Supplementary Information for

Cis and *trans*-acting variants contribute to survivorship in a naïve *Drosophila melanogaster* population exposed to ryanoid insecticides

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Figs. S1 to S4

Other supplementary materials for this manuscript include the following:

Datasets S1 to S15

Supplementary figures

Figure S1. Chlorantraniliprole phenotypes of 152 DGRP lines. (*A*) LC_{50}, calculated from a minimum of six Abbott-corrected concentration survivorship phenotypes. (*B*) The survivorship of each line on the different concentrations (coloured), ordered by LC_{50}.

Figure S2. The explanatory power of phenotype-associated DGRP variants for each chlorantraniliprole concentration compared to the number of associated variants. (*A*) the number of variants that cross the GWAS significance threshold for each concentration. (*B*) The explanatory power of 5, 10, 25 and 50 variants for each concentration using genomic prediction. This shows that more genes are required to explain the genetic architecture of the lowest concentration. For example, if the top 50 most-associated variants of the 0.5μg/mL concentration are considered they explain about the same amount of the phenotypic variation (R=0.43) as the top 5 variants of the 5μg/mL concentration.

Figure S3. q-q plot showing that correction of the LC_{50} phenotype for the effect of *Strn-Mlck* (blue) decreases the *p*-value inflation substantially but does not return the observed GWAS *p*-values (black) to expected levels (red).

Figure S4. R spider networks of GWAS candidates ($p<1x10^{-5}$) from LC_{50} (*A*) and *Strn-Mlck*-corrected LC_{50} phenotypes (*B*). GWAS candidates are annotated with minimum *p*-value (black), maximum MAF (red) and maximum effect size (blue).

Supplementary file

Files S1-S7. Individual DGRP line values for six single-concentration chlorantraniliprole phenotypes and LC_{50}.
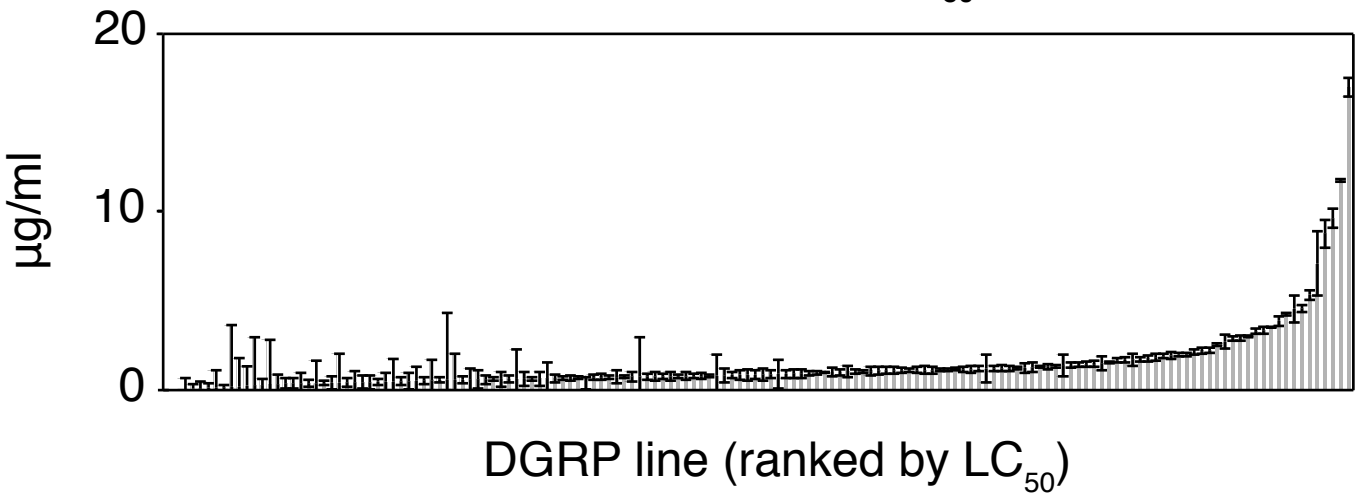
Files S8-S14. Raw Mackay Lab DGRP2 pipeline top candidate outputs for six single-concentration chlorantraniliprole phenotypes and LC_{50}.

File S15. LC_{50} phenotype to transcriptome Bonferroni-significant associations.

