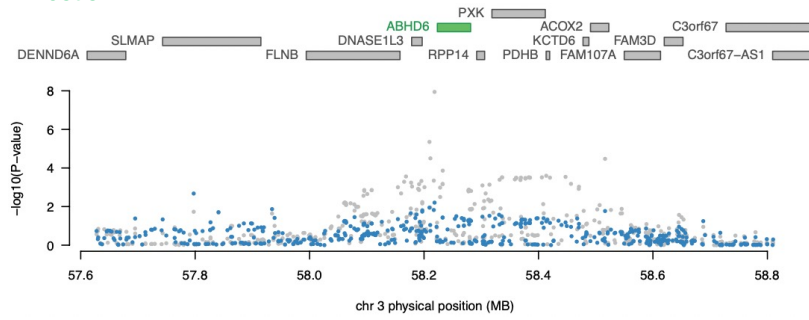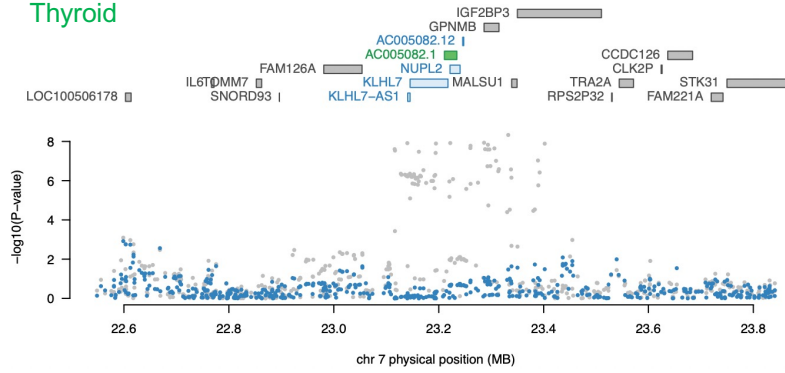(Supplementary Fig. 1.) Prediction accuracy across three linear models: BLUP (best linear unbiased predictor) , Elastic Net, LASSO regression. BSLMM (Bayesian sparse linear mixed model) was dropped due to poor convergence during cross validation. The model with the best prediction accuracy was used for imputing gene expression onto GWAS cohort.
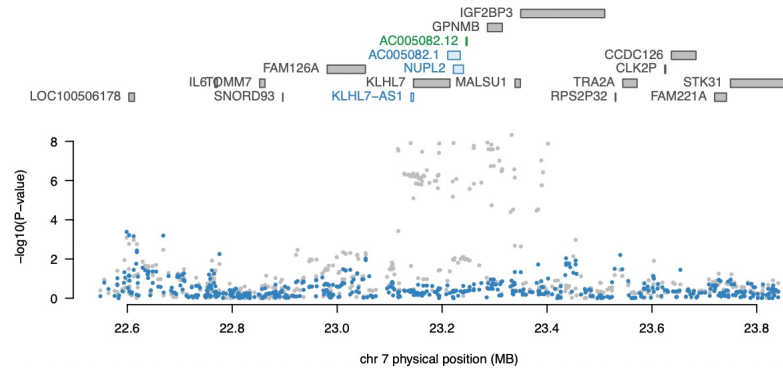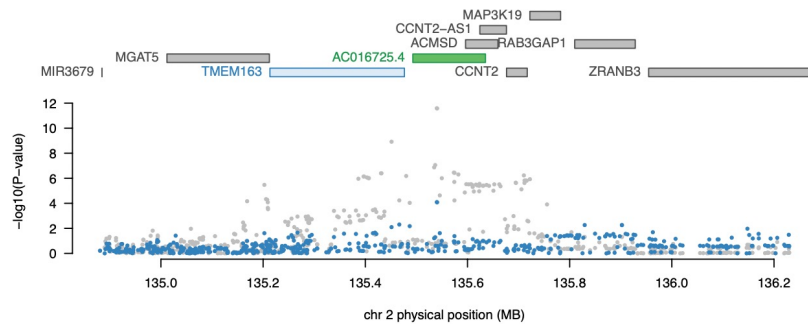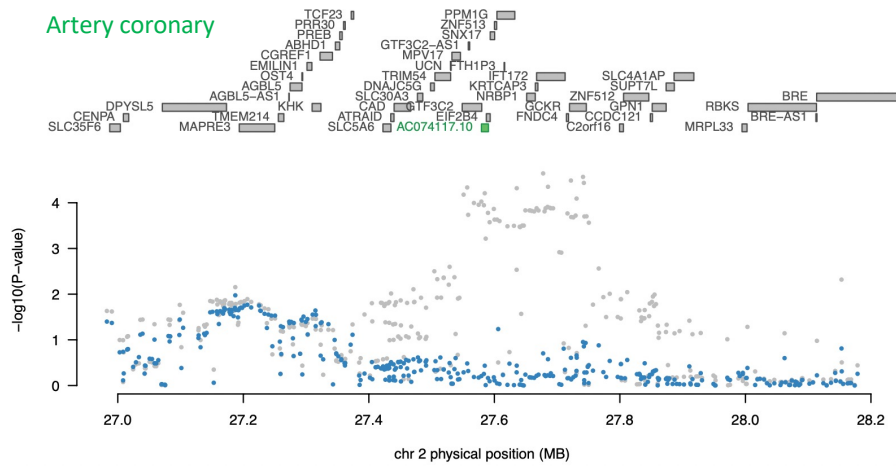
(Supplementary Fig. 2.1) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

(Supplementary Fig. 2.2) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
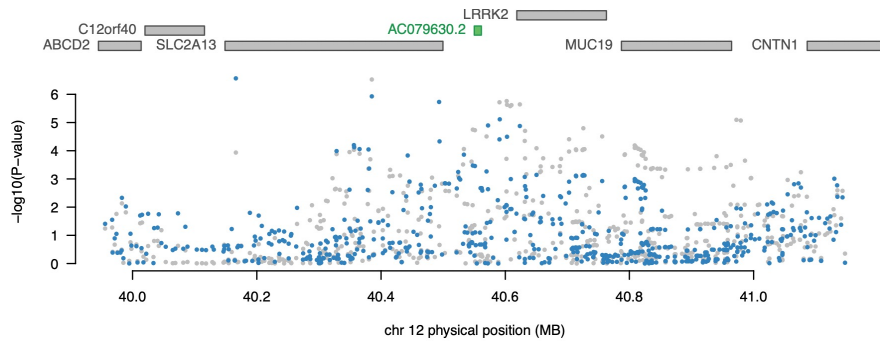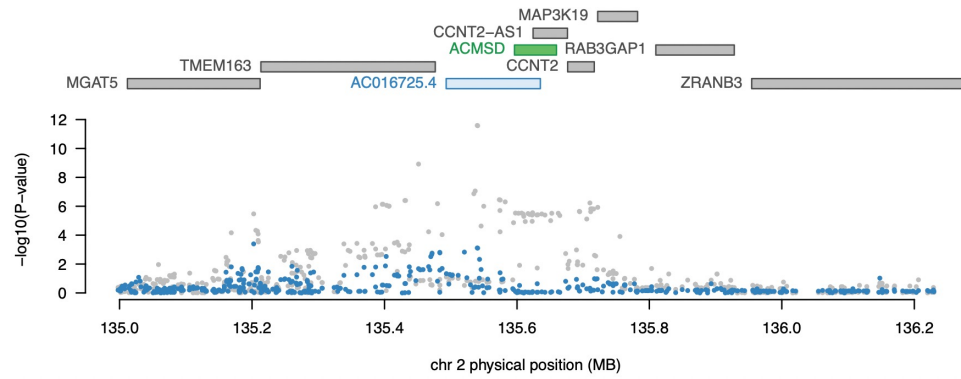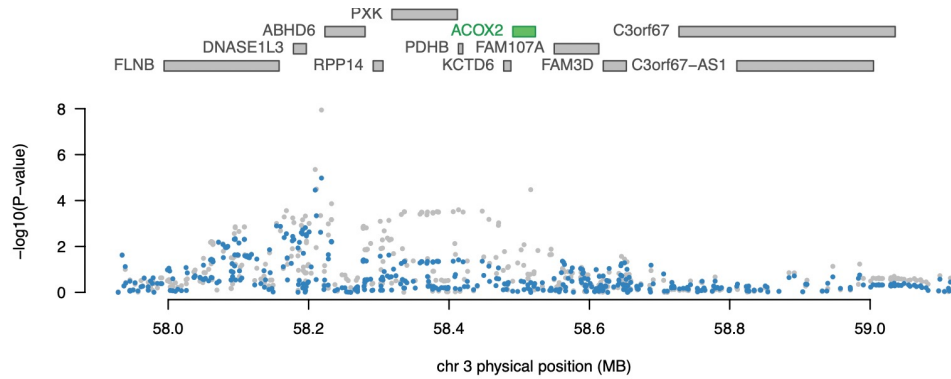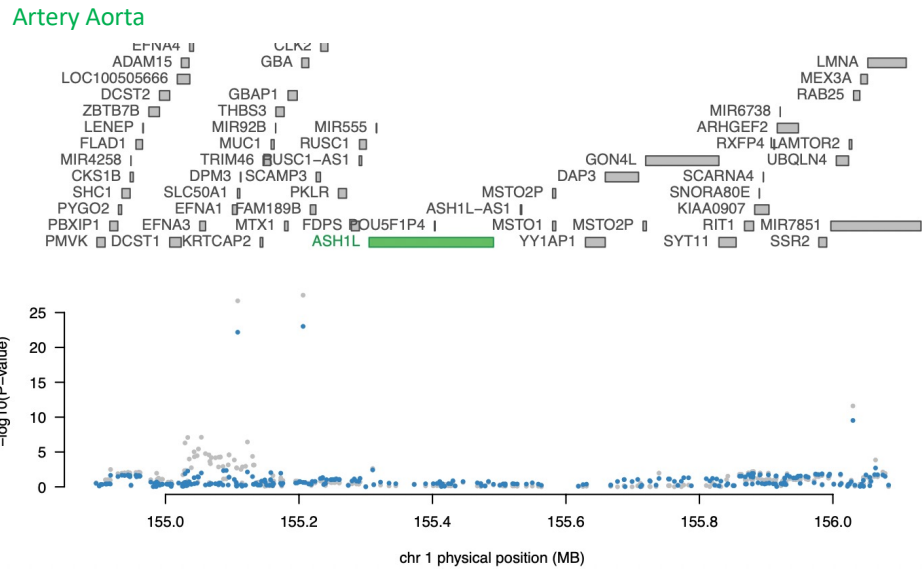
(Supplementary Fig. 2.3) FUSION plots of PD TWAS locus.
Reference panel(GTEx tissues) are shown for each plot.

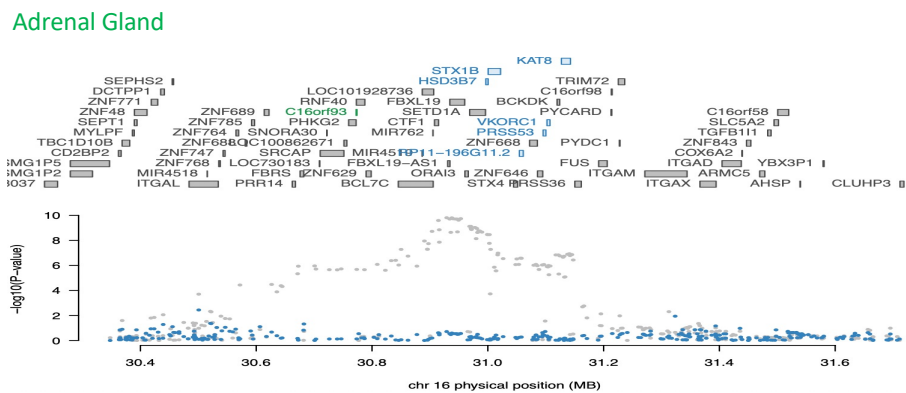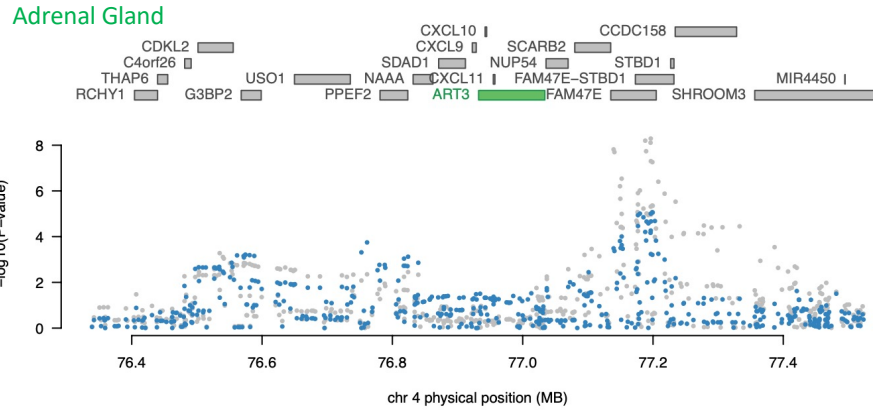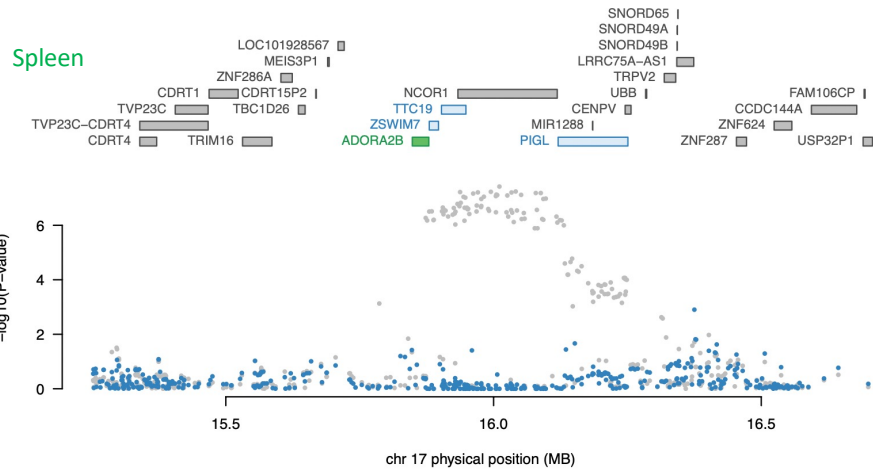(Supplementary Figure 2.4) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
