



**S1 Fig. Linkage disequilibrium matrix.** Linkage disequilibrium was assed from a genomic region of 100 kb with *MtnA* at the center. The upper and right axes show the SNPs found in the 100 kb fragment not taking into account singletons and each bin represent  $r^2$  values. The left and bottom part of the matrix show the Fisher exact test for each of the  $r^2$  values. Red boxes indicate significant p-values.