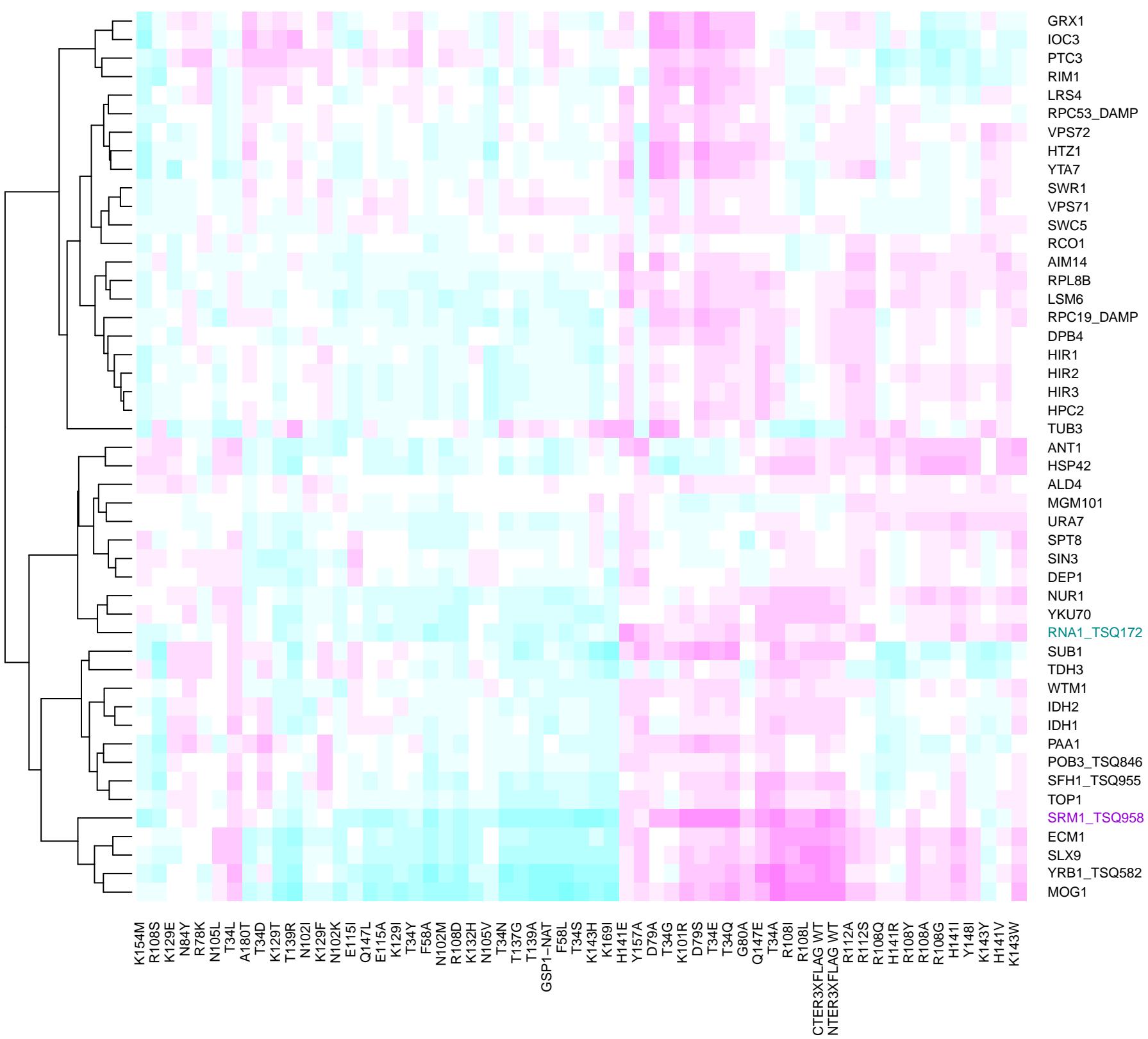
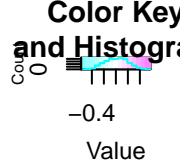
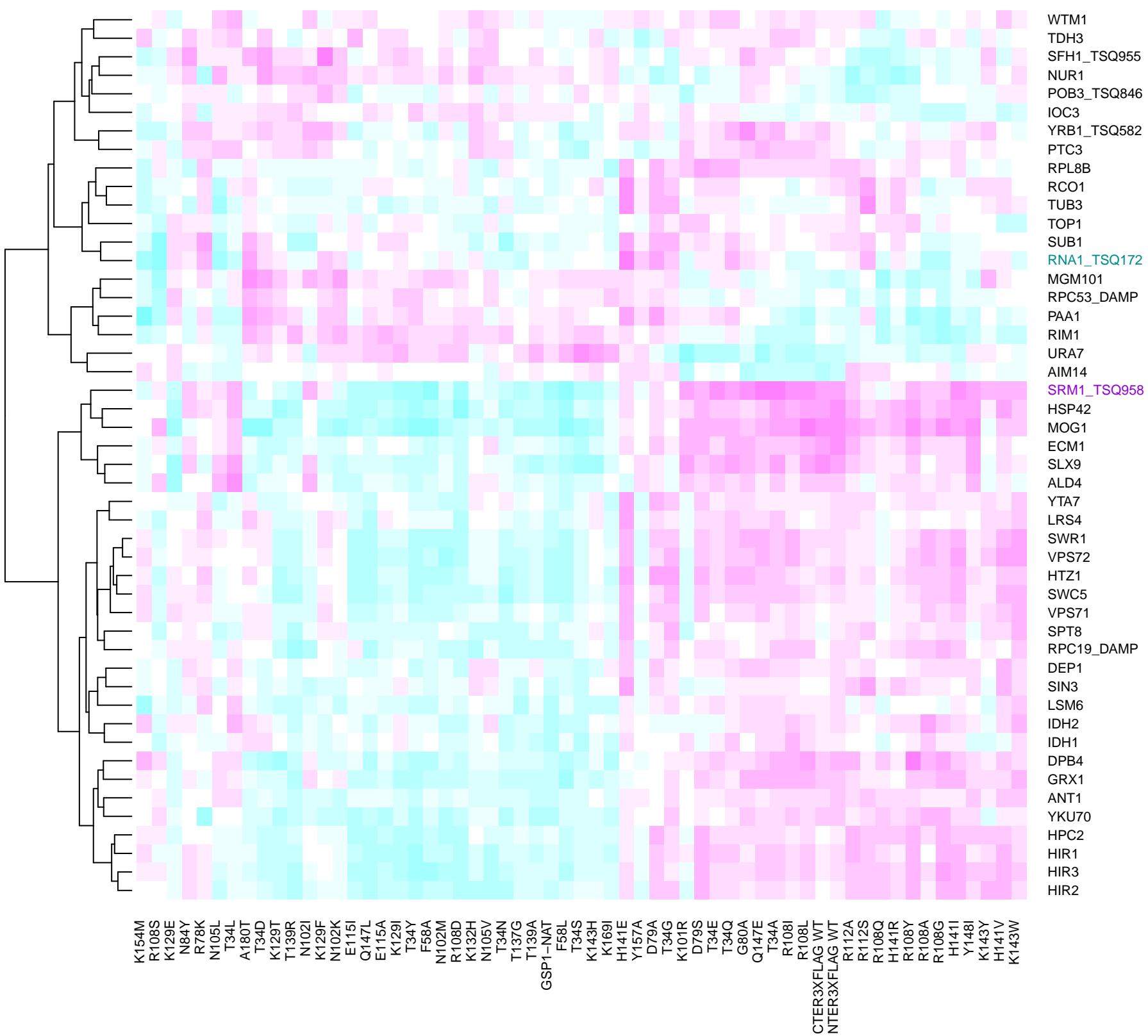


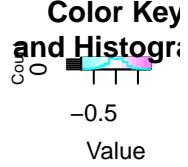
mitotic cell cycle



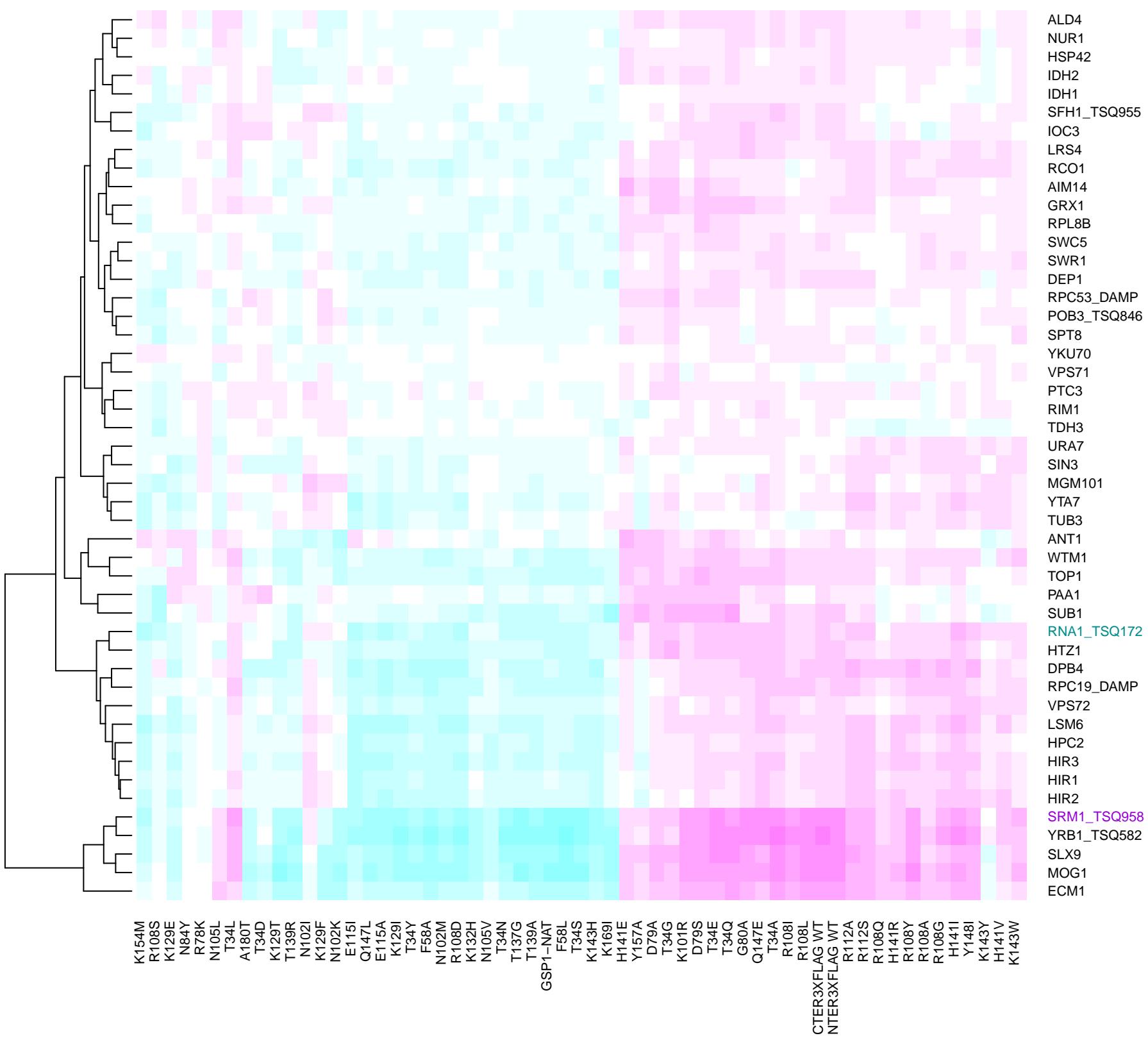


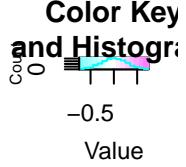
metabolic_GO_30_1



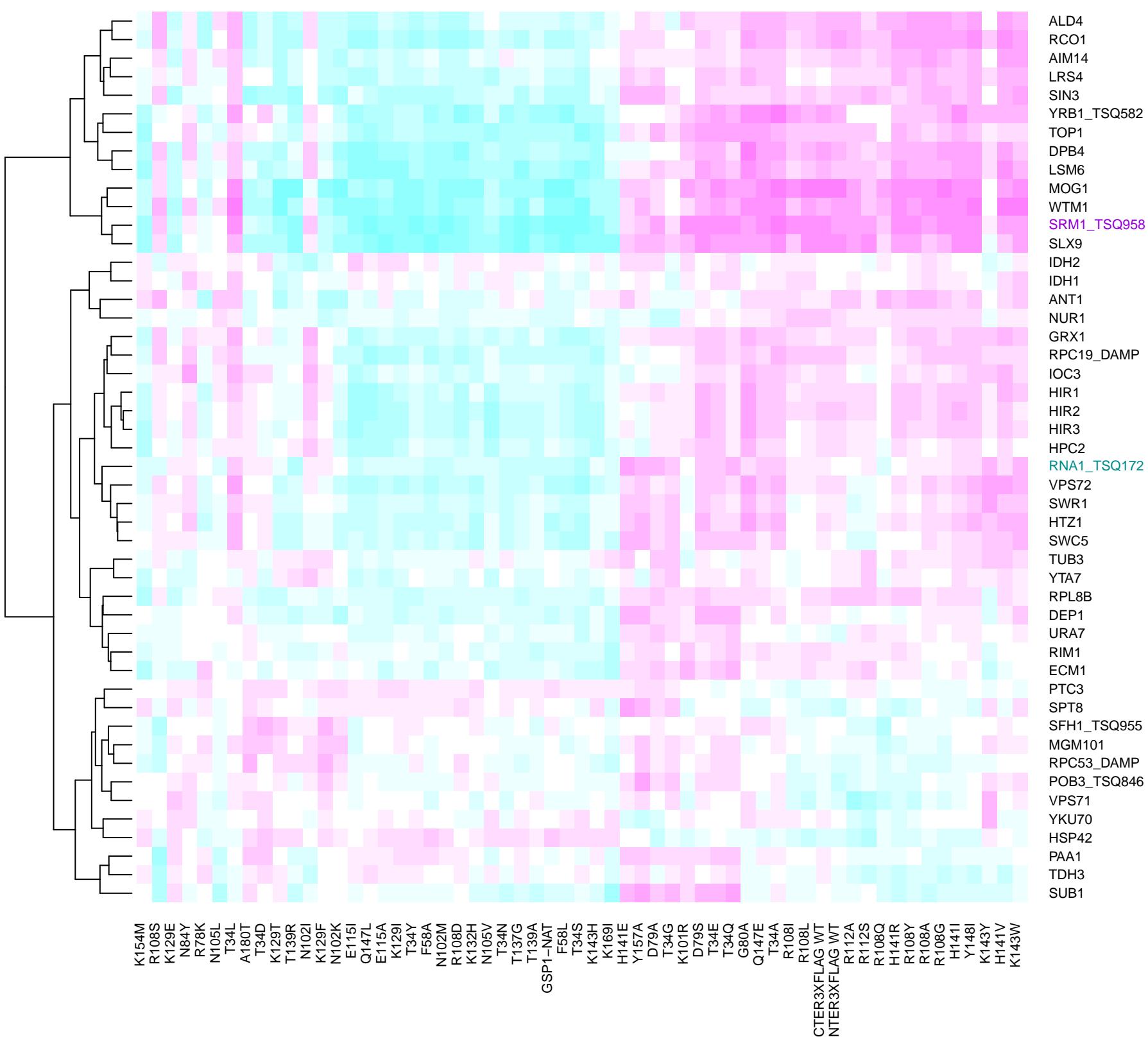


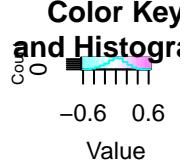
endomembrane system



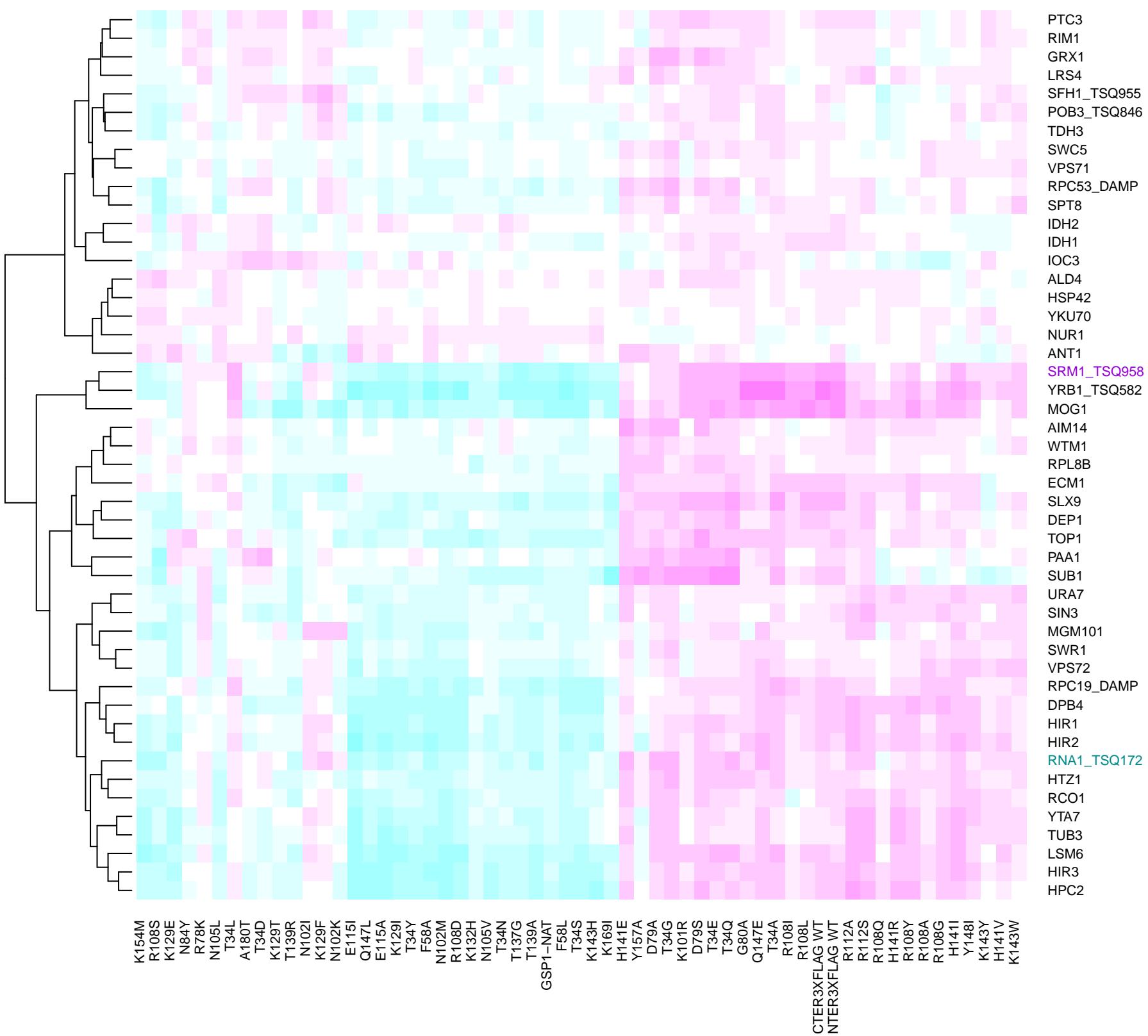


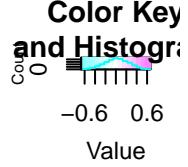
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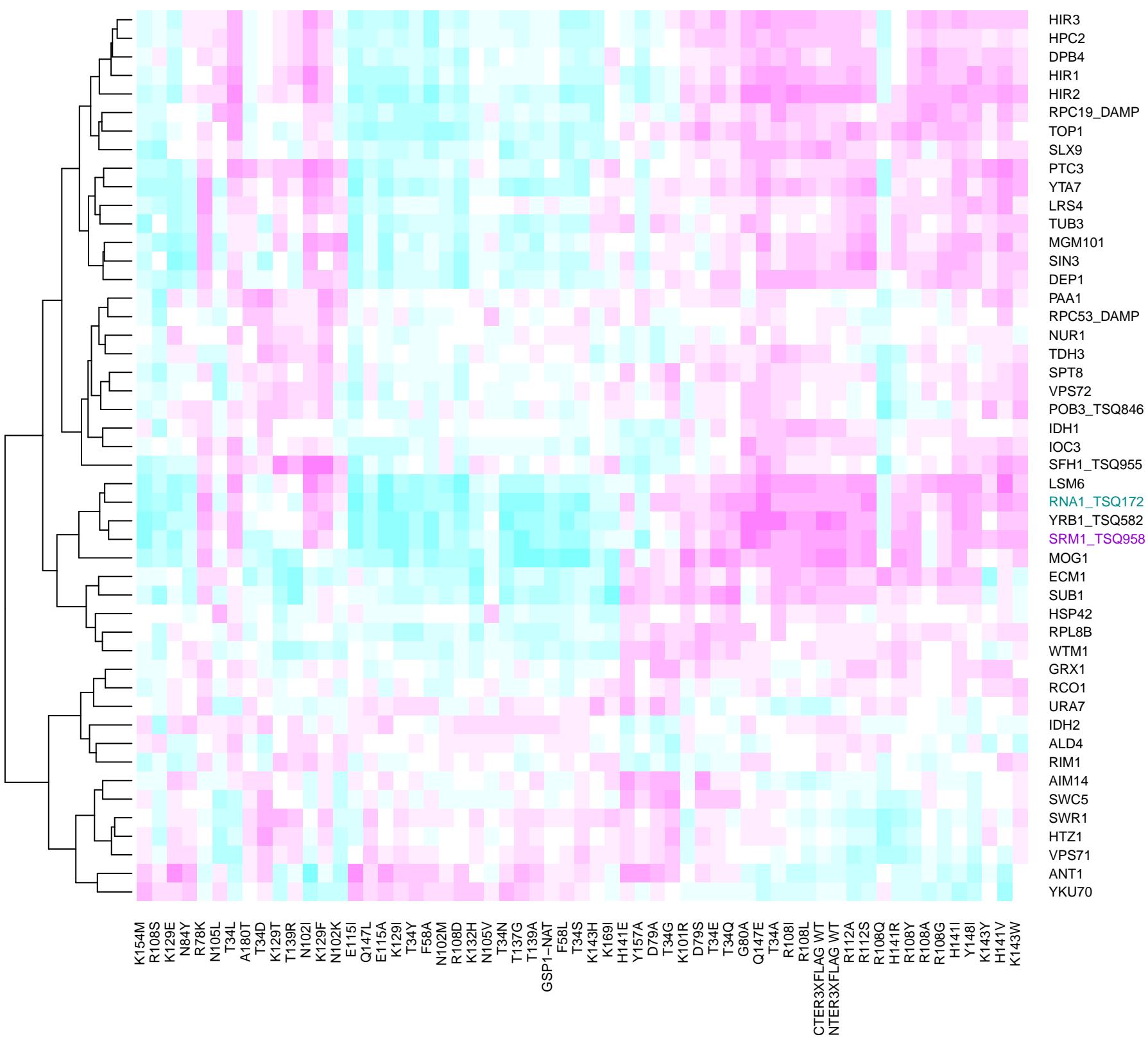


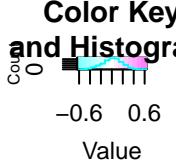
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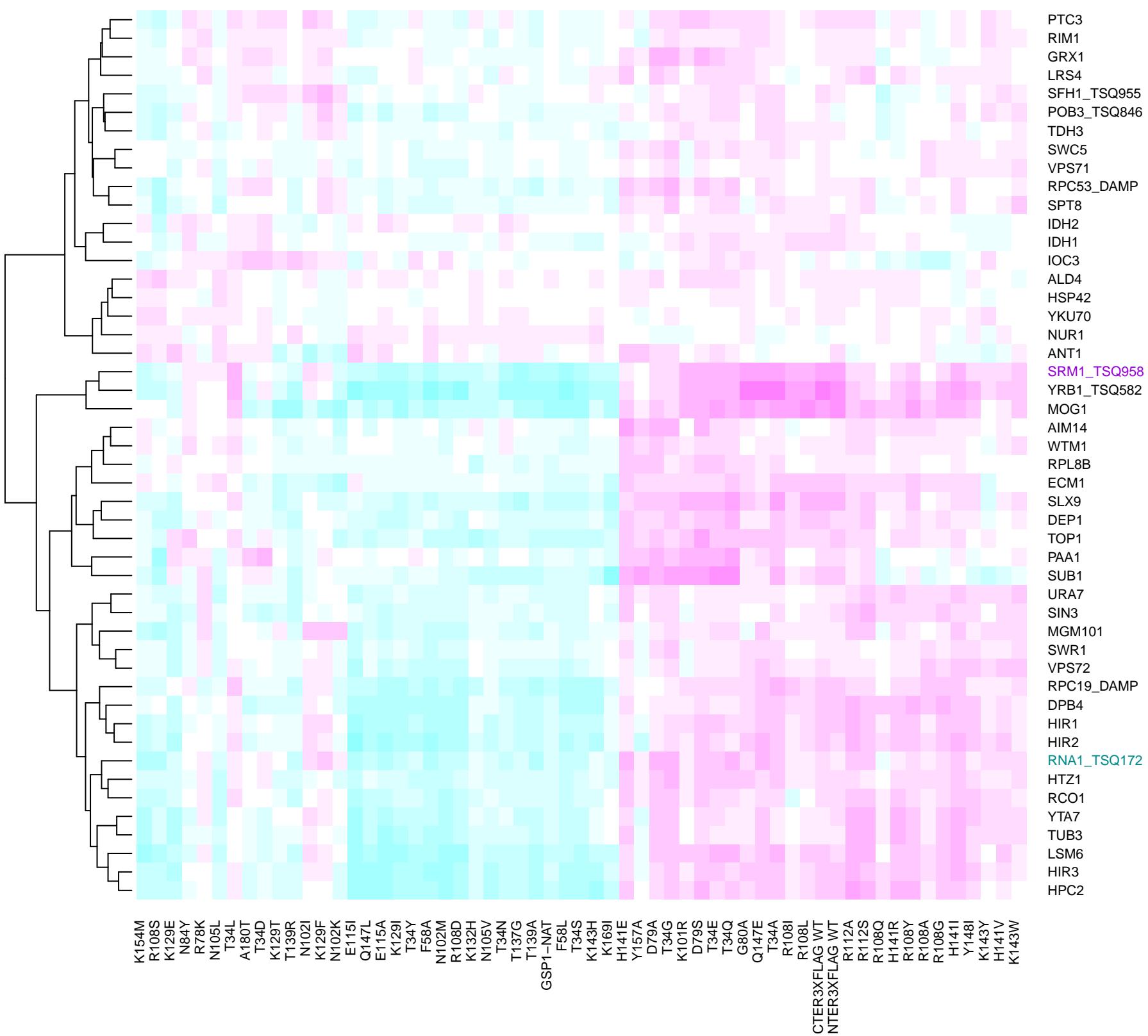


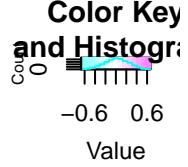
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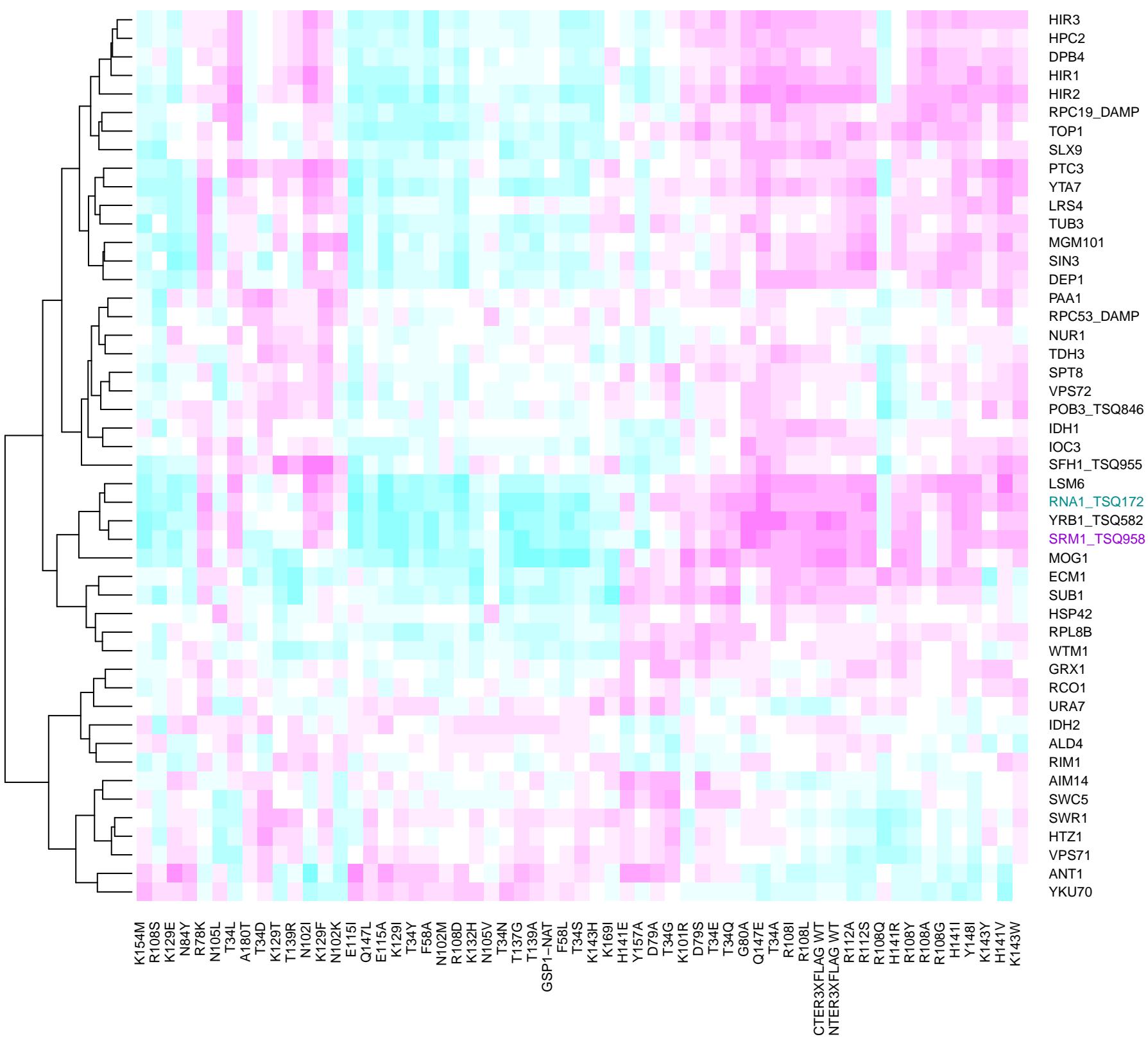


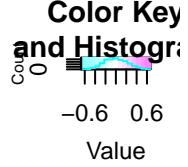
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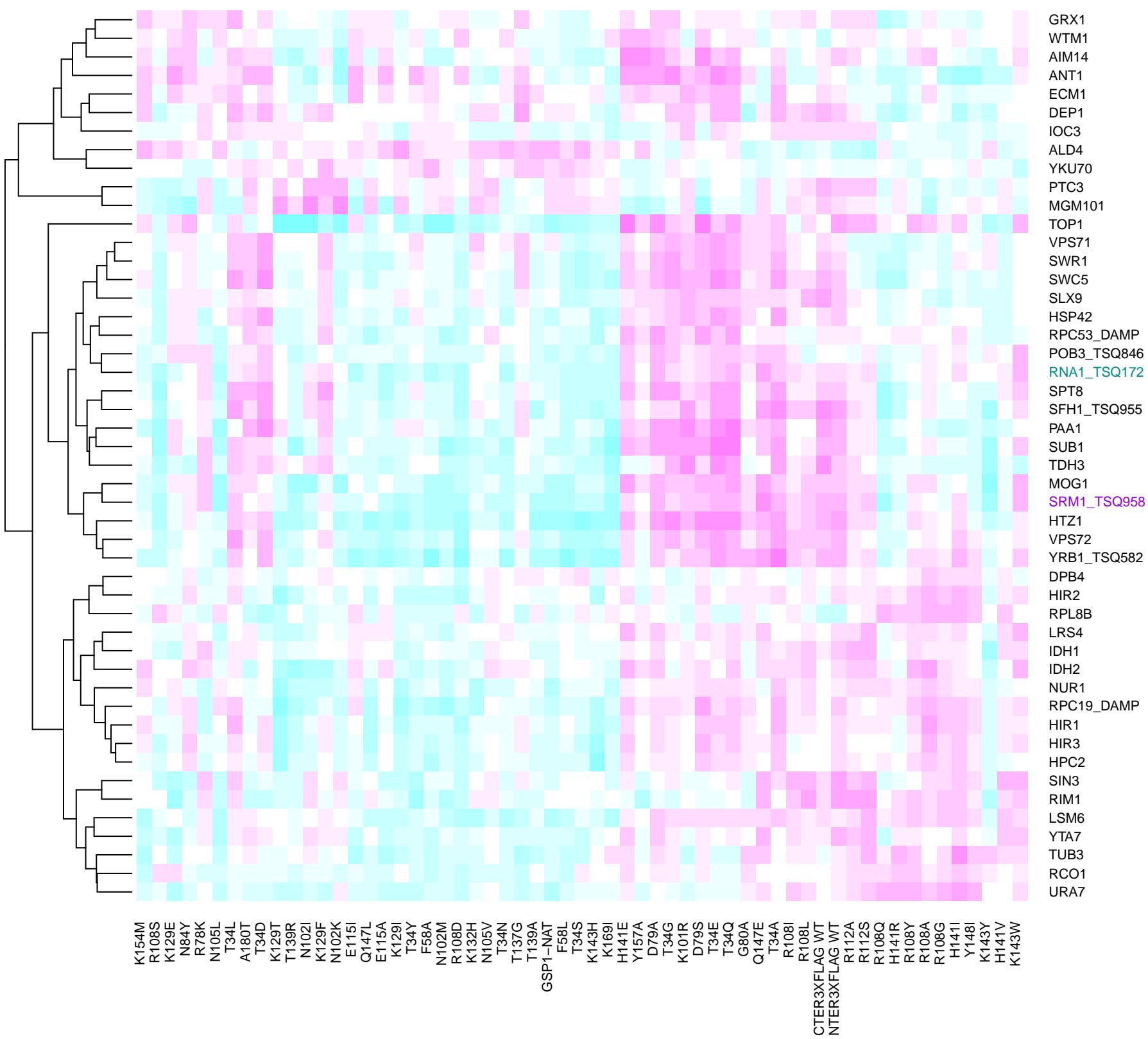


