

# NPDR Supplementary Material

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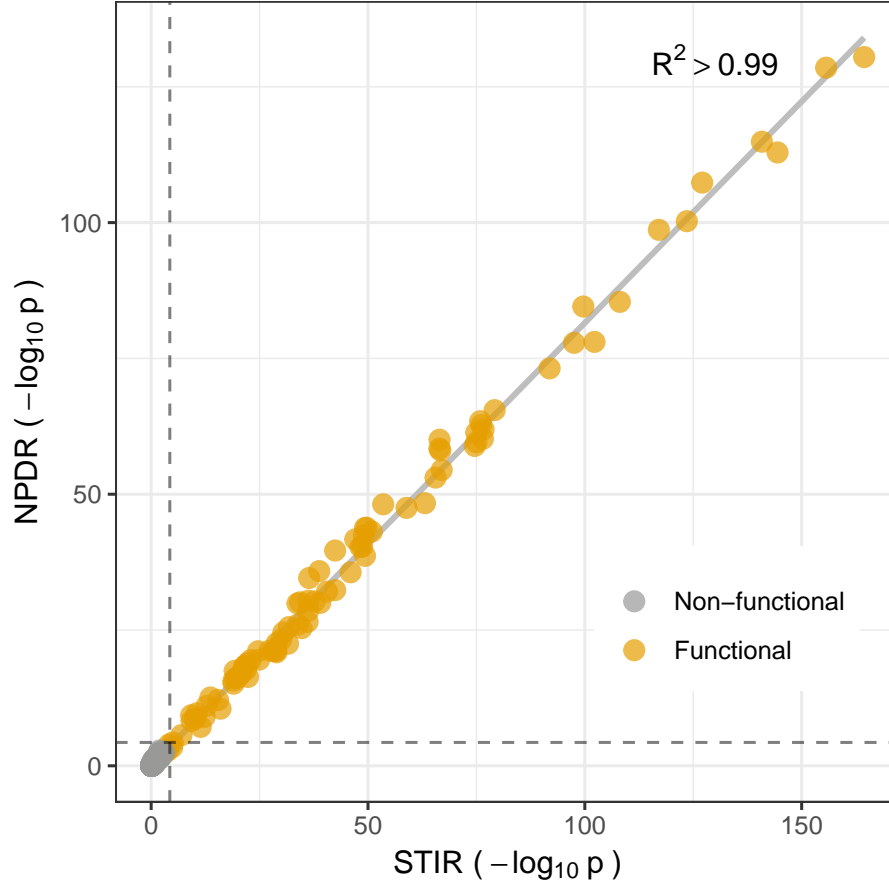


Figure S1: *Similarity between NPDR and STIR* in one simulation of  $m = 200$  samples and  $p = 1000$  attributes. In 100 replications,  $R_P^2$  ranges from 0.9827 to 0.9994.

## References

- [1] Trang T Le, Ryan J Urbanowicz, Jason H Moore, and Brett A McKinney. Statistical inference relief (stir) feature selection. *Bioinformatics*, page bty788, 2018.

