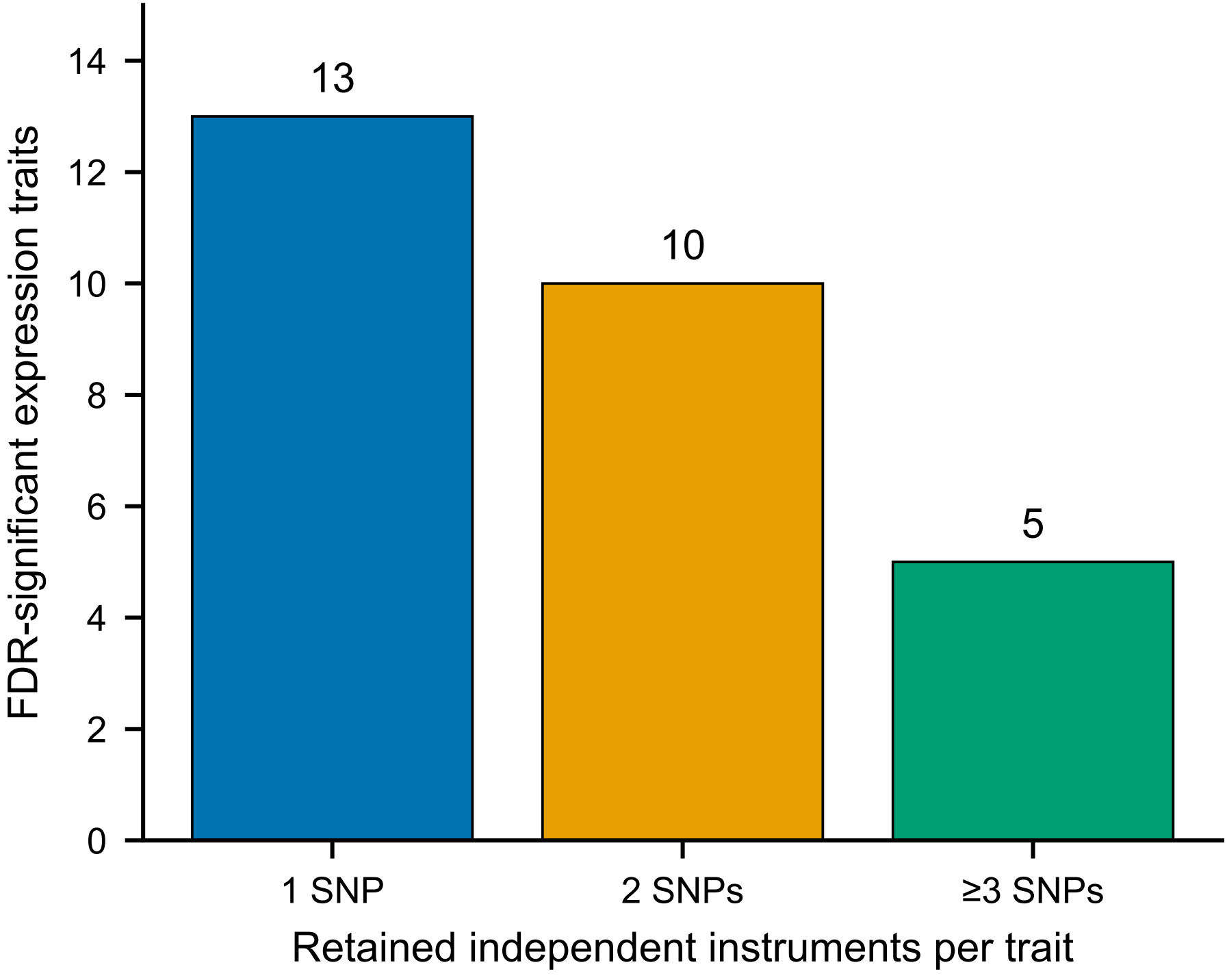
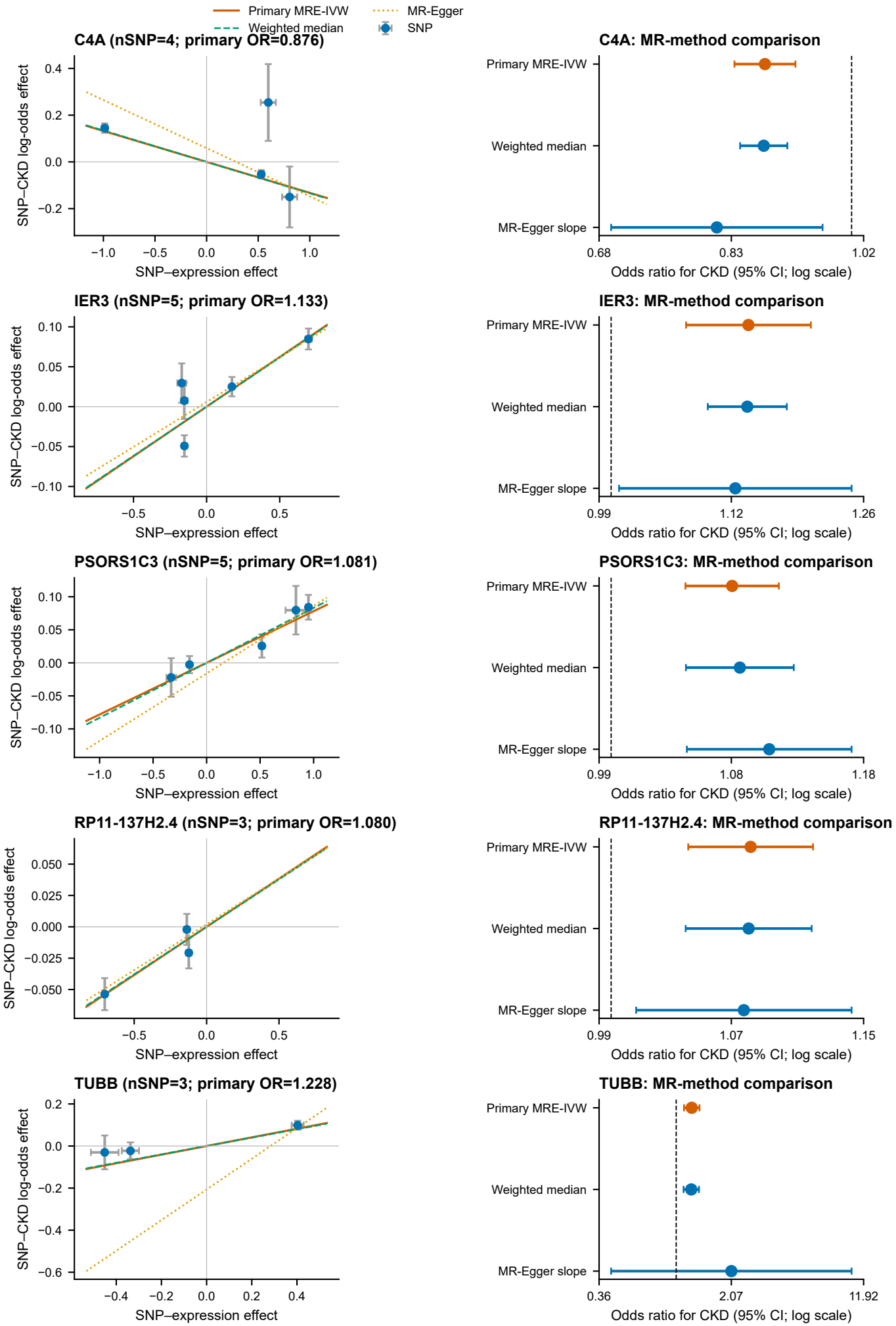
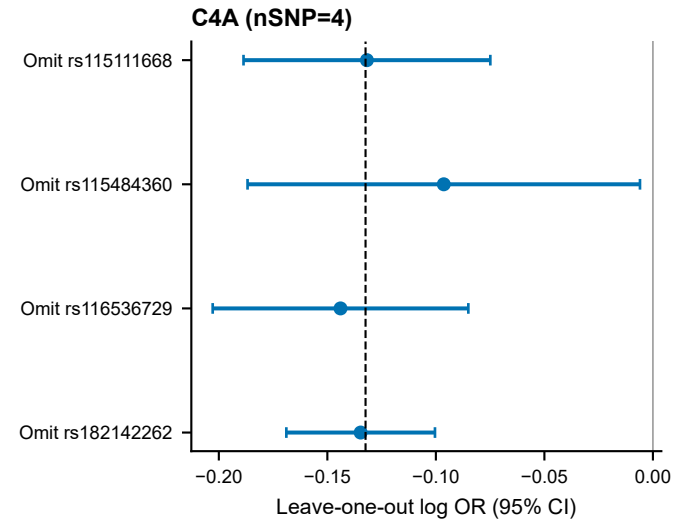
Supplementary Figure S1. Instrument-count distribution

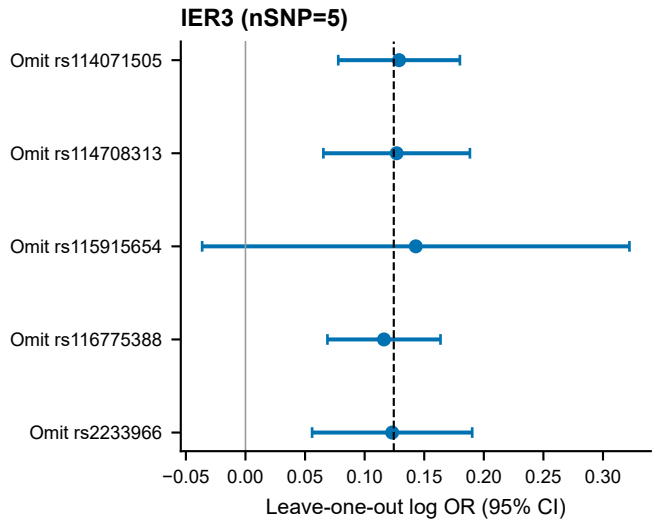


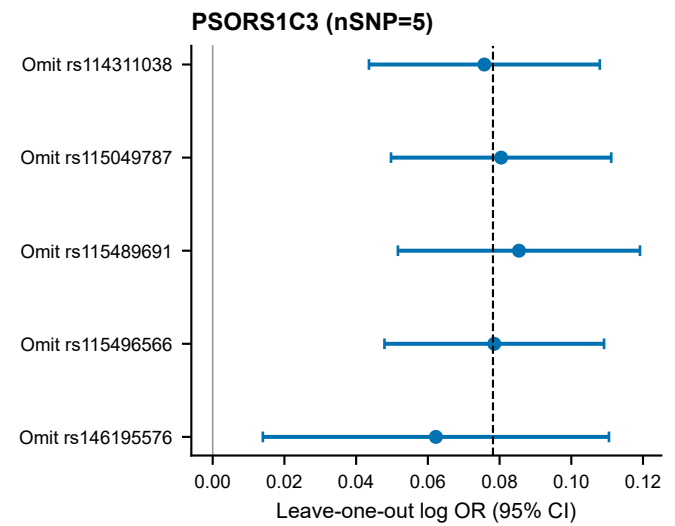
Supplementary Figure S2. MR scatter plots and MR-method comparisons

