Table 12. The top-100 differentially expressed genes in B lineage ALL vs. the NBM and normal hematopoietic cells

Accession no.	Gene name	Gene symbol	Entrez gene	Reporter ID	Score*	*P*	Sign†
BX089773	Ral guanine nucleotide dissociation stimulator-like 1	RGL1	23179	360212	1.862733	0.0002	+
AA029754	Like-glycosyltransferase	*LARGE*	9215	470092	1.853312	0.0002	+
AA683557	Ral guanine nucleotide dissociation stimulator-like 1	*RGL1*	23179	505864	1.563837	0.0002	+
AA490902	Guanylate kinase 1	*GUK1*	2987	824527	1.379727	0.0002	+
BX090758	Telomeric repeat binding factor 2	*TERF2*	7014	205335	1.345723	0.0002	+
AA708152	Transmembrane emp24 protein transport domain containing 6	*MGC23911*	146456	460798	1.345657	0.0002	+
AW073325	Down syndrome critical region gene 1	*DSCR1*	1827	2556526	1.329242	0.0002	+
AA598794	Connective tissue growth factor	*CTGF*	1490	898092	1.325661	0.0002	+
AI949742	Natriuretic peptide receptor A/guanylate cyclase A (atrionatriuretic peptide receptor A)	*NPR1*	4881	2470153	1.312974	0.0002	+
AW007634	Histidyl-tRNA synthetase 2	*HARS2*	92675	2511570	1.297933	0.0002	–
N49045	Breast cancer anti-estrogen resistance 3	*BCAR3*	8412	279670	1.247417	0.0002	+
T59334	Cysteine and glycine-rich protein 2	*CSRP2*	1466	75254	1.241858	0.0002	+
AA416817	Pleckstrin and Sec7 domain containing 3	*PSD3*	23362	731240	1.235097	0.0002	+
AA411668	Neuron navigator 1	*NAV1*	89796	753271	1.22918	0.0002	+
N63781	Chromosome 9 open reading frame 77	*C9orf77*	51104	293059	1.223212	0.0002	+
BX107803	Like-glycosyltransferase	*LARGE*	9215	197558	1.221584	0.0002	+
N47214	Transcribed locus	*0*	0	280413	1.217079	0.0002	+
AA705326	Solute carrier family 41, member 1	*SLC41A1*	254428	462849	1.217034	0.0002	+
BX092408	S100 calcium binding protein A13	*S100A13*	6284	325513	1.21287	0.0002	+
AA488889	Early B cell factor	*EBF*	1879	824886	1.210478	0.0002	+
AA897151	Testis derived transcript (3 LIM domains)	*TES*	26136	1466237	1.206966	0.0002	–
AA479132	Hypothetical protein MGC17943	*MGC17943*	90488	754192	1.206222	0.0002	+
W74533	Latrophilin 2	*LPHN2*	23266	346583	1.203971	0.0002	–
R83161	GRB2-associated binding protein 1	*GAB1*	2549	194399	1.194992	0.0002	+
CR744656	Calmodulin regulated spectrin-associated protein 1	*CAMSAP1*	157922	49228	1.194984	0.0002	+
W85766	GRB2-associated binding protein 1	*GAB1*	2549	416061	1.19398	0.0002	+
W76395	Melanoma associated gene	*D2S448*	7837	345601	1.192706	0.0002	+
AI356709	Melanoma associated gene	*D2S448*	7837	2012757	1.170167	0.0002	+
R70508	Cysteine-rich motor neuron 1	*CRIM1*	51232	141845	1.157149	0.0002	+
N68193	GRB2-associated binding protein 1	*GAB1*	2549	292272	1.154772	0.0002	+
AA707167	Early B cell factor	*EBF*	1879	451394	1.143987	0.0002	+
AA151003	Septin 11	*Sept11*	55752	505032	1.132283	0.0002	+
AI301815	Pleckstrin homology domain containing, family G (with RhoGef domain) member 1	*PLEKHG1*	57480	1901310	1.130945	0.0002	+
