Model	rs749292			rs727479		
	strata=age	strata=BMI	strata=race	strata=age	strata=BMI	strata=race
Case-Control-Level Assumption $[H = L]$						
Additive	41.5	33.7	37.7	11.3	7.8	11.2
Multiplicative	40.8	36.3	38.9	11.3	10.9	11.6
Logistic	41.3	35.1	38.5	11.3	8.8	11.5
Dominant	34.3	28.6	30.4	5.9	4.1	4.7
Recessive	21.0	16.3	19.7	8.9	6.1	9.7
Heterozygous	2.7	2.6	2.0	2.2	1.5	3.3
Population-Level Assumption $[H = J_\pi]$						
Additive	42.2	27.3	33.4	11.4	4.3	10.1
Multiplicative	41.3	35.2	38.5	11.3	8.8	11.5
Logistic	41.3	35.1	38.5	11.3	8.8	11.5
Dominant	35.1	23.3	26.0	5.9	1.9	4.1
Recessive	21.2	13.0	18.4	9.0	3.7	8.7
Heterozygous	2.9	2.3	1.3	2.2	1.2	3.1

Supplementary Table 1: Stratified trend test statistics using data on endometrial cancer risk and two estrogen-related variants in *CYP19A1*. Tests are stratified by age, body mass index (BMI), or race/ethnicity. The statistics using the population-level assumption were calculated with an assumed sampling fraction π=100; statistics were nearly equivalent to those using π=1000 (data not shown).

Stratified	High-risk Allele Freq.	Disease Freq. in Low-risk Homozygotes	Δ-GWA	Δ-CG	Label
no	0.5	0.45	0.05	0.10	unstrat, mid allele, mid disease, small eff
no	0.1	0.45	0.05	0.10	unstrat, low allele, mid disease, small eff
no	0.1	0.1	0.05	0.075	unstrat, low allele, low disease, small eff
no	0.5	0.1	0.05	0.075	unstrat, mid allele, low disease, small eff
no	0.5	0.45	0.10		unstrat, mid allele, mid disease, mid eff
yes	(0.5,0.5,0.5,0.5,0.5,0.5)	(0.01,0.025,0.0375,0.0625,0.075,0.1)	0.01	0.01	strat, constant mid allele, low disease, small eff
yes	(0.5,0.5,0.5,0.5,0.5,0.5)	(0.125,0.25,0.375,0.625,0.75,0.875)	0.05	0.05	strat, constant mid allele, mid disease, small eff
yes	(0.5,0.5,0.5,0.5,0.5,0.5)	(0.25,0.375,0.5,0.75,0.875,0.95)	0.05	0.05	strat, constant mid allele, high disease, small eff
yes	(0.03,0.08,0.13,0.29,0.40,0.65)	(0.01,0.025,0.0375,0.0625,0.075,0.1)	0.01	0.03	strat, variable low allele, low disease, small eff
yes	(0.03,0.08,0.13,0.29,0.40,0.65)	(0.125,0.25,0.375,0.625,0.75,0.875)	0.05	0.075	strat, variable low allele, mid disease, small eff
yes	(0.03,0.08,0.13,0.29,0.40,0.65)	(0.25,0.375,0.5,0.75,0.875,0.95)	0.05	0.075	strat, variable low allele, high disease, small eff
yes	(0.24,0.46,0.59,0.79,0.86,0.95)	(0.01,0.025,0.0375,0.0625,0.075,0.1)	0.01	0.01	strat, variable high allele, low disease, small eff
yes	(0.24,0.46,0.59,0.79,0.86,0.95)	(0.125,0.25,0.375,0.625,0.75,0.875)	0.05	0.075	strat, variable high allele, mid disease, small eff
yes	(0.24,0.46,0.59,0.79,0.86,0.95)	(0.25,0.375,0.5,0.75,0.875,0.95)	0.05	0.075	strat, variable high allele, high disease, small eff

Supplementary Table 2: Scenarios in which finite-sample power was investigated via simulations. Different effect sizes Δ were used in candidate-gene (CG) versus genome-wide association (GWA) simulations. Δ is the additive difference in disease probability between the low-risk and high-risk homozygotes when H is the identity function, i.e. for additive, dominant, recessive, and heterozygous truths. For multiplicative/logistic truths, Δ is the additive difference between logarithms/logits of disease probabilities in the low-risk and high-risk homozygotes for unstratified analyses. For stratified analyses with multiplicative/logistic truths, Δ is used to calculate a difference between logarithms/logits in the low-risk and high-risk homozygotes in each stratum. Then the median of these differences is used as a constant difference across strata in performing the simulations. If this choice causes a multiplicative probability to be greater than 1, then the difference between the logarithms of the highest probability in low-risk homozyogotes and 0.99 is used instead.