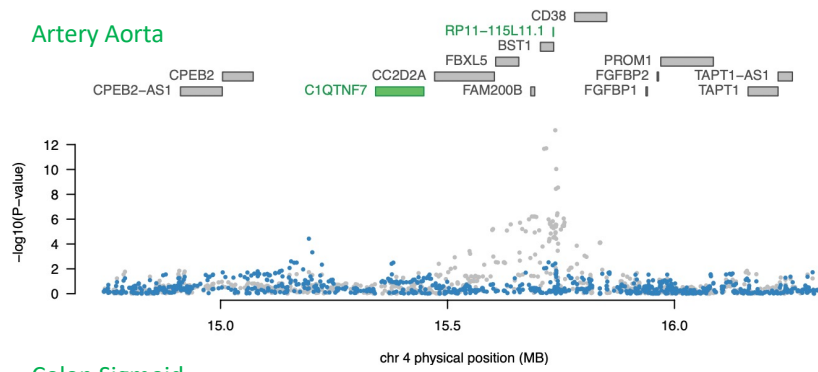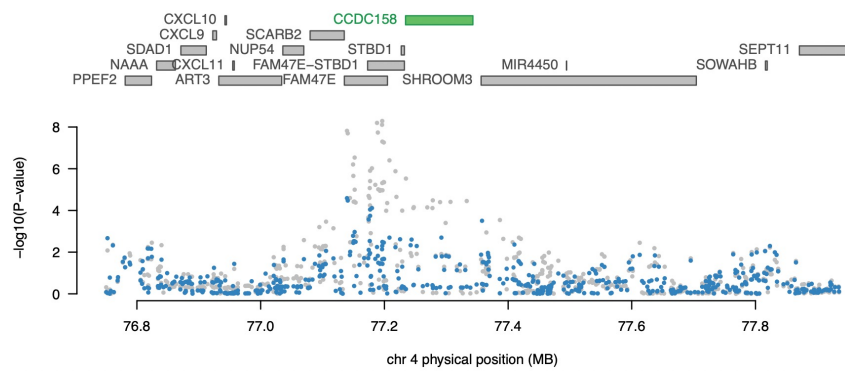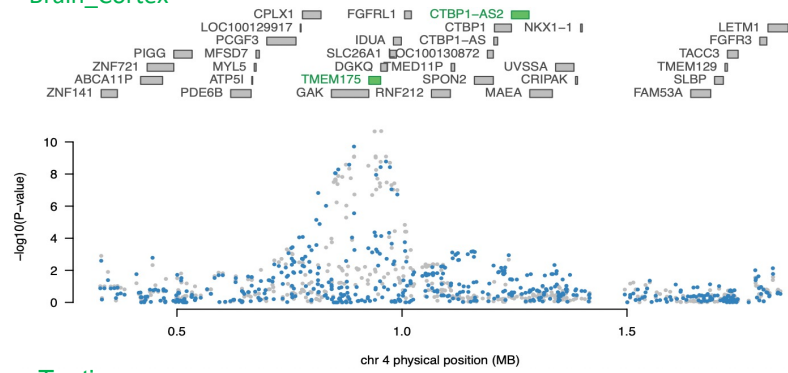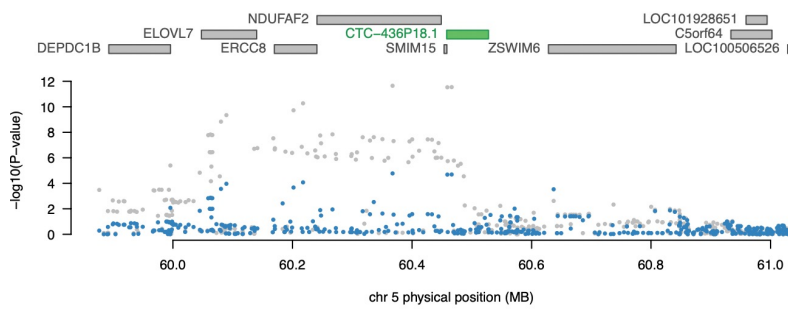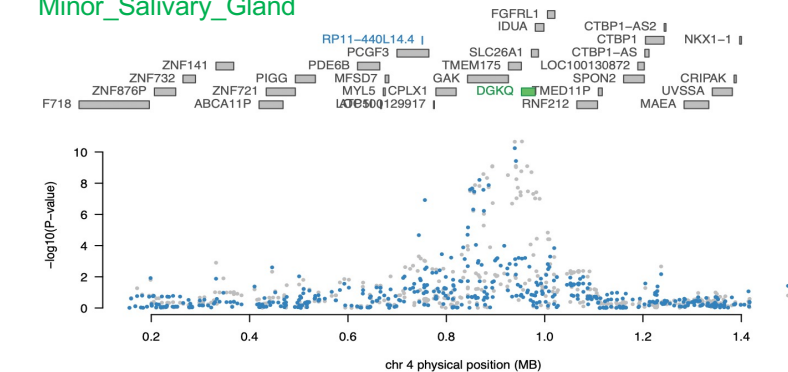
(Supplementary Fig. 2.5) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
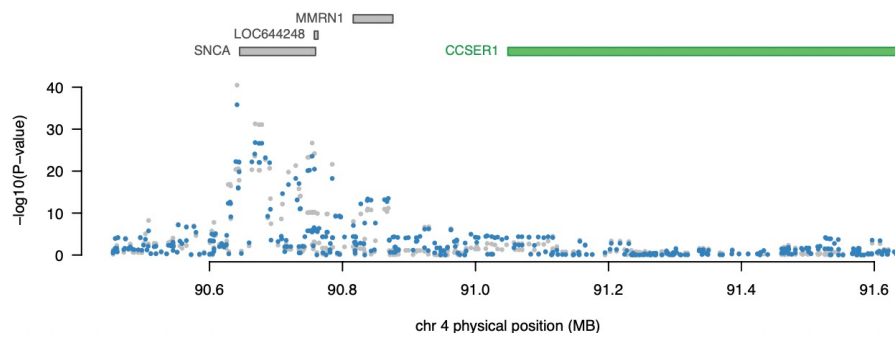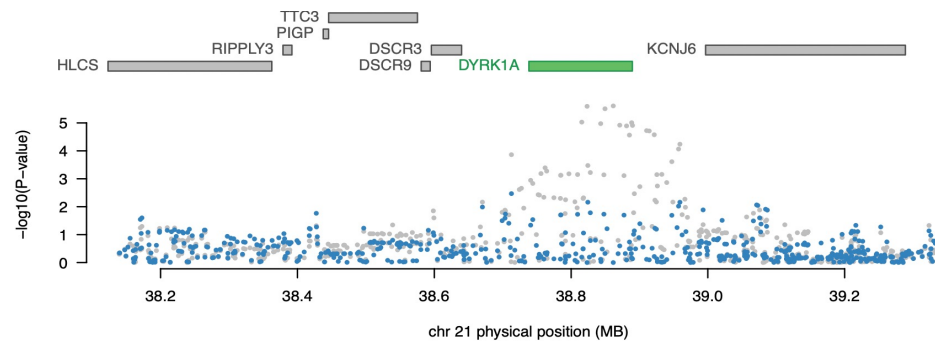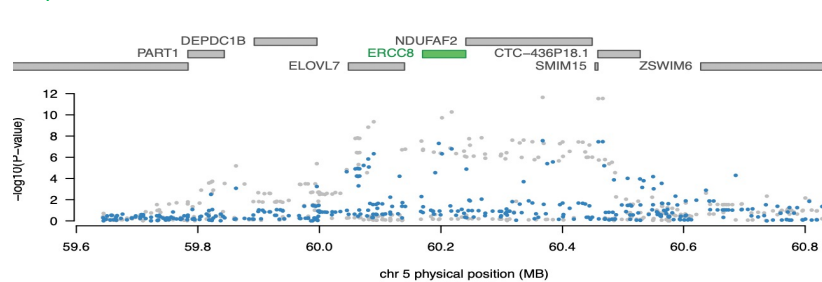
(Supplementary Fig. 2.6) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
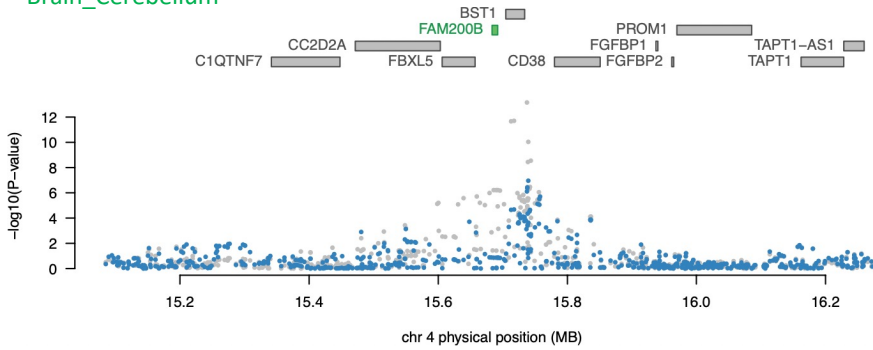
(Supplementary Fig. 2.7) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

(Supplementary Fig. 2.8) FUSION plots of PD TWAS locus.
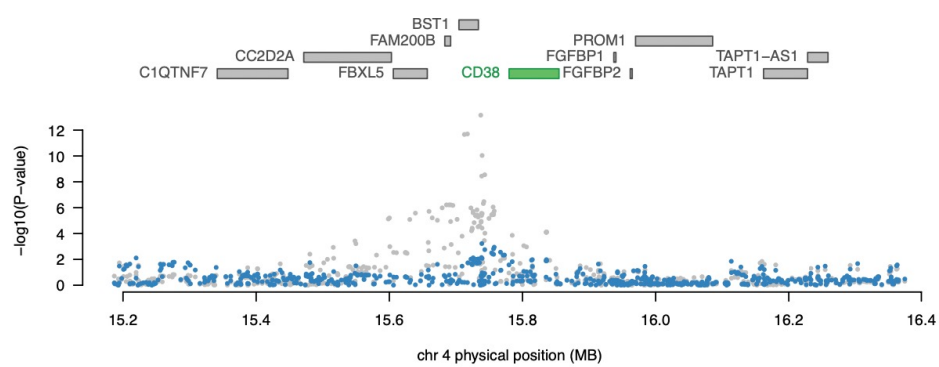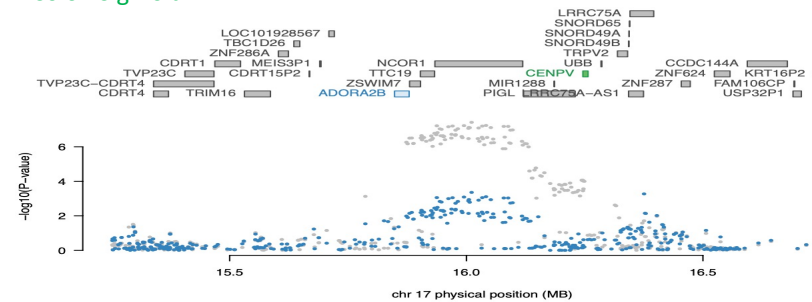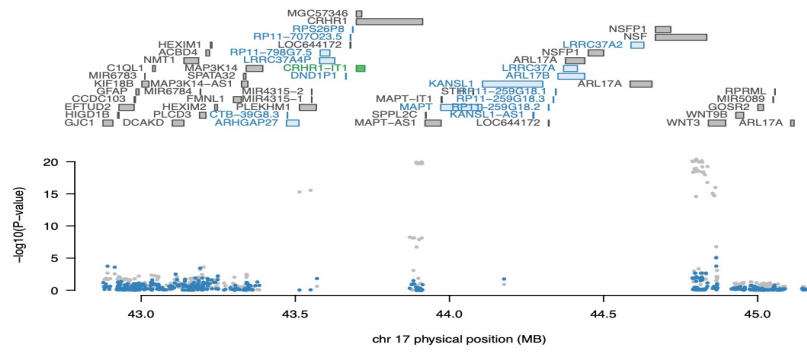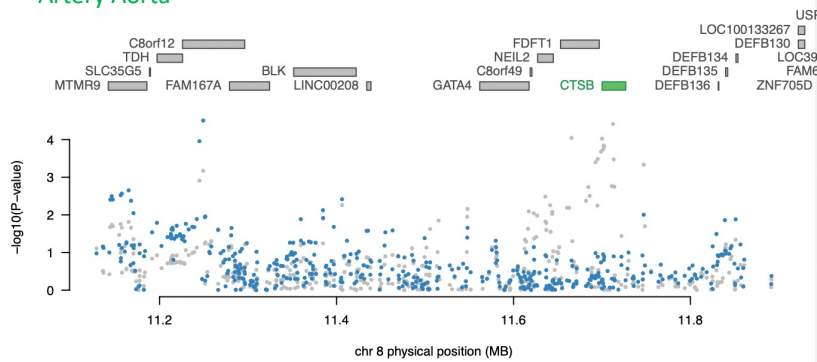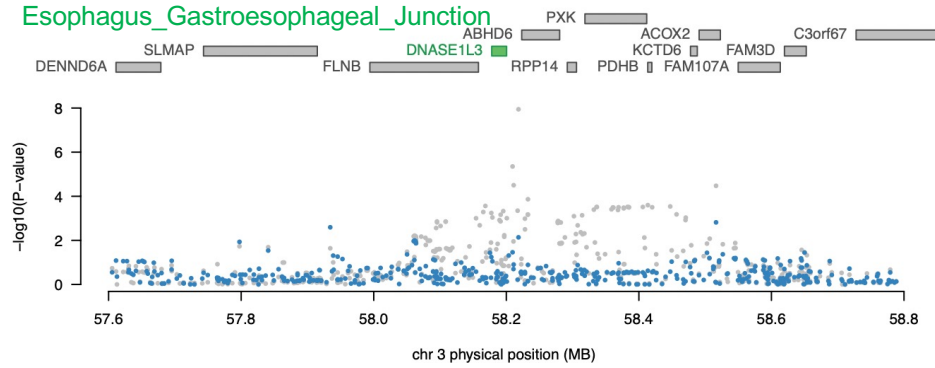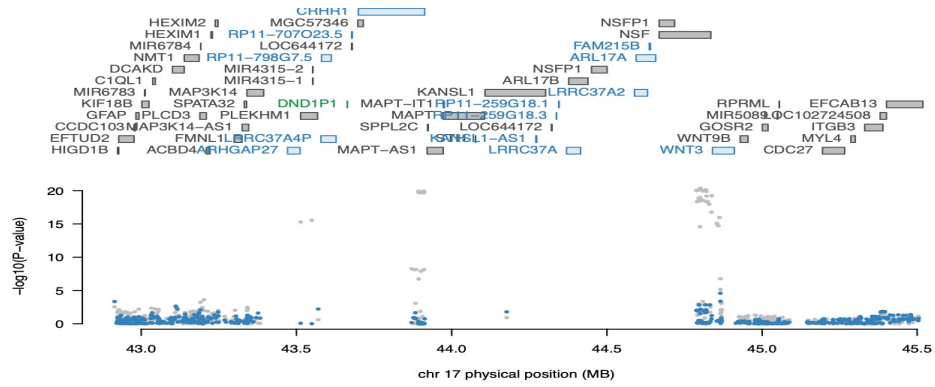Reference panel(GTEx tissues) are shown for each plot.

Supplementary Fig. 2.9) FUSION plots of PD TWAS locus.
Reference panel(GTEx tissues) are shown for each plot.
