S-Table 1: Genotype probabilities for cases and controls

Genotype	Probability
Case (1/1)	$(1-p)^2\alpha/K_p$
Case (1/2)	$2p(1-p)\gamma_1\alpha/K_p$
Case (2/2)	$p^2\gamma_2\alpha/K_p$
Control (1/1)	$(1-p)^2(1-\alpha)/(1-K_p)$
Control (1/2)	$2p(1-p)\gamma_1(1-\alpha)/(1-K_p)$
Control (2/2)	$p^2\gamma_2(1-\alpha)/(1-K_p)$

$\alpha = K_p/((1-p)^2 + 2p(1-p)\gamma_1 + p^2\gamma_2)$
p – Disease minor allele frequency
γ_1 – Heterozygous genotypic relative risk
γ_2 – Homozygous genotypic relative risk
K_p – Disease prevalence

S-Table 2: Mating type and offspring genotype probabilities conditional on offspring being affected

Mating type	Offspring genotype	Probability
1/1, 1/1	1/1	$(1-p)^4/T$
1/1, 1/2	1/1	$2(1-p)^3p/T$
1/1, 1/2	1/2	$2(1-p)^3p\gamma_1/T$
1/1, 2/2	1/2	$2(1-p)^2p^2\gamma_1/T$
1/2, 1/2	1/1	$(1-p)^2p^2/T$
1/2, 1/2	1/2	$2(1-p)^2p^2\gamma_1/T$
1/2, 1/2	2/2	$(1-p)^2p^2\gamma_2/T$
1/2, 2/2	1/2	$2(1-p)p^3\gamma_1/T$
1/2, 2/2	2/2	$2(1-p)p^3\gamma_2/T$
2/2, 2/2	2/2	$p^4\gamma_2/T$

$T=(1-p)^2+2p(1-p)\ \gamma_1+p^2\ \gamma_1$

p – Disease minor allele frequency

γ_1 – Heterozygous genotypic relative risk

γ_2 – Homozygous genotypic relative risk

S-Table 3: Model parameters for ASPFCC samples

Λ_S =1.5		LD: r^2=0.0		LD: r^2=0.1		LD: r^2=0.2	
		PC: 10^{-10}	PC: 0.5	PC: 10^{-10}	PC: 0.5	PC: 10^{-10}	PC: 0.5
Marker MAF	**Disease locus parameter**	**Dominant model**					
CC 0.1 Ped2A 0.1							
	DAF	0.28	0.075	0.28	0.075	0.28	0.075
	f_{DD}	1	1	1	1	1	1
	f_{dD}	1	1	1	1	1	1
	f_{dd}	$<10^{-10}$	0.17	$<10^{-10}$	0.17	$<10^{-10}$	0.17
	GRR_{mM}	1	1	1.89	1.89	2.39	2.38
	GRR_{MM}	1	1	2.23	2.53	2.61	3.20
CC 0.2 Ped2A 0.2							
	DAF	0.28	0.075	0.28	0.075	0.28	0.075
	f_{DD}	1	1	1	1	1	1
	f_{dD}	1	1	1	1	1	1
	f_{dd}	$<10^{-10}$	0.17	$<10^{-10}$	0.17	$<10^{-10}$	0.17
	GRR_{mM}	1	1	1.76	1.74	2.27	2.23
	GRR_{MM}	1	1	2.17	2.33	2.77	3.01
Marker MAF	**Disease locus parameter**	**Recessive model**					
CC 0.4 Ped2A 0.4							
	DAF	0.69	0.35	0.69	0.35	0.69	0.35
	f_{DD}	1	1	1	1	1	1
	f_{dD}	1	0.14	1	0.14	1	0.14
	f_{dd}	$<10^{-10}$	0.14	$<10^{-10}$	0.14	$<10^{-10}$	0.14
	GRR_{mM}	1	1	0.75	1.32	0.70	1.40
	GRR_{MM}	1	1	0.36	2.09	0.15	2.77
CC 0.5 Ped2A 0.5							
	DAF	0.69	0.35	0.69	0.35	0.69	0.35
	f_{DD}	1	1	1	1	1	1
	f_{dD}	1	0.14	1	0.14	1	0.14
	f_{dd}	$<10^{-10}$	0.14	$<10^{-10}$	0.14	$<10^{-10}$	0.14
	GRR_{mM}	1	1	0.77	1.30	0.74	1.32
	GRR_{MM}	1	1	0.42	2.04	0.25	2.64

