

Supplement C to Oron et al.:
List of Chromosomal Loci Flagged for a Significant Phenotype
Effect at the 0.1 FDR Level

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Table C-1: List of lowest-level chromosomal loci from the ALL dataset which are flagged as over-expressed by the BCR/ABL phenotype group, at the two-tailed 0.1 FDR level using the 3-covariate model (phenotype, sex, hyperdiploidy). Relative ranks and p-values under the 3-covariate and phenotype-only models are shown for each band. P-values were calculated by phenotype-label permutations, using 5000 permutations. a p-value of 0 means that the observed GS statistic was larger than any of the permutation-generated statistics.

Locus	Number of Genes	Mean Fold-Change	3-Covariate p-value	Phenotype-Only p-value
7q31	9	+21.1%	0.0000	0.0002
14q22.2	5	+29.6%	0.0000	0.0000
8p22	7	+19.8%	0.0002	0.0000
3q28	8	+12.5%	0.0004	0.0000
17q23	10	+14.8%	0.0010	0.0010
5q23	8	+22.8%	0.0010	0.0006
4p14	5	+18.6%	0.0010	0.0010
5q31.1	13	+9.6%	0.0010	0.0006
3p24.3	5	+24.1%	0.0024	0.0008

Table C-2: List of lowest-level chromosomal loci from the ALL dataset which are flagged as under-expressed by the BCR/ABL phenotype group, at the two-tailed 0.1 FDR level using the 3-covariate model. Details are as in Table 1.

Locus	Number of Genes	Mean Fold-Change	3-Covariate p-value	Phenotype-Only p-value
11q13.3	6	-14.1%	0.0002	0.0004
20q13.33	6	-10.8%	0.0004	0.0086
11p15.1	5	-14.8%	0.0006	0.0102
18q21.1	8	-9.3%	0.0012	0.0070
8p11.2	8	-6.8%	0.0020	0.0562