

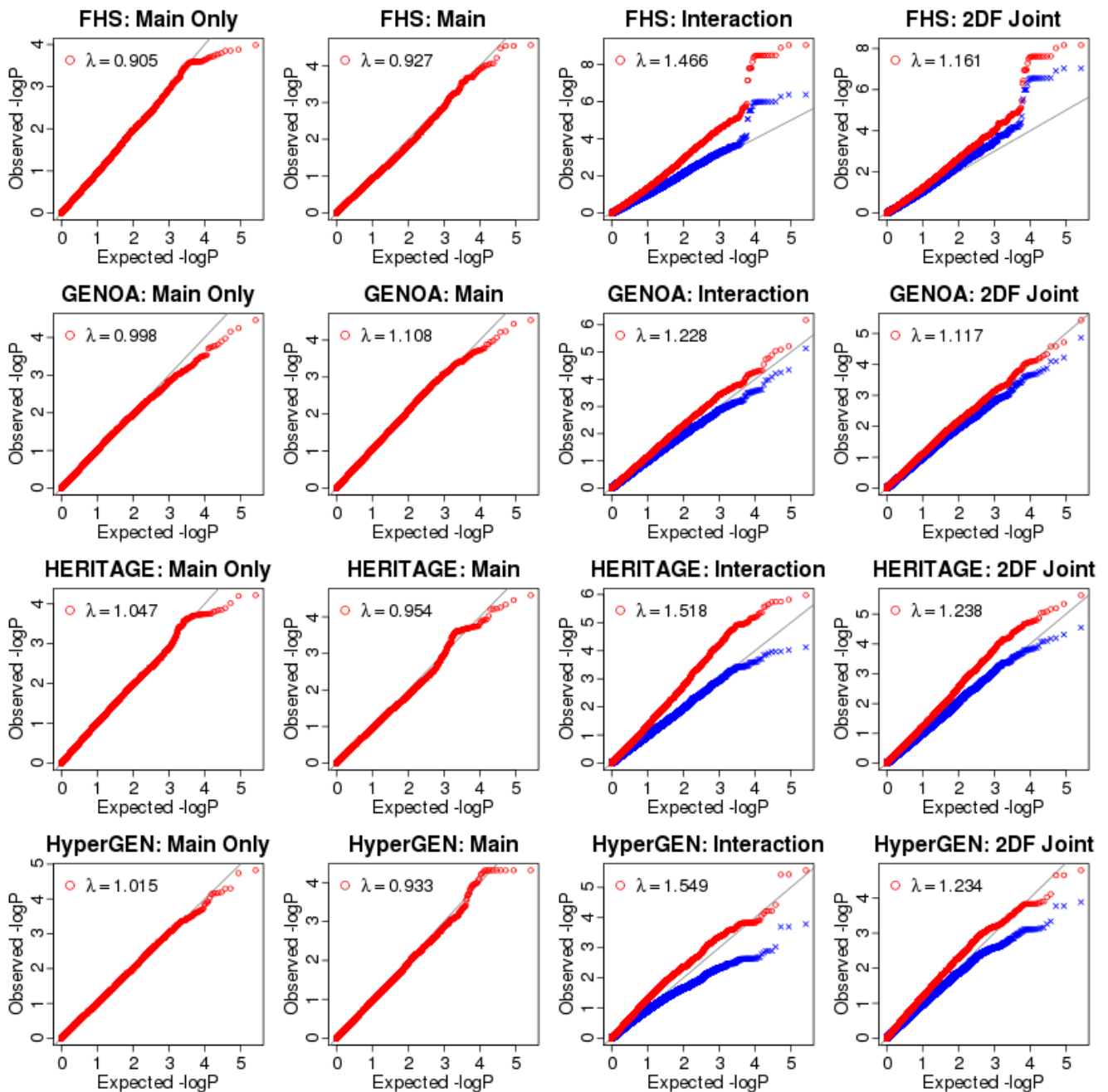
An Empirical Comparison of Meta-analysis and Mega-analysis of Individual Participant Data for Identifying Gene-Environment Interactions: Supplementary Materials

