

WORKFLOW

INPUT DATA

Find trans-eQTLs

trans_cister_eqtls()

trans_eqtls (list)

[[“sig_eqtls”]]

[[“trans_eqtls”]]

[[“cister_eqtls”]]

[[“trans_eqtls.id”]]

Various data
cleaning

Check for trans-probe
enrichment

transprobe()

gwas_pos

snp137common

probe_coord

rsid	p_snp	snpchr	snpbp

Bioconductor:
features(FDB.UCSC.snp137common.hg19)

GRangesList – one probe = one list entry

to_circleplot*

Visualise trans-eQTLs:
circle plot

circle_plot()

Circle plot

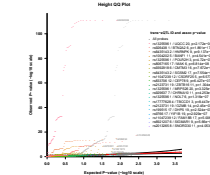
(Optional LD clumping)

qq_snps

Plot compartmentalised
QQ-plot

qqplot_comp()

QQ-plot



qq_out (list)

[[“id_ordered.row”]]

[[“colourway”]]

[[“id_ordered”]]

Plot separated
QQ-plot

sep_qq()

Separated QQ-plot

Discovery workflow summary

(see example_code.R for specifics)

Legend

Pink
Orange
Yellow
Blue
Green

input data
derived data
purpose
function
output/variable

*to_circleplot

“DERIVED” DATA (can be directly input)

rsid	p_snp	snpchr	snpbp	probe	probechr	probebp	p_eqtl	qqid

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