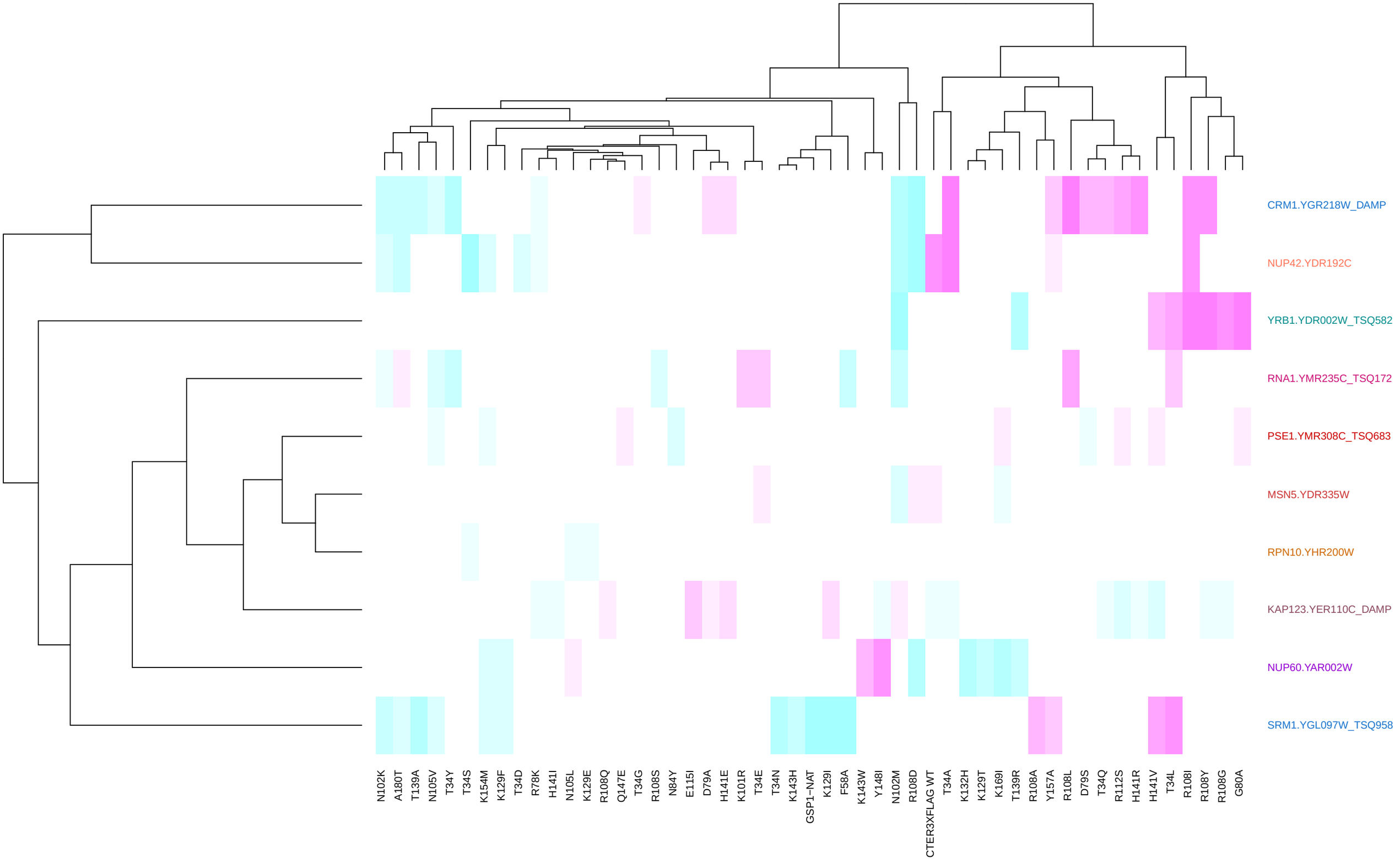
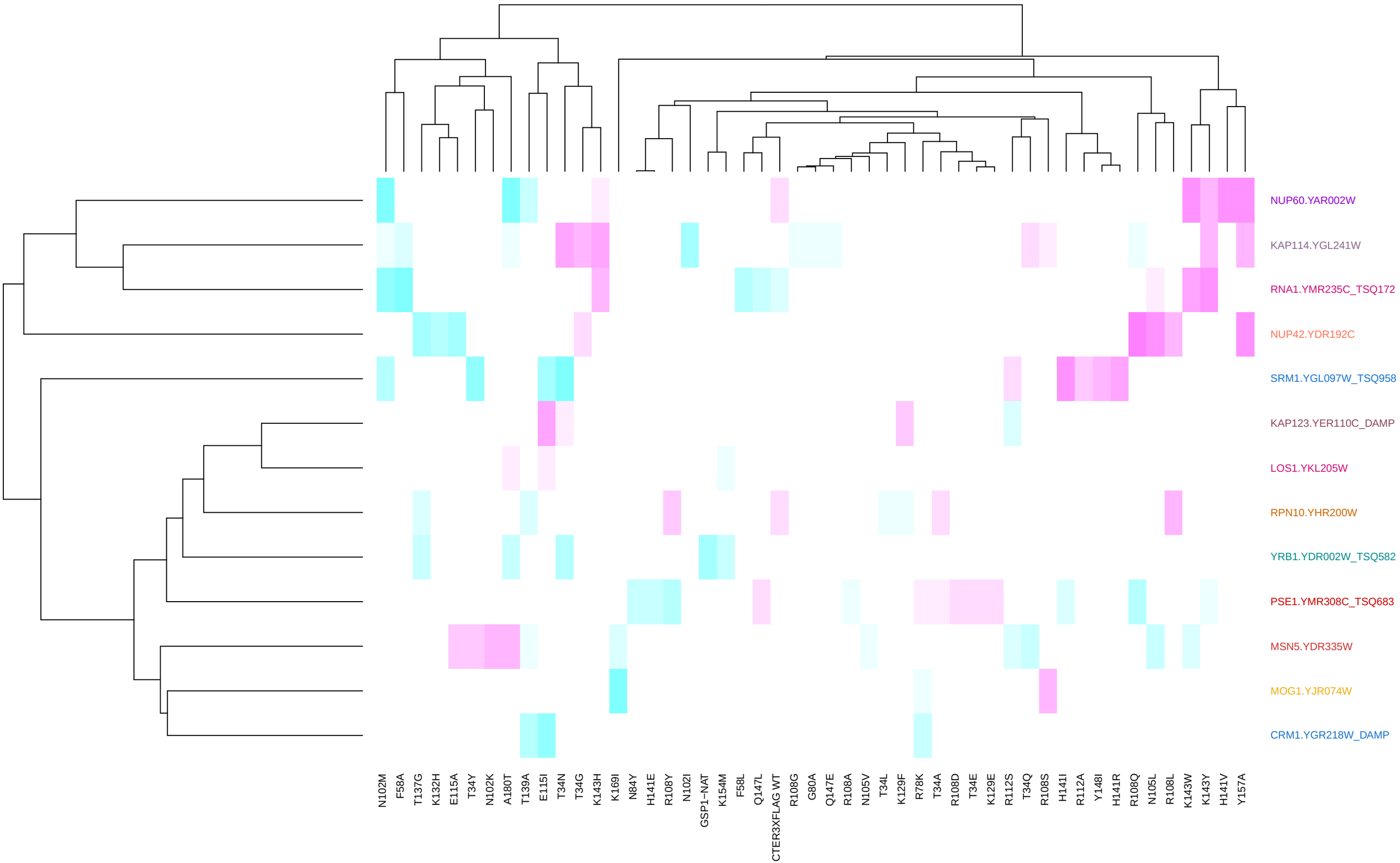
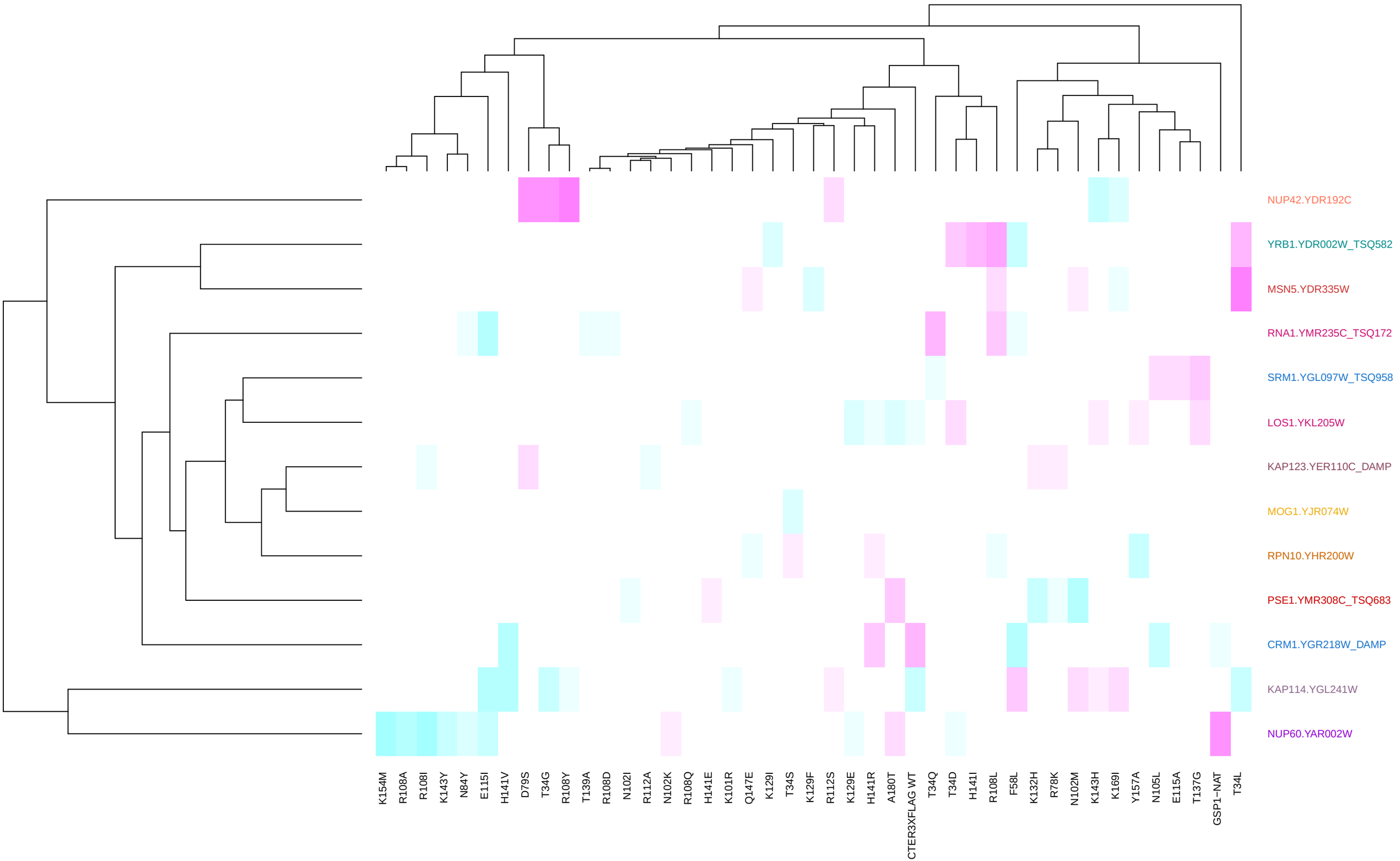
endomembrane system



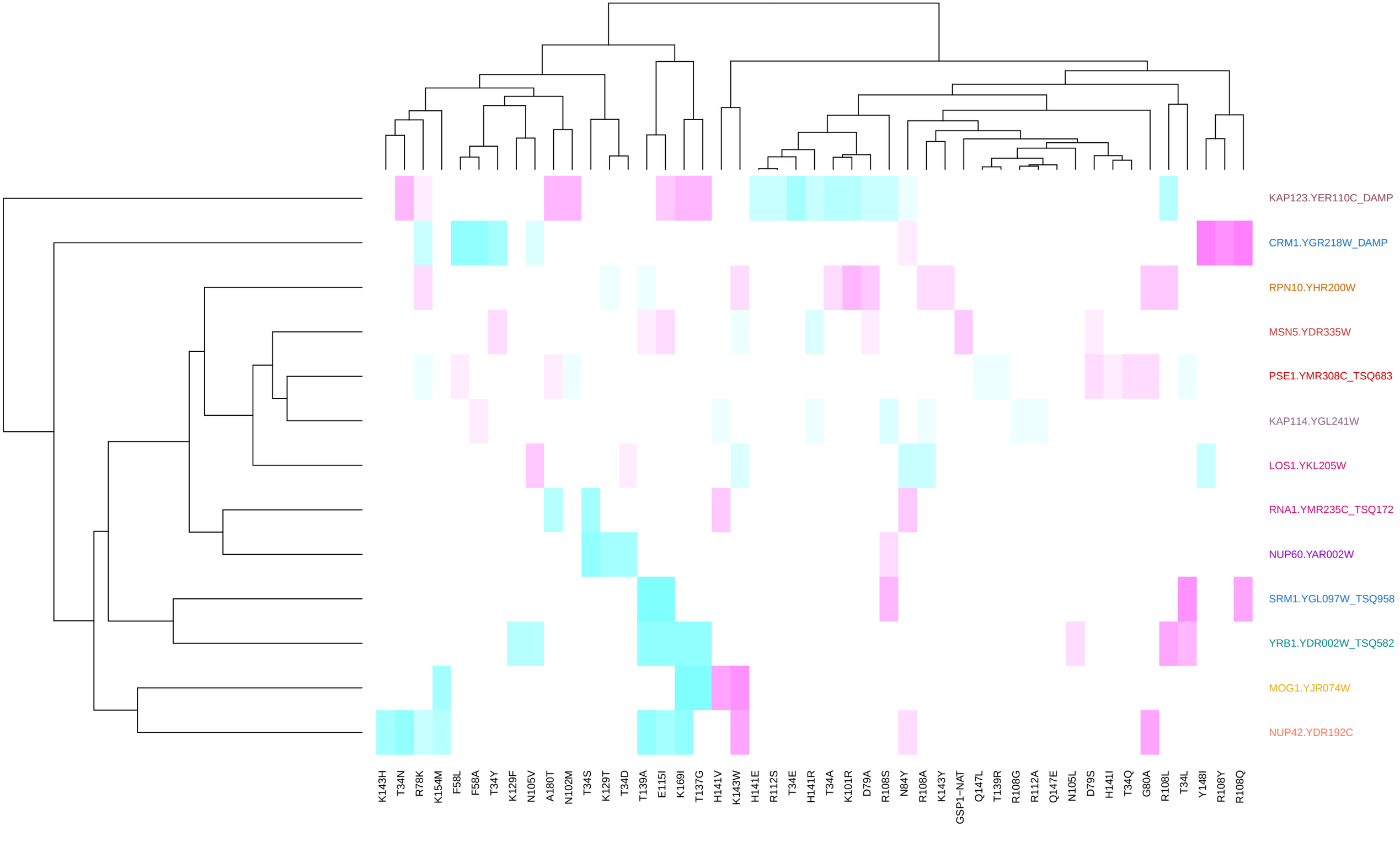
chromatin organization_GO_15_1_mut



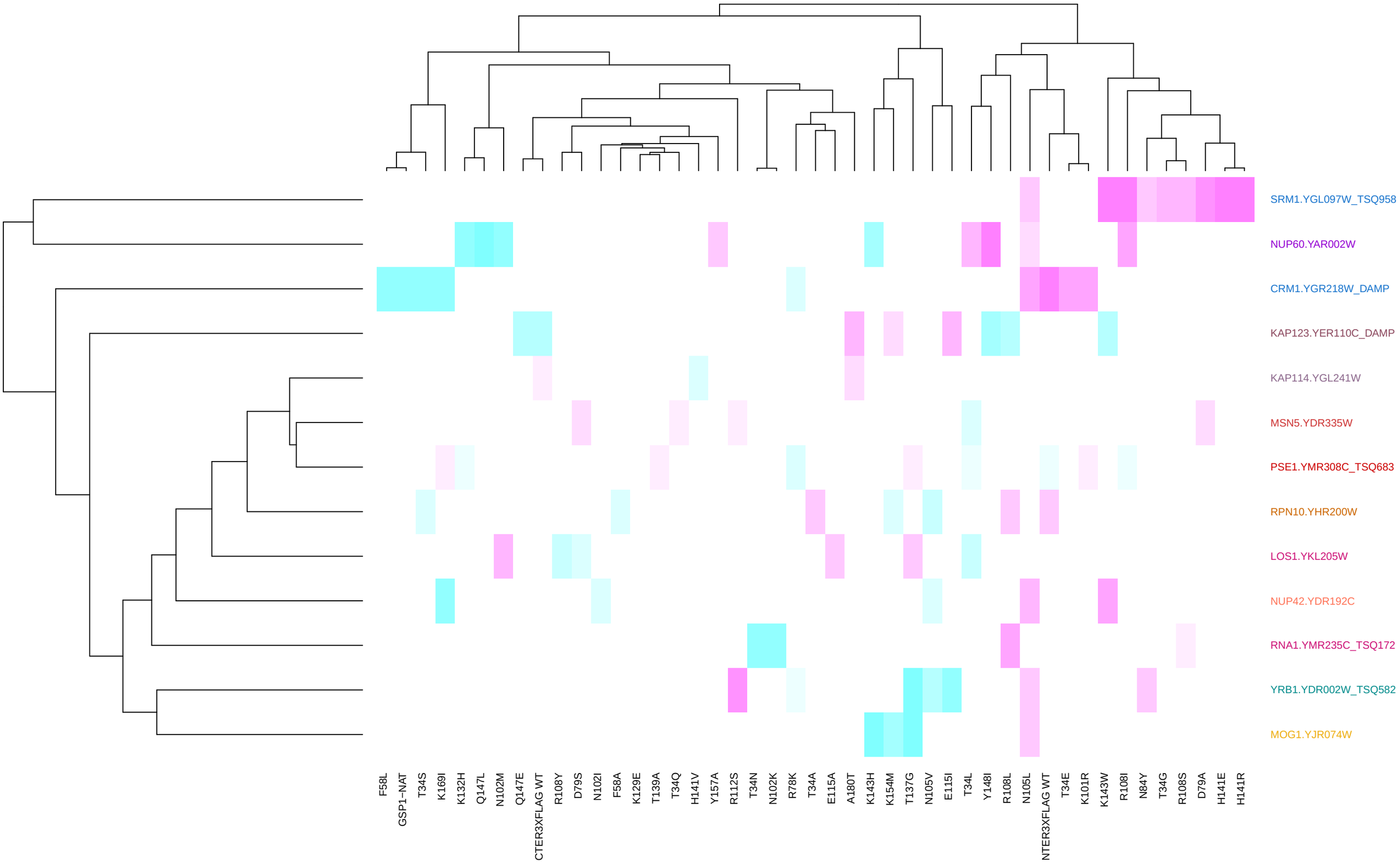
lipids_GO_15_2_all



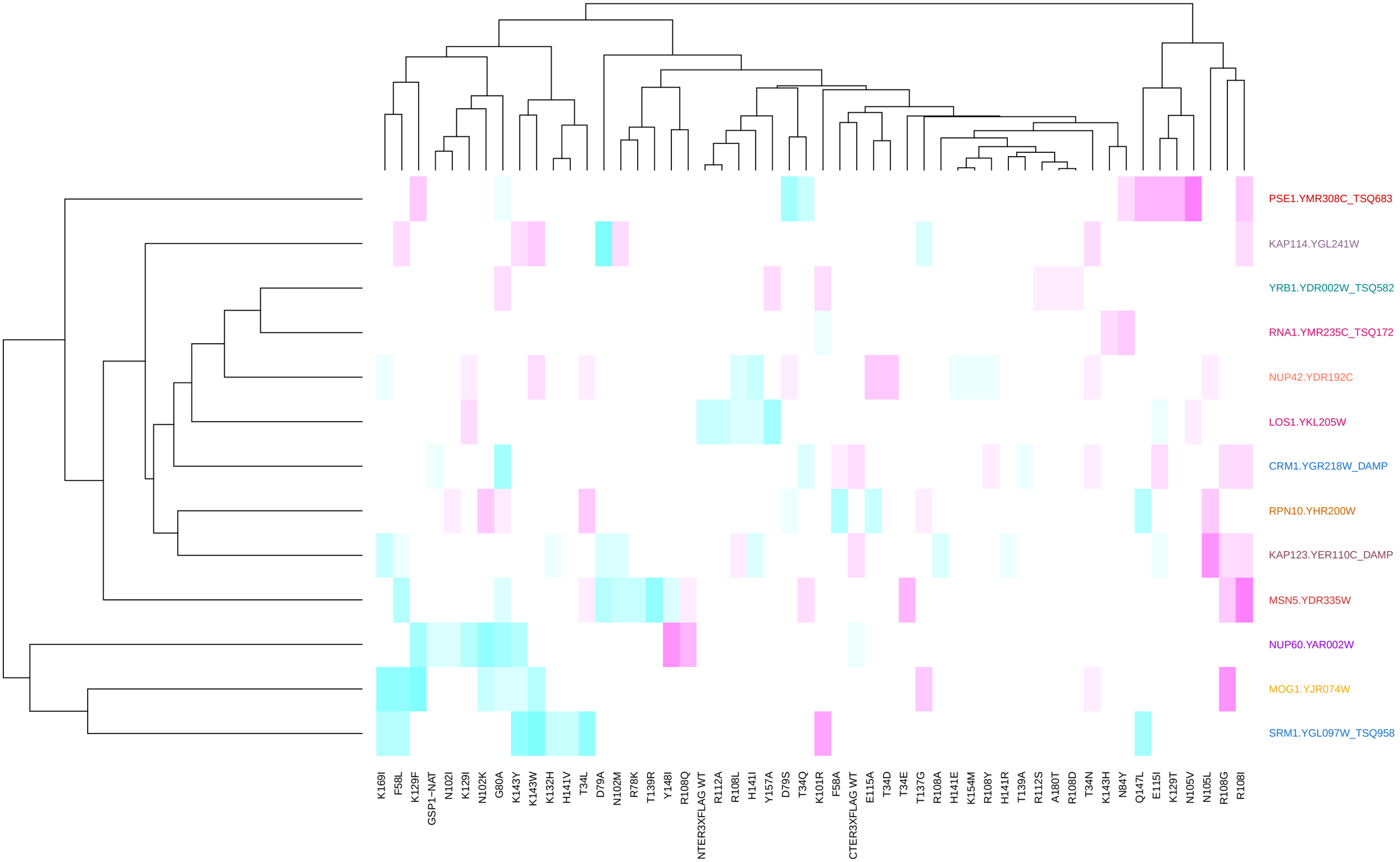
nuclear transport and organization_GO_15_1_mut



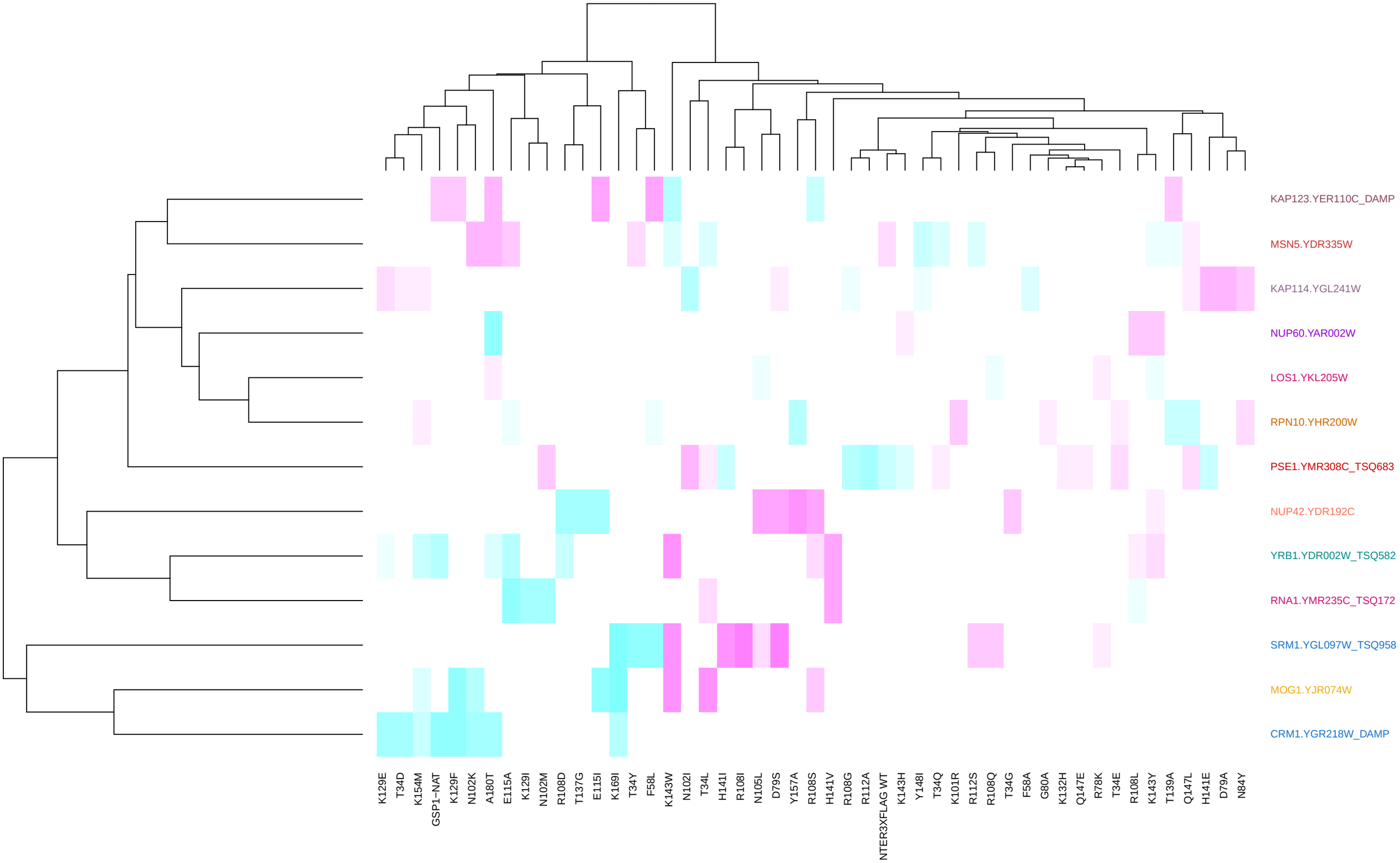
nuclear transport and organization_GO_30_1_all



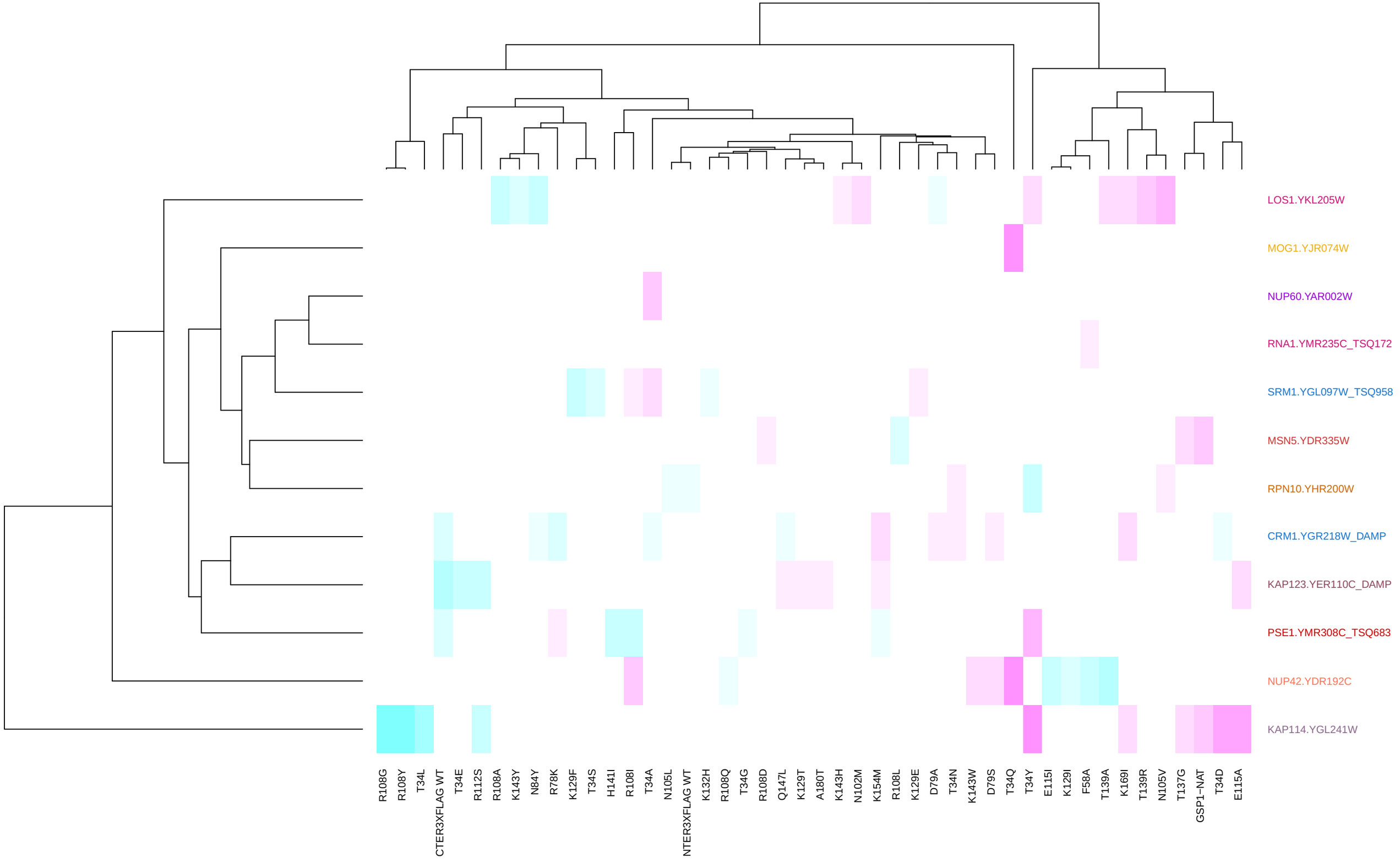
peptidyl−amino acid modification_GO_15_2_mut



