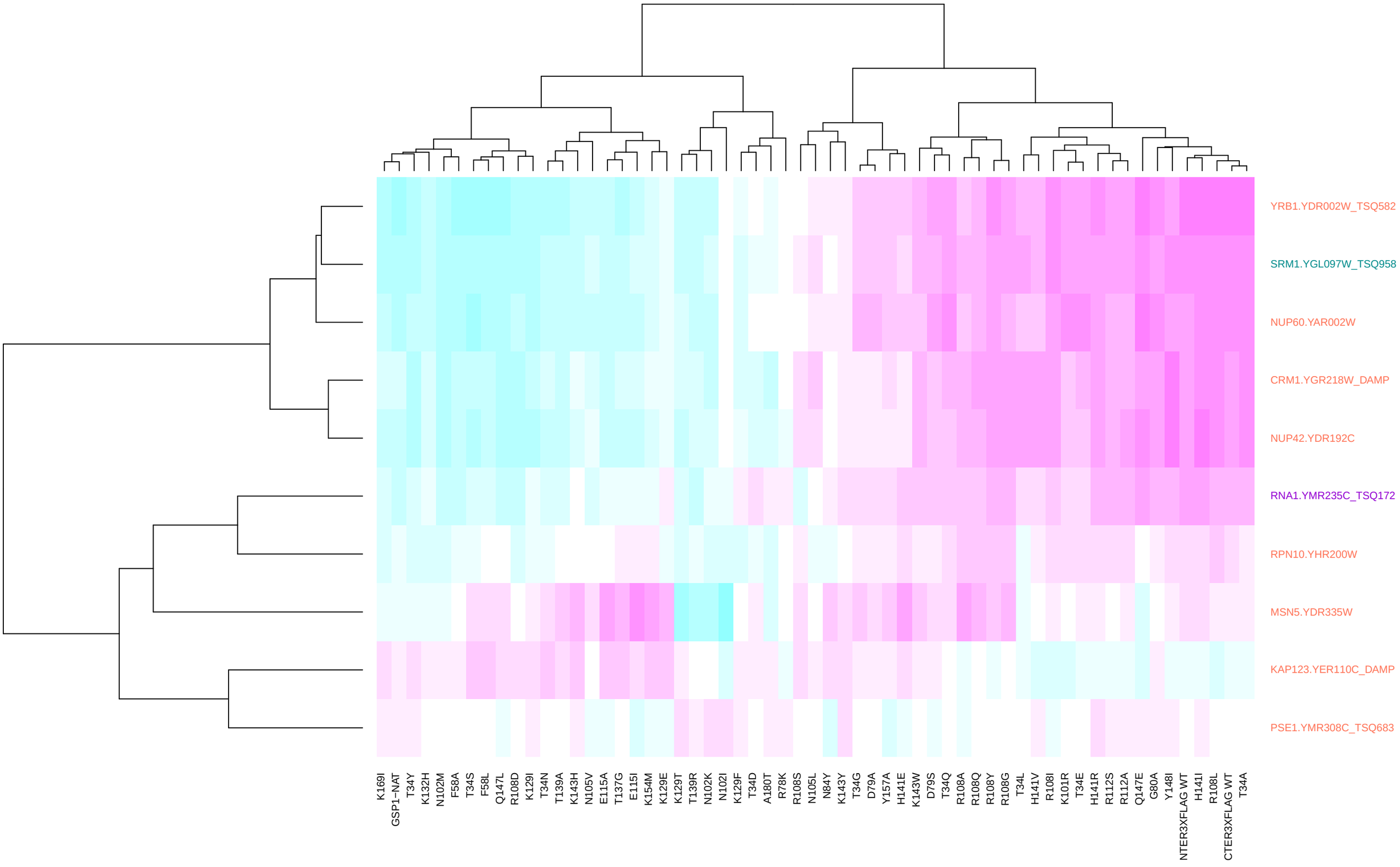
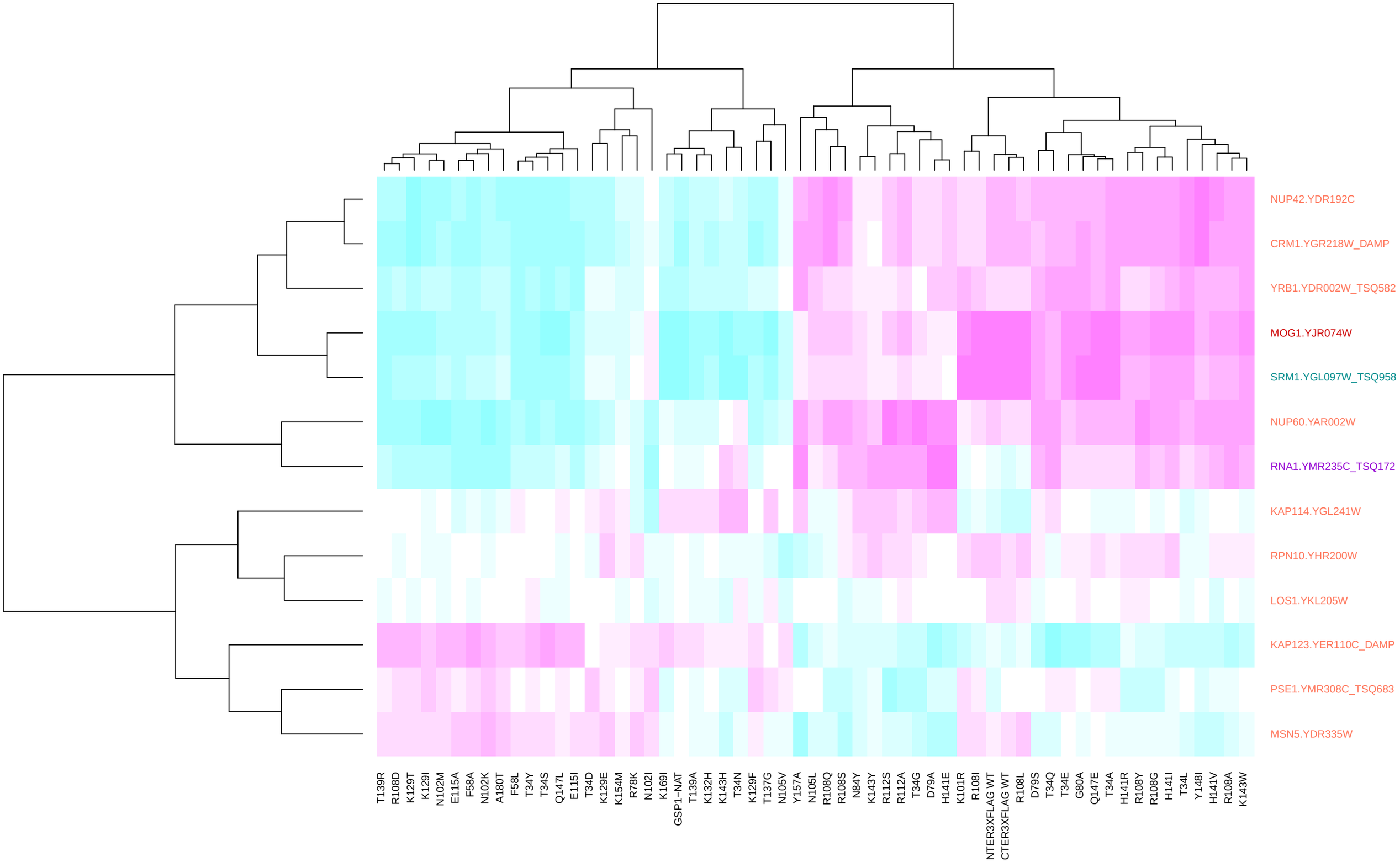
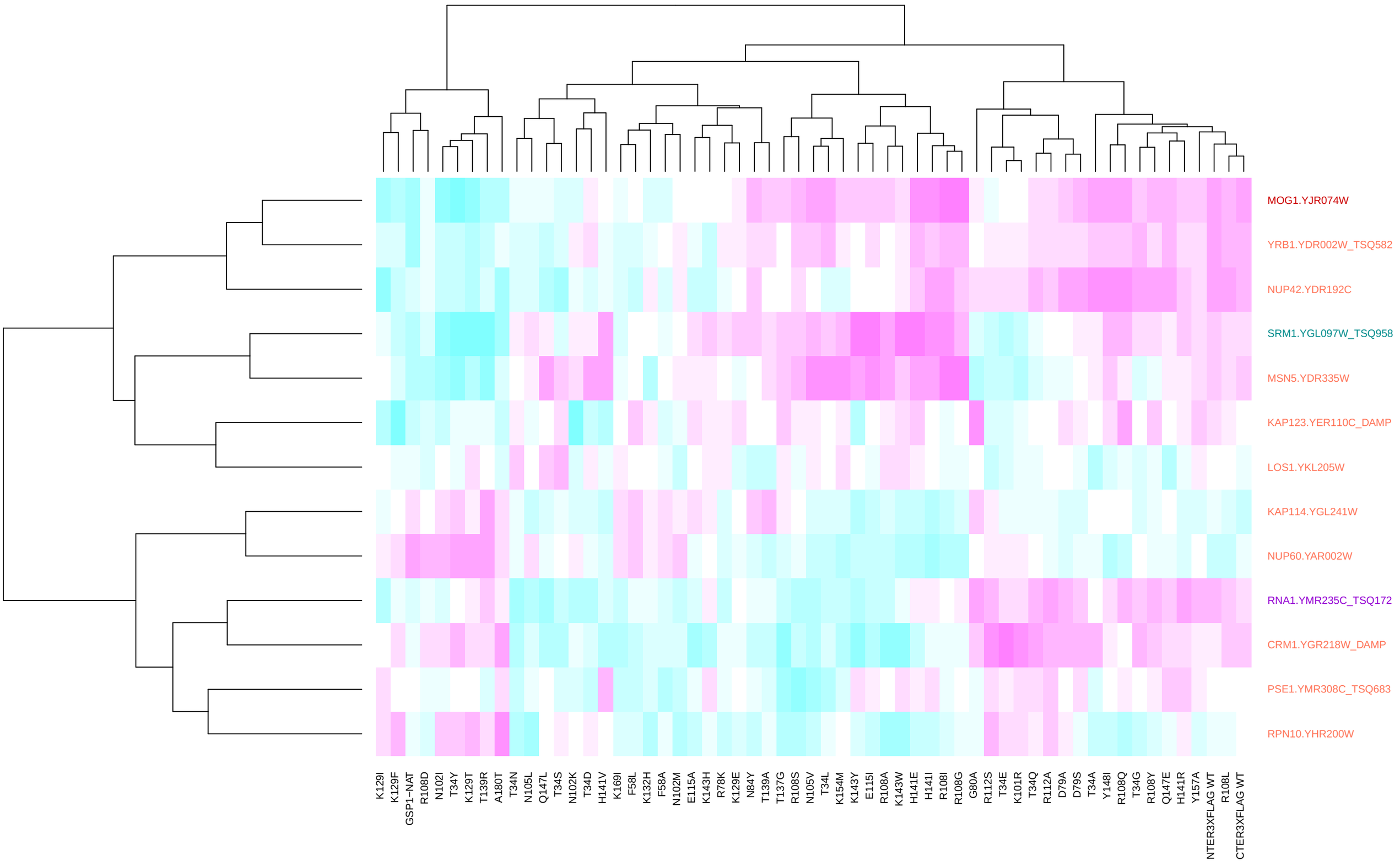
endomembrane system



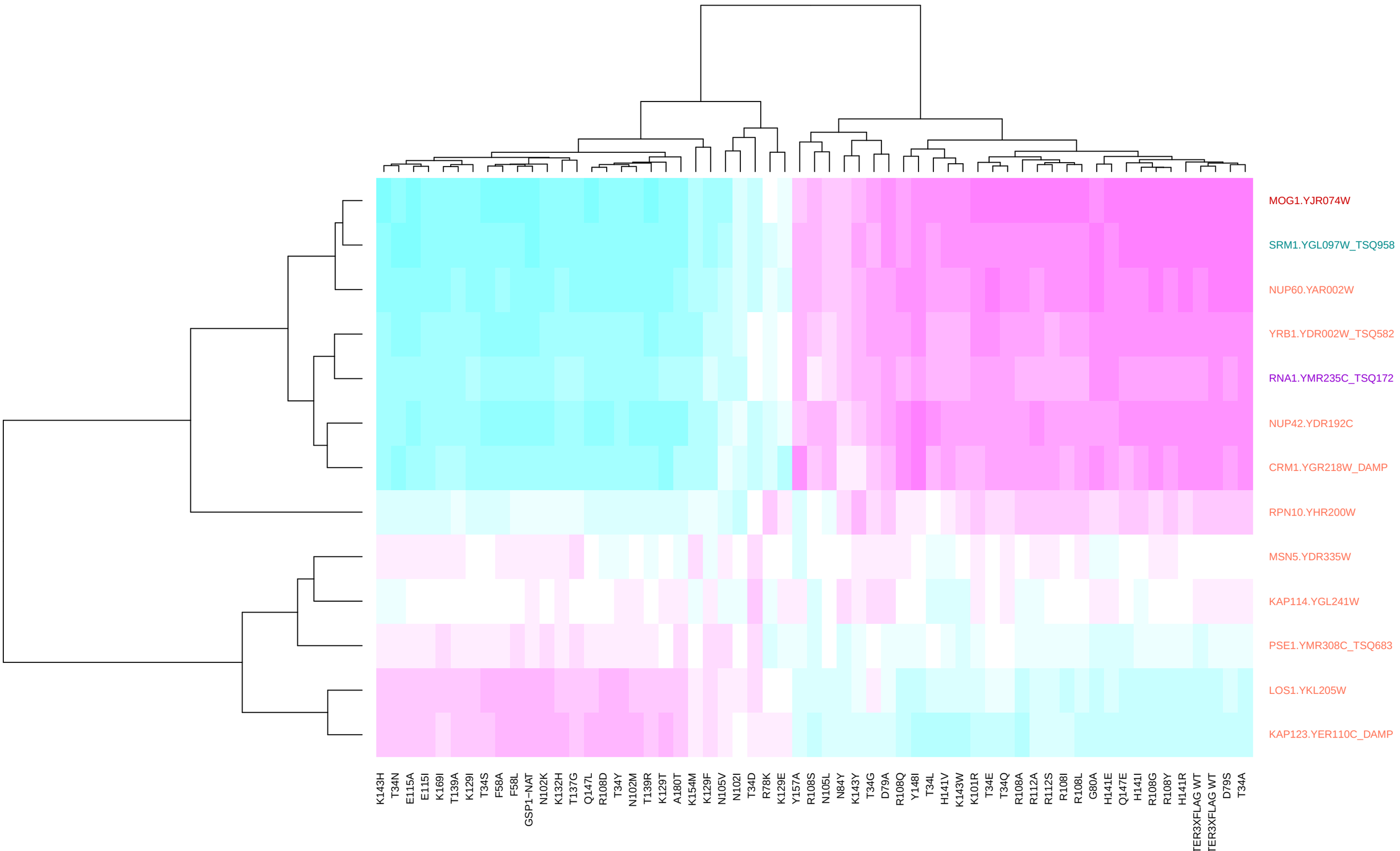
chromatin organization_GO_15_1_mut



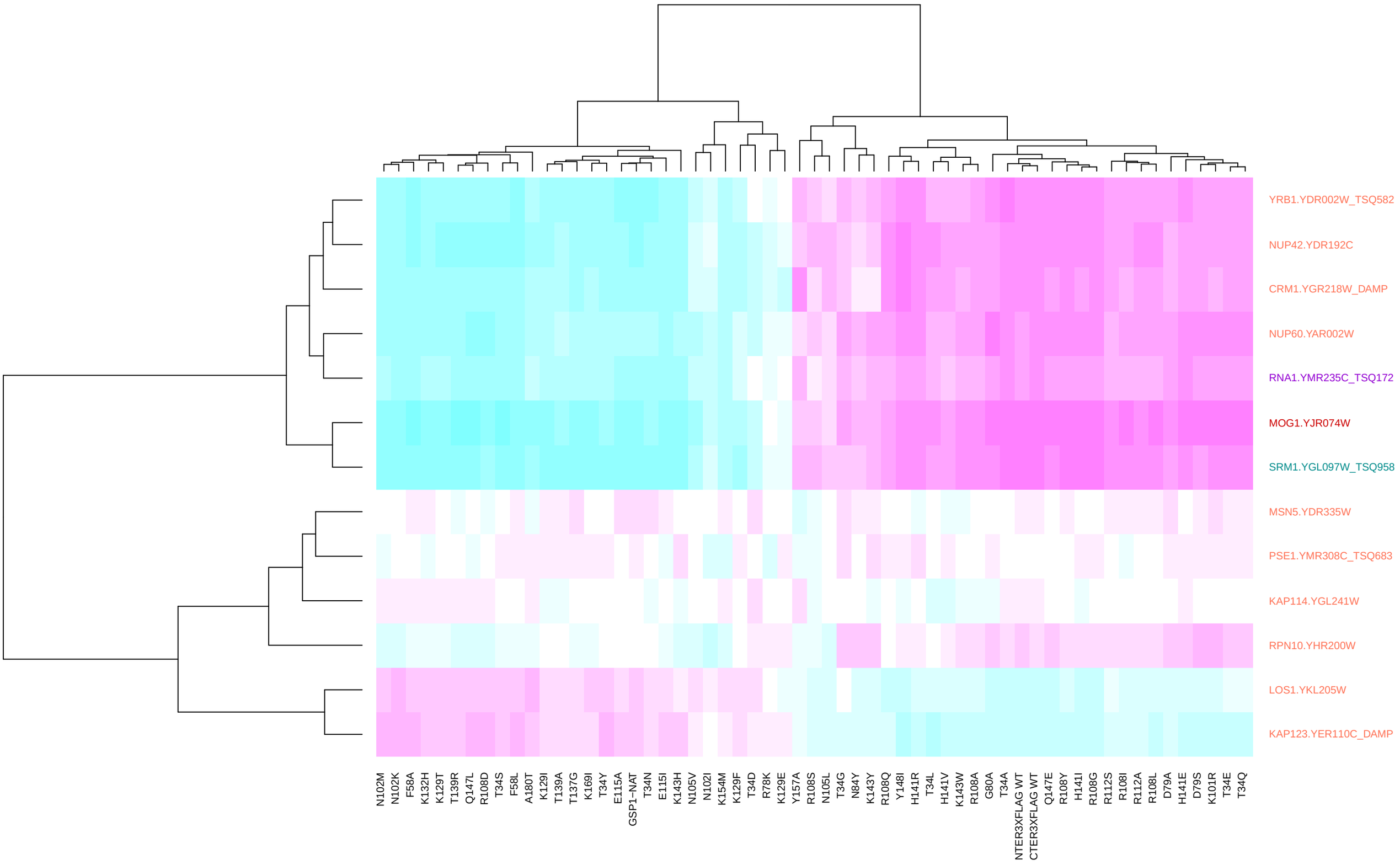
lipids_GO_15_2_all



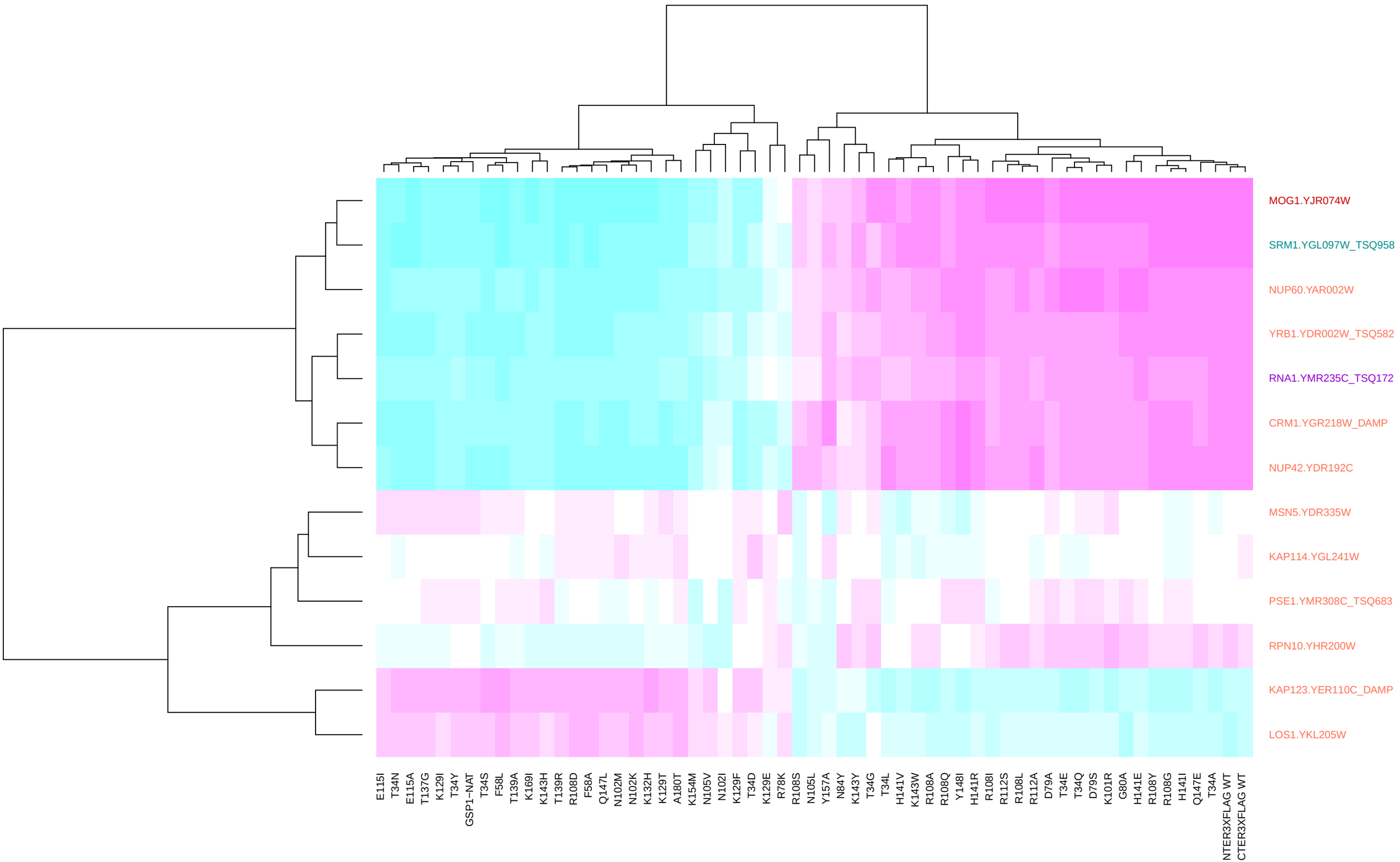
nuclear transport



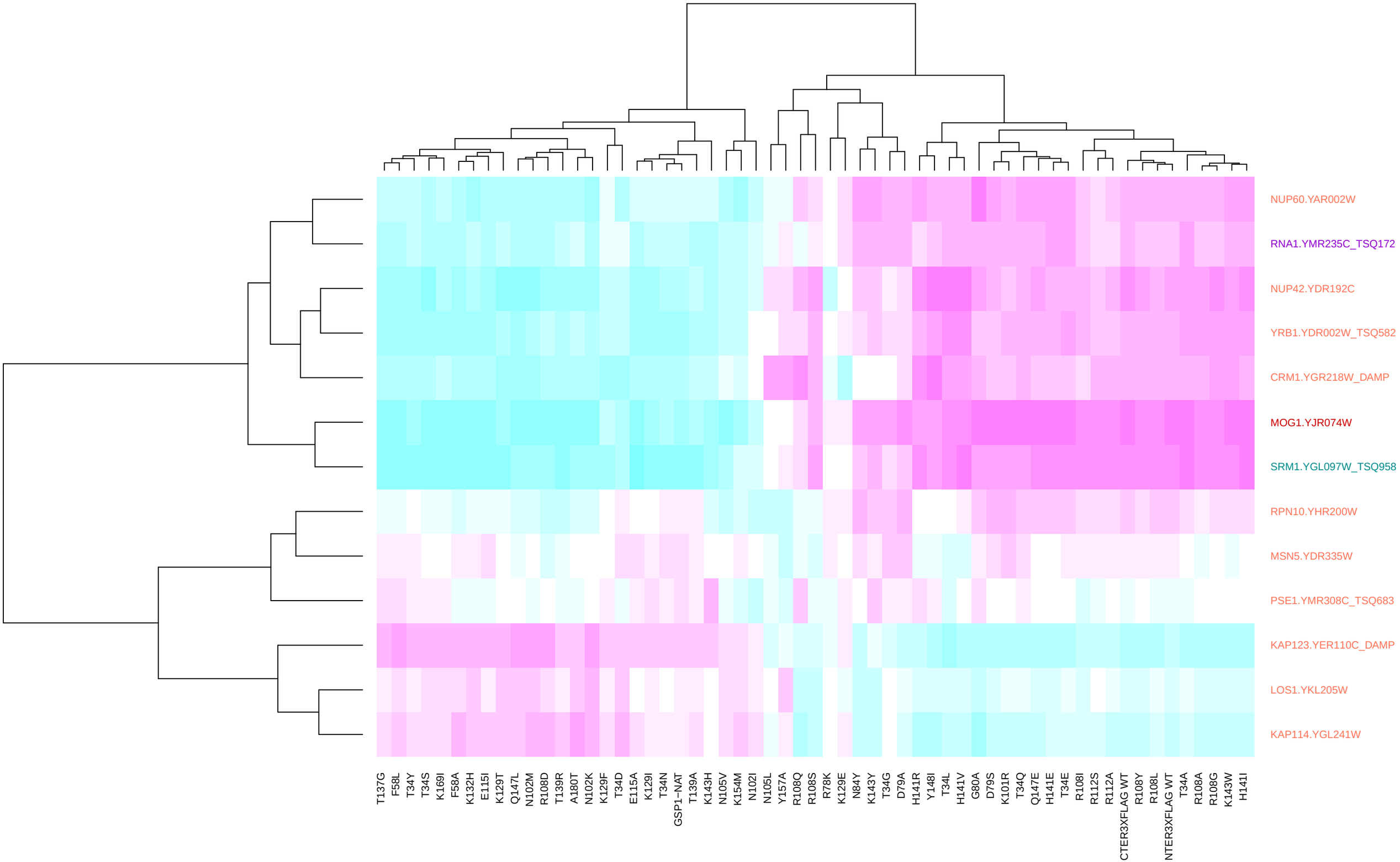
nuclear transport and organization



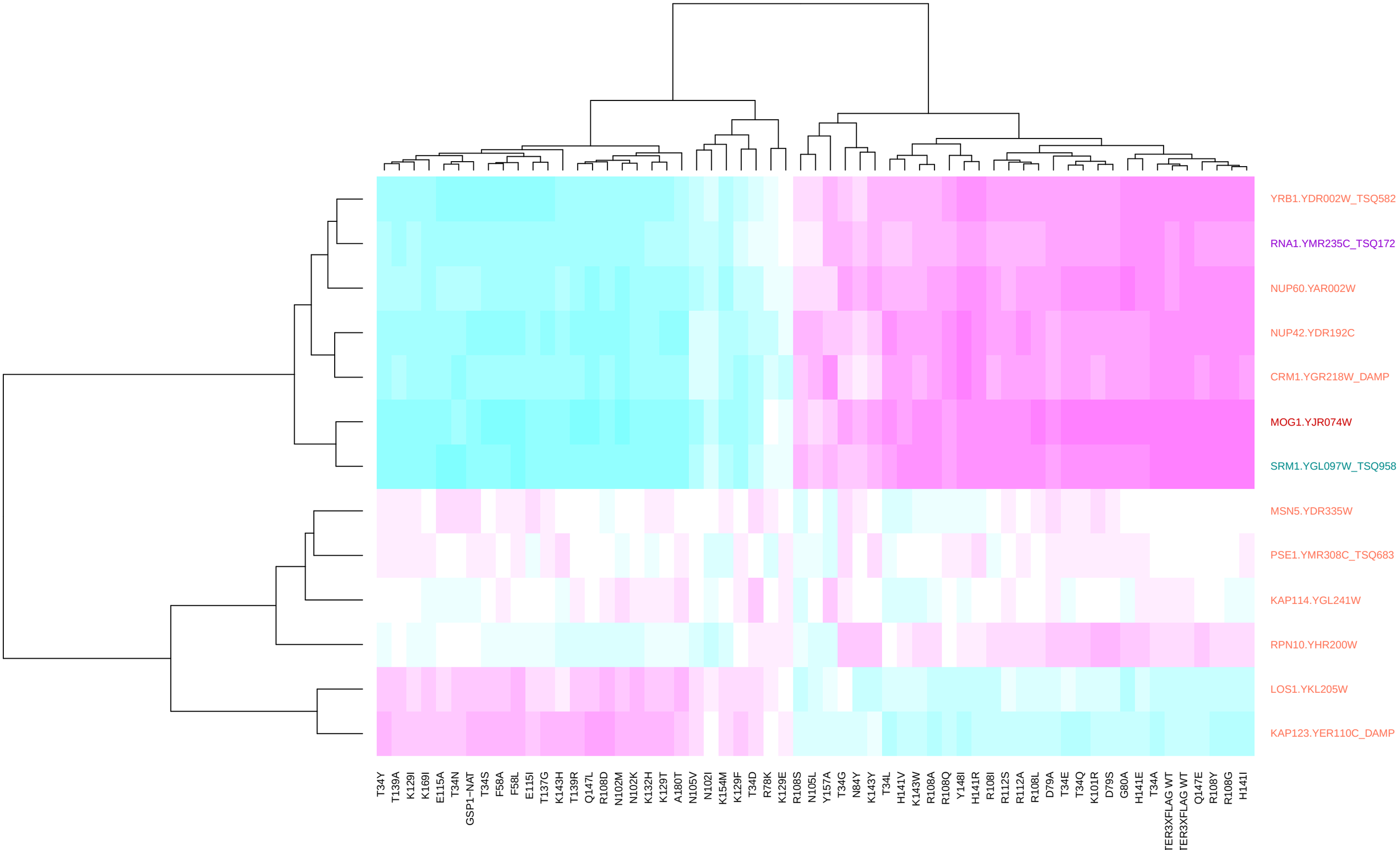
nuclear transport and organization_GO_15_1_mut



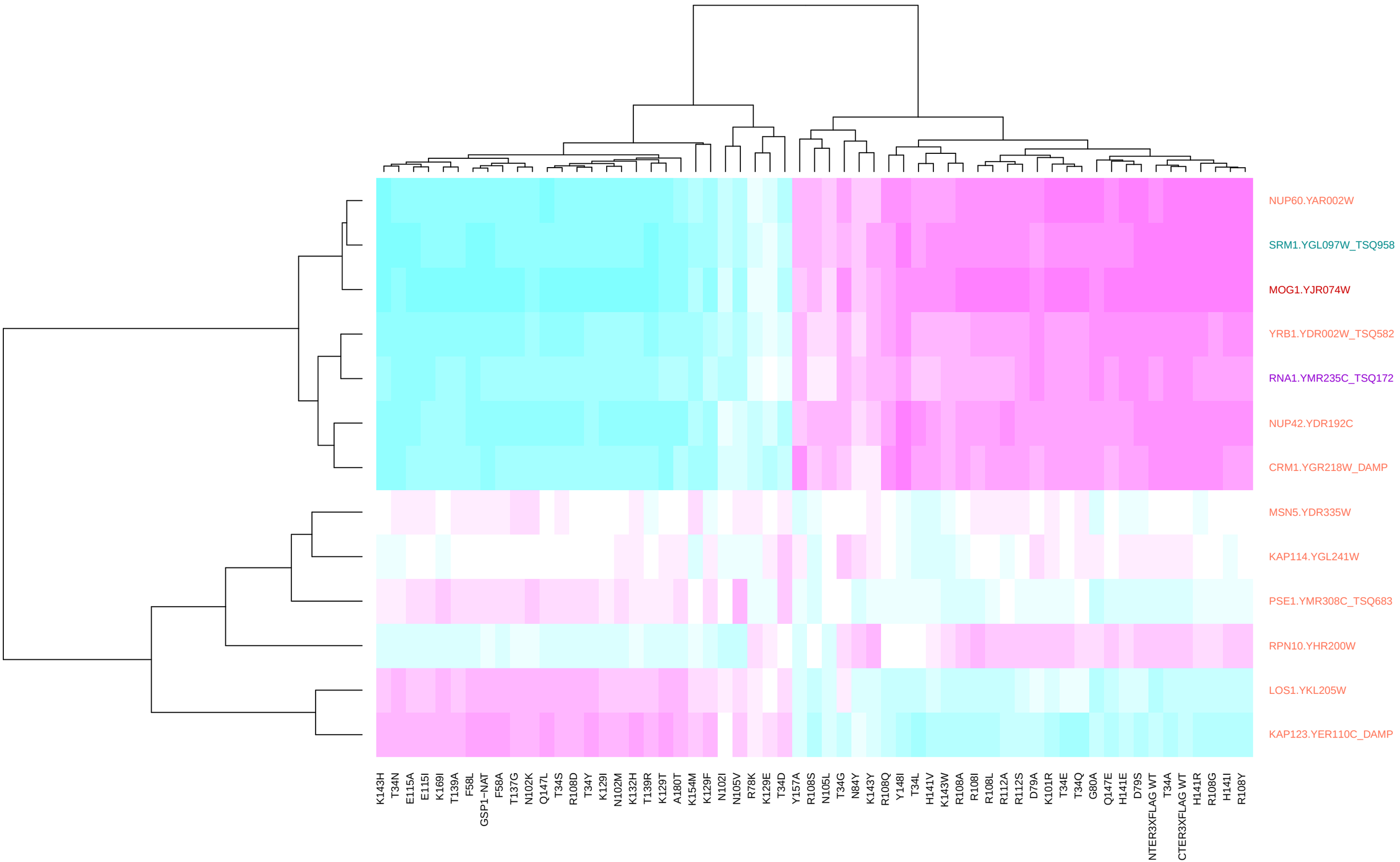
nuclear transport and organization_GO_15_2_all



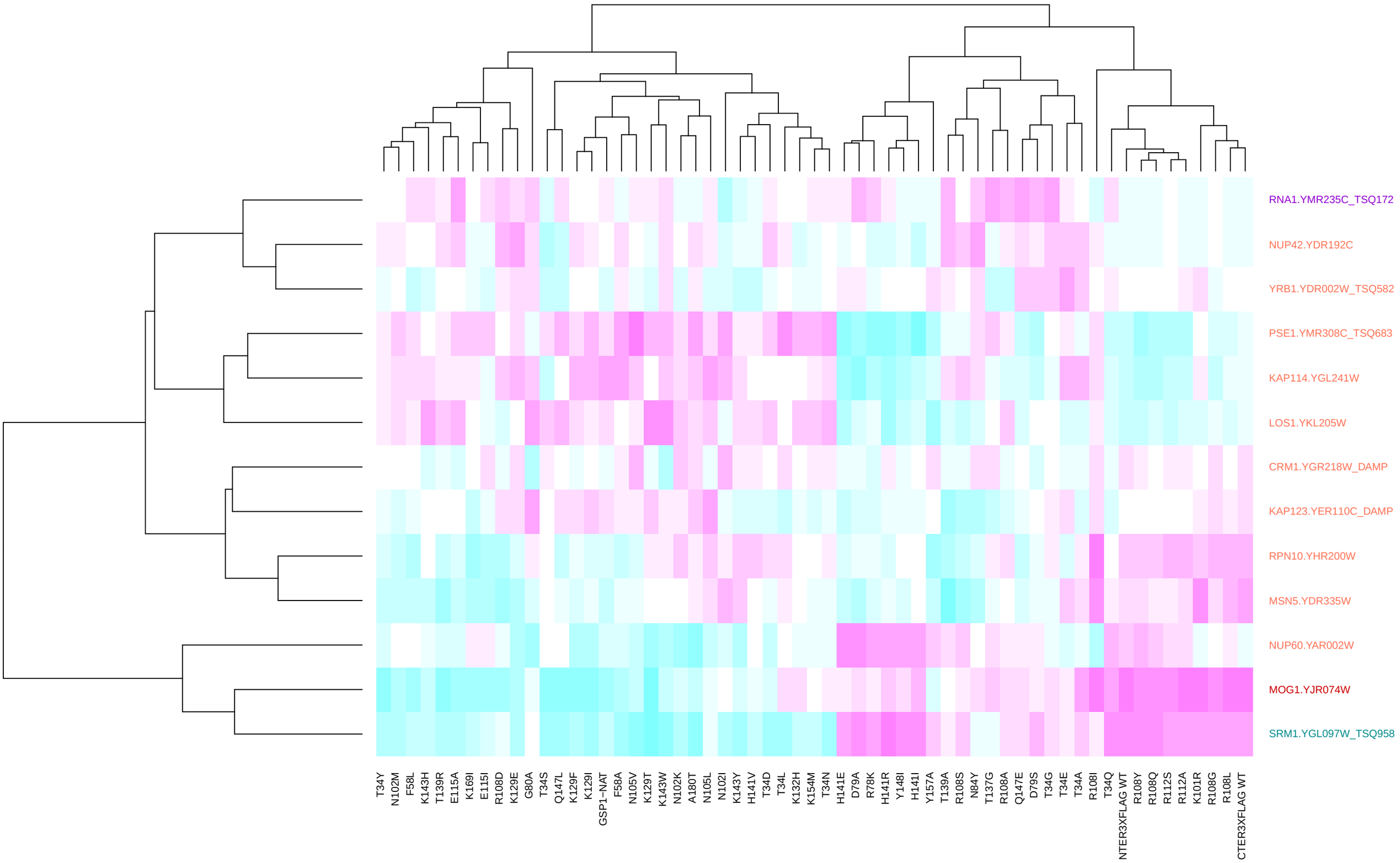
nuclear transport and organization_GO_30_1_all



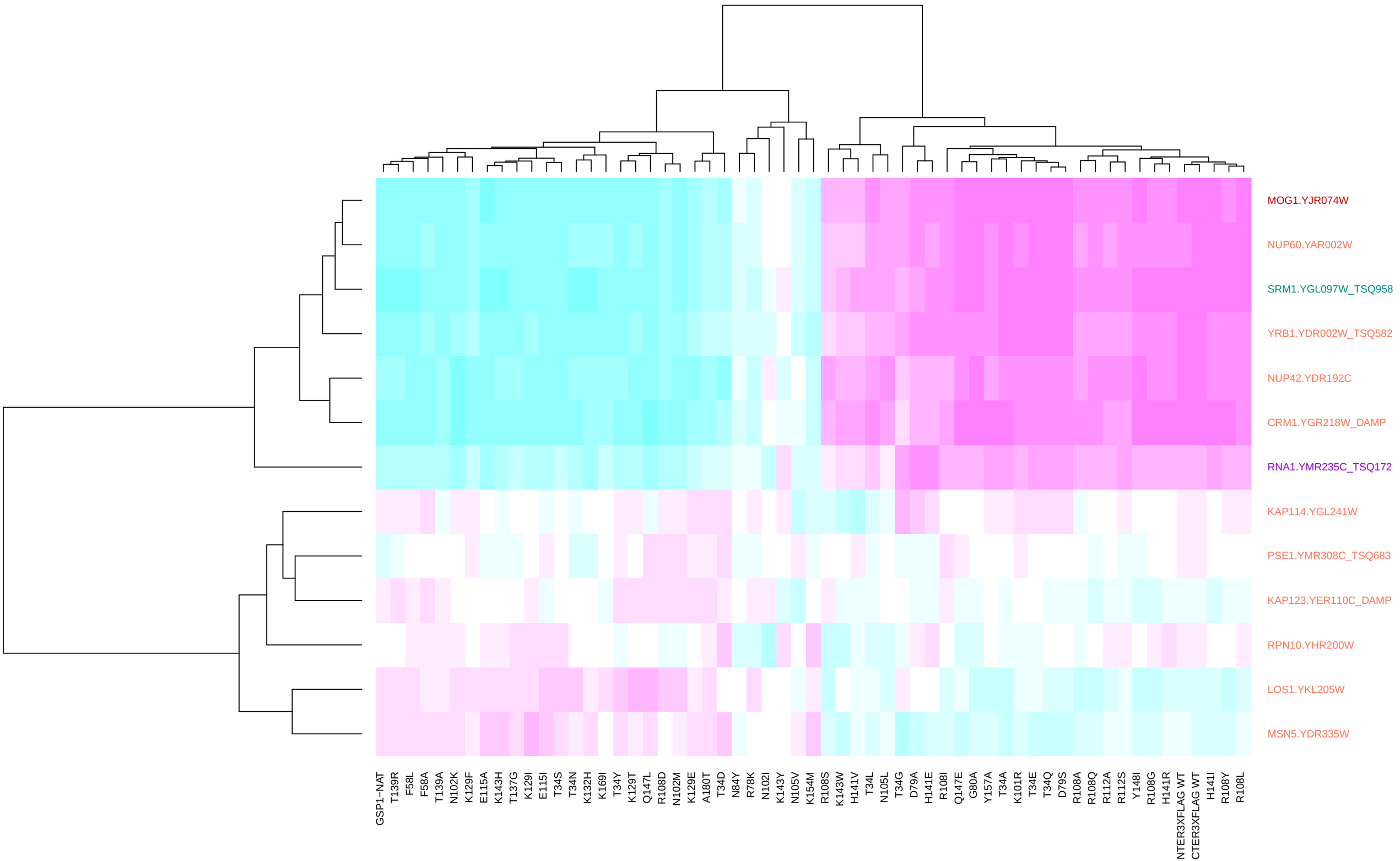
nuclear transport_GO_15_1_mut



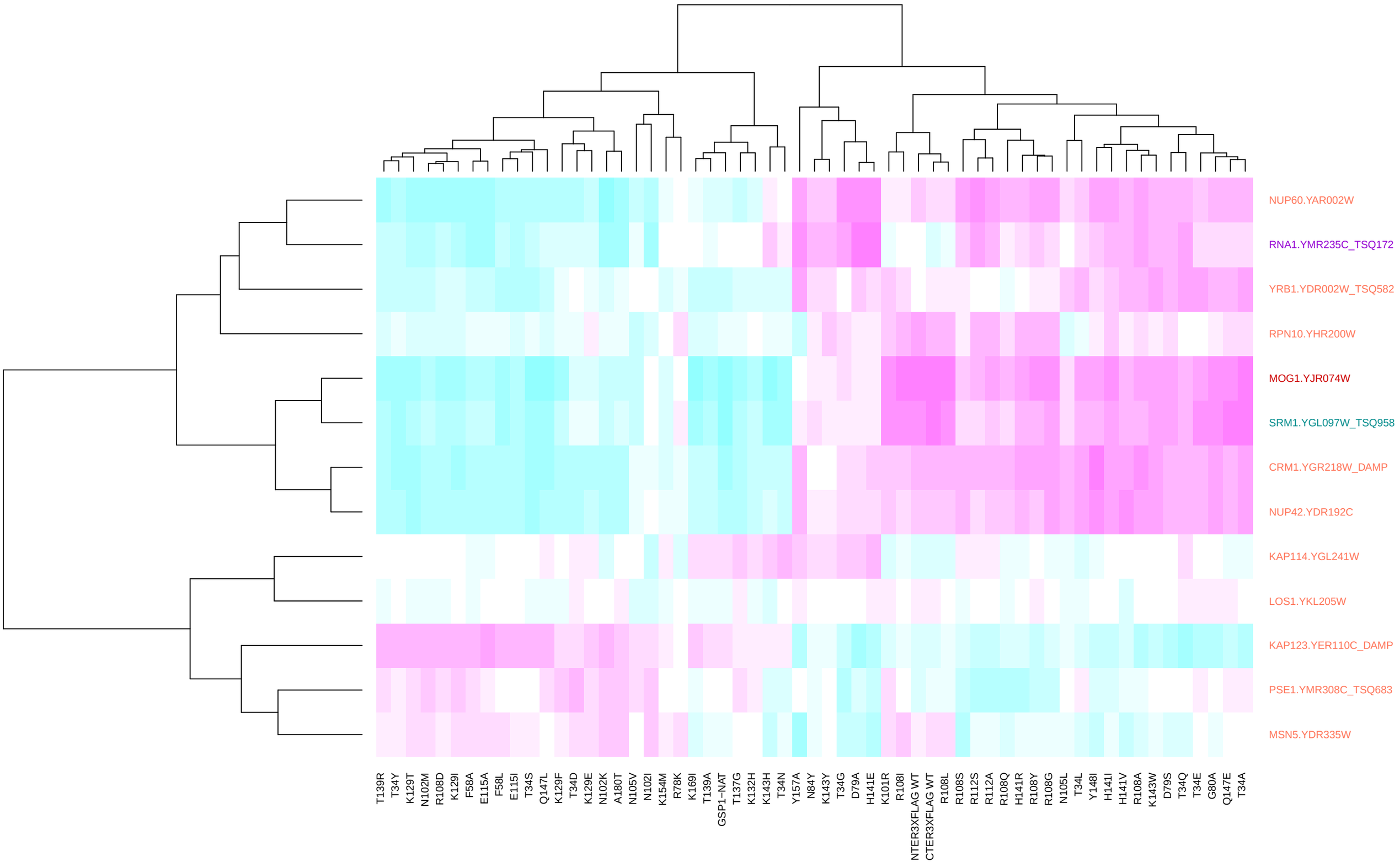
peptidyl−amino acid modification_GO_15_2_mut



