Scenario	SKAT	SKAT-O	Burden	SMT
1	0.363	0.350	0.002	0.515
4	0.565	0.554	0.006	0.715
7	0.860	0.864	0.041	0.928
8	0.388	0.406	0.002	0.190
12	0.531	0.733	0.002	0.231

S7 Table. Power estimates of the SMT and MMTs under the nominal α level of $2.5 \cdot 10^{-6}$, for a sample size of 2,000 and genes including 67 SNVs.

As genetic data, the available genotypes of the 67 SNVs of $n = 2{,}000$ individuals in the 'SKAT.example' data in the SKAT R package were used in each replicate. Data was generated under the alternative-hypothesis model described in scenarios 1, 4, 7, 8, 12 in Table 1 with size $n = 2{,}000$ for $m = 10{,}000$ replicates. 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. Power results are provided for analyses using all rare and (non-causal) common SNVs in a gene.