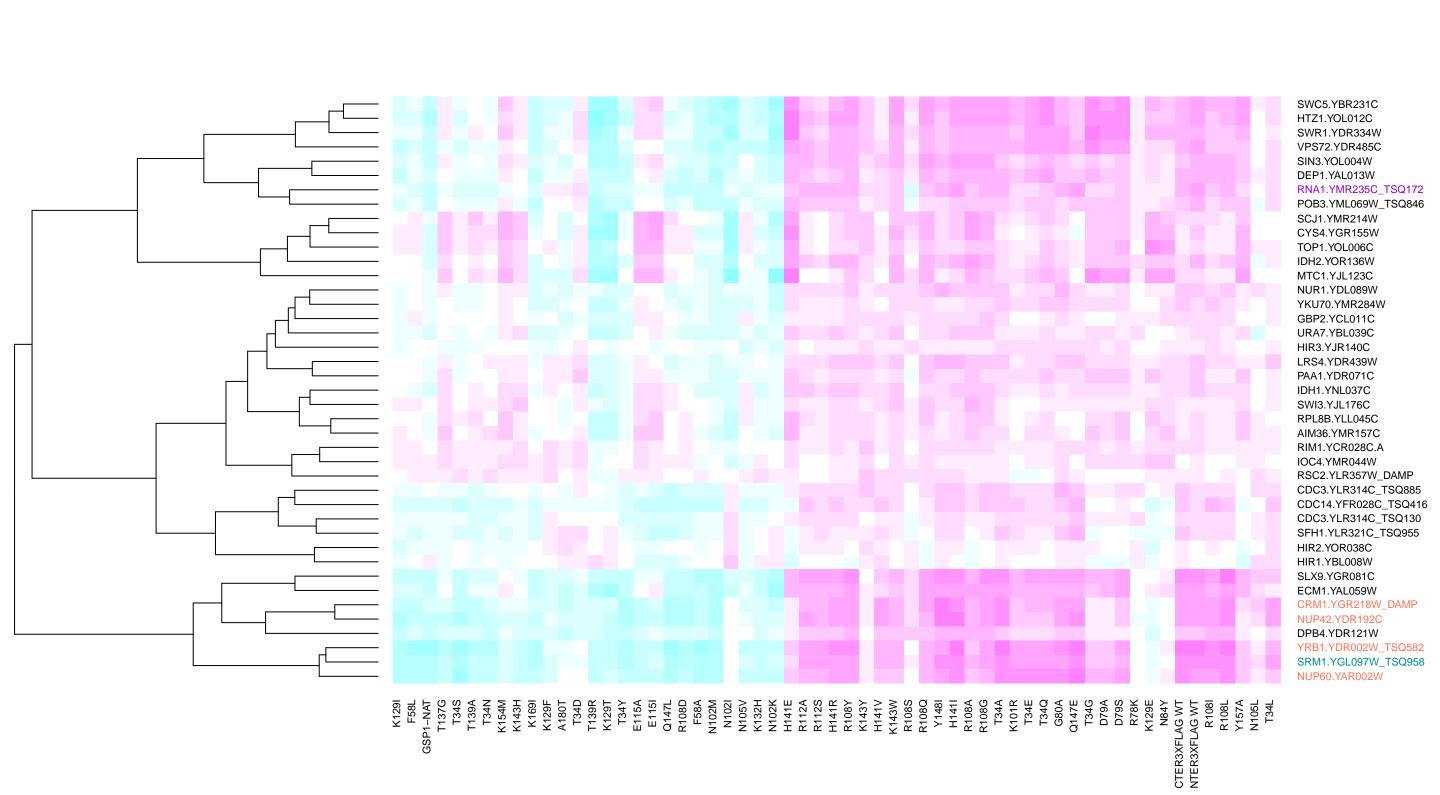
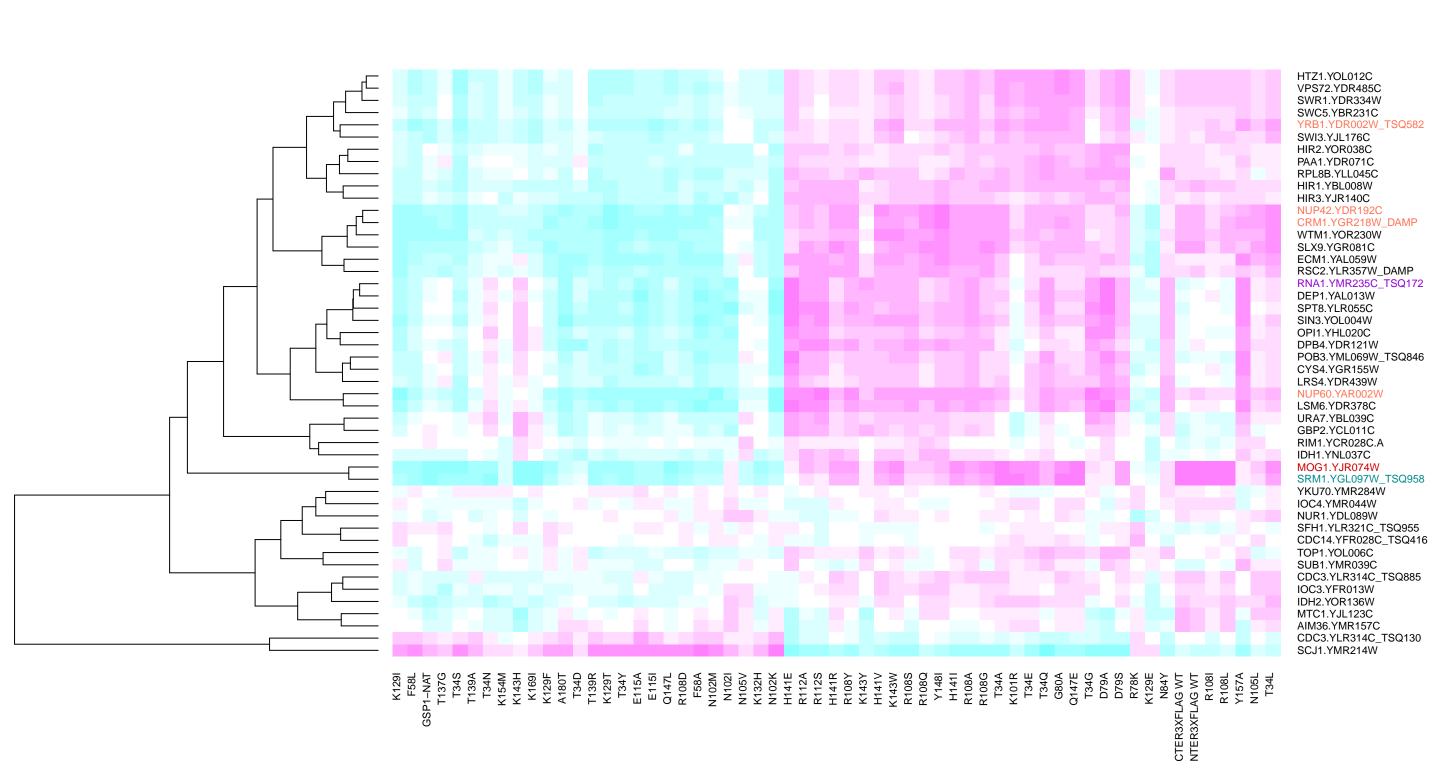
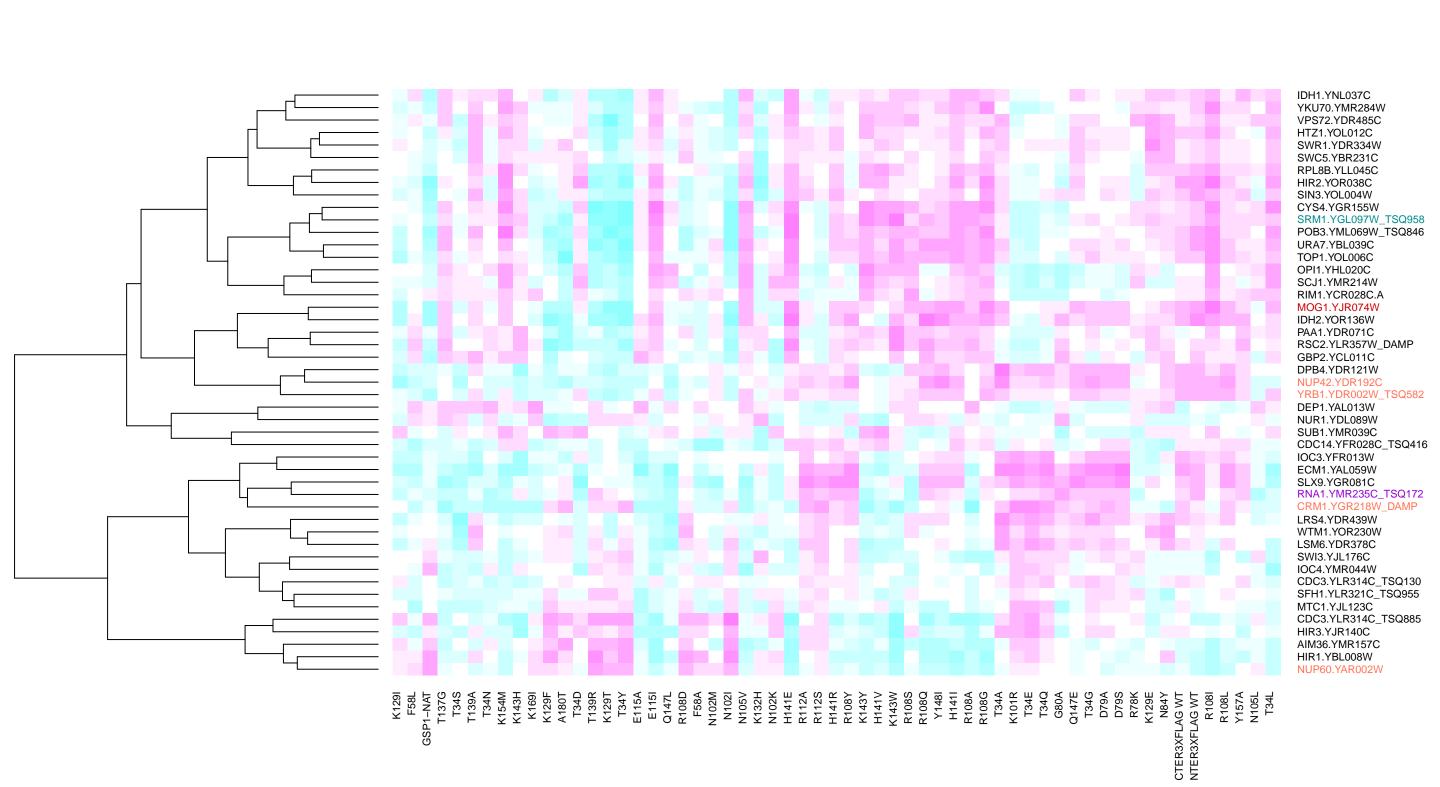
endomembrane system

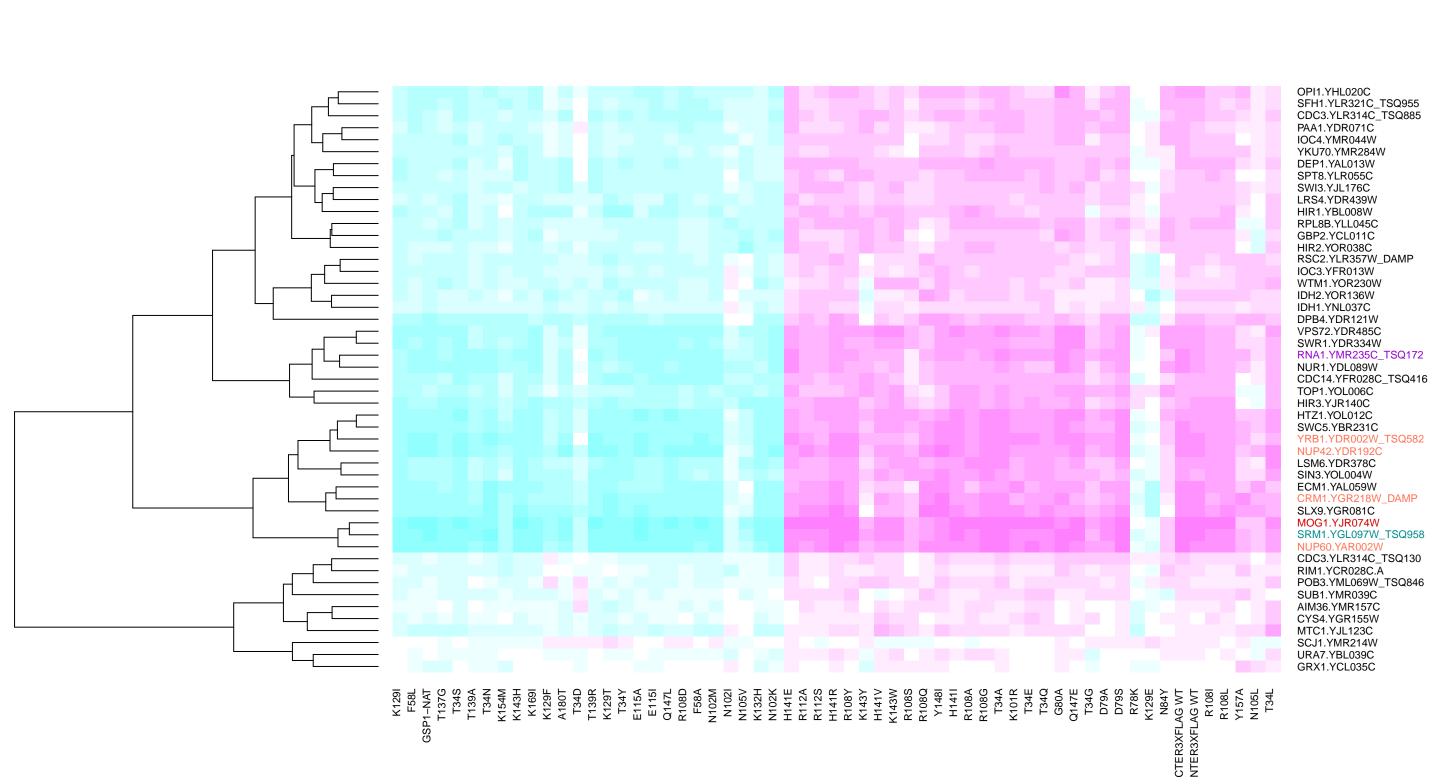


chromatin organization_GO_15_1_mut





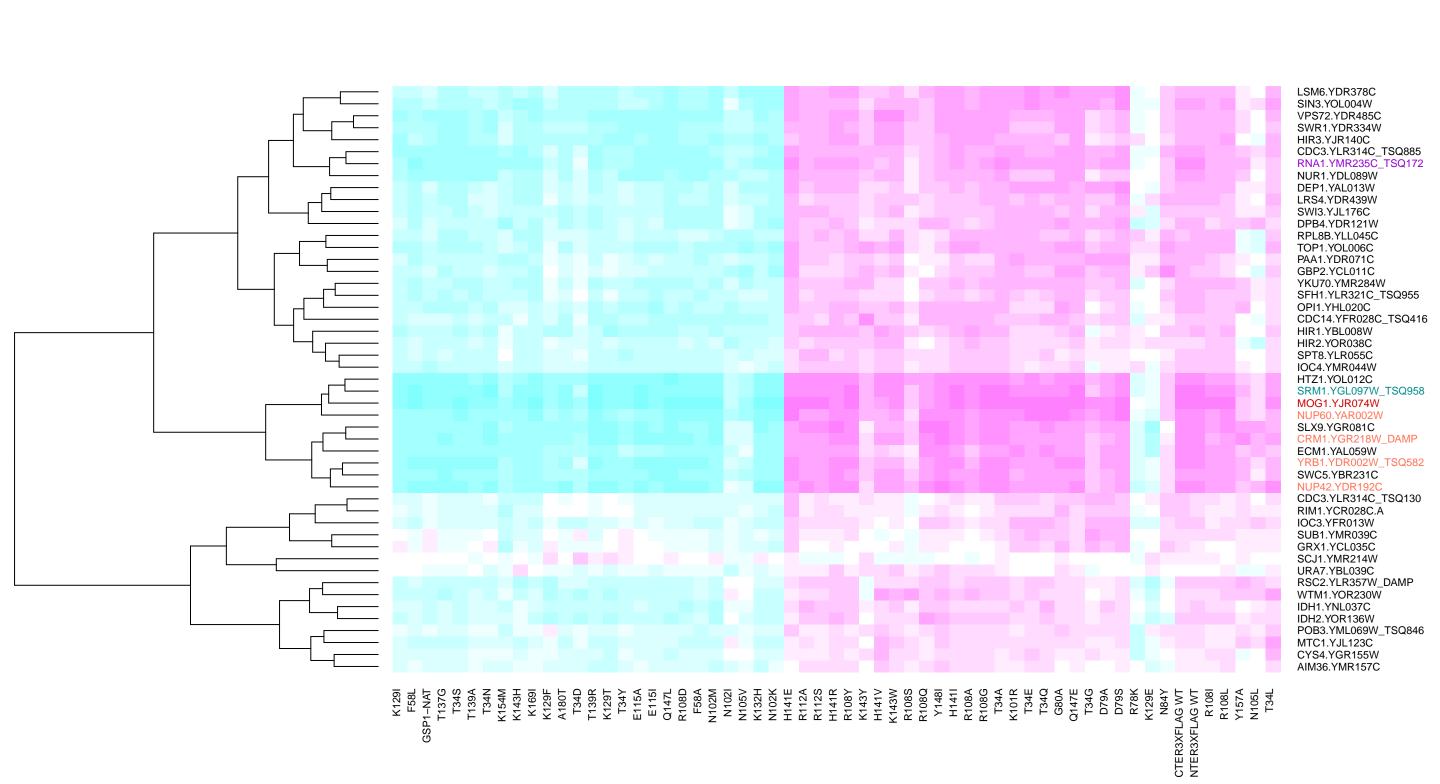
nuclear transport



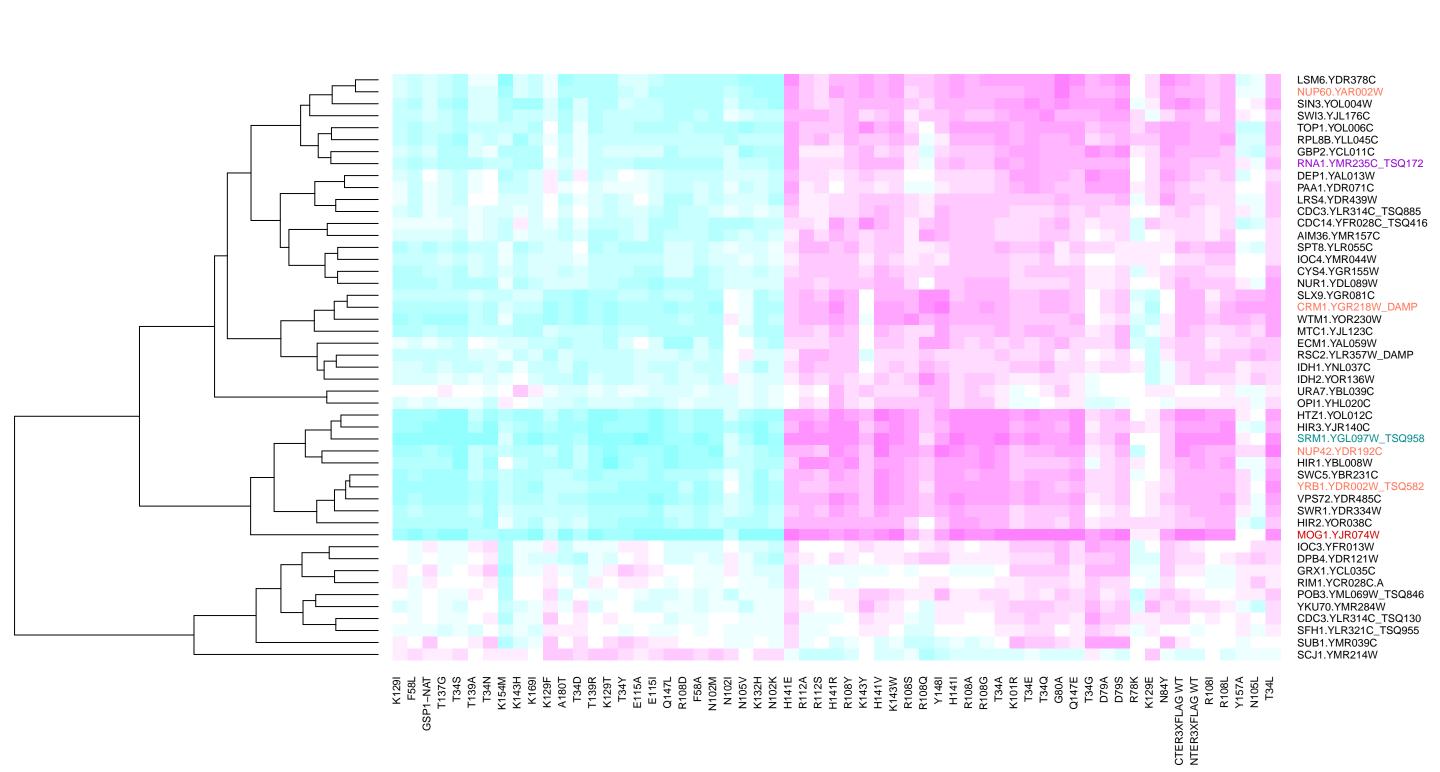
nuclear transport and organization



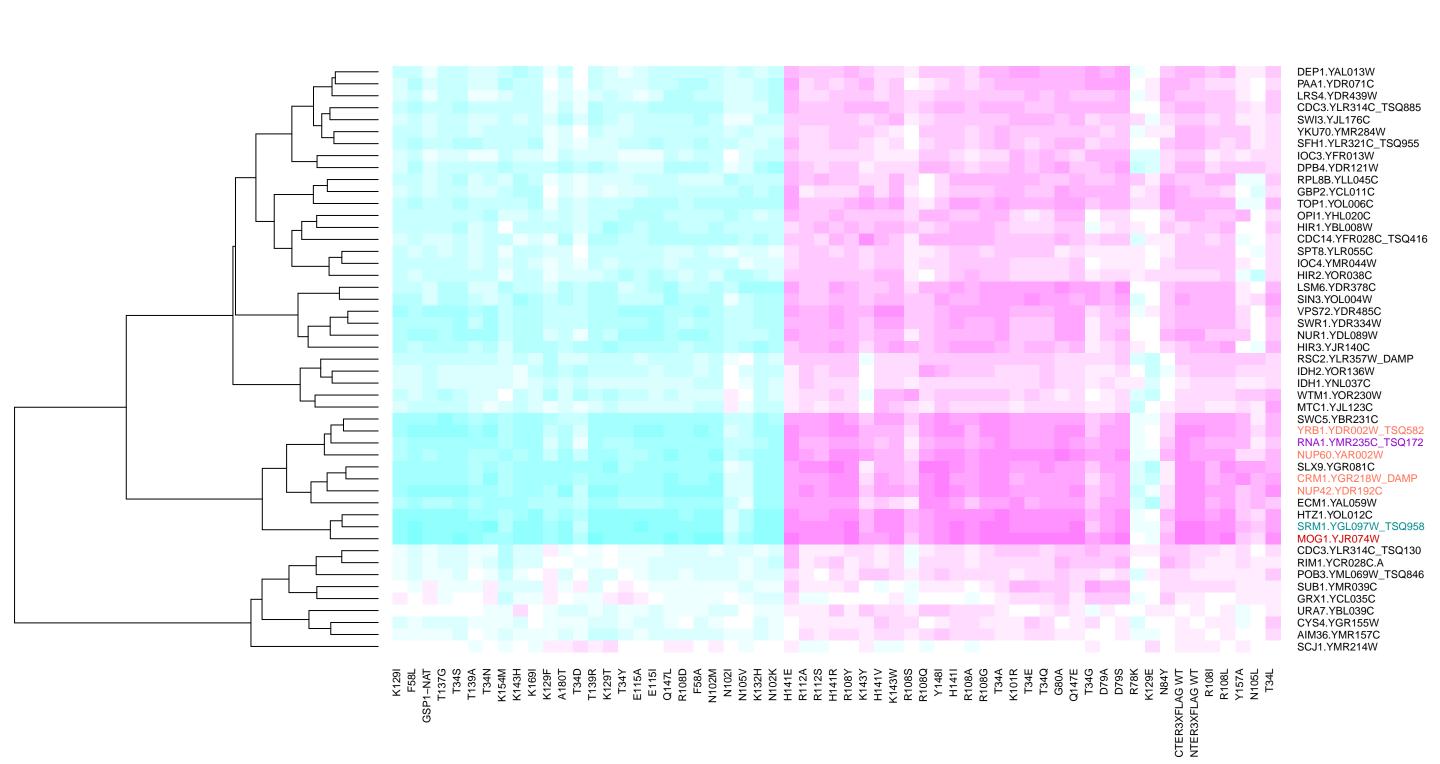
nuclear transport and organization_GO_15_1_mut



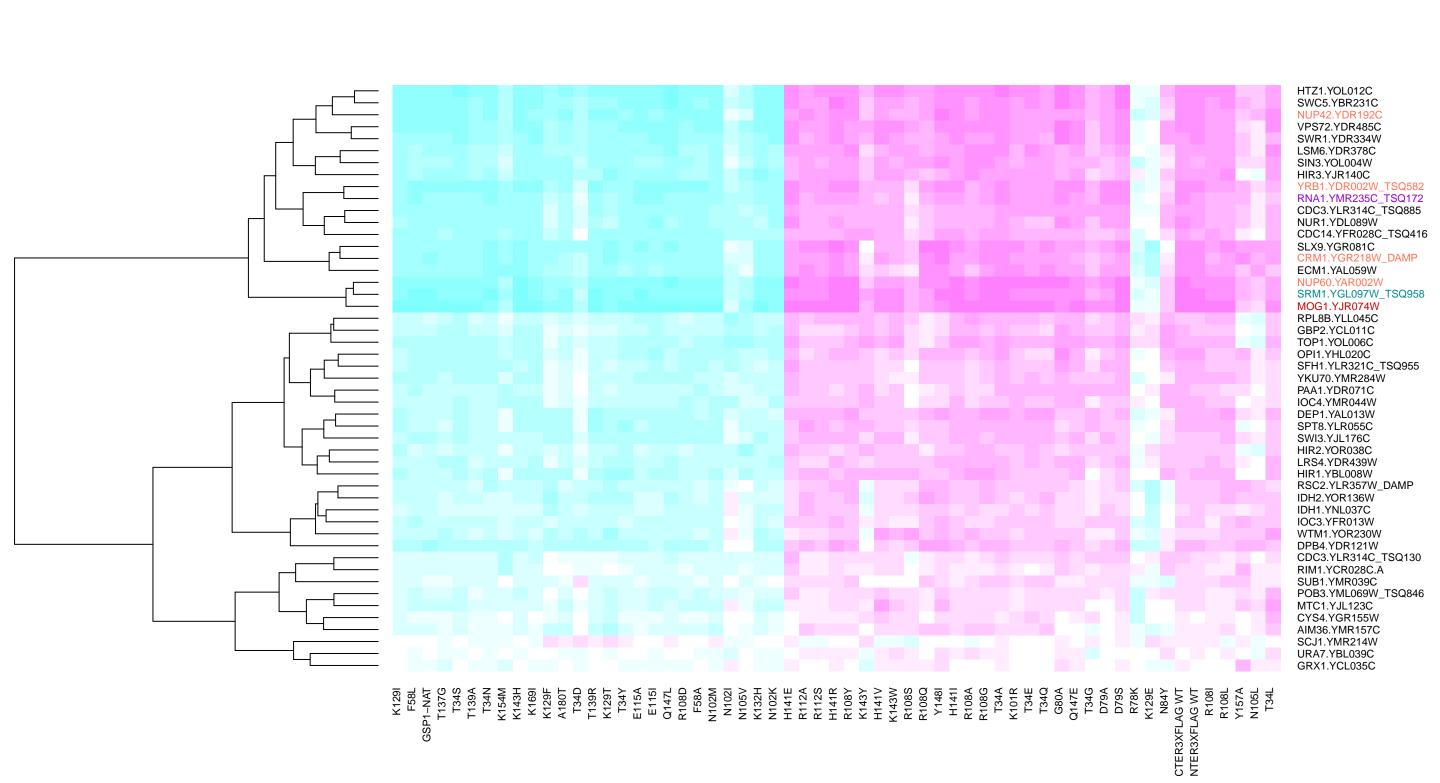
nuclear transport and organization_GO_15_2_all



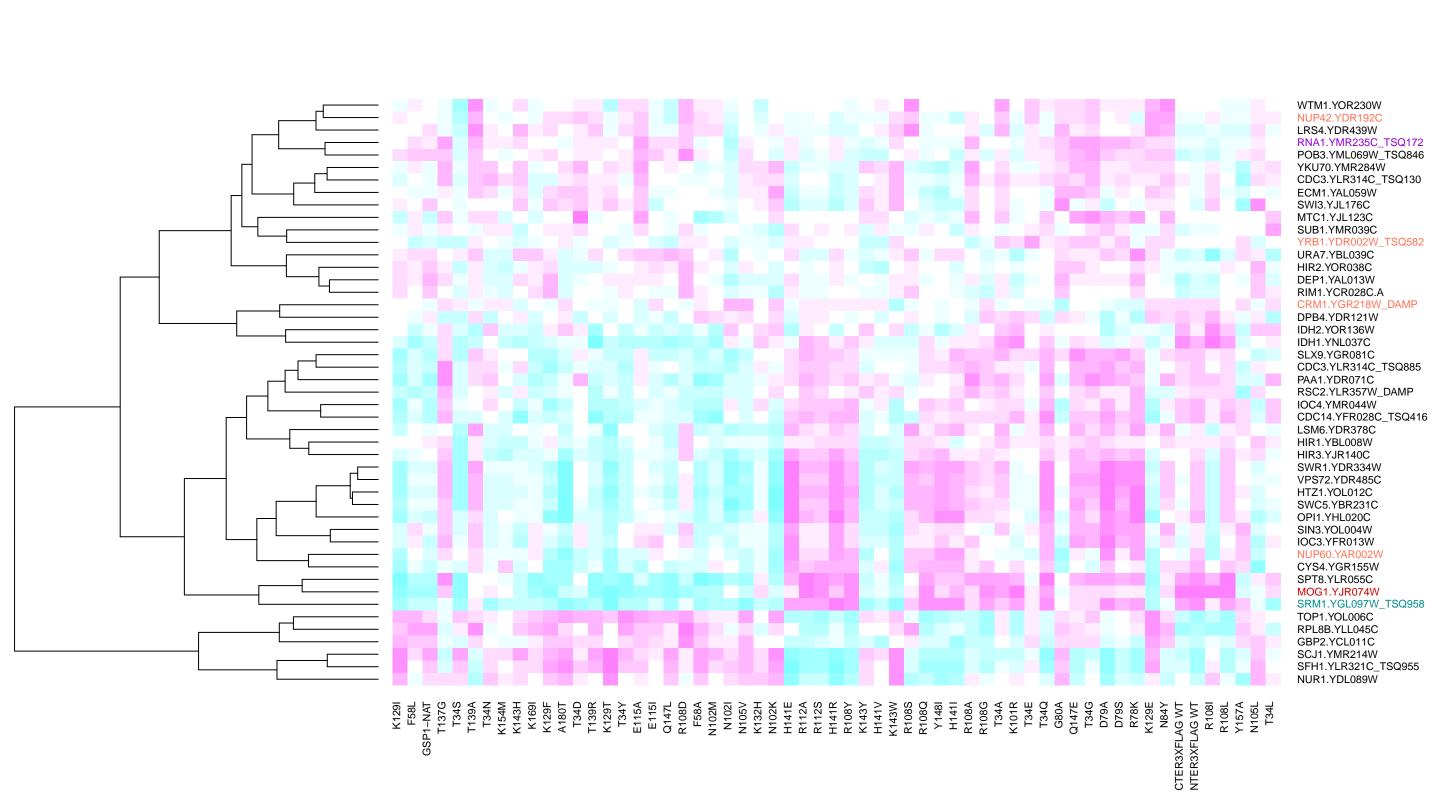
nuclear transport and organization_GO_30_1_all



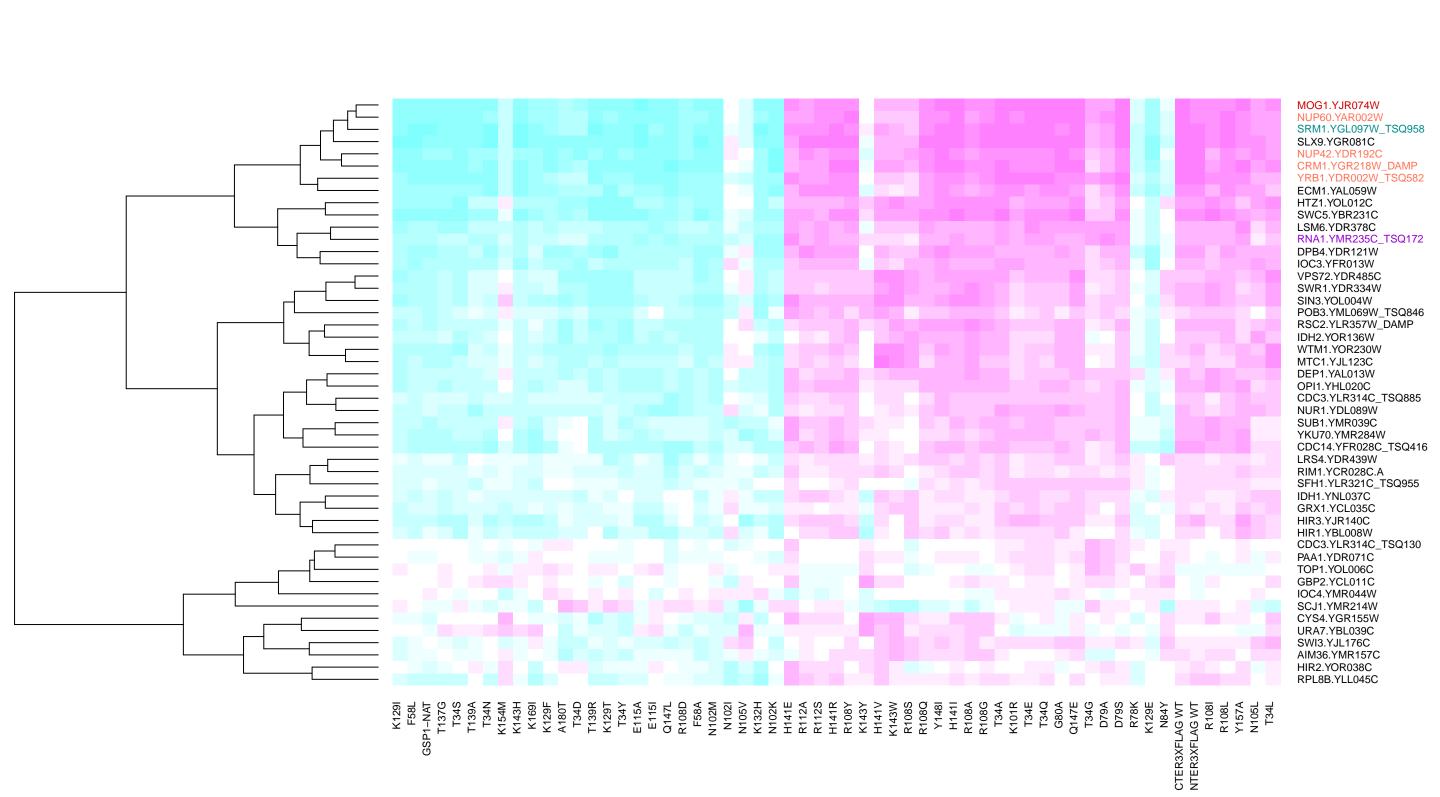
nuclear transport_GO_15_1_mut



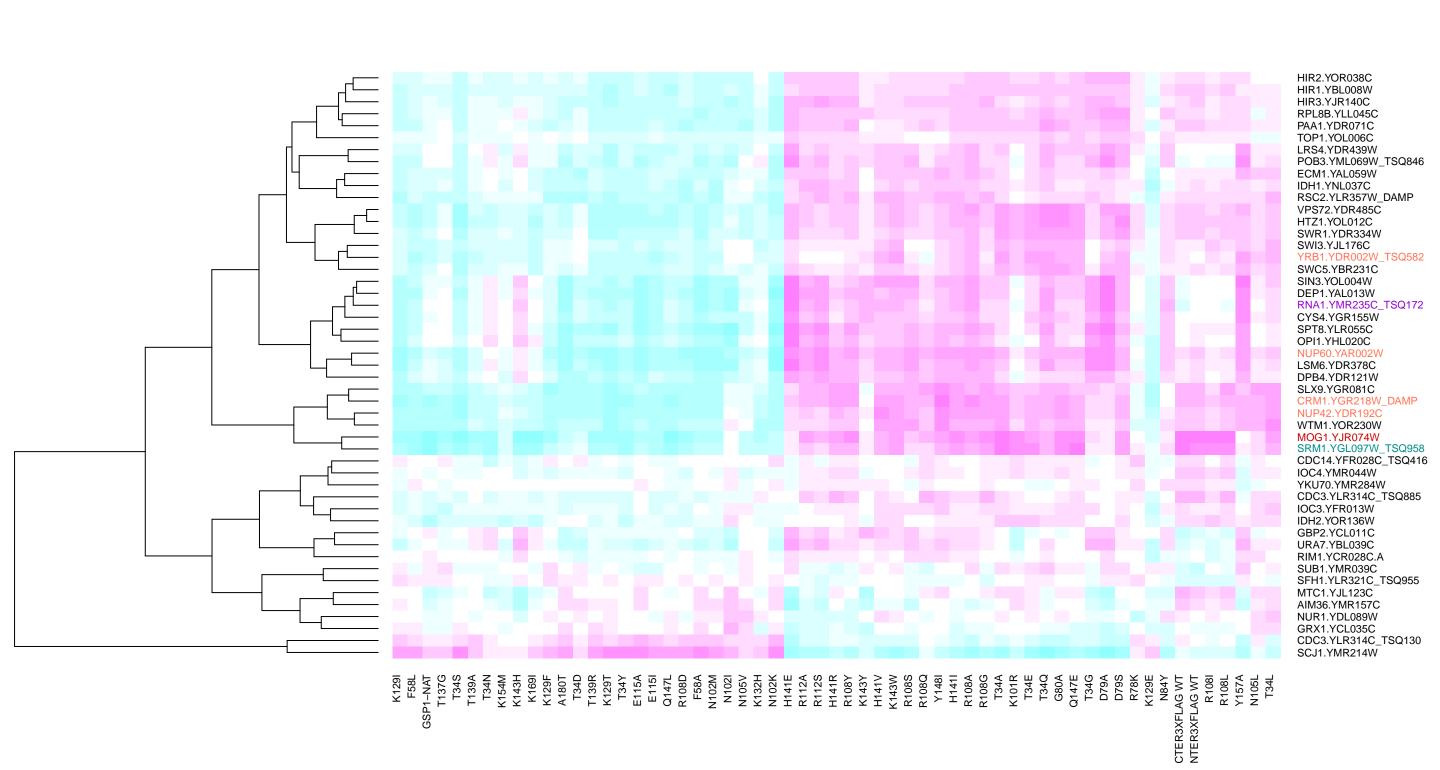
peptidyl-amino acid modification_GO_15_2_mut



