

**Table 1:** Clinical and biological database of the 95 B-lineage ALL samples evaluated by oligonucleotide microarrays.

<i>Identification code*</i>	<i>Gender</i>	<i>Age</i>	<i>Cytogenetic analysis</i>	<i>Molecular abnormalities</i>	<i>MDR</i>	<i>DNA Index</i>
01005	M	53	t(9;22)	BCR/ABL	NEG	Diploid
01010	M	19	5 Metaphases: 47xy 5 Metaphases: 46xy	NEG	POS	Diploid
03002	F	52	NE	BCR/ABL	NEG	Diploid
06002	M	15	Normal	NEG	NEG	Diploid
04006	M	38	t(4;11)	ALL1/AF4	NEG	Diploid
04007	M	57	del(6q)	NEG	NEG	Diploid
04008	M	17	10 Metaphases: 46 xy/62-78xy + X t(1;?)(p32;?) + iso (11q)	NEG	NEG	Hyperd.
04010	F	18	26 Metaphases: 46xx 4 Metaphases : 45-47xx, -2, -4, + mar 1, +mar 2	NEG	POS	Hyperd.
04016	M	16	14 Metaphases: 45-46xx, t(12;17)(p12;q12) 3 Metaphases: 46xx	NEG	NEG	Diploid
08001	M	40	NE	BCR/ABL+ (p15)	NEG	NE
08011	M	33	NE	BCR/ABL+ (p15/16)	NEG	Diploid
08012	M	55	11 Metaphases: 45xy, -5, gain(14)(q32)	p15	NEG	Diploid
08018	M	25	NE	E2A/PBX1	NEG	Diploid
08024	M	18	18 Metaphases: 46xy, der(14),t(8;14)(q11;q32)	NEG	POS	Diploid
09008	M	41	1 Metaphase: 58xy, t(9;22) x2; 13 Metaphases: 46xy	BCR/ABL	NEG	Hyperd.
09017	F	27	Normal	NEG	NEG	Diploid
11005	M	27	1 Metaphase: 46xy,add(1)(p32),del(7)(q22;q32),1(11)(q10),dic(?;12)(?;p13),-13,add(17)(p13),-17,-22,+m1,+m2,+m3	BCR/ABL	NEG	Diploid
12006	M	46	19 Metaphases: 40-46xy	BCR/ABL	NEG	Diploid
12007	M	37	t(9;22)	BCR/ABL	NEG	Diploid
12012	F	36	t(9;22)+del(9)	BCR/ABL	NEG	Diploid
12019	M	53	Normal	p15	POS	Diploid
12026	M	39	t(9;22)	BCR/ABL	UK	Diploid
14016	M	53	t(9;22)	BCR/ABL	NEG	NE
15001	M	20	Normal	p15	NEG	Hyperd.
15004	M	44	t(4;11)	ALL1/AF4	NEG	Hyperd.
15005	M	28	7 Metaphases: 53-55xy, +5,+6,t(9;22)(q34;q11),t(9;22)(q34;q11),+13,+14,+17,+19,+21; 9 Metaphases: 44-46xy	BCR/ABL	POS	Diploid
16004	F	58	t(4;11)	ALL1/AF4	NEG	Diploid
16009	F	43	NE	NEG	POS	Diploid
19005	F	48	Normal	ALL1/AF4	NEG	Diploid
20002	F	58	10 Metaphases: 46xx, t(9;22), t(7;12)	BCR/ABL	NEG	Diploid
22009	F	19	3 Metaphases: 46xx, der(12) 12 Metaphases: 46xx	NEG	NEG	Diploid
22010	F	26	t(9;22)	BCR/ABL	NEG	Diploid
22011	M	19	Normal	NEG	NEG	Diploid
22013	M	32	7 Metaphases: 46xy 4 Metaphases: 45-47xy, +1, der(1)t(1;?)(p11;?),t(9;22)	BCR/ABL	NEG	Diploid
24001	F	17	NE	BCR/ABL	NEG	Diploid
24005	F	45	t(4;11)	ALL1/AF4	NEG	Diploid
24008	F	20	Loss 6q*	NEG	NEG	Diploid
24010	F	16	t(9;22)	BCR/ABL	NEG	Diploid
24011	F	51	t(9;22)	BCR/ABL	POS	Diploid
24017	M	57	7 Metaphases: 48-51xy, +2, +6, +20, +21, t(9;22), +Ph	BCR/ABL	NEG	Hyperd.
24018	F	29	NE	NEG	POS	Diploid
24019	M	16	t(1;19)+del(6q)	E2A/PBX1	NEG	Diploid
24022	F	32	t(9;22)	BCR/ABL	POS	Diploid
25003	M	15	Metaphases: 47xy, +21 <sup>a</sup>	NEG	POS	Diploid
25006	M	19	NE	NEG	NEG	Diploid
26001	M	21	NE	p15/p16	POS	Diploid
26003	F	49	NE	BCR/ABL+ (p15/16)	NEG	Diploid
26005	M	38	NE	p15/p16	NEG	Diploid
26008	F	17	Normal	ALL1/AF4	NEG	Diploid
27003	F	26	NE	BCR/ABL	POS	Diploid
27004	F	48	t(9;22)	BCR/ABL+ (p15)	NEG	Diploid
28001	M	16	Normal	NEG	POS	Diploid

