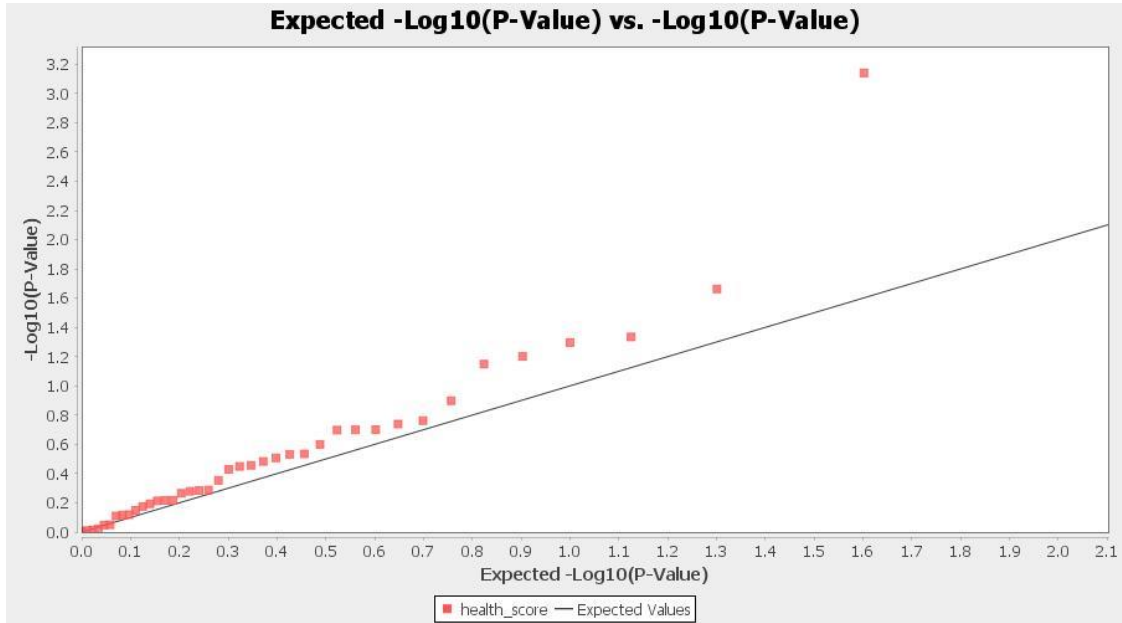


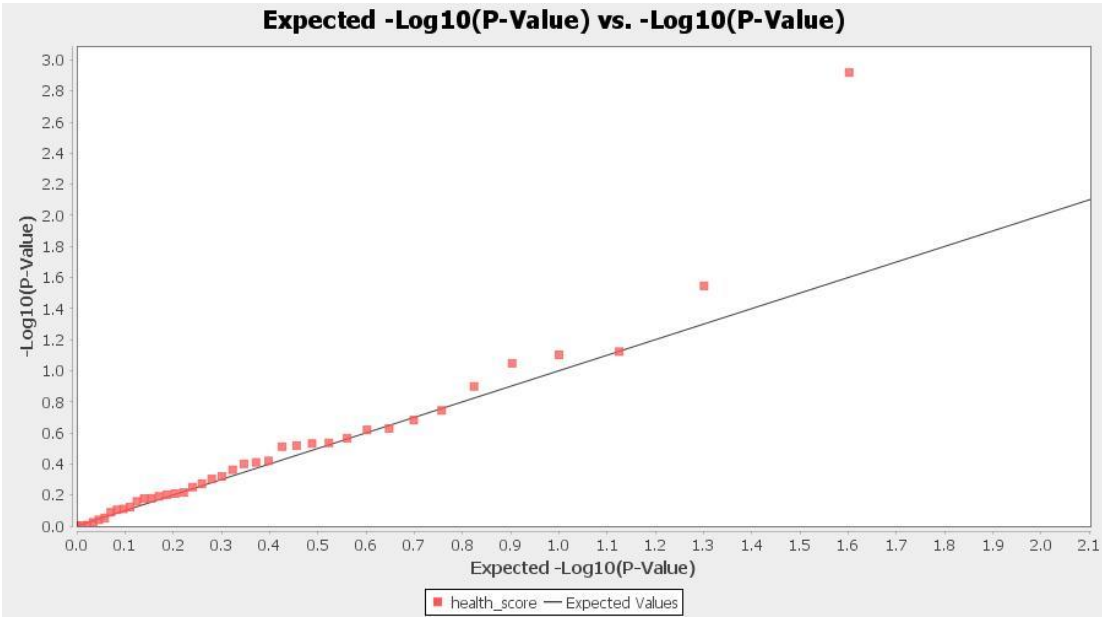
Supplementary Table 5a. Significantly associated SNP markers ( $P < 0.05$ ) and P-value adjusted after 10,000 permutations using GLM

Marker	Chr	Pos	p	padj_10000	PVE%	Annotation
SCONTIG5992_29927	Scaffold5992	29927	0.0007	0.0199	5.8	Peptidase S8, subtilisin-related Peptidase S8/S53 domain
SCONTIG6368_39377	Scaffold6368	39377	0.0220	0.5154	3.2	Leucine-rich repeat Leucine-rich repeat-containing N-terminal
SCONTIG8553_81512	Scaffold8553	81512	0.0460	0.8033	2.5	unknown
SCONTIG874_32729	Scaffold874	32729	0.0500	0.8297	2.7	cytochrome p450 94a1-like

Supplementary fig 5b: Comparison of qqplot in GLM and MLM



GLM



MLM