

Supp. Table 2. Genome-wide significance thresholds calculated by permutation.

	20 kb	100 kb
GWIS	2E-6	5E-6
minSNP	7.4E-8	4.7E-8
minSNP-P	3E-6	5E-6
BIMBAM*	3E-6	-
VEGAS**	1E-6	-
LASSO	2.1E-11	4.8E-12

Results are reported for 20 kb and 100 kb flanking transcription boundaries. Thresholds for GWIS, minSNP, minSNP-P and VEGAS are for p-values. Threshold for LASSO are for the selection index. The thresholds for minSNP and LASSO decrease because the larger threshold implies more tests. GWIS and minSNP-P already include a correction for the number of tests within a gene, and thresholds are somewhat less stringent for longer gene boundaries. *BIMBAM uses the threshold from minSNP-P because both tests provide gene-based p-values with identical uniform distributions under the null. **VEGAS is hard-coded to use ± 50 kb.