S3 Power estimates when individual variants' PAR are sampled from an exponential distribution

				PAR=0.03			PAR=0.05		
Sim. Model	Sample Size	Disease Model	#DSVs	C	WS_t	R	C	WS_t	R
1	1000	Uneq PAR	10	0.240	0.295	0.381	0.511	0.686	0.724
			20	0.214	0.256	0.337	0.469	0.597	0.705
			30	0.172	0.211	0.287	0.440	0.504	0.647
2	1000	Uneq PAR	10	0.277	0.454	0.512	0.590	0.871	0.901
			20	0.242	0.360	0.483	0.562	0.776	0.871
			30	0.241	0.300	0.448	0.519	0.716	0.864

Table S-1: Power Estimates ($\alpha = 0.05$) for the three approaches: Collapsing (C) vs. Weighted-Sum (WS_t) vs. Replication-based (R) when individual PARs are sampled from an exponential distribution. Two genetic simulation models are assumed: neutral variants (1), and mildly deleterious variants (2). Varying number of DSVs are assumed. The sample size is the total number of individuals sequenced, with equal numbers of cases and controls. All tests are two-sided, i.e., testing for the presence of risk or protective variants in the region of interest.