Maximum fold change across three RNA source

[e] Standard deviation of the subject effects

Supplementary Table 13. Key quality control parameters for 140 samples.

	LCL				PAX				PBMC			
ID	All probeset mean	PM Mean	All probeset RLE mean	Pos *vs.* neg AUC	All probeset mean	PM Mean	All probeset RLE mean	Pos *vs.* neg AUC	All probeset mean	PM Mean	All probeset RLE mean	Pos *vs.* neg AUC
1	6.33	140.68	0.43	0.90	5.68	164.57	0.31	0.82	6.02	122.12	0.38	0.85
2[a]	6.27	113.52	0.46	0.90	5.63	175.36	0.34	0.82	6.04	171.46	0.34	0.85
3	6.28	155.07	0.36	0.91	5.66	158.84	0.31	0.82	6.06	130.52	0.35	0.87
4	6.23	141.39	0.36	0.90	5.67	166.57	0.36	0.82	6.20	166.37	0.42	0.88
5	6.25	139.04	0.34	0.90	5.65	143.13	0.35	0.81	5.99	115.45	0.39	0.86
6	6.27	147.10	0.43	0.90	5.72	166.45	0.45	0.82	6.00	102.58	0.41	0.87
7	6.24	125.64	0.41	0.89	5.73	153.13	0.43	0.83	6.02	116.46	0.42	0.86
8[a]	6.17	136.99	0.44	0.89	5.58	143.97	0.37	0.81	6.19	146.71	0.43	0.88
9	6.29	177.56	0.31	0.90	5.65	146.20	0.35	0.82	6.28	213.07	0.52	0.88
10	6.15	123.64	0.50	0.88	5.57	120.62	0.42	0.80	6.09	113.19	0.47	0.86
11	6.15	124.30	0.45	0.89	5.62	129.75	0.38	0.81	6.21	155.90	0.42	0.89
12	6.22	160.17	0.40	0.90	5.56	118.20	0.45	0.80	6.27	178.31	0.49	0.89
13	6.32	197.80	0.37	0.89	5.62	144.18	0.39	0.81	6.20	205.14	0.38	0.88
14	6.37	206.14	0.43	0.90	5.63	155.02	0.35	0.80	5.96	143.38	0.41	0.86
15	6.34	179.21	0.39	0.89	5.73	176.85	0.42	0.83	6.02	157.27	0.34	0.86
16	6.24	169.70	0.39	0.89	5.63	138.49	0.40	0.81	5.98	133.38	0.37	0.86
17	6.23	196.85	0.39	0.89	5.71	209.16	0.40	0.82	6.18	259.06	0.36	0.87
18	6.31	189.93	0.37	0.89	5.63	219.86	0.30	0.81	6.06	240.33	0.32	0.88
19	6.32	242.02	0.27	0.90	5.61	211.51	0.35	0.81	6.22	231.42	0.43	0.88
20	6.25	246.33	0.31	0.90	5.67	179.40	0.34	0.82	6.17	188.69	0.37	0.88
22	6.38	229.44	0.40	0.91	5.63	169.63	0.36	0.81	6.20	203.42	0.44	0.88
24	6.16	205.42	0.43	0.90	5.66	242.93	0.34	0.82	6.16	227.32	0.35	0.88
25	6.30	334.12	0.34	0.90	5.61	190.92	0.36	0.81	5.98	191.26	0.36	0.87
26	5.96	221.71	0.66	0.88	5.63	224.18	0.30	0.82	6.16	239.11	0.34	0.89
27	6.06	229.29	0.55	0.88	5.66	256.18	0.29	0.82	6.03	223.60	0.36	0.88
28	6.31	328.28	0.28	0.90	5.62	220.94	0.29	0.81	6.19	295.34	0.35	0.88
29	6.34	366.36	0.29	0.90	5.65	206.54	0.30	0.81	6.13	211.38	0.39	0.87
30	6.36	362.74	0.42	0.90	5.65	215.49	0.32	0.81	6.23	224.78	0.46	0.88
31	6.21	334.93	0.31	0.89	5.57	193.36	0.35	0.80	6.15	259.41	0.34	0.89
32	6.29	367.30	0.34	0.89	5.65	230.79	0.32	0.81	6.40	353.21	0.63	0.90
33	6.22	268.57	0.34	0.90	5.50	166.21	0.53	0.79	6.05	287.00	0.36	0.87
34	6.30	230.65	0.31	0.90	5.61	223.89	0.31	0.81	6.13	190.64	0.38	0.88
36	6.26	210.76	0.32	0.89	5.57	150.39	0.40	0.80	5.81	217.58	0.50	0.84
37	6.35	215.27	0.36	0.90	5.45	150.94	0.51	0.78	5.46	224.12	0.88	0.79
38[b]	6.31	227.32	0.43	0.89	5.65	180.00	0.38	0.81	5.42	164.48	0.92	0.79
39[b]	6.33	219.85	0.41	0.90	5.65	195.49	0.37	0.82	5.98	192.67	0.45	0.85
40	6.38	247.91	0.40	0.89	5.55	149.03	0.44	0.80	5.36	181.78	1.00	0.77
41[b]	6.33	201.09	0.34	0.90	5.58	169.93	0.38	0.80	5.40	146.09	0.95	0.78
42[a]	6.29	216.53	0.34	0.88	5.63	155.40	0.34	0.81	5.46	174.00	0.88	0.79
43[a]	6.25	204.94	0.34	0.90	5.75	208.70	0.38	0.84	6.06	171.61	0.47	0.86
44[a]	6.34	255.79	0.29	0.90	5.72	209.89	0.39	0.83	5.53	248.37	0.78	0.80
45[c]					5.63	192.80	0.32	0.81	5.59	182.91	0.72	0.81
46[b]	6.24	218.92	0.30	0.90	5.47	232.70	0.43	0.79	5.53	197.73	0.79	0.80
47[b]	5.99	130.30	0.88	0.85	5.65	213.31	0.31	0.82	5.28	204.52	1.08	0.77
48	6.24	254.16	0.31	0.90	5.62	229.41	0.39	0.81	5.69	194.35	0.62	0.83
49	5.95	256.91	0.67	0.88	5.61	191.59	0.33	0.81	5.66	247.55	0.69	0.82
50	6.00	300.80	0.61	0.88	5.49	188.68	0.49	0.78	5.82	236.93	0.43	0.83
Min	5.95	113.52	0.27	0.85	5.45	118.20	0.29	0.78	5.28	102.58	0.32	0.77
Max	6.38	367.30	0.88	0.91	5.75	256.18	0.53	0.84	6.40	353.21	1.08	0.90

[a] Mislabeled samples

[b] Samples with all probeset RLE mean > 0.75

[c] Incomplete sample

Supplementary Table 14. Post-correction deflation rate (a one unit difference in $\log_2$ RMA value in the original data).

Correction method	PAX *vs.* LCL	PBMC *vs.* LCL	PBMC *vs.* PAX
QPN	0.9581	0.9718	0.9734
S10	0.8797	0.8855	0.8898