28003	M	18	NE	E2A/PBX1	NEG	Hyperd.
28005	M	17	10 Metaphases: 46xy/56xy, +8, +10, +10, +13, +13, +18, +18, +20, +21, +22	NEG	POS	Hyperd.
28006	M	22	del (6q)	NEG	NEG	Diploid
28007	F	47	Normal	NEG	NEG	Diploid
28019	M	21	NE	BCR/ABL	NEG	Hyperd.
28021	F	54	6 Metaphases: 53-54xx, +11, +17, +19, + 5 mar, t(9;22)	BCR/ABL	NEG	Hyperd.
28023	M	26	Normal	NEG	NEG	Diploid
28024	F	19	15 Metaphases: 46xx	NEG	NEG	Hyperd.
			15 Metaphases: 45-51xx, +1mar, +2 mar			
28028	M	47	t(4;11)	ALL1/AF4	NEG	Diploid
28031	M	18	Normal	p15/p16	NEG	Diploid
28032	F	52	t(4;11)	ALL1/AF4	NEG	Diploid
28035	M	27	Gain 10,21*	NEG	POS	Hyperd.
28036	M	52	t(9;22)	BCR/ABL	NEG	Diploid
28037	M	18	Normal	NEG	POS	Diploid
28042	M	18	Loss 5q23*	NEG	NEG	Diploid
28043	M	23	Normal	NEG	NEG	Diploid
28044	M	16	5 Metaphases: 46xy, -21, +mar1	NEG	NEG	Diploid
			5 Metaphases: 46xy, -21, -22, +mar1, +mar2			
28047	M	19	12 Metaphases: 47xy, +13	NEG	NEG	Diploid
			5 Metaphases: 46xy			
30001	F	54	1 Metaphase: 46xx;	BCR/ABL	NEG	Hyperd.
			5 Metaphases: 58xx, +x, t(9;22), +3, +4, +5, +6, iso(7q), +14, +21, +22, +3			
31007	M	25	t(4;11)	ALL1/AF4	NEG	Diploid
31011	M	31	t(9;22)	BCR/ABL	POS	Diploid
33005	F	19	12 Metaphases: 46xx / 61xx	NEG	NEG	Diploid
36001	F	24	Normal	E2A/PBX1+(p15/p16)	NEG	Diploid
36002	M	23	Normal	NEG	NEG	Hyperd.
37013	M	nk	NE	BCR/ABL+(p15/16)	NEG	Diploid
43001	M	41	t(9;22)	BCR/ABL	POS	Diploid
43004	F	37	Normal	NEG	NEG	Diploid
43007	M	54	Normal	NEG	NEG	Hyperd.
43012	M	18	Normal	NEG	NEG	Diploid
48001	M	19	7 Metaphases: 54-55xy, + 8-9 mar	NEG	NEG	Hyperd.
			4 Metaphases: 46xy			
49006	F	43	NE	BCR/ABL	NEG	Diploid
57001	F	53	Gain 1q*	NEG	NEG	Hyperd.
62001	F	50	t(9;22)	BCR/ABL	NEG	Hyperd.
62002	M	54	5 Metaphases: 46xy;	BCR/ABL	NEG	Hyperd.
			6 Metaphases: 46xy, t(9;22)(q34;q11);			
			7 Metaphases: 47xy, t(9;22)(q34;q11), +17			
62003	M	53	16 Metaphases: 44-47xy, t(9;22)(q34;q11), der(22), t(9;22)(q34;q11)	BCR/ABL	NEG	Hyperd.
63001	M	49	NE	ALL1/AF4	NEG	Diploid
64001	M	20	13 Metaphases: 46xy, t(1;8)(q12;p22-23)	NEG	NEG	Diploid
64002	F	26	Gain 1q23*	NEG	NEG	Hyperd.
65005	M	22	t(9;22)	BCR/ABL+(p15/16)	NEG	Diploid
68001	M	36	Normal	NEG	NEG	Diploid
68003	F	27	17 Metaphases: 46xx;	BCR/ABL	NEG	NE
			7 Metaphases: 46xx, t(9;22)(q34;q11);			
			1 Metaphase: 43xx, der(9)t(9;22)(q34;q11), -20,-20,-22,-22,+mar			
84004	M	50	NE	BCR/ABL	NEG	Diploid
LAL 5	M	45	UK	E2A/PBX1	POS	Diploid