		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Scenario	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
mid allele	add	3200	1.00	1.00	3200	1.00	1.00	3200	1.00	1.00	3000	0.67	0.67	3350	0.66	0.67	-	-	0.00
mid disease	mult	3200	1.00	1.00	3200	1.00	1.00	3200	1.00	1.00	3000	0.67	0.67	3350	0.66	0.67	-	-	0.00
	logit	3200	1.00	1.00	3200	1.00	1.00	3200	1.00	1.00	3000	0.67	0.67	3350	0.66	0.67		-	0.00
	dom	4650	0.69	0.67	5000	0.64	0.67	4550	0.70	0.67	2000	1.00	1.00	20500	0.11	0.11	4850	0.33	0.33
	rec	4900	0.65	0.67	4800	0.67	0.67	4900	0.65	0.67	18200	0.11	0.11	2200	1.00	1.00	4850	0.33	0.33
	hetero	-	-	0.00	-	-	0.00	-	-	0.00	6100	0.33	0.33	6500	0.34	0.33	1580	1.00	1.00
low allele	add	8700	1.00	1.00	9400	1.00	1.00	8700	1.00	1.00	2800	0.96	0.95	240000	0.18	0.18	3500	0.77	0.78
mid disease	mult	8700	1.00	1.00	9400	1.00	1.00	8700	1.00	1.00	2800	0.96	0.95	240000	0.18	0.18	3500	0.77	0.78
	logit	8700	1.00	1.00	9400	1.00	1.00	8700	1.00	1.00	2800	0.96	0.95	240000	0.18	0.18	3500	0.77	0.78
	dom	9100	0.96	0.95	10000	0.94	0.95	9050	0.96	0.95	2700	1.00	1.00	1200000	0.04	0.04	2950	0.92	0.94
	rec	49500	0.18	0.18	50000	0.19	0.18	49000	0.18	0.18	60000	0.05	0.04	42500	1.00	1.00	-	-	0.00
	hetero	10700	0.81	0.78	12000	0.78	0.78	10600	0.82	0.78	2900	0.93	0.94	-	-	0.00	2700	1.00	1.00
low allele	add	2400	1.00	1.00	3000	1.00	1.00	2920	1.00	1.00	870	0.94	0.95	64000	0.19	0.18	1080	0.77	0.78
low disease	mult	2400	1.00	1.00	3,000	1.00	1.00	2920	1.00	1.00	870	0.94	0.95	64000	0.19	0.18	1080	0.77	0.78
	logit	2400	1.00	1.00	3000	1.00	1.00	2920	1.00	1.00	870	0.94	0.95	64000	0.19	0.18	1080	0.77	0.78
	dom	2500	0.96	0.95	3200	0.94	0.95	3100	0.94	0.95	820	1.00	1.00	270000	0.05	0.04	880	0.94	0.94
	rec	15200	0.16	0.18	15000	0.20	0.18	14800	0.20	0.18	18000	0.05	0.04	12300	1.00	1.00	-	-	0.00
	hetero	3000	0.80	0.78	4000	0.75	0.78	3800	0.77	0.78	870	0.94	0.94	-	-	0.00	830	1.00	1.00
mid allele	add	1030	1.00	1.00	1020	1.00	1.00	1020	1.00	1.00	1030	0.69	0.67	980	0.67	0.67	-	-	0.00
low disease	mult	1030	1.00	1.00	1020	1.00	1.00	1020	1.00	1.00	1030	0.69	0.67	980	0.67	0.67	-	-	0.00
	logit	1030	1.00	1.00	1020	1.00	1.00	1020	1.00	1.00	1030	0.69	0.67	980	0.67	0.67	-	-	0.00
	dom	1470	0.70	0.67	1600	0.64	0.67	1590	0.64	0.67	710	1.00	1.00	5600	0.12	0.11	1500	0.35	0.33
	rec	1620	0.64	0.67	1450	0.70	0.67	1480	0.69	0.67	6500	0.11	0.11	660	1.00	1.00	1490	0.35	0.33
	hetero	-	-	0.00	-	-	0.00	-	-	0.00	2100	0.34	0.33	1900	0.35	0.33	520	1.00	1.00

Supplementary Table 3: Sample Performance of Unstratified ARE Formula in Candidate Gene Studies with Cohort Samples. N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (3). This table reflects alternatives that give reasonable sample sizes for candidate gene studies that require a p-value of 0.01 for significance.

