Supplementary Materials of "**Genotype-based Gene Signature of Glioma Risk**" by YT Huang, Y Zhang, Z Wu and DS Michaud

## I. Genotype Imputation

Because we propose to conduct multi-SNP analyses, missing genotype needs to be imputed in order to preserve the most information. Before imputing missing genotypes using IMPUTE2[1], the genotype data need to be in the same build as the reference panel. We chose the latest reference data, 1000 Genomes haplotypes Phase 3 integrated variant set release[2] in NCBI build 37 (hg19) coordinates. The eQTL genotype data was in the same build as reference data while the GWAS data are in hg18. We lifted the build of three GWAS datasets (550K, 610Q, 660W) from hg18 to hg19 using UCSC liftOver tool[3], and then merged all three with eQTL SNP data using PLINK[4]. The final merged file contained 511,126 SNPs. To increase the computation efficiency, the combined genotype data was pre-phased into haplotypes using an accurate phasing method, SHAPEIT2[5]. The estimated haplotypes were fed into IMPUTE2 program with seed 424242 and effective population size 20,000. We performed the imputation on one chunk of chromosome at a time, while the chunks were pre-defined based on hg19 cytoband positions provided by UCSC genome browser. The imputed genotype data contained non-missing genotypes of 509,100 SNPs for 372 samples in eQTL study and 4349 samples in GWAS study. SNPs with overall minor allele frequency less than 5% were excluded, resulting 482,217 SNPs. Hardy-Weinberg Equilibrium was evaluated for the 482,217 SNPs showing no inflation of disequilibrium (sFigure 9). By querying Ensemble release 75 database with use of R/Bioconductor package biomaRt[6], we were able to determine chromosome and base-pair positions for 481,664 SNPs, which were the genetic loci that we used for further analyses.

## II. Justification of using minimum p-value as the test statistic in iGWAS omnibus tests

We considered the following three models (and hypotheses): 1) the genetic effect of the gene on the glioma risk is not through its own transcription, 2) the effect is through both genetics and transcription of the gene but not their interaction, 3) effect is through both plus their interaction. The minimum p-value approach is to seek any possible evidence about the association of a gene with glioma risk given that we have three potential models. Alternatively, one may select the maximum p-value in the three models as the test statistic. The difference of the minimum p-value and the maximum p-value approaches is that the former considers the gene as a susceptibility one for glioma if any of the three has a significant effect, and the latter does so only if all three have significant effects. We think that the minimum p-value aligns better with our scientific interests. More intuitively, when one has three candidate models, the usual practice is to fit all three and see which gives us the most significant results, i.e., the smallest p-value. To take into account the fact that three models have been considered to obtain the result, the proposed perturbation procedure accounts for the multiplicity and the correlation of the three models. However, if one is interested in identifying genes with all three have significant effects, our proposed procedure can readily accommodate the maximum p-value.

## III. Sensitivity analysis by adjusting for population stratification in eQTL analyses

We conducted additional analyses adjusting for the principal components (PCs) in the eQTL modeling. Specifically, we adjusted for four PCs to account for population stratification in univariate eQTL modeling, which was then used to build multivariate eQTL models for every transcript expression, again adjusting for the four PCs. The built multivariate eQTL models for all transcripts were utilized to predict transcript expression for GWAS subjects as described in Methods. The eQTL association of the SNPs with the transcript expression with and without PCs adjustment shares extremely high correlation of 0.995

(sFigure 2a). An even higher correlation was observed in eQTL predicted transcript expression for the GWAS subjects (with vs. without PCs adjustment), 0.9999 (sFigure 2b). We then used the newly predicted transcript expression for the iGWAS analyses. The results of the 55 candidate transcripts are very similar to our previous analyses (sTables 4 and 5).

The reason that we did not adopt this strategy as our main analyses is as follows. The purpose of building eQTL models is for prediction, i.e., to predict the unknown gene expression pattern for the GWAS subjects. The adjustment of the population stratification by PCs is to seek the prediction on top of the ancestry, which may limit the performance of the prediction. The adjustment of population stratification by PCs is due to our concern about the *confounding* by ancestry in relation to the glioma risk, not the *variability* by ancestry. To predict the expression pattern based on the eQTL models adjusting for PCs tends to lose both of them, but our current strategy (not adjusting for PCs in eQTL analyses but adjusting for them in GWAS) preserves the variability and maximizes the power of predicting gene expression but still accounts for the potential confounding in the iGWAS analyses.

## IV. Exploratory validation of TCGA low-grade glioma (LGG)

We ranked the expression values of the four candidate genes (*DRD5*, *WDR1*, *NOMO1*, *PDXDC1*) in LGG tumor and normal tissue with respect to their own transcriptome, and compared whether the ranks between the LGG and normal tissues were significantly different. With this analysis, we were able to validate the two most significant genes, *DRD5* and *WDR1* (sFigure 10): *DRD5* has much lower expression level, and *WDR1* has higher expression in LGG compared to the normal tissue. This exploratory analysis is preliminary due to the lack of matched normal tissue for LGG tumor, and has the following limitations. First, the gene expression profile of the normal tissue and the LGG tumor tissue was not derived from the same project; the technical difference may contribute bias to our analyses. Secondly, the two

expression profiles were measured with different technology for expression profiling. Although we compared the ranking within their own transcriptome, the comparison with ranking does not necessarily reflect the comparison with the absolute values and it still requires assumptions to draw a valid conclusion.

## V. Discussion of *PDXDC1* and *WDR1*

Association of *PDXDC1* with lipid metabolism was reported in genome-wide association studies[7-9], and *PDXDC1* was also found significantly mutated in a subtype of non-clear cell renal carcinoma[10]. Unlike our findings in transcription, its protein expression in both normal tissue of cerebral cortex and glioma tissue is not detectable[11; 12]. *WDR1* encodes a protein containing 9 WD repeats, which are approximately 30-40 amino acid domains with conserved residues and involved in protein-protein interactions; WDR1 protein may help induce the disassembly of actin filaments[13]. Protein expression of *WDR1* is associated with breast cancer[14], thyroid cancer[15] and ovarian cancer[16]. In contrast to our findings in transcription, protein expression ranges from medium to high in both normal brain cerebral cortex and glioma tissue[11; 12].

sTable 1. Demographic characteristics of the study population.

| % | | GWAS-case (n=556) | GWAS-control (n=3647) | eQTL subjects (n=354) | TCGA case (n=473) | TCGA control (n=10) |
|---|---|---|---|---|---|---|
| Age | <30 | 2.2 | 0.1 | 31.4 | 4.9 | 0 |
| | 30-39 | 2.3 | 0.3 | 11.3 | 8.1 | 0 |
| | 40-49 | 4.1 | 3.9 | 15.8 | 14.1 | 0 |
| | 50-59 | 14.7 | 4.4 | 7.1 | 27.7 | 0 |
| | 60-69 | 35.6 | 18.3 | 5.1 | 25.3 | 33.3 |
| | 70-79 | 32.4 | 52.6 | 7.9 | 16.3 | 66.7 |
| | 80- | 8.6 | 20.4 | 21.5 | 3.7 | 0 |
| Gender | Female | 43.2 | 29.3 | 33.1 | 38.6 | 50 |
| | Male | 56.8 | 70.7 | 66.9 | 61.4 | 50 |
| Race | Caucasian | - | - | 100 | 85.1 | 75 |
| | African American | - | - | 0 | 8.6 | 25 |
| | Asian | - | - | 0 | 2.2 | 0 |
| | Other | - | - | 0 | 4.2 | 0 |

sTable 2. The iGWAS result of the 40 Ubiquitin Specific Peptidase 17-Like Family Members. They are all discovered at the significance level of omnibus $p < 0.001$ and validated at the level of omnibus $p < 0.001$.

| Illumina ID - Ensembl Gene ID | HGNC Symbol | Chromo-some | Start Position | End Position | No. of SNPs | Omnibus p-value | | |
|---|---|---|---|---|---|---|---|---|
| | | | | | | Discovery | Validation | Combined |
| ILMN_1684499-ENSG00000232399 | USP17L13 | 4 | 9212383 | 9228214 | 20 | 7.06E-47 | 3.19E-14 | 1.02E-59 |
| ILMN_1684499-ENSG00000231396 | USP17L10 | 4 | 9212383 | 9213975 | 17 | 6.96E-47 | 3.16E-14 | 9.74E-60 |
| ILMN_2335123-ENSG00000231396 | USP17L10 | 4 | 9212383 | 9213975 | 17 | 1.77E-49 | 6.54E-19 | 6.49E-67 |
| ILMN_1684499-ENSG00000233136 | USP17L11 | 4 | 9217131 | 9218723 | 17 | 7.09E-47 | 3.23E-14 | 1.10E-59 |
| ILMN_2335123-ENSG00000233136 | USP17L11 | 4 | 9217131 | 9218723 | 17 | 1.78E-49 | 6.57E-19 | 6.63E-67 |
| ILMN_1684499-ENSG00000227551 | USP17L12 | 4 | 9221878 | 9223470 | 19 | 7.06E-47 | 3.19E-14 | 1.02E-59 |
| ILMN_2335123-ENSG00000227551 | USP17L12 | 4 | 9221878 | 9223470 | 19 | 1.77E-49 | 6.54E-19 | 6.49E-67 |
| ILMN_1684499-ENSG00000223569 | USP17L15 | 4 | 9236111 | 9237700 | 13 | 7.06E-47 | 3.19E-14 | 1.02E-59 |
| ILMN_2335123-ENSG00000223569 | USP17L15 | 4 | 9236111 | 9237700 | 13 | 1.80E-49 | 6.68E-19 | 6.49E-67 |
| ILMN_1684499-ENSG00000250231 | USP17L16P | 4 | 9240856 | 9242448 | 13 | 7.06E-47 | 3.19E-14 | 1.02E-59 |
| ILMN_1684499-ENSG00000249104 | USP17L17 | 4 | 9245605 | 9247197 | 13 | 6.97E-47 | 3.13E-14 | 9.42E-60 |
| ILMN_1684499-ENSG00000250844 | USP17L18 | 4 | 9250356 | 9251948 | 13 | 7.09E-47 | 3.21E-14 | 1.04E-59 |
| ILMN_2335123-ENSG00000250844 | USP17L18 | 4 | 9250356 | 9251948 | 13 | 1.80E-49 | 6.68E-19 | 6.49E-67 |
| ILMN_1684499-ENSG00000248920 | USP17L19 | 4 | 9255104 | 9256696 | 13 | 7.14E-47 | 3.31E-14 | 1.19E-59 |
| ILMN_2335123-ENSG00000248920 | USP17L19 | 4 | 9255104 | 9256696 | 13 | 1.77E-49 | 6.44E-19 | 6.58E-67 |
| ILMN_1684499-ENSG00000250745 | USP17L20 | 4 | 9259850 | 9261442 | 14 | 7.09E-47 | 3.21E-14 | 1.04E-59 |
| ILMN_2335123-ENSG00000250745 | USP17L20 | 4 | 9259850 | 9261442 | 14 | 1.81E-49 | 6.70E-19 | 6.44E-67 |
| ILMN_1684499-ENSG00000249811 | USP17L21 | 4 | 9264598 | 9266190 | 14 | 7.17E-47 | 3.27E-14 | 1.13E-59 |
| ILMN_2335123-ENSG00000249811 | USP17L21 | 4 | 9264598 | 9266190 | 14 | 1.79E-49 | 6.63E-19 | 6.55E-67 |
| ILMN_1684499-ENSG00000248933 | USP17L22 | 4 | 9269345 | 9270937 | 14 | 7.09E-47 | 3.23E-14 | 1.10E-59 |
| ILMN_2335123-ENSG00000248933 | USP17L22 | 4 | 9269345 | 9270937 | 14 | 1.76E-49 | 6.43E-19 | 6.62E-67 |
| ILMN_1684499-ENSG00000232264 | USP17L24 | 4 | 9326891 | 9328483 | 21 | 7.06E-47 | 3.19E-14 | 1.02E-59 |
| ILMN_2335123-ENSG00000232264 | USP17L24 | 4 | 9326891 | 9328483 | 21 | 8.75E-23 | 7.24E-09 | 5.27E-32 |
| ILMN_1684499-ENSG00000230430 | USP17L25 | 4 | 9331637 | 9333229 | 22 | 6.97E-47 | 3.13E-14 | 9.42E-60 |
| ILMN_2335123-ENSG00000230430 | USP17L25 | 4 | 9331637 | 9333229 | 22 | 6.95E-19 | 2.66E-07 | 2.14E-26 |
| ILMN_1684499-ENSG00000229579 | USP17L26 | 4 | 9336384 | 9337976 | 24 | 7.09E-47 | 3.21E-14 | 1.04E-59 |

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| ILMN_2335123-ENSG00000229579 | USP17L26 | 4 | 9336384 | 9337976 | 24 | 3.28E-18 | 1.08E-06 | 7.10E-25 |
| ILMN_1684499-ENSG00000227140 | USP17L5 | 4 | 9341129 | 9342721 | 24 | 7.06E-47 | 3.19E-14 | 1.02E-59 |
| ILMN_2335123-ENSG00000227140 | USP17L5 | 4 | 9341129 | 9342721 | 24 | 3.15E-18 | 1.07E-06 | 7.22E-25 |
| ILMN_1684499-ENSG00000235780 | USP17L27 | 4 | 9345874 | 9347466 | 25 | 7.17E-47 | 3.27E-14 | 1.13E-59 |
| ILMN_2335123-ENSG00000235780 | USP17L27 | 4 | 9345874 | 9347466 | 25 | 3.43E-17 | 4.07E-06 | 4.34E-23 |
| ILMN_1684499-ENSG00000231051 | USP17L28 | 4 | 9350619 | 9352211 | 26 | 7.27E-47 | 3.33E-14 | 1.24E-59 |
| ILMN_2335123-ENSG00000231051 | USP17L28 | 4 | 9350619 | 9352211 | 26 | 2.77E-17 | 3.90E-06 | 4.60E-23 |
| ILMN_1684499-ENSG00000231637 | USP17L29 | 4 | 9355364 | 9356956 | 26 | 6.92E-47 | 3.11E-14 | 8.99E-60 |
| ILMN_2335123-ENSG00000231637 | USP17L29 | 4 | 9355364 | 9356956 | 26 | 2.97E-17 | 3.95E-06 | 4.58E-23 |
| ILMN_1684499-ENSG00000251694 | USP17L9P | 4 | 9360109 | 9361701 | 27 | 7.17E-47 | 3.27E-14 | 1.13E-59 |
| ILMN_2335123-ENSG00000251694 | USP17L9P | 4 | 9360109 | 9361701 | 27 | 4.00E-15 | 2.53E-05 | 3.45E-20 |
| ILMN_1684499-ENSG00000228856 | USP17L30 | 4 | 9364855 | 9366447 | 30 | 6.92E-47 | 3.11E-14 | 8.99E-60 |
| ILMN_2335123-ENSG00000228856 | USP17L30 | 4 | 9364855 | 9366447 | 30 | 2.32E-13 | 0.000116 | 1.49E-17 |
| ILMN_2335123-ENSG00000205946 | USP17L6P | 4 | 9369600 | 9370796 | 30 | 2.39E-13 | 0.000116 | 1.47E-17 |

sTable 3. The p-values of the 55 validated transcripts in SNP-only models, main effect-only models and interaction models.

| | | | Discovery Set | | | Validation Set | | | Combined | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Illumina ID - Ensembl ID | HGNC Symbol | Ch | Interac-tion | Main Effect | SNP only | Interaction | Main Effect | SNP only | Interac-tion | Main Effect | SNP only |
| ILMN_1684499-ENSG00000232399 | USP17L13 | 4 | 3.52E-37 | 5.35E-32 | 8.18E-46 | 7.66E-11 | 1.79E-09 | 2.15E-13 | 9.03E-46 | 2.68E-39 | 7.58E-57 |
| ILMN_1684499-ENSG00000231396 | USP17L10 | 4 | 4.21E-37 | 6.89E-32 | 8.18E-46 | 8.06E-11 | 1.92E-09 | 2.15E-13 | 1.15E-45 | 3.74E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000231396 | USP17L10 | 4 | 2.03E-47 | 2.29E-45 | 1.56E-47 | 2.23E-18 | 3.50E-17 | 8.50E-19 | 7.20E-68 | 1.66E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000233136 | USP17L11 | 4 | 2.43E-37 | 3.17E-32 | 8.18E-46 | 6.90E-11 | 1.54E-09 | 2.15E-13 | 5.51E-46 | 1.34E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000233136 | USP17L11 | 4 | 2.28E-47 | 2.68E-45 | 1.56E-47 | 2.29E-18 | 3.64E-17 | 8.50E-19 | 8.45E-68 | 2.05E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000227551 | USP17L12 | 4 | 3.52E-37 | 5.35E-32 | 8.18E-46 | 7.66E-11 | 1.79E-09 | 2.15E-13 | 9.03E-46 | 2.68E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000227551 | USP17L12 | 4 | 2.03E-47 | 2.29E-45 | 1.56E-47 | 2.23E-18 | 3.50E-17 | 8.50E-19 | 7.20E-68 | 1.66E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000223569 | USP17L15 | 4 | 3.52E-37 | 5.35E-32 | 8.18E-46 | 7.66E-11 | 1.79E-09 | 2.15E-13 | 9.03E-46 | 2.68E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000223569 | USP17L15 | 4 | 2.70E-47 | 3.32E-45 | 1.56E-47 | 2.38E-18 | 3.85E-17 | 8.50E-19 | 1.06E-67 | 2.77E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000250231 | USP17L16P | 4 | 3.52E-37 | 5.35E-32 | 8.18E-46 | 7.66E-11 | 1.79E-09 | 2.15E-13 | 9.03E-46 | 2.68E-39 | 7.58E-57 |
| ILMN_1684499-ENSG00000249104 | USP17L17 | 4 | 5.01E-37 | 8.83E-32 | 8.18E-46 | 8.47E-11 | 2.06E-09 | 2.15E-13 | 1.44E-45 | 5.18E-39 | 7.58E-57 |
| ILMN_1684499-ENSG00000250844 | USP17L18 | 4 | 2.93E-37 | 4.13E-32 | 8.18E-46 | 7.27E-11 | 1.66E-09 | 2.15E-13 | 7.07E-46 | 1.90E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000250844 | USP17L18 | 4 | 2.70E-47 | 3.32E-45 | 1.56E-47 | 2.38E-18 | 3.85E-17 | 8.50E-19 | 1.06E-67 | 2.77E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000248920 | USP17L19 | 4 | 1.66E-37 | 1.86E-32 | 8.18E-46 | 6.19E-11 | 1.32E-09 | 2.15E-13 | 3.32E-46 | 6.59E-40 | 7.58E-57 |
| ILMN_2335123-ENSG00000248920 | USP17L19 | 4 | 1.76E-47 | 1.90E-45 | 1.56E-47 | 2.15E-18 | 3.33E-17 | 8.50E-19 | 5.93E-68 | 1.29E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000250745 | USP17L20 | 4 | 2.93E-37 | 4.13E-32 | 8.18E-46 | 7.27E-11 | 1.66E-09 | 2.15E-13 | 7.07E-46 | 1.90E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000250745 | USP17L20 | 4 | 2.81E-47 | 3.51E-45 | 1.56E-47 | 2.41E-18 | 3.91E-17 | 8.50E-19 | 1.12E-67 | 2.98E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000249811 | USP17L21 | 4 | 2.01E-37 | 2.43E-32 | 8.18E-46 | 6.54E-11 | 1.43E-09 | 2.15E-13 | 4.28E-46 | 9.42E-40 | 7.58E-57 |
| ILMN_2335123-ENSG00000249811 | USP17L21 | 4 | 2.48E-47 | 2.98E-45 | 1.56E-47 | 2.34E-18 | 3.74E-17 | 8.50E-19 | 9.45E-68 | 2.38E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000248933 | USP17L22 | 4 | 2.43E-37 | 3.17E-32 | 8.18E-46 | 6.90E-11 | 1.54E-09 | 2.15E-13 | 5.51E-46 | 1.34E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000248933 | USP17L22 | 4 | 1.70E-47 | 1.82E-45 | 1.56E-47 | 2.14E-18 | 3.30E-17 | 8.50E-19 | 5.68E-68 | 1.21E-64 | 5.16E-68 |
| ILMN_1684499-ENSG00000232264 | USP17L24 | 4 | 3.52E-37 | 5.35E-32 | 8.18E-46 | 7.66E-11 | 1.79E-09 | 2.15E-13 | 9.03E-46 | 2.68E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000232264 | USP17L24 | 4 | 2.11E-19 | 5.42E-17 | 9.78E-23 | 4.73E-08 | 3.54E-07 | 6.13E-09 | 9.11E-27 | 2.25E-23 | 3.94E-31 |
| ILMN_1684499-ENSG00000230430 | USP17L25 | 4 | 5.01E-37 | 8.83E-32 | 8.18E-46 | 8.47E-11 | 2.06E-09 | 2.15E-13 | 1.44E-45 | 5.18E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000230430 | USP17L25 | 4 | 2.28E-16 | 2.09E-14 | 4.07E-19 | 1.11E-06 | 5.65E-06 | 2.01E-07 | 3.65E-22 | 1.99E-19 | 9.72E-26 |
| ILMN_1684499-ENSG00000229579 | USP17L26 | 4 | 2.93E-37 | 4.13E-32 | 8.18E-46 | 7.27E-11 | 1.66E-09 | 2.15E-13 | 7.07E-46 | 1.90E-39 | 7.58E-57 |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| ILMN_2335123-ENSG00000229579 | USP17L26 | 4 | 5.84E-16 | 3.20E-14 | 3.37E-18 | 2.55E-06 | 9.21E-06 | 7.71E-07 | 1.55E-21 | 3.77E-19 | 2.31E-24 |
| ILMN_1684499-ENSG00000227140 | USP17L5 | 4 | 3.52E-37 | 5.35E-32 | 8.18E-46 | 7.66E-11 | 1.79E-09 | 2.15E-13 | 9.03E-46 | 2.68E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000227140 | USP17L5 | 4 | 1.50E-15 | 1.14E-13 | 3.37E-18 | 3.71E-06 | 1.55E-05 | 7.71E-07 | 6.10E-21 | 2.39E-18 | 2.31E-24 |
| ILMN_1684499-ENSG00000235780 | USP17L27 | 4 | 2.01E-37 | 2.43E-32 | 8.18E-46 | 6.54E-11 | 1.43E-09 | 2.15E-13 | 4.28E-46 | 9.42E-40 | 7.58E-57 |
| ILMN_2335123-ENSG00000235780 | USP17L27 | 4 | 4.29E-15 | 1.52E-13 | 4.95E-17 | 7.59E-06 | 2.16E-05 | 2.99E-06 | 3.11E-20 | 3.93E-18 | 1.19E-22 |
| ILMN_1684499-ENSG00000231051 | USP17L28 | 4 | 1.37E-37 | 1.41E-32 | 8.18E-46 | 5.86E-11 | 1.23E-09 | 2.15E-13 | 2.57E-46 | 4.60E-40 | 7.58E-57 |
| ILMN_2335123-ENSG00000231051 | USP17L28 | 4 | 1.30E-13 | 1.54E-11 | 4.95E-17 | 2.82E-05 | 0.00013364 | 2.99E-06 | 4.07E-18 | 2.89E-15 | 1.19E-22 |
| ILMN_1684499-ENSG00000231637 | USP17L29 | 4 | 5.94E-37 | 1.12E-31 | 8.18E-46 | 8.88E-11 | 2.21E-09 | 2.15E-13 | 1.81E-45 | 7.10E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000231637 | USP17L29 | 4 | 4.45E-14 | 3.59E-12 | 4.95E-17 | 1.87E-05 | 7.58E-05 | 2.99E-06 | 8.83E-19 | 3.64E-16 | 1.19E-22 |
| ILMN_1684499-ENSG00000251694 | USP17L9P | 4 | 2.01E-37 | 2.43E-32 | 8.18E-46 | 6.54E-11 | 1.43E-09 | 2.15E-13 | 4.28E-46 | 9.42E-40 | 7.58E-57 |
| ILMN_2335123-ENSG00000251694 | USP17L9P | 4 | 2.50E-14 | 2.76E-13 | 3.82E-15 | 1.67E-05 | 2.93E-05 | 1.65E-05 | 4.73E-19 | 1.07E-17 | 7.22E-20 |
| ILMN_1684499-ENSG00000228856 | USP17L30 | 4 | 5.94E-37 | 1.12E-31 | 8.18E-46 | 8.88E-11 | 2.21E-09 | 2.15E-13 | 1.81E-45 | 7.10E-39 | 7.58E-57 |
| ILMN_2335123-ENSG00000228856 | USP17L30 | 4 | 1.67E-11 | 3.59E-10 | 1.98E-13 | 0.00021852 | 0.00054221 | 7.48E-05 | 5.57E-15 | 3.32E-13 | 2.22E-17 |
| ILMN_2335123-ENSG00000205946 | USP17L6P | 4 | 7.45E-12 | 1.20E-10 | 1.98E-13 | 0.00016193 | 0.0003549 | 7.48E-05 | 1.79E-15 | 7.05E-14 | 2.22E-17 |
| ILMN_2079225-ENSG00000250884 | OR7E85P | 4 | 2.58E-47 | 2.96E-50 | 7.56E-37 | 2.08E-15 | 3.88E-16 | 2.04E-12 | 6.31E-62 | 1.72E-65 | 1.79E-48 |
| ILMN_1738406-ENSG00000109667 | SLC2A9 | 4 | 1.32E-18 | 1.76E-21 | 5.18E-10 | 6.26E-05 | 1.19E-05 | 0.004389 | 4.15E-23 | 1.36E-26 | 1.07E-12 |
| ILMN_1723803-ENSG00000109667 | SLC2A9 | 4 | 1.76E-58 | 7.12E-54 | 6.75E-58 | 1.50E-17 | 1.34E-16 | 8.29E-17 | 1.08E-73 | 1.04E-67 | 3.68E-73 |
| ILMN_1689043-ENSG00000169676 | DRD5 | 4 | 3.65E-46 | 2.64E-59 | 1.08E-15 | 2.98E-12 | 1.45E-15 | 0.000178 | 1.32E-59 | 6.44E-77 | 3.11E-20 |
| ILMN_1780036-ENSG00000071127 | WDR1 | 4 | 7.16E-40 | 3.15E-44 | 6.27E-25 | 1.50E-12 | 2.40E-13 | 9.99E-09 | 1.00E-52 | 3.35E-57 | 3.14E-34 |
| ILMN_1675844-ENSG00000071127 | WDR1 | 4 | 1.32E-52 | 2.42E-59 | 1.12E-32 | 4.30E-17 | 8.76E-19 | 3.40E-11 | 1.18E-70 | 2.93E-79 | 7.84E-44 |
| ILMN_1804935-ENSG00000093134 | VNN3 | 6 | 2.44E-08 | 3.39E-08 | 1.04E-07 | 4.43E-05 | 2.36E-05 | 0.00041 | 6.56E-13 | 4.86E-13 | 4.38E-11 |
| ILMN_2096747-ENSG00000221500 | SNORD100 | 6 | 2.23E-09 | 4.88E-12 | 0.000591 | 0.00405293 | 0.00040858 | 0.197477 | 5.67E-12 | 3.64E-16 | 0.000737 |
| ILMN_2096747-ENSG00000200534 | SNORA33 | 6 | 2.91E-09 | 7.54E-12 | 0.000591 | 0.00448741 | 0.00048439 | 0.197477 | 8.48E-12 | 7.06E-16 | 0.000737 |
| ILMN_2126957-ENSG00000103512 | NOMO1 | 16 | 9.51E-20 | 7.88E-20 | 8.72E-17 | 2.35E-07 | 5.03E-08 | 3.12E-05 | 2.71E-25 | 3.93E-26 | 6.40E-20 |
| ILMN_1702114-ENSG00000103512 | NOMO1 | 16 | 4.52E-18 | 7.06E-18 | 1.21E-17 | 1.32E-05 | 1.63E-05 | 1.40E-05 | 7.89E-22 | 1.87E-21 | 1.45E-21 |
| ILMN_1703969-ENSG00000179889 | PDXDC1 | 16 | 4.70E-19 | 6.88E-19 | 6.55E-16 | 4.30E-06 | 1.02E-06 | 0.000326 | 4.77E-24 | 1.27E-24 | 1.70E-18 |
| ILMN_1815552-ENSG00000157045 | NTAN1 | 16 | 8.20E-14 | 5.95E-12 | 3.48E-15 | 0.00374158 | 0.01380299 | 0.000529 | 3.02E-15 | 1.32E-12 | 7.63E-18 |
| ILMN_1728645-ENSG00000197457 | STMN3 | 20 | 4.29E-05 | 0.00062463 | 6.76E-07 | 0.00139136 | 0.00515311 | 0.000214 | 1.57E-08 | 1.61E-06 | 1.86E-11 |
| ILMN_2344079-ENSG00000203896 | LIME1 | 20 | 6.79E-05 | 0.0007056 | 4.59E-06 | 0.00101493 | 0.00287834 | 0.000401 | 2.26E-08 | 1.08E-06 | 4.37E-10 |

sTable 4. The p-values of the 55 validated transcripts in SNP-only models, main effect-only models and interaction models. Results of sensitivity analyses by adjusting for population stratification in eQTL analyses.

| Illumina ID - Ensembl ID | HGNC Symbol | Ch | Omnibus p-value | | |
|---|---|---|---|---|---|
| | | | Discovery | Validation | Combined |
| ILMN_1684499-ENSG00000232399 | USP17L13 | 4 | 2.85E-51 | 1.27E-13 | 9.51E-71 |
| ILMN_1684499-ENSG00000231396 | USP17L10 | 4 | 2.58E-51 | 1.27E-13 | 9.15E-71 |
| ILMN_2335123-ENSG00000231396 | USP17L10 | 4 | 2.46E-51 | 6.23E-19 | 1.28E-70 |
| ILMN_1684499-ENSG00000233136 | USP17L11 | 4 | 2.91E-51 | 1.25E-13 | 8.19E-71 |
| ILMN_2335123-ENSG00000233136 | USP17L11 | 4 | 2.02E-51 | 6.79E-19 | 1.21E-70 |
| ILMN_1684499-ENSG00000227551 | USP17L12 | 4 | 2.85E-51 | 1.27E-13 | 9.51E-71 |
| ILMN_2335123-ENSG00000227551 | USP17L12 | 4 | 2.46E-51 | 6.23E-19 | 1.28E-70 |
| ILMN_1684499-ENSG00000223569 | USP17L15 | 4 | 2.85E-51 | 1.27E-13 | 9.51E-71 |
| ILMN_2335123-ENSG00000223569 | USP17L15 | 4 | 2.23E-51 | 7.17E-19 | 1.22E-70 |
| ILMN_1684499-ENSG00000250231 | USP17L16P | 4 | 2.85E-51 | 1.27E-13 | 9.51E-71 |
| ILMN_1684499-ENSG00000249104 | USP17L17 | 4 | 2.08E-51 | 1.25E-13 | 1.14E-70 |
| ILMN_1684499-ENSG00000250844 | USP17L18 | 4 | 2.67E-51 | 1.28E-13 | 8.34E-71 |
| ILMN_2335123-ENSG00000250844 | USP17L18 | 4 | 2.23E-51 | 7.17E-19 | 1.22E-70 |
| ILMN_1684499-ENSG00000248920 | USP17L19 | 4 | 4.31E-51 | 1.25E-13 | 7.84E-71 |
| ILMN_2335123-ENSG00000248920 | USP17L19 | 4 | 2.41E-51 | 5.67E-19 | 1.32E-70 |
| ILMN_1684499-ENSG00000250745 | USP17L20 | 4 | 2.67E-51 | 1.28E-13 | 8.34E-71 |
| ILMN_2335123-ENSG00000250745 | USP17L20 | 4 | 2.21E-51 | 7.26E-19 | 1.22E-70 |
| ILMN_1684499-ENSG00000249811 | USP17L21 | 4 | 4.16E-51 | 1.24E-13 | 7.86E-71 |
| ILMN_2335123-ENSG00000249811 | USP17L21 | 4 | 2.12E-51 | 6.92E-19 | 1.22E-70 |
| ILMN_1684499-ENSG00000248933 | USP17L22 | 4 | 2.91E-51 | 1.25E-13 | 8.19E-71 |
| ILMN_2335123-ENSG00000248933 | USP17L22 | 4 | 2.38E-51 | 5.59E-19 | 1.32E-70 |
| ILMN_1684499-ENSG00000232264 | USP17L24 | 4 | 2.85E-51 | 1.27E-13 | 9.51E-71 |
| ILMN_2335123-ENSG00000232264 | USP17L24 | 4 | 1.23E-24 | 3.32E-09 | 8.05E-35 |
| ILMN_1684499-ENSG00000230430 | USP17L25 | 4 | 2.08E-51 | 1.25E-13 | 1.14E-70 |
| ILMN_2335123-ENSG00000230430 | USP17L25 | 4 | 3.38E-20 | 1.82E-07 | 3.83E-29 |
| ILMN_1684499-ENSG00000229579 | USP17L26 | 4 | 2.67E-51 | 1.28E-13 | 8.34E-71 |

| | | | | | |
|---|---|---|---|---|---|
| ILMN_2335123-ENSG00000229579 | USP17L26 | 4 | 3.13E-20 | 1.26E-06 | 2.49E-27 |
| ILMN_1684499-ENSG00000227140 | USP17L5 | 4 | 2.85E-51 | 1.27E-13 | 9.51E-71 |
| ILMN_2335123-ENSG00000227140 | USP17L5 | 4 | 3.42E-20 | 1.10E-06 | 2.21E-27 |
| ILMN_1684499-ENSG00000235780 | USP17L27 | 4 | 4.16E-51 | 1.24E-13 | 7.86E-71 |
| ILMN_2335123-ENSG00000235780 | USP17L27 | 4 | 2.97E-19 | 4.50E-06 | 5.45E-25 |
| ILMN_1684499-ENSG00000231051 | USP17L28 | 4 | 4.22E-51 | 1.21E-13 | 9.35E-71 |
| ILMN_2335123-ENSG00000231051 | USP17L28 | 4 | 2.10E-19 | 4.47E-06 | 7.83E-25 |
| ILMN_1684499-ENSG00000231637 | USP17L29 | 4 | 1.93E-51 | 1.24E-13 | 1.25E-70 |
| ILMN_2335123-ENSG00000231637 | USP17L29 | 4 | 2.36E-19 | 4.44E-06 | 6.28E-25 |
| ILMN_1684499-ENSG00000251694 | USP17L9P | 4 | 4.16E-51 | 1.24E-13 | 7.86E-71 |
| ILMN_2335123-ENSG00000251694 | USP17L9P | 4 | 6.57E-17 | 2.23E-05 | 2.25E-21 |
| ILMN_1684499-ENSG00000228856 | USP17L30 | 4 | 1.93E-51 | 1.24E-13 | 1.25E-70 |
| ILMN_2335123-ENSG00000228856 | USP17L30 | 4 | 2.87E-15 | 0.000124 | 2.48E-19 |
| ILMN_2335123-ENSG00000205946 | USP17L6P | 4 | 2.98E-15 | 0.000124 | 3.29E-19 |
| ILMN_2079225-ENSG00000250884 | OR7E85P | 4 | 3.43E-57 | 1.78E-18 | 7.69E-79 |
| ILMN_1738406-ENSG00000109667 | SLC2A9 | 4 | 7.38E-22 | 1.51E-05 | 3.09E-29 |
| ILMN_1723803-ENSG00000109667 | SLC2A9 | 4 | 1.80E-71 | 3.88E-21 | 4.06E-81 |
| ILMN_1689043-ENSG00000169676 | DRD5 | 4 | 3.86E-62 | 5.39E-14 | 1.02E-64 |
| ILMN_1780036-ENSG00000071127 | WDR1 | 4 | 2.13E-46 | 1.48E-13 | 1.17E-60 |
| ILMN_1675844-ENSG00000071127 | WDR1 | 4 | 5.84E-78 | 3.30E-21 | 4.80E-97 |
| ILMN_1804935-ENSG00000093134 | VNN3 | 6 | 7.88E-08 | 6.96E-06 | 3.02E-12 |
| ILMN_2096747-ENSG00000221500 | SNORD100 | 6 | 3.50E-11 | 0.002429 | 3.36E-13 |
| ILMN_2096747-ENSG00000200534 | SNORA33 | 6 | 5.70E-11 | 0.002845 | 6.13E-13 |
| ILMN_2126957-ENSG00000103512 | NOMO1 | 16 | 8.76E-24 | 4.50E-07 | 1.99E-30 |
| ILMN_1702114-ENSG00000103512 | NOMO1 | 16 | 9.12E-21 | 1.77E-05 | 1.18E-27 |
| ILMN_1703969-ENSG00000179889 | PDXDC1 | 16 | 9.09E-24 | 2.82E-06 | 7.30E-29 |
| ILMN_1815552-ENSG00000157045 | NTAN1 | 16 | 1.10E-19 | 0.000159 | 4.57E-25 |
| ILMN_1728645-ENSG00000197457 | STMN3 | 20 | 6.50E-07 | 0.000326 | 2.71E-10 |
| ILMN_2344079-ENSG00000203896 | LIME1 | 20 | 2.39E-06 | 0.000530 | 3.86E-10 |

sTable 5. The p-values of the 55 validated transcripts in SNP-only models, main effect-only models and interaction models. Results of sensitivity analyses by adjusting for population stratification in eQTL analyses.