Figure S1

A

Chlorantraniliprole LC$_{50}$

μg/ml

DGRP line (ranked by LC$_{50}$)

B

Chlorantraniliprole concentration response

- 0.5μg/ml
- 1.0μg/ml
- 2.0μg/ml
- 3.0μg/ml
- 4.0μg/ml
- 5.0μg/ml

Survivorship (%)

DGRP line (ranked by LC$_{50}$)
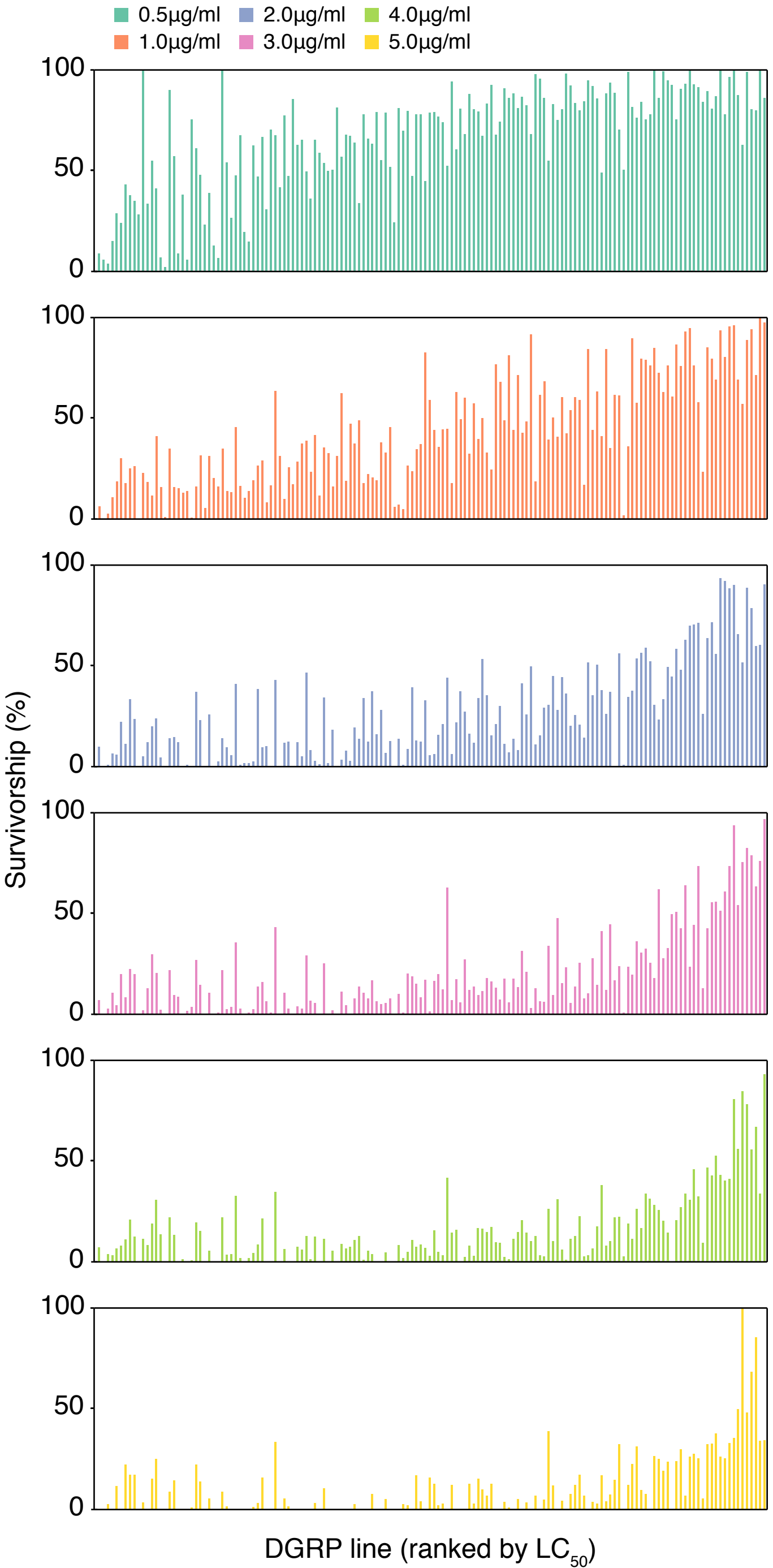
Figure S2