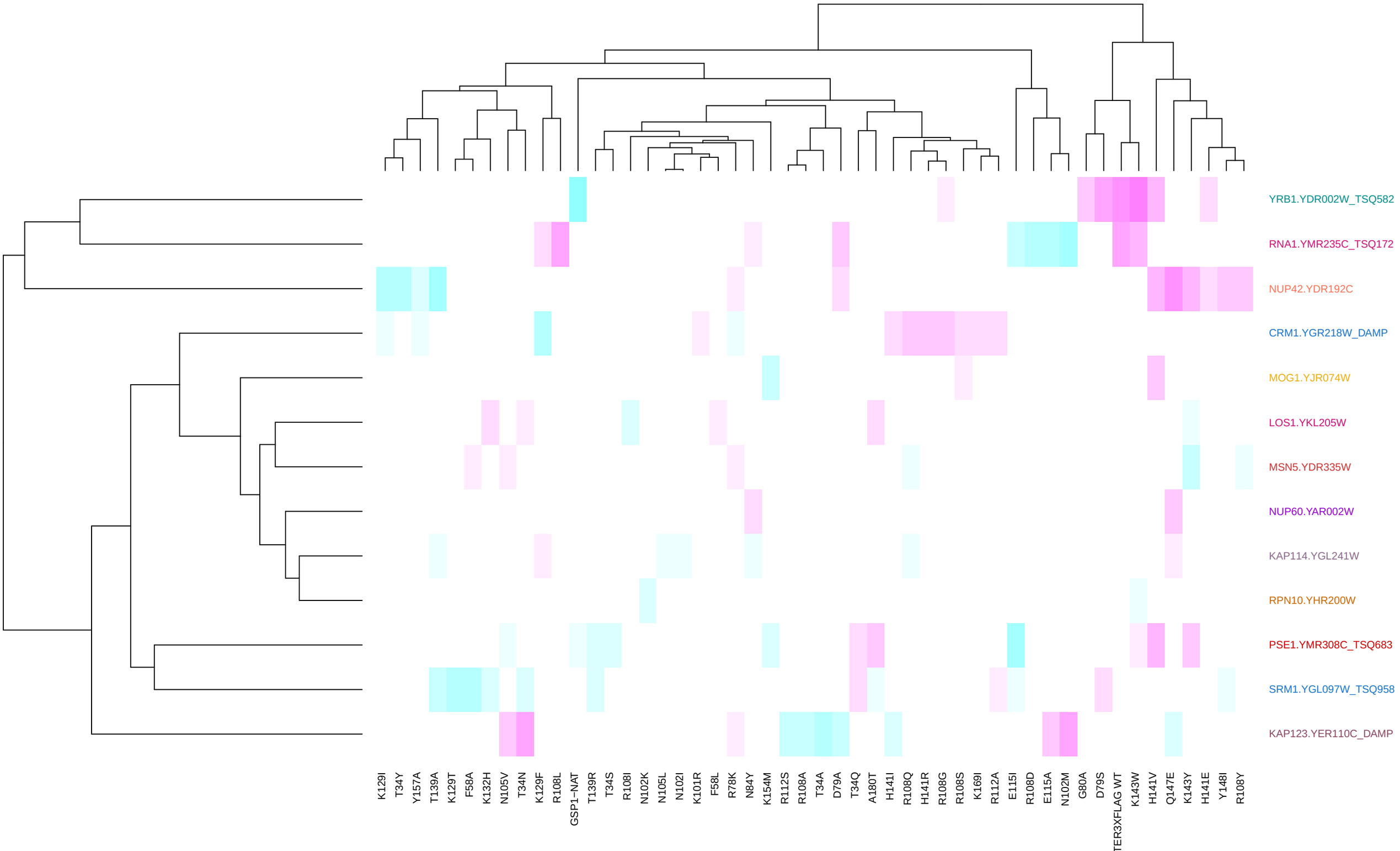
chromatin organization_GO_30_1_mut



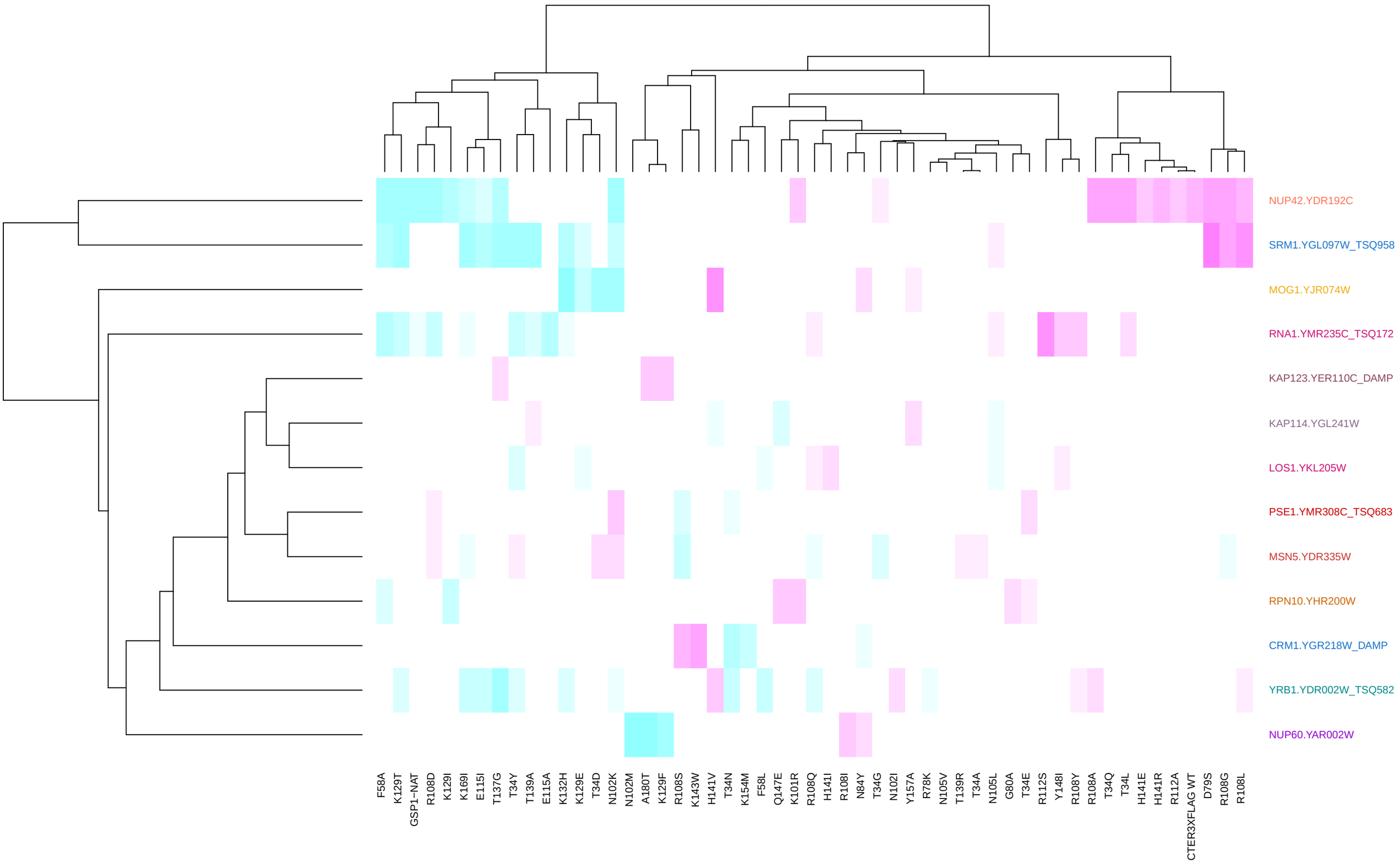
telomere organization



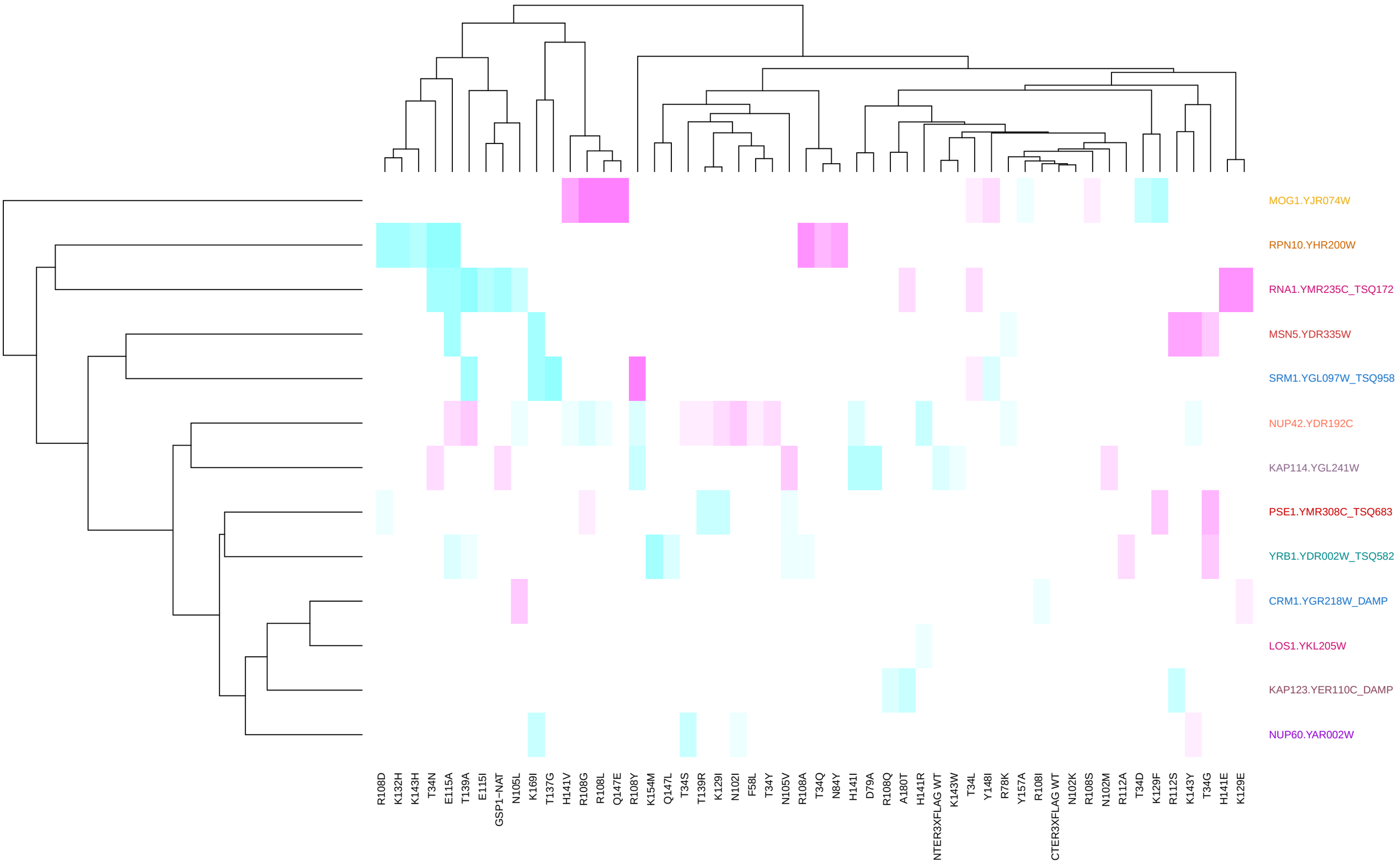
budding_GO_30_1_mut



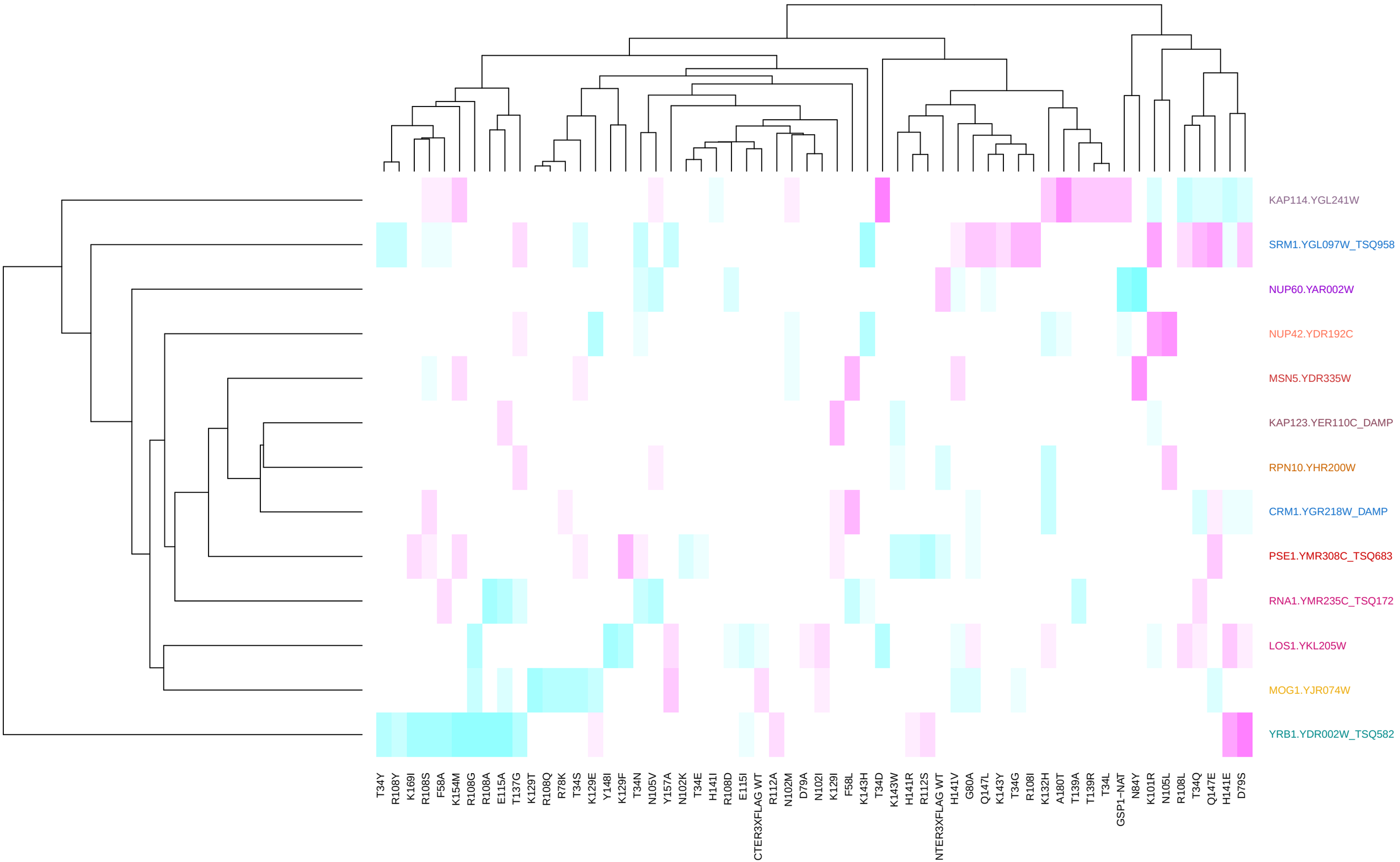
chromatin_GO_30_3_mut



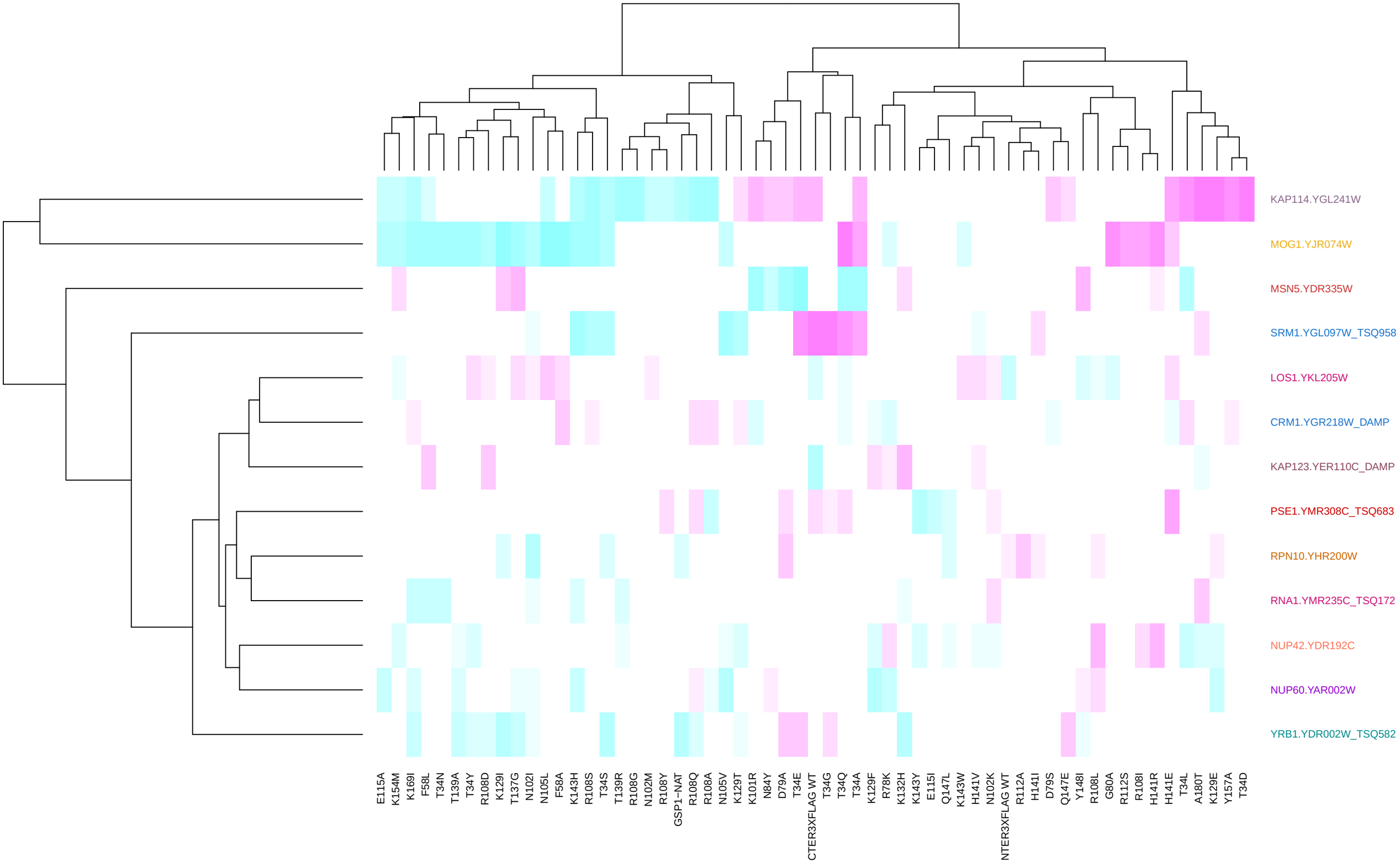
regulation of cell cycle_GO_15_2_mut



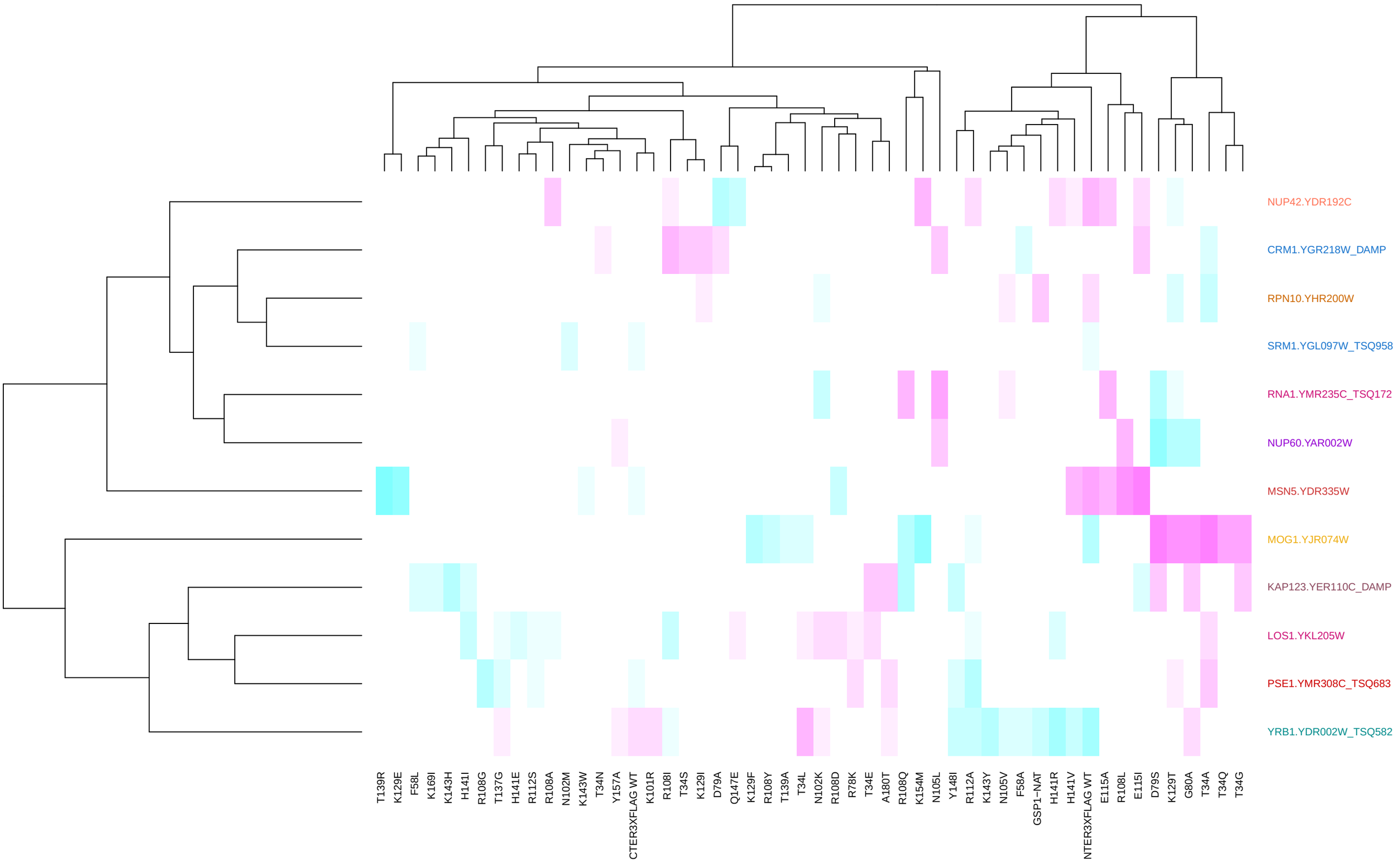
sig_Gsp1_GI_15_5_all



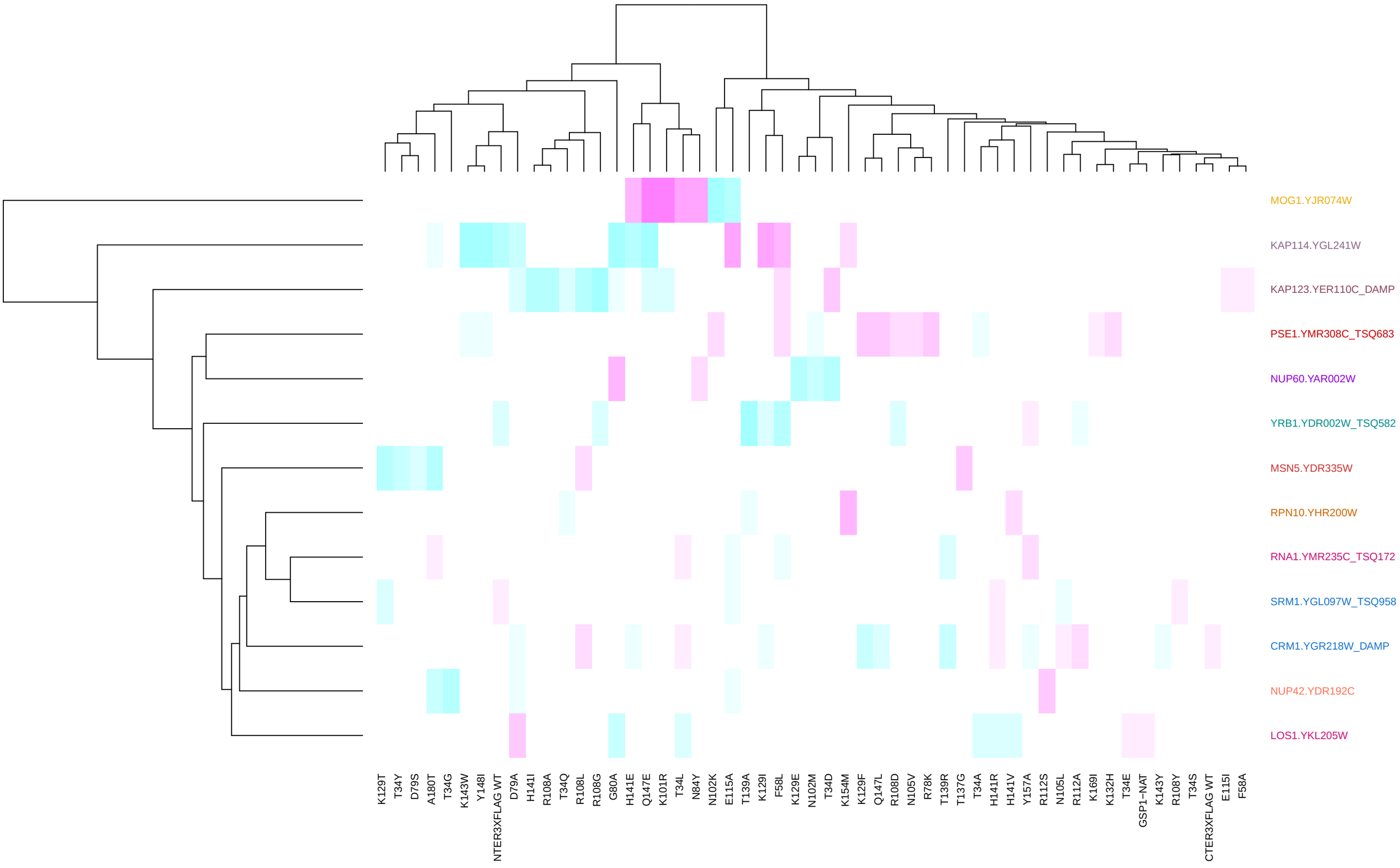
sig_Gsp1_GI_15_6_mut



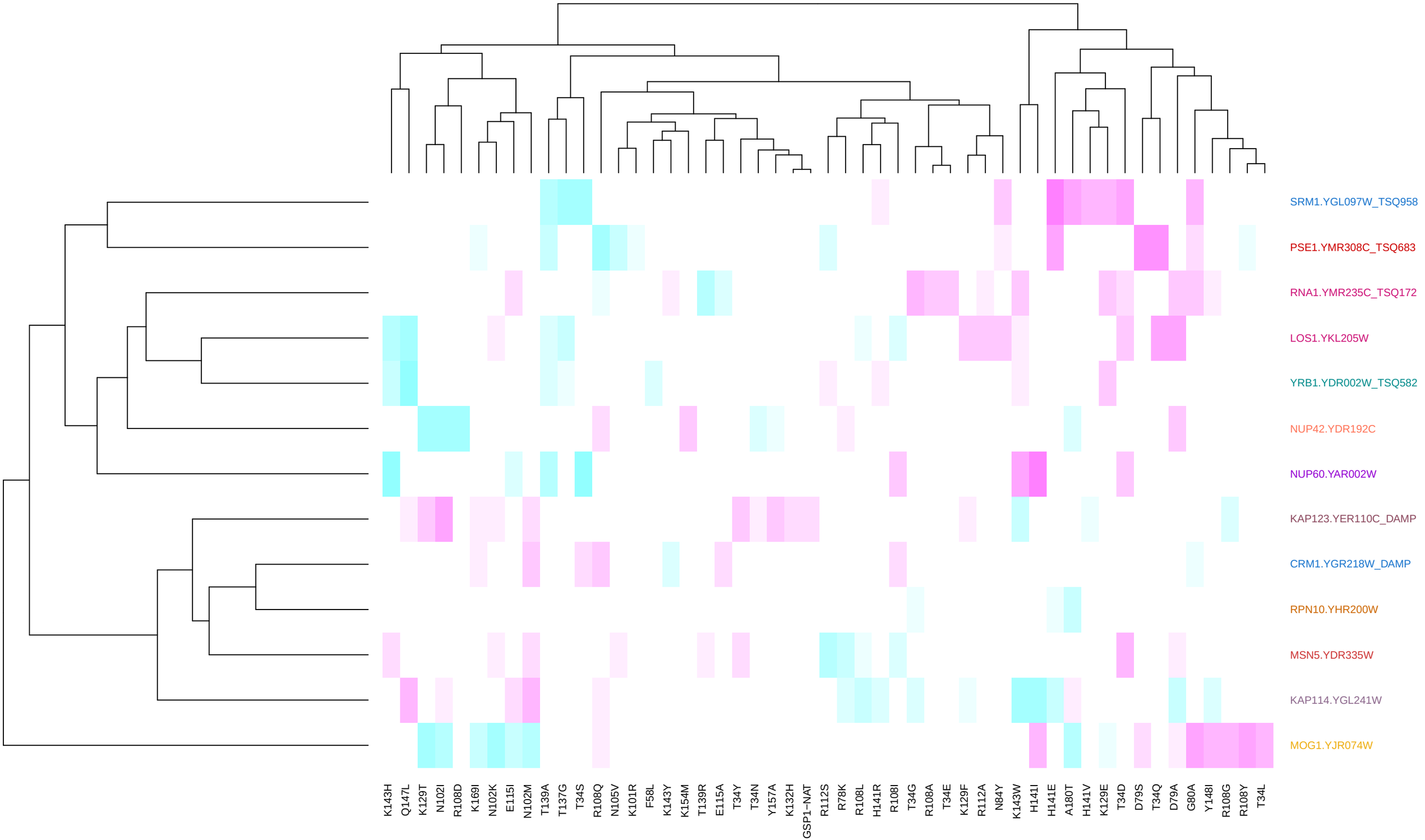
chromatin_GO_15_3_mut



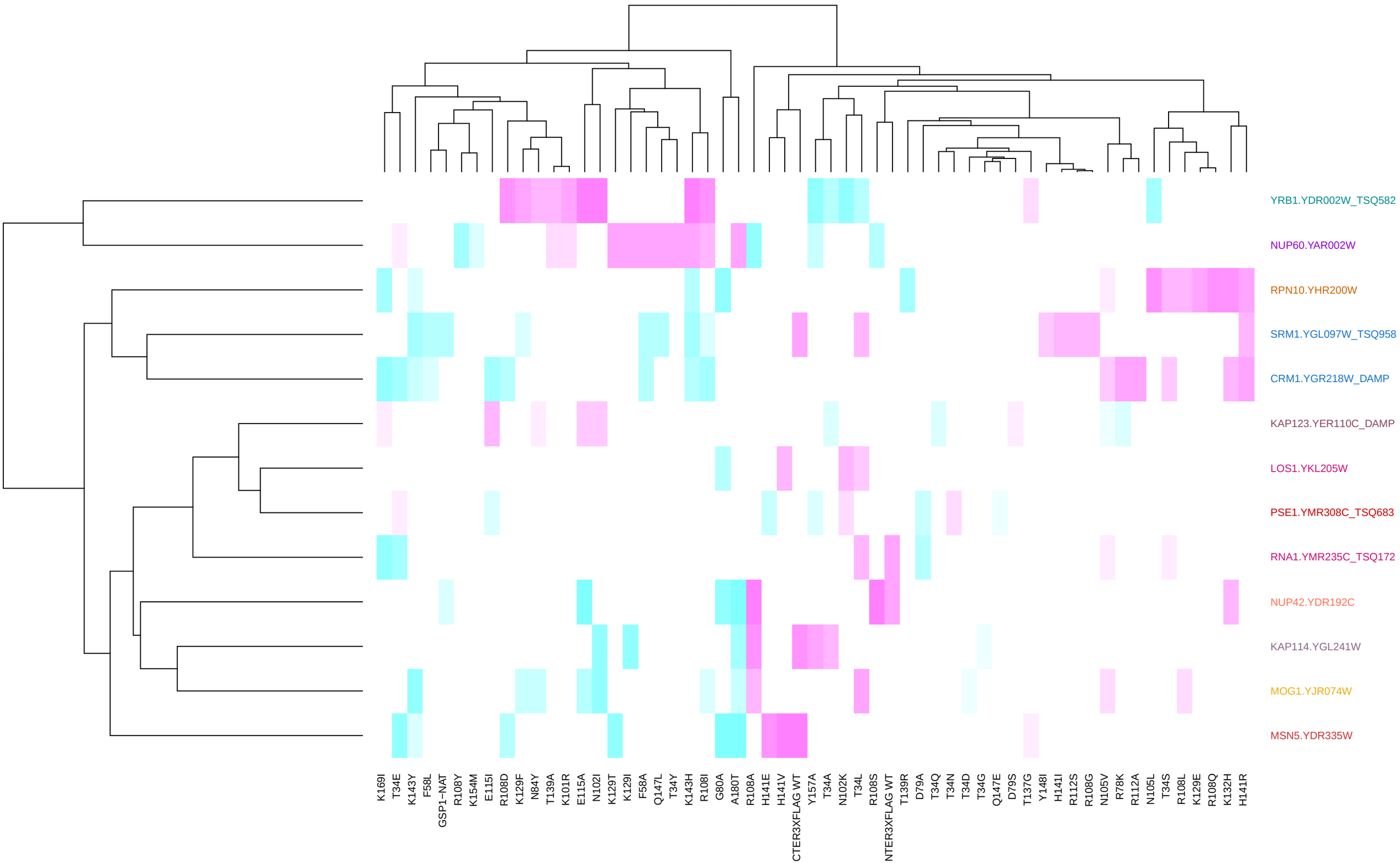
DNA−templated transcription, elongation_GO_15_1_all



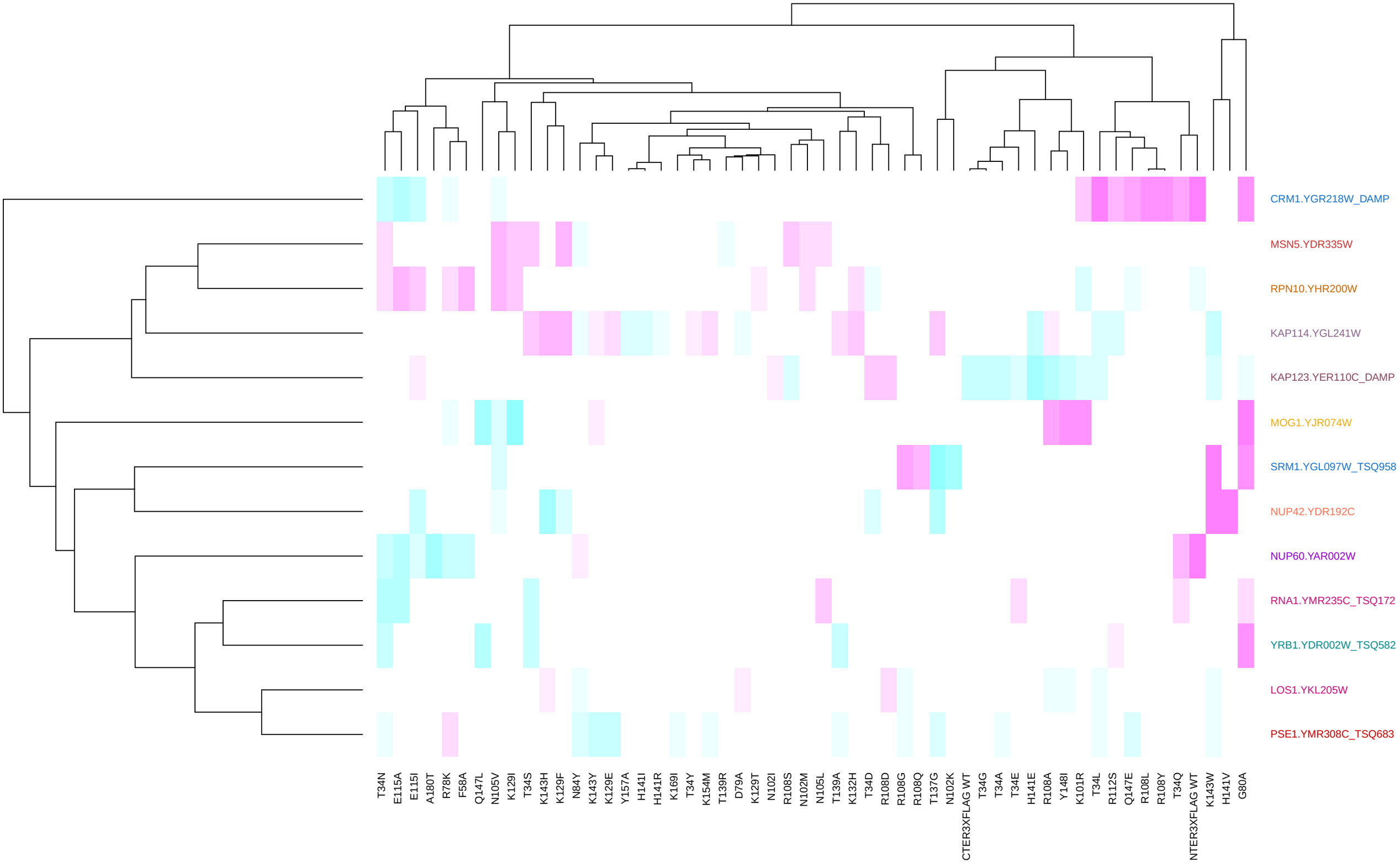
transcription and mRNA processing_GO_15_3_all



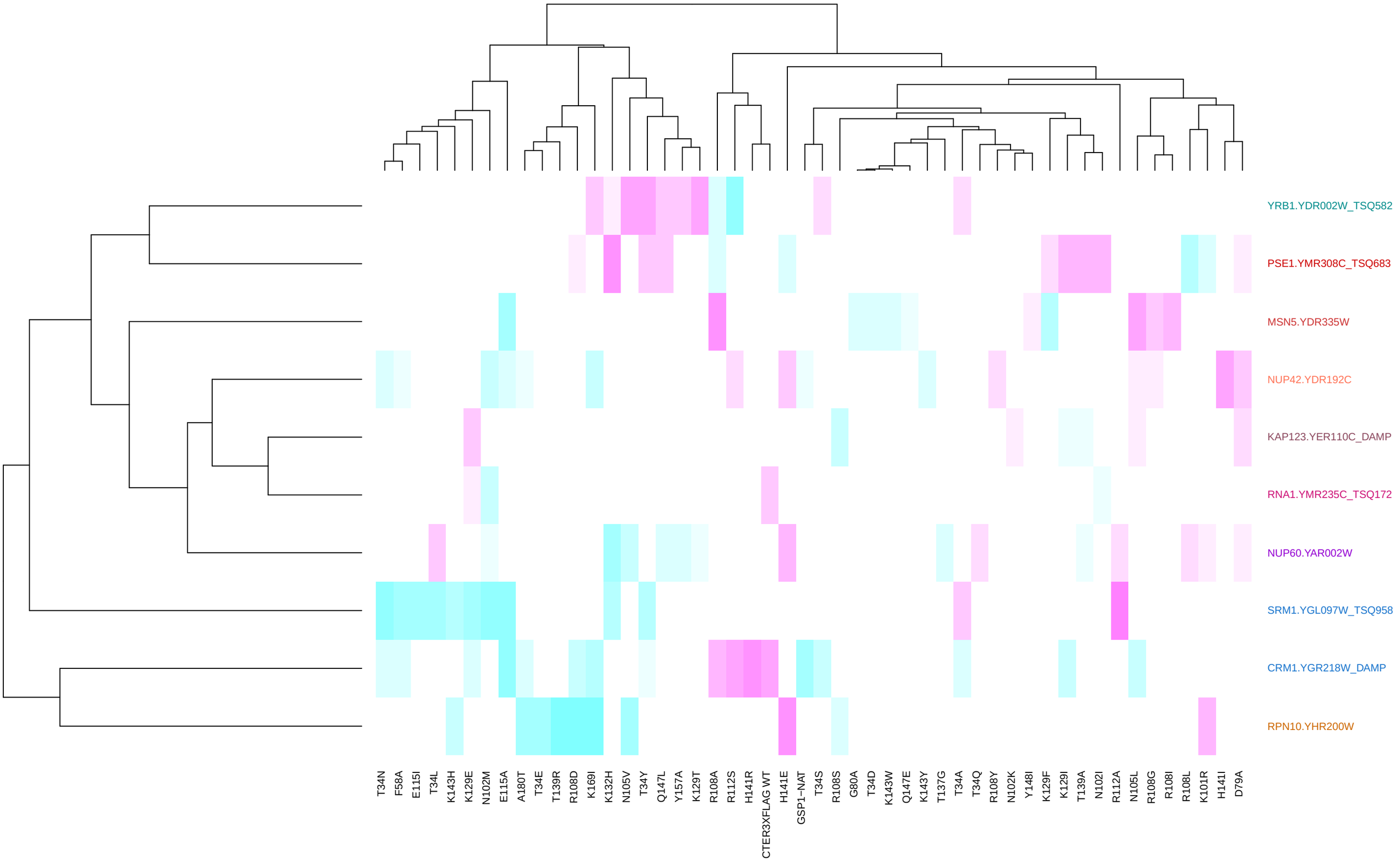
RNA modification_GO_15_1_mut



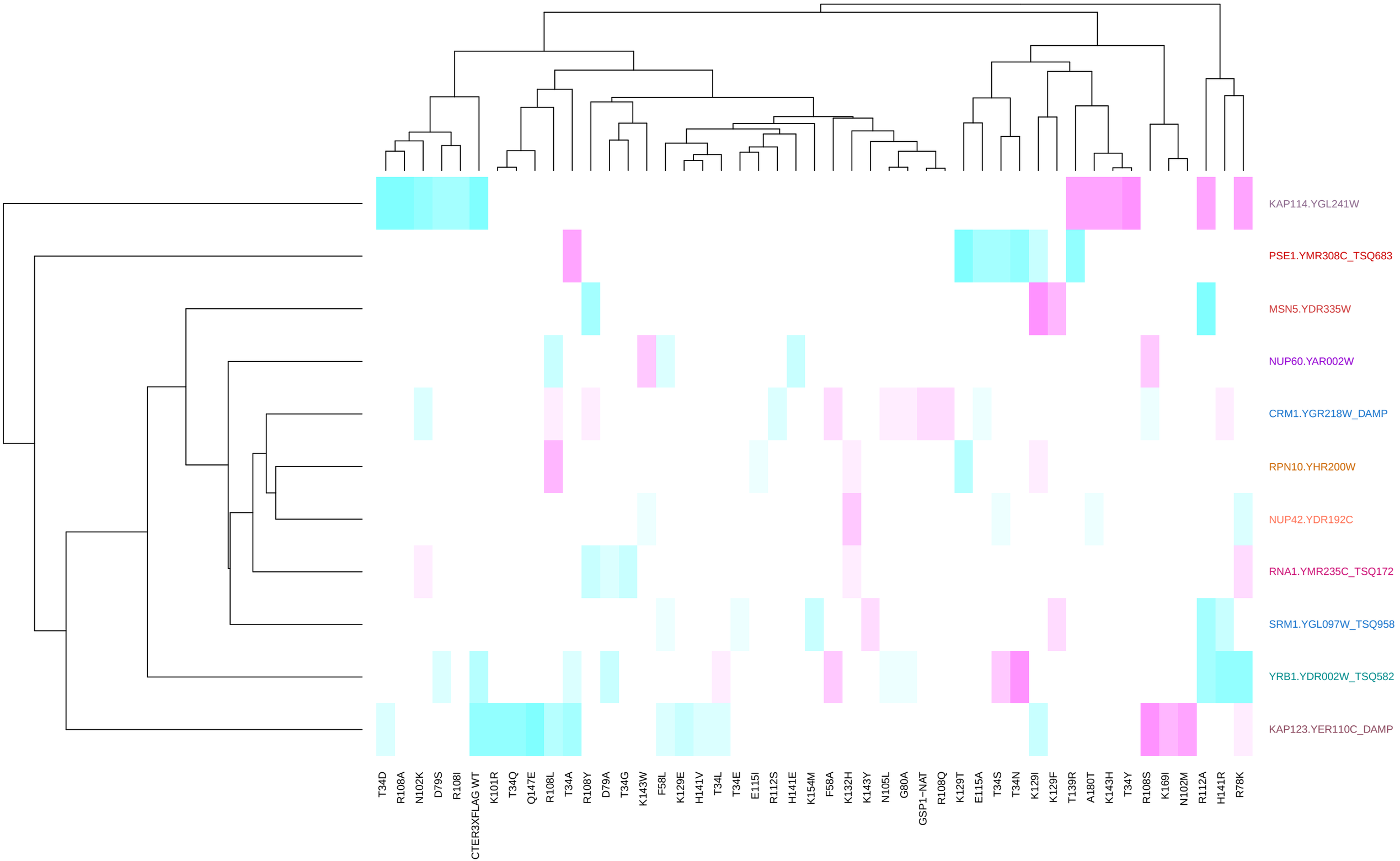
transcription and mRNA processing_GO_30_1_all



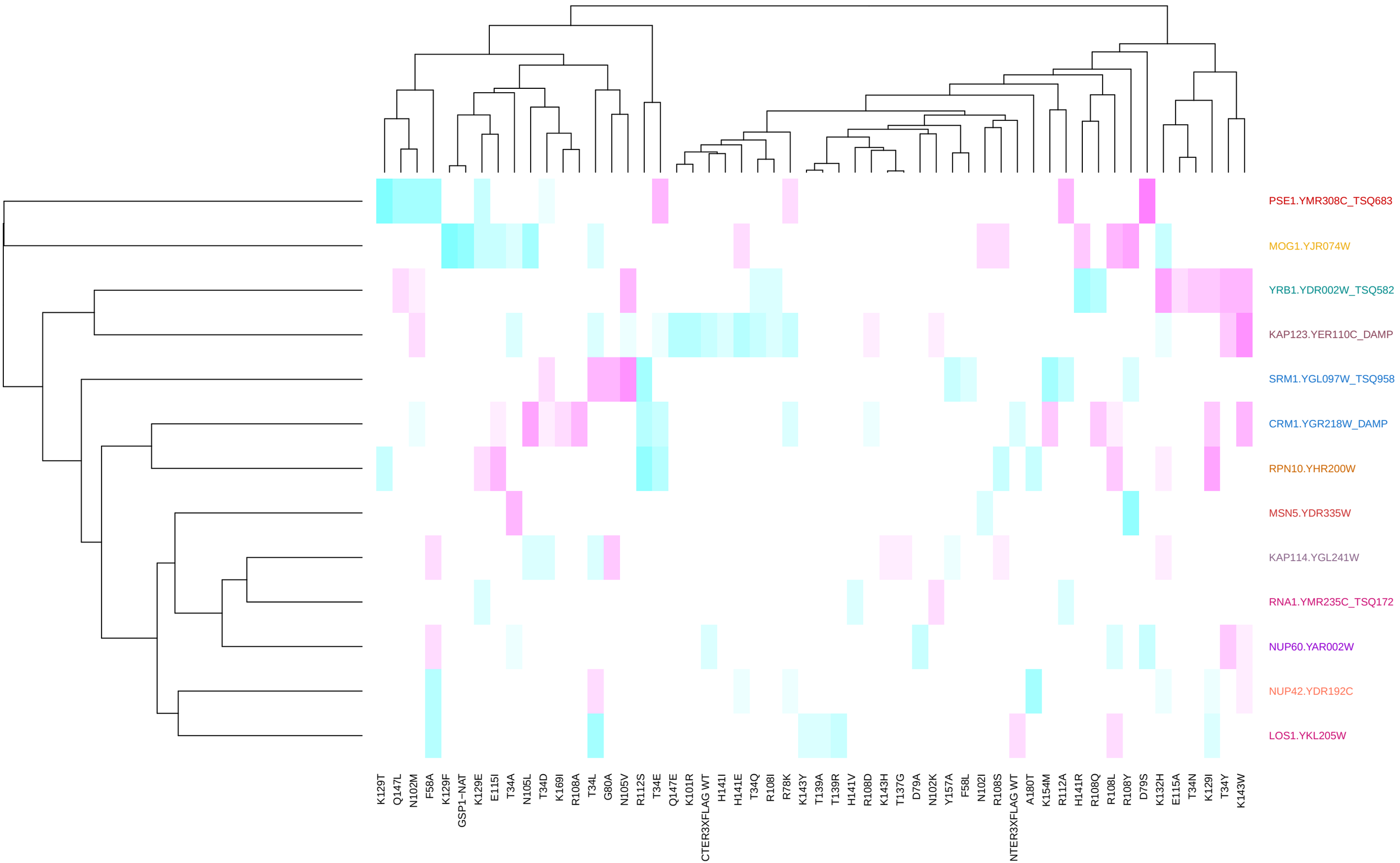
whole_library_15_24_mut



cytoplasmic translation



ribosome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CRM1.YGR218W_DAMP
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MSN5.YDR335W
KAP114.YGL241W
RNA1.YMR235C_TSQ172
NUP60.YAR002W
NUP42.YDR192C
LOS1.YKL205W
K129T
Q147L
N102M
F58A
K129F
GSP1−NAT
K129E
E115I
T34A
N105L
T34D
K169I
R108A
T34L
G80A
N105V
R112S
T34E
Q147E
K101R
CTER3XFLAG WT
H141I
H141E
T34Q
R108I
R78K
K143Y
T139A
T139R
H141V
R108D
K143H
T137G
D79A
N102K
Y157A
F58L
N102I
R108S
NTER3XFLAG WT
A180T
K154M
R112A
H141R
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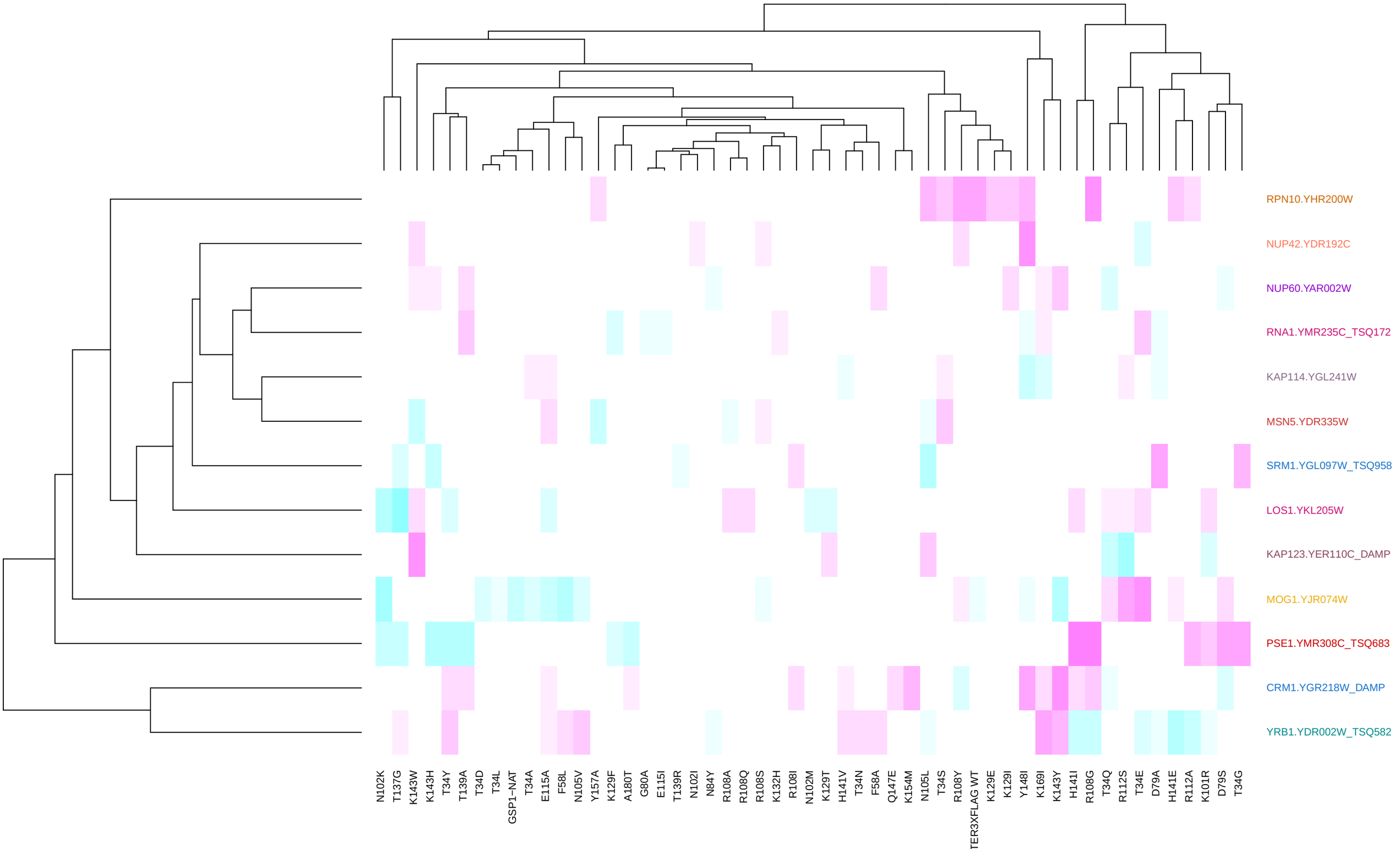
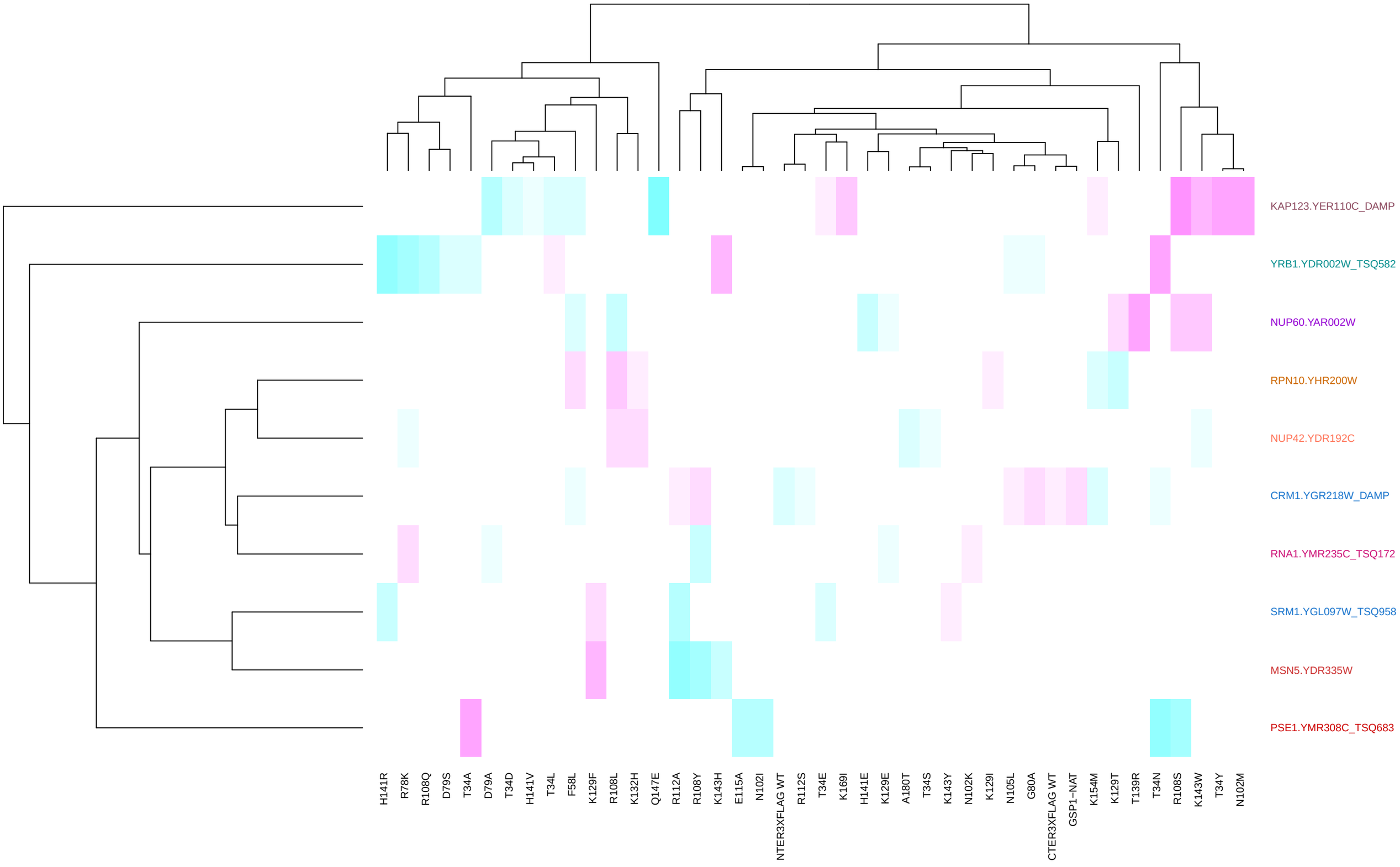
K143W

