Table 21. The differentially expressed genes in *MLL* vs. B lineage ALL

Accession no.	Gene name	Gene symbol	Entrez gene	Reporter ID	Score*	*P*	Sign†
BX112951	Meis1, myeloid ecotropic viral integration site 1 homolog (mouse)	*MEIS1*	4211	307506	13.01914	0.0002	+
AA953229	Homeo box A10	*HOXA10*	3206	1592006	7.32839	0.0002	+
AA479883	Hypothetical protein FLJ21127	*FLJ21127*	79600	772880	4.298862	0.0002	+
N67262	Zinc finger protein 135 (clone pHZ-17)	*ZNF135*	7694	286378	4.223683	0.0002	–
AA047441	Protein phosphatase 1H (PP2C domain containing)	*PPM1H*	57460	488431	4.195039	0.0002	+
BX115990	Chromosome 9 open reading frame 52	*C9orf52*	158219	2110547	4.098576	0.0002	+
BX105581	Lymphocyte antigen 86	*LY86*	9450	2333826	3.400301	0.0002	+
AI984983	Phospholipase A2, group IVA (cytosolic, calcium-dependent)	*PLA2G4A*	5321	2494805	3.295743	0.0002	+
AI021905	Adducin 1 (alpha)	*ADD1*	118	1654651	3.293293	0.0002	+
R22219	Phosphate cytidylyltransferase 2, ethanolamine	*PCYT2*	5833	130884	3.291428	0.0004	+
AA975680	SVAP1 protein	*IMAGE3451454*	116841	1588973	3.287576	0.0004	+
AA194765	Forkhead box O1A (rhabdomyosarcoma)	*FOXO1A*	2308	628955	3.284992	0.0002	–
R06246	Multiple cluster hits:30258 & 486548	*0 & MAP7*	0 & 9053	126218	3.252799	0.0002	+
AA147540	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 9	*SERPINB9*	5272	505385	3.214267	0.0002	–
AA486067	Transducin (beta)-like 1X-linked	*TBL1X*	6907	840766	3.205819	0.0002	–
AA453898	Sialyltransferase 4C (beta-galactoside alpha-2,3-sialyltransferase)	*SIAT4C*	6484	813751	3.137125	0.0002	+
AA128156	RunT related transcription factor 2	*RUNX2*	860	501989	3.097915	0.0006	+
AI927284	Lectin, galactoside-binding, soluble, 1 (galectin 1)	*LGALS1*	3956	2461050	3.039644	0.0002	+
AA453774	Regulator of G-protein signalling 16	*RGS16*	6004	813707	2.999767	0.0002	+
AA431426	Ribosomal protein L23a pseudogene 7	*RPL23AP7*	118433	782434	2.975902	0.0002	+
W45031	Mitochondria-associated protein involved in granulocyte-macrophage colony-stimulating factor signal transduction	*Magmas*	51025	322923	2.9567	0.0008	+
R12636	Hypothetical gene LOC401431	*LOC401431*	401431	26149	2.89011	0.0002	–
AA928660	Protease, serine, 12 (neurotrypsin, motopsin)	*PRSS12*	8492	1553054	2.838338	0.0004	+
AA449654	Formin binding protein 1	*FNBP1*	23048	785907	2.821136	0.0002	+
AI278206	RAB1A, member RAS oncogene family	*RAB1A*	5861	1878917	2.814022	0.0002	–
AA683557	Ral guanine nucleotide dissociation stimulator-like 1	*RGL1*	23179	505864	2.80546	0.0004	–
AA953973	Spastic paraplegia 20, spartin (Troyer syndrome)	*SPG20*	23111	1573305	2.796572	0.001	+
N98832	Spleen focus forming virus (SFFV) proviral integration oncogene spi1	*SPI1*	6688	278808	2.786428	0.0002	–
AA633658	Amyloid beta (A4) precursor protein (protease nexin-II, Alzheimer disease)	*APP*	351	856575	2.769163	0.0002	–
N71061	Chromosome 10 open reading frame 58	*C10orf58*	84293	294591	2.736423	0.0002	–
W52082	Mitochondrial ribosomal protein L33	*MRPL33*	9553	325520	2.698654	0.0002	+
AA459614	Tyrosylprotein sulfotransferase 2	*TPST2*	8459	810937	2.686035	0.0002	–
R77251	Microtubule-associated protein 7	*MAP7*	9053	144834	2.676695	0.0002	+
BX095299	Fragile histidine triad gene	*FHIT*	2272	125273	2.662129	0.0002	–
AA857015	Ephrin-A1	*EFNA1*	1942	1474684	2.646903	0.0002	–
AA782337	Ankyrin 2, neuronal	*ANK2*	287	857603	2.628807	0.0002	+
AA482594	Kelch-like 5 (Drosophila)	*KLHL5*	51088	746080	2.587484	0.0004	–
AA400292	Disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)	*DAB2*	1601	742685	2.58302	0.0002	–
AA669136	Transcription factor 4	*TCF4*	6925	854581	2.575075	0.0002	–
N36927	CDNA FLJ33419 fis, clone BRACE2019877	*0*	0	273536	2.527296	0.0004	+
N46717	Syntaxin binding protein 6 (amisyn)	*STXBP6*	29091	277042	2.516744	0.0002	+
AA428394	HtrA serine peptidase 3	*HTRA3*	94031	773558	2.509196	0.0008	+
AA043163	ELK3, ETS-domain protein (SRF accessory protein 2)	*ELK3*	2004	486102	2.494976	0.0008	–
AW087156	Nuclear phosphoprotein similar to S. cerevisiae PWP1	*PWP1*	11137	2578263	2.470165	0.0002	+
AA158540	TBC1 domain family, member 14	*TBC1D14*	57533	592458	2.457798	0.001	+
T60664	AHNAK nucleoprotein (desmoyokin)	*AHNAK*	195	79216	2.422263	0.0006	+
AI268273	Mitogen-activated protein kinase kinase kinase 5	*MAP3K5*	4217	1880757	2.421493	0.0008	+