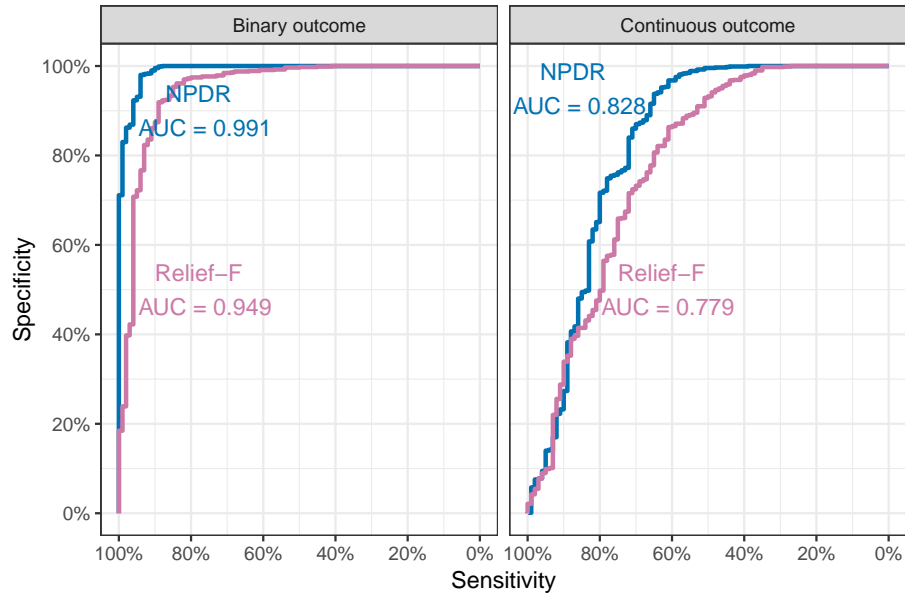


Figure S2: *auROC of Relief-F and NPDR for binary and continuous outcome data.*

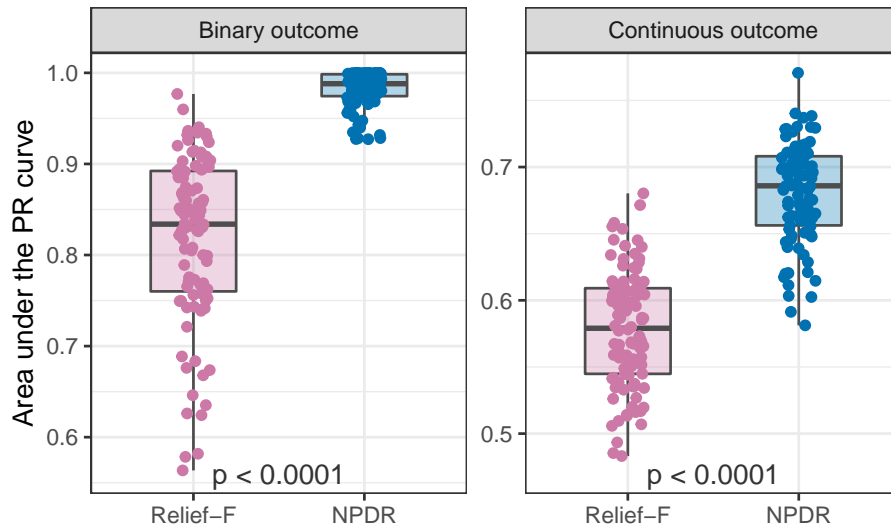


Figure S3: *auPRC of Relief-F and NPDR for binary and continuous outcome data.* In both cases, across 100 simulations of  $m = 200$  samples and  $p = 1000$  attributes, NPDR yields significantly higher auPRC.

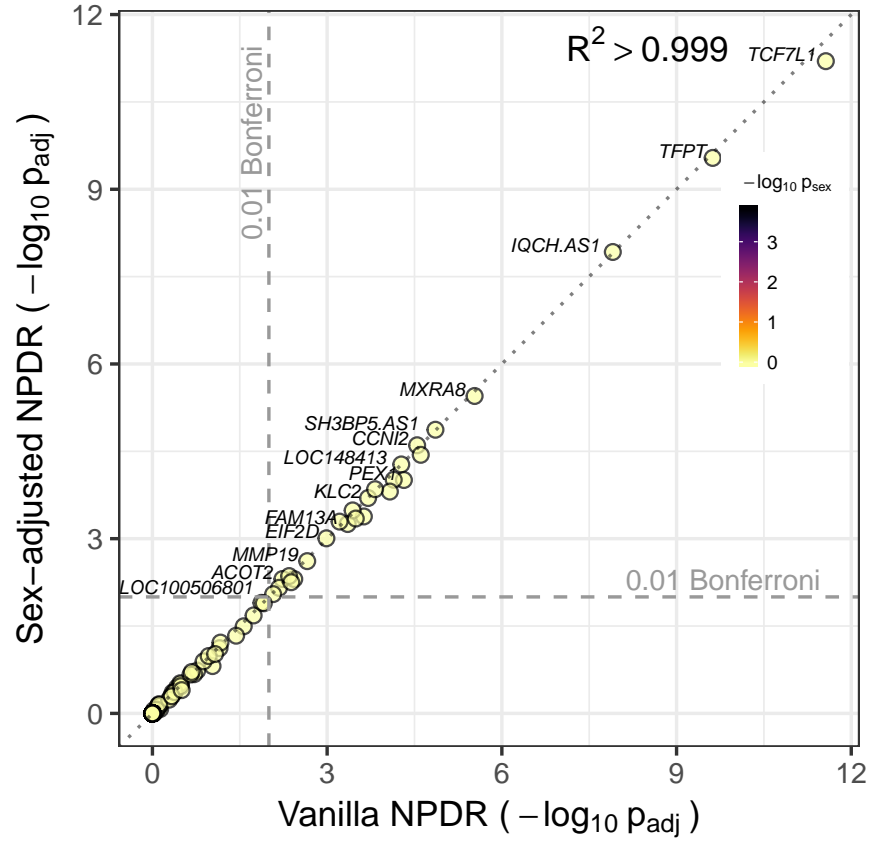


Figure S4: NPDR with and without sex adjustment to analyze MDD-associated genes in Le et al.'s RNASeq dataset. Adjustment of the sex covariate does not make a big difference in the resulting P values for each important gene. Both methods yield consistent results with STIR from previous study (Fig. 4 of Ref. [1])

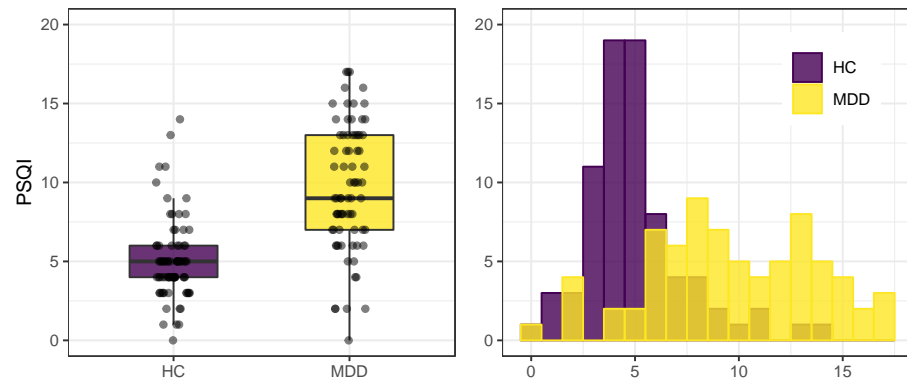


Figure S5: *The distribution of the PSQI scores among individuals with and without MDD.*