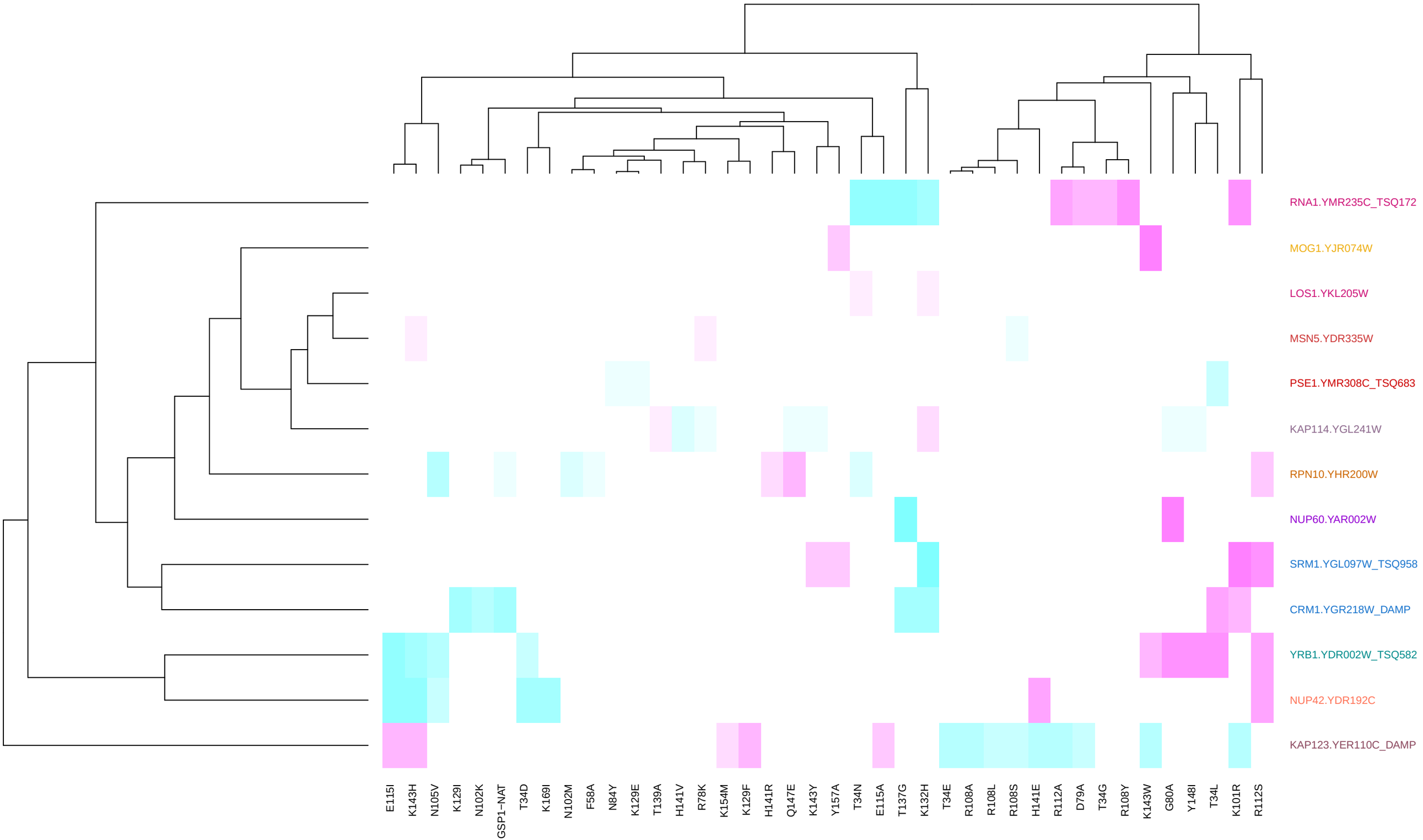
ribosome_GO_15_1_all



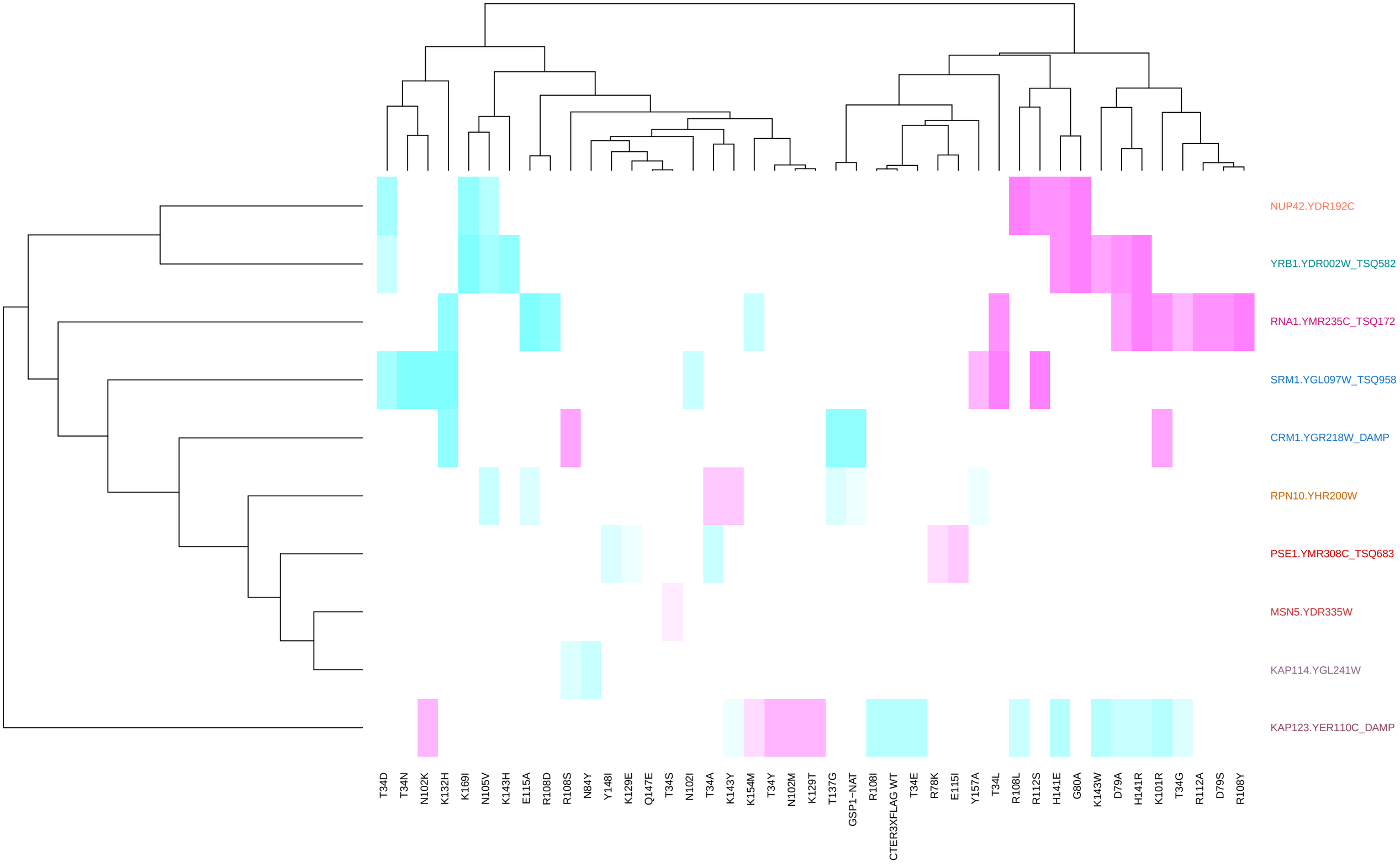
structural constituent of ribosome



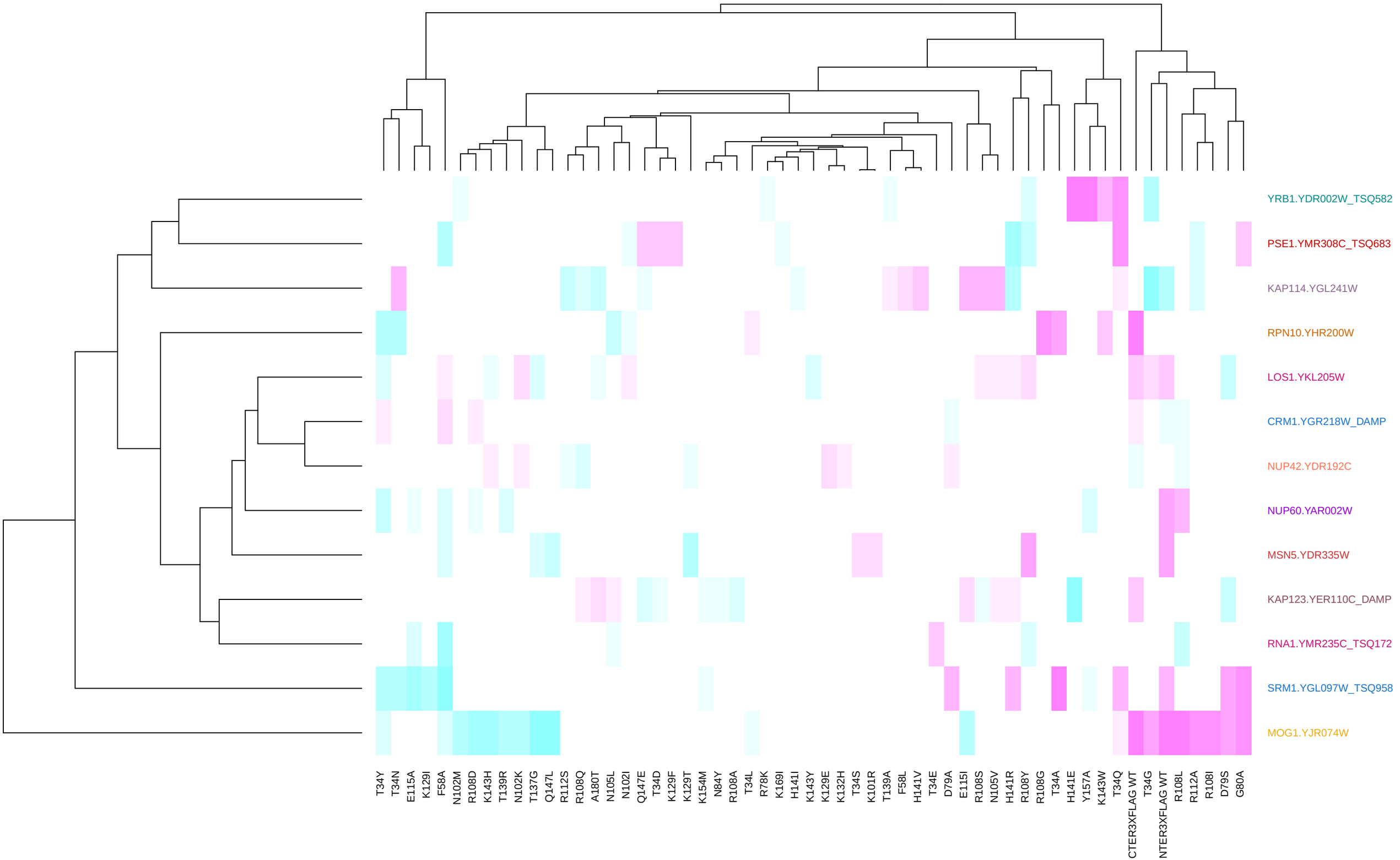
whole_library_15_14_mut



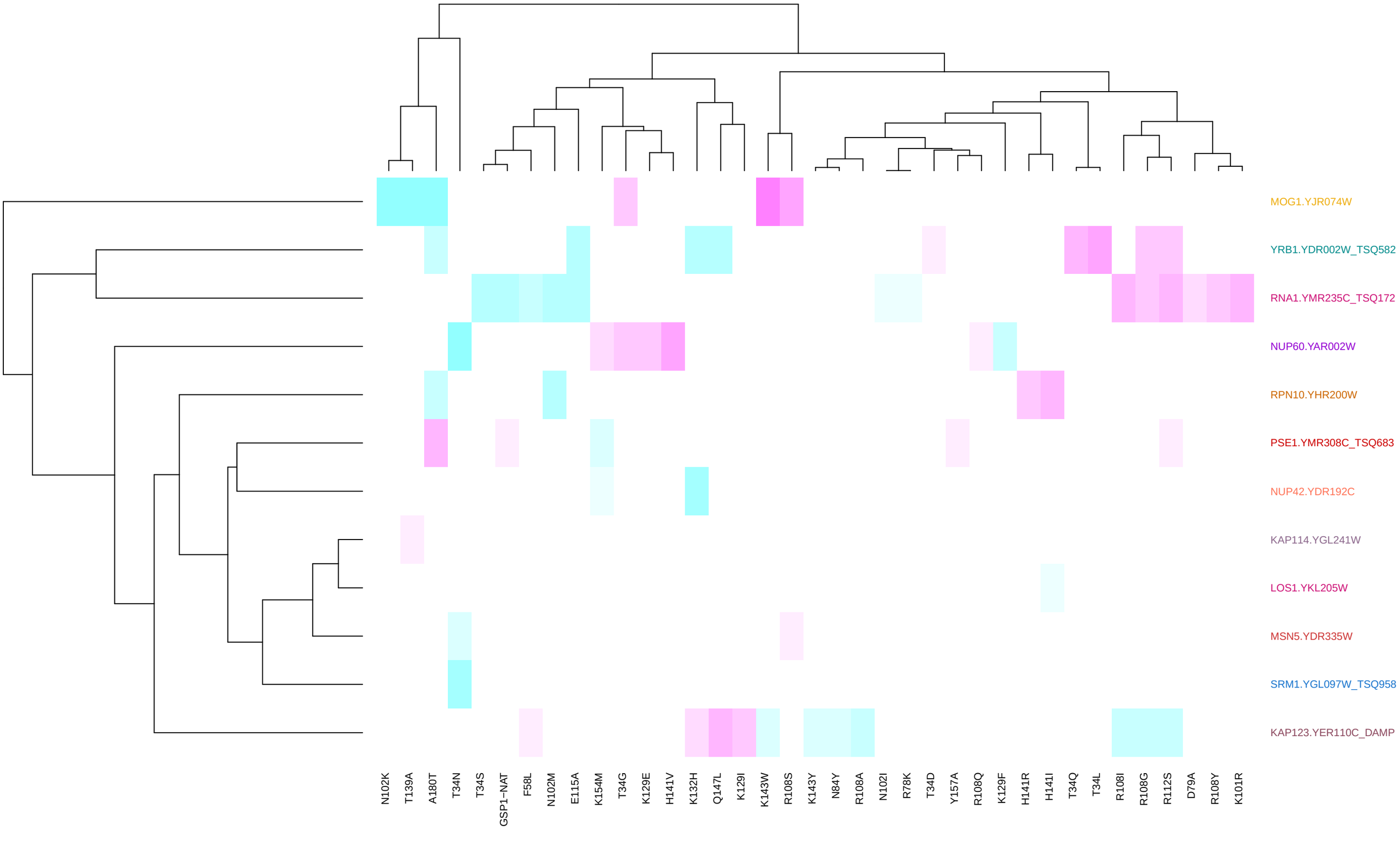
whole_library_30_12_mut



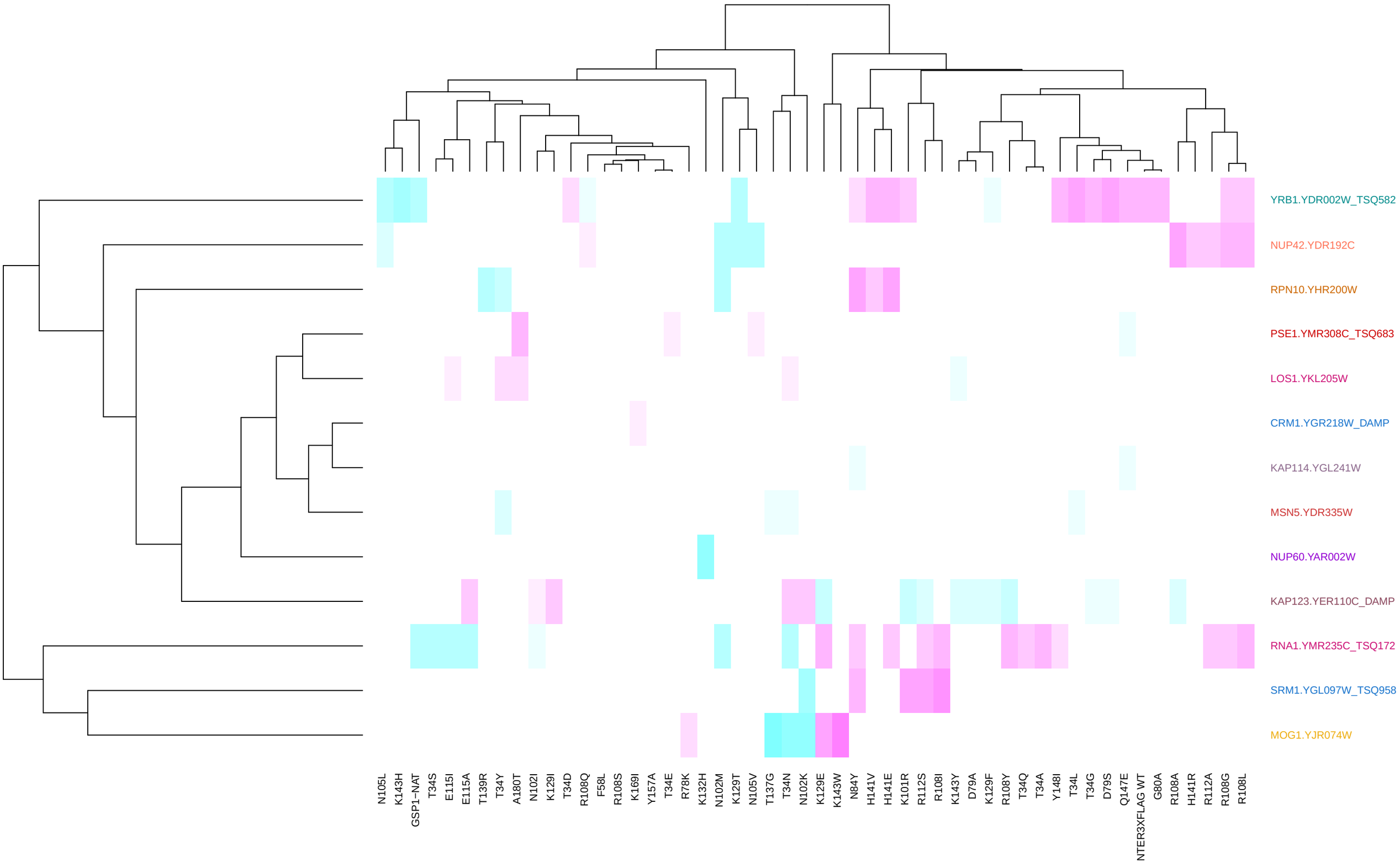
histone modification_GO_15_1_all



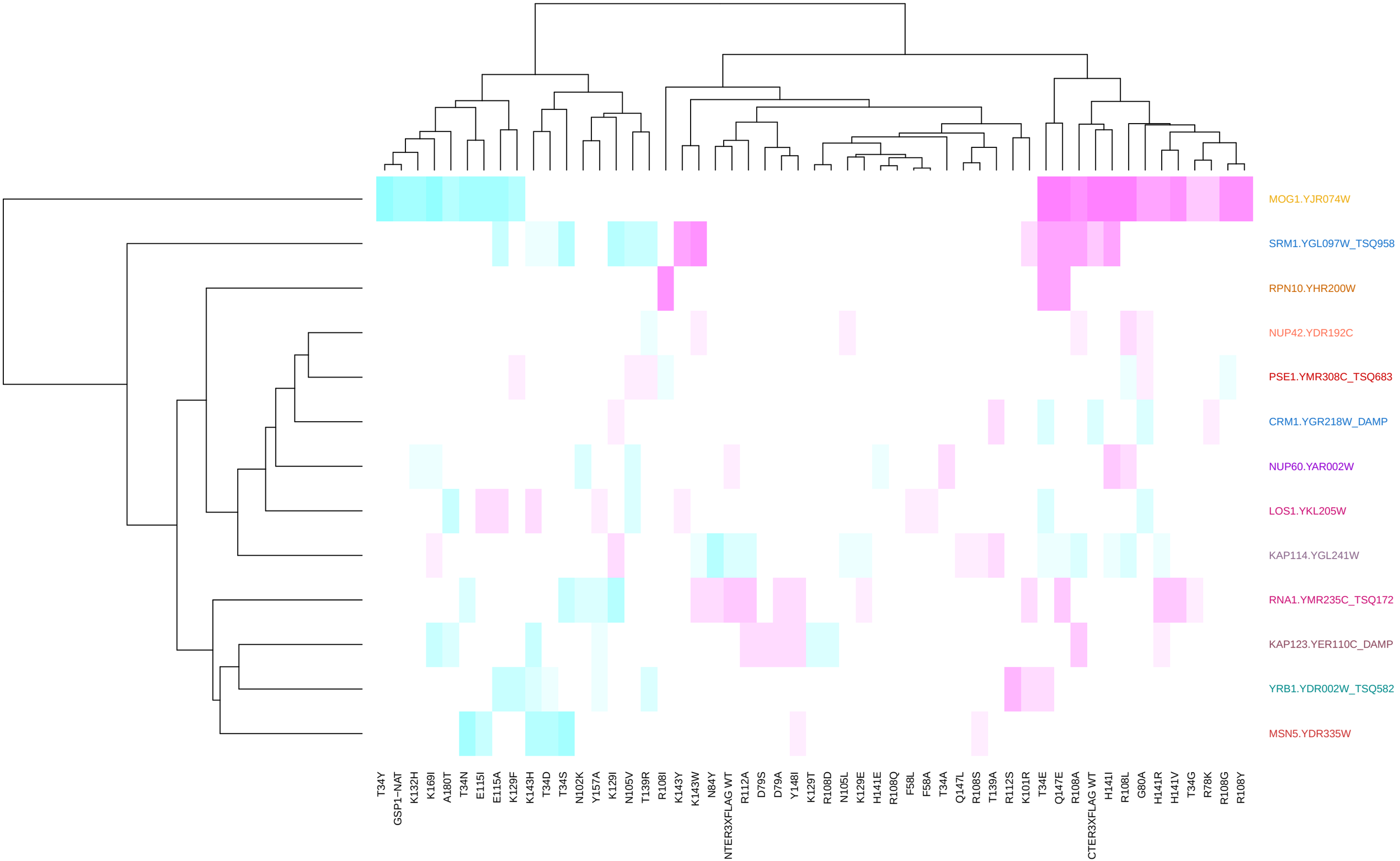
cell cycle_GO_15_9_mut



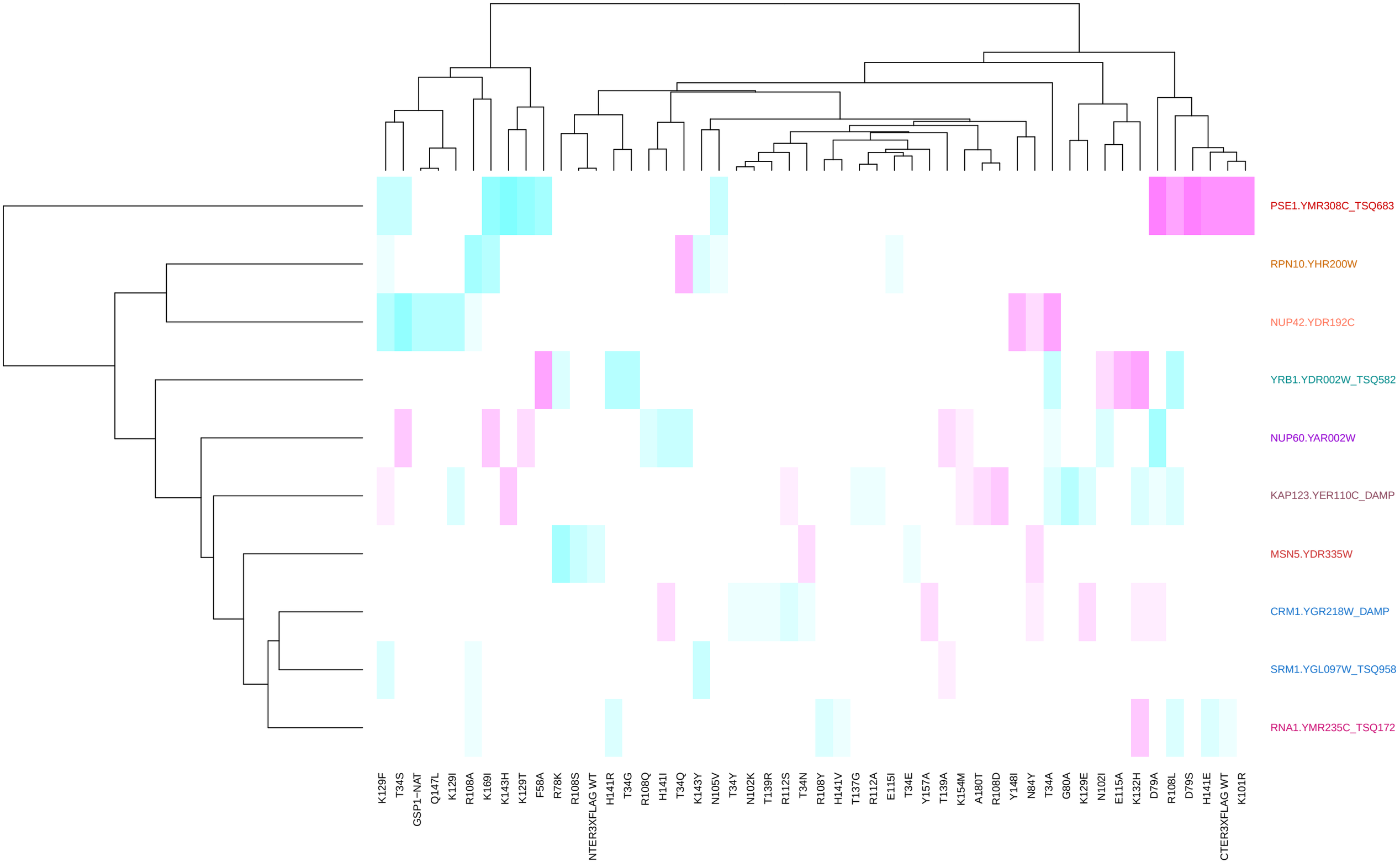
cell cycle_GO_30_3_mut



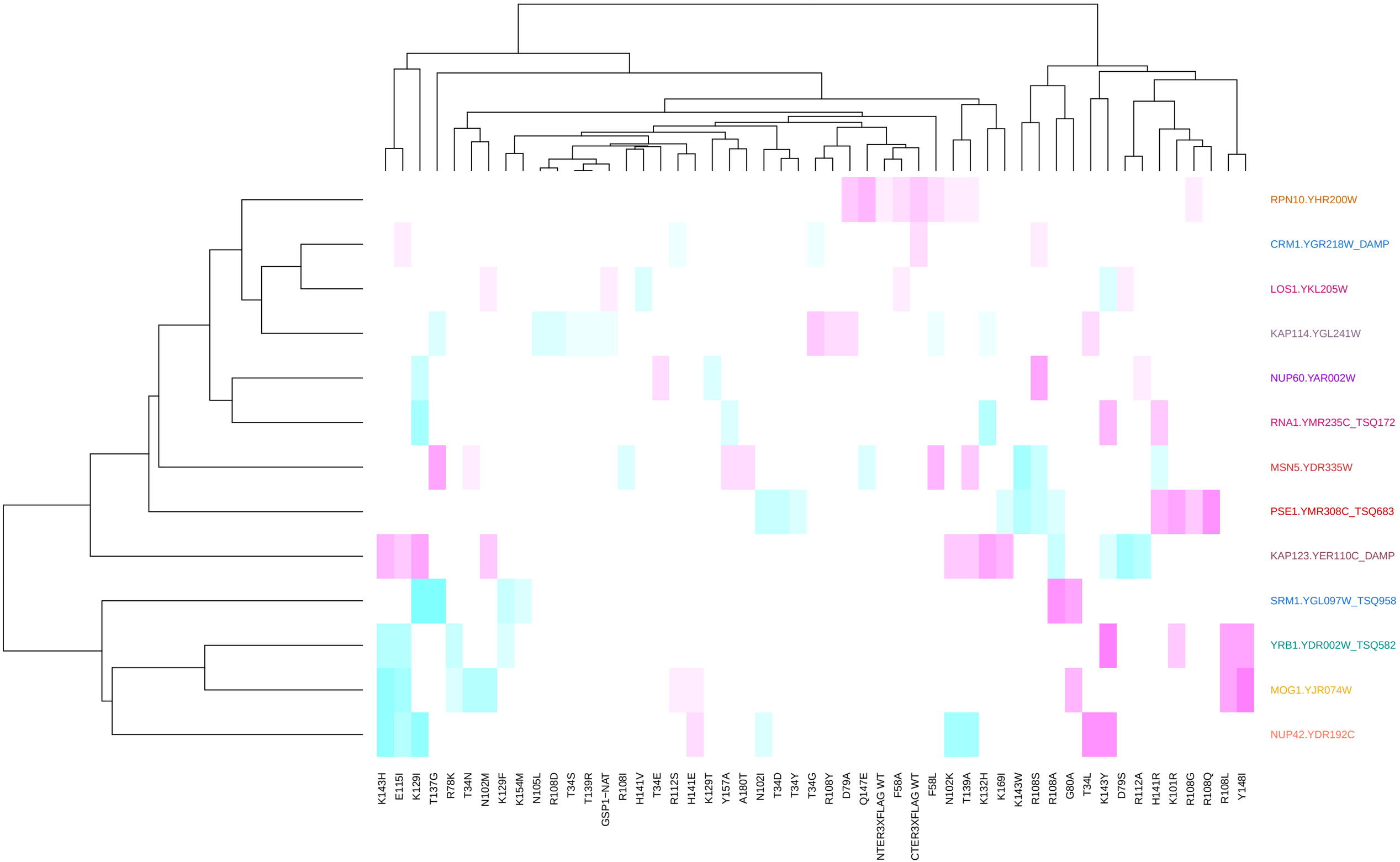
proteolysis involved in cellular protein catabolic process_GO_15_2_mut



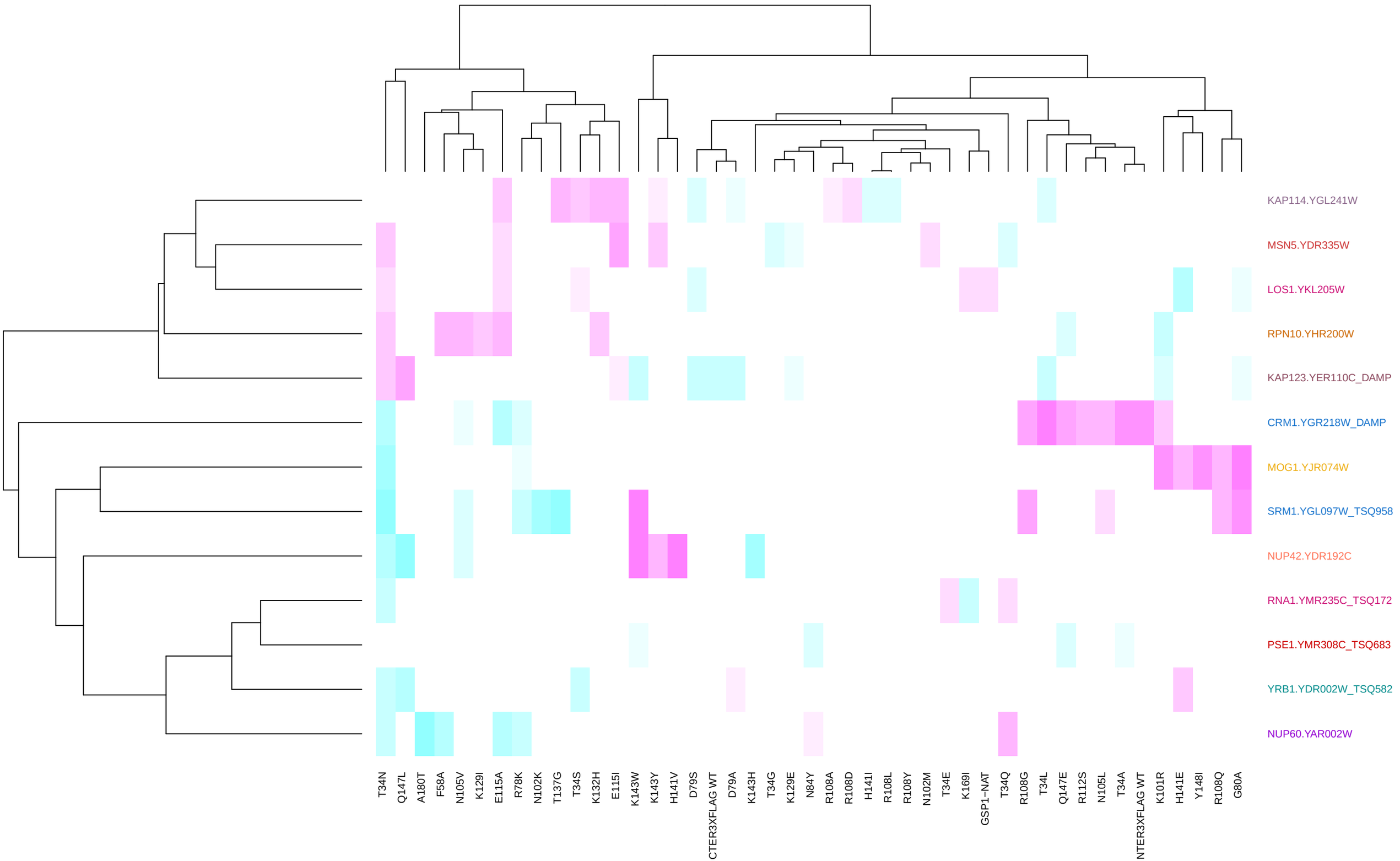
cytoplasmic translation_GO_15_1_all



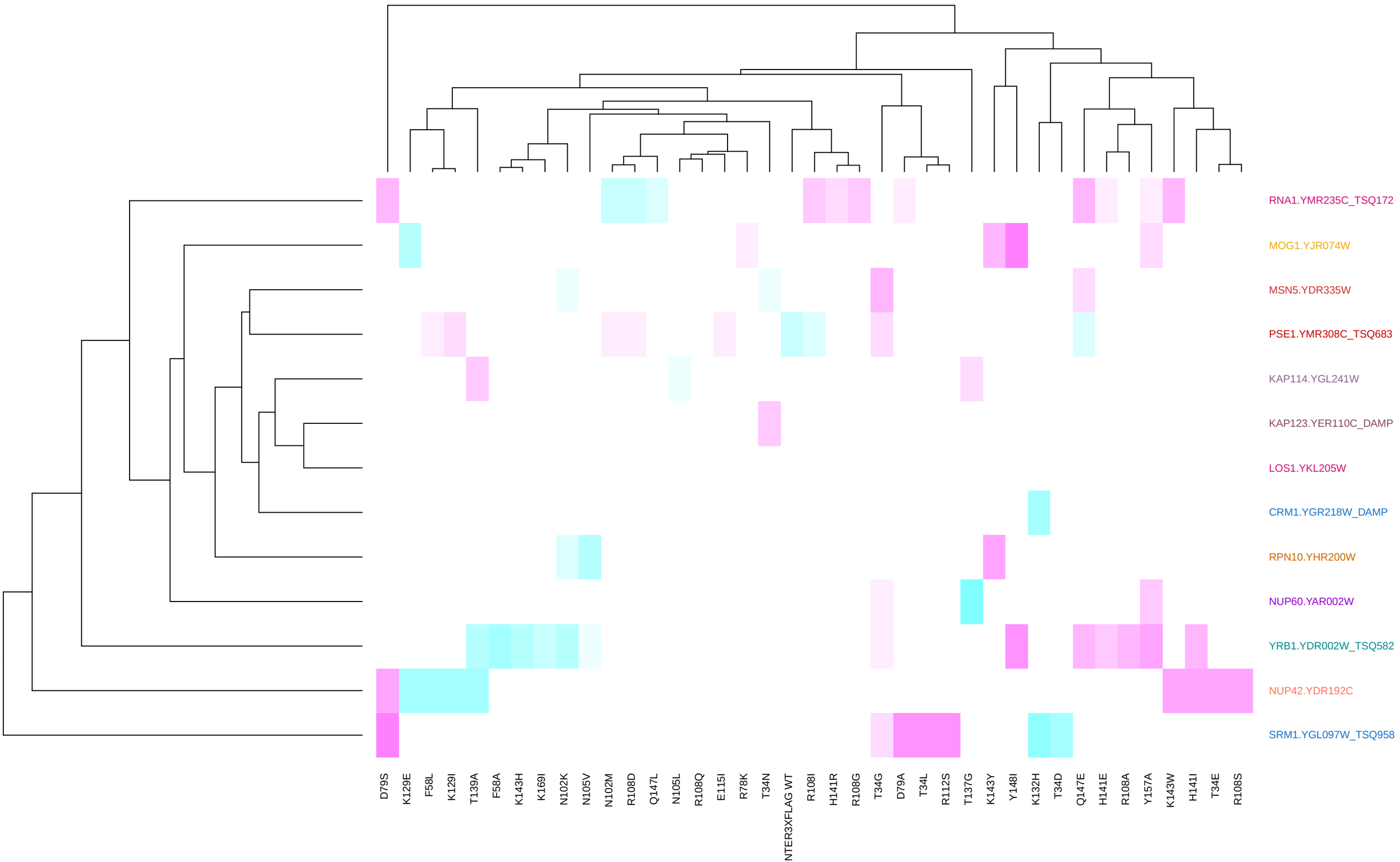
ribosomes and translation_GO_15_2_mut



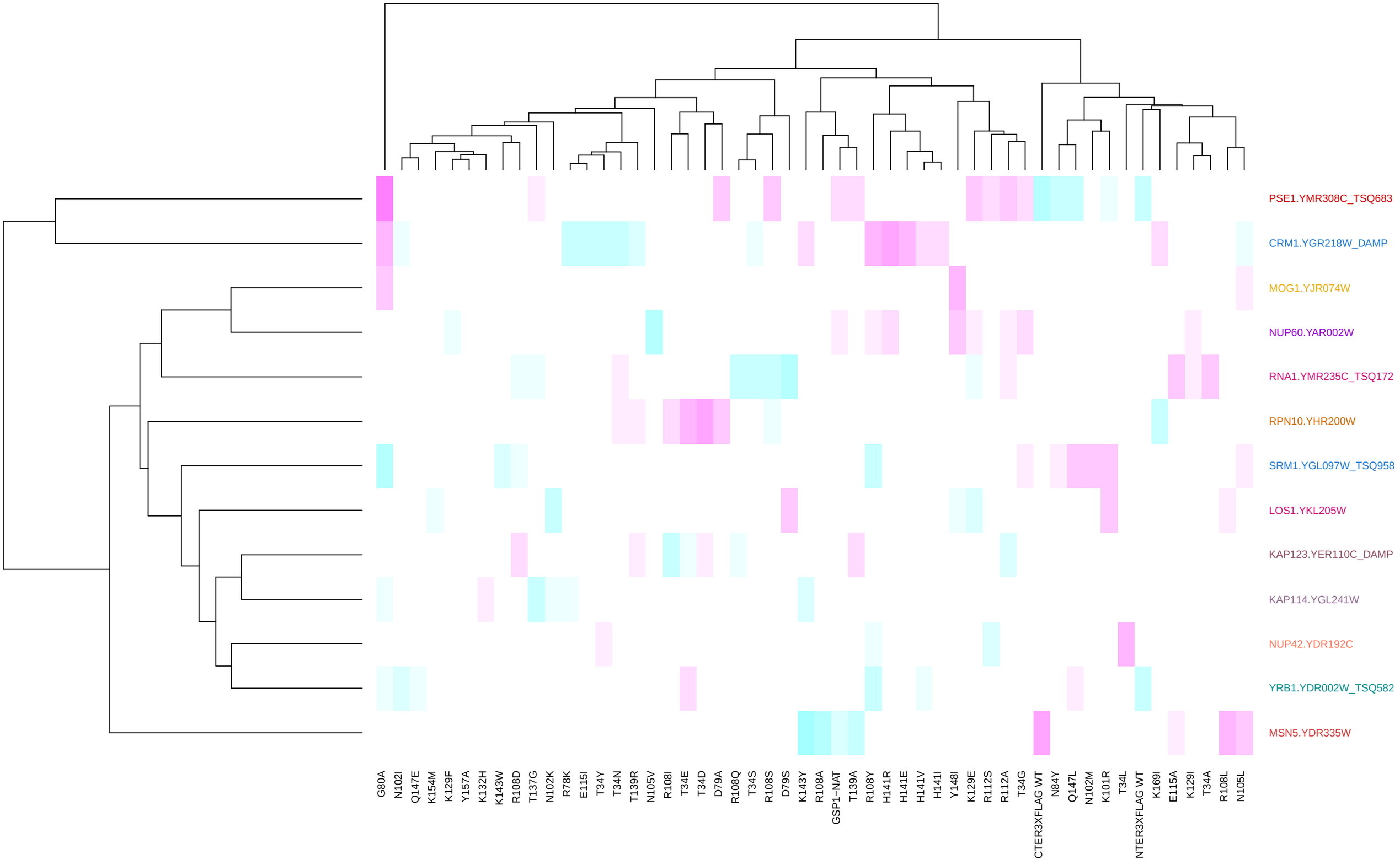
transcription and mRNA processing_GO_15_1_all



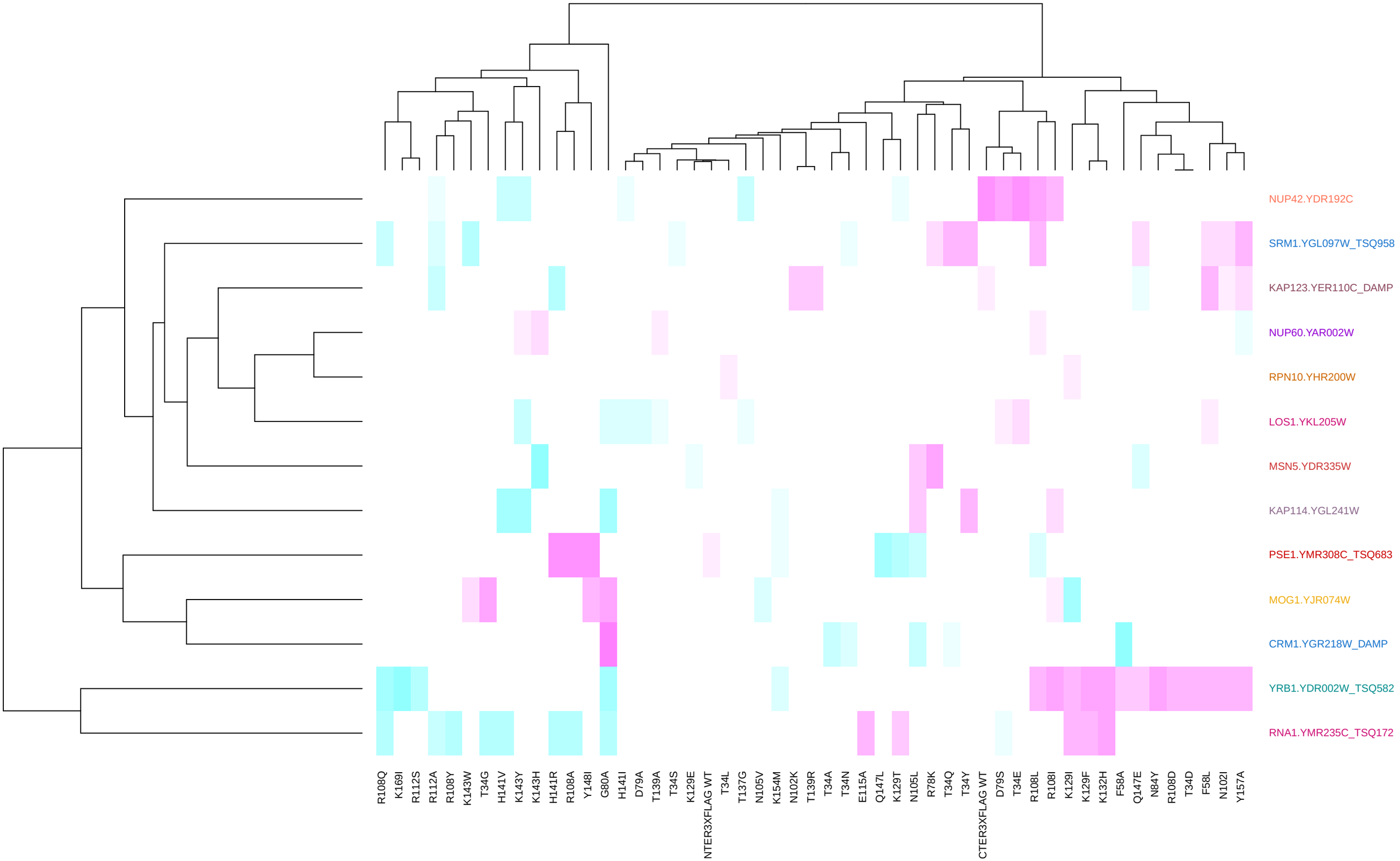
chromatin_GO_15_7_mut



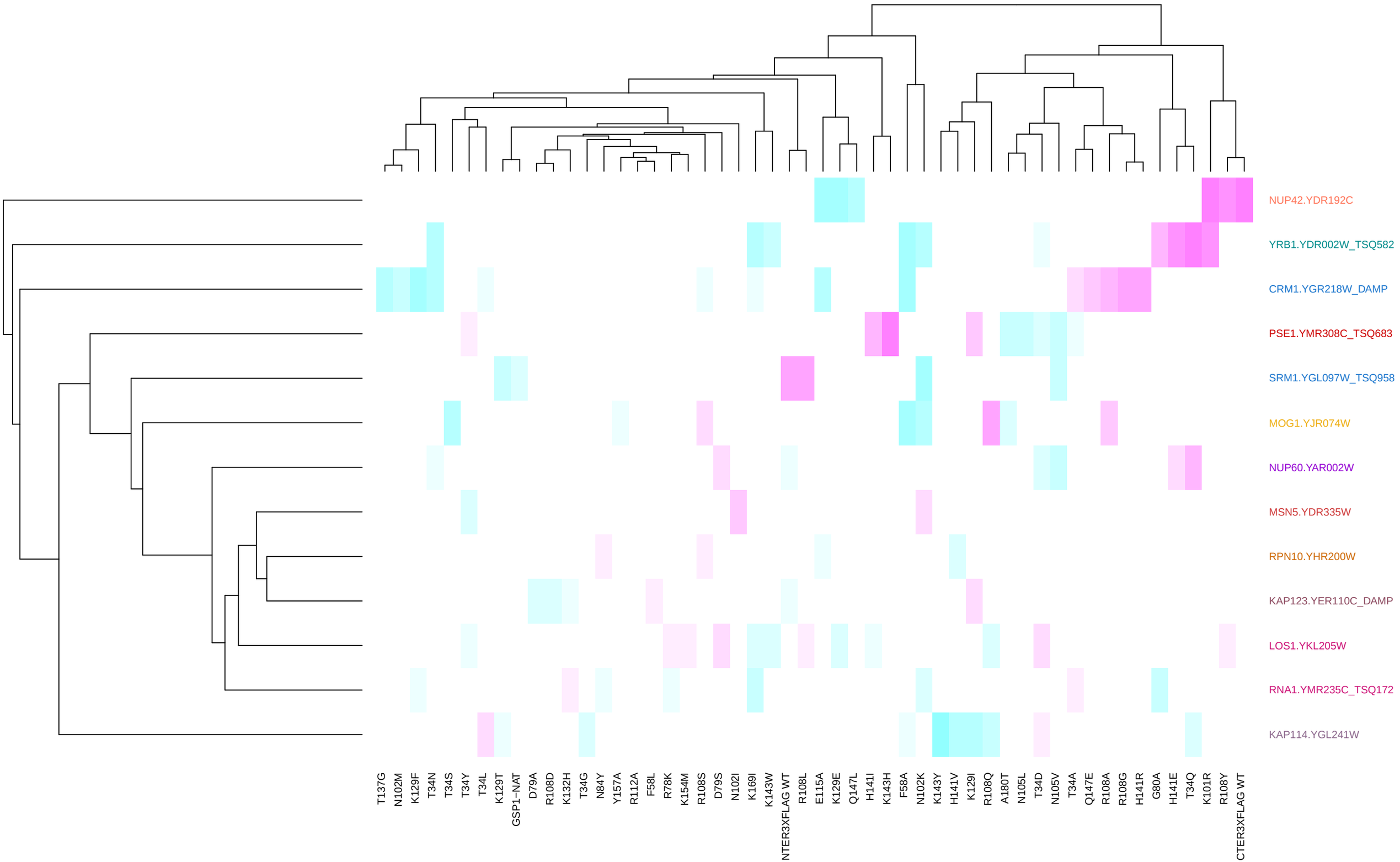
chromosome segregation_GO_15_1_all



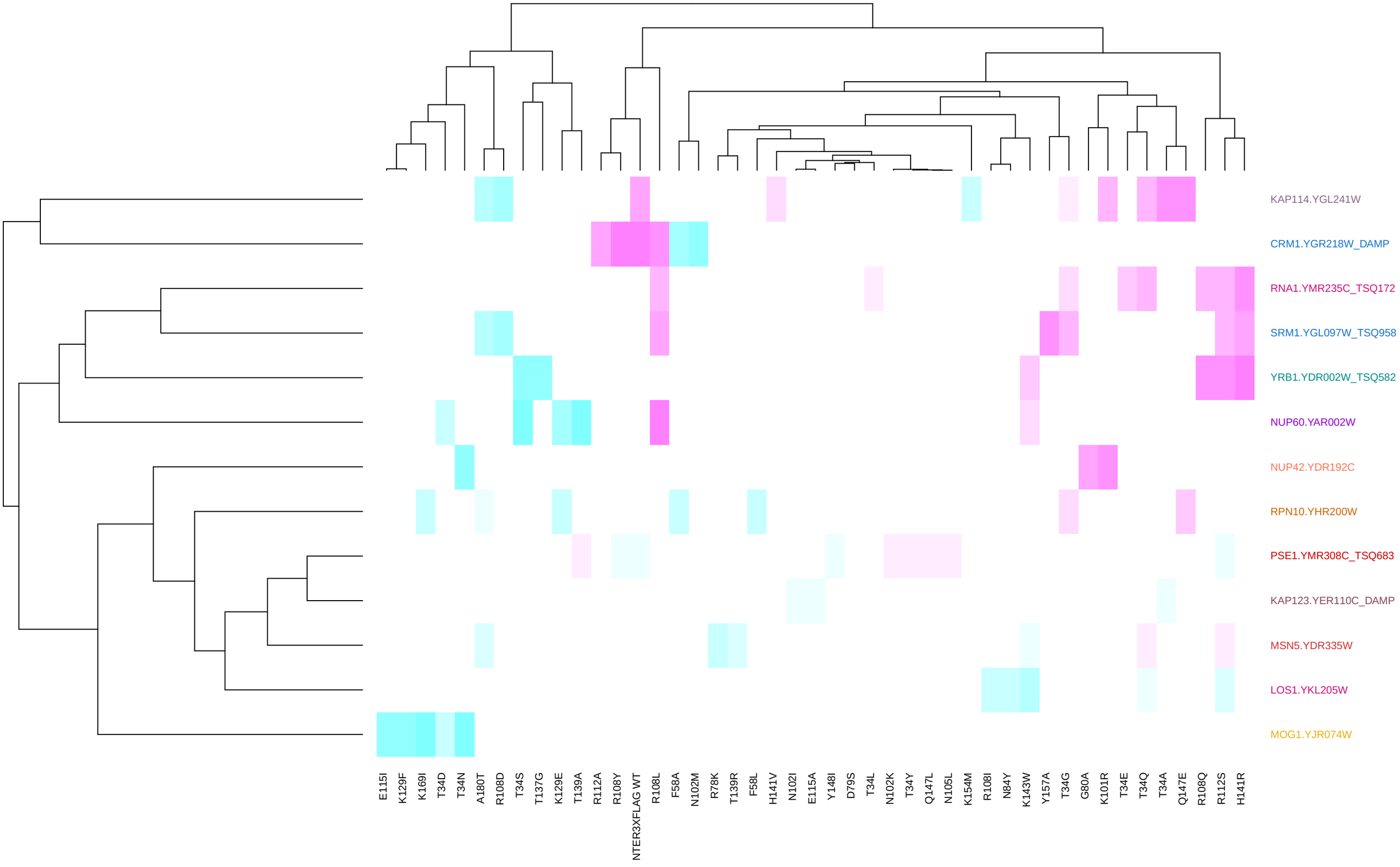
cytoskeleton and microtubules_GO_15_2_mut



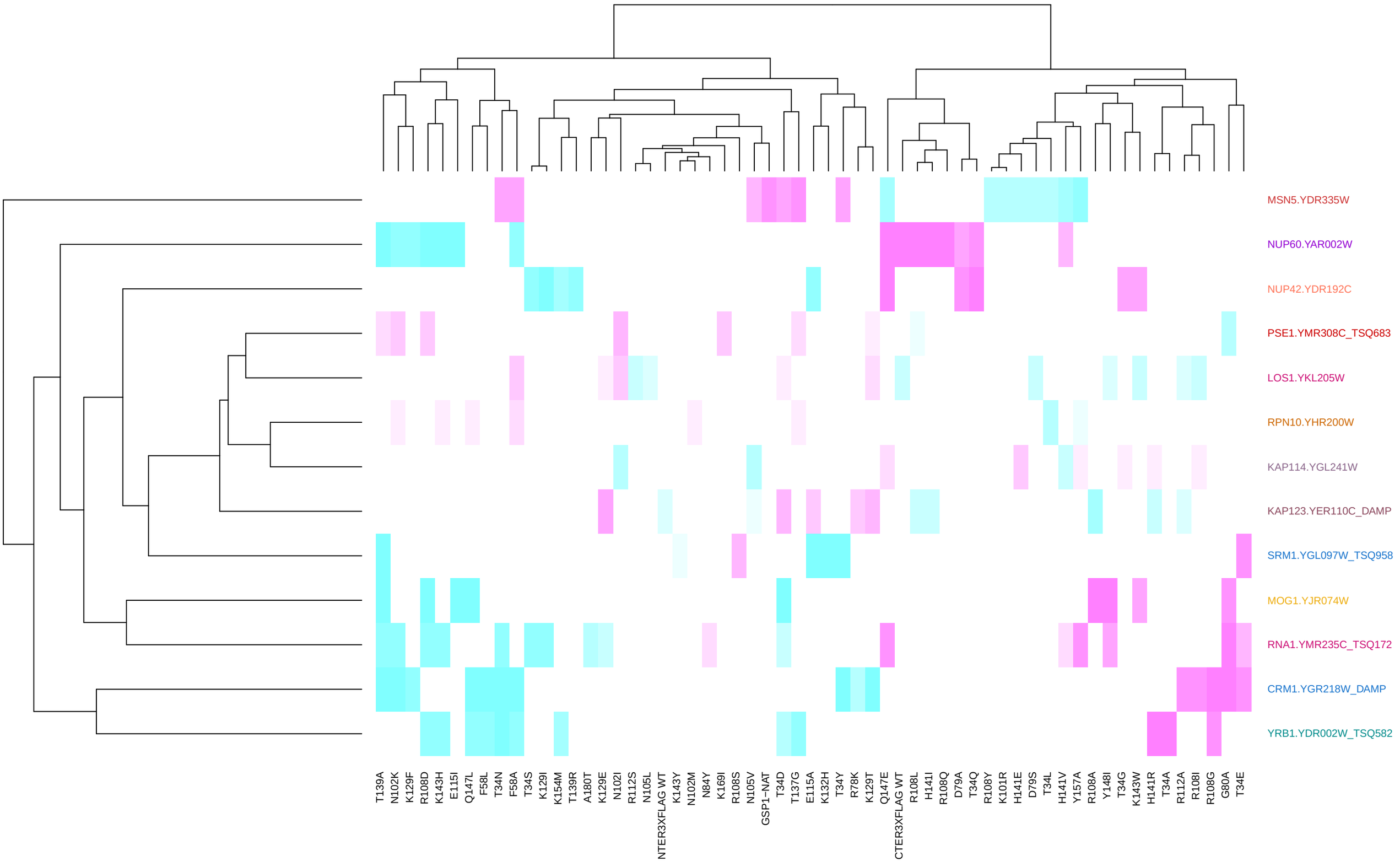
cytoskeleton and microtubules_GO_15_3_all



