S5 Fig. A. Enrichment of DNase hypersensitive (DHS) sites in 34 tissue categories for variants in $r^2 > 0.1$ with 11 replicated SNPs reaching genome-wide significance using FGWAS **B**. Causal probabilities of variants at the *LLPH/TMBIM4* locus. The most probably causal variant rs12426813 overlaps a DHS site active in blood and cardiovascular cells