N30348	Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	*FLT1*	2321	258101	2.397606	0.0006	–
AI440513	Villin 2 (ezrin)	*VIL2*	7430	2072783	2.352864	0.0008	+
W58161	Pinin, desmosome associated protein	*PNN*	5411	341051	2.349005	0.0002	–
AA634300	IGF-II mRNA-binding protein 2	*IMP-2*	10644	743774	2.346936	0.0002	+
N67762	Chromosome 9 open reading frame 21	*C9orf21*	195827	291403	2.345112	0.0002	+
AA630100	Hypothetical protein MGC17299	*MGC17299*	128218	854691	2.323185	0.0002	–
AA864840	Retinoic acid induced 14	*RAI14*	26064	1460073	2.309665	0.0008	–
R76277	Calmodulin 1 (phosphorylase kinase, delta)	*CALM1*	801	144801	2.295832	0.0008	–
AA668595	Tumor protein p53 inducible protein 3	*TP53I3*	9540	859359	2.290491	0.0002	+
BX098767	Seryl-tRNA synthetase 2	*SARS2*	54938	809467	2.281401	0.001	+
AA425588	Integrin, alpha E (antigen CD103, human mucosal lymphocyte antigen 1; alpha polypeptide)	*ITGAE*	3682	773332	2.26545	0.0002	+
BX099263	Prominin 1	*PROM1*	8842	27544	2.246197	0.0004	+
H46554	Transcription factor 8 (represses interleukin 2 expression)	*TCF8*	6935	178463	2.24379	0.0002	–
N23340	Hypothetical protein LOC152485	*LOC152485*	152485	267186	2.230099	0.0004	–
R01824	Myofibrillogenesis regulator 1	*MR-1*	25953	124447	2.227693	0.0002	+
AA486275	Serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 1	*SERPINB1*	1992	842836	2.226654	0.0008	+
AA187045	Sialyltransferase 10 (alpha-2,3-sialyltransferase VI)	*SIAT10*	10402	624372	2.226331	0.0006	–
T58146	HLA complex P5	*HCP5*	10866	79254	2.225294	0.0004	–
N32639	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 8	*SLC7A8*	23428	267666	2.220183	0.0004	+
T47228	X 009 protein	*MDS009*	56986	75919	2.217918	0.001	+
BX112066	Hypothetical protein FLJ38984	*FLJ38984*	127703	770380	2.213171	0.0002	+
AA630534	Kruppel-like factor 11	*KLF11*	8462	854789	2.193718	0.0006	–
N57610	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	*HACE1*	57531	283430	2.180532	0.0002	–
AA134531	Hypothetical protein BC018415	*LOC130617*	130617	502558	2.171082	0.0002	+
AA886199	Chromosome 1 open reading frame 34	*C1orf34*	22996	1492468	2.157518	0.0008	+
AA293453	Sideroflexin 3	*SFXN3*	81855	726236	2.156278	0.001	+
W02342	Ceroid-lipofuscinosis, neuronal 5	*CLN5*	1203	292071	2.144411	0.001	+
AW057757	Palladin	*KIAA0992*	23022	2542582	2.113065	0.0004	+
AA228130	PC4 and SFRS1 interacting protein 1	*PSIP1*	11168	667598	2.112296	0.001	–
N31532	Potassium channel tetramerisation domain containing 15	*KCTD15*	79047	266019	2.092832	0.0004	+
AA999901	Guanine nucleotide binding protein (G protein), gamma 11	*GNG11*	2791	1636447	2.086228	0.001	–
AA412217	Anaphase promoting complex subunit 1	*ANAPC1*	64682	731433	2.085086	0.0002	+
AA464028	Hypothetical protein FLJ14525	*FLJ14525*	84886	810603	2.081352	0.0002	–
N94362	Solute carrier family 35, member E3	*SLC35E3*	55508	309486	2.060098	0.0006	–
AA629596	Nipsnap homolog 3A (C. elegans)	*NIPSNAP3A*	25934	884765	2.033848	0.0002	+
AA479995	Discs, large homolog 5 (Drosophila)	*DLG5*	9231	753969	2.000836	0.0006	–
AA464688	OCIA domain containing 2	*OCIAD2*	132299	810218	1.977171	0.0008	–
AA460890	Nedd4 family interacting protein 1	*NDFIP1*	80762	796739	1.93092	0.0008	–
AI374985	Growth arresT specific 2	*GAS2*	2620	2047854	1.862829	0.0008	–
N63635	Pim-1 oncogene	*PIM1*	5292	292726	1.850285	0.0002	–
AA626846	Hypothetical LOC389025	*0*	389025	745190	1.849095	0.0002	–
AI986457	Serine (or cysteine) proteinase inhibitor, clade F (alpha-2 antiplasmin, pigment epithelium derived factor), member 1	*SERPINF1*	5176	2562939	1.844415	0.0002	–
AA457731	SNARE protein Ykt6	*YKT6*	10652	810762	1.734551	0.0004	–
N21237	SAM and SH3 domain containing 1	*SASH1*	23328	264938	1.727895	0.0008	–
R83161	GRB2-associated binding protein 1	*GAB1*	2549	194399	1.719901	0.001	–

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