

Study	Data-type	p_1, p_2	p_{12}	Notes
44	eQTL-methQTL	empirical ¹	empirical ²	
27	GWAS-eQTL	default	default	MS lead SNPs with eQTL signals; independent snps in each region
43	GWAS-molQTL	default	default	
36	GWAS-eQTL	default	default	
25	GWAS-methQTL	default	default	
40	GWAS-GWAS ³	default	default	tested in 50kb windows around each of 6472 snps in HLA region
24	GWAS-chromQTL	default	empirical ⁴	
20	GWAS-eQTL	default	default	post-TWAS;
28	GWAS-eQTL ⁵	default	default	45 reQTL samples only
29	GWAS-eQTL	default	default	
32	GWAS-methQTL	default	default	
26	GWAS-eQTL			
33	GWAS-eQTL			
35	eQTL-pQTL			
41	GWAS-eQTL	gwas-pw ⁵⁰	gwas-pw ⁵⁰	implemented in coloc2 https://github.com/Stahl-Lab-MSSM/coloc2
23	GWAS-eQTL			
31	GWAS-eQTL	not stated	not stated	
39	GWAS-eQTL	not stated	not stated	used to confirm primary SMR analysis
38	GWAS-eQTL	default	default	
21	GWAS-eQTL	default	default	
22	GWAS-chromQTL	not stated	not stated	

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Table S1: Applied studies which used coloc in 2018

¹set by #indep signals/#tests

²considered range of p12 and compared prior mean of H4 to posterior mean of H4

³pediatric vs adult disease

⁴The default prior on sharing ($P = 1 \times 10^5$) was used for all primary analyses, with priors $P = 1 \times 10^{-4}$ and $P = 1 \times 10^3$ evaluated separately with all other parameters unchanged.

⁵response eQTL

Study	Data-type	p_1, p_2	p_{12}	Notes
³⁷	GWAS-pQTL	default	default	
⁴²	eQTL-pQTL	estimated ⁶	$p_{12}/(p_{12}+p_1)=0.75$	used data to inform p_1, p_2 . used conditioning and prior beliefs to inform p_{12}
³⁰	GWAS-eQTL	not stated	not stated	
³⁴	GWAS-eQTL	default	default	

Table S1: Applied studies which used coloc in 2018. eQTL = expression QTL; mQTL = methylation QTL; pQTL = protein QTL; chromQTL = chromatin mark QTL; molQTL = selection of molecular QTLs

⁶#eqtl or #pqt1 snps/number tested