‡: Patients codes as reported in the cell.files from Affymetrix; UK: Unknown; NE: Not evaluable; \*: Evaluated by CGH;  
 □: Down syndrome.

**Table 2:** 167 genes selected by ANOVA for differential expression between E2A/PBX1, ALL1/AF4, BCR/ABL and NEG.

<i>Gene symbol</i>	<i>Locuslink ID</i>	<i>Probe set ID</i>	<i>Adjusted p-value</i>	<i>Average expression in ALL1/AF4</i>	<i>Average expression in BCR/ABL</i>	<i>Average expression in E2A/PBX1</i>	<i>Average expression in NEG</i>
<b>High in ALL1/AF4</b>							
HOXA9	3205	37809_at	<e-13	957	59	54	66
HOXA10	3206	41448_at	<e-13	234	41	55	41
VLDLR	7436	36873_at	<e-13	318	40	43	59
MEIS1	4211	40763_at	<e-13	112	5	9	4
DPYSL3	1809	36149_at	<e-13	163	53	52	53
PALLADIN	23022	41191_at	1e-13	224	63	47	55
KIAA1157	57460	33358_at	1.5e-12	374	113	111	149
PROM1	8842	41470_at	2.4e-12	1554	151	57	115
CCNA1	8900	1914_at	1.3e-11	431	56	54	125
LGALS1	3956	33412_at	2.3e-10	1666	313	167	201
PRSS12	8492	34247_at	3.2e-10	115	43	49	43
NPTX2	4885	35663_at	4.4e-10	253	33	32	30
FUT4	2526	39210_at	1e-9	192	124	124	115
TBC1D8	11138	38223_at	4.8e-9	296	95	59	74
DIAPH2	1730	34262_at	8e-9	166	98	103	89
DAD1	1603	38413_at	1.2e-7	870	218	167	255
HOXA5	3202	873_at	1.5e-7	226	46	40	58
RHOBTB3	22836	32215_i_at	3.7e-7	108	26	24	25
KIAA0125	9834	33528_at	4.3e-7	265	66	90	63
TRIM9	114088	36903_at	9.2-07	110	58	65	56
CSRP2	1466	41401_at	1.5e-6	428	165	99	142
PIK3C3	5289	35665_at	1.5e-6	307	111	88	109
SPINK2	6691	41071_at	1.6e-6	522	100	98	194
D12S2489E	22914	36777_at	1.8e-6	327	147	139	182
SPN	6693	36798_g_at	2.1e-6	1490	791	688	682
ADCY9	115	33800_at	2.1e-6	382	209	207	211
QPR1	23475	37978_at	2.2e-6	473	320	382	310
CD72	971	37479_at	2.4e-6	321	171	268	210
WT1	7490	1500_at	7.6e-6	208	82	80	92
ITGAE	3682	1140_at	8.5e-6	505	181	199	275
EBI2	1880	931_at	1e-5	285	60	42	77
PPP2R5	5527	40785_g_at	1e-5	510	230	295	256
GPM6B	2824	37251_s_at	1.3e-5	357	81	111	116
DSTN	11034	38385_at	1.8e-5	545	147	320	212
NA	NA	41478_at	2.1e-5	212	109	111	145
BID	637	32725_at	1.8e-5	281	207	260	198
MAP3K5	4217	1327_s_at	2.1e-5	180	75	45	50
IMP-3	10643	37558_at	2.1e-5	541	116	46	153
CTGF	1490	36628_at	2.1e-5	2648	1307	256	706
RNASE3	6037	33979_at	2.3e-5	200	77	64	68
DKFZP434H132	56905	32915_at	2.7e-5	409	289	264	285
GNA12	2768	919_at	3.8e-5	371	208	251	235
RUNX1	861	2026_at	4.8e-5	230	129	103	117
TPD52L2	7165	40076_at	5.4e-5	607	285	380	466
PKIG	11142	34376_at	5.9e-5	364	173	356	250
CD44	960	40493_at	6.1e-5	2289	874	961	843
KIAA1025	23389	34785_at	6.5e-5	499	241	103	205
IGFBP7	3490	2062_at	7.1e-5	1463	617	706	397
SLC1A4	6509	41126_at	7.5e-5	312	194	207	187
FLT3	2322	34583_at	7.7e-5	2083	765	328	1125
PPP2R5C	5527	40784_at	1.e-4	317	147	202	166
<b>High in E2A/PBX1</b>							
PBX1	5087	32063_at	<e-13	225	213	815	240
FAT	2195	40454_at	<e-13	192	205	874	204
KANK	23189	37225_at	2.5e-12	454	125	1422	112
FGF9	2254	1616_at	1.7e-11	70	34	227	45
CRYM	1428	38285_at	2.2e-11	103	105	382	112
NID2	22795	753_at	2.3e-11	26	53	538	48
KIAA0802	23255	39614_at	8.7e-11	63	97	837	108

