α	pairedT	sign
0.01	0.0118	0.0066
0.005	0.0053	0.0025
0.001	0.0004	0.0012
1e-04	0.0000	0.0000

Table 1: **Type I error results.** Proportion of 5,000 tests that are rejected at a given α level (rows) for each of the proposed methods. These correspond to samples simulated under the null hypothesis, for which the random ancestry effect has the same mean and standard deviation for chromosomes 1 and 2.

α		sd_0.01	sd_0.02	sd_0.03	sd_0.04	sd_0.05
0.001	pairedT	0.0015	0.0010	0.0025	0.0040	0.0035
	sign	0.0015	0.0000	0.0015	0.0005	0.0010
1e-4	pairedT	0.0000	0.0000	0.0000	0.0000	0.0005
	sign	0.0000	0.0000	0.0000	0.0000	0.0000

Table 2: **Type I error results.** Proportion of 2,000 tests that are rejected at a given α level for each of the proposed methods. These correspond to simulated samples under the null hypothesis, for which the random ancestry effect has the same mean for chromosomes 1 and 2, but the standard deviation for chromosome 1 is 0.01, while the standard deviation for chromosome 2 is as listed in the column names.
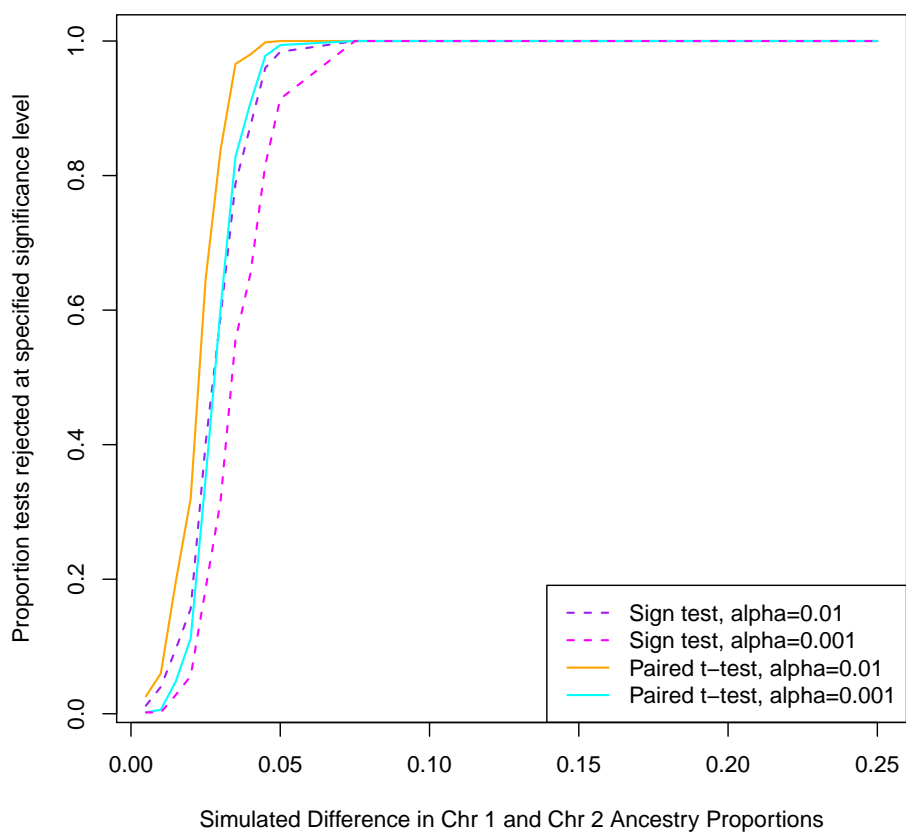
Figure 1: **Power results.** Plot of values presented in Table 3.

	$\alpha = 0.01$		$\alpha = 0.001$	
	pairedT	signT	pairedT	signT
0.005	0.0260	0.0120	0.0020	0.0020
0.01	0.0600	0.0400	0.0060	0.0020
0.015	0.1960	0.0960	0.0480	0.0280
0.02	0.3200	0.1560	0.1120	0.0560
0.025	0.6460	0.4020	0.3500	0.1860
0.03	0.8380	0.5900	0.6020	0.3160
0.035	0.9660	0.7880	0.8280	0.5560
0.04	0.9800	0.8740	0.9080	0.6540
0.045	0.9980	0.9600	0.9780	0.8160
0.05	1.0000	0.9840	0.9940	0.9140
0.075	1.0000	1.0000	1.0000	1.0000
0.1	1.0000	1.0000	1.0000	1.0000
0.12	1.0000	1.0000	1.0000	1.0000
0.125	1.0000	1.0000	1.0000	1.0000
0.13	1.0000	1.0000	1.0000	1.0000
0.14	1.0000	1.0000	1.0000	1.0000
0.15	1.0000	1.0000	1.0000	1.0000
0.175	1.0000	1.0000	1.0000	1.0000
0.2	1.0000	1.0000	1.0000	1.0000
0.225	1.0000	1.0000	1.0000	1.0000
0.25	1.0000	1.0000	1.0000	1.0000

Table 3: **Power results.** Proportion of 500 tests that are rejected at a given α level. The rows correspond to the mean of the random ancestry effect for chromosome 2, i.e. the simulated difference in means between chromosome 1 and 2. Figure 1 shows these results in a plot.

	alpha	sd_01	sd_02	sd_03	sd_04	sd_05
ttest	0.01	0.0095	0.0135	0.0155	0.0120	0.0135
sign	0.01	0.0085	0.0095	0.0103	0.0090	0.0100
ttest	0.001	0.0000	0.0020	0.0013	0.0015	0.0020
sign	0.001	0.0005	0.0020	0.0008	0.0010	0.0010
ttest	0.005	0.0055	0.0065	0.0067	0.0065	0.0070
sign	0.005	0.0040	0.0050	0.0030	0.0040	0.0030
ttest	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000
sign	0.0001	0.0000	0.0000	0.0000	0.0000	0.0000