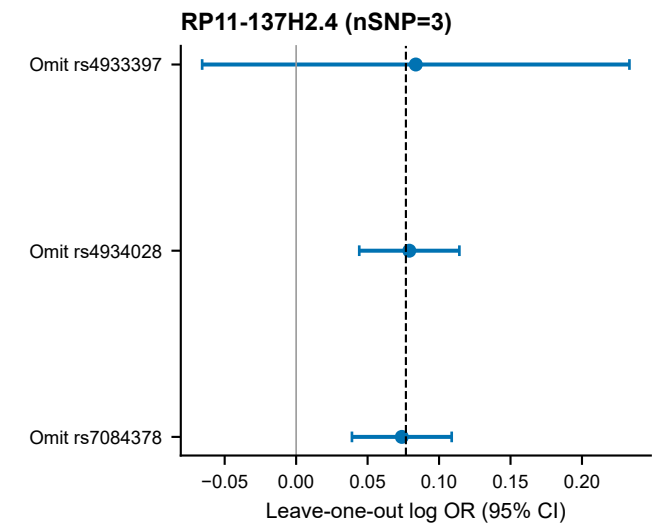


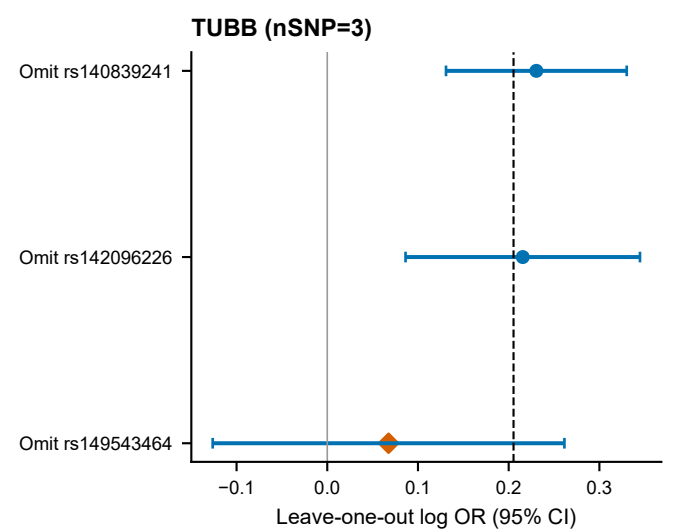
Supplementary Figure S3. Leave-one-out analyses



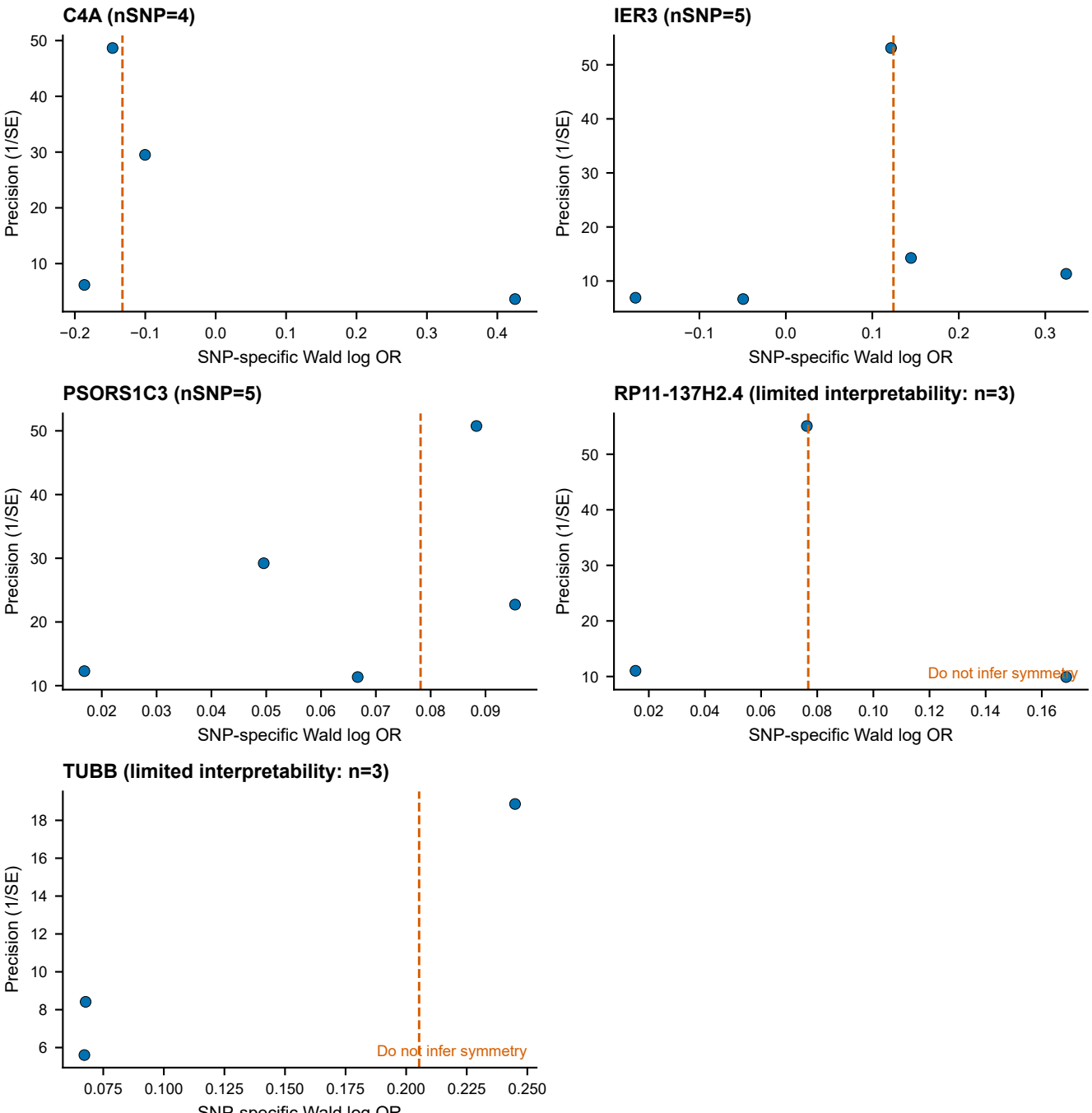




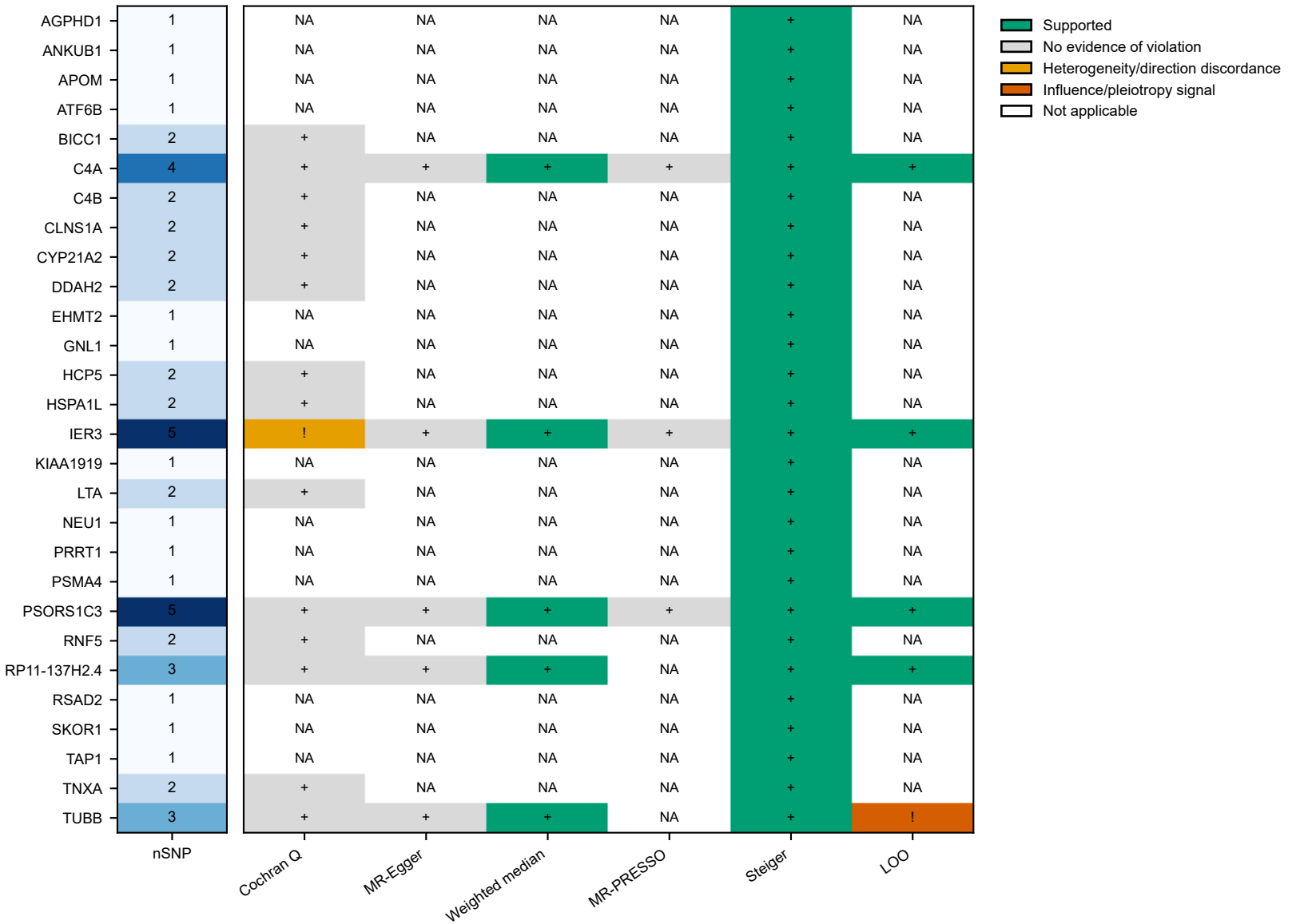




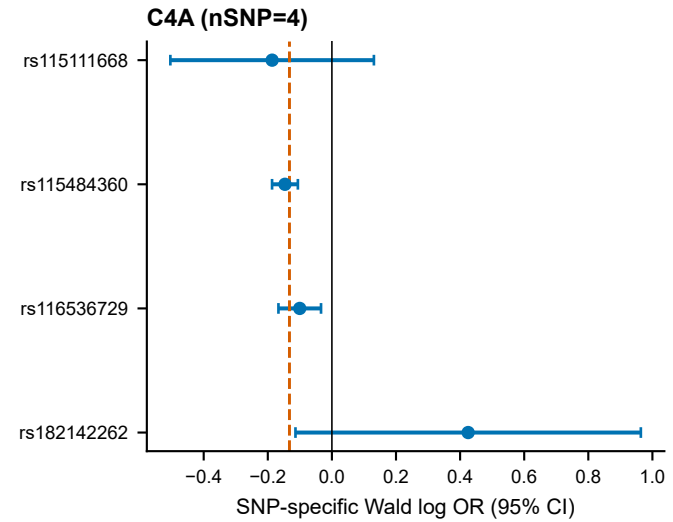
Supplementary Figure S4. Funnel plots for eligible multi-instrument traits

