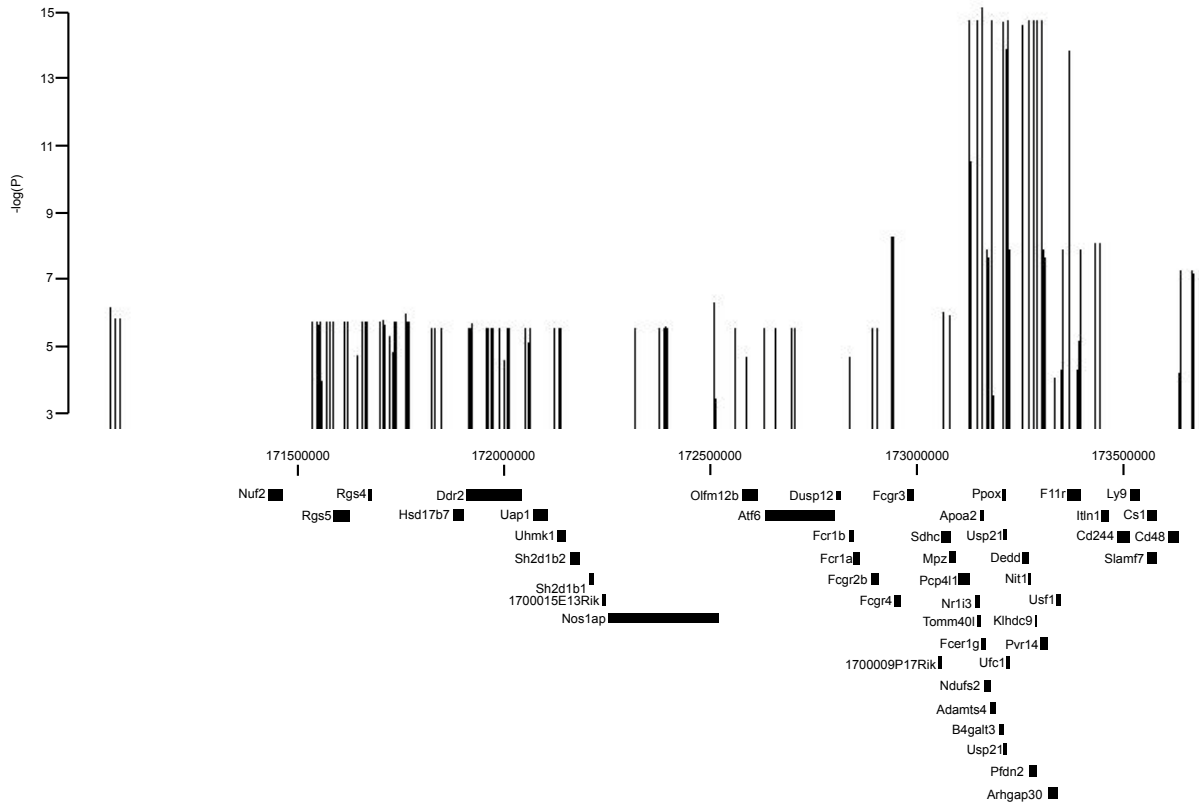
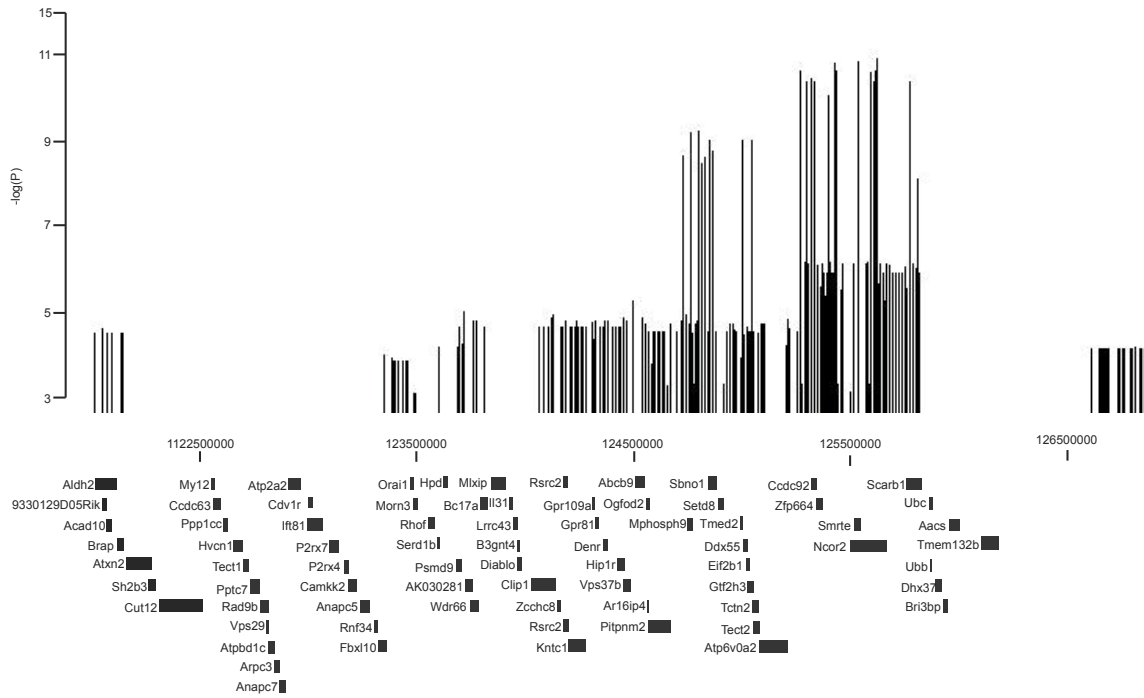


A



B



**Figure S6** (A) Detail of the genome-wide association scan for HDL spanning significant ( $P < 10^{-3}$ ) SNPs in the region around 173 Mb on Chromosome 1. The  $-\log(P)$  statistics are taken from the mixed model (EMMA). Annotated protein coding gene from UCSC are shown below for reference. (B) Detail of the genome-wide association scan for HDL spanning significant ( $P < 10^{-3}$ ) SNPs in the region around 125 Mb on Chromosome 5. The  $-\log(P)$  statistics are taken from the mixed model (EMMA). Annotated protein coding gene from UCSC are shown below for reference.