protein targeting_GO_15_3_all



chromatin organization_GO_30_1_mut



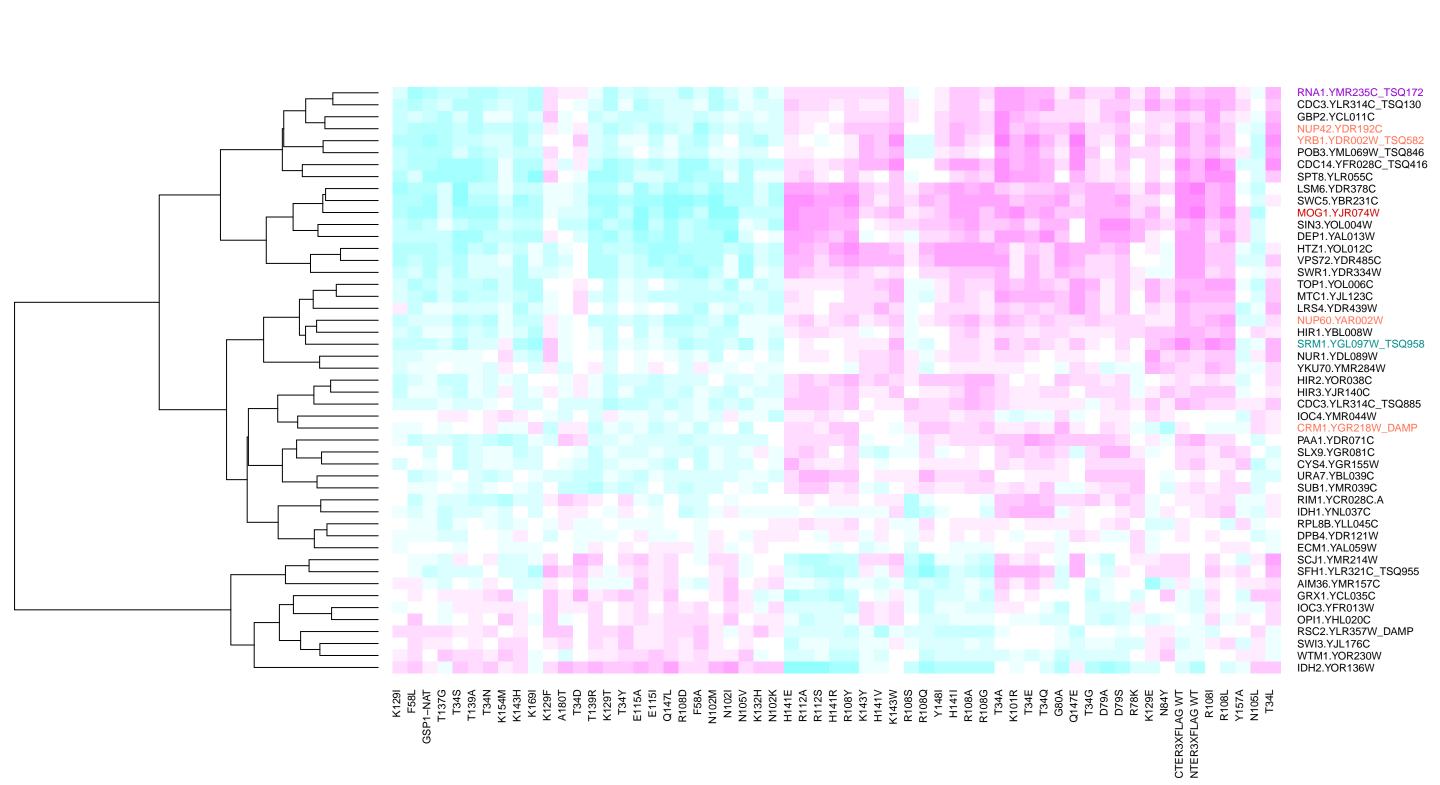
histone modification_GO_15_1_mut



telomere organization



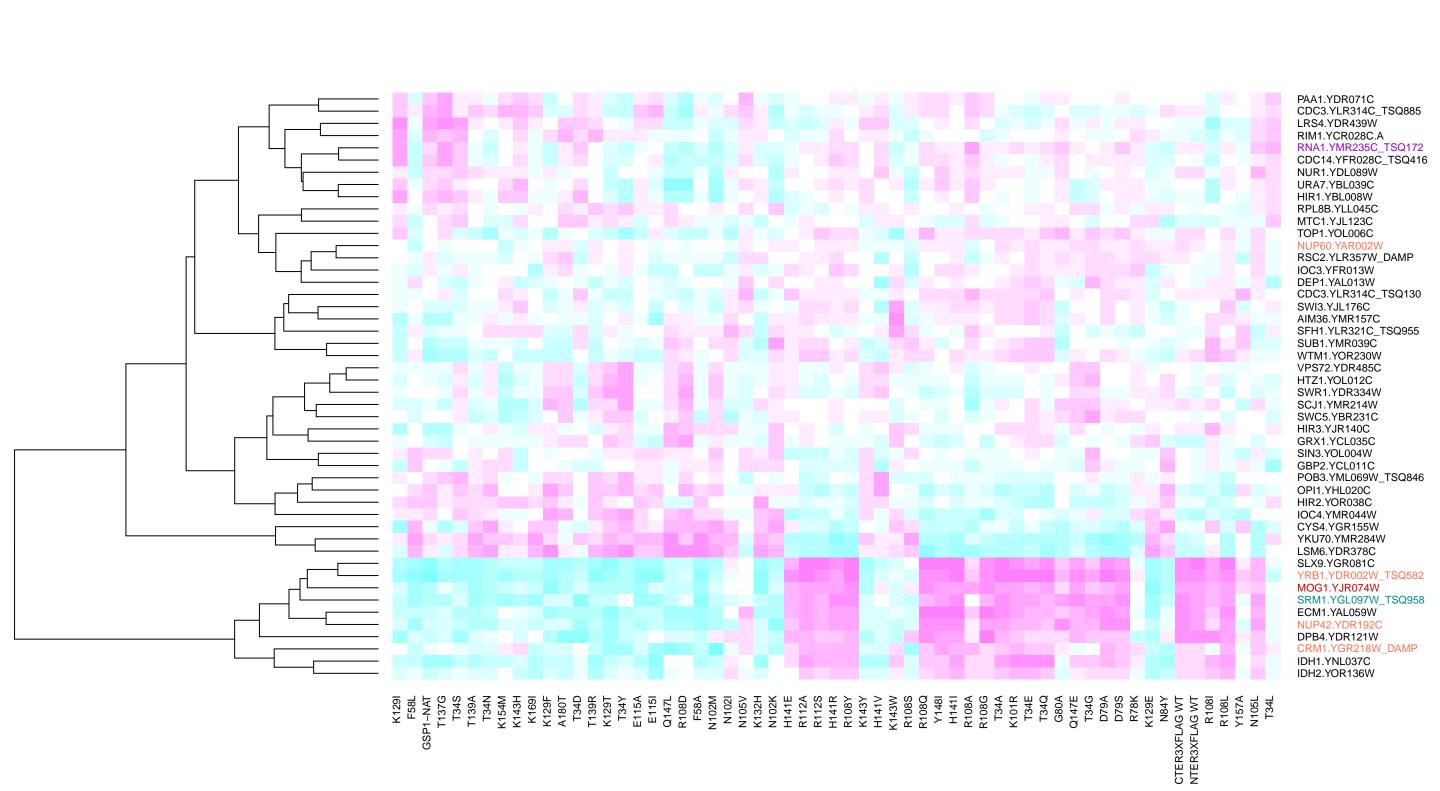
budding_GO_30_1_mut



cytoskeleton organization_GO_15_1_mut



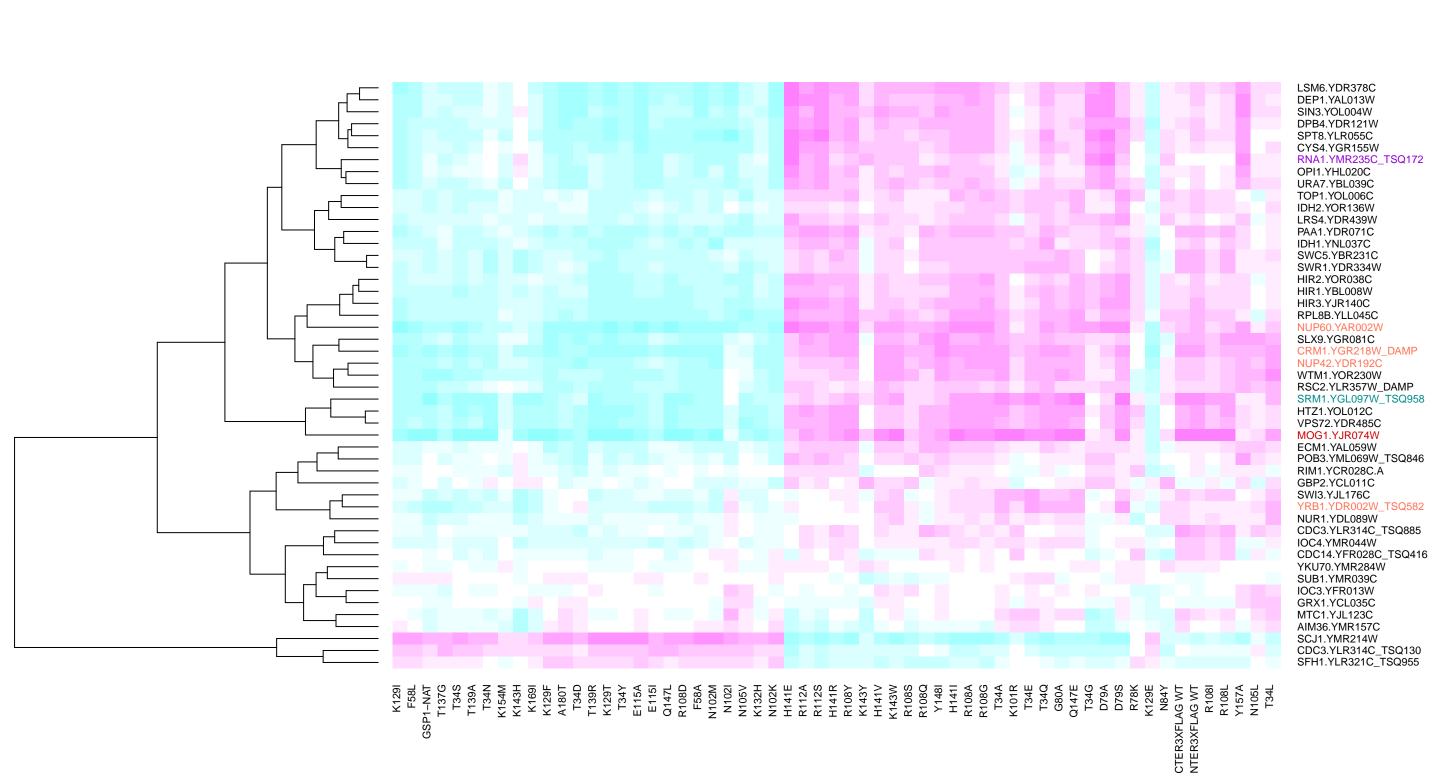
cytoskeleton organization_GO_15_3_all



cytoskeleton organization_GO_30_1_mut

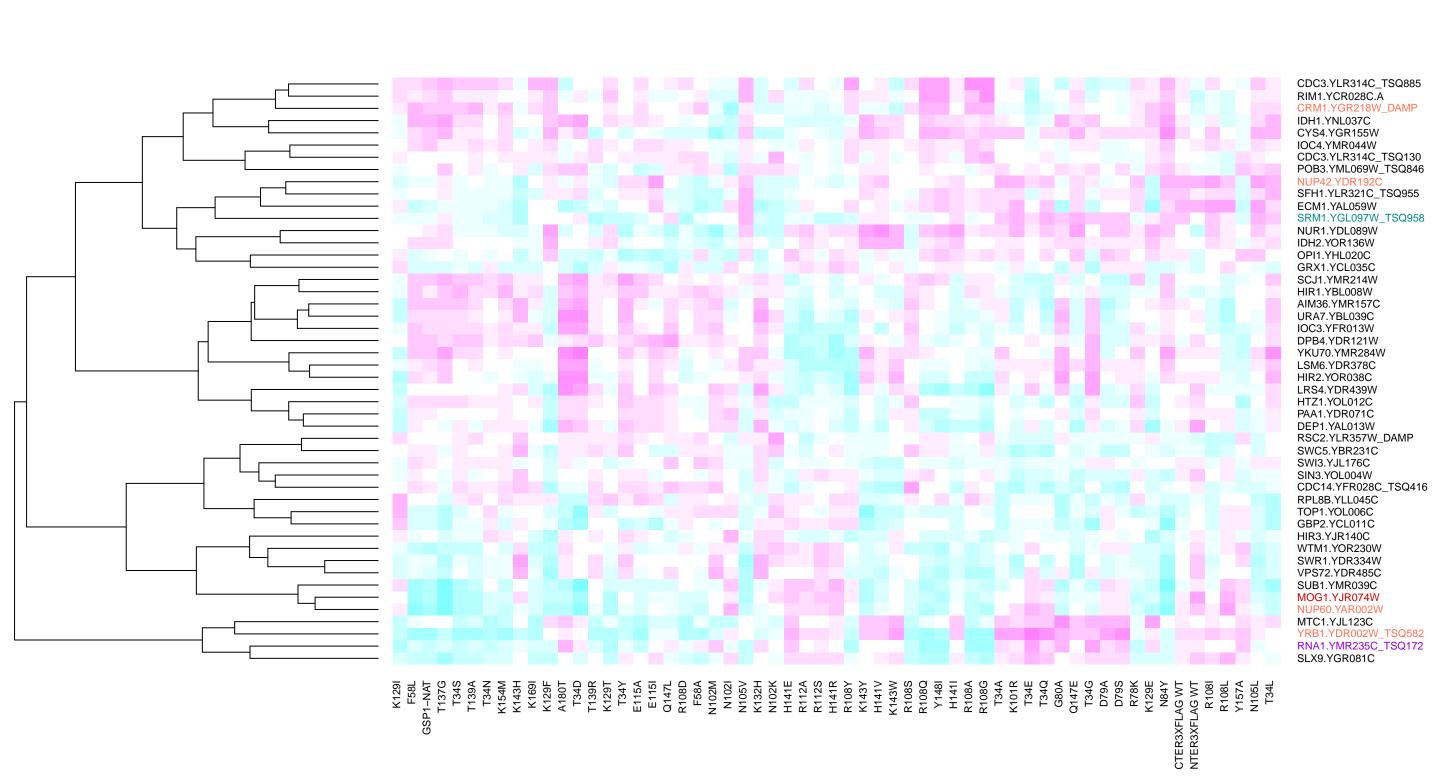


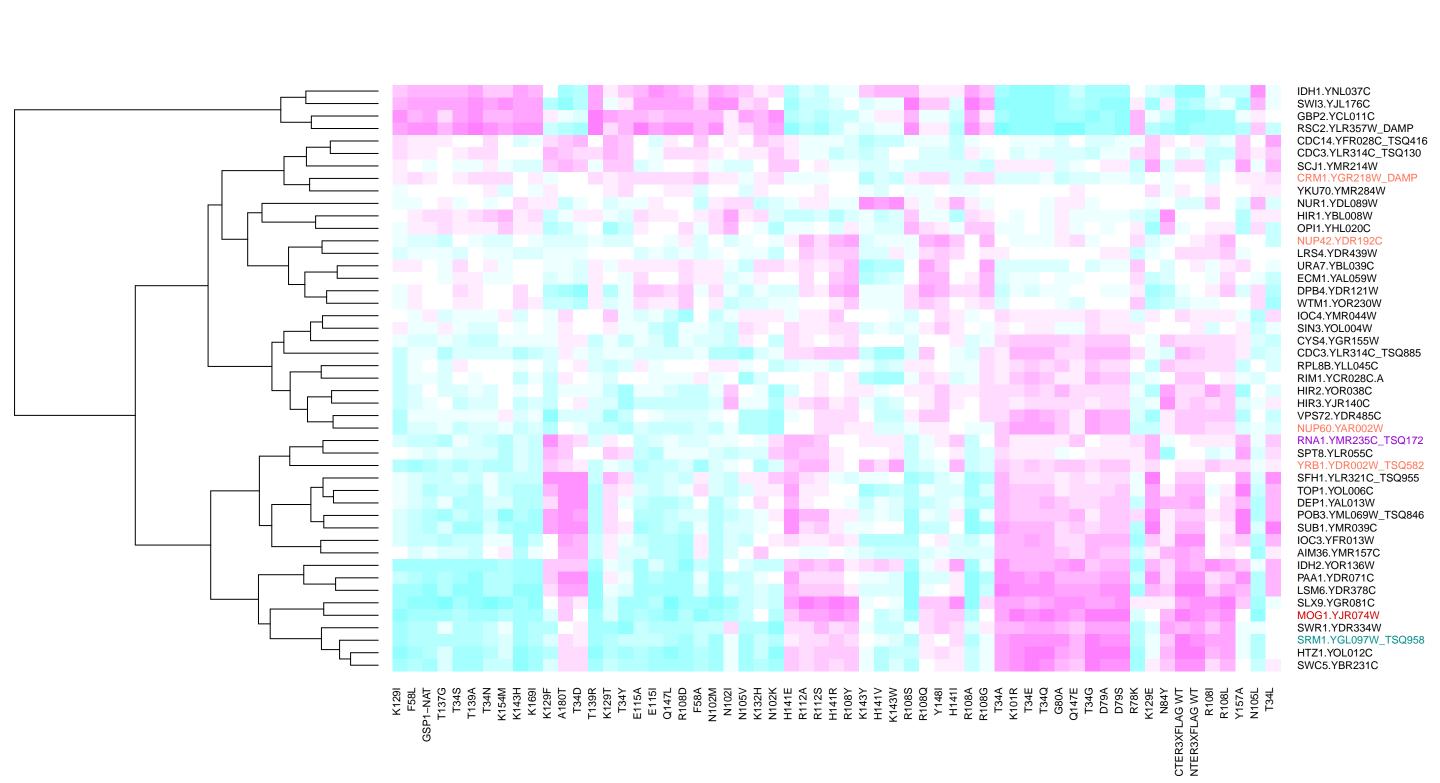
chromatin_GO_30_3_mut



regulation of cell cycle_GO_15_2_mut





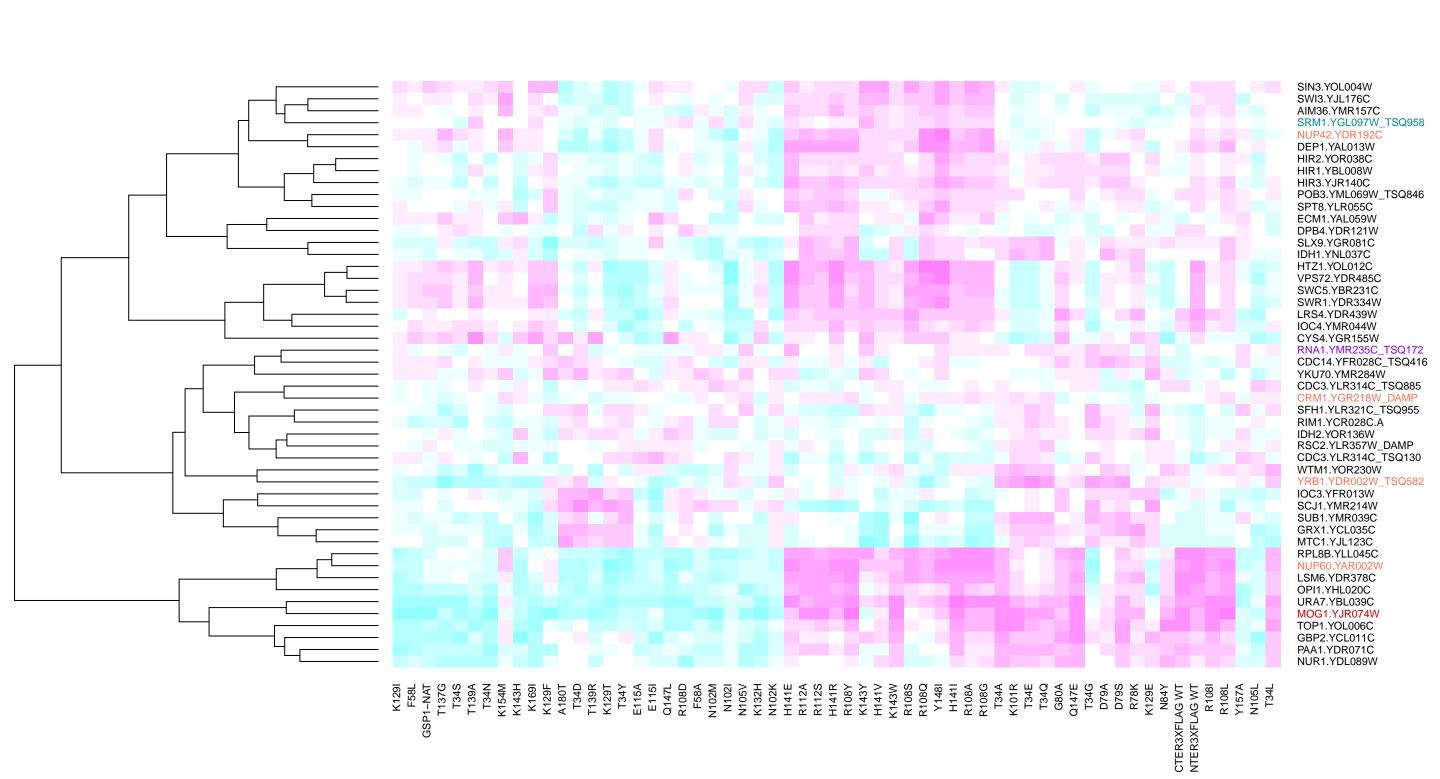




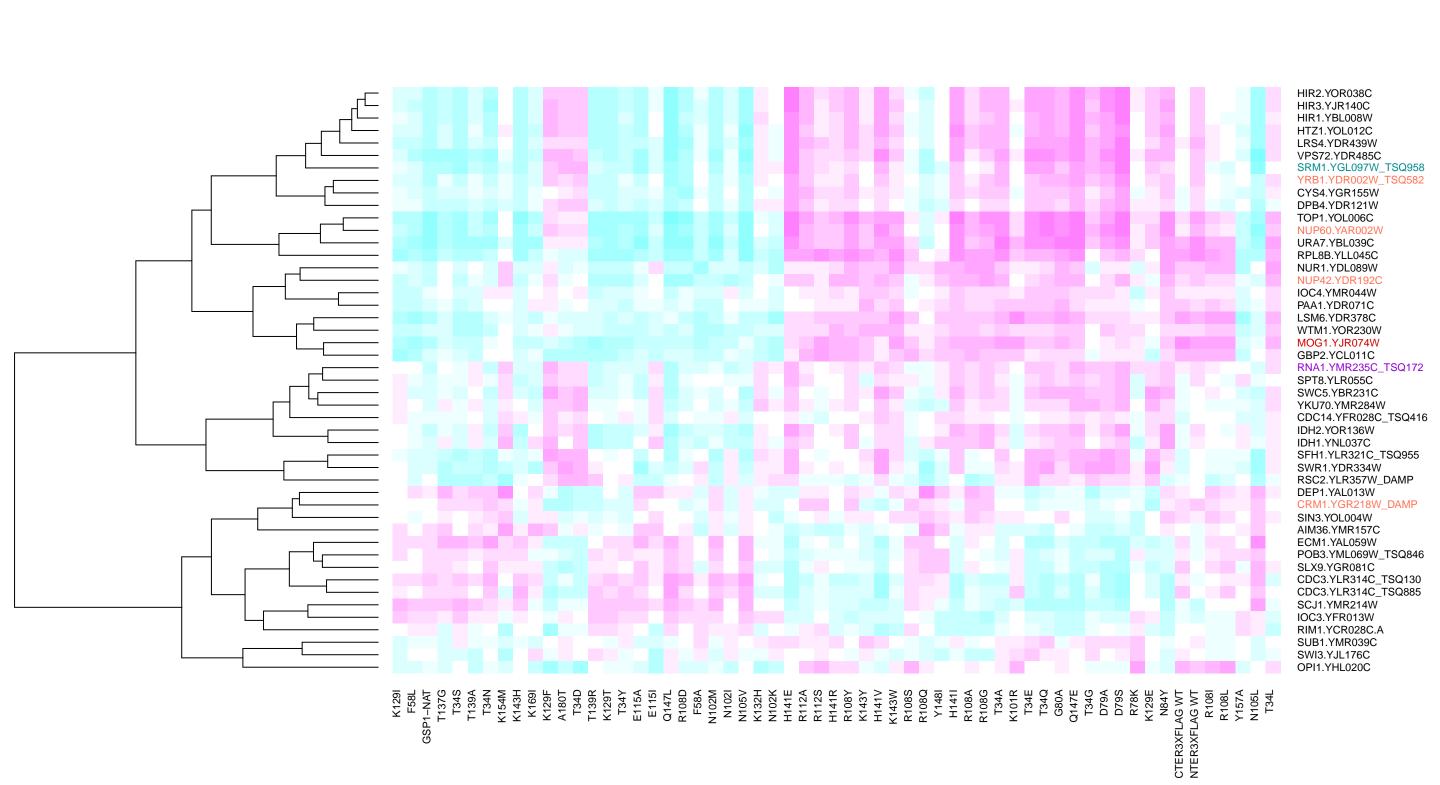
chromatin_GO_15_3_mut



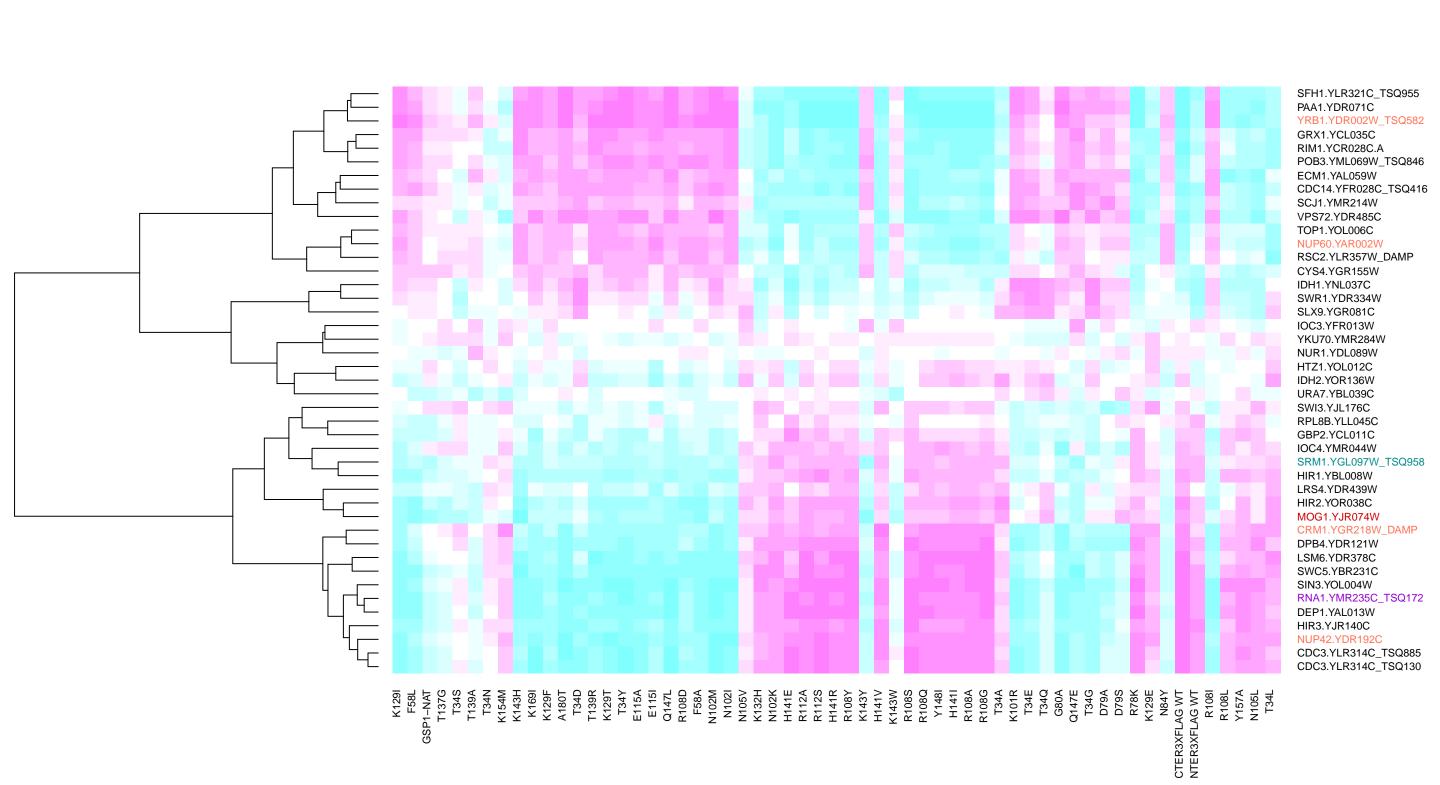
DNA-templated transcription, elongation_GO_15_1_all



transcription and mRNA processing_GO_15_3_all



RNA modification_GO_15_1_mut



transcription and mRNA processing_GO_30_1_all



chromosome



whole_library_15_24_mut



cytoplasmic translation

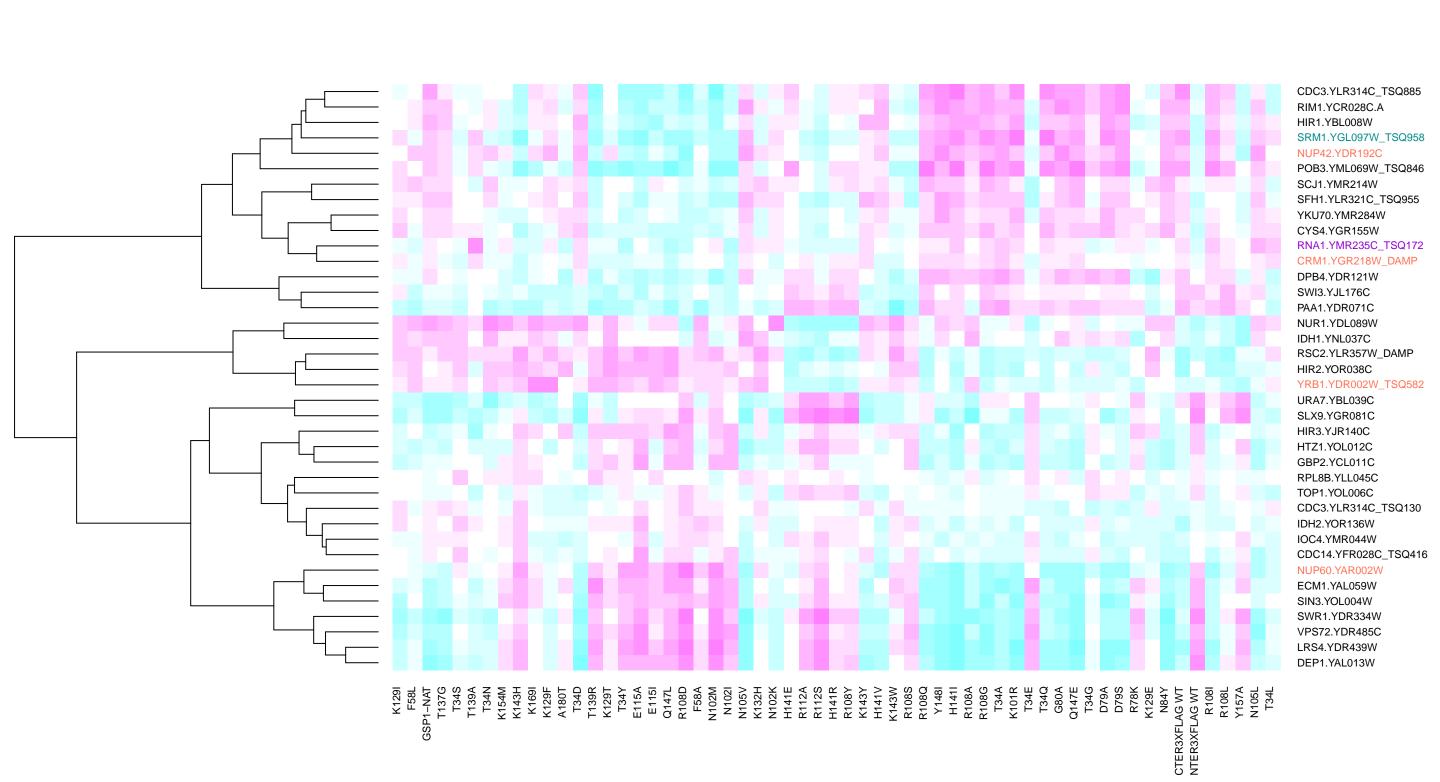


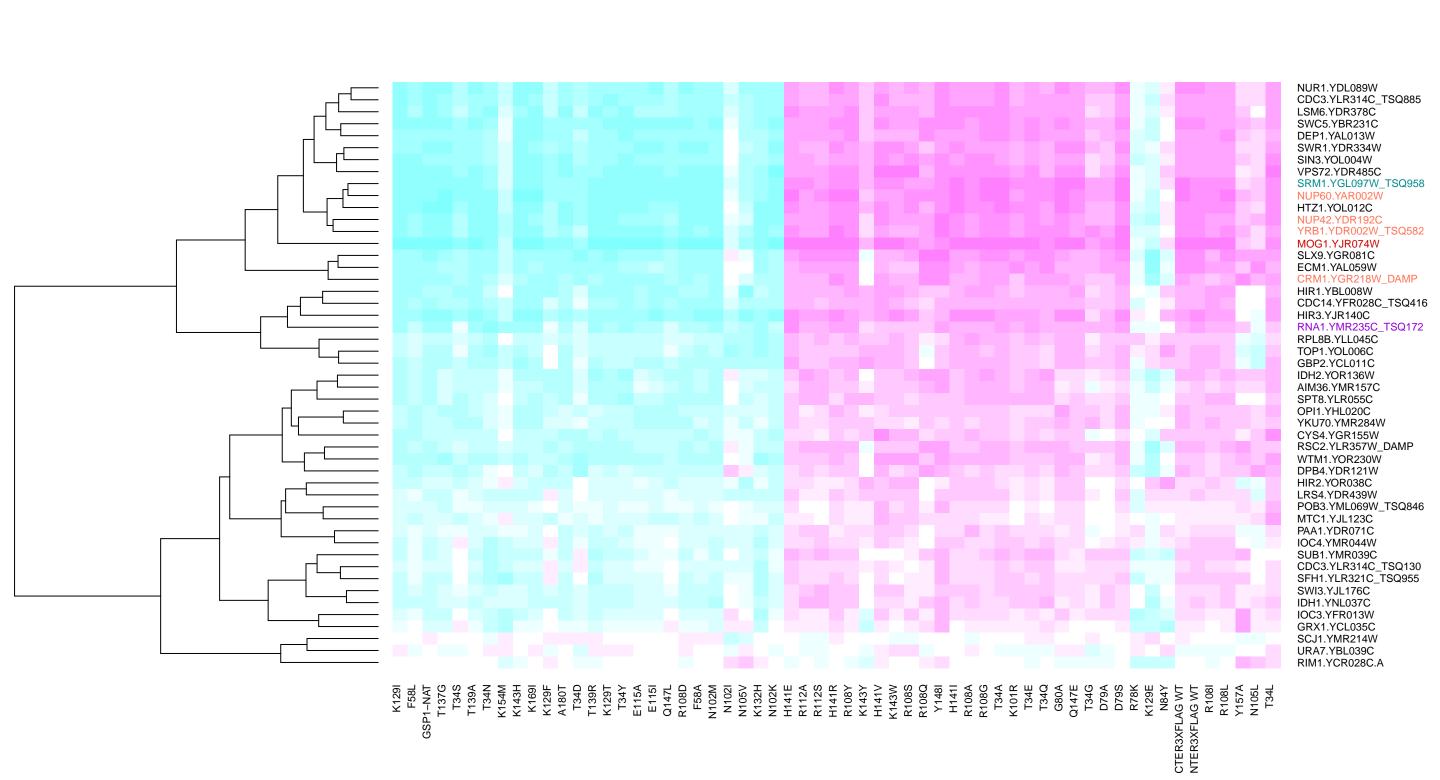
ribosome



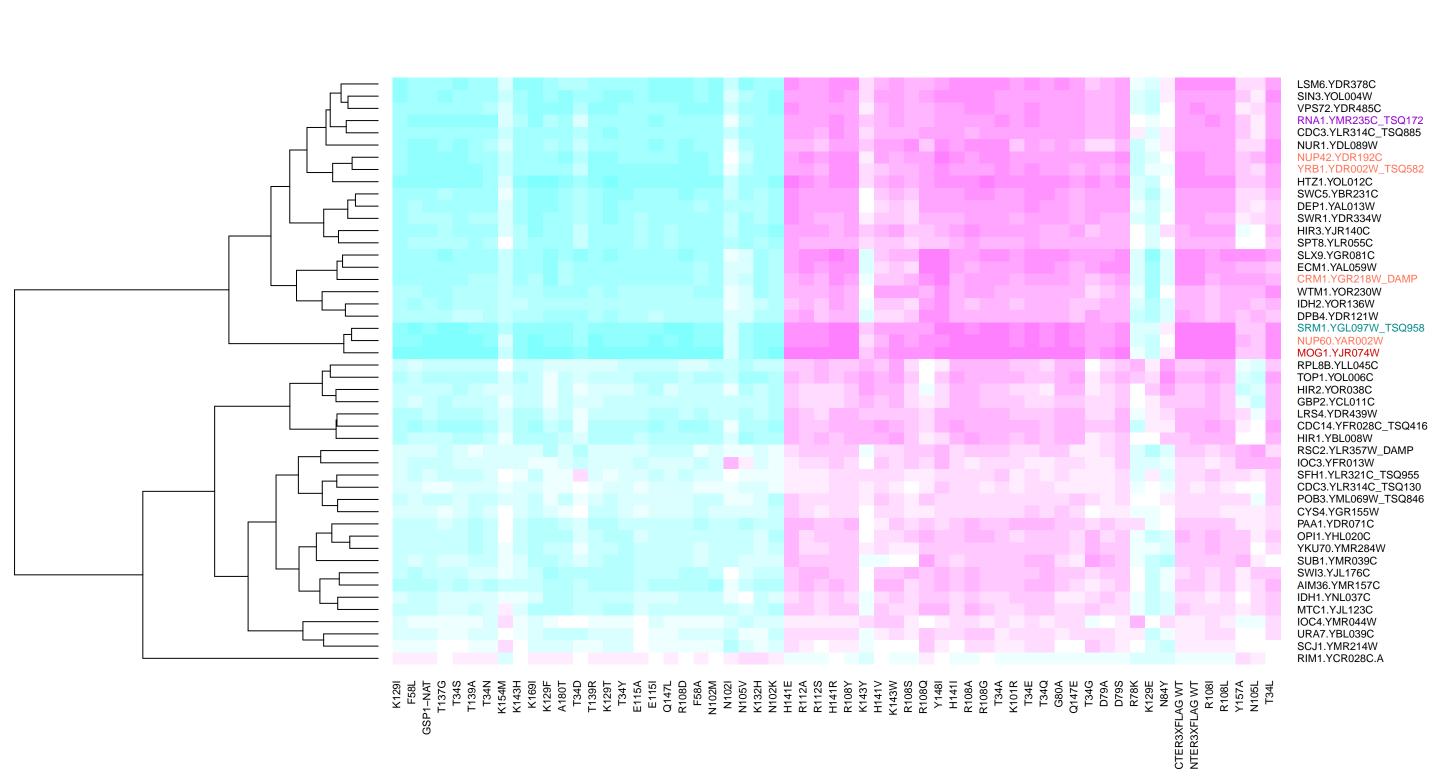


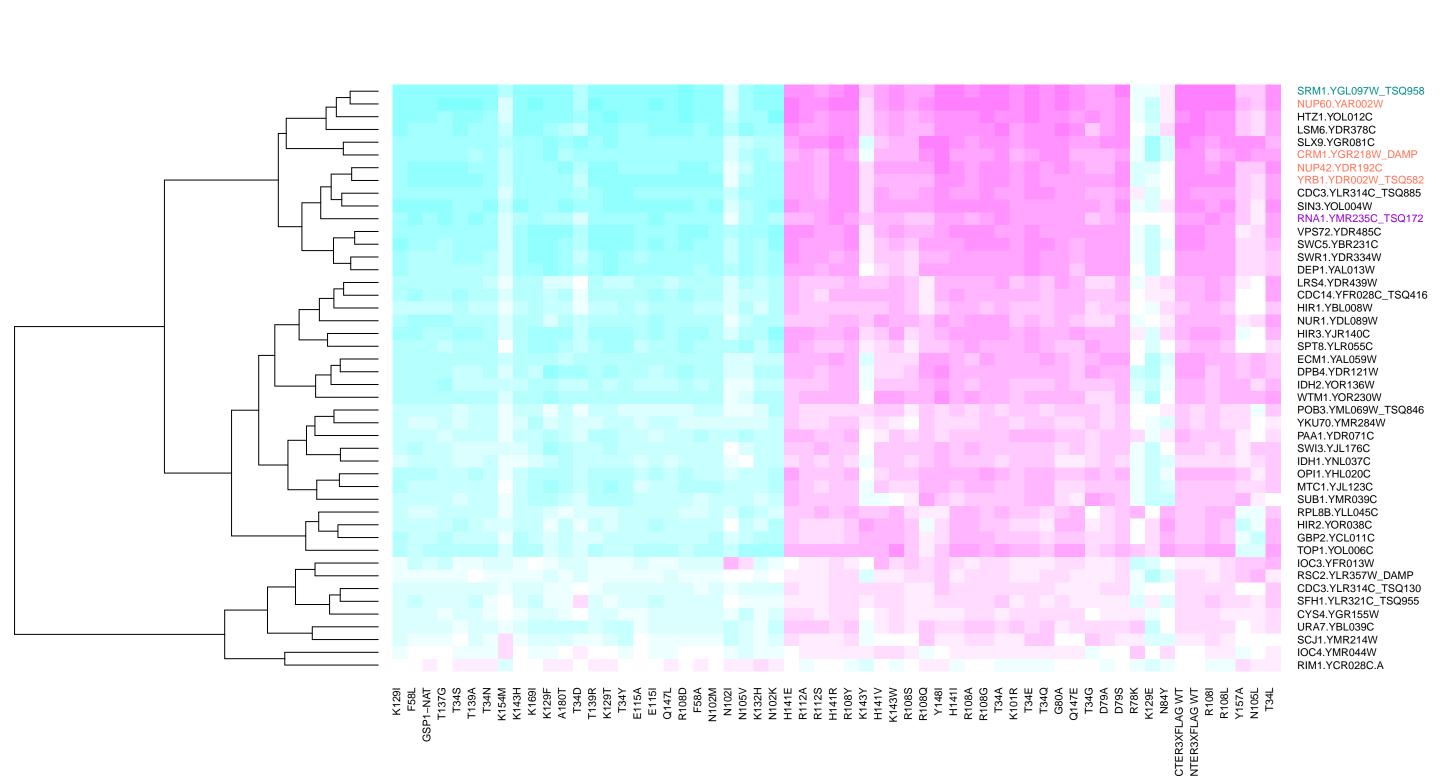
structural constituent of ribosome





whole_library_15_14_mut

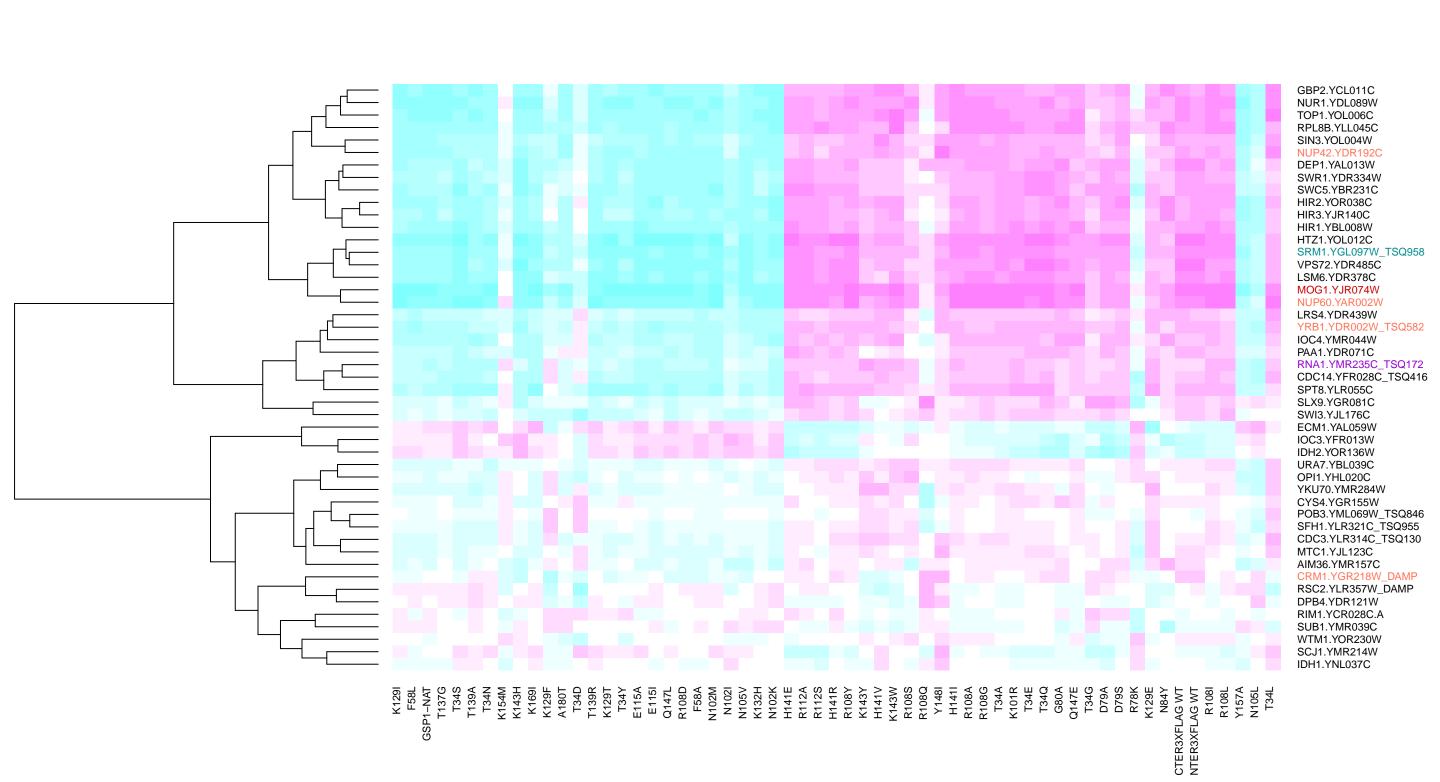




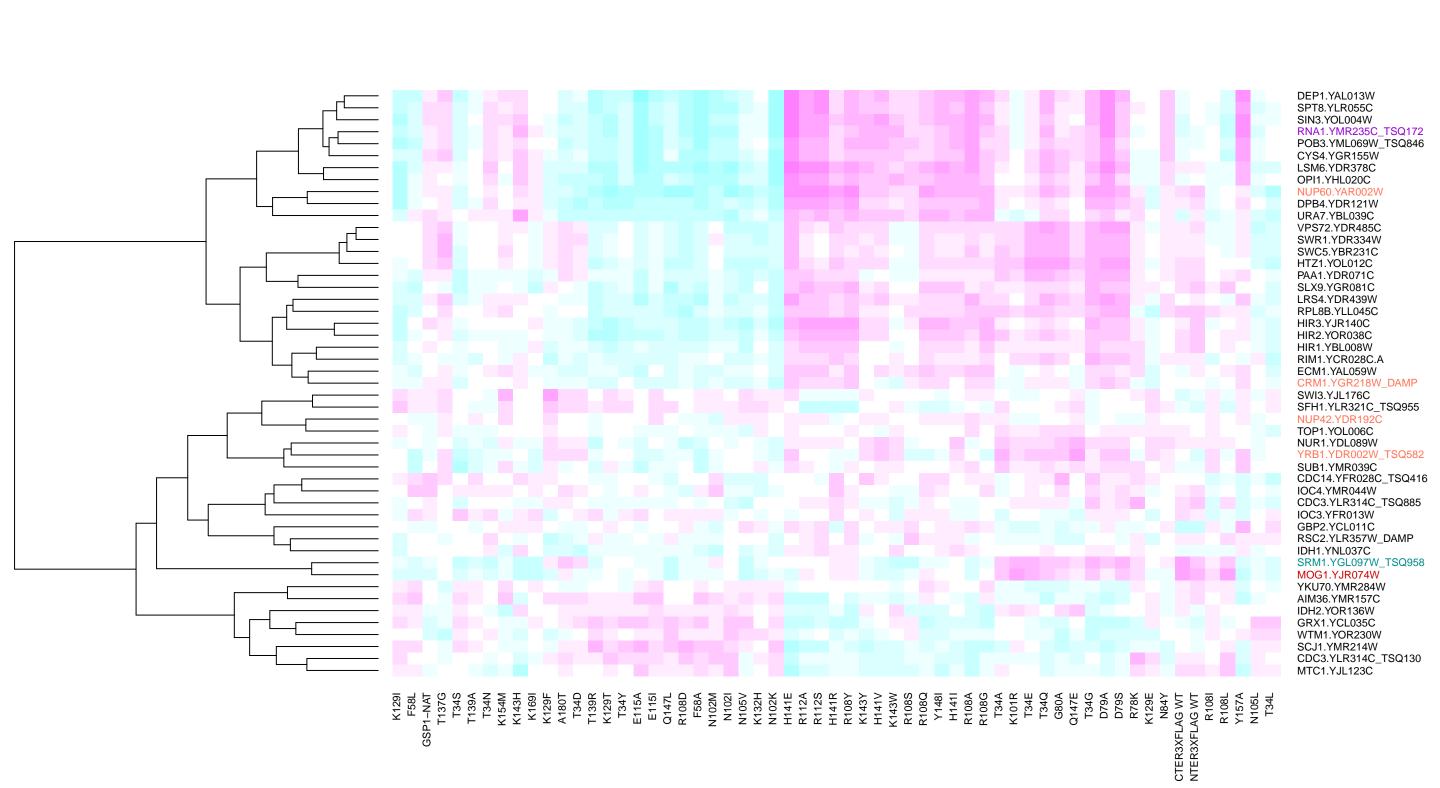
histone modification_GO_15_1_all

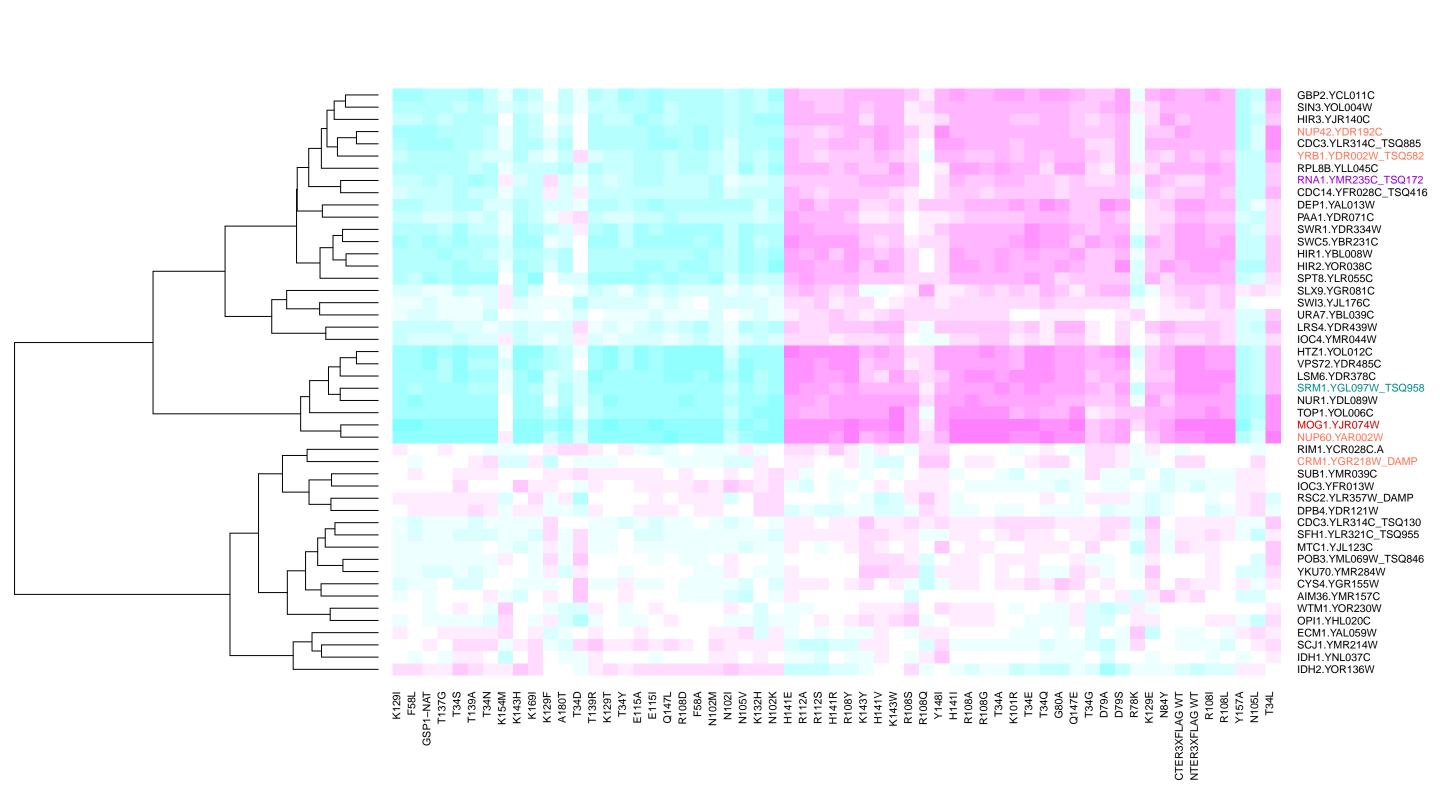


cell cycle_GO_15_9_mut

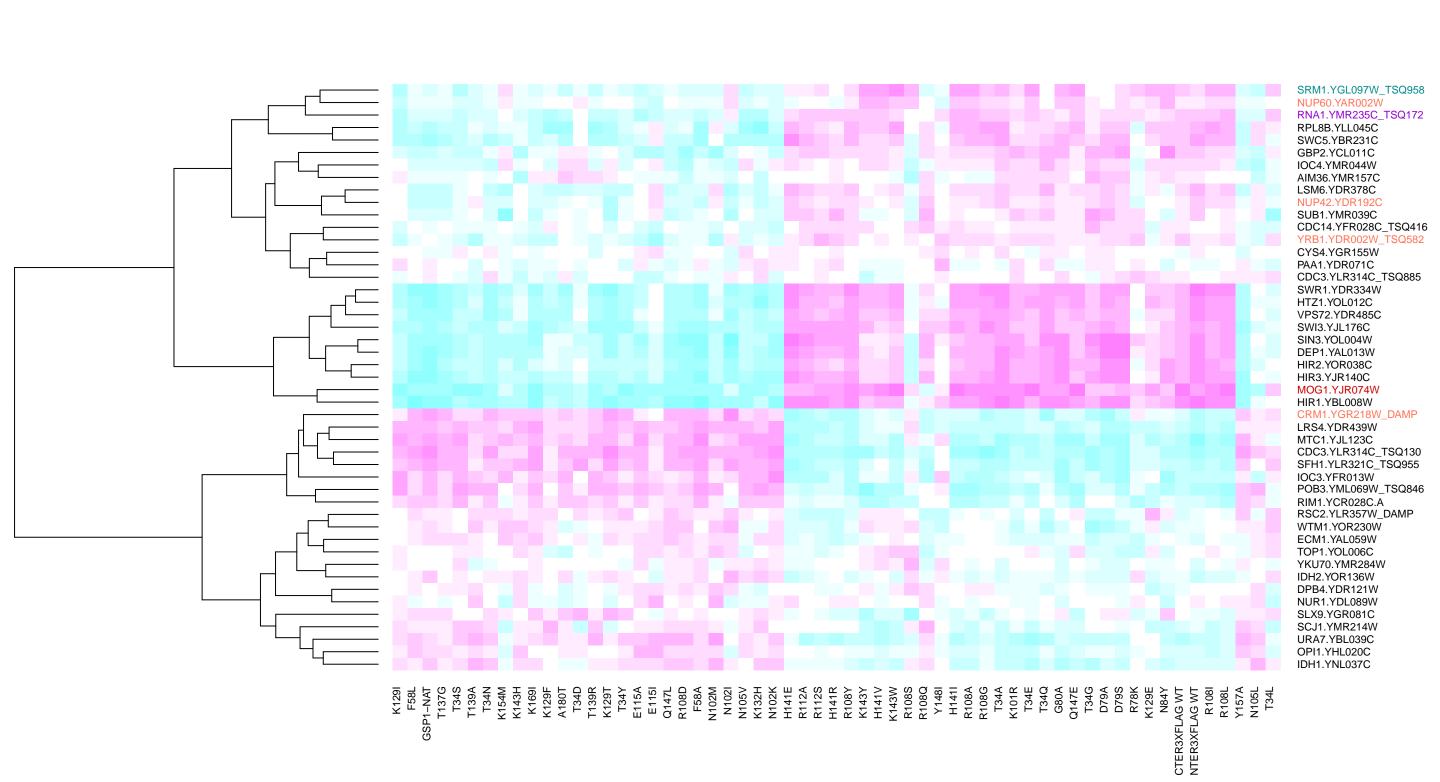


chromosome_GO_30_1_mut





proteolysis involved in cellular protein catabolic process_GO_15_2_mut

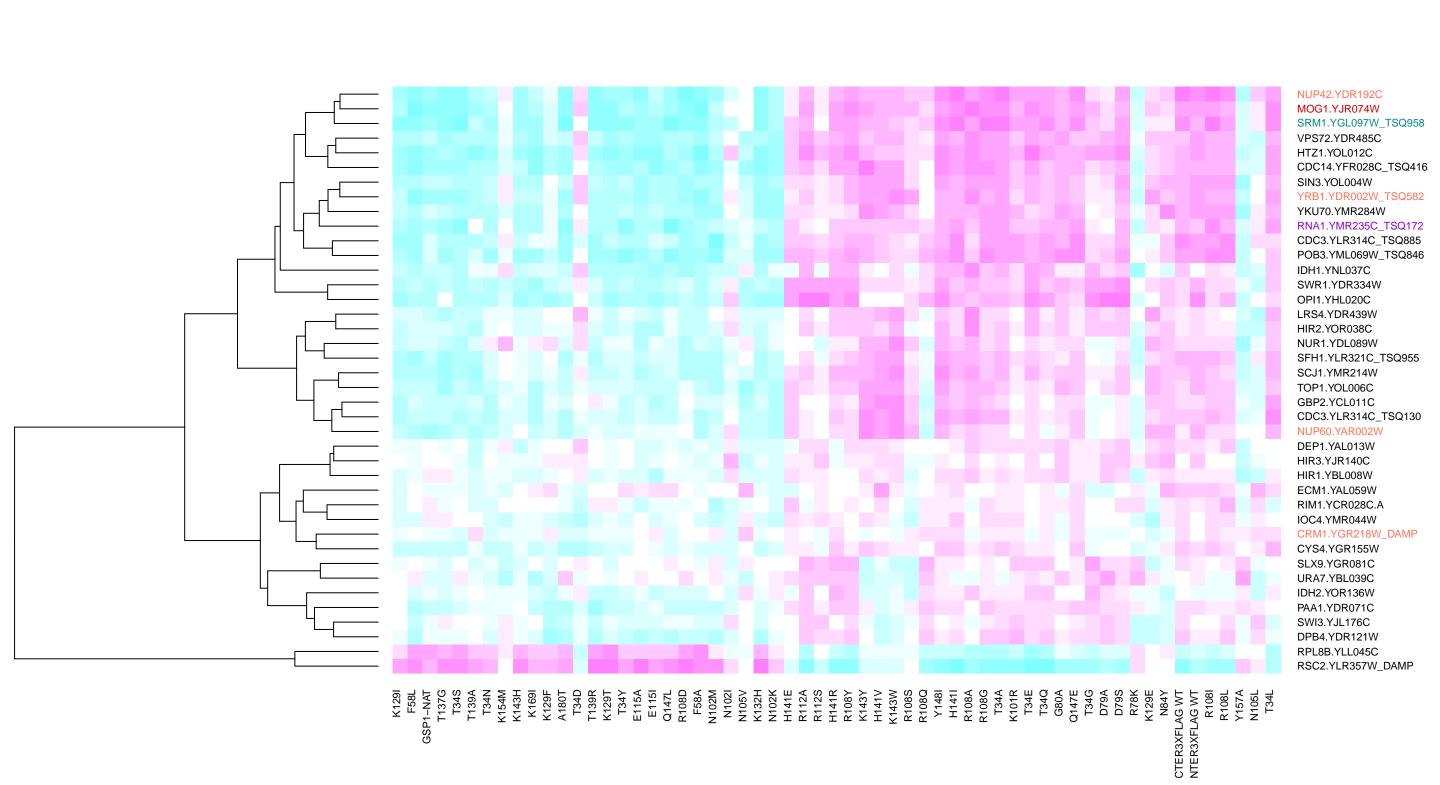




cytoplasmic translation_GO_15_1_all



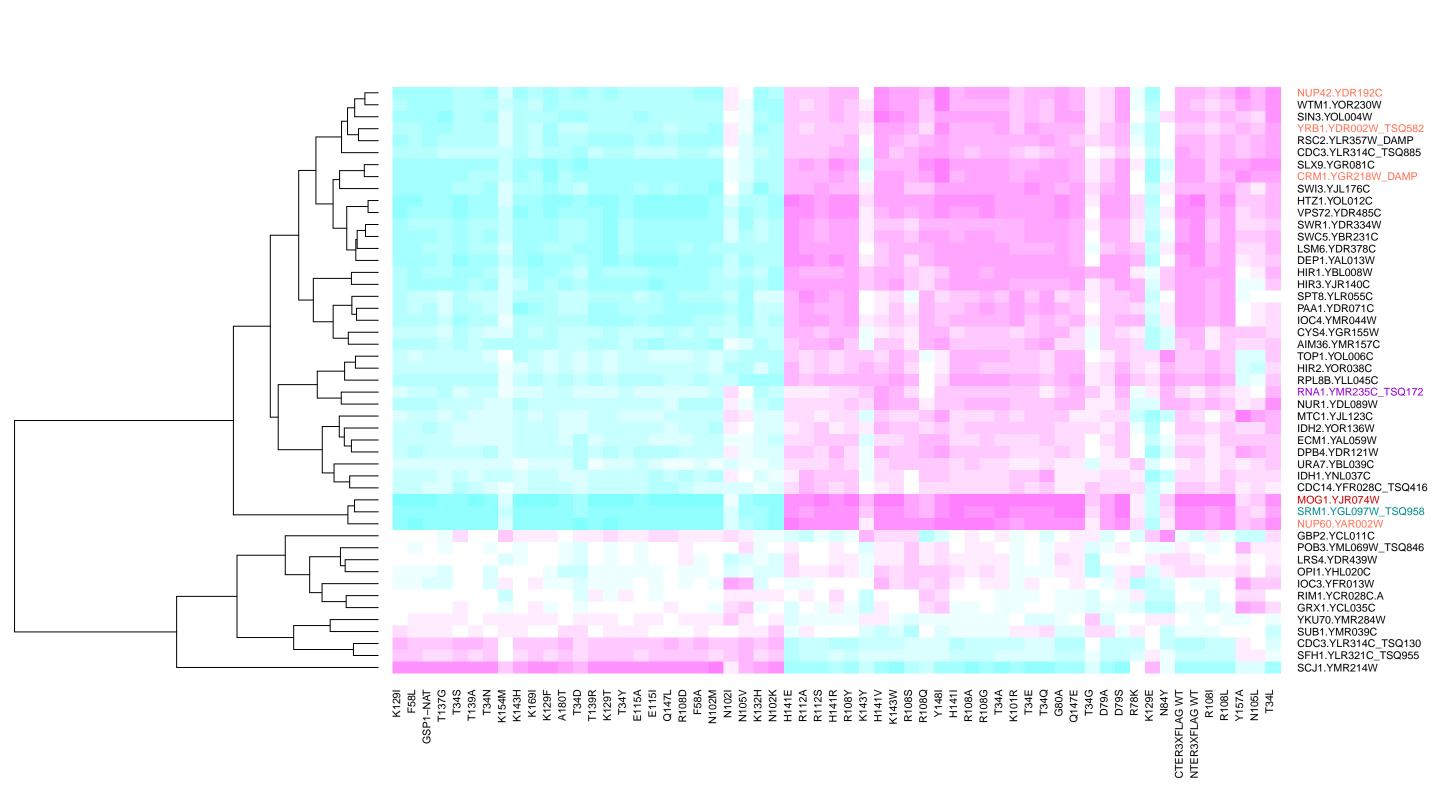
ribosomes and translation_GO_15_2_mut



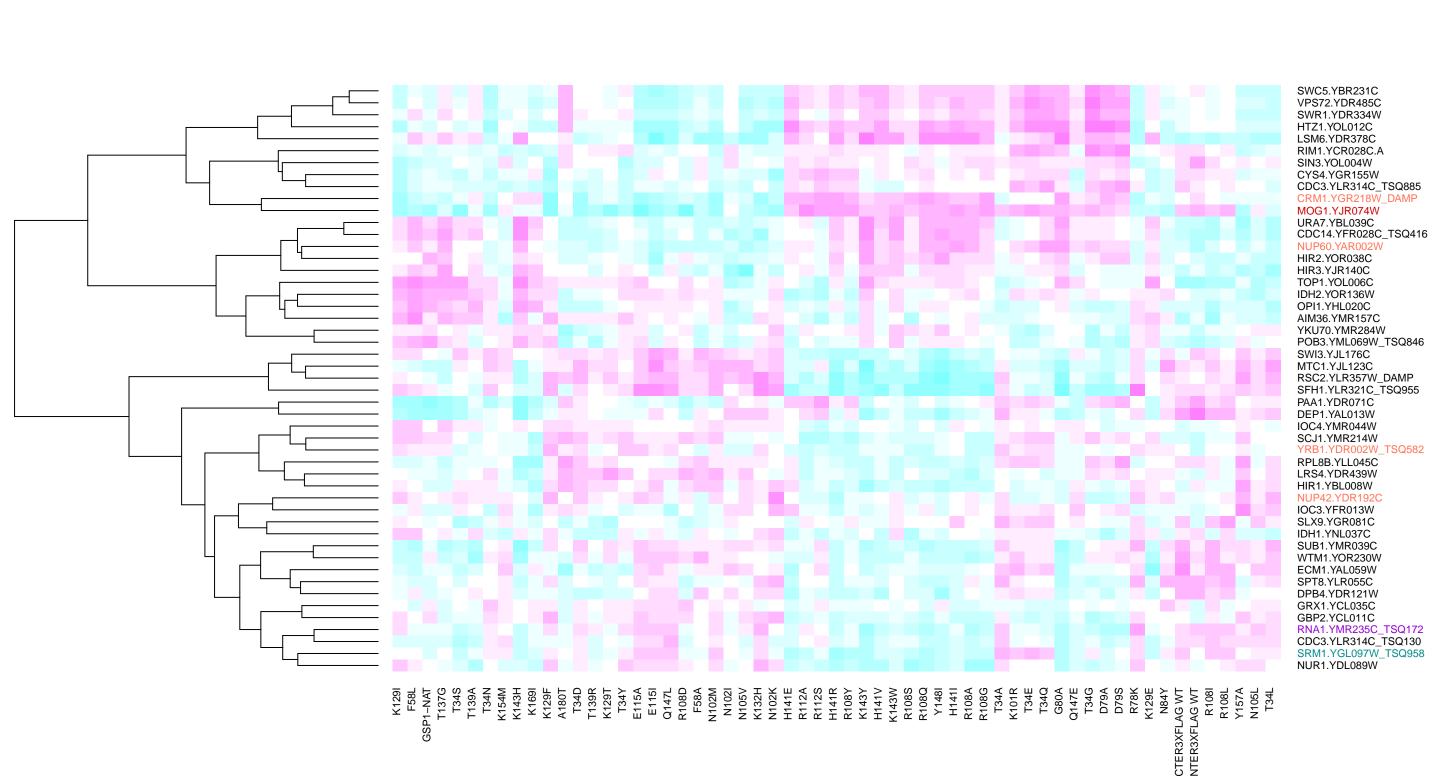
transcription and mRNA processing_GO_15_1_all