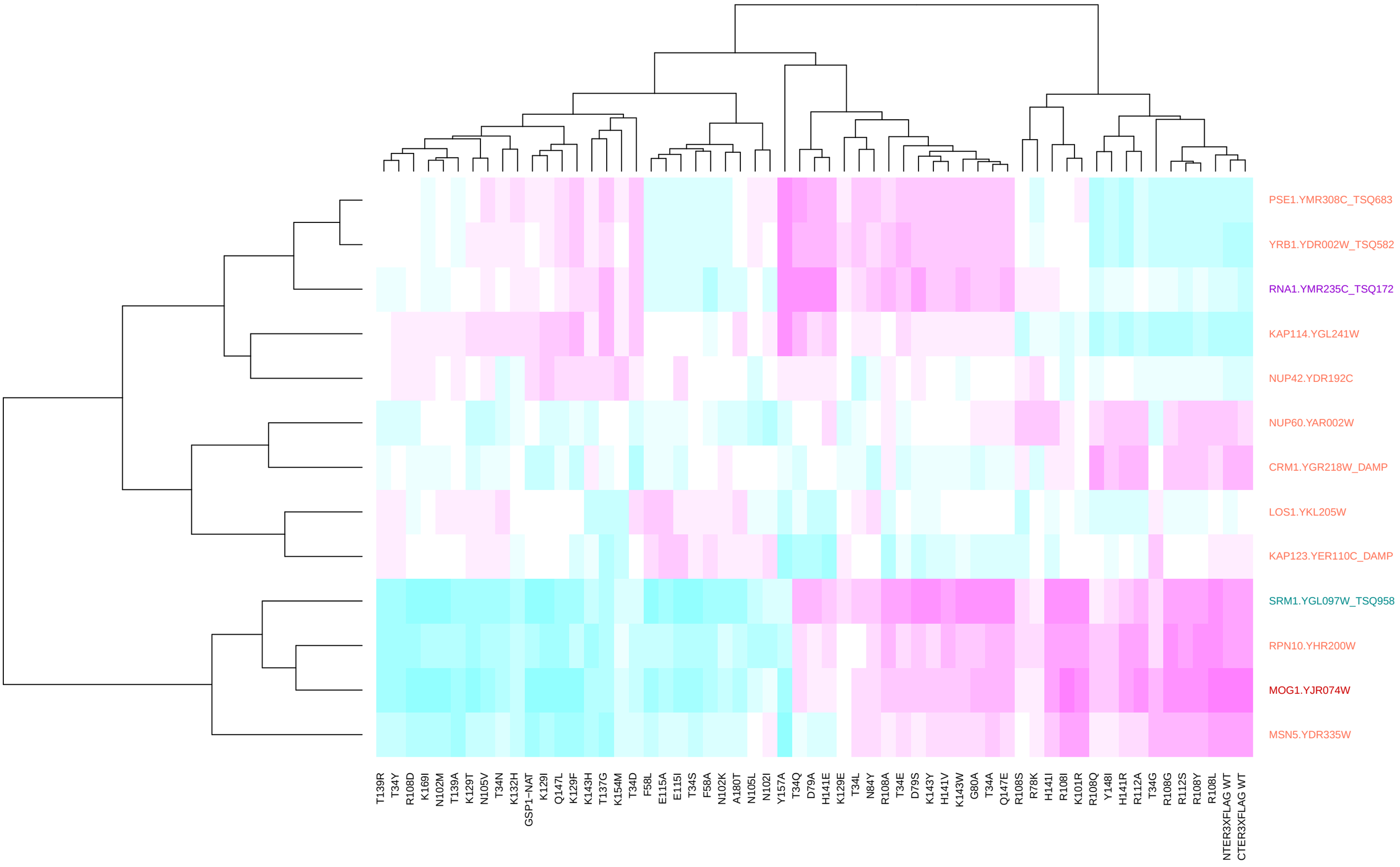
protein targeting_GO_15_3_all



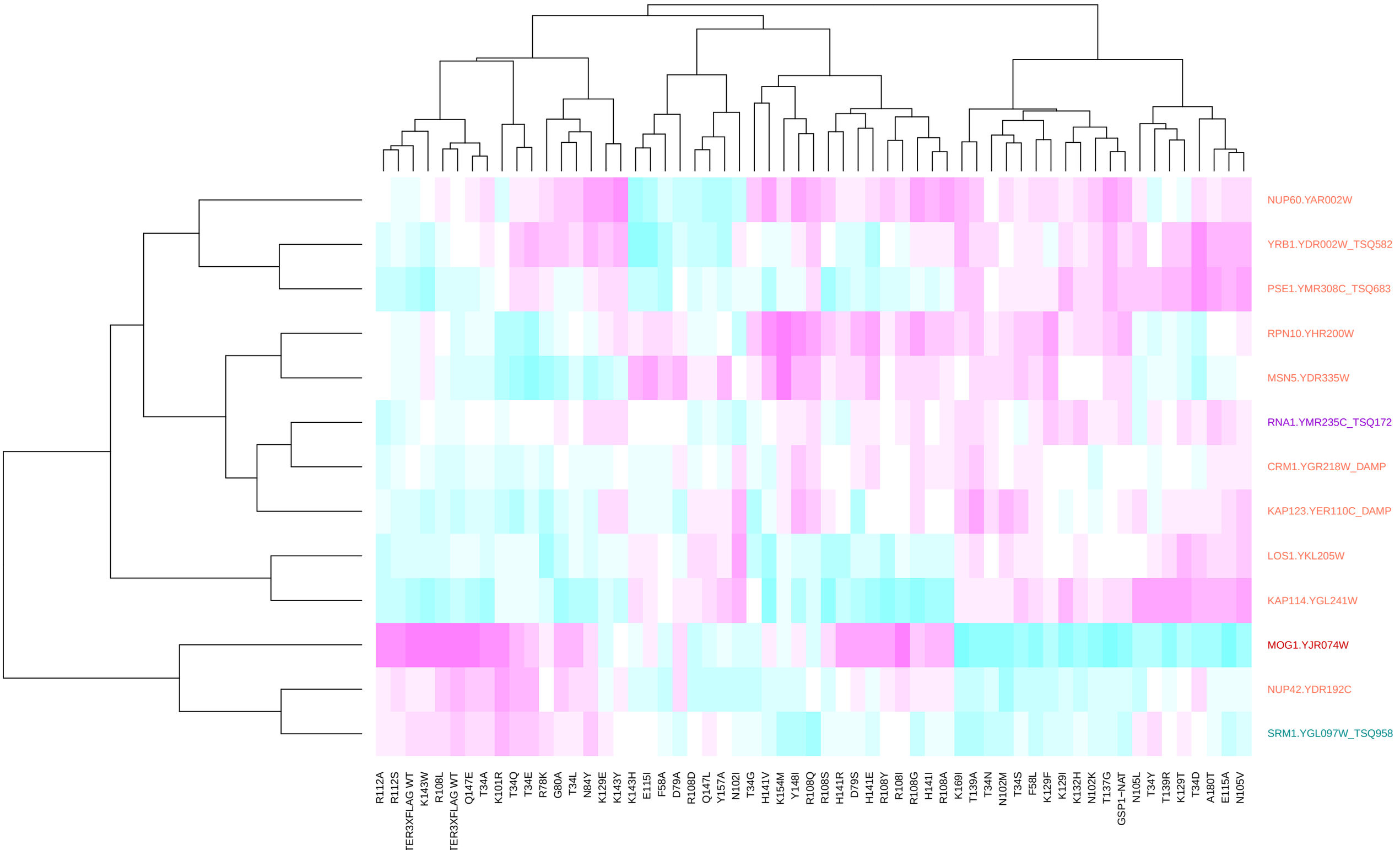
chromatin organization_GO_30_1_mut



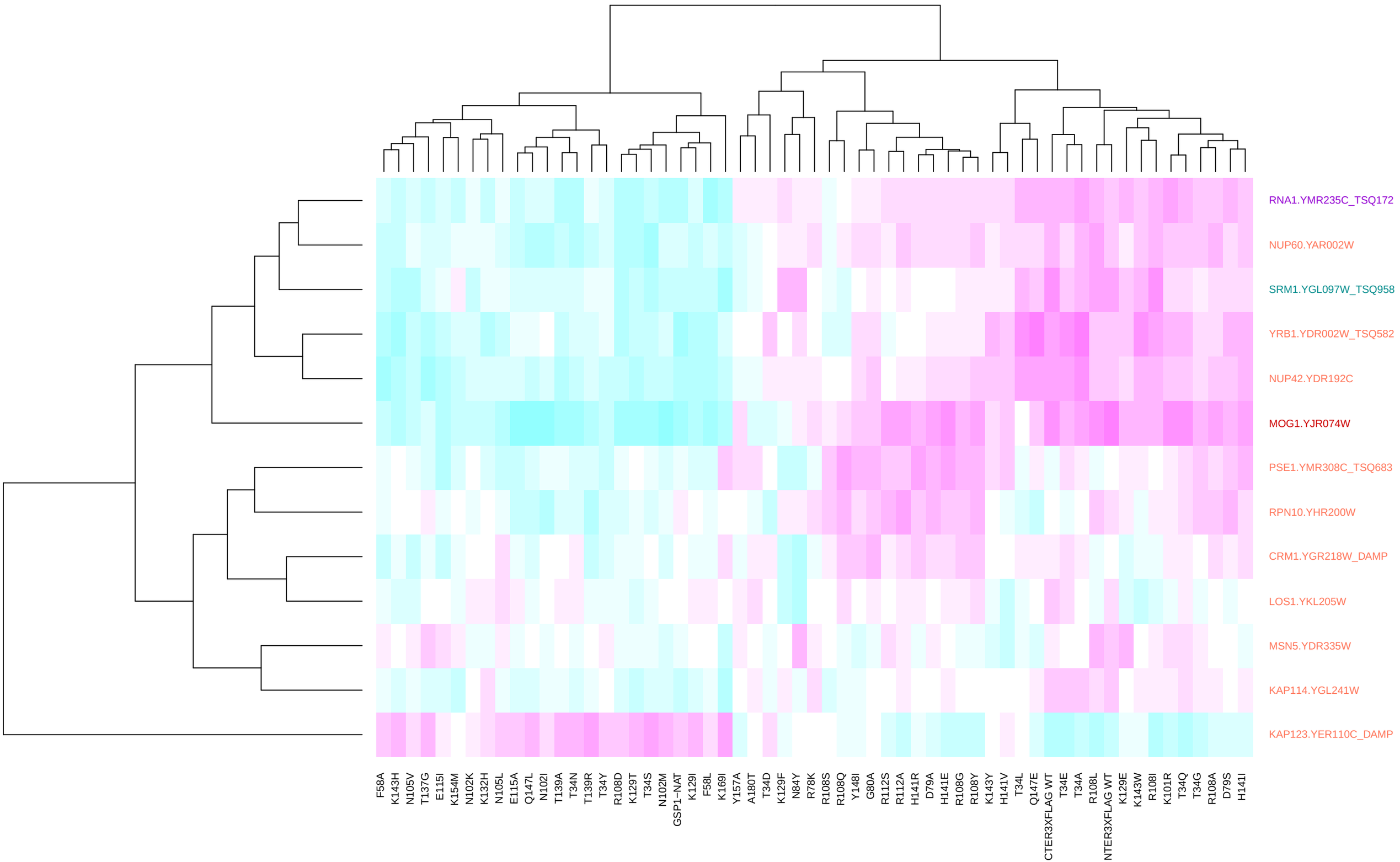
histone modification_GO_15_1_mut



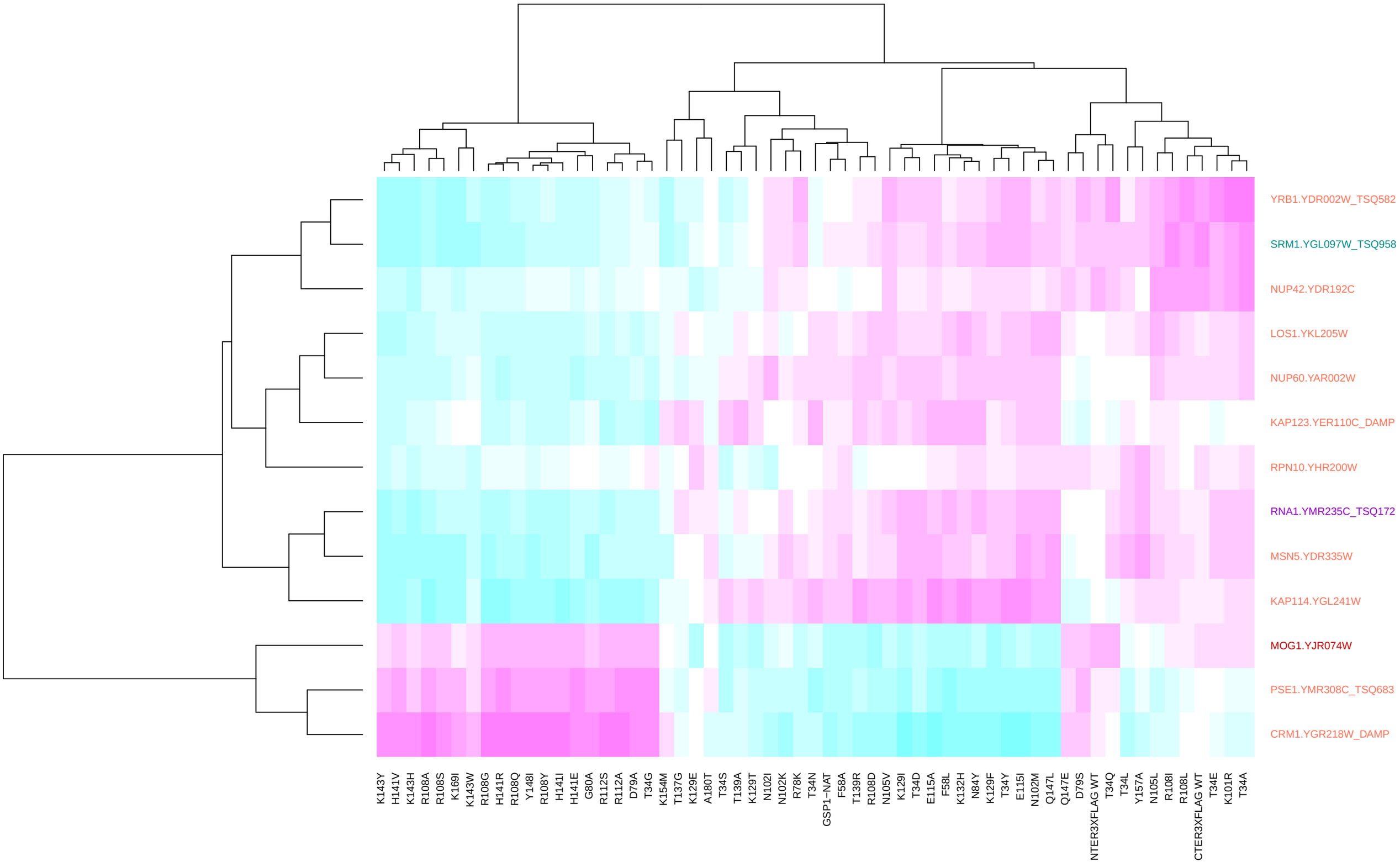
telomere organization



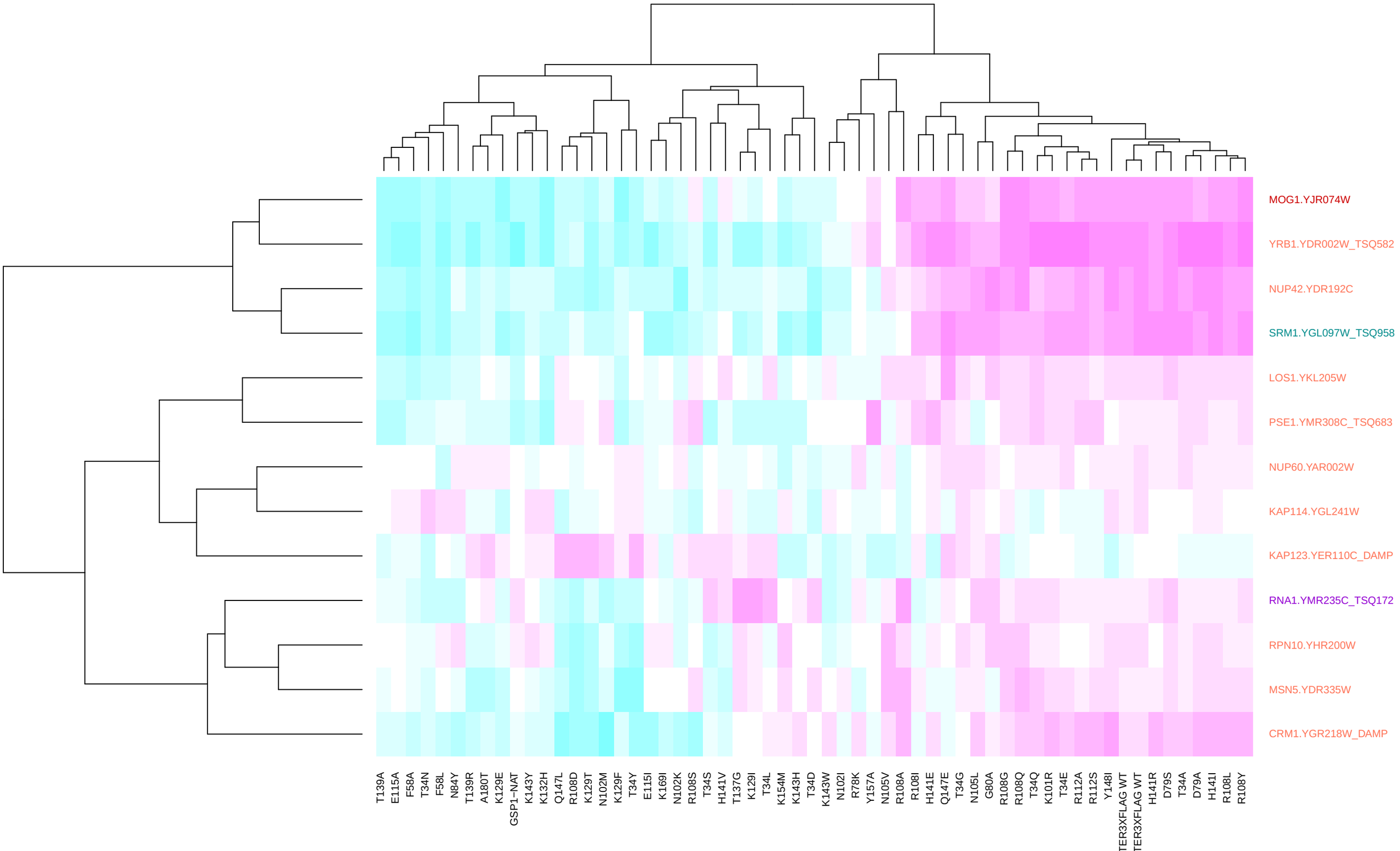
budding_GO_30_1_mut



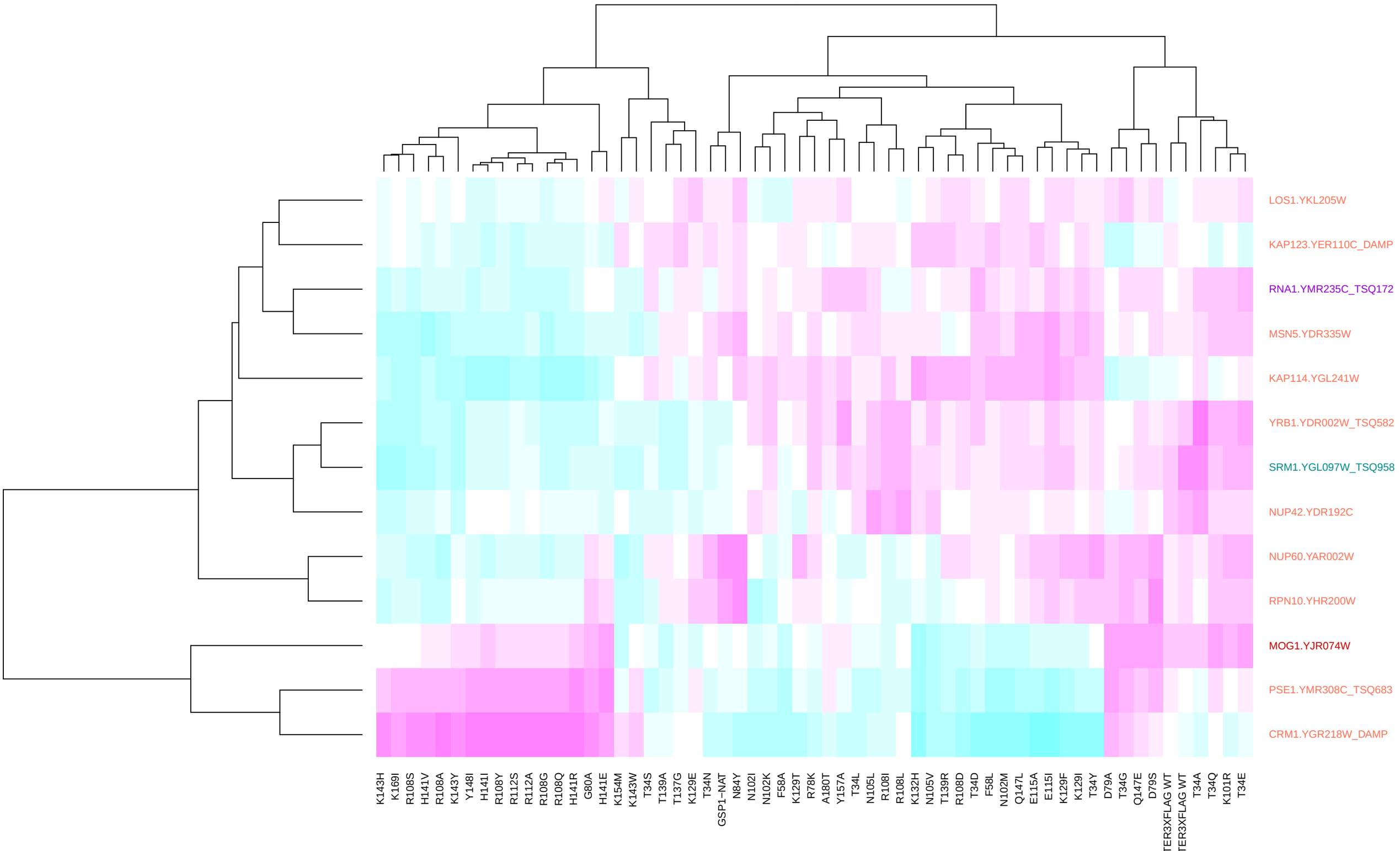
cytoskeleton organization_GO_15_1_mut



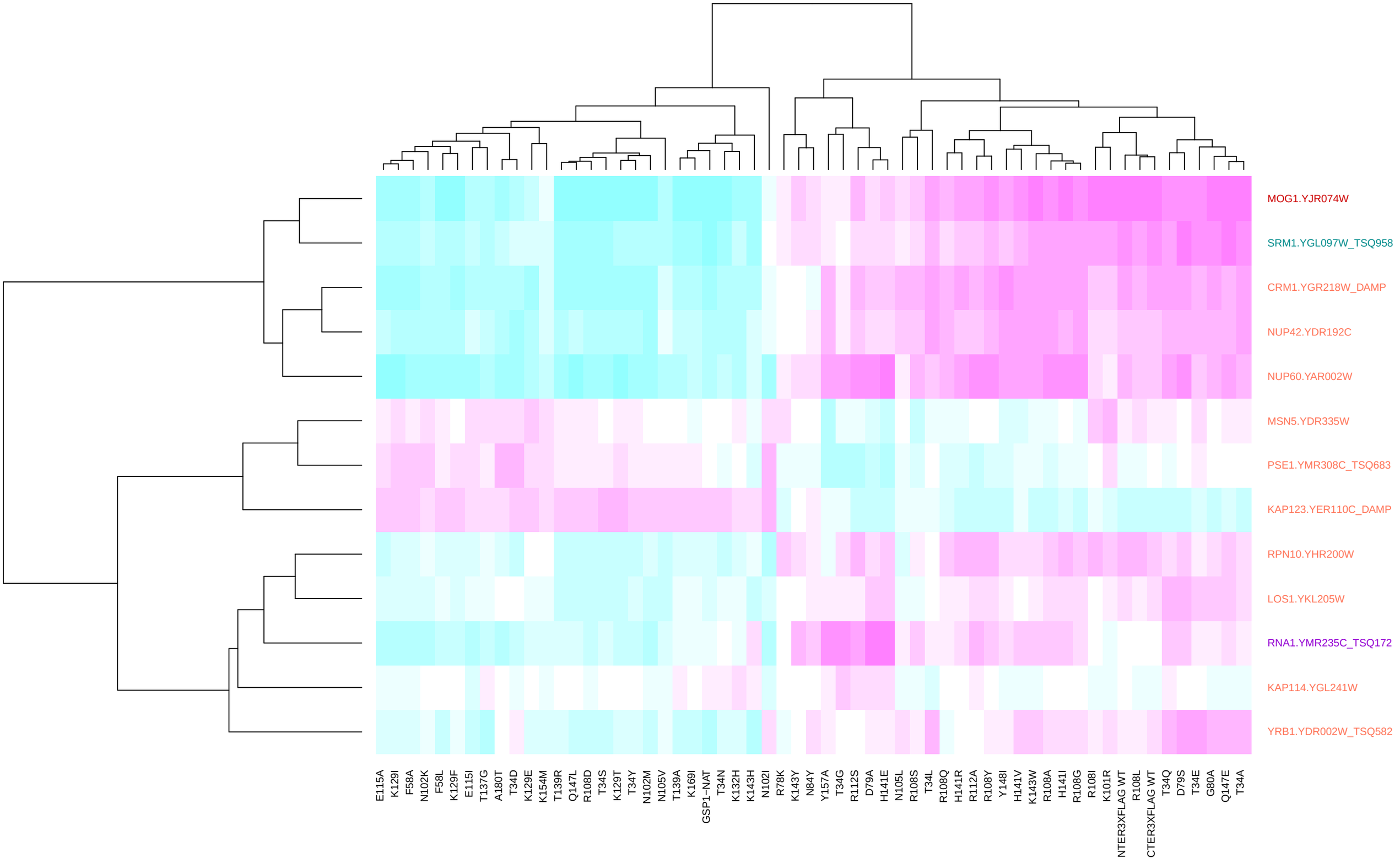
cytoskeleton organization_GO_15_3_all



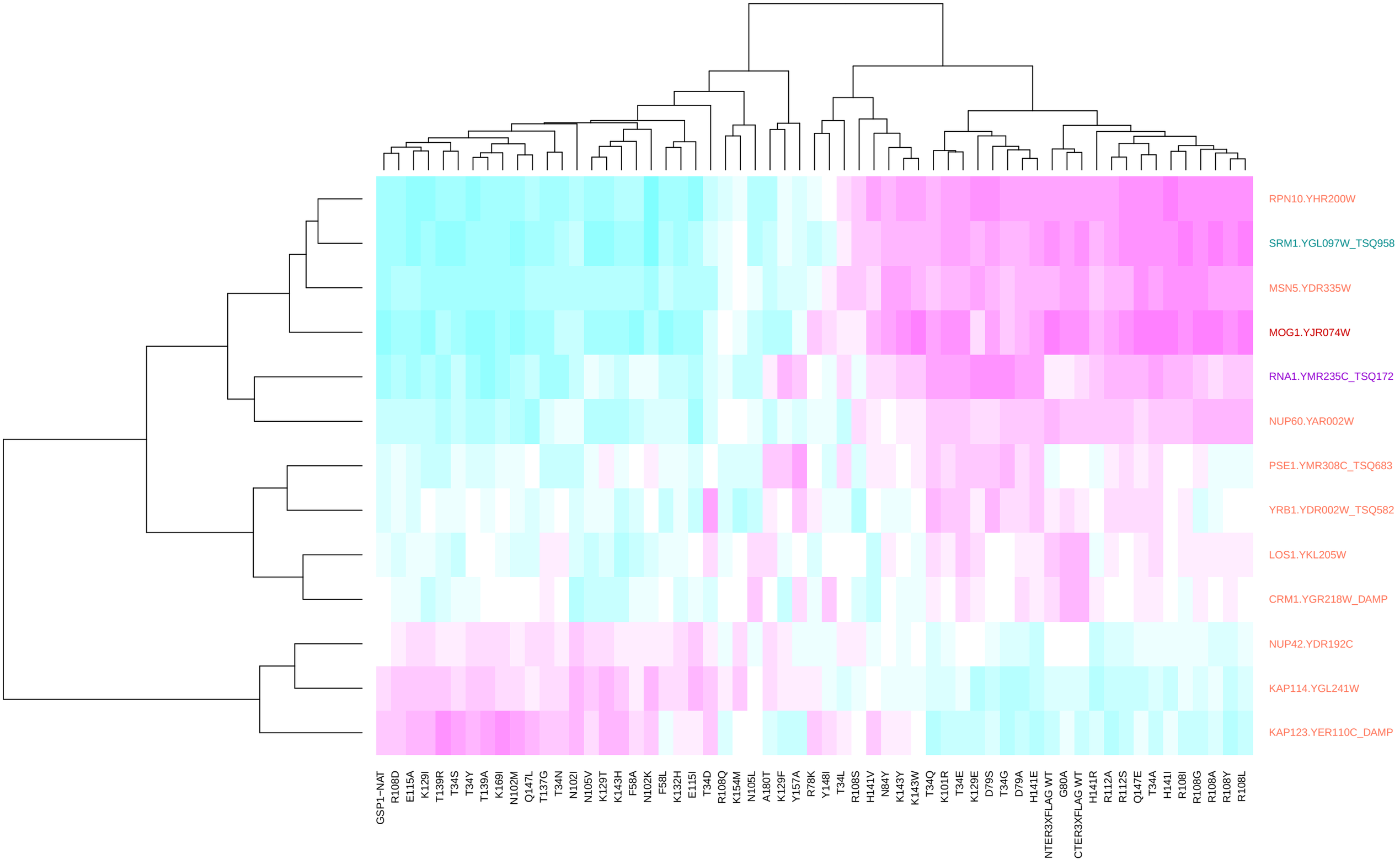
cytoskeleton organization_GO_30_1_mut



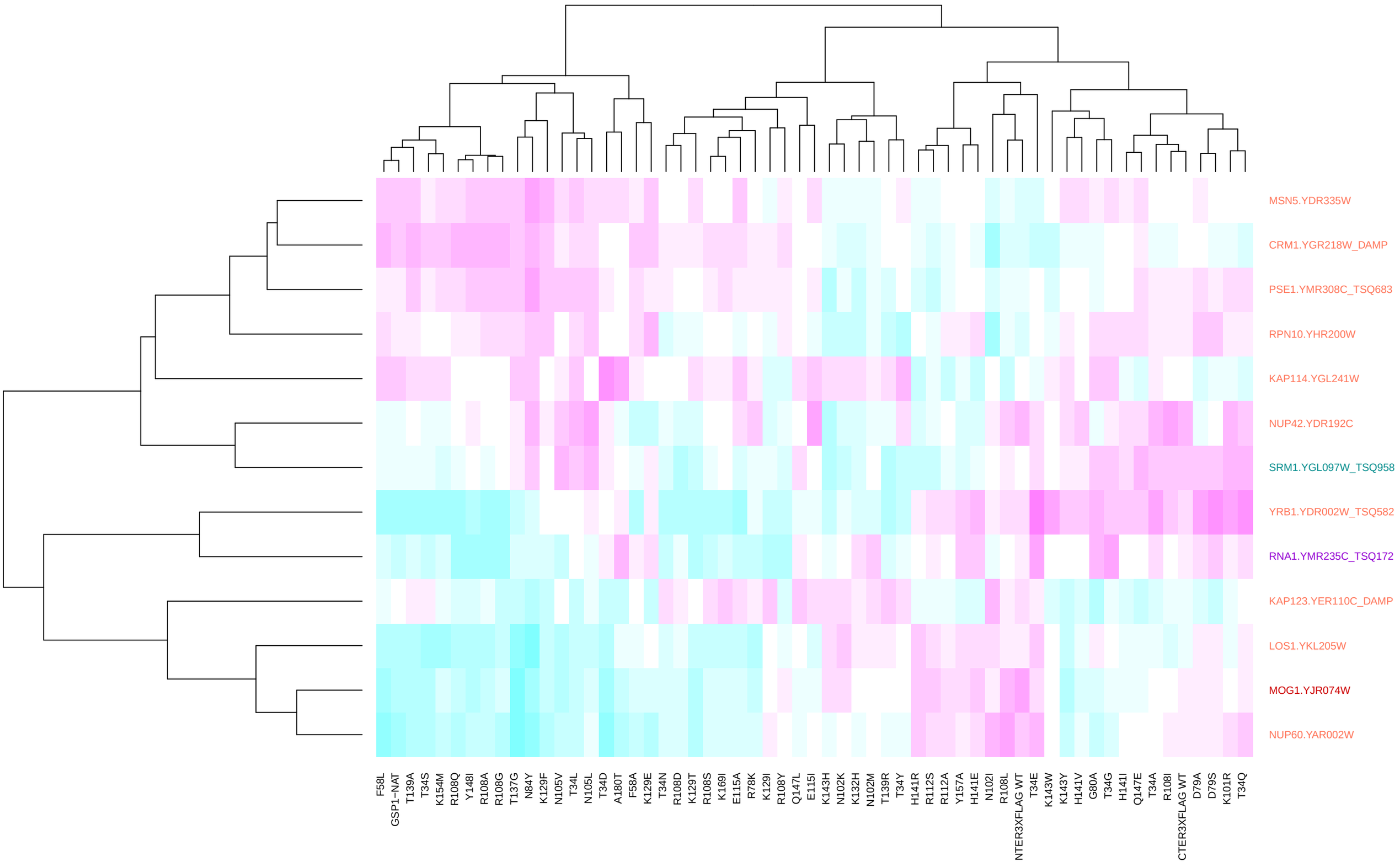
chromatin_GO_30_3_mut



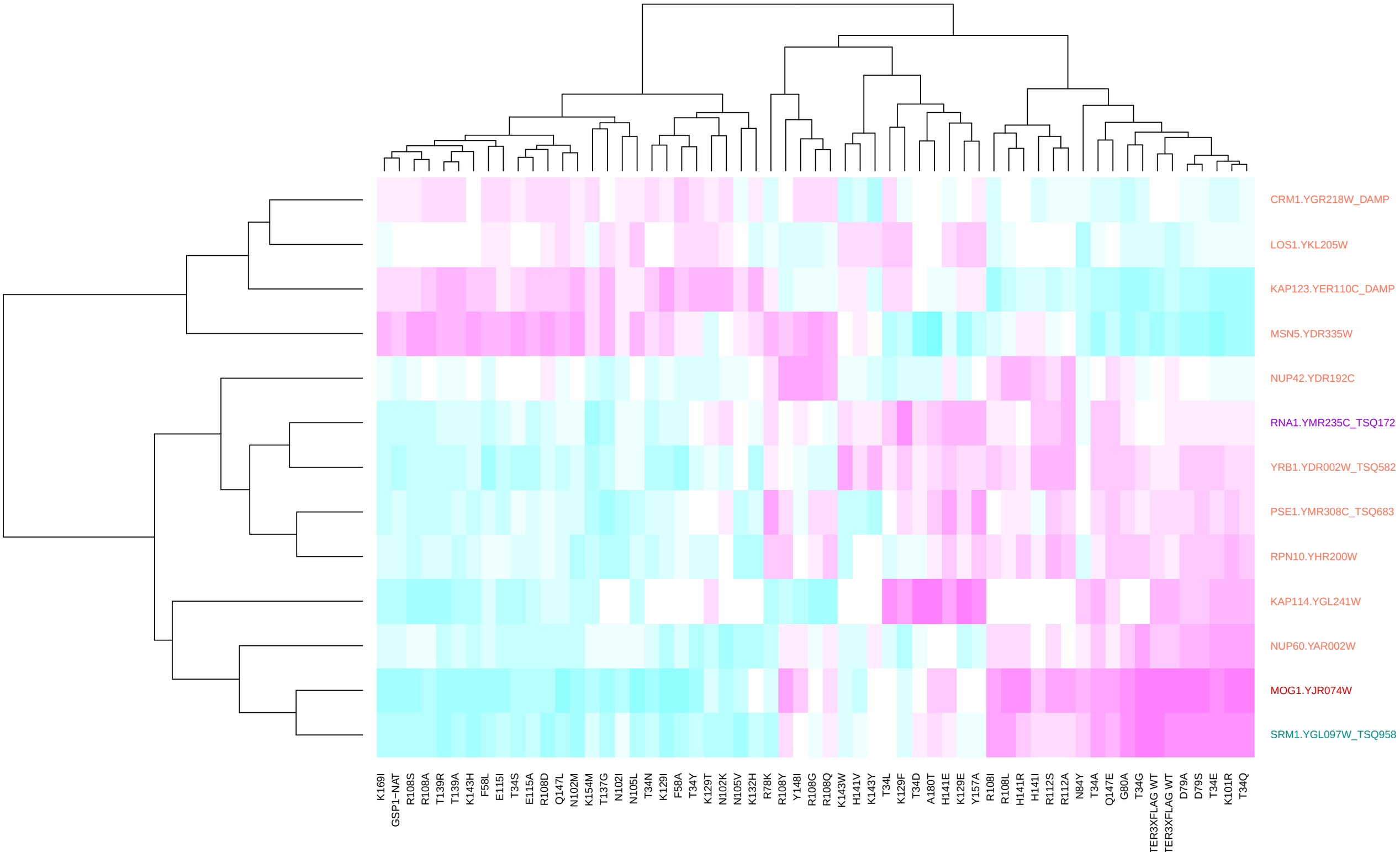
regulation of cell cycle_GO_15_2_mut



sig_Gsp1_GI_15_5_all



sig_Gsp1_GI_15_6_mut



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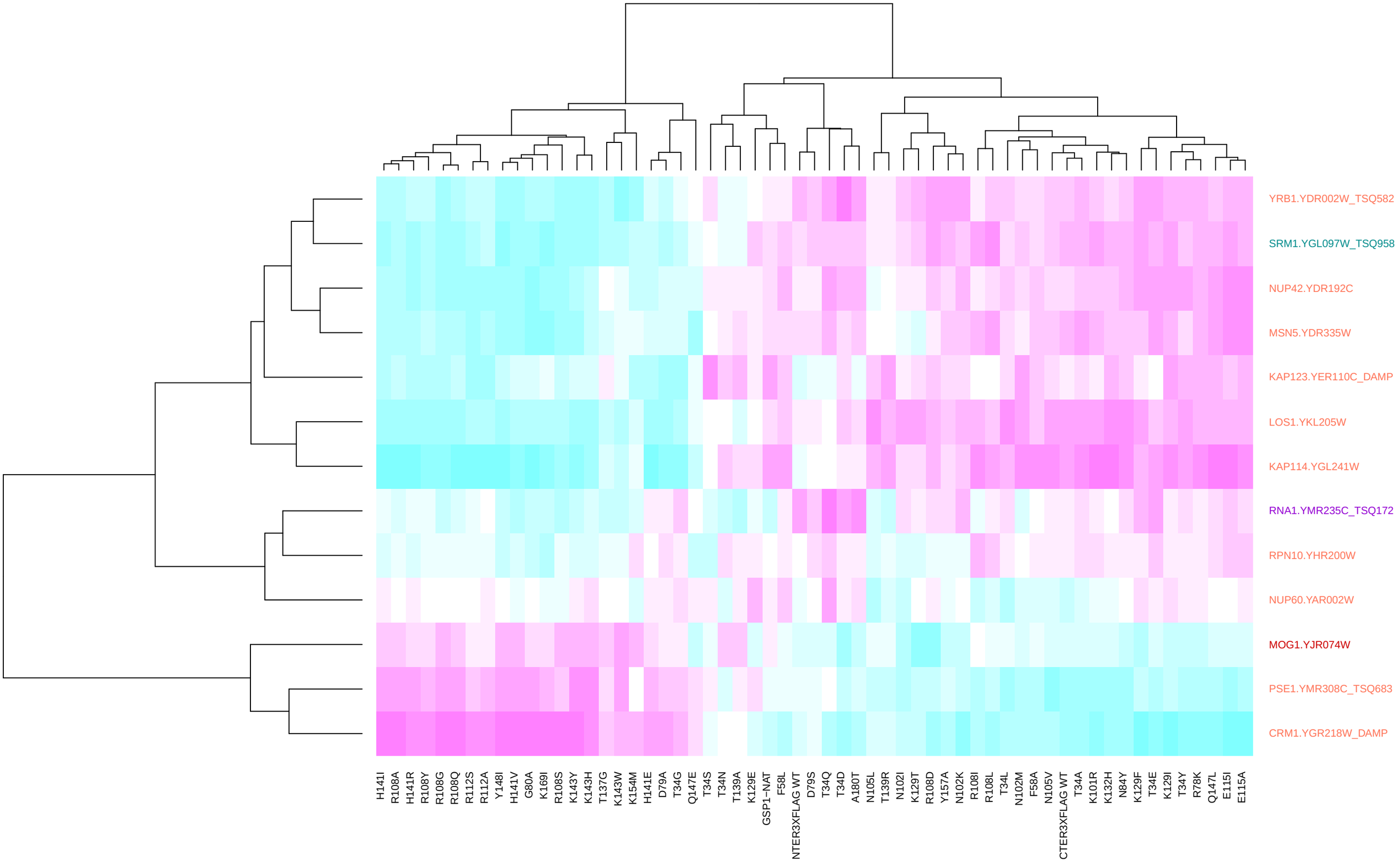
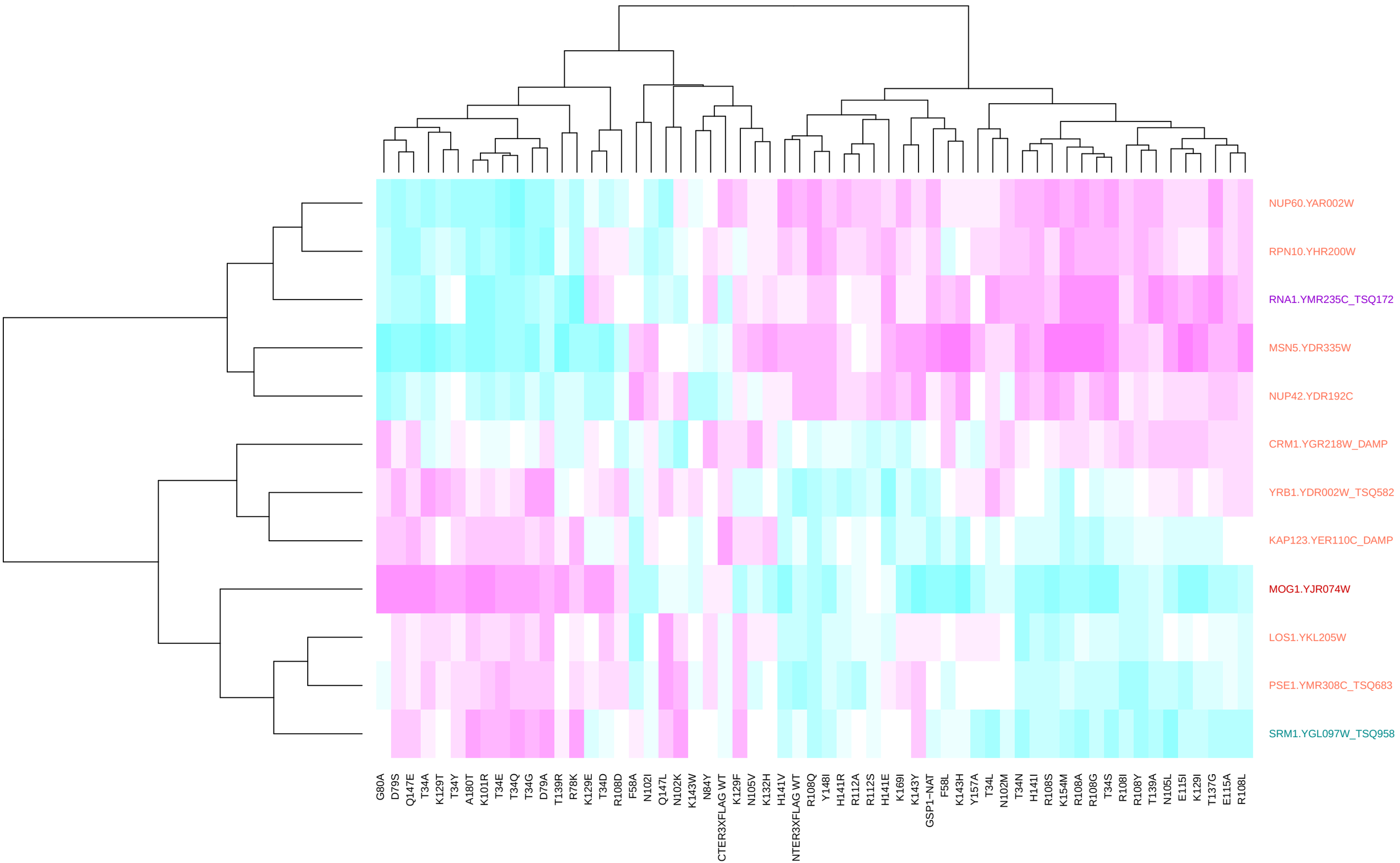
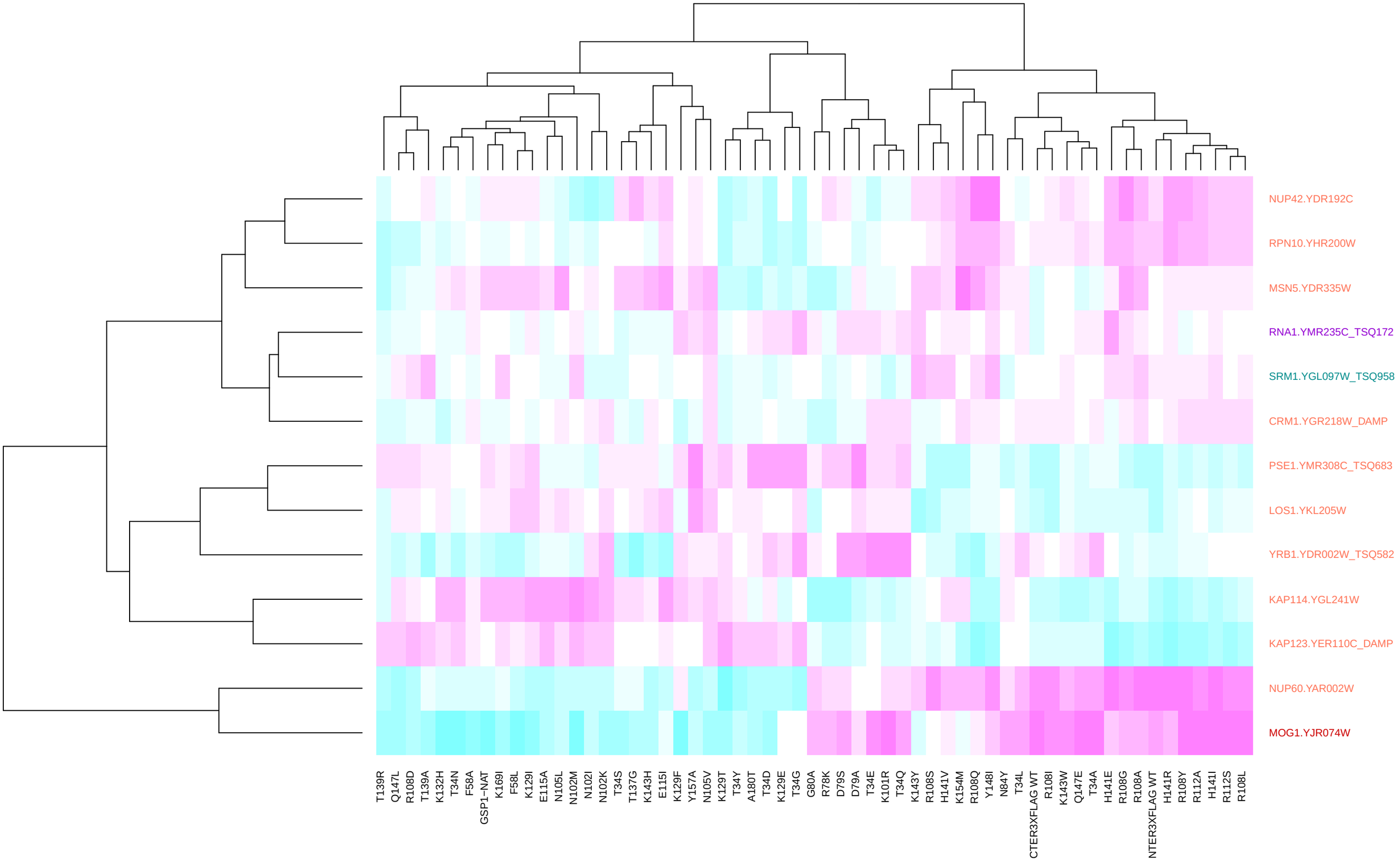


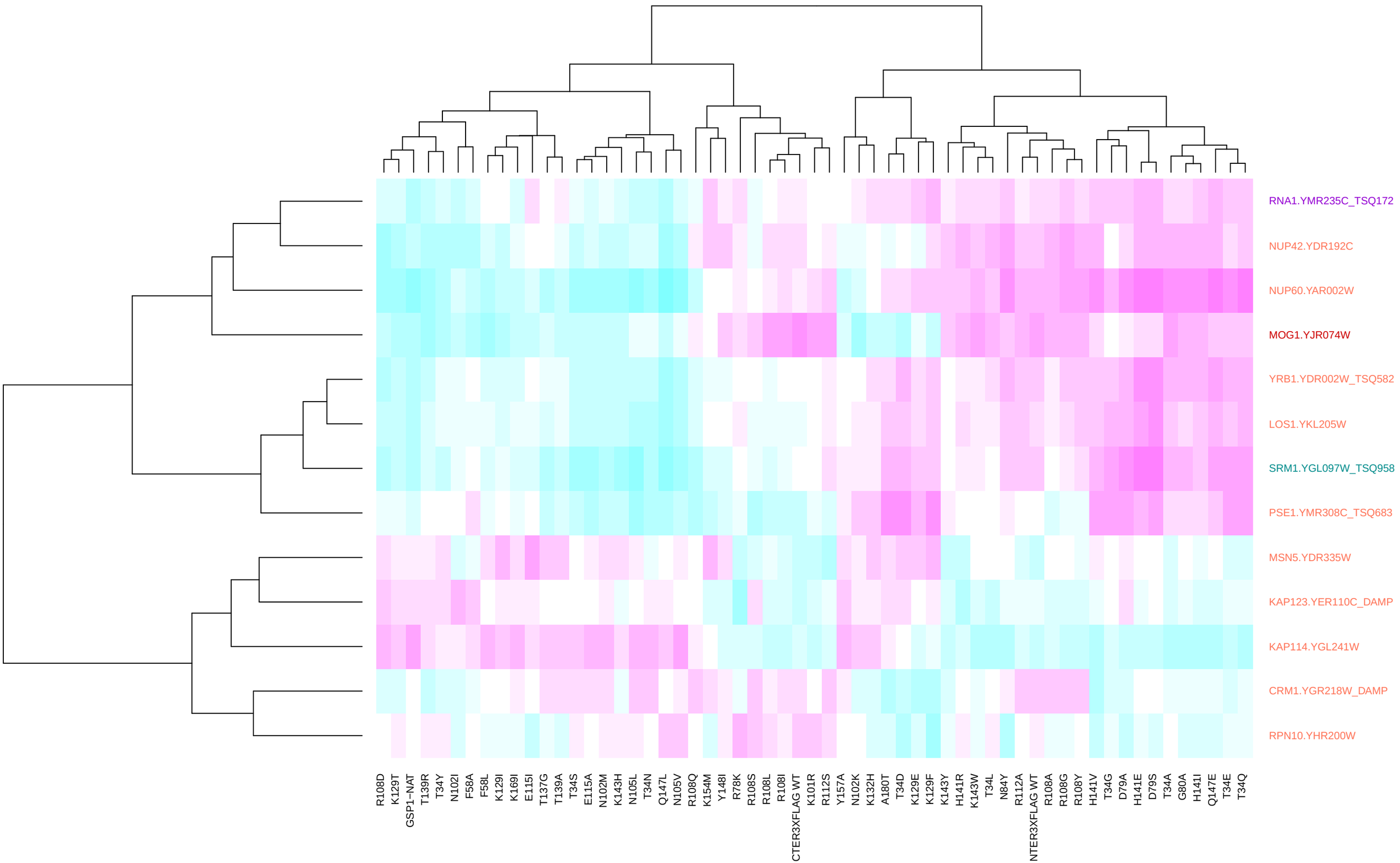
chromatin_GO_15_3_mut



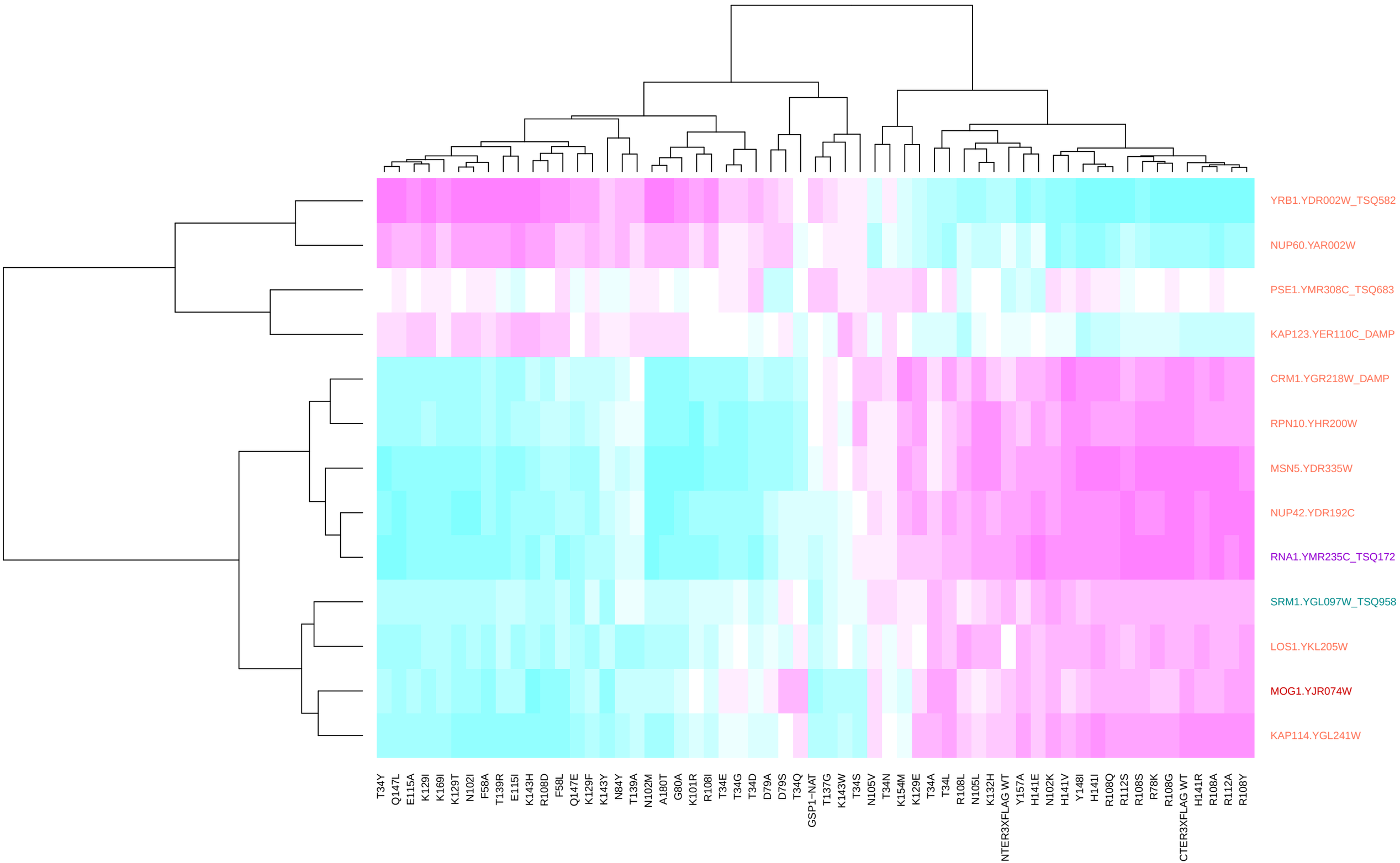
DNA−templated transcription, elongation_GO_15_1_all



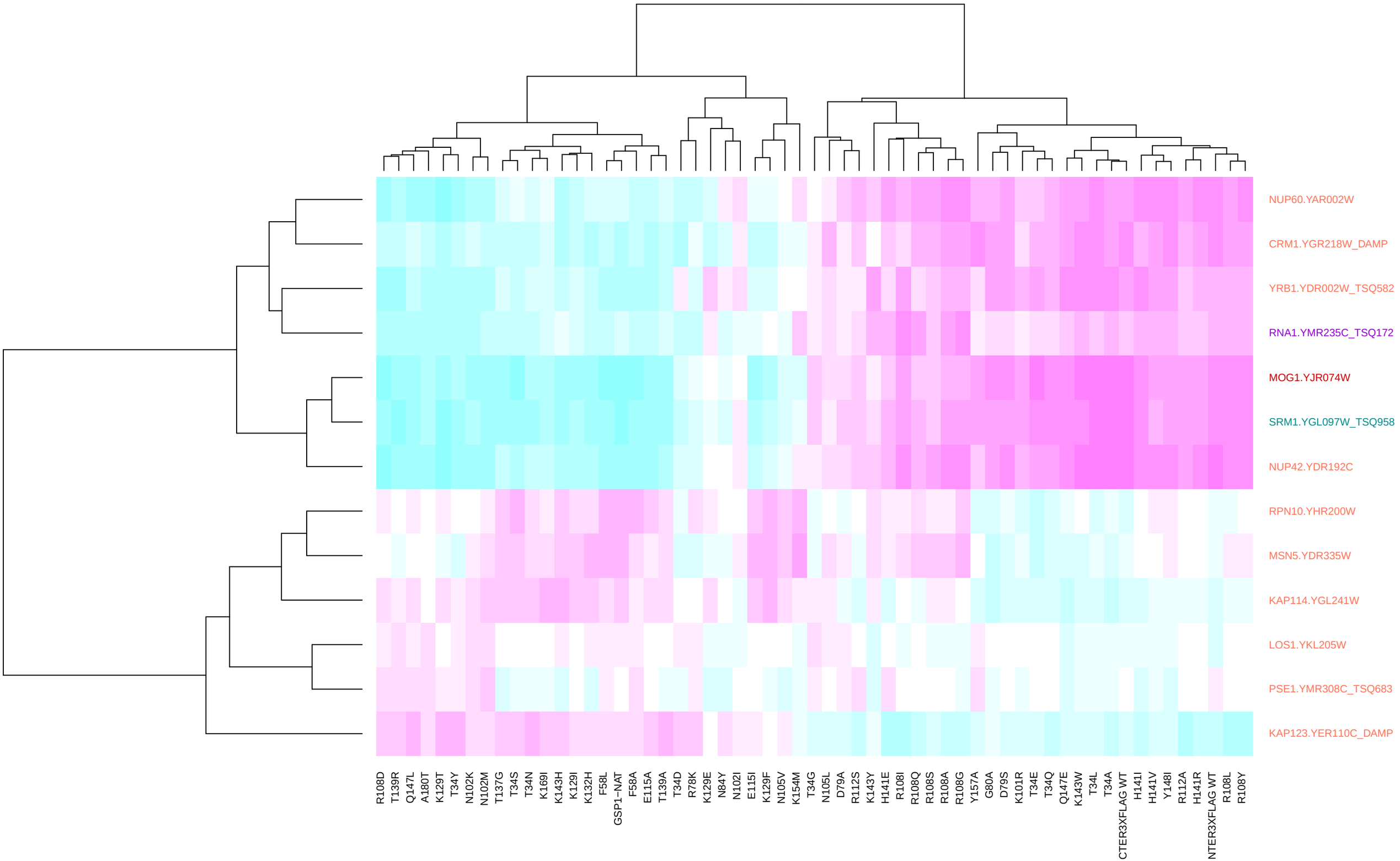
transcription and mRNA processing_GO_15_3_all



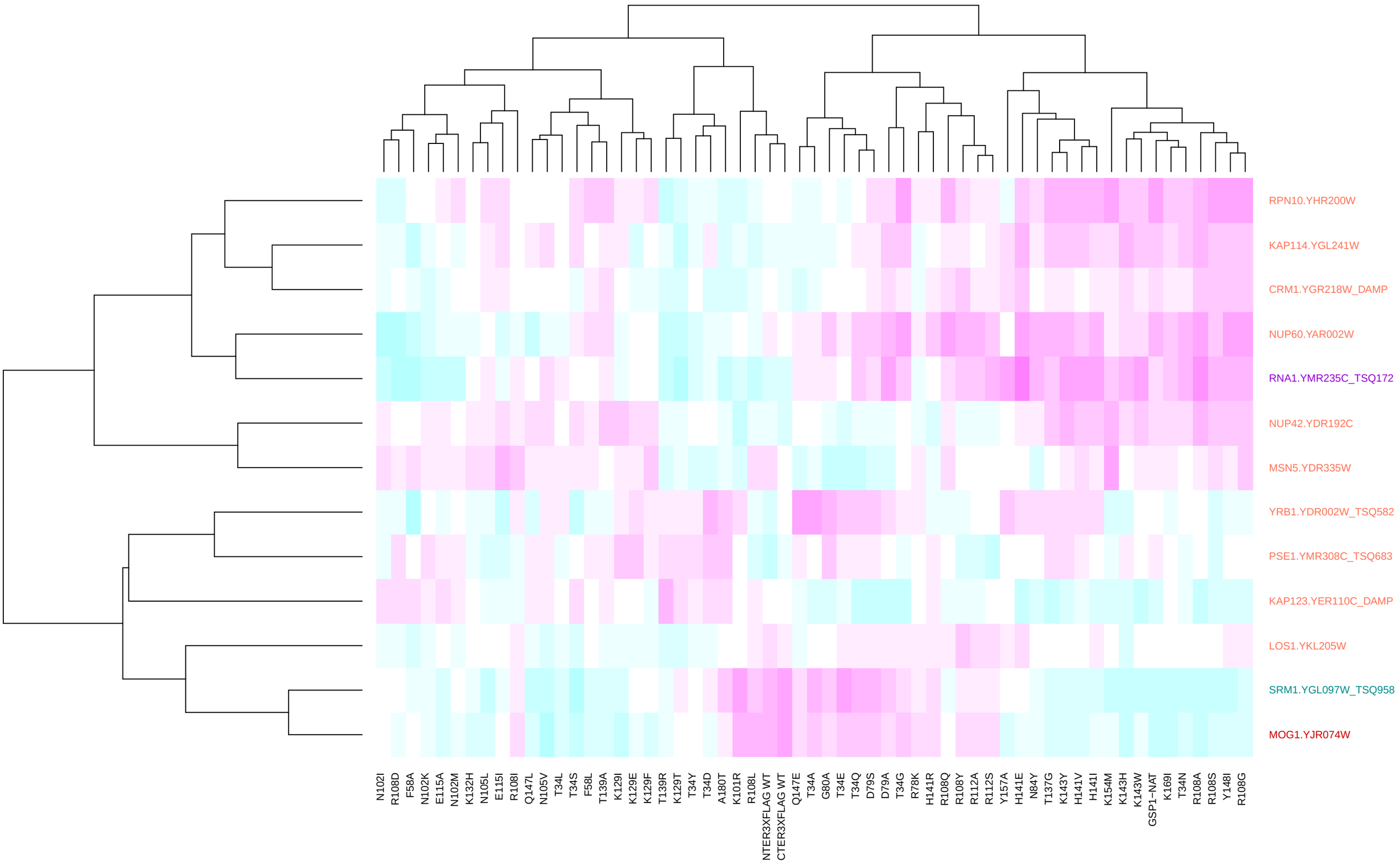
RNA modification_GO_15_1_mut



transcription and mRNA processing_GO_30_1_all



chromosome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KAP114.YGL241W
CRM1.YGR218W_DAMP
NUP60.YAR002W
RNA1.YMR235C_TSQ172
NUP42.YDR192C
MSN5.YDR335W
YRB1.YDR002W_TSQ582
PSE1.YMR308C_TSQ683
KAP123.YER110C_DAMP
LOS1.YKL205W
SRM1.YGL097W_TSQ958
MOG1.YJR074W
N102I
R108D
F58A
N102K
E115A
N102M
K132H
N105L
E115I
R108I
Q147L
N105V
T34L
T34S
F58L
T139A
K129I
K129E
K129F
T139R
K129T
T34Y
T34D
A180T
K101R
R108L
NTER3XFLAG WT
CTER3XFLAG WT
Q147E
T34A
G80A
T34E
T34Q
D79S
D79A
T34G
R78K
H141R
R108Q
R108Y
R112A
R112S
Y157A
H141E
N84Y
T137G
K143Y
H141V
H141I
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K143H
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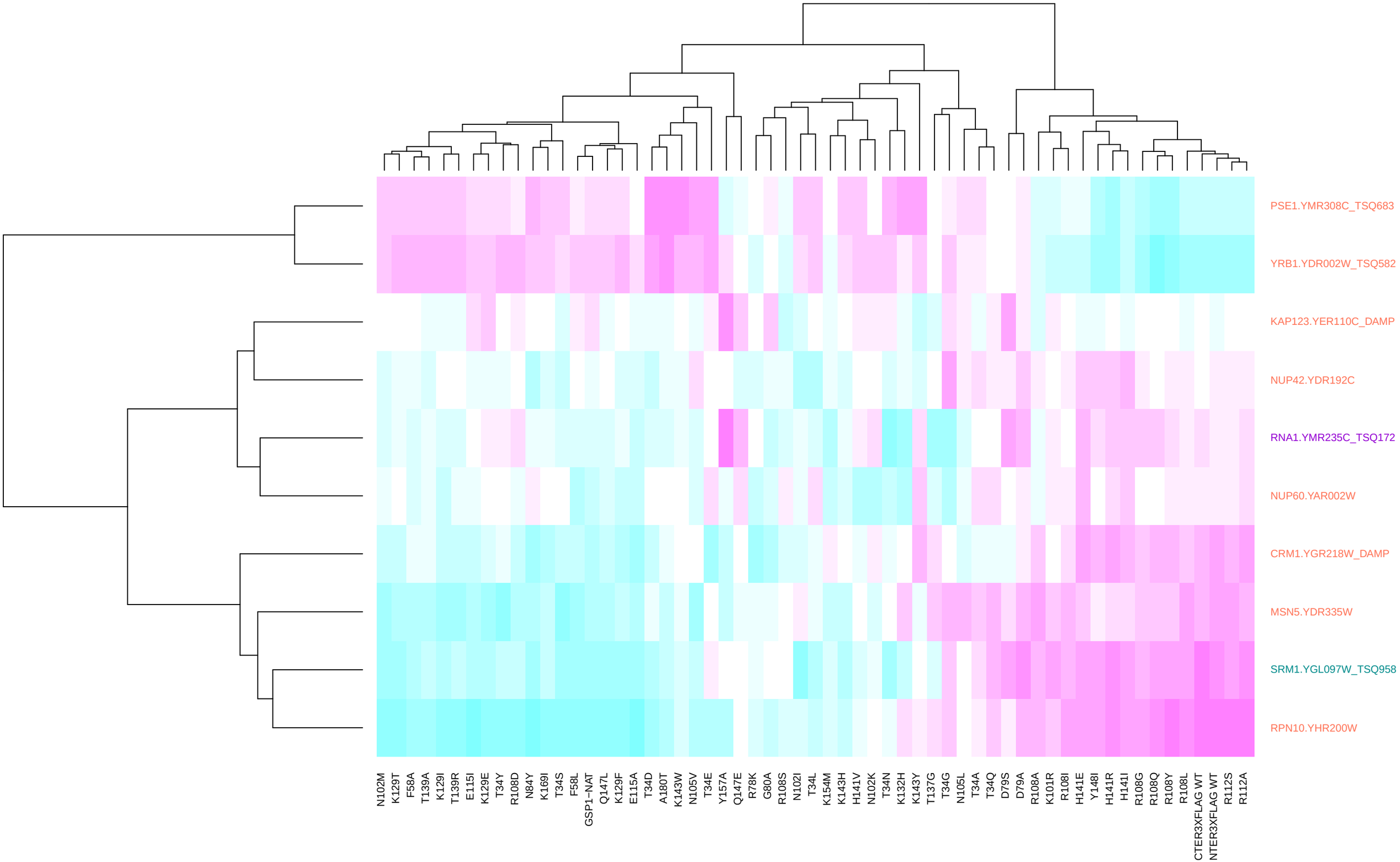
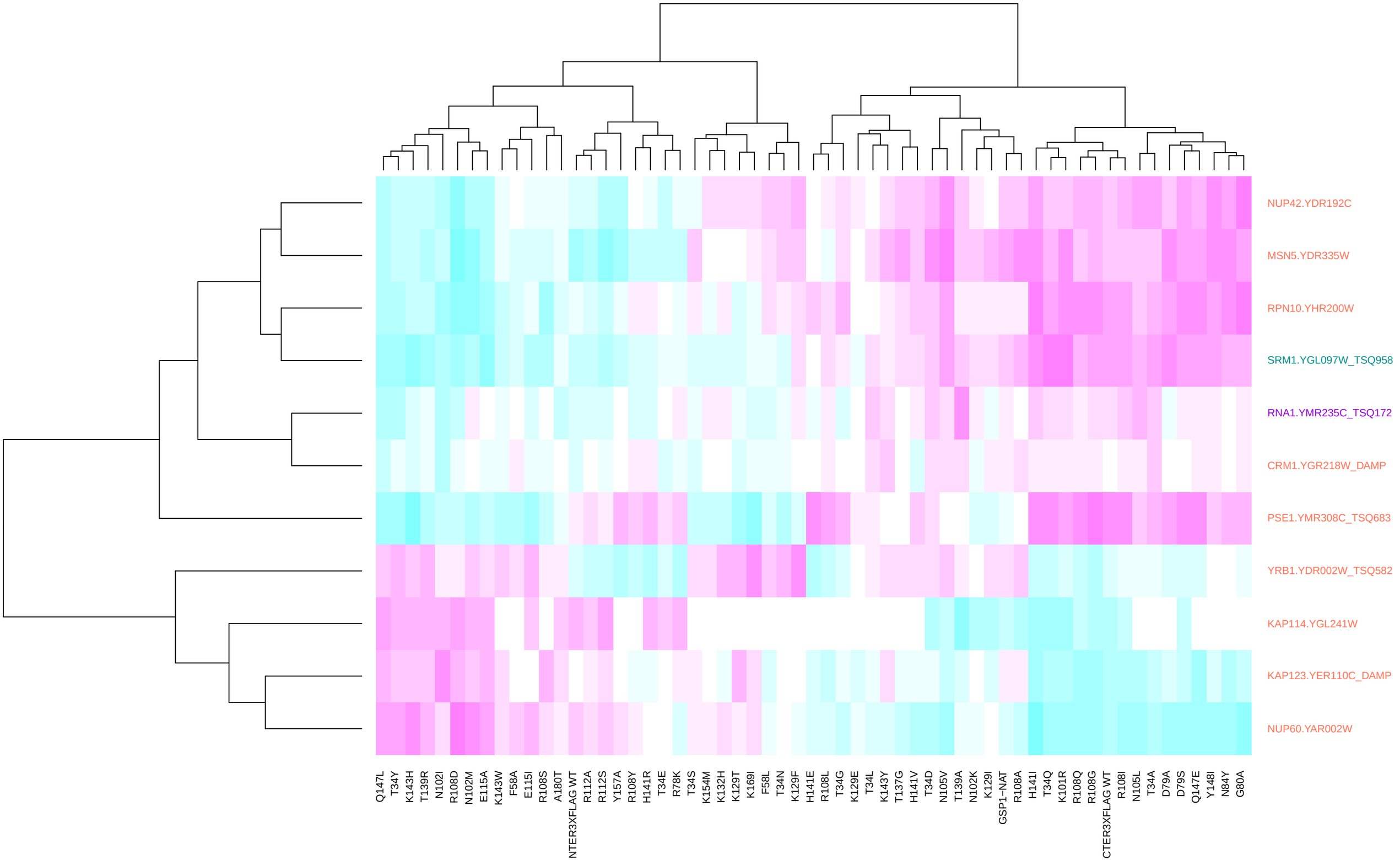
R108S
Y148I
R108G

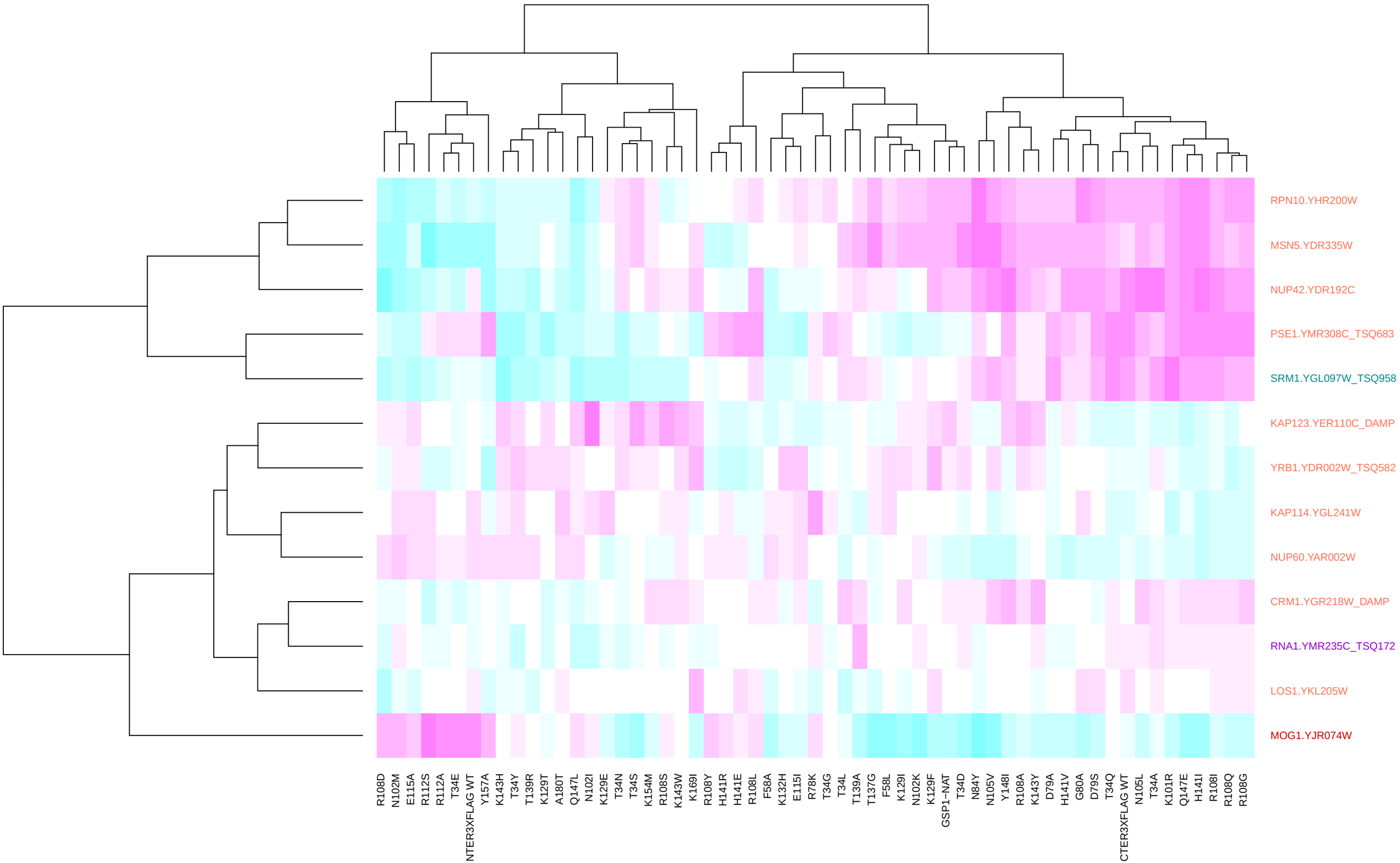
whole_library_15_24_mut



cytoplasmic translation



ribosome


RPN10.YHR200W
MSN5.YDR335W
NUP42.YDR192C
PSE1.YMR308C_TSQ683
SRM1.YGL097W_TSQ958
KAP123.YER110C_DAMP
YRB1.YDR002W_TSQ582
KAP114.YGL241W
NUP60.YAR002W
CRM1.YGR218W_DAMP
RNA1.YMR235C_TSQ172
LOS1.YKL205W
MOG1.YJR074W
R108D
N102M
E115A
R112S
R112A
T34E
NTER3XFLAG WT
Y157A
K143H
T34Y
T139R
K129T
A180T
Q147L
N102I
K129E
T34N
T34S
K154M
R108S
K143W
K169I
R108Y
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T137G
F58L
K129I
N102K
K129F
GSP1−NAT
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R108A
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H141V
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D79S
T34Q
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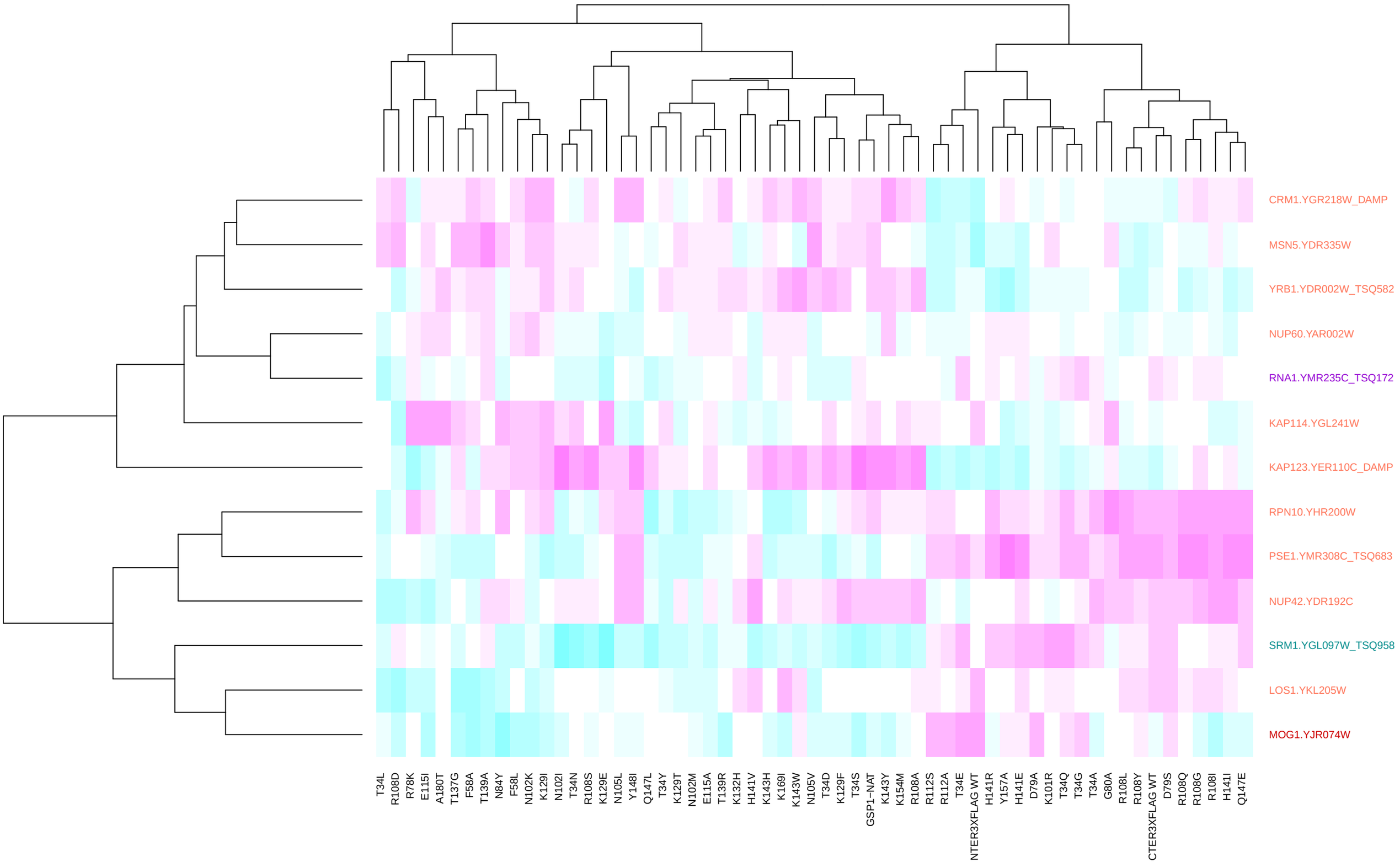
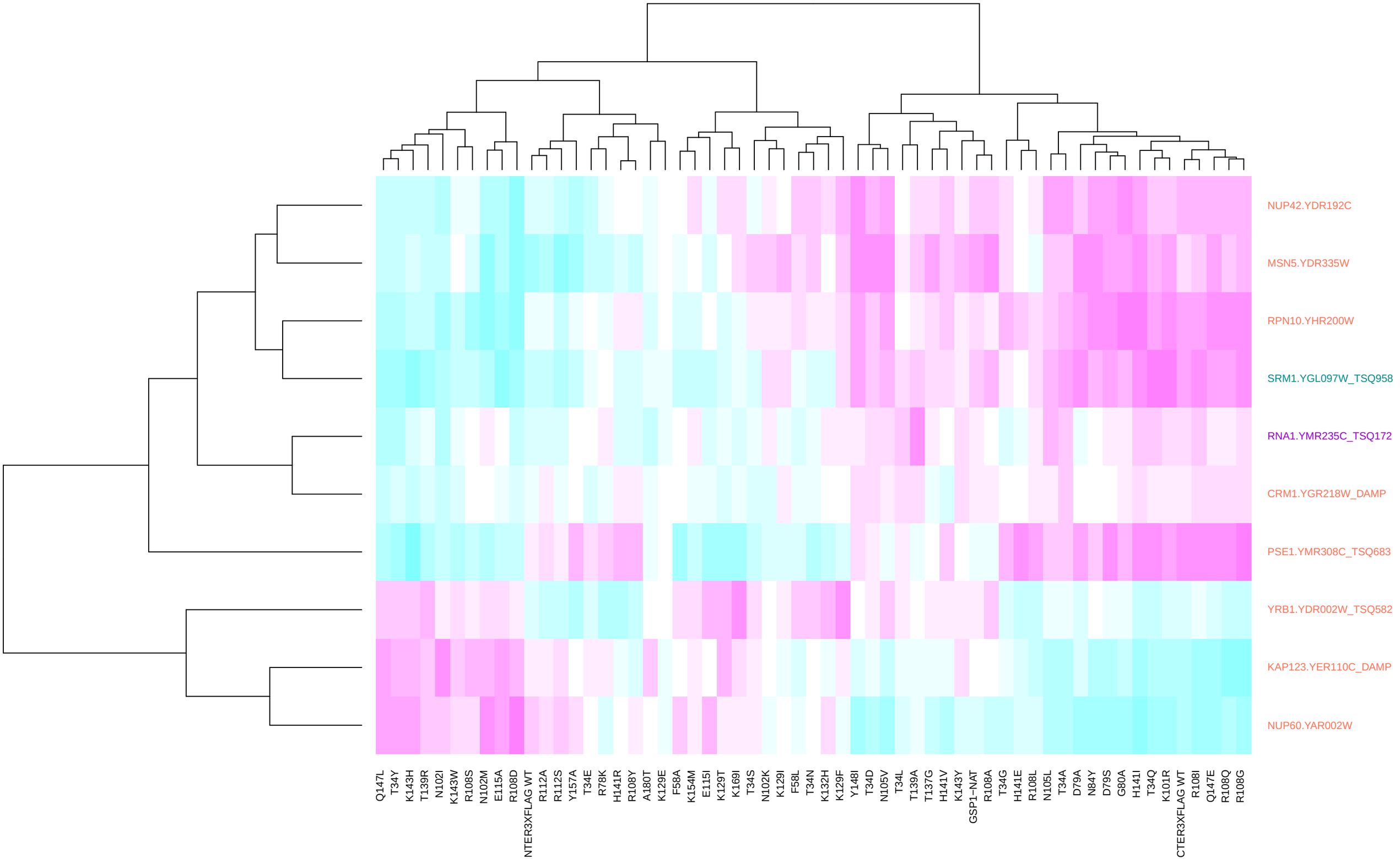
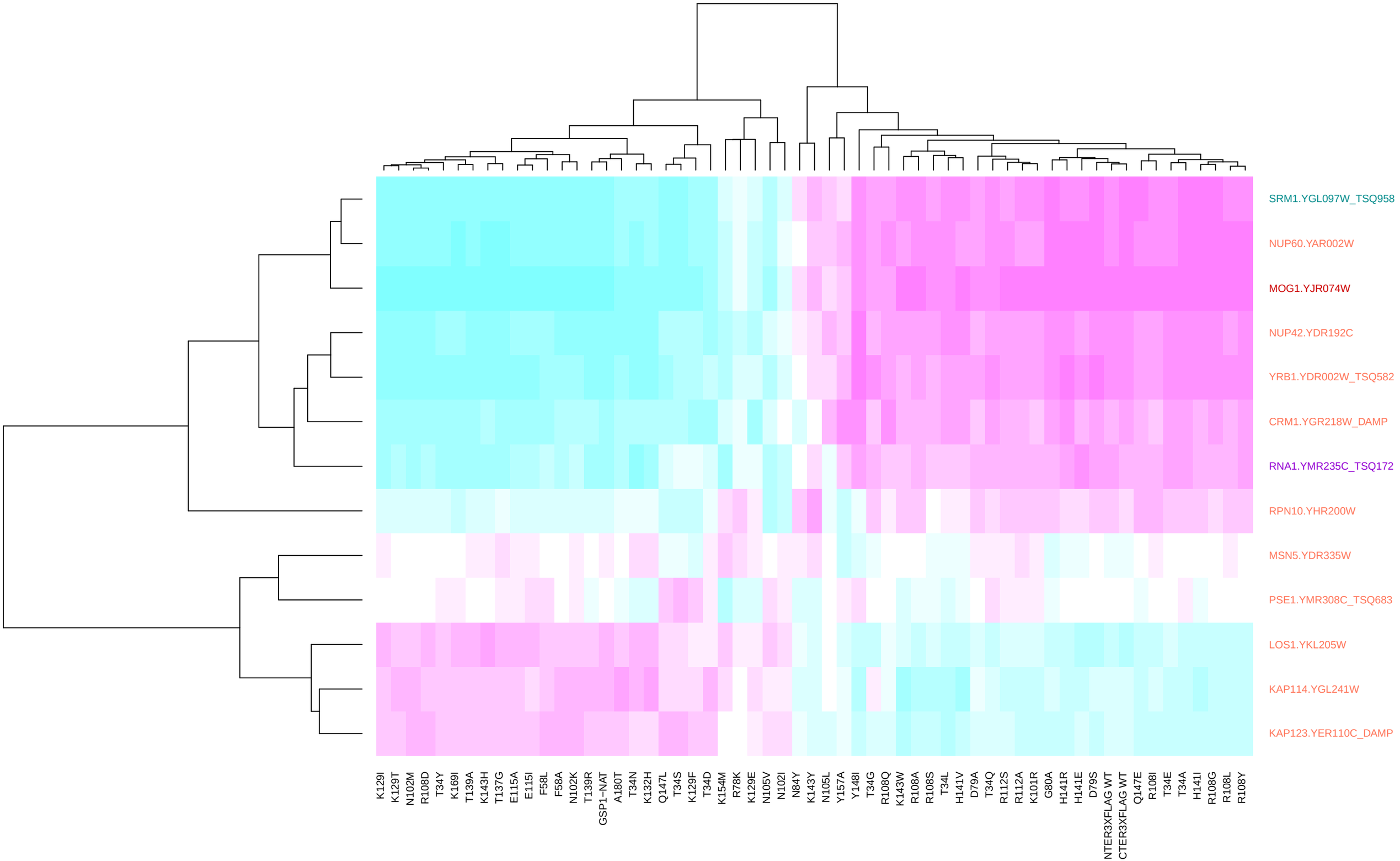
ribosome_GO_15_1_all