All		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Freq	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
0.5	add	6200	1.00	1.00	4700	0.70	0.71	8200	0.91	0.90	6000	0.65	0.67	6000	0.68	0.67	-	-	0.00
	mult	8100	0.77	0.74	3300	1.00	1.00	11000	0.68	0.69	7600	0.51	0.51	8300	0.49	0.47	-	-	0.00
	logit	6500	0.95	0.90	5500	0.60	0.61	7500	1.00	1.00	6500	0.60	0.60	6600	0.62	0.60	-	-	0.00
	dom	8800	0.70	0.67	7100	0.46	0.47	12200	0.61	0.60	3900	1.00	1.00	35000	0.12	0.11	9100	0.33	0.33
	rec	9300	0.67	0.67	7100	0.46	0.47	12200	0.61	0.60	35000	0.11	0.11	4100	1.00	1.00	8900	0.34	0.33
	hetero	-	-	0.00	-	-	0.00	-	-	0.00	11500	0.34	0.33	12000	0.34	0.33	3000	1.00	1.00
vary	add	5000	1.00	1.00	2000	0.90	0.90	6100	0.93	0.93	3400	0.71	0.70	7600	0.55	0.53	31000	0.06	0.06
low	mult	5700	0.88	0.89	1800	1.00	1.00	7500	0.76	0.77	4900	0.49	0.49	6500	0.65	0.66	-	-	0.00
	logit	5450	0.92	0.91	2800	0.64	0.62	5700	1.00	1.00	3200	0.75	0.75	10100	0.42	0.41	18500	0.11	0.11
	dom	6650	0.75	0.71	3900	0.46	0.47	7300	0.78	0.75	2400	1.00	1.00	65000	0.06	0.06	3900	0.51	0.53
	rec	8400	0.60	0.54	2400	0.75	0.69	14000	0.41	0.41	36000	0.07	0.06	4200	1.00	1.00	8200	0.24	0.23
	hetero	90000	0.06	0.05	-	-	0.00	43000	0.13	0.11	4600	0.52	0.50	17600	0.24	0.23	2000	1.00	1.00
vary	add	3800	1.00	1.00	4300	0.60	0.66	4800	0.94	0.91	5100	0.55	0.57	3300	0.67	0.65	250000	0.01	0.01
high	mult	5500	0.69	0.70	2600	1.00	1.00	5500	0.82	0.75	16500	0.17	0.18	2800	0.79	0.75	13000	0.15	0.15
	logit	4300	0.88	0.92	5100	0.51	0.54	4500	1.00	1.00	6300	0.44	0.47	3100	0.71	0.69	50000	0.04	0.04
	dom	7000	0.54	0.58	25000	0.10	0.12	11000	0.41	0.44	2800	1.00	1.00	43000	0.05	0.06	5200	0.38	0.33
	rec	6200	0.61	0.66	3500	0.74	0.77	6500	0.69	0.69	55000	0.05	0.05	2200	1.00	1.00	4400	0.45	0.43
	hetero	380000	0.01	0.01	12000	0.22	0.25	120000	0.04	0.04	10500	0.27	0.30	5400	0.41	0.43	2000	1.00	1.00

Supplementary Table 4: Sample Performance of Stratified ARE Formula in Candidate Gene Studies with Cohort Samples (mid disease frequency). N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (4). Simulations reflect data from a sample with equal numbers of subjects in each stratum. The mid disease frequency scenario is used throughout, and the first column indicates which high-risk allele frequency is used. This table reflects alternatives that give reasonable sample sizes for candidate gene studies that require a p-value of 0.01 for significance.