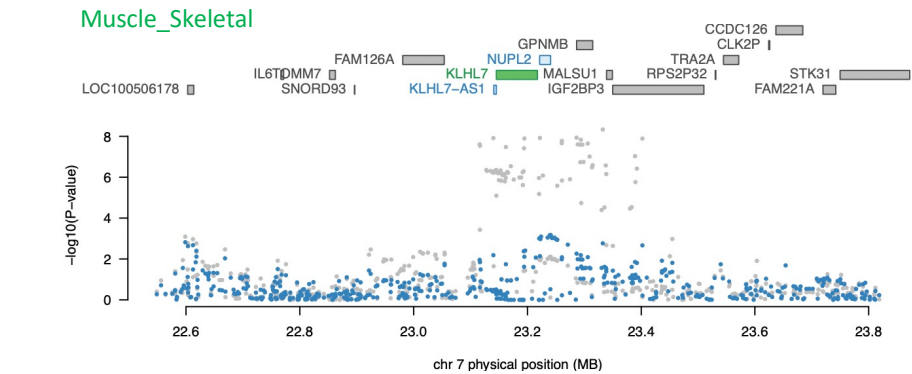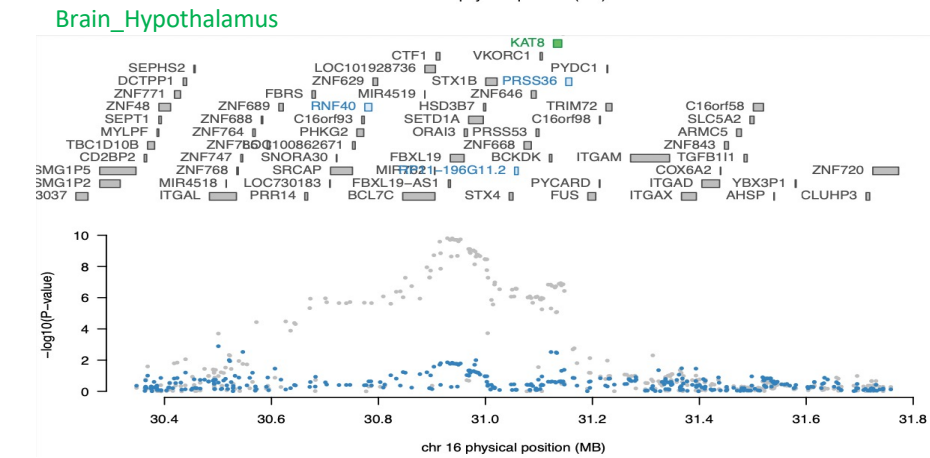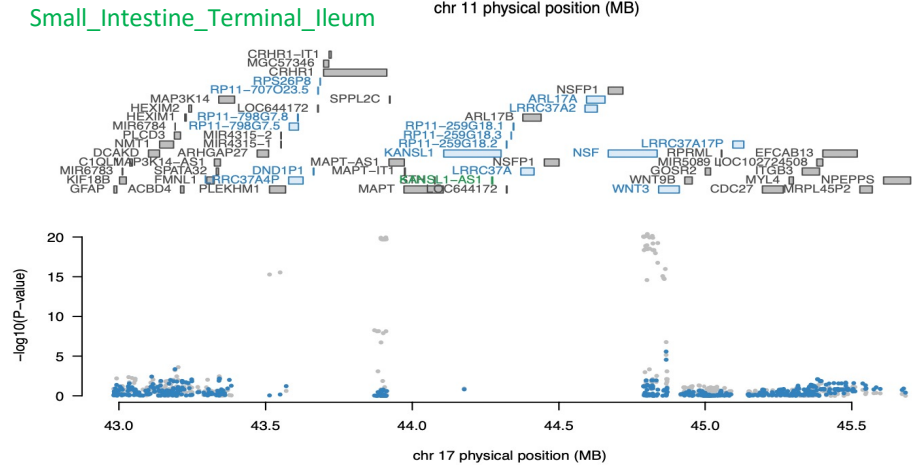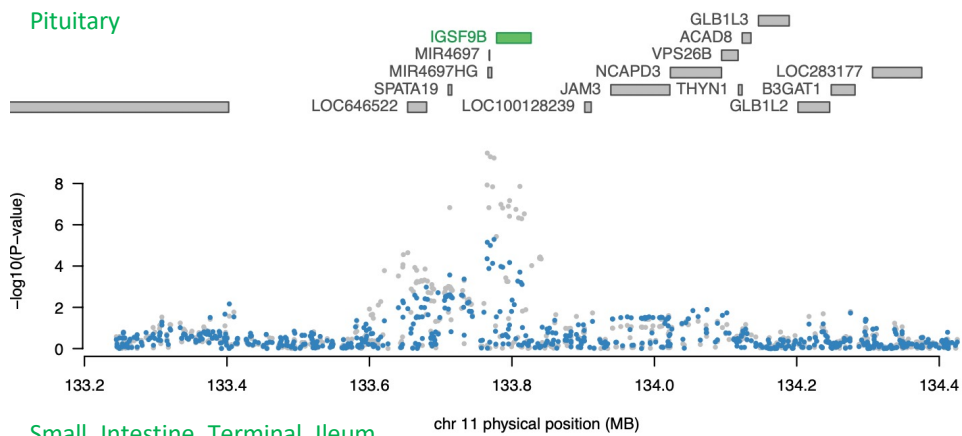
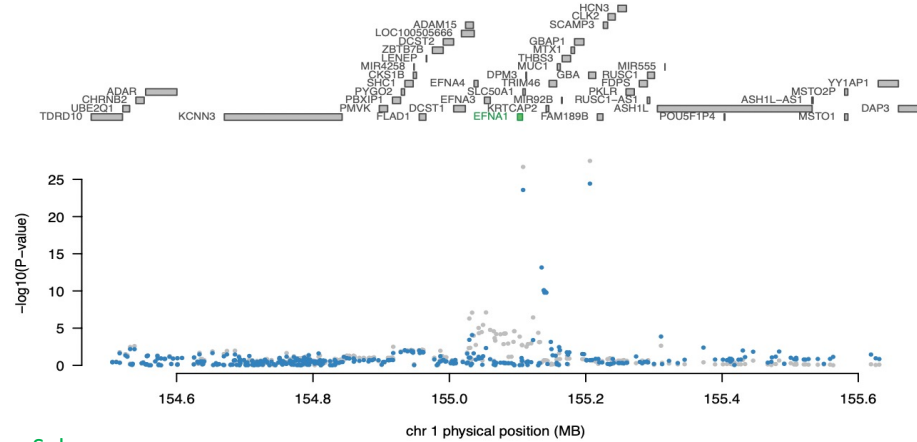(Supplementary Fig. 2.10) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
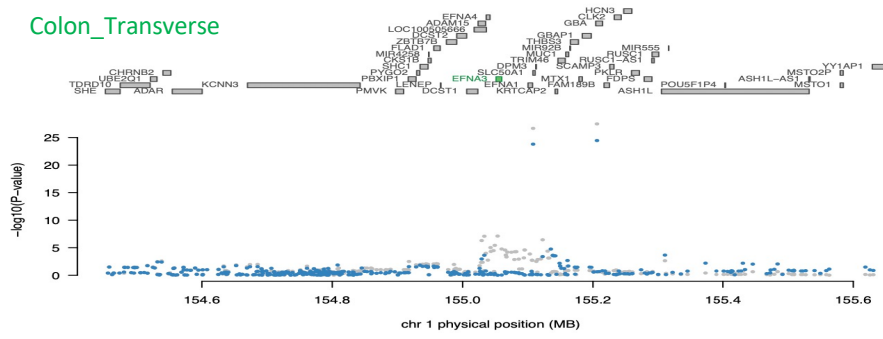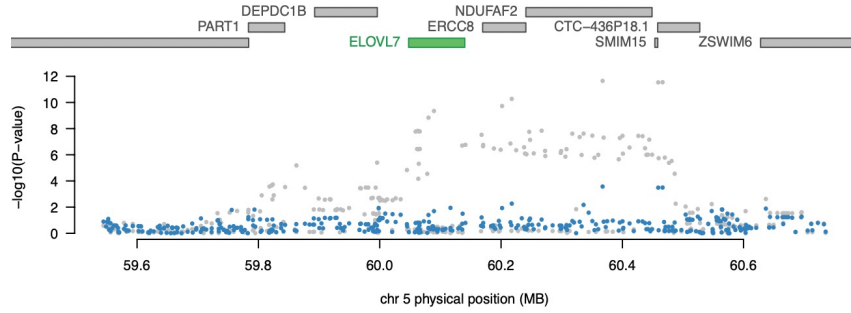
(Supplementary Fig. 2.11) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

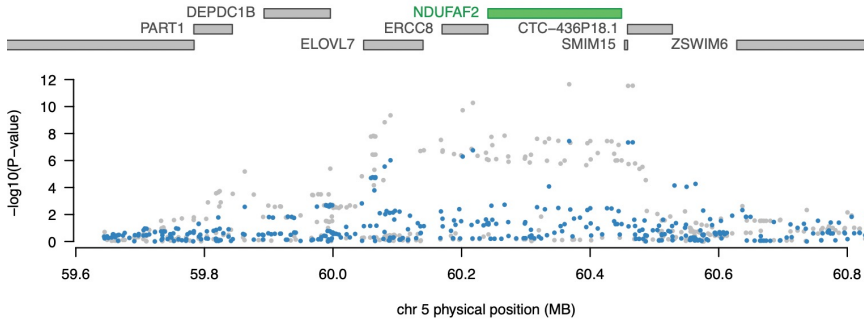(Supplementary Fig. 2.12) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

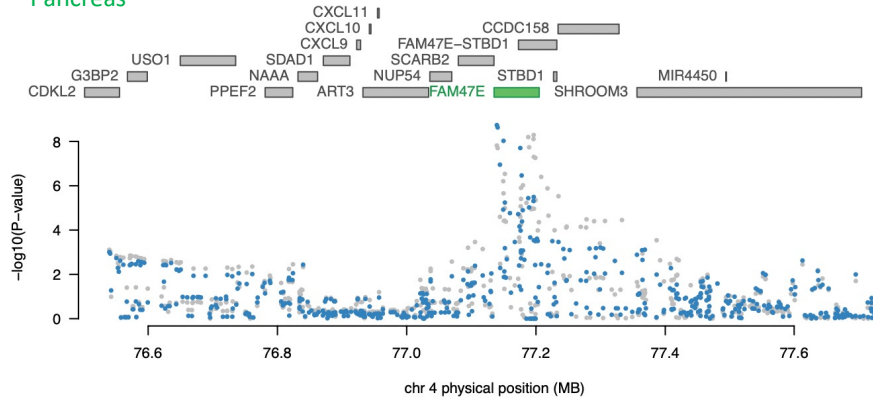(Supplementary Fig. 2.13) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
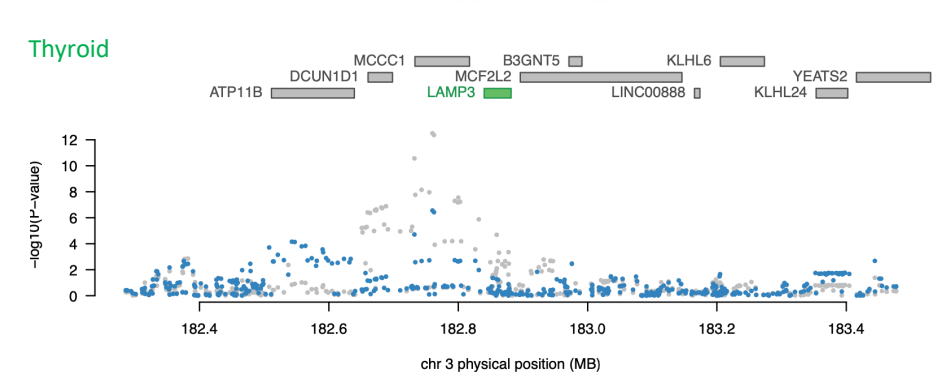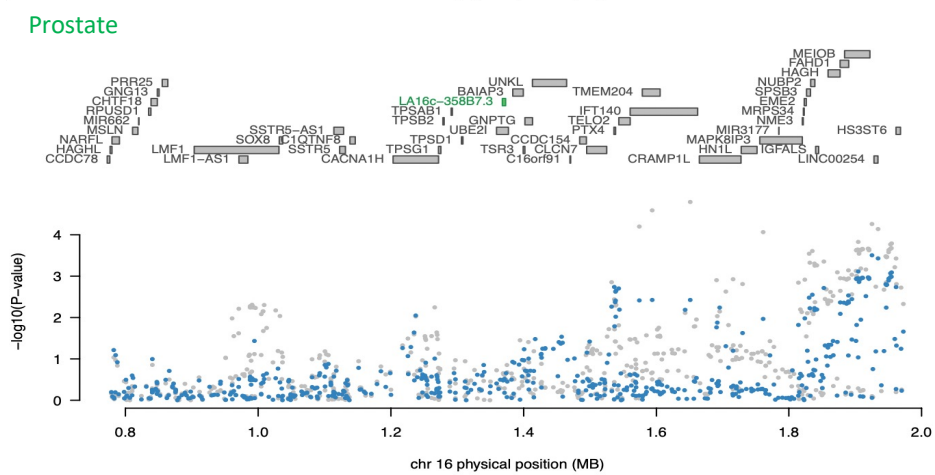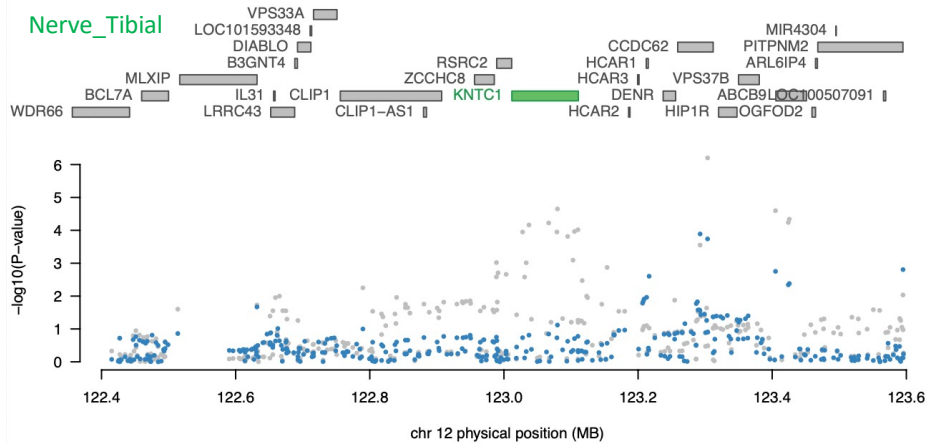
(Supplementary Fig. 2.14) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
