Table S5. Selection of terms used for the gene ontology analysis.

This selection was based on list of 164 predefined GO slims restricted to the yeast taxonomy (https://www.ebi.ac.uk/QuickGO/slimming; accessed: May 2023, revised: November 2023)

Domain	Gene Ontology term
Cellular Component (CC)	GO:0005634 – nucleus GO:0005694 – chromosome GO:0005730 – nucleolus GO:0005737 – cytoplasm GO:0005739 – mitochondrion GO:0005773 – vacuole GO:0005783 – endoplasmic reticulum GO:0005794 – Golgi apparatus GO:0005840 – ribosome GO:0005886 – plasma membrane
Biological Process (BP)	GO:0000278 – mitotic cell cycle GO:0006281 – DNA repair GO:0006325 – chromatin organization GO:0006457 – protein folding GO:0006260 – DNA replication GO:0006310 – DNA recombination GO:0006352 – DNA-templated transcription initiation GO:0006353 – DNA-templated transcription termination GO:0006354 – DNA-templated transcription elongation GO:0006360 – transcription by RNA polymerase I GO:0006366 – transcription by RNA polymerase II GO:0006383 – transcription by RNA polymerase III GO:0006417 – regulation of translation GO:0006974 – DNA damage response GO:0006997 – nucleus organization GO:0007059 – chromosome segregation GO:0016570 – histone modification GO:0023052 – signaling GO:0031399 – regulation of protein modification process GO:0042221 – response to chemical GO:0051052 – regulation of DNA metabolic process GO:0051169 – nuclear transport GO:0051726 – regulation of cell cycle GO:0070647 – protein modification by small protein conjugation or removal
Molecular Function (MF)	GO:0003677 – DNA binding GO:0003682 – chromatin binding GO:0003700 – DNA-binding transcription factor activity GO:0003723 – RNA binding GO:0003729 – mRNA binding GO:0004386 – helicase activity GO:0004518 – nuclease activity

	GO:0008134 – transcription factor binding GO:0016874 – ligase activity GO:0019899 – enzyme binding GO:0030234 – enzyme regulator activity GO:0032182 – ubiquitin-like protein binding GO:0042393 – histone binding GO:0140657 – ATP-dependent activity