# Supplemental Figures

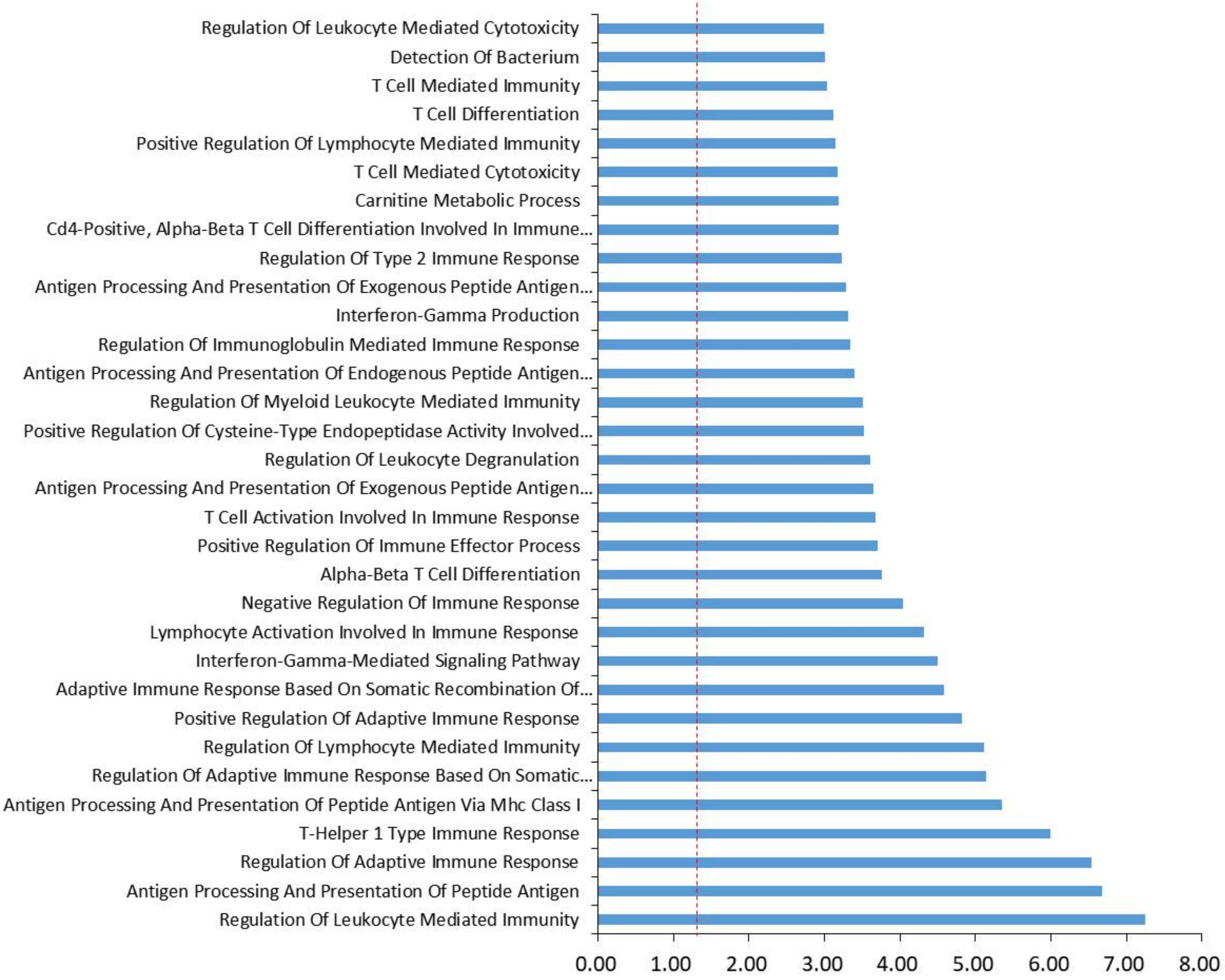
**Supplemental Figure S1. GO-terms of biological process enrichment analysis for 228 identified genes.** The red vertical line represents that the threshold of the P-value after the Bonferroni step down correction.

**Supplemental Figure S2. Violin plots show the expression profiles of identified genes among control, notSA, and SA group. a**) for *STAT6*, b) for *MPI*, c) for *GNGT2*, d) for *DECR2*.