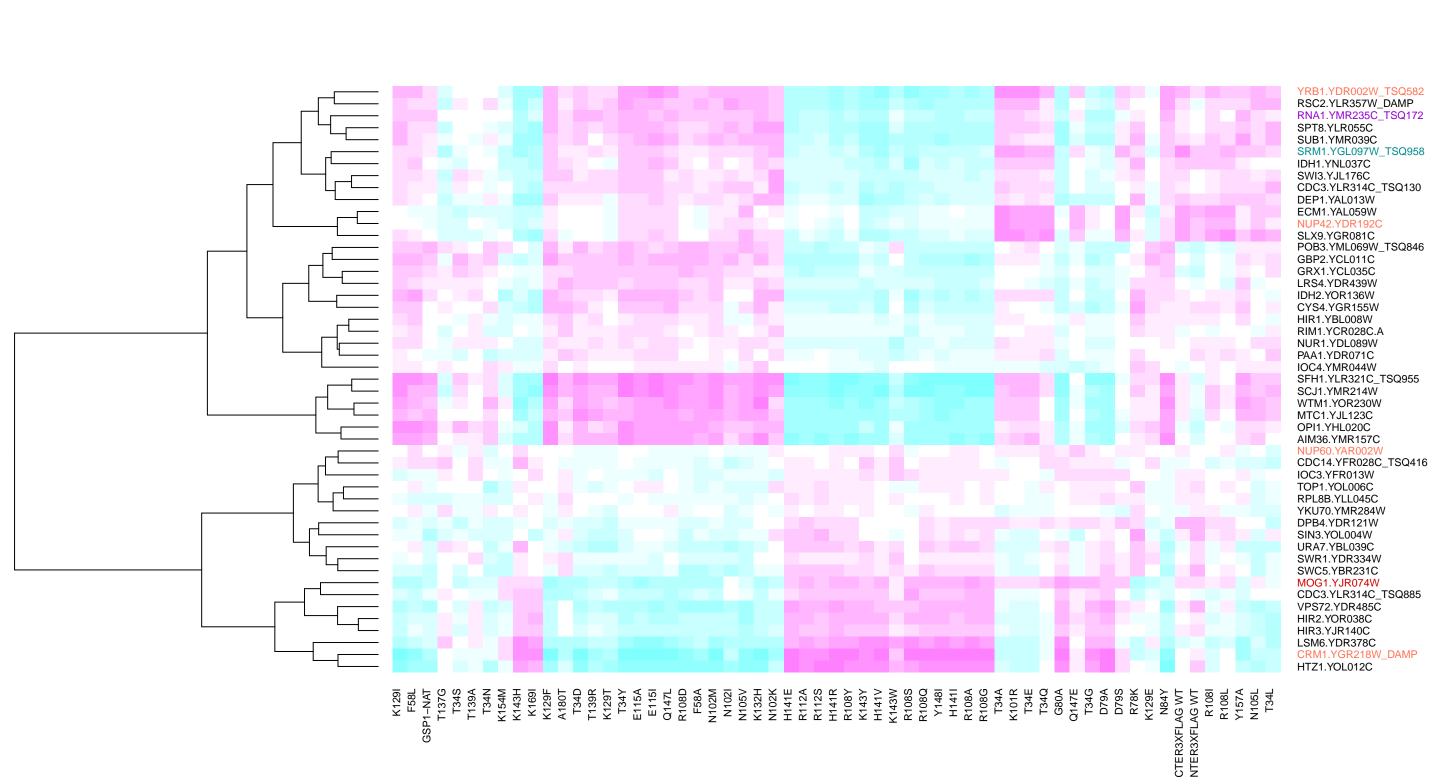
chromatin_GO_15_7_mut



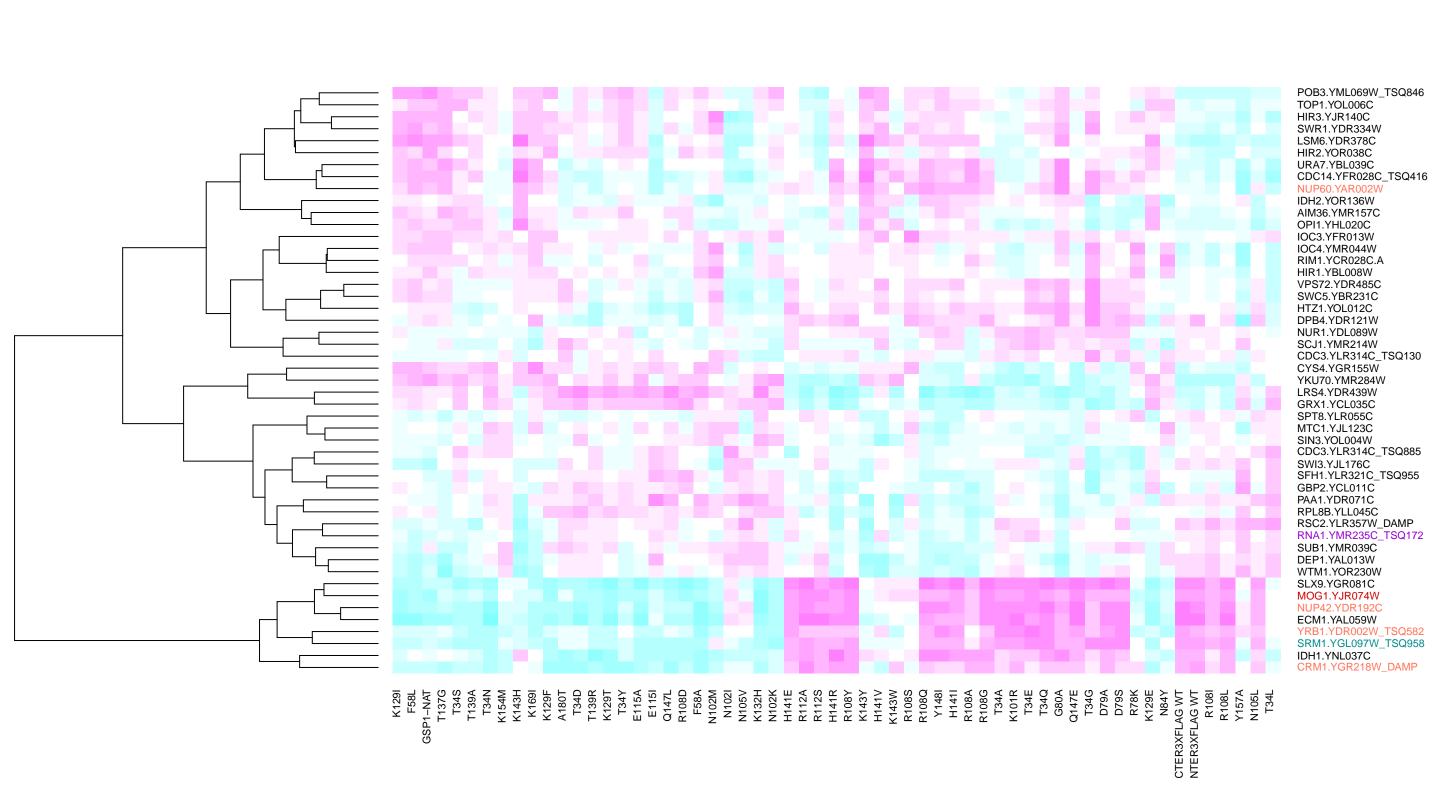
chromosome segregation_GO_15_1_all

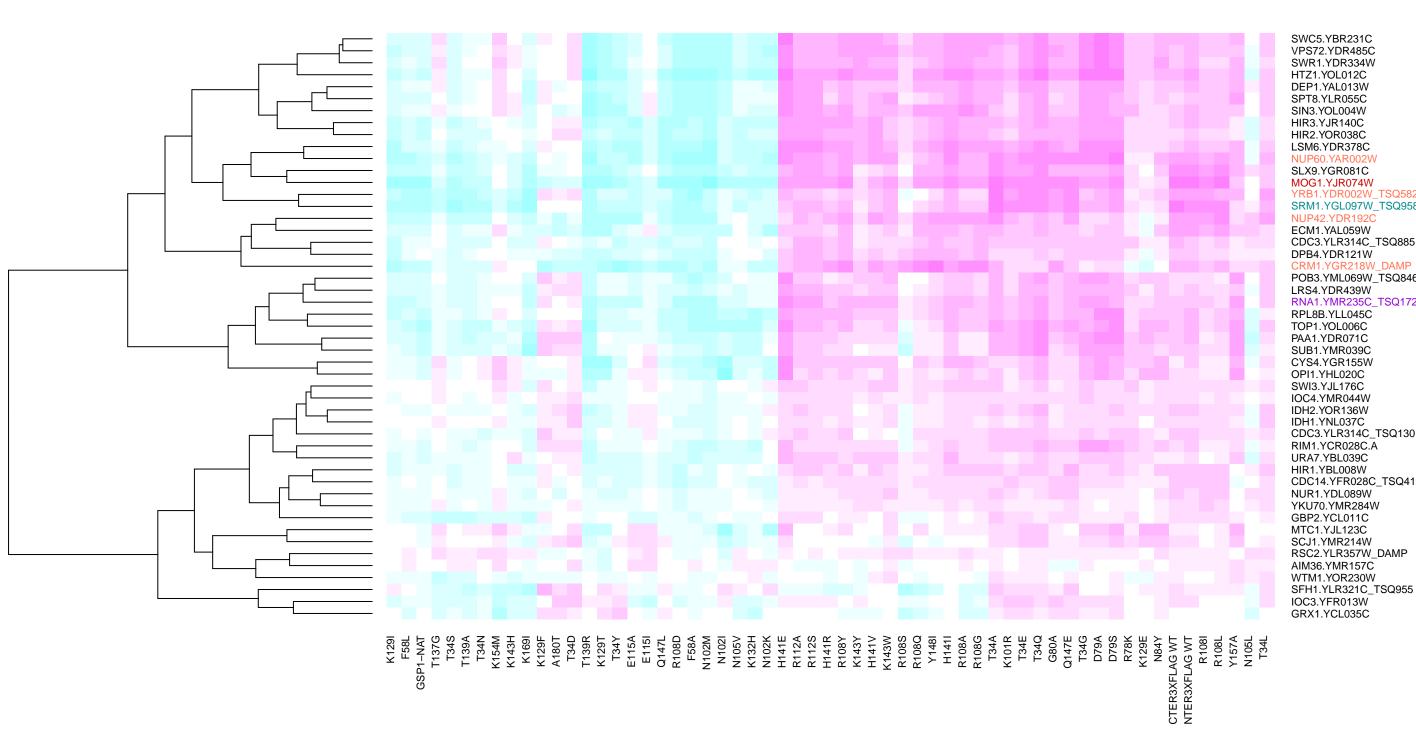


cytoskeleton and microtubules_GO_15_2_mut



cytoskeleton and microtubules_GO_15_3_all



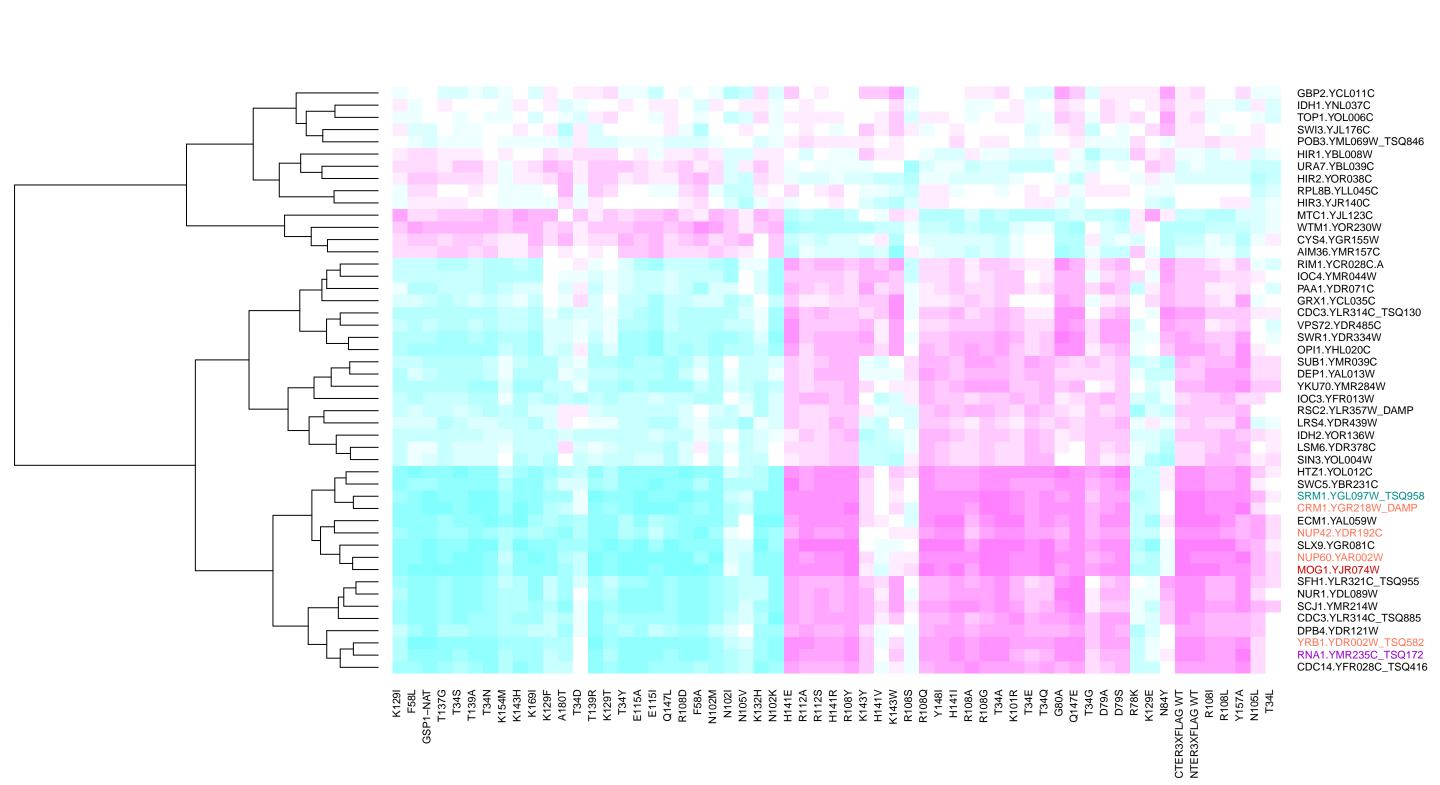


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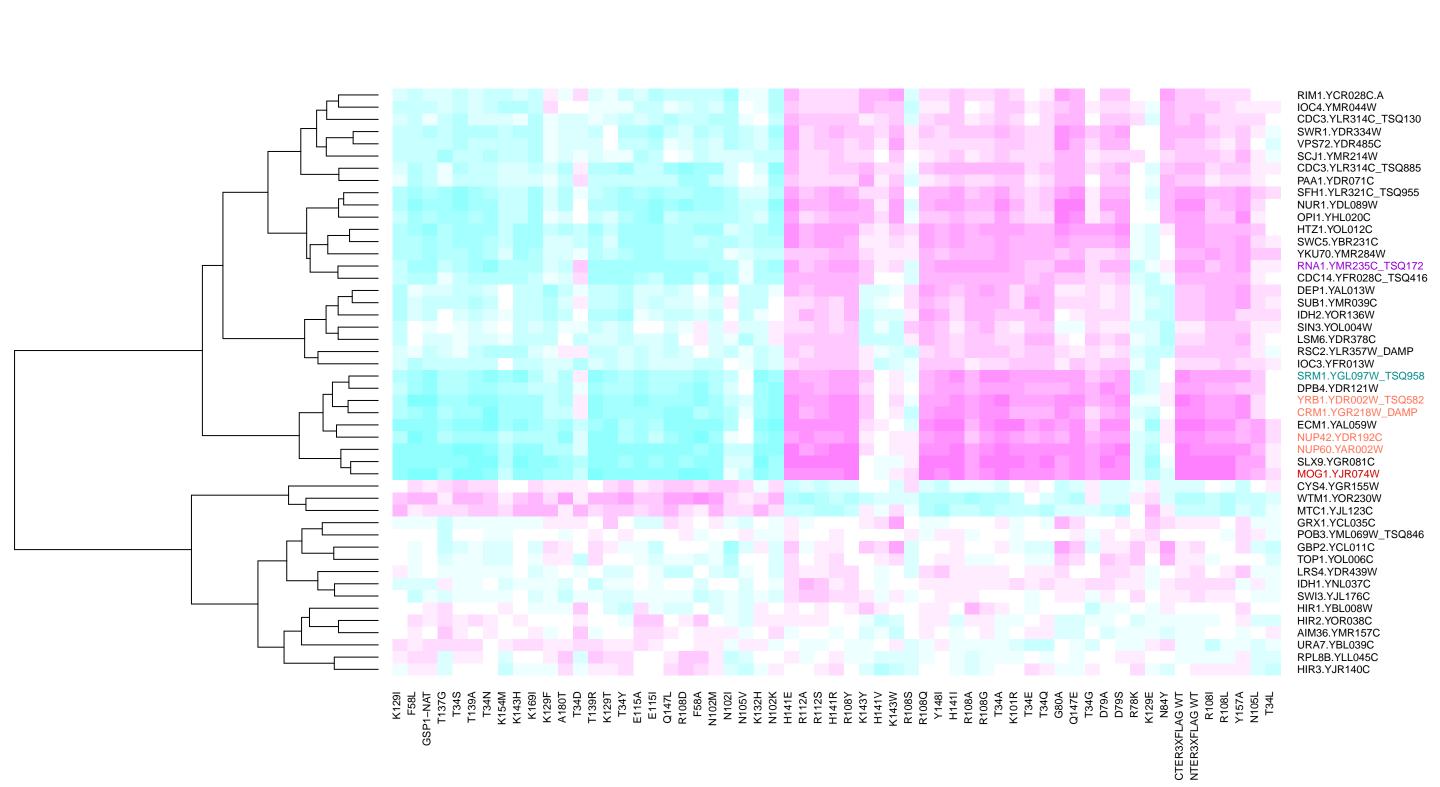
cytoskeleton and microtubules_GO_30_3_all



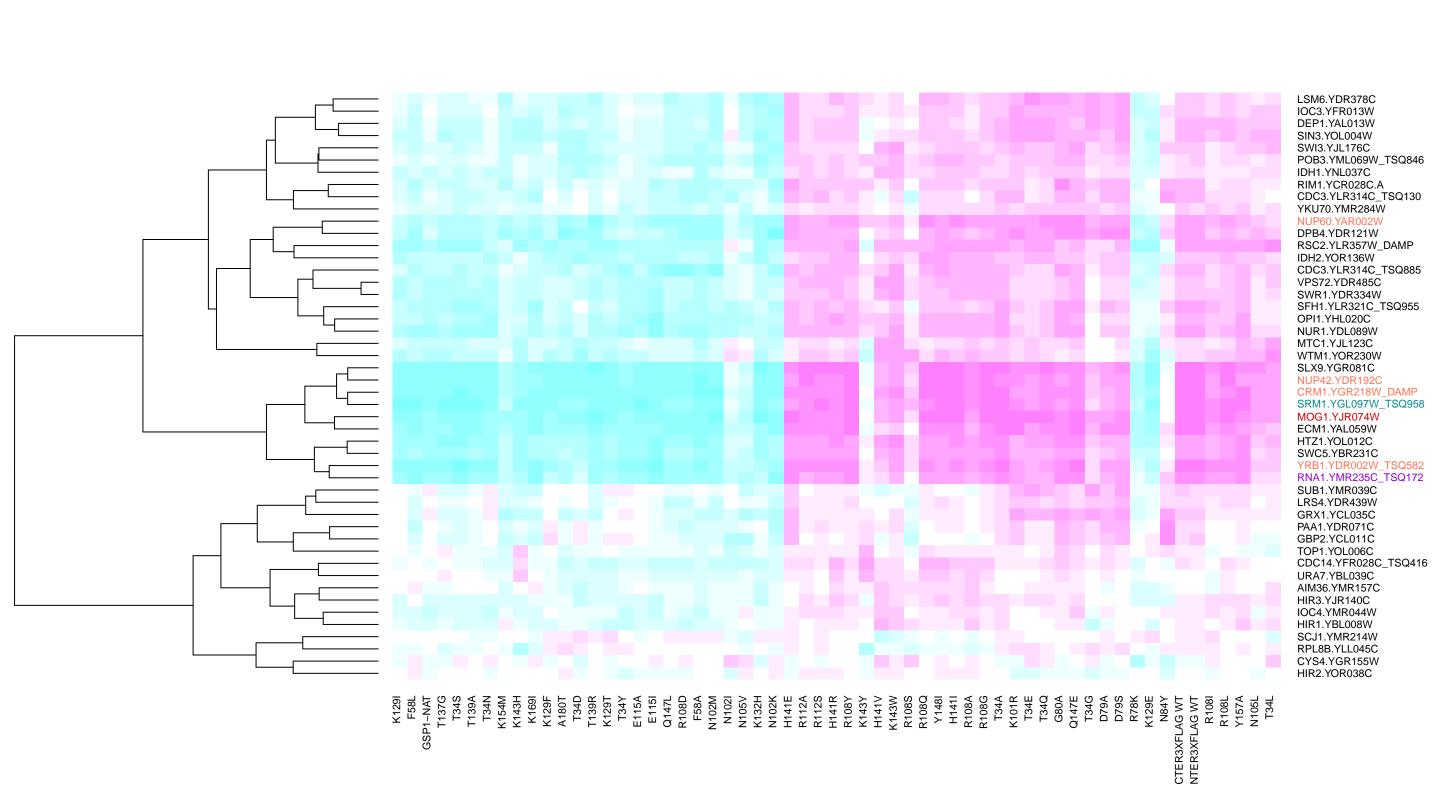
nuclear transport and organization_GO_15_3_all



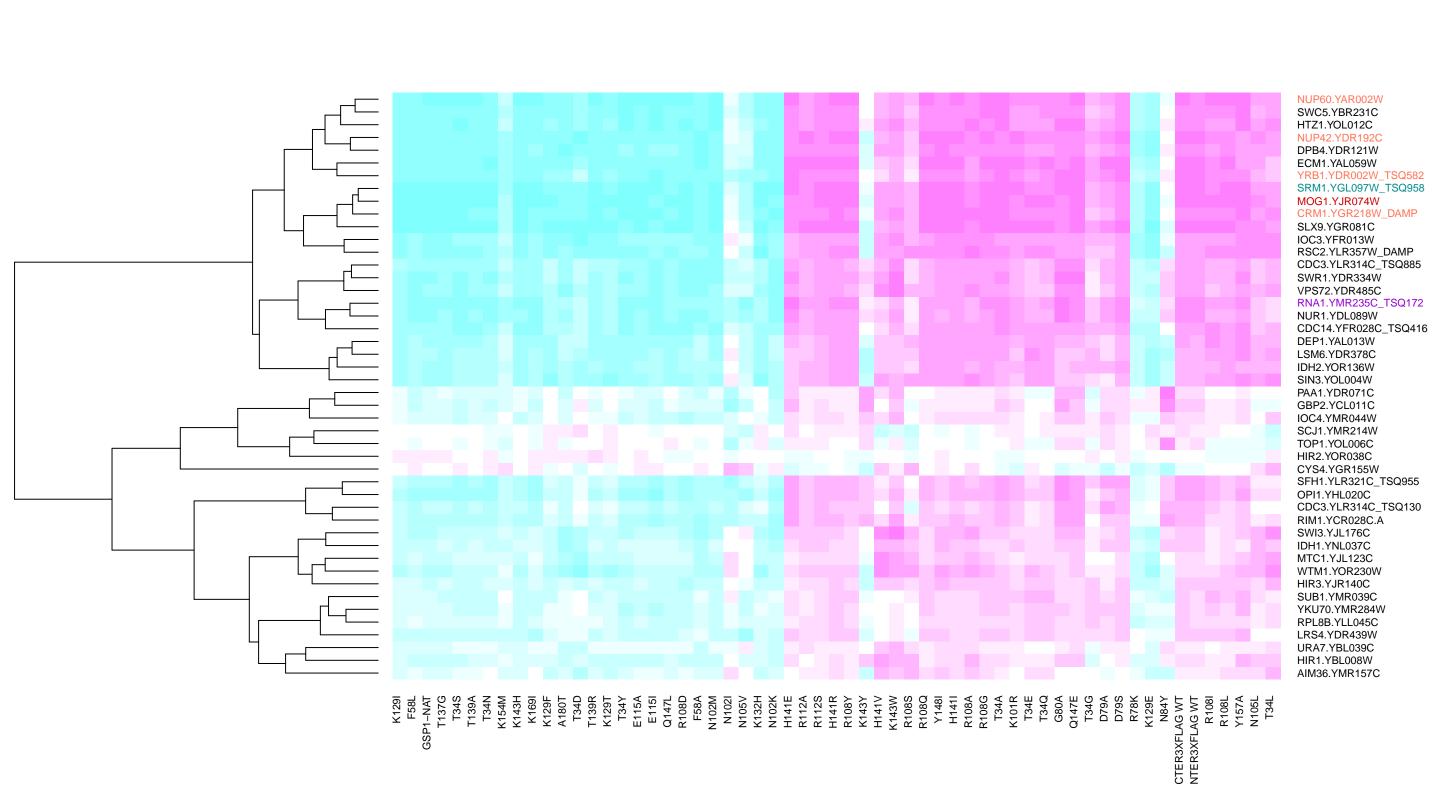
nuclear transport_GO_15_1_all

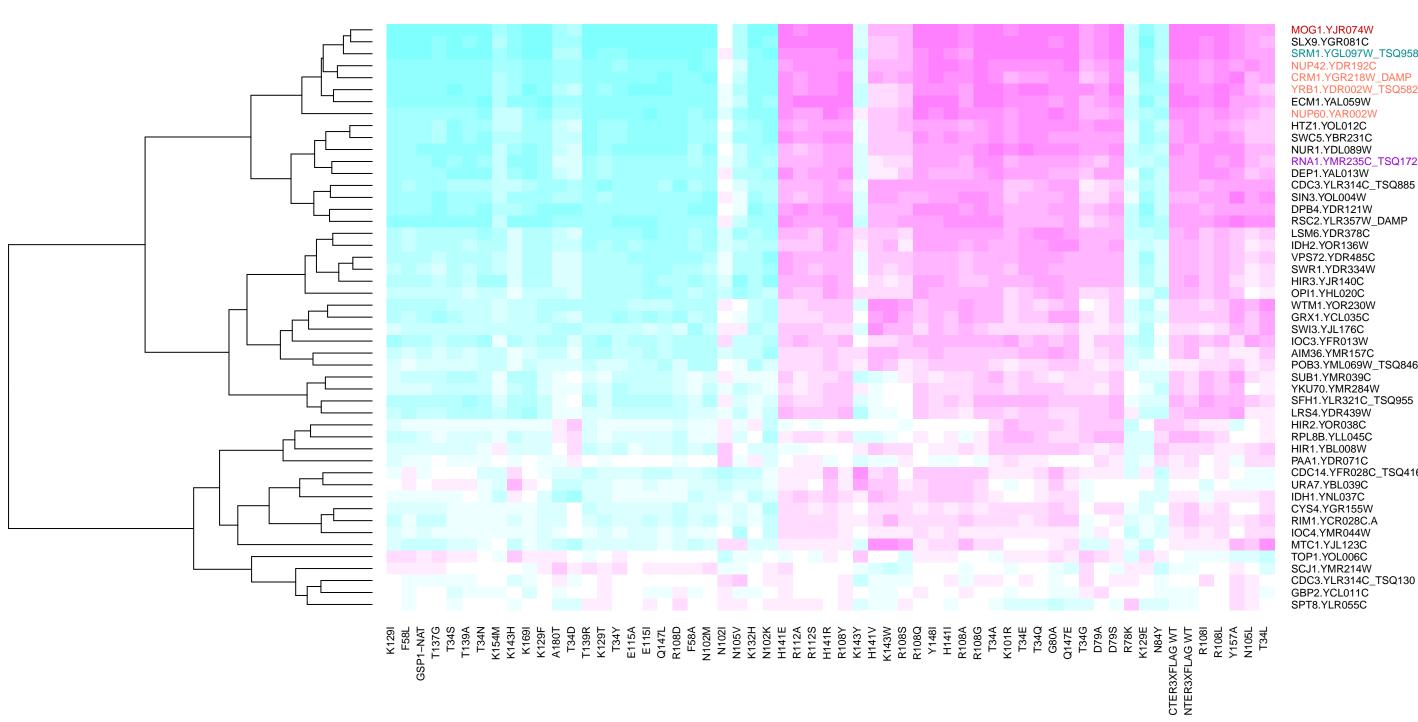


nucleus organization



nucleus organization_GO_15_1_all

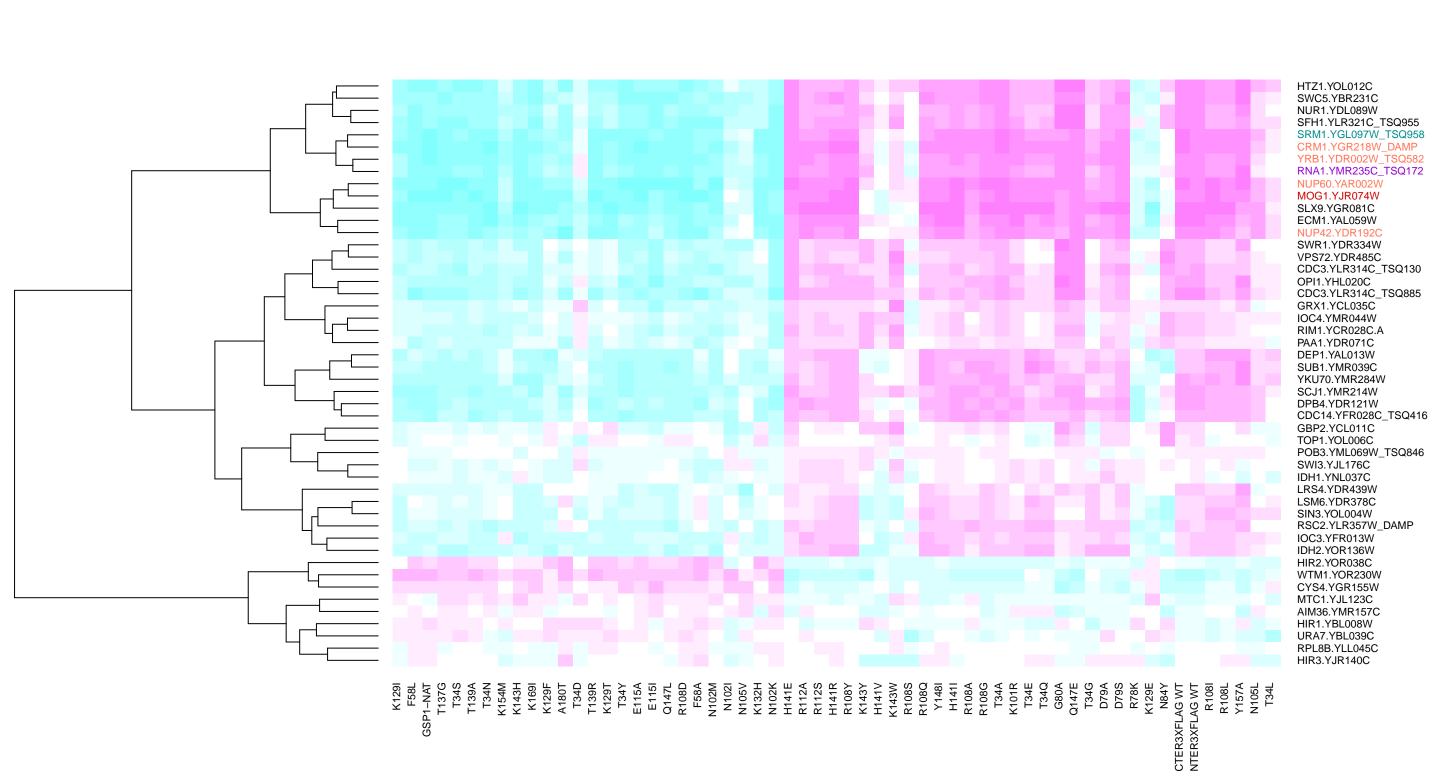




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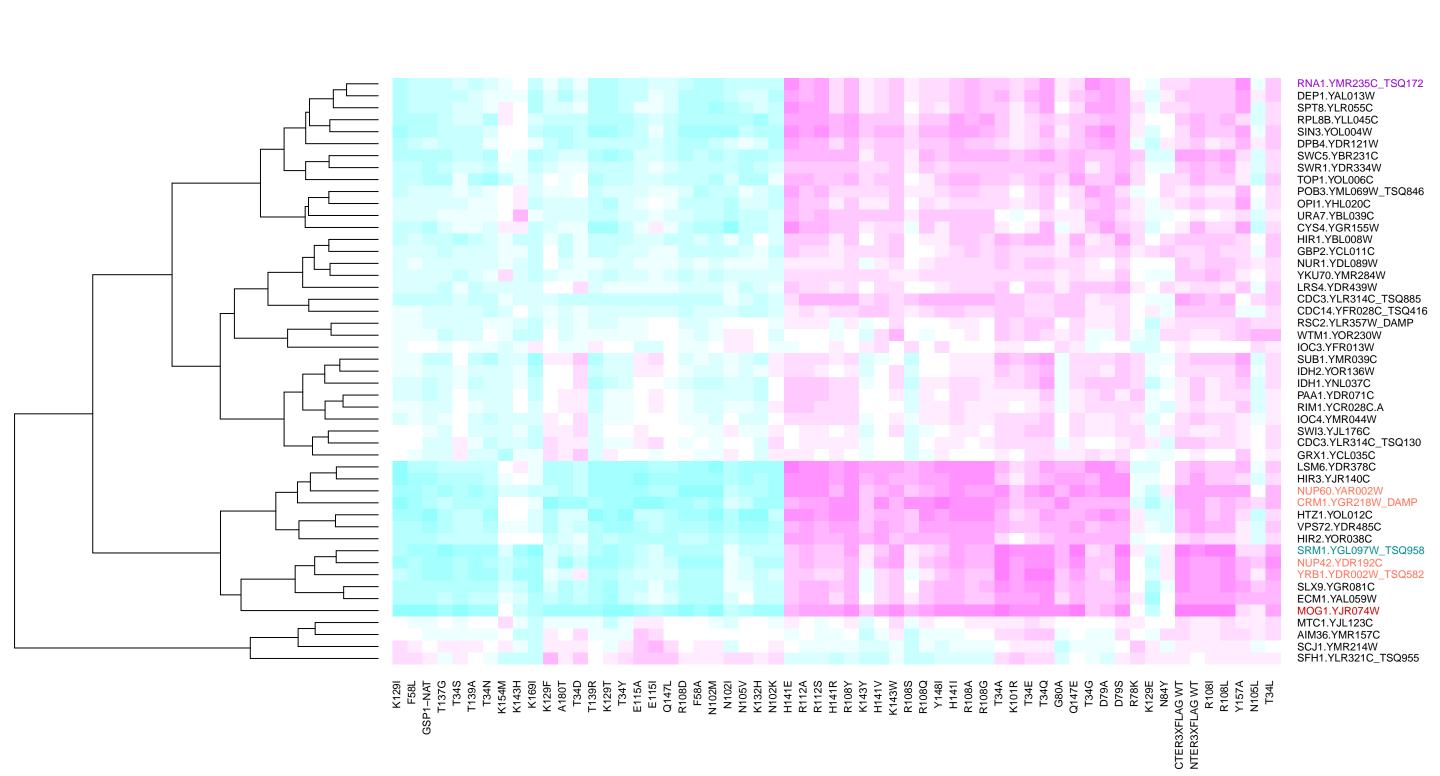
ECM1.YAL059W NUP60.YAR002W HTZ1.YOL012C SWC5.YBR231C NUR1.YDL089W RNA1.YMR235C_TSQ172 DEP1.YAL013W CDC3.YLR314C_TSQ885 SIN3.YOL004W DPB4.YDR121W RSC2.YLR357W_DAMP LSM6.YDR378C IDH2.YOR136W VPS72.YDR485C SWR1.YDR334W HIR3.YJR140C OPI1.YHL020C WTM1.YOR230W GRX1.YCL035C SWI3.YJL176C IOC3.YFR013W AIM36.YMR157C POB3.YML069W_TSQ846 SUB1.YMR039C YKU70.YMR284W SFH1.YLR321C_TSQ955 LRS4.YDR439W HIR2.YOR038C RPL8B.YLL045C HIR1.YBL008W PAA1.YDR071C CDC14.YFR028C_TSQ416 URA7.YBL039C IDH1.YNL037C CYS4.YGR155W RIM1.YCR028C.A IOC4.YMR044W MTC1.YJL123C



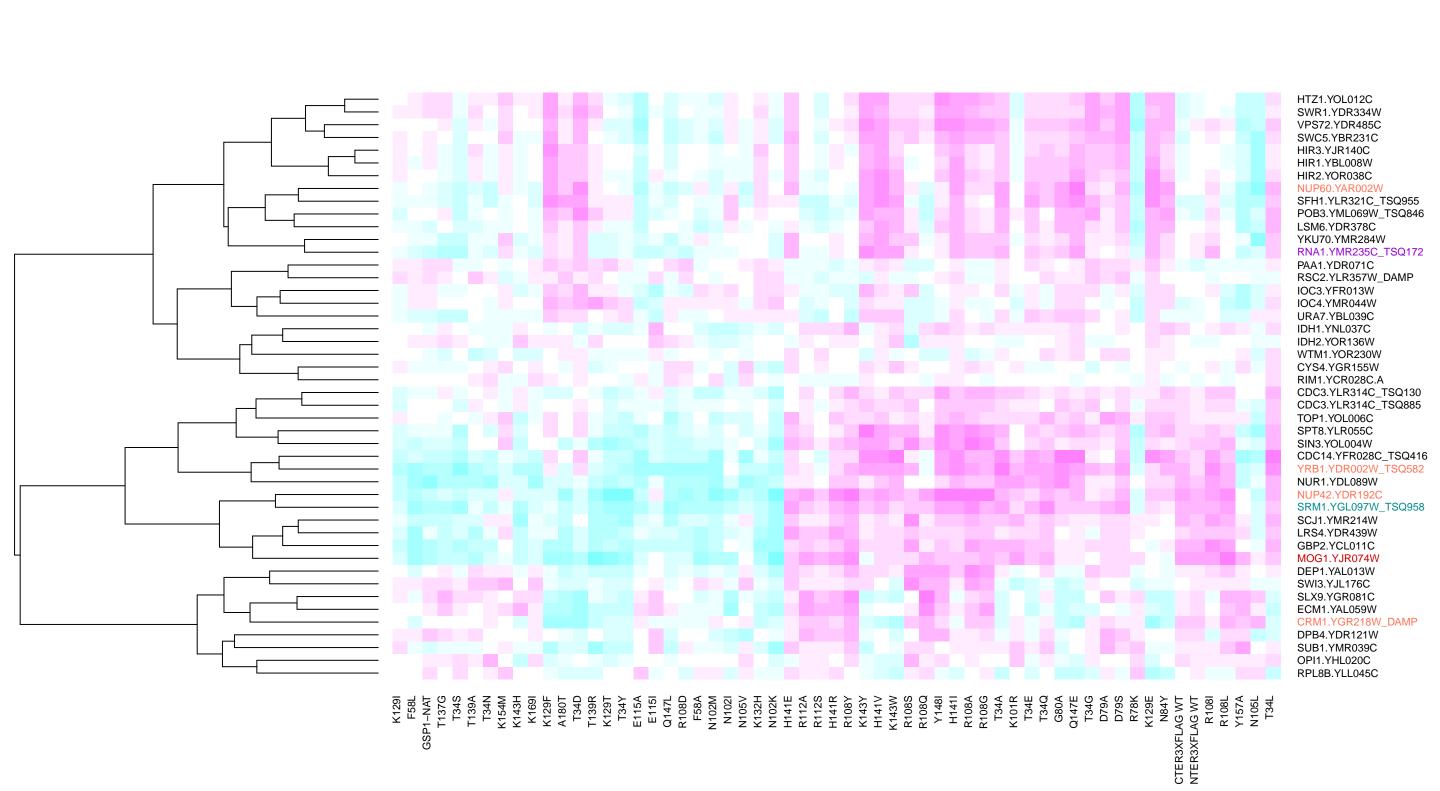


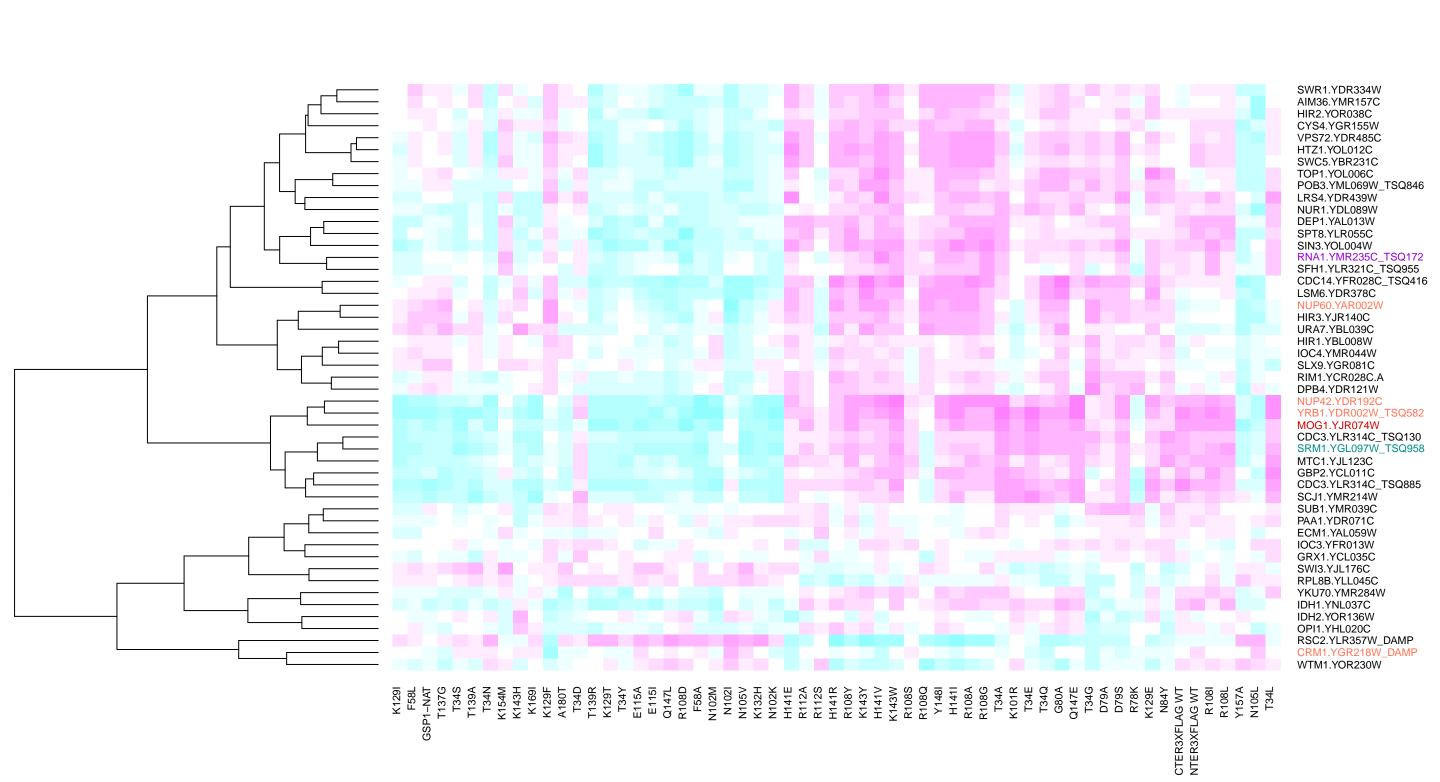
transcription and mRNA processing_GO_15_7_all



