

a Complex diseases and traits

Biobank Japan (BBJ)
79 complex traits

Japanese
($n = 178,726$)

FinnGen (FG) release 6
67 complex traits

Finnish
($n = 271,341$)

UK Biobank (UKBB)
119 complex traits

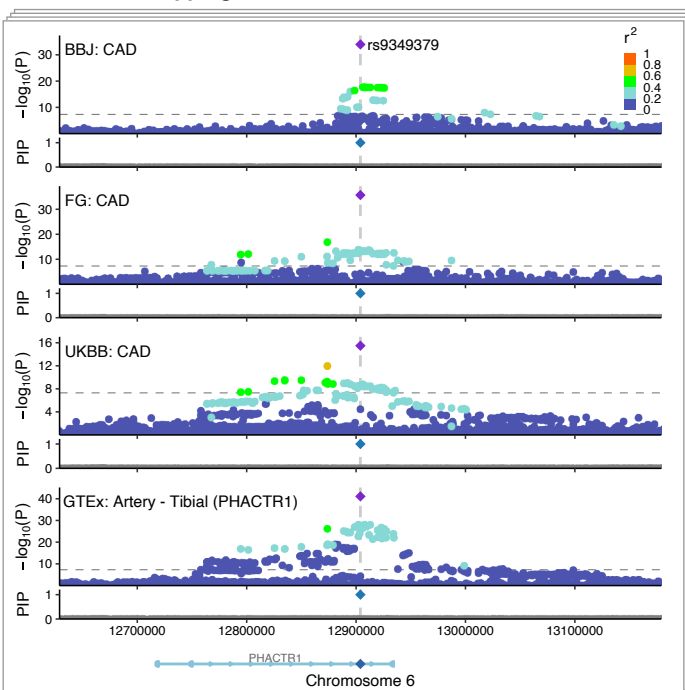
White British
($n = 361,194$)

Expression QTL (*cis*-eQTL)

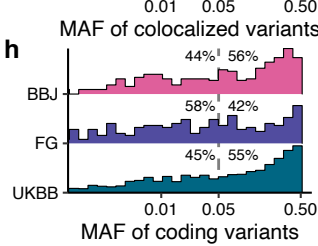
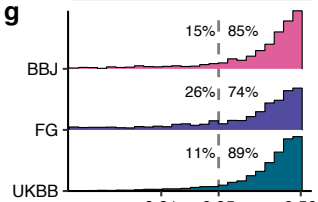
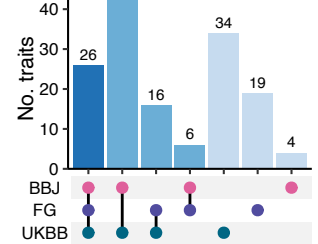
GTEx v8 eQTL Catalogue r^2
49 tissues 66 cell types/tissues

Predominantly Europeans
($n_{\text{donors}} = 5,714$)

b Atlas of fine-mapping and *cis*-eQTL colocalization



c No. traits



c BBJ

BBJ					
1		2		3 4 ≥5	
1,765			405	116573	
3,558 independent 95% CS in 2,406 regions of 79 traits					
1	2-5	6-10	11-20	21-50	>50
479	773	473	586	668	579
2,979 CS of 79 traits fine-mapped to ≤50 variants					
>90%	50-90%	10-50%		1-10%	≤1%
471	416	1,407		1,103	161
2,294 CS of 79 traits have a variant with PIP >10%					
>90%50-90%		10-50%			
476	455	5,397			
6,328 variant-trait pairs have PIP >10%					

d FG

FG	1	2	3	4	≥5
	1,071	266	93	35	52
2,348 independent 95% CS in 1,517 regions of 67 traits					
1	2-5	6-10	11-20	21-50	>50
343	534	375	393	440	263
2,085 CS of 67 traits fine-mapped to ≤50 variants					
>90%	50-90%	10-50%	1-10%	≤1%	
337	188	936	730	157	
1,461 CS of 63 traits have a variant with PIP >10%					
>90%	50-90%	10-50%			
342	232	3,774			
4,348 variant-trait pairs have PIP >10%					

e UKBB

UKBB	1	2	3	4	≥5
	6,640	2,861	1,450	763	1,145
27,276 independent 95% CS in 12,859 regions of 119 traits					
1	2-5	6-10	11-20	21-50	>50
3,835	5,459	3,574	4,138	5,350	4,920
22,356 CS of 119 traits fine-mapped to ≤50 variants					
>90%	50-90%	10-50%	1-10%	≤1%	
3,670	2,456	10,667	8,902	1,581	
16,793 CS of 117 traits have a variant with PIP >10%					
>90%	50-90%	10-50%			
3,846	2,935	39,184			
45,965 variant-trait pairs have PIP >10%					

f Colocalization

>90%	50-90%	10-50%	1-10%
14,151	6,033	7,054	1,441
27,238 genes have an eQTL variant with PIP >10% in ≥1 tissue(s)			
>90%50-90%	10-50%		
29,448	41,671	364,054	
435,173 variants have PIP >10% in ≥1 tissue(s)			
>90%	50-90%	10-50%	
712	440	2,785	
3,937 gene-trait pairs have an eQTL variant with coloc PIP >10% in ≥1 tissue(s)			
>90%	50-90%	10-50%	
720	445	3,792	
4,957 variant-trait-gene triples have coloc PIP >10% in ≥1 tissue(s)			