Supplementary table III - Effect of addition of more informative genomes on accuracy and coverage scores. We calculated the accuracy and coverage after addition of *N. crassa* and *S. pombe* genomes, for different conservation scores. The analysis is only for putative target motifs within predicted unstructured protein regions in the *S. cerevisiae* proteome and for a probing region of 210.

<table>
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<th>Conservation Level</th>
<th>Calculated with Gold Positives (Total Positives = 59)</th>
<th>Calculated with Platinum Positives (Total Positives = 19)</th>
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