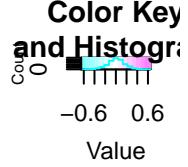
ER_GO_30_3



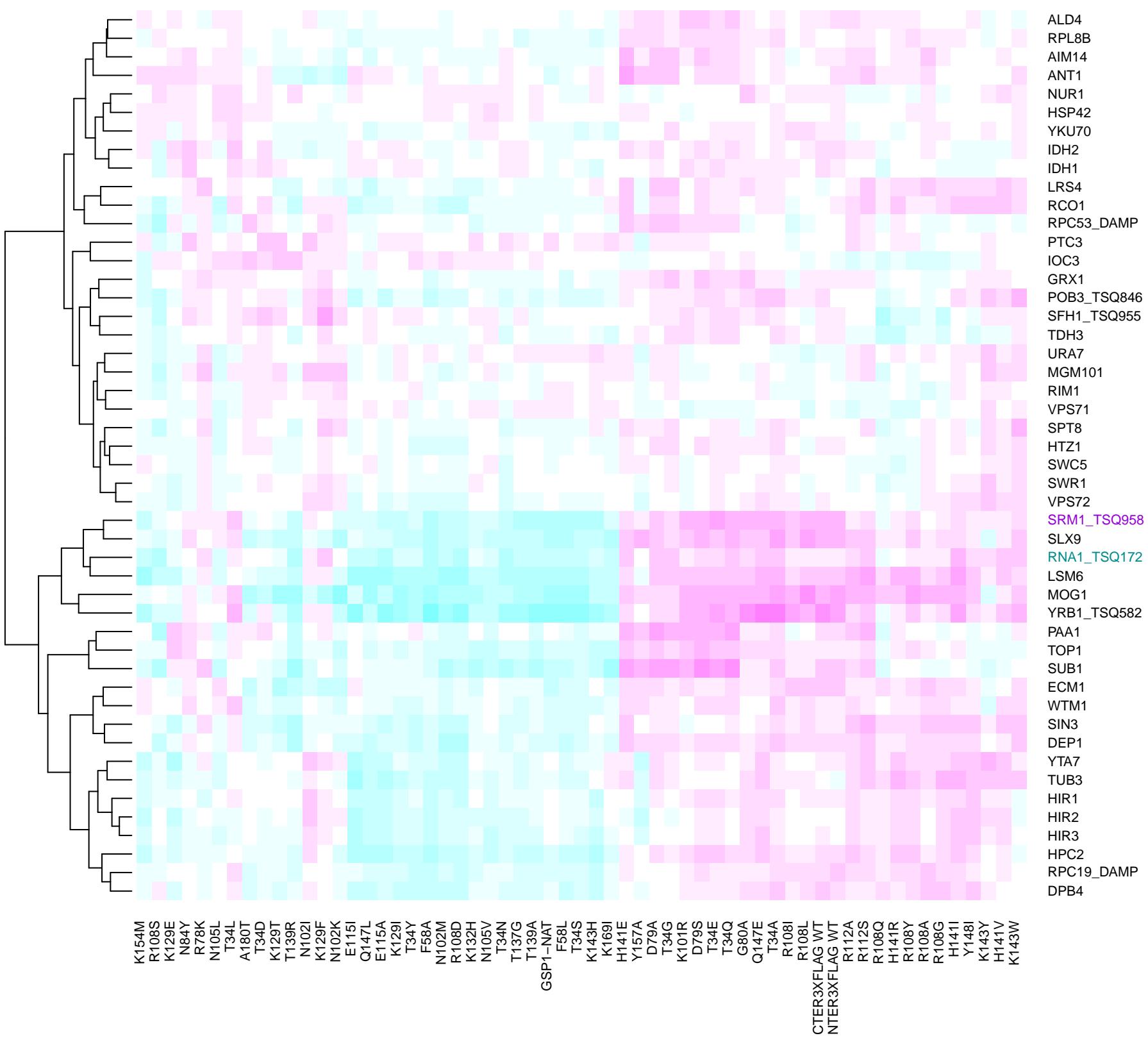


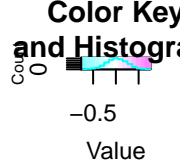
Golgi and ER_GO_30_7



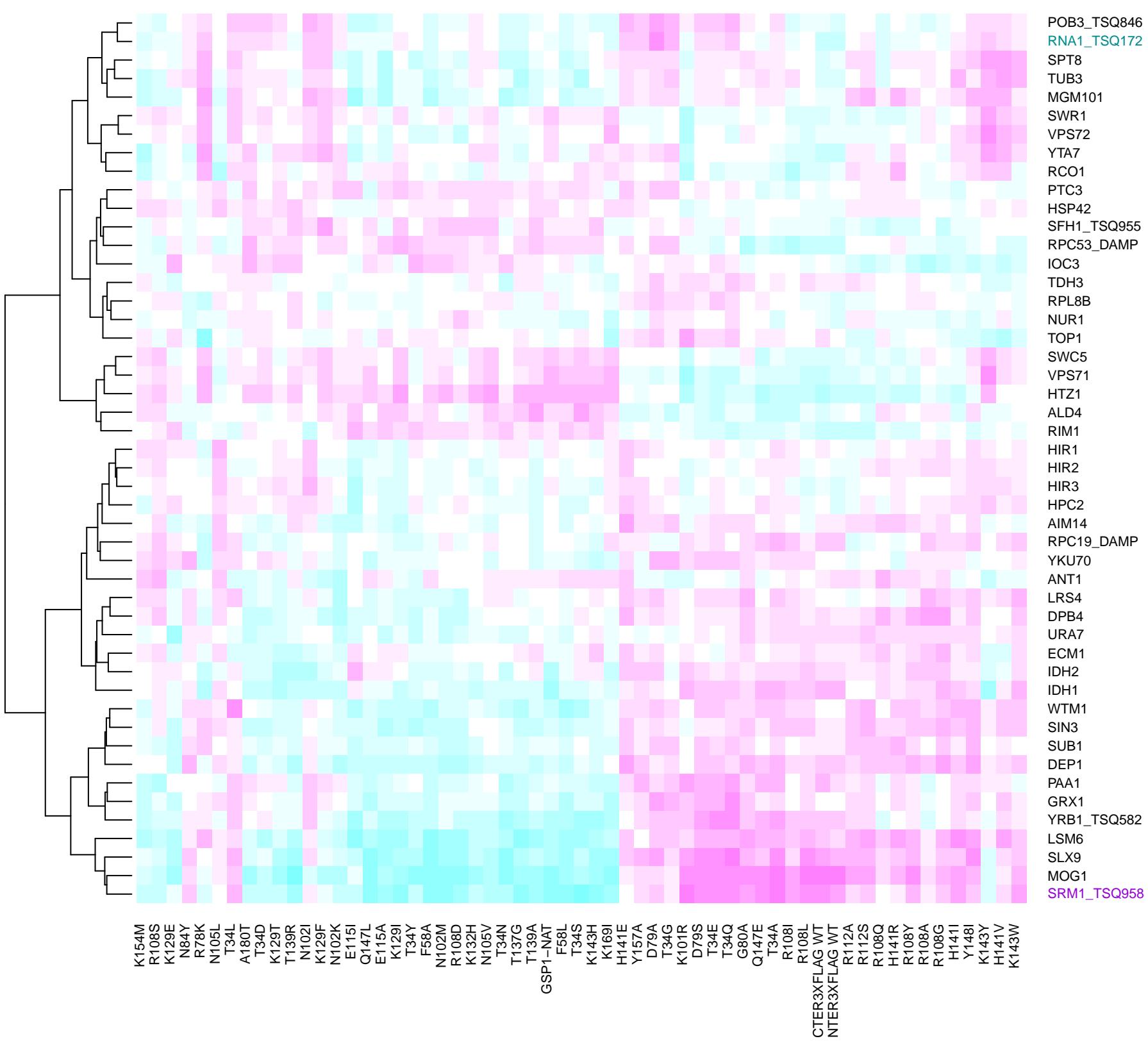


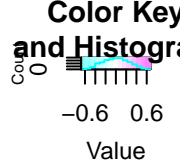
lipid metabolic process



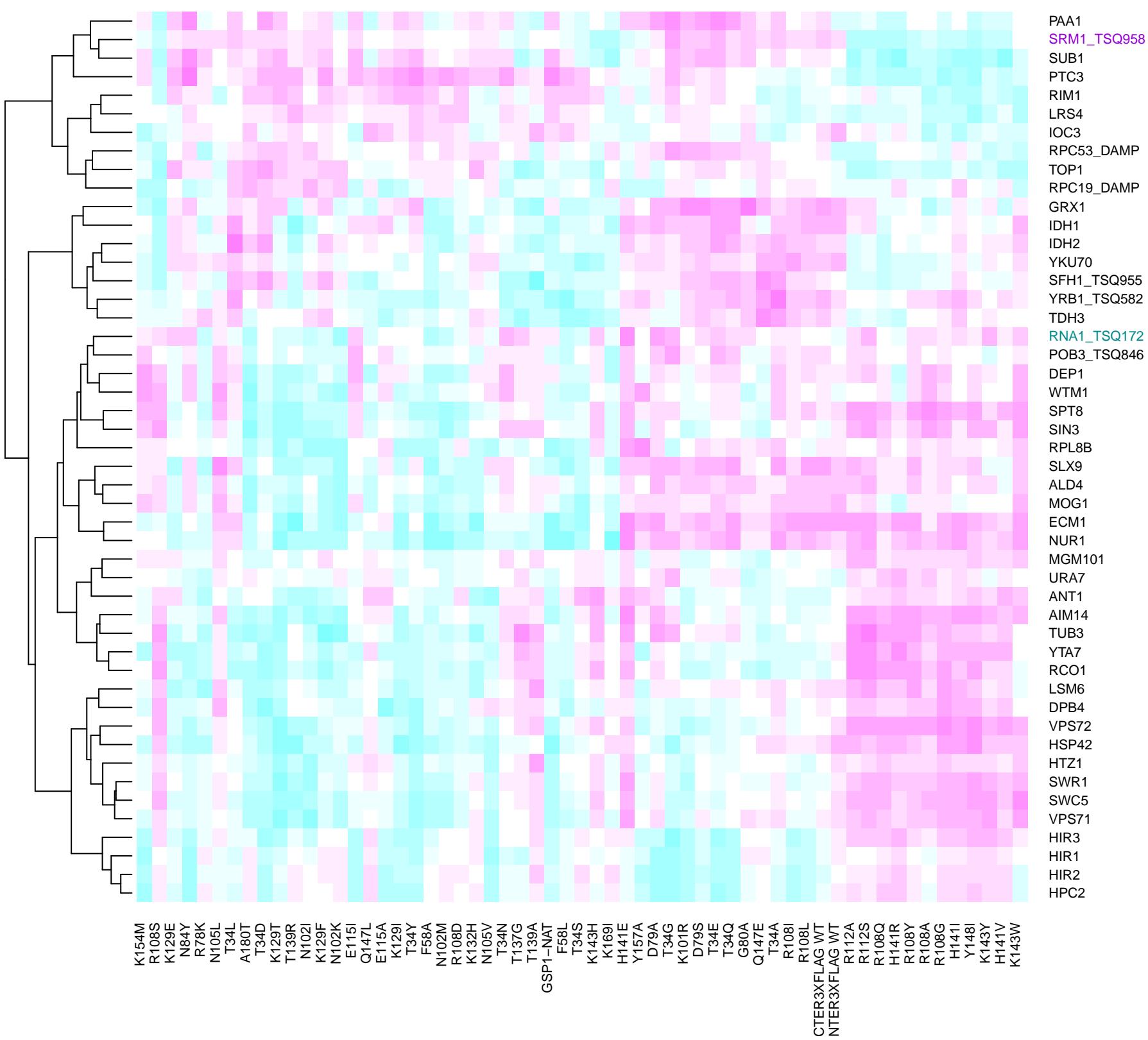


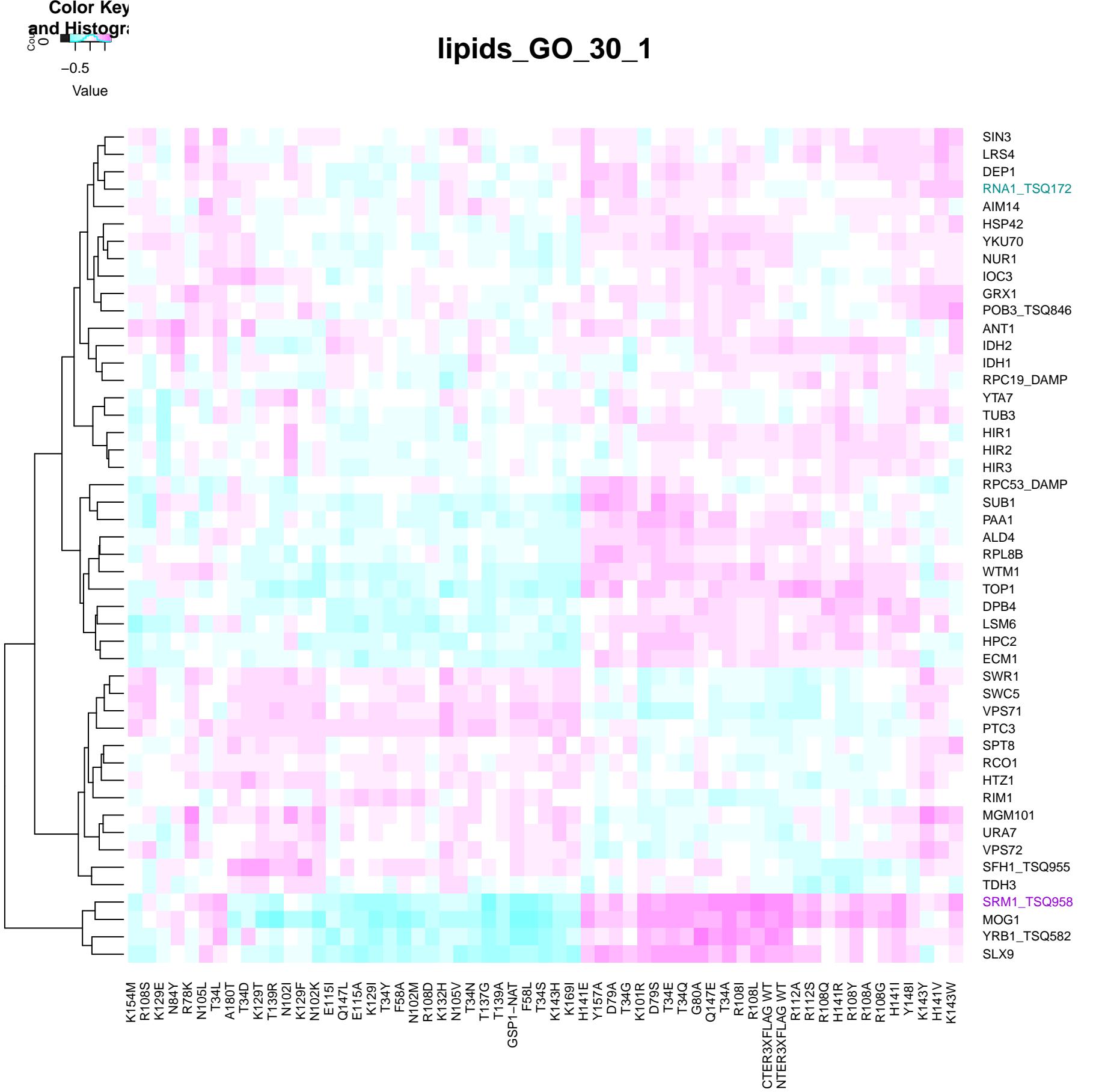
lipid metabolic process_GO_30_4

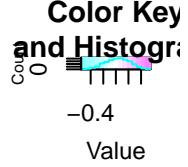




mitotic cell cycle_GO_30_6

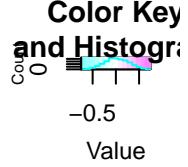




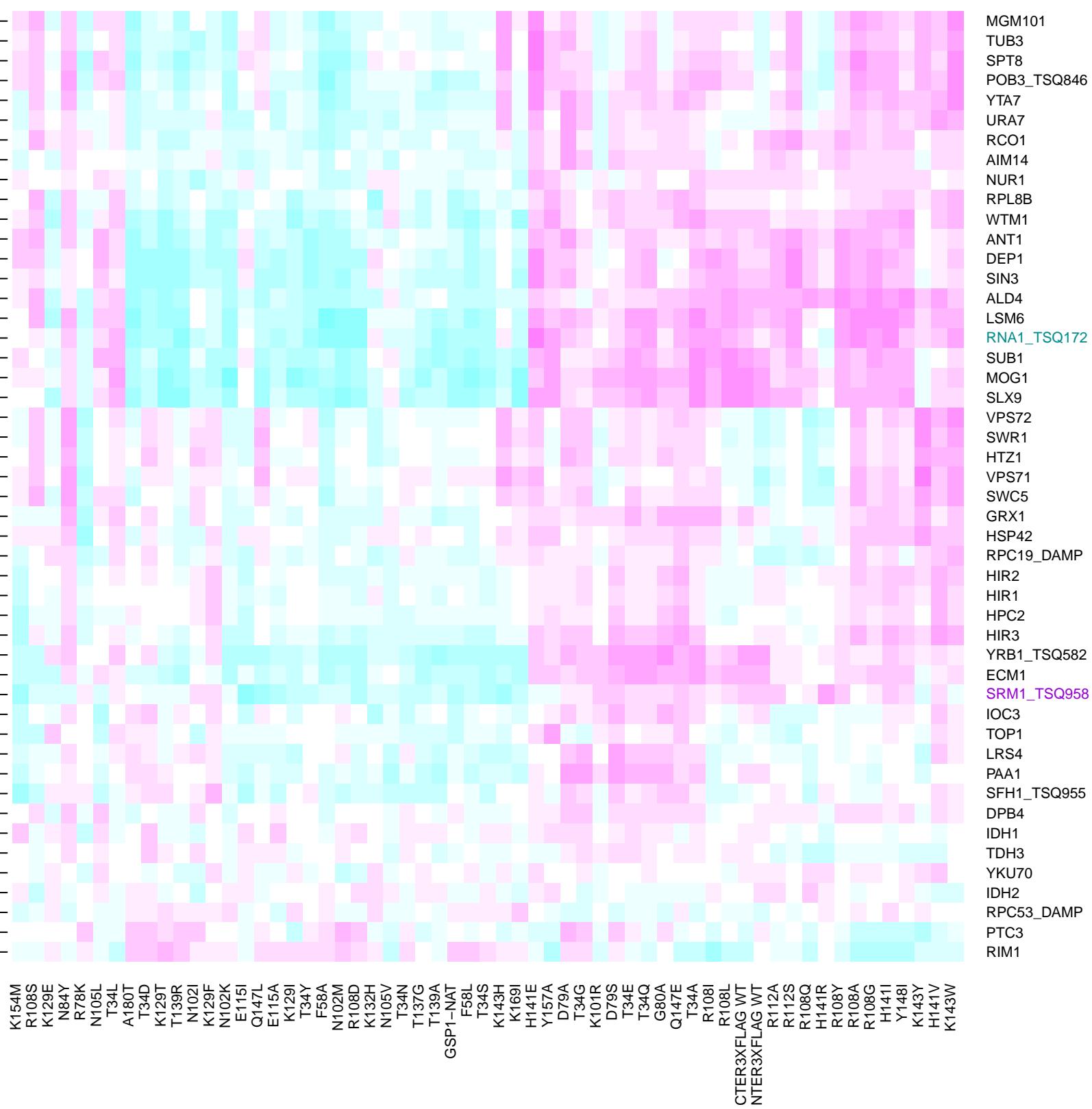


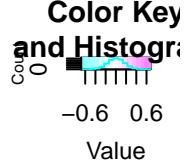
metabolic_GO_30_9



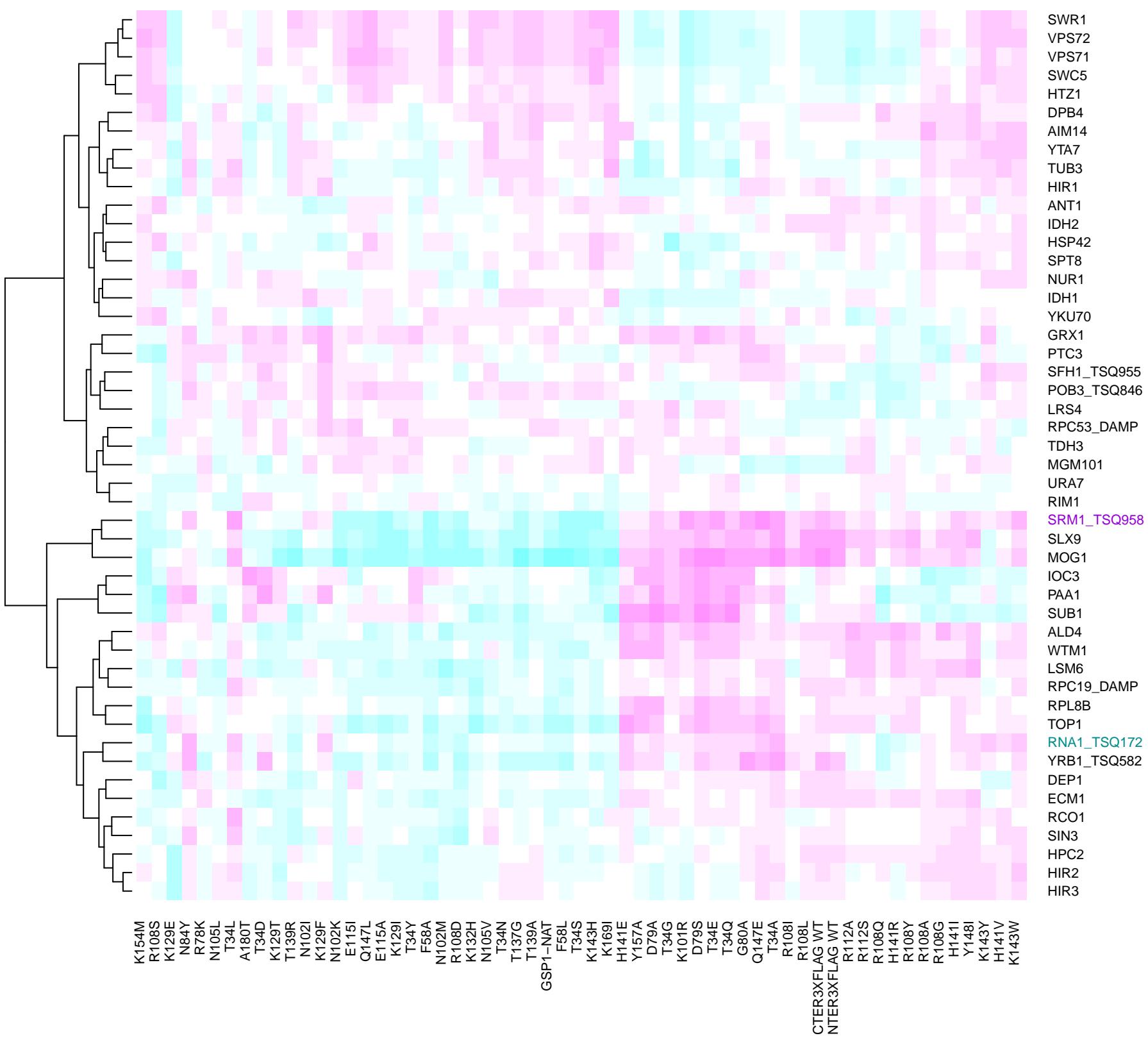


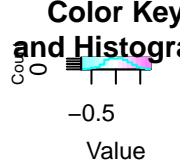
cell cycle_GO_30_4



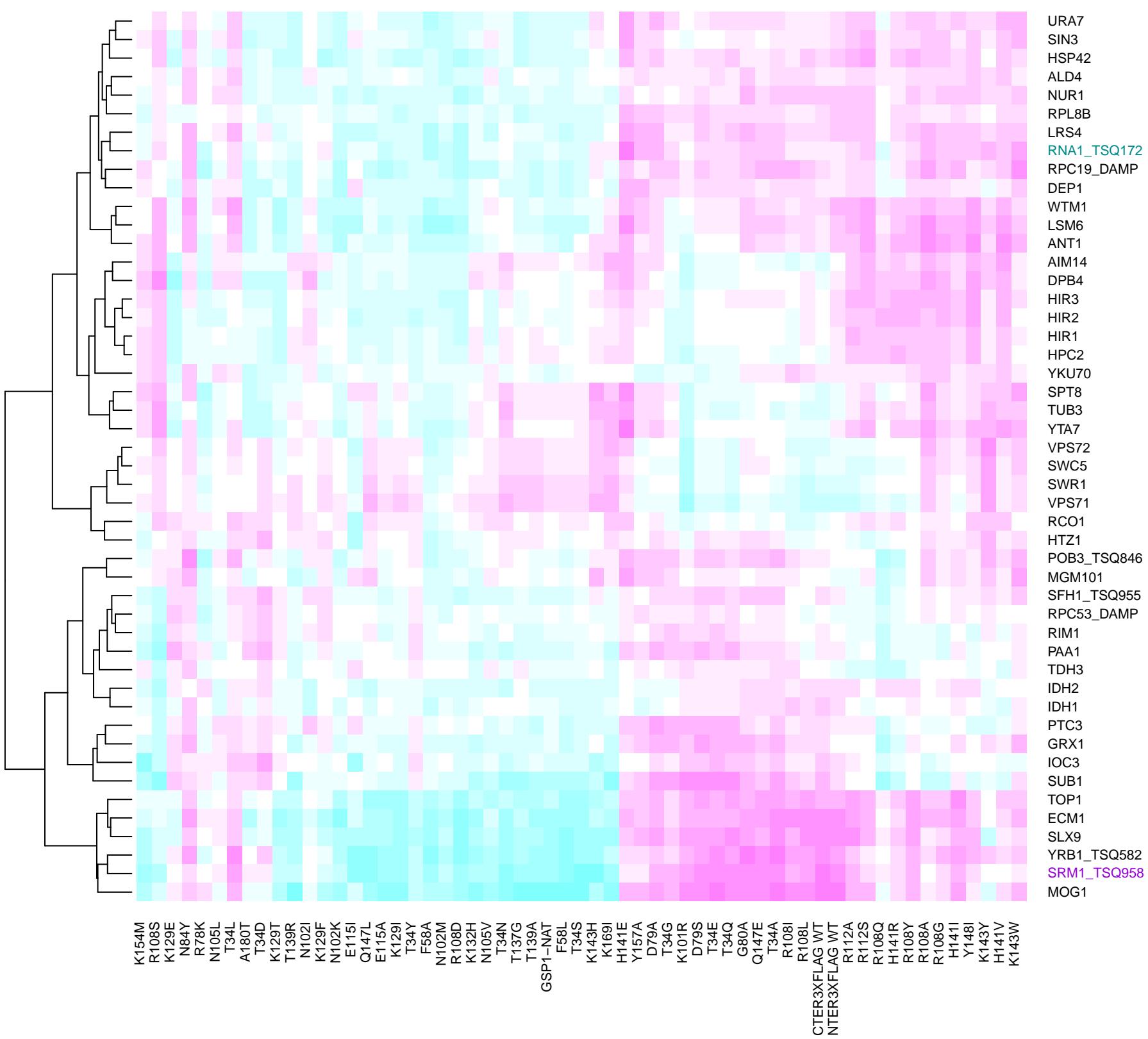


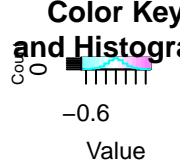
cellular bud_GO_30_1



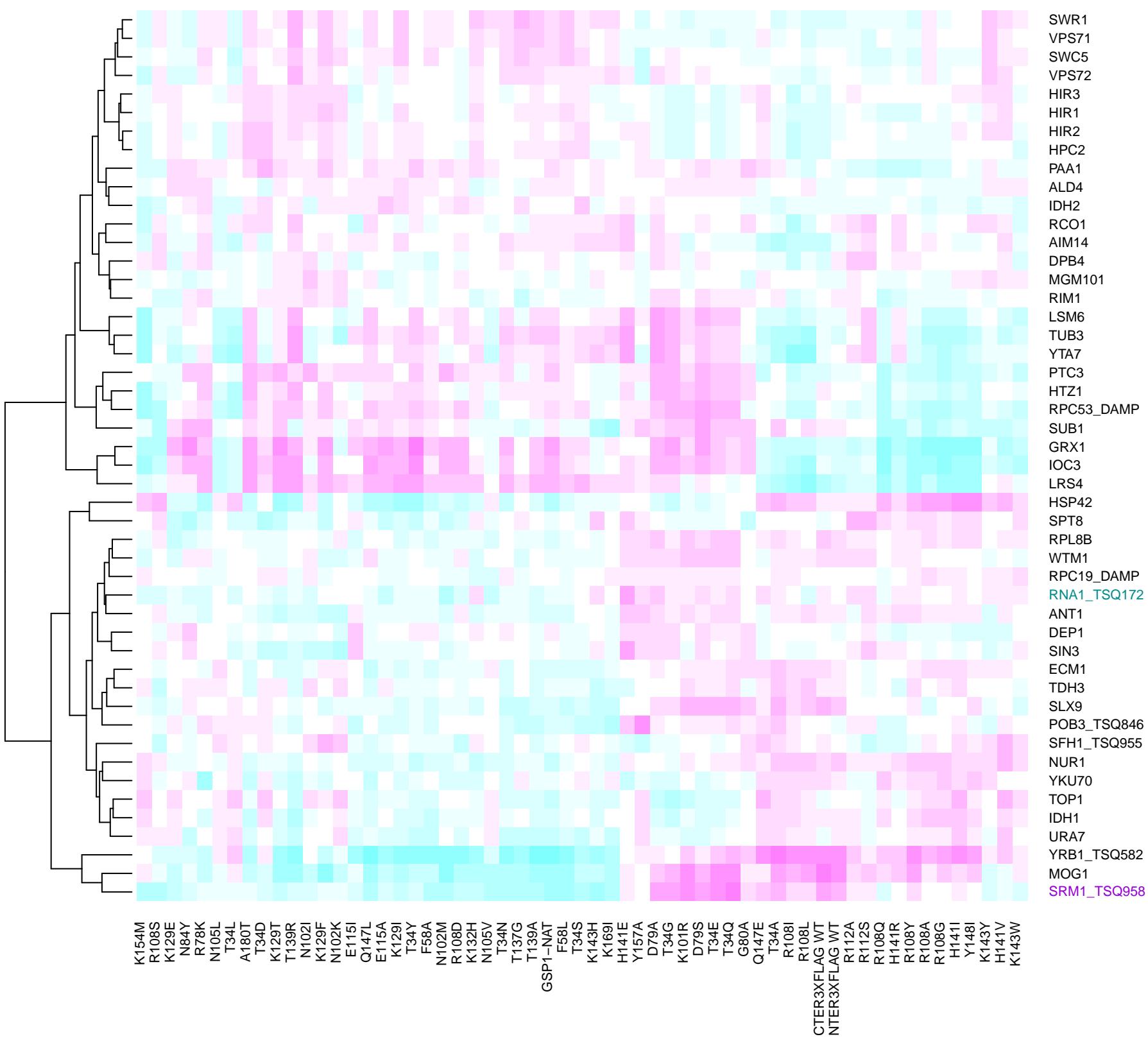


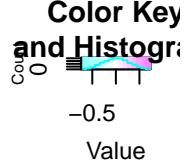
chromatin_GO_30_2



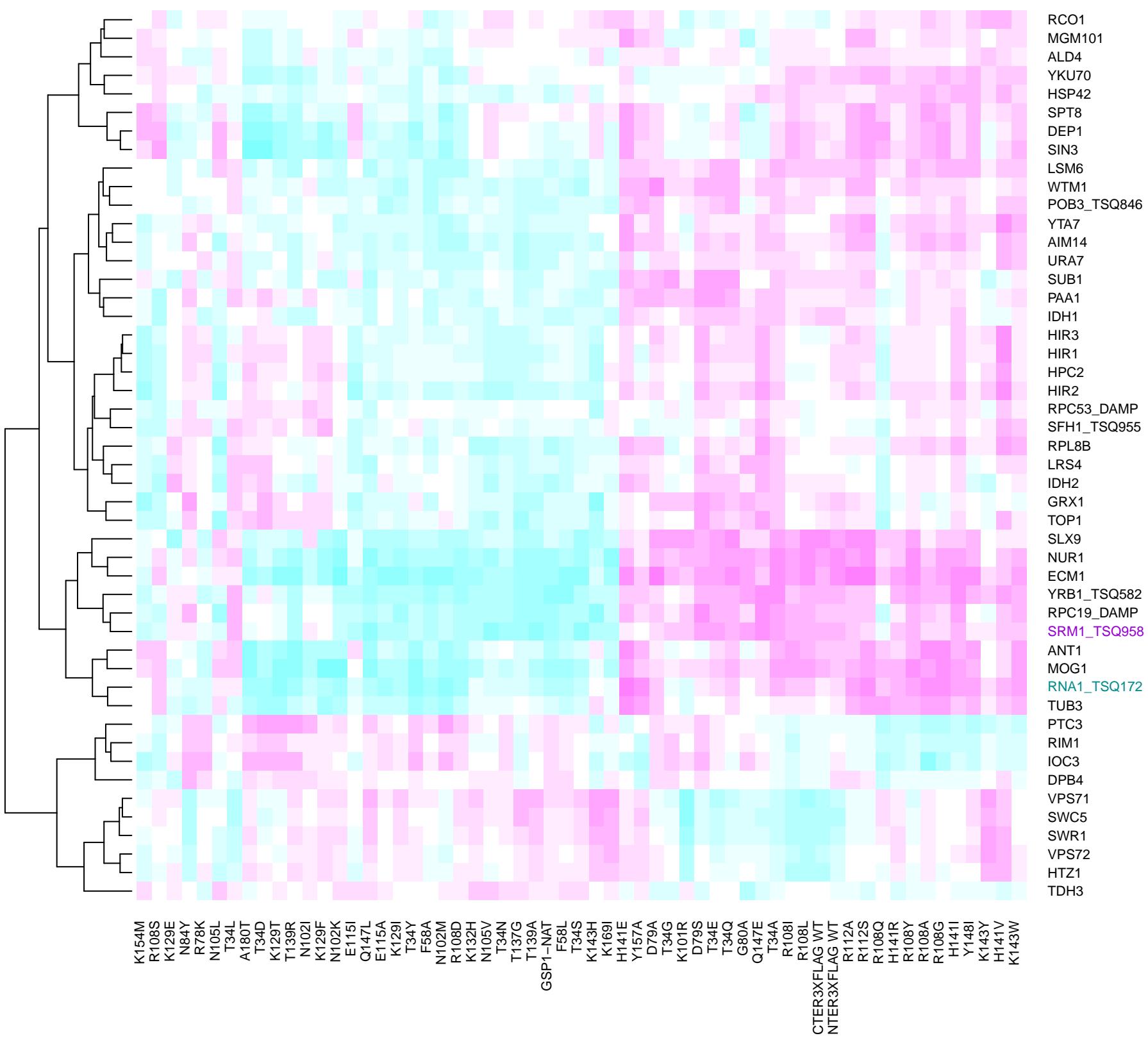


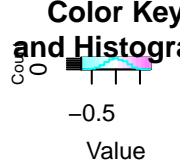
chromosome segregation_GO_30_1



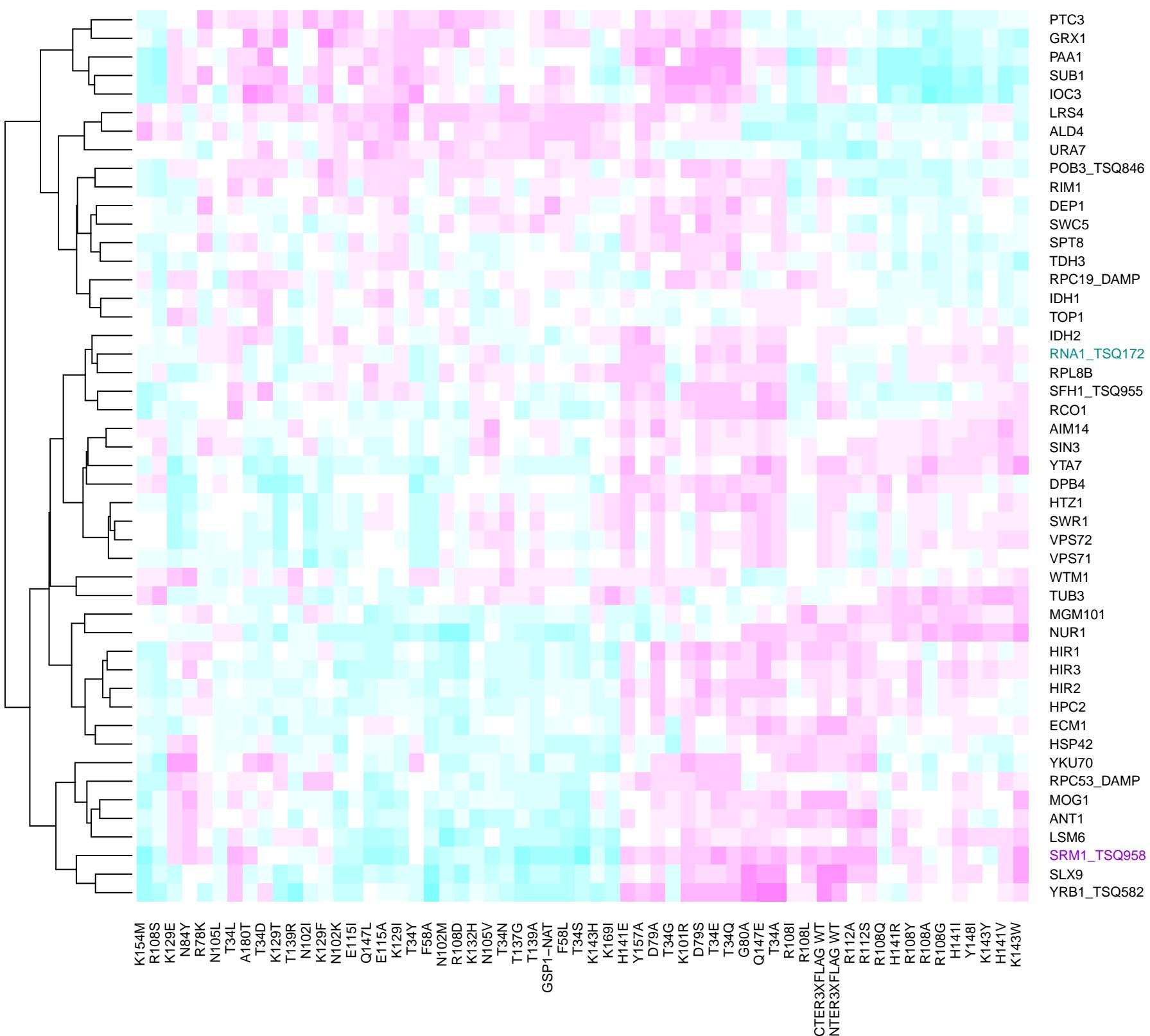


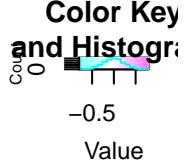
organelle fission_GO_30_4



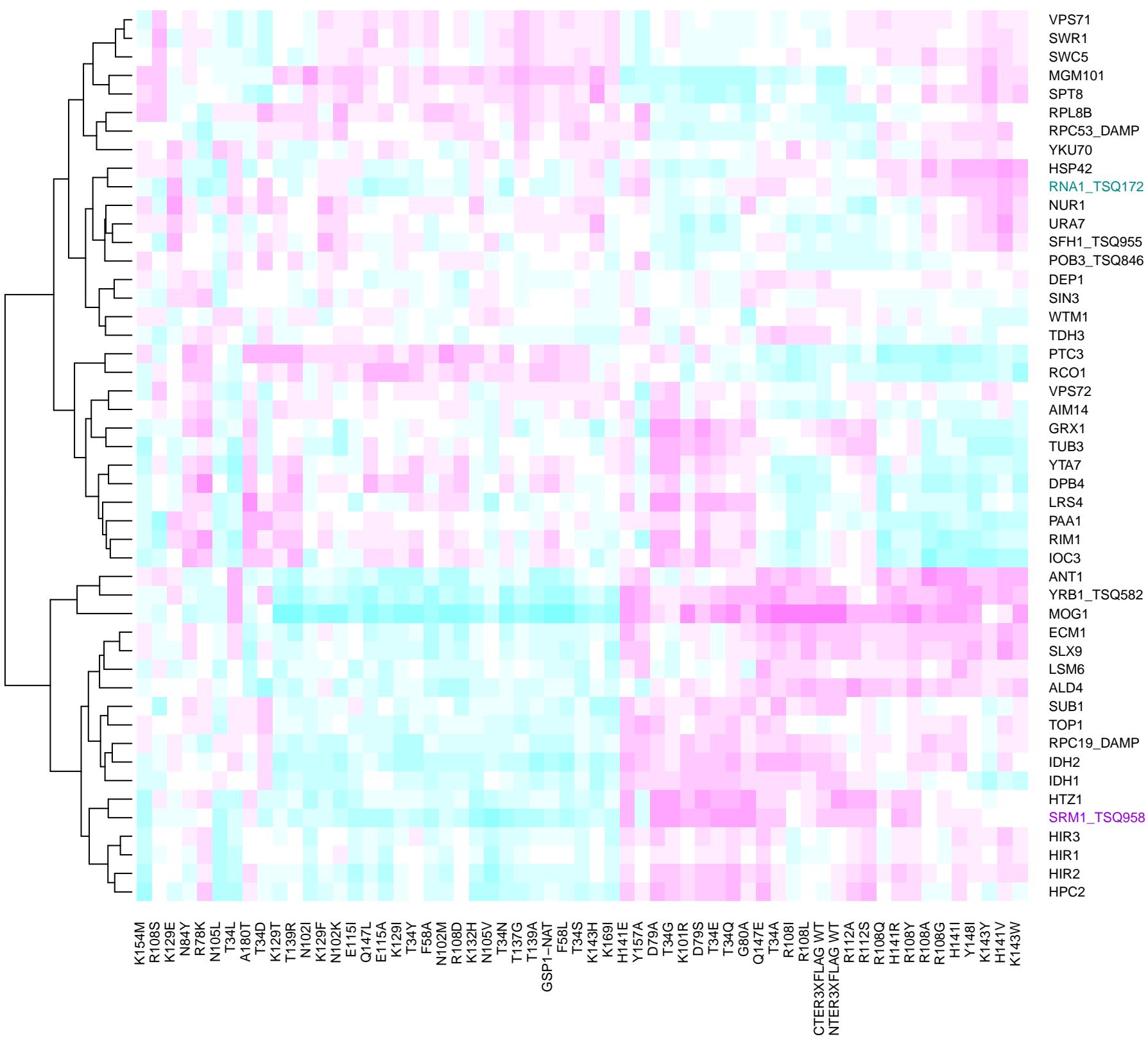


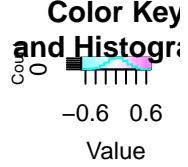
site of polarized growth_GO_30_2



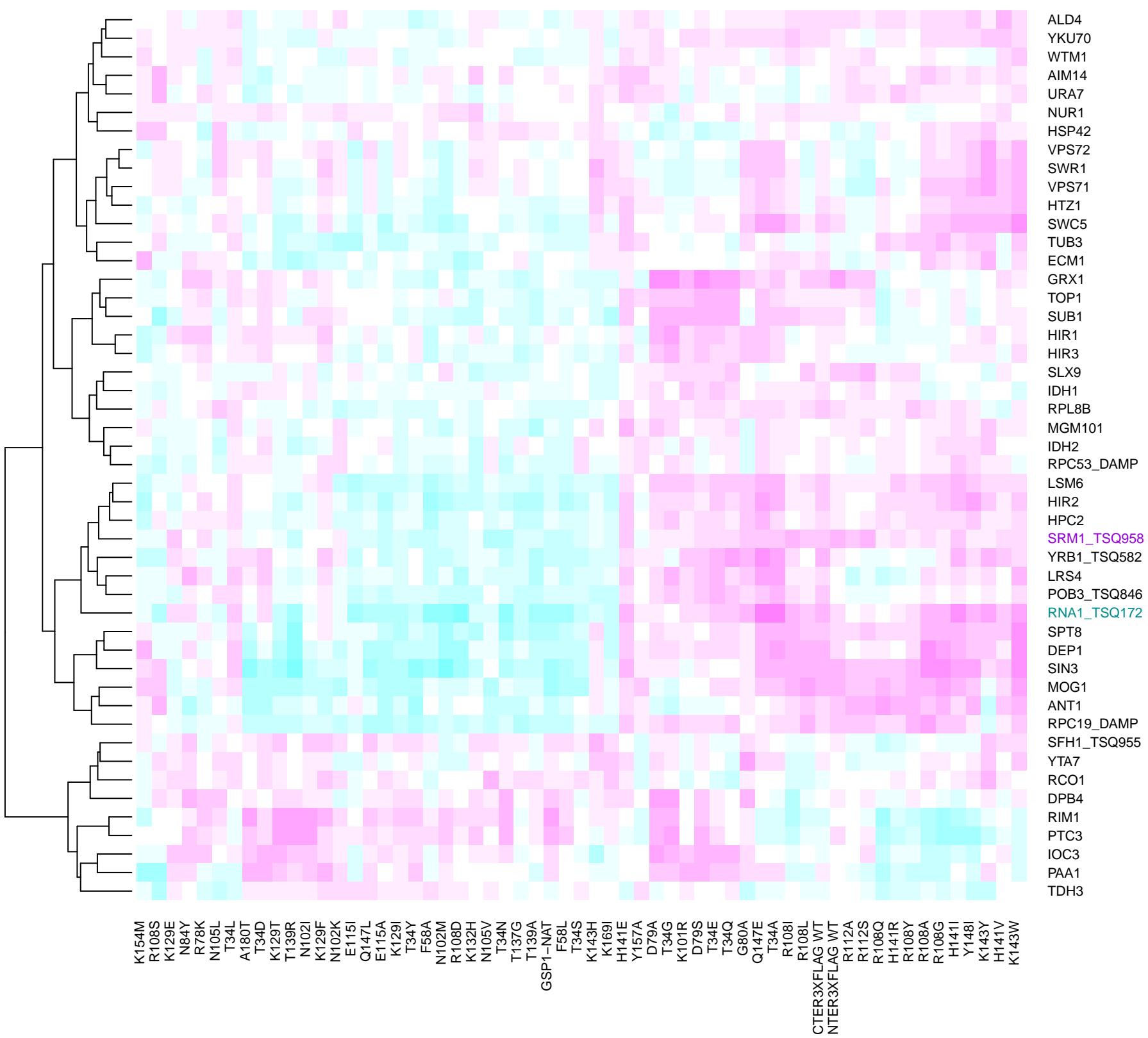


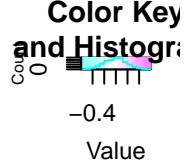
cytoskeleton and microtubules_GO_30_8



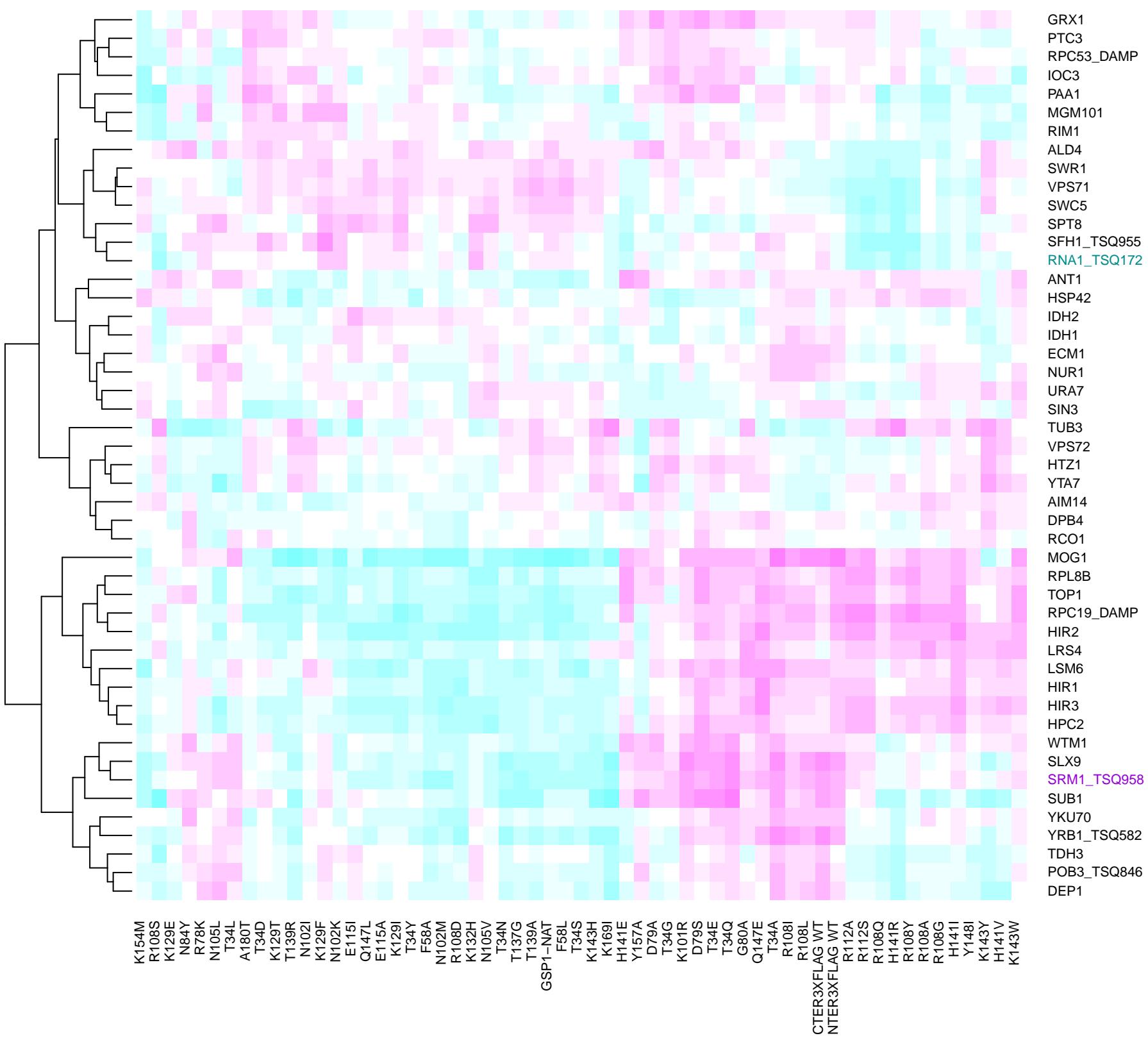


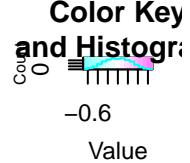
metabolic_GO_30_4



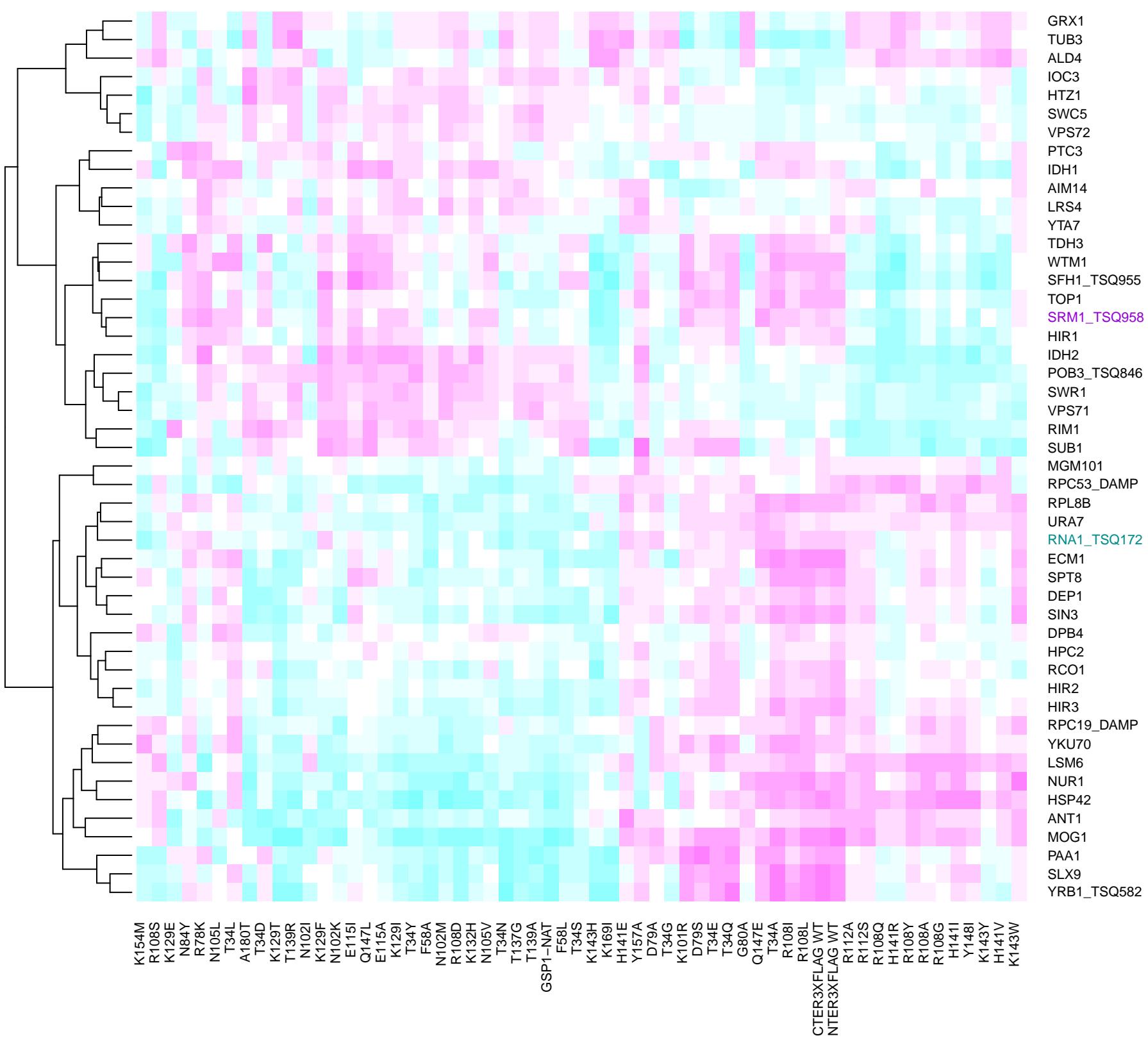


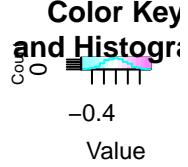
organelle assembly



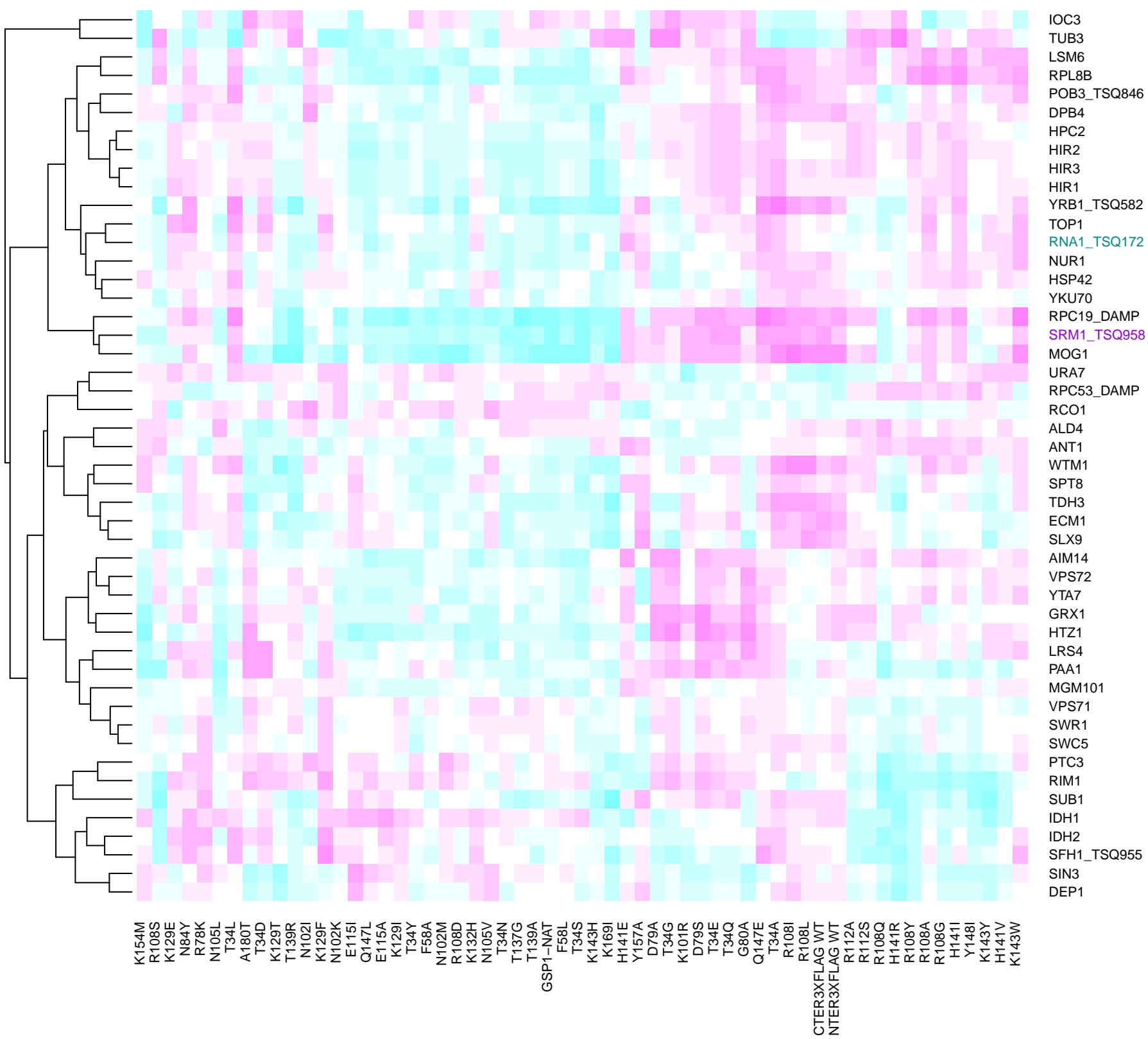


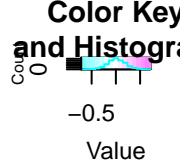
cell cycle_GO_30_6



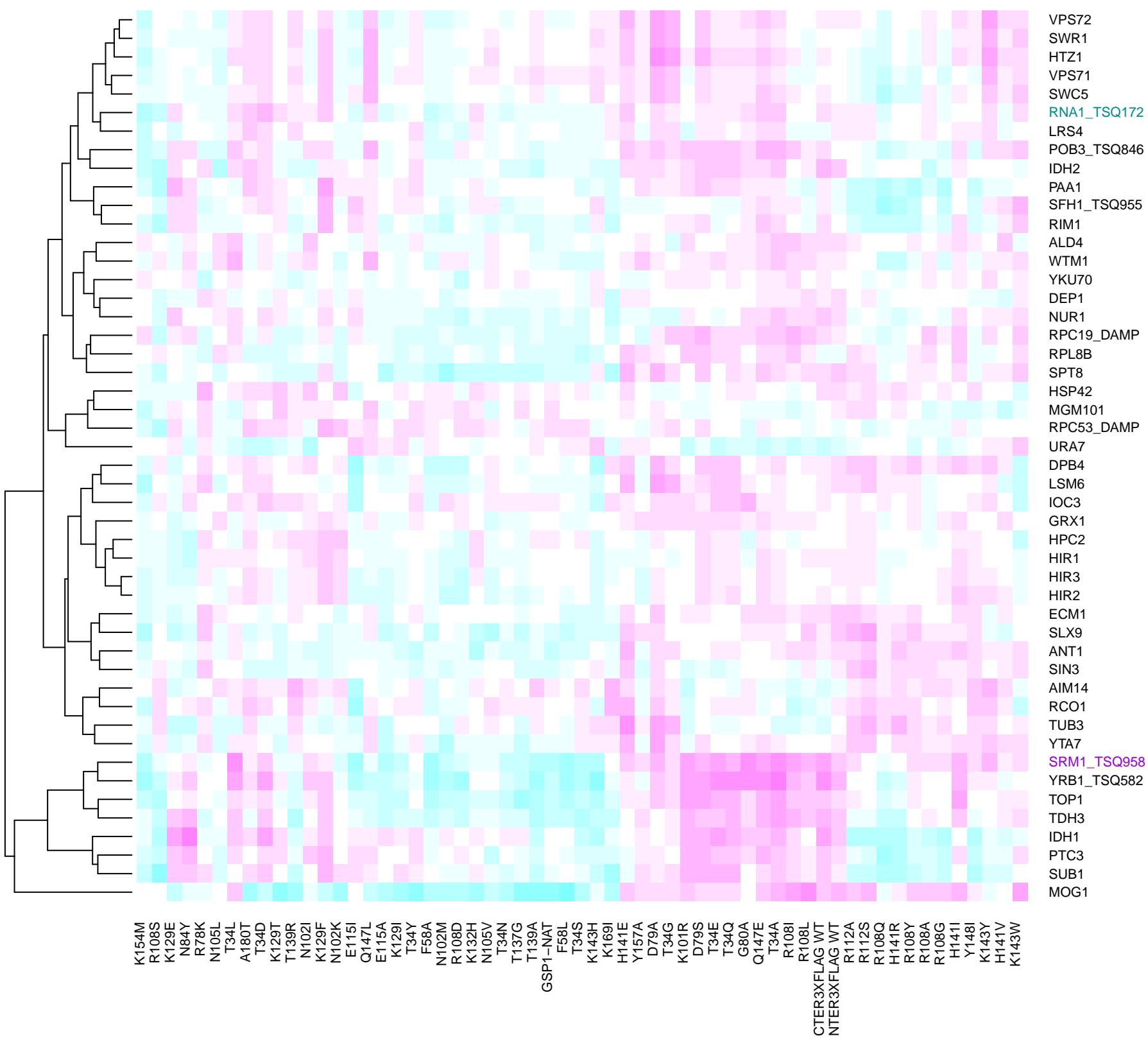


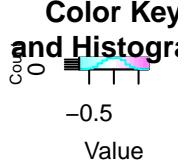
chromatin_GO_30_1



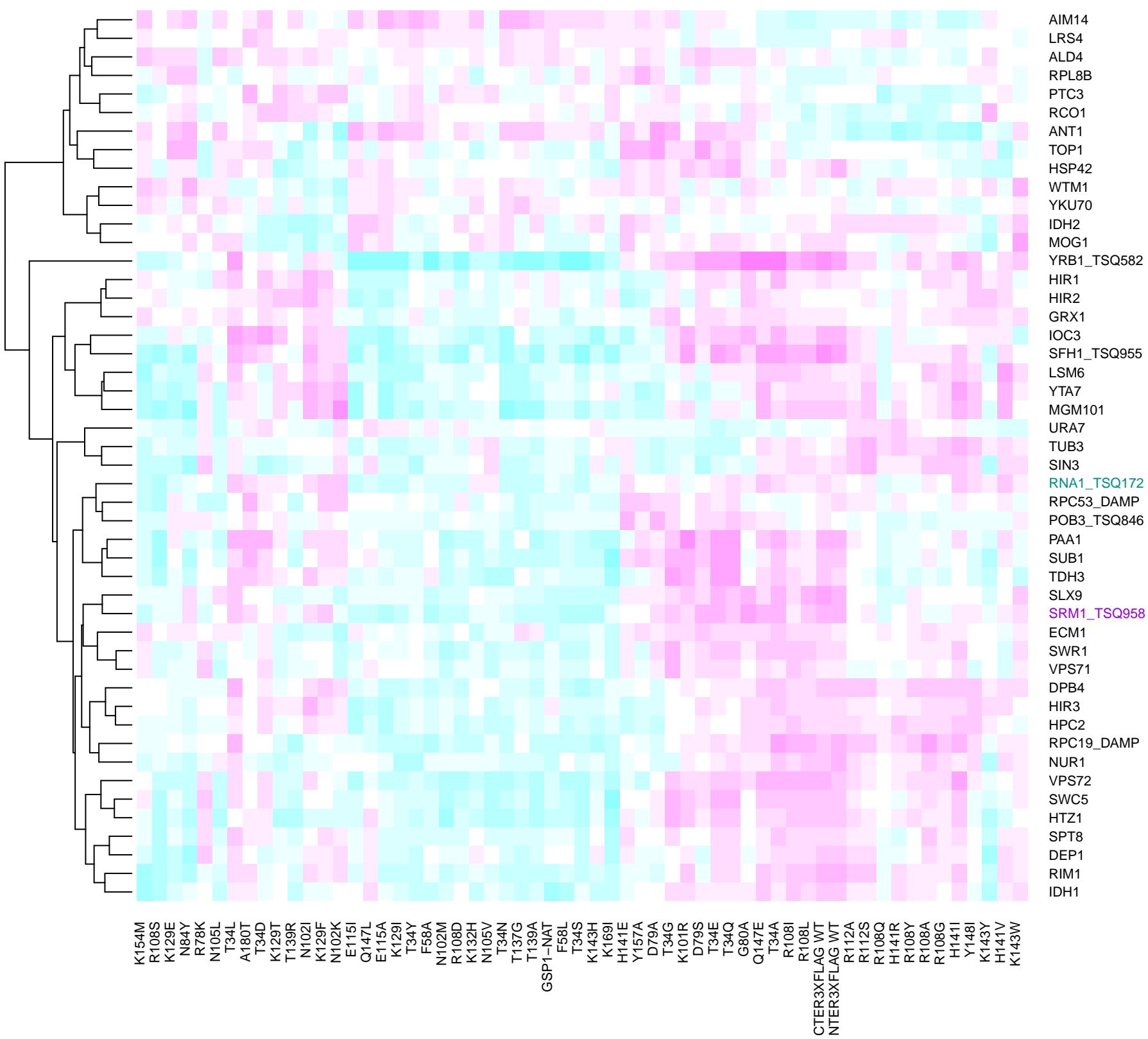


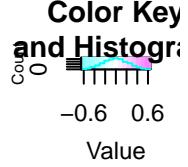
DNA repair_GO_30_2



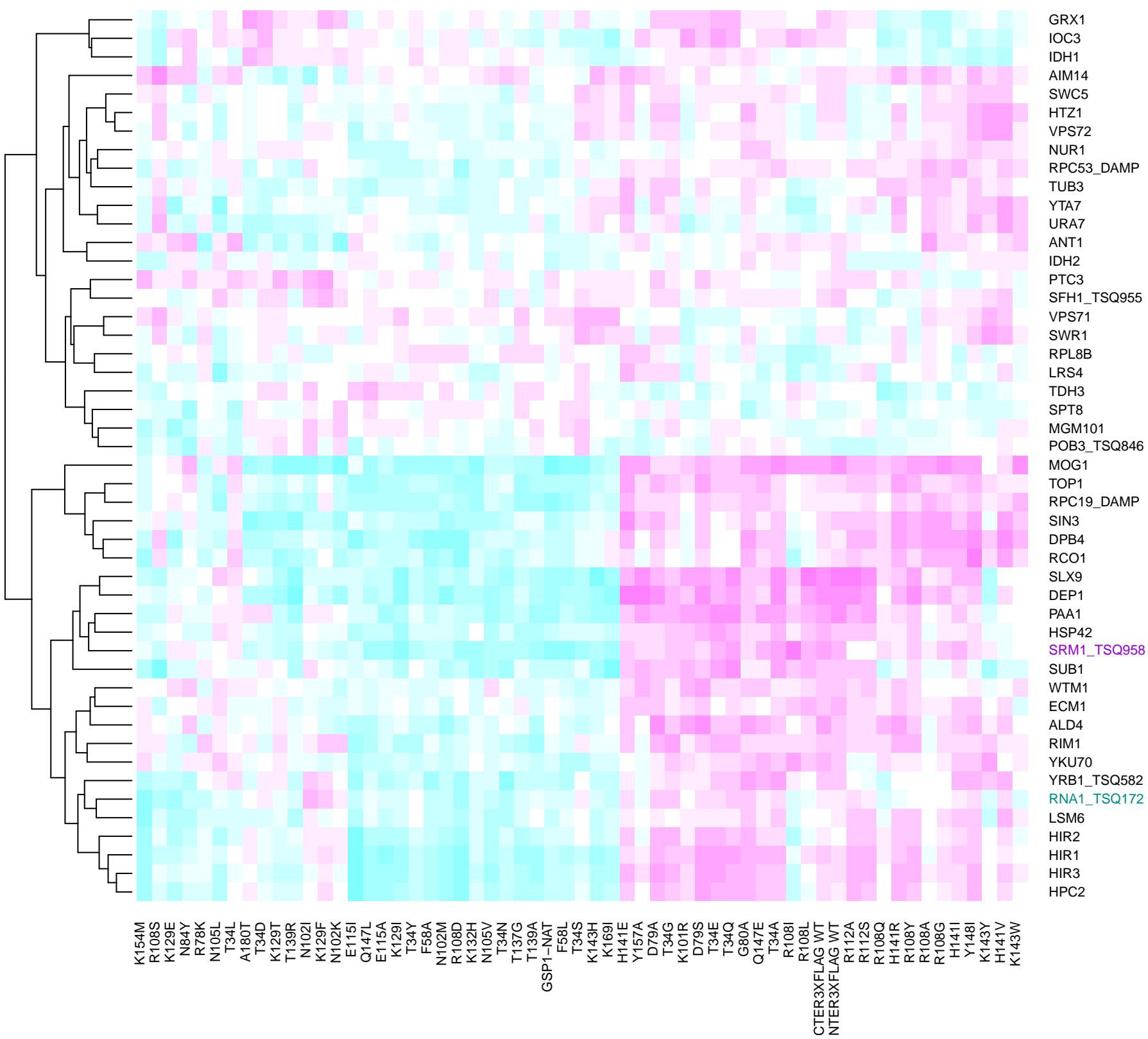


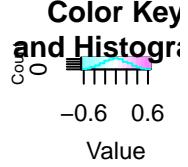
endomembrane system_GO_30_2



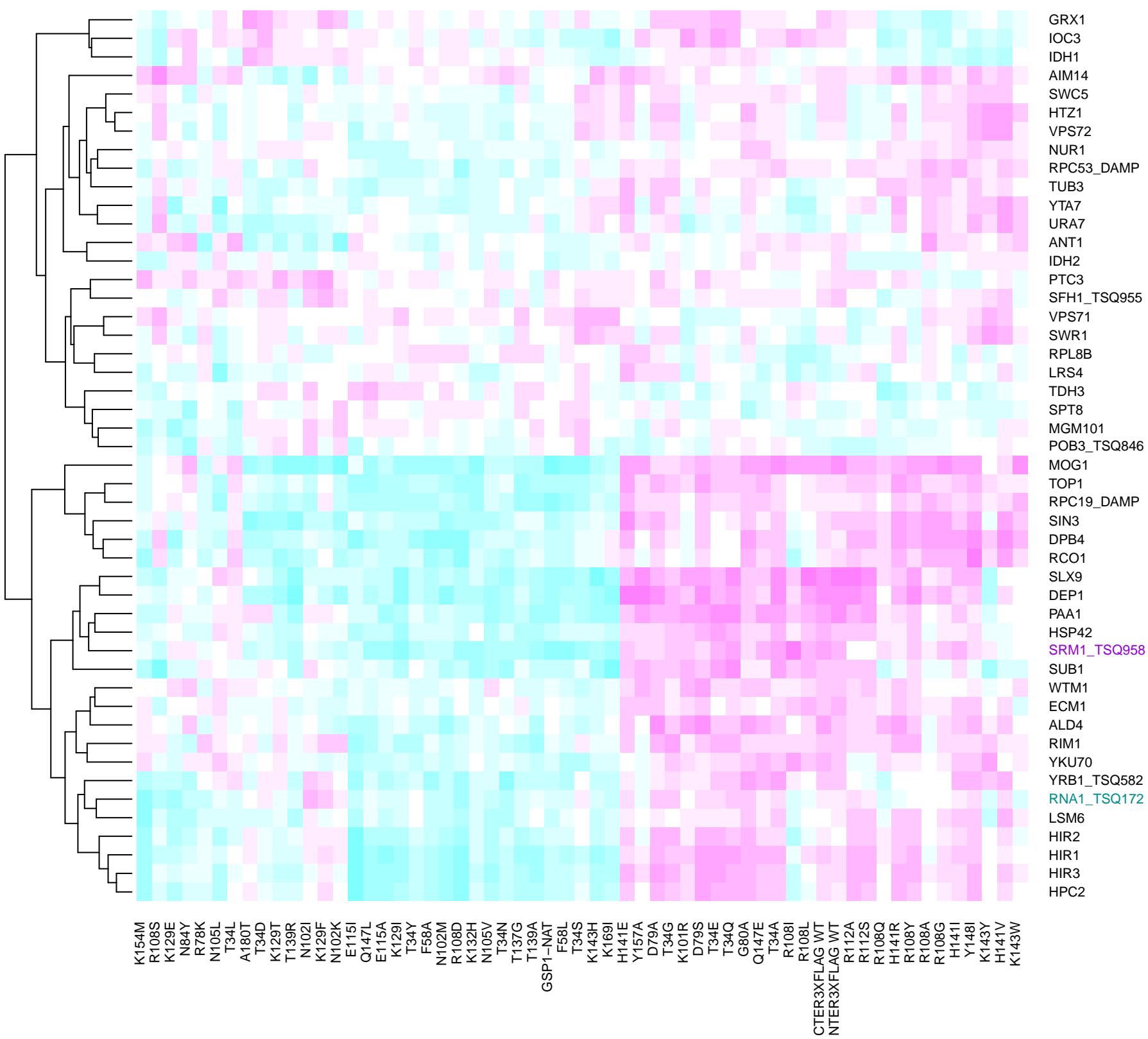


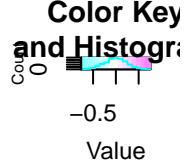
endoplasmic reticulum_GO_30_6



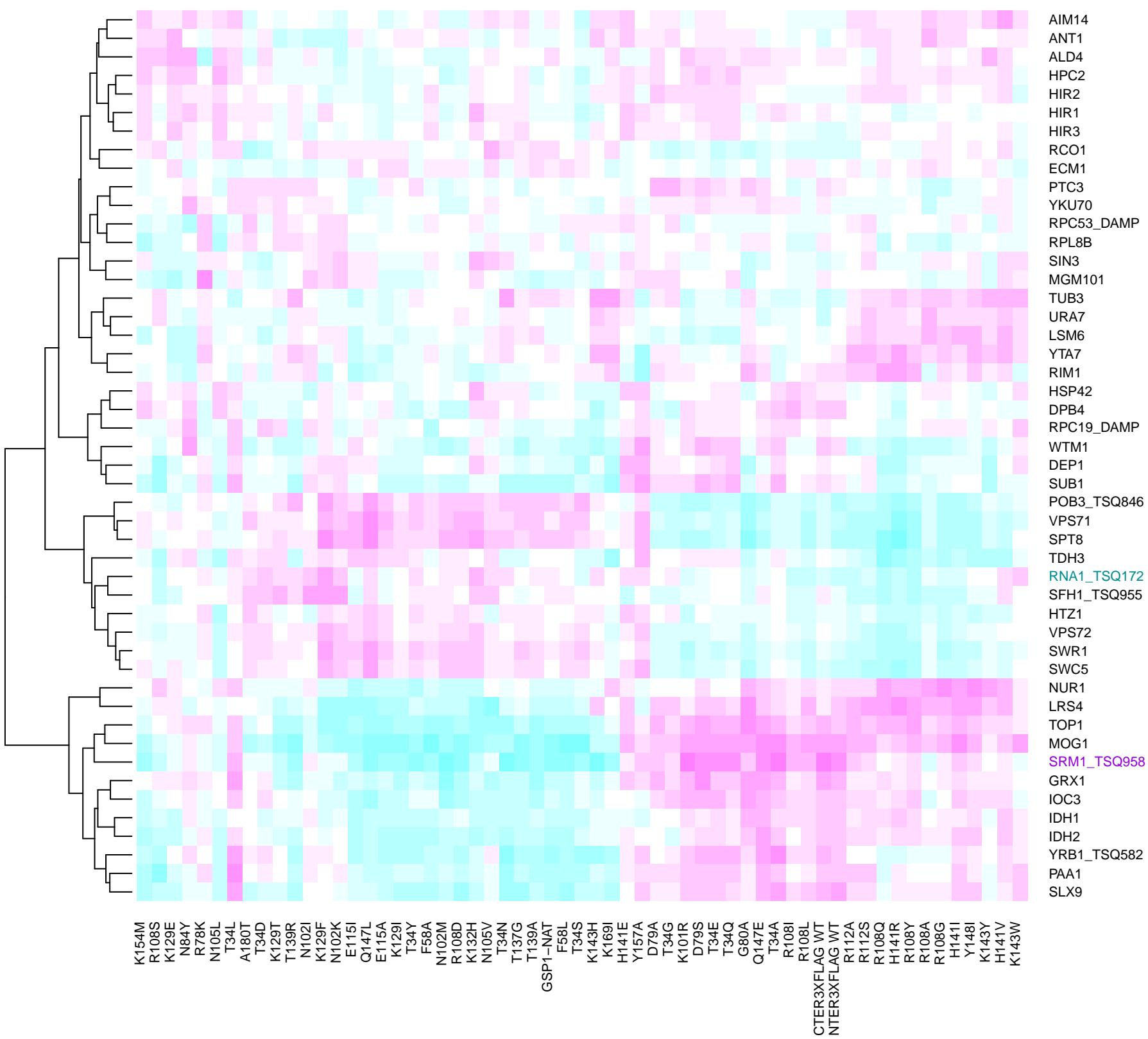


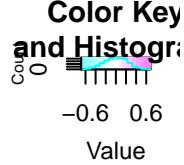
ER_GO_30_6



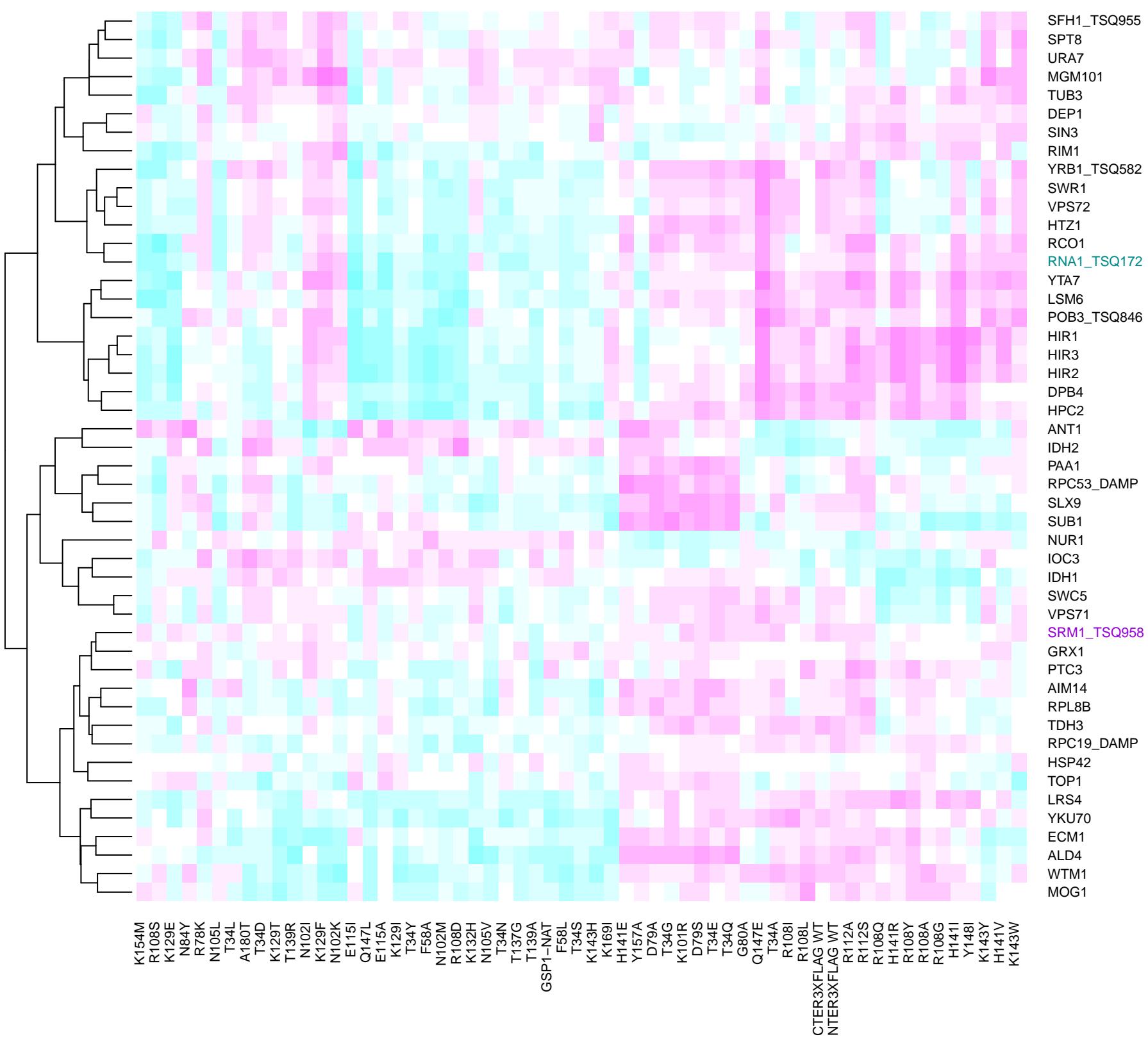


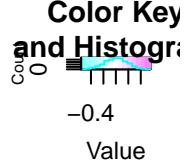
Golgi and ER_GO_30_15





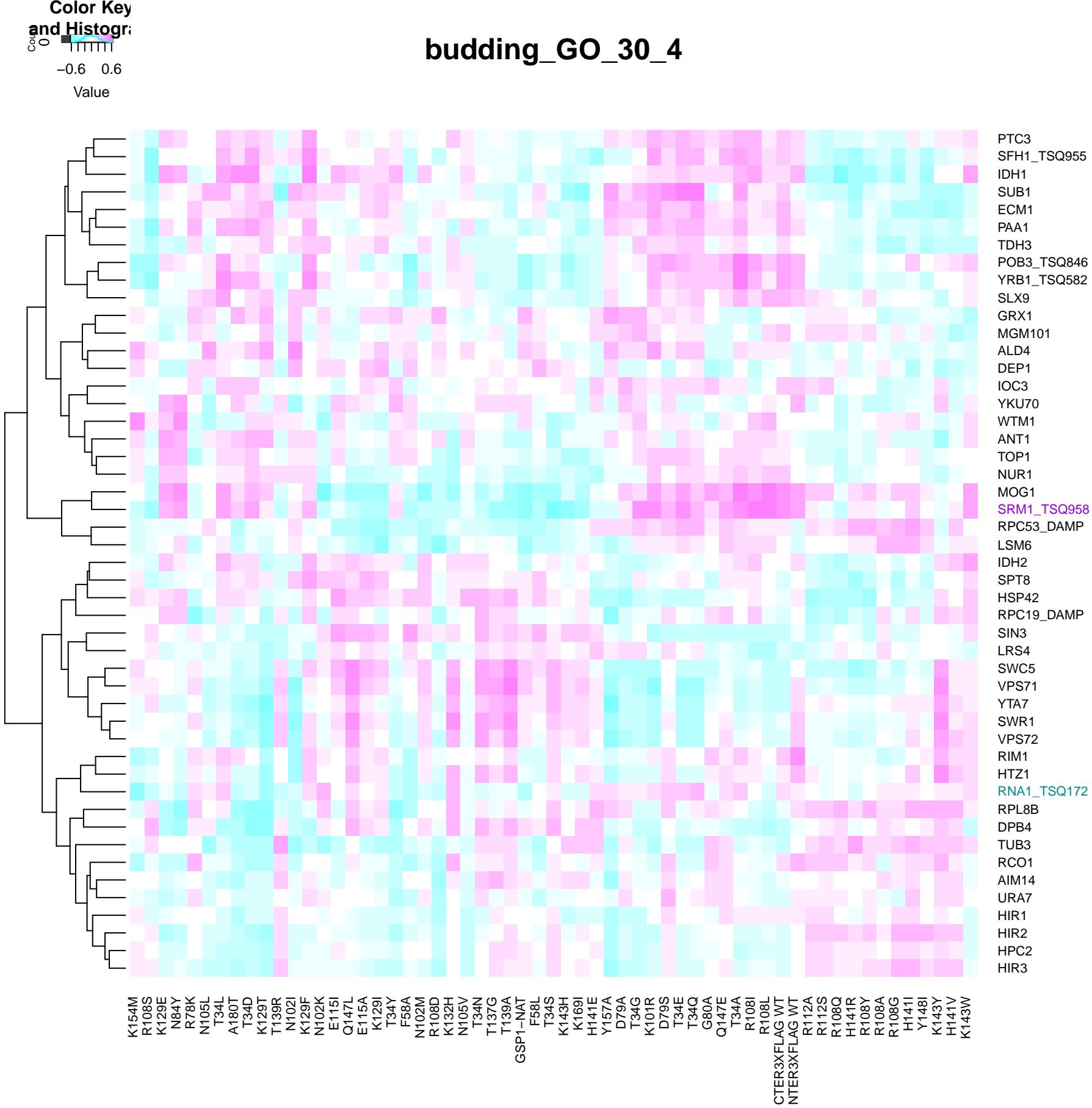
lipid metabolic process_GO_30_3

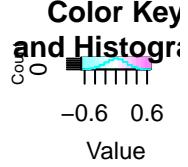




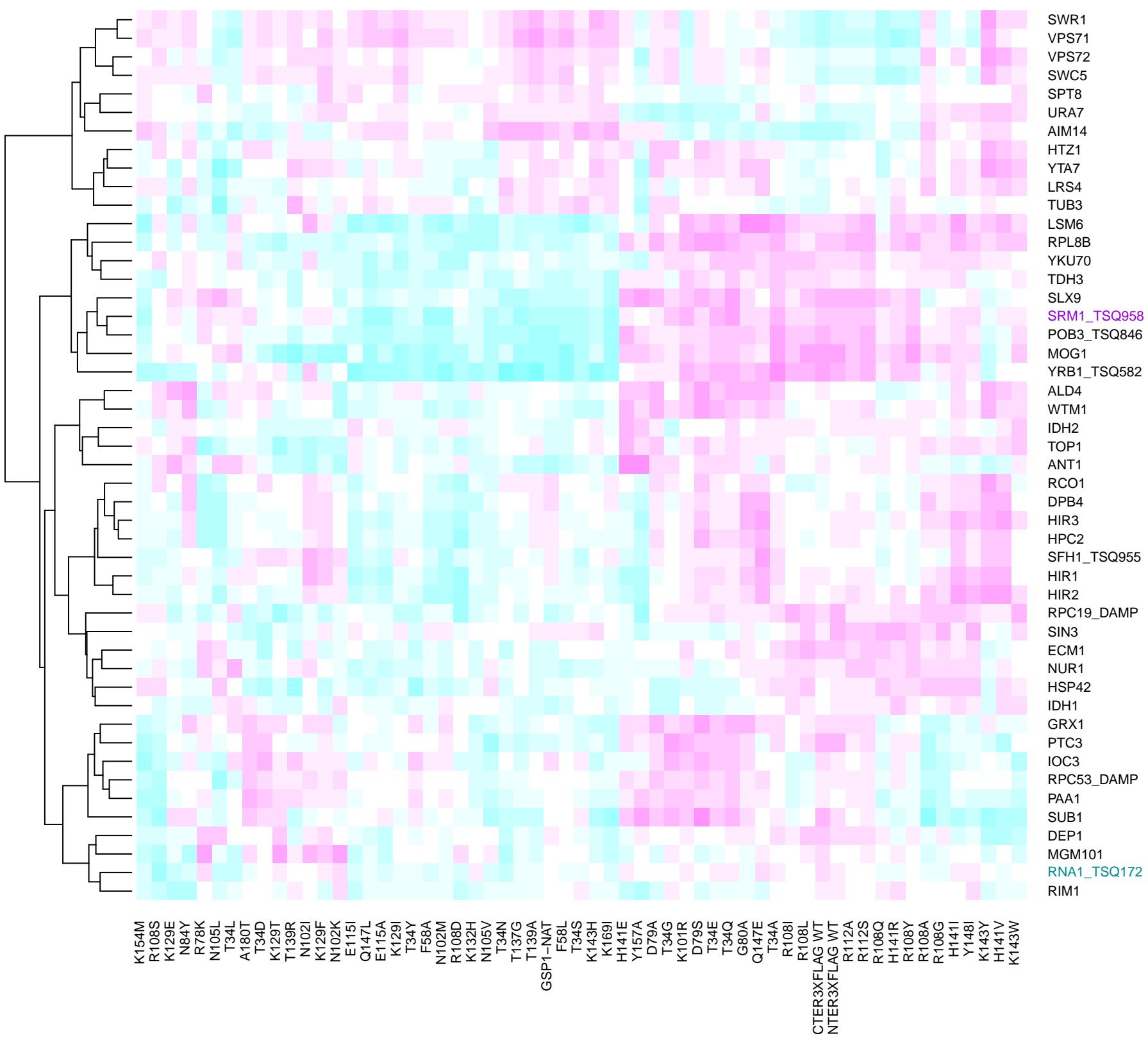
metabolic_GO_30_2

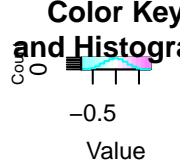




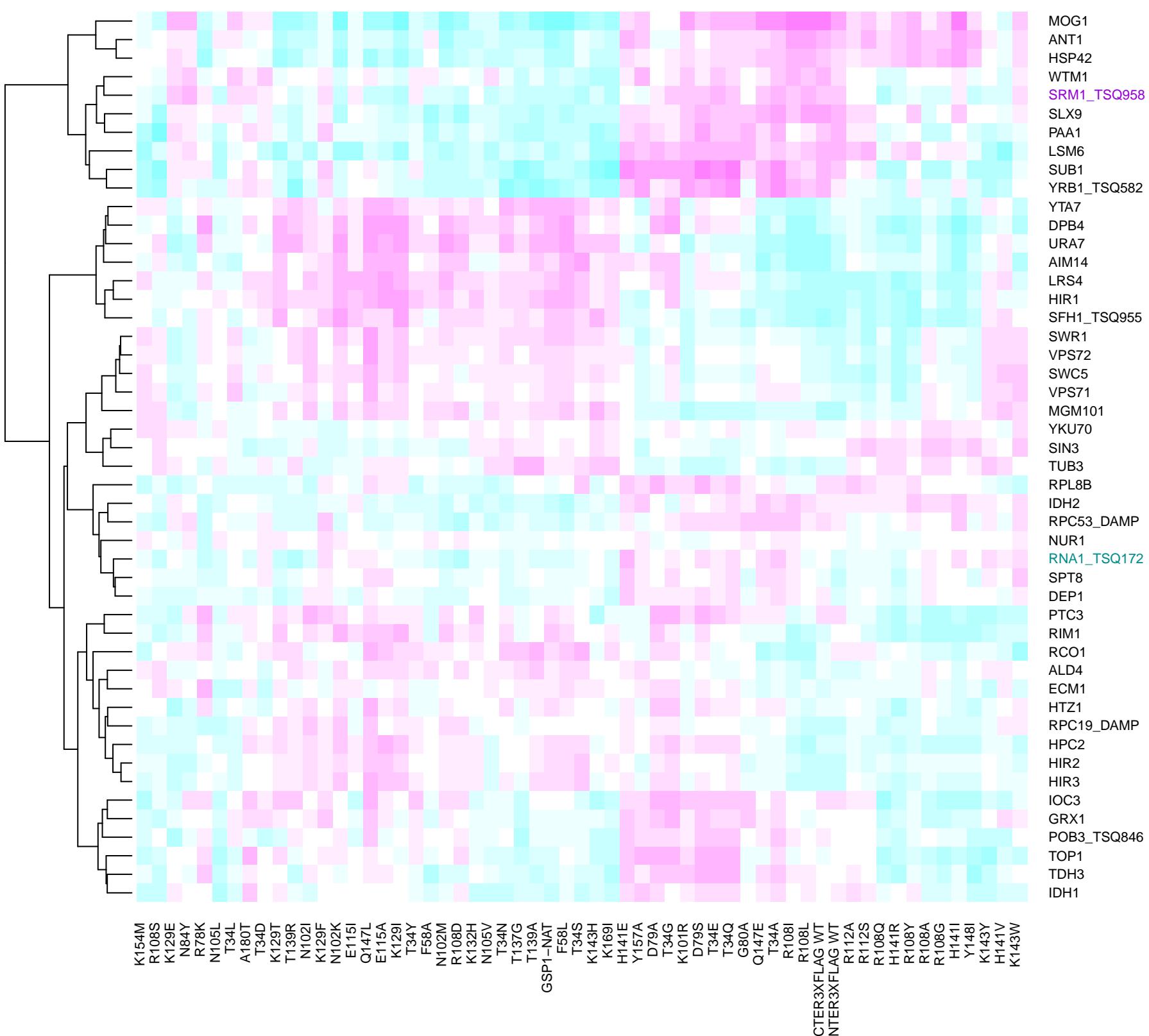


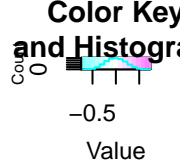
organelle assembly_GO_30_1



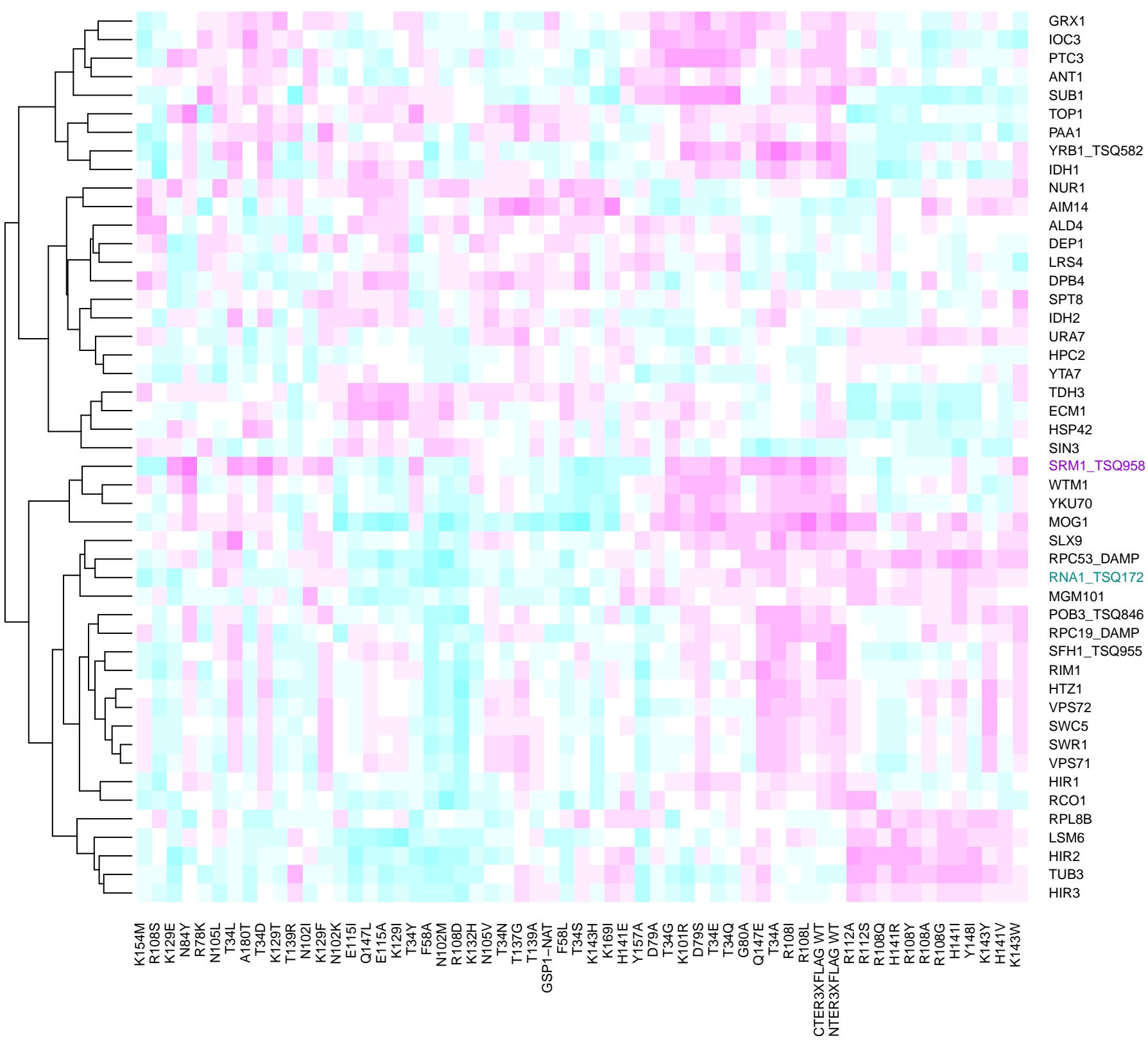


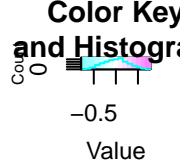
chromatin_GO_30_5



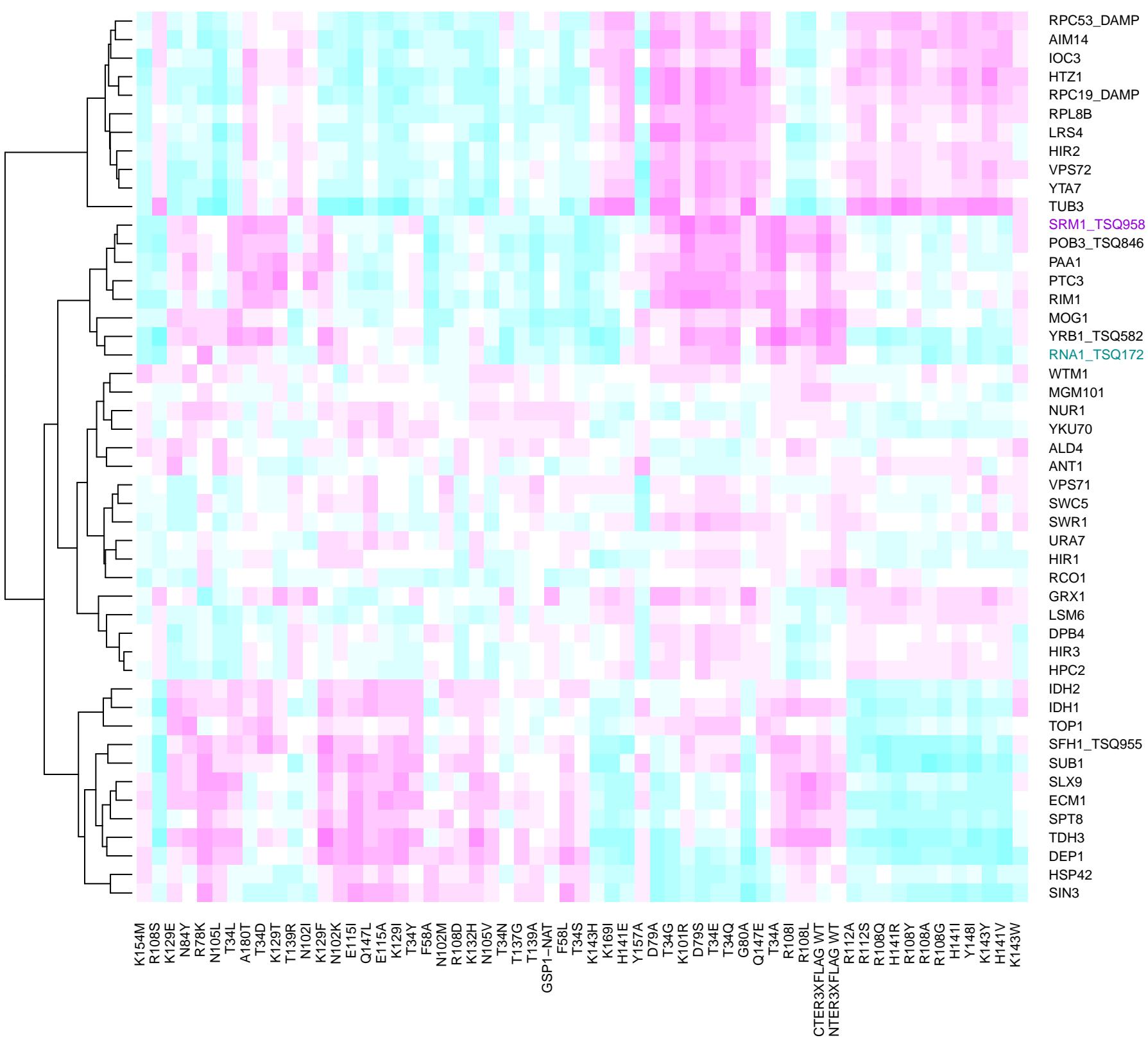


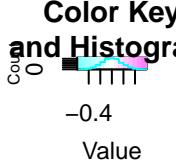
cytoskeleton and microtubules_GO_30_7



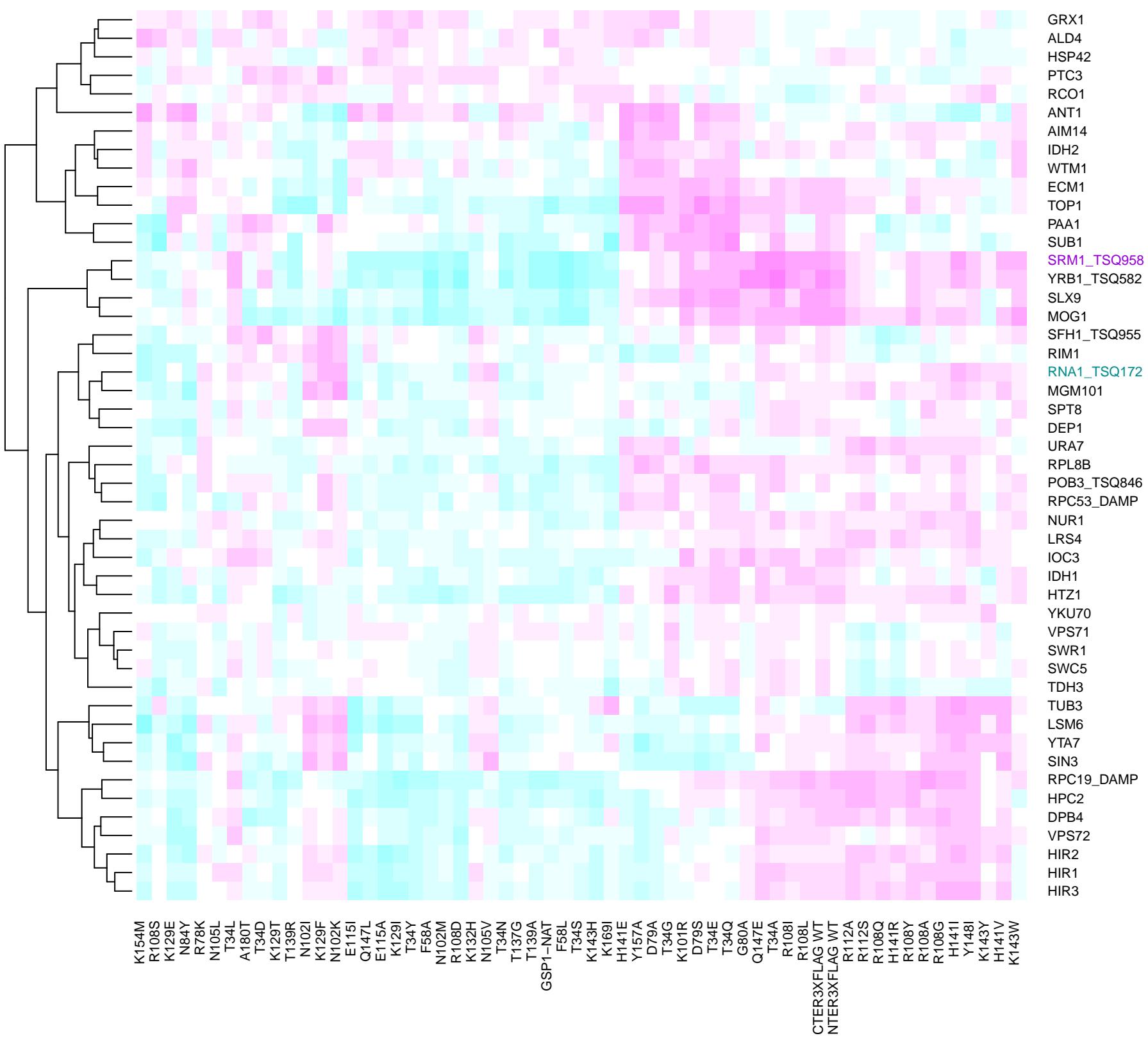


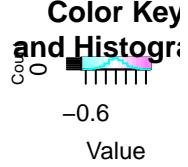
cytoskeleton_GO_30_1



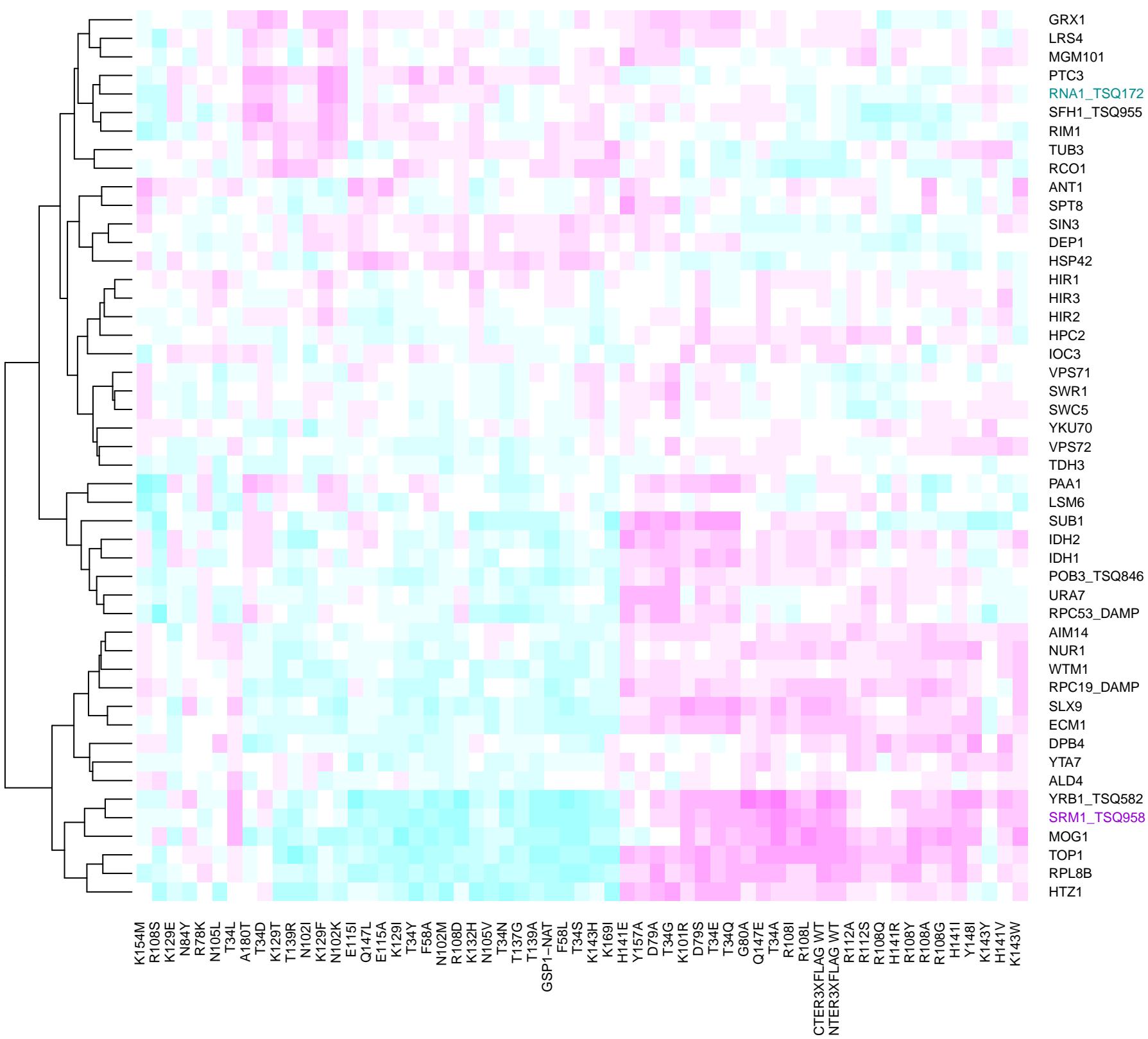


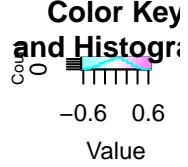
cytoplasmic vesicle



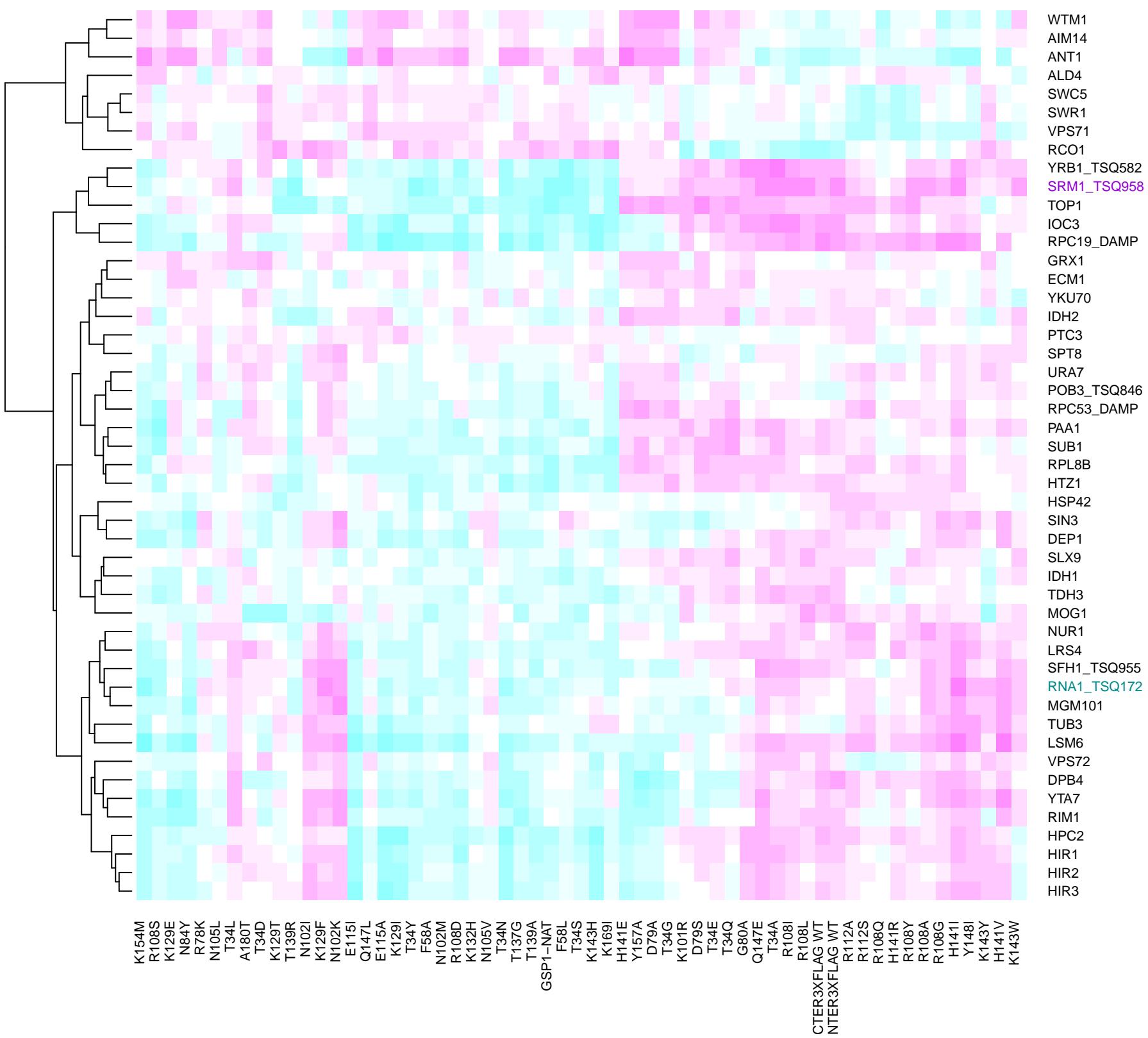


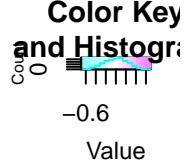
cytoplasmic vesicle_GO_30_1



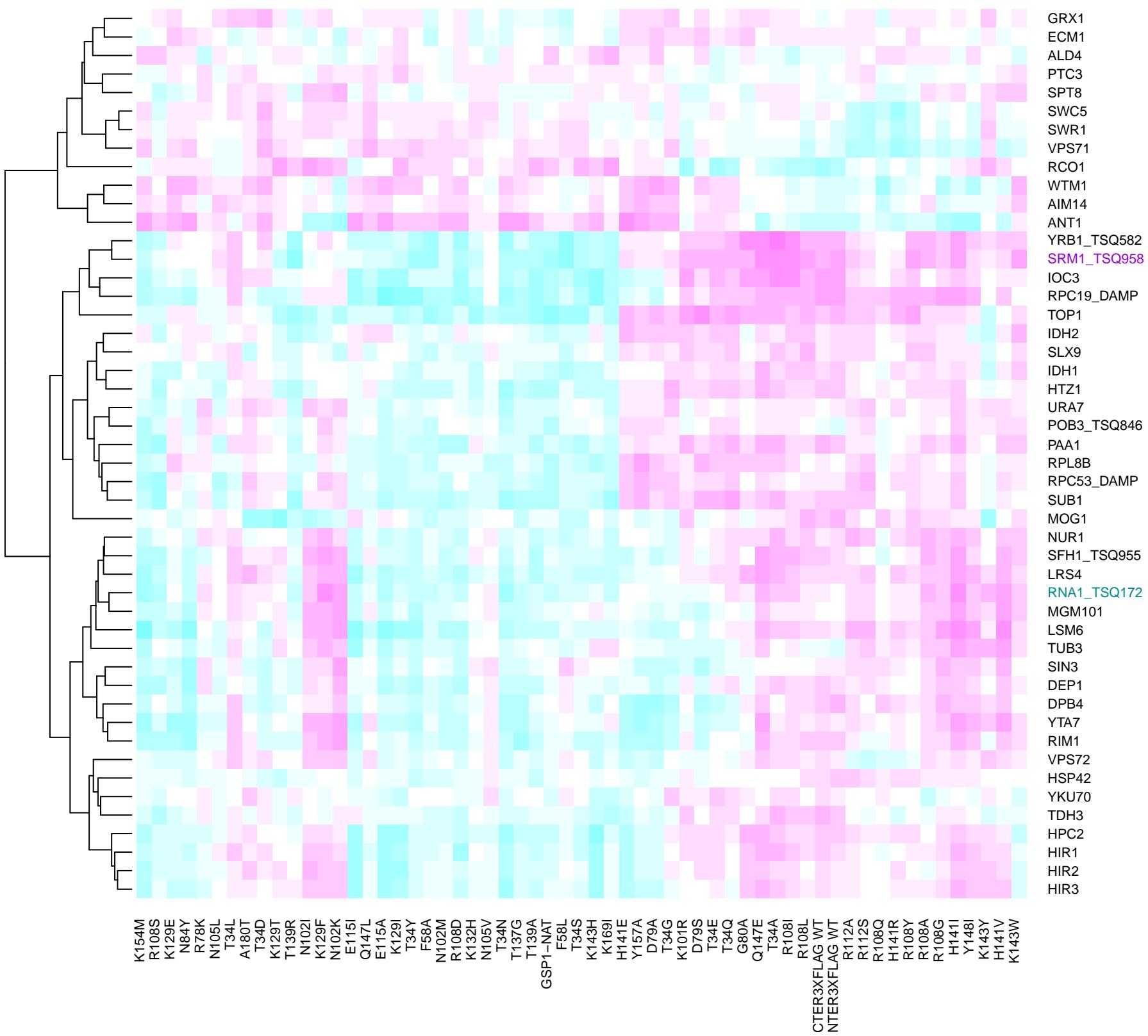


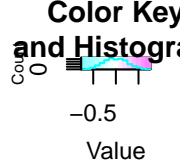
endosomal transport



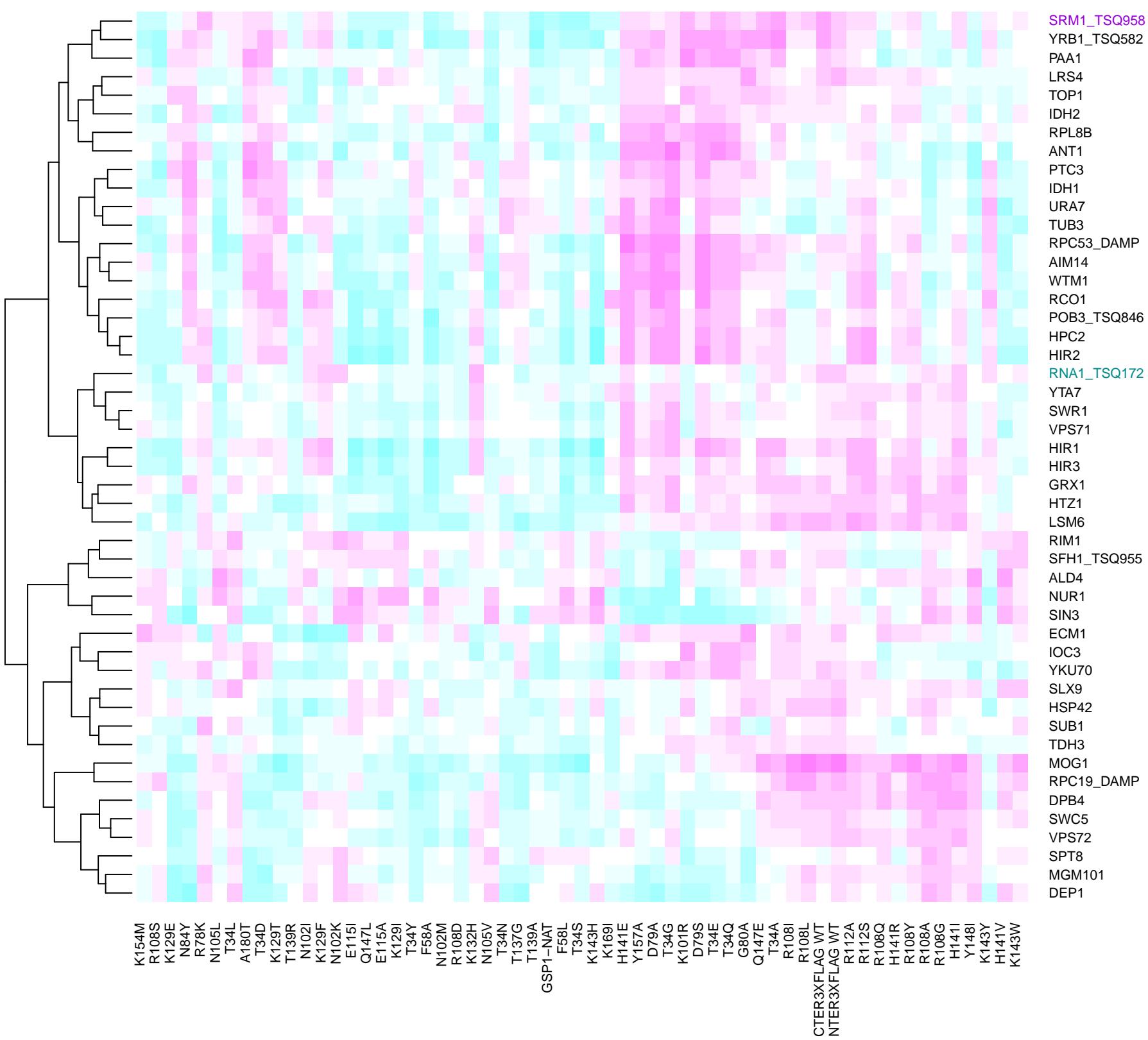


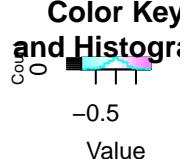
endosomal transport_GO_30_1



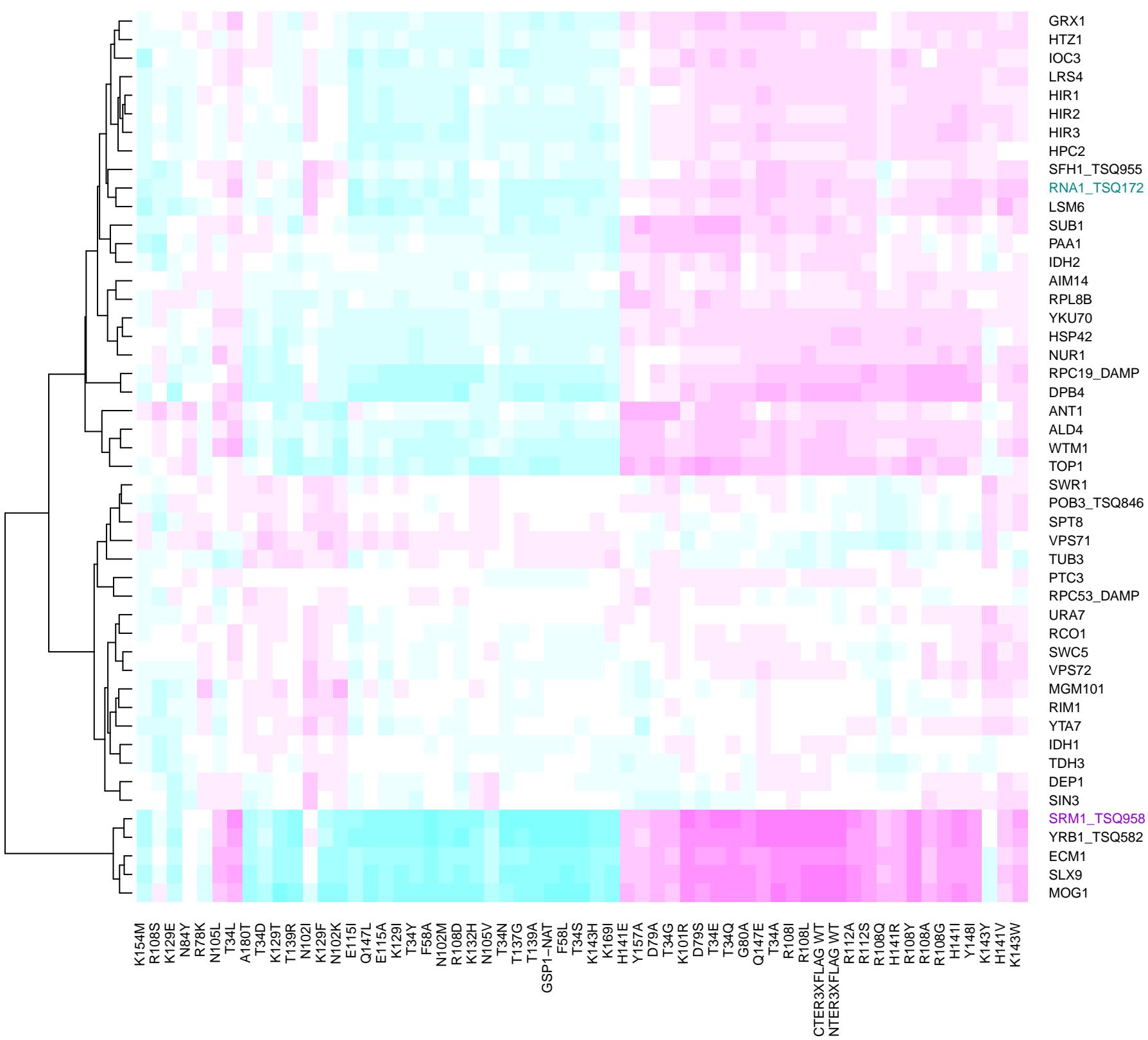


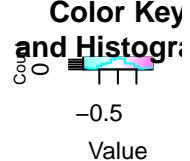
Golgi and ER_GO_30_10



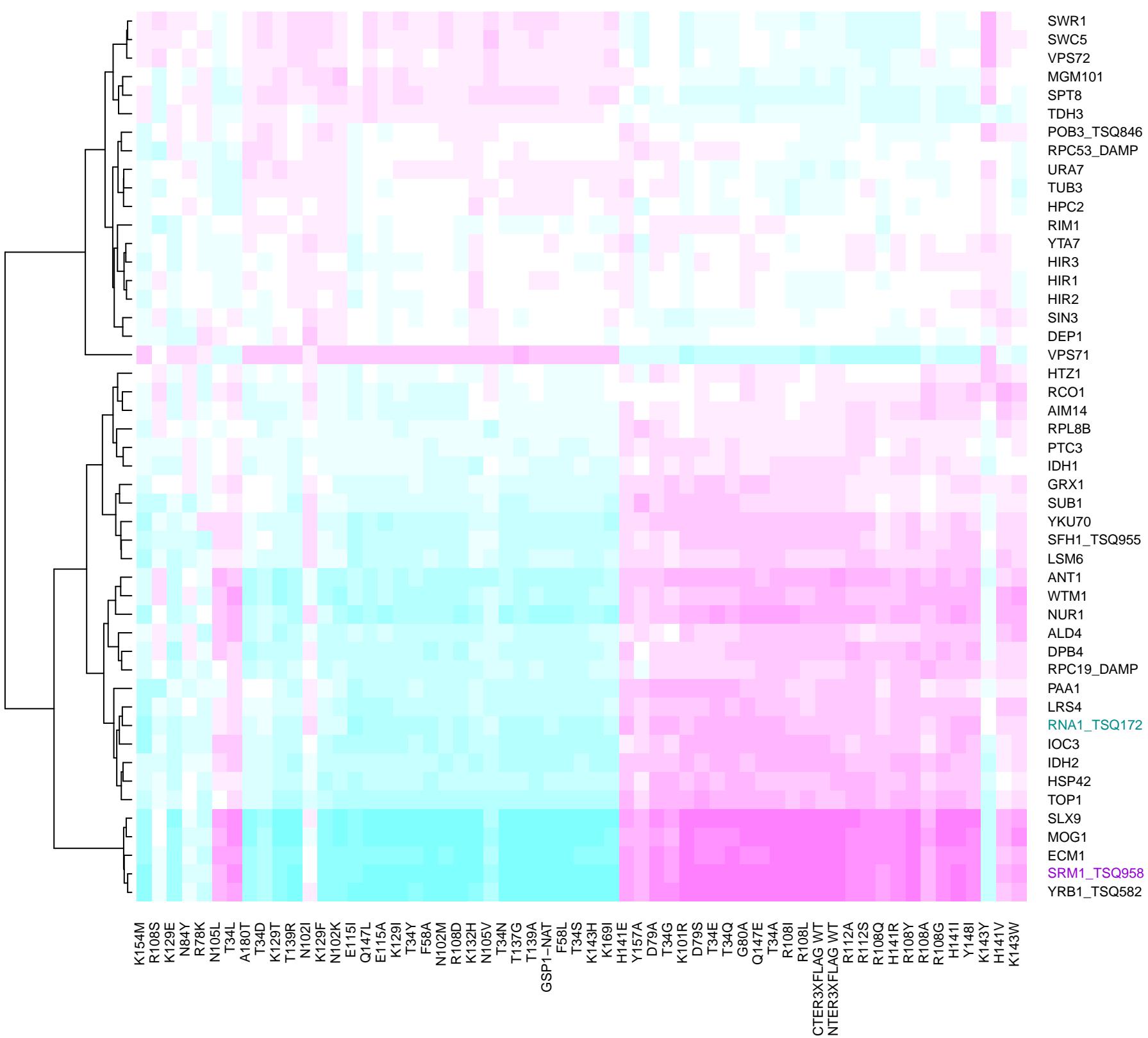


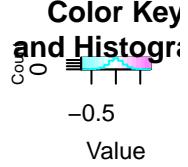
protein targeting



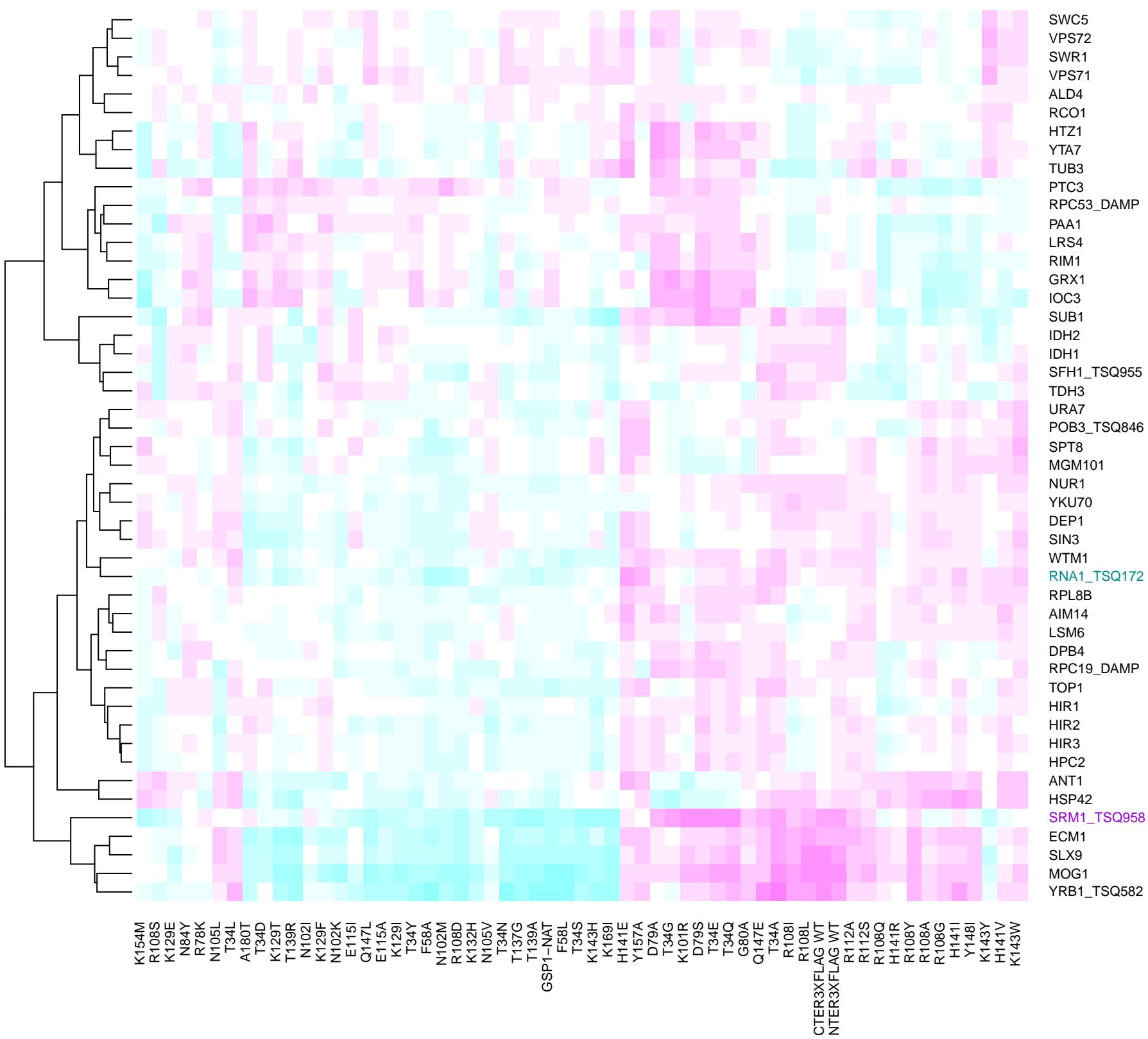


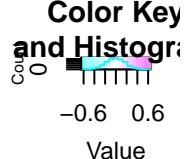
protein targeting_GO_30_1



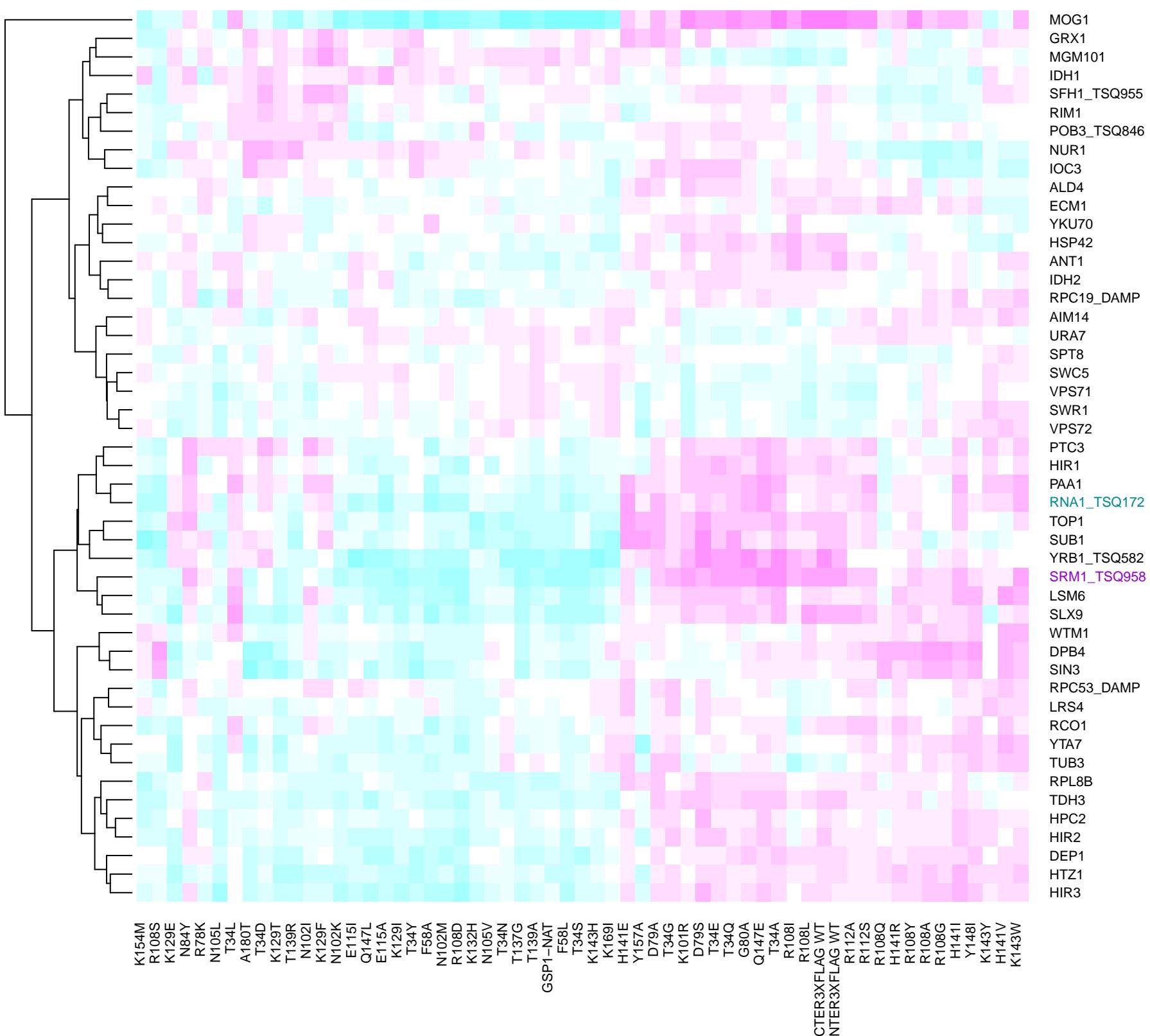


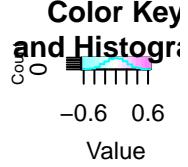
organelle fission



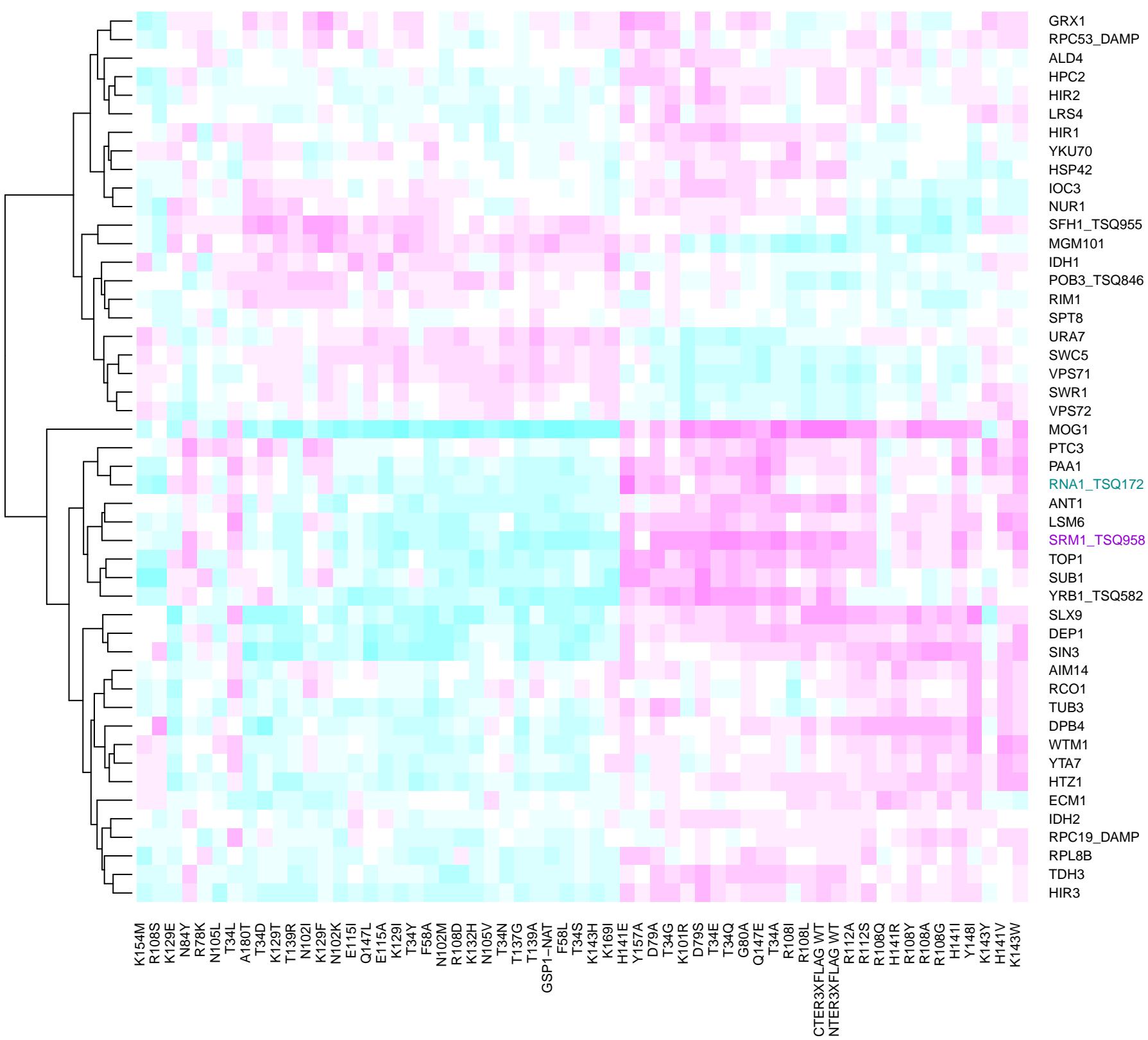


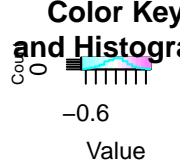
cell wall



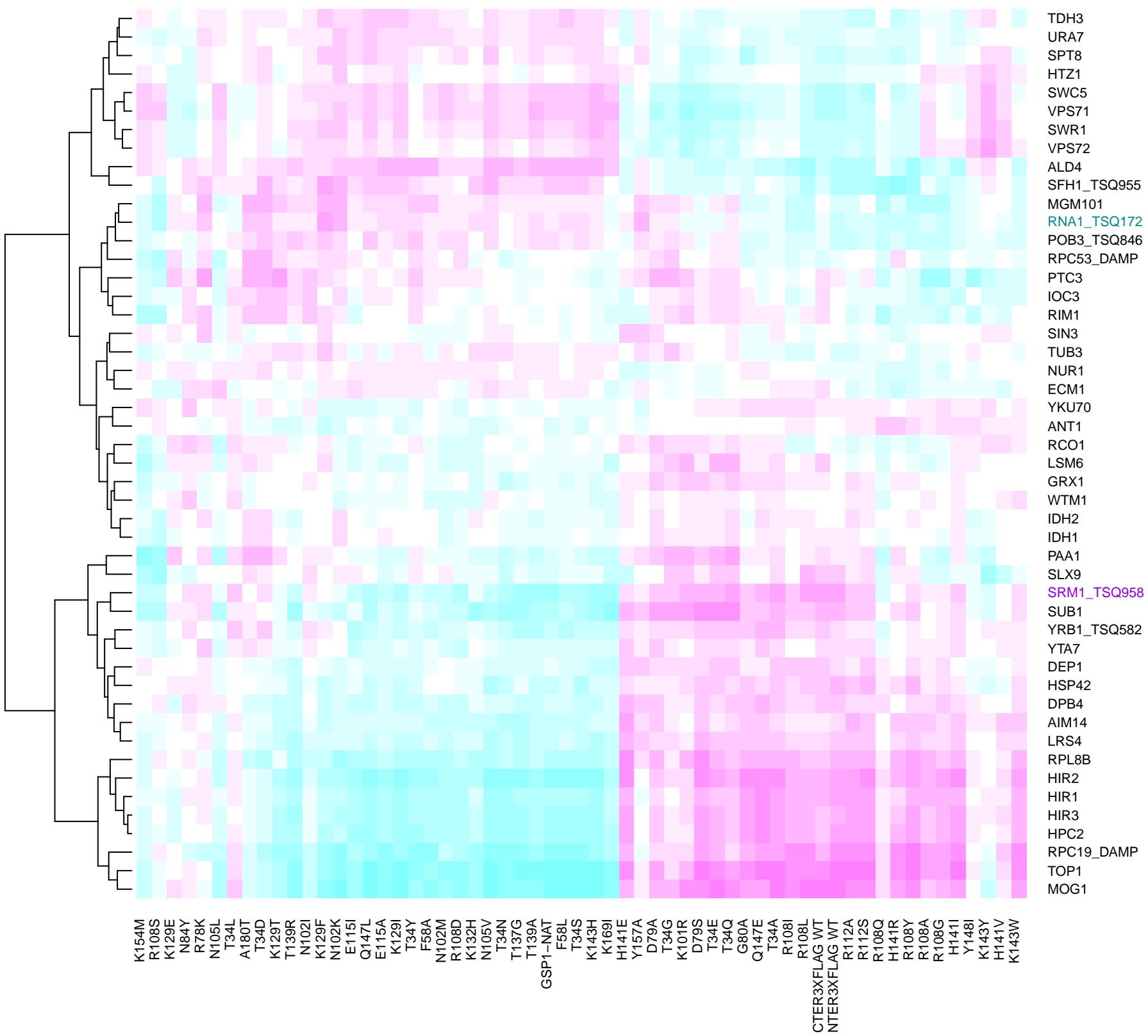


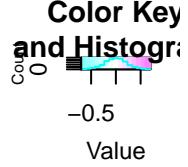
cell wall_GO_30_1



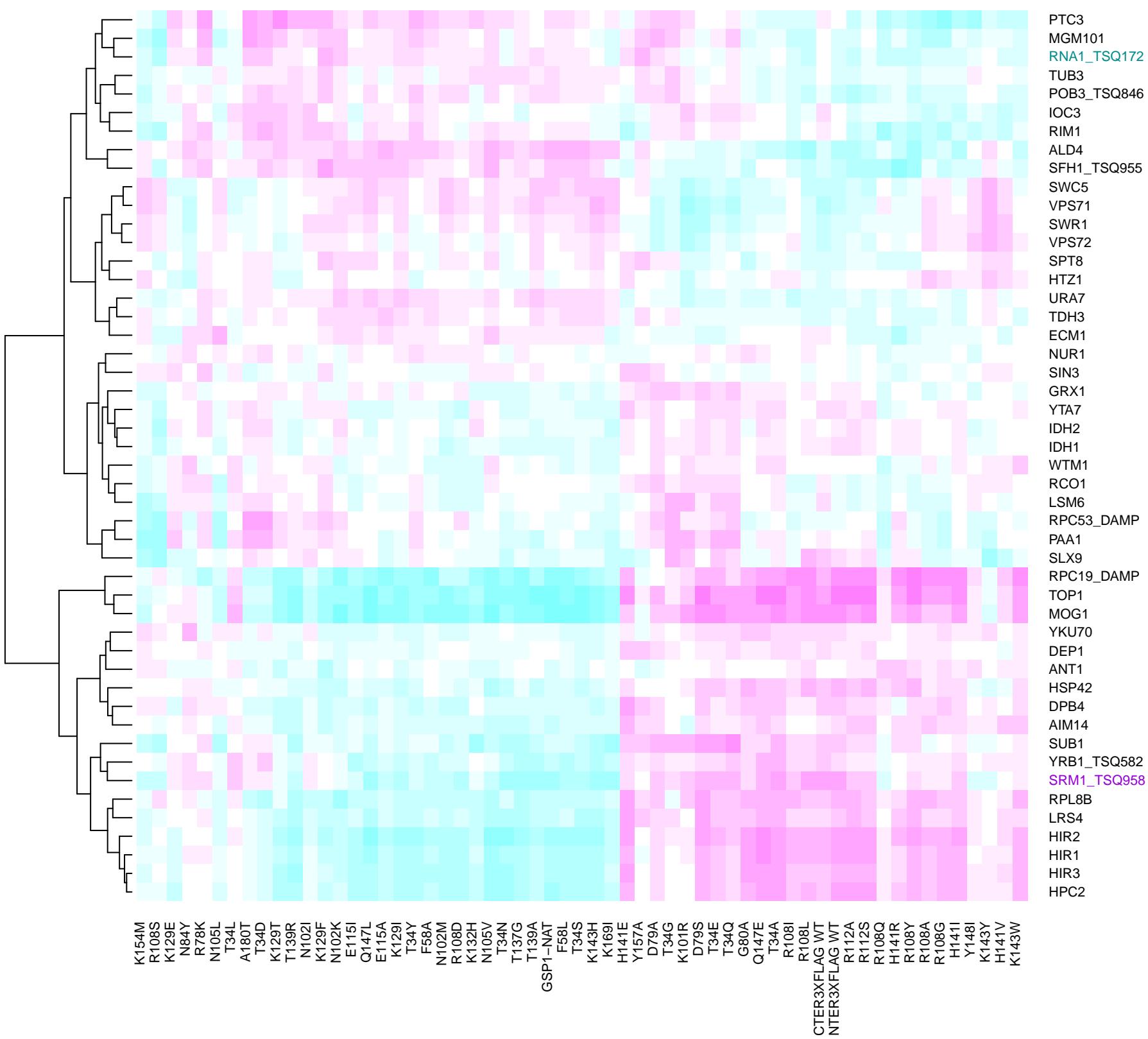


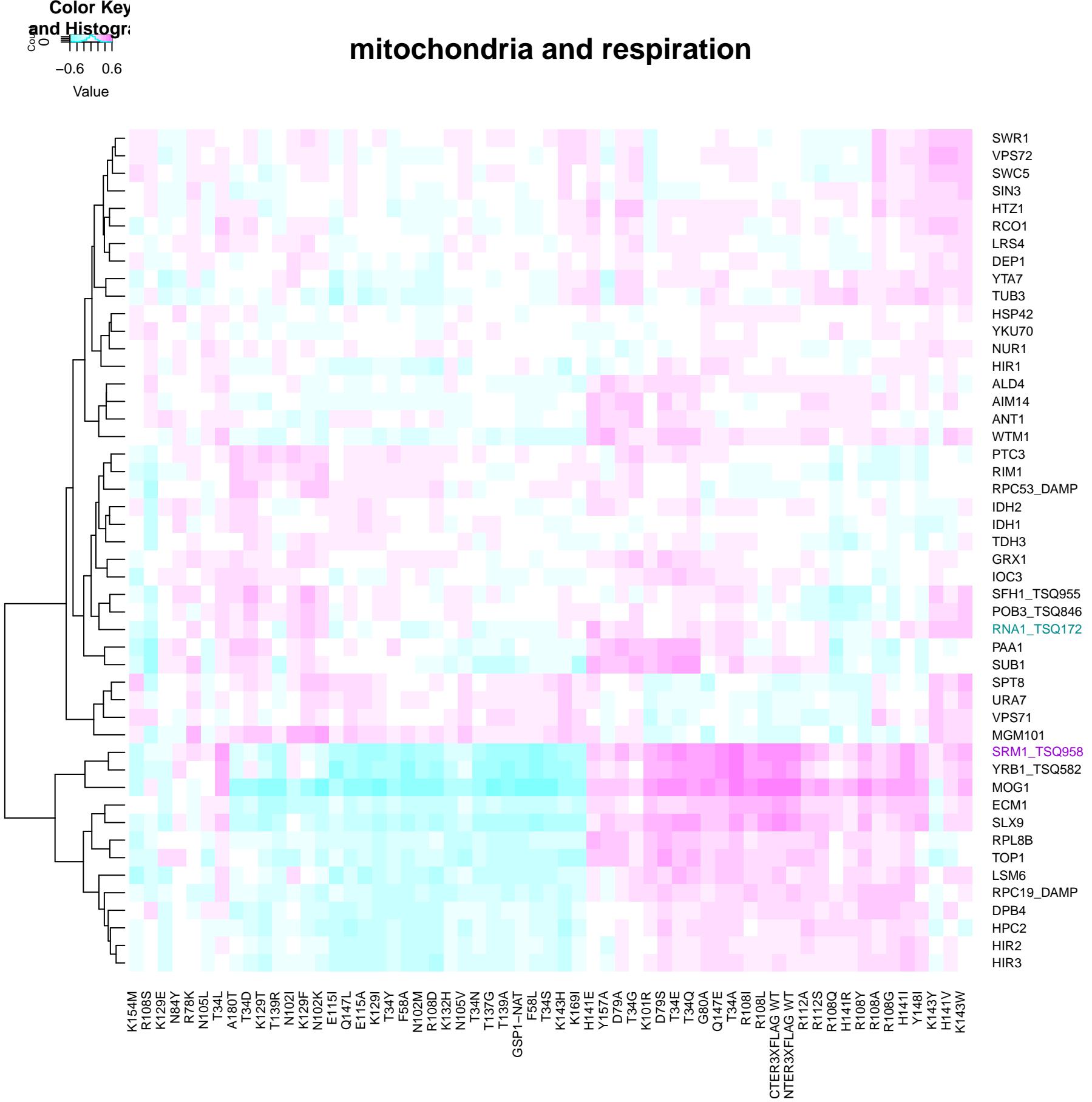
cytoplasmic translation

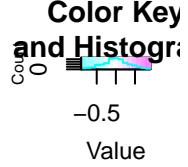




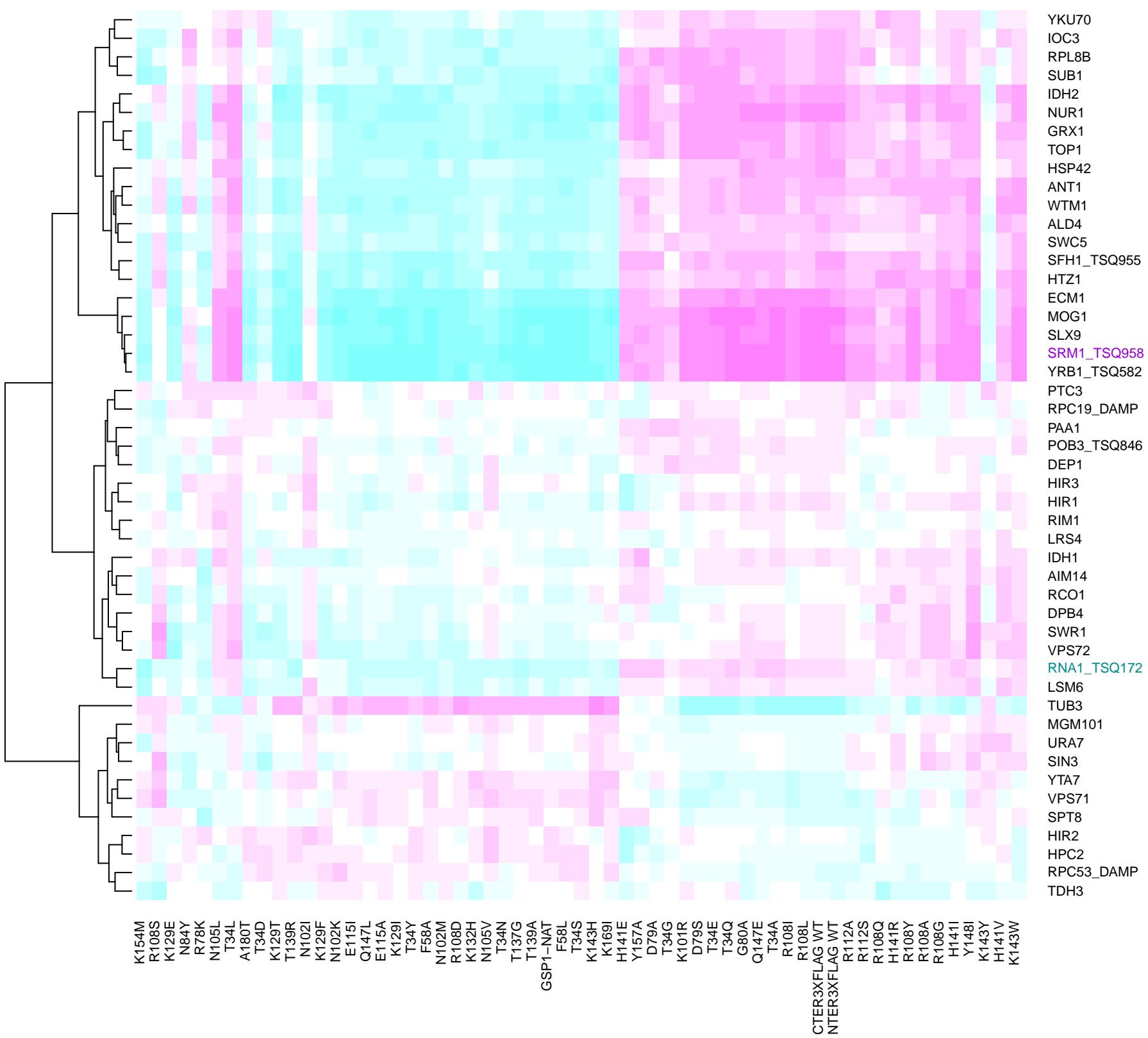
cytoplasmic translation_GO_30_1

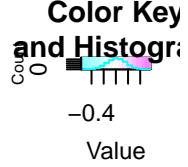




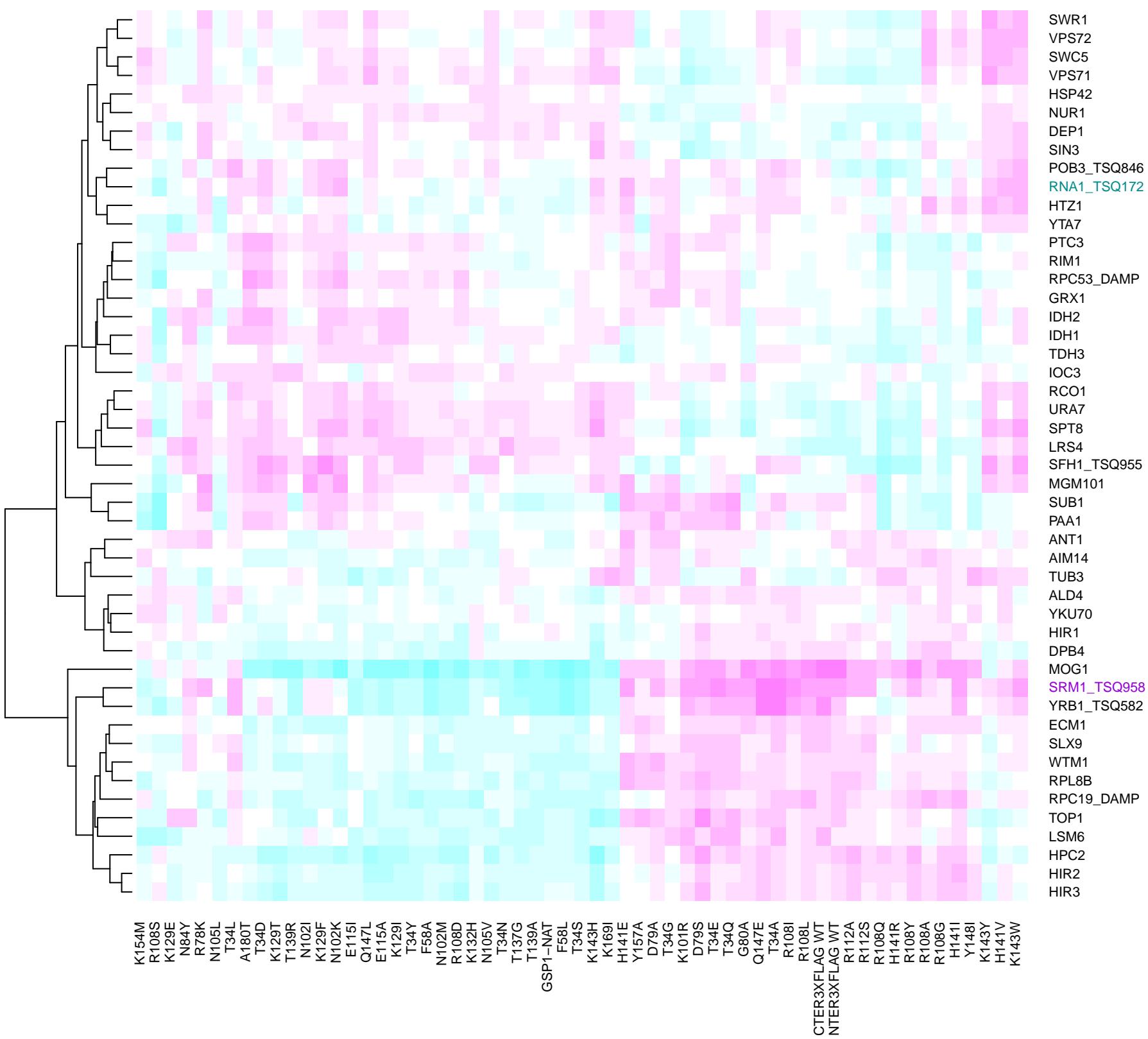


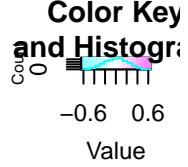
mitochondria and respiration_GO_30_13



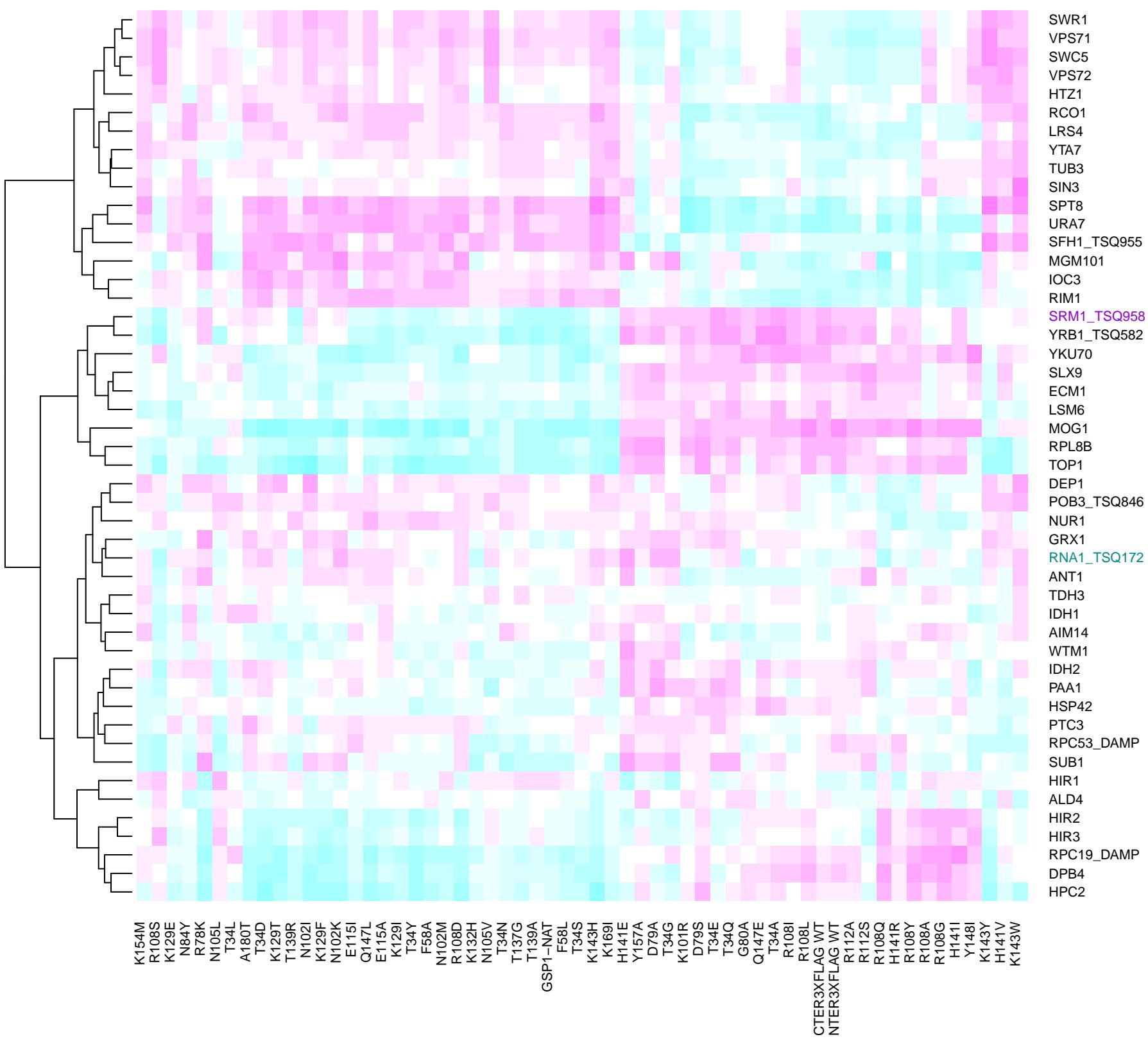


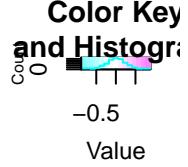
mitochondrion organization



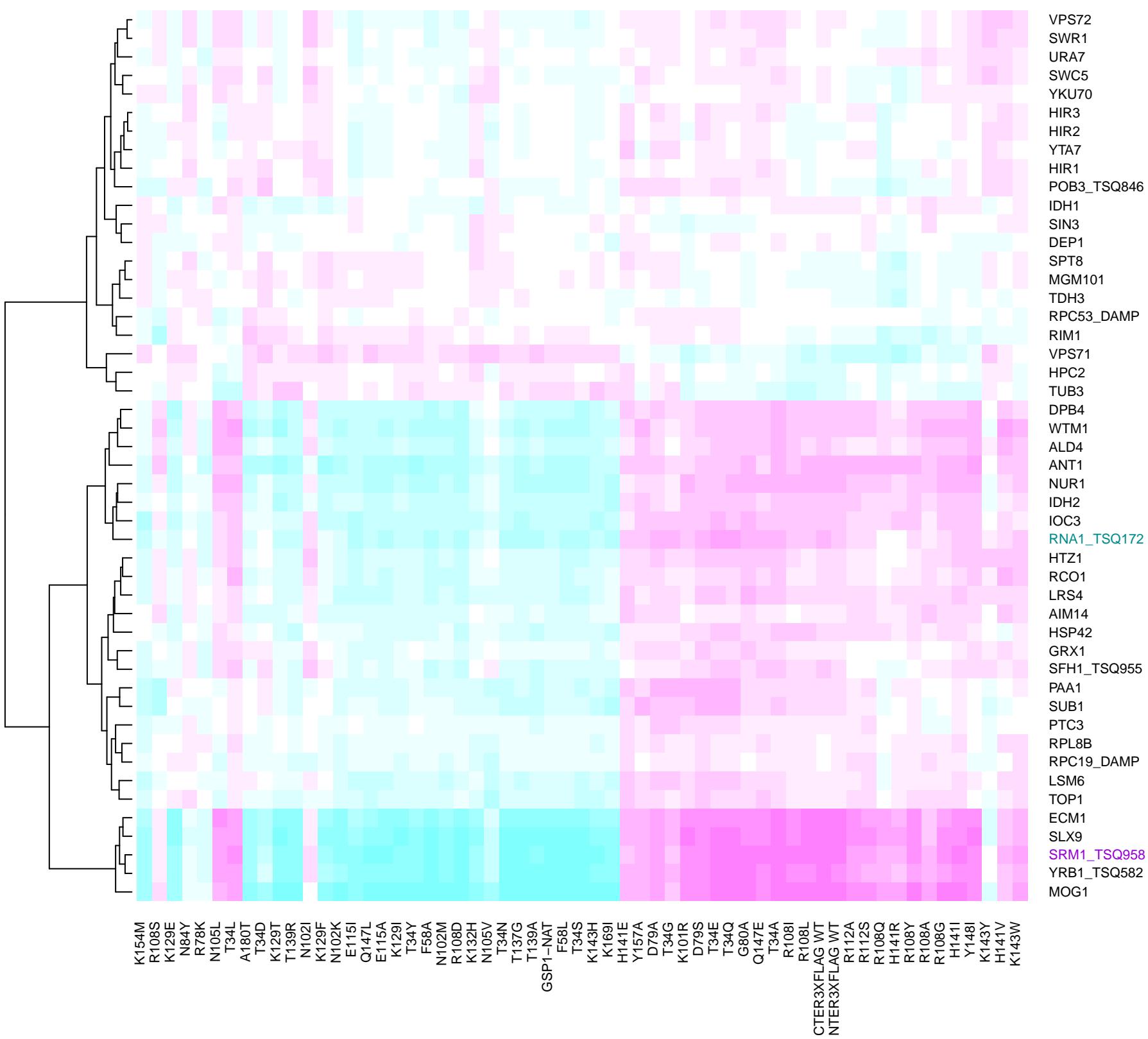


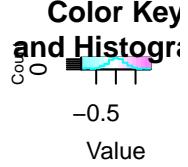
mitochondrion organization_GO_30_2



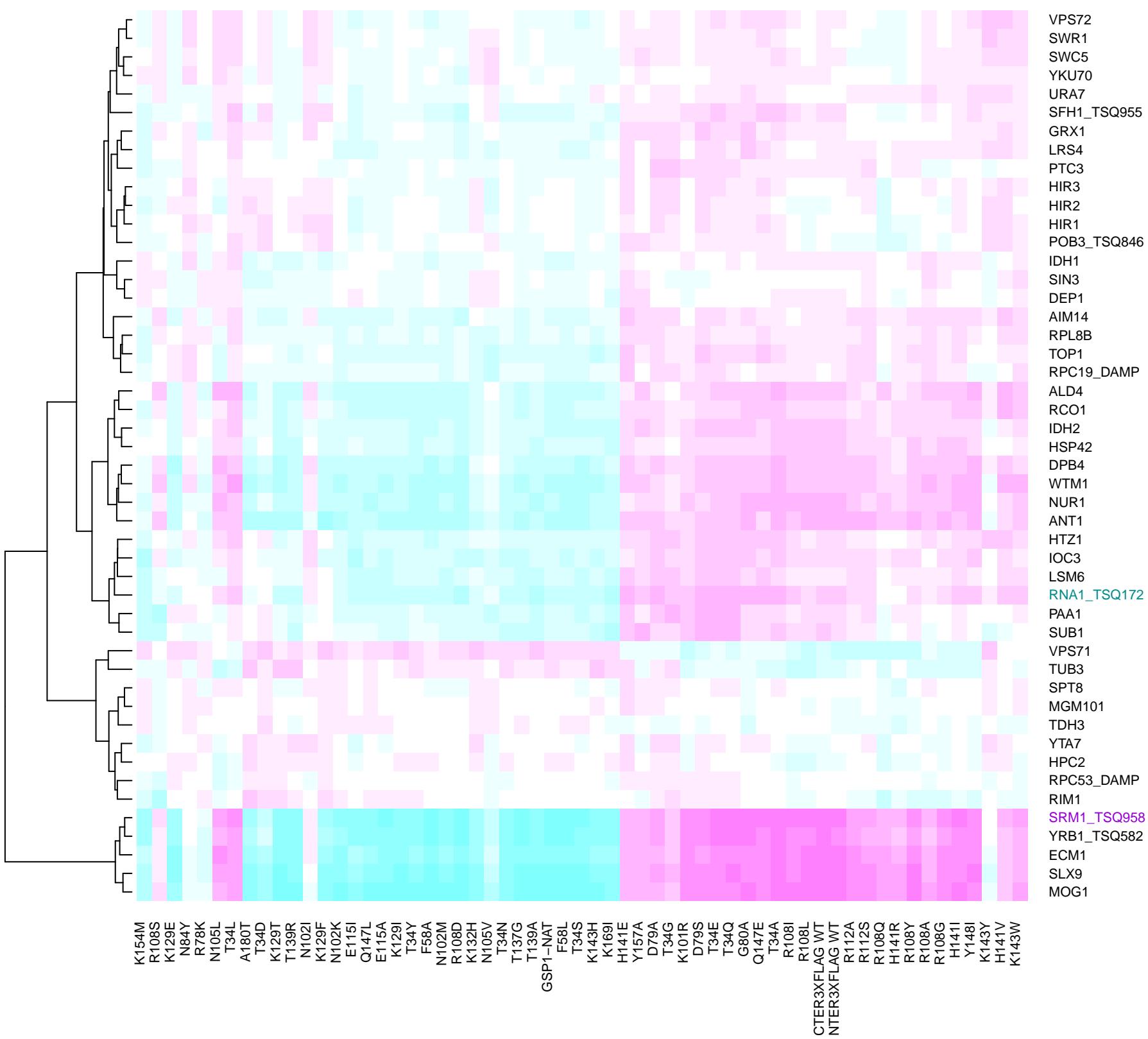


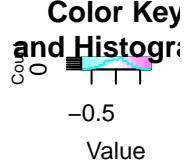
nuclear transport



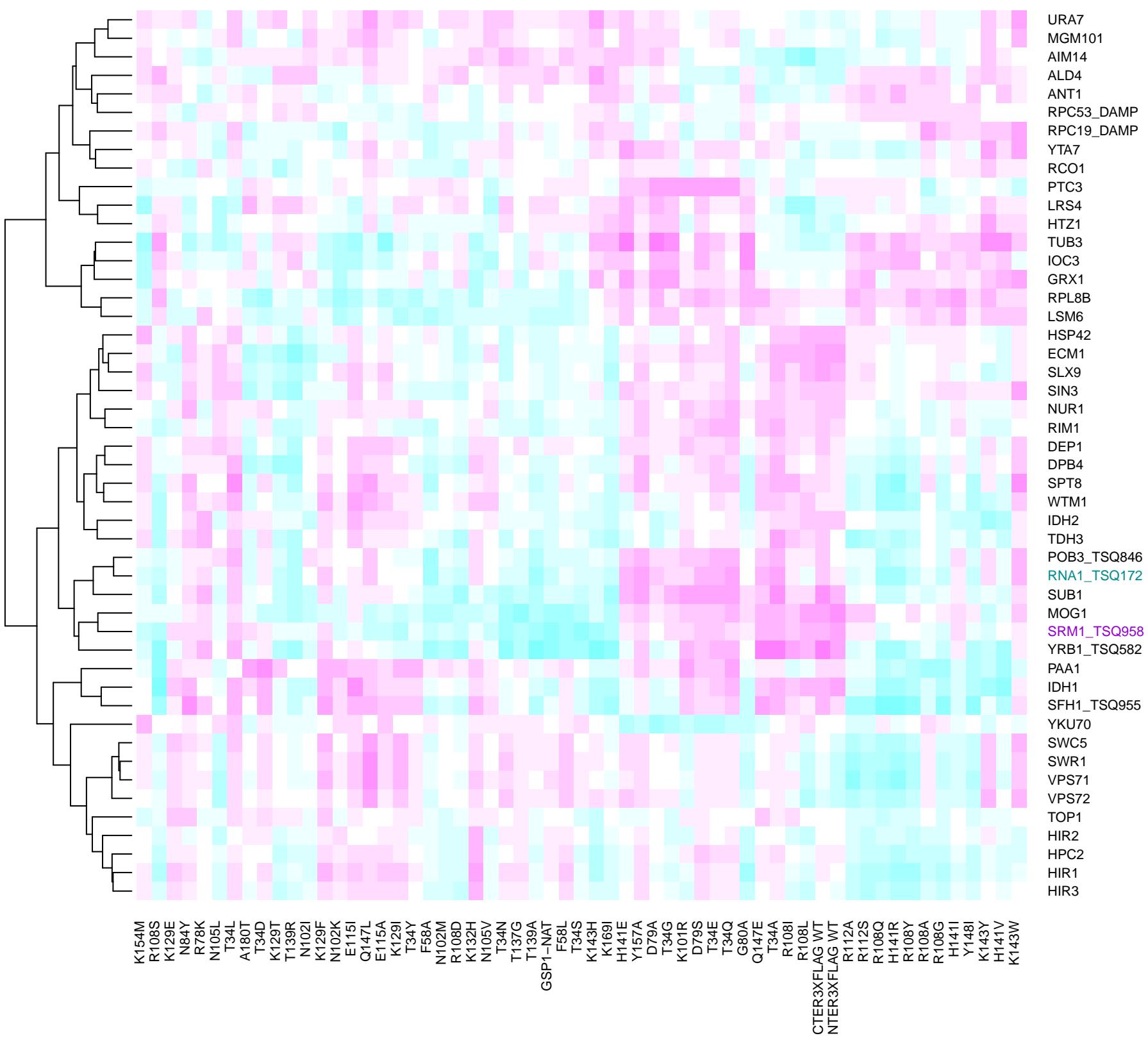


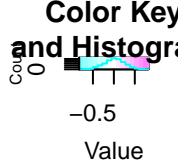
nuclear transport and organization



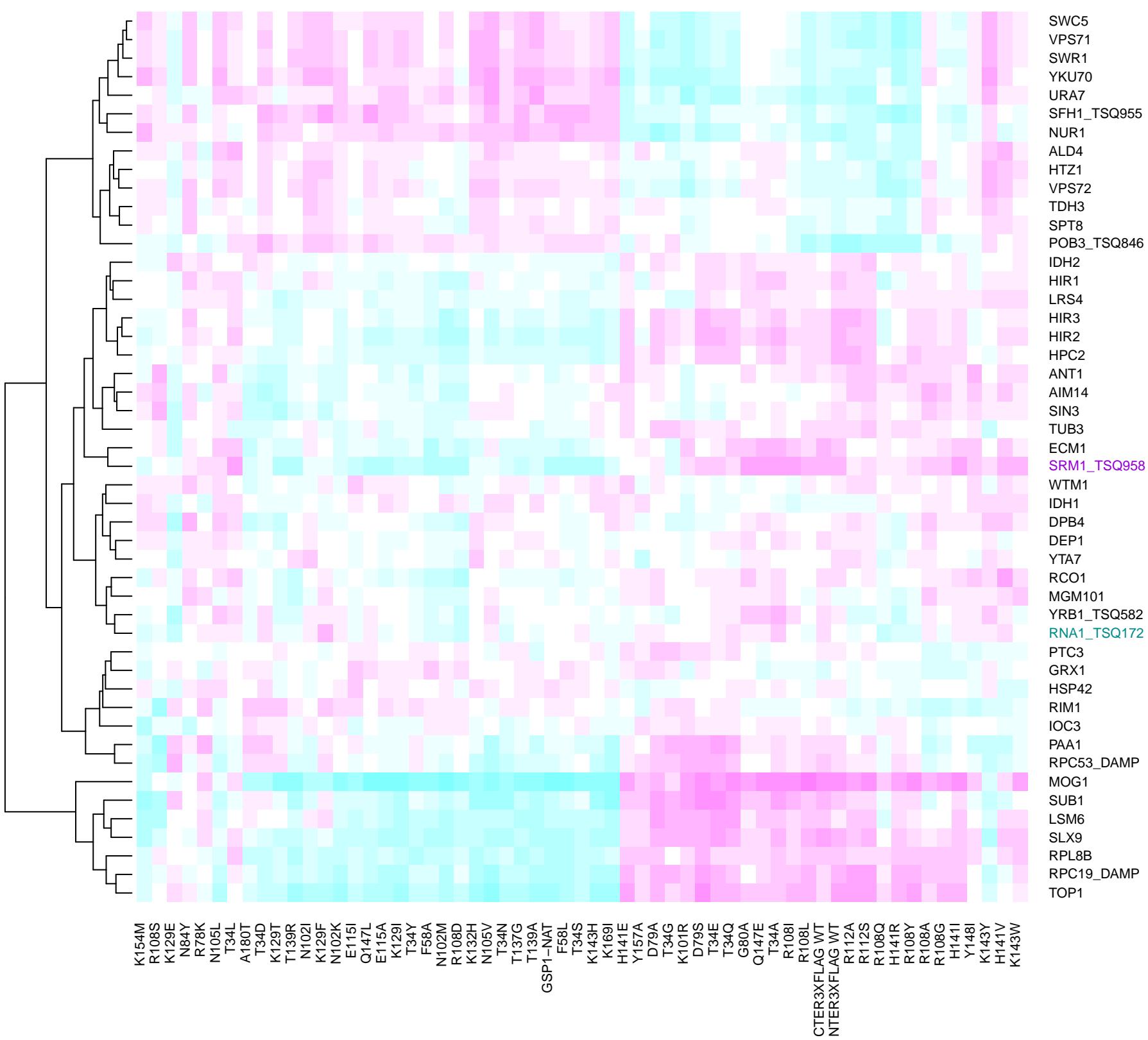


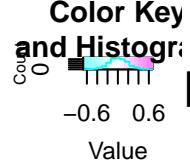
organelle fission_GO_30_3



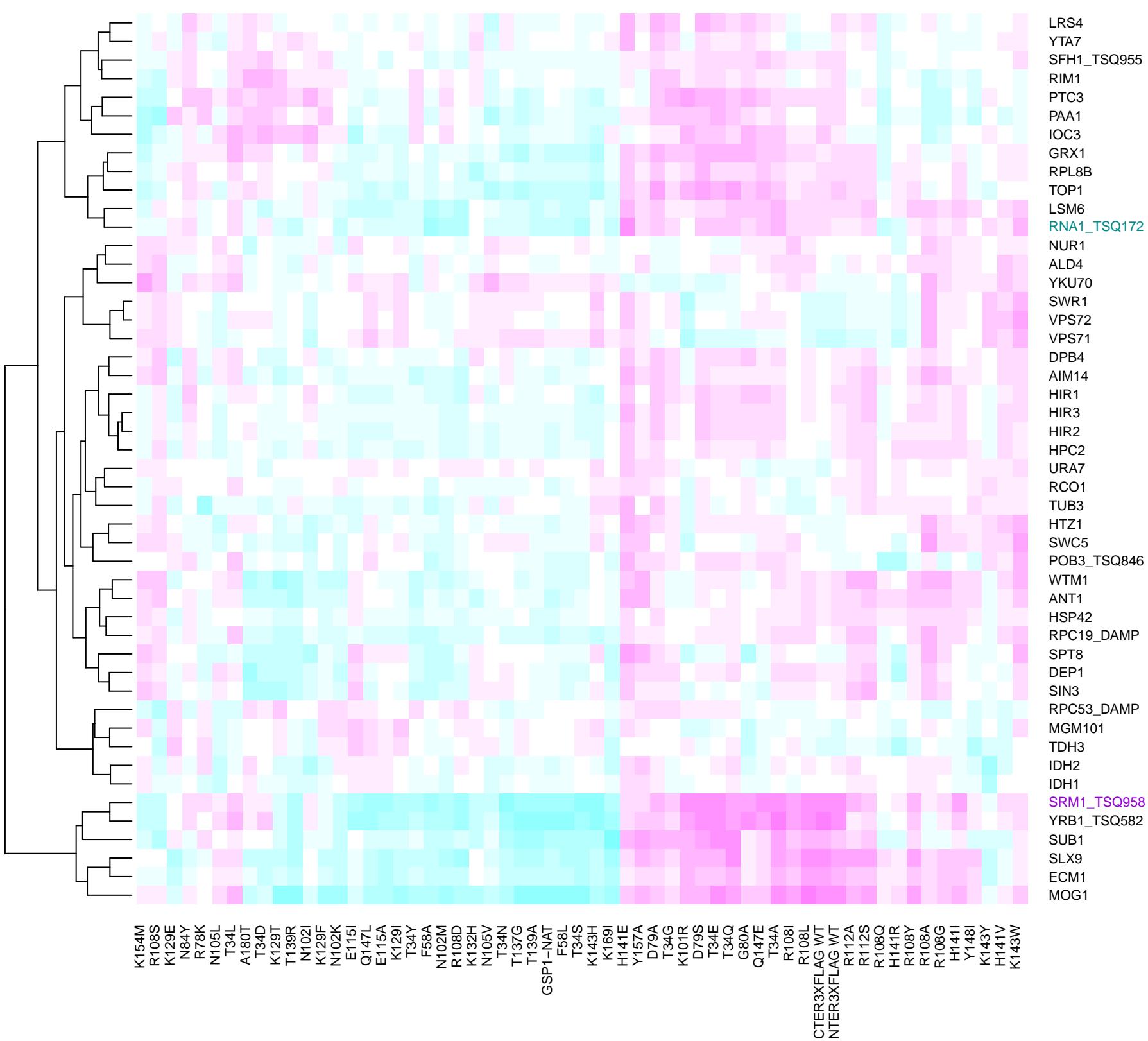


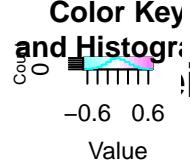
nuclear transport and organization_GO_30_3



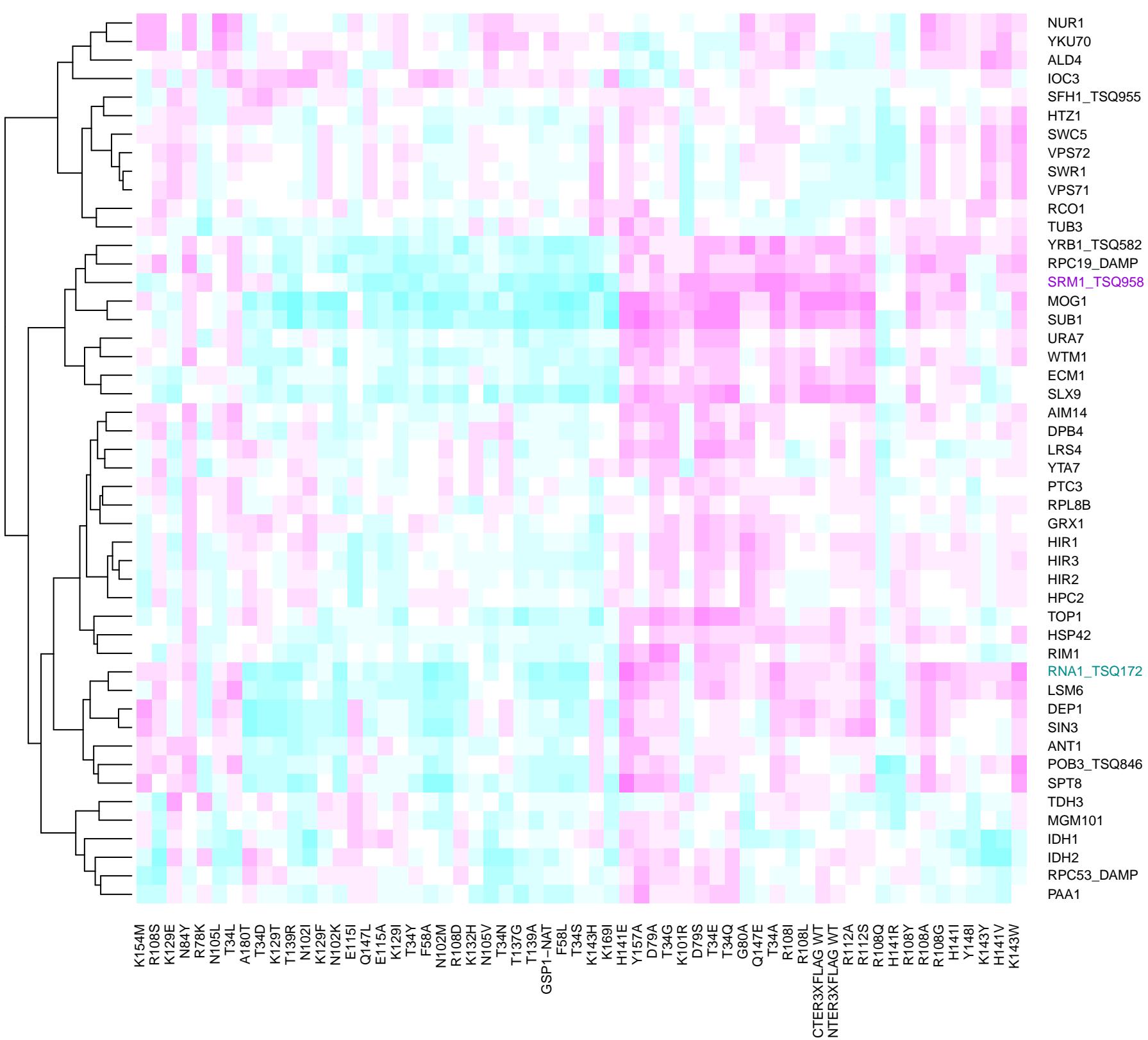


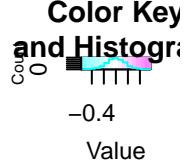
protein modification by small protein conjugation or removal



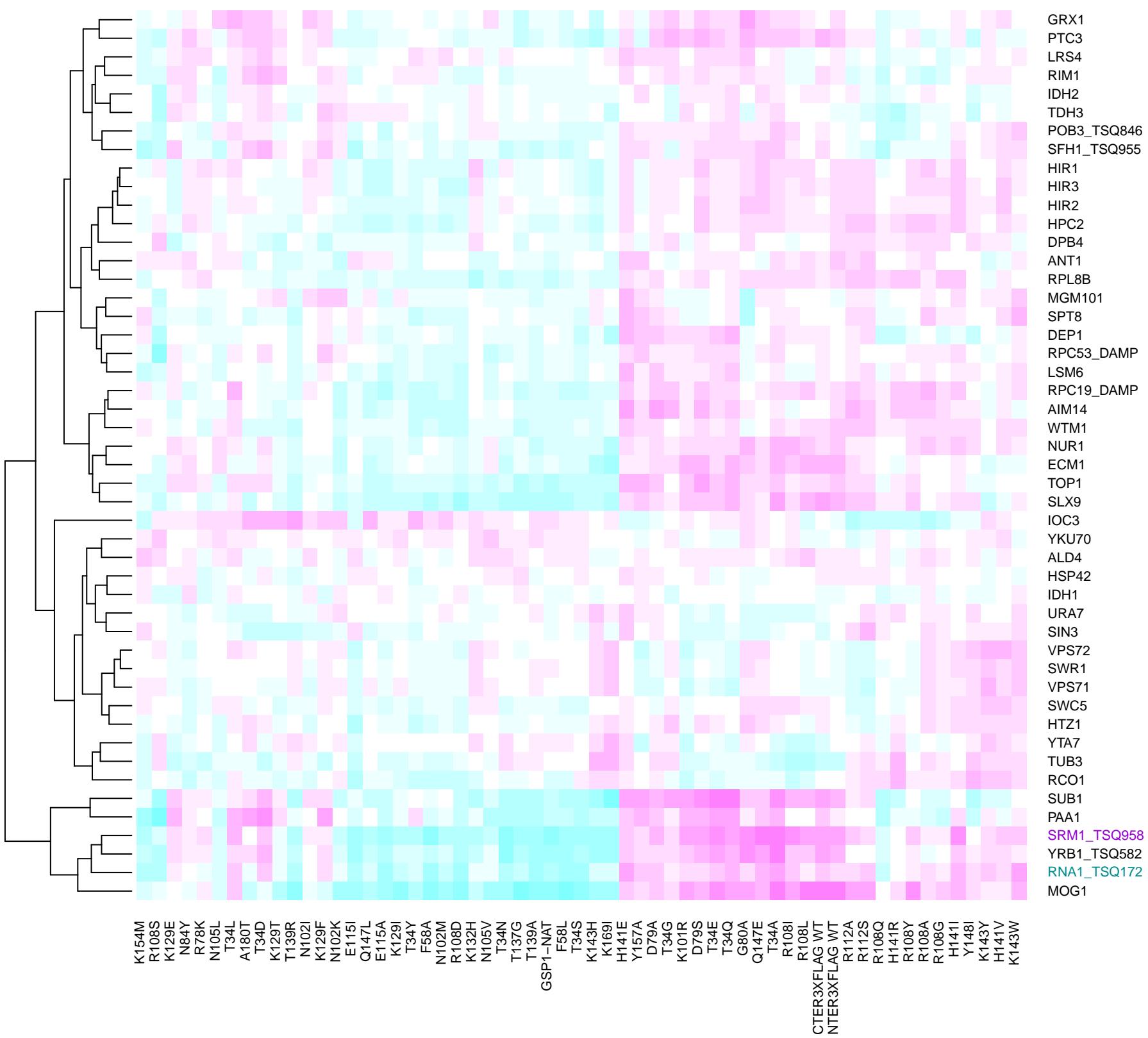


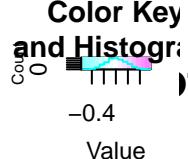
in modification by small protein conjugation or removal_GO_30_1



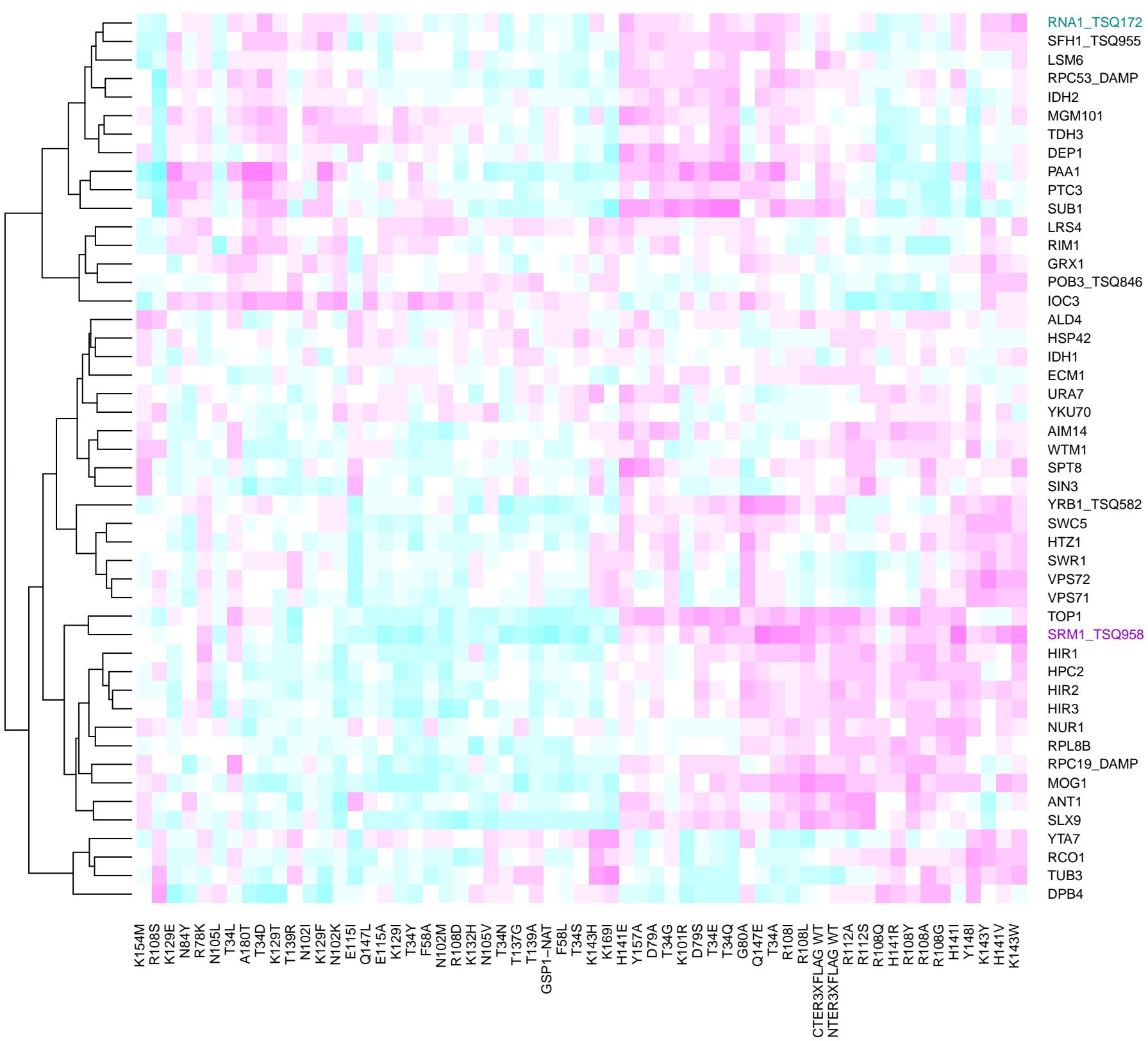


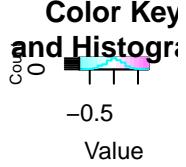
proteolysis involved in cellular protein catabolic process



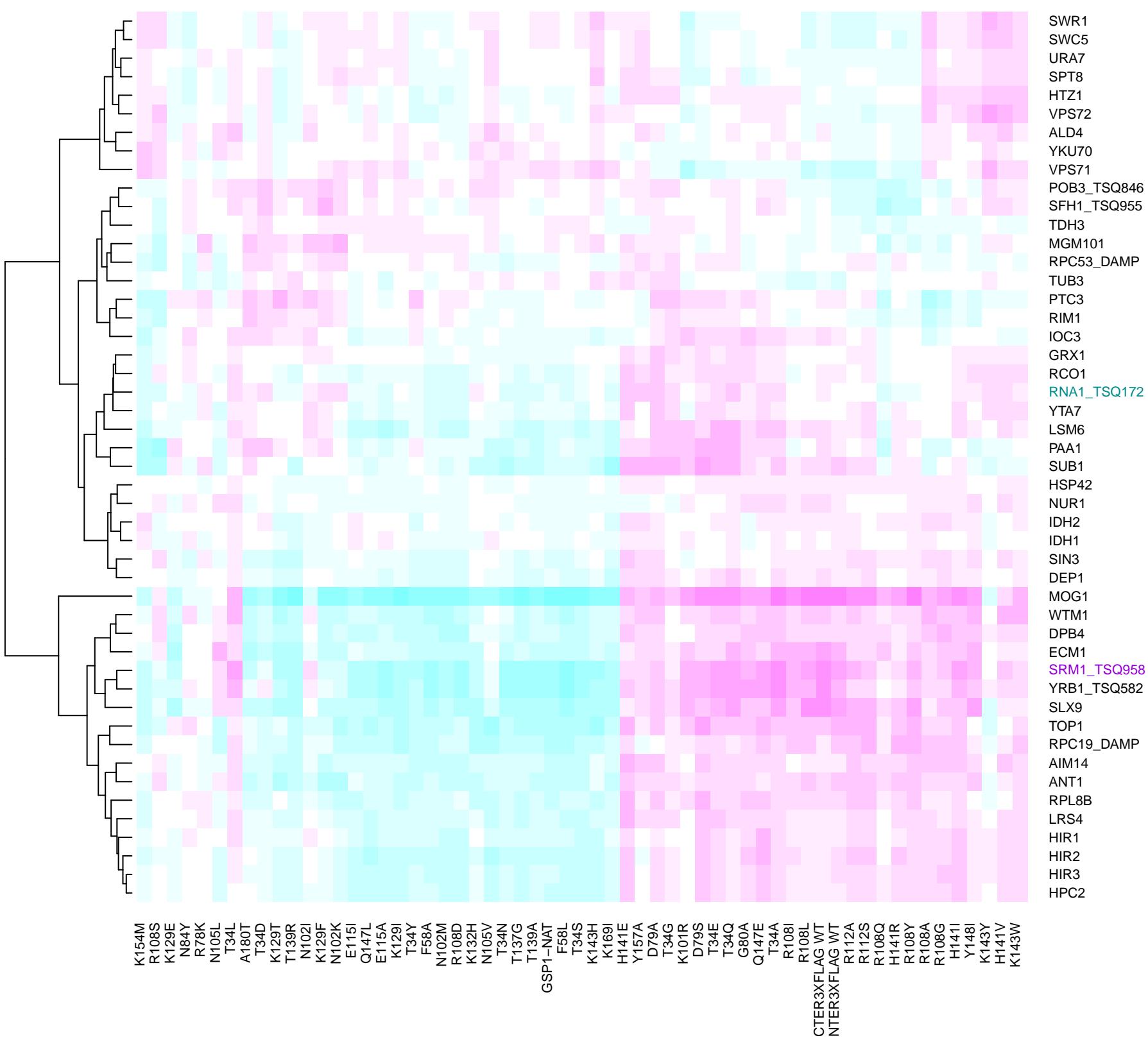


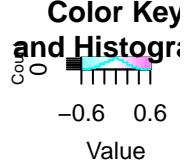
Proteolysis involved in cellular protein catabolic process_GO_30_1



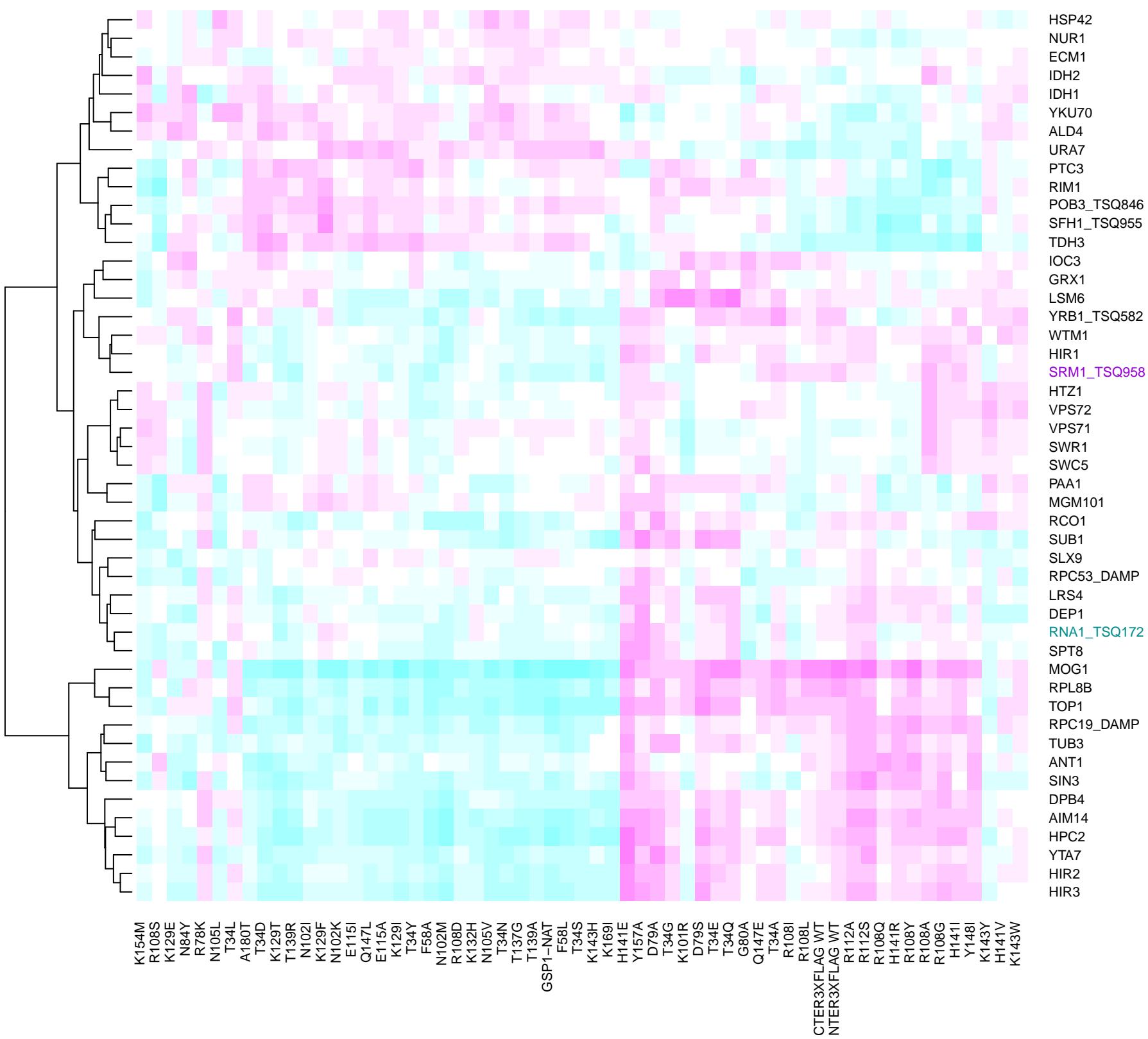


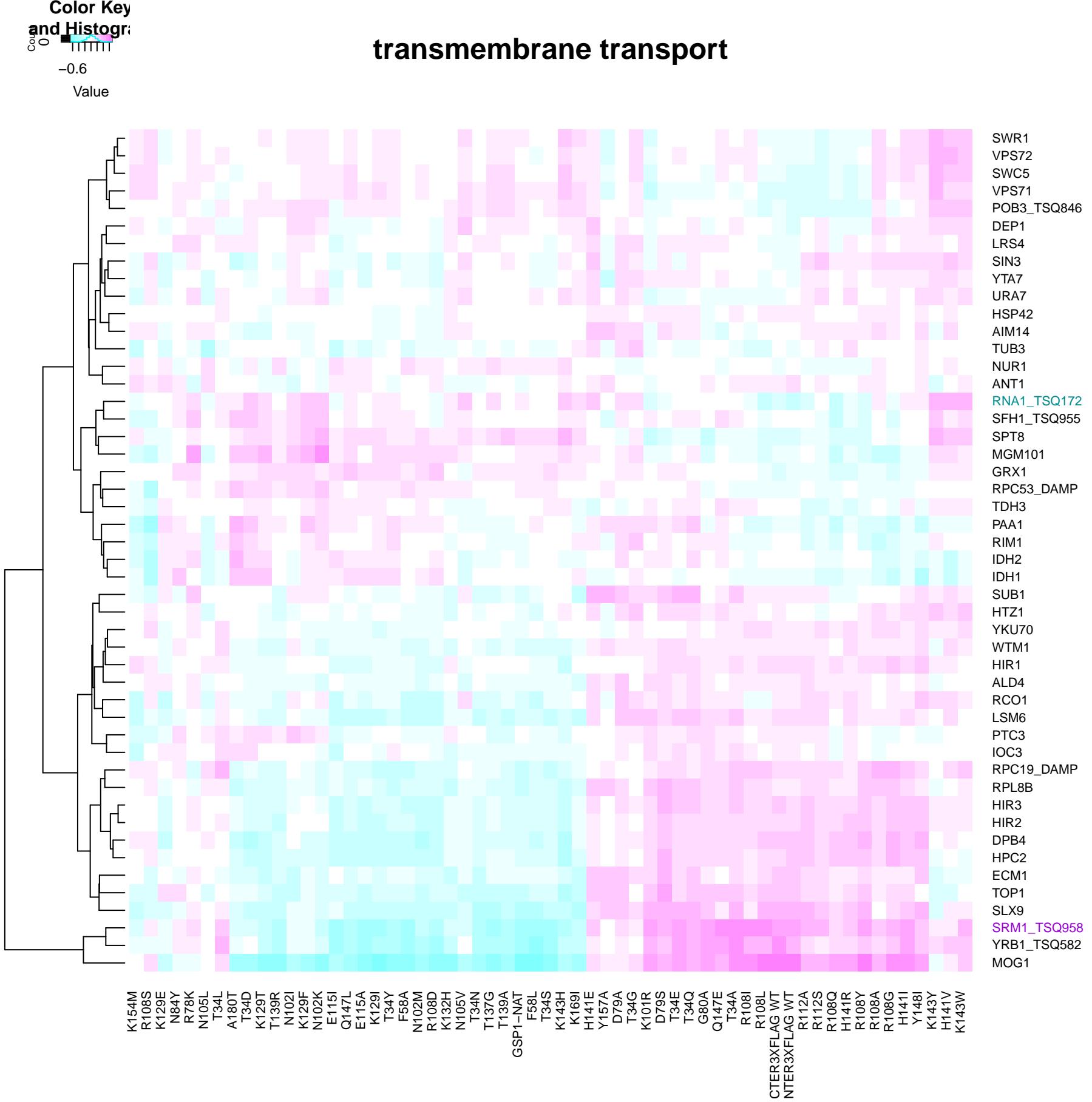
ribosomes and translation

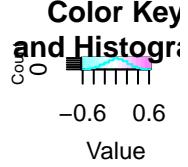




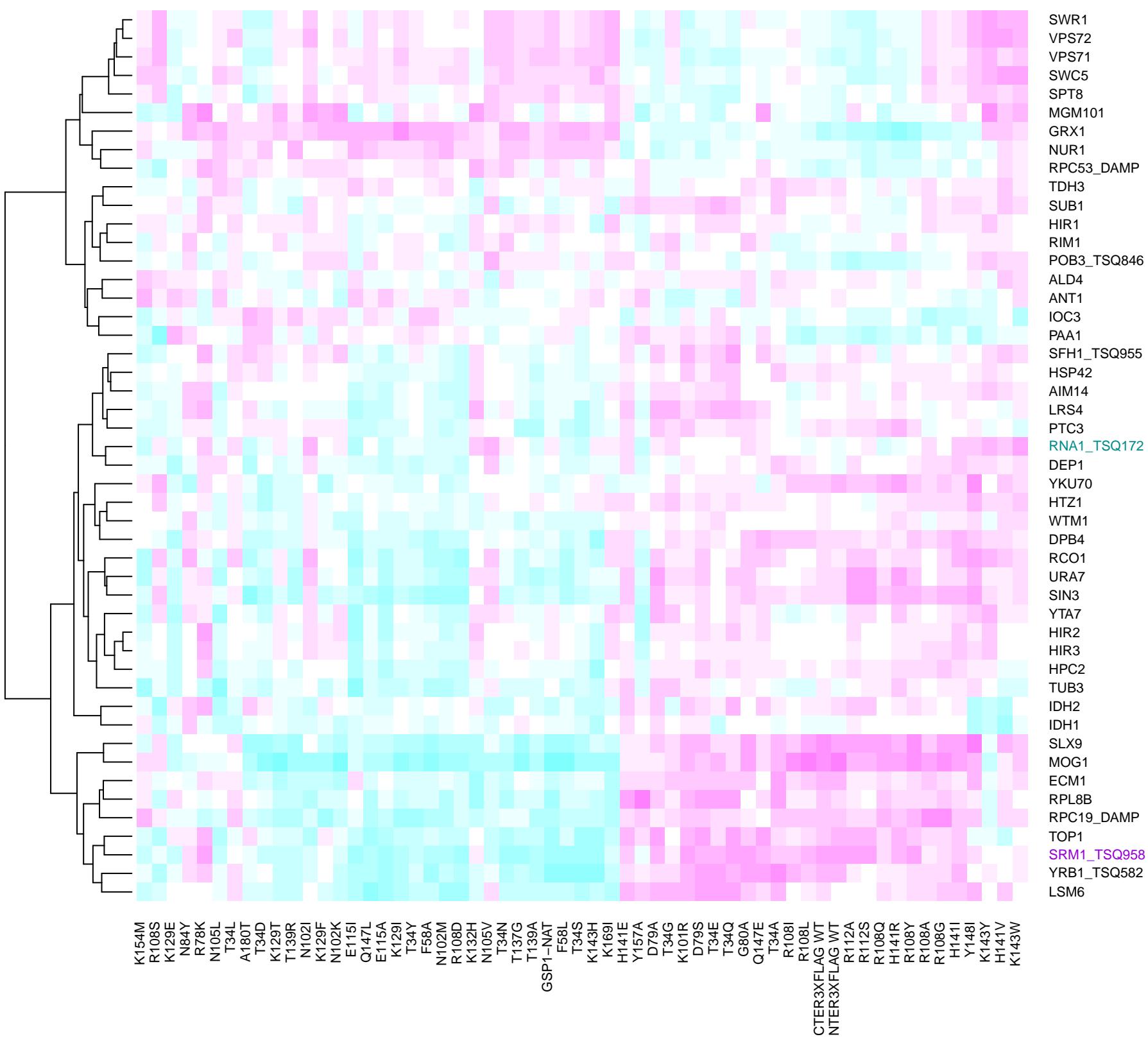
ribosomes and translation_GO_30_1

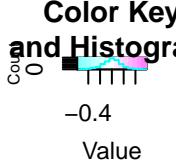




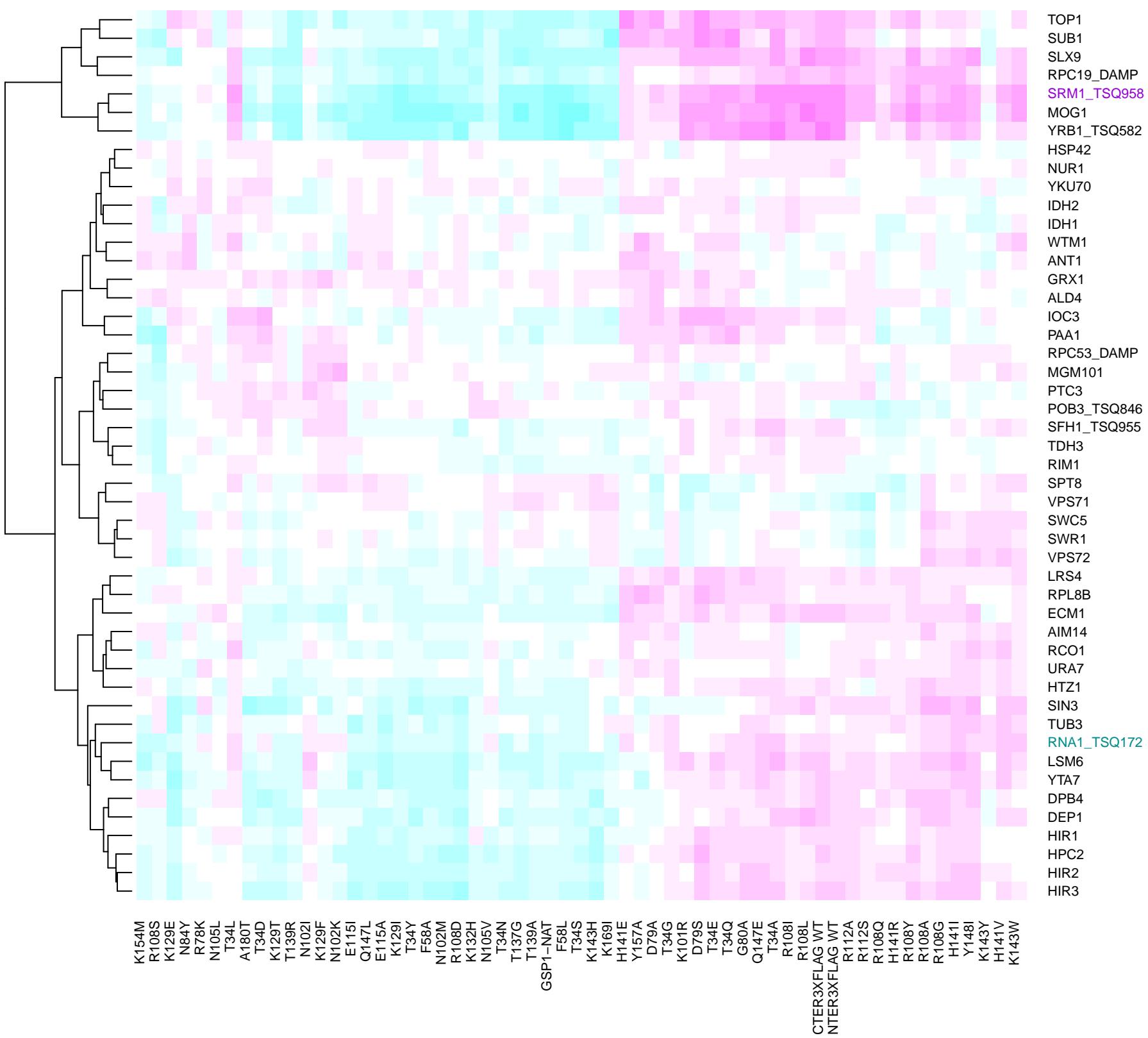


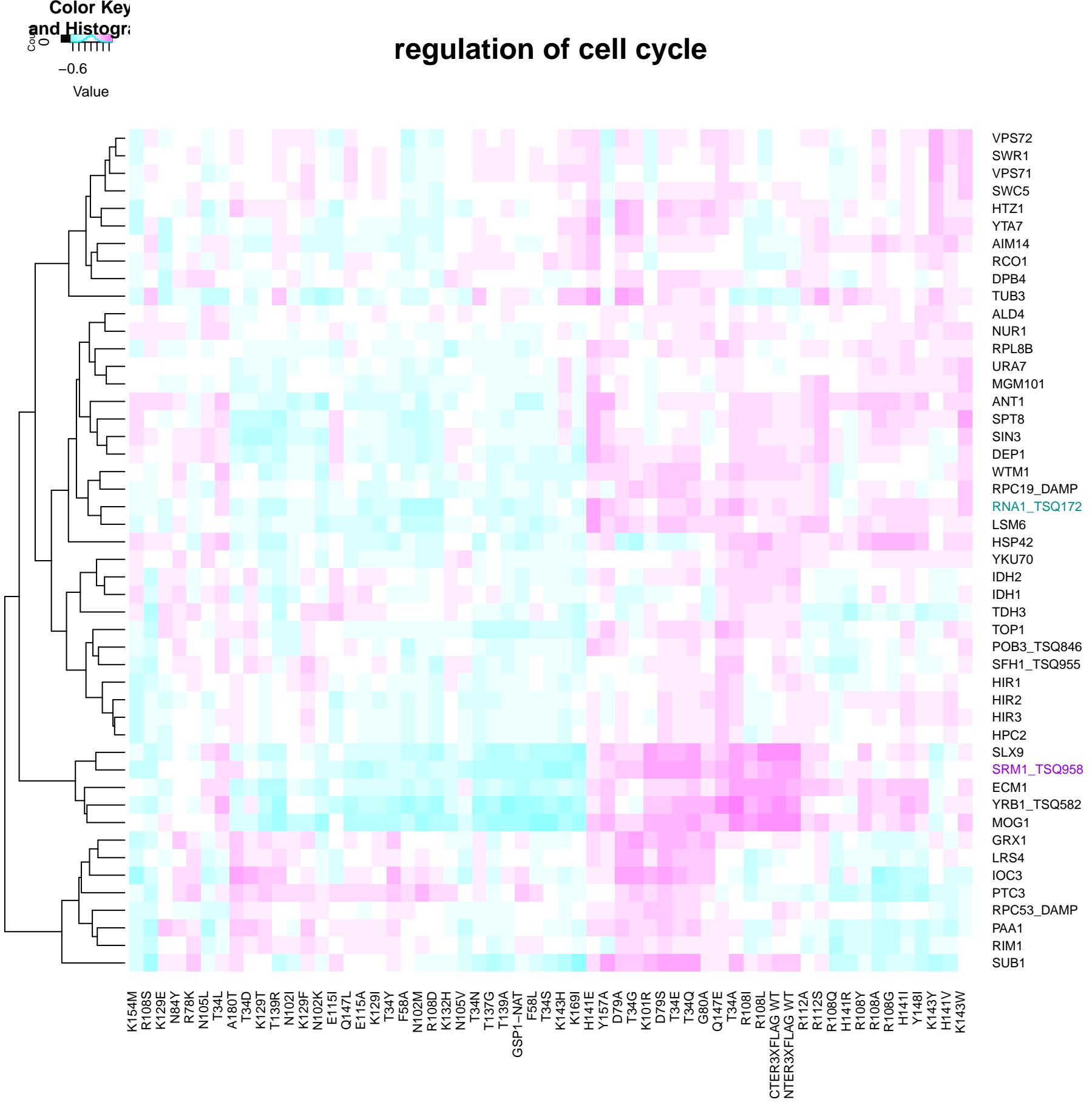
transmembrane transport_GO_30_1

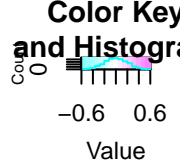




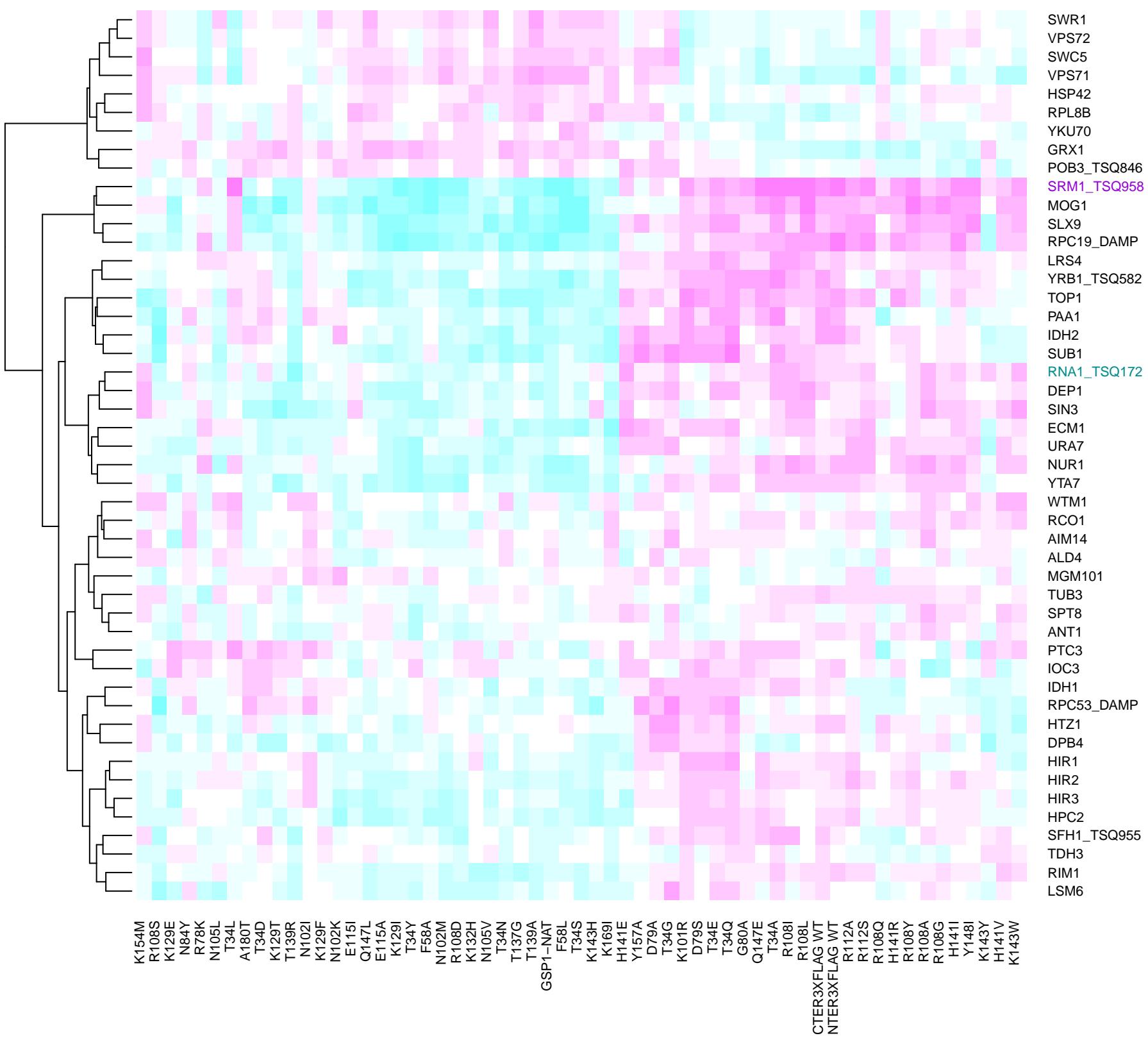
vacuole

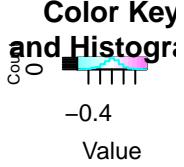




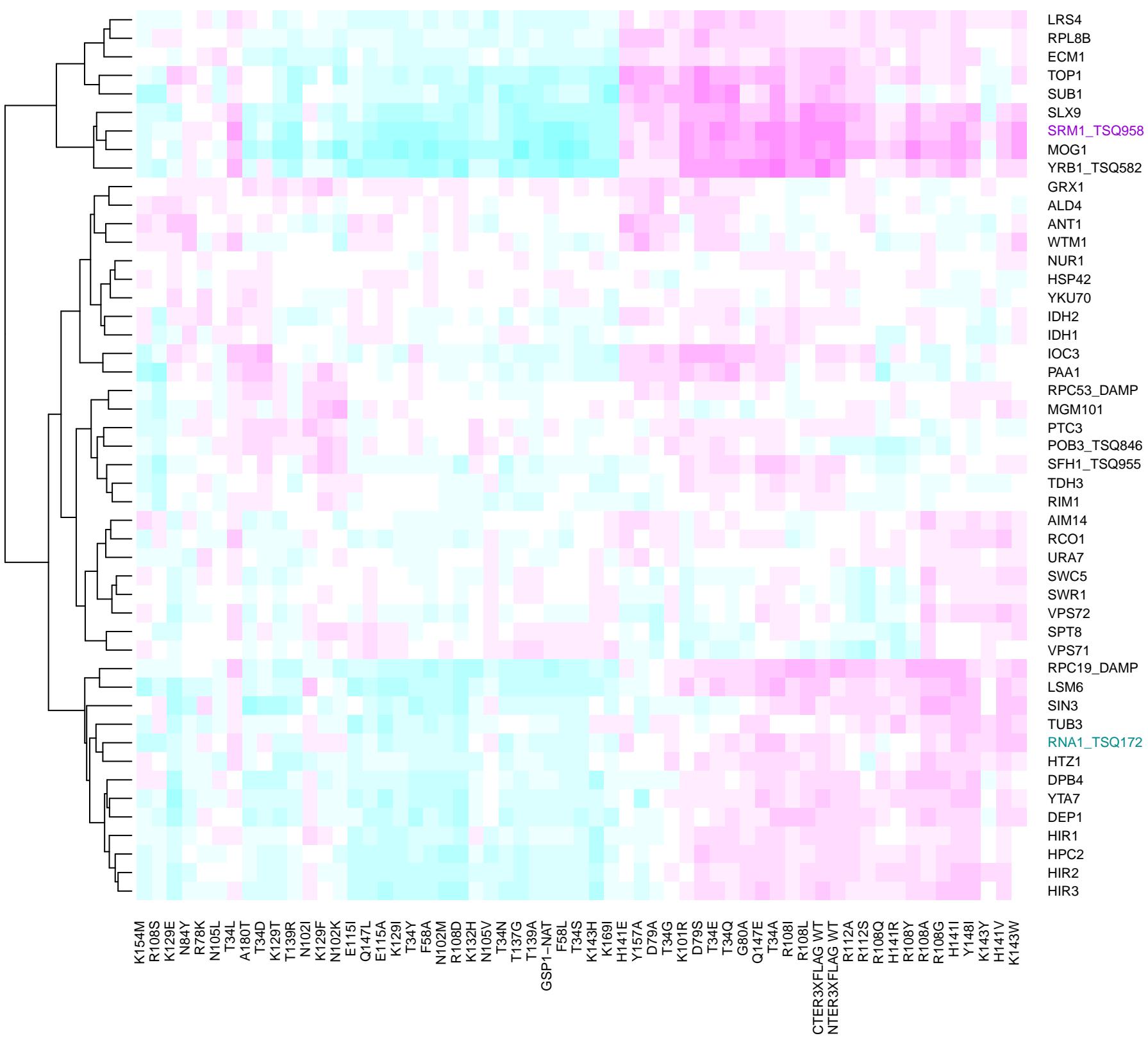


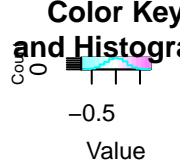
vacuole_GO_30_4



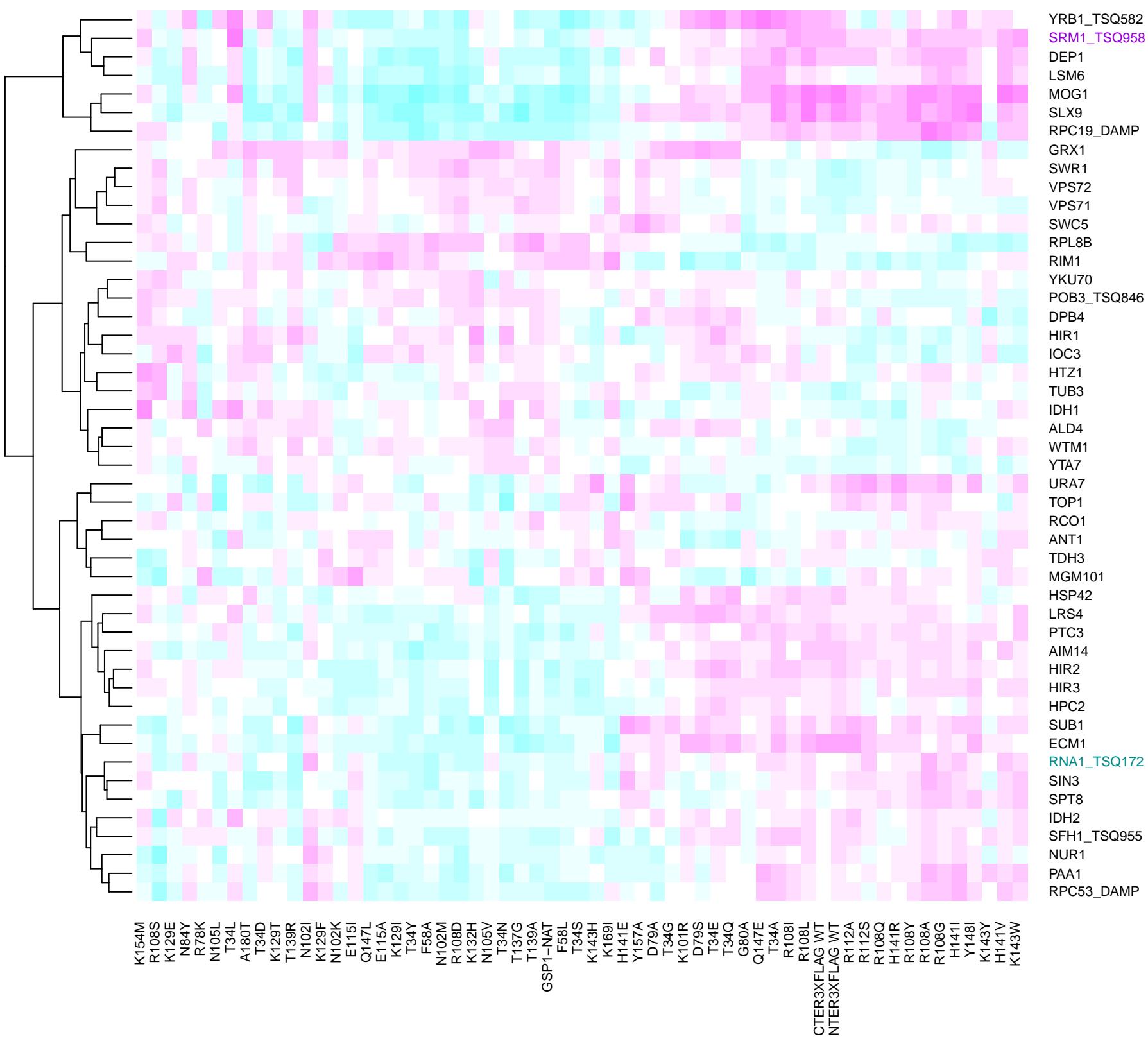


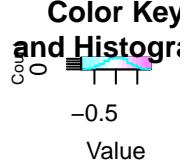
vacuoles



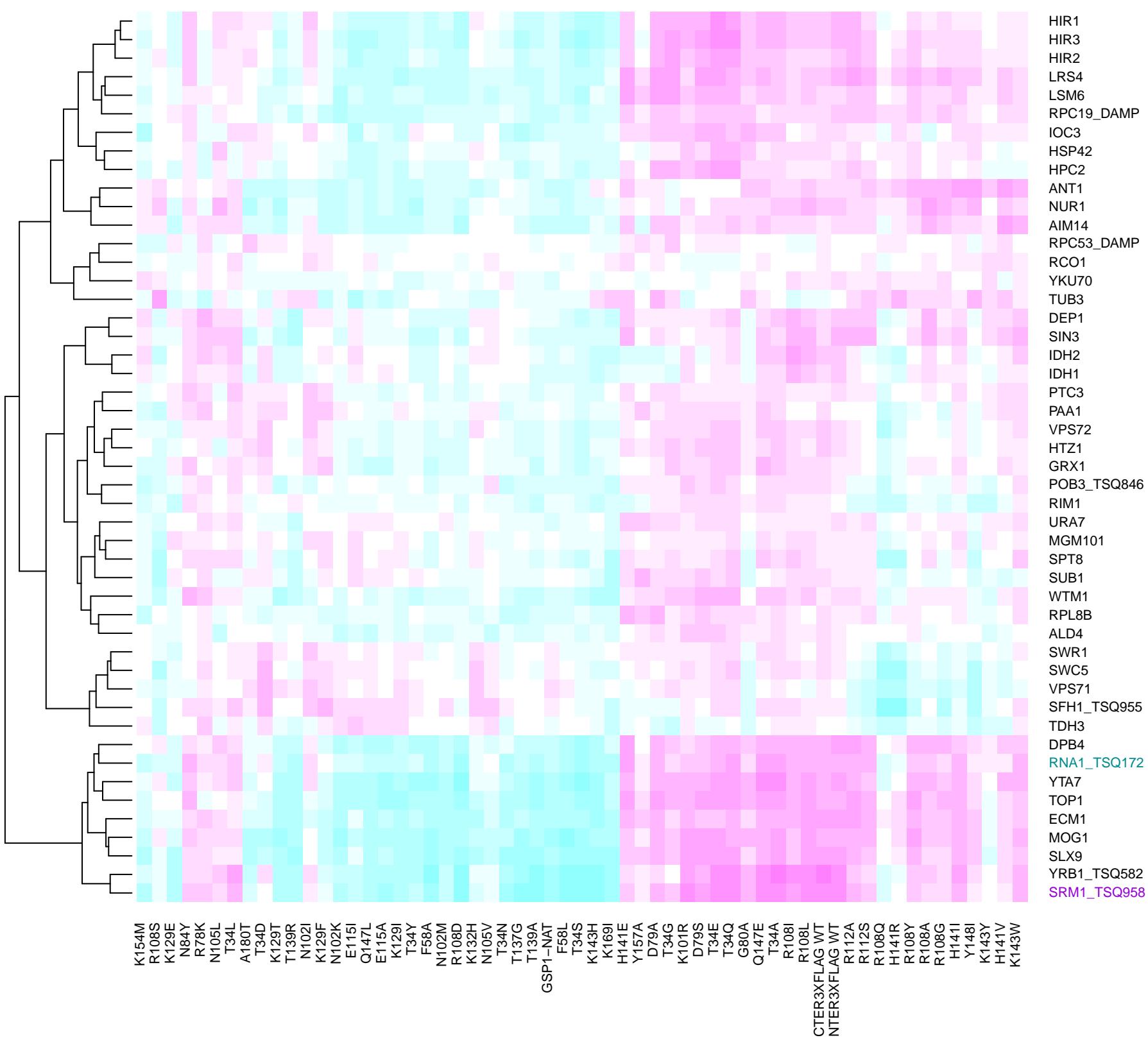


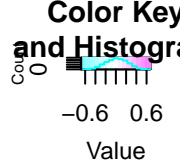
vacuoles_GO_30_8



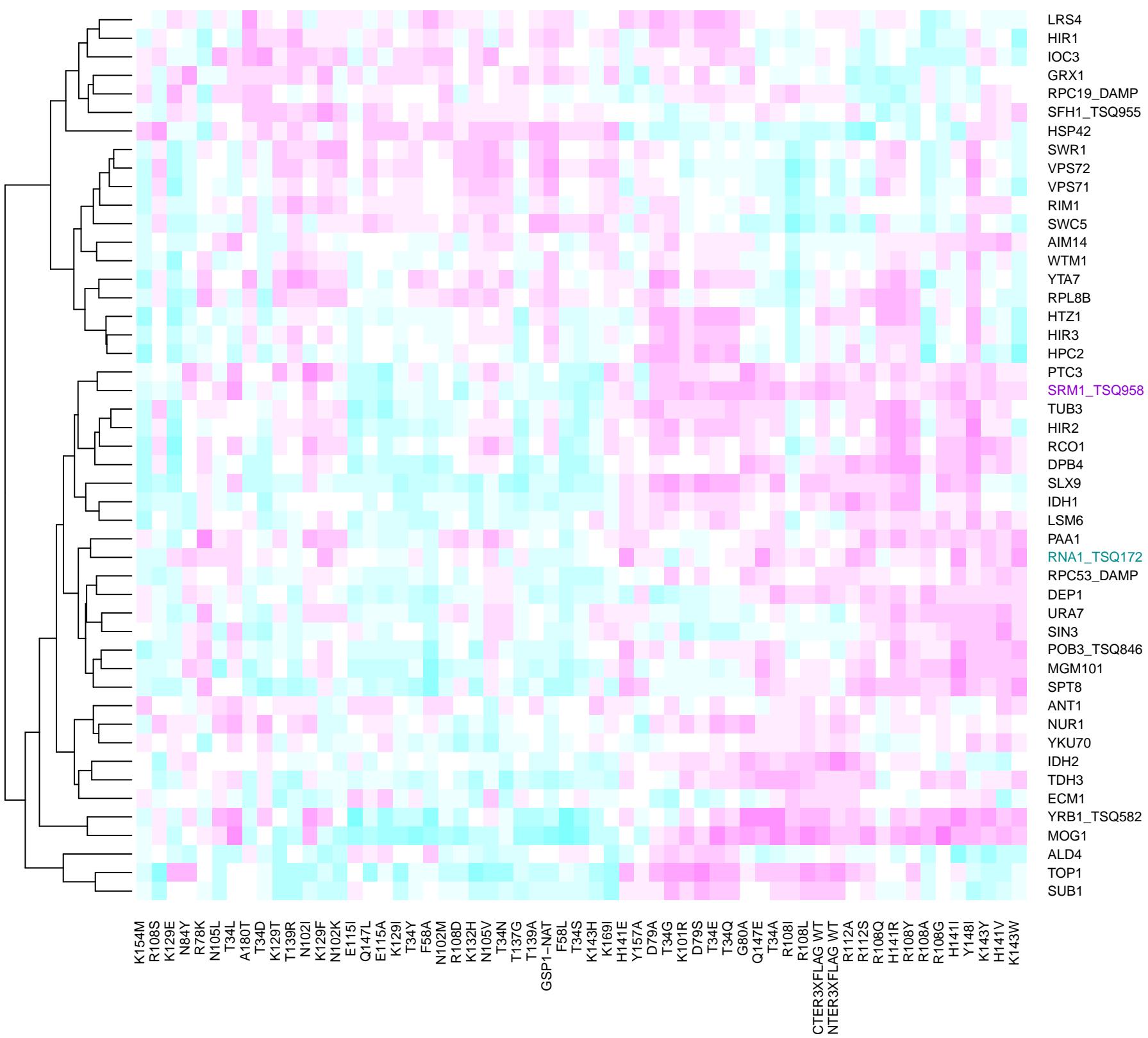


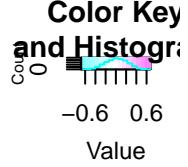
endomembrane system_GO_30_7



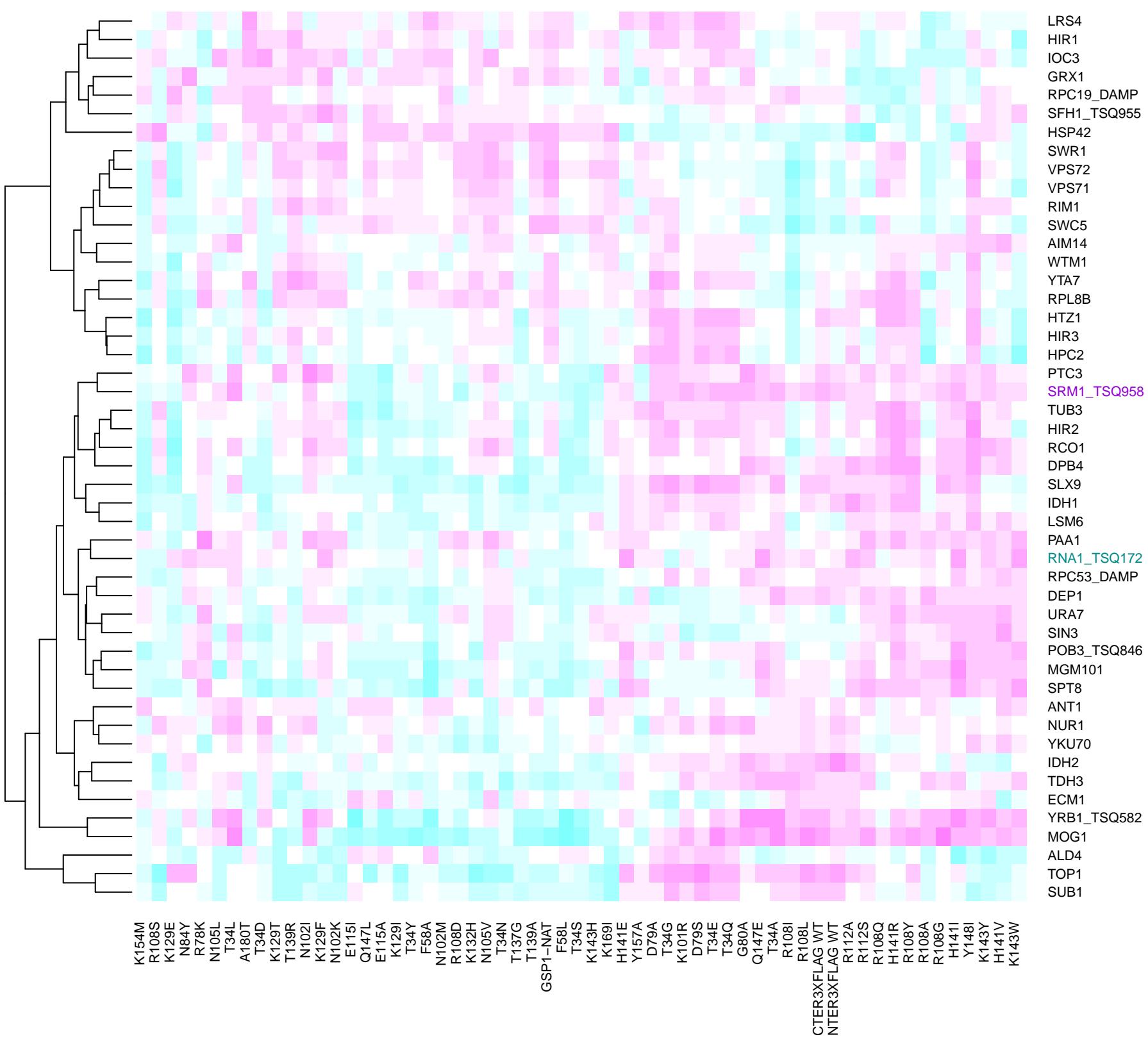


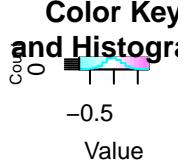
endoplasmic reticulum_GO_30_8



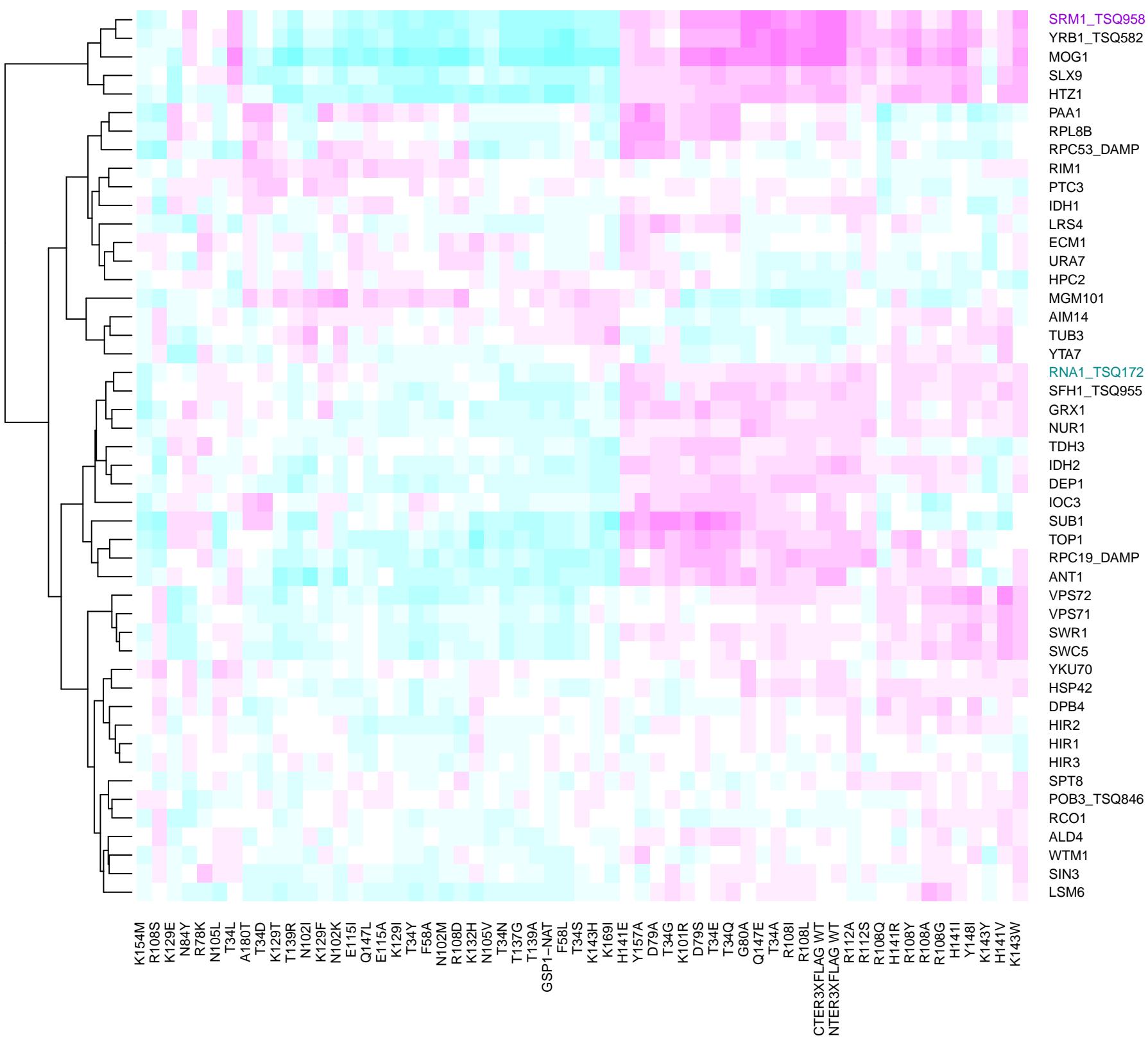


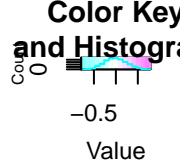
ER_GO_30_8



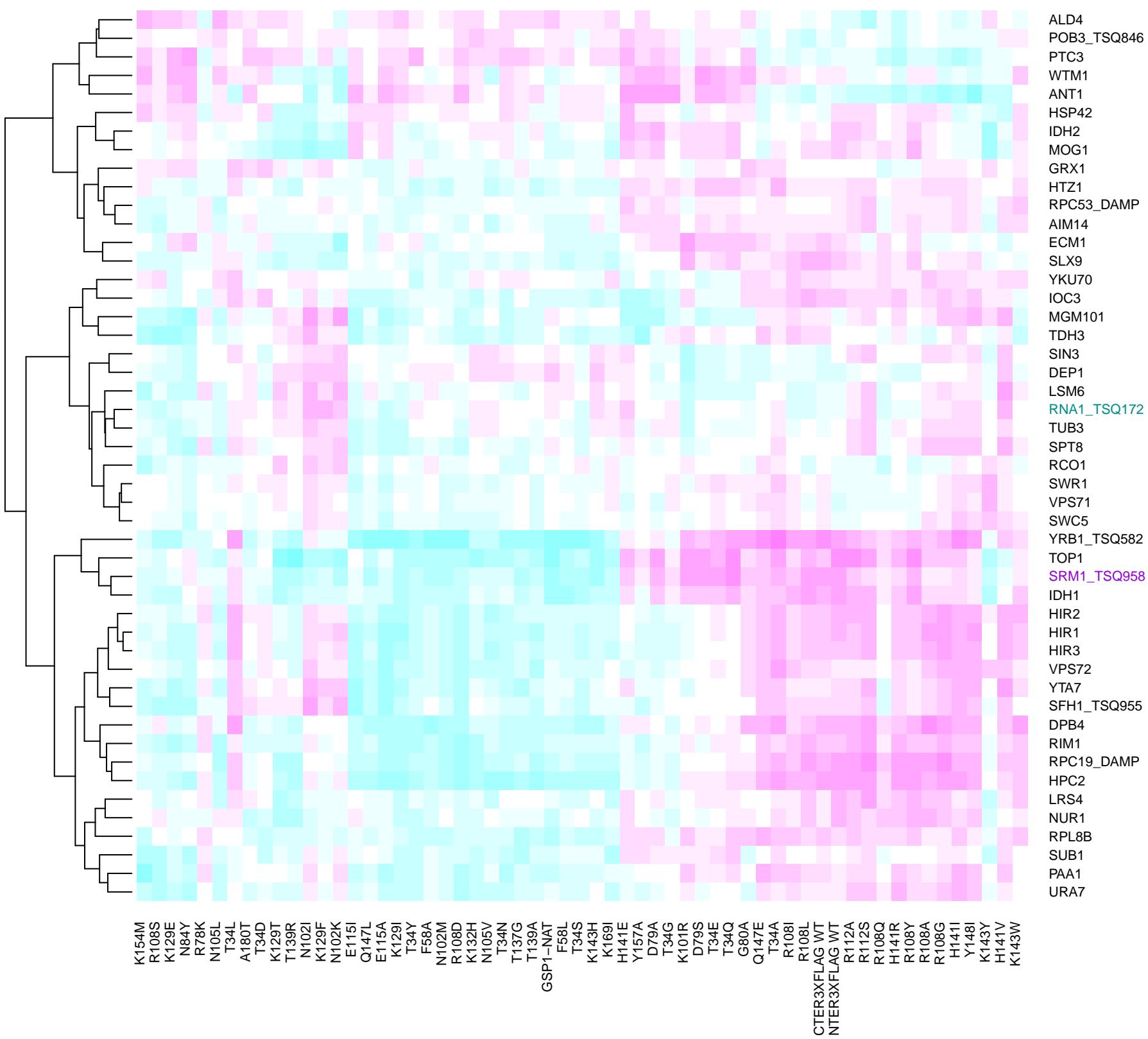


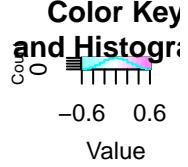
Golgi and ER_GO_30_5



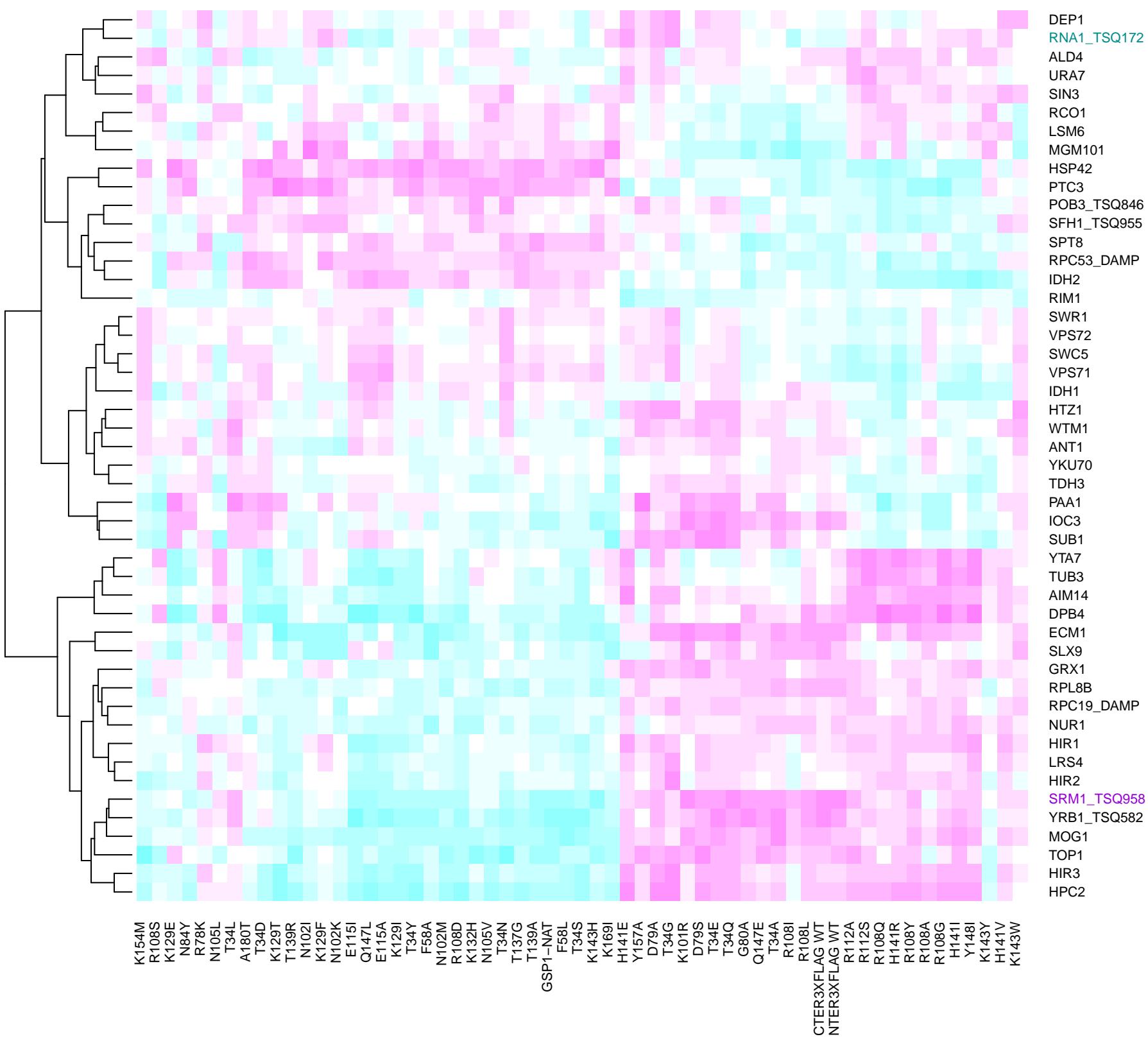


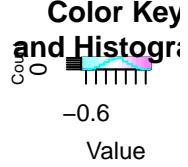
Golgi vesicle transport_GO_30_1



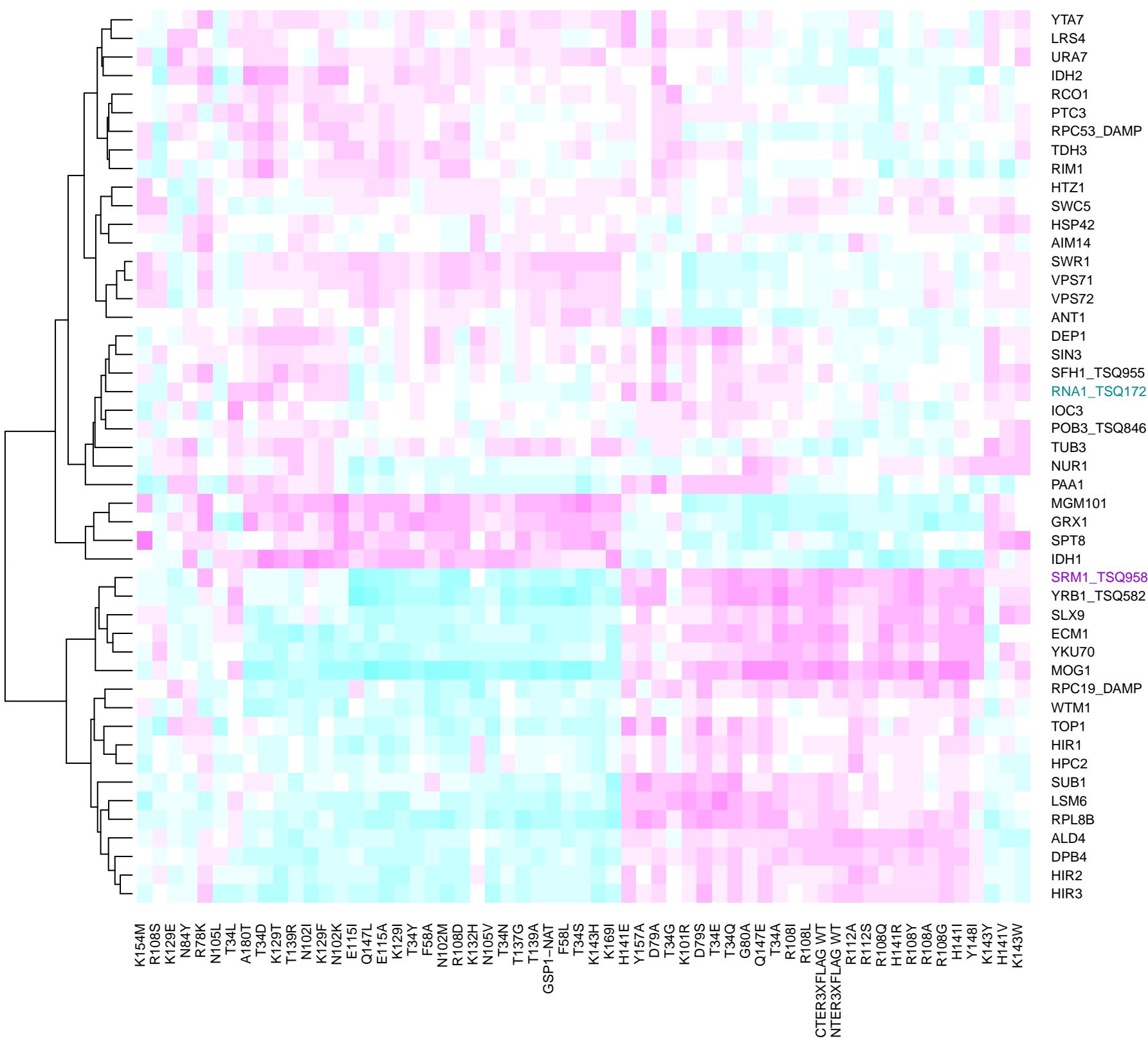


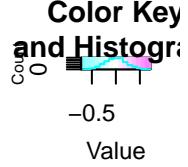
Golgi_GO_30_3



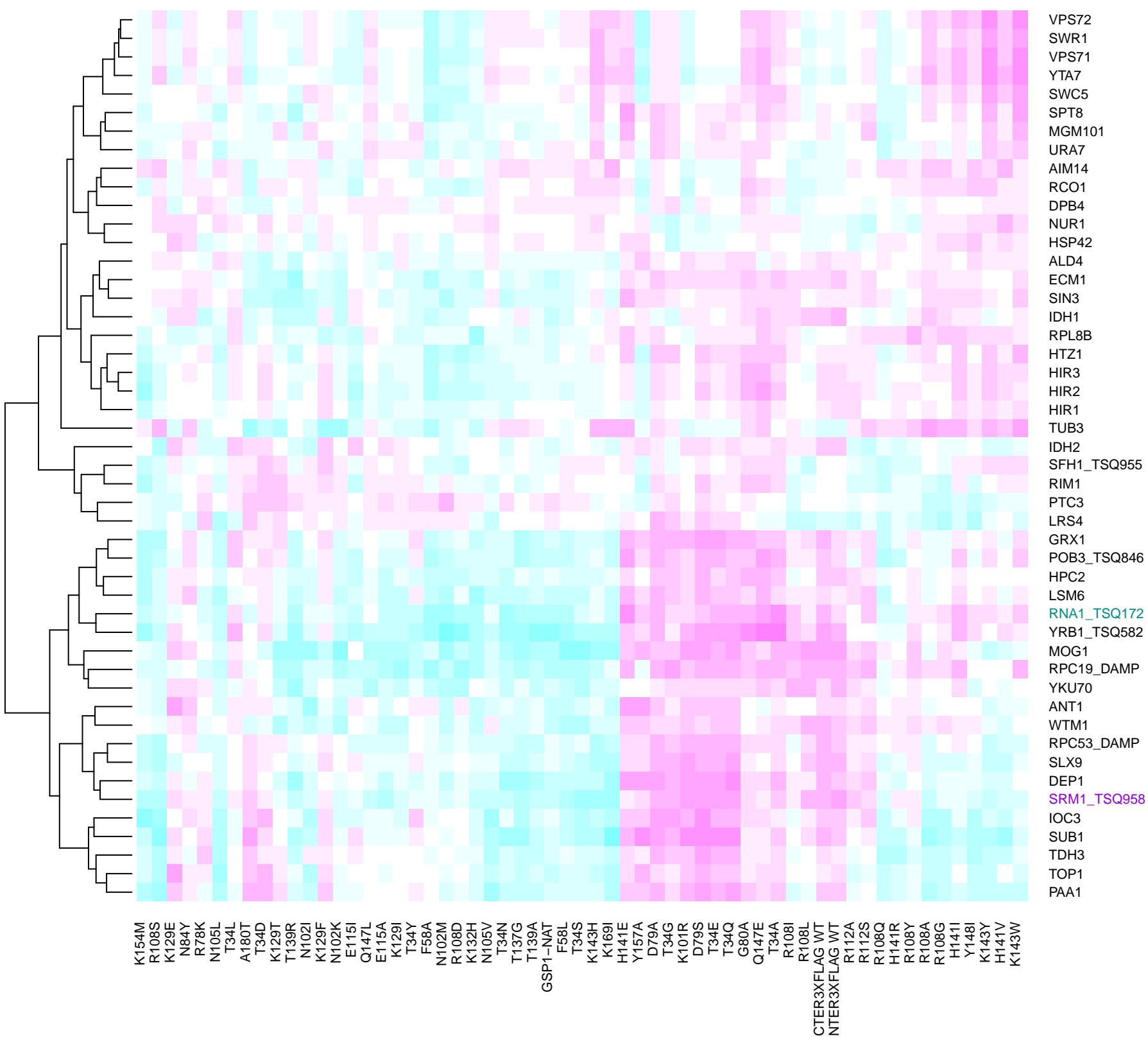


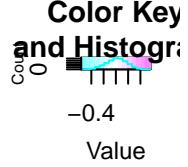
mitochondria and respiration_GO_30_7



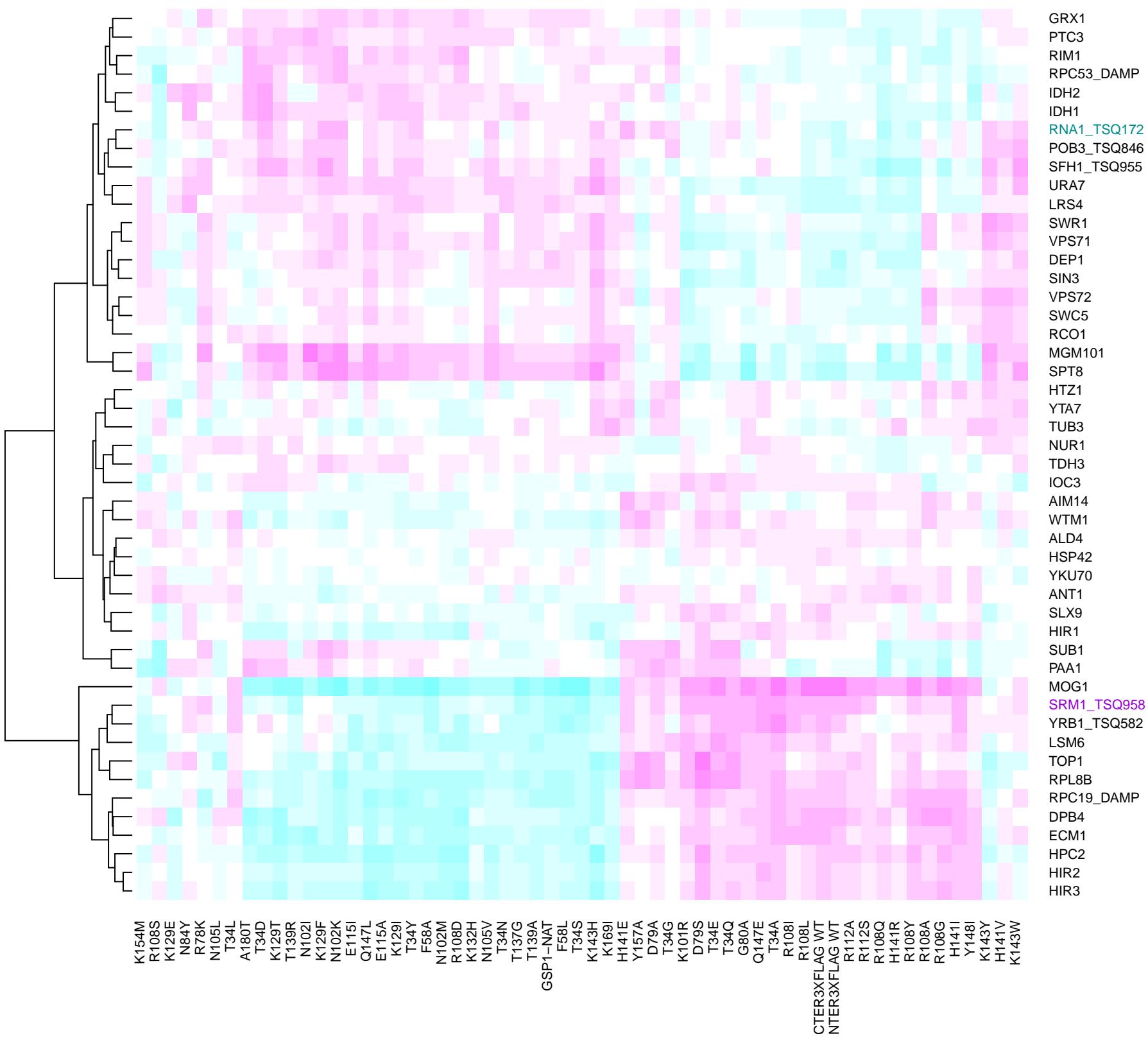


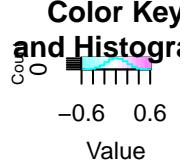
regulation of cell cycle_GO_30_2



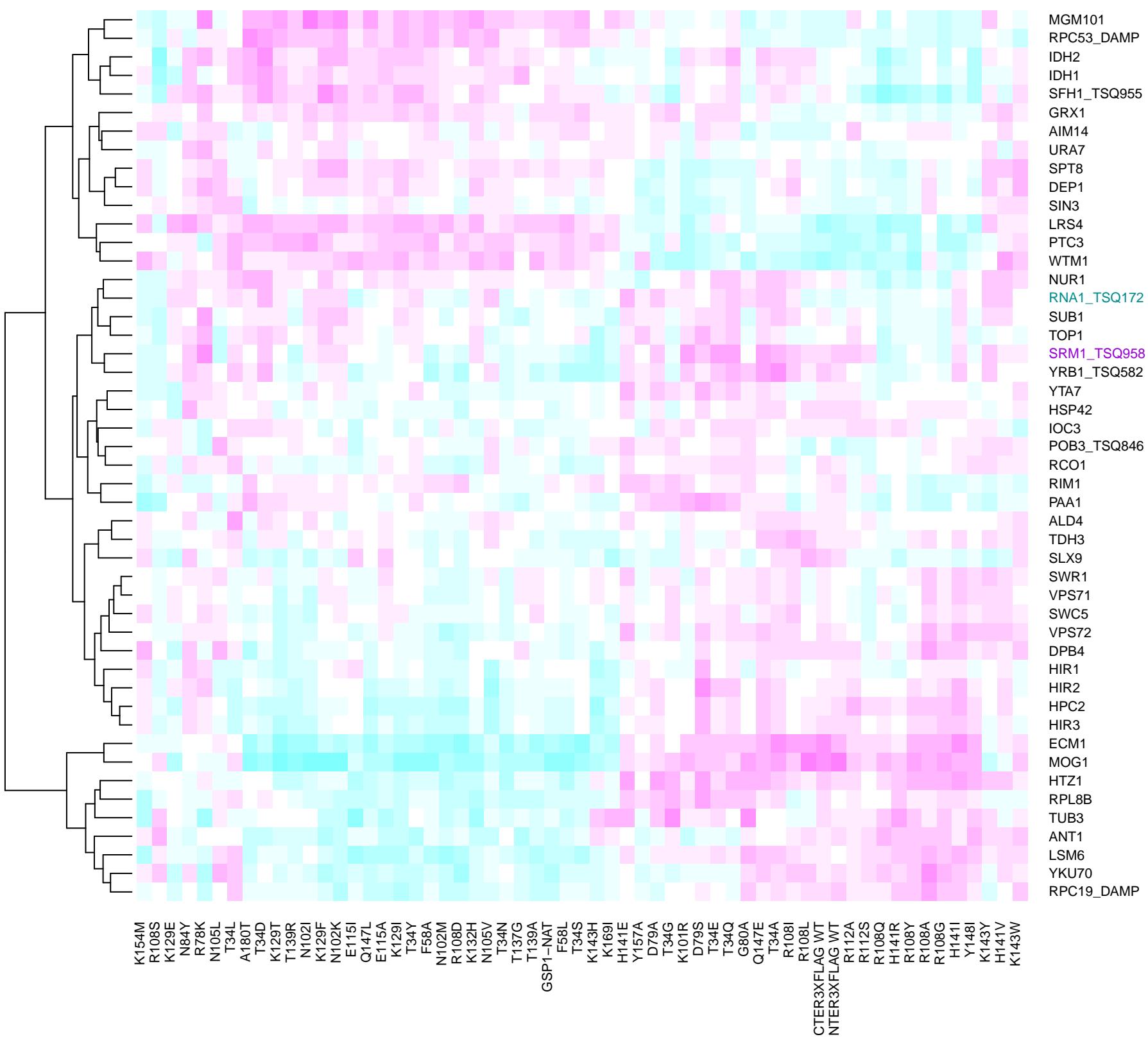


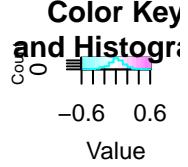
mitochondrial envelope



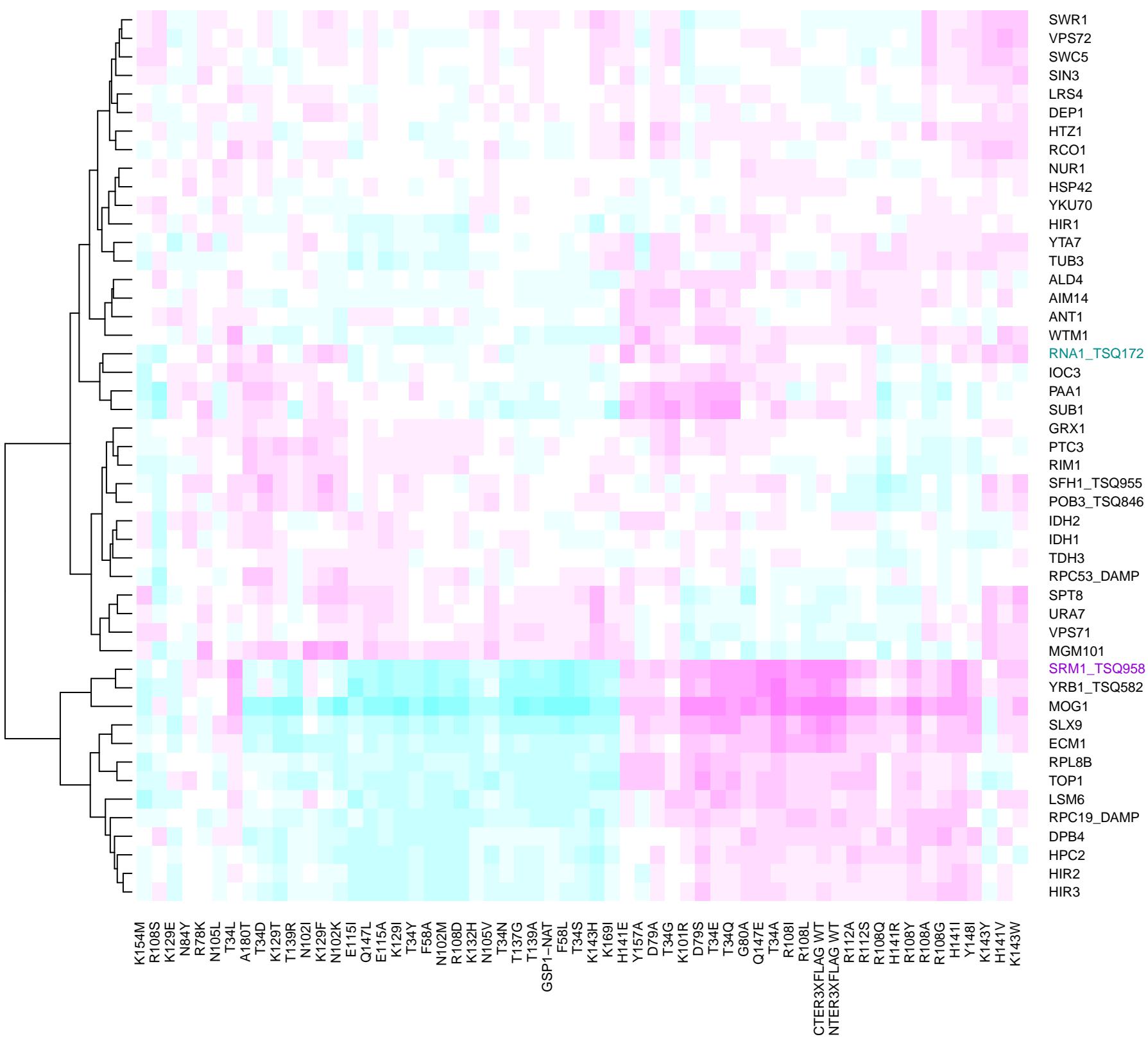


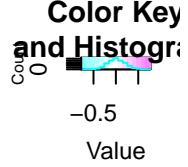
mitochondrial envelope_GO_30_2



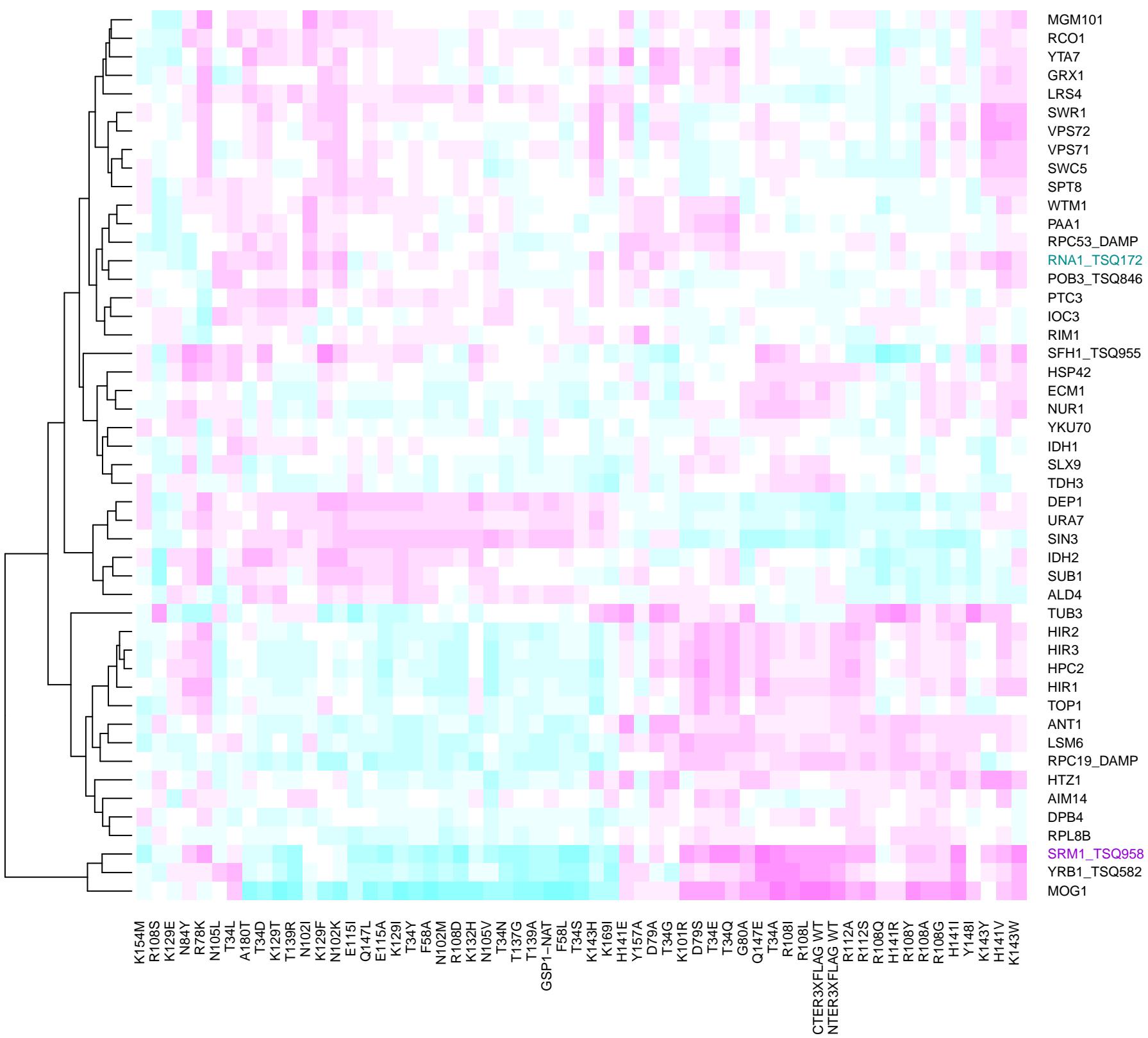


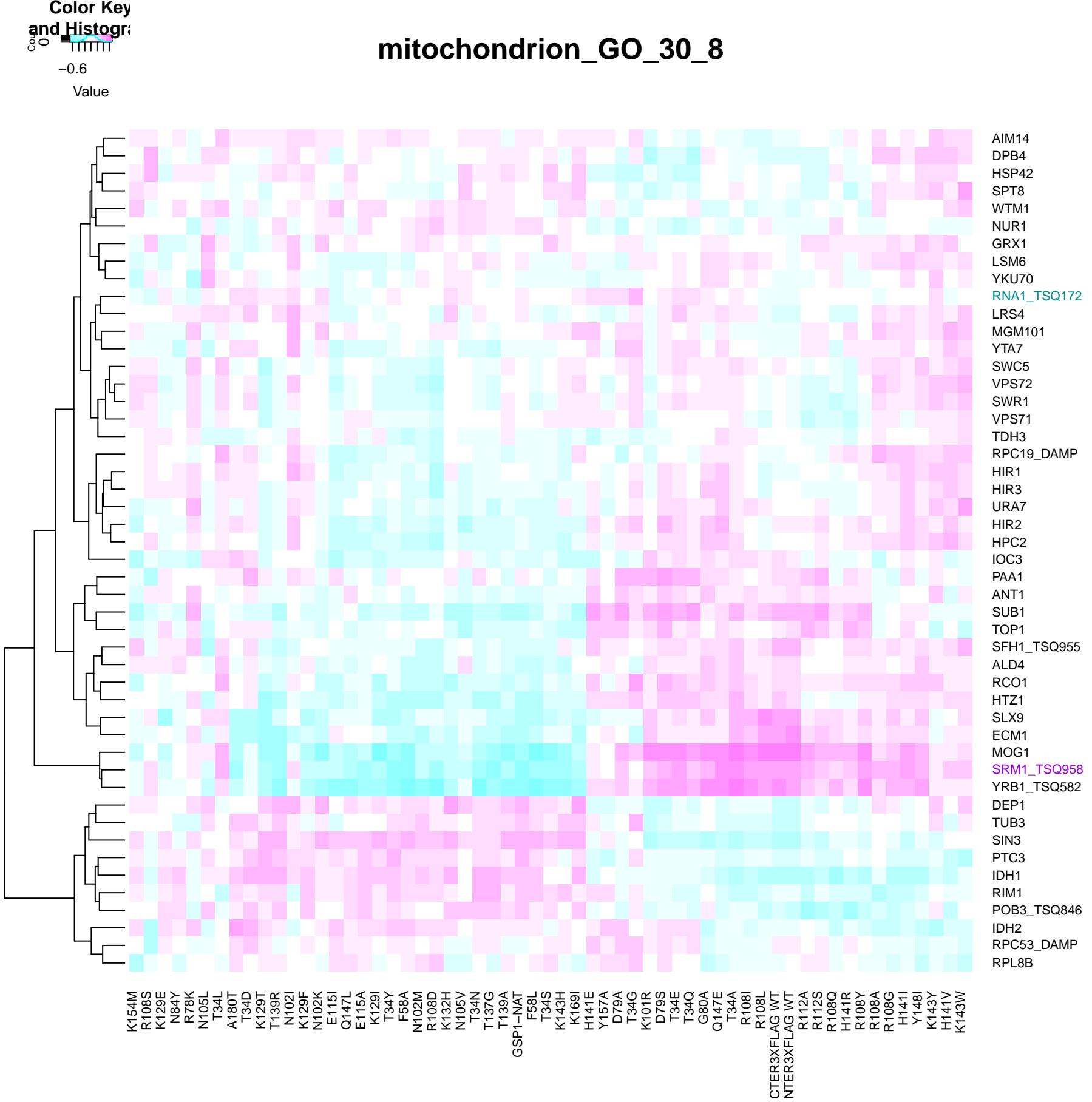
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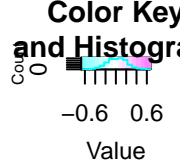




