

Corrigendum: Joint analysis is more efficient than replication-based analysis for two-stage genome-wide association studies

Andrew D Skol, Laura J Scott, Gonçalo R Abecasis & Michael Boehnke
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In Table 1 of the versions of this article initially published online and in print, the significance thresholds for C_2 were incorrect, and the significance thresholds for C_{joint} in the case of $\pi_{\text{samples}} = 0.20$ were incorrect. The error has been corrected in the HTML and PDF versions of the article. This correction has been appended to the PDF version.

Table 1 Significance thresholds and power of joint analysis for two-stage genome-wide association designs

π_{samples}	π_{markers}	Proportion of genotypes ^a	Significance threshold			Power					
			C_1	C_2	C_{joint}	GRR = 1.30		GRR = 1.35		GRR = 1.40	
						Joint	Rep	Joint	Rep	Joint	Rep
1.0	0	1.00	—	—	5.23	0.26	—	0.51	—	0.75	—
0.50	0.10	0.55	1.64	4.65	5.23	0.26	0.08	0.51	0.17	0.75	0.31
	0.05	0.53	1.96	4.50	5.23	0.26	0.09	0.51	0.21	0.75	0.36
	0.01	0.51	2.58	4.15	5.23	0.26	0.14	0.50	0.29	0.74	0.48
0.40	0.10	0.46	1.64	4.65	5.23	0.26	0.12	0.51	0.27	0.75	0.46
	0.05	0.43	1.96	4.50	5.23	0.26	0.14	0.50	0.30	0.74	0.51
	0.01	0.41	2.58	4.15	5.20	0.24	0.17	0.48	0.36	0.71	0.58
0.30	0.10	0.37	1.64	4.65	5.22	0.25	0.17	0.50	0.36	0.73	0.58
	0.05	0.34	1.96	4.50	5.21	0.24	0.18	0.48	0.37	0.72	0.60
	0.01	0.31	2.58	4.15	5.16	0.21	0.18	0.42	0.37	0.64	0.58
0.20	0.10	0.28	1.64	4.65	5.19	0.23	0.19	0.46	0.39	0.68	0.62
	0.05	0.24	1.96	4.50	5.16	0.21	0.18	0.42	0.38	0.63	0.59
	0.01	0.21	2.58	4.15	5.06	0.15	0.14	0.31	0.29	0.47	0.46

Shown is analysis of 1,000 cases and 1,000 controls, $M = 300,000$ markers, genome-wide significance level $\alpha_{\text{genome}} = 0.05$, multiplicative model, control risk allele frequency = 0.40 and prevalence = 0.10.

^a(Number of genotypes required for two-stage design) / (number of genotypes required when all markers are genotyped on all samples).