

Scenario	SKAT	SKAT-O	Burden	SMT – BH	SMT – Bonferroni
1	0.118	0.111	0.012	0.156	0.153
2	0.007	0.008	0.002	0.005	0.004
3	0.001	0.001	<0.001	0.001	<0.001
4	0.223	0.215	0.024	0.263	0.259
5	0.021	0.021	0.004	0.014	0.011
6	0.004	0.004	<0.001	0.002	0.002
7	0.410	0.414	0.065	0.422	0.415
8	0.063	0.071	0.012	0.043	0.040
9	0.014	0.016	0.003	0.009	0.007
10	0.797	0.867	0.207	0.698	0.692
11	0.248	0.350	0.070	0.155	0.147
12	0.093	0.128	0.036	0.059	0.053

S8 Table. Power estimates of the SMT and MMTs under the nominal  $\alpha$  level of  $2.5 \cdot 10^{-6}$  to compare the BH and Bonferroni correction for SMTs.

Data was generated under the alternative-hypothesis model described in scenarios 1-12 in Table 1 with size  $n = 1,000$  for  $m = 10,000$  replicates. The nominal  $\alpha$  level was set to  $2.5 \cdot 10^{-6}$ . Adjustments for multiple testing of all SNVs in a gene with the SMT were done using the BH or the Bonferroni correction. Power results are provided for analyses using all rare and (non-causal) common SNVs in a gene.