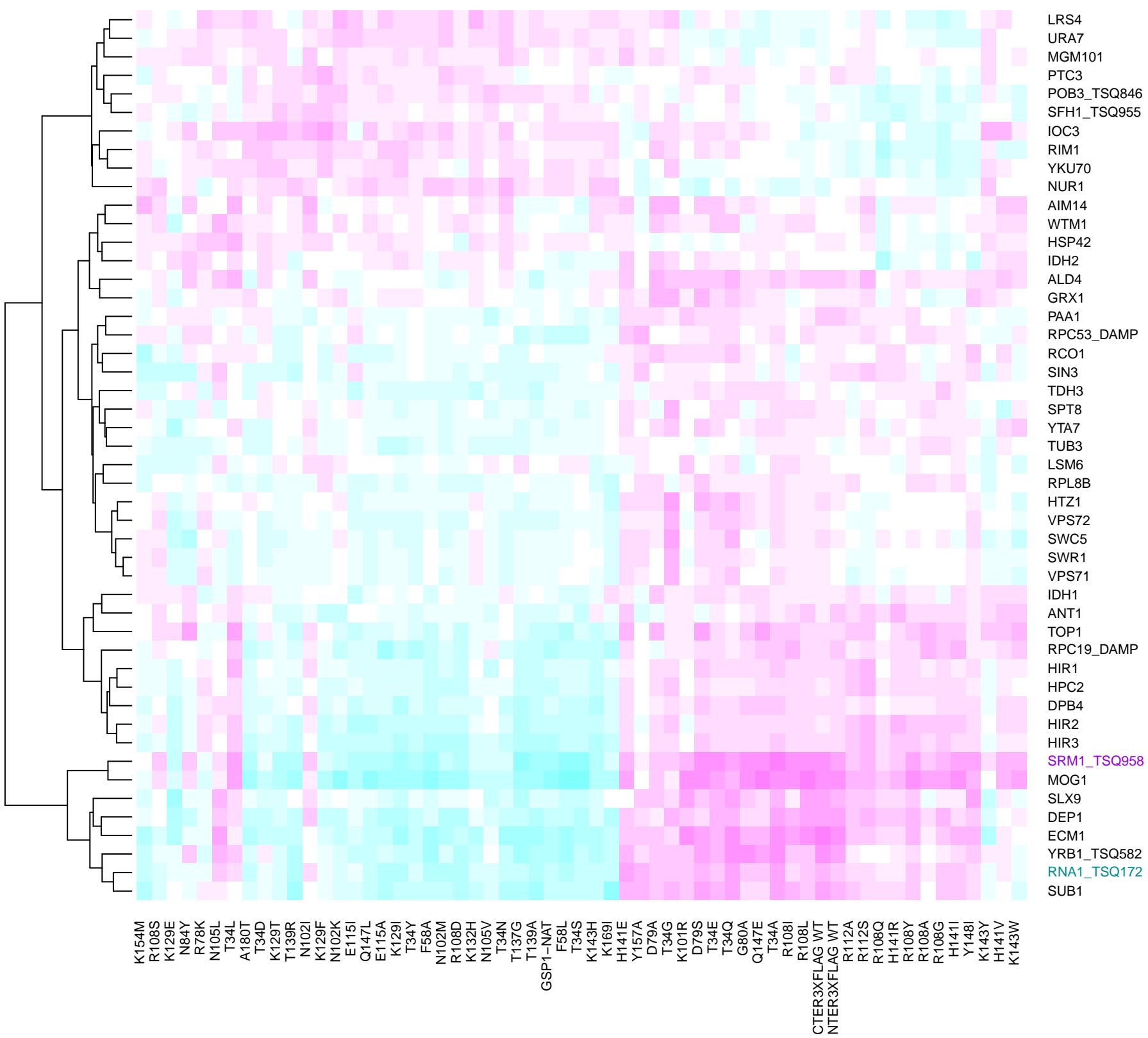
mitochondrion organization_GO_30_3

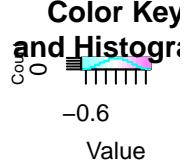




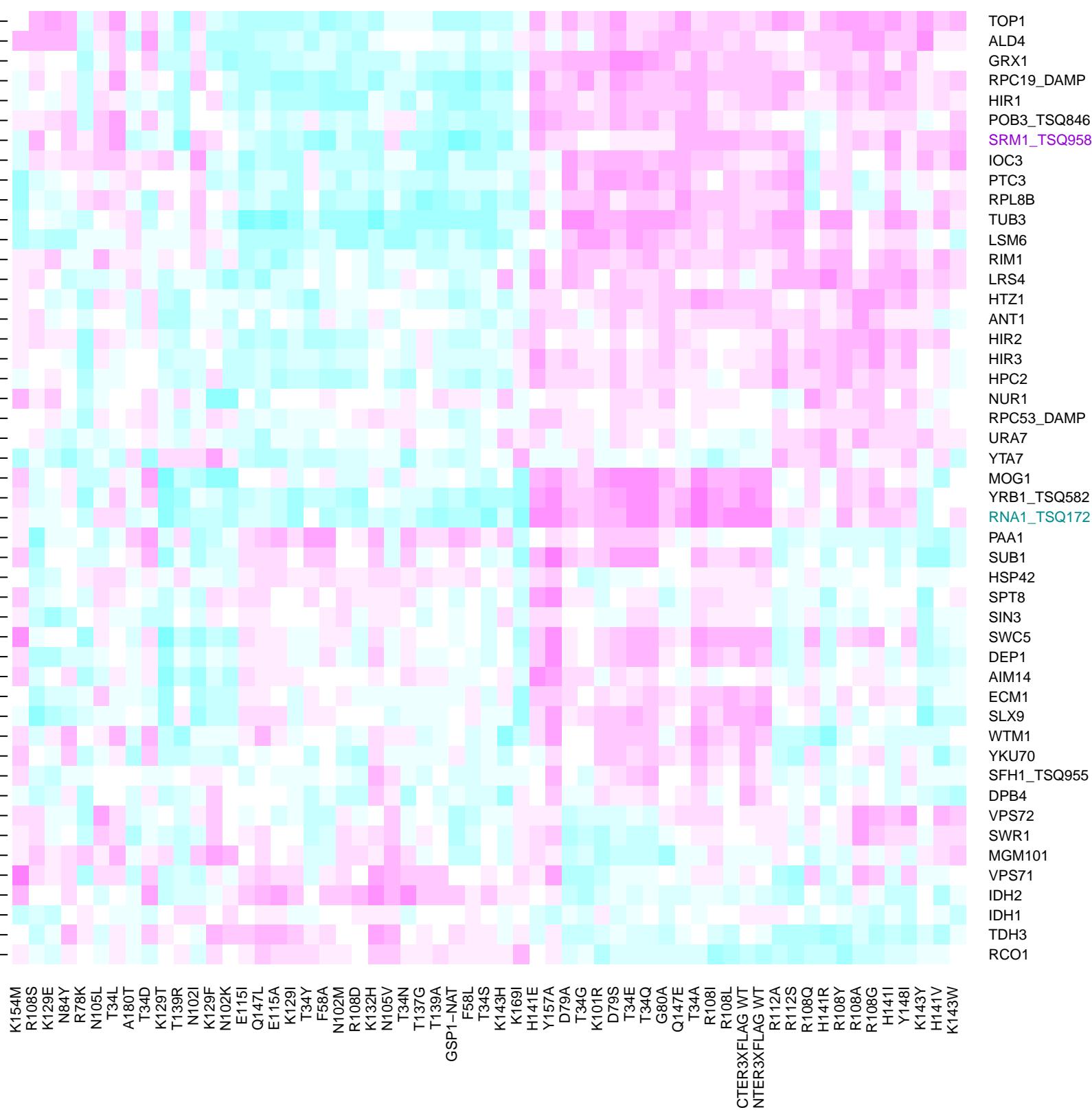


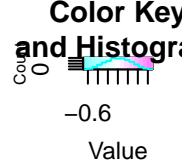
endomembrane system_GO_30_3



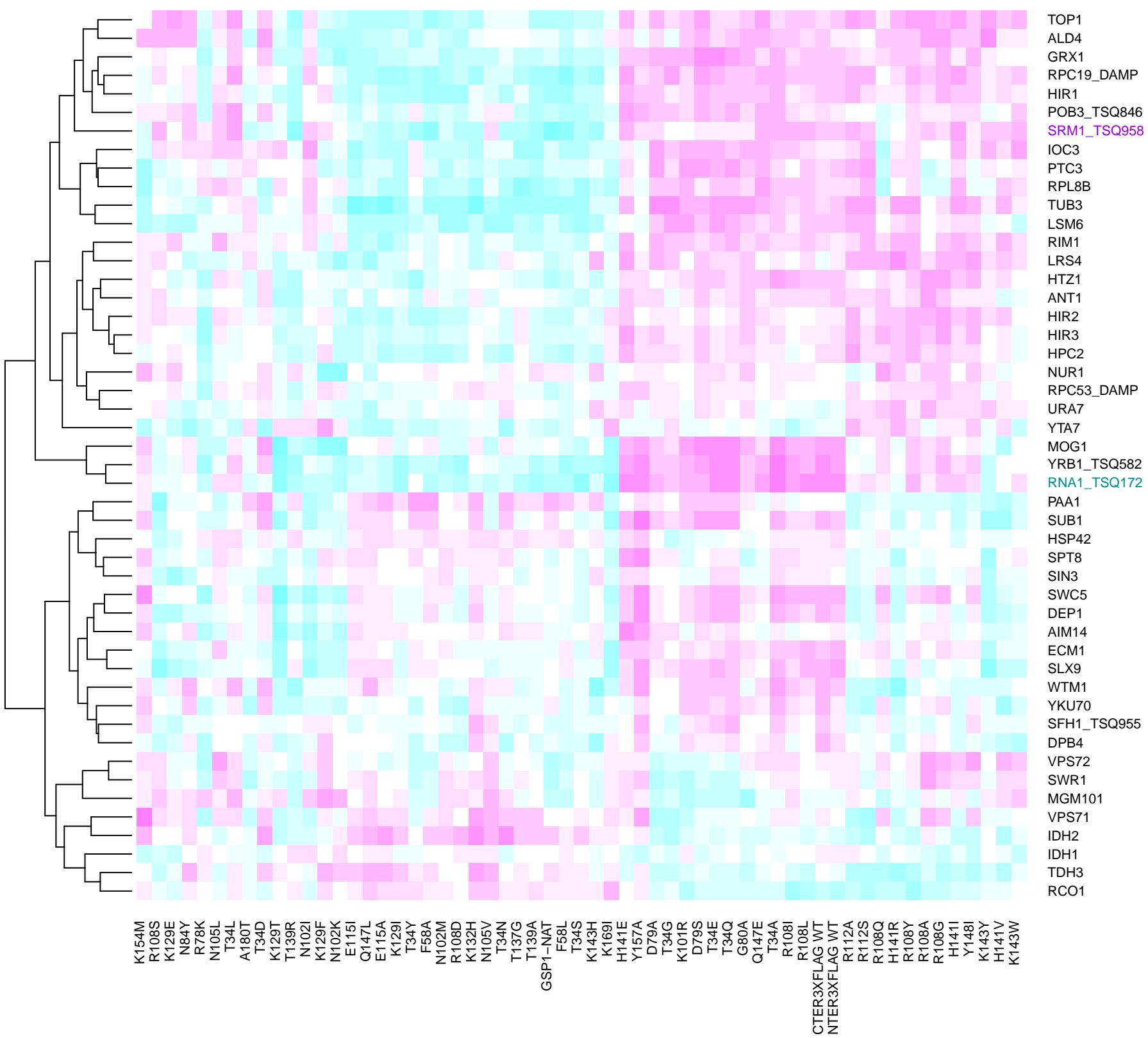


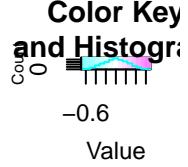
endoplasmic reticulum_GO_30_12



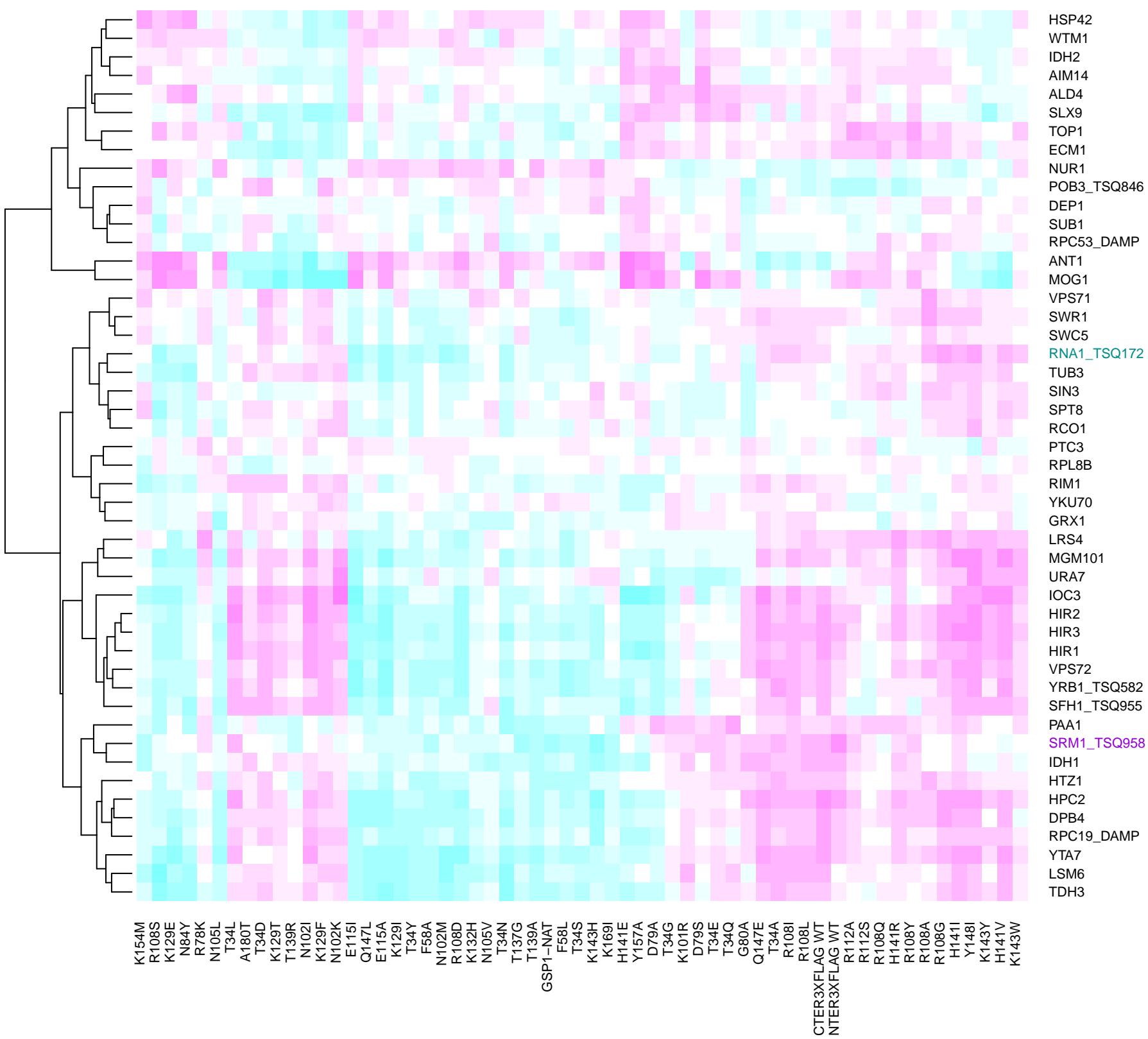


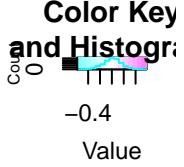
ER_GO_30_12



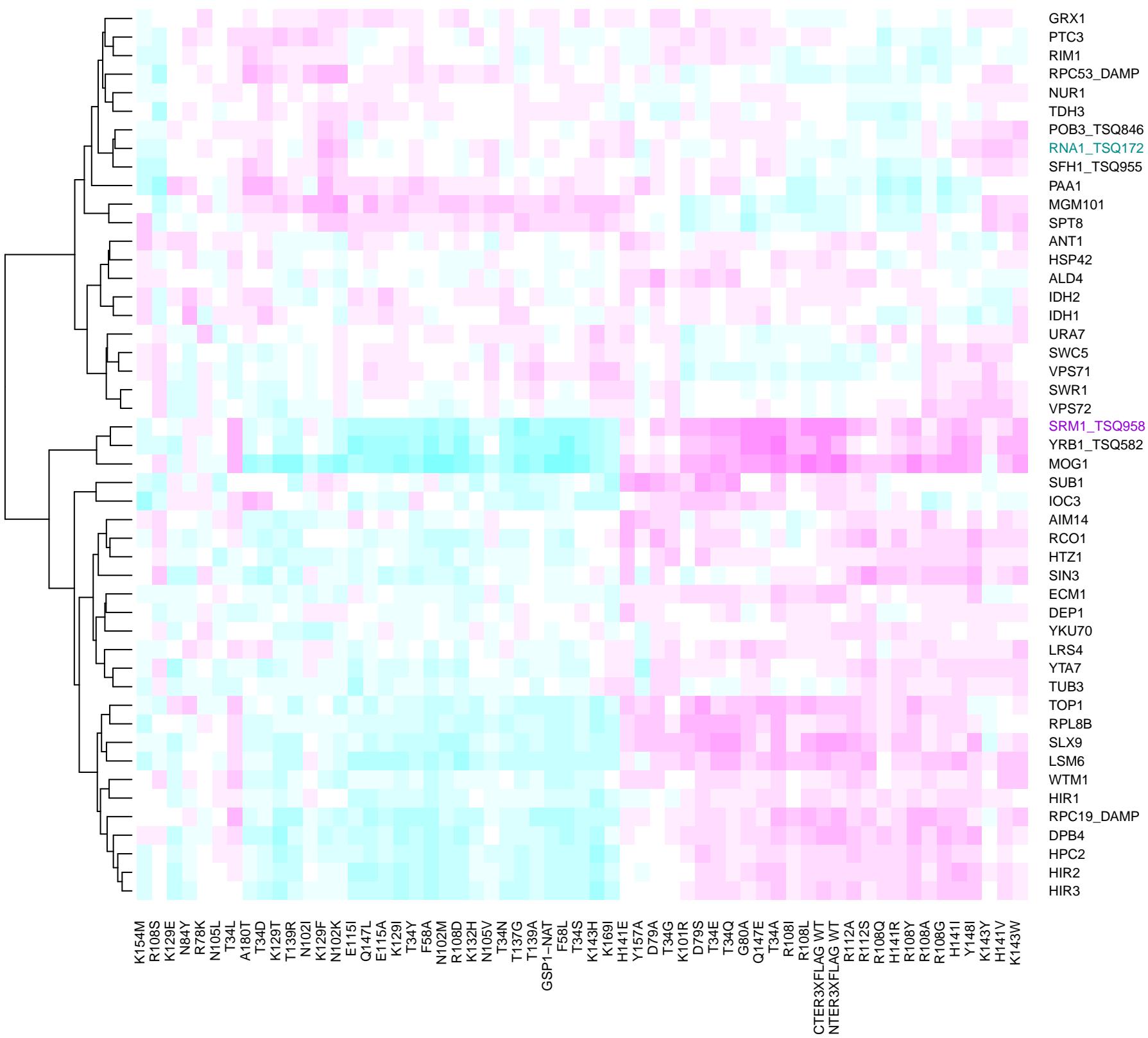


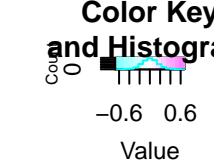
Golgi and ER_GO_30_6



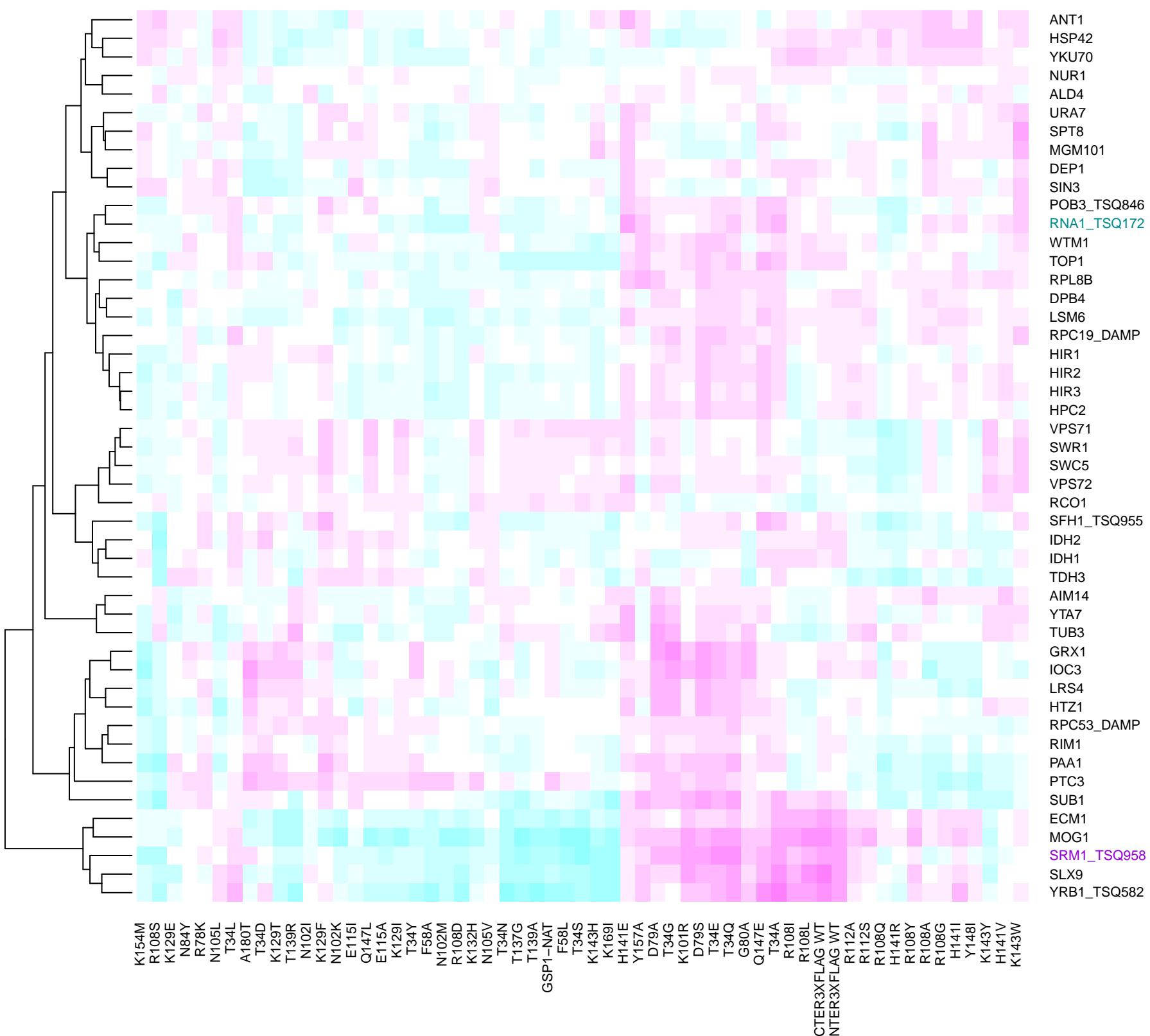


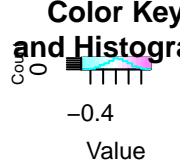
ion transport



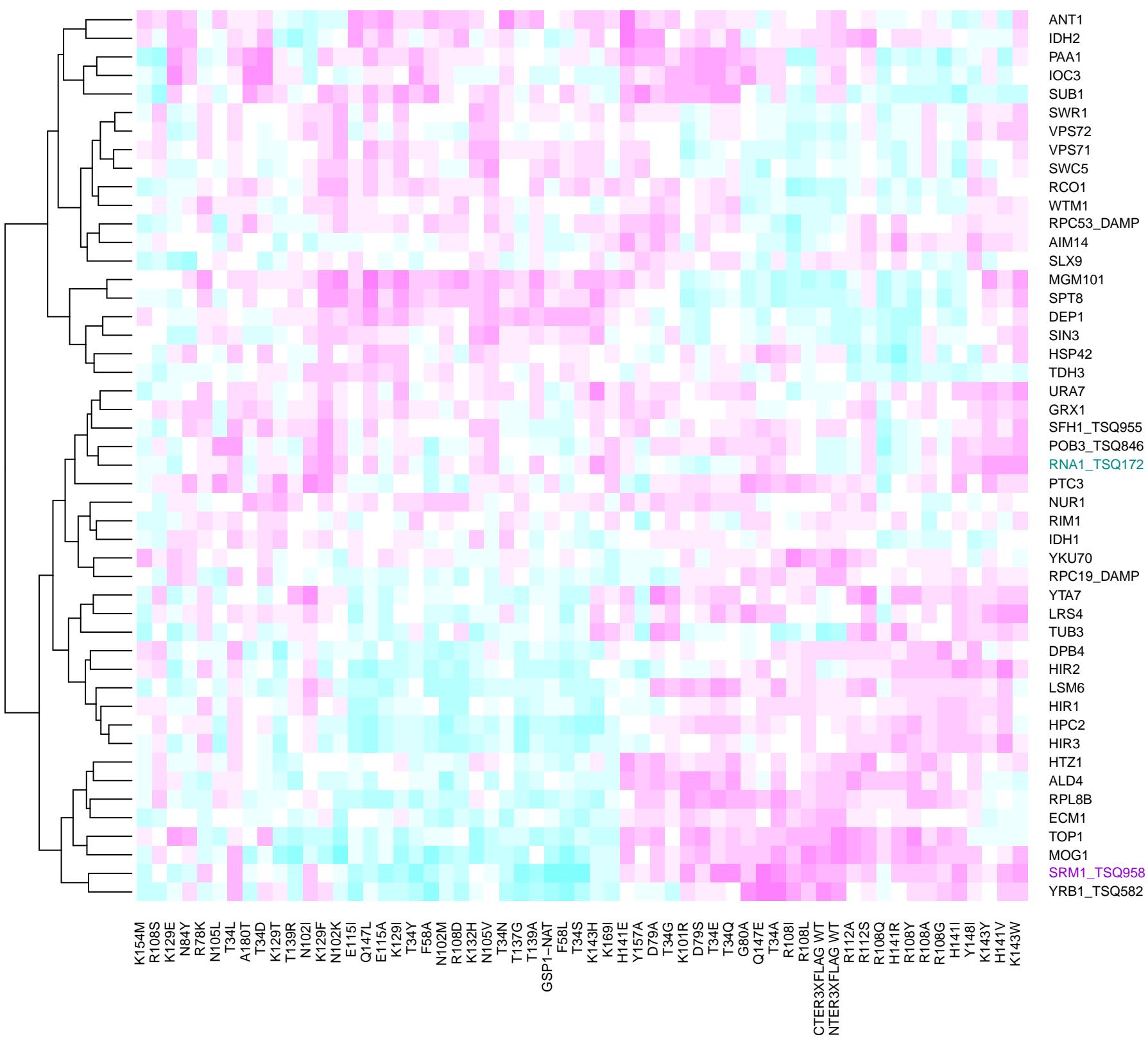


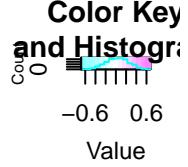
regulation of organelle organization



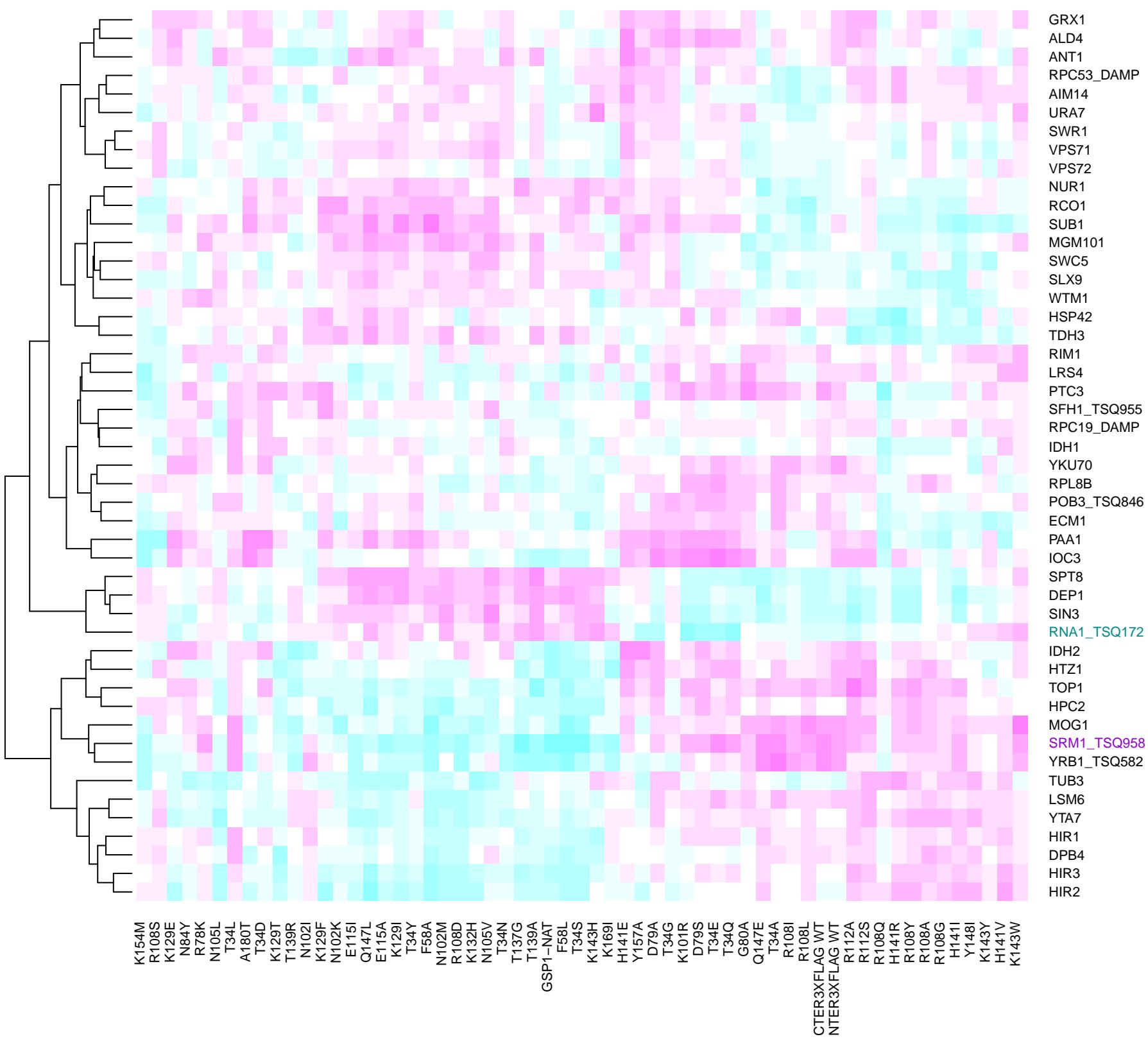


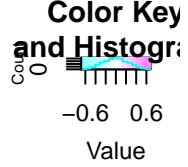
lipid transport



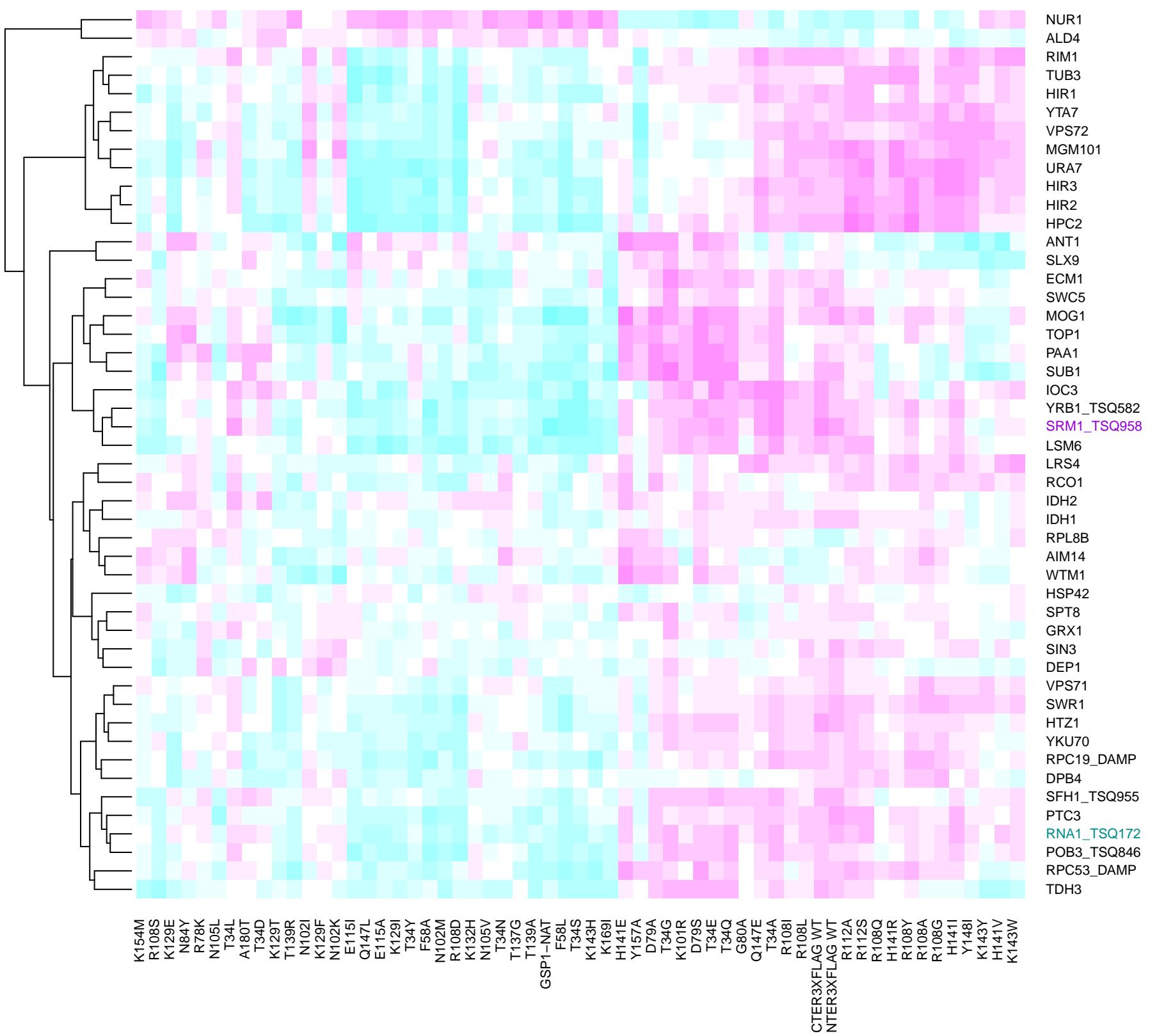


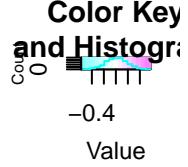
lipid transport_GO_30_1



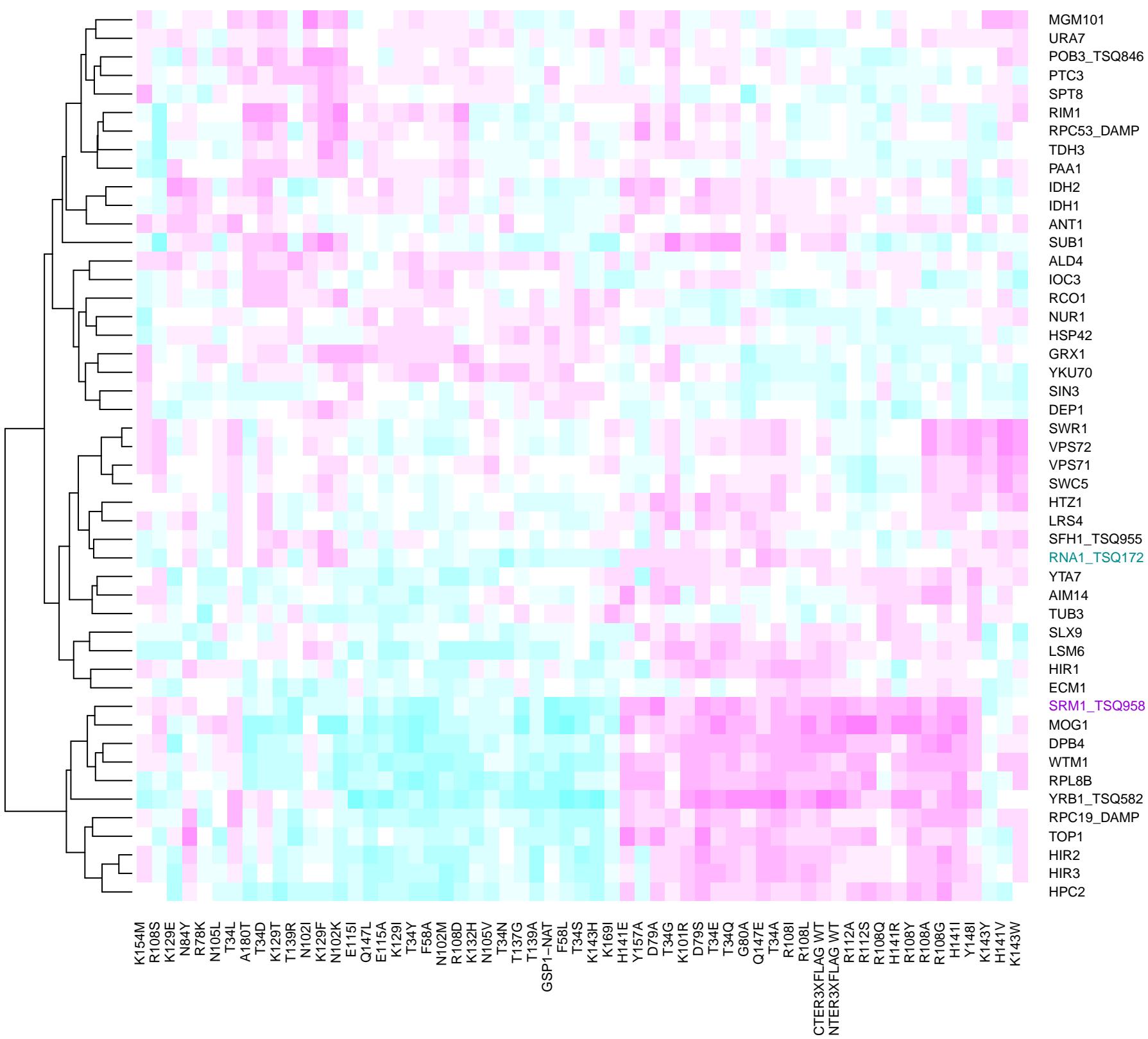


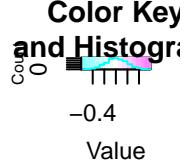
mitochondria and respiration_GO_30_8



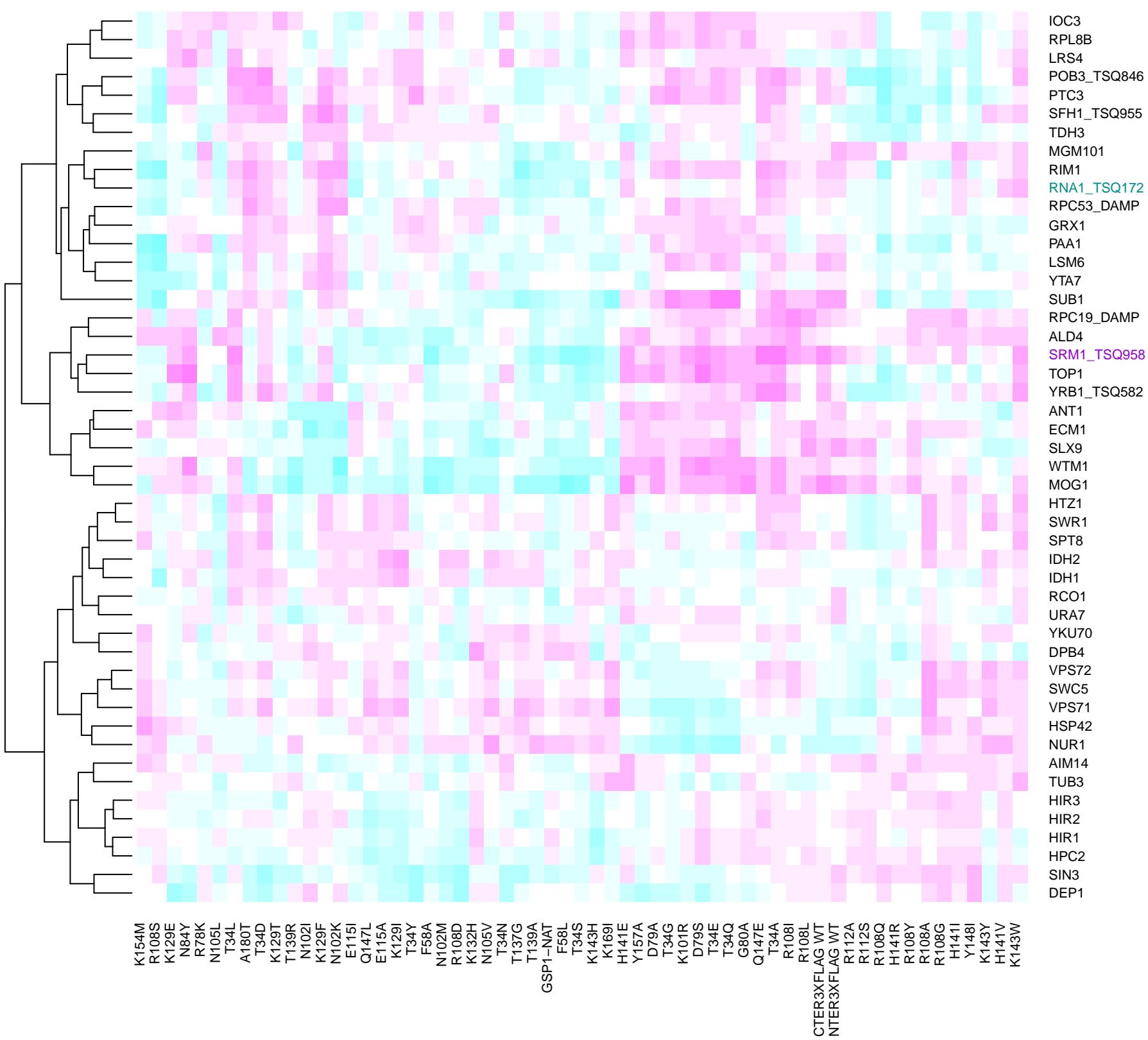


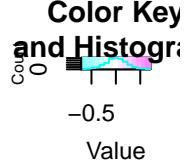
mitochondrial envelope_GO_30_1



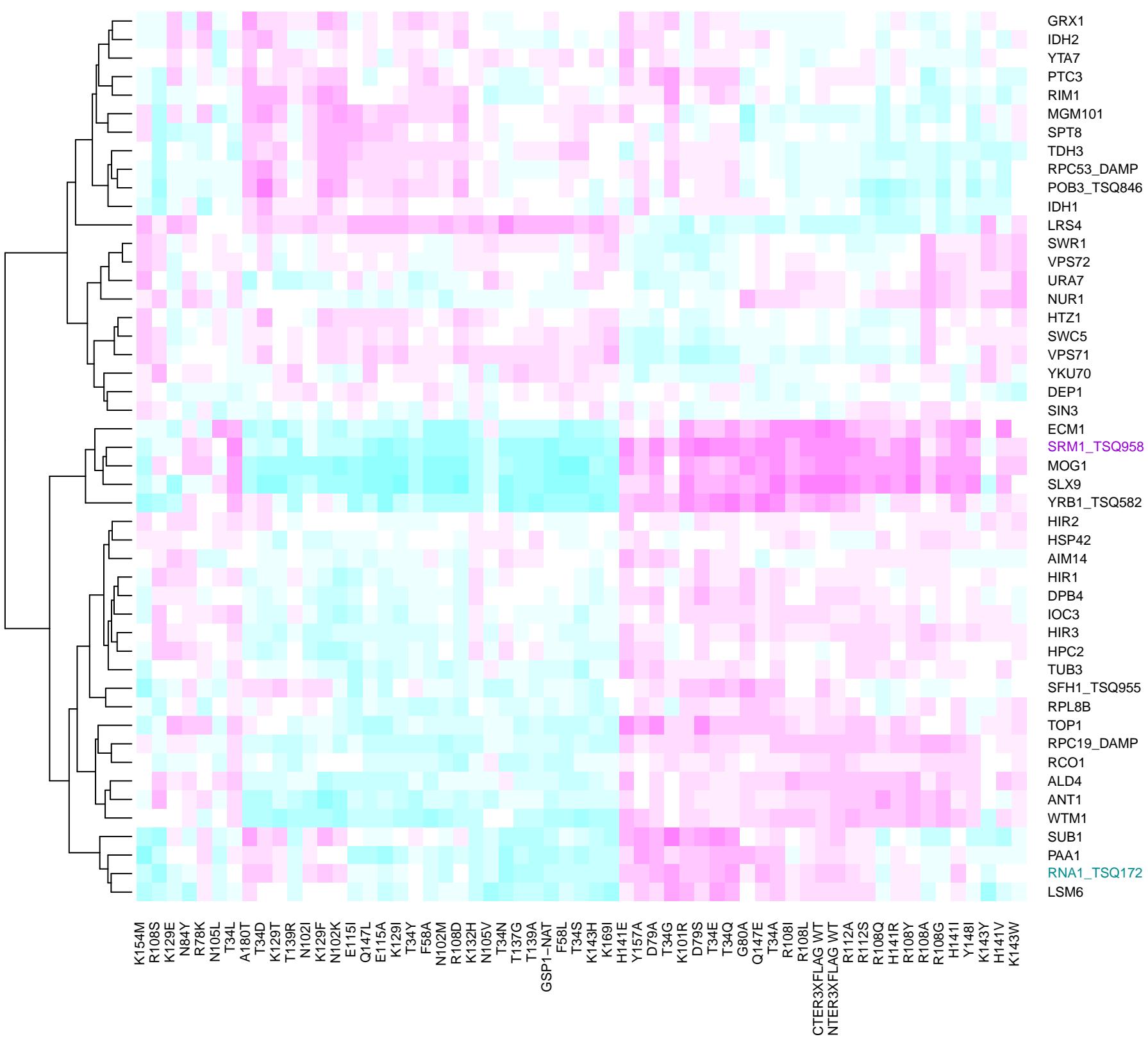


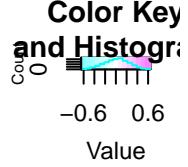
mitochondrion organization_GO_30_1



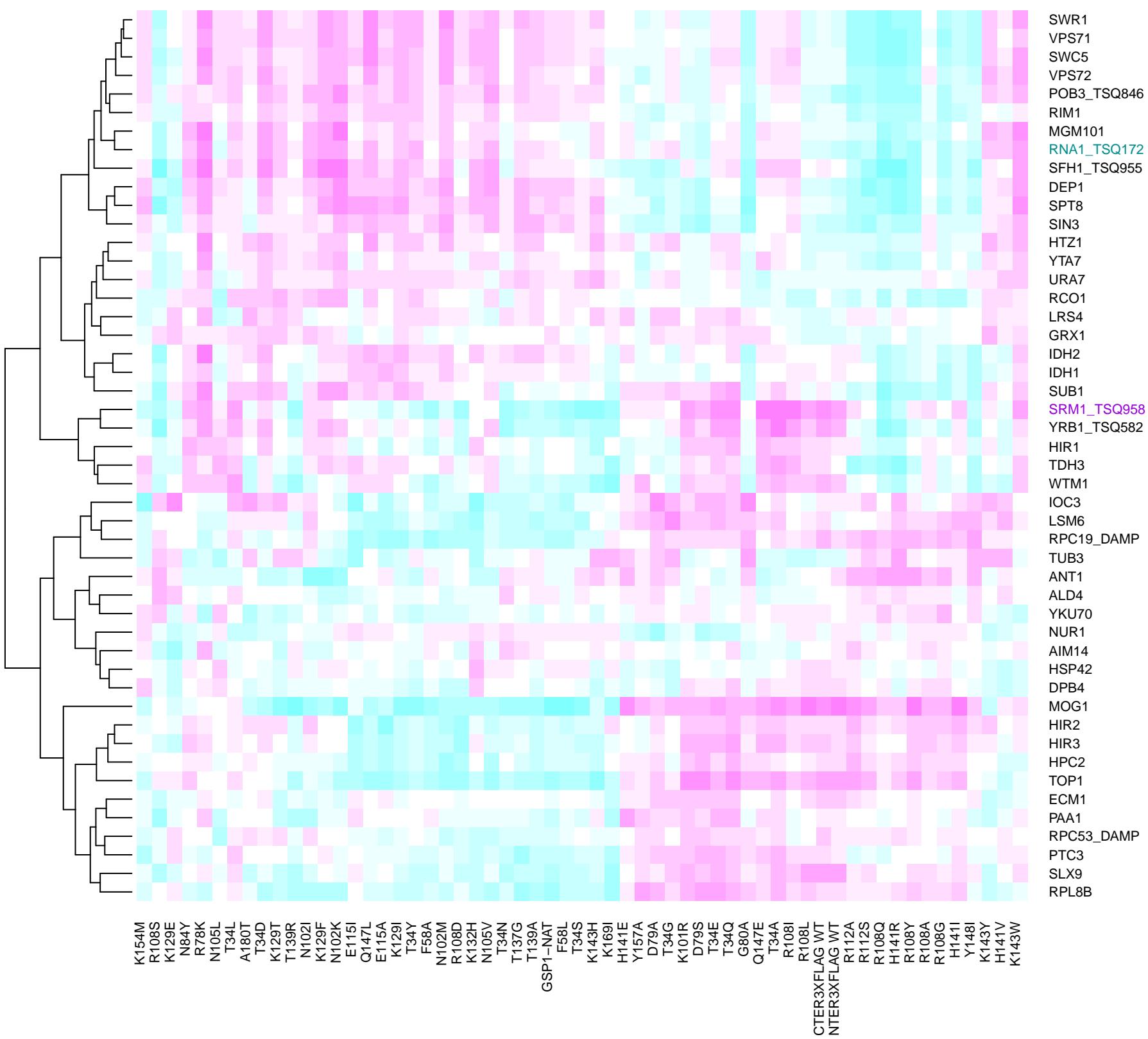


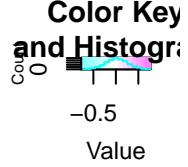
mitochondrion_GO_30_5



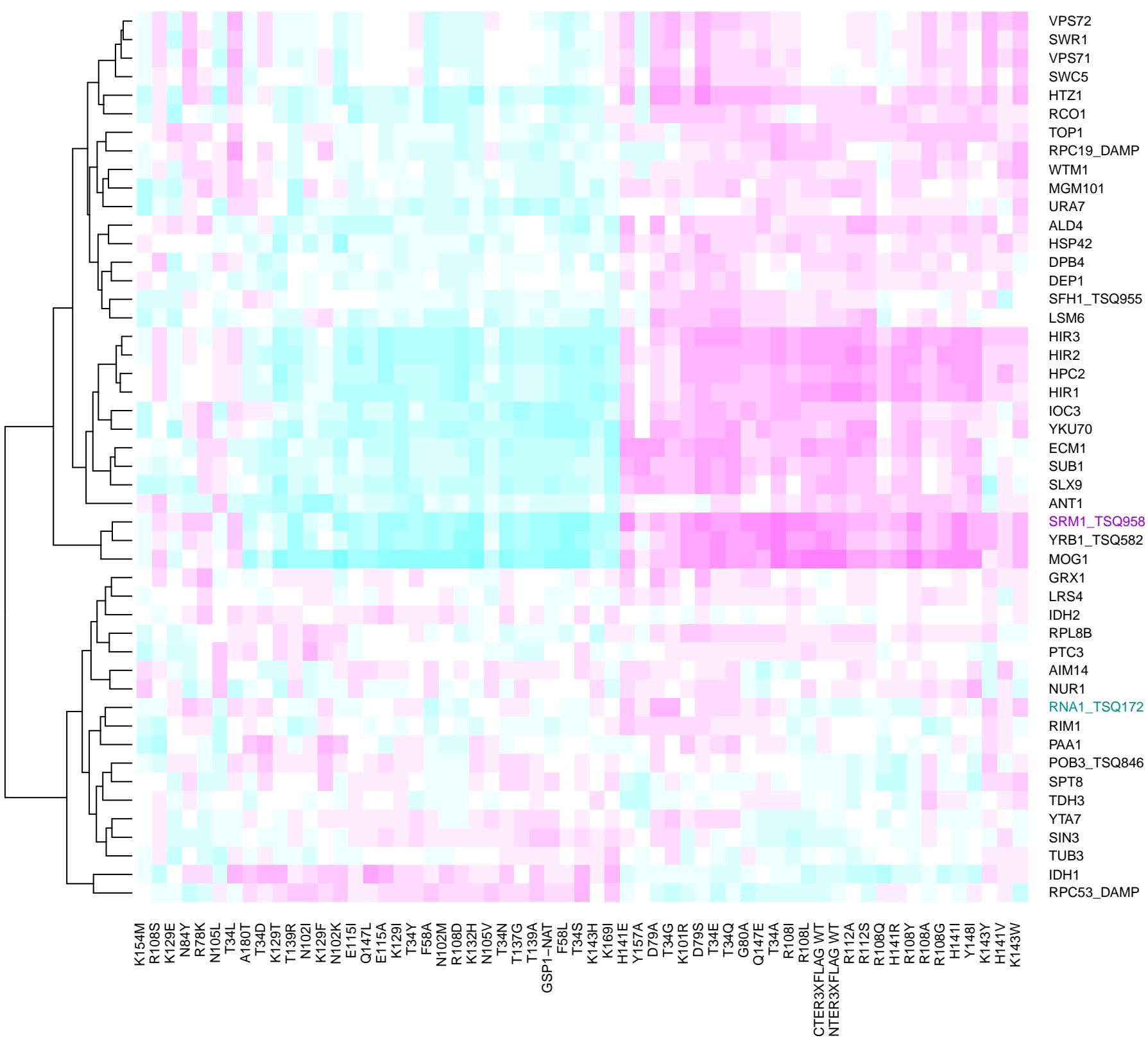


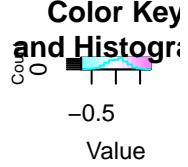
protein targeting_GO_30_3



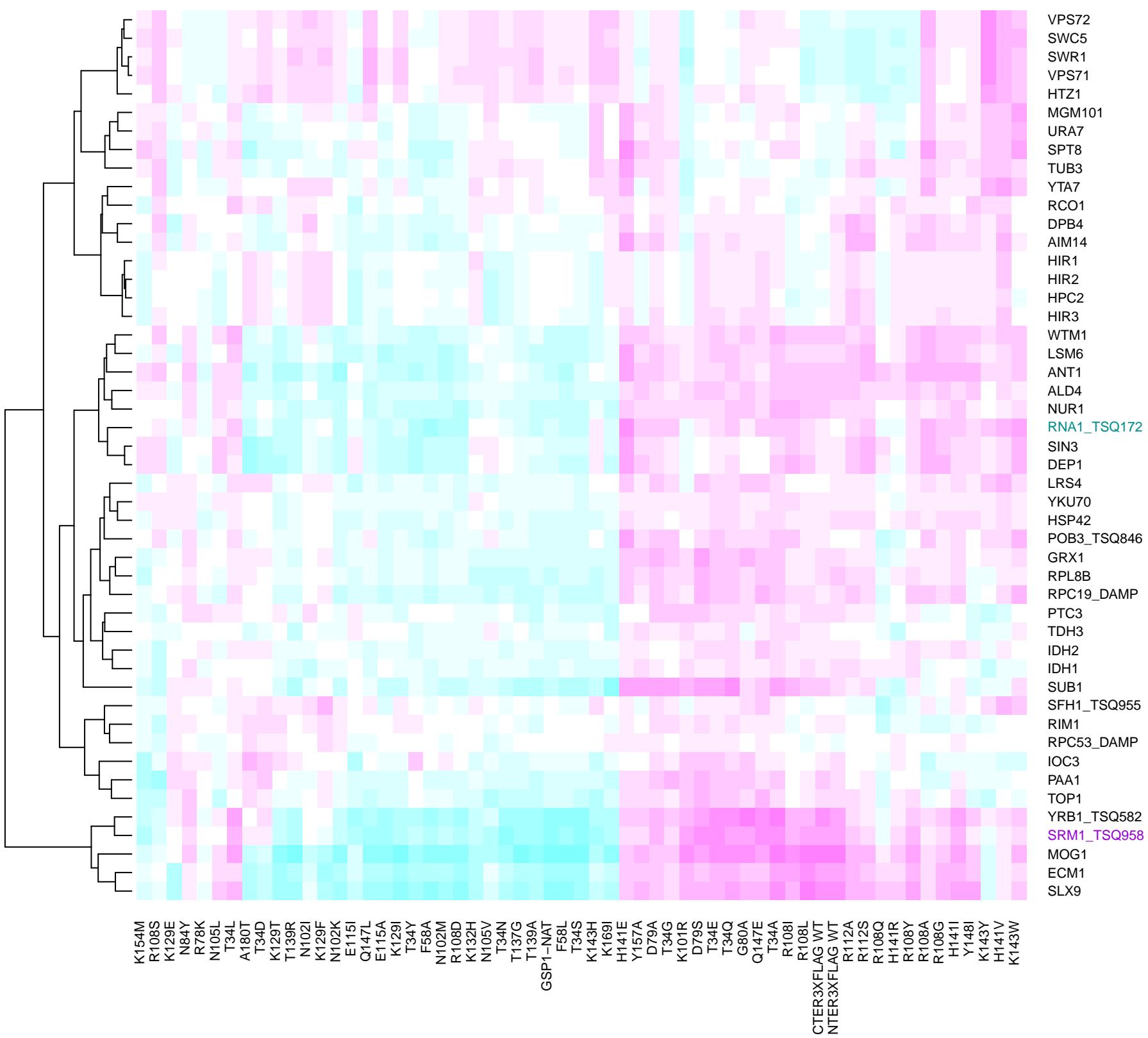


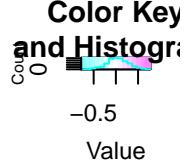
transmembrane transport_GO_30_3



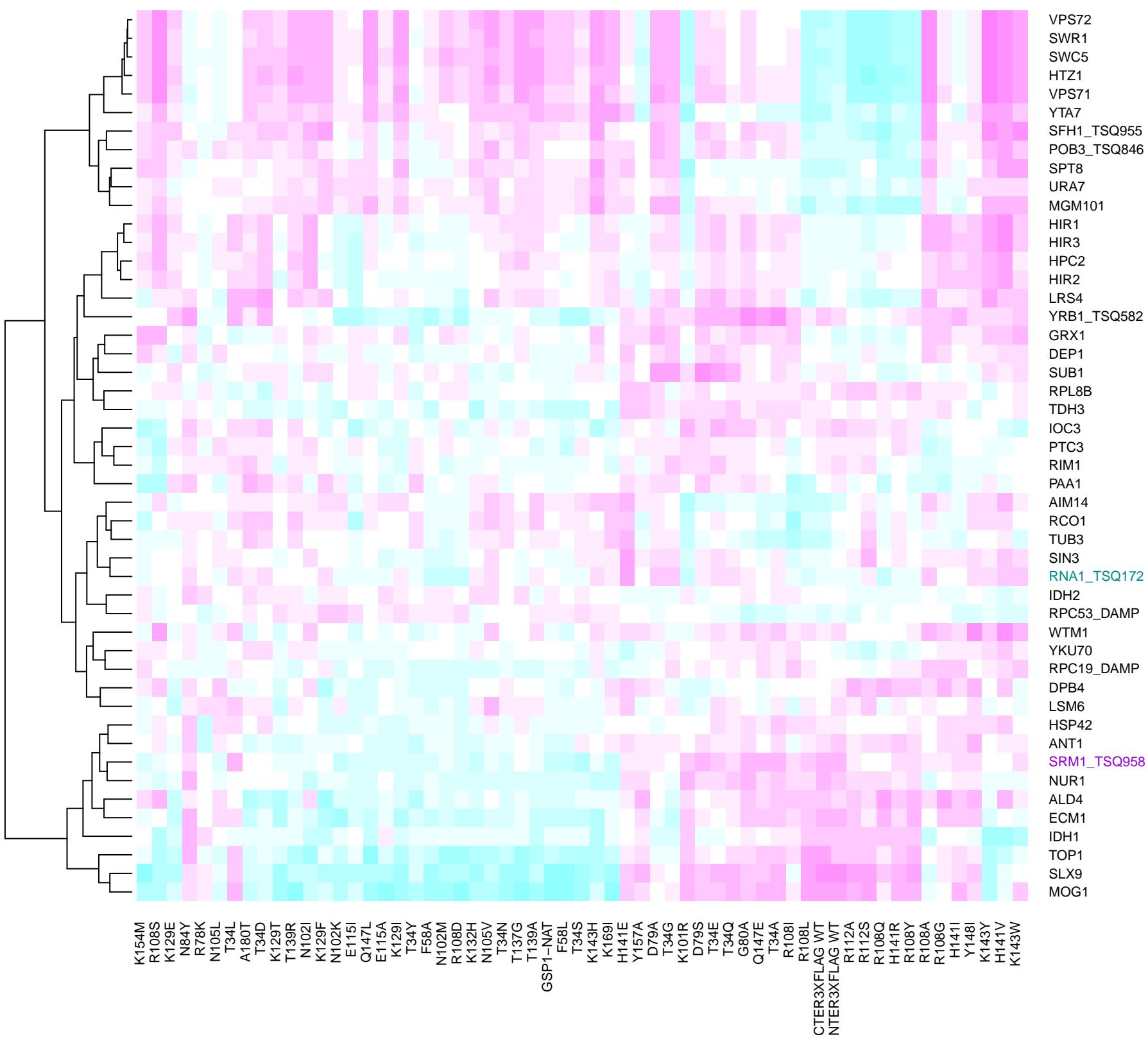


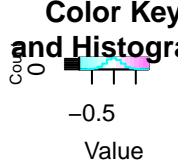
chromatin organization





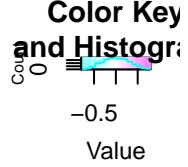
chromatin organization_GO_30_2



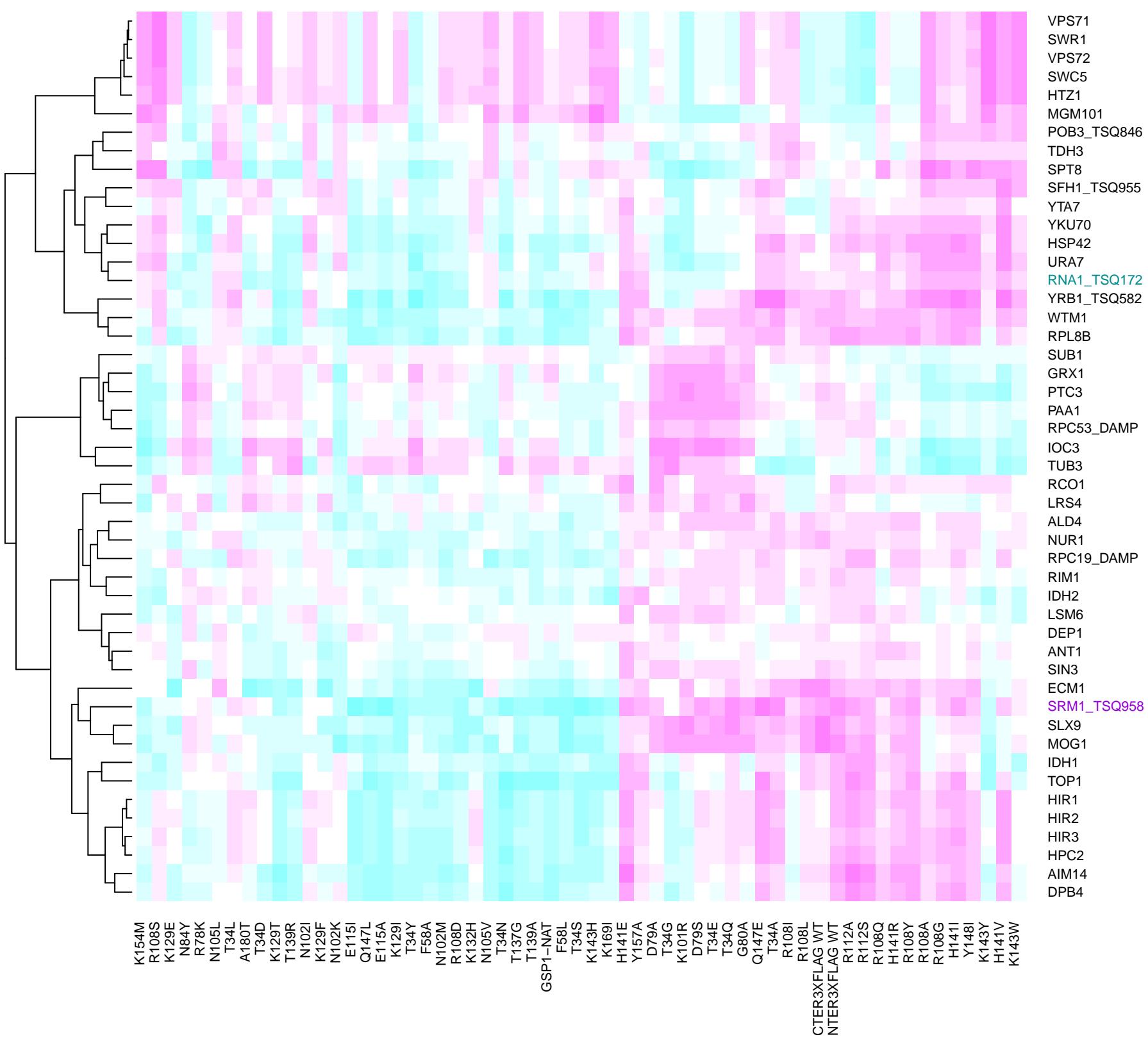


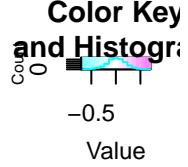
regulation of organelle organization_GO_30_1



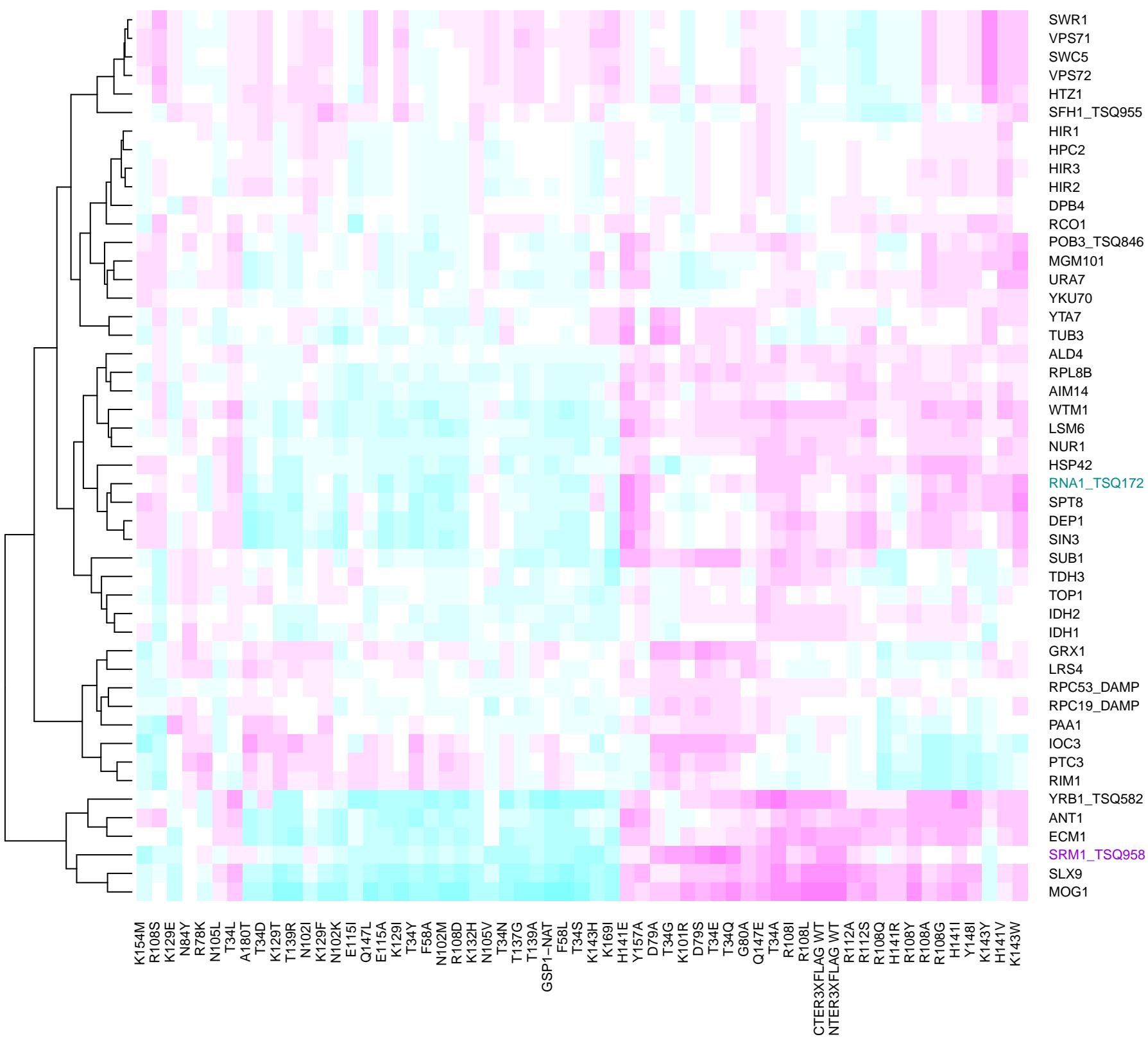


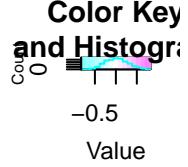
chromatin_GO_30_4



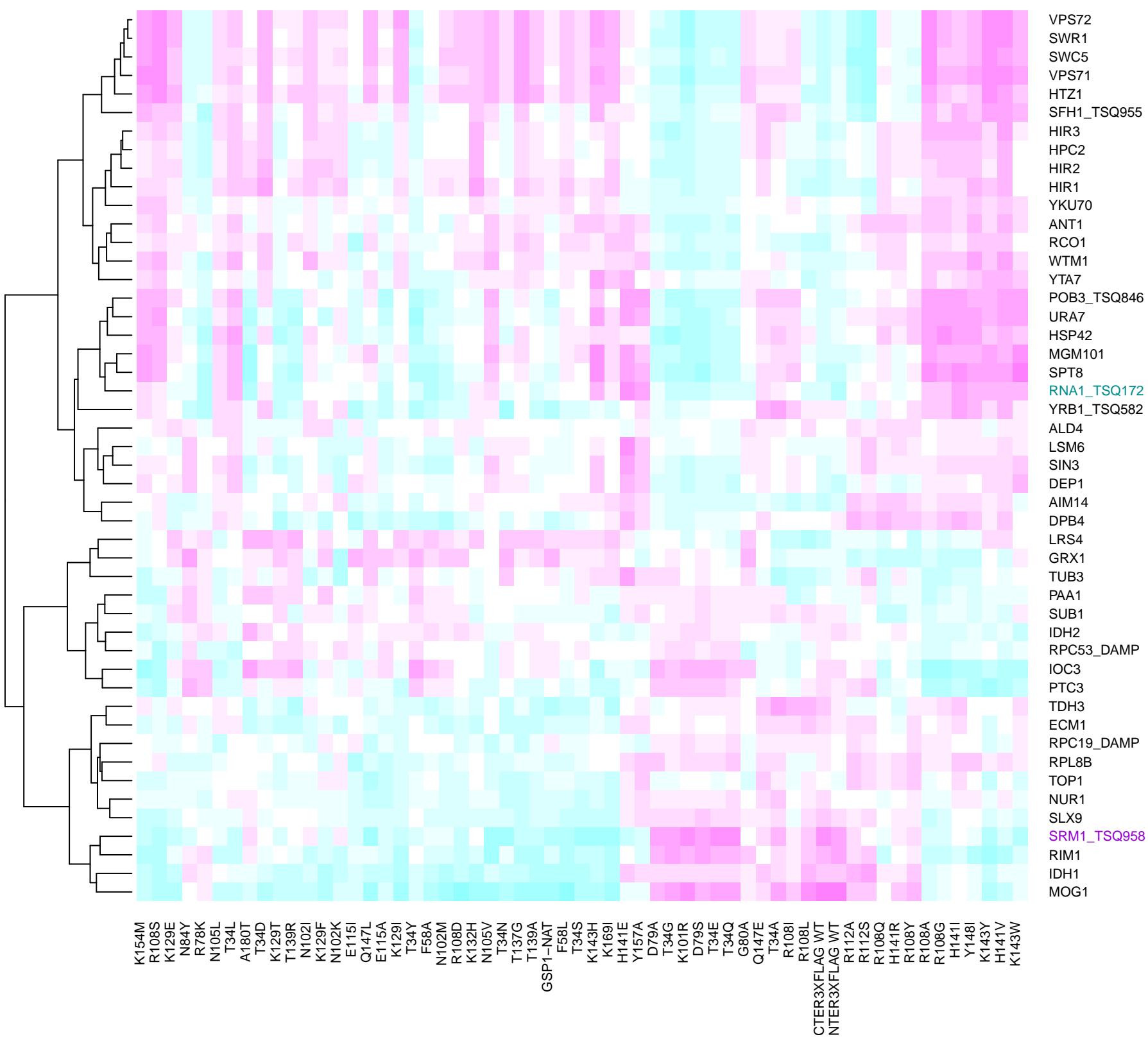


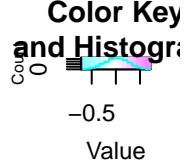
chromosome



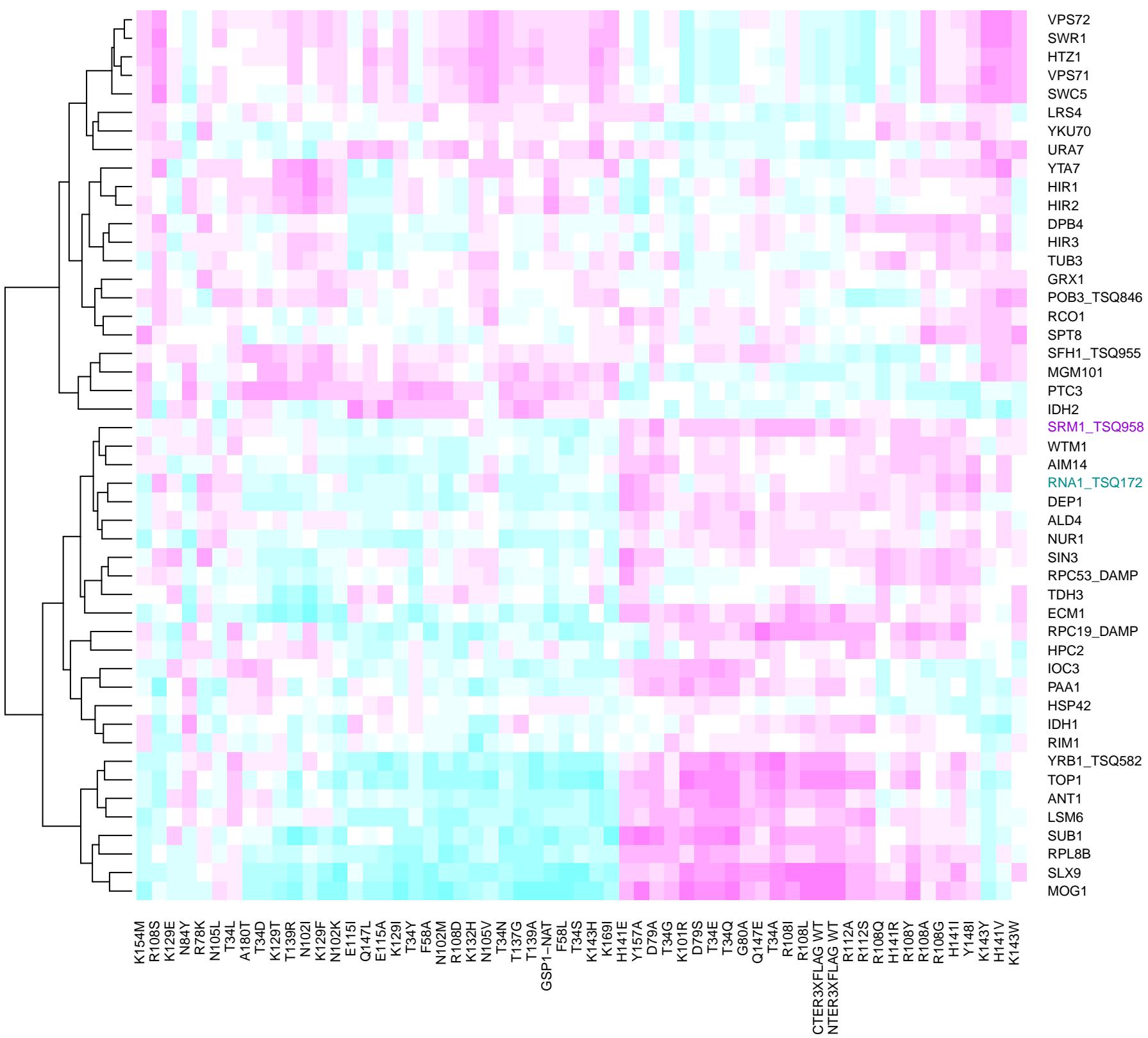


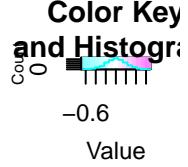
chromosome_GO_30_2



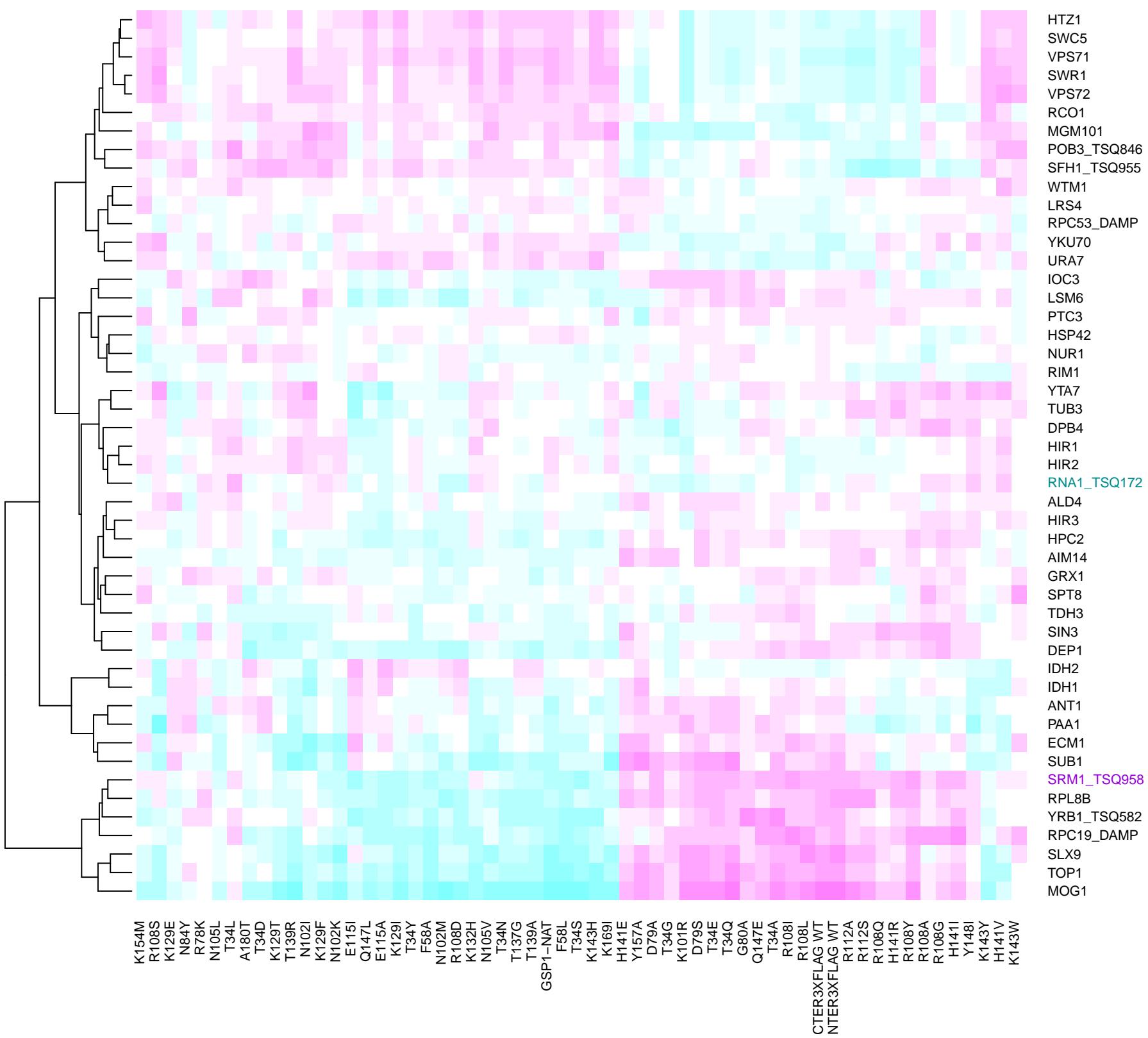


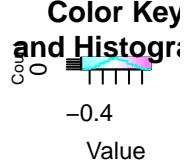
mitochondria and respiration_GO_30_10



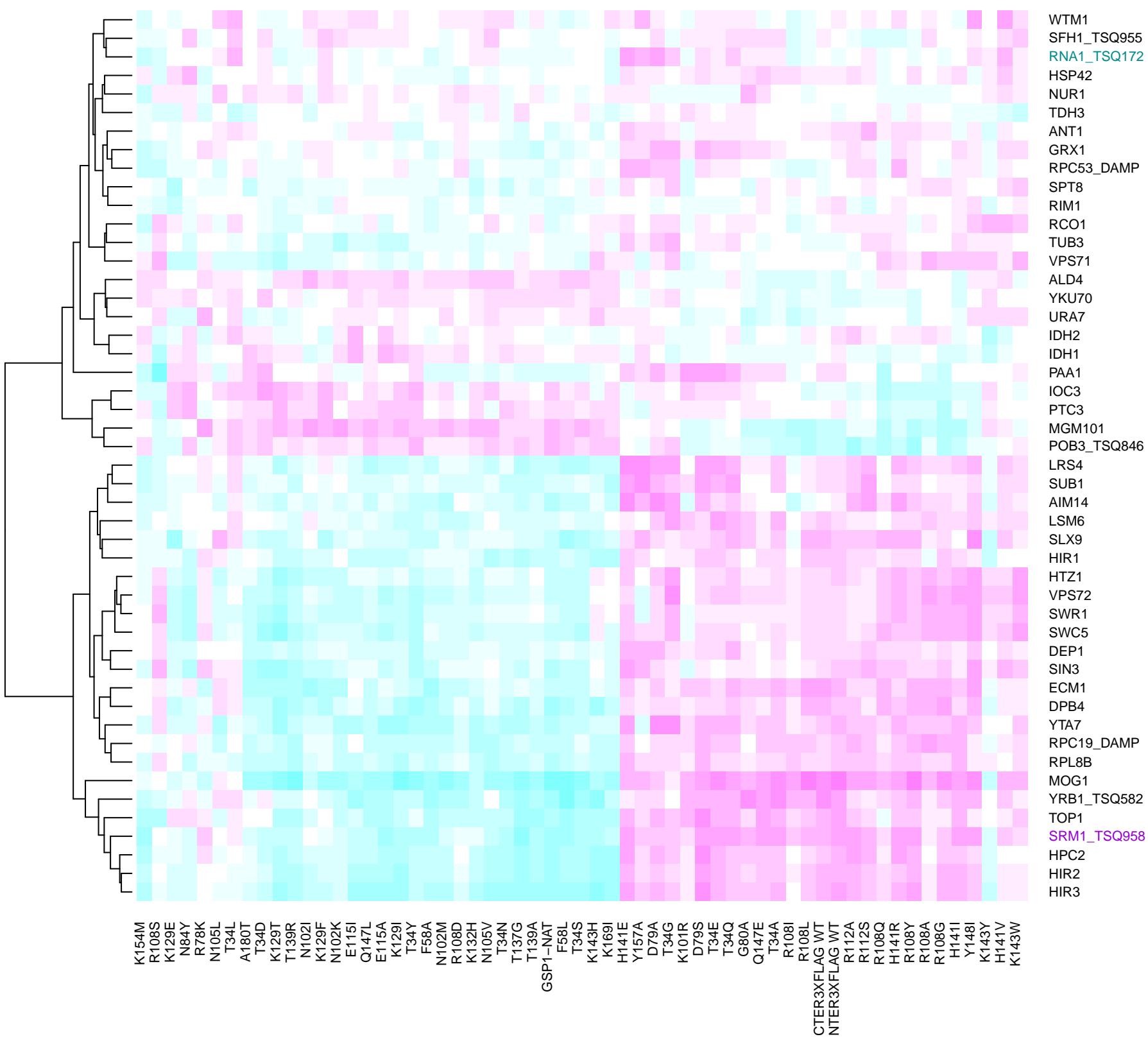


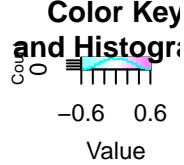
mitochondrion_GO_30_4



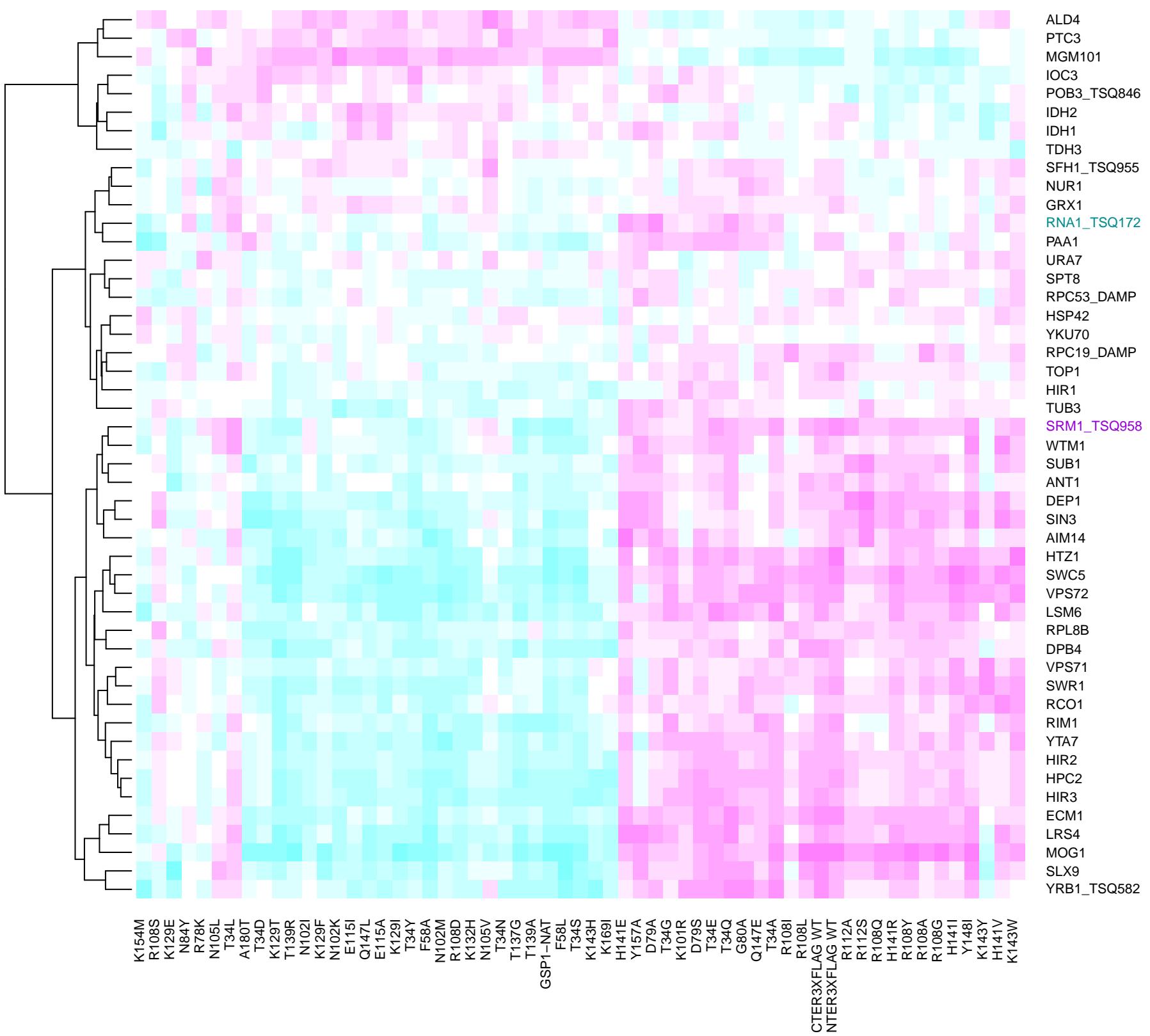


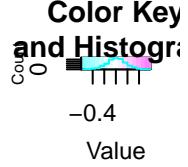
cellular amino acid metabolic process



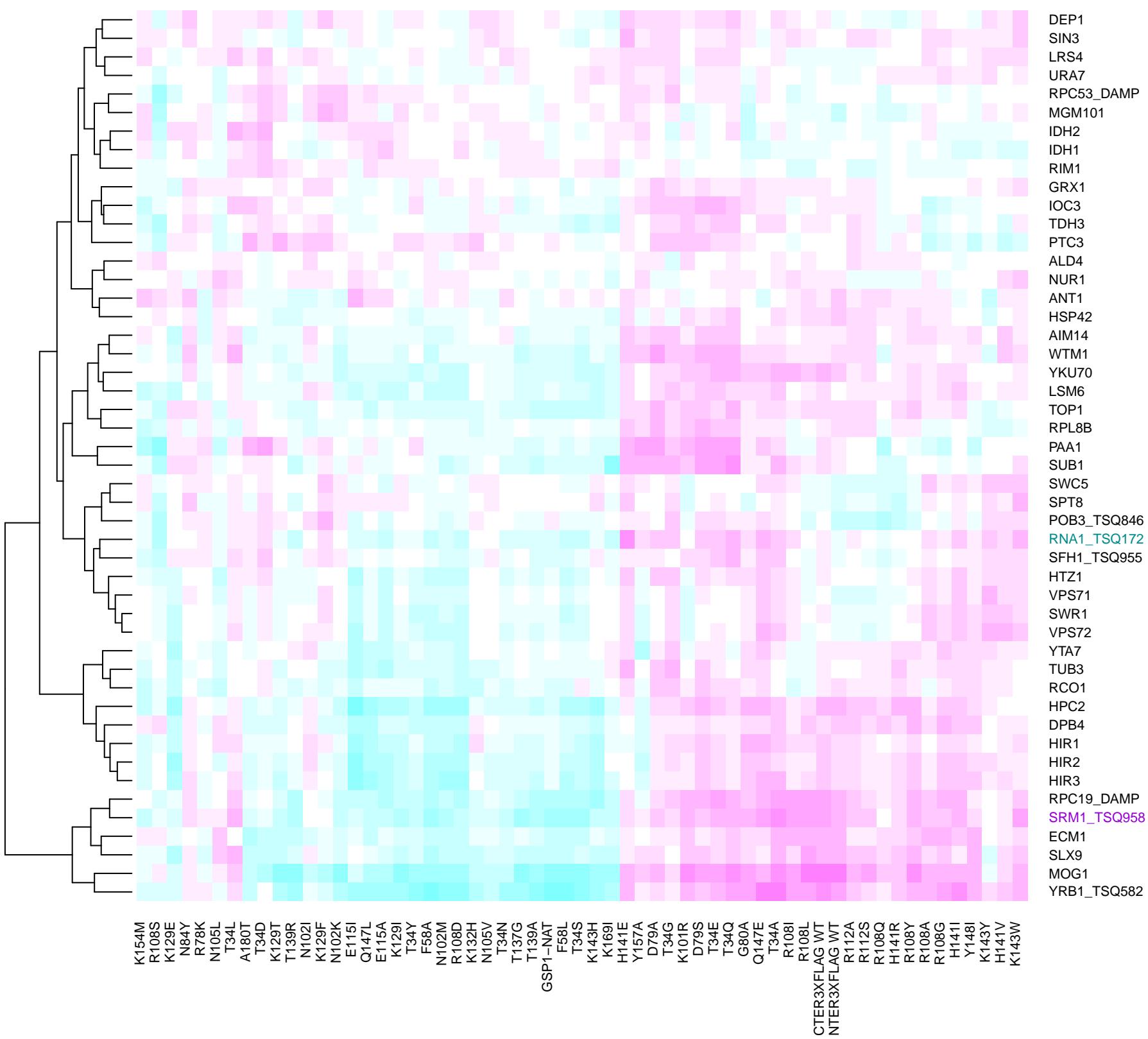


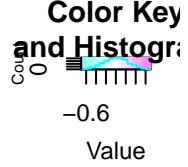
cellular amino acid metabolic process_GO_30_1



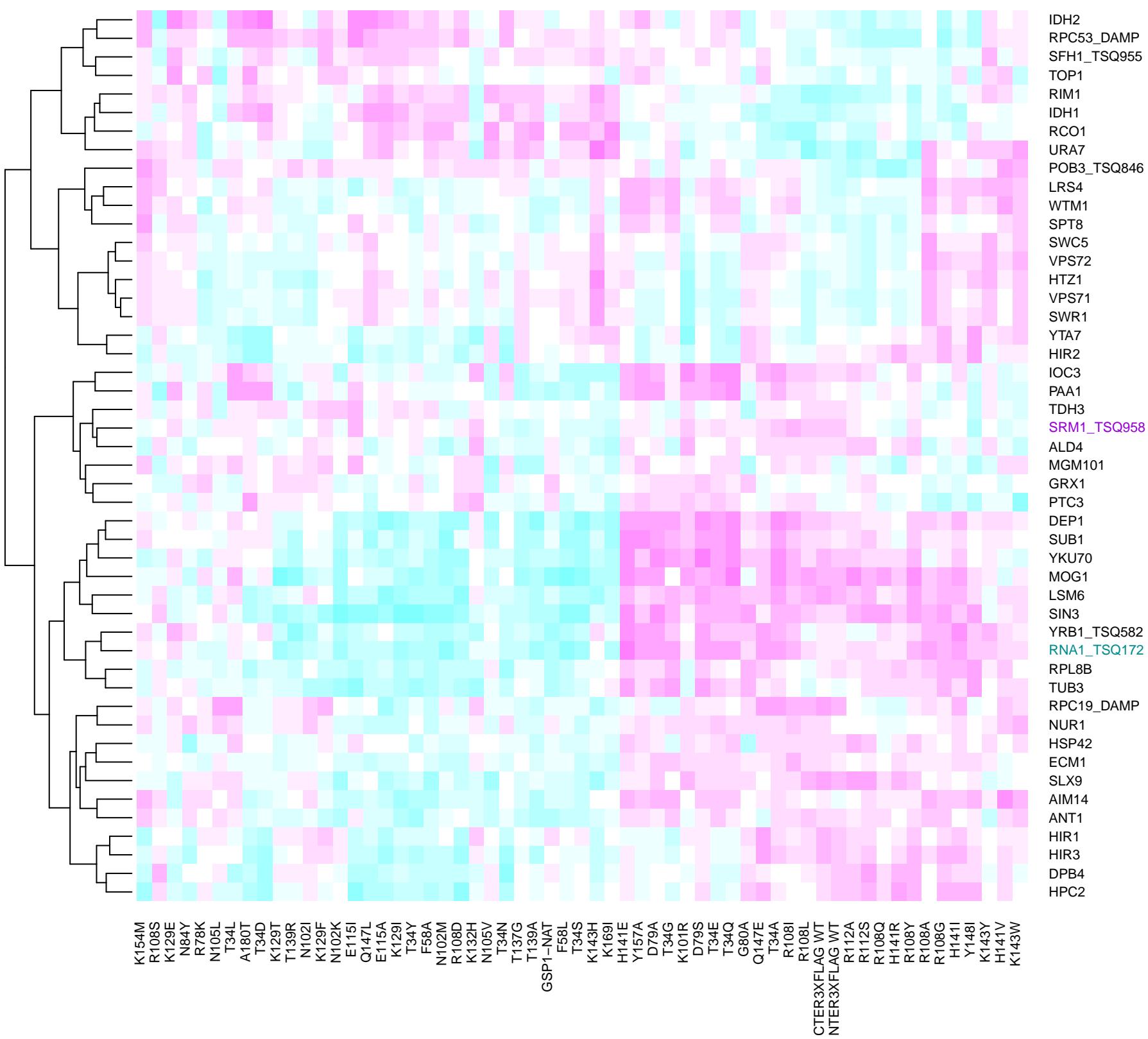


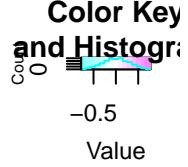
carbohydrate metabolic process



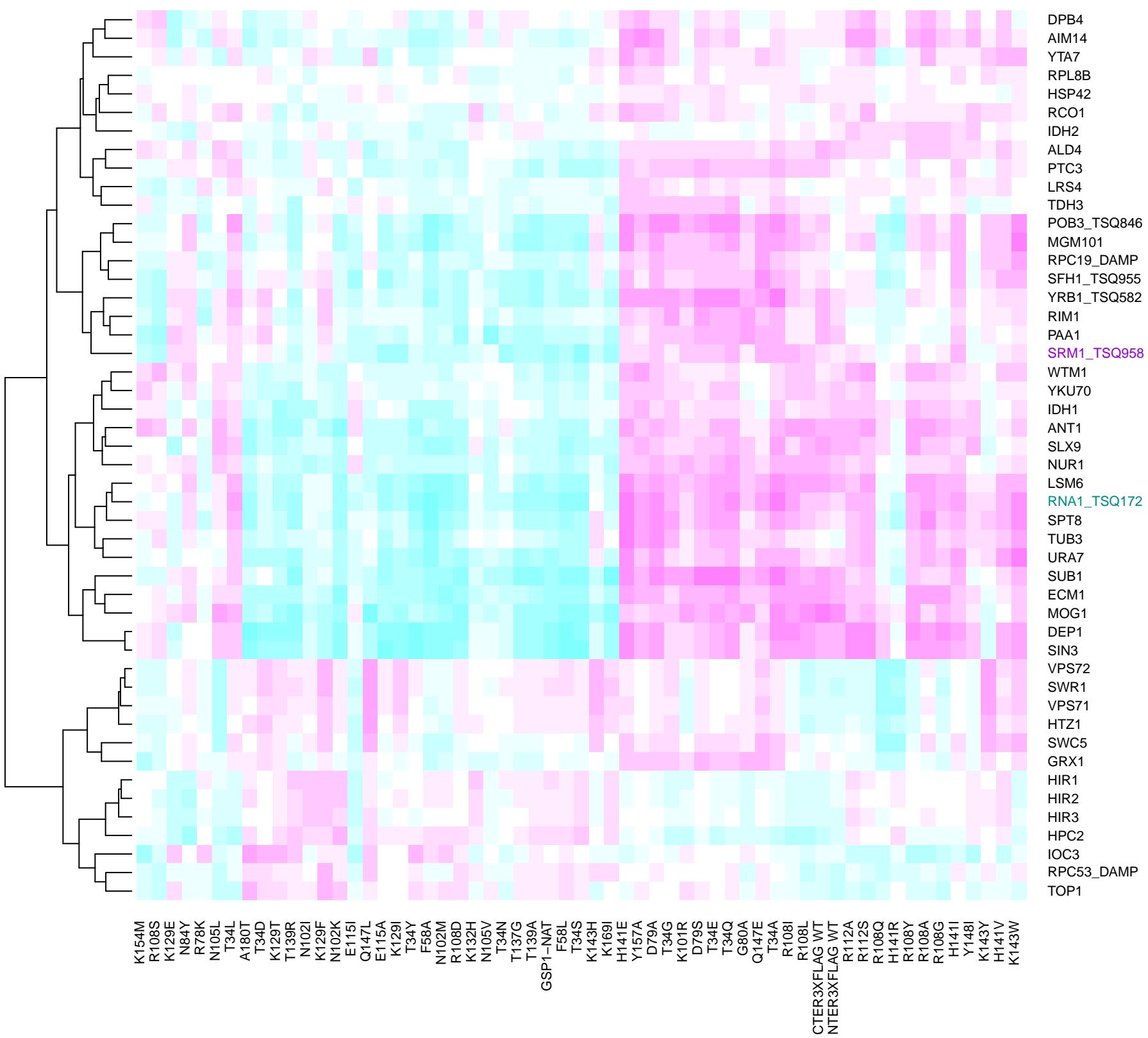


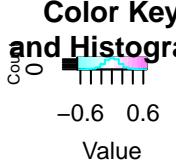
carbohydrate metabolic process_GO_30_4



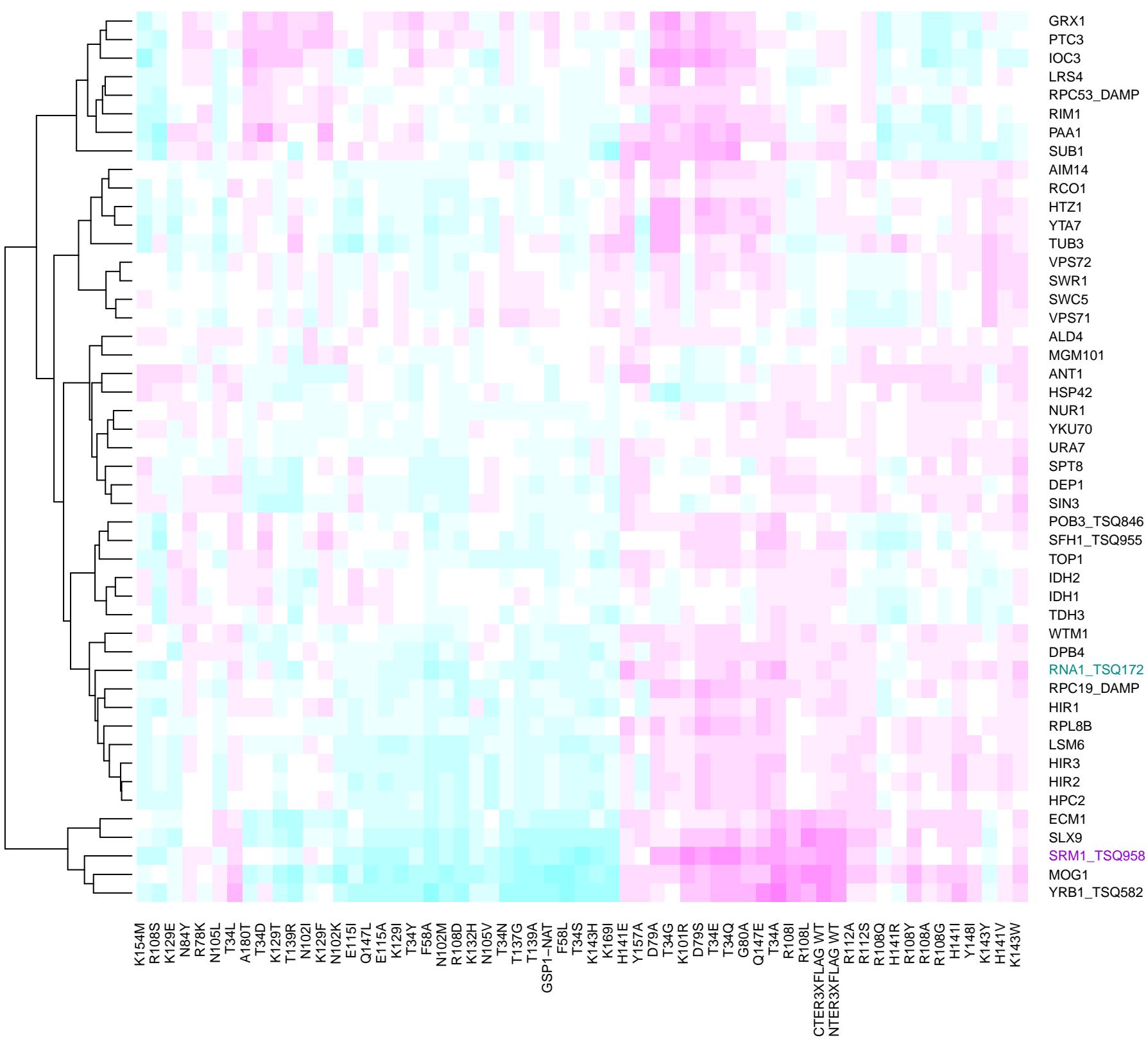


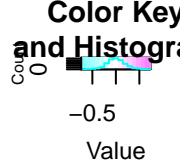
chromatin organization_GO_30_1



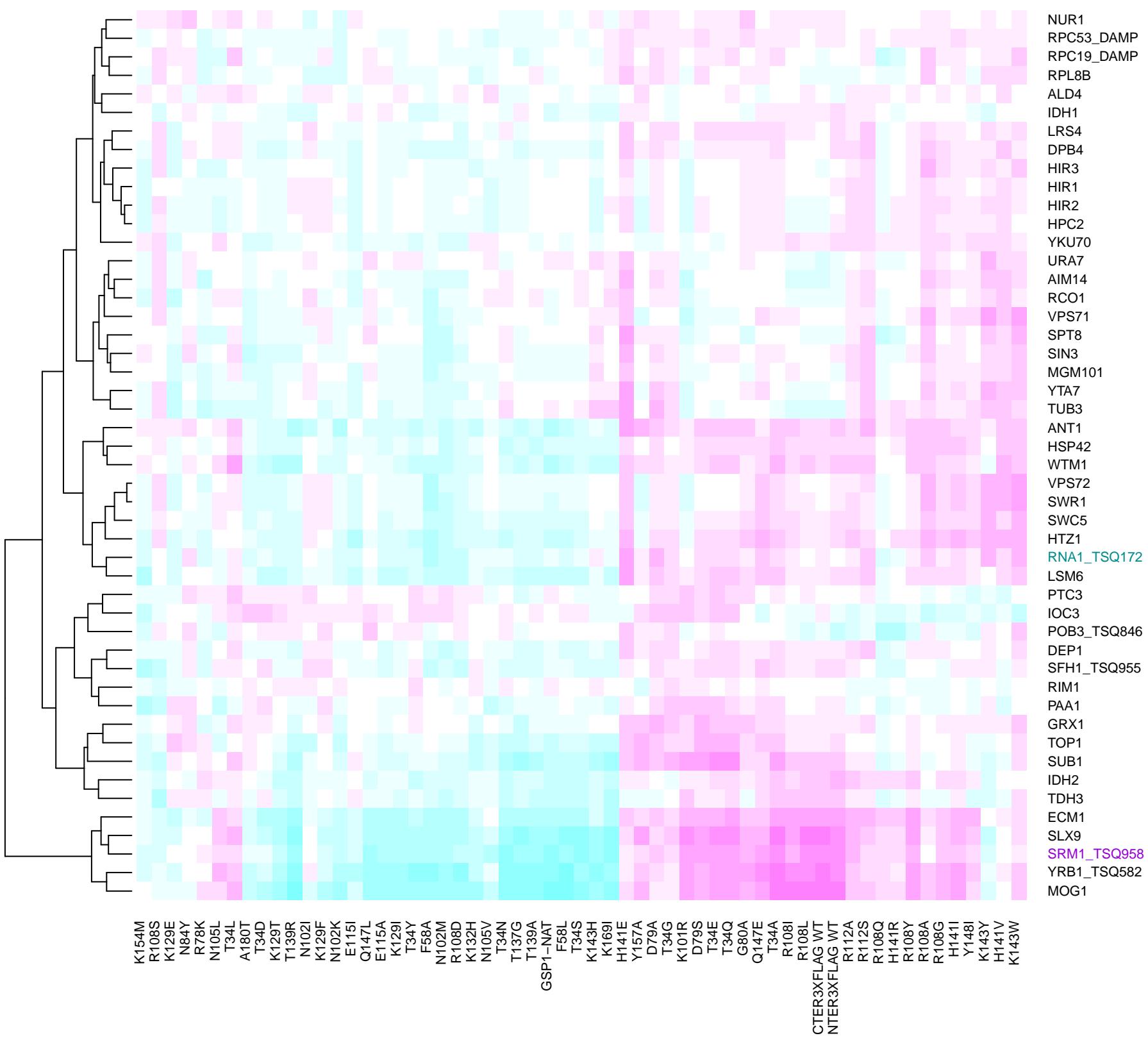


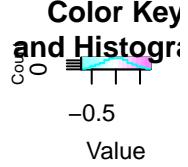
budding



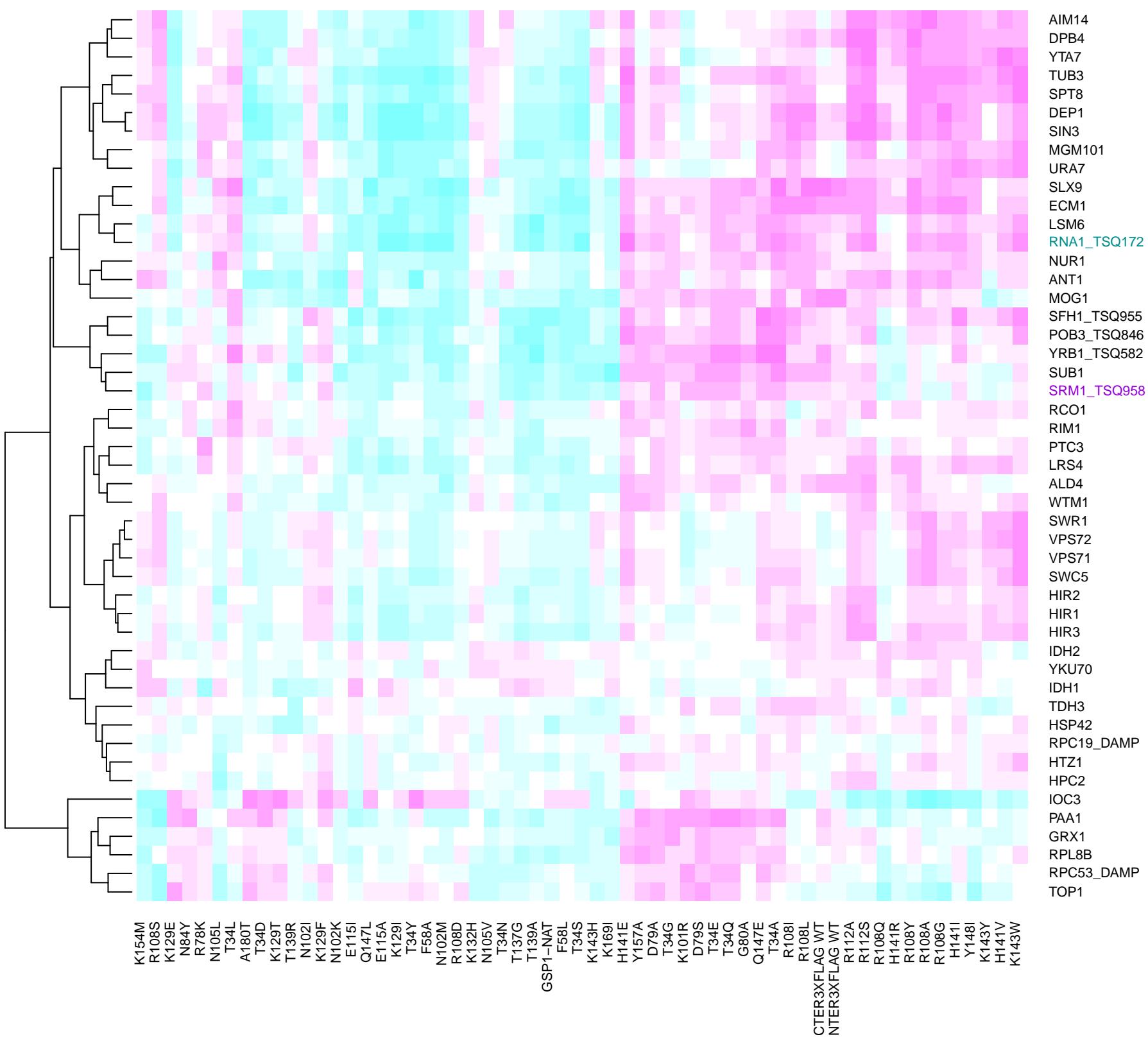


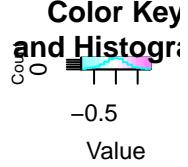
regulation of protein modification process



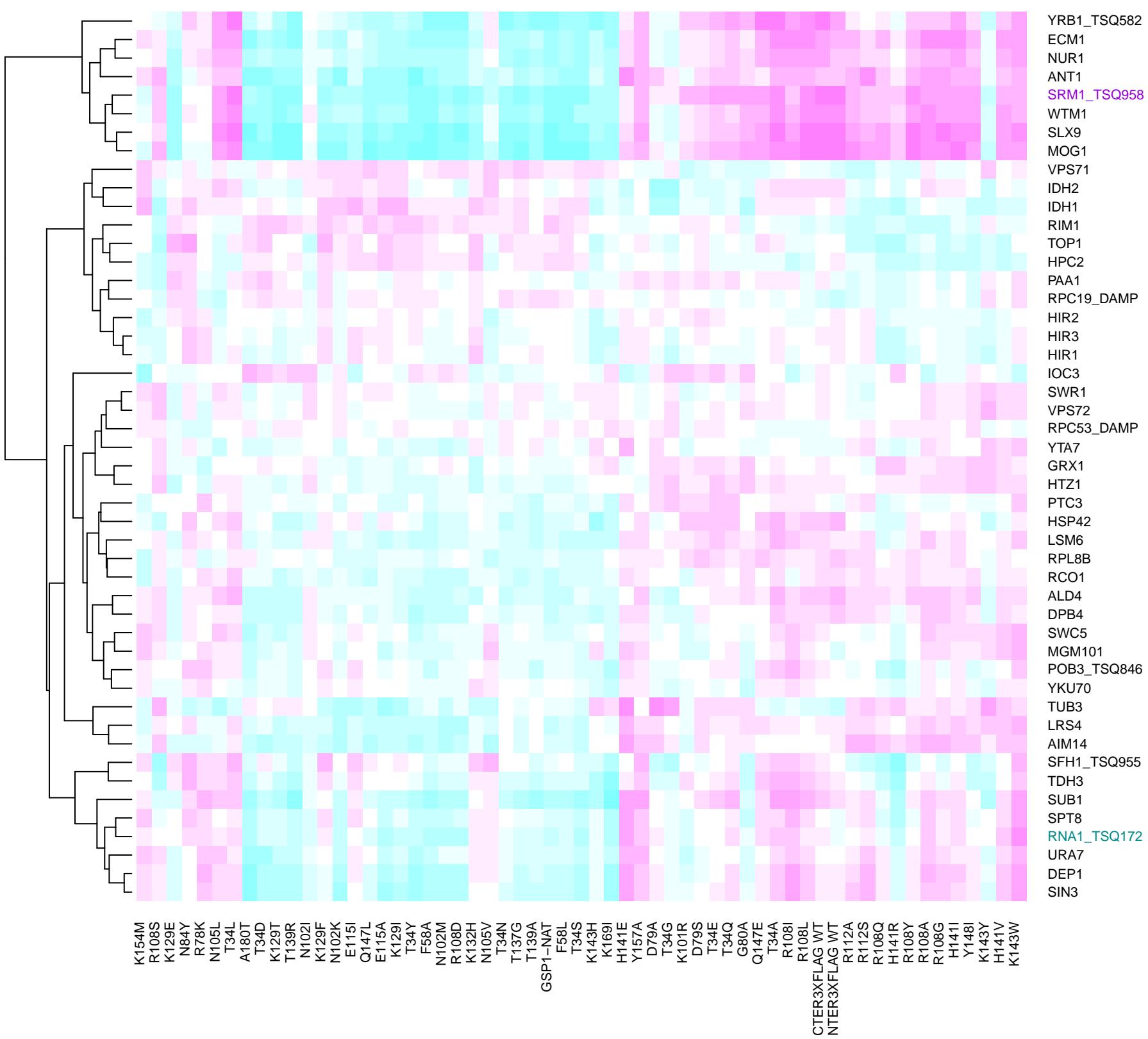


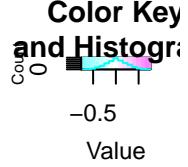
chromatin_GO_30_3



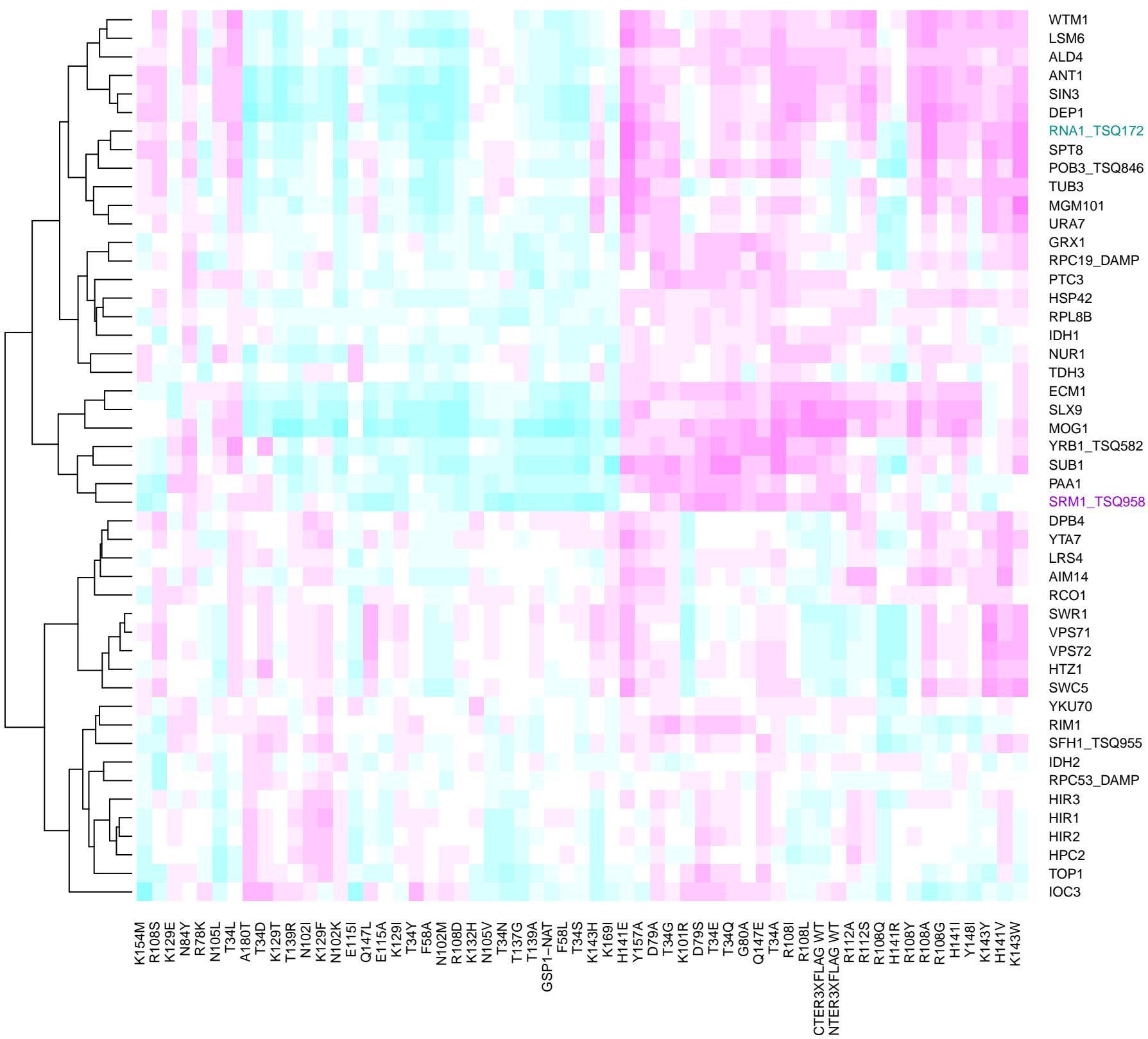


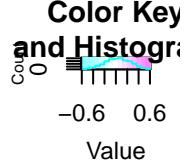
chromosome_GO_30_4



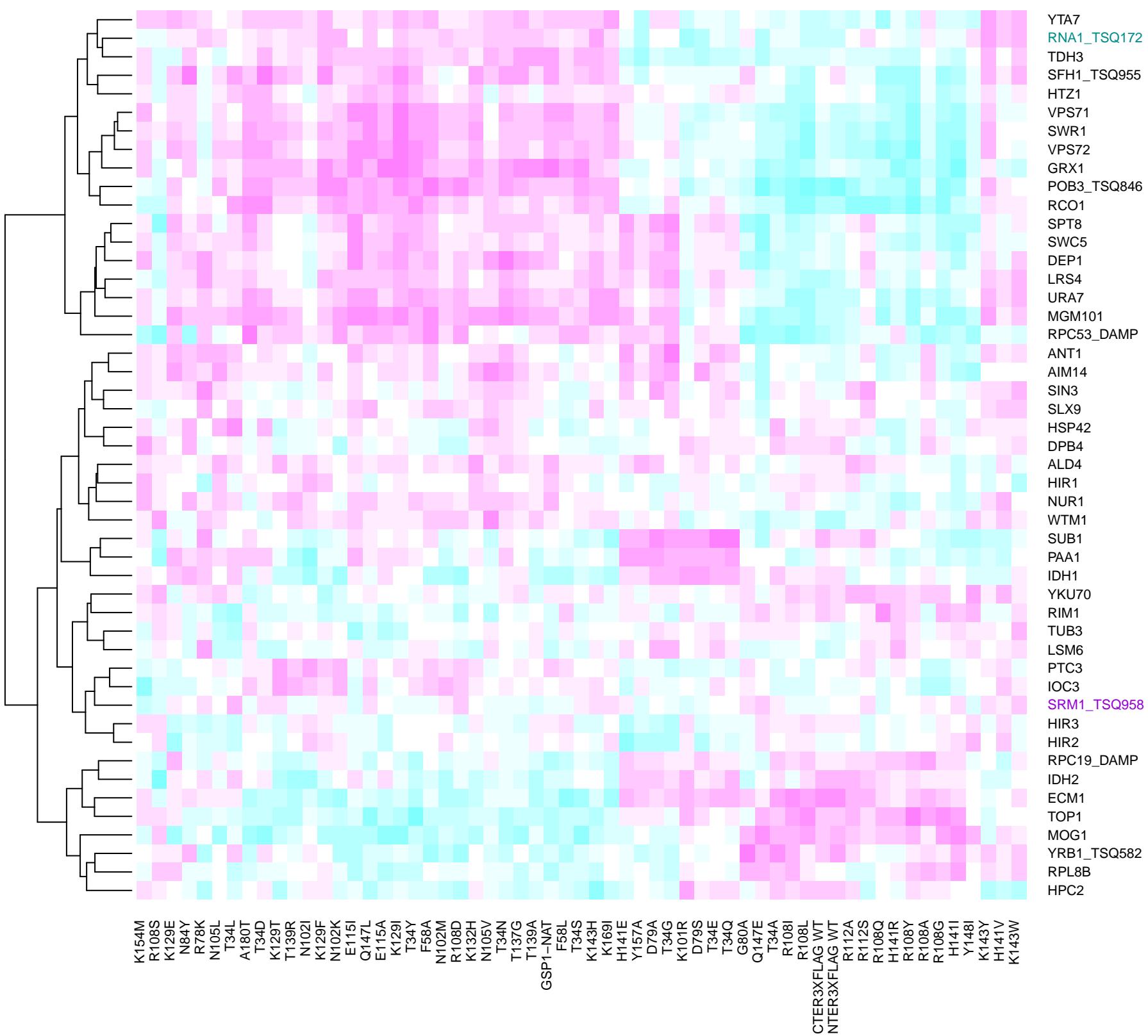


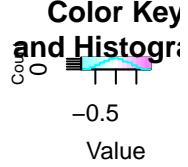
histone modification



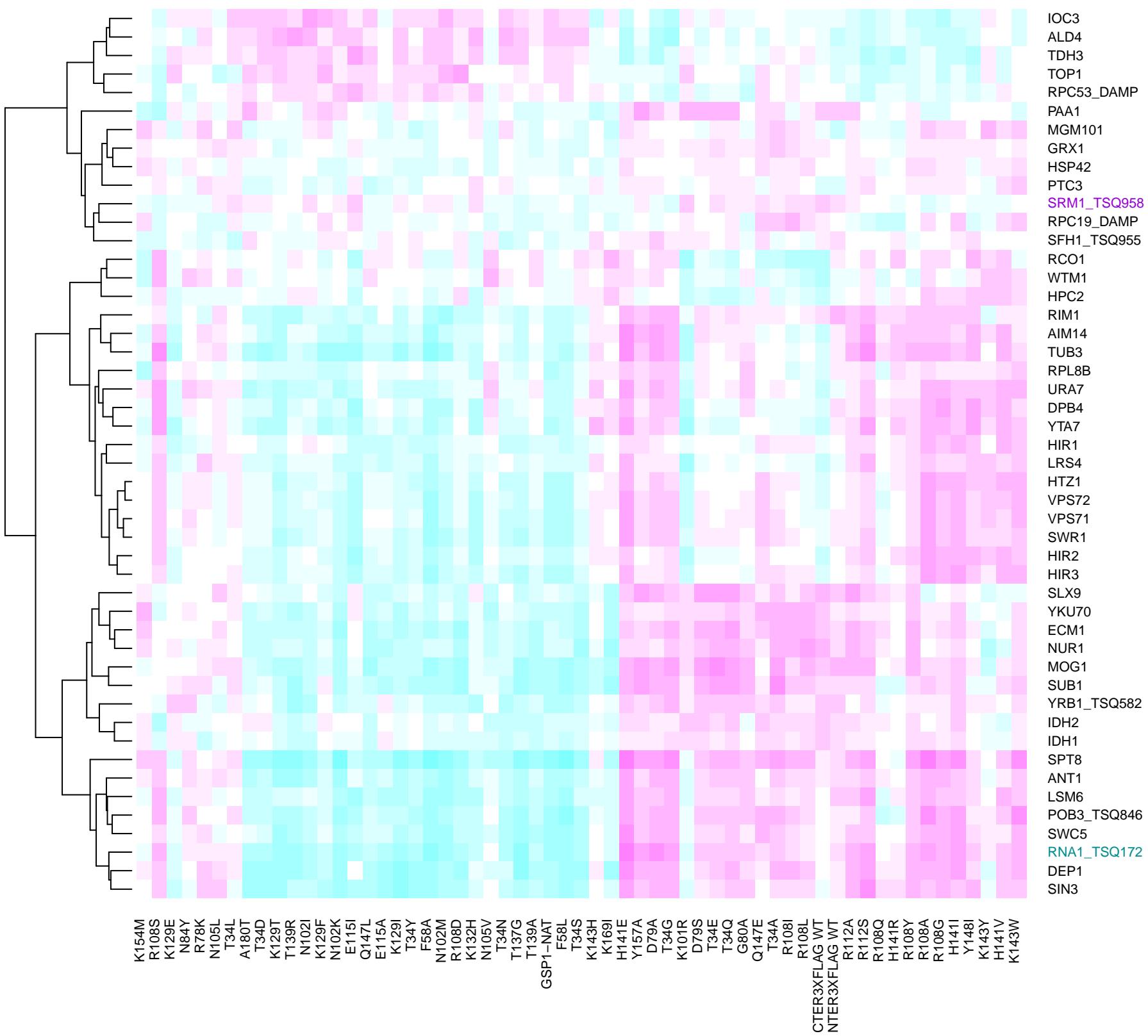


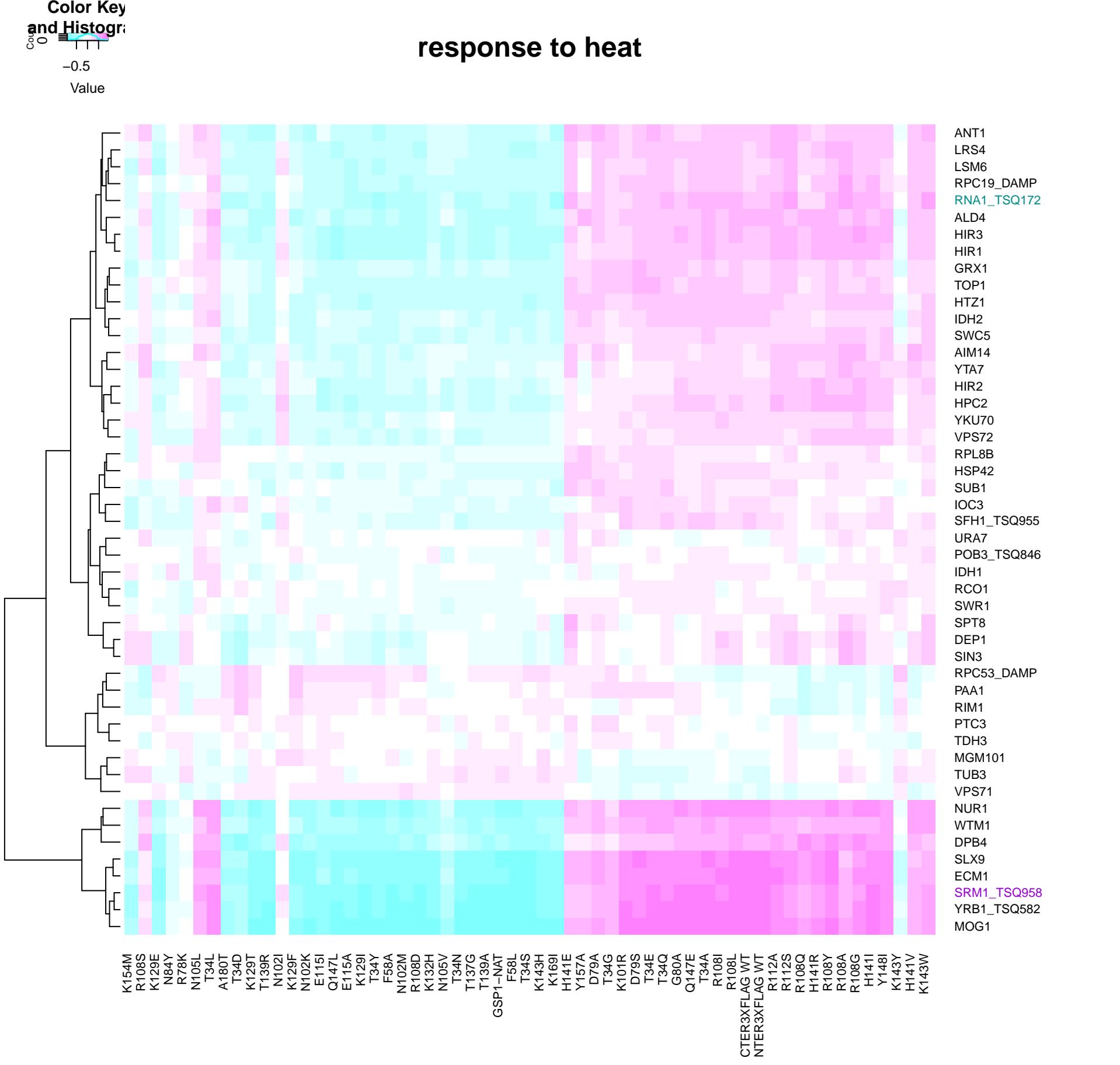
lipids_GO_30_6

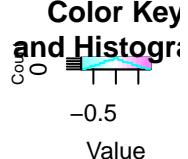




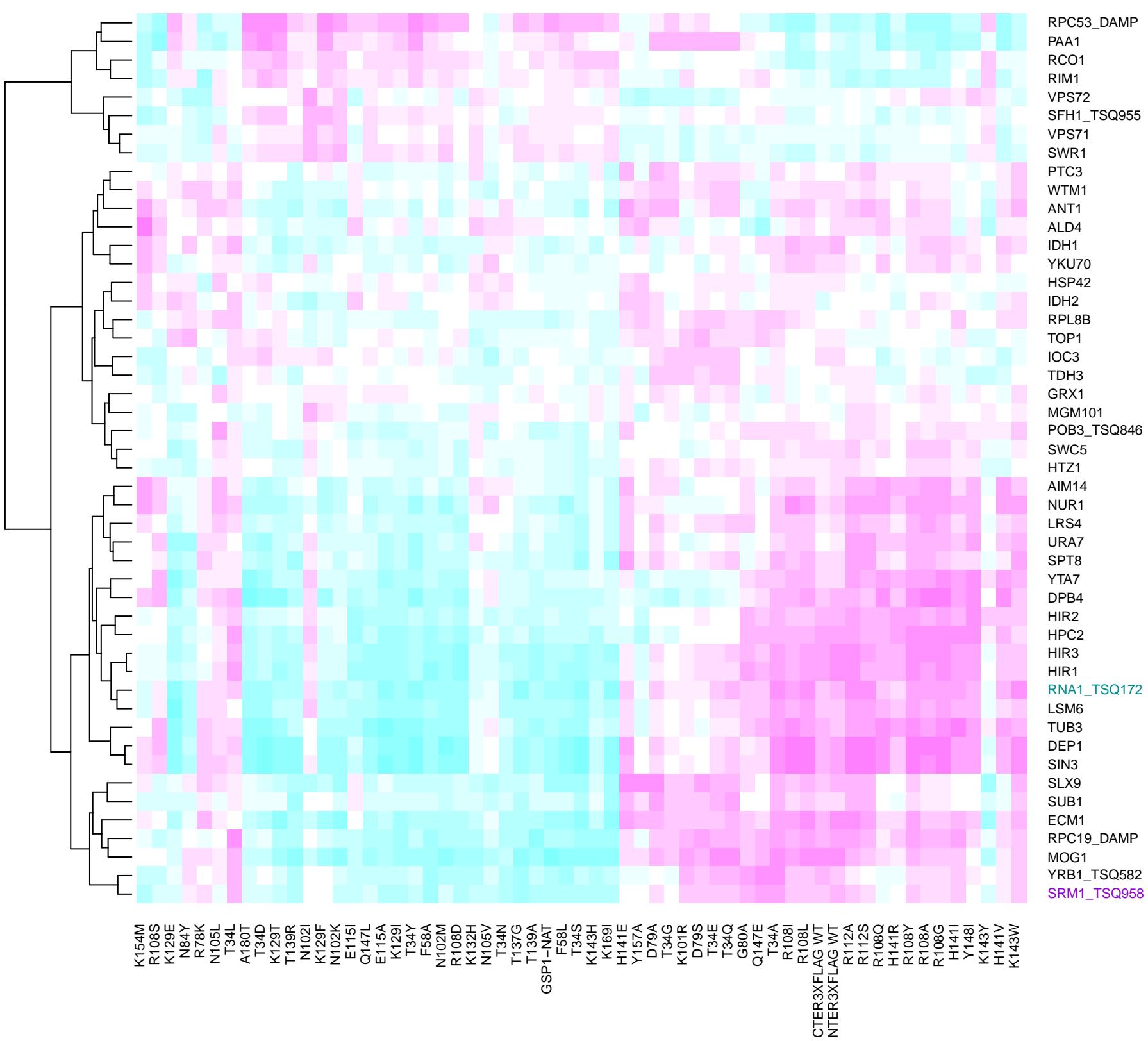
metabolic_GO_30_11

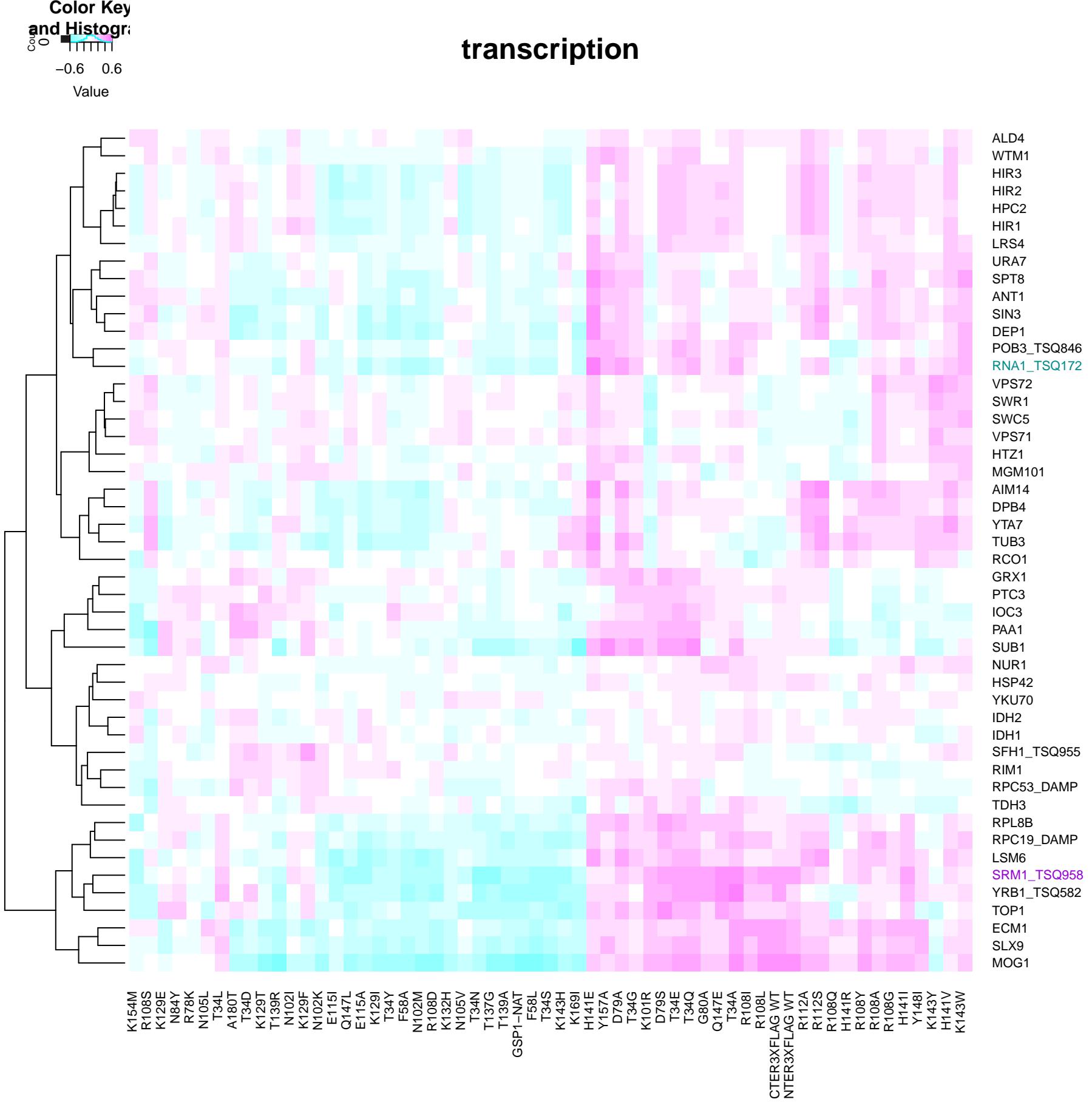


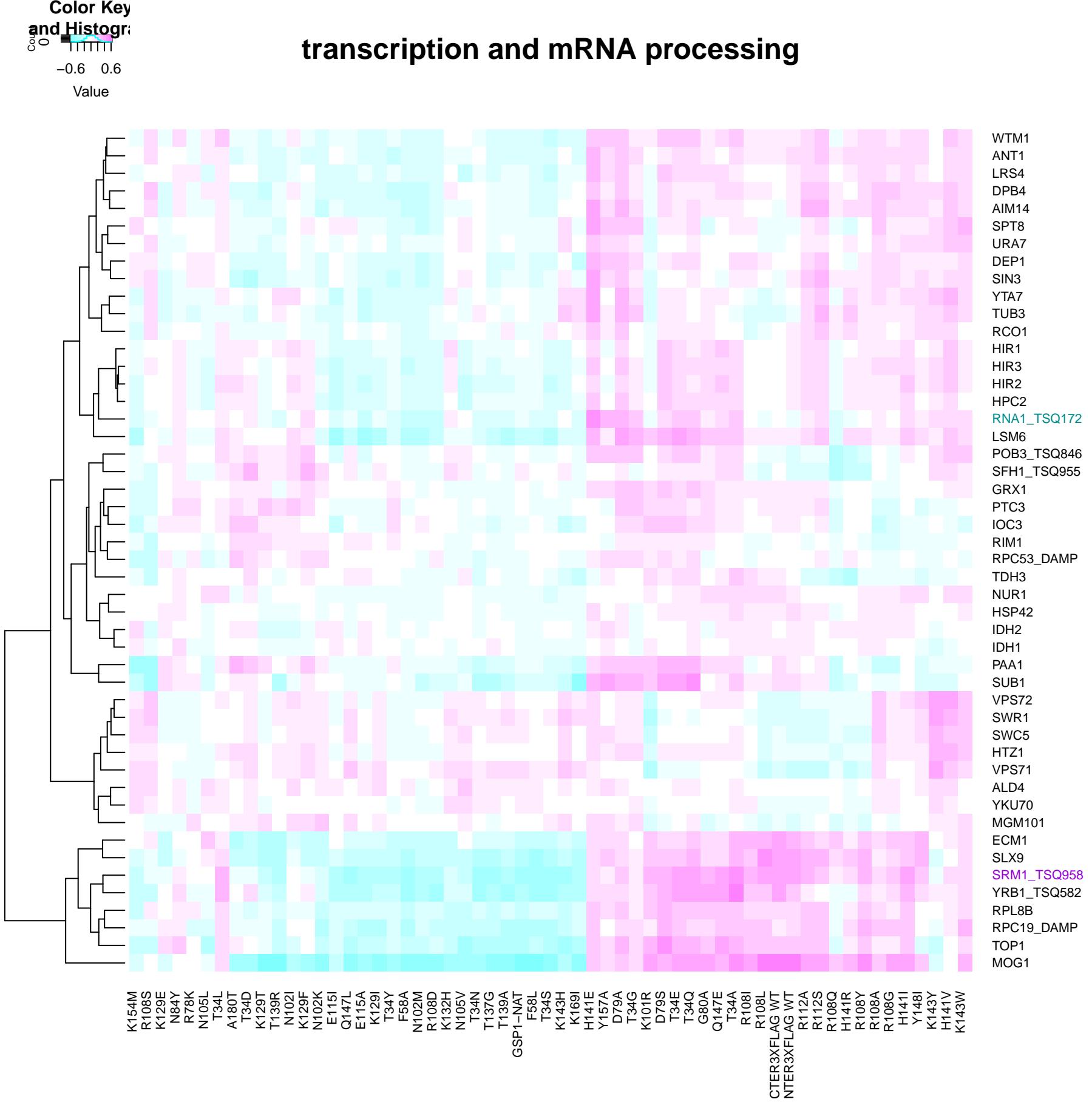


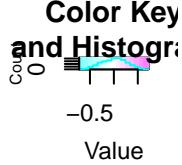


response to heat_GO_30_1

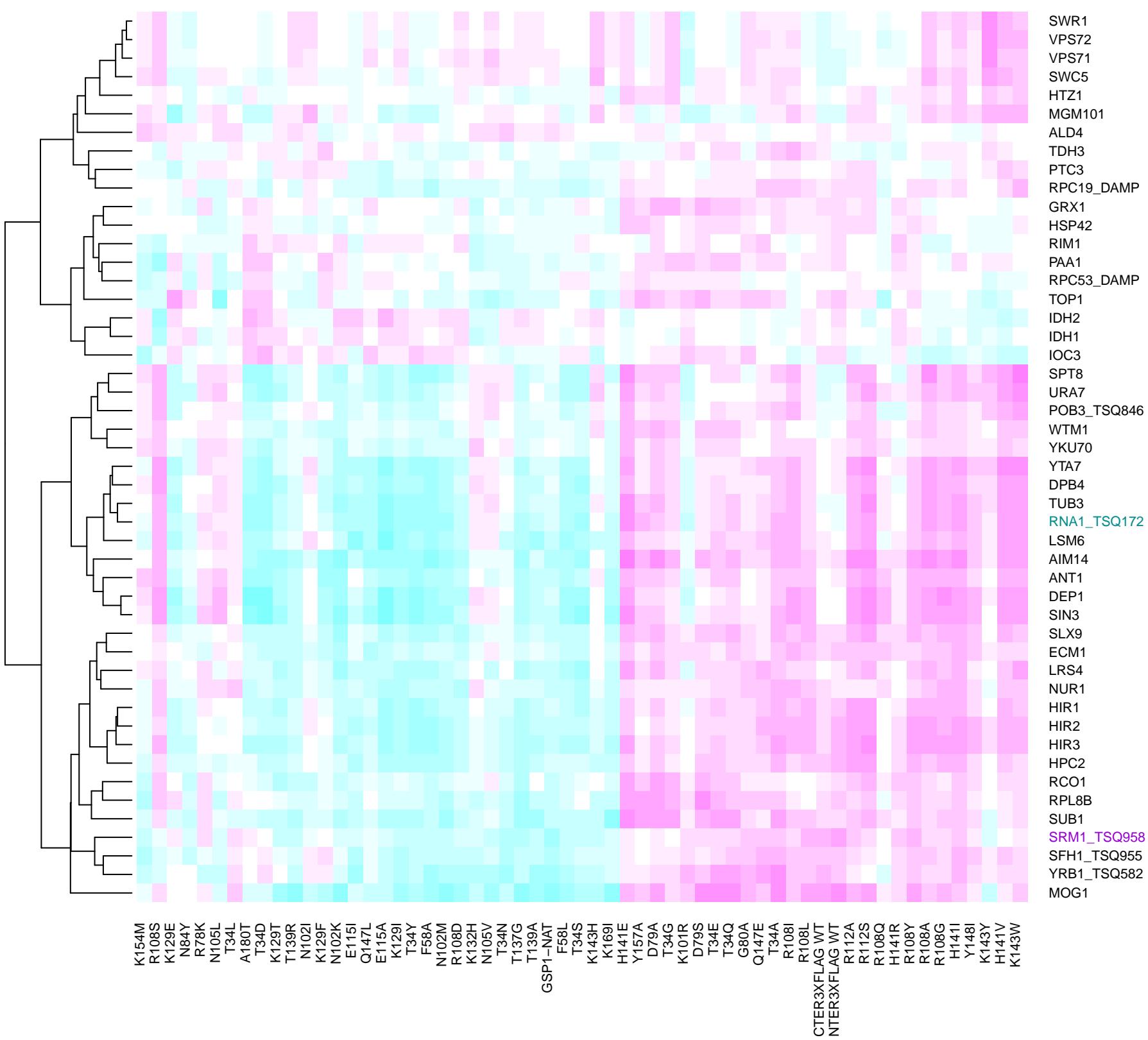


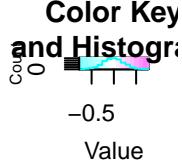




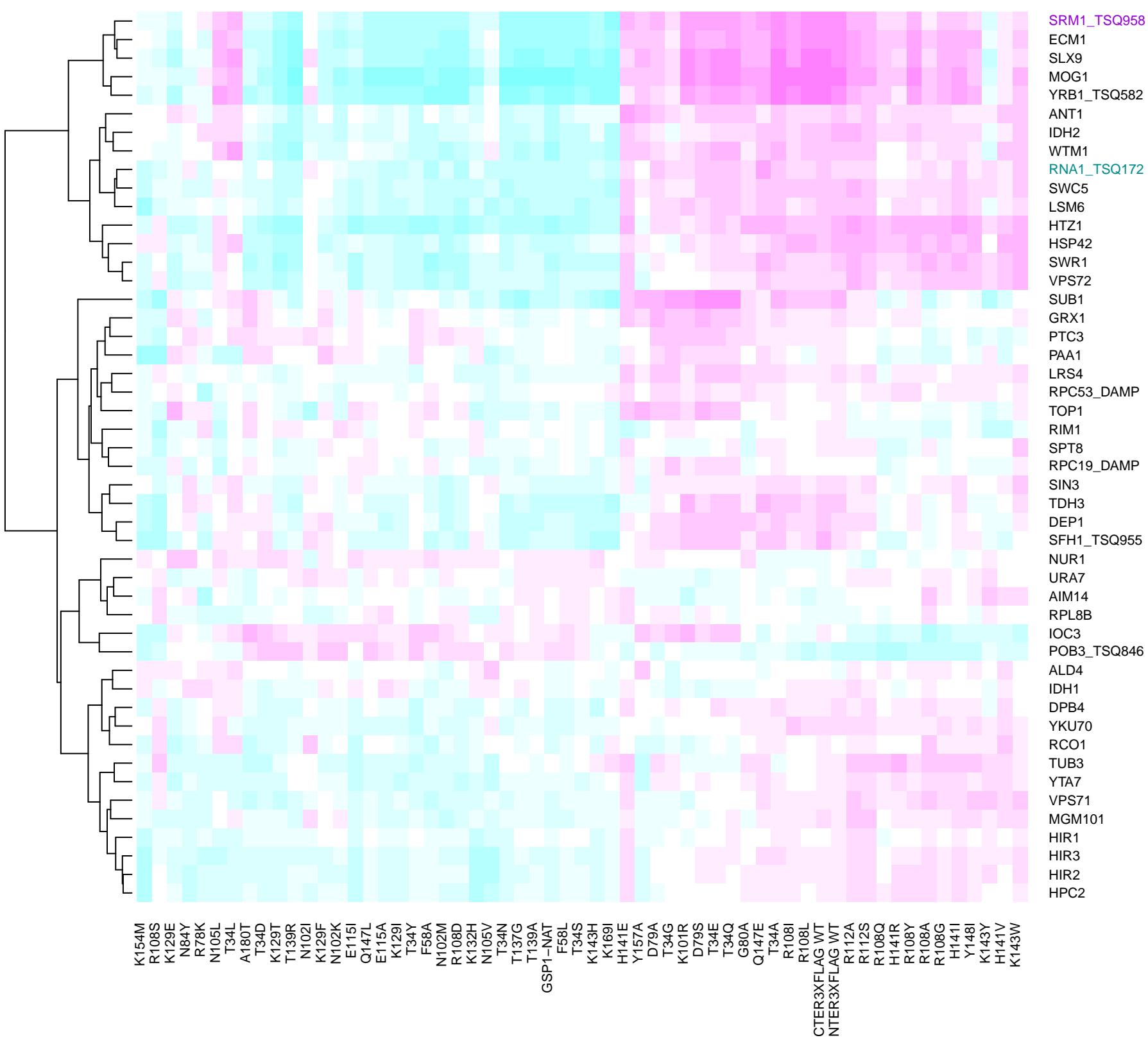


transcription and mRNA processing_GO_30_2

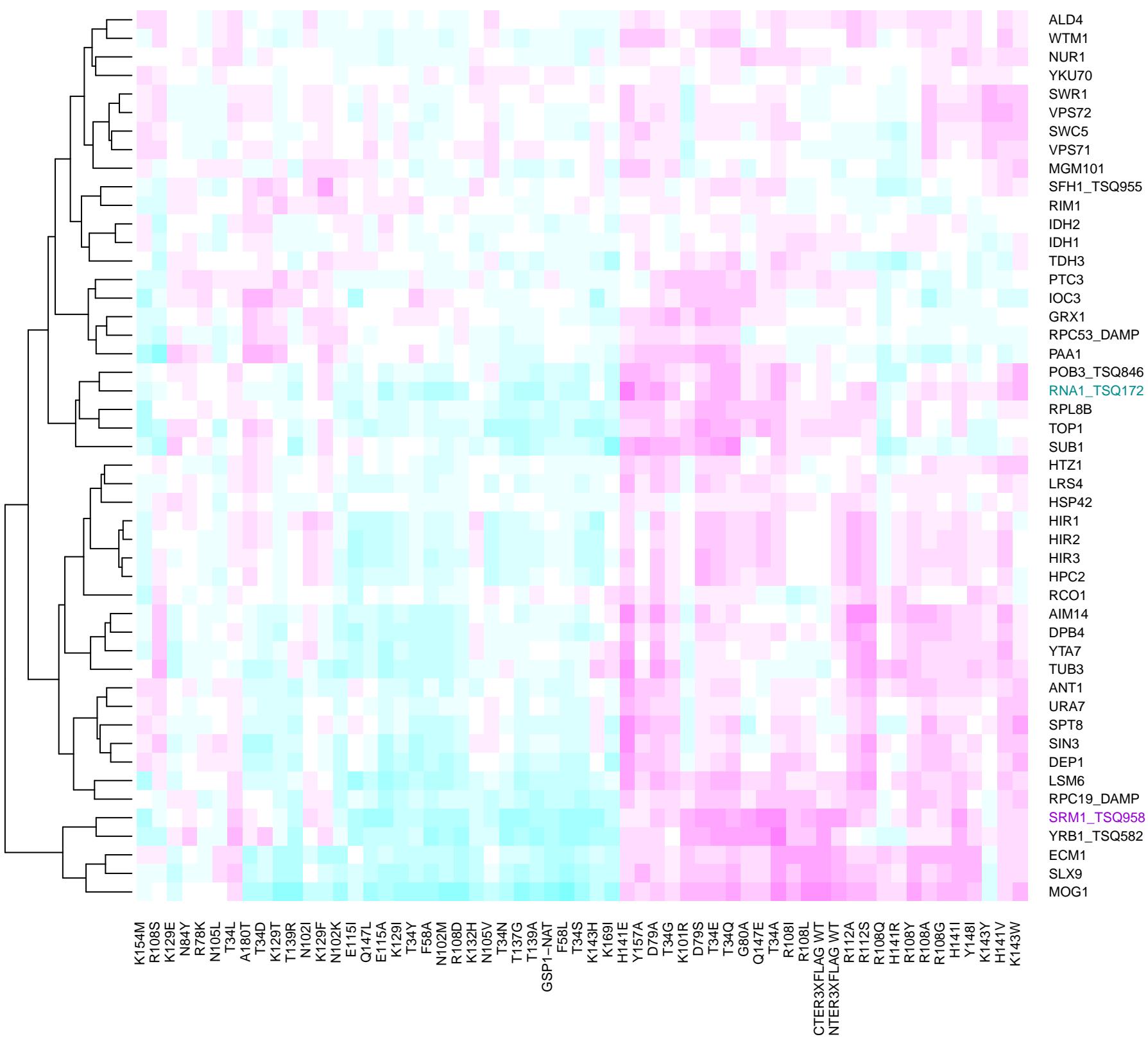
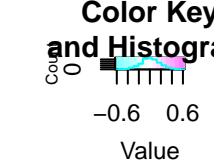