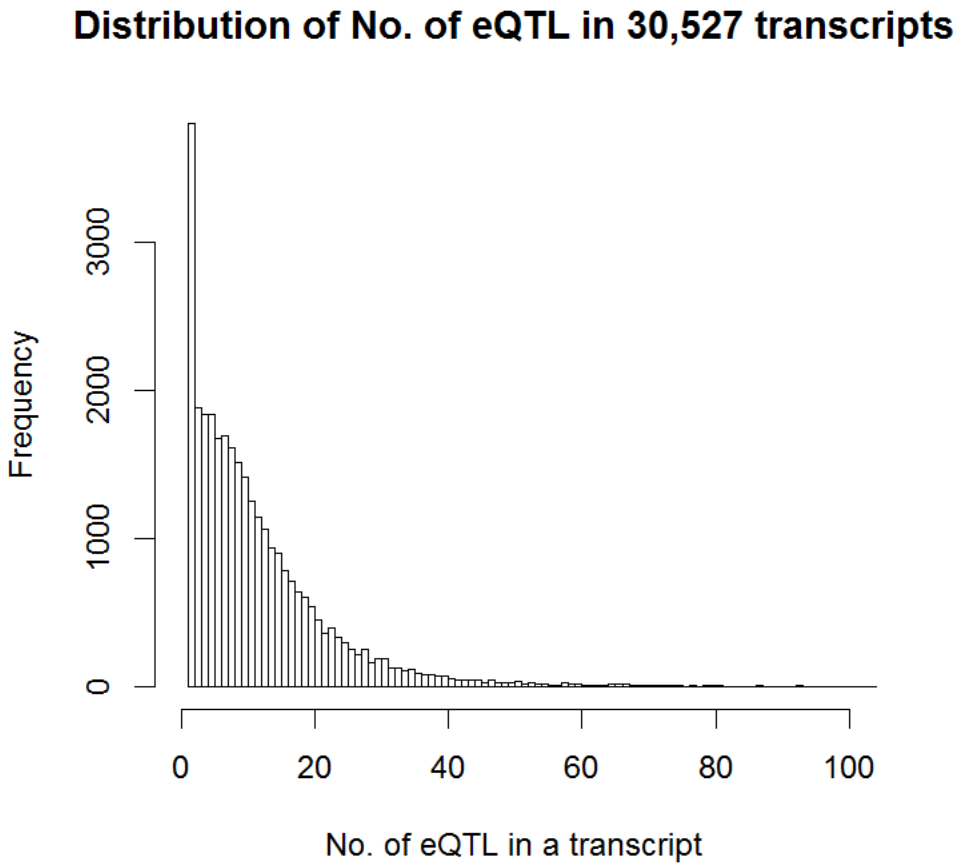
| | | | Discovery Set | | | Validation Set | | | Combined | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| Illumina ID - Ensembl ID | HGNC Symbol | Ch | Interac-tion | Main Effect | SNP only | Interaction | Main Effect | SNP only | Interac-tion | Main Effect | SNP only |
| ILMN_1684499-ENSG00000232399 | USP17L13 | 4 | 1.03E-38 | 3.64E-33 | 8.28E-48 | 2.46E-10 | 4.95E-09 | 9.05E-13 | 5.44E-53 | 1.51E-45 | 2.01E-65 |
| ILMN_1684499-ENSG00000231396 | USP17L10 | 4 | 1.25E-38 | 4.75E-33 | 8.28E-48 | 2.58E-10 | 5.31E-09 | 9.05E-13 | 7.20E-53 | 2.23E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000231396 | USP17L10 | 4 | 2.64E-47 | 5.40E-45 | 4.97E-48 | 3.95E-18 | 2.28E-17 | 9.97E-18 | 4.44E-63 | 3.95E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000233136 | USP17L11 | 4 | 6.99E-39 | 2.10E-33 | 8.28E-48 | 2.22E-10 | 4.28E-09 | 9.05E-13 | 3.05E-53 | 6.71E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000233136 | USP17L11 | 4 | 3.03E-47 | 6.43E-45 | 4.97E-48 | 4.07E-18 | 2.38E-17 | 9.97E-18 | 5.30E-63 | 4.94E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000227551 | USP17L12 | 4 | 1.03E-38 | 3.64E-33 | 8.28E-48 | 2.46E-10 | 4.95E-09 | 9.05E-13 | 5.44E-53 | 1.51E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000227551 | USP17L12 | 4 | 2.64E-47 | 5.40E-45 | 4.97E-48 | 3.95E-18 | 2.28E-17 | 9.97E-18 | 4.44E-63 | 3.95E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000223569 | USP17L15 | 4 | 1.03E-38 | 3.64E-33 | 8.28E-48 | 2.46E-10 | 4.95E-09 | 9.05E-13 | 5.44E-53 | 1.51E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000223569 | USP17L15 | 4 | 3.66E-47 | 8.22E-45 | 4.97E-48 | 4.24E-18 | 2.54E-17 | 9.97E-18 | 6.77E-63 | 6.75E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000250231 | USP17L16P | 4 | 1.03E-38 | 3.64E-33 | 8.28E-48 | 2.46E-10 | 4.95E-09 | 9.05E-13 | 5.44E-53 | 1.51E-45 | 2.01E-65 |
| ILMN_1684499-ENSG00000249104 | USP17L17 | 4 | 1.50E-38 | 6.16E-33 | 8.28E-48 | 2.71E-10 | 5.69E-09 | 9.05E-13 | 9.46E-53 | 3.26E-45 | 2.01E-65 |
| ILMN_1684499-ENSG00000250844 | USP17L18 | 4 | 8.52E-39 | 2.77E-33 | 8.28E-48 | 2.34E-10 | 4.61E-09 | 9.05E-13 | 4.08E-53 | 1.01E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000250844 | USP17L18 | 4 | 3.66E-47 | 8.22E-45 | 4.97E-48 | 4.24E-18 | 2.54E-17 | 9.97E-18 | 6.77E-63 | 6.75E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000248920 | USP17L19 | 4 | 4.67E-39 | 1.19E-33 | 8.28E-48 | 1.99E-10 | 3.69E-09 | 9.05E-13 | 1.68E-53 | 2.92E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000248920 | USP17L19 | 4 | 2.24E-47 | 4.37E-45 | 4.97E-48 | 3.81E-18 | 2.16E-17 | 9.97E-18 | 3.60E-63 | 3.01E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000250745 | USP17L20 | 4 | 8.52E-39 | 2.77E-33 | 8.28E-48 | 2.34E-10 | 4.61E-09 | 9.05E-13 | 4.08E-53 | 1.01E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000250745 | USP17L20 | 4 | 3.84E-47 | 8.74E-45 | 4.97E-48 | 4.28E-18 | 2.58E-17 | 9.97E-18 | 7.20E-63 | 7.30E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000249811 | USP17L21 | 4 | 5.72E-39 | 1.58E-33 | 8.28E-48 | 2.10E-10 | 3.97E-09 | 9.05E-13 | 2.26E-53 | 4.44E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000249811 | USP17L21 | 4 | 3.33E-47 | 7.27E-45 | 4.97E-48 | 4.15E-18 | 2.46E-17 | 9.97E-18 | 5.98E-63 | 5.77E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000248933 | USP17L22 | 4 | 6.99E-39 | 2.10E-33 | 8.28E-48 | 2.22E-10 | 4.28E-09 | 9.05E-13 | 3.05E-53 | 6.71E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000248933 | USP17L22 | 4 | 2.16E-47 | 4.17E-45 | 4.97E-48 | 3.78E-18 | 2.13E-17 | 9.97E-18 | 3.43E-63 | 2.83E-59 | 2.85E-65 |
| ILMN_1684499-ENSG00000232264 | USP17L24 | 4 | 1.03E-38 | 3.64E-33 | 8.28E-48 | 2.46E-10 | 4.95E-09 | 9.05E-13 | 5.44E-53 | 1.51E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000232264 | USP17L24 | 4 | 5.53E-20 | 1.30E-17 | 4.78E-23 | 6.21E-08 | 3.38E-07 | 1.23E-08 | 9.24E-29 | 3.06E-25 | 1.00E-32 |
| ILMN_1684499-ENSG00000230430 | USP17L25 | 4 | 1.50E-38 | 6.16E-33 | 8.28E-48 | 2.71E-10 | 5.69E-09 | 9.05E-13 | 9.46E-53 | 3.26E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000230430 | USP17L25 | 4 | 1.47E-16 | 1.16E-14 | 4.05E-19 | 1.52E-06 | 6.24E-06 | 3.46E-07 | 1.70E-23 | 1.14E-20 | 7.06E-27 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ILMN_1684499-ENSG00000229579 | USP17L26 | 4 | 8.52E-39 | 2.77E-33 | 8.28E-48 | 2.34E-10 | 4.61E-09 | 9.05E-13 | 4.08E-53 | 1.01E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000229579 | USP17L26 | 4 | 2.08E-16 | 1.10E-14 | 1.67E-18 | 3.37E-06 | 9.64E-06 | 1.36E-06 | 6.50E-23 | 1.84E-20 | 1.82E-25 |
| ILMN_1684499-ENSG00000227140 | USP17L5 | 4 | 1.03E-38 | 3.64E-33 | 8.28E-48 | 2.46E-10 | 4.95E-09 | 9.05E-13 | 5.44E-53 | 1.51E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000227140 | USP17L5 | 4 | 5.39E-16 | 4.03E-14 | 1.67E-18 | 4.91E-06 | 1.66E-05 | 1.36E-06 | 2.73E-22 | 1.29E-19 | 1.82E-25 |
| ILMN_1684499-ENSG00000235780 | USP17L27 | 4 | 5.72E-39 | 1.58E-33 | 8.28E-48 | 2.10E-10 | 3.97E-09 | 9.05E-13 | 2.26E-53 | 4.44E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000235780 | USP17L27 | 4 | 1.08E-15 | 4.13E-14 | 1.52E-17 | 9.32E-06 | 2.10E-05 | 5.11E-06 | 1.75E-21 | 2.41E-19 | 1.40E-23 |
| ILMN_1684499-ENSG00000231051 | USP17L28 | 4 | 3.81E-39 | 8.97E-34 | 8.28E-48 | 1.89E-10 | 3.42E-09 | 9.05E-13 | 1.24E-53 | 1.92E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000231051 | USP17L28 | 4 | 3.43E-14 | 4.60E-12 | 1.52E-17 | 3.54E-05 | 0.000141 | 5.11E-06 | 2.92E-19 | 2.54E-16 | 1.40E-23 |
| ILMN_1684499-ENSG00000231637 | USP17L29 | 4 | 1.80E-38 | 7.92E-33 | 8.28E-48 | 2.84E-10 | 6.08E-09 | 9.05E-13 | 1.23E-52 | 4.73E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000231637 | USP17L29 | 4 | 1.16E-14 | 1.04E-12 | 1.52E-17 | 2.33E-05 | 7.81E-05 | 5.11E-06 | 5.86E-20 | 2.85E-17 | 1.40E-23 |
| ILMN_1684499-ENSG00000251694 | USP17L9P | 4 | 5.72E-39 | 1.58E-33 | 8.28E-48 | 2.10E-10 | 3.97E-09 | 9.05E-13 | 2.26E-53 | 4.44E-46 | 2.01E-65 |
| ILMN_2335123-ENSG00000251694 | USP17L9P | 4 | 8.47E-15 | 9.60E-14 | 1.53E-15 | 2.07E-05 | 2.99E-05 | 2.51E-05 | 4.07E-20 | 9.59E-19 | 1.07E-20 |
| ILMN_1684499-ENSG00000228856 | USP17L30 | 4 | 1.80E-38 | 7.92E-33 | 8.28E-48 | 2.84E-10 | 6.08E-09 | 9.05E-13 | 1.23E-52 | 4.73E-45 | 2.01E-65 |
| ILMN_2335123-ENSG00000228856 | USP17L30 | 4 | 7.49E-12 | 1.69E-10 | 9.61E-14 | 0.00027 | 0.000601 | 0.000106 | 1.01E-15 | 6.73E-14 | 4.72E-18 |
| ILMN_2335123-ENSG00000205946 | USP17L6P | 4 | 3.29E-12 | 5.51E-11 | 9.61E-14 | 0.0002 | 0.00039 | 0.000106 | 3.07E-16 | 1.32E-14 | 4.72E-18 |
| ILMN_2079225-ENSG00000250884 | OR7E85P | 4 | 4.07E-50 | 4.77E-52 | 1.70E-40 | 1.02E-16 | 3.48E-17 | 6.05E-14 | 3.83E-64 | 1.24E-69 | 3.44E-48 |
| ILMN_1738406-ENSG00000109667 | SLC2A9 | 4 | 1.45E-20 | 6.93E-24 | 3.37E-11 | 6.29E-05 | 1.32E-05 | 0.003856 | 4.76E-26 | 1.05E-29 | 2.26E-14 |
| ILMN_1723803-ENSG00000109667 | SLC2A9 | 4 | 4.57E-67 | 2.13E-62 | 4.68E-65 | 4.87E-19 | 1.47E-18 | 2.64E-17 | 1.96E-79 | 7.26E-73 | 2.64E-78 |
| ILMN_1689043-ENSG00000169676 | DRD5 | 4 | 1.16E-47 | 2.89E-60 | 1.91E-17 | 1.20E-10 | 2.64E-13 | 0.000252 | 4.20E-55 | 1.55E-69 | 1.58E-20 |
| ILMN_1780036-ENSG00000071127 | WDR1 | 4 | 1.08E-39 | 1.01E-43 | 1.73E-25 | 4.80E-12 | 3.94E-13 | 4.43E-08 | 3.70E-51 | 8.92E-55 | 1.76E-34 |
| ILMN_1675844-ENSG00000071127 | WDR1 | 4 | 5.35E-66 | 5.83E-71 | 1.26E-45 | 6.04E-18 | 1.55E-19 | 2.29E-12 | 6.22E-85 | 3.31E-94 | 1.13E-55 |
| ILMN_1804935-ENSG00000093134 | VNN3 | 6 | 3.05E-08 | 4.19E-08 | 2.19E-07 | 1.95E-05 | 1.02E-05 | 0.000313 | 3.98E-12 | 2.28E-12 | 7.53E-10 |
| ILMN_2096747-ENSG00000221500 | SNORD100 | 6 | 1.01E-07 | 4.96E-10 | 0.004345 | 0.014624 | 0.00131 | 0.511956 | 1.30E-10 | 1.10E-14 | 0.002368 |
| ILMN_2096747-ENSG00000200534 | SNORA33 | 6 | 1.28E-07 | 7.28E-10 | 0.004345 | 0.016062 | 0.001542 | 0.511956 | 1.83E-10 | 1.95E-14 | 0.002368 |
| ILMN_2126957-ENSG00000103512 | NOMO1 | 16 | 3.21E-21 | 5.08E-21 | 1.35E-19 | 5.36E-07 | 3.14E-07 | 7.07E-06 | 6.24E-29 | 3.15E-29 | 3.59E-25 |
| ILMN_1702114-ENSG00000103512 | NOMO1 | 16 | 5.23E-19 | 4.61E-19 | 3.12E-17 | 2.33E-05 | 2.25E-05 | 6.07E-05 | 1.59E-27 | 2.04E-27 | 6.68E-25 |
| ILMN_1703969-ENSG00000179889 | PDXDC1 | 16 | 3.75E-21 | 6.02E-21 | 9.84E-18 | 7.44E-06 | 3.09E-06 | 0.000316 | 6.47E-26 | 9.61E-26 | 8.40E-21 |
| ILMN_1815552-ENSG00000157045 | NTAN1 | 16 | 1.99E-15 | 5.49E-13 | 2.16E-17 | 0.001191 | 0.005791 | 0.000142 | 1.63E-19 | 4.04E-16 | 1.72E-22 |
| ILMN_1728645-ENSG00000197457 | STMN3 | 20 | 5.69E-05 | 0.000581 | 2.55E-06 | 0.00158 | 0.005448 | 0.000306 | 1.69E-07 | 5.90E-06 | 1.44E-09 |
| ILMN_2344079-ENSG00000203896 | LIME1 | 20 | 5.37E-05 | 0.000597 | 4.41E-06 | 0.001157 | 0.003581 | 0.000359 | 1.39E-08 | 8.65E-07 | 2.72E-10 |

sTable 6. The p-values of the SNPs reported in previous GWAS of glioma.

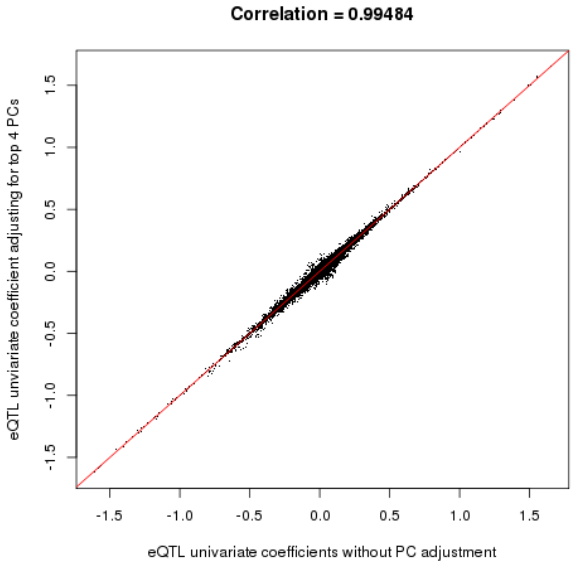
| SNP ID | Gene | Cytoband | *p*-value |
|---|---|---|---|
| rs1920116 | *TERC* | 3q26.2 | 0.0993 |
| rs2736100 | *TERT* | 5p15.33 | 1.46E-05 |
| rs2853676 | *TERT* | 5p15.33 | 0.00152 |
| rs11979158 | *EGFR* | 7p11.2 | 0.233 |
| rs2252586 | *EGFR* | 7p11.2 | 3.12E-05 |
| rs4295627 | *CCDC26* | 8q24.21 | 0.537 |
| rs10464870 | *CCDC26* | 8q24.21 | 0.208 |
| rs891835 | *CCDC26* | 8q24.21 | 0.535 |
| rs6470745 | *CCDC26* | 8q24.21 | 0.991 |
| rs16904140 | *CCDC26* | 8q24.21 | 0.521 |
| rs4977756 | *CDKN2BAS* | 9p21.3 | 8.63E-05 |
| rs1412829 | *CDKN2BAS* | 9p21.3 | 1.08E-05 |
| rs1063192 | *CDKN2A/B* | 9p21.3 | 1.36E-07 |
| rs2157719 | *CDKN2A/B* | 9p21.3 | 6.44E-07 |
| rs111696067 | *VTI1A* | 10q25.2 | NA |
| rs648044 | *ZBTB16* | 11q23.2 | NA |
| rs498872 | *ARCN;PHLDB1* | 11q23.3 | 0.710 |
| rs12230172 | *NA* | 12q21.2 | NA |
| rs3851634 | *POLR3B* | 12q23.3 | 0.0129 |
| rs1801591 | *ETFA* | 15q24.2 | 0.109 |
| rs2297440 | *RTEL1* | 20q13.33 | 1.01E-08 |
| rs4809324 | *RTEL1;TNFRSF6B* | 20q13.33 | 0.0570 |
| rs6010620 | *RTEL1;TNFRSF6B* | 20q13.33 | 3.36E-08 |

sFigure 1. Distribution of number of eQTL in 30,527 transcripts. 24 transcripts with more than 100 eQTL are not shown in the plot.

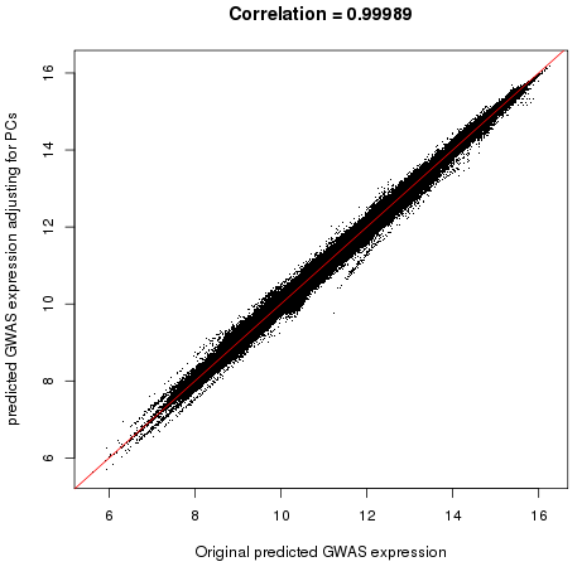


sFigure 2. Comparison of eQTL association (a) and predicted transcript expression (b) with and without adjustment of principal components of population stratification.

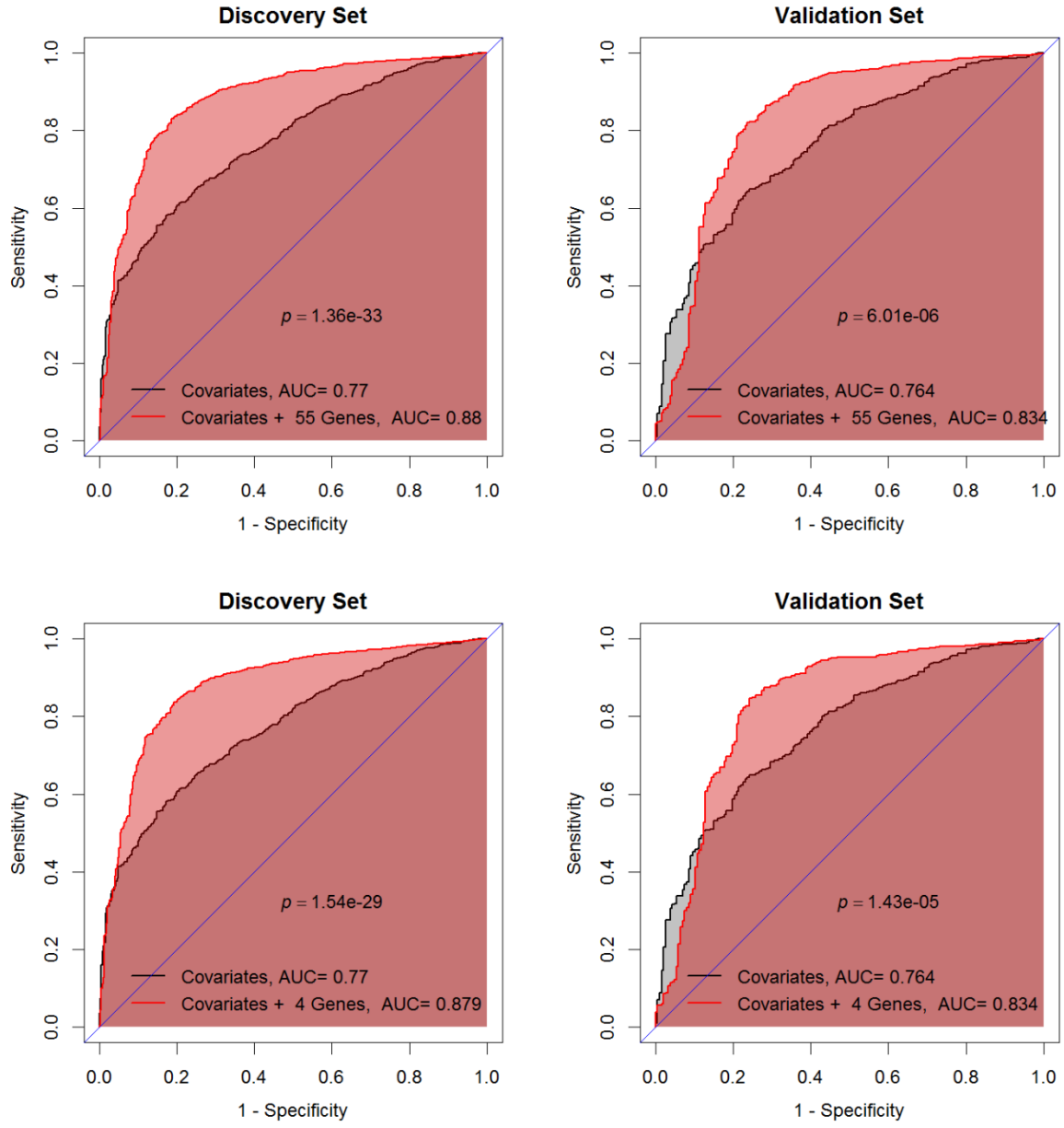
a



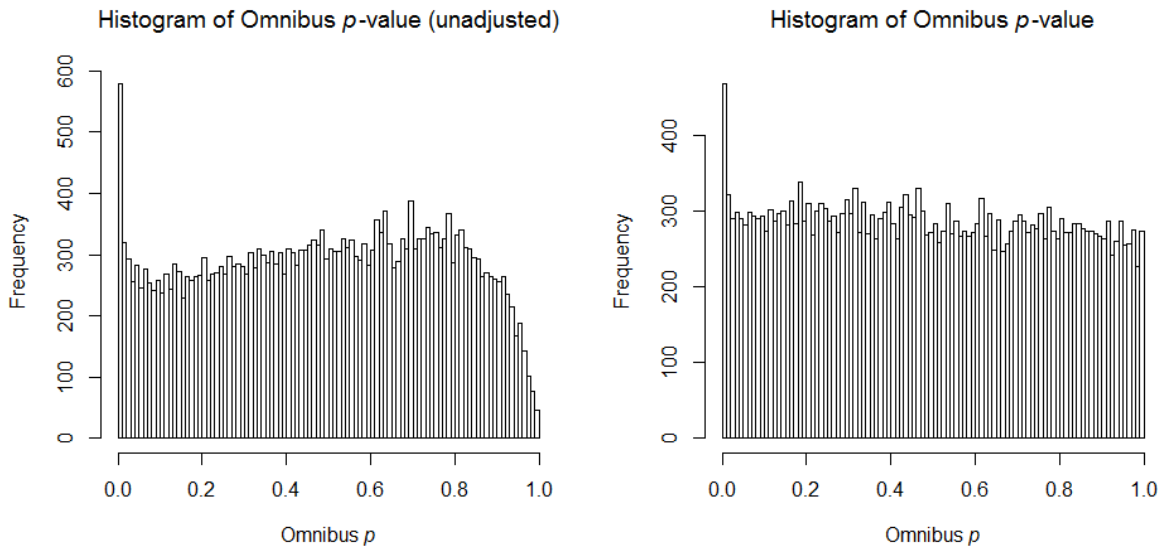

b



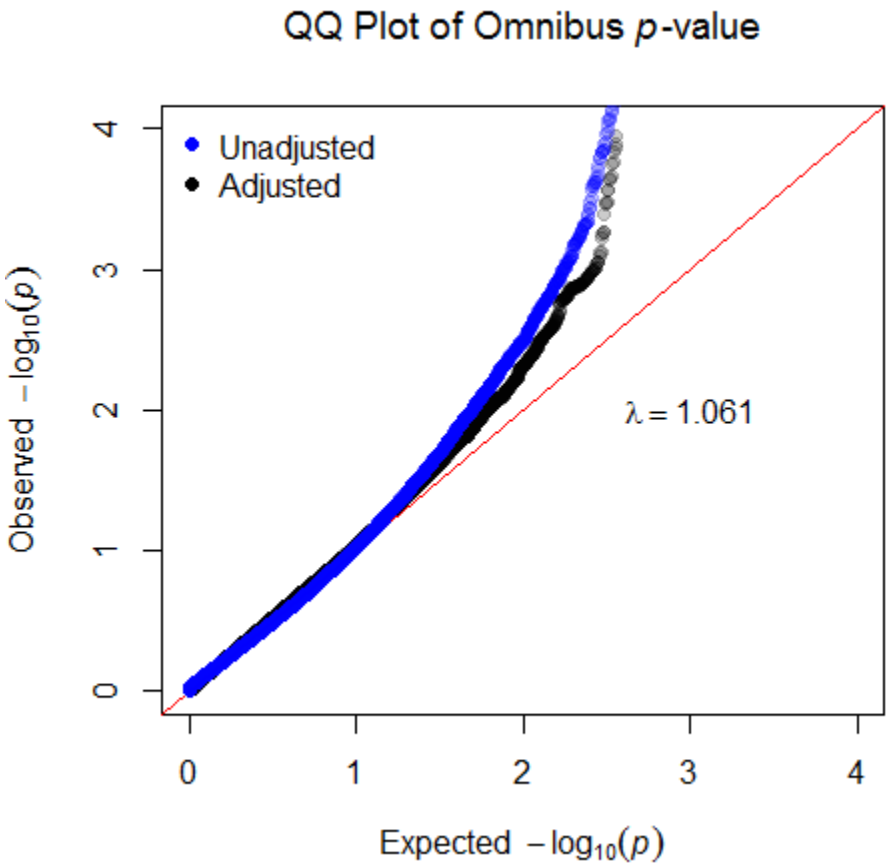
sFigure 3. The gene signature of glioma risk with eQTL analyses adjusting for population stratification. (a) and (b), the ROC curve and its area under the curve (AUC) of the model with only covariates (black curve) and that with covariates and the 55 transcripts (red curve) in Discovery Set (a) and Validation Set (b). (c) and (d), the ROC curve and its area under the curve (AUC) of the model with only covariates (black curve) and that with covariates and the 4 genes: *DRD5*, *WDR1*, *NOMO1* and *PDXDC1* (red curve) in Discovery Set (c) and Validation Set (d).



