

SUPPLEMENTARY DATA

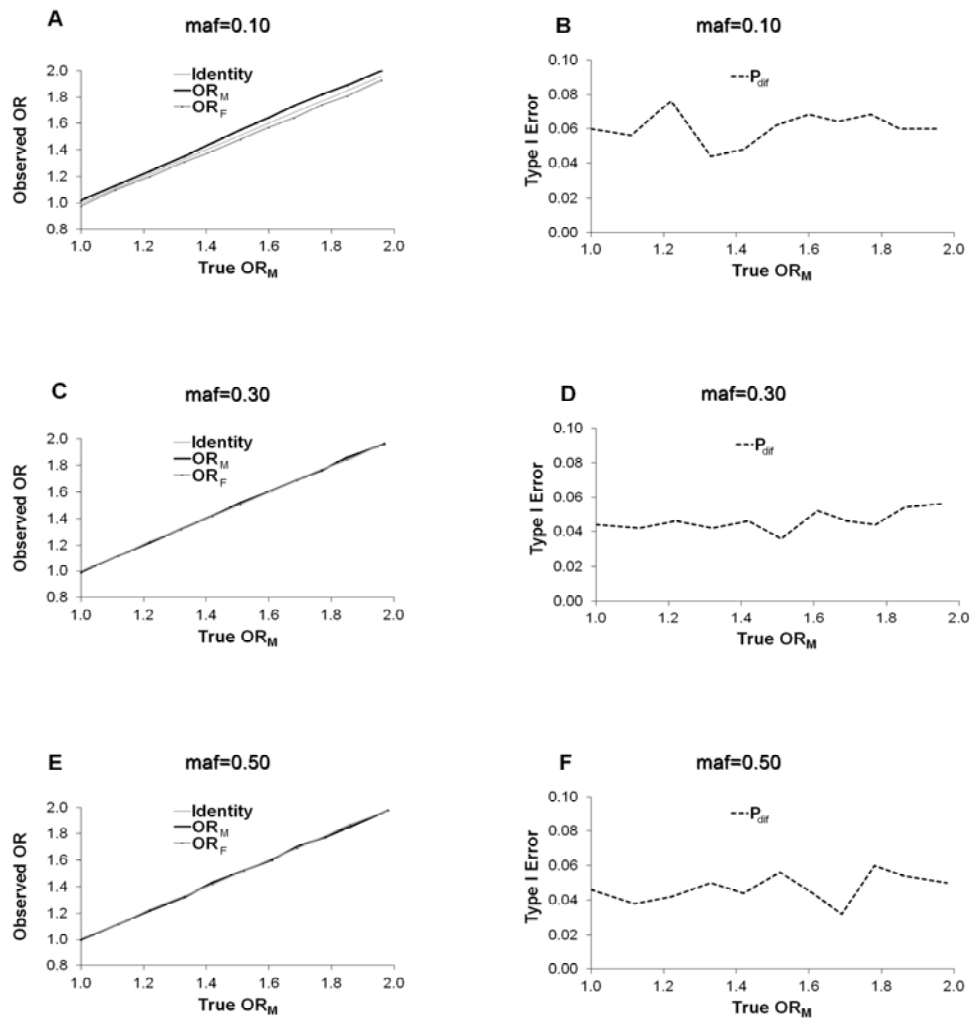
Supplementary Table 1. Calculation of G_M and G_F for different combinations of genotypes for parent and child.

Mother	Father	Child	G_M	G_F
RR	RR	RR	1	1
RR	RL	RR	1	1
RR	RL	RL	1	0
RR	LL	RL	1	0
RR	UU	RR	1	1
RR	UU	RL	1	0
RL	RR	RR	1	1
RL	RR	RL	0	1
RL	RL	RR	1	1
RL	RL	RL	1/2	1/2
RL	RL	LL	0	0
RL	LL	RL	1	0
RL	LL	LL	0	0
RL	UU	RR	1	1
RL	UU	RL	$1 - P_{FRR} - 1/2 P_{FRL}$	$P_{FRR} + 1/2 P_{FRL}$
RL	UU	LL	0	0
LL	RR	RL	0	1
LL	RL	RL	0	1
LL	RL	LL	0	0
LL	UU	RL	0	1
LL	UU	LL	0	0
UU	RR	RR	1	1
UU	RR	RL	0	1
UU	RL	RR	1	1
UU	RL	RL	$P_{MRR} + 1/2 P_{MRL}$	$1 - P_{MRR} - 1/2 P_{MRL}$
UU	RL	LL	0	0
UU	LL	RL	1	0
UU	LL	LL	0	0
UU	UU	RR	1	1
UU	UU	RL	1/2	1/2
UU	UU	LL	0	0

Genotypes for mother, father and child are given as two-letter combinations. Letters designate alleles- R is the risk allele, L is the low-risk allele and U is unknown. G_M designates the number of risk alleles inherited from the mother, while G_F represents the number of risk alleles inherited from the father. In ambiguous cases involving heterozygous children, the expected values are calculated from the population allele frequencies and the genotypes of family members. P_{FRR} is the probability the father is genotype “RR”, P_{FRL} is the probability the father is genotype “RL”; P_{MRR} and P_{MRL} are the corresponding probabilities for the mother’s genotypes. These probabilities are calculated by the MLINK program (16).

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Supplementary Figure 1. Results of simulation studies assessing the performance of methods for analyzing parent-of-origin effects in the present families for models simulated without parent-of-origin effects ($OR_M=OR_F$): Panels A, C, and E show values of OR_M and OR_F obtained from applying the present method against the true value of OR_M (or OR_F since they are equal) for various values of minor allele frequency (maf). Panels B, D and F show the type I error at $P<0.05$ for these simulations (i.e., the proportion of replicates with $P_{dif}<0.05$). Apart from a slight tendency at $maf=0.10$ to overestimate the odds ratio for the maternal allele (genotypes were available for more mothers than fathers), the geometric mean values of OR_M and OR_F are nearly identical to their true values (and nearly identical to each other). Each point represents the analysis of 500 replicates.



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Supplementary Figure 2. Results of simulation studies assessing the performance of methods for analyzing parent-of-origin effects in the present families for models simulated with parent-of-origin effects ($OR_M > 1$, $OR_F = 1$): Panels A, C, and E show values of OR_M and OR_F obtained from applying the present method against the true value of OR_M for various values of minor allele frequency (maf). Panels B, D and F show the proportion of replicates for which OR_M was significantly different from 1 at $P < 0.05$ (P_M), the proportion for which OR_F was significantly different from 1 (P_F) and for which OR_M and OR_F were significantly different (P_{dif}). For P_M and P_{dif} this represents power, whereas for P_F it represents type I error. Apart from a slight tendency at $maf = 0.10$ to overestimate the odds ratio for the maternal allele (genotypes were available for more mothers than fathers), the geometric mean values of OR_M and OR_F are nearly identical to their true values. Each point represents the analysis of 500 replicates.