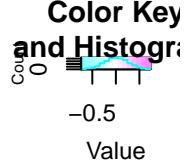


regulation of protein modification process_GO_30_1

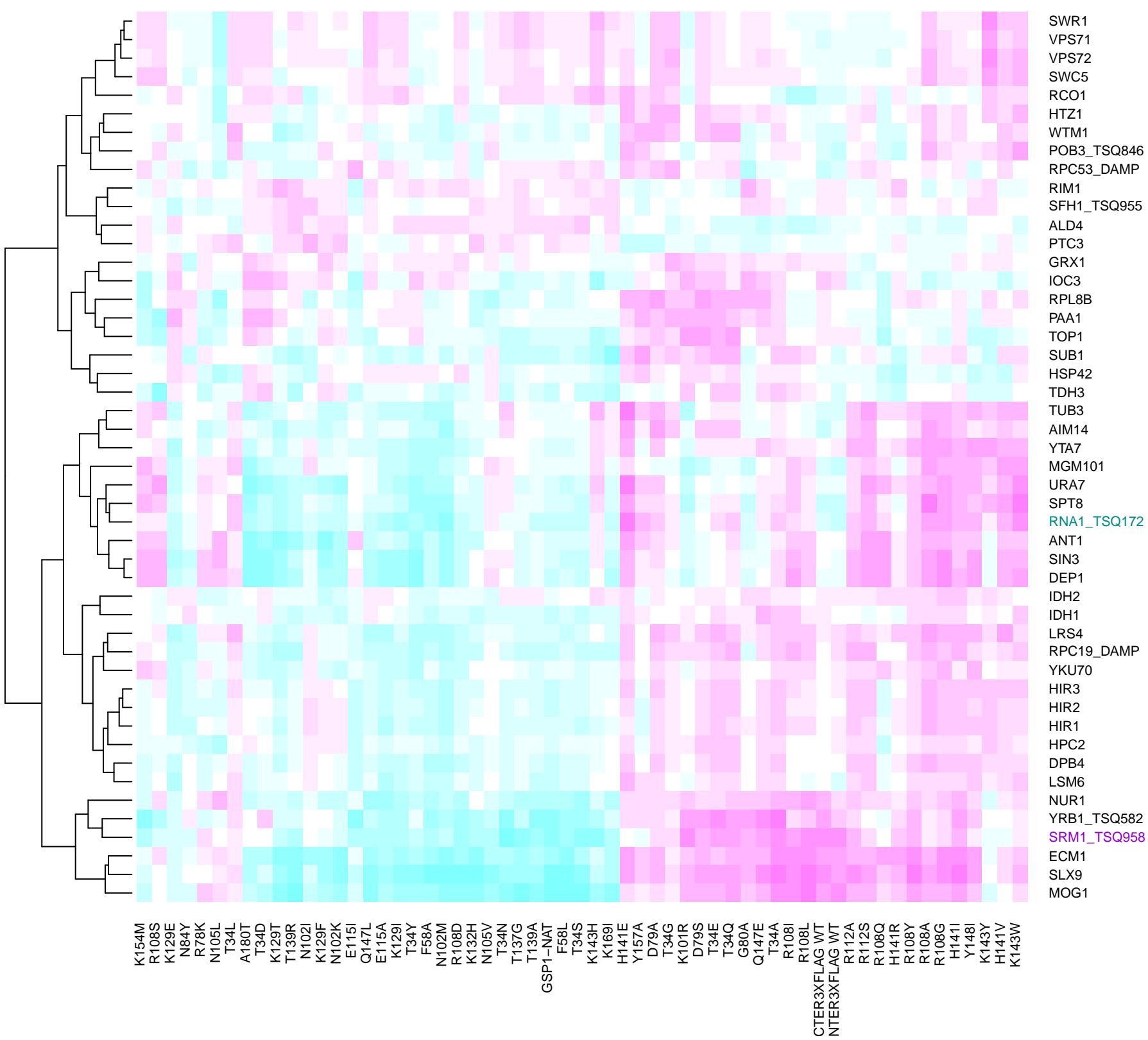


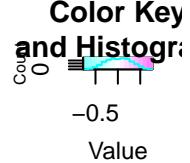
transcription from RNA polymerase II promoter



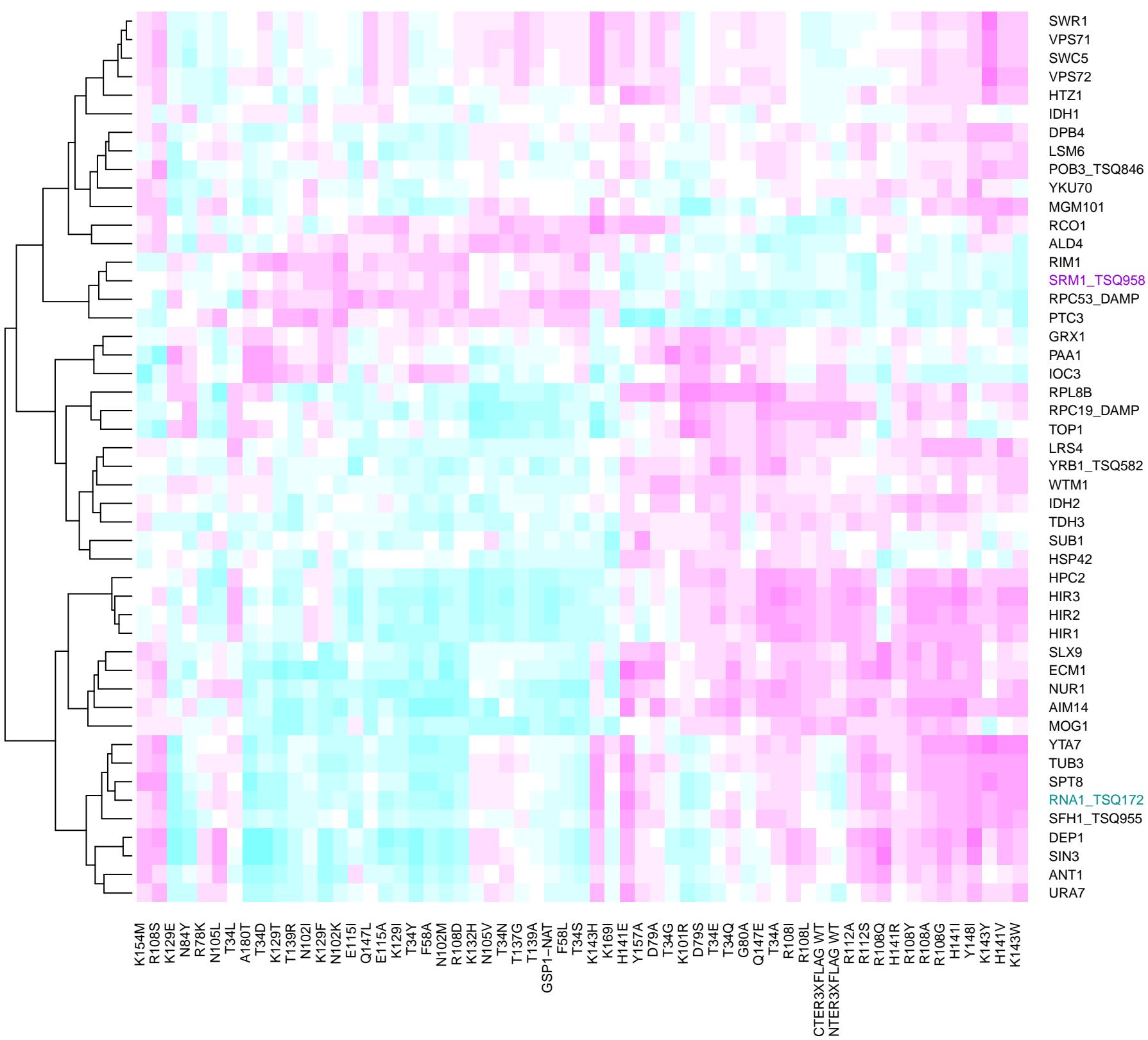


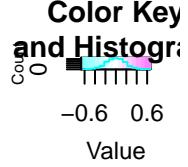
transcription from RNA polymerase II promoter_GO_30_4



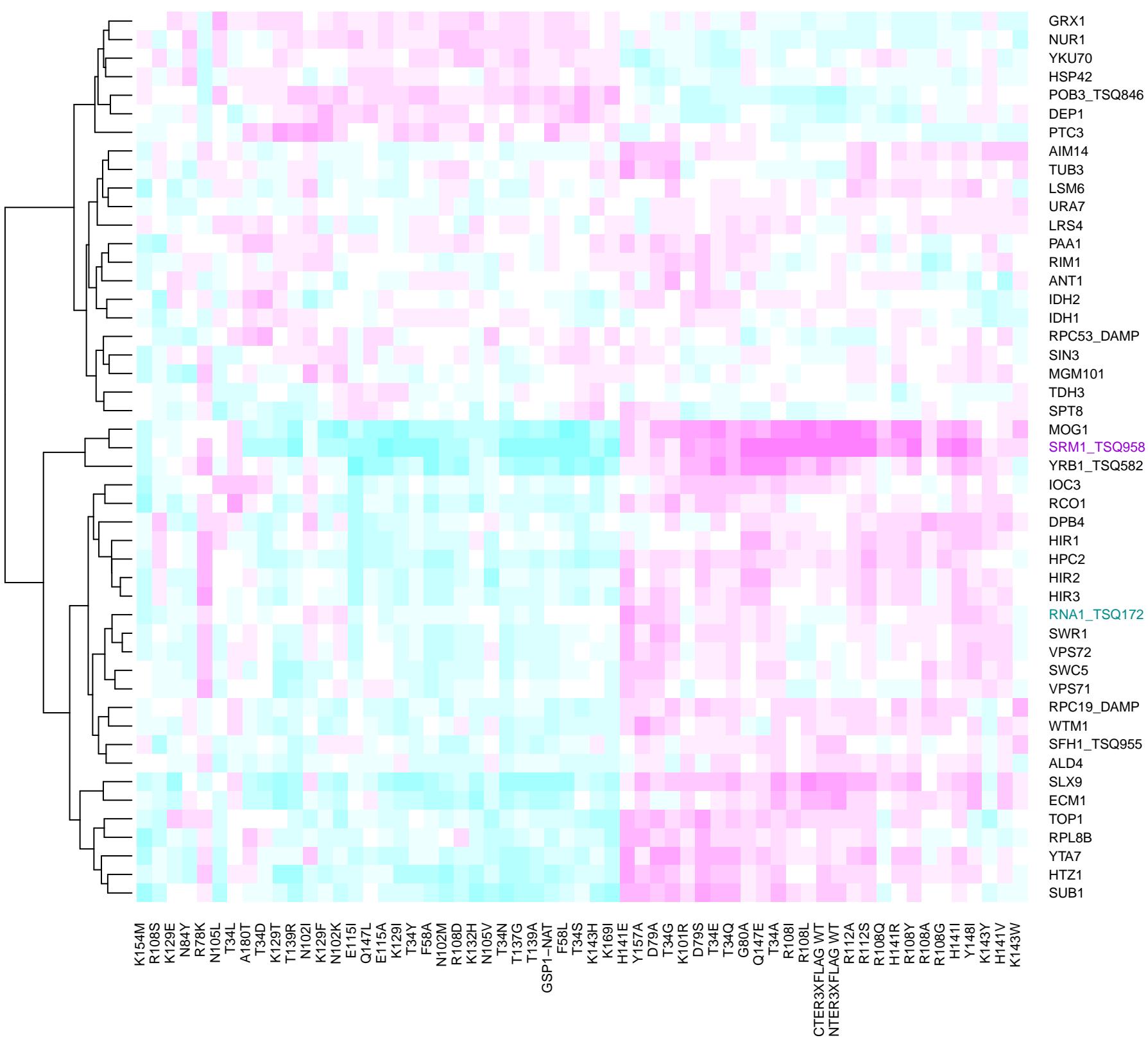


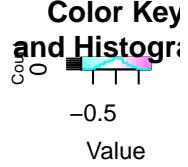
transcription_GO_30_6



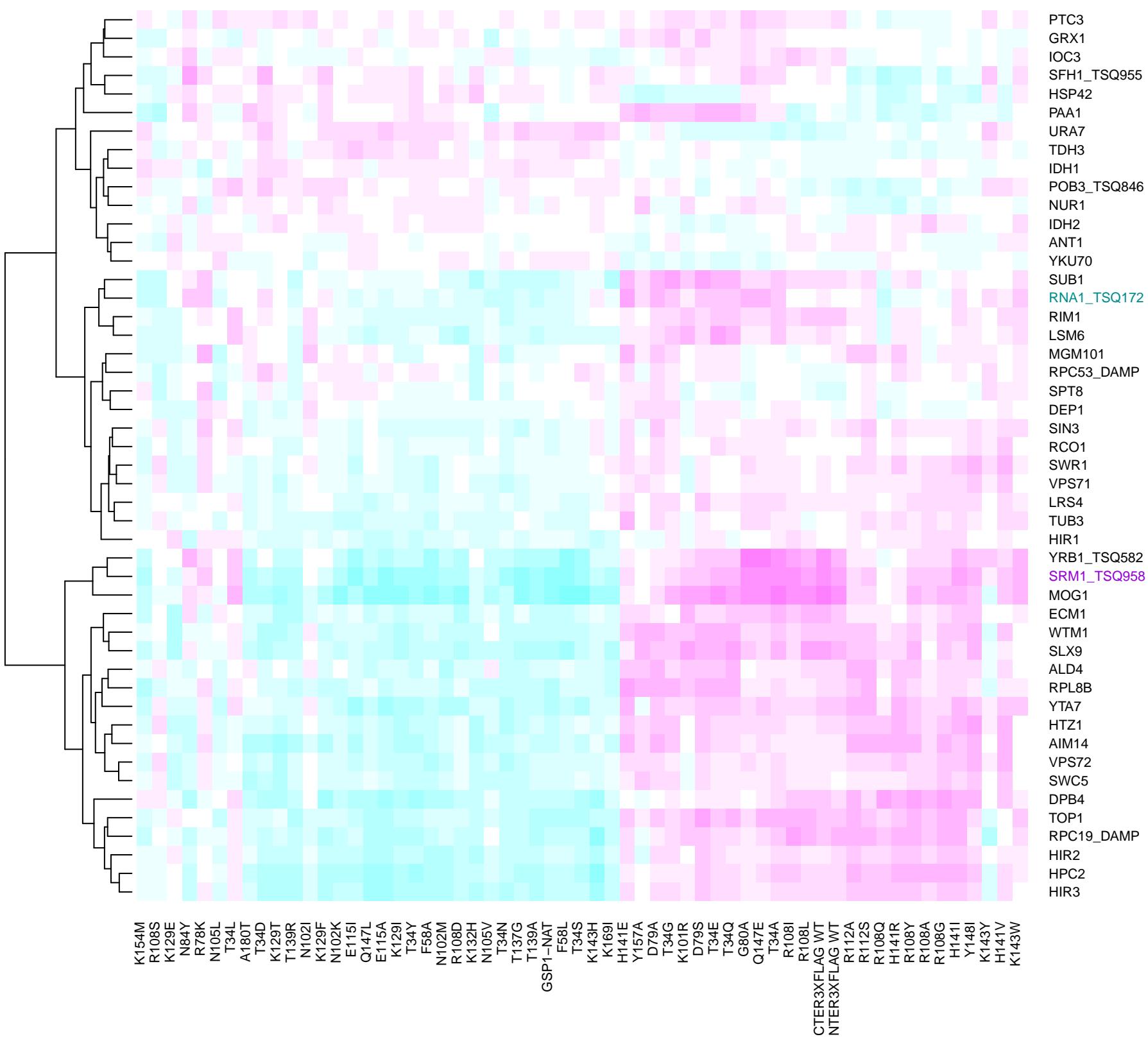


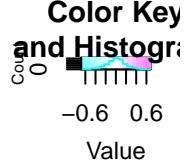
mitochondria and respiration_GO_30_6



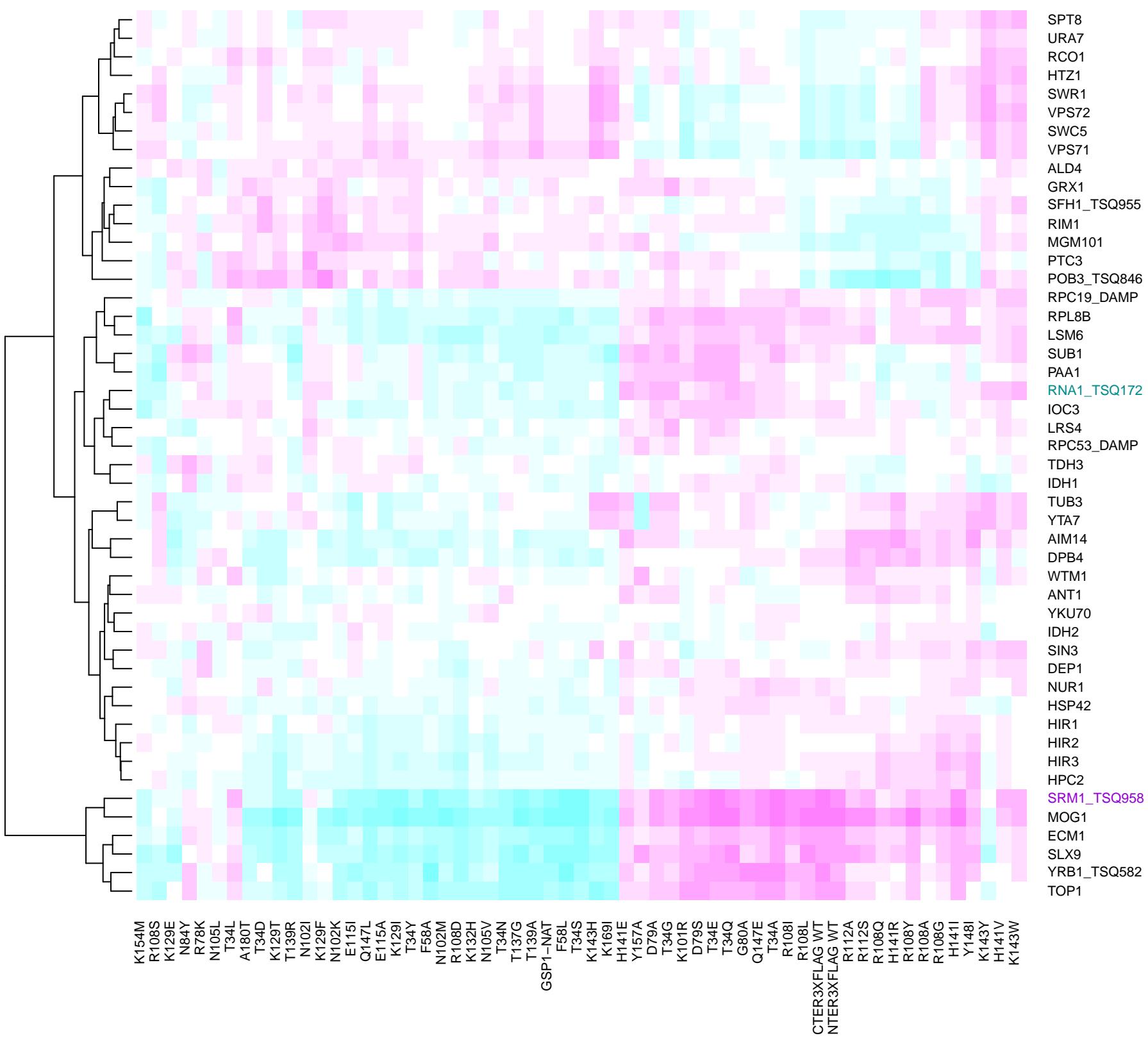


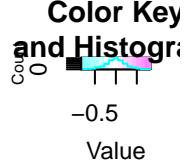
mitochondrion_GO_30_3



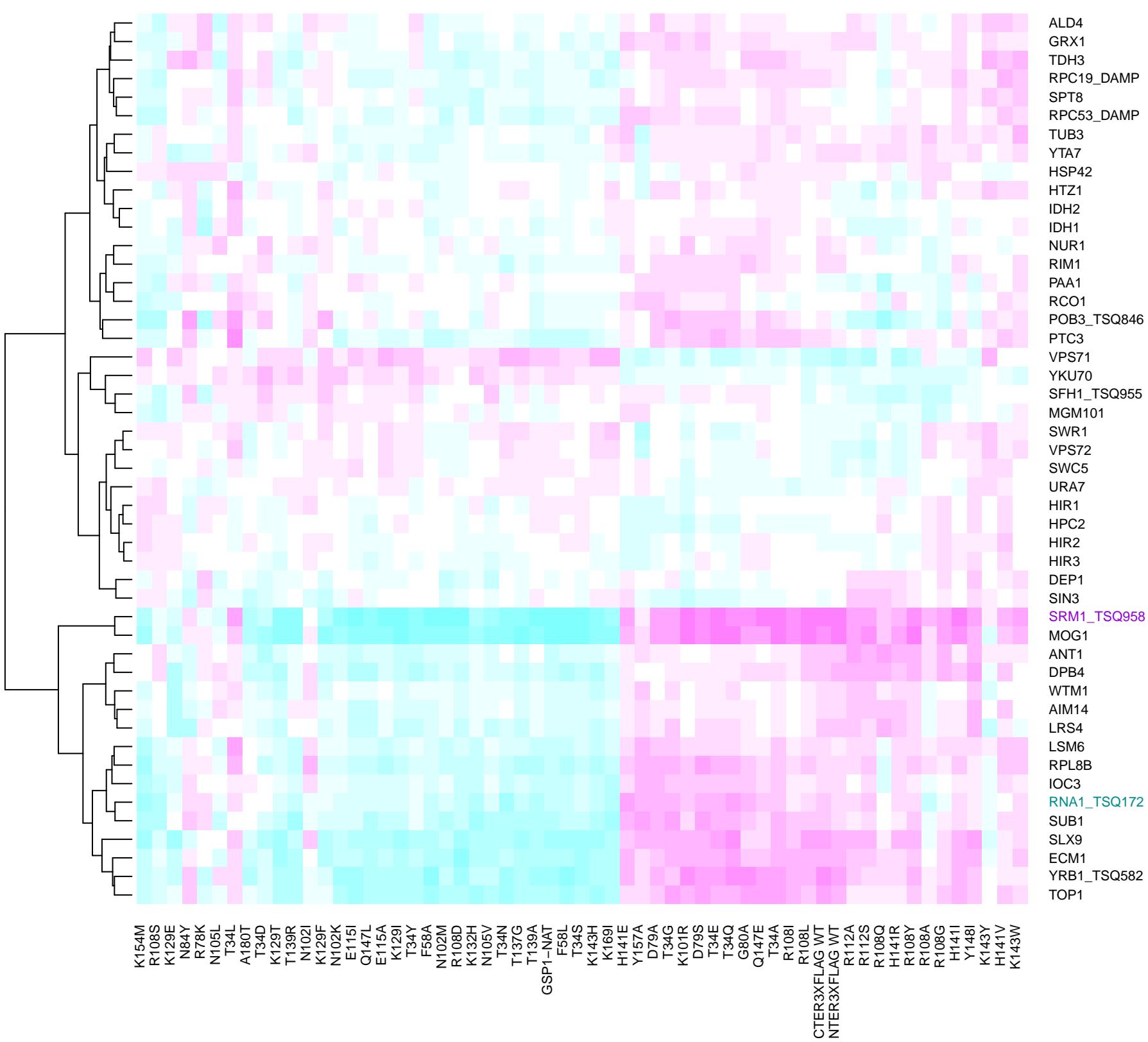


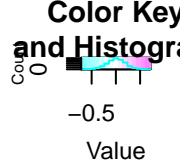
response to oxidative stress





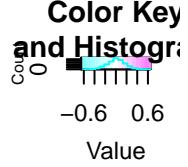
response to oxidative stress_GO_30_2



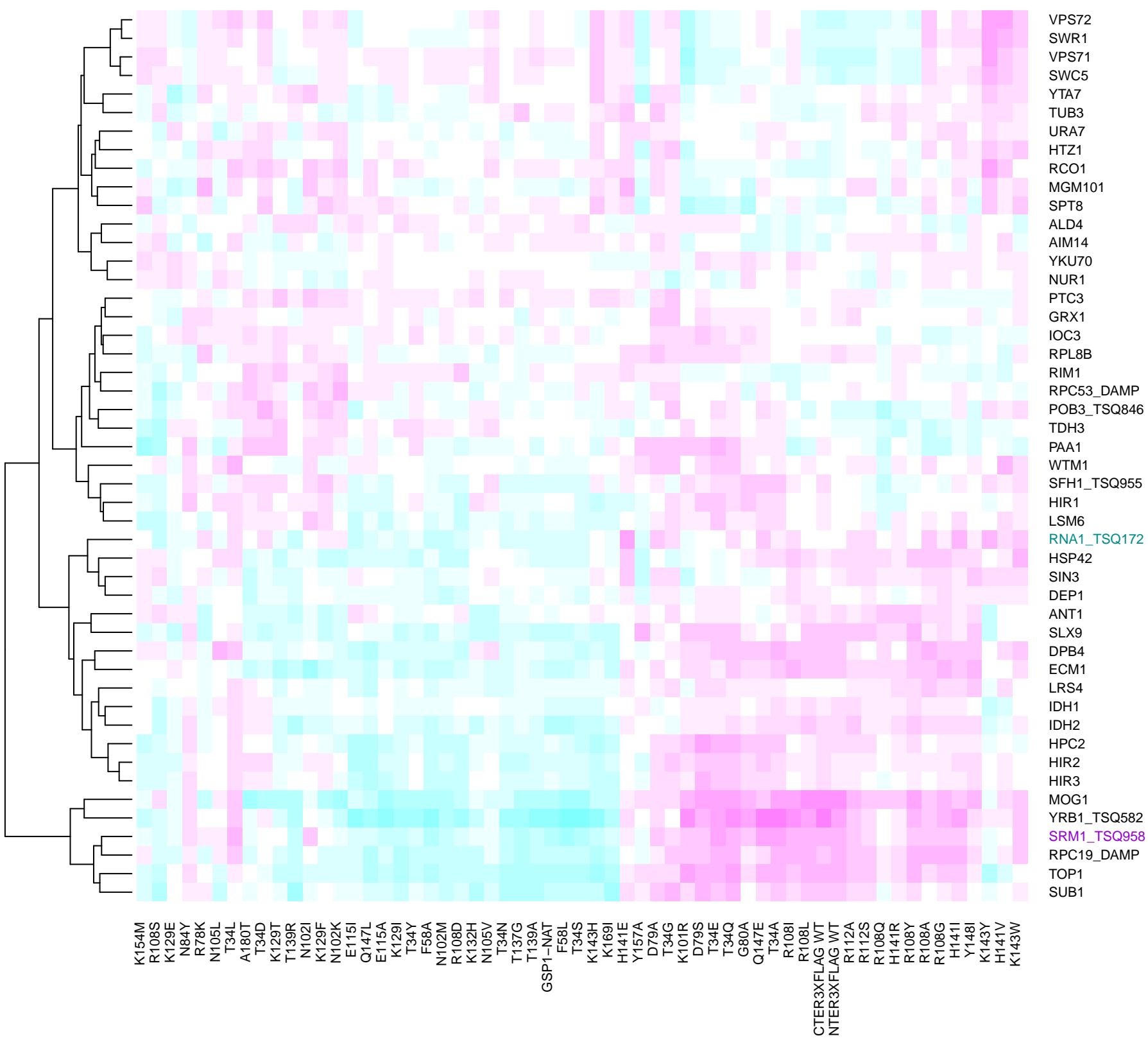


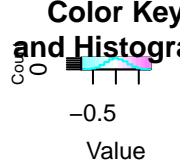
carbohydrate metabolic process_GO_30_2



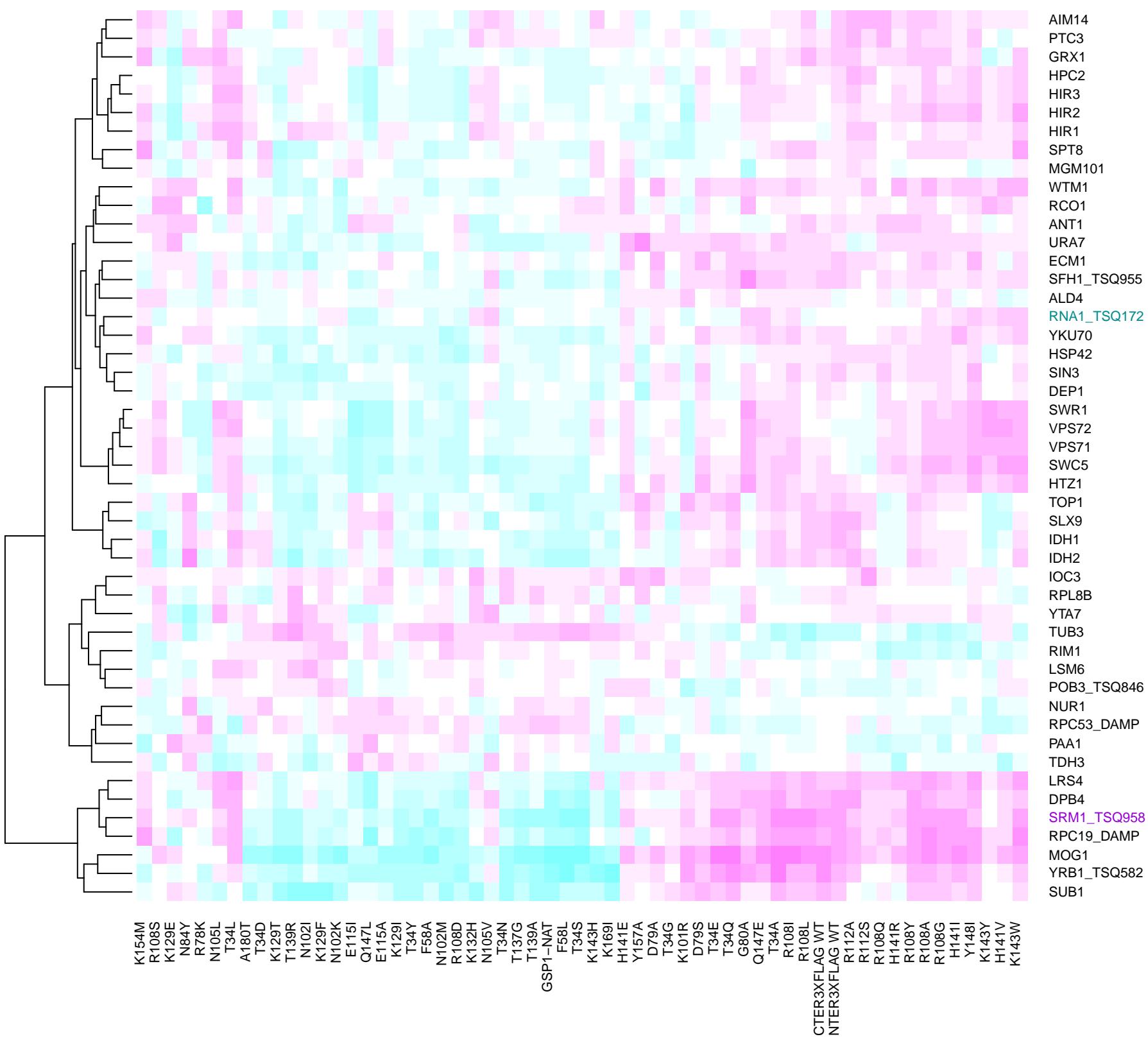


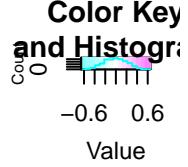
generation of precursor metabolites and energy



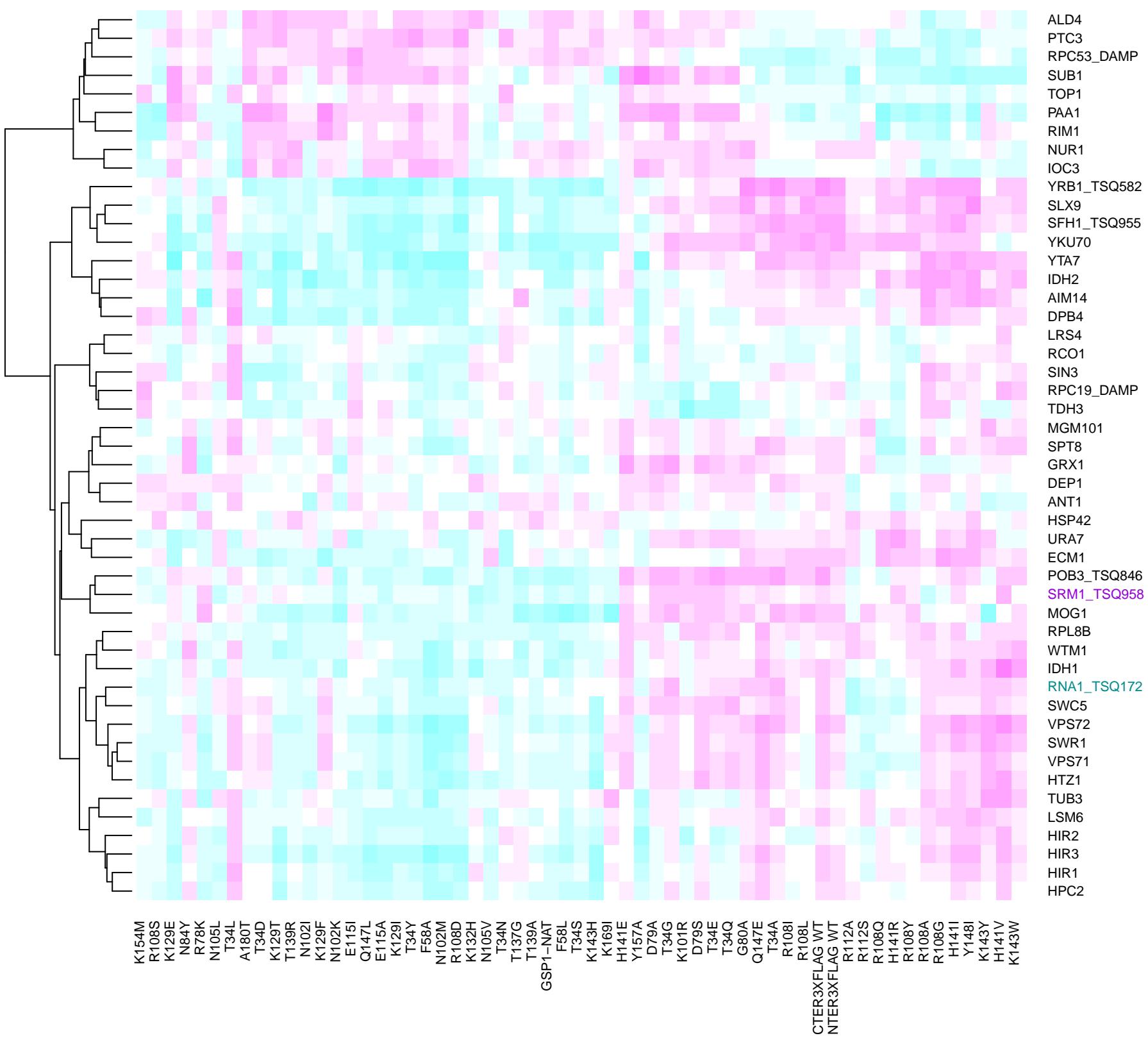


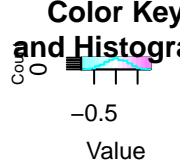
generation of precursor metabolites and energy_GO_30_3



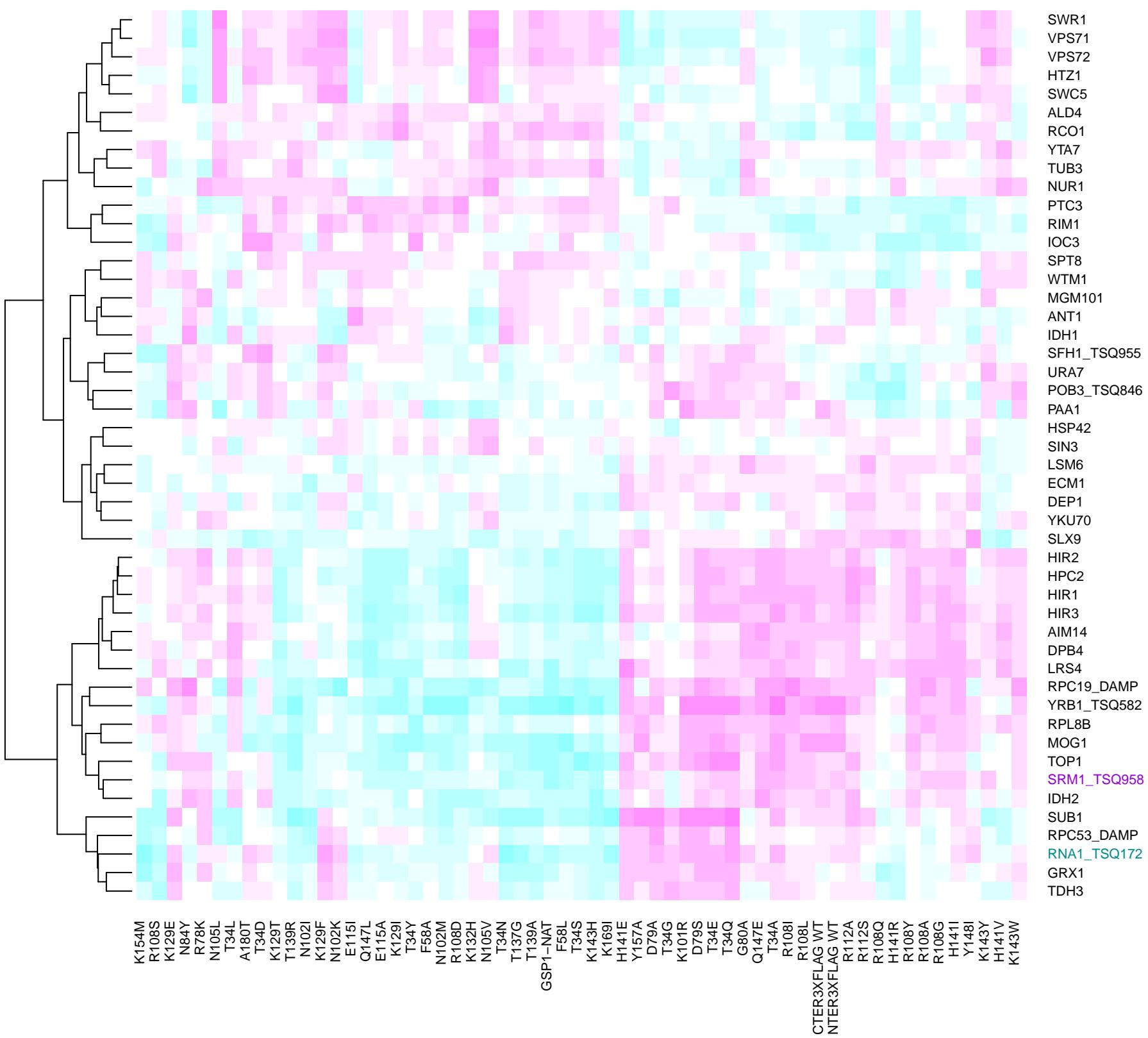


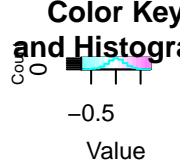
budding_GO_30_6



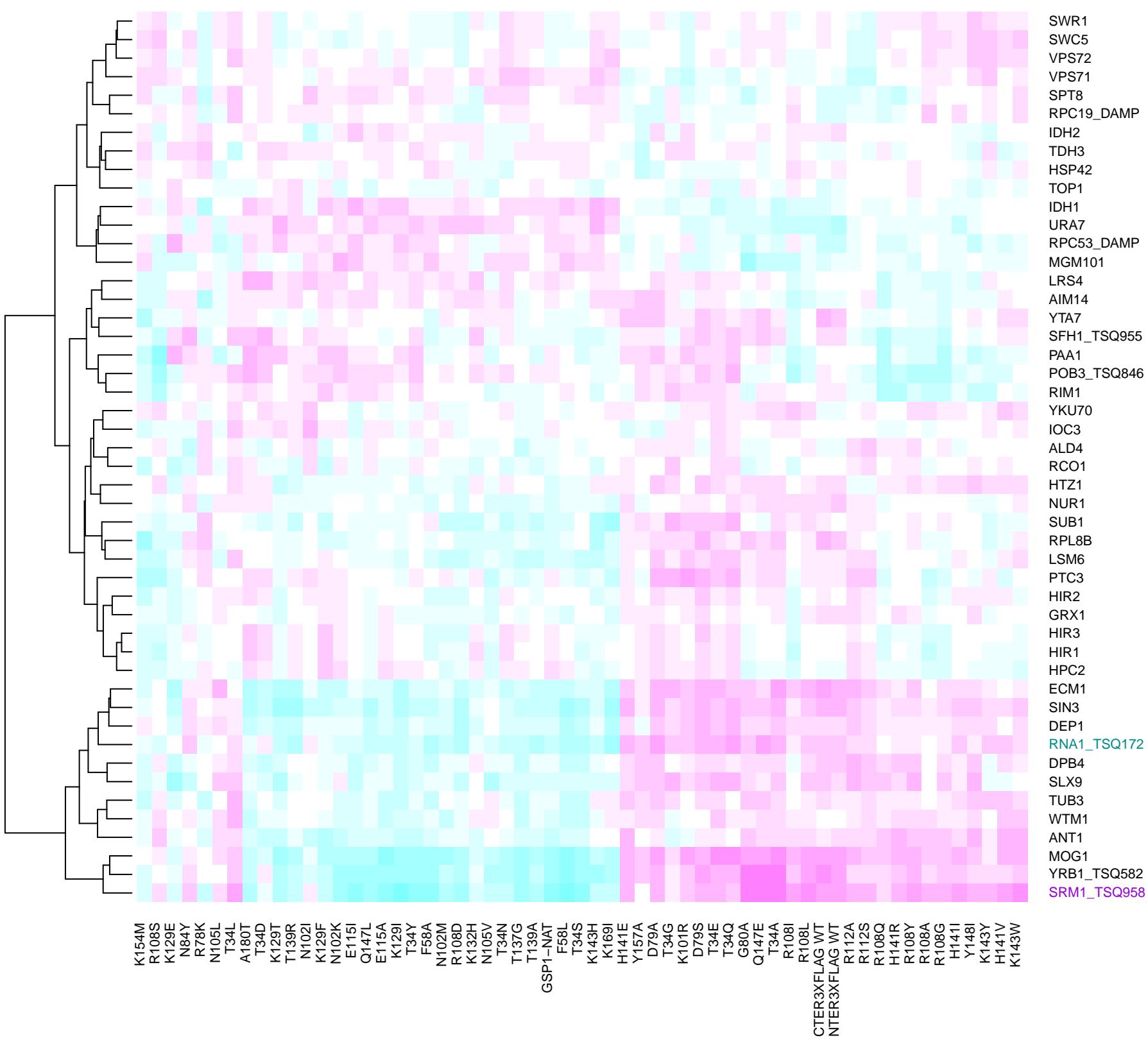


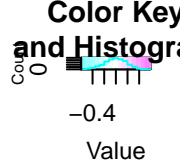
metabolic_GO_30_17



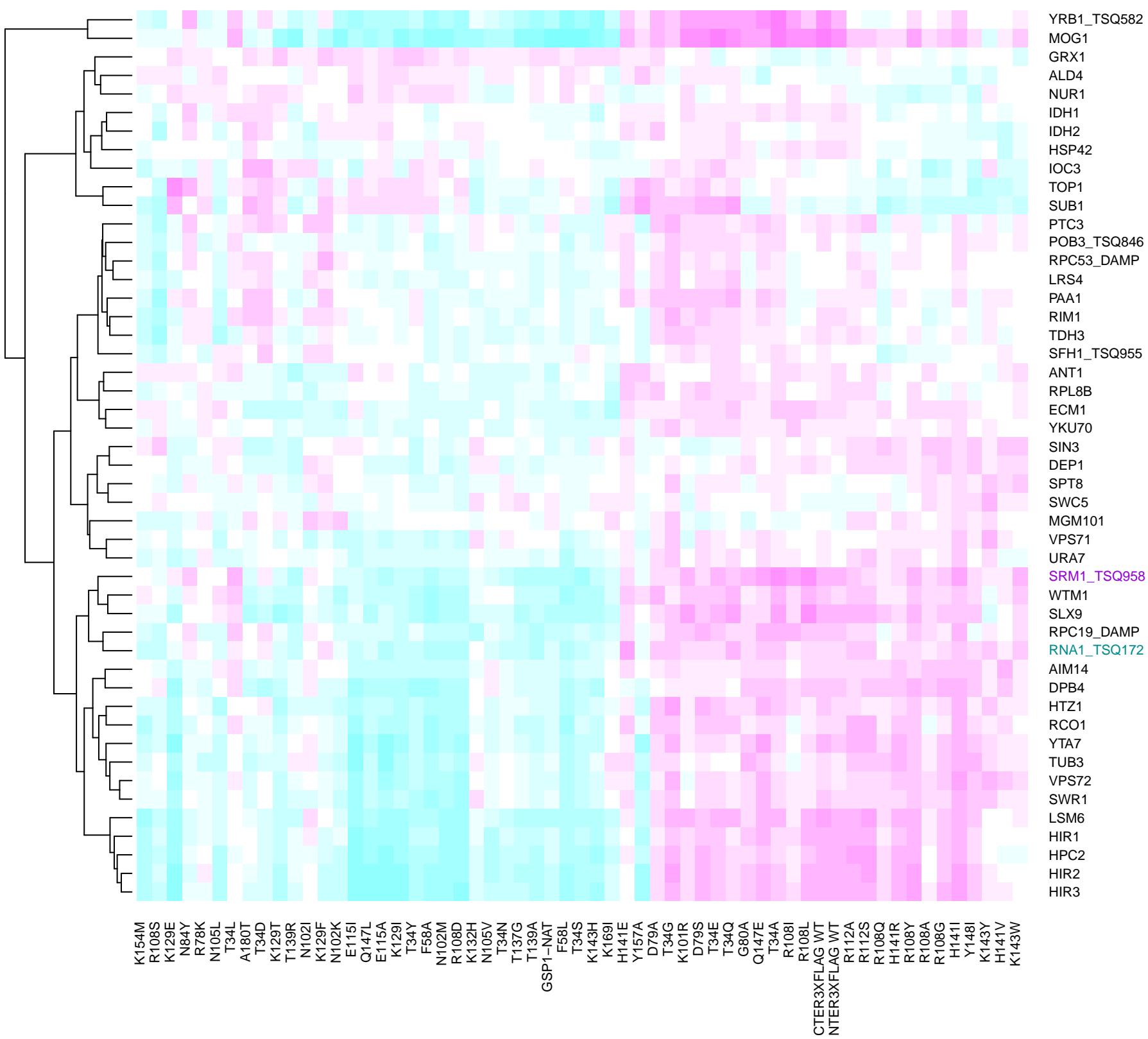


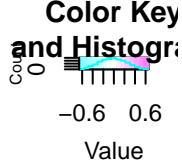
budding_GO_30_3



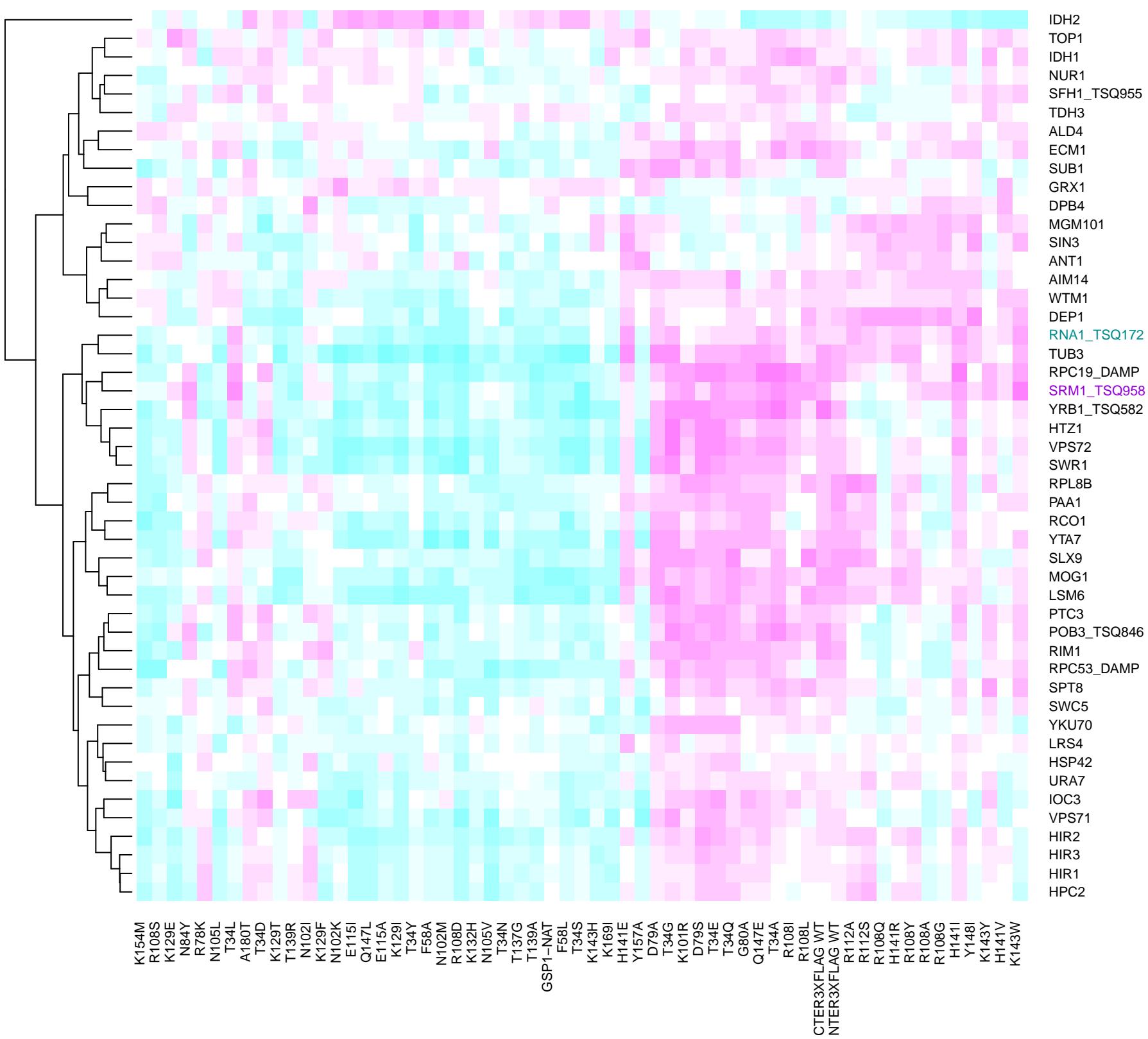


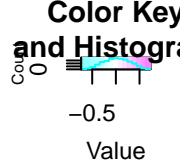
cell wall organization or biogenesis



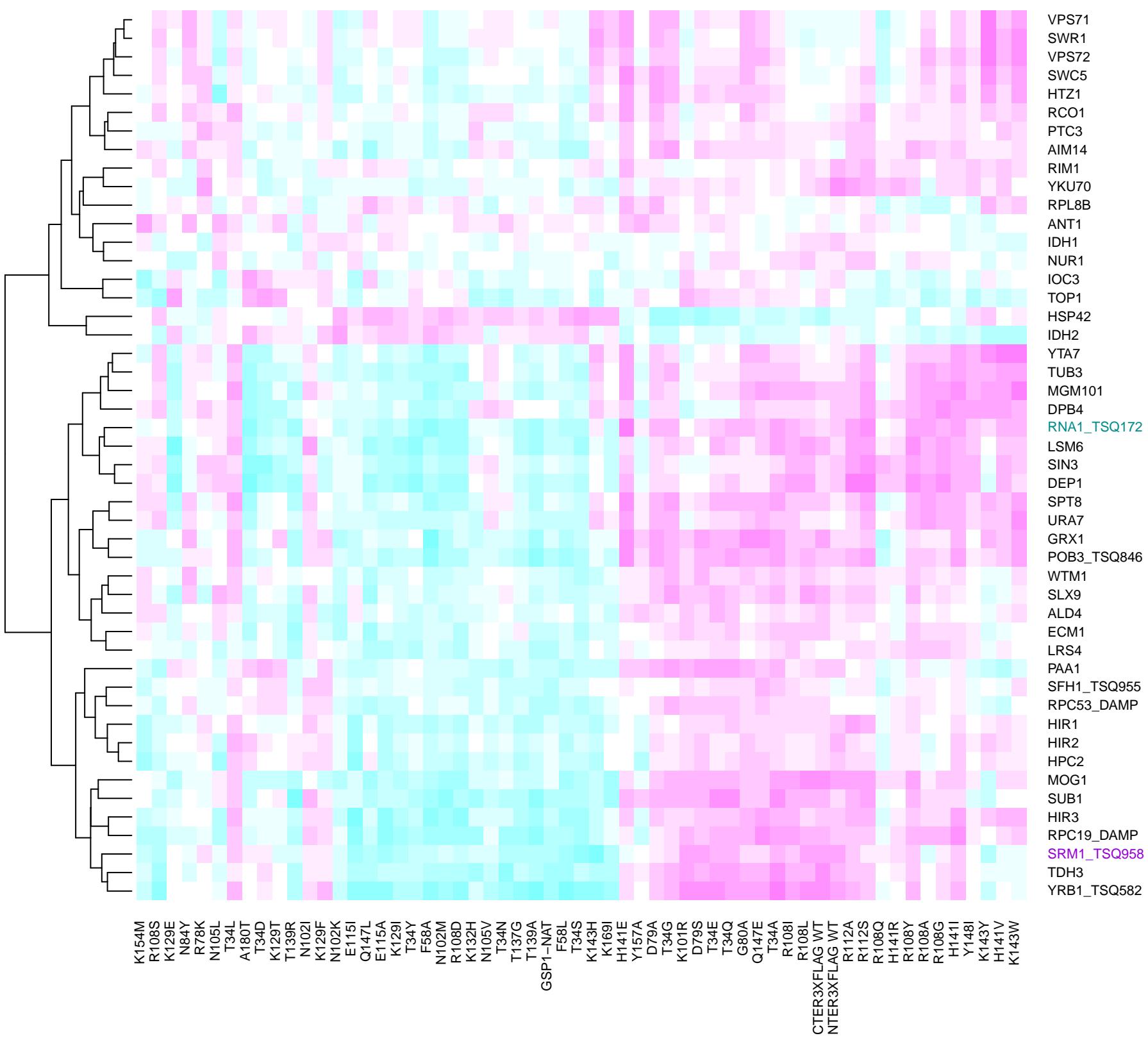


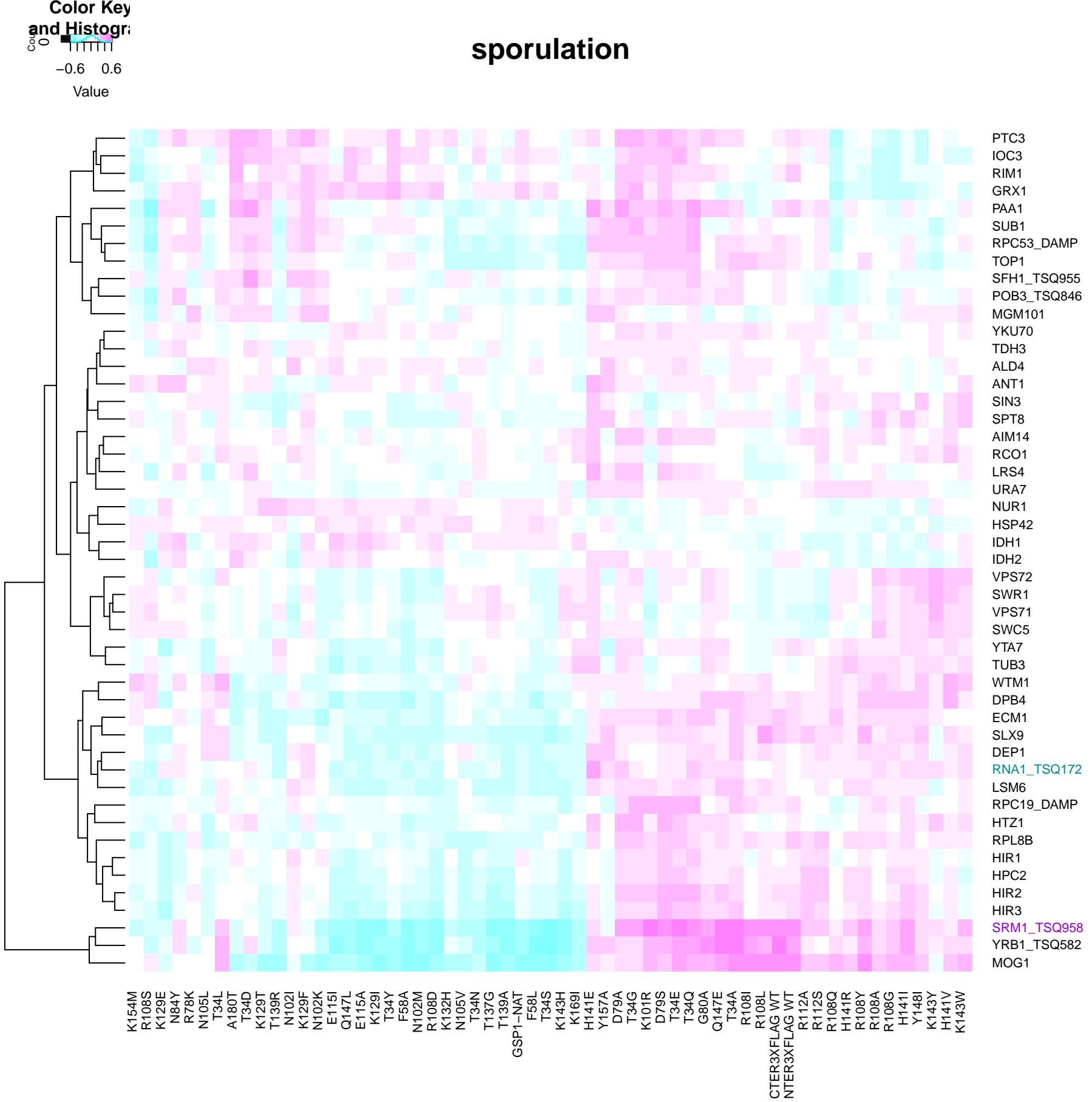
cell wall organization or biogenesis_GO_30_2

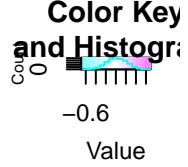




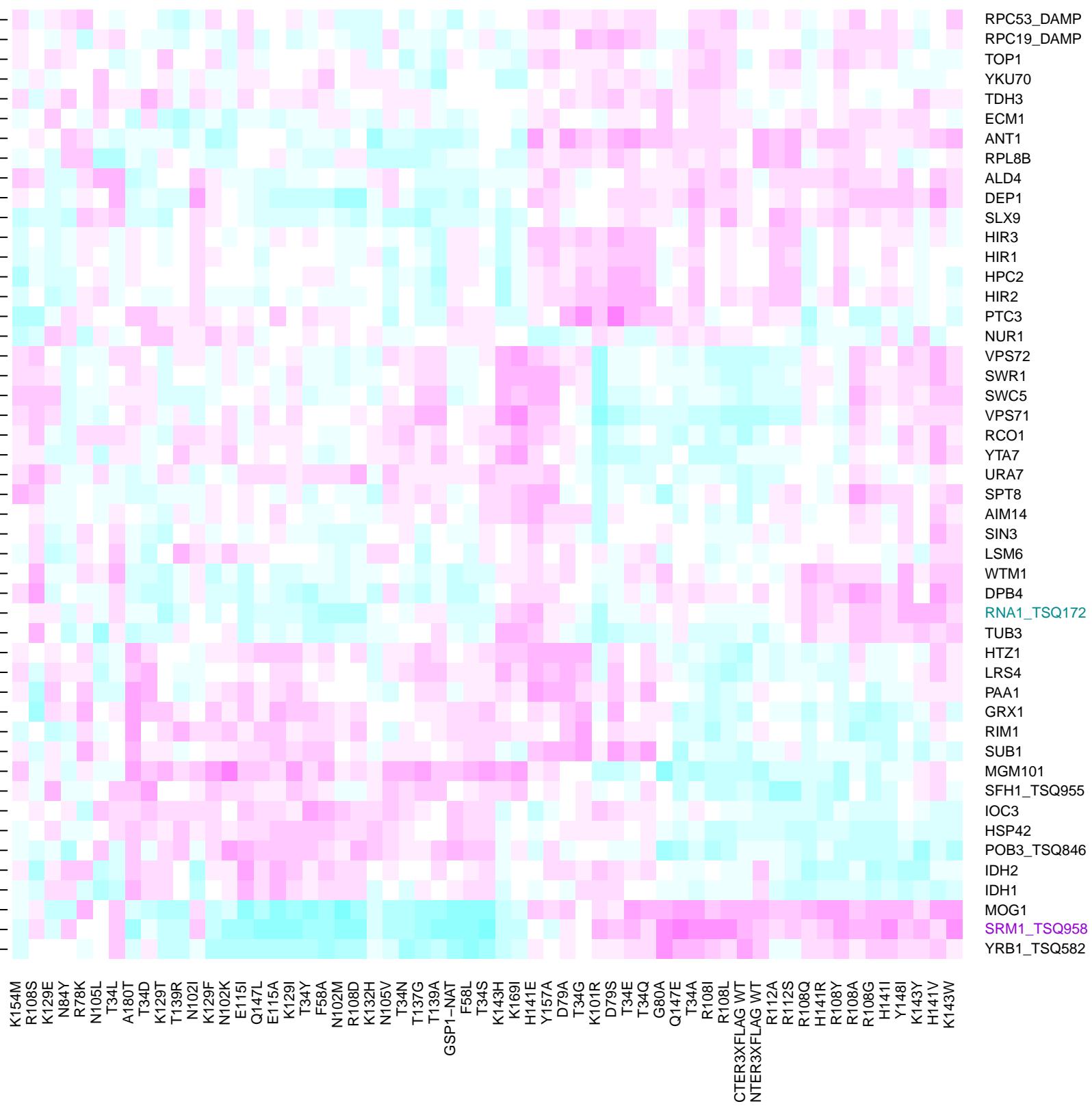
meiotic cell cycle_GO_30_5

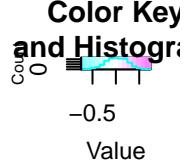




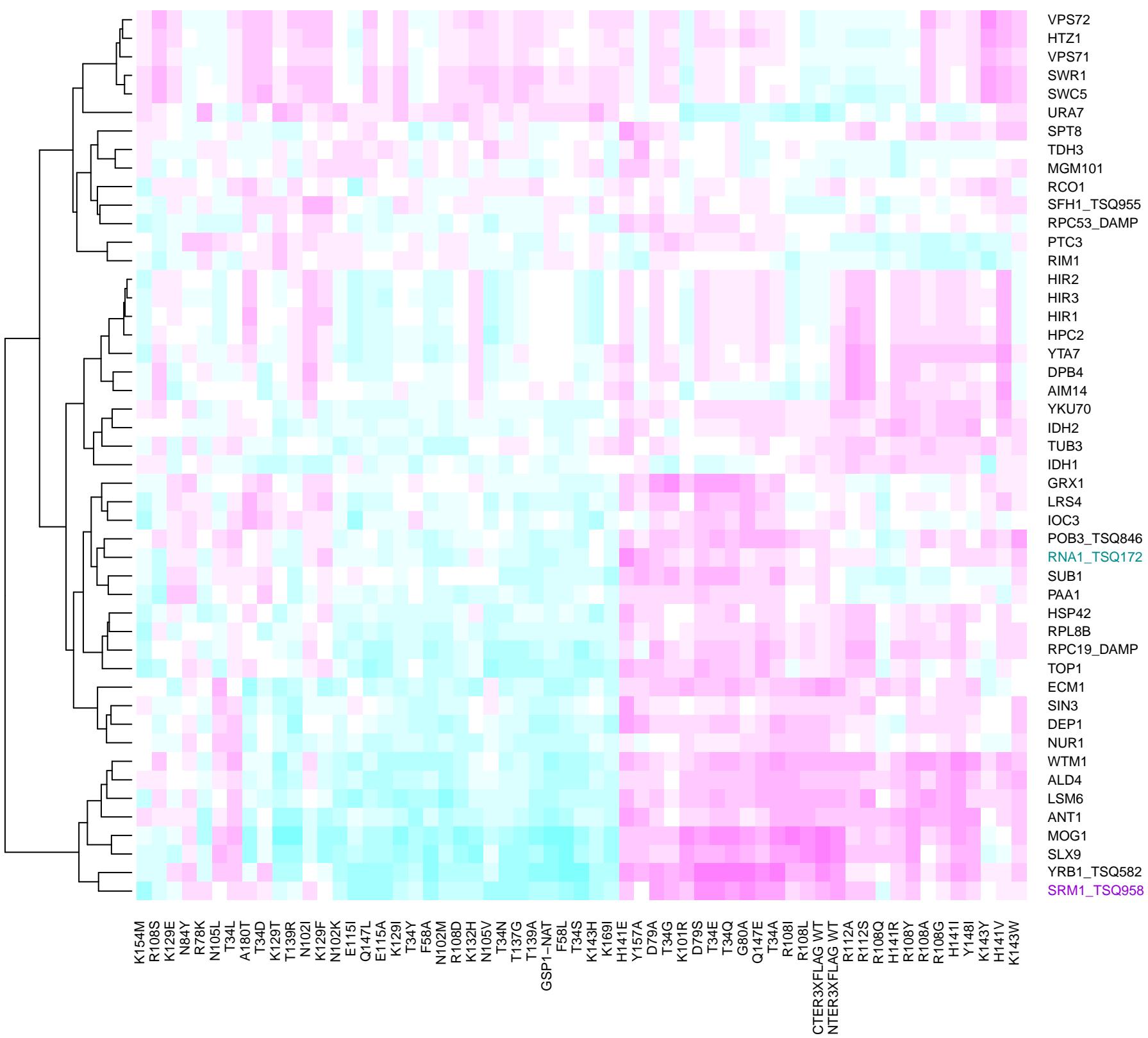


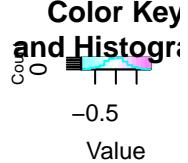
sporulation_GO_30_2



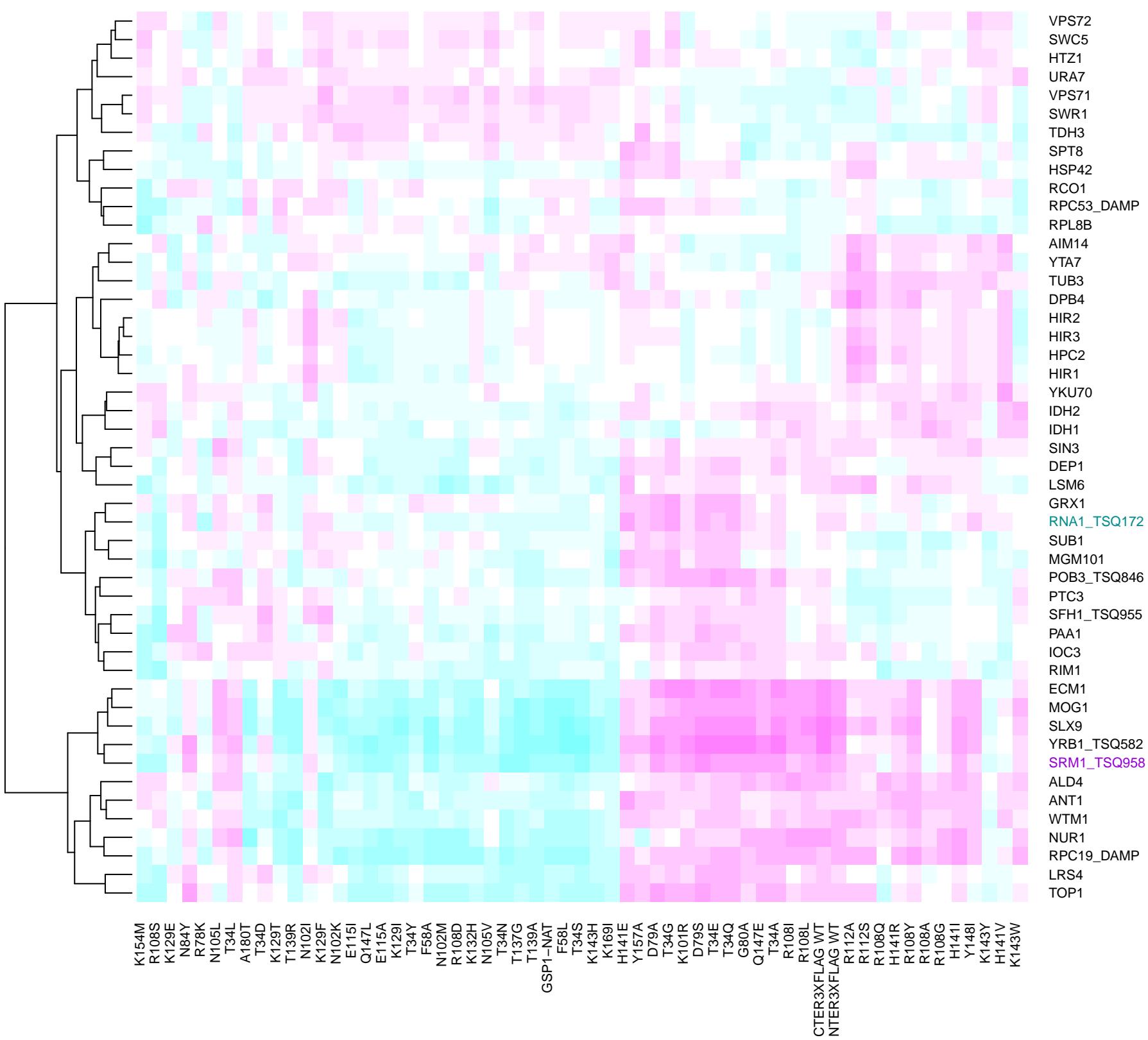


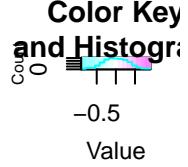
chromatin binding



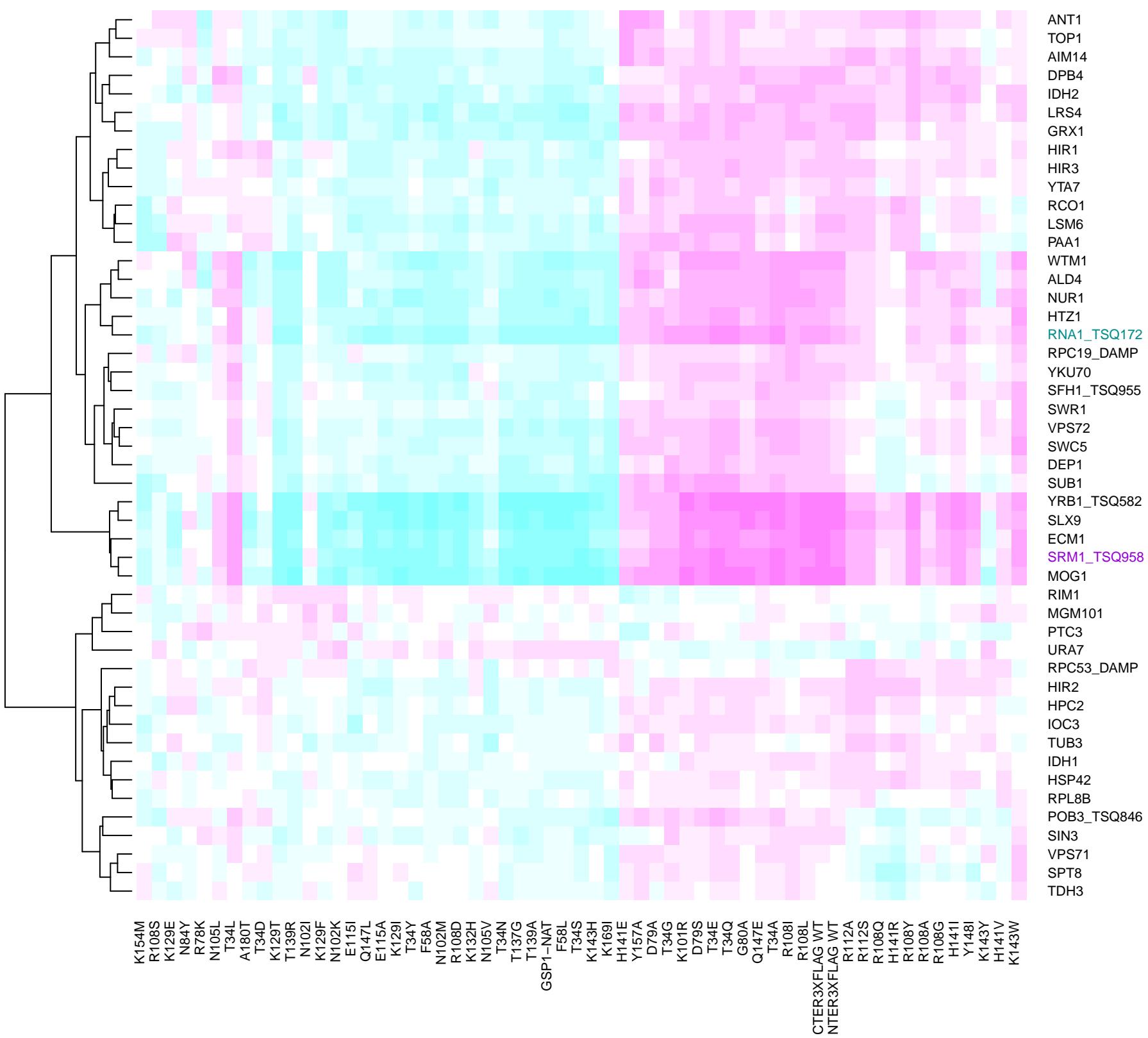


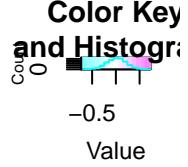
chromatin binding_GO_30_2



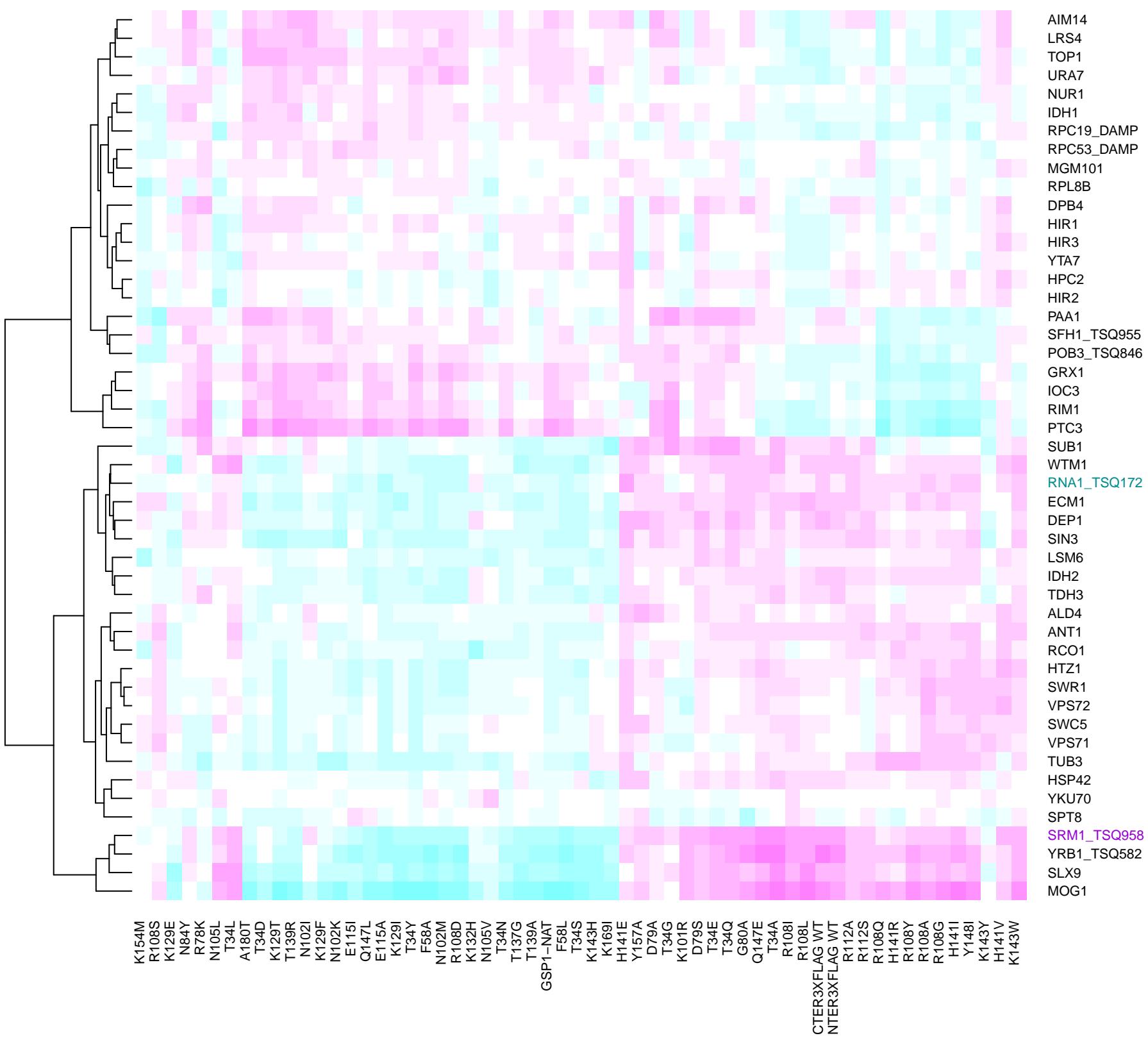


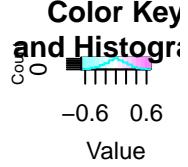
chromatin organization_GO_30_4



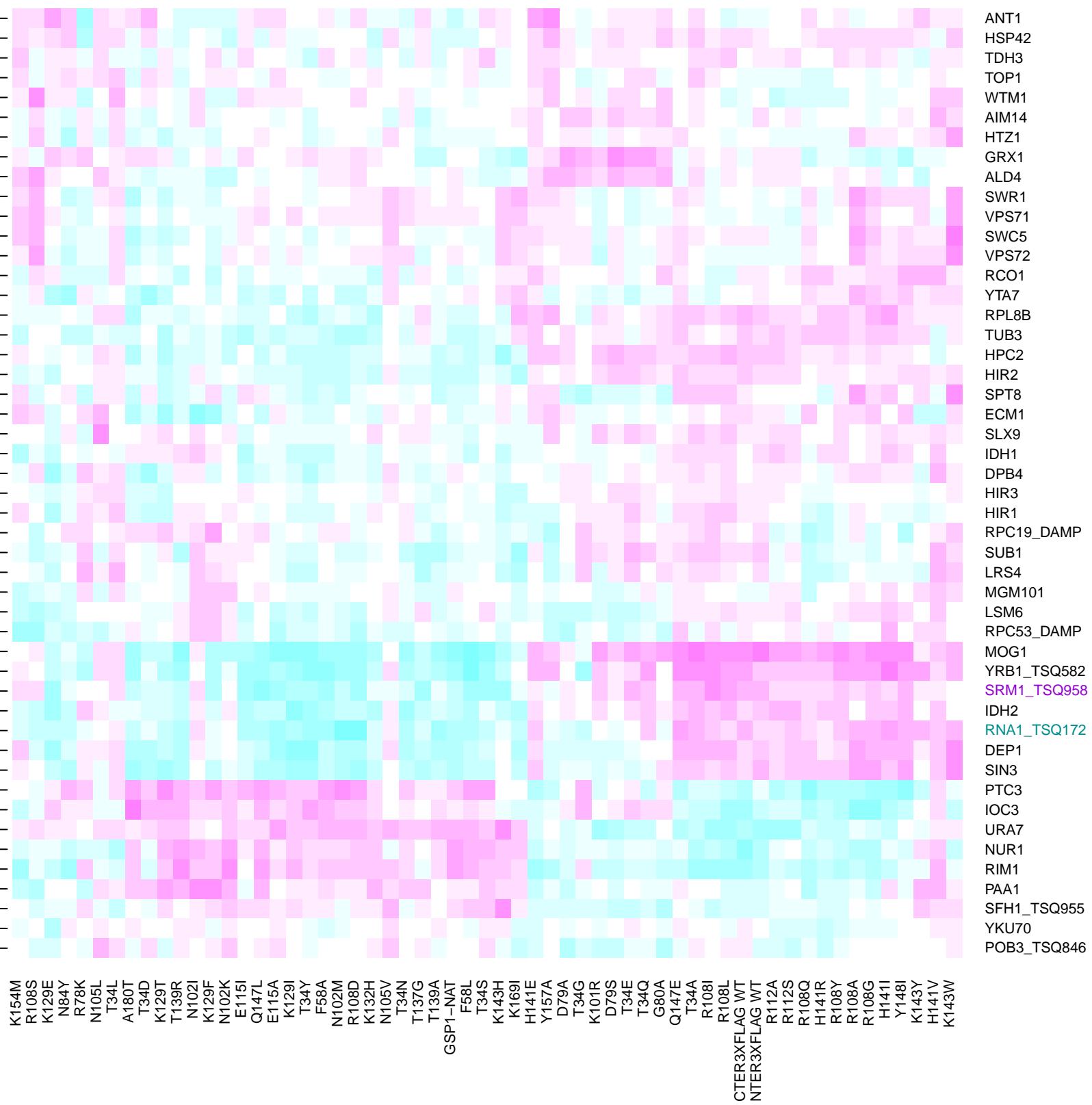


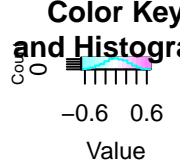
cell cycle_GO_30_2



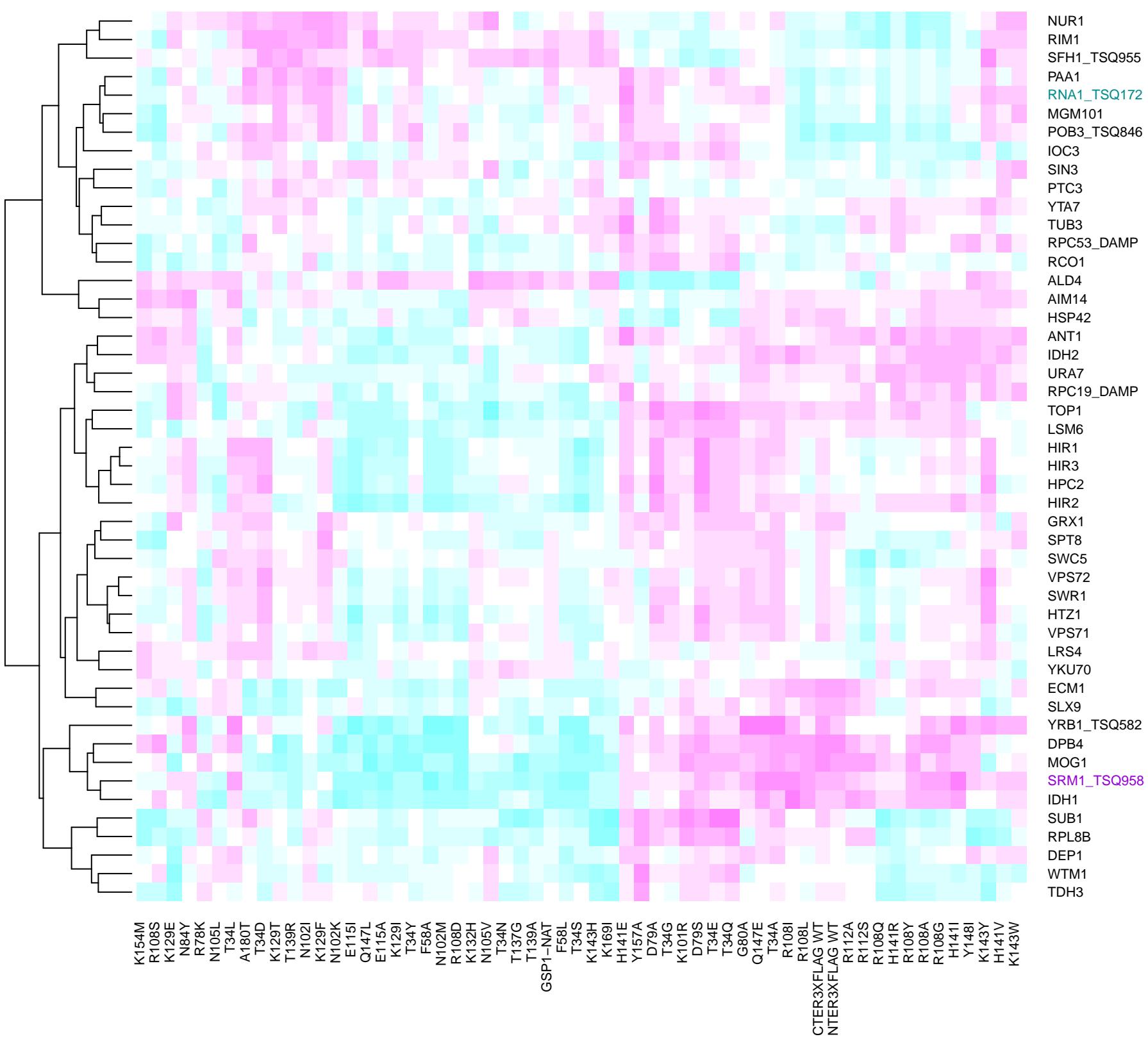


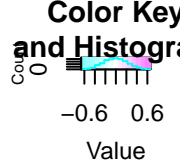
mitochondria and respiration_GO_30_12



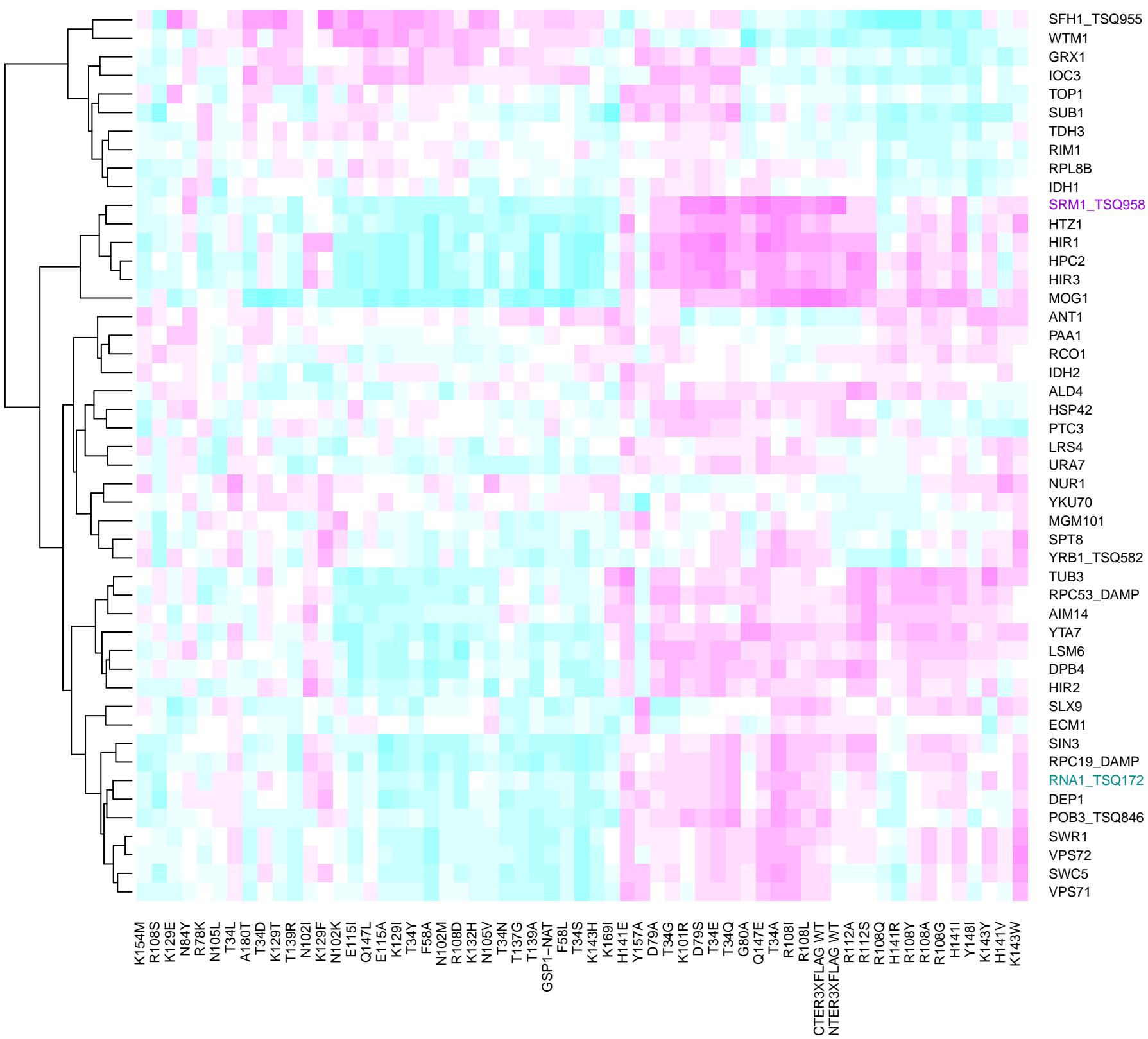


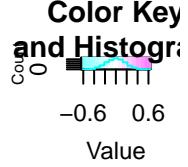
transcription and mRNA processing_GO_30_12



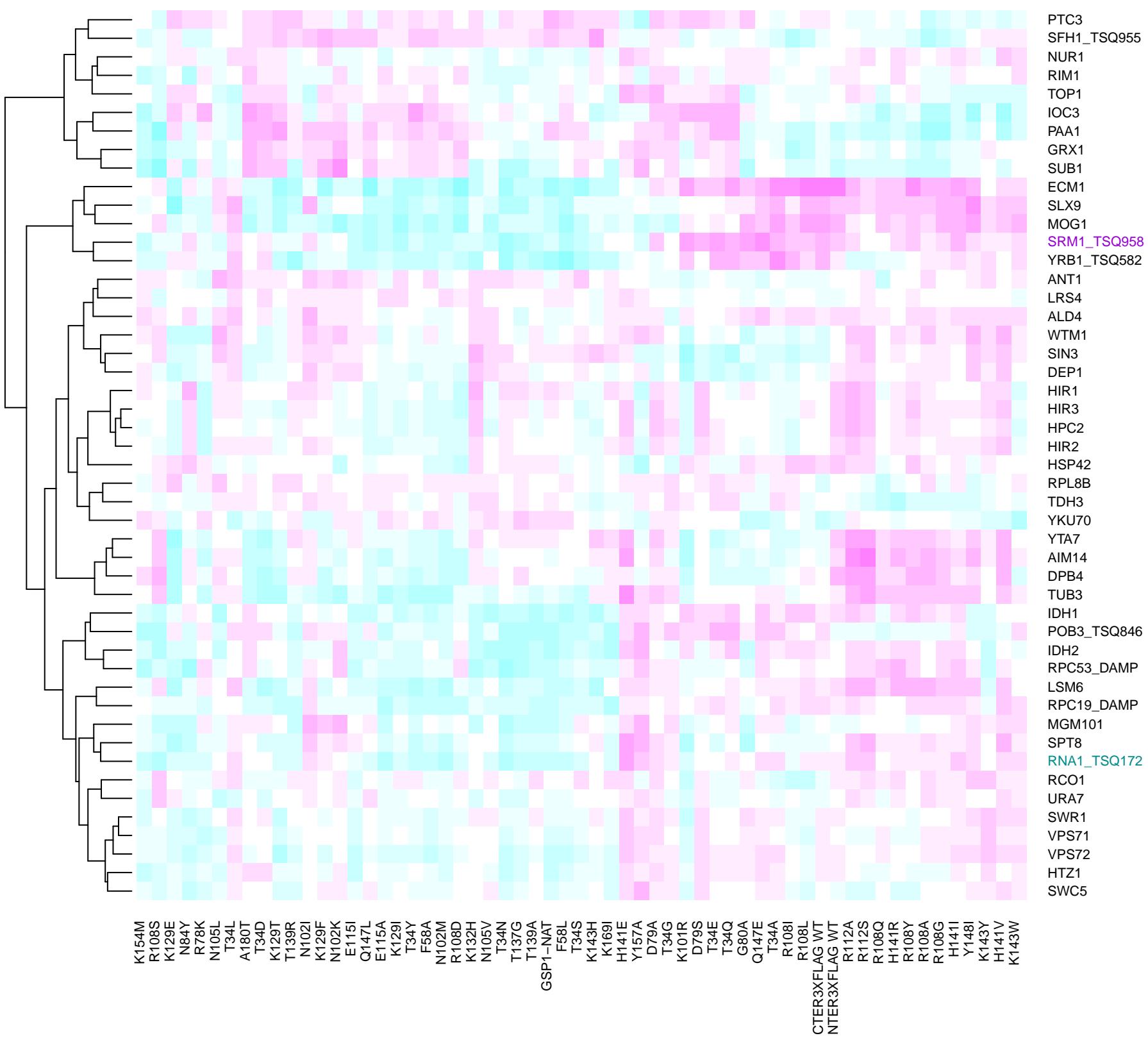


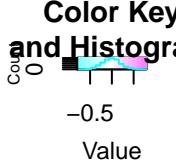
transcription from RNA polymerase II promoter_GO_30_6



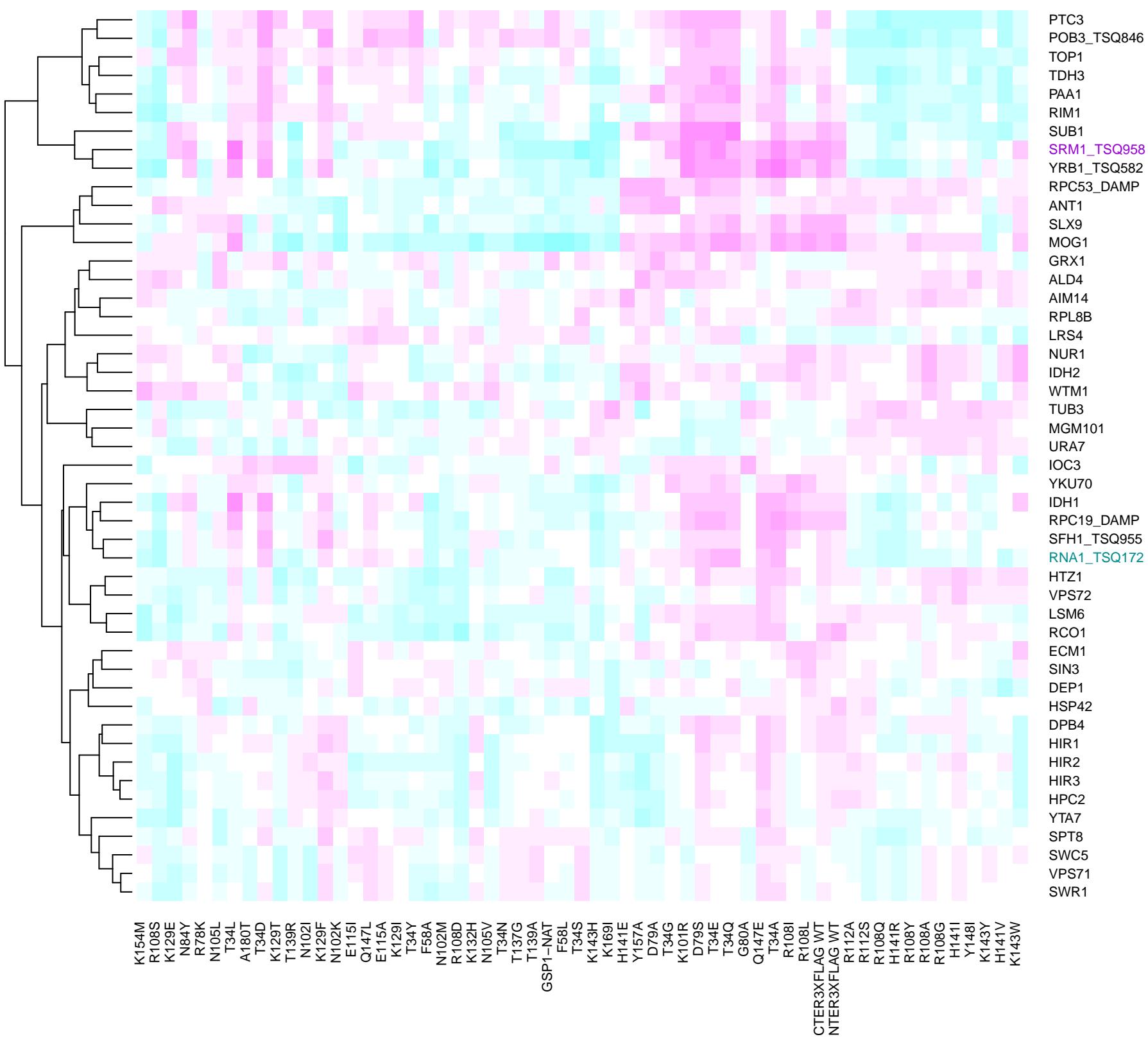


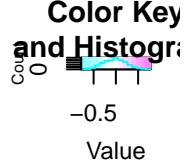
transcription_GO_30_2



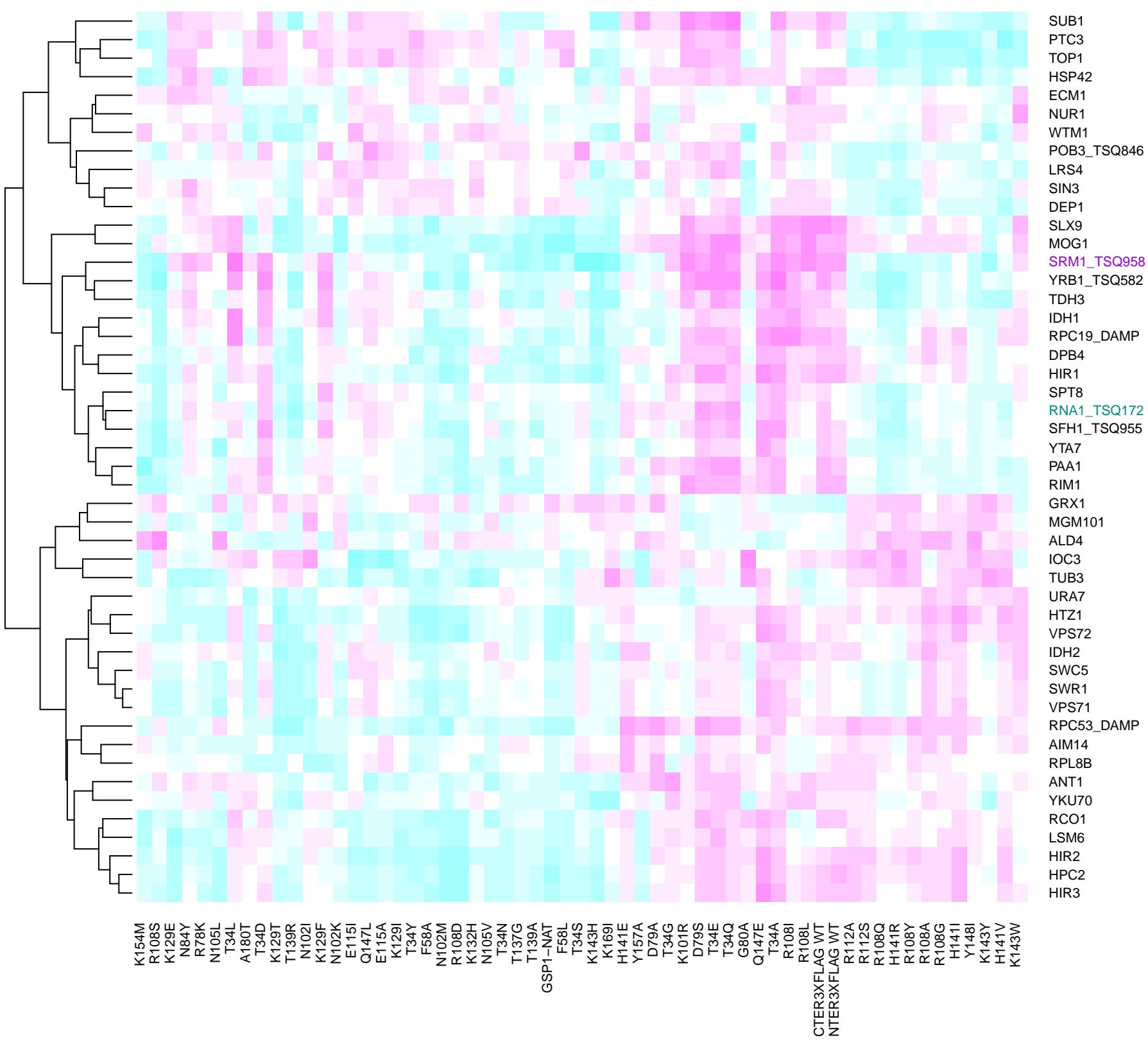


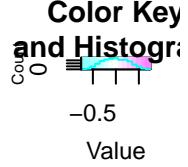
cell budding



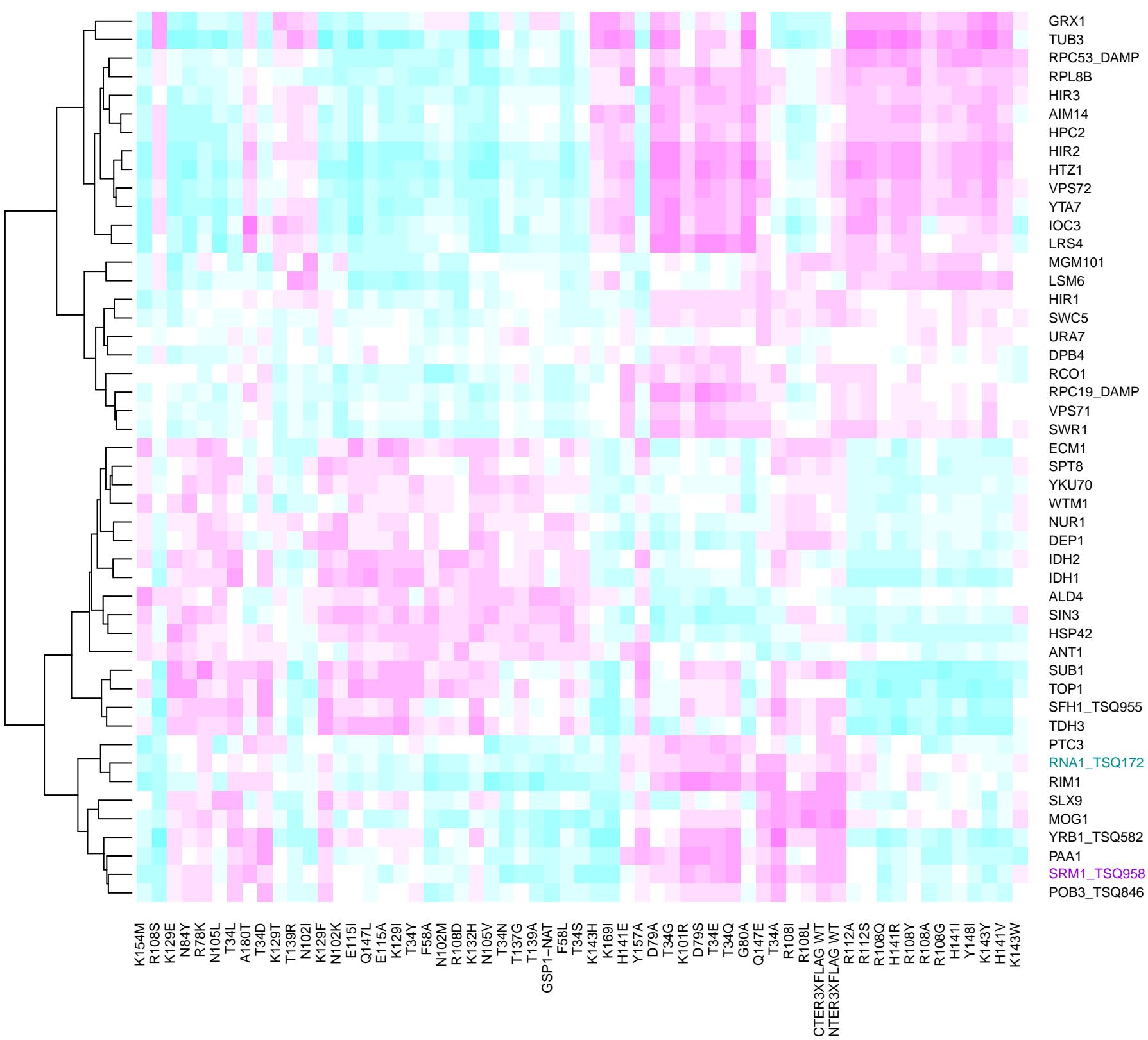


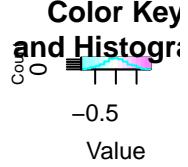
cell budding_GO_30_1



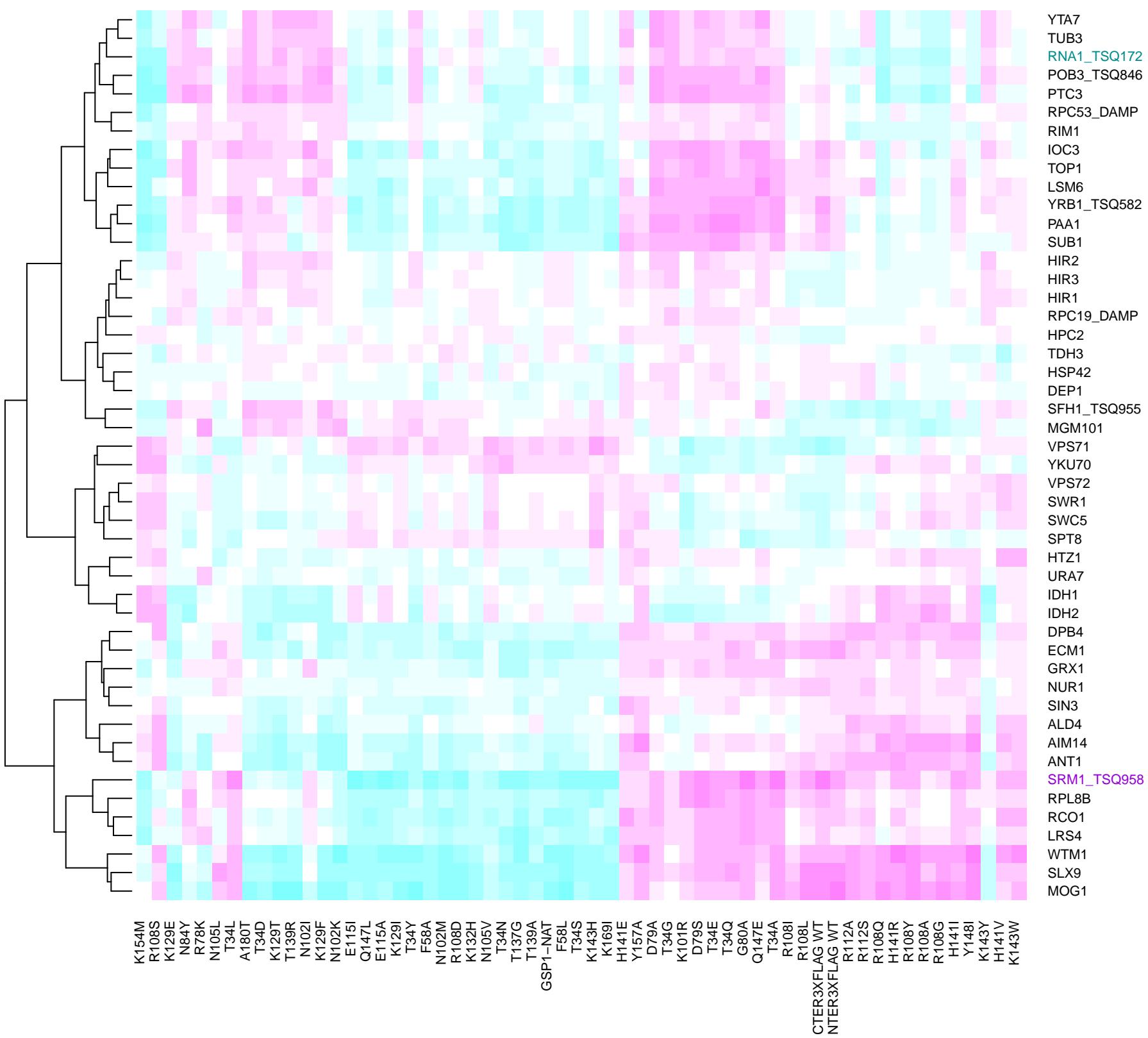


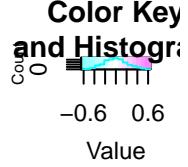
cytoskeleton organization_GO_30_2



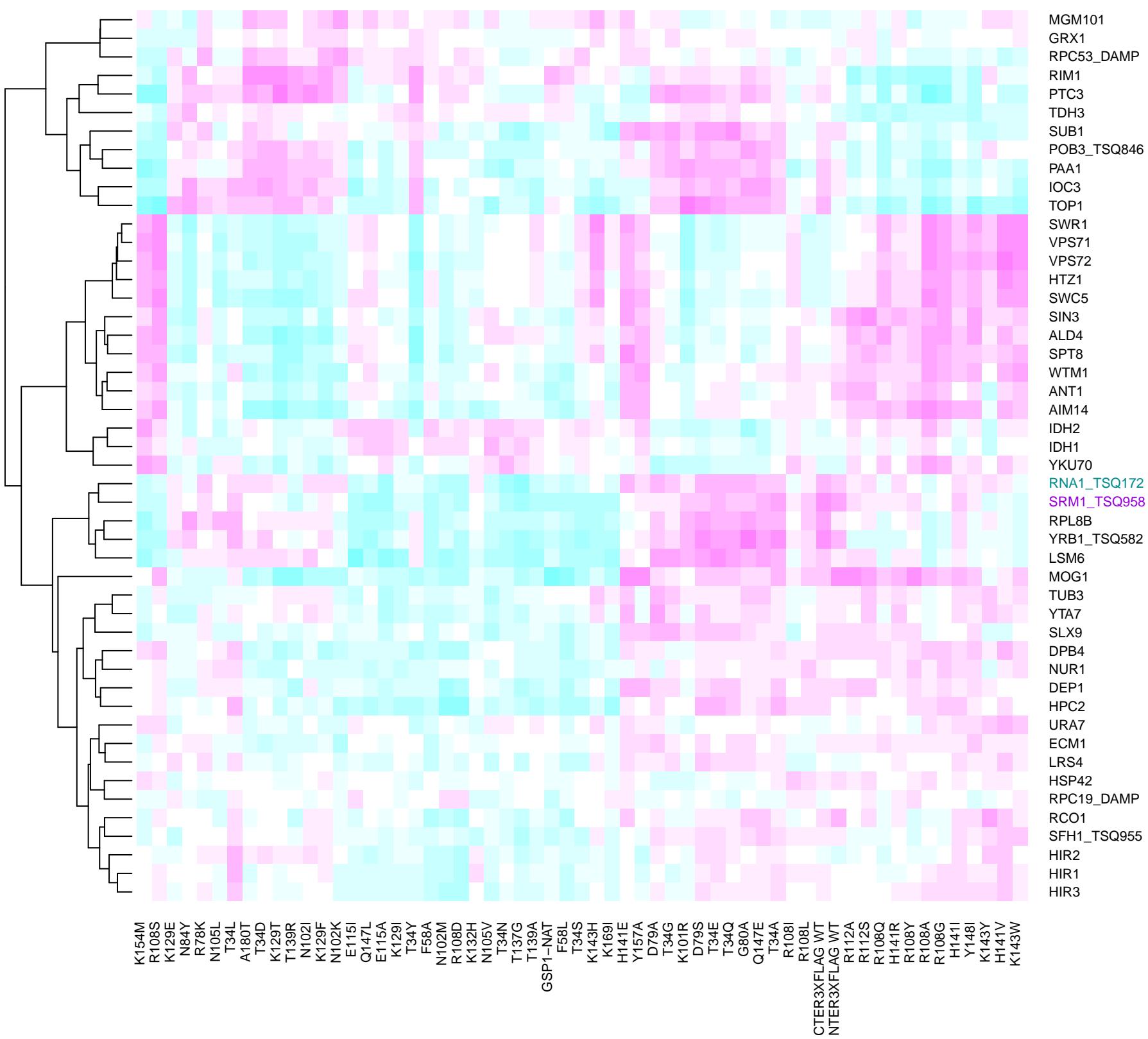


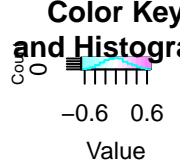
ribosomes and translation_GO_30_3



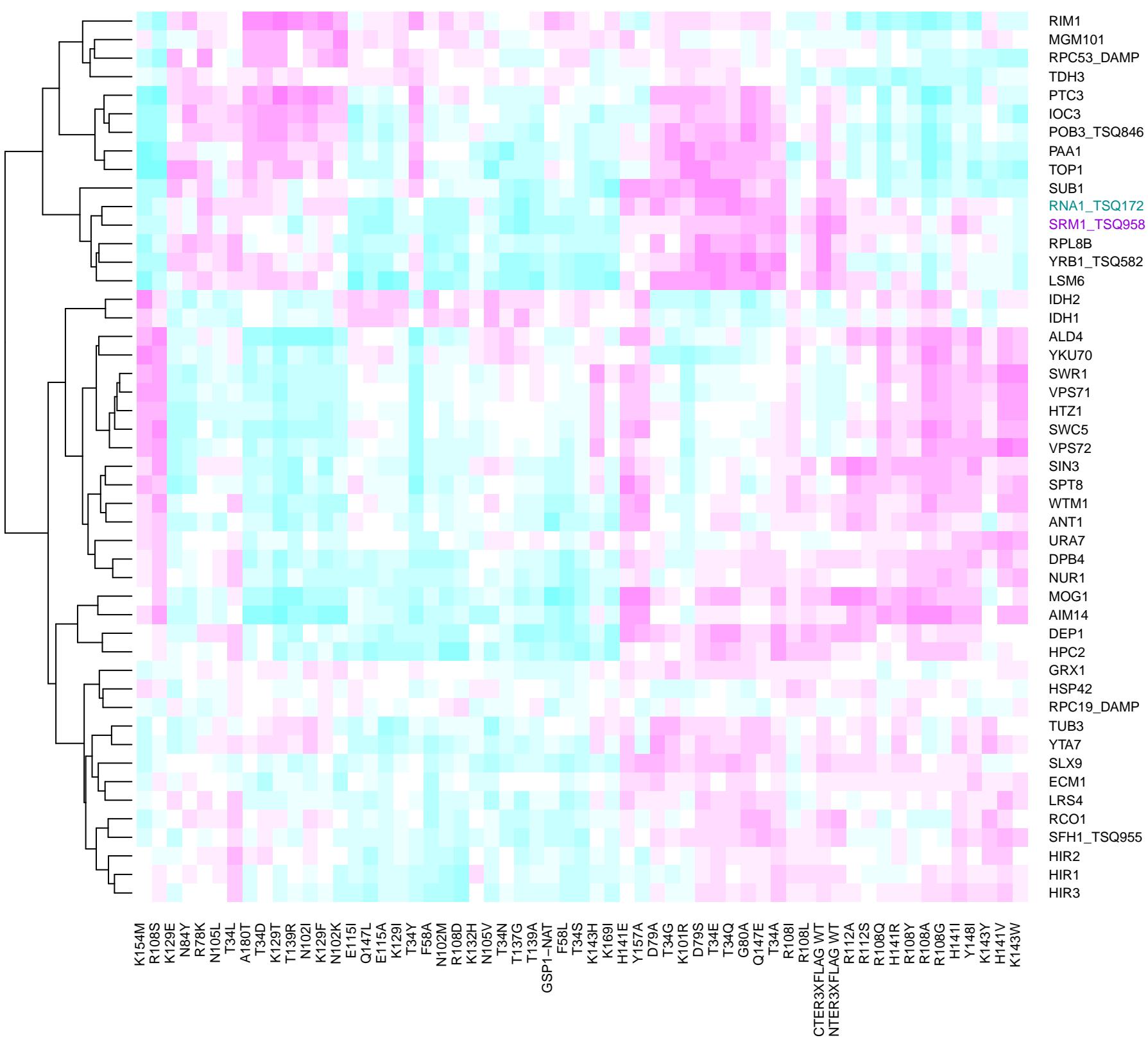


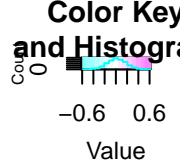
RNA modification



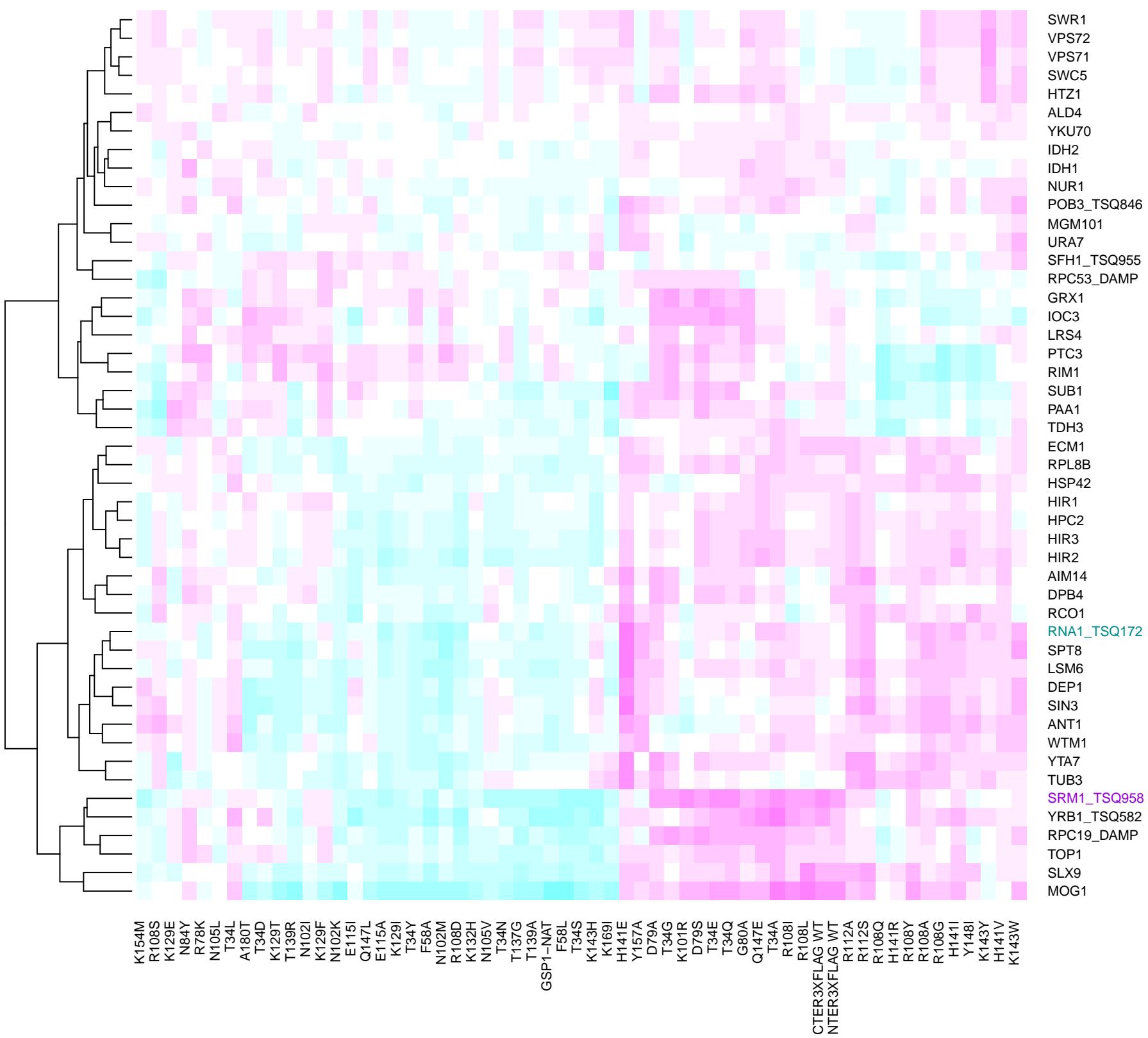


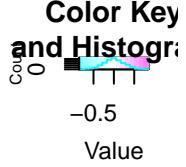
RNA modification_GO_30_1



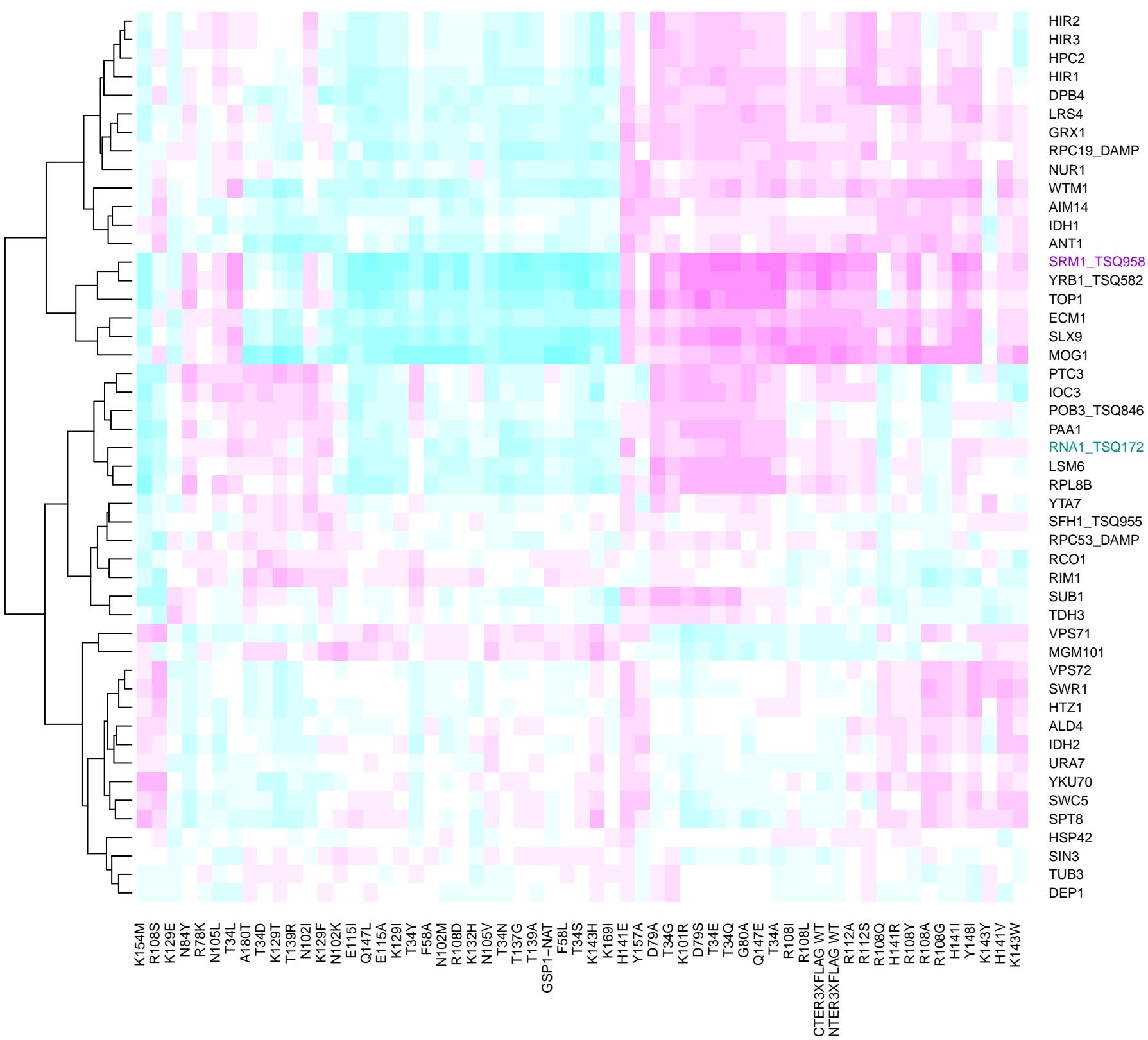


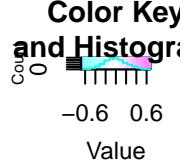
cellular response to DNA damage stimulus



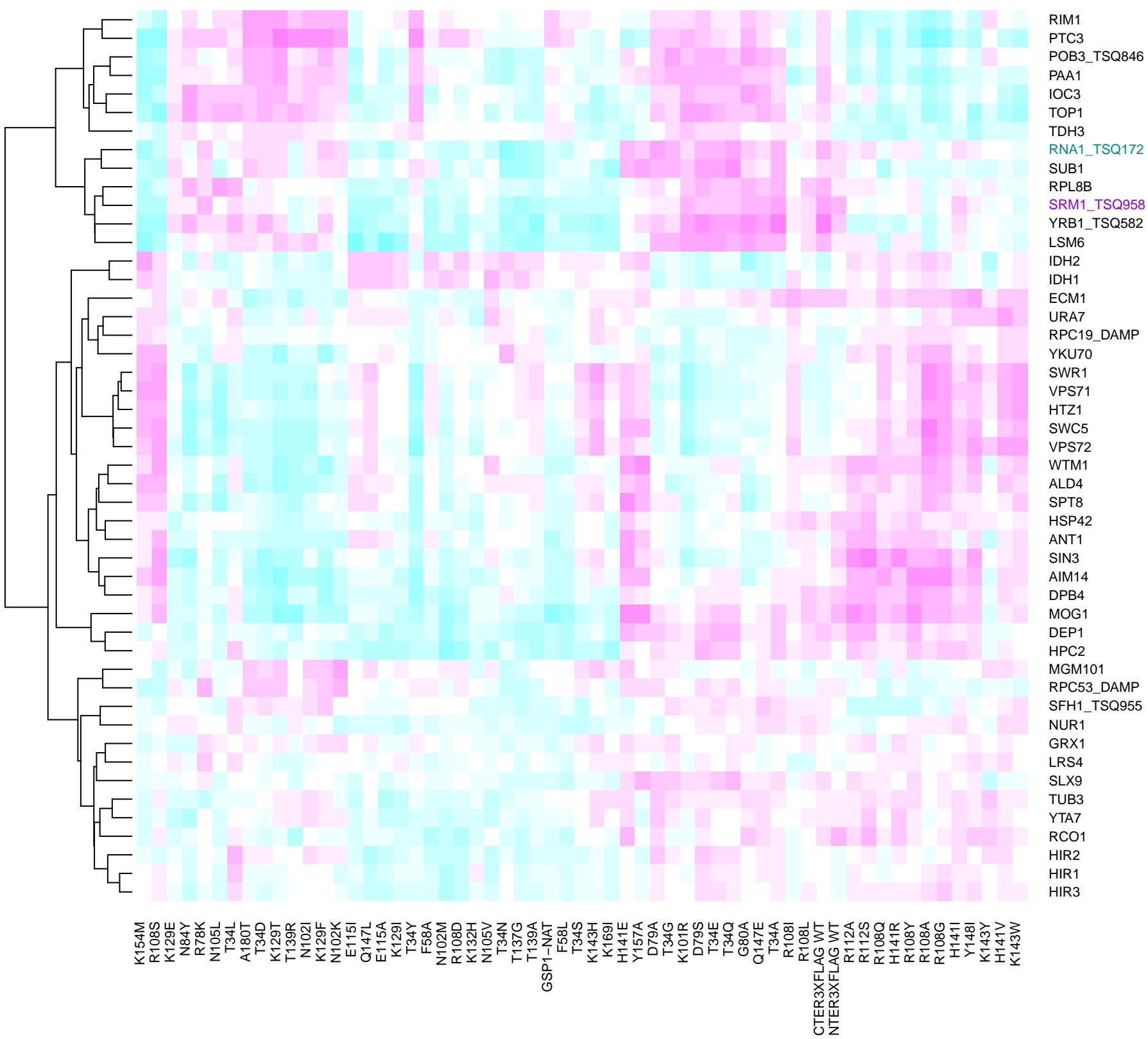


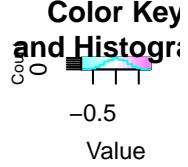
transcription and mRNA processing_GO_30_4