FGF9	2254	35081_at	2.3e-10	73	36	164	44
LAMA5	3911	41610_at	1.8e-9	51	58	282	68
AOX1	316	37599_at	1.9e-9	89	78	233	81
SLAM	6504	33513_at	3.1e-9	184	50	288	67
PRKCZ	5590	362_at	5.8e-8	44	46	222	51
MERTK	10461	40648_at	1.3e-7	75	99	271	82
ALDH1A1	216	37015_at	1.5e-7	134	210	419	148
MERTK	10461	1786_at	4.1e-7	107	128	314	114
PKM2	5315	32378_at	4.3e-7	541	1127	1423	1119
NA	NA	32872_at	1.4e-6	84	218	462	211
ACK1	10188	1134_at	1.4e-6	298	433	523	366
NCBP2	22916	32790_at	1.6e-6	147	109	197	113
BLK	640	854_at	2.1e-6	673	365	1065	456
TMSNB	11013	36491_at	2.4e-6	90	52	215	63
TRIB2	28951	40113_at	1.5e-5	228	341	937	337
CGI-49	51097	34863_s_at	1.6e-5	202	120	328	143
LRMP	4033	35974_at	1.7e-5	1405	745	3060	686
TRB2	28951	717_at	1.8e-5	194	169	619	169
KIAA0889	25781	32406_at	2.1e-5	57	56	111	62
E2F5	1875	41275_at	2.1e-5	108	147	474	189
CSF2RB	1439	37493_at	2.2e-5	100	129	599	136
E2F5	1875	1044_s_at	2.8e-5	98	130	444	175
CYFIP1	23191	37306_at	3.5e-5	146	222	477	166
DBN1	1627	37981_at	3.5e-5	354	476	683	554
ARL7	10123	39829_at	5.6e-5	79	120	571	130
GP5	2814	34632_r_at	7.2e-5	63	52	160	50

**High in  
BCR/ABL**

CDW52	1043	34210_at	9.4e-13	144	1380	528	1050
ABL1	25	39730_at	1.3e-11	689	1199	603	621
ABL1	25	1636_g_at	2.2e-11	721	1260	687	684
YES1	7525	1674_at	6.1e-10	41	280	42	83
SOCS2	8835	38994_at	5.7e-10	566	567	33	358
CCND2	894	36650_at	3e-9	115	759	59	556
HLA-DPA1	3113	38833_at	4.8e-9	1512	3954	1575	3319
ABL1	25	1635_at	9.8e-9	199	496	210	215
HLA-DOA	3111	31728_at	3.6e-8	195	546	224	482
CD2AP	23607	34699_at	4e-8	64	251	233	231
TCF8	6935	33440_at	5e-8	35	278	110	117
HLA-C	3107	37383_f_at	5.9e-8	4638	7312	5167	6849
FYN	2534	40480_s_at	1e-7	231	626	279	389
HLA-DPB1	3115	38095_i_at	1.3e-7	1369	3967	1958	3430
GAB1	2549	32979_at	1.6e-7	65	184	52	100
FYN	2534	2039_s_at	2.1e-7	228	584	275	391
HLA-DPB1	3115	38096_f_at	2.2e-7	620	2079	1088	1950
GAB1	2549	1249_at	3e-7	59	203	53	102
IFITM1	8519	675_at	3.6e-7	364	2498	697	1702
OPTN	10133	41742_s_at	4.1e-7	85	231	102	172
ITGA6	3655	41266_at	5.9e-7	131	1471	183	1427
HLA-A	3105	41237_at	7.1e-7	2347	4764	3178	4181
PSAP	5660	36795_at	9.2e-7	958	2375	1325	1635
E2F2	1870	37043_at	1.1e-6	244	1904	926	1049
CD24	934	266_s_at	1.8e-6	182	1315	1212	1154
BTEB1	687	40202_at	1.8e-6	714	1579	314	669
SCHIP1	29970	36536_at	1.9e-6	89	529	69	297
WSB2	55884	40167_s_at	2e-6	138	282	205	186
CD74	972	35016_at	2.1e-6	2413	4488	3093	4367
NRIP1	8204	40088_at	2.3e-6	205	580	305	465
DUSP6	1848	41193_at	2.3e-6	152	766	301	505
MARCKS	4082	32434_at	2.4e-6	29	191	71	54
ITPR1	3708	32778_at	3.2e-6	69	180	29	134
HLA-DRA	3122	37039_at	3.9e-6	3950	6920	4272	6092
ITGA5	3678	39753_at	5.2e-6	313	531	354	400
FZD6	8323	34472_at	5.6e-6	88	246	83	12
SEMA6A	57556	36275_at	6.8e-6	97	449	98	218
TLE4	7091	40692_at	1e-5	137	275	194	219
CASP8	841	33774_at	1.1e-5	426	1246	607	652
RGL	23179	37539_at	1.3e-5	74	307	139	193
GNAI1	2770	33809_at	1.3e-5	60	199	134	165
UGCG	7357	40215_at	1.4e-5	147	531	234	415

