

Table 1. Genes differentially expressed between adult T-ALL overexpressing ABL1 and the remaining T-ALL cases. Genes are rank-ordered according to their p-value.

| Probeset ID | Gene symbol | p-value | FC | GenBank ID | Gene function | Chromosome location | Expression in “high” ABL1 cases |
|-------------|-------------|-------------------|------|--------------|---|---------------------|---------------------------------|
| 38847_at | MELK | <10 ⁻⁴ | 2.79 | NM_014791 | Protein amino acid phosphorylation | 9p13.2 | High |
| 37999_at | CPOX | <10 ⁻⁴ | 2.86 | NM_000097 | Heme biosynthesis | 3q12 | High |
| 38711_at | CLASP2 | <10 ⁻⁴ | 2.33 | NM_015097 | Cell division | 3p23 | High |
| 40822_at | NFATC3 | 0.00011 | 2.06 | NM_004555 | Regulation of transcription from RNA polymerase II promoter | 16q22.2 | High |
| 41638_at | PPWD1 | 0.00025 | 2.13 | NM_015342 | Protein folding | 5q12.3 | High |
| 41278_at | BAF53 | 0.00085 | 2.08 | NM_004301 | Regulation of transcription, DNA-dependent | 3q26.33 | High |
| 39388_at | CAMK2G | 0.00088 | 2.32 | NM_001222 | Protein amino acid phosphorylation | 10q22 | High |
| 32916_at | PTPRE | 0.0011 | 2.13 | NM_006504 | Protein amino acid dephosphorylation | 10q26 | High |
| 36511_at | SACM1L | 0.0014 | 2.16 | NM_014016 | Unknown | 3p21.3 | High |
| 38834_at | TOPBP1 | 0.0015 | 2.55 | NM_007027 | DNA replication and chromosome cycle | 3q22.1 | High |
| 33301_g_at | CDC2L1 | 0.0017 | 2.16 | NM_001787 | Regulation of transcription, DNA-dependent | 1p36 | High |
| 32767_at | SIL | 0.0025 | 2.23 | NM_003035 | Cell proliferation | 1p32 | High |
| 40828_at | ARHGEF7 | 0.0025 | 2.08 | NM_003899 | Signal transduction | 13q34 | High |
| 38431_at | MAPK9 | 0.0026 | 2.24 | NM_002752 | Protein amino acid phosphorylation | 5q35 | High |
| 35663_at | NPTX2 | 0.0028 | 3.68 | NM_002523 | Synaptic transmission | 7q21.3-q22.1 | High |
| 38325_at | MINPP1 | 0.003 | 2.58 | NM_004897 | Multiple inositol-polyphosphate phosphatase activity | 10q23 | High |
| 35747_at | SDFR1 | 0.0035 | 2.28 | NM_012428 | Receptor | 15q22 | High |
| 32954_at | RIF1 | 0.0038 | 2.54 | NM_018151 | Response to DNA damage stimulus | 2q23.3 | High |
| 34893_at | NDUFV2 | 0.0043 | 2.02 | NM_021074 | Mitochondrial electron transport | 18p11.31-p11.2 | High |
| 35364_at | APPBP1 | 0.0044 | 2.02 | NM_001018159 | Ubiquitin cycle | 16q22 | High |
| 40334_at | CSTF2 | 0.0072 | 2.34 | NM_001325 | mRNA processing | Xq22.1 | High |
| 40082_at | ACSL1 | 0.0081 | 3.04 | NM_001995 | Lipid metabolism | 4q34-q35 | High |
| 38353_at | TUBGCP3 | 0.0085 | 2.2 | NM_006322 | Microtubule cytoskeleton organization | 13q34 | High |
| 39379_at | C1orf121 | 0.0094 | 2.06 | NM_016076 | Unknwon | 1q44 | High |
