

Supplementary data of  
 “Prioritizing *de novo* autism risk variants with calibrated gene-  
 and variant-scoring models”

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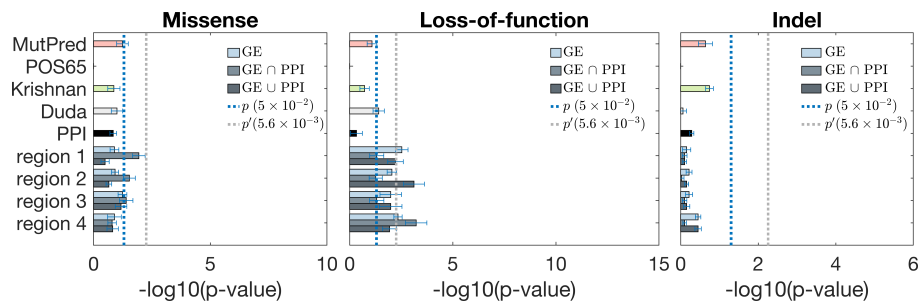


Figure 1: Same as Figure 3 in the main manuscript, but we exclude variants from genes in the list of POS65 from the  $p$ -value calculation.

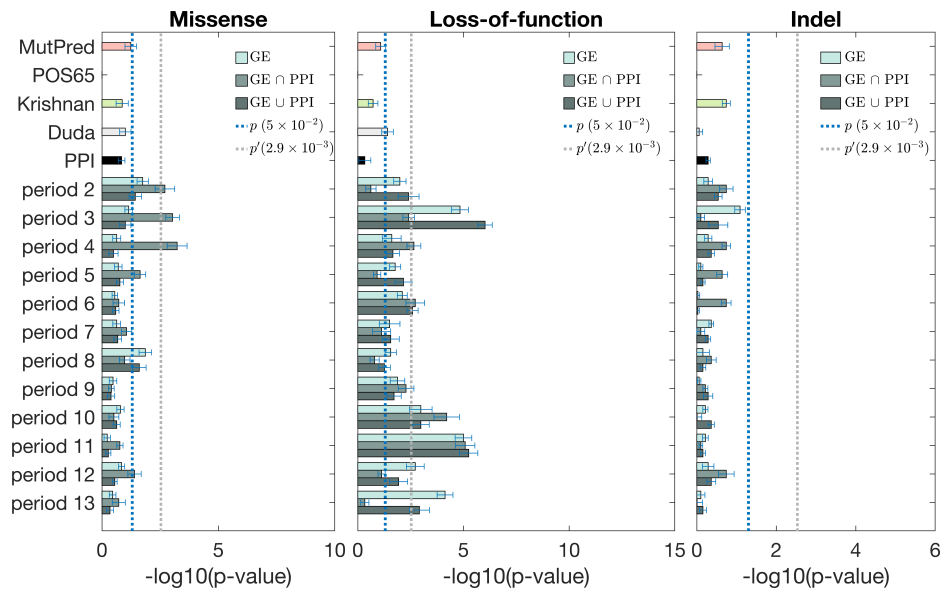


Figure 2: Same as Figure 4 in the main manuscript, but we exclude variants from genes in the list of POS65 from the  $p$ -value calculation.

