Supplementary information:

model 1			*% of missing data*							
		expected	*0%*	*1%*	*5%*	*10%*	*20%*	*30%*	*40%*	*50%*
	number of complete families		500	486.4	434.4	374.7	271.9	189.8	125.8	77.8
without multiple imputation	*GRR2*	1	0.006	0.006	0.007	0.008	0.008	0.001	0.010	0.040
	GRR3	1.5	0.007	0.006	0.006	0.006	0.007	-0.009	-0.005	0.053
	coverage 2	0.95	0.938	0.940	0.930	0.946	0.936	0.942	0.966	0.960
	coverage 3	0.95	0.928	0.924	0.926	0.940	0.948	0.958	0.954	0.966
with multiple imputation	*GRR2*	1	0.006	0.007	0.012	0.018	0.033	0.055	0.096	0.154
	GRR3	1.5	0.007	0.008	0.013	0.015	0.022	0.027	0.036	0.045
	coverage 2	0.95	0.938	0.936	0.938	0.934	0.928	0.932	0.906	0.843
	coverage 3	0.95	0.928	0.928	0.936	0.936	0.928	0.922	0.926	0.896

model 2			*% of missing data*							
		expected	*0%*	*1%*	*5%*	*10%*	*20%*	*30%*	*40%*	*50%*
	number of complete families		500	486.2	434.3	374.6	272.1	189.5	125.2	78.4
without multiple imputation	*GRR2*	1.5	0.008	0.007	0.010	0.014	0.017	0.019	0.015	0.008
	GRR3	1.5	-0.001	-0.002	0.000	0.006	0.004	0.006	-0.006	0.000
	coverage 2	0.95	0.960	0.958	0.960	0.956	0.952	0.962	0.976	0.958
	coverage 3	0.95	0.962	0.952	0.958	0.960	0.952	0.948	0.962	0.952
with multiple imputation	*GRR2*	1.5	0.008	0.009	0.014	0.020	0.036	0.054	0.084	0.129
	GRR3	1.5	-0.001	0.001	0.006	0.012	0.017	0.023	0.021	0.018
	coverage 2	0.95	0.960	0.954	0.952	0.952	0.950	0.948	0.942	0.910
	coverage 3	0.95	0.962	0.958	0.954	0.968	0.958	0.960	0.928	0.938

model 3			*% of missing data*							
		expected	*0%*	*1%*	*5%*	*10%*	*20%*	*30%*	*40%*	*50%*
	number of complete families		500	486.7	434.3	374.6	271.6	188.6	126.4	77.6
without multiple imputation	*GRR2*	1.5	0.009	0.008	0.007	0.007	0.015	0.016	0.001	0.045
	GRR3	1.5	0.003	0.002	0.004	0.005	0.011	0.014	0.023	0.096
	coverage 2	0.95	0.922	0.924	0.912	0.938	0.940	0.942	0.932	0.964
	coverage 3	0.95	0.934	0.930	0.932	0.930	0.938	0.940	0.940	0.954
with multiple imputation	*GRR2*	1.5	0.009	0.010	0.015	0.023	0.040	0.068	0.116	0.179
	GRR3	1.5	0.003	0.005	0.009	0.015	0.022	0.032	0.049	0.058
	coverage 2	0.95	0.922	0.920	0.916	0.922	0.924	0.918	0.898	0.830
	coverage 3	0.95	0.934	0.934	0.938	0.936	0.924	0.930	0.922	0.904

model 4			% of missing data							
		expected	*0%*	*1%*	*5%*	*10%*	*20%*	*30%*	*40%*	*50%*
	number of complete families		500	486.1	433.6	375.2	272.9	189.6	125.6	78.1
without multiple imputation	*GRR2*	1.5	0.012	0.013	0.009	0.016	0.017	0.039	0.070	0.285
	GRR3	1.5	-0.002	0.000	-0.007	-0.001	0.006	0.010	0.056	0.247
	coverage 2	0.95	0.946	0.958	0.962	0.974	0.956	0.942	0.950	0.966
	coverage 3	0.95	0.958	0.956	0.956	0.956	0.960	0.970	0.968	0.952
with multiple imputation	*GRR2*	1.5	0.012	0.014	0.016	0.025	0.036	0.050	0.084	0.137
	GRR3	1.5	-0.002	0.000	0.003	0.010	0.014	0.008	0.015	0.033
	coverage 2	0.95	0.946	0.944	0.954	0.954	0.964	0.956	0.948	0.922
	coverage 3	0.95	0.958	0.954	0.964	0.960	0.970	0.958	0.948	0.934