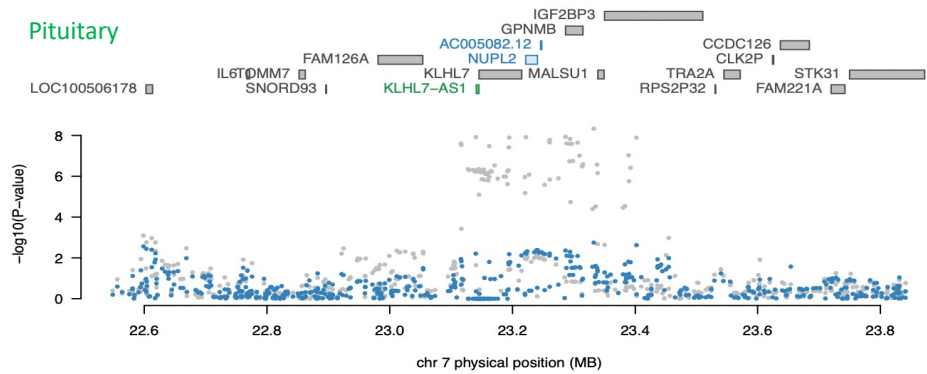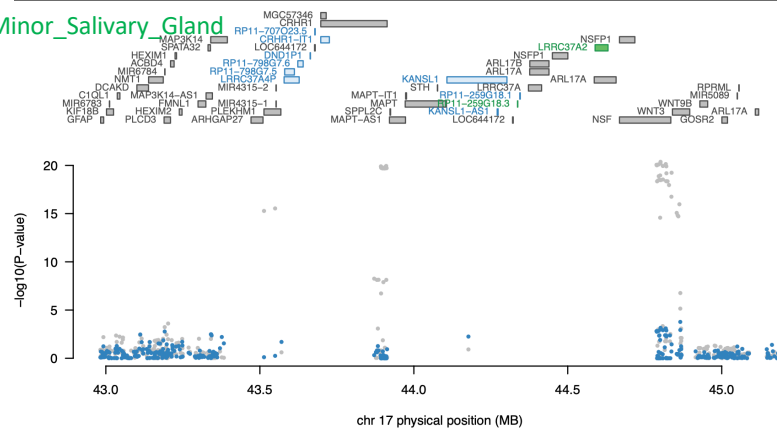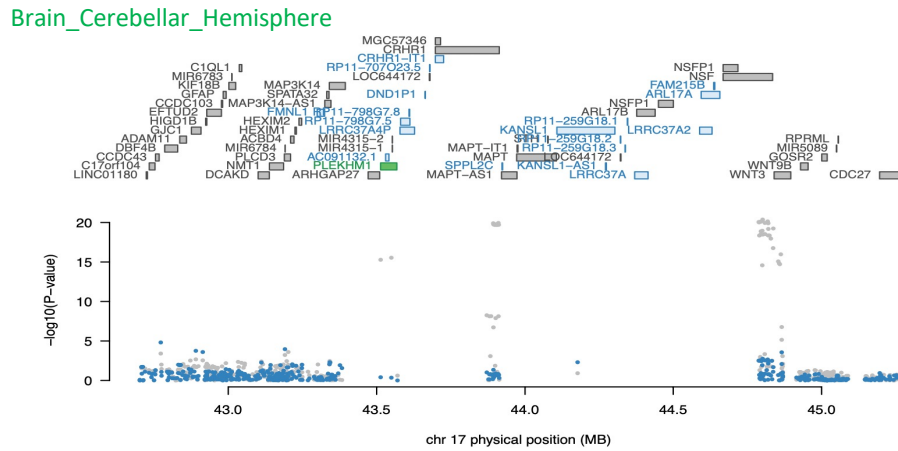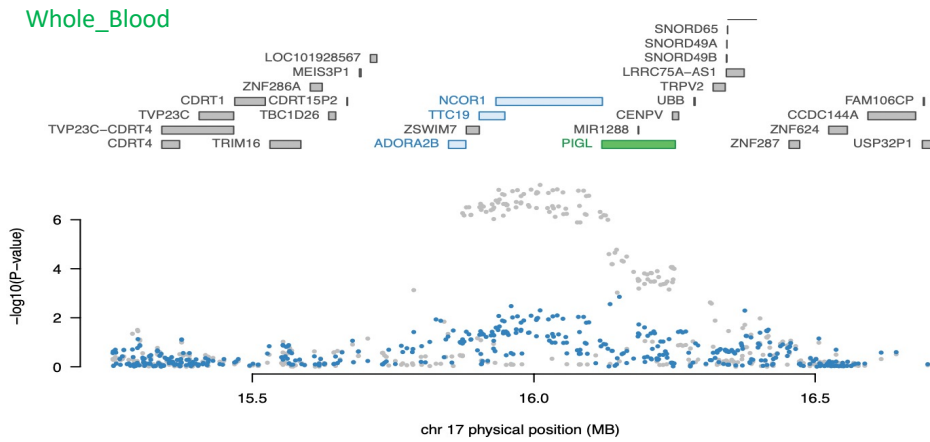
(Supplementary Fig. 2.15) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

(Supplementary Fig. 2.16) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
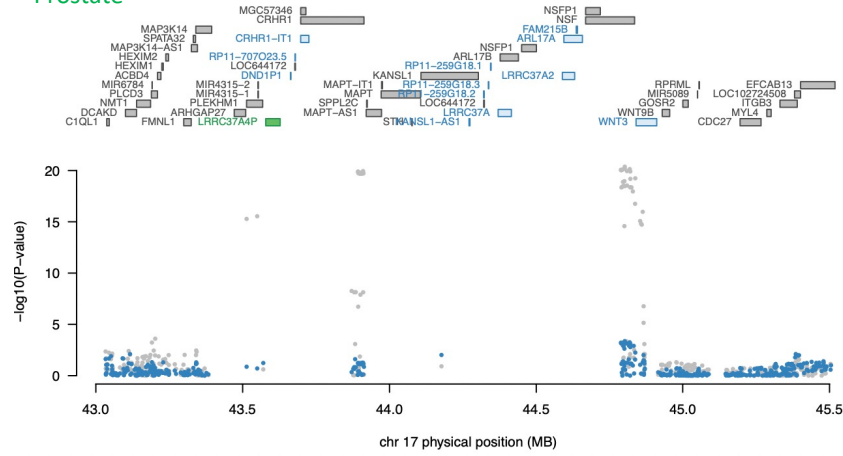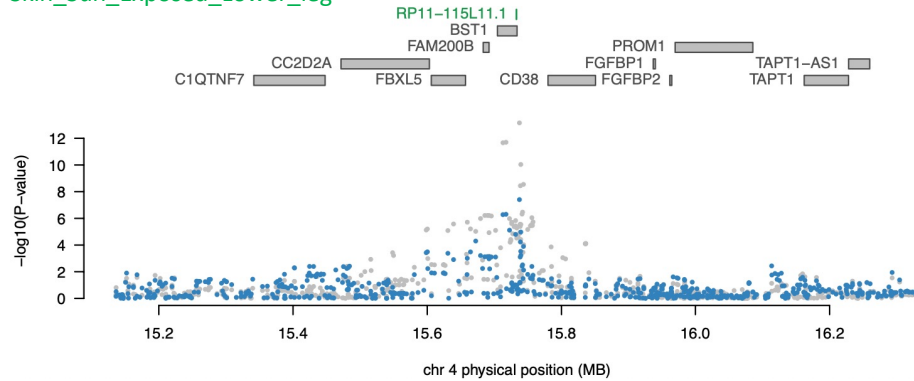
(Supplementary Fig. 2.17) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
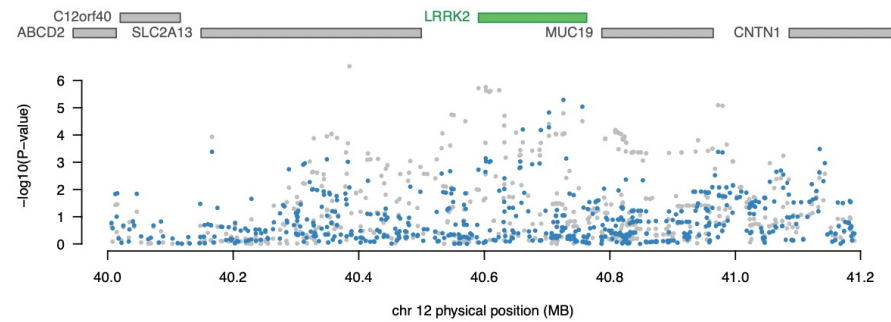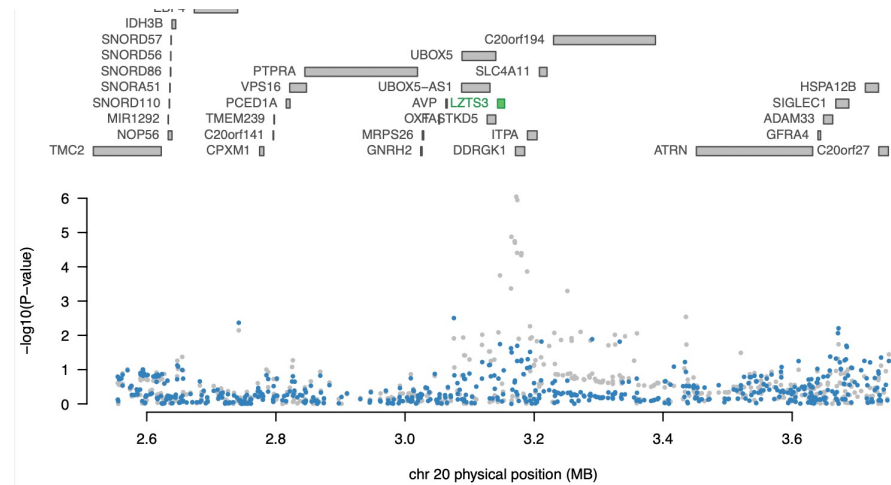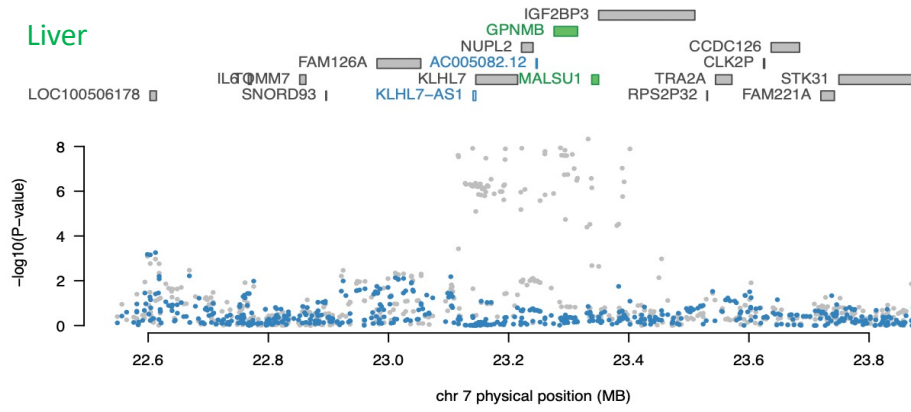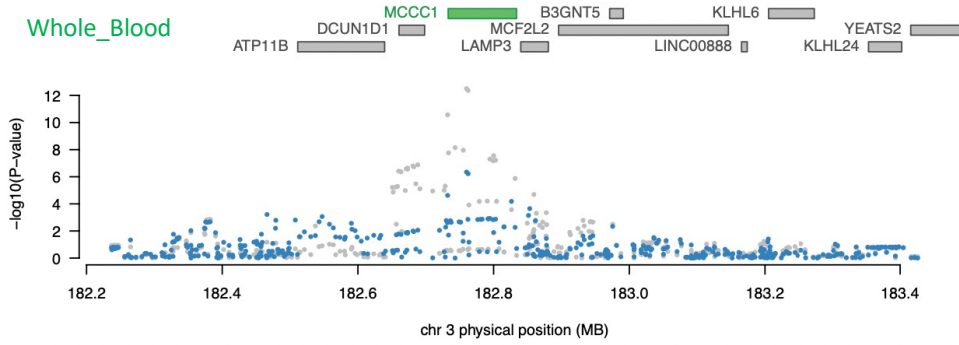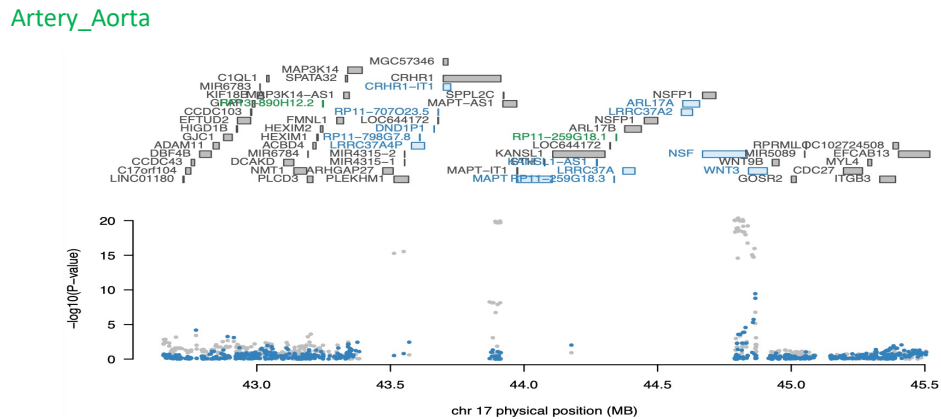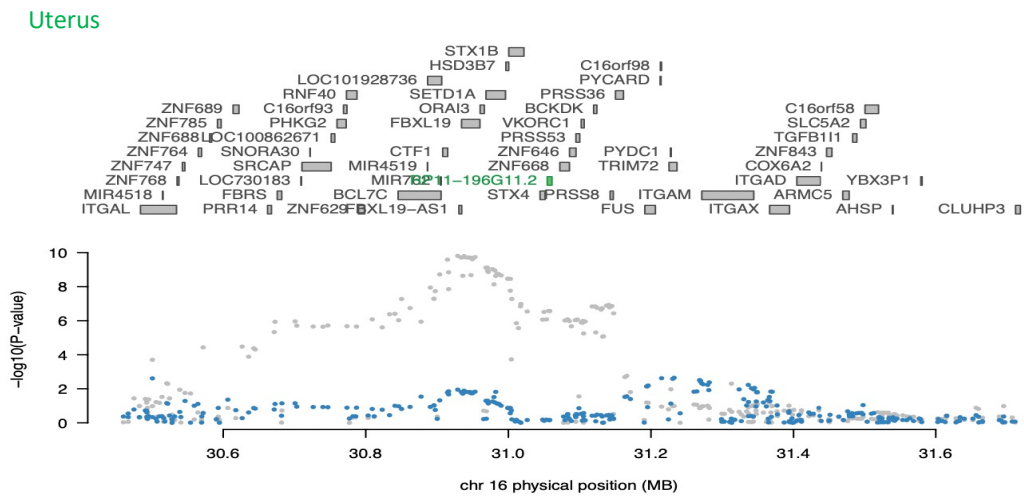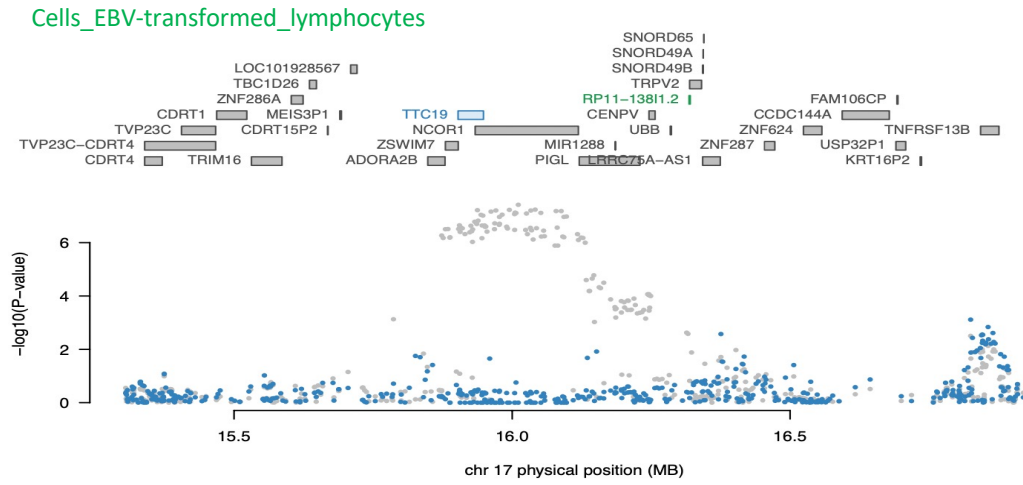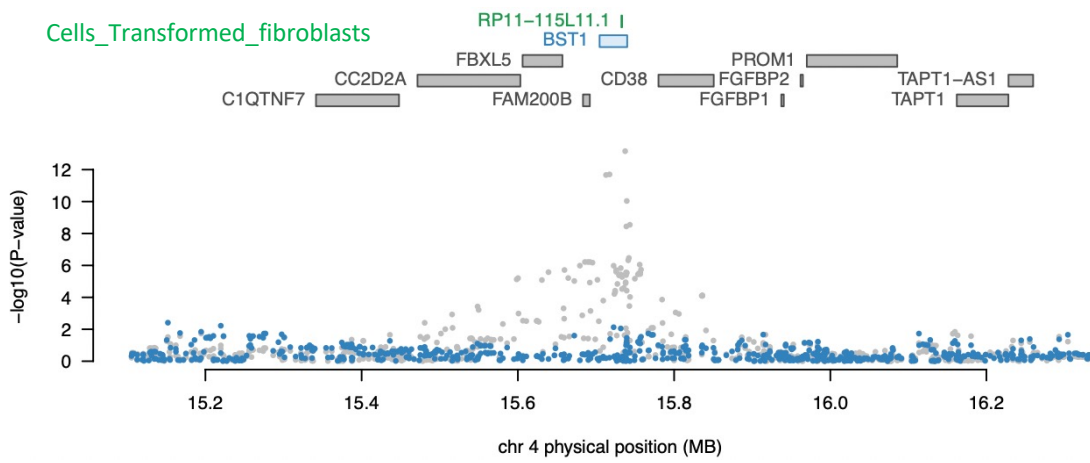
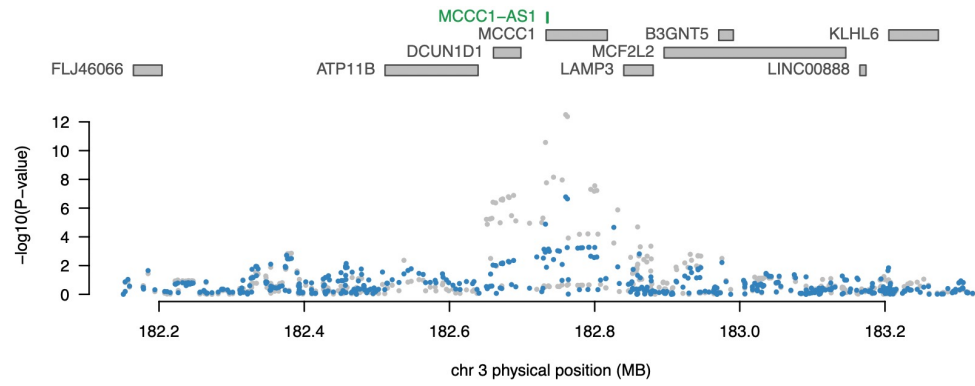(Supplementary Fig. 2.18) FUSION plots of PD TWAS locus.
Reference panel(GTEx tissues) are shown for each plot.
