Supplementary information, Figure S1

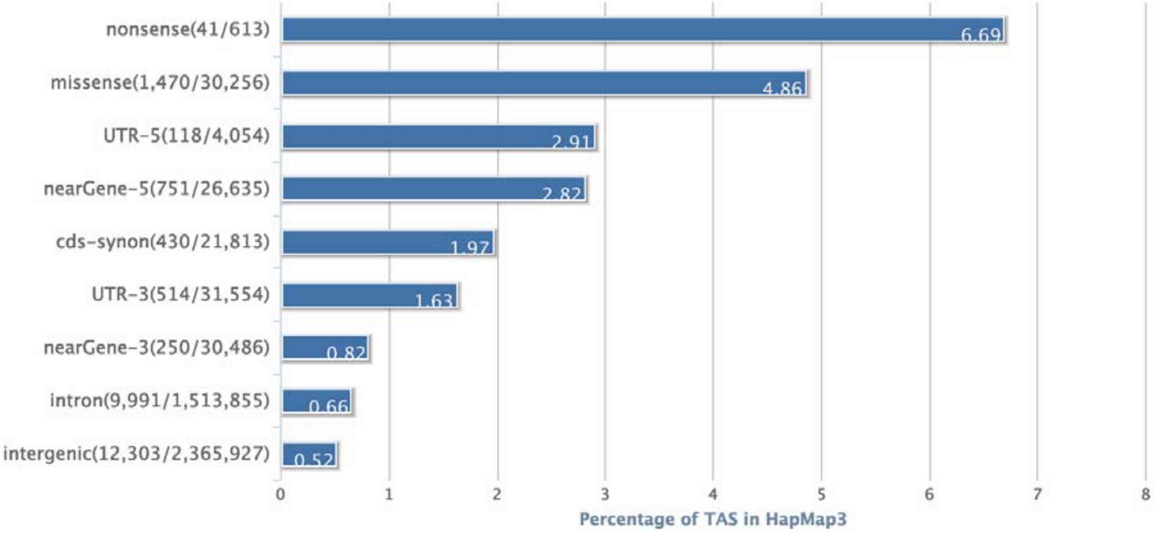

Figure S1. The percentage of TASs in GWASdb and in HapMap3 for different types of genetic variants. A total of 25872 TASs collected from GWASdb with P-value $< 1.0 \times 10^{-5}$ were mapped into reference genome (hg19) and were compared with the HapMap3 dataset. The likelihood of disease associations for each type of genetic variants (such as nonsense and missense) was estimated.