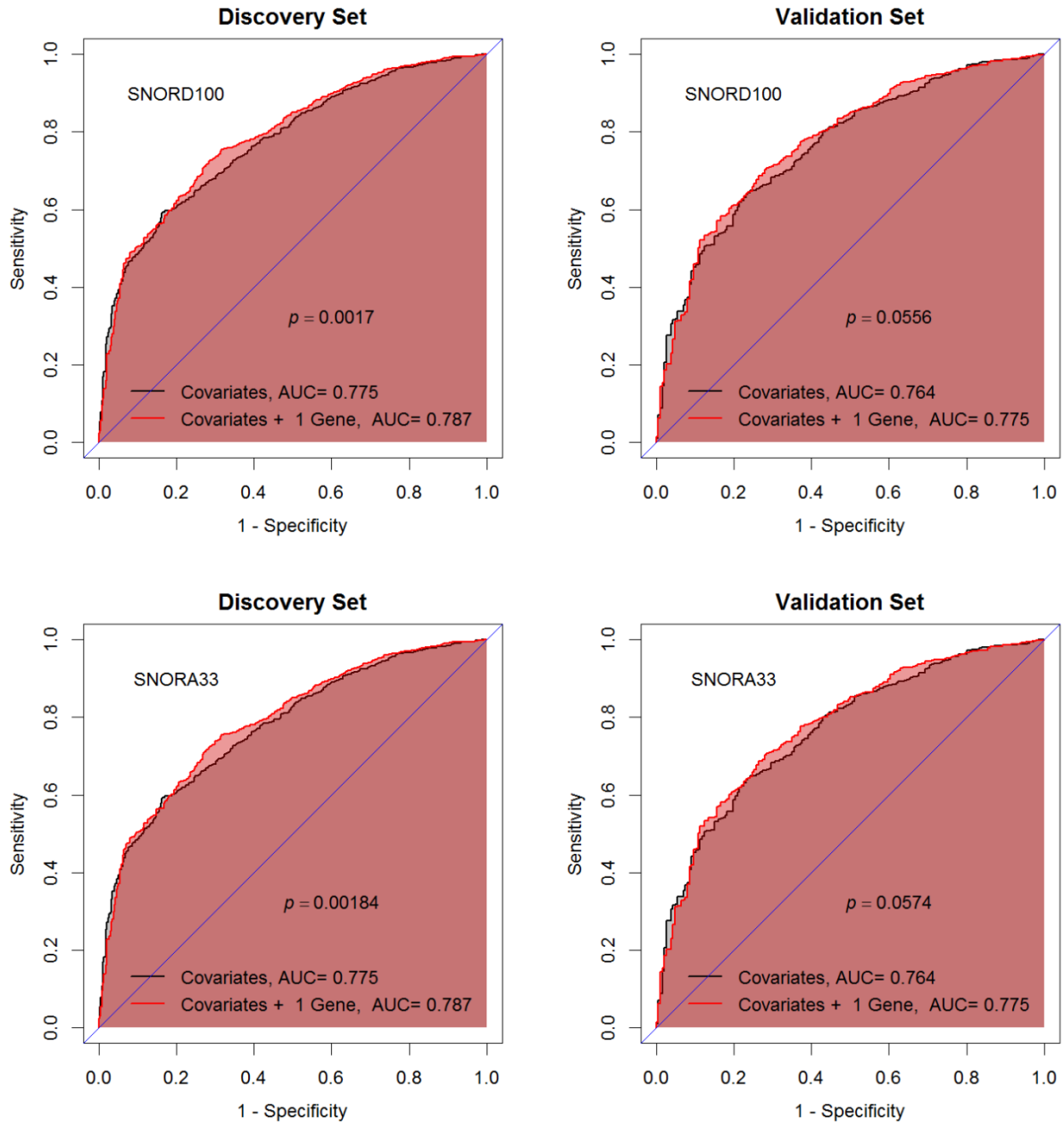
sFigure 4. Histogram of iGWAS omnibus p-value for the association of 30,527 transcripts with glioma risk. Left, p-values without adjusting for age, gender and population stratification; right: adjusted p-values.

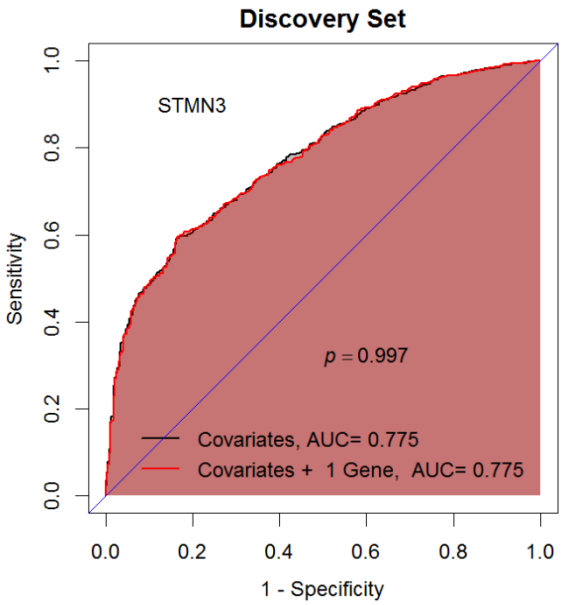


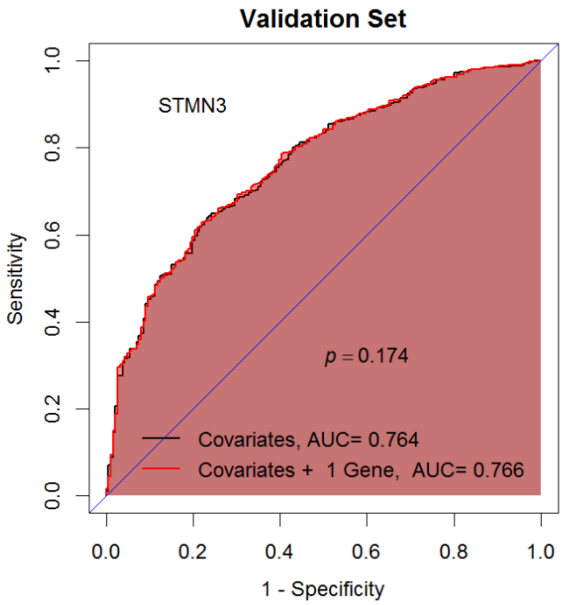
sFigure 5. Quantile-quantile plot of iGWAS omnibus p-value for the association of 30,527 transcripts with glioma risk, with genomic inflation factor $\lambda$ of 1.061. Blue dots indicate the p-values from analyses without adjusting for age, gender and population stratification.

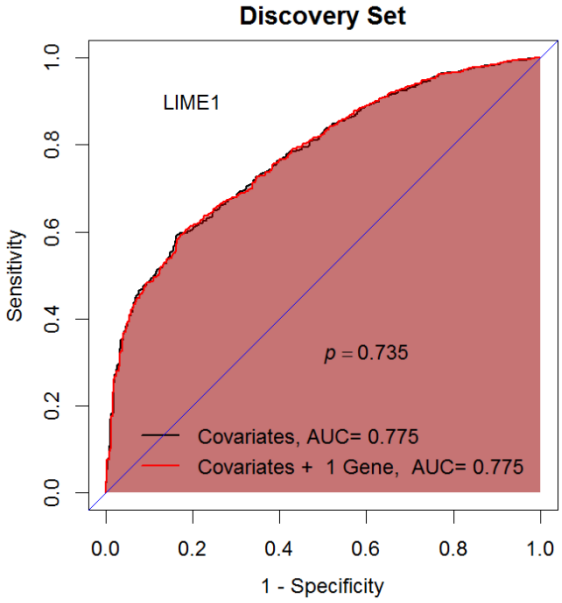


sFigure 6. The ROC curves for the 55 validated transcripts and its AUC of the model with only covariates (black curve) and that with covariates plus the estimated expression values of one transcript (red curve) in Discovery Set (left) and Validation Set (right).




Discovery Set
STMN3
p = 0.997
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.775
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Validation Set
STMN3
p = 0.174
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.766
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
LIME1
p = 0.735
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.775
Sensitivity
1 - Specificity
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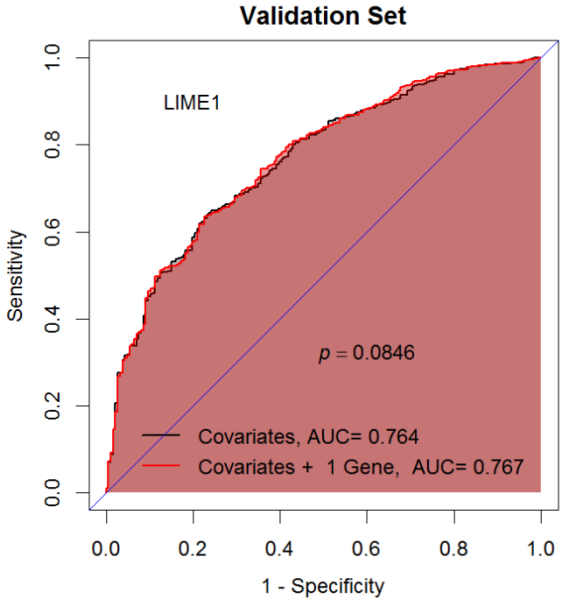
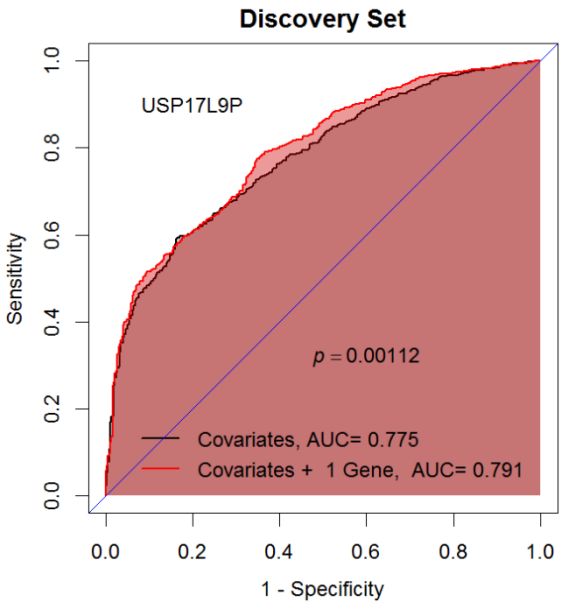
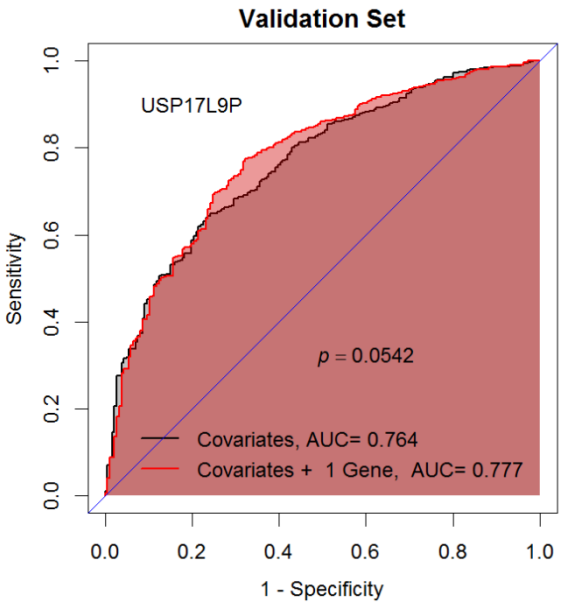
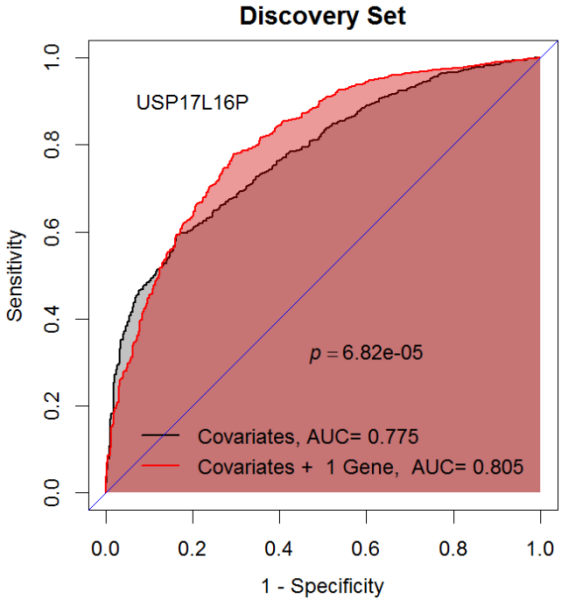
0.2
0.4
0.6
0.8
1.0


Validation Set
LIME1
p = 0.0846
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.767
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L9P
p = 0.00112
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.791
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L9P
p = 0.0542
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.777
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L16P
p = 6.82e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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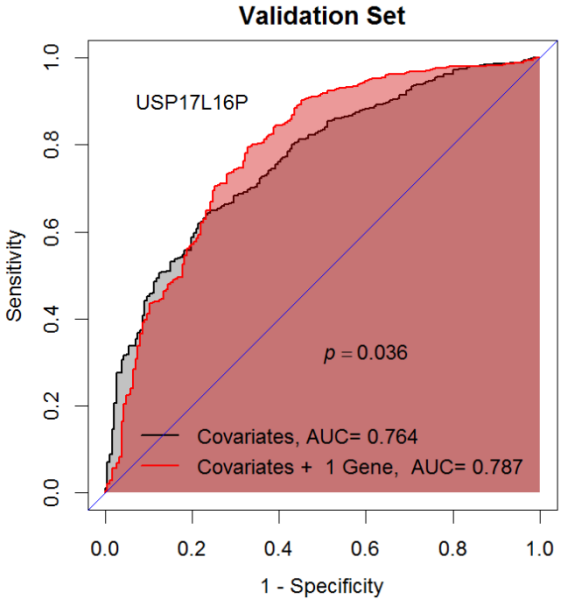
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L16P
p = 0.036
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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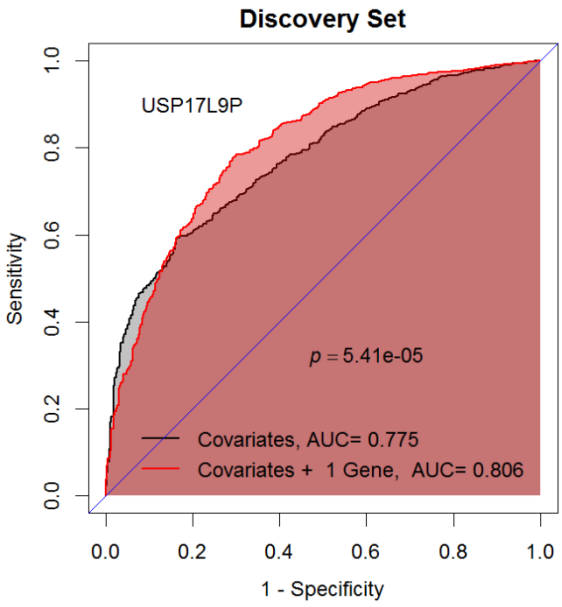
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L9P
p = 5.41e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
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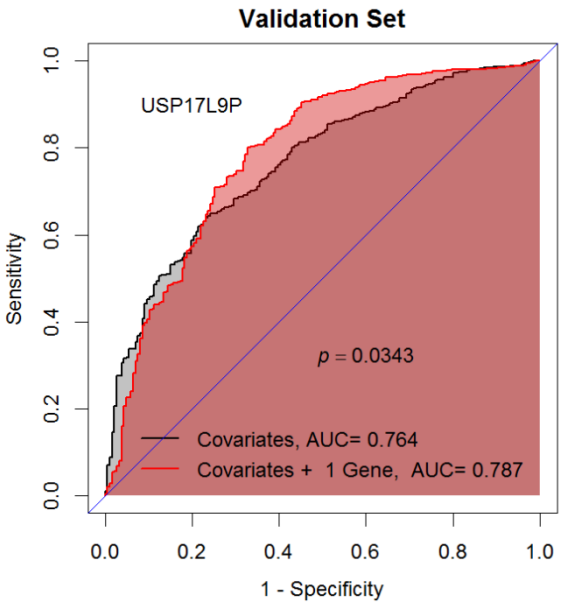
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L9P
p = 0.0343
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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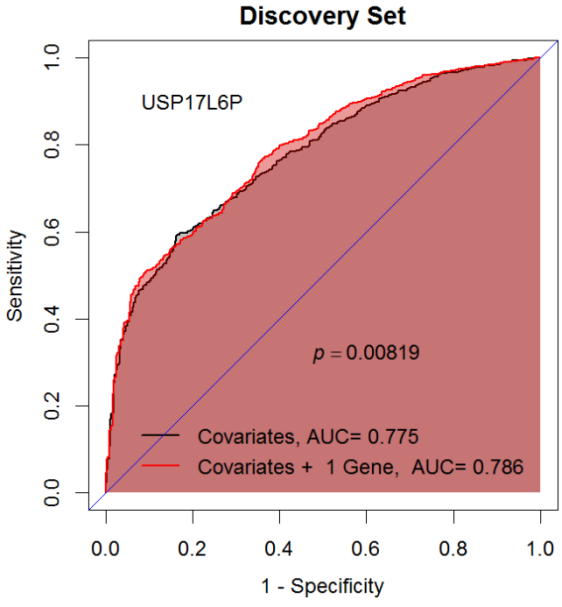
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L6P
p = 0.00819
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.786
Sensitivity
1 - Specificity
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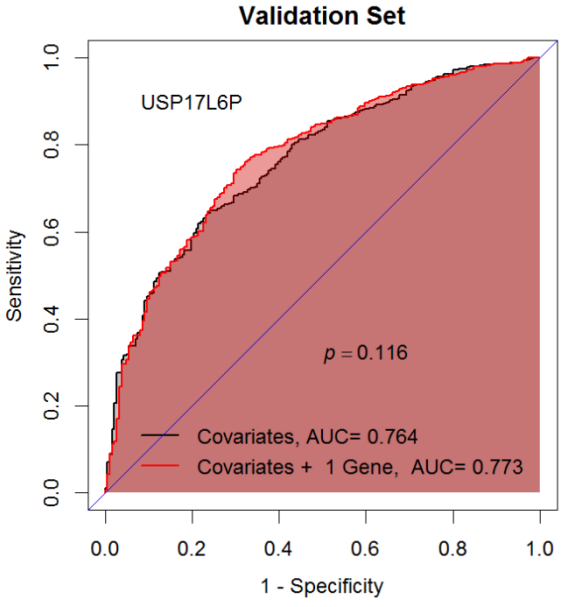
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L6P
p = 0.116
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.773
Sensitivity
1 - Specificity
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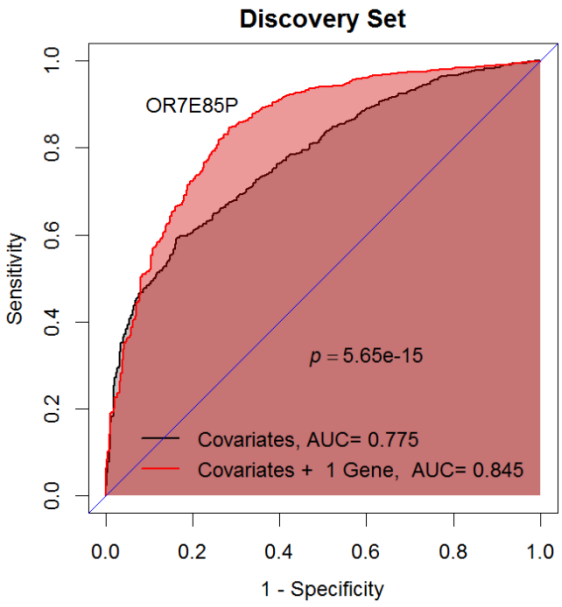
0.2
0.4
0.6
0.8
1.0


Discovery Set
OR7E85P
p = 5.65e-15
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.845
Sensitivity
1 - Specificity
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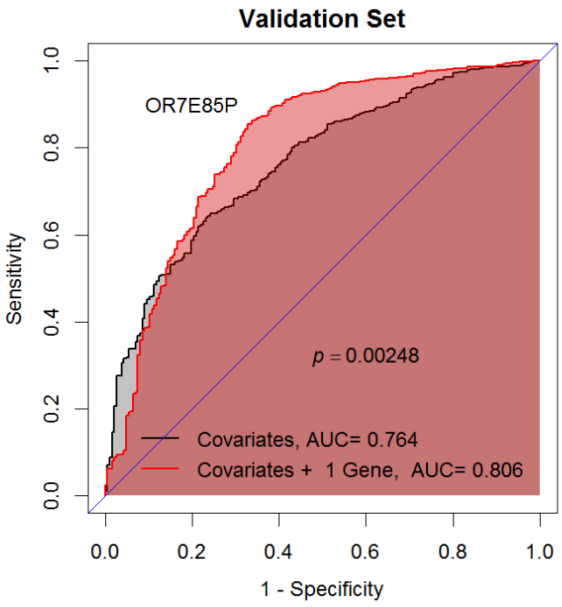
0.2
0.4
0.6
0.8
1.0


Validation Set
OR7E85P
p = 0.00248
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
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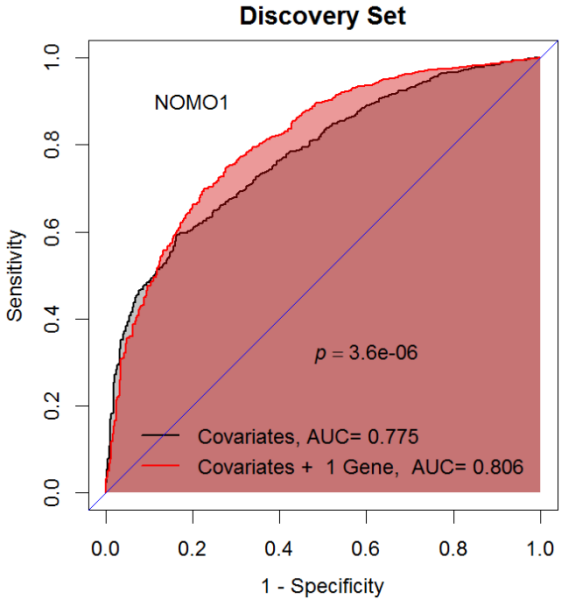
0.2
0.4
0.6
0.8
1.0


Discovery Set
NOMO1
p = 3.6e-06
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
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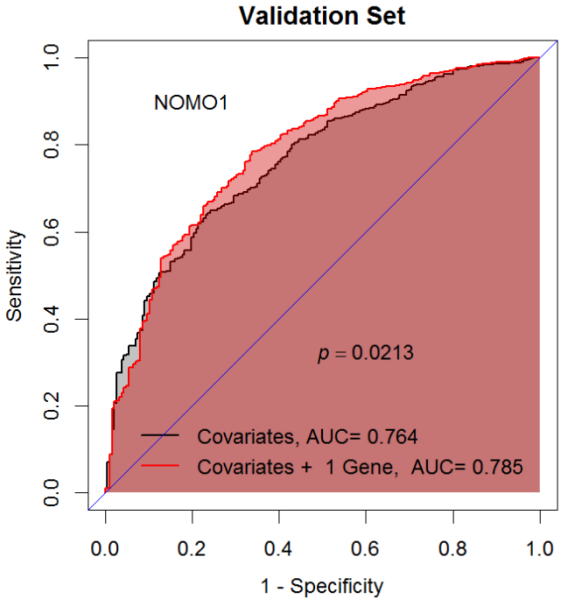
0.2
0.4
0.6
0.8
1.0


Validation Set
NOMO1
p = 0.0213
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.785
Sensitivity
1 - Specificity
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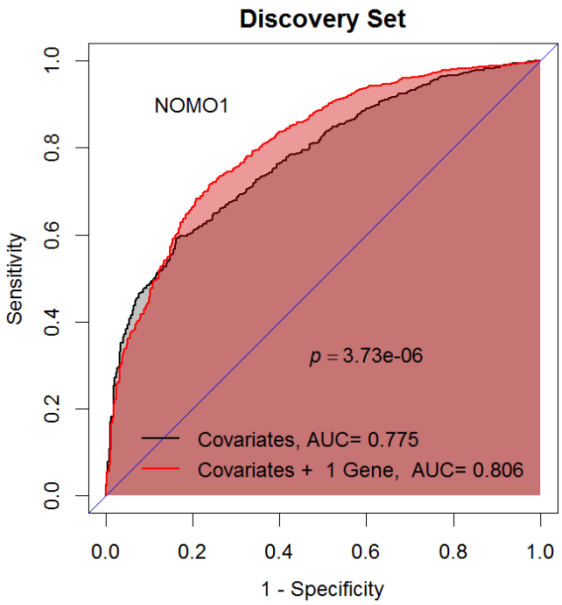
0.2
0.4
0.6
0.8
1.0


Discovery Set
NOMO1
p = 3.73e-06
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
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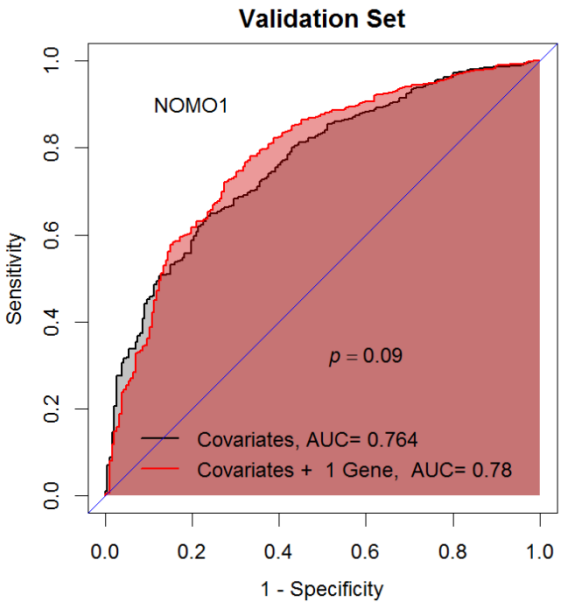
0.2
0.4
0.6
0.8
1.0


Validation Set
NOMO1
p = 0.09
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.78
Sensitivity
1 - Specificity
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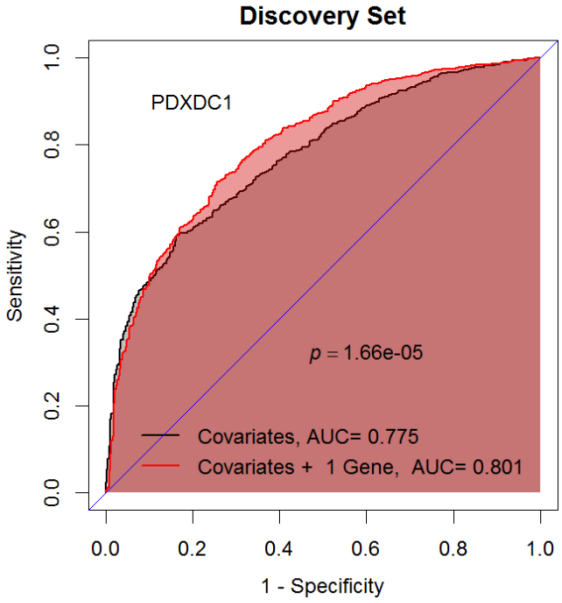
0.2
0.4
0.6
0.8
1.0


Discovery Set
PDXDC1
p = 1.66e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.801
Sensitivity
1 - Specificity
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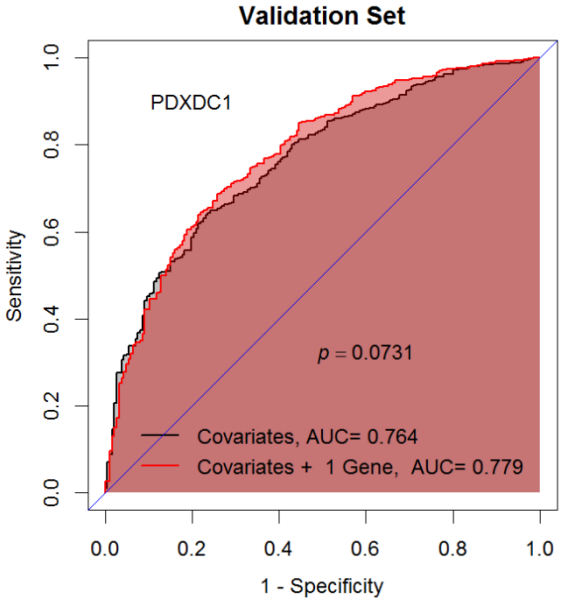
0.2
0.4
0.6
0.8
1.0


Validation Set
PDXDC1
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Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.779
Sensitivity
1 - Specificity
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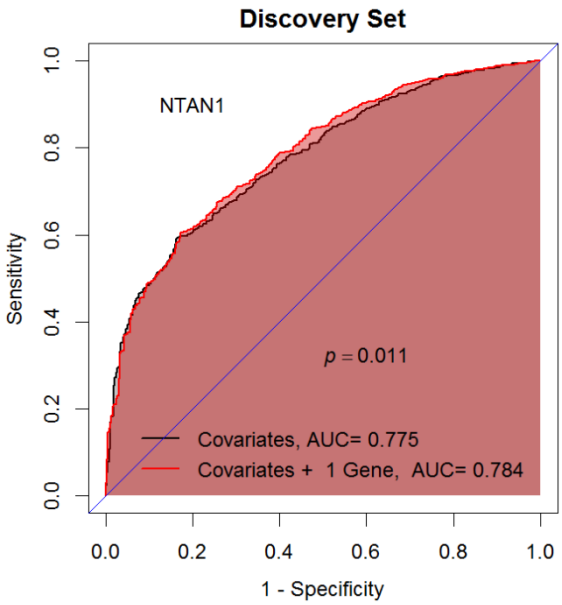
0.2
0.4
0.6
0.8
1.0


Discovery Set
NTAN1
p = 0.011
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.784
Sensitivity
1 - Specificity
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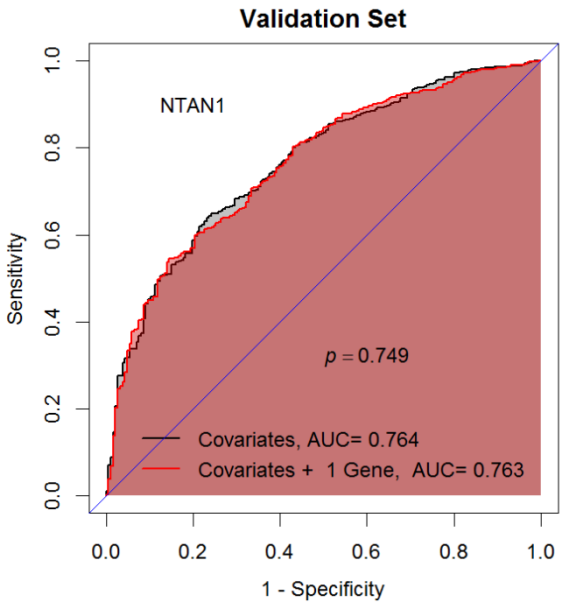
0.2
0.4
0.6
0.8
1.0