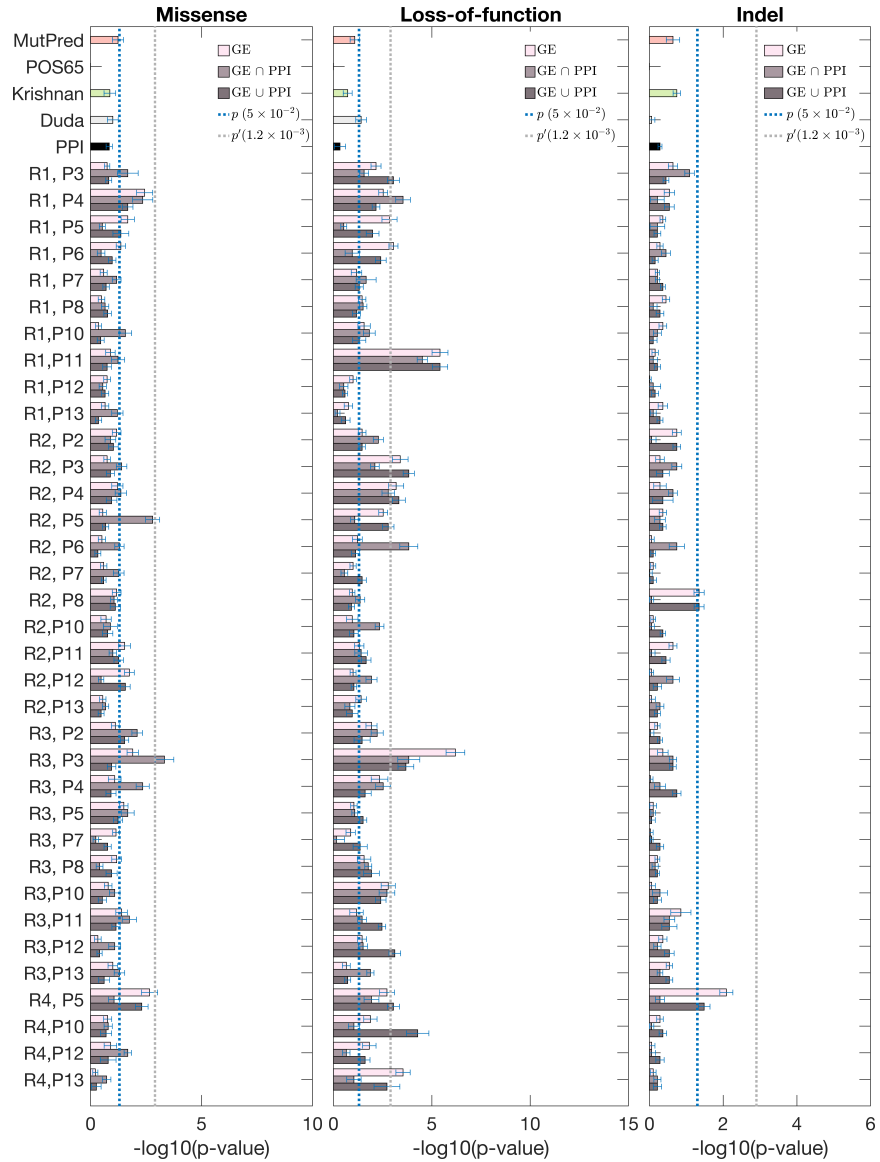


Figure 3: Same as Figure 5 in the main manuscript, but we exclude variants from genes in the list of POS65 from the  $p$ -value calculation.

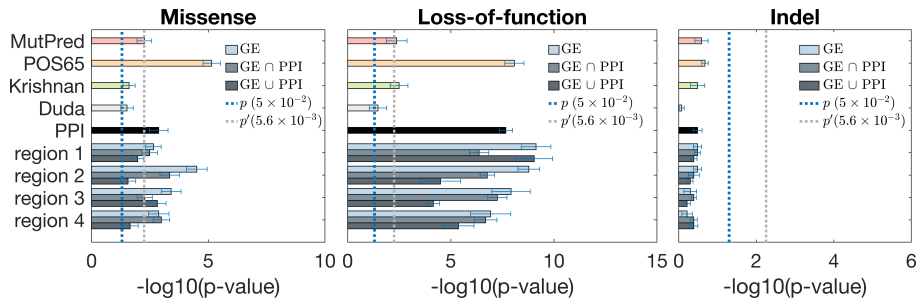


Figure 4: Same as Figure 3 in the main manuscript, but using 95% of control variants scores to determine the “right-tail” for the  $F$ -test.

