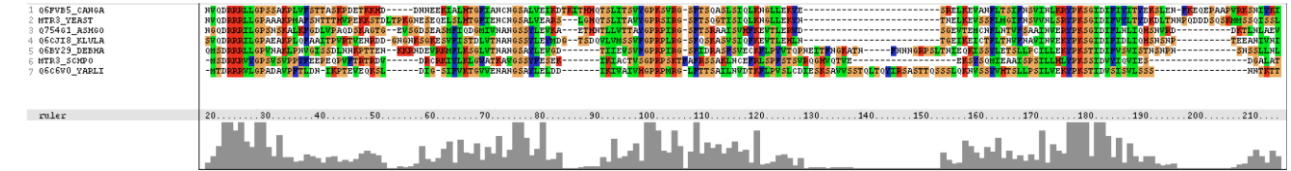


Supplementary Table10: Distant ortholog prediction alignments

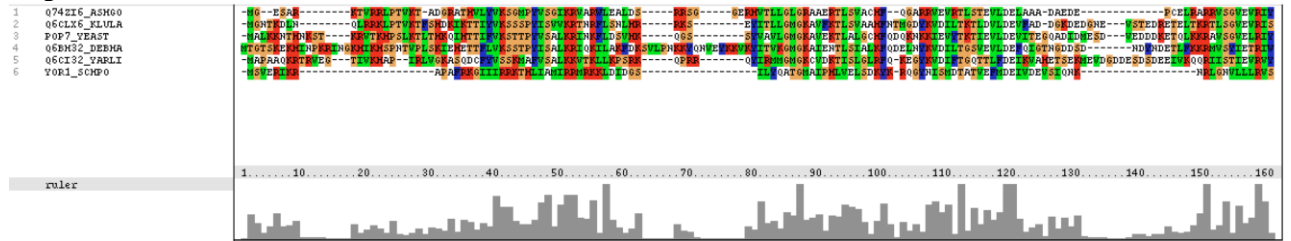
Mtr3

(Larger image link: <http://pombe.kaist.ac.kr/nbtsupp/data/imgs/Mtr3.tif>)



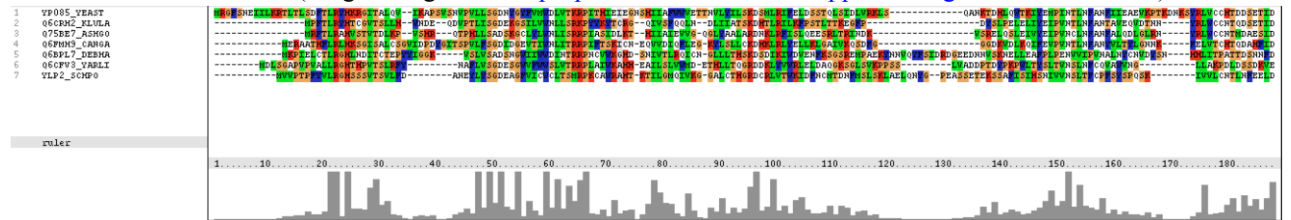
Pop7

(Larger image link: <http://pombe.kaist.ac.kr/nbtsupp/data/imgs/Pop7.tif>)



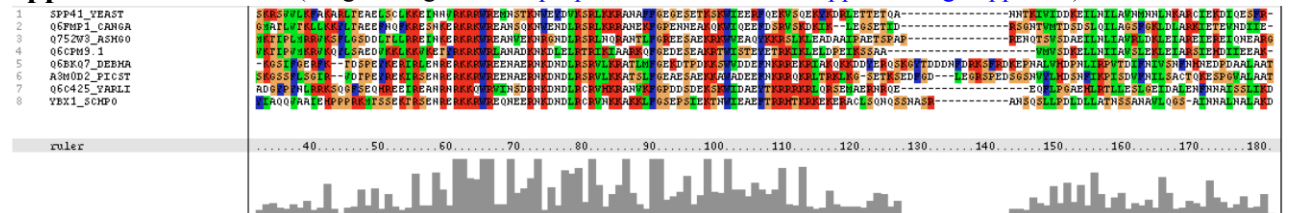
SPAC1006.02

(Larger image link: <http://pombe.kaist.ac.kr/nbtsupp/data/imgs/SPAC1006.02.tif>)



Spp41

(Larger image link: <http://pombe.kaist.ac.kr/nbtsupp/data/imgs/Spp41.tif>)



Multiple alignments of the conserved regions of the distant orthologs detected, demonstrating conservation between fungal species. These protein families representing orthologous clusters with copy number 1:1 is included in Pfam Release Version 24.0. The Pfam release has been generated using HMMER3, which is more sensitive than previous versions for detecting distant similarities.

Full alignment data links:

1. Mtr3 http://pombe.kaist.ac.kr/nbtsupp/data/Mtr3_aln.pdf
2. Pop7 http://pombe.kaist.ac.kr/nbtsupp/data/Pop7_aln.pdf
3. SPAC1006.02 http://pombe.kaist.ac.kr/nbtsupp/data/SPAC1006.02_aln.pdf
4. Spp41 http://pombe.kaist.ac.kr/nbtsupp/data/Spp41_aln.pdf