A · Associations with concentration phenotypes

Legend:
- 0.5µg/ml (H²=0.73)
- 1.0µg/ml (H²=0.85)
- 2.0µg/ml (H²=0.81)
- 3.0µg/ml (H²=0.83)
- 4.0µg/ml (H²=0.84)
- 5.0µg/ml (H²=0.82)

Y-axis: Associated variants ($p<1\times10^{-5}$)

X-axis: Phenotype (µg/ml chlorantraniliprole)
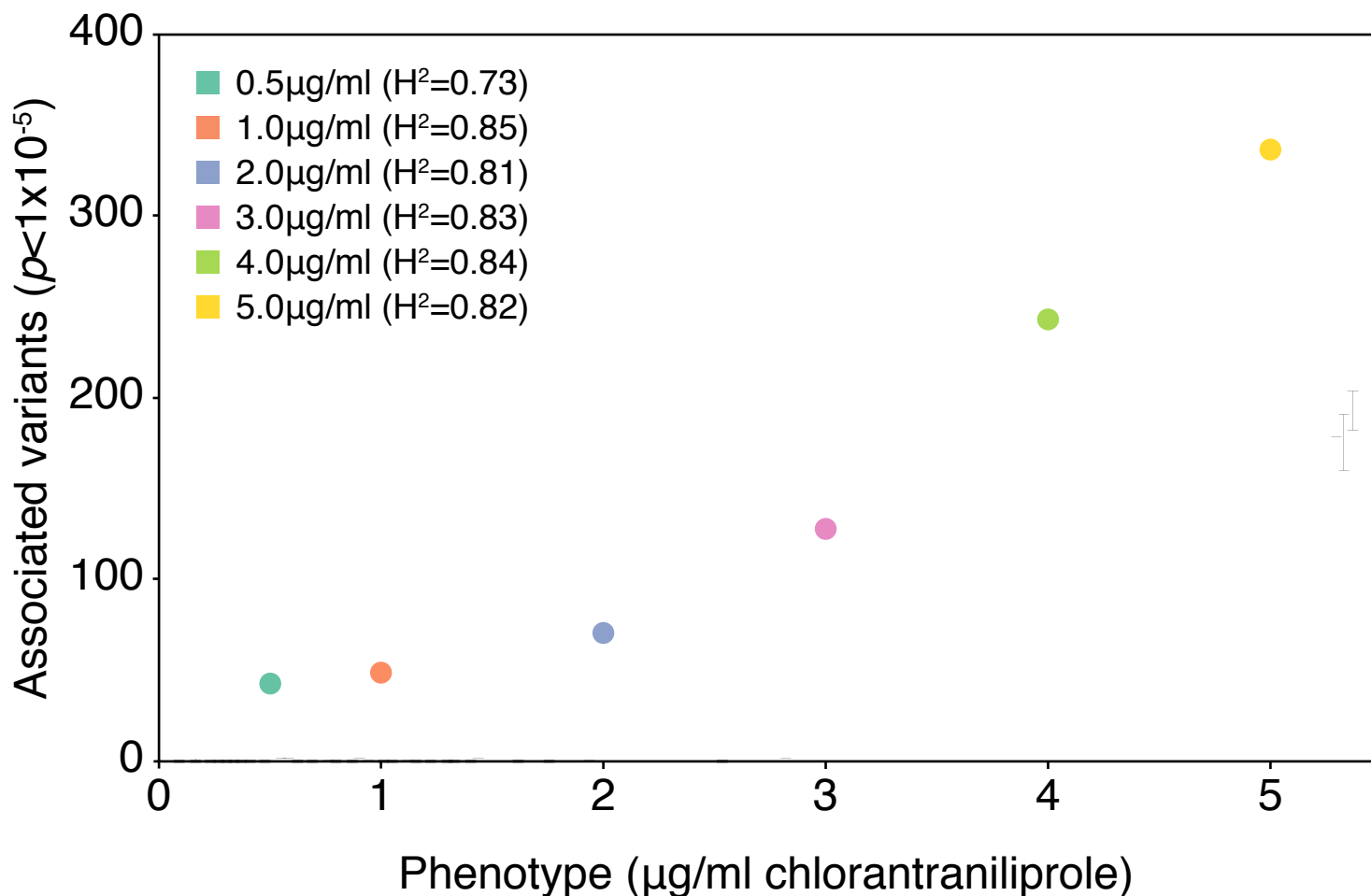
B · Explanatory power of associated variants