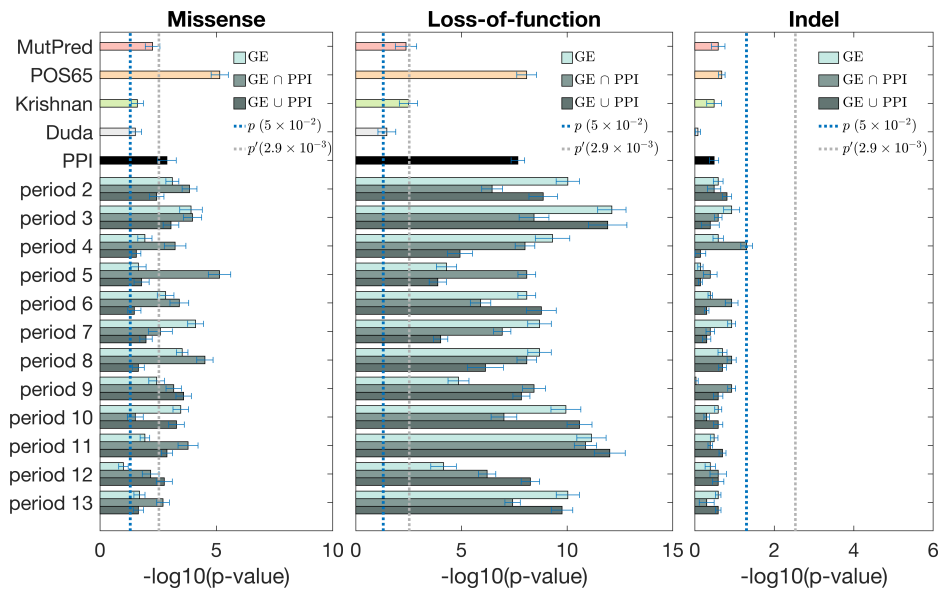


Figure 5: Same as Figure 4 in the main manuscript, but using 95% of control variants scores to determine the “right-tail” for the  $F$ -test.

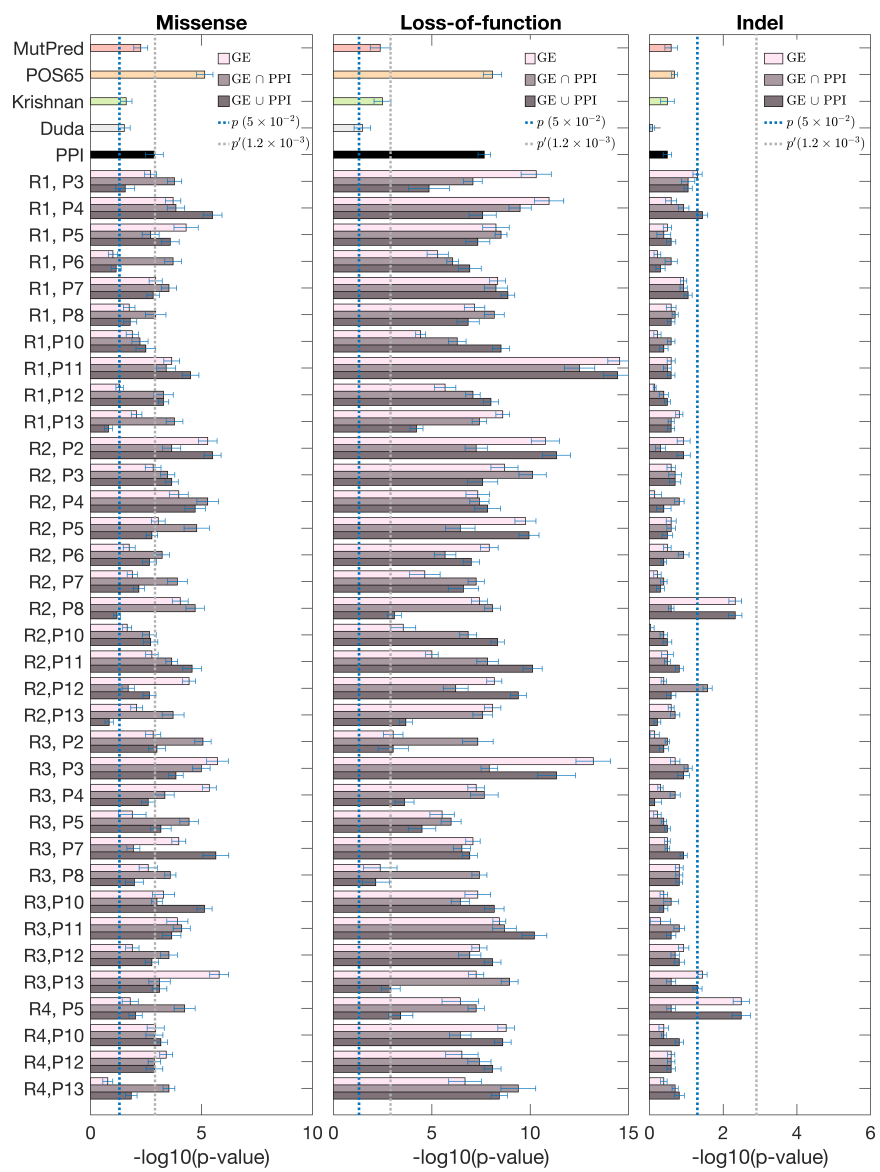


Figure 6: Same as Figure 5 in the main manuscript, but using 95% of control variants scores to determine the “right-tail” for the  $F$ -test.