All		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Freq	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
0.5	add	4700	1.00	1.00	4100	0.88	0.90	9500	0.79	0.79	4100	0.66	0.67	5000	0.68	0.67	-	-	0.00
	mult	5100	0.92	0.90	3600	1.00	1.00	15000	0.50	0.51	4700	0.57	0.61	5600	0.61	0.59	-	-	0.00
	logit	6400	0.73	0.72	8900	0.40	0.39	7500	1.00	1.00	6200	0.44	0.42	6500	0.52	0.52	-	-	0.00
	dom	6900	0.68	0.67	6200	0.58	0.60	14000	0.54	0.53	2700	1.00	1.00	32000	0.11	0.11	6800	0.31	0.33
	rec	7000	0.67	0.67	5400	0.67	0.60	14000	0.54	0.53	23000	0.12	0.11	3400	1.00	1.00	6900	0.30	0.33
	hetero	-	-	0.00	-	-	0.00	-	-	0.00	8000	0.34	0.33	10600	0.32	0.33	2100	1.00	1.00
vary	add	2900	1.00	1.00	2260	0.96	0.96	8400	0.81	0.82	2500	0.62	0.62	4700	0.57	0.60	-	-	0.00
low	mult	3000	0.97	0.96	2160	1.00	1.00	10200	0.67	0.66	2800	0.55	0.54	4200	0.64	0.67	-	-	0.00
	logit	4300	0.67	0.69	4800	0.45	0.47	6800	1.00	1.00	2500	0.62	0.61	8700	0.31	0.29	14700	0.09	0.10
	dom	4500	0.64	0.65	4300	0.50	0.54	9000	0.76	0.74	1540	1.00	1.00	39000	0.07	0.07	3300	0.39	0.42
	rec	4600	0.63	0.62	2800	0.77	0.70	22500	0.30	0.31	18000	0.09	0.08	2700	1.00	1.00	4000	0.33	0.31
	hetero	-	-	0.00	200000	0.01	0.01	55000	0.12	0.10	4100	0.38	0.33	9000	0.30	0.31	1300	1.00	1.00
vary	add	3100	1.00	1.00	650	0.66	0.90	4500	0.93	0.91	7000	0.44	0.44	2100	0.71	0.74	26000	0.08	0.08
high	mult	3600	0.86	0.85	430	1.00	1.00	5600	0.75	0.64	19000	0.16	0.20	1400	1.07	0.84	9300	0.23	0.23
	logit	4700	0.66	0.84	5200	0.08	0.18	4200	1.00	1.00	6300	0.49	0.58	3500	0.43	0.51	55000	0.04	0.04
	dom	7600	0.41	0.46	10500	0.04	0.10	7500	0.56	0.57	3100	1.00	1.00	40000	0.04	0.05	7800	0.27	0.23
	rec	5100	0.61	0.75	1080	0.40	0.92	7600	0.55	0.57	85000	0.04	0.04	1500	1.00	1.00	3900	0.54	0.55
	hetero	31000	0.10	0.14	2500	0.17	0.63	130000	0.03	0.03	23000	0.13	0.18	3600	0.42	0.61	2100	1.00	1.00

Supplementary Table 5: Sample Performance of Stratified ARE Formula in Candidate Gene Studies with Cohort Samples (high disease frequency). N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (4). Simulations reflect data from a sample with equal numbers of subjects in each stratum. The high disease frequency scenario is used throughout, and the first column indicates which high-risk allele frequency is used. This table reflects alternatives that give reasonable sample sizes for candidate gene studies that require a p-value of 0.01 for significance.