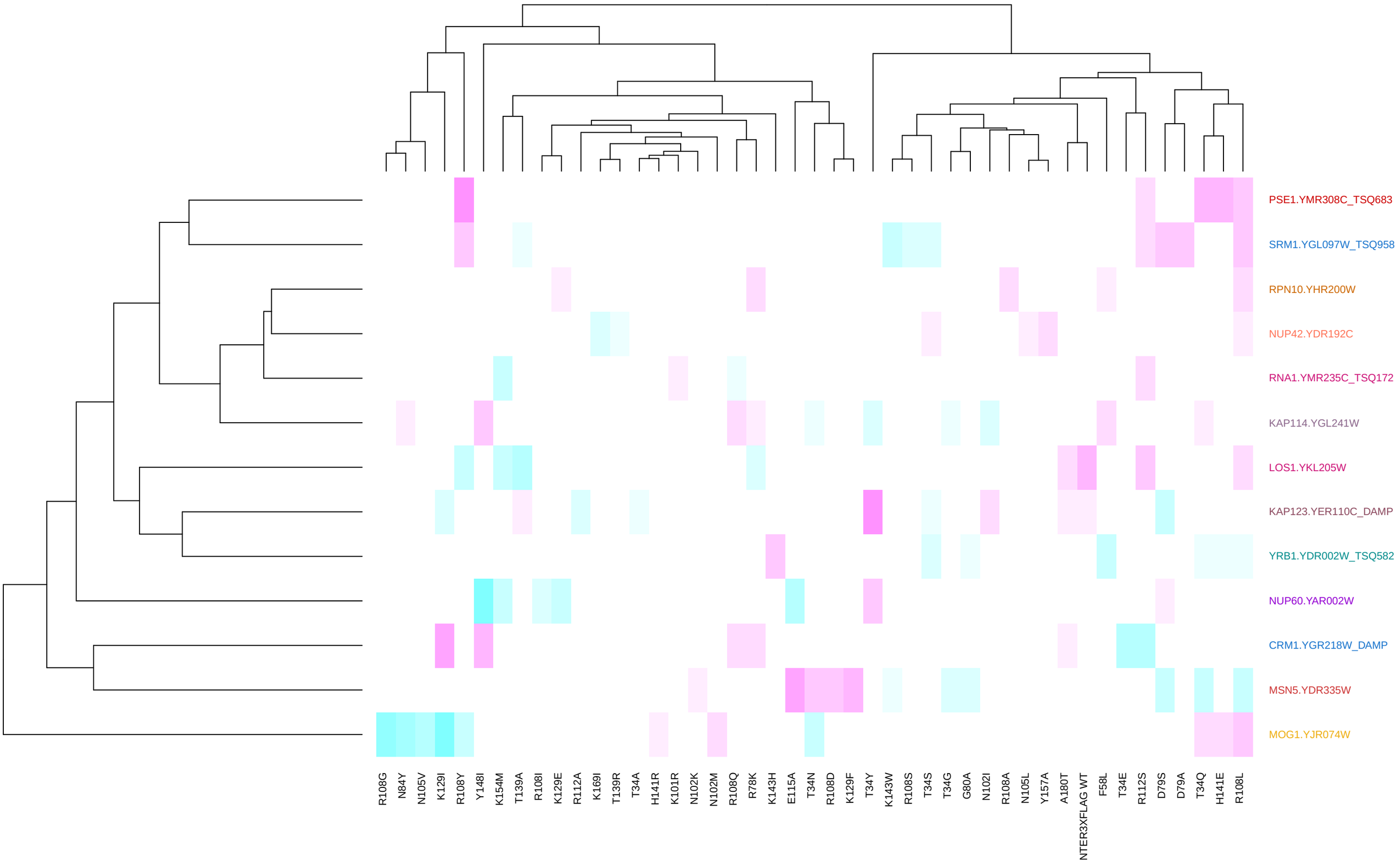
nuclear transport_GO_15_1_all



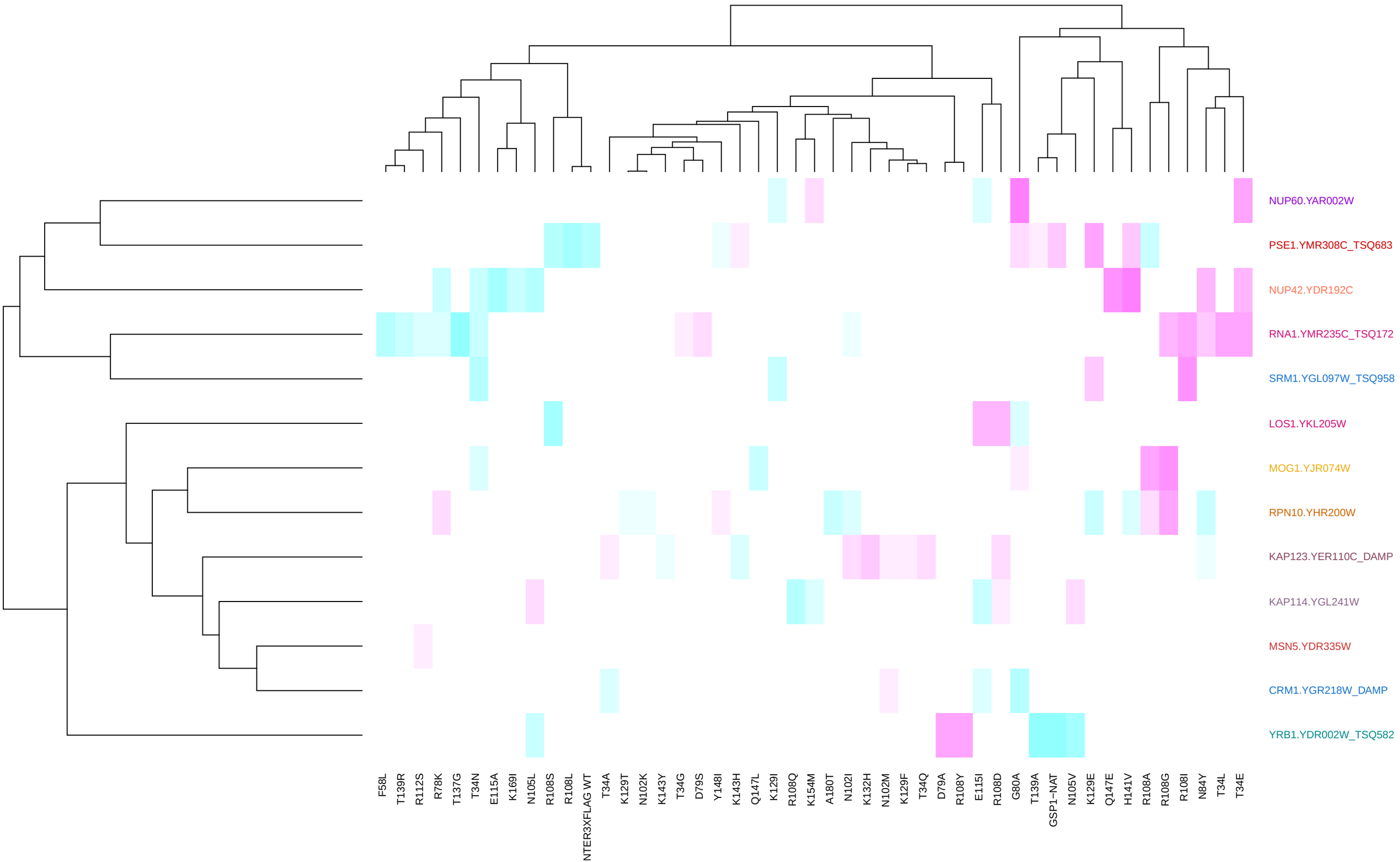
nucleus organization_GO_15_1_all



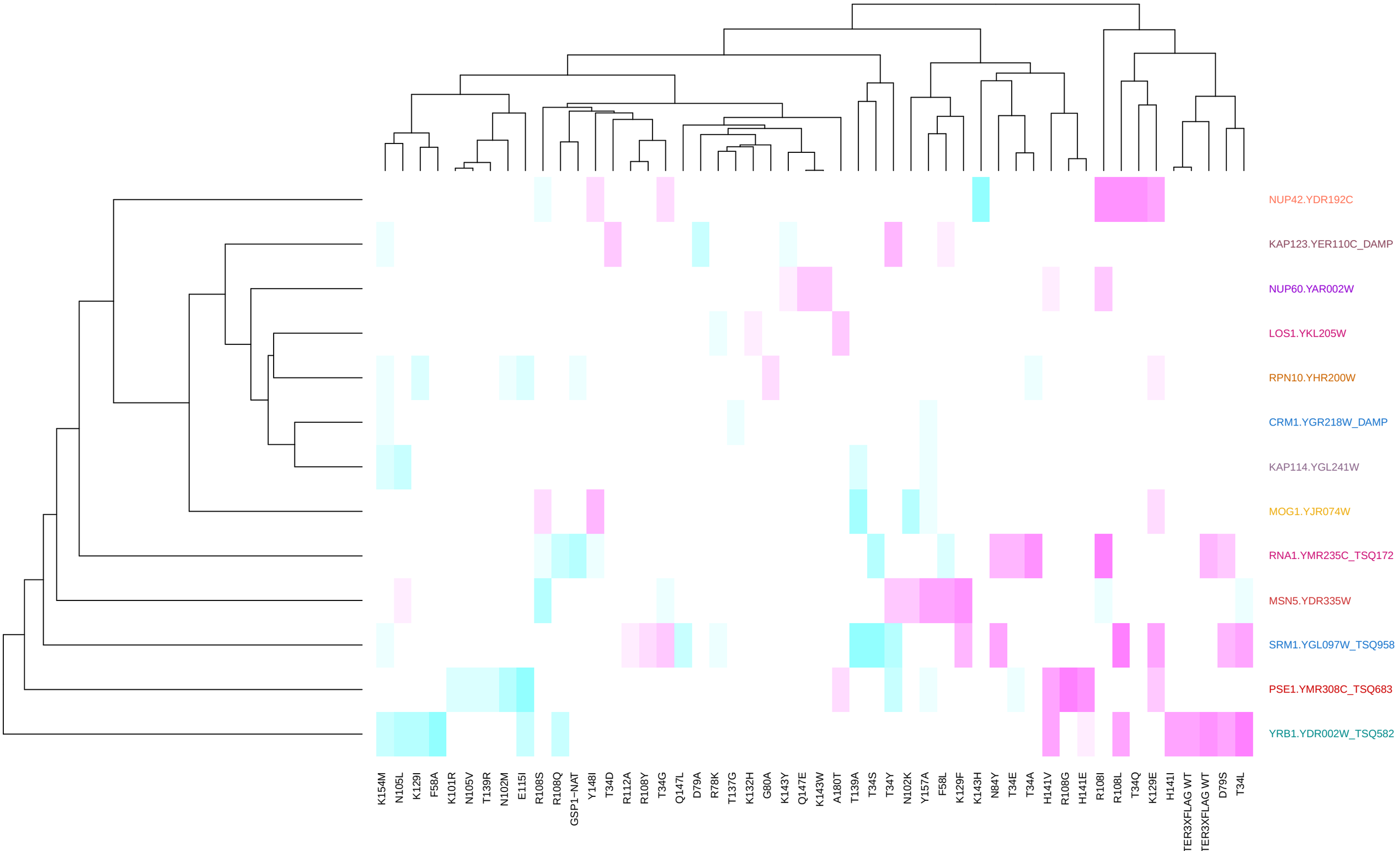
transcription and mRNA processing_GO_15_7_all



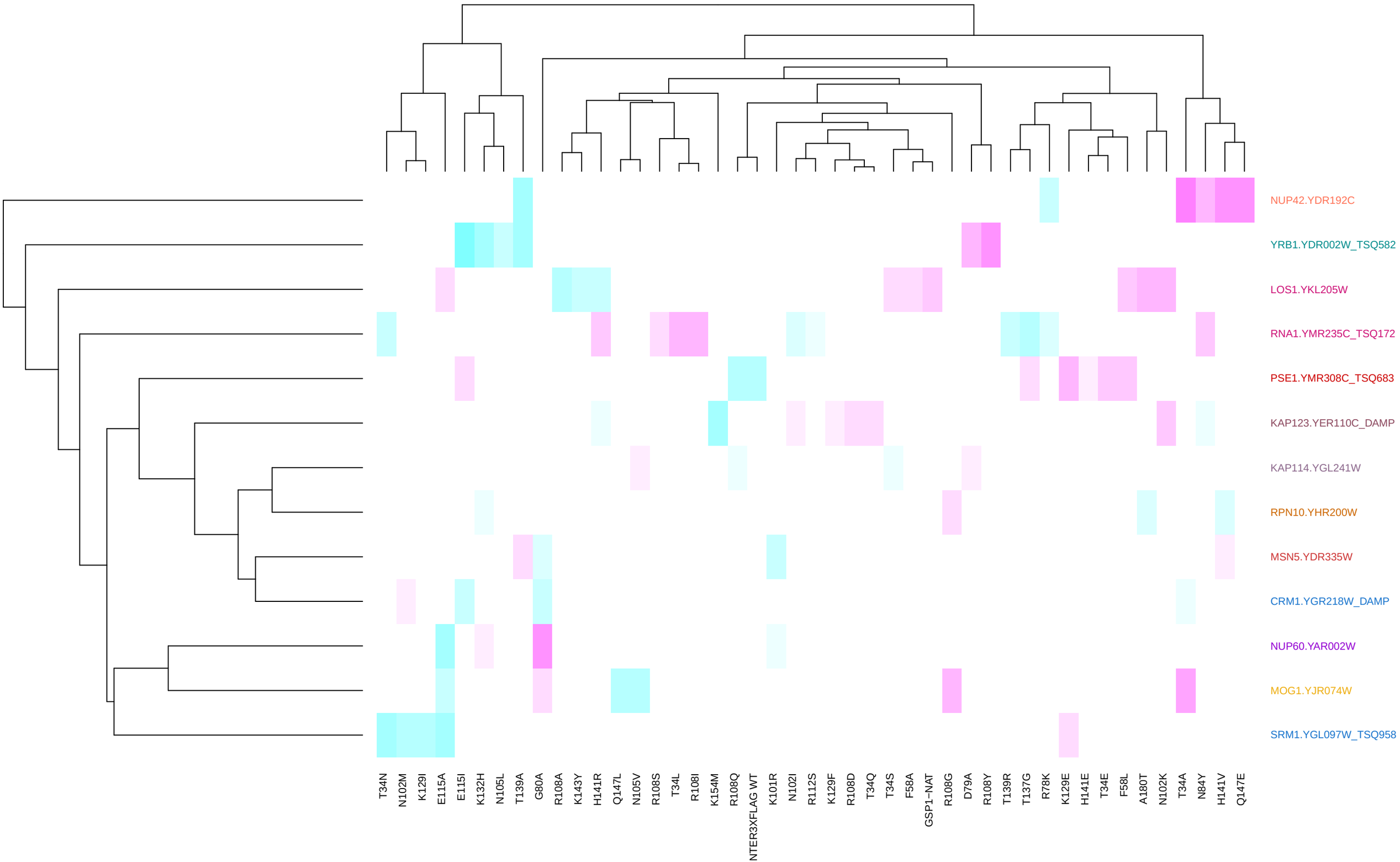
RNA processing



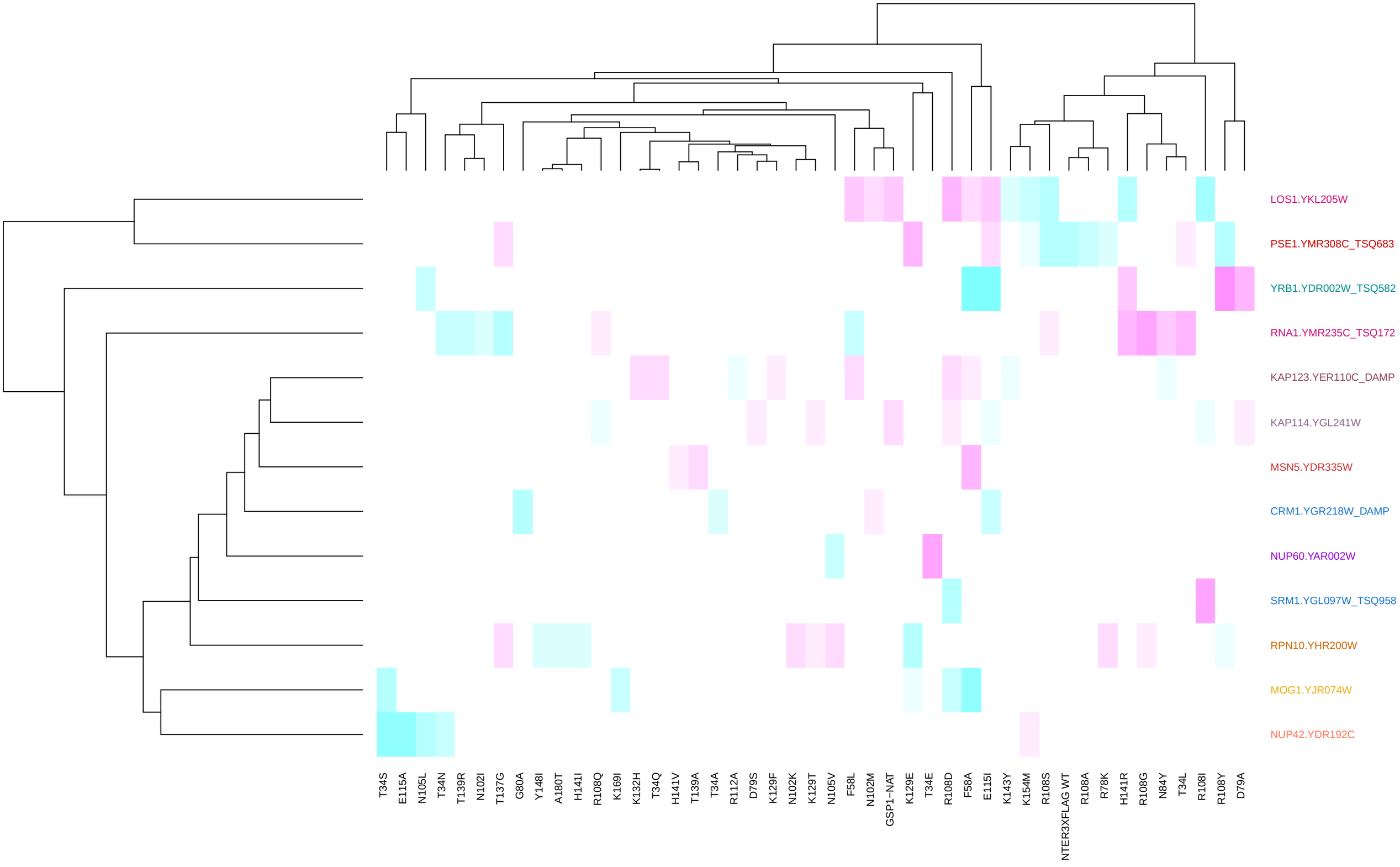
organelle fission_GO_30_1_mut



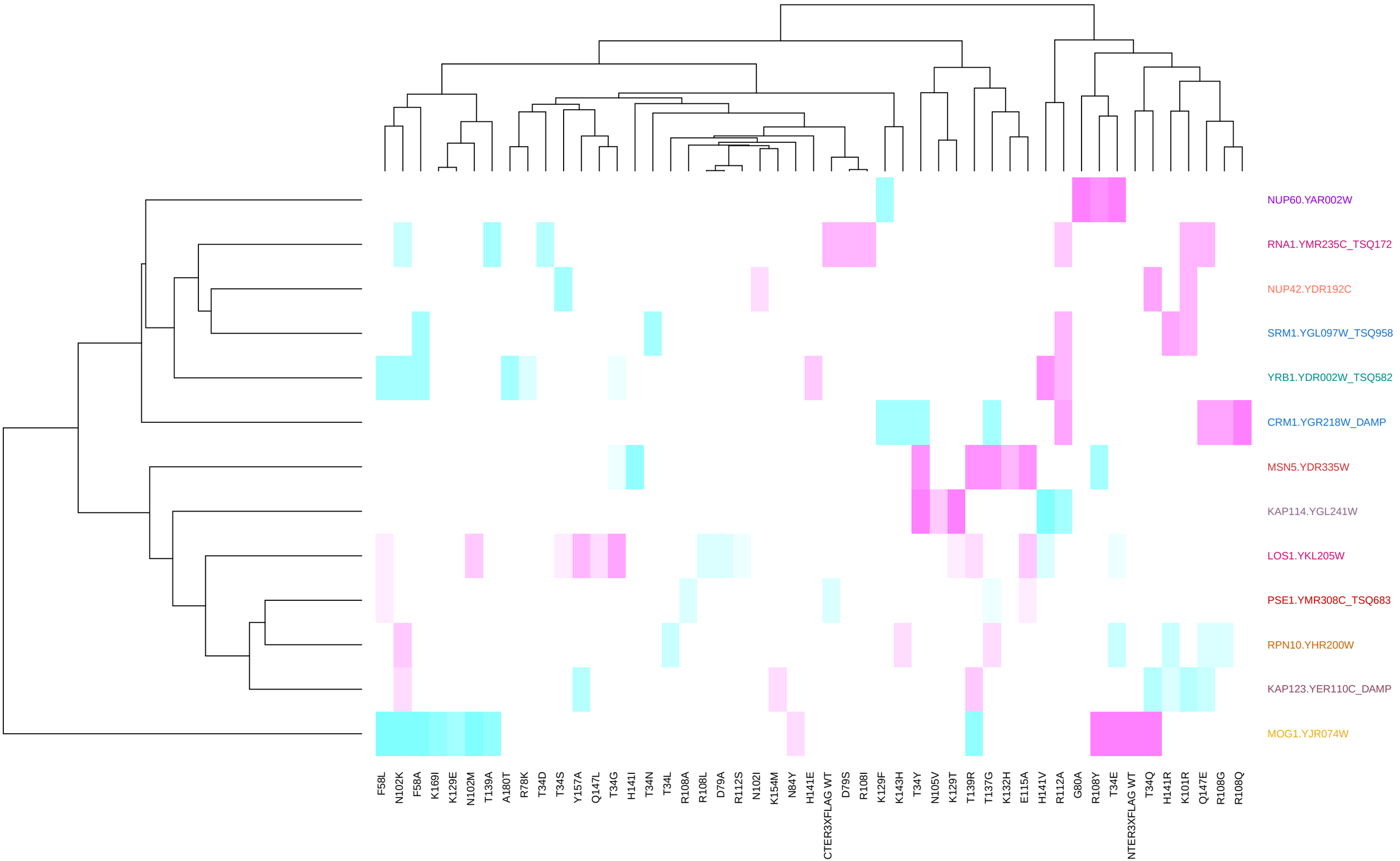
mRNA processing



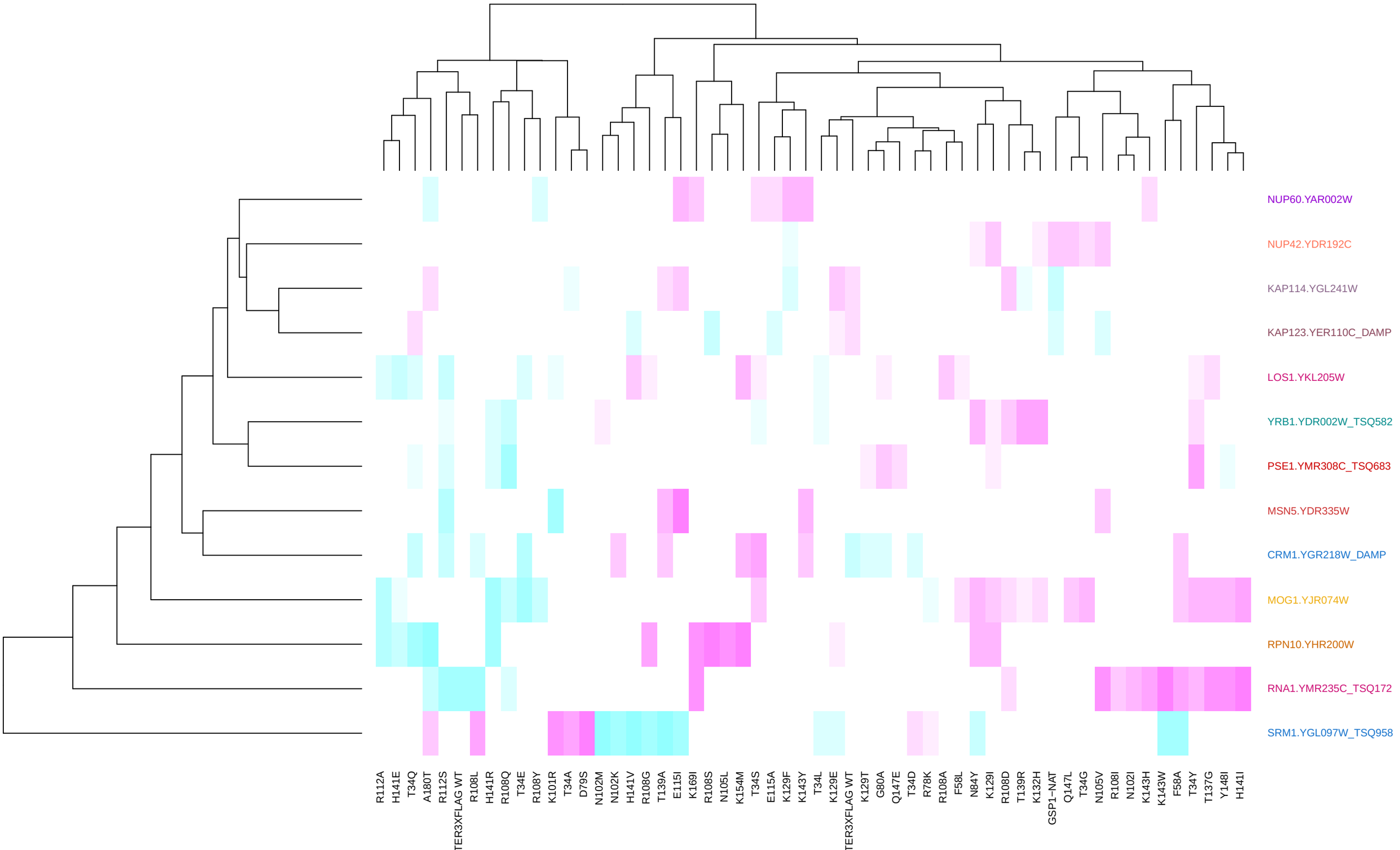
RNA processing_GO_15_1_all



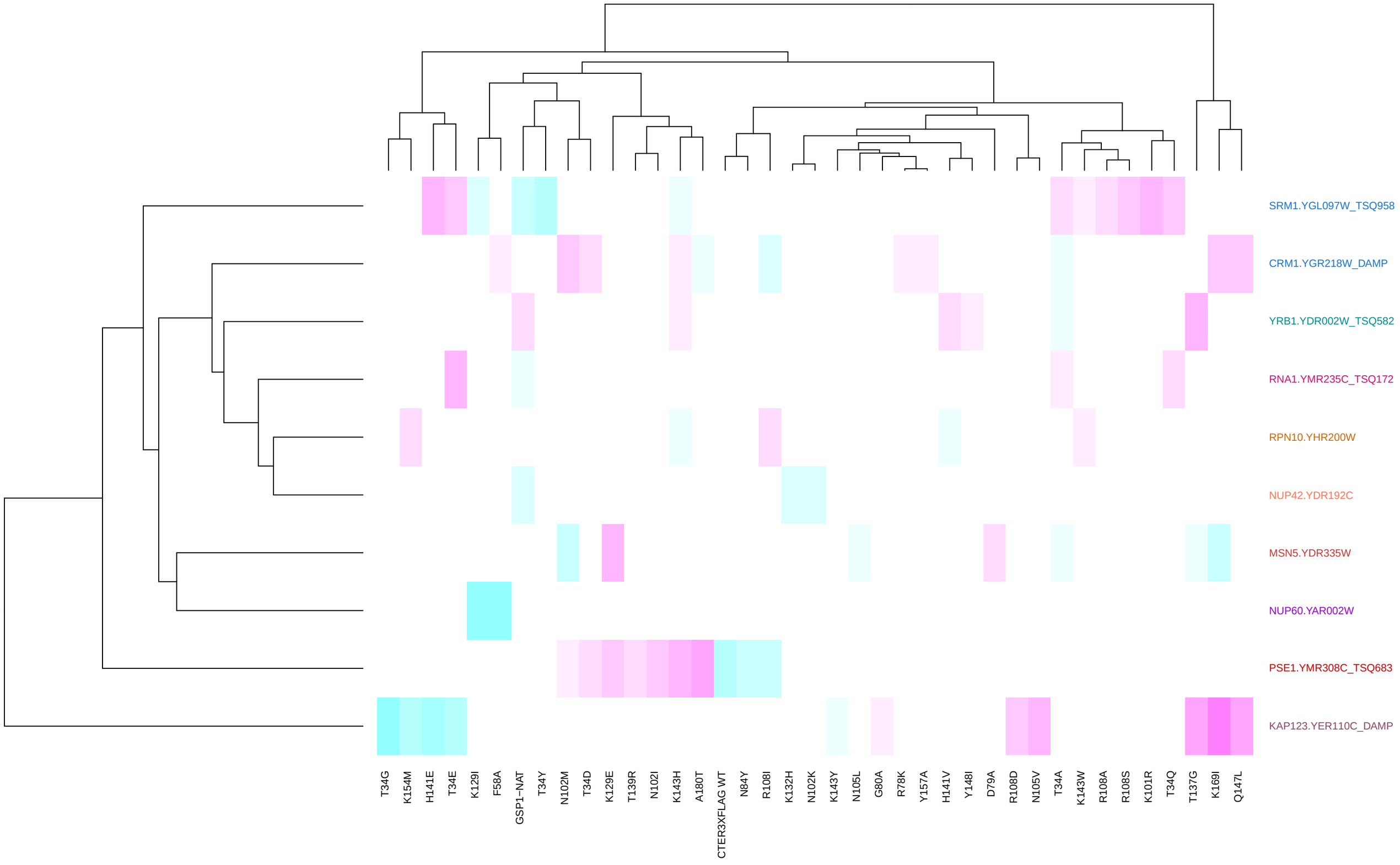
transcription from RNA polymerase II promoter_GO_15_4_all



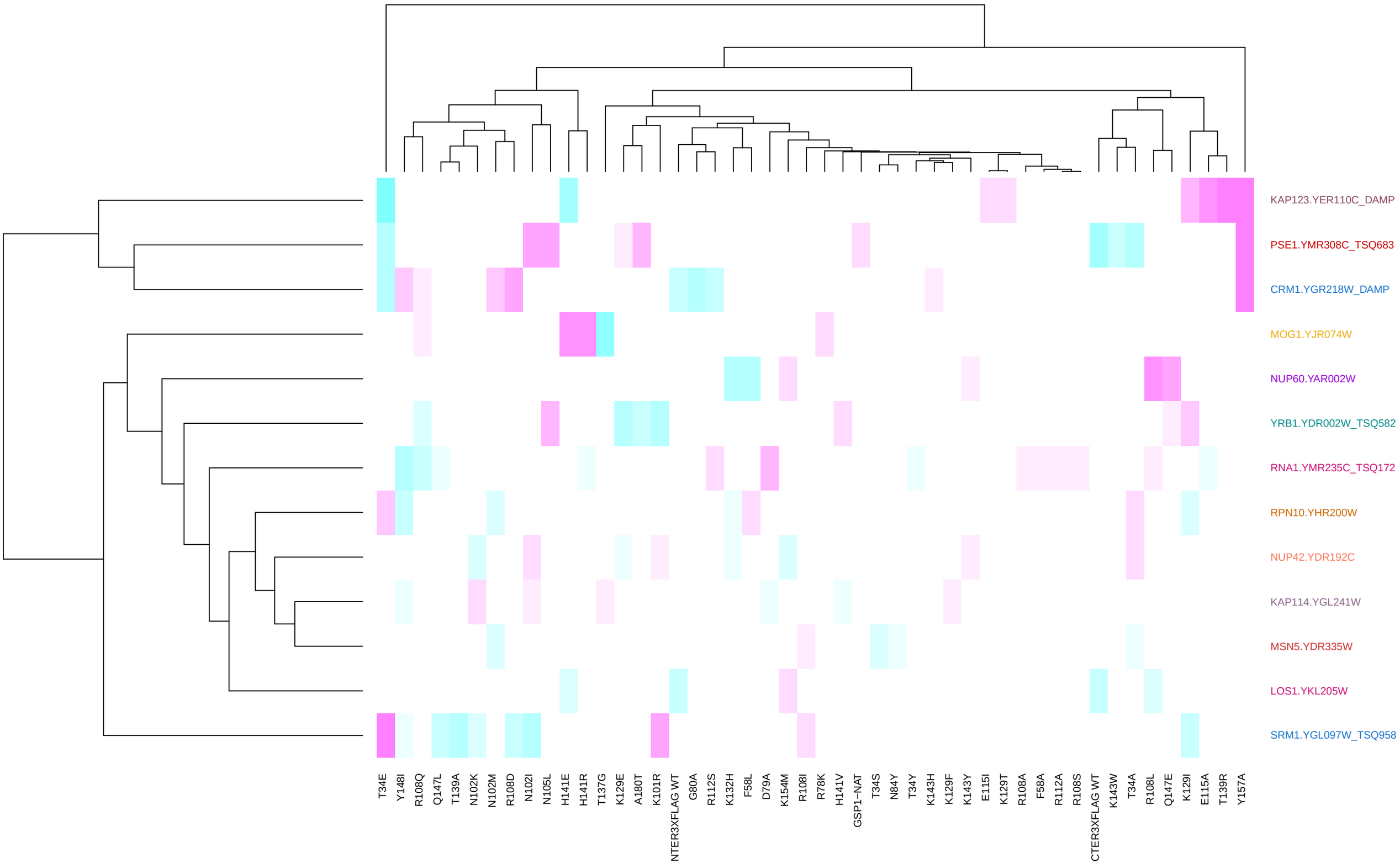
sig_Gsp1_GI_15_7_mut



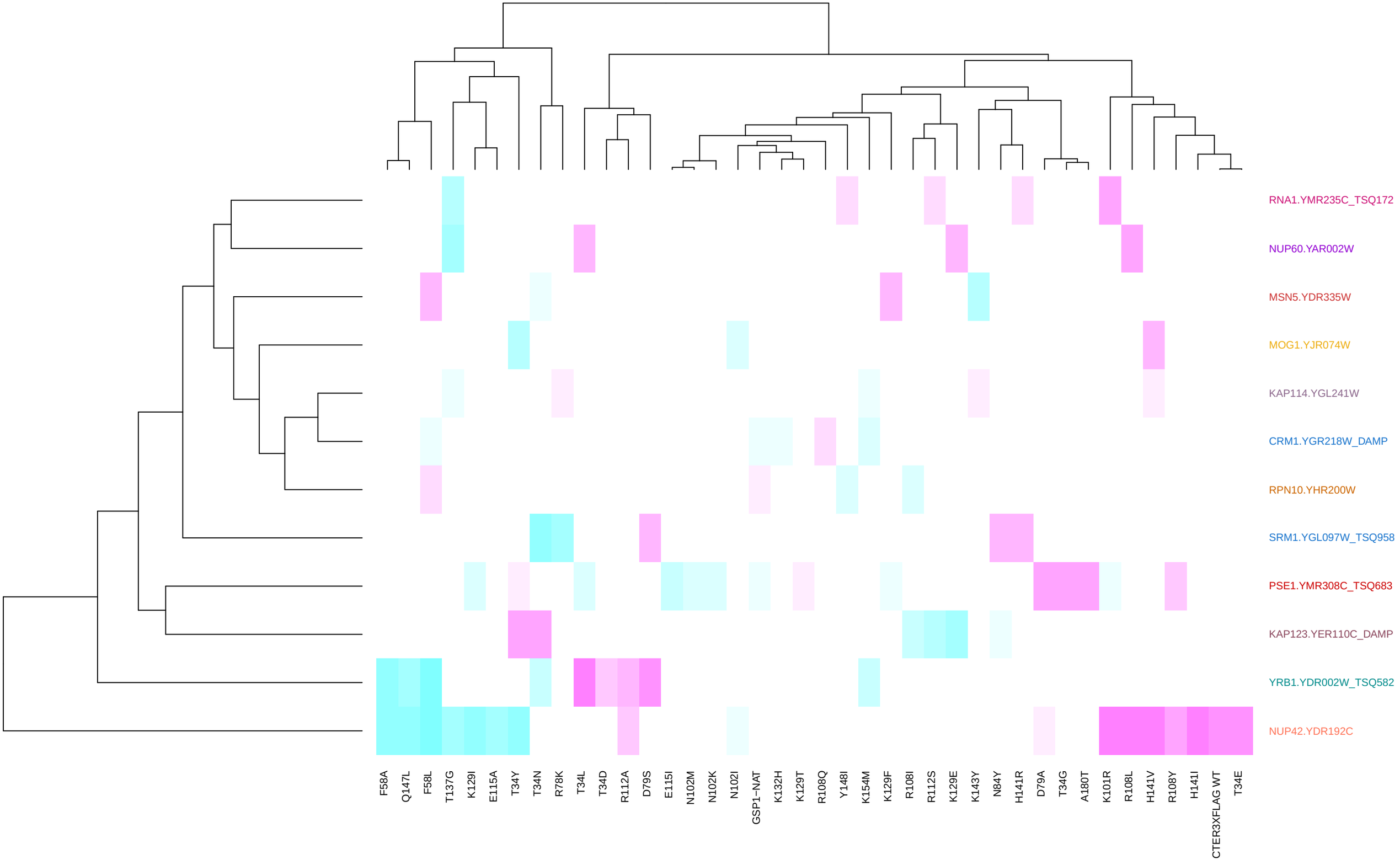
DNA recombination_GO_15_1_mut



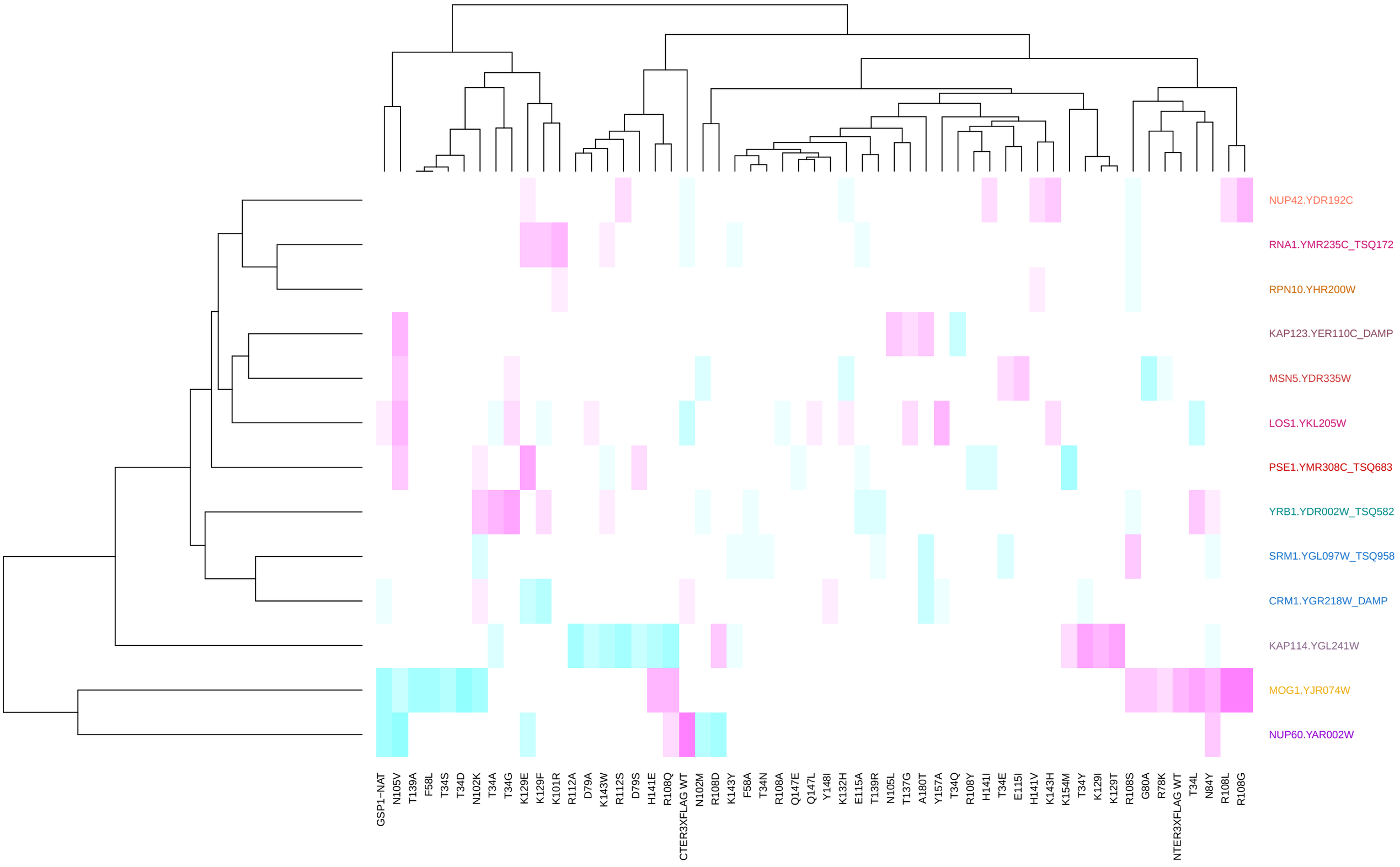
DNA recombination_GO_30_1_mut



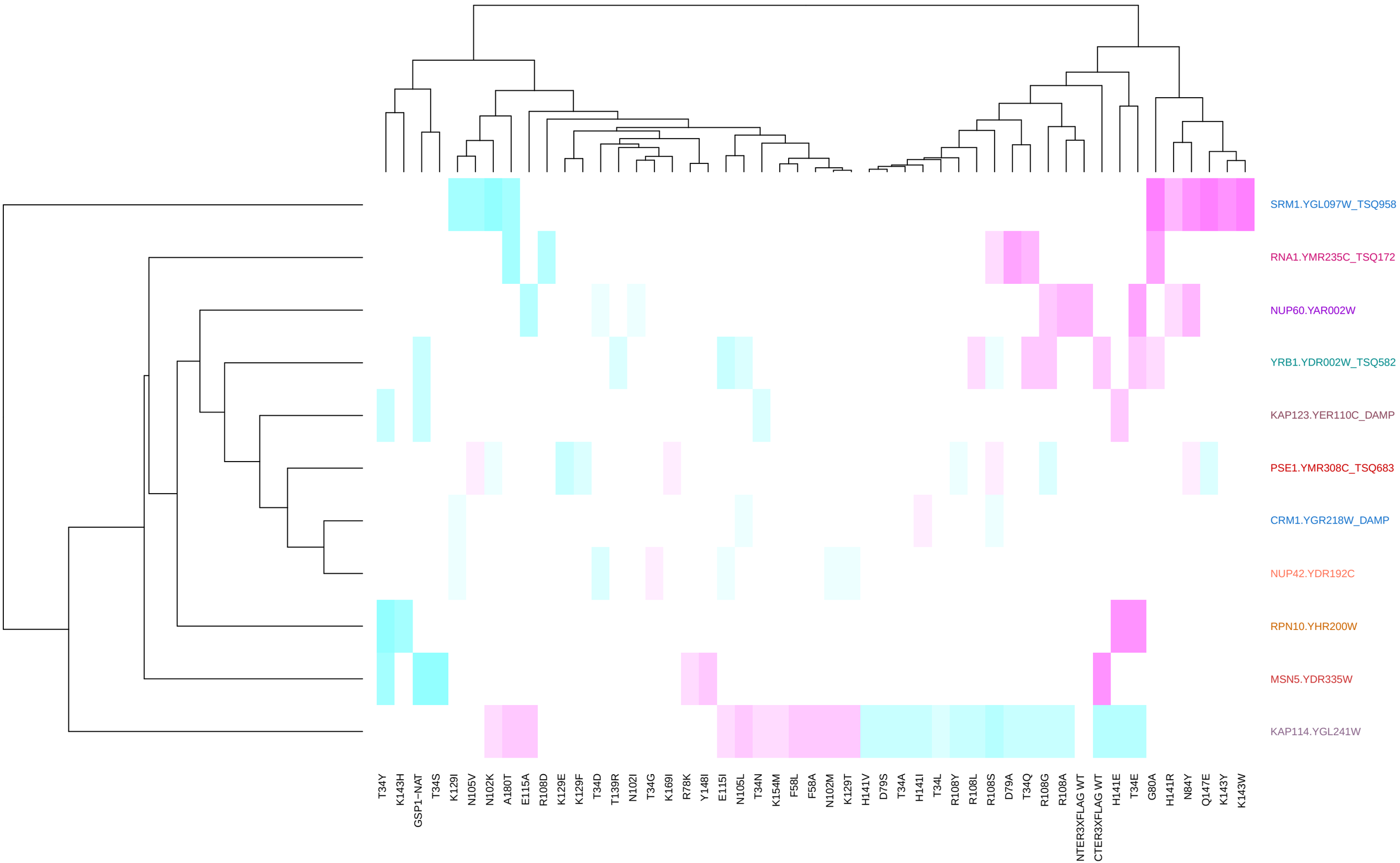
organelle fission_GO_15_3_mut



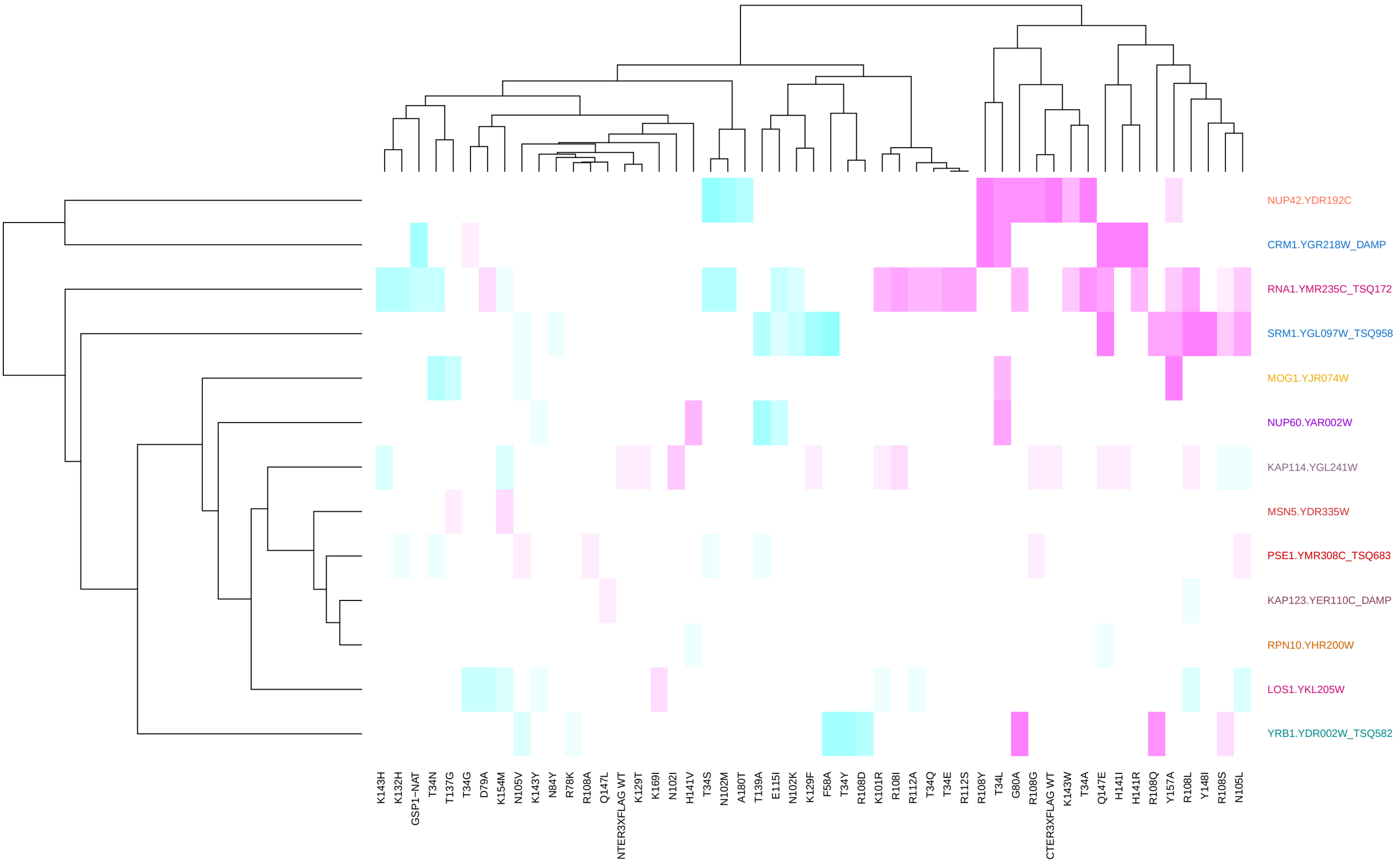
DNA−templated transcription, elongation_GO_15_1_mut



