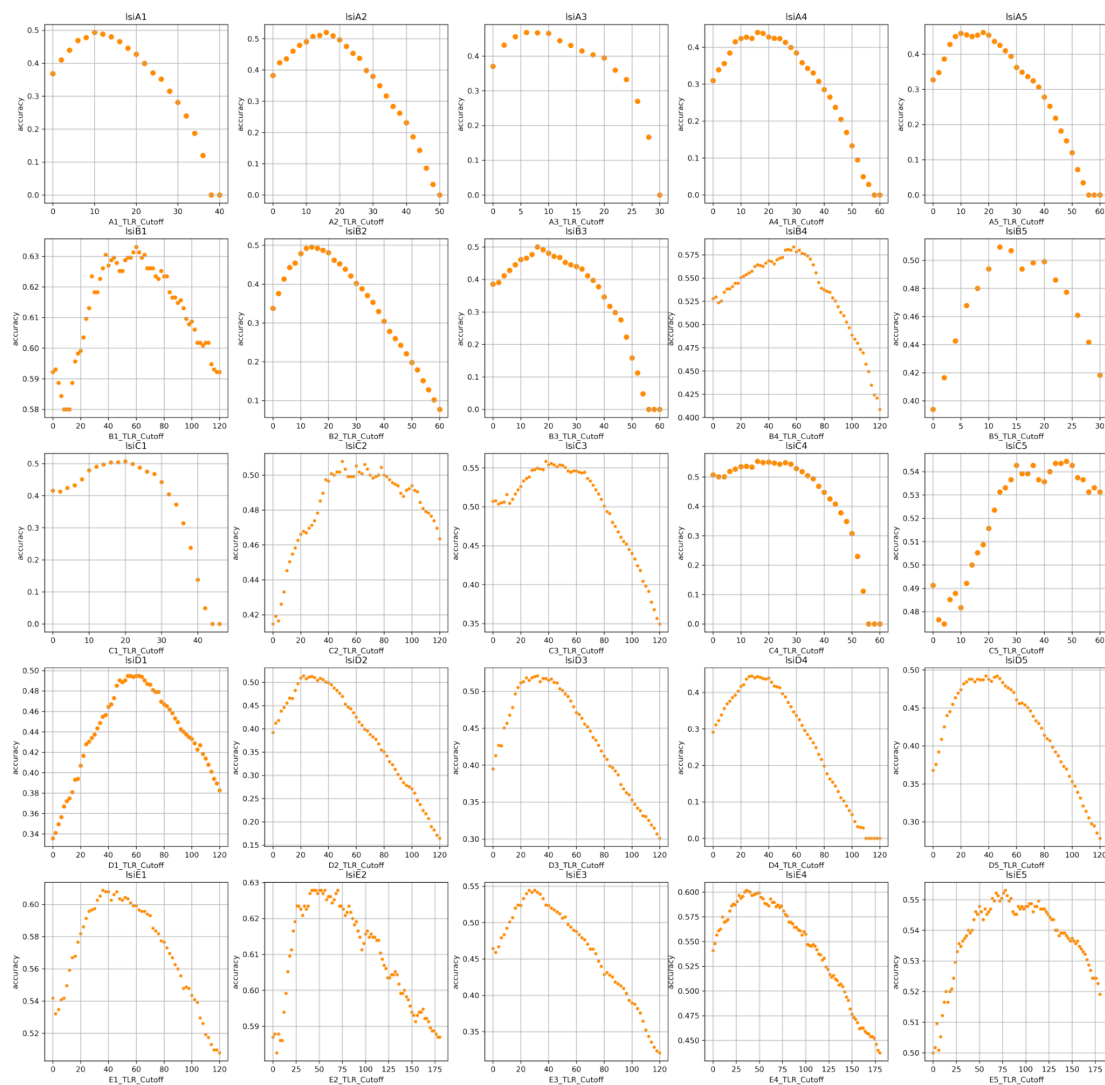
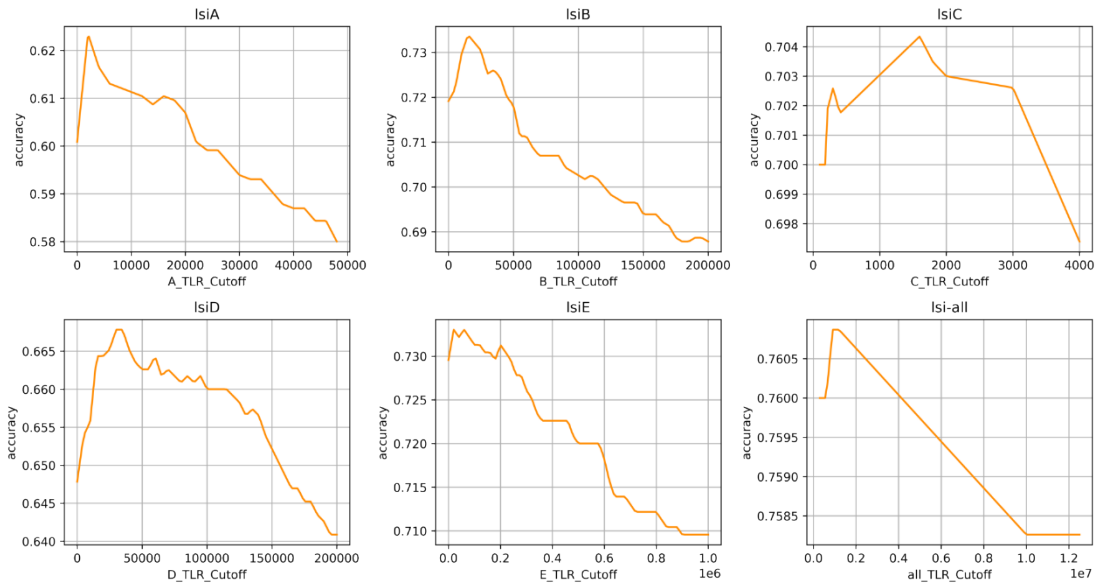