All		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Freq	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
0.5	add	5500	1.00	1.00	15000	1.17	1.19	15000	0.83	0.84	5400	0.63	0.67	5200	0.70	0.67	-	-	0.00
	mult	9300	0.59	0.62	17500	1.00	1.00	18000	0.69	0.69	8200	0.41	0.46	10500	0.35	0.35	-	-	0.00
	logit	2600	2.12	2.08	13000	1.35	1.39	12500	1.00	1.00	2500	1.36	1.33	2700	1.35	1.41	-	-	0.00
	dom	6900	0.80	0.67	21500	0.81	0.80	22000	0.57	0.56	3400	1.00	1.00	32000	0.11	0.11	8100	0.33	0.33
	rec	9800	0.56	0.67	22500	0.78	0.80	23000	0.54	0.56	33000	0.10	0.11	3650	1.00	1.00	8100	0.33	0.33
	het	-	-	0.00	-	-	0.00	-	-	0.00	10500	0.32	0.33	10900	0.33	0.33	2650	1.00	1.00
vary	add	5300	1.00	1.00	5200	1.02	1.07	5500	0.89	0.86	3400	0.65	0.58	17500	0.63	0.64	10600	0.20	0.27
low	mult	6500	0.82	0.79	5300	1.00	1.00	5700	0.86	0.81	4300	0.51	0.44	17300	0.64	0.63	15000	0.14	0.17
	logit	3500	1.51	1.83	5000	1.06	1.21	4900	1.00	1.00	2100	1.05	1.35	22000	0.50	0.61	4300	0.49	0.81
	dom	4500	1.18	1.18	5950	0.89	0.91	6000	0.82	0.75	2200	1.00	1.00	108000	0.10	0.12	2900	0.72	0.86
	rec	23000	0.23	0.20	13000	0.41	0.45	13400	0.37	0.35	65000	0.03	0.02	11000	1.00	1.00	26500	0.08	0.05
	het	12200	0.43	0.41	34000	0.16	0.12	31000	0.16	0.11	3300	0.67	0.64	52000	0.21	0.19	2100	1.00	1.00
vary	add	5200	1.00	1.00	16500	1.15	1.17	15300	0.96	0.86	4800	0.42	0.38	7200	0.97	0.99	135000	0.02	0.02
high	mult	8300	0.63	0.66	19000	1.00	1.00	18000	0.82	0.73	7200	0.28	0.24	9000	0.78	0.75	-	-	0.00
	logit	3300	1.58	1.68	15000	1.27	1.33	14700	1.00	1.00	2600	0.77	0.76	6200	1.13	1.35	25000	0.12	0.13
	dom	3600	1.44	1.29	24200	0.79	0.82	22500	0.65	0.62	2000	1.00	1.00	40000	0.18	0.23	3000	1.02	0.87
	rec	19000	0.27	0.32	28000	0.68	0.69	29000	0.51	0.50	82000	0.02	0.02	7000	1.00	1.00	17000	0.18	0.19
	het	115000	0.05	0.03	420000	0.05	0.05	510000	0.03	0.03	8400	0.24	0.24	17800	0.39	0.40	3060	1.00	1.00

Supplementary Table 6: Sample Performance of Stratified ARE Formula in Candidate Gene Studies with Case-Control Samples (low disease frequency). N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (5). Simulations reflect data from a sample with equal numbers of subjects in each stratum. The sampling ratio π is 100, meaning that cases are 100 times more likely to be sampled than controls. The low disease frequency scenario is used throughout, and the first column indicates which high-risk allele frequency is used. This table reflects alternatives that give reasonable sample sizes for candidate gene studies that require a p-value of 0.01 for significance.

Dis		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Scenario	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
mid allele	add	31500	1.00	1.00	32000	1.00	1.00	31700	1.00	1.00	31700	0.66	0.67	31800	0.66	0.67	-	-	0.00
mid disease	mult	31500	1.00	1.00	32000	1.00	1.00	31700	1.00	1.00	31700	0.66	0.67	31800	0.66	0.67	-	-	0.00
small eff	logit	31500	1.00	1.00	32000	1.00	1.00	31700	1.00	1.00	31700	0.66	0.67	31800	0.66	0.67	-	-	0.00
	dom	47600	0.66	0.67	48500	0.66	0.67	48000	0.66	0.67	21000	1.00	1.00	190000	0.11	0.11	47100	0.34	0.33
	rec	46500	0.68	0.67	46500	0.69	0.67	46400	0.68	0.67	190000	0.11	0.11	20900	1.00	1.00	47100	0.34	0.33
	het	-	-	0.00	-	-	0.00	-	-	0.00	62800	0.33	0.33	62000	0.34	0.33	15900	1.00	1.00
low allele	add	87800	1.00	1.00	90500	1.00	1.00	88200	1.00	1.00	27300	0.94	0.95	2200000	0.18	0.18	34100	0.78	0.78
mid disease	mult	87800	1.00	1.00	90500	1.00	1.00	88200	1.00	1.00	27300	0.94	0.95	2200000	0.18	0.18	34100	0.78	0.78
small eff	logit	87800	1.00	1.00	90500	1.00	1.00	88200	1.00	1.00	27300	0.94	0.95	2200000	0.18	0.18	34100	0.78	0.78
	dom	93700	0.94	0.95	94500	0.96	0.95	91400	0.96	0.95	25600	1.00	1.00	9500000	0.04	0.04	28800	0.92	0.94
	rec	480000	0.18	0.18	475000	0.19	0.18	475000	0.19	0.18	600000	0.04	0.04	405000	1.00	1.00	-	-	0.00
	het	113000	0.78	0.78	118000	0.77	0.78	112500	0.78	0.78	27000	0.95	0.94	-	-	0.00	26500	1.00	1.00
low allele	add	34000	1.00	1.00	40500	1.00	1.00	38800	1.00	1.00	10800	0.95	0.95	820000	0.19	0.18	13500	0.79	0.78
low disease	mult	34000	1.00	1.00	40500	1.00	1.00	38800	1.00	1.00	10800	0.95	0.95	820000	0.19	0.18	13500	0.79	0.78
small eff	logit	34000	1.00	1.00	40500	1.00	1.00	38800	1.00	1.00	10800	0.95	0.95	820000	0.19	0.18	13500	0.79	0.78
	dom	36000	0.94	0.95	42600	0.95	0.95	41000	0.95	0.95	10300	1.00	1.00	3500000	0.04	0.04	11500	0.93	0.94
	rec	185000	0.18	0.18	190000	0.21	0.18	185000	0.21	0.18	245000	0.04	0.04	157000	1.00	1.00	-	-	0.00
	het	43000	0.79	0.78	53700	0.75	0.78	51000	0.76	0.78	10900	0.94	0.94	-	-	0.00	10700	1.00	1.00
mid allele	add	13800	1.00	1.00	14000	1.00	1.00	14000	1.00	1.00	14900	0.66	0.67	12800	0.68	0.67	-	-	0.00
low disease	mult	13800	1.00	1.00	14000	1.00	1.00	14000	1.00	1.00	14900	0.66	0.67	12800	0.68	0.67	-	-	0.00
small eff	logit	13800	1.00	1.00	14000	1.00	1.00	14000	1.00	1.00	14900	0.66	0.67	12800	0.68	0.67	-	-	0.00
	dom	20300	0.68	0.67	22200	0.63	0.67	22100	0.63	0.67	9800	1.00	1.00	75400	0.12	0.11	20600	0.33	0.33
	rec	21100	0.65	0.67	18900	0.74	0.67	19000	0.74	0.67	91100	0.11	0.11	8700	1.00	1.00	20200	0.34	0.33
	het	-	-	0.00	-	-	0.00	-	-	0.00	30300	0.32	0.33	25200	0.35	0.33	6900	1.00	1.00