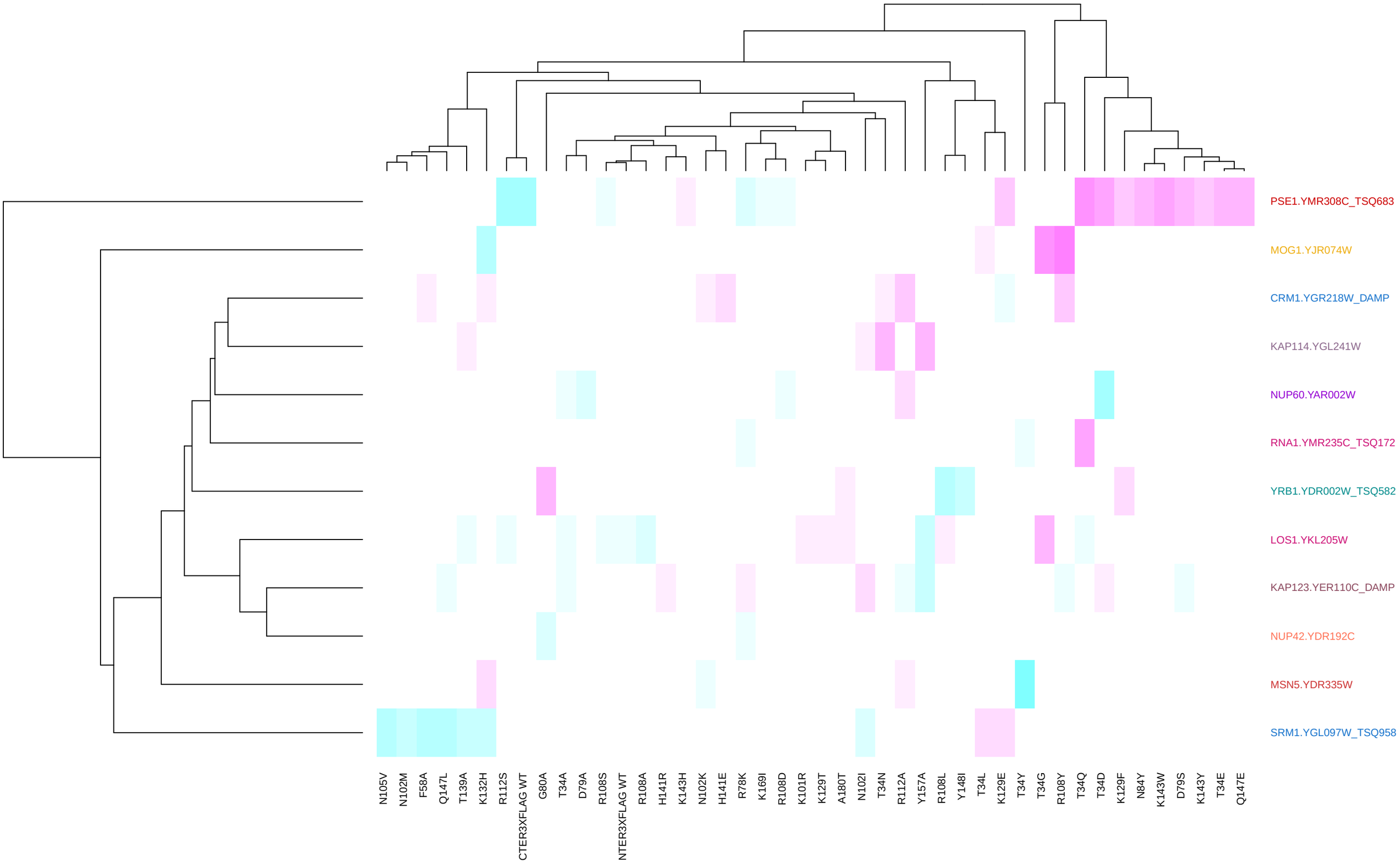
whole_library_15_13_all



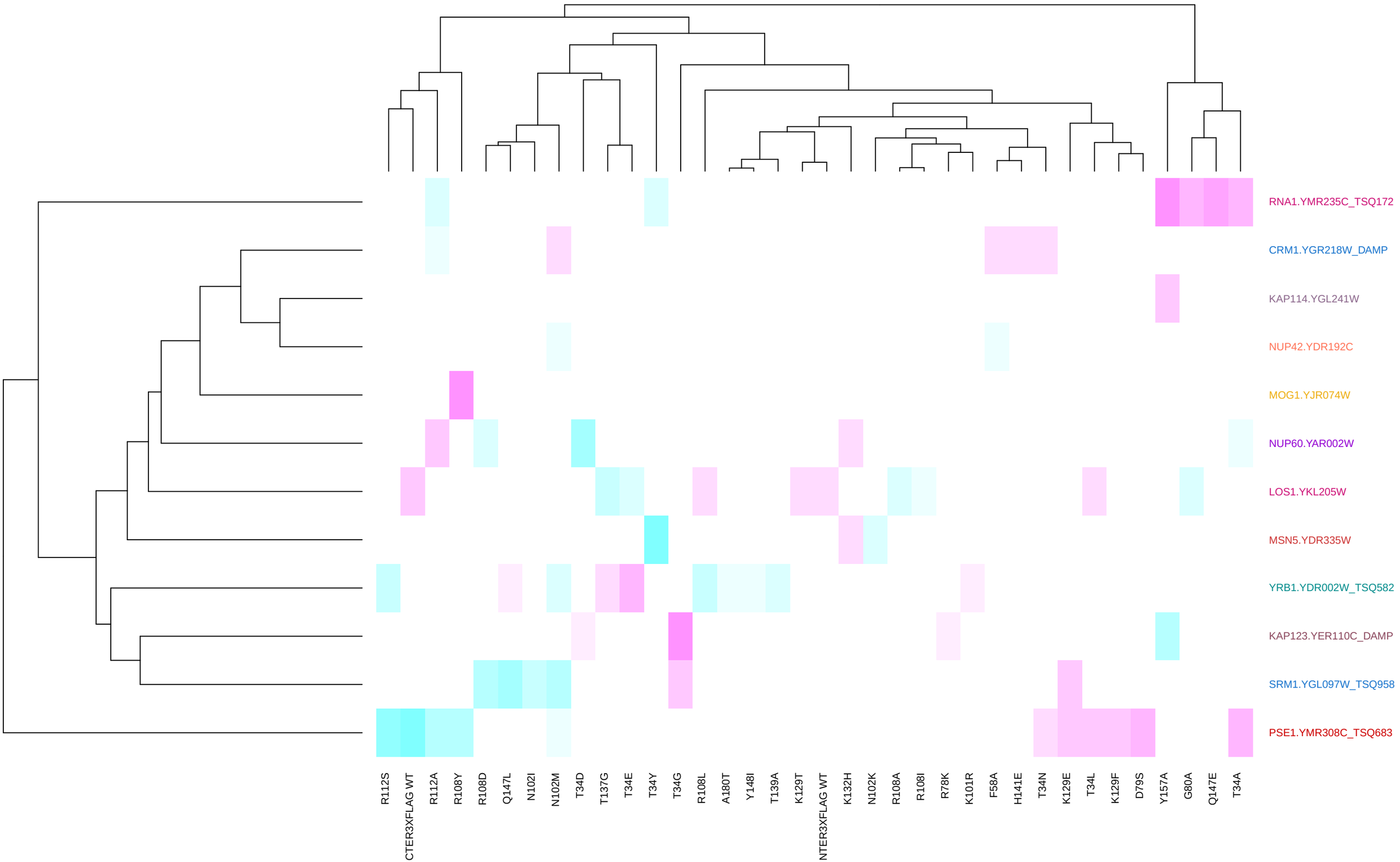
protein targeting



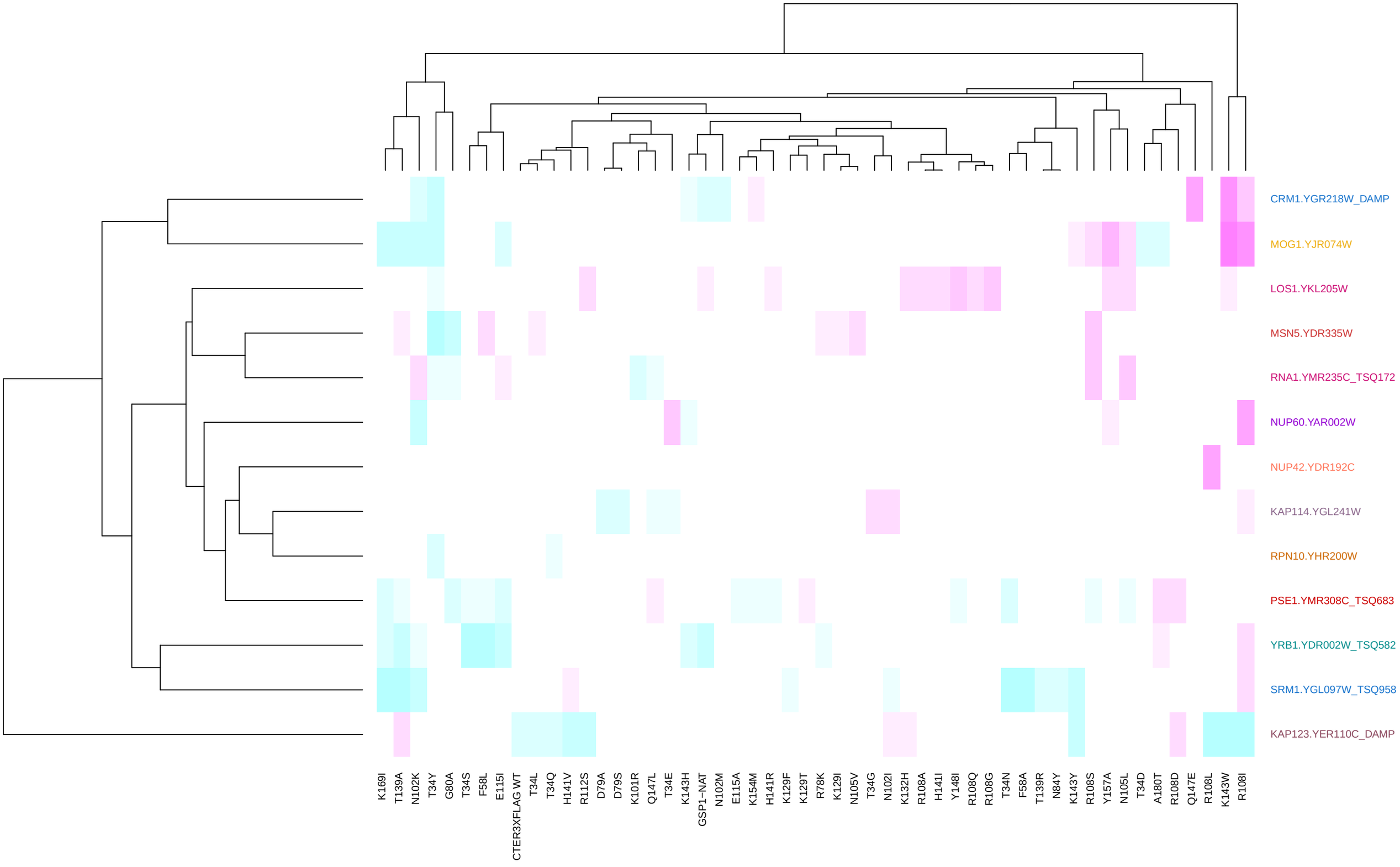
histone modification



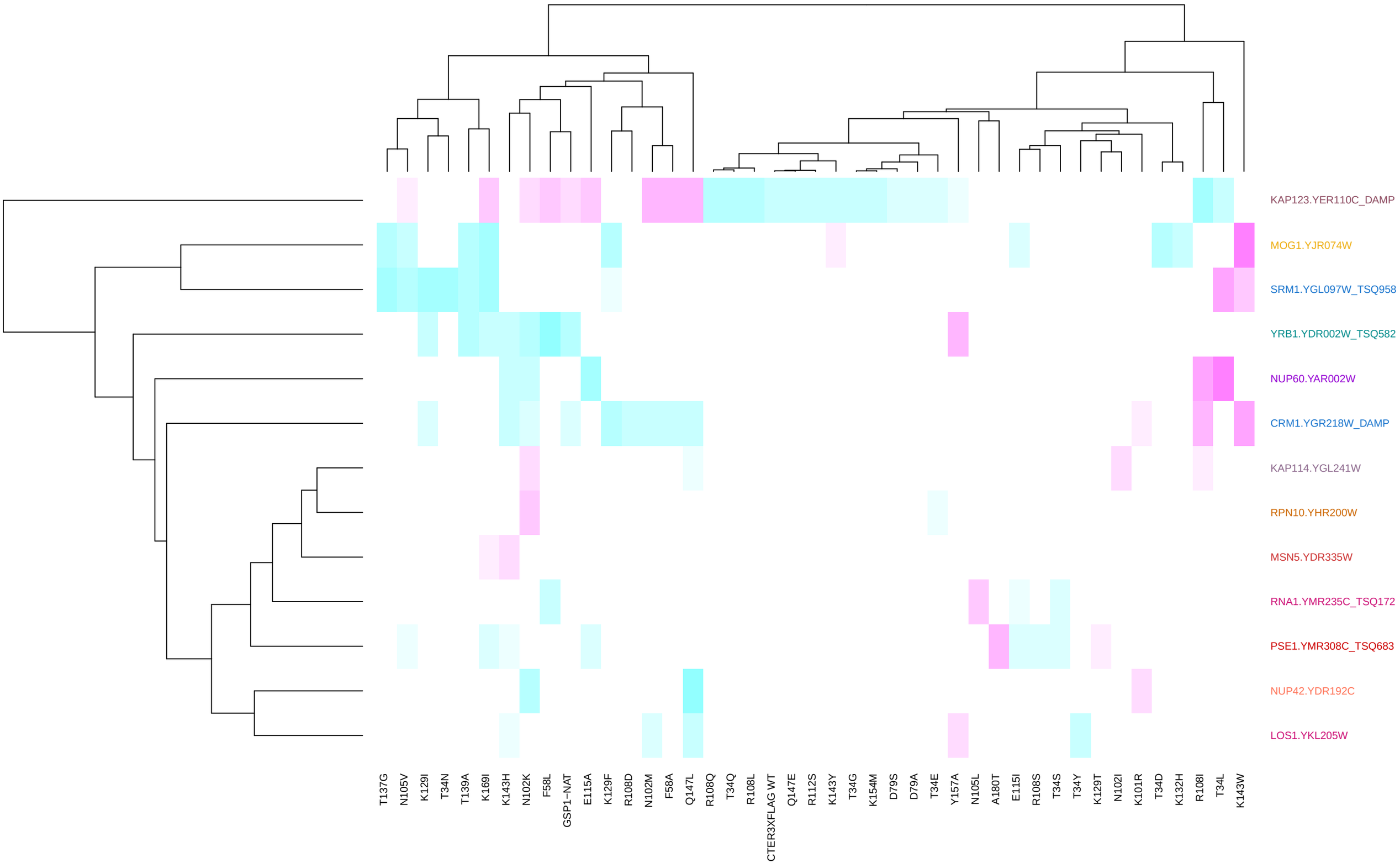
histone modification_GO_30_1_all



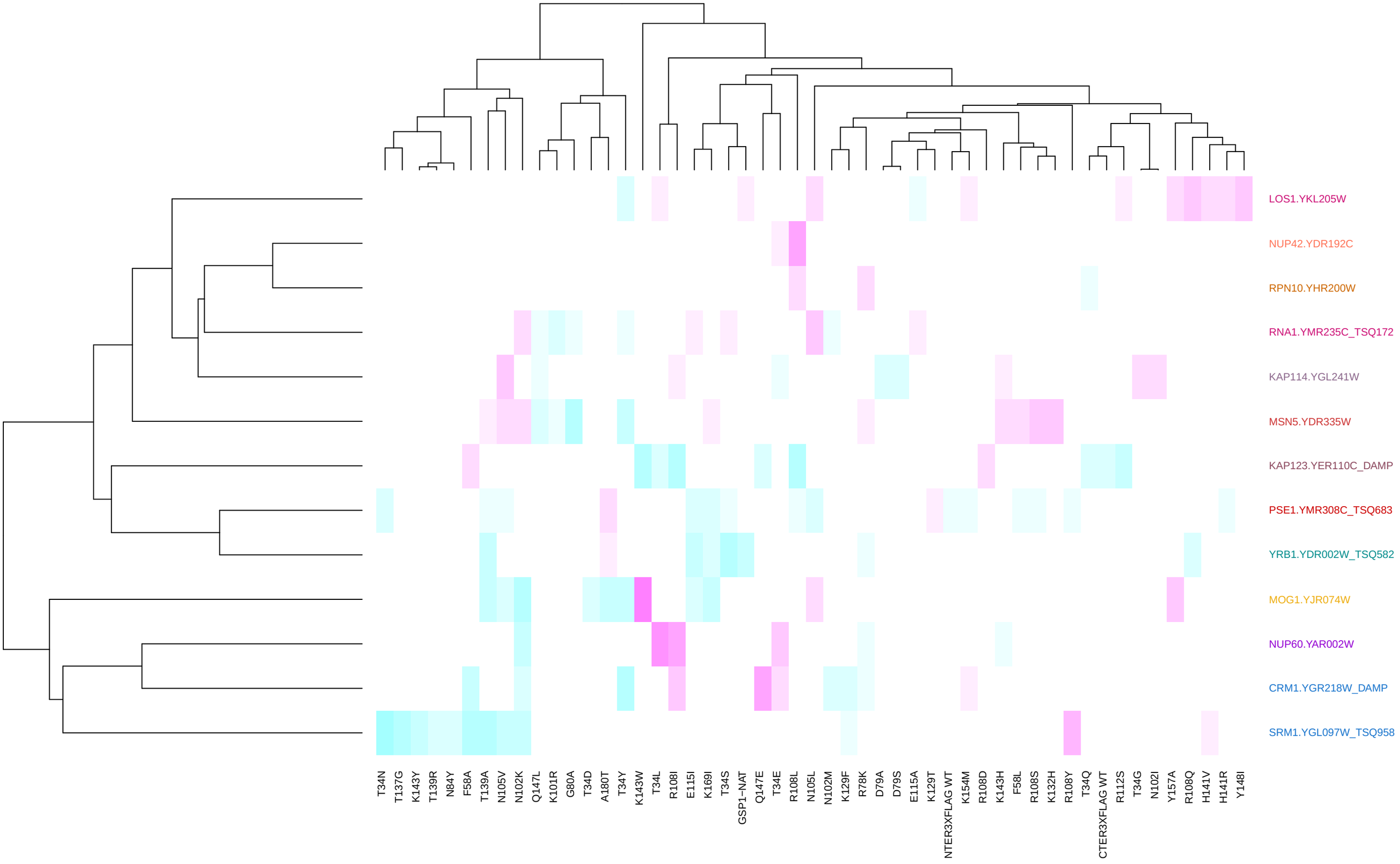
transcription



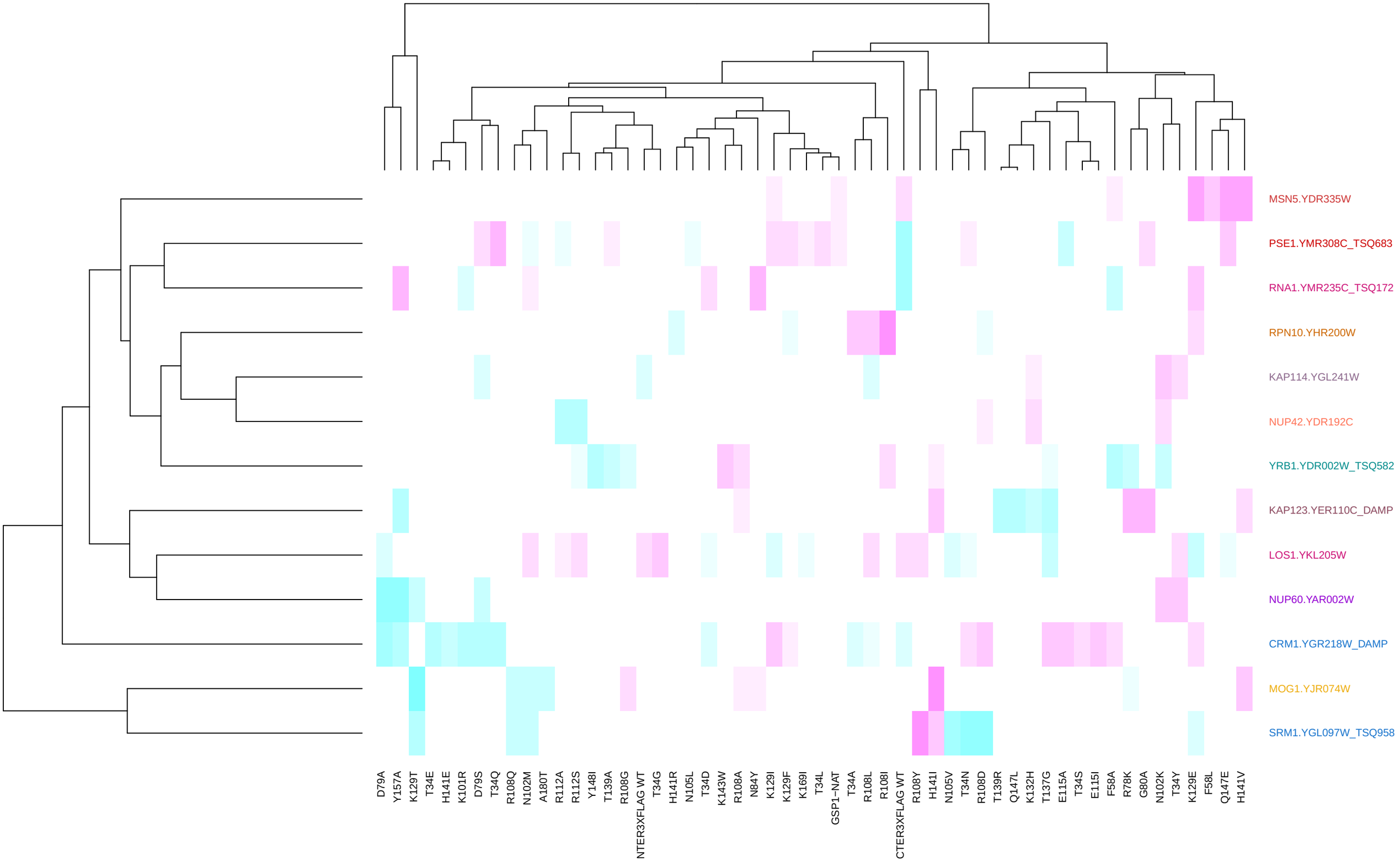
transcription and mRNA processing



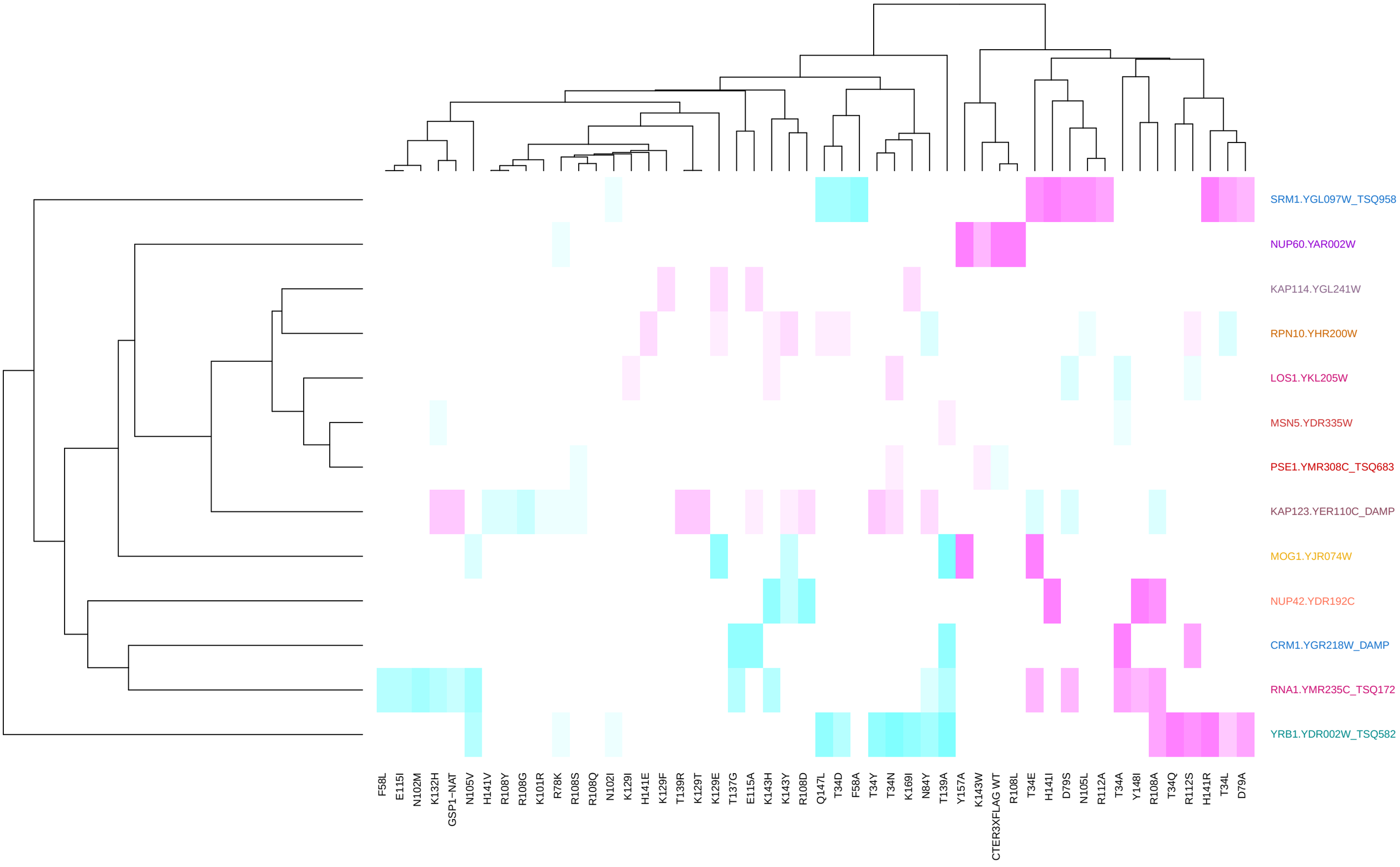
transcription from RNA polymerase II promoter



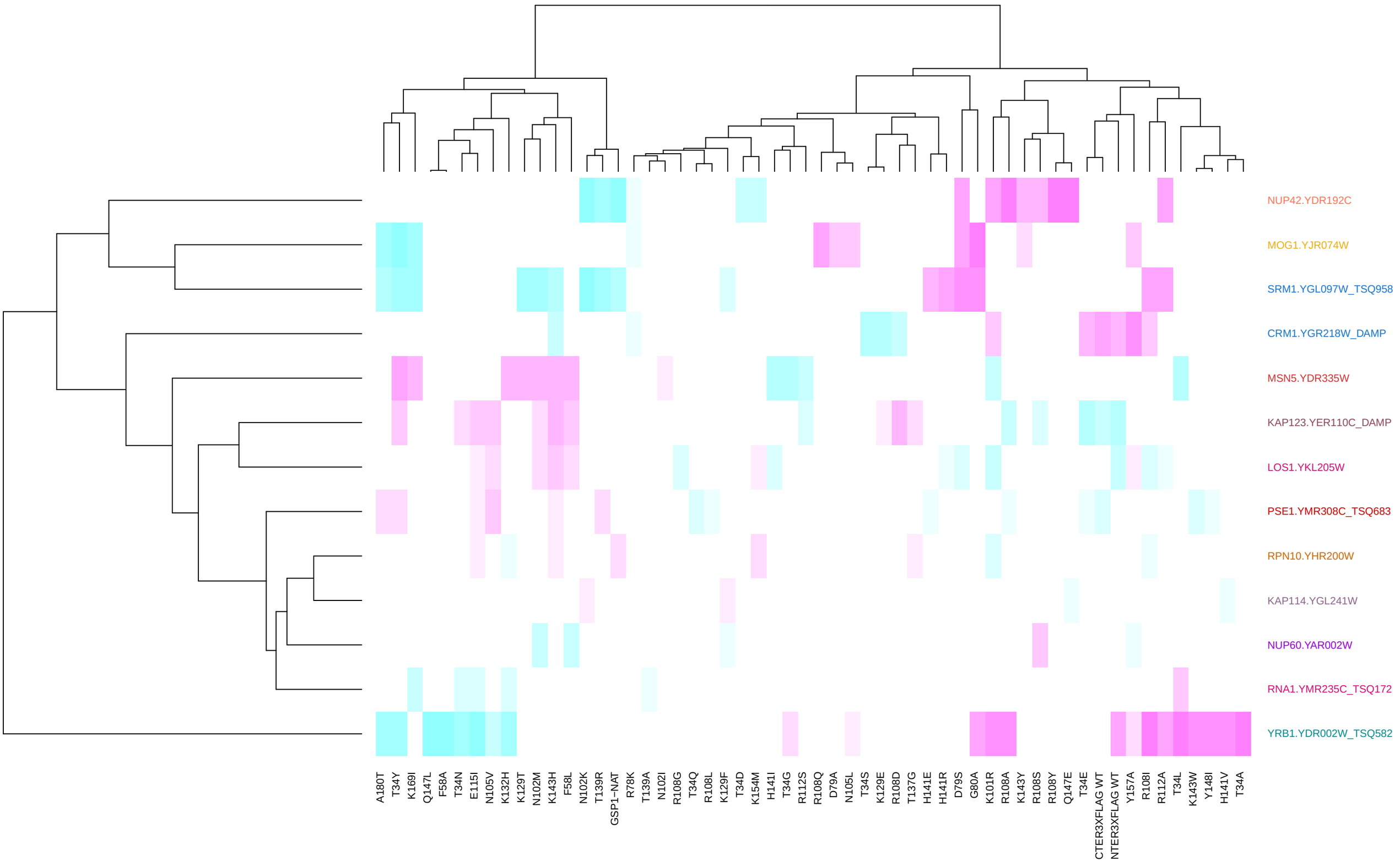
whole_library_30_1_all



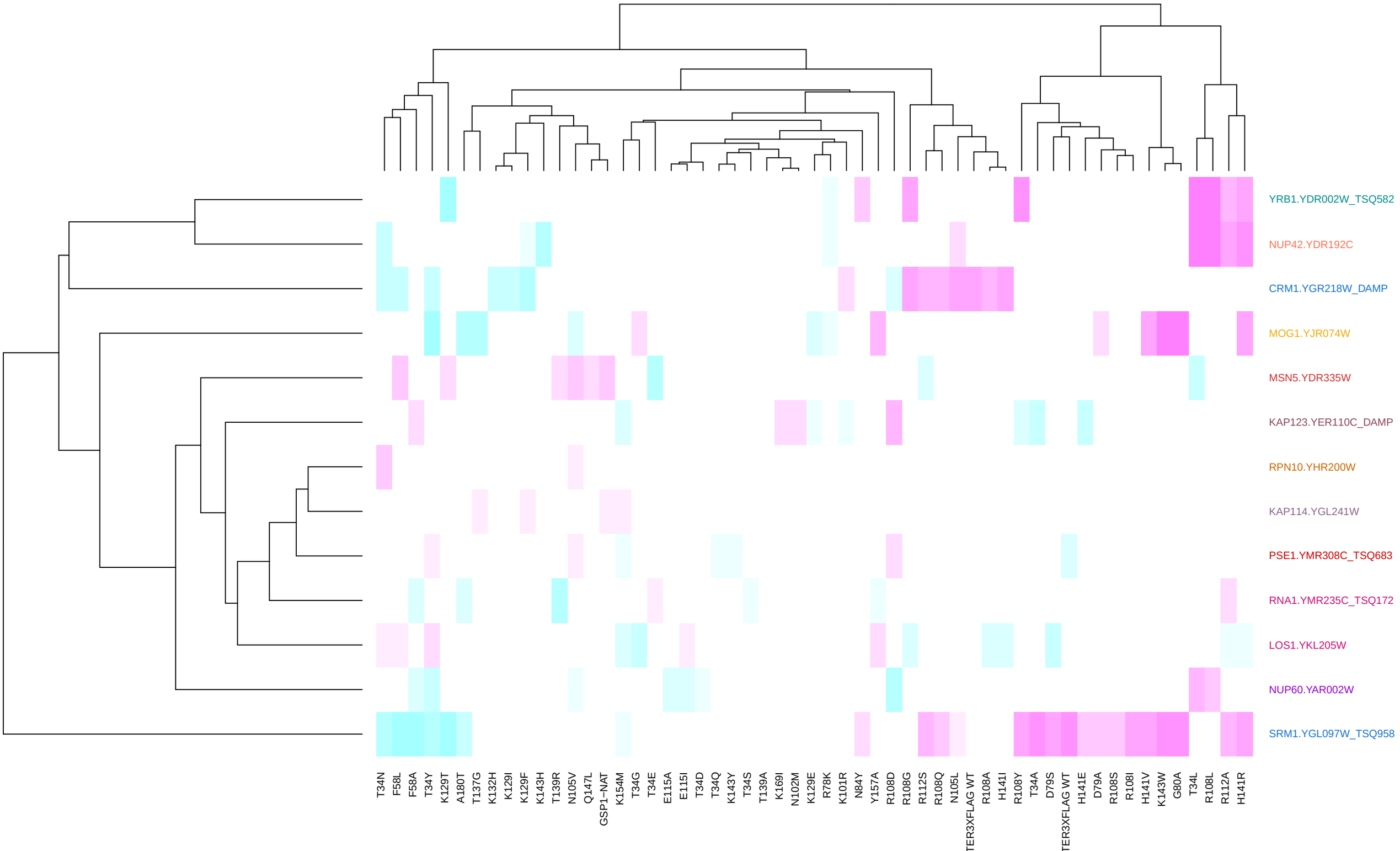
protein targeting_GO_15_2_mut



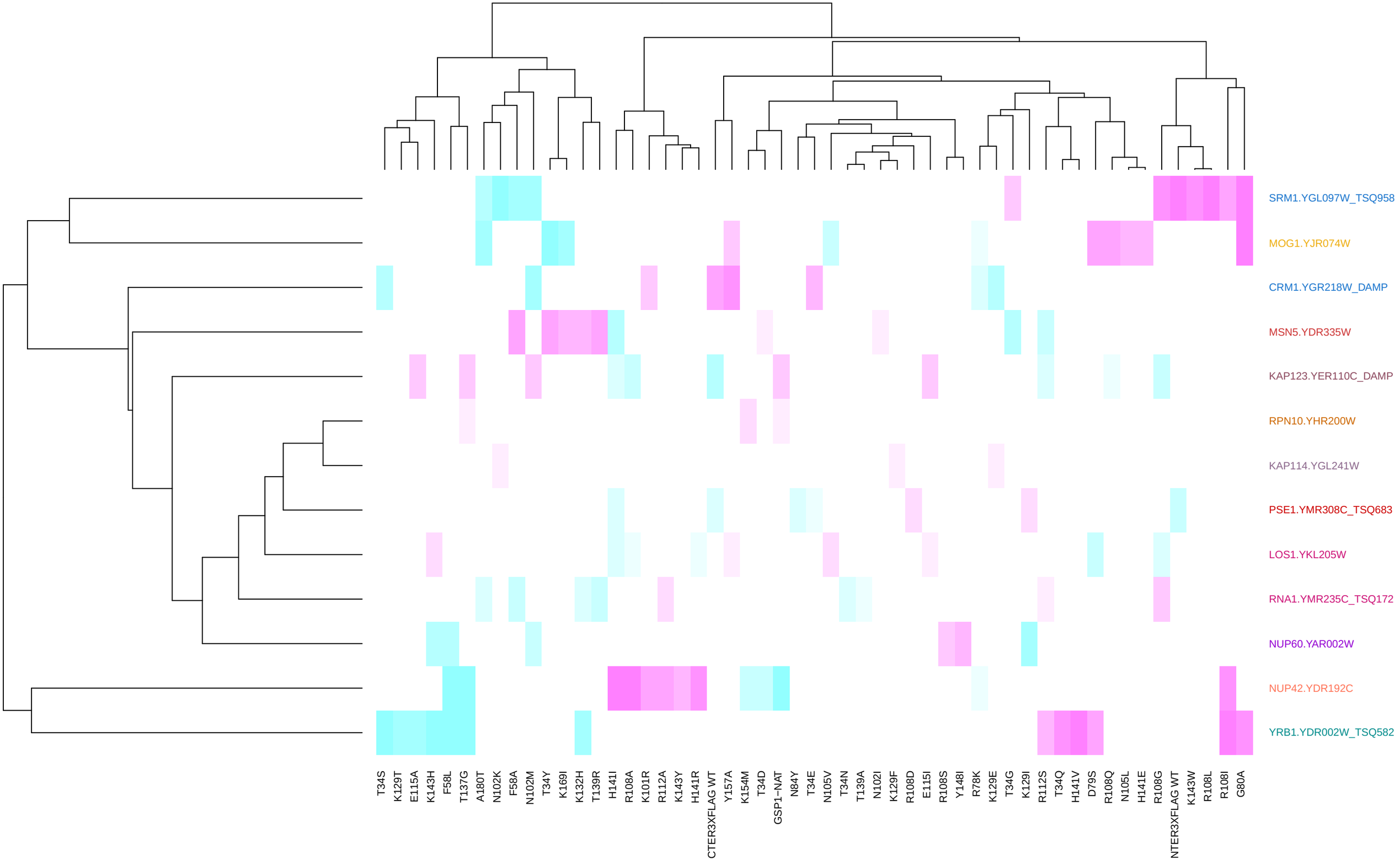
cellular response to DNA damage stimulus_GO_30_1_mut



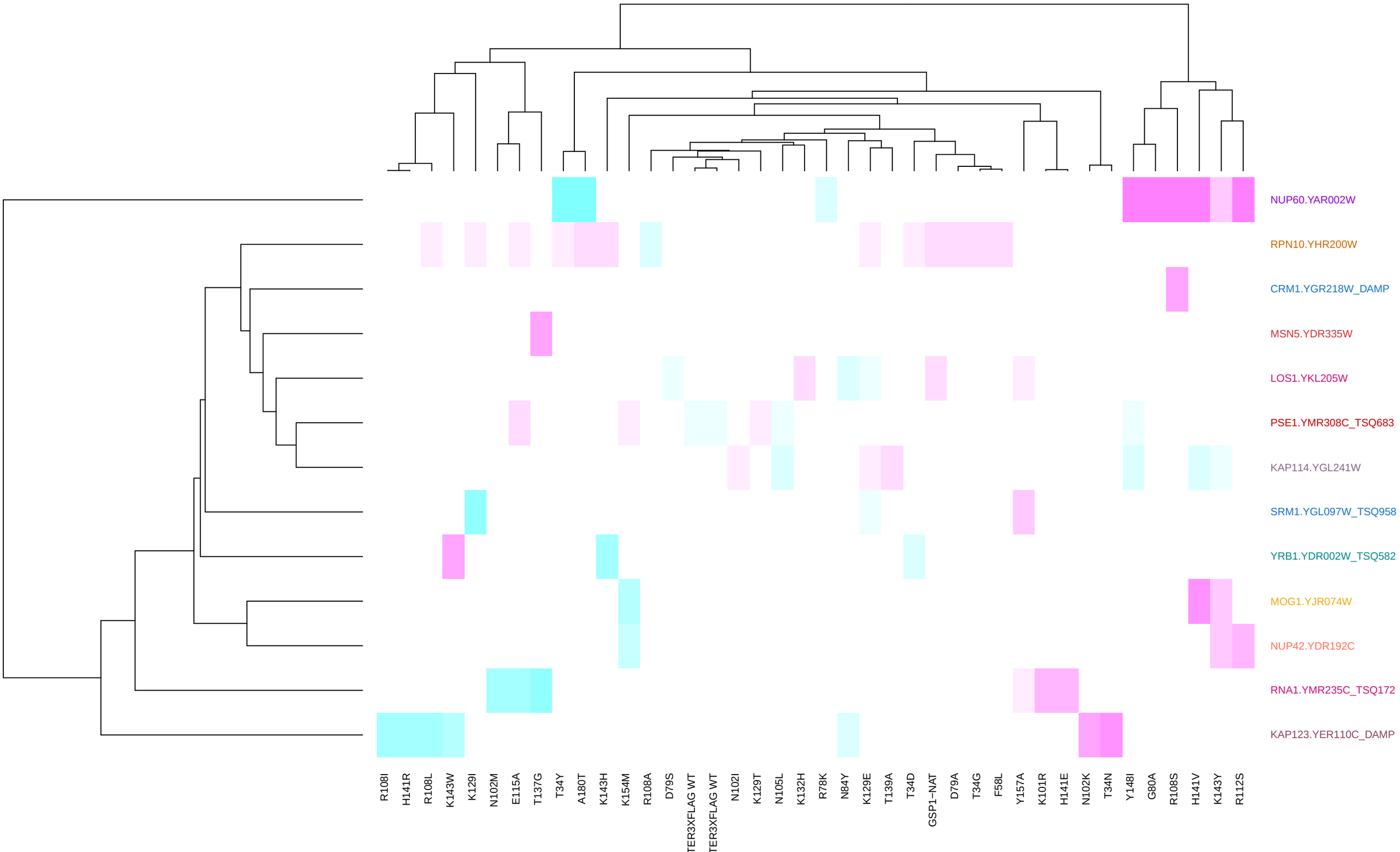
DNA repair


YRB1.YDR002W_TSQ582
NUP42.YDR192C
CRM1.YGR218W_DAMP
MOG1.YJR074W
MSN5.YDR335W
KAP123.YER110C_DAMP
RPN10.YHR200W
KAP114.YGL241W
PSE1.YMR308C_TSQ683
RNA1.YMR235C_TSQ172
LOS1.YKL205W
NUP60.YAR002W
SRM1.YGL097W_TSQ958
T34N
F58L
F58A
T34Y
K129T
A180T
T137G
K132H
K129I
K129F
K143H
T139R
N105V
Q147L
GSP1−NAT
K154M
T34G
T34E
E115A
E115I
T34D
T34Q
K143Y
T34S
T139A
K169I
N102M
K129E
R78K
K101R
N84Y
Y157A
R108D
R108G
R112S
R108Q
N105L
CTER3XFLAG WT
R108A
H141I
R108Y
T34A
D79S
NTER3XFLAG WT
H141E
D79A
R108S
R108I
H141V
K143W
G80A
T34L
R108L
R112A
H141R

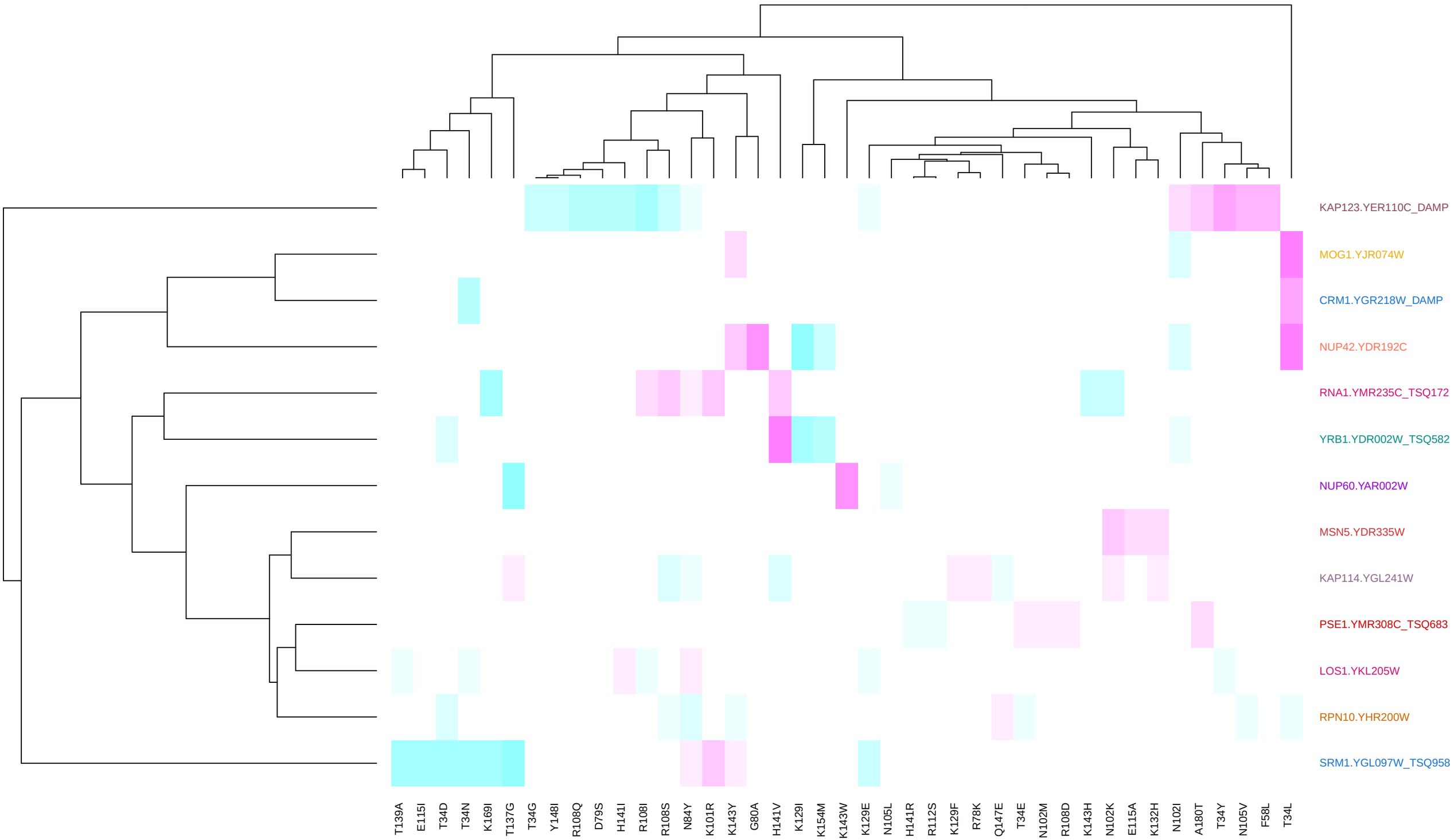
DNA repair_GO_30_1_mut



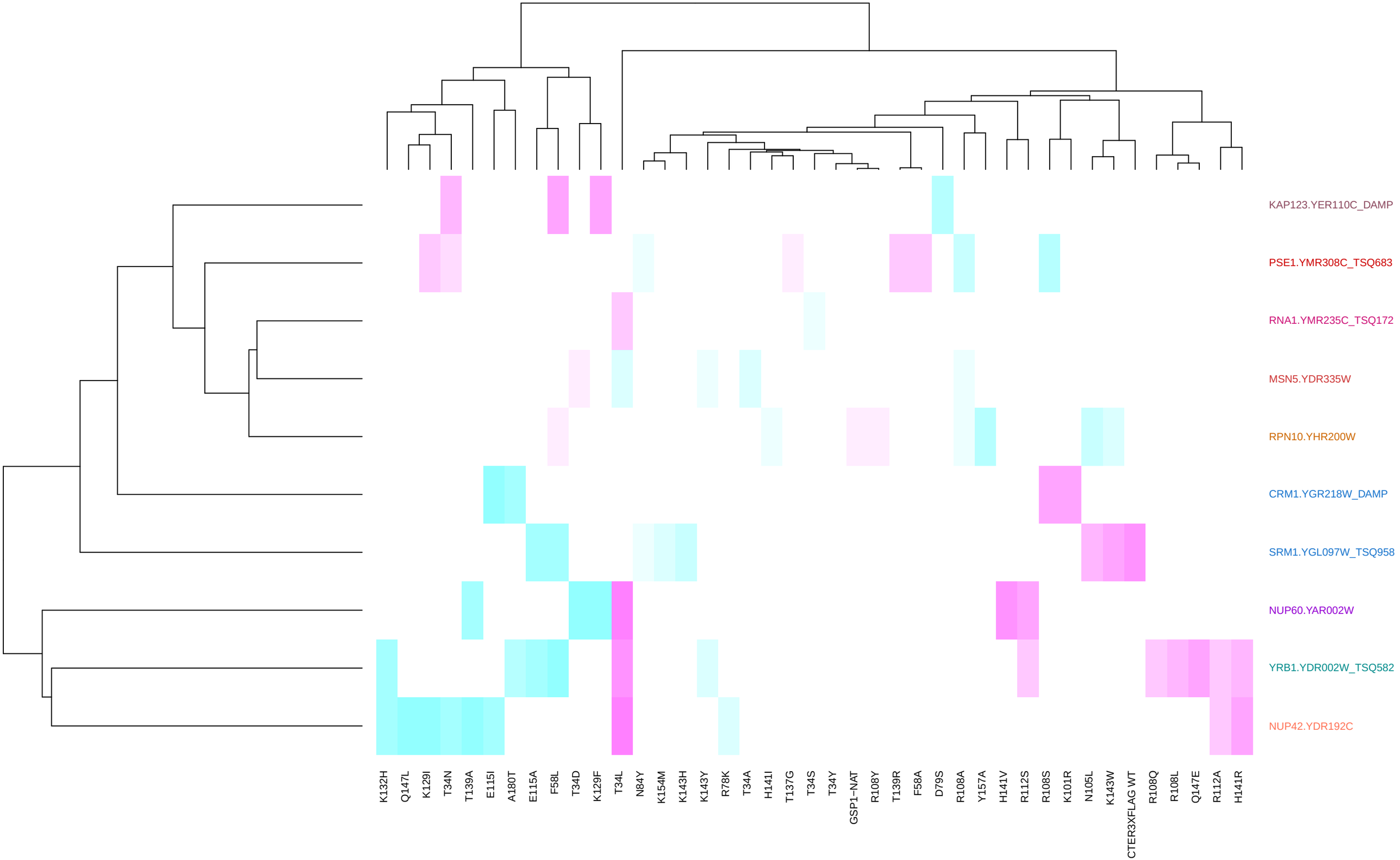
transcription and mRNA processing_GO_15_14_mut