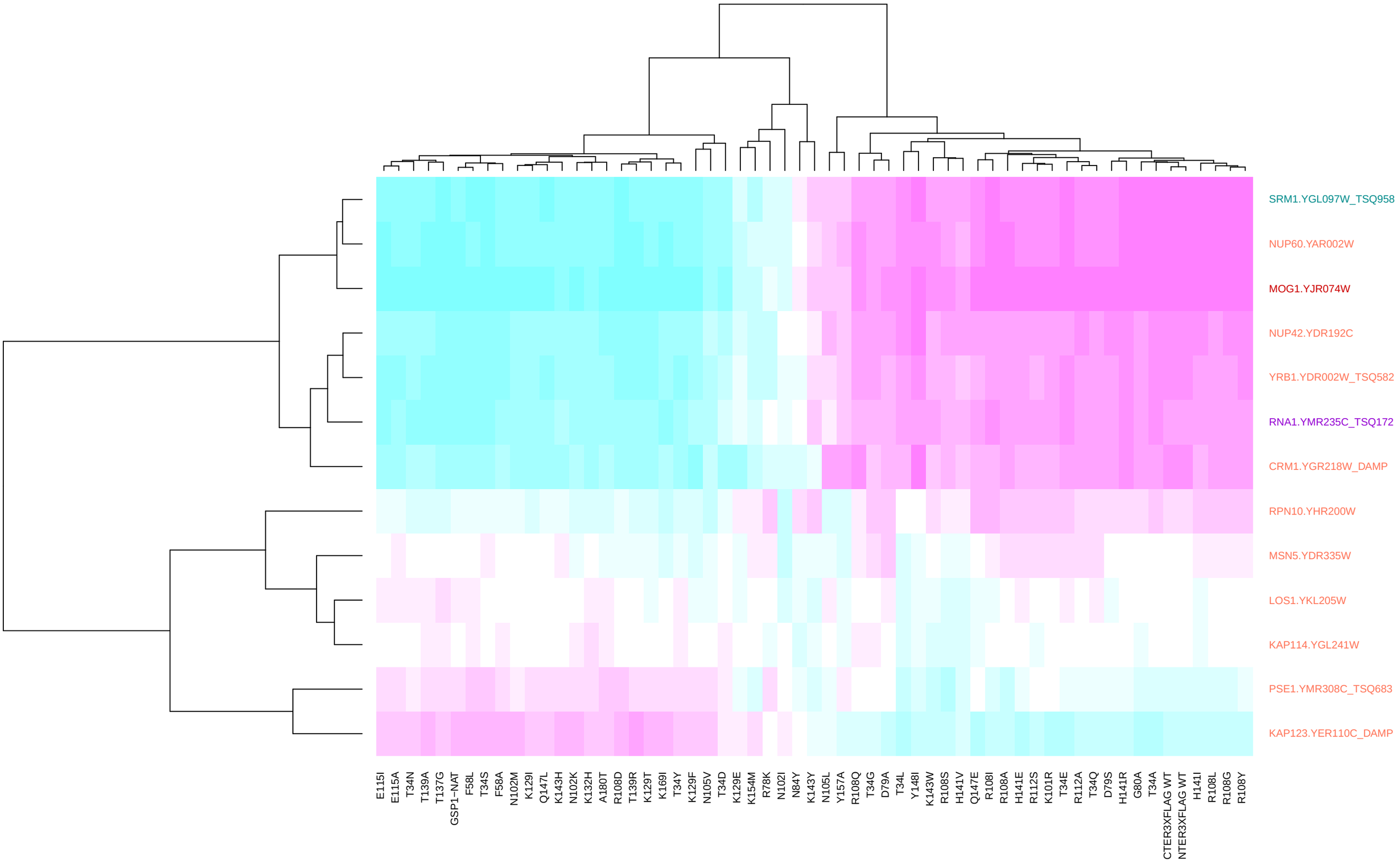
structural constituent of ribosome



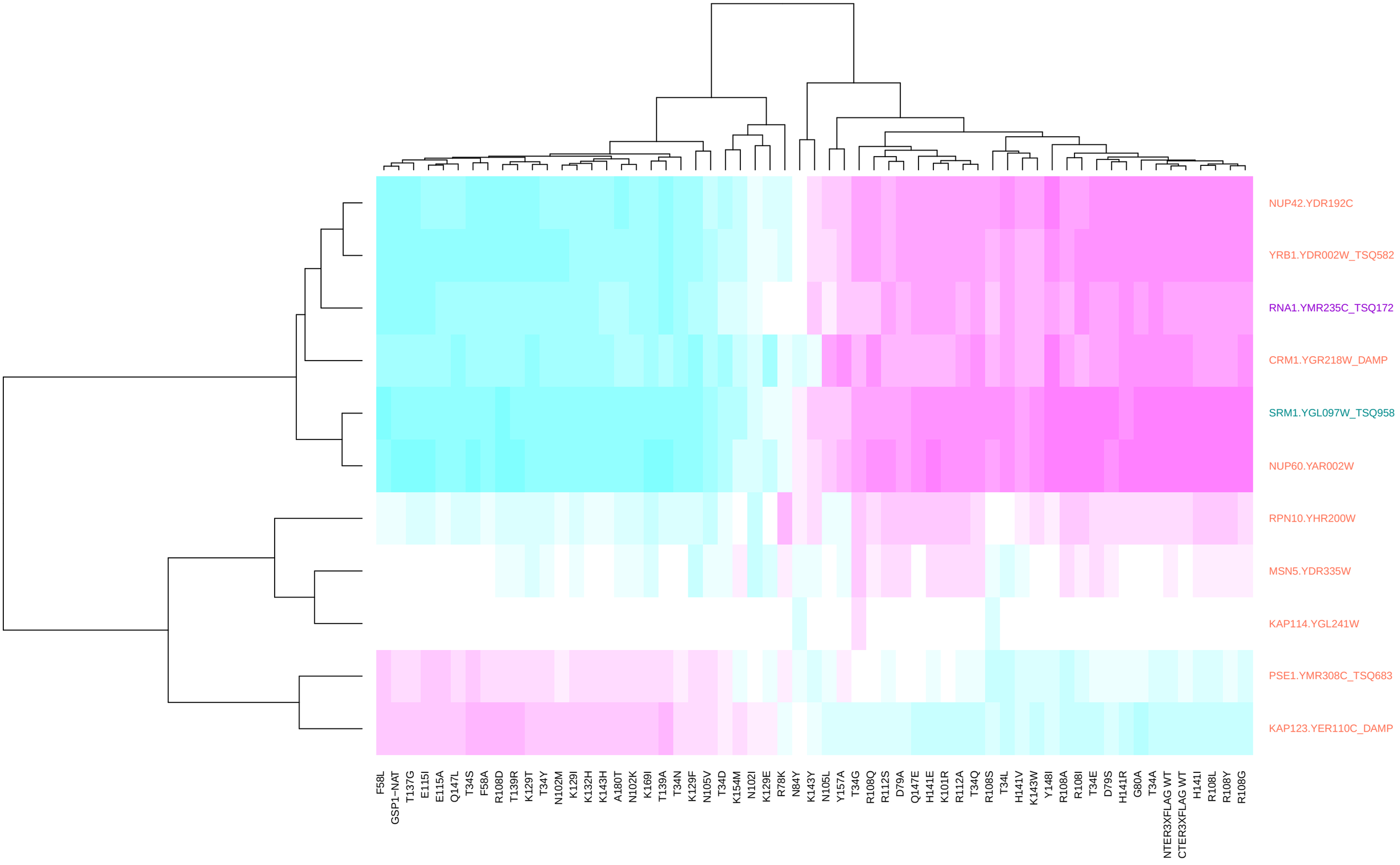
sig_Gsp1_GI_15_4_mut



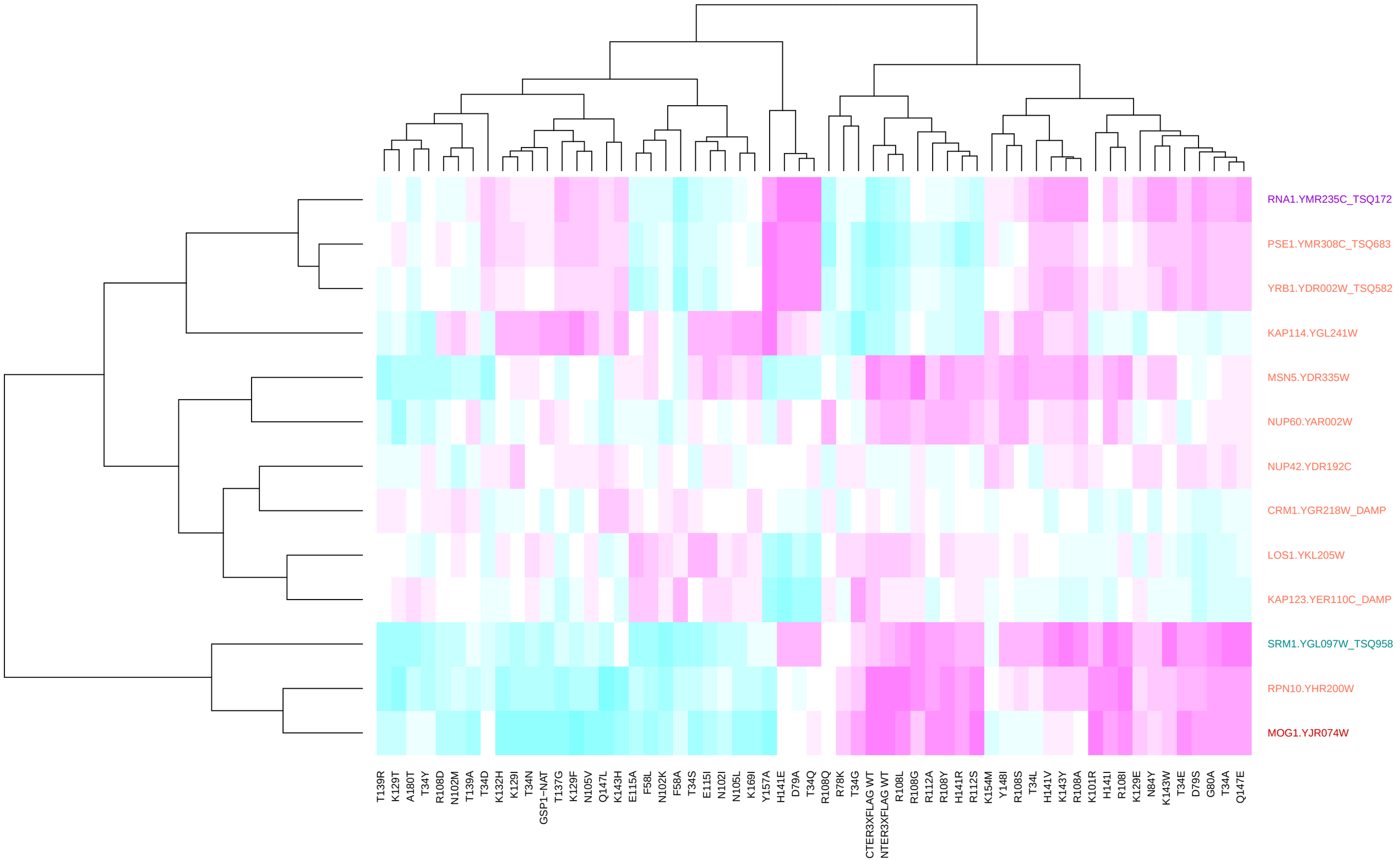
whole_library_15_14_mut



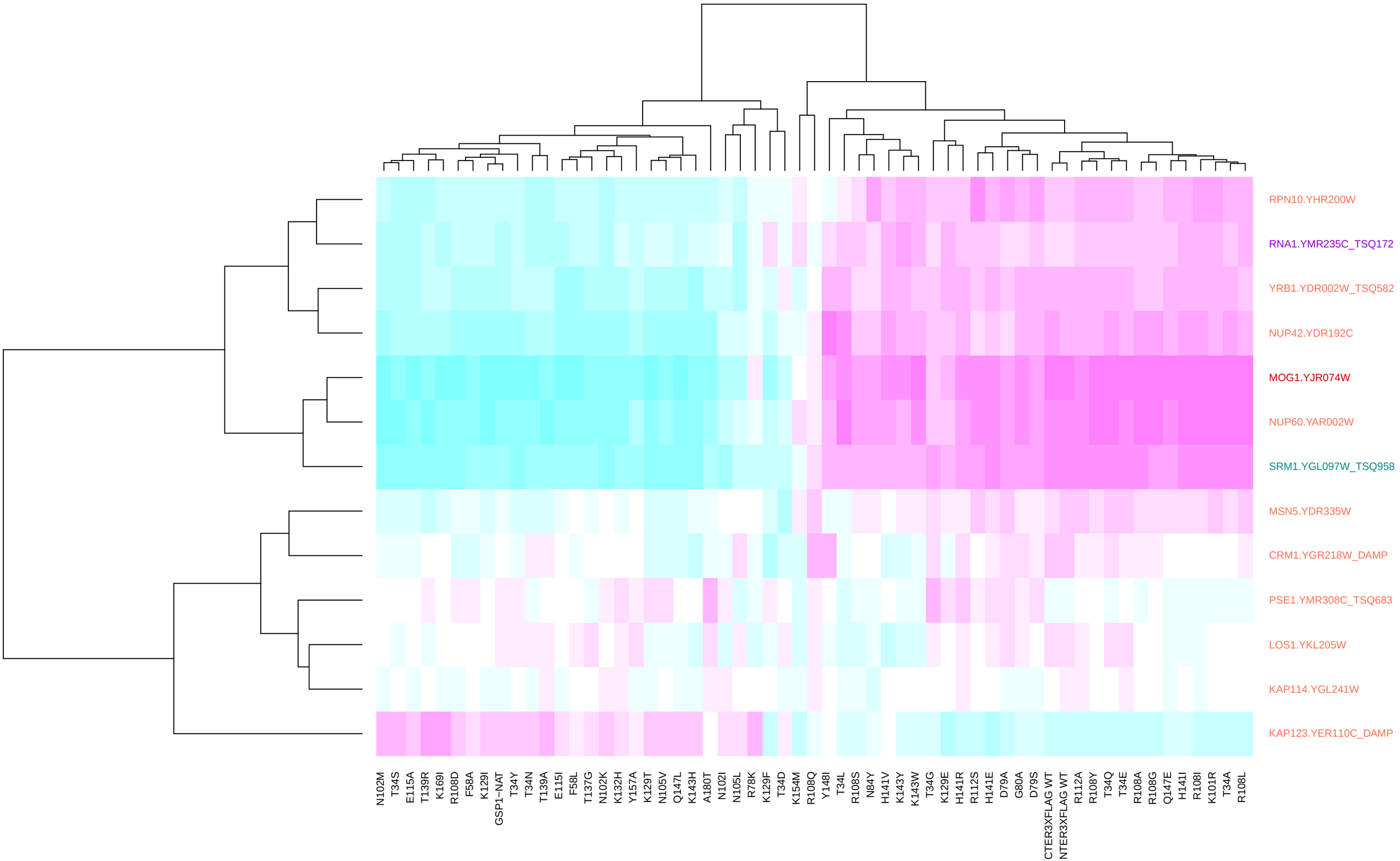
whole_library_30_12_mut



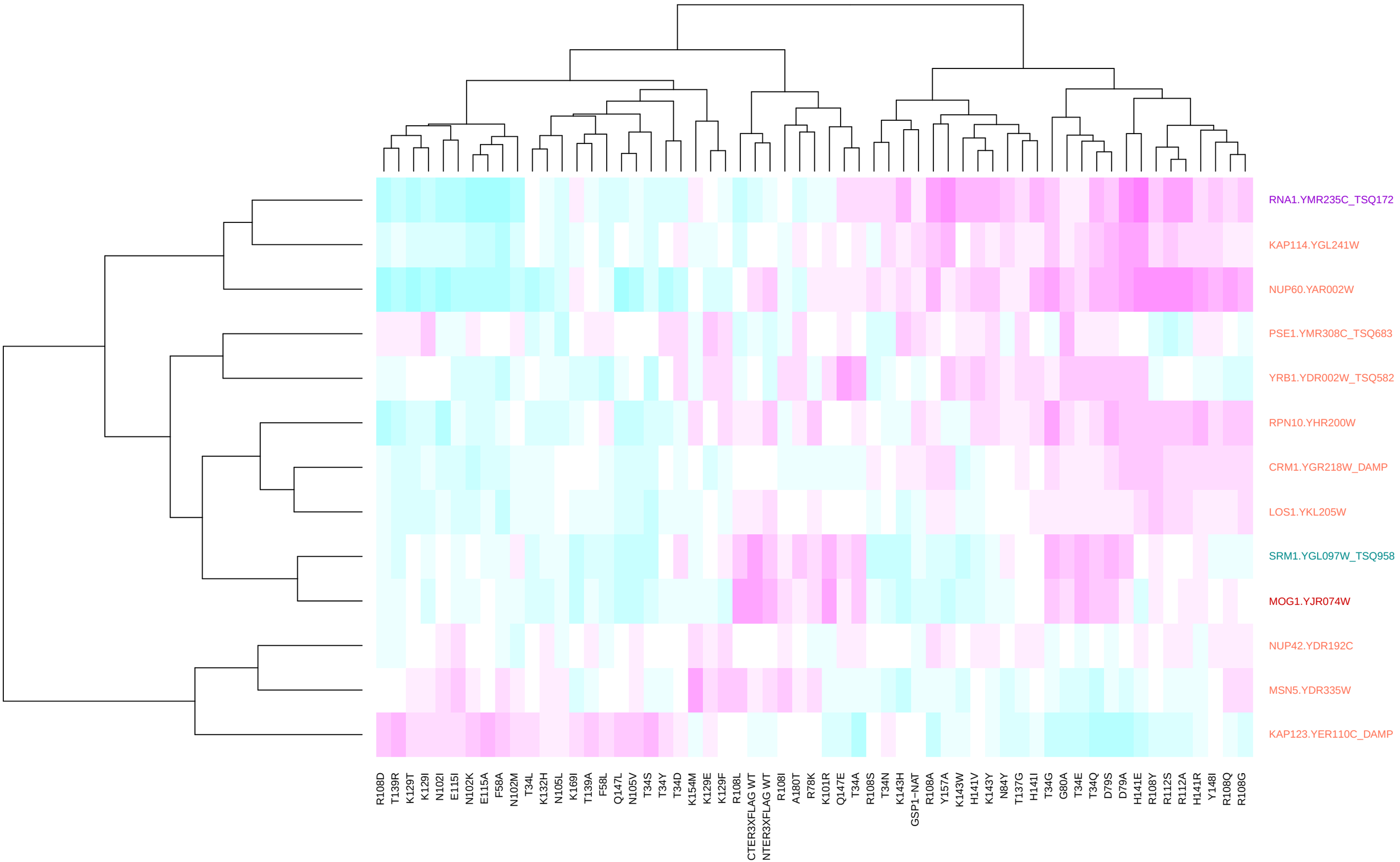
histone modification_GO_15_1_all



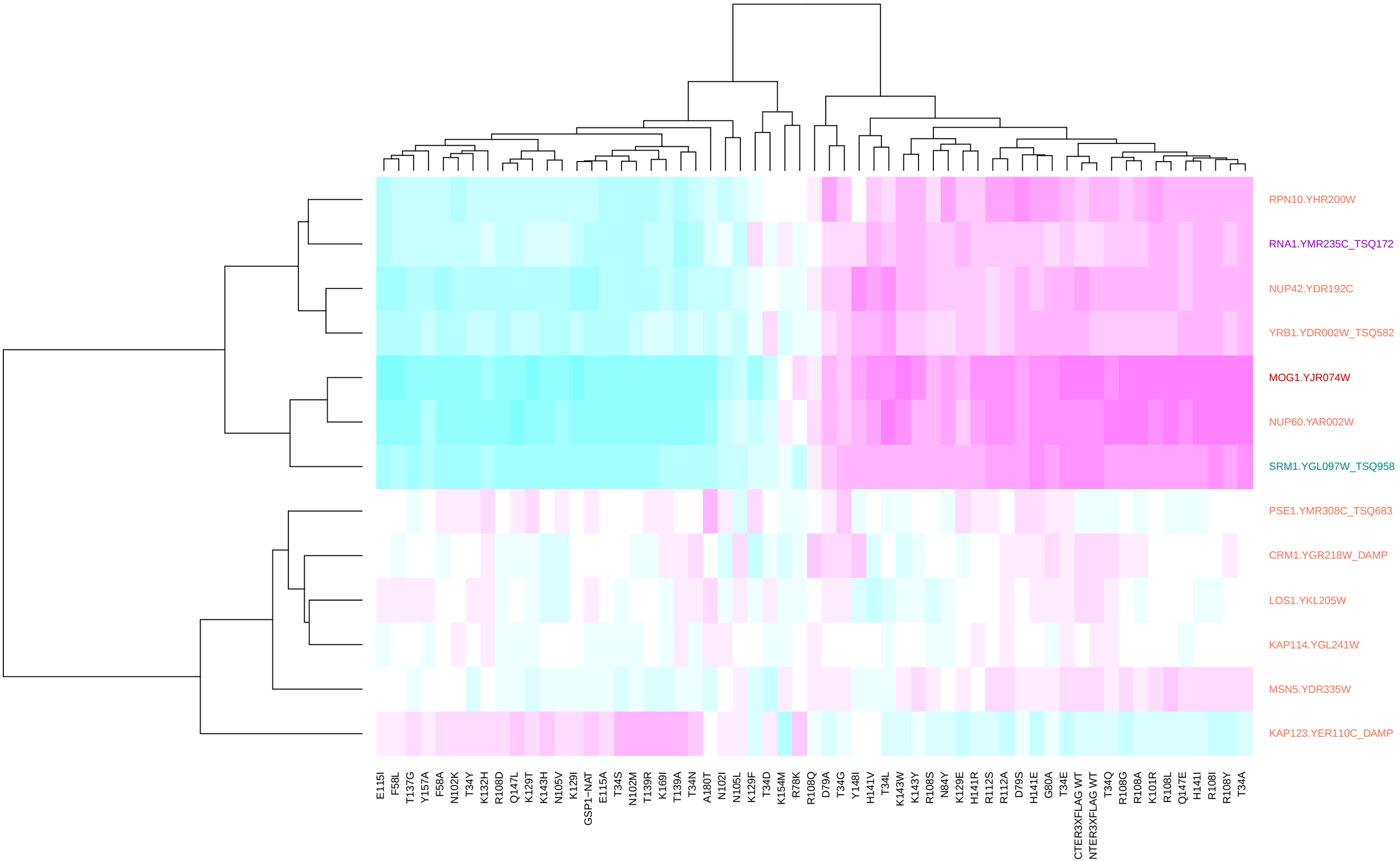
cell cycle_GO_15_9_mut



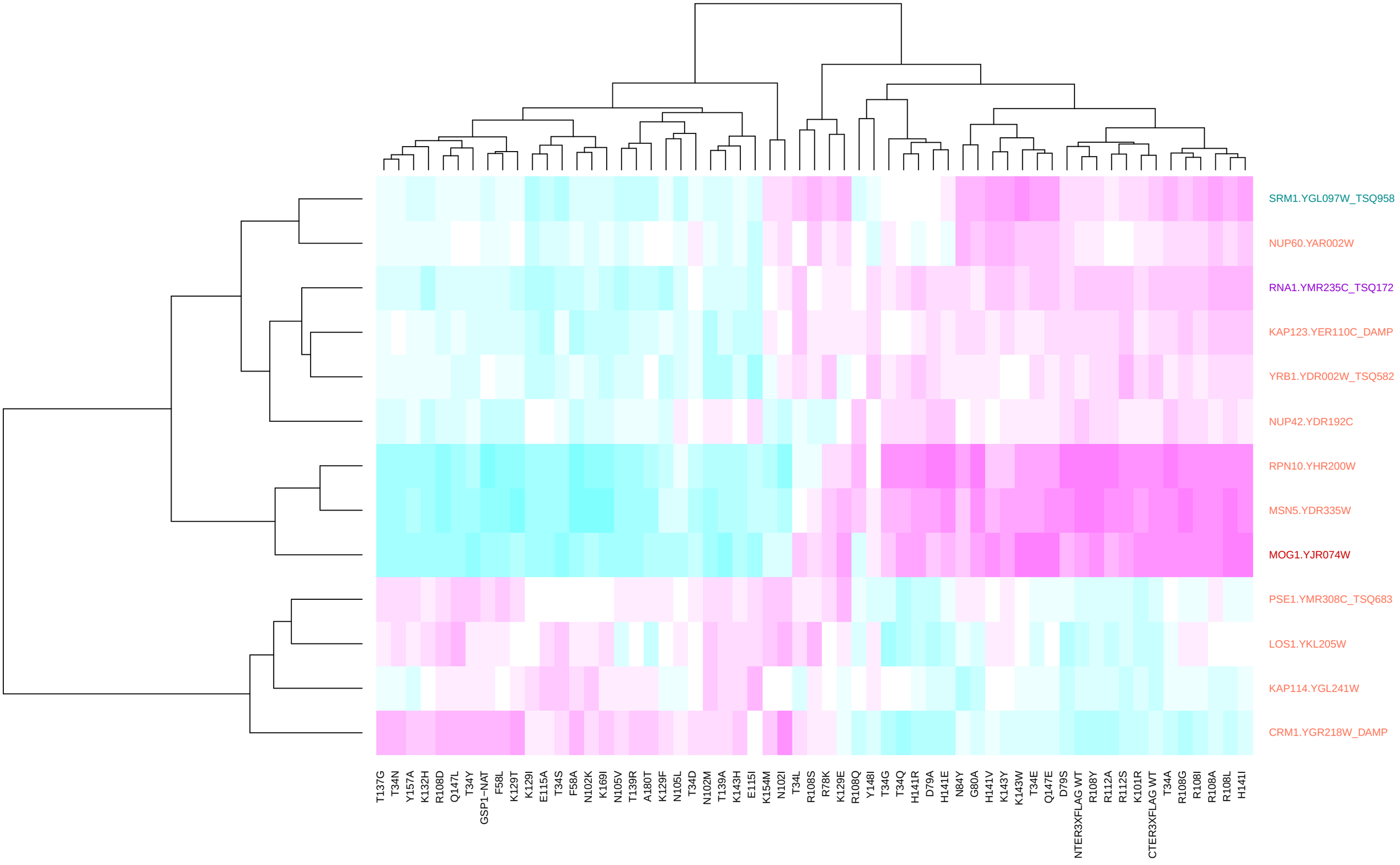
chromosome_GO_30_1_mut



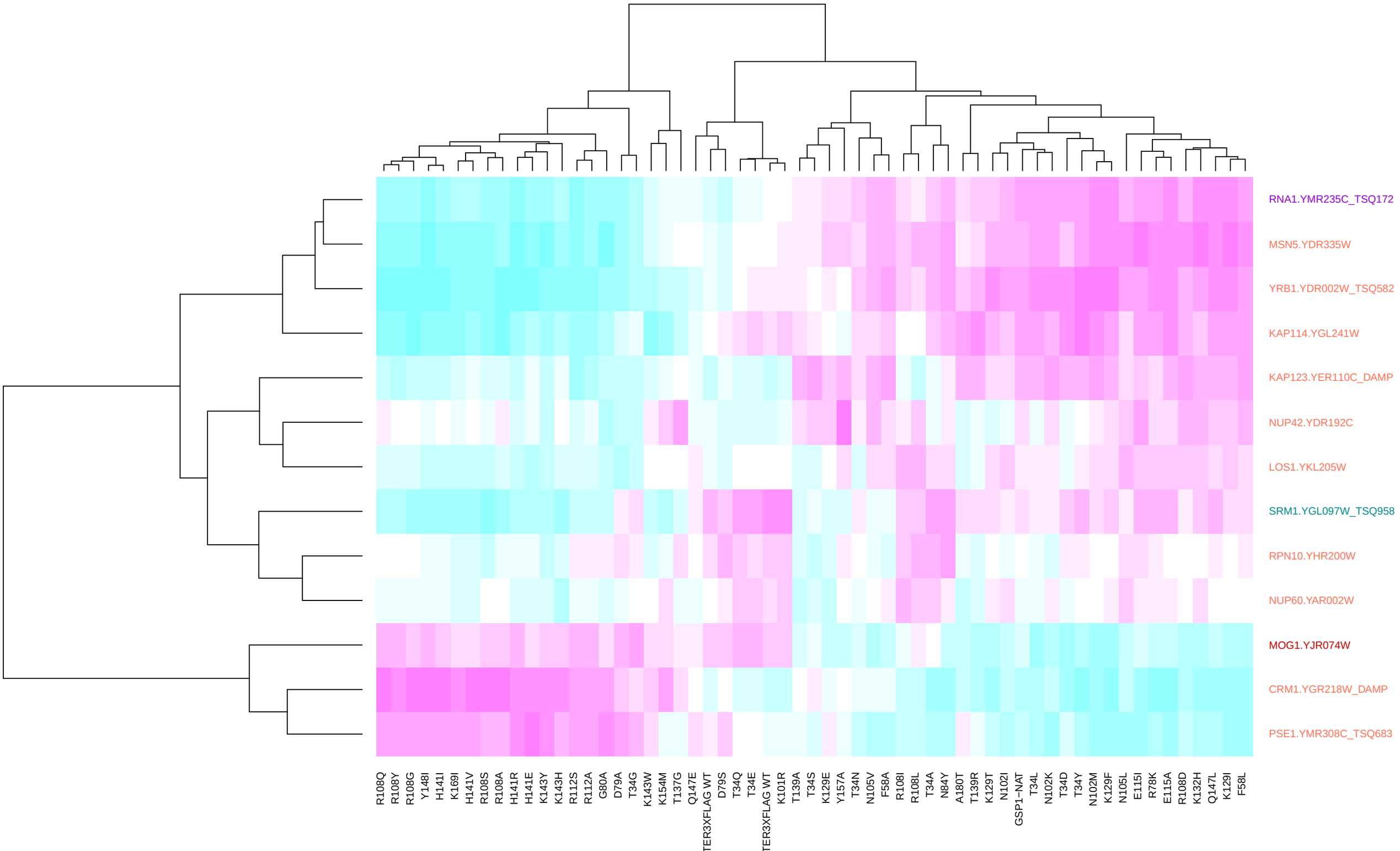
cell cycle_GO_30_3_mut



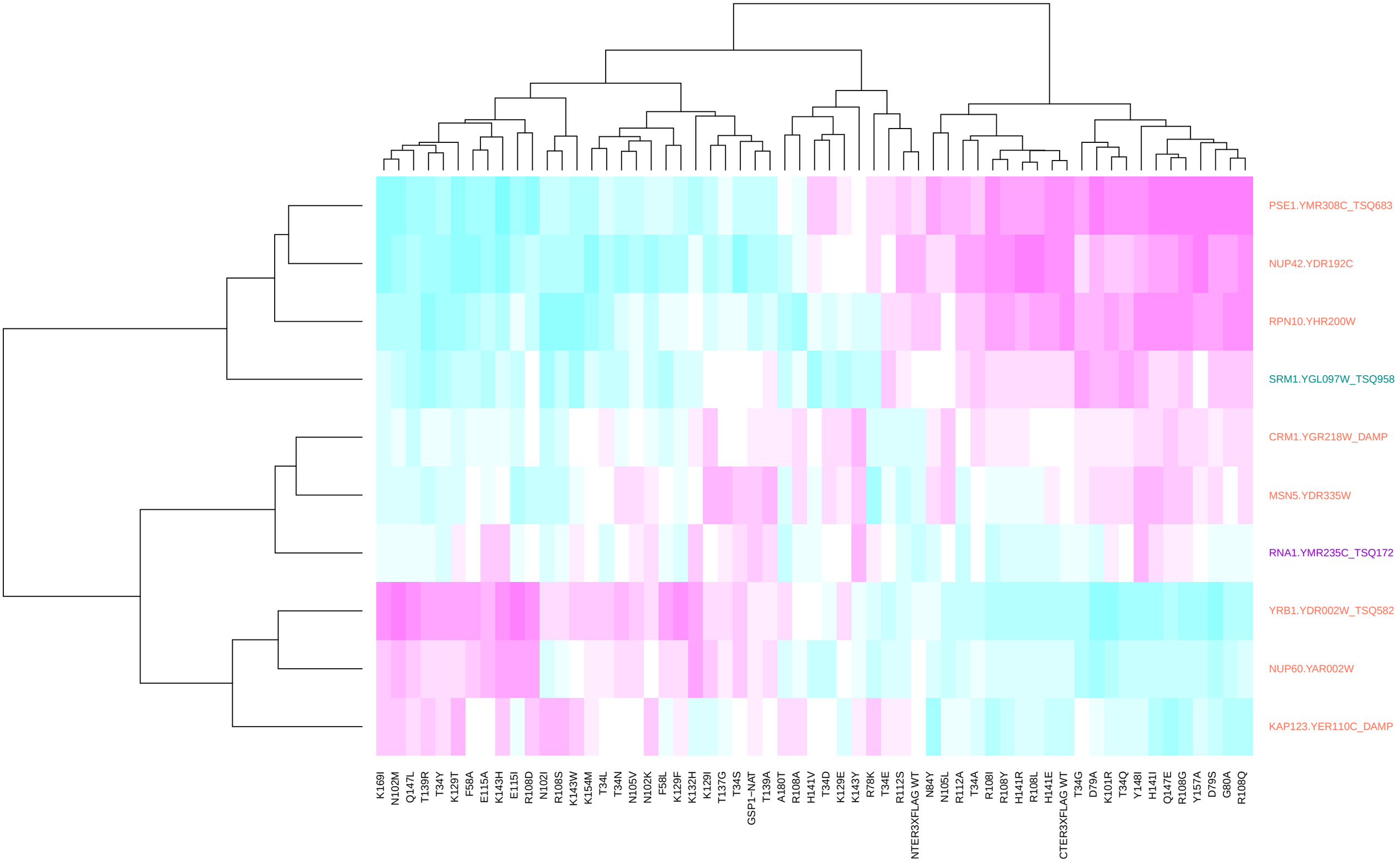
proteolysis involved in cellular protein catabolic process_GO_15_2_mut



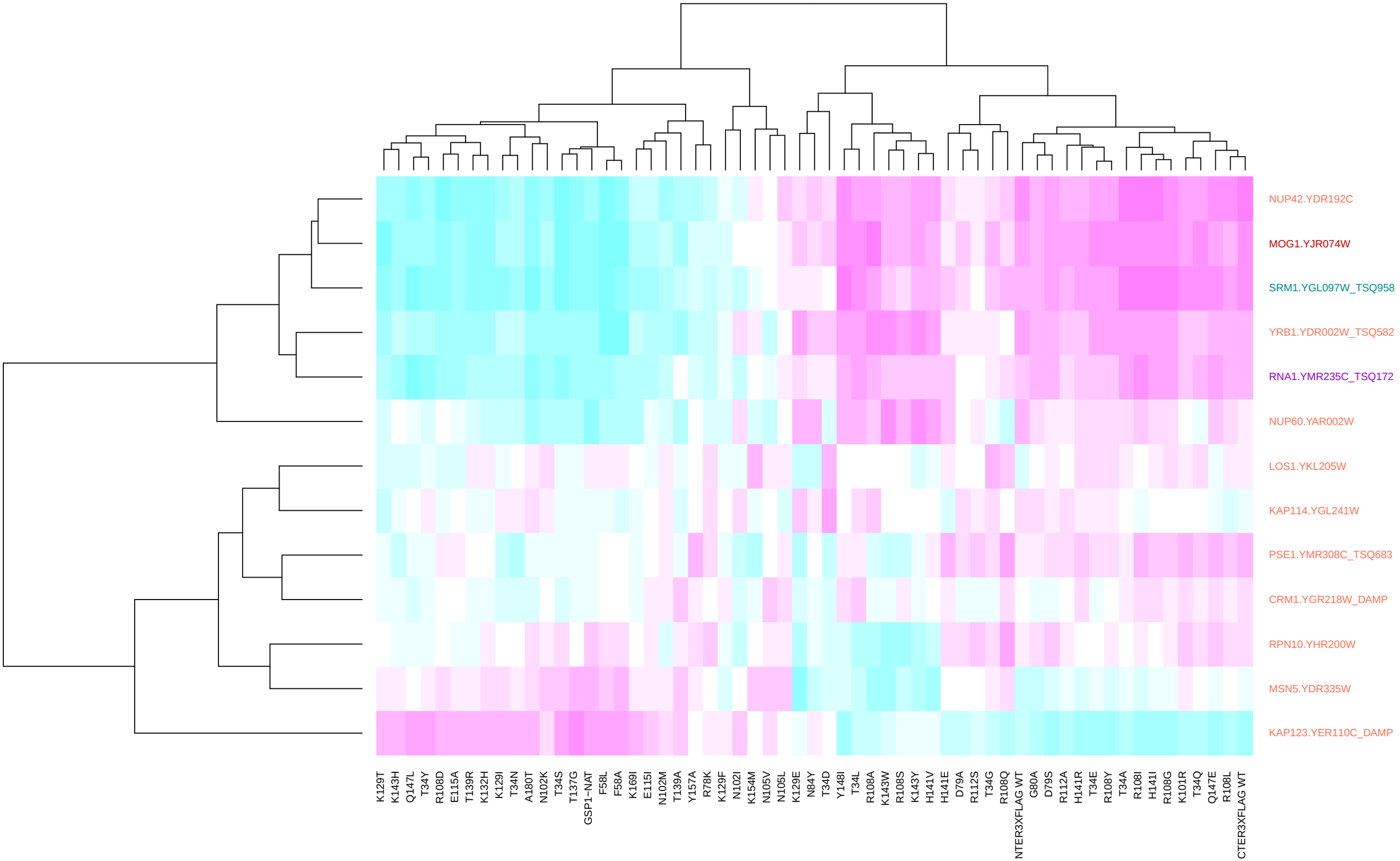
sig_Gsp1_GI_15_1_all



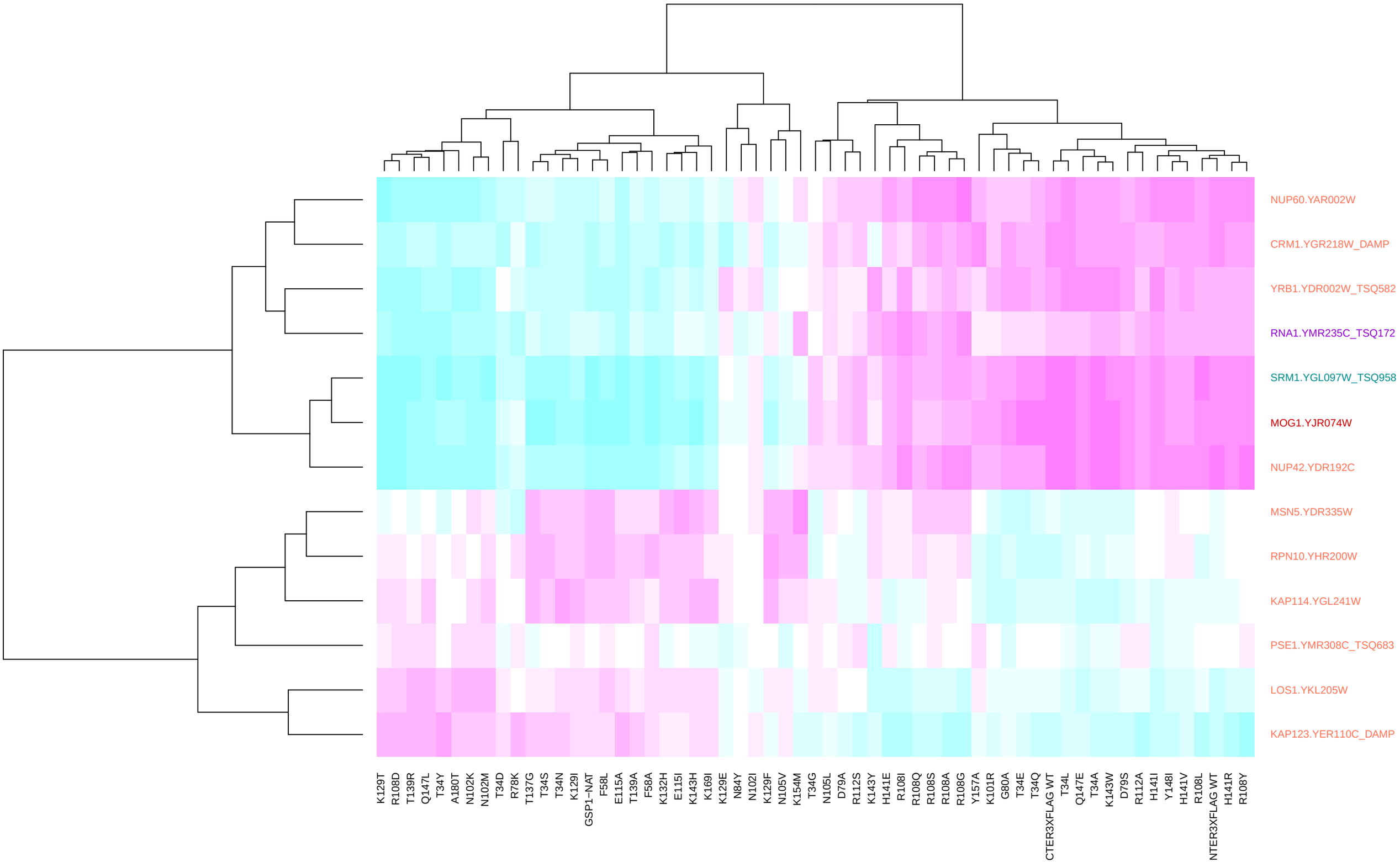
cytoplasmic translation_GO_15_1_all



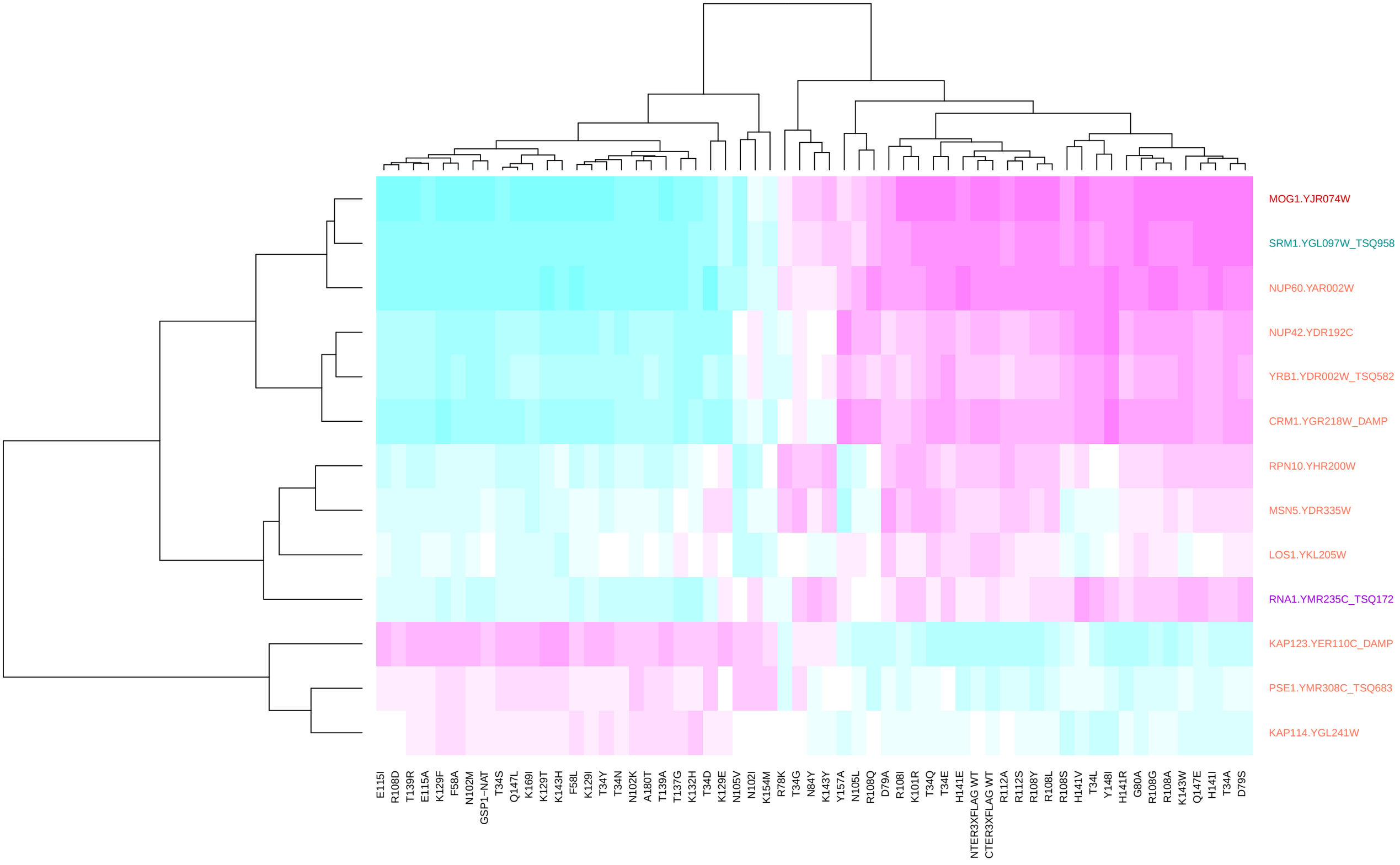
ribosomes and translation_GO_15_2_mut



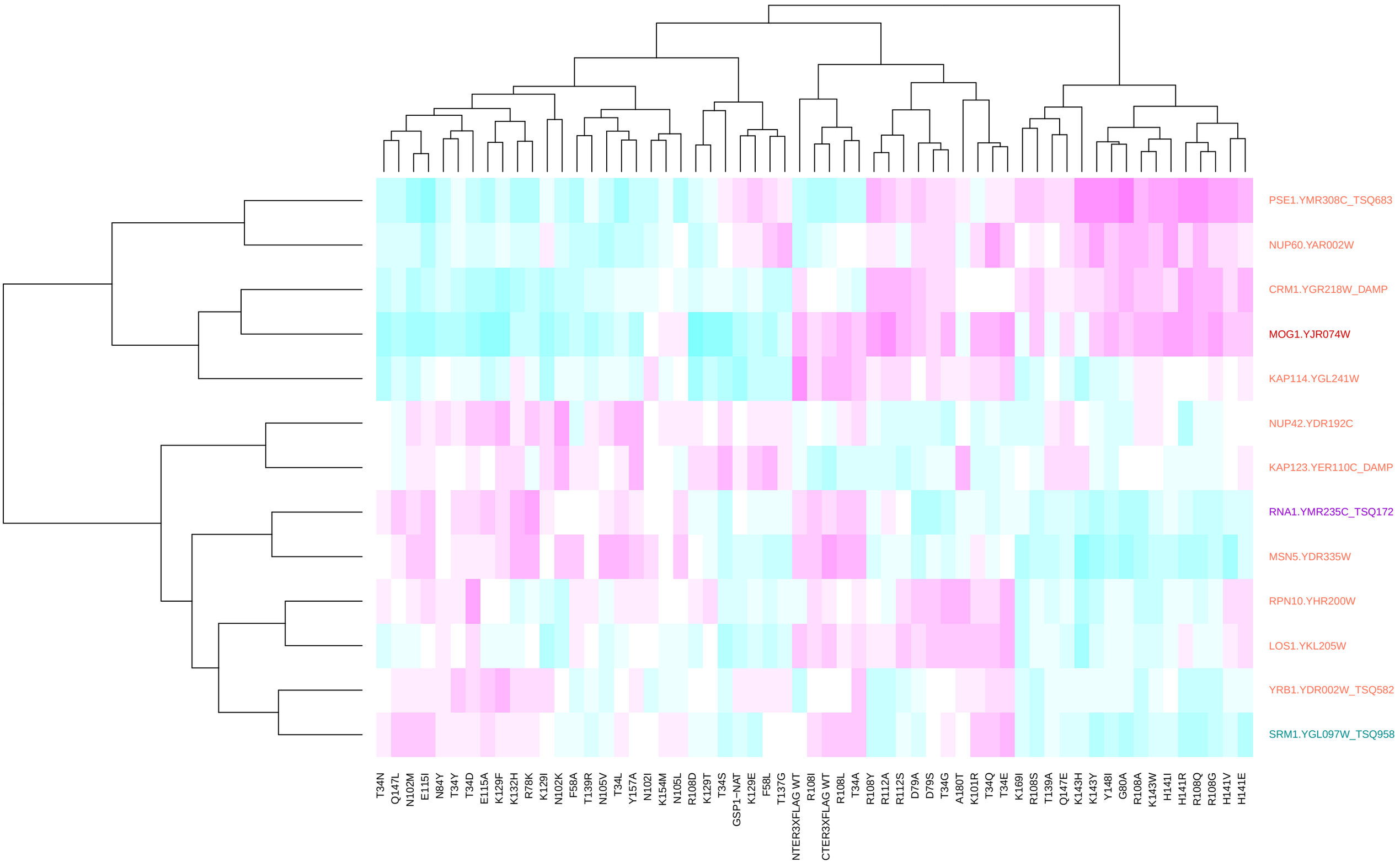
transcription and mRNA processing_GO_15_1_all



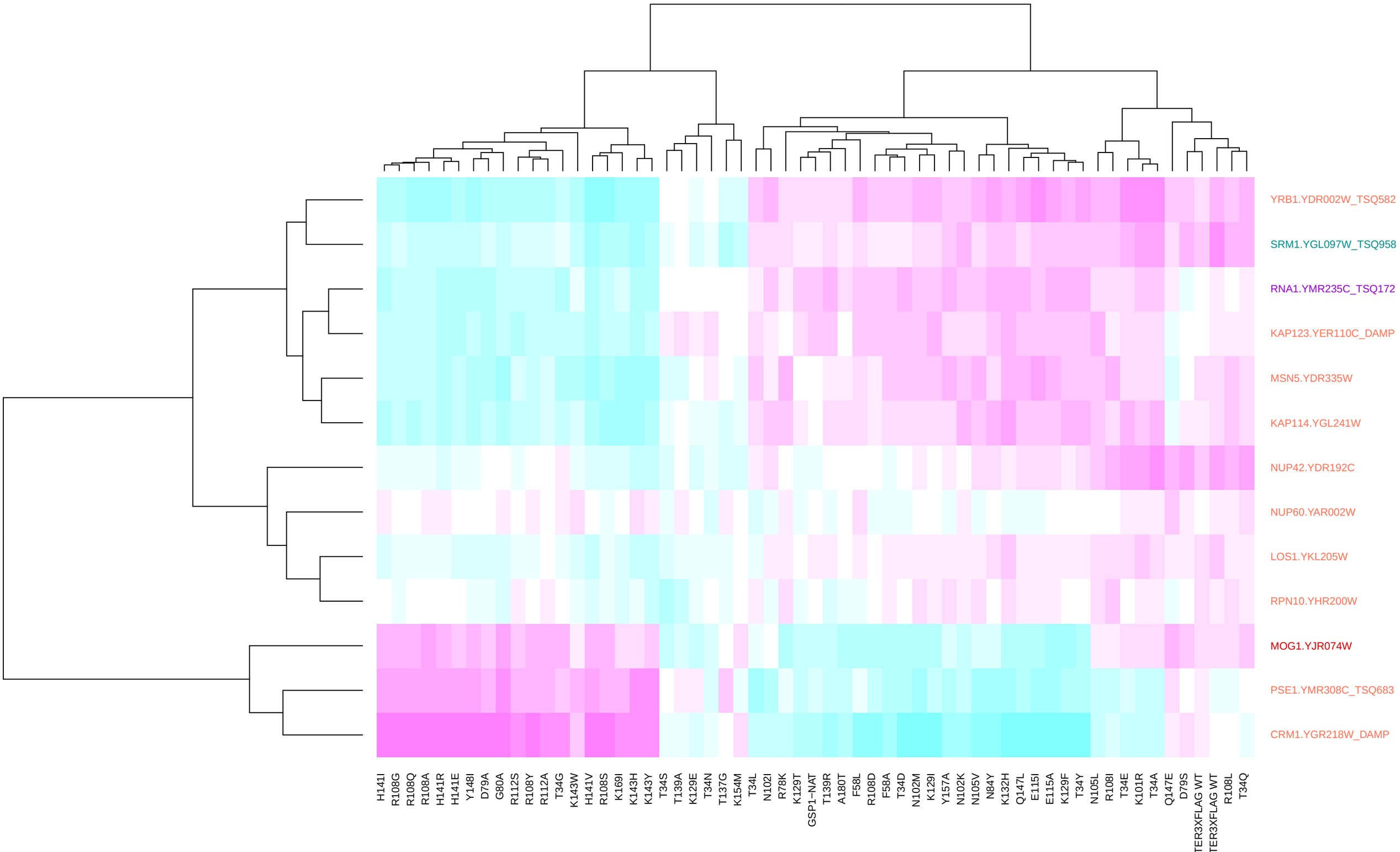
chromatin_GO_15_7_mut



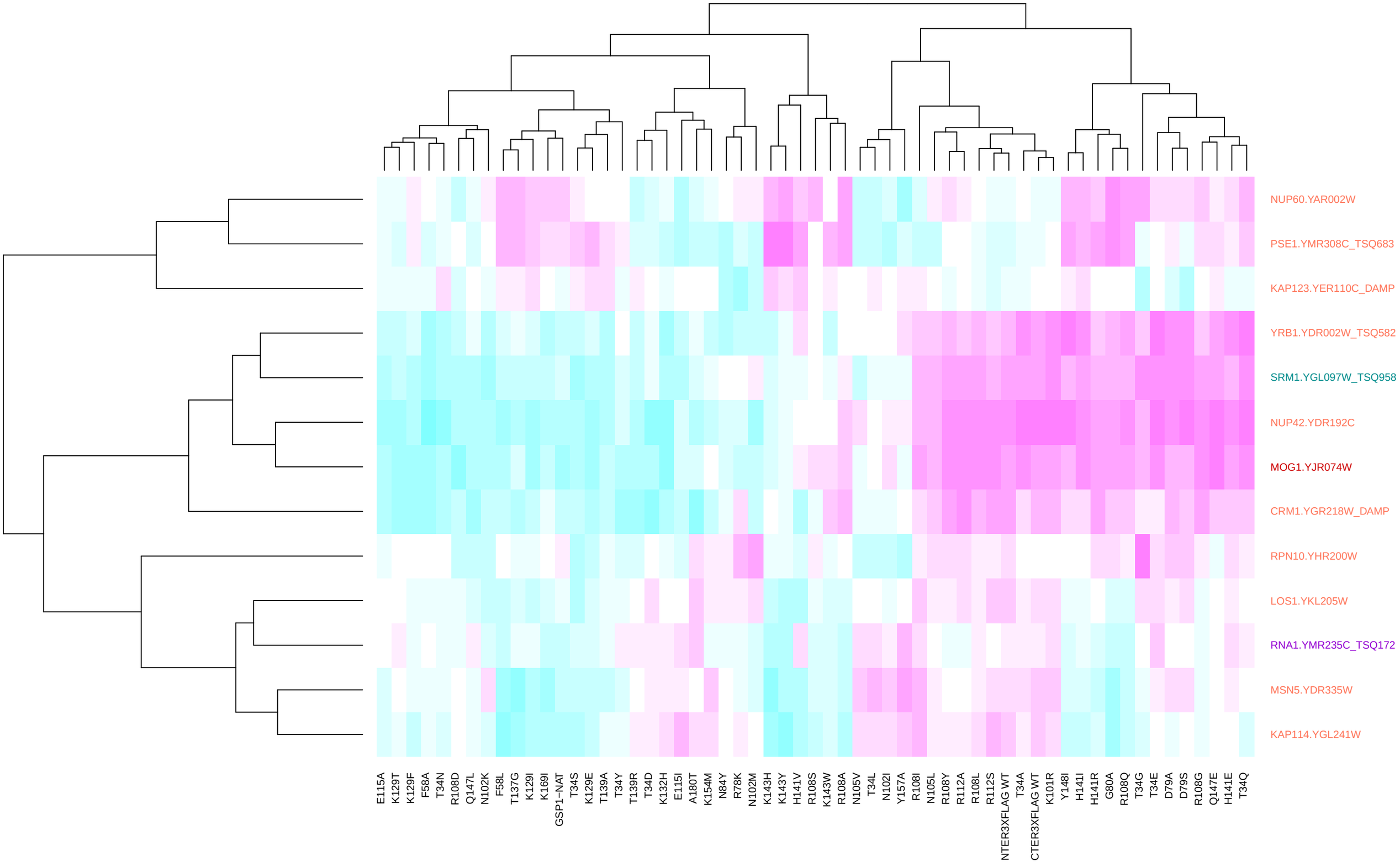
chromosome segregation_GO_15_1_all



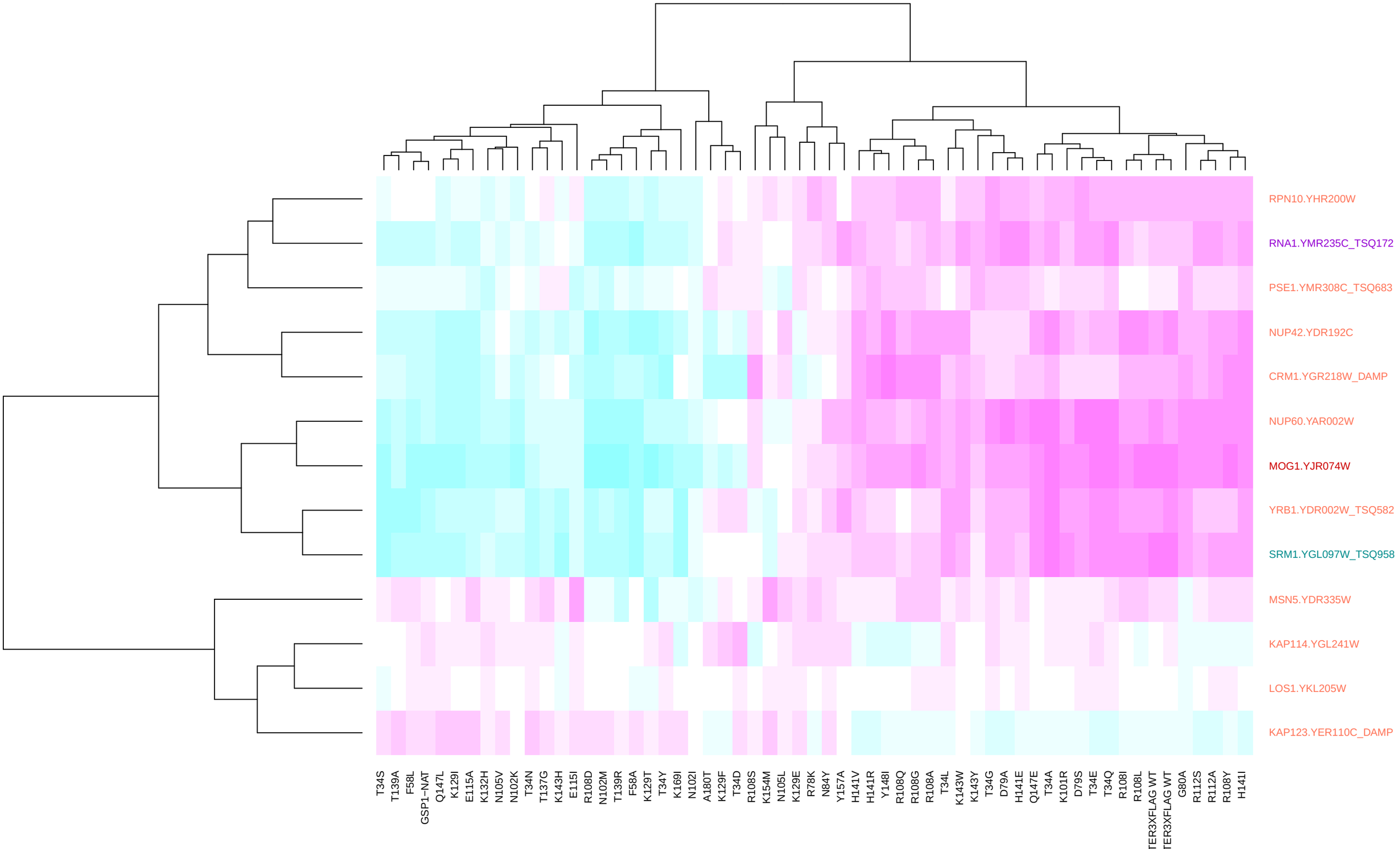
cytoskeleton and microtubules_GO_15_2_mut



cytoskeleton and microtubules_GO_15_3_all



sig_Gsp1_GI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MSN5.YDR335W
KAP114.YGL241W
LOS1.YKL205W
KAP123.YER110C_DAMP
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T139A
F58L
GSP1−NAT
Q147L
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K132H
N105V
N102K
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T137G
K143H
E115I
R108D
N102M
T139R
F58A
K129T
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A180T
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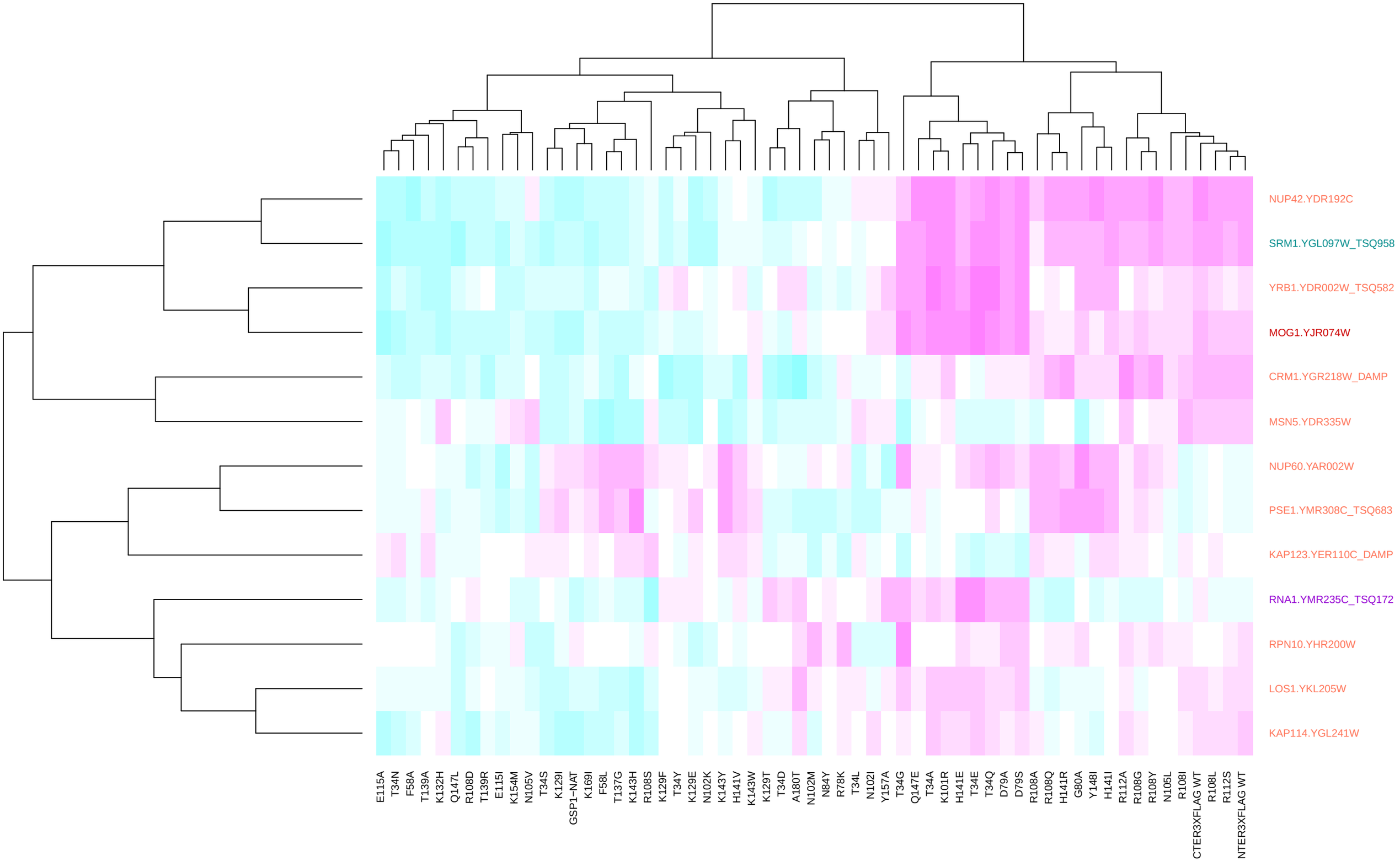
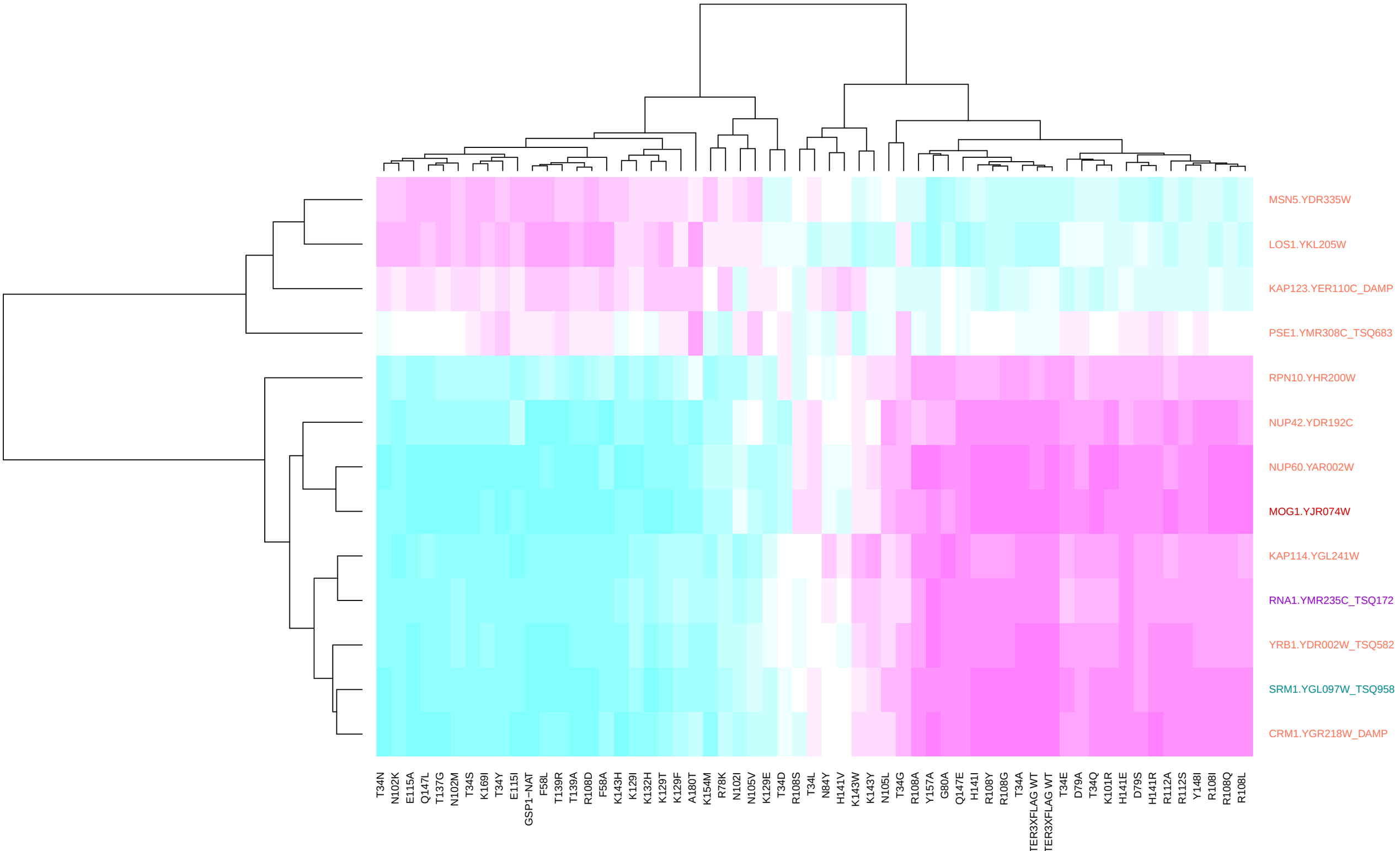
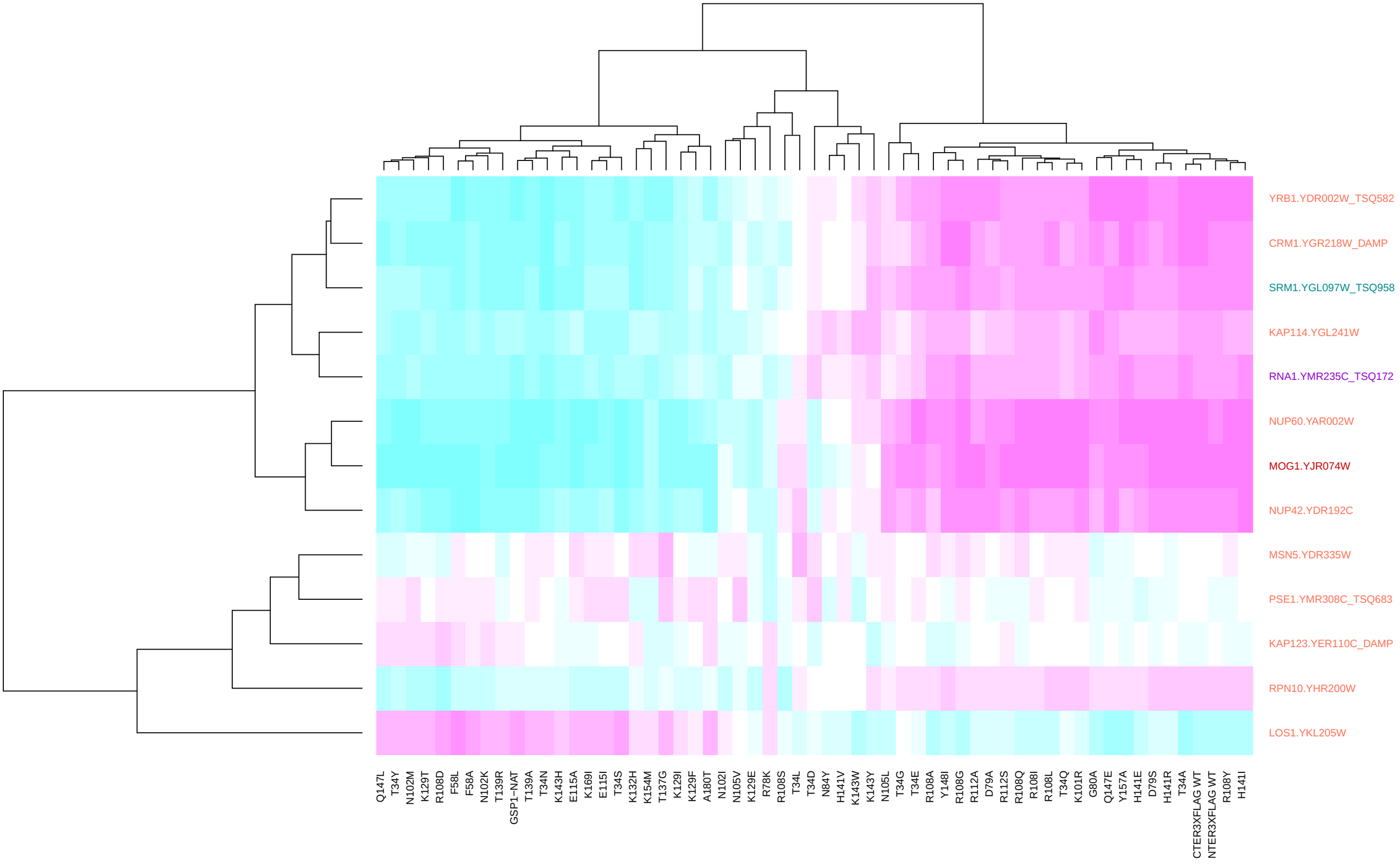
cytoskeleton and microtubules_GO_30_3_all



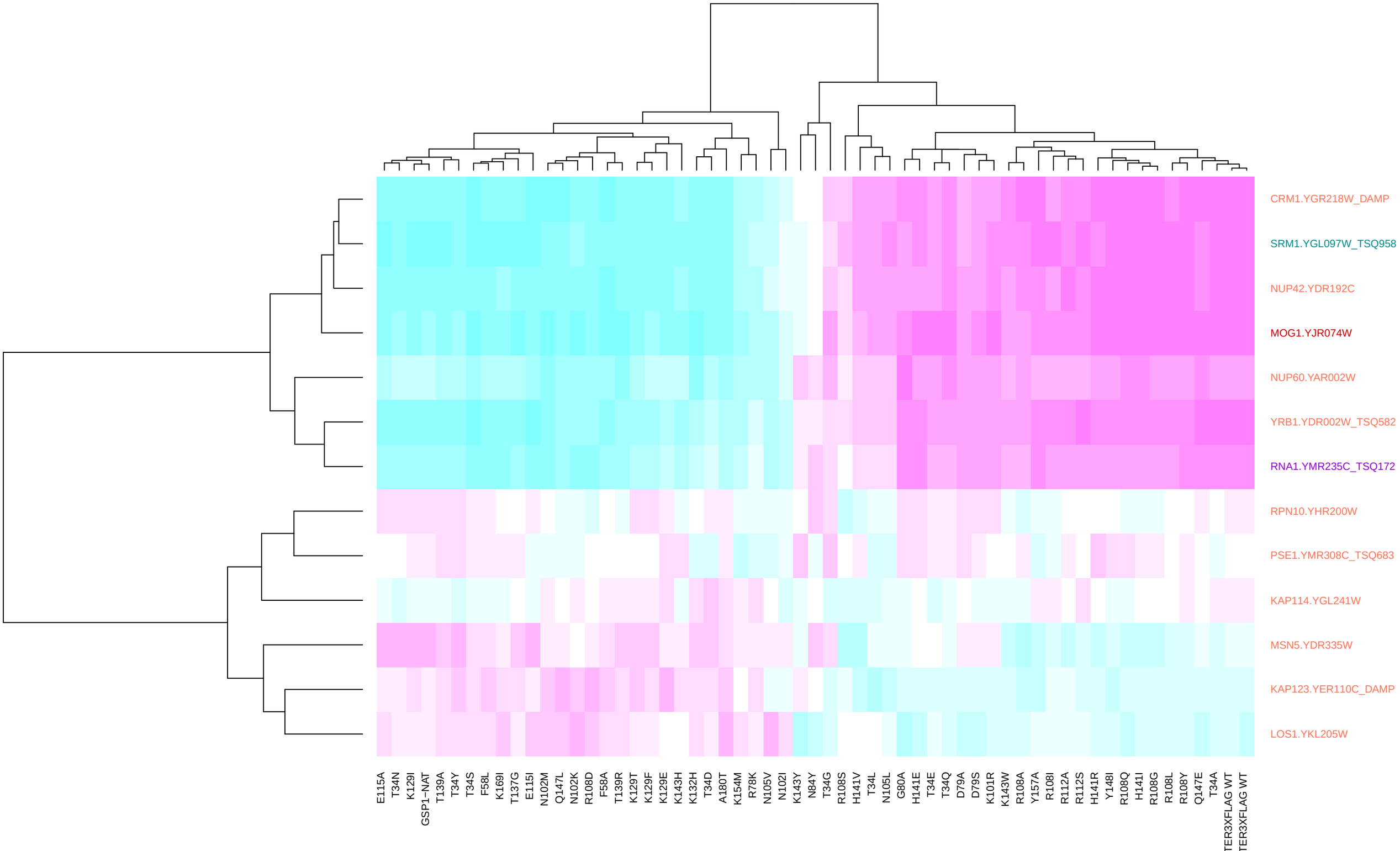
nuclear transport and organization_GO_15_3_all