PC – Phenocopy rate; DAF – Disease allele frequency; MAF – Marker minor allele frequency; $f_{DD}/f_{dD}/f_{dd}$ – Disease penetrances; RR_{mM}/RR_{MM} – Heterozygous and homozygous genotypic relative risks for marker; Λ_S – Sibling recurrence risk ratio

S-Table 4: Power under the TDTCC scenario - Dominant model

		GRR: CC 2 Trios 1			GRR: CC 1 Trios 2			GRR: CC 2 Trios 2		
MAF	**Method**	**0.05**	**0.01**	**0.001**	**0.05**	**0.01**	**0.001**	**0.05**	**0.01**	**0.001**
CC 0.1	**CC-$\chi^{2\#}$**	0.99	0.96	0.86	0.03	0.01	0.00	0.99	0.96	0.85
Trios 0.1	**TDT-$\chi^{2\#}$**	0.02	0.00	0.00	0.99	0.95	0.85	0.99	0.96	0.84
Comb 0.1	**Pooled-χ^2**	0.99	0.96	0.83	0.99	0.95	0.81	1.00	1.00	1.00
	KF	0.93	0.78	0.51	0.91	0.75	0.46	1.00	1.00	1.00
	SR	0.93	0.80	0.56	0.92	0.79	0.53	1.00	1.00	1.00
	N(P)	0.94	0.82	0.58	0.91	0.76	0.48	1.00	1.00	1.00
	N(NP)	0.93	0.80	0.55	0.92	0.78	0.53	1.00	1.00	1.00
	D	0.93	0.80	0.55	0.92	0.79	0.52	1.00	1.00	1.00
	E	0.00	0.00	0.00	0.00	0.00	0.00	0.90	0.90	0.90
	E*	NA_2	NA_2	NA_2	NA_2	NA_2	NA_2	1.00	1.00	1.00
	A	0.99	0.93	0.79	0.75	0.52	0.25	1.00	1.00	1.00
CC 0.5	**CC-$\chi^{2\#}$**	0.86	0.68	0.41	0.02	0.01	0.00	0.86	0.68	0.41
Trios 0.5	**TDT-$\chi^{2\#}$**	0.03	0.01	0.00	0.84	0.66	0.39	0.85	0.67	0.39
Comb 0.5	**Pooled-χ^2**	0.83	0.63	0.36	0.84	0.64	0.35	0.99	0.96	0.84
	KF	0.61	0.37	0.15	0.61	0.35	0.14	1.00	0.98	0.91
	SR	0.65	0.40	0.17	0.63	0.38	0.15	1.00	0.98	0.91
	N(P)	0.64	0.39	0.16	0.62	0.37	0.14	1.00	0.98	0.91
	N(NP)	0.65	0.40	0.16	0.62	0.37	0.14	1.00	0.98	0.91
	D	0.63	0.39	0.15	0.63	0.38	0.15	1.00	0.98	0.90
	E	0.05	0.04	0.02	0.05	0.03	0.01	0.91	0.90	0.83
	E*	0.68	0.47	0.22	0.65	0.38	0.15	1.00	0.98	0.91
	A	0.77	0.55	0.26	0.44	0.23	0.08	0.99	0.97	0.88

MAF – Marker minor allele frequency; GRR – Homozygous genotypic relative risk; 0.05/0.01/0.001 – p-value thresholds; CC – Case-control sample; Comb – Combined sample; Pooled χ^2–from single samples; KF – Kazeem & Farrall; SR – Schaid & Rowland; NK –Nagelkerke with (P) and without parental information (NP); D – Dudbridge; E – Epstein ; E* – Adjusted power of E; NA_1 – Not designed for stratified samples; NA_2 – Number of joint association tests for E ≤ 100; A – Allen-Brady (1000 simulations); # Corrected for multiple testing