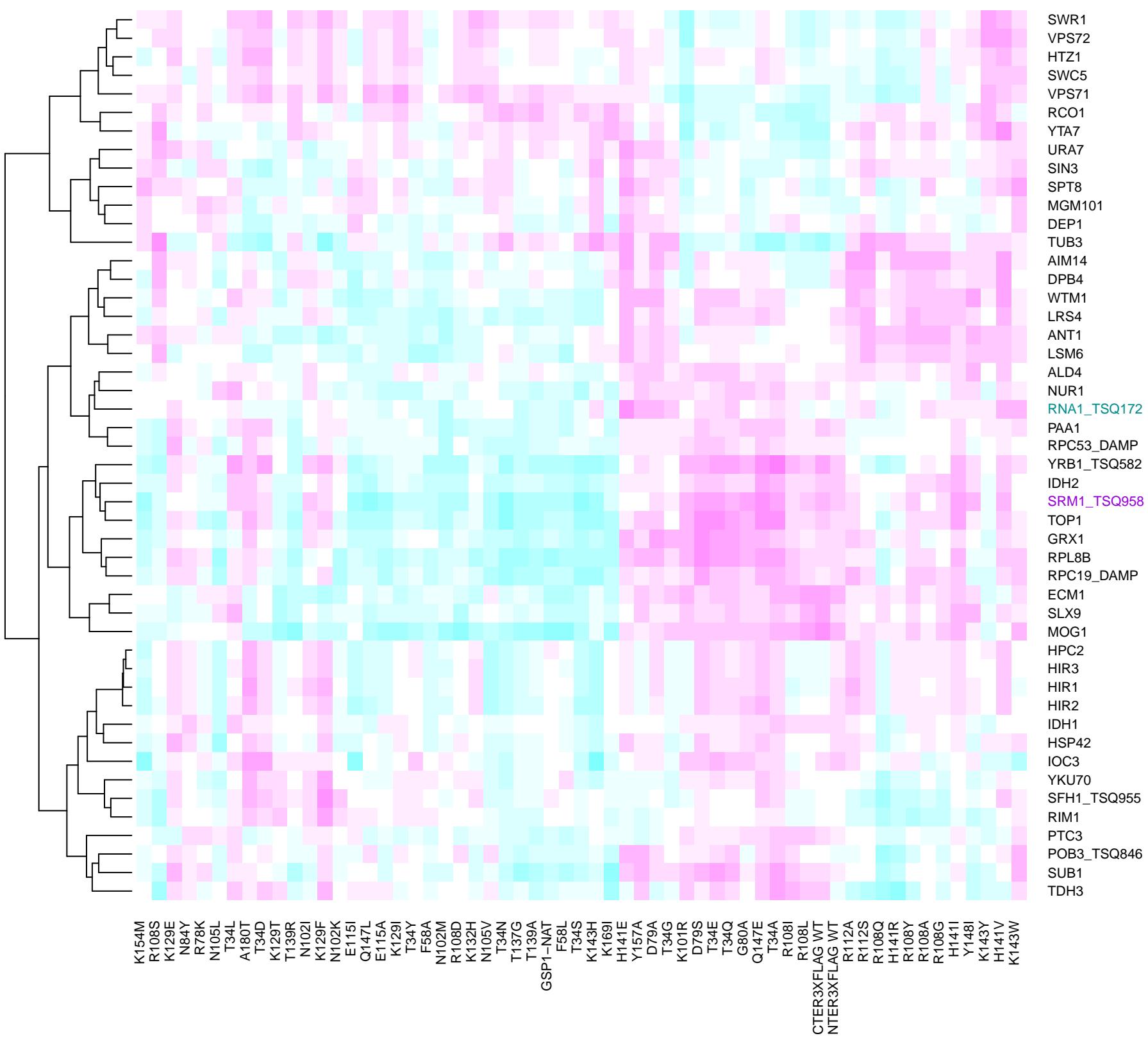


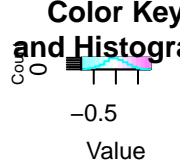
tRNA processing



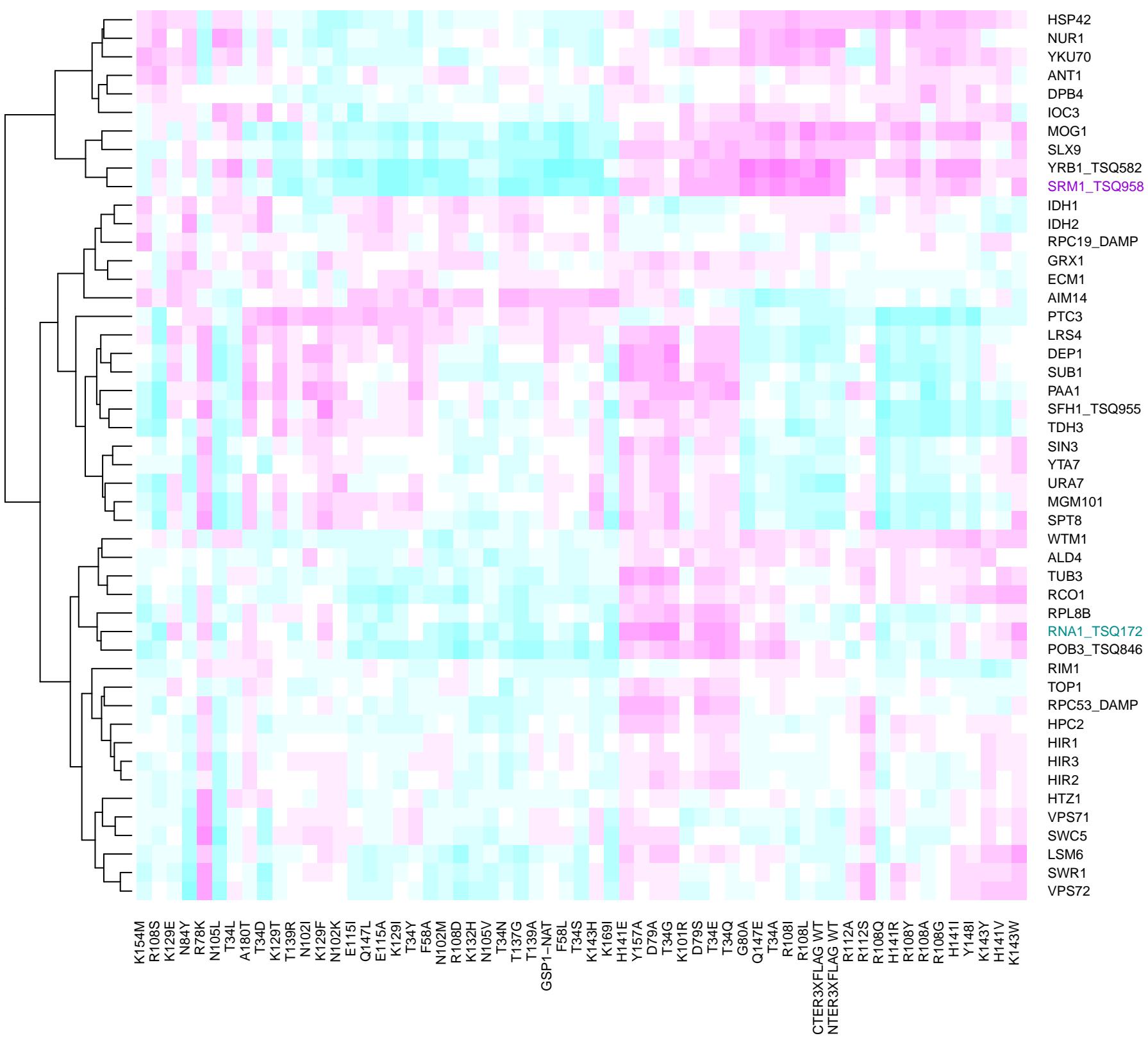


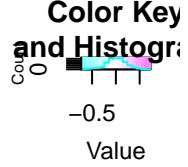
DNA-templated transcription, elongation



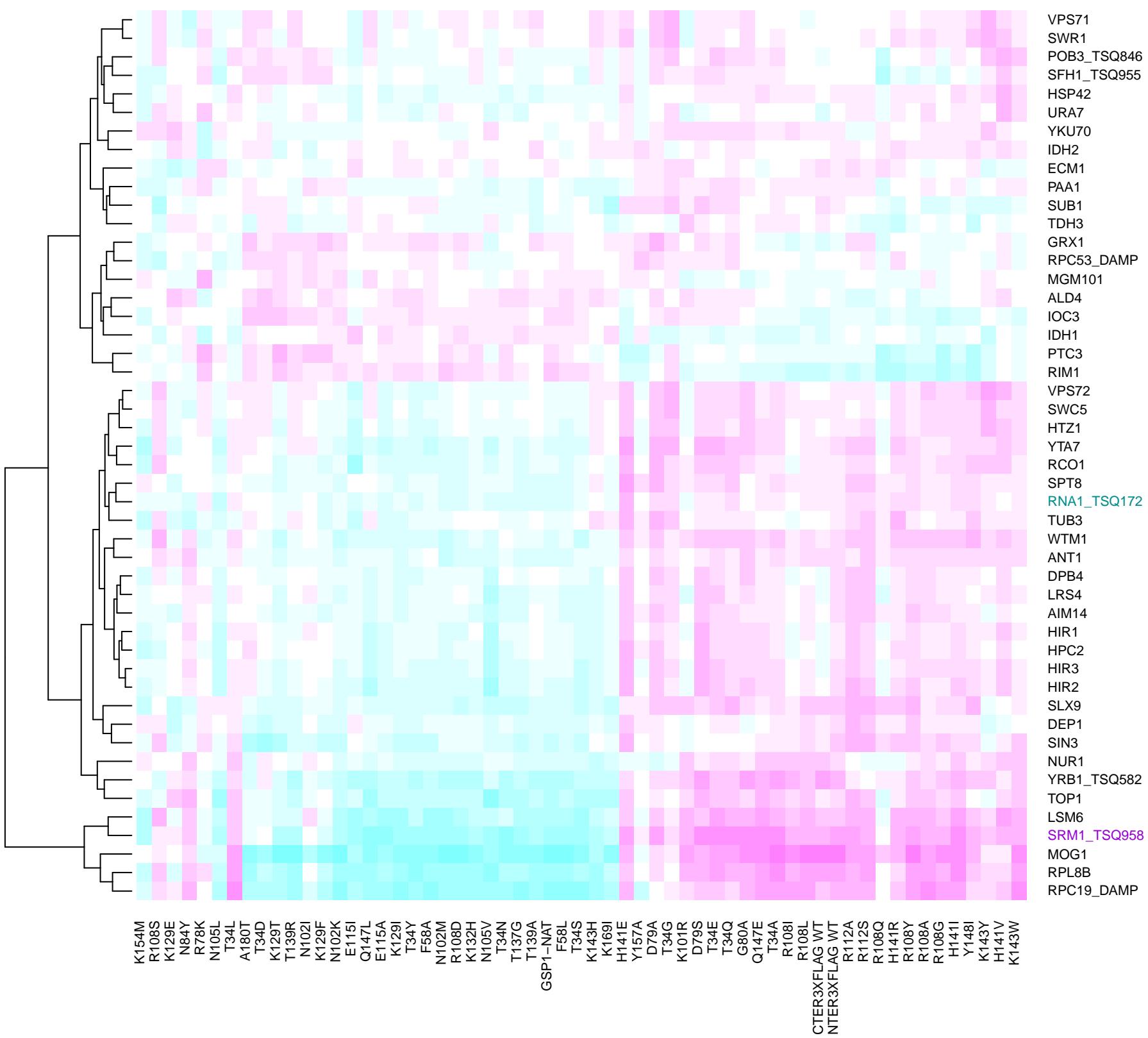


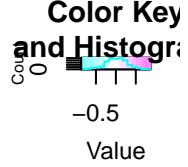
metabolic_GO_30_14



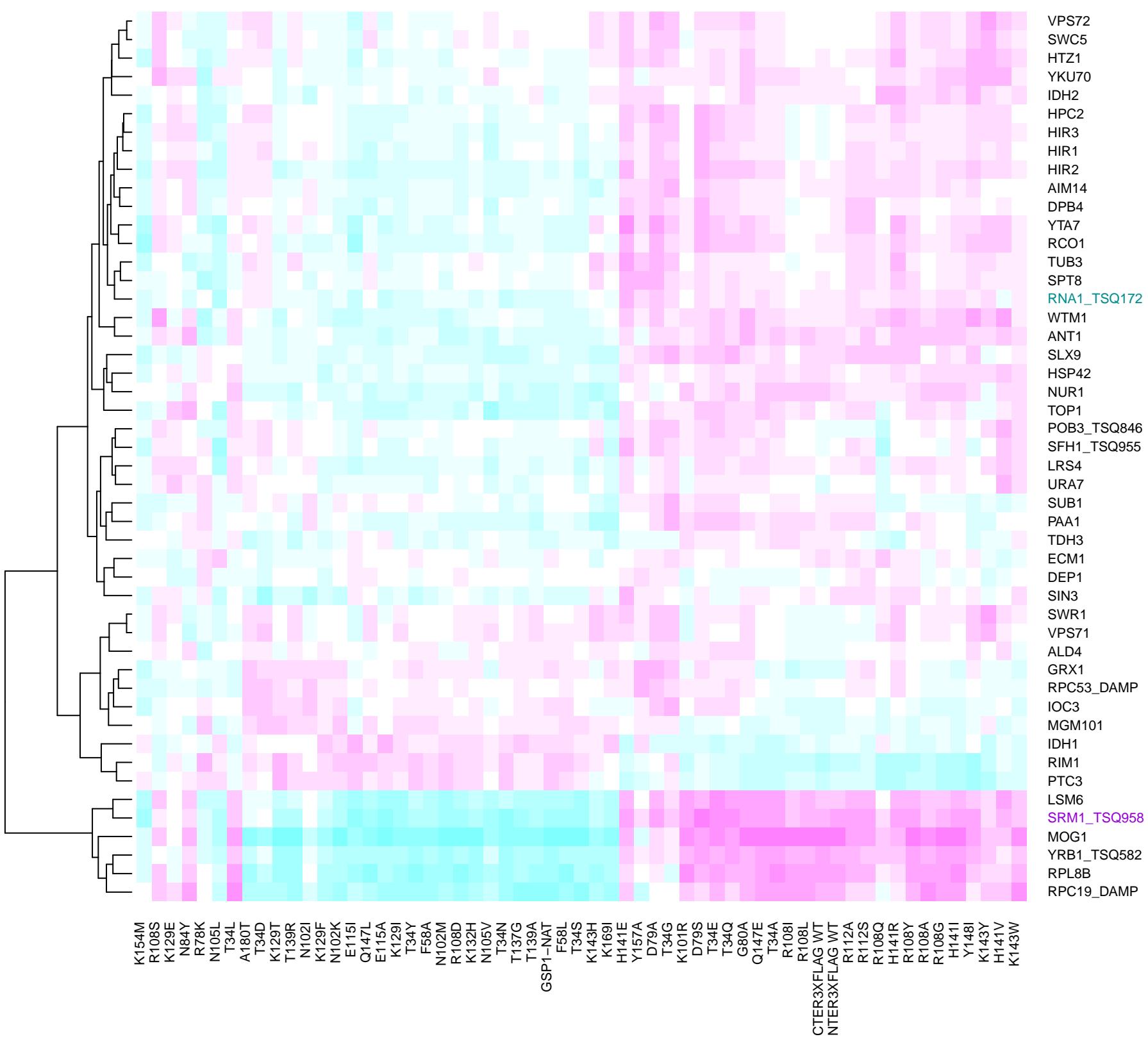


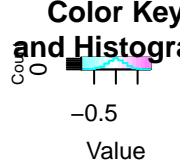
RNA catabolic process



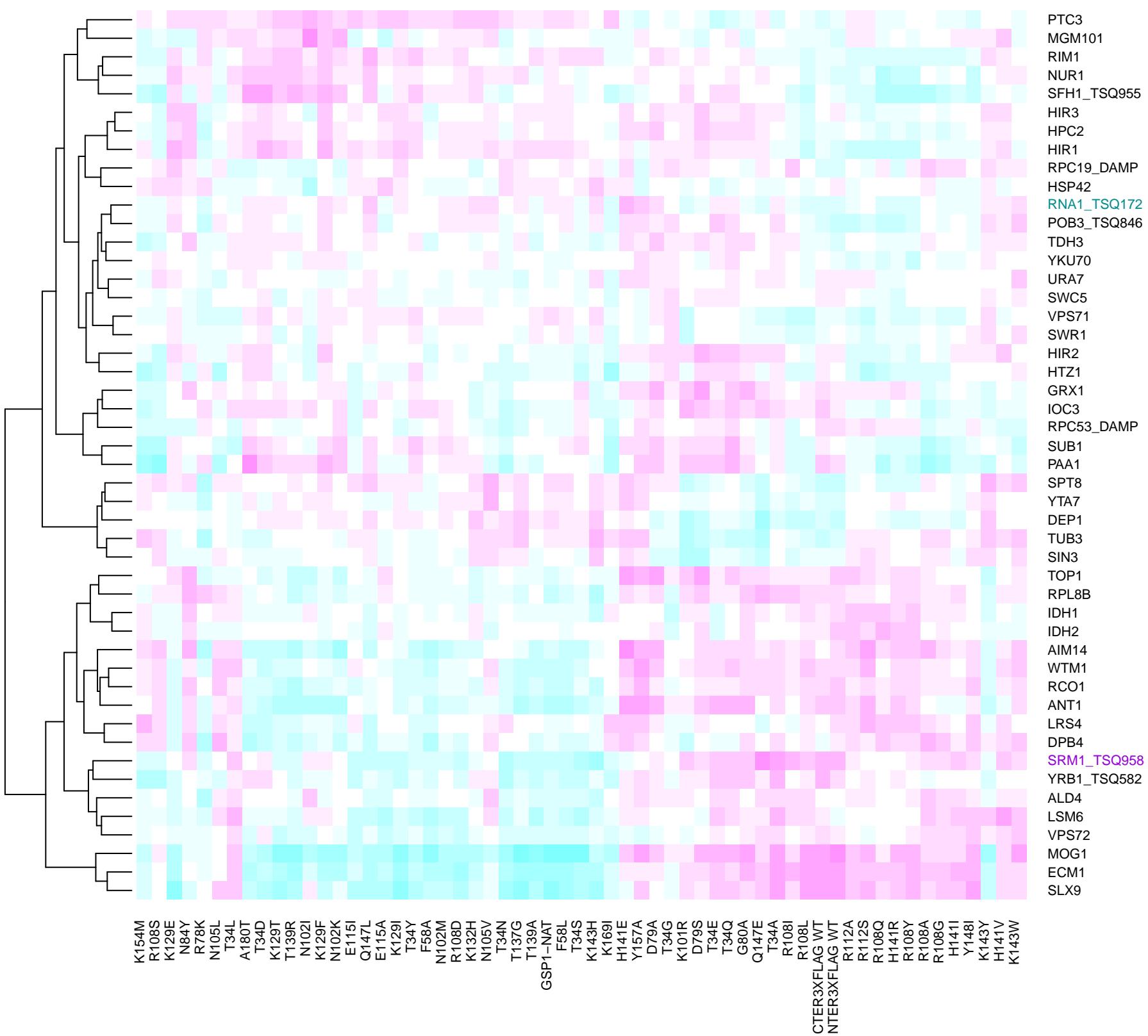


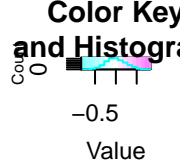
RNA catabolic process_GO_30_1



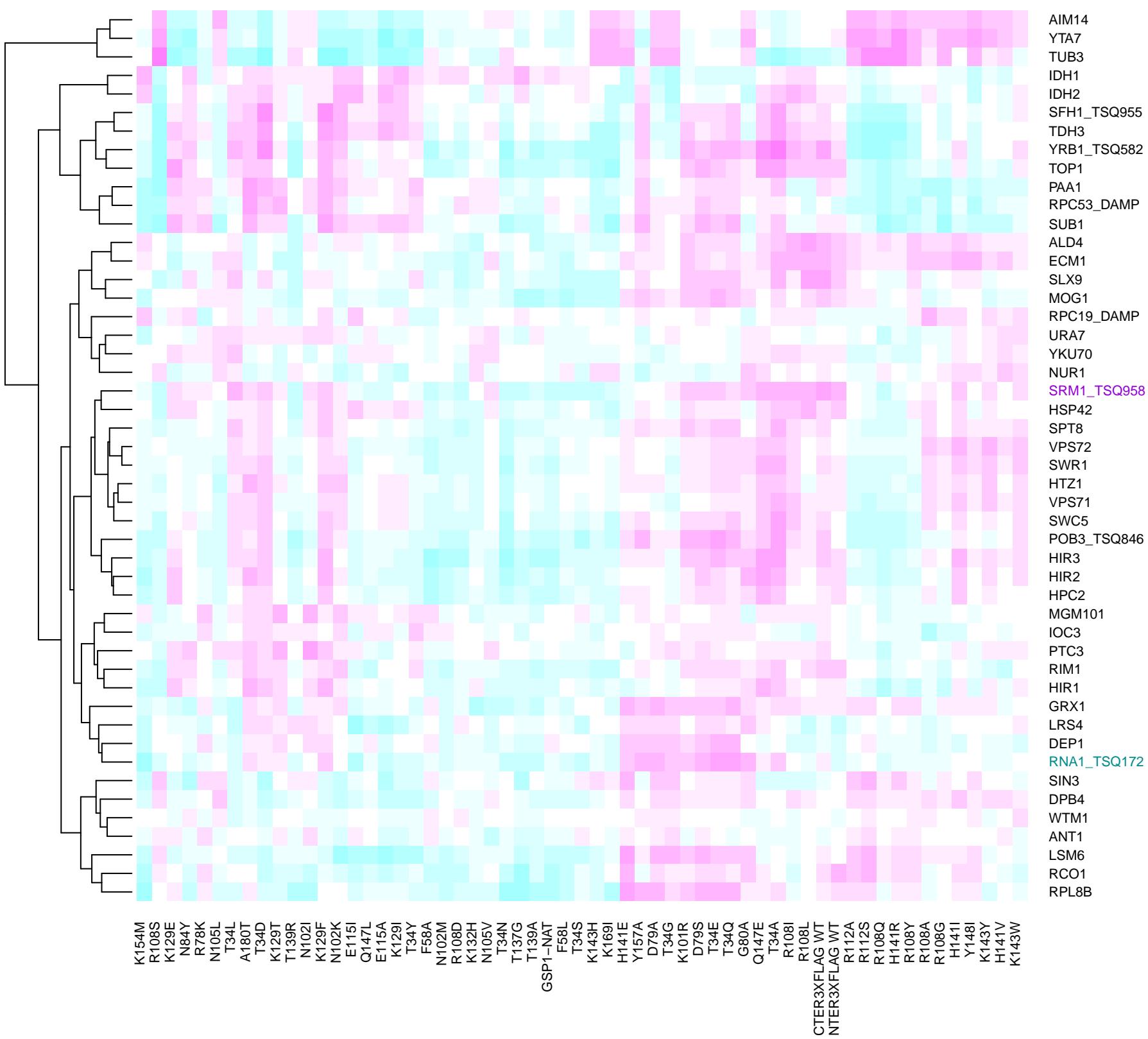


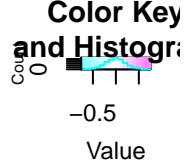
transcription and mRNA processing_GO_30_10



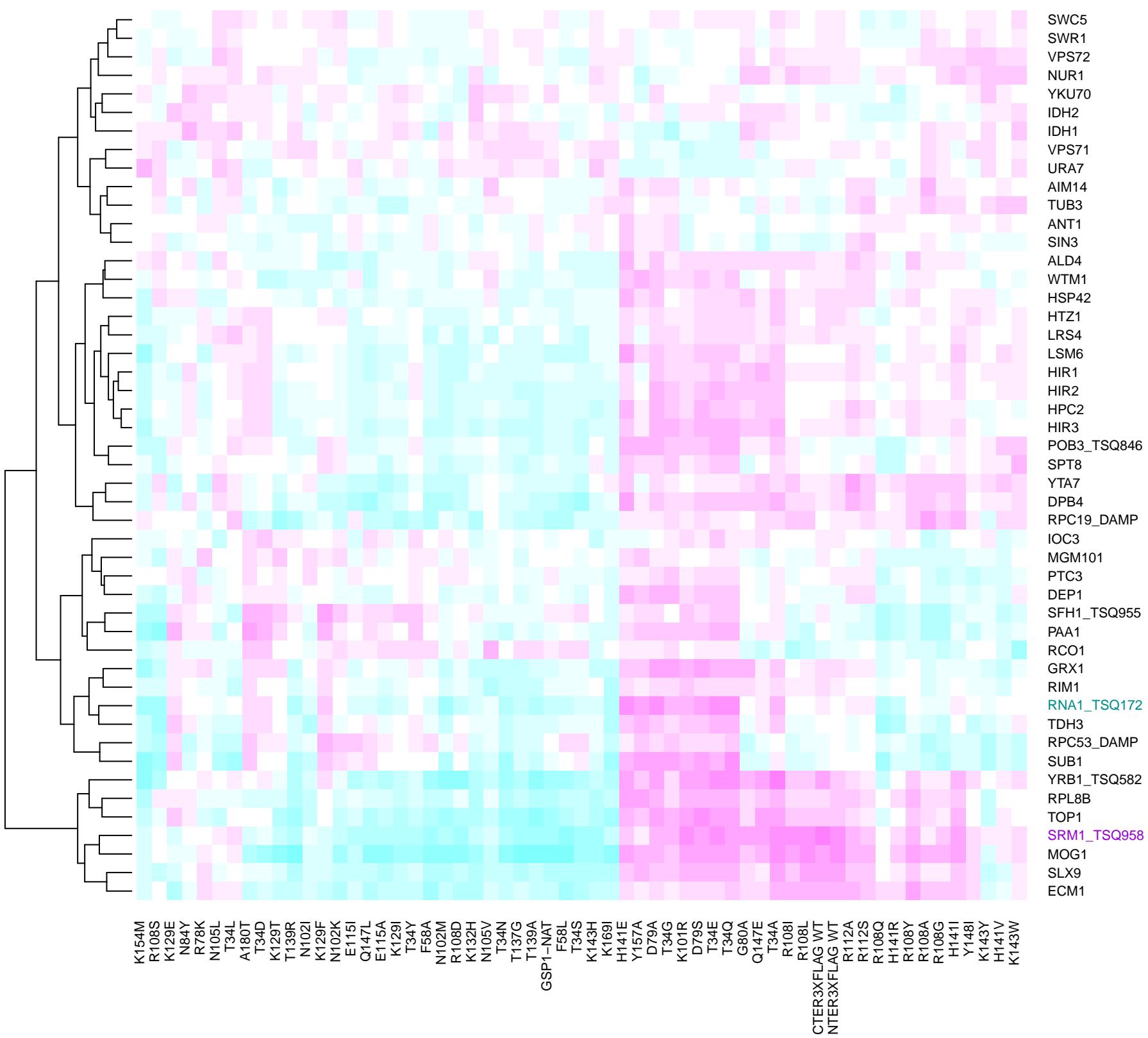


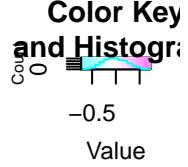
transcription from RNA polymerase II promoter_GO_30_3



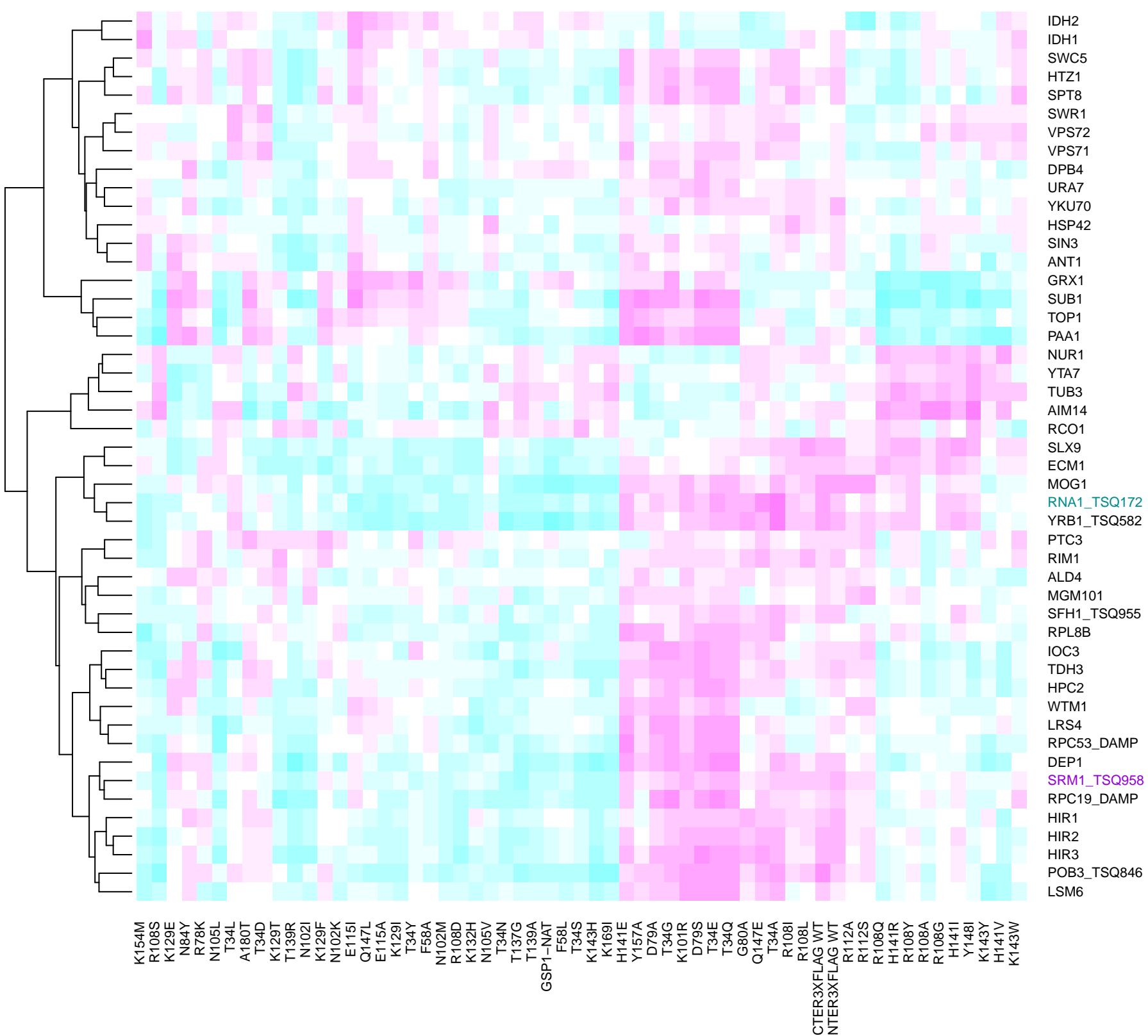


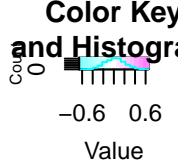
transcription_GO_30_3



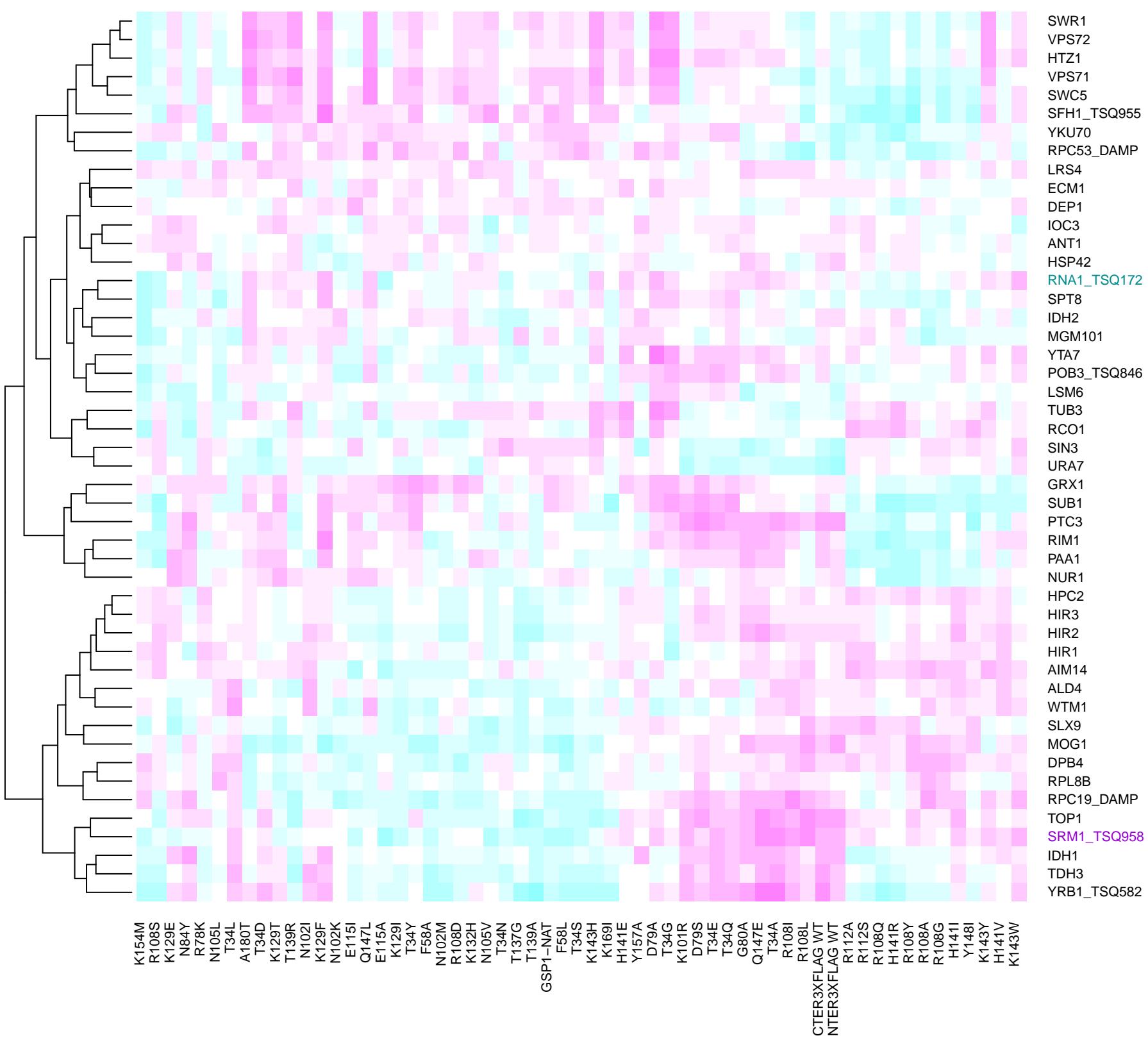


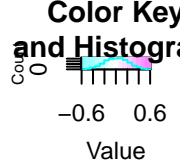
cell cycle_GO_30_9



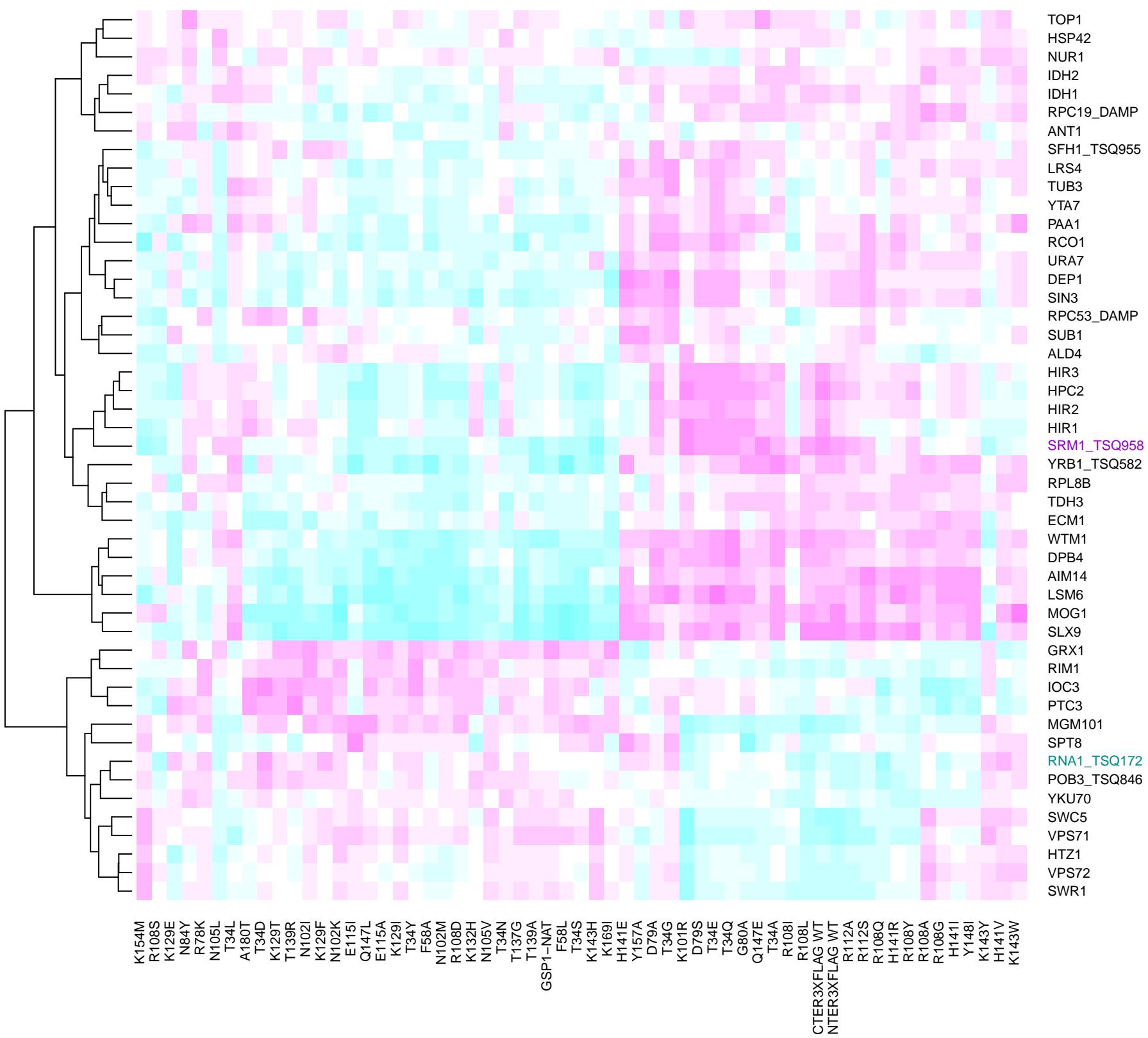


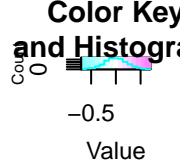
cellular response to DNA damage stimulus_GO_30_3



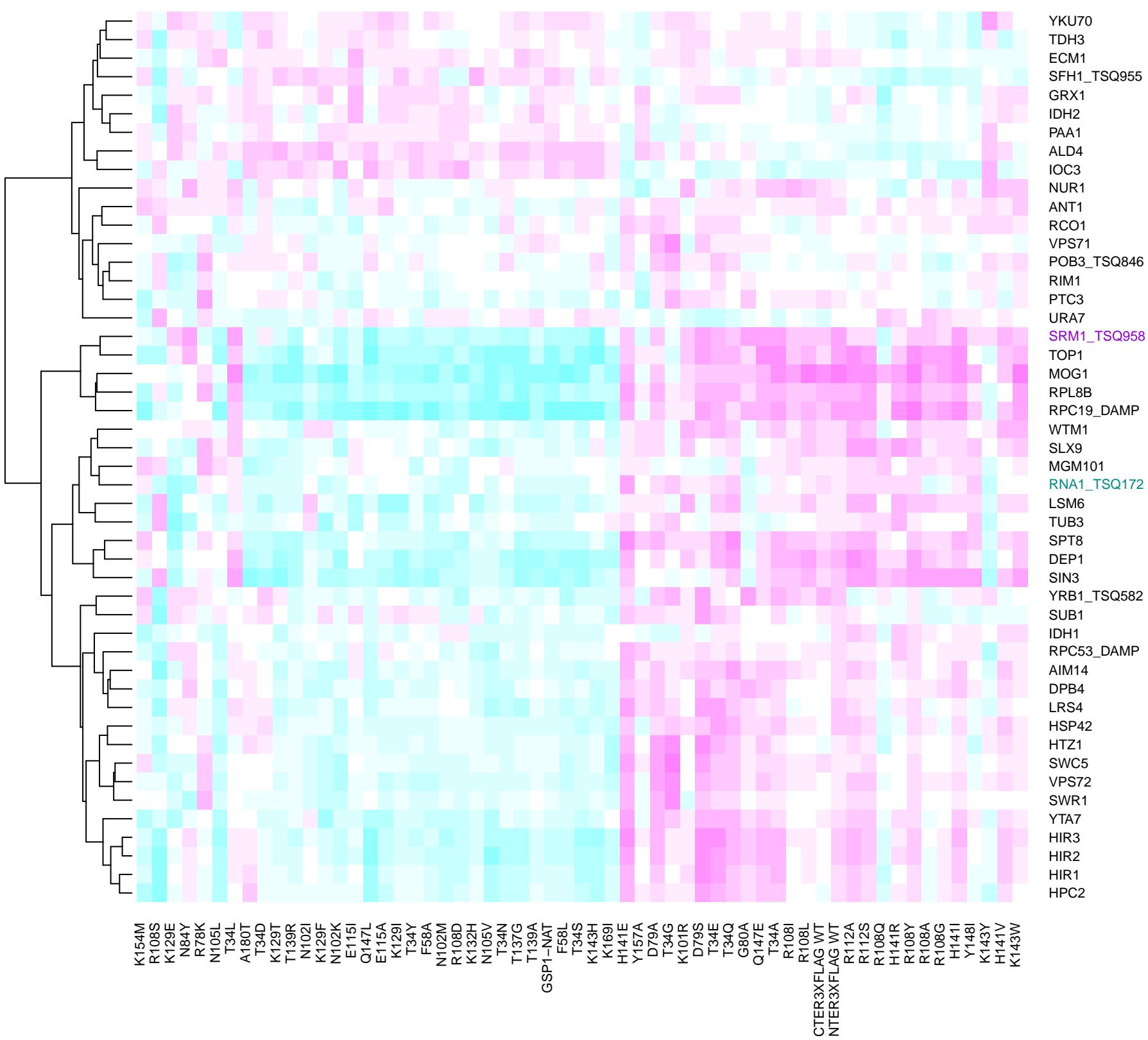


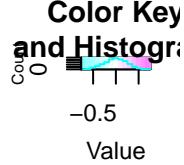
metabolic_GO_30_7



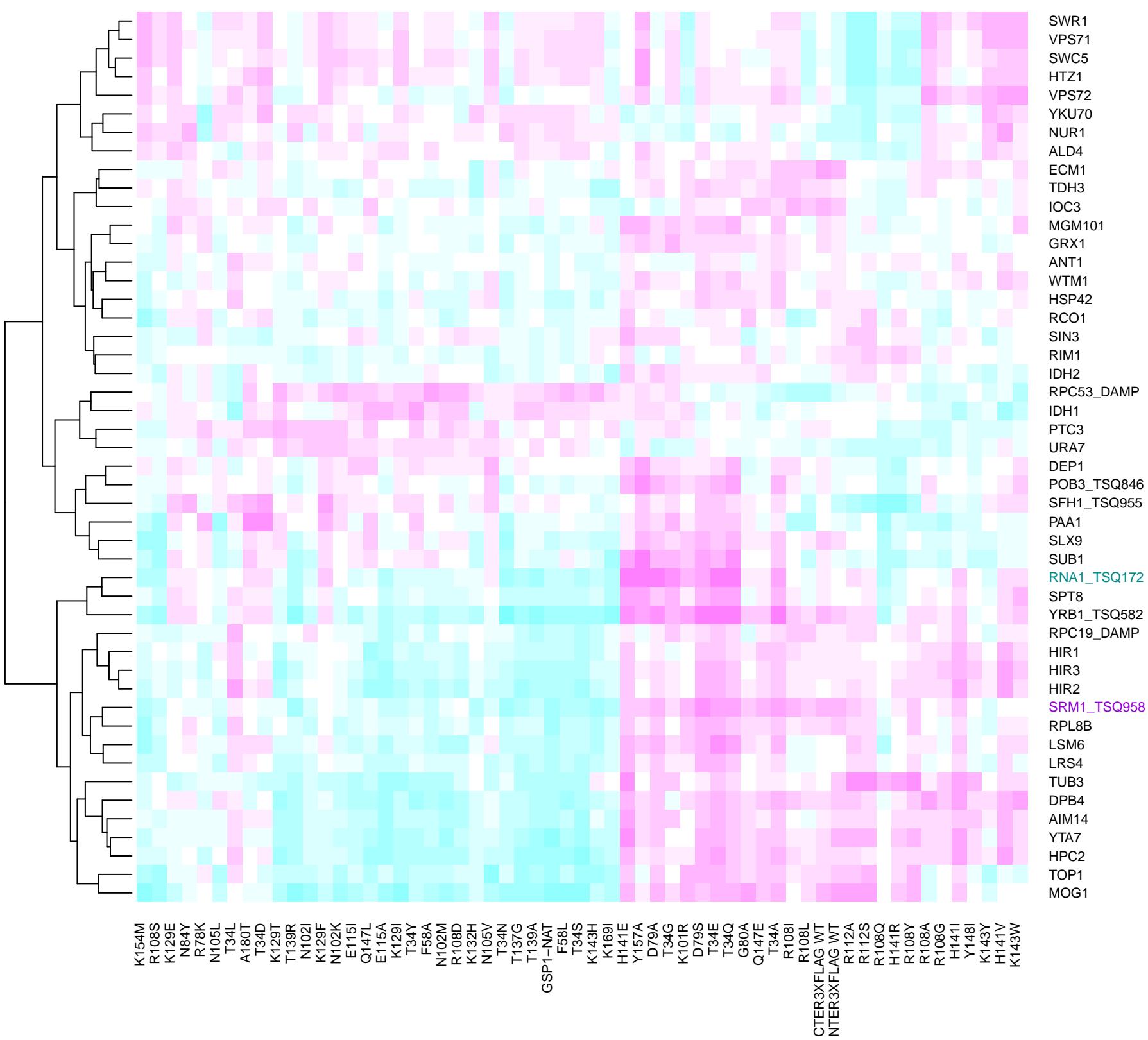


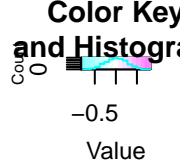
RNA catabolic process_GO_30_2



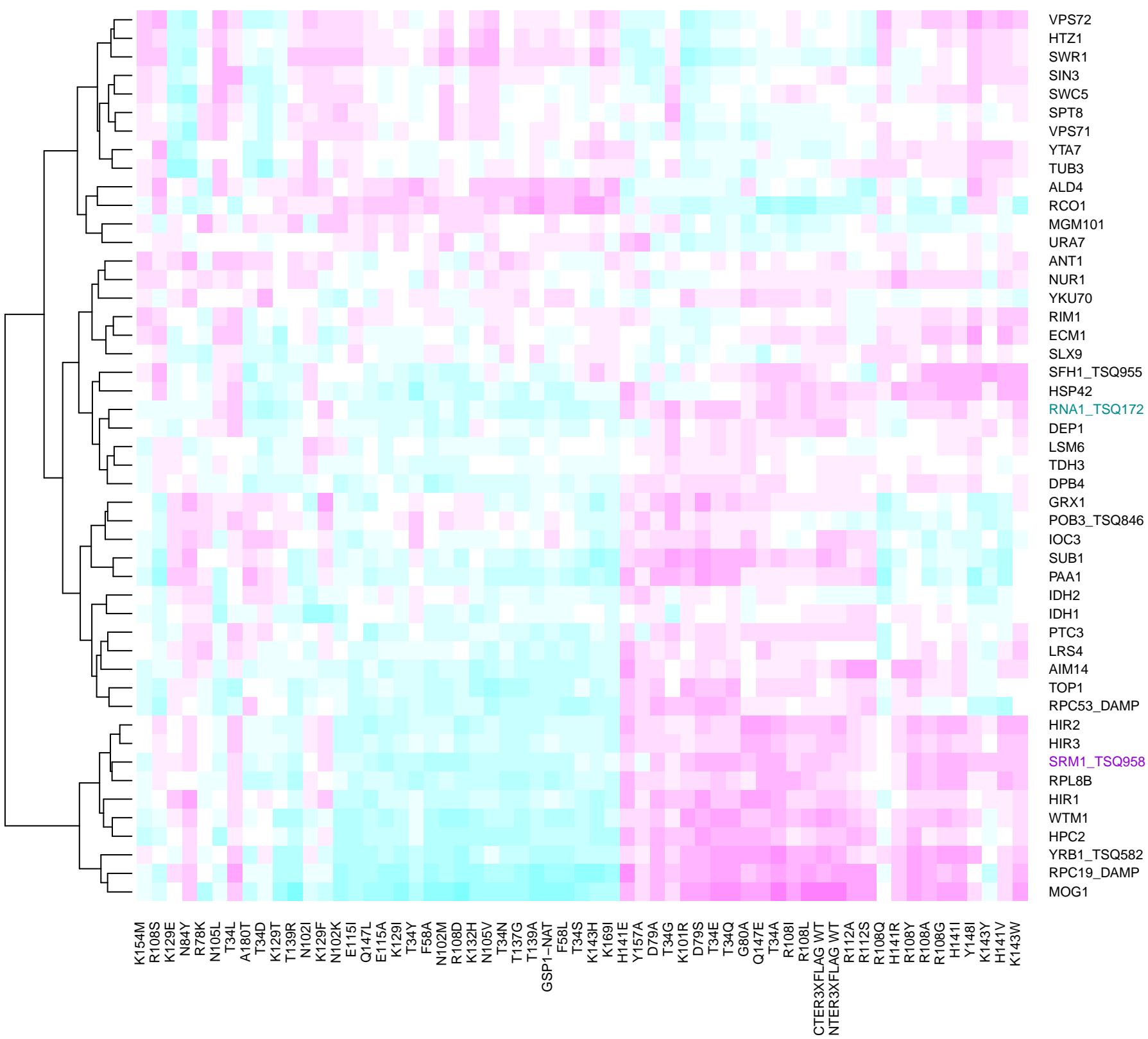


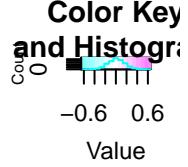
transcription and mRNA processing_GO_30_11



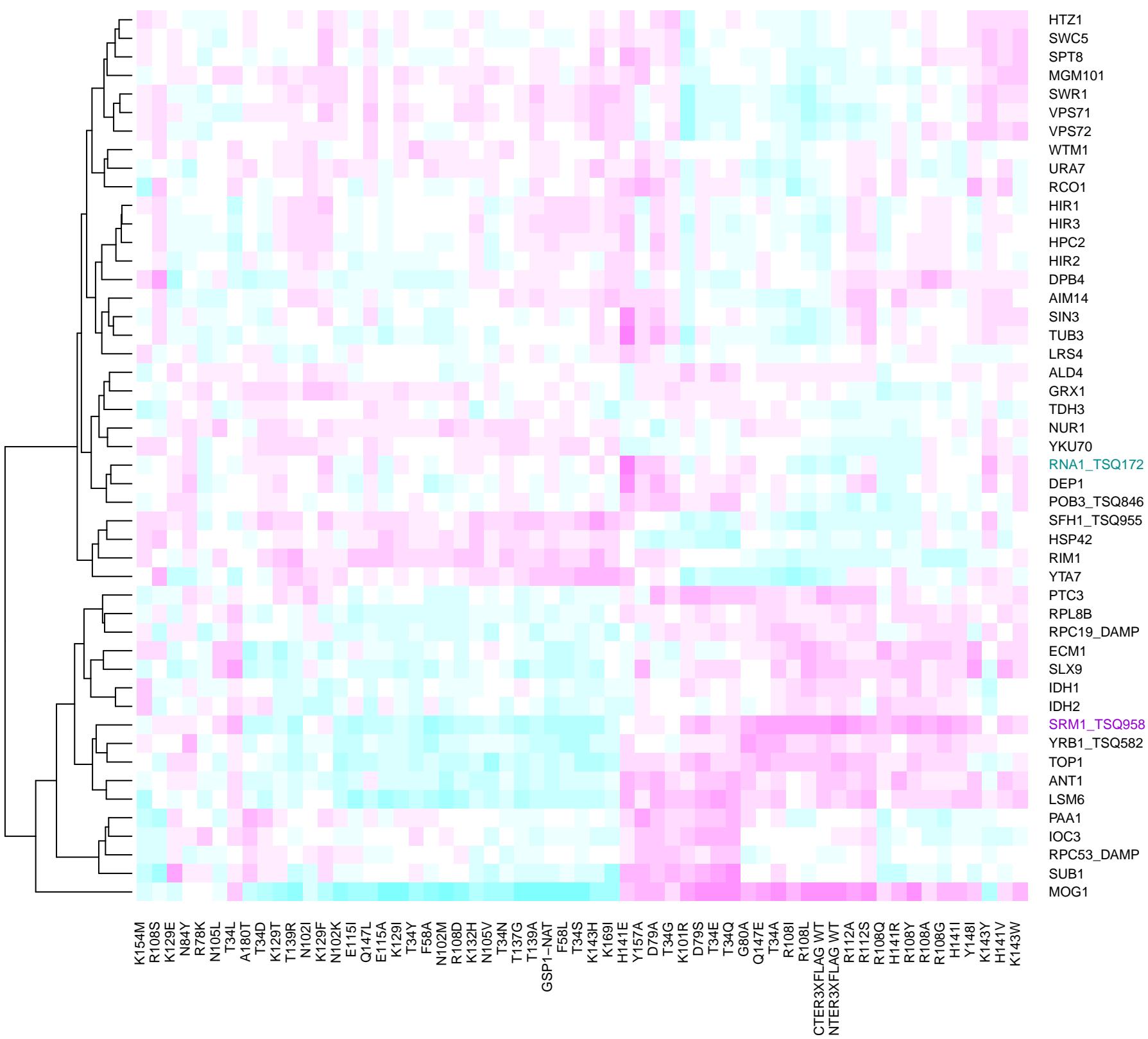


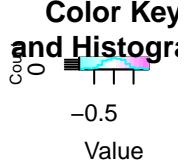
transcription from RNA polymerase II promoter_GO_30_7



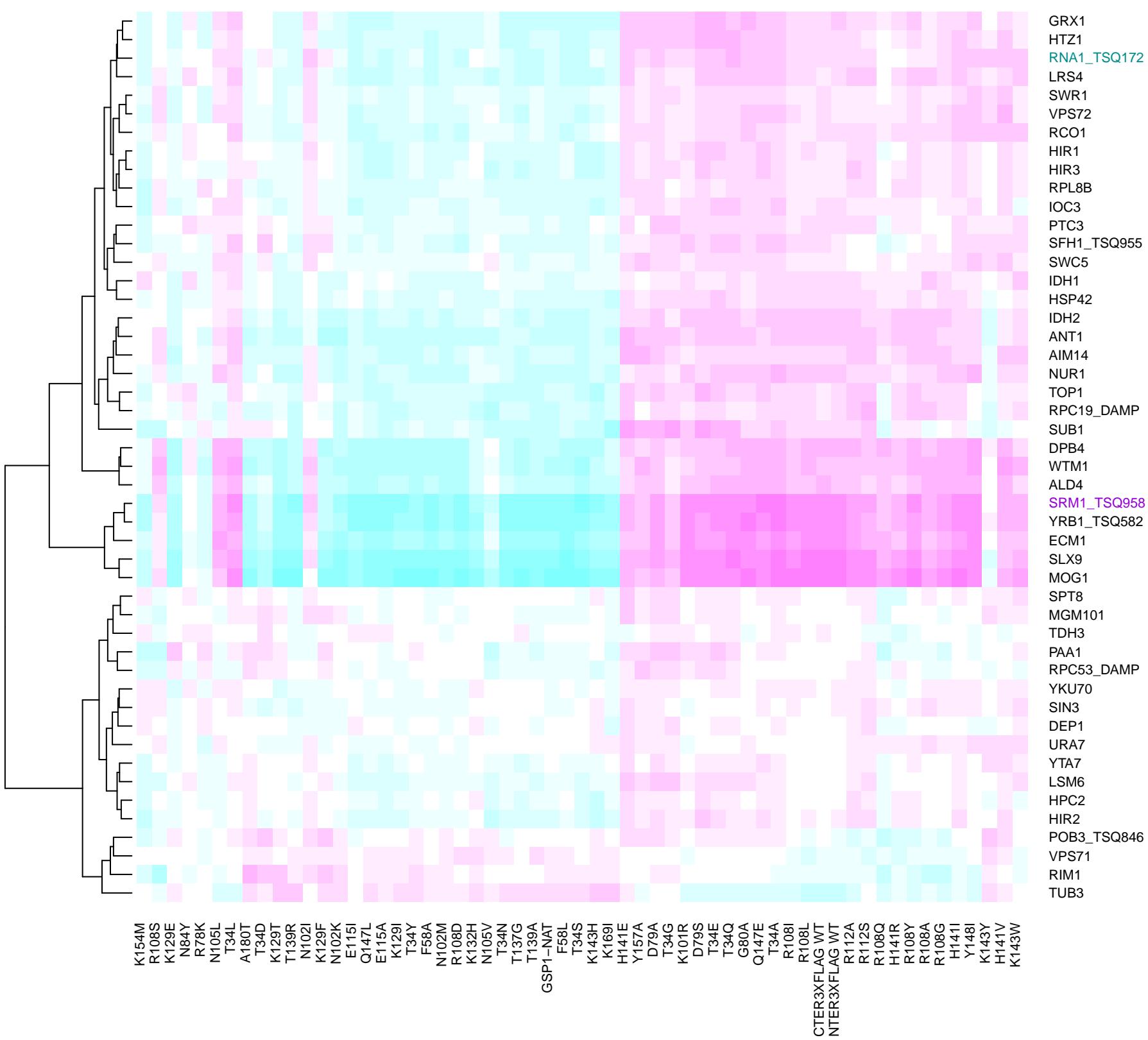


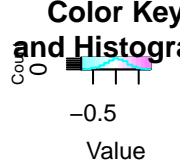
transcription_GO_30_1



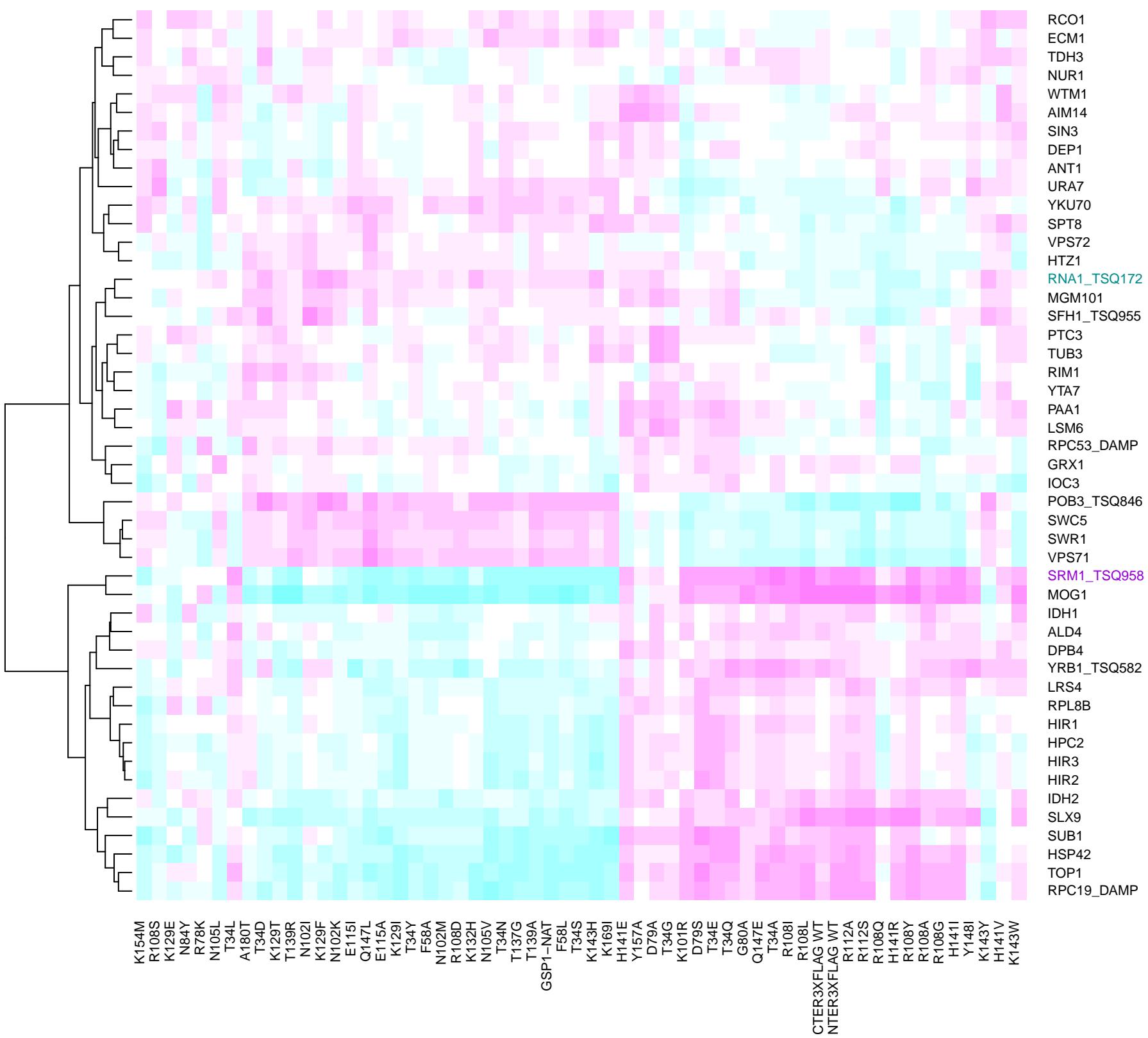


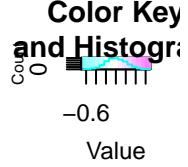
nucleobase-containing compound transport



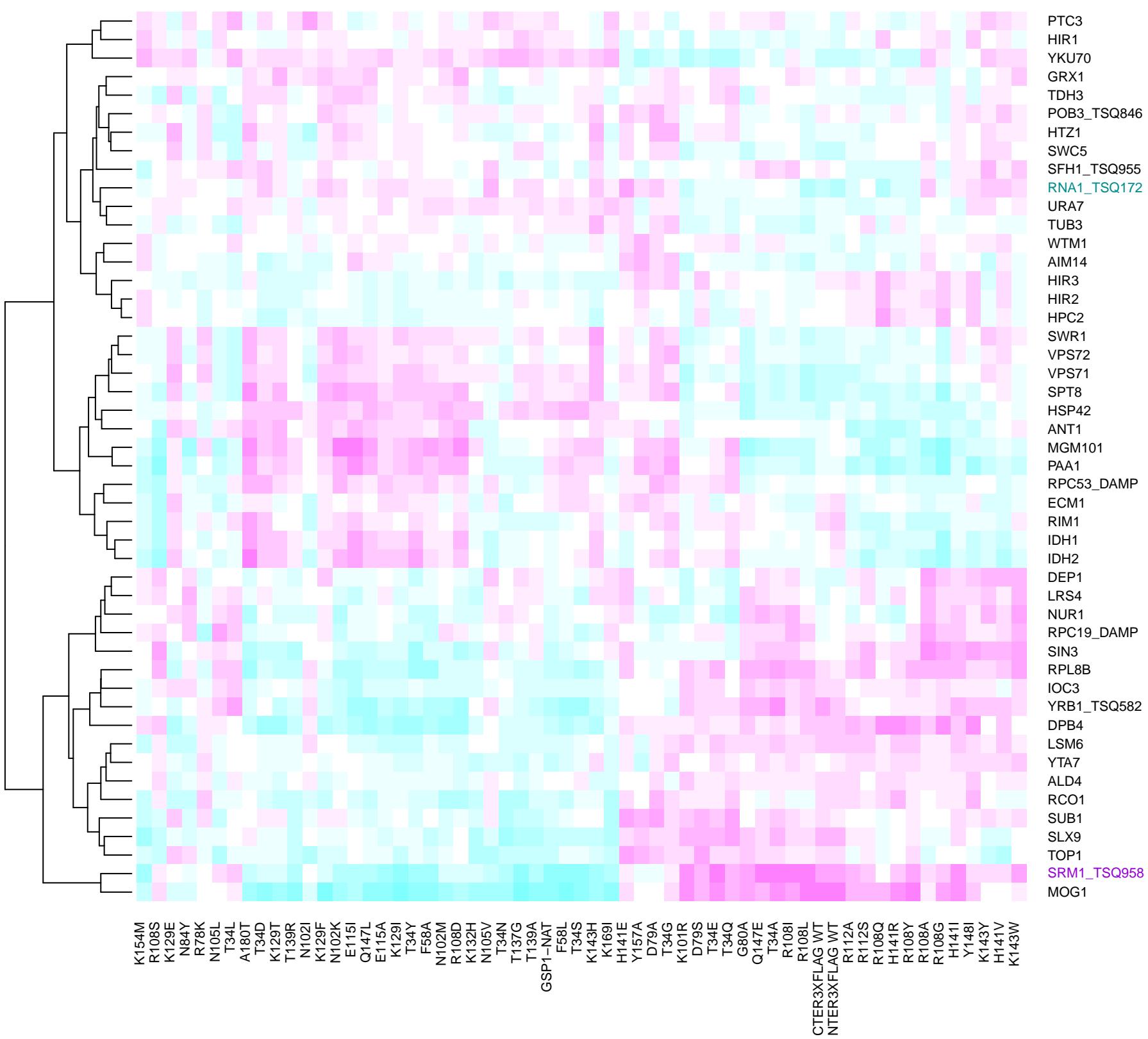


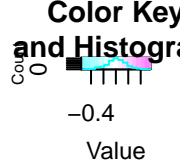
nucleobase-containing compound transport_GO_30_2



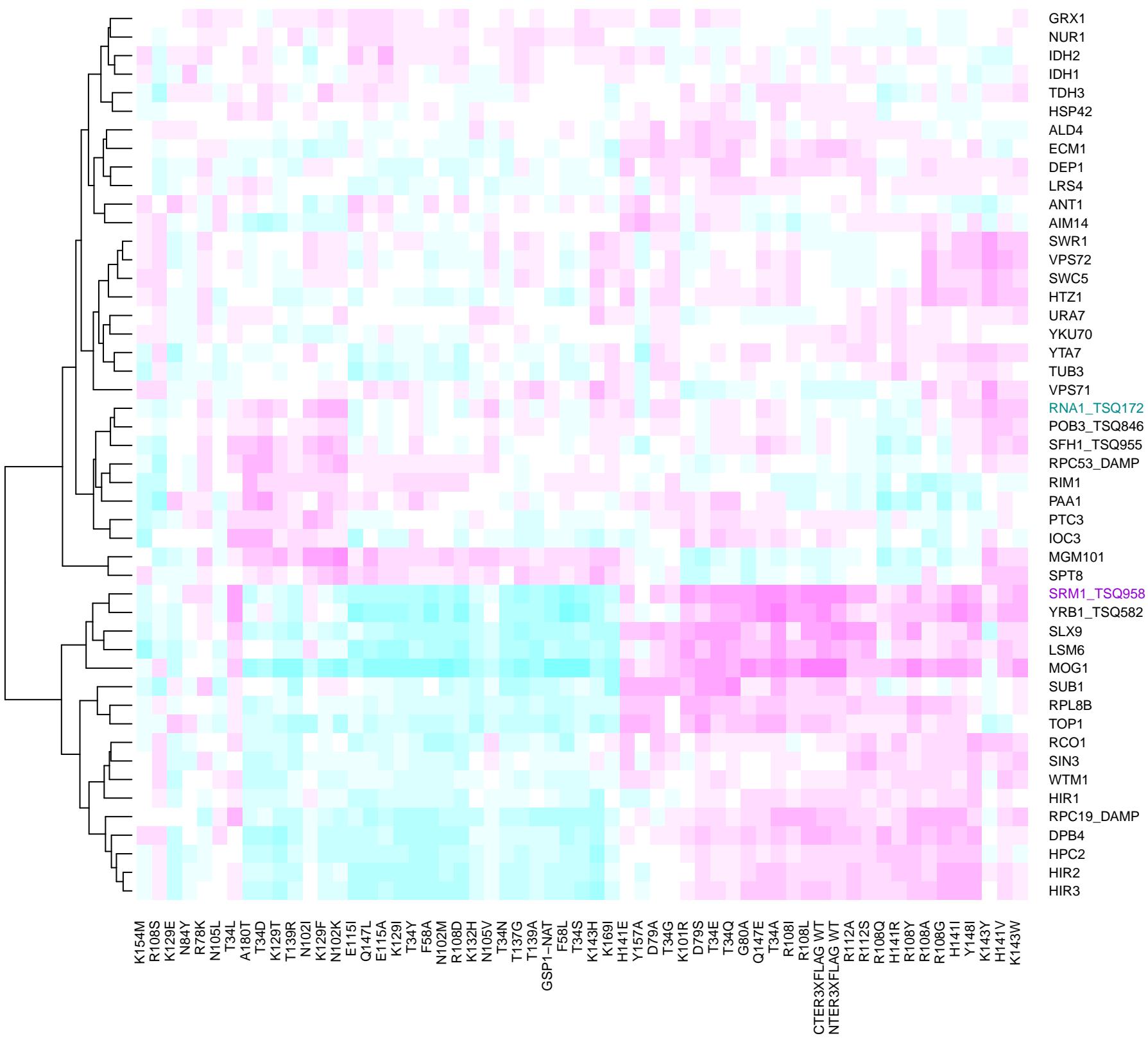


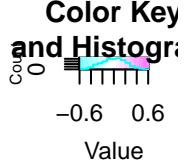
transmembrane transport_GO_30_2



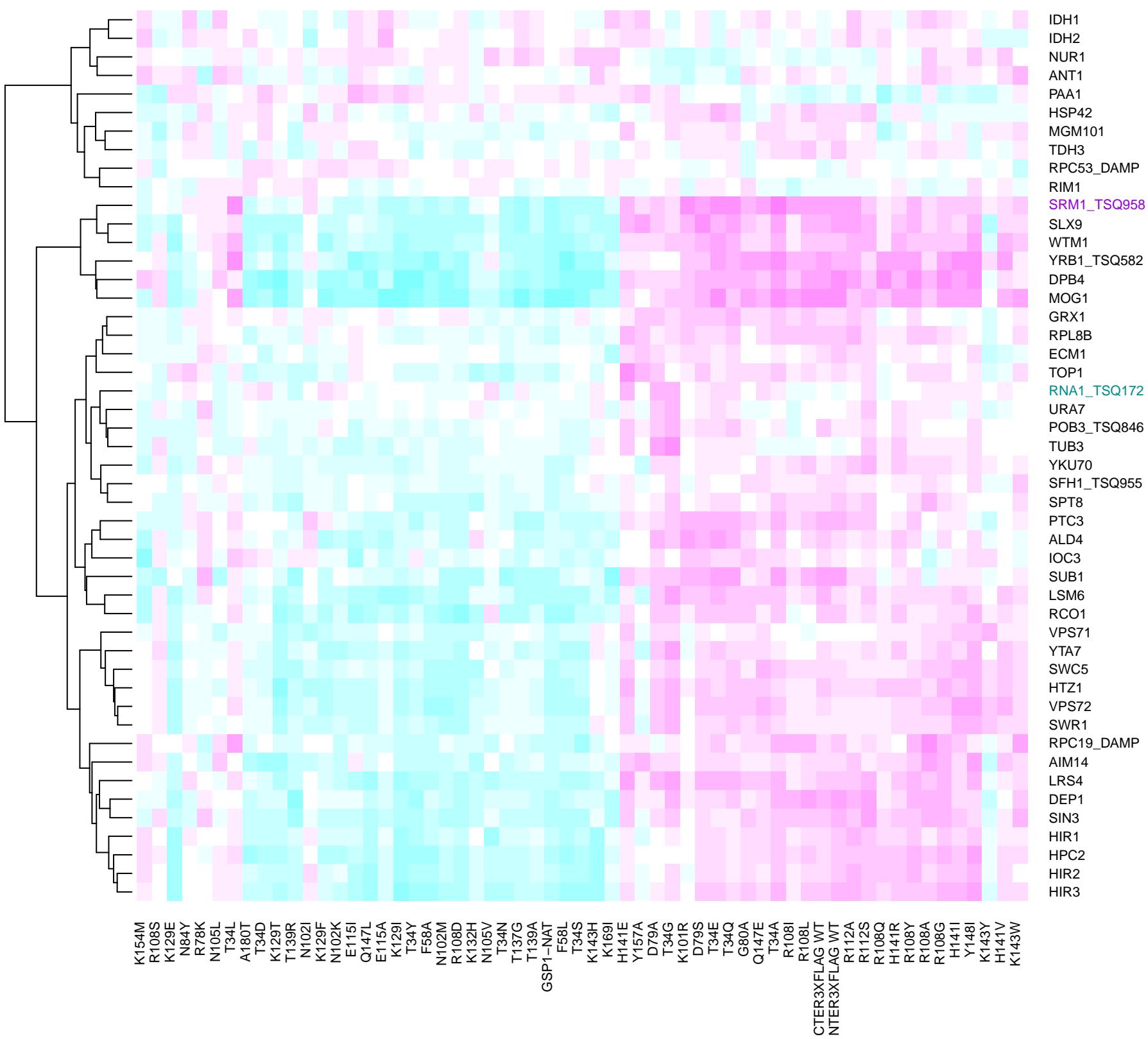


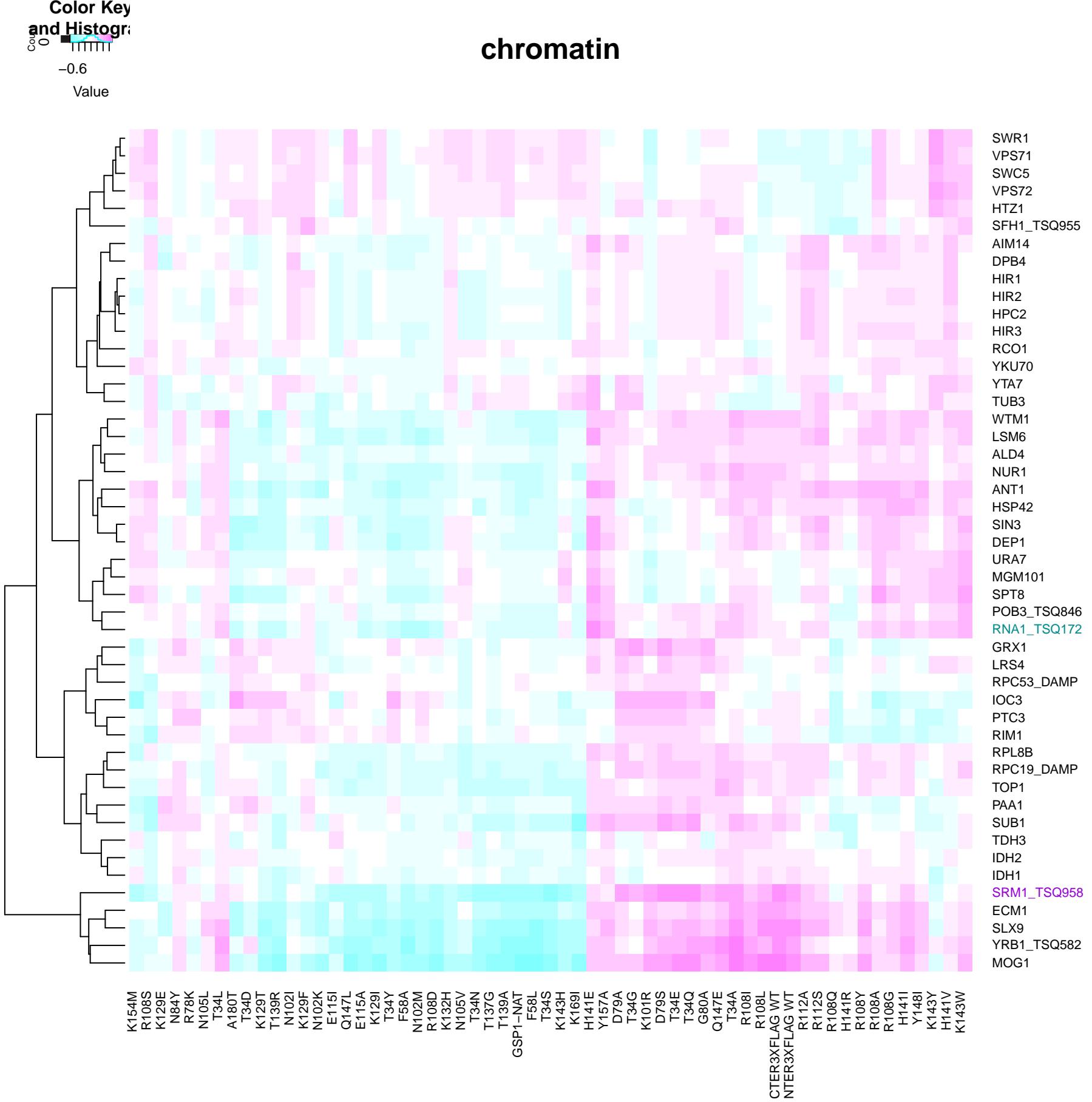
transmembrane transporter activity

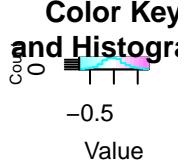




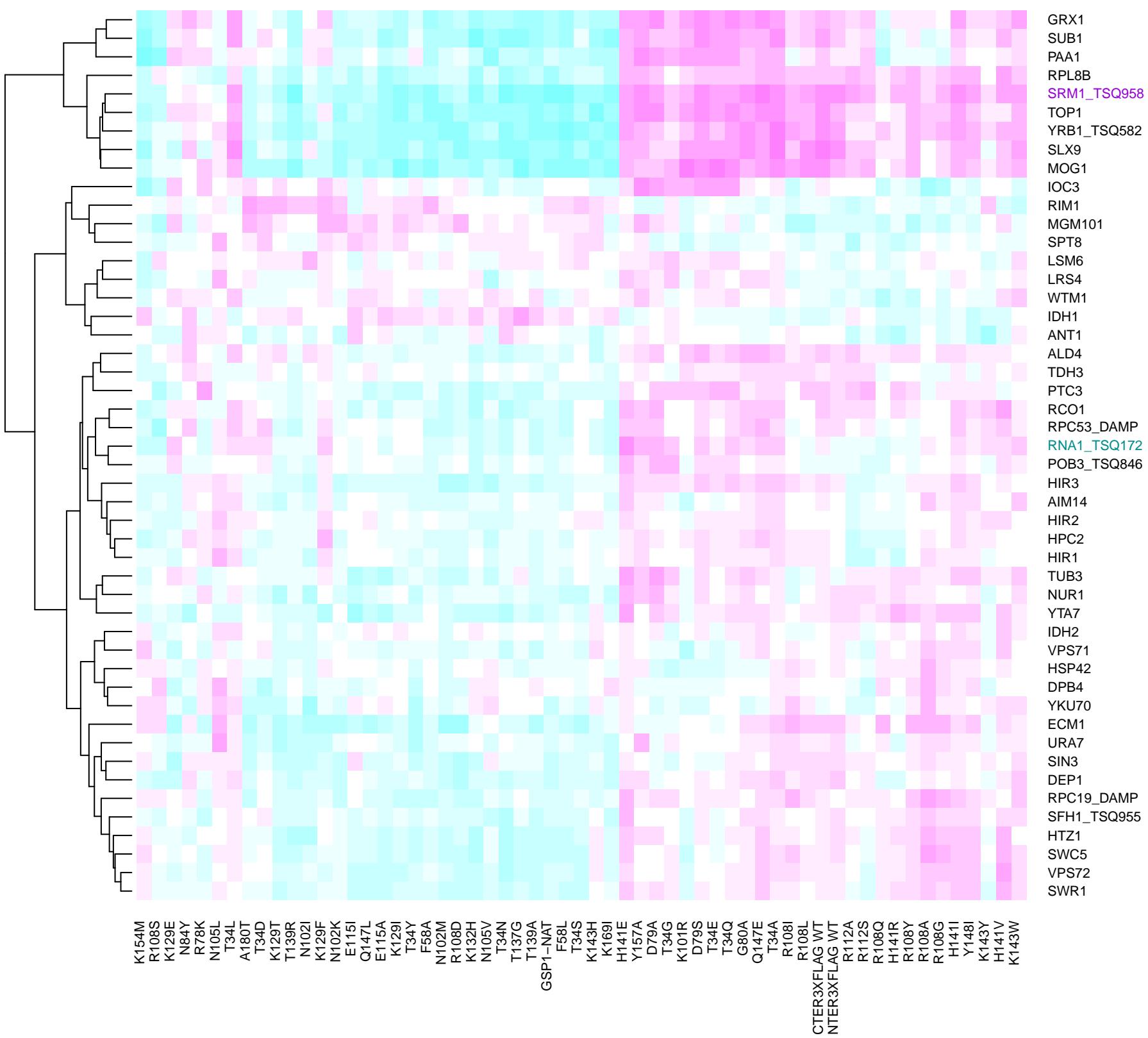
transmembrane transporter activity_GO_30_1

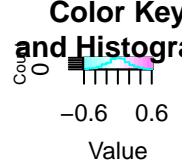




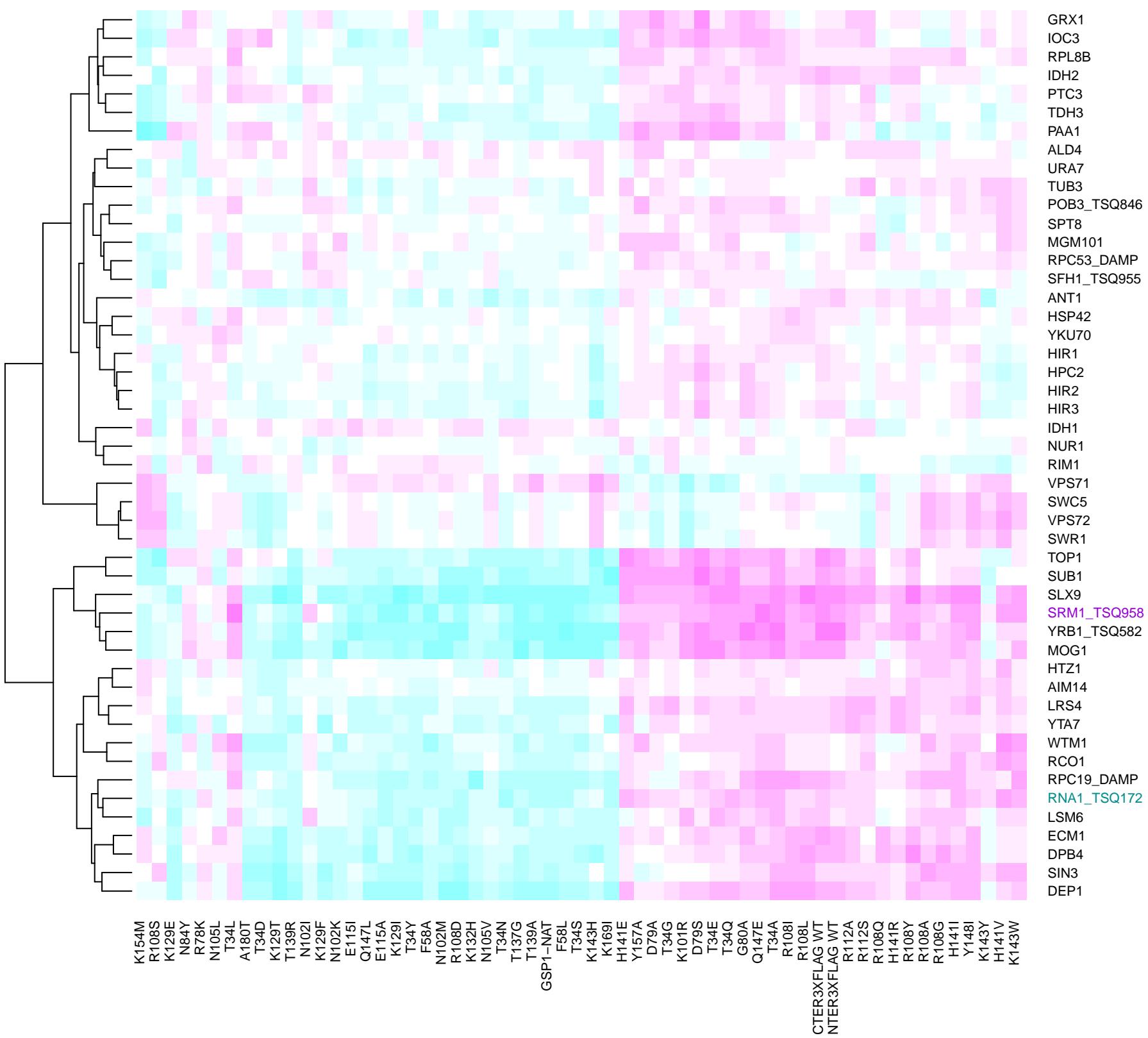


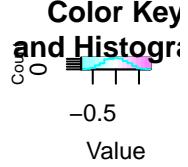
vacuole_GO_30_6



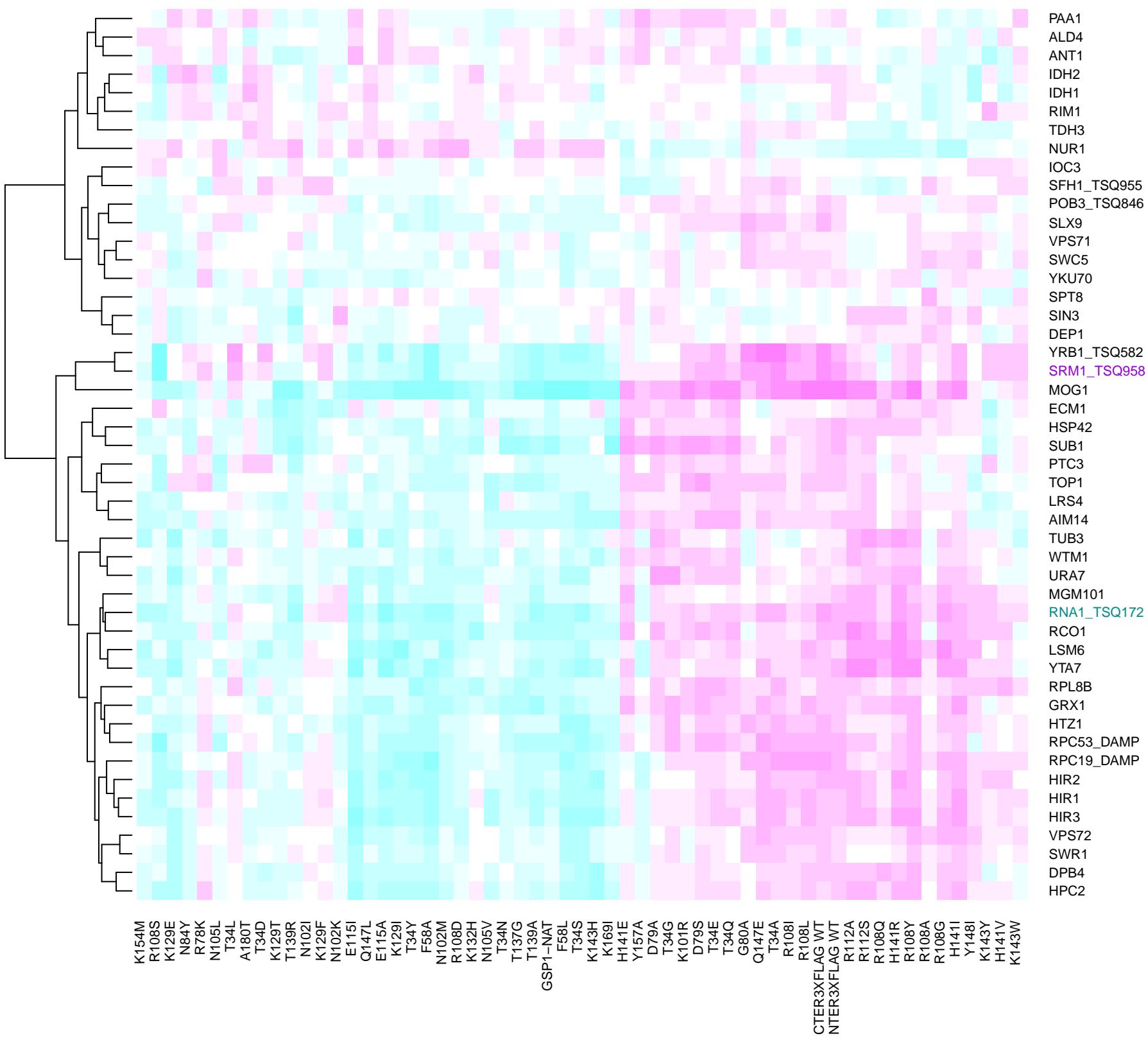


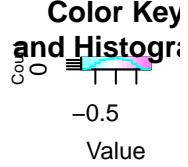
vacuoles_GO_30_1



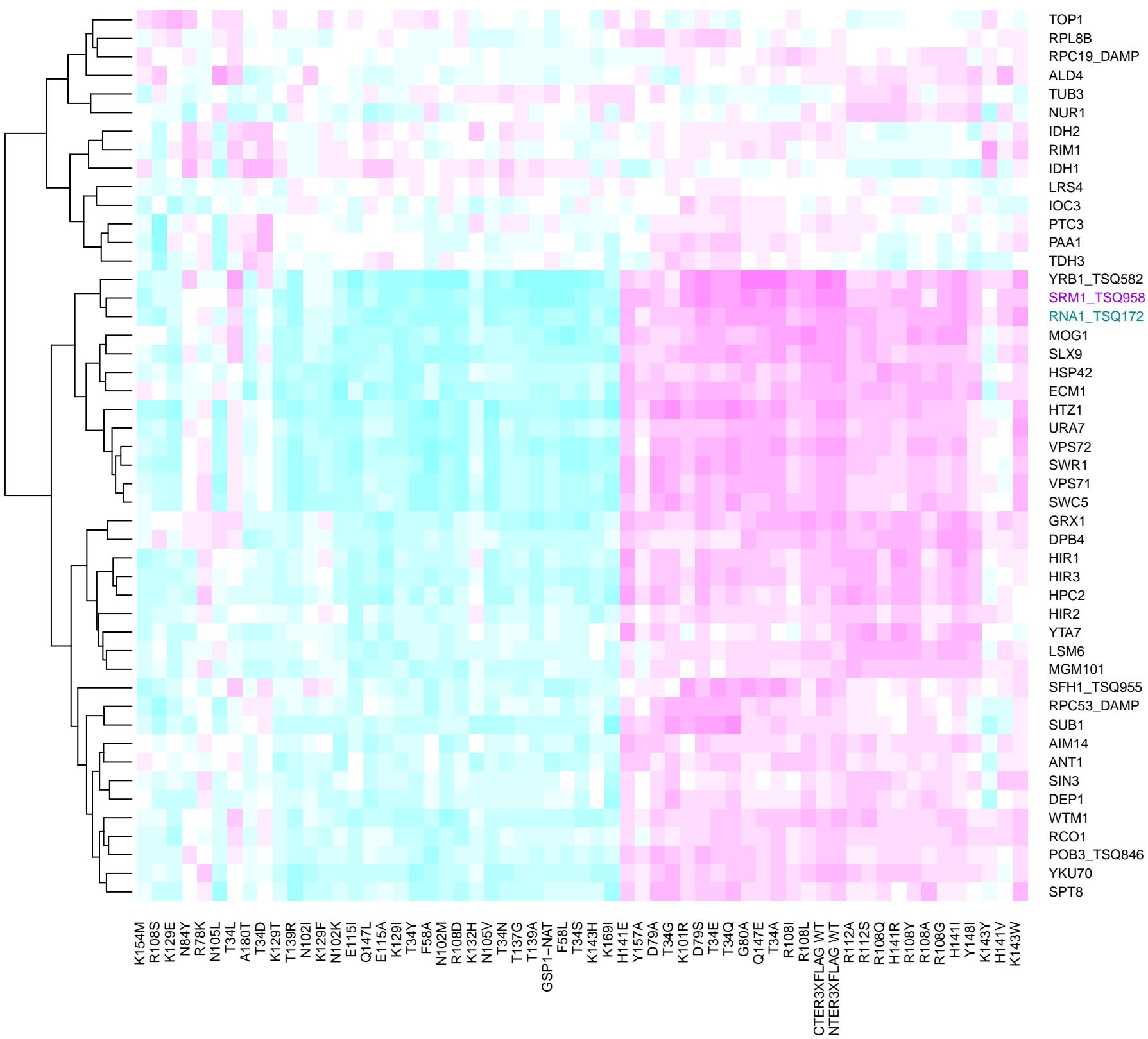


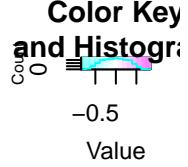
endomembrane system_GO_30_6



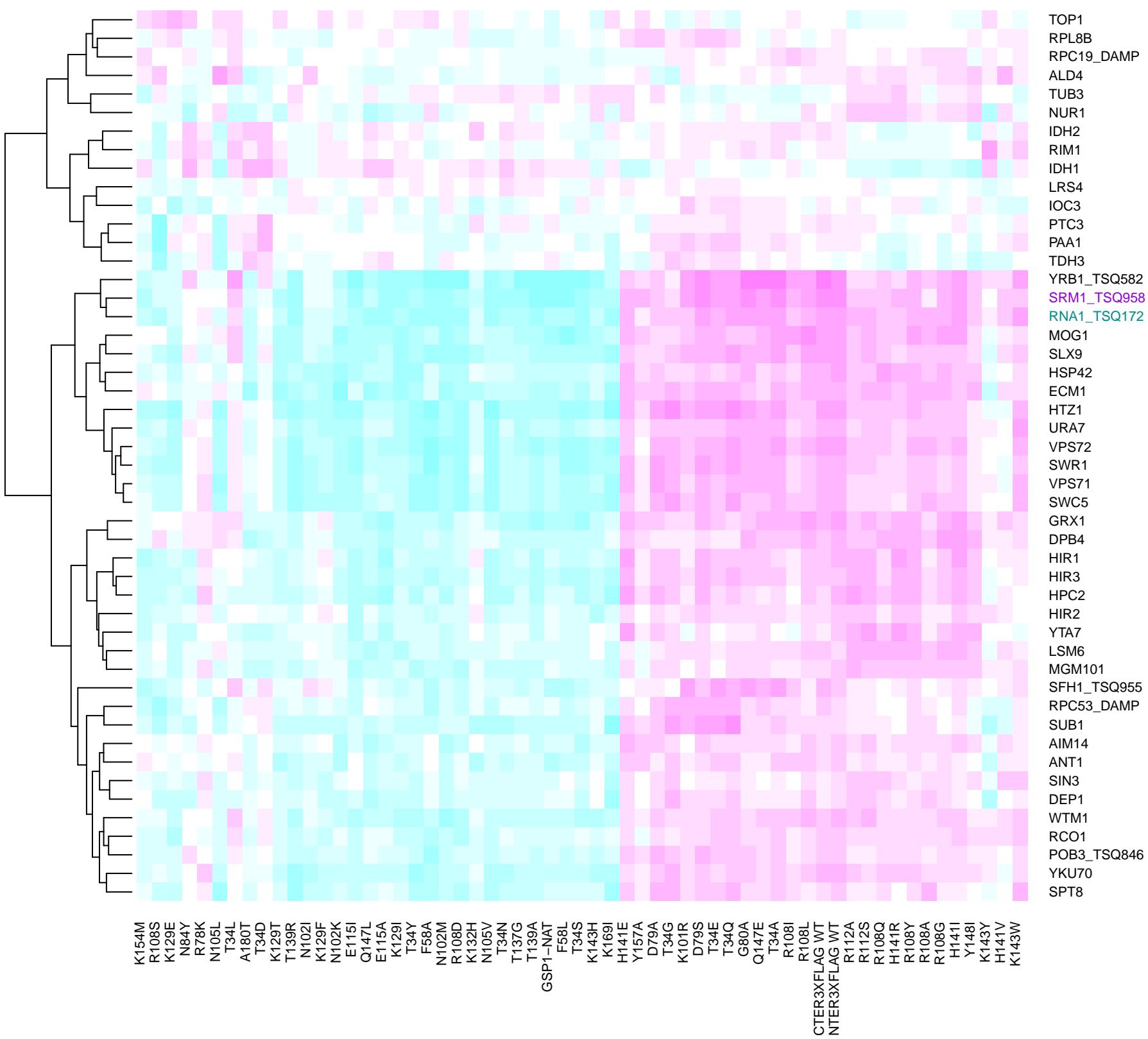


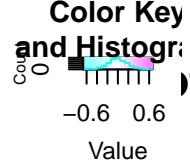
endoplasmic reticulum_GO_30_2





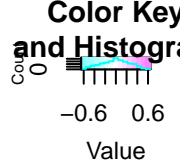
ER_GO_30_2



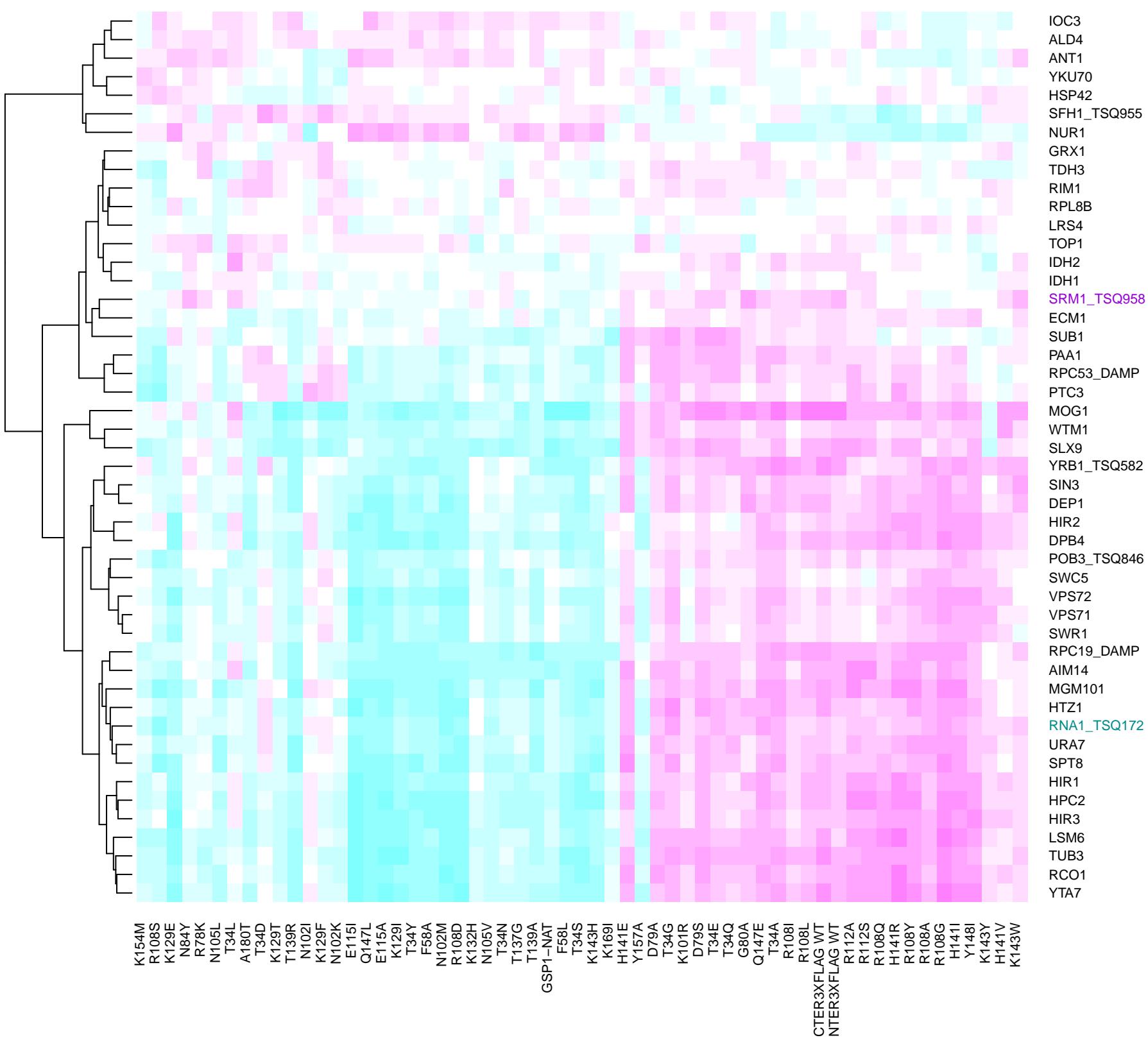


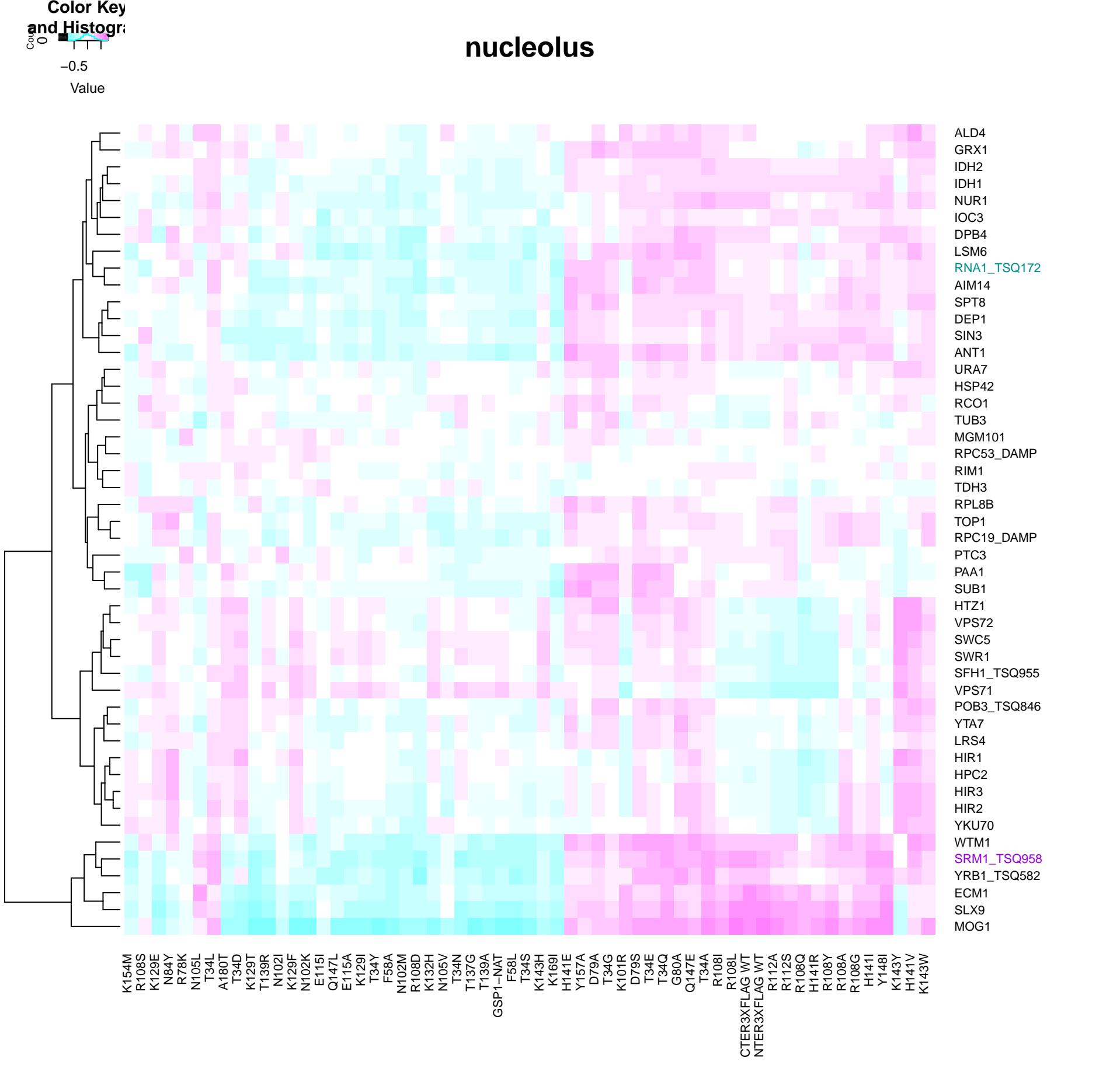
Proteolysis involved in cellular protein catabolic process_GO_30_2

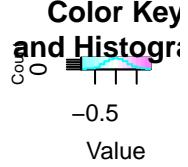




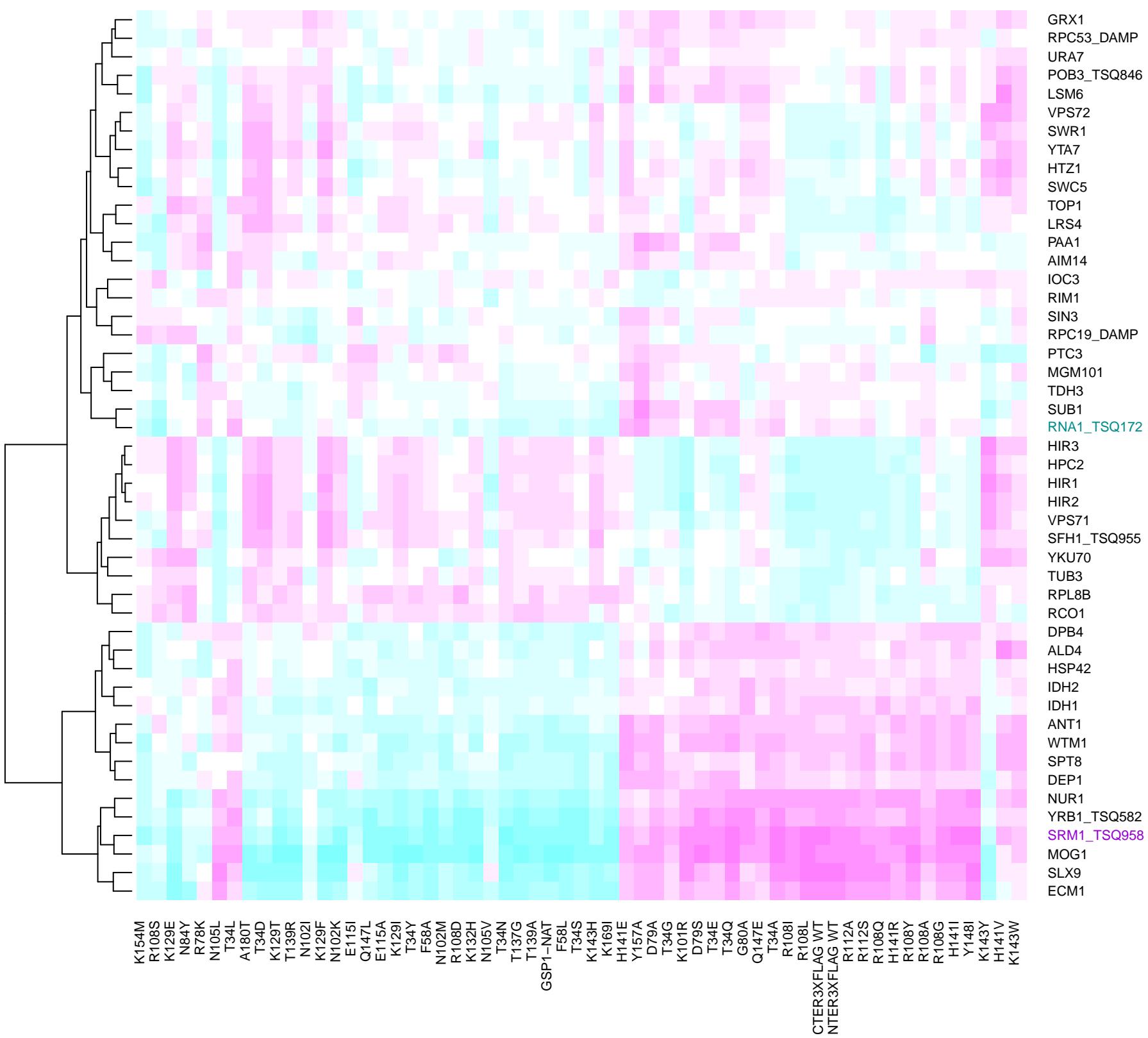
transferase activity, transferring glycosyl groups

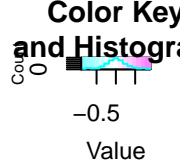




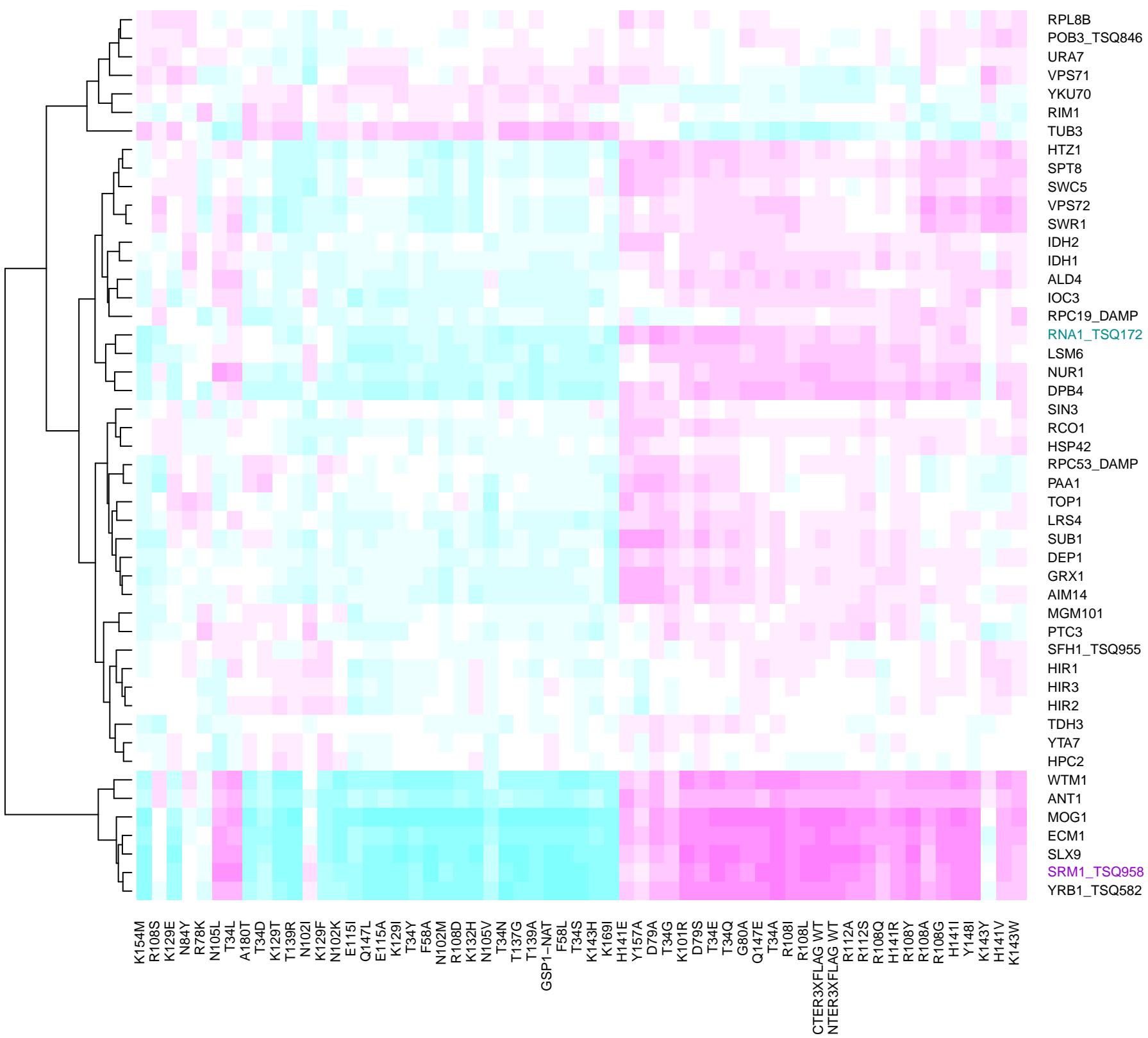


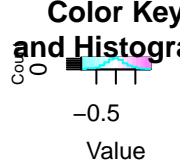
nucleolus_GO_30_2



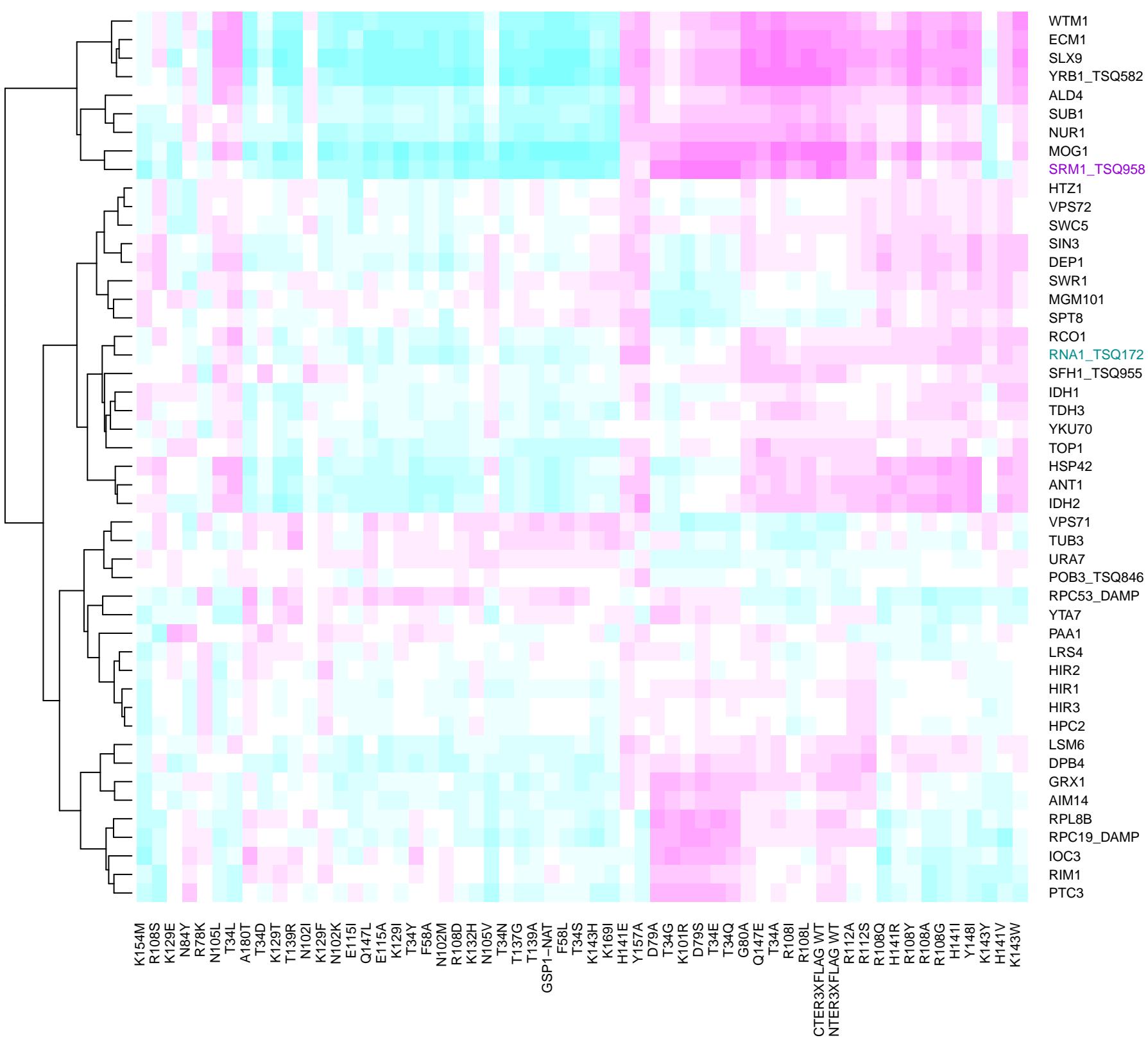


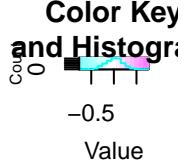
ribosomes and translation_GO_30_4



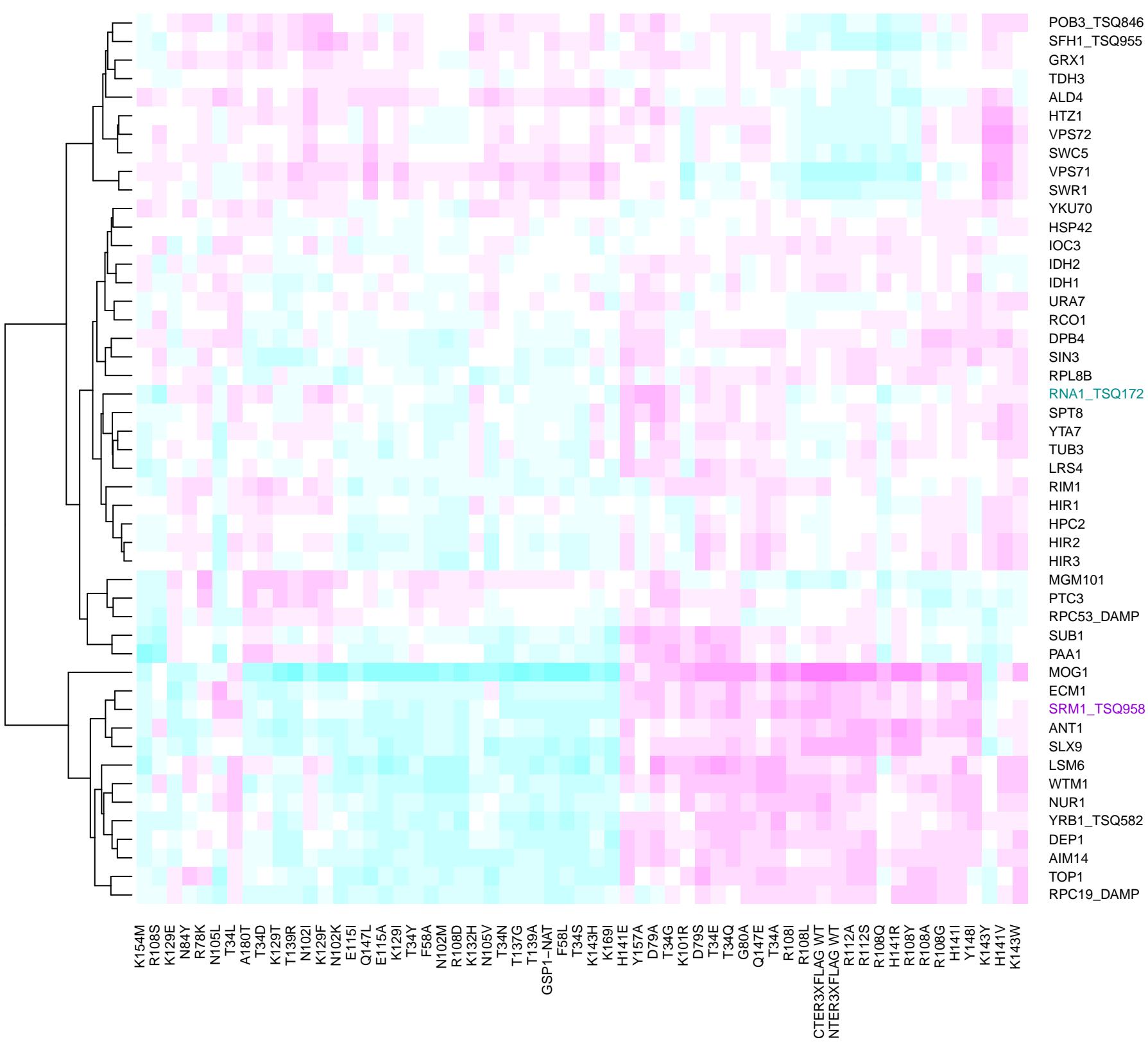


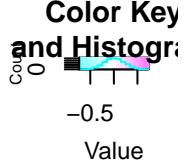
chromatin_GO_30_6



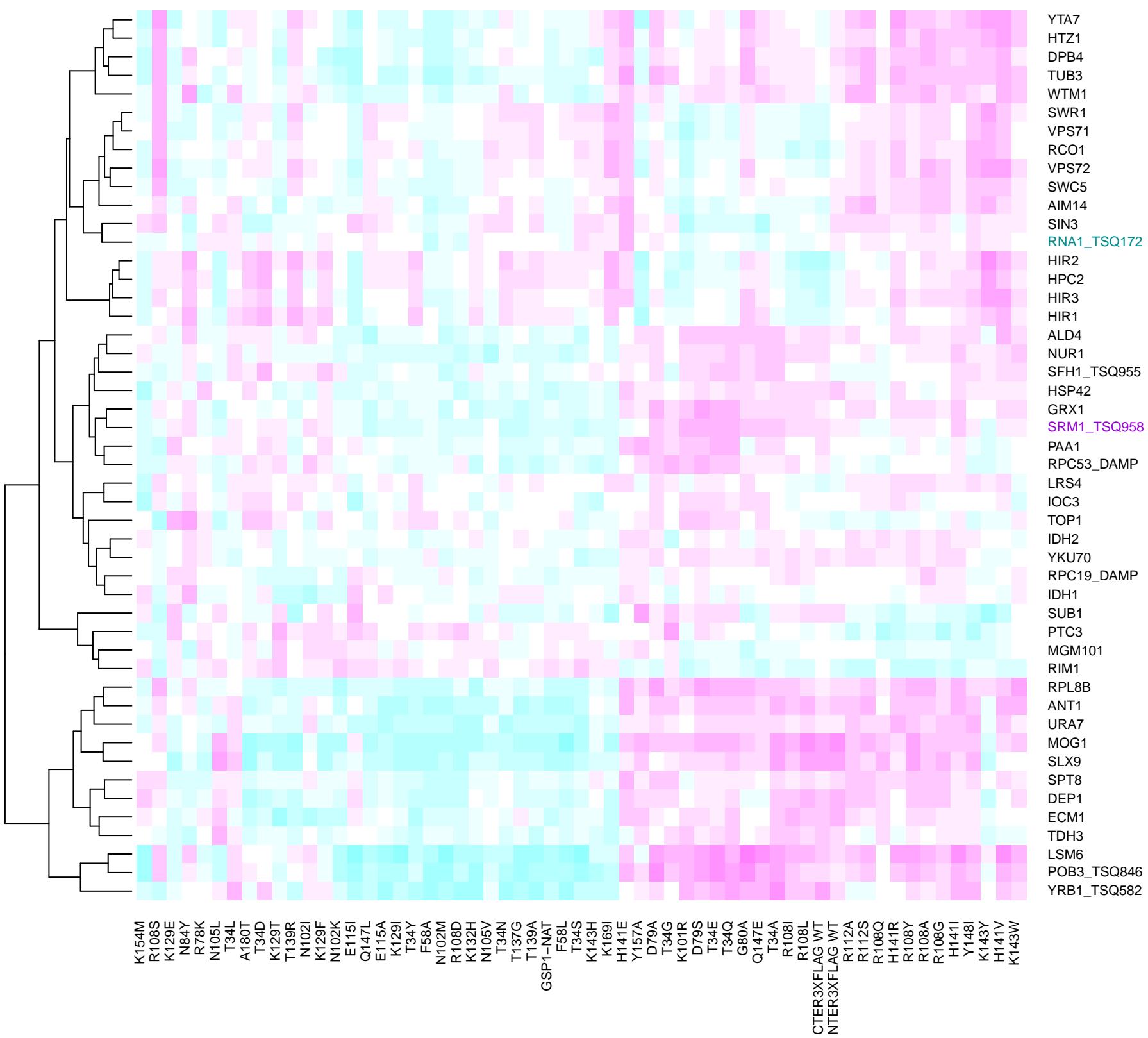


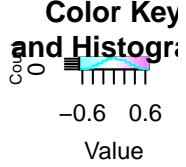
rRNA processing



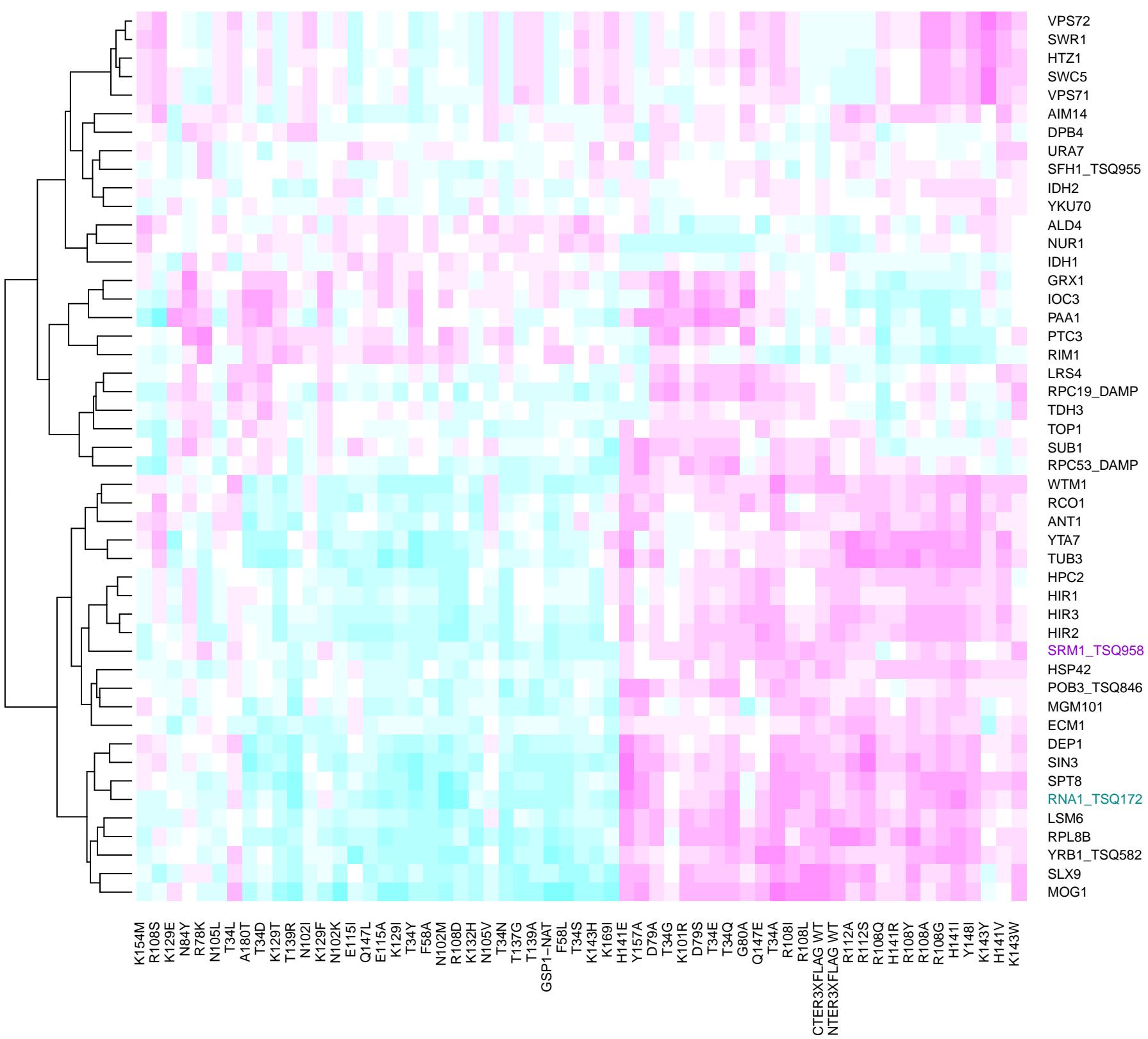


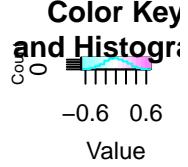
transcription and mRNA processing_GO_30_5



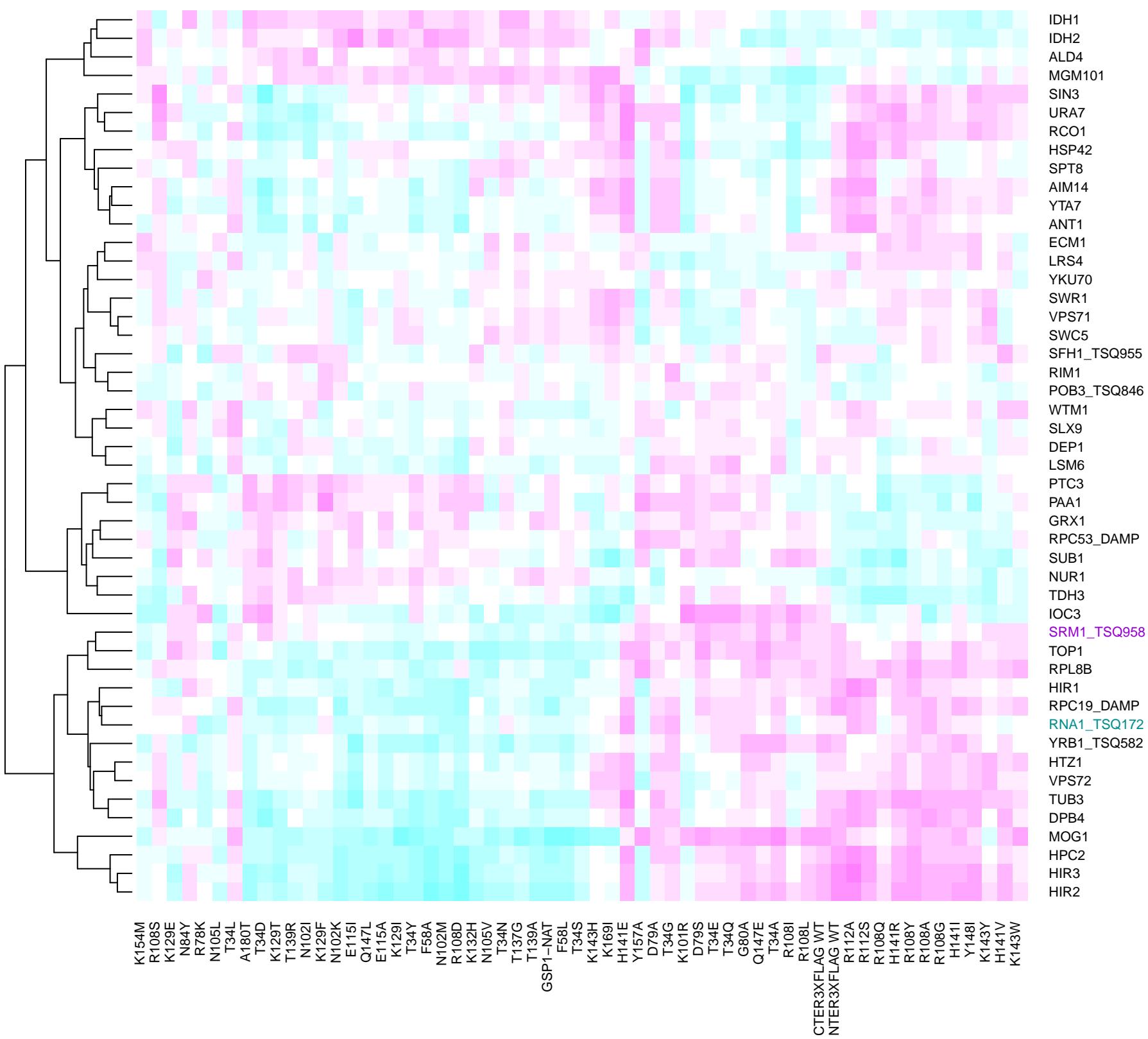


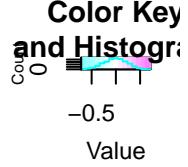
cellular response to DNA damage stimulus_GO_30_2



