

Table 3. Summary of gene and pathway level extrapolation performance of the S1500 and S1500+ gene sets using independent test set.

	Pearson Correlation	Concordance Rate	Significance Overlap	Mean Squared Error
Gene level Performance				
S1500	0.72	0.93	0.33	0.22
Random 1500	0.72 (0.72, 0.73)	0.93 (0.93, 0.93)	0.34 (0.33, 0.34)	0.24 (0.24, 0.25)
S1500+ (2739 genes)	0.75	0.94	0.37	0.2
Random 2739	0.76 (0.75, 0.76)	0.93 (0.93, 0.93)	0.38 (0.37, 0.38)	0.22 (0.22, 0.22)
Pathway level performance				
S1500	0.81	0.87	0.52	0.07
Random 1500	0.74 (0.73, 0.75)	0.84 (0.84, 0.84)	0.39 (0.37, 0.40)	0.10 (0.09, 0.10)
S1500+ (2739 genes)	0.87	0.9	0.6	0.05
Random 2739	0.78 (0.77, 0.79)	0.86 (0.86, 0.86)	0.44 (0.42, 0.46)	0.08 (0.08, 0.08)

Note: for the evaluation of random gene lists, a random set of genes was selected 20 times then averaged. The values presented for random gene lists are the mean followed by the minimum and maximum values in brackets.