

Supporting Information S2. The benchmark dataset S(2) for *S. cerevisiae*.

It is formed by 314 Ψ -site-containing sequences and 314 false ψ -site-containing sequences. Each of these samples is 31-bp long with the uridine located at the center. None of the sequences included here has $\geq 60\%$ pairwise sequence identity to any other in a same subset.

I. 314 Ψ -site-containing sequences (positive samples)

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II. 314 false Ψ -site-containing sequences (negative samples)

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