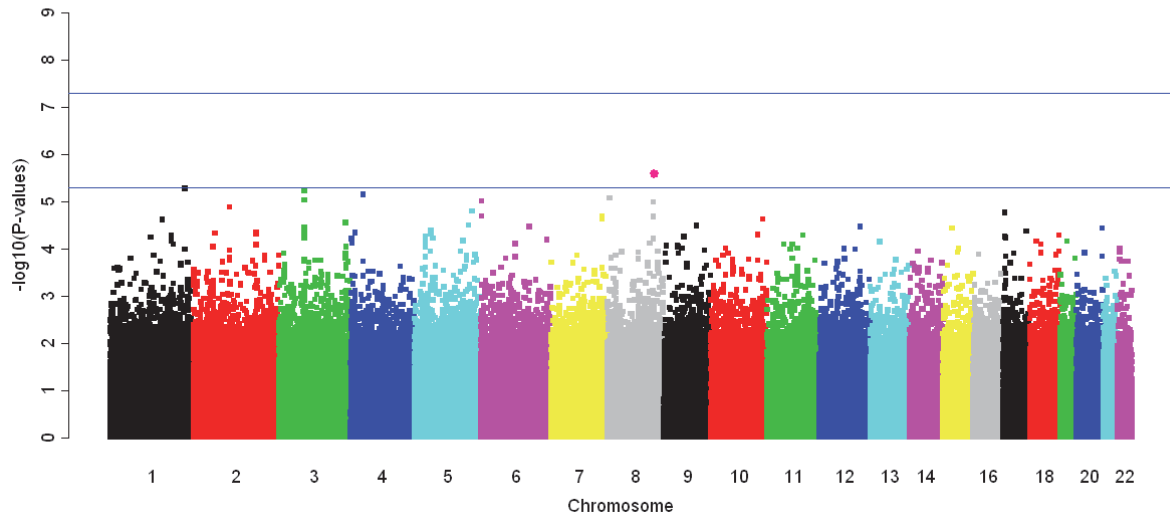
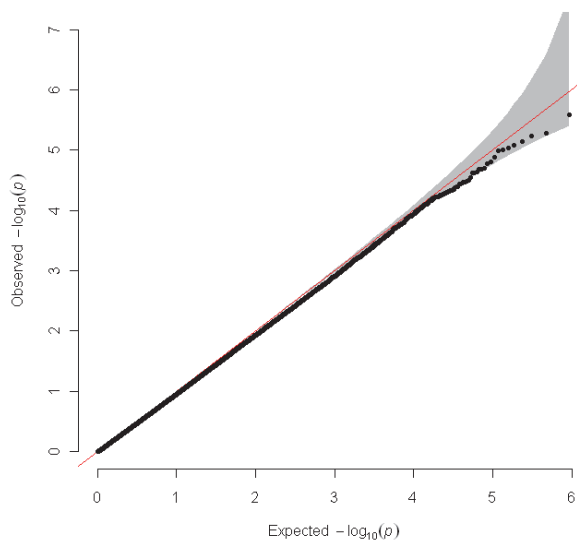


Supplementary Figure 1: Manhattan plot from p-values of genome-wide association analysis of major depression under a recessive model.



Supplementary Figure 2: QQ plot of p-values from genome-wide association analysis of major depression under a recessive model.



Supplementary Table 1:

Predictor	R ²	F _{ROH} increased in:	p-value
Percentage of recurrent cases	0.01	Controls	0.84
German study binary variable	0.58	Cases	0.02
US study binary variable	0.41	Controls	0.06
Australian study binary variable	0.04	Controls	0.59
Binary variable for if study was genotyped on Illumina	0.45	Cases	0.05
Binary variable for if copy number variant probes were available on the genotyping platform	0.01	Controls	0.79
Mean F _{ROH}	0.18	Cases	0.25
Mean genome-wide homozygosity	0.01	Controls	0.77