NPDR Supplementary Material

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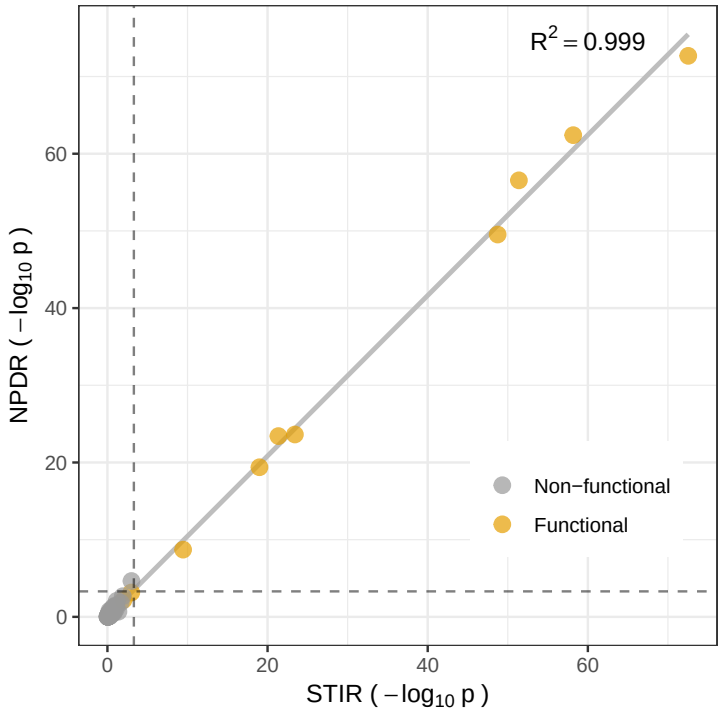

Figure S1: *Similarity between NPDR and STIR* in one simulation of $m = 100$ samples and $p = 100$ attributes. In 100 replications, R^2_P ranges from 0.9827 to 0.9994.

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.

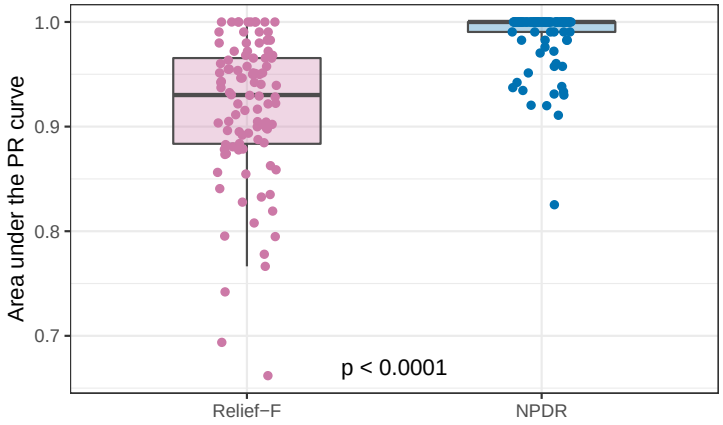

Figure S2: *auPRC of Relief-F and NPDR for binary outcome data.* Across 100 simulations of $m = 100$ samples and $p = 100$ attributes, NPDR yields significantly higher auPRC.

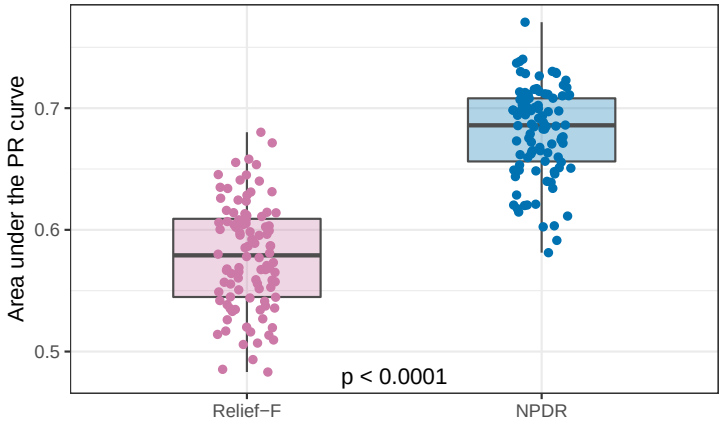

Figure S3: *auPRC of Relief-F and NPDR for continuous outcome data.* Across 100 simulations of $m = 100$ samples and $p = 100$ attributes, NPDR yields significantly higher auPRC.

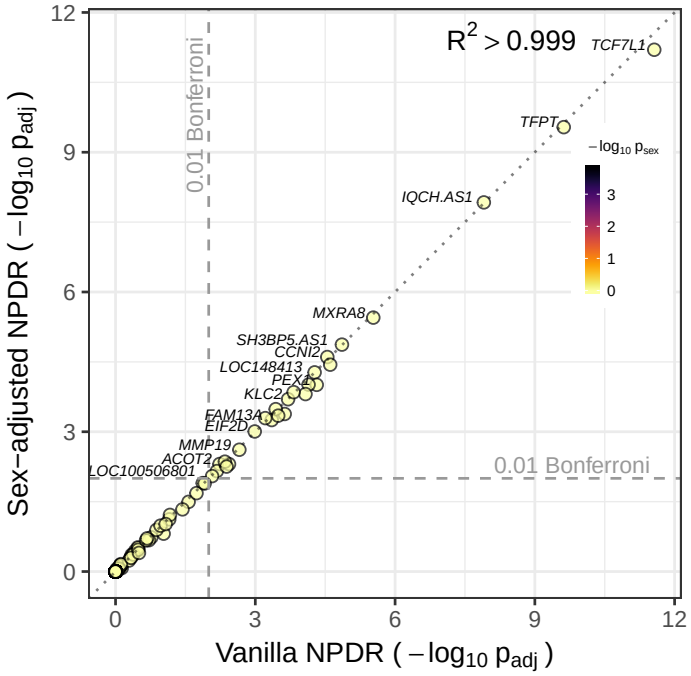

Figure S4: *NPDR with and without sex adjustment to analyze MDD-associated genes in Le et al.'s RNASeq dataset.* Adjustment of the sex covariate does not make a big difference in the resulting P values for each important gene. Both methods yield consistent results with STIR from previous study (Fig.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