Validation Set
NTAN1
p = 0.749
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.763
Sensitivity
1 - Specificity
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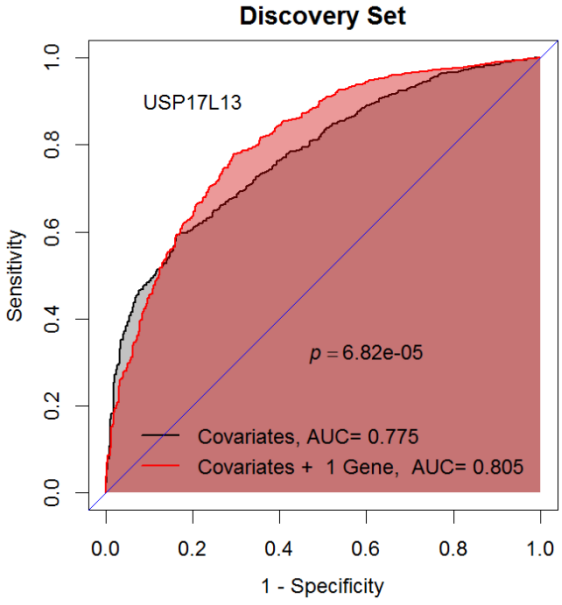
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L13
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Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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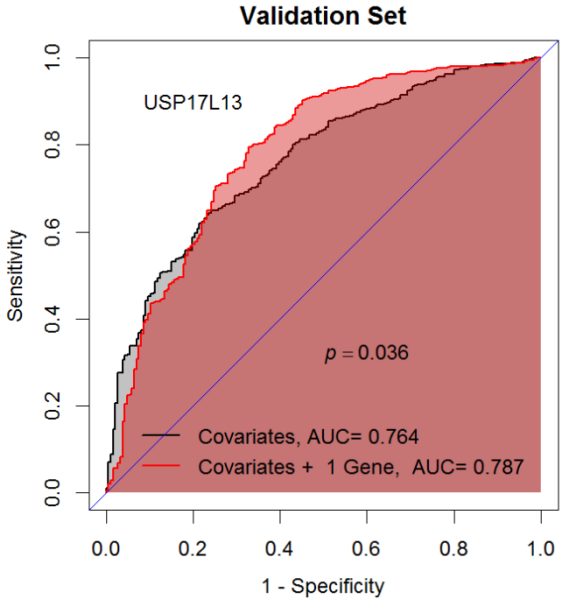
0.2
0.4
0.6
0.8
1.0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USP17L13
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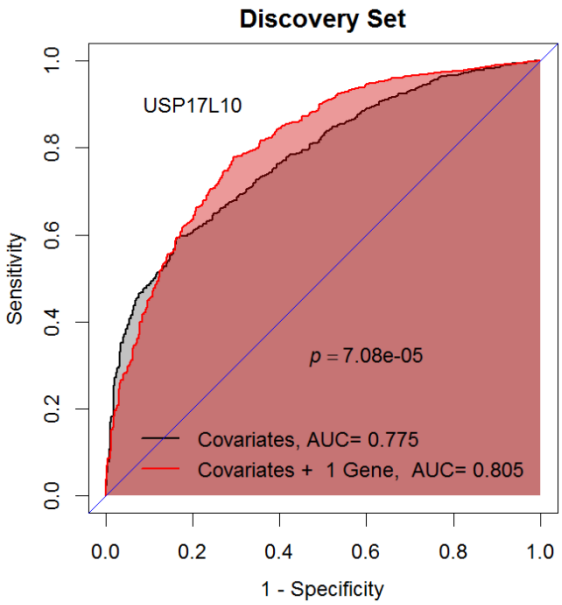
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L10
p = 7.08e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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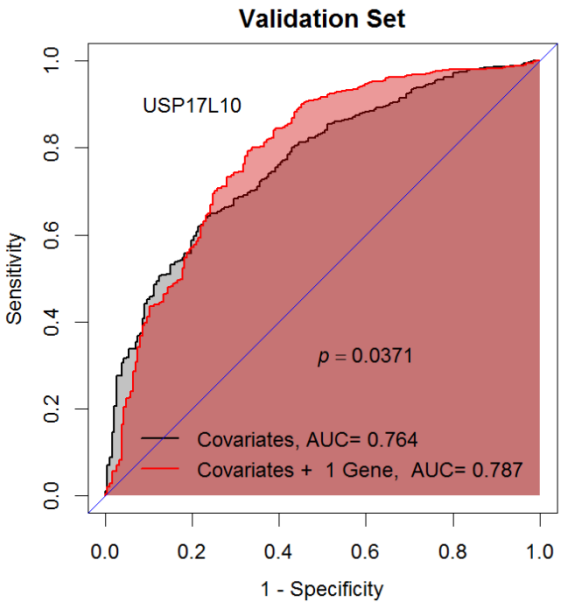
Validation Set
USP17L10
p = 0.0371
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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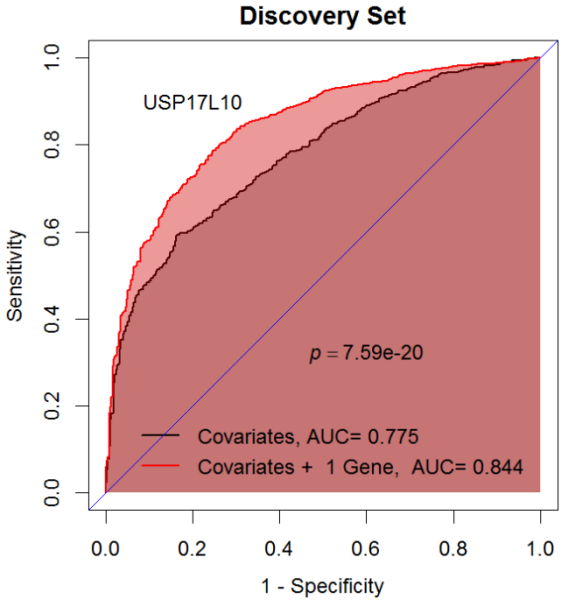
Discovery Set
USP17L10
p = 7.59e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
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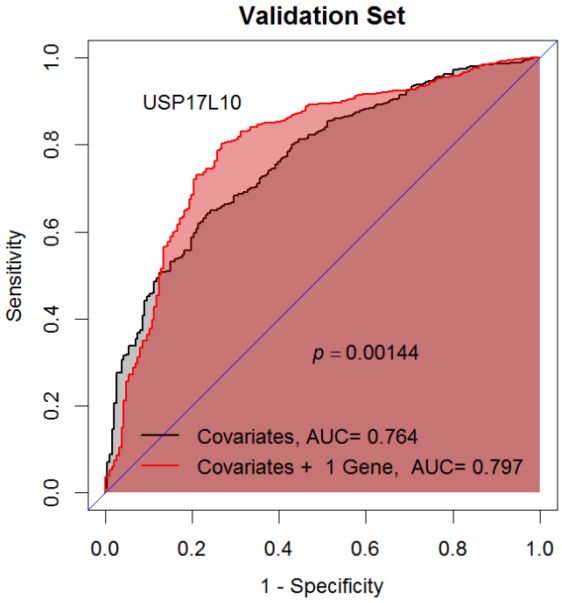
Validation Set
USP17L10
p = 0.00144
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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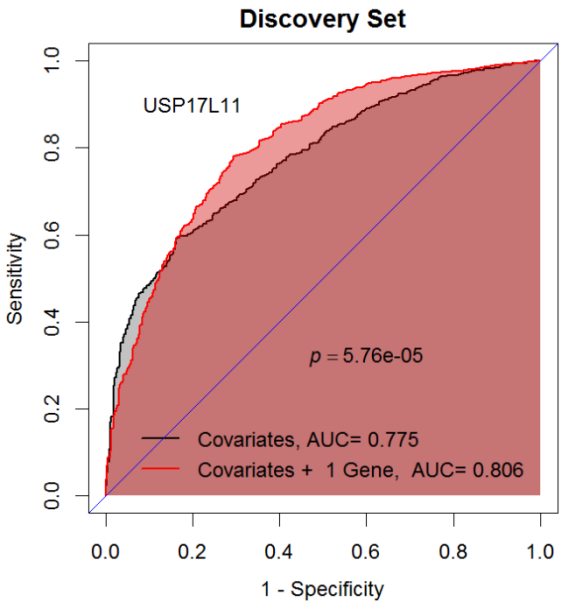
Discovery Set
USP17L11
p = 5.76e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
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0.8
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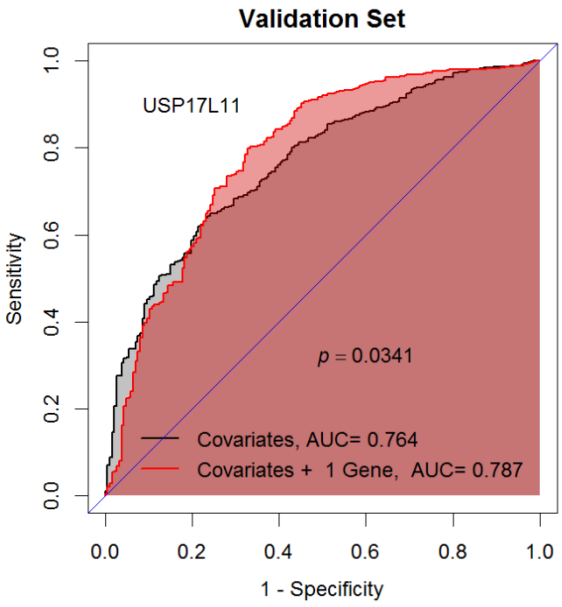
Validation Set
USP17L11
p = 0.0341
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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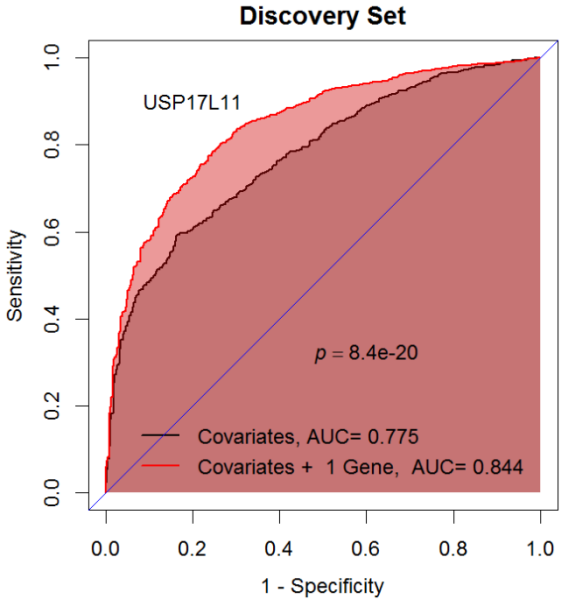
0.8
1.0


Discovery Set
USP17L11
p = 8.4e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
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0.2
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0.8
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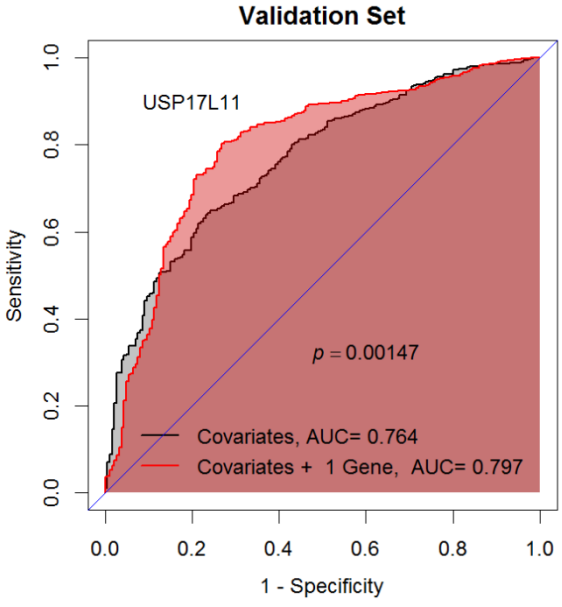
Validation Set
USP17L11
p = 0.00147
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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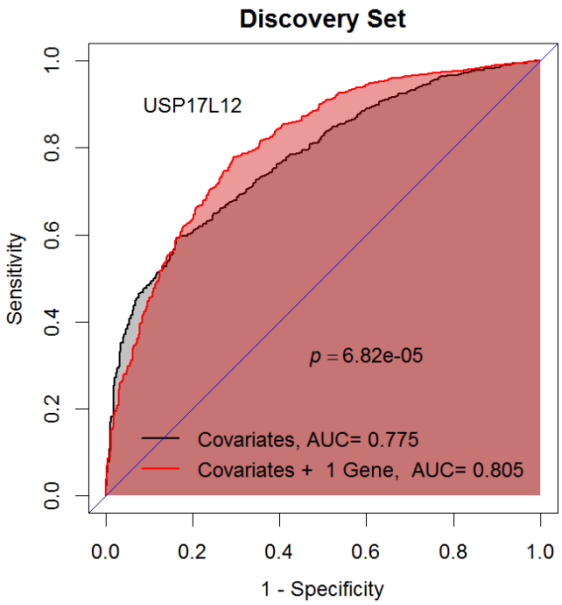
Discovery Set
USP17L12
p = 6.82e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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0.2
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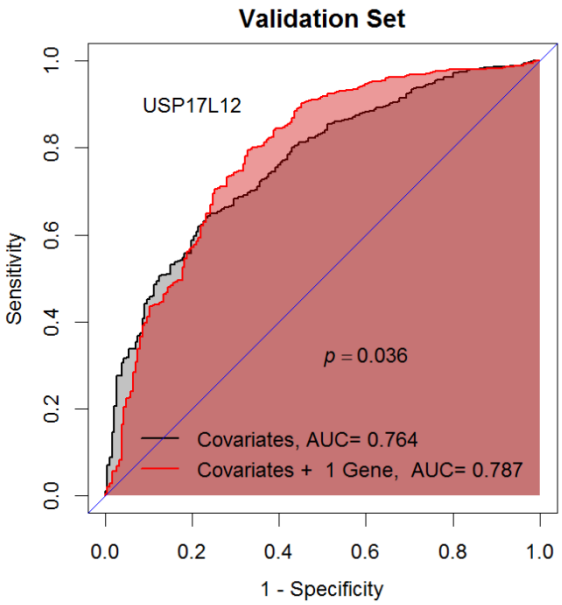
0.8
1.0


Validation Set
USP17L12
p = 0.036
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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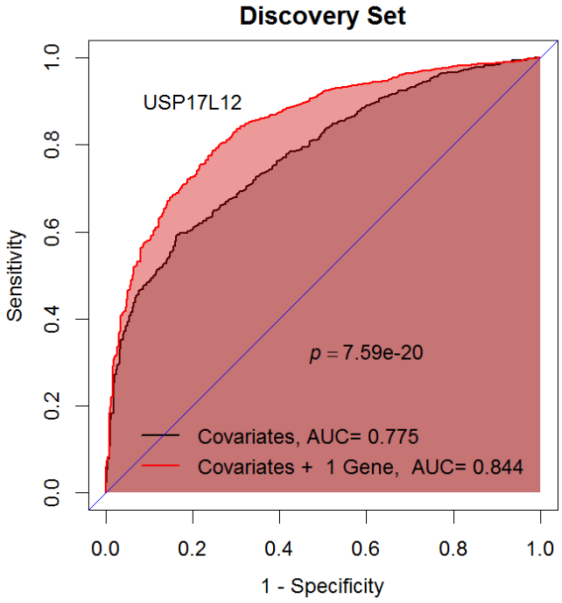
0.8
1.0


Discovery Set
USP17L12
p = 7.59e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
0.0
0.2
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0.8
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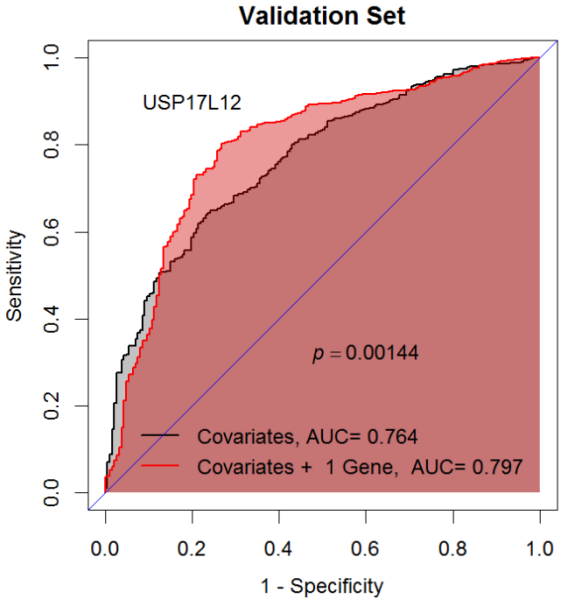
Validation Set
USP17L12
p = 0.00144
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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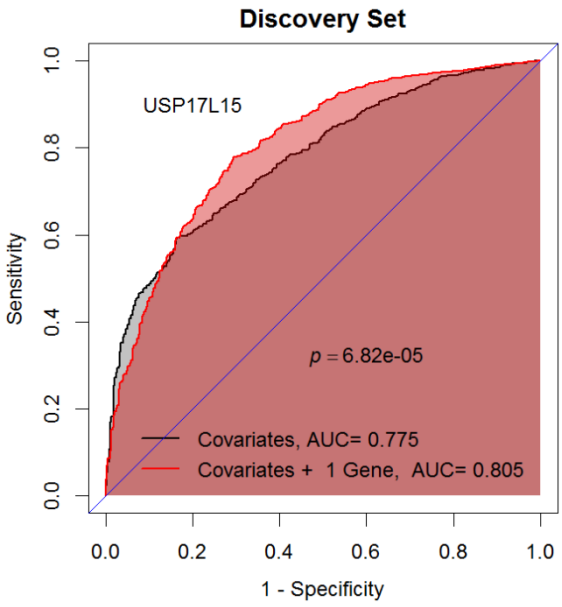
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L15
p = 6.82e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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0.2
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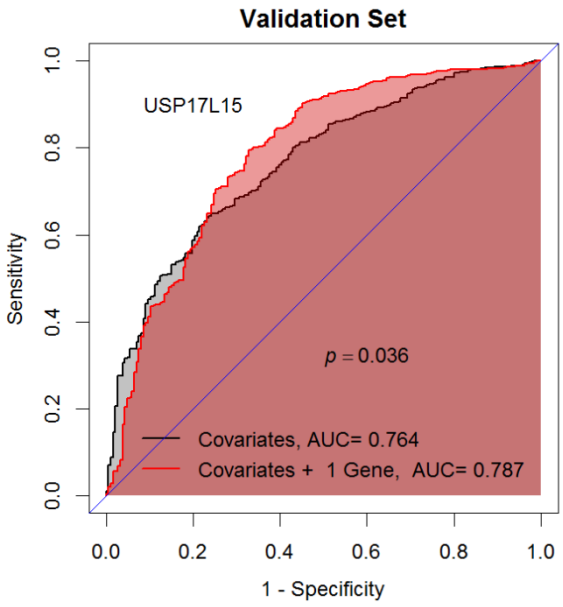
0.6
0.8
1.0


Validation Set
USP17L15
p = 0.036
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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0.2
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0.8
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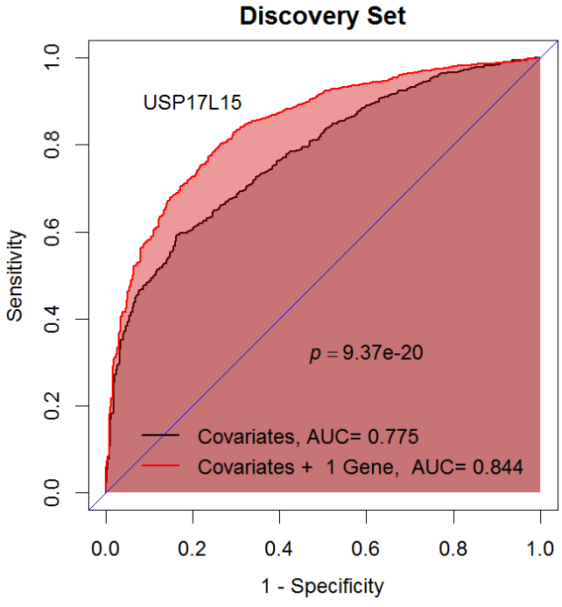
Discovery Set
USP17L15
p = 9.37e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
0.0
0.2
0.4
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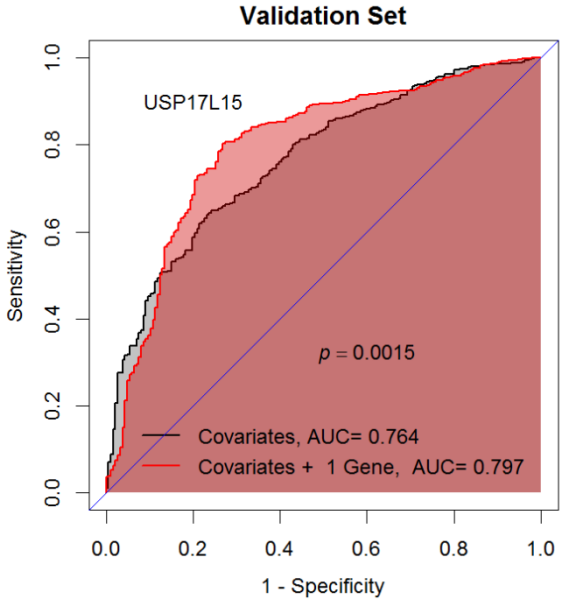
0.8
1.0


Validation Set
USP17L15
p = 0.0015
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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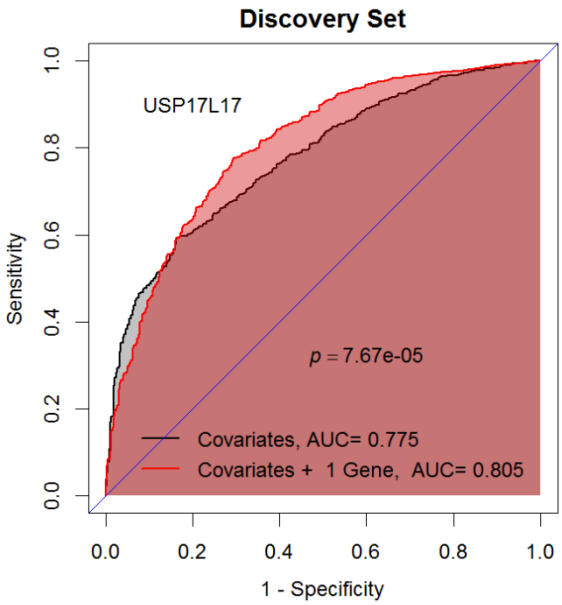
0.6
0.8
1.0


Discovery Set
USP17L17
p = 7.67e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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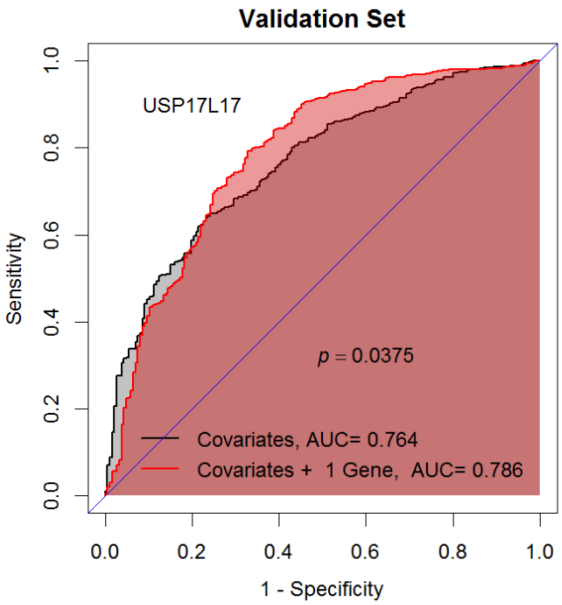
0.6
0.8
1.0


Validation Set
USP17L17
p = 0.0375
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.786
Sensitivity
1 - Specificity
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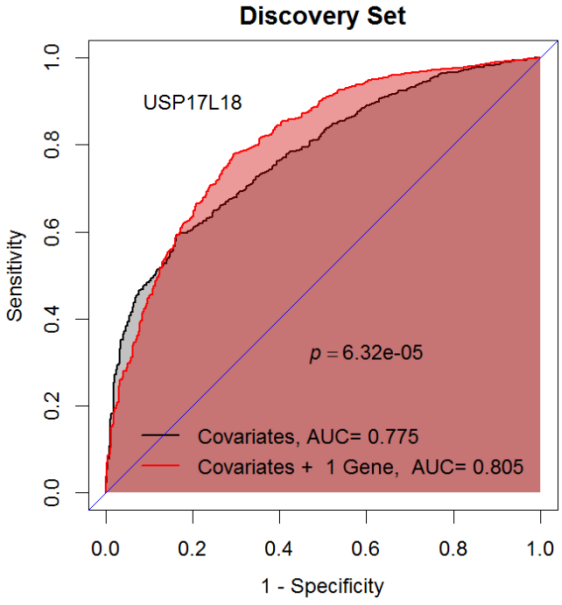
0.8
1.0


Discovery Set
USP17L18
p = 6.32e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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0.2
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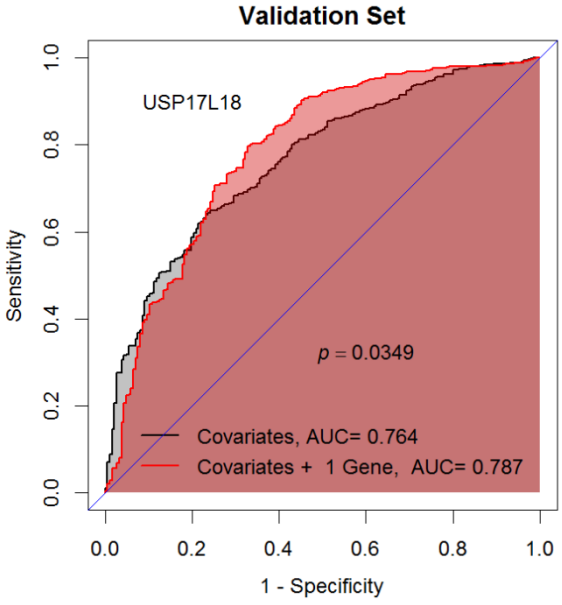
0.6
0.8
1.0


Validation Set
USP17L18
p = 0.0349
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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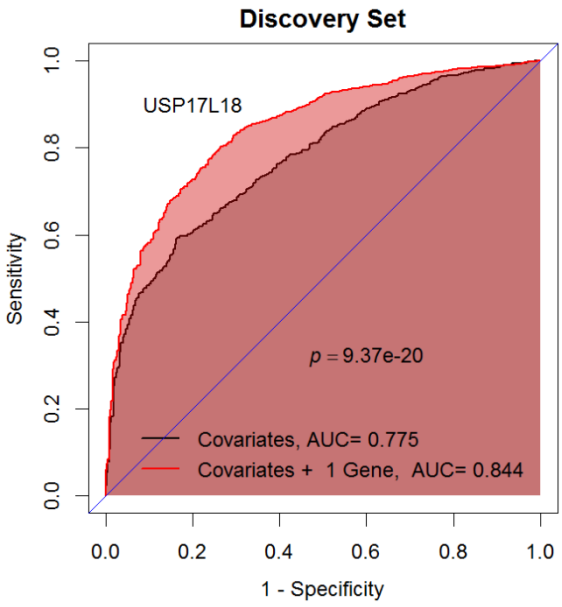
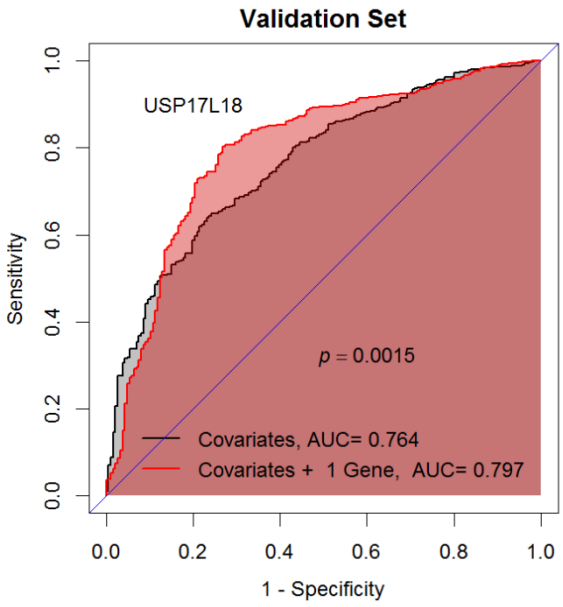
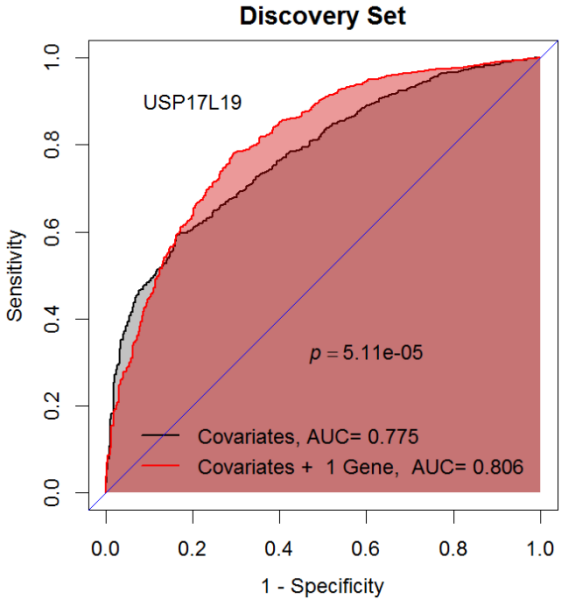
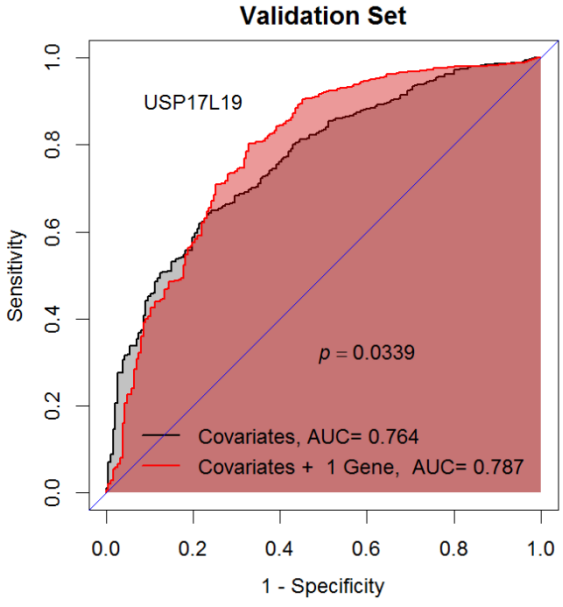
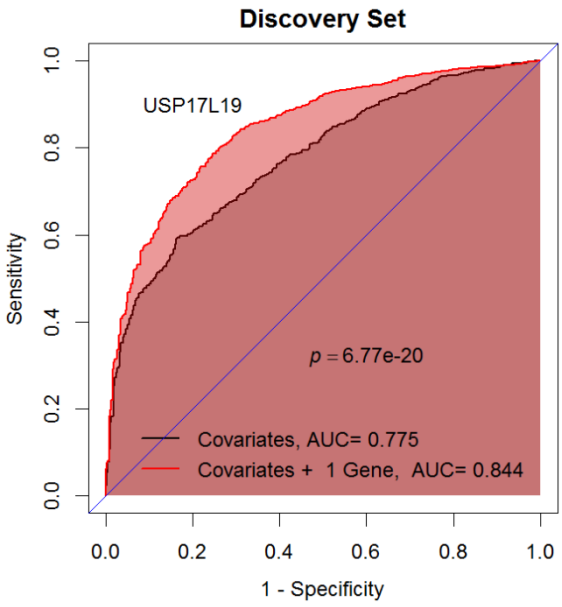
0.6
0.8
1.0


Discovery Set
USP17L18
Sensitivity
1 - Specificity
p = 9.37e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844


Validation Set
USP17L18
Sensitivity
1 - Specificity
p = 0.0015
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797


Discovery Set
USP17L19
Sensitivity
1 - Specificity
p = 5.11e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806


Validation Set
USP17L19
Sensitivity
1 - Specificity
p = 0.0339
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787


Discovery Set
USP17L19
p = 6.77e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
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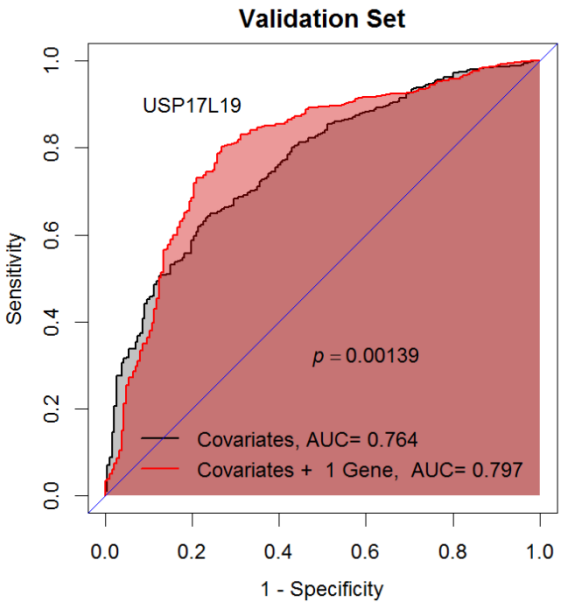
0.8
1.0


Validation Set
USP17L19
p = 0.00139
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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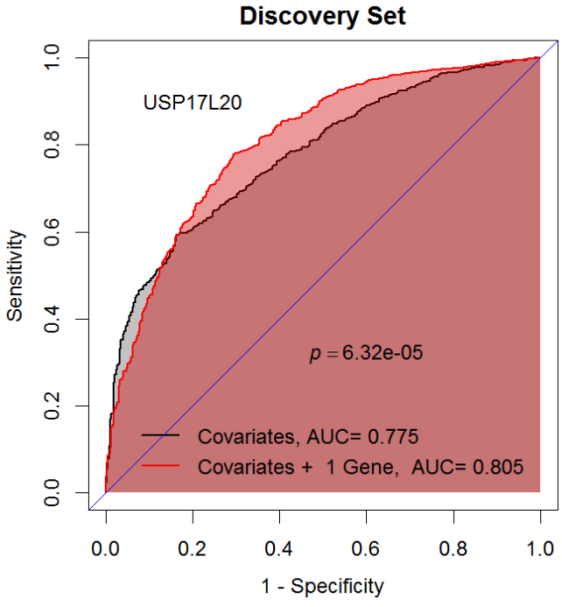
0.8
1.0


Discovery Set
USP17L20
p = 6.32e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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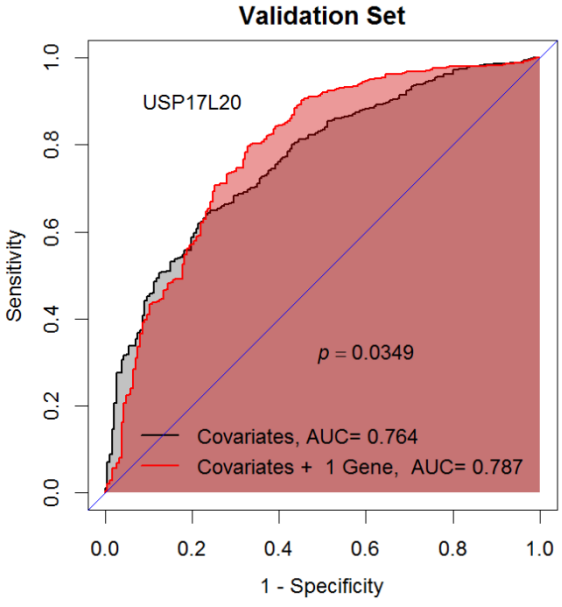
0.6
0.8
1.0


Validation Set
USP17L20
p = 0.0349
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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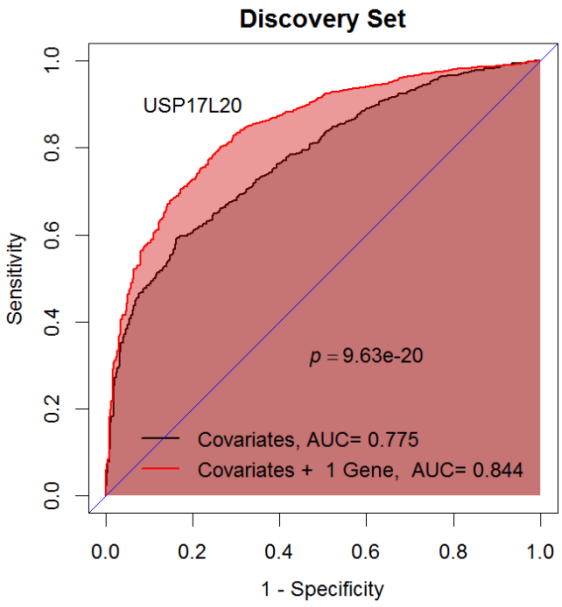
0.8
1.0


Discovery Set
USP17L20
p = 9.63e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
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0.2
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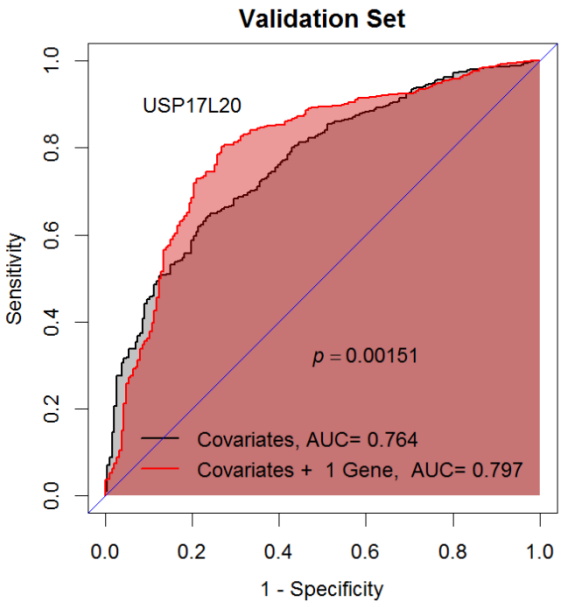
0.6
0.8
1.0