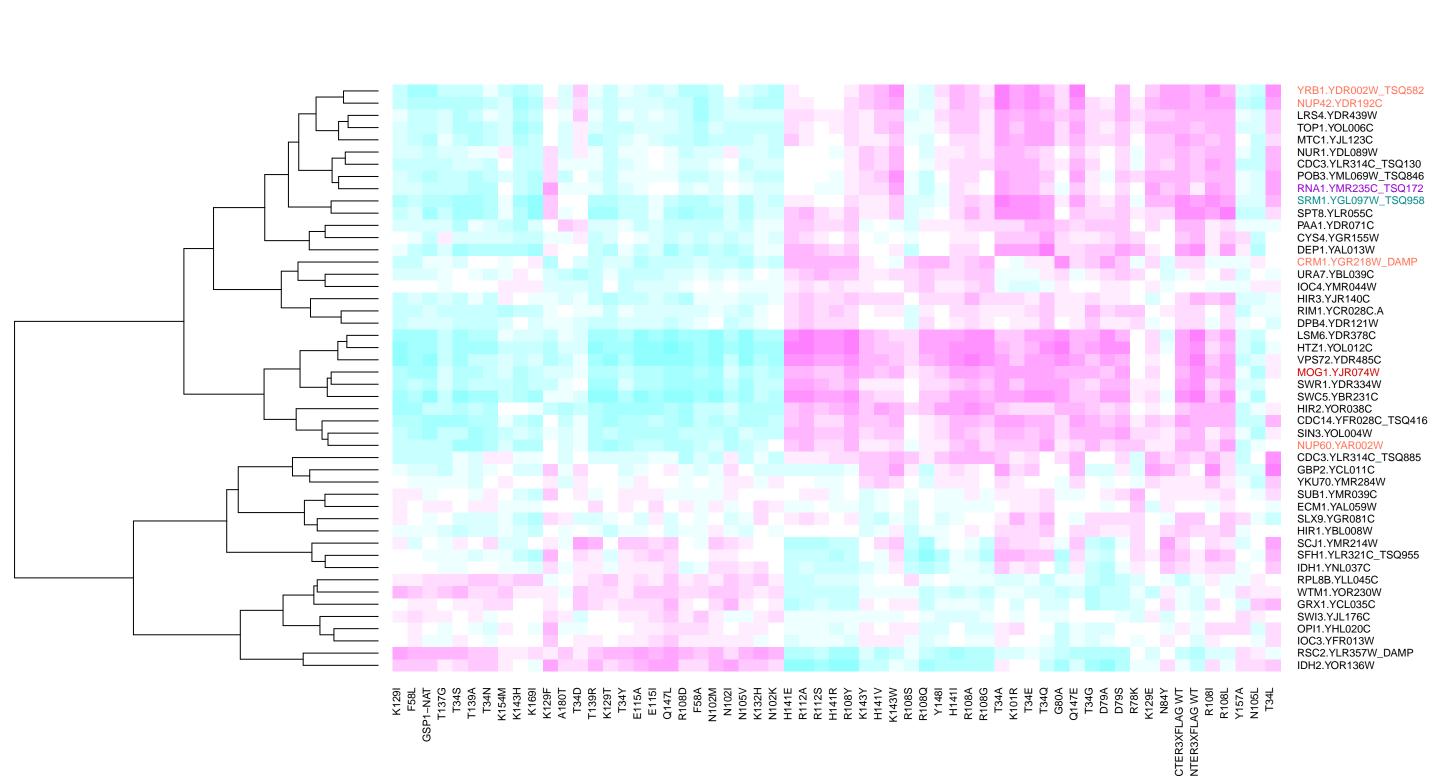


RNA processing





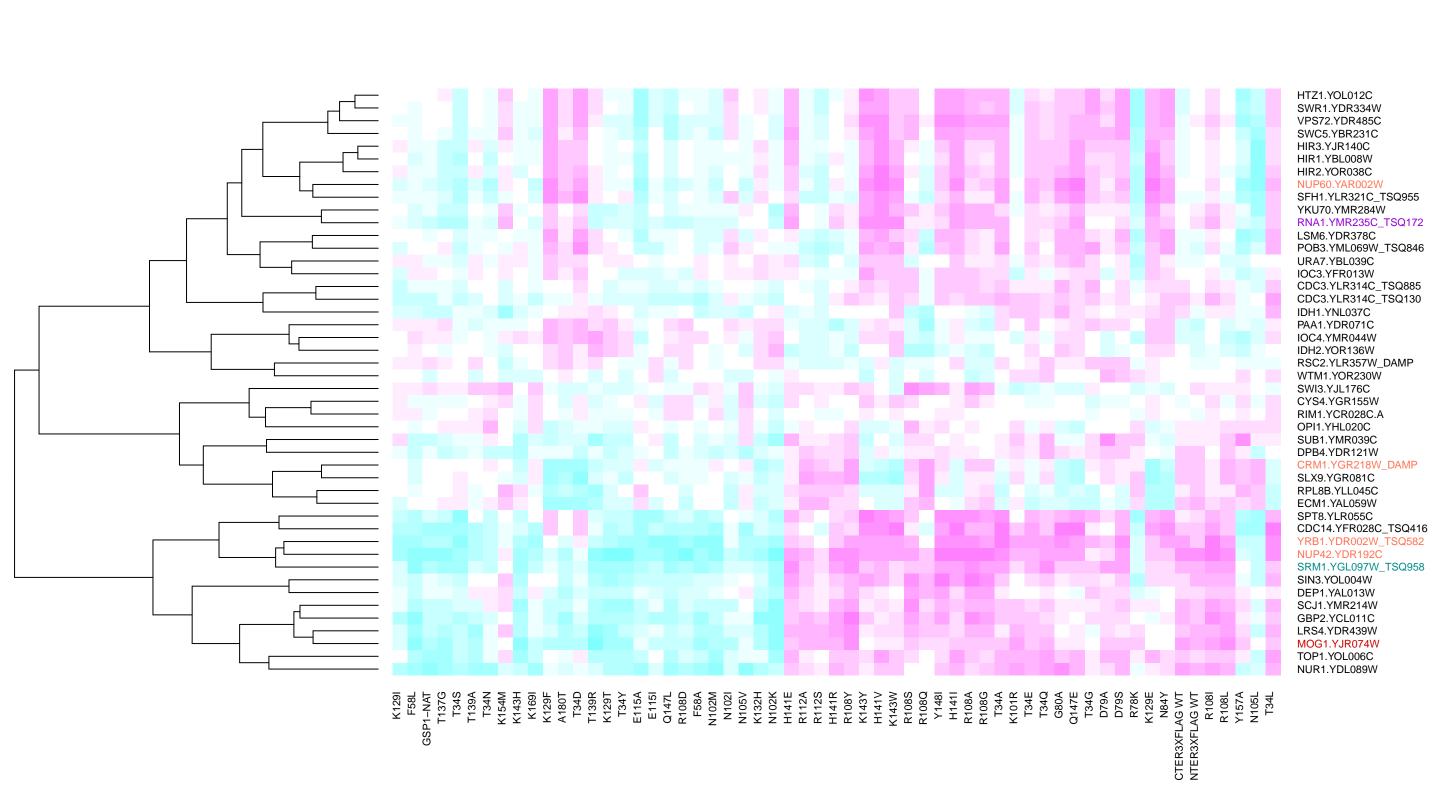
organelle fission_GO_30_1_mut



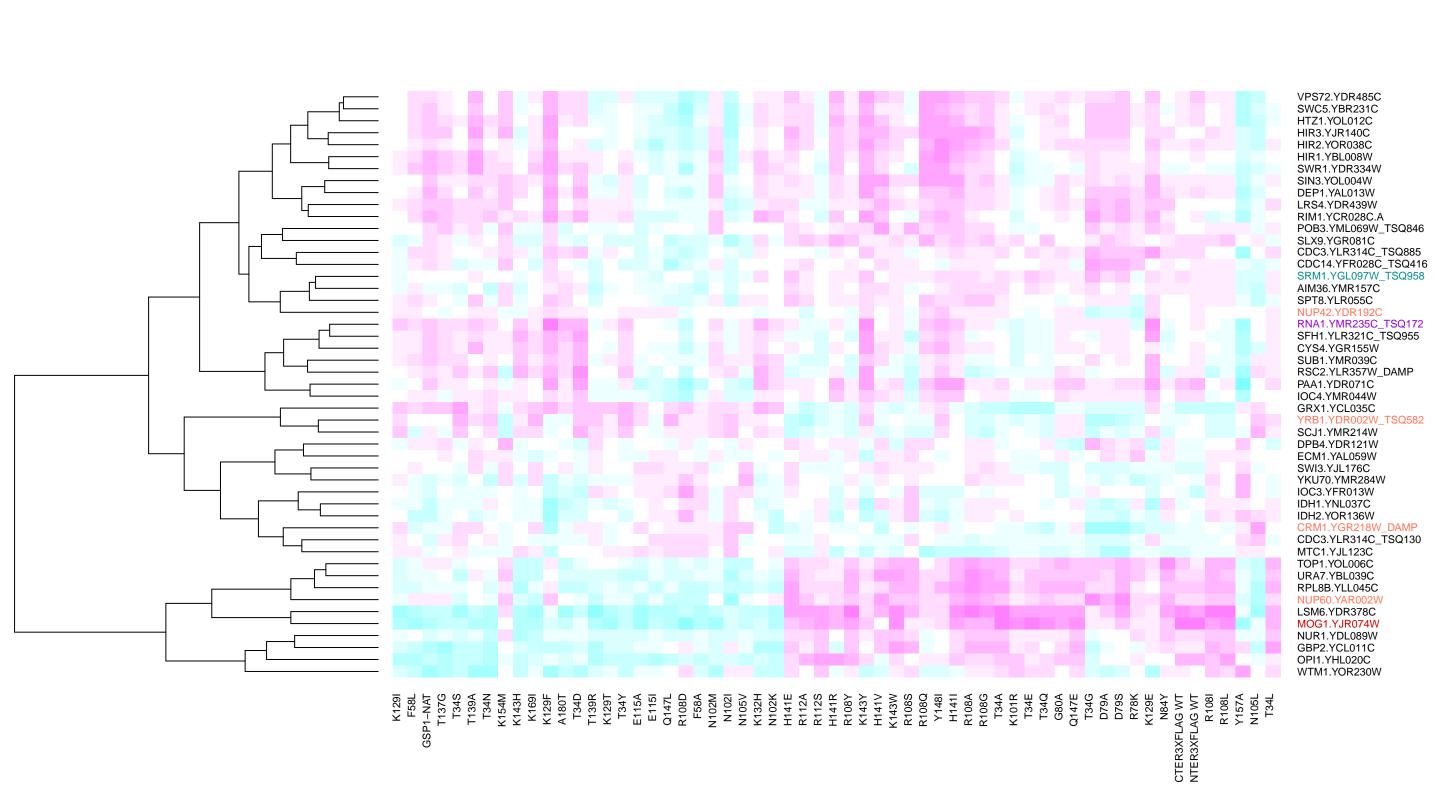
mRNA processing



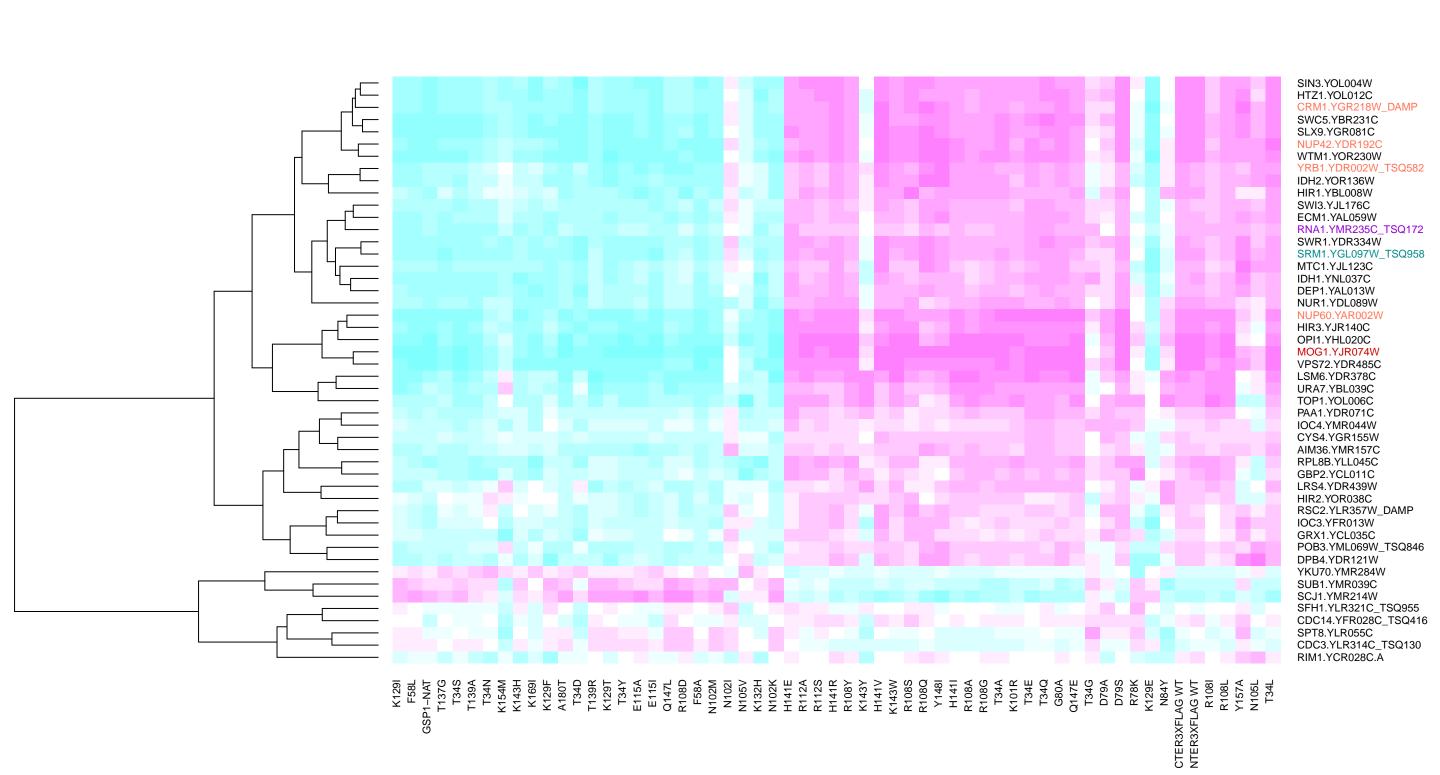
RNA processing_GO_15_1_all

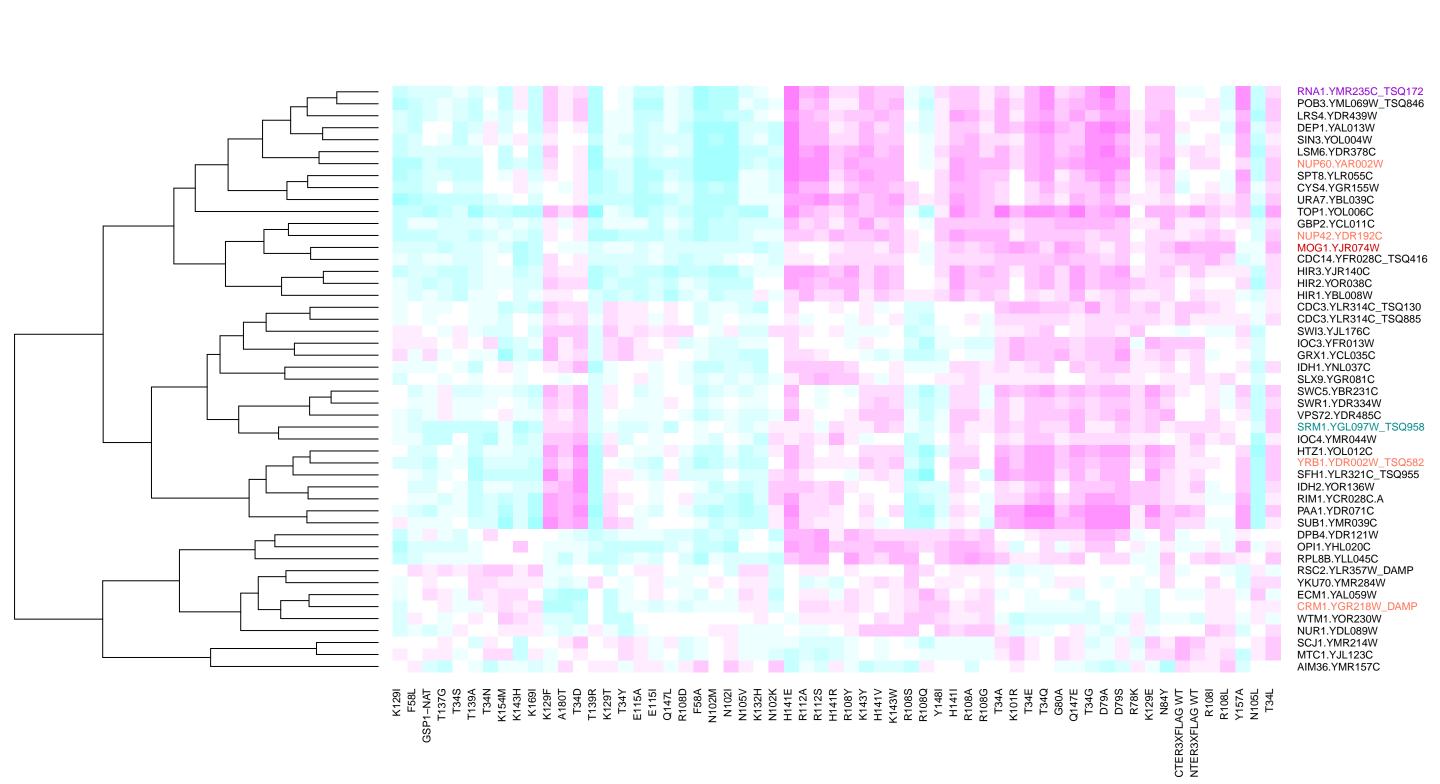


DNA recombination

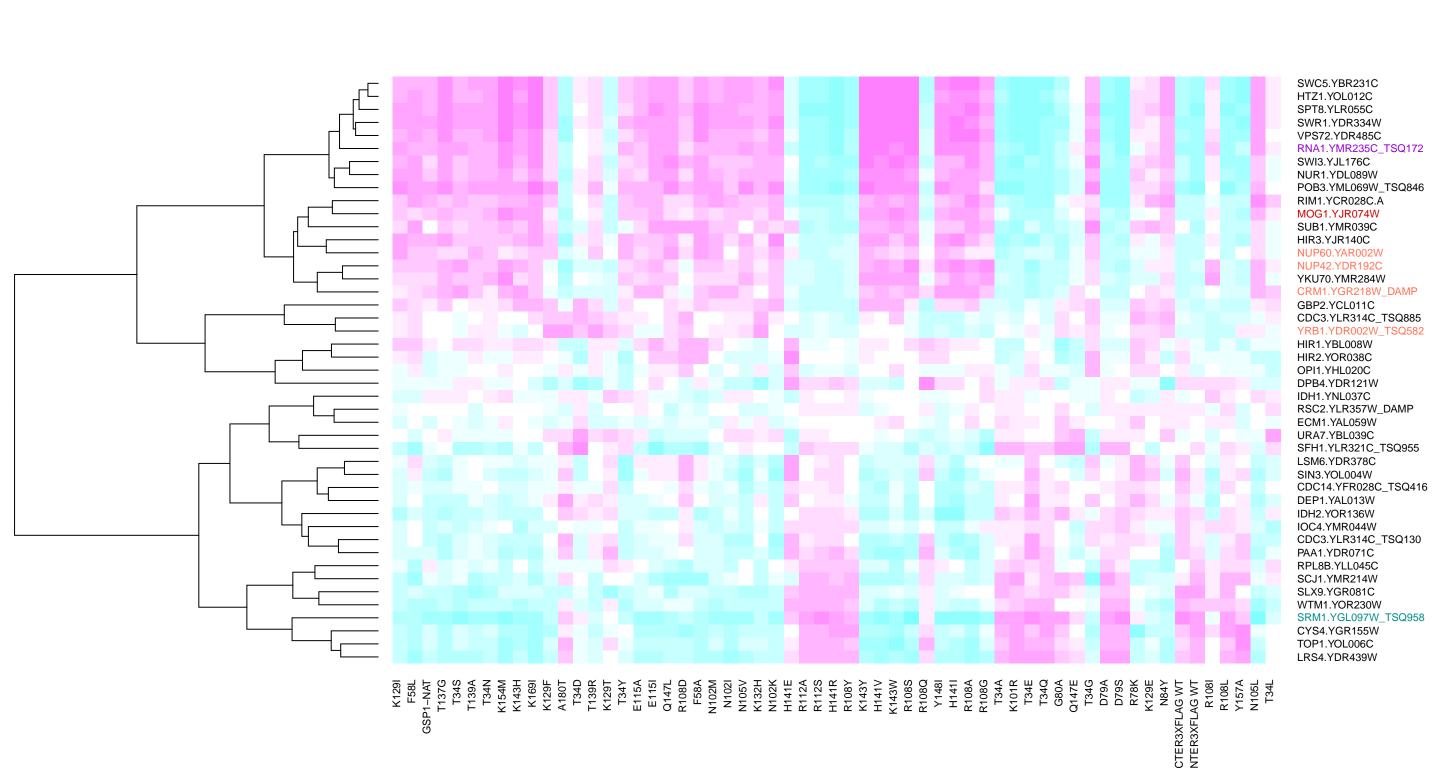


transcription from RNA polymerase II promoter_GO_15_4_all

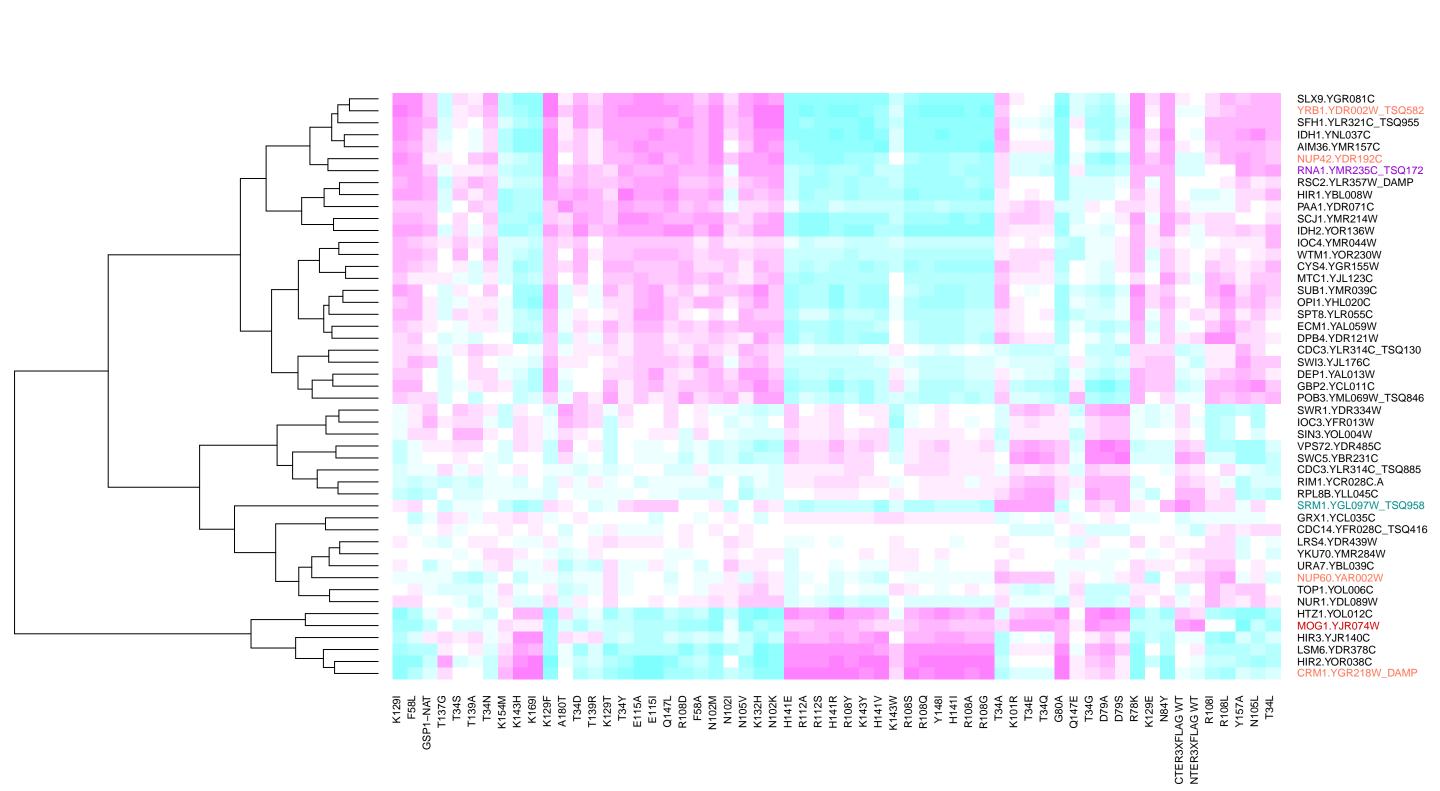


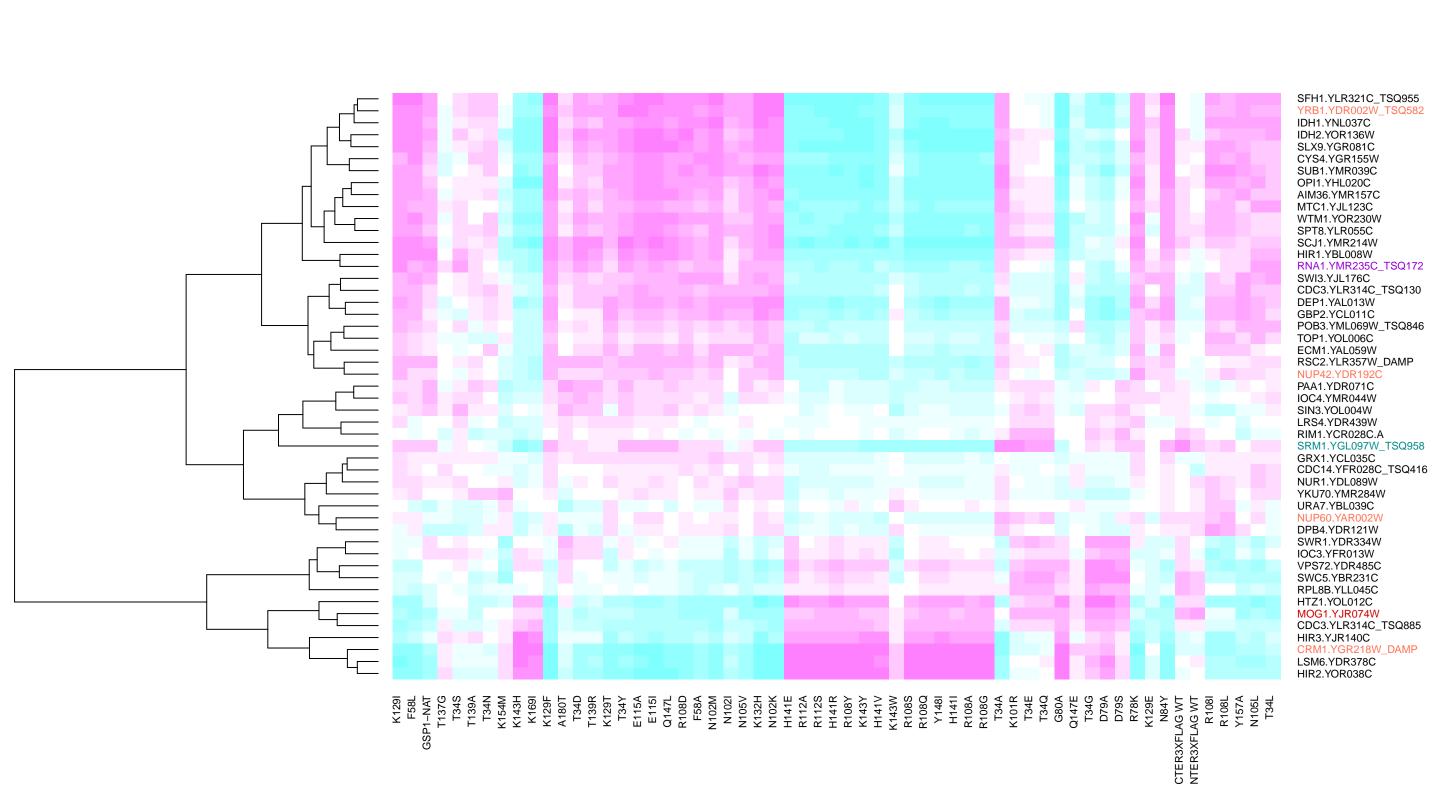


sig_Gsp1_Gl_15_7_mut

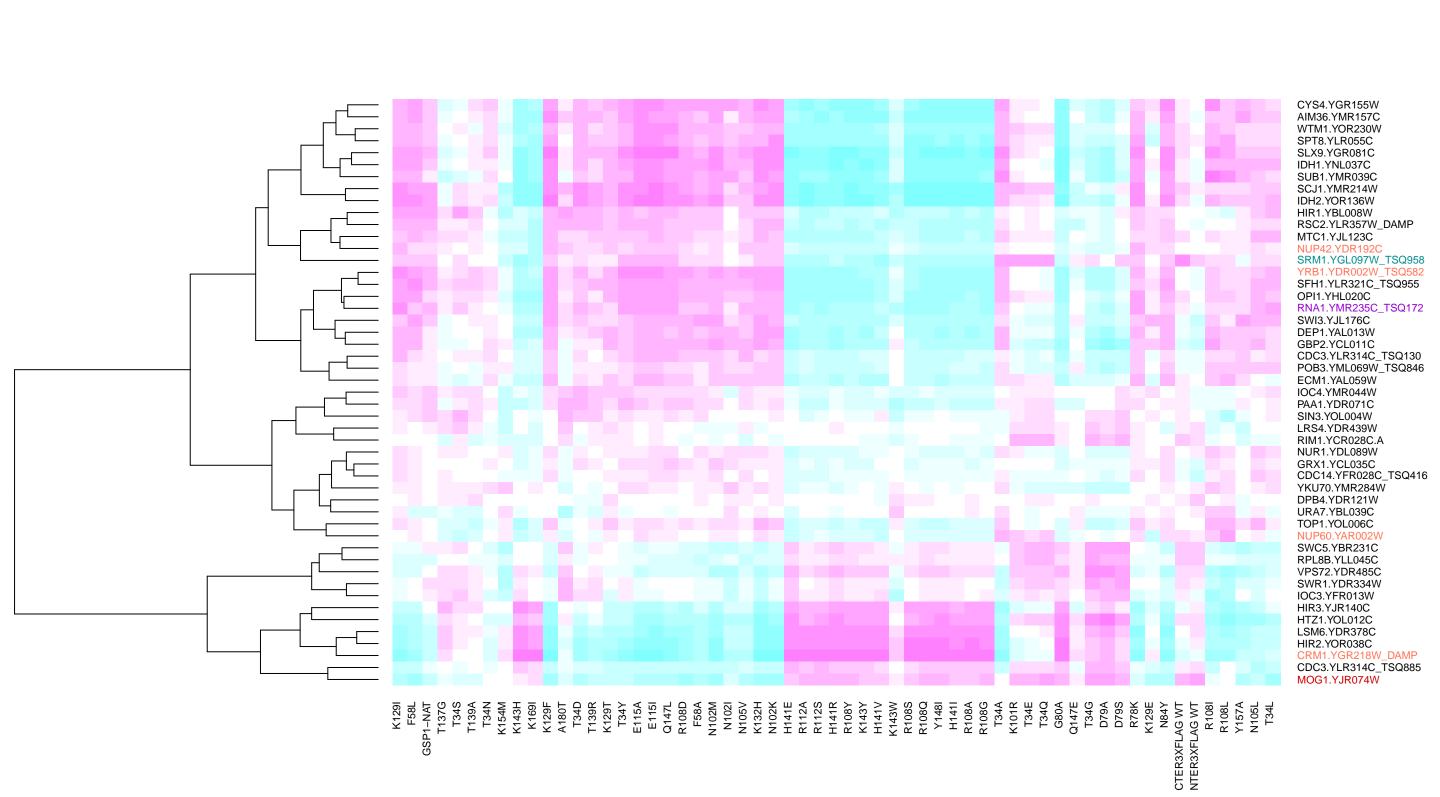


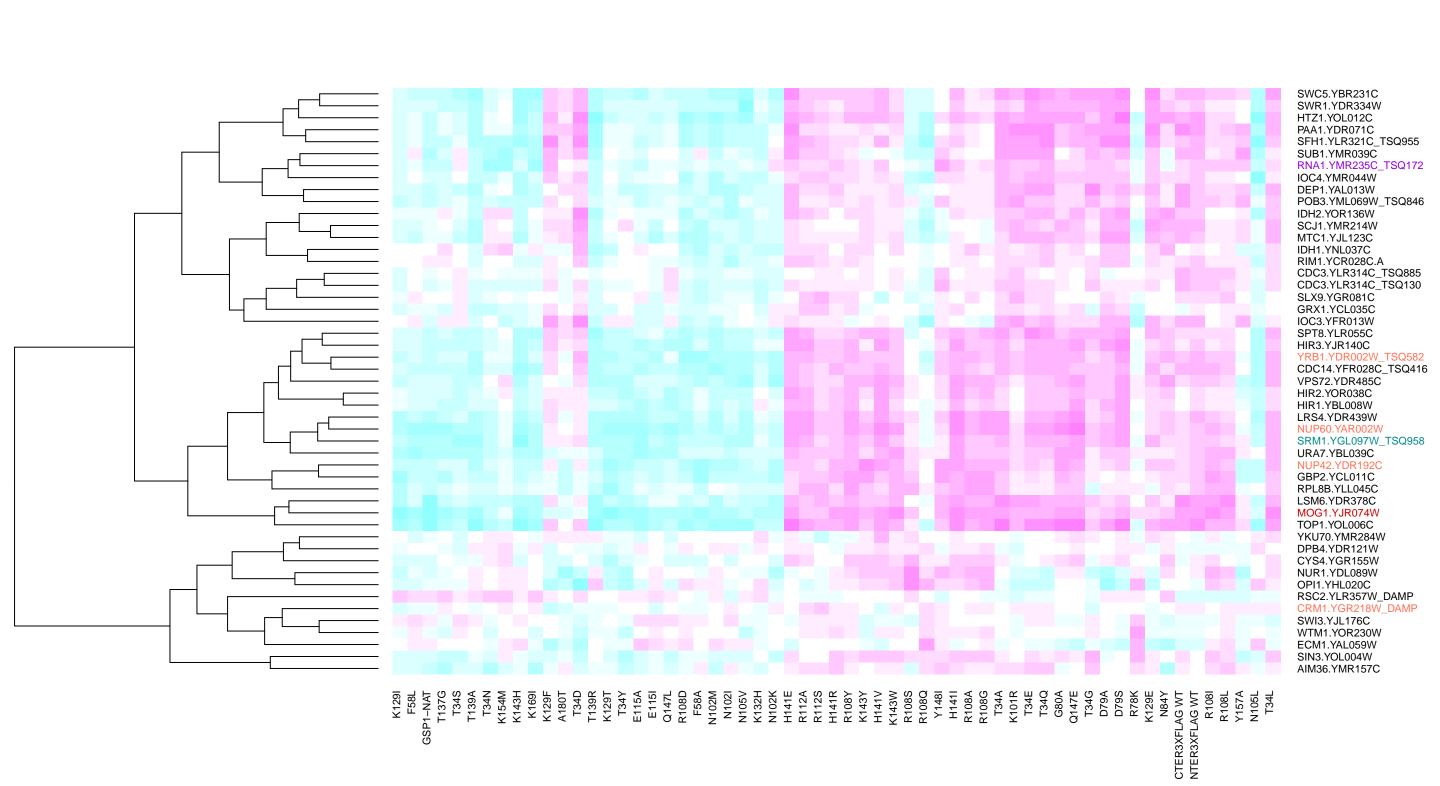
mitotic cell cycle_GO_15_2_all

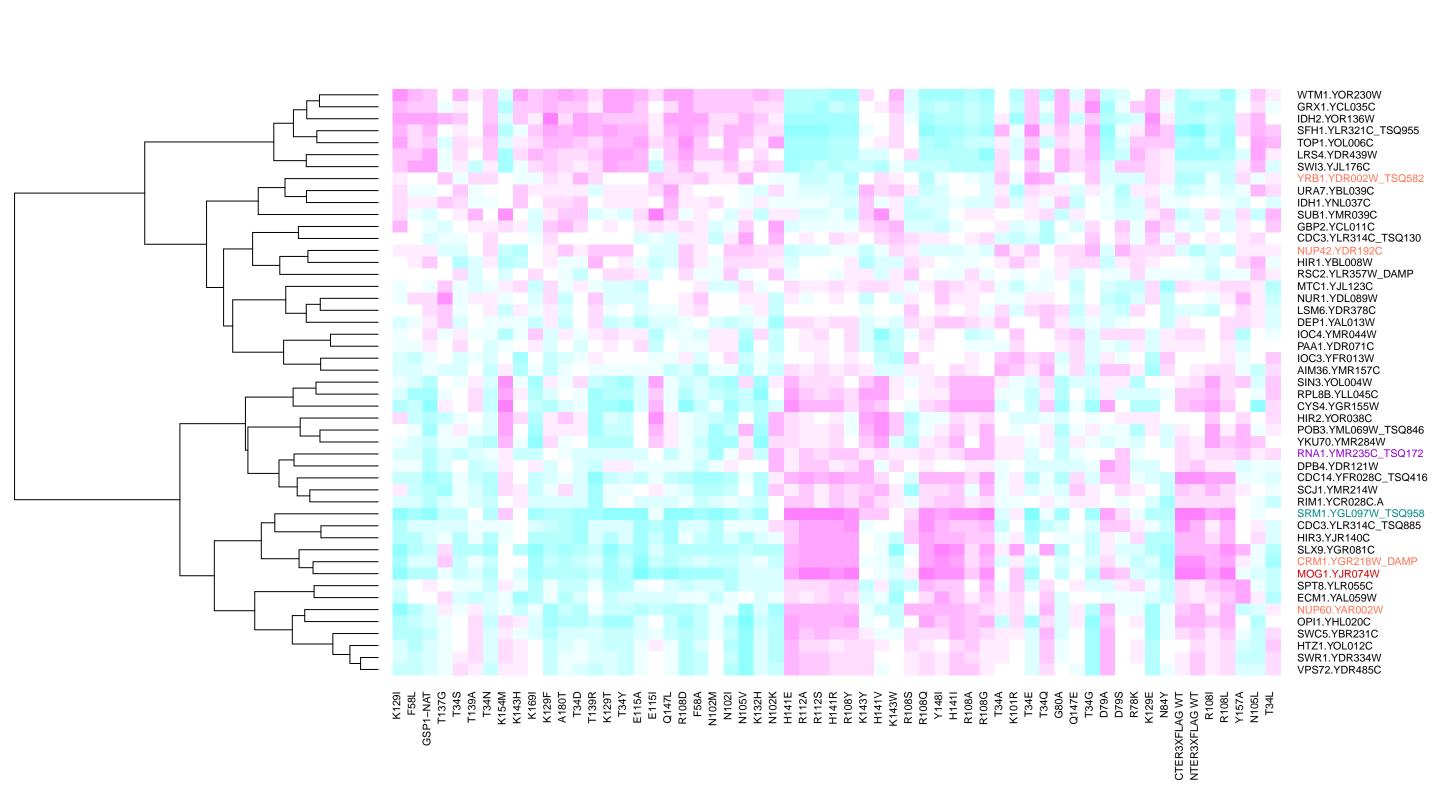




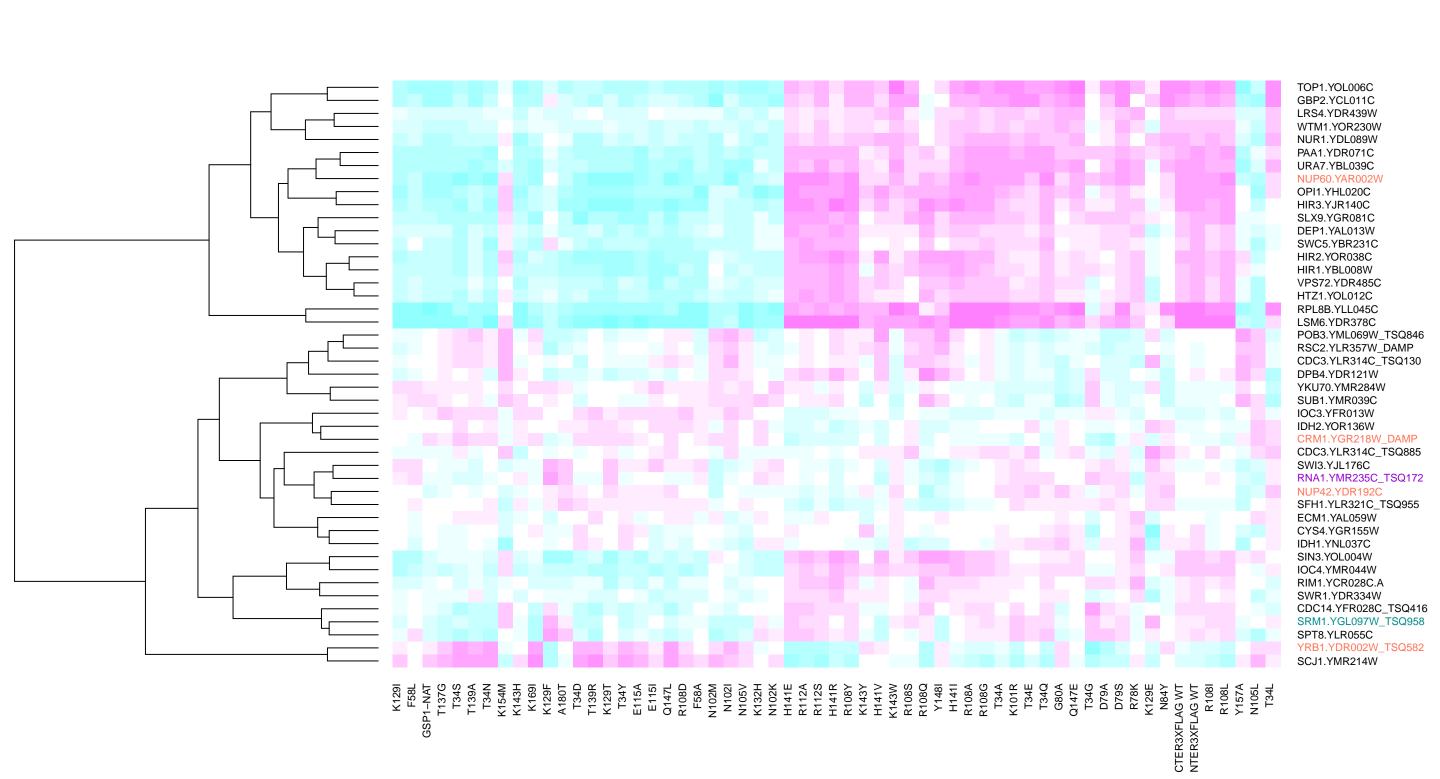
whole_library_30_9_all







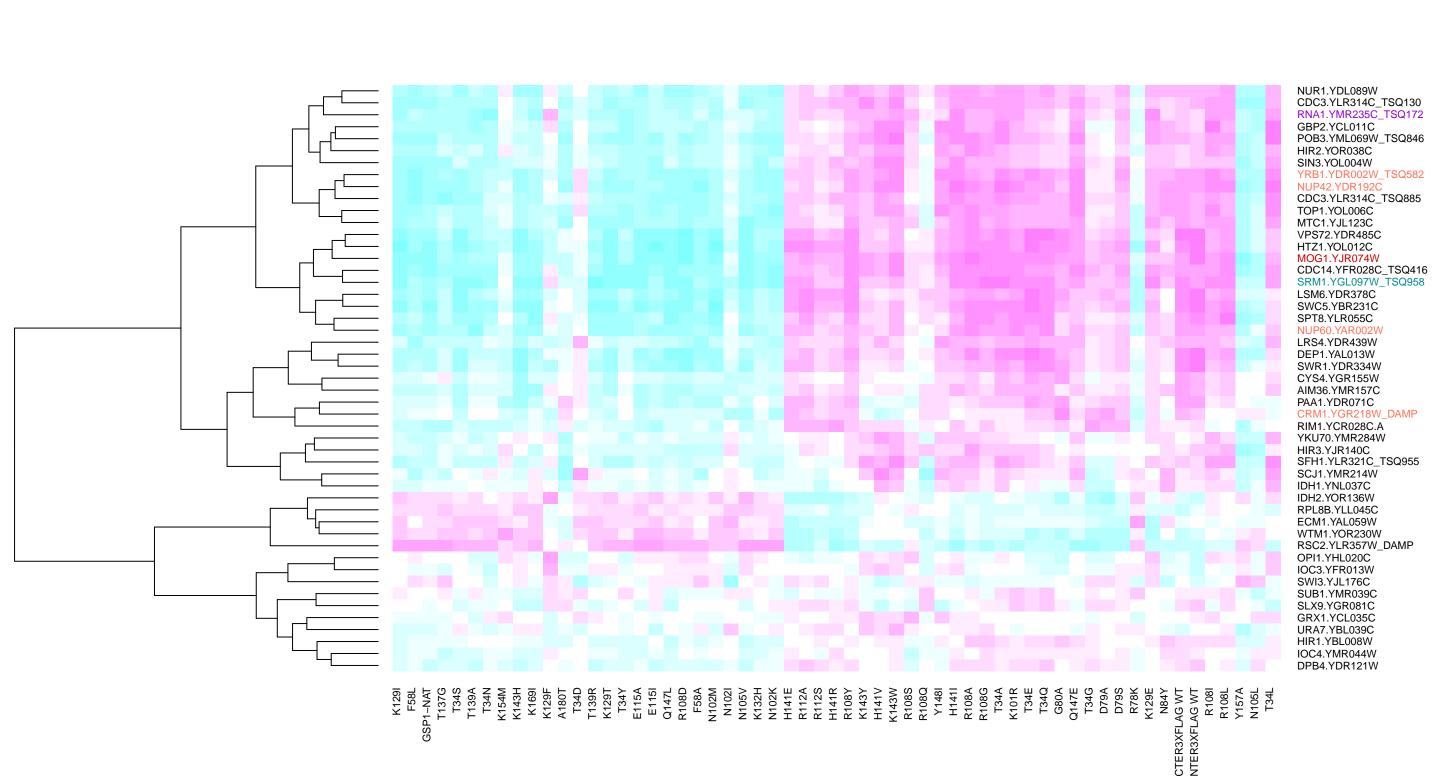
DNA recombination_GO_15_1_mut



DNA recombination_GO_30_1_mut



organelle fission_GO_15_3_mut



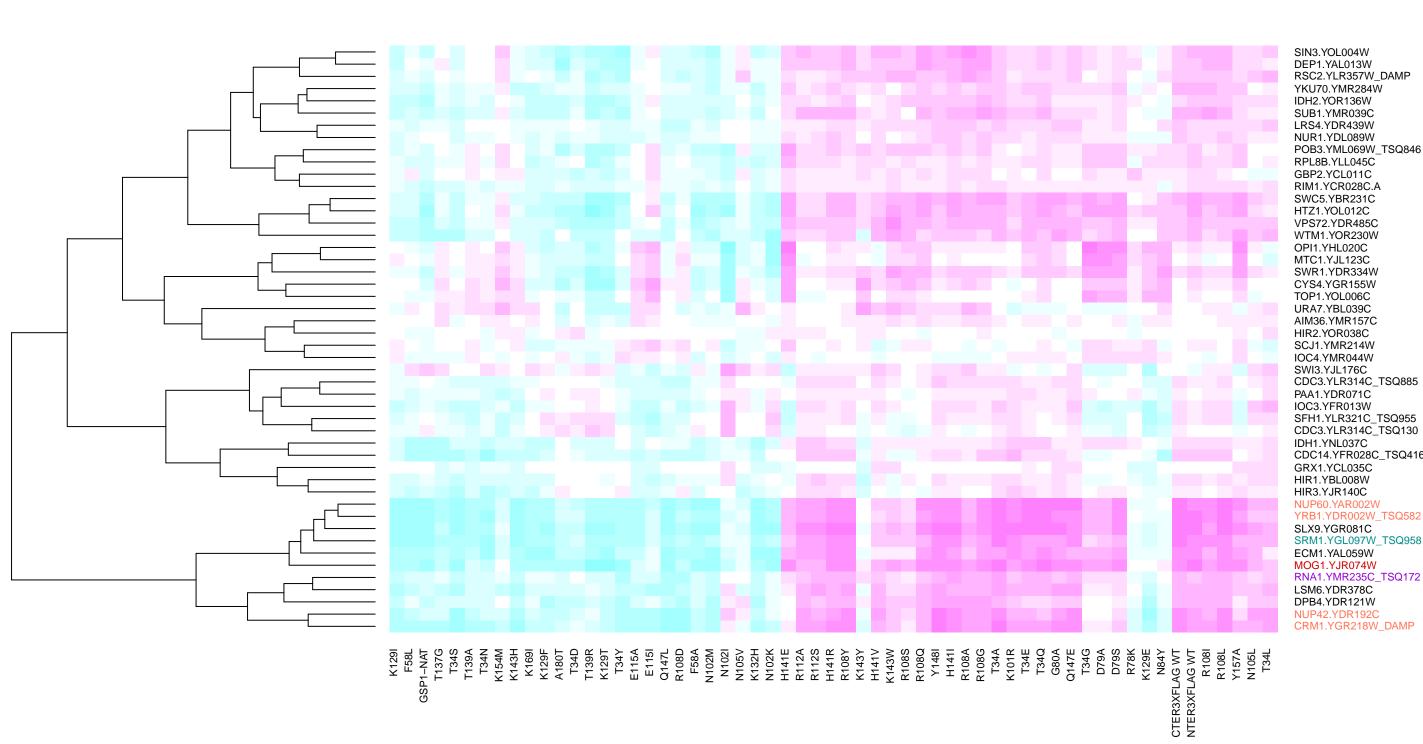
DNA-templated transcription, elongation_GO_15_1_mut





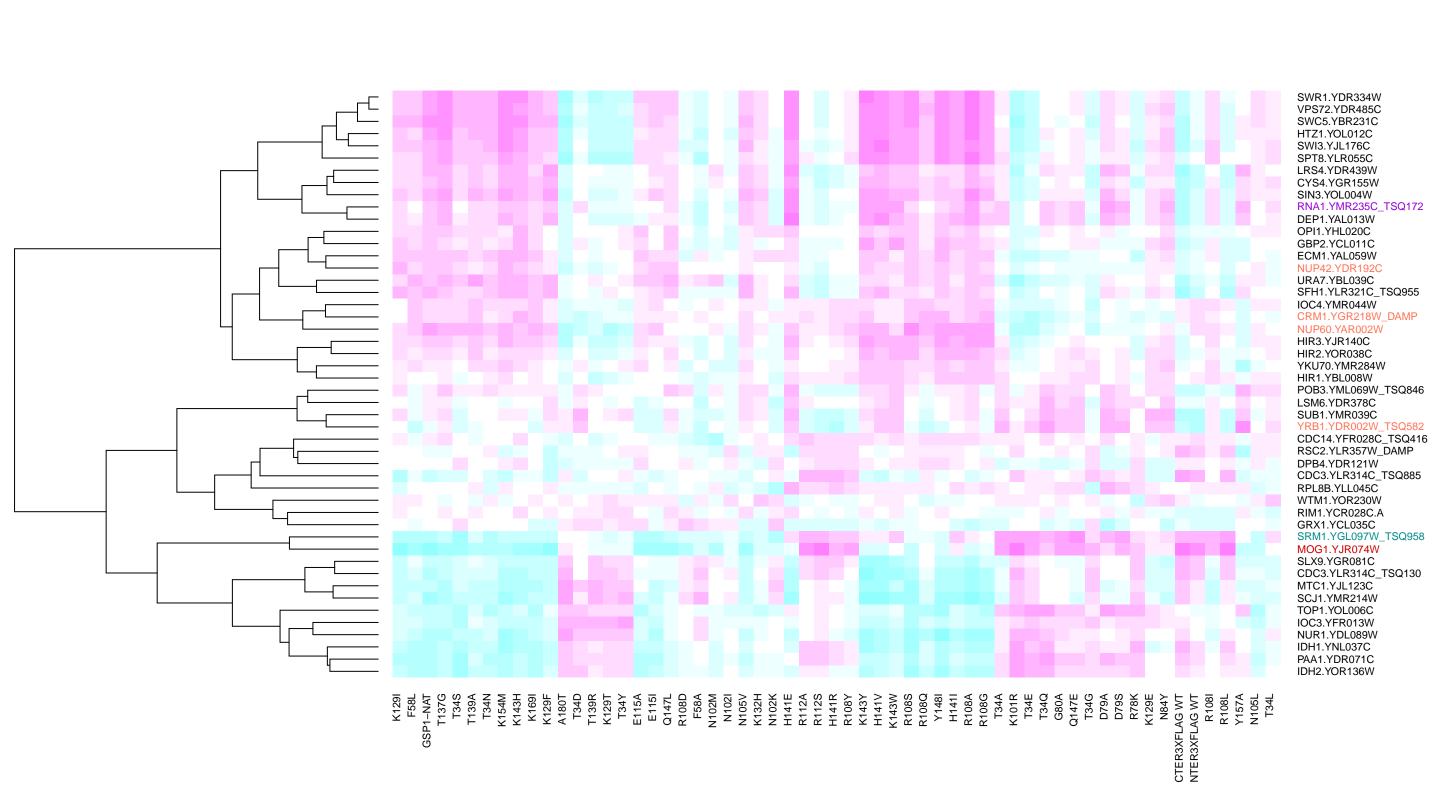


protein targeting

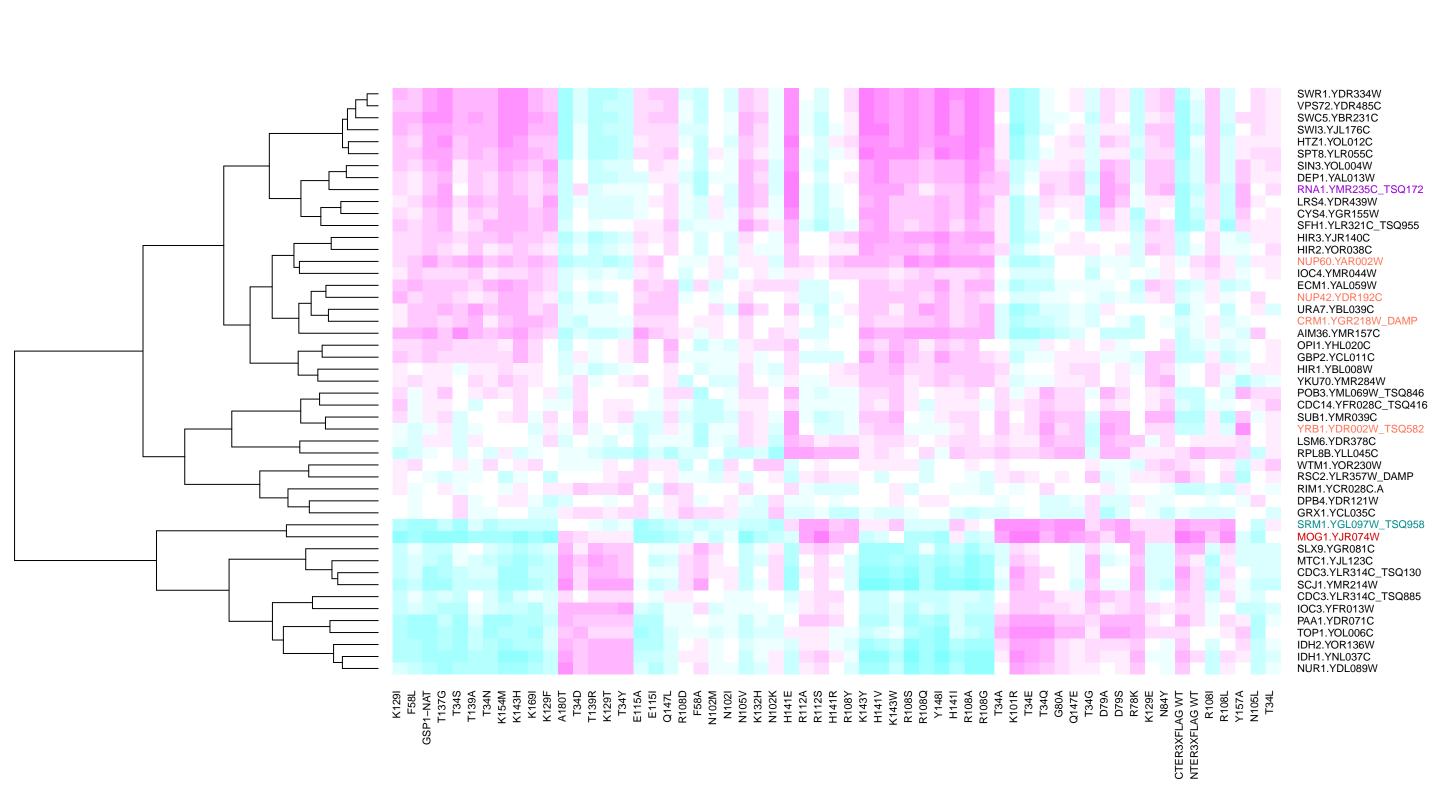


RSC2.YLR357W_DAMP YKU70.YMR284W POB3.YML069W_TSQ846 CDC3.YLR314C_TSQ885 SFH1.YLR321C_TSQ955 CDC3.YLR314C_TSQ130 CDC14.YFR028C_TSQ416 YRB1.YDR002W_TSQ582