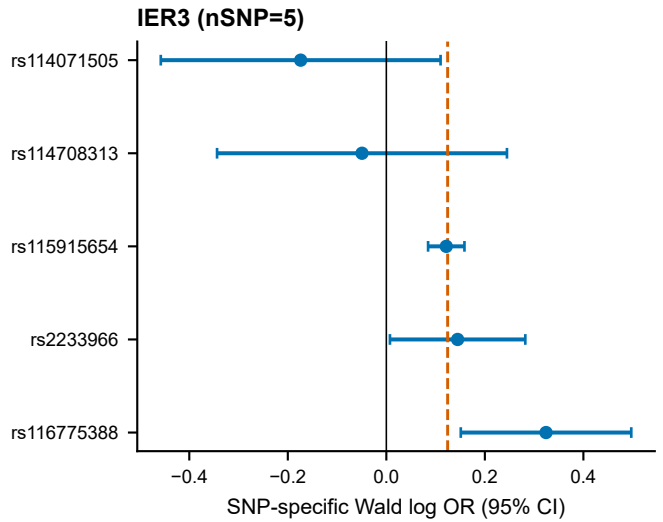


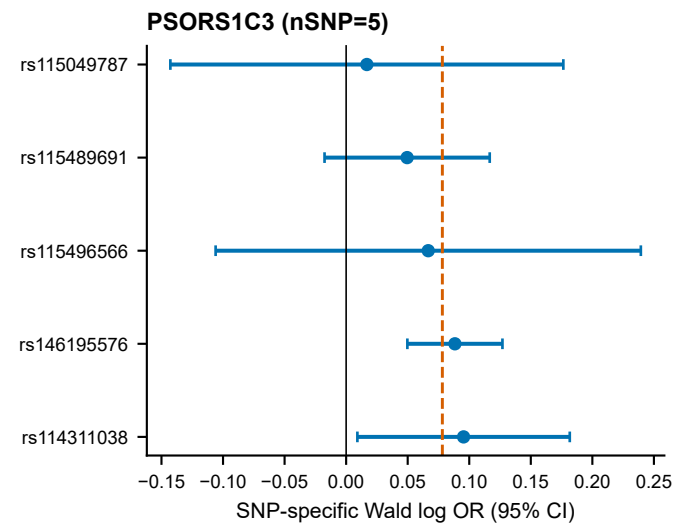
Supplementary Figure S5. MR sensitivity matrix for all 28 FDR-significant traits

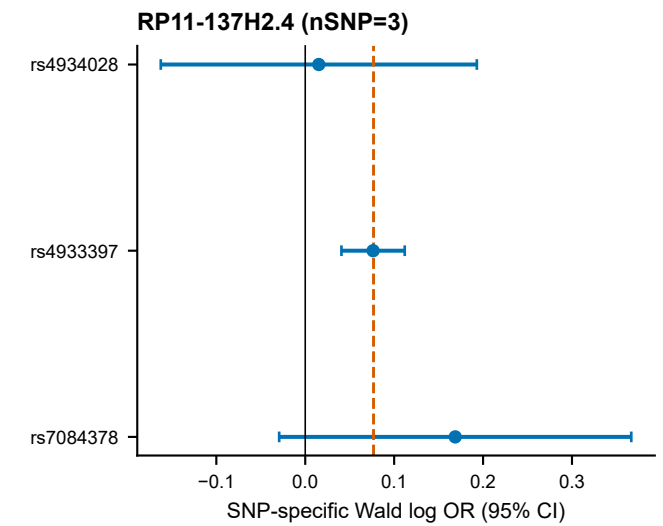


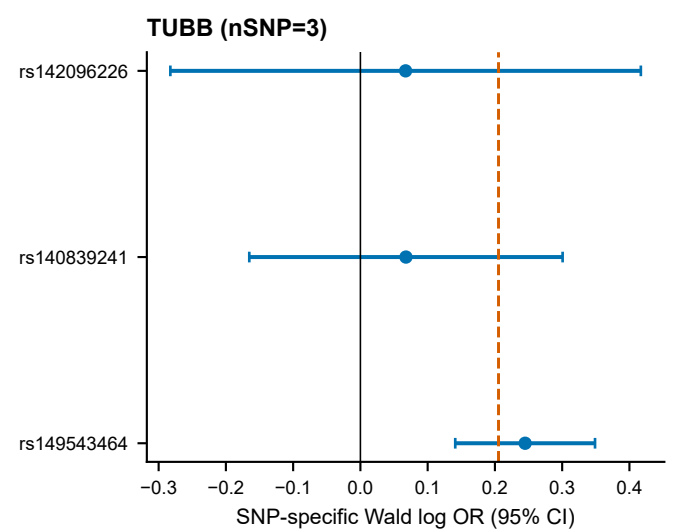
Supplementary Figure S6. SNP-level MR forest plots for eligible multi-instrument traits