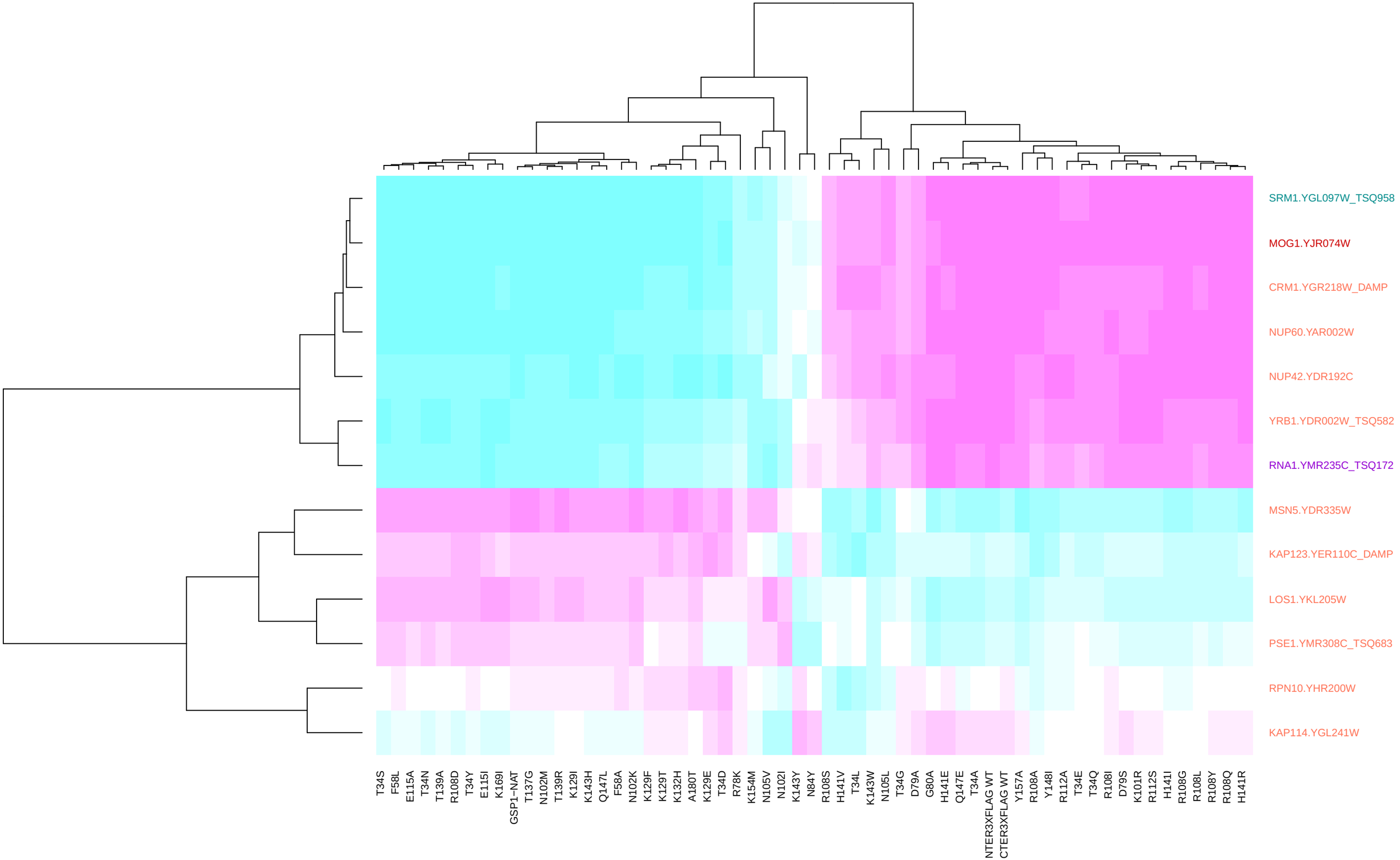
nuclear transport_GO_15_1_all



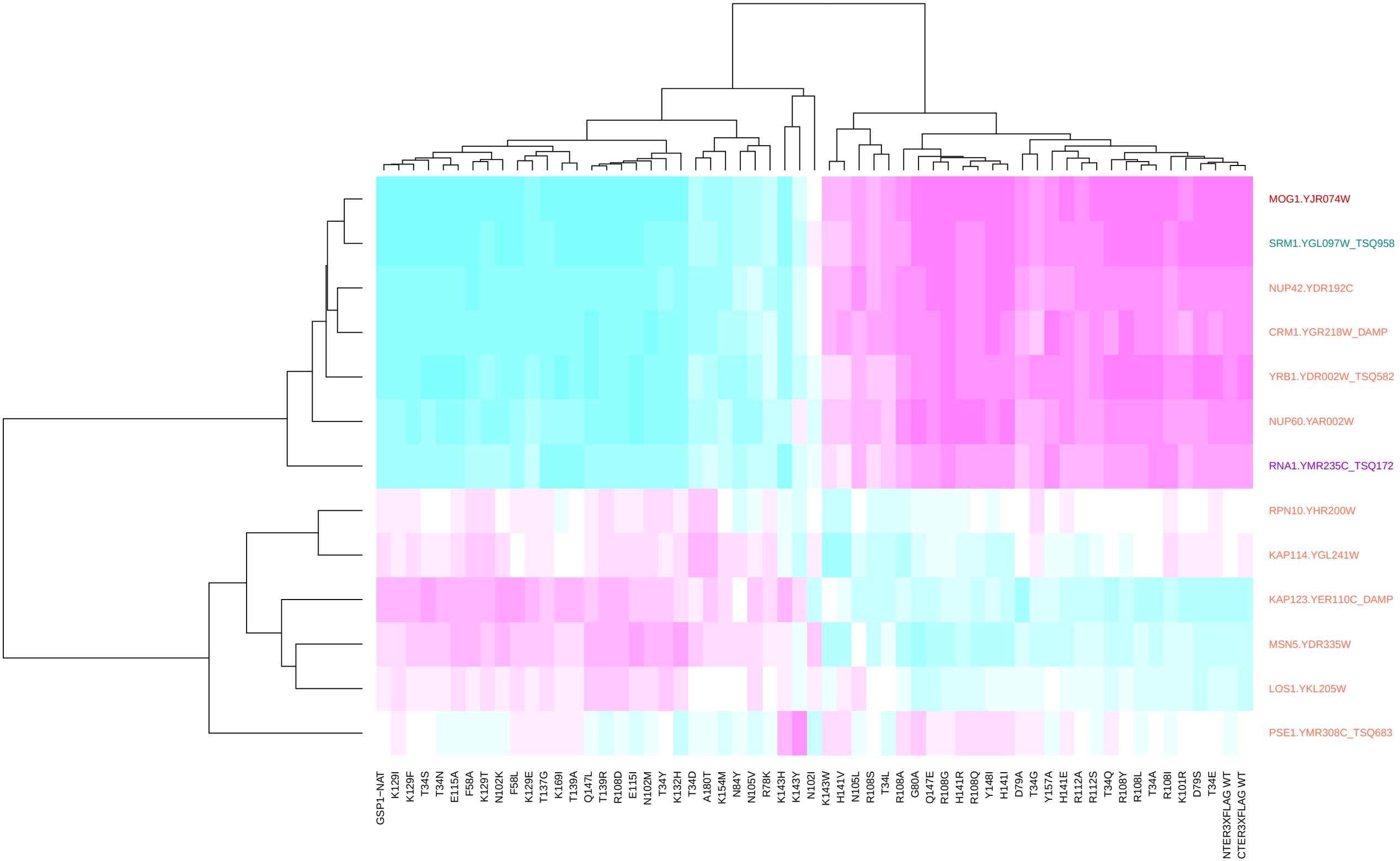
nucleus organization



nucleus organization_GO_15_1_all



sig_Gsp1_GI_15_9_all



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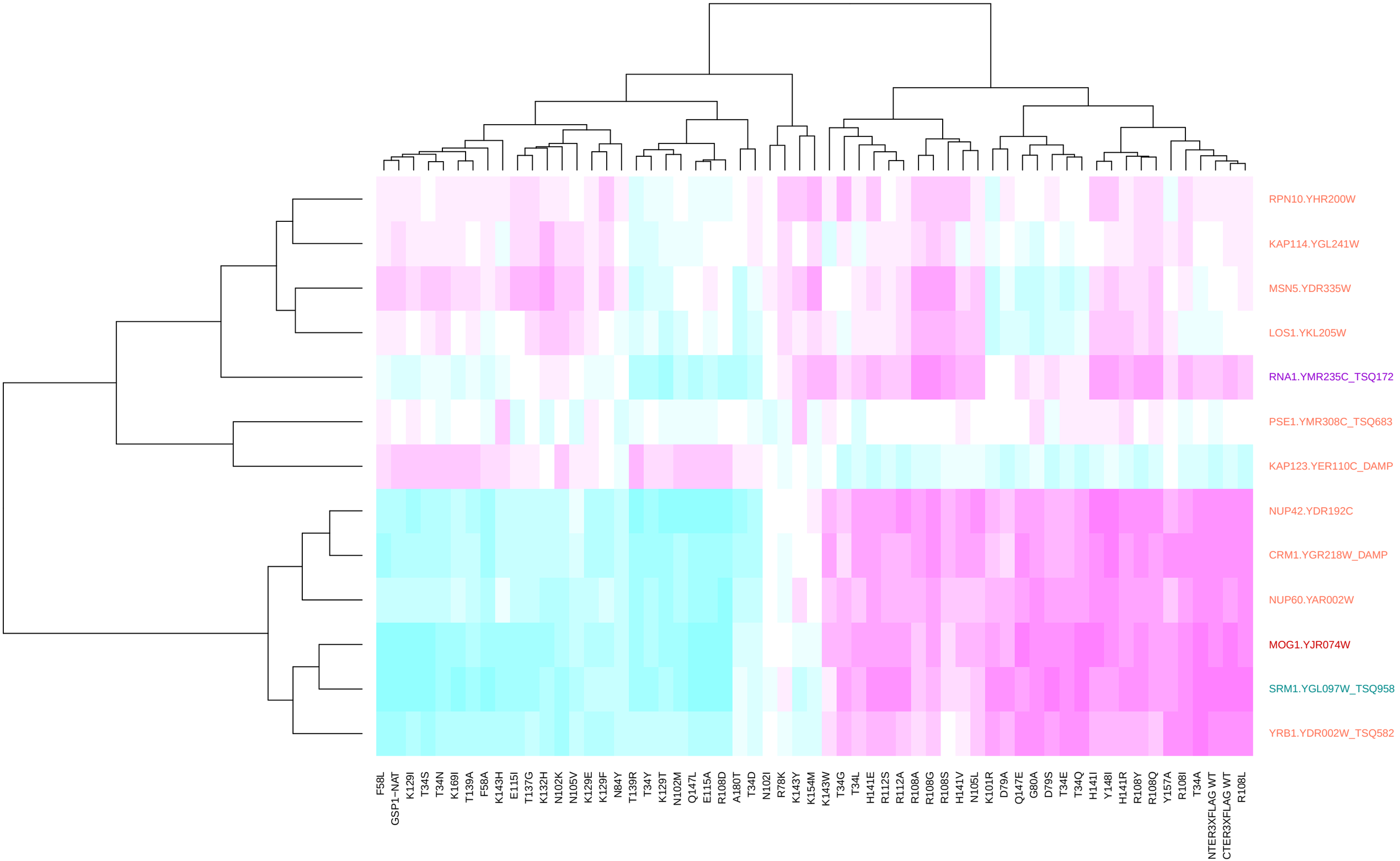
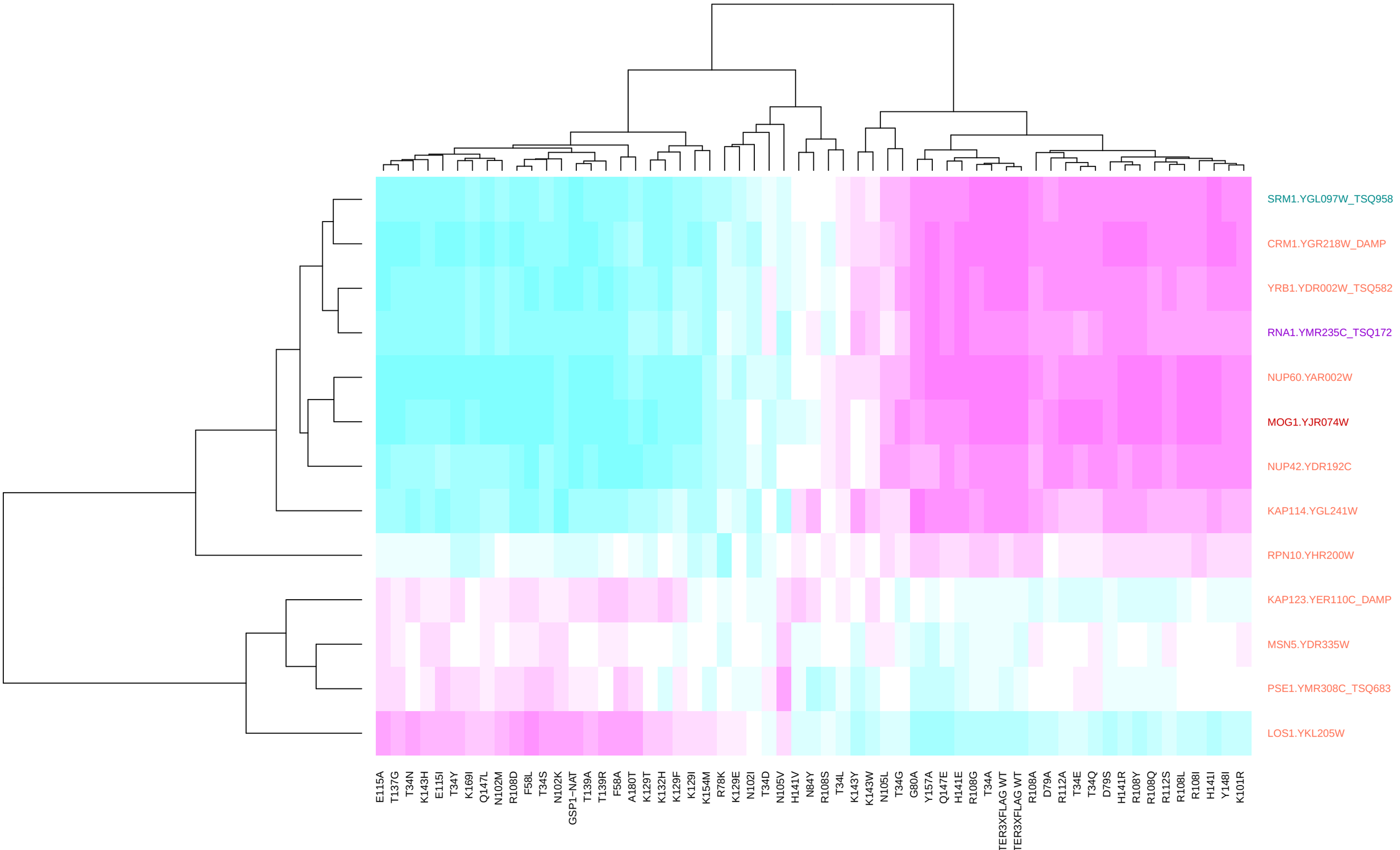
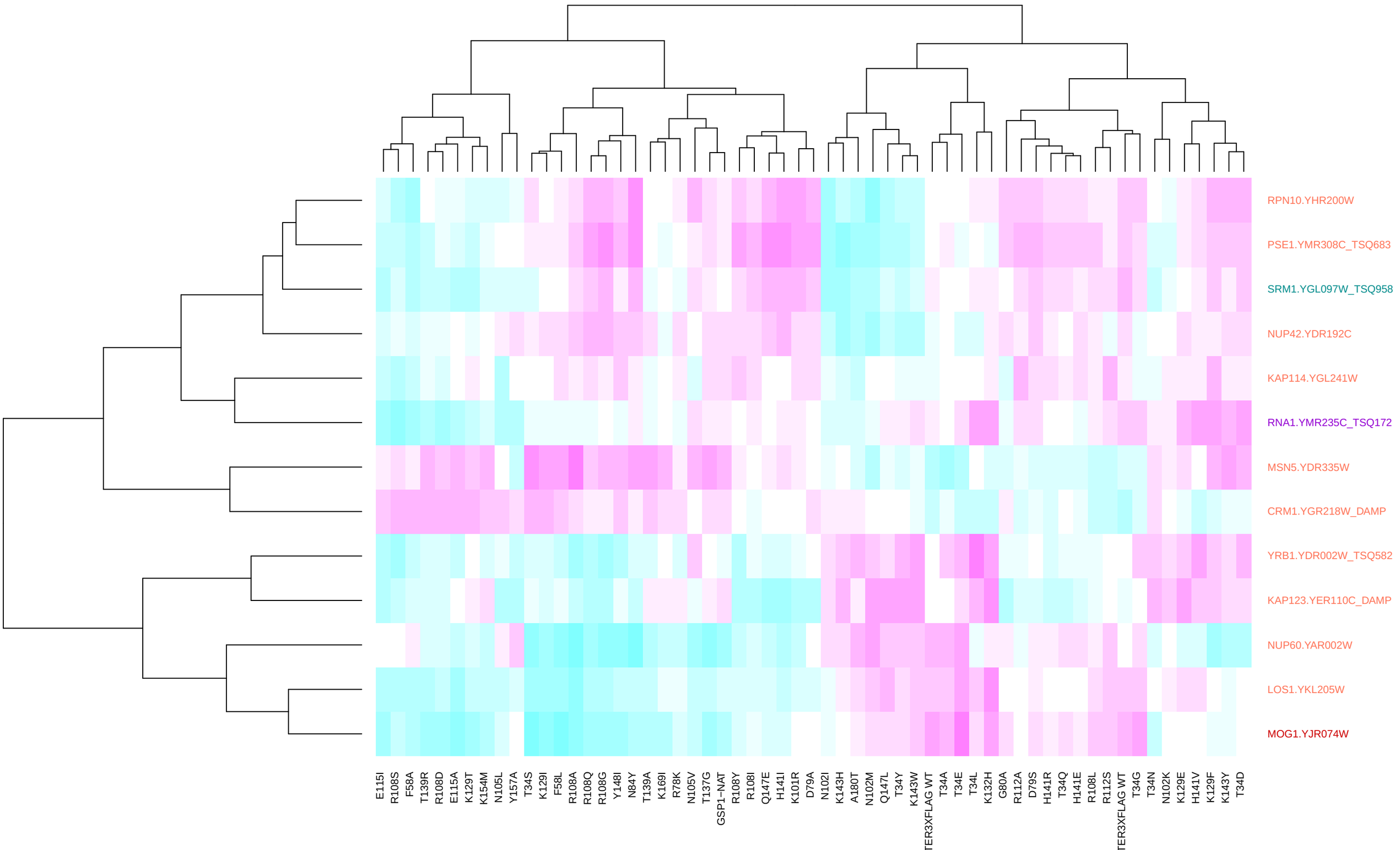


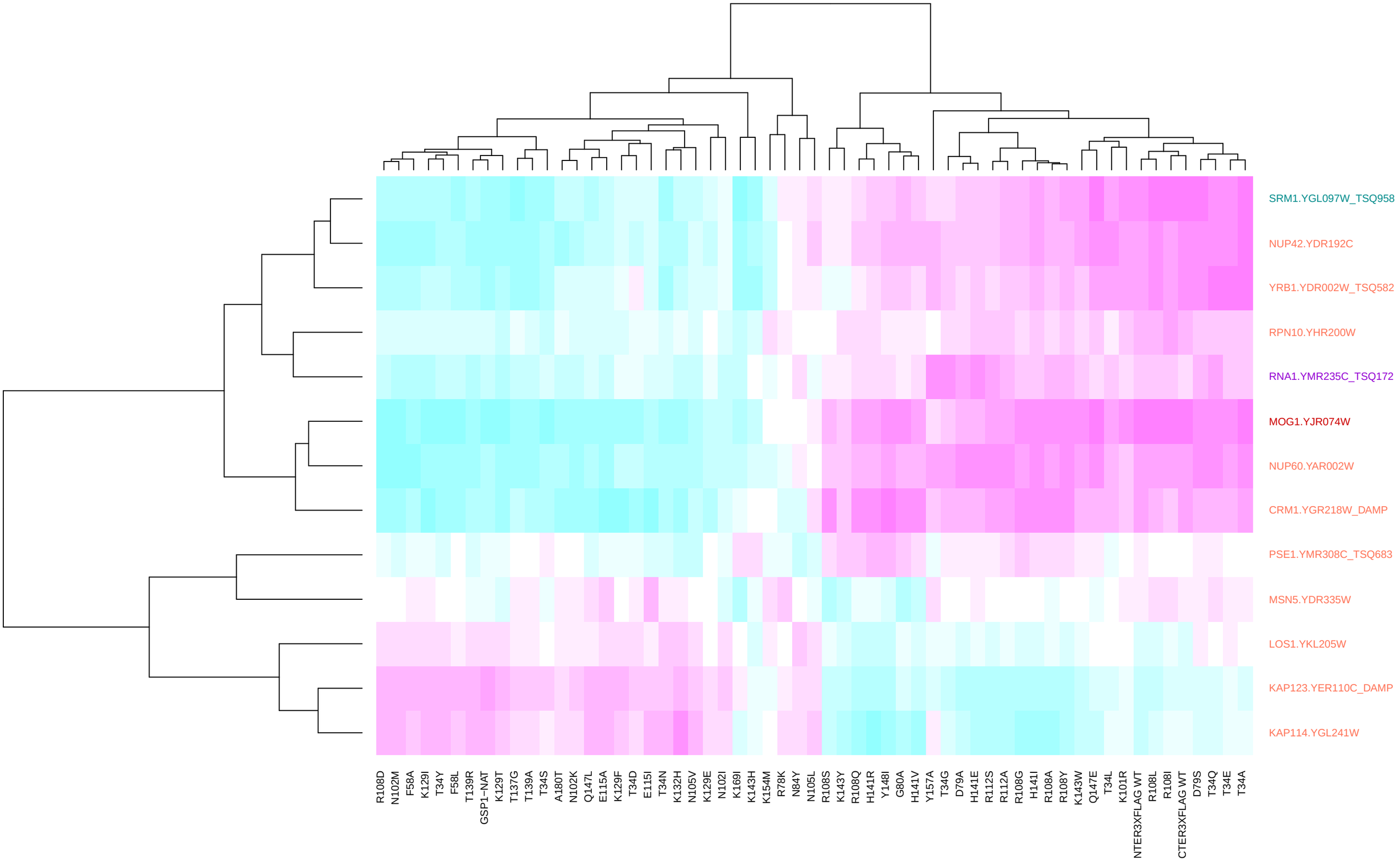
whole_library_15_36_all



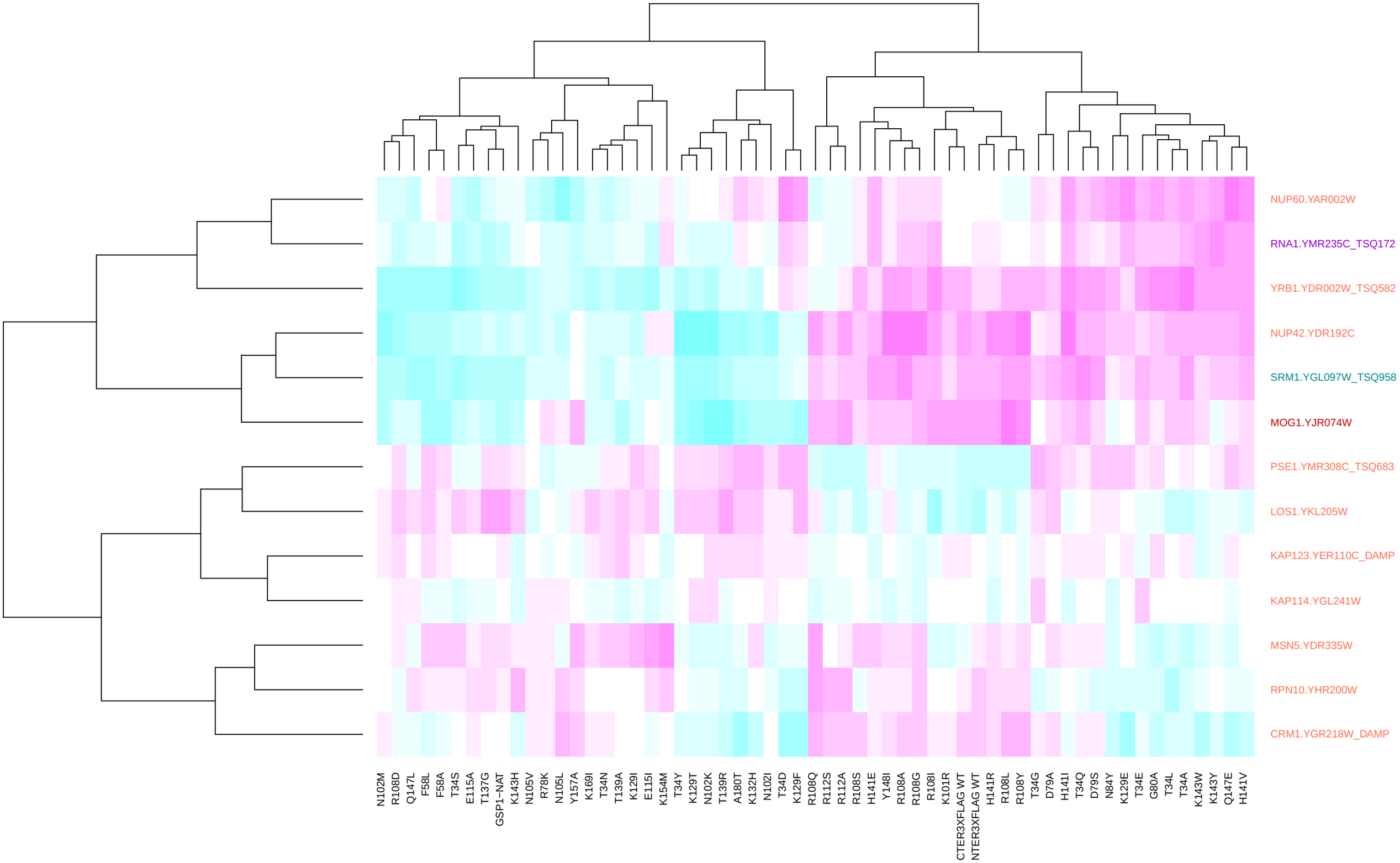
transcription and mRNA processing_GO_15_7_all



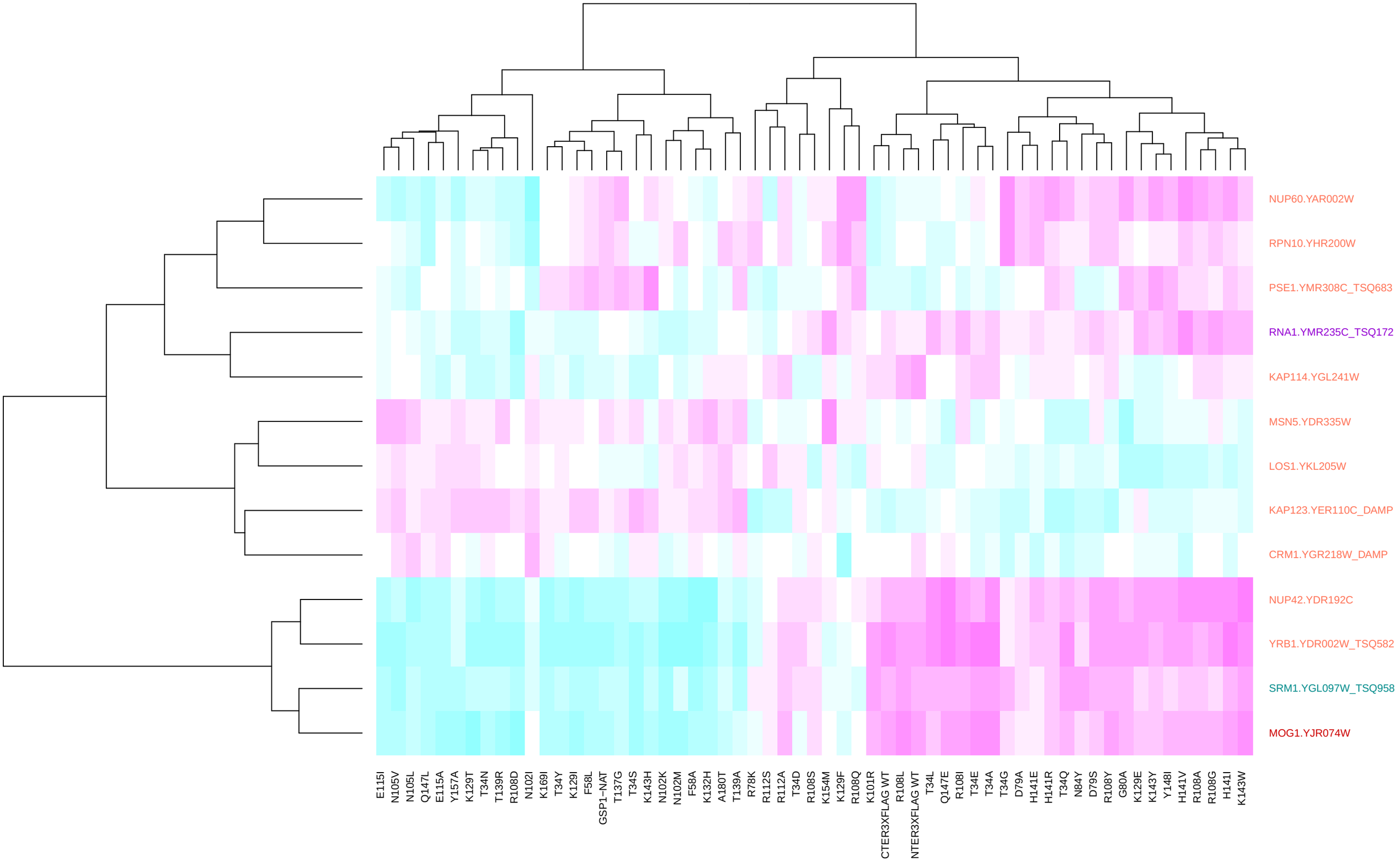
sig_Gsp1_GI_30_1_mut



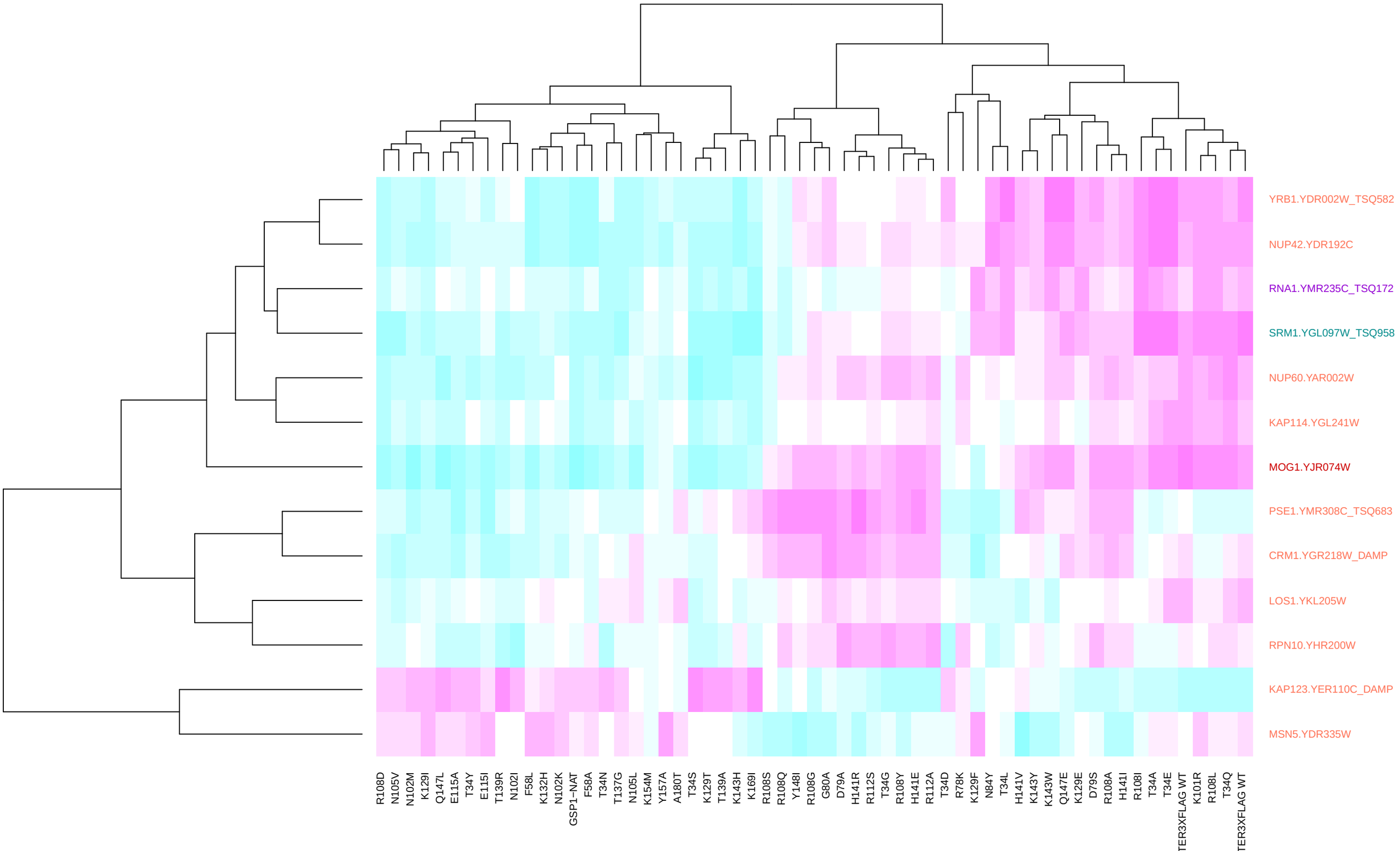
RNA processing



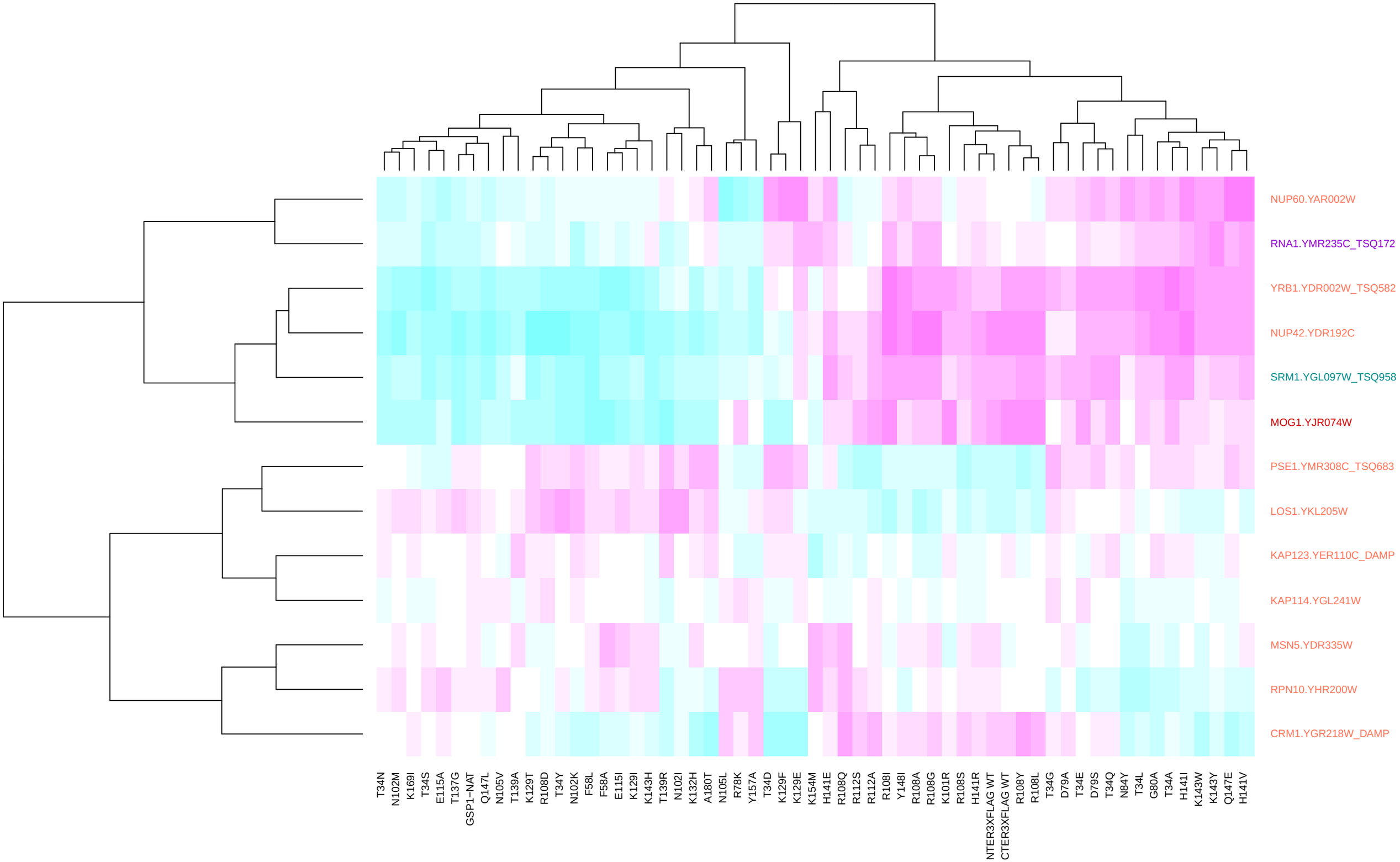
budding_GO_15_1_all



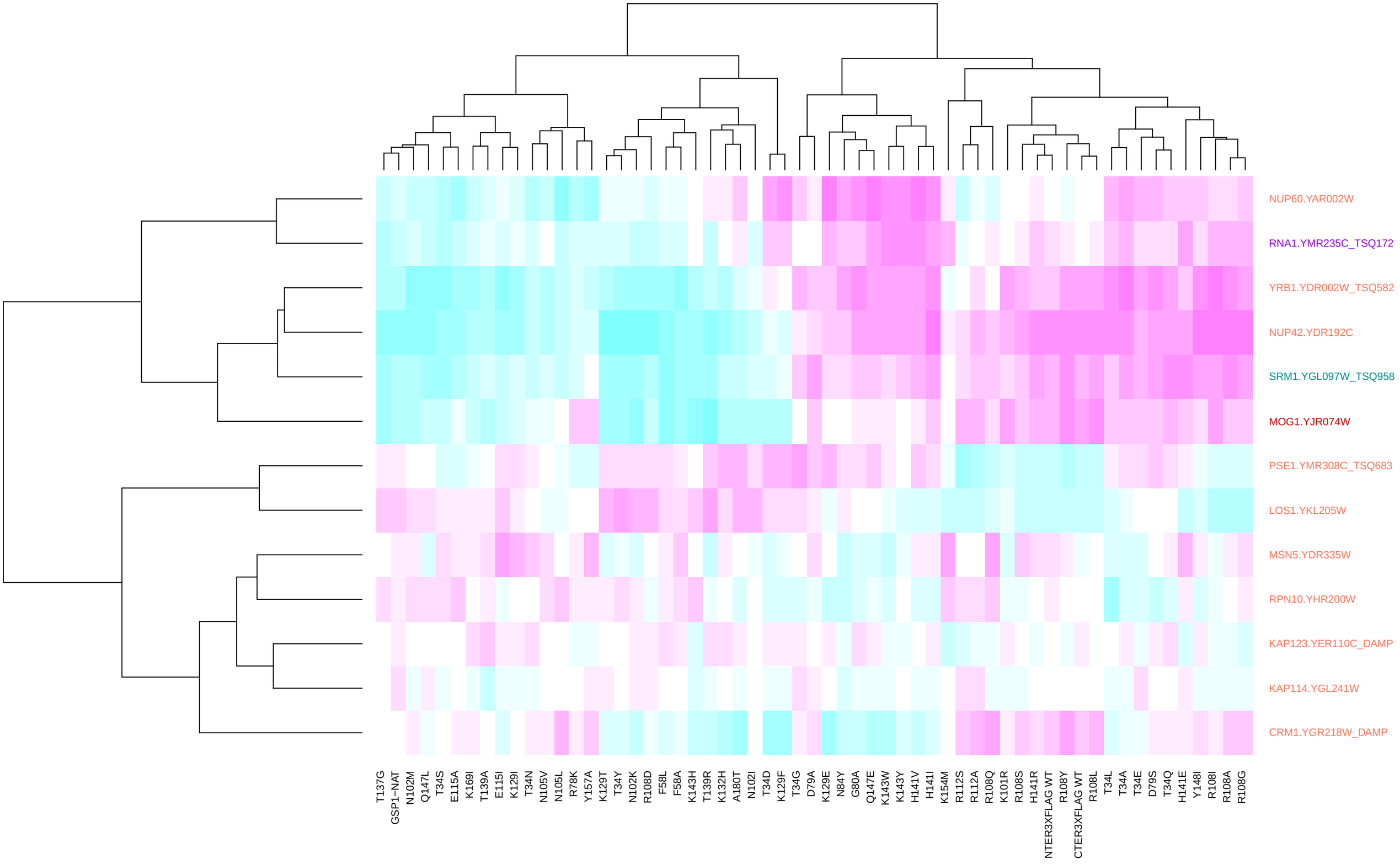
organelle fission_GO_30_1_mut



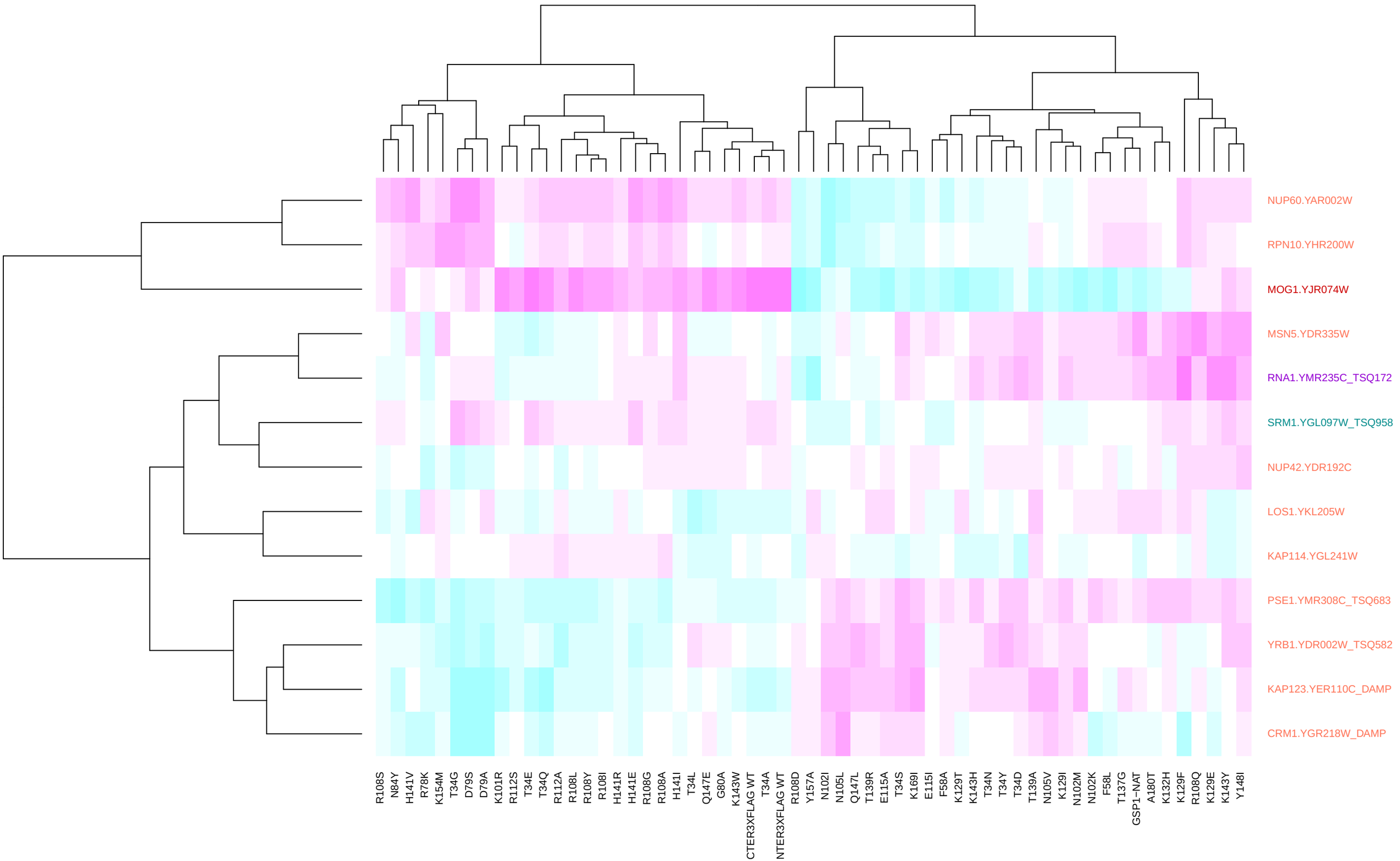
mRNA processing



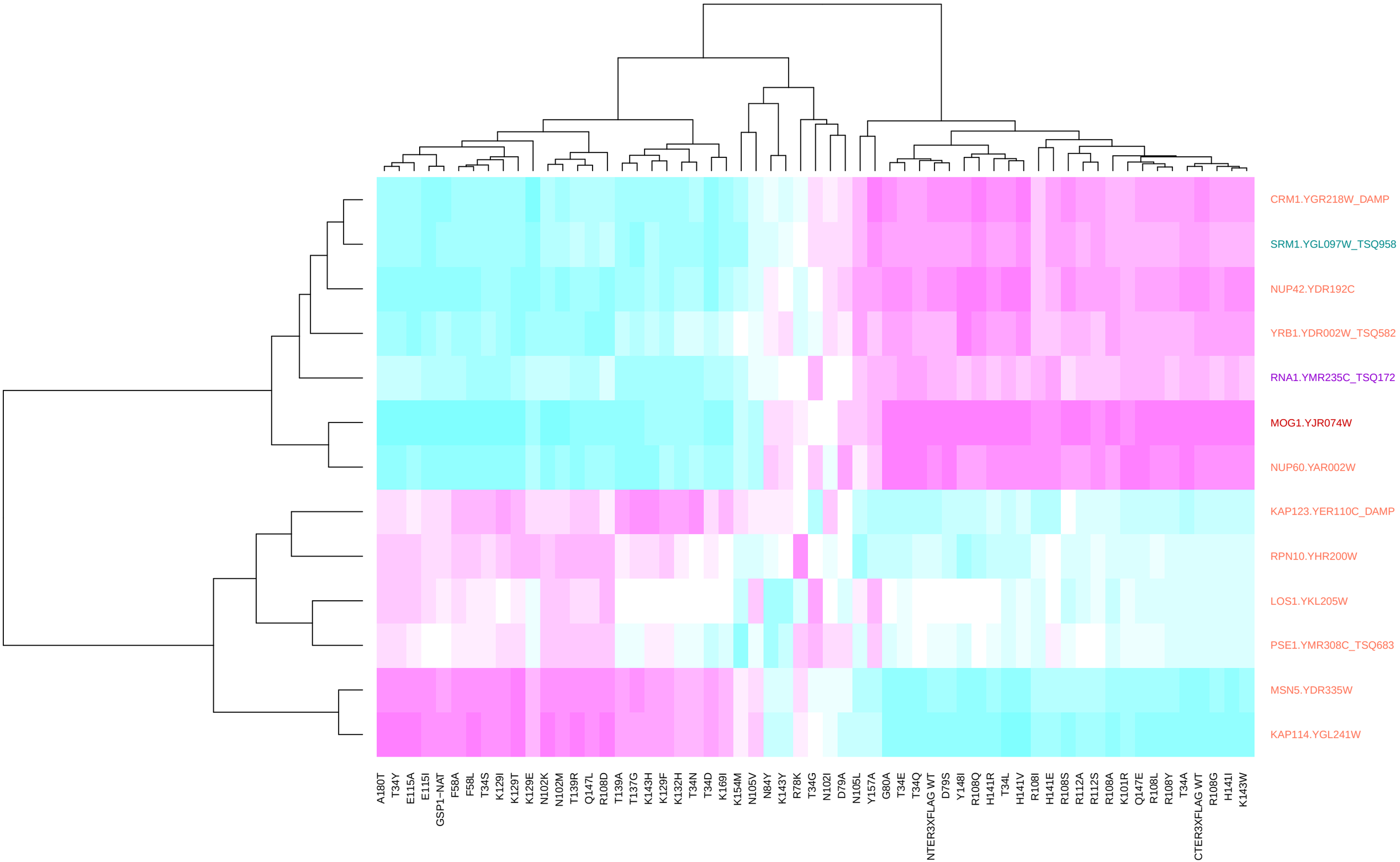
RNA processing_GO_15_1_all



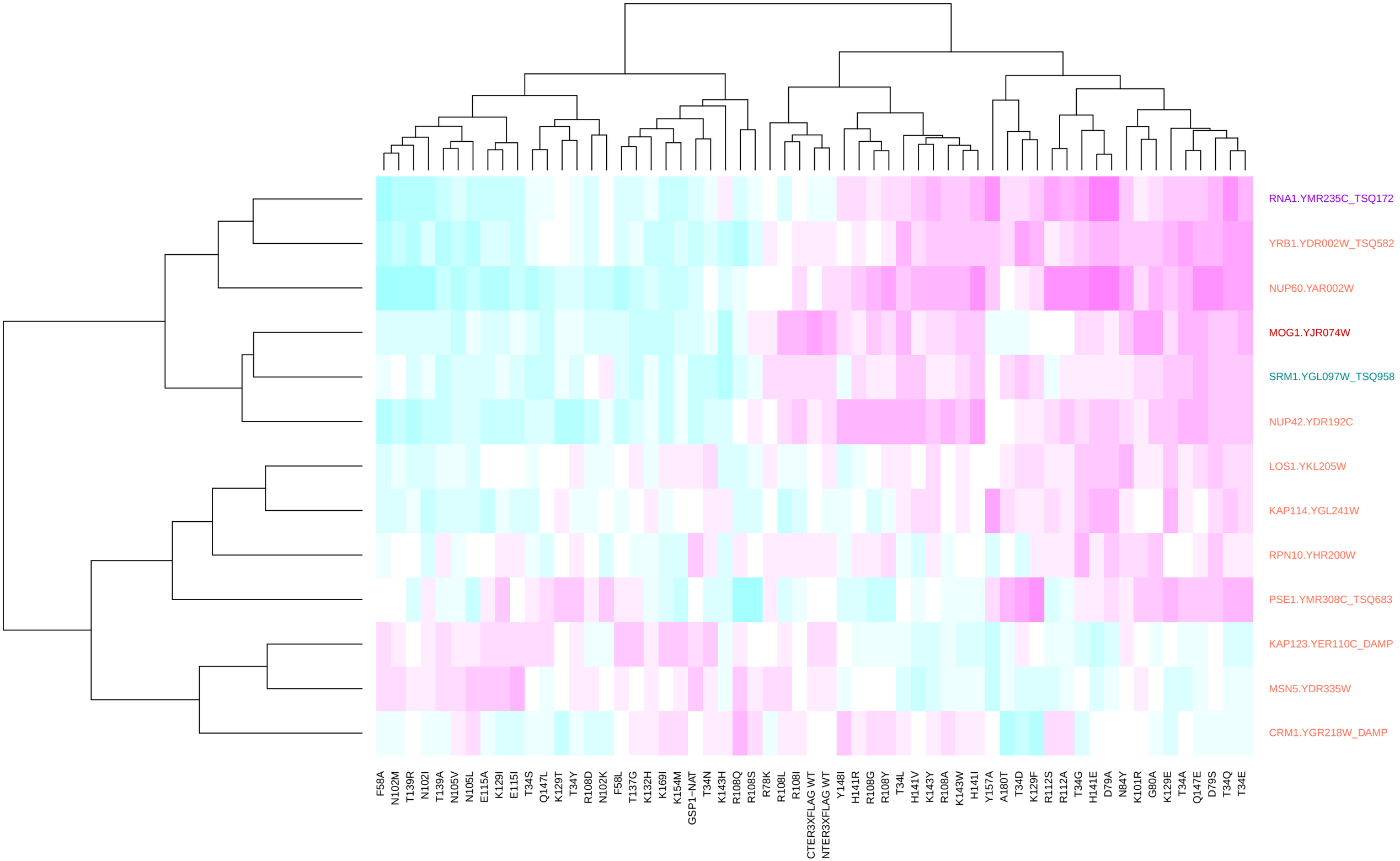
DNA recombination



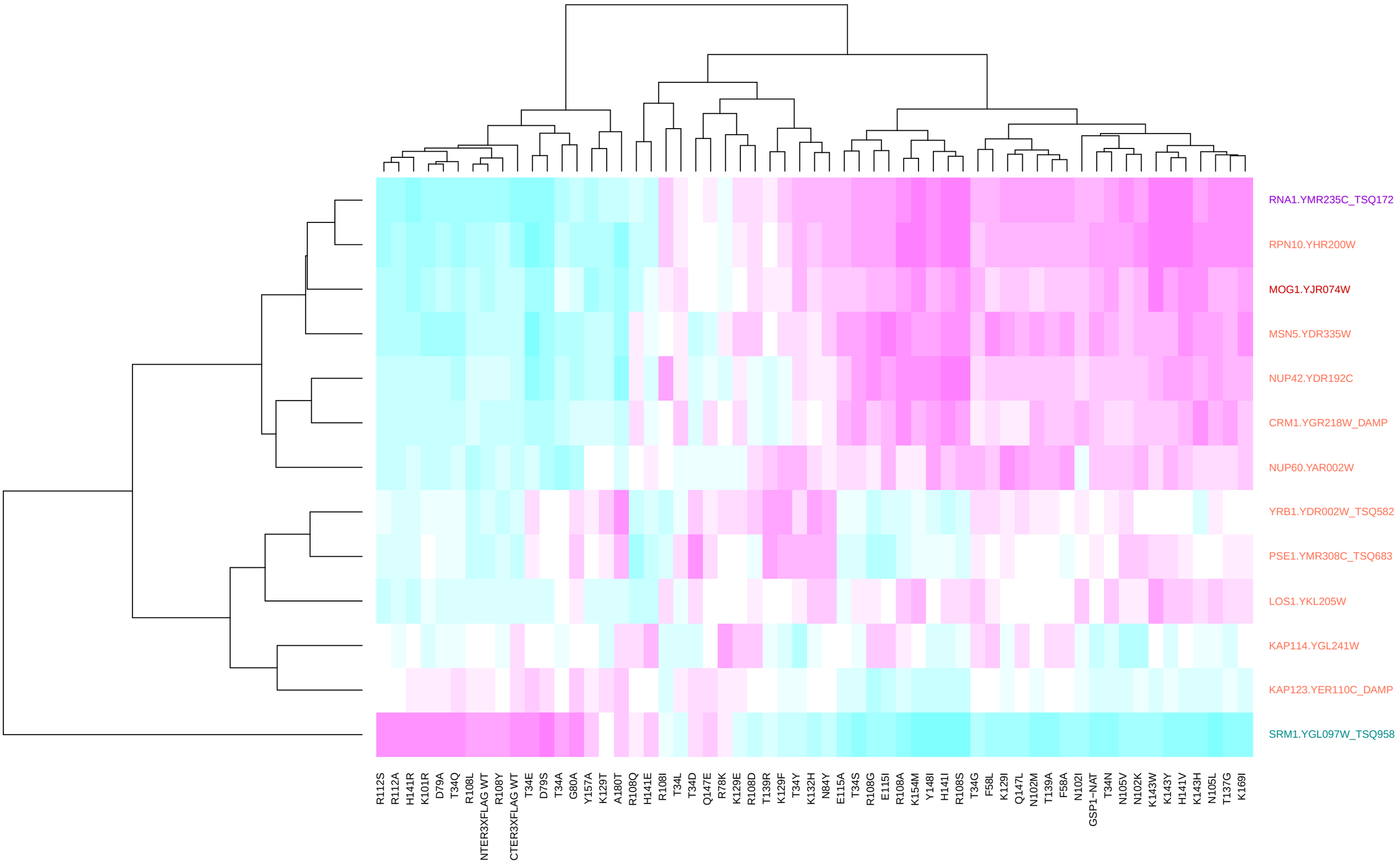
transcription from RNA polymerase II promoter_GO_15_4_all