Y-axis: R value

X-axis: Number of explanatory variants
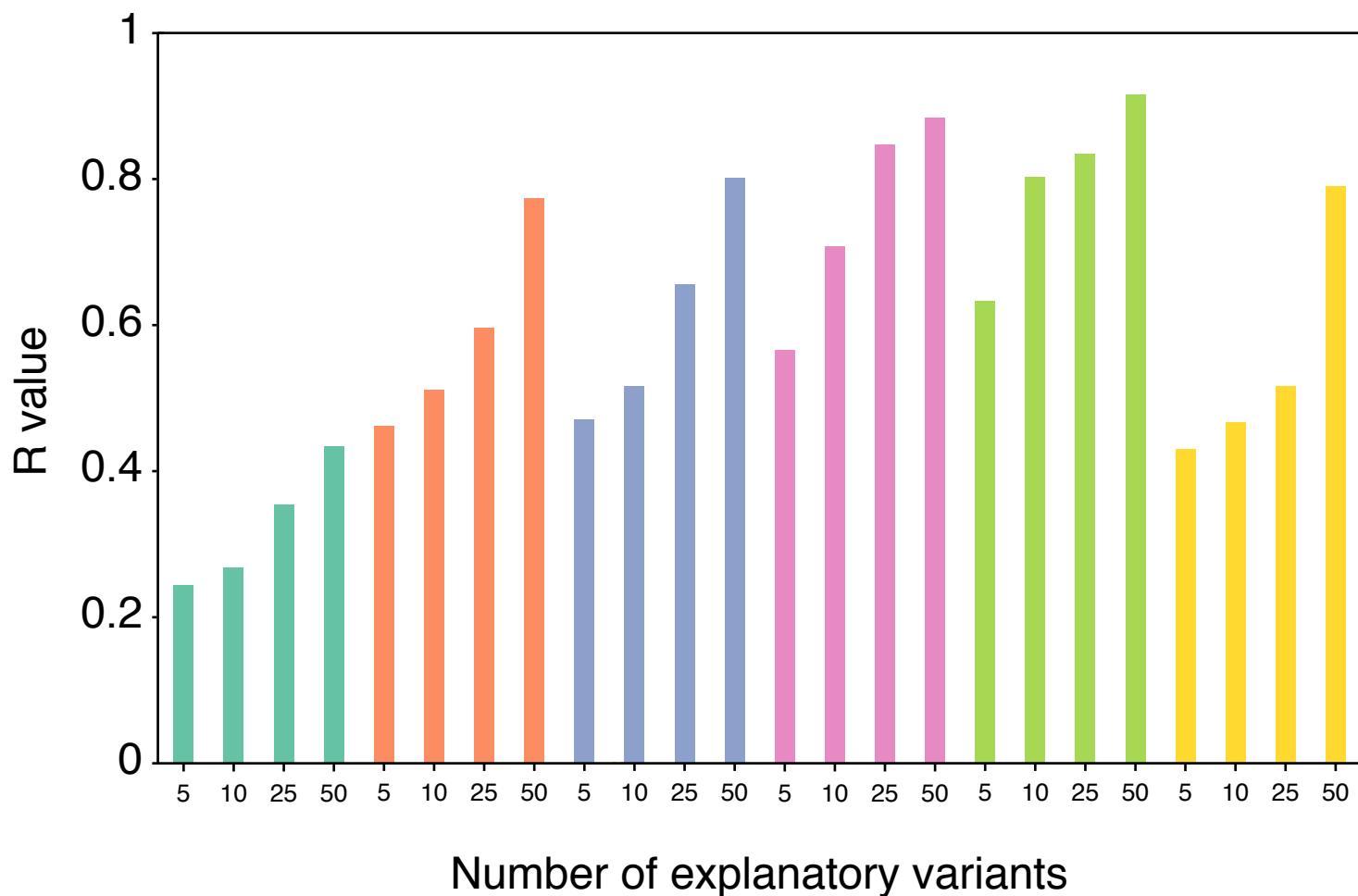
Figure S3