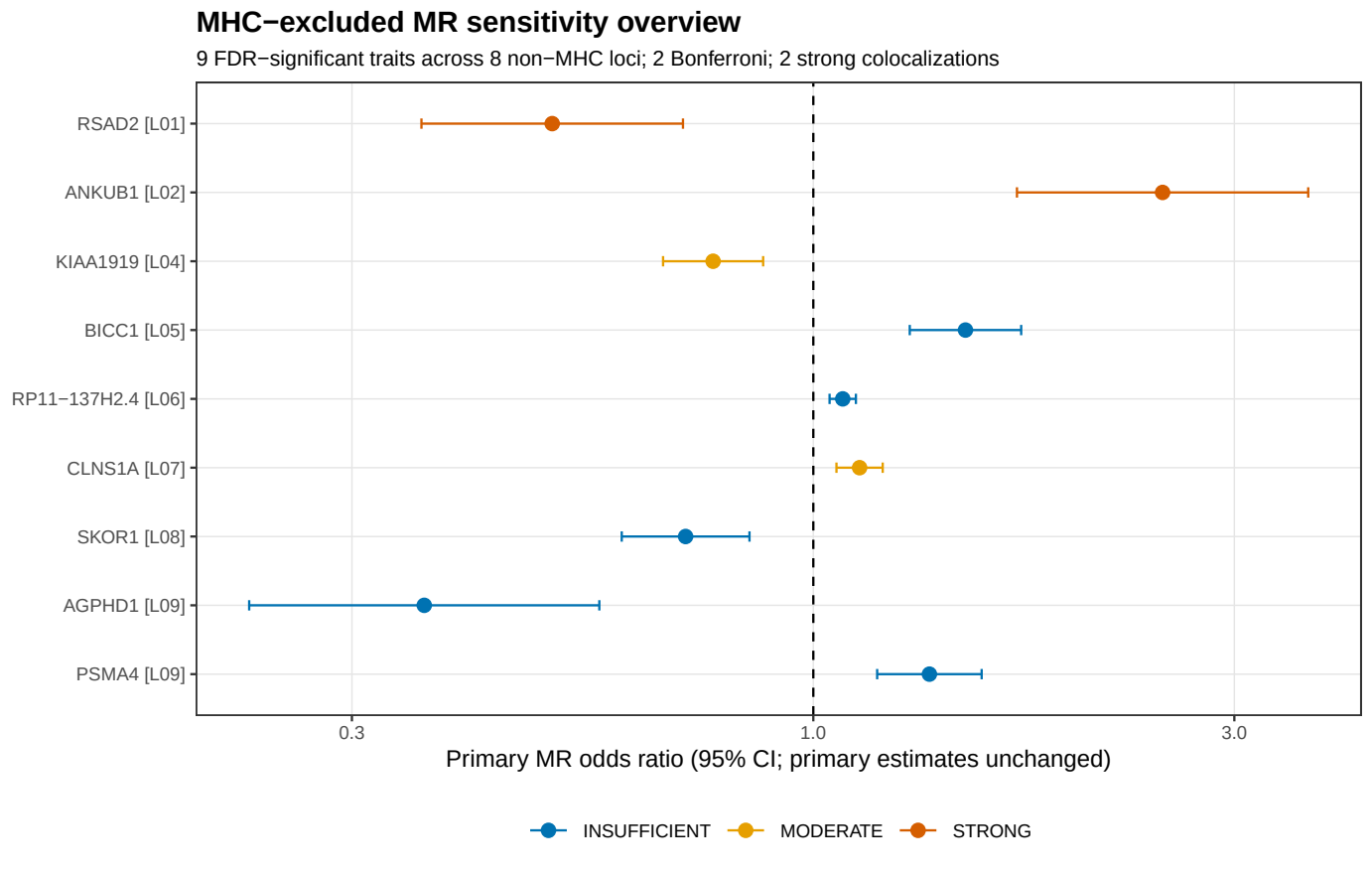


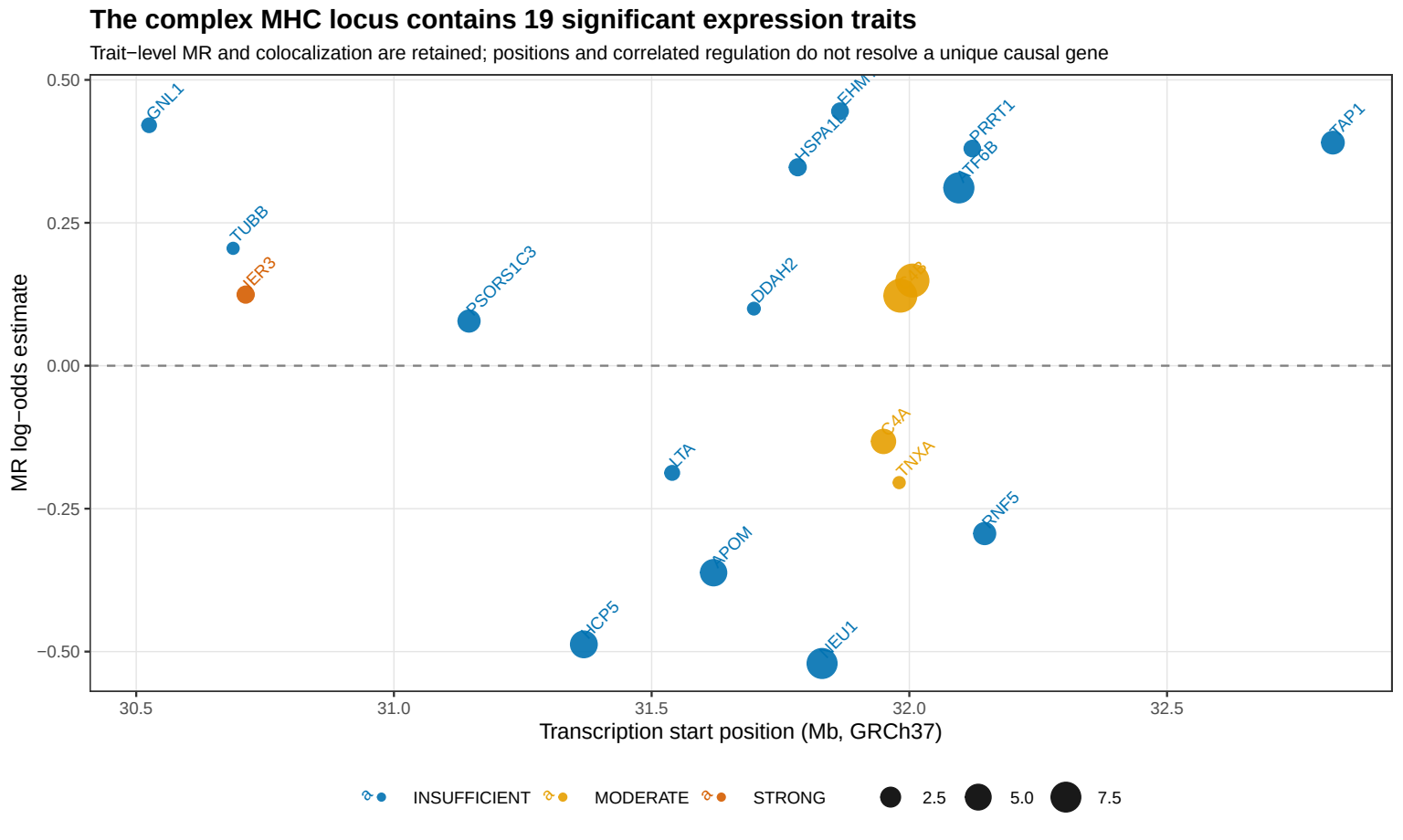


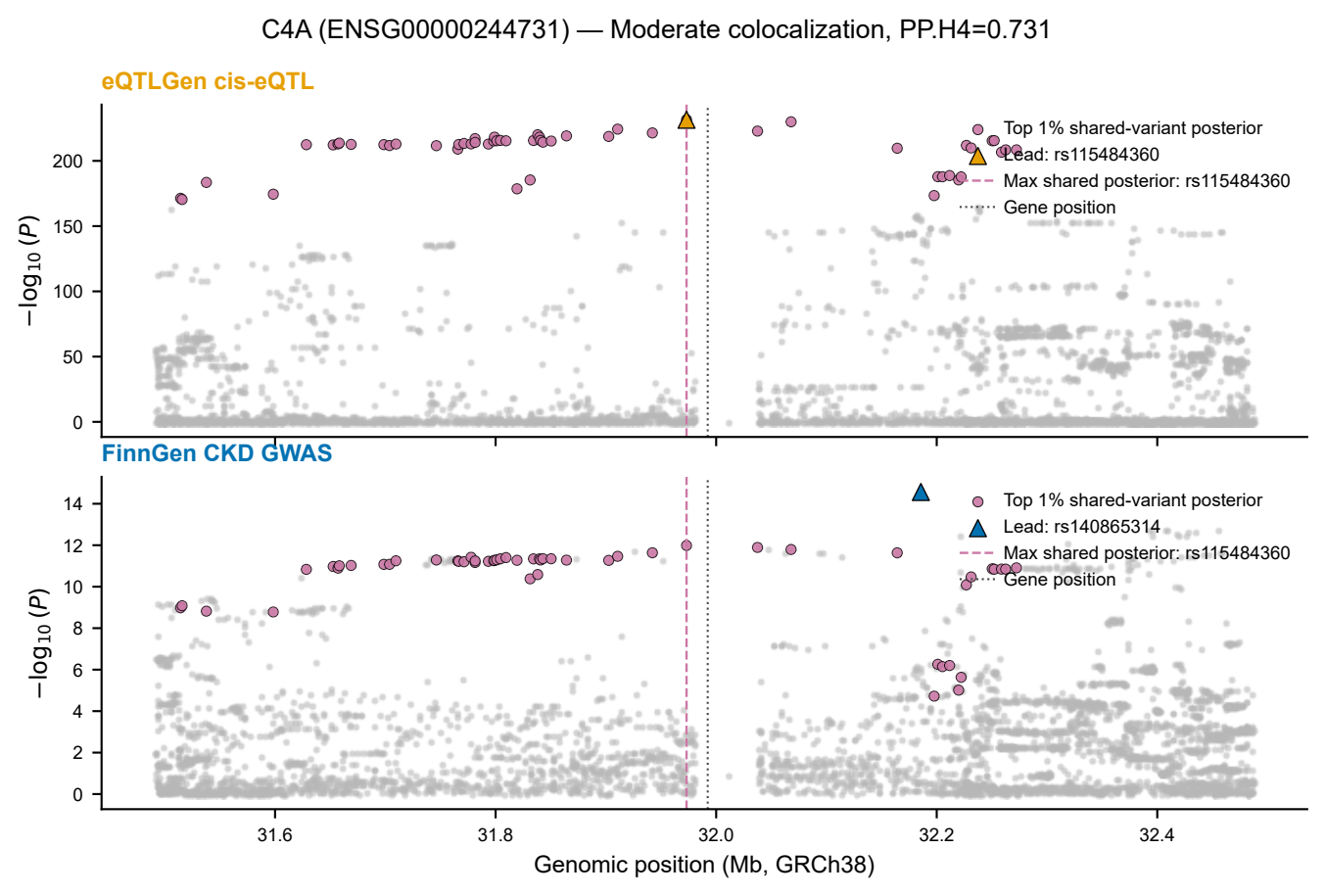


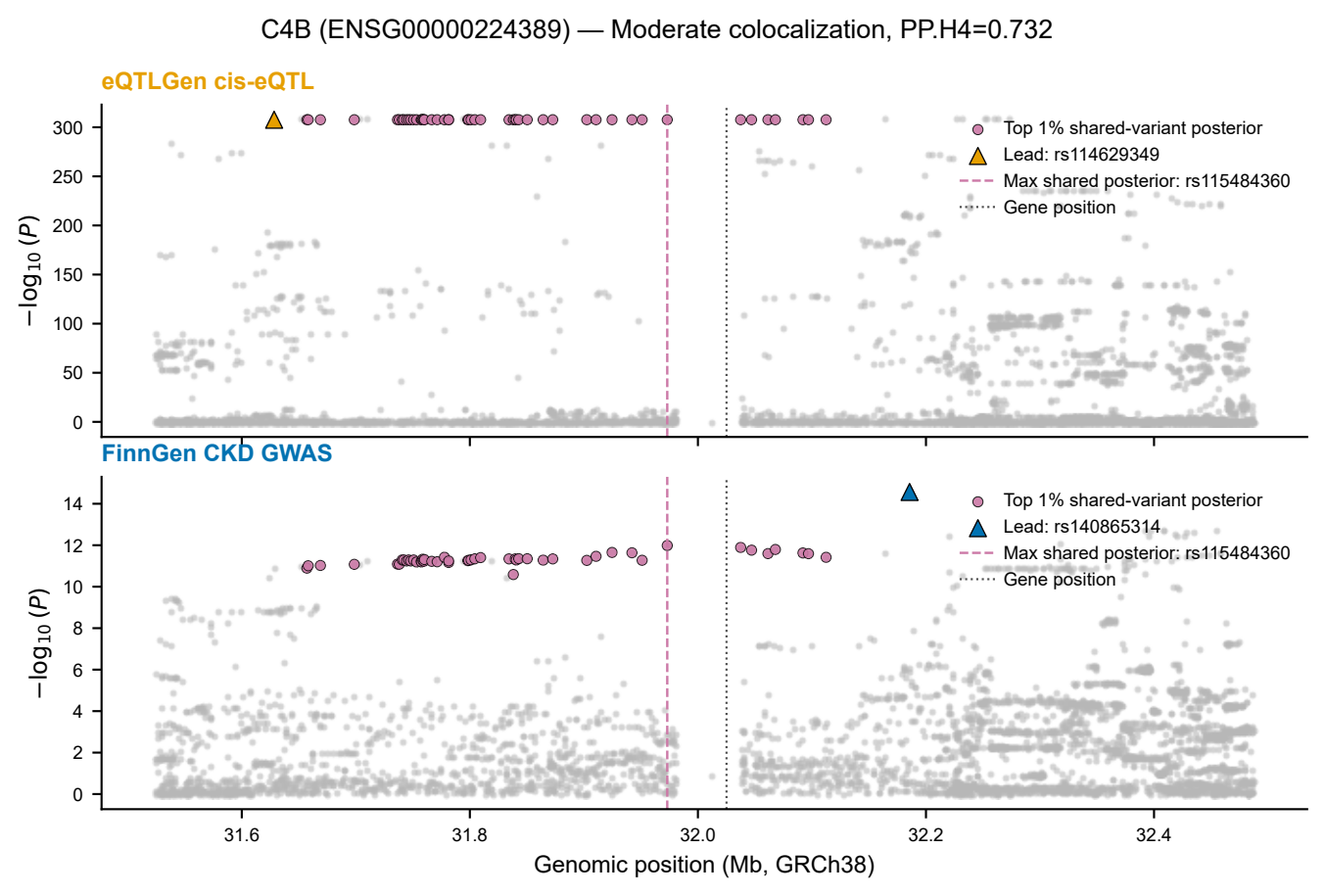


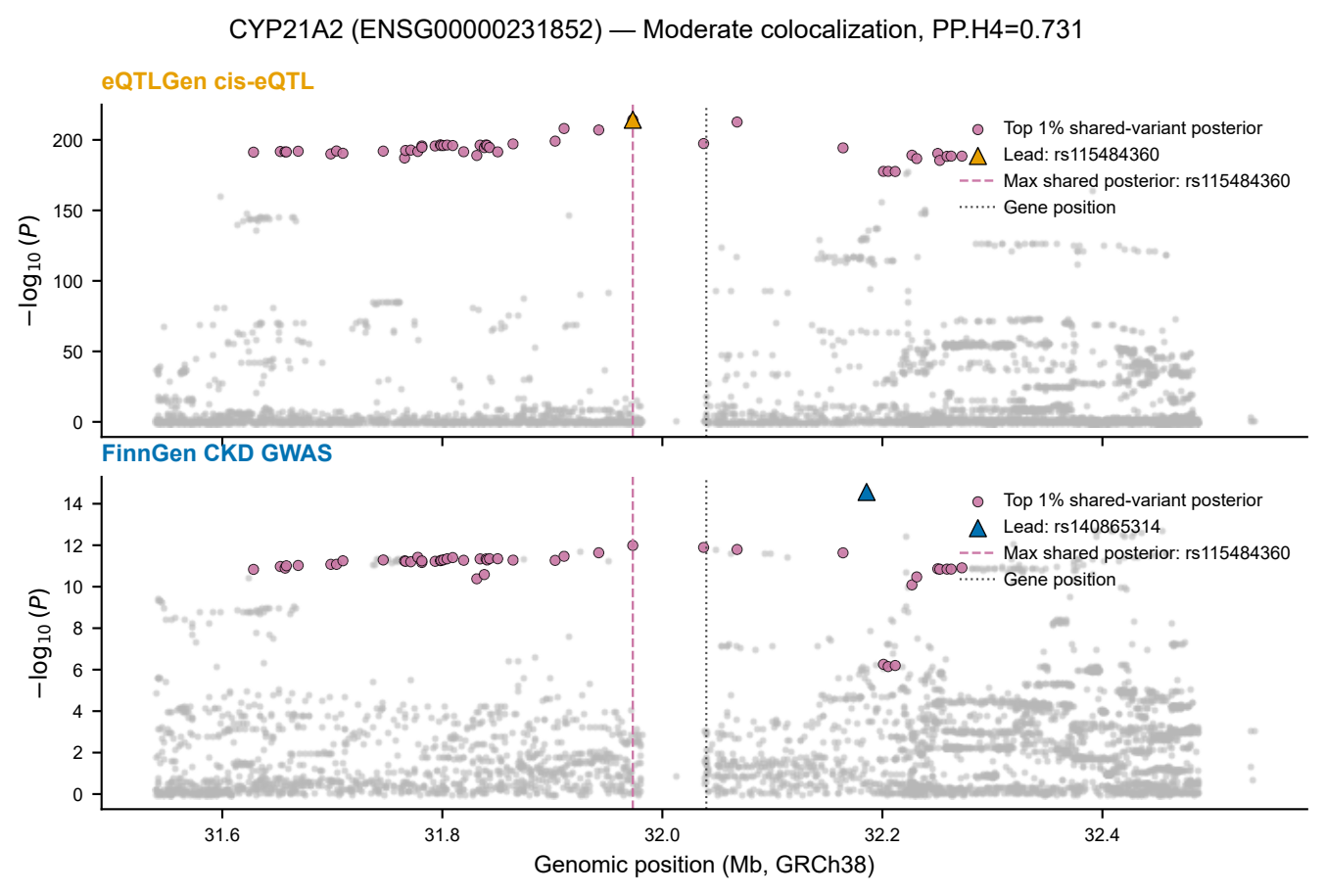


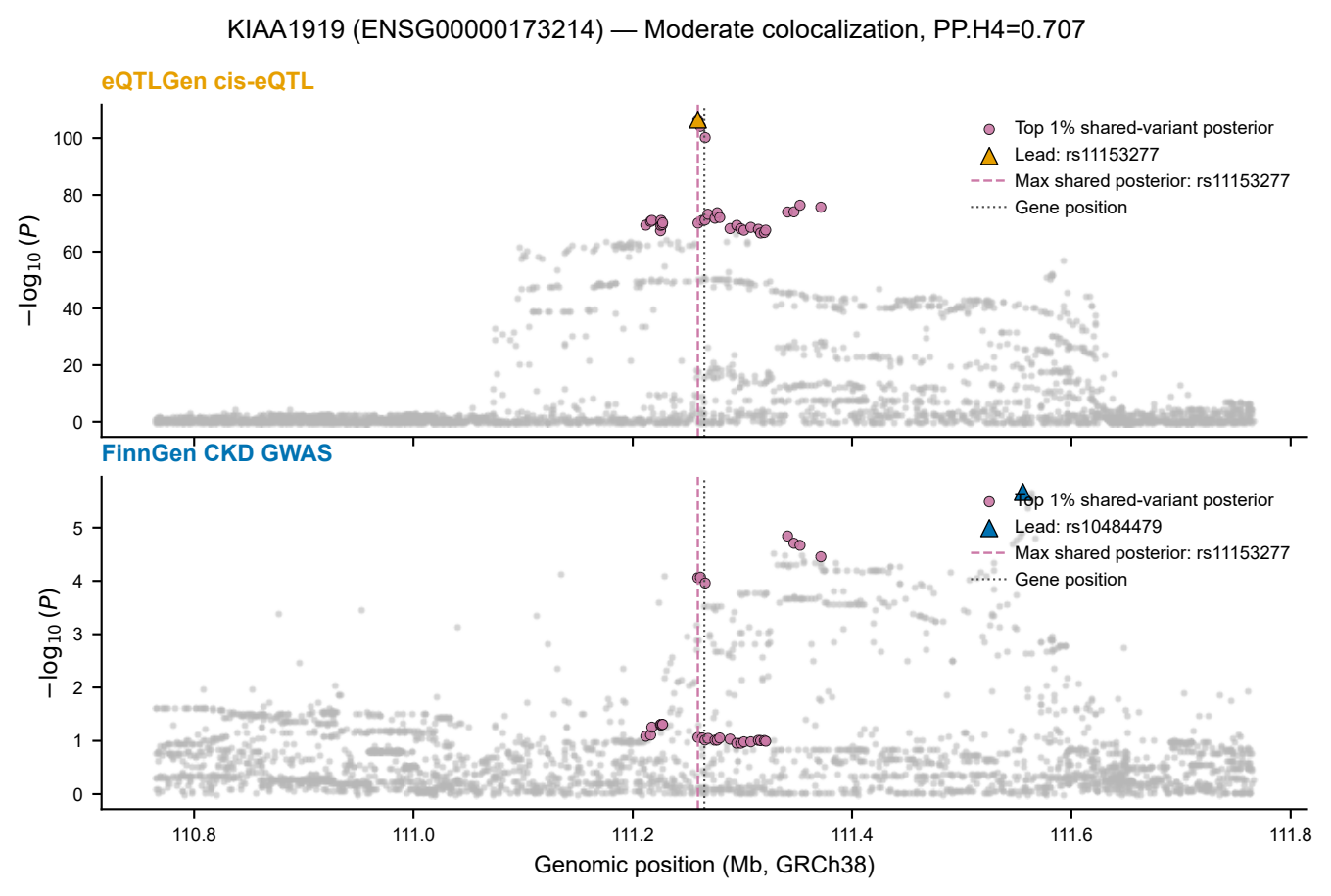

MHC−excluded MR sensitivity overview
9 FDR−significant traits across 8 non−MHC loci; 2 Bonferroni; 2 strong colocalizations
RSAD2 [L01]
ANKUB1 [L02]
KIAA1919 [L04]
BICC1 [L05]
RP11−137H2.4 [L06]
CLNS1A [L07]
SKOR1 [L08]
AGPHD1 [L09]
PSMA4 [L09]
0.3
1.0
3.0