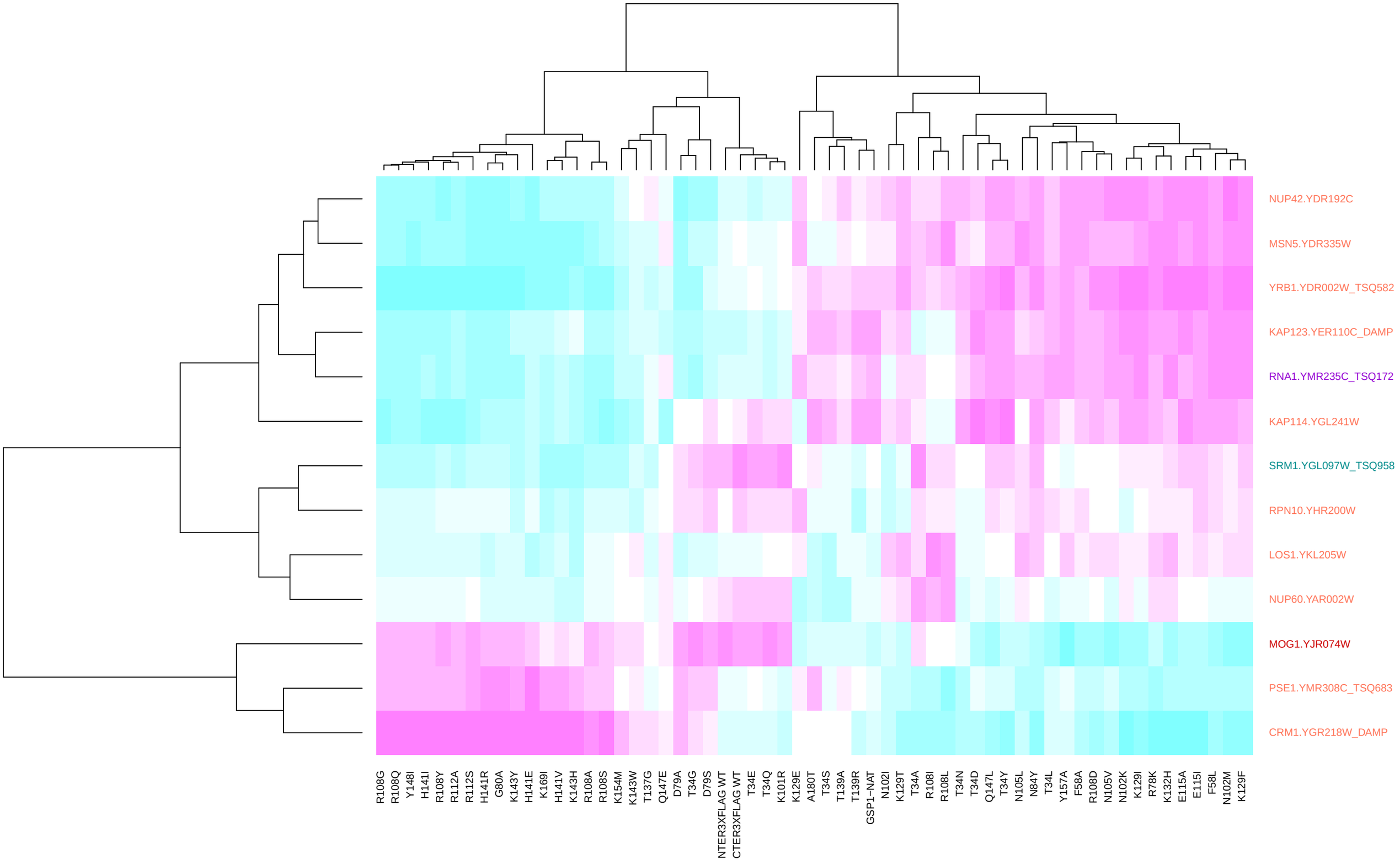
sig_Gsp1_GI_30_2_all



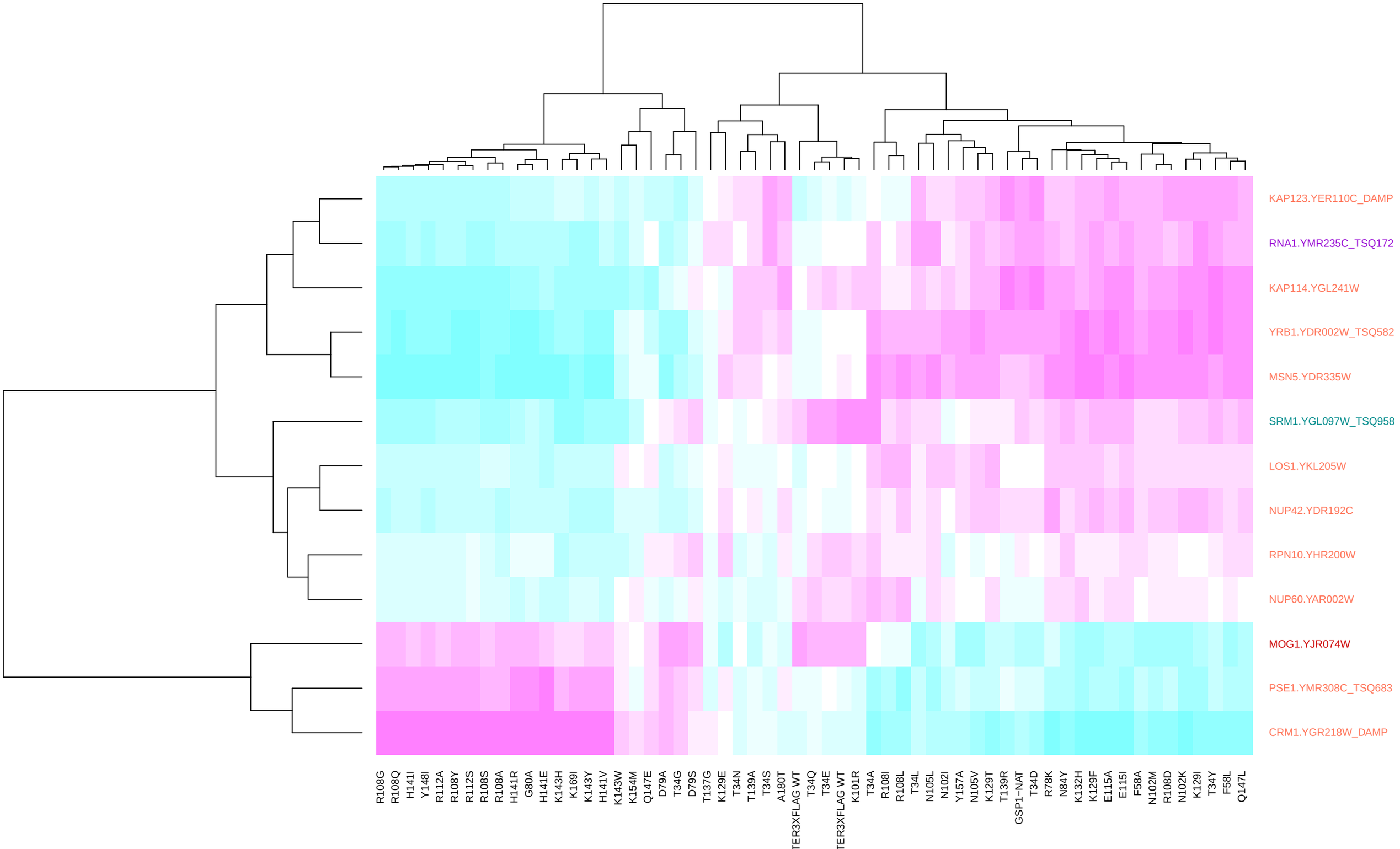
sig_Gsp1_GI_15_7_mut



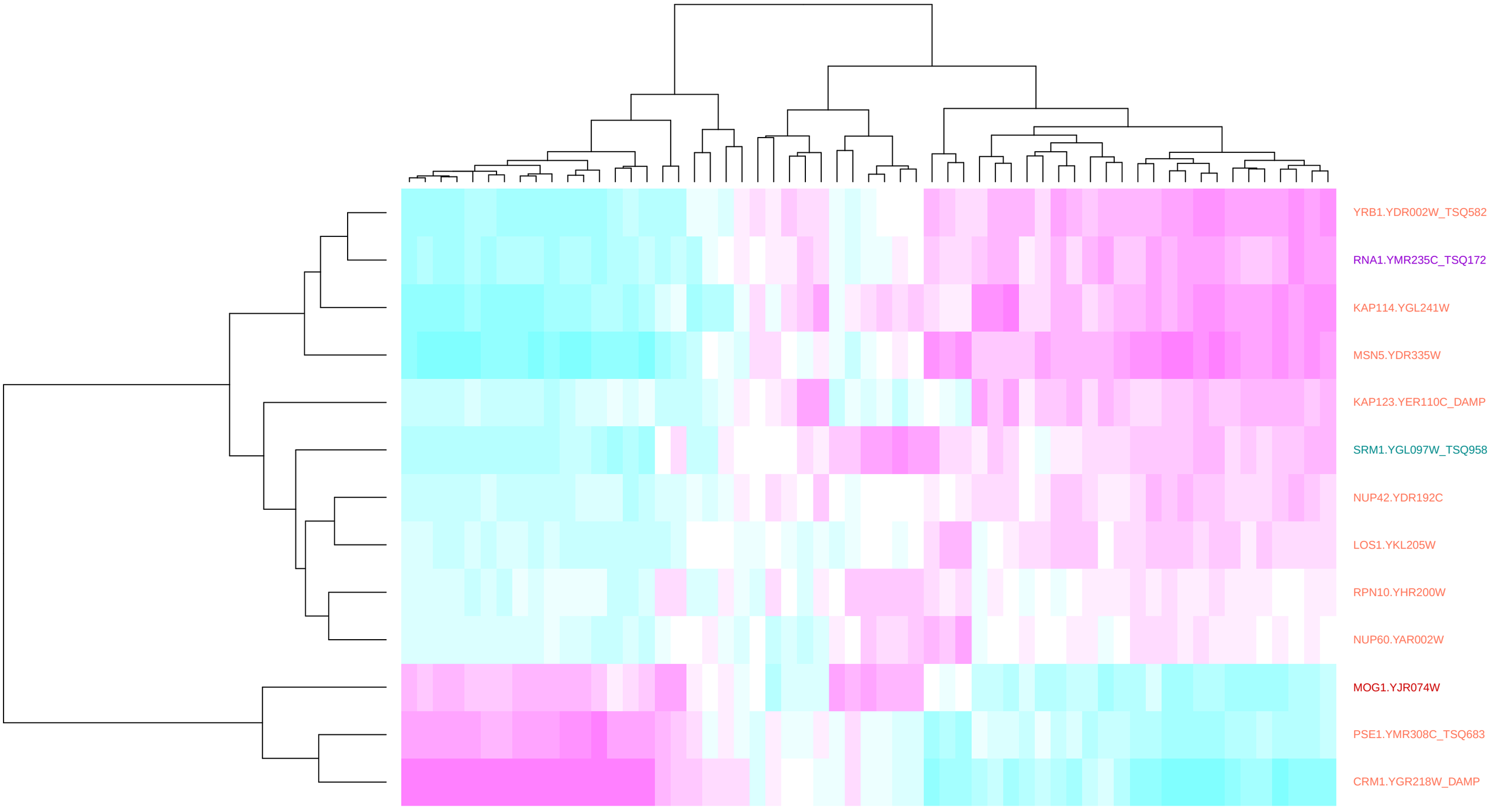
mitotic cell cycle_GO_15_2_all



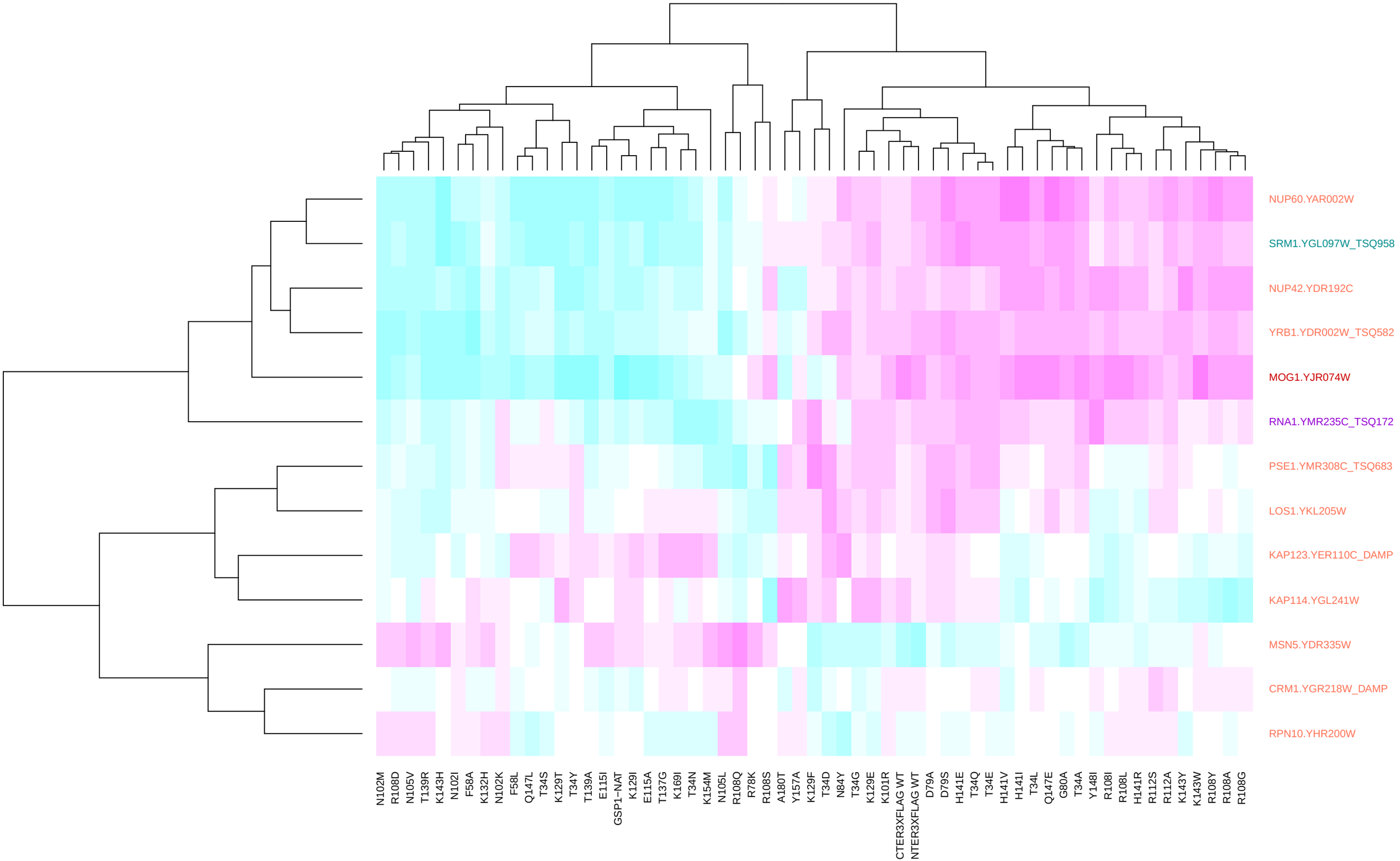
whole_library_15_3_all



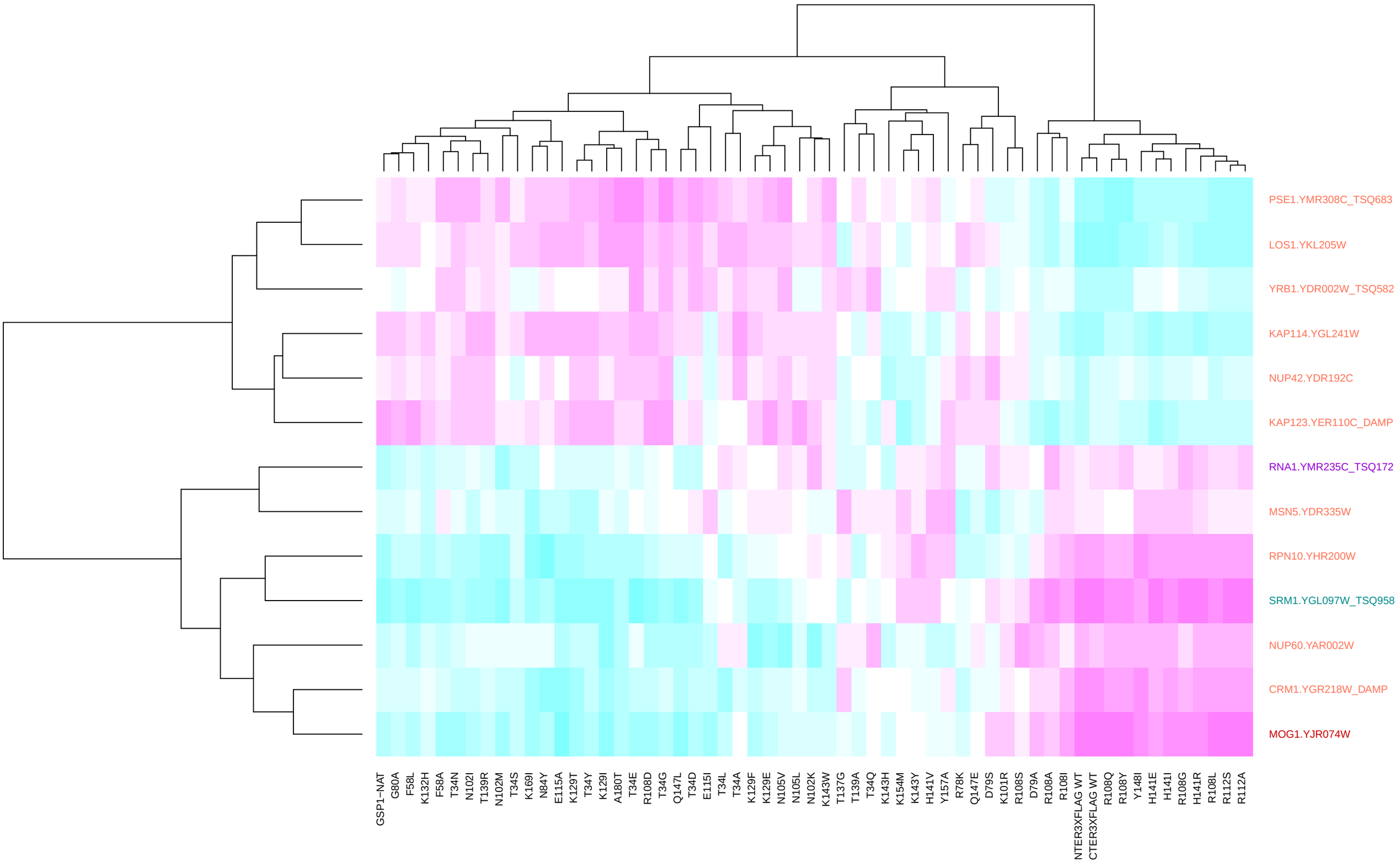
whole_library_30_9_all



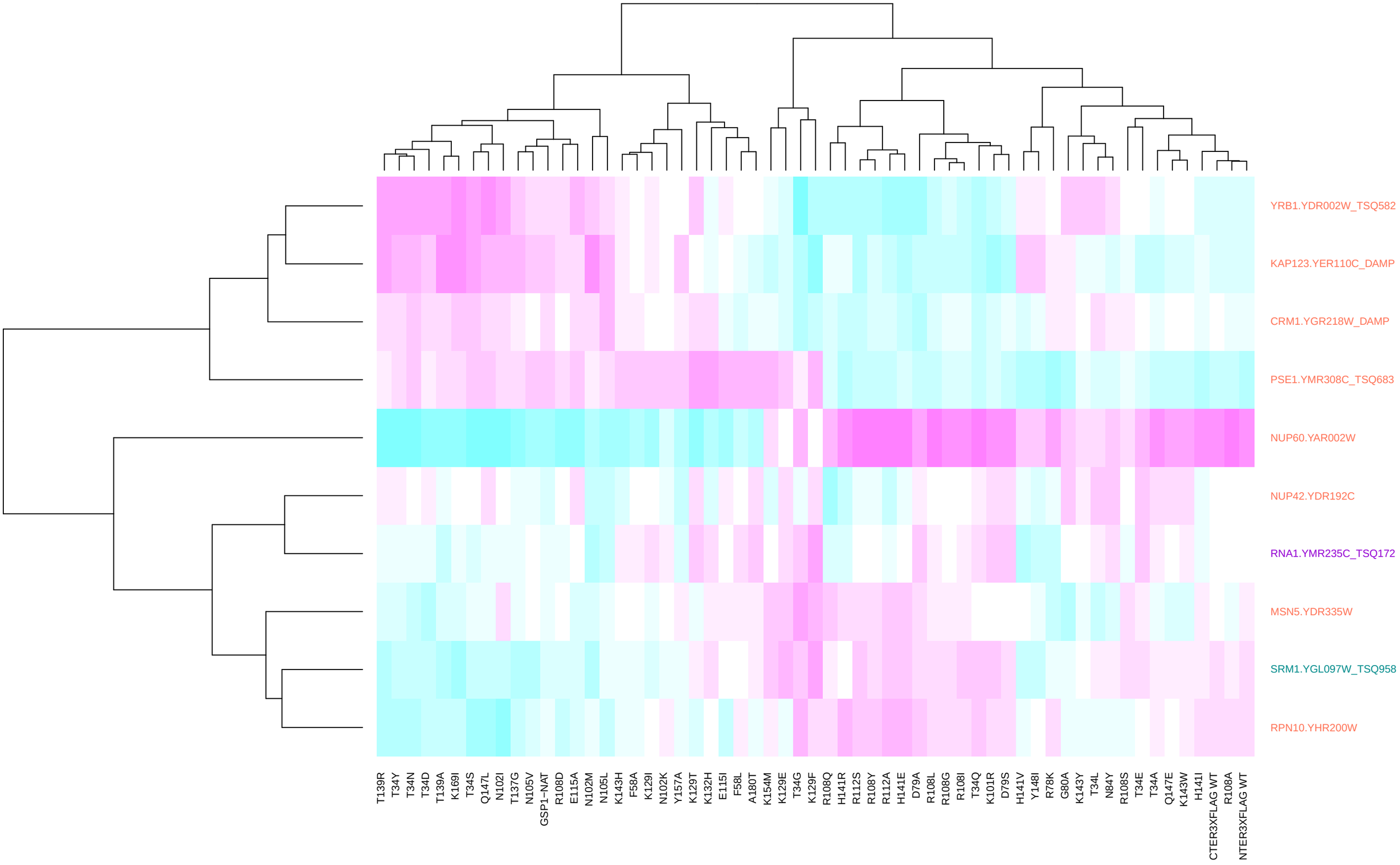
sig_Gsp1_GI_15_3_all



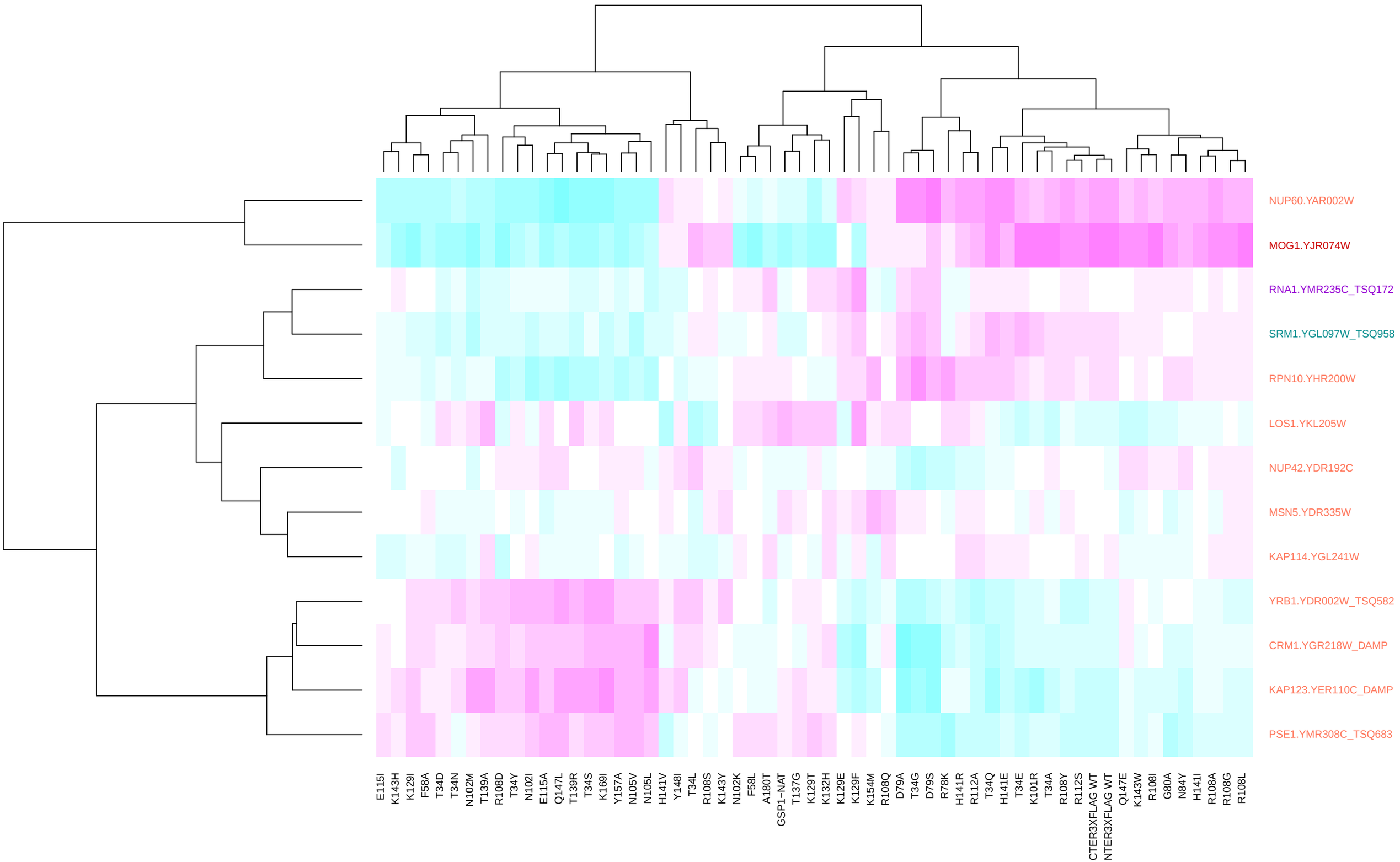
sig_Gsp1_GI_15_9_mut



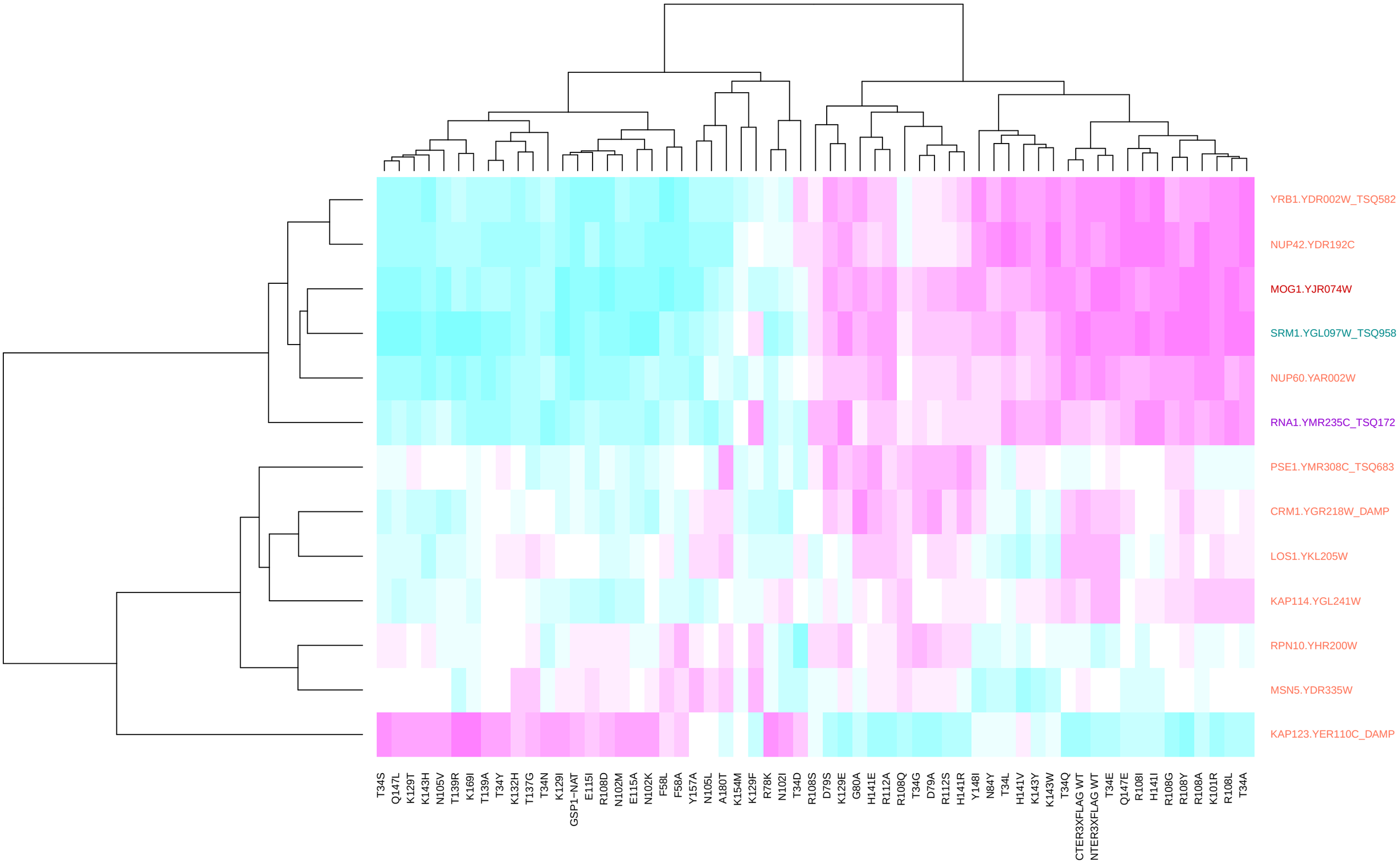
DNA recombination_GO_15_1_mut



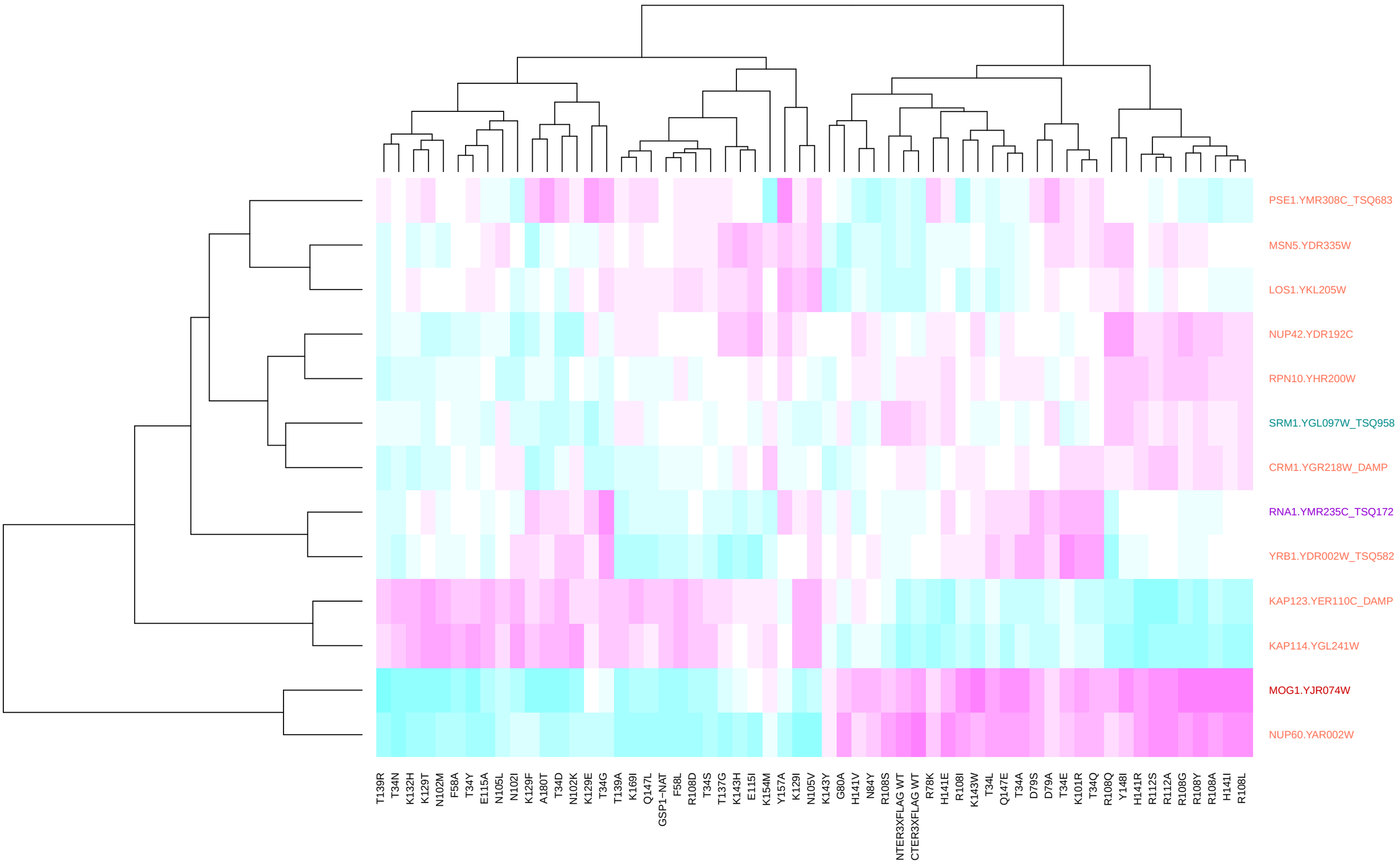
DNA recombination_GO_30_1_mut



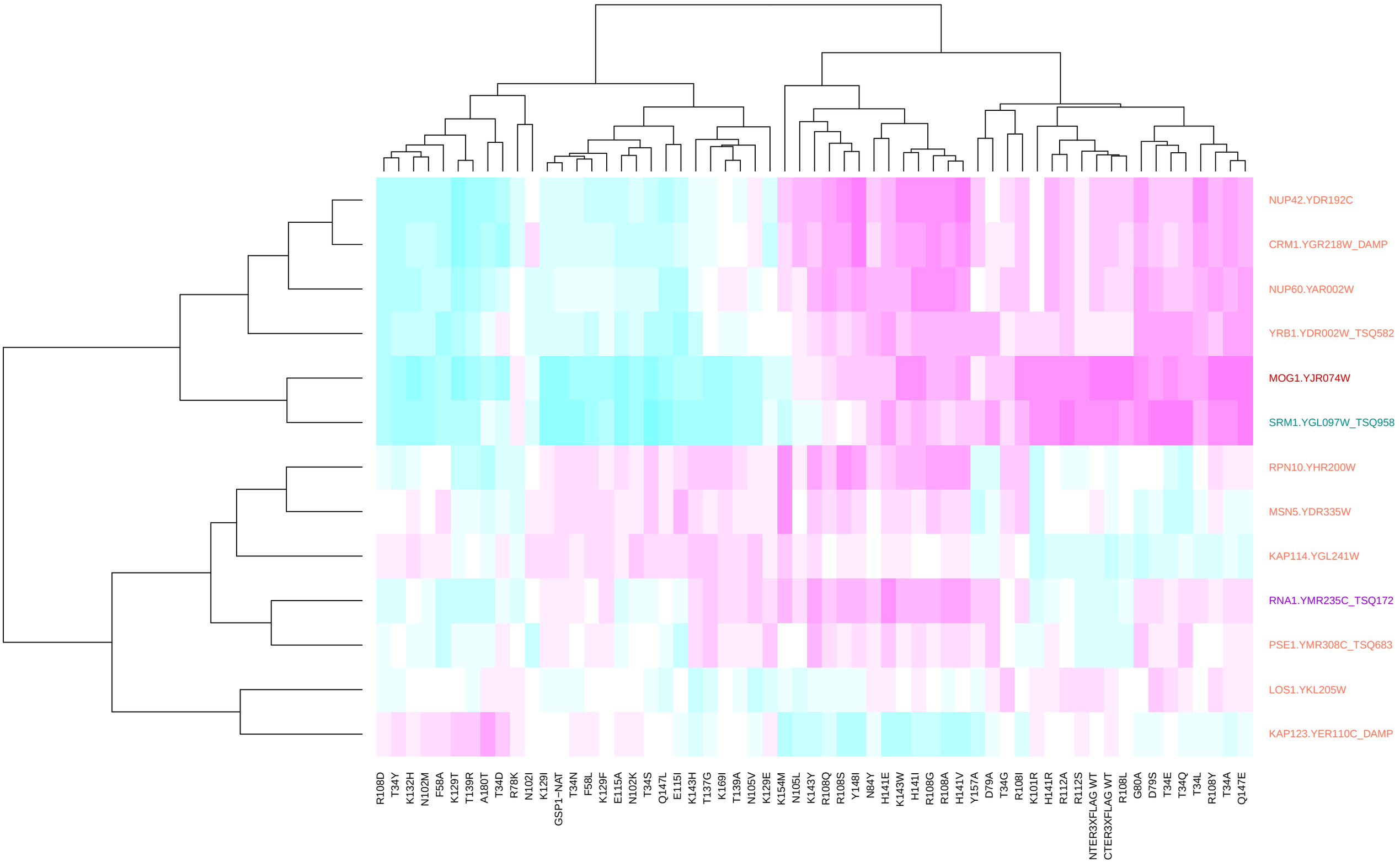
organelle fission_GO_15_3_mut



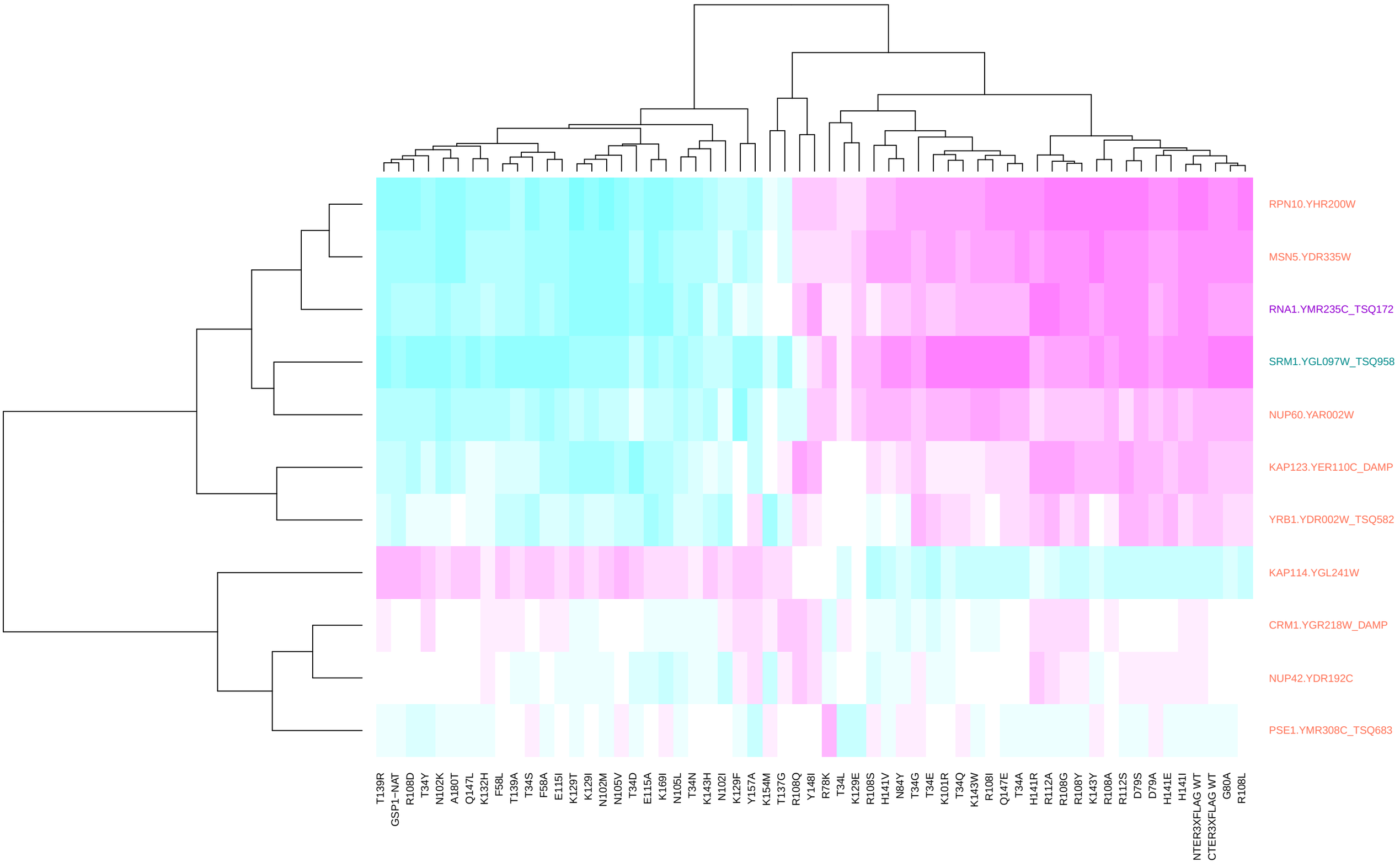
DNA−templated transcription, elongation_GO_15_1_mut



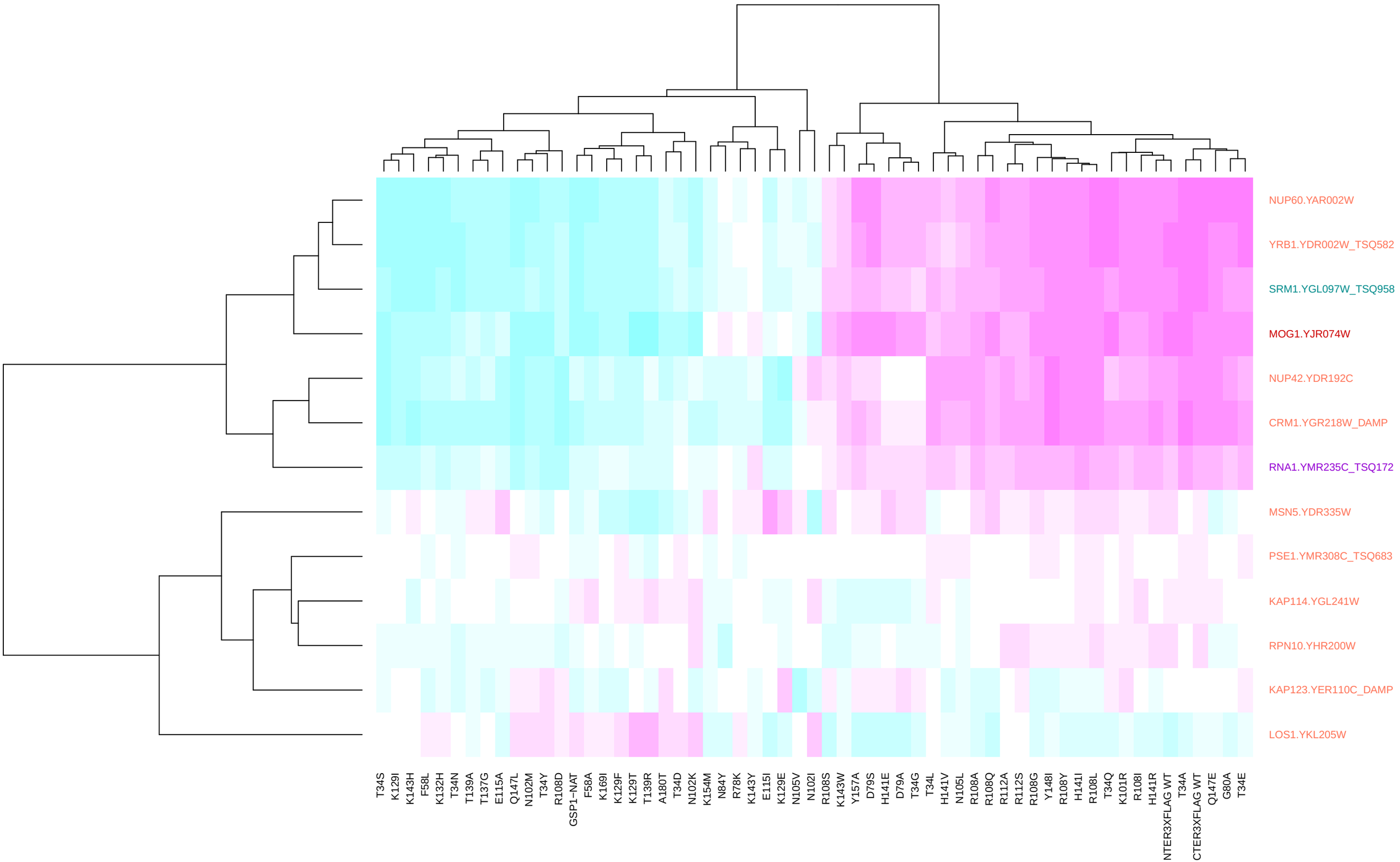
chromatin_GO_30_2_all



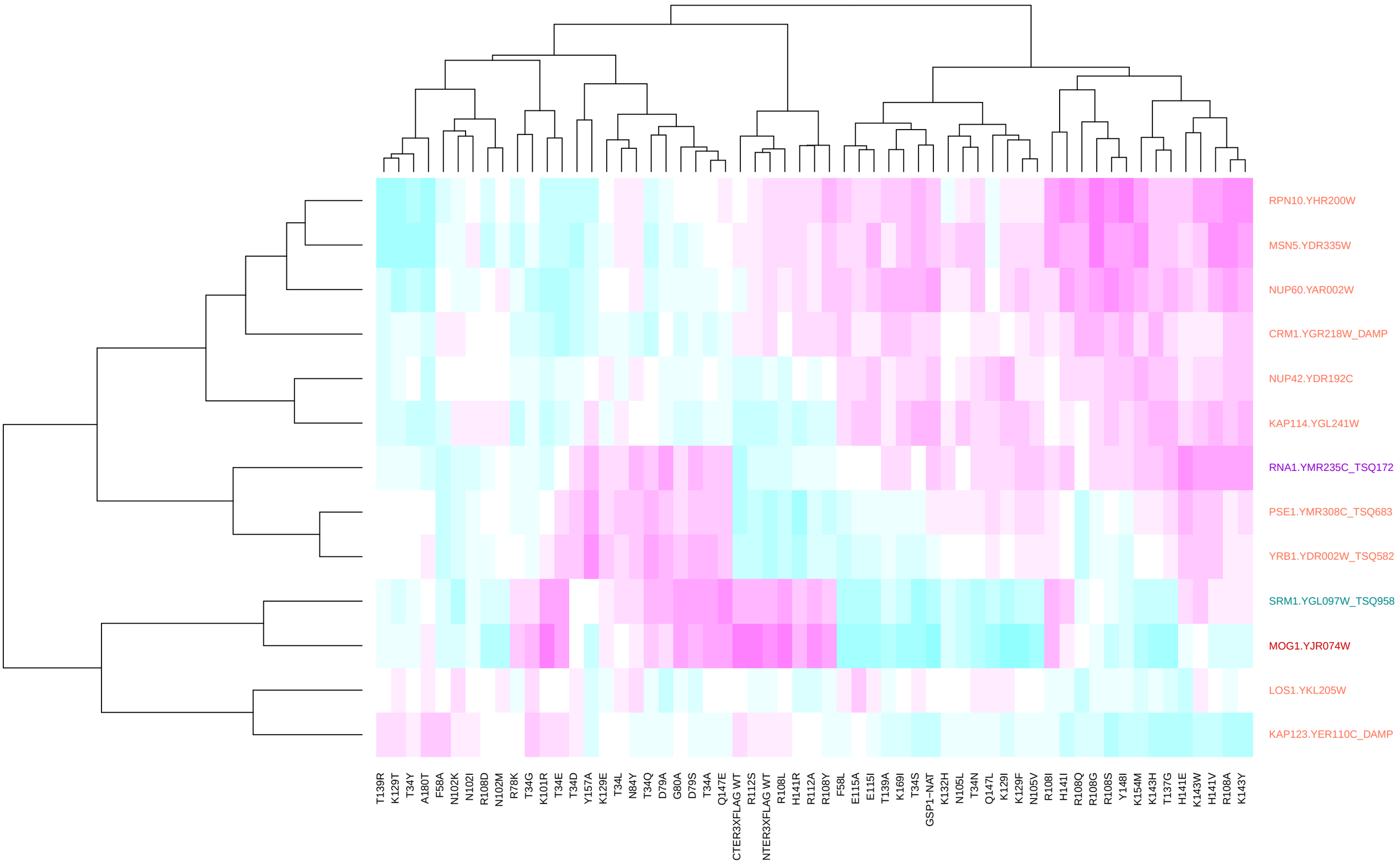
whole_library_15_13_all



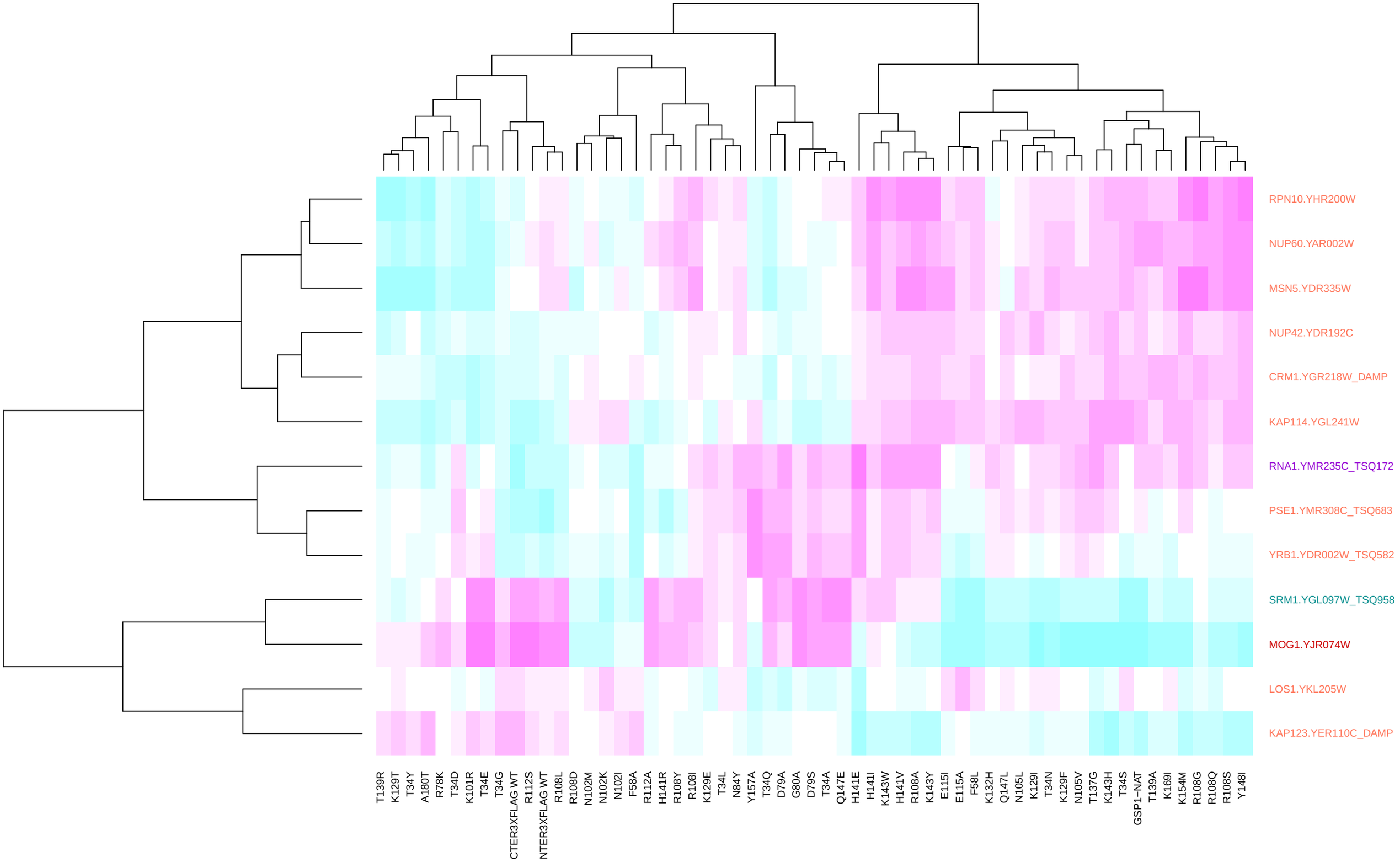
protein targeting



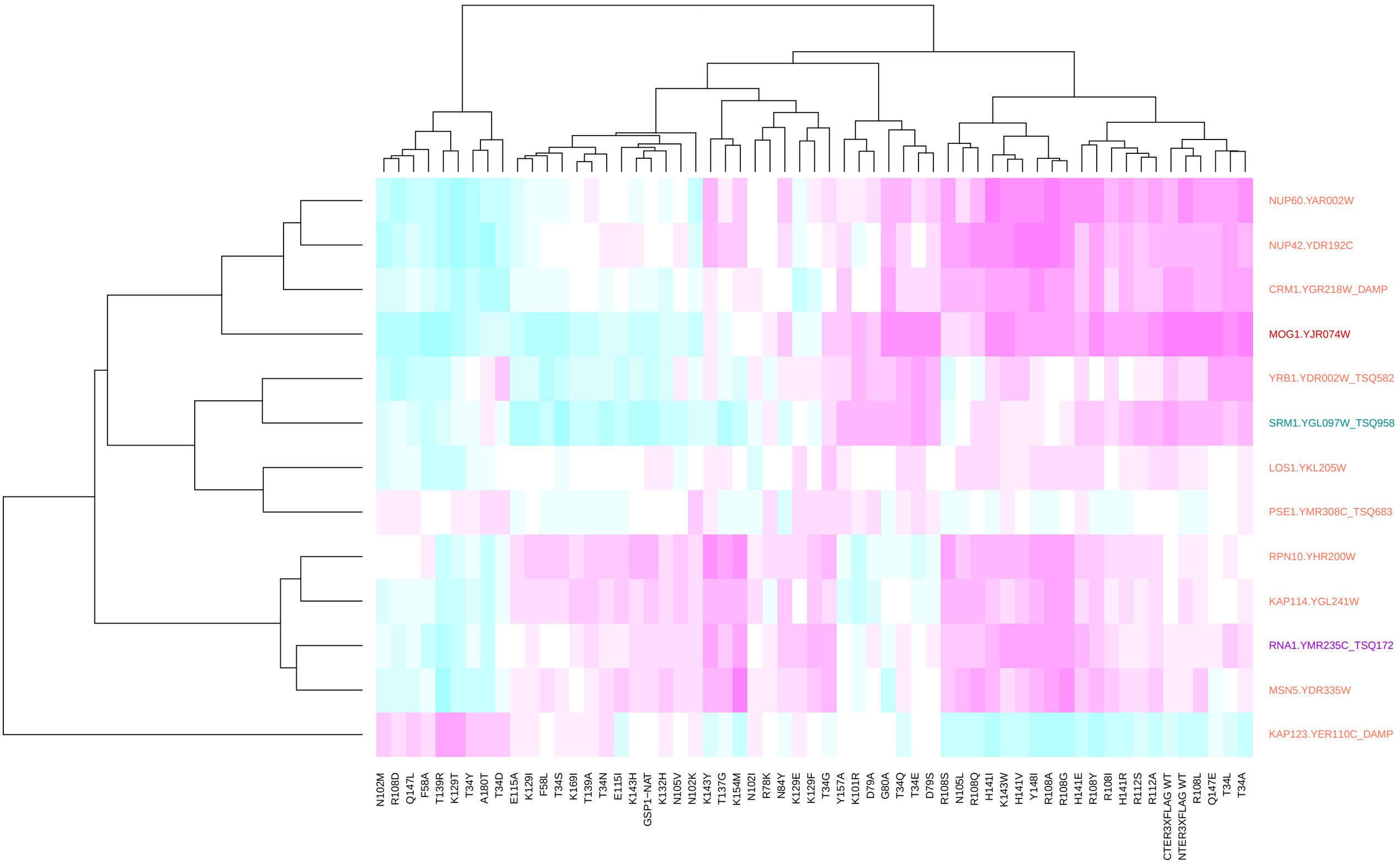
histone modification



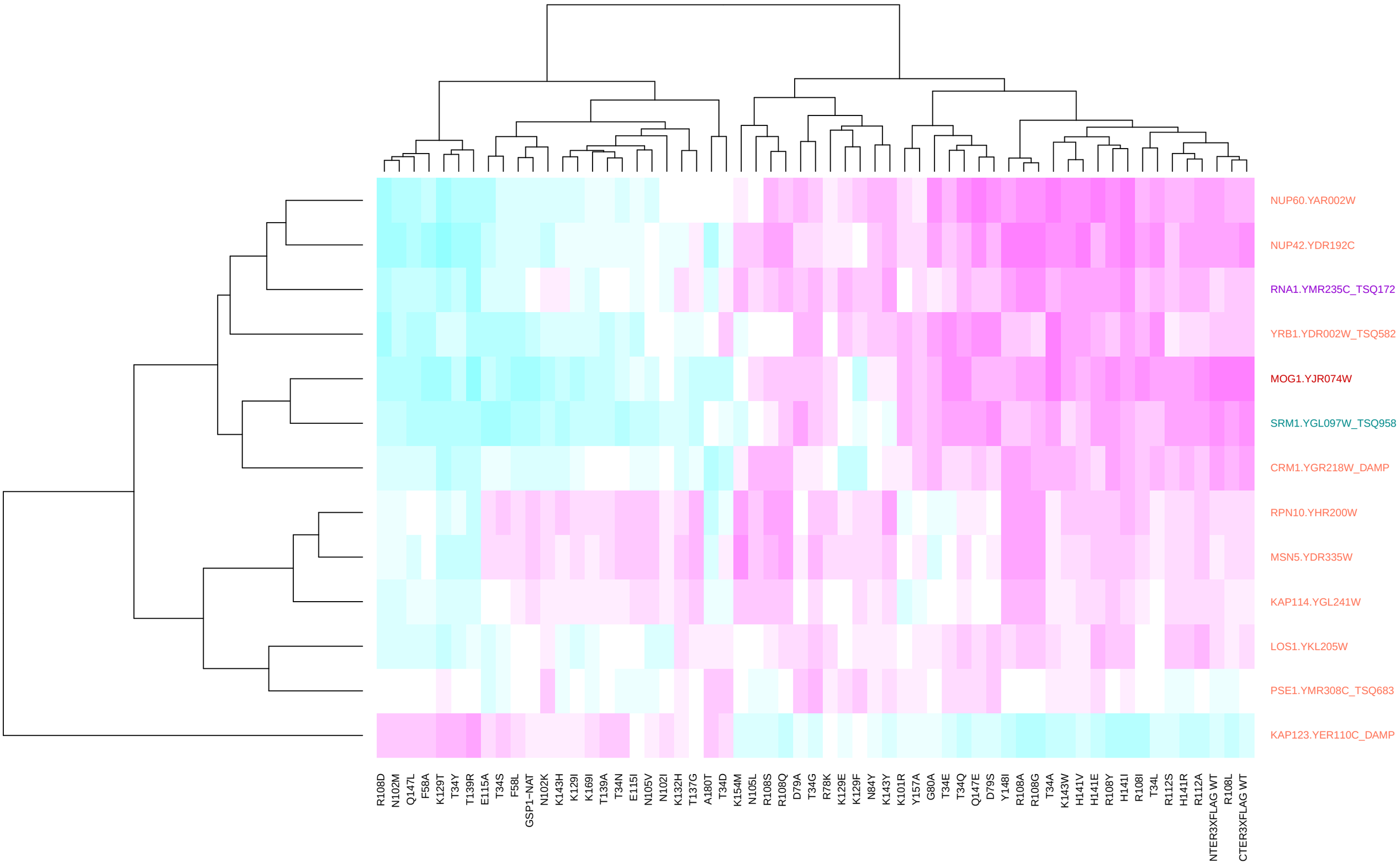
histone modification_GO_30_1_all



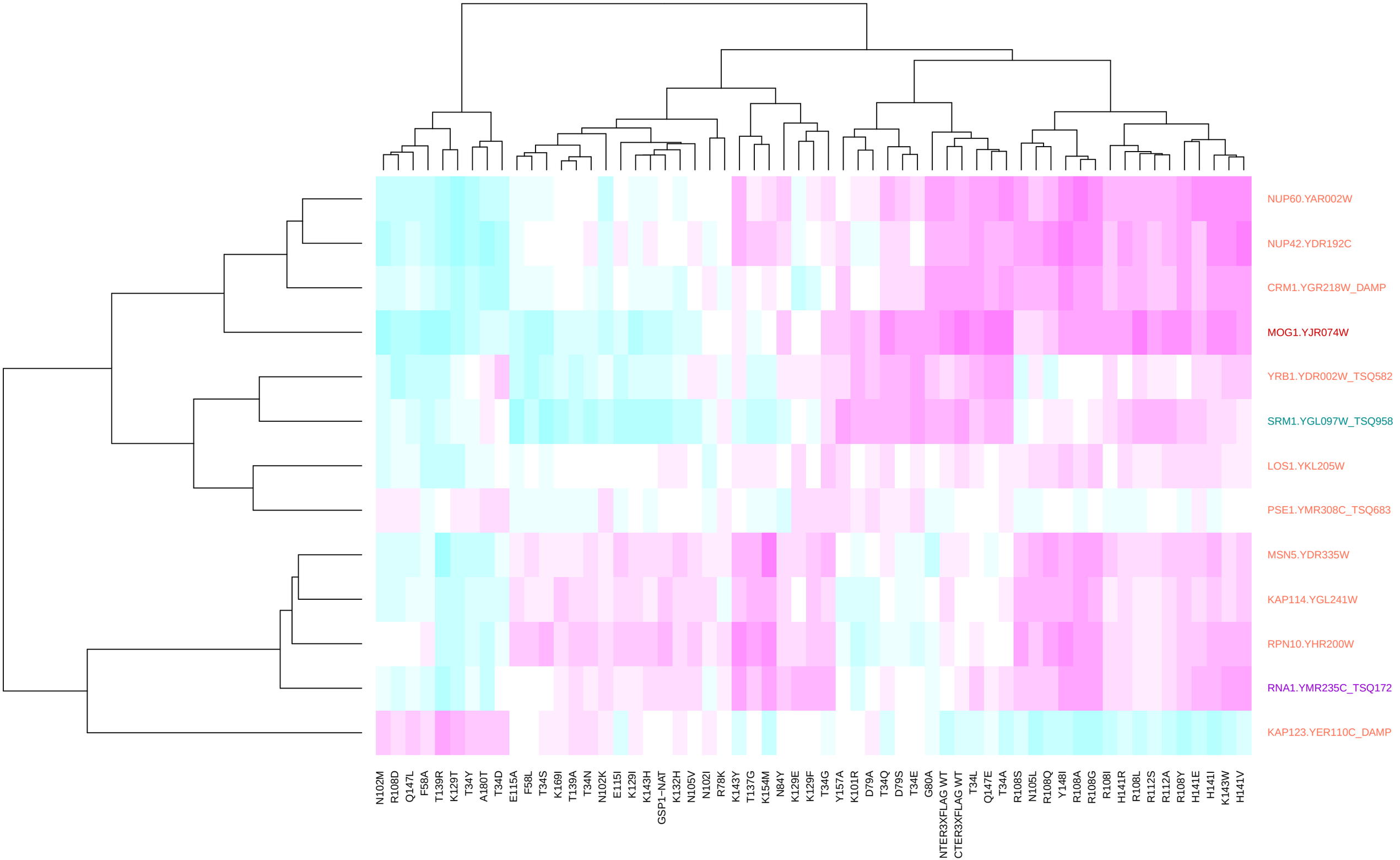
transcription



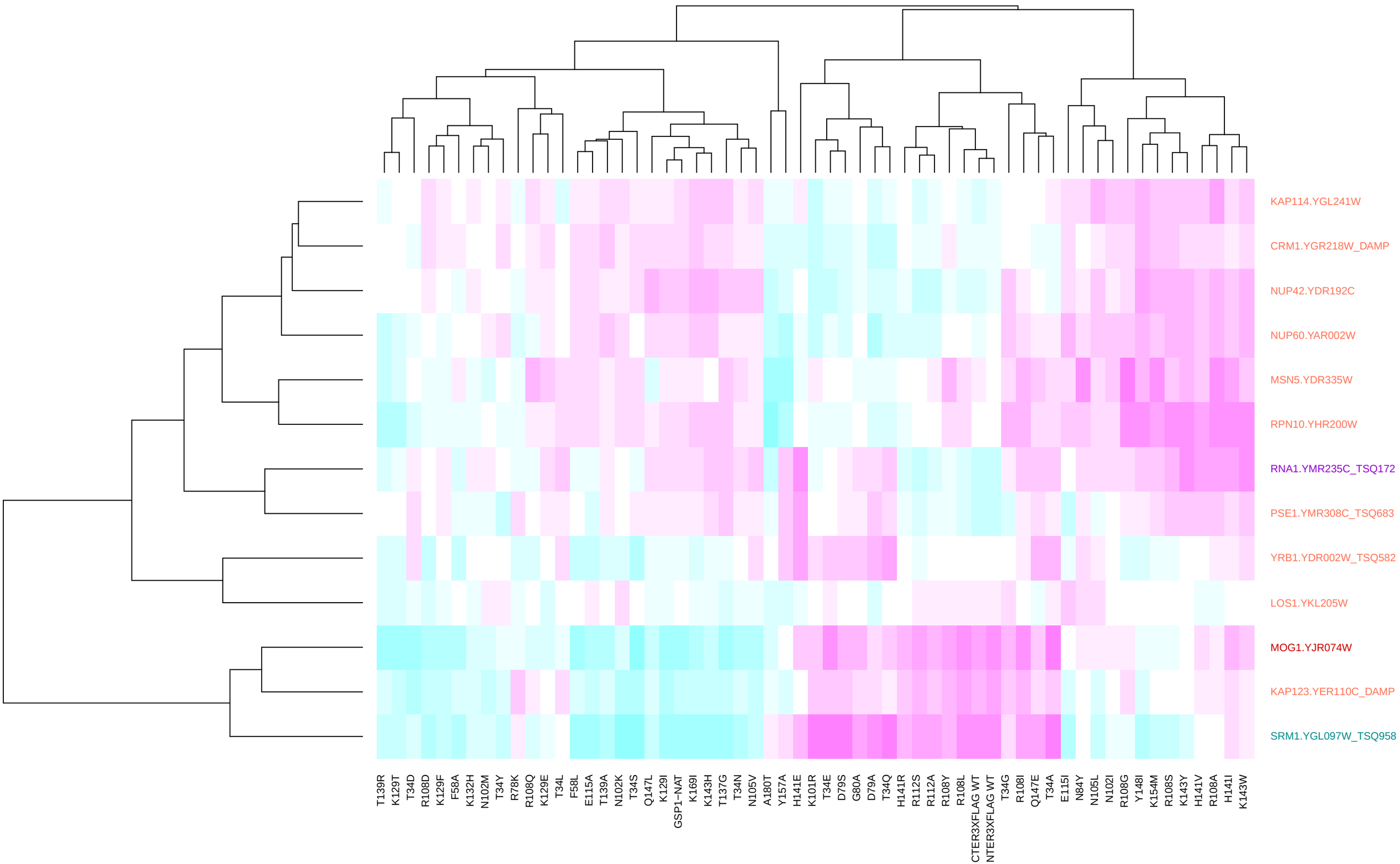
transcription and mRNA processing



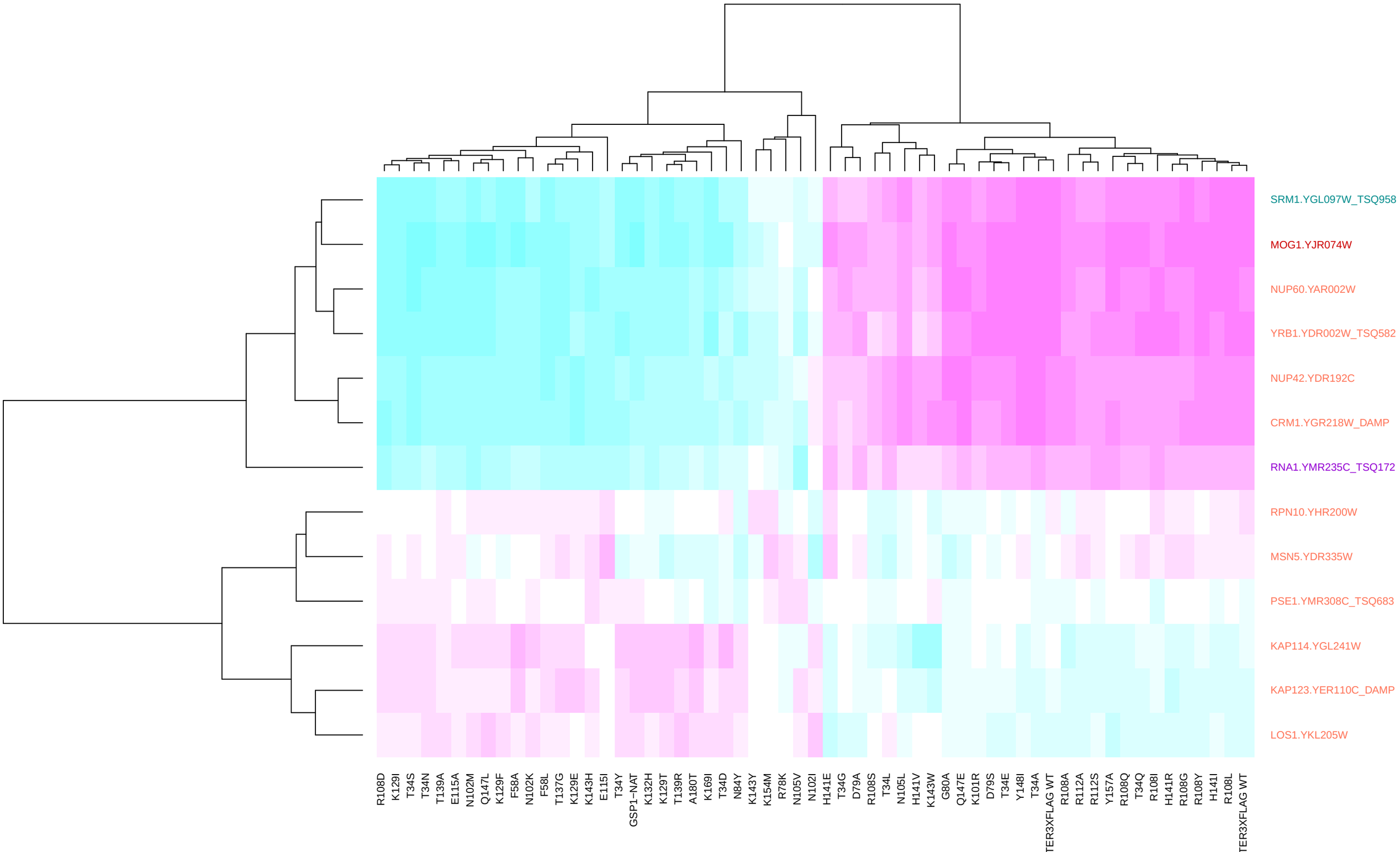
transcription from RNA polymerase II promoter



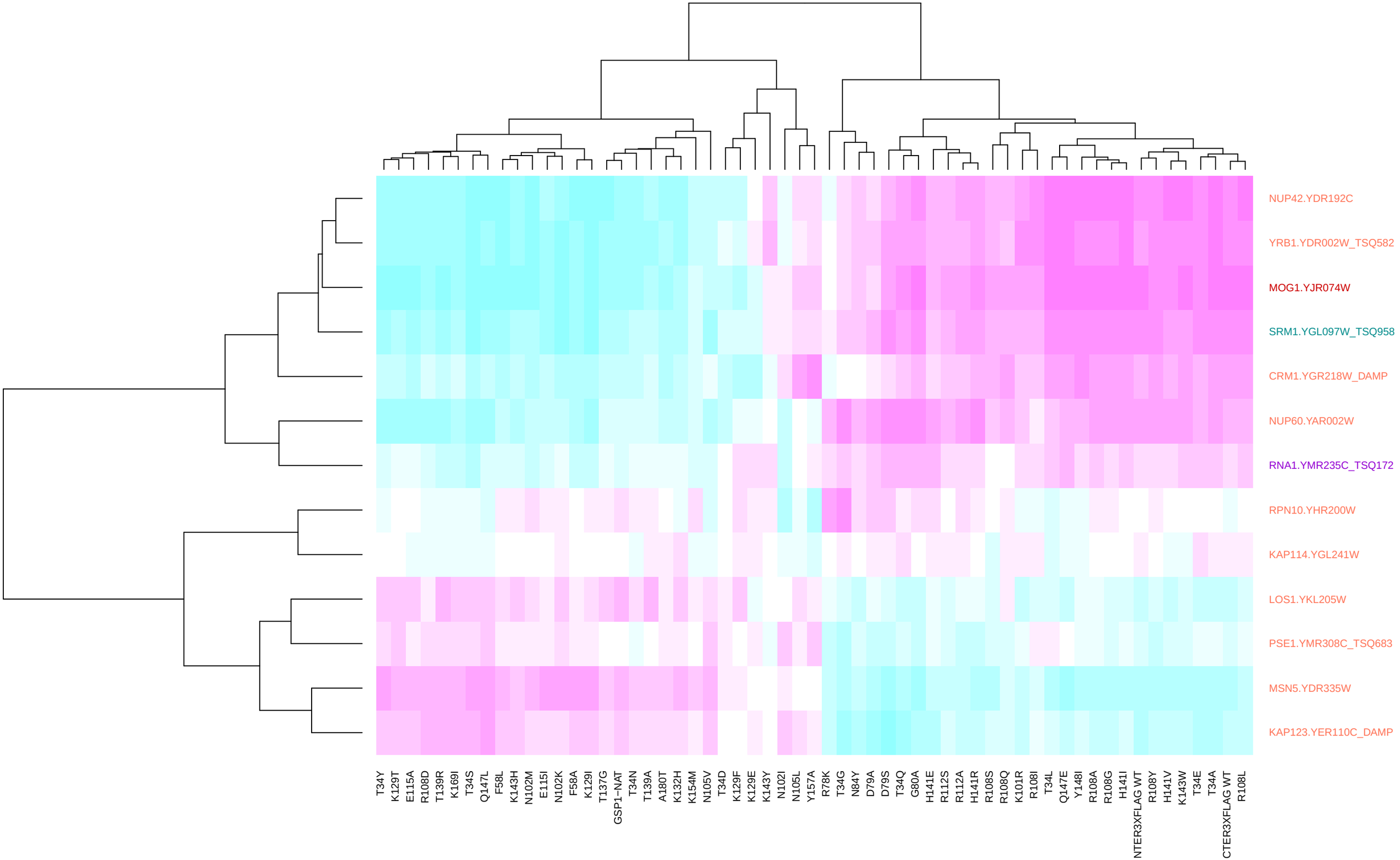
whole_library_30_1_all



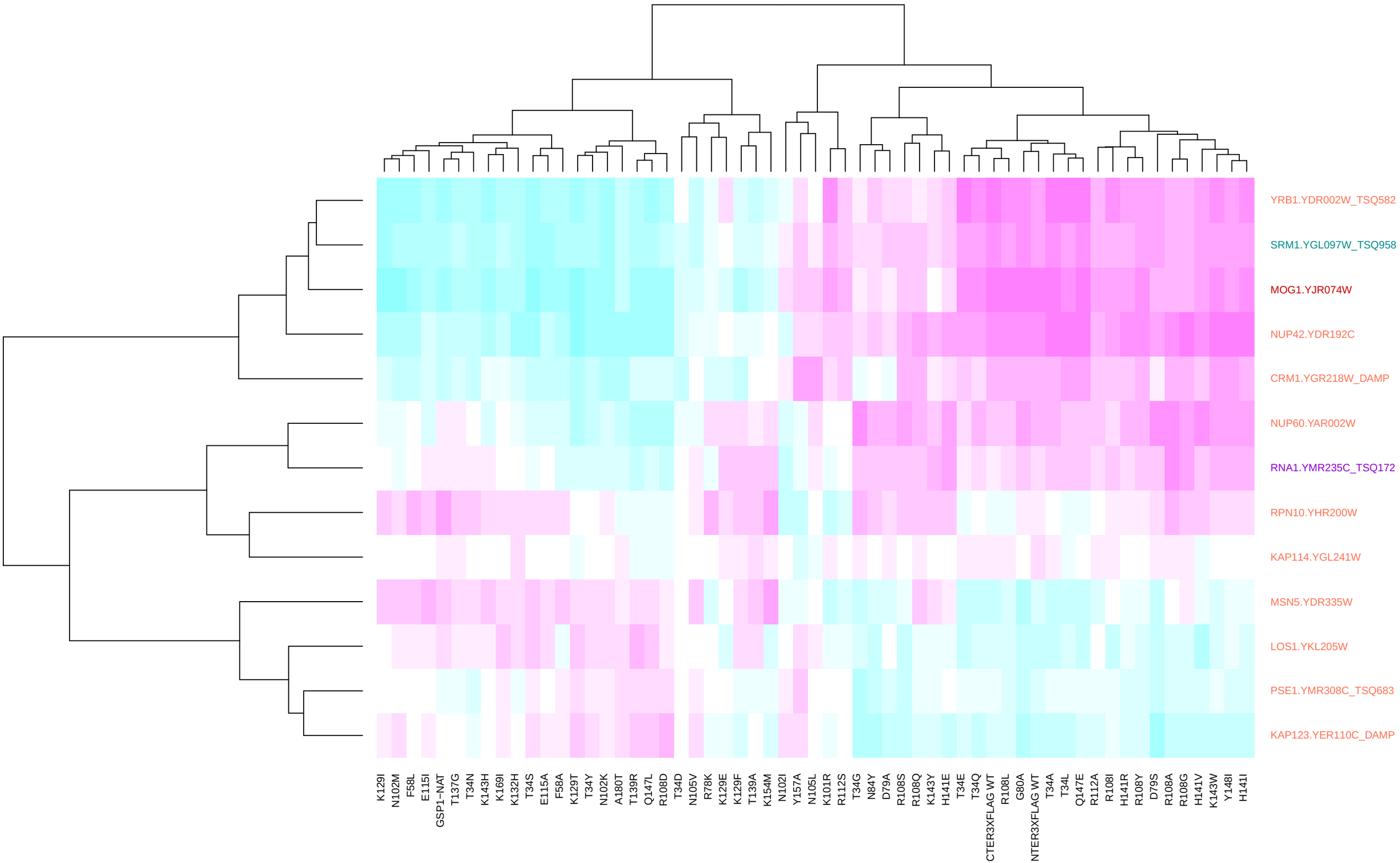
protein targeting_GO_15_2_mut



cellular response to DNA damage stimulus_GO_30_1_mut



DNA repair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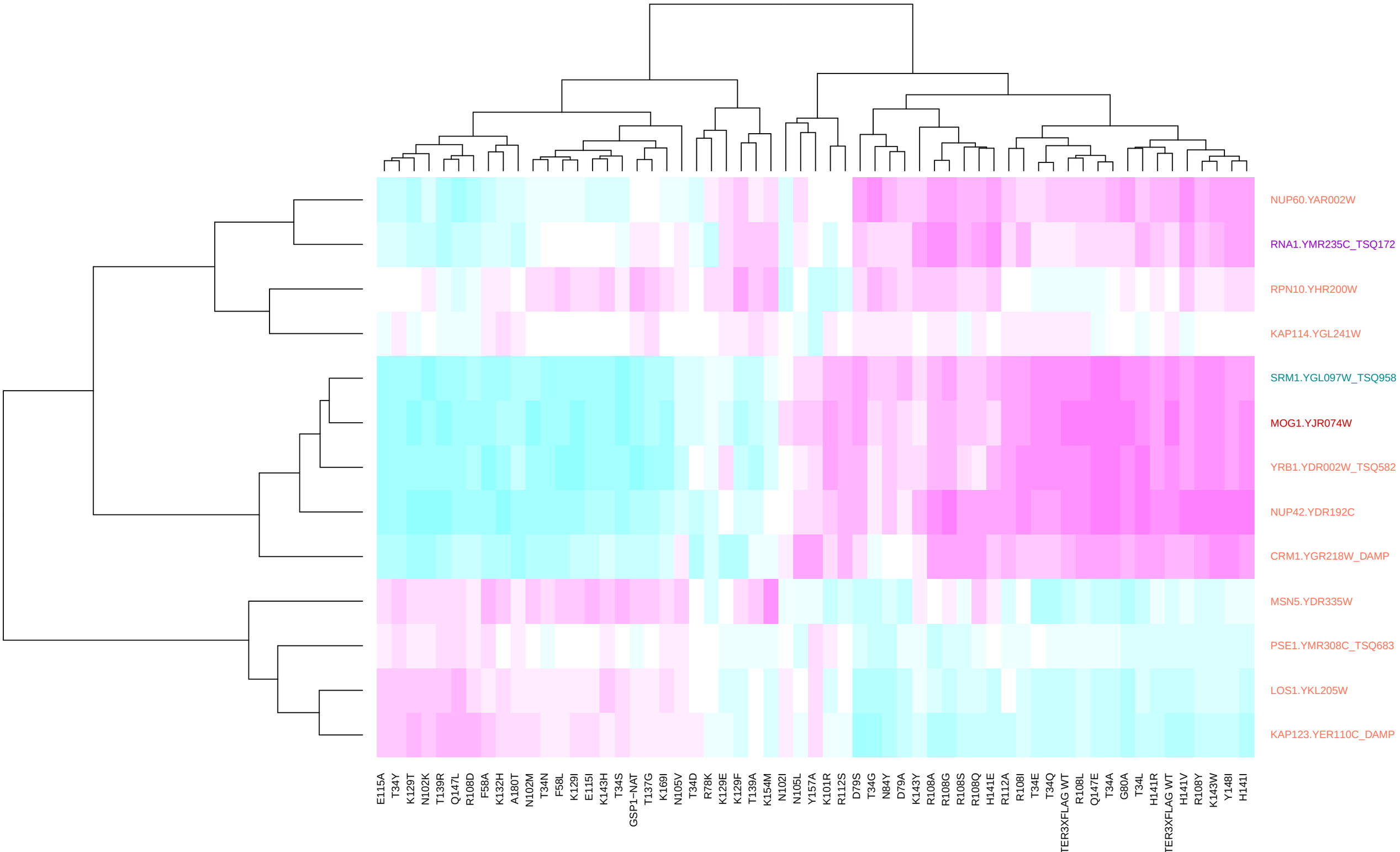
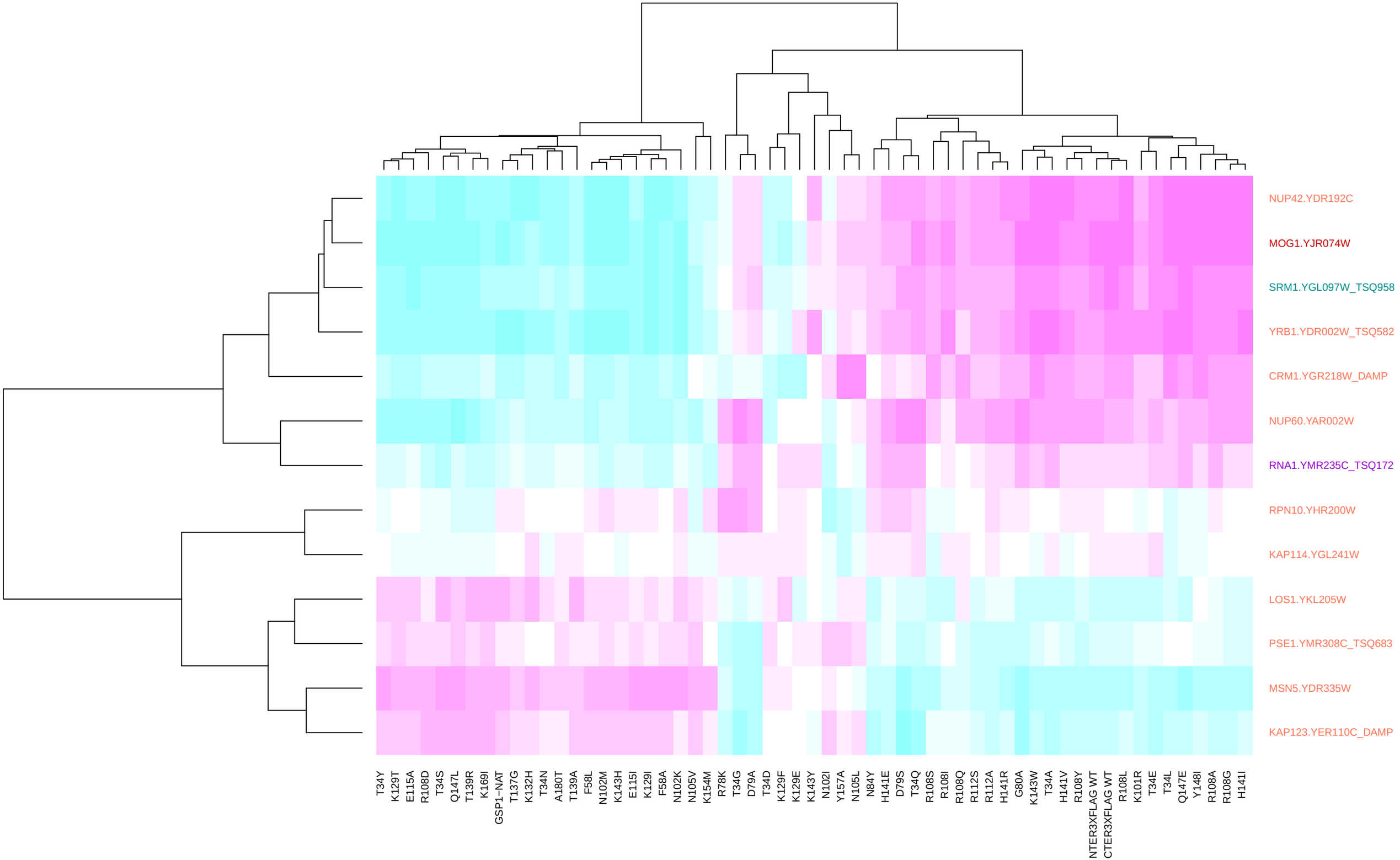
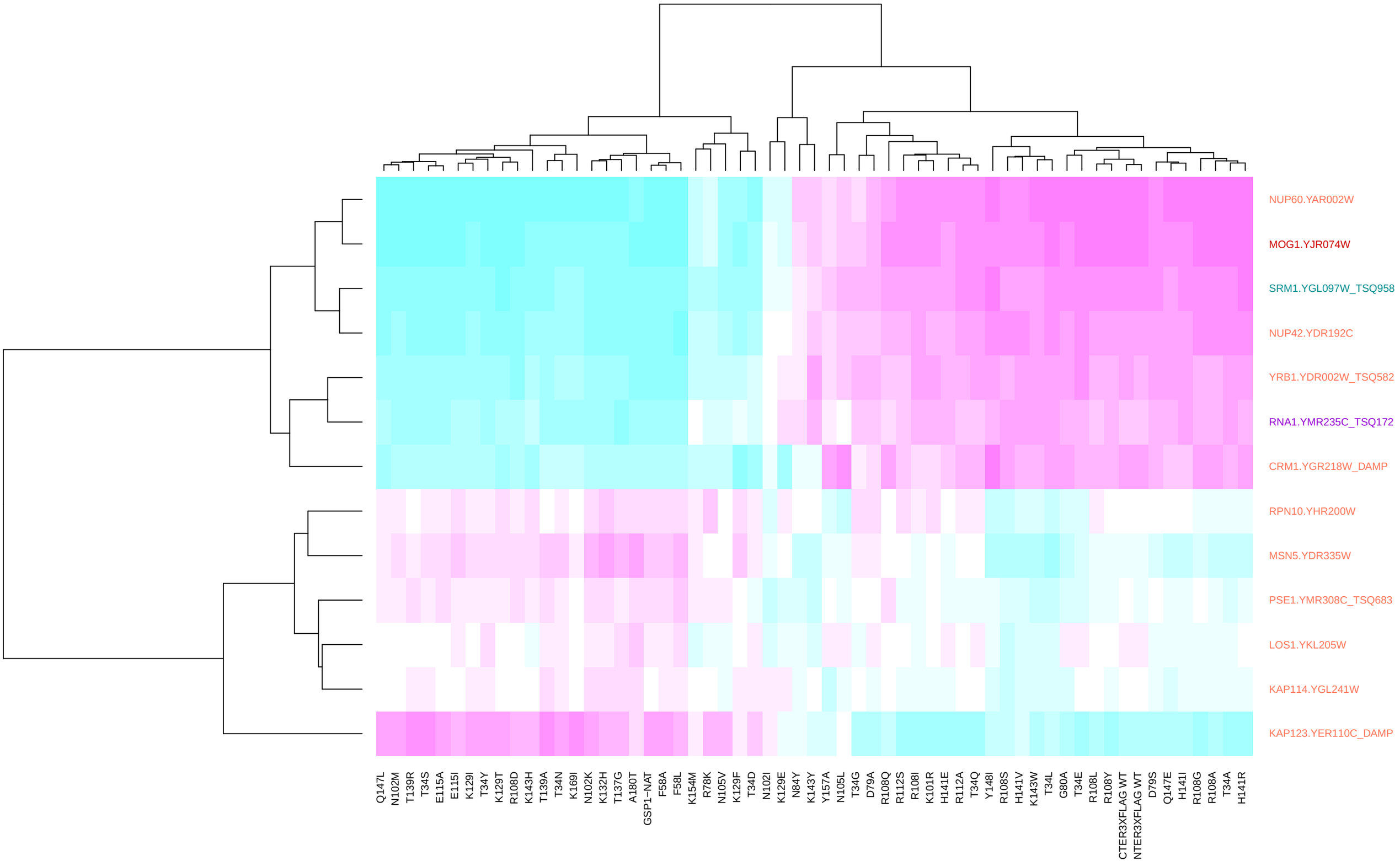
DNA repair_GO_15_1_all



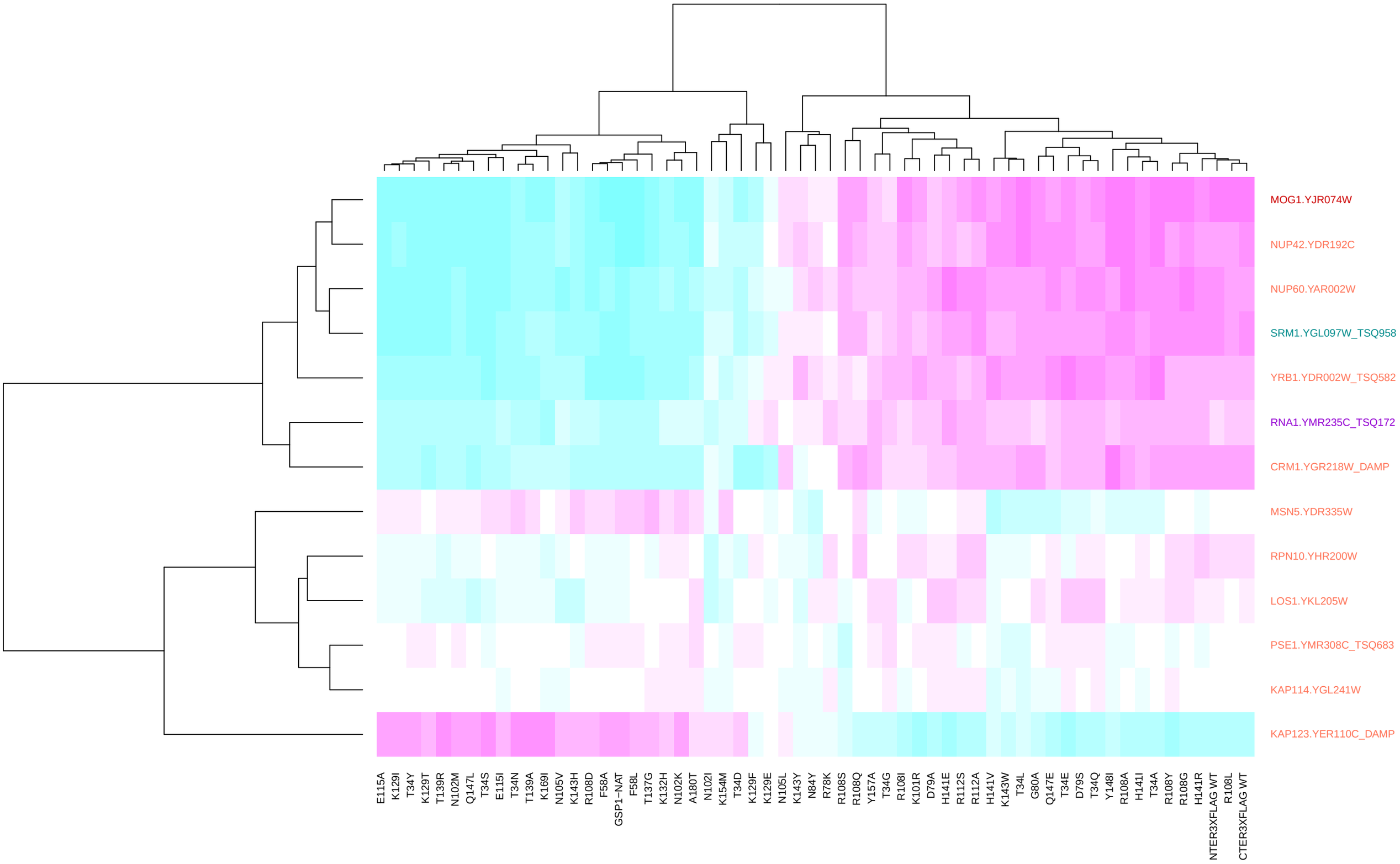
DNA repair_GO_30_1_mut



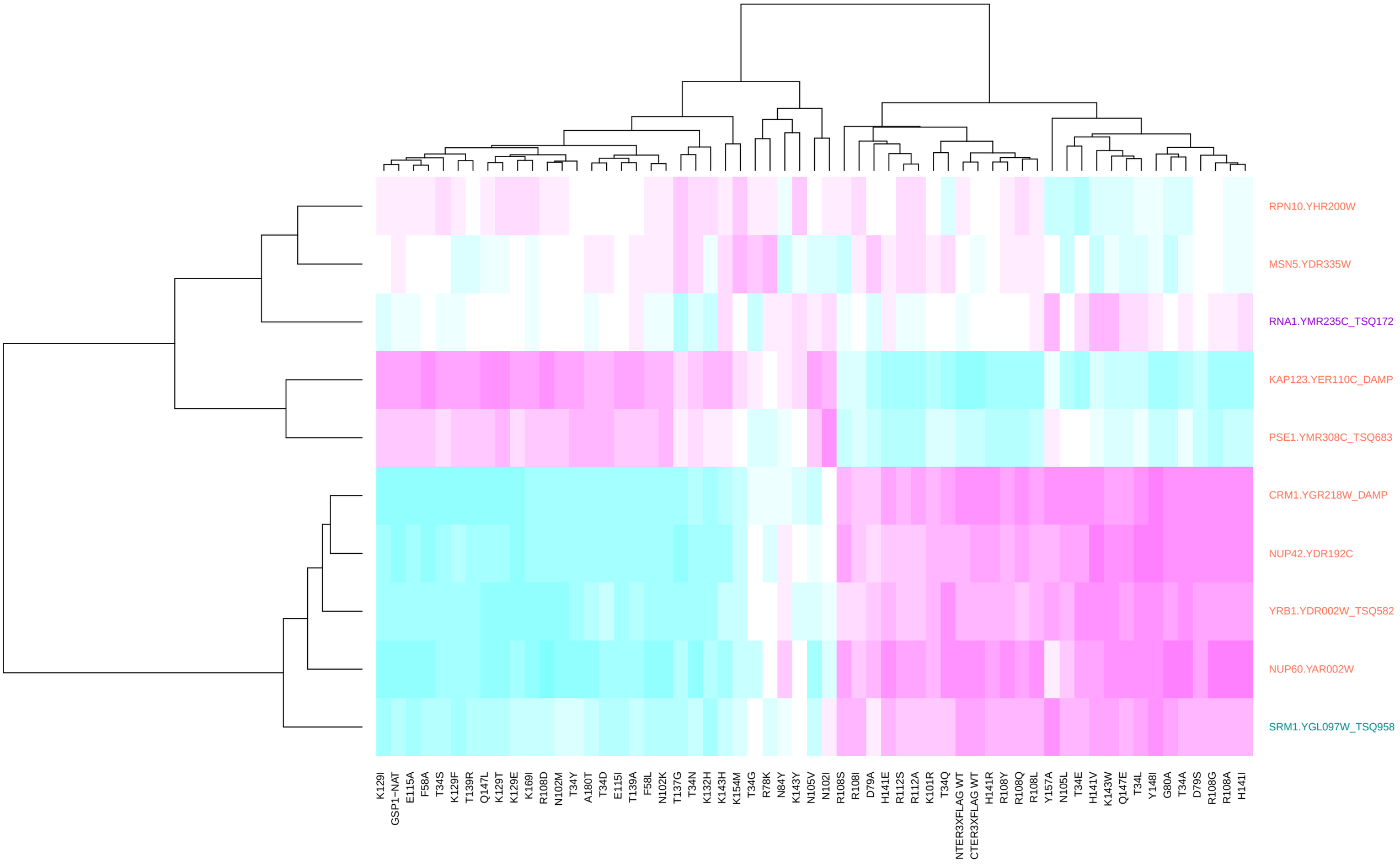
transcription and mRNA processing_GO_15_14_mut



