S1 TABLE: POWER AND TYPE I ERROR TABLES

Table A. Type I error results at nominal level α=5% based on 10,000 replicates.

	Type I error
CAST	0.0399
WSS	0.0472
VT	0.0455
aSum	0.0461
C-alpha	0.0412
SKAT	0.0398
SKAT-O	0.0428
KBAC	0.0467
ADA	0.0455
DBM	0.0436
CLUSTER	0.048
KERNEL	0.0433
PODKAT	0.0426
BOMP	0.0504
DoEstRare	0.0452

Table B. Power results for the scenario 1 at nominal level α=5% based on 1000 replicates.

	P5	P10	P15	P20
CAST	0.176	0.395	0.612	0.794
WSS	0.262	0.511	0.726	0.881
VT	0.245	0.462	0.642	0.802
aSum	0.258	0.524	0.699	0.835
C-alpha	0.36	0.636	0.791	0.888
SKAT	0.35	0.632	0.798	0.892
SKAT-O	0.328	0.625	0.793	0.895
KBAC	0.328	0.62	0.822	0.941
ADA	0.189	0.391	0.607	0.763
DBM	0.165	0.352	0.546	0.726
CLUSTER	0.177	0.363	0.583	0.728
KERNEL	0.286	0.526	0.682	0.761
PODKAT	0.25	0.508	0.663	0.8
BOMP	0.321	0.62	0.795	0.914
DoEstRare	0.369	0.657	0.828	0.92

P5, P10, P15 and P20 correspond to 5%, 10%, 15% and 20% of DRVs in the gene. DRVs: disease-risk variants.

Table C. Power results for the scenario 2 at nominal level α=5% based on 1000 replicates.

	P5	P10	P15	P20
CAST	0.166	0.408	0.638	0.796
WSS	0.259	0.537	0.748	0.868
VT	0.224	0.451	0.668	0.791
aSum	0.258	0.521	0.726	0.836
C-alpha	0.348	0.639	0.792	0.89
SKAT	0.335	0.633	0.797	0.887
SKAT-O	0.317	0.612	0.799	0.904
KBAC	0.33	0.64	0.83	0.927
ADA	0.167	0.375	0.592	0.739
DBM	0.155	0.353	0.57	0.715
CLUSTER	0.181	0.413	0.635	0.783
KERNEL	0.313	0.592	0.768	0.868
PODKAT	0.267	0.626	0.831	0.931
BOMP	0.333	0.619	0.798	0.912
DoEstRare	0.378	0.707	0.865	0.944

P5, P10, P15 and P20 correspond to 5%, 10%, 15% and 20% of DRVs in the gene. DRVs: disease-risk variants.

Table D. Power results for the scenario 3 at nominal level α=5% based on 1000 replicates.

	P5	P10	P15	P20
CAST	0.154	0.399	0.619	0.791
WSS	0.237	0.514	0.729	0.876
VT	0.207	0.466	0.655	0.814
aSum	0.26	0.509	0.709	0.835
C-alpha	0.361	0.623	0.78	0.876
SKAT	0.352	0.623	0.782	0.881
SKAT-O	0.339	0.601	0.775	0.89
KBAC	0.324	0.65	0.823	0.931
ADA	0.196	0.394	0.593	0.736
DBM	0.192	0.394	0.569	0.743
CLUSTER	0.195	0.393	0.606	0.782
KERNEL	0.317	0.566	0.714	0.83
PODKAT	0.28	0.591	0.787	0.909
BOMP	0.341	0.624	0.795	0.906
DoEstRare	0.387	0.689	0.841	0.933

P5, P10, P15 and P20 correspond to 5%, 10%, 15% and 20% of DRVs in the gene. DRVs: disease-risk variants.