Supplementary table 1: Bias and coverage of genetic parameter estimates from one-locus simulation study as a function of the percentage of missing data. The average number of informative families for the analysis without MI is noted on the third row.

	haplotype frequencies				number of families
	11	**12**	**21**	**22**	
population1	0.5	0.1	0.25	0.15	100
population 2	0.2	0.3	0.3	0.2	400

Supplementary table 2: Haplotype frequencies for simulations under population stratification

Supplementary Figure 1: LD pattern between the five loci considered in the simulations. Gradation of greys represents the level of the r^2 and numbers are the D' values. This LD pattern is similar to the one observed in the CTLA4 gene in a sample of 450 multiple sclerosis trios [23].

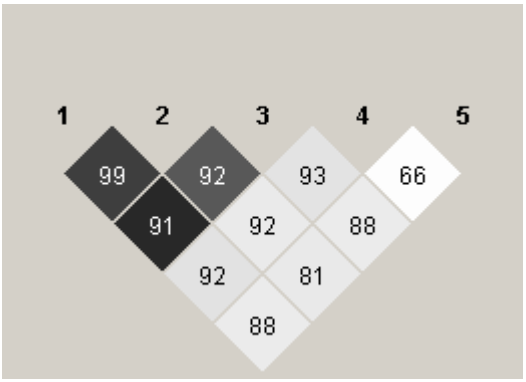
Supplementary Figure 2: Correlation plot between the logarithm of the p-value obtained on the complete data file and data with 5, 30 and 50% of missing data when using MI approach on the recessive model 1 (a, b and c respectively) and the dominant model 2 (d, e and f) with genotype relative risks 1.5. For a better understanding of these graphs, the linear equation y=x has been plotted.

Supplementary Figure 3: Correlation plot between the genotype relative risk of the homozygous 2/2 obtained on the complete data file and data with 5, 30 and 50% of missing data when using MI approach on the recessive model 1 (a, b and c respectively) and the dominant model 2 (d, e and f) with genotype relative risk 1.5. For a better understanding of these graph, the linear equation y=x has been plotted.

Supplementary Figure 4: mean difference between the true p-value from complete datasets and p-values obtained by TRANSMIT or conditional logistic regression when using or not MI approach from datasets with different levels of missing data.

Supplementary Figure 5: Type one error rate obtained at α=0.05 on data simulated under population stratification as a function of the percentage of missing data when using TRANSMIT program or conditional logistic regression with or without MI.

Supplementary information, figure1



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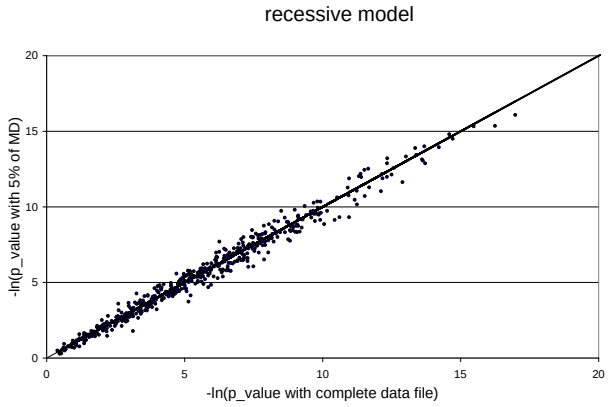

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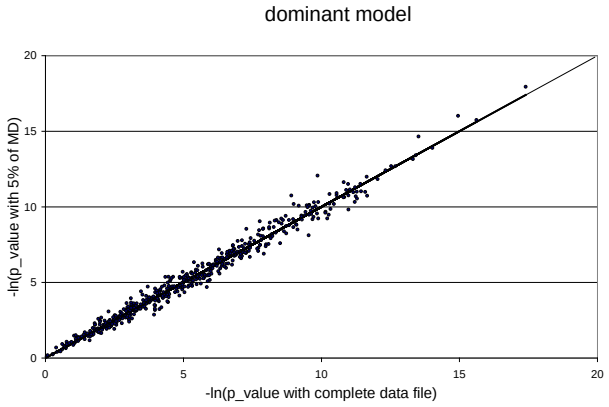