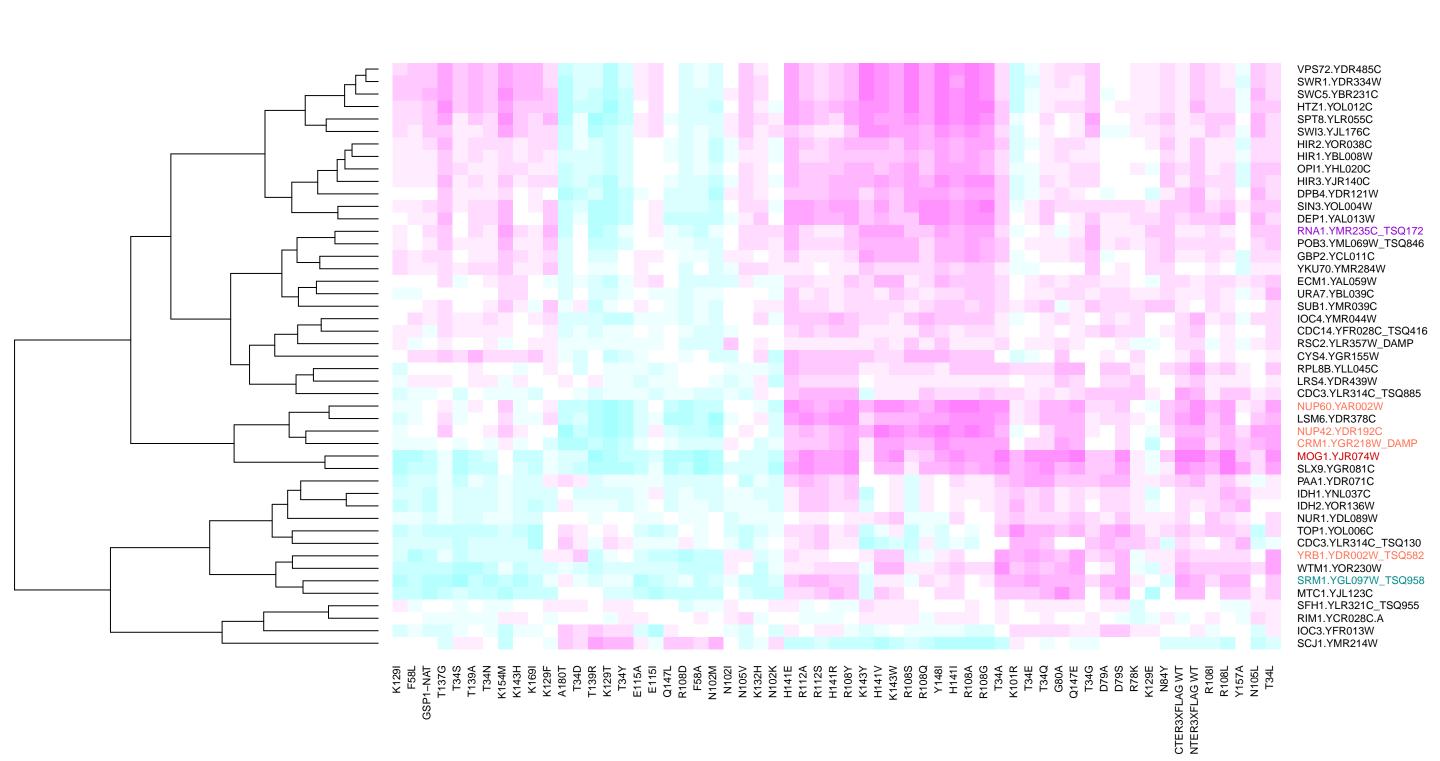
histone modification



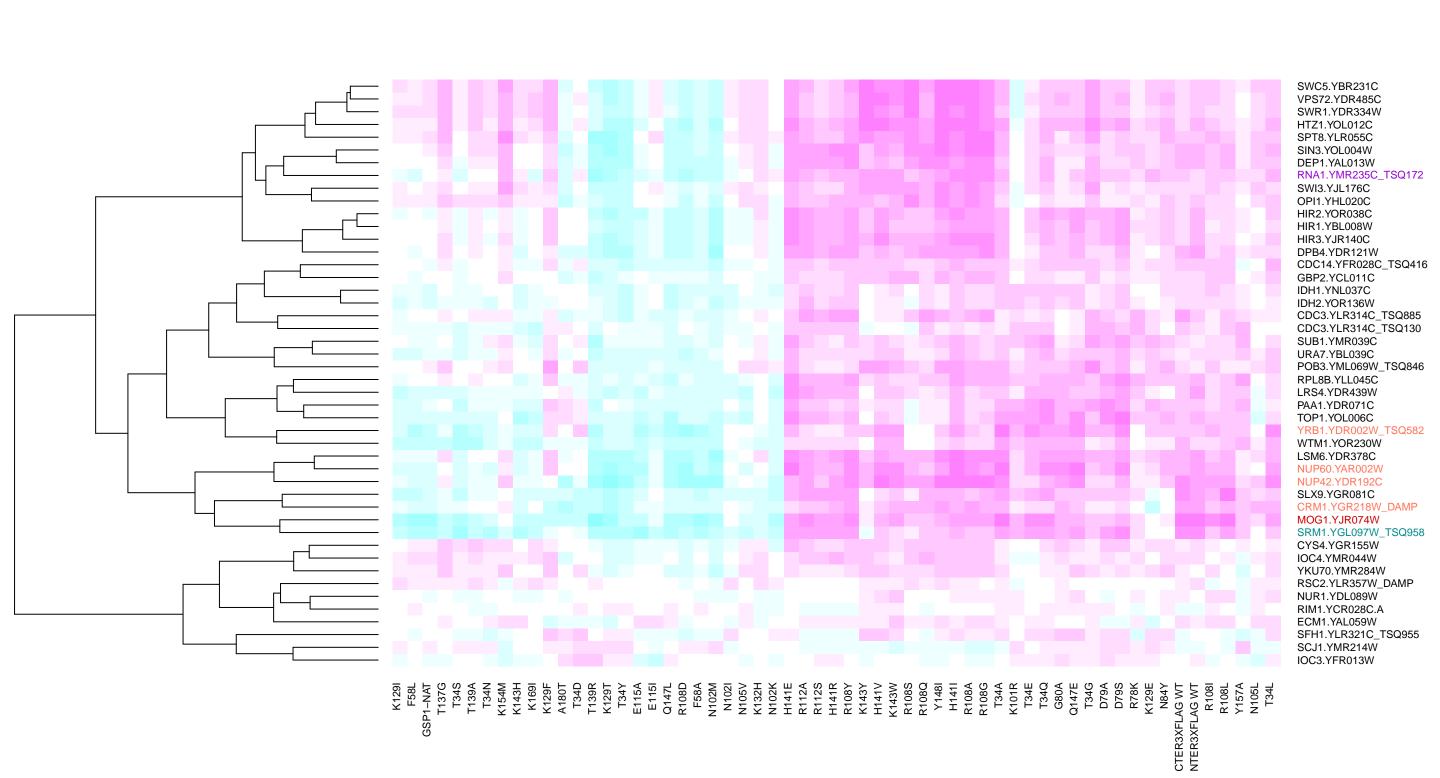
histone modification_GO_30_1_all



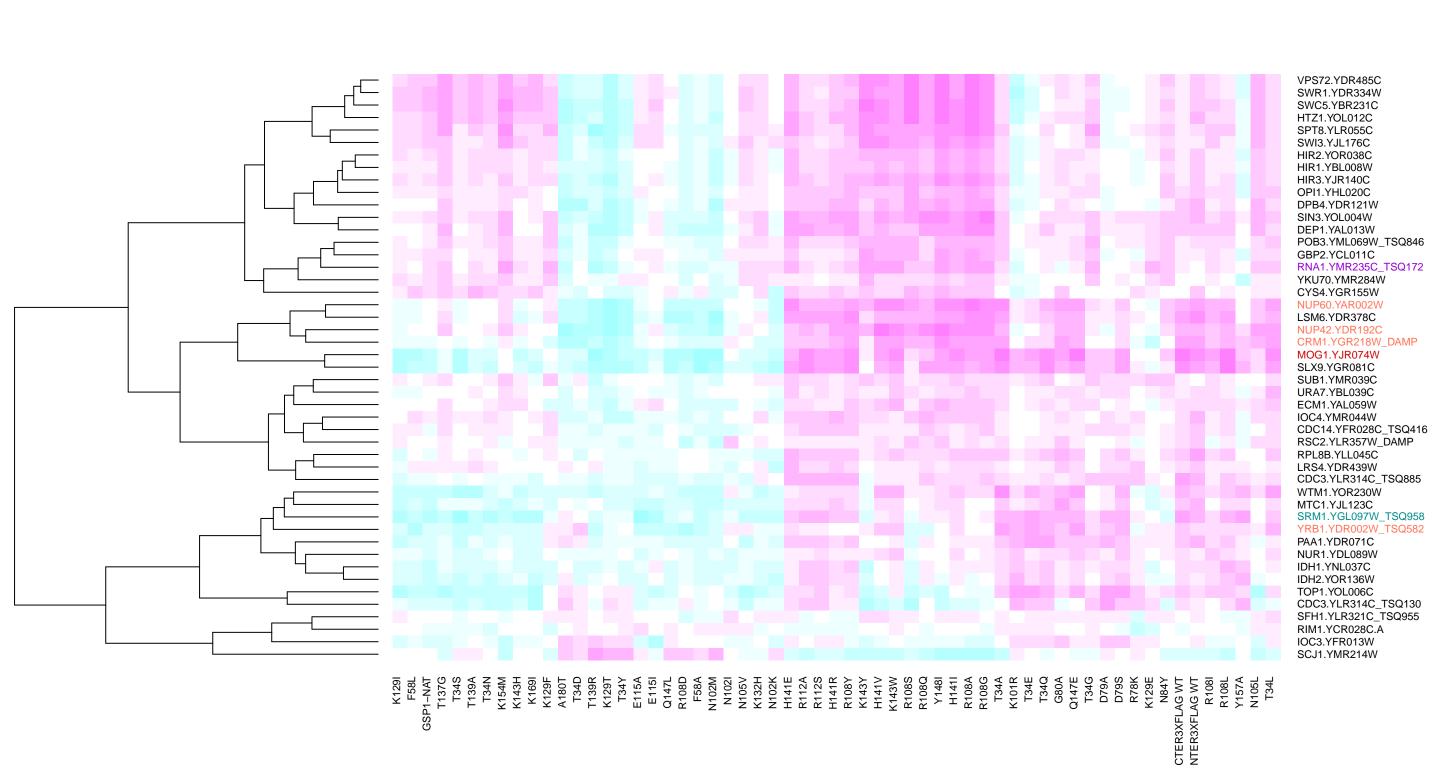
transcription



transcription and mRNA processing

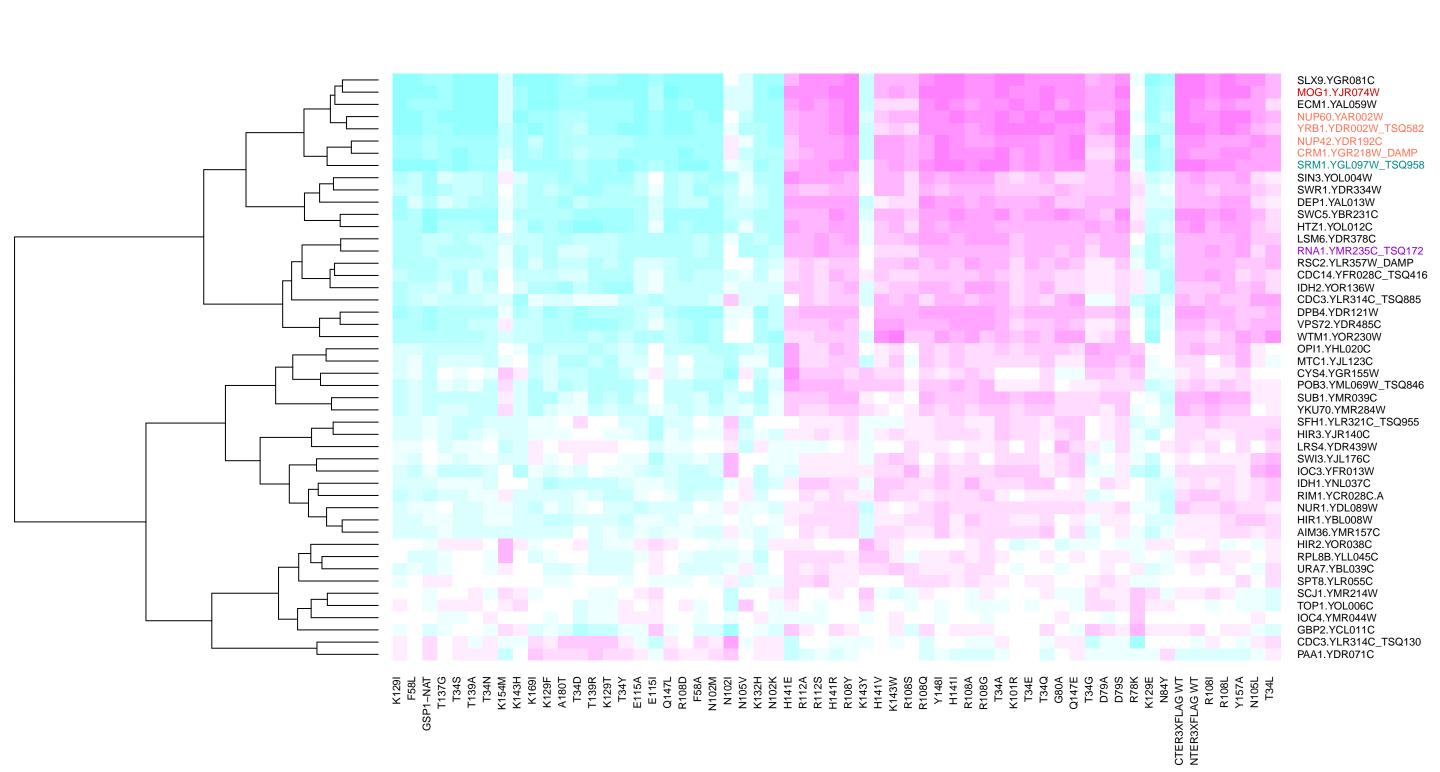


transcription from RNA polymerase II promoter





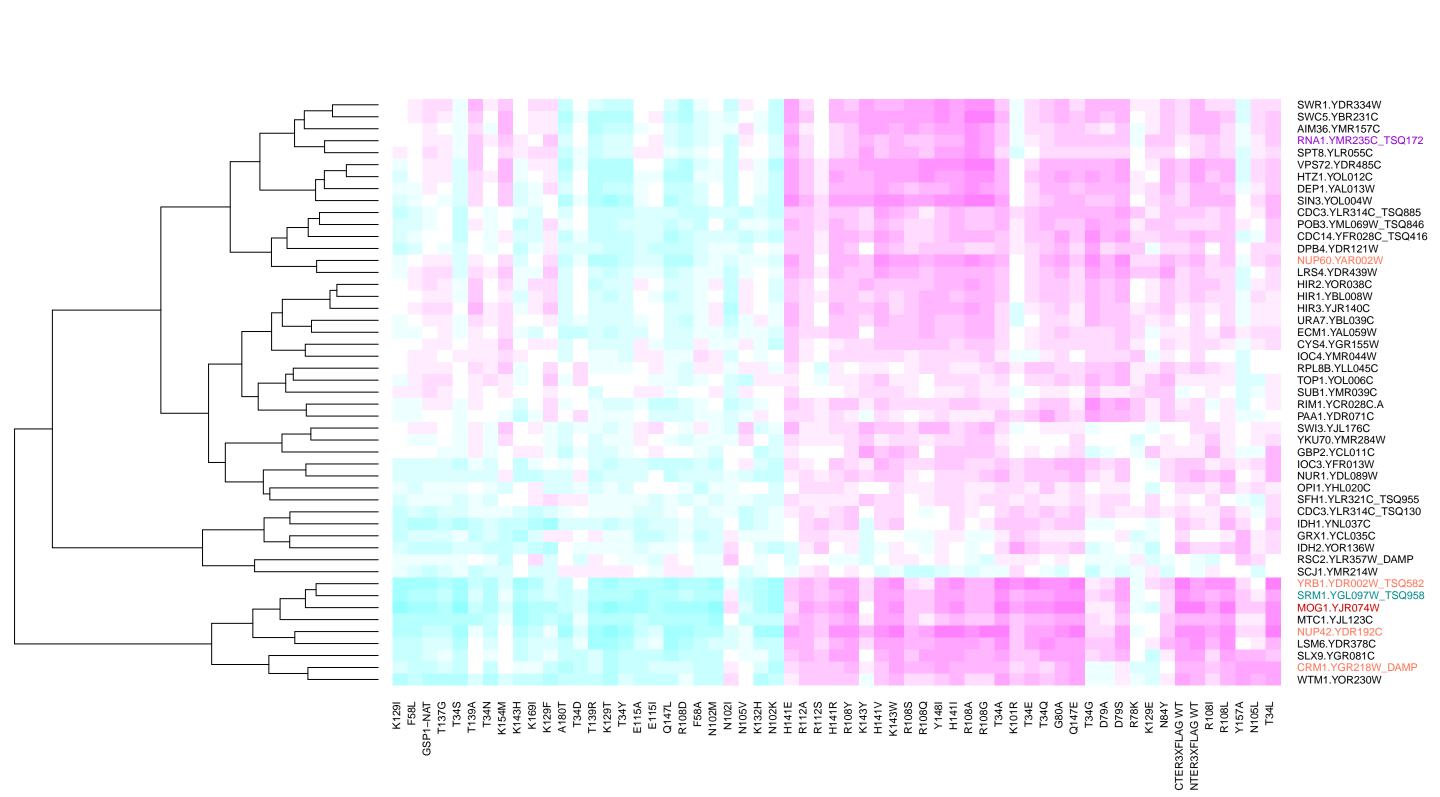
protein targeting_GO_15_2_mut

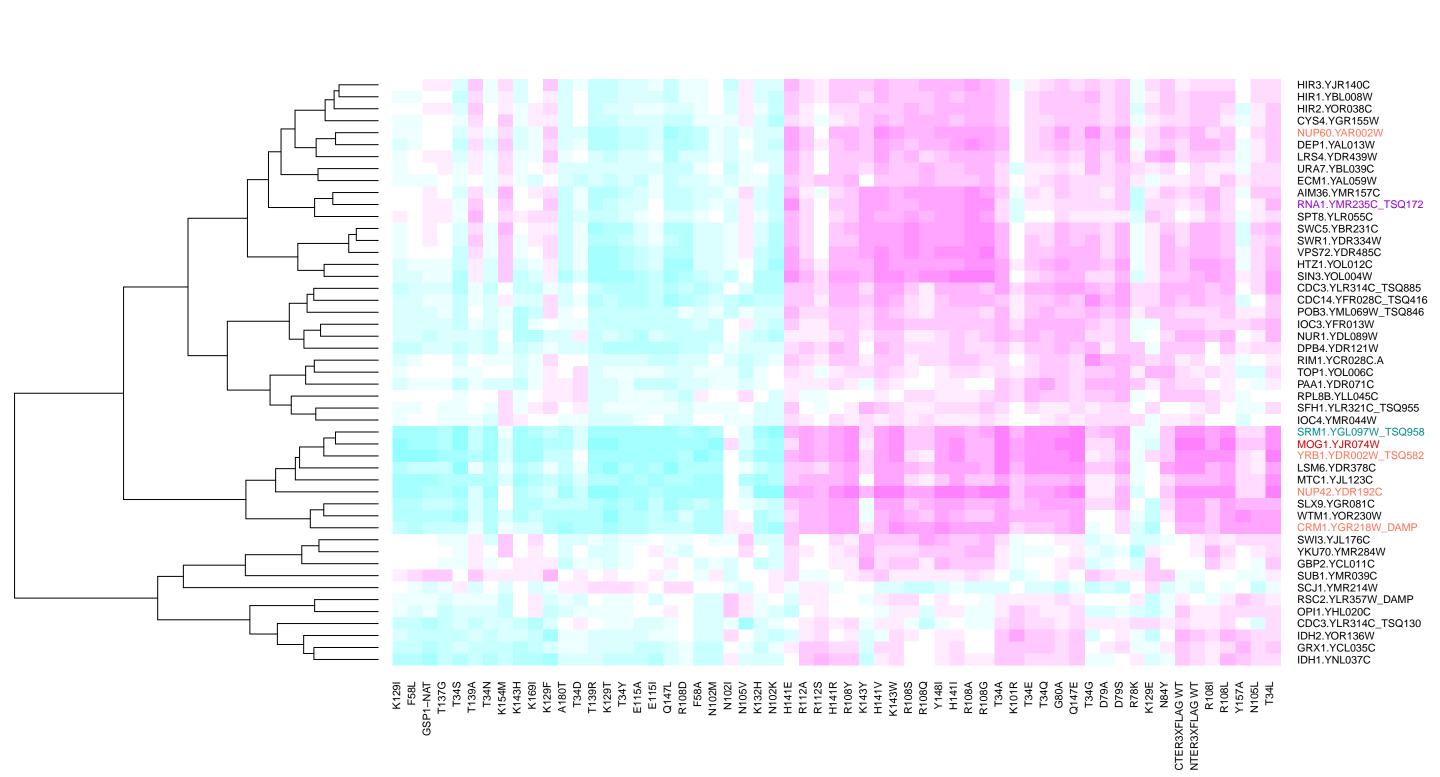


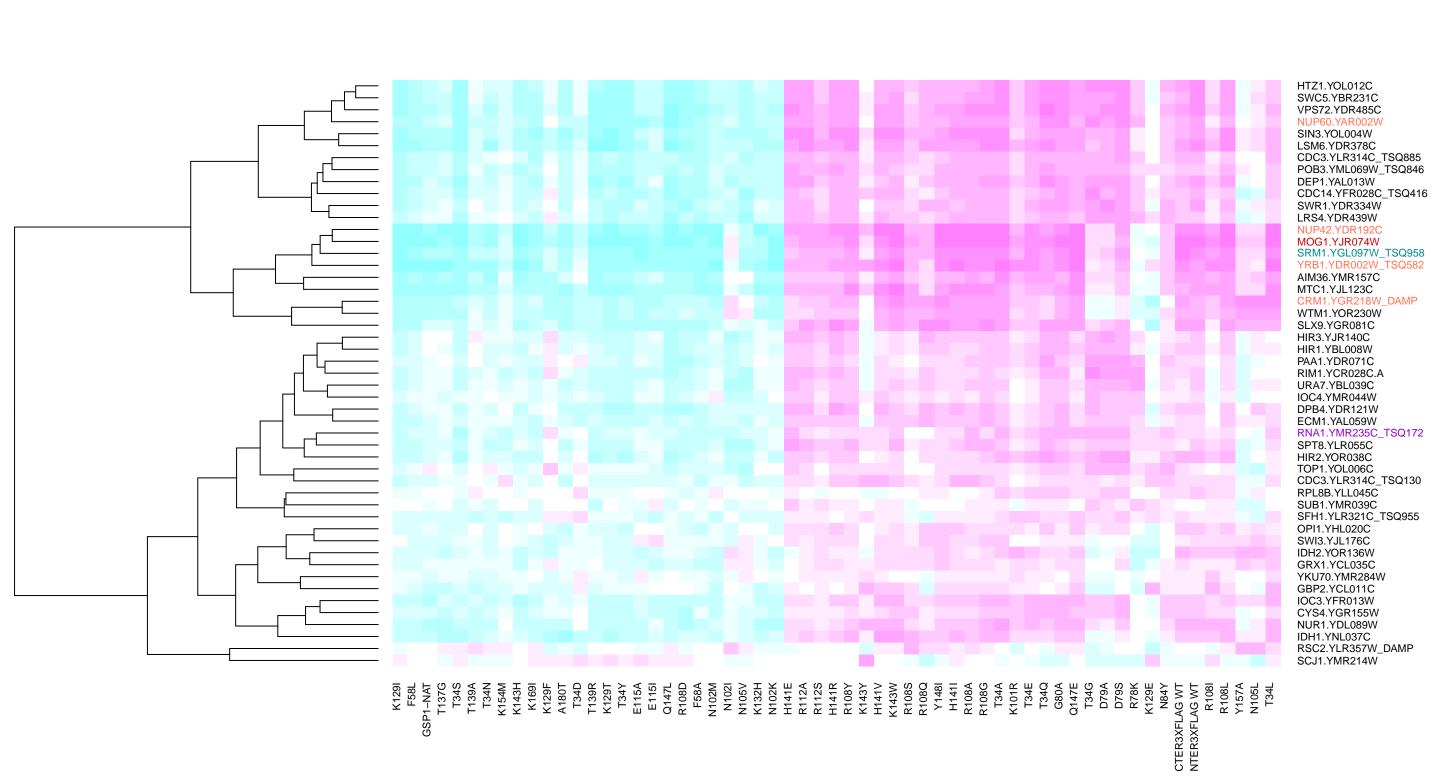
cellular response to DNA damage stimulus_GO_30_1_mut



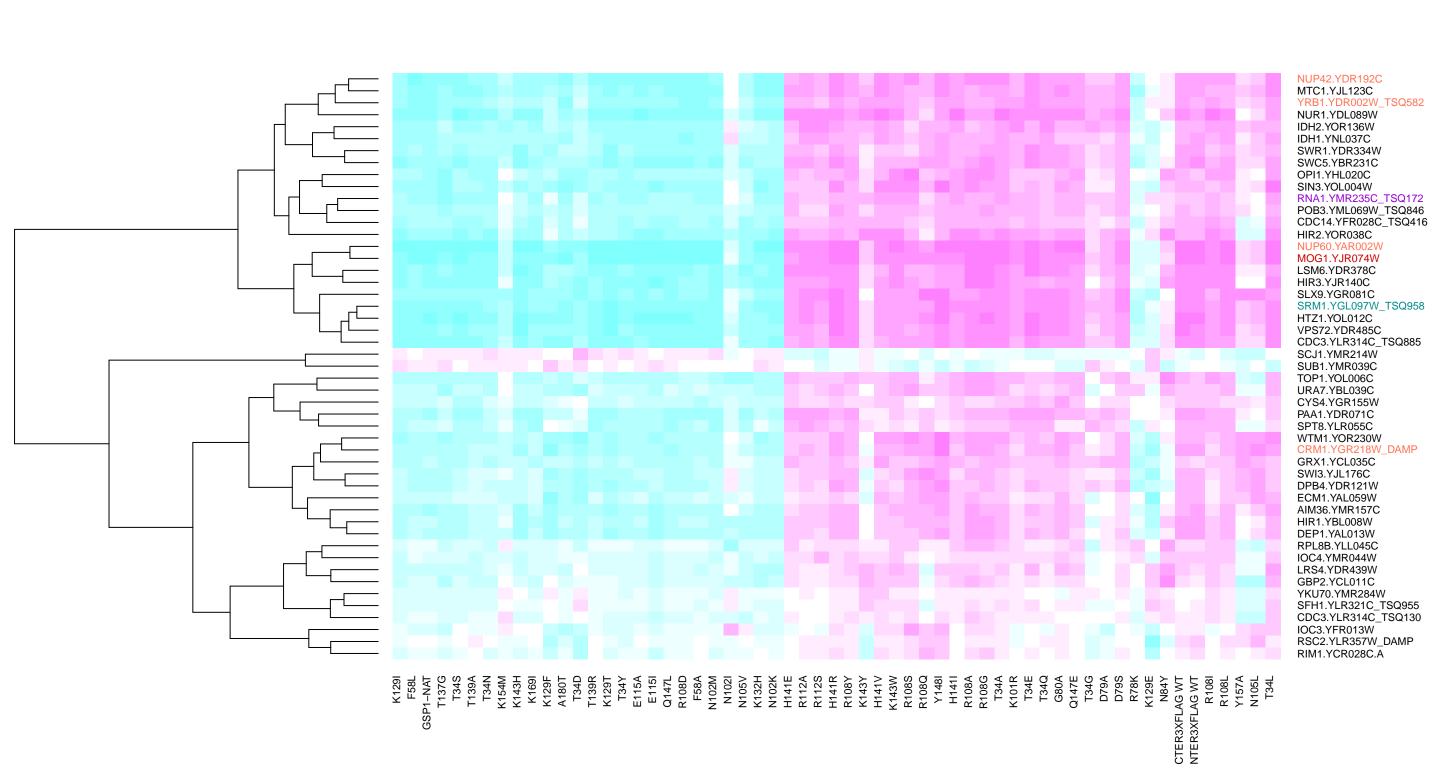
DNA repair



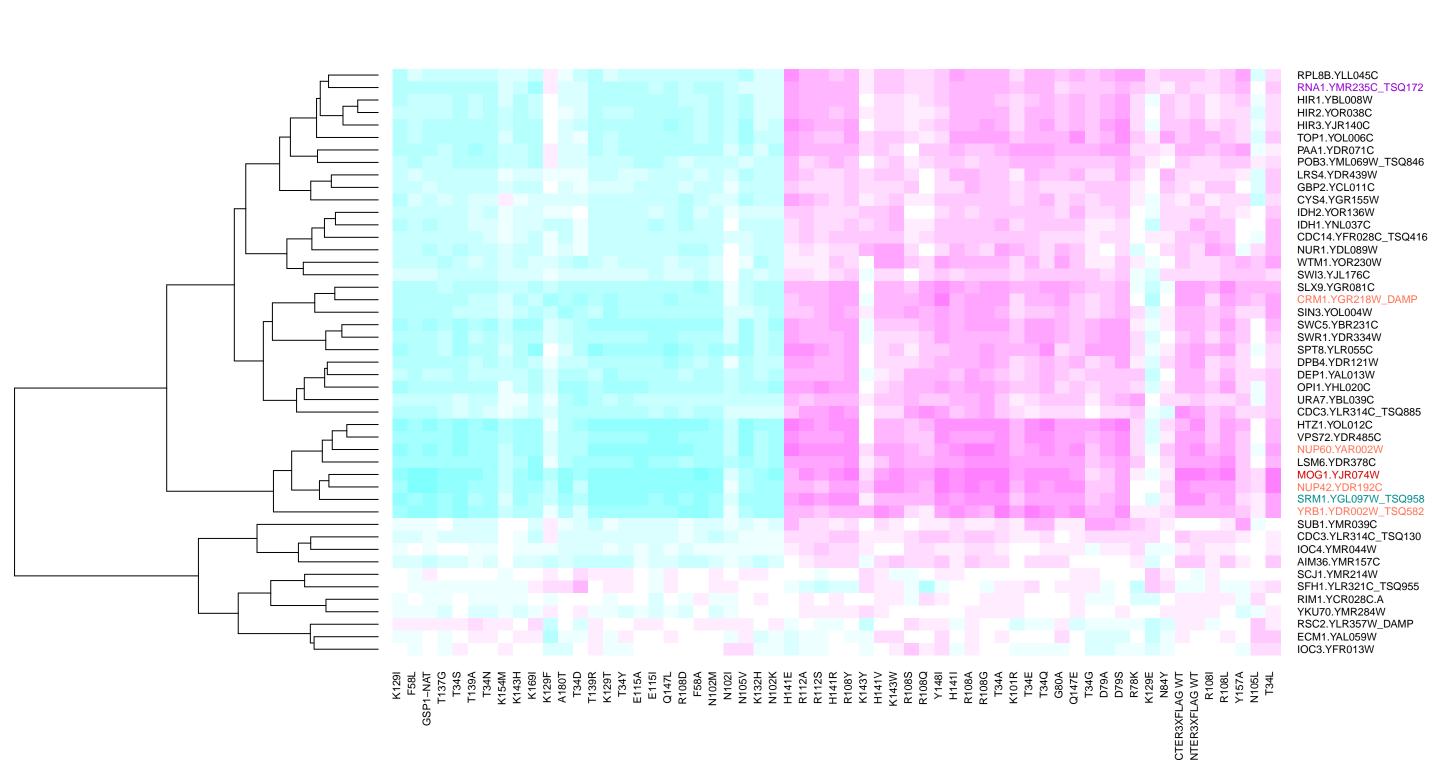




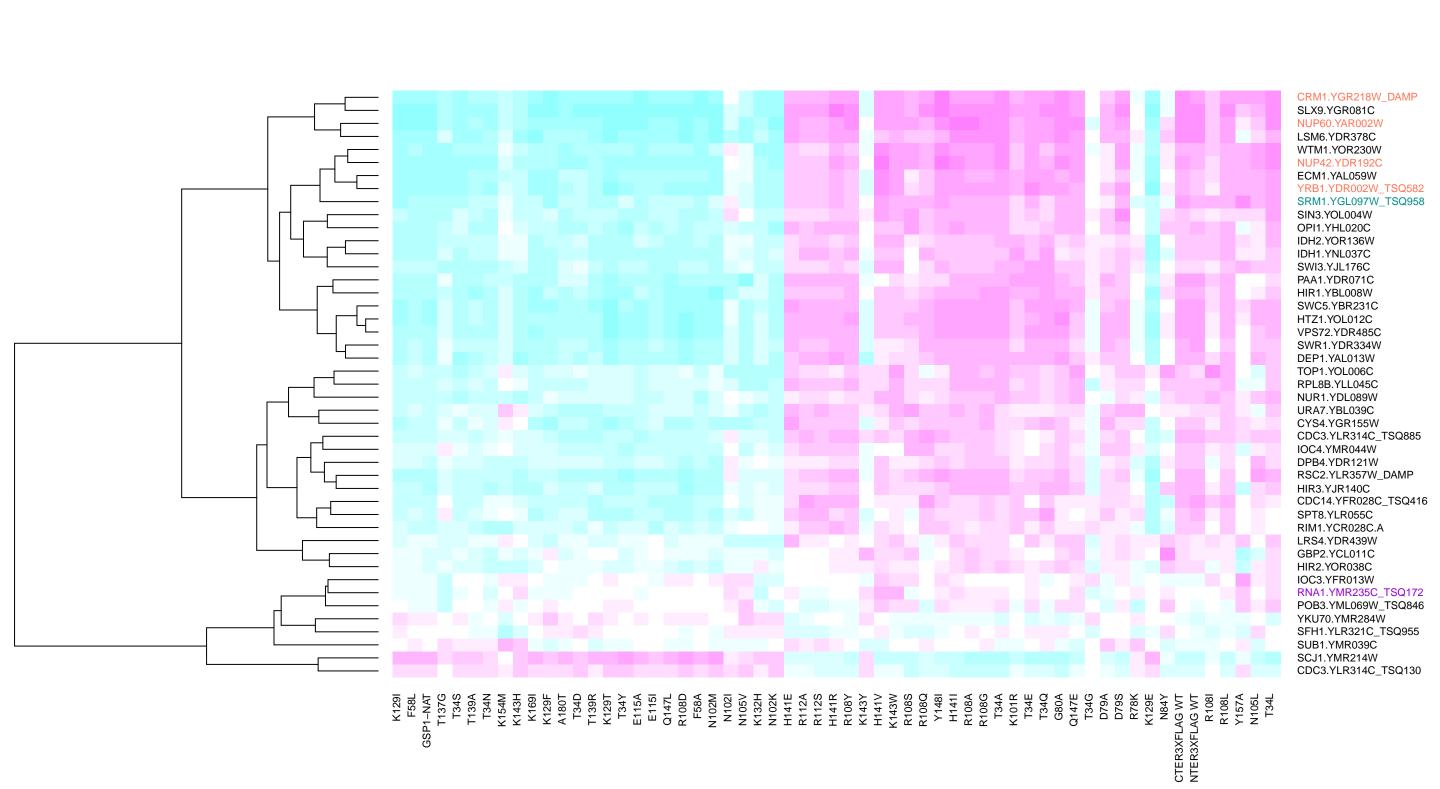
transcription and mRNA processing_GO_15_14_mut



transcription and mRNA processing_GO_30_2_mut



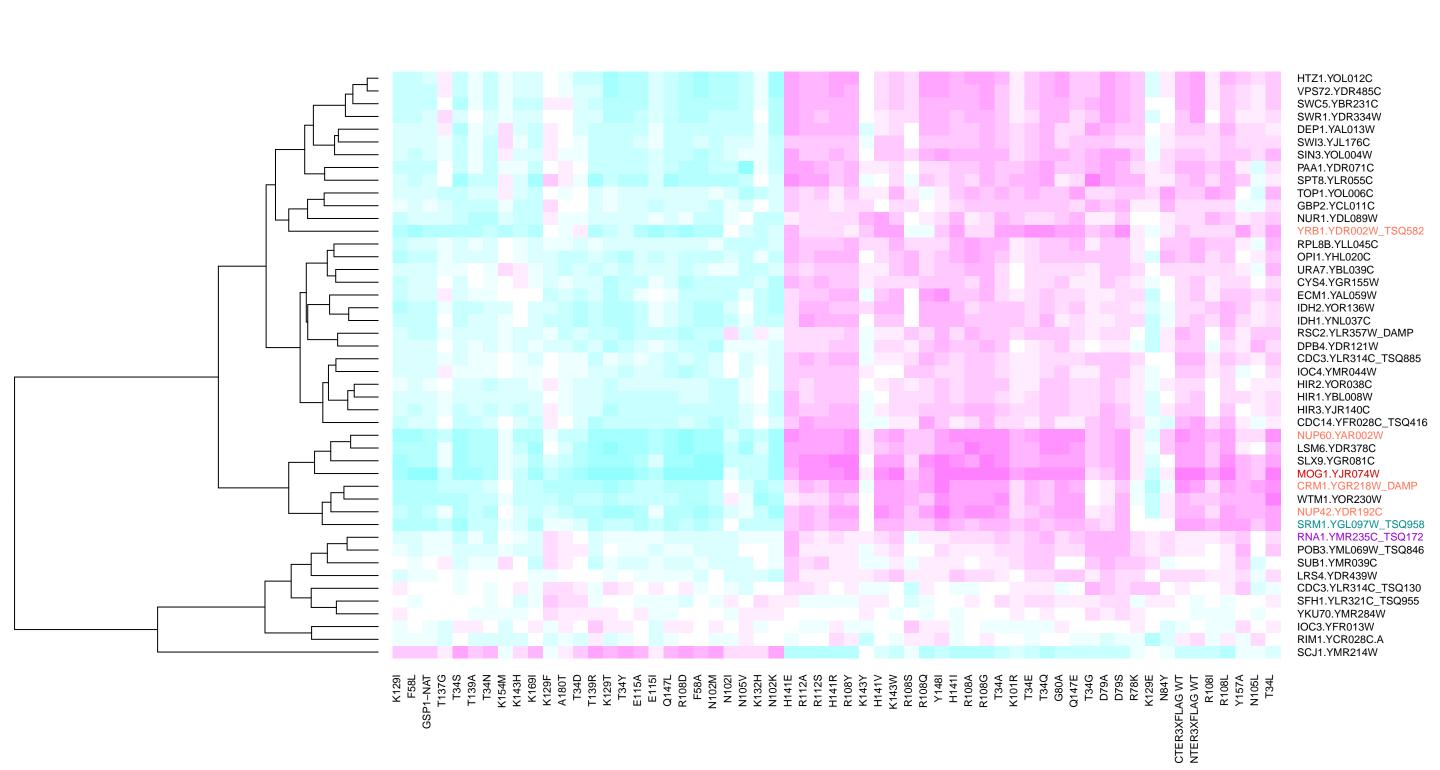
transcription from RNA polymerase II promoter_GO_15_3_mut



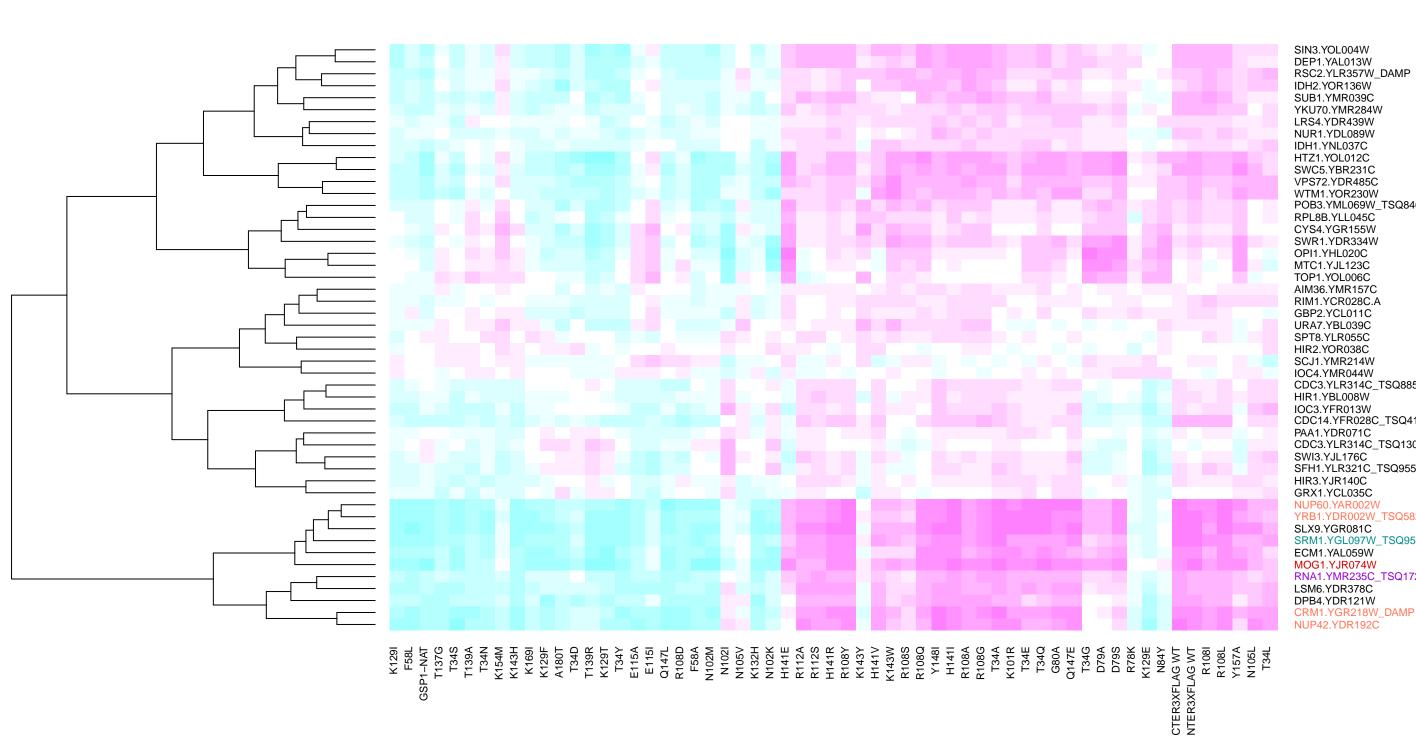
transcription from RNA polymerase II promoter_GO_30_1_all



transcription from RNA polymerase II promoter_GO_30_1_mut

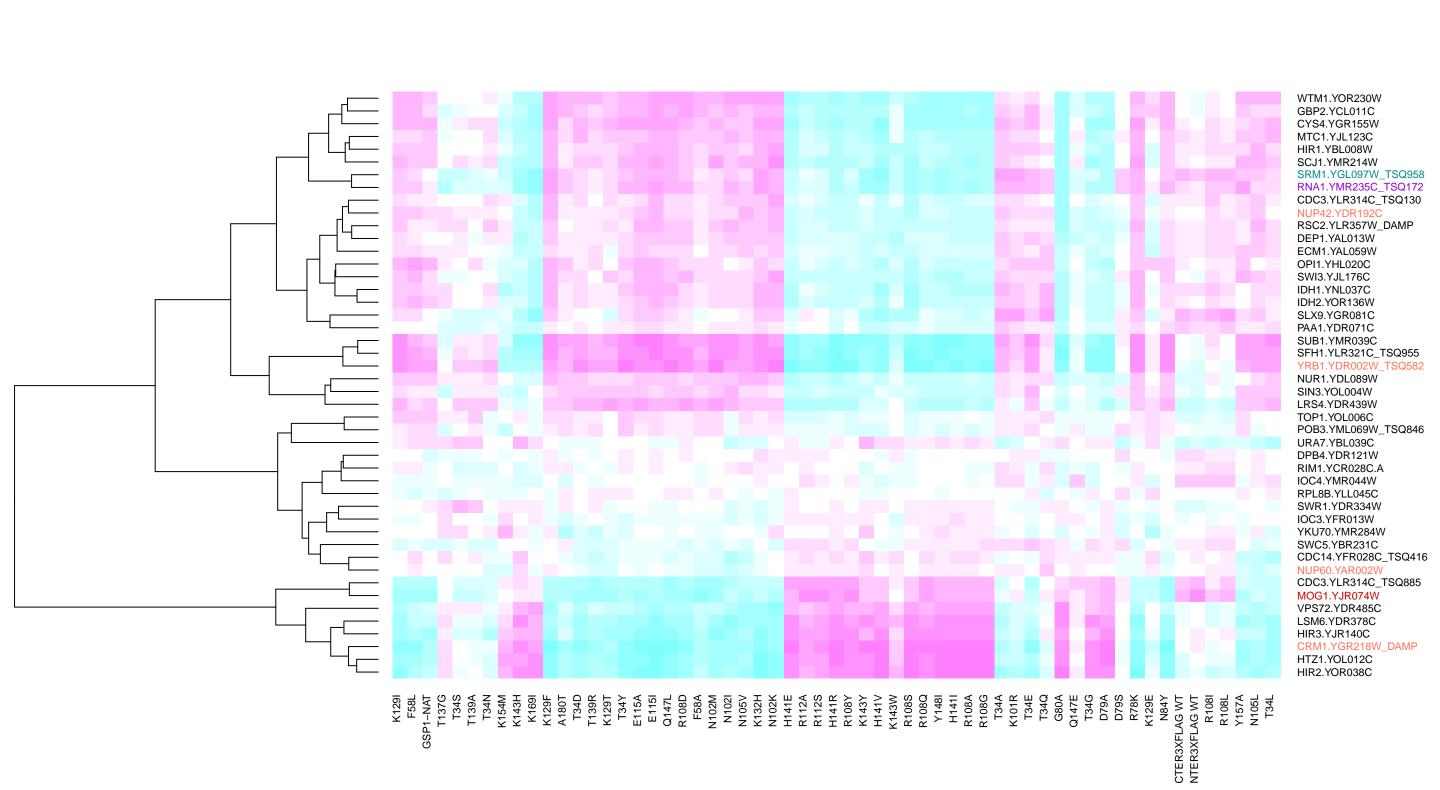


protein targeting_GO_30_1_all

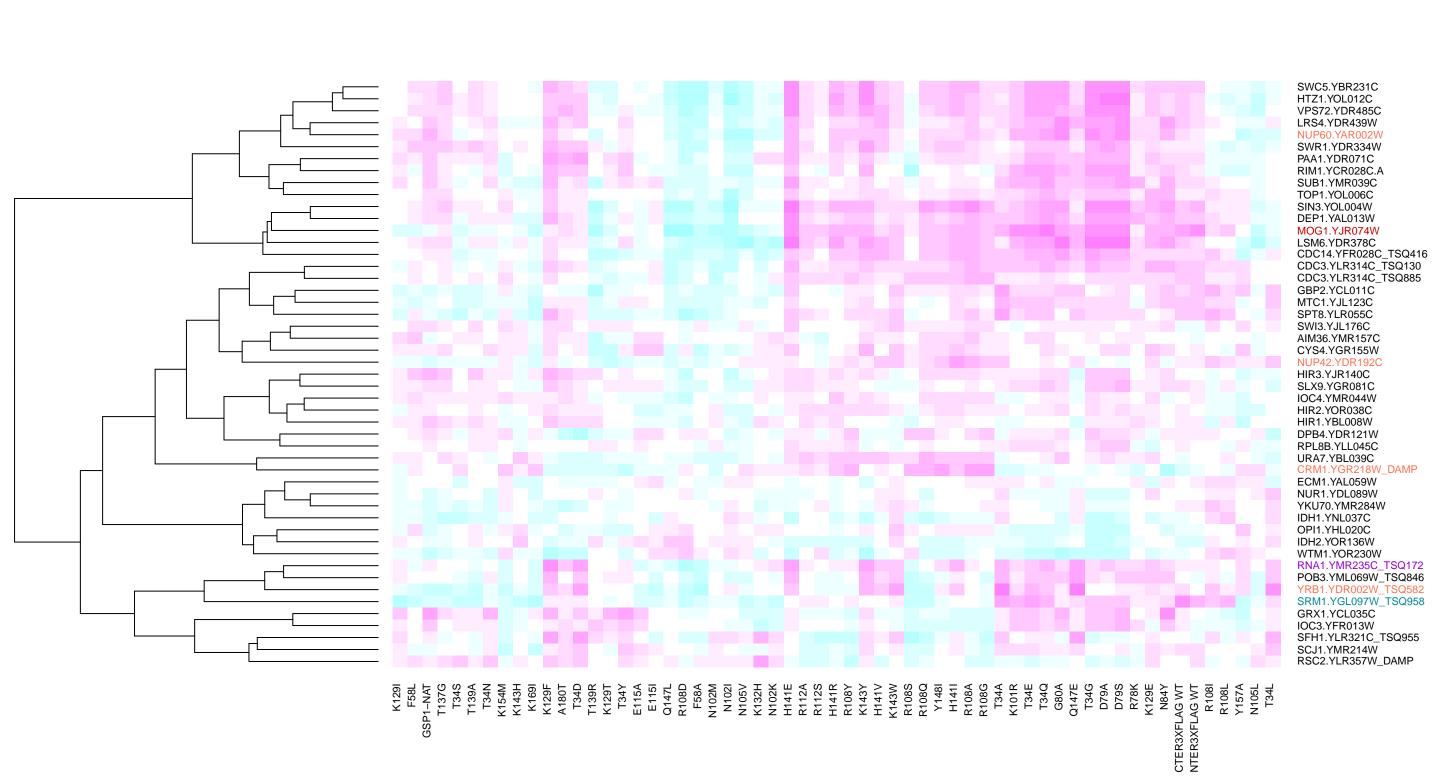


RSC2.YLR357W_DAMP YKU70.YMR284W POB3.YML069W_TSQ846 CDC3.YLR314C_TSQ885 CDC14.YFR028C_TSQ416 CDC3.YLR314C_TSQ130 SFH1.YLR321C_TSQ955 YRB1.YDR002W_TSQ582 SRM1.YGL097W_TSQ958 RNA1.YMR235C_TSQ172

