

**Table 18. The top-100 differentially expressed genes in hyperdiploid vs. B lineage ALL**

Accession no.	Gene name	Gene symbol	Entrez Gene	Reporter ID	Score*	P	Sign <sup>†</sup>
AA099522	Zinc finger, CW type with coiled-coil domain 2	<i>ZCWCC2</i>	79710	489594	0.920107	0.0002	+
AA464528	Proteolipid protein 2 (colonic epithelium-enriched)	<i>PLP2</i>	5355	810504	0.916328	0.0002	+
AA504303	Multiple cluster hits:435933 & 495960	<i>PHF10 &amp; ATP6AP2</i>	55274 & 10159	825076	0.882042	0.0002	+
AA496795	Intersectin 1 (SH3 domain protein)	<i>ITSN1</i>	6453	897652	0.871029	0.0002	+
AI983274	ATPase, H <sup>+</sup> transporting, lysosomal accessory protein 2	<i>ATP6AP2</i>	10159	2517344	0.861921	0.0002	+
BX099233	Down syndrome critical region gene 5	<i>DSCR5</i>	51227	785642	0.855825	0.0002	+
R67222	Chromosome 6 open reading frame 192	<i>C6orf192</i>	116843	140852	0.854382	0.0002	+
AA151486	Phosphoribosyl pyrophosphate synthetase 2	<i>PRPS2</i>	5634	503097	0.853556	0.0002	+
AA989257	SH3-domain kinase binding protein 1	<i>SH3KBP1</i>	30011	1604005	0.826585	0.0002	+
AA188661	SH3-domain binding protein 5 (BTK-associated)	<i>SH3BP5</i>	9467	626343	0.824351	0.0002	+
AA488237	Hypothetical protein MGC23937 similar to CG4798	<i>MGC23937</i>	139596	877637	0.820576	0.0002	+
AA669443	Eukaryotic translation initiation factor 5	<i>EIF5</i>	1983	884867	0.810772	0.0002	+
AA251026	Transmembrane protein 32	<i>TMEM32</i>	93380	684539	0.804051	0.0002	+
BX099263	Prominin 1	<i>PROM1</i>	8842	27544	0.800393	0.0002	+
R59936	Potassium inwardly-rectifying channel, subfamily J, member 6	<i>KCNJ6</i>	3763	43101	0.798717	0.0002	+
AI537061	Sex comb on midleg-like 1 (Drosophila)	<i>SCML1</i>	6322	2184814	0.795694	0.0002	+
R89905	Ubiquitin specific protease 9, X-linked (fat facets-like, Drosophila)	<i>USP9X</i>	8239	194706	0.794274	0.0002	+
N48017	CDNA clone IMAGE:4686928, partial cds	<i>0</i>	0	272049	0.793969	0.0002	+
N49204	Acylphosphatase 2, muscle type	<i>ACYP2</i>	98	280252	0.792266	0.0002	-
H23561	Deltex homolog 1 (Drosophila)	<i>DTX1</i>	1840	52120	0.786572	0.0002	-
AA167328	Implantation-associated protein	<i>DKFZp564K142</i>	84061	595620	0.785457	0.0002	+
BX108537	Multiple cluster hits:2815 & 369761	<i>POU6F1 &amp; DAZAP2</i>	5463 & 9802	289447	0.783708	0.0002	+
AA482326	Leucine zipper, down-regulated in cancer 1-like	<i>LDOC1L</i>	84247	840884	0.776053	0.0002	-
AA670134	Tetrapeptide repeat domain 3	<i>TTC3</i>	7267	844725	0.772243	0.0002	+
AA446730	Upstream regulatory element binding protein 1	<i>UREB1</i>	10075	783681	0.771771	0.0002	+
N22323	Mst3 and SOK1-related kinase	<i>MST4</i>	51765	254029	0.77065	0.0002	+
AA621510	Zinc finger protein 219	<i>ZNF219</i>	51222	1055297	0.770246	0.0002	-
AI948893	SH3-domain binding protein 2	<i>SH3BP2</i>	6452	2471503	0.763598	0.0002	+
AI523637	Protocadherin 9	<i>PCDH9</i>	5101	2116531	0.7611	0.0002	-
W40257	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylglucosaminyltransferase 3 (GalNAc-T3)	<i>GALNT3</i>	2591	328542	0.758871	0.0002	+
BX116655	Follicular lymphoma variant translocation 1	<i>FVT1</i>	2531	233765	0.754143	0.0002	+
AA278240	Haloacid dehalogenase-like hydrolase domain containing 1A	<i>HDHD1A</i>	8226	703479	0.750802	0.0002	+