Validation Set
USP17L20
p = 0.00151
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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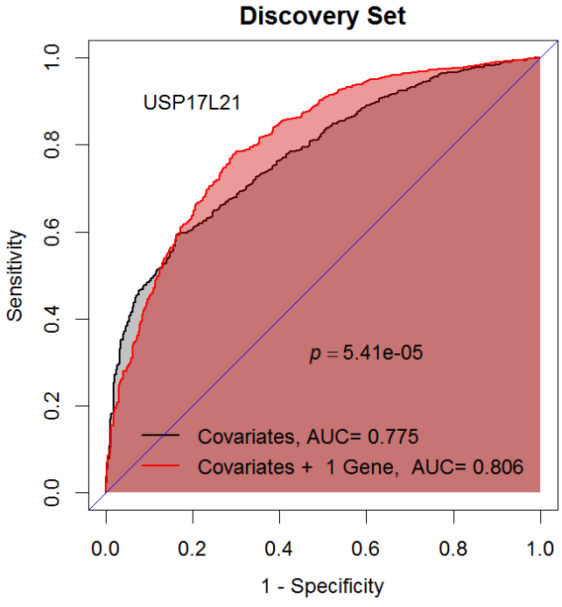
0.6
0.8
1.0


Discovery Set
USP17L21
p = 5.41e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
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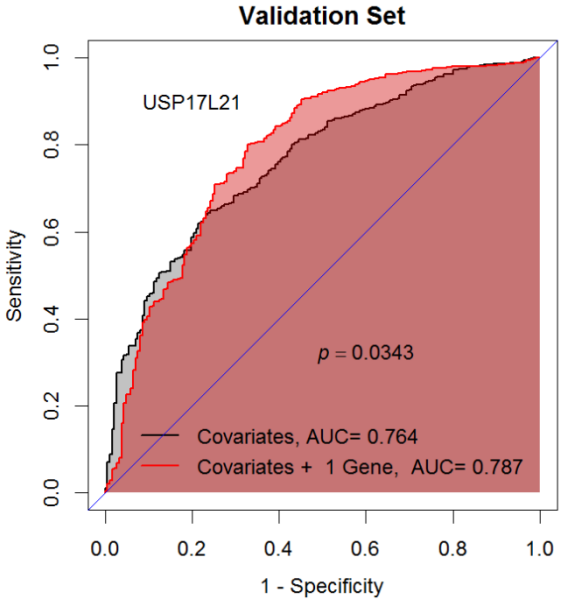
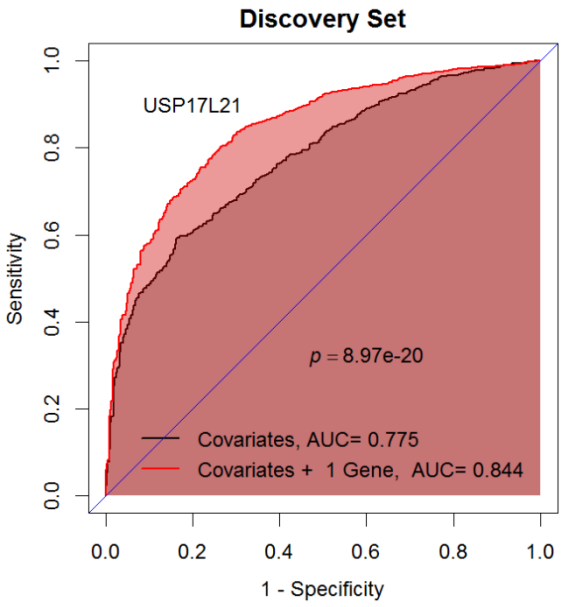
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L21
p = 0.0343
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L21
p = 8.97e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
0.0
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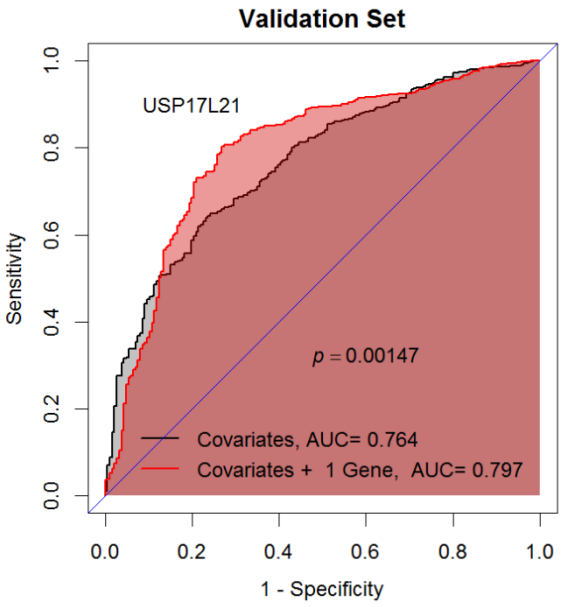
0.6
0.8
1.0


Validation Set
USP17L21
p = 0.00147
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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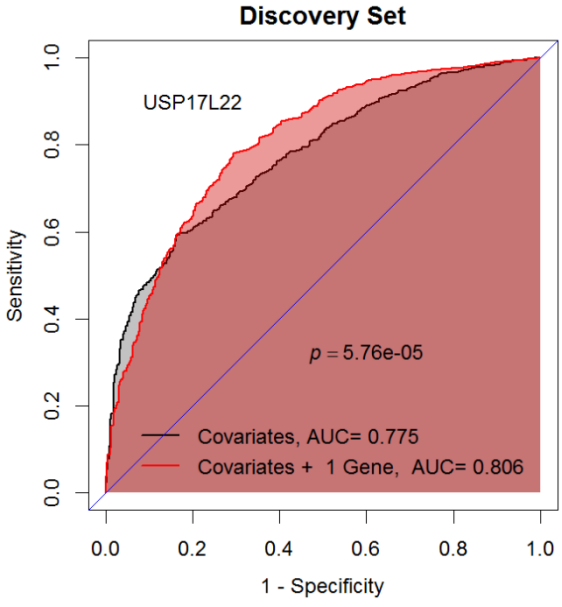
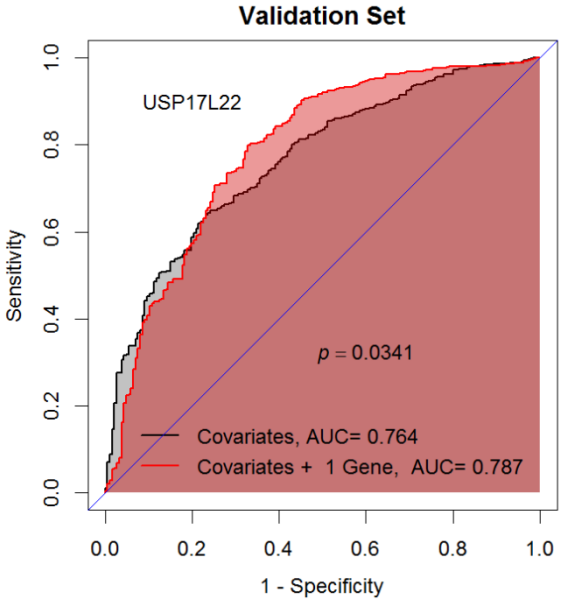
0.6
0.8
1.0


Discovery Set
USP17L22
p = 5.76e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L22
p = 0.0341
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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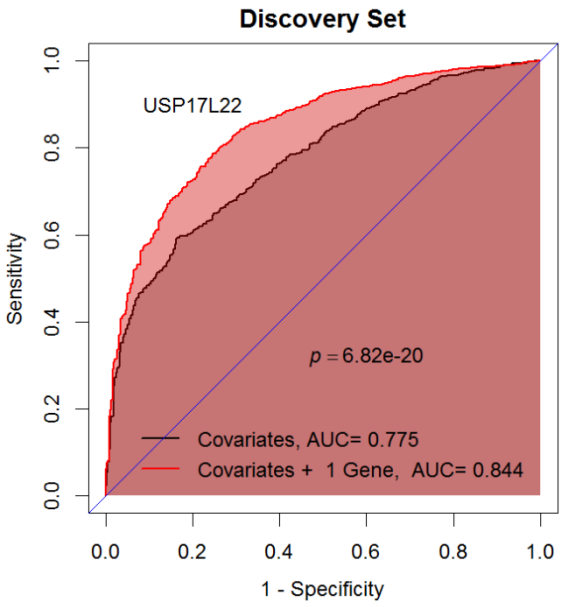
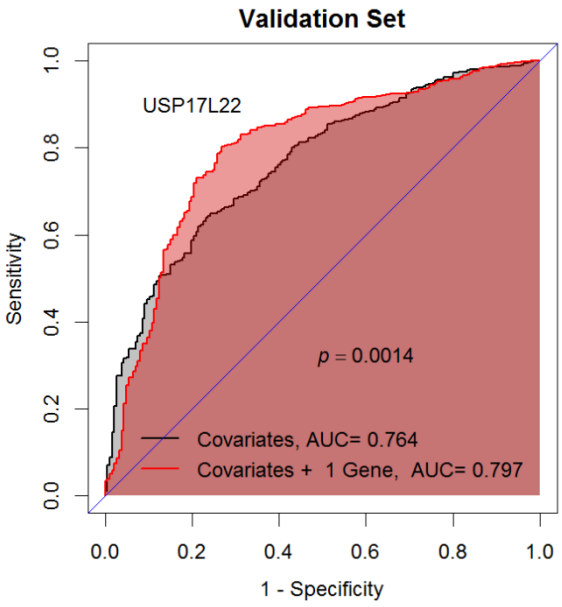
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L22
p = 6.82e-20
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.844
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L22
p = 0.0014
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.797
Sensitivity
1 - Specificity
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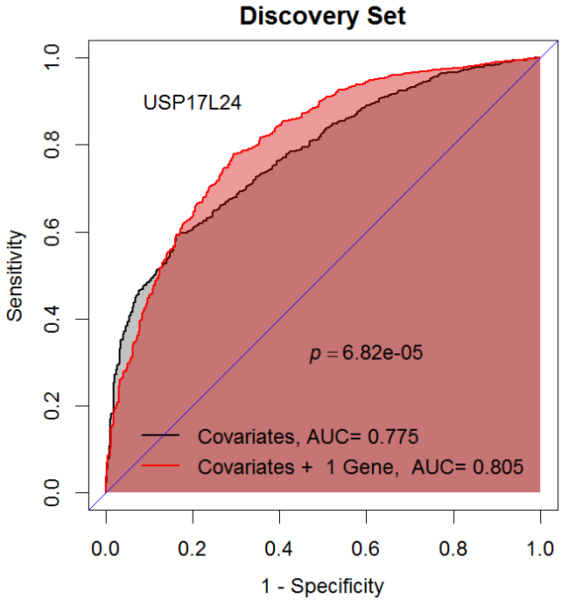
Discovery Set
USP17L24
p = 6.82e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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0.2
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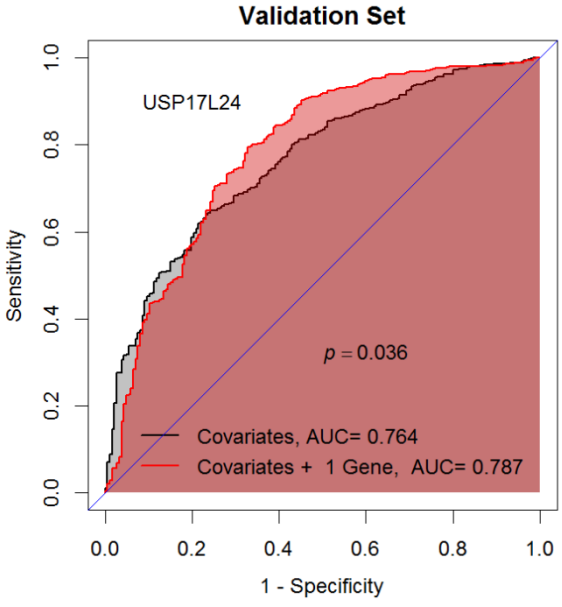
0.8
1.0


Validation Set
USP17L24
p = 0.036
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
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0.2
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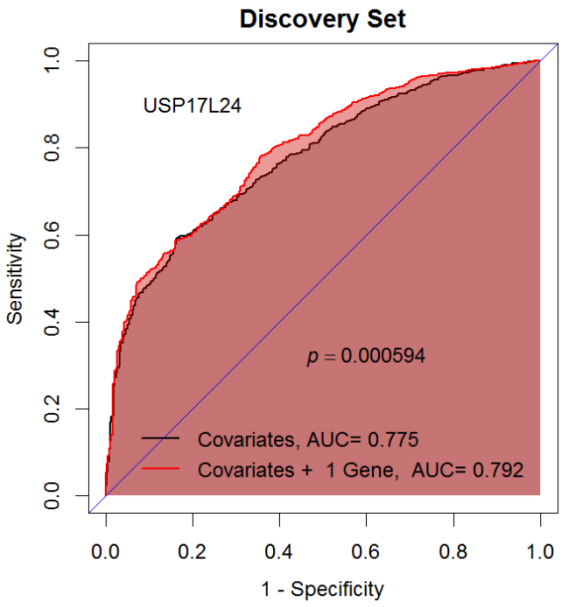
0.8
1.0


Discovery Set
USP17L24
p = 0.000594
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.792
Sensitivity
1 - Specificity
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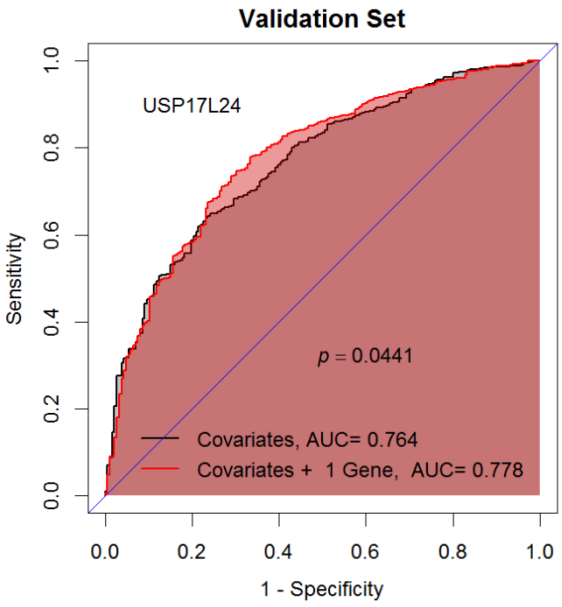
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L24
p = 0.0441
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.778
Sensitivity
1 - Specificity
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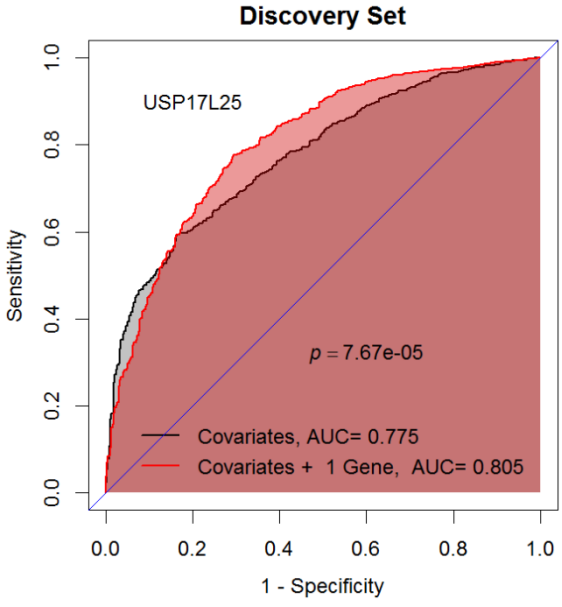
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L25
p = 7.67e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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0.2
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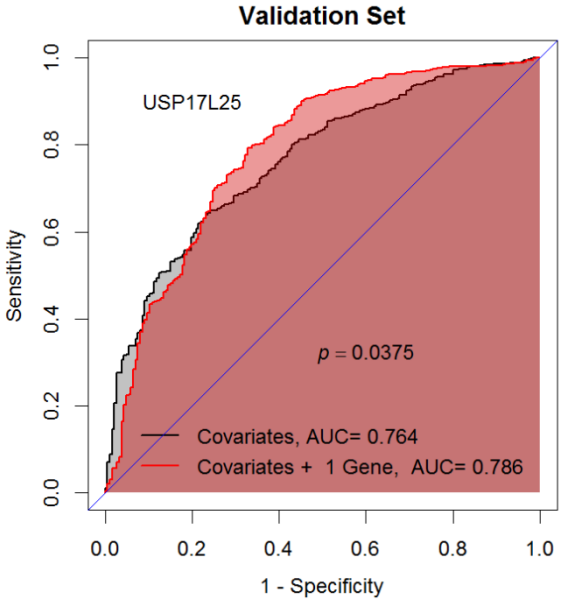
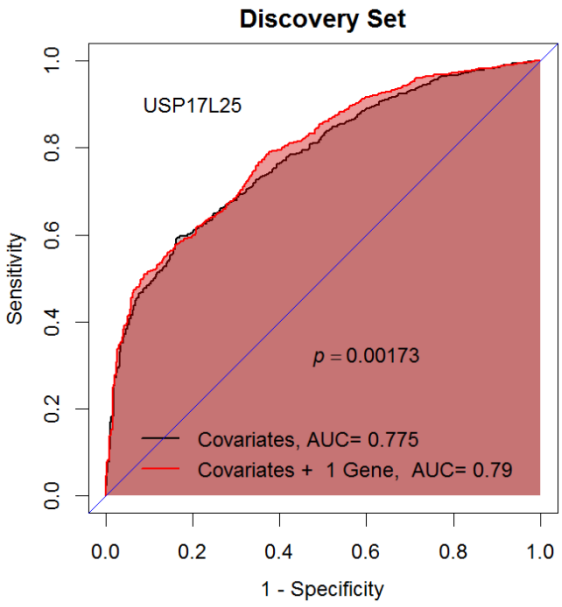
0.8
1.0


Validation Set
USP17L25
p = 0.0375
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.786
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L25
p = 0.00173
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.79
Sensitivity
1 - Specificity
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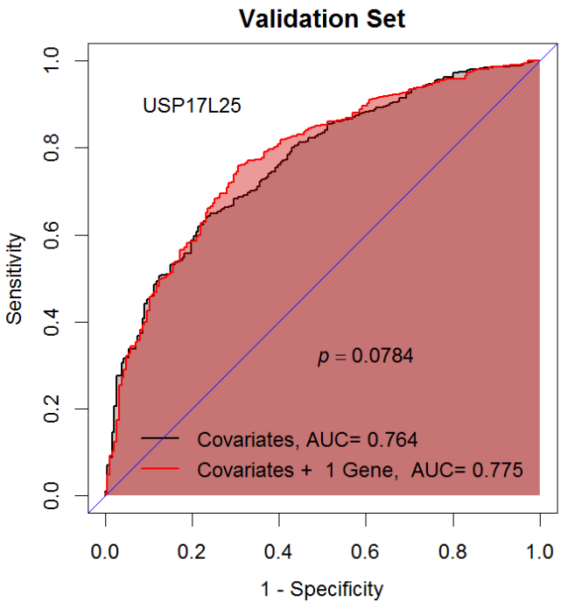
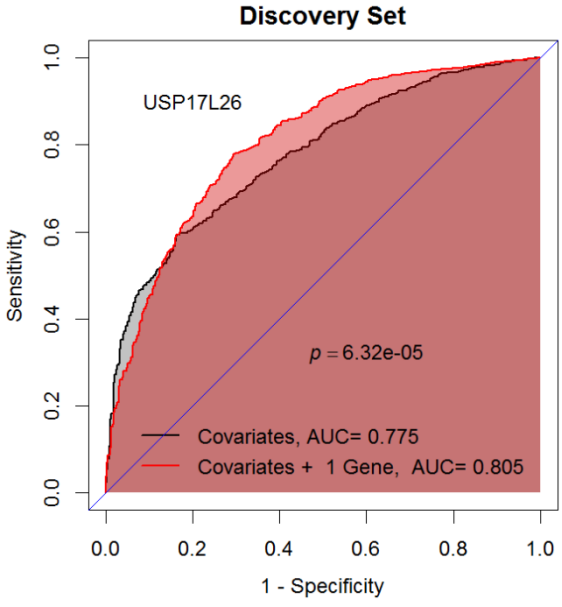
0.2
0.4
0.6
0.8
1.0


Validation Set
USP17L25
p = 0.0784
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.775
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
USP17L26
p = 6.32e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
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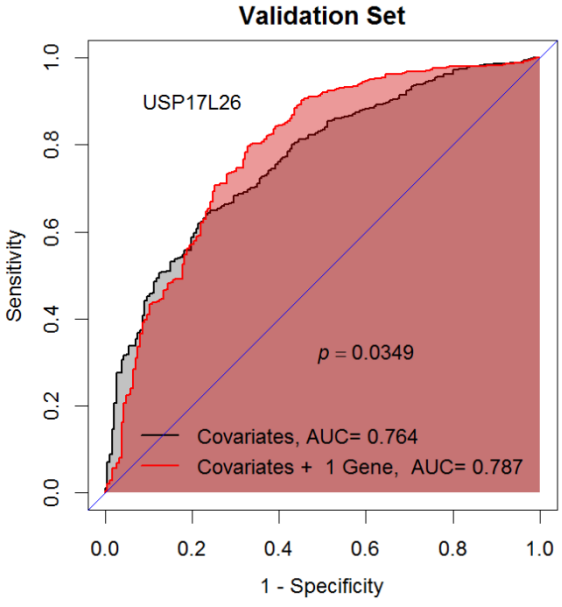
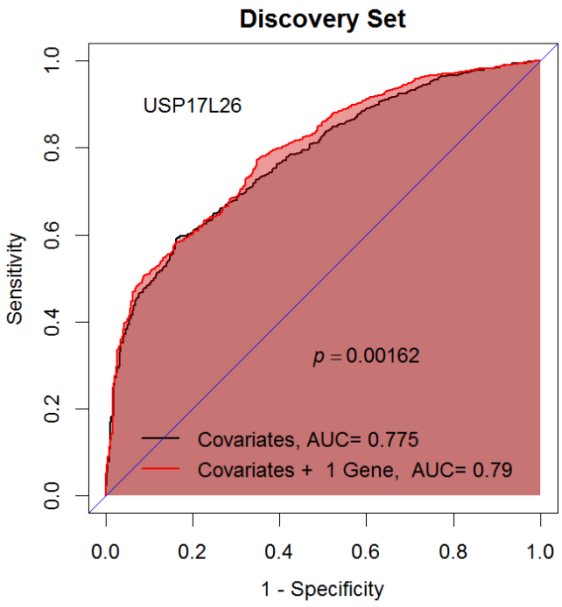
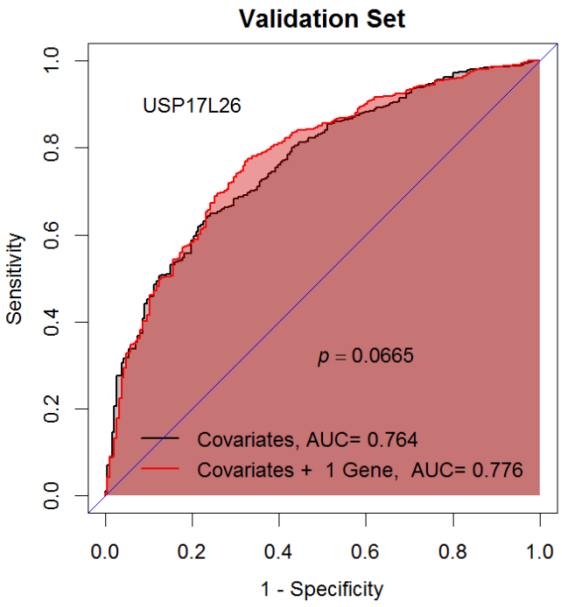
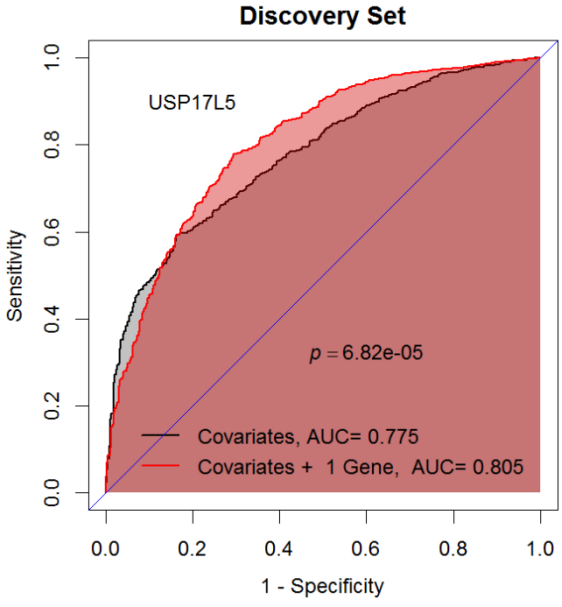
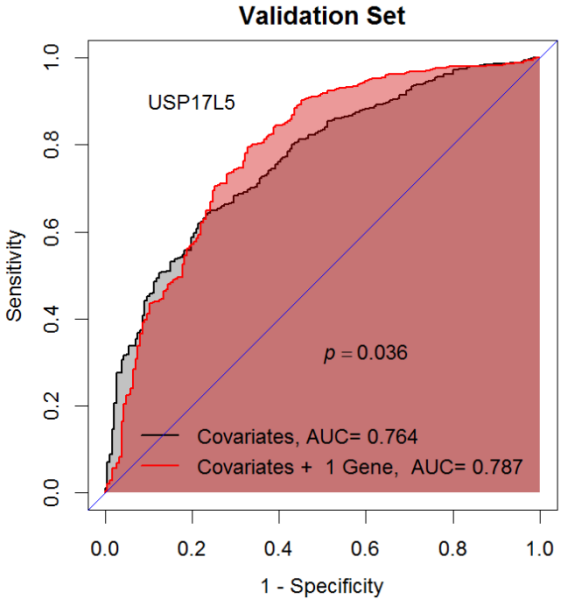
0.2
0.4
0.6
0.8
1.0

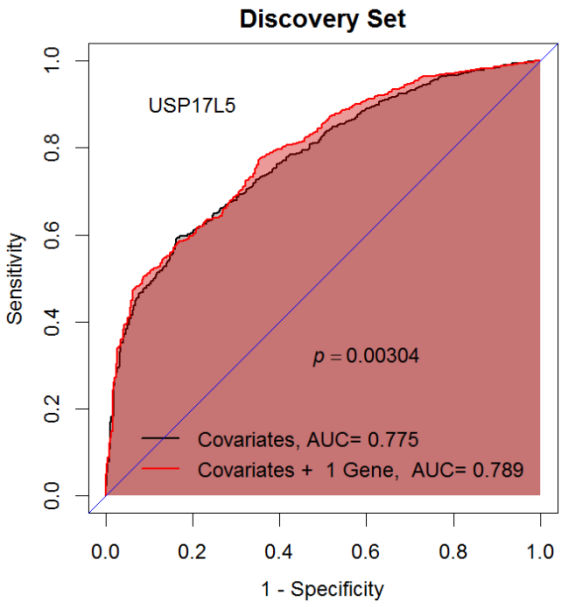

Validation Set
USP17L26
p = 0.0349
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

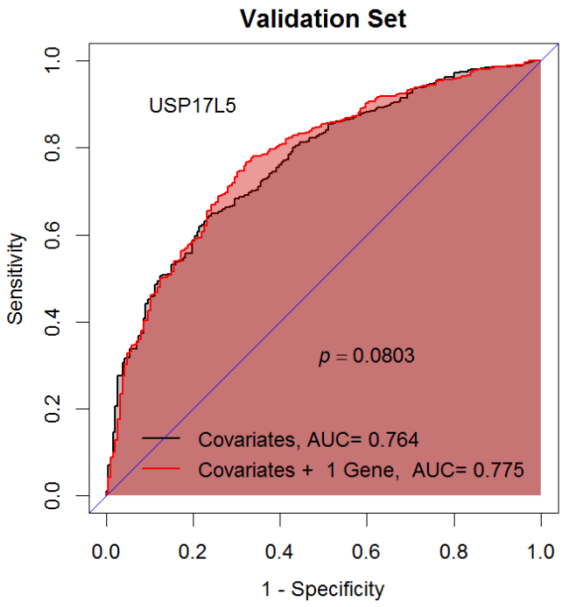

Discovery Set
USP17L26
p = 0.00162
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.79
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

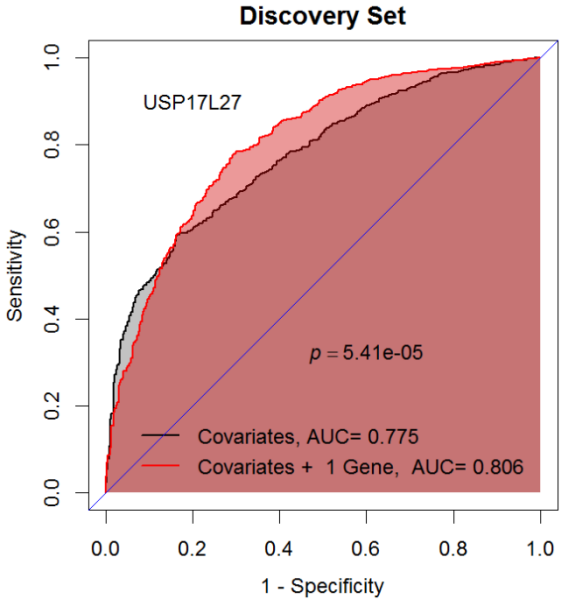

Validation Set
USP17L26
p = 0.0665
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.776
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

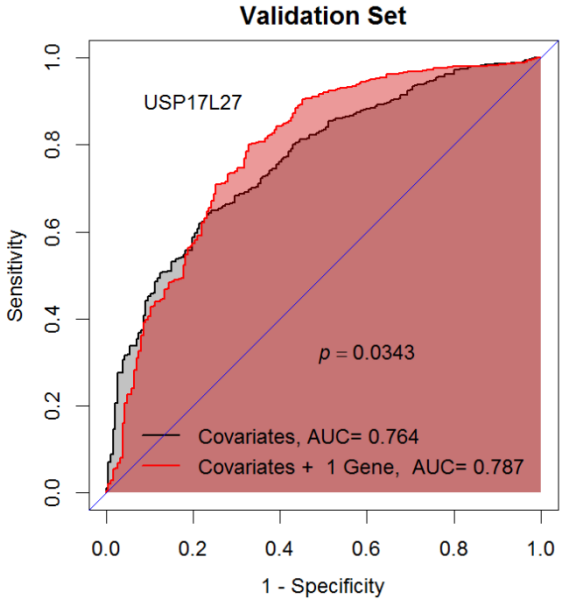

Discovery Set
USP17L5
p = 6.82e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

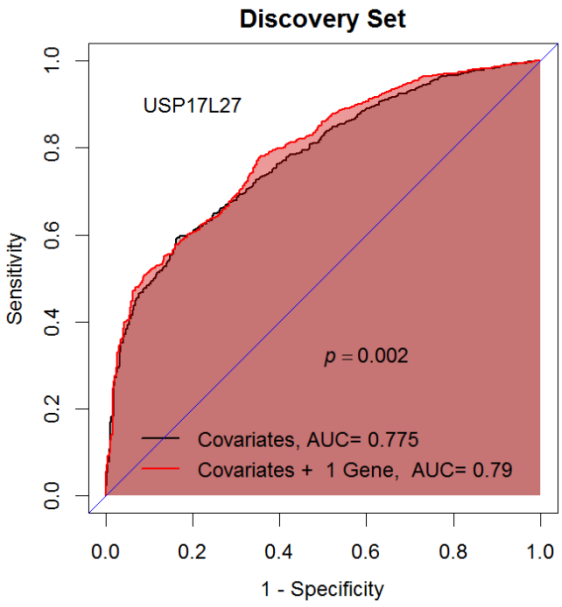

Validation Set
USP17L5
p = 0.036
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

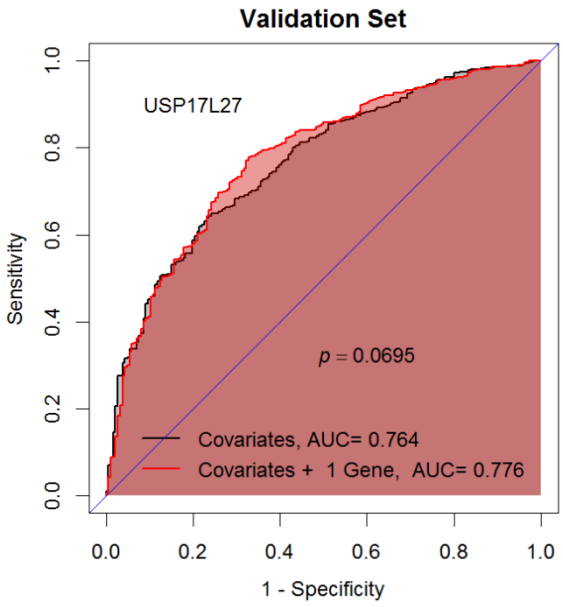

Discovery Set
USP17L5
Sensitivity
1 - Specificity
p = 0.00304
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.789

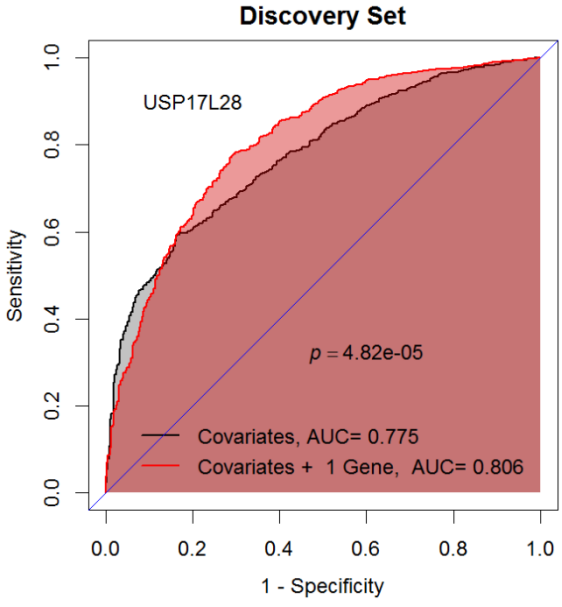

Validation Set
USP17L5
Sensitivity
1 - Specificity
p = 0.0803
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.775