| 37305_at | EZH2 | 0.011 | 2.16 | NM_004456 | Regulation of transcription, DNA-dependent | 7q35-q36 | High |
| 39677_at | PSF1 | 0.011 | 2.58 | NM_021067 | DNA replication | 20p11.21 | High |
| 33772_at | PTGER4 | 0.013 | 3.09 | NM_000958 | Immune response | 5p13.1 | High |
| 818_s_at | ATRX | 0.013 | 2.12 | NM_000489 | Regulation of transcription, DNA-dependent | Xq13.1-q21.1 | High |
| 582_g_at | NR2C1 | 0.014 | 2.63 | NM_001032287 | Regulation of transcription, DNA-dependent | 12q22 | High |
| 40018_at | NUPL1 | 0.014 | 2.58 | NM_001008564 | Transport | 13q12.13 | High |
| 33219_at | USP33 | 0.018 | 2.03 | NM_015017 | Protein deubiquitination | 1p31.1 | High |
| 41129_at | TMEM41B | 0.02 | 2.45 | NM_015012 | Integral to membrane | 11p15.4 | High |
| 38992_at | DEK | 0.021 | 2.17 | NM_003472 | Regulation of transcription from RNA polymerase II promoter | 6p23 | High |
| 32223_at | SFRS14 | 0.021 | 2.04 | NM_001017392 | Nuclear mRNA splicing | 19p12 | High |
| 41716_at | DMXL2 | 0.021 | 2.42 | NM_015263 | Translational initiation | 15q21.2 | High |

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| 39147_g_at | ATRX | 0.021 | 2.28 | NM_000489 | Regulation of transcription, DNA-dependent | Xq13.1-q21.1 | High |
| 40818_at | RBPSUH | 0.022 | 2.13 | NM_005349 | Regulation of transcription, DNA-dependent | 4p15.2 | High |
| 40801_at | GAPVD1 | 0.023 | 2.26 | NM_015635 | Unknown | 9q33.3 | High |
| 603_at | NR2C1 | 0.024 | 2.29 | NM001032287 | Regulation of transcription, DNA-dependent | 12q22 | High |
| 36787_at | GATA1 | 0.025 | 2.18 | NM002049 | Regulation of transcription from RNA polymerase II promoter | Xp11.23 | High |
| 35802_at | FNBP4 | 0.026 | 2.2 | NM015308 | Cell adhesion | 11p11.2 | High |
| 32635_at | TRIM33 | 0.028 | 2.58 | NM_015906 | Regulation of transcription, DNA-dependent | 1p13.1 | High |
| 36935_at | RASA1 | 0.03 | 2.03 | NM_002890 | Intracellular cascade signalling | 5q13.3 | High |
| 36998_s_at | ATXN2 | 0.03 | 2.08 | NM_002973 | Protein binding | 12q24.1 | High |
| 37333_at | DNMT1 | 0.03 | 2.42 | NM_001379 | DNA methylation | 19p13.2 | High |
| 38764_at | DICER1 | 0.03 | 2.23 | NM_030621 | RNA processing | 14q32.13 | High |
| 1675_at | RASA1 | 0.031 | 2.08 | NM_002890 | Intracellular cascade signalling | 5q13.3 | High |
| 32130_at | Unknown | 0.033 | 2.02 | NM_017432 | Unknown | unknown | High |
| 1055_g_at | RFC4 | 0.035 | 2.26 | NM_002916 | DNA replication | 3q27 | High |
| 36814_at | KIAA1109 | 0.038 | 2.19 | XM_371706 | Unknown | 4q27 | High |
| 1809_at | CDC7 | 0.04 | 3.59 | NM_003503 | DNA replication/initiation | 1p22 | High |
| 33291_at | RASGRP1 | 0.041 | 2.4 | NM_005739 | Intracellular signaling cascade | 15q15 | High |
