Enrichment and null distribution computation:

Enrichment was calculated as the ratio between the proportion of SNPs close to candidate genes and/or overlapped by at least 1 QTL among SNPs above a defined threshold (i.e. number of top SNPs chosen) and the proportion of SNPs of the same category over the whole genome.

To test the significance of enrichment, we generated a null distribution using permutations. The algorithm used is detailed below:

- Lists of SNP positions and associated p-values for each chromosome were reordered, pasting the chromosomes in a random orientation.

- The same procedure was applied to the annotations (*i.e.* whether the SNP is close to a candidate gene and/or overlapped by at least 1 QTL).

- These 2 newly formed lists were rotated randomly with respect to one another.

- Enrichment in SNPs close to candidate genes and/or overlapped by QTLs was calculated for the defined number of top SNPs.

These 4 steps were repeated 500 times in order to produce the null distribution for each number of top SNPs to be tested. A 5% confidence threshold was then assessed from the null distribution.