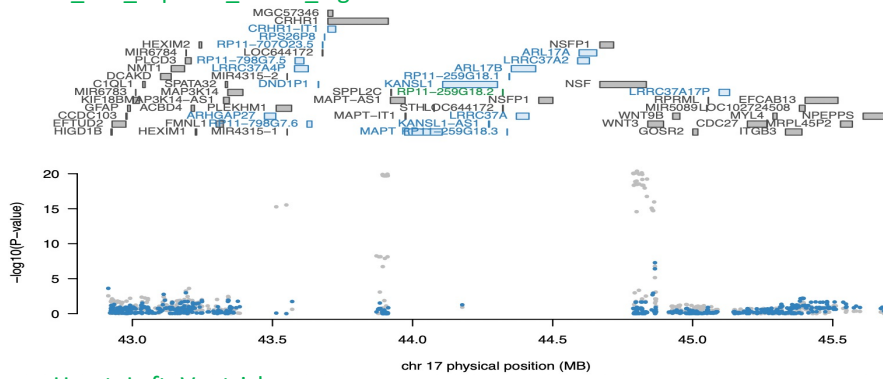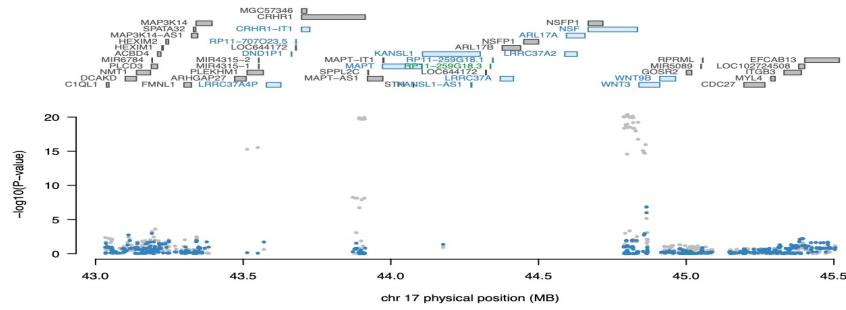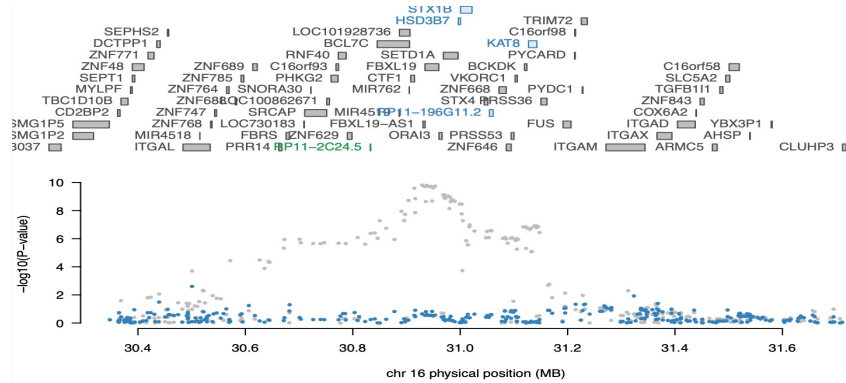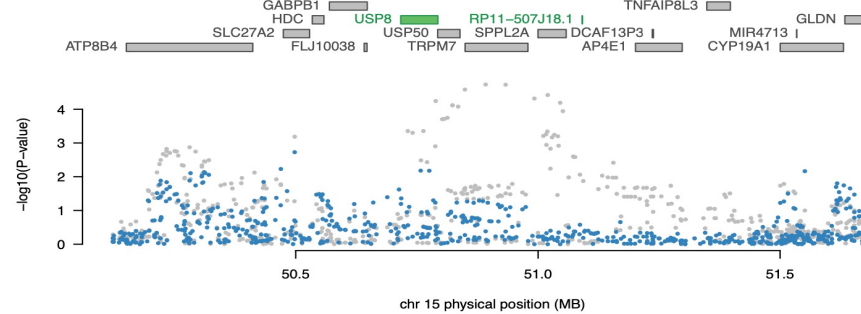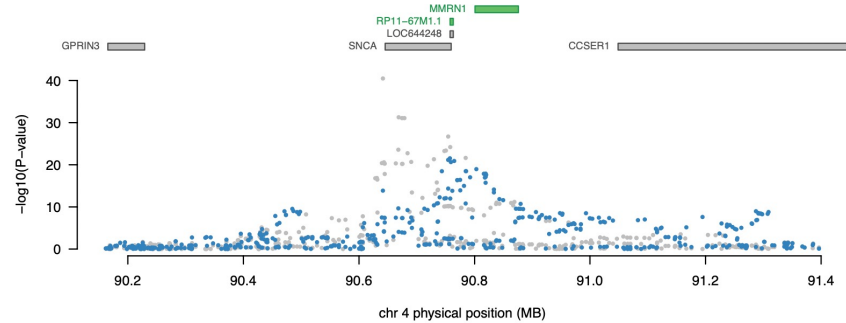
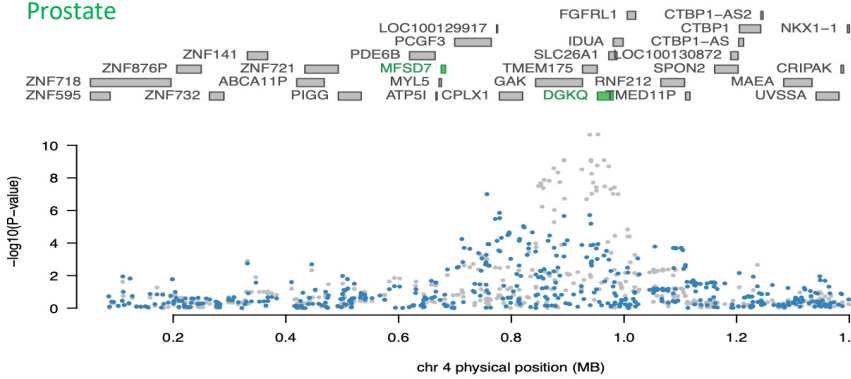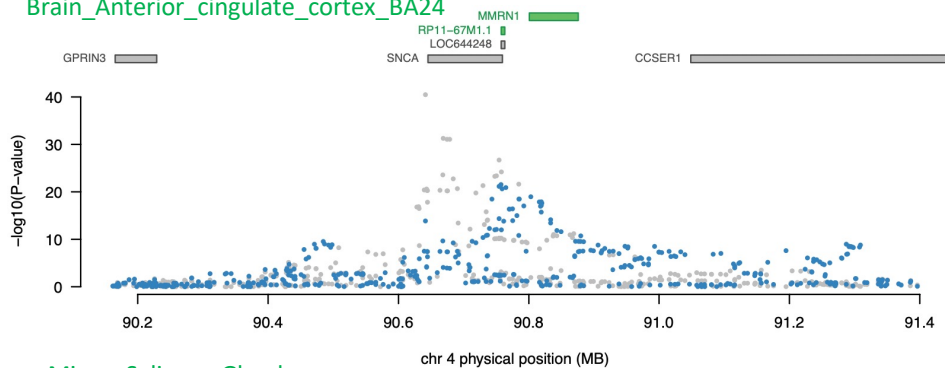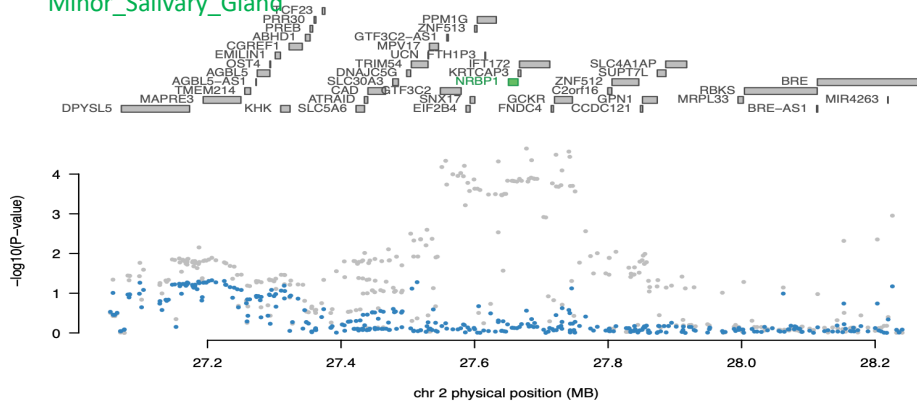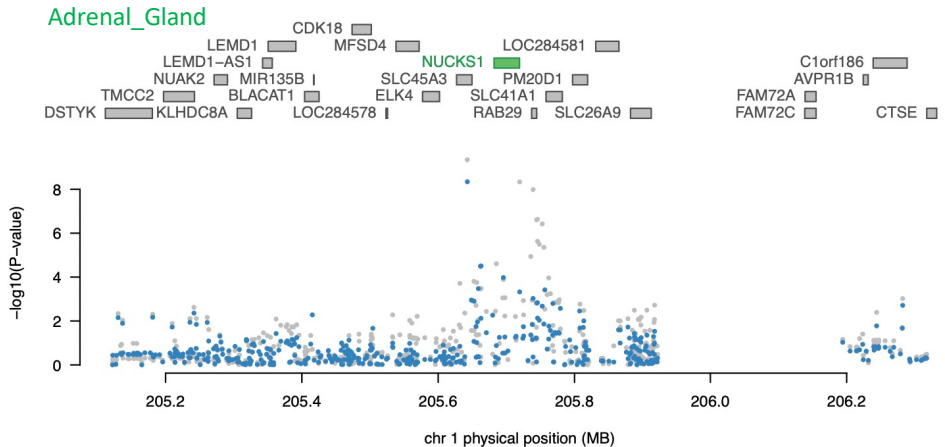(Supplementary Fig. 2.19) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
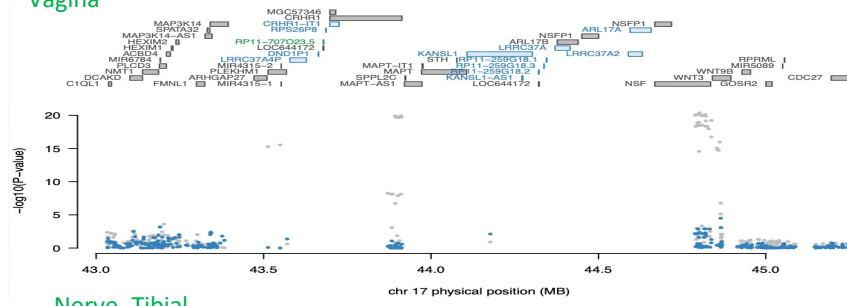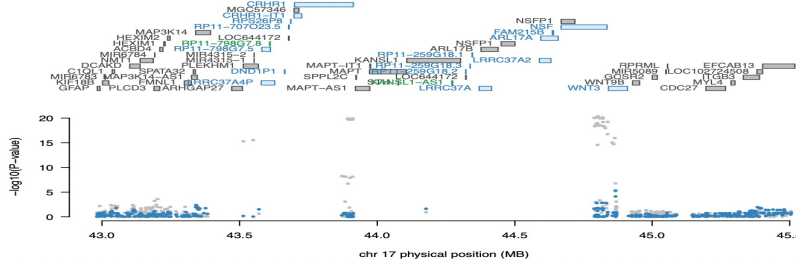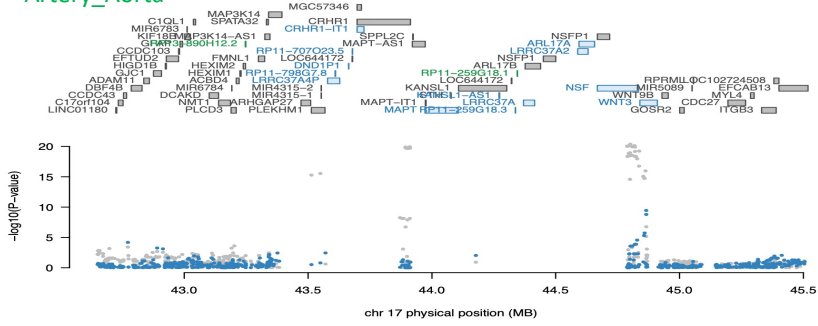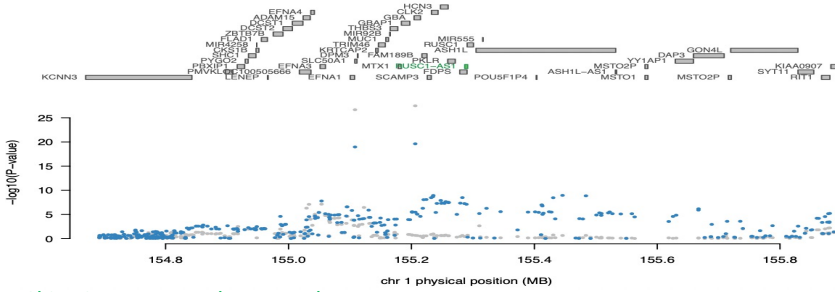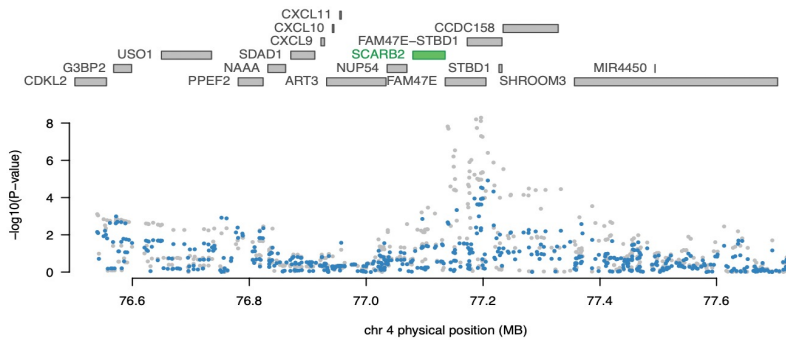
(Supplementary Fig. 2.20) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.
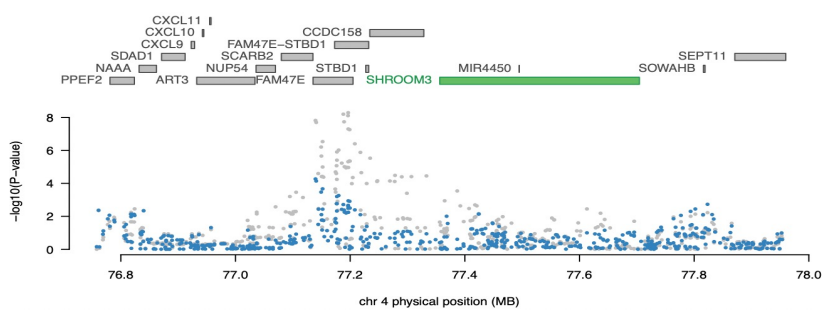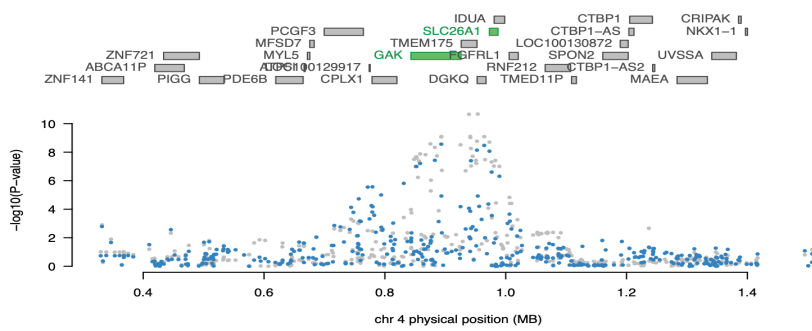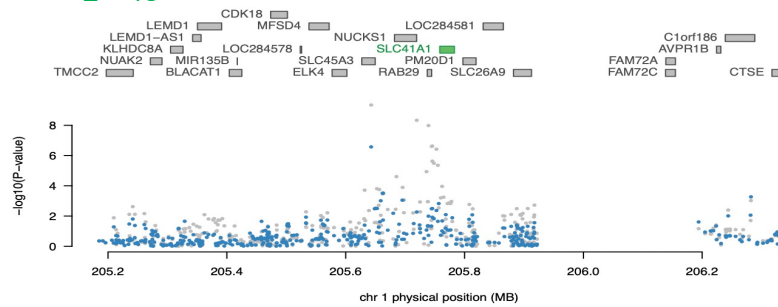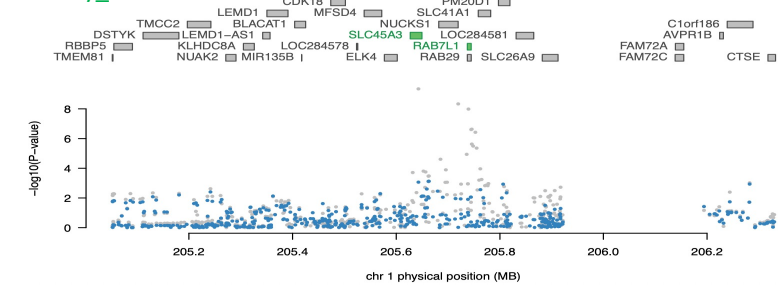
(Supplementary Fig. 2.21) FUSION plots of PD TWAS locus.
