Table 2. Summary of gene and pathway level extrapolation performance of S1500 gene set on cross-validated training set.

	Pearson Correlation[a]	Concordance Rate[b]	Significance Overlap[c]	Mean Squared Error[d]
Gene level performance				
S1500	0.79 (0.64, 0.99)	0.94 (0.91, 1.00)	0.34 (0.27, 0.50)	0.22 (0.12, 0.32)
Random 1500	0.79 (0.65, 0.99)	0.93 (0.91, 1.00)	0.33 (0.26, 0.51)	0.23 (0.12, 0.31)
Pathway level performance				
S1500	0.79 (0.44, 0.91)	0.85 (0.55, 0.93)	0.51 (0.43, 0.72)	0.10 (0.02, 0.62)
Random 1500	0.75 (0.51, 0.89)	0.82 (0.55, 0.92)	0.41 (0.34, 0.68)	0.12 (0.03, 0.56)

Note: values represent mean and range (min, max) across 20-fold cross validation. Gene-level analyses were conducted using fold change. Pathway-level analyses were conducted on GSEA scores.