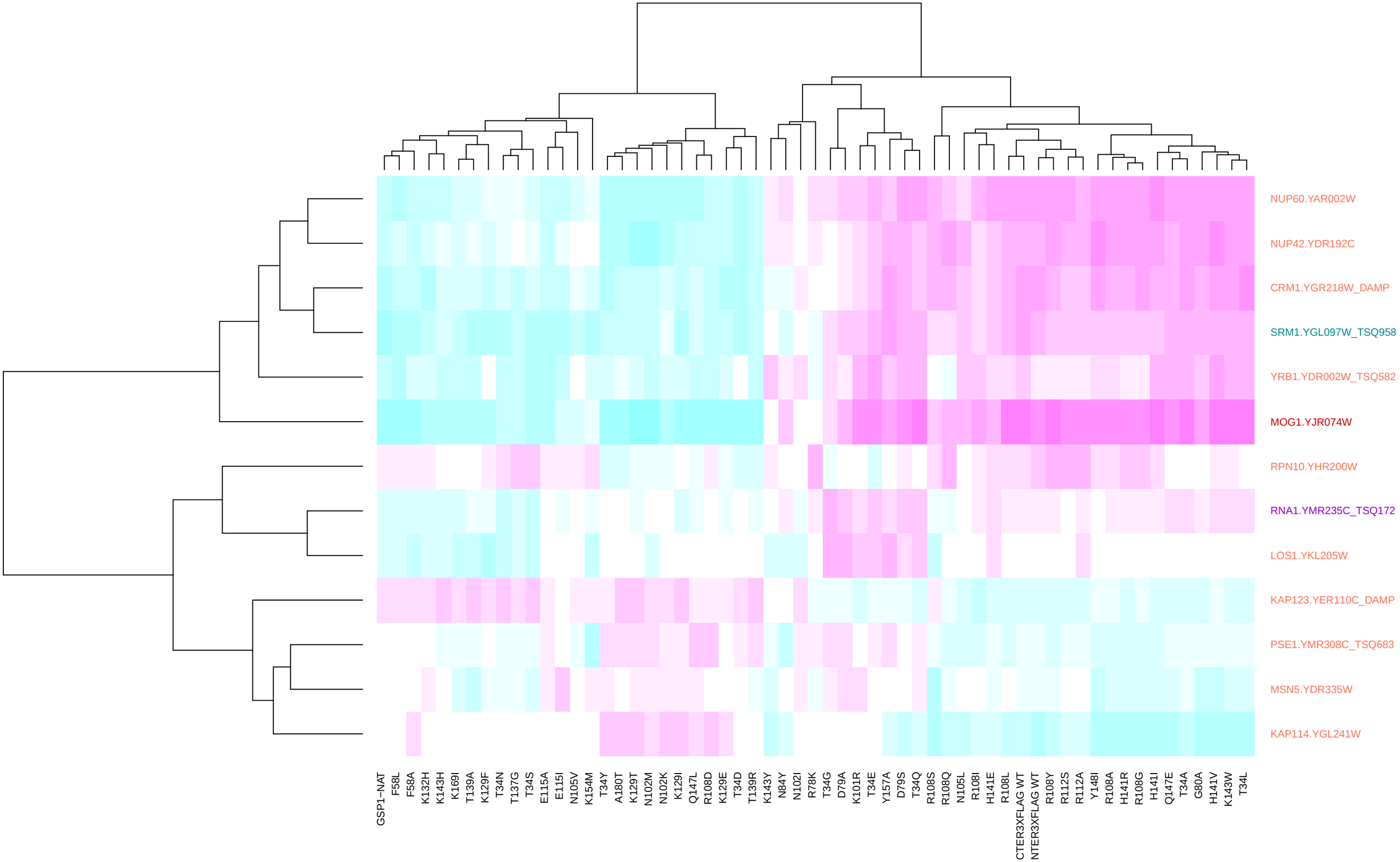
transcription and mRNA processing_GO_30_2_mut



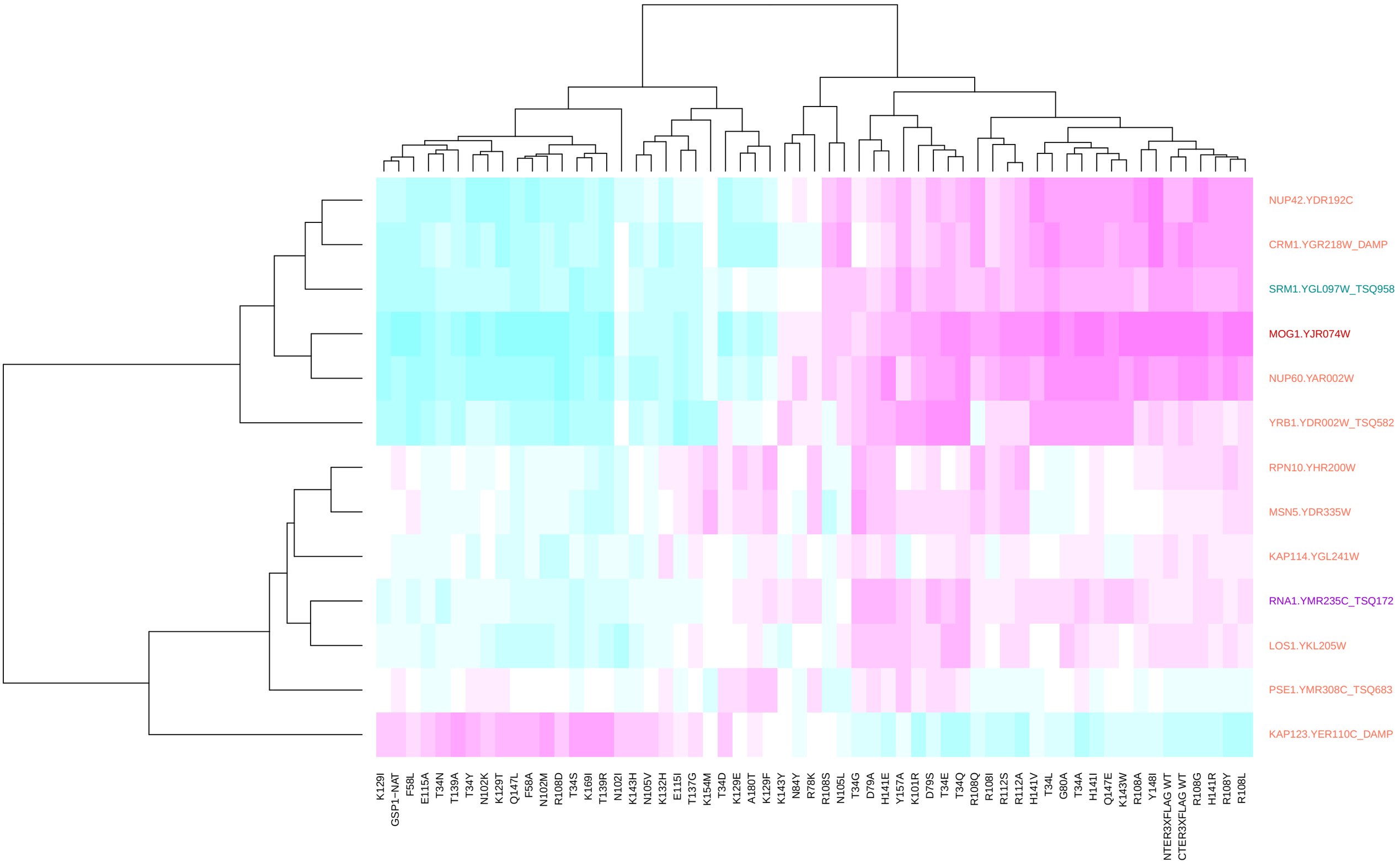
transcription from RNA polymerase II promoter_GO_15_3_mut



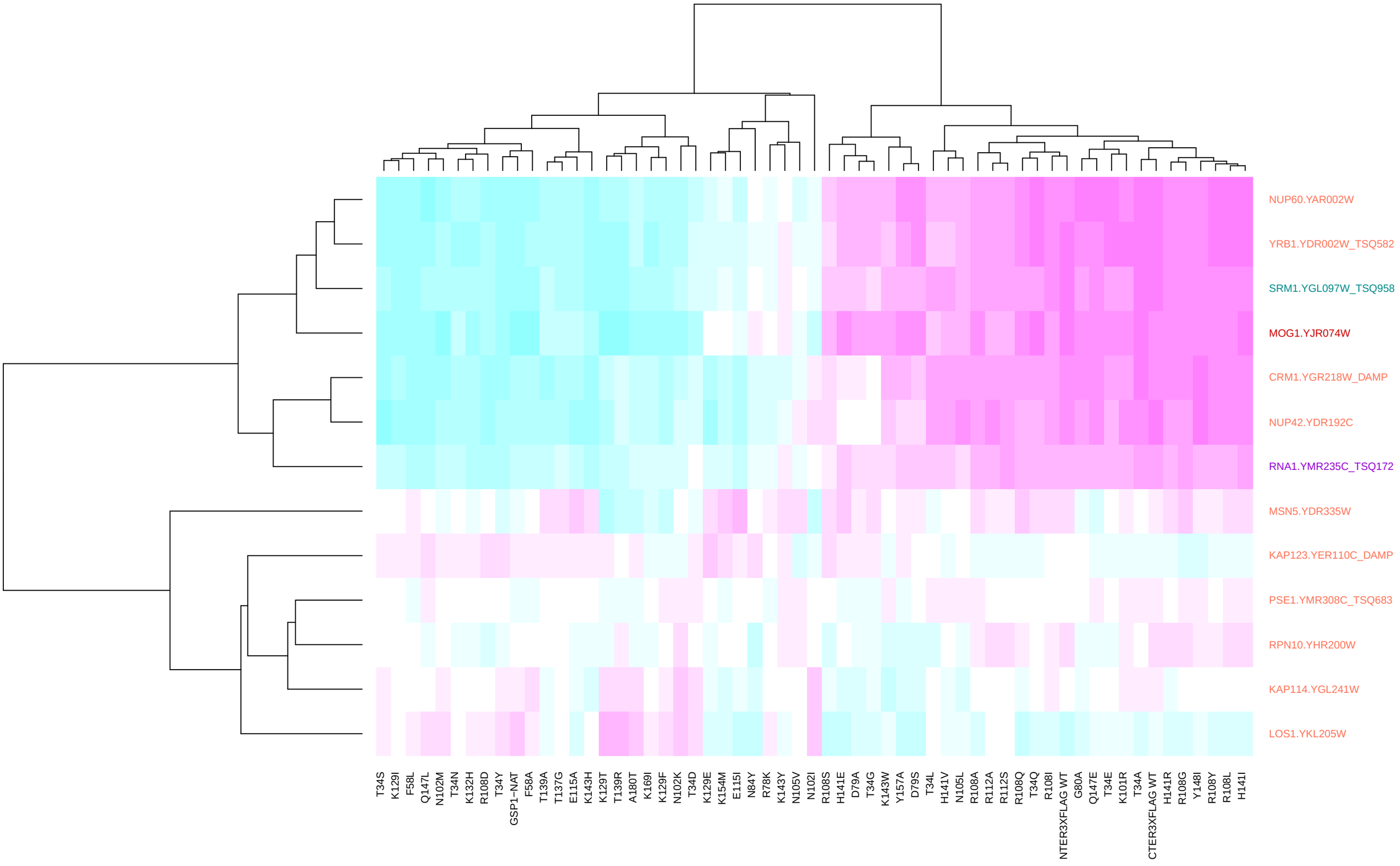
transcription from RNA polymerase II promoter_GO_30_1_all



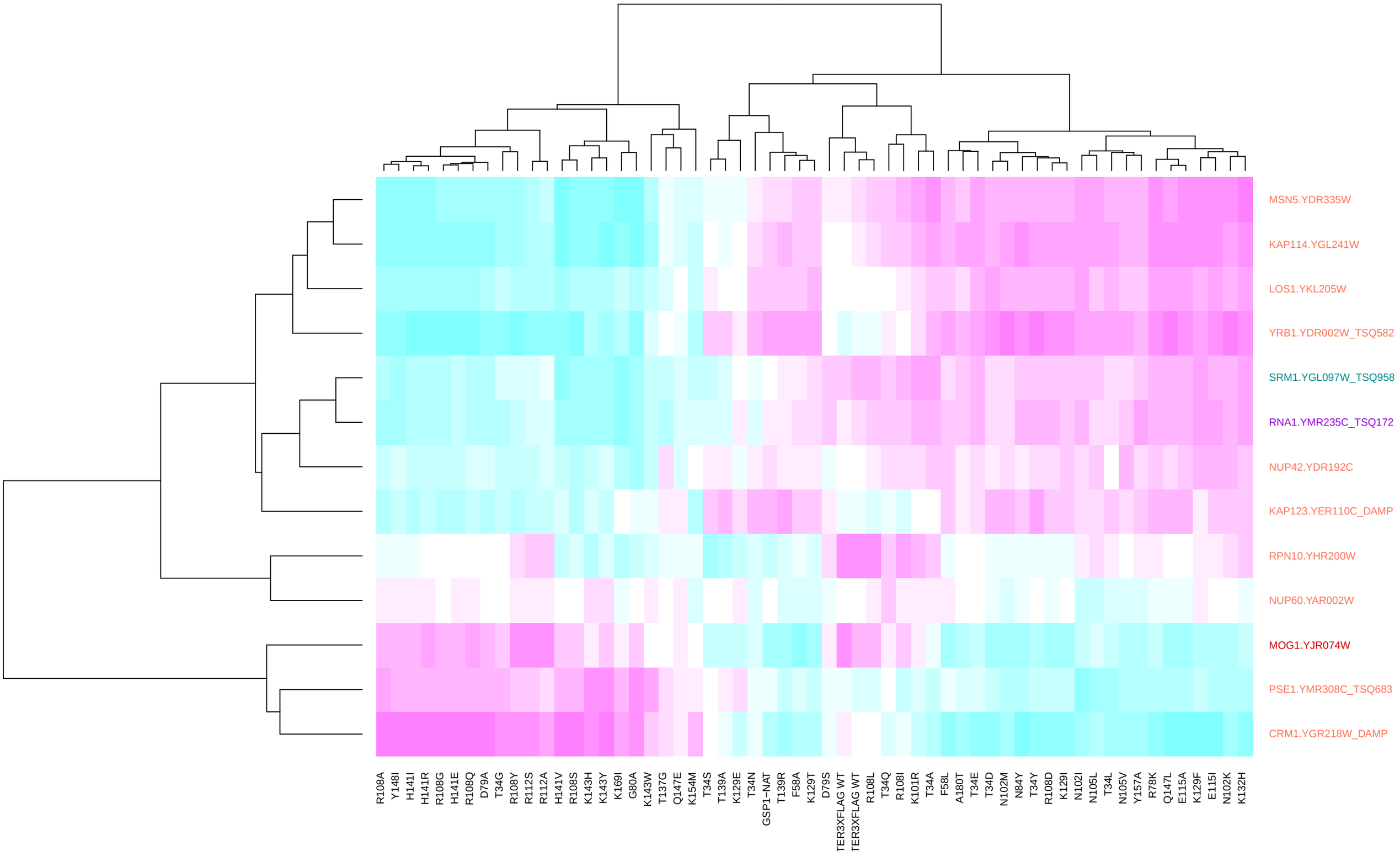
transcription from RNA polymerase II promoter_GO_30_1_mut



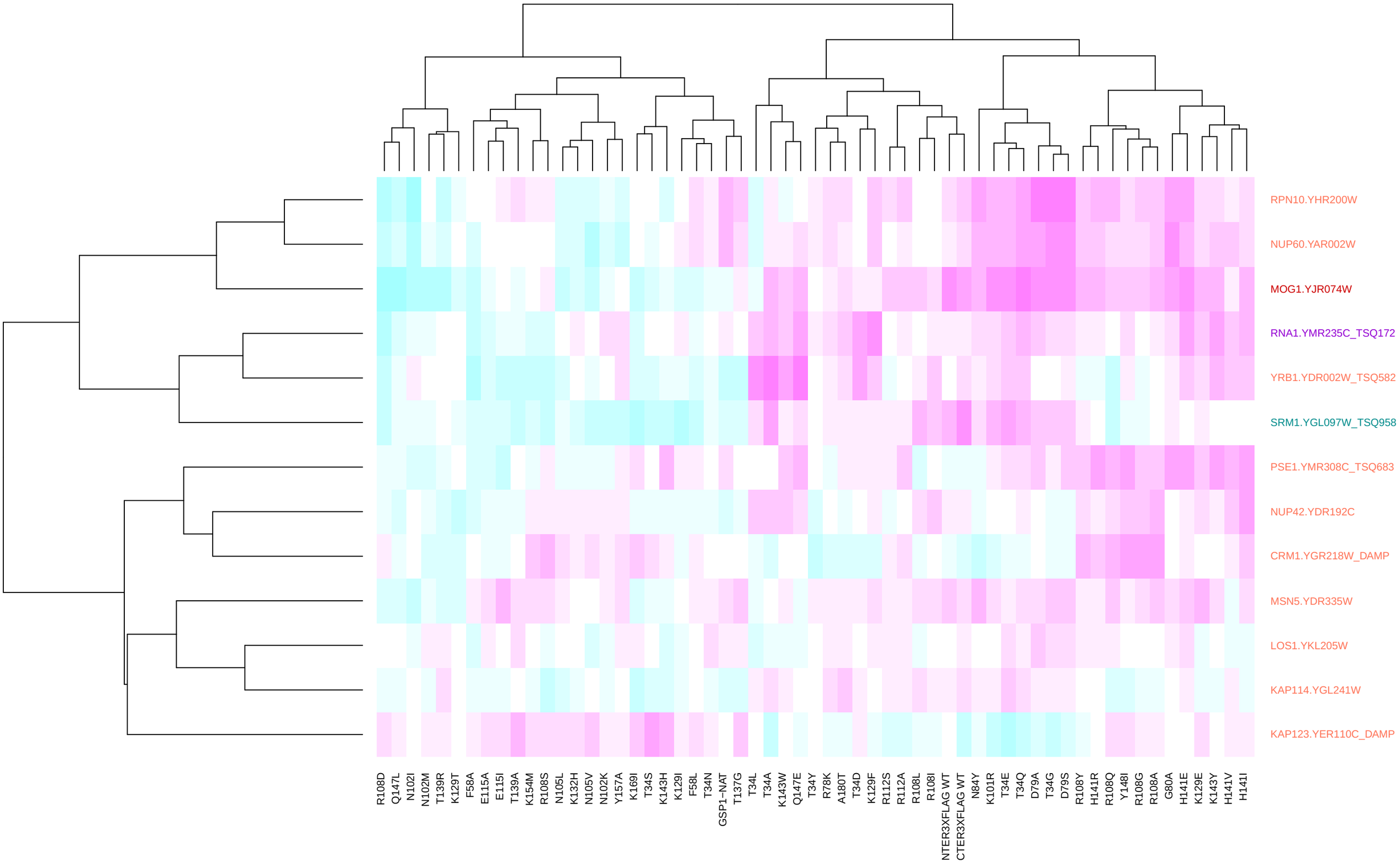
protein targeting_GO_30_1_all



whole_library_30_14_mut



budding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NUP42.YDR192C
CRM1.YGR218W_DAMP
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LOS1.YKL205W
KAP114.YGL241W
KAP123.YER110C_DAMP
R108D
Q147L
N102I
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GSP1−NAT
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T34L
T34A
K143W
Q147E
T34Y
R78K
A180T
T34D
K129F
R112S
R112A
R108L
R108I
NTER3XFLAG WT
CTER3XFLAG WT
N84Y
K101R
T34E
T34Q
D79A
T34G
D79S
R109Y
H141R
R108Q
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R108G
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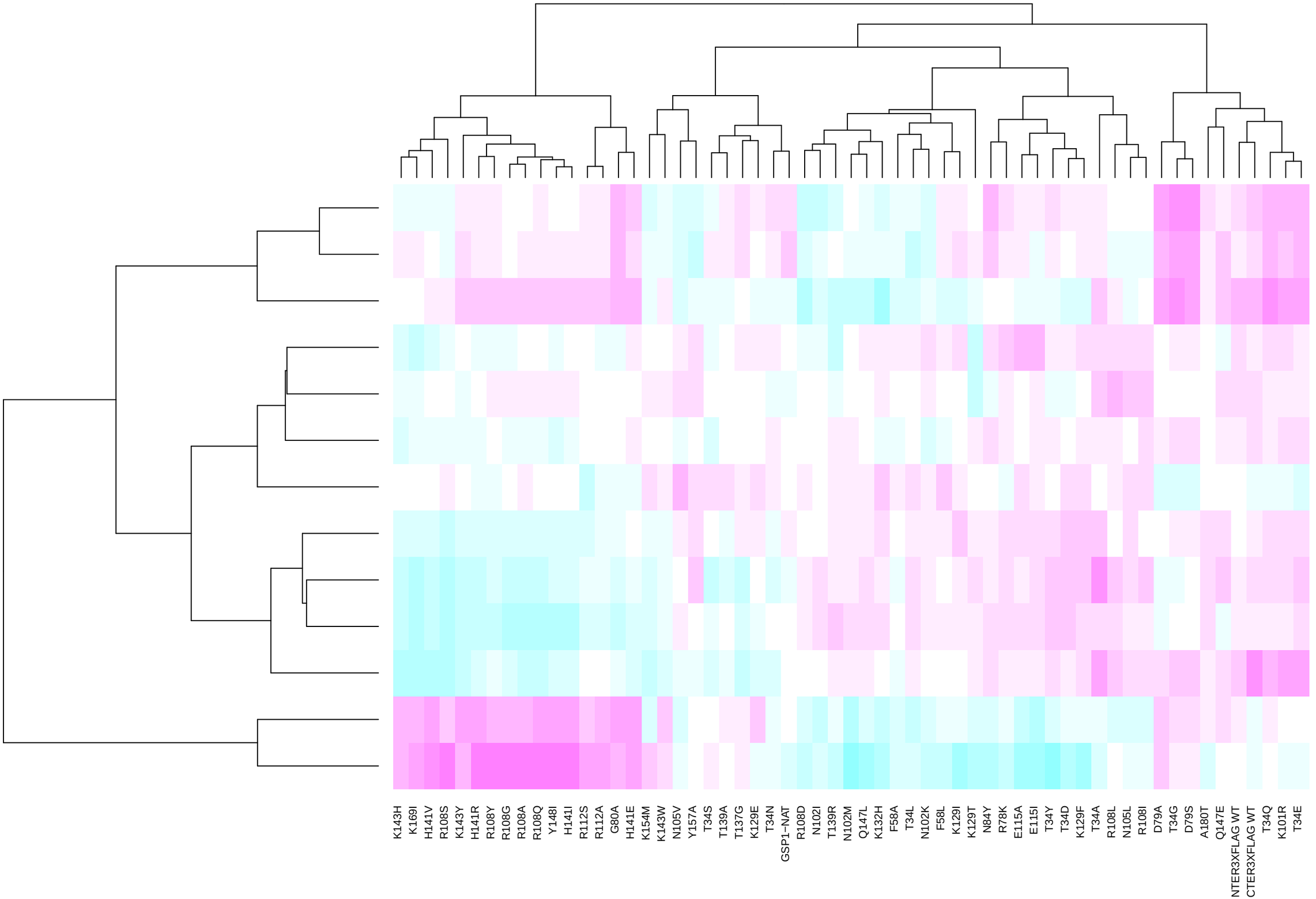
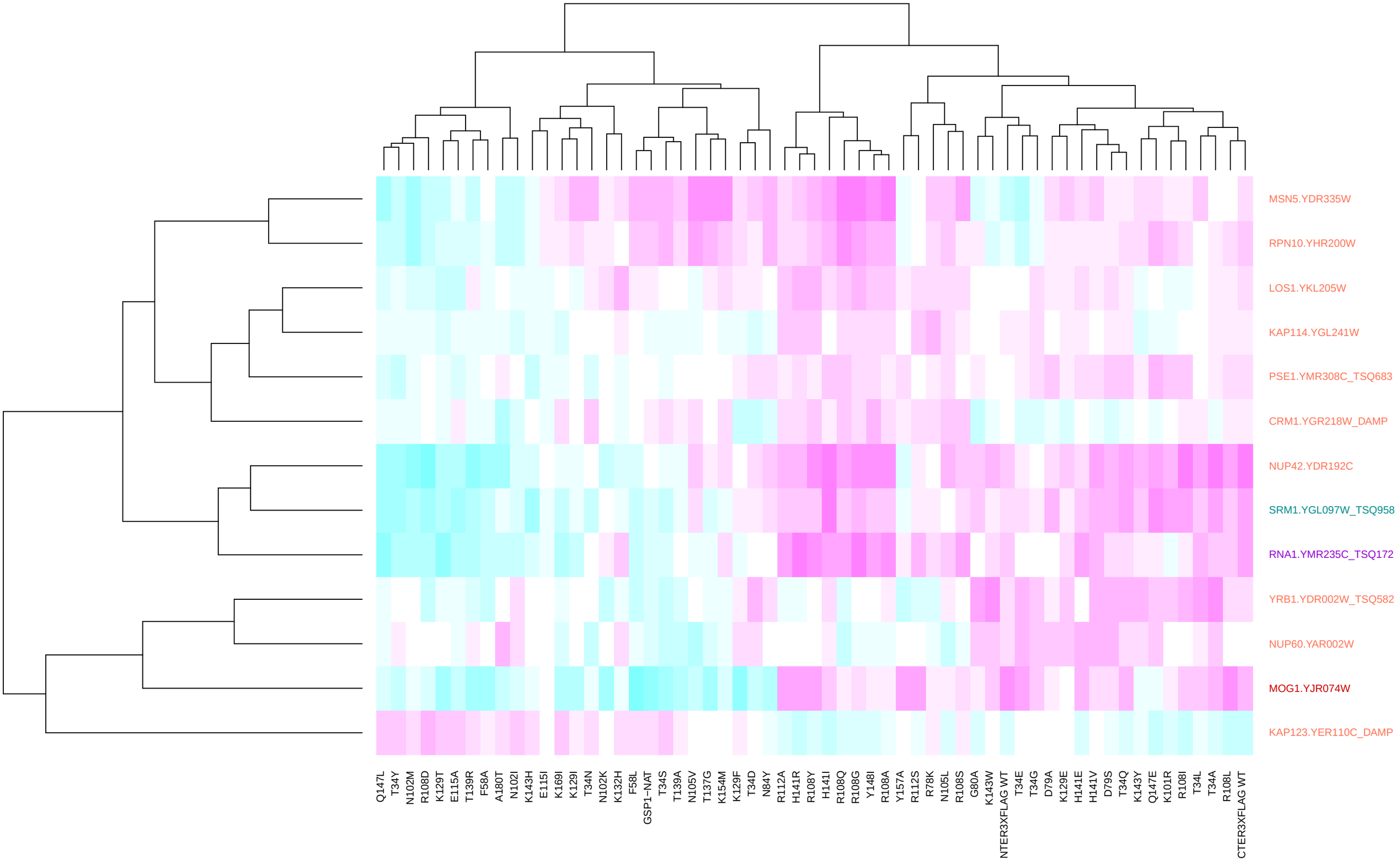
G80A
H141E
K129E
K143Y
H141V
H141I

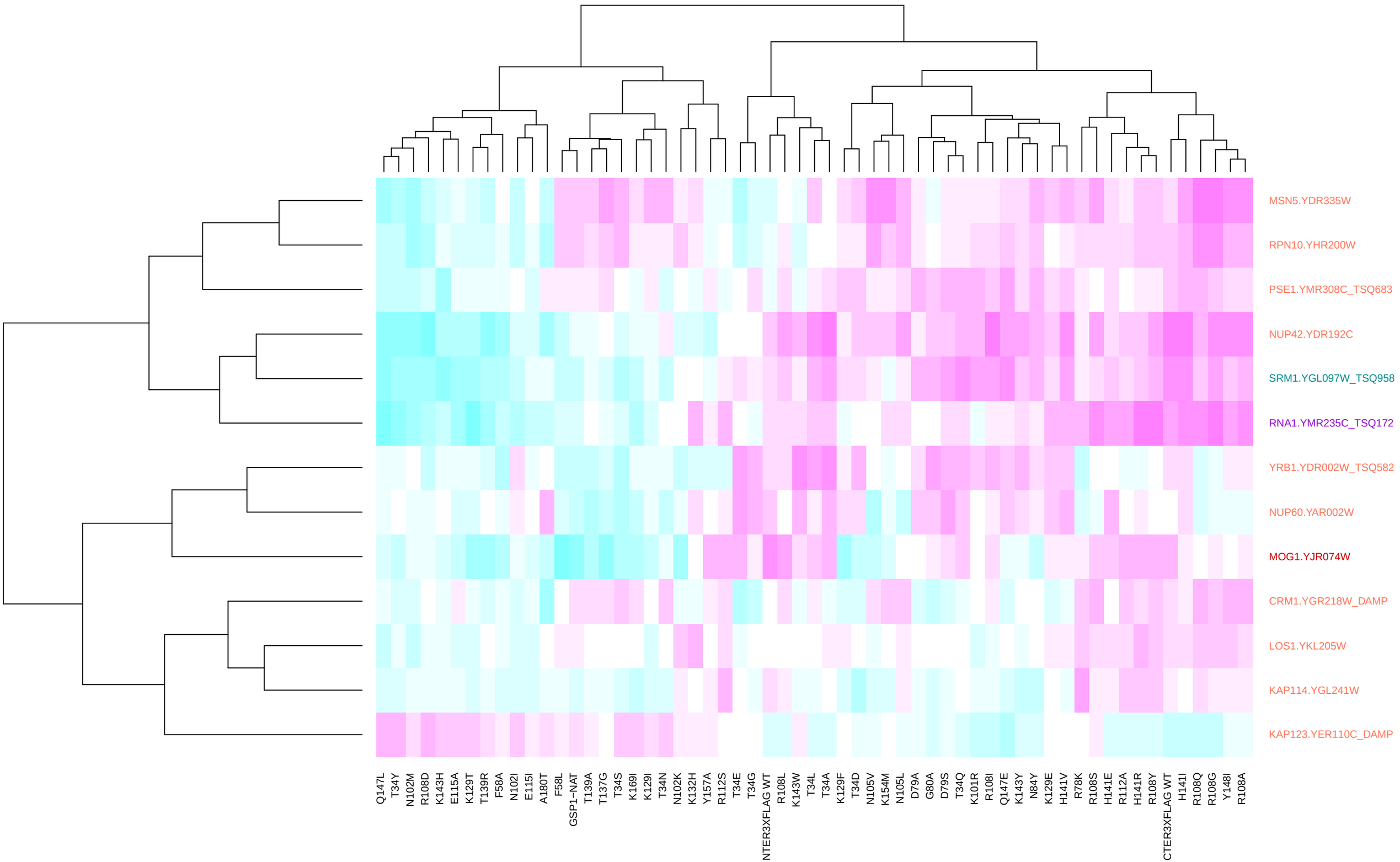
cytoskeleton and microtubules



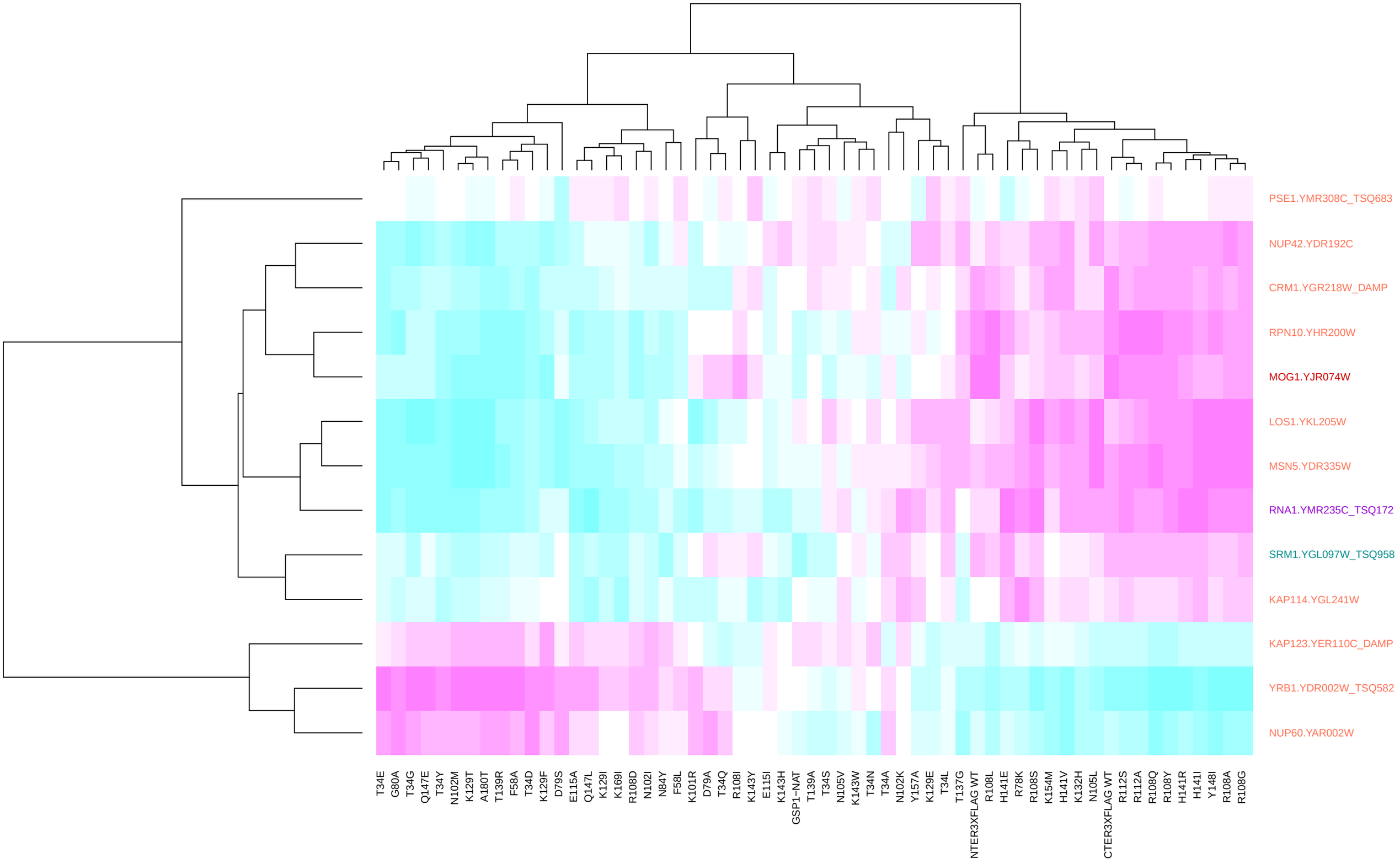
ribosomes and translation



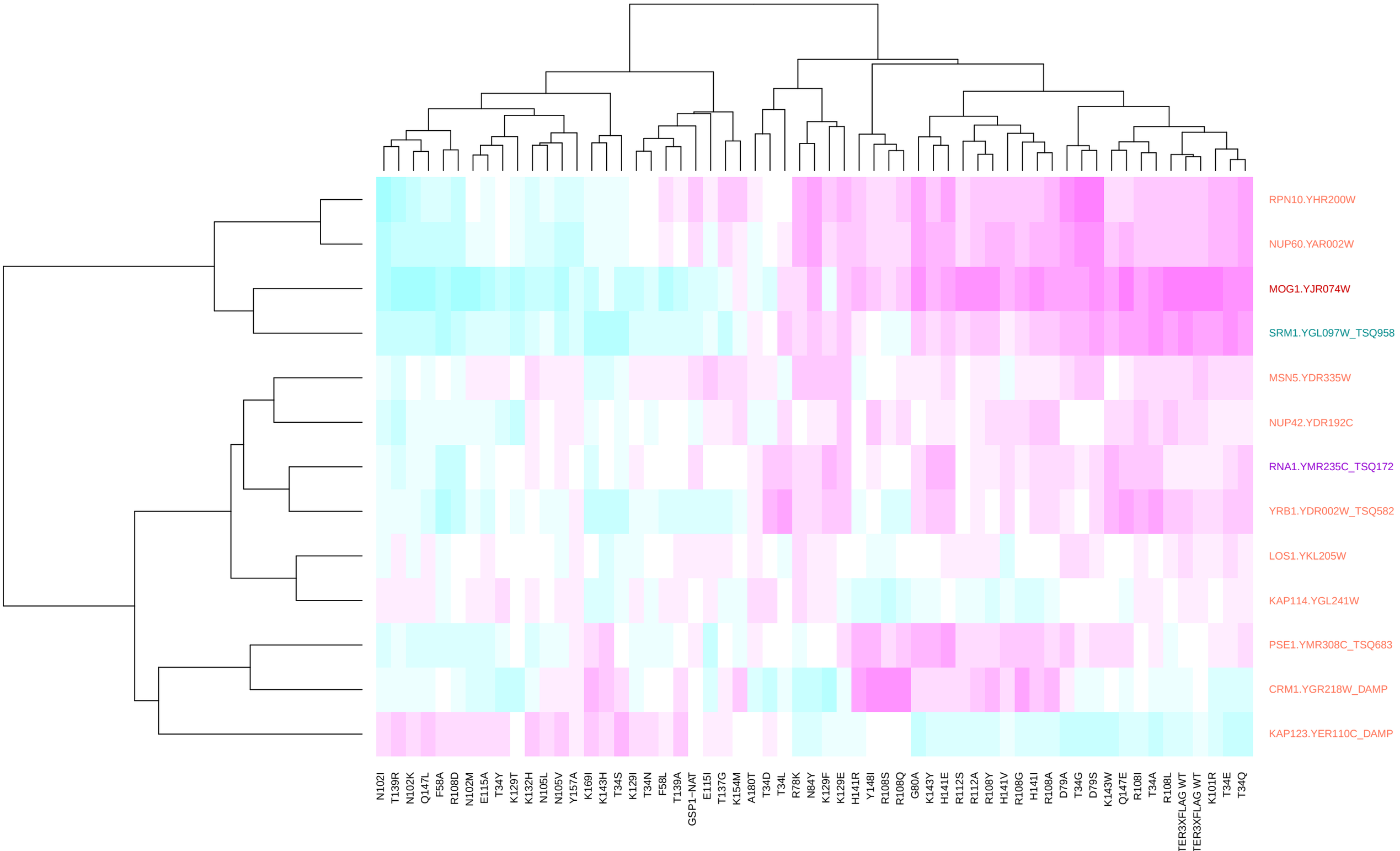
ribosomes and translation_GO_30_1_all



transcription and mRNA processing_GO_15_8_all



cell cycle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MSN5.YDR335W
NUP42.YDR192C
RNA1.YMR235C_TSQ172
YRB1.YDR002W_TSQ582
LOS1.YKL205W
KAP114.YGL241W
PSE1.YMR308C_TSQ683
CRM1.YGR218W_DAMP
KAP123.YER110C_DAMP
N102I
T139R
N102K
Q147L
F58A
R108D
N102M
E115A
T34Y
K129T
K132H
N105L
N105V
Y157A
K169I
K143H
T34S
K129I
T34N
F58L
T139A
GSP1−NAT
E115I
T137G
K154M
A180T
T34D
T34L
R78K
N84Y
K129F
K129E
H141R
Y148I
R108S
R108Q
G80A
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H141E
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H141I
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D79A
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D79S
K143W
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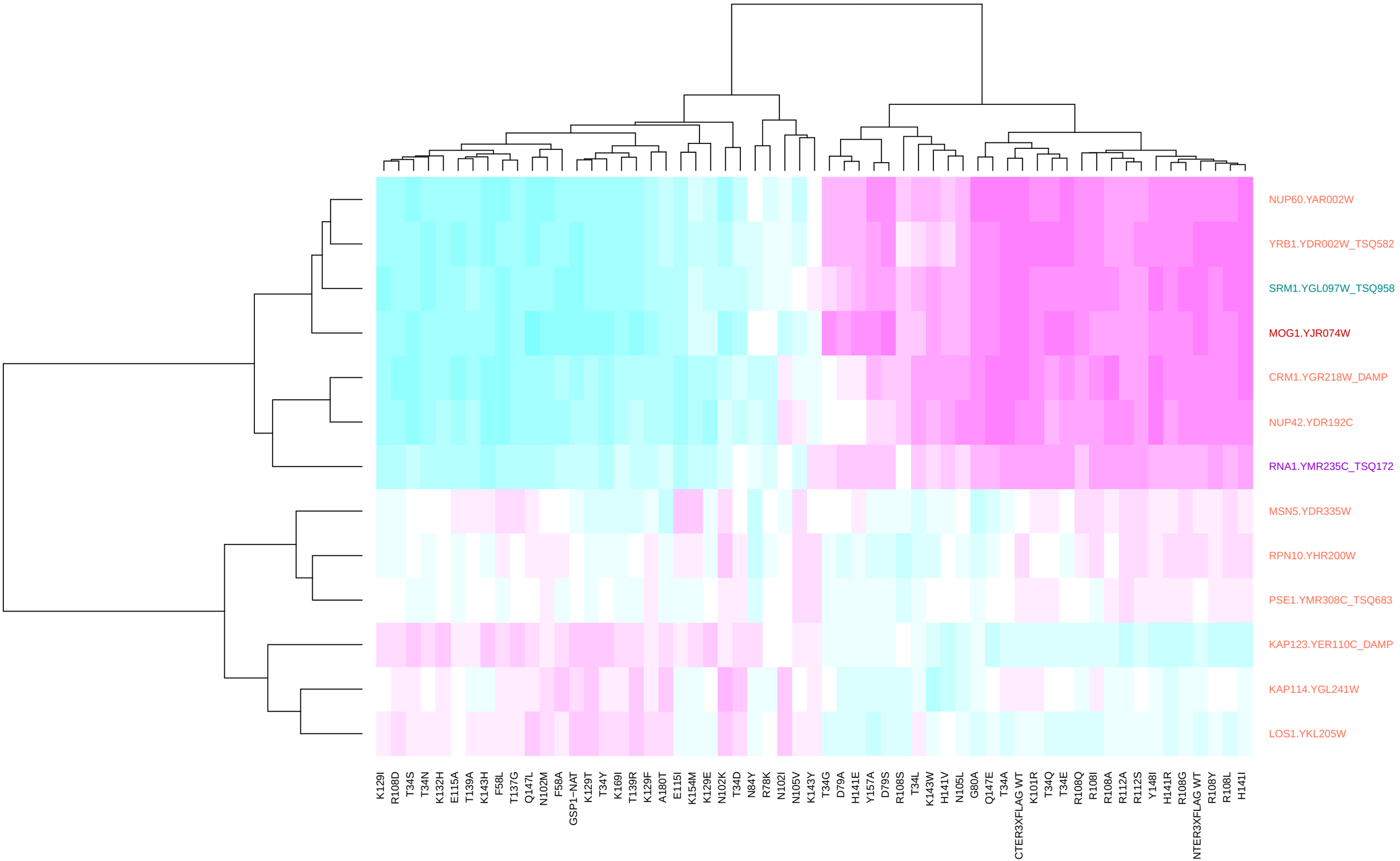
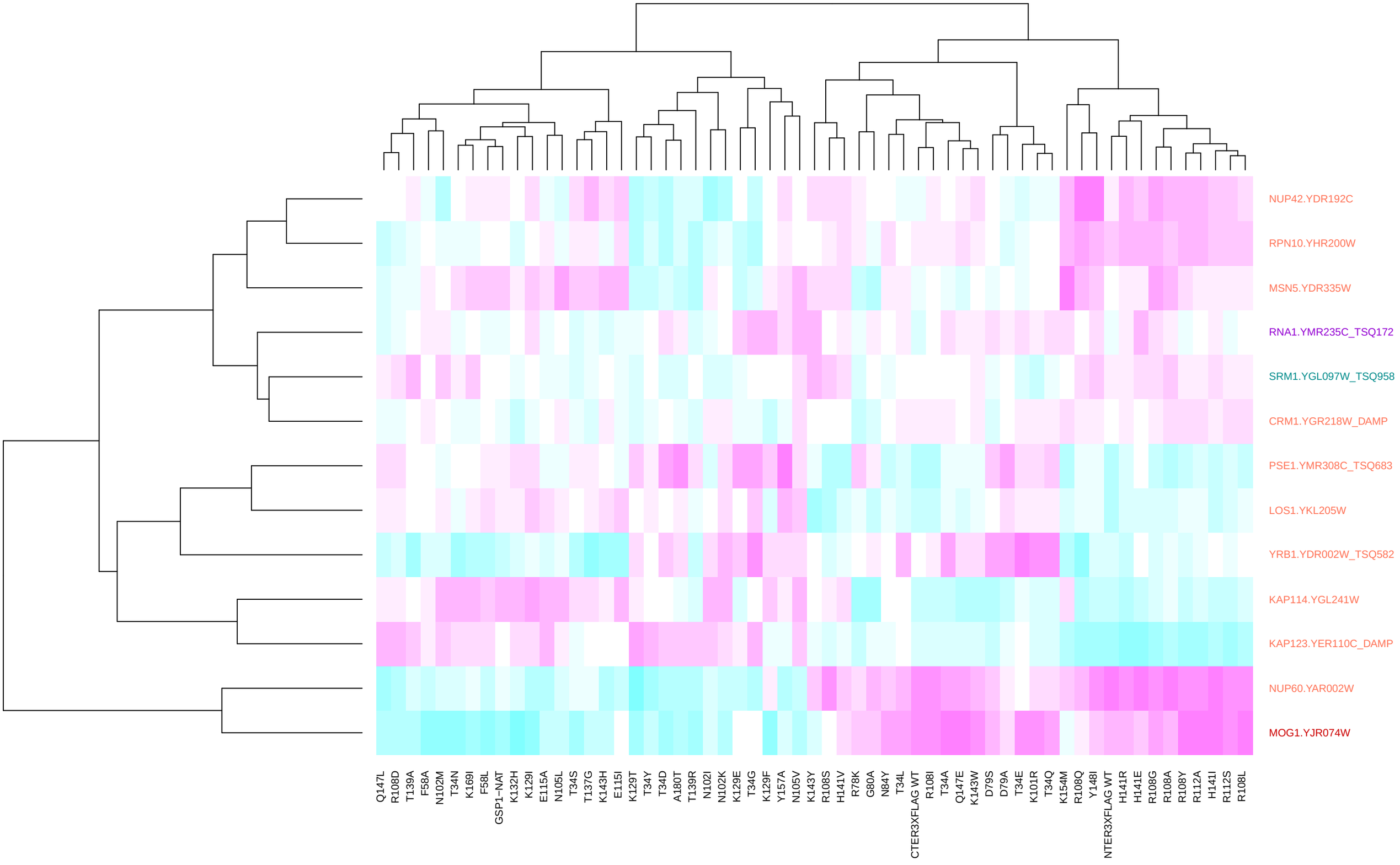
T34E
T34Q

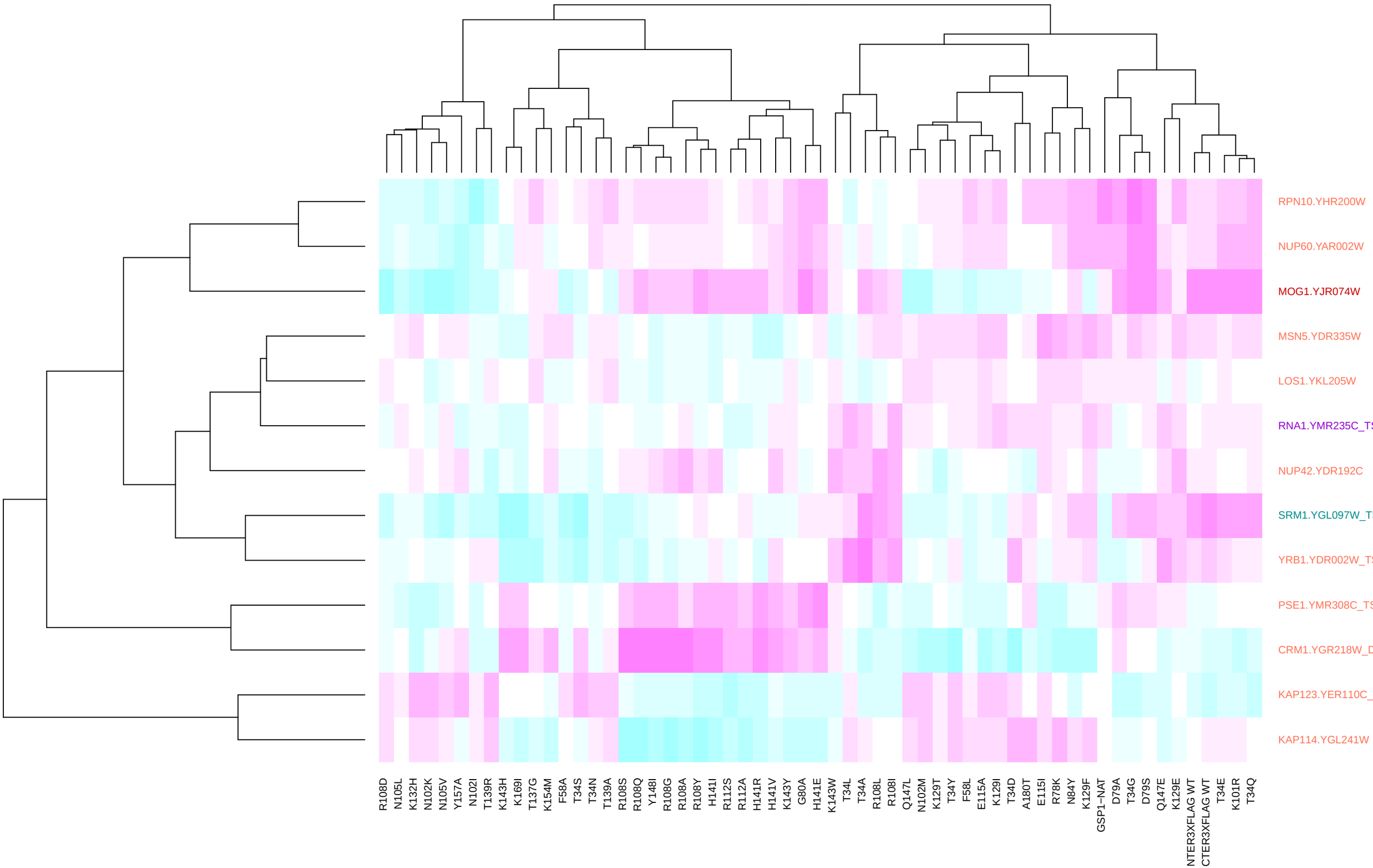
protein targeting_GO_30_1_mut



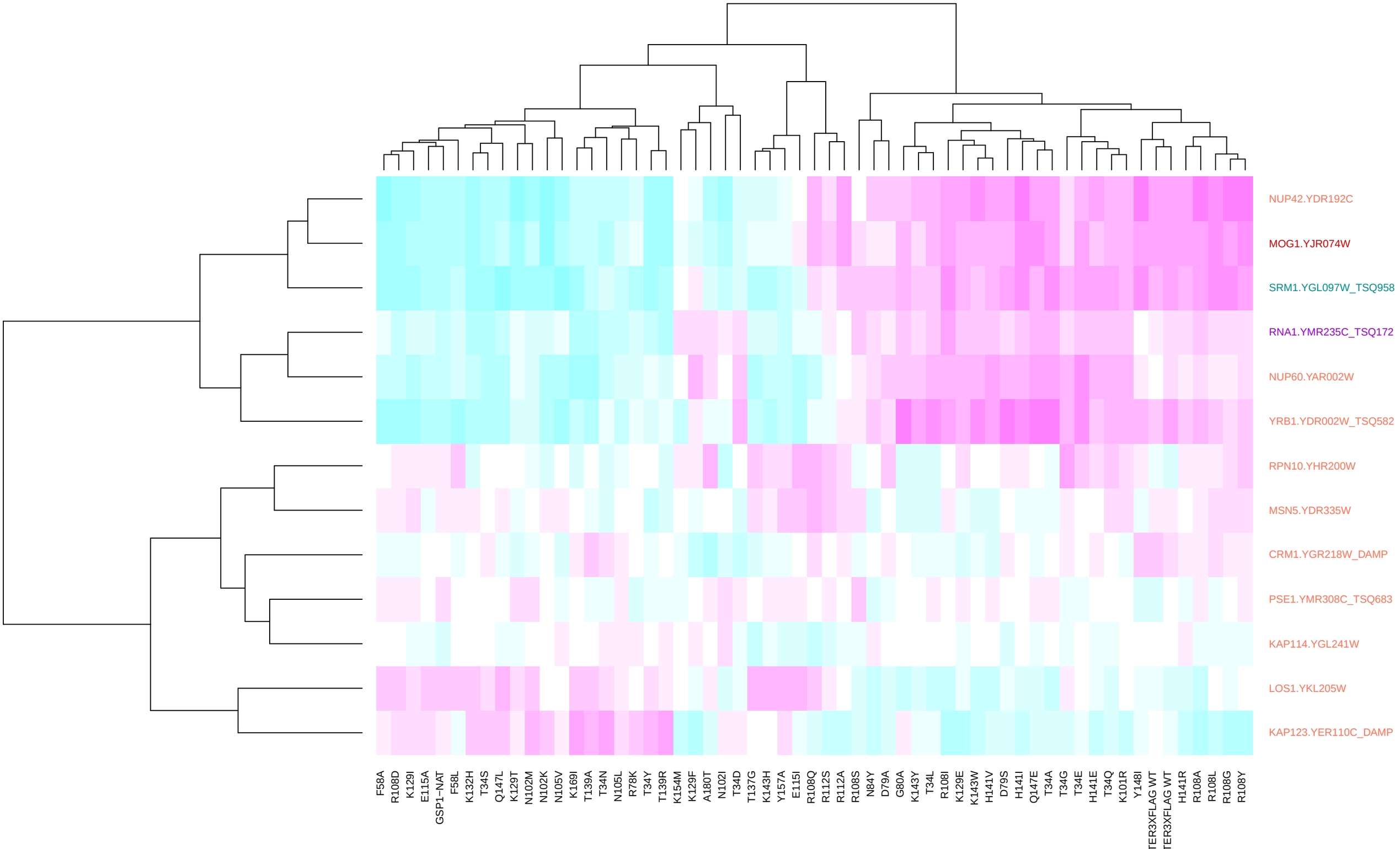
DNA−templated transcription, elongation



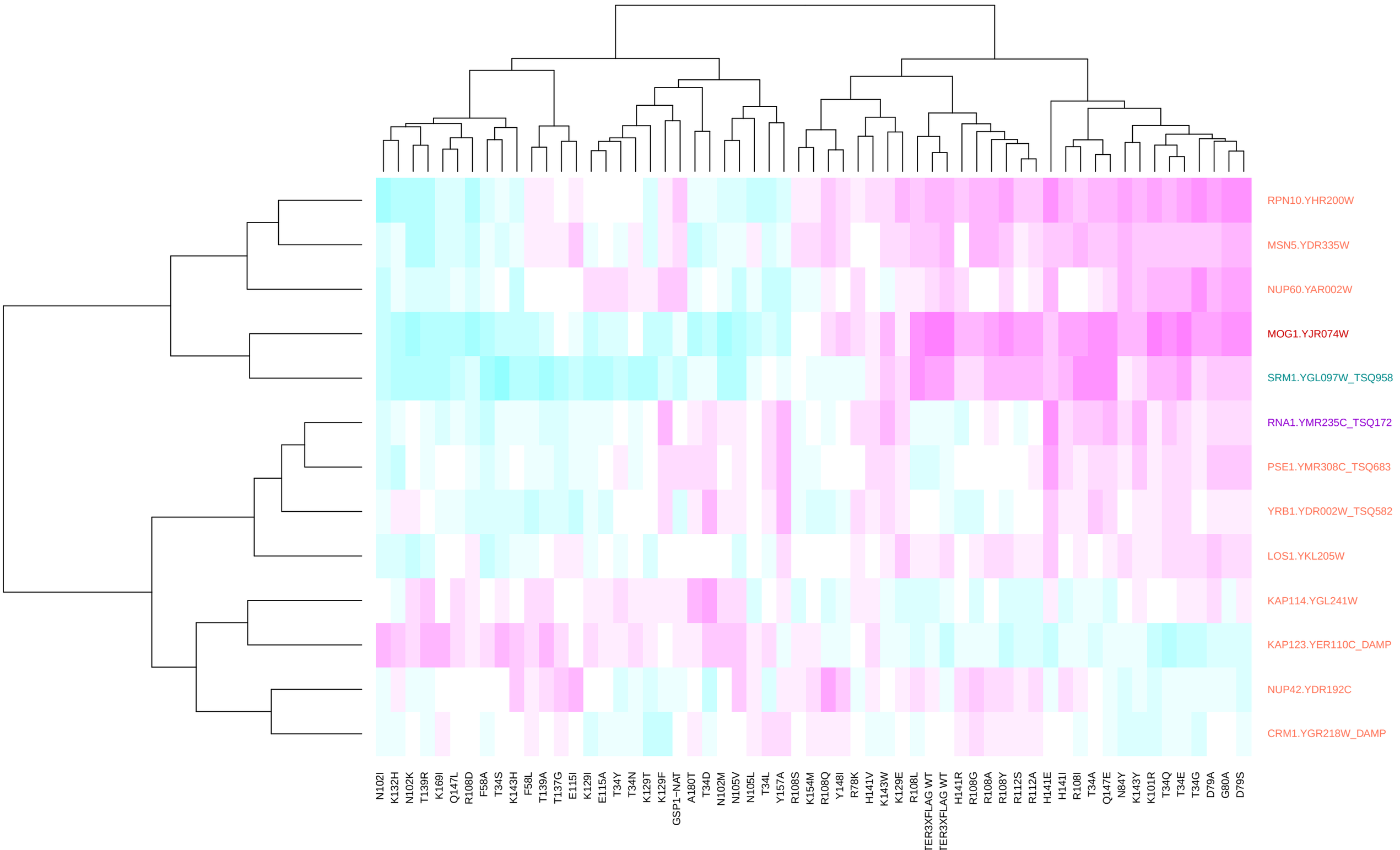
mitotic cell cycle



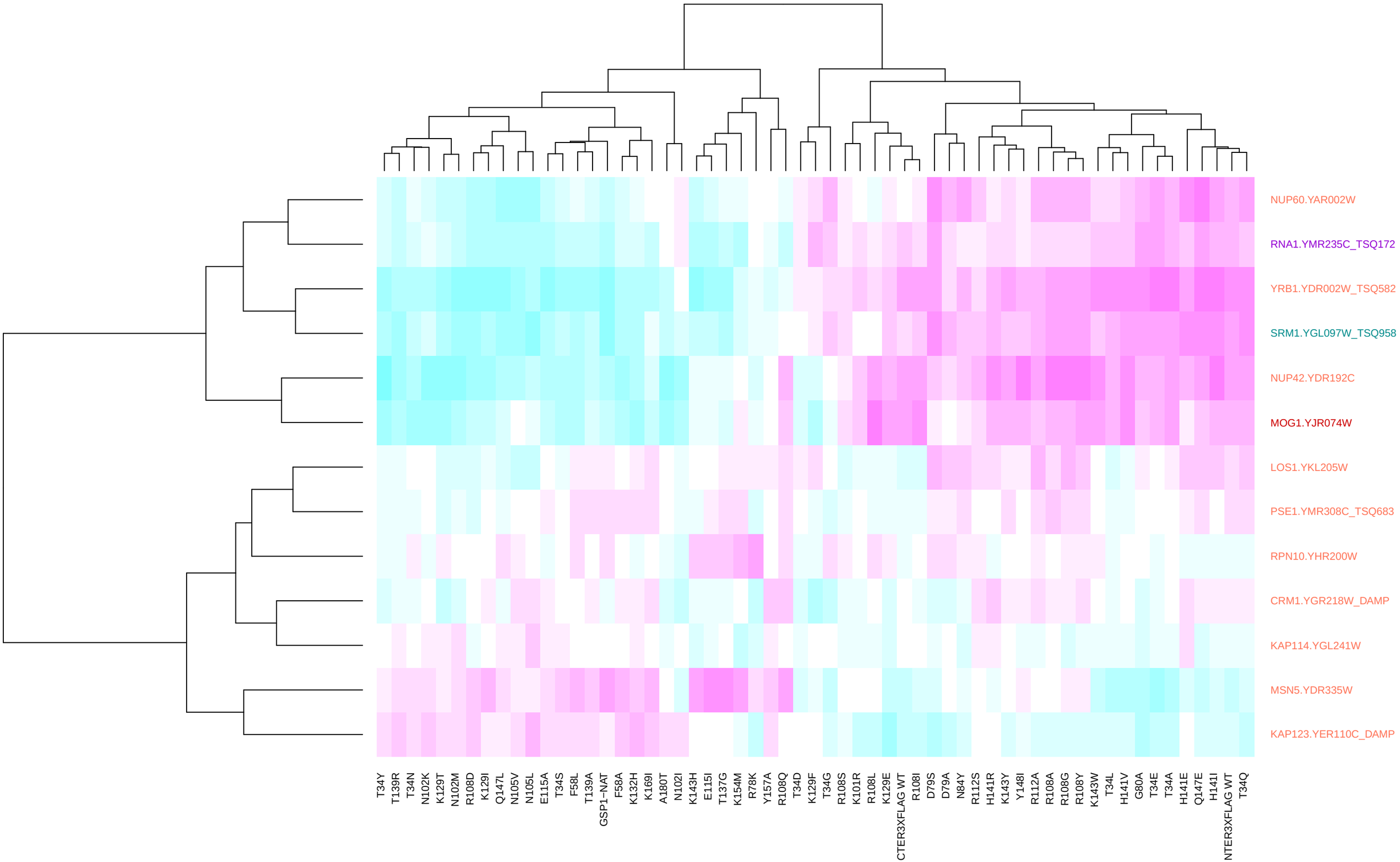
mitotic cell cycle_GO_15_1_all



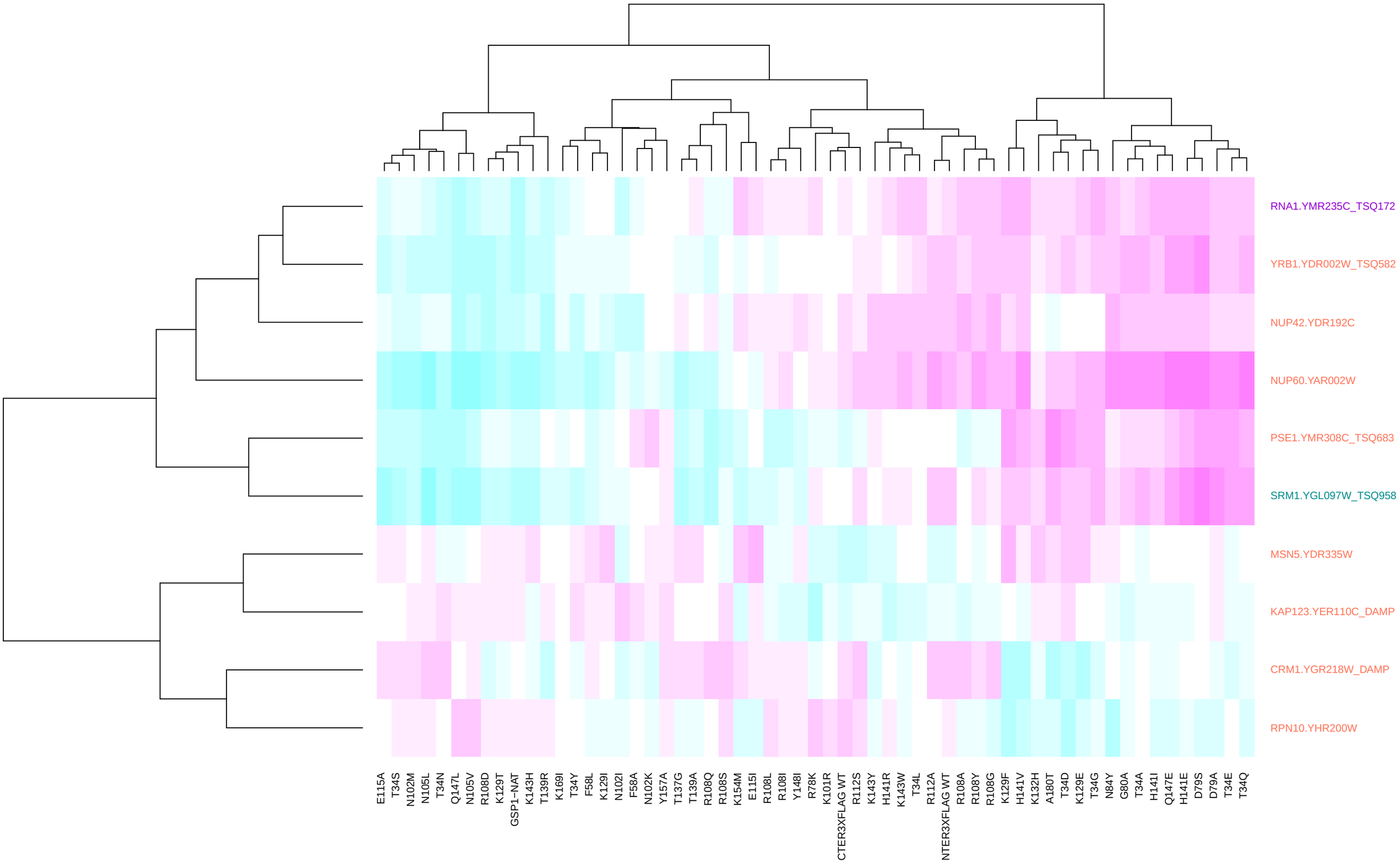
regulation of cell cycle



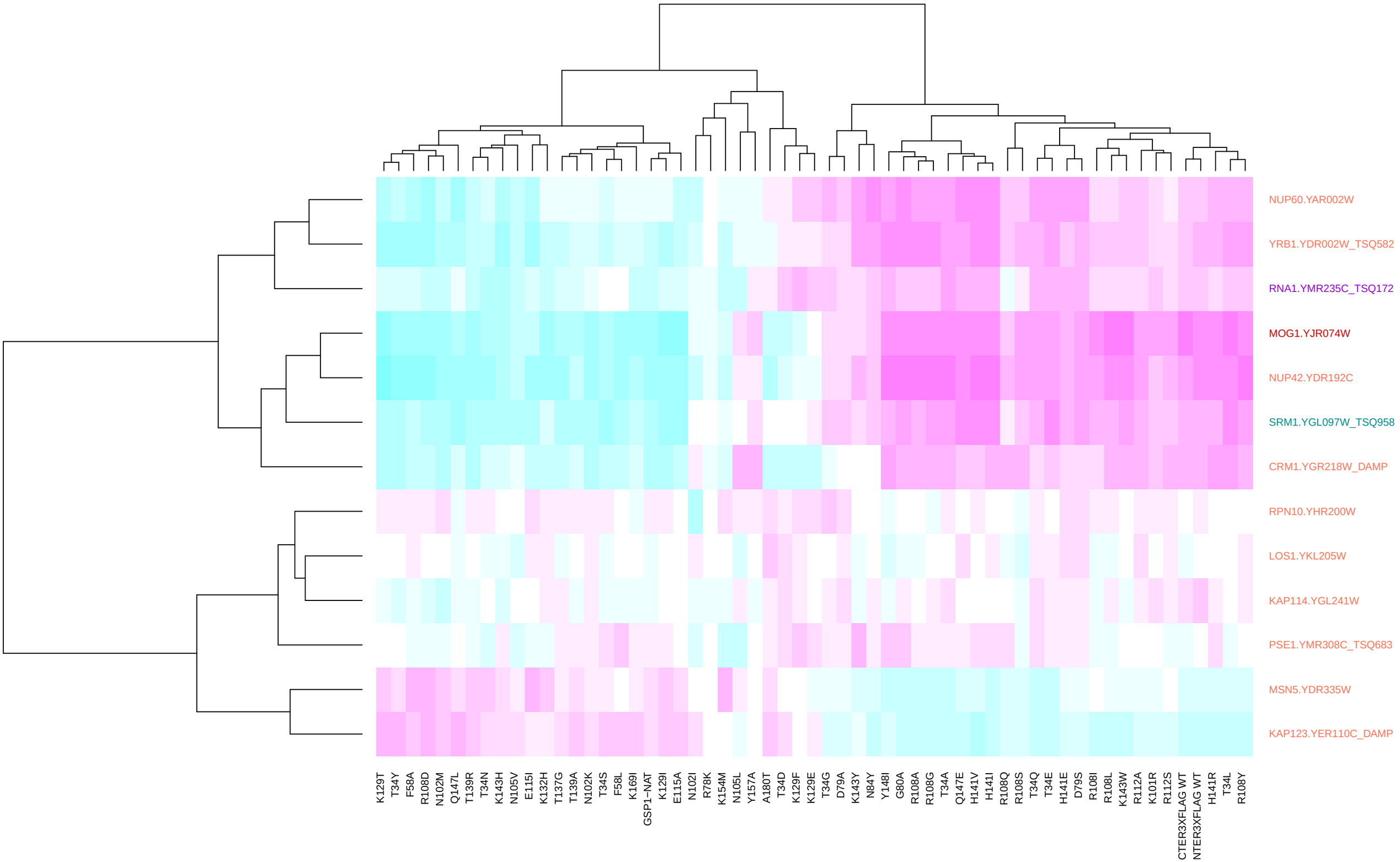
RNA catabolic process



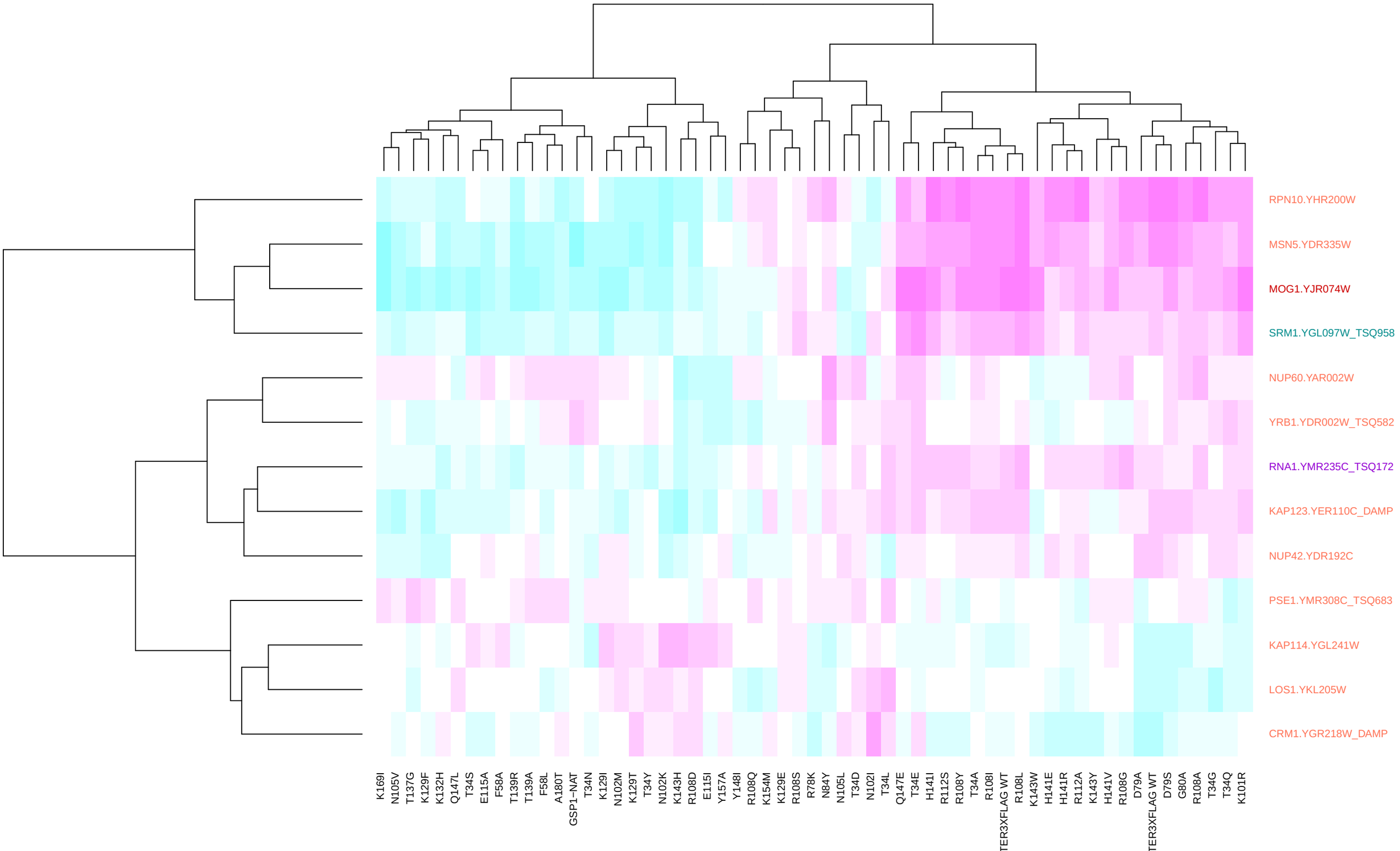
transcription and mRNA processing_GO_30_2_all