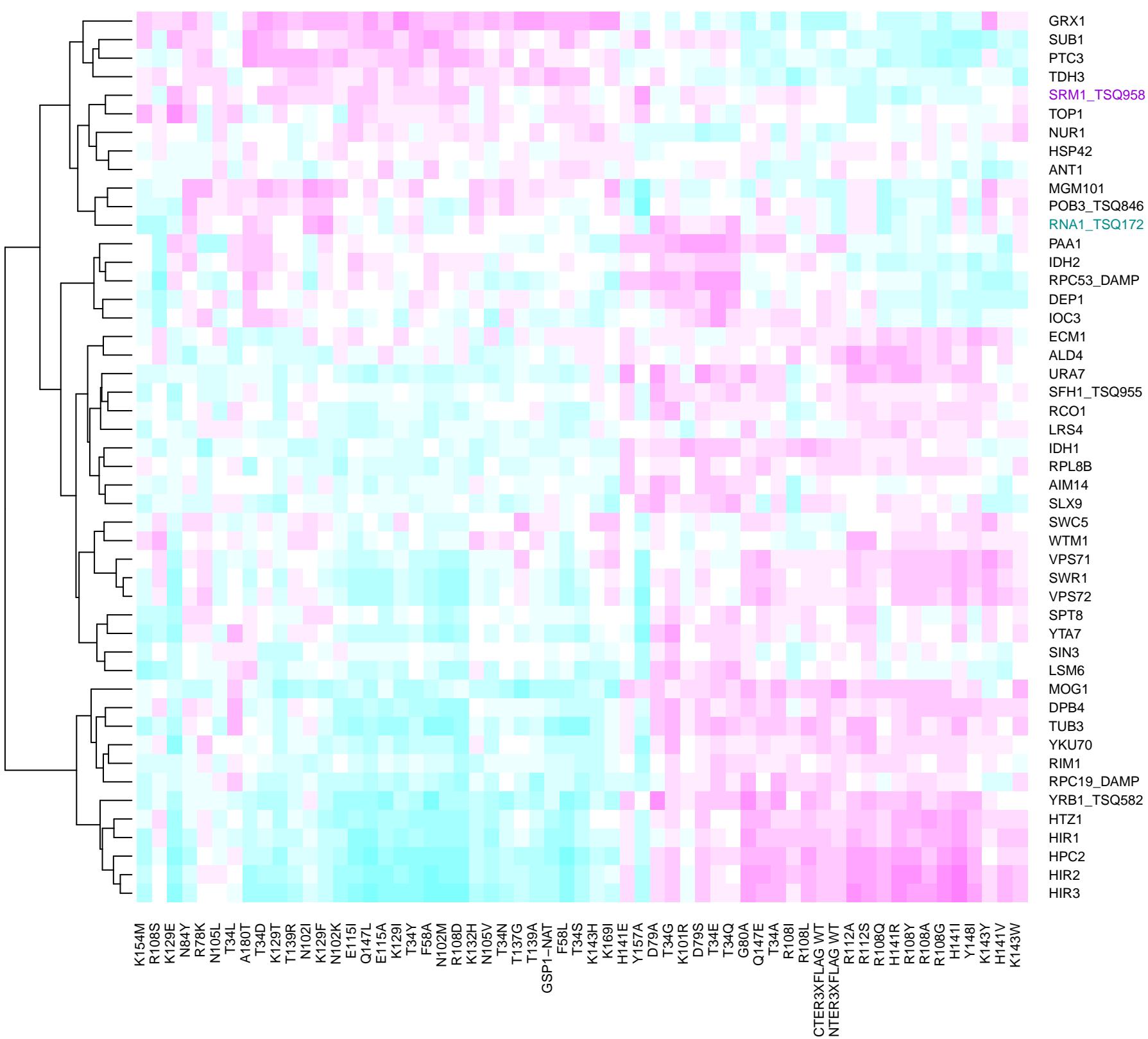


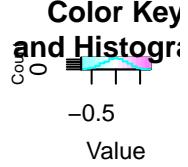
endomembrane system_GO_30_13



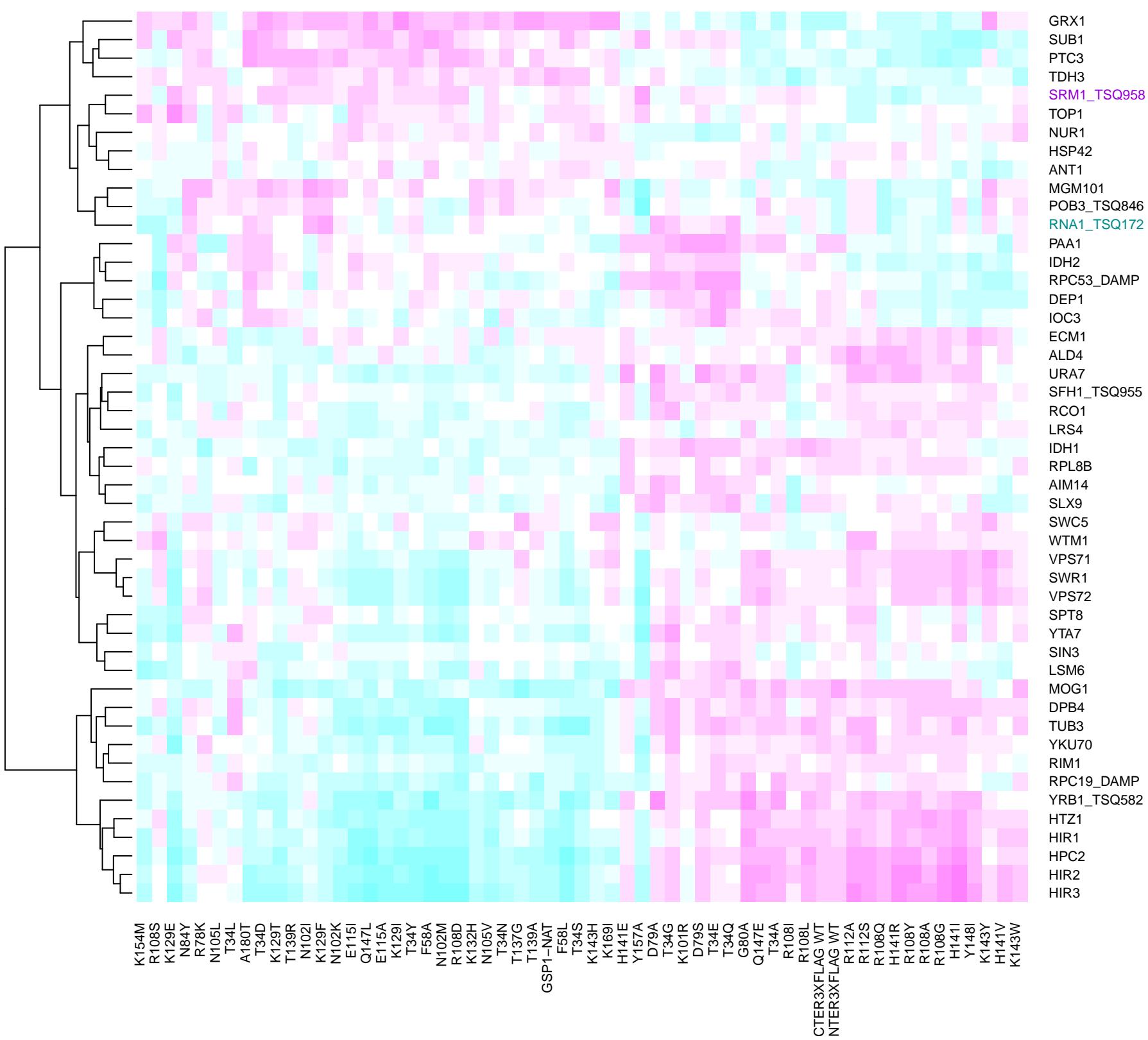


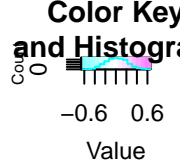
endoplasmic reticulum_GO_30_9



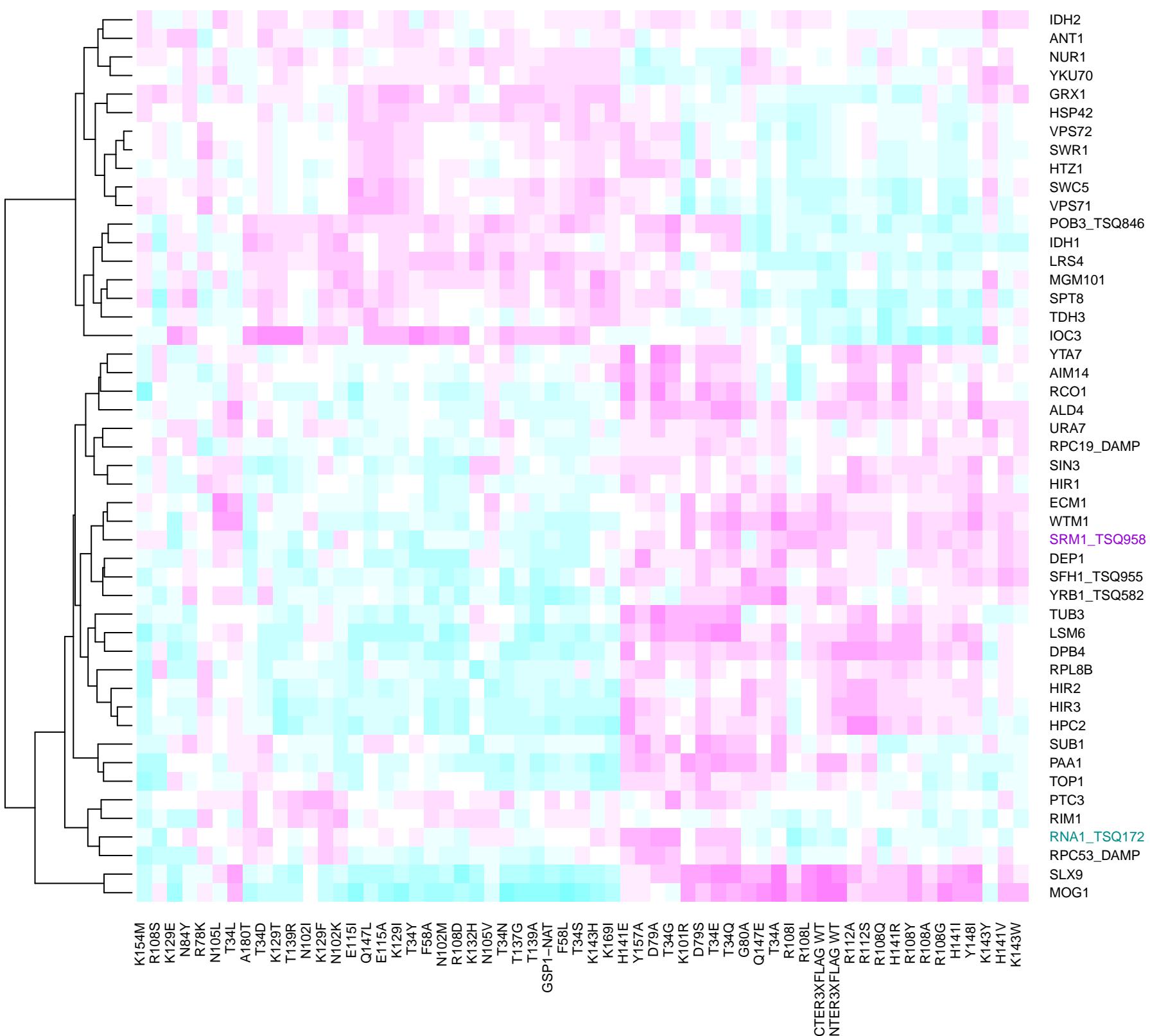


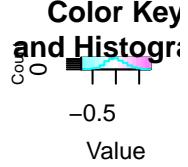
ER_GO_30_9



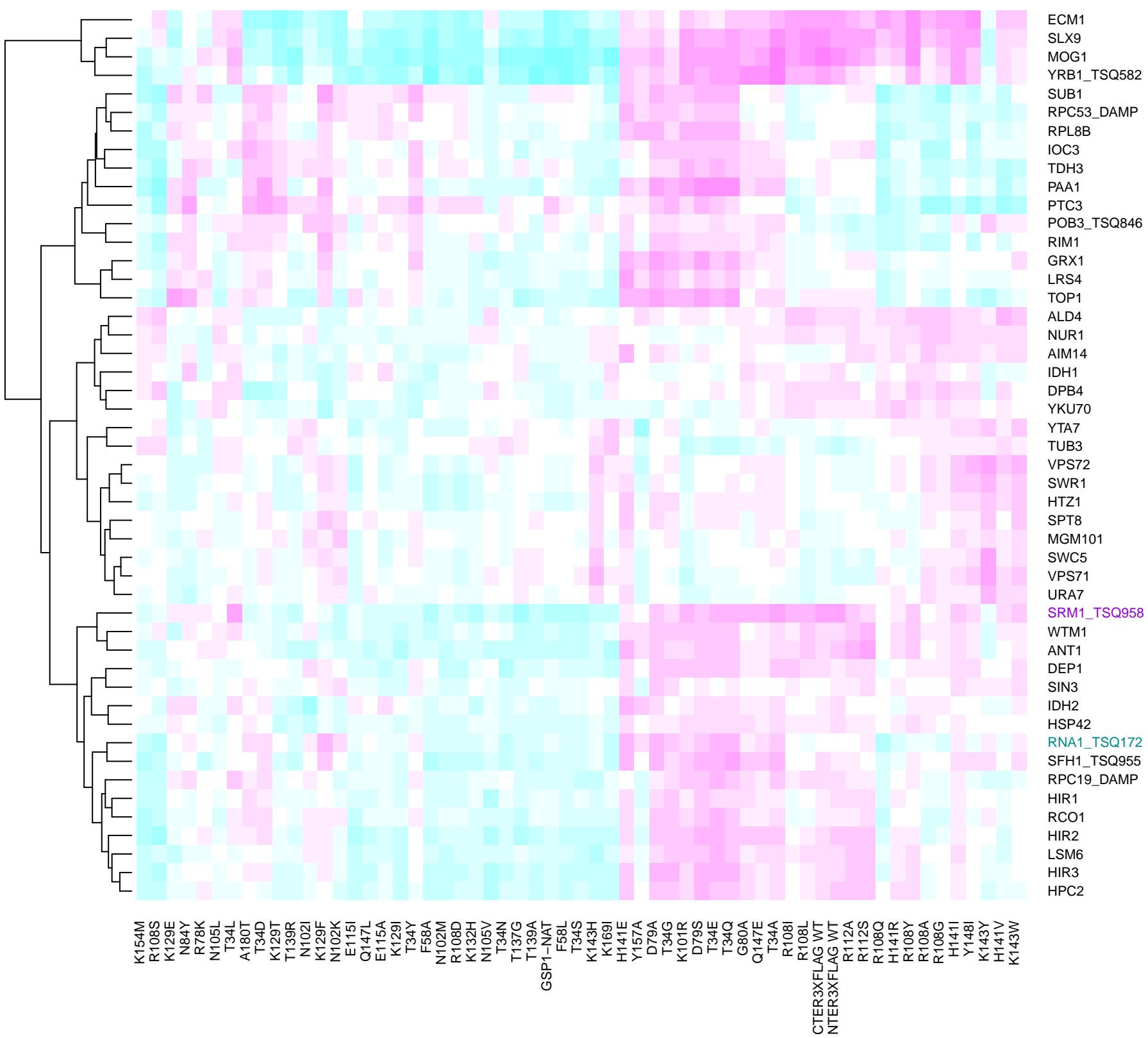


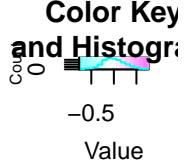
Golgi and ER_GO_30_9



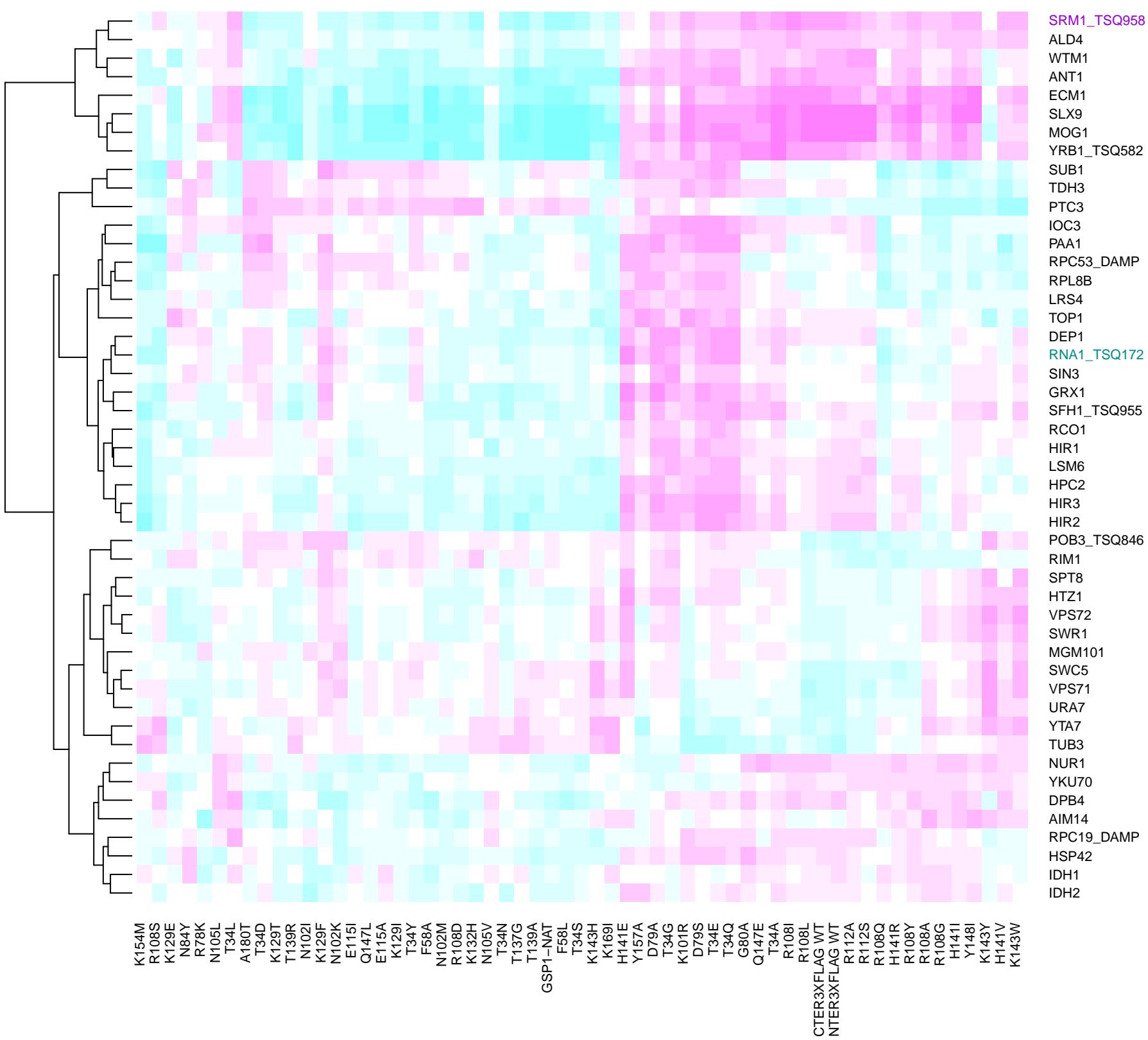


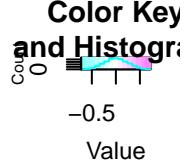
response to osmotic stress



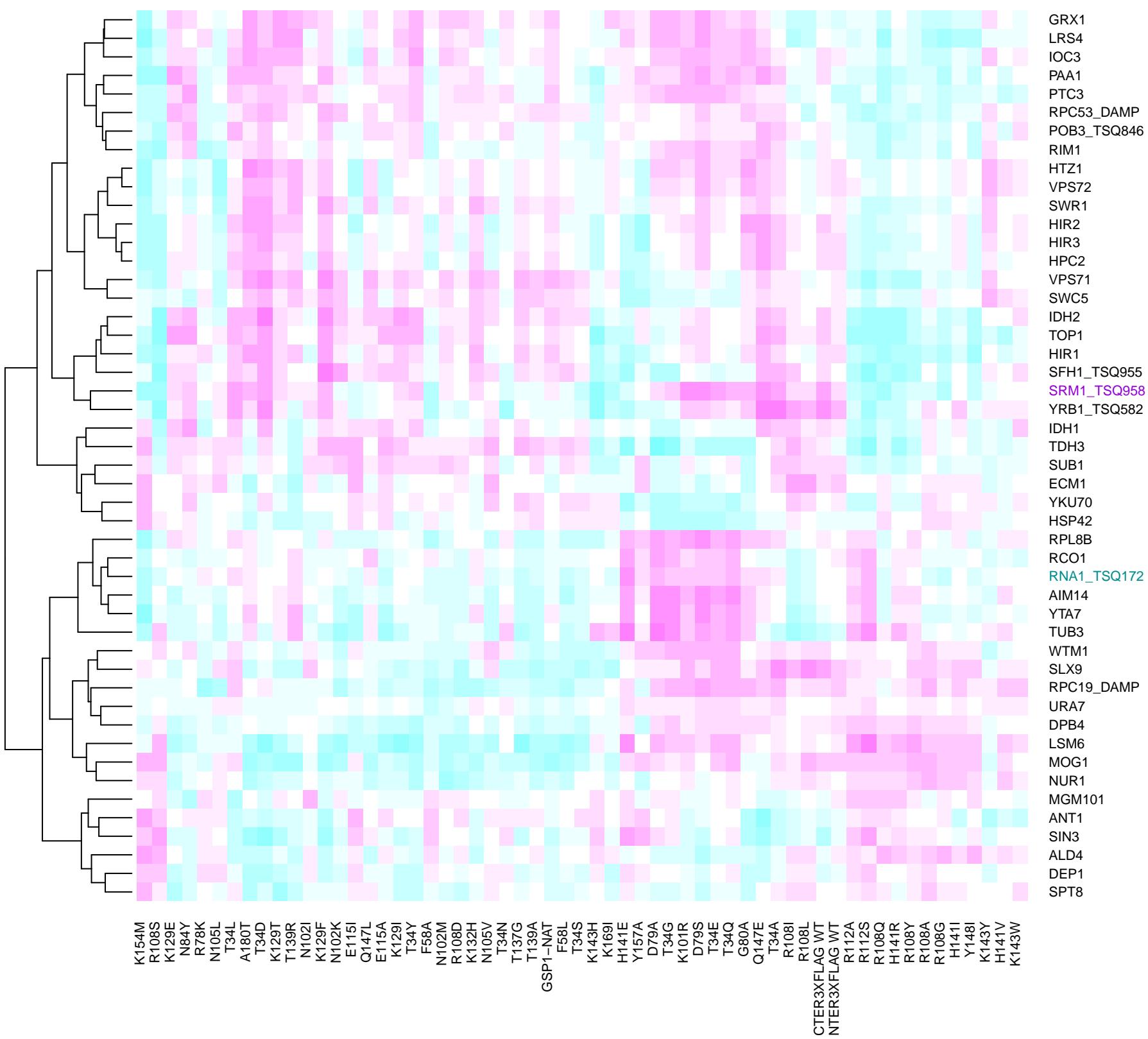


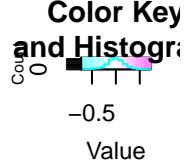
response to osmotic stress_GO_30_1



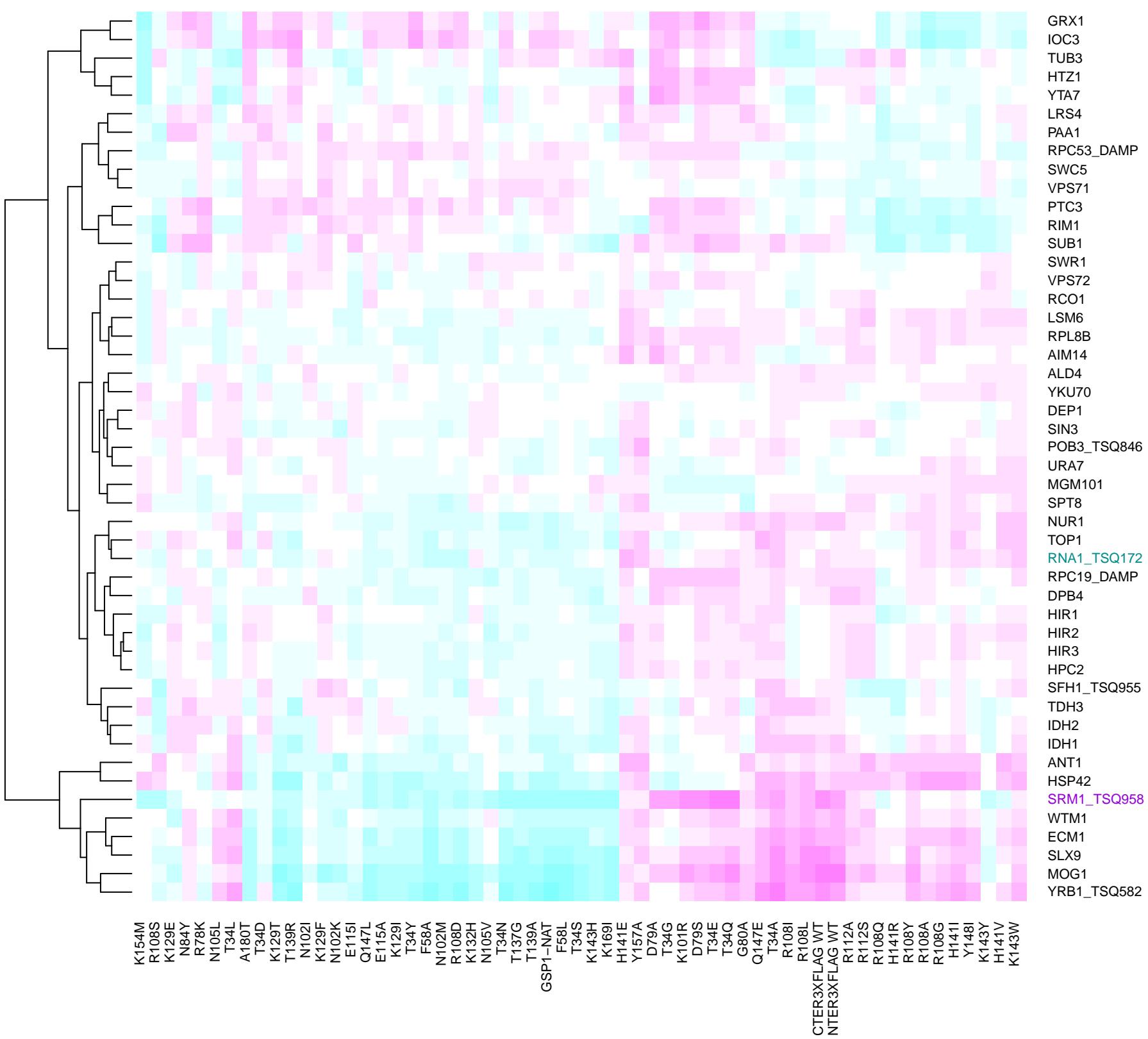


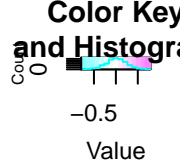
cytoskeletal protein binding



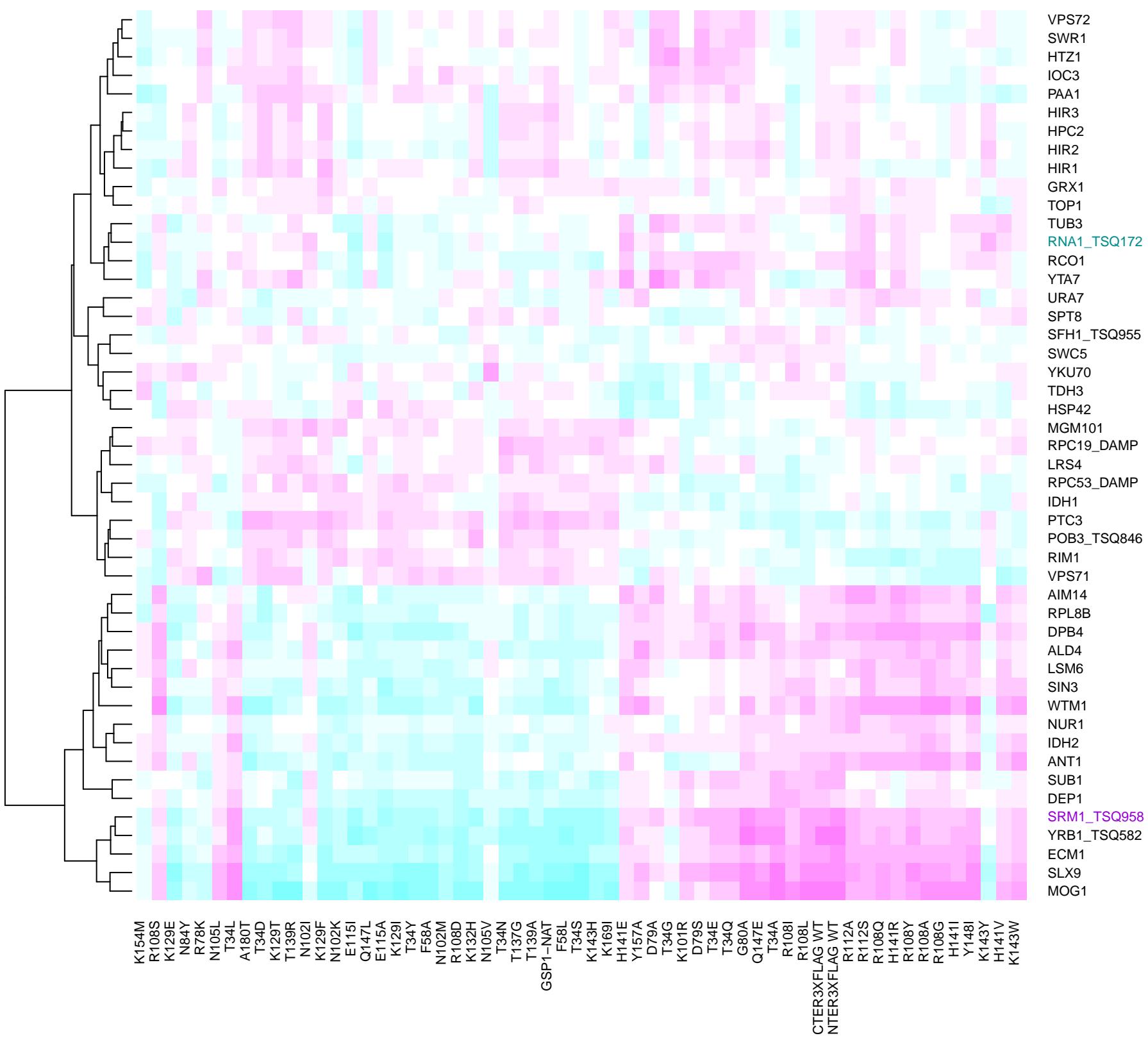


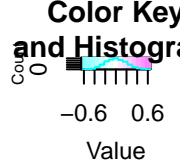
chromosome segregation



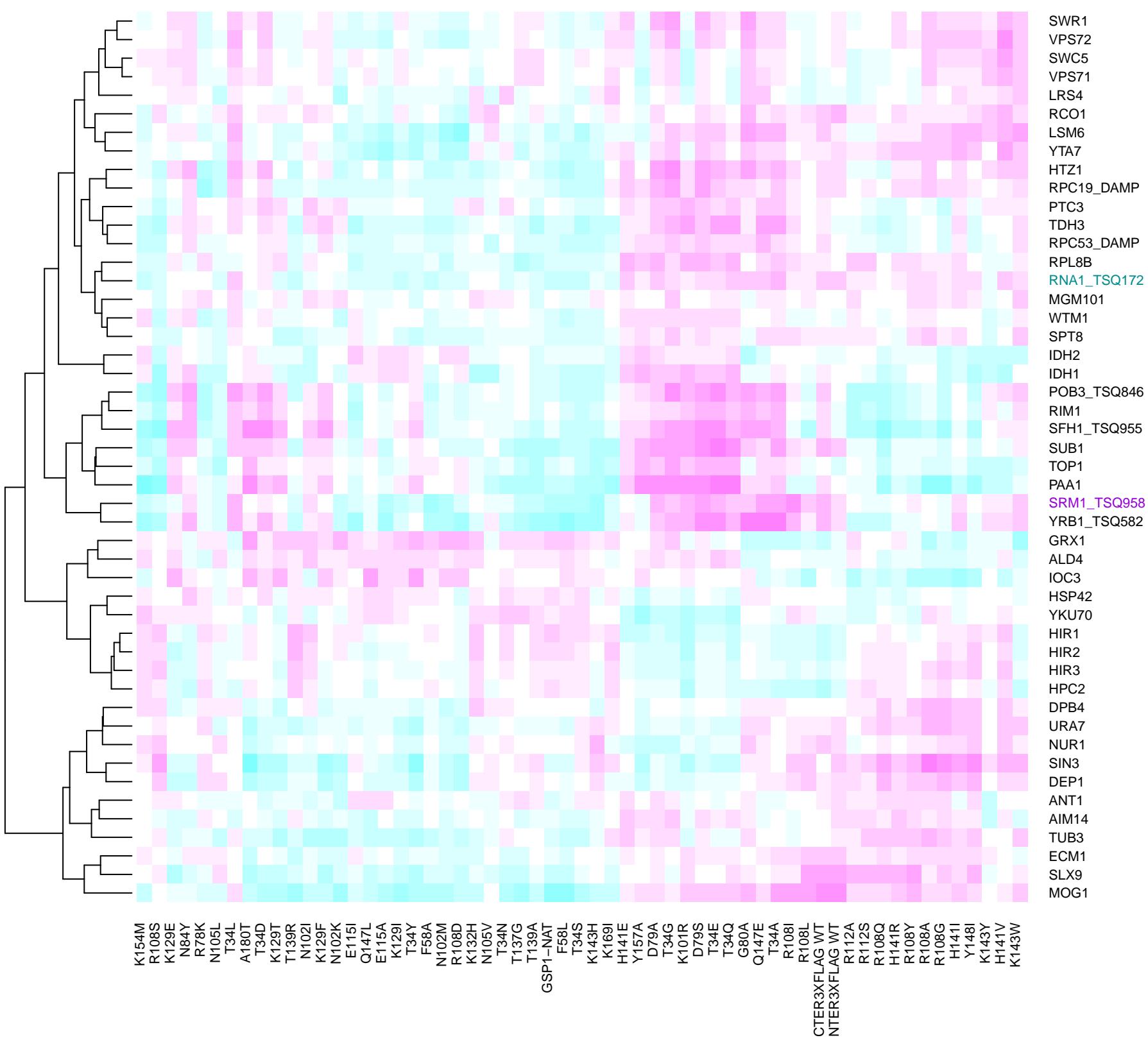


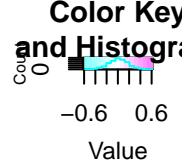
cytoskeleton_GO_30_3



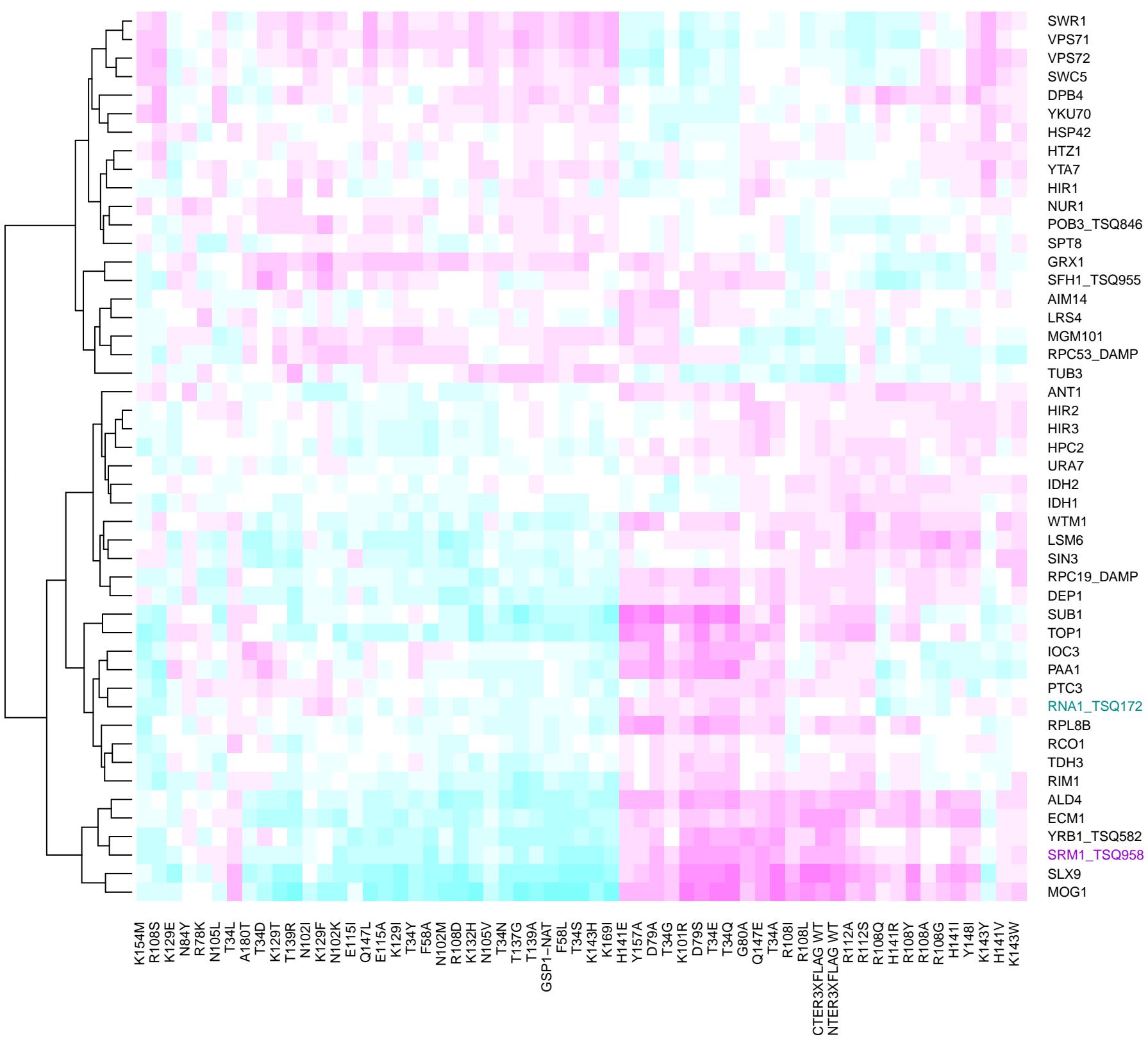


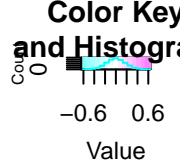
mitochondria and respiration_GO_30_4



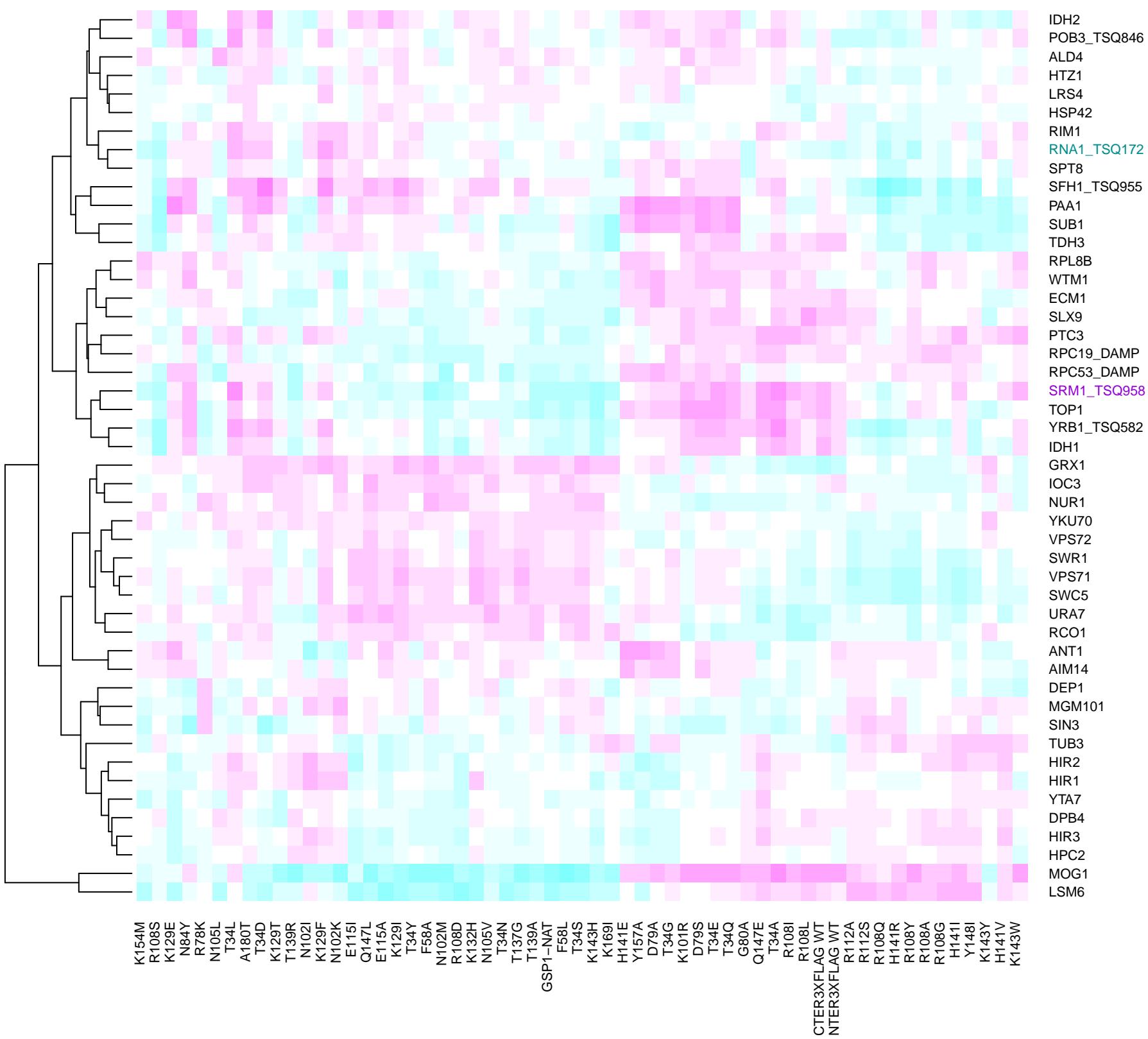


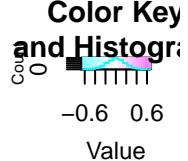
site of polarized growth_GO_30_1



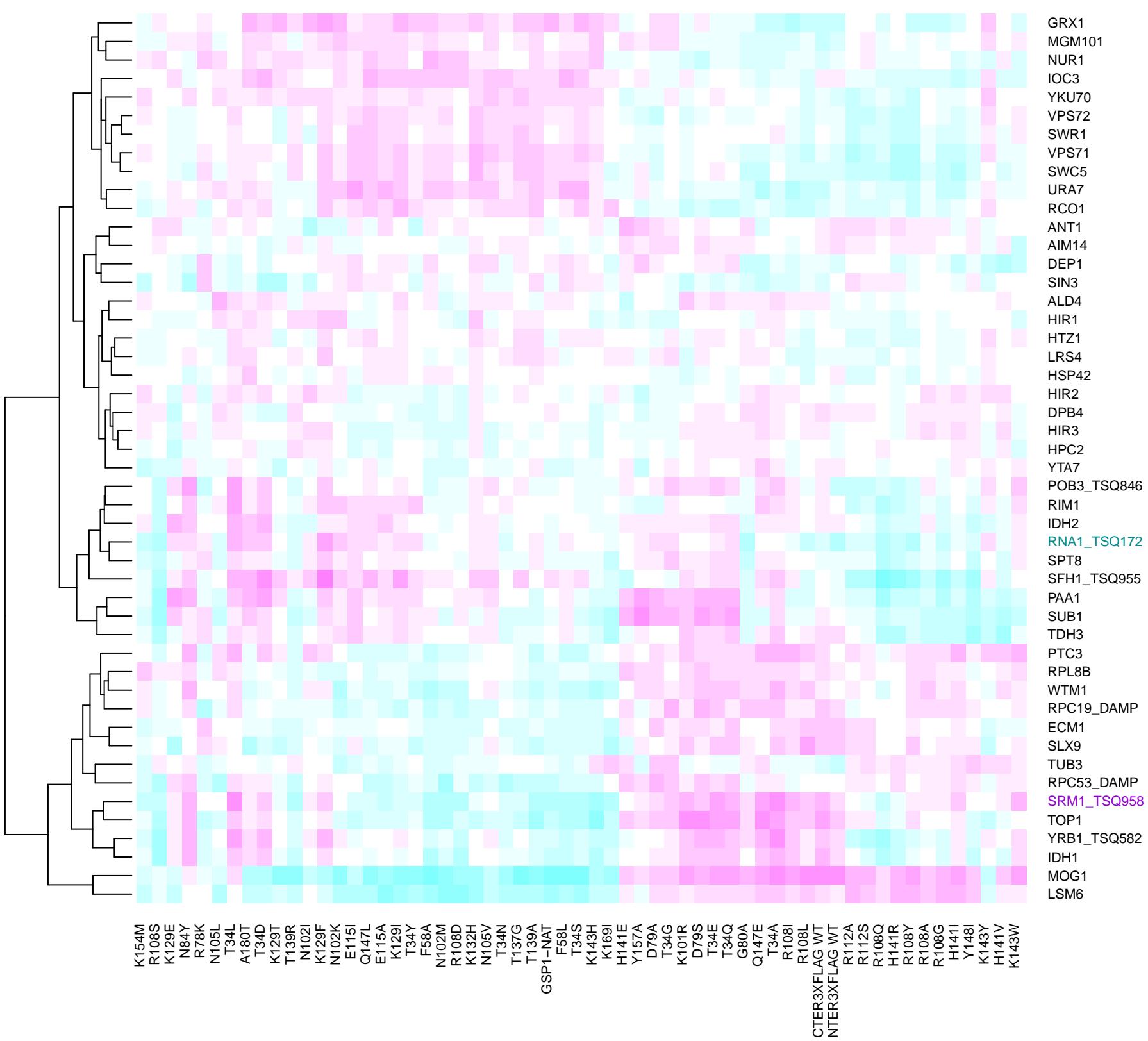


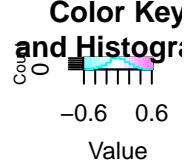
endocytosis



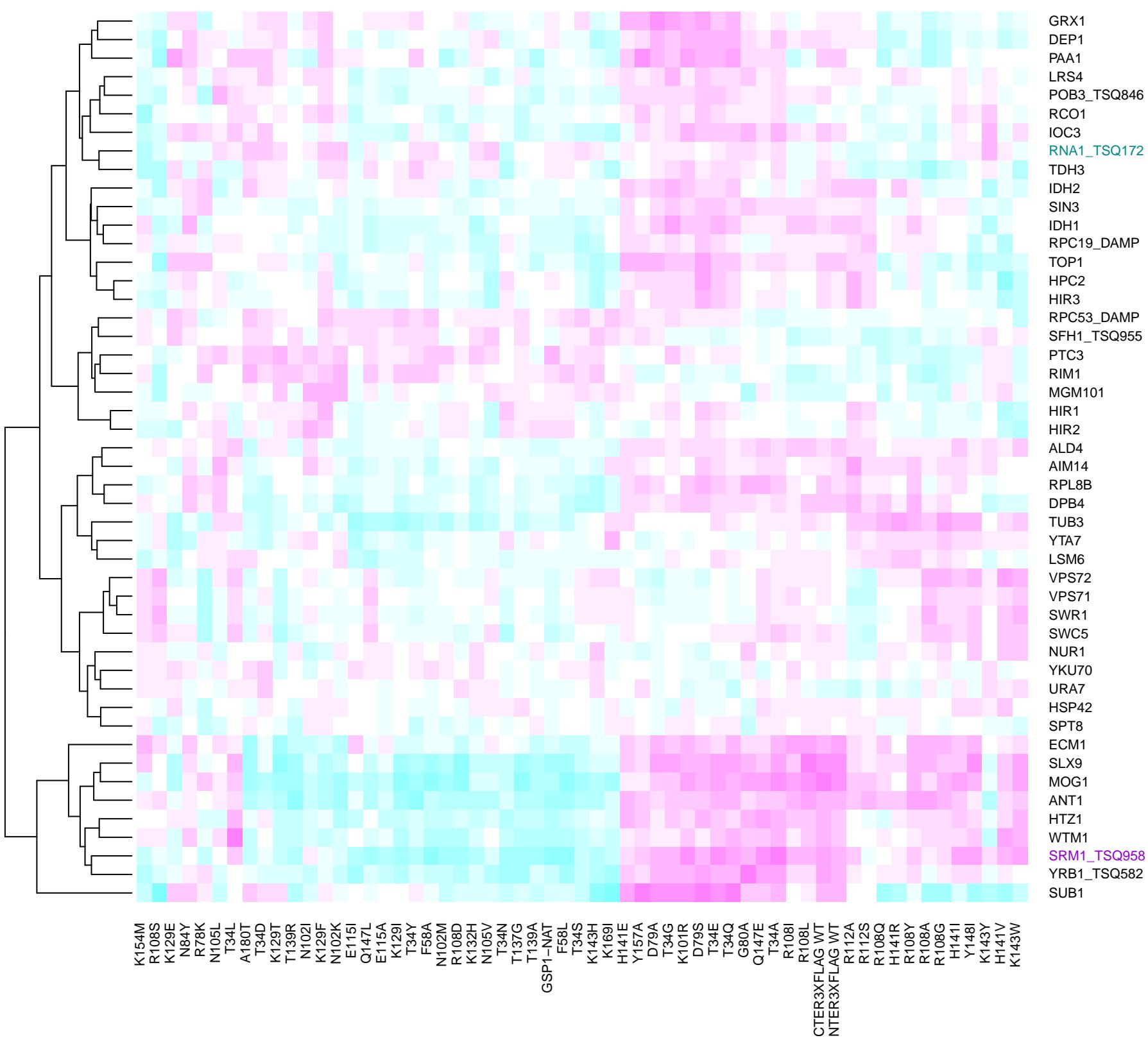


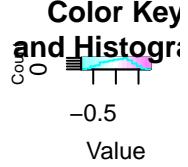
endocytosis_GO_30_1





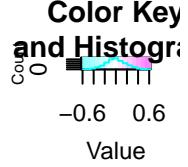
endomembrane system_GO_30_4



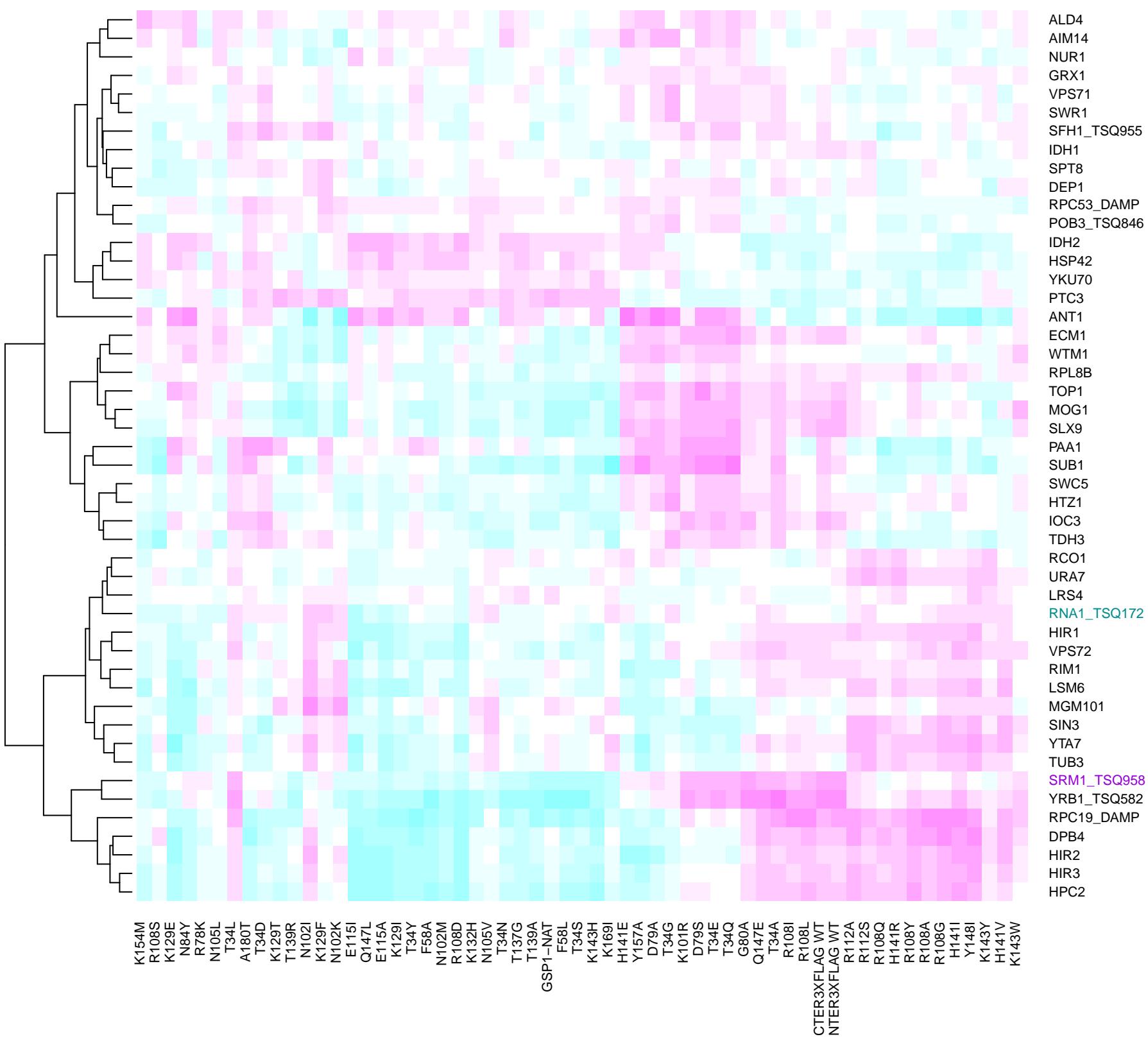


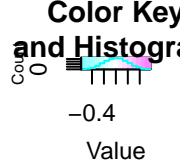
Golgi and ER_GO_30_3



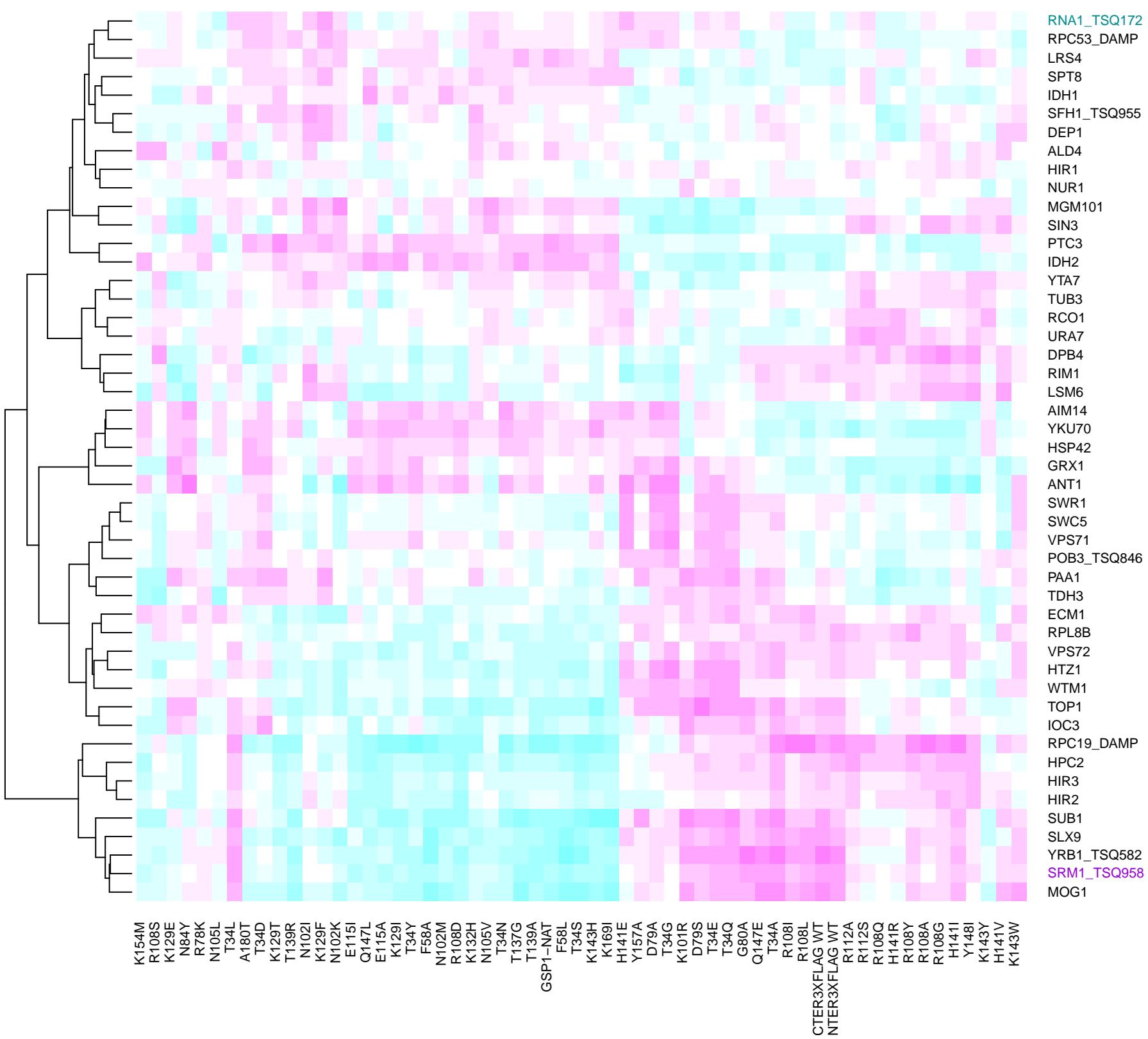


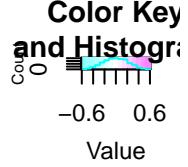
Golgi apparatus



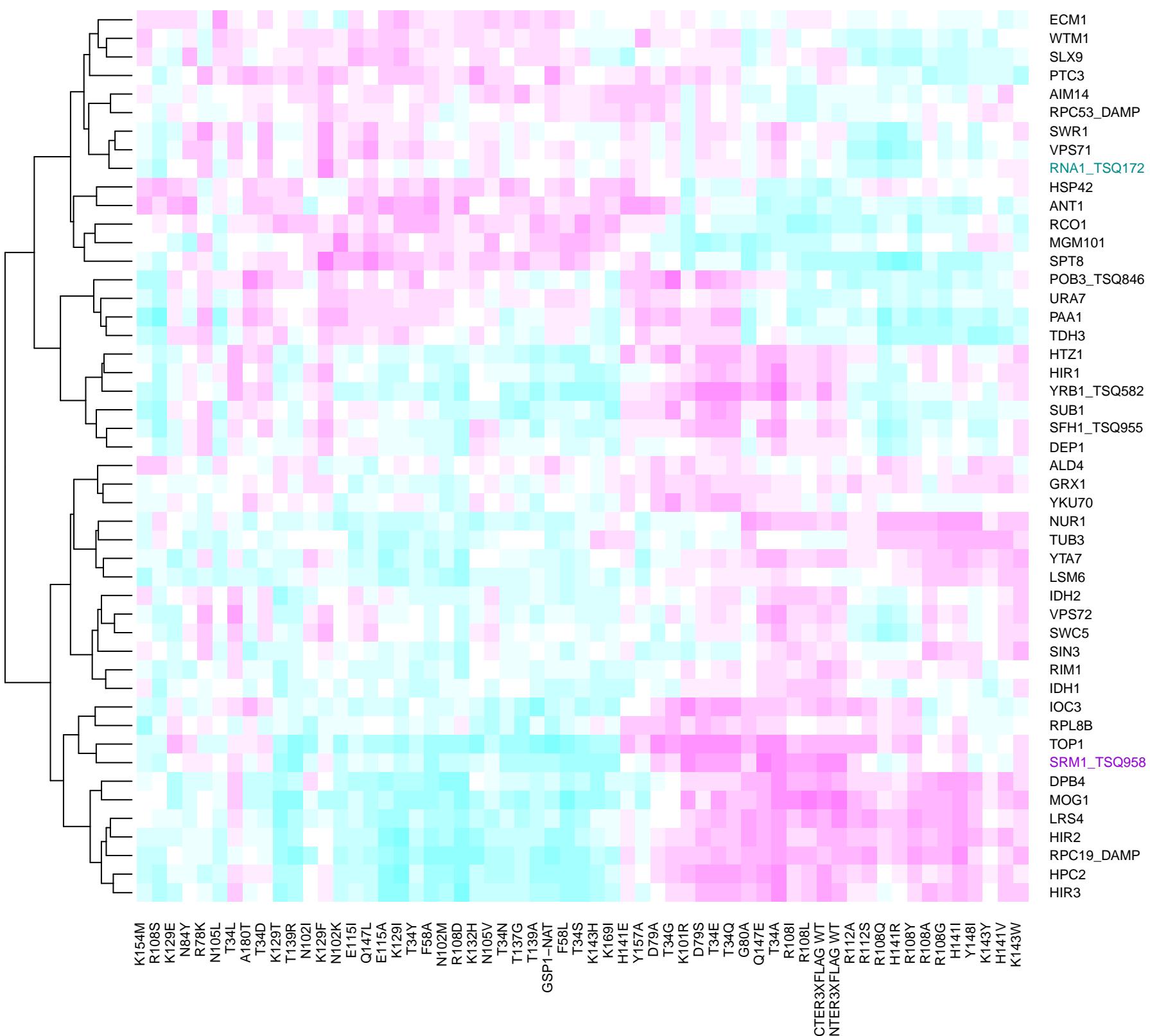


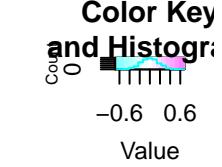
Golgi apparatus_GO_30_1



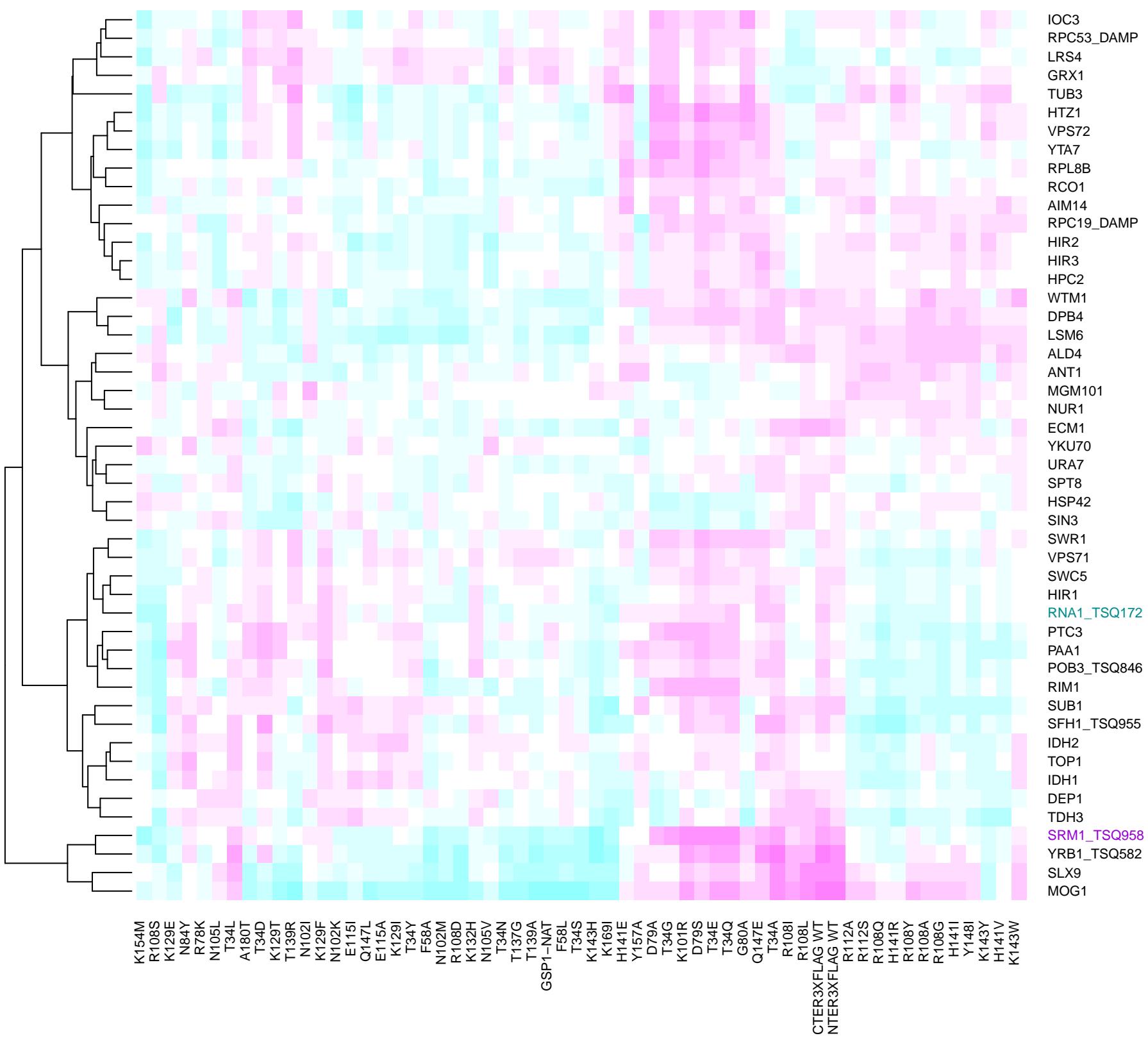


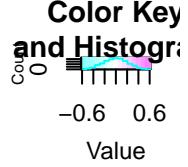
membrane fusion



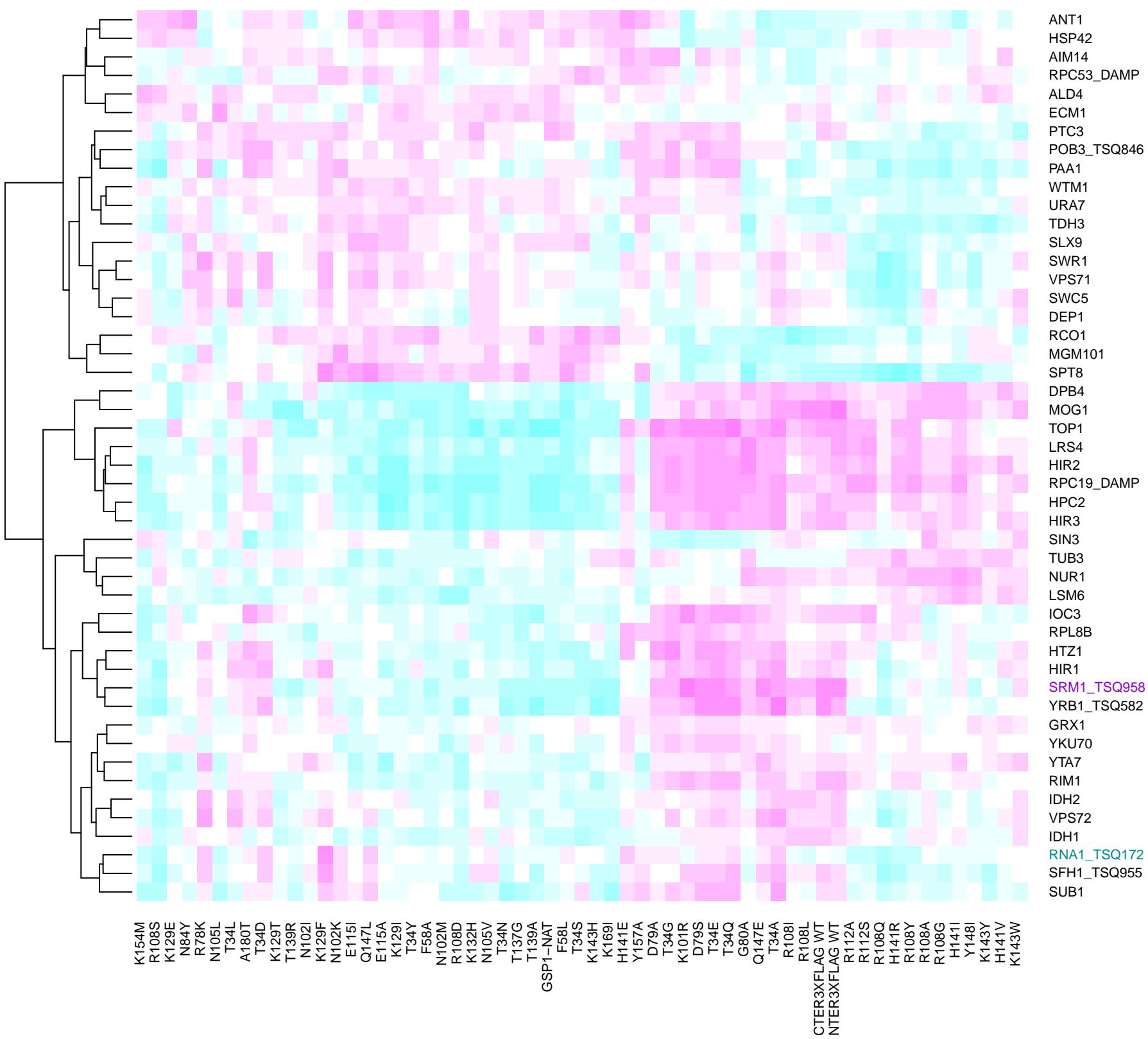


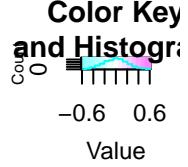
cytoskeleton



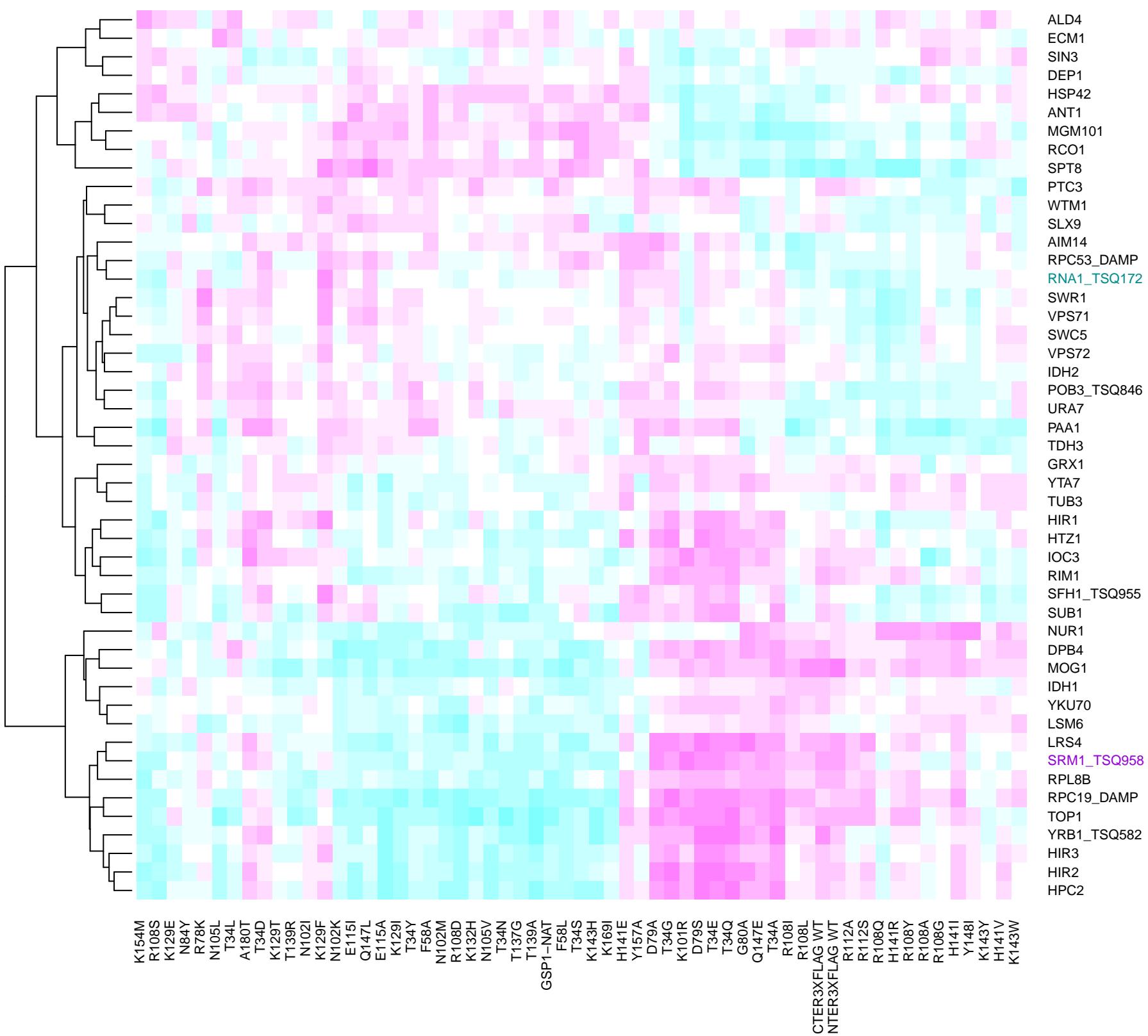


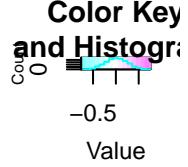
organelle fusion



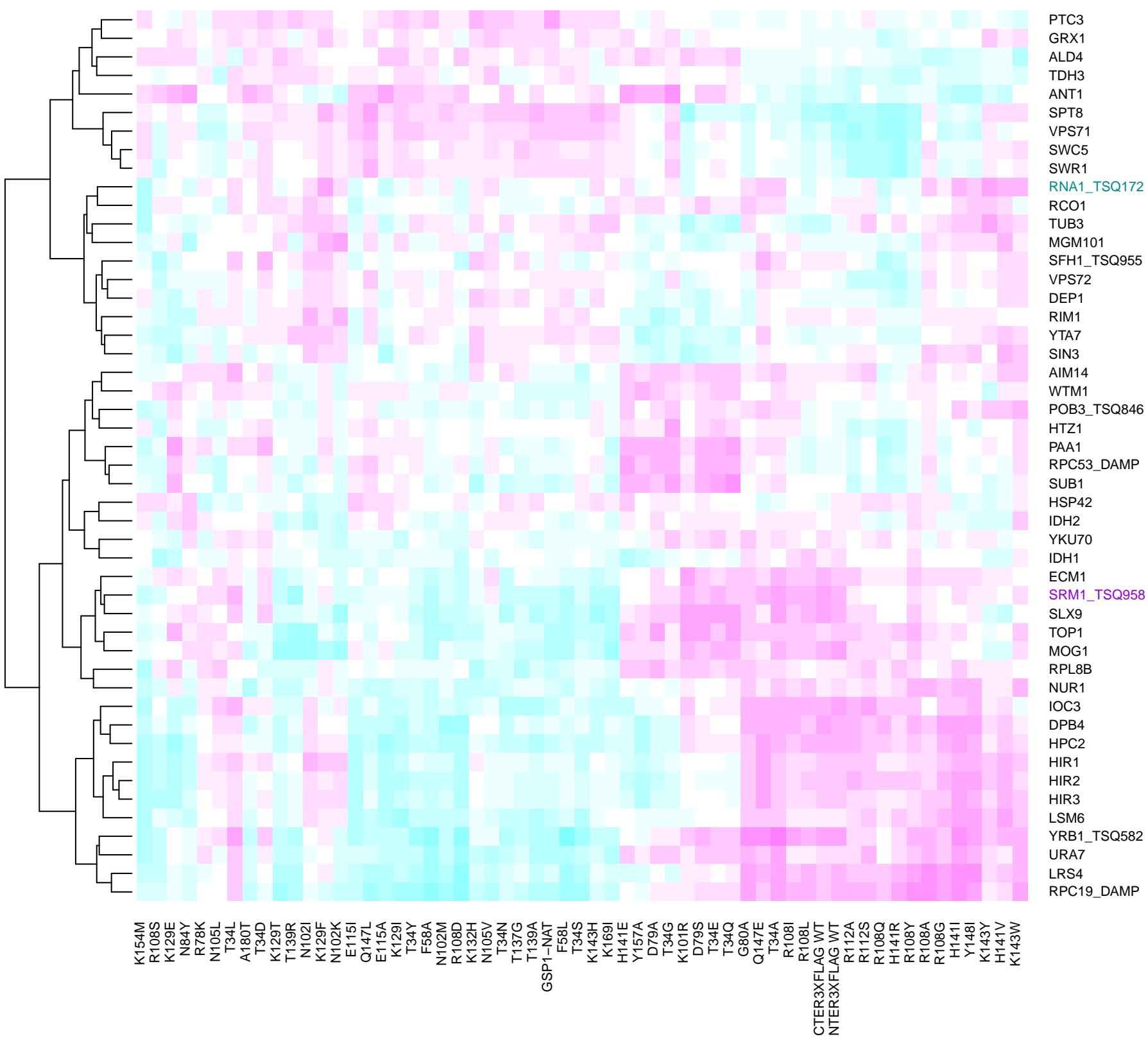


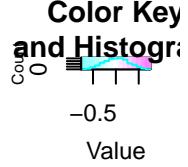
organelle fusion_GO_30_1



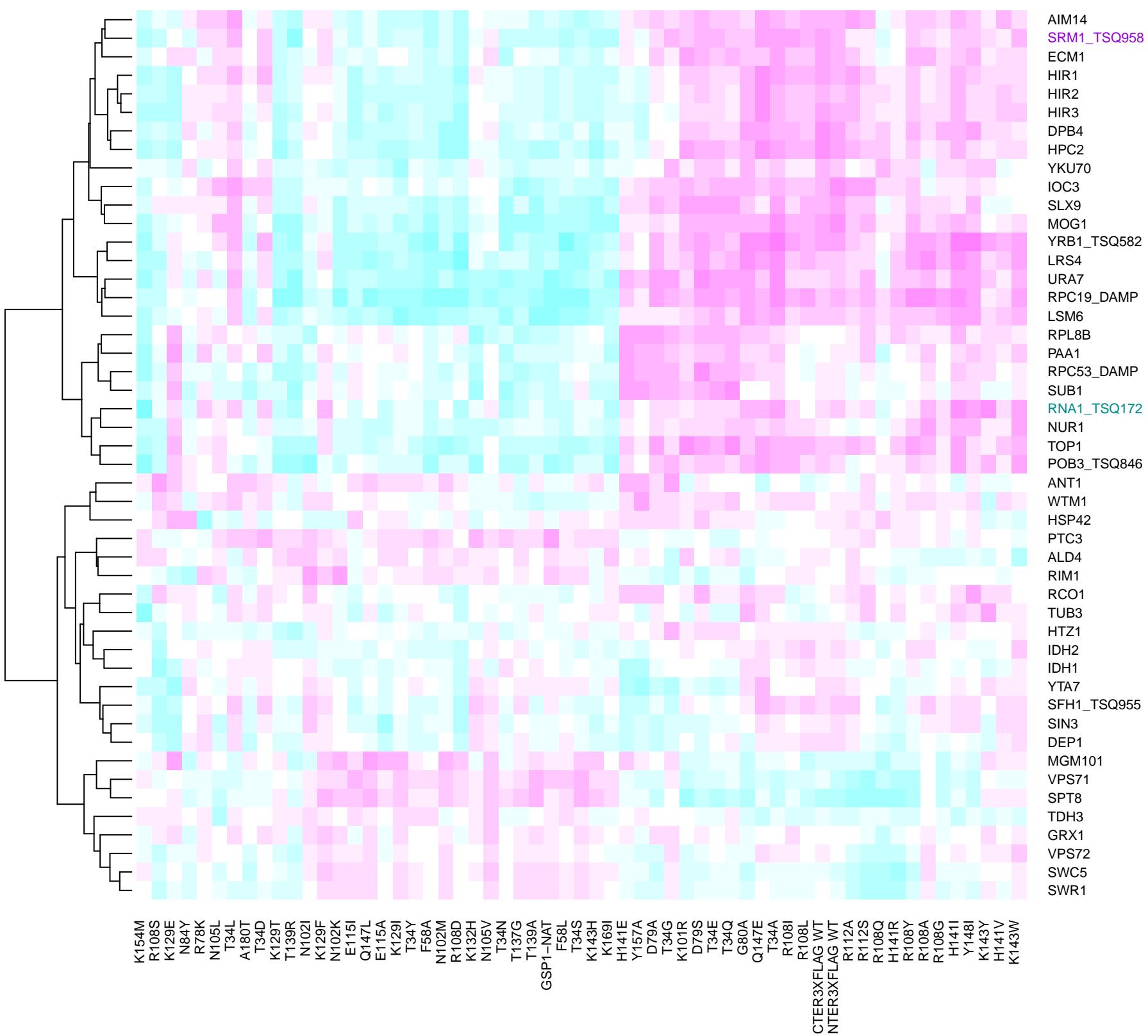


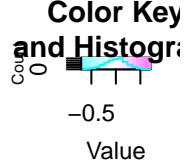
vesicle organization



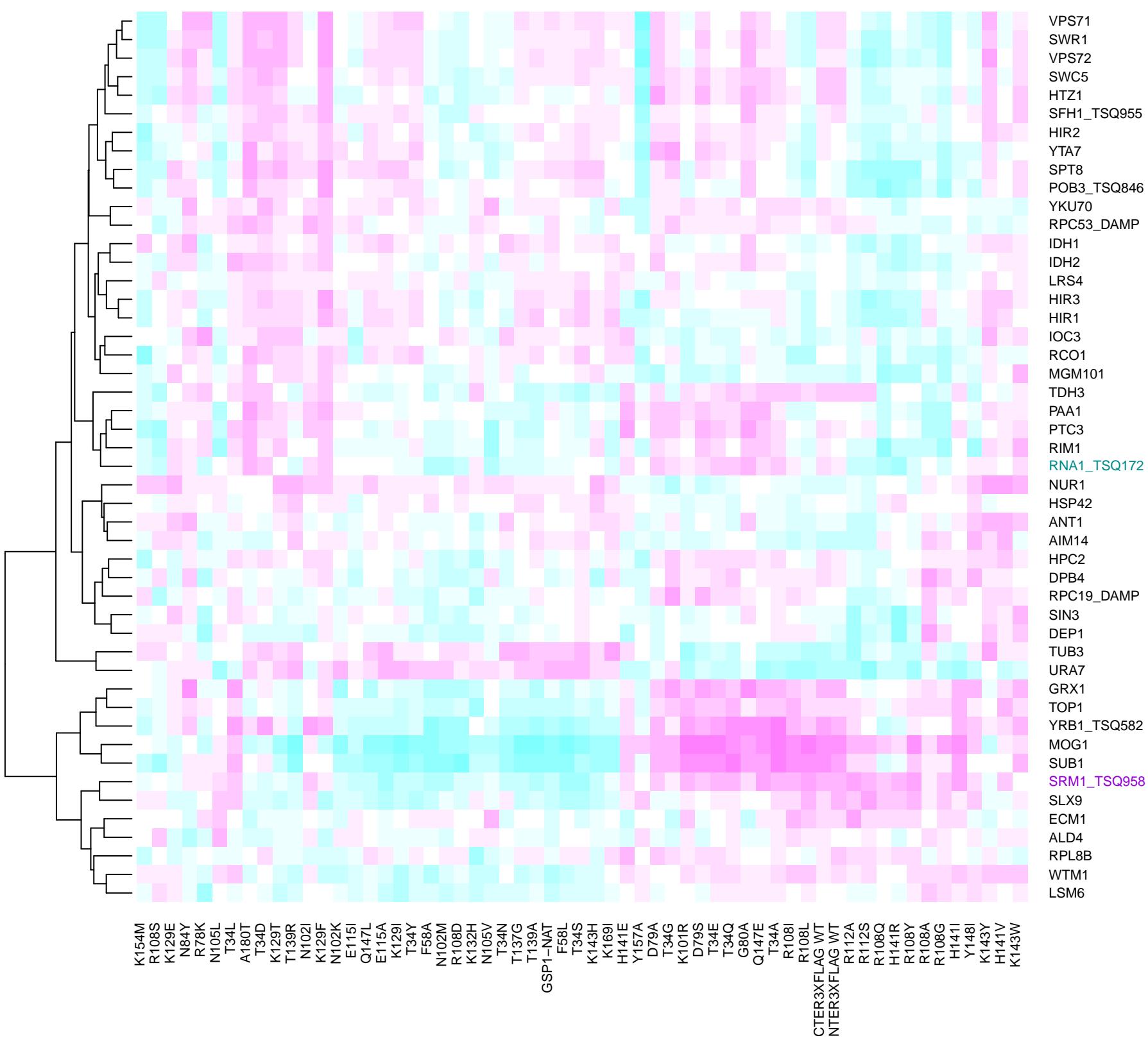


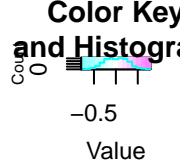
vesicle organization_GO_30_1



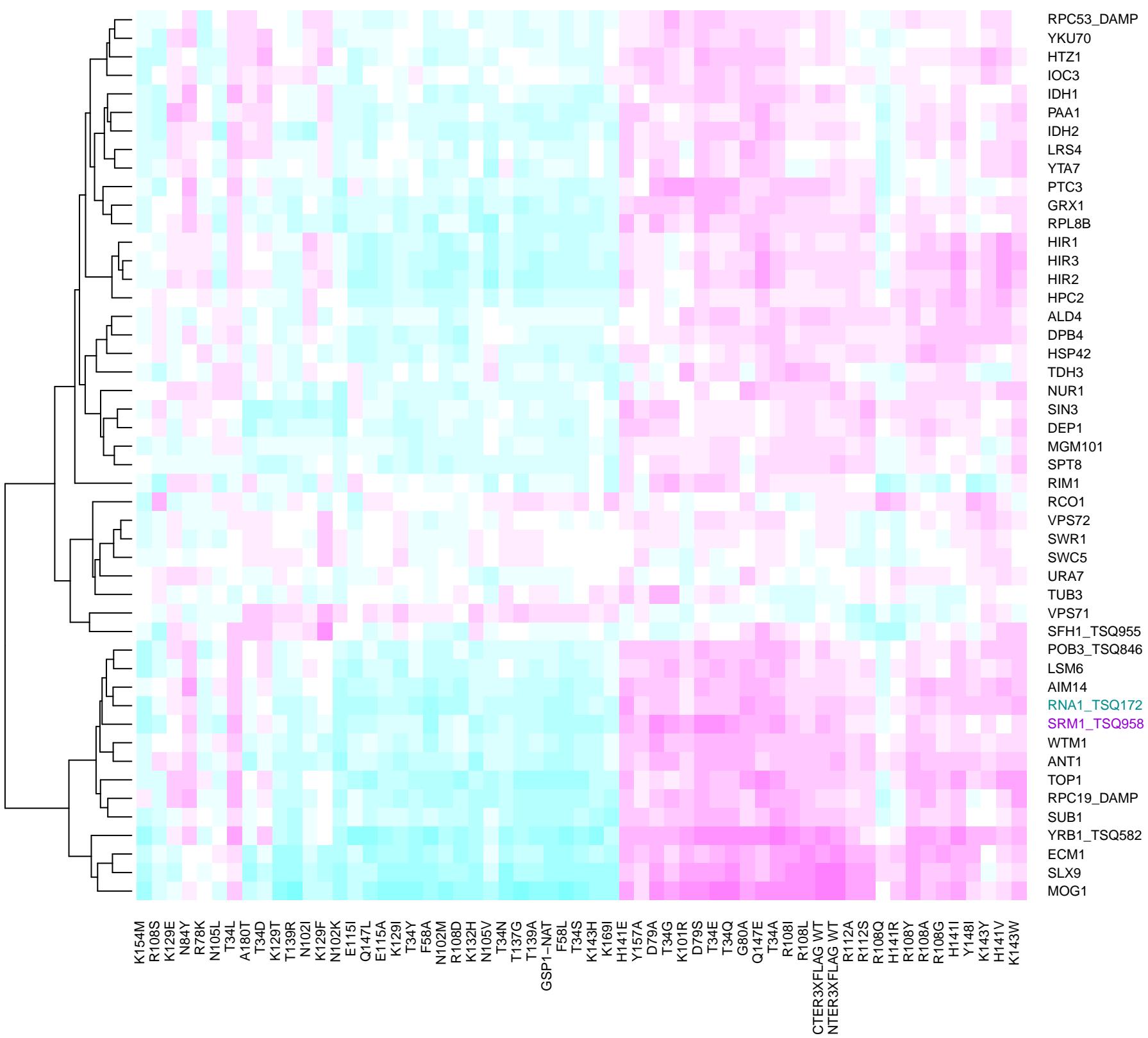


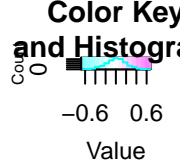
cell cycle_GO_30_7



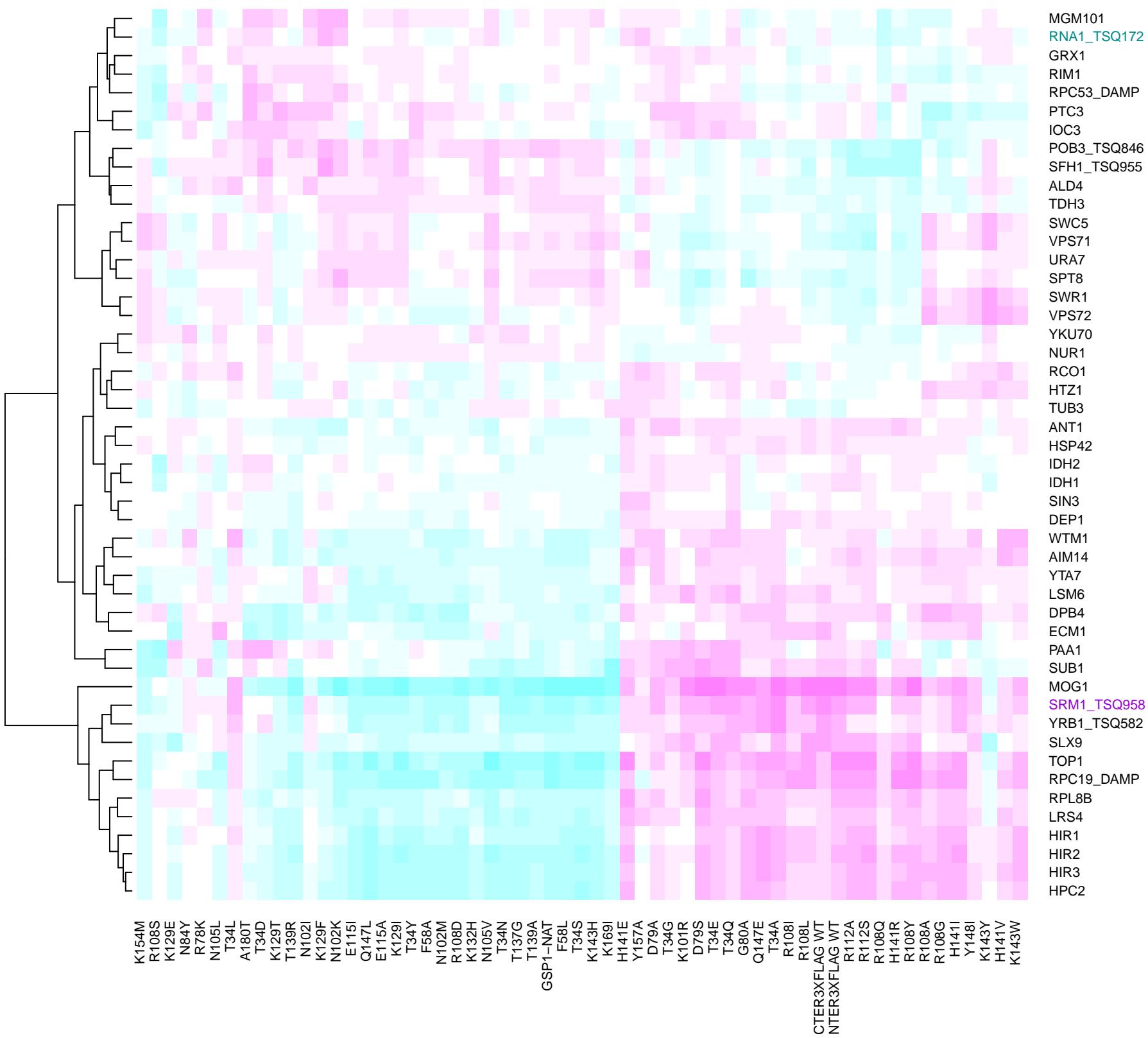


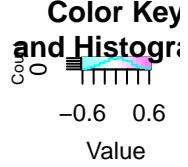
chromosome_GO_30_3



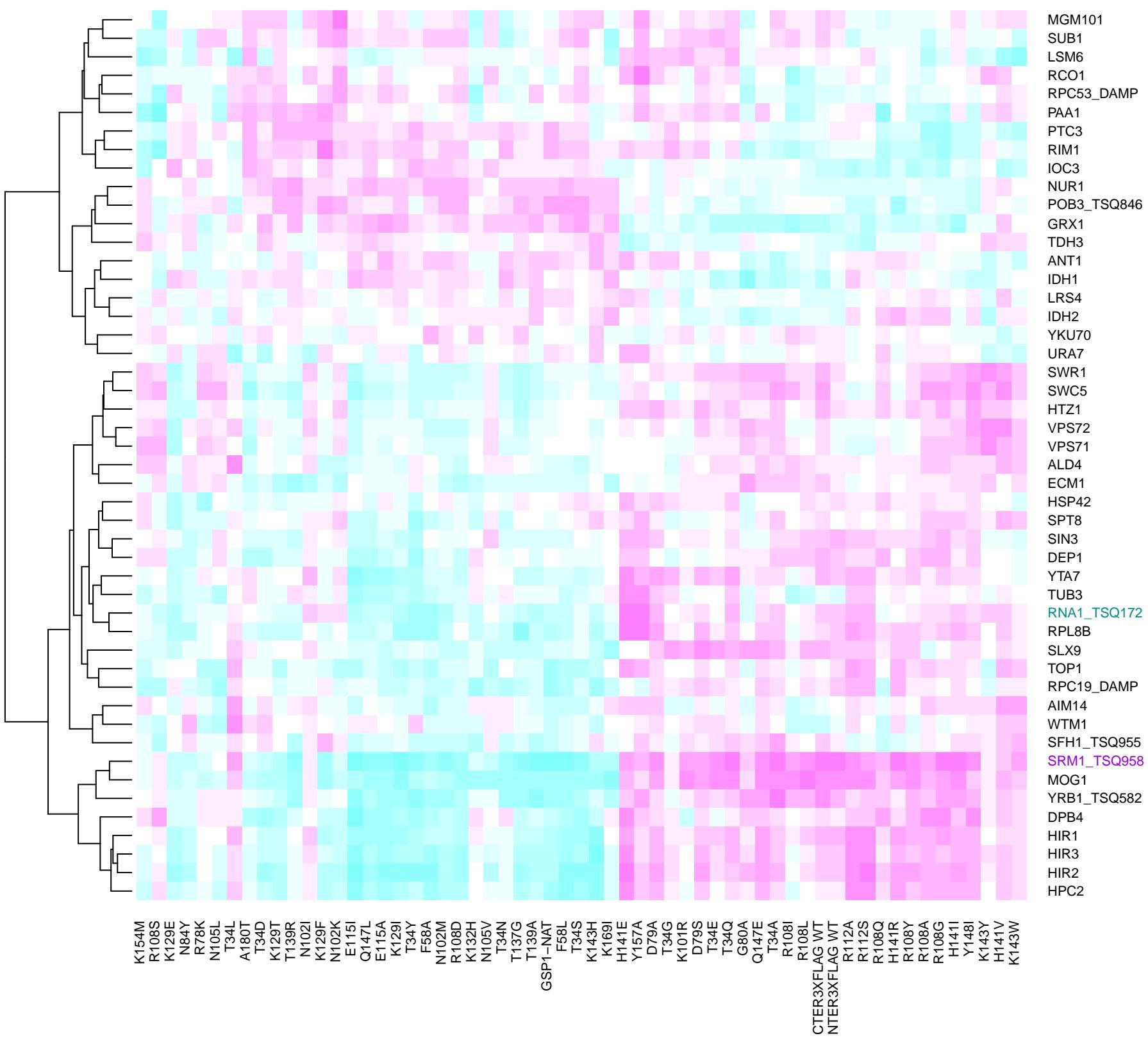


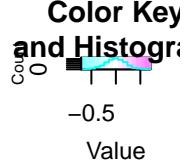
ribosome



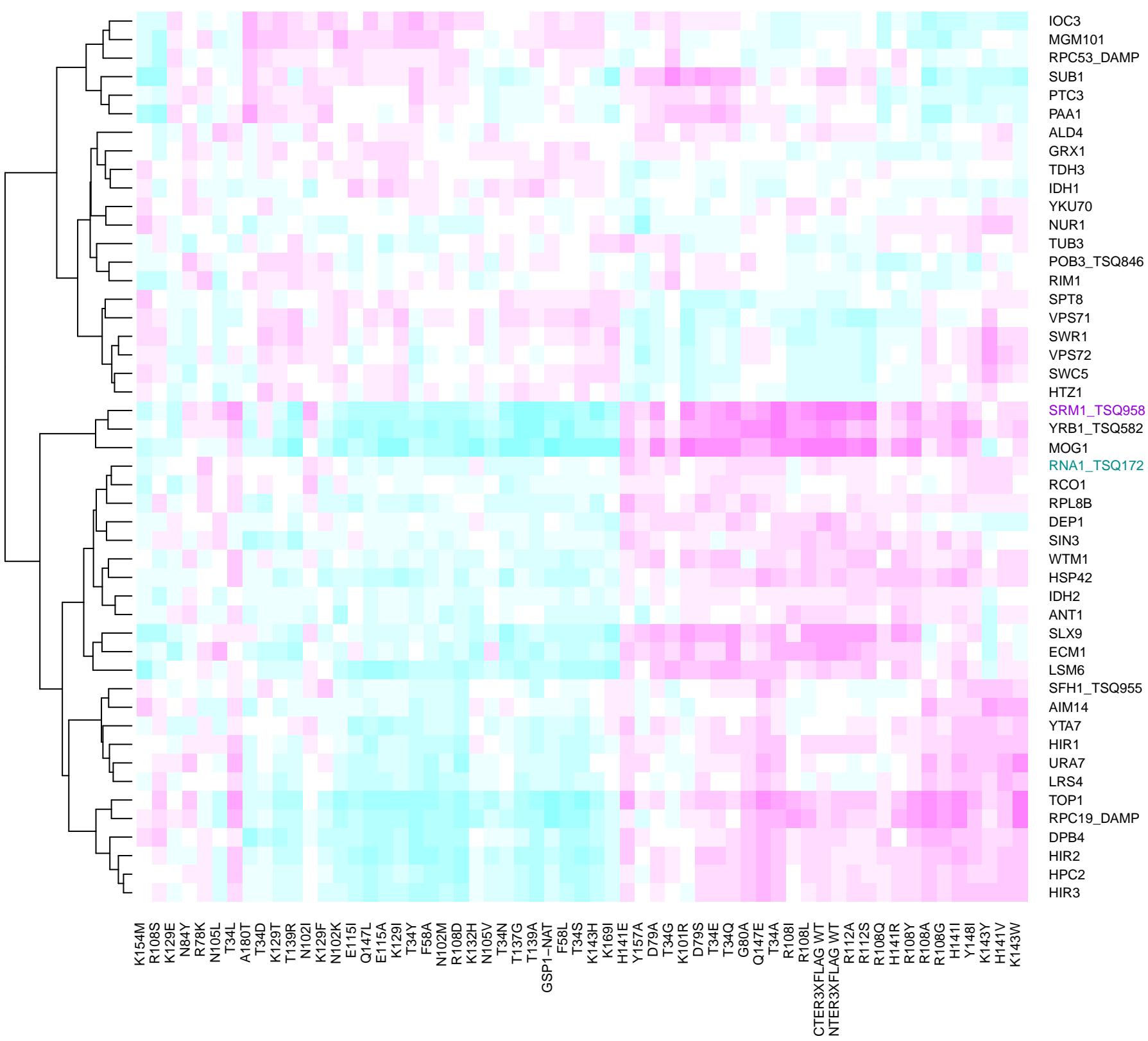


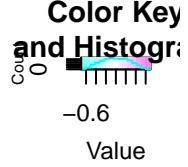
ribosome_GO_30_3



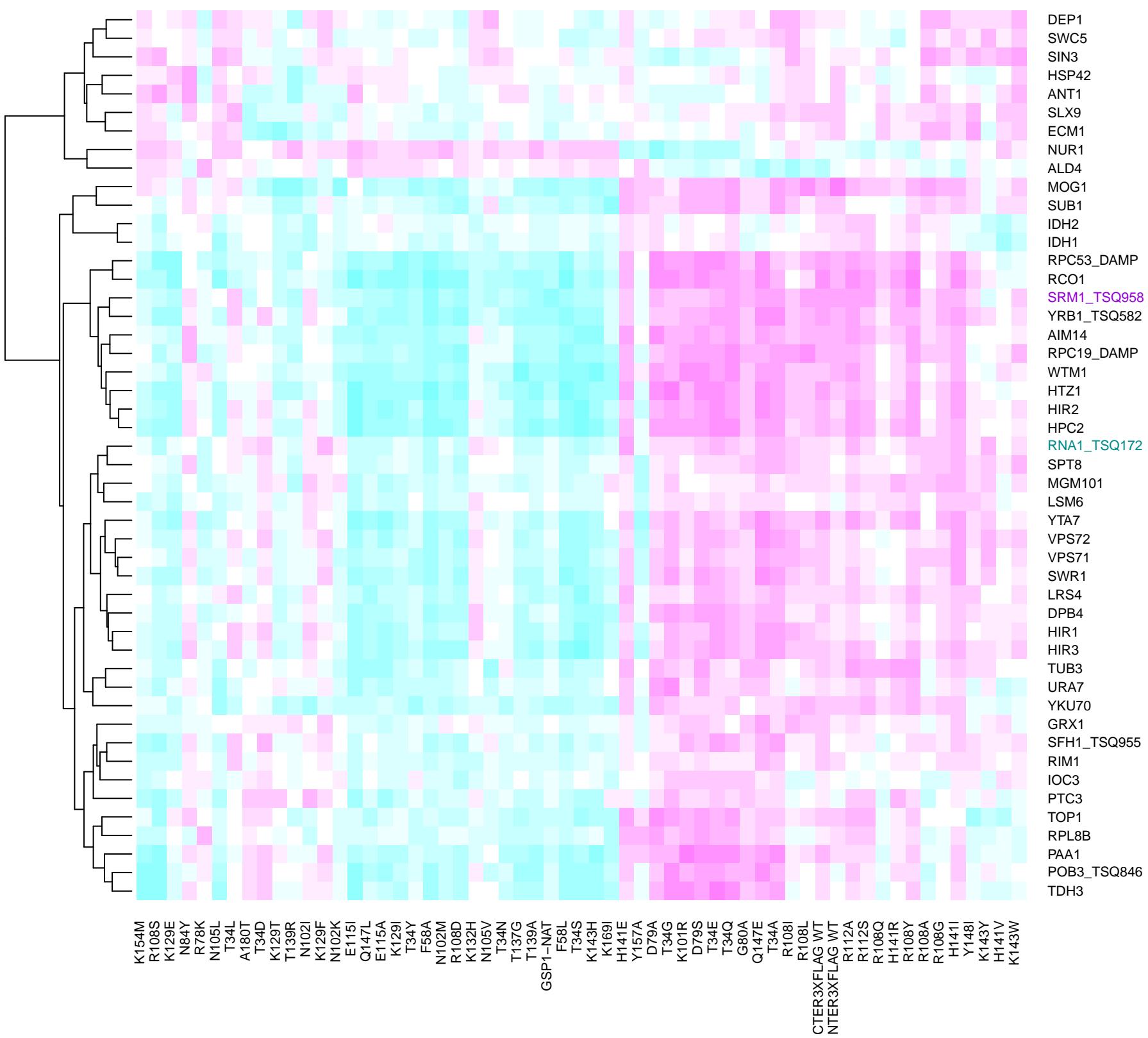


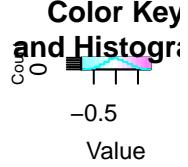
ribosomes and translation_GO_30_2





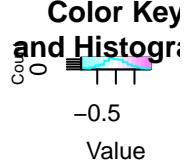
carbohydrate metabolic process_GO_30_3



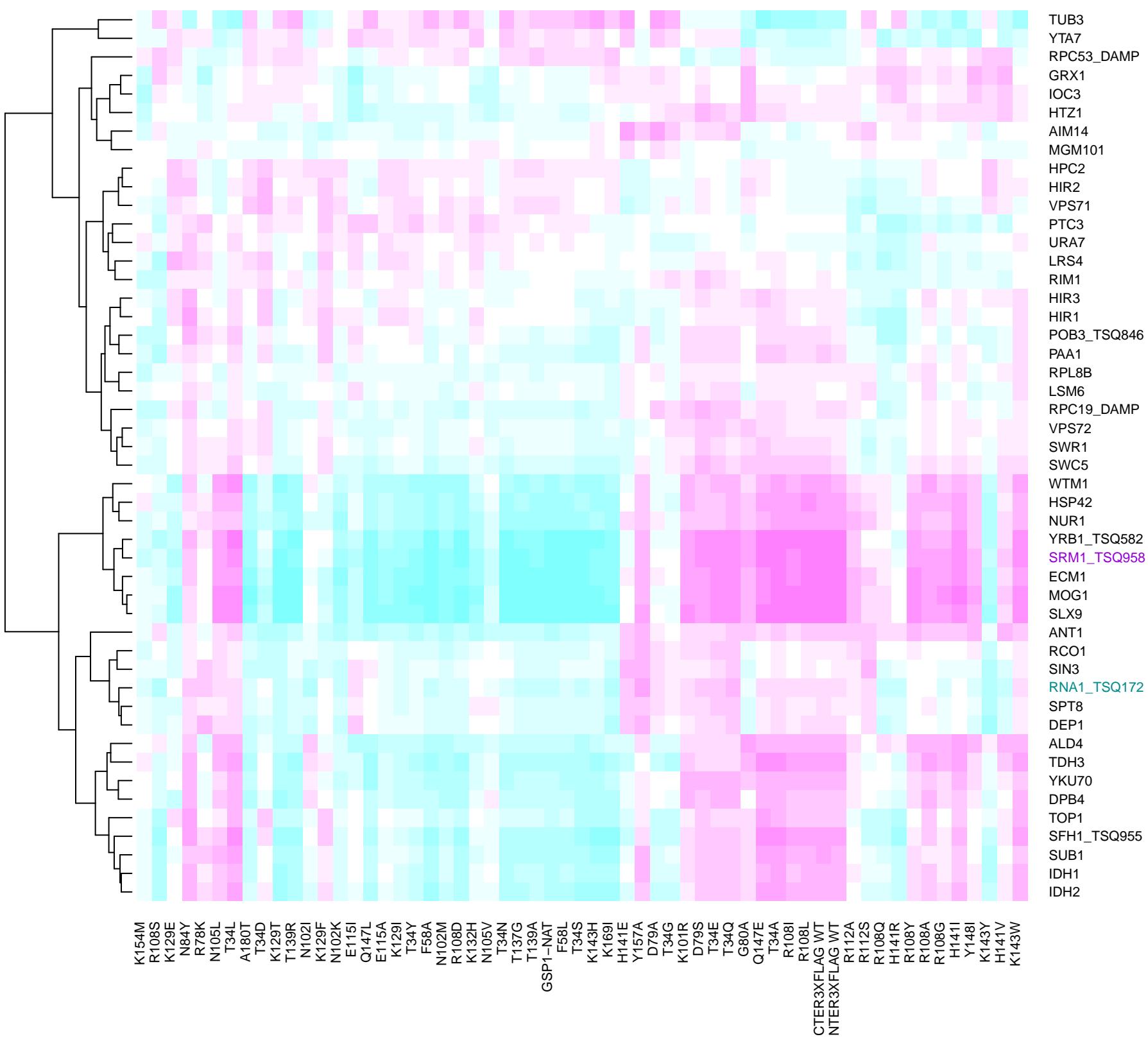


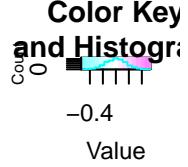
budding_GO_30_8



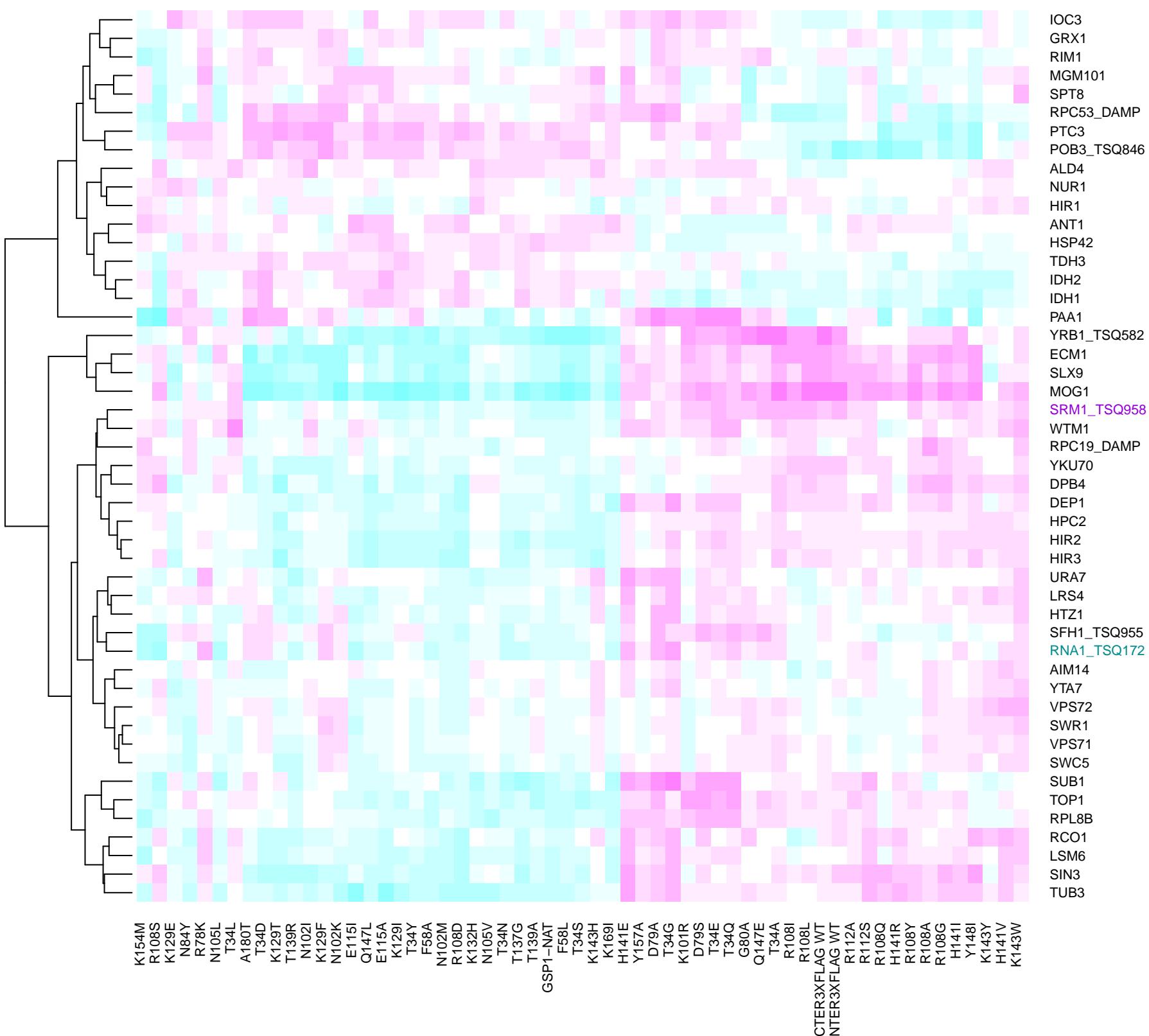


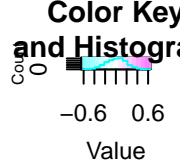
cytoskeleton and microtubules_GO_30_5



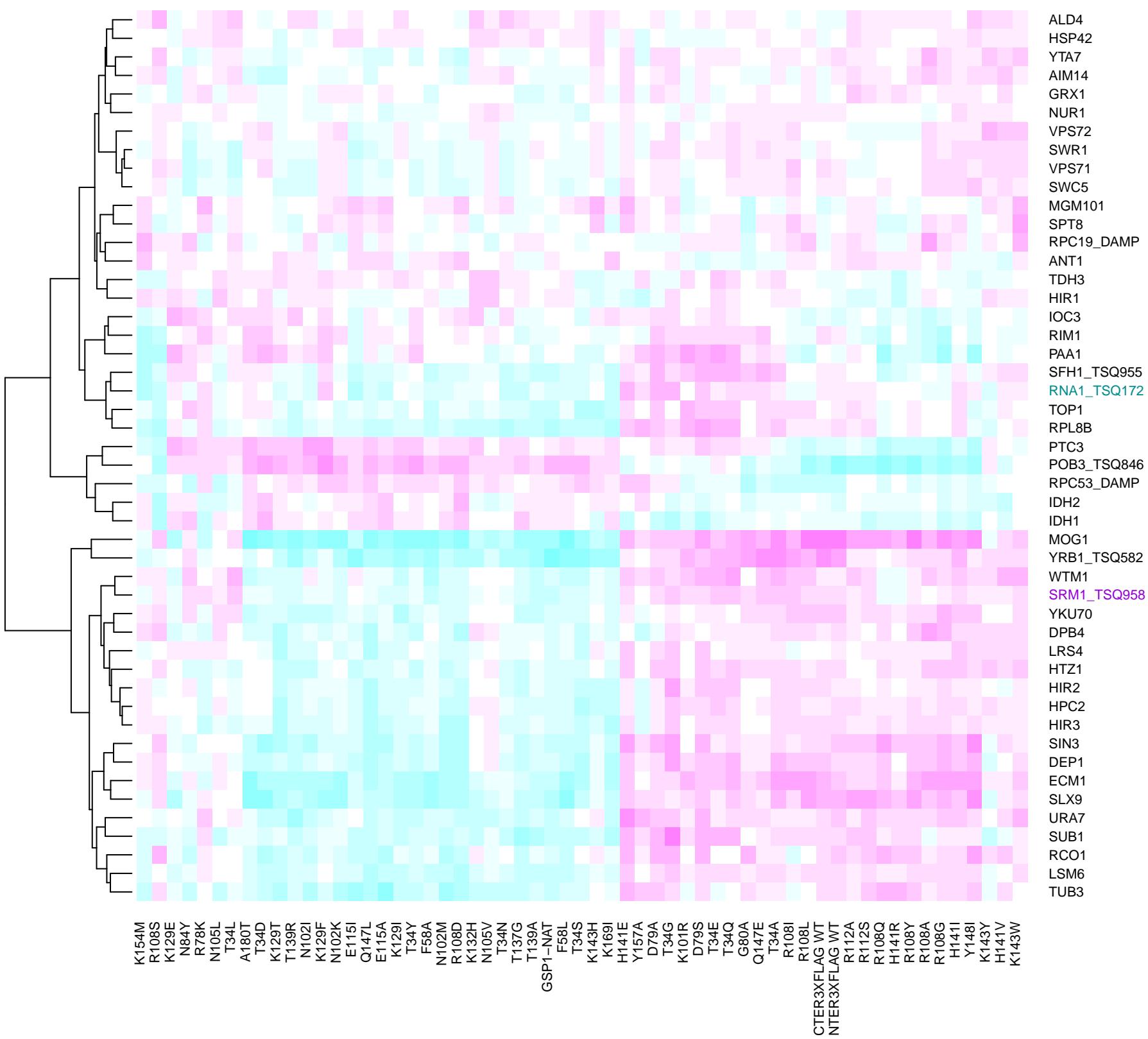


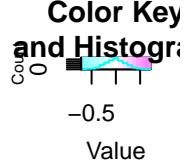
cofactor metabolic process



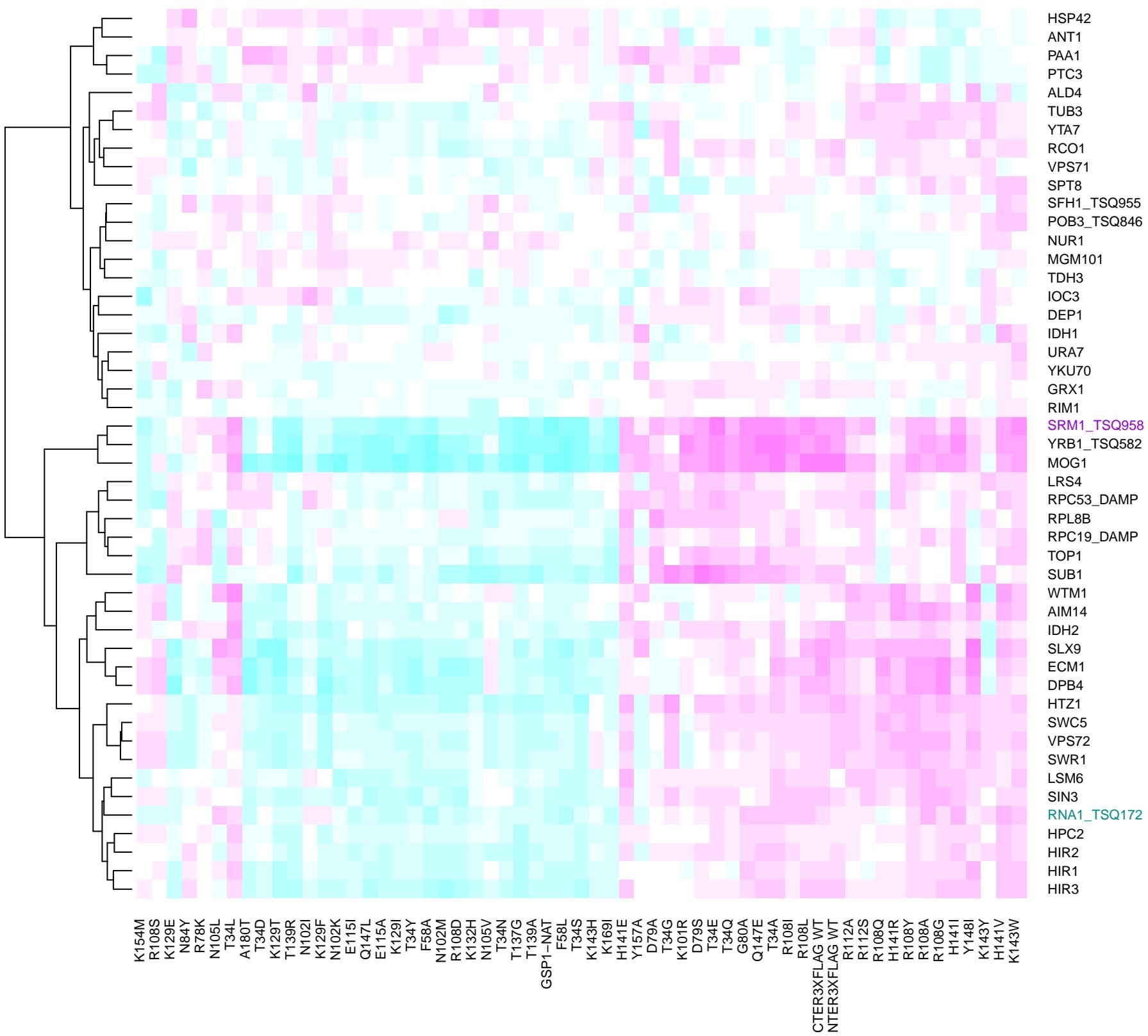


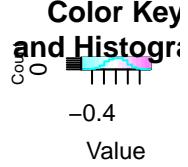
cofactor metabolic process_GO_30_1



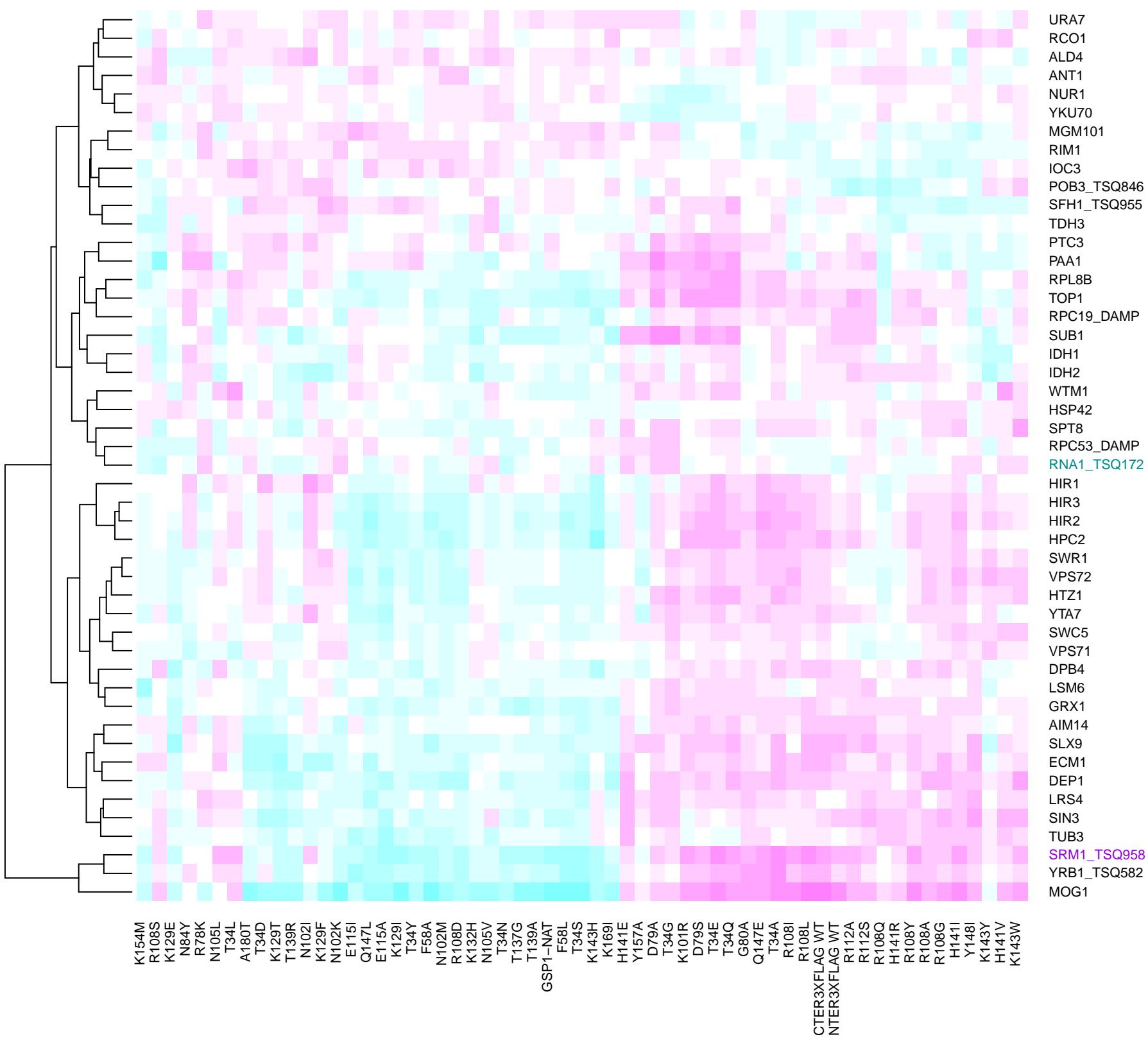


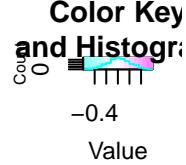
metabolic_GO_30_5



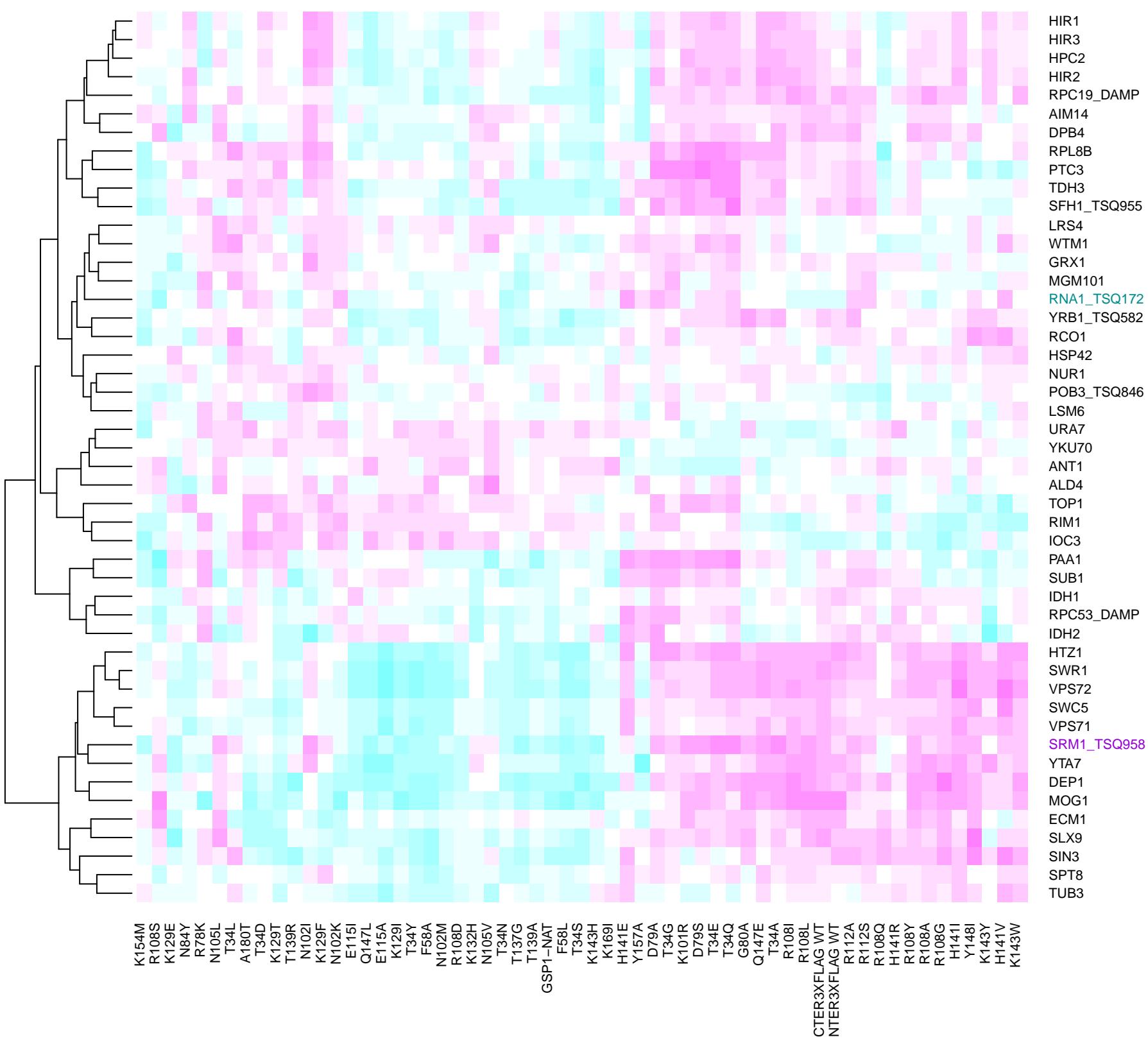


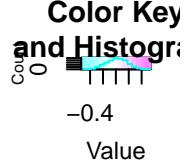
monocarboxylic acid metabolic process



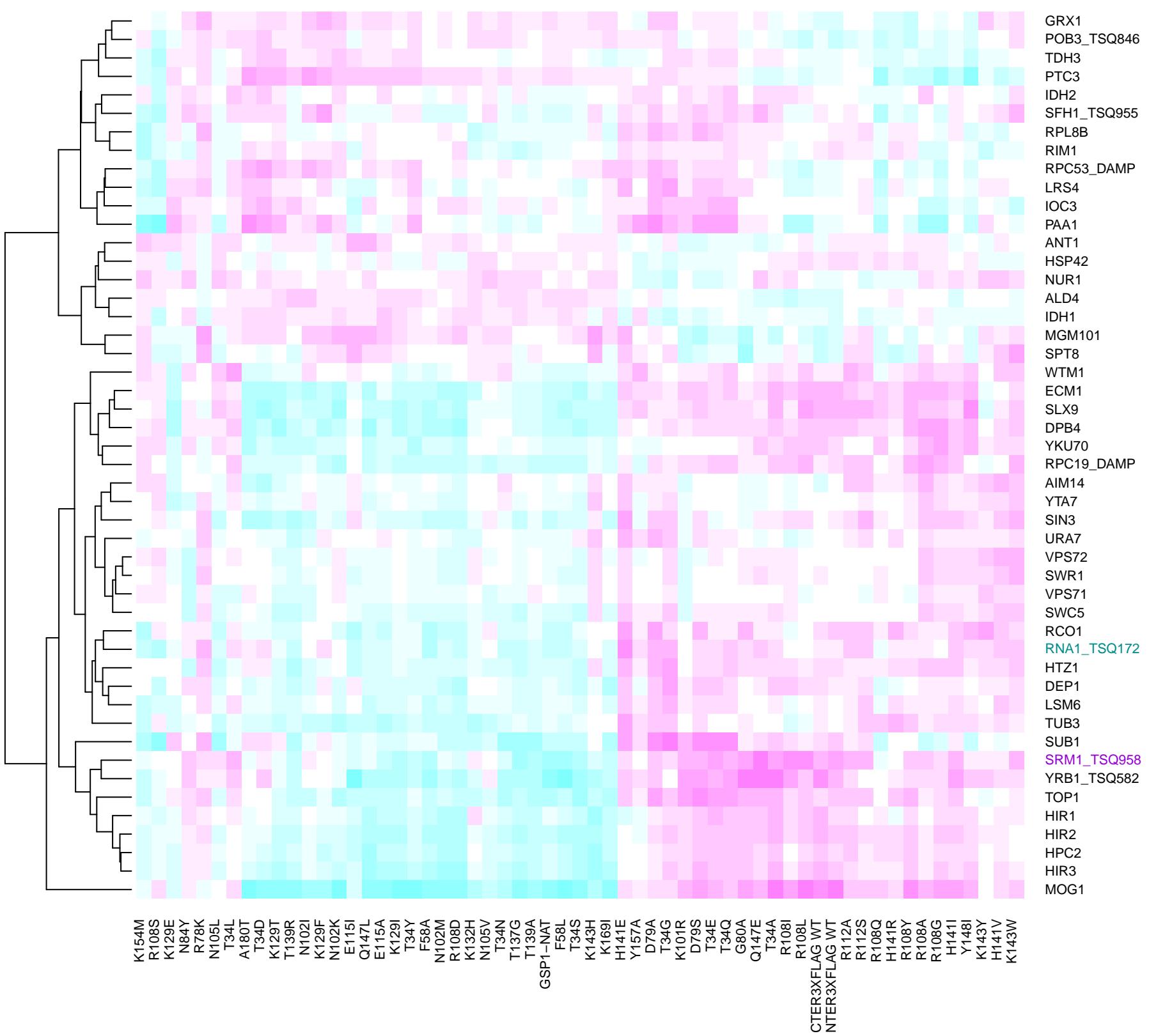


monocarboxylic acid metabolic process_GO_30_1





nucleobase-containing small molecule metabolic process

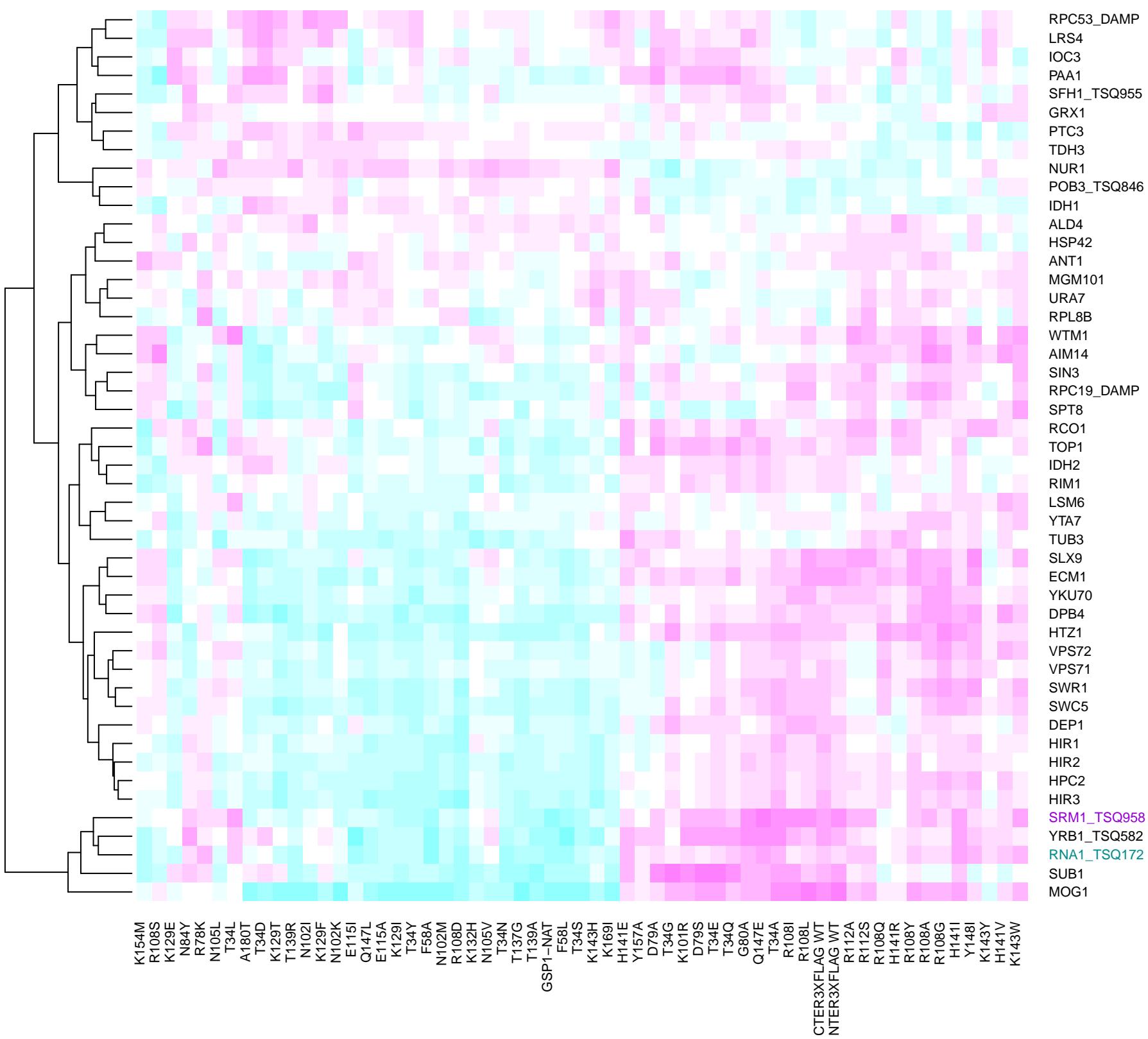


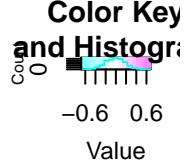
Color Key
and Histogram

-0.6 0.6

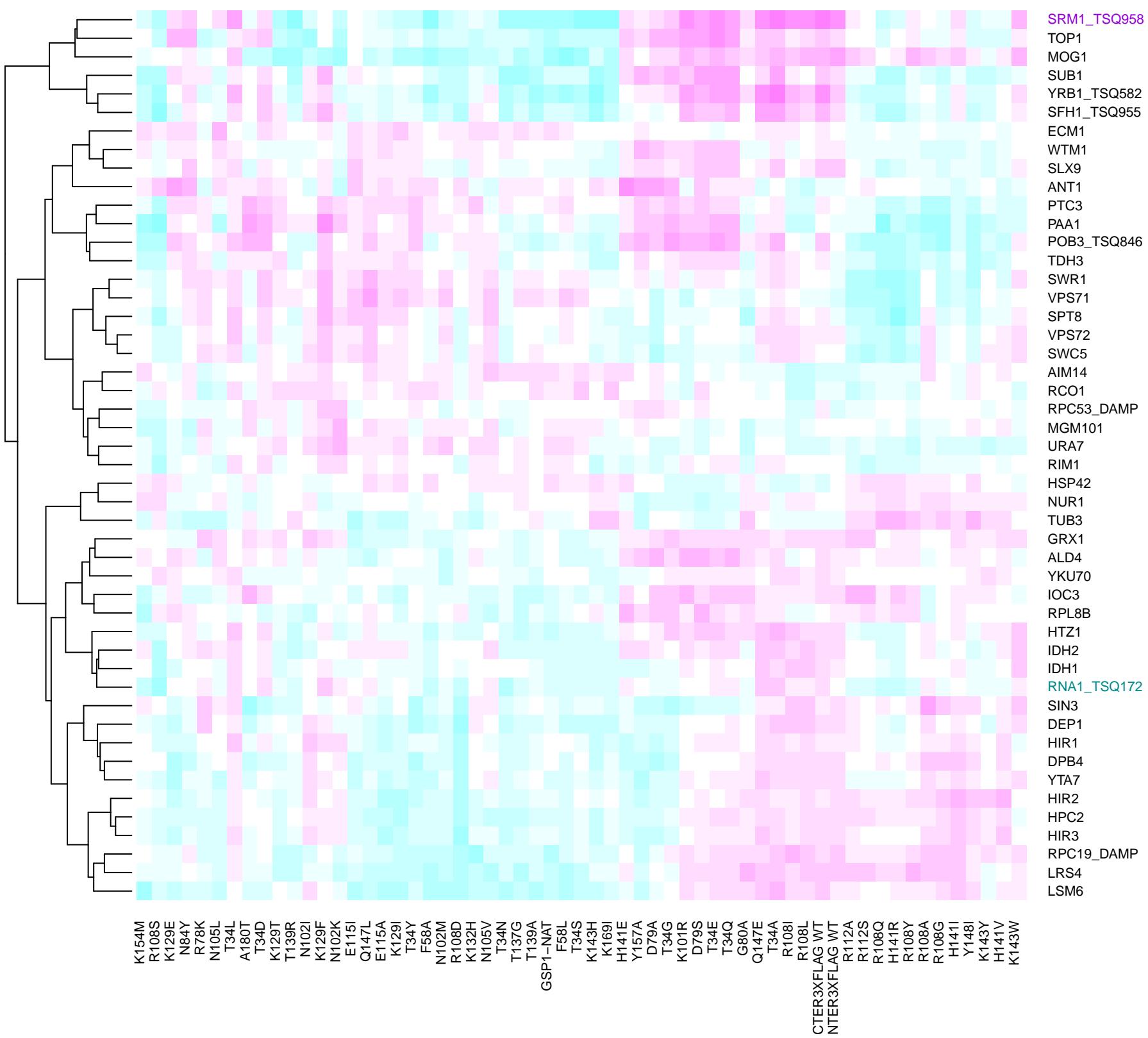
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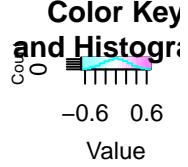
leobase-containing small molecule metabolic process_GO_30_2



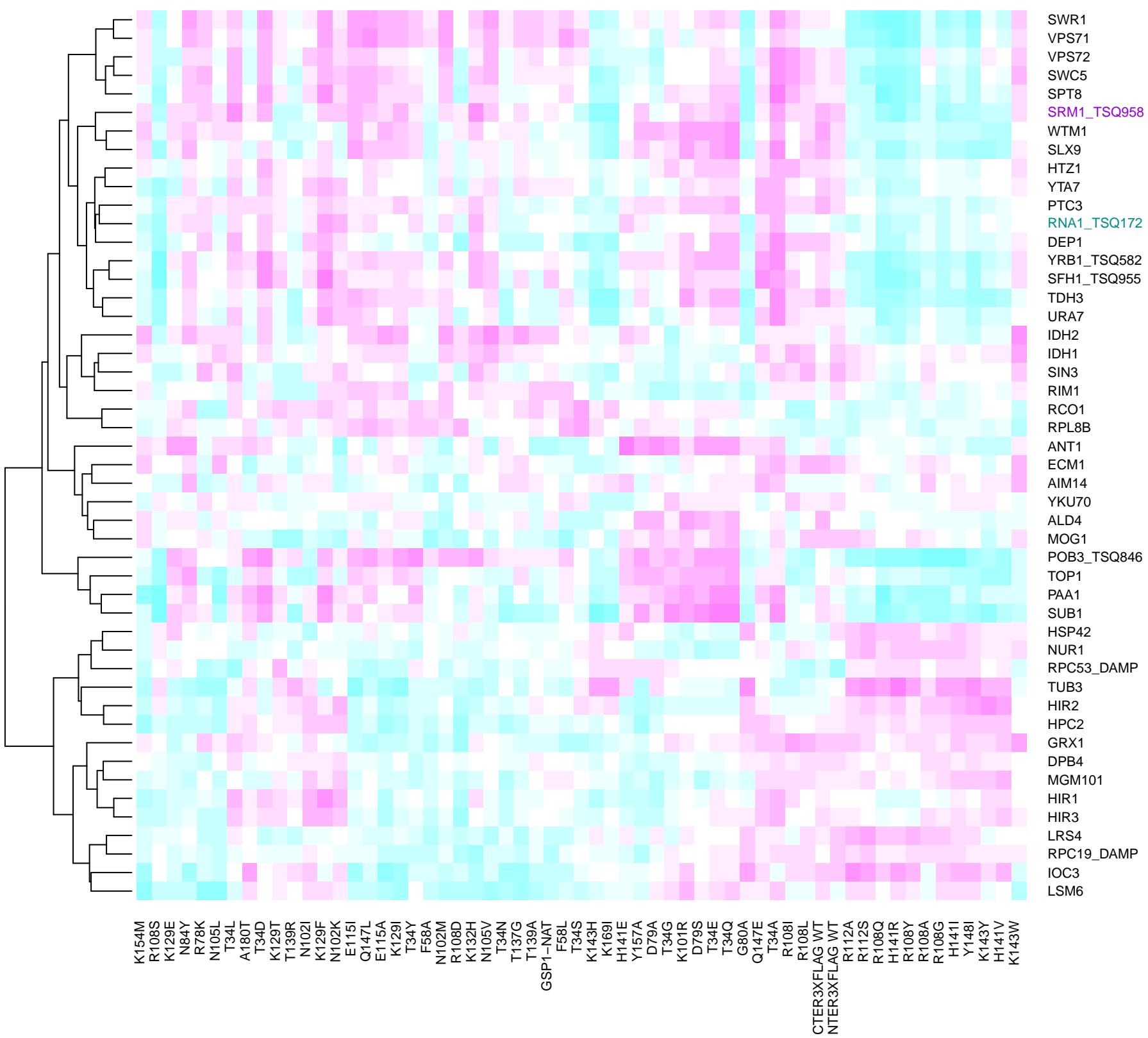


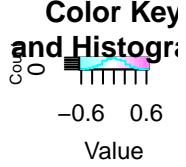
vacuole organization





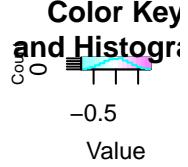
vacuole organization_GO_30_2



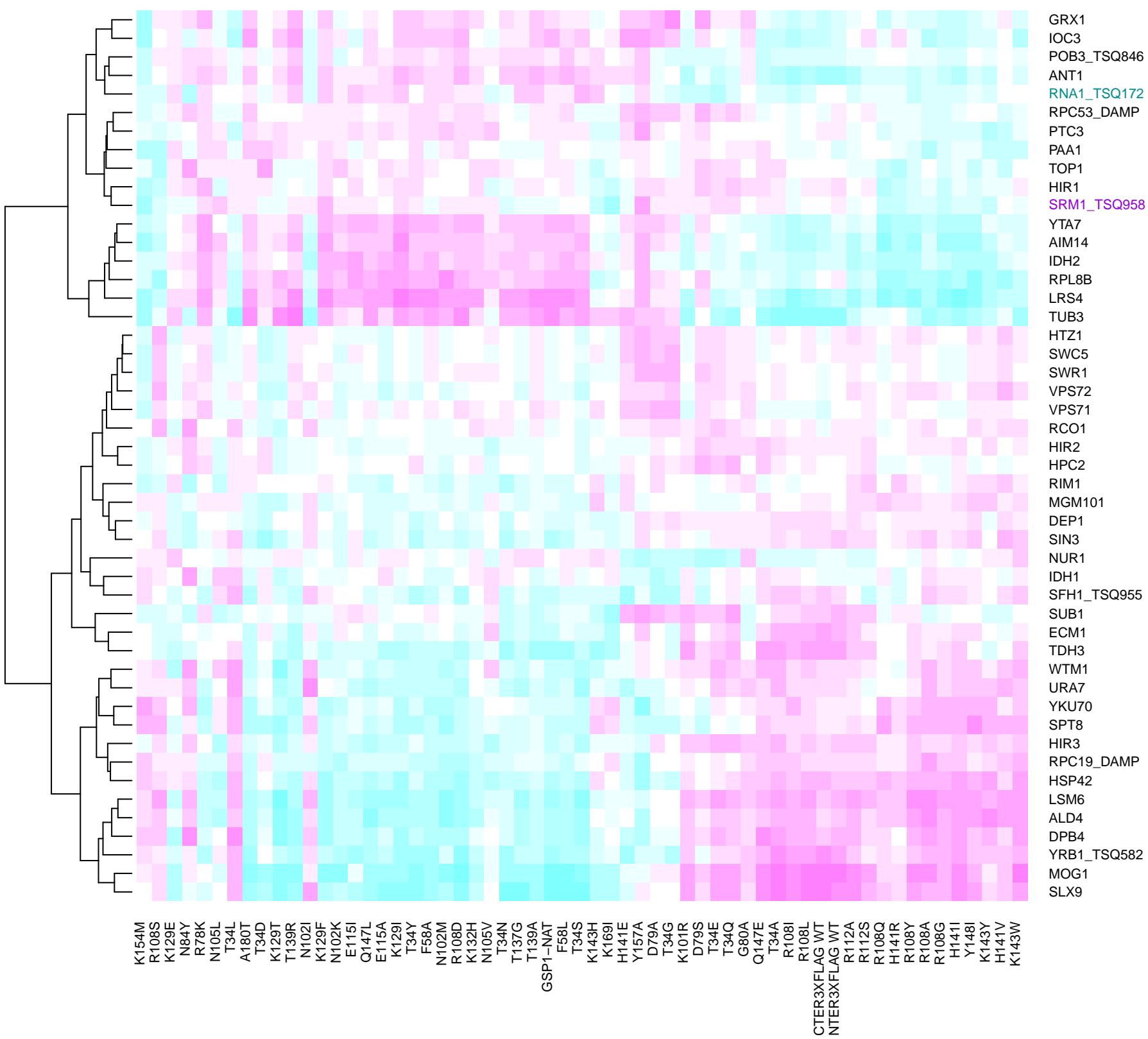


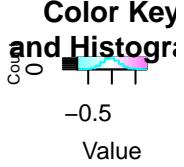
vacuoles_GO_30_4



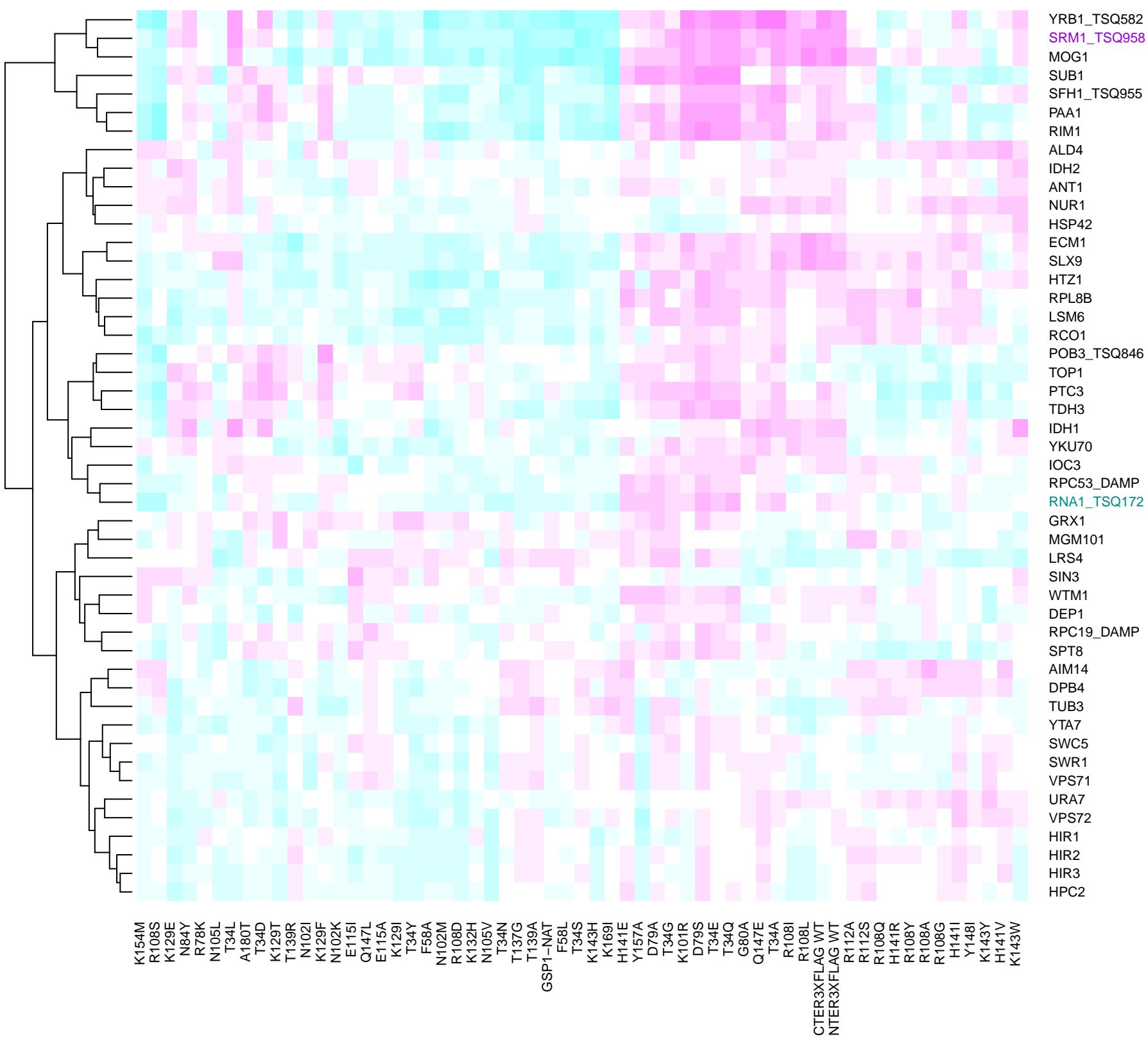


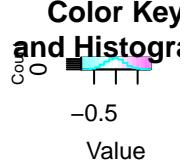
cytoskeleton_GO_30_4



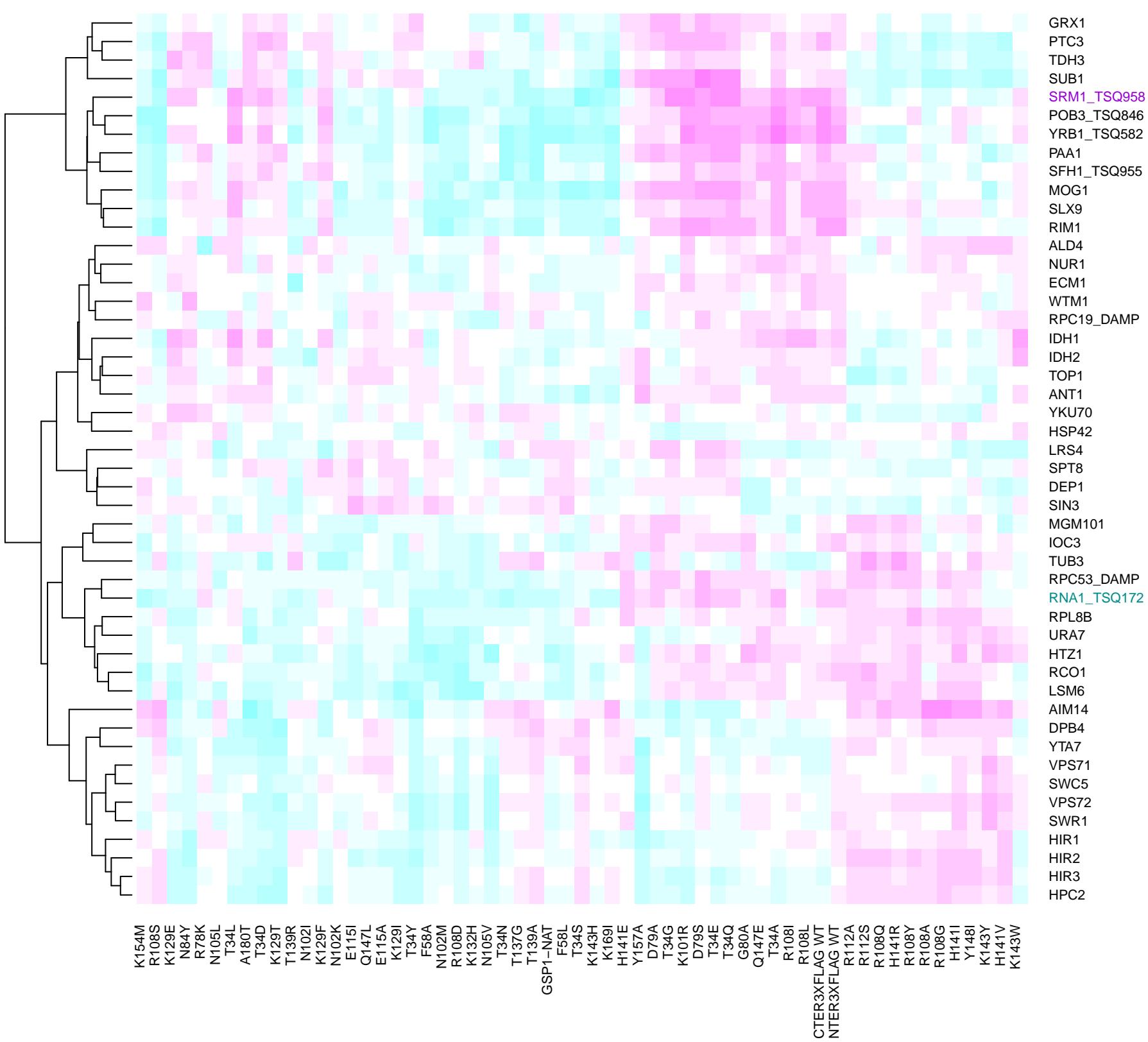


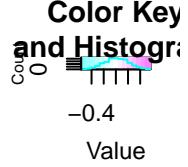
cytokinesis



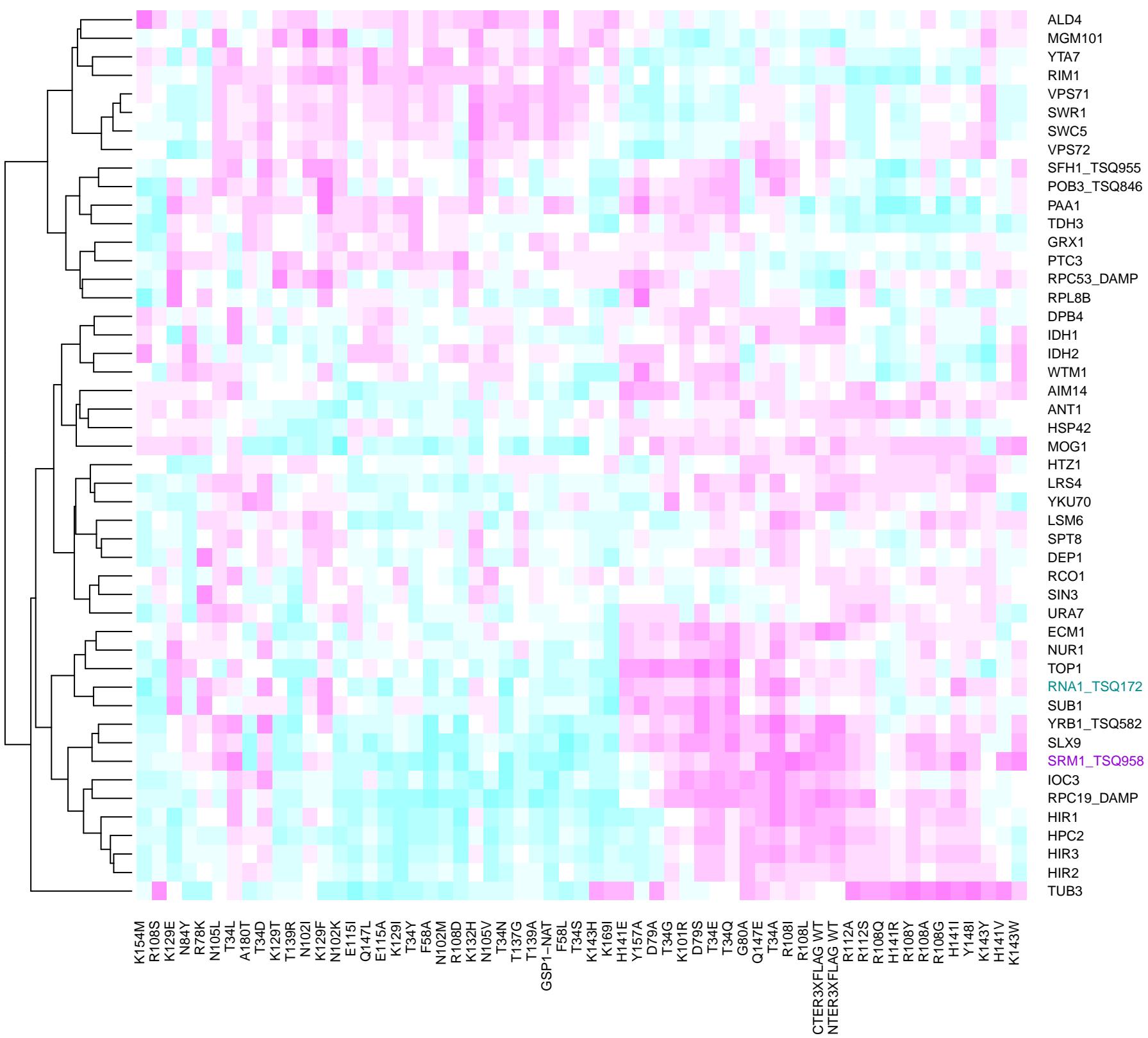


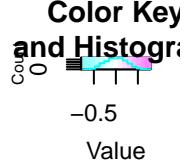
cytokinesis_GO_30_1



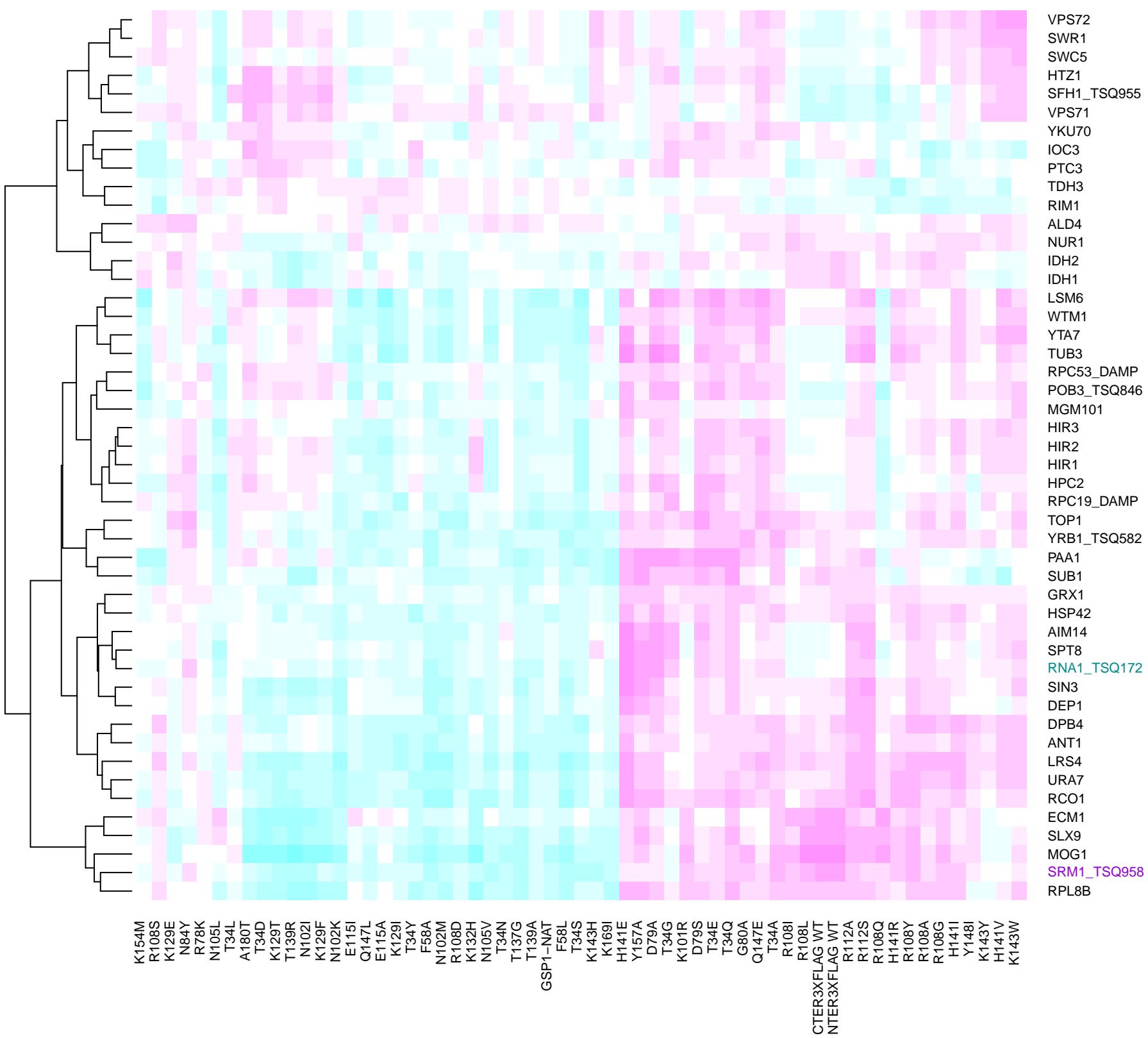


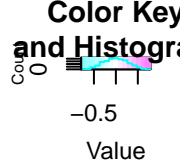
cytoplasmic vesicle_GO_30_3



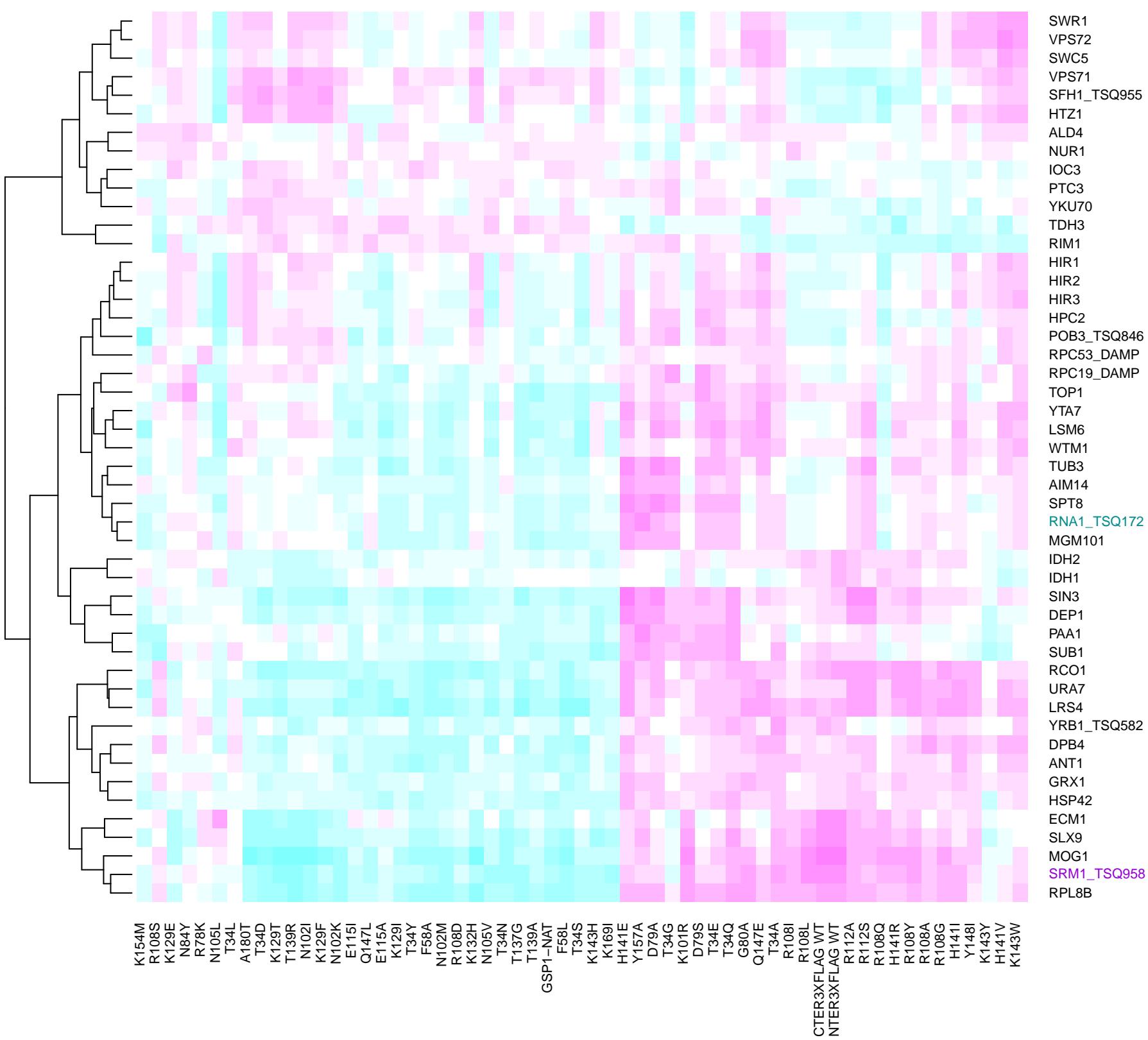


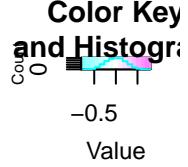
mRNA processing



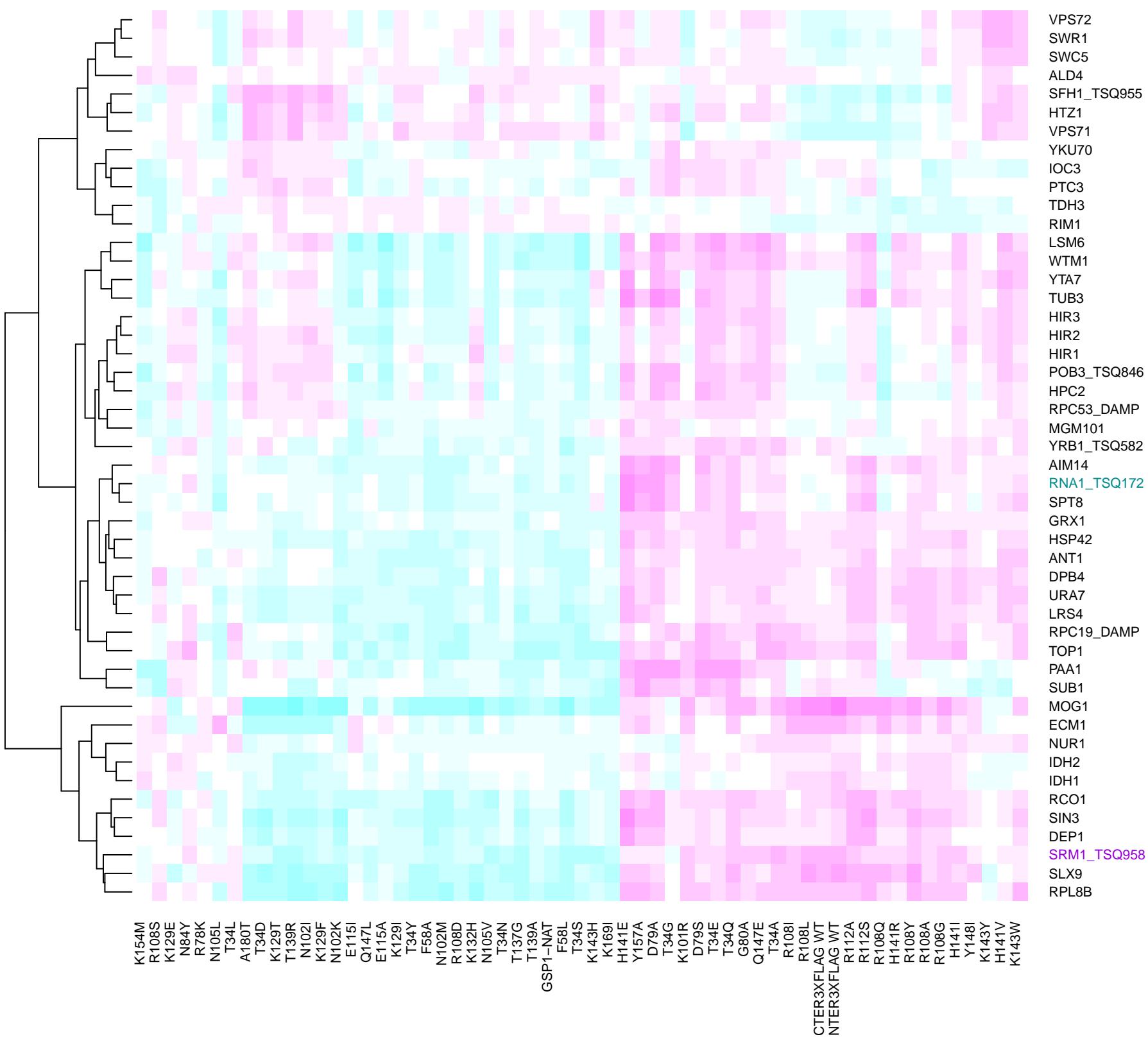


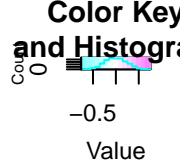
mRNA processing_GO_30_1



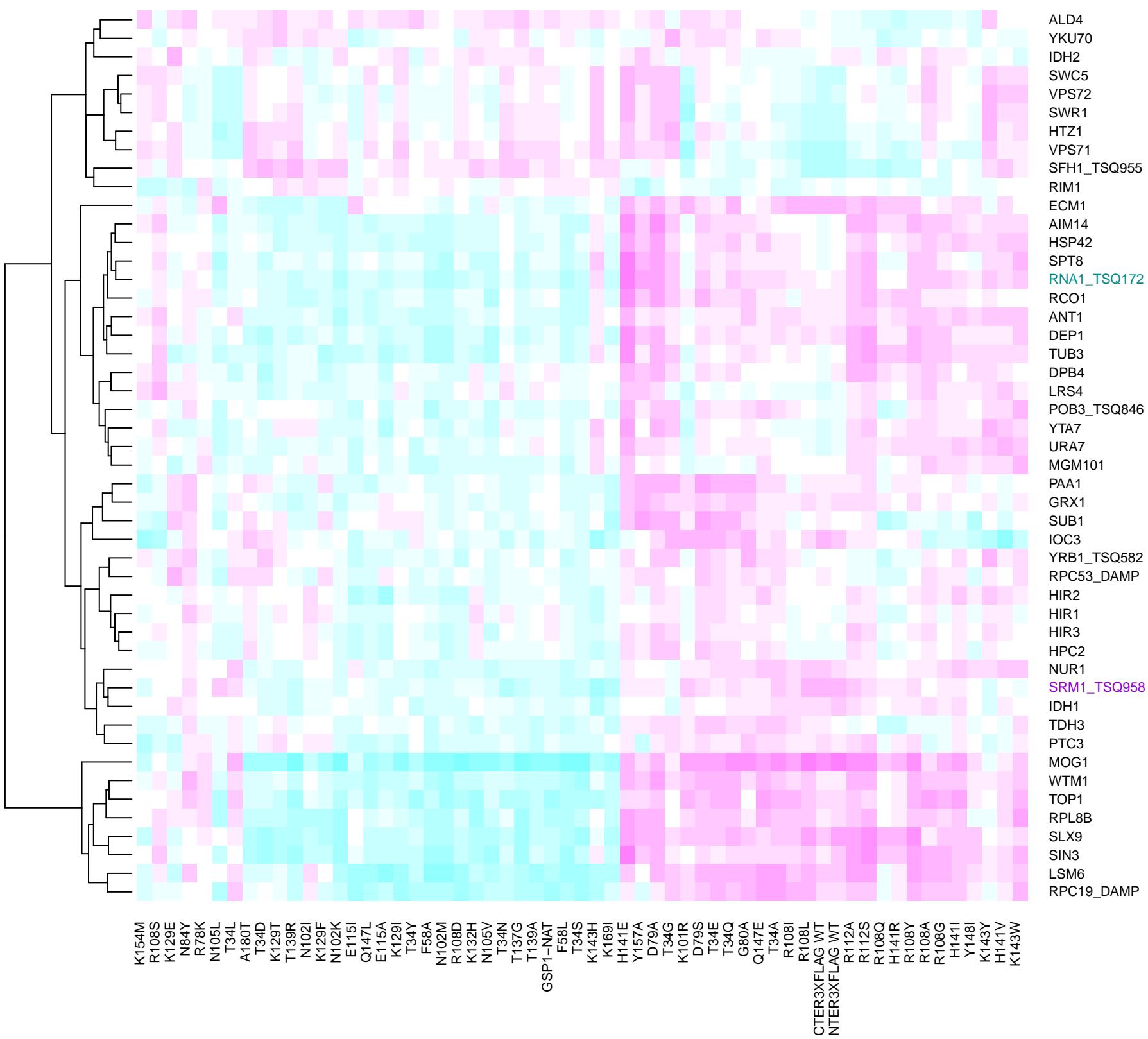


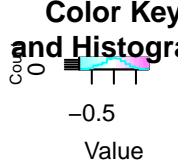
RNA processing



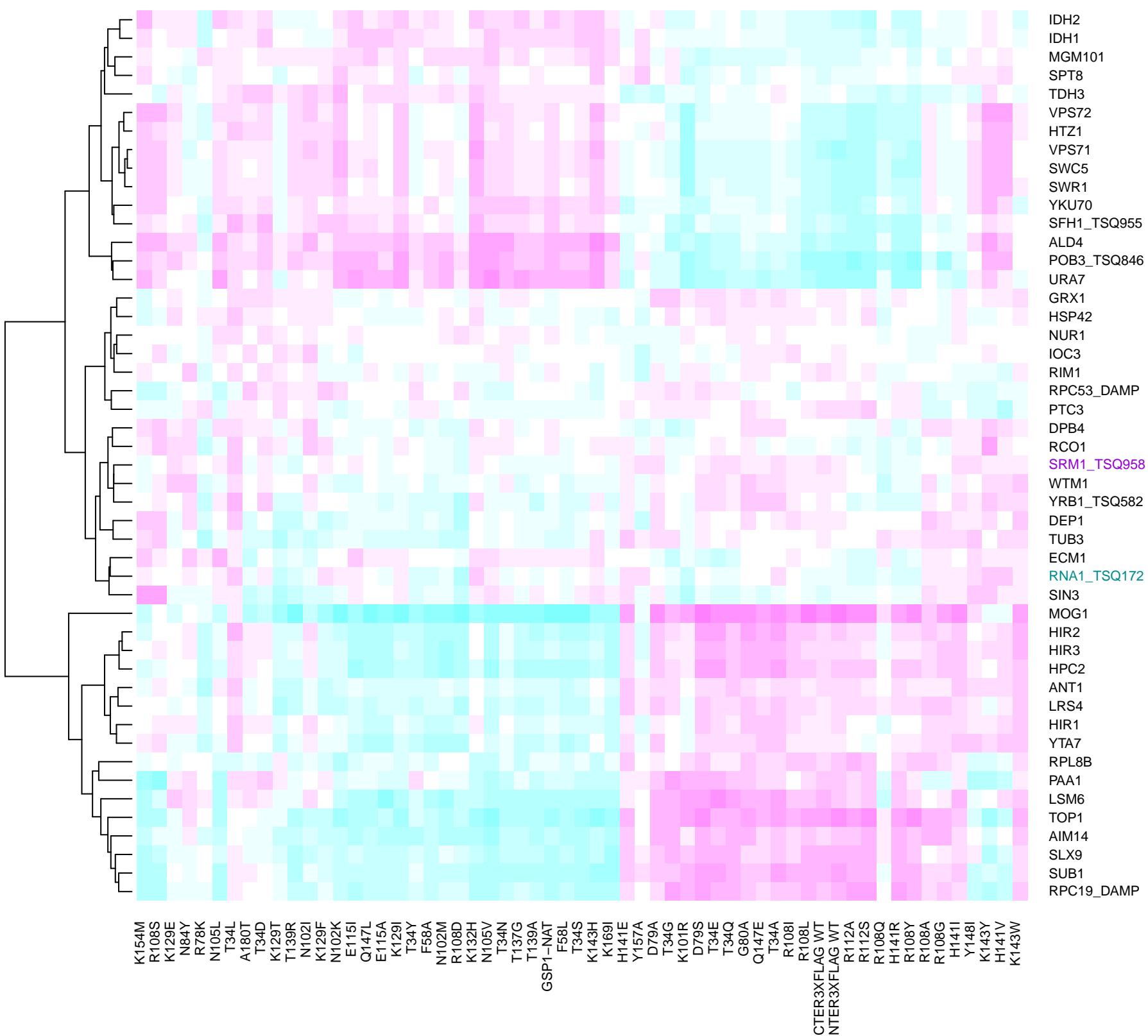


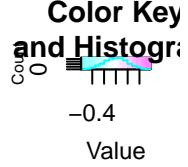
RNA processing_GO_30_1



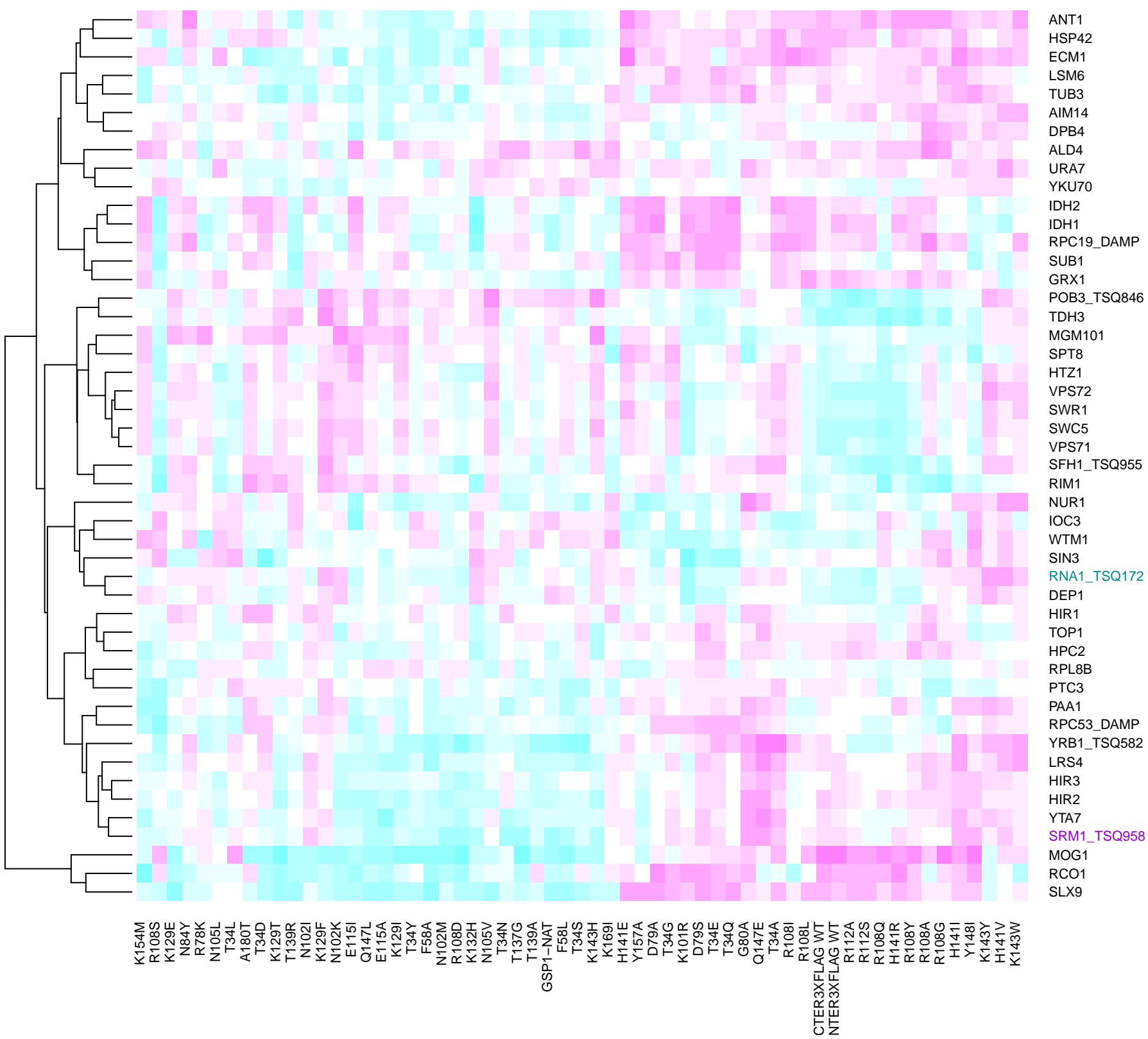


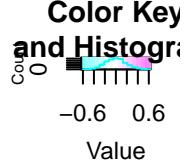
transcription and mRNA processing_GO_30_6