Primary MR odds ratio (95% CI; primary estimates unchanged)
INSUFFICIENT
MODERATE
STRONG

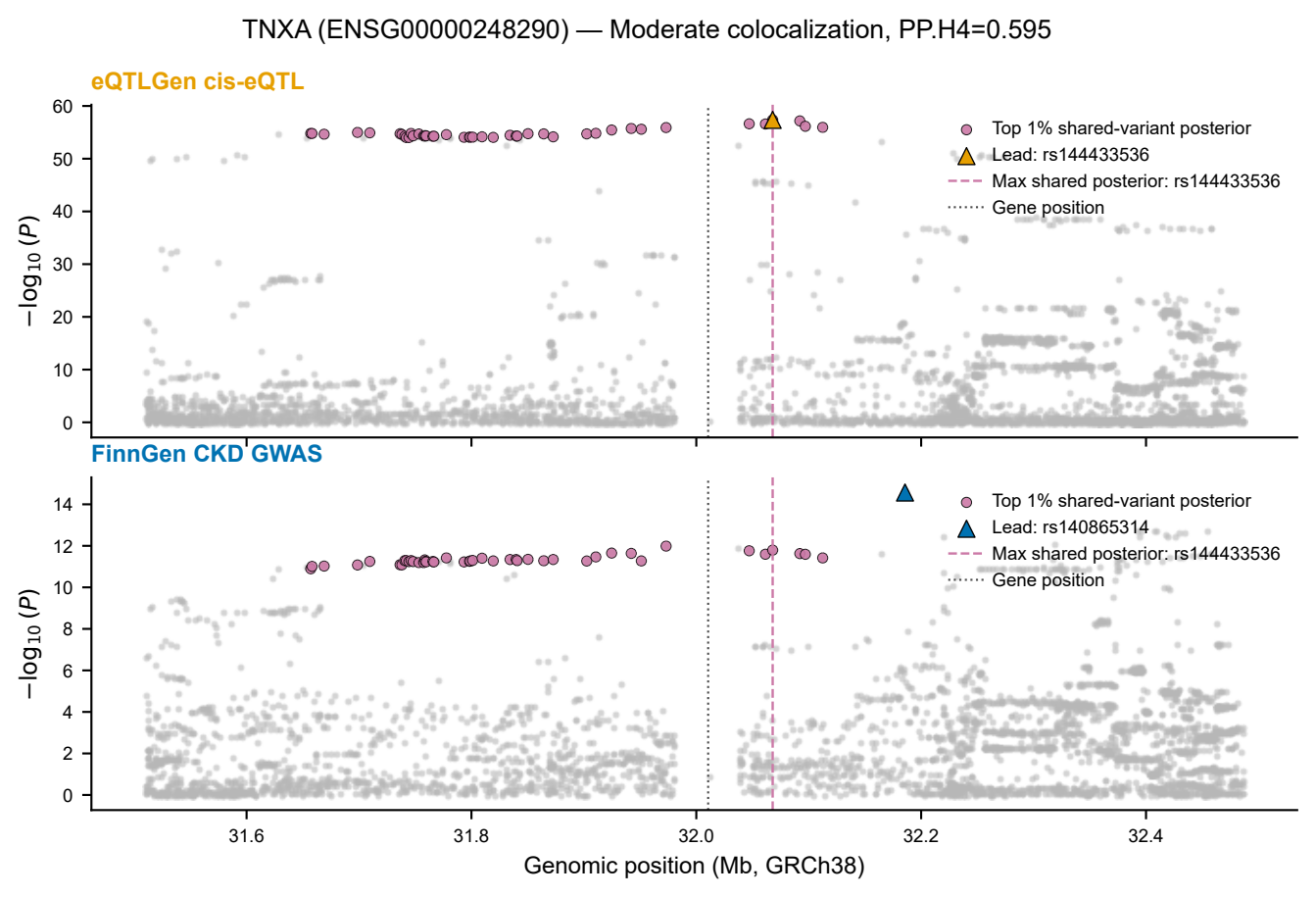

The complex MHC locus contains 19 significant expression traits
Trait−level MR and colocalization are retained; positions and correlated regulation do not resolve a unique causal gene
MR log−odds estimate
0.50
0.25
0.00
−0.25
−0.50
GNL1
TUBB
IER3
PSORS1C3
HSPA1B
EHMT2
DDAH2
PRRT1
ATF6B
TAP1
C4A
TNXA
LTA
RNF5
APOM
NCP5
NEU1
30.5
31.0
31.5
32.0
32.5
Transcription start position (Mb, GRCh37)
INSUFFICIENT
MODERATE
STRONG
2.5
5.0
7.5