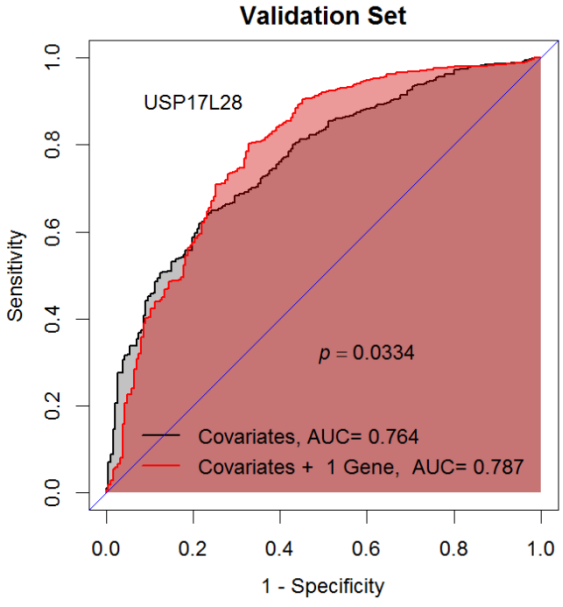

Discovery Set
USP17L27
Sensitivity
1 - Specificity
p = 5.41e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806

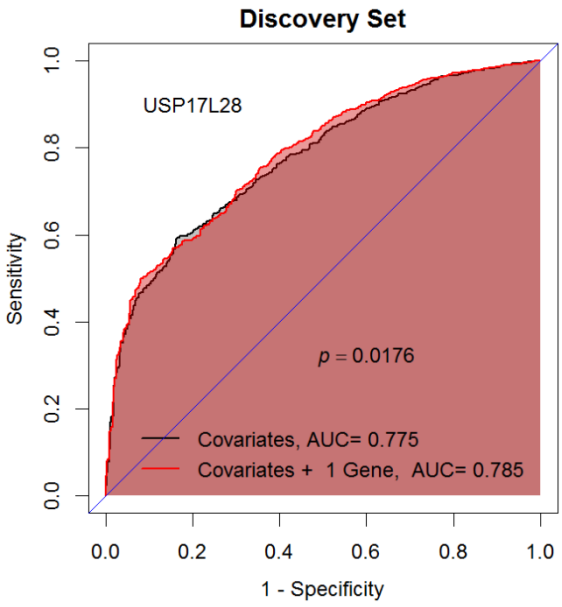

Validation Set
USP17L27
Sensitivity
1 - Specificity
p = 0.0343
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787

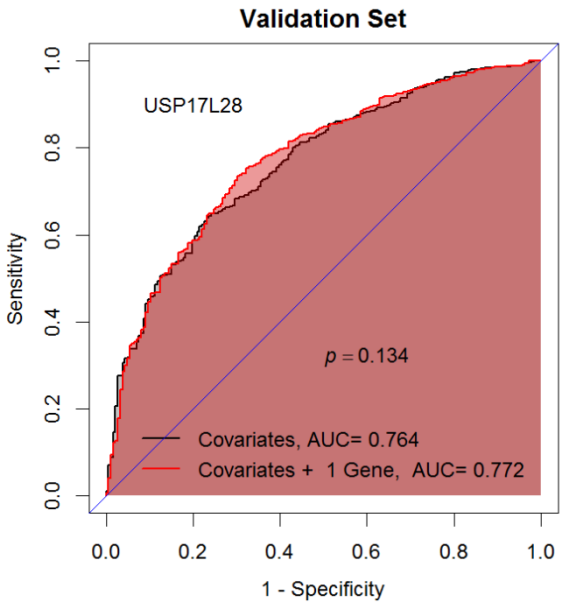

Discovery Set
USP17L27
p = 0.002
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.79
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

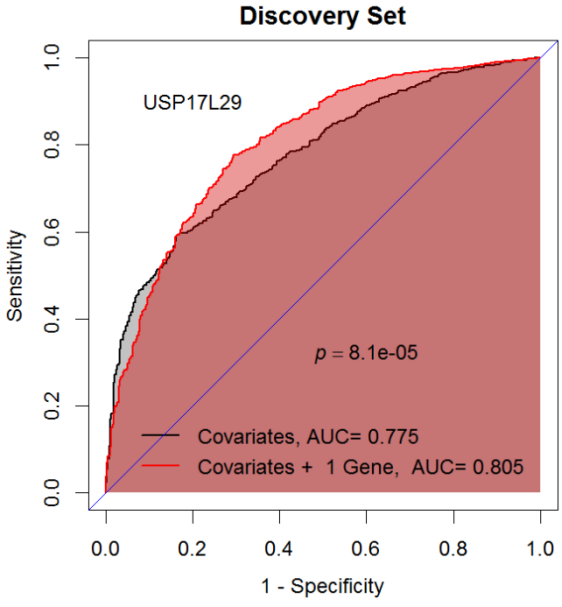

Validation Set
USP17L27
p = 0.0695
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.776
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

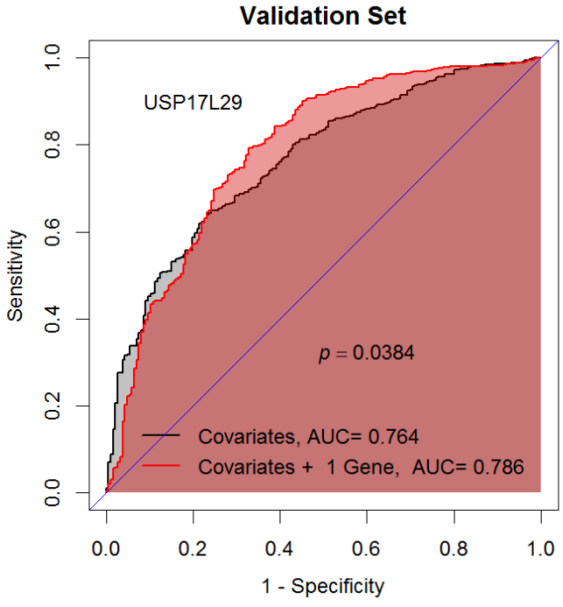

Discovery Set
USP17L28
p = 4.82e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.806
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

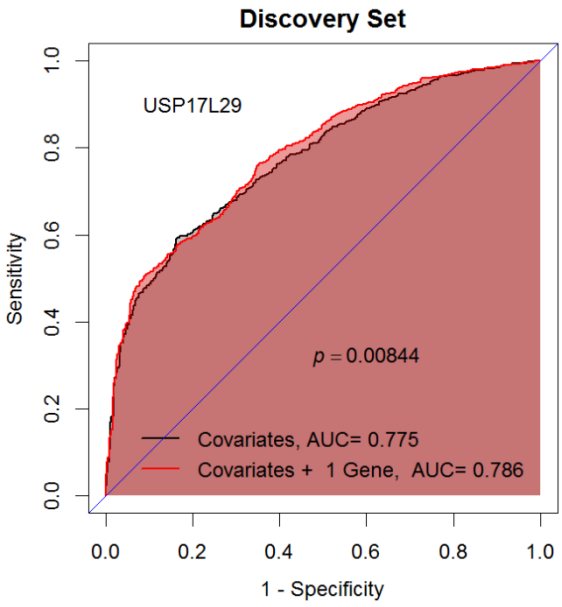

Validation Set
USP17L28
p = 0.0334
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.787
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

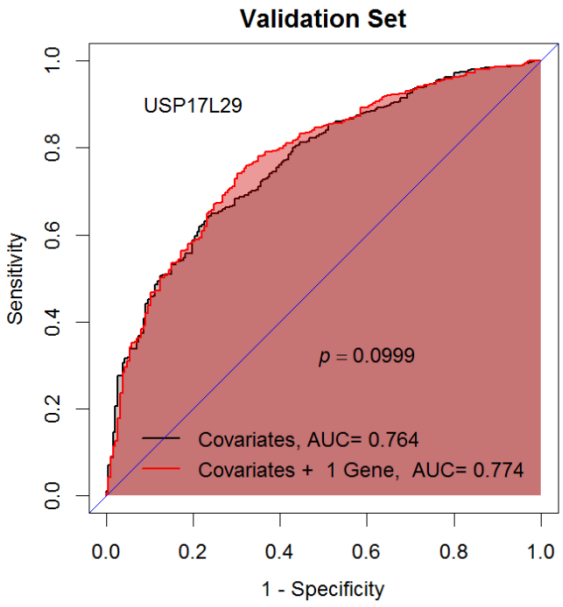

Discovery Set
USP17L28
p = 0.0176
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.785
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

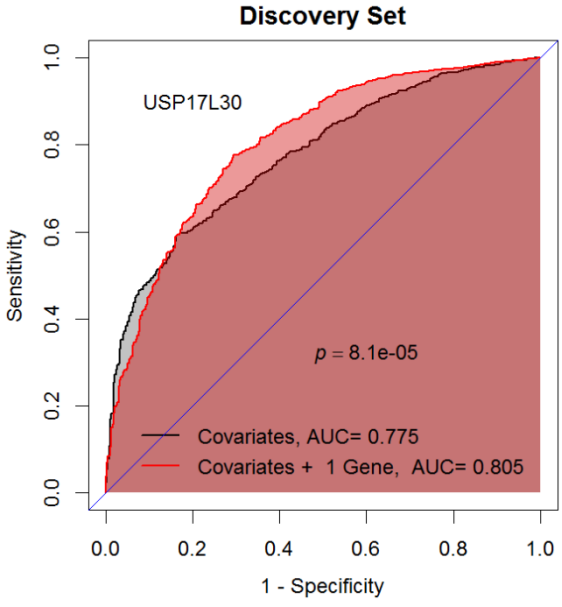

Validation Set
USP17L28
p = 0.134
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.772
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

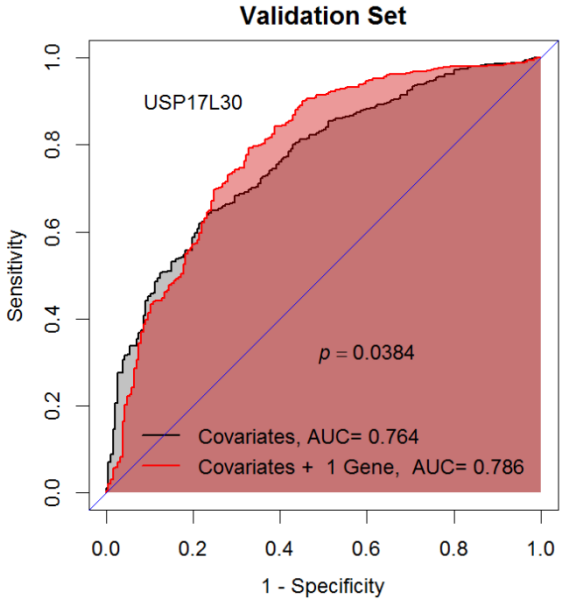

Discovery Set
USP17L29
p = 8.1e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

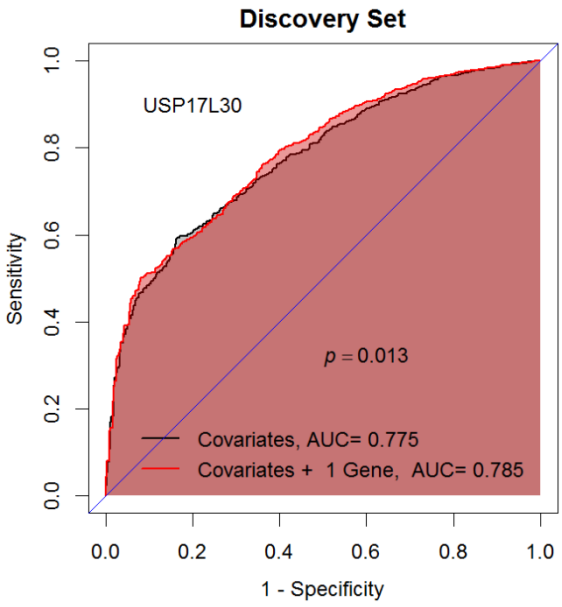

Validation Set
USP17L29
p = 0.0384
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.786
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

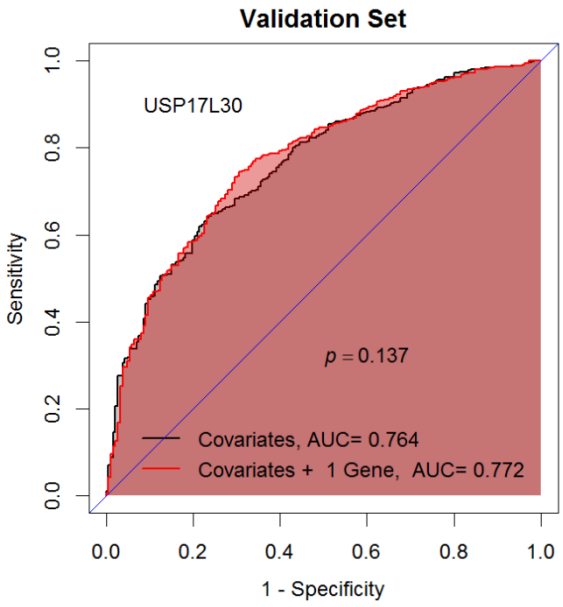

Discovery Set
USP17L29
p = 0.00844
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.786
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

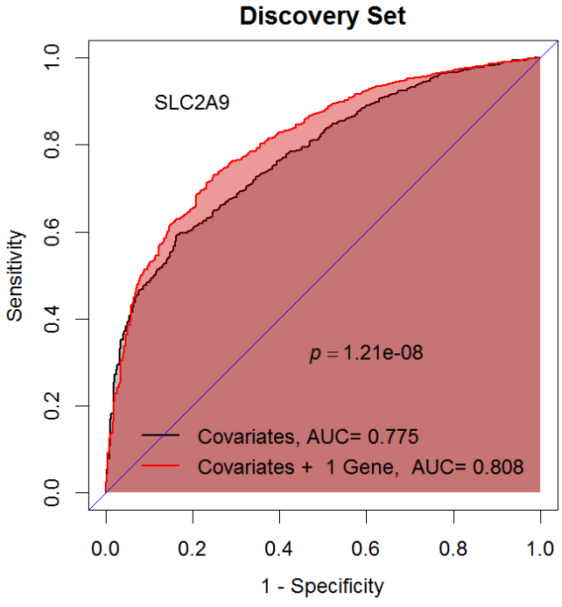

Validation Set
USP17L29
p = 0.0999
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.774
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

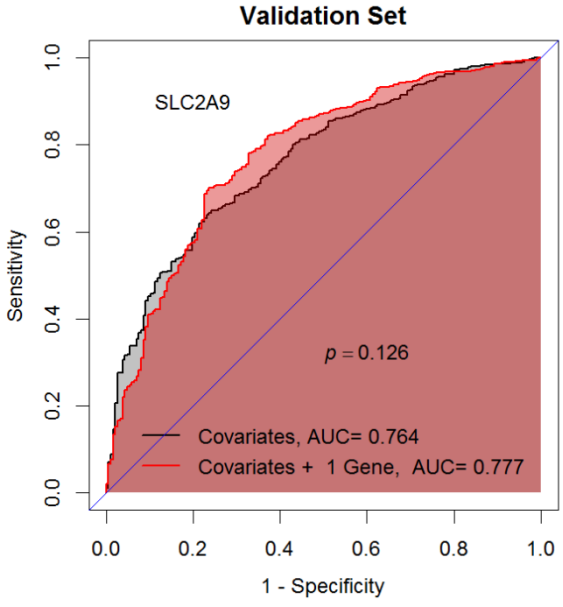

Discovery Set
USP17L30
p = 8.1e-05
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

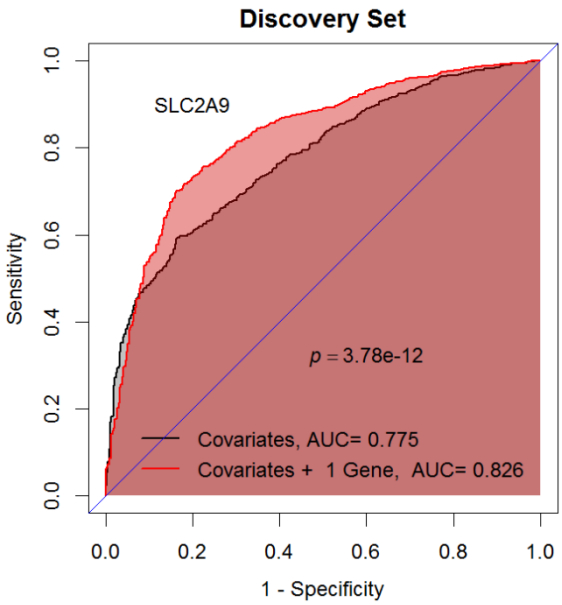

Validation Set
USP17L30
p = 0.0384
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.786
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

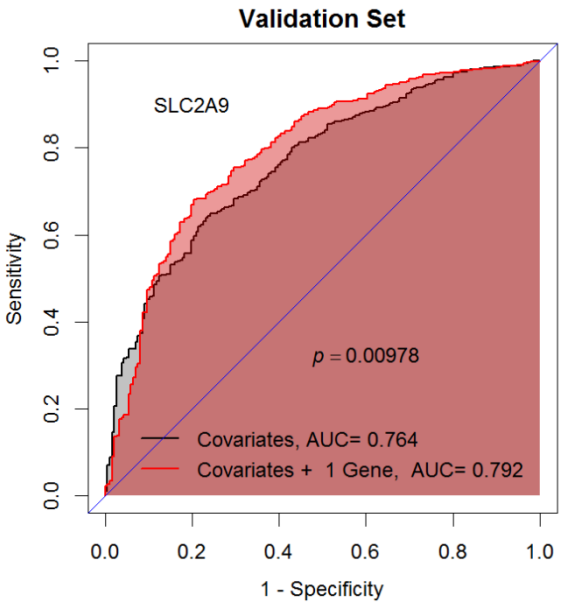

Discovery Set
USP17L30
p = 0.013
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.785
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

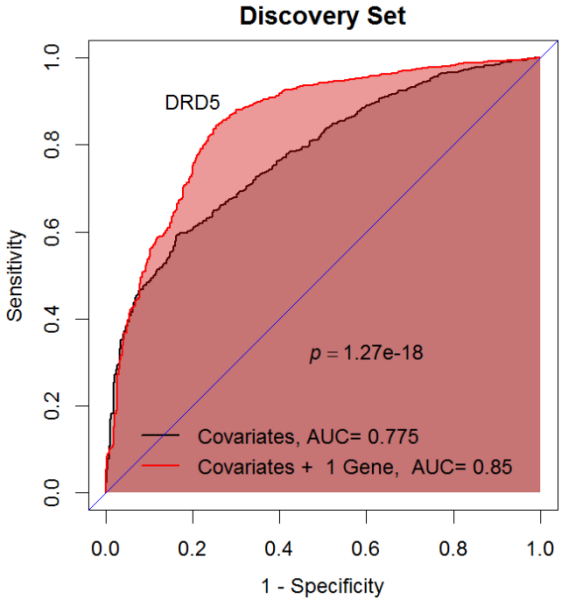

Validation Set
USP17L30
p = 0.137
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.772
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

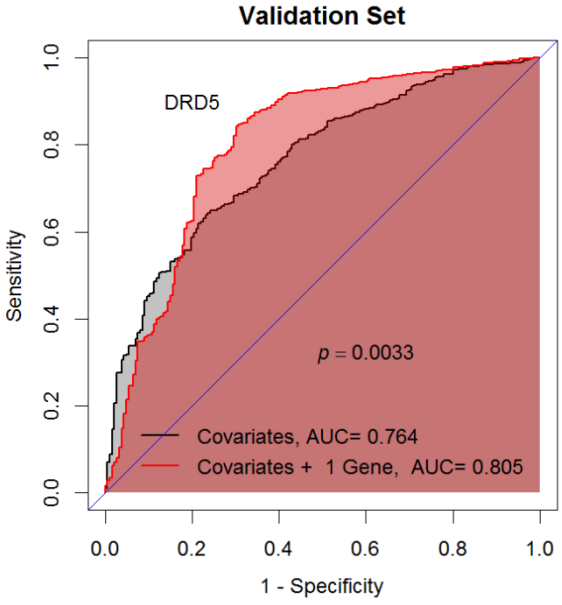

Discovery Set
SLC2A9
p = 1.21e-08
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.808
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

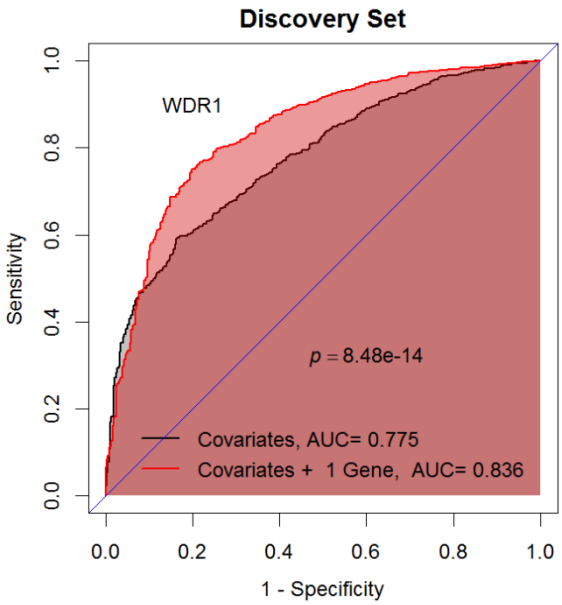

Validation Set
SLC2A9
p = 0.126
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.777
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

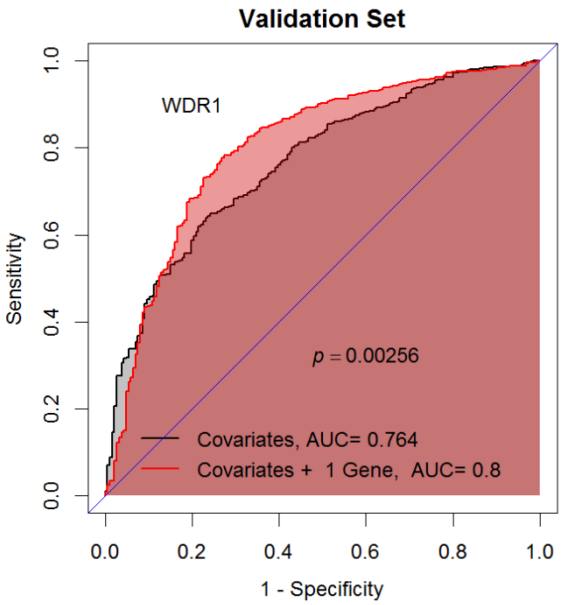

Discovery Set
SLC2A9
p = 3.78e-12
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.826
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

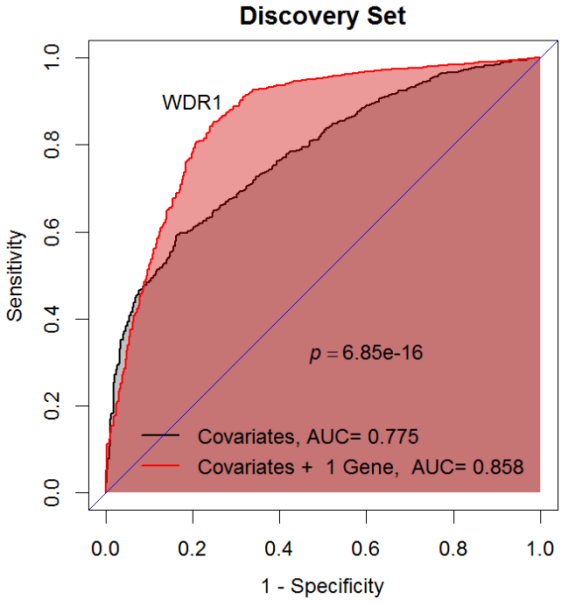

Validation Set
SLC2A9
p = 0.00978
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.792
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

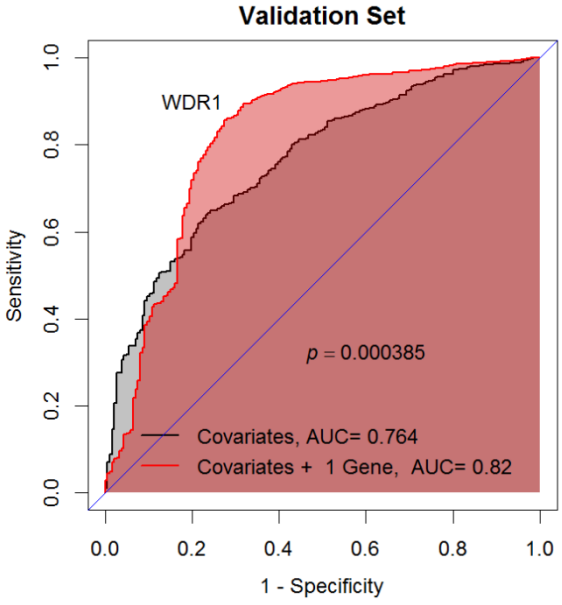

Discovery Set
DRD5
p = 1.27e-18
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.85
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

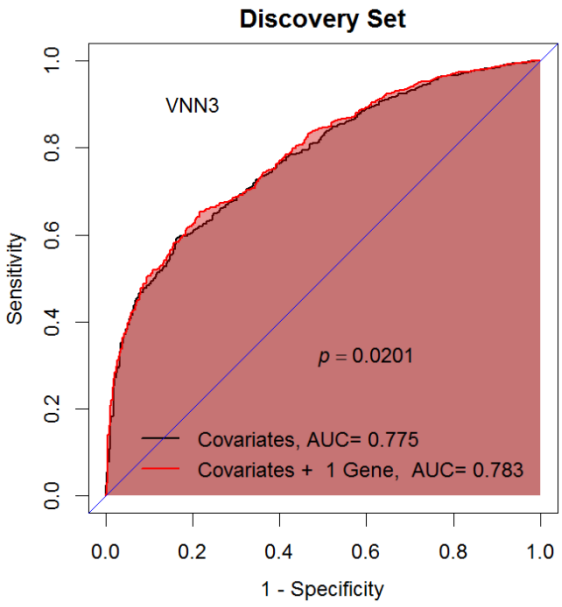

Validation Set
DRD5
p = 0.0033
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.805
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

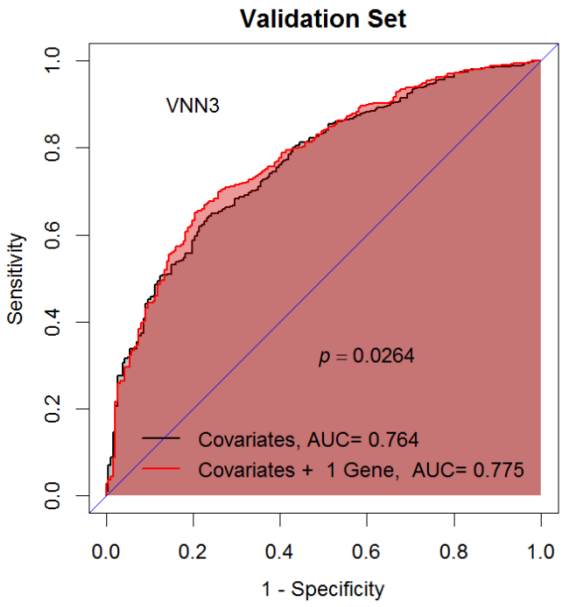

Discovery Set
WDR1
p = 8.48e-14
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.836
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Validation Set
WDR1
p = 0.00256
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.8
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
WDR1
p = 6.85e-16
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.858
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0

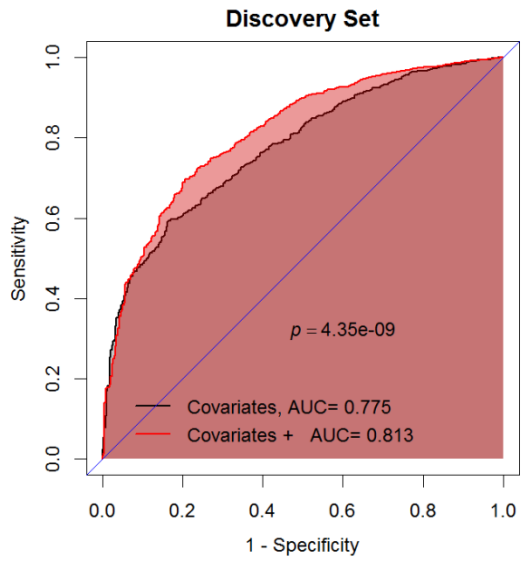

Validation Set
WDR1
p = 0.000385
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.82
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0


Discovery Set
VNN3
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0
p = 0.0201
Covariates, AUC= 0.775
Covariates + 1 Gene, AUC= 0.783

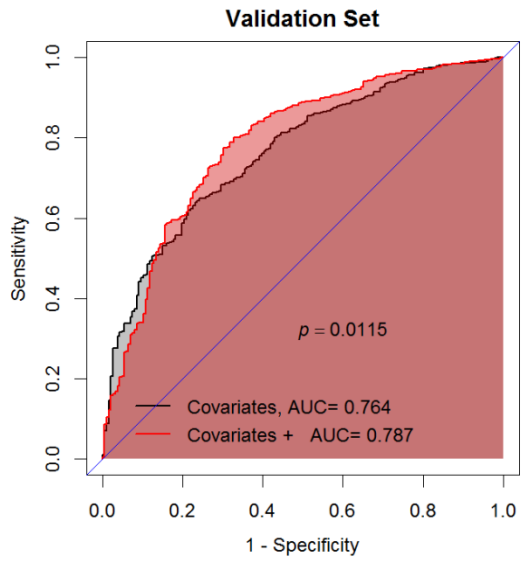

Validation Set
VNN3
Sensitivity
1 - Specificity
0.0
0.2
0.4
0.6
0.8
1.0
p = 0.0264
Covariates, AUC= 0.764
Covariates + 1 Gene, AUC= 0.775

sFigure 7. The ROC curve and its AUC of the model with only covariates (black curve) and that with covariates plus the estimated expression values of LIME1, SLC2A9, STMN3 and VNN3 (red curve) in Discovery Set (a) and Validation Set (b).

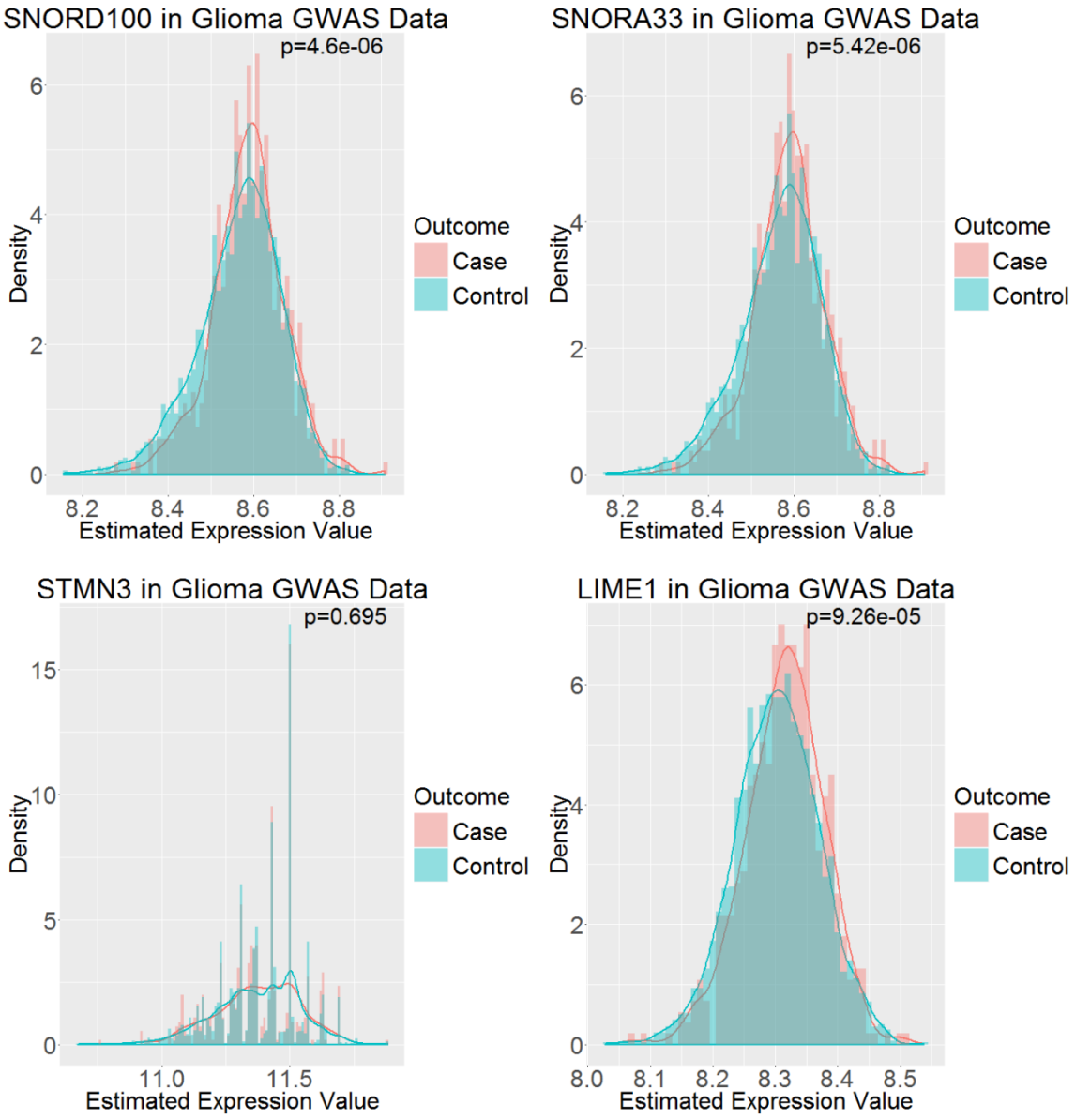
a

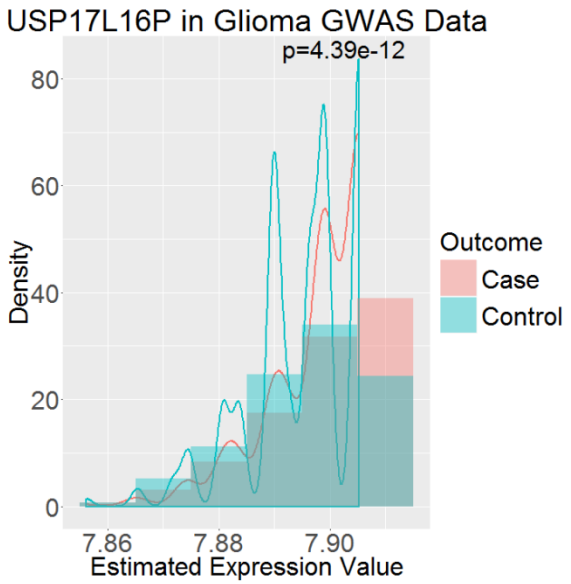


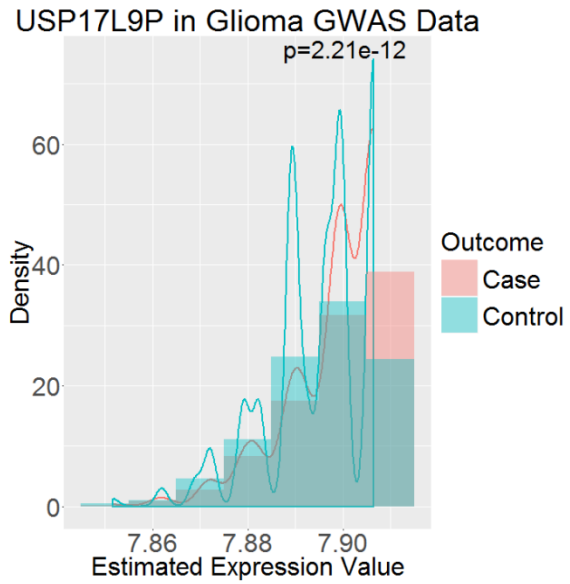

b

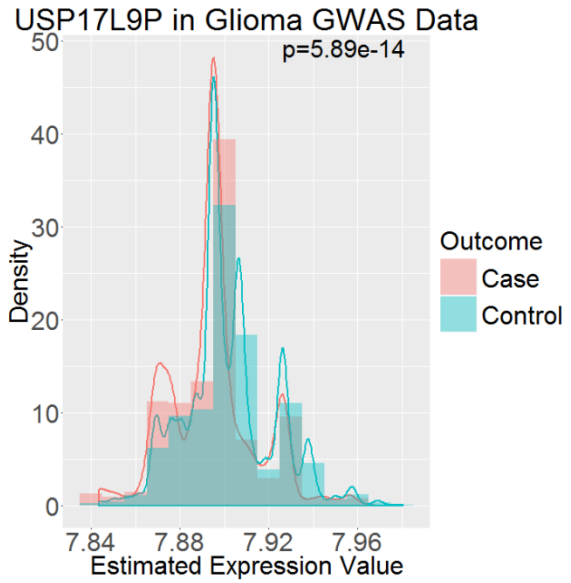


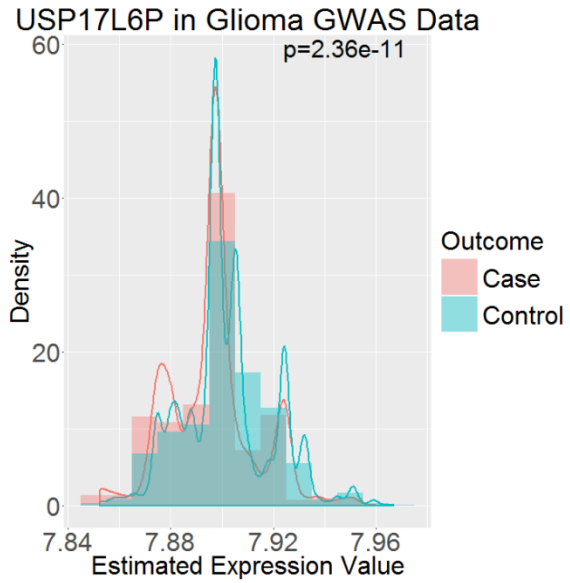
sFigure 8. The distribution of estimated expression values of the 55 validated transcripts (see sTable 3) between cases and controls.