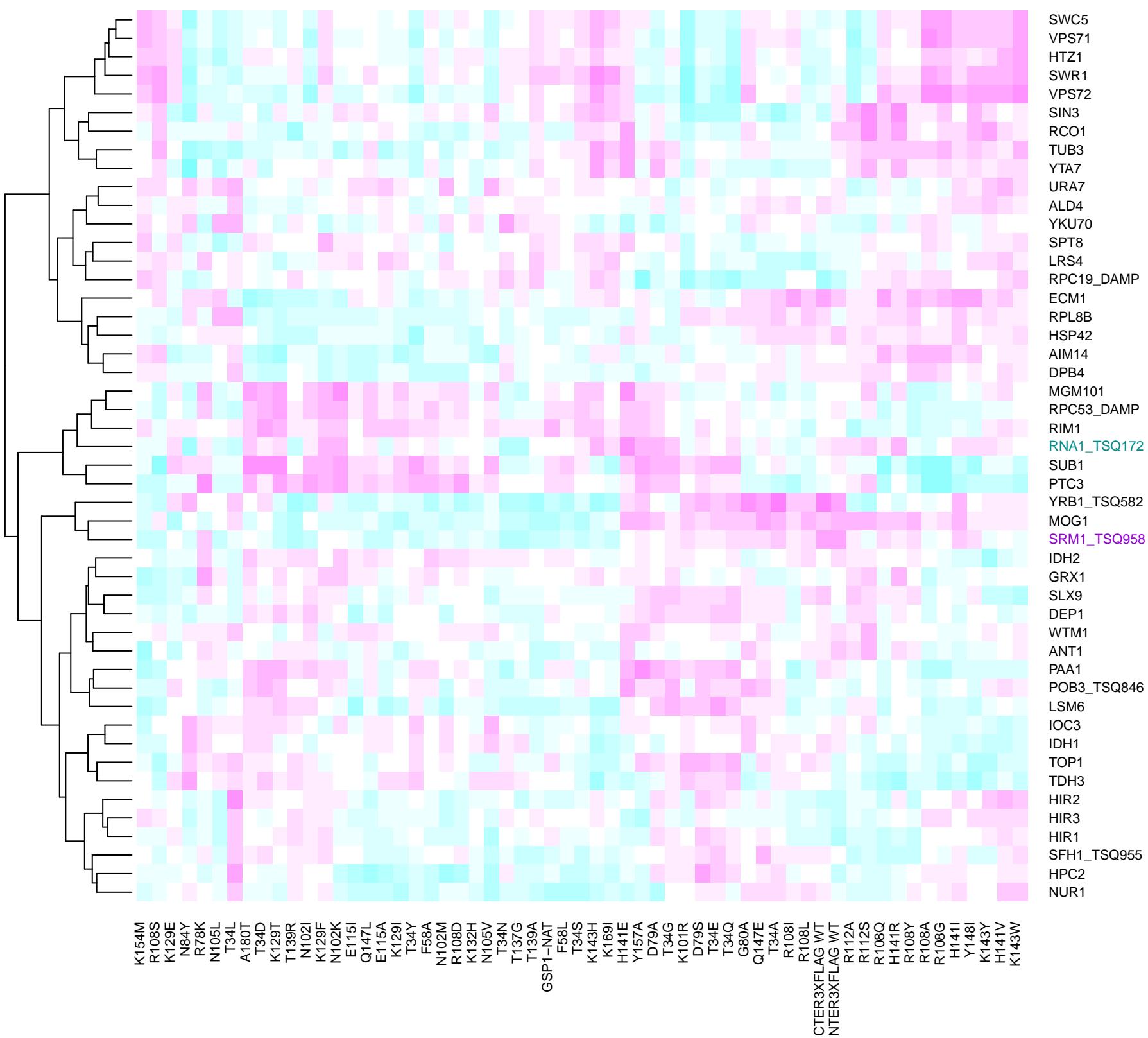


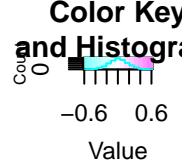
transcription_GO_30_5



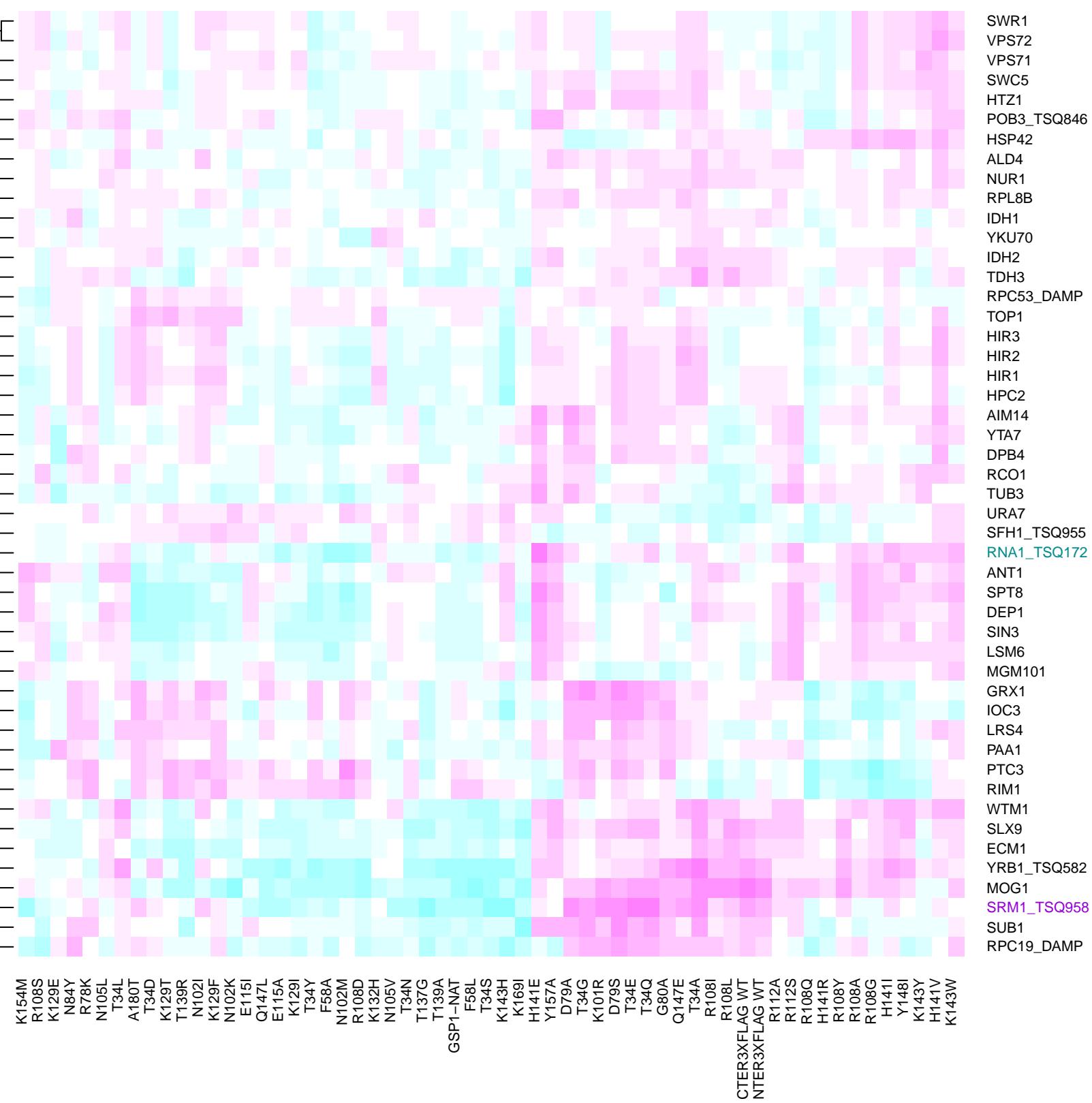


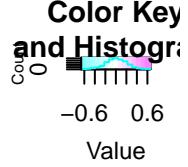
tRNA processing_GO_30_1



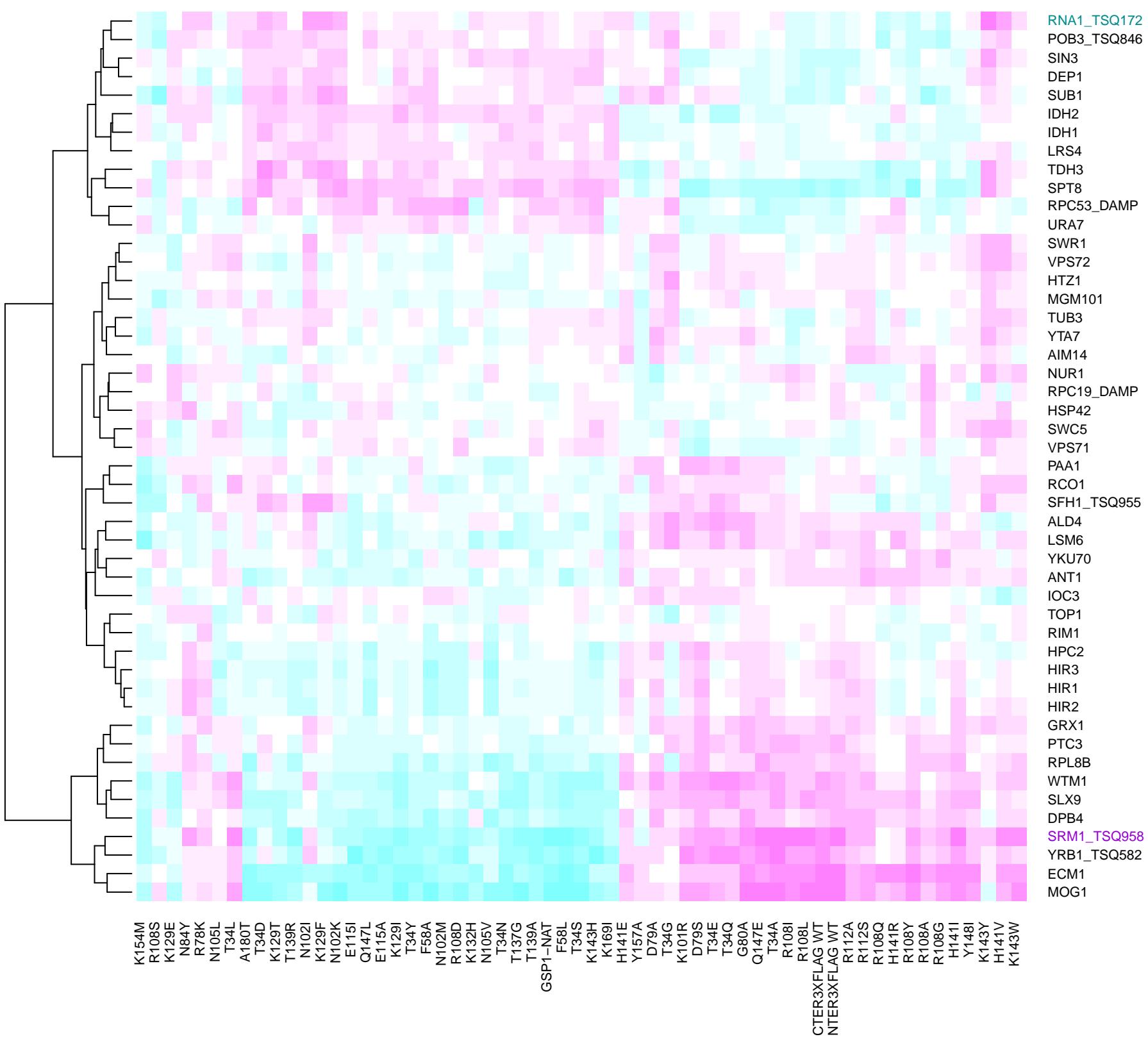


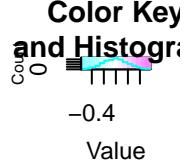
DNA recombination



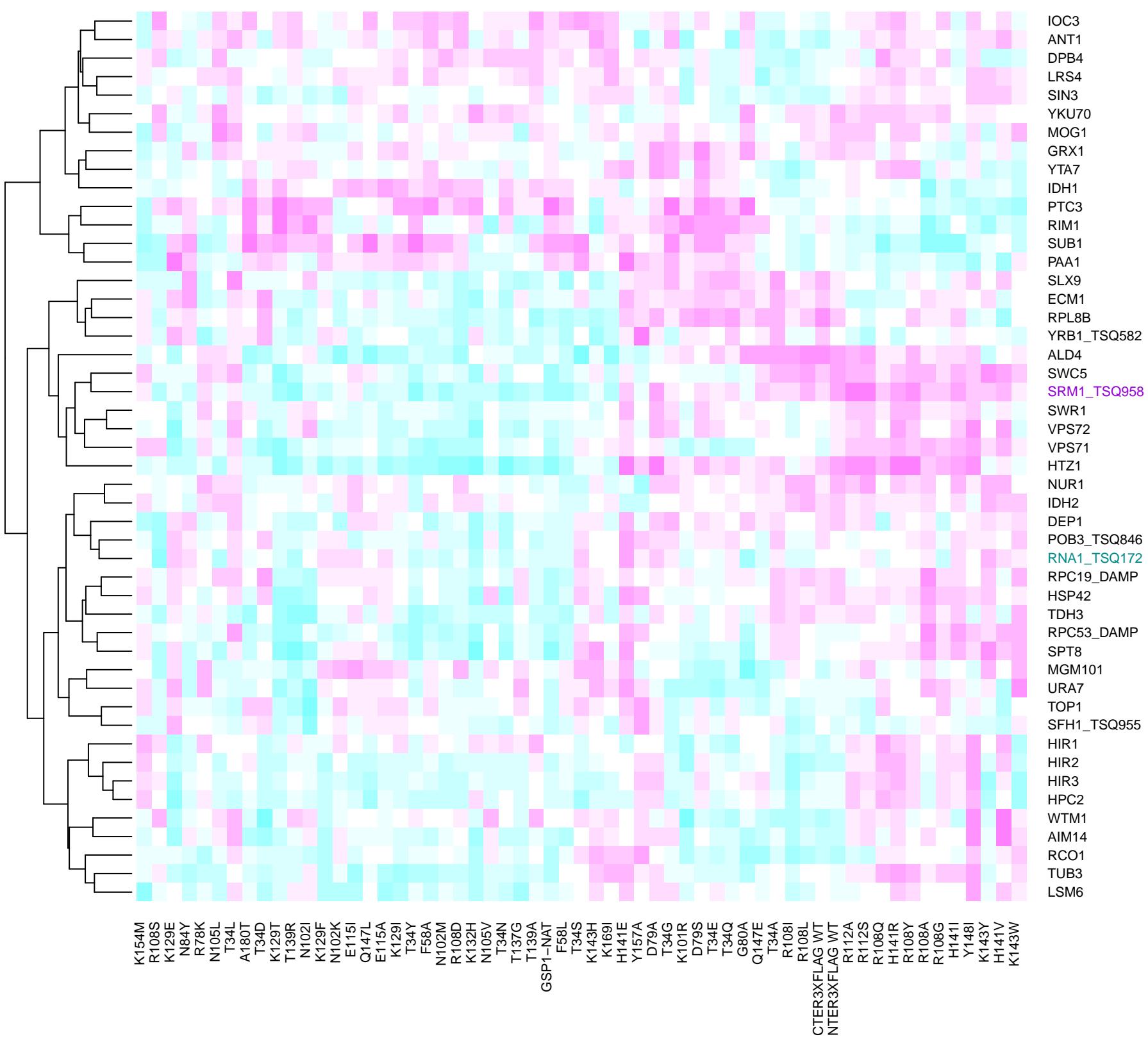


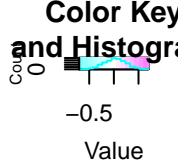
mitochondria and respiration_GO_30_11



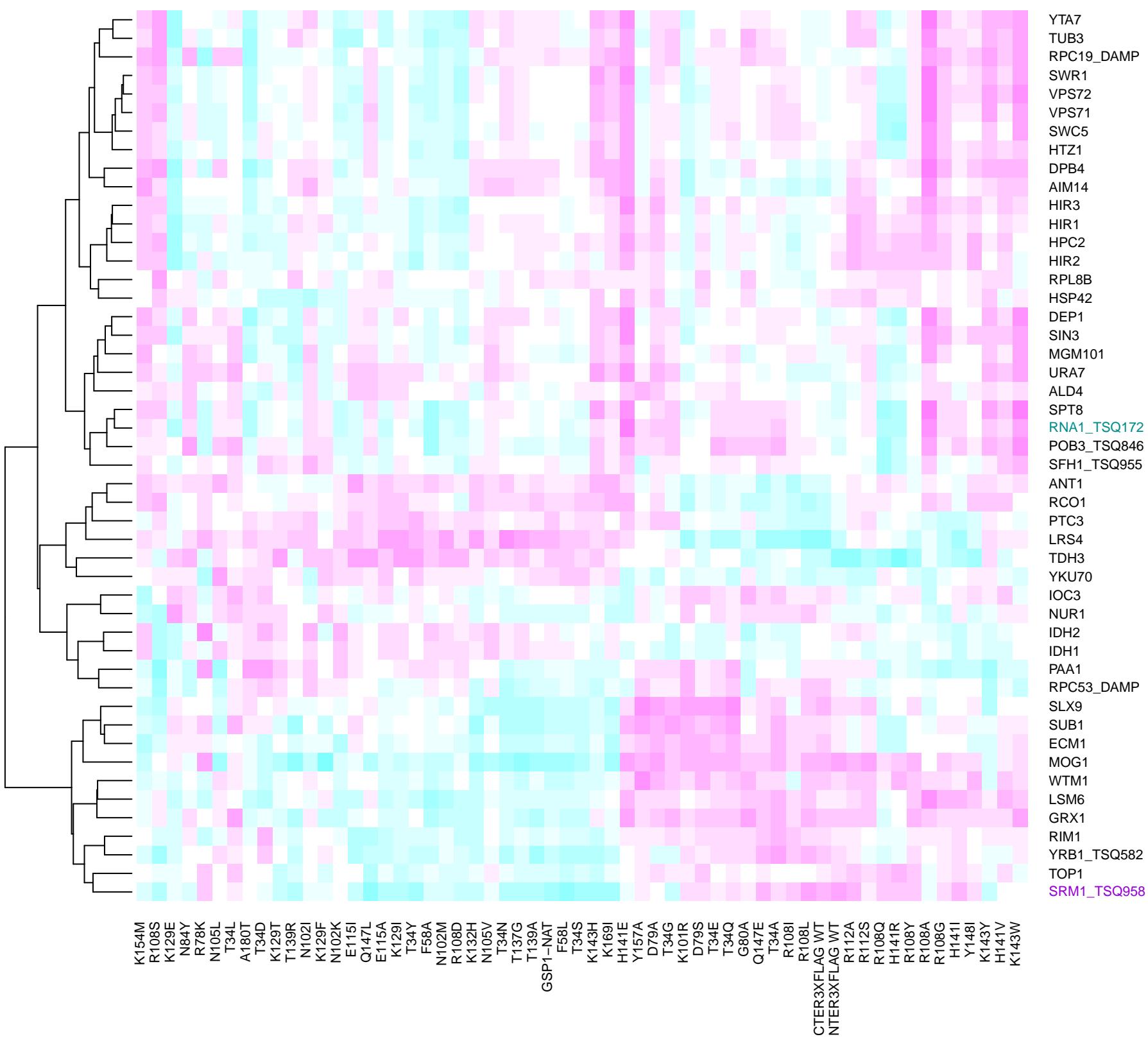


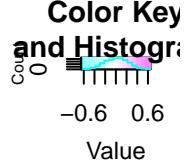
mitochondrion_GO_30_15



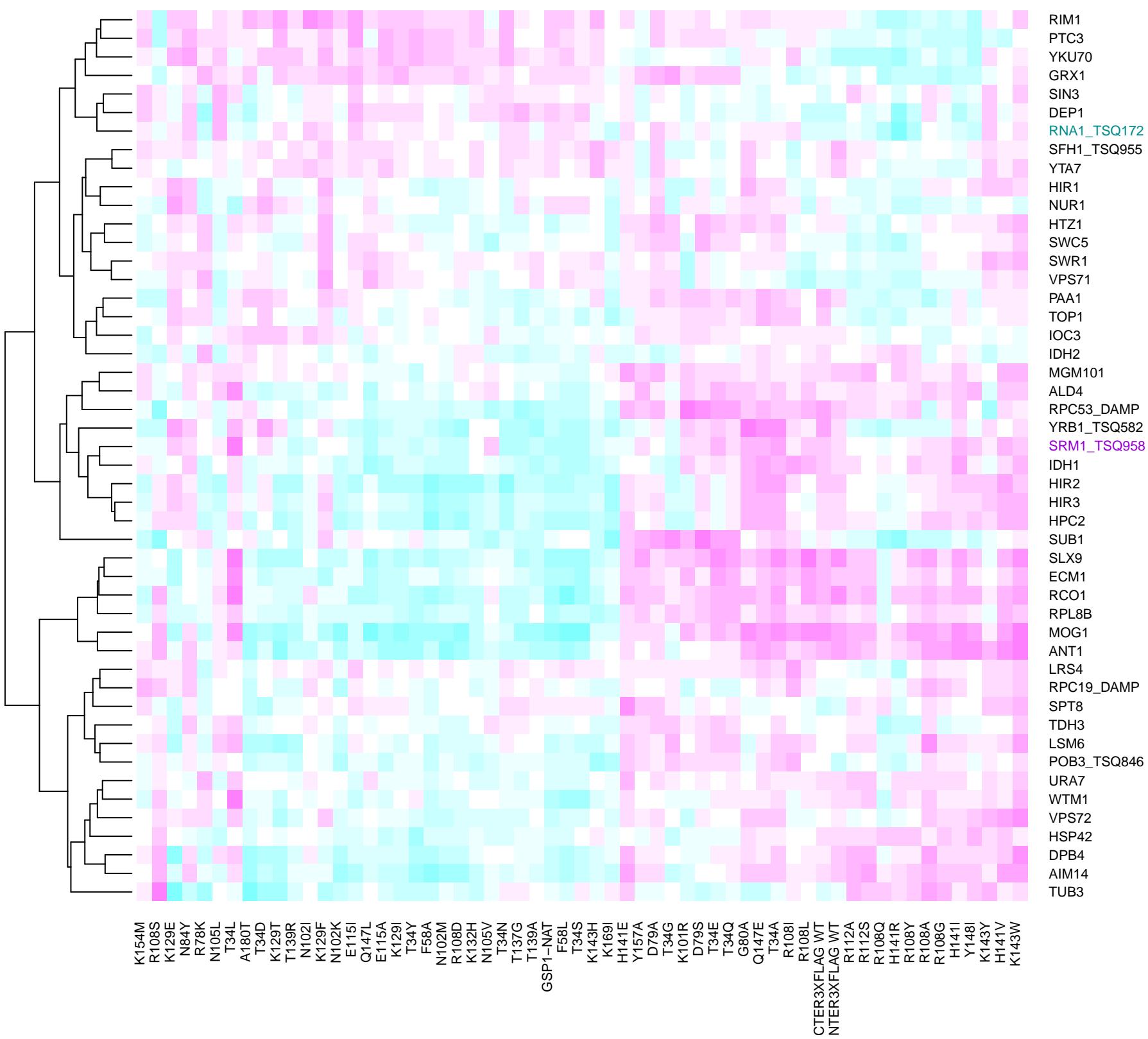


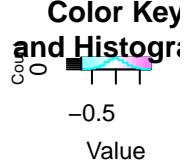
regulation of organelle organization_GO_30_3



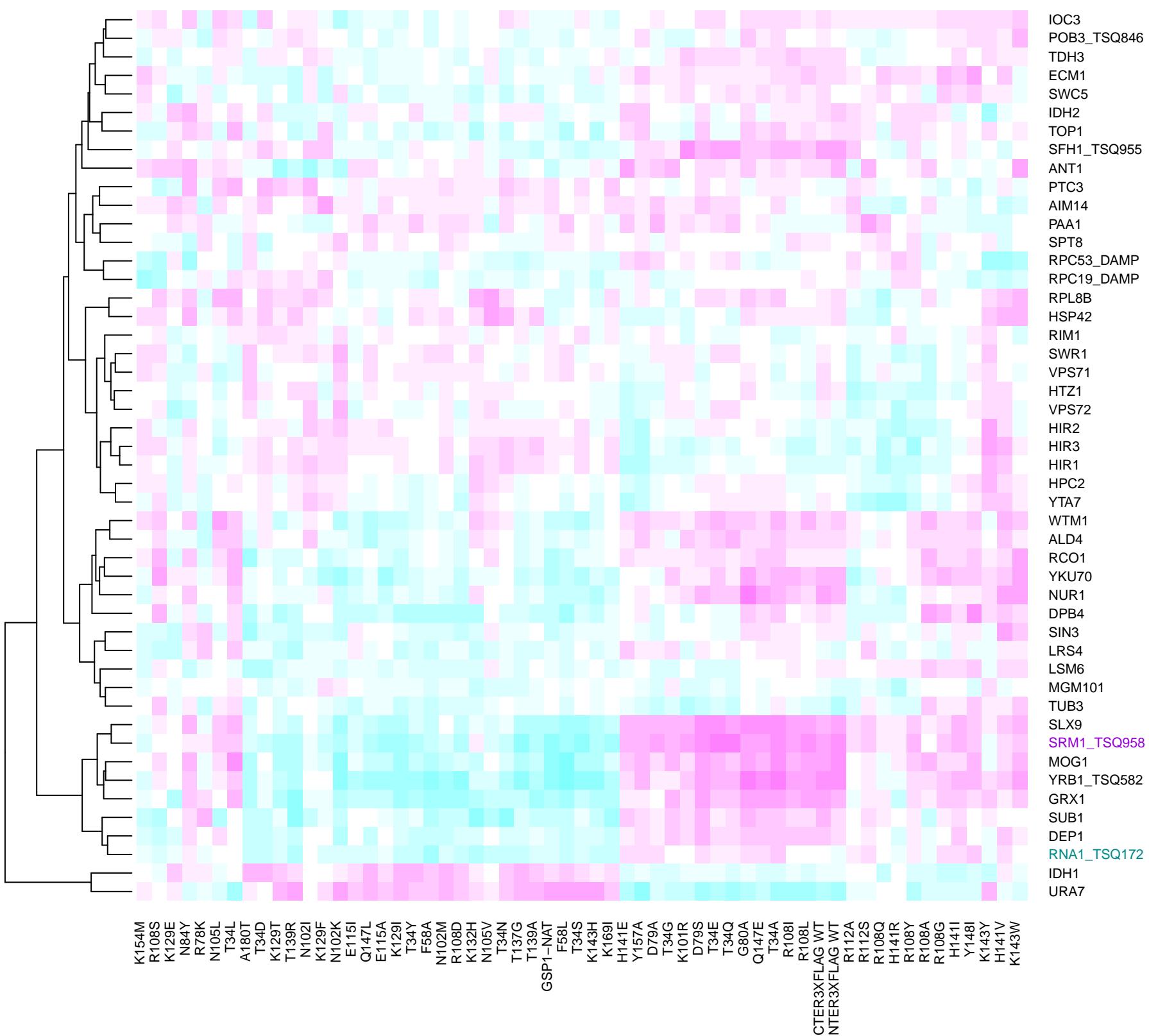


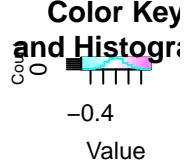
chromatin organization_GO_30_5



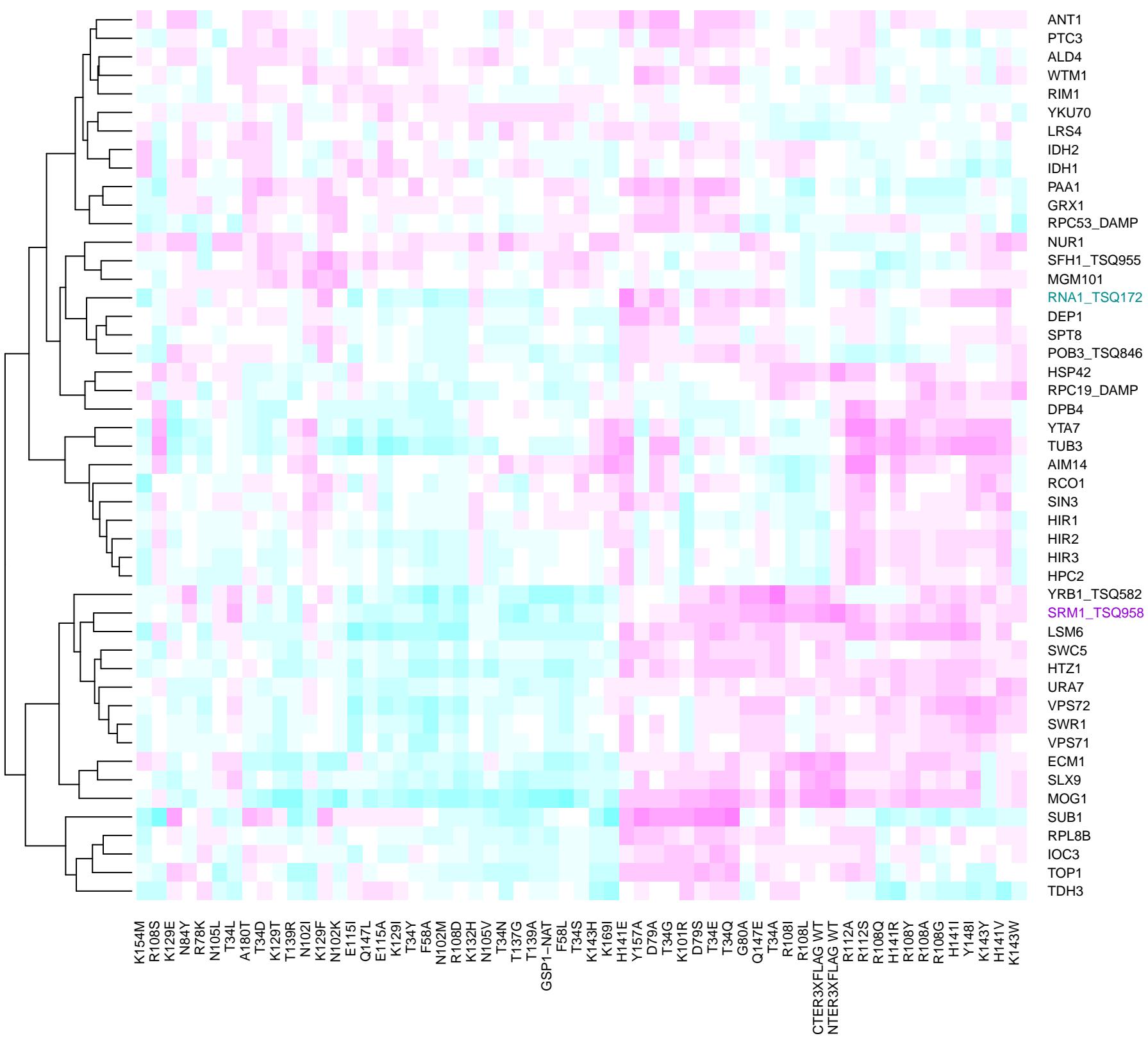


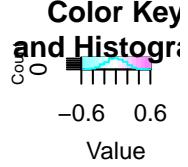
lipid metabolic process_GO_30_5



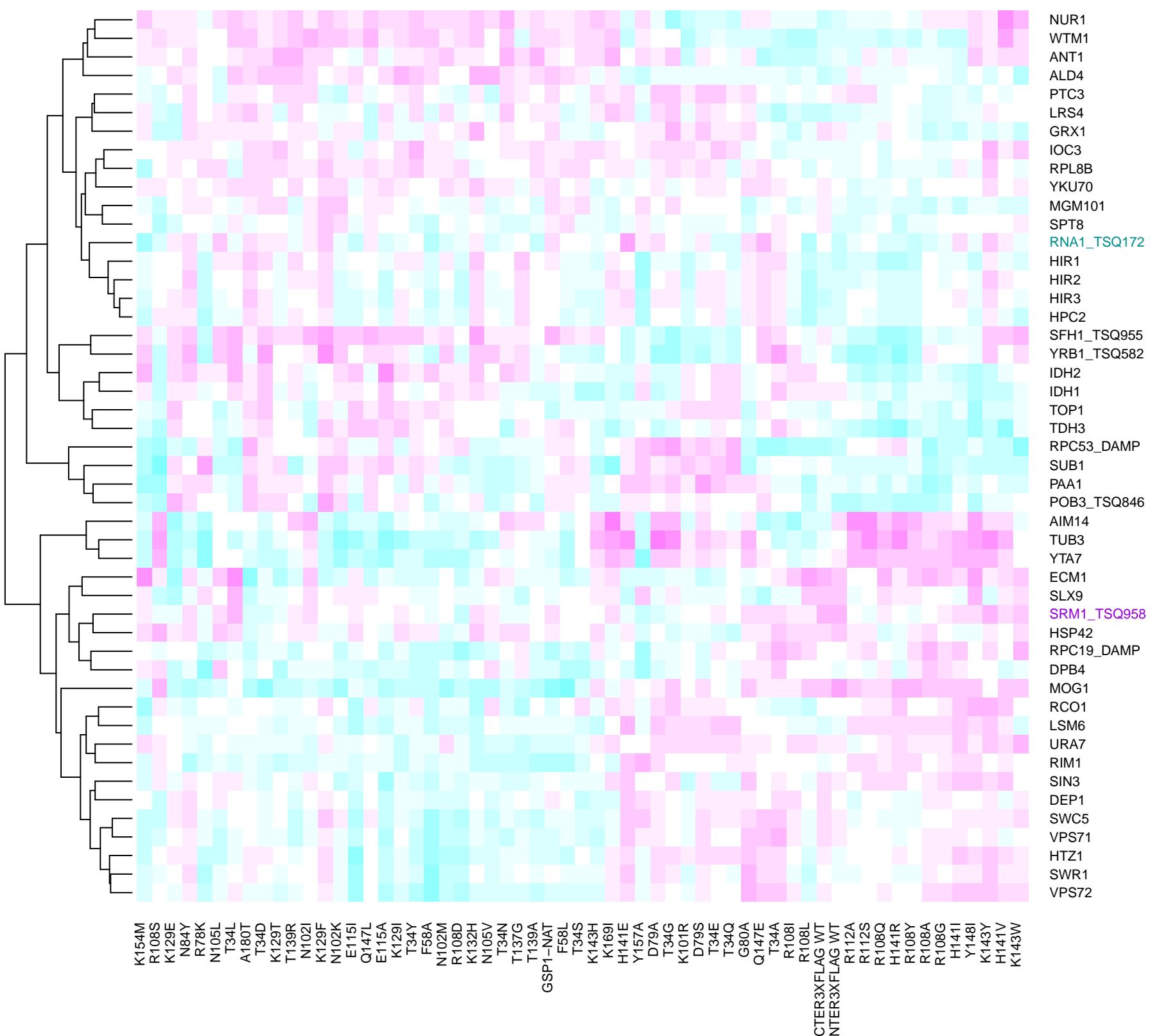


nucleic acid binding transcription factor activity

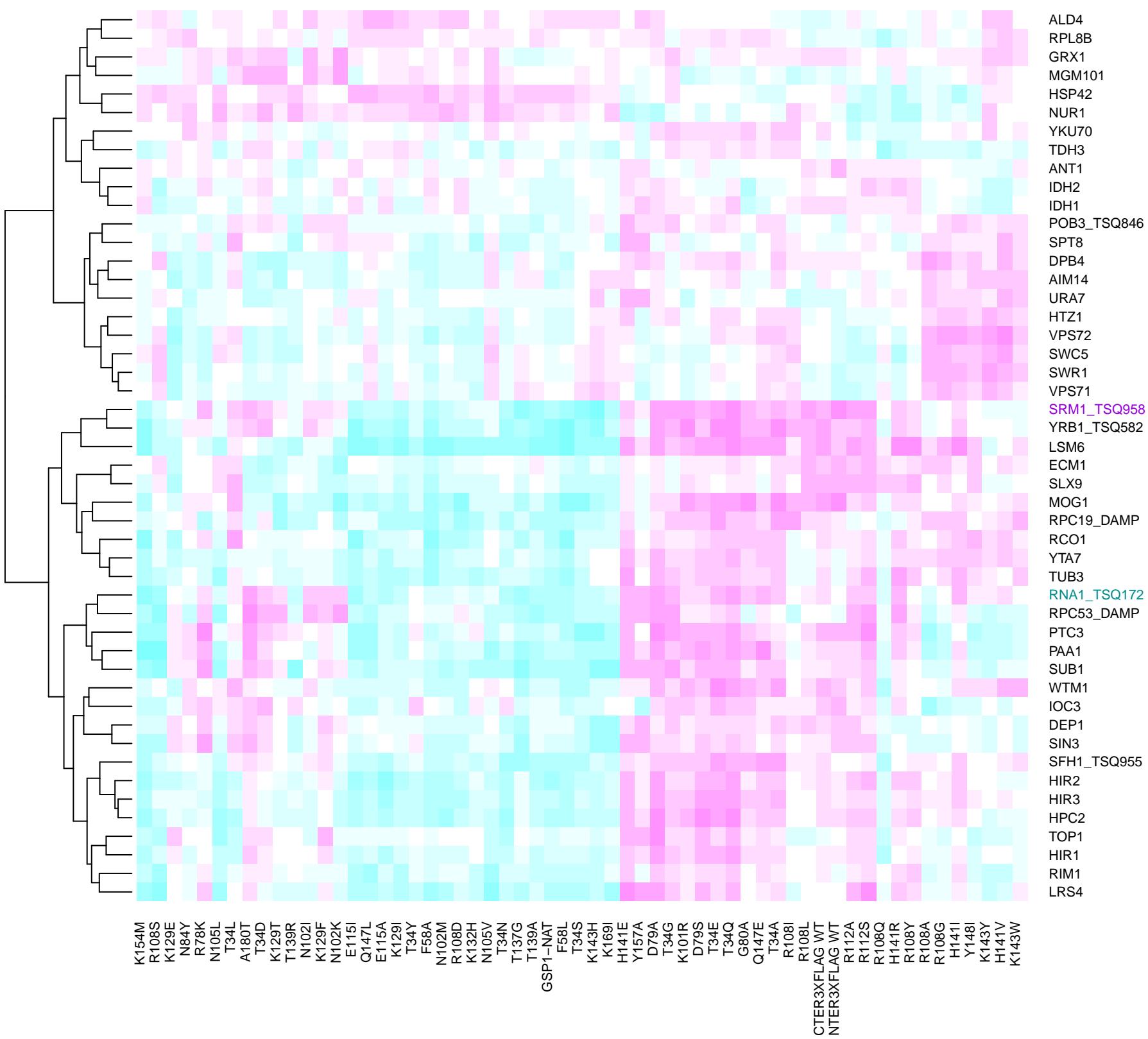
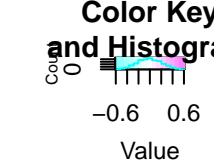


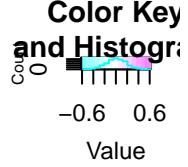


nucleic acid binding transcription factor activity_GO_30_1

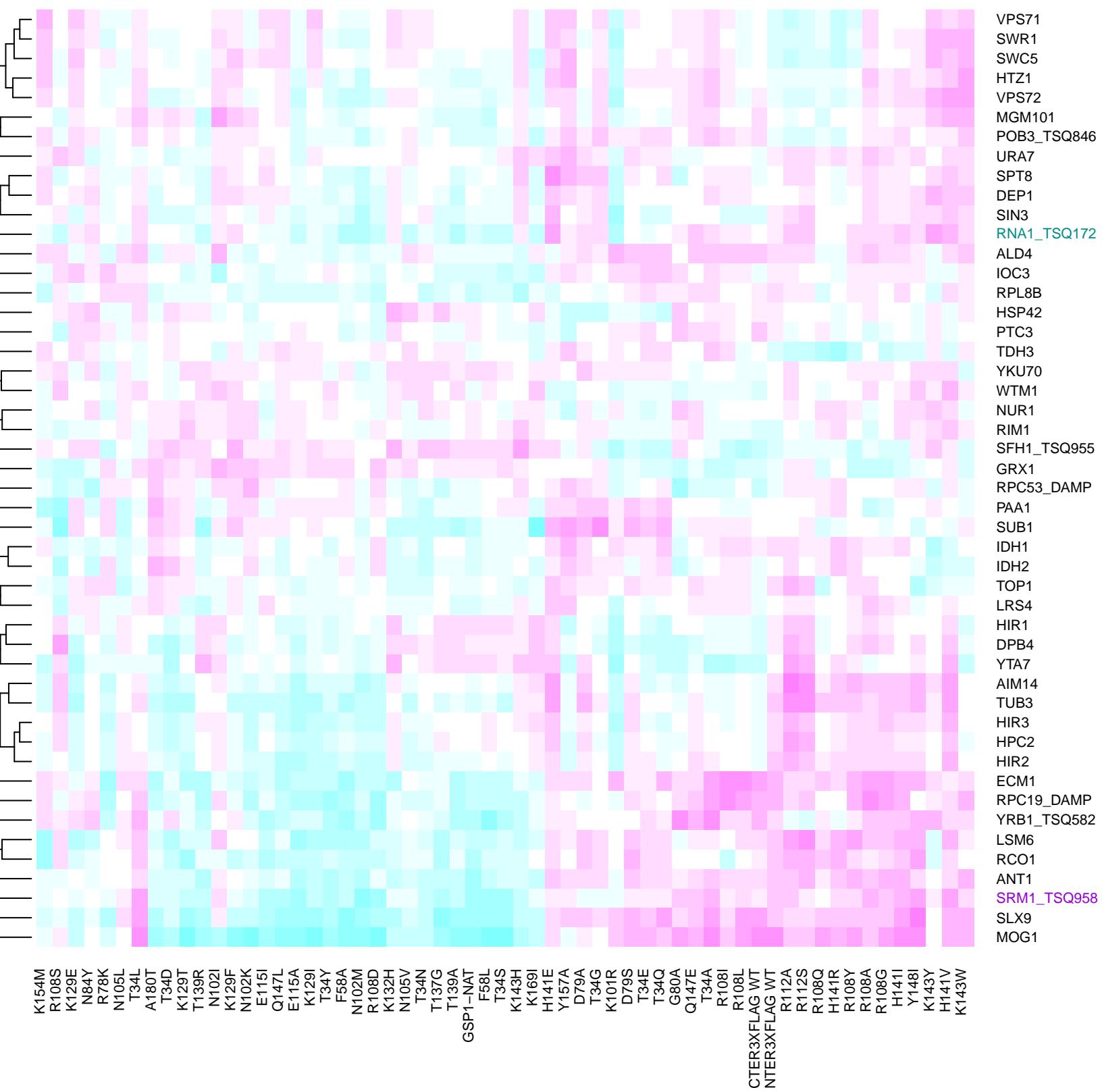


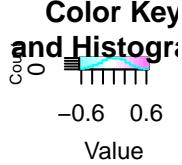
transcription and mRNA processing_GO_30_7



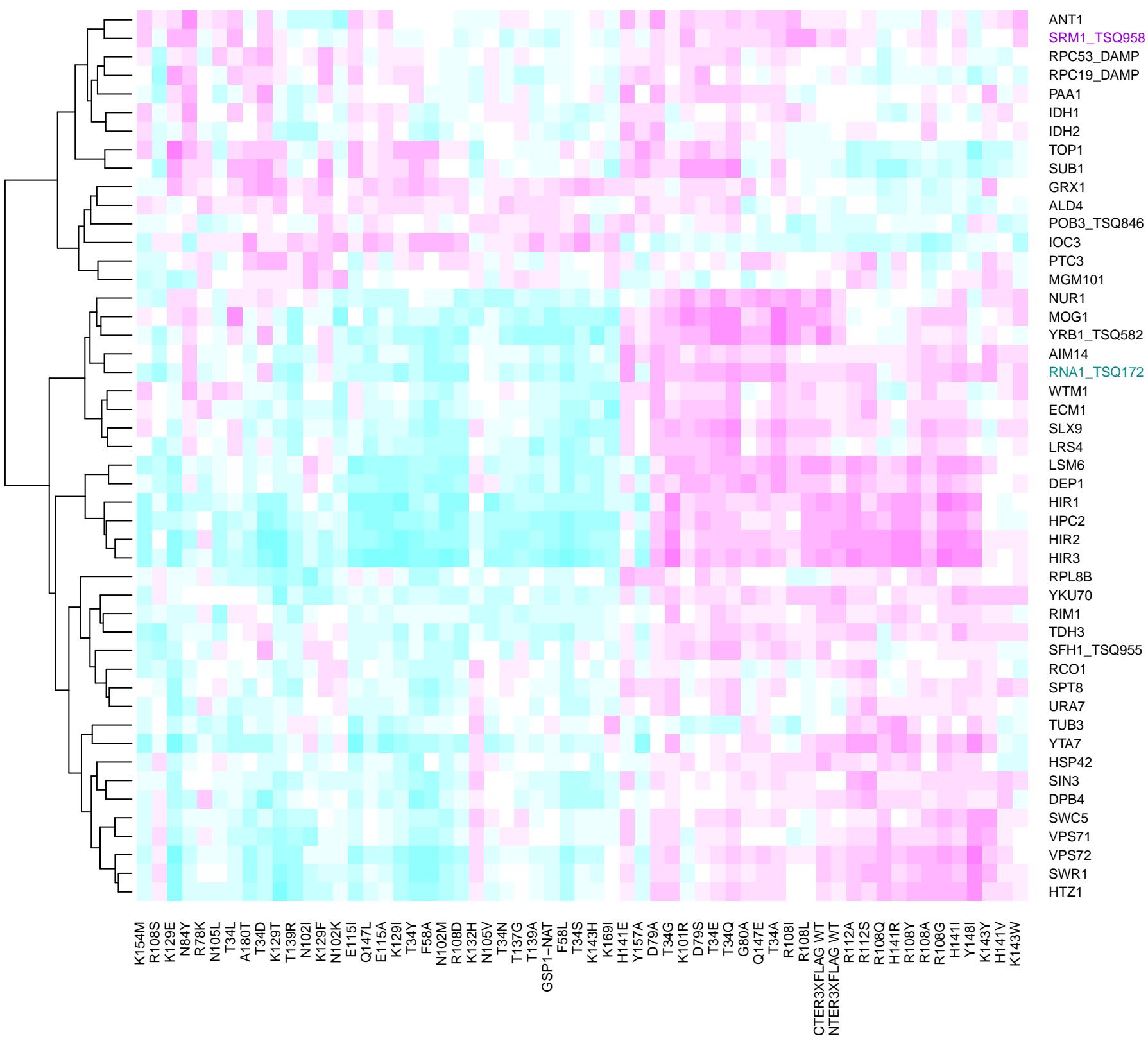


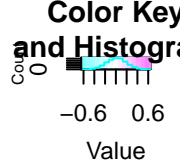
transcription from RNA polymerase II promoter_GO_30_1



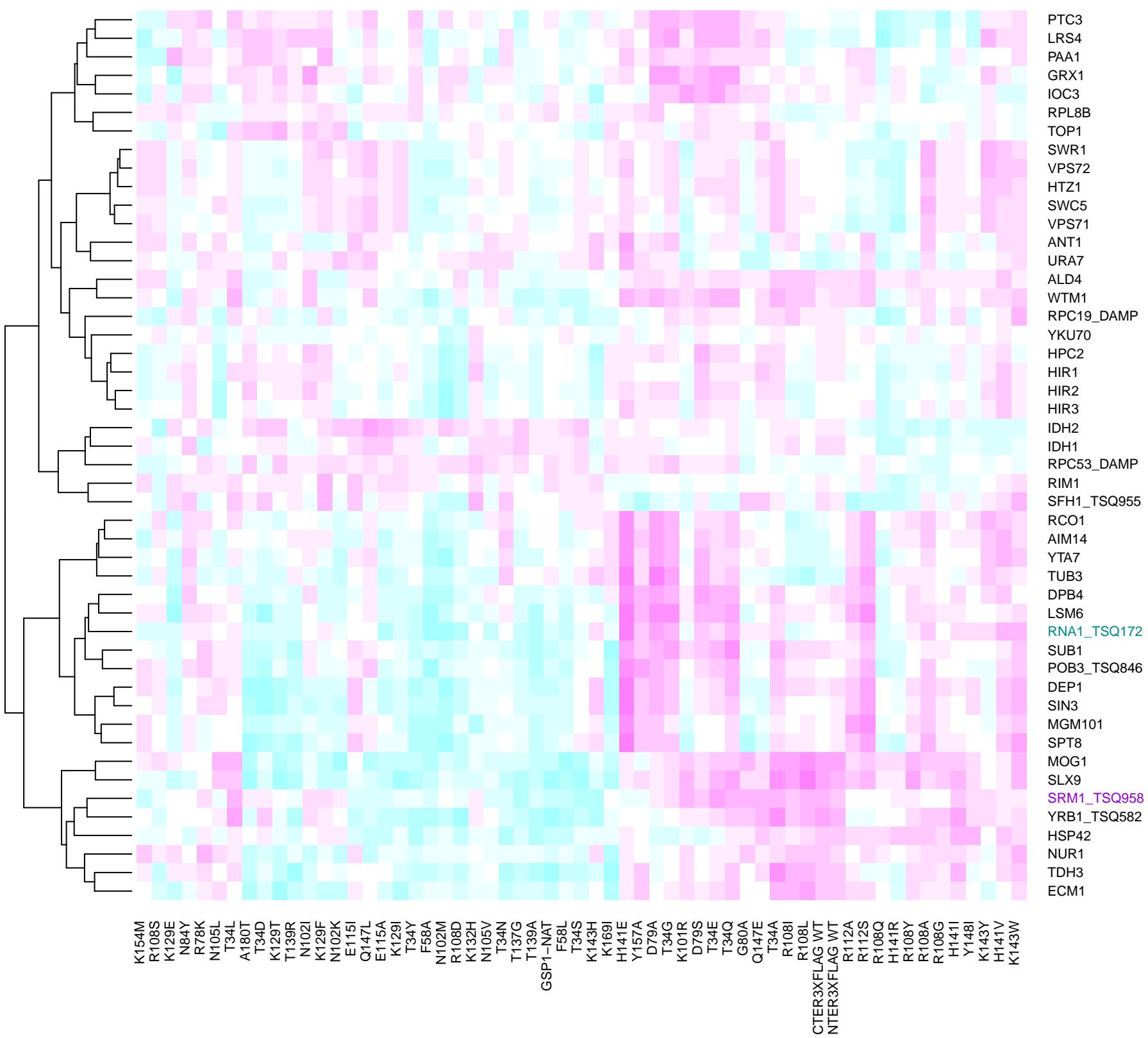


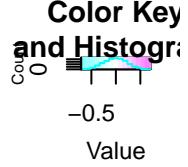
cell wall organization or biogenesis_GO_30_1



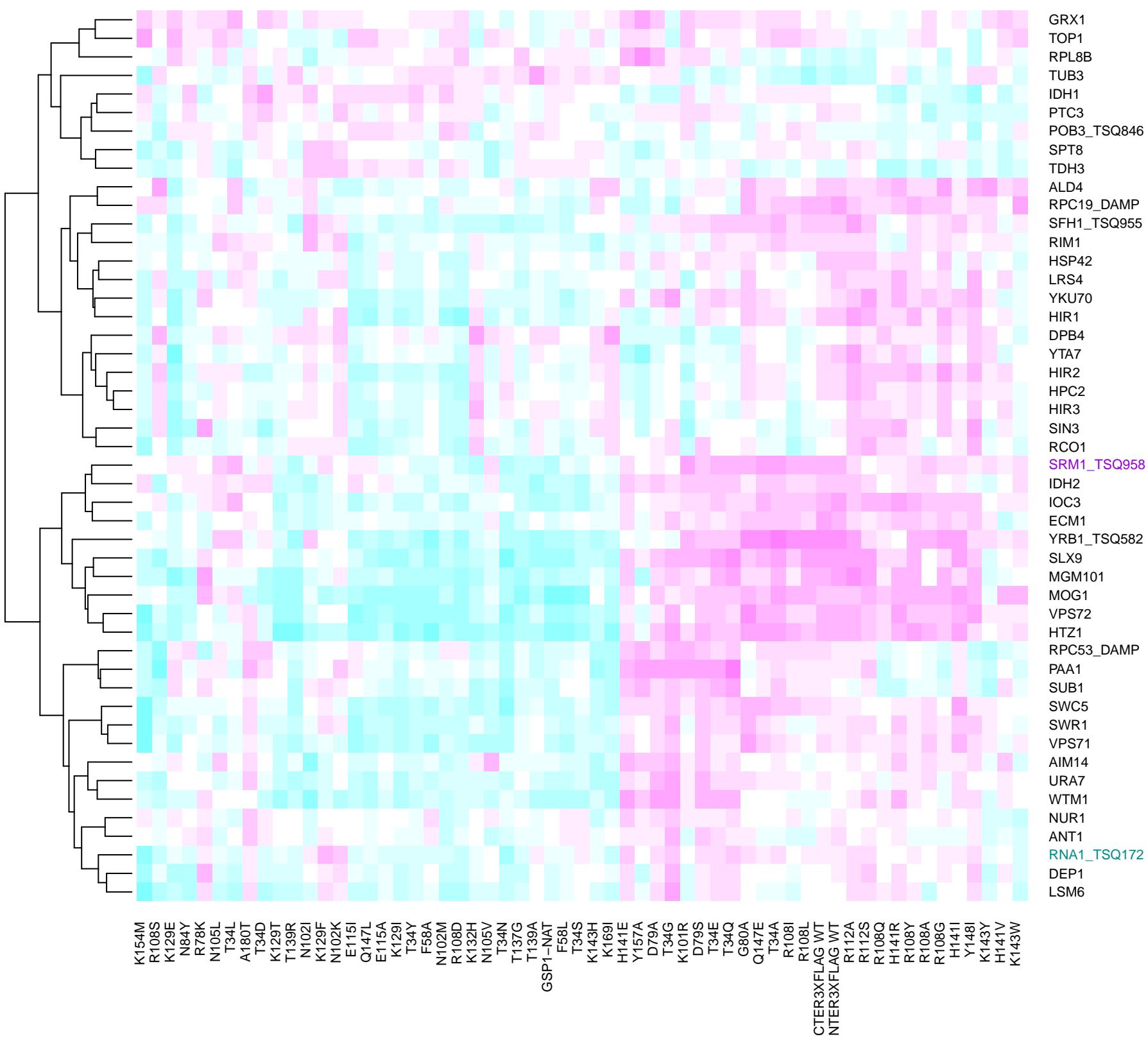


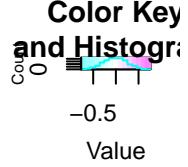
DNA recombination_GO_30_2



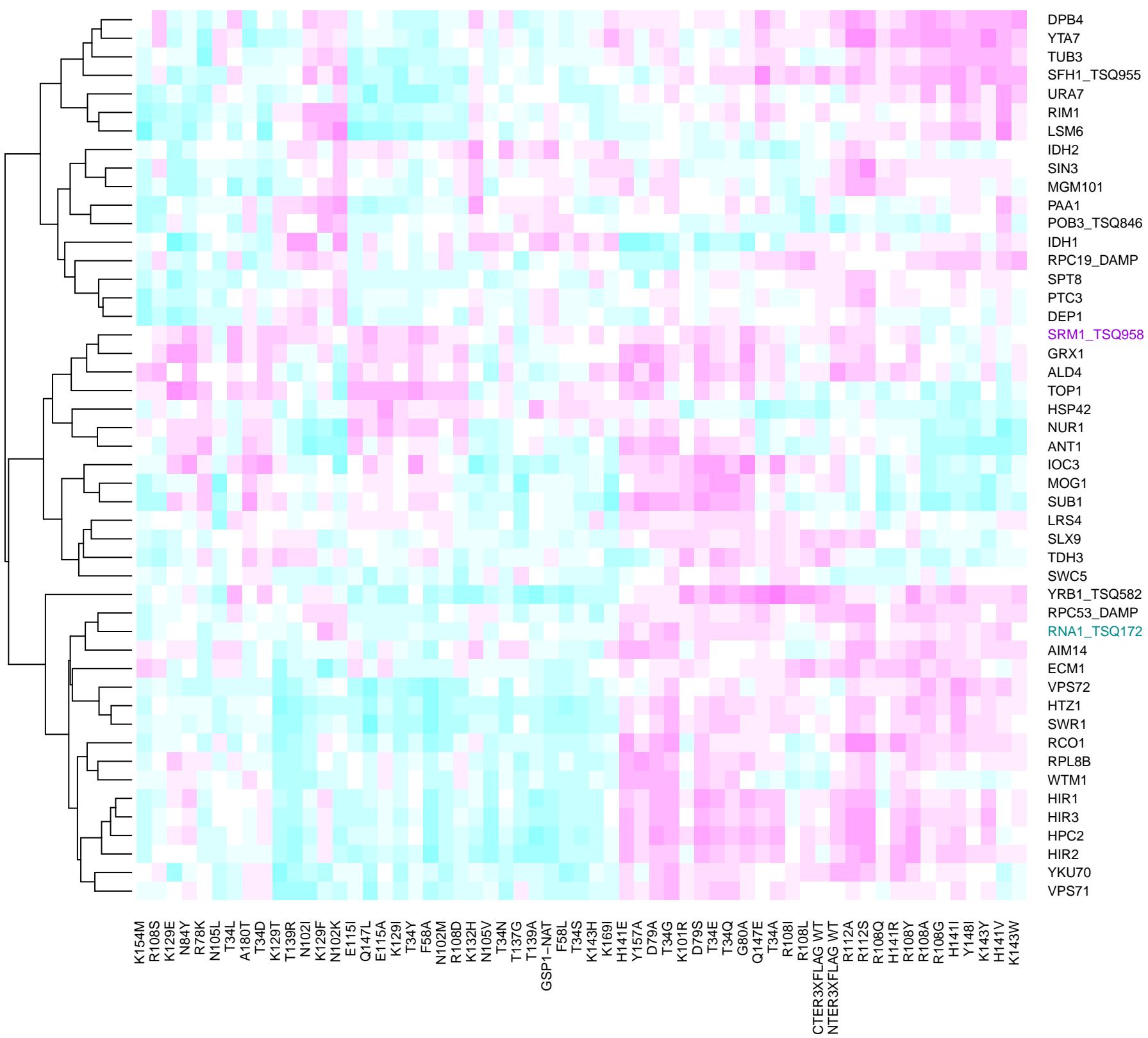


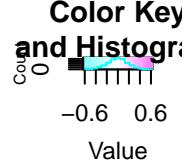
endomembrane system_GO_30_12



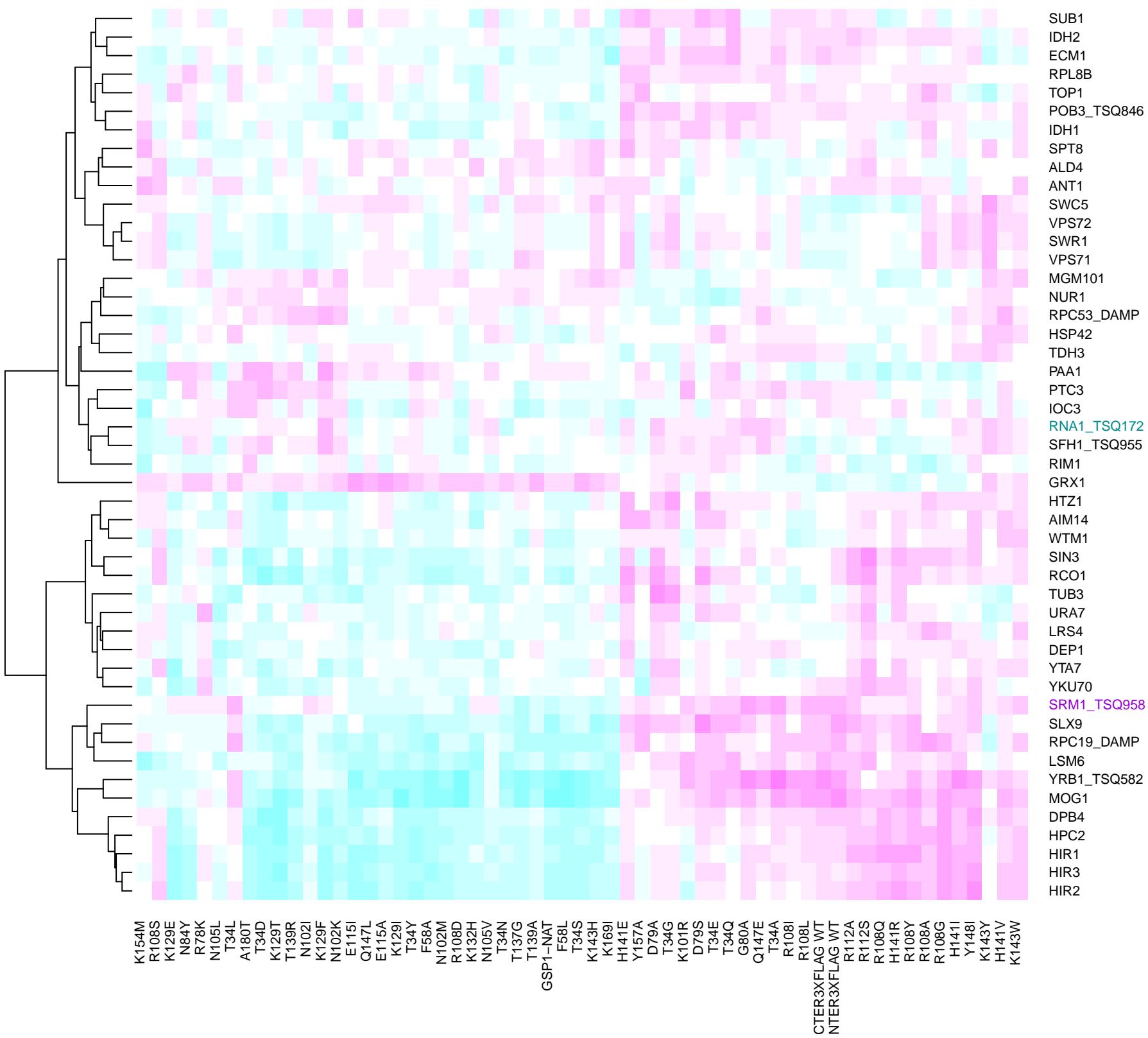


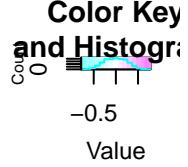
Golgi and ER_GO_30_16



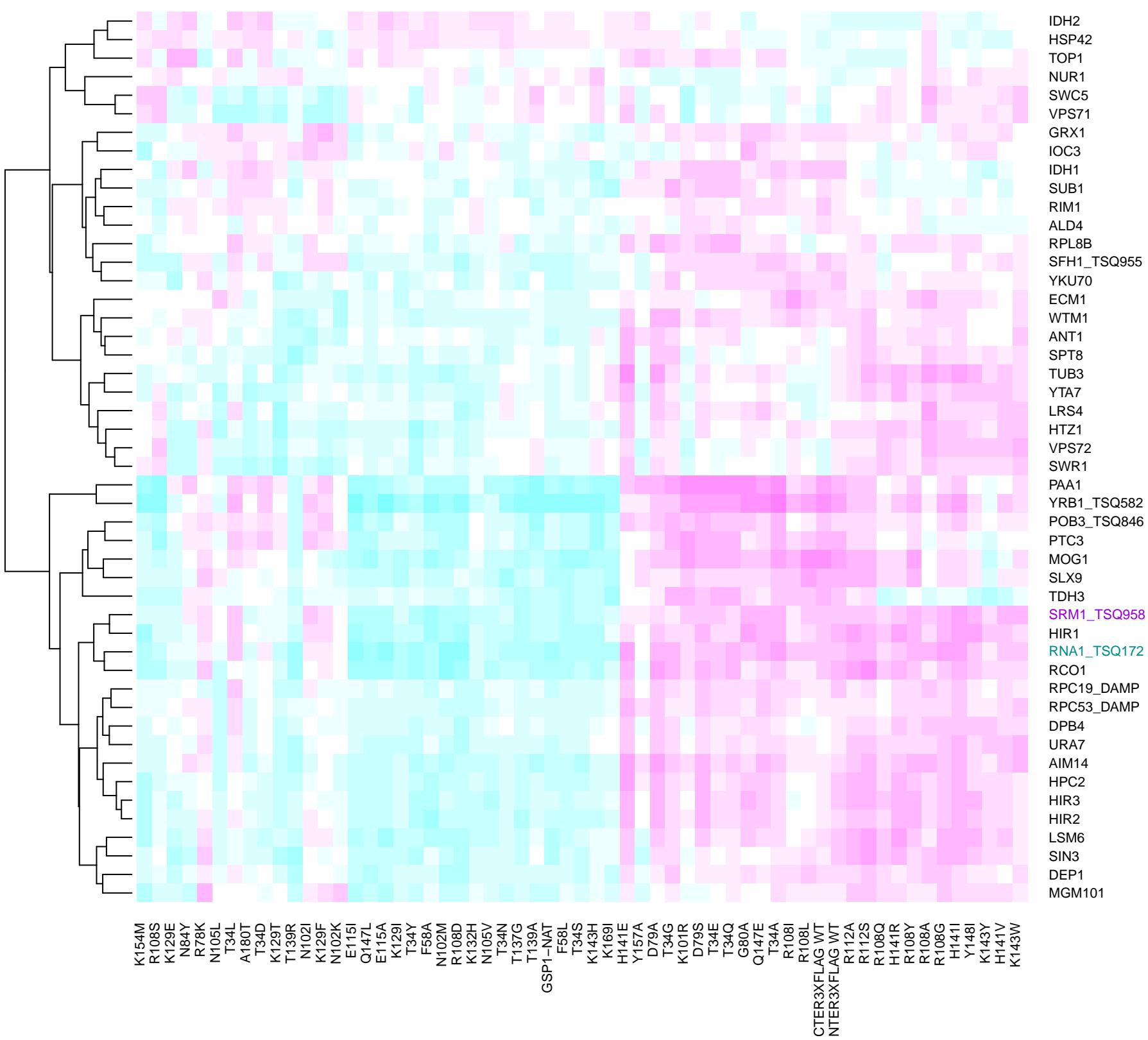


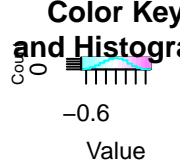
ion transport_GO_30_1



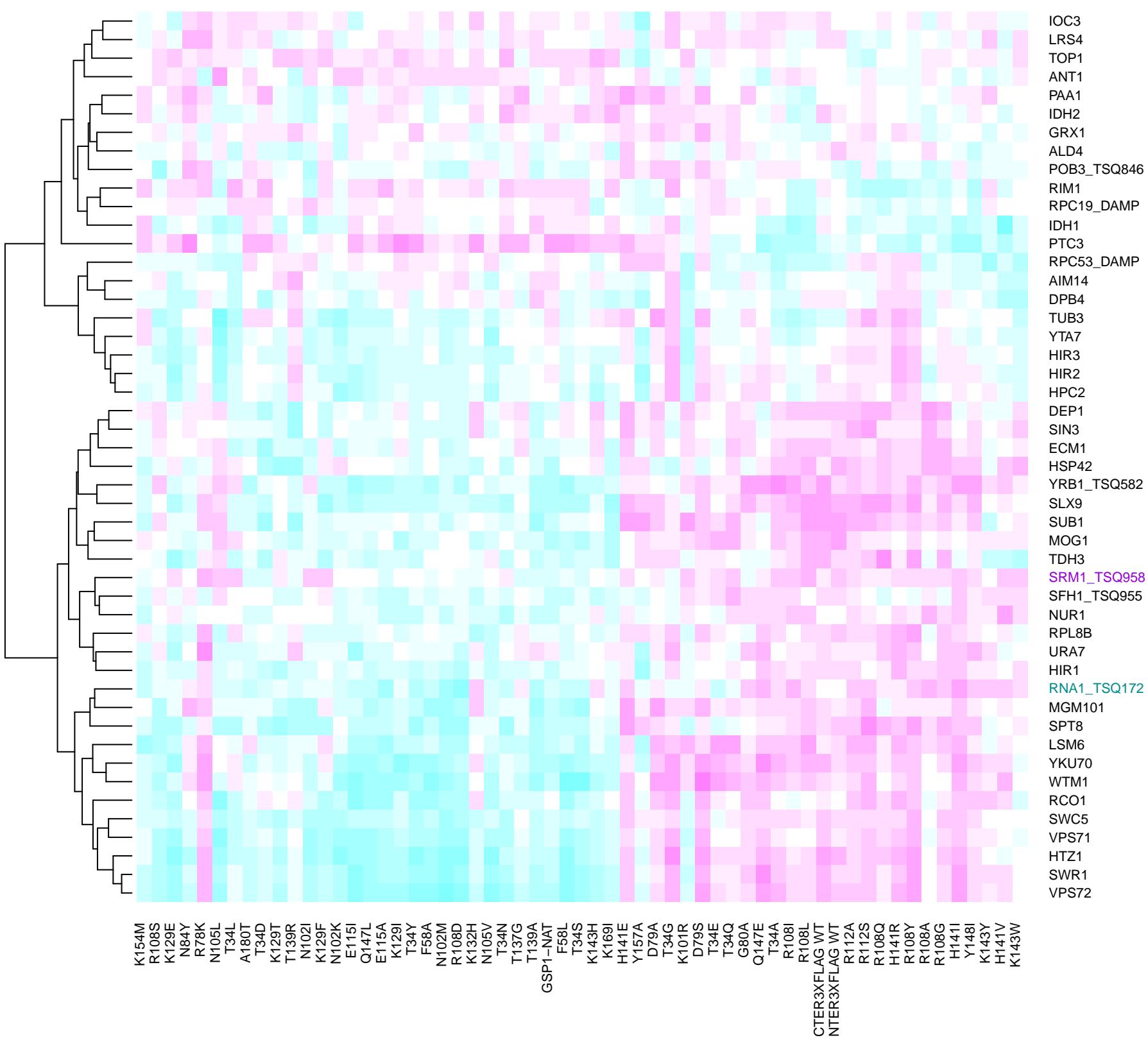


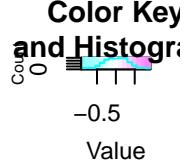
lipids_GO_30_3



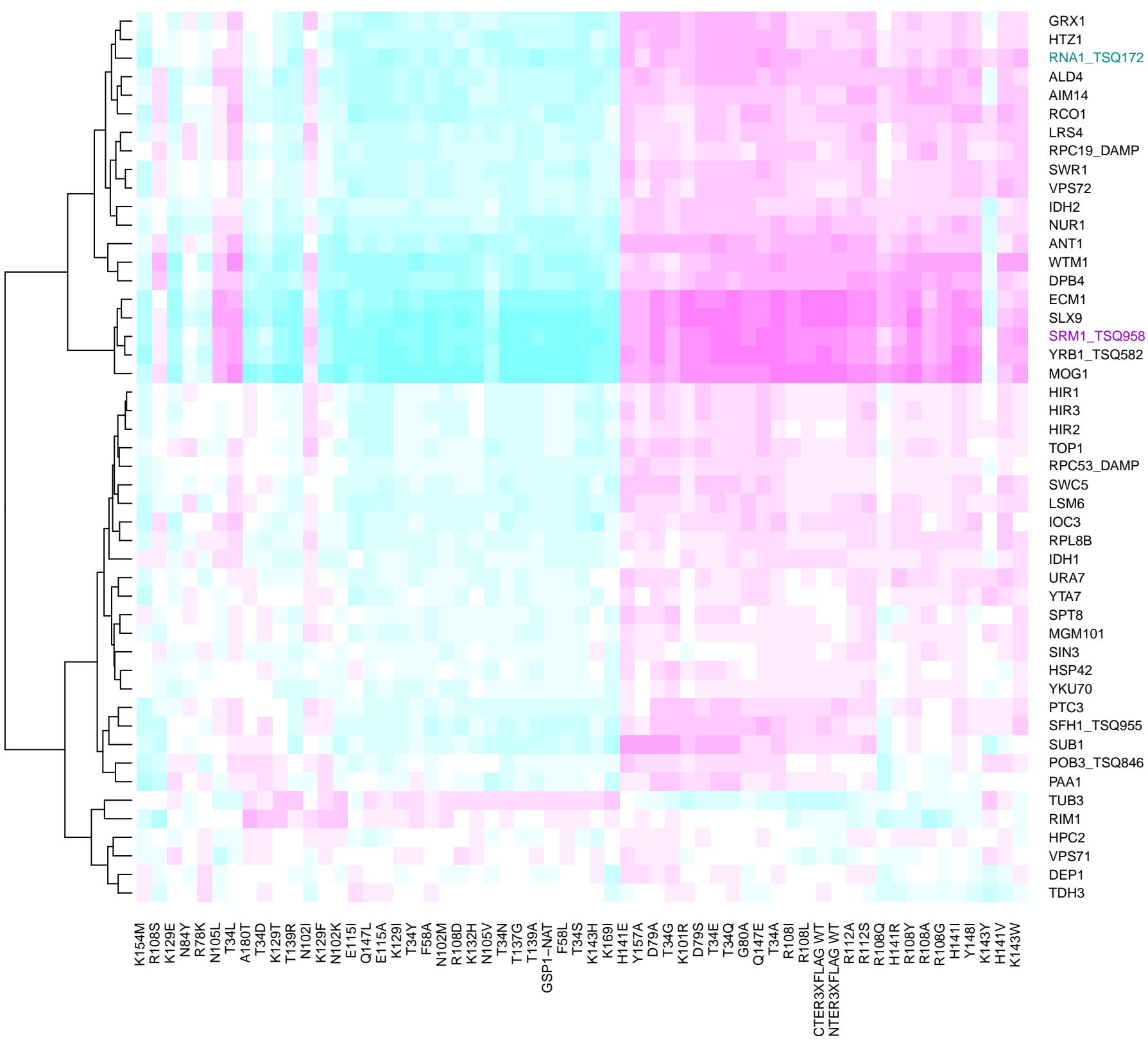


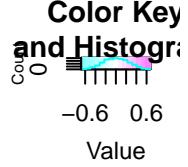
metabolic_GO_30_15



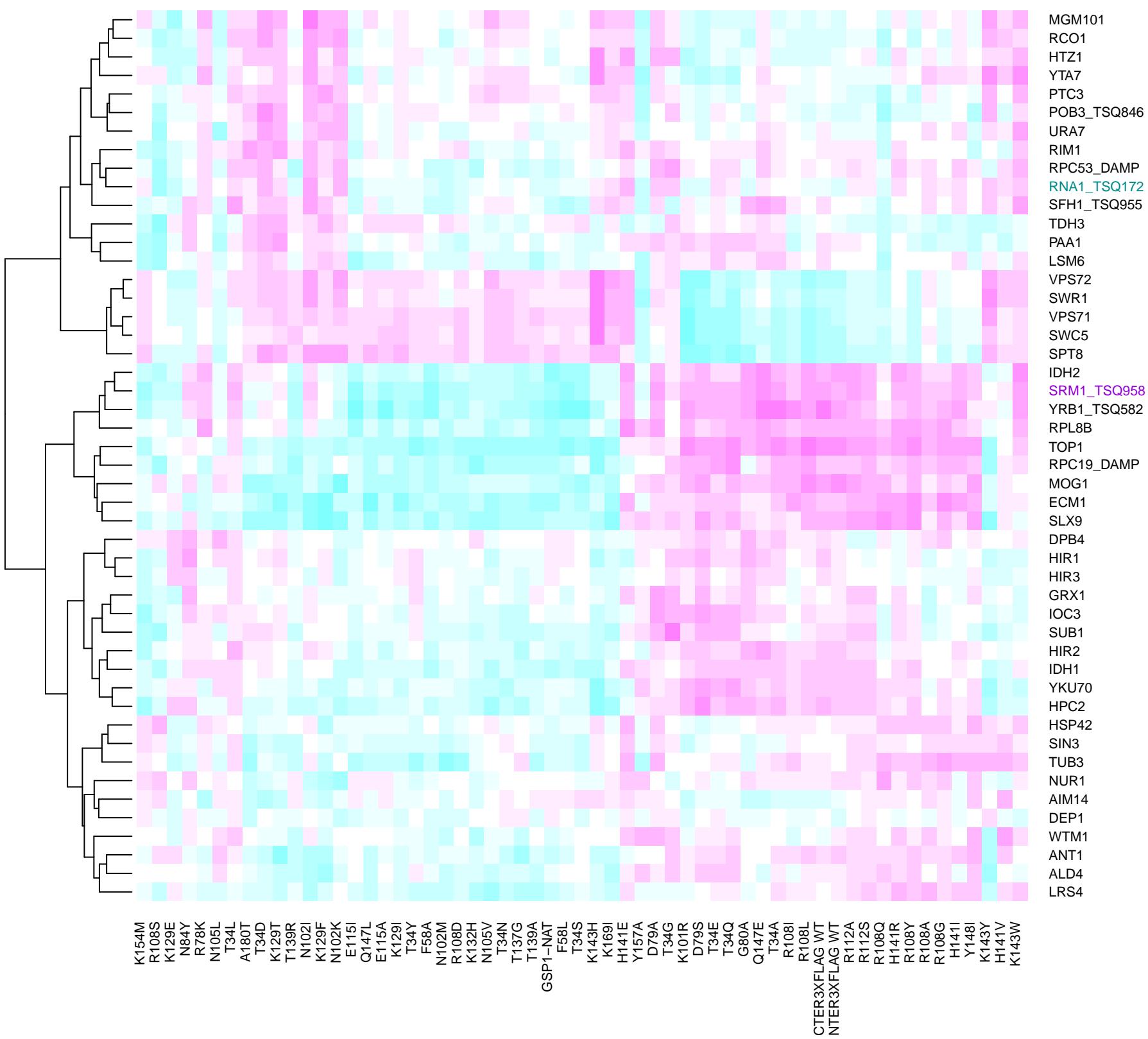


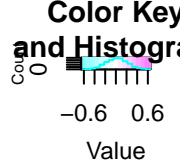
nucleobase-containing compound transport_GO_30_1



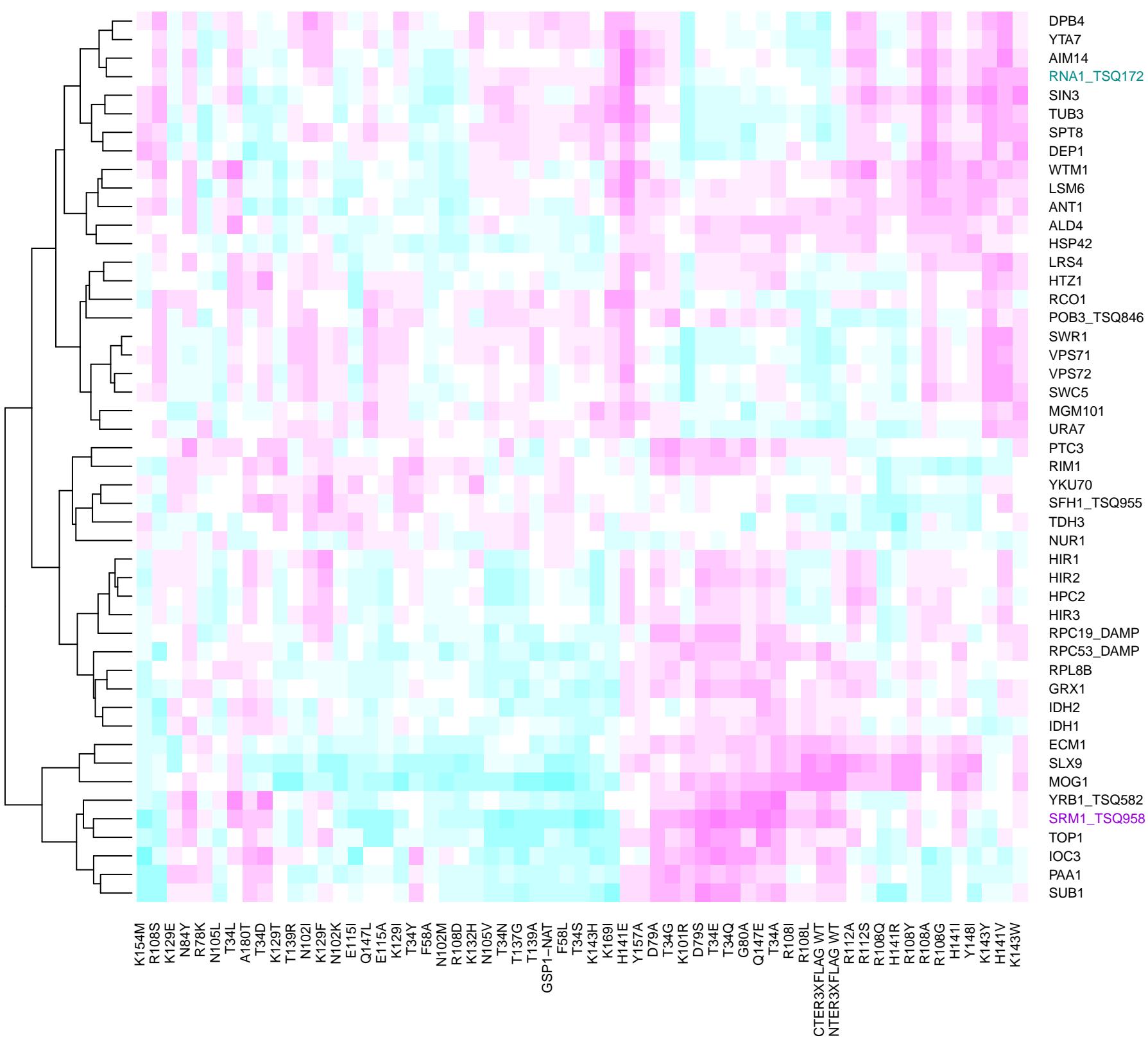


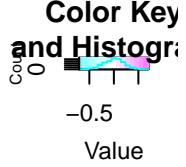
generation of precursor metabolites and energy_GO_30_1



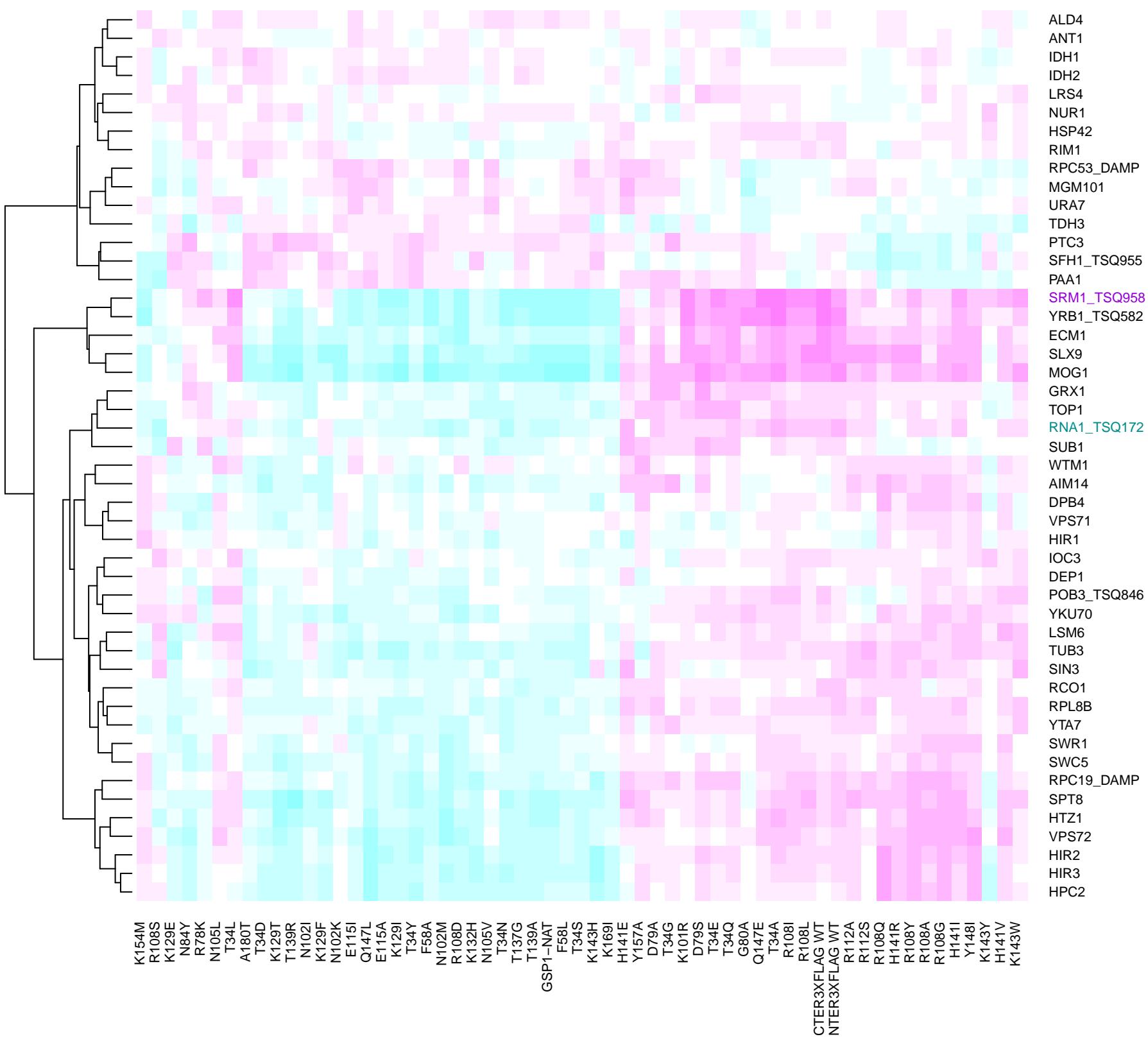


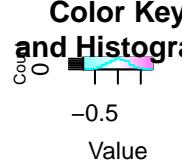
histone modification_GO_30_1



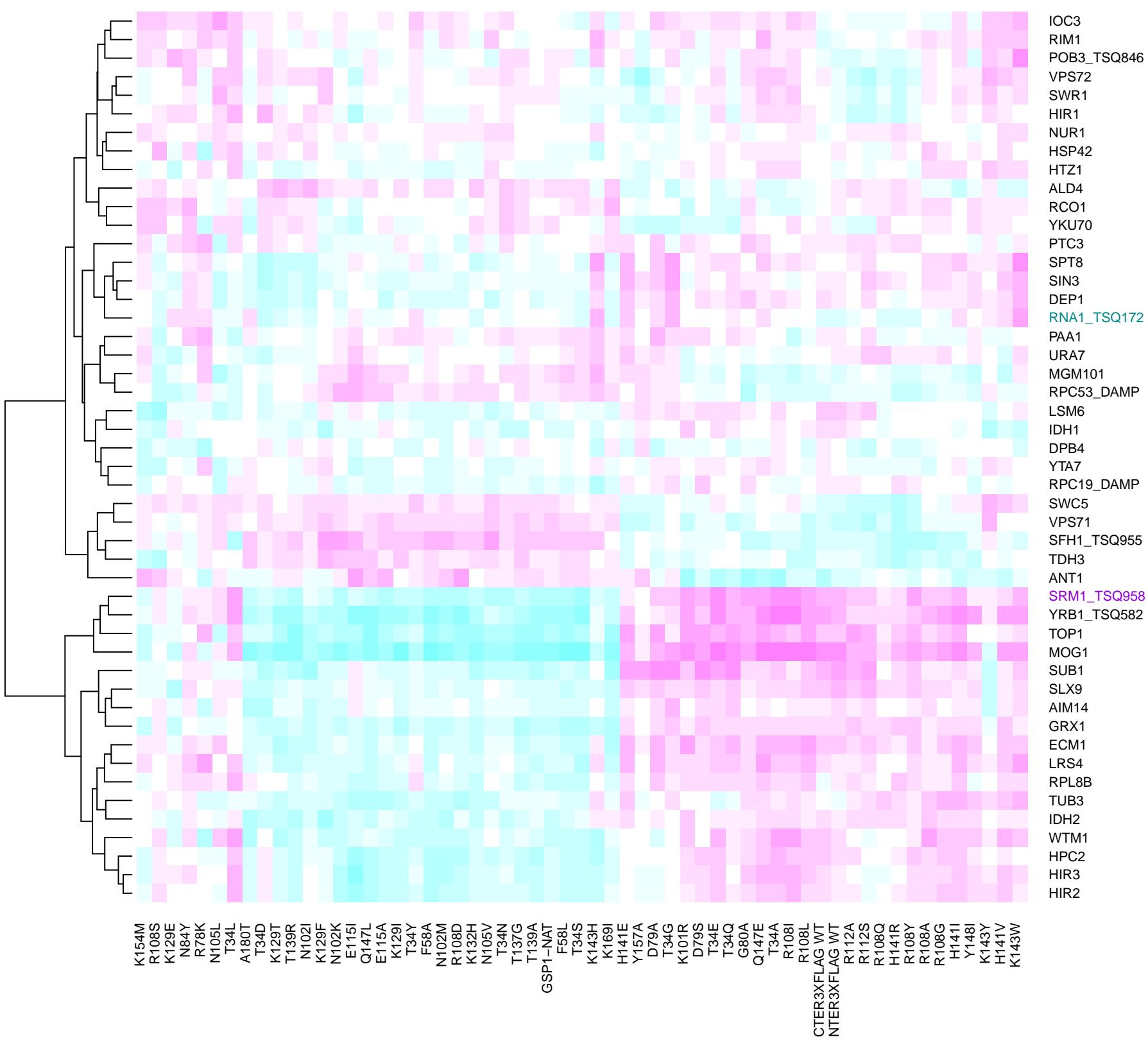


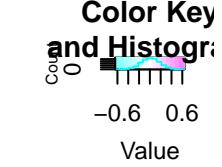
mitochondria and respiration_GO_30_3



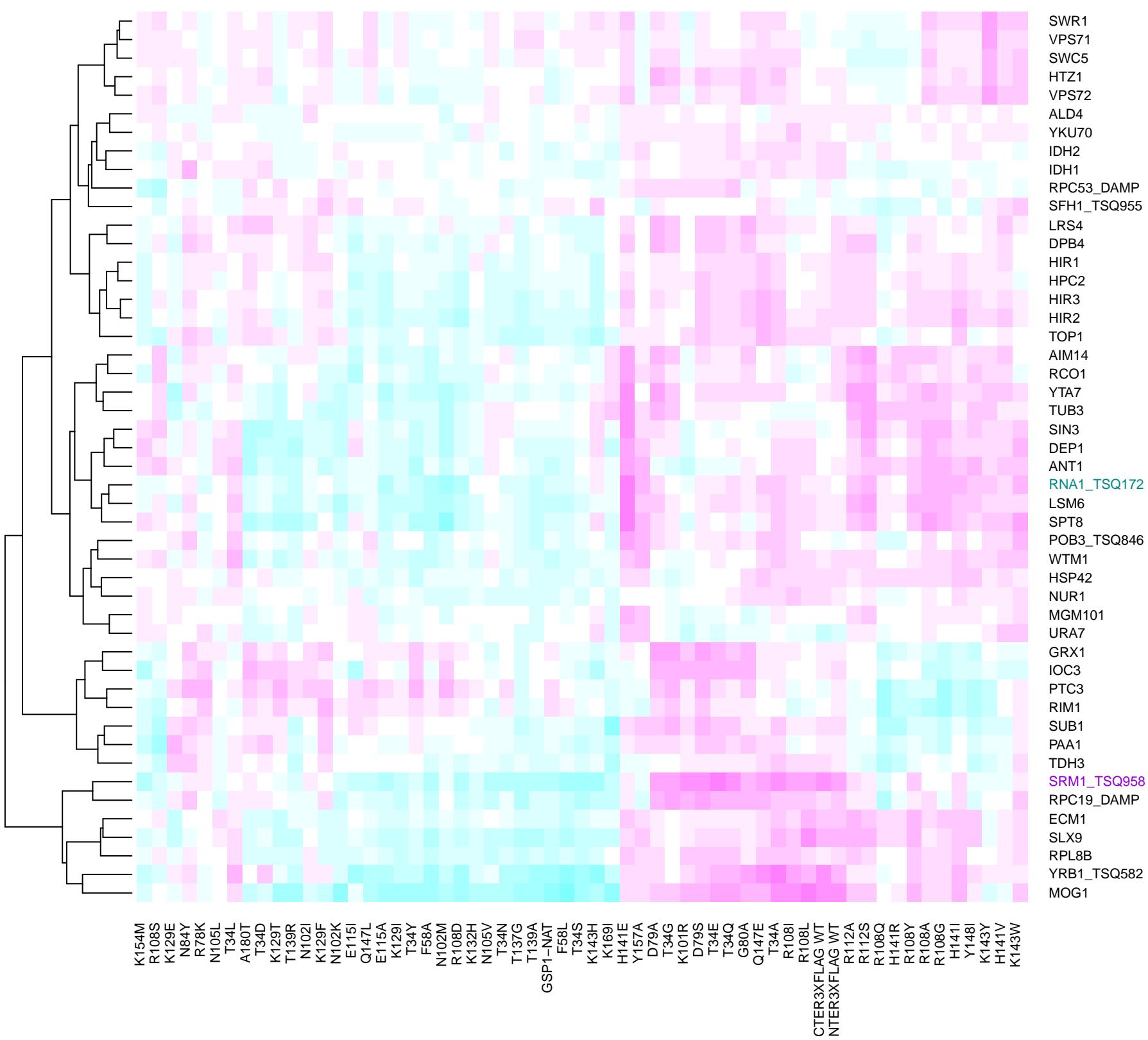


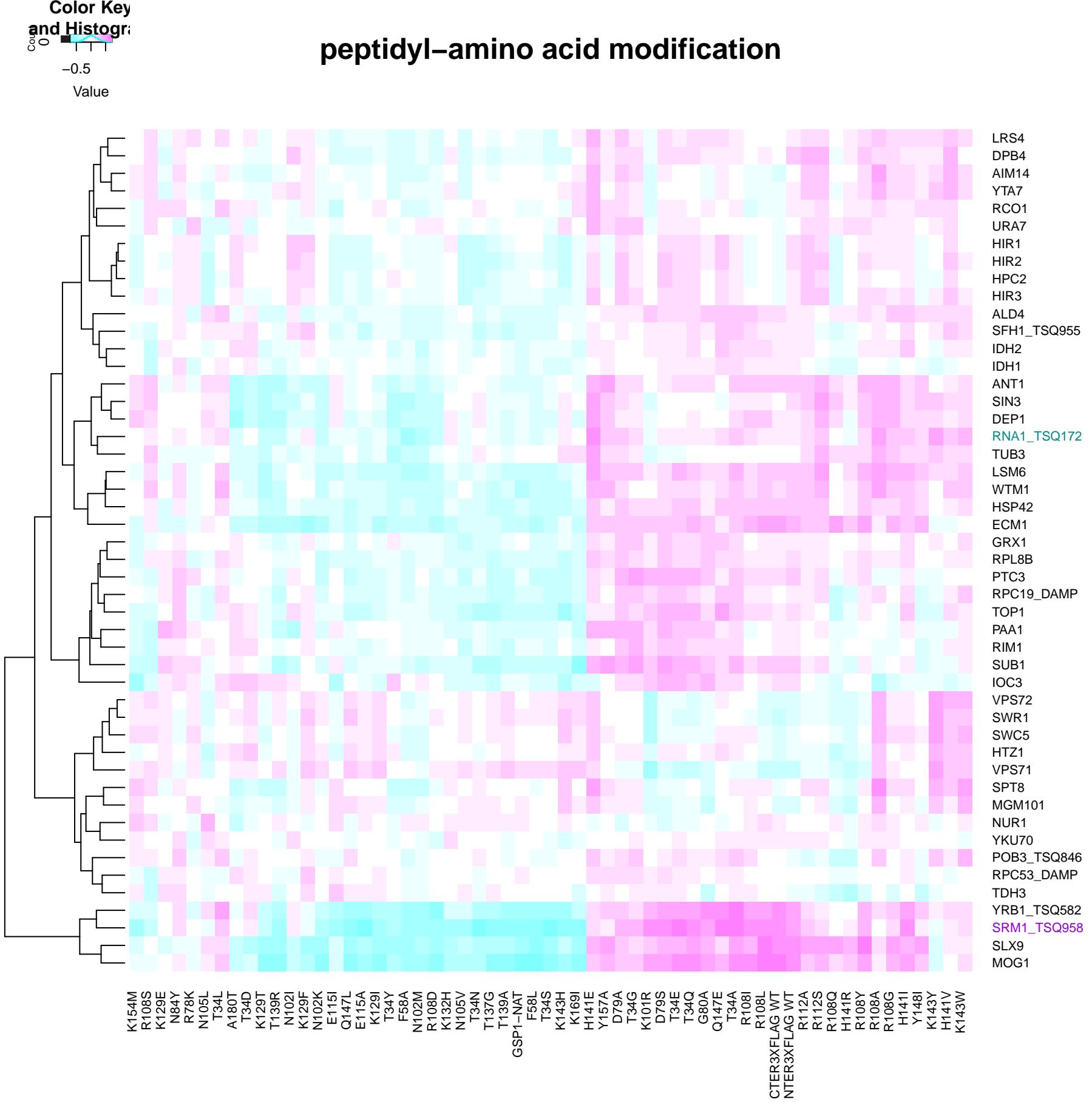
monocarboxylic acid metabolic process_GO_30_3

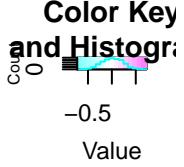




DNA repair

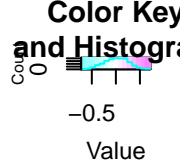




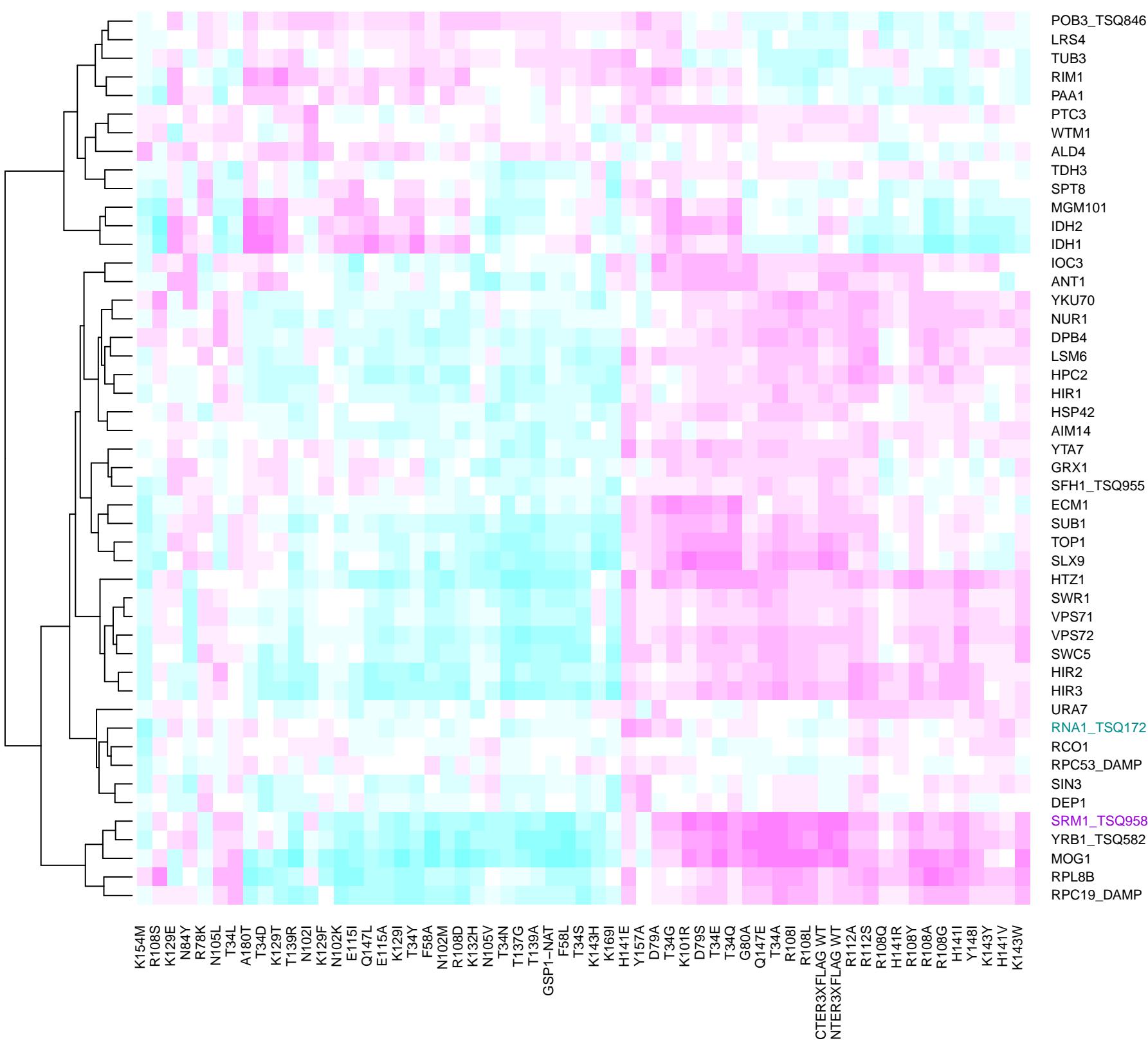


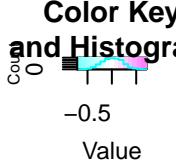
peroxisome



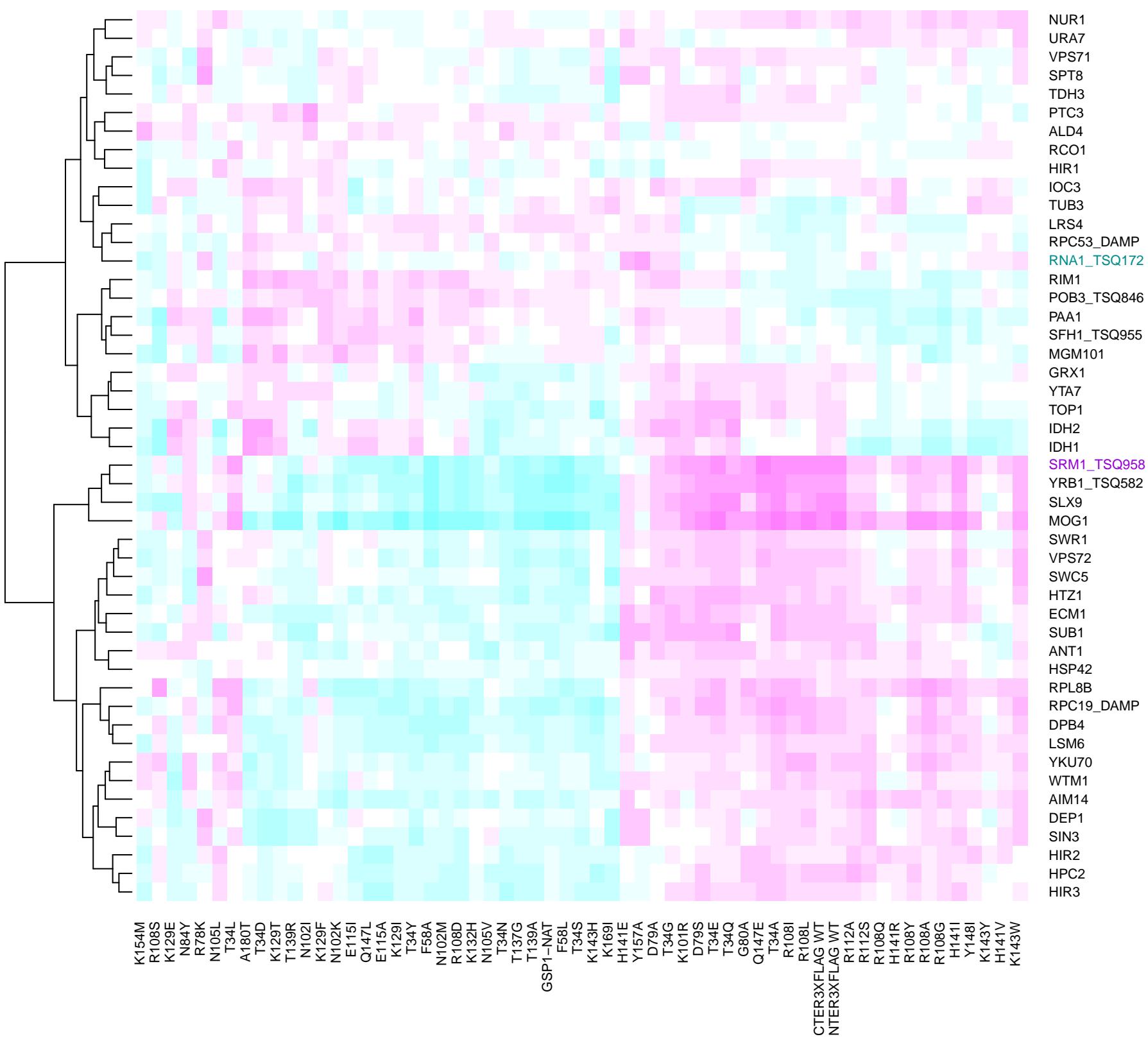


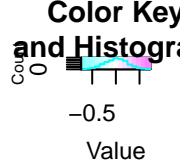
peroxisome_GO_30_1



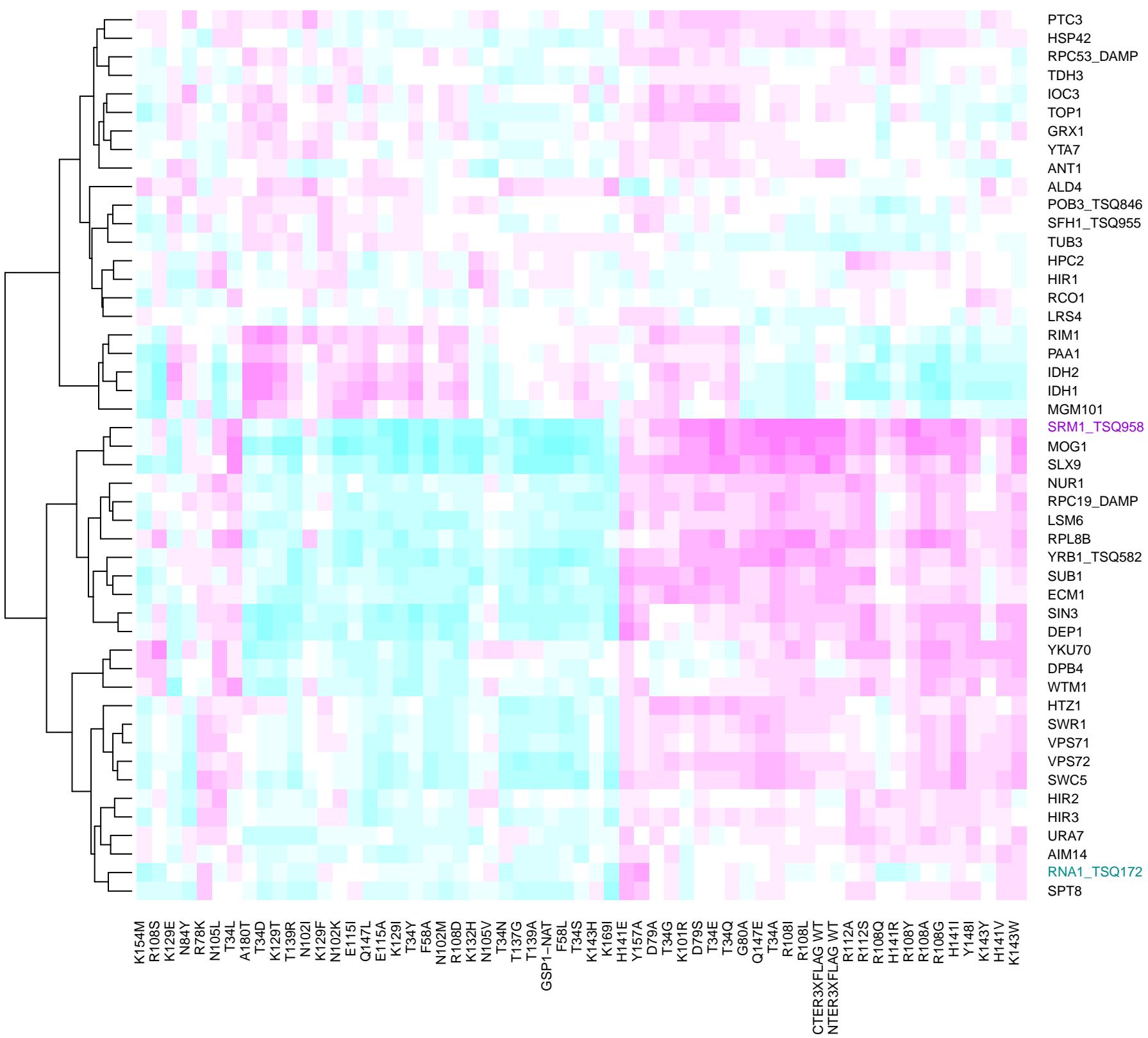


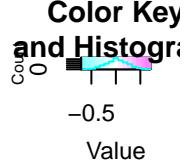
peroxisomes



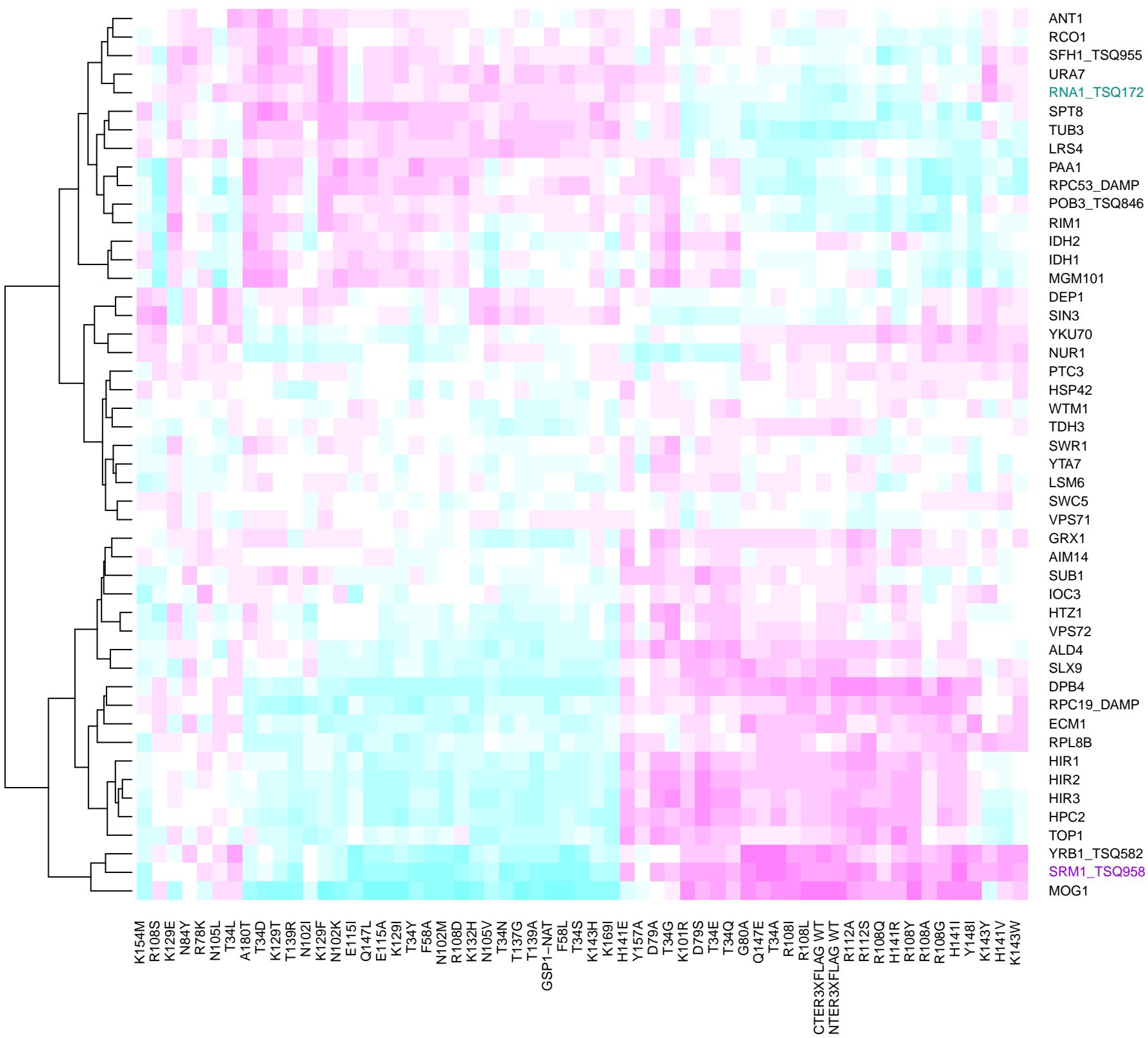


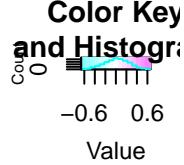
peroxisomes_GO_30_1



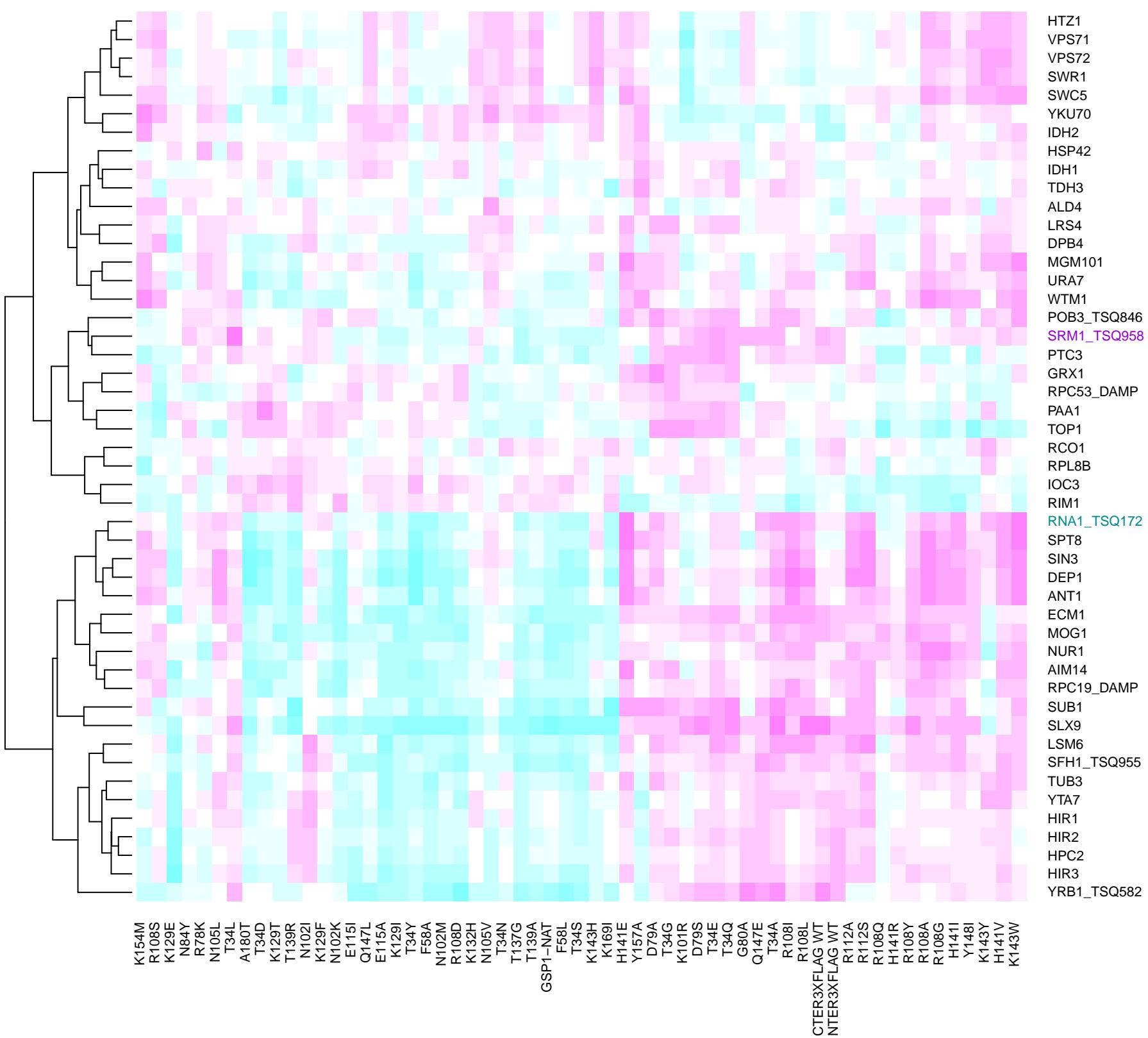


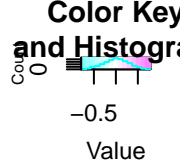
protein targeting_GO_30_2



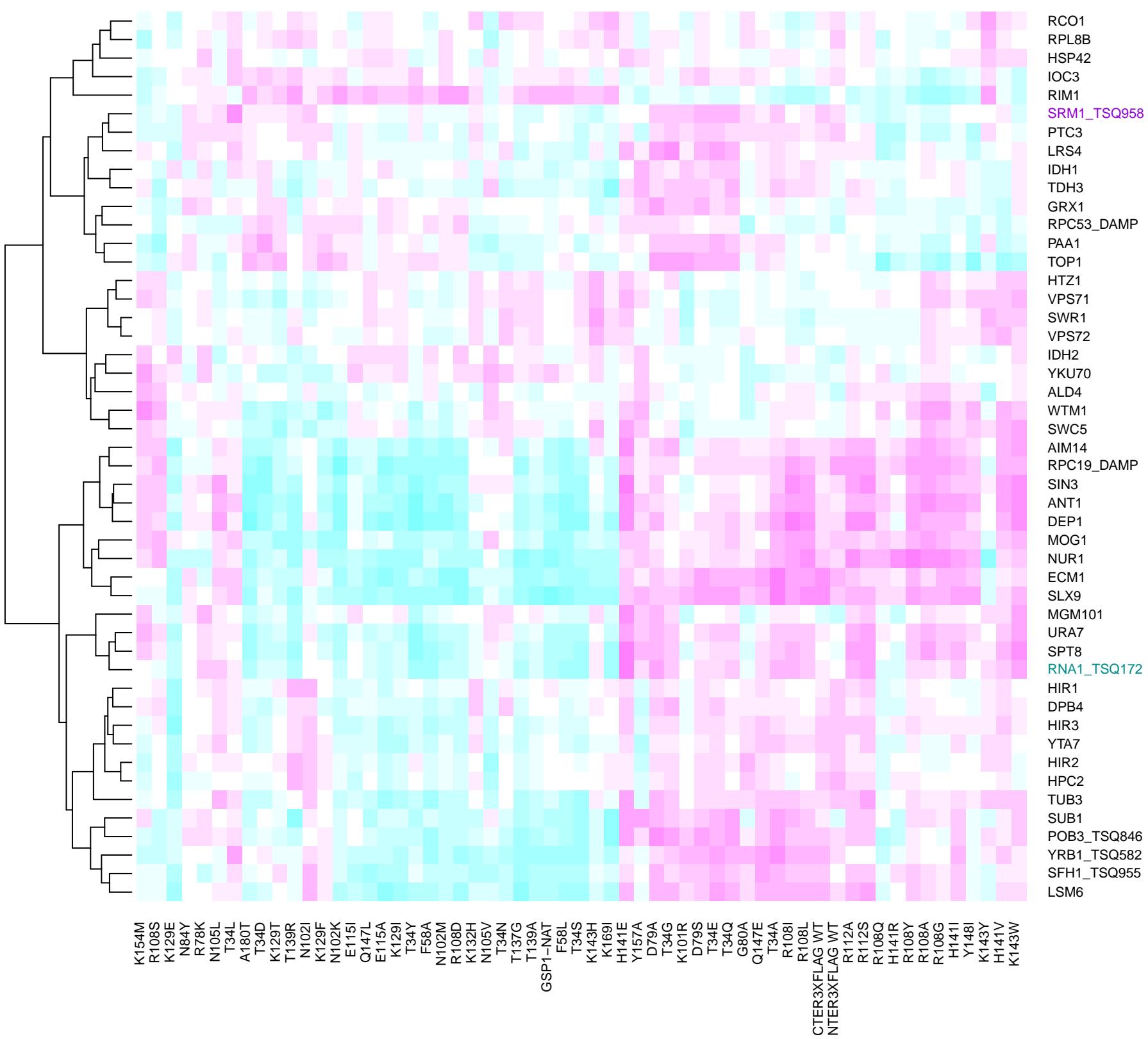


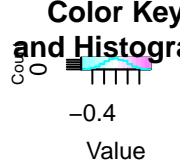
invasive growth in response to glucose limitation



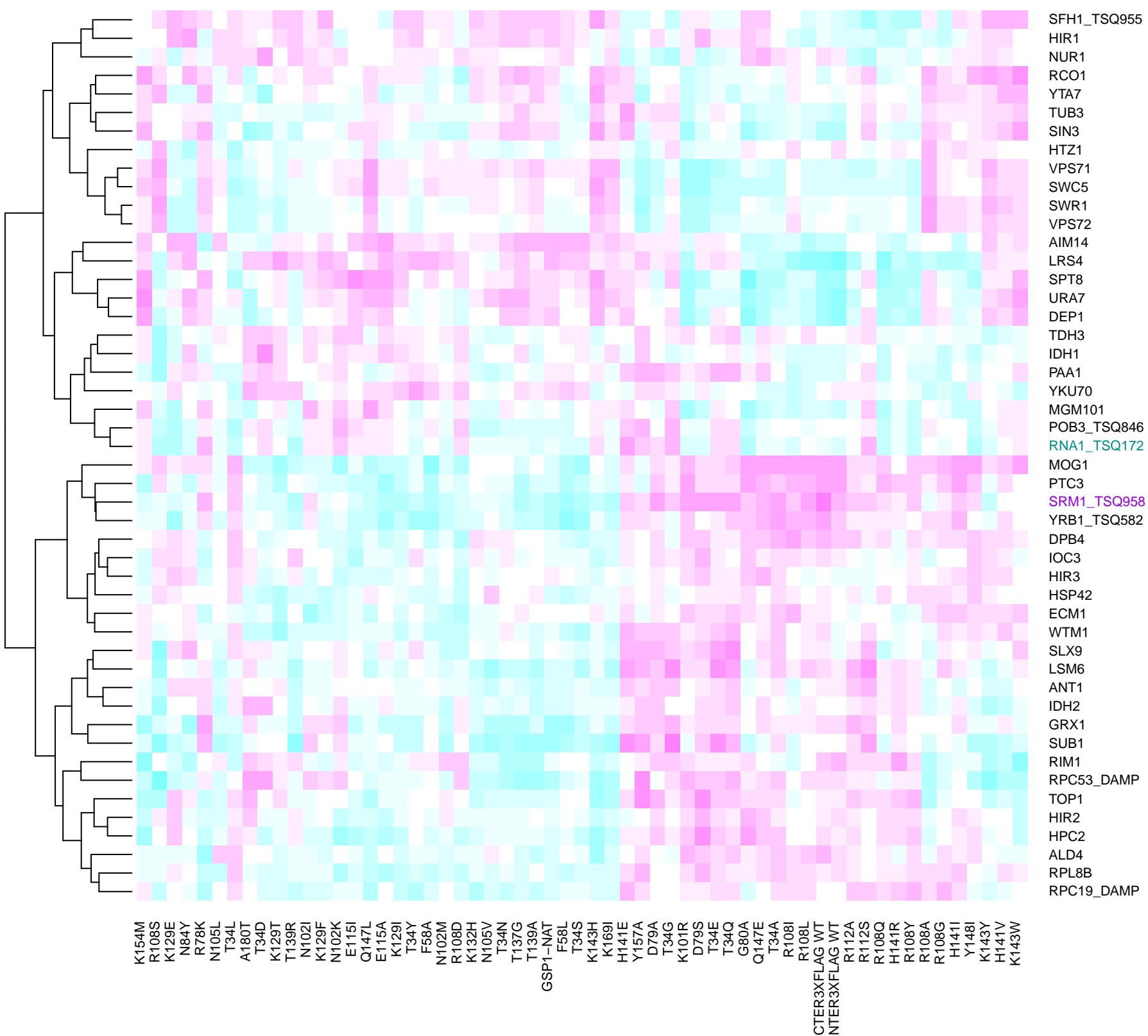


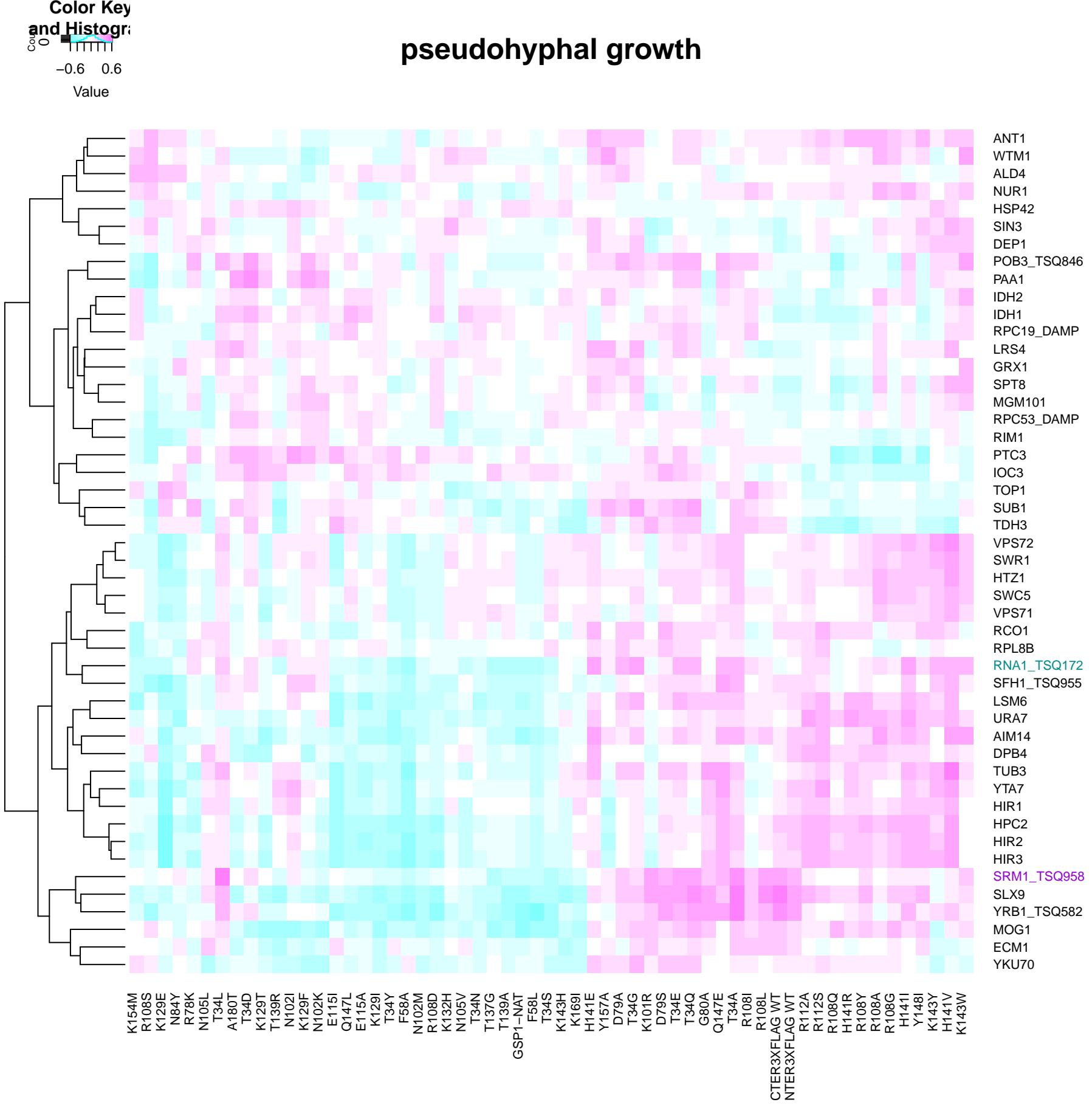
invasive growth in response to glucose limitation_GO_30_1

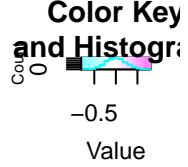




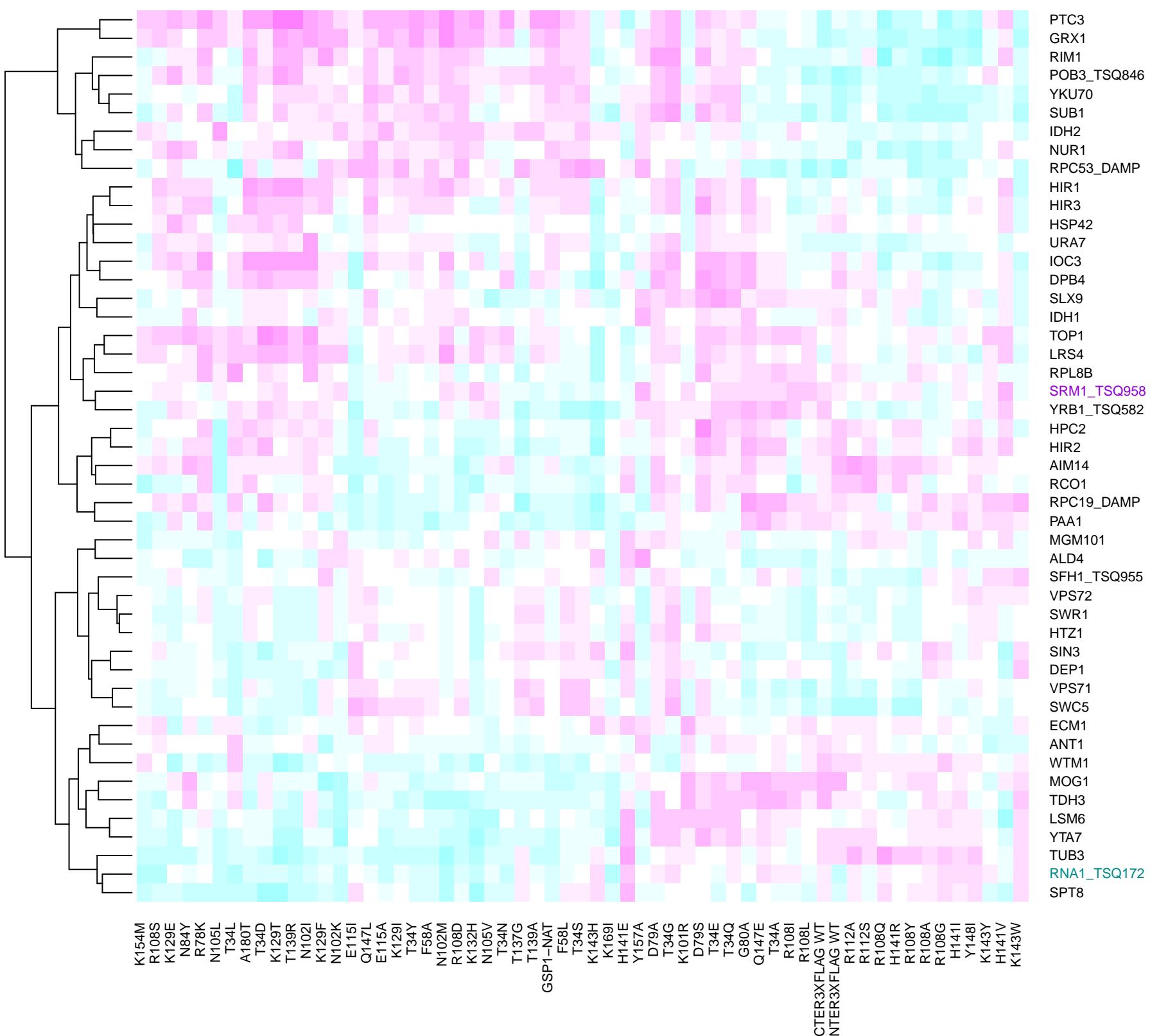
mitochondria and respiration_GO_30_5

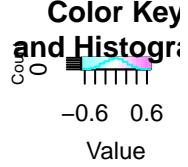




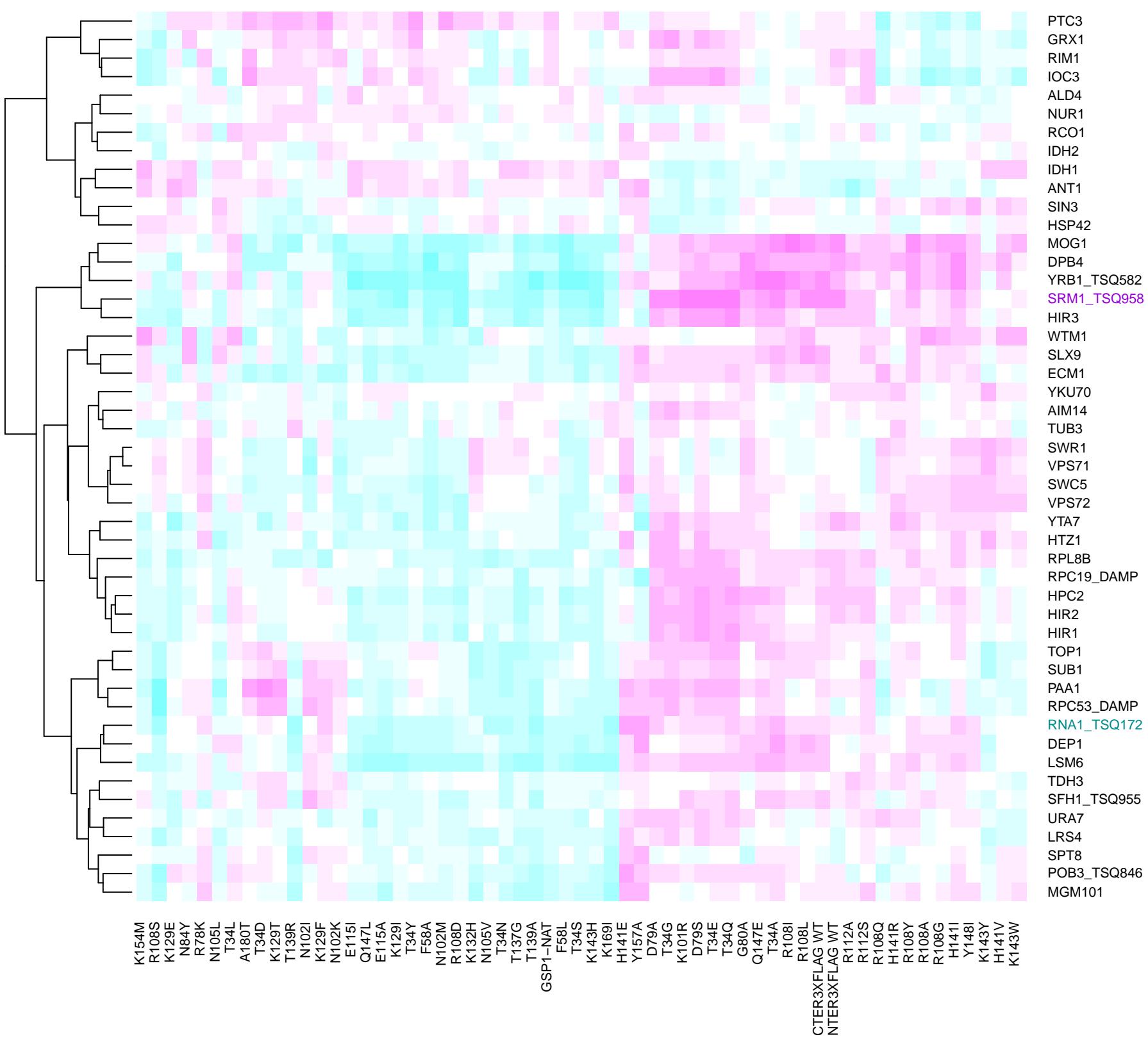


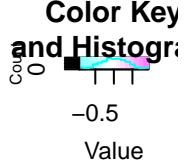
DNA repair_GO_30_3



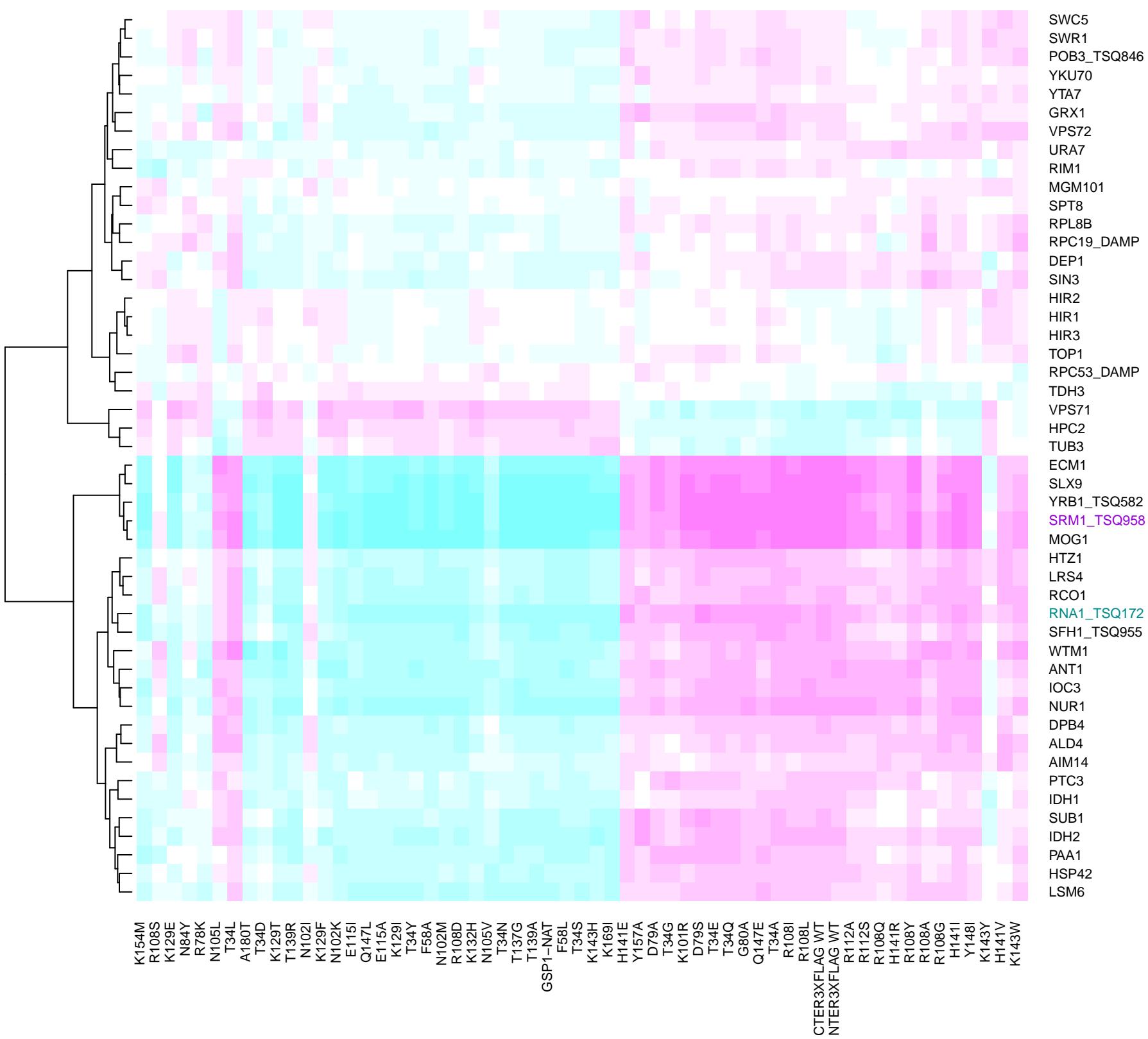


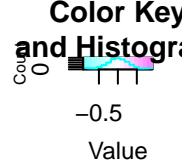
sporulation_GO_30_1



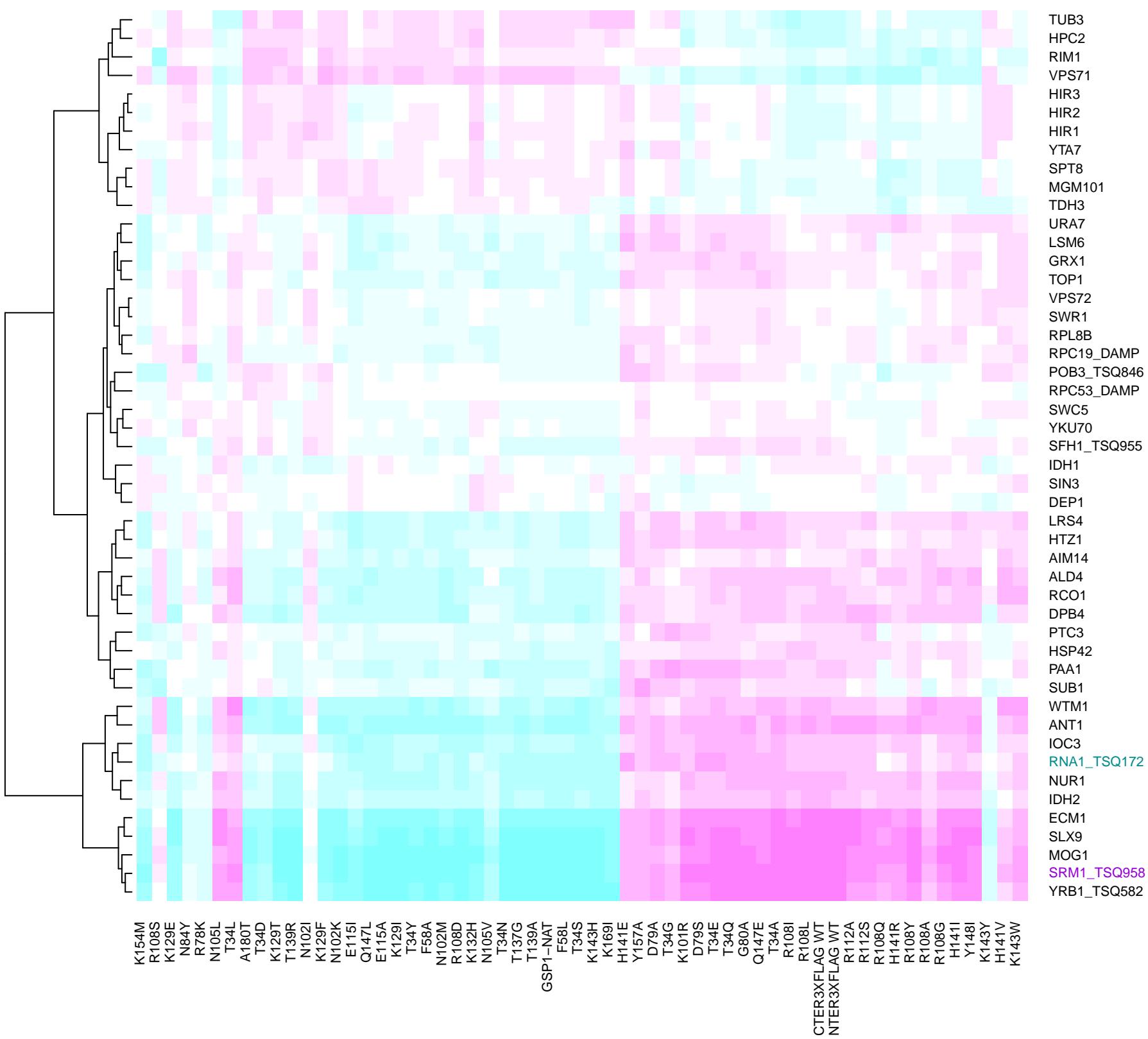


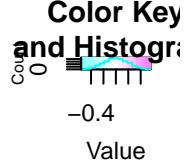
nuclear transport and organization_GO_30_1



