Supplemental Table 1: The effect of incomplete LD on HWE. Displayed for $r^2 = 1.0$, 0.8 and 0.5 is the maximum deviation from HWE (D) and the population allele frequency (freq) at which it occurs for a genotypic RR of for $\gamma_1 = 1.5$ for parental and unaffected sibling genotype data under an additive, multiplicative, dominant and recessive model.

	Parental Genotype Data							
	Additive		Multiplicative		Dominant		Recessive	
LD	D	freq	D	freq	D	freq	D	freq
r^2=1.0	-0.00184	0.41	-0.00255	0.45	-0.00086	0.29	-0.00094	0.63
r^2=0.8	-0.00147	0.41	-0.00204	0.45	-0.00069	0.29	-0.00075	0.63
r^2=0.5	-0.00092	0.41	-0.00128	0.45	-0.00043	0.29	-0.00047	0.63
	Unaffected Siblings Genotype Data							
r^2=1.0	-0.00175	0.4	0.00023	0.8	-0.00596	0.45	0.00603	0.45
r^2=0.8	-0.00139	0.4	0.00024	0.79	-0.00476	0.45	0.00483	0.45
r^2=0.5	-0.00084	0.39	0.00025	0.77	-0.00296	0.45	0.00303	0.45

Supplemental Table 2: The effect of incomplete LD on the power to reject HWE. Displayed for $r^2 = 1.0$, 0.8 and 0.5 is the maximum power to reject HWE and the population allele frequency (freq) at which it occurs for a genotypic RR of for $\gamma_1 = 1.5$ for parental and unaffected sibling genotype data under an additive, multiplicative, dominant and recessive model.

	Parental Genotype Data							
	Additive		Multiplicative		Dominant		Recessive	
LD	D	freq	D	freq	D	freq	D	freq
r^2=1.0	2.32E-06	0.37	8.30E-06	0.45	4.68E-07	0.21	5.22E-07	0.71
r^2=0.8	1.14E-06	0.37	3.24E-06	0.44	3.13E-07	0.21	3.32E-07	0.71
r^2=0.5	3.77E-07	0.36	7.36E-07	0.44	1.75E-07	0.21	1.76E-07	0.71
	Unaffected Siblings Genotype Data							
r^2=1.0	7.21E-07	0.36	1.55E-07	0.95	0.000141	0.42	0.000151	0.43
r^2=0.8	4.31E-07	0.35	1.54E-07	0.95	3.58E-05	0.42	3.86E-05	0.43
r^2=0.5	2.03E-07	0.33	1.51E-07	0.95	3.72E-06	0.41	4.03E-06	0.43

Supplemental Table 3: The effect of genotyping error on HWE. Displayed is the effect of three genotyping error models: random genotyping error (M1), homozygote to heterozygote genotyping error (M2) and heterozygote to homozygote genotyping error (M3) on the maximum deviation from HWE (D) and the population allele frequency (freq) at which it occurs for a genotypic RR of for $\gamma_1 = 1.5$ for parental and unaffected sibling genotype data under an additive, multiplicative, dominant and recessive model.

	Parental Genotype Data							
	Additive		Multiplicative		Dominant		Recessive	
Model	D	freq	D	freq	D	freq	D	freq
M1	-0.00177	0.41	-0.00245	0.45	-0.00082	0.29	-0.00090	0.63
M2	-0.00431	0.43	-0.00503	0.45	-0.00319	0.38	-0.00330	0.55
M3	0.00103	0.73	0.000623	0.83	0.00208	0.59	0.00198	0.35
	Unaffected Siblings Genotype Data							
M1	-0.00168	0.40	0.00023	0.79	-0.00572	0.45	0.00579	0.45
M2	-0.00421	0.42	-0.00251	0.42	-0.00839	0.45	0.00348	0.45
M3	0.00120	0.72	0.00251	0.49	-0.00341	0.44	0.00846	0.46

Supplemental Table 4: The effect of genotyping error on the power to reject HWE. Displayed is the effect of three genotyping error models: random genotyping error (M1), homozygote to heterozygote genotyping error (M2) and heterozygote to homozygote genotyping error (M3) on the maximum power to reject HWE and the population allele frequency (freq) at which it occurs for a genotypic RR of for $\gamma_1 = 1.5$ for parental and unaffected sibling genotype data under an additive, multiplicative, dominant and recessive model.

	Parental Genotype Data							
	Additive		Multiplicative		Dominant		Recessive	
Model	D	freq	D	freq	D	freq	D	freq
M1	2.01E-06	0.38	6.91E-06	0.45	4.19E-07	0.22	4.67E-07	0.7
M2	1.67E-04	0.38	4.56E-04	0.45	4.48E-05	0.22	4.92E-05	0.7
M3	0.001029	0.95	0.000625	0.95	0.002081	0.95	0.001979	0.05
	Unaffected Siblings Genotype Data							
M1	6.47E-07	0.36	1.36E-07	0.94	0.000108	0.42	0.000116	0.43
M2	1.90E-05	0.36	2.13E-06	0.24	0.00163	0.42	7.21E-06	0.43
M3	2.24E-06	0.95	4.61E-06	0.95	6.64E-06	0.42	0.001733	0.43

Supplemental Table 5: The effect of population substructure on HWE. Displayed is the ratio of the allele frequency in population 1 and 2, maximum deviation from HWE (D) and the population 2 allele frequency (freq) at which it occurs for a genotypic RR offor $\gamma_1 = 1.5$ for parental and unaffected sibling genotype data under an additive, multiplicative, dominant and recessive model.

Parental Genotype Data								
	Additive		Multiplicative		Dominant		Recessive	
Ratio	D	freq	D	freq	D	freq	D	freq
r=0.9	-0.00157	0.39	-0.00222	0.43	0.00136	0.95	0.00099	0.95
r=0.8	0.00447	0.95	0.00407	0.95	0.00535	0.95	0.00448	0.95
r=0.6	0.01894	0.95	0.01802	0.95	0.02086	0.95	0.02025	0.95
Unaffected Siblings Genotype Data								
r=0.9	-0.00149	0.38	0.00120	0.95	-0.00565	0.44	0.00640	0.48
r=0.8	0.00459	0.95	0.00455	0.95	-0.00475	0.41	0.00775	0.54
r=0.6	0.01914	0.95	0.01881	0.95	0.01978	0.95	0.02177	0.95

Supplemental Table 6: The effect of population substructure on the power to rejected HWE. Displayed is the ratio of the allele frequency in population 1 and 2, maximum power to reject HWE and the population 2 allele frequency (freq) at which it occurs for a genotypic RR of for $\gamma_1 = 1.5$ for parental and unaffected sibling genotype data under an additive, multiplicative, dominant and recessive model.

Parental Genotype Data								
	Additive		Multiplicative		Dominant		Recessive	
Ratio	D	freq	D	freq	D	freq	D	freq
r=0.9	0.00025	0.95	0.000125	0.95	0.000742	0.95	0.000197	0.95
r=0.8	0.813977	0.95	0.714577	0.95	0.92767	0.95	0.84634	0.95
r=0.6	>.999	0.95	>.999	0.95	>.999	0.95	>.999	0.95
Unaffected Siblings Genotype Data								
r=0.9	0.00025	0.95	0.000125	0.95	0.000742	0.95	0.000197	0.95
r=0.8	0.202151	0.95	0.233738	0.95	0.130639	0.95	0.508447	0.95
r=0.6	>.999	0.91	>.999	0.95	>.999	0.95	>.999	0.95