Uncorrected and corrected GWAS q-q plots
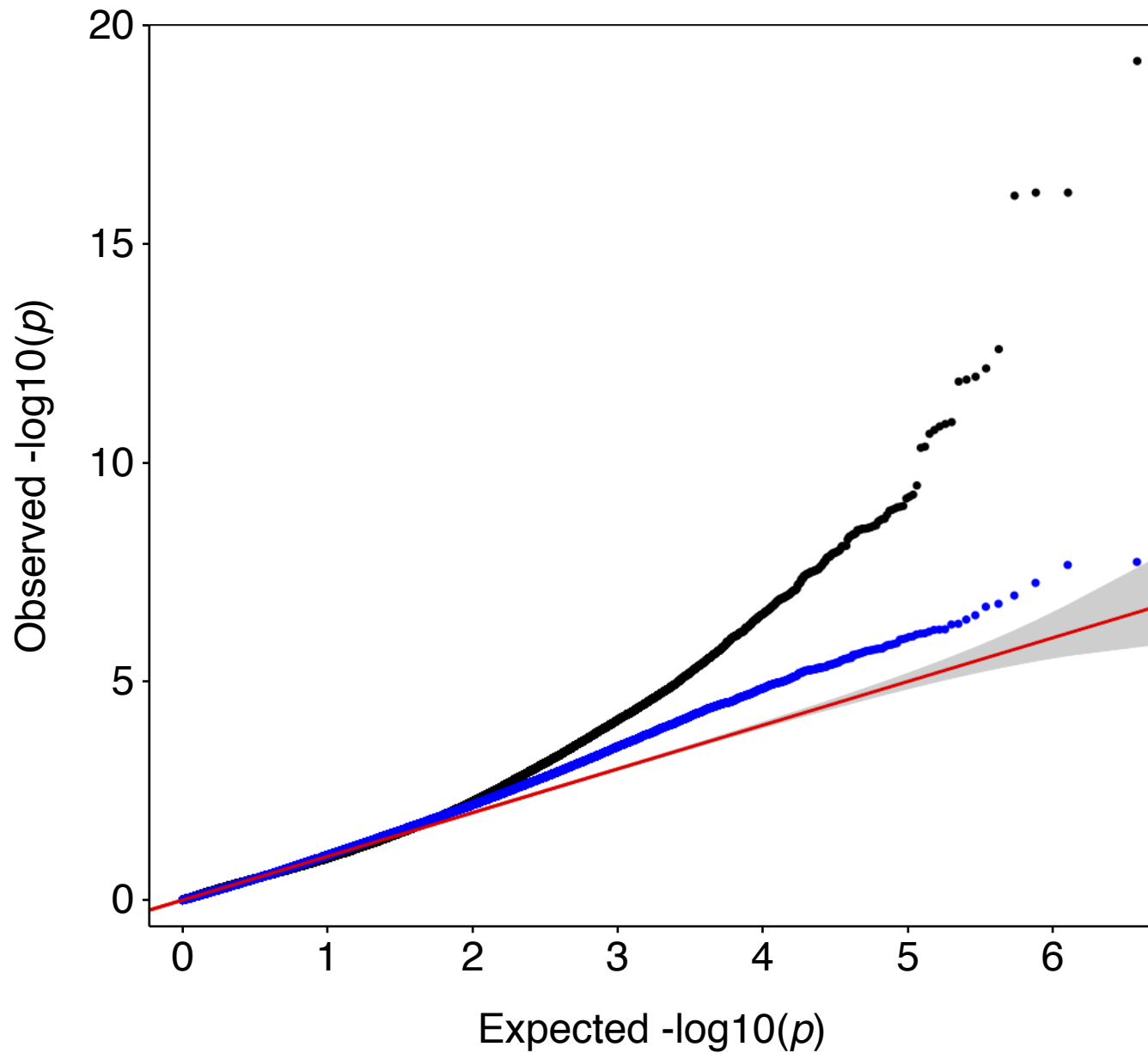
Figure S4