| 37901_at | PIK3R4 | 0.041 | 2.35 | NM_014602 | Protein amino acid phosphorylation | 3q21.3 | High |
| 33810_at | TRRAP | 0.042 | 2.14 | NM_003496 | Regulation of transcription, DNA-dependent | 7q21.2-q22.1 | High |
| 35995_at | ZWINT | 0.043 | 2.33 | NM_001005413 | Spindle organization | 10q21-q22 | High |
| 41436_at | ZNF198 | 0.043 | 2.39 | NM_003453 | Regulation of transcription, DNA-dependent | 13q11-q12 | High |
| 31853_at | EED | 0.046 | 2.66 | NM_003797 | Negative regulation of transcription | 11q14.2-q22.3 | High |
| 38908_s_at | REV3L | 0.047 | 2.13 | NM_002912 | DNA replication | 6q21 | High |
| 35320_at | SLC11A2 | 0.049 | 2.58 | NM_000617 | Ttransport | 12q13 | High |
| 38854_at | CEP4 | 0.049 | 2.11 | NM_025009 | Unknown | 4q12 | High |
| 35810_at | ARPC3 | 0 | 2.18 | NM_005719 | Cell motility | 12q24.11 | Low |
| 35985_at | PALM2-AKAP2 | 0 | 2.92 | NM_001004065 | Regulation of cell shape | 9q31-q33 | Low |
| 36846_s_at | LSM7 | <10 ⁻⁴ | 2.62 | NM_016199 | mRNA processing | 19p13.3 | Low |
| 286_at | HIST2H2AA | <10 ⁻⁴ | 5.22 | NM_001040874 | Chromosome organization | 1q21.2 | Low |
| 39180_at | FUS | <10 ⁻⁴ | 2 | NM_001010850 | Immune repsonse | 16p11.2 | Low |
| 32583_at | JUN | <10 ⁻⁴ | 2.88 | NM_002228 | Regulation of transcription, DNA-dependent | 1p32-p31 | Low |
| 36629_at | TSC22D3 | <10 ⁻⁴ | 2.73 | NM_0001015881 | Regulation of transcription, DNA-dependent | Xq22.3 | Low |
| 38313_at | ABCA2 | <10 ⁻⁴ | 2.41 | NM_001606 | Lipid metabolism | 9q34 | Low |
| 32609_at | HIST2H2AA | <10 ⁻⁴ | 3.14 | NM_001040074 | Chromosome organization | 1q21.2 | Low |
| 32749_s_at | FLNA | 0.00011 | 2.46 | NM_001456 | Cell motility | Xq28 | Low |
| 32134_at | TES | 0.00014 | 2.64 | NM_015641 | Zinc ion binding | 7q31.2 | Low |
| 1984_s_at | ARHGDI | 0.00016 | 2.28 | NM_001175 | Actin cytoskeleton organization and biogenesis | 12p12.3 | Low |
| 41399_at | PHF8 | 0.00028 | 2.21 | NM_015107 | Regulation of transcription, DNA-dependent | Xp11.22 | Low |
| 39081_at | MT2A | 0.00030 | 2.29 | NM_005953 | Copper ion homeostasis | 16q13 | Low |
| 38555_at | DUSP10 | 0.00033 | 2.47 | NM_007207 | Protein amino acid dephosphorylation | 1q41 | Low |

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| 33146_at | MCL1 | 0.00033 | 2.07 | NM_021960 | Regulation of apoptosis | 1q21 | Low |
| 38994_at | SOCS2 | 0.00037 | 3.61 | NM_003877 | Regulation of cell growth | 12q | Low |
| 36234_at | EIF4A1 | 0.00042 | 2.01 | NM_001416 | Protein biosynthesis | 17p13 | Low |
| 32855_at | LDLR | 0.00045 | 2.2 | NM_000527 | Lipid metabolism | 19p13.3 | Low |
| 32542_at | FHL1 | 0.00046 | 2.2 | NM_001449 | Cell differentiation | Xq26 | Low |