whole_library_30_14_mut



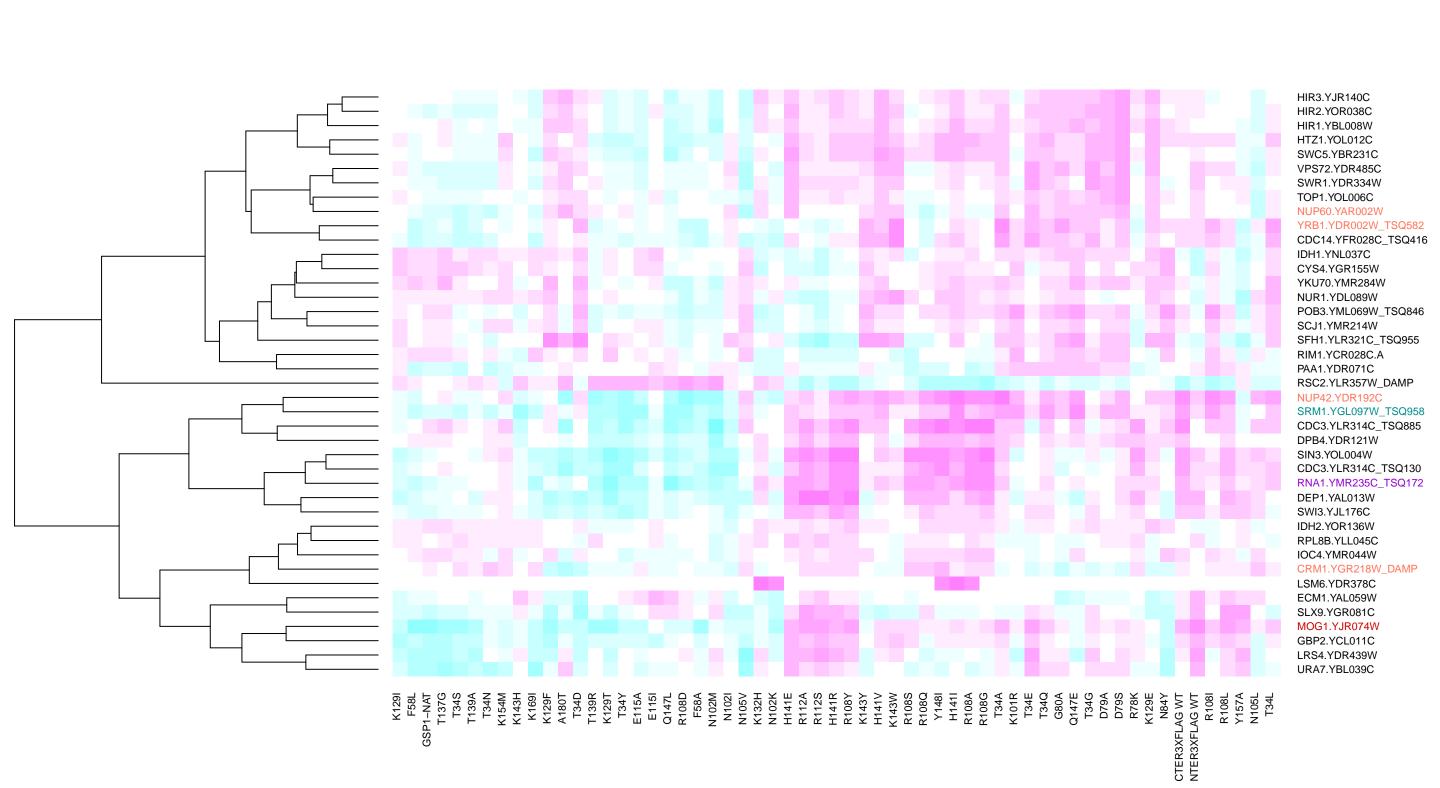
budding



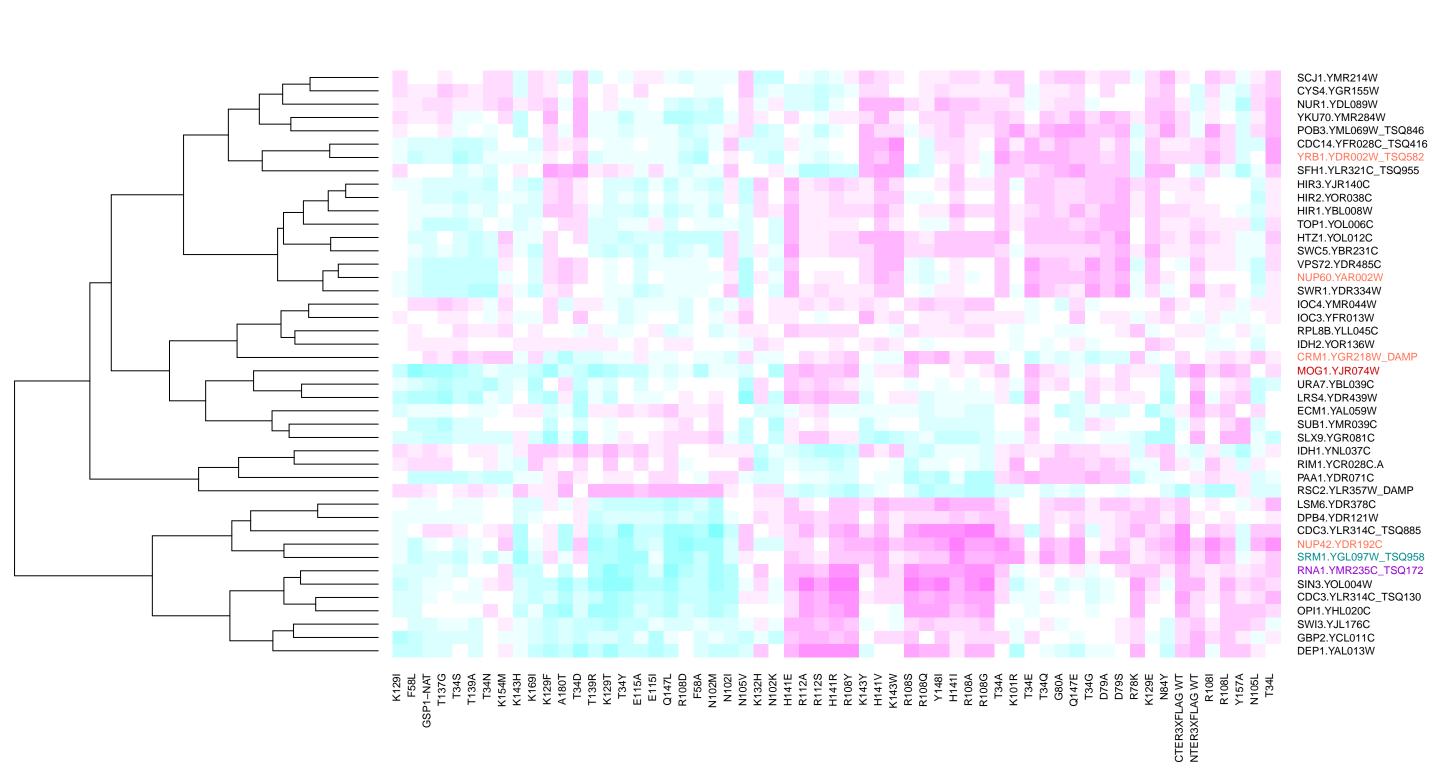
cytoskeleton and microtubules



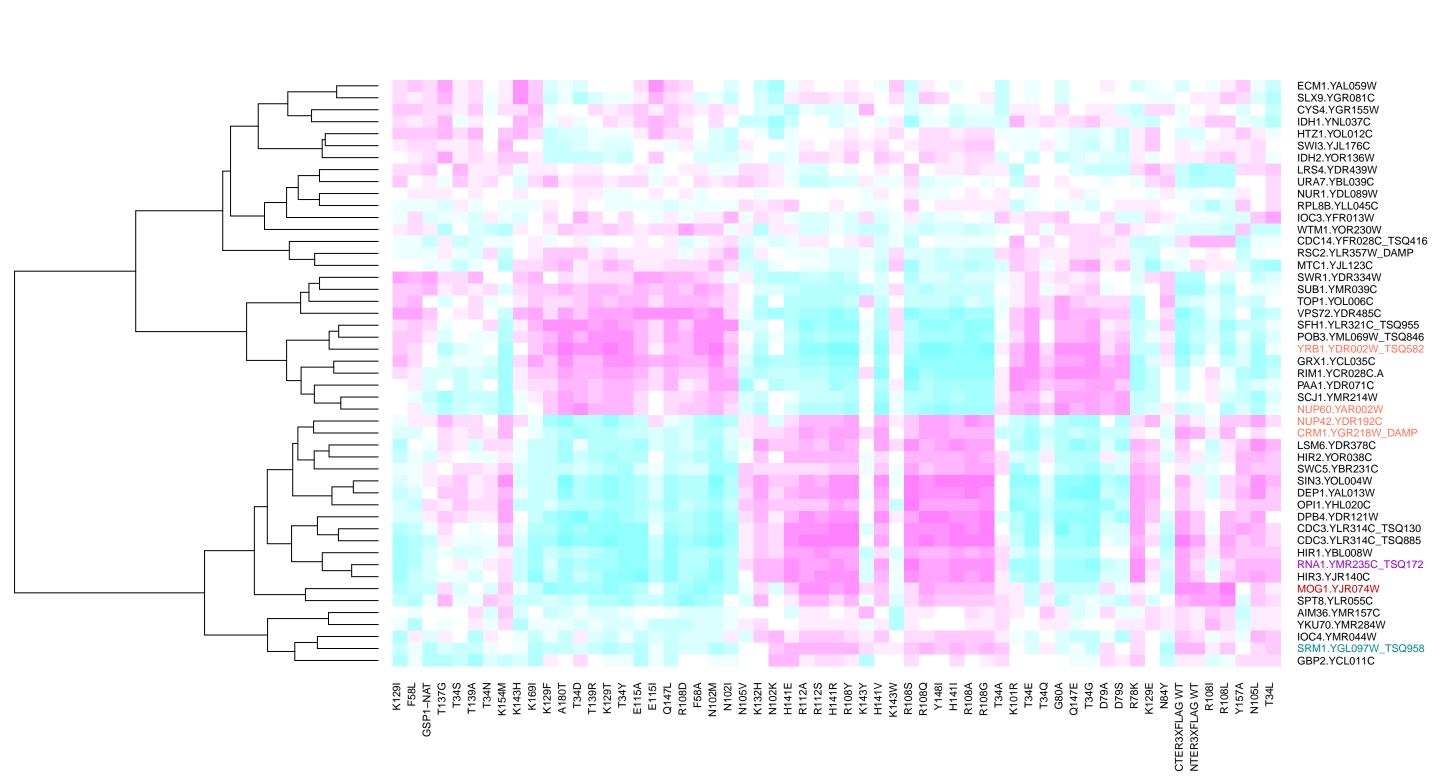
ribosomes and translation



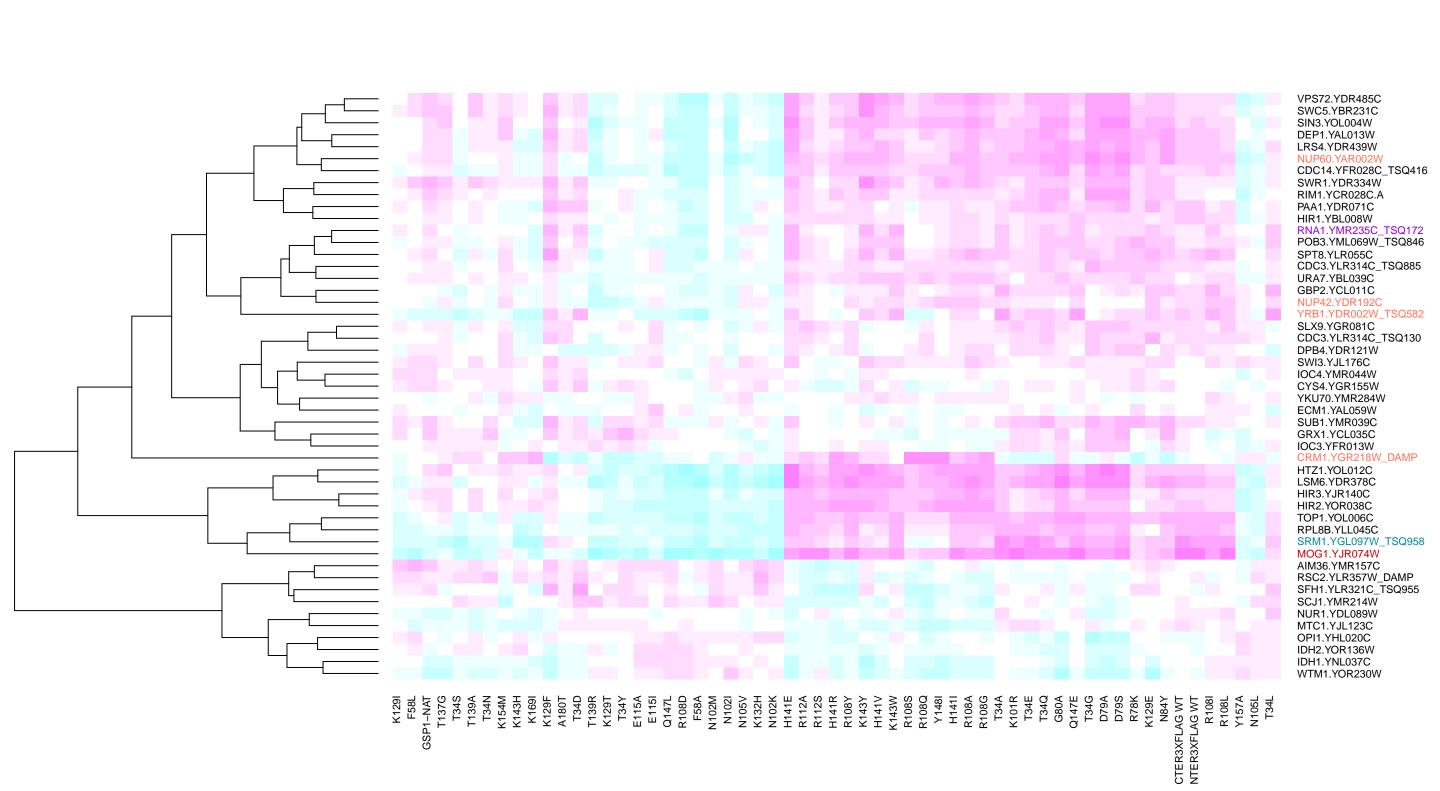
ribosomes and translation_GO_30_1_all



transcription and mRNA processing_GO_15_8_all



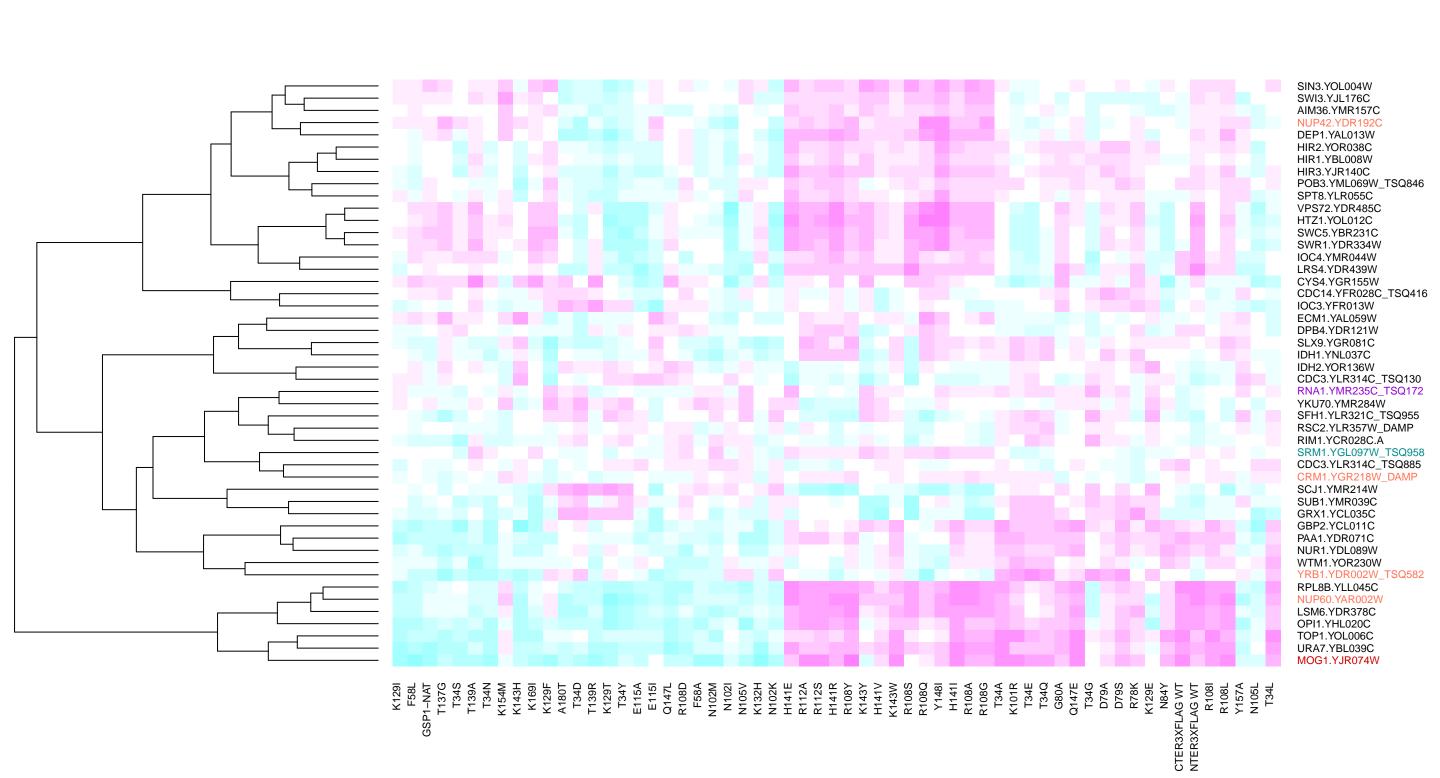
cell cycle



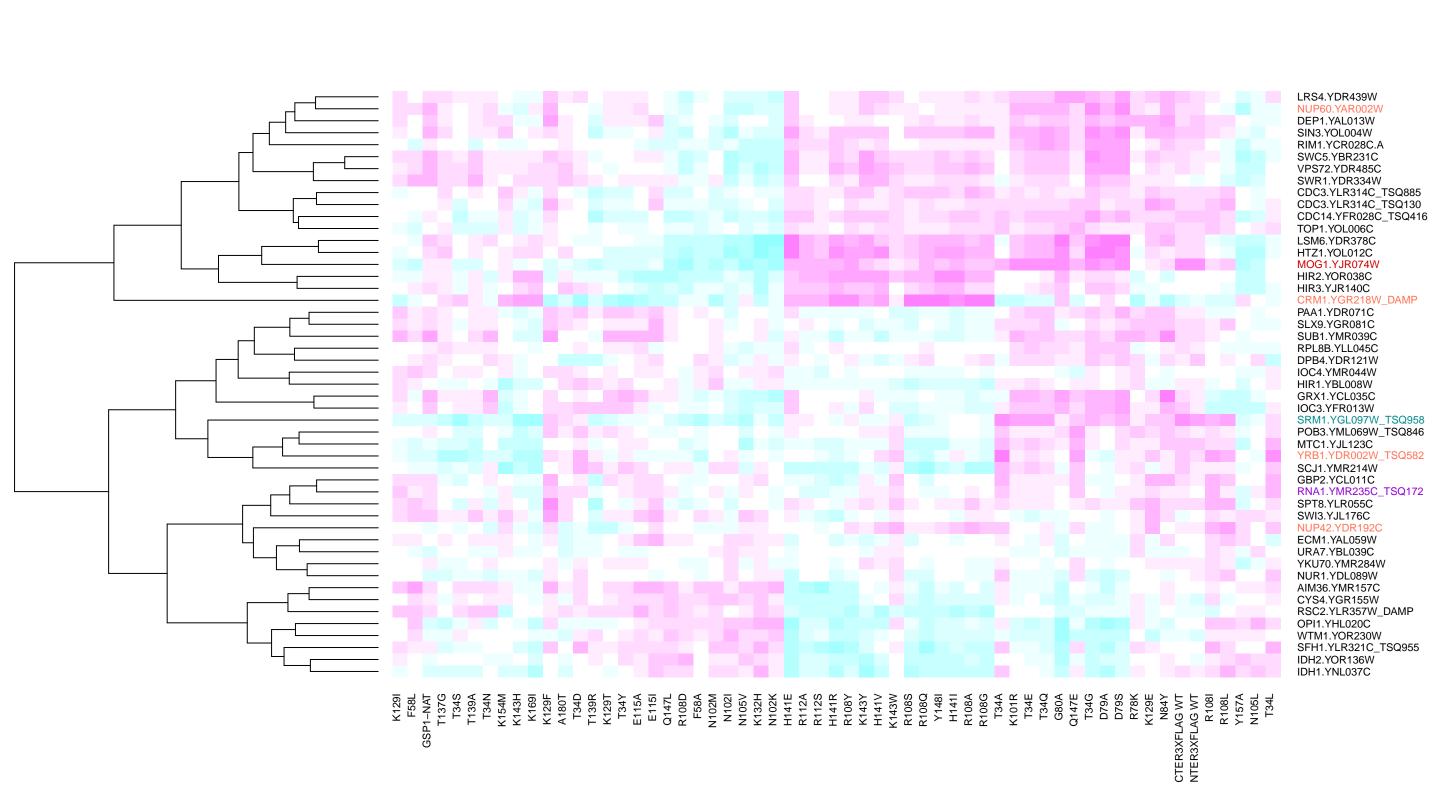
protein targeting_GO_30_1_mut



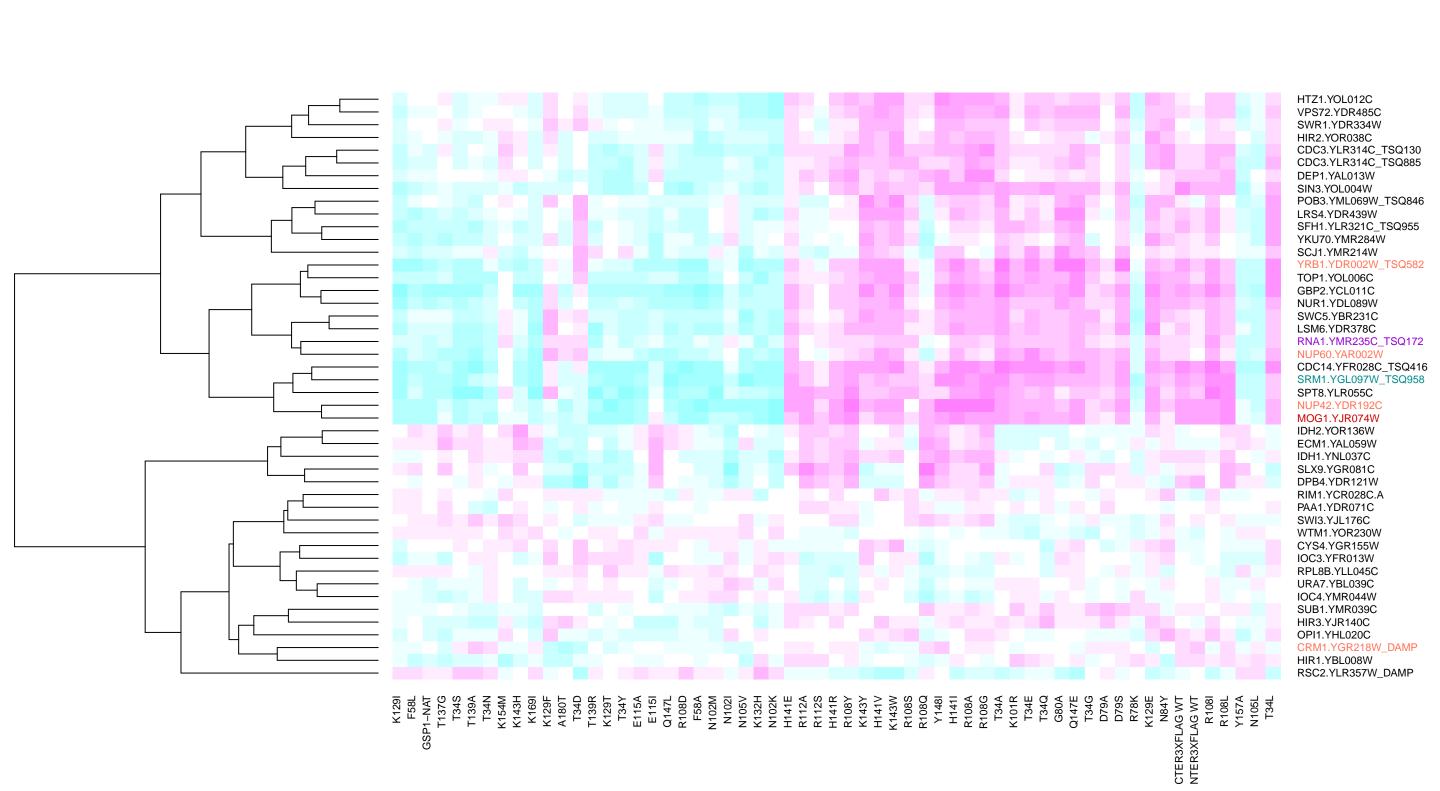
DNA-templated transcription, elongation



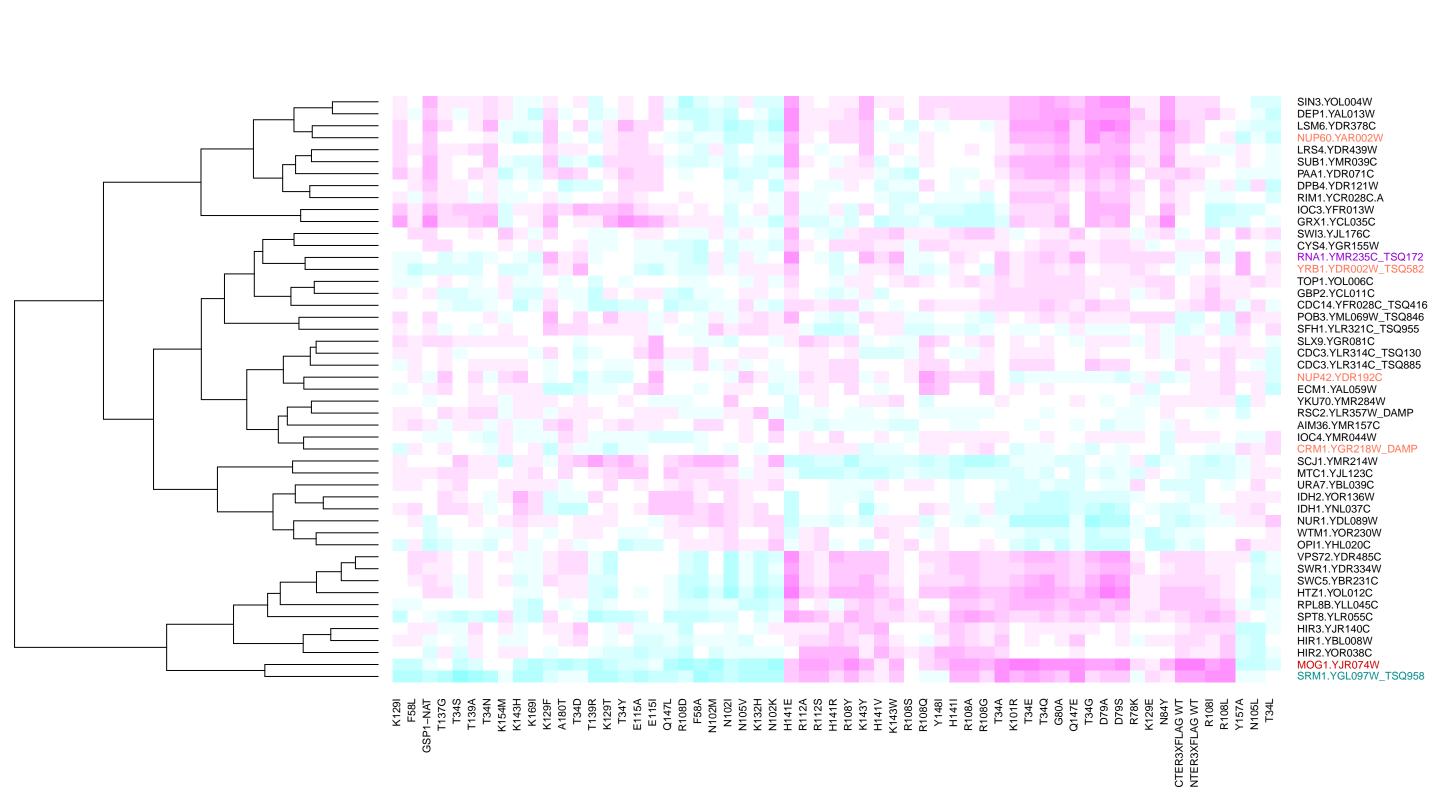
mitotic cell cycle



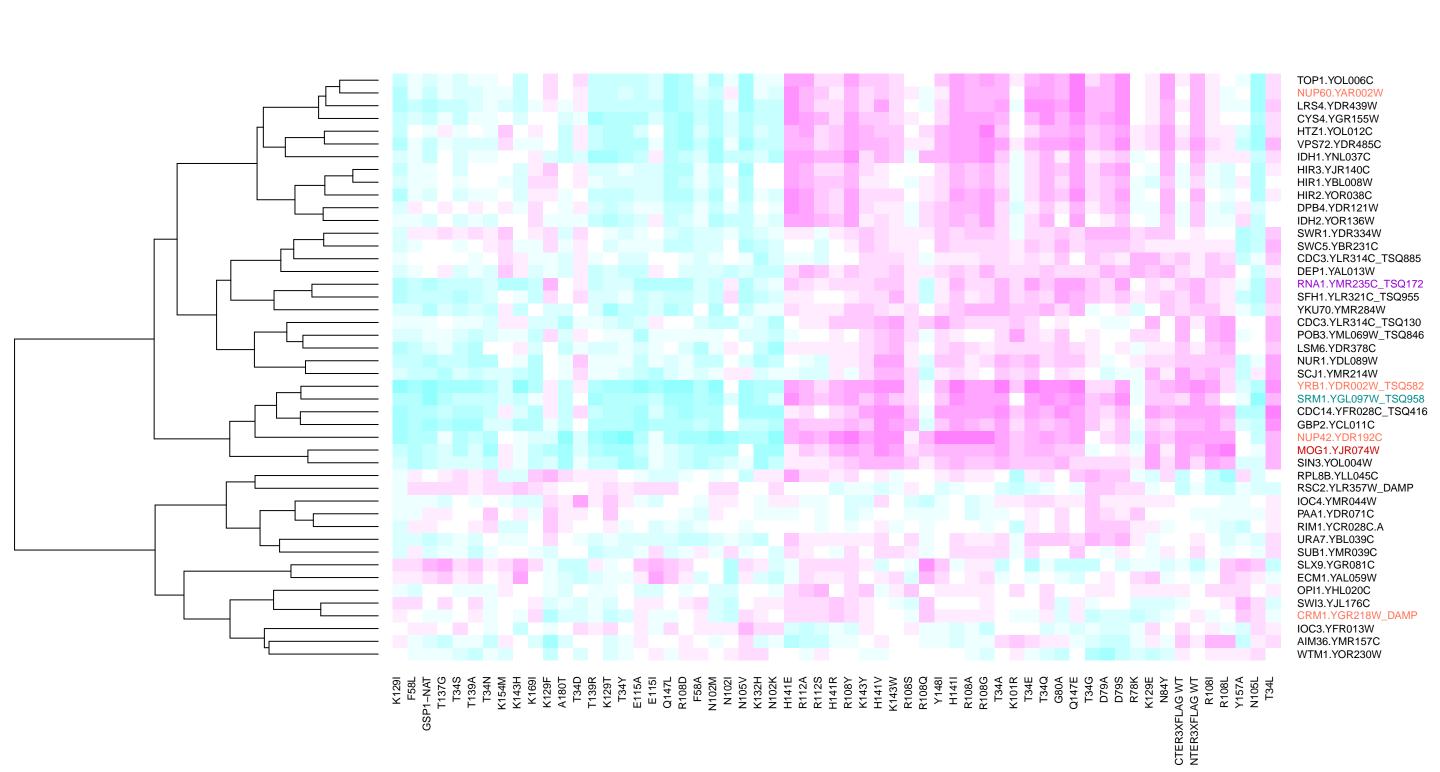
mitotic cell cycle_GO_15_1_all



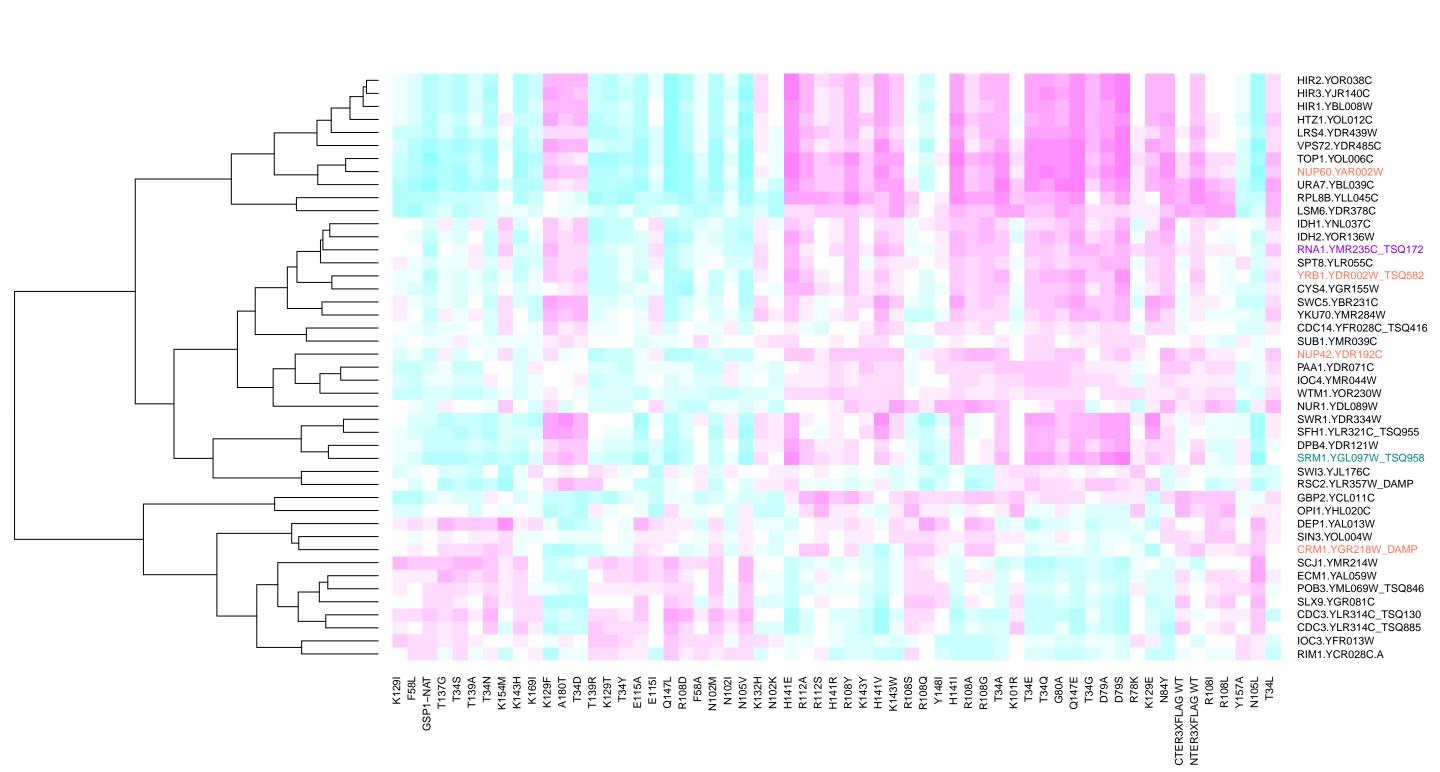
regulation of cell cycle



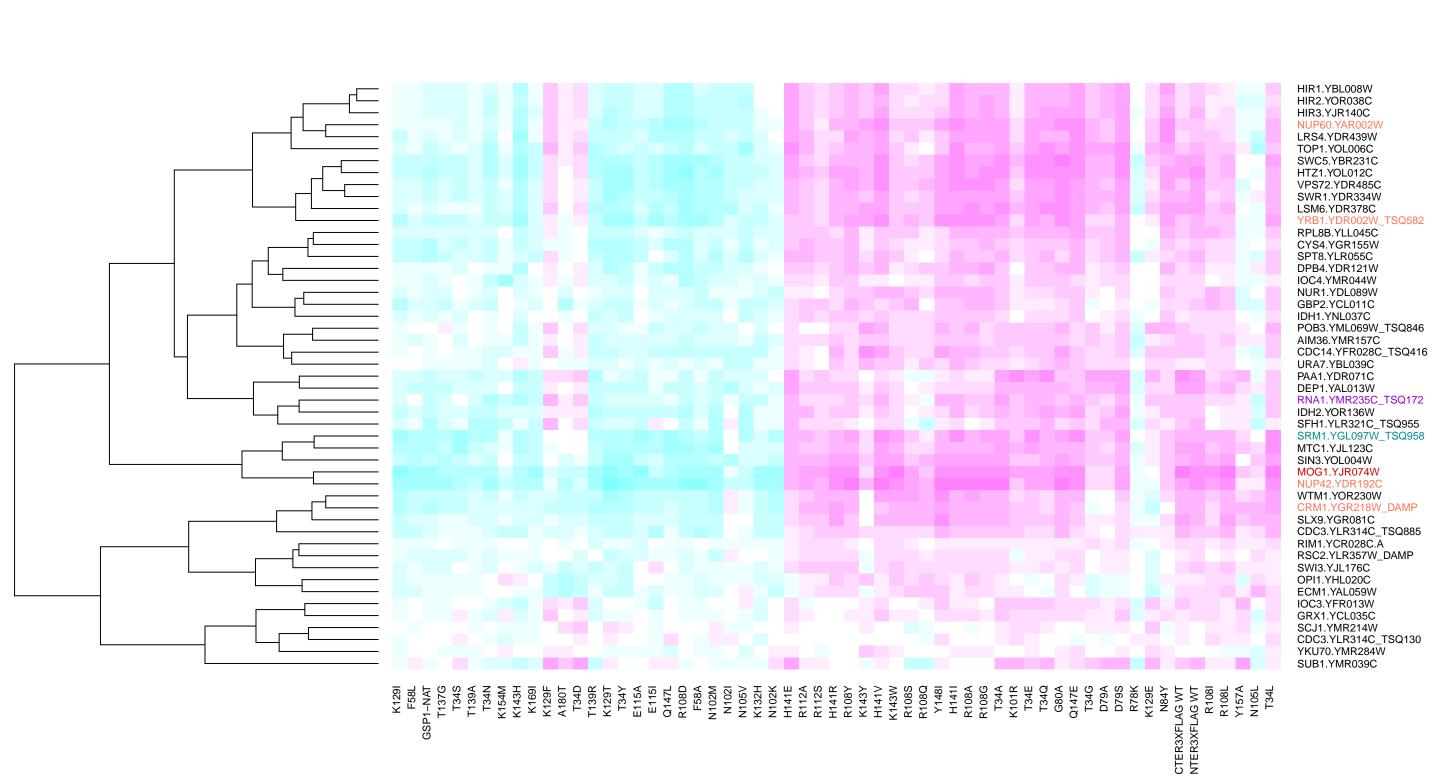
RNA catabolic process



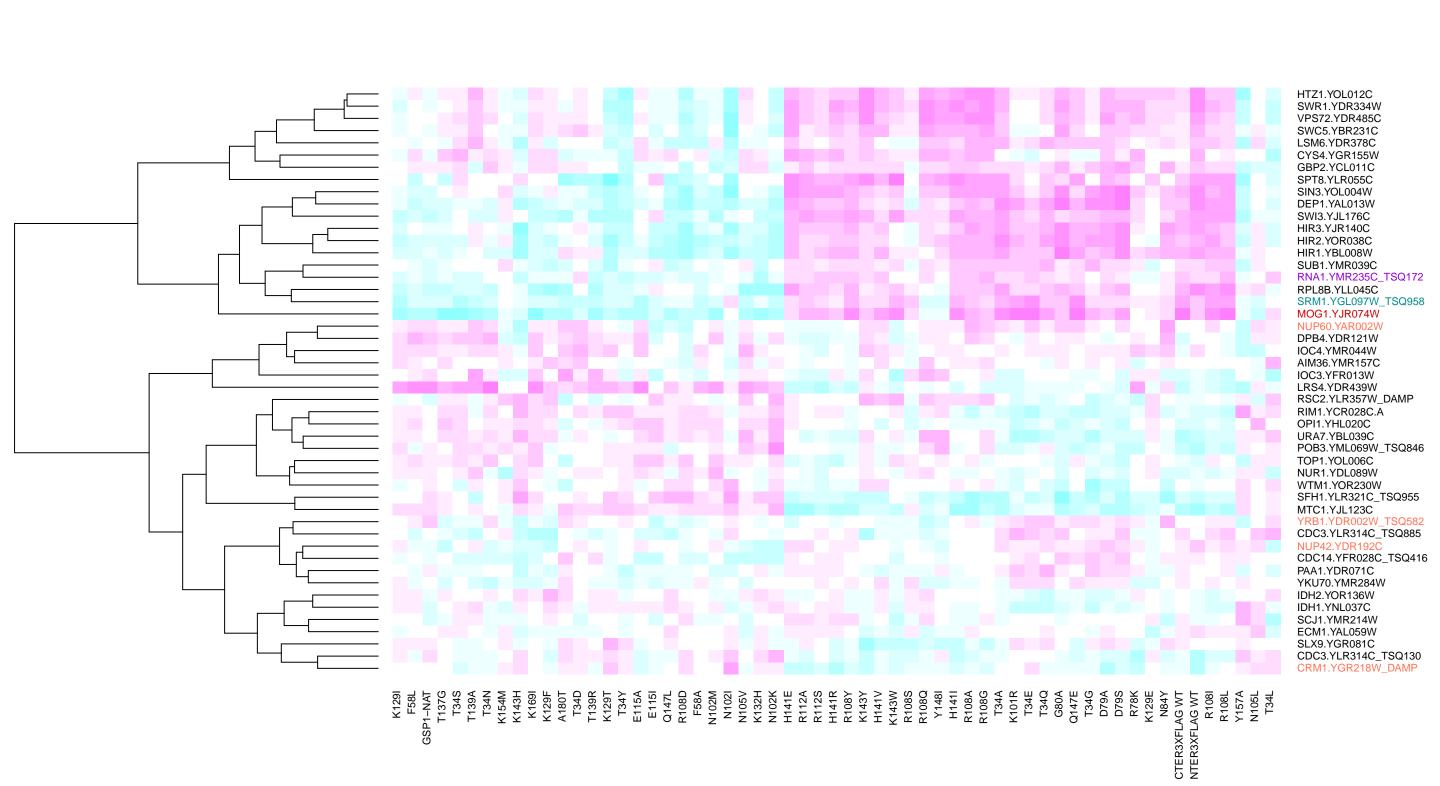
transcription and mRNA processing_GO_30_2_all



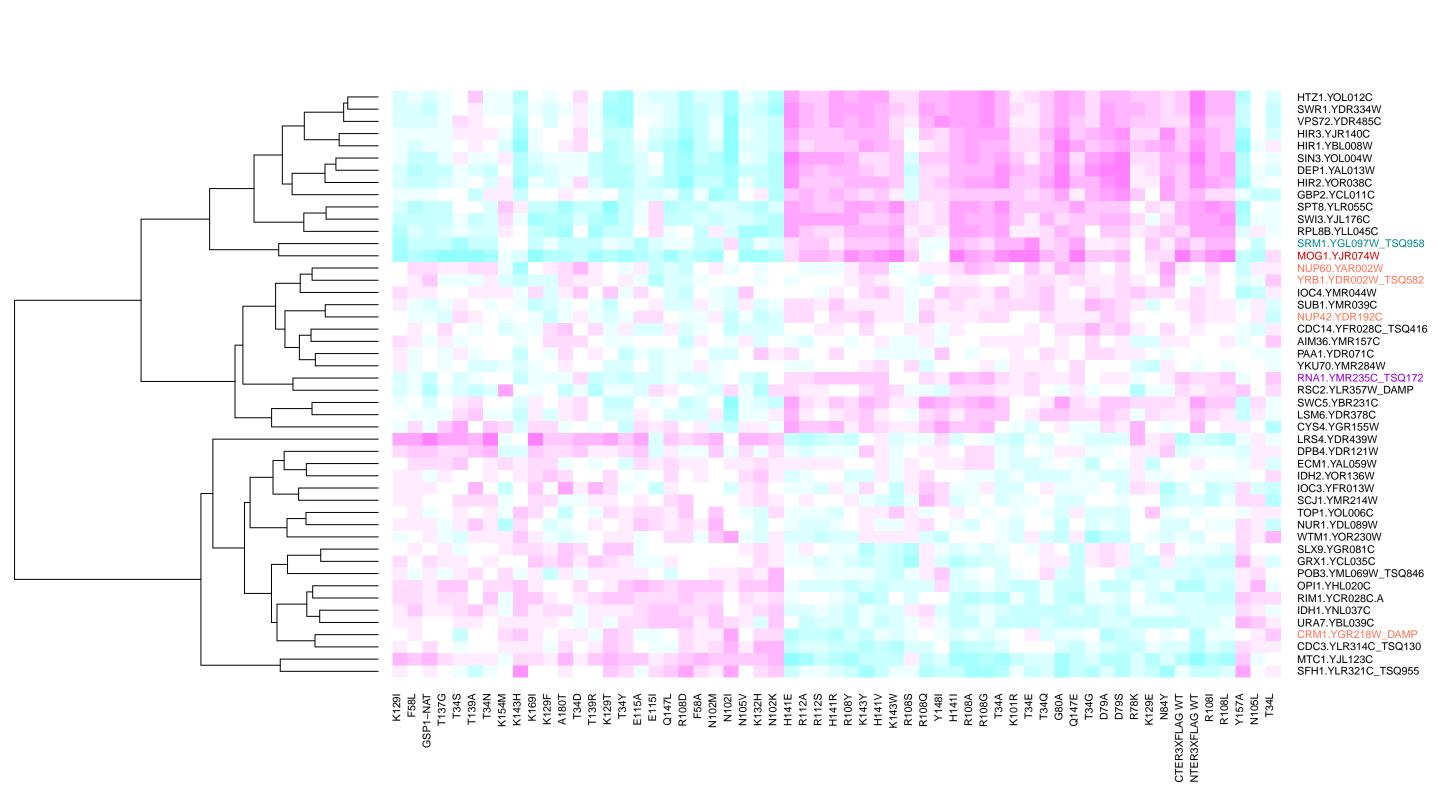
whole_library_30_3_all

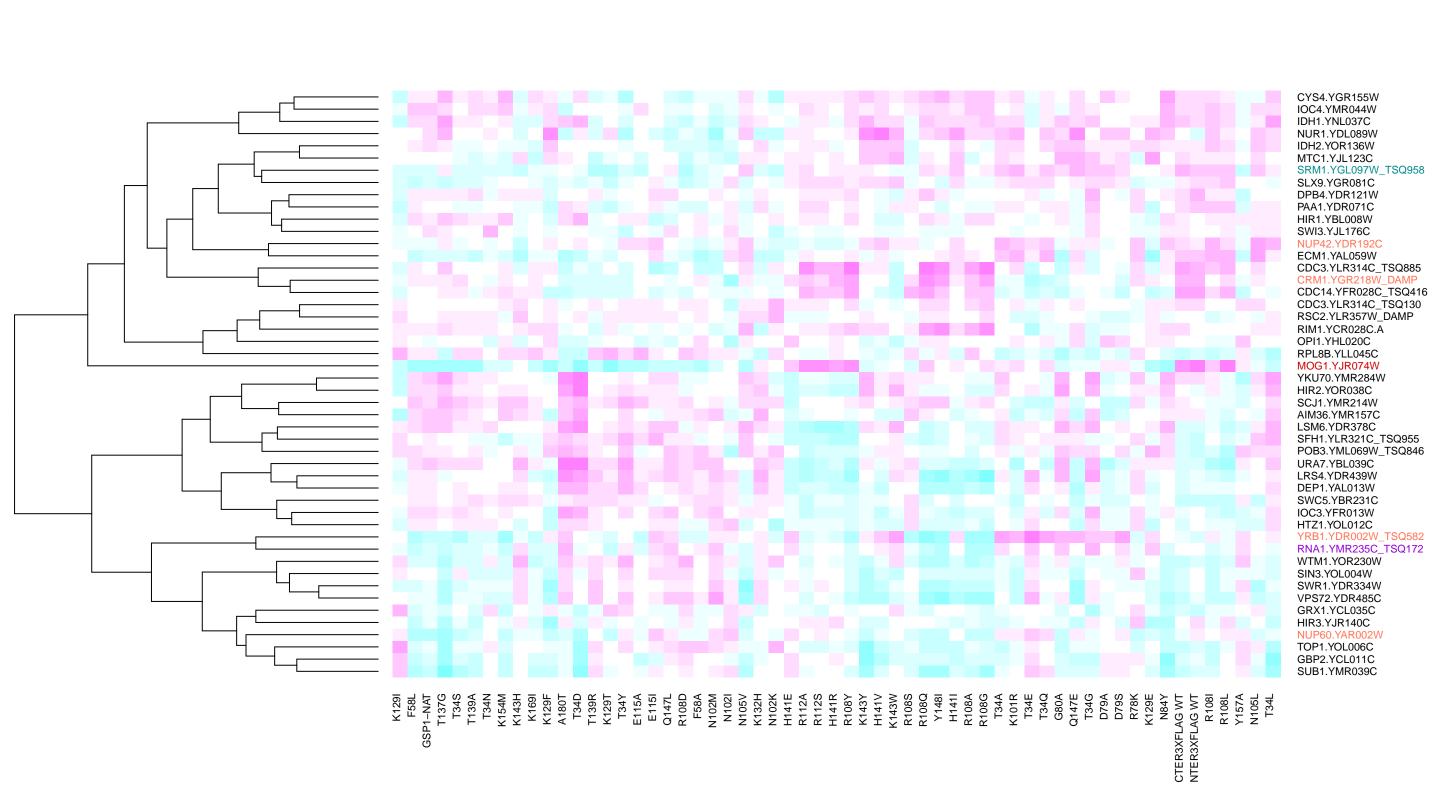


proteolysis involved in cellular protein catabolic process

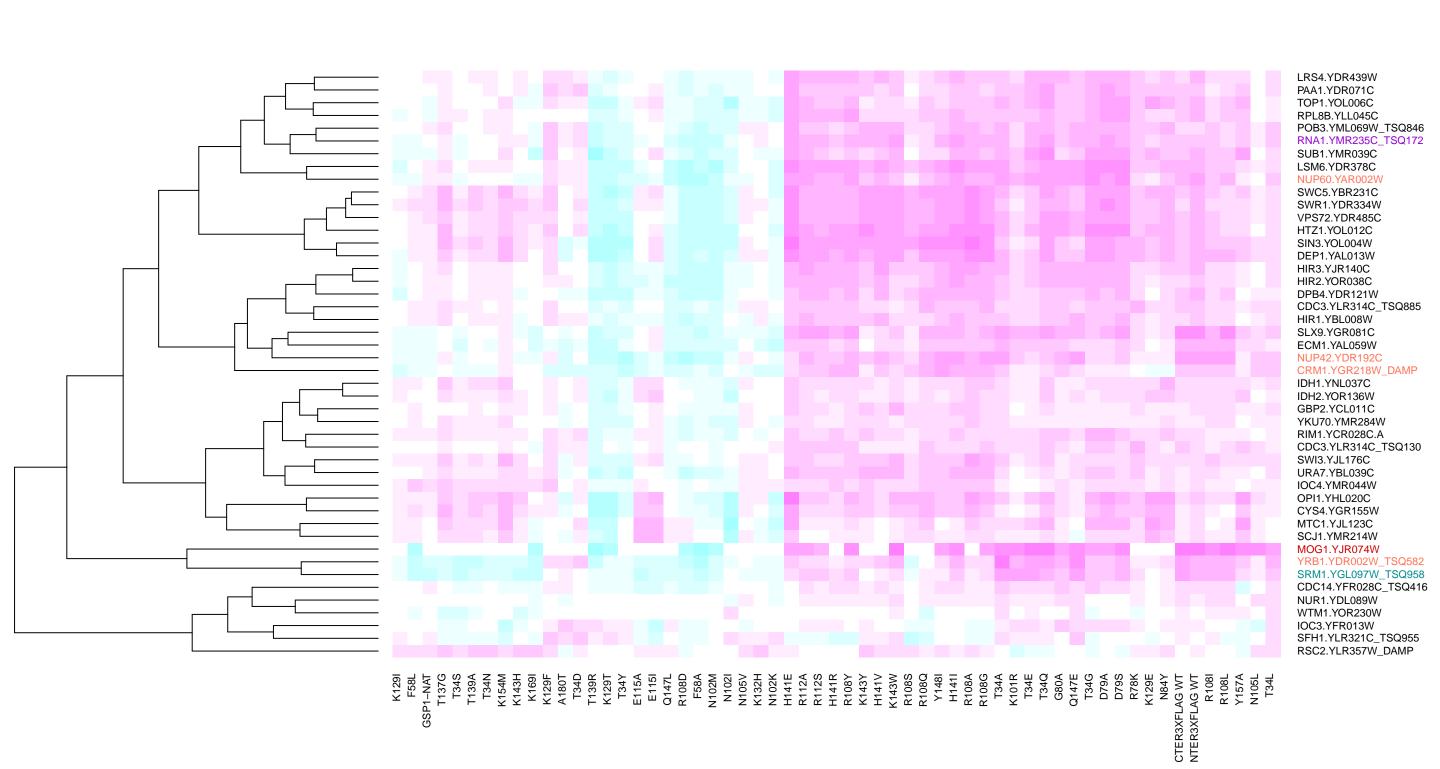


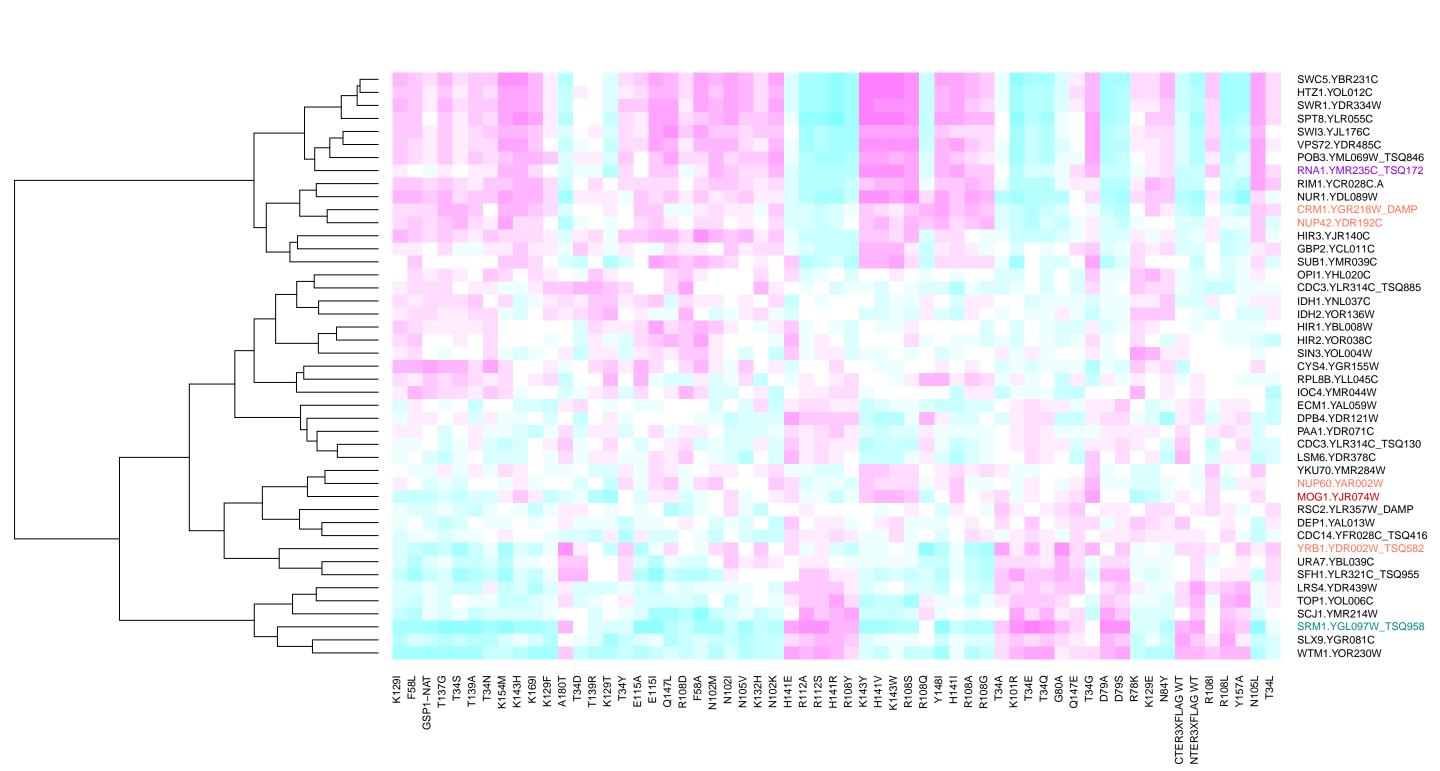
proteolysis involved in cellular protein catabolic process_GO_15_1_all

