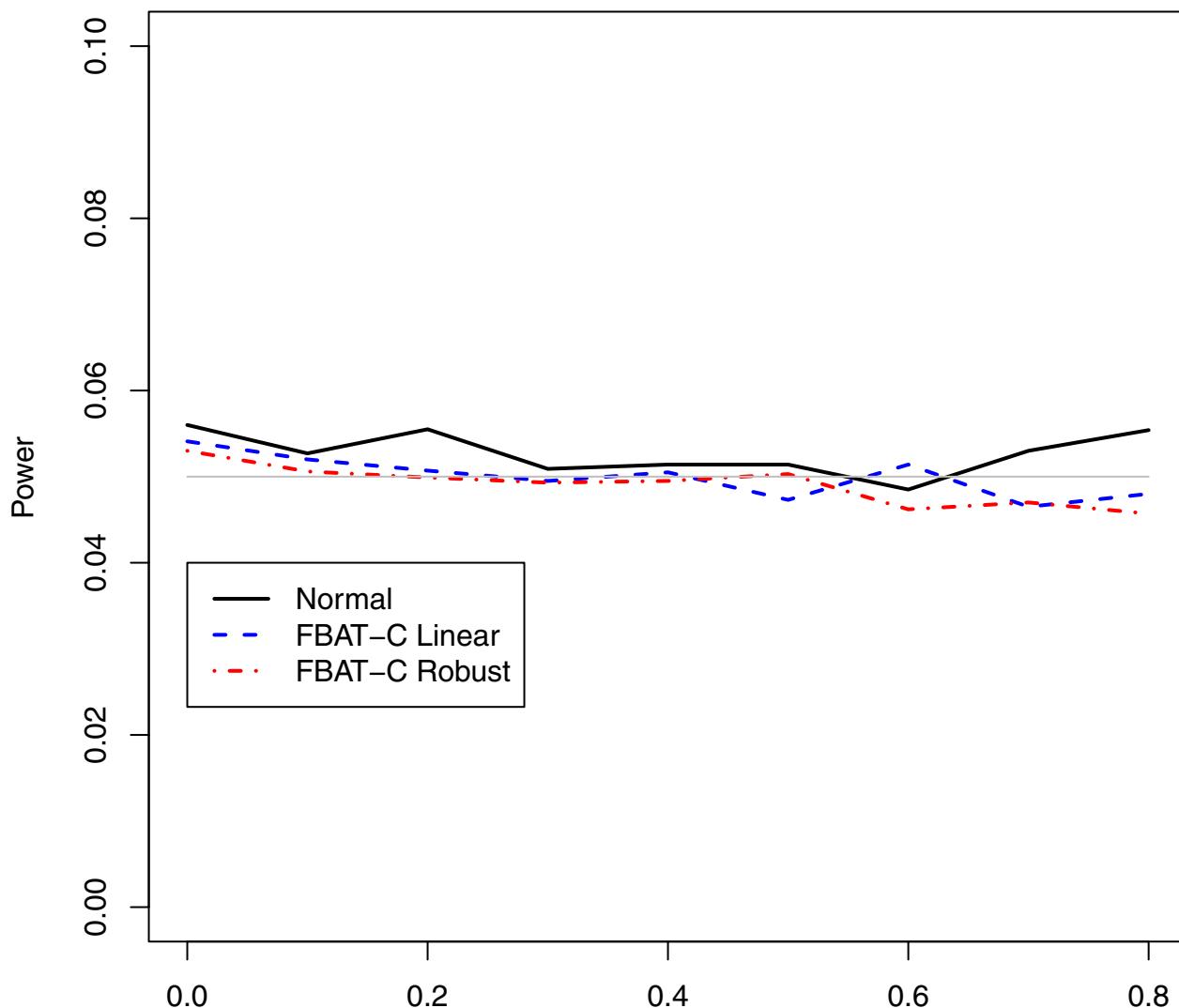


Figure VII: Power for discordant sibpairs of the test of  $X_m$  conditional on  $X_c$  for a continuous trait. Results are only shown for  $R^2$  up to 0.8, as the normal model is unstable for higher values.

## Sibpair QTL Validity with Population Stratification



$$\begin{aligned} R^2 \\ \beta_m = 0, \beta_c = 0.35, p_m = 0.2, 0.8, p_c = 0.2, 0.8 \end{aligned}$$

Figure VIII: Empirical type I error rate for discordant sibpairs under population substructure. Results are only shown for  $R^2$  up to 0.8, as the normal model is unstable for higher values.

$\beta_0$	$e^{\beta_m}$	$e^{\beta_c}$	$K$	$R^2$	FBAT-C Log-Linear	FBAT-C Robust
-2	1	0.16	0	0	0.0518	0.0516
				0.2	0.0482	0.0497
				0.5	0.0398	0.0480
				0.8	0.0247	0.0523
	3	0.27	0	0.0503	0.0499	
				0.2	0.0480	0.0497
				0.5	0.0457	0.0538
				0.8	0.0333	0.0517
	-4	1.5	0.022	0	0.0514	0.0518
				0.2	0.0479	0.0500
				0.5	0.0425	0.0502
				0.8	0.0244	0.0519
-4	3	0.035	0	0.0510	0.0519	
				0.2	0.0518	0.0505
				0.5	0.0462	0.0520
				0.8	0.0394	0.0555

Table VI: FBAT-C validity results for model misspecification under a logistic model, with empirical type I error rate 0.05. Trios were simulated with the allele frequency of all markers 0.2, and the pairwise  $R^2$  between each of the markers and the population prevalence  $K$  is as specified in the table.