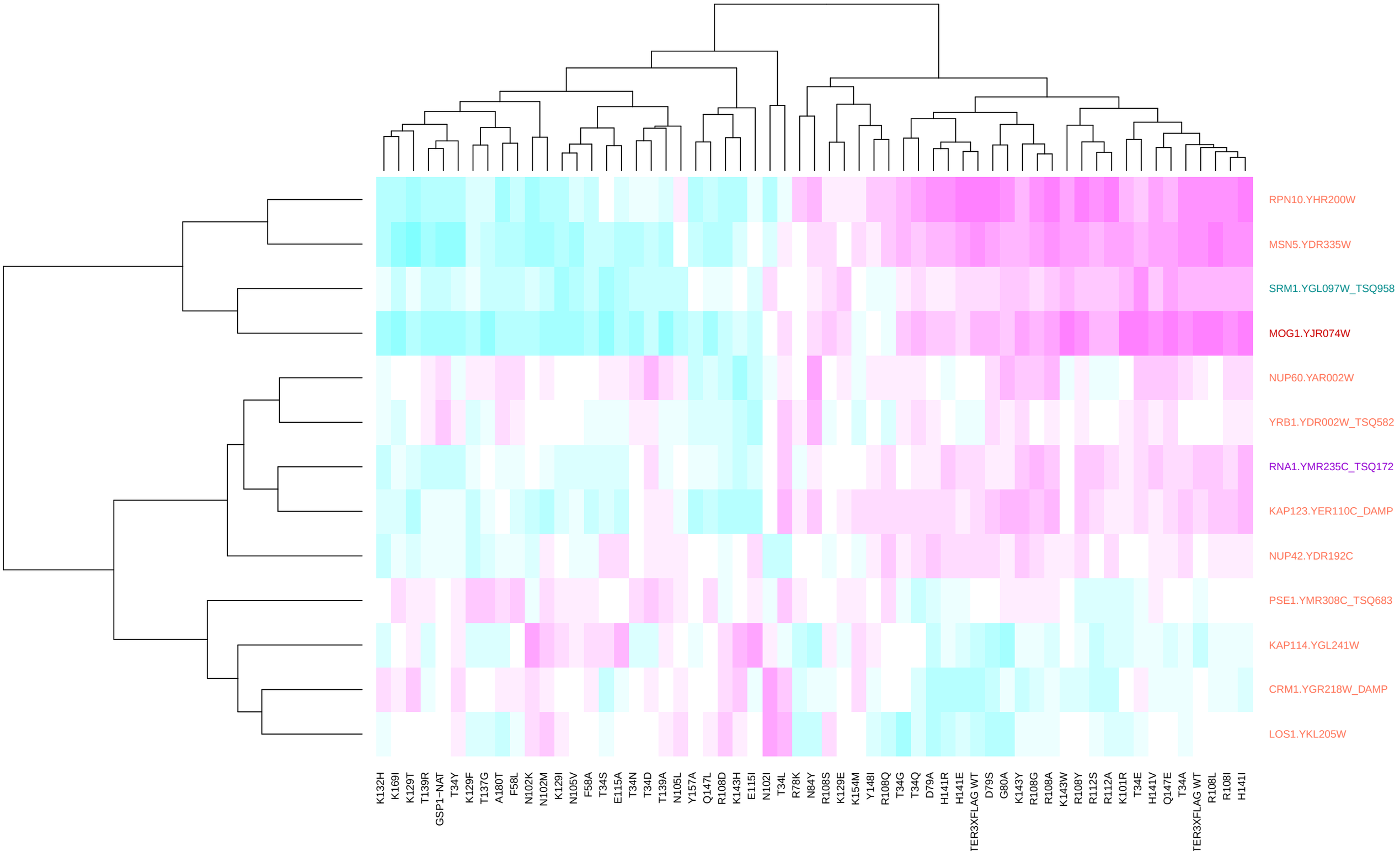
whole_library_30_3_all



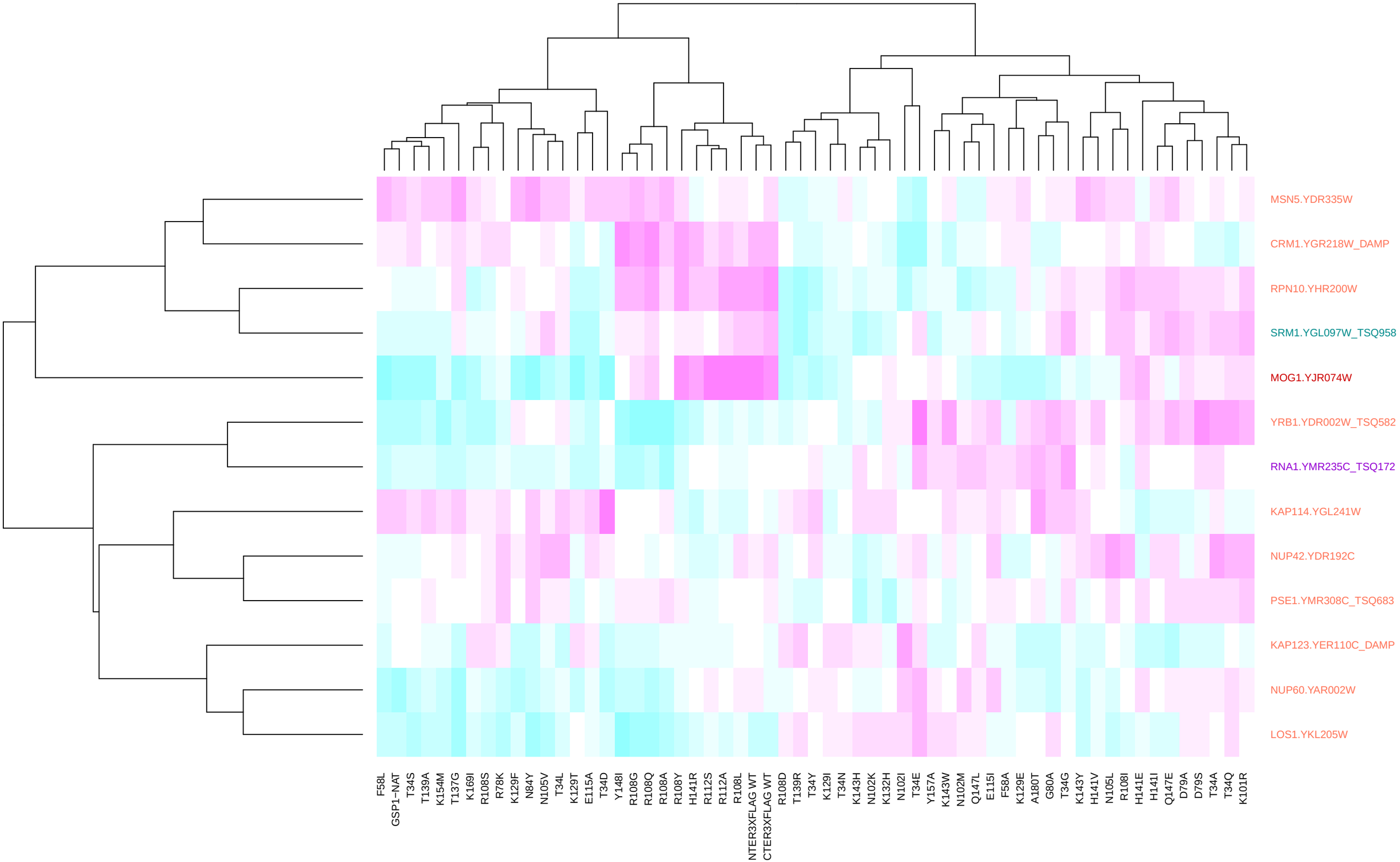
proteolysis involved in cellular protein catabolic process



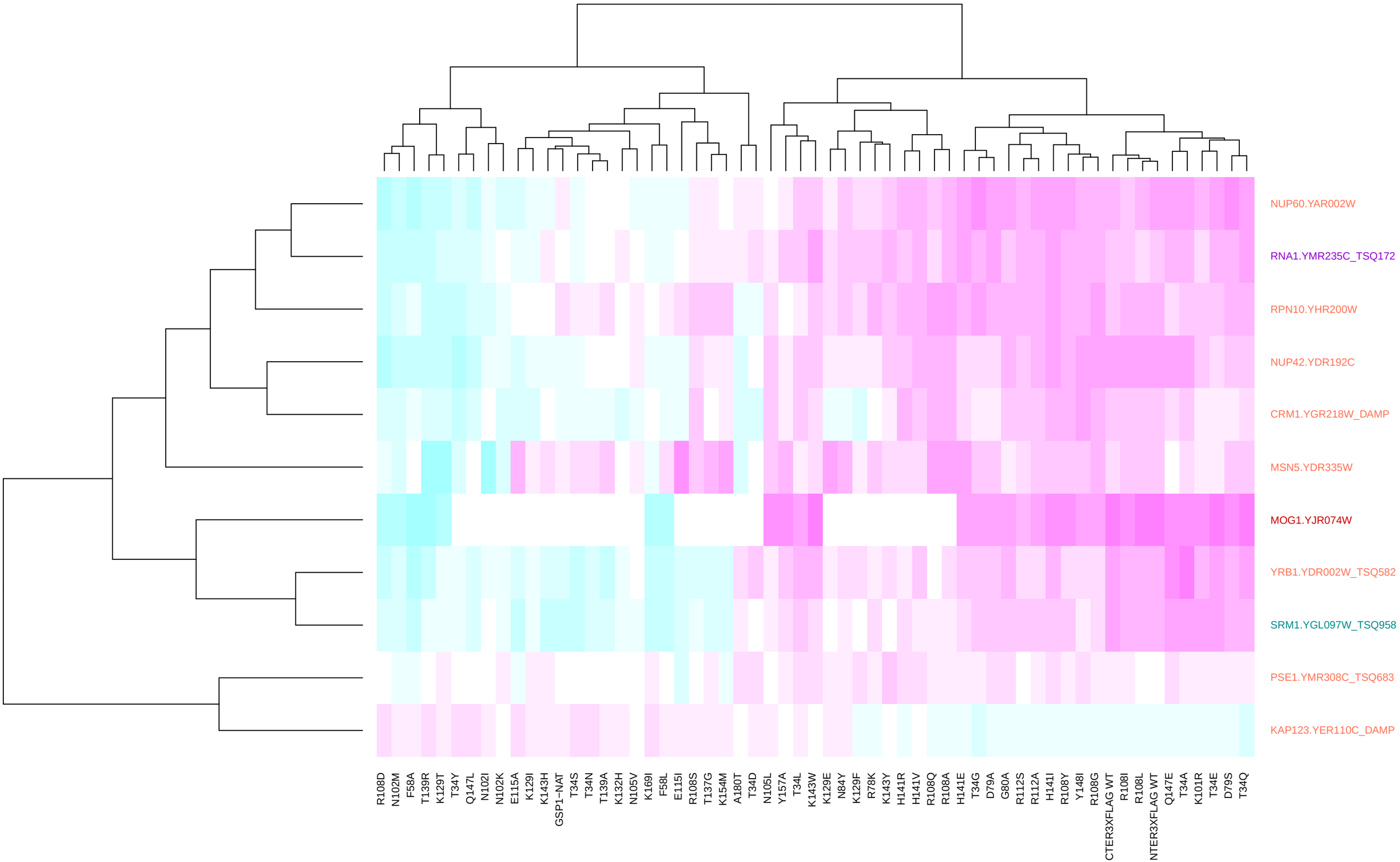
proteolysis involved in cellular protein catabolic process_GO_15_1_all



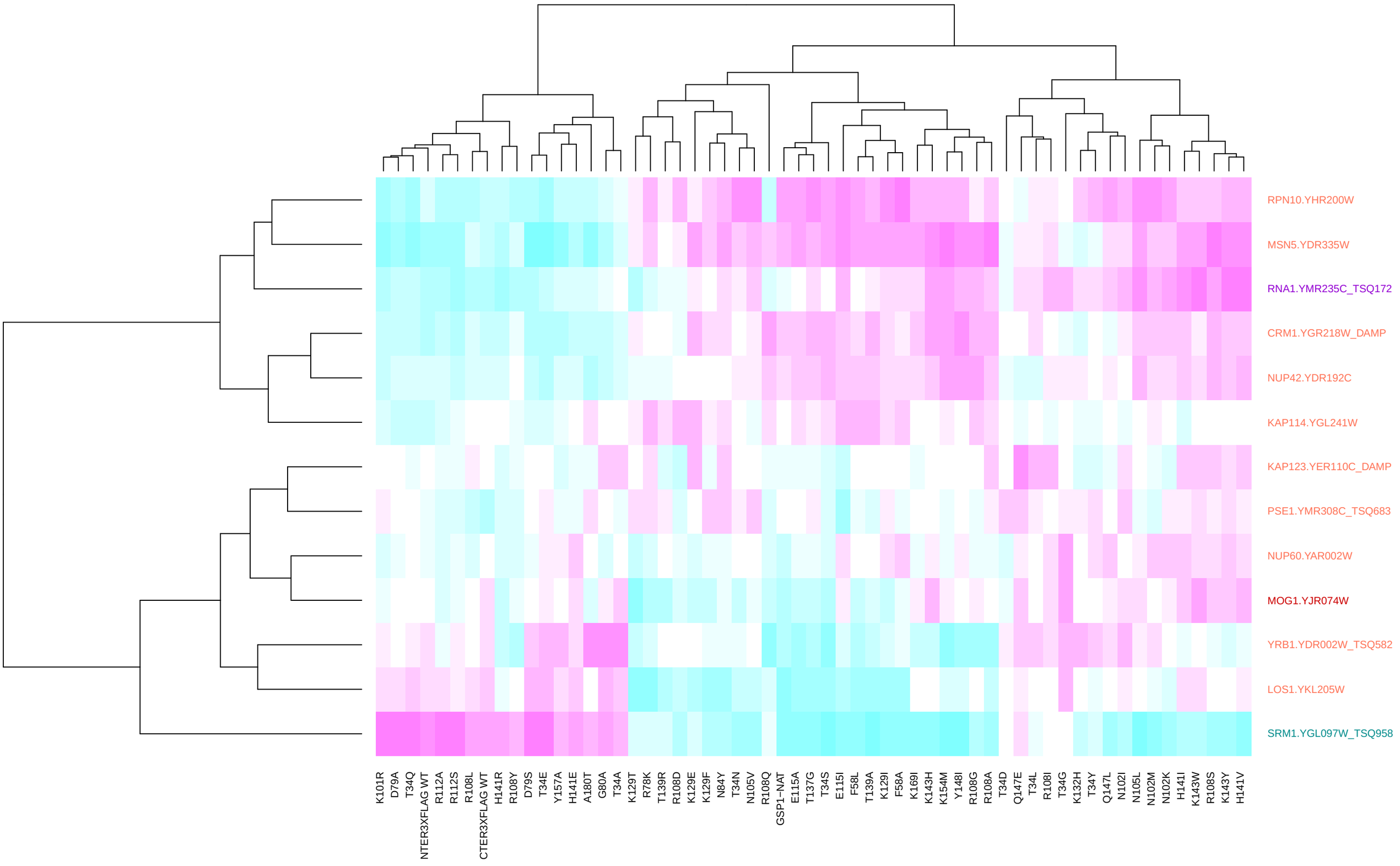
sig_Gsp1_GI_30_4_all



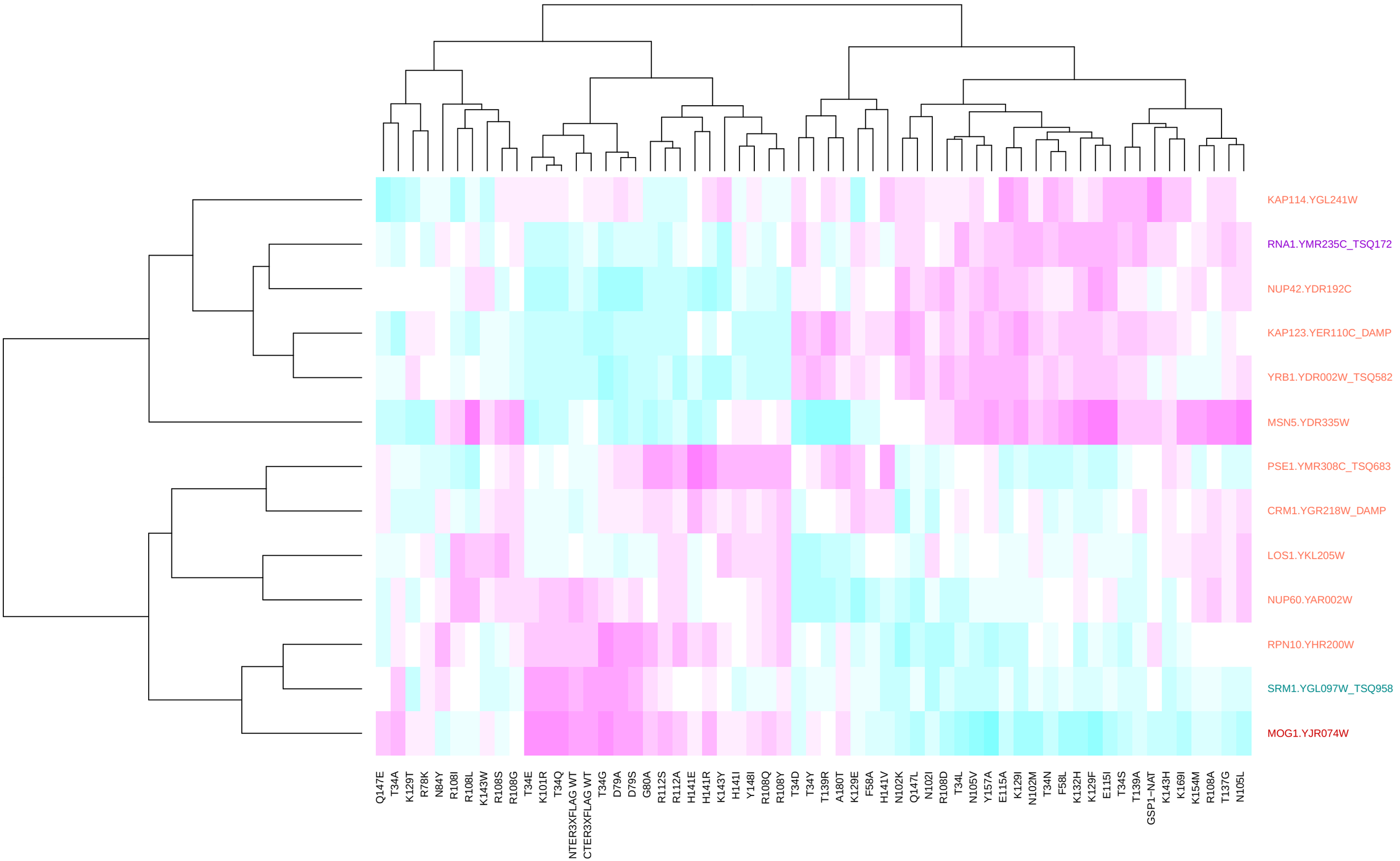
whole_library



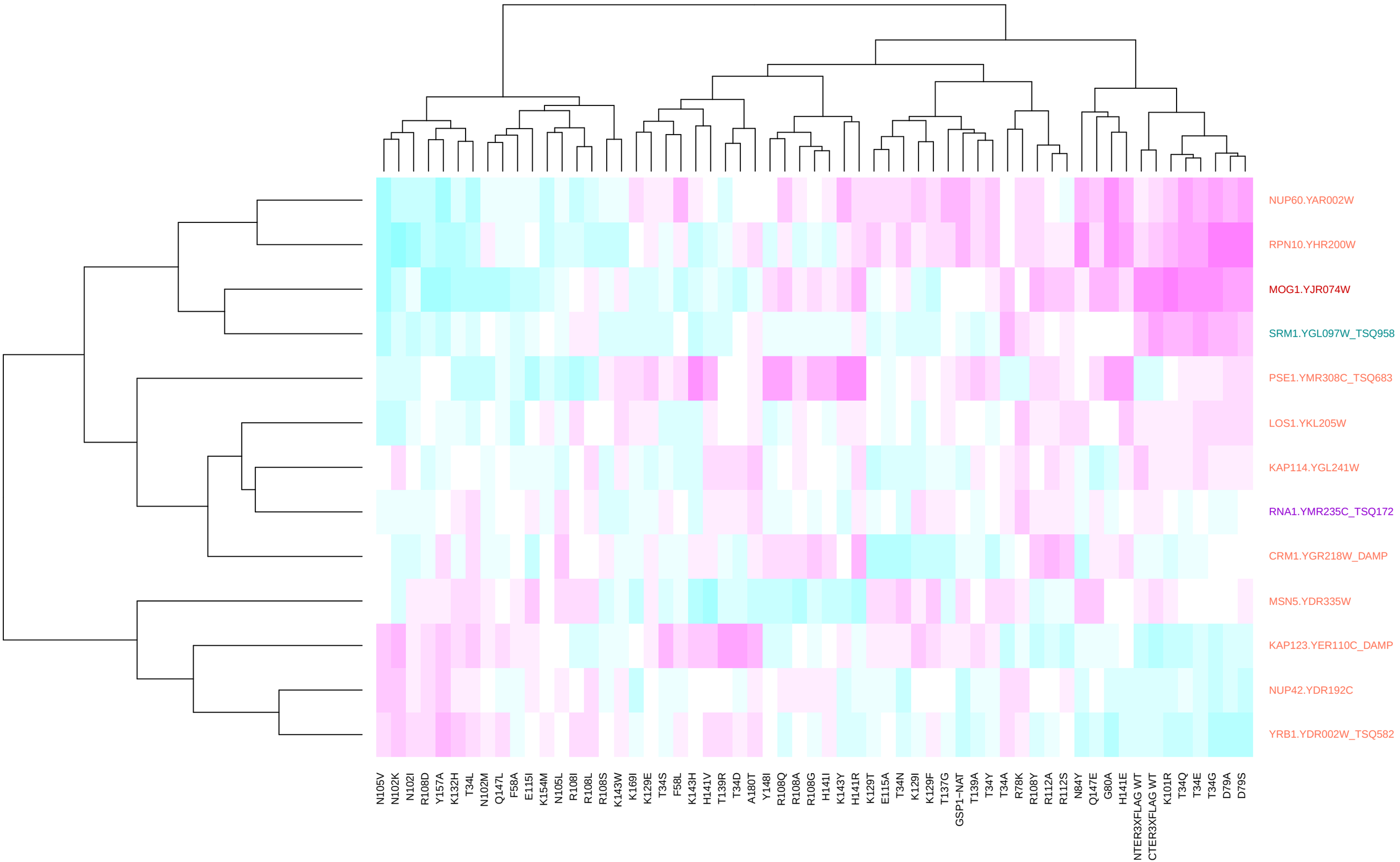
sig_Gsp1_GI_30_5_mut



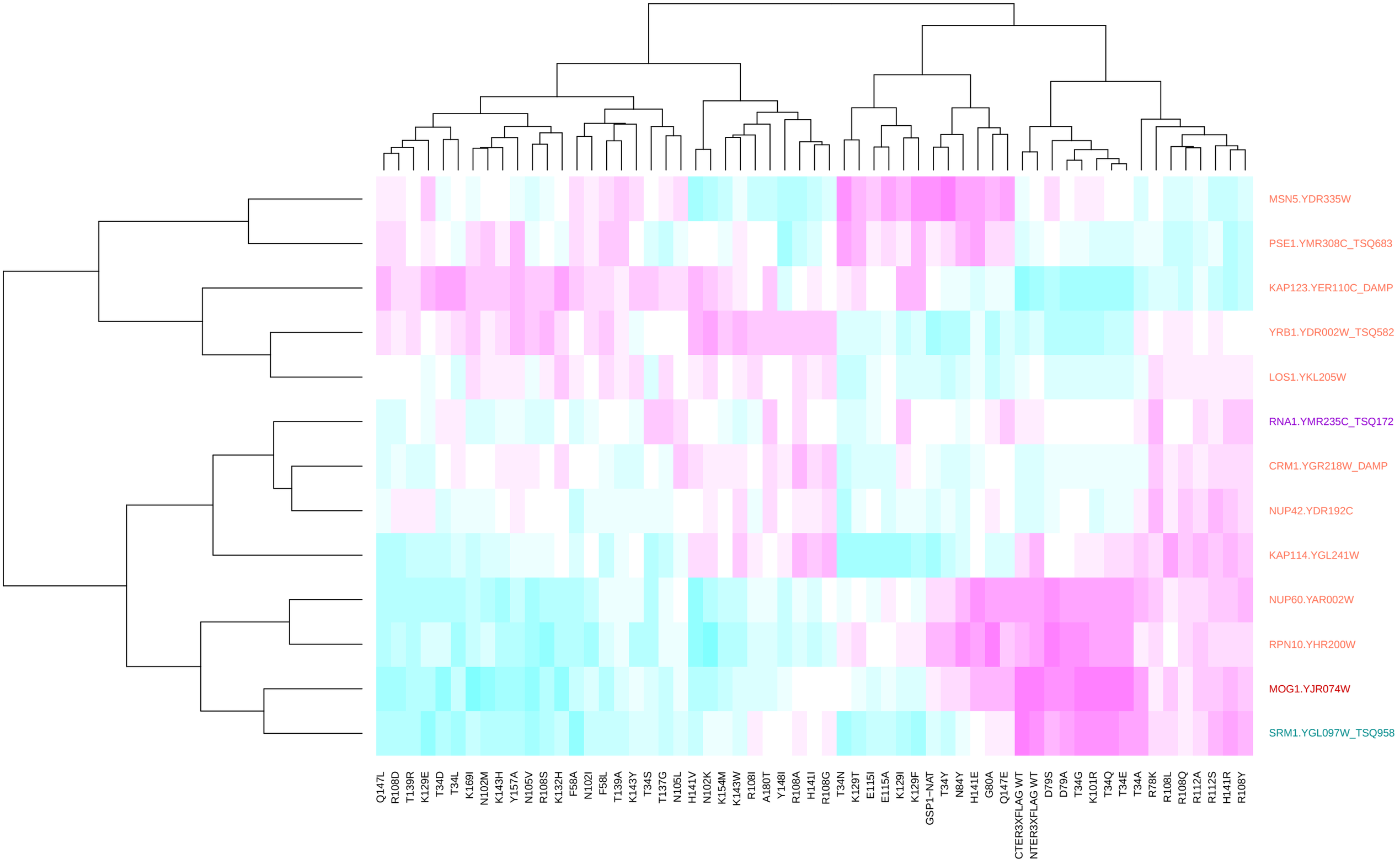
chromatin_GO_15_1_all



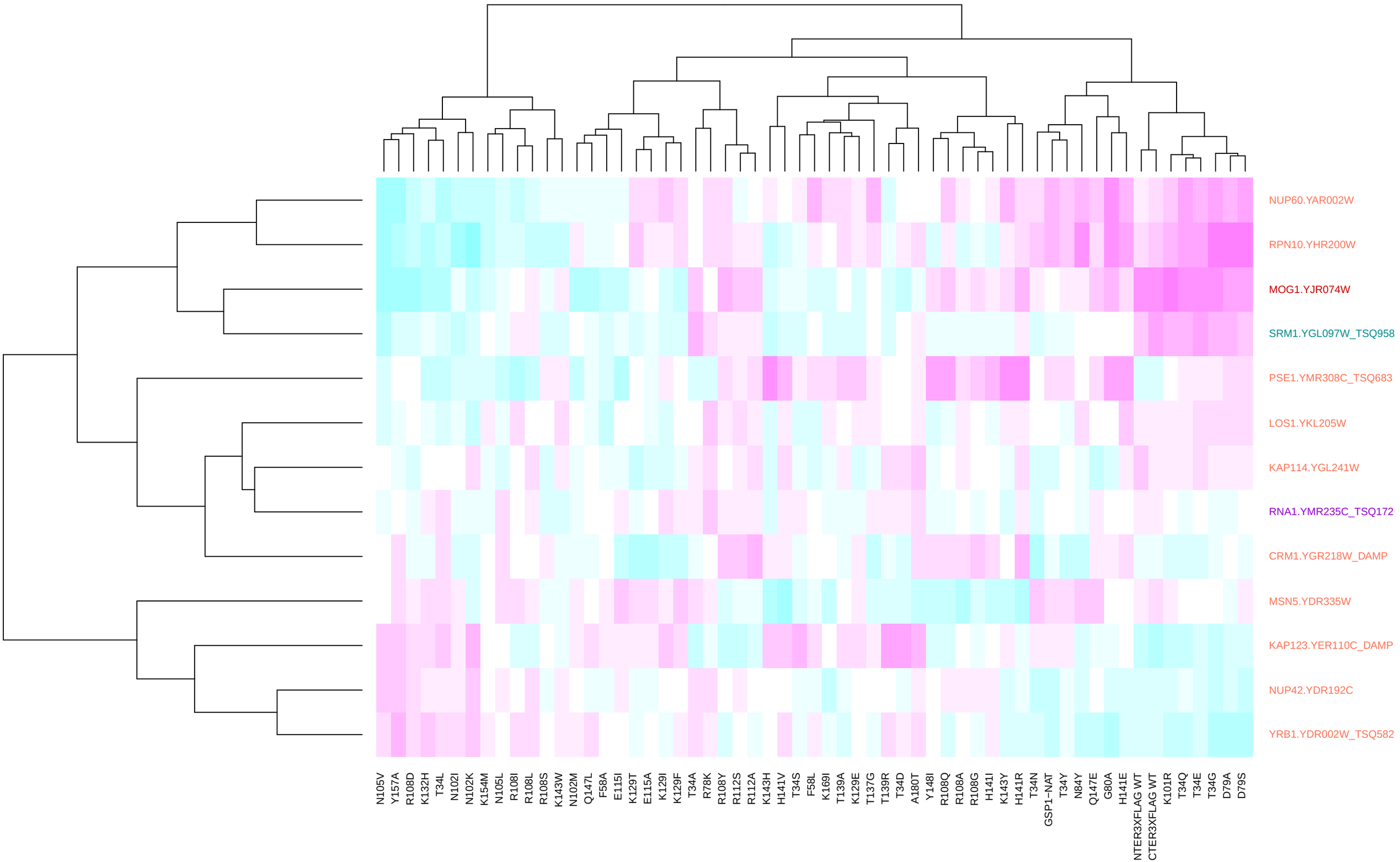
chromosome segregation



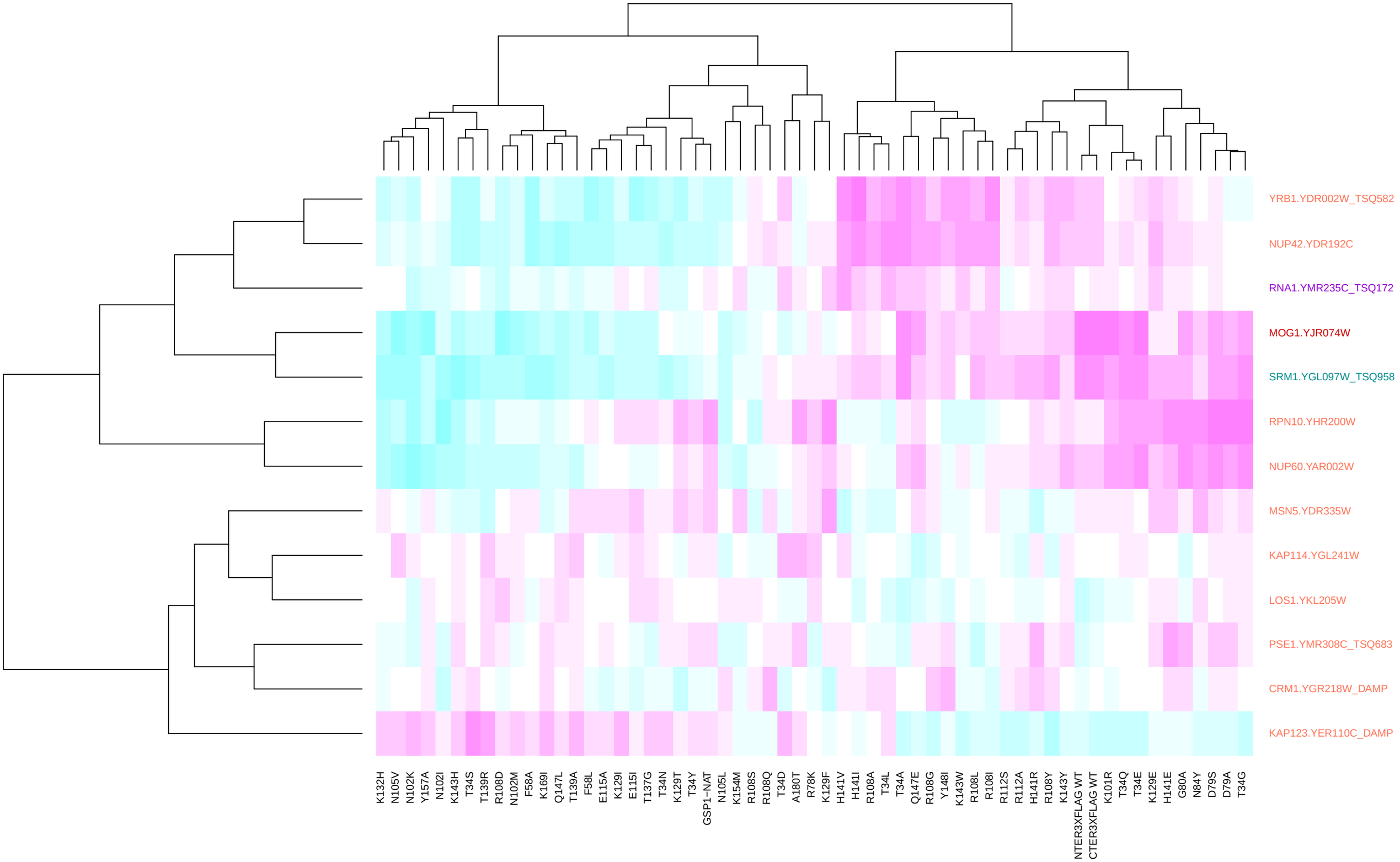
chromosome segregation_GO_15_1_mut



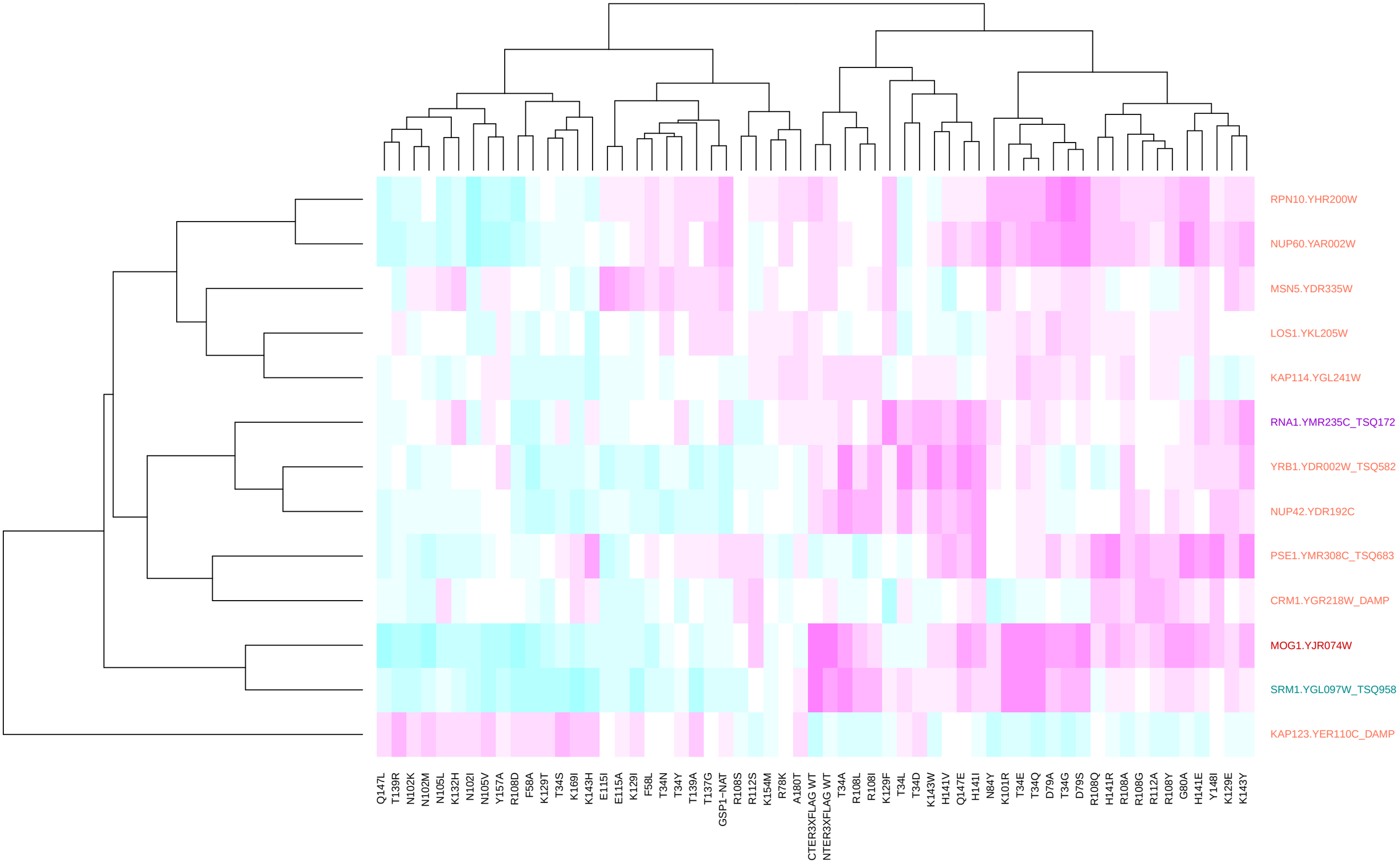
chromosome segregation_GO_30_1_all



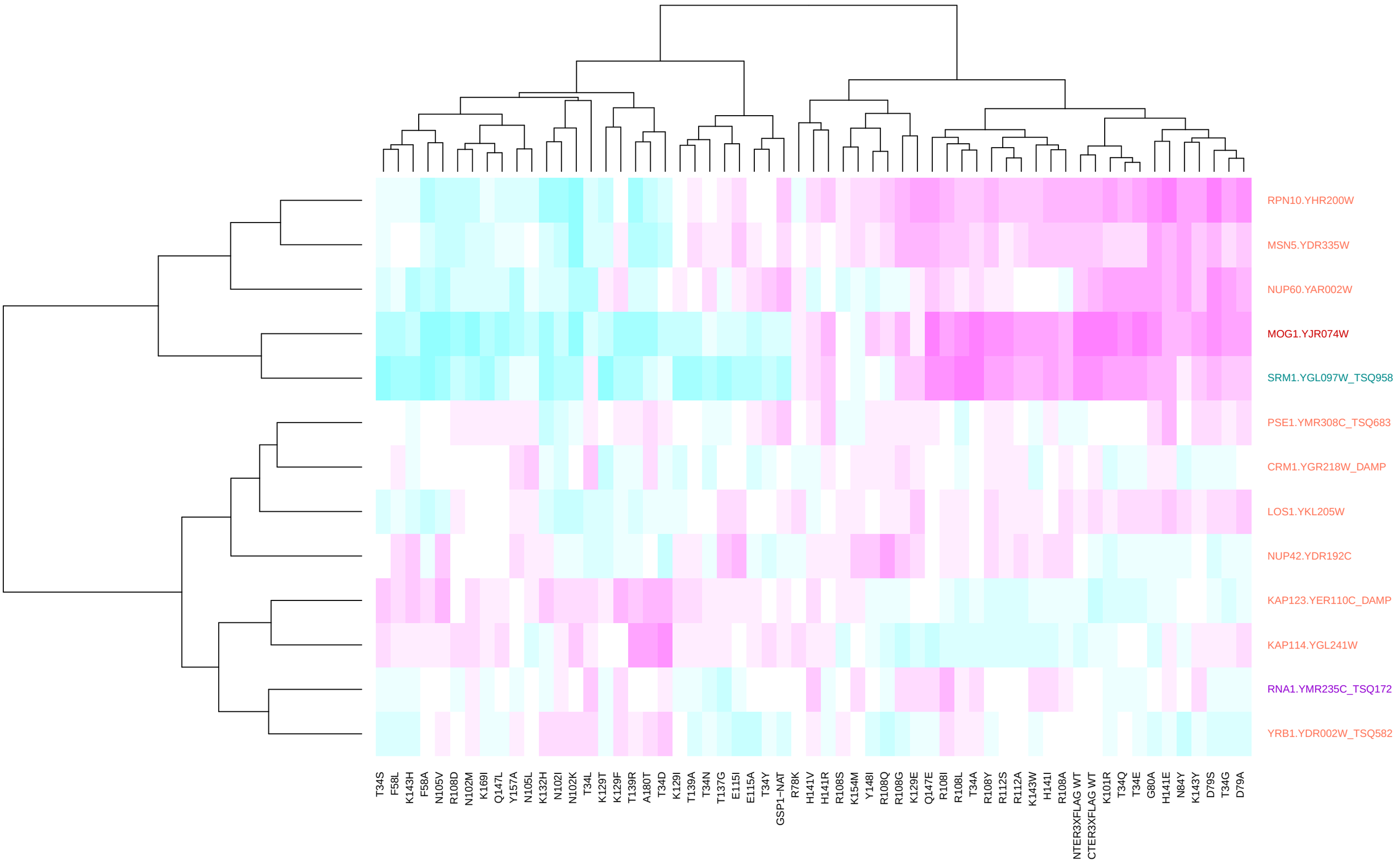
mitotic cell cycle_GO_30_1_mut



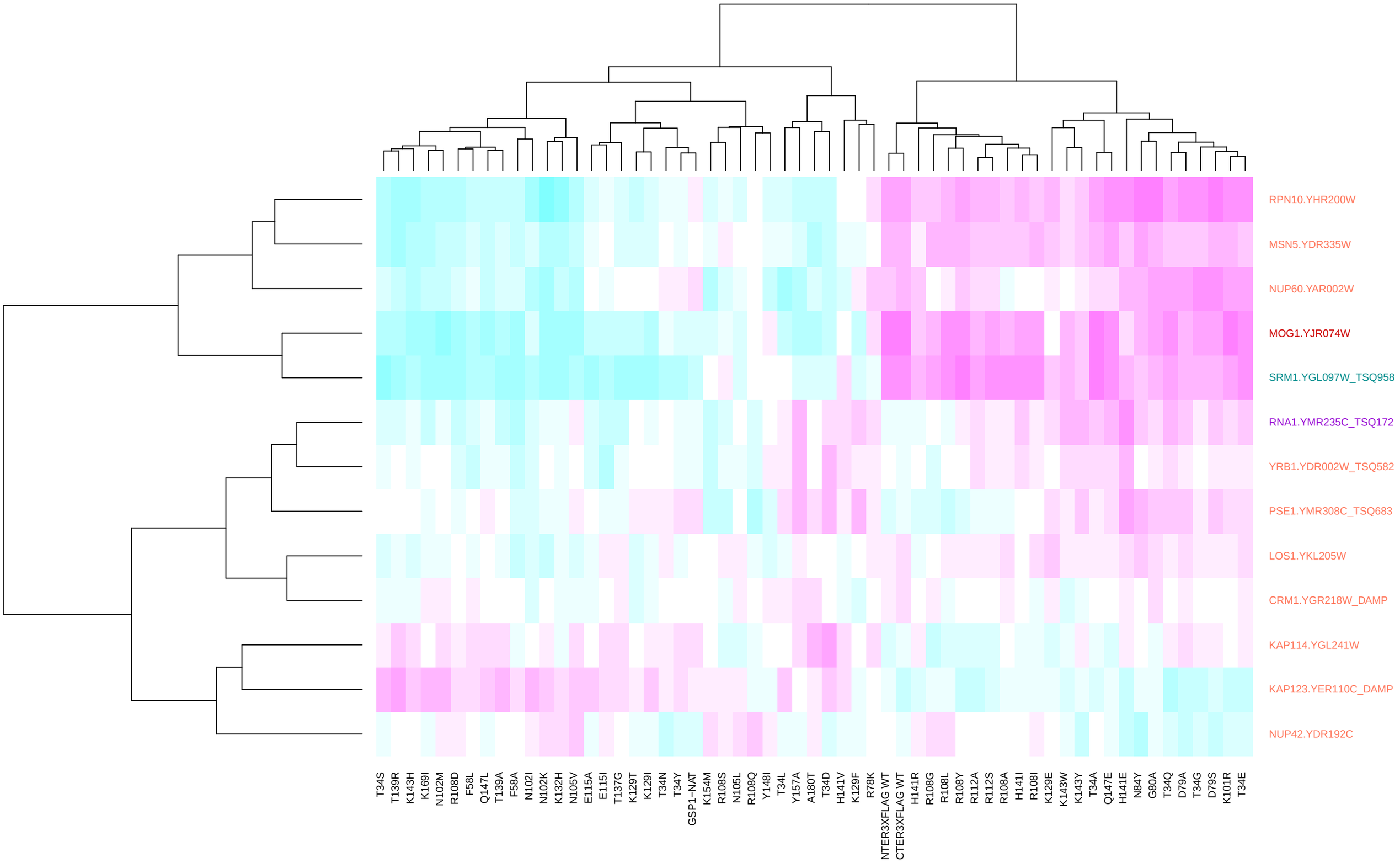
organelle fission



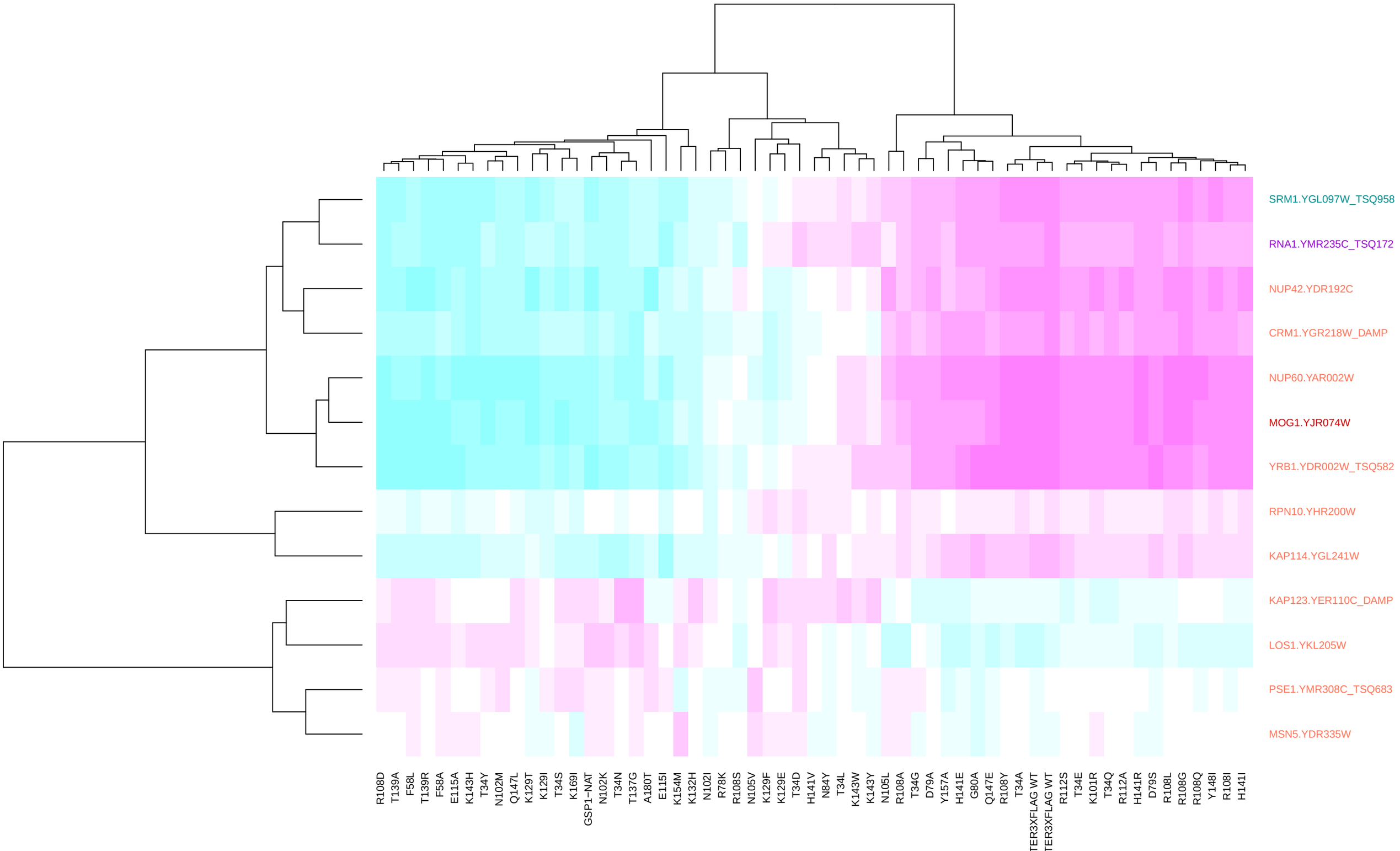
regulation of cell cycle_GO_30_1_all



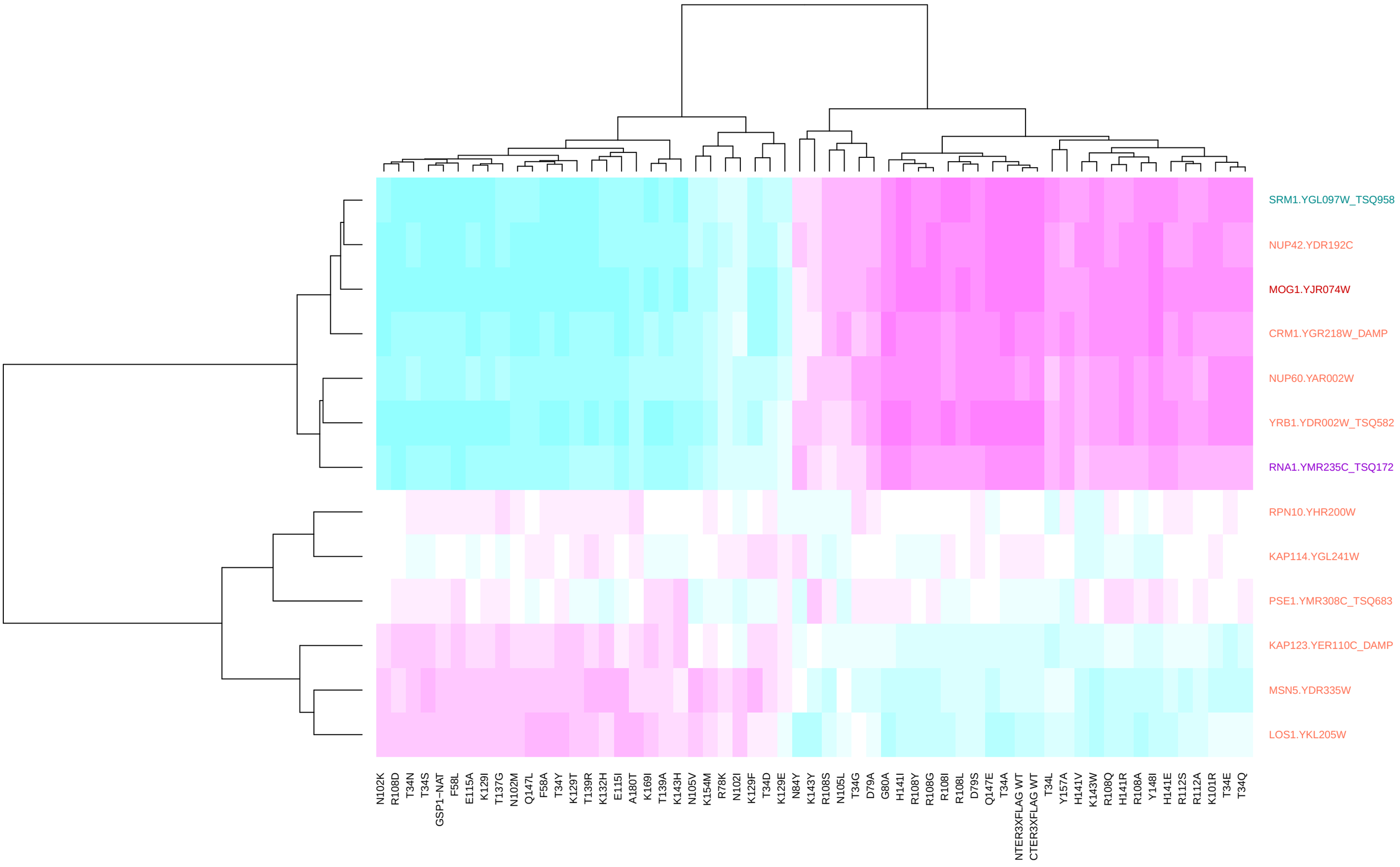
regulation of cell cycle_GO_30_1_mut



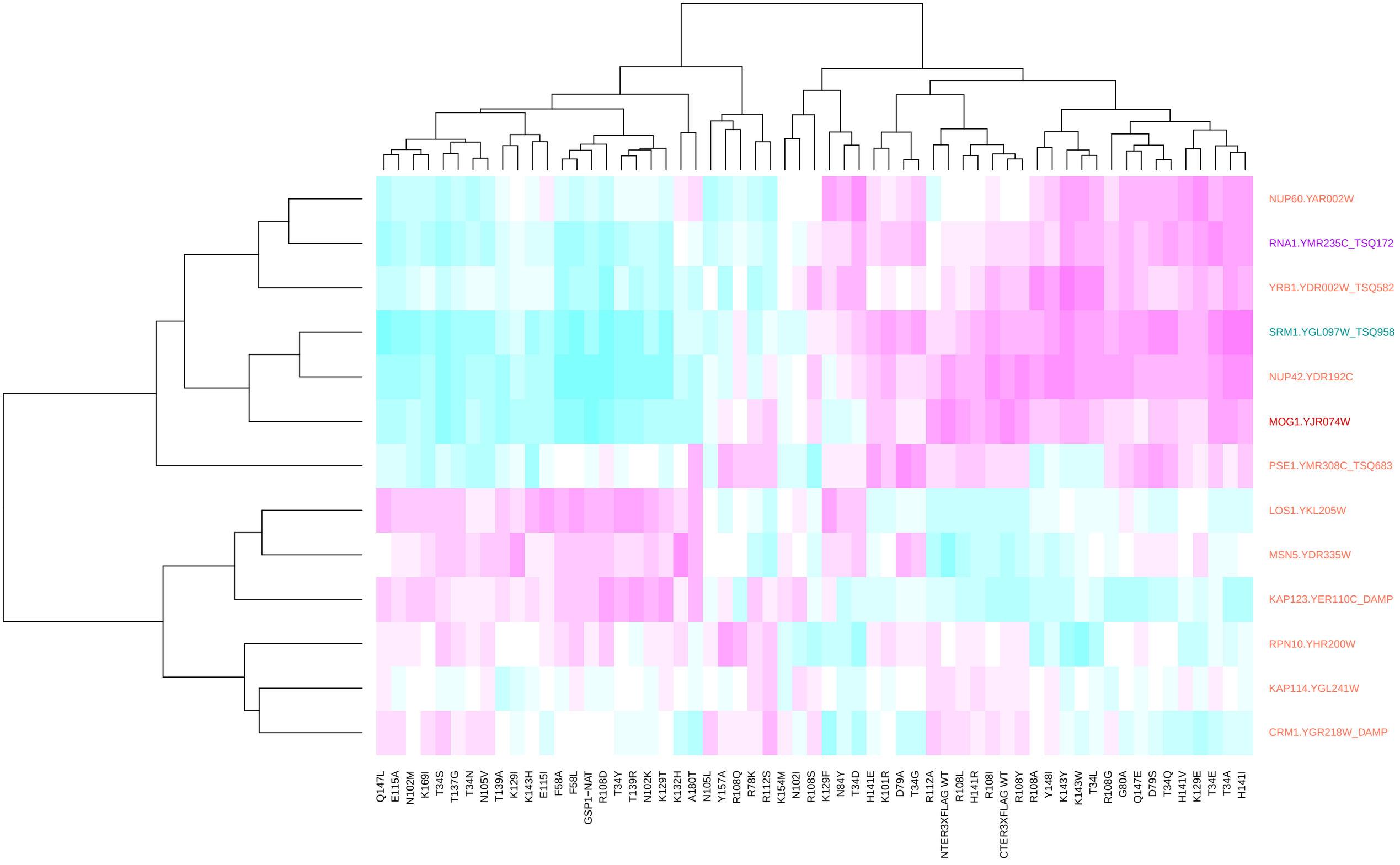
whole_library_30_5_all



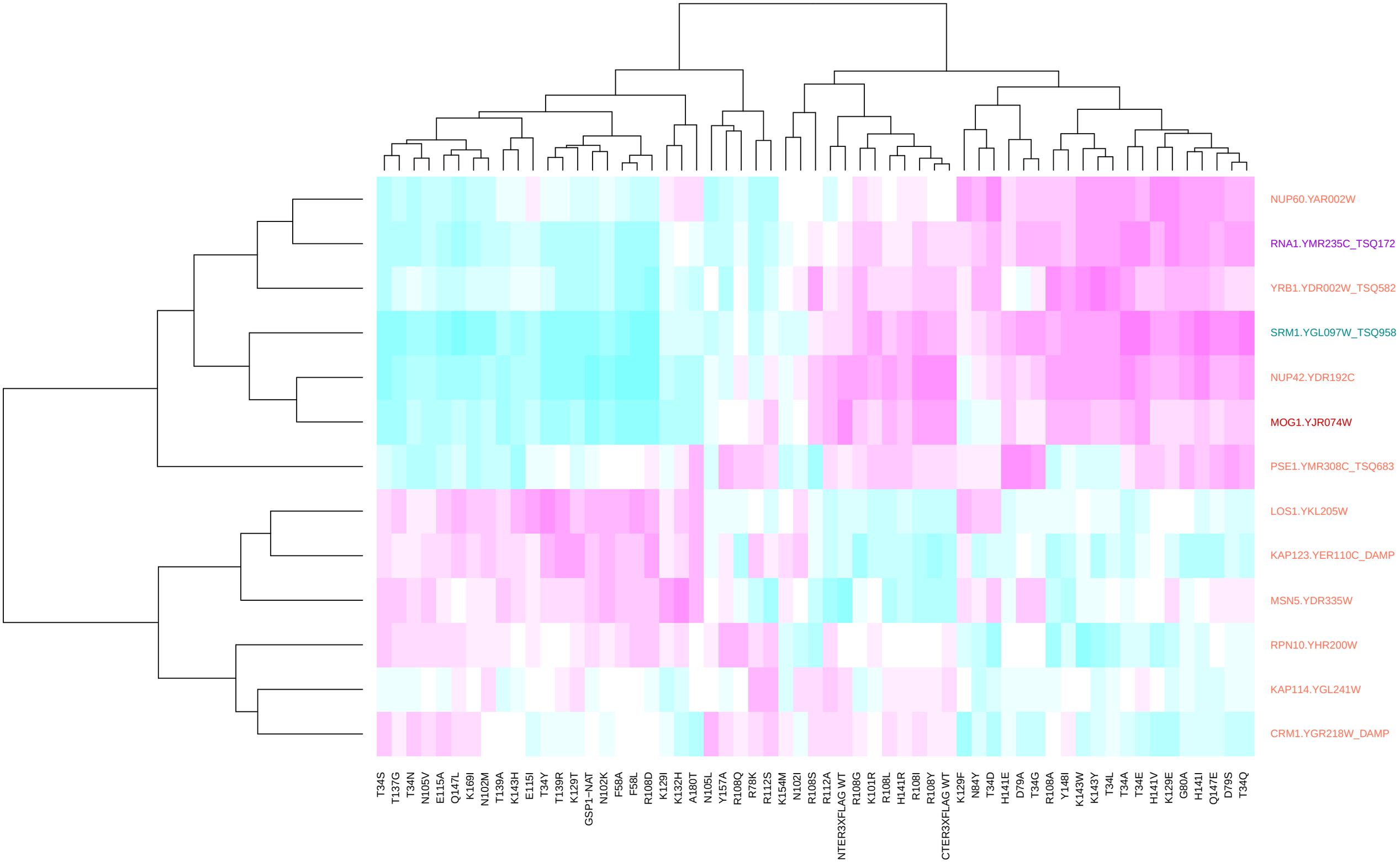
endomembrane system_GO_30_3_all



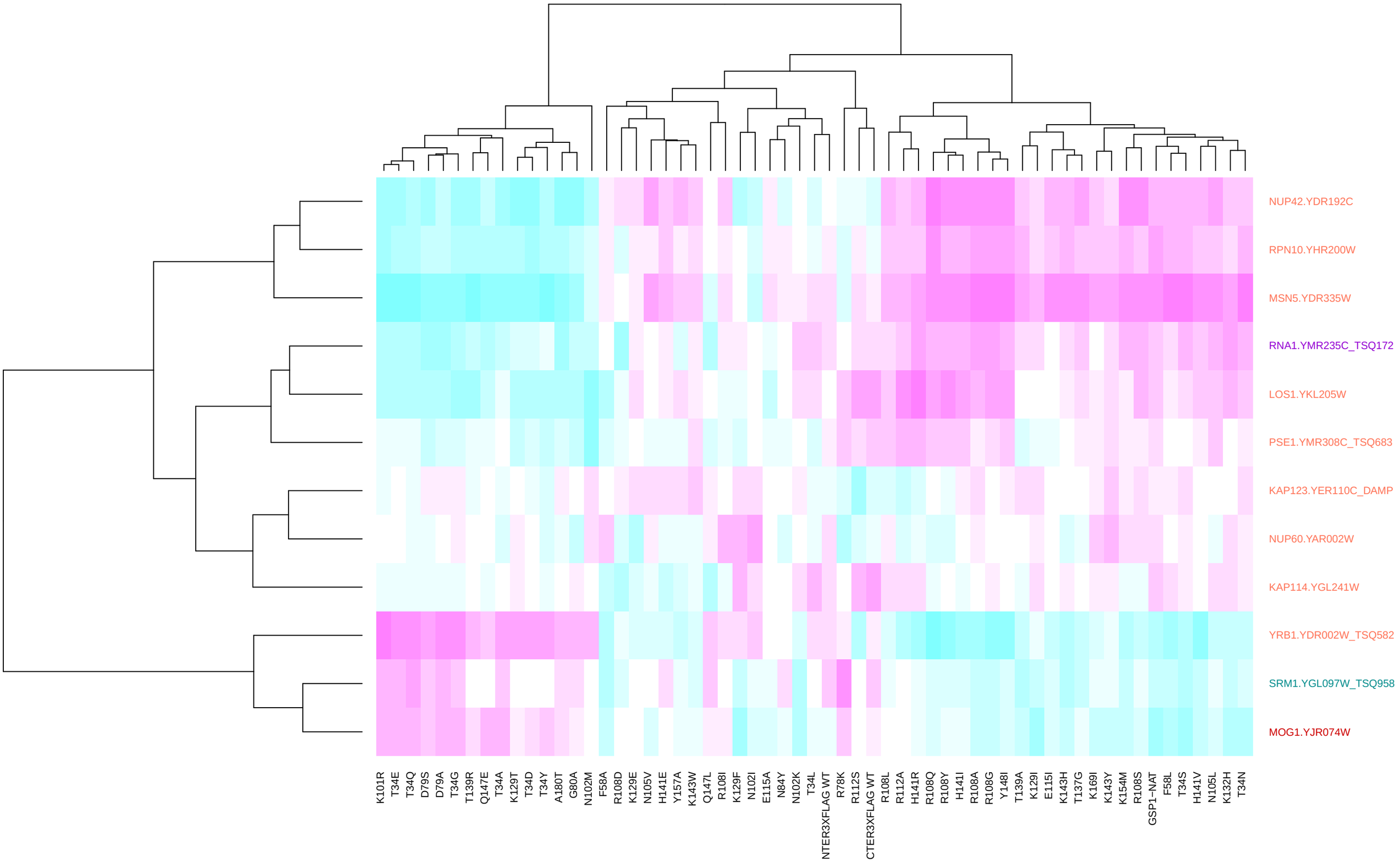
ribosomal small subunit biogenesis



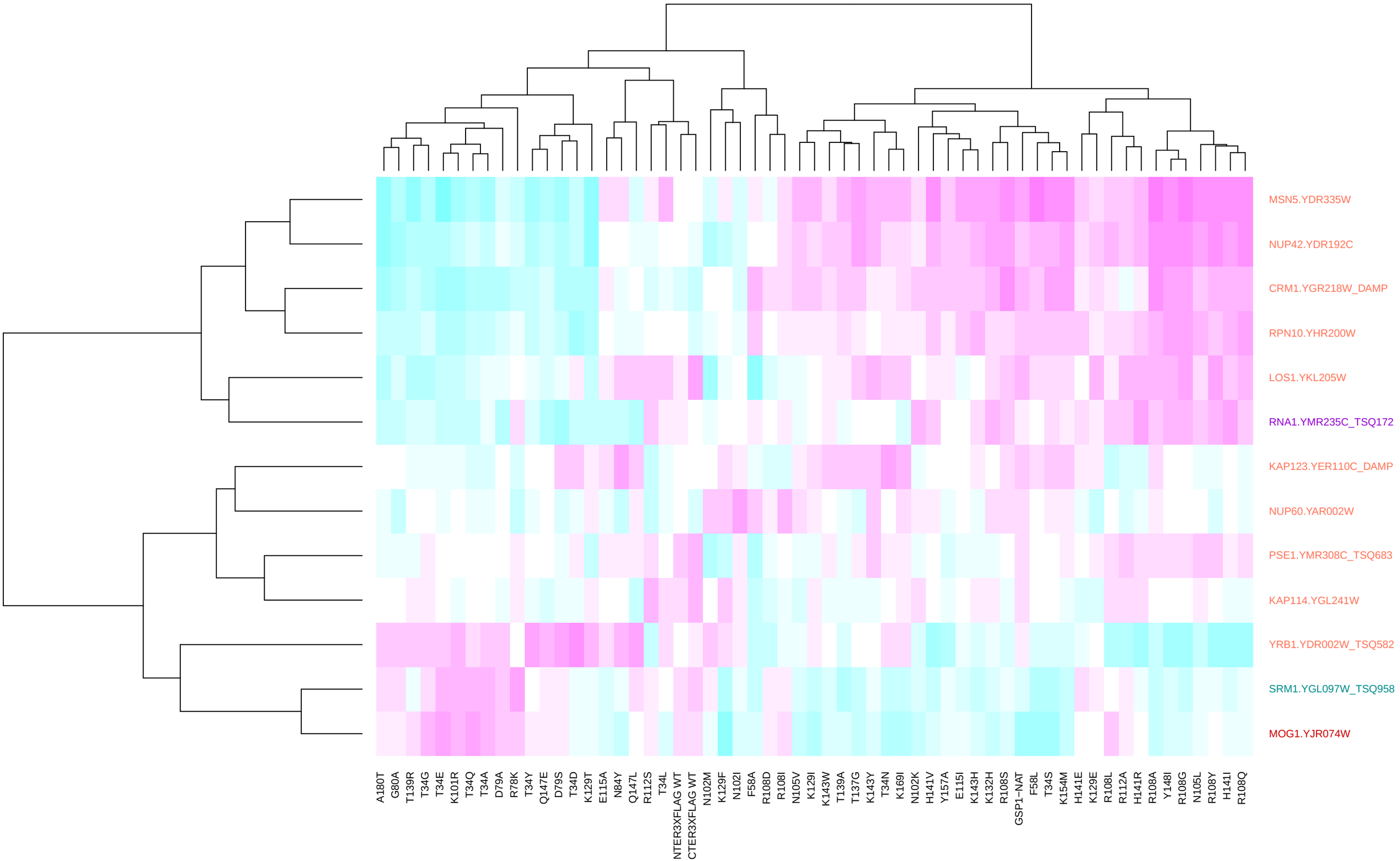
ribosomal small subunit biogenesis_GO_15_1_all