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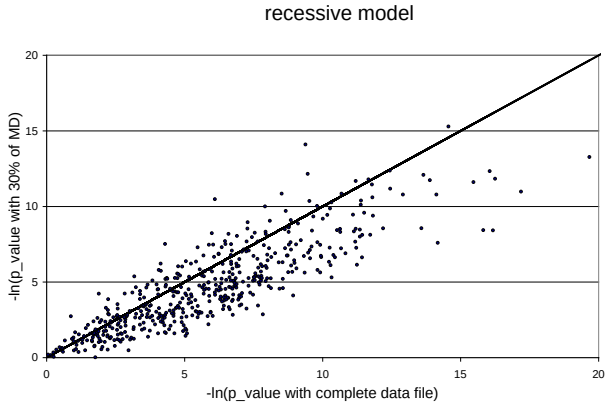

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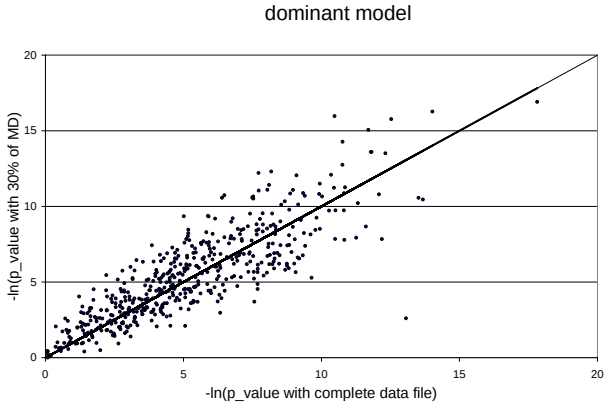

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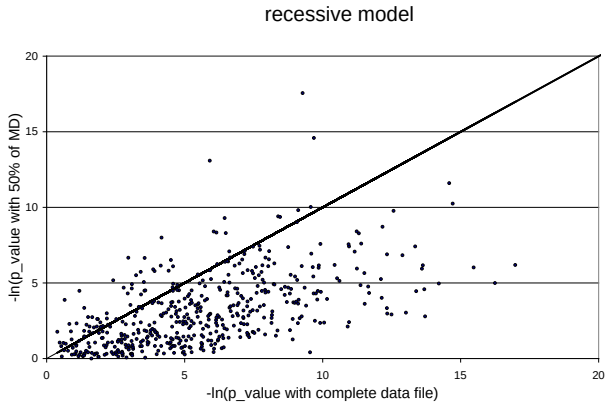

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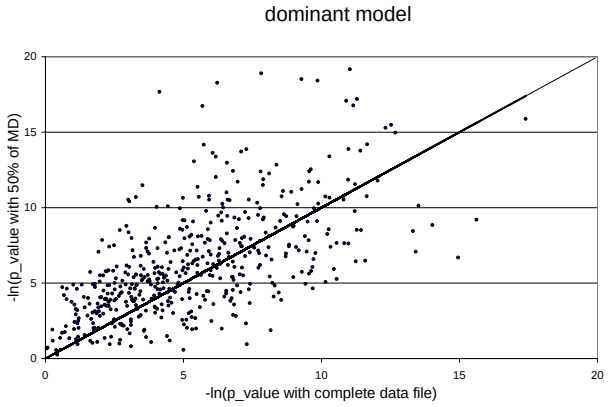
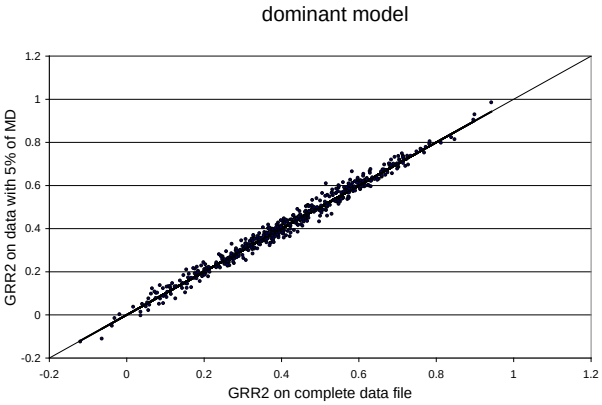