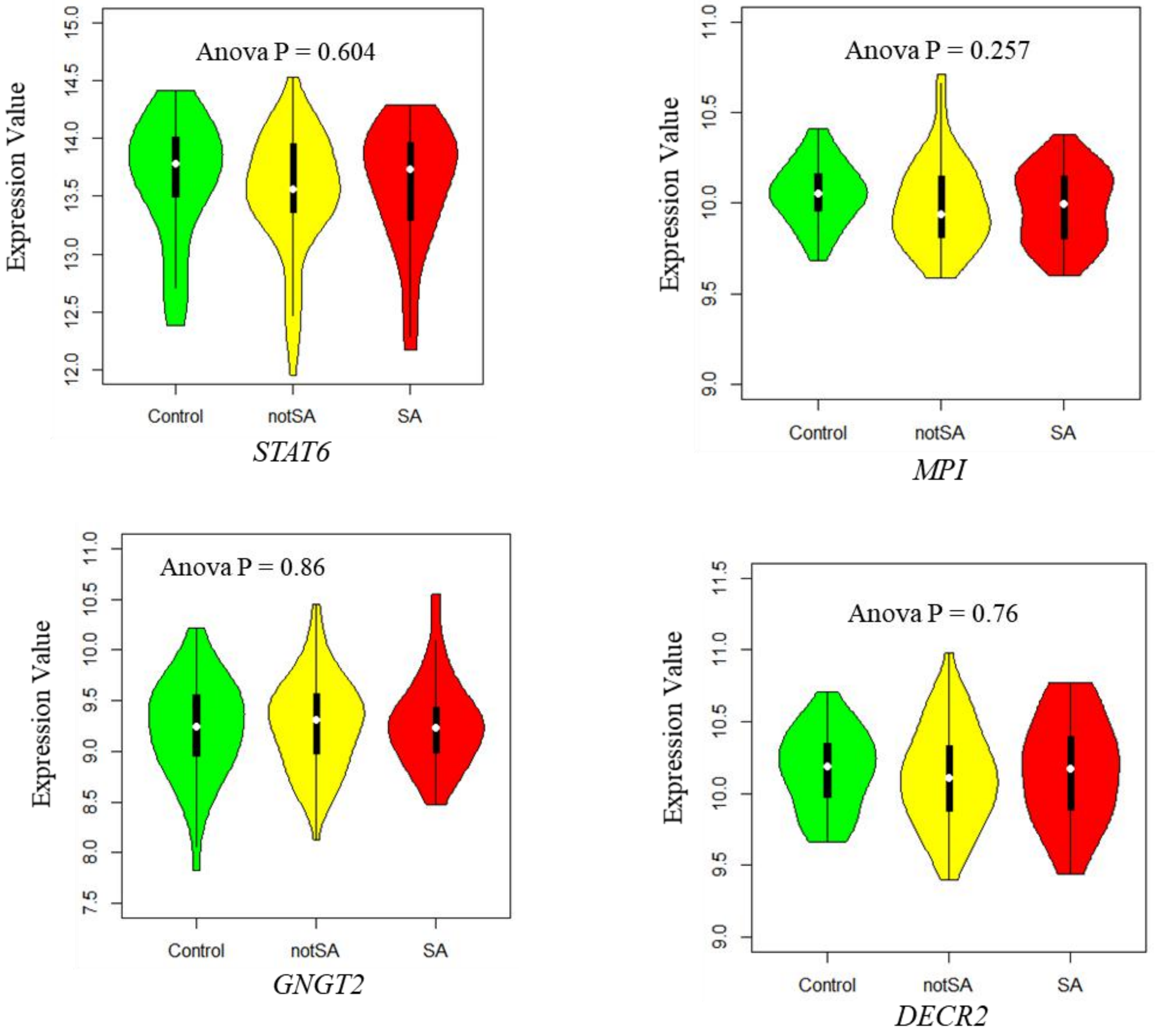
**Supplemental Figure S3. Boxplots show the differential gene expressions between vehicle and various glucocorticoids including VSG158, VSG159, FF, and DEX.** a) for stat6, b) for Decr2, c) for Slc22a5, d) for Lnpep, e) for Ttc19, f) for Mpi.