Supplementary Table 7: Sample Performance of Unstratified ARE Formula in GWA studies with Cohort Samples. N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (3). This table reflects genome-wide association studies that use a p-value of $5 * 10^{-8}$ for significance.

All		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Freq	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
0.5	add	20000	1.00	1.00	15900	0.71	0.71	28000	0.90	0.90	20100	0.67	0.67	20200	0.68	0.67	-	-	0.00
	mult	26000	0.77	0.74	11300	1.00	1.00	36000	0.70	0.69	27400	0.49	0.51	28400	0.48	0.47	-	-	0.00
	logit	22650	0.88	0.90	18300	0.62	0.61	25300	1.00	1.00	22200	0.60	0.60	22500	0.61	0.60	-	-	0.00
	dom	30000	0.67	0.67	24600	0.46	0.47	42000	0.60	0.60	13400	1.00	1.00	120000	0.11	0.11	30000	0.34	0.33
	rec	30500	0.66	0.67	23000	0.49	0.47	42000	0.60	0.60	120000	0.11	0.11	13700	1.00	1.00	30100	0.34	0.33
	het	-	-	0.00	-	-	0.00	-	-	0.00	40000	0.34	0.33	41000	0.33	0.33	10200	1.00	1.00
vary	add	35000	1.00	1.00	15300	0.90	0.89	45000	0.96	0.92	25300	0.69	0.70	55000	0.54	0.53	260000	0.06	0.06
low	mult	39000	0.90	0.89	13700	1.00	1.00	54500	0.79	0.76	35800	0.49	0.49	45000	0.66	0.66	-	-	0.00
	logit	39000	0.90	0.91	20300	0.67	0.66	43000	1.00	1.00	23700	0.74	0.75	73000	0.40	0.40	135000	0.11	0.11
	dom	50000	0.70	0.71	29500	0.46	0.47	56500	0.76	0.75	17500	1.00	1.00	500000	0.06	0.06	28300	0.51	0.53
	rec	65000	0.54	0.54	19500	0.70	0.68	105000	0.41	0.40	280000	0.06	0.06	29500	1.00	1.00	61500	0.24	0.24
	het	700000	0.05	0.05	-	-	0.00	353000	0.12	0.11	34800	0.50	0.50	125000	0.24	0.24	14500	1.00	1.00
vary	add	32000	1.00	1.00	40000	0.66	0.67	39200	0.92	0.92	40000	0.58	0.57	27700	0.66	0.65	1650000	0.01	0.01
high	mult	46500	0.69	0.70	26500	1.00	1.00	47200	0.76	0.74	125000	0.18	0.18	23300	0.79	0.75	89500	0.16	0.16
	logit	34800	0.92	0.92	44000	0.60	0.62	36000	1.00	1.00	50500	0.46	0.46	26500	0.69	0.69	380000	0.04	0.04
	dom	56000	0.57	0.58	192000	0.14	0.14	82000	0.44	0.44	23100	1.00	1.00	330000	0.06	0.05	41700	0.34	0.33
	rec	50000	0.64	0.66	35000	0.76	0.77	52000	0.69	0.69	435000	0.05	0.05	18300	1.00	1.00	32100	0.45	0.44
	het	2800000	0.01	0.01	125000	0.21	0.22	900000	0.04	0.04	75000	0.31	0.31	41500	0.44	0.44	14300	1.00	1.00