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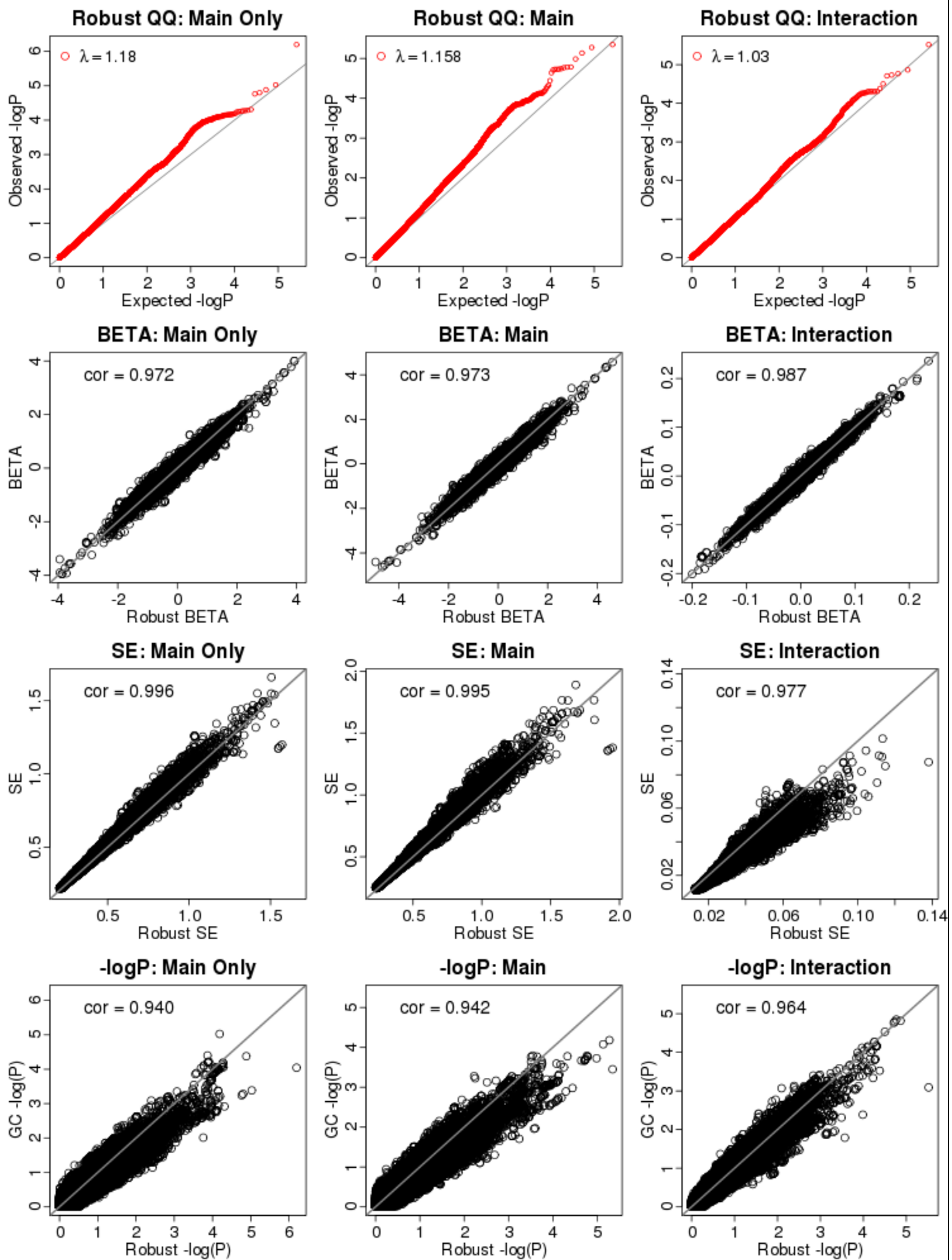
Supplemental Table I. Summary statistics of $-\log(P)$ differences between mega- and meta-analysis.

	Analysis	Minimum	1st Quartile	Median	Mean	3rd Quartile	Max.
Mega vs. Meta	1df Main Only	-1.433	-0.098	0.009	0.016	0.125	1.810
	1 df Main	-1.254	-0.101	0.010	0.017	0.128	2.056
	1 df Interaction	-1.826	-0.131	0.003	0.006	0.139	1.847
	2 df Joint	-1.711	-0.101	0.009	0.014	0.122	1.790
Mega-GC vs. Meta-GC	1df Main Only	-1.525	-0.112	-0.002	-0.003	0.109	1.682
	1 df Main	-1.370	-0.120	-0.001	-0.002	0.115	2.021
	1 df Interaction	-1.304	-0.102	0.002	0.003	0.107	1.321
	2 df Joint	-1.605	-0.102	-0.002	-0.007	0.088	1.368

For Mega-GC and Meta-GC, GC correction was applied after mega-analysis and meta-analysis, respectively.



Supplemental Figure I. Study-specific quantile-quantile (QQ) plots for the 4 analysis options: main effect only analysis (1st column), main effect in the presence of interaction (2nd column), interaction in the presence of main effect (3rd column), and 2 df joint test of main and interaction effects (4th column). The red circle points are p-values and the blue cross points are genomic controlled p-values. The genomic control value for the blue cross points is 1. QQ plots for meta- and mega-analyses are shown in Figure III.



Supplemental Figure II. Results using the robust option in ProbABEL: QQ plots (1st row), comparison of effect size estimates (2nd row) and standard errors (3rd row) between the regular analysis and robust analysis. The comparison of $-\log(P)$ values between the genomic controlled and robust analysis are shown in the 4th row.