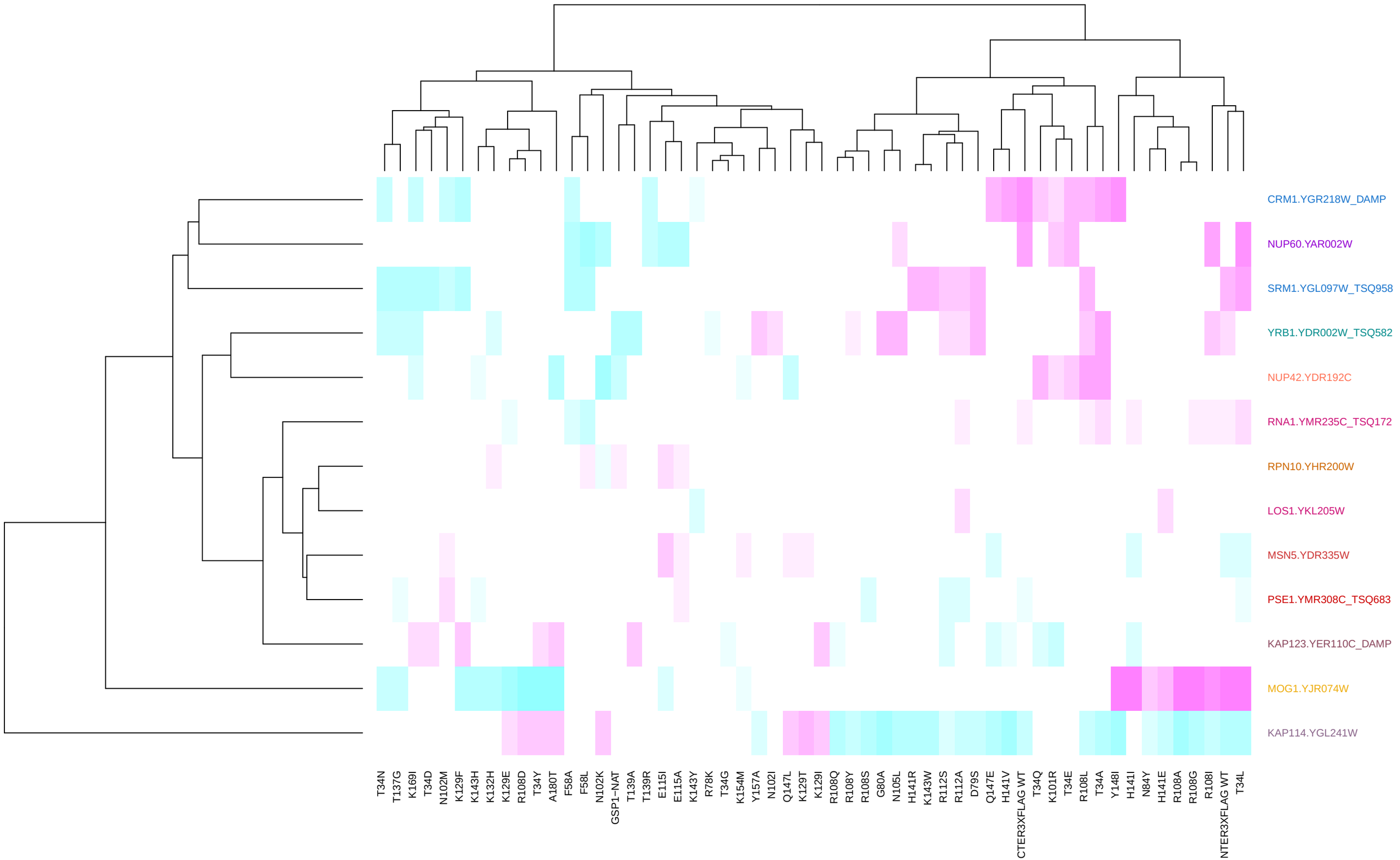
transcription and mRNA processing_GO_30_2_mut



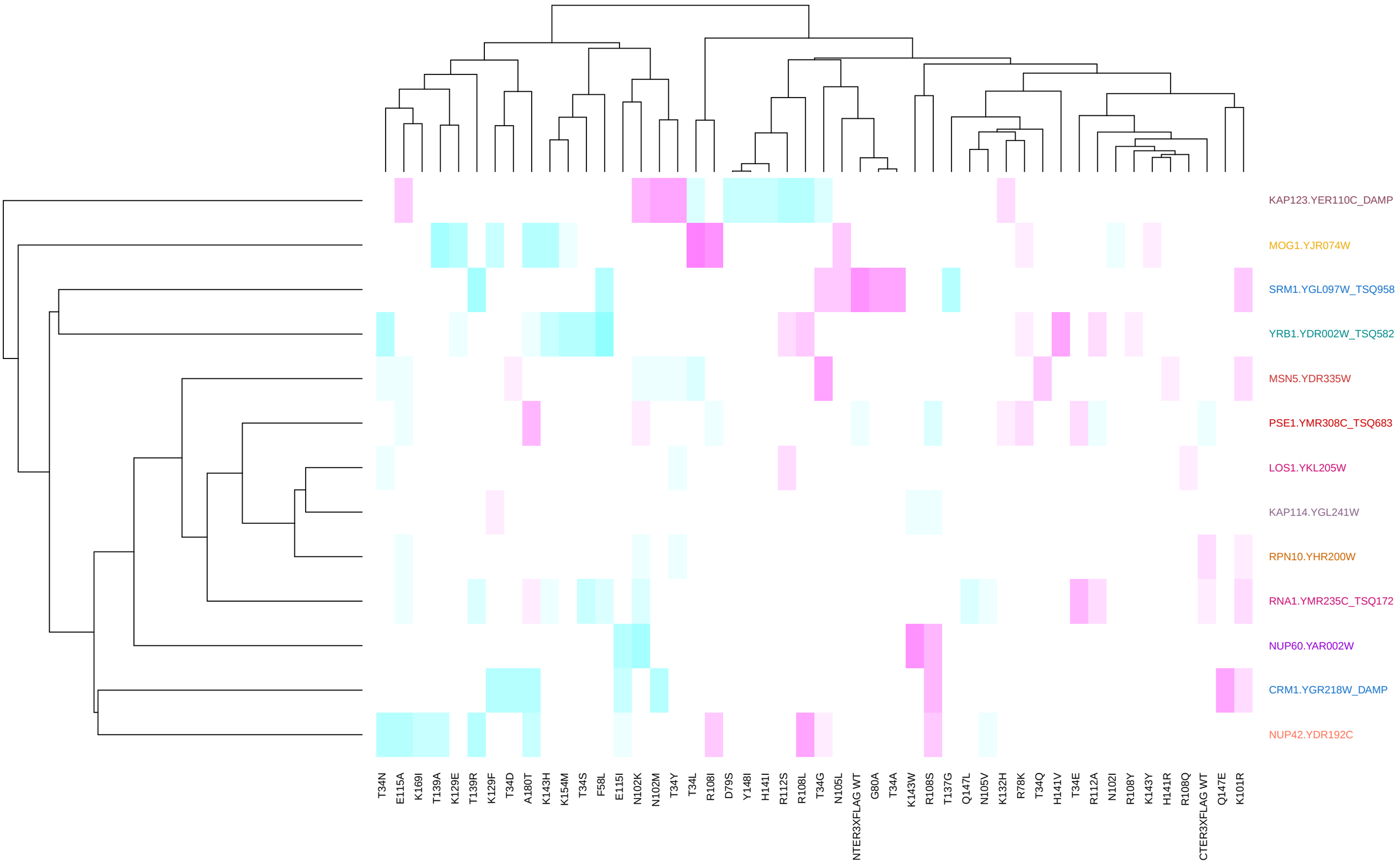
transcription from RNA polymerase II promoter_GO_15_3_mut



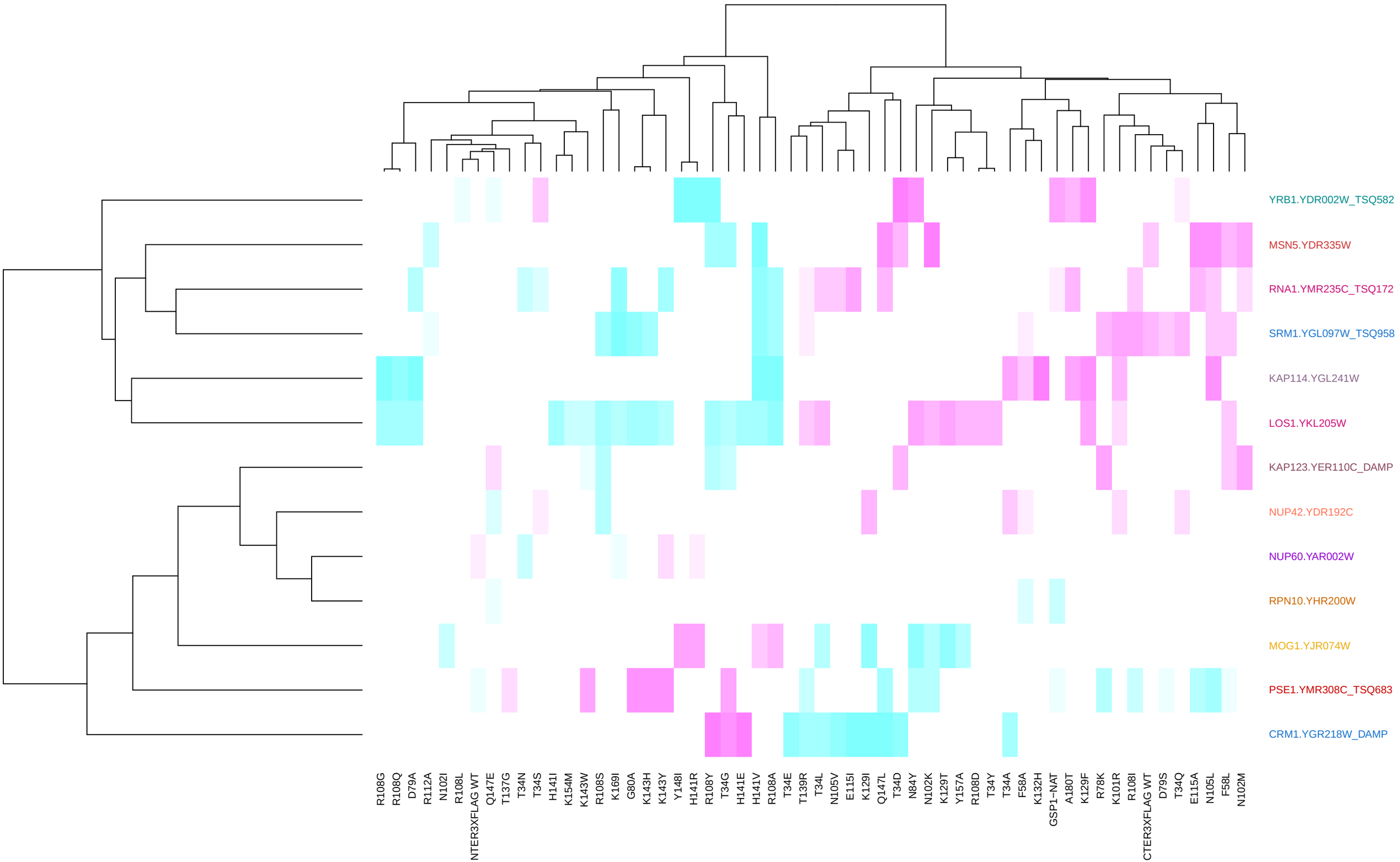
transcription from RNA polymerase II promoter_GO_30_1_all



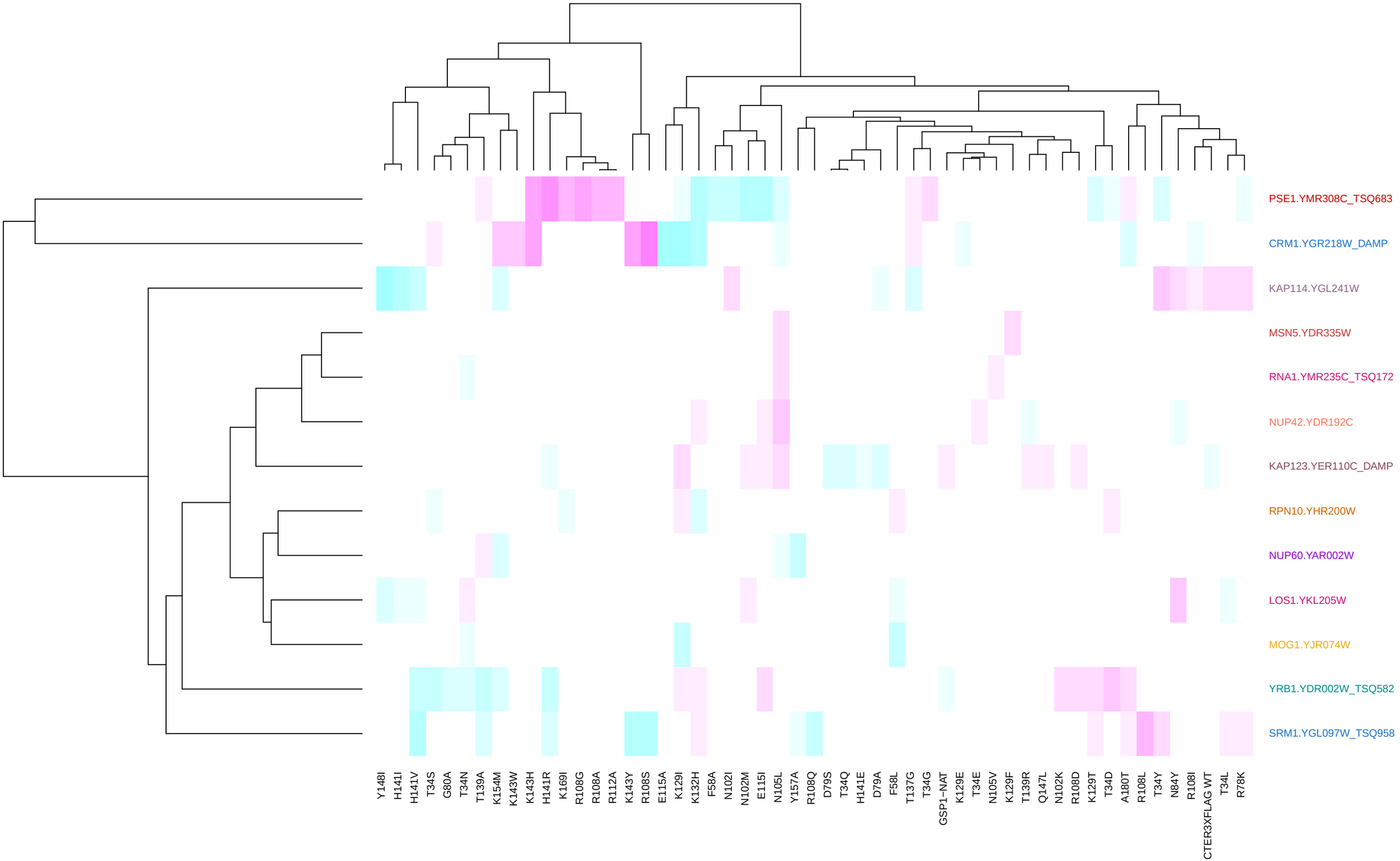
transcription from RNA polymerase II promoter_GO_30_1_mut



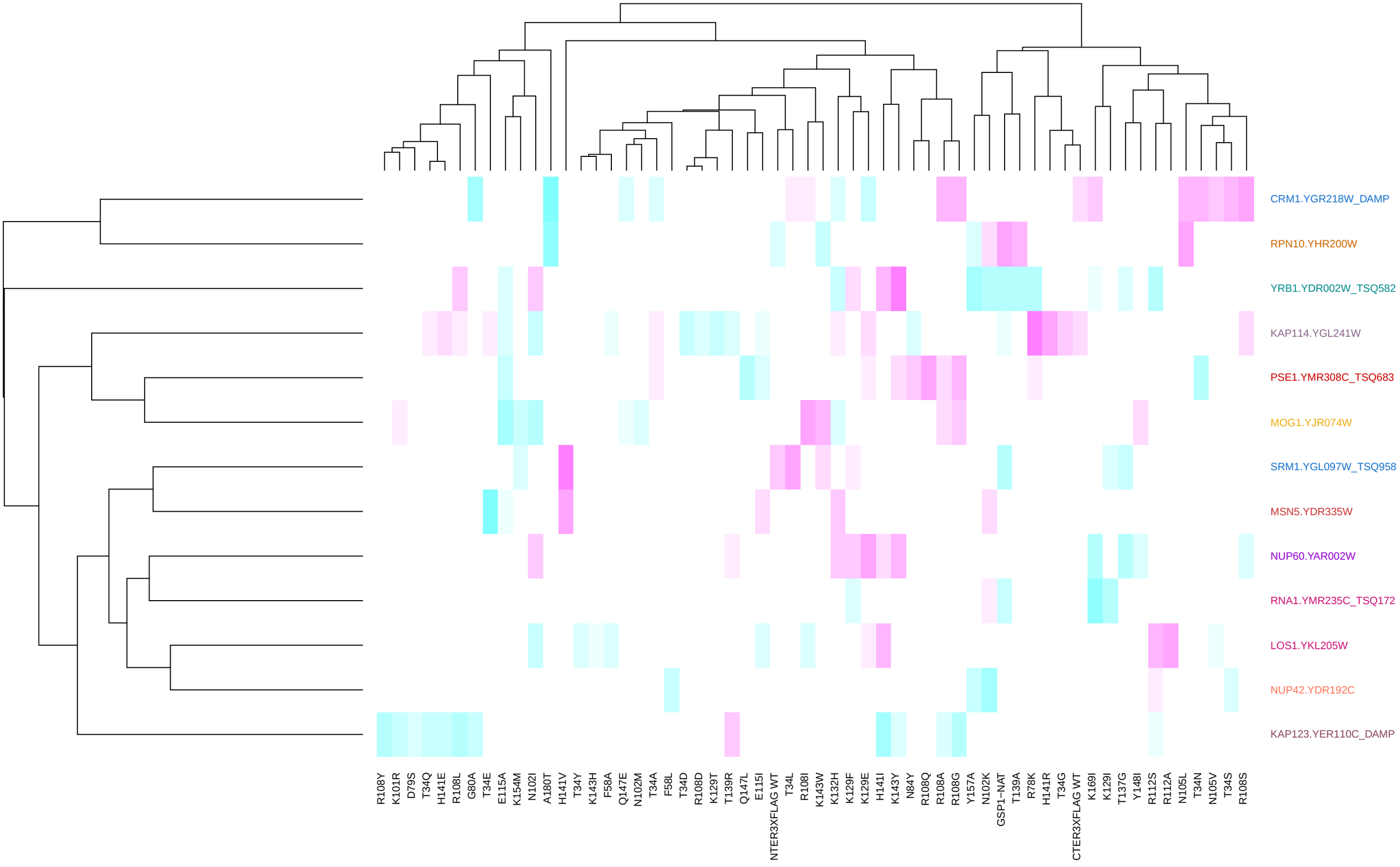
whole_library_30_14_mut



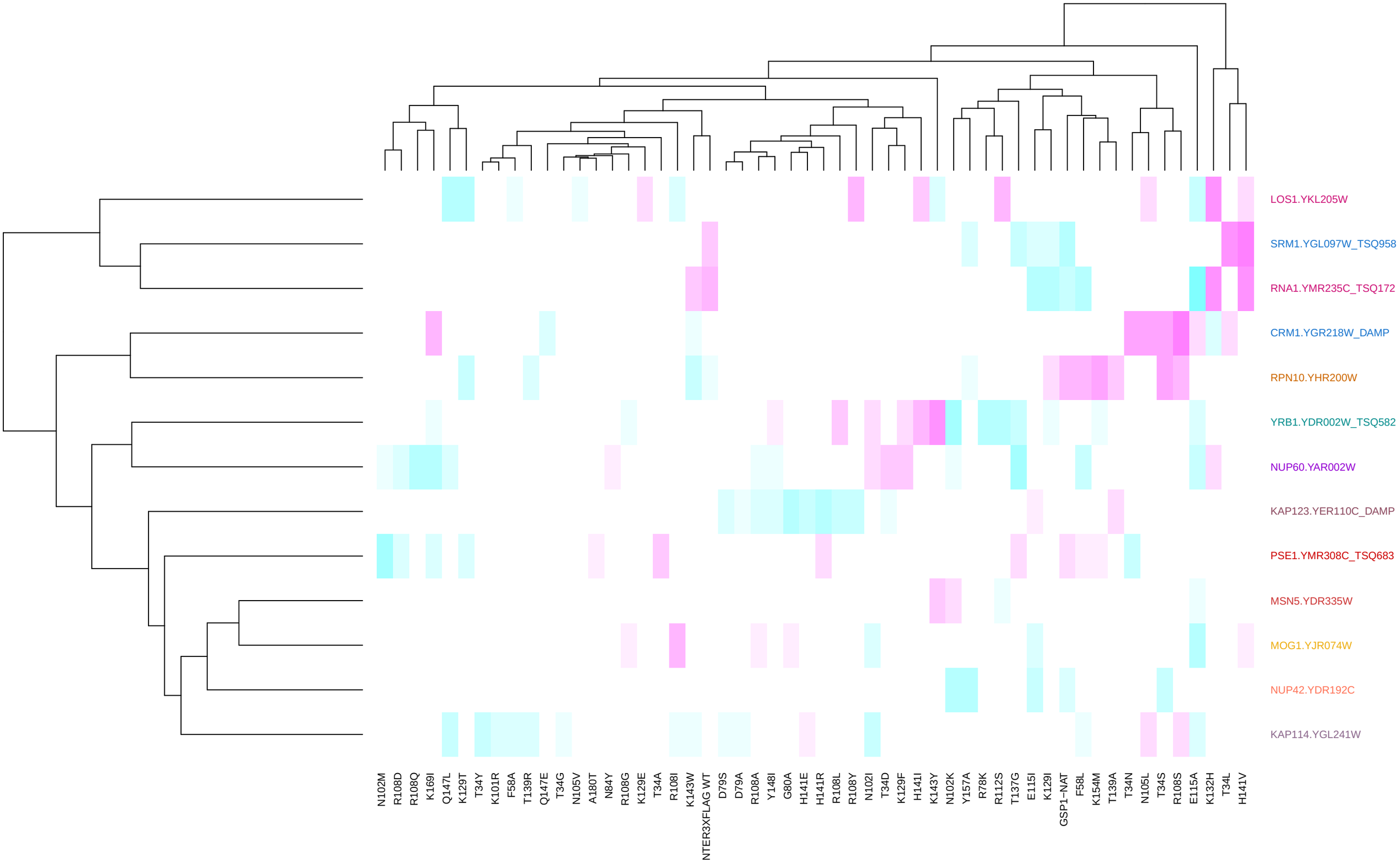
cytoskeleton and microtubules



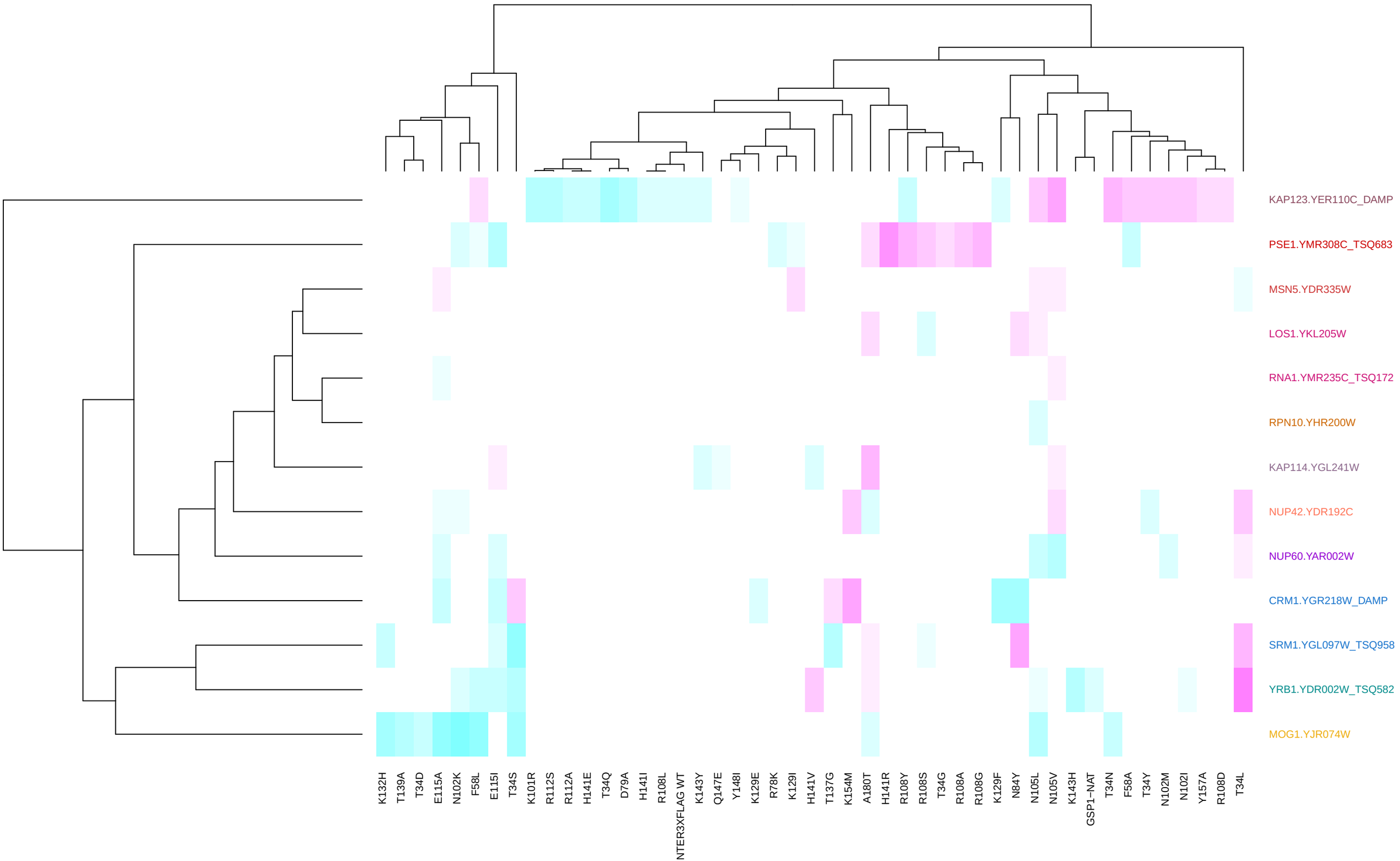
ribosomes and translation



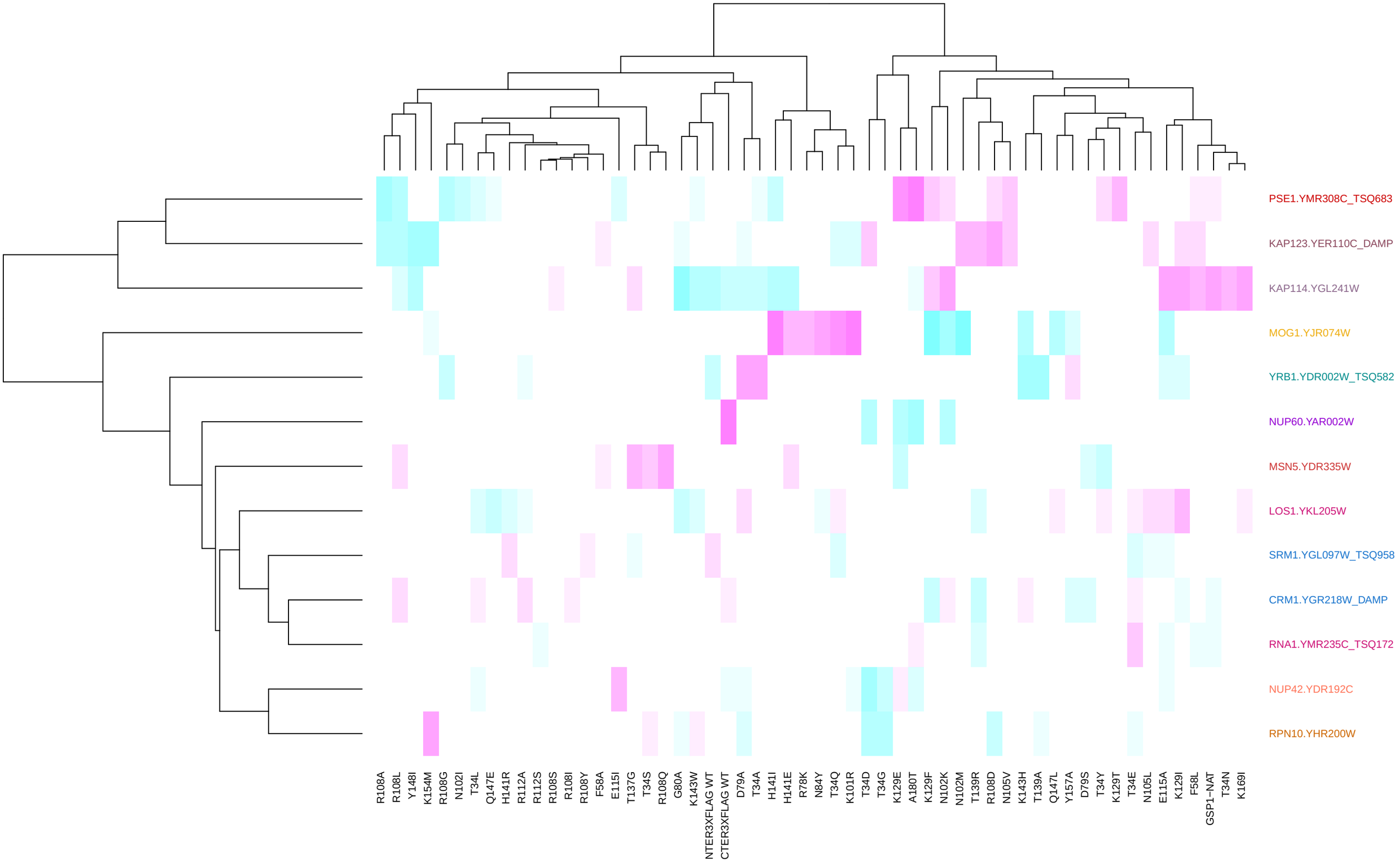
ribosomes and translation_GO_30_1_all



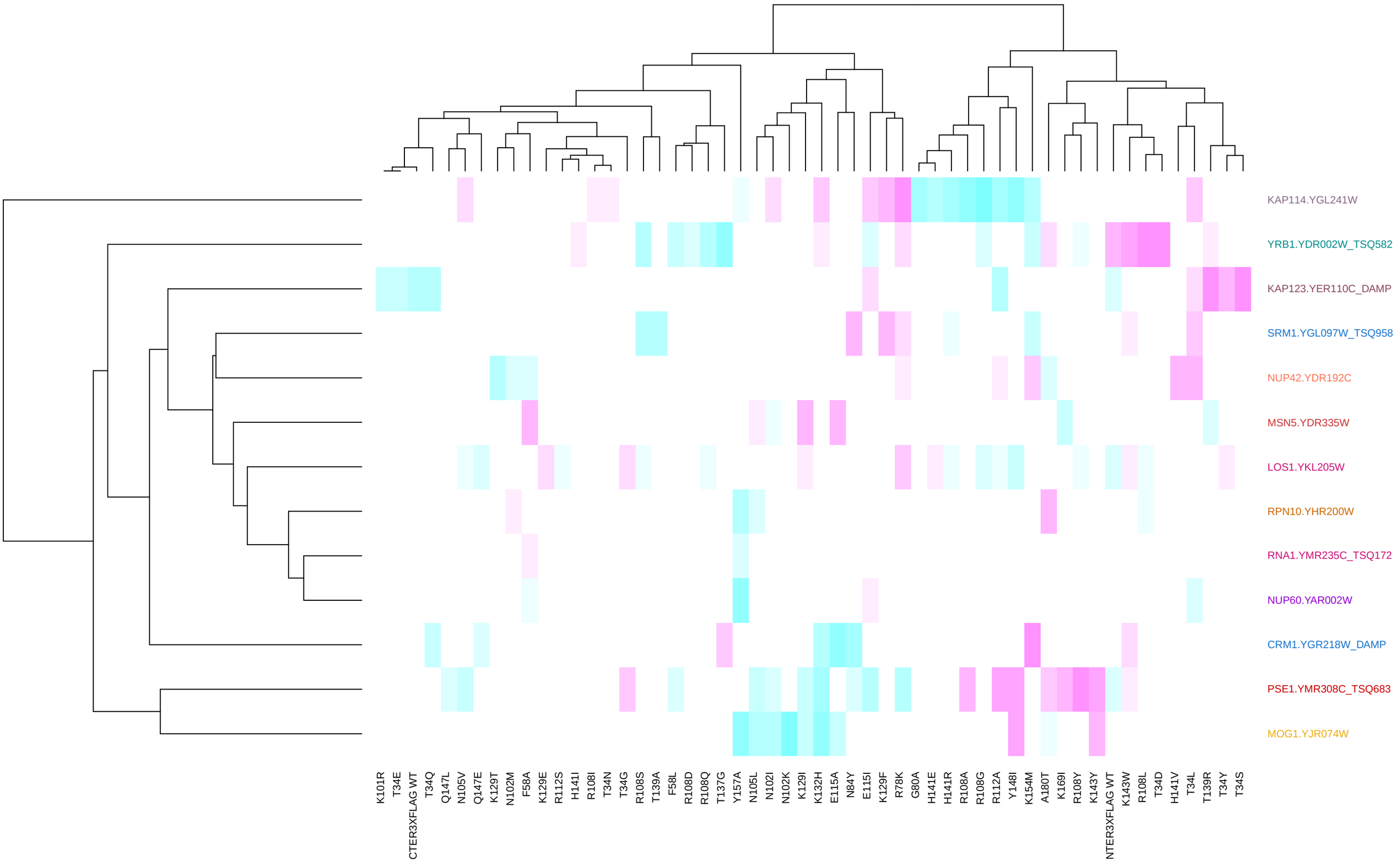
cell cycle


KAP123.YER110C_DAMP
PSE1.YMR308C_TSQ683
MSN5.YDR335W
LOS1.YKL205W
RNA1.YMR235C_TSQ172
RPN10.YHR200W
KAP114.YGL241W
NUP42.YDR192C
NUP60.YAR002W
CRM1.YGR218W_DAMP
SRM1.YGL097W_TSQ958
YRB1.YDR002W_TSQ582
MOG1.YJR074W
K132H
T139A
T34D
E115A
N102K
F58L
E115I
T34S
K101R
R112S
R112A
H141E
T34Q
D79A
H141I
R108L
NTER3XFLAG WT
K143Y
Q147E
Y148I
K129E
R78K
K129I
H141V
T137G
K154M
A180T
H141R
R108Y
R108S
T34G
R108A
R108G
K129F
N84Y
N105L
N105V
K143H
GSP1−NAT
T34N
F58A
T34Y
N102M
N102I
Y157A
R108D
T34L

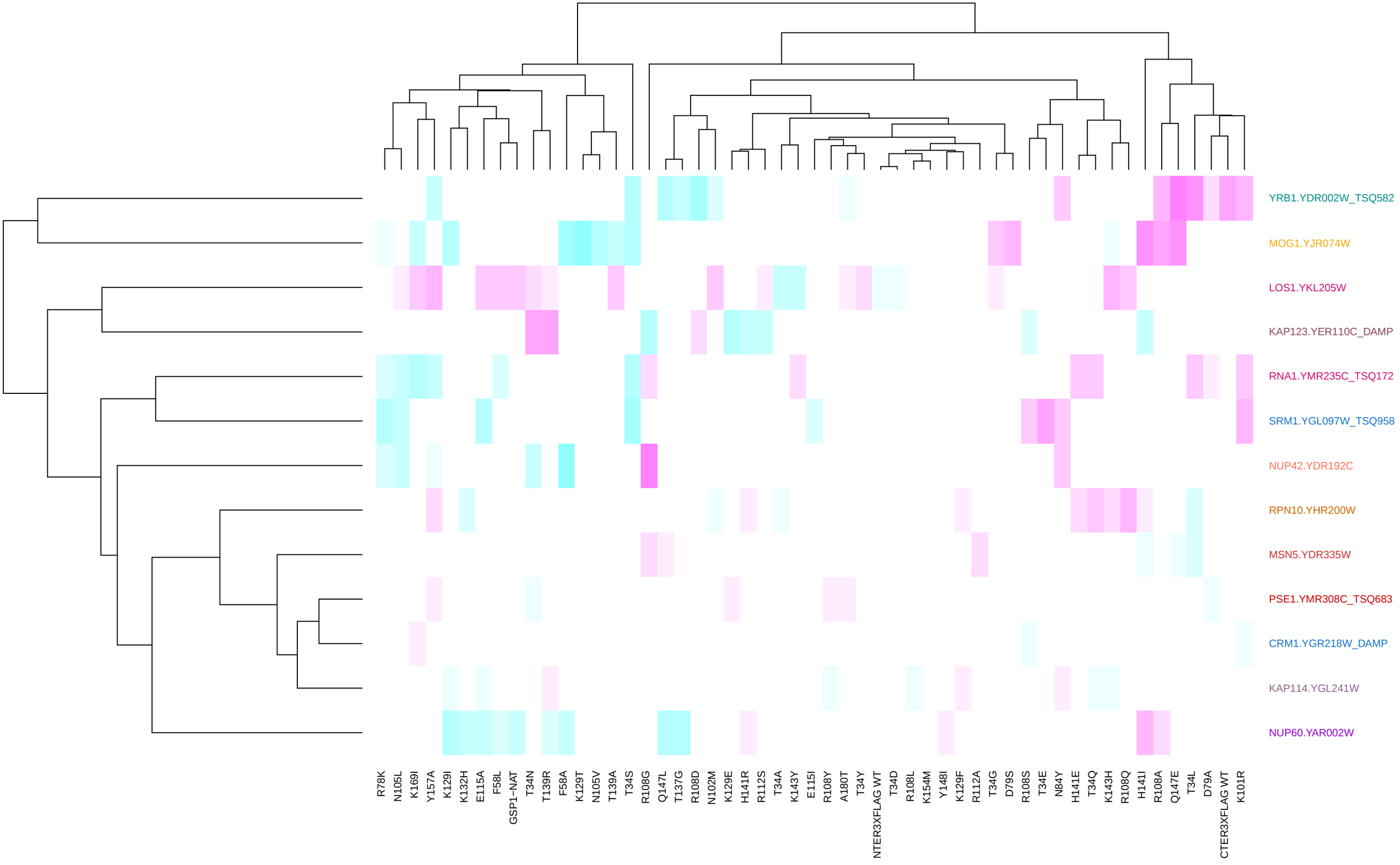
DNA−templated transcription, elongation



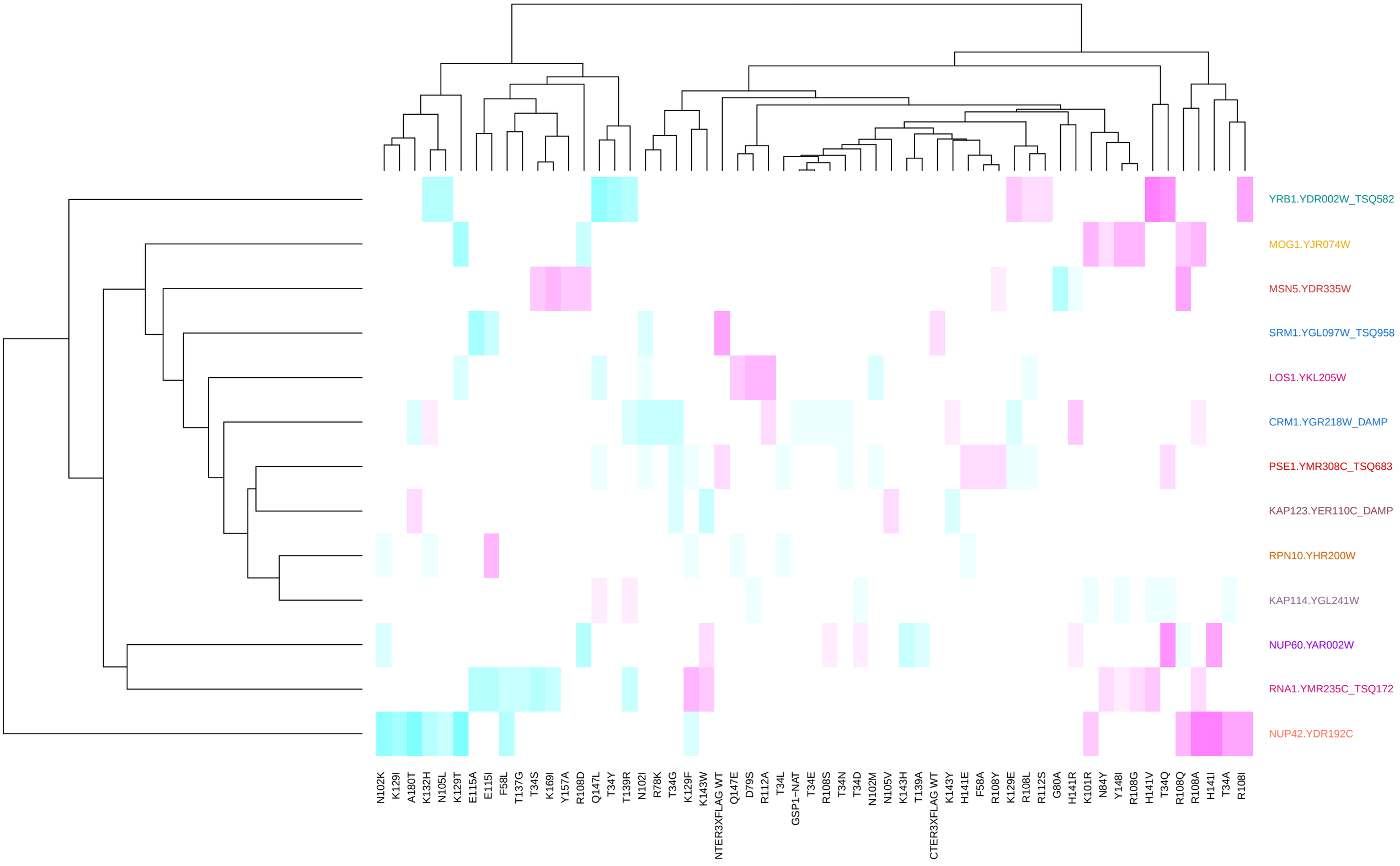
mitotic cell cycle



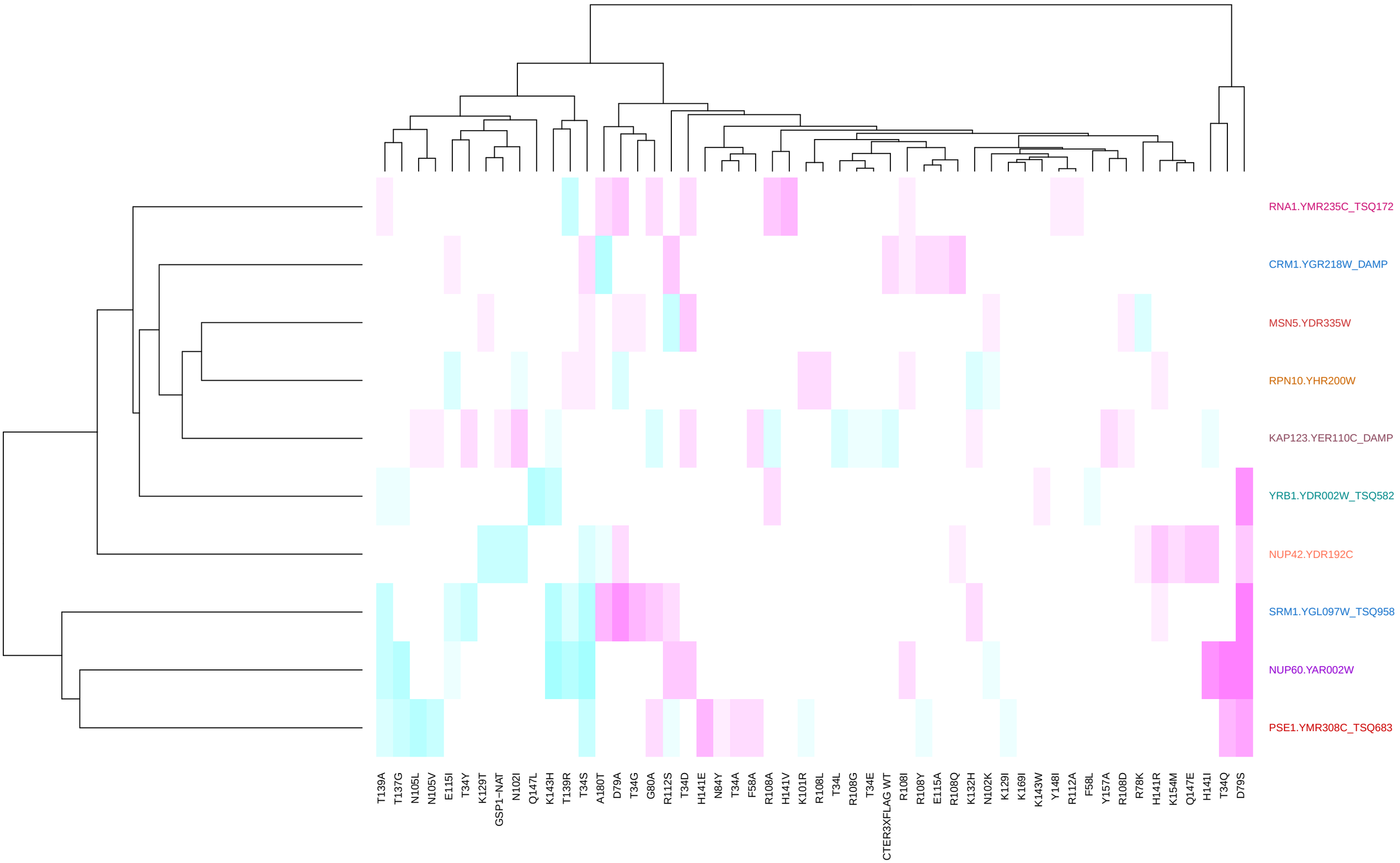
mitotic cell cycle_GO_15_1_all



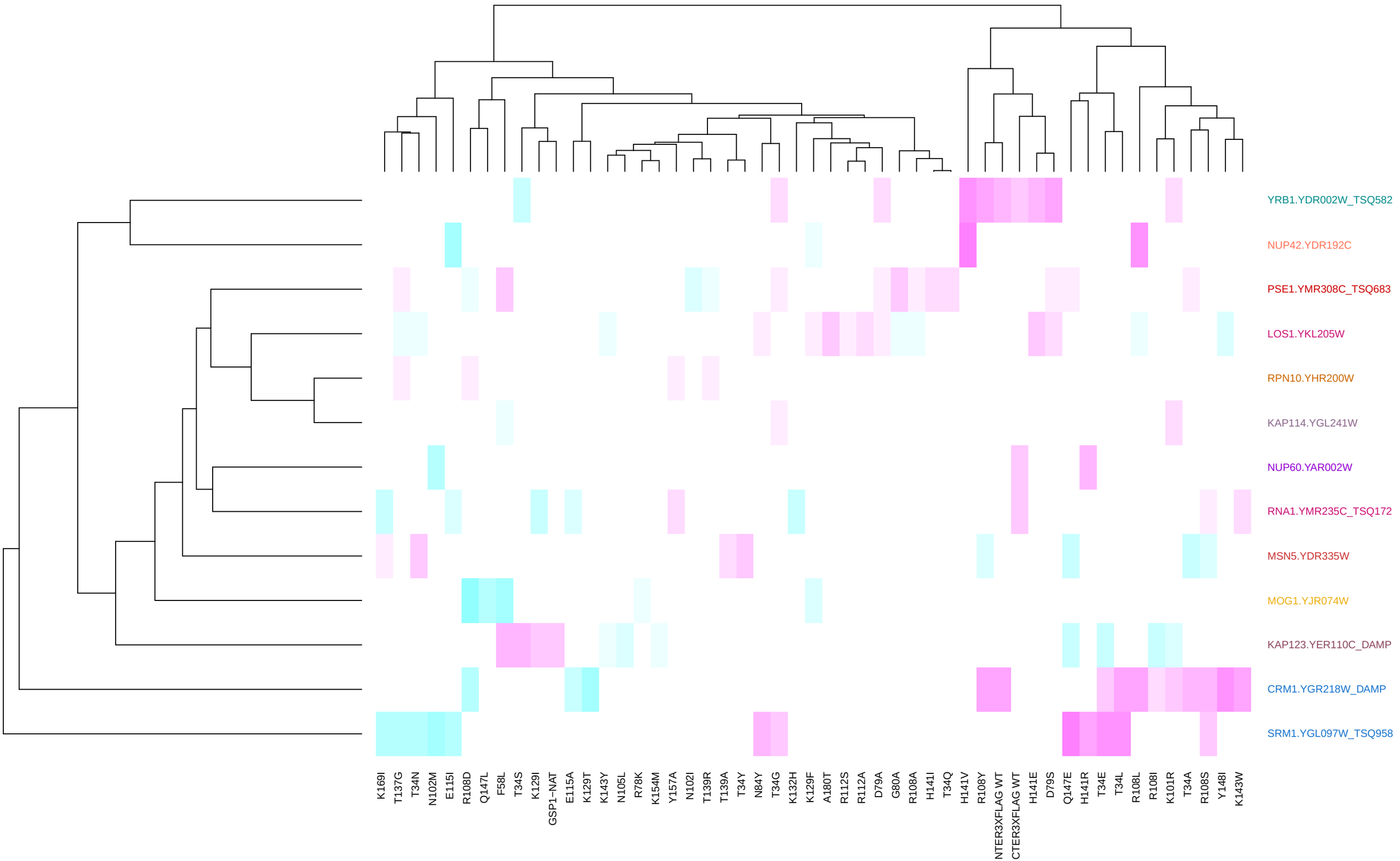
RNA catabolic process



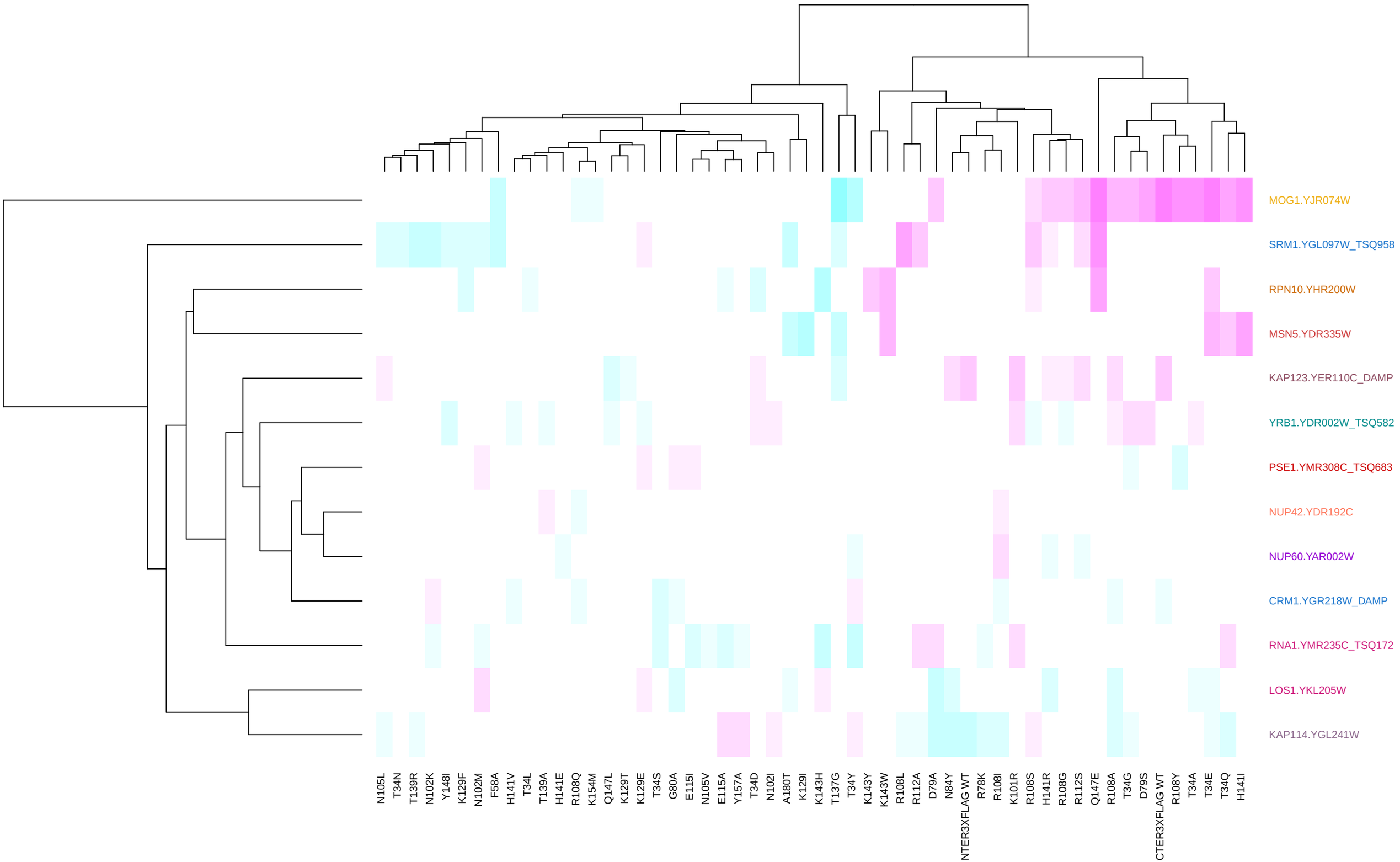
transcription and mRNA processing_GO_30_2_all