Supplementary Table 8: Sample Performance of Stratified ARE Formula in GWA studies with Cohort Samples (mid disease frequency). N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (4). Simulations reflect data from a sample with equal numbers of subjects in each stratum. The mid disease frequency scenario is used throughout, and the first column indicates which high-risk allele frequency is used. This table reflects genome-wide association studies that use a p-value of $5 * 10^{-8}$ for significance.

All		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Freq	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
0.5	add	15500	1.00	1.00	13600	0.88	0.90	32000	0.80	0.79	14000	0.66	0.67	16600	0.68	0.67	-	-	0.00
	mult	17400	0.89	0.90	11900	1.00	1.00	51000	0.50	0.51	14800	0.63	0.61	19000	0.59	0.59	-	-	0.00
	logit	21500	0.72	0.72	30000	0.40	0.39	25500	1.00	1.00	21300	0.43	0.42	21800	0.52	0.52	-	-	0.00
	dom	23500	0.66	0.67	21300	0.56	0.60	48600	0.52	0.53	9250	1.00	1.00	100000	0.11	0.11	23500	0.32	0.33
	rec	22800	0.68	0.67	19100	0.62	0.60	48600	0.52	0.53	80000	0.12	0.11	11300	1.00	1.00	23500	0.32	0.33
	het	-	-	0.00	-	-	0.00	-	-	0.00	26600	0.35	0.33	34500	0.33	0.33	7500	1.00	1.00
vary	add	21100	1.00	1.00	7900	0.96	0.97	65700	0.79	0.79	19000	0.63	0.63	26100	0.61	0.61	-	-	0.00
low	mult	22050	0.96	0.96	7600	1.00	1.00	83000	0.63	0.62	22000	0.55	0.54	23000	0.70	0.68	-	-	0.00
	logit	31000	0.68	0.69	19000	0.40	0.40	52000	1.00	1.00	18400	0.65	0.64	60000	0.27	0.27	108000	0.09	0.09
	dom	33200	0.64	0.65	15000	0.51	0.53	70000	0.74	0.73	12000	1.00	1.00	225000	0.07	0.07	24000	0.41	0.41
	rec	33000	0.64	0.62	10200	0.75	0.71	180000	0.29	0.30	150000	0.08	0.07	16000	1.00	1.00	31000	0.32	0.32
	het	-	-	0.00	390000	0.02	0.02	470000	0.11	0.10	32000	0.38	0.35	50000	0.32	0.32	9800	1.00	1.00
vary	add	30700	1.00	1.00	18500	0.88	0.86	38000	0.92	0.90	64600	0.46	0.45	18800	0.72	0.74	155000	0.09	0.09
high	mult	36500	0.84	0.85	16200	1.00	1.00	54000	0.65	0.62	150000	0.20	0.19	16500	0.82	0.85	54600	0.26	0.25
	logit	37000	0.83	0.84	45300	0.36	0.35	35000	1.00	1.00	52000	0.58	0.57	27100	0.50	0.51	403000	0.04	0.03
	dom	68500	0.45	0.46	111000	0.15	0.15	60700	0.58	0.57	30000	1.00	1.00	307000	0.04	0.05	63000	0.23	0.22
	rec	41000	0.75	0.75	19000	0.85	0.88	61700	0.57	0.55	660000	0.05	0.05	13600	1.00	1.00	24700	0.58	0.57
	het	230000	0.13	0.14	37000	0.44	0.46	1000000	0.04	0.03	168000	0.18	0.18	23100	0.59	0.61	14300	1.00	1.00

Supplementary Table 9: Sample Performance of Stratified ARE Formula in GWA studies with Cohort Samples (high disease frequency). N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (4). Simulations reflect data from a sample with equal numbers of subjects in each stratum. The high disease frequency scenario is used throughout, and the first column indicates which high-risk allele frequency is used. This table reflects genome-wide association studies that use a p-value of $5 * 10^{-8}$ for significance.

