

**Supplementary Table 2a****Classification results for reduced sets comprising all modifications and K most important TFs**

Classification results

Number of Tfs in the feature set	Classification error
125	2,7%
100	2,6%
80	2,4%
64	2,4%
52	2,3%
42	2,3%
34	2,2%
27	2,2%
22	2,1%
18	2,1%
15	2,1%
12	2,0%
10	2,0%
8	2,1%
7	2,1%
6	2,1%
5	2,1%
4	2,1%
3	2,0%
2	2,0%
1	2,1%

The inspection of the influence of individual modifications reveals that three modifications are non-redundant – their removal from the feature set results in increase of classification error, see Supplementary Table 2b.

**Supplementary Table 2b****Classification results for reduced sets comprising all TFs and all but one ribosome modification**

Modification removed from the feature set	Classification error
A	2,8%
B	2,9%
C	3,0%
D	3,3%
E	2,9%
F	2,8%
G	4,8%
H	2,8%

The analysis of redundancy between ribosomal modifications shows that removal of the most important modifications from the feature set leads to rapid degradation of the model quality, see Supplementary Table 2a.