Supplementary information, figure 2

a

d



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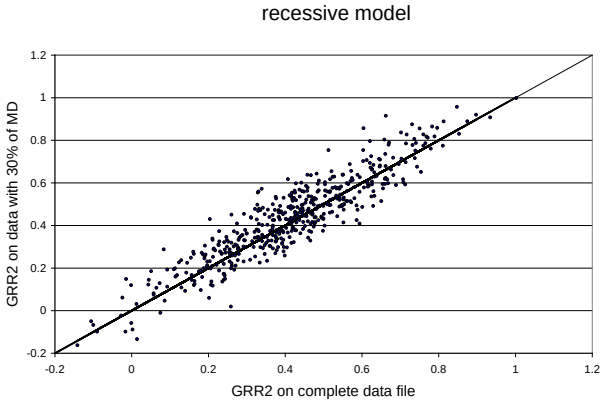

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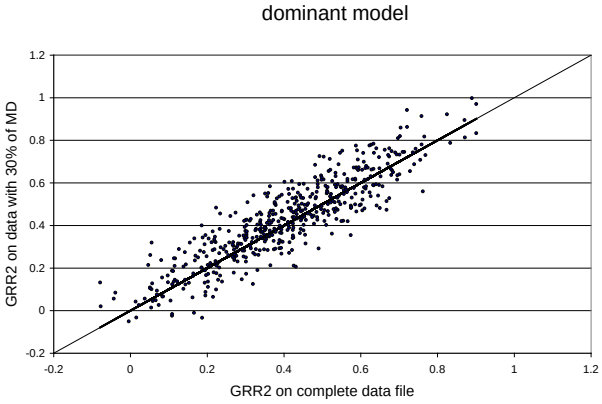

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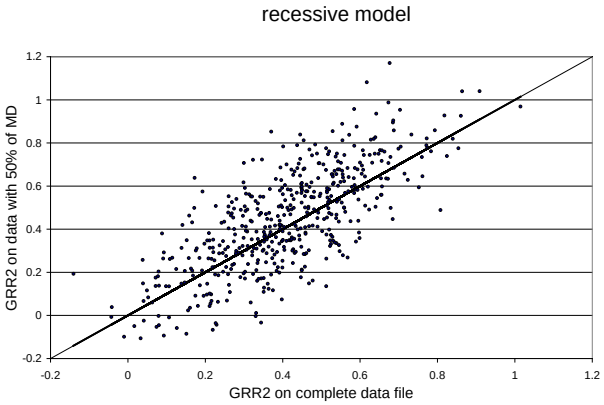