BX104021	Synuclein, alpha (non A4 component of amyloid precursor)	<i>SNCA</i>	6622	418328	0.747027	0.0002	+
AA906438	Hypothetical protein BC007772	<i>LOC93109</i>	93109	1505998	0.744796	0.0002	-
AA491107	Multiple cluster hits:449098 & 549611	<i>KIAA0685 &amp; 0</i>	9701 & 0	824557	0.741599	0.0002	+
AW008840	Nephroblastoma overexpressed gene	<i>NOV</i>	4856	2502789	0.738042	0.0002	+
AA630138	Zinc finger protein 185 (LIM domain)	<i>ZNF185</i>	7739	855079	0.737008	0.0002	+
R48131	Multiple cluster hits:167679 & 537269	<i>SH3BP2 &amp; 0</i>	6452 & 0	153694	0.735089	0.0002	+
BX105795	Ephrin-B1	<i>EFNB1</i>	1947	756968	0.734999	0.0002	+
AA425612	Solute carrier family 16 (monocarboxylic acid transporters), member 2	<i>SLC16A2</i>	6567	773344	0.733934	0.0002	+
AI401528	Hypothetical protein MGC34646	<i>MGC34646</i>	157807	2110073	0.732217	0.0002	+
N47922	FLJ10378 protein	<i>FLJ10378</i>	55132	260181	0.729115	0.0002	+
AI682474	Nuclear transport factor 2-like export factor 2	<i>NXT2</i>	55916	2322396	0.727954	0.0002	+
CR742982	Multiple cluster hits:257761 & 410969	<i>SH3BP5 &amp; NTRK3</i>	9467 & 4916	35356	0.723647	0.0002	+
AI299482	Hairy/enhancer-of-split related with YRPW motif 2	<i>HEY2</i>	23493	1895748	0.720416	0.0002	-

W01926	Membrane-spanning 4-domains, subfamily A, member 6A	<i>MS4A6A</i>	64231	294535	0.71719	0.0002	+
AA663941	LOC387882 hypothetical protein	<i>LOC387882</i>	387882	855707	0.716953	0.0002	+
AA629796	Sorting nexin 12	<i>SNX12</i>	29934	884540	0.715941	0.0002	+
H02929	Ring finger protein 153	<i>RNF153</i>	54708	151755	0.713692	0.0002	+
AA706929	Protein phosphatase 1F (PP2C domain containing)	<i>PPM1F</i>	9647	451855	0.712116	0.0002	+
H09375	Cellular repressor of E1A-stimulated genes 2	<i>CREG2</i>	200407	45999	0.710153	0.0002	+
AA194201	Bradykinin receptor B2	<i>BDKRB2</i>	624	665674	0.699995	0.0002	+
AA679345	Heterogeneous nuclear ribonucleoprotein H2 (H')	<i>HNRPH2</i>	3188	866874	0.699454	0.0002	+
AW004620	Calcium/calmodulin-dependent protein kinase I	<i>CAMK1</i>	8536	2505310	0.697136	0.0002	+
N73975	Transcription elongation factor A (SII)-like 4	<i>TCEAL4</i>	79921	296616	0.69489	0.0002	+
W55967	MAP3K12 binding inhibitory protein 1	<i>MBIP</i>	51562	340555	0.693368	0.0002	+
H09456	Target of myb1-like 2 (chicken)	<i>TOMIL2</i>	146691	46278	0.693016	0.0002	+
H61901	Ribosomal protein S6 kinase, 90kDa, polypeptide 3	<i>RPS6KA3</i>	6197	204148	0.692303	0.0002	+
H24099	Cystatin B (stefin B)	<i>CSTB</i>	1476	51814	0.691051	0.0002	+
N48804	Forkhead box P1	<i>FOXP1</i>	27086	279482	0.689329	0.0002	-
BX102980	Moesin	<i>MSN</i>	4478	814265	0.688239	0.0002	+
R92281	Cytochrome B 5	<i>CYB5</i>	1528	196189	0.687899	0.0002	+
BX103653	Breast cancer membrane protein 101	<i>NSE2</i>	157638	278572	0.686955	0.0002	+
AA429946	Dehydrogenase/reductase (SDR family) member 4	<i>DHRS4</i>	10901	781295	0.679879	0.0002	+
AA029842	Mature T cell proliferation 1	<i>MTCPI1</i>	4515	470175	0.67954	0.0002	+
AA782314	Hypothetical protein MGC35440	<i>LOC147991</i>	147991	857574	0.679373	0.0002	-
AA459420	Hypothetical protein FLJ20699	<i>FLJ20699</i>	55020	810981	0.677223	0.0002	+