## SUPPLEMENTARY DATA

### Predicting Novel Targets with Bayesian Machine Learning by Integrating Multiple Biological Signatures

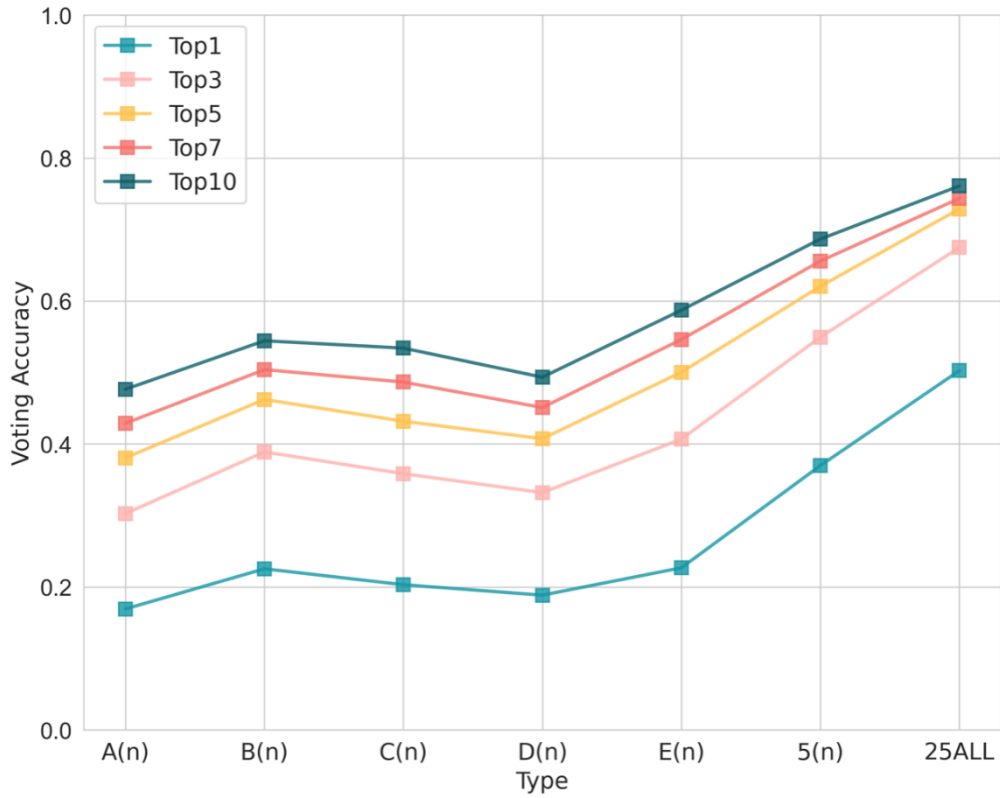


(A)



(B)

**Supplementary Figure 1 (A)** Result of the top 10 target predictions across 25 levels at varying thresholds. Accuracy was calculated by leave-one-out cross-validation under each TLR. (B) The results include the top 10 target predictions at various thresholds across 5 main levels, integrating corresponding sub-levels, as well as the top 10 target predictions integrating all 25 levels at varying thresholds.



**Supplementary Figure 2** The predictive capability for target identification across multiple levels. A(n) represents the average target prediction accuracy within a single layer of level A, and similarly for BCDE. 5(n) denotes the average target prediction accuracy when integrating the five main levels with their respective sub-levels. 25all indicates the target prediction accuracy after integrating information from all 25 levels.

Additional\_file1.xlsx

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