Supplementary Figure 4
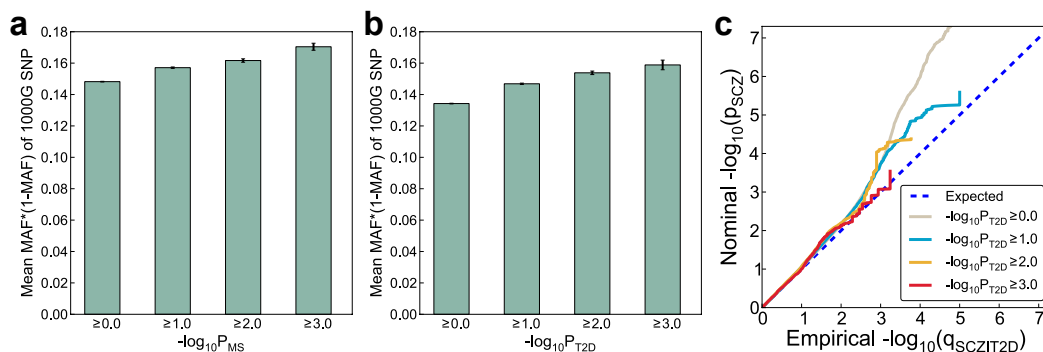

a.) The SNPs from 1000 Genome data which correspond to the common SNPs between SCZ and MS in the current study were extracted and stratified by the significant level of MS (x axis). SNPs in each stratum were prune at LD-r^2 > 0.2 with the most significant SNPs remained. The average genetic variance tagged by the remaining SNPs (y axis, MAF*(1-MAF)) in each stratum were plotted as the height of each bar. **b.)** The 1000 Genome SNPs which corresponds to the common SNPs between SCZ and T2D were extracted and stratified by the significant level of T2D (x axis). SNPs in each stratum were prune at LD-r^2 > 0.2 with the most significant SNPs remained. The average genetic variance tagged by the remaining SNPs (y axis, MAF*(1-MAF)) in each stratum were plotted as the height of each bar. **c.)** The conditional Q-Q plots of SCZ conditioning on T2D. The standard errors were shown by small intervals on the top of each bar after adjusting by the number of remaining SNPs in each stratum.