| 32793_at | TRBC1 | 0.00047 | 5.19 | | Immune response | 7q34 | Low |
| 33386_at | H1F0 | 0.00054 | 3.7 | NM_005318 | Chromosome organization | 22q13.1 | Low |
| 33412_at | LGALS1 | 0.00054 | 3.15 | NM_002305 | Apoptosis | 22q13.1 | Low |
| 33700_at | SPRY2 | 0.00057 | 2.99 | NM_005842 | Cell-cell signalling | 13q31.1 | Low |
| 37026_at | KLF6 | 0.00059 | 2.89 | NM_001008490 | Regulation of transcription, DNA-dependent | 10p15 | Low |
| 39411_at | TIPARP | 0.00063 | 2.08 | NM_015508 | Protein amino acid phosphorylation | 3q25.31 | Low |
| 34308_at | HIST1H2AC | 0.00067 | 2.96 | NM_003512 | Chromosome organization | 6p21.3 | Low |
| 31481_s_at | TMSB10 | 0.00074 | 2.4 | NM_021103 | Cytoskeleton organization and biogenesis | 2p11.2 | Low |
| 41504_s_at | MAF | 0.00085 | 7.4 | NM_001031804 | Regulation of transcription, DNA-dependent | 16q22-q23 | Low |
| 676_g_at | IFITM1 | 0.0010 | 2.78 | NM_003641 | Immune response | 11p15.15 | Low |
| 38750_at | NOTCH3 | 0.0010 | 2.93 | NM_000435 | Regulation of transcription, DNA-dependent | 19p13.2-p13.1 | Low |
| 34168_at | DNNT | 0.0013 | 3.81 | NM_001017520 | DNA replication | 10q23-q24 | Low |
| 40698_at | CLEC2B | 0.0016 | 3.26 | NM_005127 | Sugar binding | 12p13.12 | Low |
| 37027_at | AHNAK | 0.0020 | 2.4 | NM_001620 | Signal transduction | 11q12.2 | Low |
| 38968_at | SH3BP5 | 0.0022 | 2.21 | NM_001018009 | Signal transduction | 3p24.3 | Low |
| 2049_s_at | JUNB | 0.0026 | 2.41 | NM_002229 | Regulation of transcription, DNA-dependent | 19p13.2 | Low |
| 37403_at | ANXA1 | 0.003 | 2.33 | NM_000700 | Cell motility | 9q12-q21 | Low |
| 41356_at | BCL11A | 0.004 | 3.1 | NM_018014 | Regulation of transcription, DNA-dependent | 2p16.1 | Low |
| 37524_at | STK17B | 0.0053 | 2.61 | NM_004226 | Protein amino acid phosphorylation | 2q32.3 | Low |
| 35277_at | SPON1 | 0.01 | 2.9 | NM_006108 | Cell adhesion | 11p15.2 | Low |
| 742_at | HABP2 | 0.012 | 2.22 | NM_004132 | Cell adhesion | 10q25.3 | Low |
| 38894_g_at | NCF4 | 0.013 | 2.07 | NM_000631 | Intracellular signalling cascade | 22q13.1 | Low |
| 36618_g_at | ID1 | 0.013 | 2.31 | NM_002165 | Regulation of transcription from RNA polymerase II promoter | 20q11 | Low |
| 37018_at | HIST1H1C | 0.016 | 2.24 | NM_005319 | Chromosome organization | 6p21.3 | Low |
| 37544_at | NFIL3 | 0.02 | 2.01 | NM_005384 | Regulation of transcription, DNA-dependent | 9q22 | Low |
| 40951_at | LOC348162 | 0.025 | 2.11 | XM_496125 | Kinase activity | 16p11.2 | Low |
| 36617_at | ID1 | 0.028 | 3.87 | NM_002165 | Regulation of transcription from RNA polymerase II promoter | 20q11 | Low |
| 182_at | ITPR3 | 0.04 | 3.55 | NM_002224 | Calcium ion transport | 6p21 | Low |