AA705153	Hypothetical protein FLJ10357	<i>FLJ10357</i>	55701	461613	0.676399	0.0002	-
AA070661	S100 calcium binding protein A13	<i>S100A13</i>	6284	530035	0.676162	0.0002	+
R35848	Membrane-bound transcription factor protease, site 2	<i>MBTPS2</i>	51360	38450	0.676029	0.0002	+
R43580	Ubiquilin 2	<i>UBQLN2</i>	29978	23018	0.675635	0.0002	+
AA056375	Hypothetical protein from clone 643	<i>LOC57228</i>	57228	509458	0.675332	0.0002	+
AA464059	Coagulation factor VIII-associated (intronic transcript) 1	<i>F8A1</i>	8263	810264	0.674808	0.0002	+
AW051907	KIAA0179	<i>KIAA0179</i>	23076	2557117	0.673702	0.0002	+
AA169699	Hypothetical protein FLJ11171	<i>FLJ11171</i>	55783	609910	0.671402	0.0002	+
AA491271	Hypothetical protein FLJ12525	<i>FLJ12525</i>	81887	824622	0.66928	0.0002	+
H94063	Chromosome 13 open reading frame 1	<i>C13orf1</i>	57213	242840	0.667141	0.0002	+
AA045399	Hypothetical protein LOC162073	<i>LOC162073</i>	162073	487831	0.666409	0.0002	+
AA872379	SMT3 suppressor of mif two 3 homolog 3 (yeast)	<i>SUMO3</i>	6612	1472719	0.666257	0.0002	+
AA486239	Filamin B, beta (actin binding protein 278)	<i>FLNB</i>	2317	840818	0.666244	0.0002	+
N71286	Tripartite motif-containing 10	<i>TRIM10</i>	10107	294655	0.664245	0.0002	-
AA102454	Calpain 2, (m/II) large subunit	<i>CAPN2</i>	824	549728	0.659665	0.0002	+
AA701368	Carbonic anhydrase VB like	<i>CA5BL</i>	340591	435510	0.658644	0.0002	+
AA677340	Phosphorylase kinase, alpha 2 (liver)	<i>PHKA2</i>	5256	454475	0.658351	0.0002	+
N52162	Protein kinase (cAMP-dependent, catalytic) inhibitor alpha	<i>PKIA</i>	5569	284401	0.657349	0.0002	-
R52176	Multiple cluster hits:180257 & 407983	<i>ZNF550 &amp; SFMBT2</i>	162972 & 57713	40296	0.656336	0.0002	+
AA630381	Chromosome 14 open reading frame 147	<i>C14orf147</i>	171546	855345	0.654548	0.0002	+
AA099515	Signal sequence receptor, alpha (translocon-associated protein alpha)	<i>SSR1</i>	6745	510679	0.652463	0.0002	+
BX112916	RAB40C, member RAS oncogene family	<i>RAB40C</i>	57799	136303	0.651194	0.0002	+
AA489238	Multiple cluster hits:21388 & 460499	<i>ZDHHC21 &amp; ATXN2L</i>	340481 & 11273	825088	0.650119	0.0002	-
N53133	Spermatid perinuclear RNA binding protein	<i>STRBP</i>	55342	246620	0.647345	0.0002	+
AA056693	Phosphatidic acid phosphatase type 2B	<i>PPAP2B</i>	8613	489201	0.647171	0.0002	+
N78101	Cyclin I	<i>CCNI</i>	10983	248295	0.646068	0.0002	+
AA004975	Development and differentiation enhancing factor 1	<i>DDEF1</i>	50807	428936	0.64329	0.0002	+
AA047623	Progesterone receptor membrane component 2	<i>PGRMC2</i>	10424	376785	0.64271	0.0002	+

AW005979	Interleukin-1 receptor-associated kinase 1	<i>IRAK1</i>	3654	2566158	0.642416	0.0002	+
AA928142	Porcupine homolog (Drosophila)	<i>PORCN</i>	64840	1541827	0.641004	0.0002	+
BX090714	Pyruvate dehydrogenase kinase, isoenzyme 3	<i>PKD3</i>	5165	278242	0.640593	0.0002	+
R74171	Rap2 interacting protein x	<i>RIPX</i>	22902	143310	0.639547	0.0002	-
AI349234	Family with sequence similarity 26, member B	<i>FAM26B</i>	51063	2049813	0.637868	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 hyperdiploid ALL, the minus (-) sign indicates up-regulation in B lineage ALLs.