Scenario	SKAT	SKAT-O	Burden	SMT
1	0.003	0.003	<0.001	0
4	0.009	0.009	0.001	0
7	0.029	0.032	0.005	<0.001
8	0.002	0.002	<0.001	0
12	0.003	0.005	<0.001	0

S10 Table. Power estimates of the SMT and MMTs for analyzing a binary trait under the nominal α level of $2.5 \cdot 10^{-6}$.

Case-control data was generated under the alternative-hypothesis model described in scenarios 1, 4, 7, 8, 12 in Table 1 with size $n = 1{,}000$ for $m = 10{,}000$ replicates for a binary trait. The nominal α 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 correction. All rare and (non-causal) common SNVs were incorporated in the analysis.