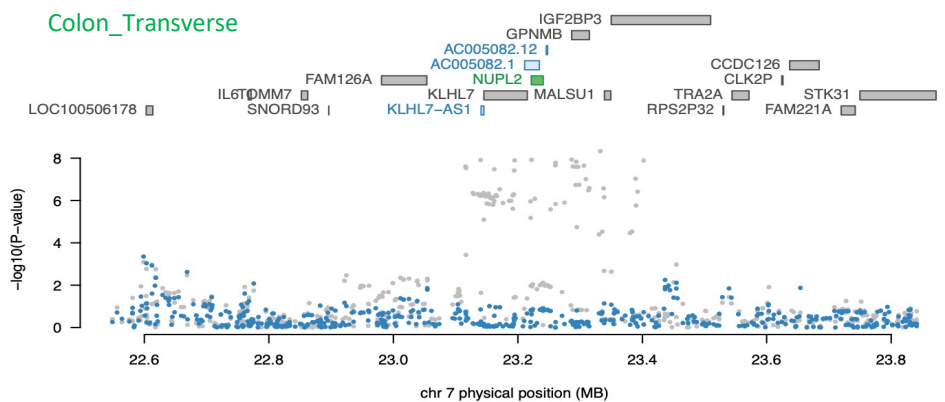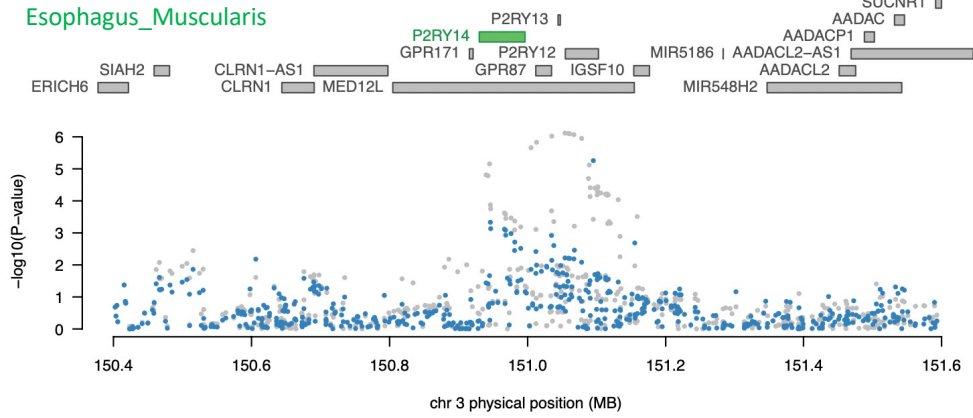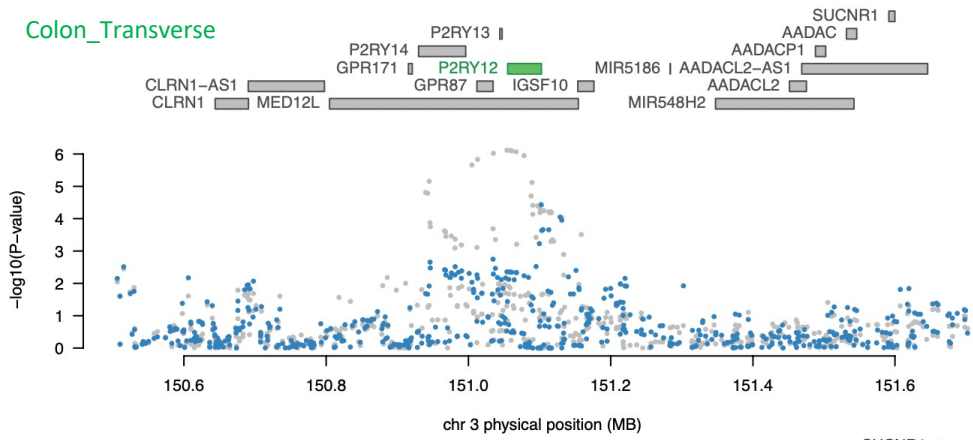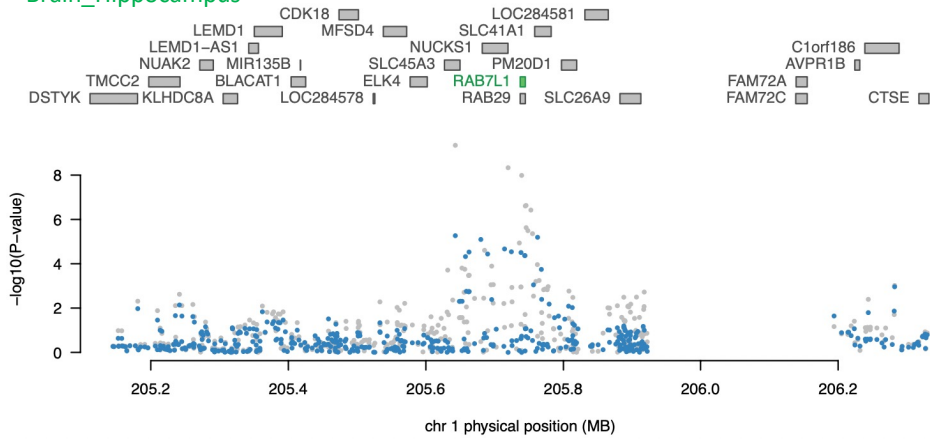Reference panel(GTEx tissues) are shown for each plot.
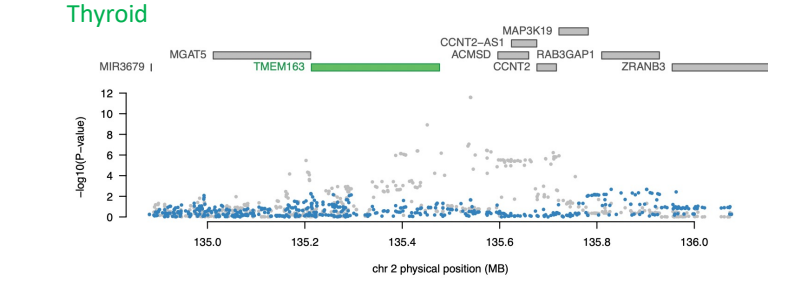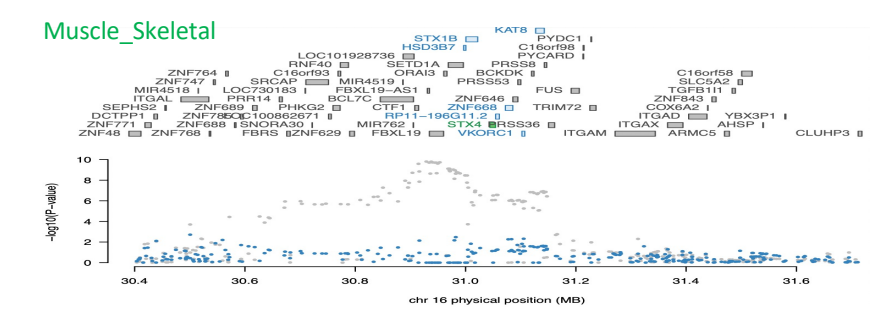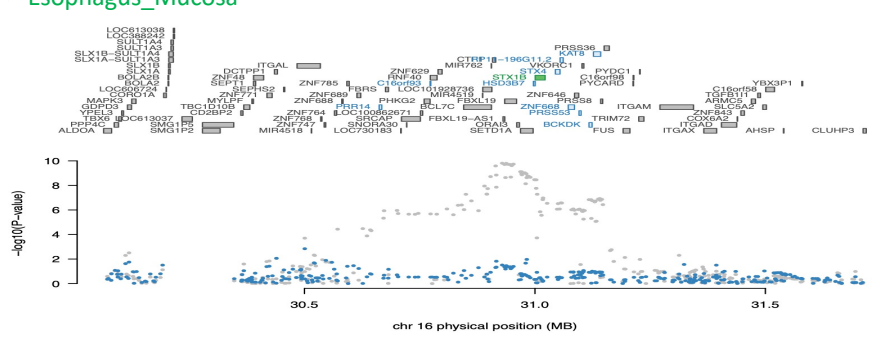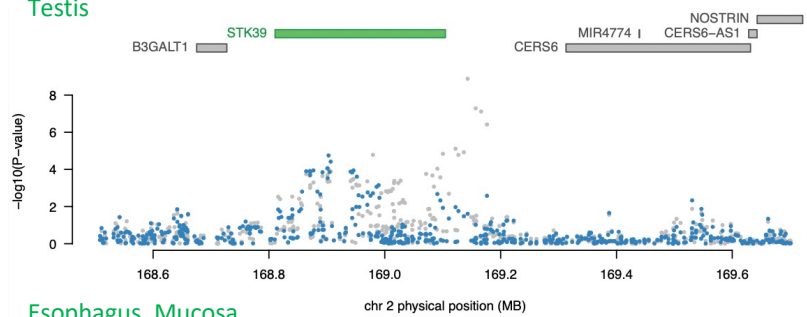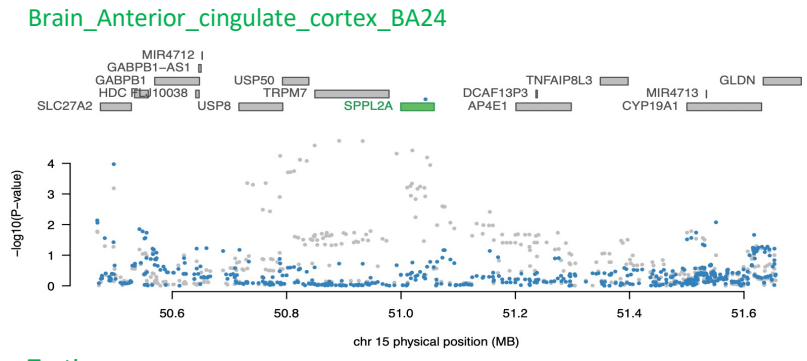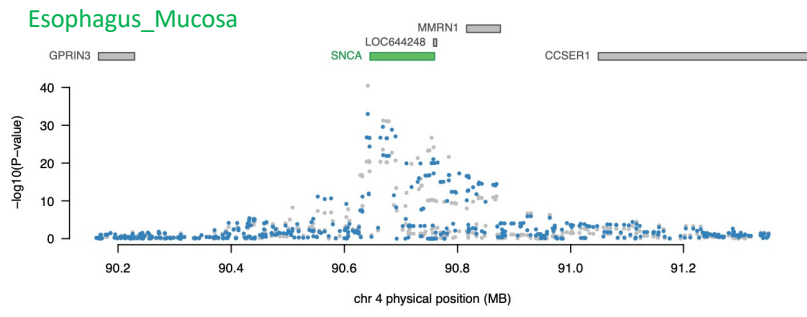
(Supplementary Fig. 2.22) FUSION plots of PD TWAS locus.
Reference panel(GTEx tissues) are shown for each plot.
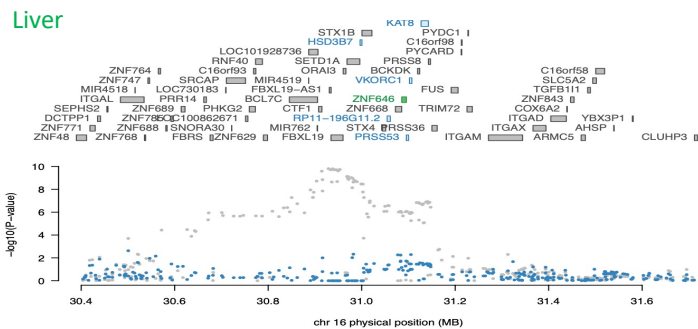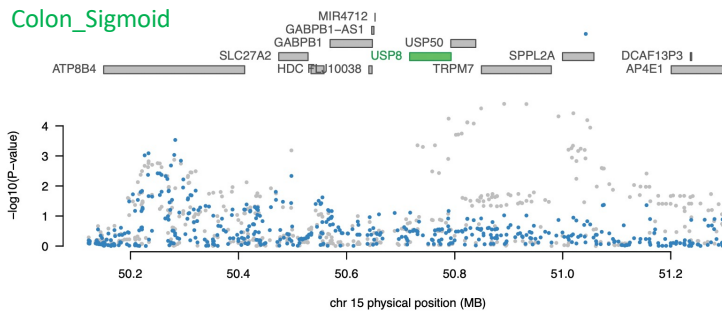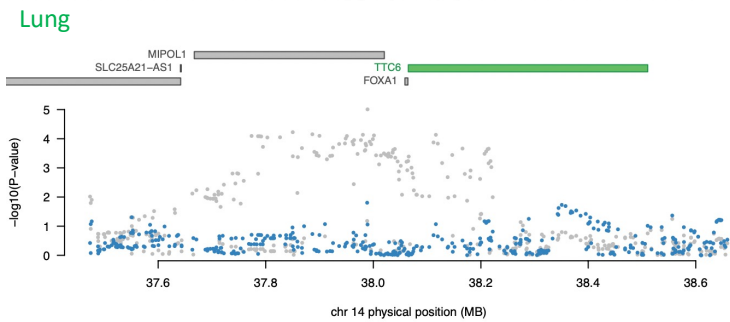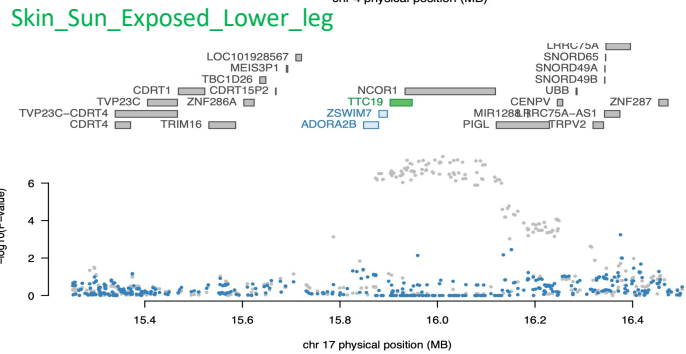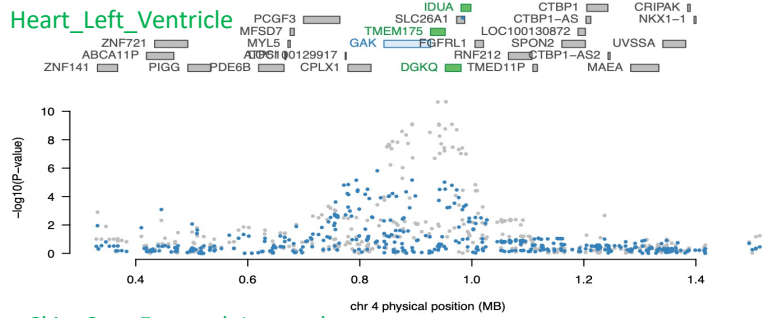
(Supplementary Fig. 2.23) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

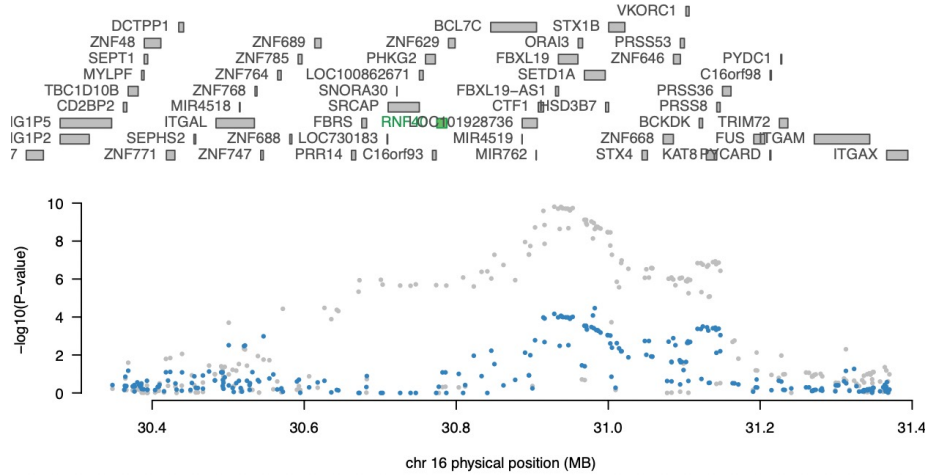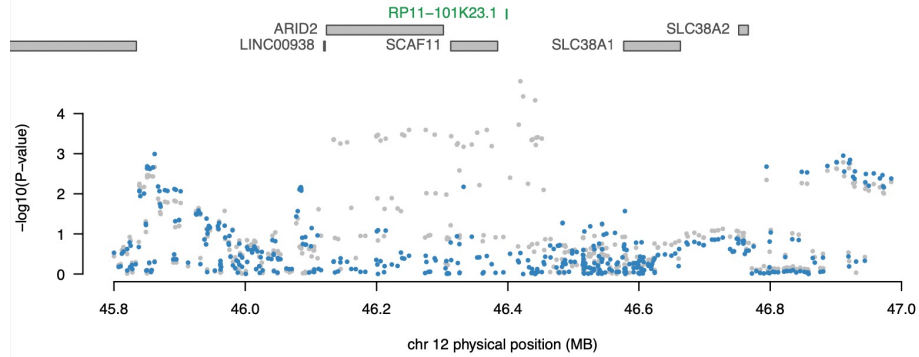(Supplementary Fig. 2.24) FUSION plots of PD TWAS locus. Reference panel(GTEx tissues) are shown for each plot.