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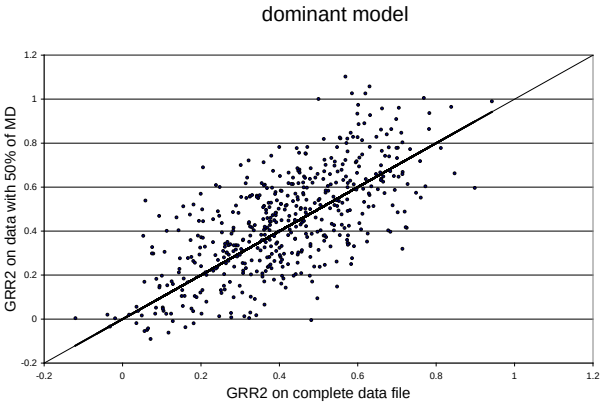
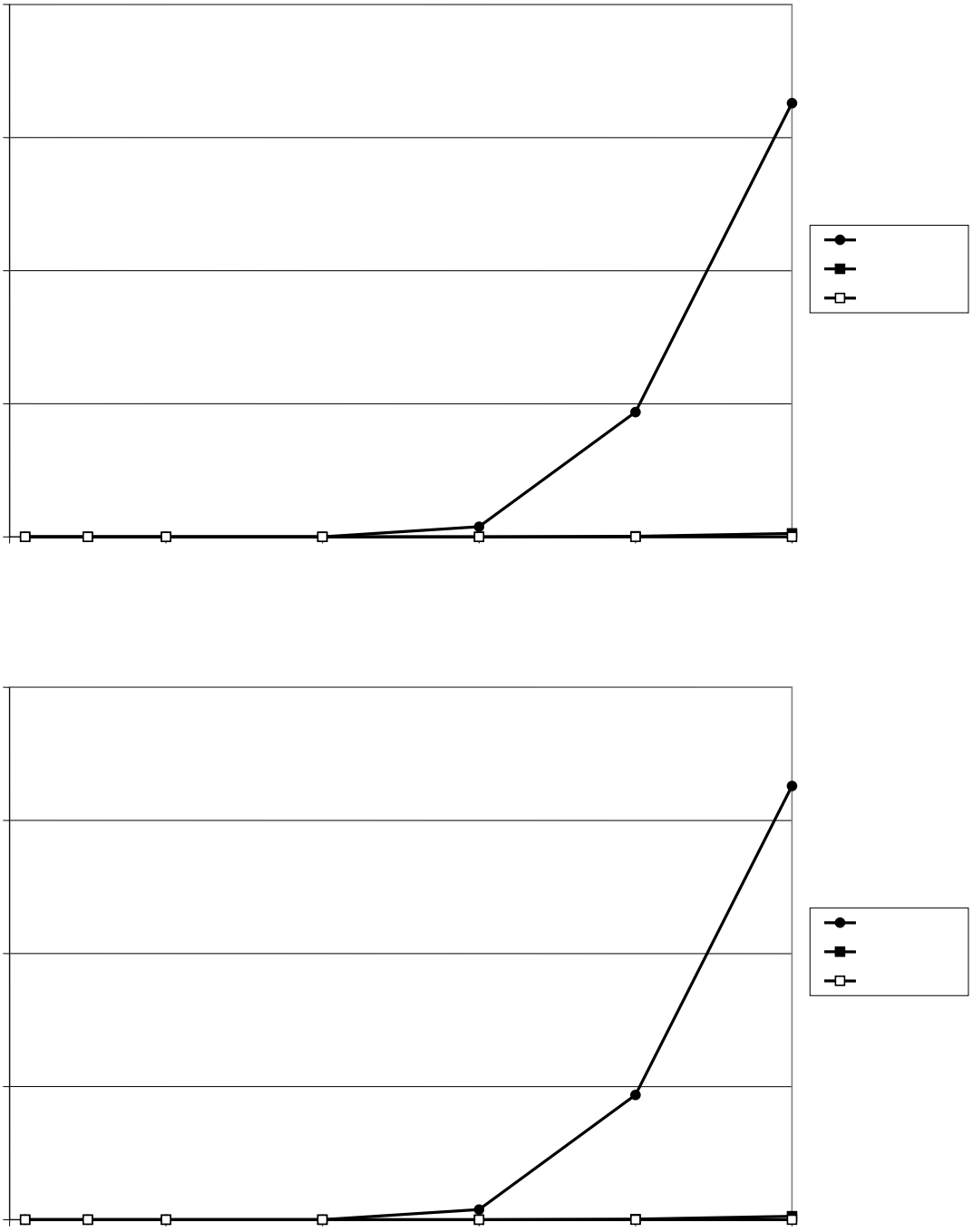
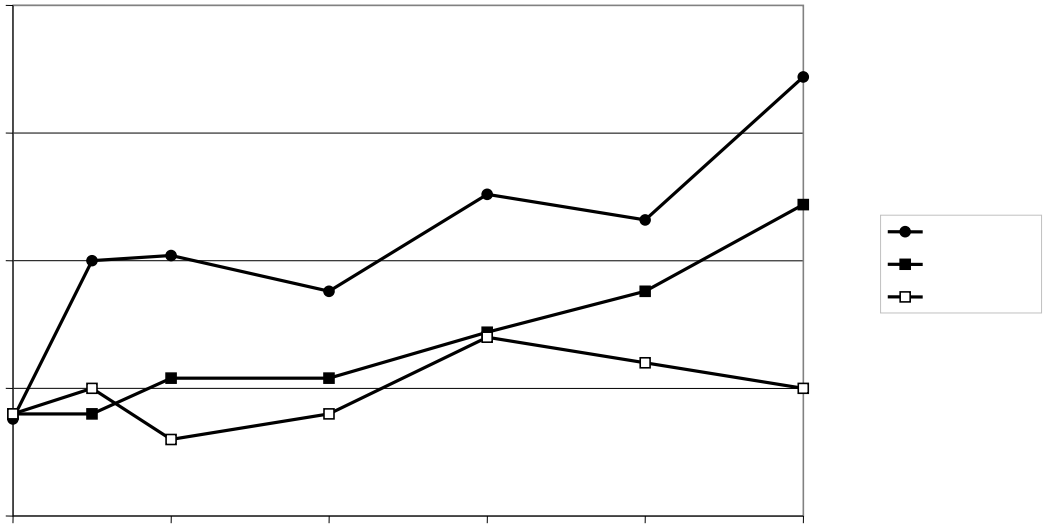


Supplementary information, figure 3



Supplementary information, figure 4



Supplementary information, figure 5