(A) Roll back to a simpler model.

(B) Exclude incomplete cases.
(C) Expectation-maximisation algorithm.

(D) Multiple imputation.
(E) Median imputation.

Figure S3  FPR < 0.1 AUC distribution across all combinations of gene properties, using 5 missing value handling methods. Methods for missing value treatment include (A) rolling back to a simpler model, (B) excluding incomplete cases, (C) the expectation-maximisation algorithm, (D) multiple imputation, and (E) median imputation. The three letter codes identify gene properties and are described in the legend. Distributions are for 100 ROC curves generated during cross validation (see Methods). Whiskers represent lowest point within 1.5 interquartile range (IQR) of the lower quartile, and highest point within 1.5 IQR of the upper quartile. Dots represent outliers of the aforementioned ranges. The black horizontal line represents the random expectation from the ROC plot.

<table>
<thead>
<tr>
<th>Abbreviation</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>gdg</td>
<td>Genetic interaction network degree</td>
</tr>
<tr>
<td>mxv</td>
<td>mRNA expression variation through the yeast cell cycle</td>
</tr>
<tr>
<td>odi</td>
<td>ORF DNA percentage between S. cerevisiae and S. kudriavzevii</td>
</tr>
<tr>
<td>pdg</td>
<td>Protein interaction network degree</td>
</tr>
<tr>
<td>pdi</td>
<td>Promoter sequence DNA identity between S. cerevisiae and S. paradoxus</td>
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<td>psi</td>
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