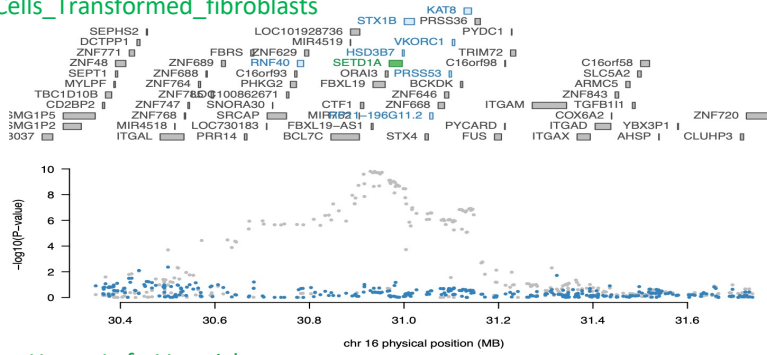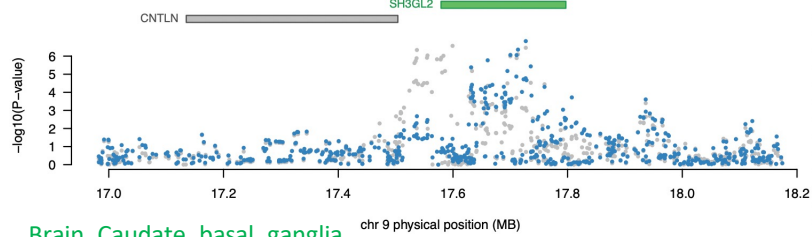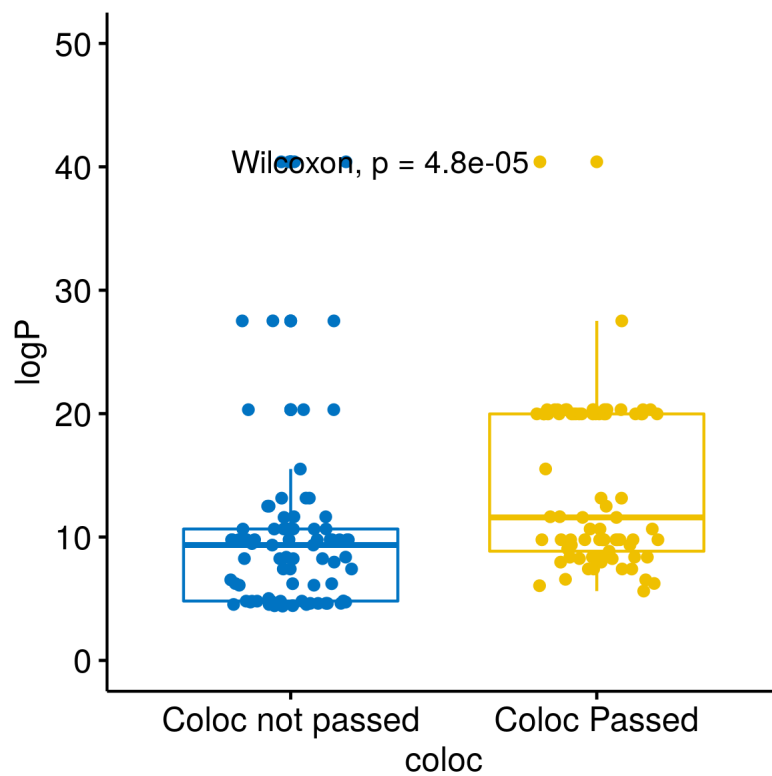(Supplementary Fig. 3.) TWAS-prioritized genes whose GWAS signals colocalized with eQTL signals have more GWAS significance compared to genes that do not show colocalize with eQTLs. Wilcoxon test was used to access the difference.
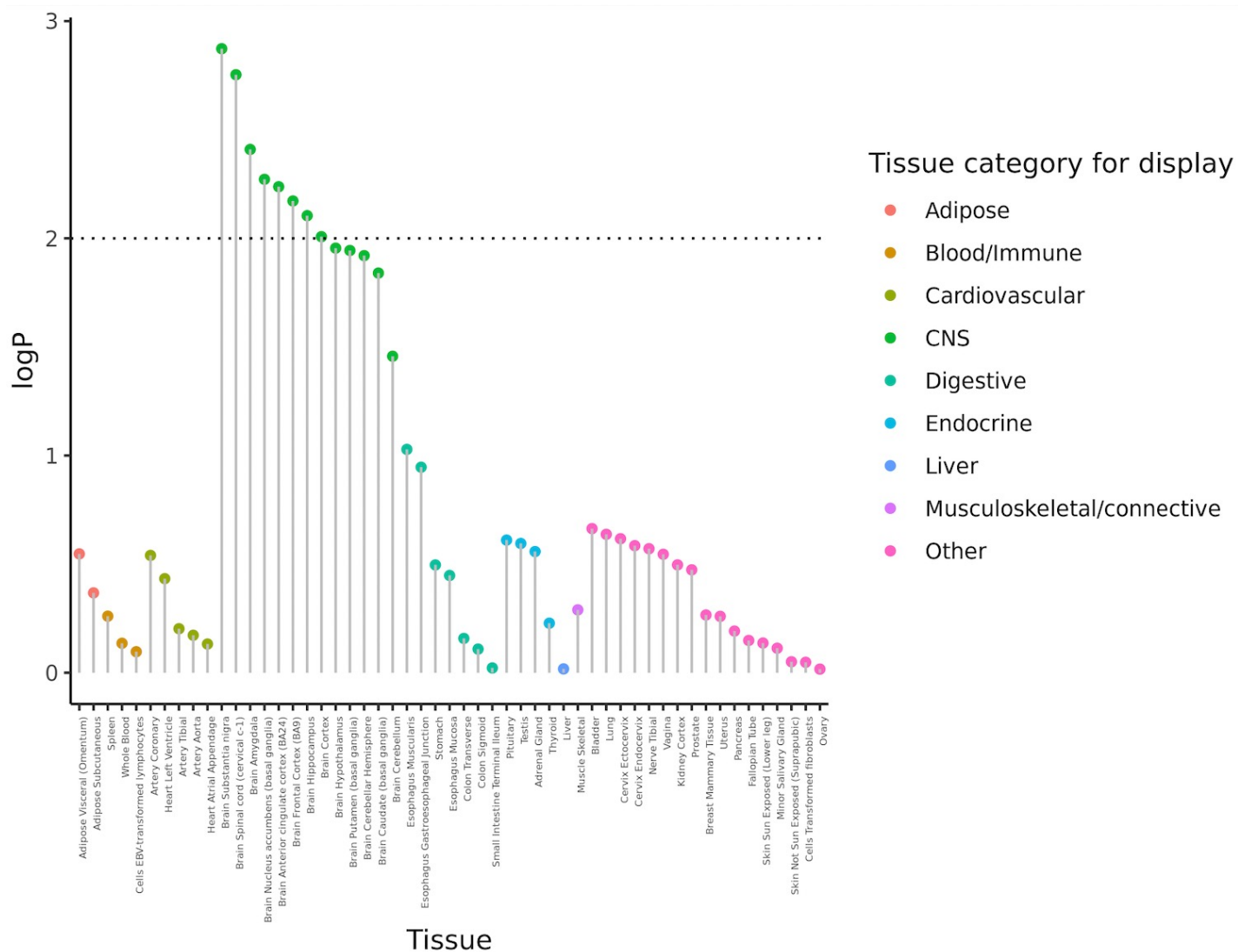
(Supplementary Fig. 4.) Multi-tissue analysis to select PD-relevant tissues via linkage disequilibrium (LD) score regression in specifically expressed genes. Among 53 tissues accessed in the GTEx project, 8 brain-derived tissues were significantly enriched (p < 0.05) for PD heritability in regions surrounding specifically expressed genes.
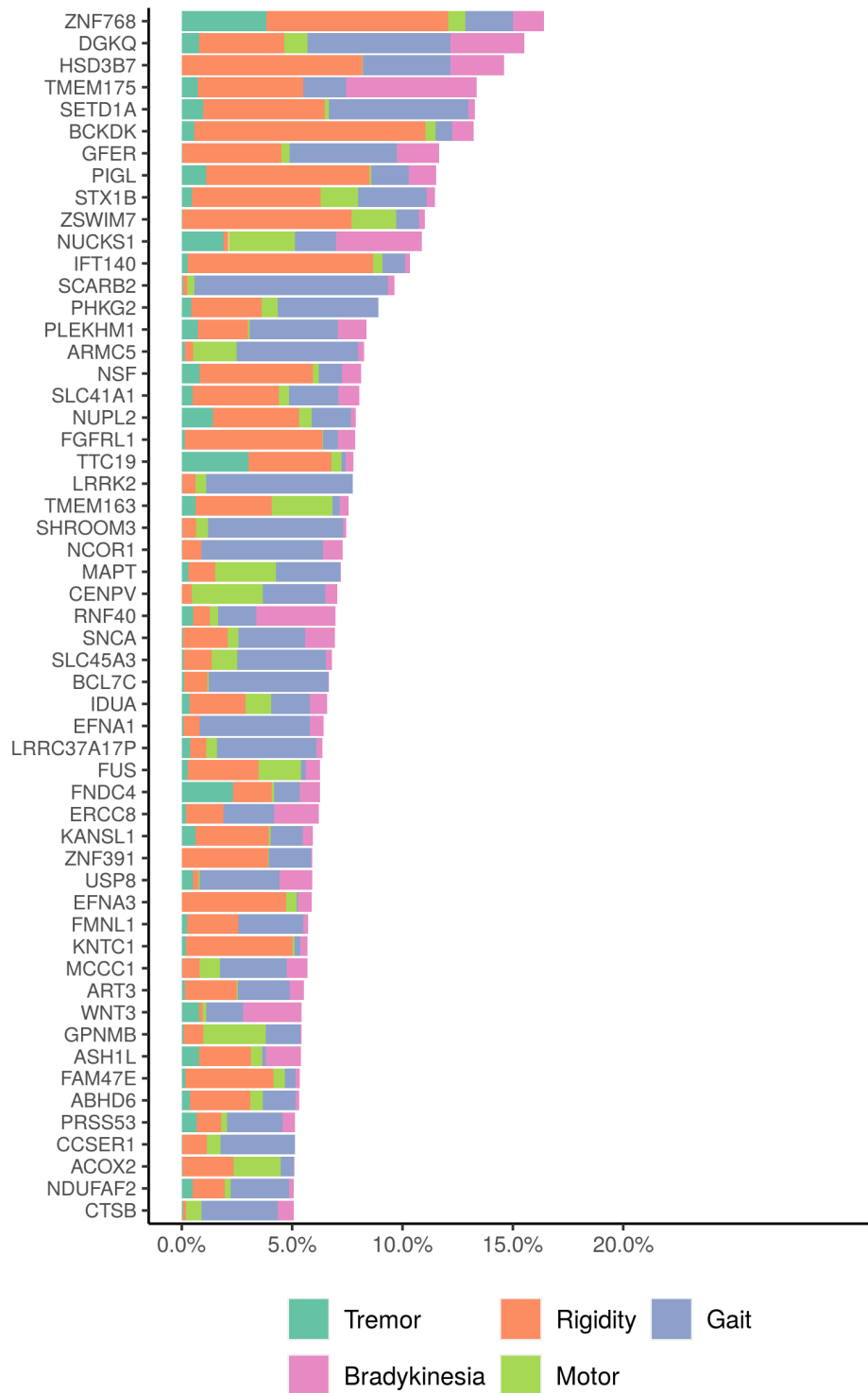
Supplementary Fig. 5. Result of applying a linear mixed model to correlate genes expression with clinical traits. The 55 shown PD candidates correspond to genes whose differences in expression are correlated with 5% or more of the summed variance of the indicated clinical traits among defined PD cases and controls.
