

The American Journal of Human Genetics, Volume 108

## Supplemental information

### **Closing the gap: Systematic integration of multiplexed functional data resolves variants of uncertain significance in *BRCA1*, *TP53*, and *PTEN***

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Figure S1:

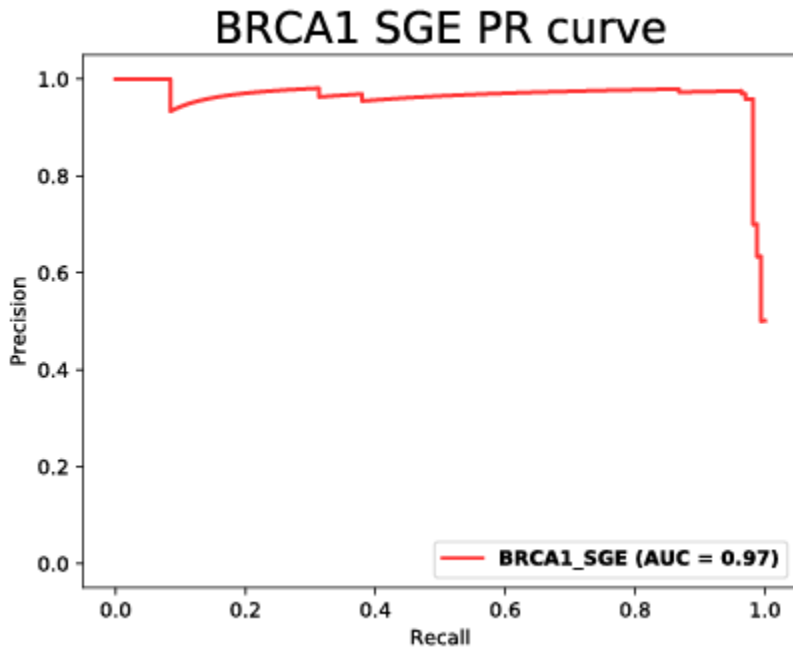


Figure S1 legend: precision recall curve for *BRCA1* MAVE data validated on all assayed variants with benign/likely benign and pathogenic/likely pathogenic interpretations in ClinVar.

Figure S2:

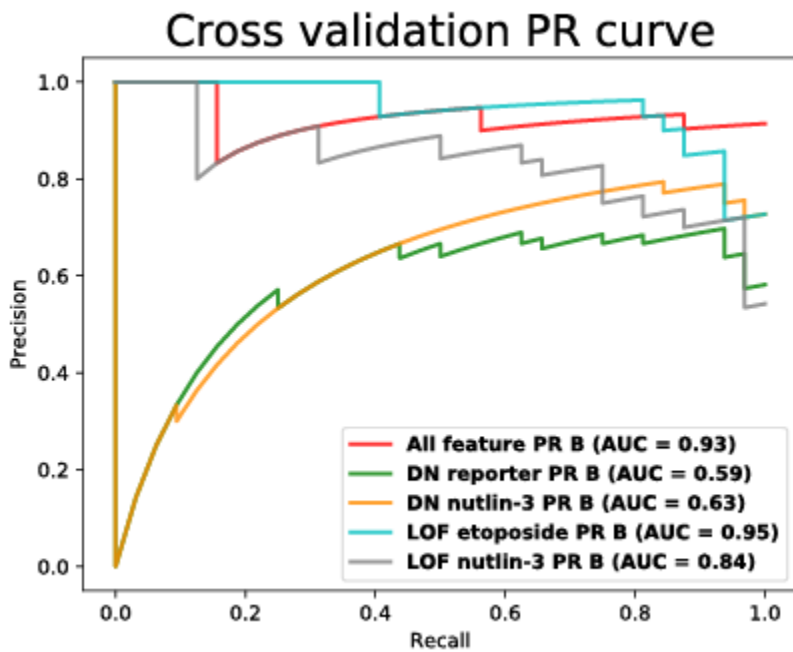


Figure S2 legend: precision recall curves for leave-one-out cross validation for *TP53* naive Bayes classifiers trained on all benign/likely benign and pathogenic/likely pathogenic variants in ClinVar. Classifiers were trained on either all four *TP53* MAVEs used in this analysis or each