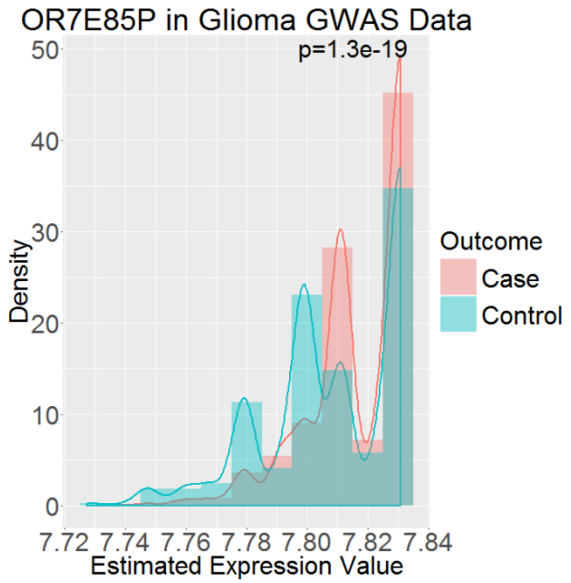


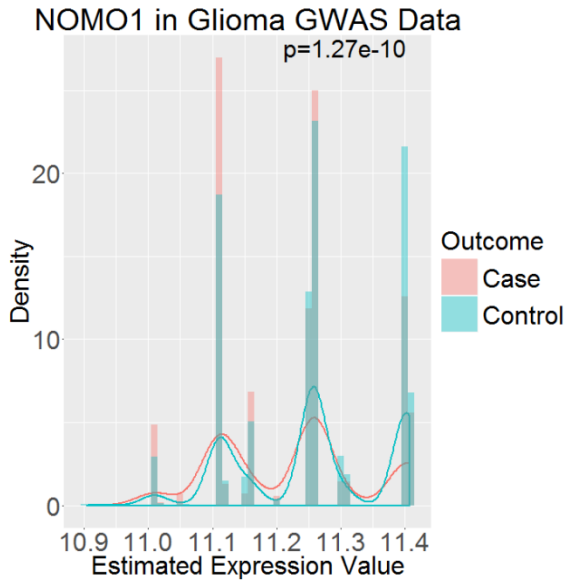

USP17L16P in Glioma GWAS Data
p=4.39e-12
Density
Estimated Expression Value
Outcome
Case
Control

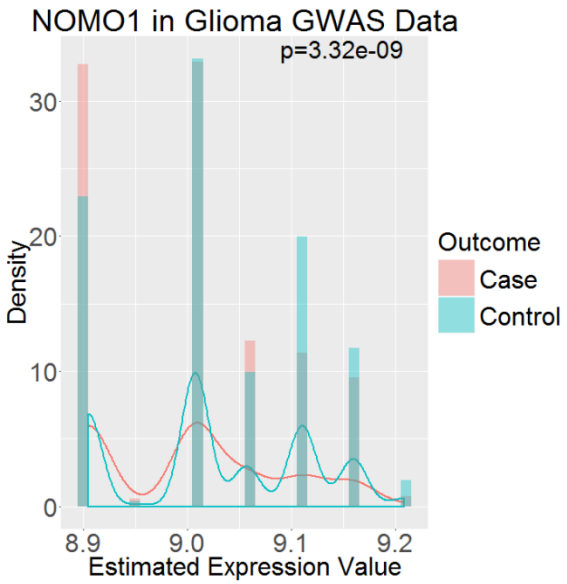

USP17L9P in Glioma GWAS Data
p=2.21e-12
Density
Estimated Expression Value
Outcome
Case
Control

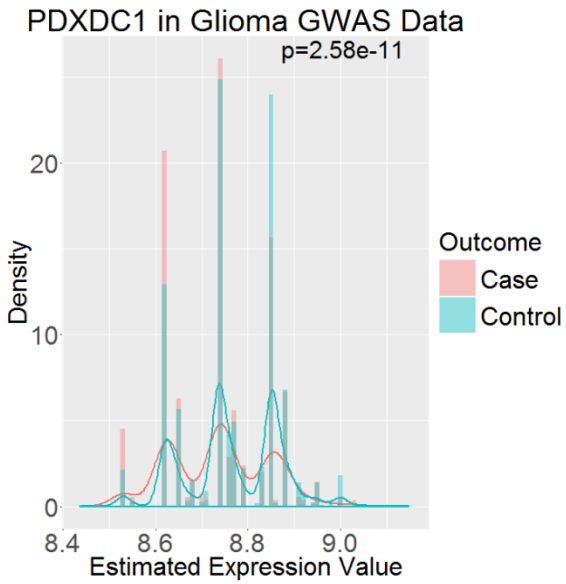

USP17L9P in Glioma GWAS Data
p=5.89e-14
Density
Estimated Expression Value
Outcome
Case
Control

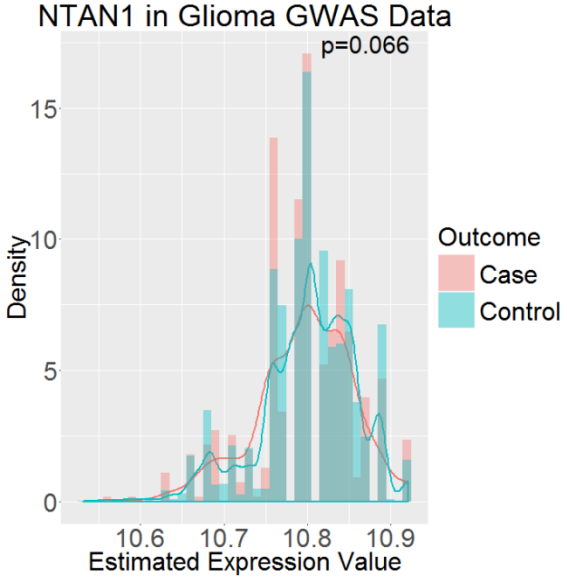

USP17L6P in Glioma GWAS Data
p=2.36e-11
Density
Estimated Expression Value
Outcome
Case
Control

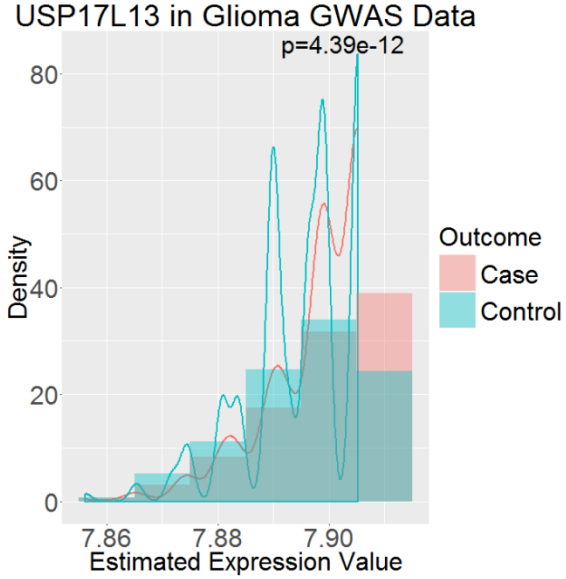

OR7E85P in Glioma GWAS Data
p=1.3e-19
Density
Estimated Expression Value
Outcome
Case
Control

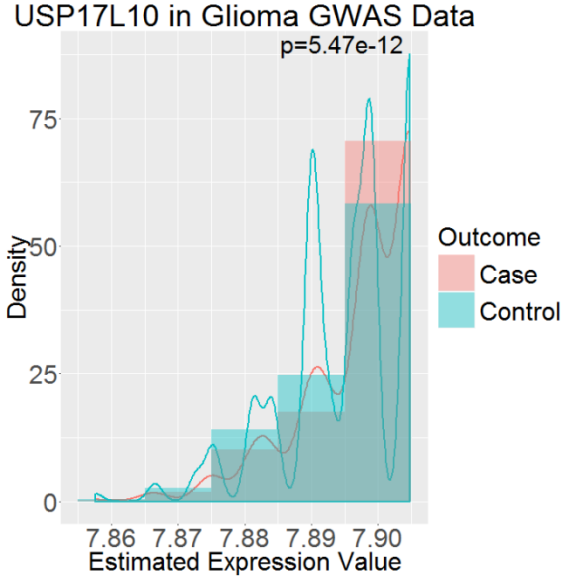

NOMO1 in Glioma GWAS Data
p=1.27e-10
Density
Estimated Expression Value
Outcome
Case
Control

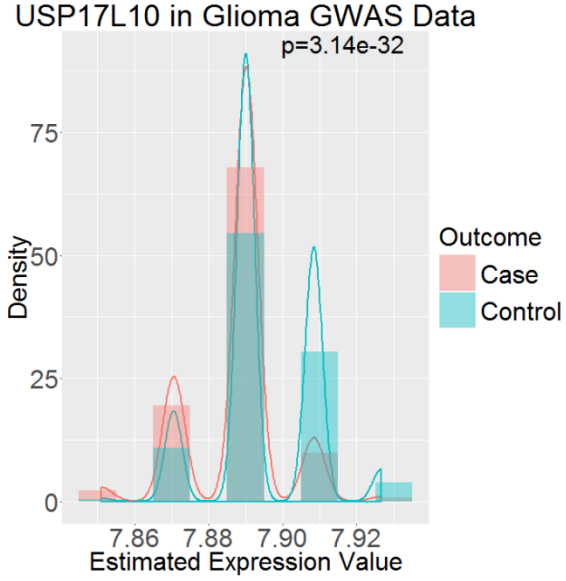

NOMO1 in Glioma GWAS Data
p=3.32e-09
Density
Estimated Expression Value
Outcome
Case
Control

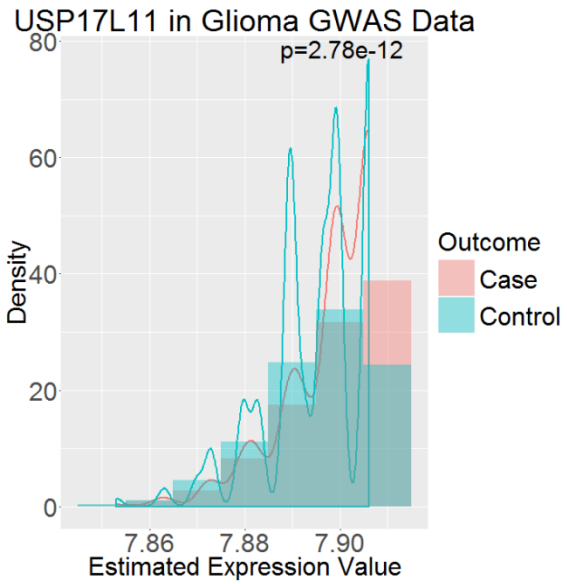

PDXDC1 in Glioma GWAS Data
p=2.58e-11
Density
Estimated Expression Value
Outcome
Case
Control

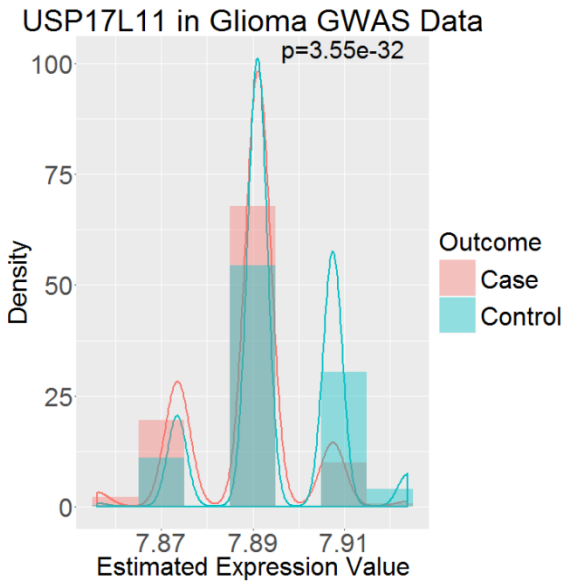

NTAN1 in Glioma GWAS Data
p=0.066
Density
Estimated Expression Value
Outcome
Case
Control

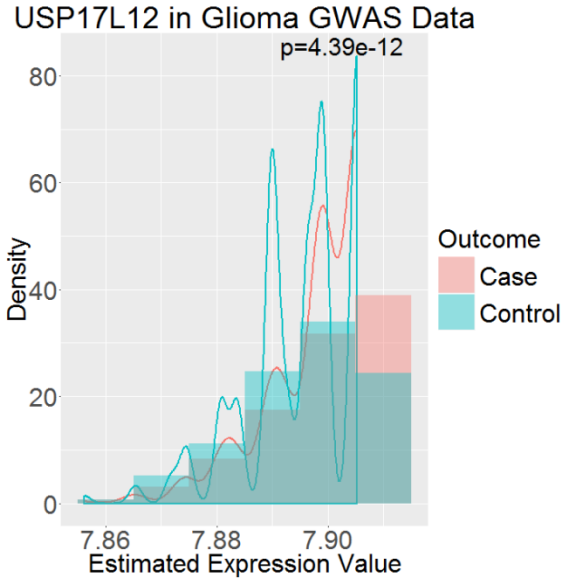

USP17L13 in Glioma GWAS Data
p=4.39e-12
Density
Estimated Expression Value
Outcome
Case
Control

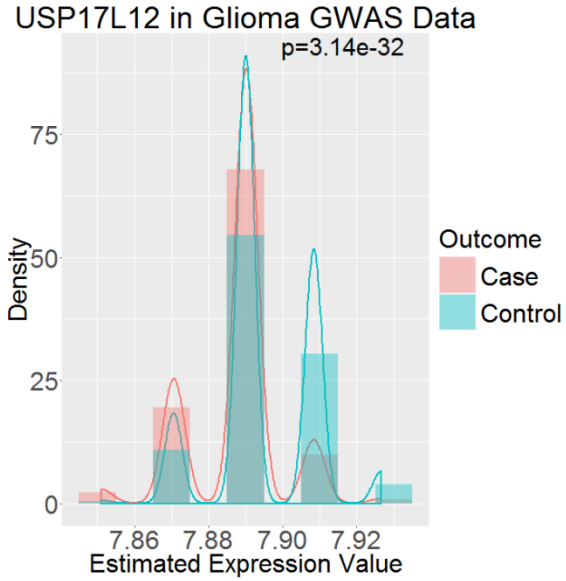

USP17L10 in Glioma GWAS Data
p=5.47e-12
Density
Estimated Expression Value
Outcome
Case
Control

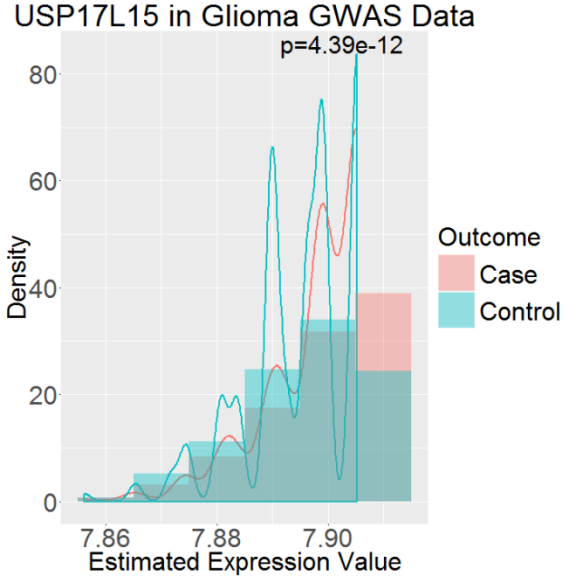

USP17L10 in Glioma GWAS Data
p=3.14e-32
Density
Estimated Expression Value
Outcome
Case
Control

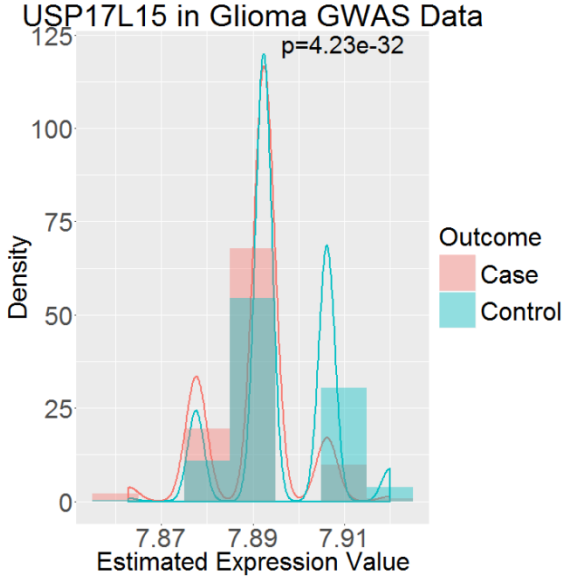

USP17L11 in Glioma GWAS Data
p=2.78e-12
Density
Estimated Expression Value
Outcome
Case
Control

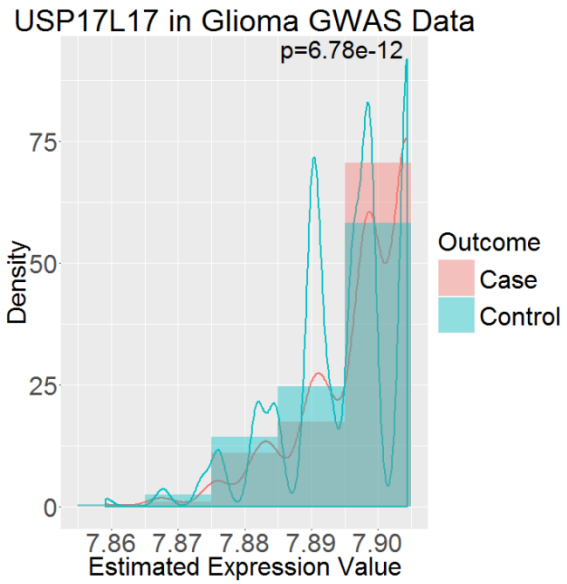

USP17L11 in Glioma GWAS Data
p=3.55e-32
Density
Estimated Expression Value
Outcome
Case
Control

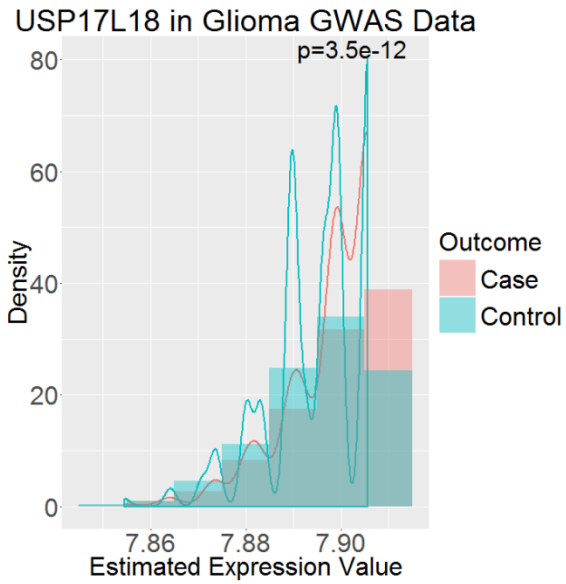

USP17L12 in Glioma GWAS Data
p=4.39e-12
Density
Estimated Expression Value
Outcome
Case
Control

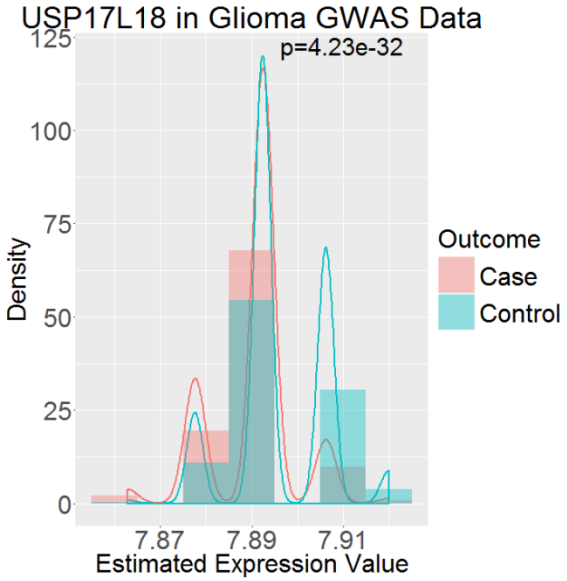

USP17L12 in Glioma GWAS Data
p=3.14e-32
Density
Estimated Expression Value
Outcome
Case
Control

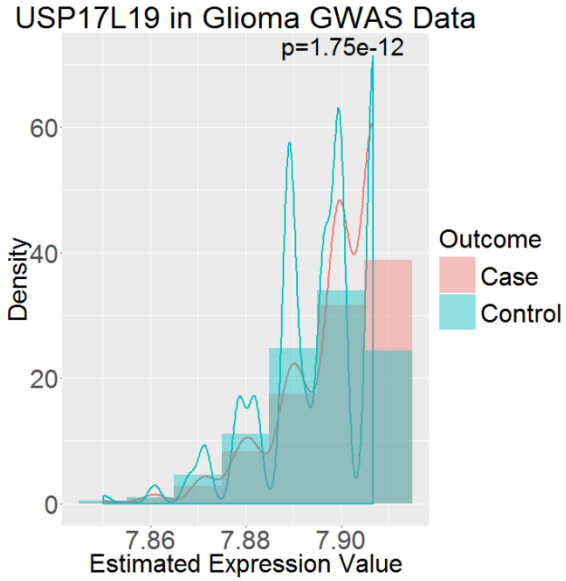

USP17L15 in Glioma GWAS Data
p=4.39e-12
Density
Estimated Expression Value
Outcome
Case
Control

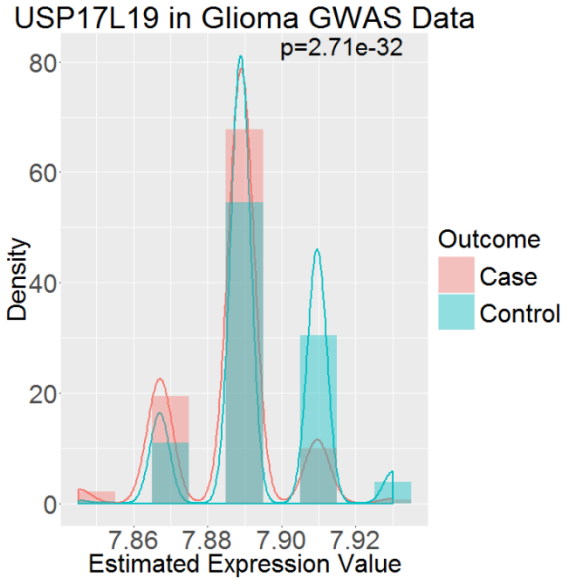

USP17L15 in Glioma GWAS Data
p=4.23e-32
Density
Estimated Expression Value
Outcome
Case
Control

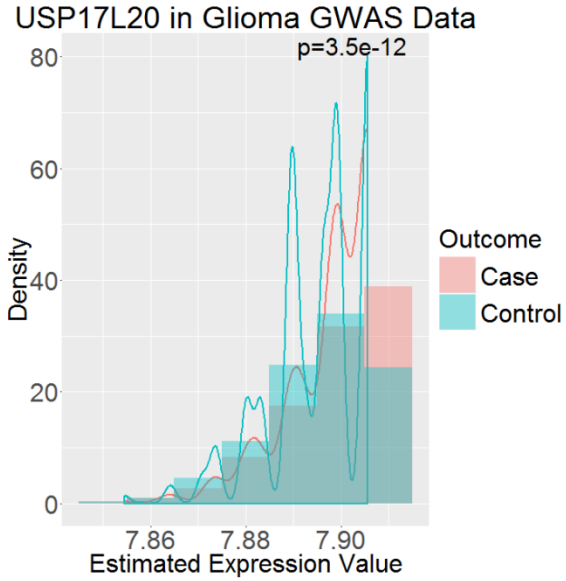

USP17L17 in Glioma GWAS Data
p=6.78e-12
Density
Estimated Expression Value
Outcome
Case
Control

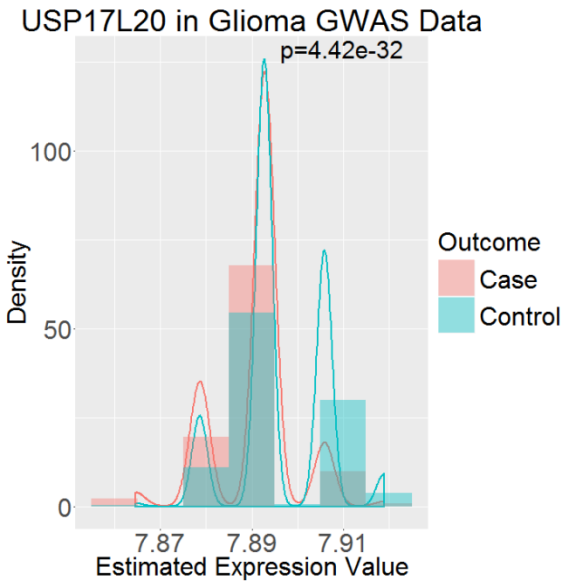

USP17L18 in Glioma GWAS Data
p=3.5e-12
Density
Estimated Expression Value
Outcome
Case
Control

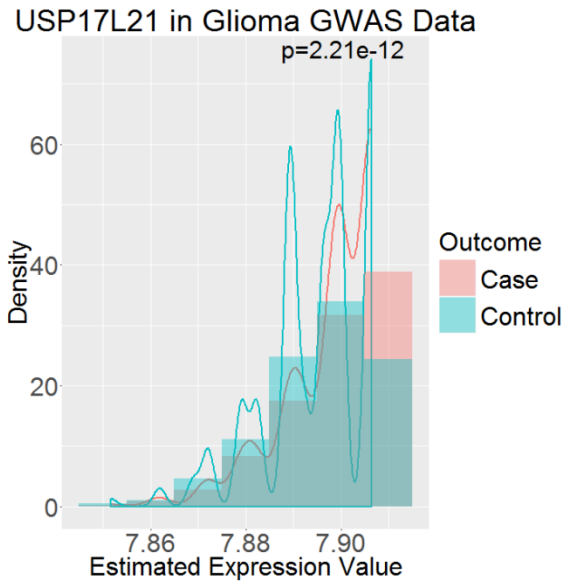

USP17L18 in Glioma GWAS Data
p=4.23e-32
Density
Estimated Expression Value
Outcome
Case
Control

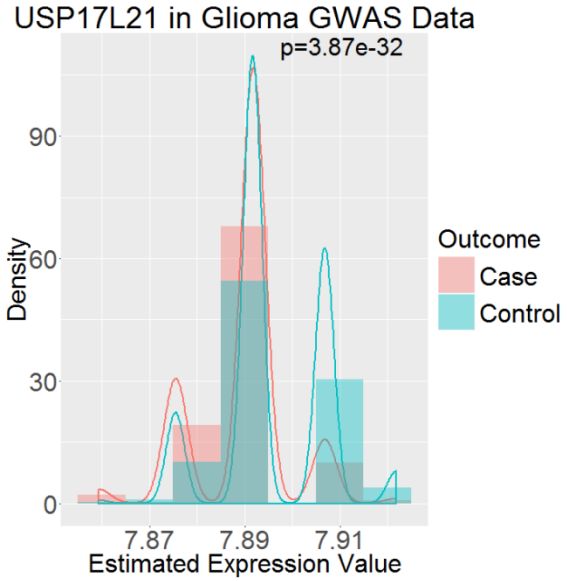

USP17L19 in Glioma GWAS Data
p=1.75e-12
Density
Estimated Expression Value
Outcome
Case
Control

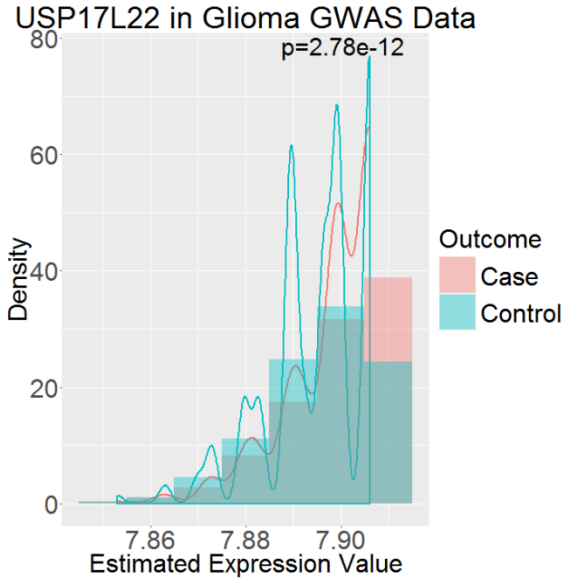

USP17L19 in Glioma GWAS Data
p=2.71e-32
Density
Estimated Expression Value
Outcome
Case
Control

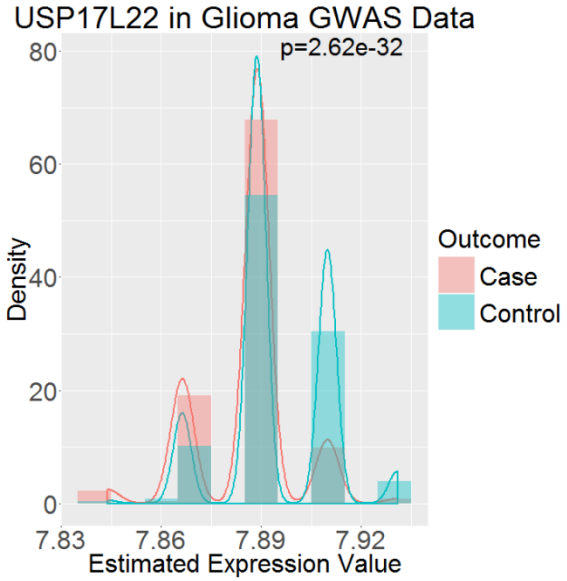

USP17L20 in Glioma GWAS Data
p=3.5e-12
Density
Estimated Expression Value
Outcome
Case
Control