AA448464	Multiple cluster hits:381214 & 432419	*C21orf56 & MGC4677*	84221 & 112597	782446	1.130311	0.0002	–
AA005196	Zinc finger protein 138 (clone pHZ-32)	*ZNF138*	7697	429086	1.121234	0.0002	+
AI015577	Homolog of yeast INO80	*INO80*	54617	1636837	1.117714	0.0002	+
AI380933	CDNA FLJ34248 fis, clone FCBBF4000446	*0*	0	2109112	1.11521	0.0002	+
AA491191	Interferon, gamma-inducible protein 16	*IFI16*	3428	824602	1.107342	0.0002	+
AA678226	Talin 1	*TLN1*	7094	430894	1.104417	0.0002	–
BX093830	CDNA FLJ37485 fis, clone BRAWH2014379	*0*	0	786612	1.102379	0.0002	+
AA404694	PTK2 protein tyrosine kinase 2	*PTK2*	5747	724892	1.099251	0.0002	+
AA448270	Hypothetical protein MGC33630	*MGC33630*	144406	782838	1.095011	0.0002	+
AA599005	Laminin, gamma 1 (formerly LAMB2)	*LAMC1*	3915	897760	1.092641	0.0002	+
T60135	Monoglyceride lipase	*MGLL*	11343	81394	1.091577	0.0002	–

AA487460	Stromal cell-derived factor 2-like 1	*DPYSL2*	1808	841620	1.090863	0.0002	+
AA490735	Cytochrome c oxidase subunit Va	*COX5A*	9377	824068	1.080635	0.0002	+
H23338	Protein kinase C, epsilon	*PRKCE*	5581	51986	1.079515	0.0002	+
R10947	Cytochrome *c* oxidase subunit VIIa polypeptide 2 like	*COX7A2L*	9167	129146	1.073208	0.0002	—-
AA976561	Asparaginase like 1	*ASRGL1*	80150	1558655	1.073004	0.0002	—
R56808	Multiple cluster hits:26579 & 444619	*0 & DXS9879E*	0 & 8270	41225	1.070818	0.0002	+
AA495935	Microsomal glutathione S-transferase 1	*MGST1*	4257	768443	1.070522	0.0002	—
N99711	Histone 1, H2bk	*HIST1H2BK*	85236	290841	1.066153	0.0002	+
AA453304	Transcribed locus, strongly similar to NP_005927.1 myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 4 [Homo sapiens]	*0*	0	788155	1.061896	0.0002	+
T69562	Pyroglutamyl-peptidase I	*PGPEP1*	54858	83506	1.059634	0.0002	—
AA456435	GRB2-associated binding protein 1	*GAB1*	2549	788405	1.058575	0.0002	+
AI830988	B cell linker	*BLNK*	29760	2409188	1.058467	0.0002	+
N80054	Full length insert cDNA clone ZA91F08	*0*	0	299943	1.05708	0.0002	+
AA486151	Neuron navigator 1	*NAV1*	89796	840777	1.056286	0.0002	+
AA863424	Dipeptidase 1 (renal)	*DPEP1*	1800	1456900	1.054641	0.0002	+
AA047338	Proteasome (prosome, macropain) subunit, alpha type, 6	*PSMA6*	5687	509495	1.054629	0.0002	+
AA456845	Phosphatase and actin regulator 2	*PHACTR2*	9749	815588	1.05081	0.0002	-
AA011266	Multiple cluster hits:87385 & 432616	*C7orf30 & IMP-3*	115416 & 10643	429494	1.048869	0.0002	+
AA991507	Selectin P ligand	*SELPLG*	6404	1609625	1.045794	0.0002	—
AA071235	Aurora kinase B	*AURKB*	9212	531319	1.042825	0.0002	+
H45966	Cyclin-dependent kinase 9 (CDC2-related kinase)	*CDK9*	1025	184365	1.041096	0.0002	+
AA700164	Phosphatase and actin regulator 2	*PHACTR2*	9749	452417	1.039226	0.0002	—
AI824948	Telomerase reverse transcriptase	*TERT*	7015	2304672	1.038918	0.0002	+
AA987959	Transcription factor 4	*TCF4*	6925	1603442	1.033538	0.0002	+