All		Additive Truth			Multiplicative Truth			Logistic Truth			Dominant Truth			Recessive Truth			Heterozygous Truth		
Freq	Stat	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE	N	RE	ARE
0.5	add	18700	1.00	1.00	50000	1.22	1.19	51000	0.83	0.84	18300	0.67	0.67	17500	0.71	0.67	-	-	0.00
	mult	32000	0.58	0.62	61000	1.00	1.00	61000	0.70	0.69	29000	0.42	0.46	35400	0.35	0.35	-	-	0.00
	logit	8800	2.13	2.08	43000	1.42	1.39	42500	1.00	1.00	8600	1.42	1.33	9000	1.38	1.41	-	-	0.00
	dom	24000	0.78	0.67	73000	0.84	0.80	74000	0.57	0.56	12200	1.00	1.00	110000	0.11	0.11	28000	0.33	0.33
	rec	34000	0.55	0.67	77000	0.79	0.80	77000	0.55	0.56	108000	0.11	0.11	12400	1.00	1.00	27500	0.33	0.33
	het	-	-	0.00	-	-	0.00	-	-	0.00	36500	0.33	0.33	36000	0.34	0.33	9200	1.00	1.00
vary	add	128000	1.00	1.00	113000	1.04	1.06	120000	0.89	0.88	70000	0.59	0.58	460000	0.65	0.64	180000	0.24	0.28
low	mult	160000	0.80	0.79	117000	1.00	1.00	125000	0.86	0.83	89000	0.47	0.43	470000	0.64	0.63	270000	0.16	0.18
	logit	75000	1.71	1.83	103000	1.14	1.18	107000	1.00	1.00	34500	1.20	1.31	520000	0.58	0.60	61000	0.72	0.85
	dom	109000	1.17	1.18	130000	0.90	0.90	135000	0.79	0.76	41500	1.00	1.00	2650000	0.11	0.12	52500	0.84	0.88
	rec	610000	0.21	0.20	275000	0.43	0.45	300000	0.36	0.36	1750000	0.02	0.02	300000	1.00	1.00	820000	0.05	0.04
	het	310000	0.41	0.41	940000	0.12	0.12	880000	0.12	0.11	64000	0.65	0.64	1500000	0.20	0.19	44000	1.00	1.00
vary	add	20000	1.00	1.00	59000	1.16	1.17	57000	0.88	0.86	17500	0.38	0.38	27800	0.97	0.99	475000	0.02	0.02
high	mult	30000	0.67	0.66	68500	1.00	1.00	65000	0.77	0.73	28800	0.23	0.24	34300	0.79	0.75	-	-	0.00
	logit	12300	1.63	1.68	53000	1.29	1.33	50000	1.00	1.00	9000	0.74	0.76	22000	1.23	1.35	82000	0.12	0.13
	dom	15000	1.33	1.29	83000	0.83	0.82	77000	0.65	0.62	6700	1.00	1.00	136000	0.20	0.23	11100	0.90	0.87
	rec	70000	0.29	0.32	101000	0.68	0.69	101000	0.50	0.50	290000	0.02	0.02	27000	1.00	1.00	55000	0.18	0.19
	het	390000	0.05	0.03	1400000	0.05	0.05	1700000	0.03	0.03	29800	0.22	0.24	60000	0.45	0.40	10000	1.00	1.00

Supplementary Table 10: Sample Performance of Stratified ARE Formula in GWA studies with Case-Control Samples (low disease frequency). N represents the sample size needed to get 80% power in simulations, RE represents the simulated efficiency of a given test relative to the one that reflects the truth, and ARE is calculated using equation (5). Simulations reflect data from a sample with equal numbers of subjects in each stratum. The sampling ratio π is 100, meaning that cases are 100 times more likely to be sampled than controls. The low disease frequency scenario is used throughout, and the first column indicates which high-risk allele frequency is used. This table reflects genome-wide association studies that use a p-value of $5 * 10^{-8}$ for significance.