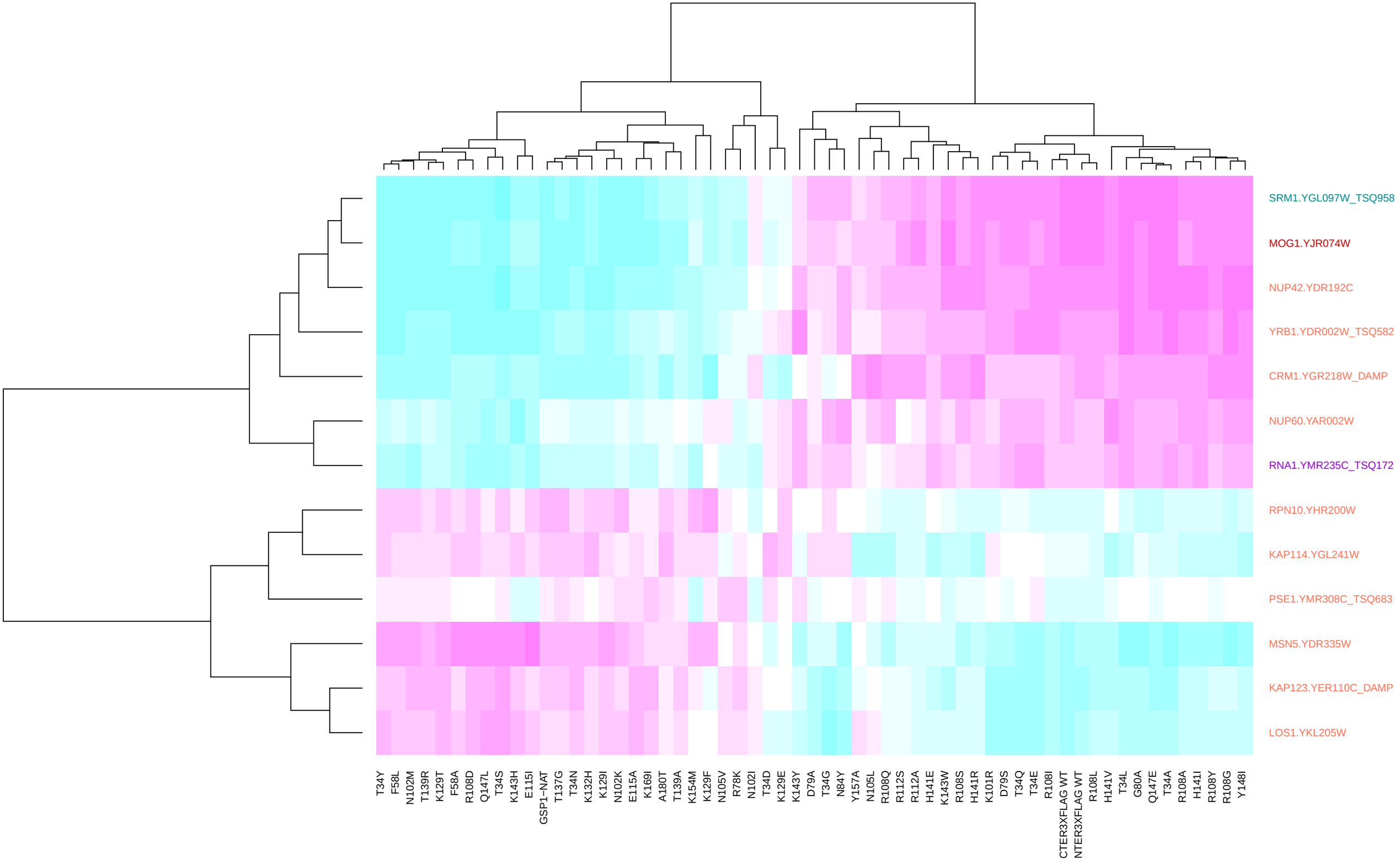
sig_Gsp1_GI_15_1_mut



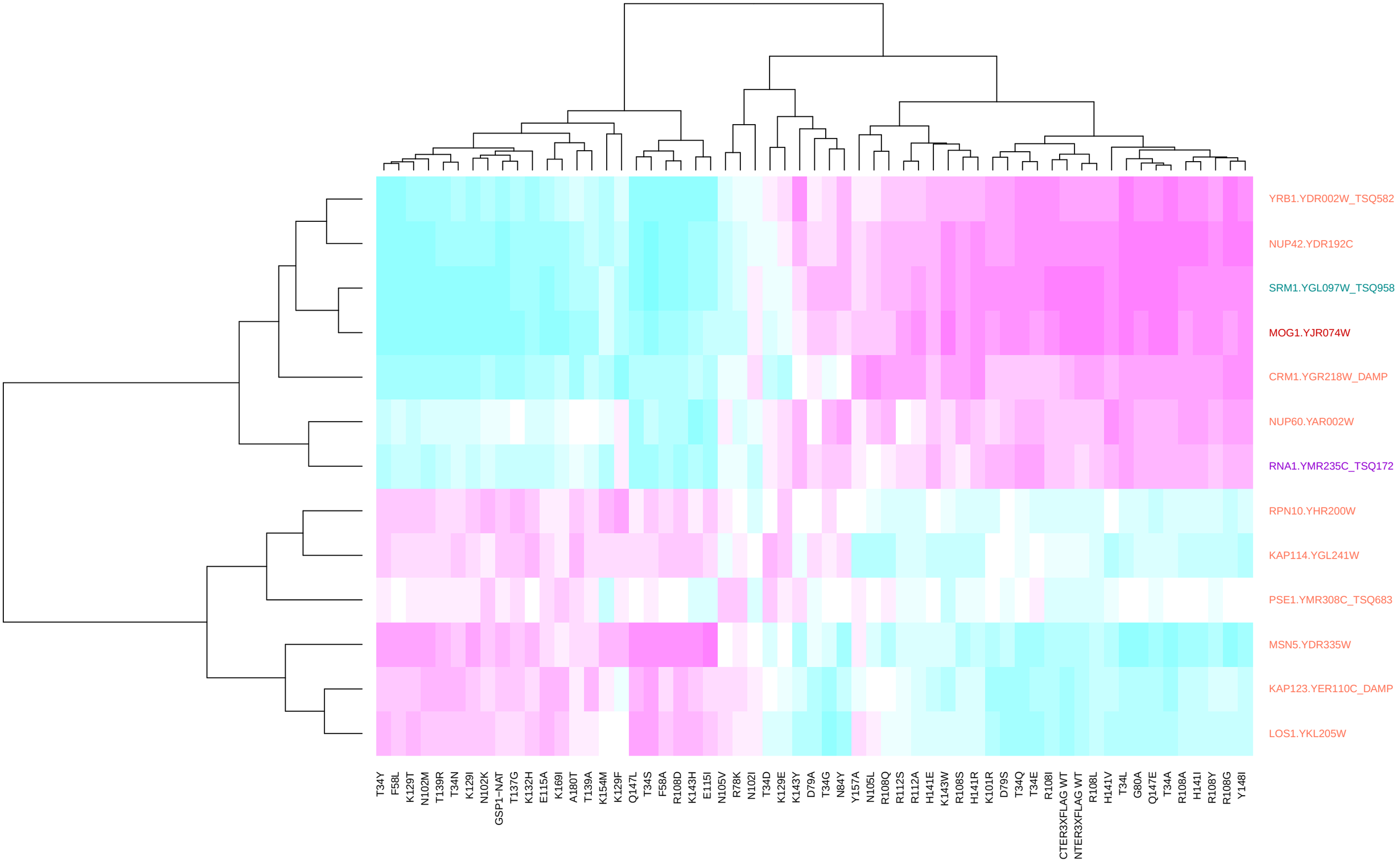
sig_Gsp1_GI_30_3_mut



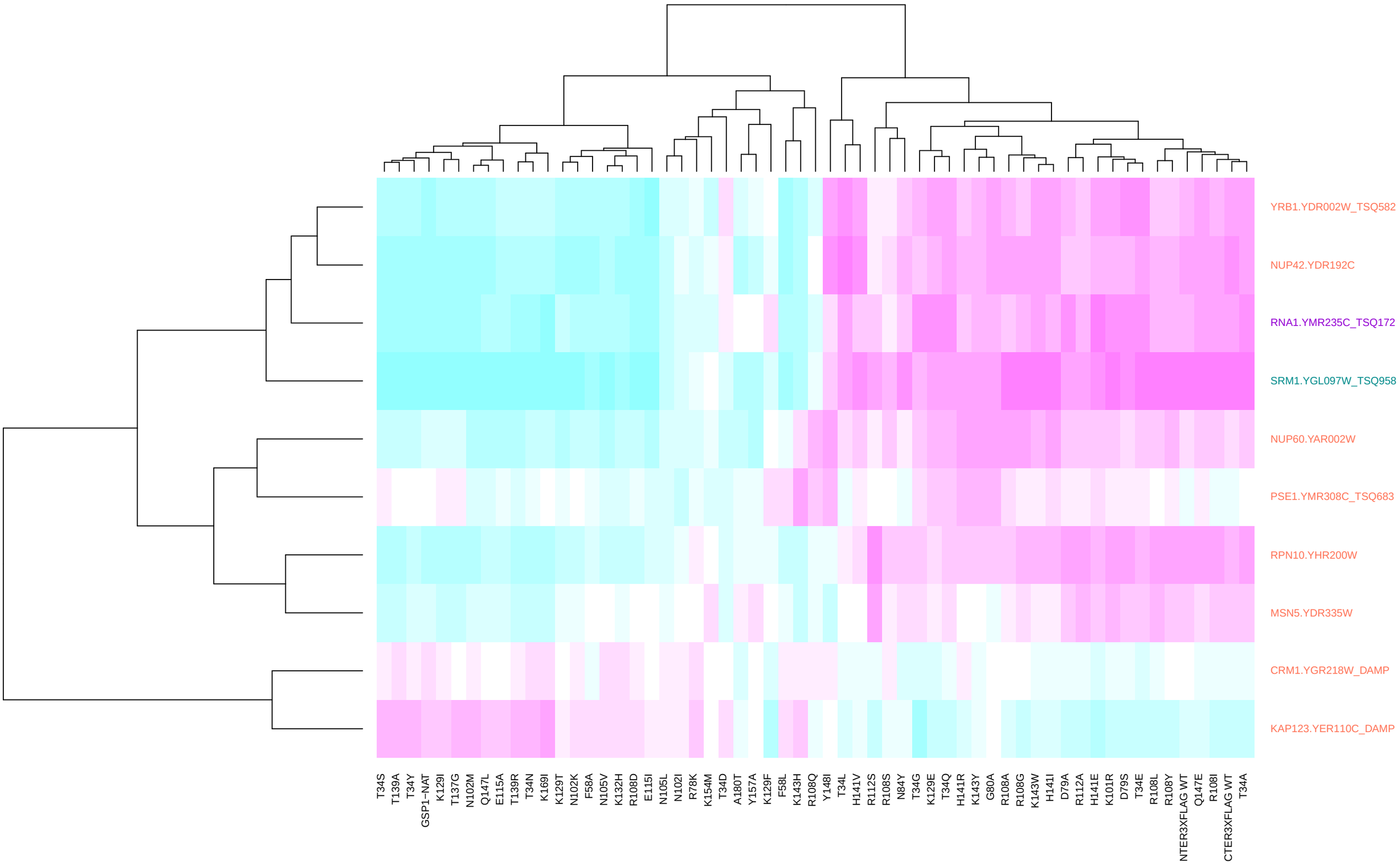
cellular response to DNA damage stimulus_GO_15_1_all



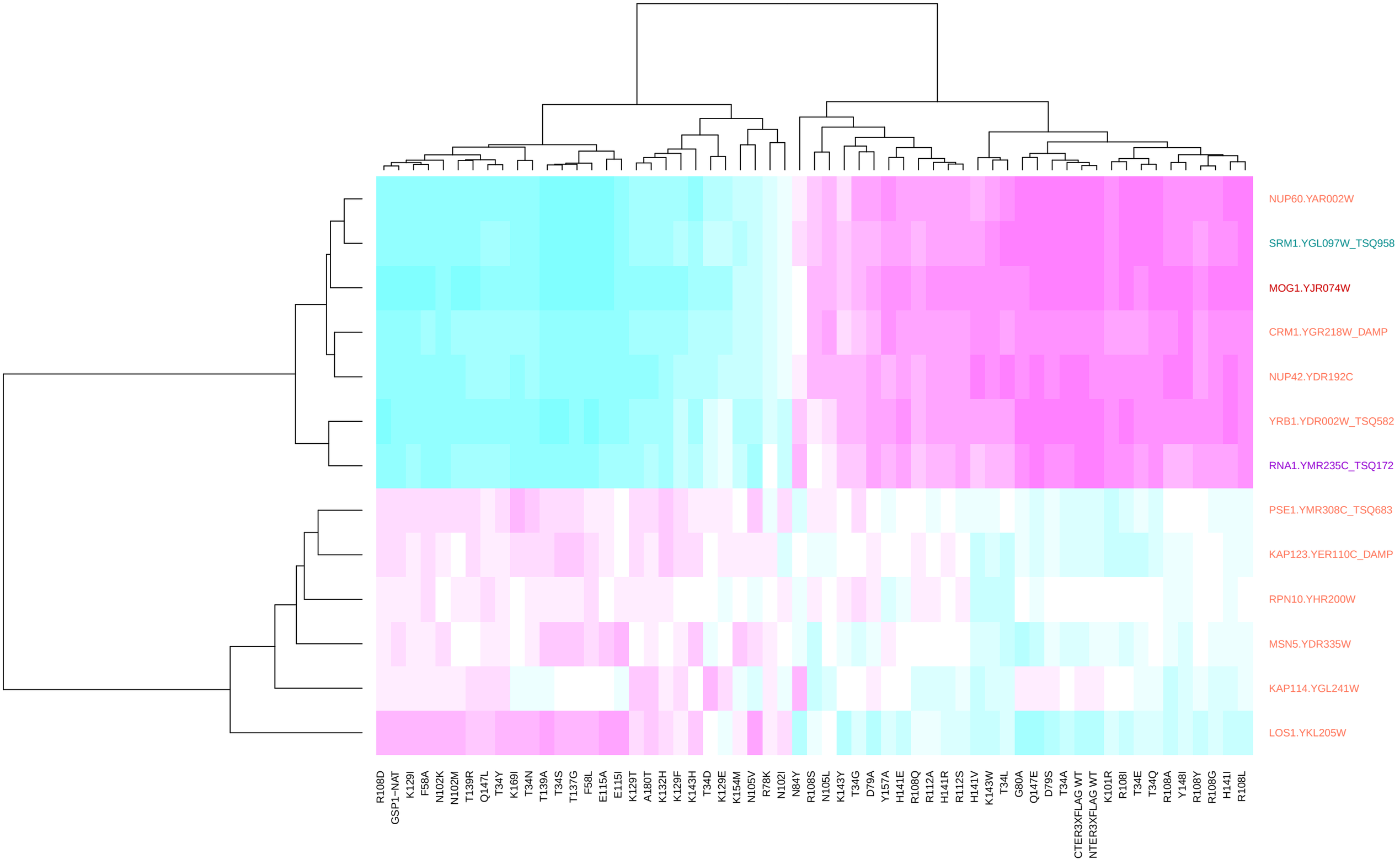
cellular response to DNA damage stimulus_GO_30_3_all



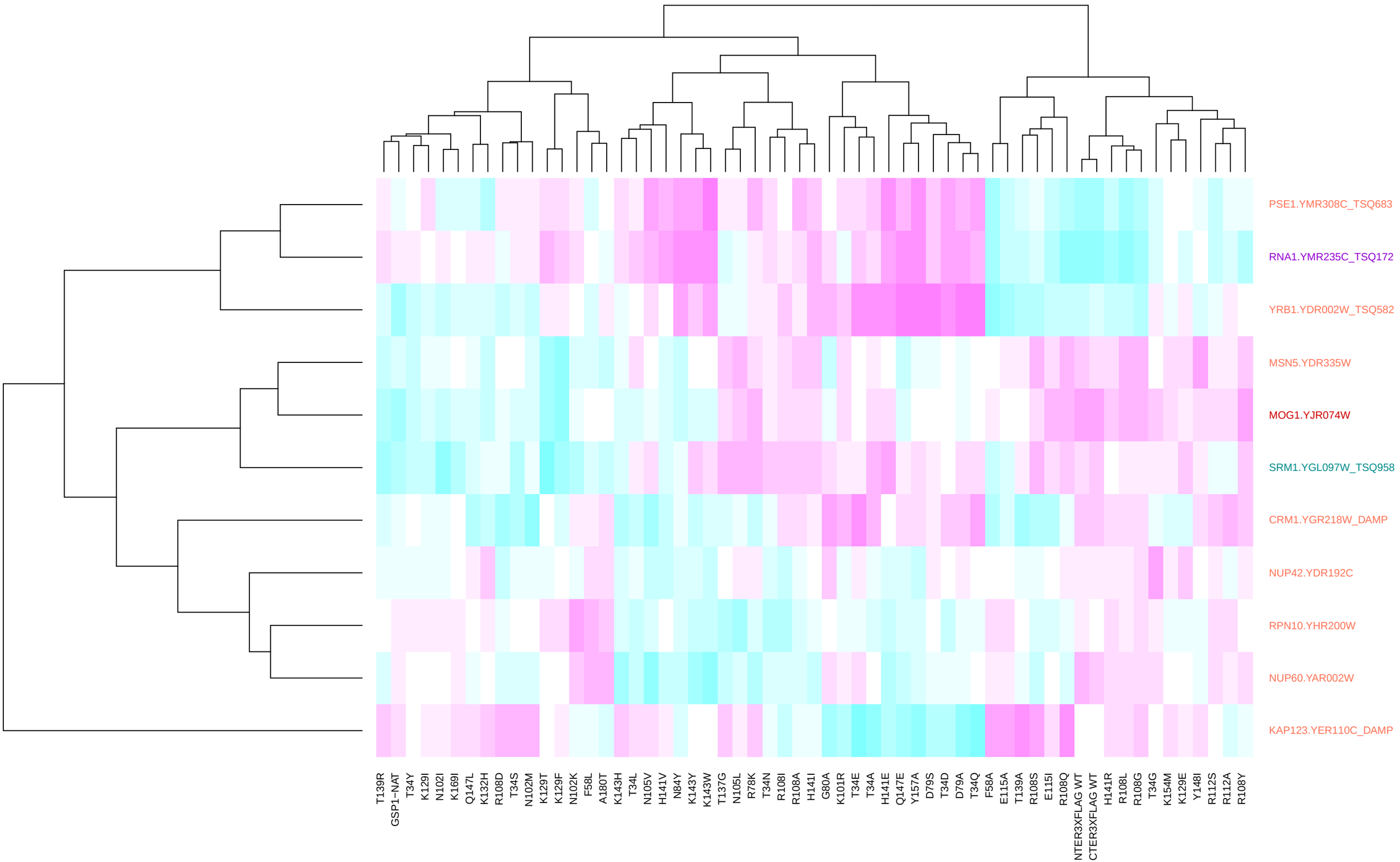
cell cycle_GO_15_3_all



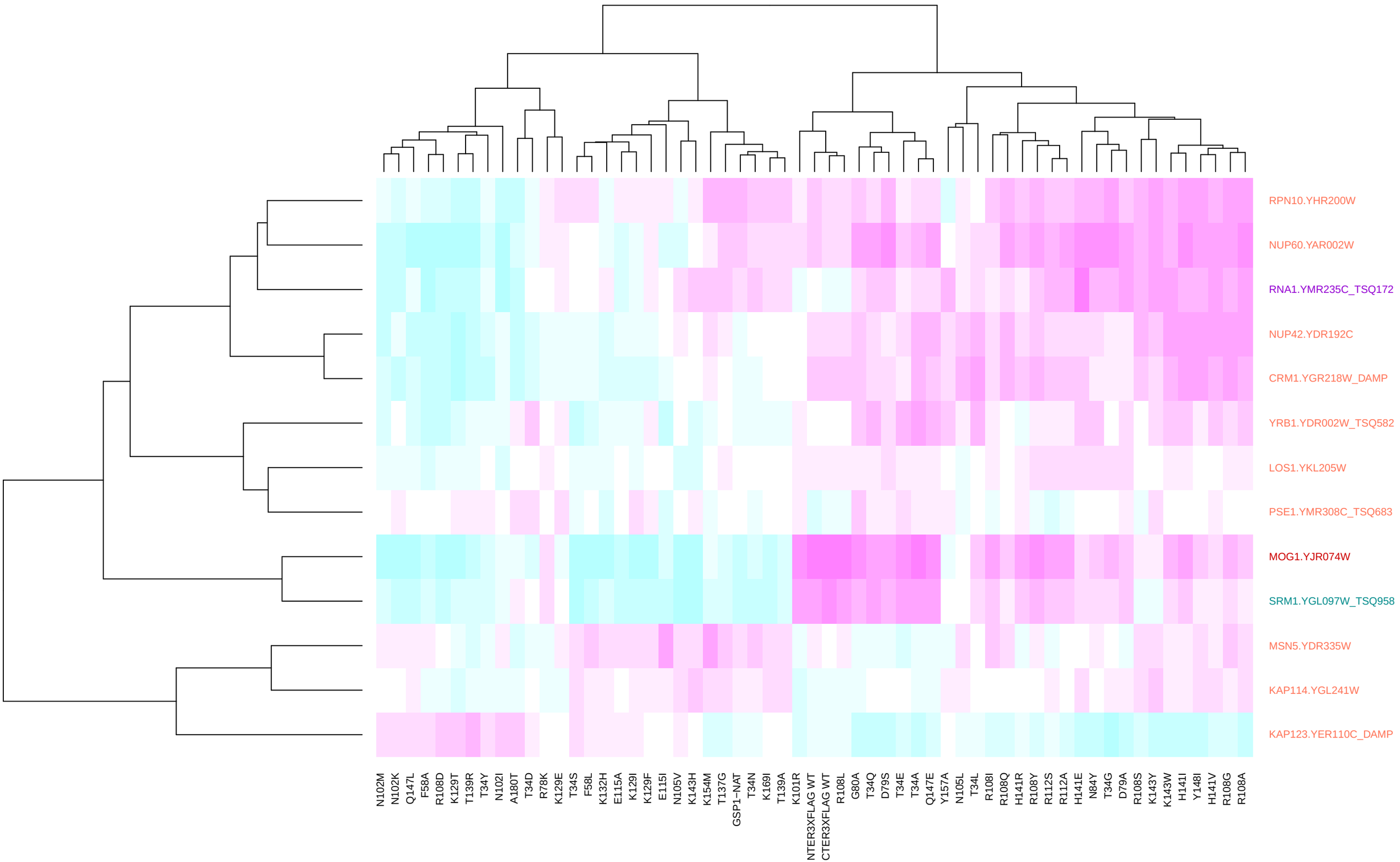
endomembrane system_GO_15_3_mut



regulation of organelle organization_GO_15_1_all



chromatin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GSP1−NAT
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CTER3XFLAG WT
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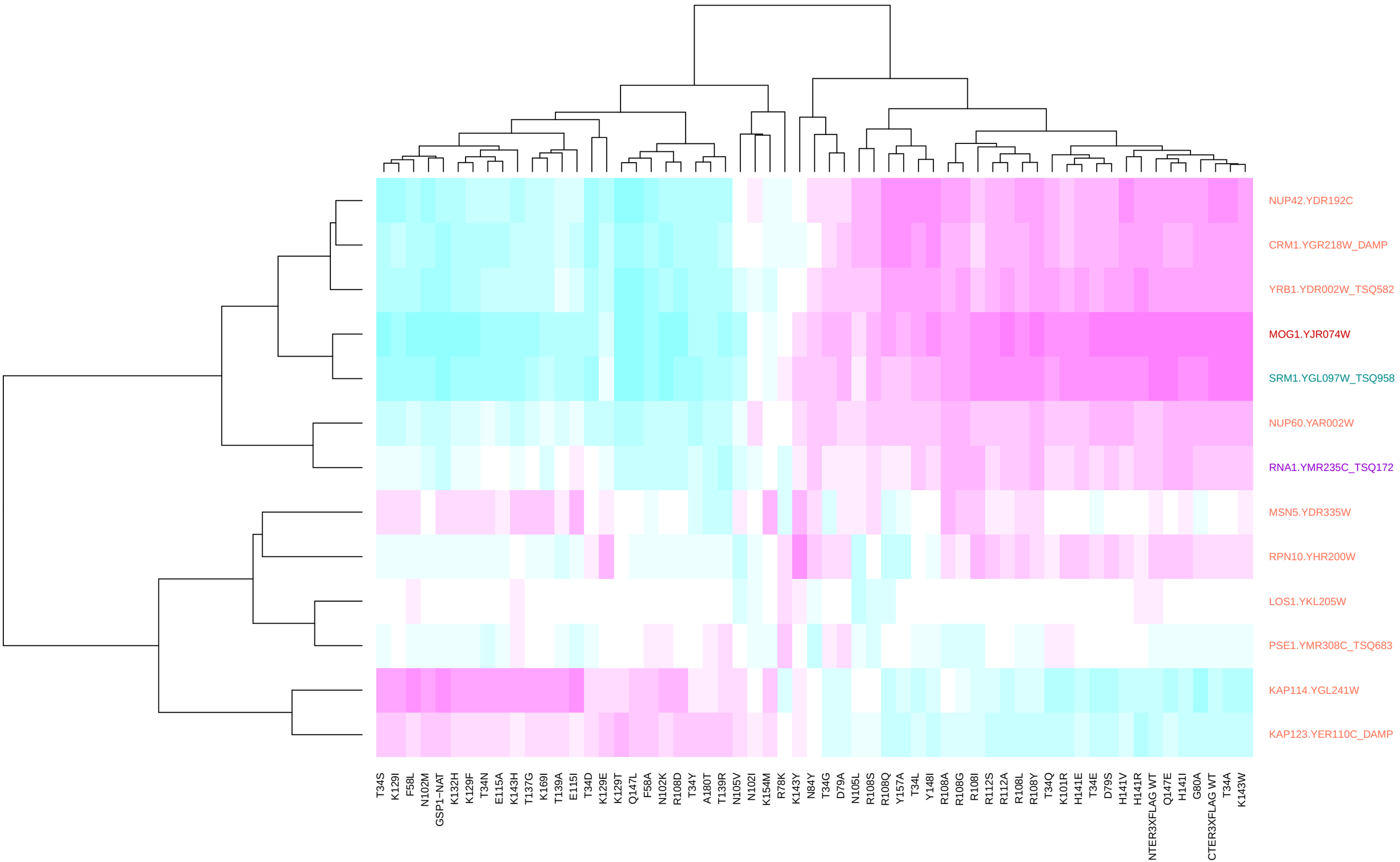
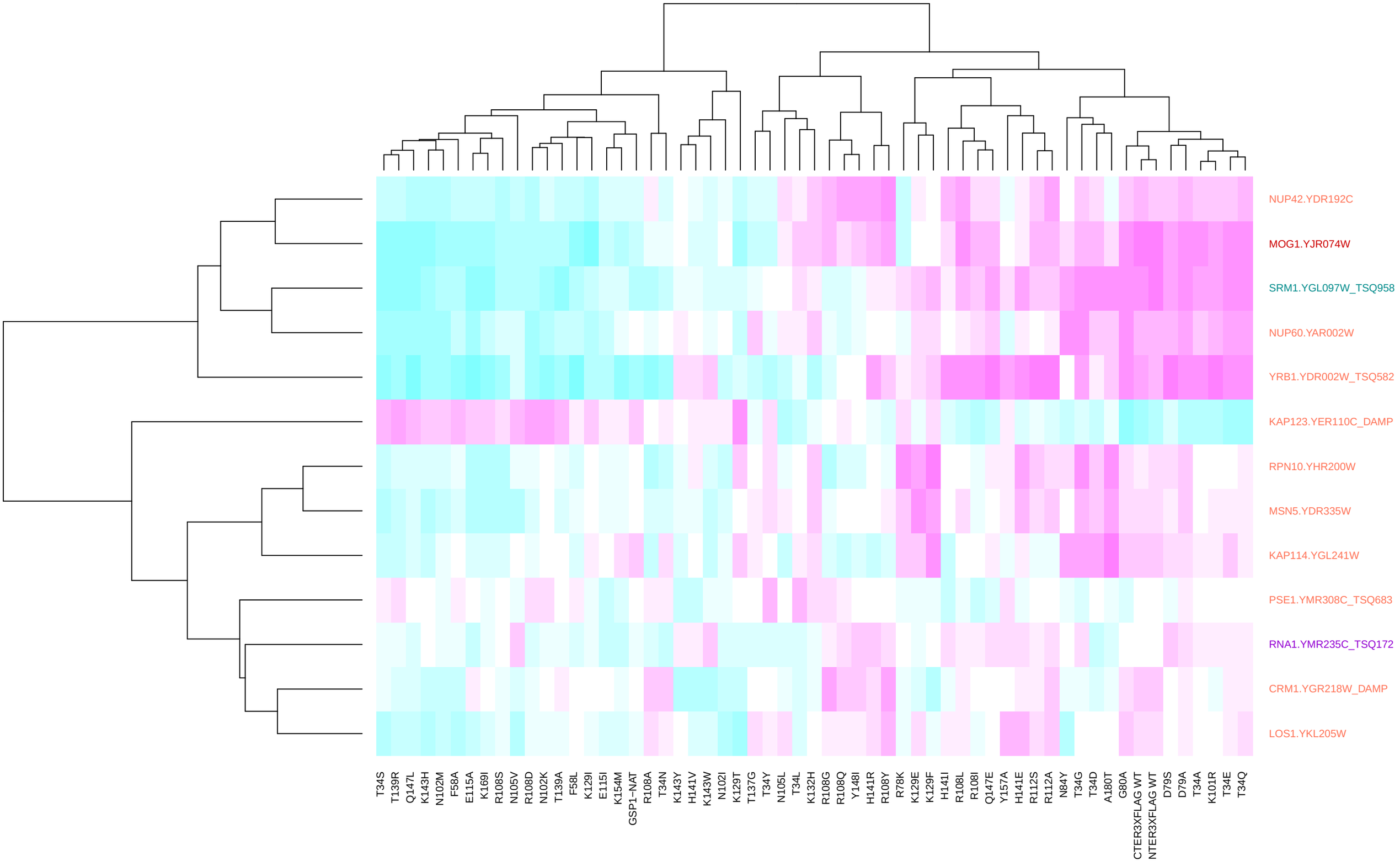
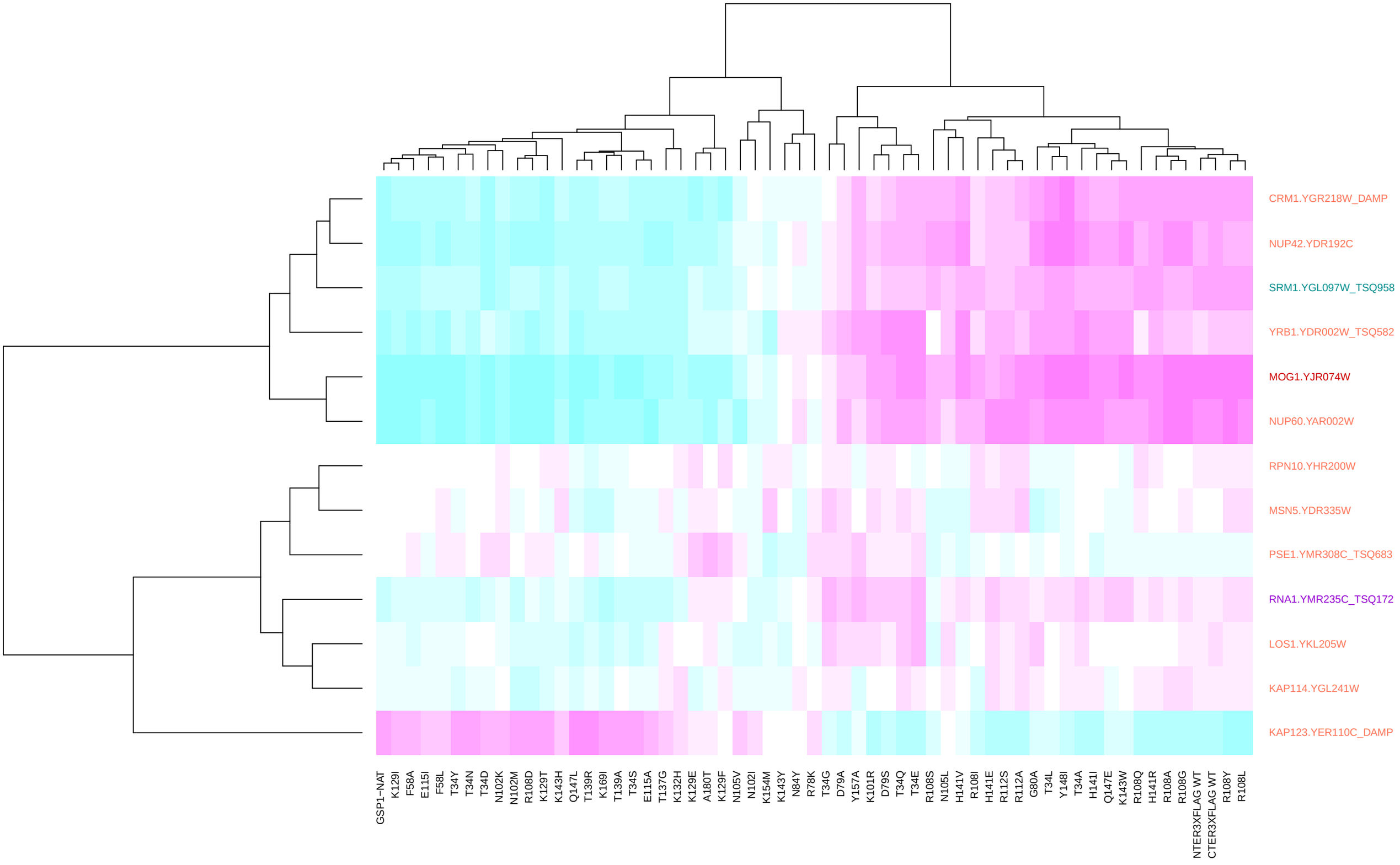
chromatin organization_GO_30_2_all



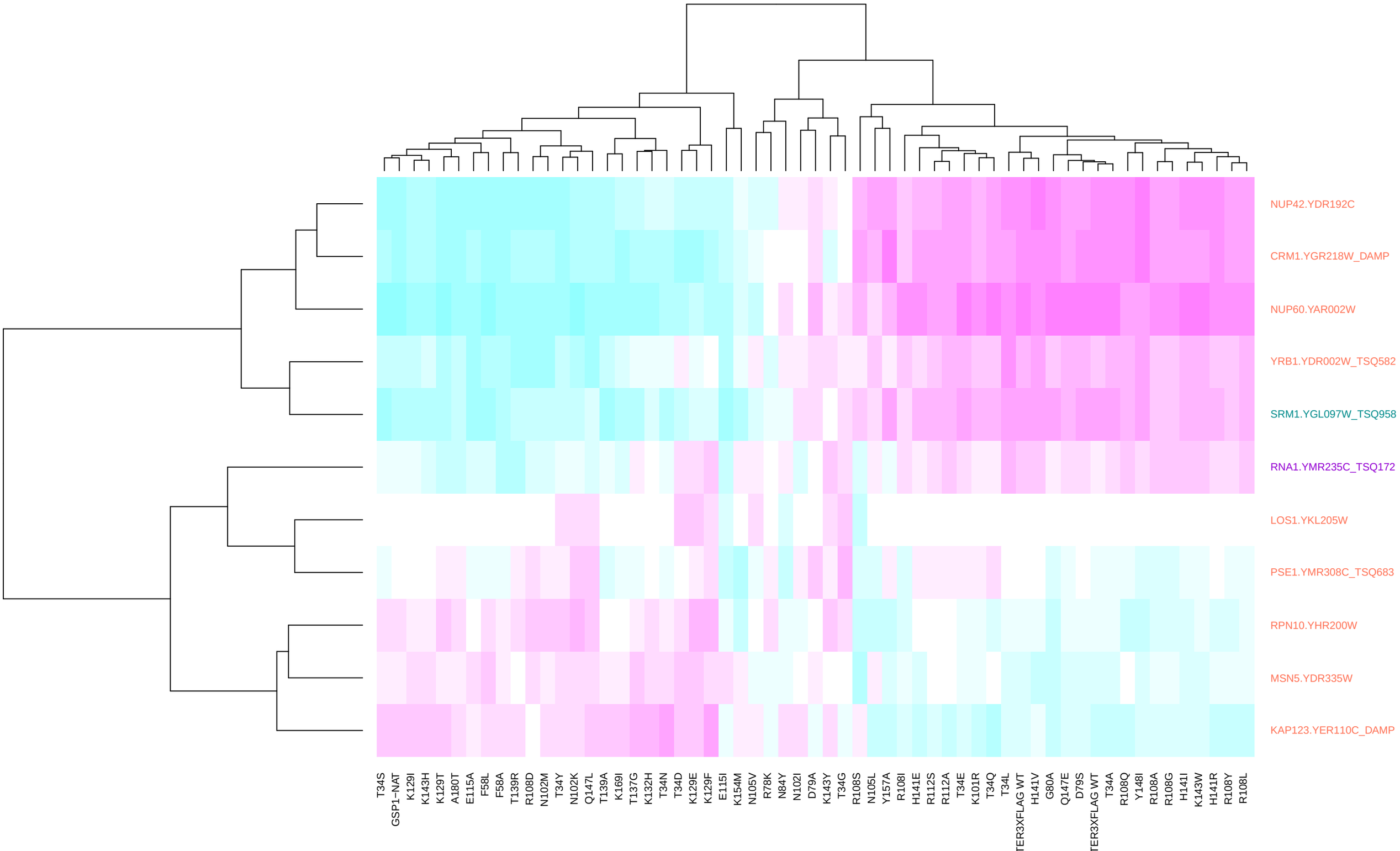
DNA binding_GO_15_3_mut



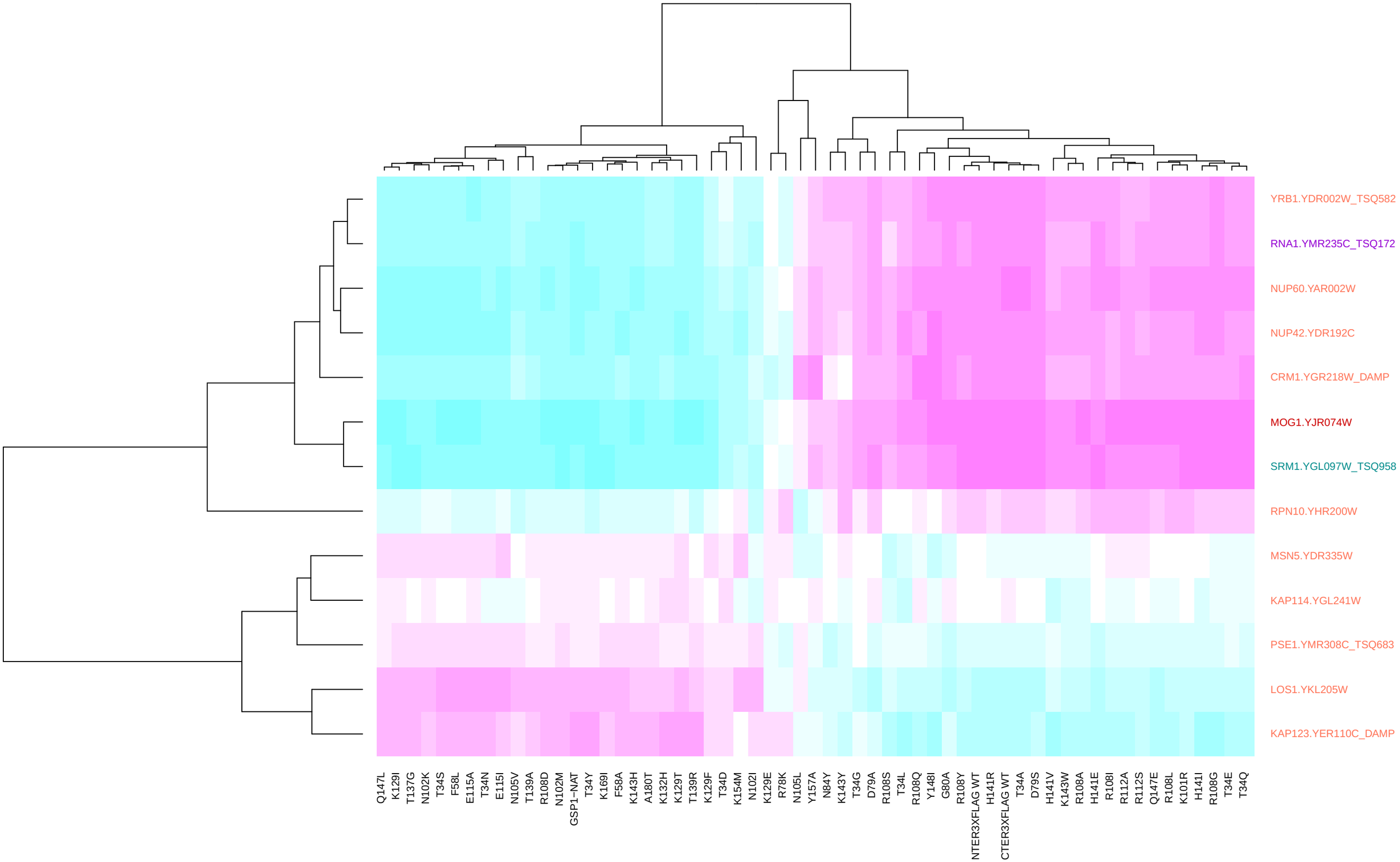
transcription_GO_15_1_mut



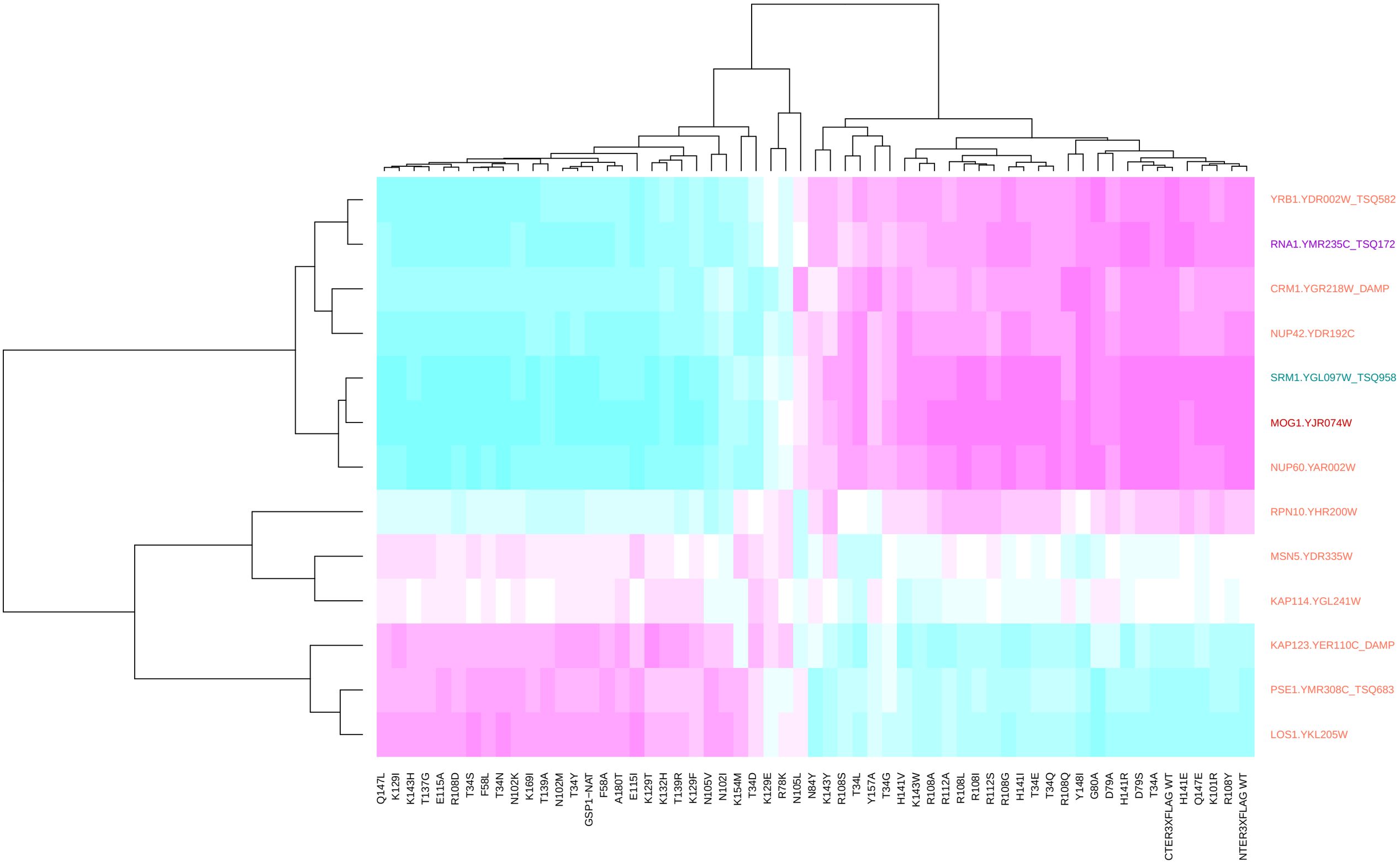
transcription_GO_30_4_all



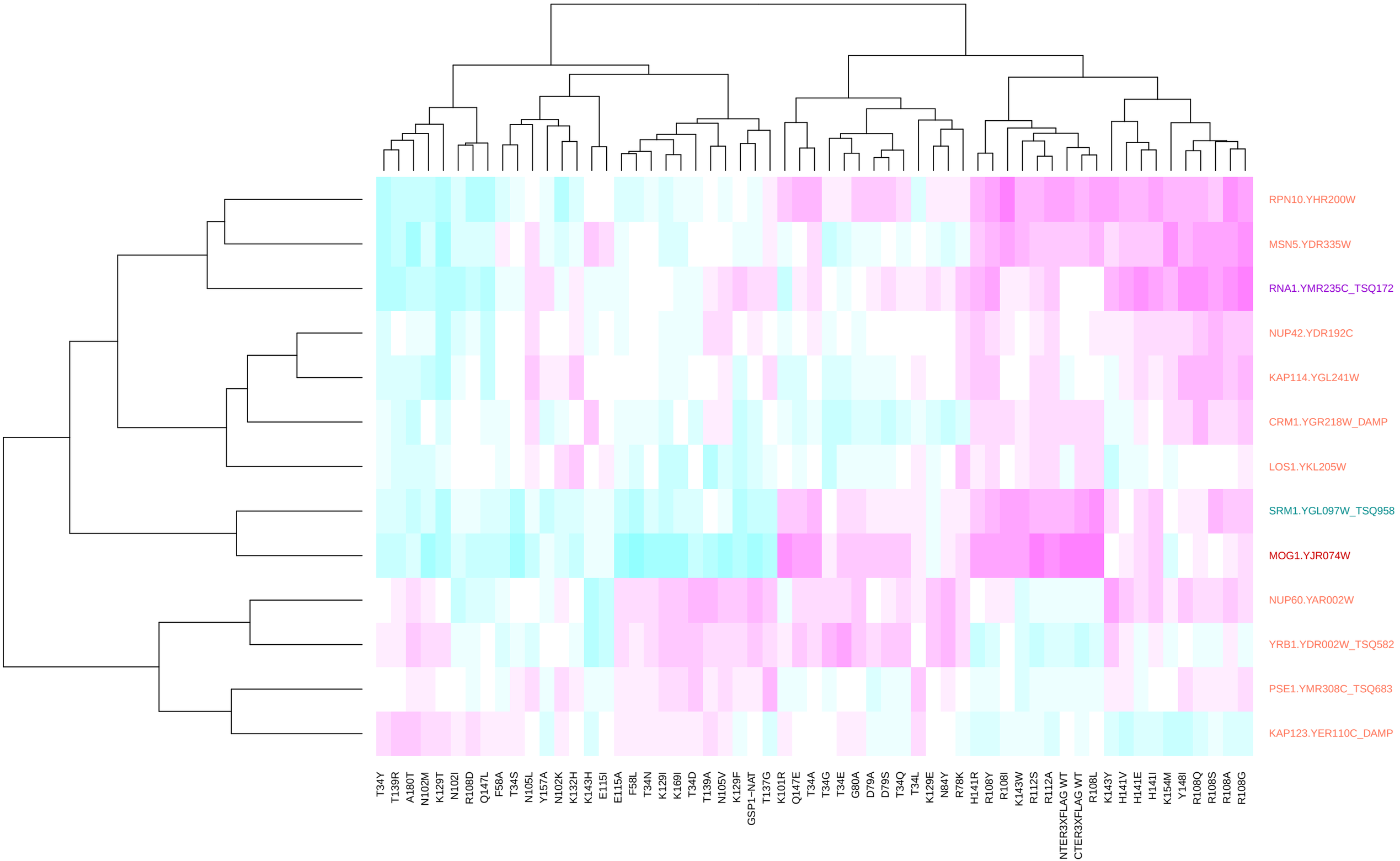
nucleobase−containing compound transport



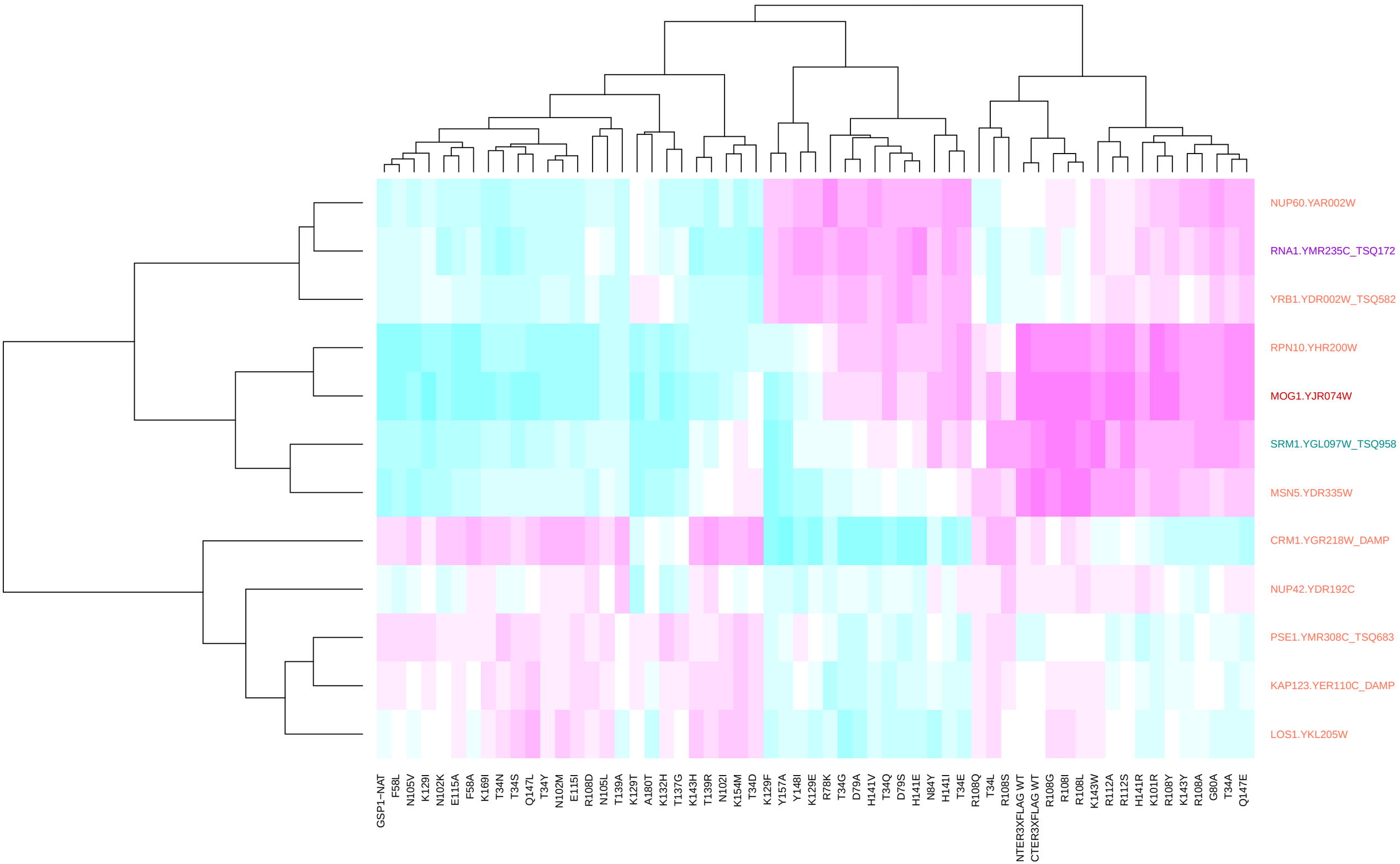
nucleobase−containing compound transport_GO_15_1_mut



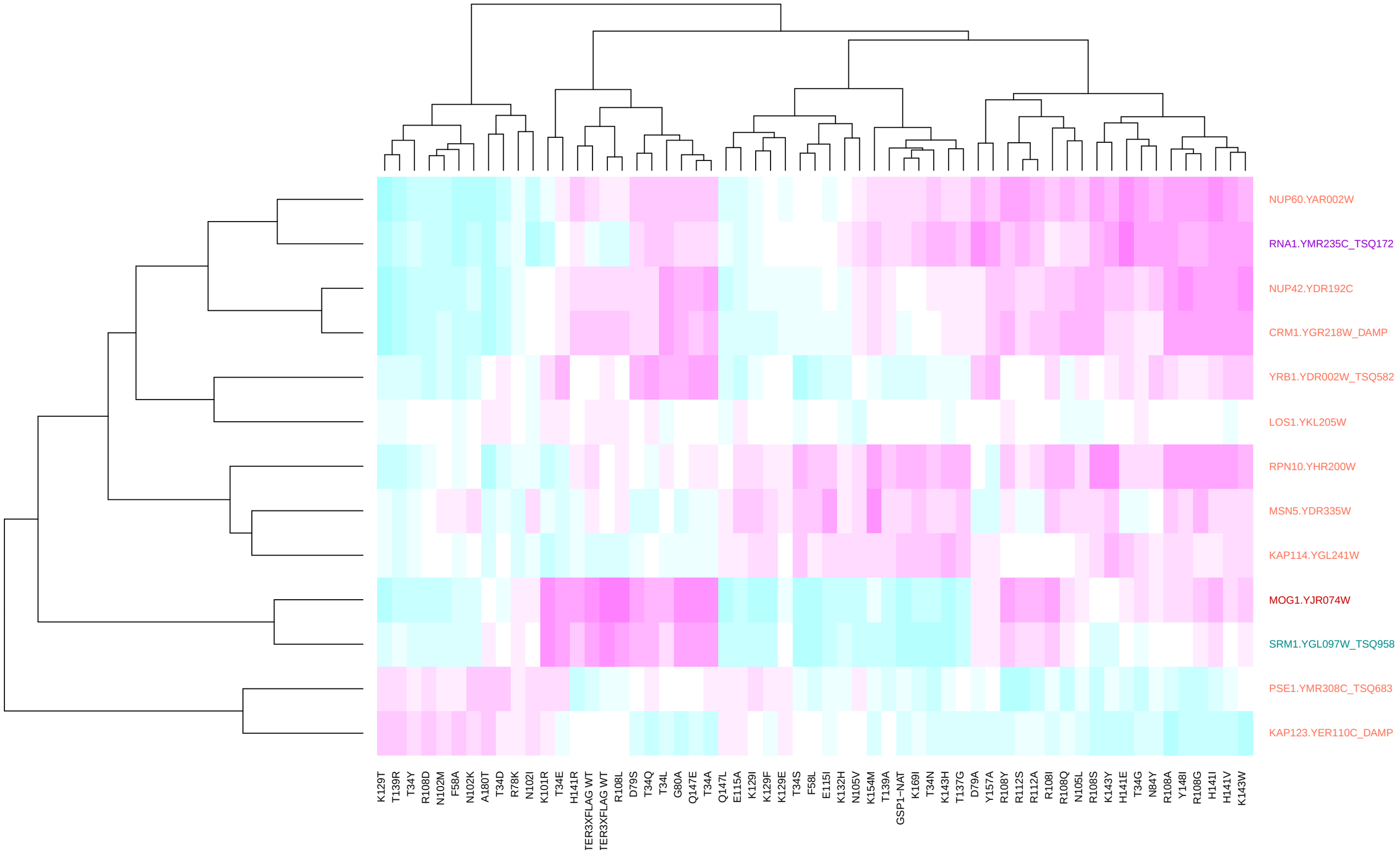
protein modification by small protein conjugation or removal



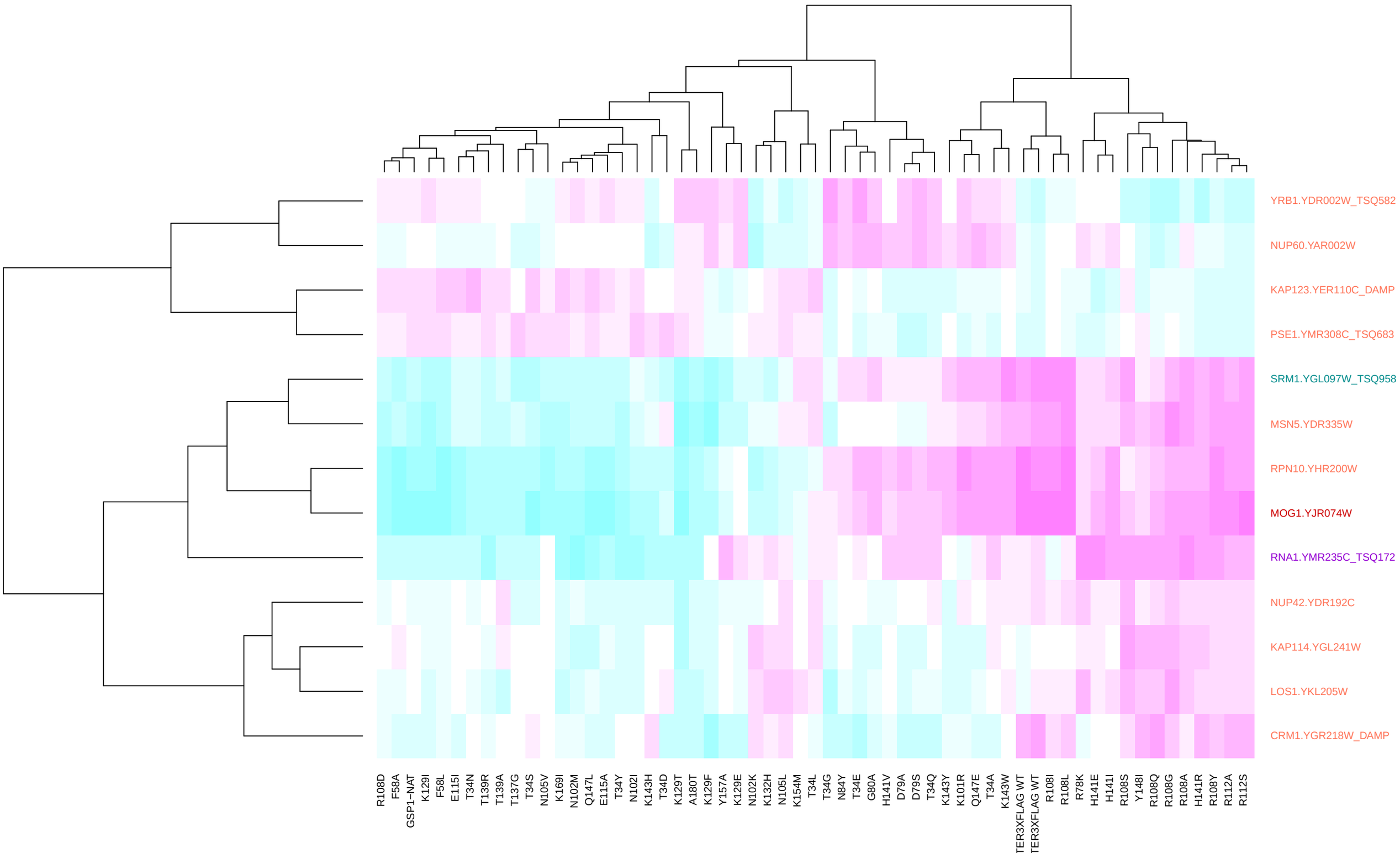
protein modification by small protein conjugation or removal_GO_15_1_mut



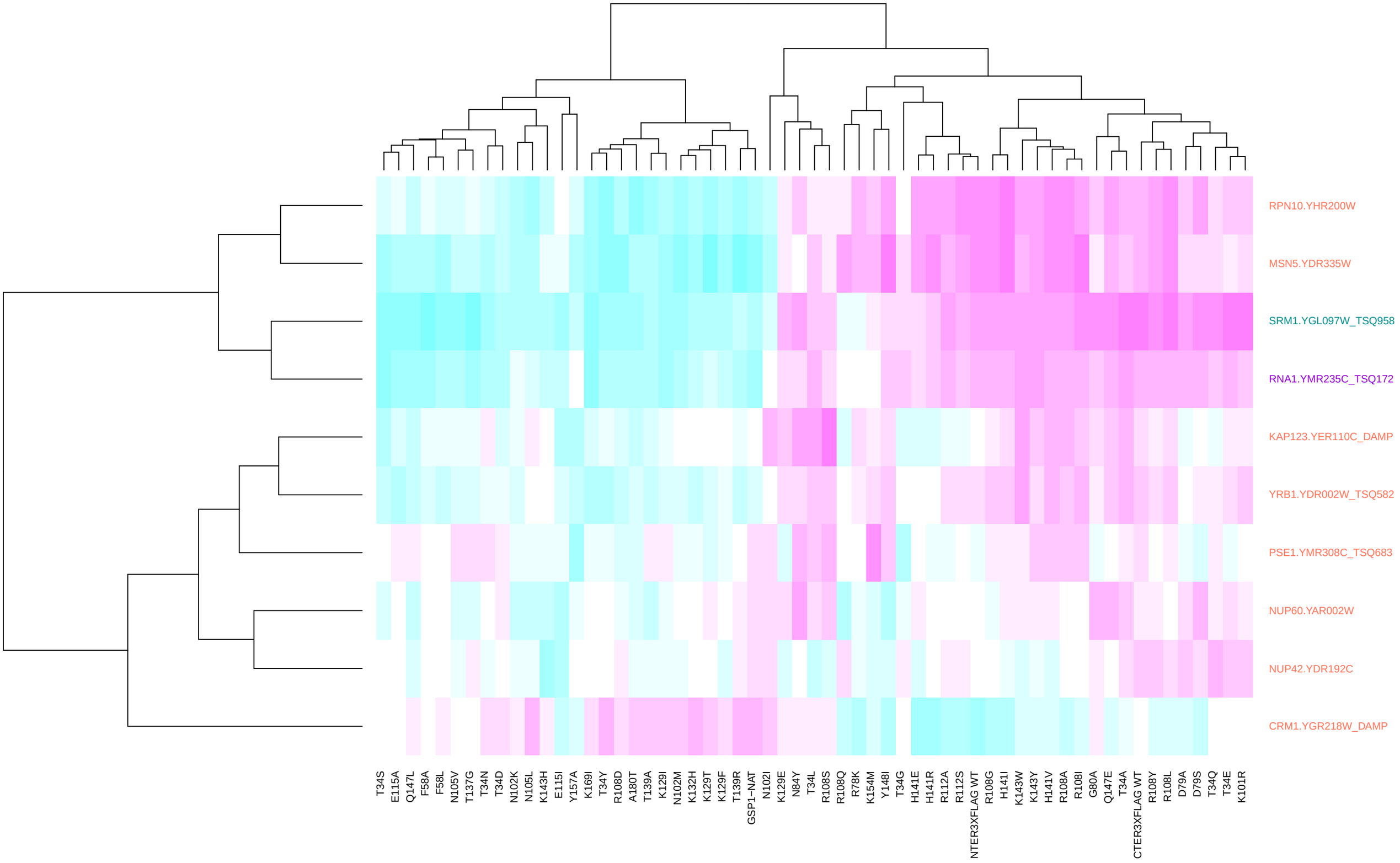
chromatin organization



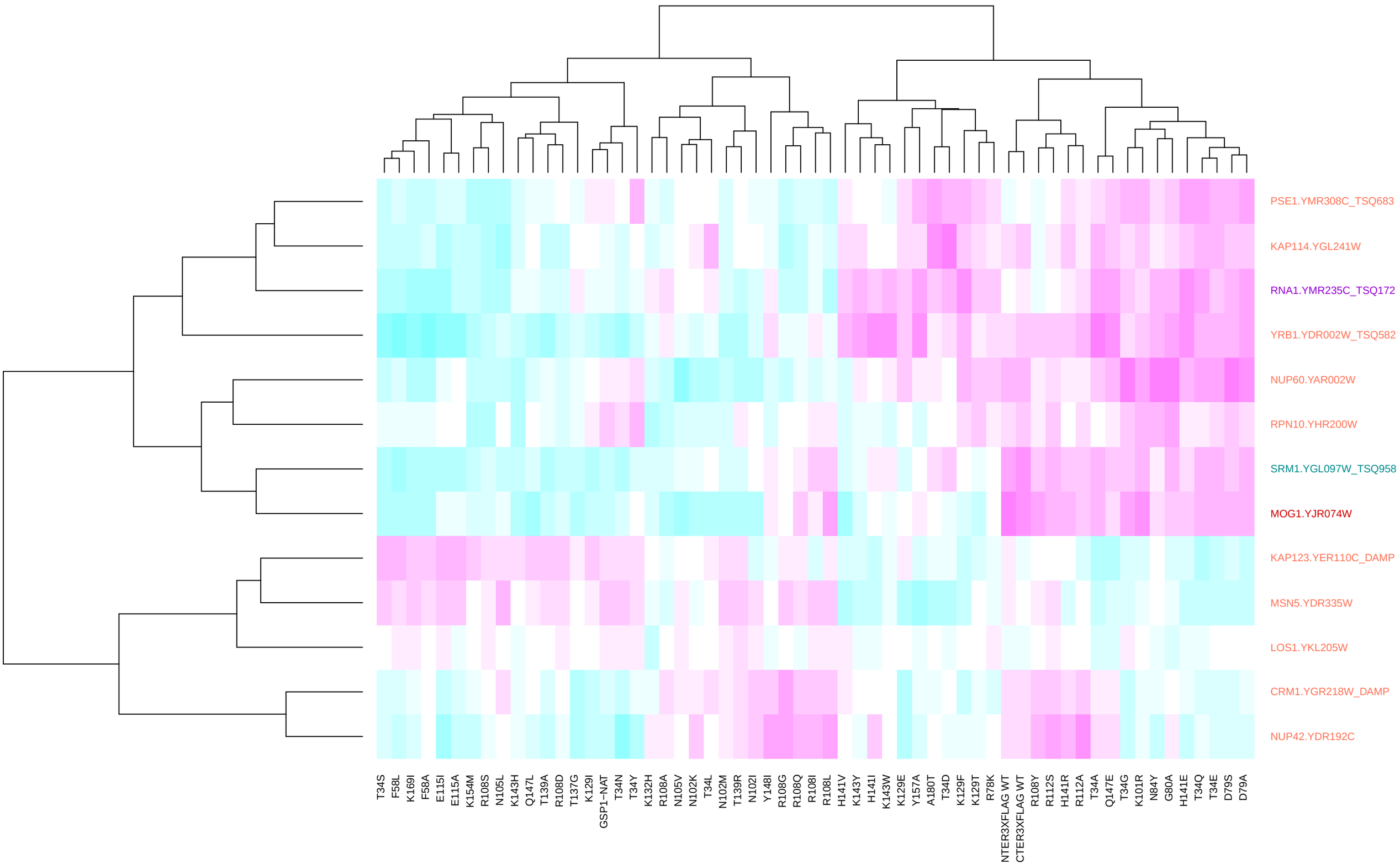
protein modification by small protein conjugation or removal_GO_30_1_mut



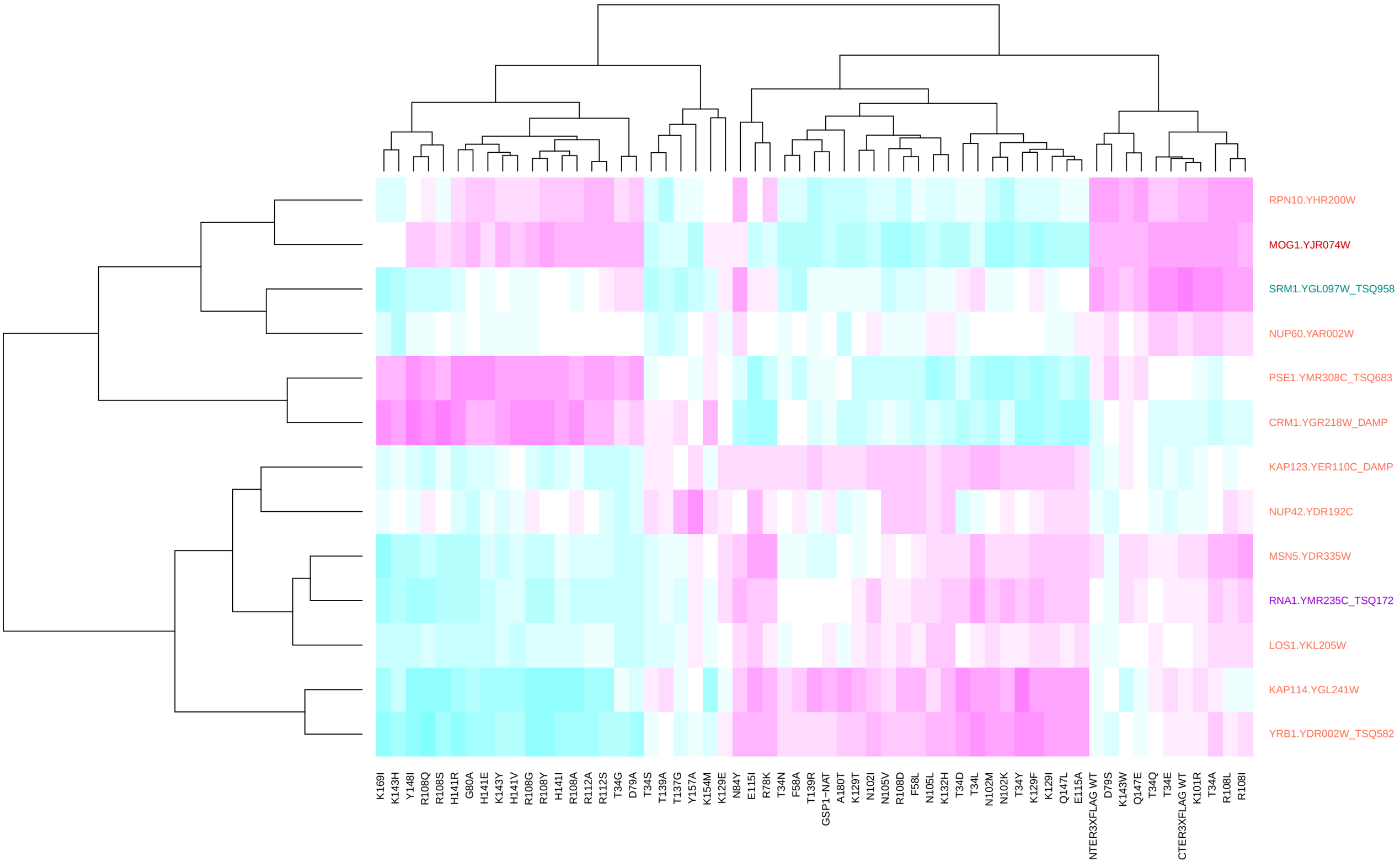
sig_Gsp1_GI_15_11_all



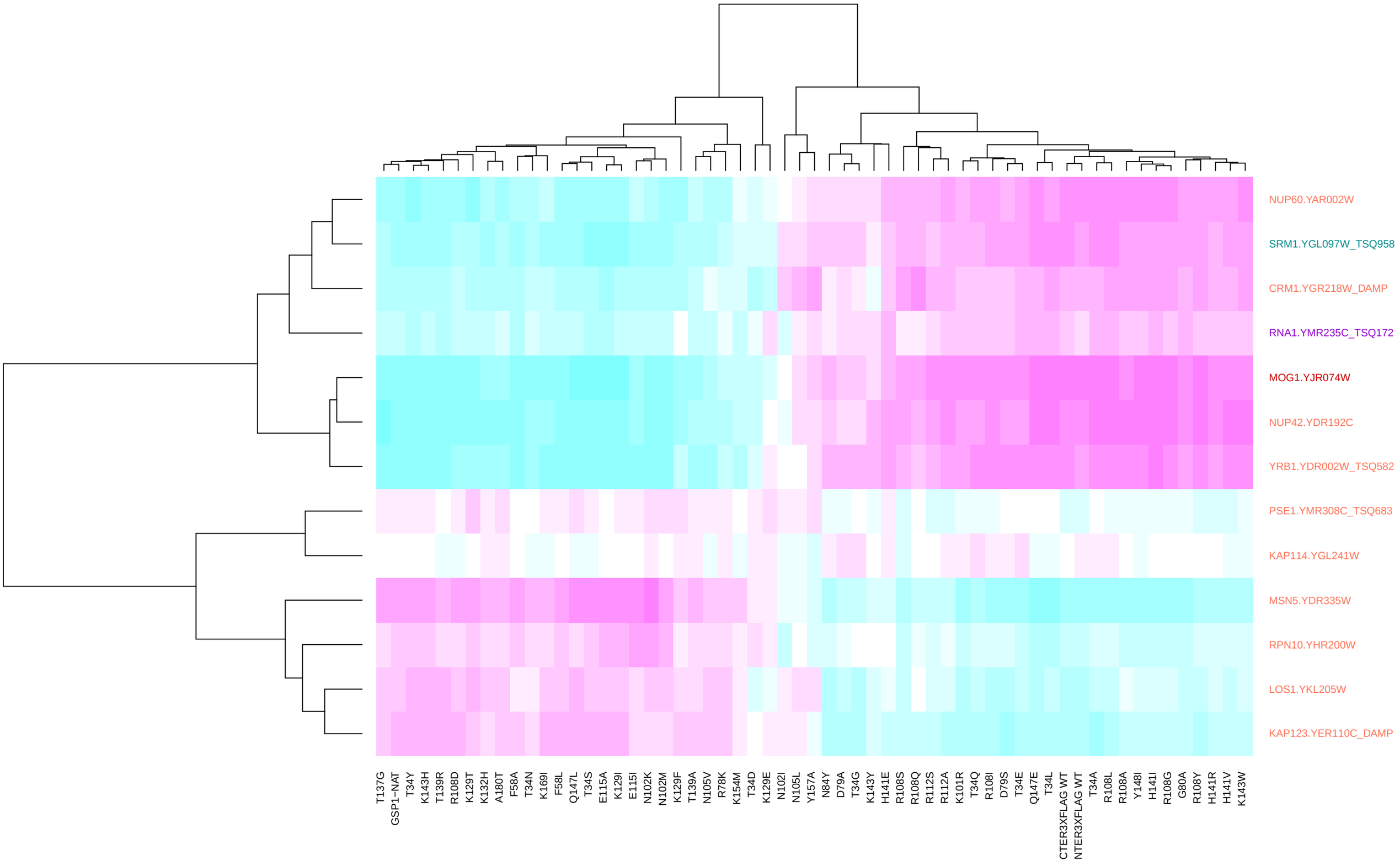
sig_Gsp1_GI_30_2_mut



sig_Gsp1_GI_30_3_all



cellular response to DNA damage stimulus_GO_15_3_mut



lipid binding_GO_15_2_all