S-Table 5: Power under the TDTCC scenario - Recessive model

		GRR: CC 2 Trios 1			GRR: CC 1 Trios 2			GRR: CC 2 Trios 2		
MAF	**Method**	**0.05**	**0.01**	**0.001**	**0.05**	**0.01**	**0.001**	**0.05**	**0.01**	**0.001**
CC 0.1	**CC-$\chi^{2\#}$**	0.07	0.02	0.00	0.02	0.00	0.00	0.06	0.02	0.00
Trios 0.1	**TDT-$\chi^{2\#}$**	0.03	0.01	0.00	0.06	0.02	0.00	0.06	0.02	0.00
Comb 0.1	**Pooled-χ^2**	0.09	0.02	0.00	0.08	0.02	0.00	0.12	0.04	0.01
	KF	0.07	0.02	0.00	0.07	0.02	0.00	0.15	0.04	0.01
	SR	0.08	0.02	0.00	0.08	0.02	0.00	0.15	0.05	0.01
	N(P)	0.07	0.02	0.00	0.08	0.02	0.00	0.16	0.06	0.01
	N(NP)	0.07	0.01	0.00	0.08	0.02	0.00	0.15	0.05	0.01
	D	0.08	0.02	0.00	0.08	0.02	0.00	0.16	0.05	0.01
	E	0.07	0.02	0.00	0.07	0.02	0.00	0.13	0.05	0.01
	E*	0.08	0.02	0.00	0.08	0.02	0.00	0.15	0.05	0.01
	A	0.09	0.02	0.00	0.05	0.01	0.00	0.15	0.05	0.01
CC 0.5	**CC-$\chi^{2\#}$**	0.99	0.95	0.85	0.03	0.01	0.00	0.99	0.95	0.84
Trios 0.5	**TDT-$\chi^{2\#}$**	0.02	0.01	0.00	0.99	0.94	0.84	0.99	0.95	0.85
Comb 0.5	**Pooled-χ^2**	0.99	0.95	0.82	0.98	0.93	0.80	1.00	1.00	1.00
	KF	0.89	0.73	0.47	0.87	0.70	0.43	1.00	1.00	1.00
	SR	0.89	0.71	0.44	0.88	0.72	0.45	1.00	1.00	1.00
	N(P)	0.88	0.72	0.44	0.88	0.71	0.44	1.00	1.00	1.00
	N(NP)	0.88	0.70	0.43	0.88	0.72	0.44	1.00	1.00	1.00
	D	0.89	0.74	0.48	0.88	0.72	0.46	1.00	1.00	1.00
	E	0.01	0.01	0.00	0.01	0.00	0.00	0.88	0.88	0.88
	E*	NA_2	NA_2	NA_2	NA_2	NA_2	NA_2	NA_2	NA_2	NA_2
	A	0.96	0.88	0.54	0.71	0.49	0.23	1.00	1.00	0.99

MAF – Marker minor allele frequency; GRR – Homozygous genotypic relative risk; 0.05/0.01/0.001 – p-value thresholds; CC – Case-control sample; Comb – Combined sample; Pooled χ^2–from single samples; KF – Kazeem & Farrall; SR – Schaid & Rowland; NK –Nagelkerke with (P) and without parental information (NP); D – Dudbridge; E – Epstein ; E* – Adjusted power of E; NA_1 – Not designed for stratified samples; NA_2 – Number of joint association tests for $E \leq 100$; A – Allen-Brady (1000 simulations); # Corrected for multiple testing

S-Table 6: Coverage of the true genetic effect under the TDTCC scenario

	MAF: CC 0.1 Trios 0.1		MAF: CC 0.5 Trios 0.5	
Method	**OR/RR (95%CI)**	**Coverage**	**OR/RR (95%CI)**	**Coverage**
CC-OR	1.42(1.08-1.87)	0.95	1.42(1.19-1.69)	0.95
TDT-OR	1.42(1.08-1.87)	0.95	1.41(1.18-1.68)	0.95
KF	1.42(1.17-1.72)	0.95	1.41(1.25-1.60)	0.95
N(P)	1.42(1.17-1.73)	0.95	1.42(1.25-1.61)	0.95
N(NP)	1.42(1.17-1.73)	0.95	1.42(1.25-1.61)	0.95
D	1.43(1.17-1.73)	0.95	1.42(1.25-1.61)	0.95
E	1.42	-	1.42	-

MAF – Marker minor allele frequency; Average ORs/RRs and their 95% CI across all simulations; CC-OR – Allelic case-control-OR ; TDT-OR – Allelic TDT-OR; KF – Kazeem & Farrall; NK – Nagelkerke with (P) and without parental information (NP); D – Dudbridge; E – Epstein (no Confidence intervals given)