

Supplementary Table S2. Panel-size sensitivity analysis.

Mean nested CV AUC ($\pm$ SD) across 15 outer folds as a function of top-N genes per model, for each dataset. Values shown as mean $\pm$ SD. Green = AUC $\geq$ 0.80; amber = 0.60-0.79; red = $<$ 0.60. Dark red column header (GSE276531) indicates negative result; grey column headers (GSE14951, GSE15480) indicate exploratory datasets (n < 30).

Top-N	GSE112713	GSE276531	GSE12720	GSE14951	GSE15480	GSE151648 TIME	GSE151648 IRI
5	0.756 $\pm$ 0.187	0.369 $\pm$ 0.195	0.957 $\pm$ 0.066	1.000 $\pm$ 0.000	1.000 $\pm$ 0.000	0.969 $\pm$ 0.037	0.662 $\pm$ 0.154
10	0.784 $\pm$ 0.161	0.369 $\pm$ 0.195	0.961 $\pm$ 0.062	1.000 $\pm$ 0.000	1.000 $\pm$ 0.000	0.952 $\pm$ 0.052	0.721 $\pm$ 0.151
15	0.812 $\pm$ 0.137	0.376 $\pm$ 0.182	0.965 $\pm$ 0.062	1.000 $\pm$ 0.000	1.000 $\pm$ 0.000	0.959 $\pm$ 0.051	0.753 $\pm$ 0.179
20	0.829 $\pm$ 0.138	0.369 $\pm$ 0.195	0.965 $\pm$ 0.059	1.000 $\pm$ 0.000	1.000 $\pm$ 0.000	0.958 $\pm$ 0.050	0.768 $\pm$ 0.188
30	0.842 $\pm$ 0.124	0.402 $\pm$ 0.164	0.965 $\pm$ 0.059	1.000 $\pm$ 0.000	1.000 $\pm$ 0.000	0.959 $\pm$ 0.052	0.783 $\pm$ 0.208
40	0.845 $\pm$ 0.129	0.385 $\pm$ 0.171	0.968 $\pm$ 0.057	1.000 $\pm$ 0.000	1.000 $\pm$ 0.000	0.959 $\pm$ 0.052	0.777 $\pm$ 0.198

* GSE14951 (n=10) and GSE15480 (n=24) are exploratory only; results should not be interpreted as reliable performance estimates.

† GSE276531 (n=32) yielded near-chance performance at all panel sizes, confirming absence of reliable transcriptomic signal regardless of compression strategy.