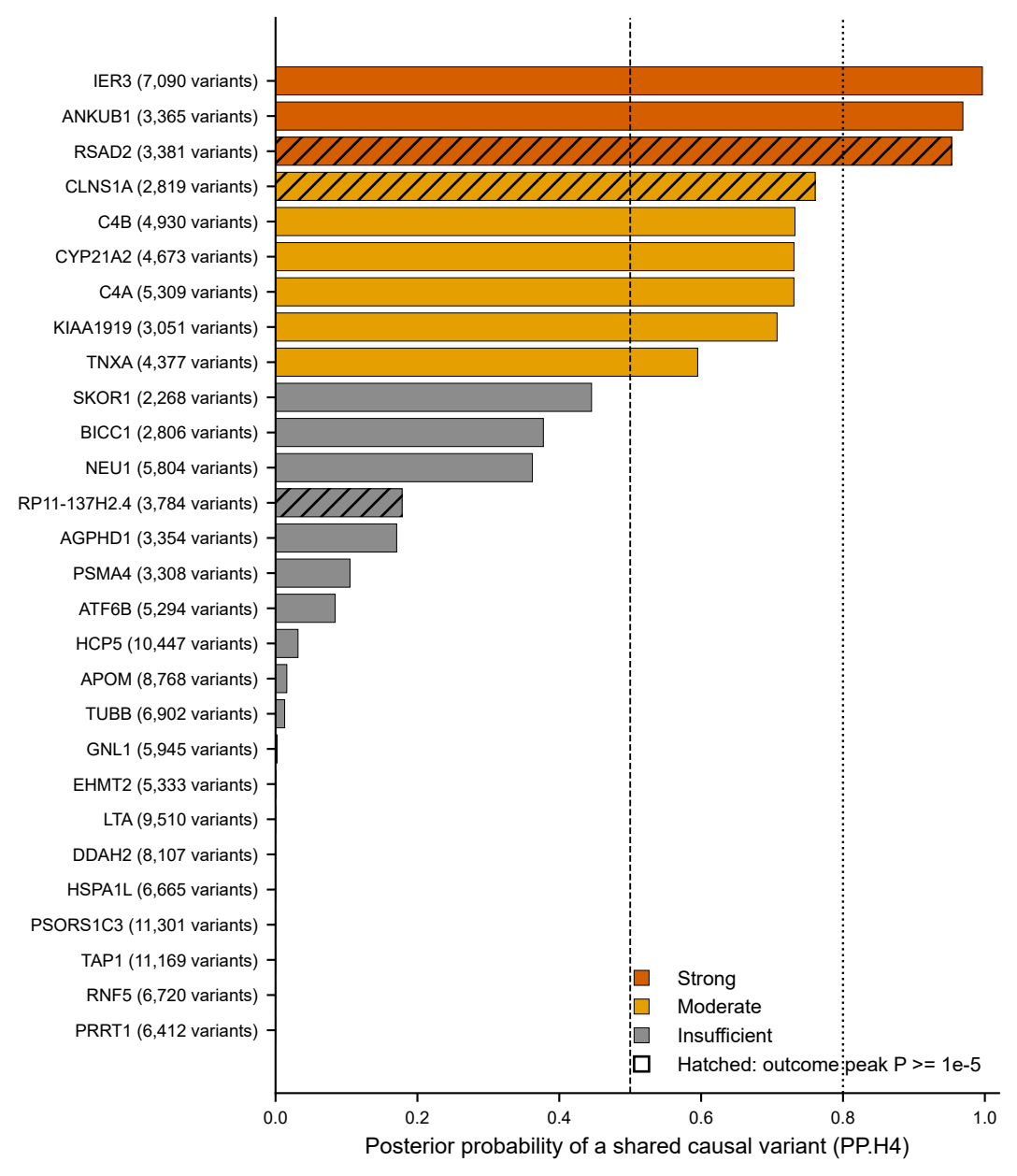

C4A (ENSG00000244731) — Moderate colocalization, PP.H4=0.731
eQTLGen cis-eQTL
−log10 (P)
Top 1% shared-variant posterior
Lead: rs115484360
Max shared posterior: rs115484360
Gene position
FinnGen CKD GWAS
−log10 (P)
Top 1% shared-variant posterior
Lead: rs140865314
Max shared posterior: rs115484360
Gene position
31.6
31.8
32.0
32.2
32.4
Genomic position (Mb, GRCh38)


C4B (ENSG00000224389) — Moderate colocalization, PP.H4=0.732
eQTLGen cis-eQTL
−log10 (P)
Top 1% shared-variant posterior
Lead: rs114629349
Max shared posterior: rs115484360
Gene position
FinnGen CKD GWAS
−log10 (P)
Top 1% shared-variant posterior
Lead: rs140865314
Max shared posterior: rs115484360
Gene position
31.6
31.8
32.0
32.2
32.4
Genomic position (Mb, GRCh38)

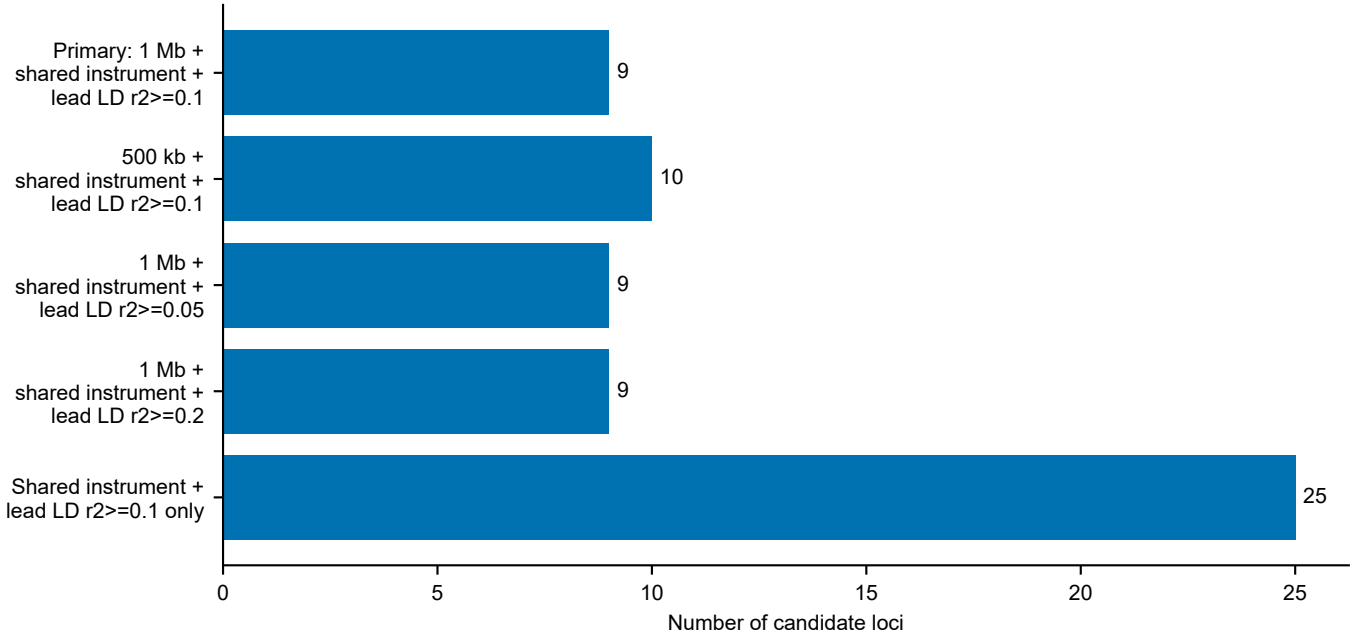

CYP21A2 (ENSG00000231852) — Moderate colocalization, PP.H4=0.731
eQTLGen cis-eQTL
−log10 (P)
Top 1% shared-variant posterior
Lead: rs115484360
Max shared posterior: rs115484360
Gene position
FinnGen CKD GWAS
−log10 (P)
Top 1% shared-variant posterior
Lead: rs140865314
Max shared posterior: rs115484360
Gene position
31.6
31.8
32.0
32.2
32.4
Genomic position (Mb, GRCh38)


KIAA1919 (ENSG00000173214) — Moderate colocalization, PP.H4=0.707
eQTLGen cis-eQTL
−log10 (P)
Top 1% shared-variant posterior
Lead: rs11153277
Max shared posterior: rs11153277
Gene position
FinnGen CKD GWAS
−log10 (P)
Top 1% shared-variant posterior
Lead: rs10484479
Max shared posterior: rs11153277
Gene position
110.8
111.0
111.2
111.4
111.6
111.8
Genomic position (Mb, GRCh38)


TNXA (ENSG00000248290) — Moderate colocalization, PP.H4=0.595
eQTLGen cis-eQTL
FinnGen CKD GWAS
Top 1% shared-variant posterior
Lead: rs144433536
Max shared posterior: rs144433536
Gene position
Top 1% shared-variant posterior
Lead: rs140865314
Max shared posterior: rs144433536
Gene position
−log10 (P)
−log10 (P)
Genomic position (Mb, GRCh38)
31.6
31.8
32.0
32.2
32.4

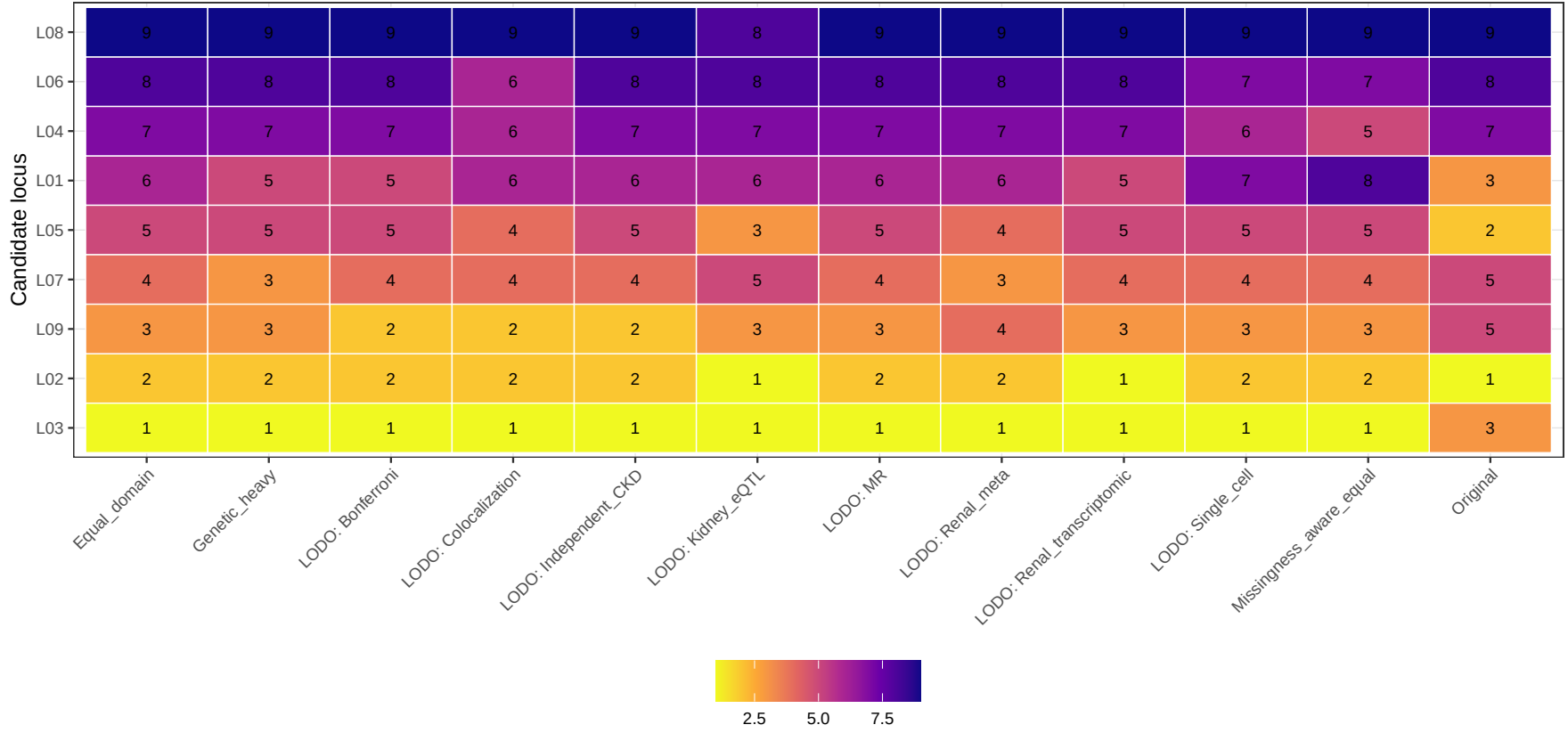

IER3 (7,090 variants)
ANKUB1 (3,365 variants)
RSAD2 (3,381 variants)
CLNS1A (2,819 variants)
C4B (4,930 variants)
CYP21A2 (4,673 variants)
C4A (5,309 variants)
KIAA1919 (3,051 variants)
TNXA (4,377 variants)
SKOR1 (2,268 variants)
BICC1 (2,806 variants)
NEU1 (5,804 variants)
RP11-137H2.4 (3,784 variants)
AGPHD1 (3,354 variants)
PSMA4 (3,308 variants)
ATF6B (5,294 variants)
HCP5 (10,447 variants)
APOM (8,768 variants)
TUBB (6,902 variants)
GNL1 (5,945 variants)
EHMT2 (5,333 variants)
LTA (9,510 variants)
DDAH2 (8,107 variants)
HSPA1L (6,665 variants)
PSORS1C3 (11,301 variants)
TAP1 (11,169 variants)
RNF5 (6,720 variants)
PRRT1 (6,412 variants)
Strong
Moderate
Insufficient
Hatched: outcome peak P >= 1e-5
0.0
0.2
0.4
0.6
0.8
1.0
Posterior probability of a shared causal variant (PP.H4)