A   GWAS candidate R spider network

G-IALPHA65A

AC78C

cGMP

norpA
2.11E-11
0.073
-1.65

PKCDELTA

FRA

dlp
7.1E-10
0.054
-1.7

sli
1.37E-13
0.054
-2.53
3 variants

Pde9
1.64E-9
0.113
-1.48

DCP-1

PAK

▲ R spider
■ GWAS candidate

LamC
5.49E-9
0.066
-1.84

DECAY
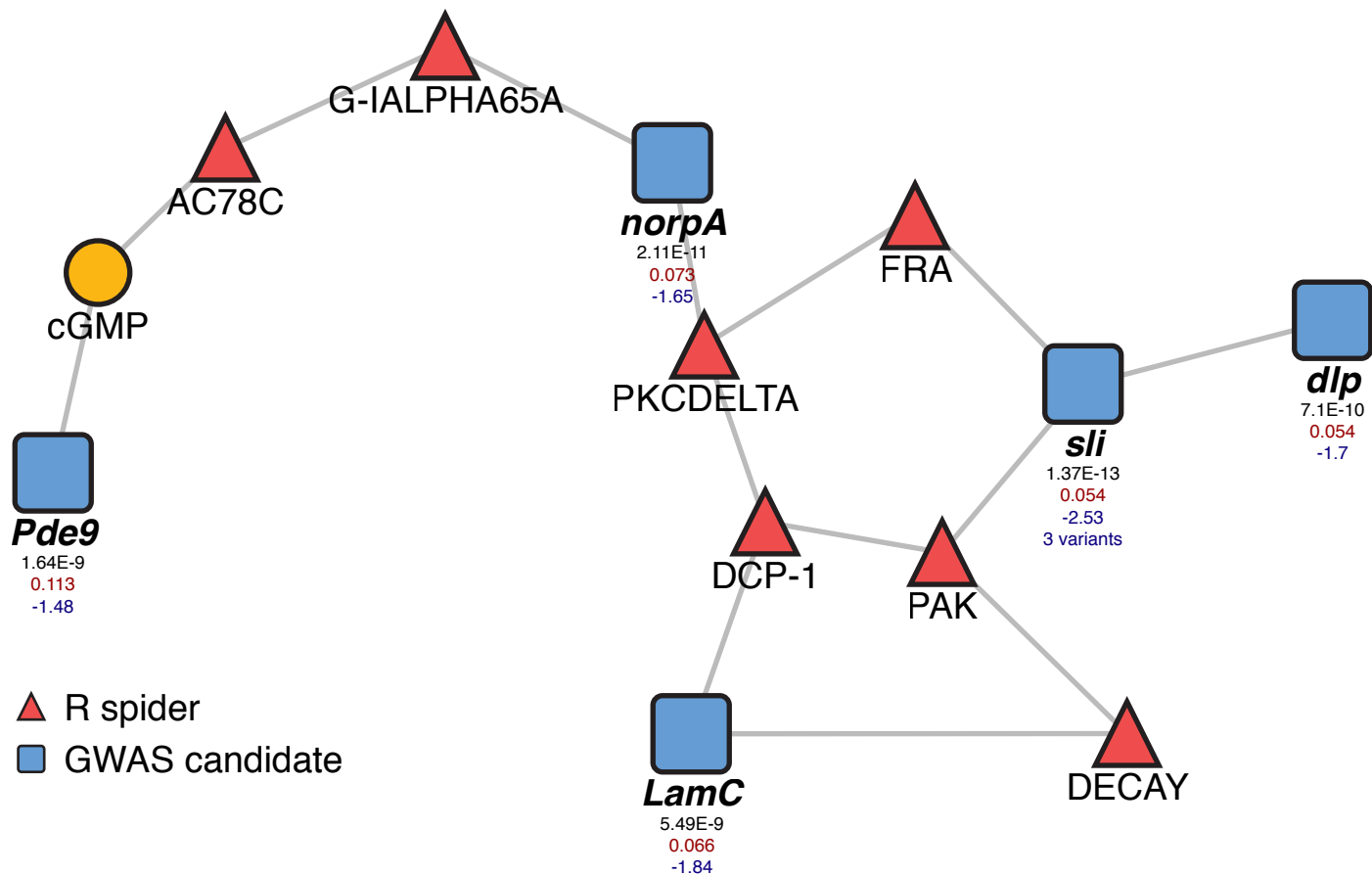
B   Corrected GWAS candidate R spider network

robo3
5.84E-6
0.076
-1.4

FRA

sli
1.99E-6
0.054
-1.29

norpA
2.07E-6
0.054
-1.36

PKCDELTA

SOS

PK61C

RHEA

Strn-Mlck

foxo
1.57E-7
0.054
-1.36

zip
8.8E-7
0.054
-1.4
3 variants