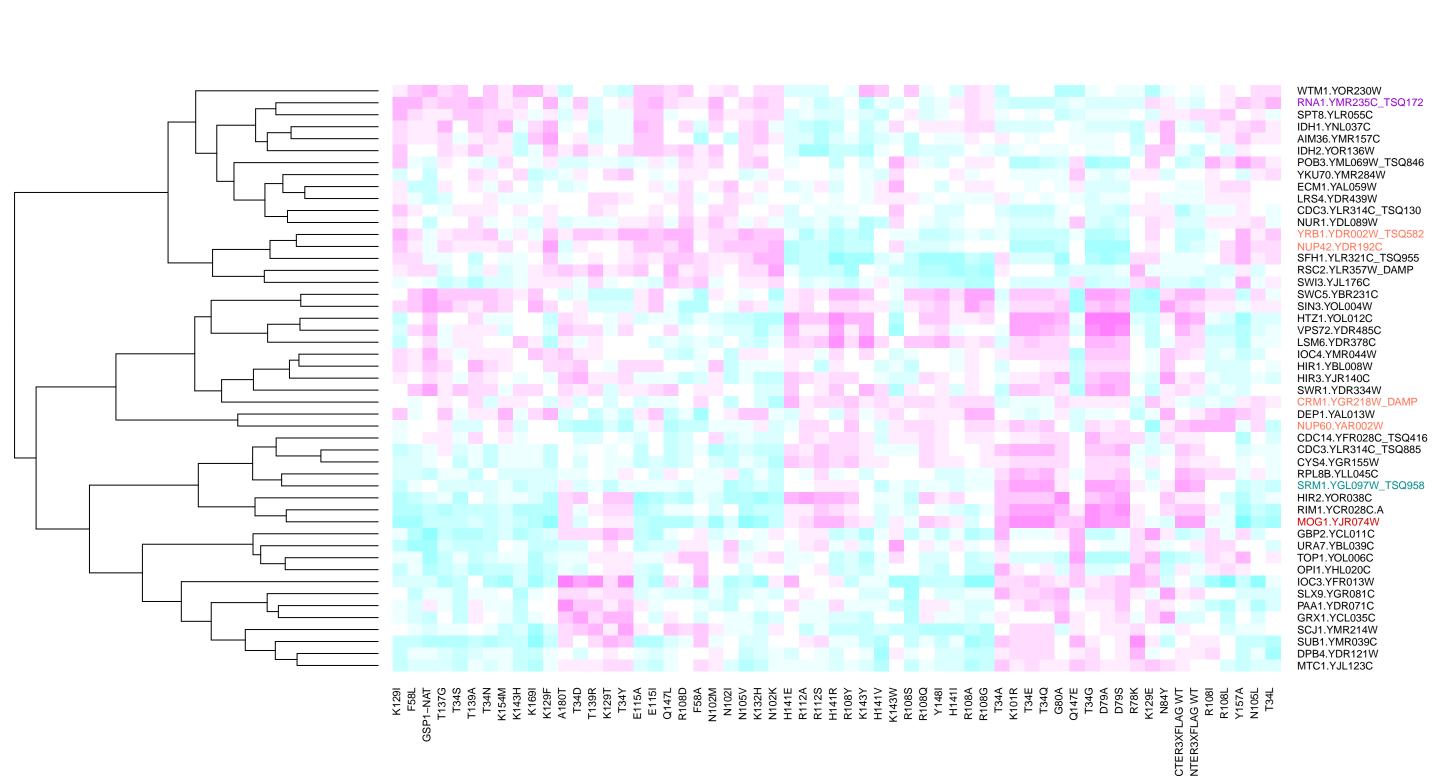




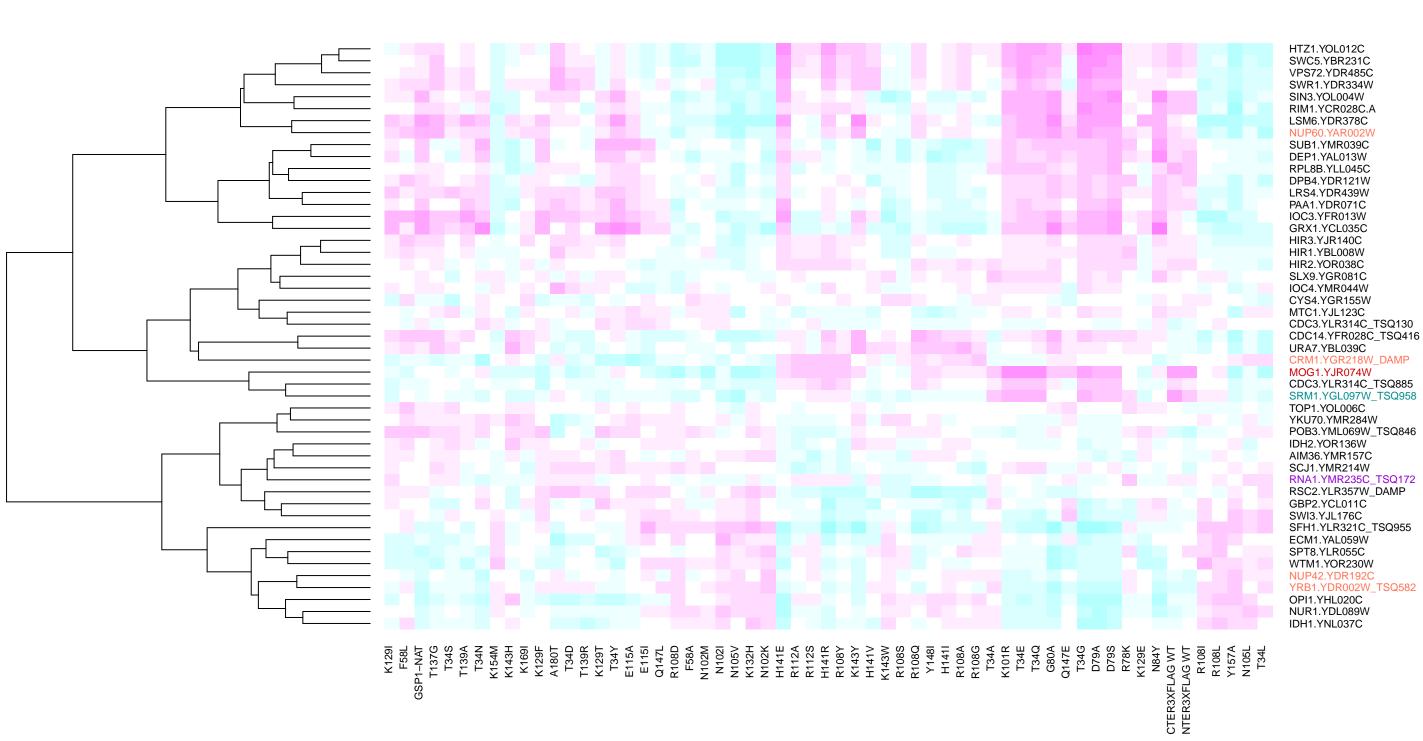
whole_library







chromosome segregation



CRM1.YGR218W_DAMP

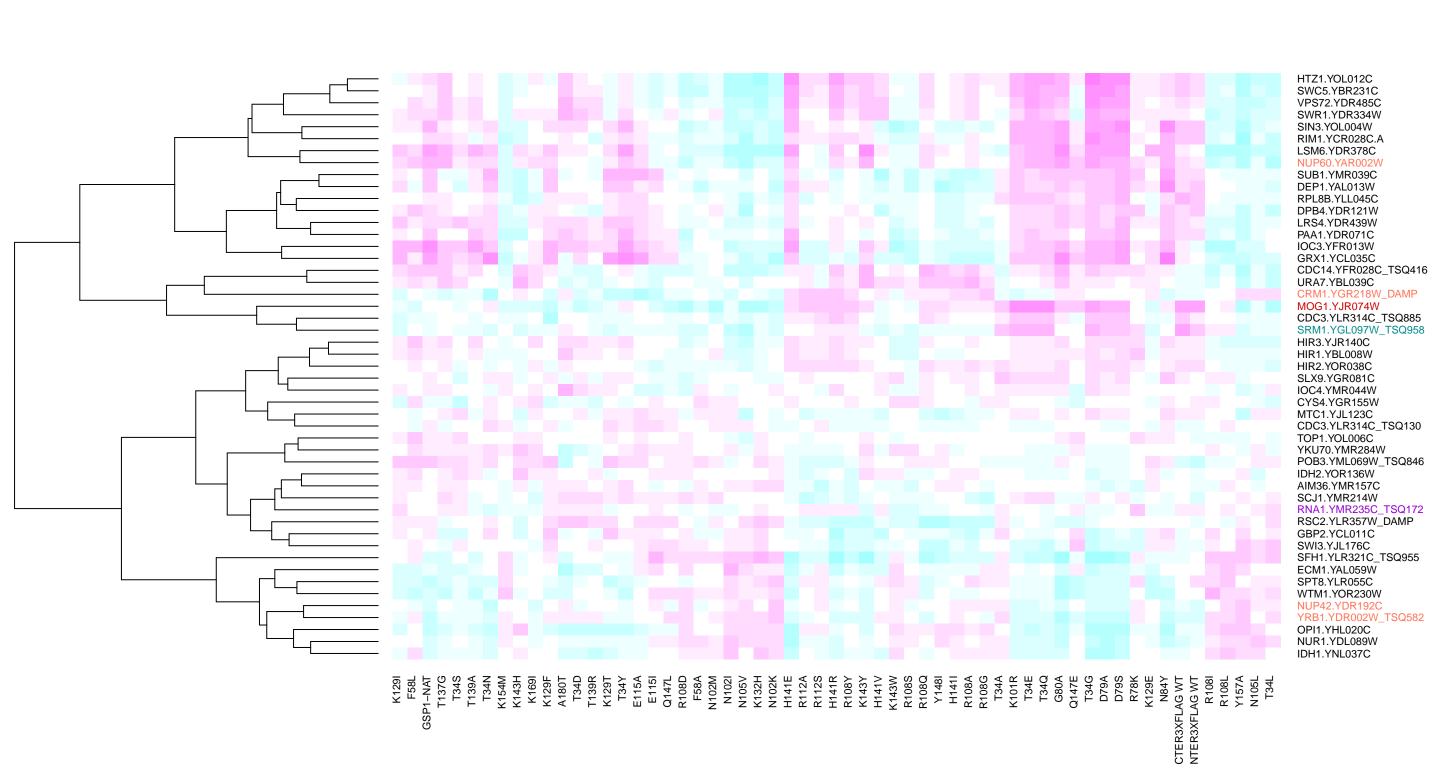
POB3.YML069W_TSQ846 RNA1.YMR235C_TSQ172

SFH1.YLR321C_TSQ955

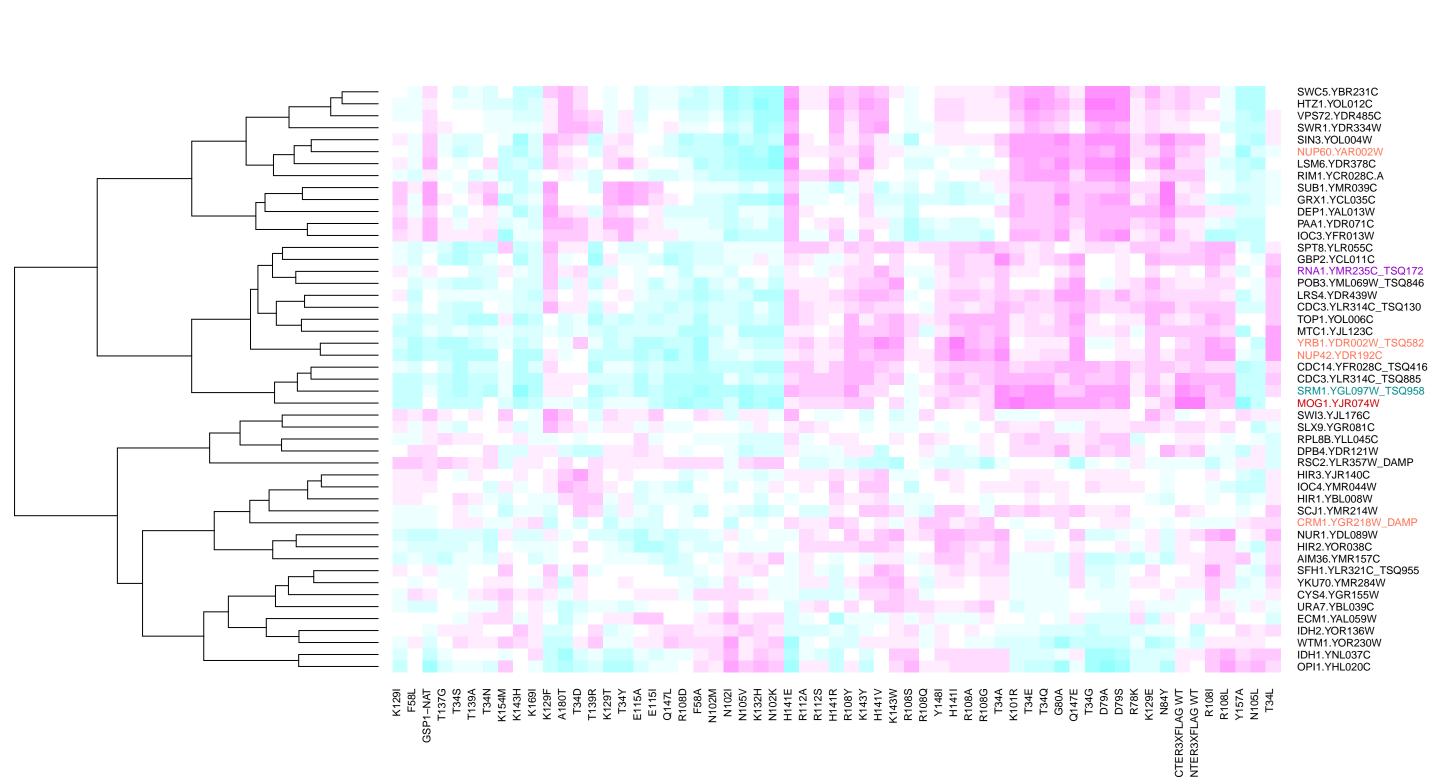
chromosome segregation_GO_15_1_mut



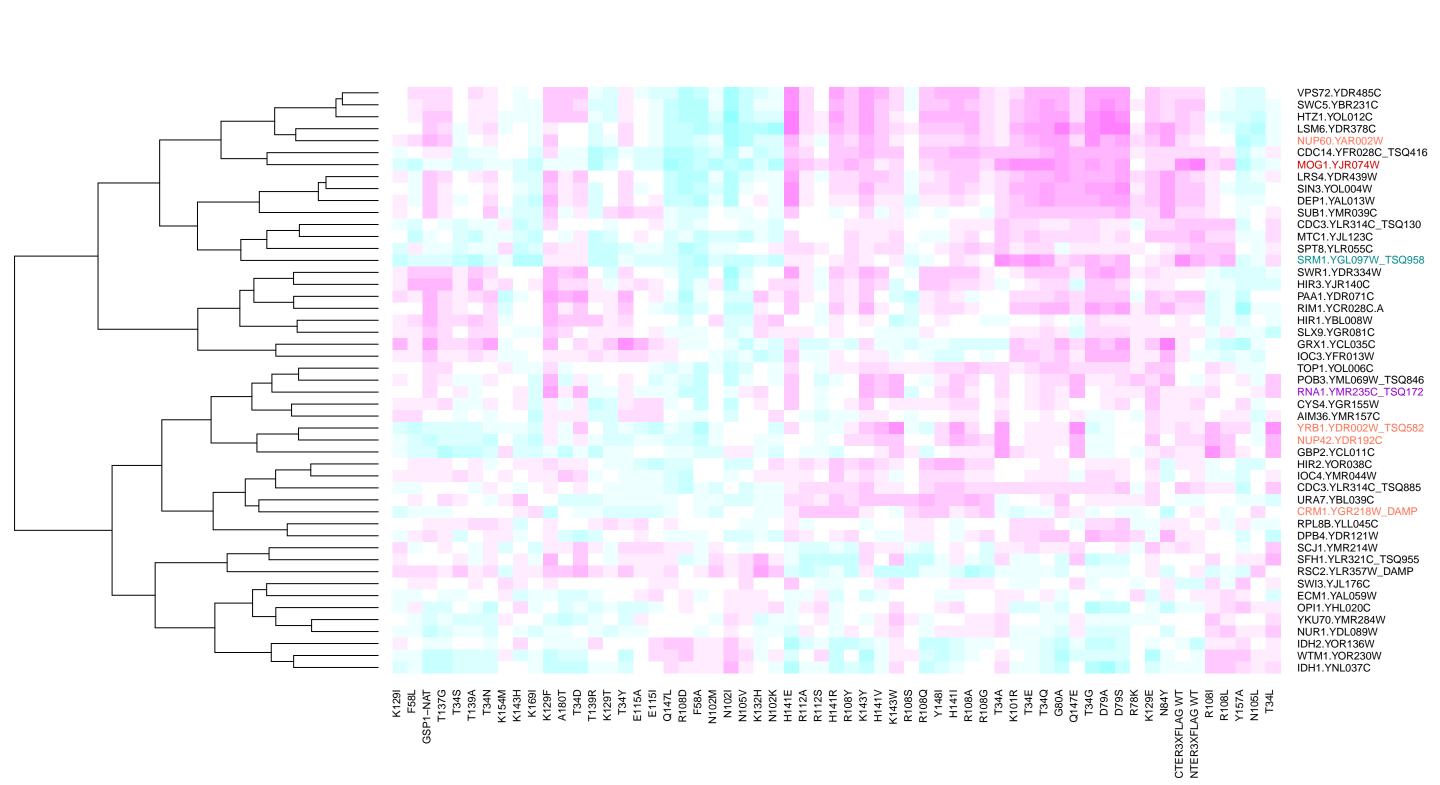
chromosome segregation_GO_30_1_all



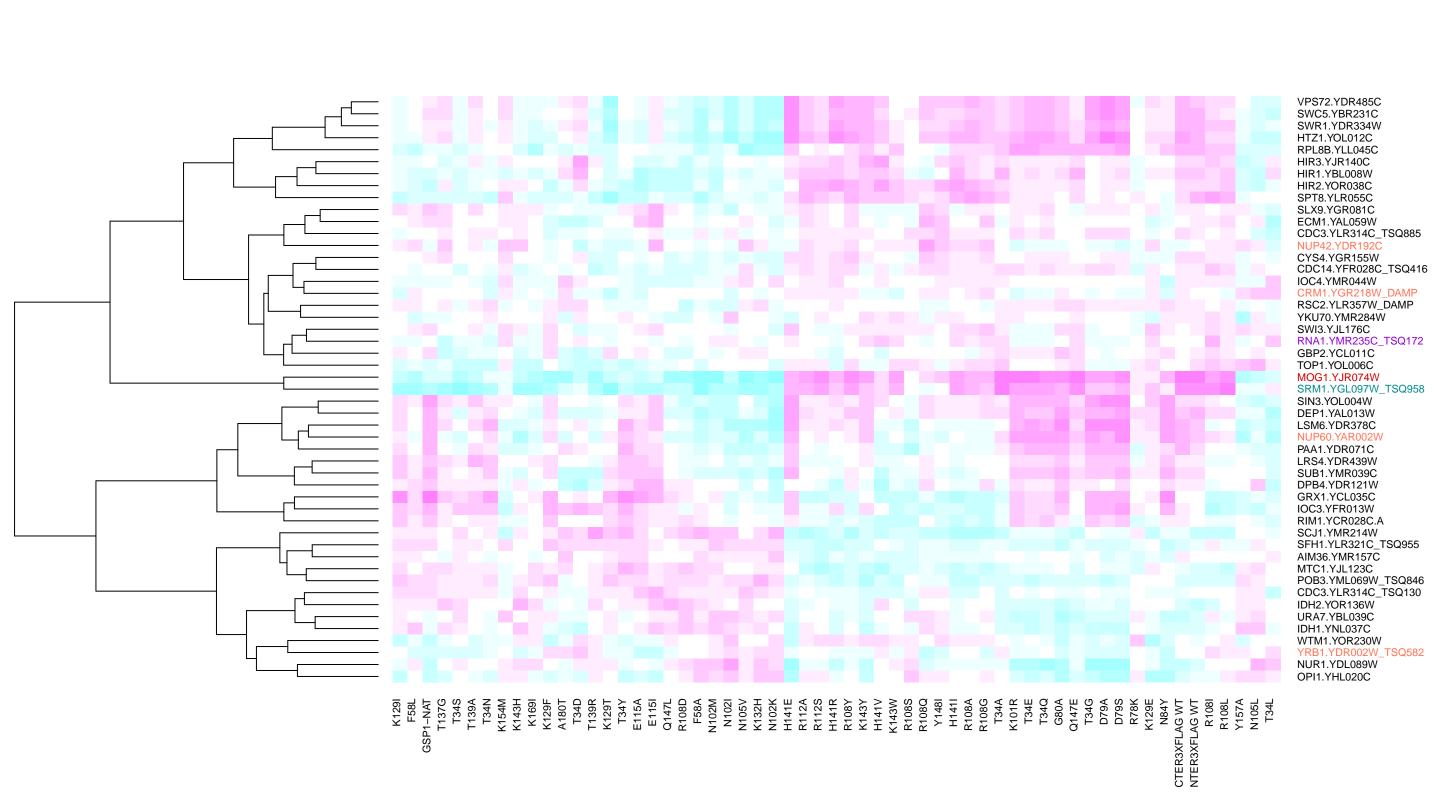
mitotic cell cycle_GO_30_1_mut



organelle fission



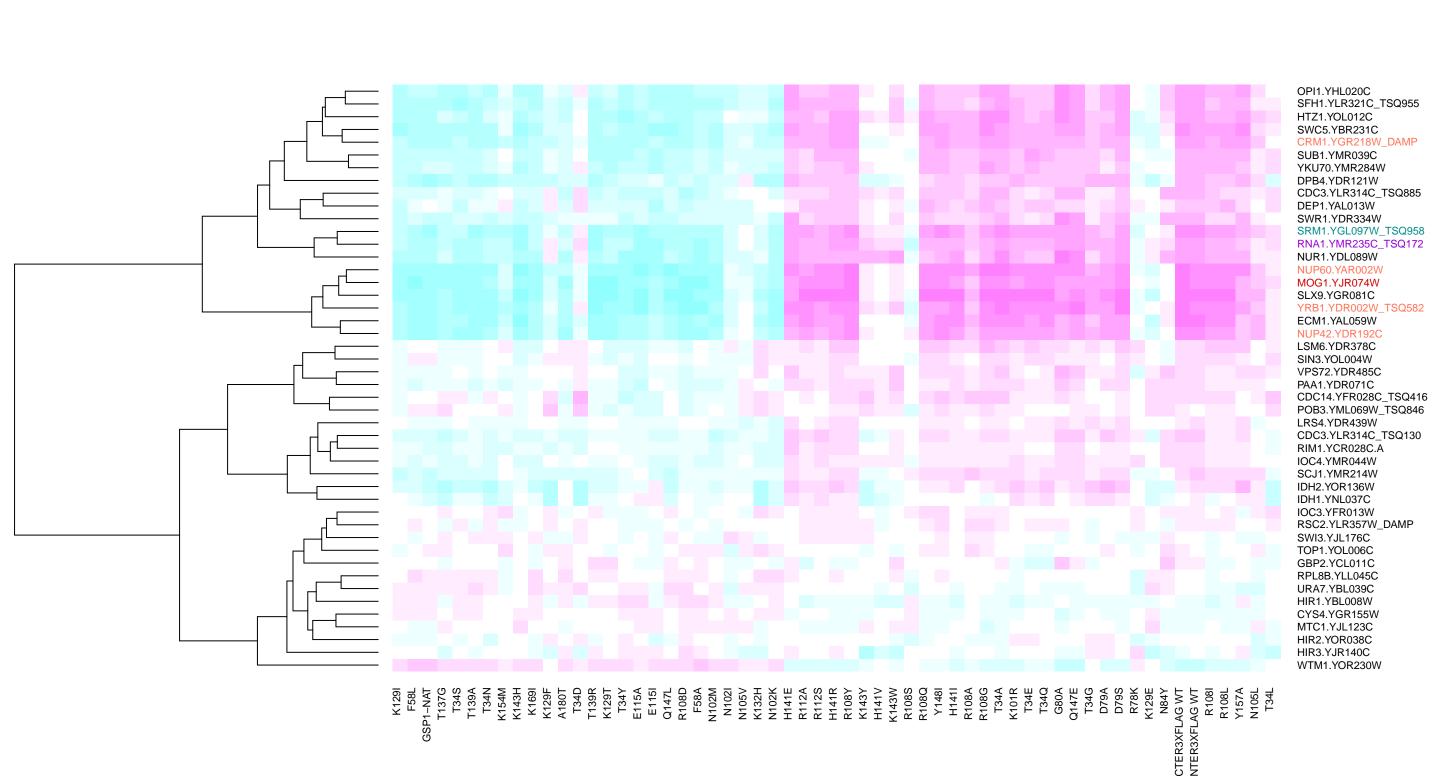
regulation of cell cycle_GO_30_1_all



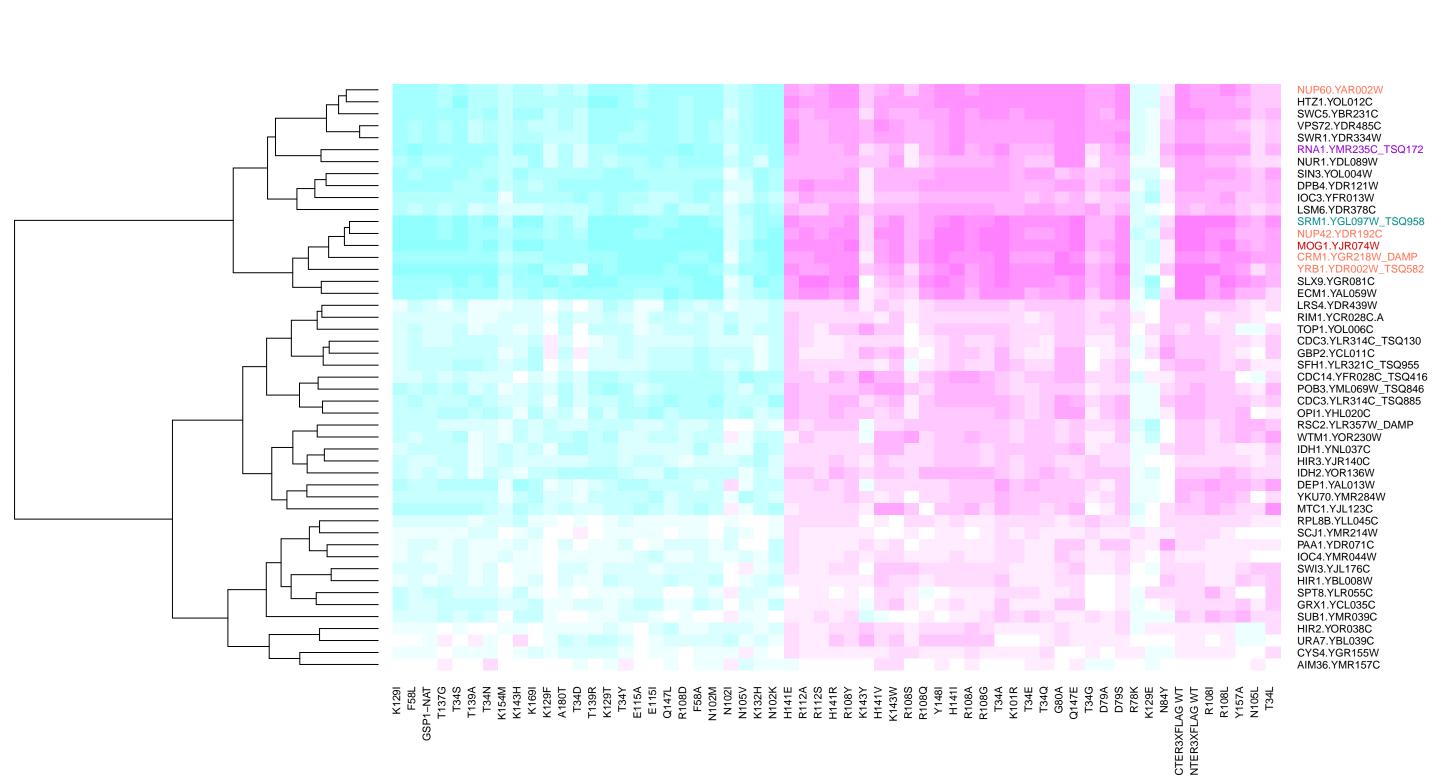
regulation of cell cycle_GO_30_1_mut



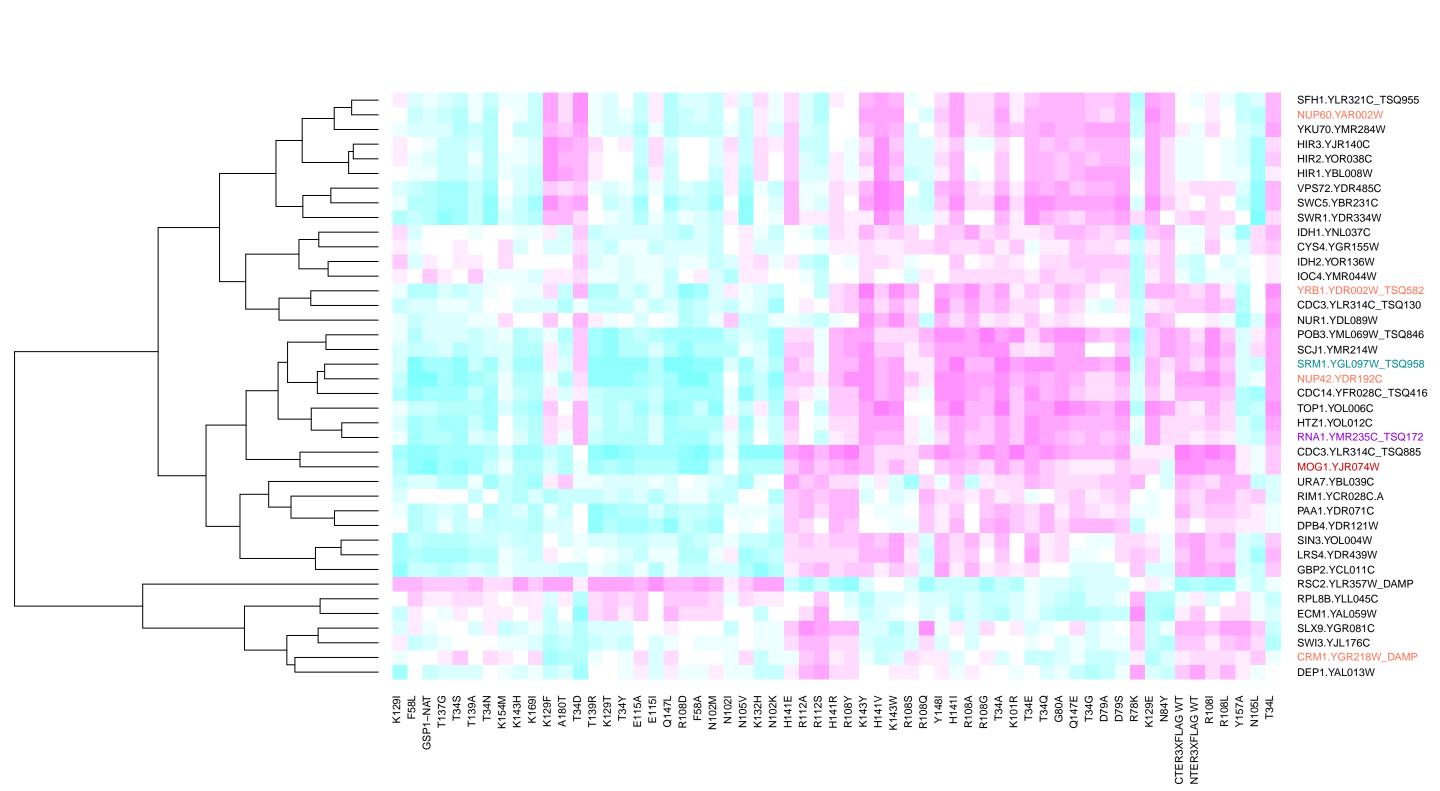
whole_library_30_5_all



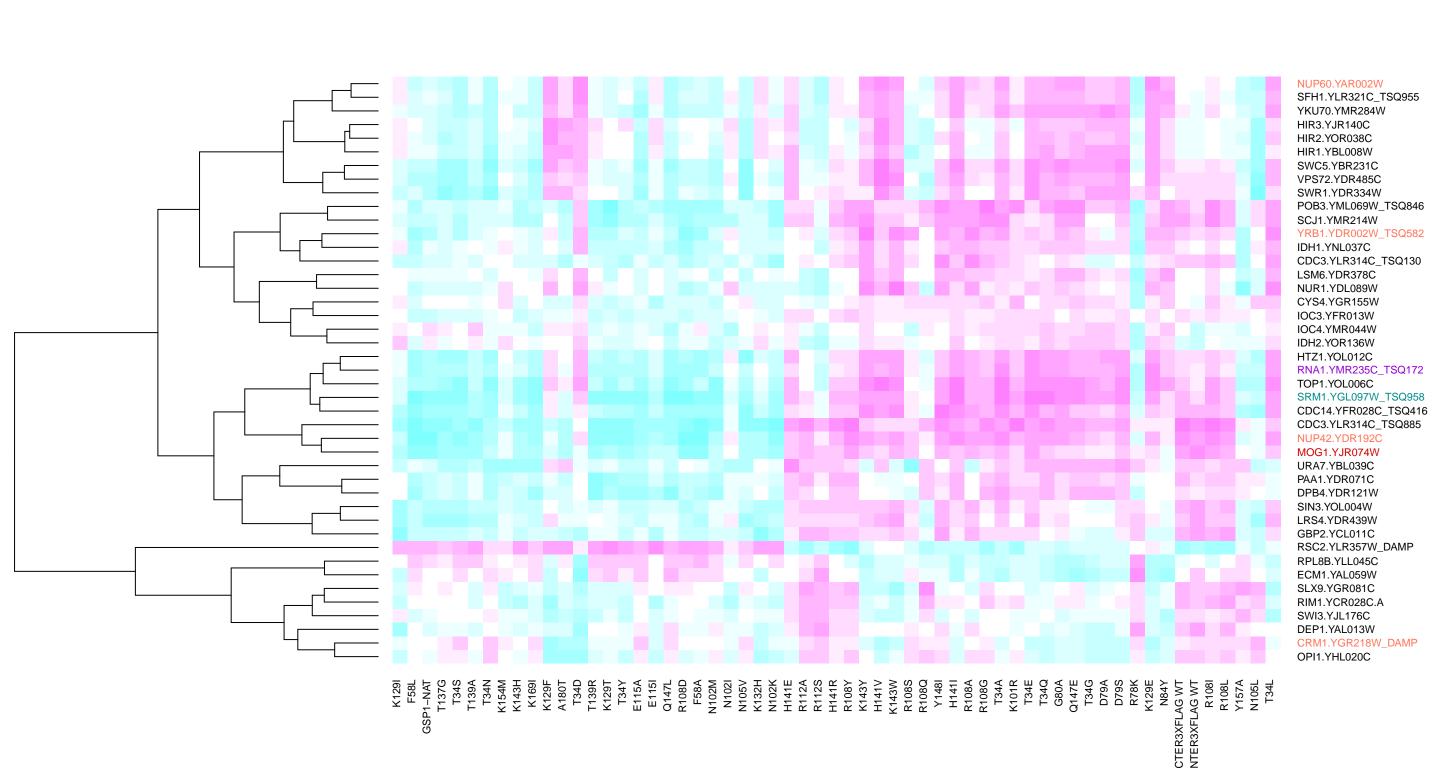
endomembrane system_GO_30_3_all

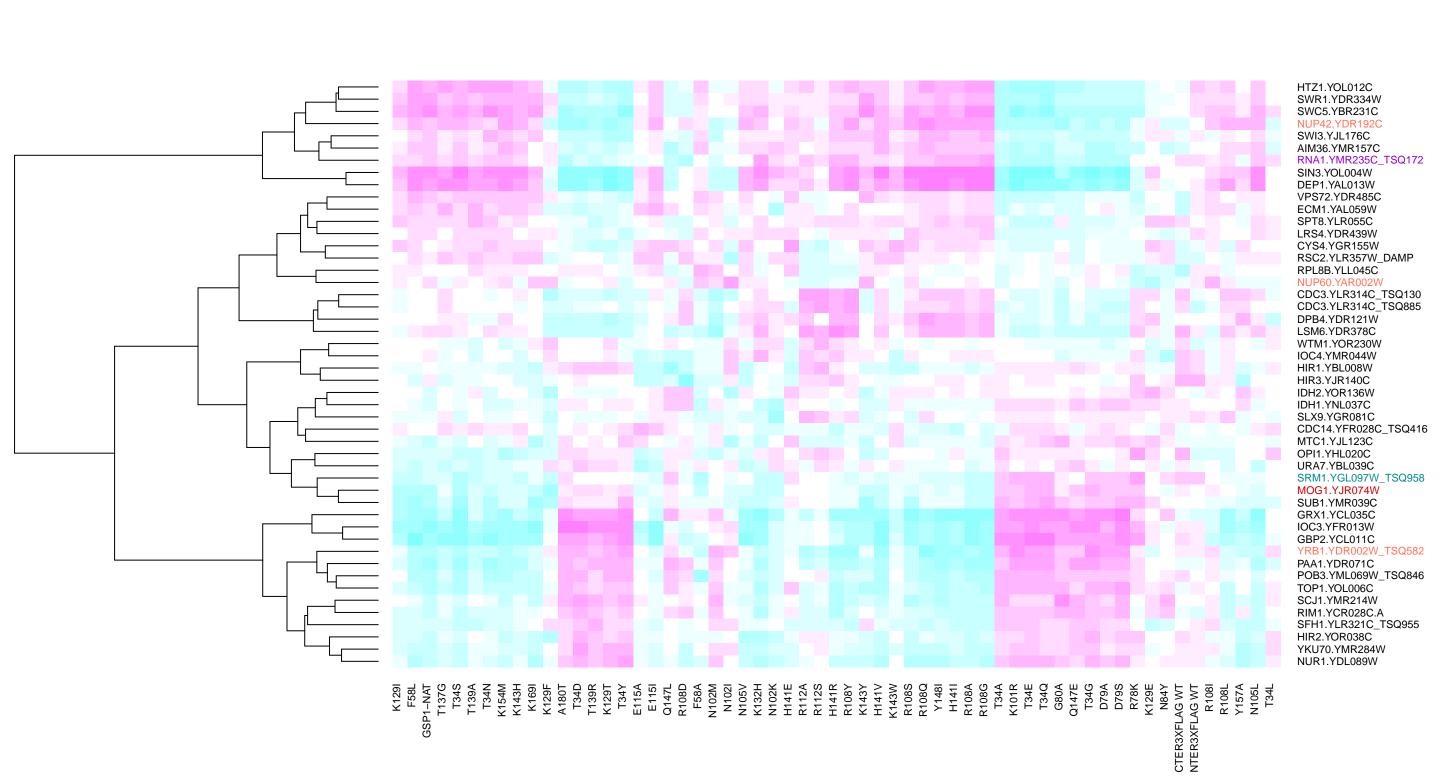


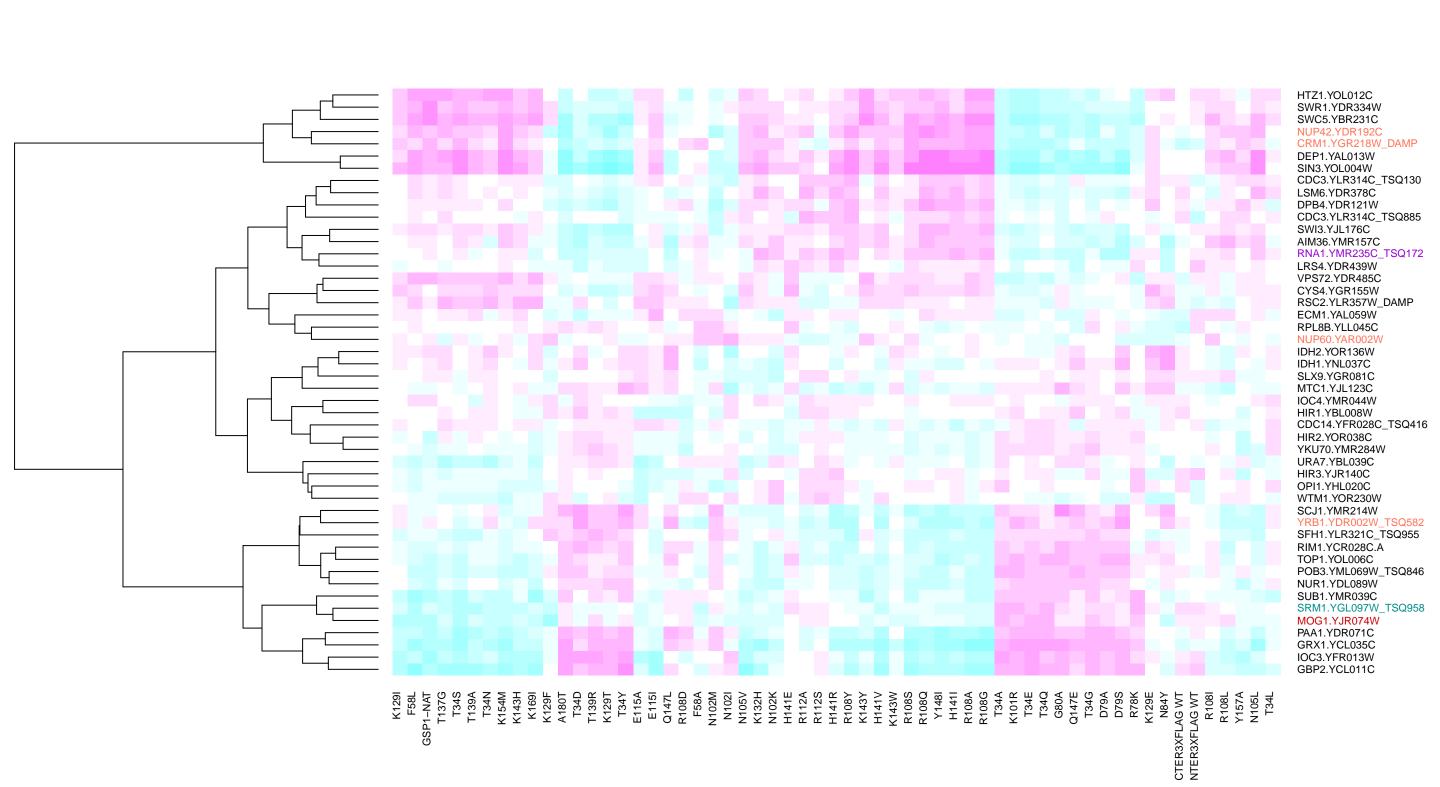
ribosomal small subunit biogenesis



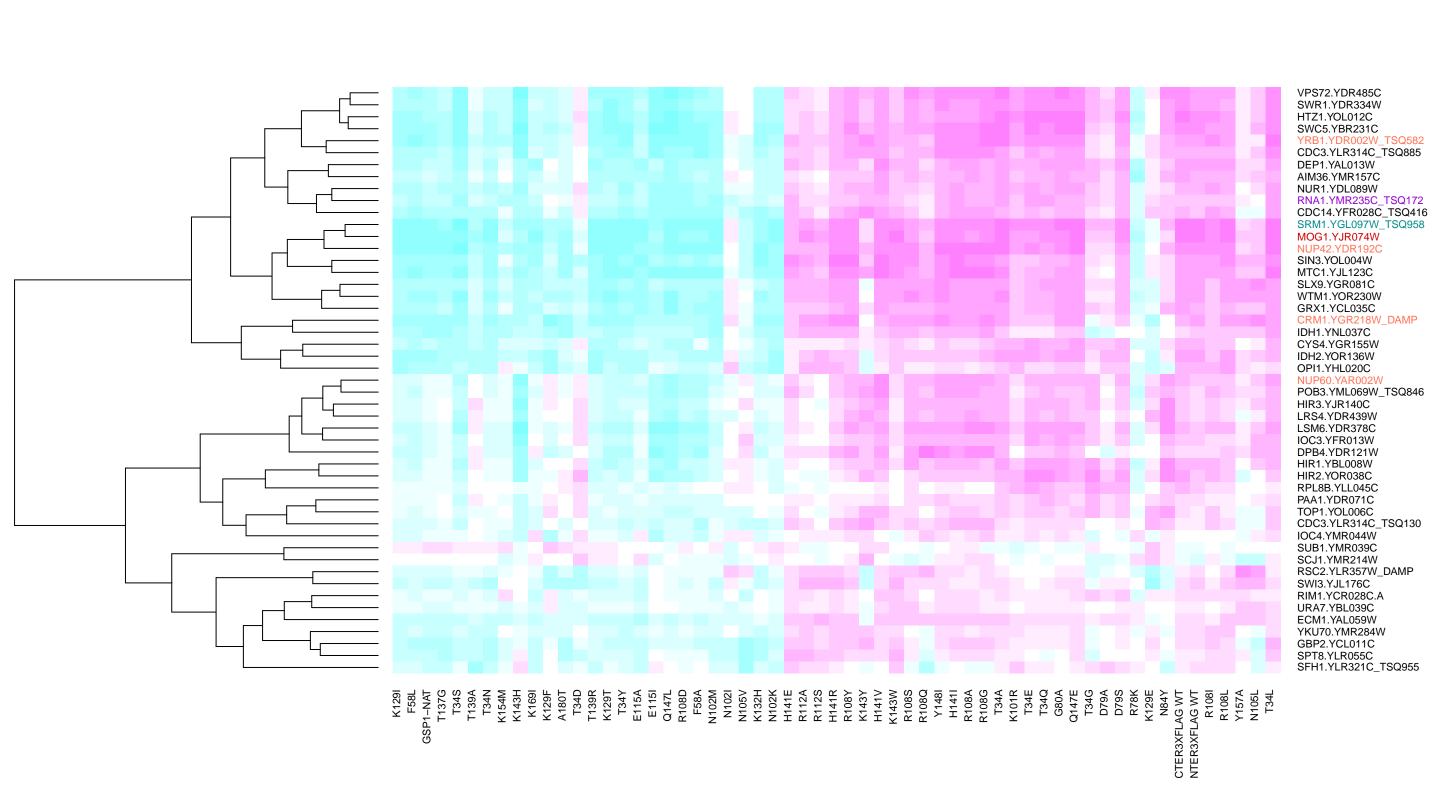
ribosomal small subunit biogenesis_GO_15_1_all