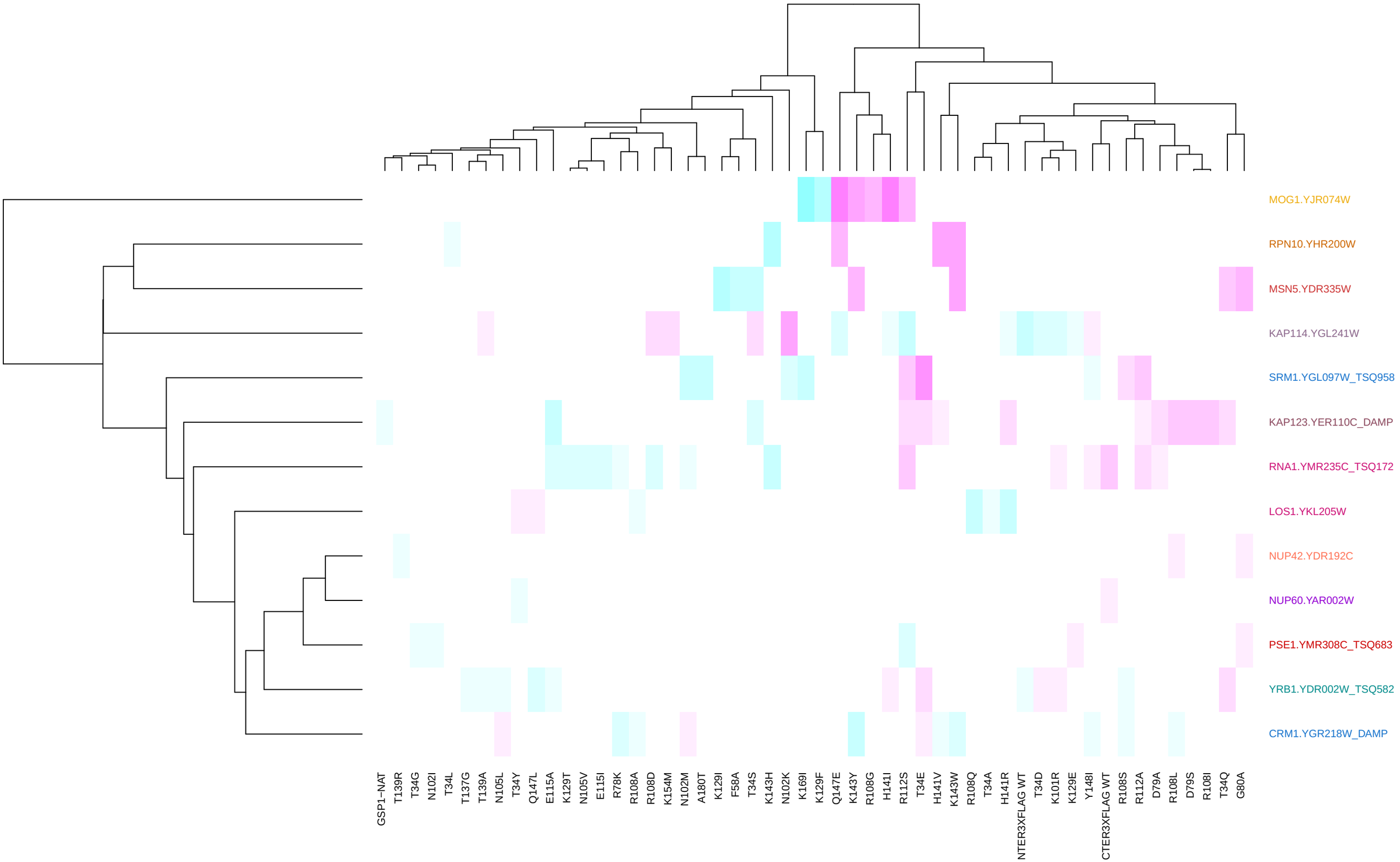
whole_library_30_3_all



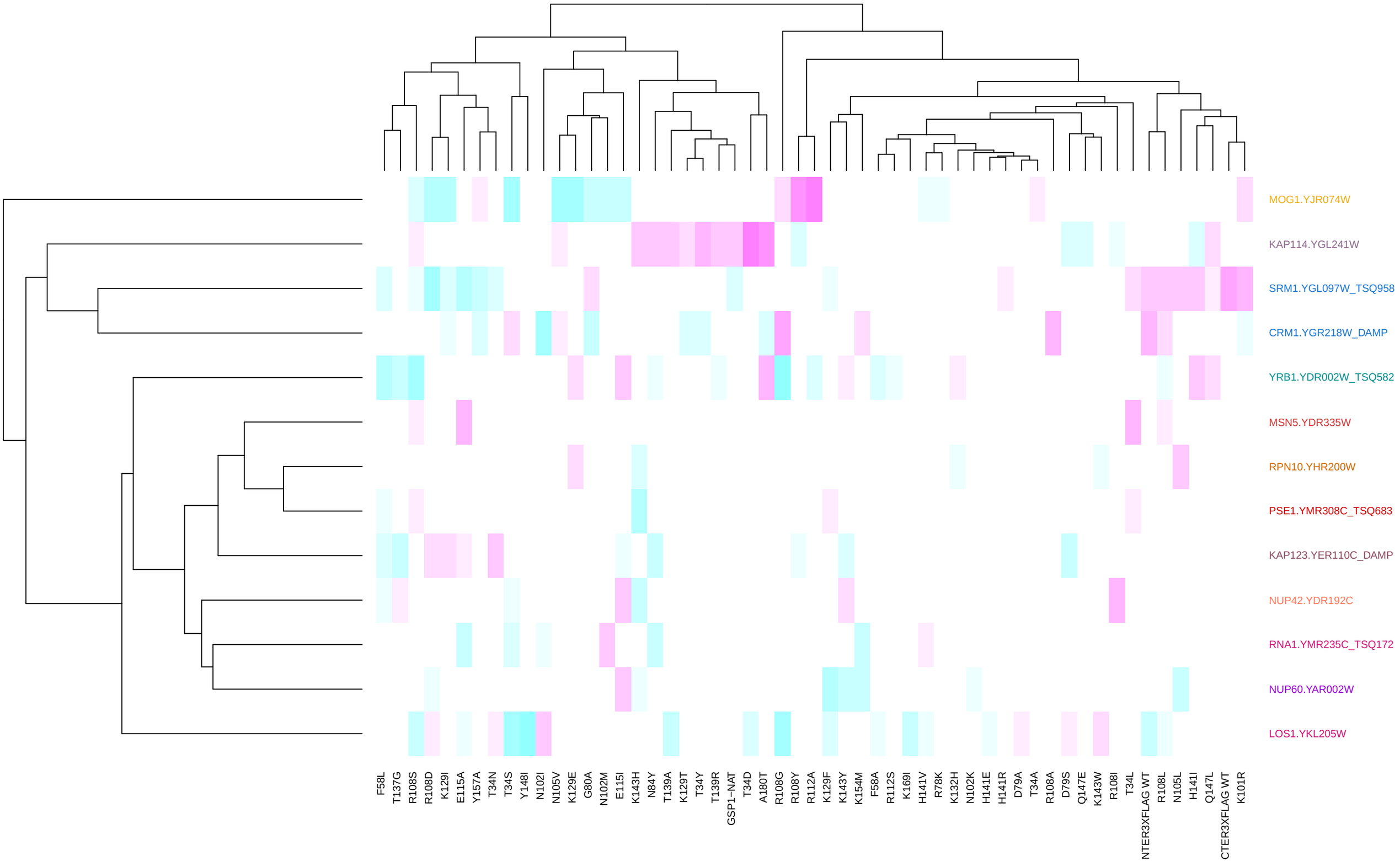
proteolysis involved in cellular protein catabolic process



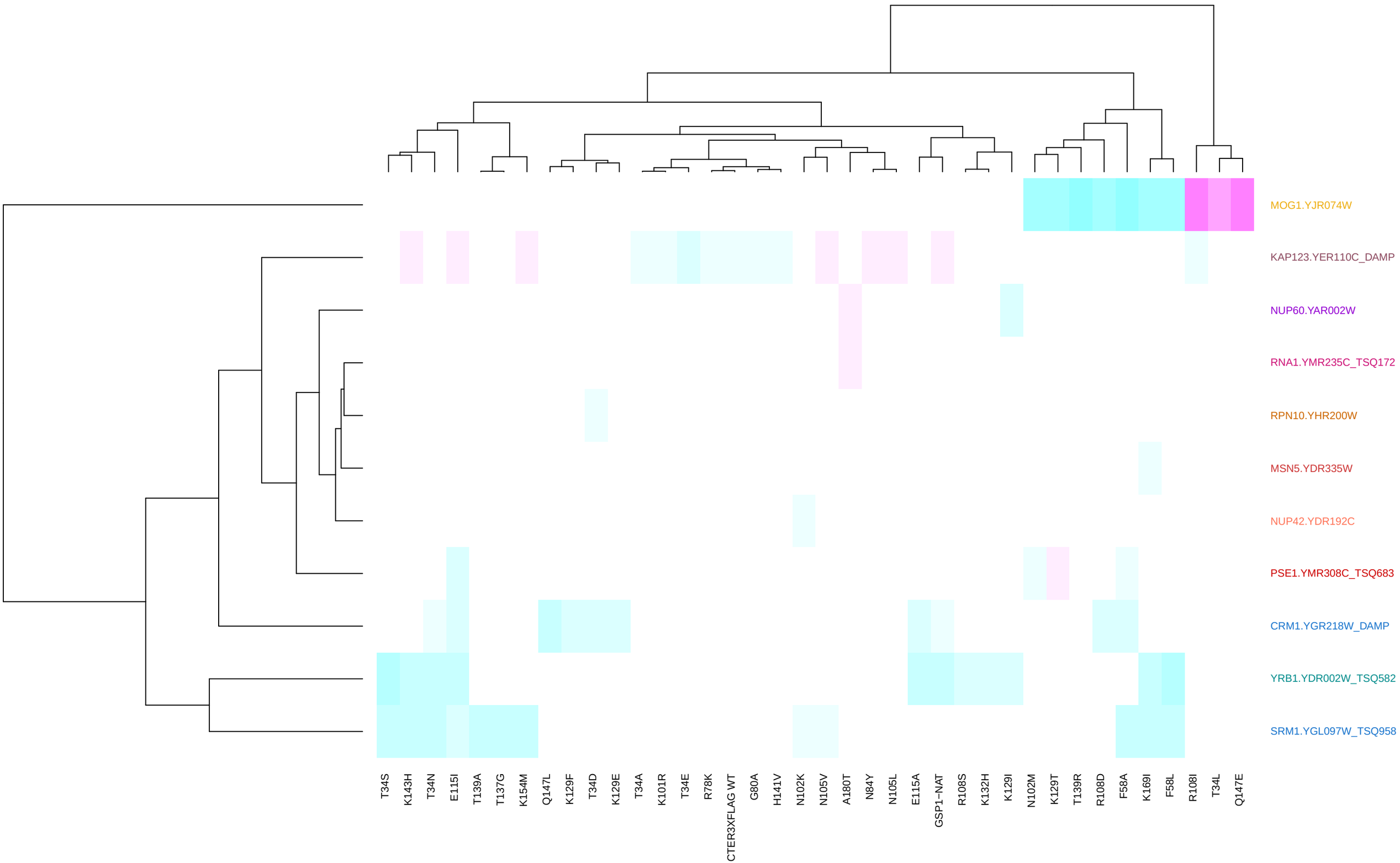
proteolysis involved in cellular protein catabolic process_GO_15_1_all



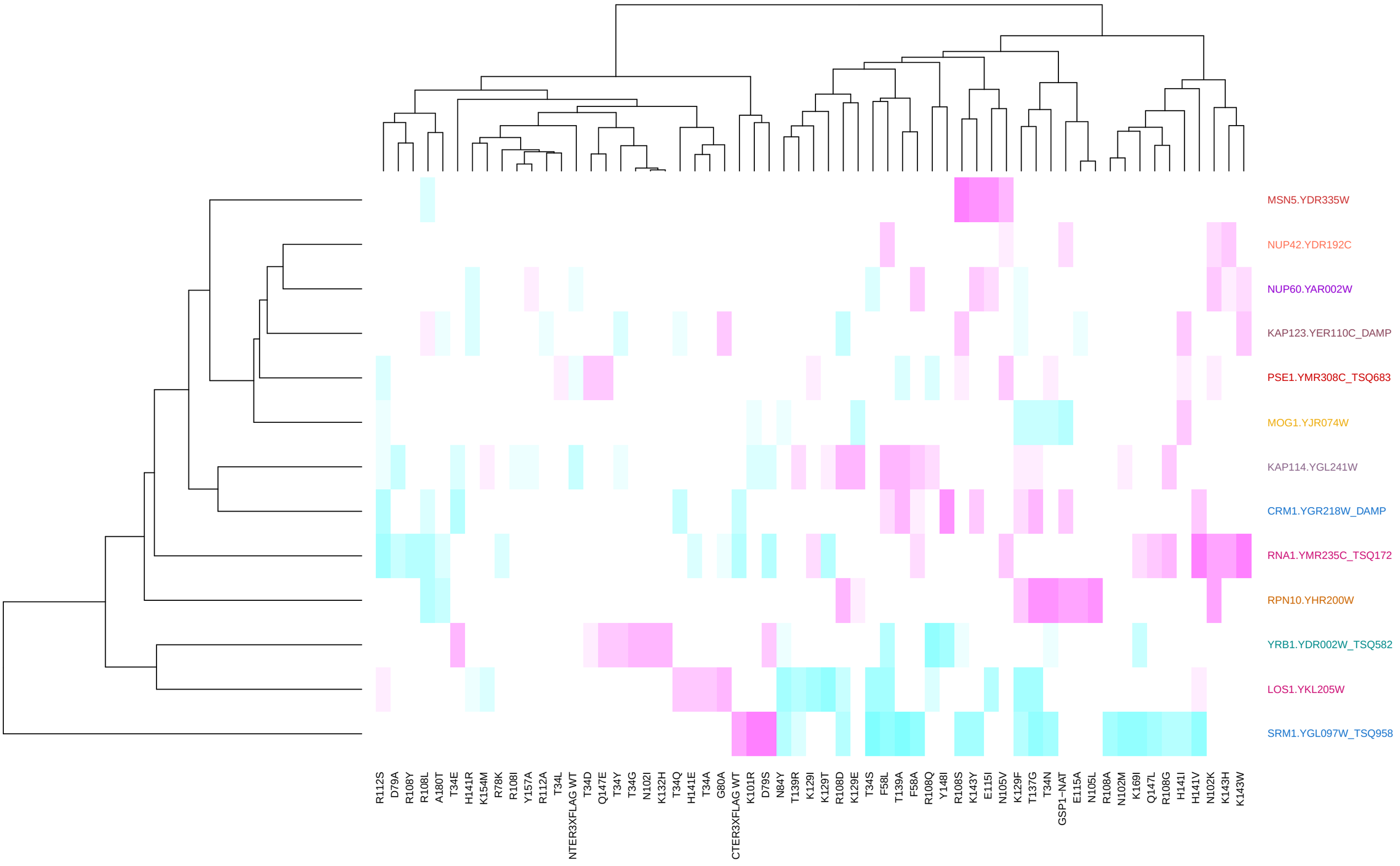
sig_Gsp1_GI_30_4_all



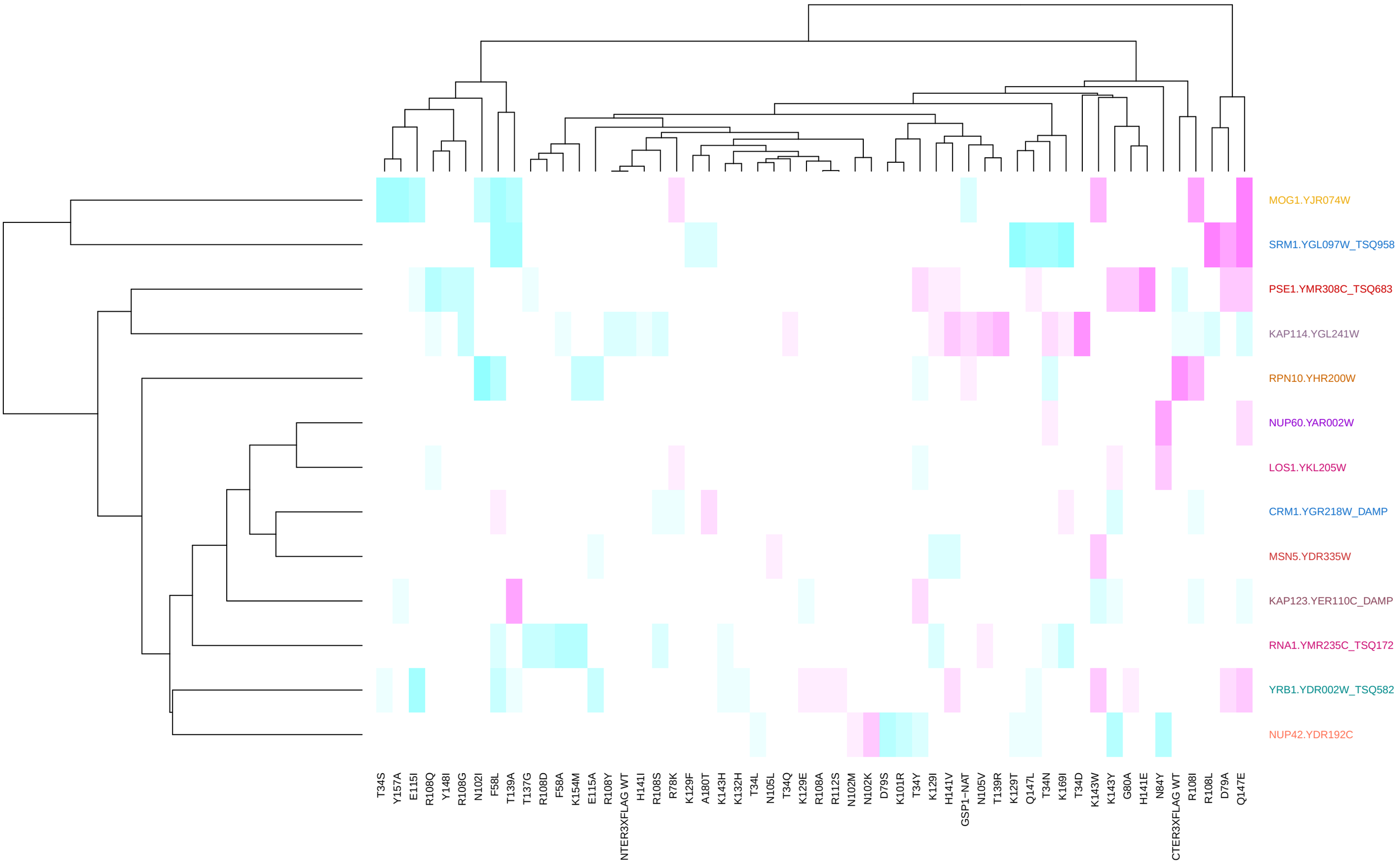
whole_library



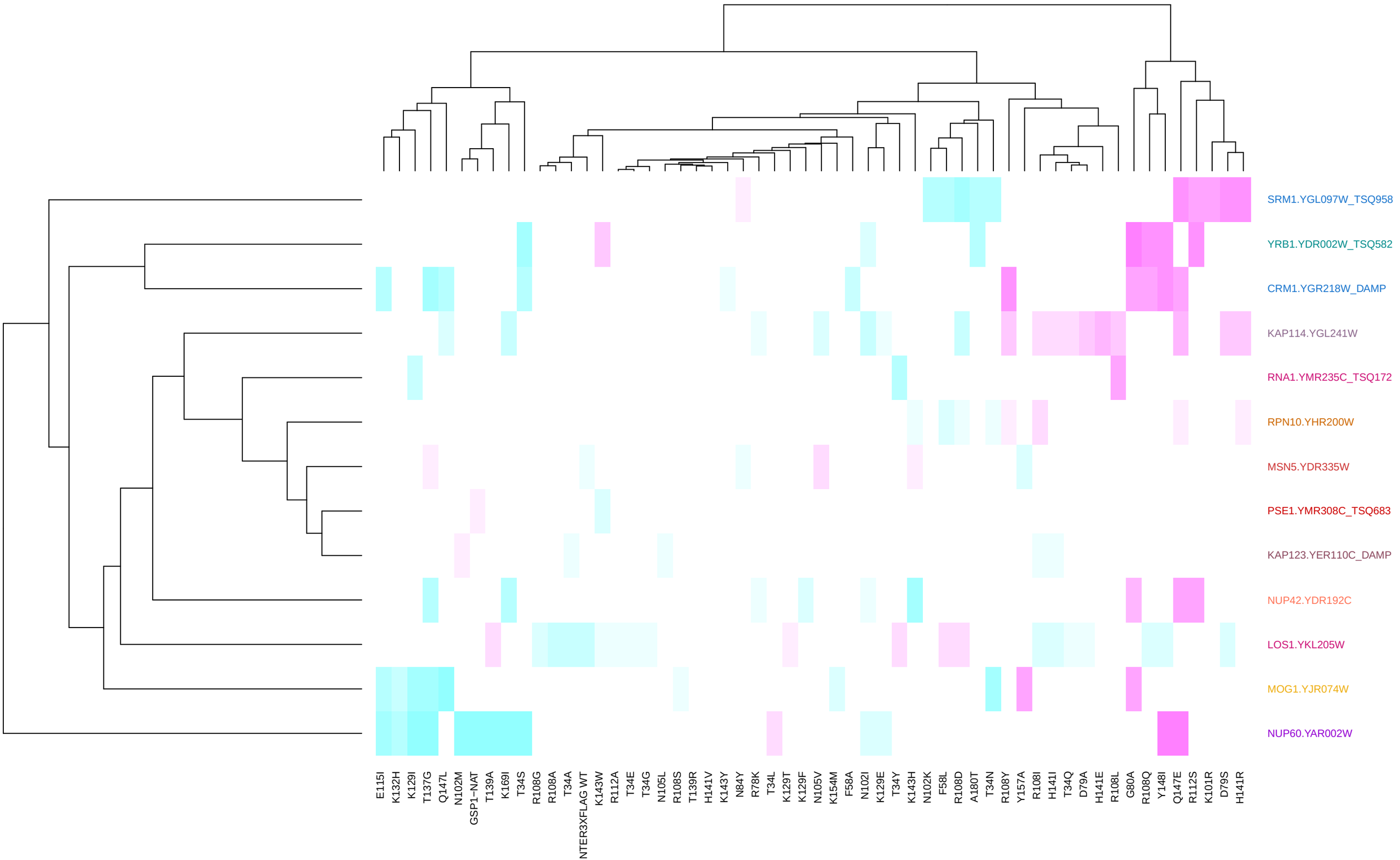
sig_Gsp1_GI_30_5_mut



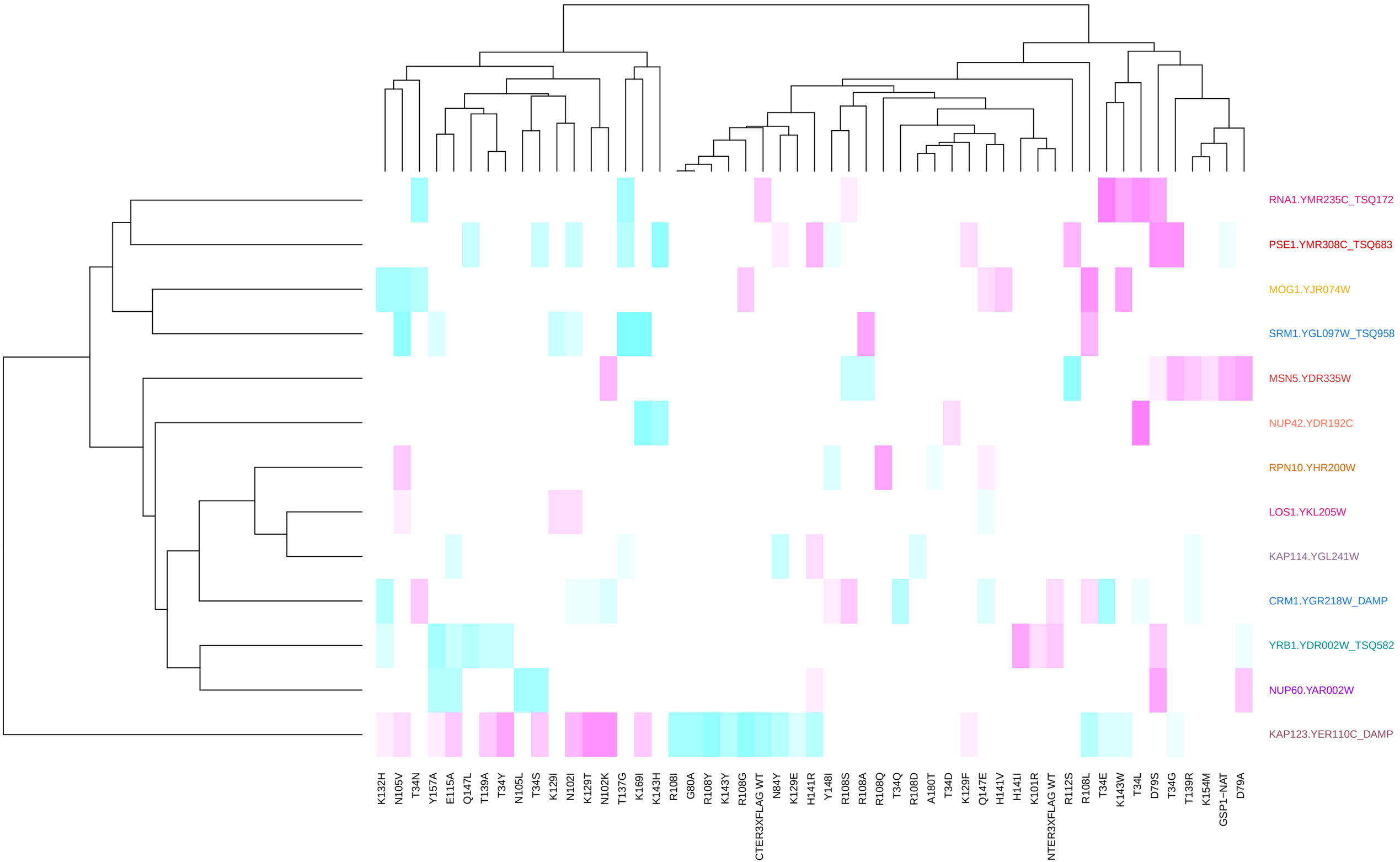
regulation of cell cycle_GO_30_1_mut



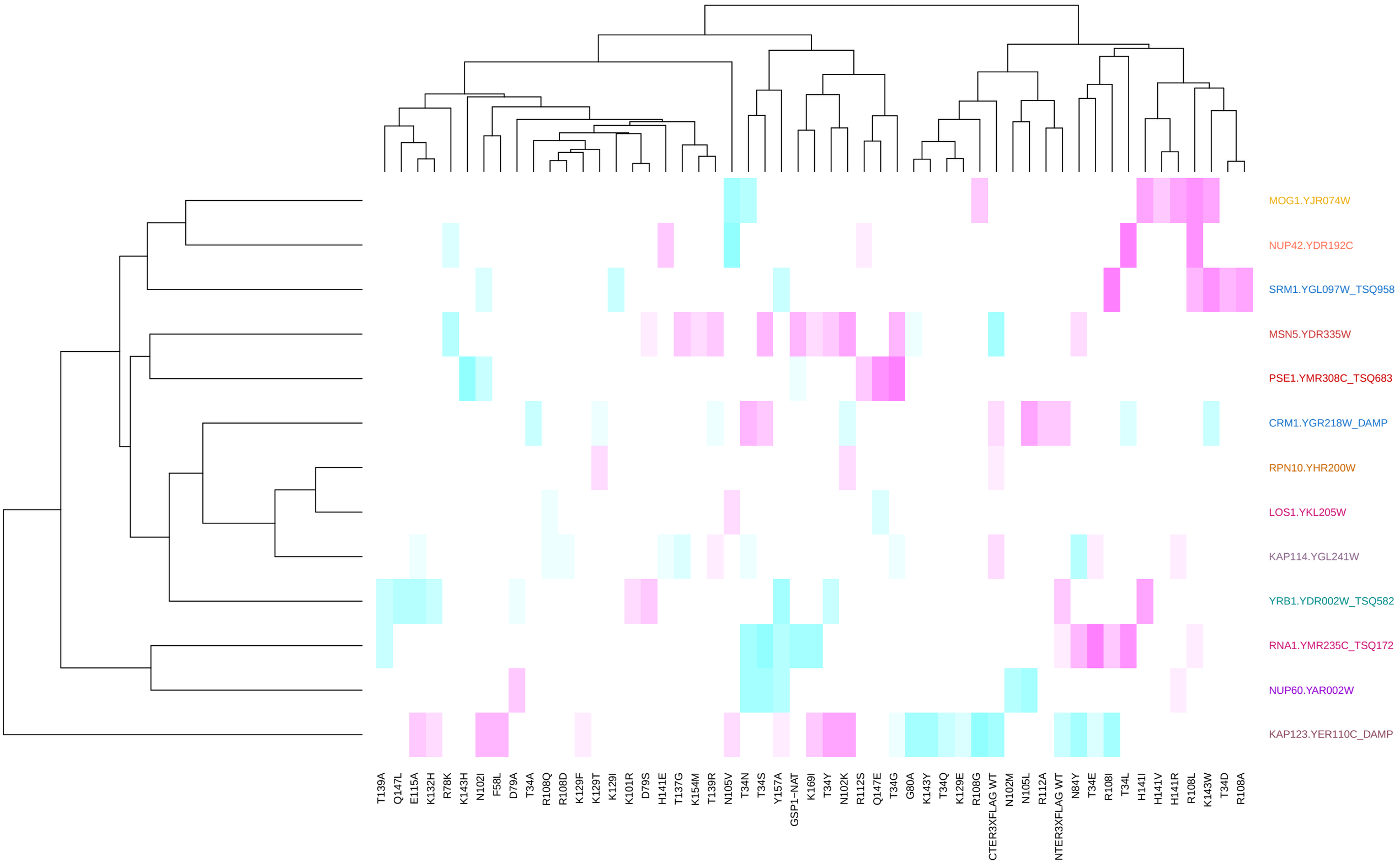
whole_library_30_5_all



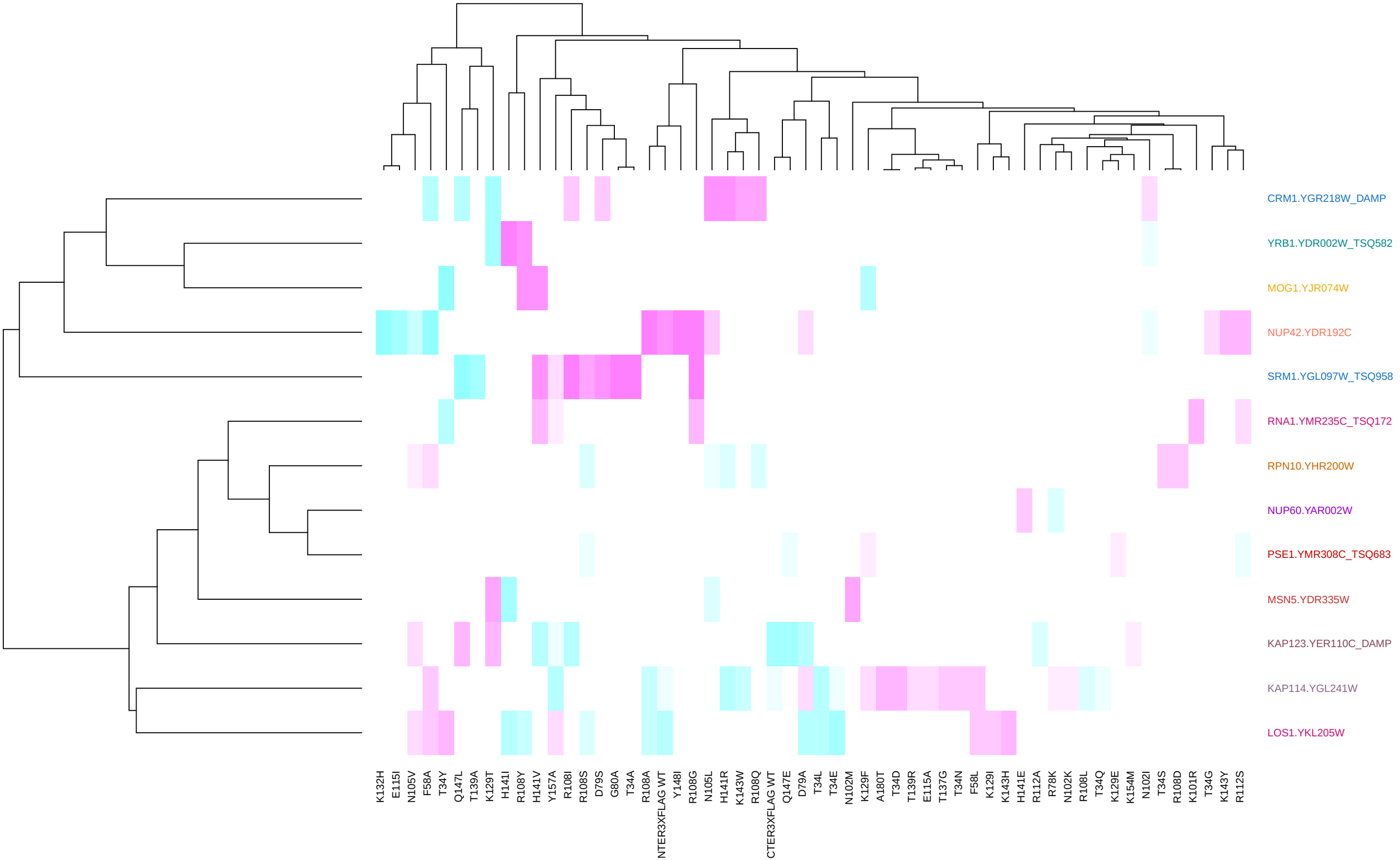
ribosomal small subunit biogenesis



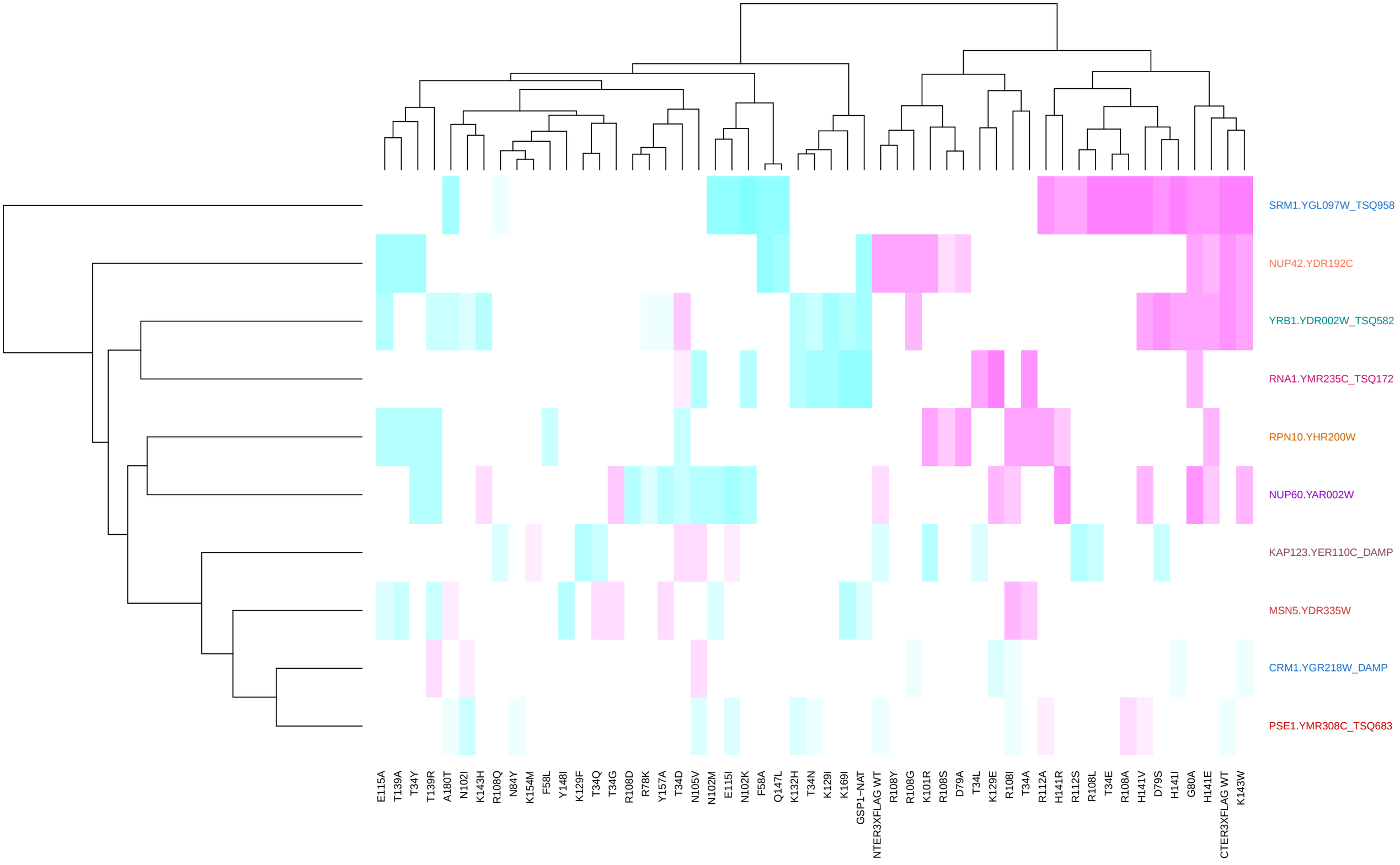
ribosomal small subunit biogenesis_GO_15_1_all



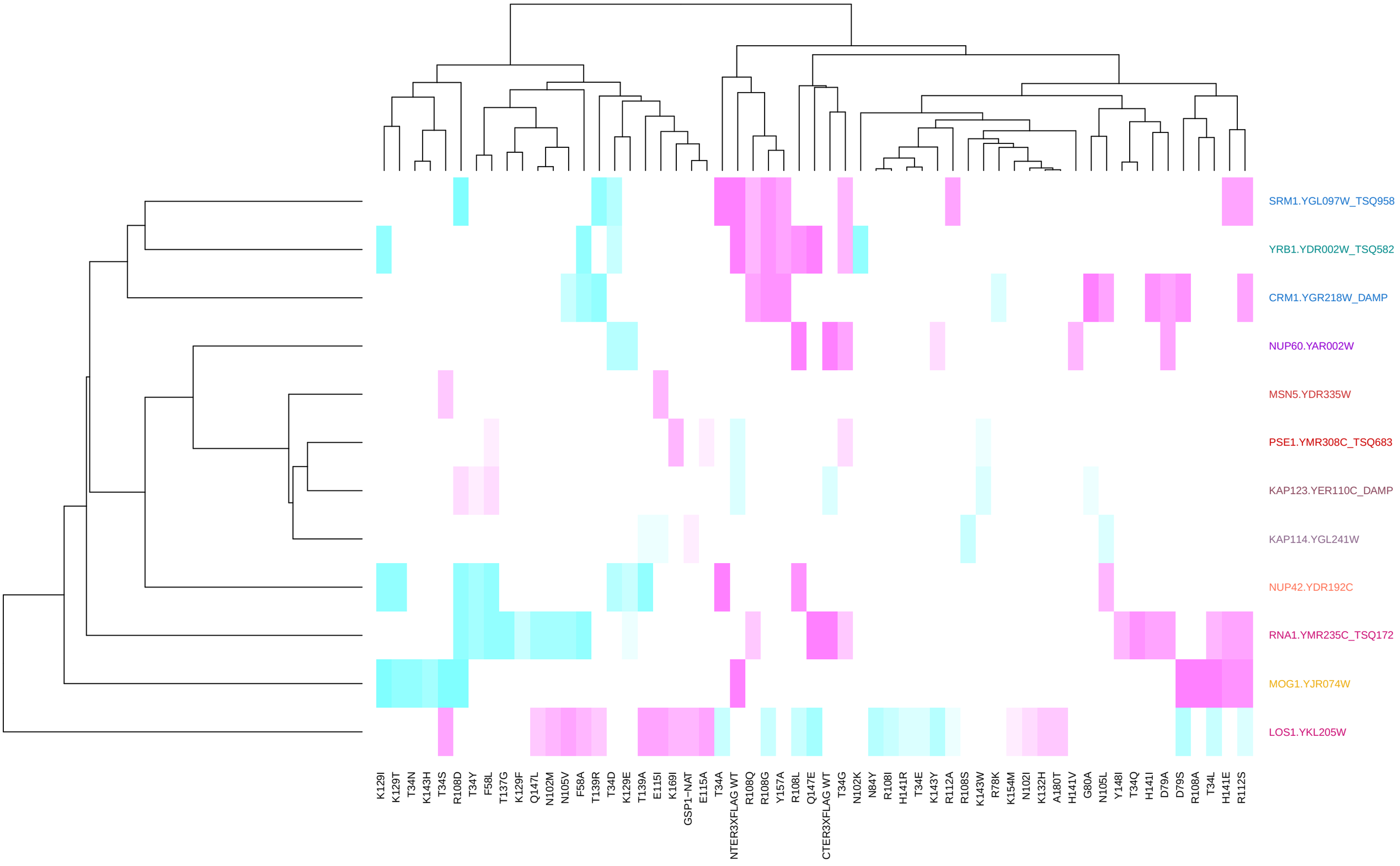
cellular response to DNA damage stimulus_GO_30_3_all