**Supplemental Figure S4. Co-expression patterns of identified genes between vehicle and various glucocorticoids including VSG158, VSG159, FF, and DEX.** a) Co-expression patterns of identified genes in vehicle group; b) Co-expression patterns of identified genes in DEX; c) Co-expression patterns of identified genes in FF; d) Co-expression patterns of identified genes in VSG158; e) Co-expression patterns of identified genes in VSG159.

**Supplemental Figure S5. Regional plot shows risk SNPs mapped into the severe asthma-associated gene of *GNGT2* based on the GWAS dataset of Dataset #1.**



Supplemental Figure S1



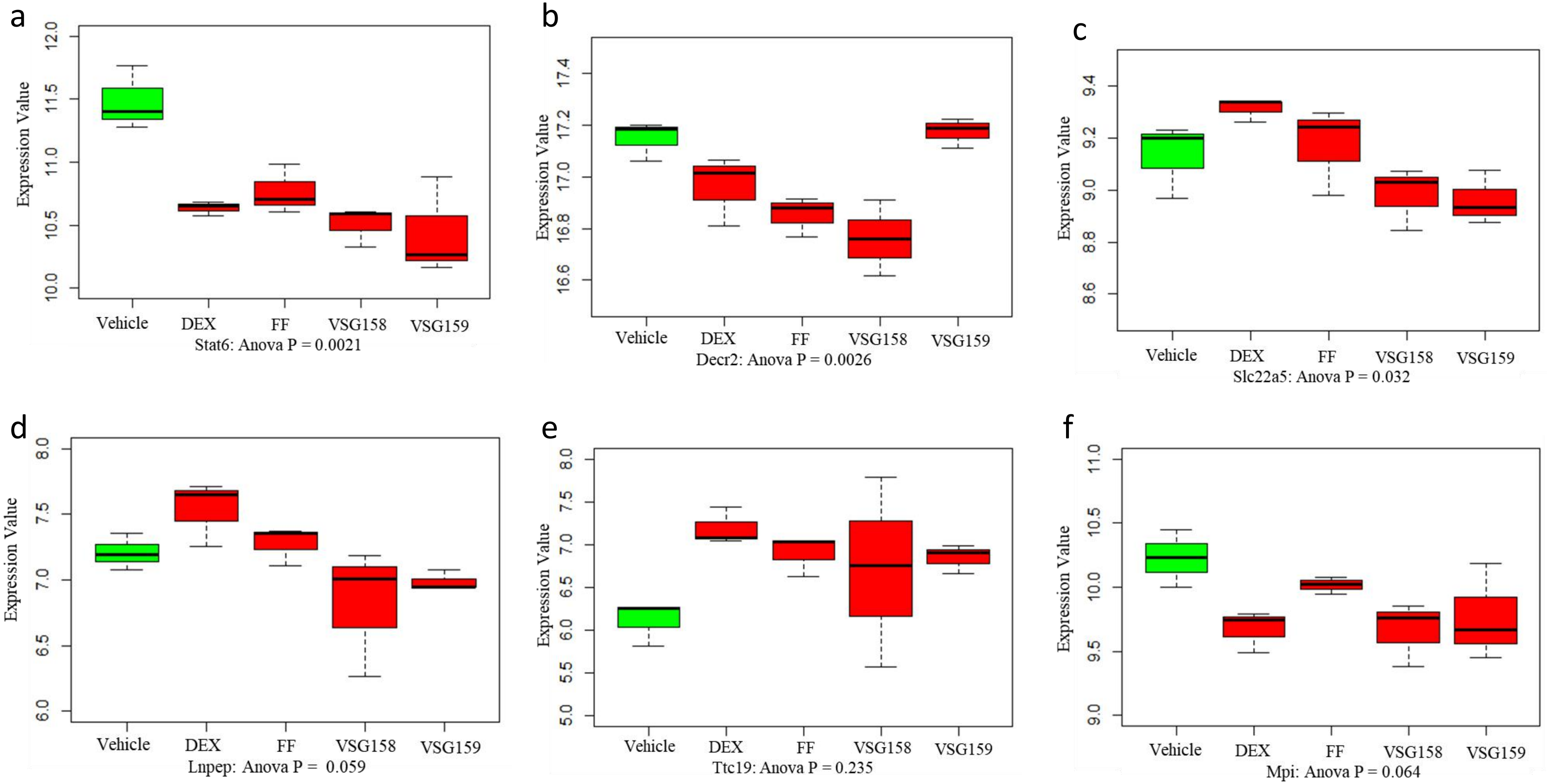
*STAT6*

*MPI*

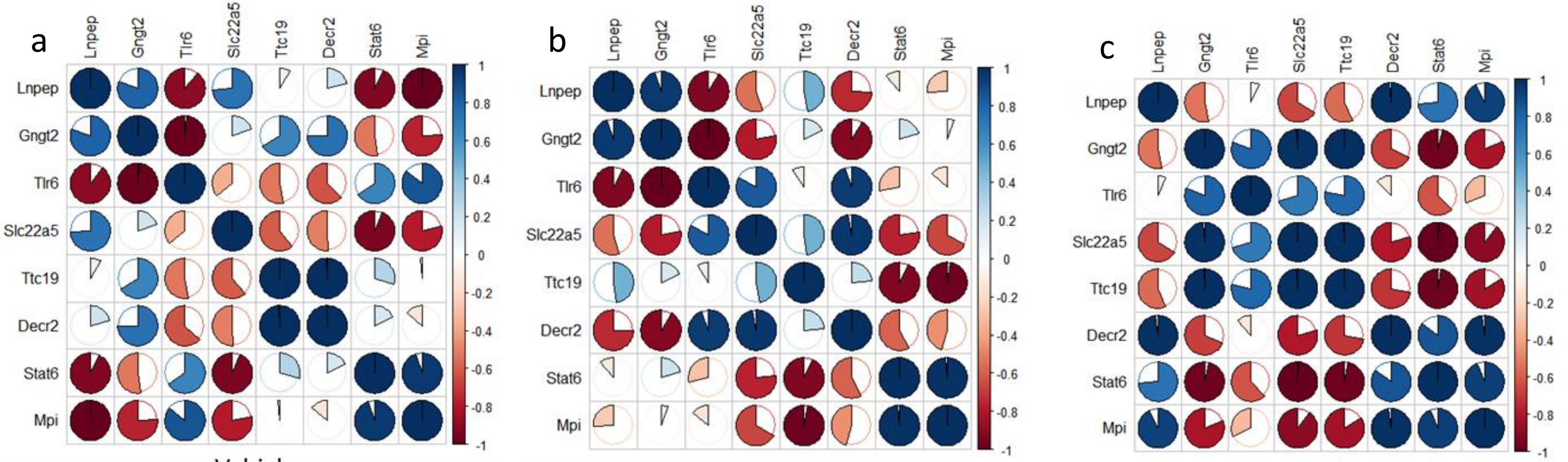
*GNGT2*

*DECR2*

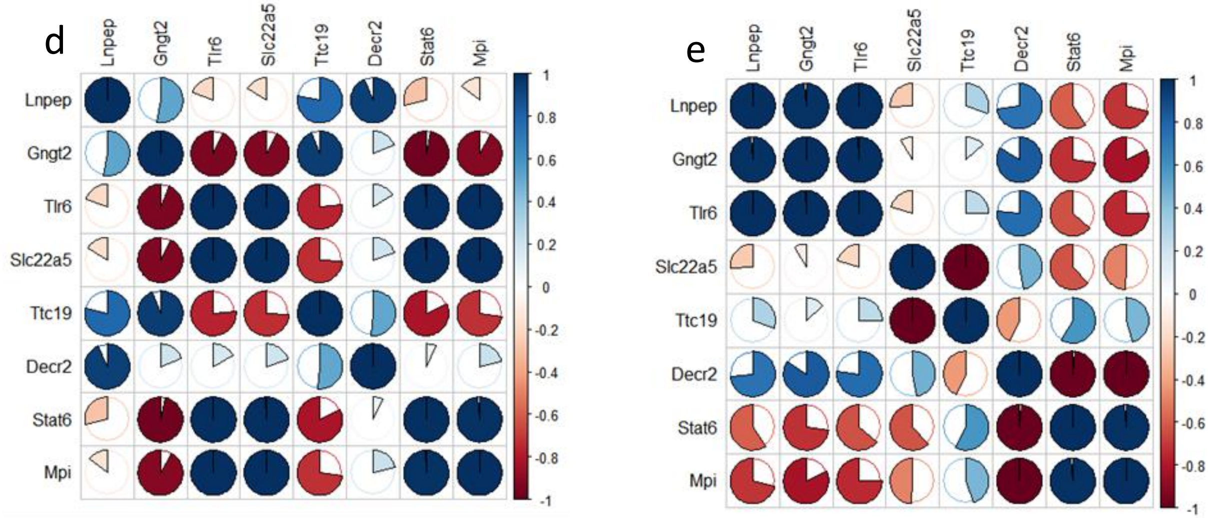
Supplemental Figure S2



Supplemental Figure S3

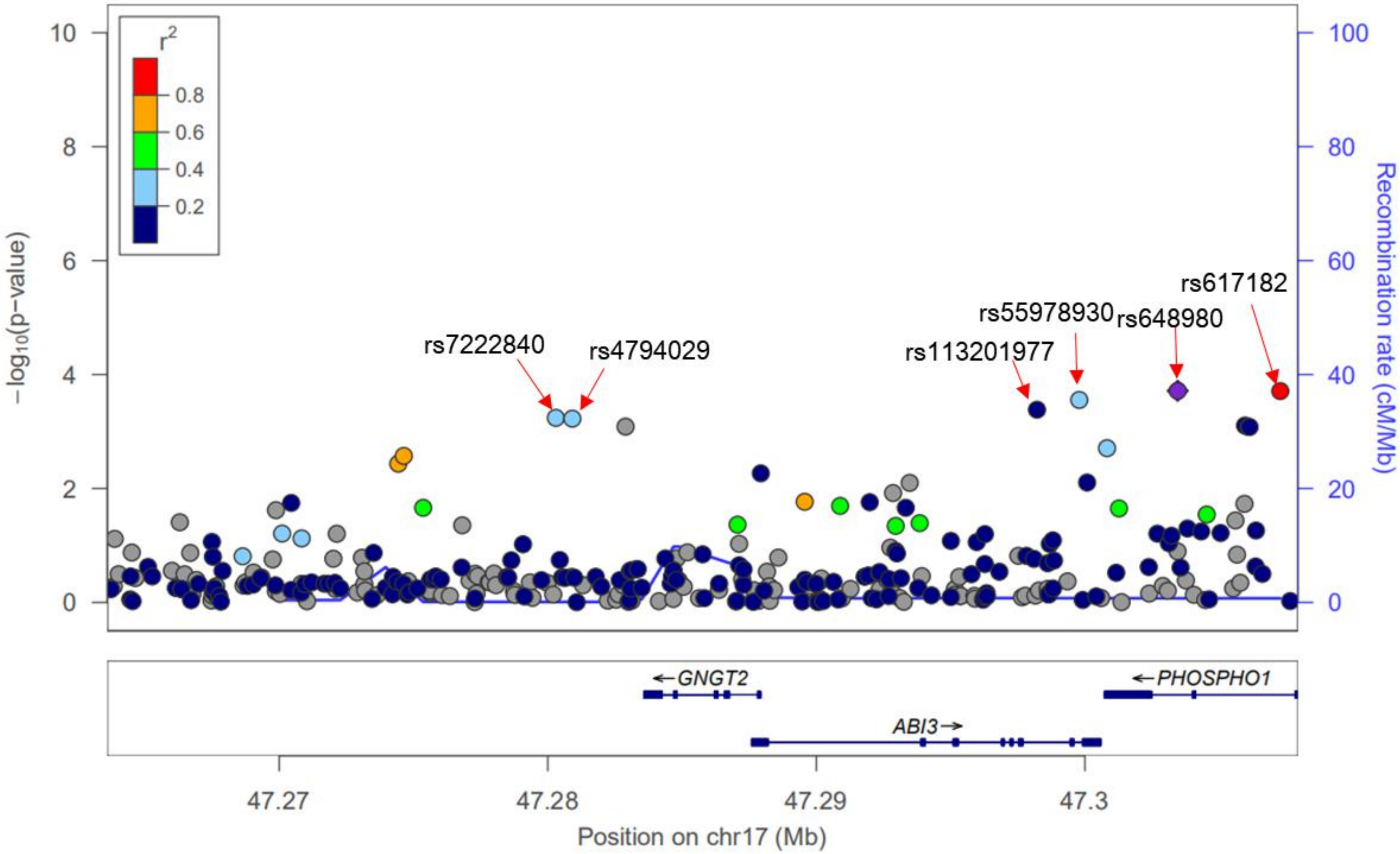


Vehicle DEX FF



VSG158 VSG159

Supplemental Figure S4



Supplemental Figure S5