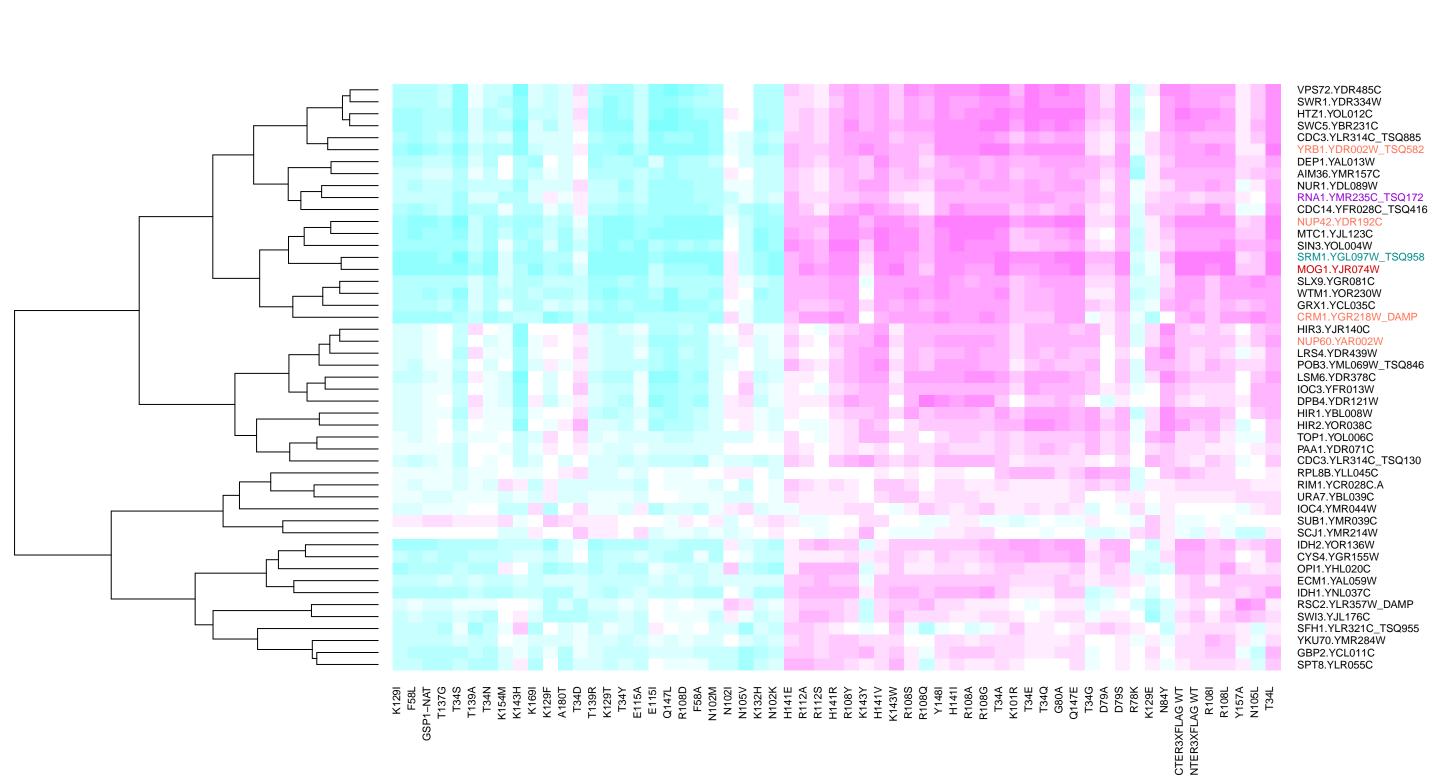


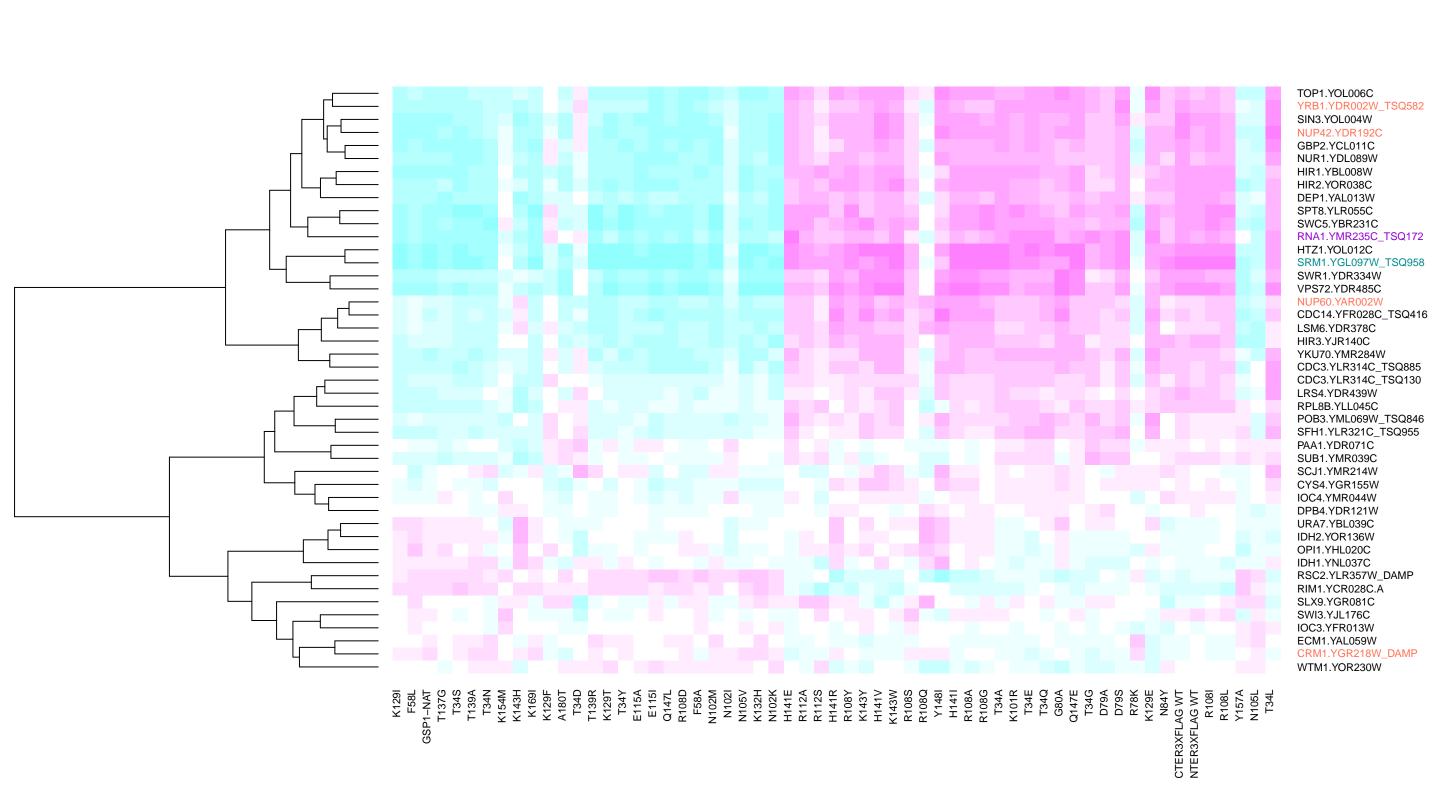


cellular response to DNA damage stimulus_GO_15_1_all

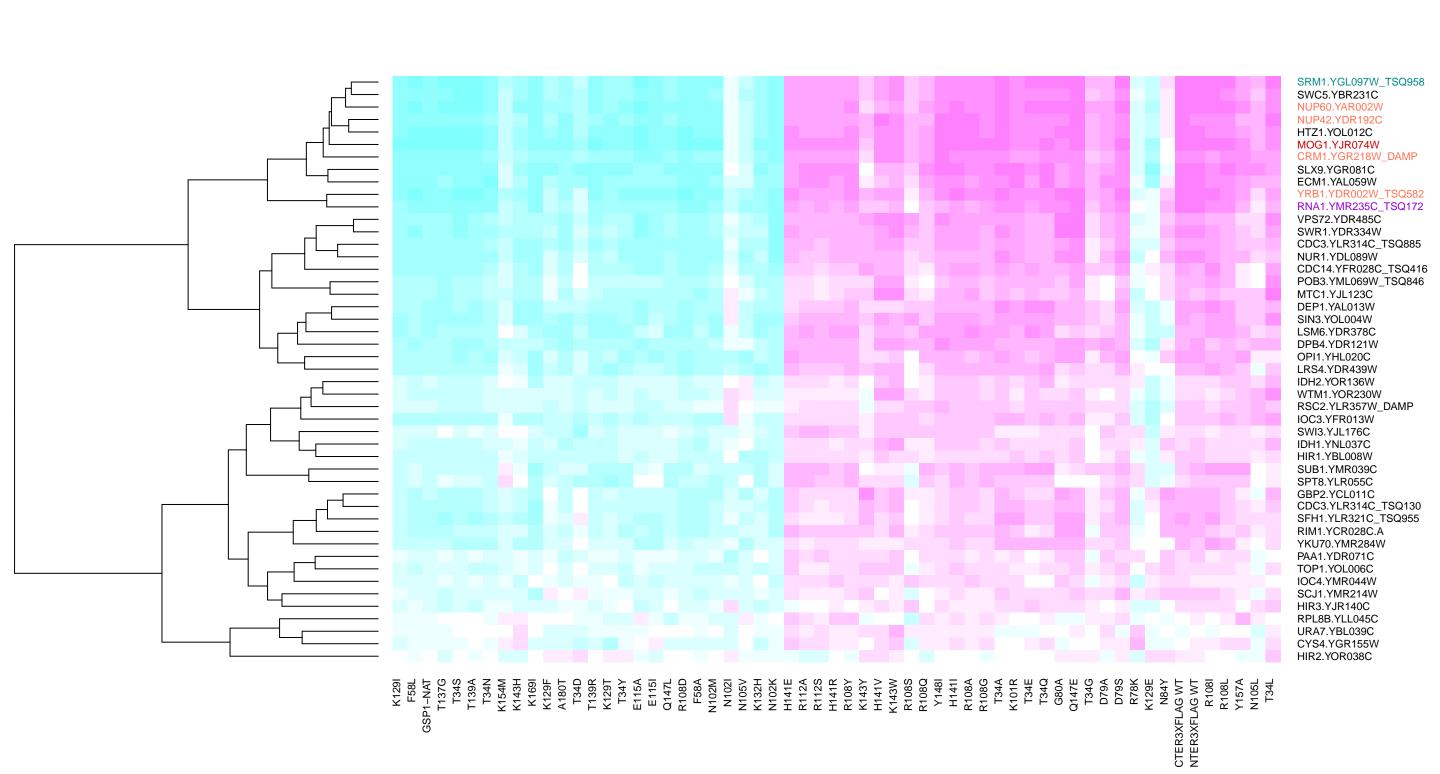


cellular response to DNA damage stimulus_GO_30_3_all

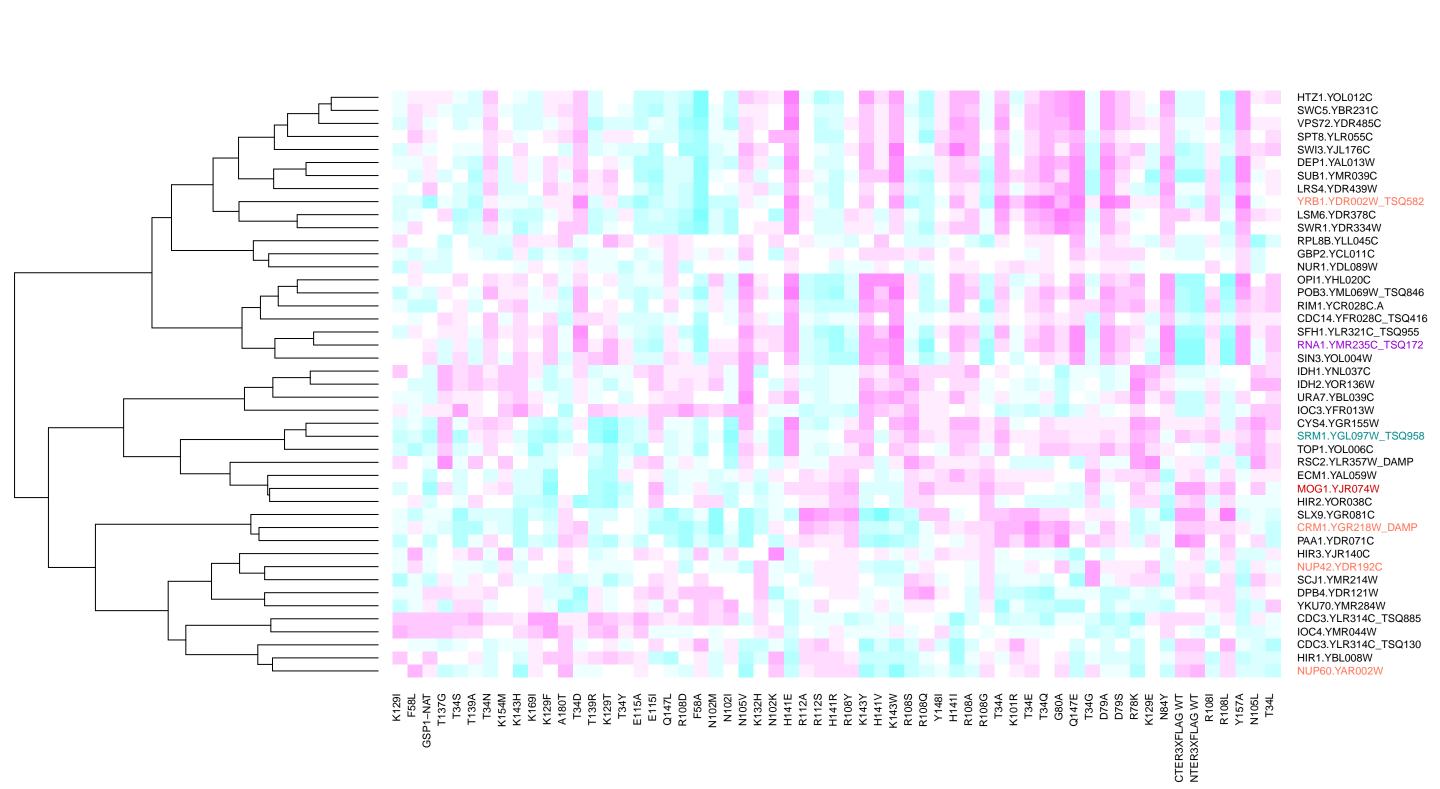




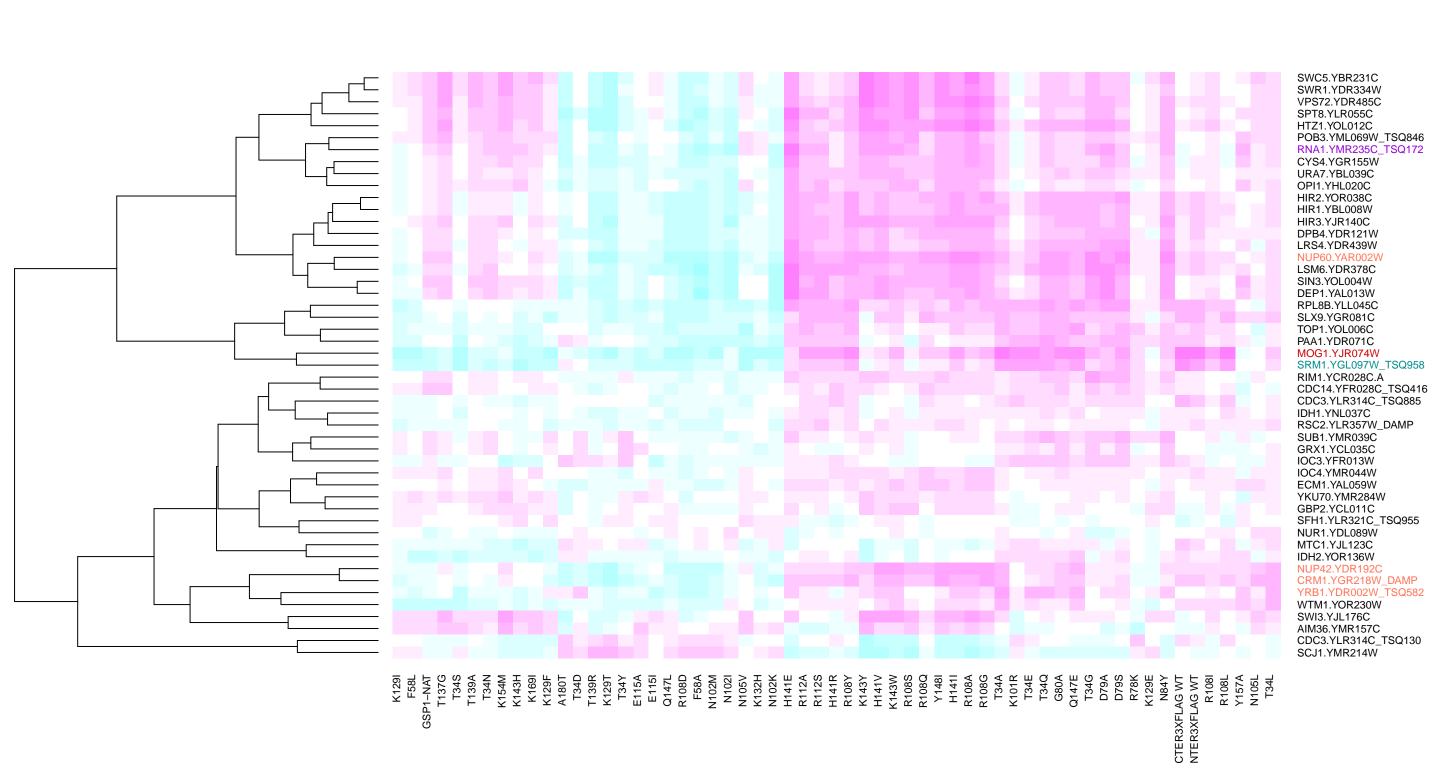
endomembrane system_GO_15_3_mut



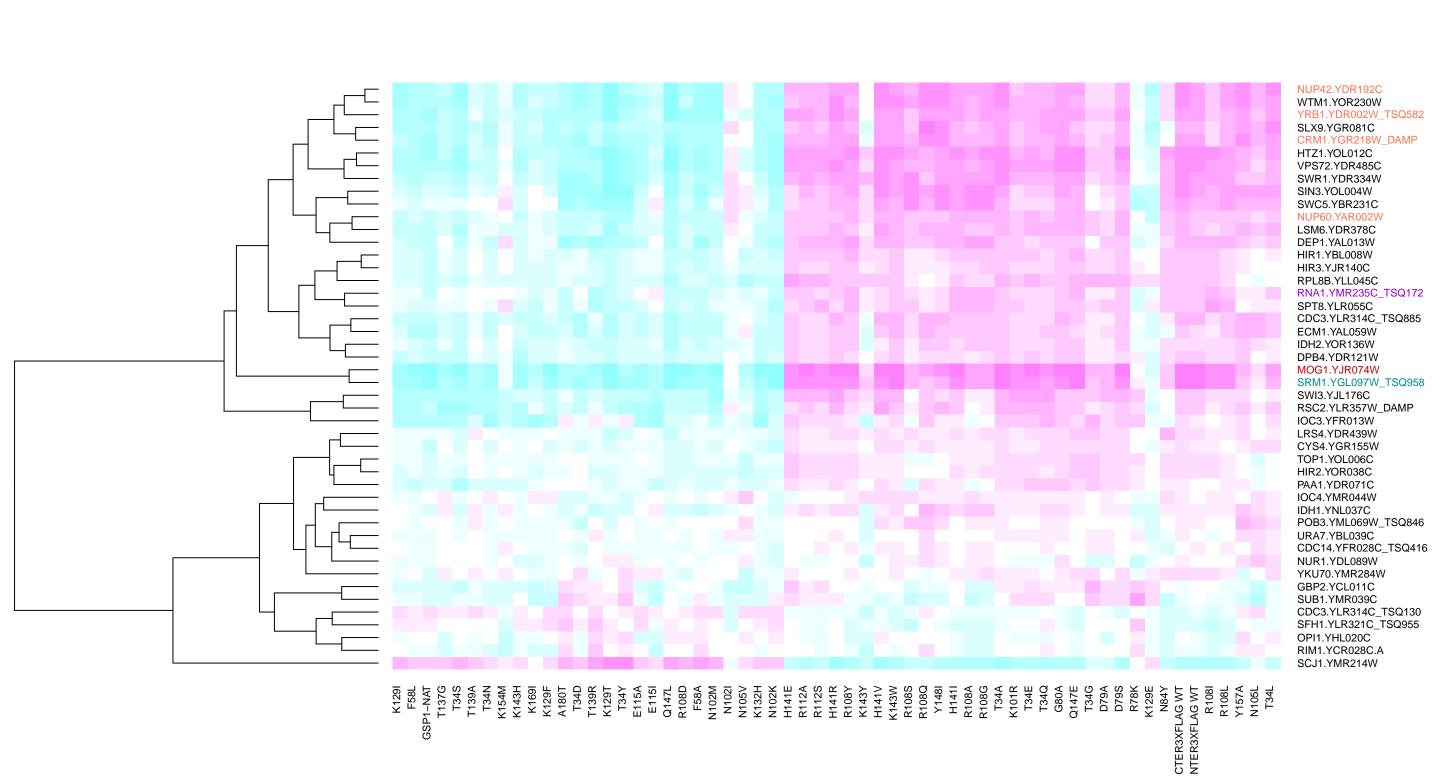
regulation of organelle organization_GO_15_1_all



chromatin



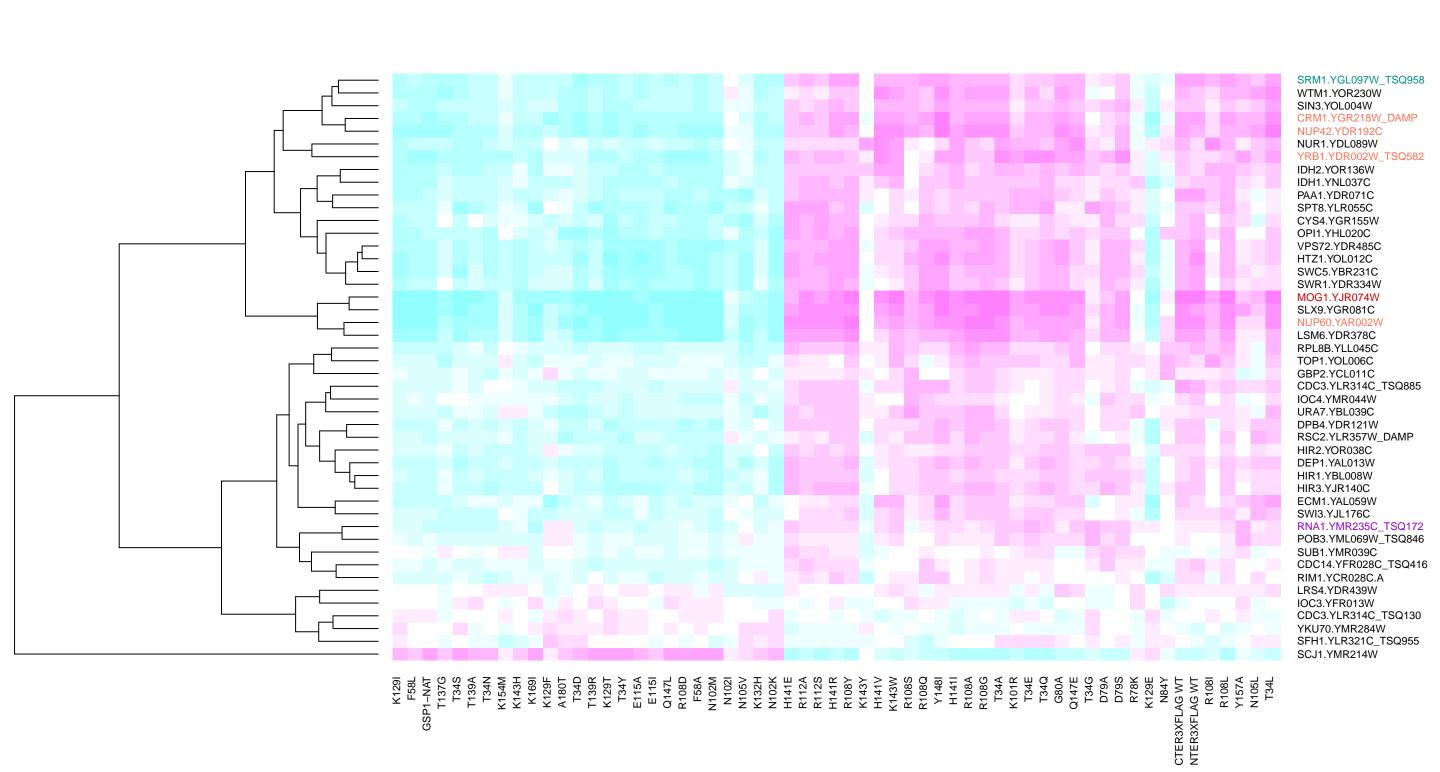
chromatin organization_GO_30_2_all



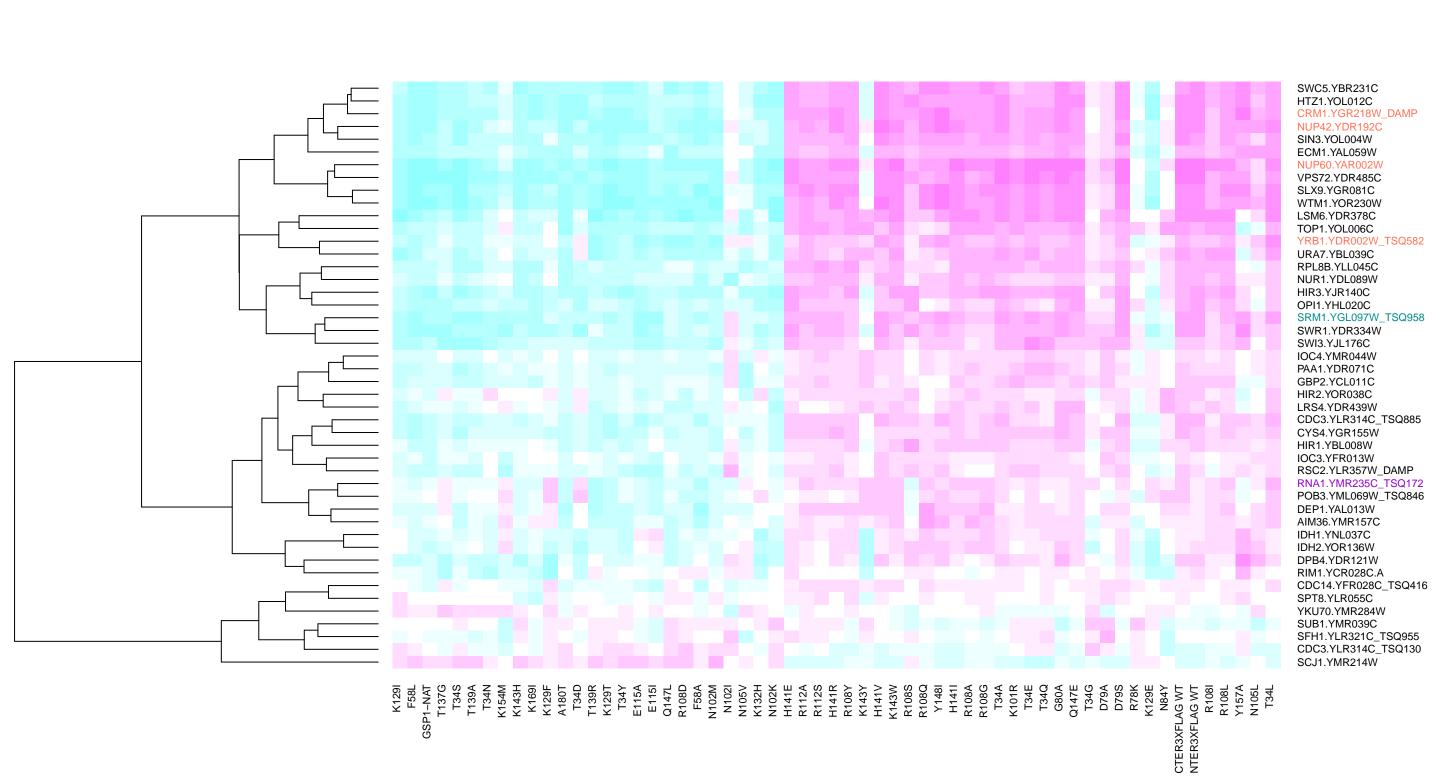
DNA binding_GO_15_3_mut



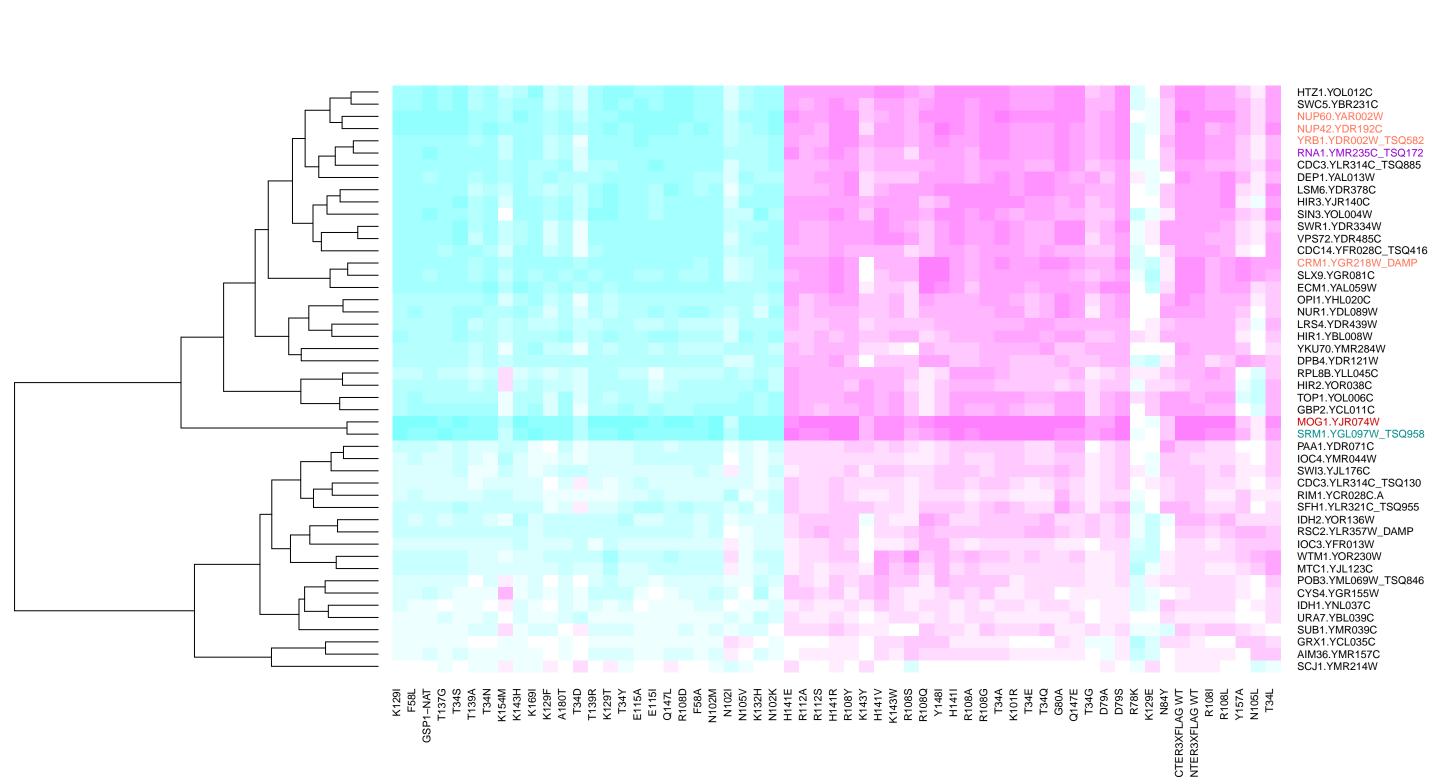
transcription_GO_15_1_mut



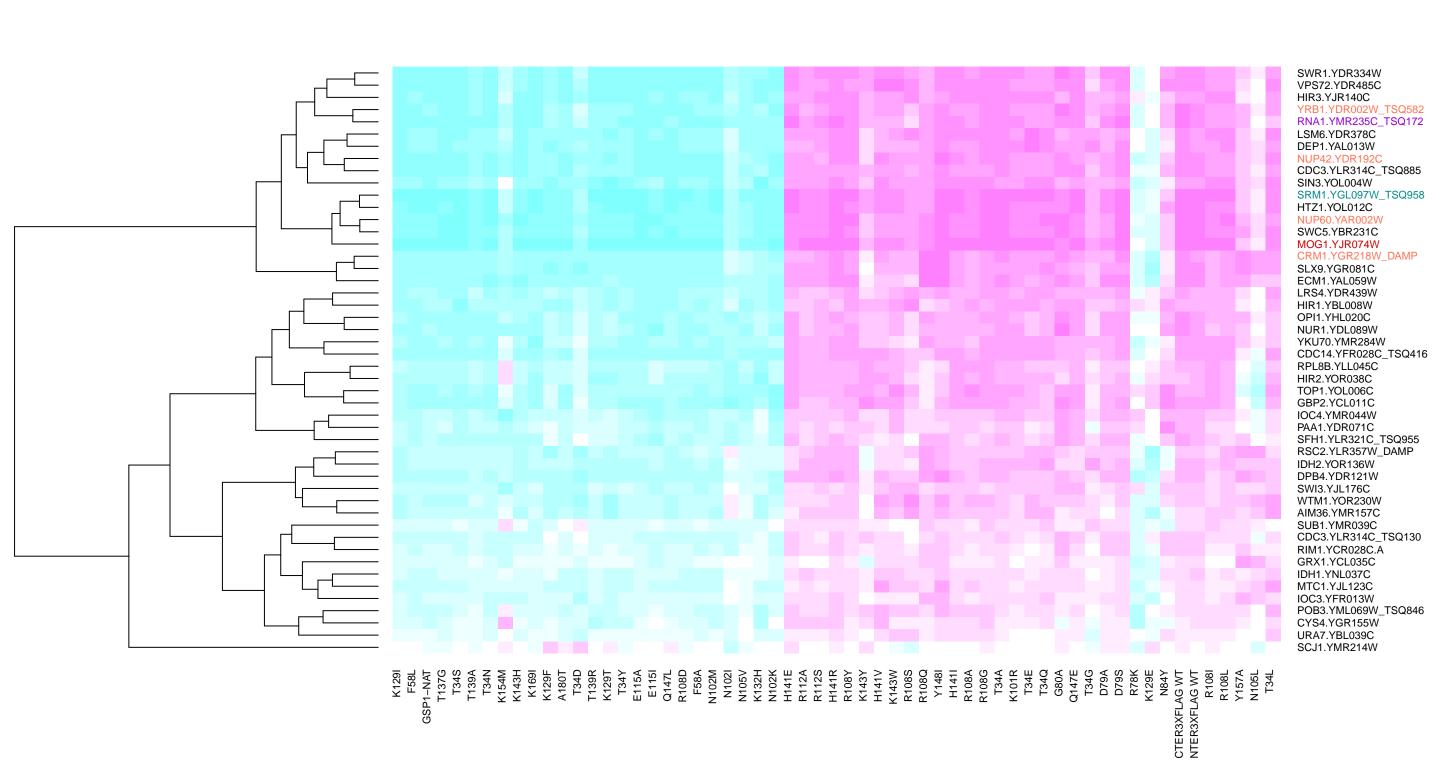
transcription_GO_30_4_all



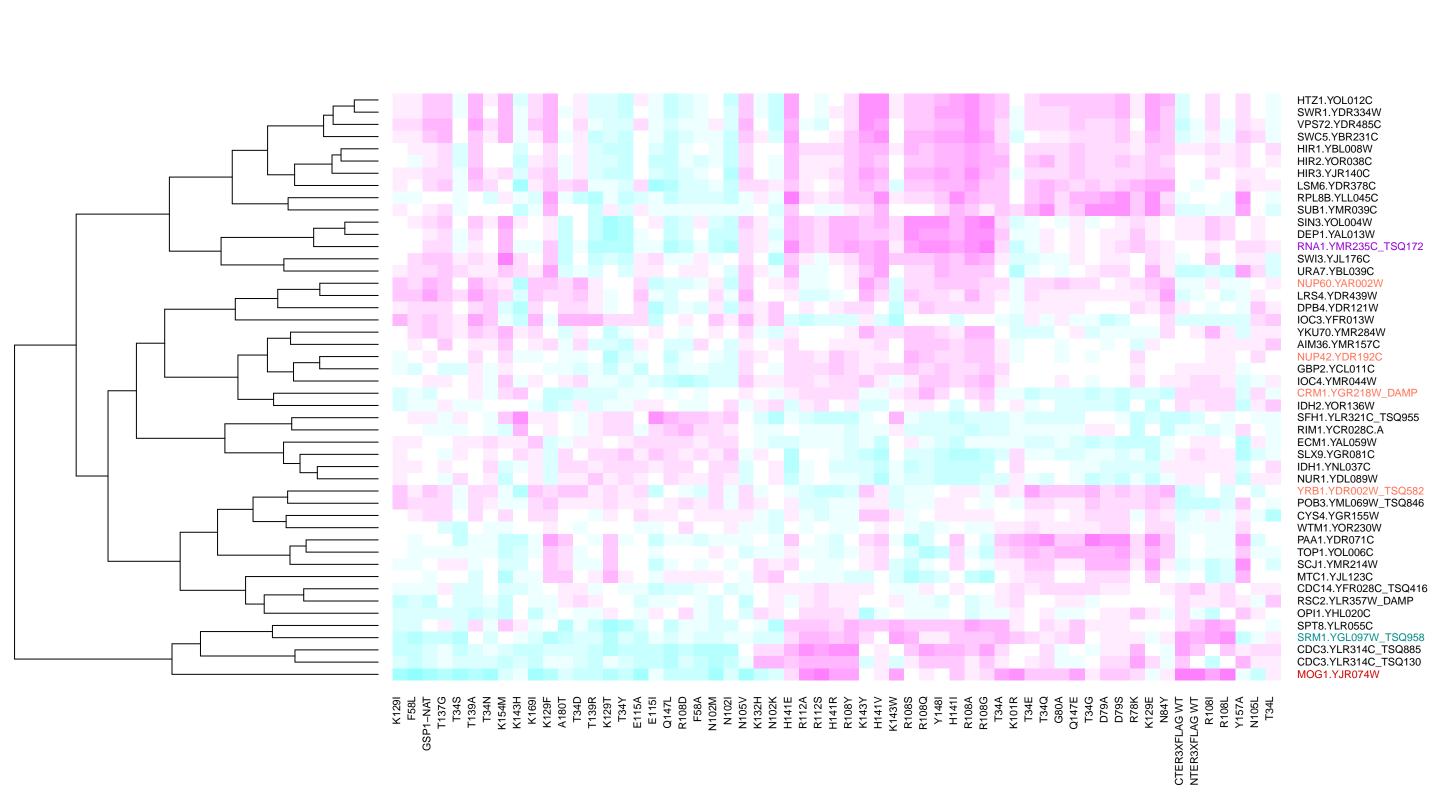
nucleobase-containing compound transport



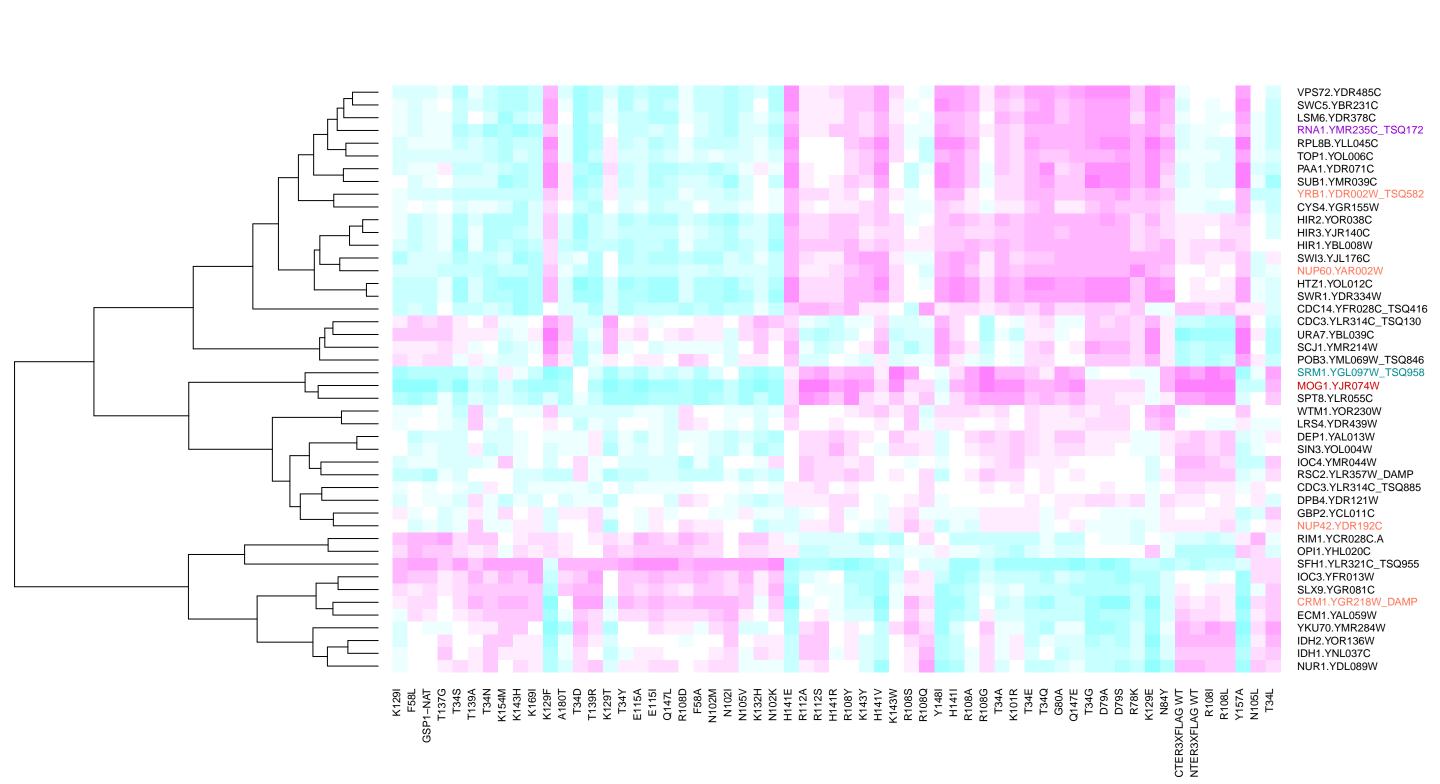
nucleobase-containing compound transport_GO_15_1_mut



protein modification by small protein conjugation or removal



protein modification by small protein conjugation or removal_GO_15_1_mut



chromatin organization

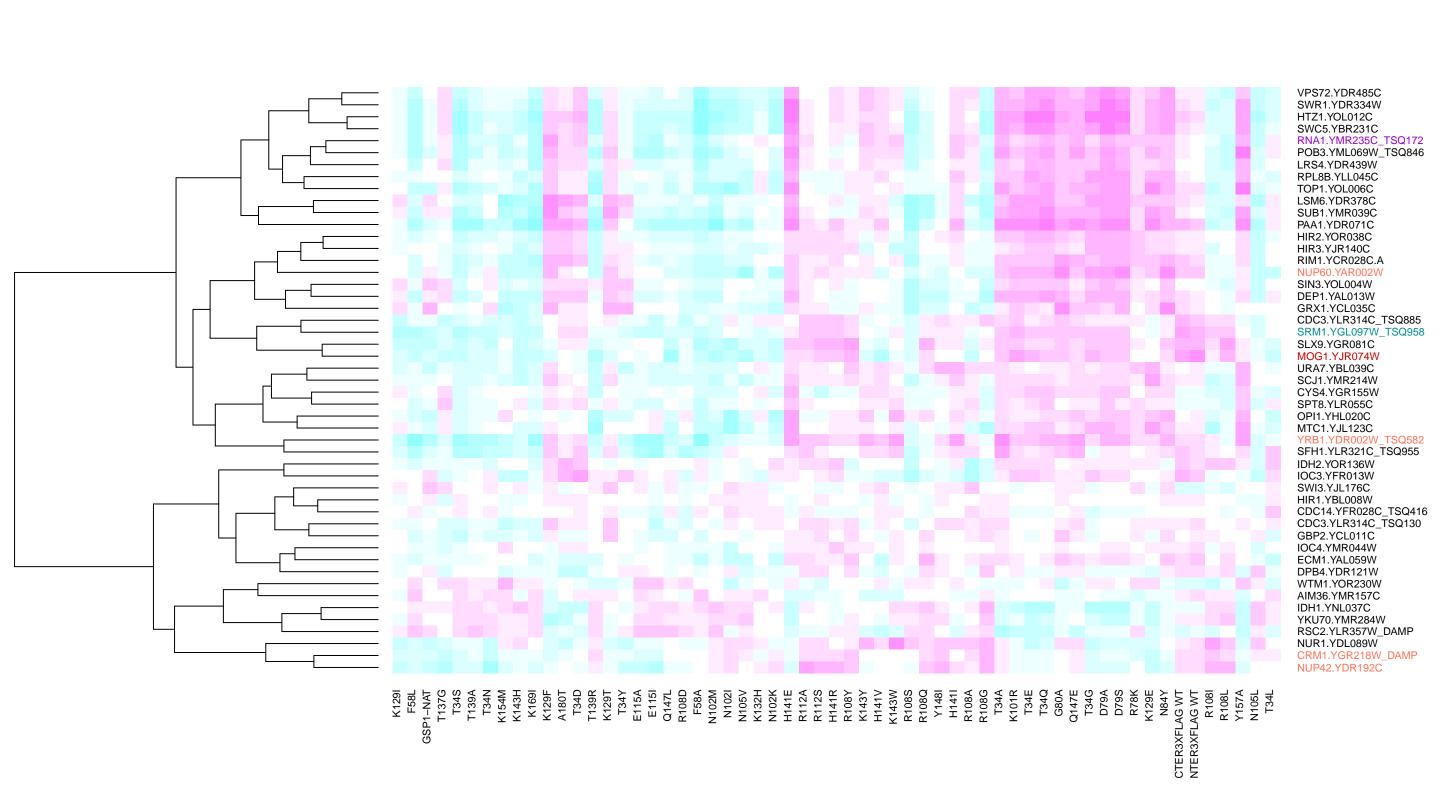


protein modification by small protein conjugation or removal_GO_30_1_mut



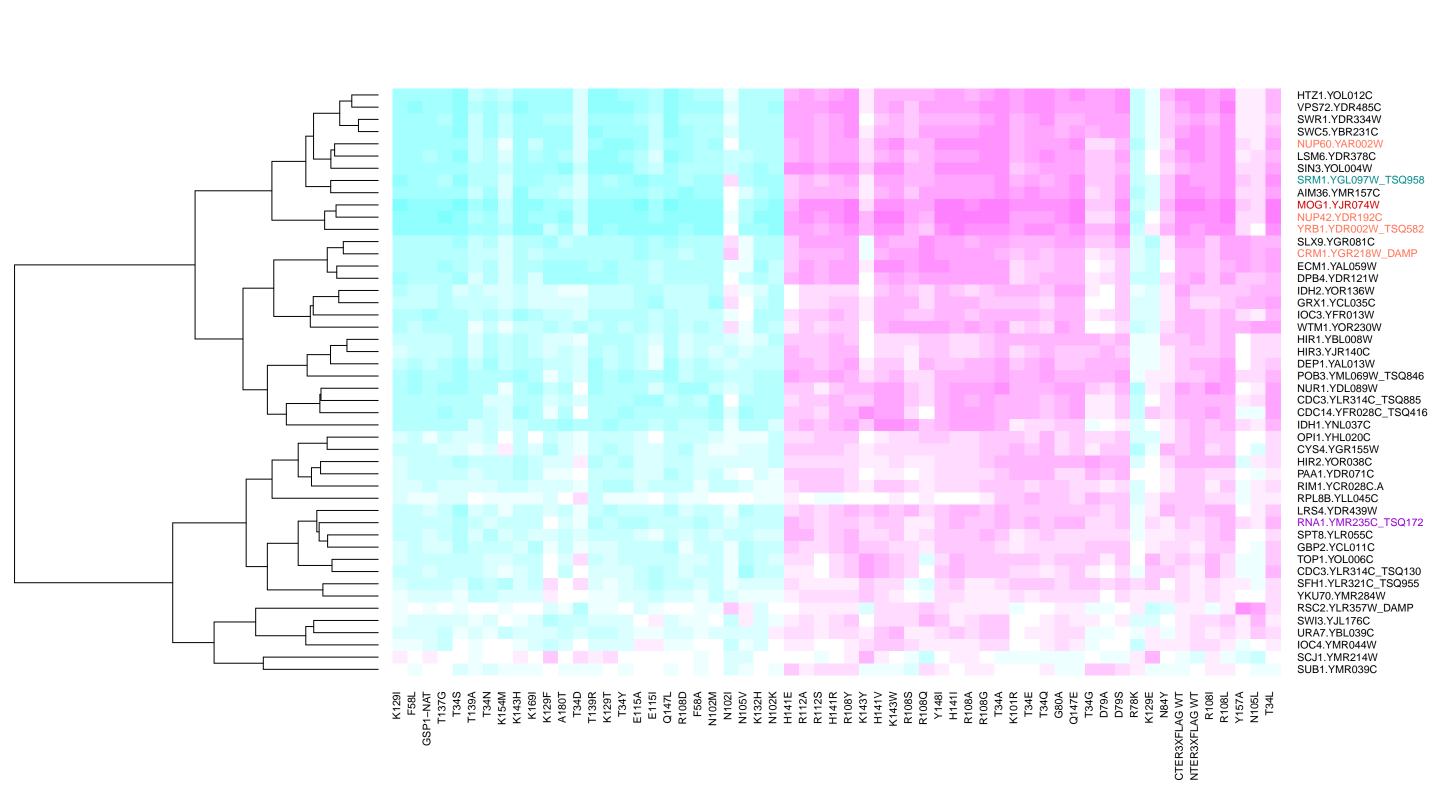
sig_Gsp1_Gl_15_11_all







cellular response to DNA damage stimulus_GO_15_3_mut



lipid binding_GO_15_2_all