R33200	Spastic paraplegia 20, spartin (Troyer syndrome)	*SPG20*	23111	135800	1.031475	0.0002	—
AA021132	Transcribed locus	*0*	0	364098	1.02752	0.0002	+
BX100113	Intercellular adhesion molecule 3	*ICAM3*	3385	754080	1.027461	0.0002	—
AA699652	RALBP1 associated Eps domain containing 2	*REPS2*	9185	436455	1.023902	0.0002	+
N94362	Solute carrier family 35, member E3	*SLC35E3*	55508	309486	1.022697	0.0002	+
AA457138	Frizzled homolog 8 (Drosophila)	*FZD8*	8325	810459	1.022	0.0002	+
AA036649	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	*TAF7*	6879	365930	1.019557	0.0002	+
AI675889	Neuropeptide Y	*NPY*	4852	2314420	1.018292	0.0002	+
AA453028	Paired immunoglobin-like type 2 receptor beta	*PILRB*	29990	788355	1.016402	0.0002	+
AA933641	Hypothetical protein FLJ20674	*FLJ20674*	54621	1551151	1.016044	0.0002	+
AI686016	GRB2-associated binding protein 1	*GAB1*	2549	2248902	1.009668	0.0002	+
AI538546	Histidyl-tRNA synthetase 2	*HARS2*	92675	2075029	1.008811	0.0002	—
AA490922	Hypothetical protein BC018415	*LOC130617*	130617	824553	1.006749	0.0002	—
N68512	Hermansky-Pudlak syndrome 4	*HPS4*	89781	294089	1.005311	0.0002	+
AA708756	Hect domain and RLD 6	*HERC6*	55008	384526	1.003075	0.0002	+
AA911661	Homeo box B2	*HOXB2*	3212	1526826	1.002989	0.0002	—
AA446789	LIM protein (similar to rat protein kinase C-binding enigma)	*LIM*	10611	784168	1.000501	0.0002	—
CR741637	Transducin (beta)-like 1X-linked	*TBL1X*	6907	712454	0.999427	0.0002	+
AA670123	KH domain containing, RNA binding, signal transduction associated 3	*KHDRBS3*	10656	844703	0.998818	0.0002	+
AA928451	Hypothetical protein FLJ36674	*FLJ36674*	284040	1486534	0.998722	0.0002	—
AA026692	CDNA FLJ12931 fis, clone NT2RP2004861	*0*	0	366591	0.997925	0.0002	+
AA461518	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	*TAF7*	6879	795850	0.997269	0.0002	+
AI360342	RAB33A, member RAS oncogene family	*RAB33A*	9363	2019211	0.99195	0.0002	—
R15978	Similar to RIKEN cDNA 2210021J22	*LOC150383*	150383	53245	0.991427	0.0002	+
R23318	Suppressor of cytokine signaling 2	*SOCS2*	8835	131073	0.991062	0.0002	+

AI927284	Lectin, galactoside-binding, soluble, 1 (galectin 1)	*LGALS1*	3956	2461050	0.990076	0.0002	–
N71462	Sex comb on midleg-like 2 (Drosophila)	*SCML2*	10389	294913	0.990004	0.0002	+
AA452955	Solute carrier family 38, member 1	*SLC38A1*	81539	788541	0.98639	0.0002	+
BX113432	Gamma-glutamyltransferase 2	*GGT2*	2679	2061465	0.986187	0.0002	–
N51097	Zinc finger protein 545	*ZNF545*	284406	281982	0.985471	0.0002	+
H08899	Isopentenyl-diphosphate delta isomerase	*IDI1*	3422	44975	0.985334	0.0002	+
AA278839	Zinc finger protein (ZFD25)	*ZFD25*	51427	703844	0.985318	0.0002	+

*Value from discriminatory analysis, with a high value indicating a high correlation with the classes.
†The plus (+) sign indicates relative up-regulation in B lineage ALL, the minus (–) sign indicates up-regulation in normal cells.