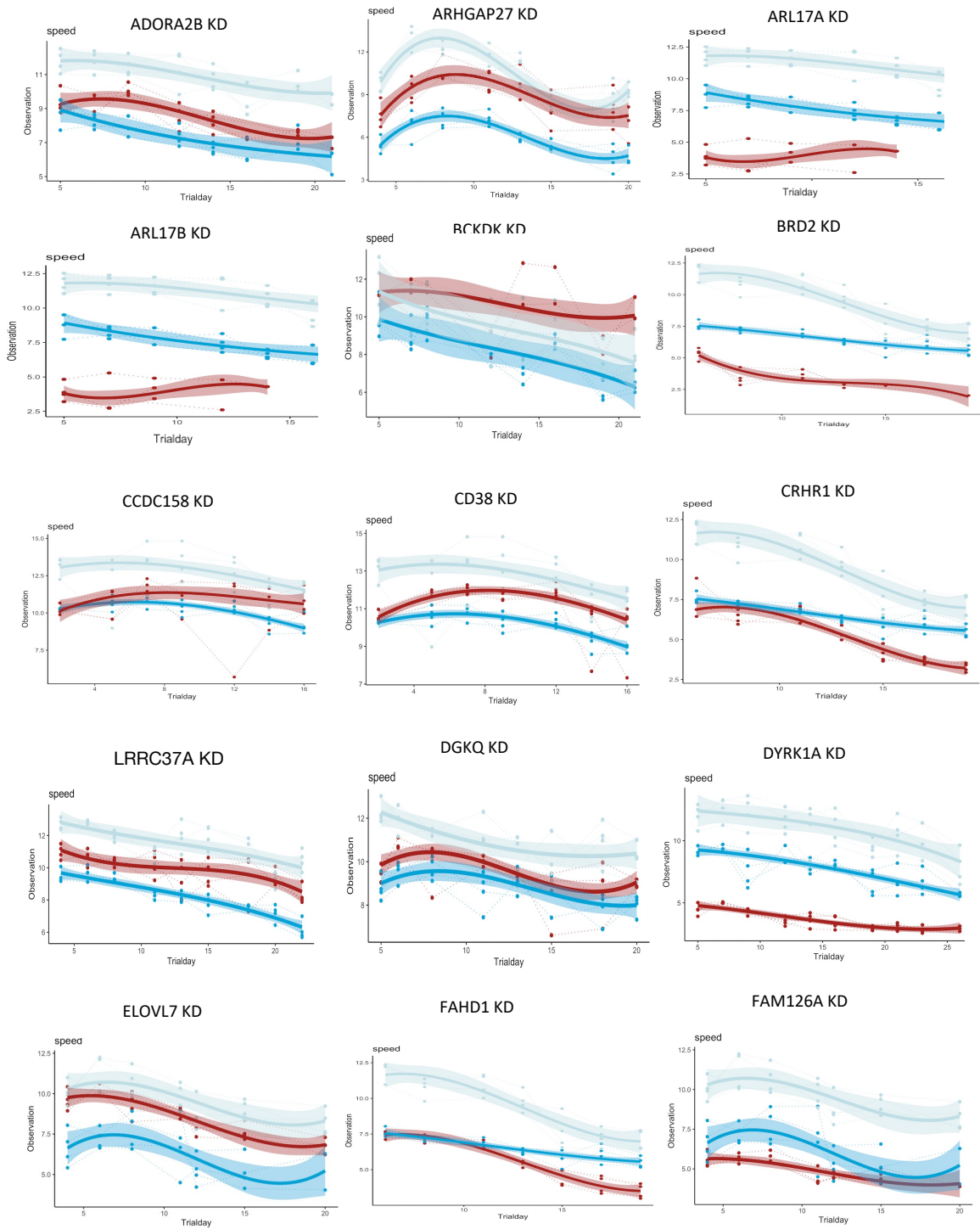
Supplementary figure 6.1
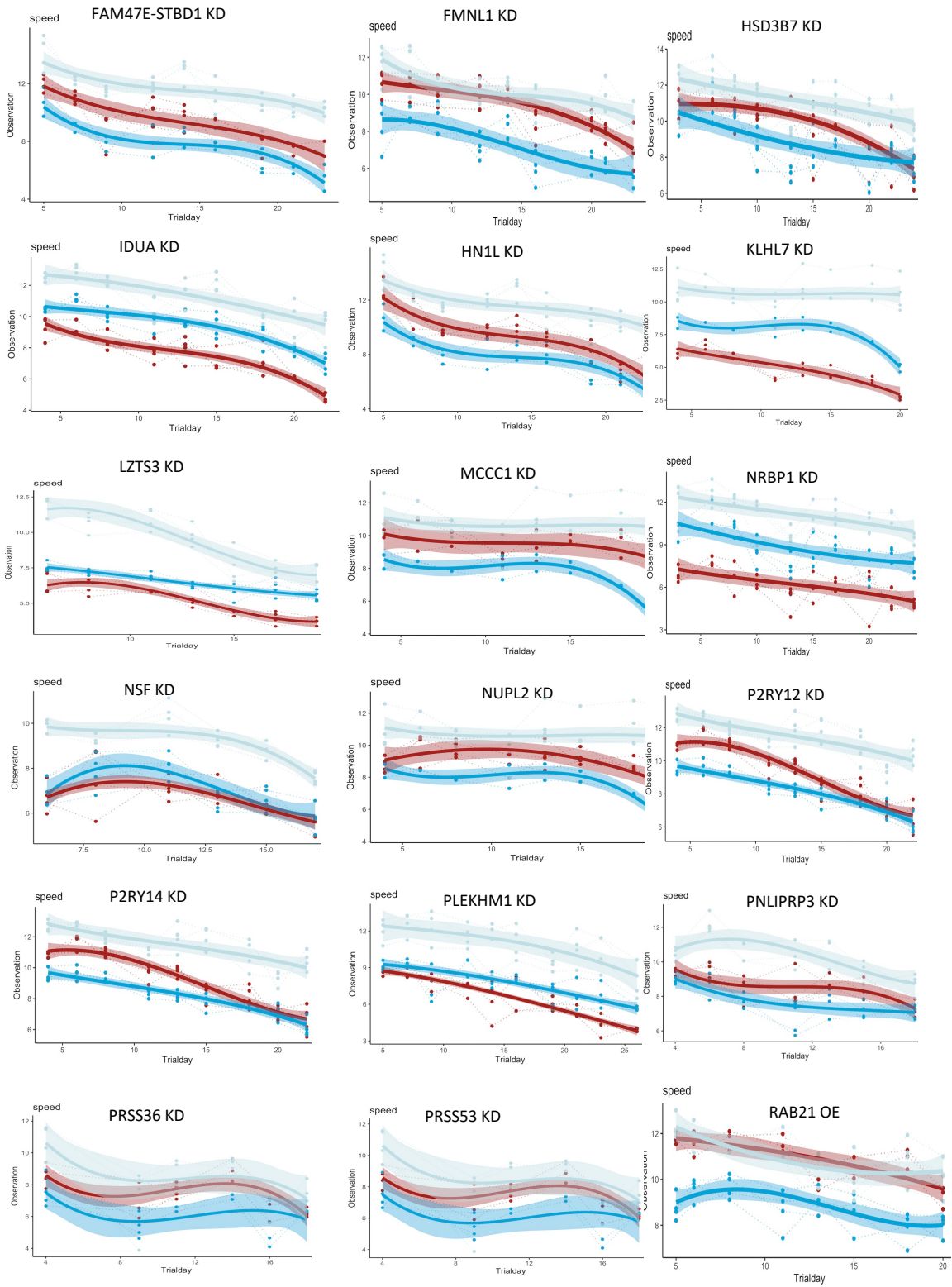
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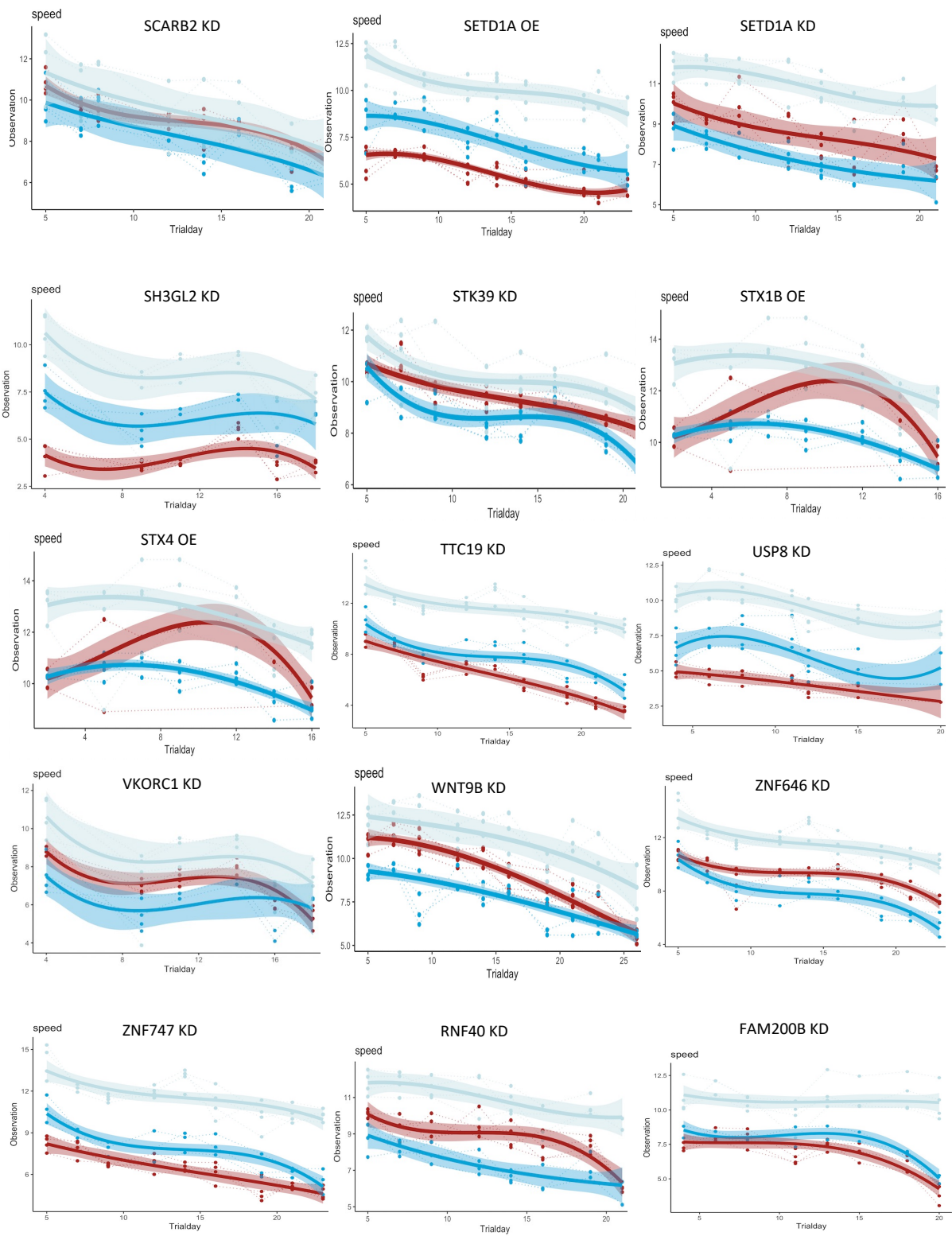
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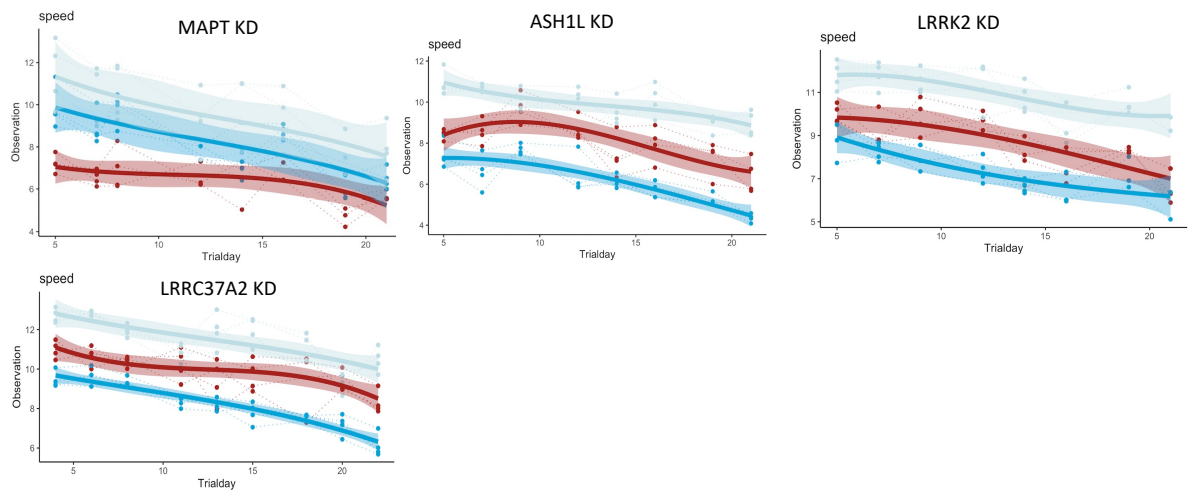
Supplementary figure 6.1-6.4. Specific graphs depicting speed as a function of age for the alleles listed in Figure 4B, which match to the modifiers. Negative controls with scrambled hp-RNA are shown in grey. Blue depicts the age-related performance of α-syn/scramble. The performance of animals harboring the allele indicated on top and α-syn is shown in red. Third degree polynomial regressions (lines), confidence intervals (shaded area), and individual data are shown in the graphs (dots). When examined using the linear mixed effect model ANOVA, all studies shown are statistically substantially different (p<0.05).
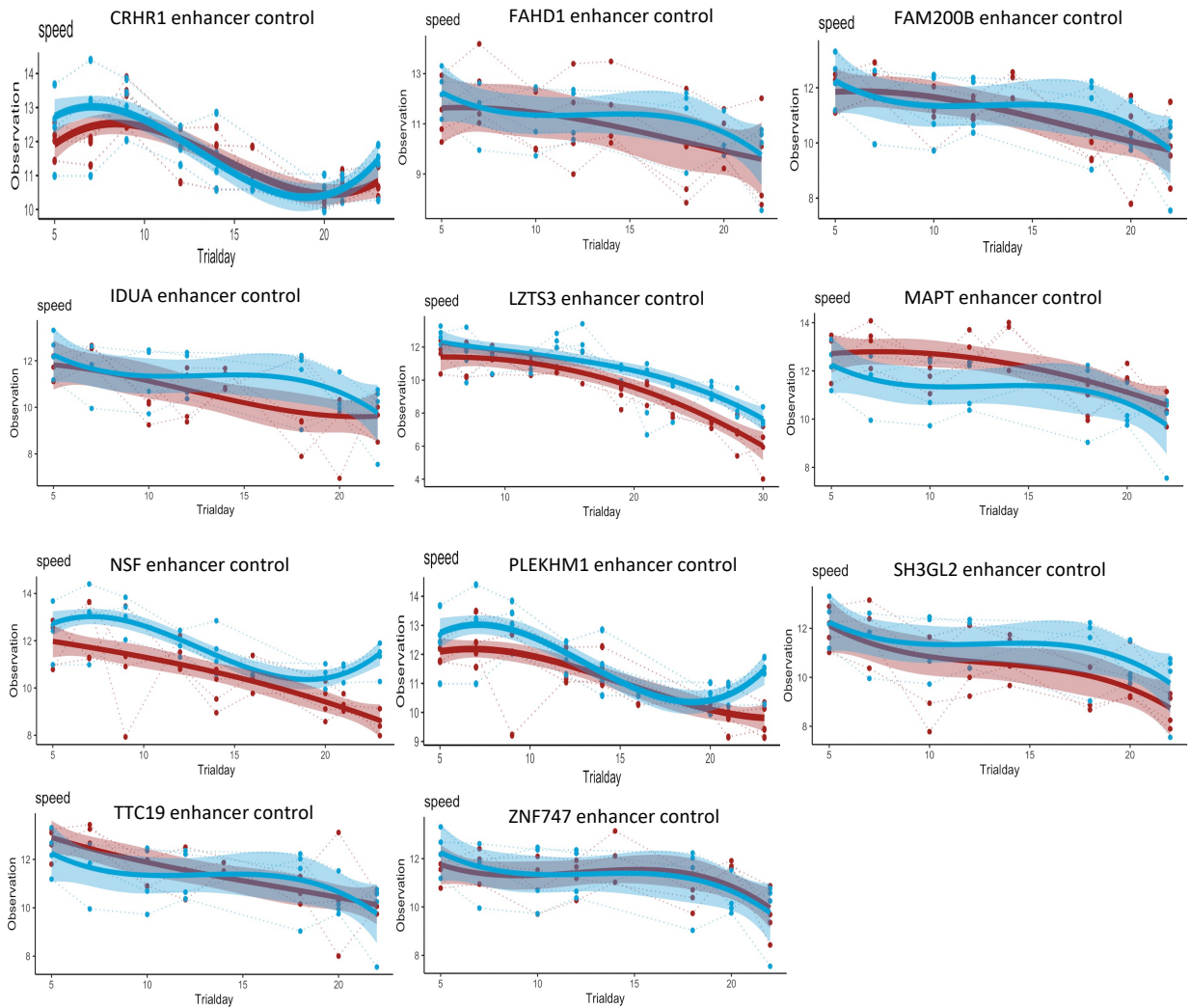
Supplementary figure 6.5. Specific graphs depicting speed as a function of age for the alleles listed in Figure 4B, which match to the enhancers. Blue lines indicate the motor performance of negative controls (*elav_{C155}/w1118*). Red line shows motor performance of animals carrying the indicated modifier alleles but not expressing human α-syn. Note that some modifiers impair motor performance of both the negative controls (*elav_{C155}/w1118*) and the PD animals