Supplementary Figure S15. Locus-definition sensitivity

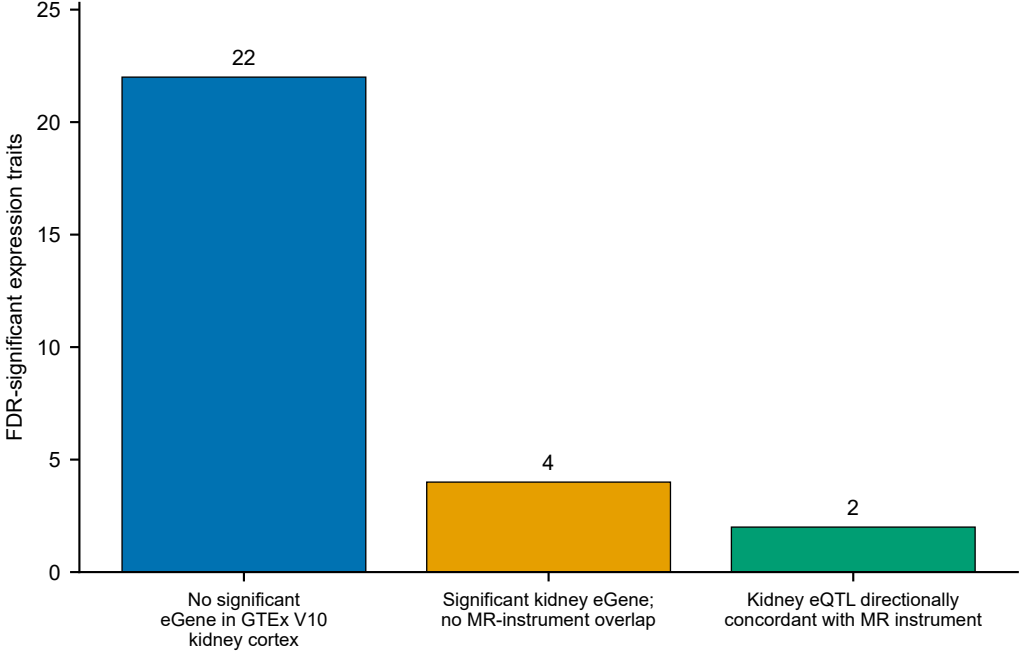


Locus−level evidence ranking is weighting−sensitive

Fixed ordinal rank claims are therefore not used

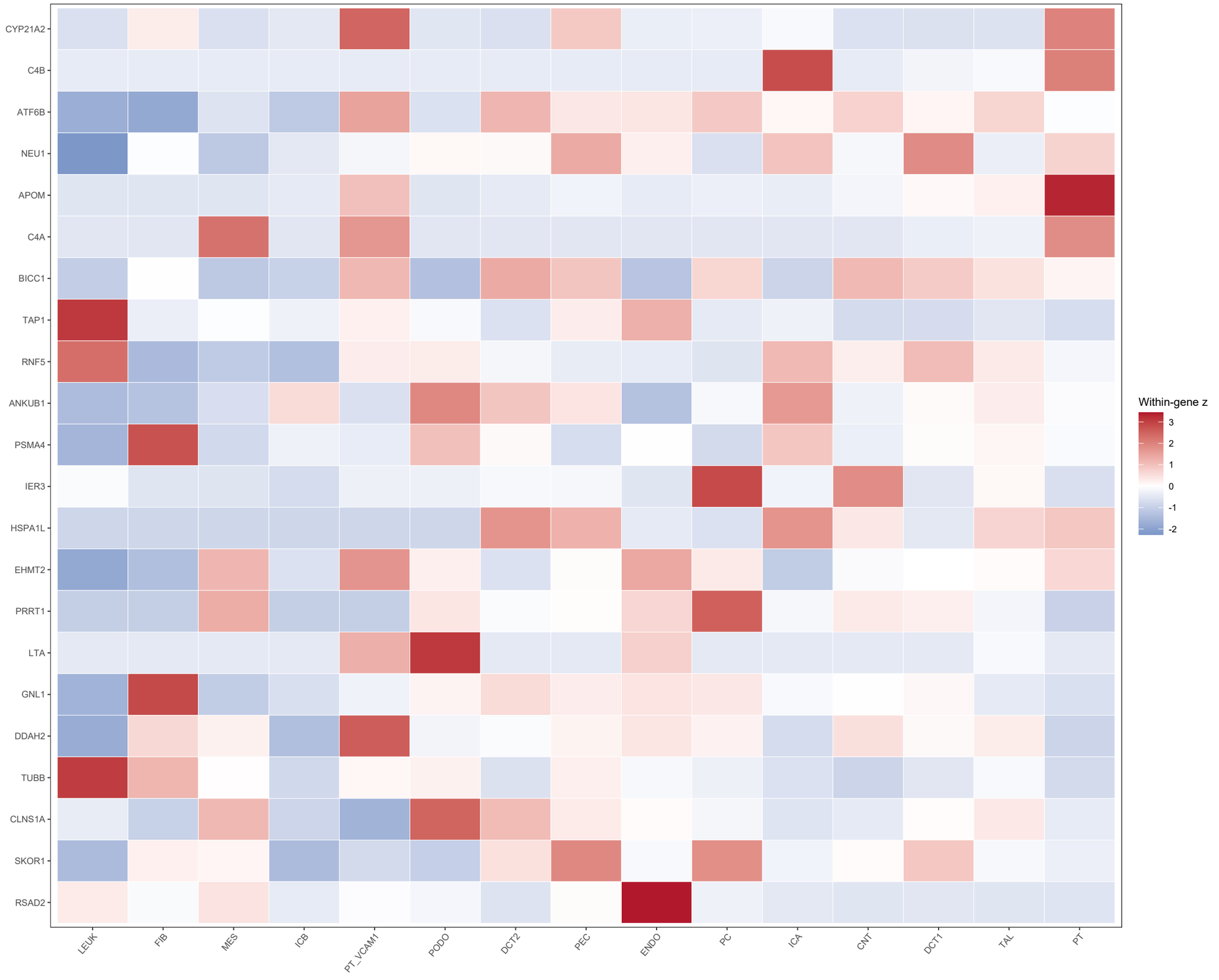


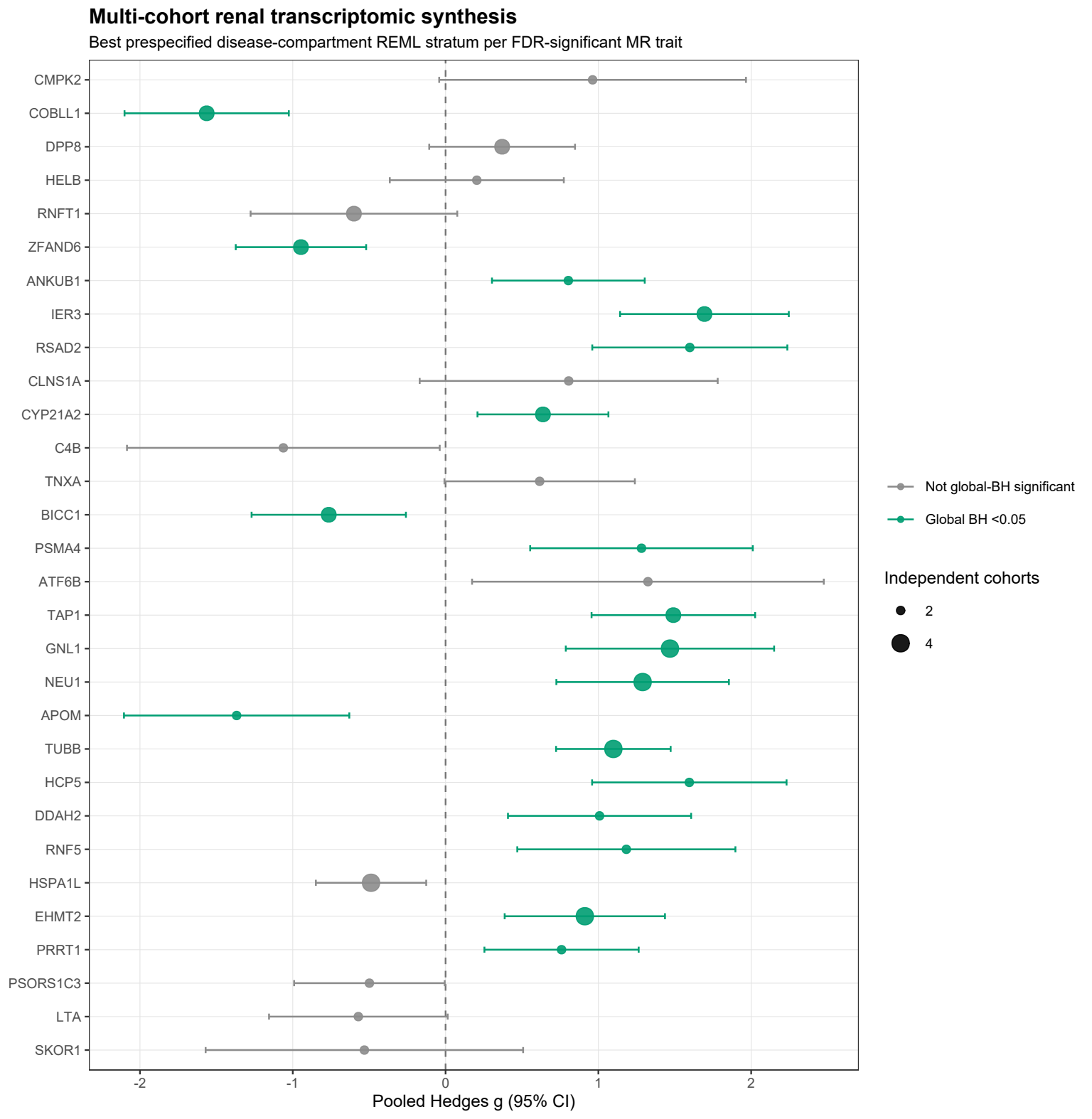
Supplementary Figure S17. GTEx V10 kidney-cortex eQTL support