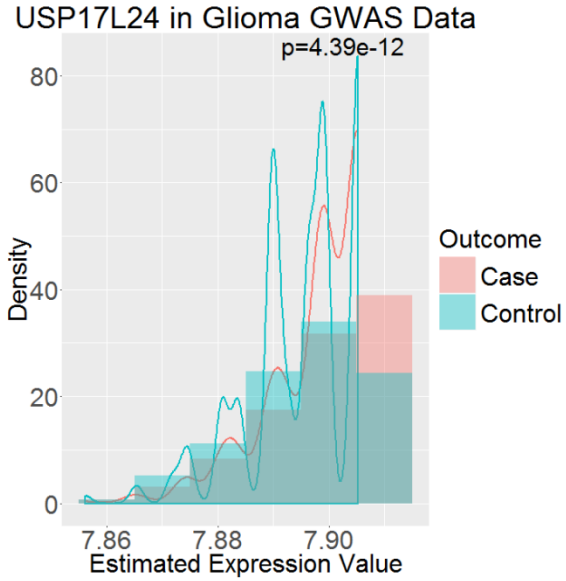

USP17L20 in Glioma GWAS Data
p=4.42e-32
Density
100
50
0
7.87
7.89
7.91
Estimated Expression Value
Outcome
Case
Control

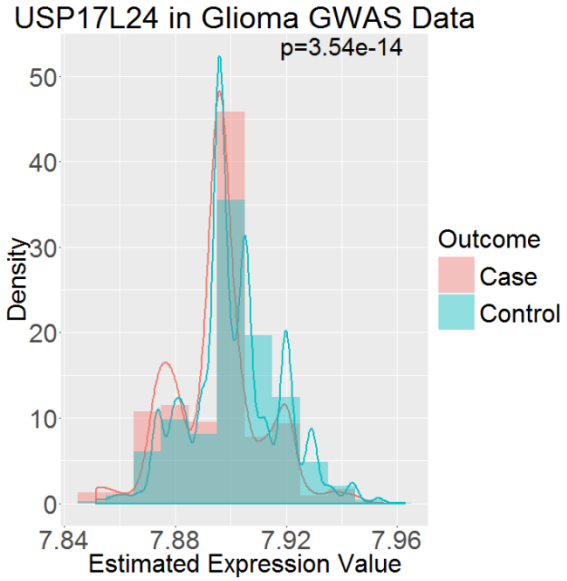

USP17L21 in Glioma GWAS Data
p=2.21e-12
Density
60
40
20
0
7.86
7.88
7.90
Estimated Expression Value
Outcome
Case
Control

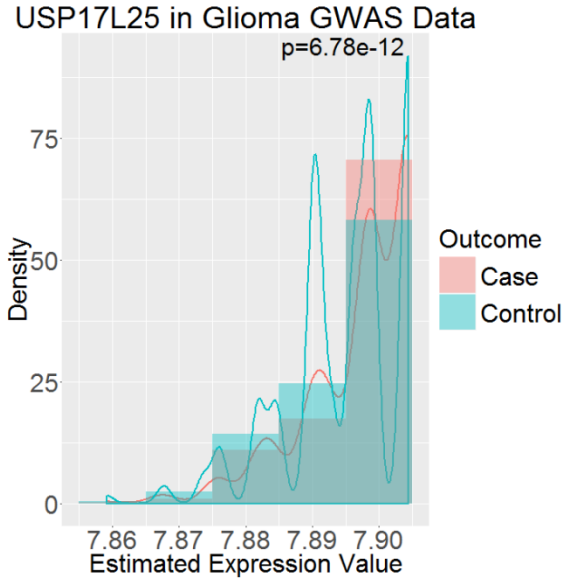

USP17L21 in Glioma GWAS Data
p=3.87e-32
Density
90
60
30
0
7.87
7.89
7.91
Estimated Expression Value
Outcome
Case
Control

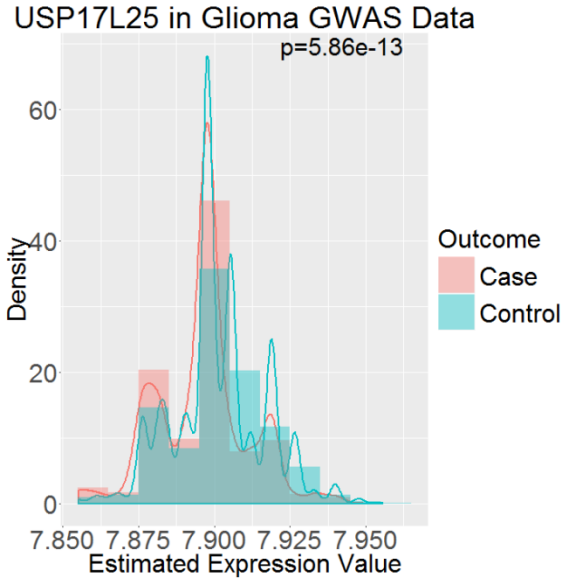

USP17L22 in Glioma GWAS Data
p=2.78e-12
Density
80
60
40
20
0
7.86
7.88
7.90
Estimated Expression Value
Outcome
Case
Control

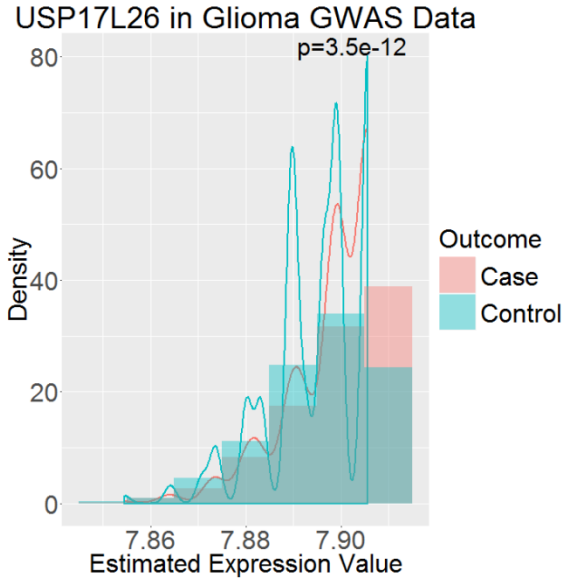

USP17L22 in Glioma GWAS Data
p=2.62e-32
Density
80
60
40
20
0
7.83
7.86
7.89
7.92
Estimated Expression Value
Outcome
Case
Control

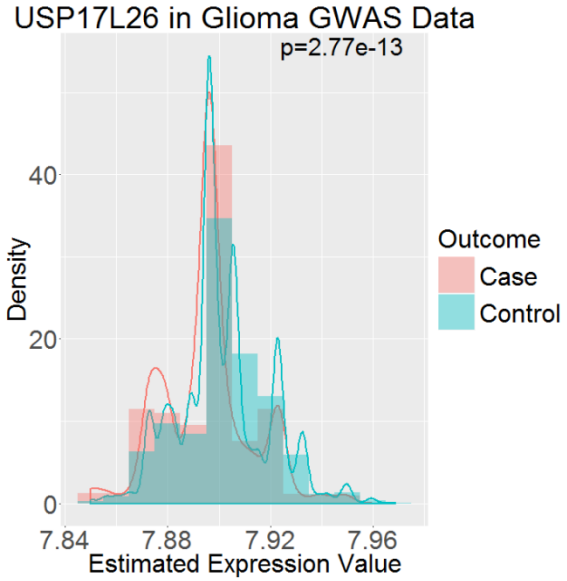

USP17L24 in Glioma GWAS Data
p=4.39e-12
Density
80
60
40
20
0
7.86
7.88
7.90
Estimated Expression Value
Outcome
Case
Control

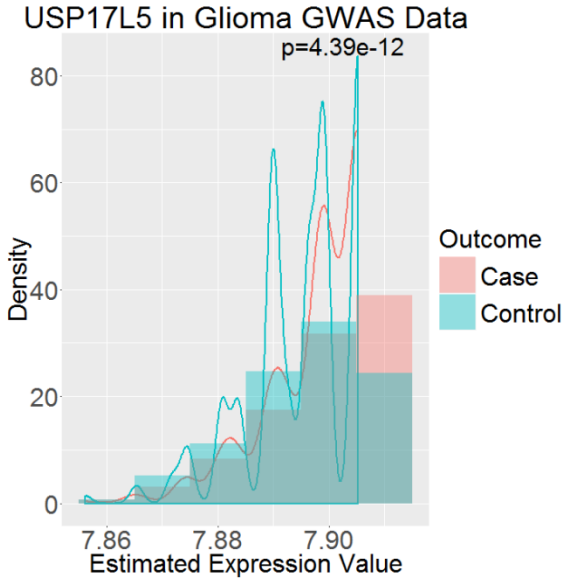

USP17L24 in Glioma GWAS Data
p=3.54e-14
Density
Estimated Expression Value
Outcome
Case
Control

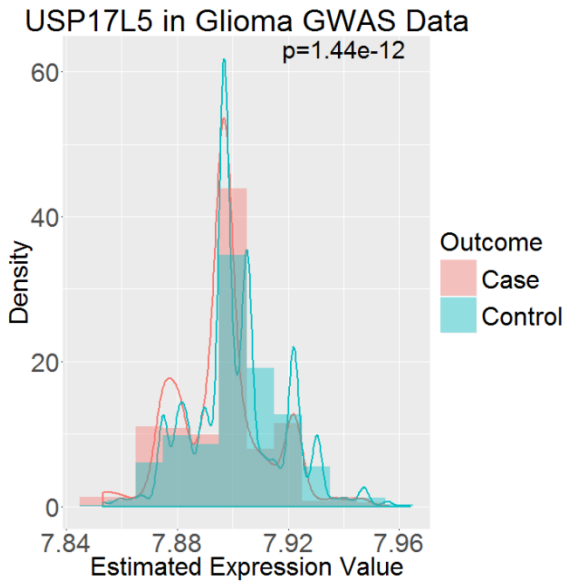

USP17L25 in Glioma GWAS Data
p=6.78e-12
Density
Estimated Expression Value
Outcome
Case
Control

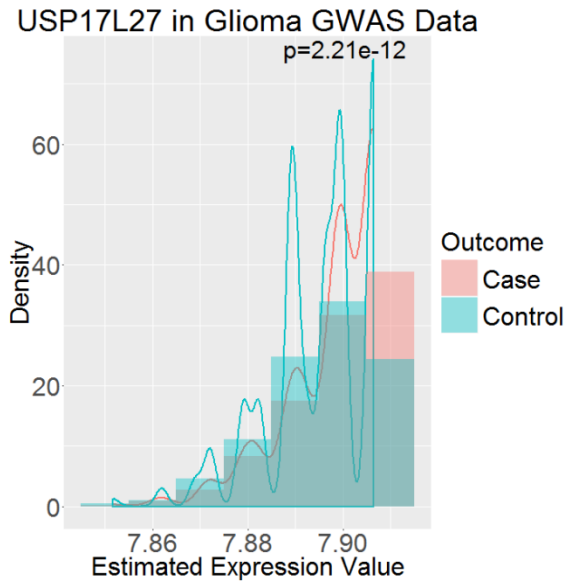

USP17L25 in Glioma GWAS Data
p=5.86e-13
Density
Estimated Expression Value
Outcome
Case
Control

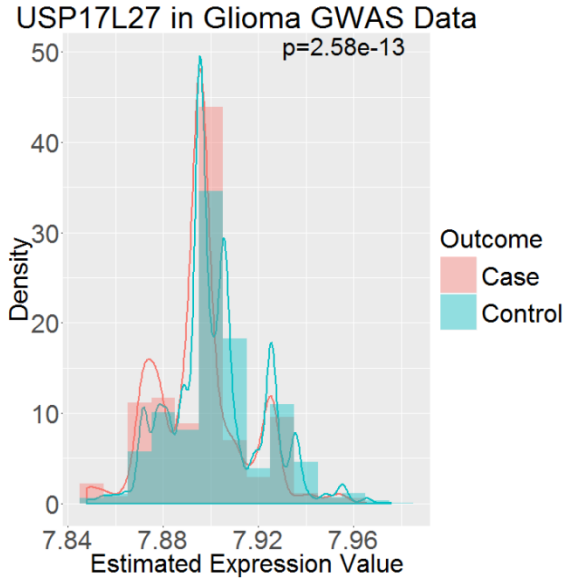

USP17L26 in Glioma GWAS Data
p=3.5e-12
Density
Estimated Expression Value
Outcome
Case
Control

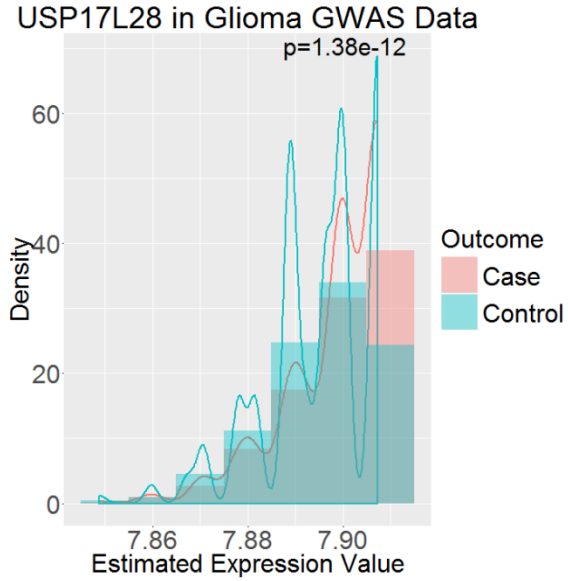

USP17L26 in Glioma GWAS Data
p=2.77e-13
Density
Estimated Expression Value
Outcome
Case
Control

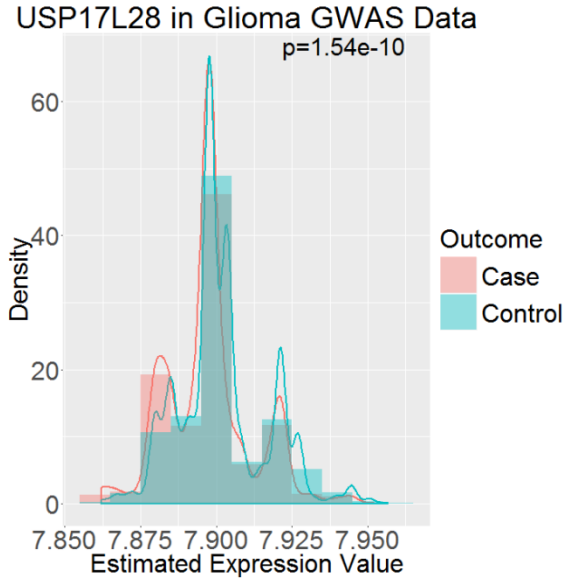

USP17L5 in Glioma GWAS Data
p=4.39e-12
Density
Estimated Expression Value
Outcome
Case
Control


USP17L5 in Glioma GWAS Data
p=1.44e-12
Density
Estimated Expression Value
Outcome
Case
Control


USP17L27 in Glioma GWAS Data
p=2.21e-12
Density
Estimated Expression Value
Outcome
Case
Control


USP17L27 in Glioma GWAS Data
p=2.58e-13
Density
Estimated Expression Value
Outcome
Case
Control


USP17L28 in Glioma GWAS Data
p=1.38e-12
Density
Estimated Expression Value
Outcome
Case
Control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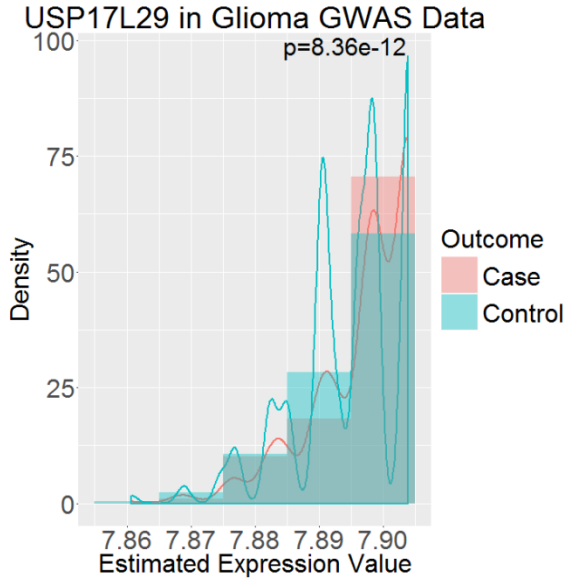
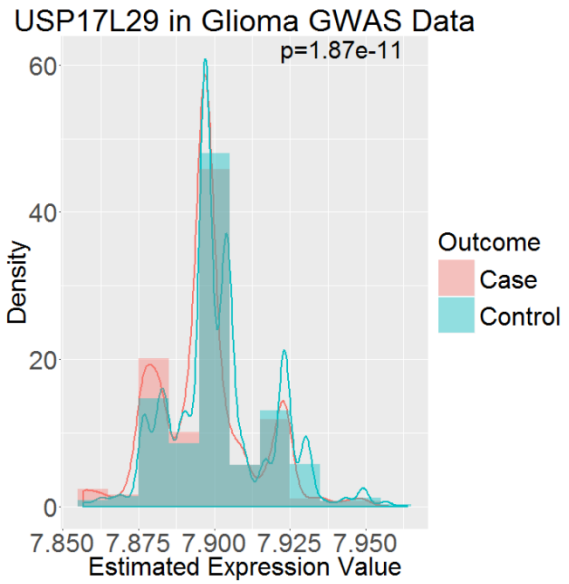
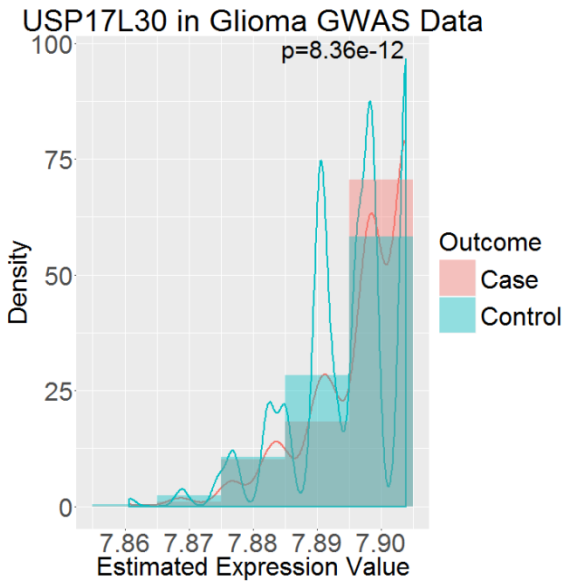
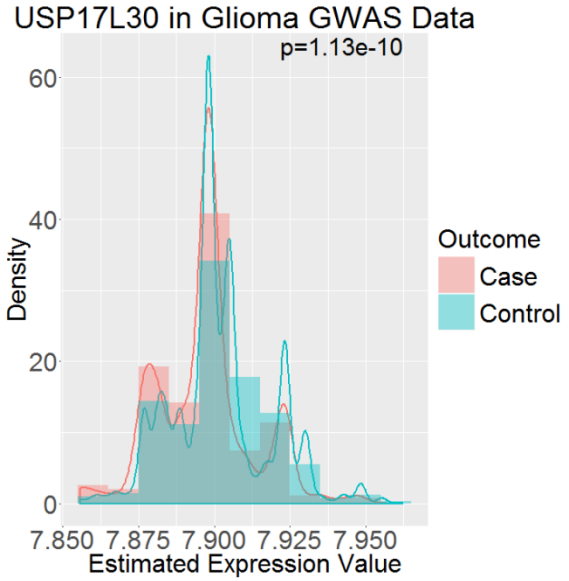
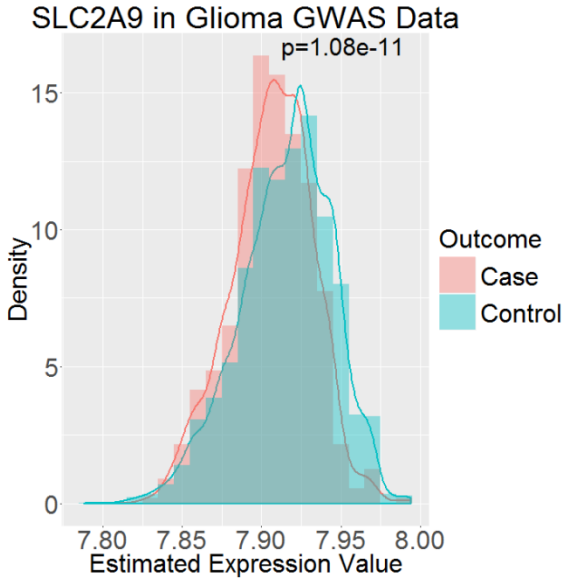
Density
Estimated Expression Value
Outcome
Case
Control

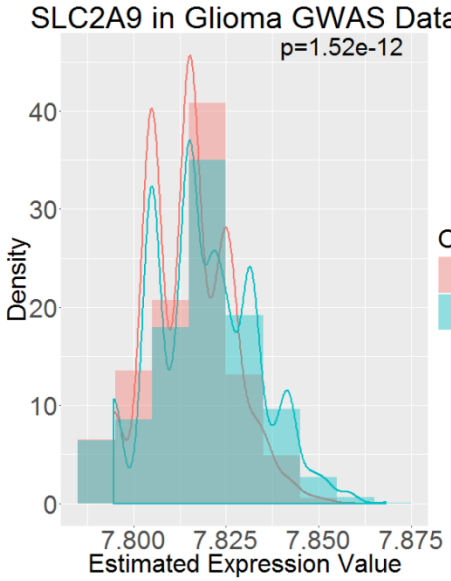

USP17L29 in Glioma GWAS Data
p=8.36e-12
Density
Estimated Expression Value
Outcome
Case
Control


USP17L29 in Glioma GWAS Data
p=1.87e-11
Density
Estimated Expression Value
Outcome
Case
Control


USP17L30 in Glioma GWAS Data
p=8.36e-12
Density
Estimated Expression Value
Outcome
Case
Control


USP17L30 in Glioma GWAS Data
p=1.13e-10
Density
Estimated Expression Value
Outcome
Case
Control


SLC2A9 in Glioma GWAS Data
p=1.08e-11
Density
Estimated Expression Value
Outcome
Case
Control


SLC2A9 in Glioma GWAS Data
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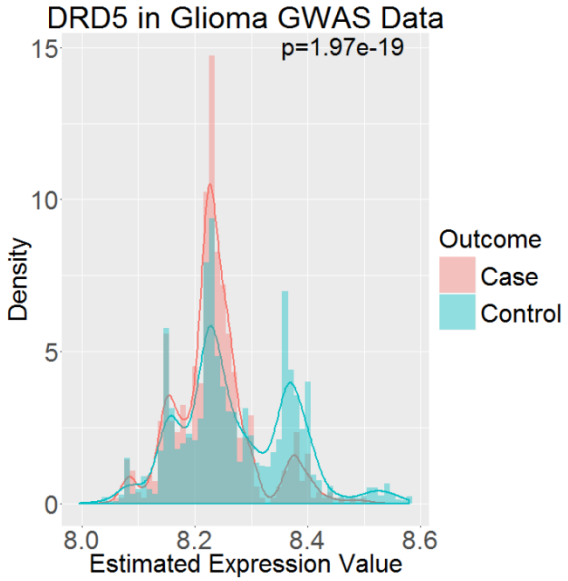
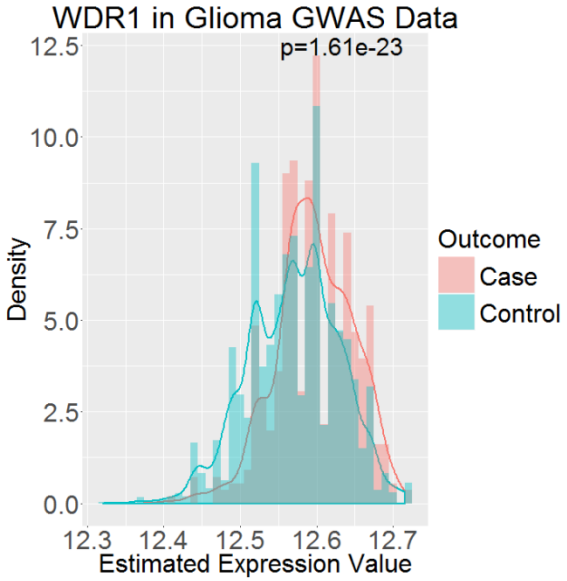
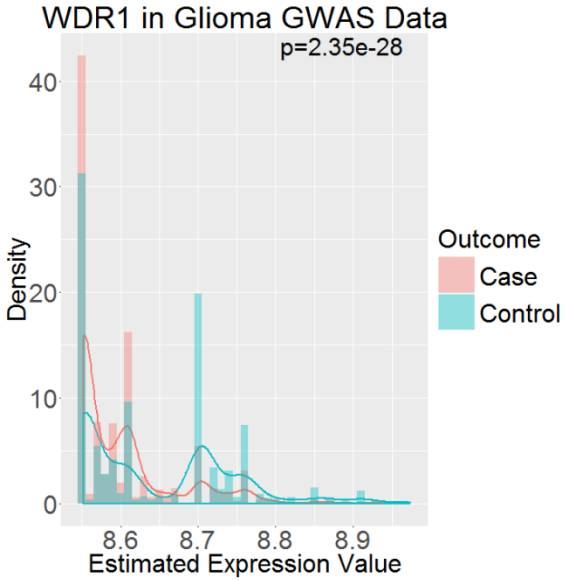
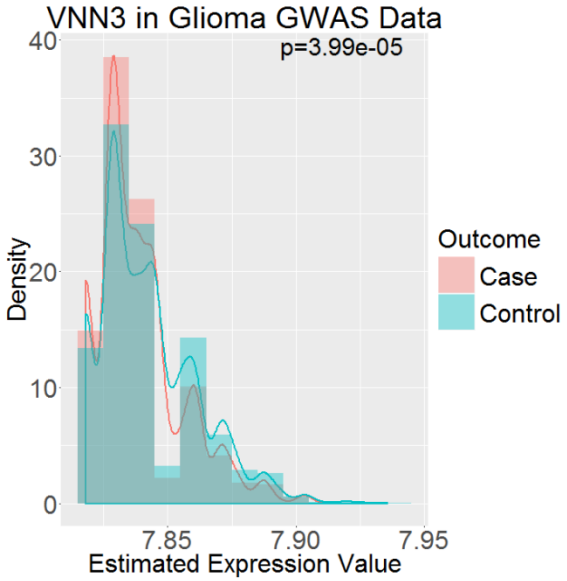
Density
Estimated Expression Value
Outcome
Case
Control

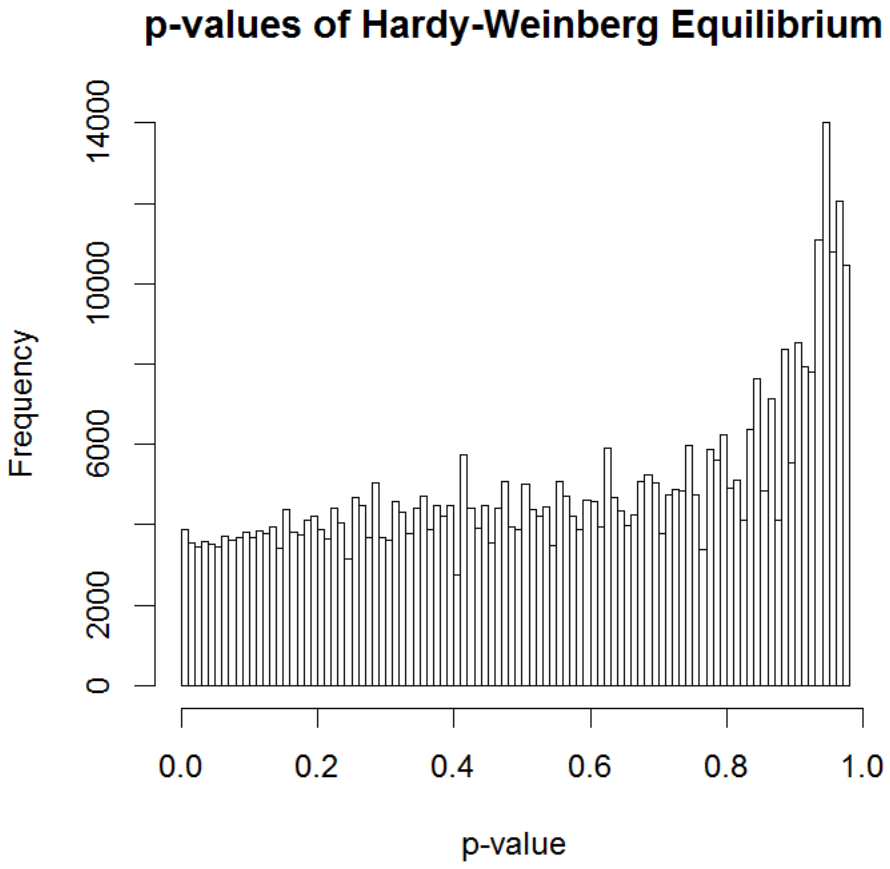

DRD5 in Glioma GWAS Data
p=1.97e-19
Density
Estimated Expression Value
Outcome
Case
Control


WDR1 in Glioma GWAS Data
p=1.61e-23
Density
Estimated Expression Value
Outcome
Case
Control


WDR1 in Glioma GWAS Data
p=2.35e-28
Density
Estimated Expression Value
Outcome
Case
Control

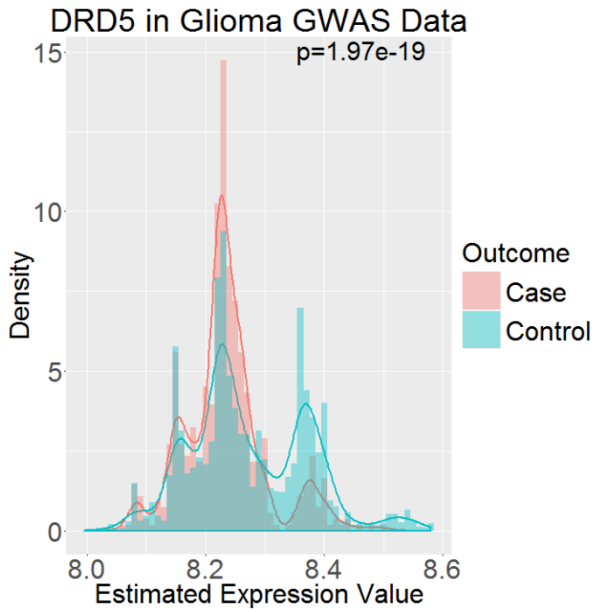

VNN3 in Glioma GWAS Data
p=3.99e-05
Density
Estimated Expression Value
Outcome
Case
Control

sFigure 9. Histogram of Hardy-Weinberg Equilibrium p-value.

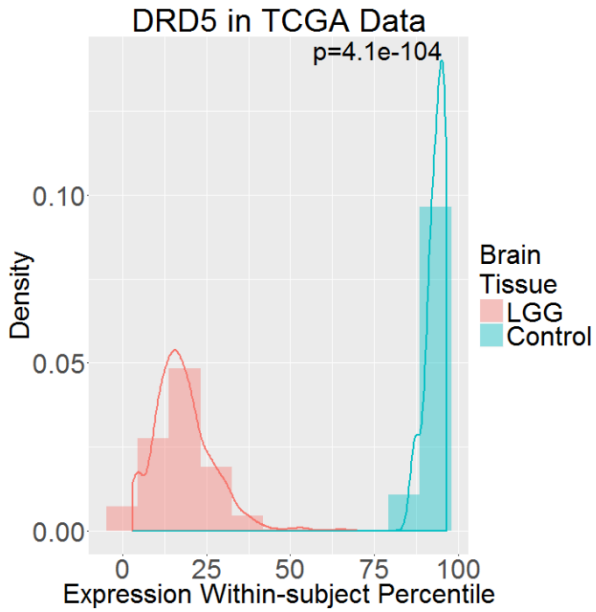


sFigure 10. Gene expression in glioma GWAS data and TCGA LGG (low grade glioma) data. (a), The estimated gene expression level of DRD5 estimated for glioma cases and controls in our glioma GWAS data ((a) *DRD5*, (c) *WDR1*). The relative gene expression level (measured as within subject percentile) of brain tissue from LGG patients and organ-specific controls from TCGA GBM project ((b) *DRD5*, (d) *WDR1*).

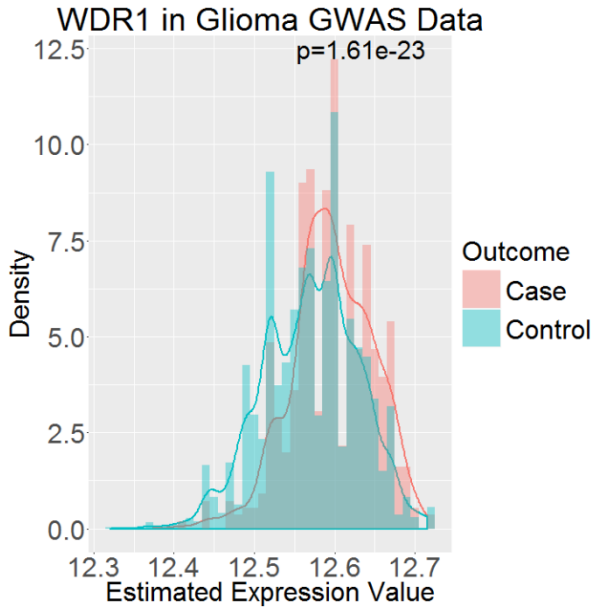
a



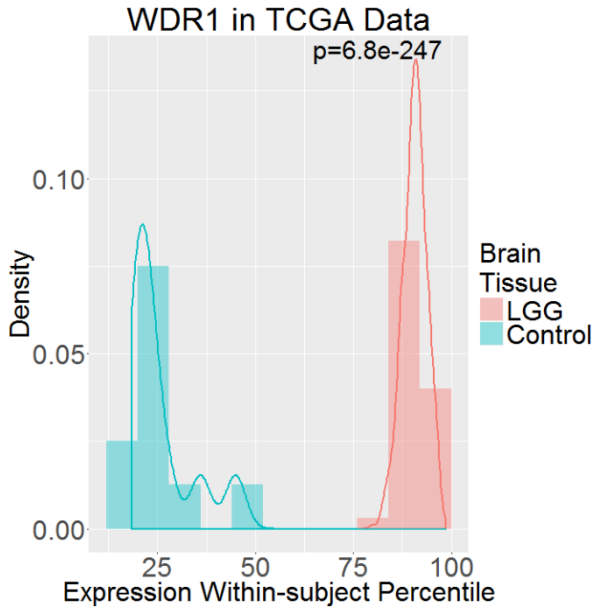

b




c




d



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