Table 19. The differentially expressed genes in NK vs. B lineage ALL

Accession no. r	Gene name	Gene symbol	Entrez gene	Reporter ID	Score*	*P*	Sign†
BX090123	Chromatin assembly factor 1, subunit B (p60)	*CHAF1B*	8208	756769	0.97783	0.0002	–
R72365	ORF	*LOC51035*	51035	155896	0.897056	0.0002	+
AA126419	Inositol polyphosphate-4-phosphatase, type I, 107kDa	*INPP4A*	3631	490471	0.896319	0.0002	+
AA455693	COP9 constitutive photomorphogenic homolog subunit 3 (Arabidopsis)	*COPS3*	8533	813983	0.88703	0.0002	–
R23687	Golgi autoantigen, golgin subfamily a, 1	*GOLGA1*	2800	34102	0.8847	0.0002	+
AA485983	MCM4 minichromosome maintenance deficient 4 (S. cerevisiae)	*MCM4*	4173	843049	0.882806	0.0004	–
AA043501	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	*MAF*	4094	487793	0.872188	0.0002	+
AA455261	Chromobox homolog 7	*CBX7*	23492	814815	0.861587	0.0002	+
AA505067	Multiple cluster hits:126655 & 155983	*LOC92017 & JMJD2A*	92017 & 9682	825649	0.857942	0.0004	+
N63894	LOC440461	*0*	440461	293759	0.854021	0.0002	+
AA005350	Hypothetical protein MGC26694	*MGC26694*	284439	428377	0.847288	0.0006	+
AA491015	Integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	*ITGA4*	3676	823964	0.838276	0.0006	+
N34436	V-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	*MAF*	4094	277414	0.837416	0.0002	+
AA481076	MAD2 mitotic arrest deficienT like 1 (yeast)	*MAD2L1*	4085	814701	0.836135	0.0004	–
W05762	Chromosome 14 open reading frame 147	*C14orf147*	171546	299664	0.831883	0.0004	–
AI795996	X-ray repair complementing defective repair in Chinese hamster cells 4	*XRCC4*	7518	2383277	0.829554	0.0004	+
R38306	Nuclear factor of activated T cells, cytoplasmic, calcineurin-dependent 3	*NFATC3*	4775	137457	0.823186	0.0004	+
CR742119	Multiple cluster hits:144496 & 370292	*GMDS & BCCIP*	2762 & 56647	112576	0.805223	0.0008	–
AA703117	3' exoribonuclease	*3'HEXO*	90459	434828	0.7985	0.0004	–
AA293819	Nuclear factor of activated T cells, cytoplasmic, calcineurin-dependent 3	*NFATC3*	4775	727192	0.790428	0.0004	+
H85311	Stress 70 protein chaperone, microsome-associated, 60kDa	*STCH*	6782	222025	0.783004	0.0004	–
BX113198	Microtubule associated serine/threonine kinase-like	*MASTL*	84930	1070324	0.78294	0.0008	–
N47311	Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)	*HPRT1*	3251	280507	0.780259	0.0004	–
AA252014	Galactosidase, alpha	*GLA*	2717	684879	0.77791	0.0008	–
AI222059	Follistatin-like 4	*FSTL4*	23105	1843488	0.768948	0.0002	+
AA404486	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 5	*SLC25A5*	292	772304	0.757738	0.0004	–
AA521490	Limkain b1	*LKAP*	9665	826622	0.753162	0.001	+
R21638	Multiple cluster hits:460184 & 547153	*MCM4 & 0*	4173 & 0	130204	0.744934	0.0006	–
AA464291	Ubiquitin specific protease 19	*USP19*	10869	809848	0.742805	0.001	+
R43956	Pleckstrin homology, Sec7 and coiled-coil domains 4	*PSCD4*	27128	33293	0.741404	0.0006	+
AA019203	High-mobility group box 2	*HMGB2*	3148	363103	0.739436	0.0006	–
AA454912	Vacuolar protein sorting 52 (yeast)	*VPS52*	6293	809961	0.738125	0.0008	+
AA918089	Ras homolog gene family, member T2	*RHOT2*	89941	1536013	0.737092	0.0008	+
AA426341	Von Hippel-Lindau binding protein 1	*VBP1*	7411	757404	0.736667	0.0008	–
H59203	CDC6 cell division cycle 6 homolog (S. cerevisiae)	*CDC6*	990	204214	0.729547	0.001	–
BX103899	Hypothetical protein MGC29956	*MGC29956*	131616	754112	0.727237	0.0006	+
BX100912	Basophilic leukemia expressed protein BLES03	*Bles03*	83638	151371	0.724993	0.001	+
AA453497	Rap guanine nucleotide exchange factor (GEF) 3	*RAPGEF3*	10411	795382	0.722959	0.0006	+
R19544	Multiple cluster hits:143805 & 530075	*0 & 0*	0 & 0	33510	0.719607	0.0006	+
AA935719	Hypothetical protein LOC283357	*LOC283357*	283357	1557318	0.705155	0.0004	+

*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.