ACVR2	92	35162_s_at	1.8e-5	50	114	50	61
OPTN	10133	41744_at	1.8e-5	91	173	92	140
CD99	4267	41138	1.8e-5	1704	3522	820	2288
HIF1A	3091	1039_s_at	2e-5	93	284	135	250
UBE2E3	10477	34850_at	2.1e-5	99	277	170	197
ENG	2022	32562_at	2.2e-5	263	539	258	361
IFITM3	10410	41475_at	2.2e-5	1377	3294	1297	2802
ACTN1	12087	39329_at	2.3e-5	313	782	164	418
MADH1	4086	1325_at	2.4e-5	32	442	139	438
AHNAK	195	37027_at	2.5e-5	1783	2014	627	956
MYO1B	4430	41439_at	2.8e-5	40	123	35	72
TM4SF2	7102	38408_at	2.8e-5	265	751	337	492
TUBA1	7277	36591_at	2.8e-5	865	1535	362	795
NT5E	4907	31886_at	3e-5	37	273	100	141
IFITM1	8519	676_g_at	3e-5	1633	4071	1676	3606
LSP1	4046	36493_at	3.1e-5	107	329	93	512
IGJ	3512	37006_at	3.1e-5	79	958	127	542
HLA-DRB1	3123	41723_s_at	3.1e-5	690	2131	921	1810
CDC42EP3	10602	33362_at	3.3e-5	126	242	56	130
HLA-DQB1	3119	36878_f_at	3.5e-5	716	1840	759	1452
PDE4B	5142	33705_at	4.4e-5	250	661	203	777
FHL1	2273	32542_at	4.6e-5	1047	1390	367	758
PRKCH	5583	1267_at	4.8e-5	133	242	185	208
DDR1	780	36643_at	4.8e-5	67	333	280	220
LCP2	3937	39319_at	5.2e-5	97	214	108	137
LST1	7940	37967_at	5.5e-5	894	1719	1007	1547
ANXA1	301	37403_at	5.6e-5	381	425	163	182
XPNPEP1	7511	35305_at	5.7e-5	551	847	377	598
GTAR	26057	39380_at	5.9e-5	297	629	322	570
ENPP2	5168	41123_s_at	5.9e-5	42	185	40	83
TNFAIP2	7127	38631_at	7.9e-5	136	312	181	209
SLC2A5	6518	34362_at	8.1e-5	160	711	116	538
MTSS1	9788	37363_at	9.0e-5	75	149	39	59
TXNIP	10628	31508_at	9.5e-5	1729	3709	1485	3025
MADH1	4086	37280_at	9.5e-5	54	512	179	509
MME	4311	1389_at	9.5e-5	326	2065	1542	1646
<b>High in NEG</b>							
DAPK1	1612	40049_at	4.5e-5	27	101	23	144
MX1	4599	37014_at	5.5e-5	201	265	215	851
APP	351	41136_s_at	2.30E-06	60	261	244	272
MADH2	4087	1928_s_at	5.3e-6	46	86	72	111