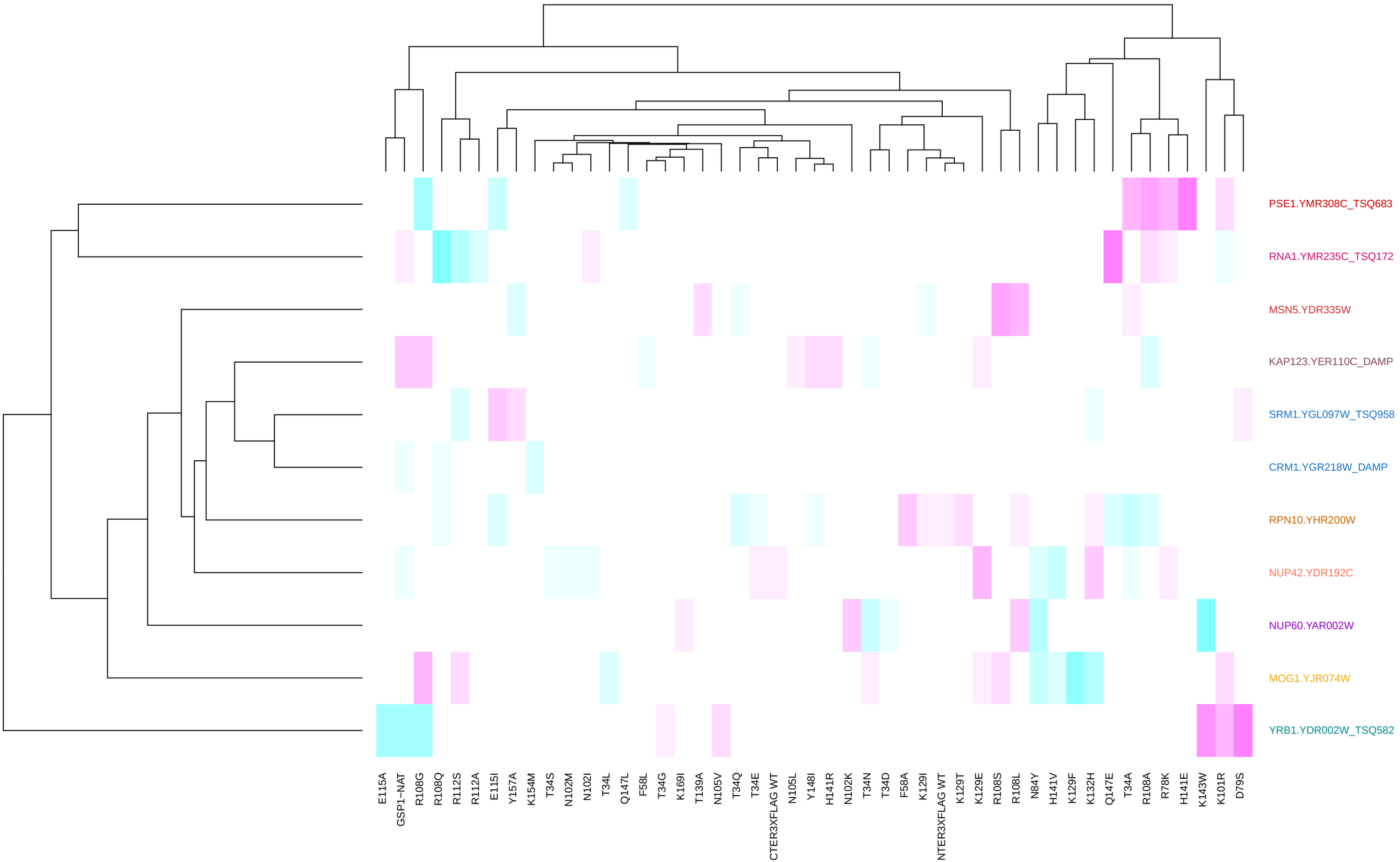
cell cycle_GO_15_3_all



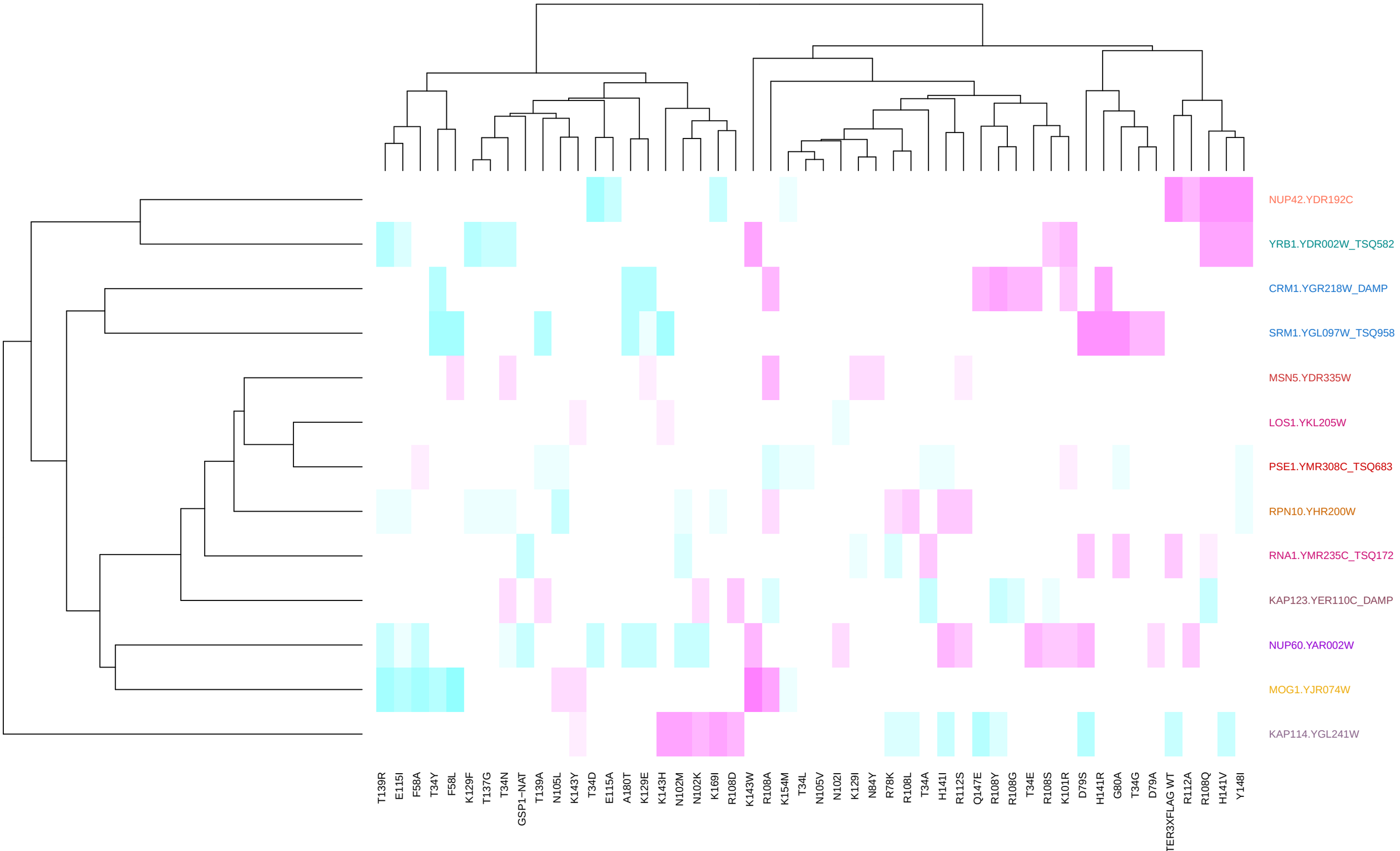
endomembrane system_GO_15_3_mut



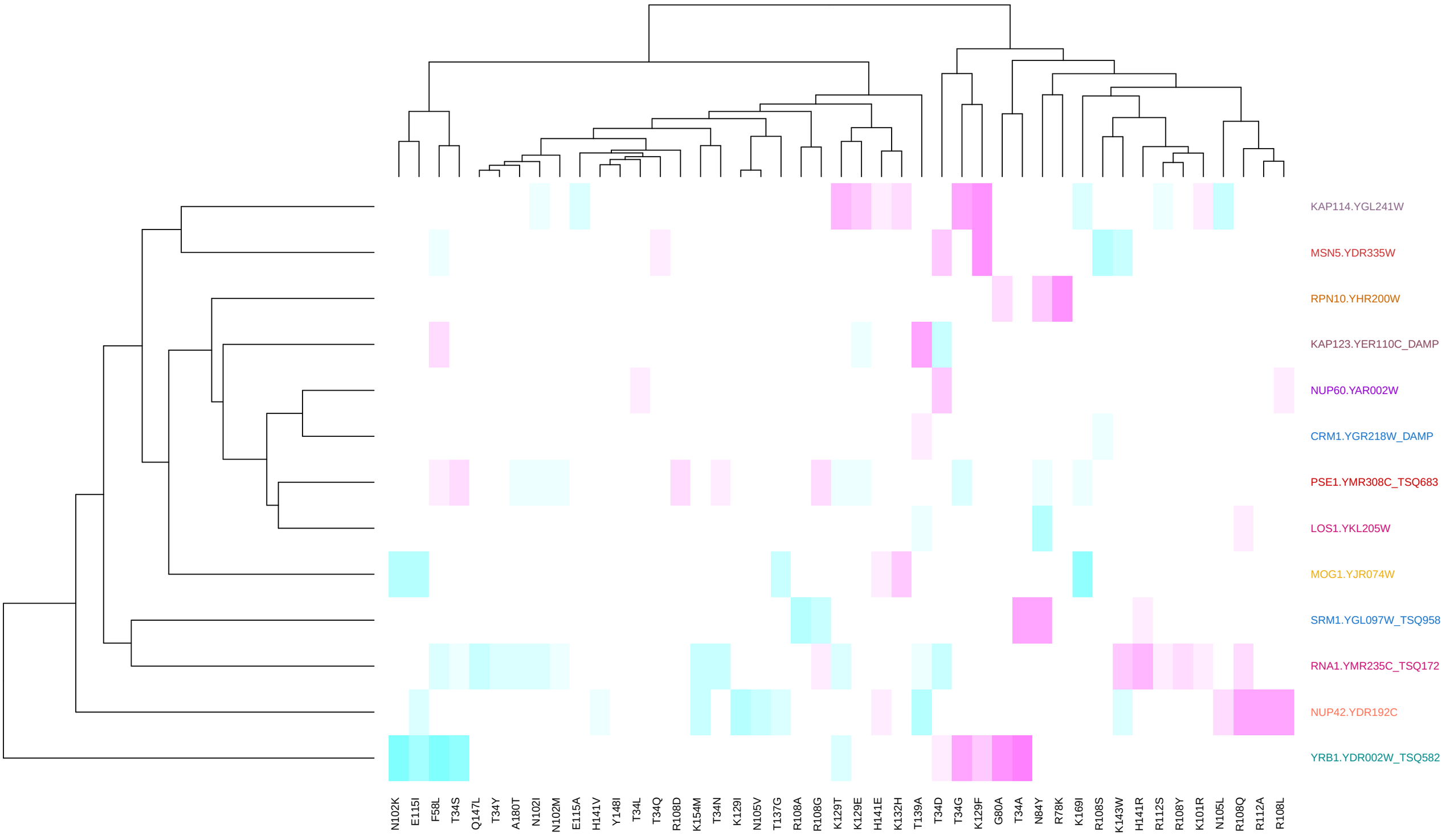
regulation of organelle organization_GO_15_1_all



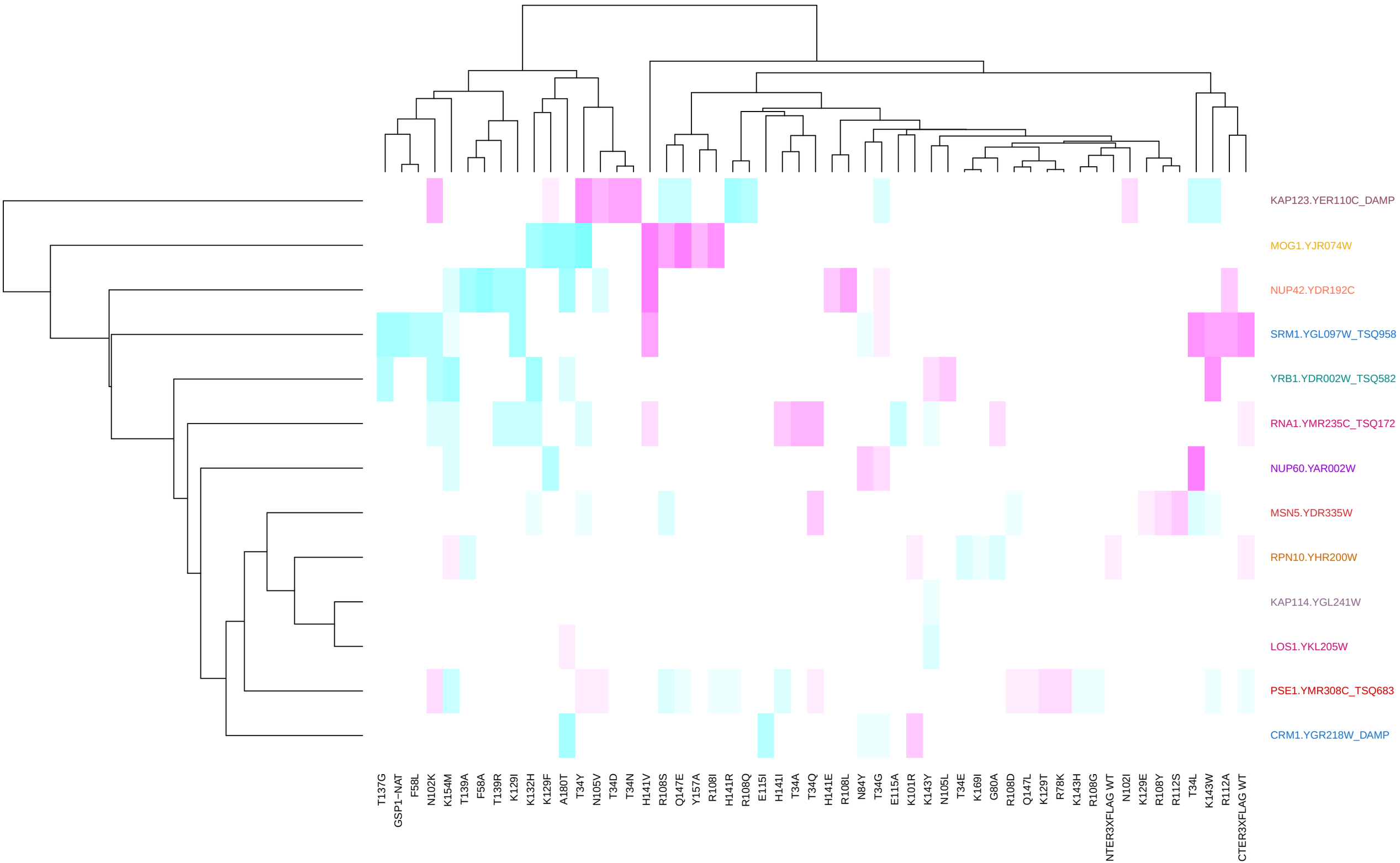
chromatin organization_GO_30_2_all



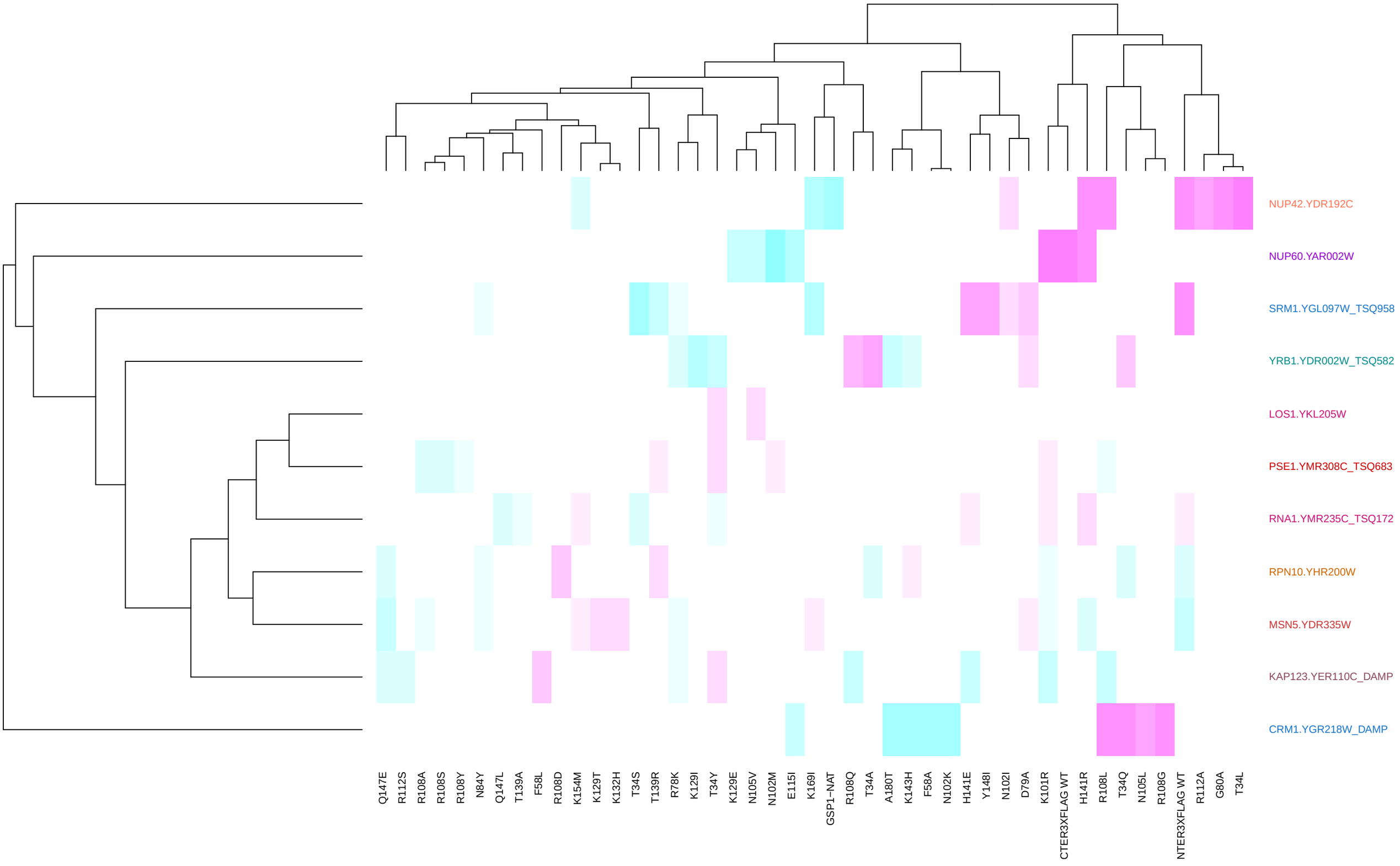
DNA binding_GO_15_3_mut



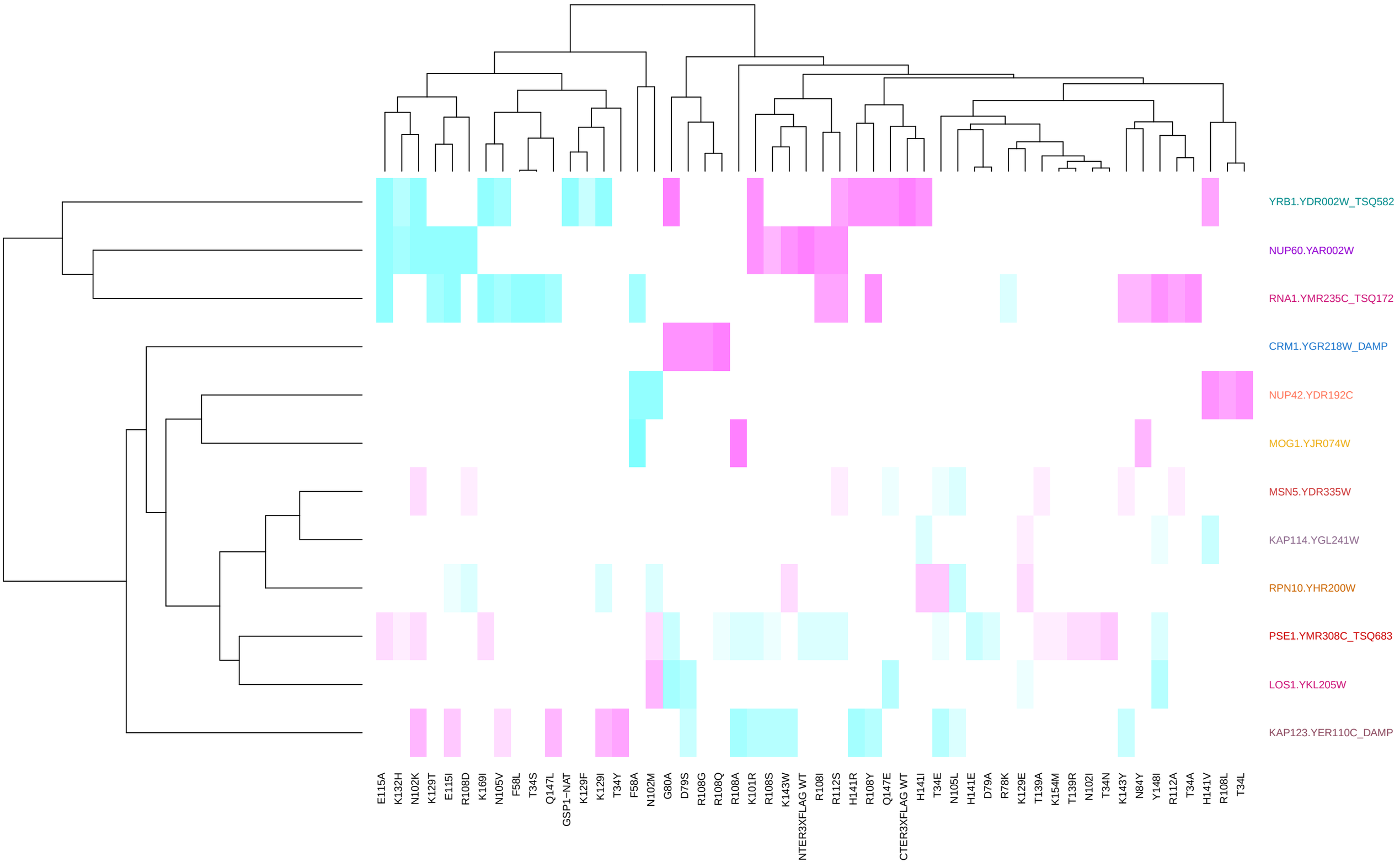
transcription_GO_15_1_mut



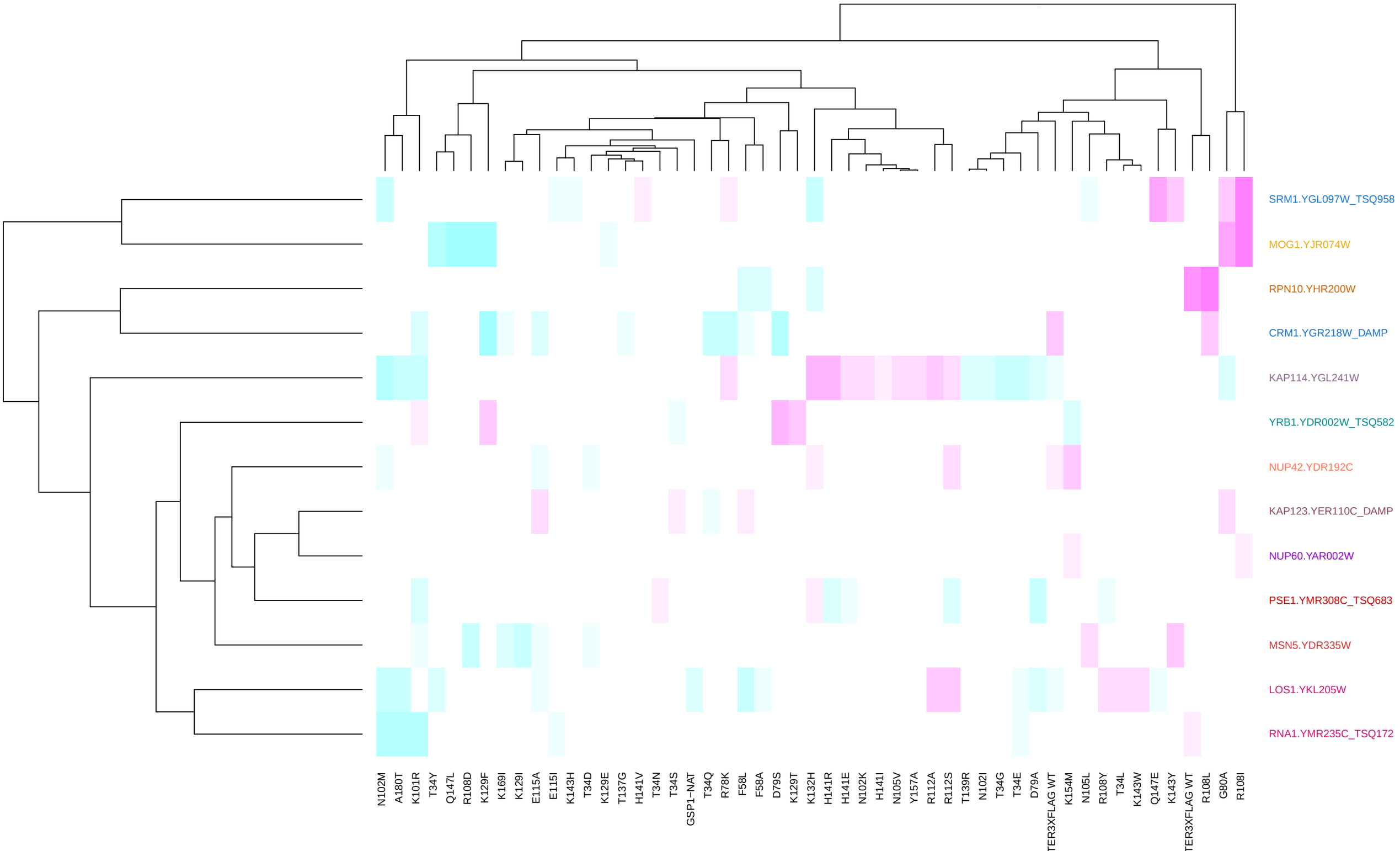
transcription_GO_30_4_all



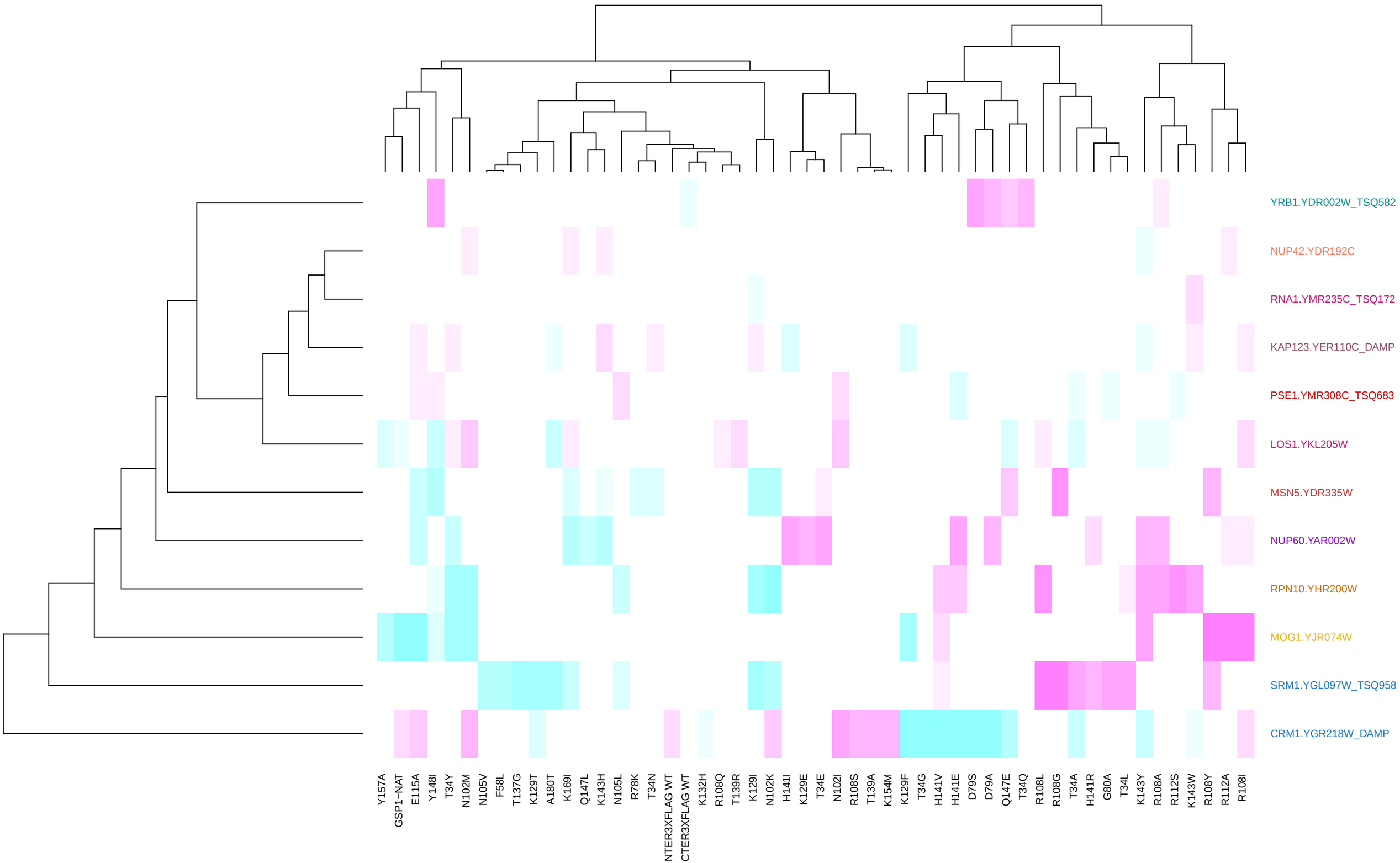
nucleobase−containing compound transport



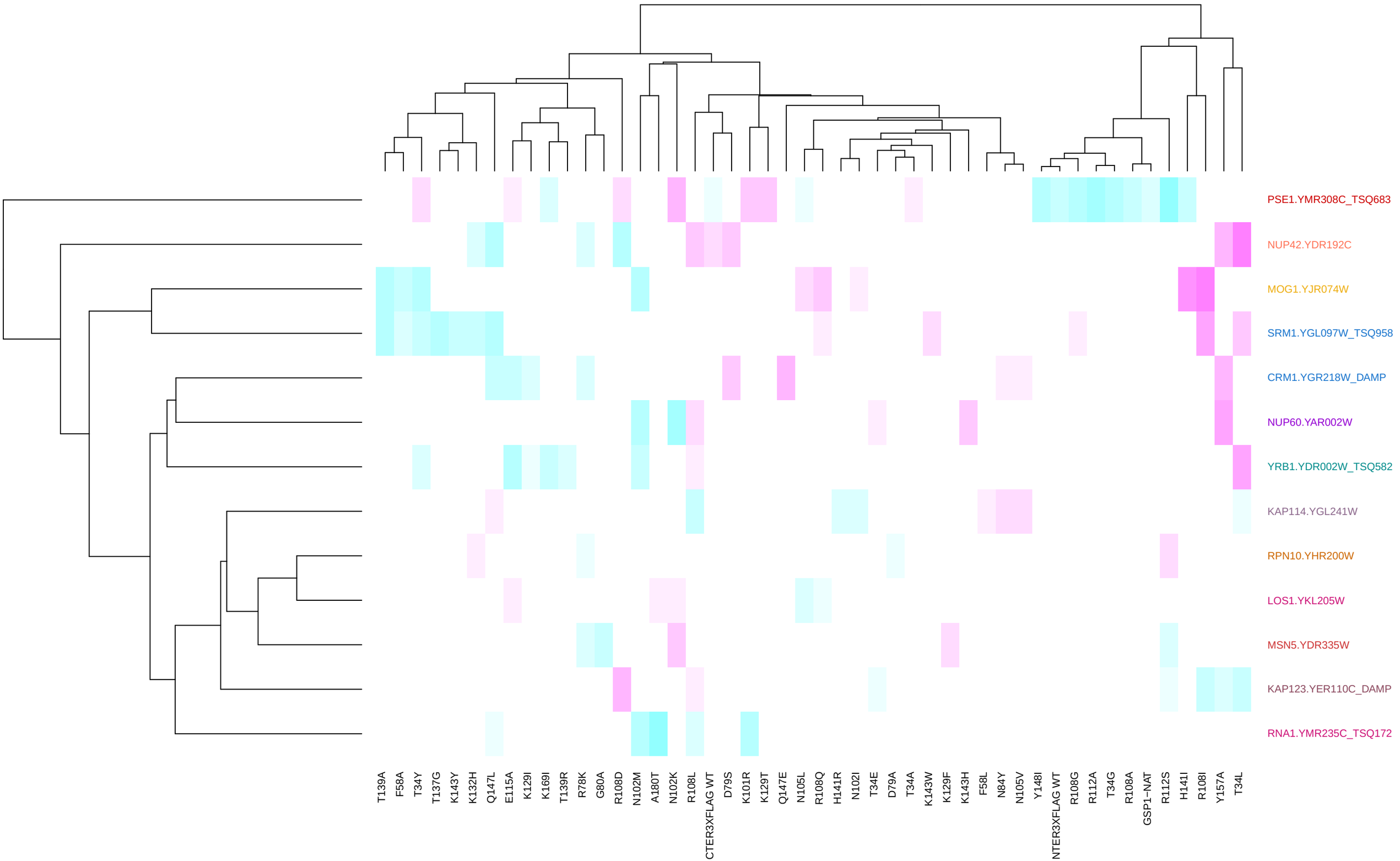
protein modification by small protein conjugation or removal



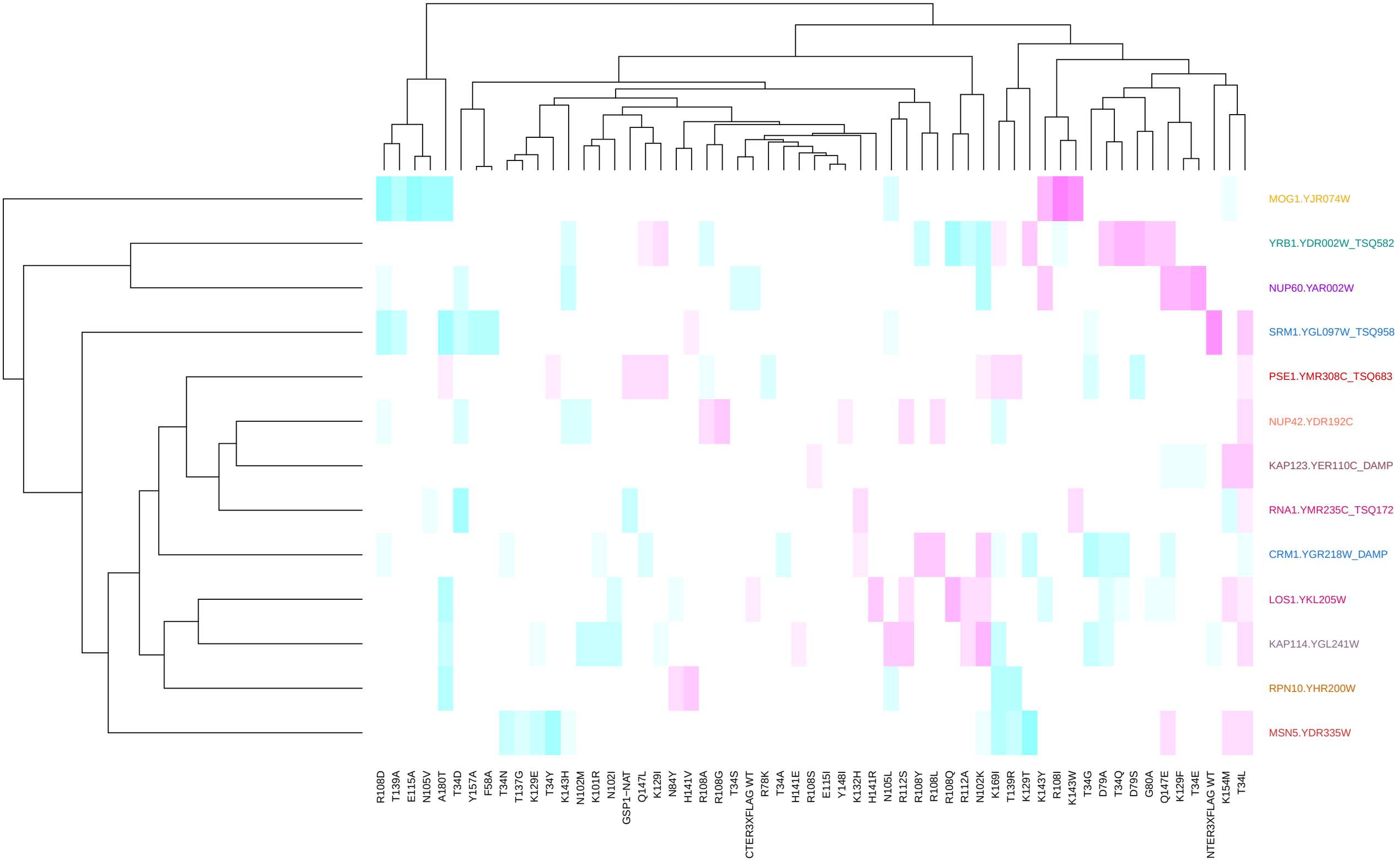
protein modification by small protein conjugation or removal_GO_15_1_mut



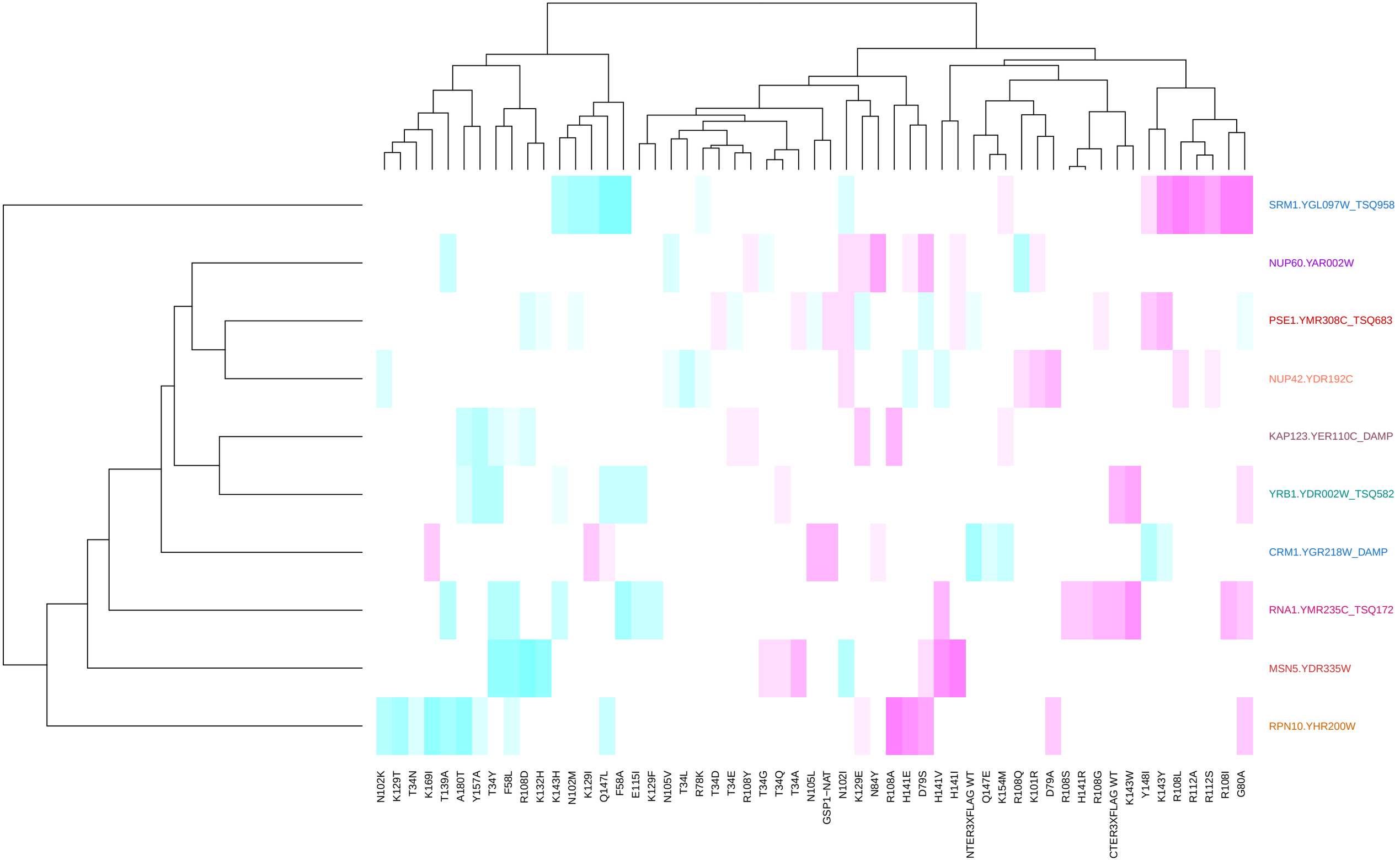
chromatin organization



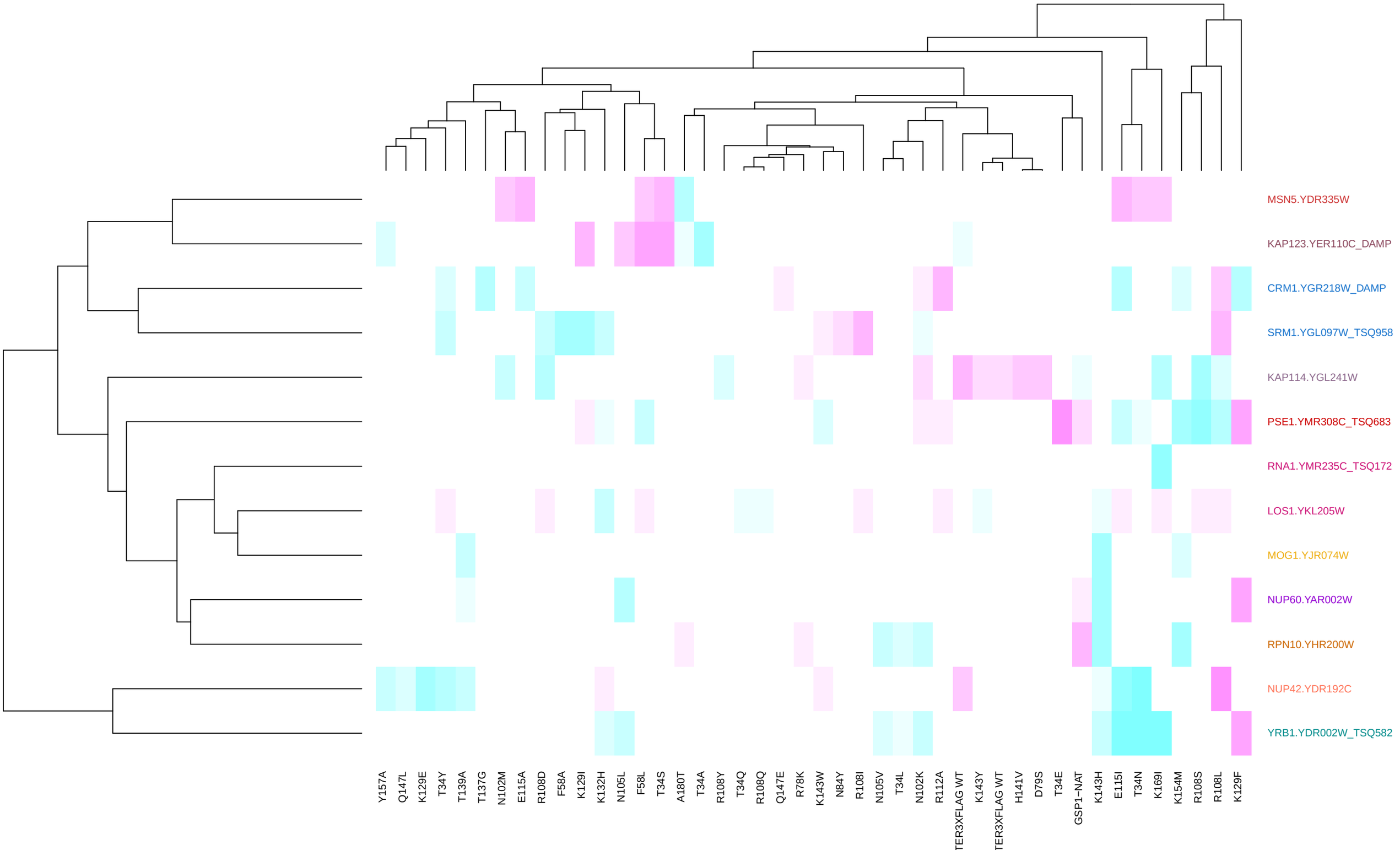
protein modification by small protein conjugation or removal_GO_30_1_mut



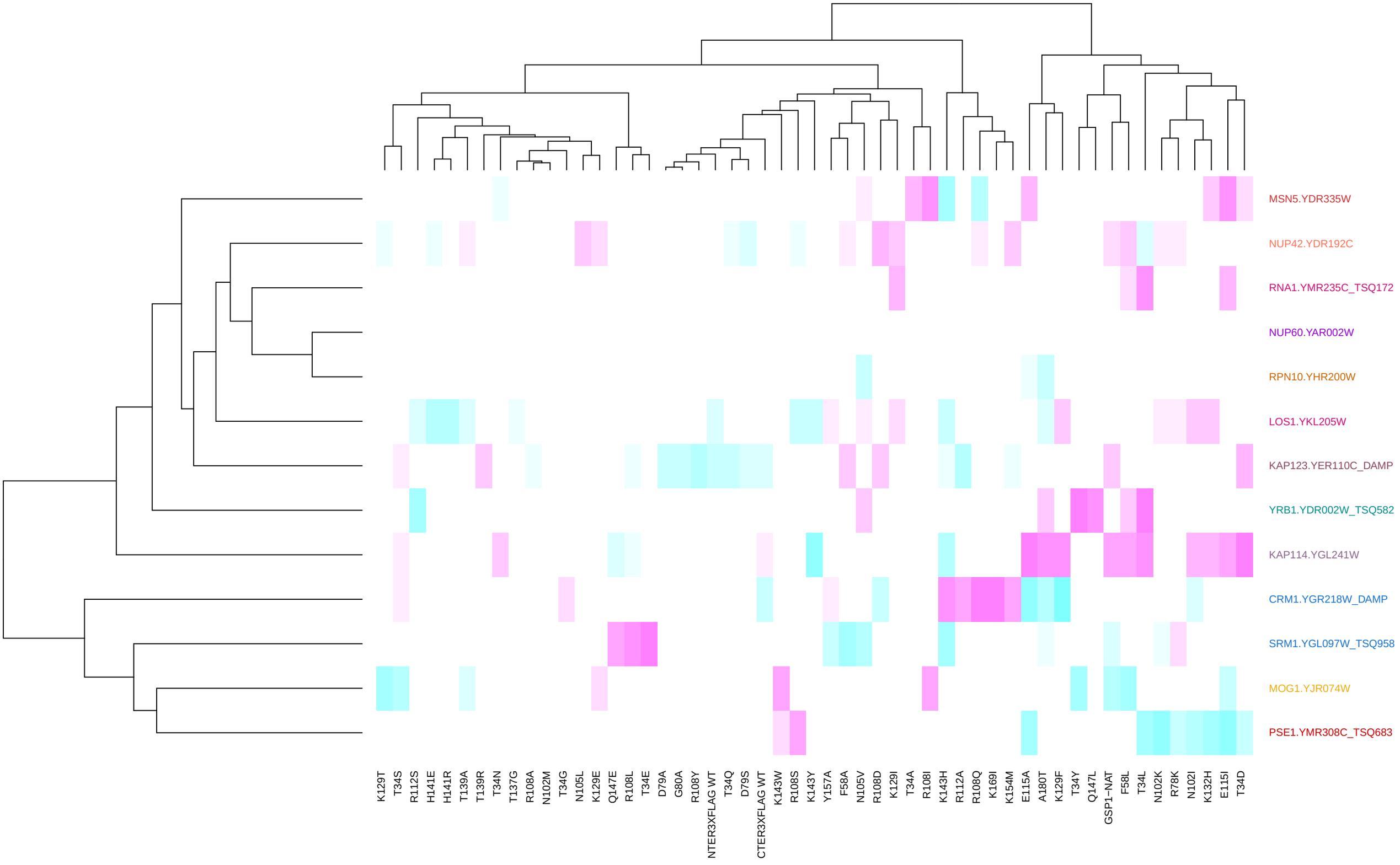
sig_Gsp1_GI_15_11_all



sig_Gsp1_GI_30_2_mut



sig_Gsp1_GI_30_3_all



cellular response to DNA damage stimulus_GO_15_3_mut