



Additional File 15: Distribution of the number of variants predicted to have functional consequences in QTL intervals (indicated by the red bar) and in 1000 sets of randomly selected non-QTL regions of similar size. **A.** The distribution of amino-acid changing mutations predicted to be damaging by at least one algorithm (LRT, PolyPhen, SIFT); $p < 2.2e^{-16}$. **B.** The distributions of variants falling in transcription factor binding site motifs that are predicted to have a high impact (predictions generated by MOODS software); $p < 2.2e^{-16}$.