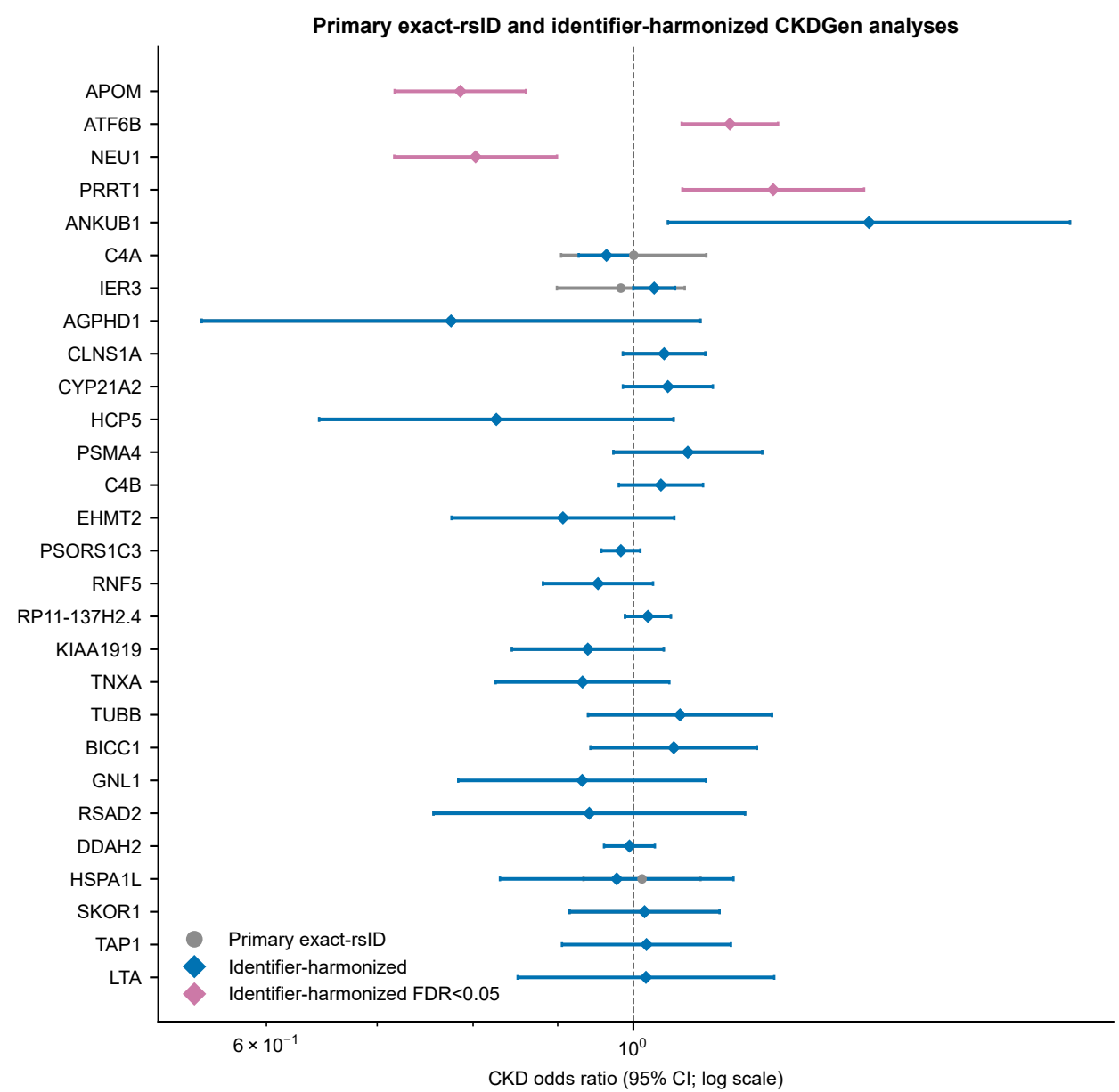


Corrected FDR28 expression localization across adult kidney cell types

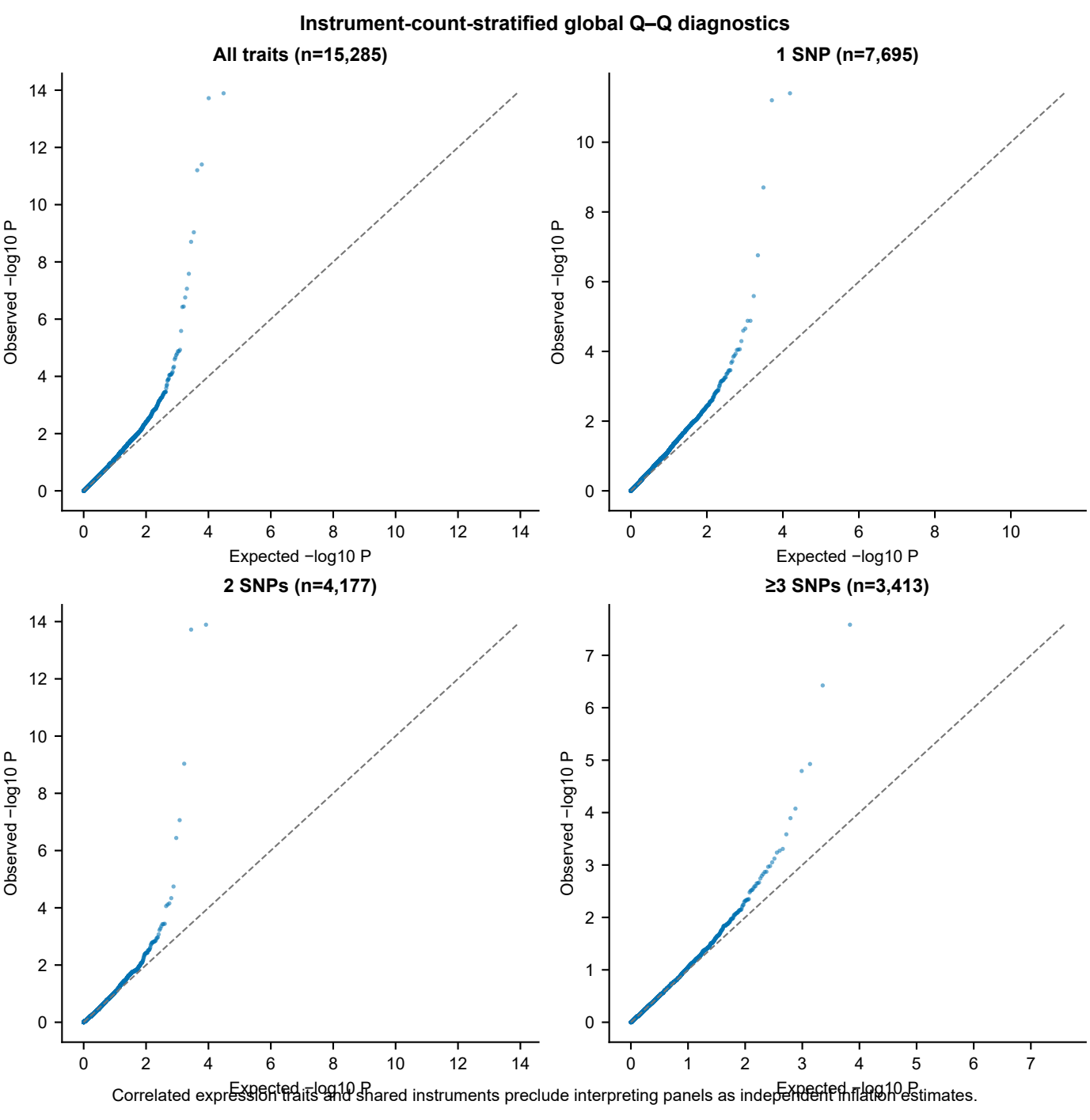
Donor-balanced mean log1p(CP10K), scaled within each gene

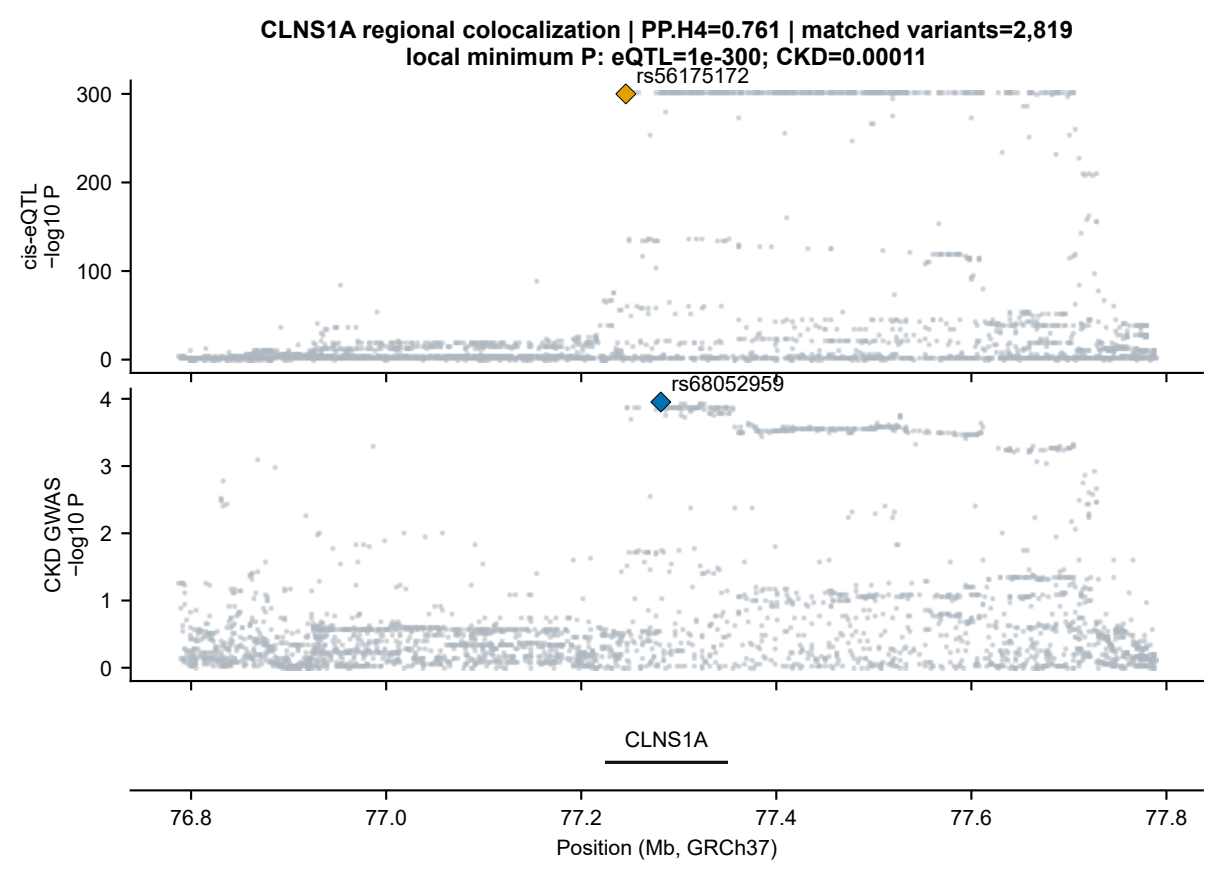



Multi-cohort renal transcriptomic synthesis
Best prespecified disease-compartment REML stratum per FDR-significant MR trait
CMPK2
COBLL1
DPP8
HELB
RNFT1
ZFAND6
ANKUB1
IER3
RSAD2
CLNS1A
CYP21A2
C4B
TNXA
BICC1
PSMA4
ATF6B
TAP1
GNL1
NEU1
APOM
TUBB
HCP5
DDAH2
RNF5
HSPA1L
EHMT2
PRRT1
PSORS1C3
LTA
SKOR1
-2
-1
0
1
2
Pooled Hedges g (95% CI)
Not global-BH significant
Global BH <0.05
Independent cohorts
2
4



Secondary recovery used the same GRCh37 coordinate and alleles only; no LD proxies or nearest variants were used.


Instrument-count-stratified global Q–Q diagnostics
All traits (n=15,285)
1 SNP (n=7,695)
2 SNPs (n=4,177)
≥3 SNPs (n=3,413)
Observed −log10 P
Expected −log10 P
Correlated expression traits and shared instruments preclude interpreting panels as independent inflation estimates.


CLNS1A regional colocalization | PP.H4=0.761 | matched variants=2,819
local minimum P: eQTL=1e-300; CKD=0.00011
rs56175172
rs68052959
cis-eQTL
−log10 P
CKD GWAS
−log10 P
CLNS1A
Position (Mb, GRCh37)