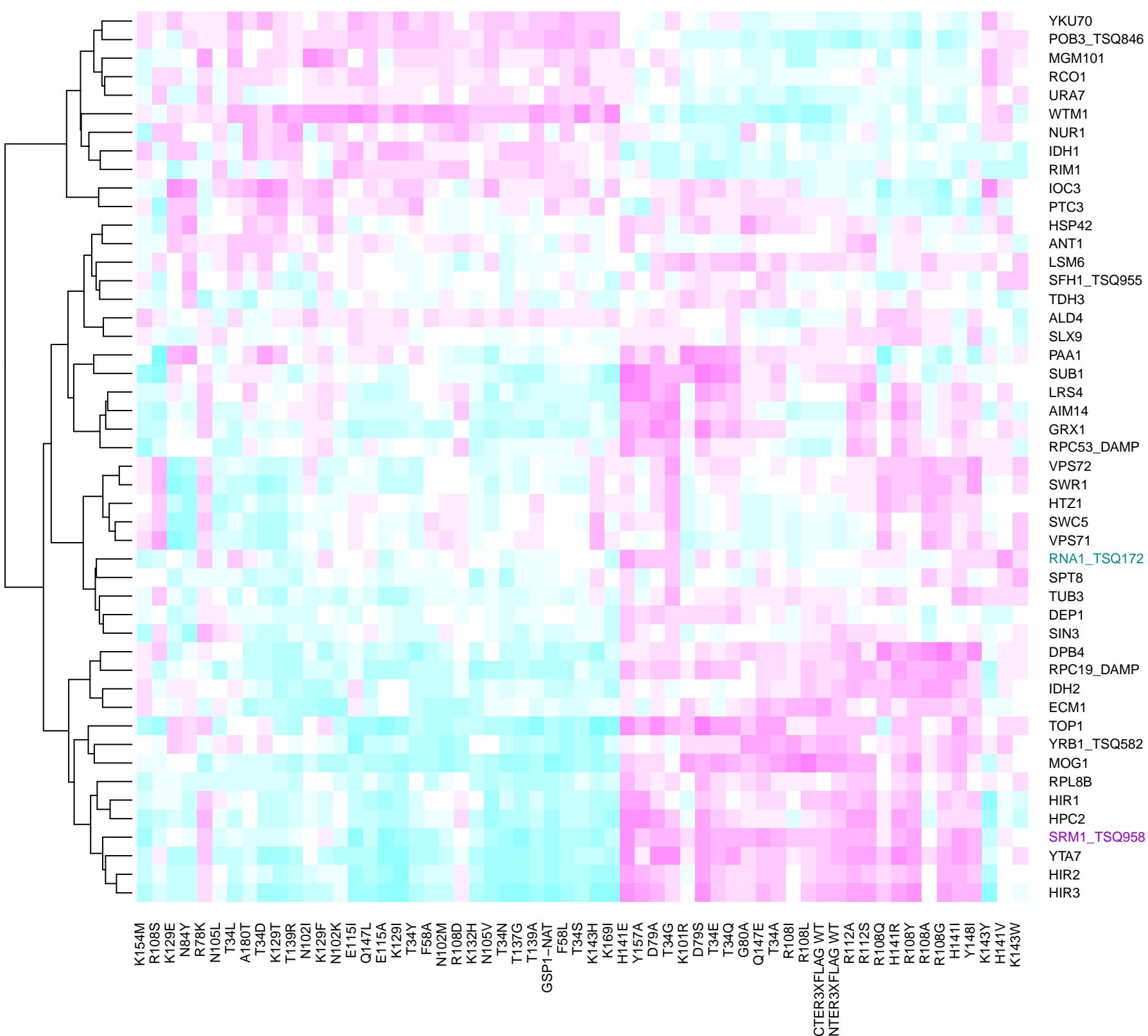


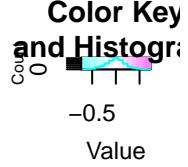
nuclear transport_GO_30_1





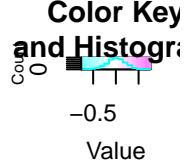
cellular amino acid metabolic process_GO_30_2



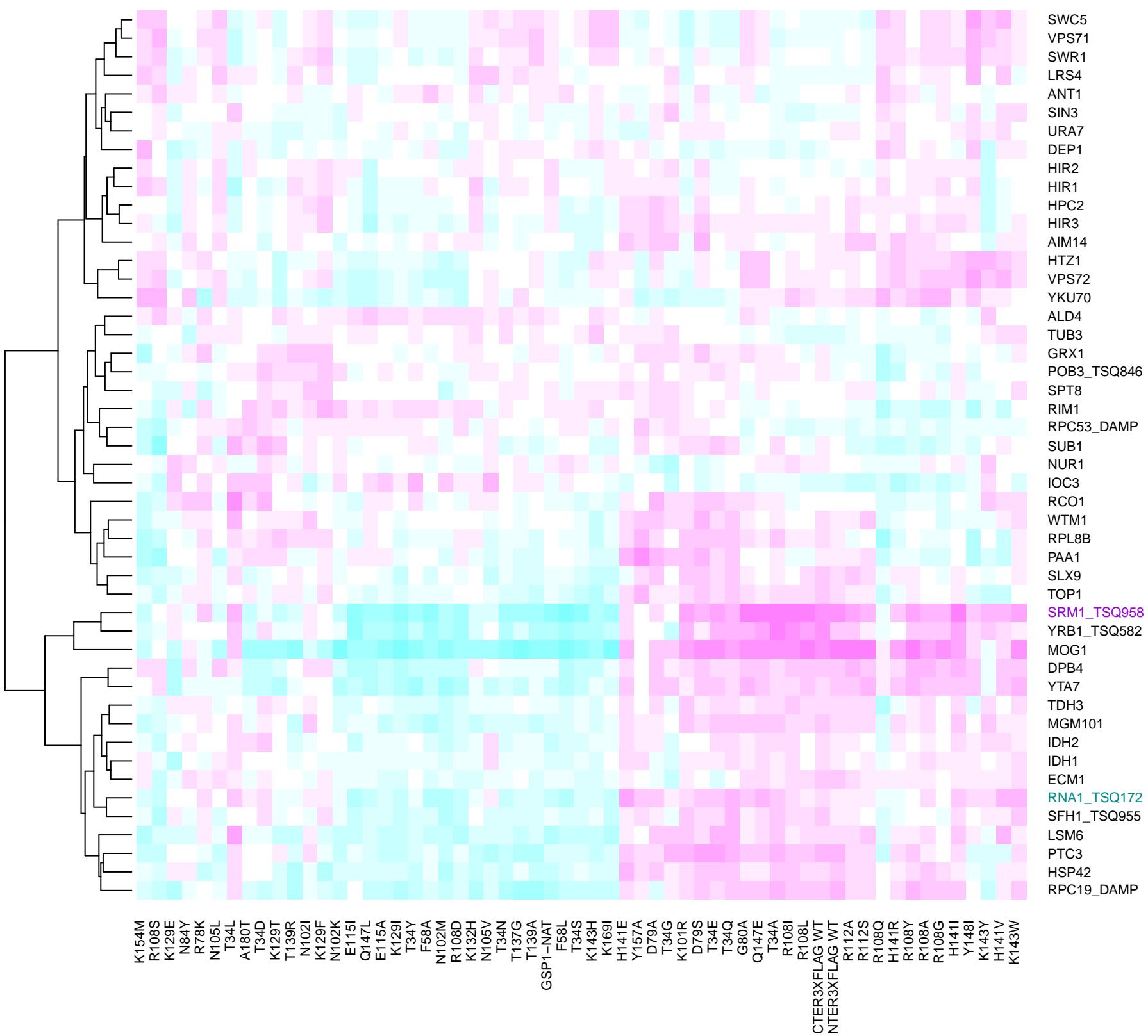


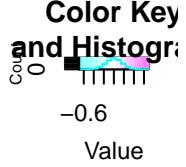
metabolic_GO_30_13



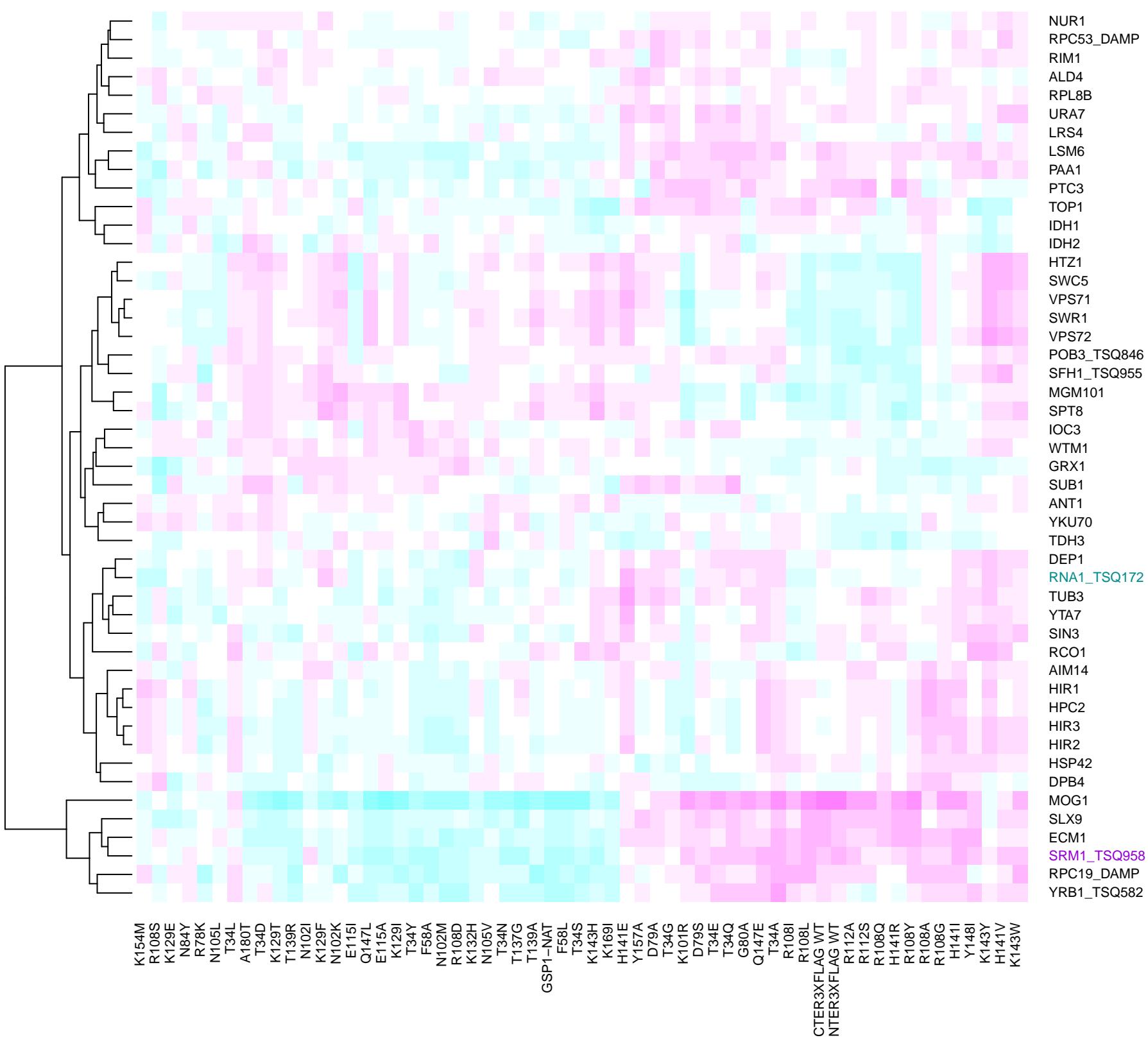


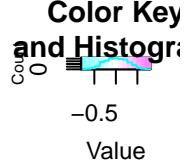
mitochondrion_GO_30_10



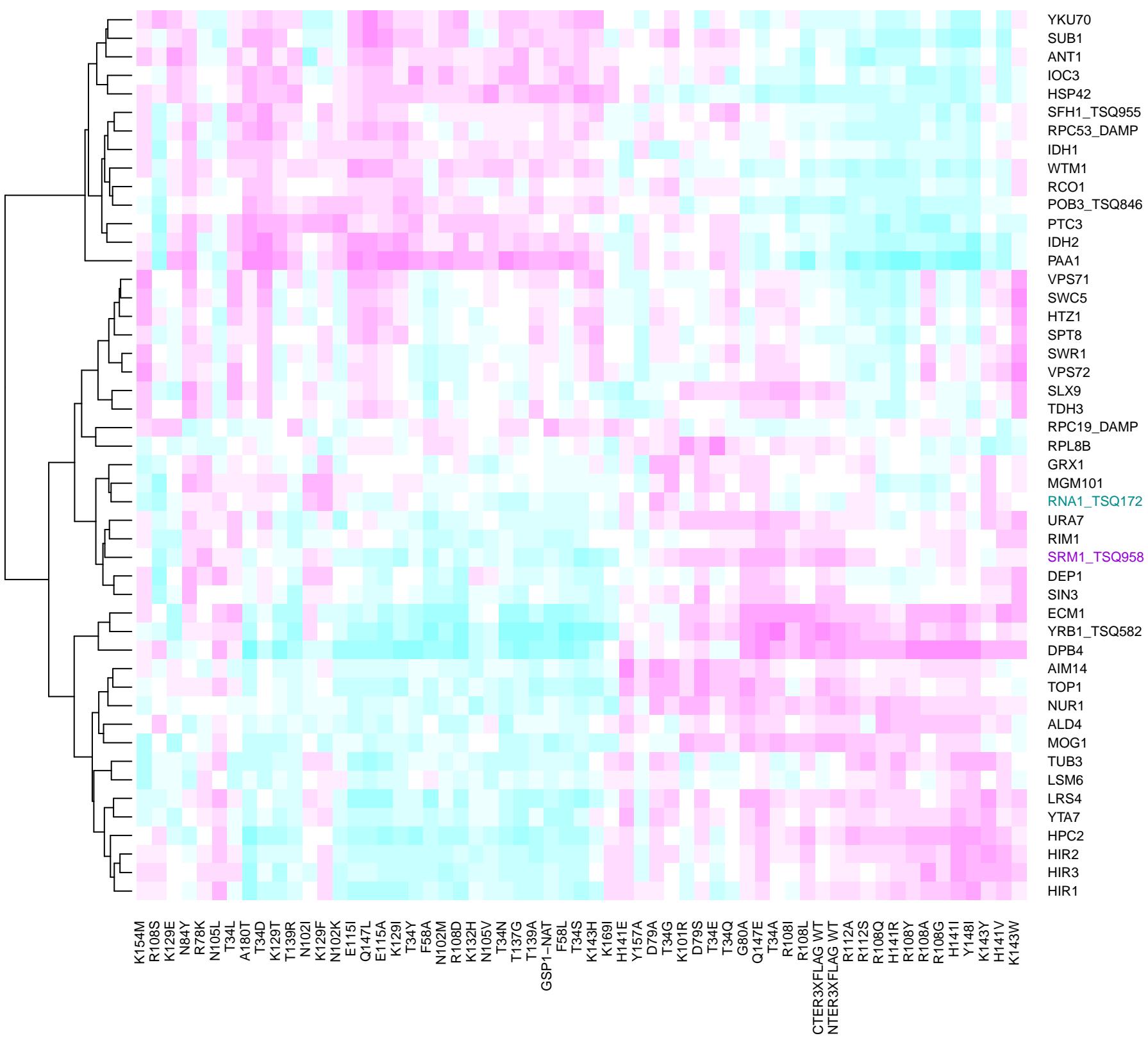


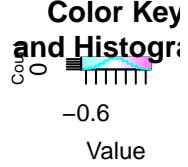
transcription and mRNA processing_GO_30_1



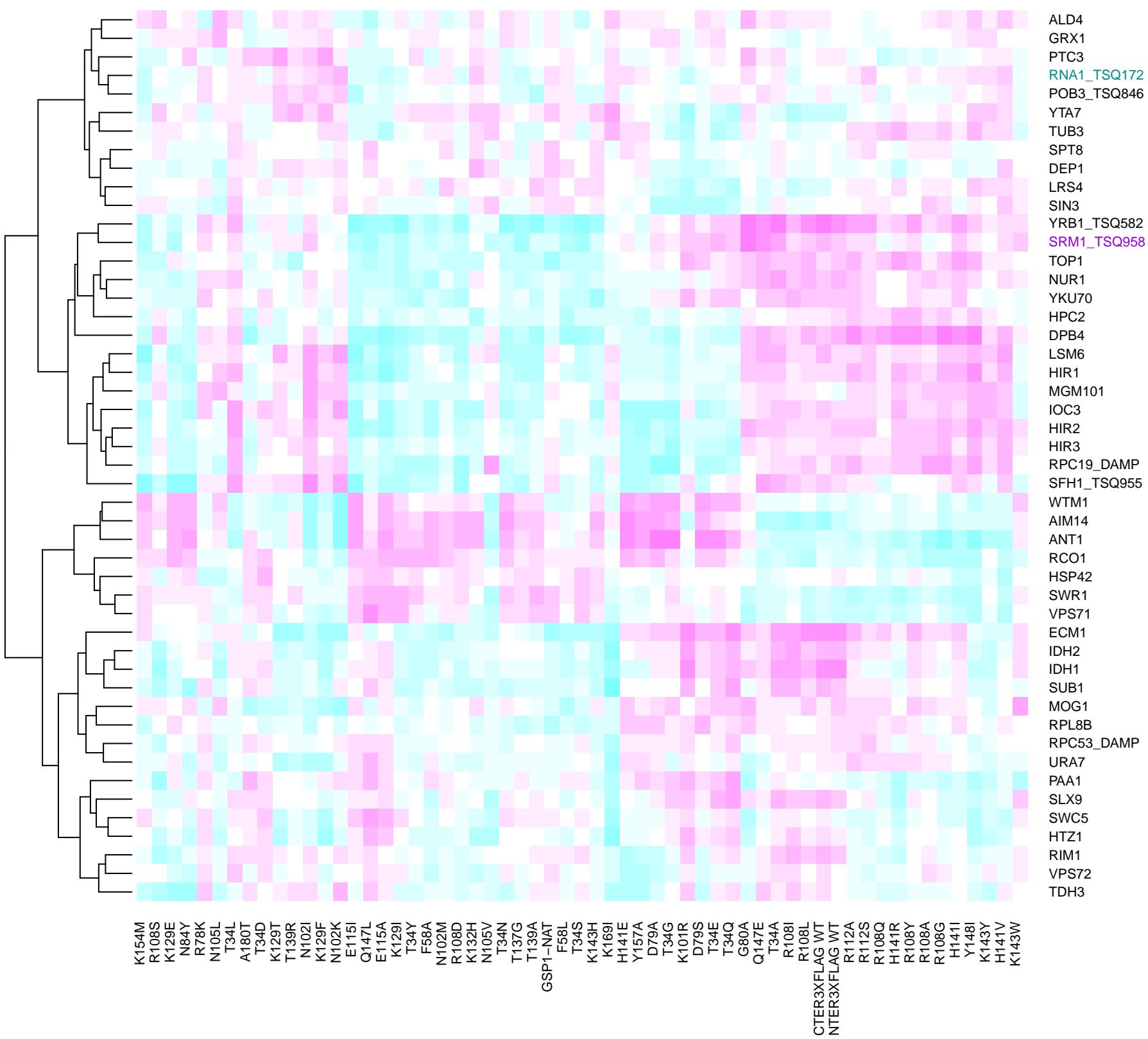


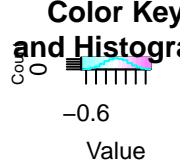
endomembrane system_GO_30_14



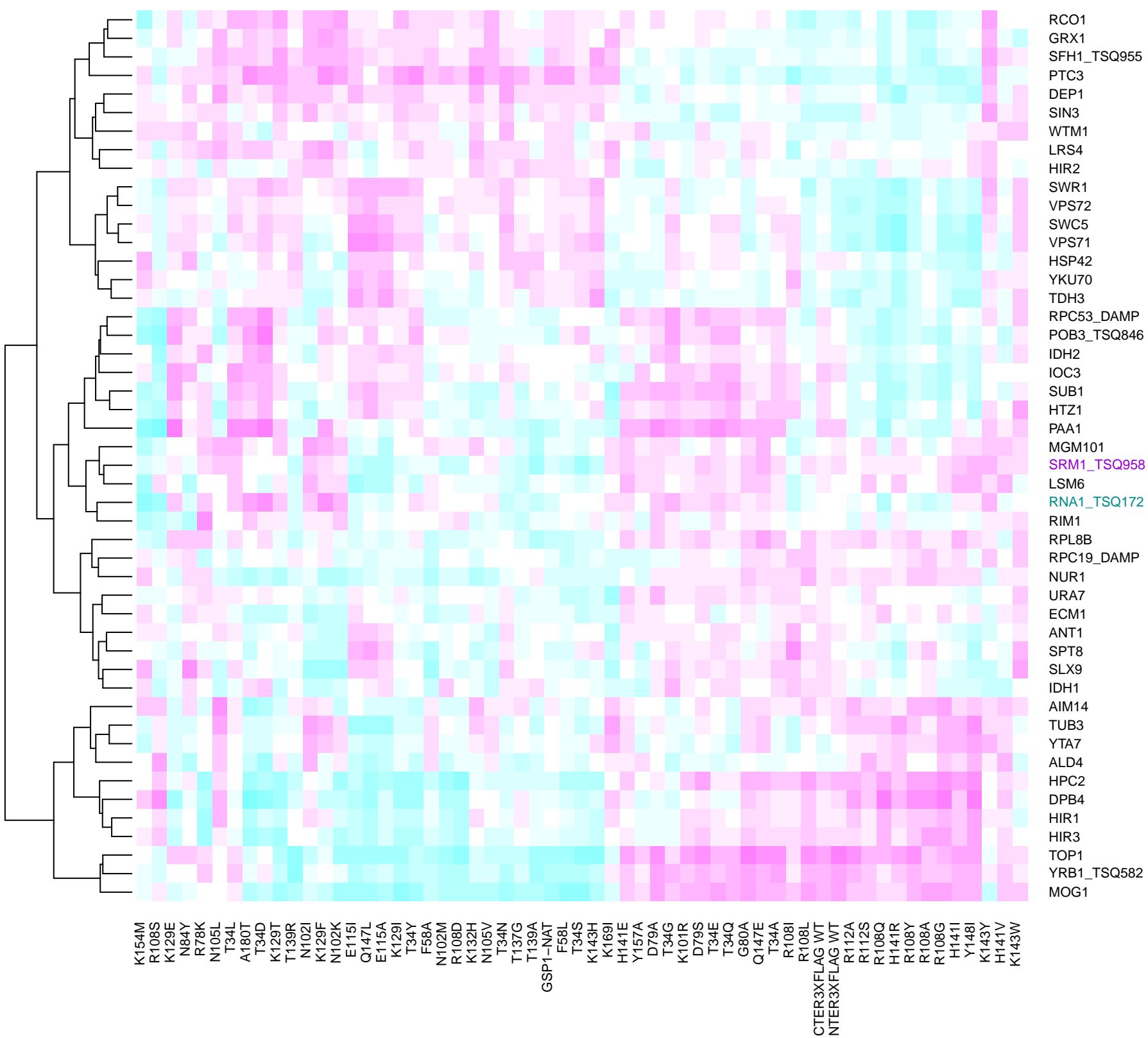


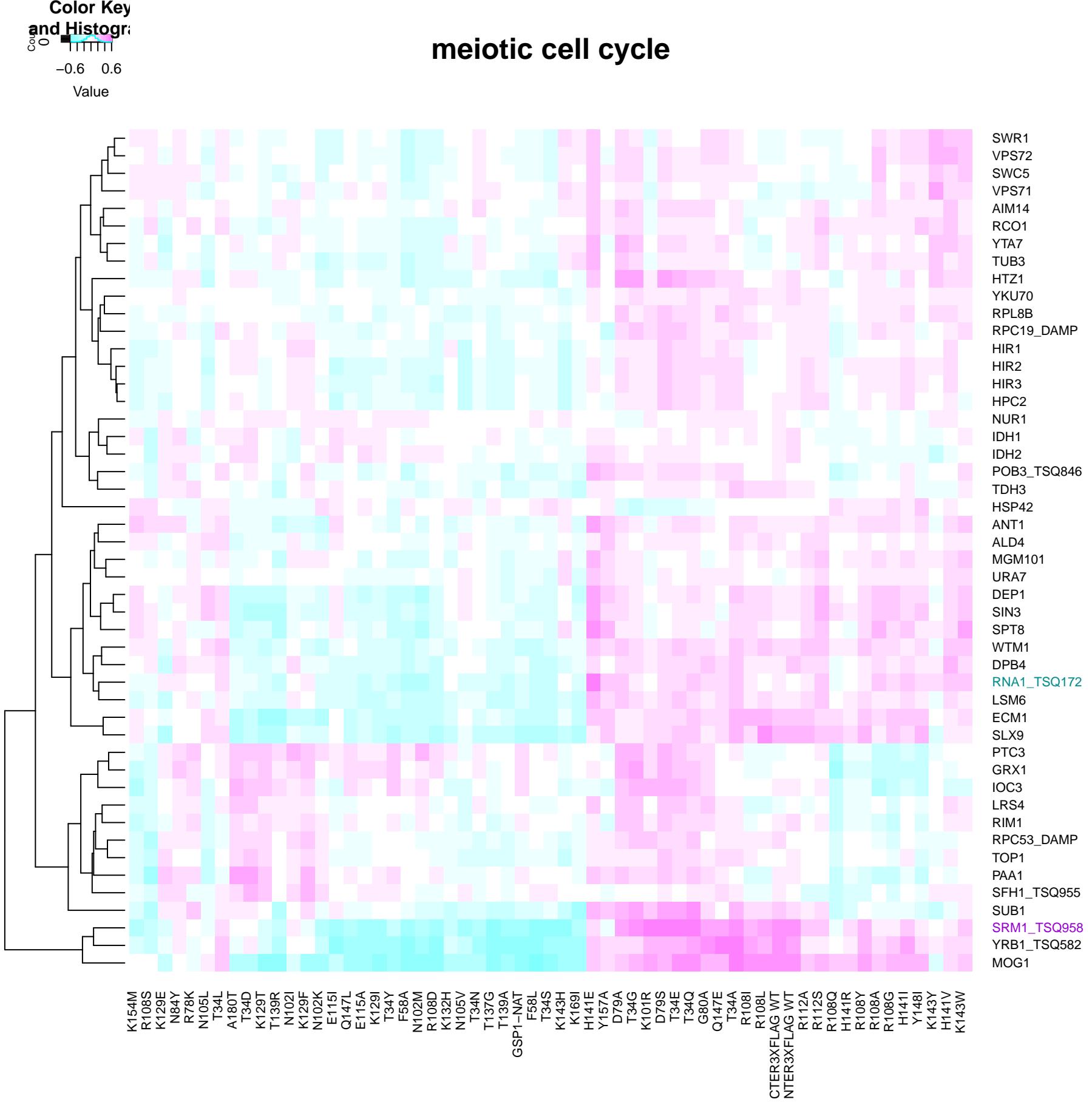
Golgi and ER_GO_30_8

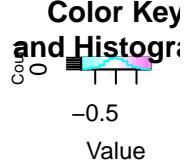




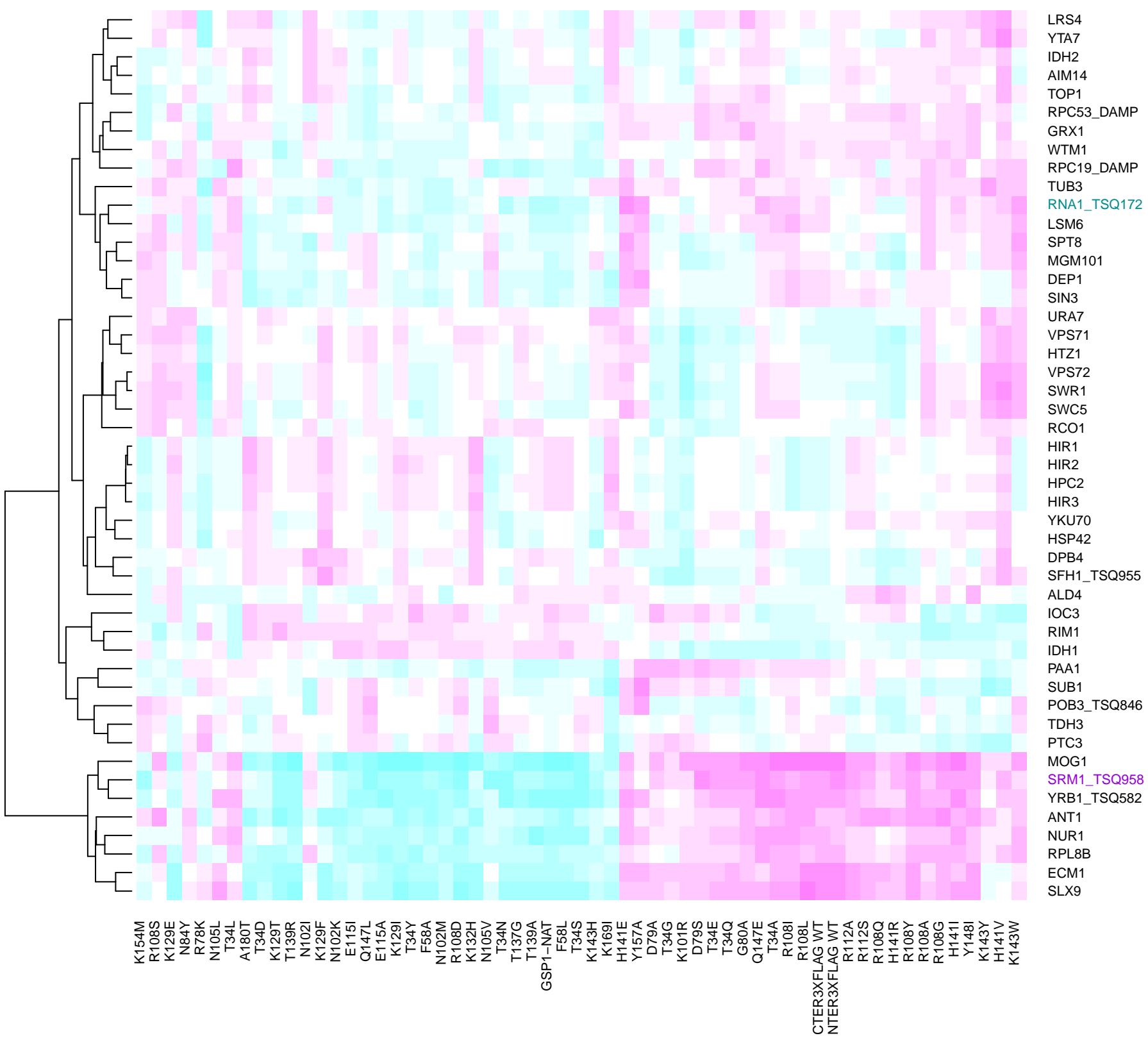
Golgi vesicle transport_GO_30_3

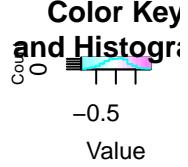




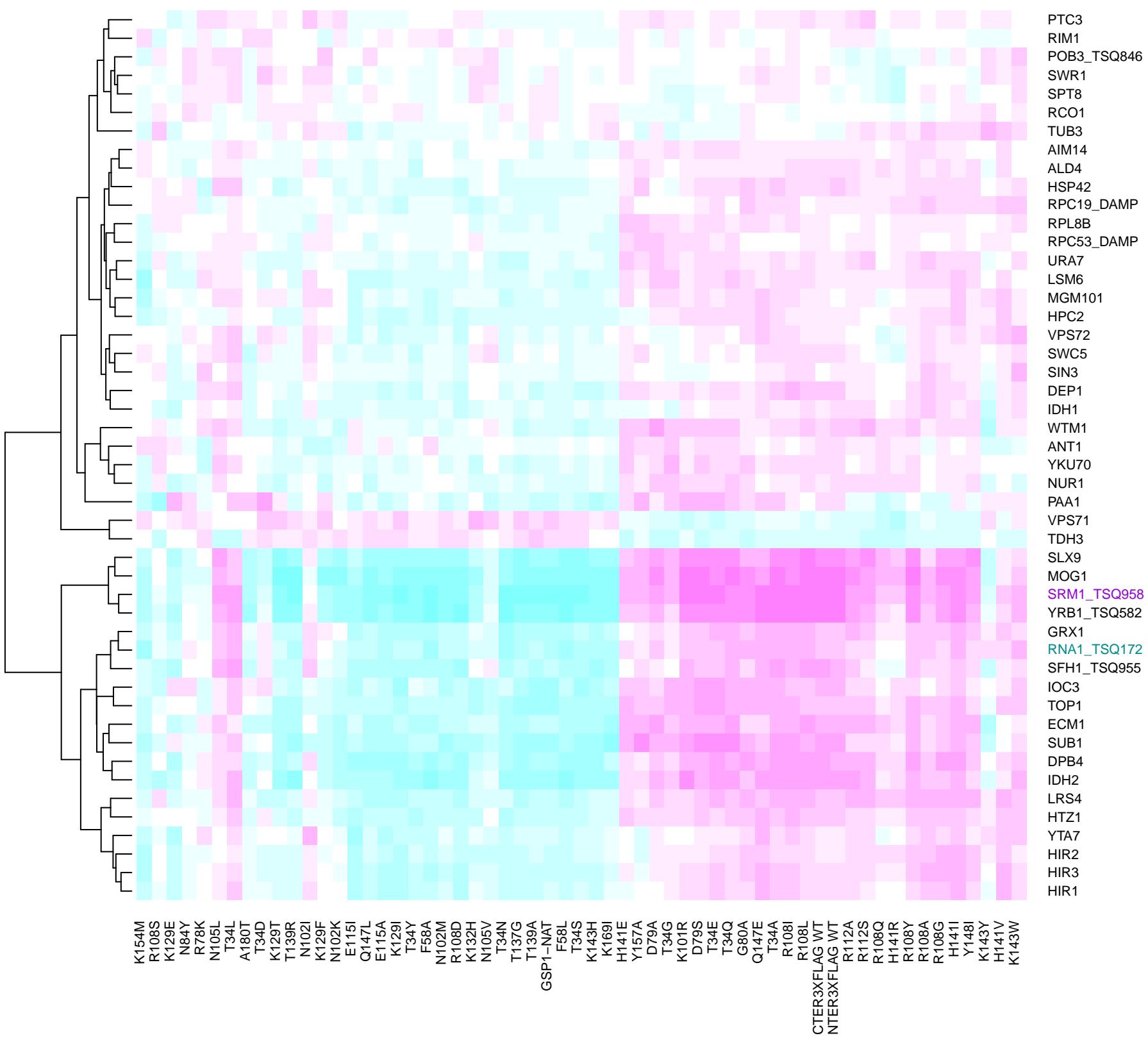


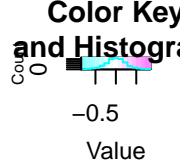
chromatin organization_GO_30_3



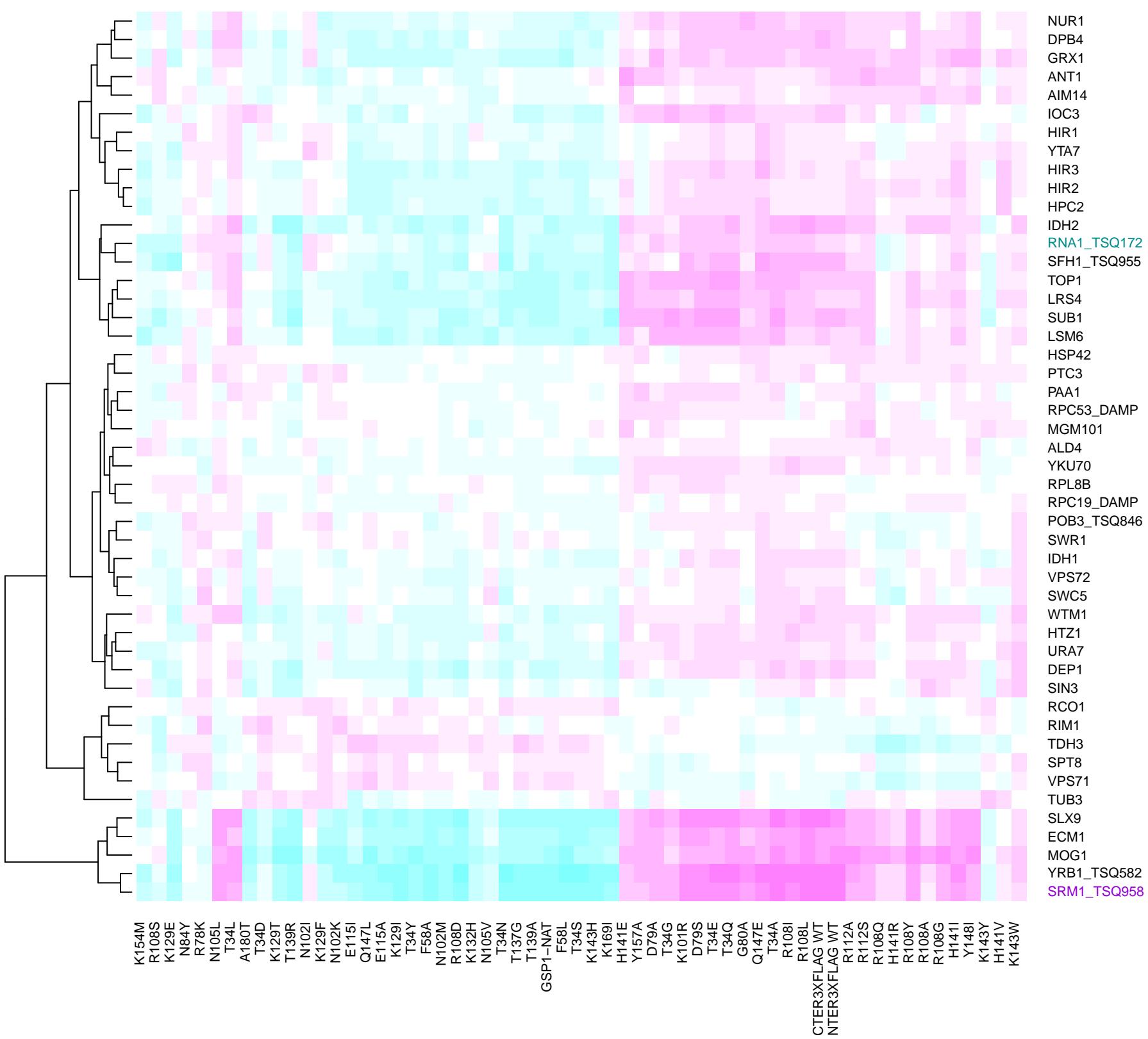


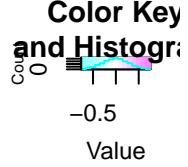
lipid binding_GO_30_2



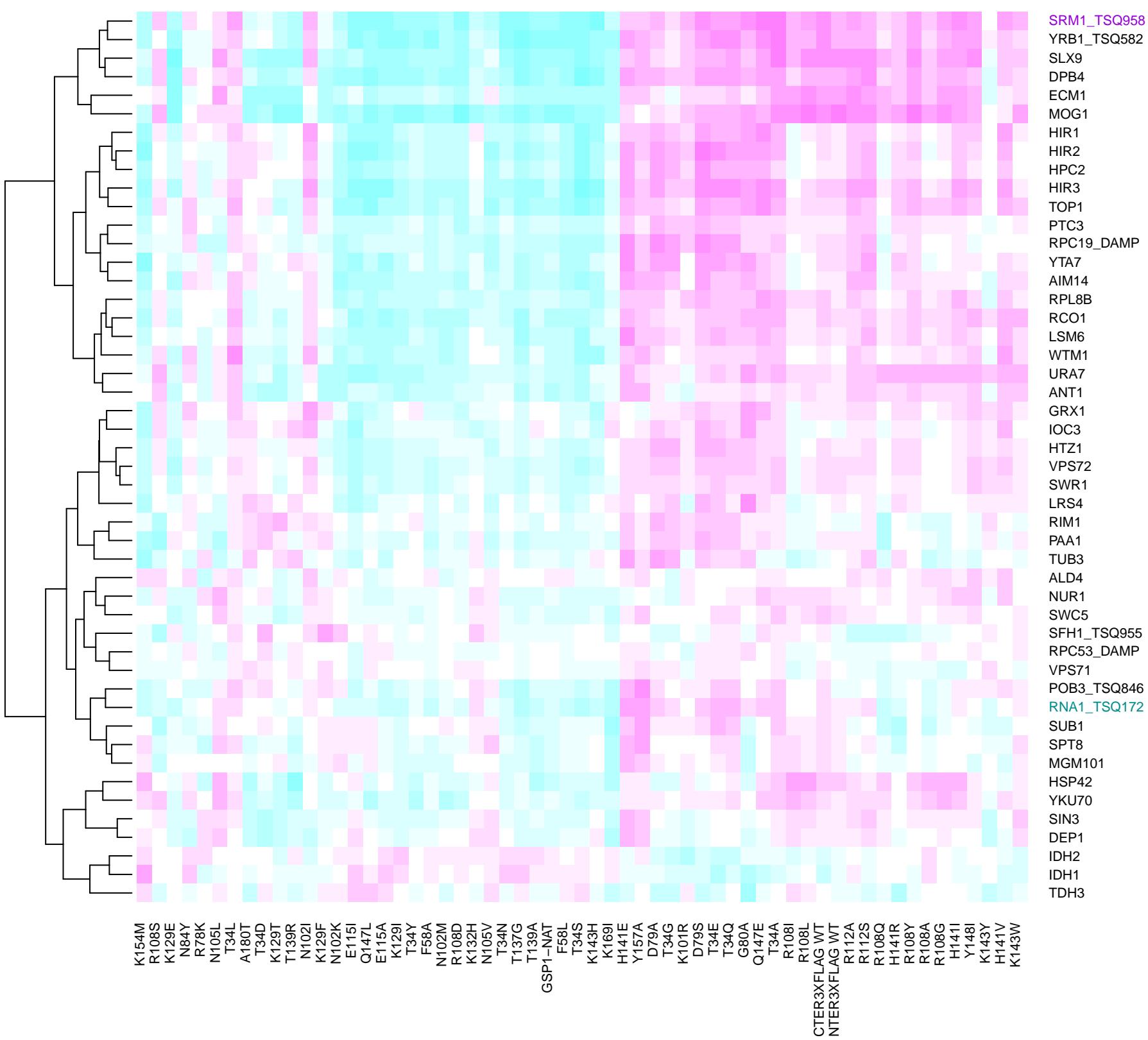


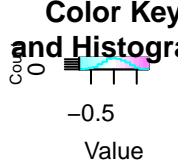
lipids_GO_30_2



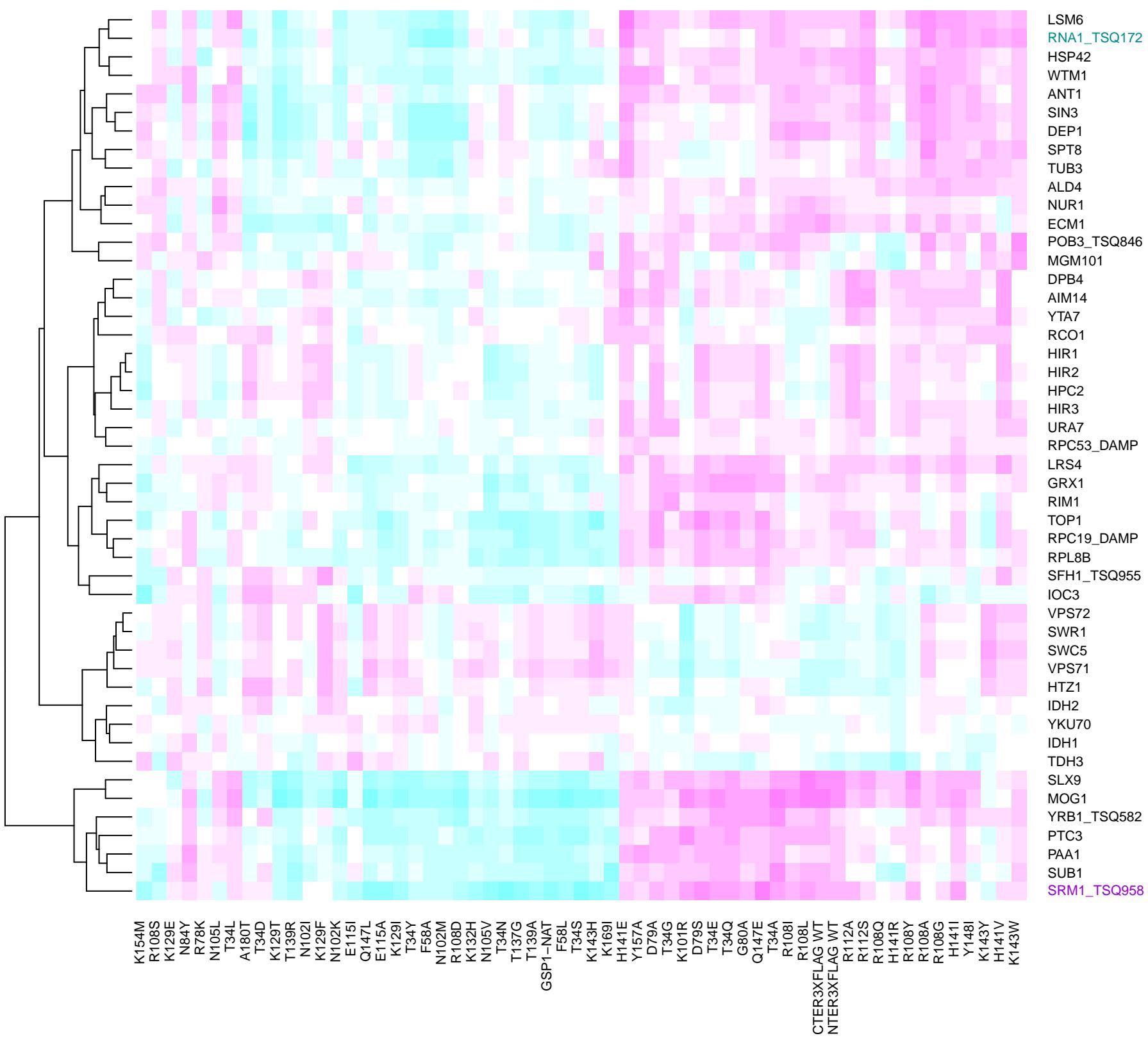


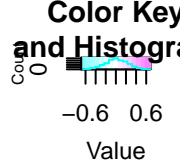
nuclear transport and organization_GO_30_2



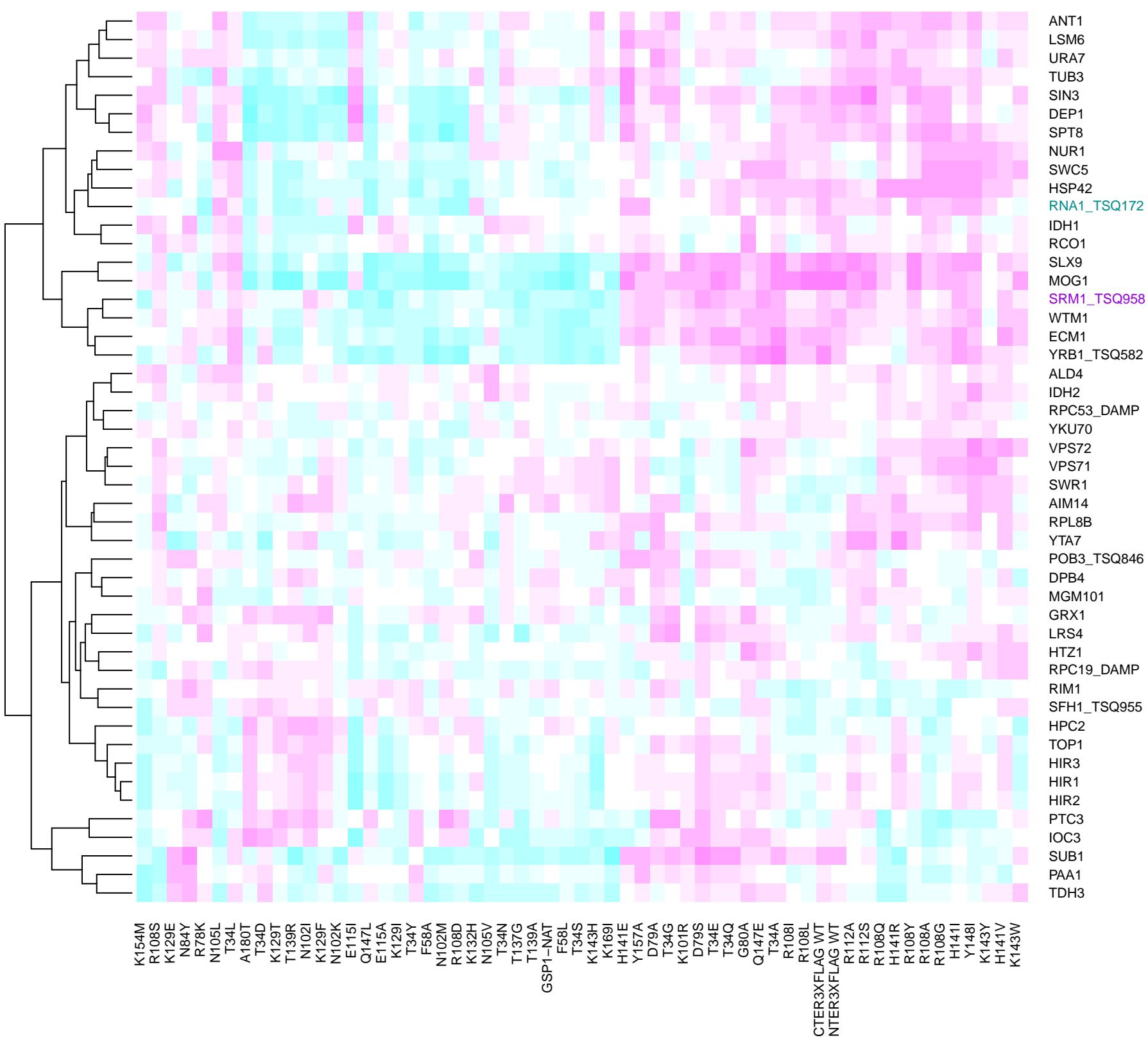


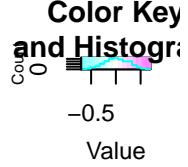
peptidyl-amino acid modification_GO_30_1



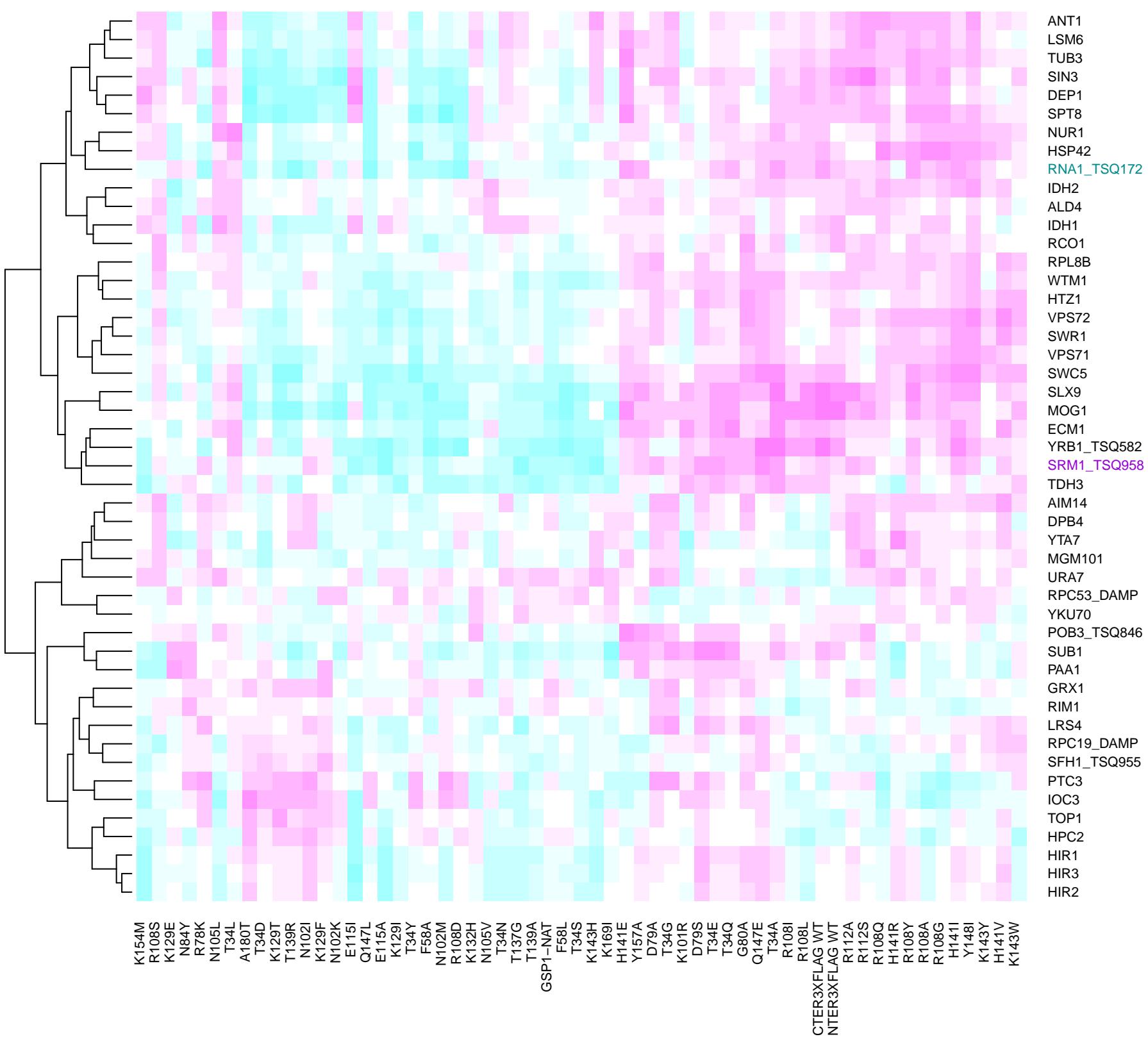


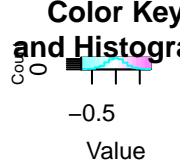
telomere organization



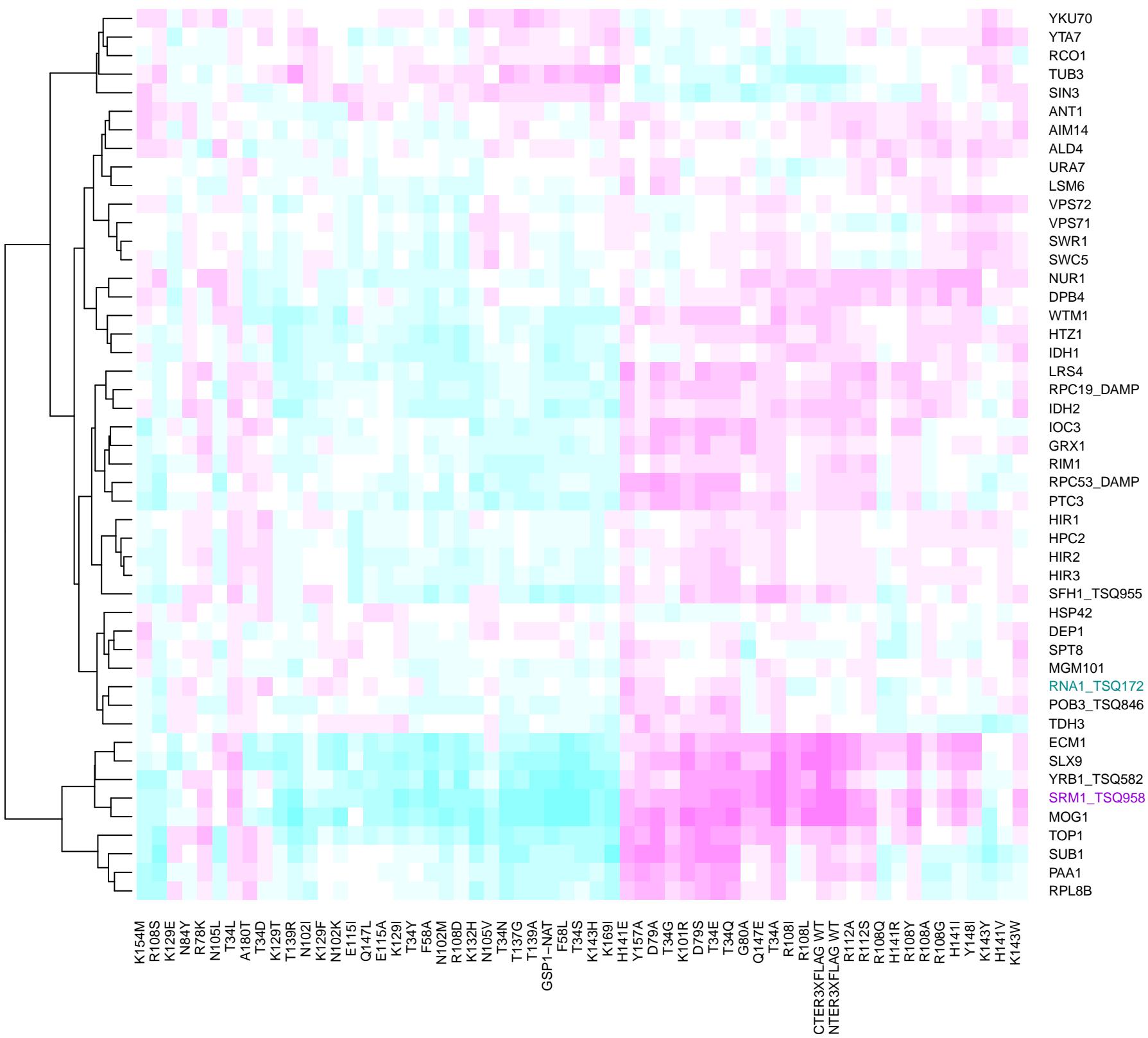


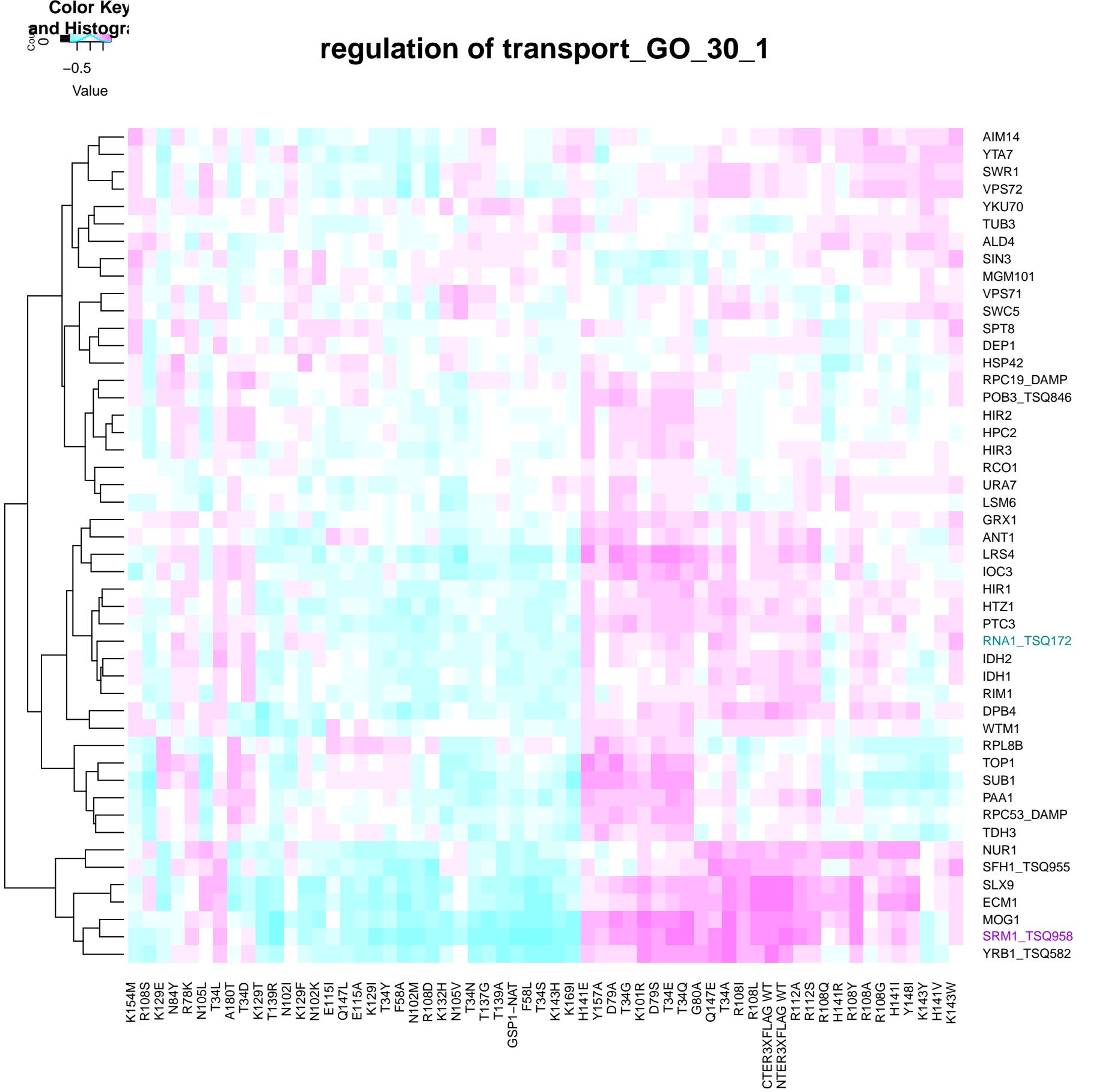
telomere organization_GO_30_1

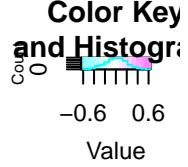




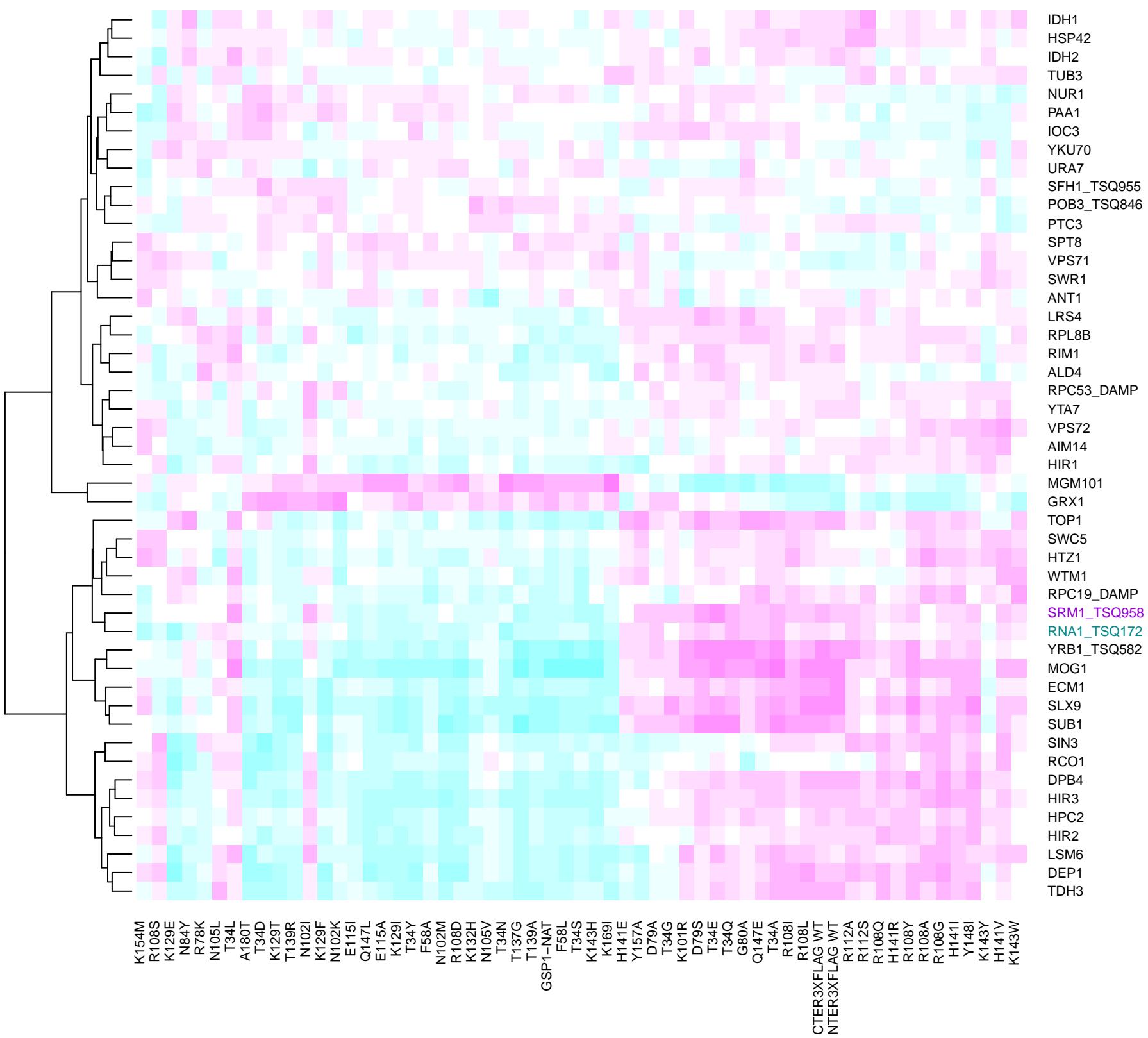
regulation of transport

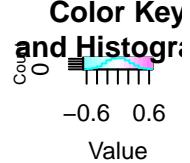




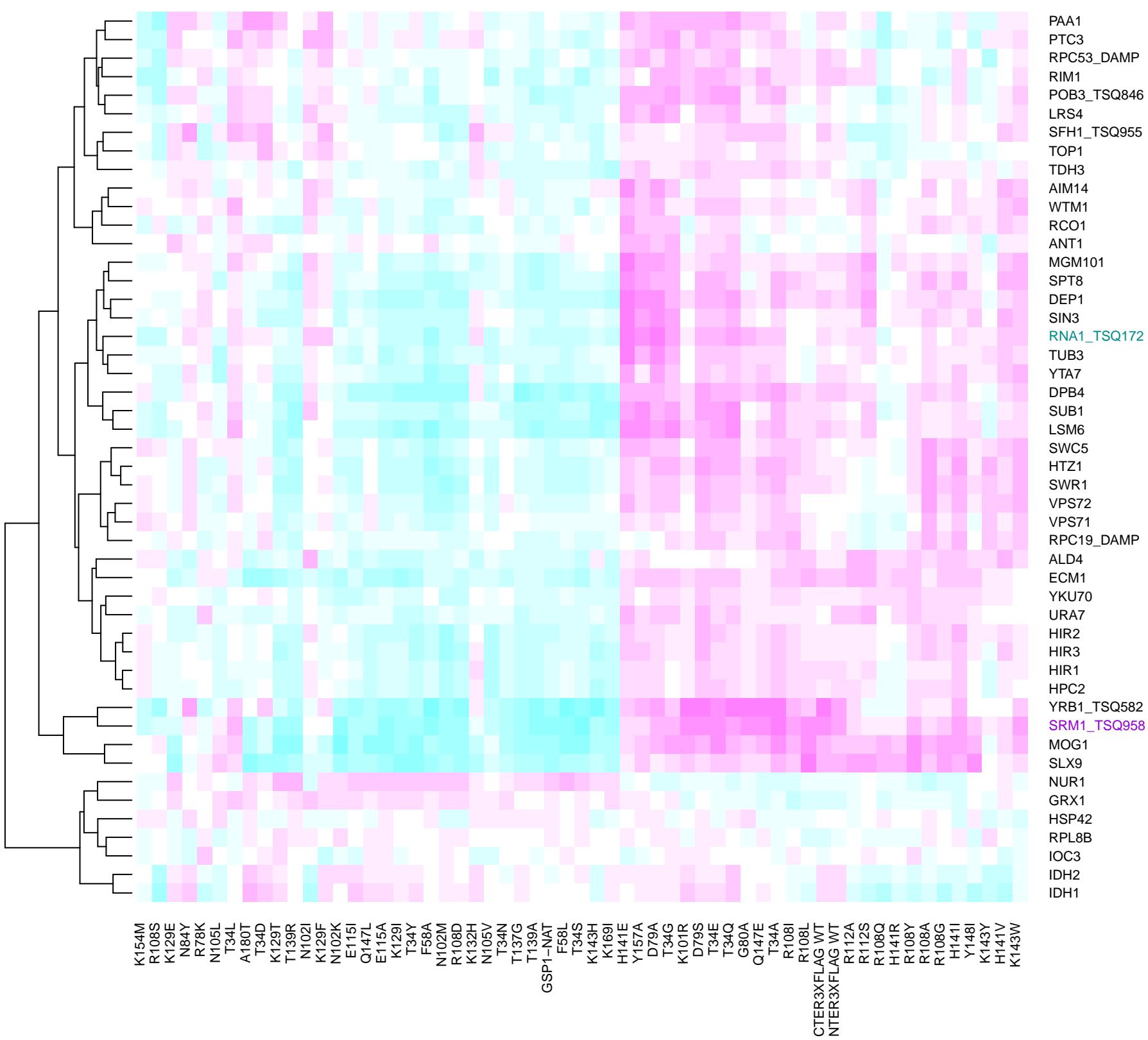


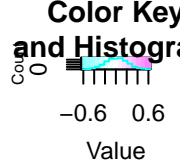
vacuole_GO_30_3



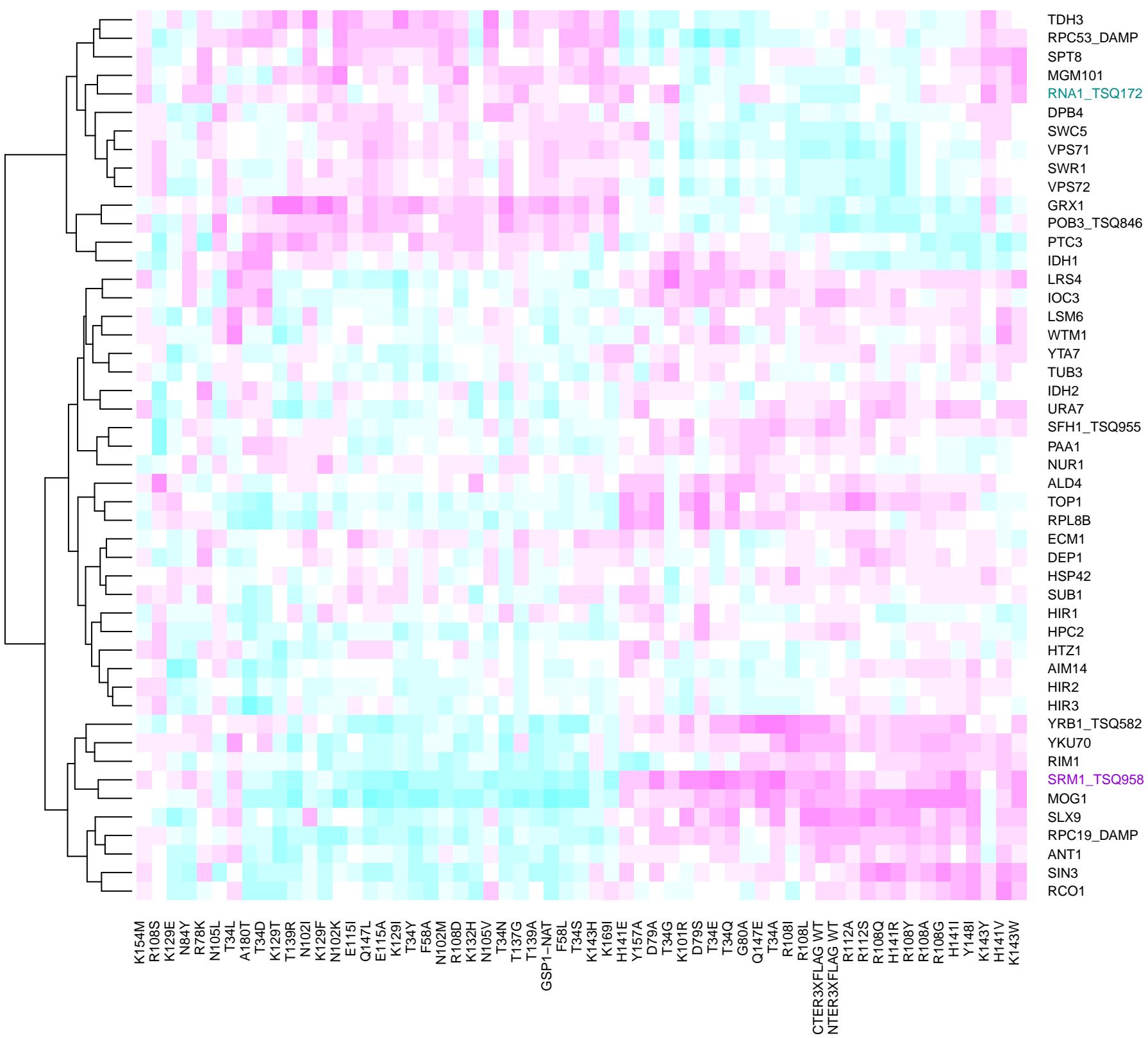


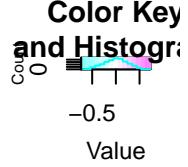
meiotic cell cycle_GO_30_2



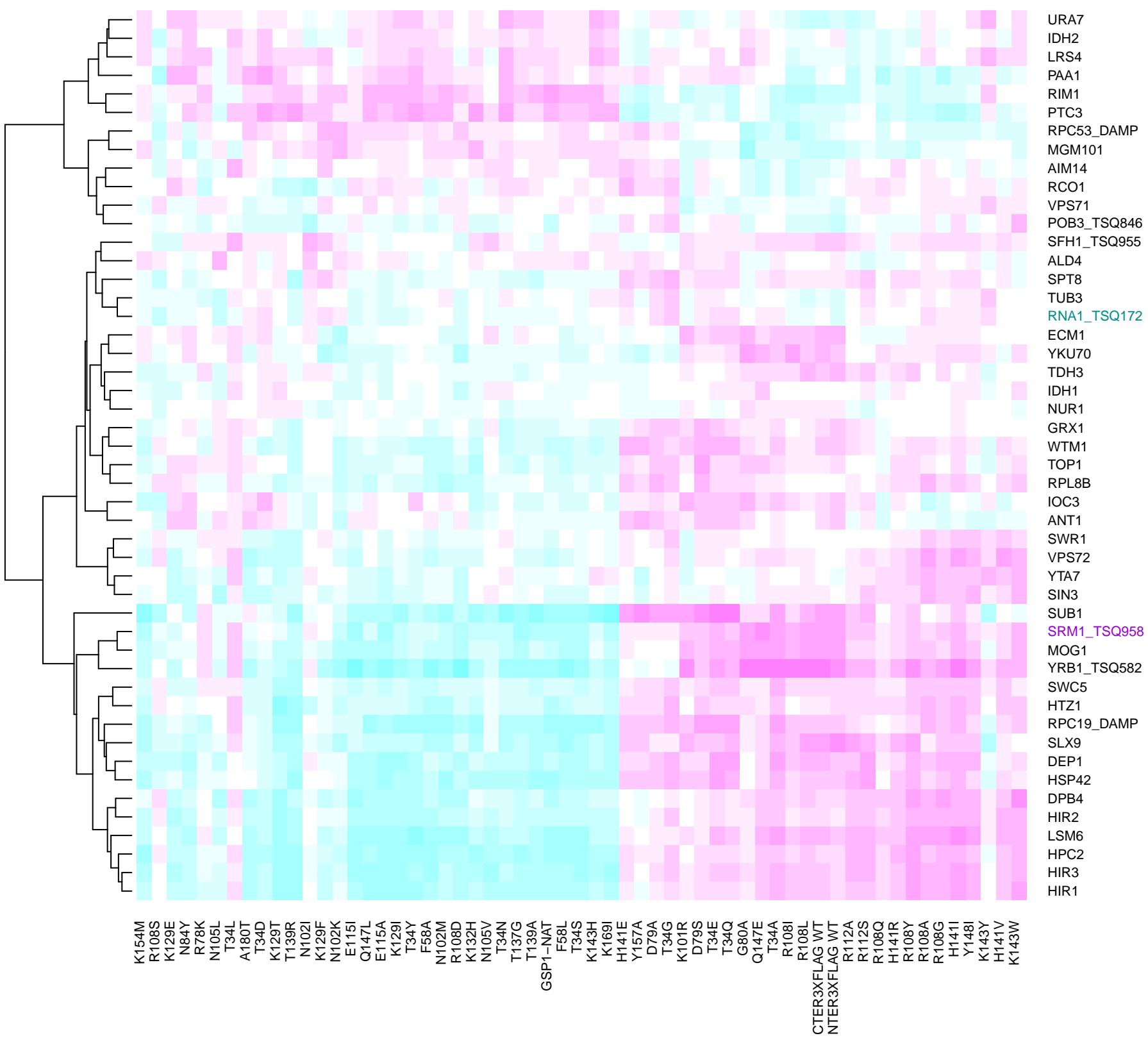


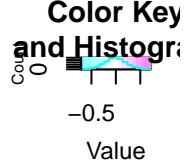
vacuoles_GO_30_6



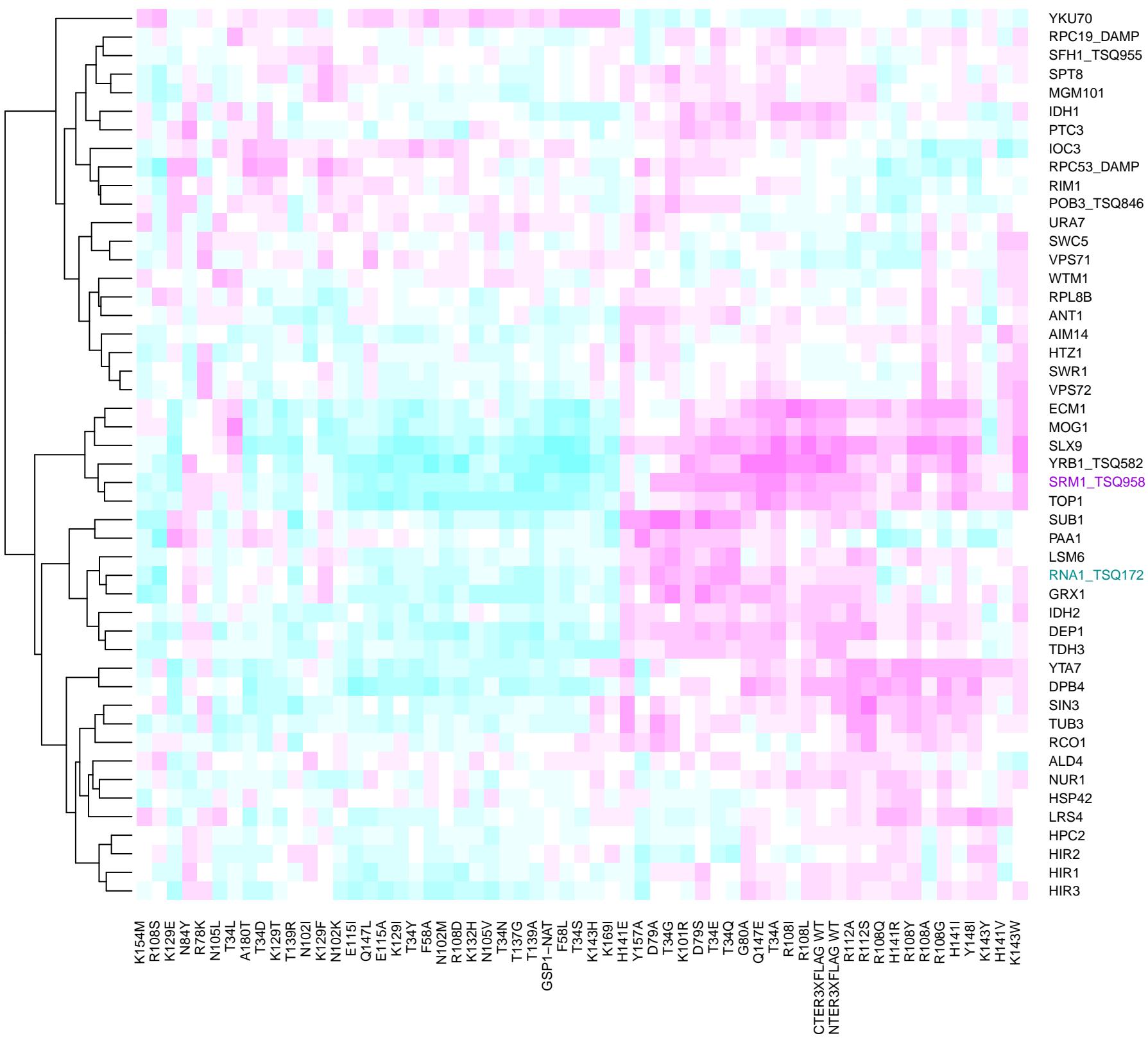


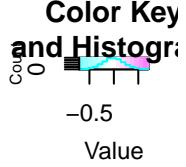
endomembrane system_GO_30_10



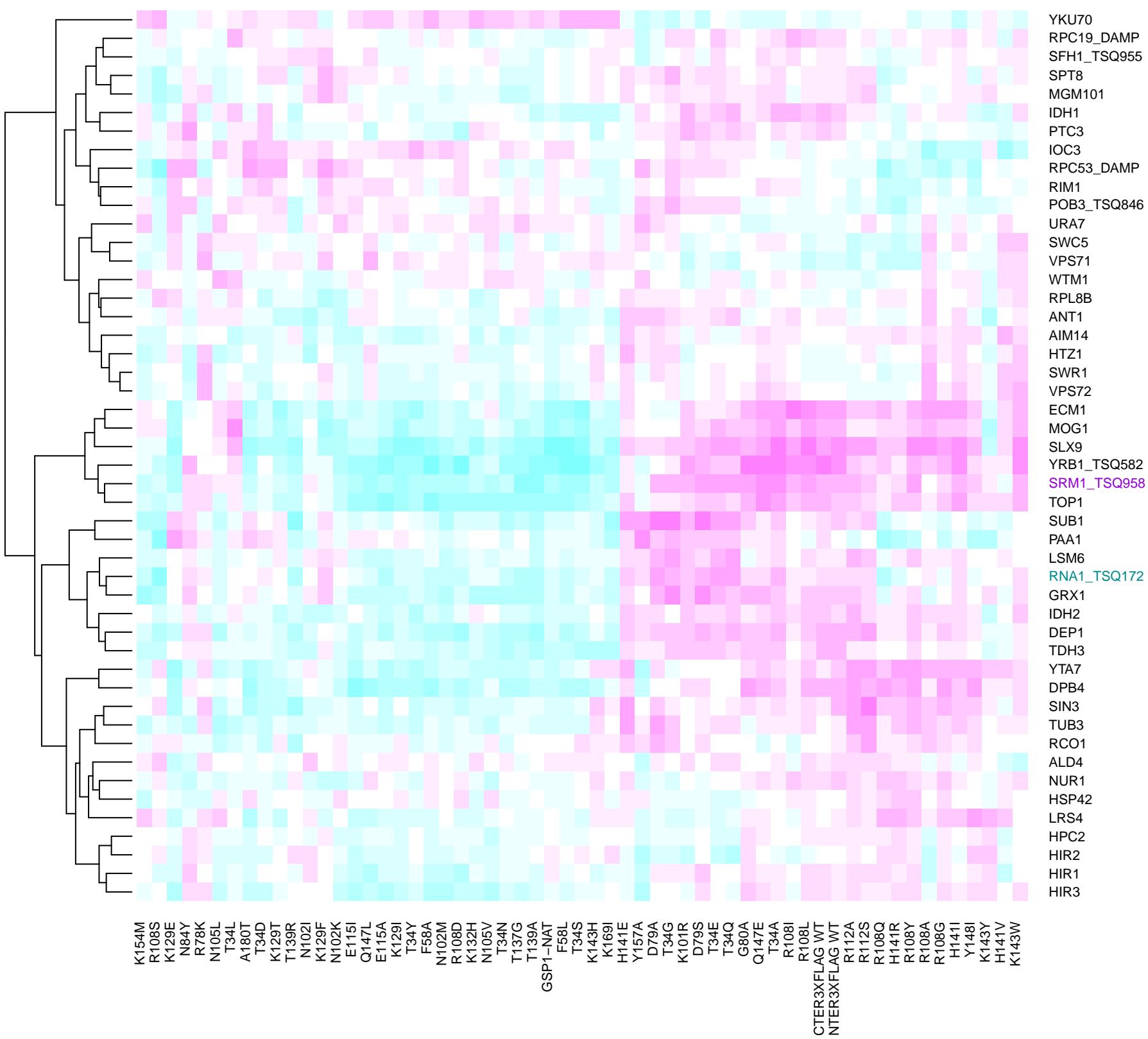


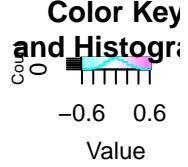
endoplasmic reticulum_GO_30_5



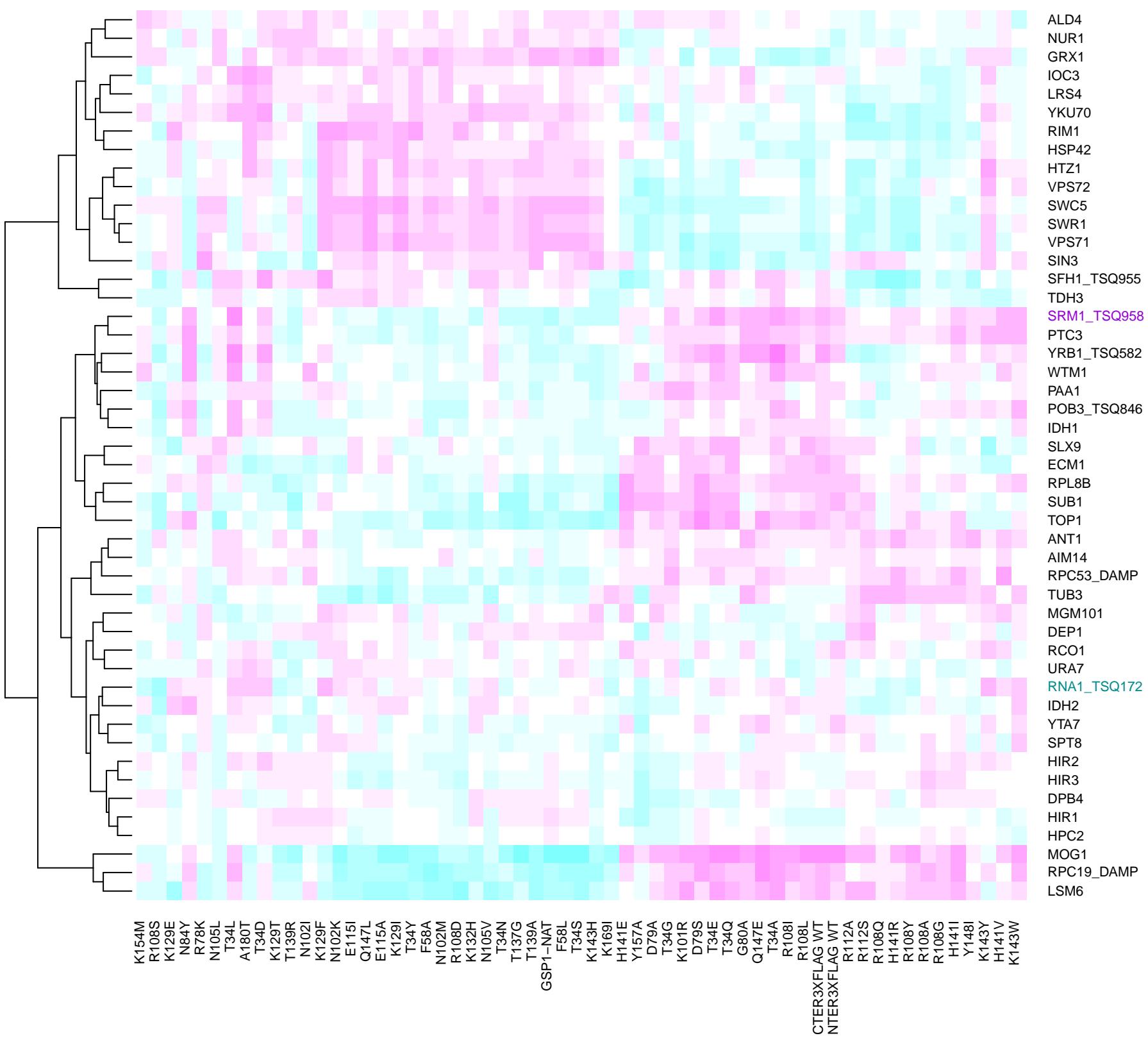


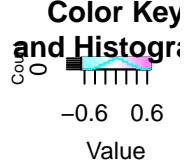
ER_GO_30_5



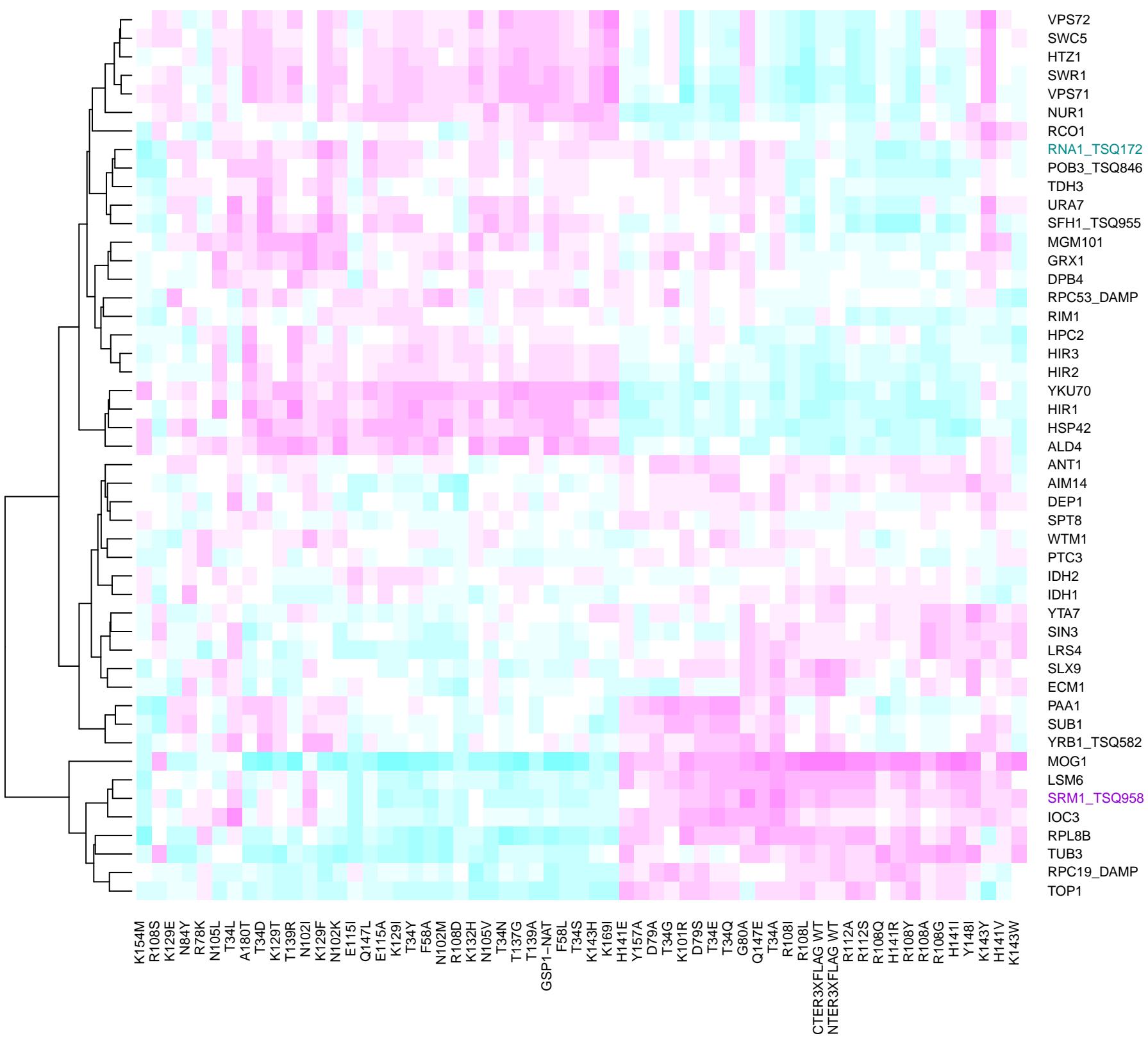


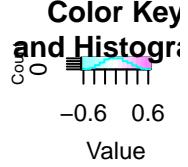
Golgi and ER_GO_30_1





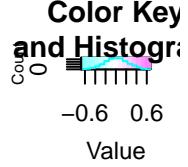
mitochondrion_GO_30_6



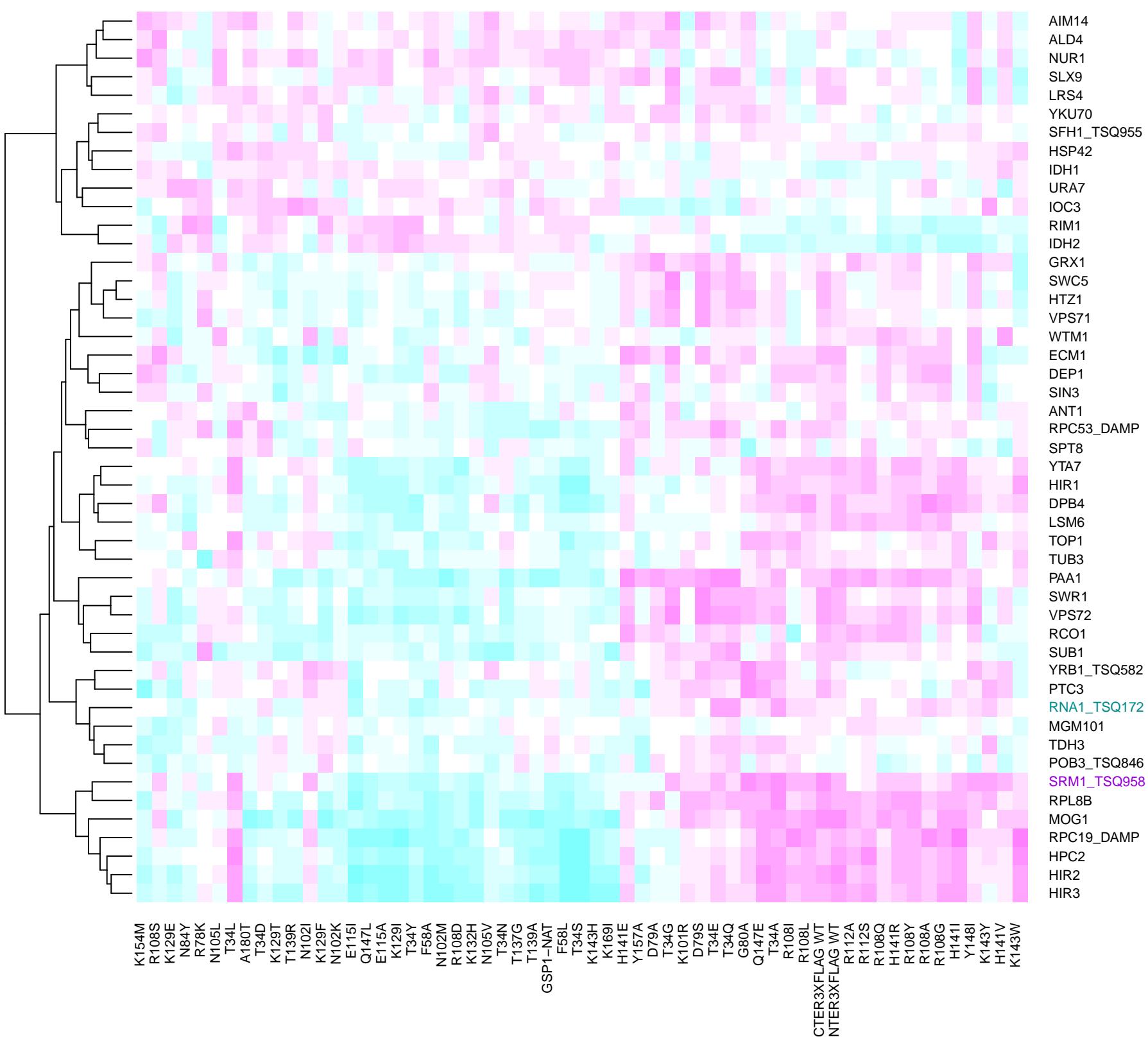


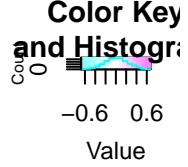
cytoplasmic vesicle_GO_30_2



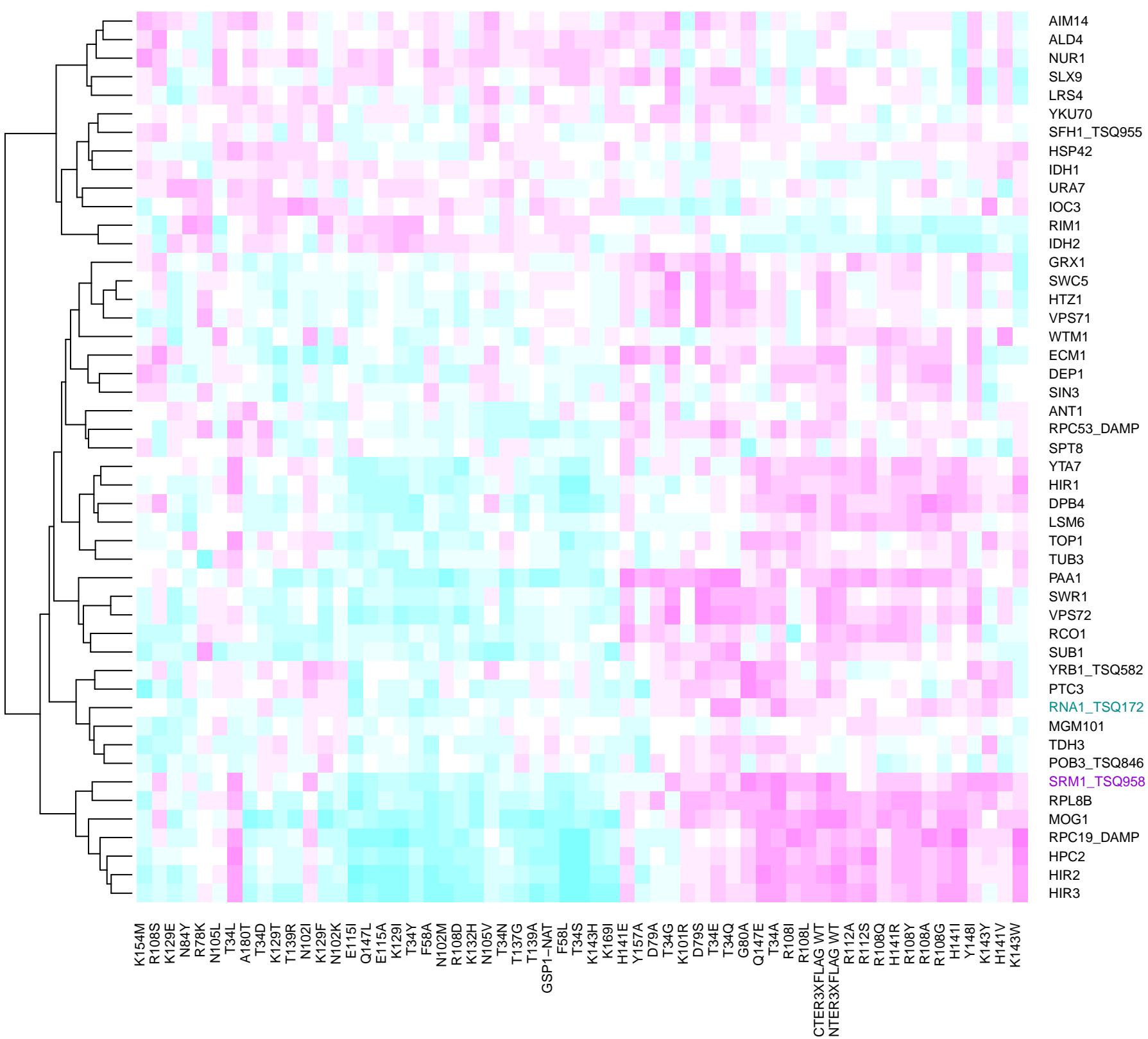


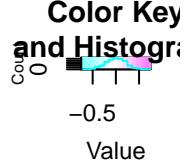
endoplasmic reticulum_GO_30_11



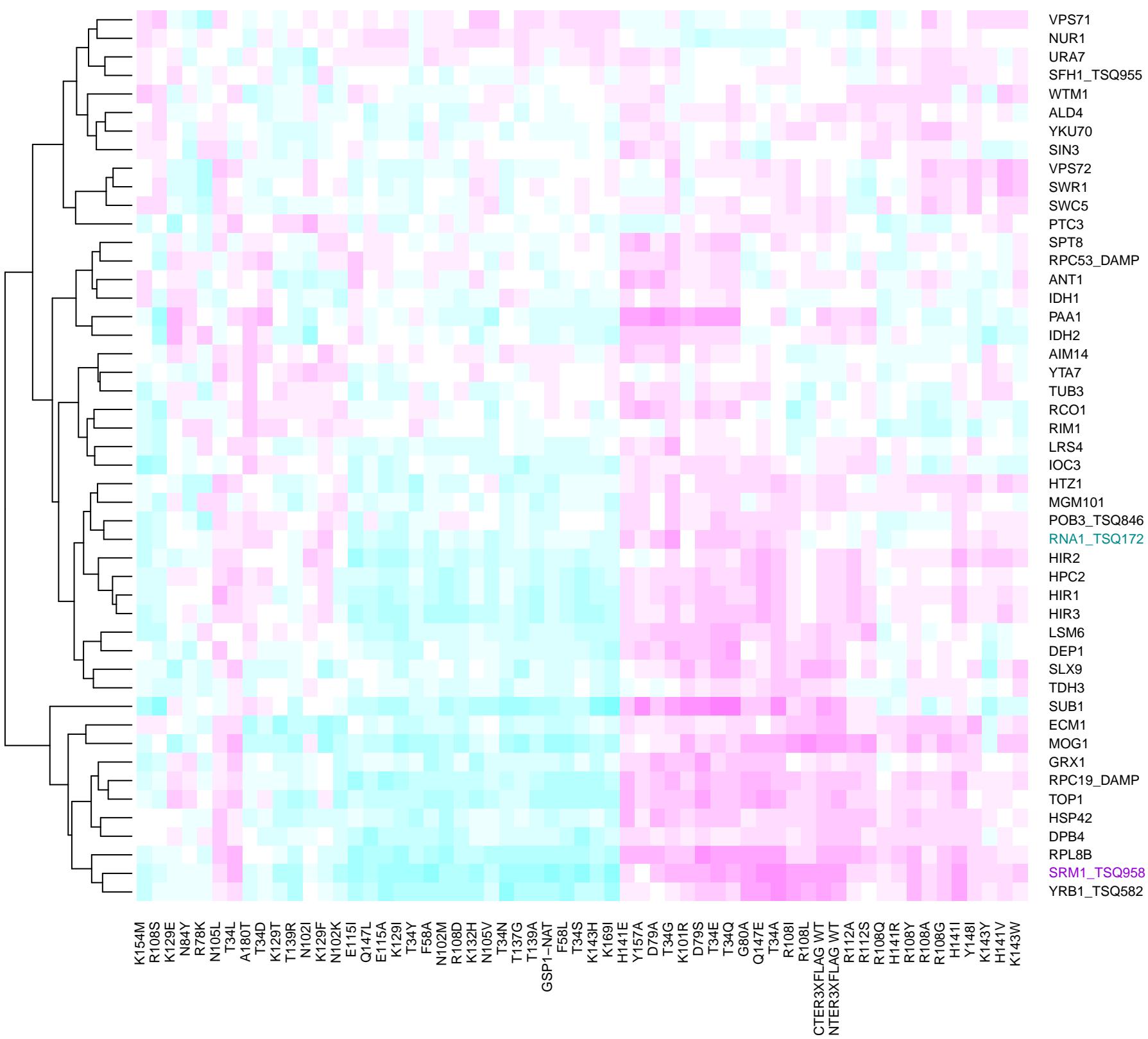


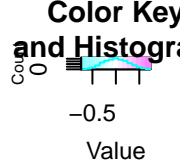
ER_GO_30_11



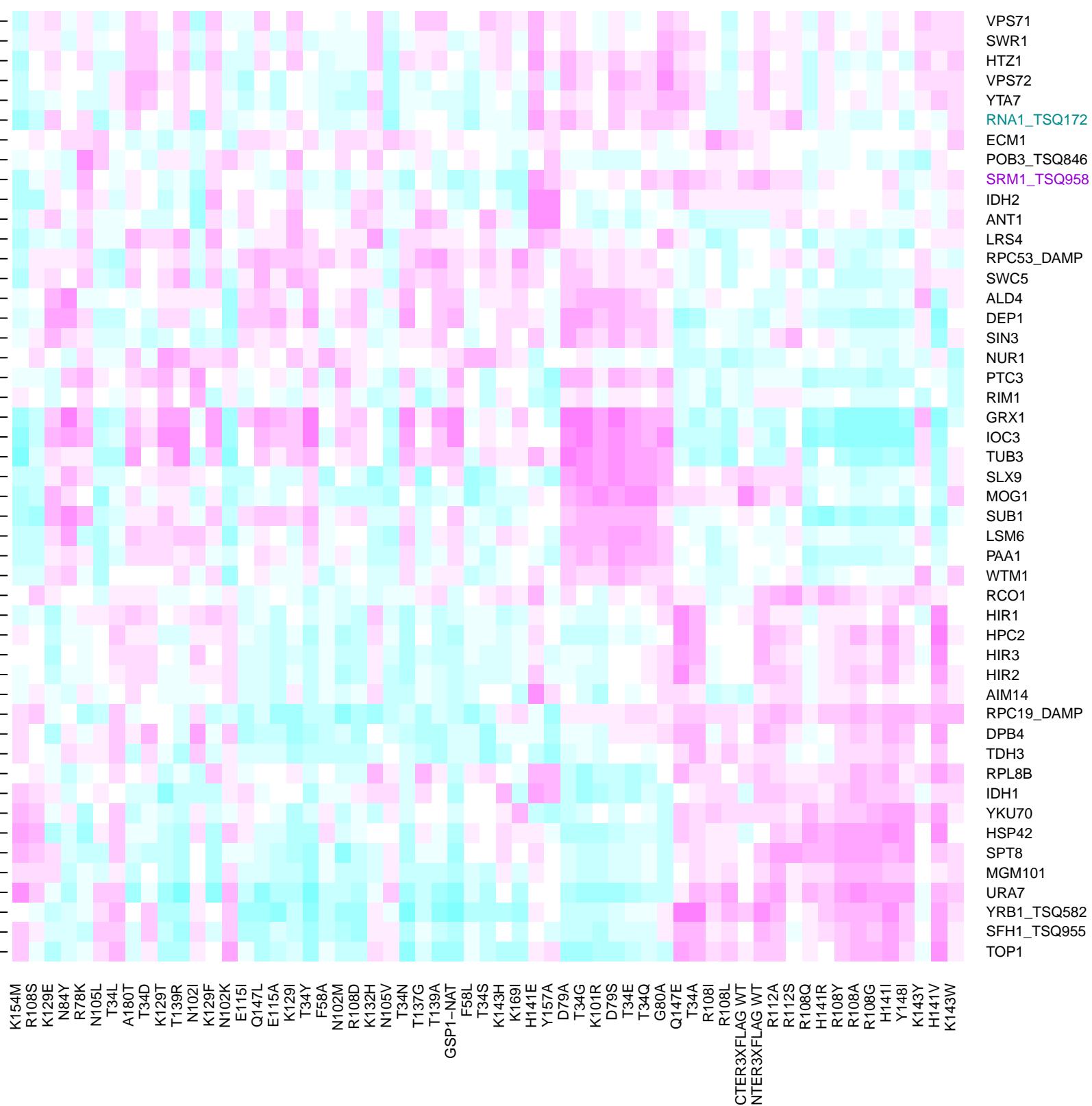


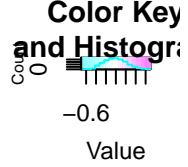
Golgi and ER_GO_30_4



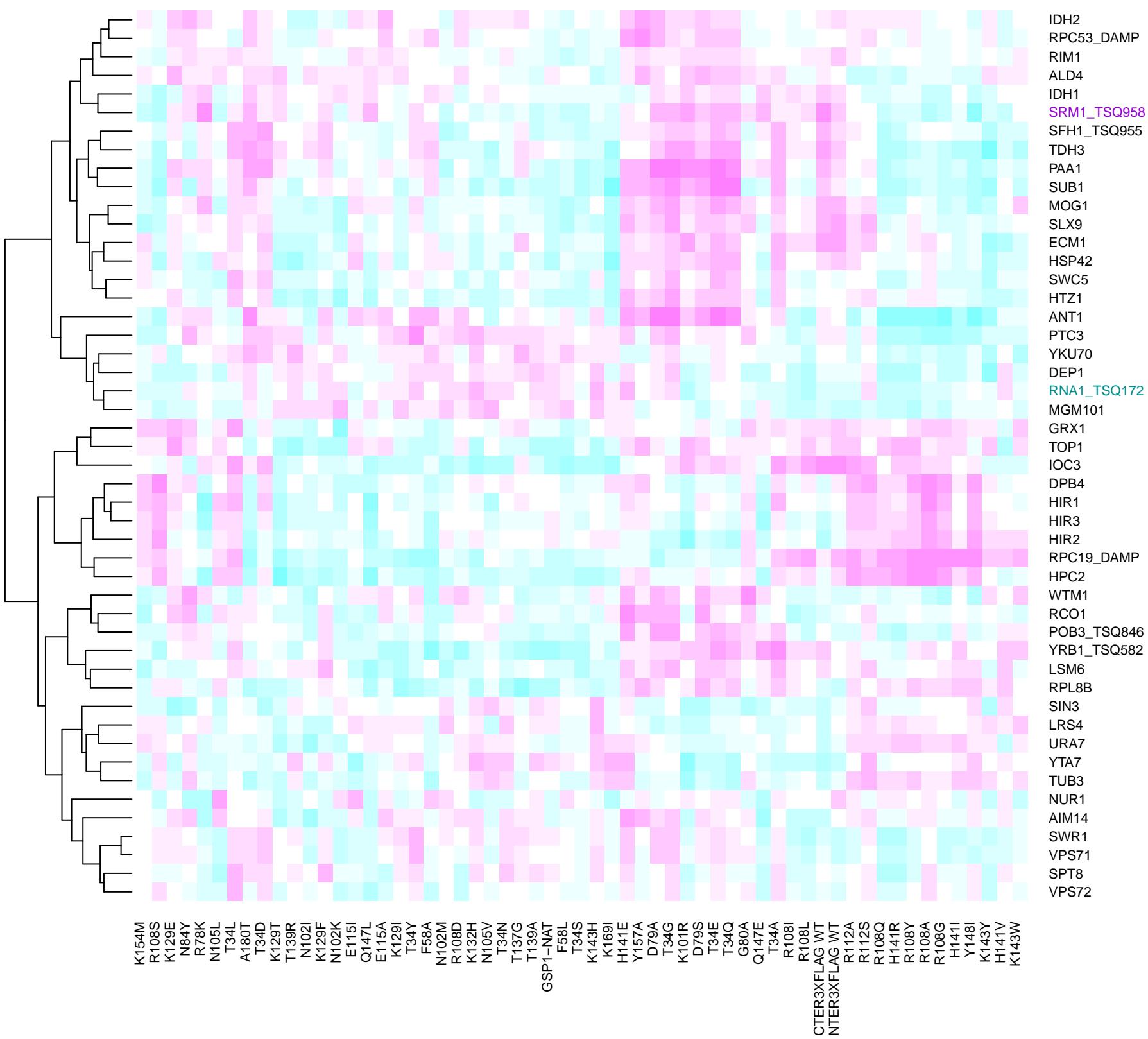


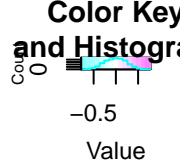
mitotic cell cycle_GO_30_4



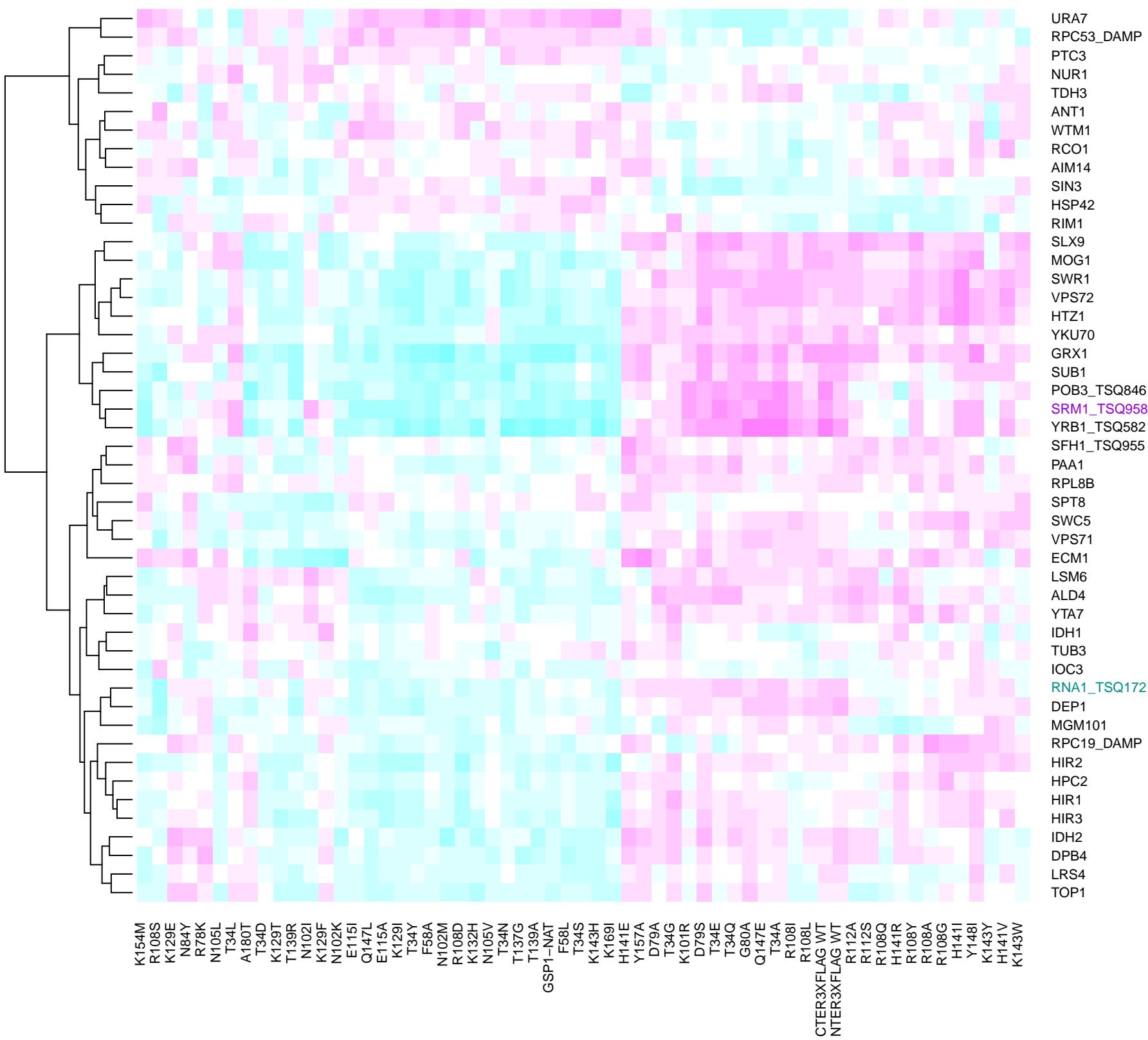


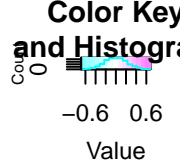
Golgi_GO_30_5



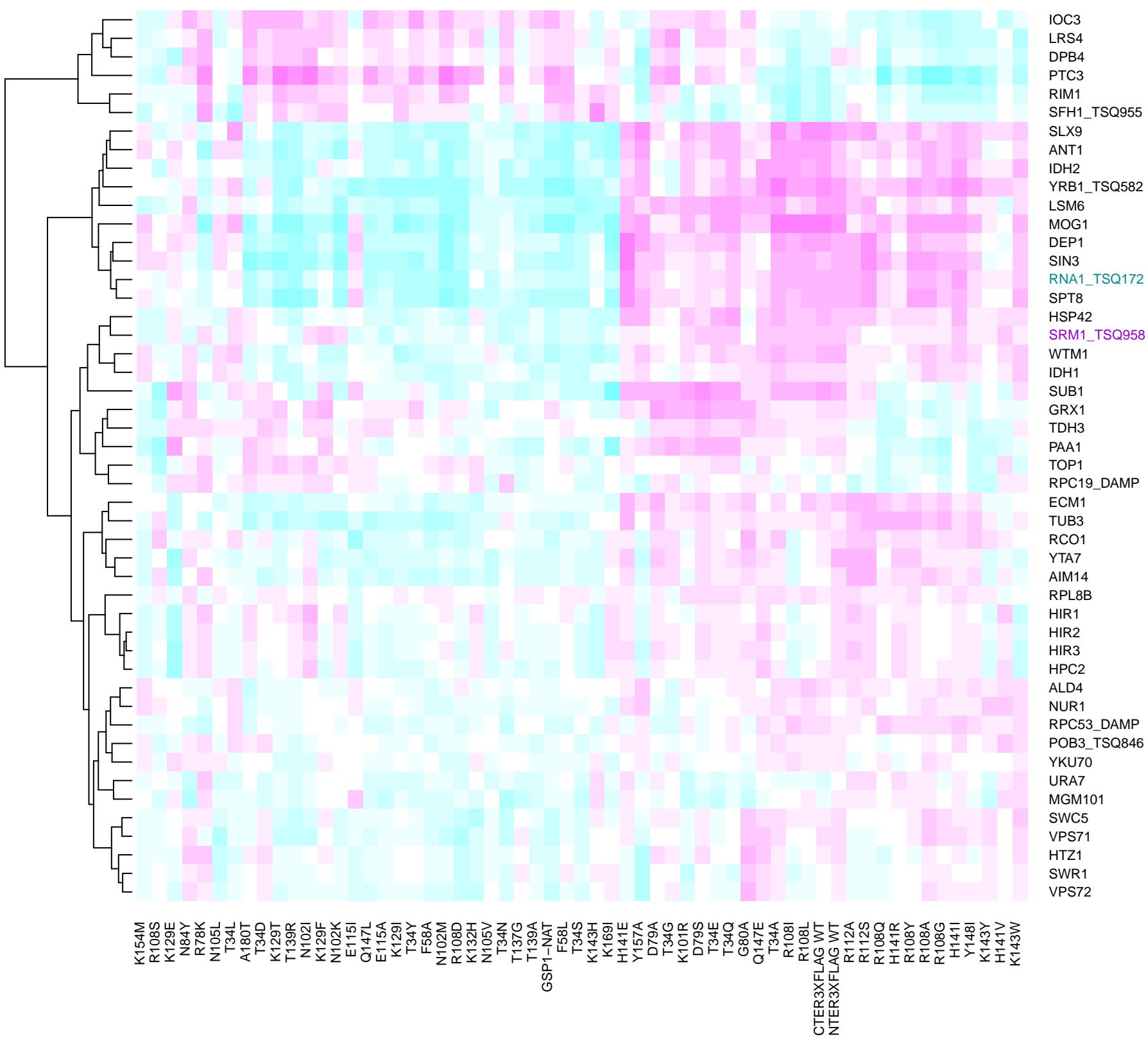


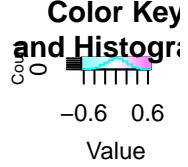
lipids_GO_30_8



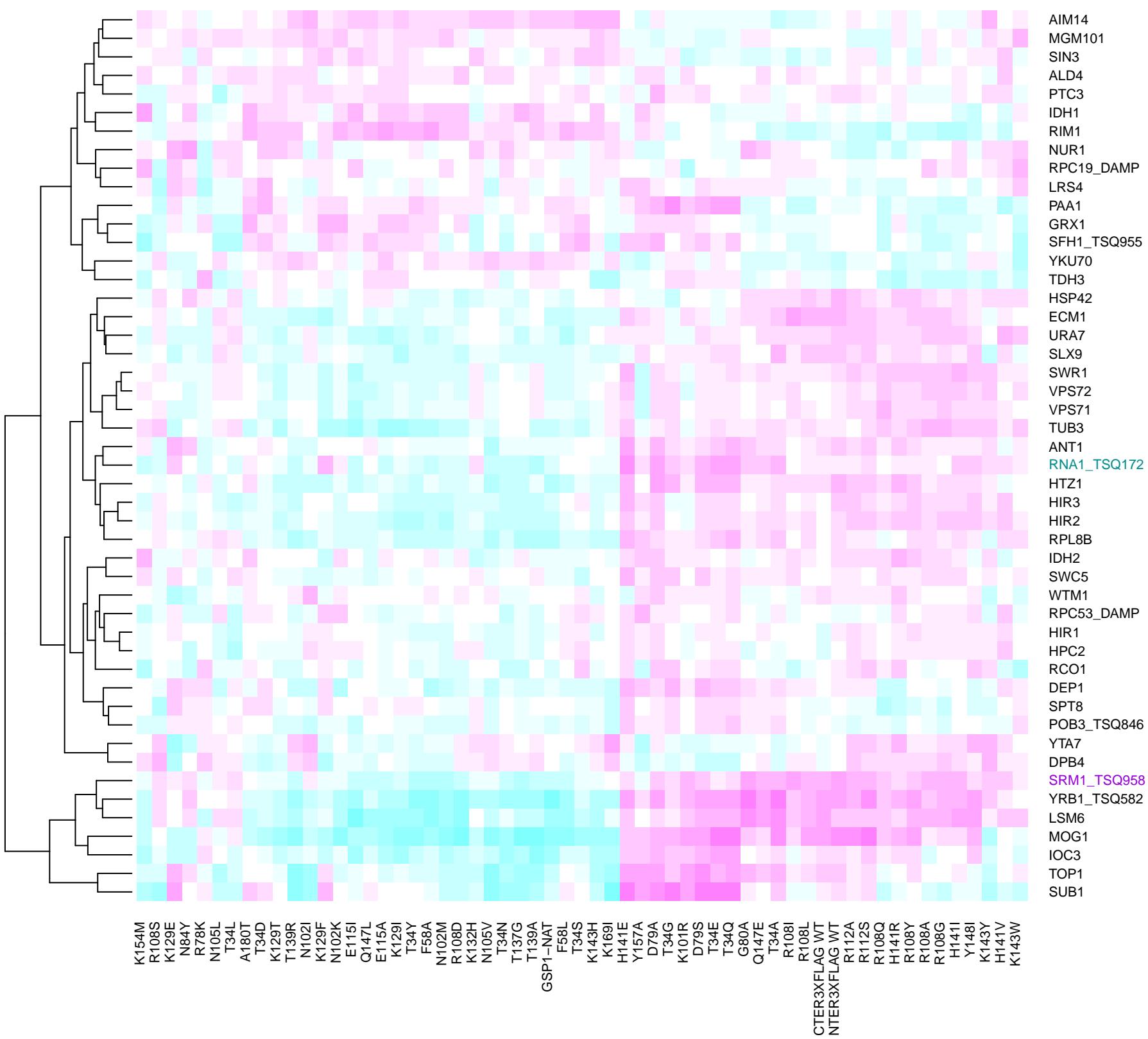


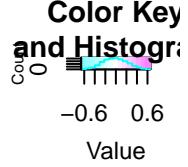
chromosome_GO_30_1



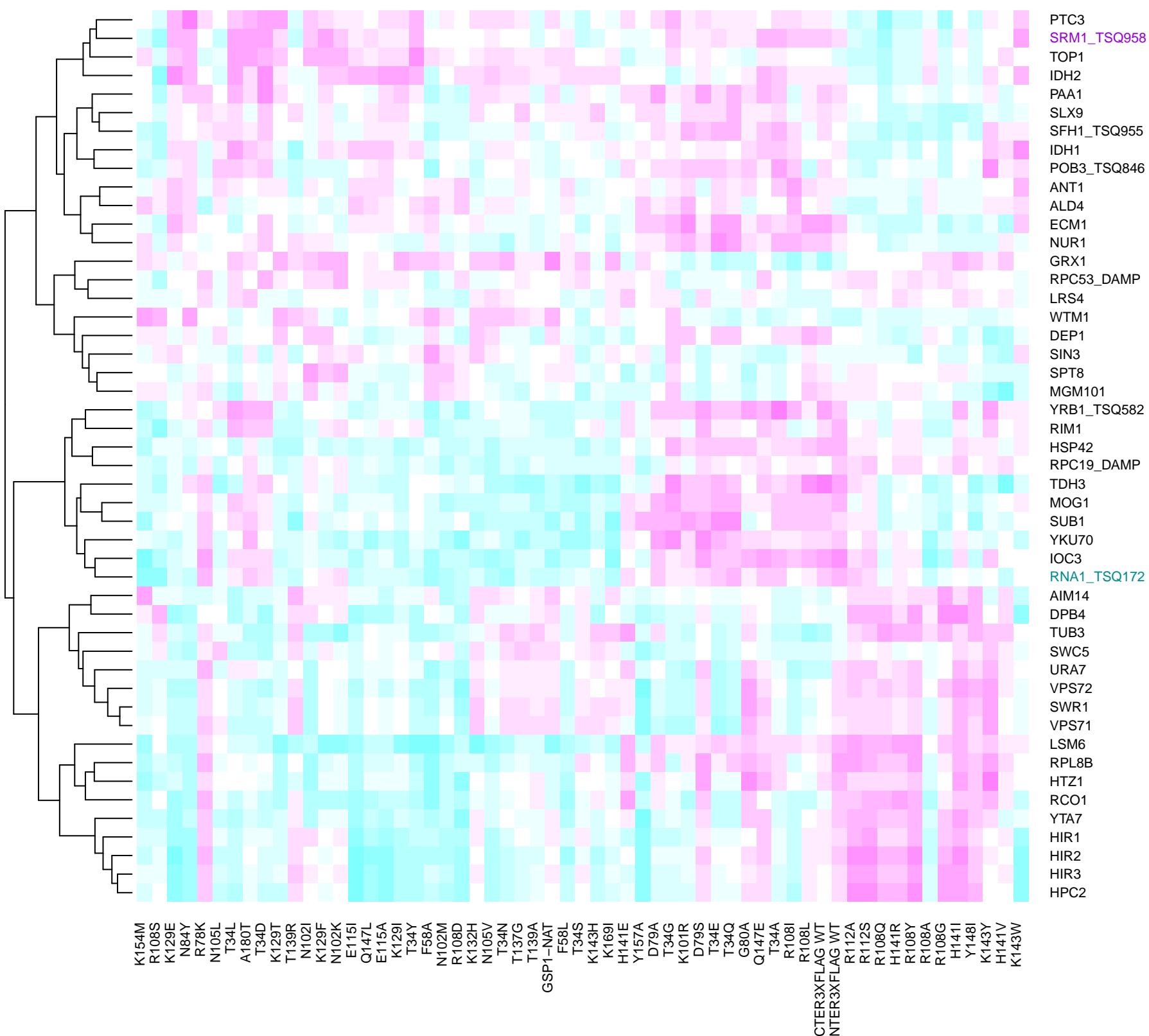


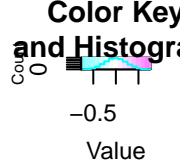
nucleic acid binding transcription factor activity_GO_30_2





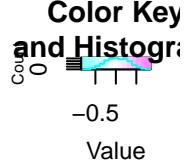
cellular bud_GO_30_4



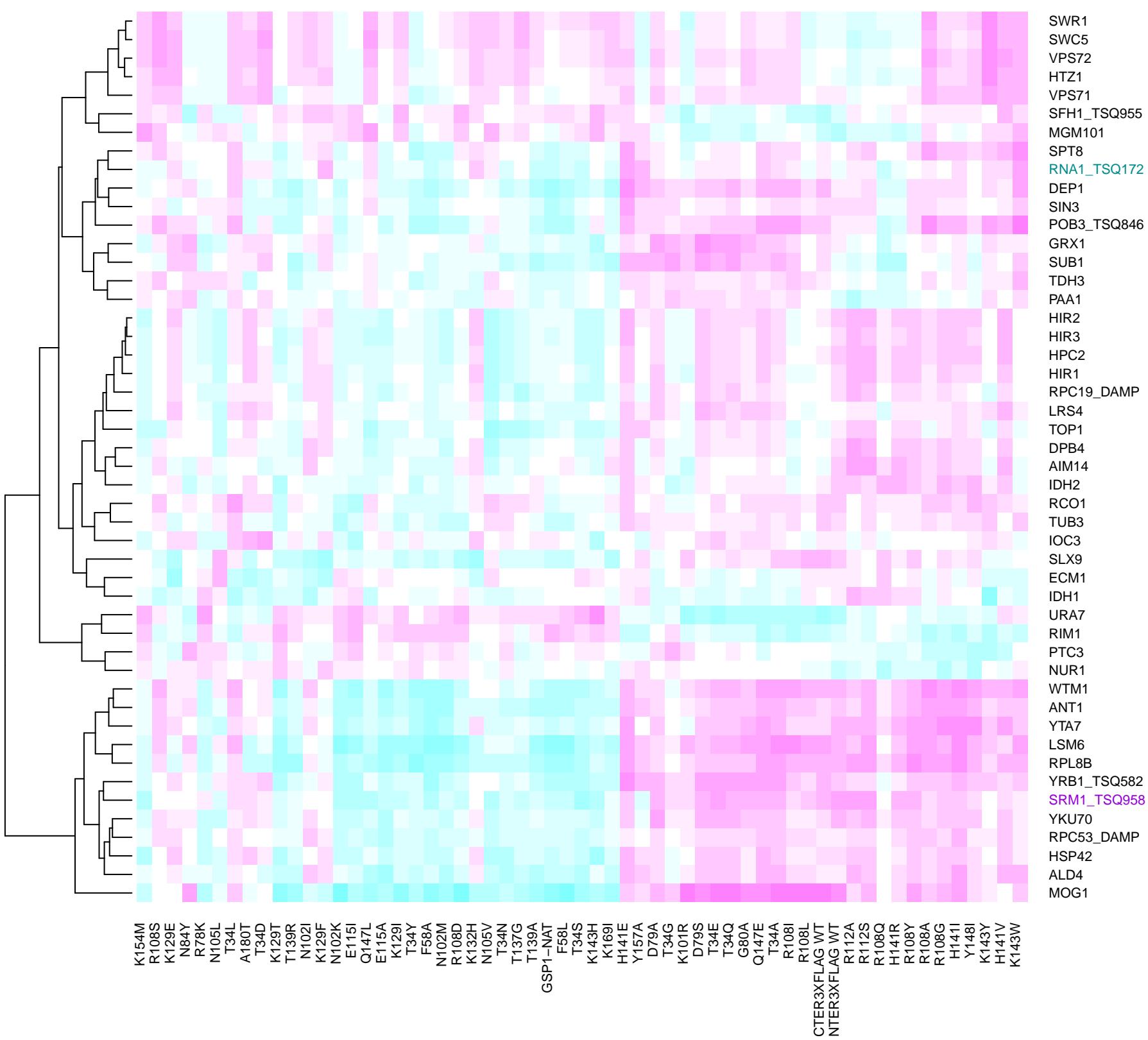


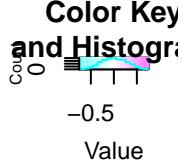
Golgi and ER_GO_30_14



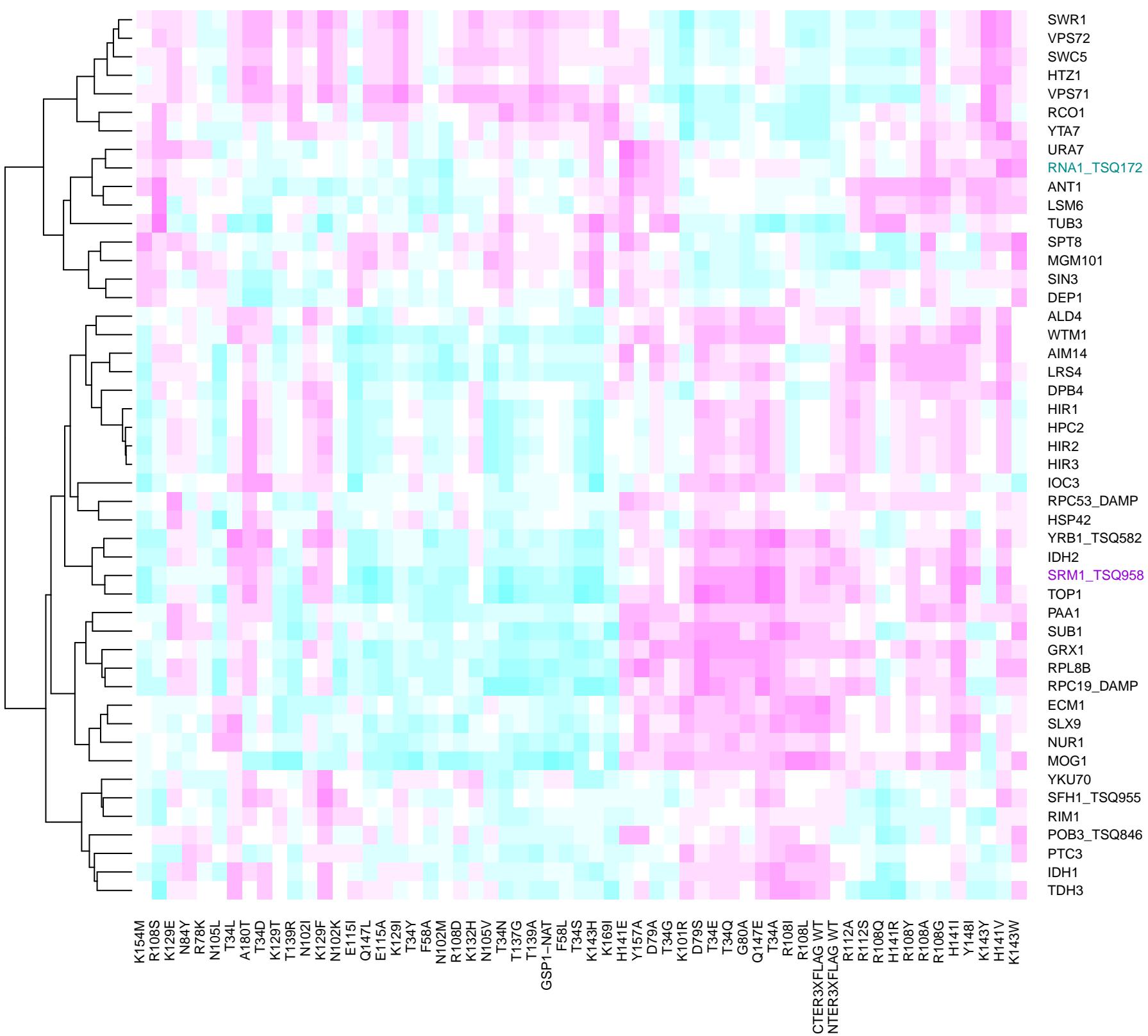


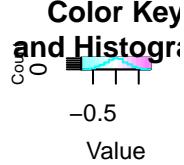
chromatin binding_GO_30_1



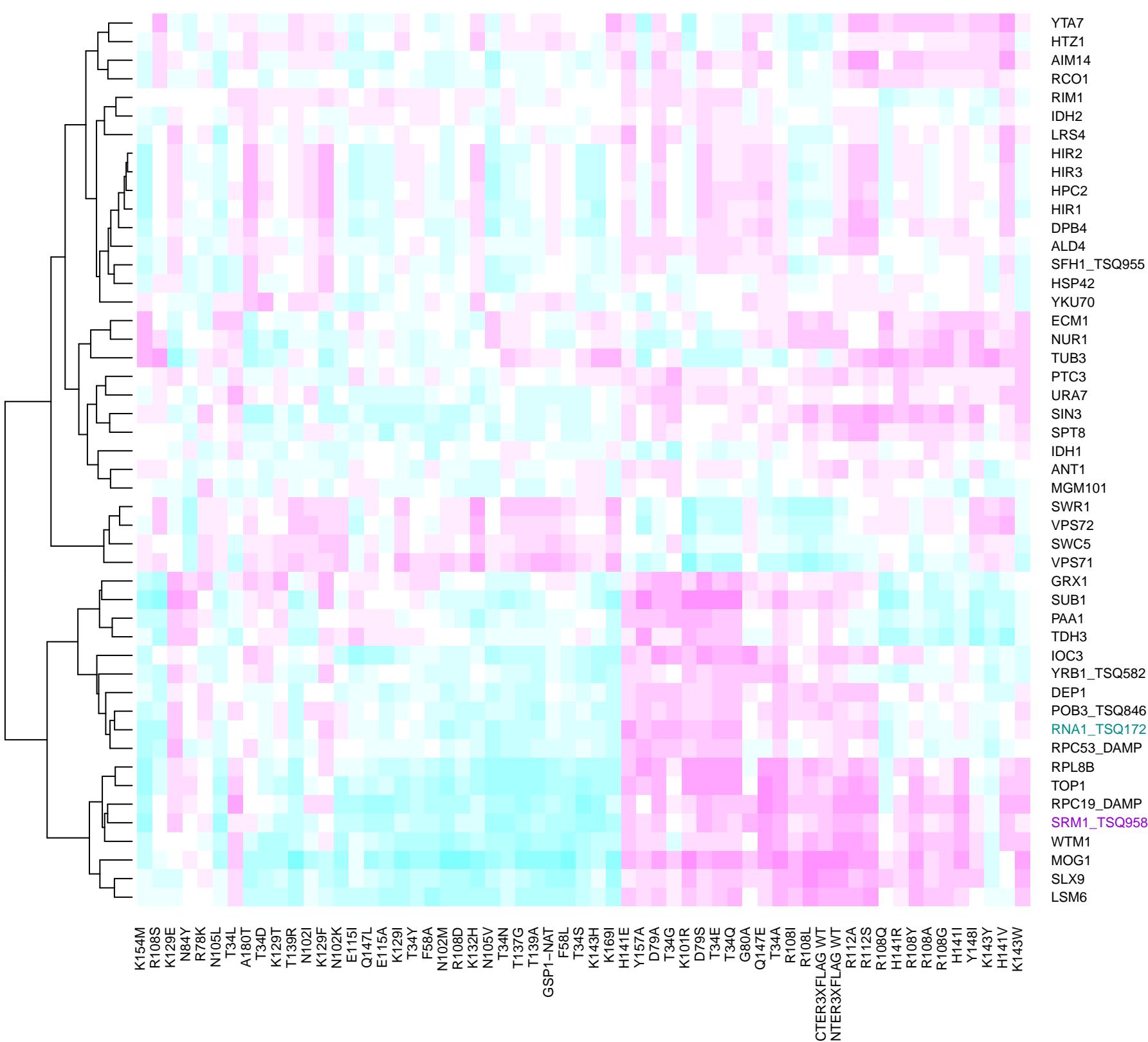


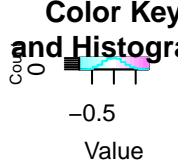
DNA-templated transcription, elongation_GO_30_1



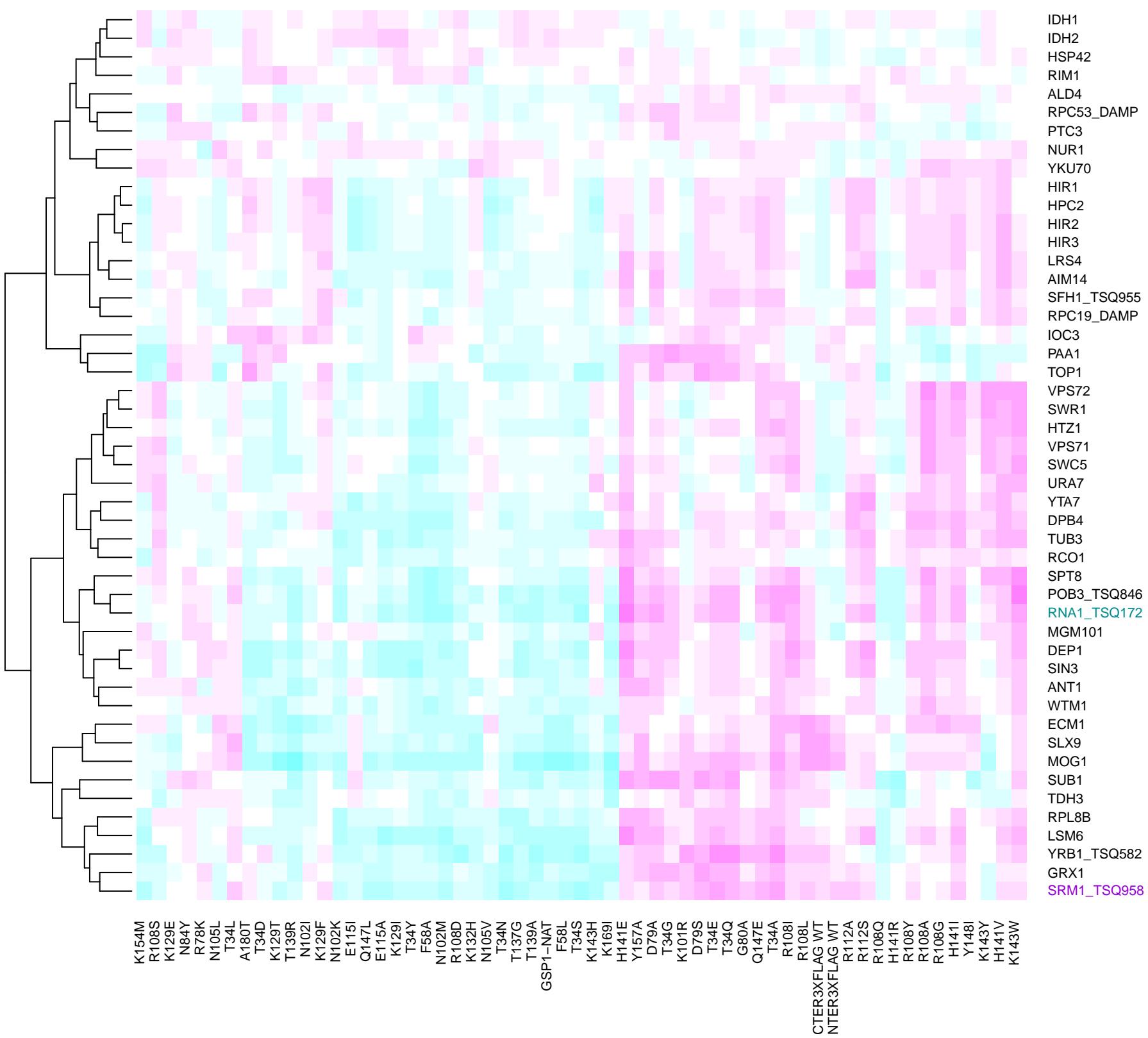


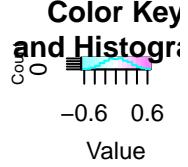
transcription and mRNA processing_GO_30_8



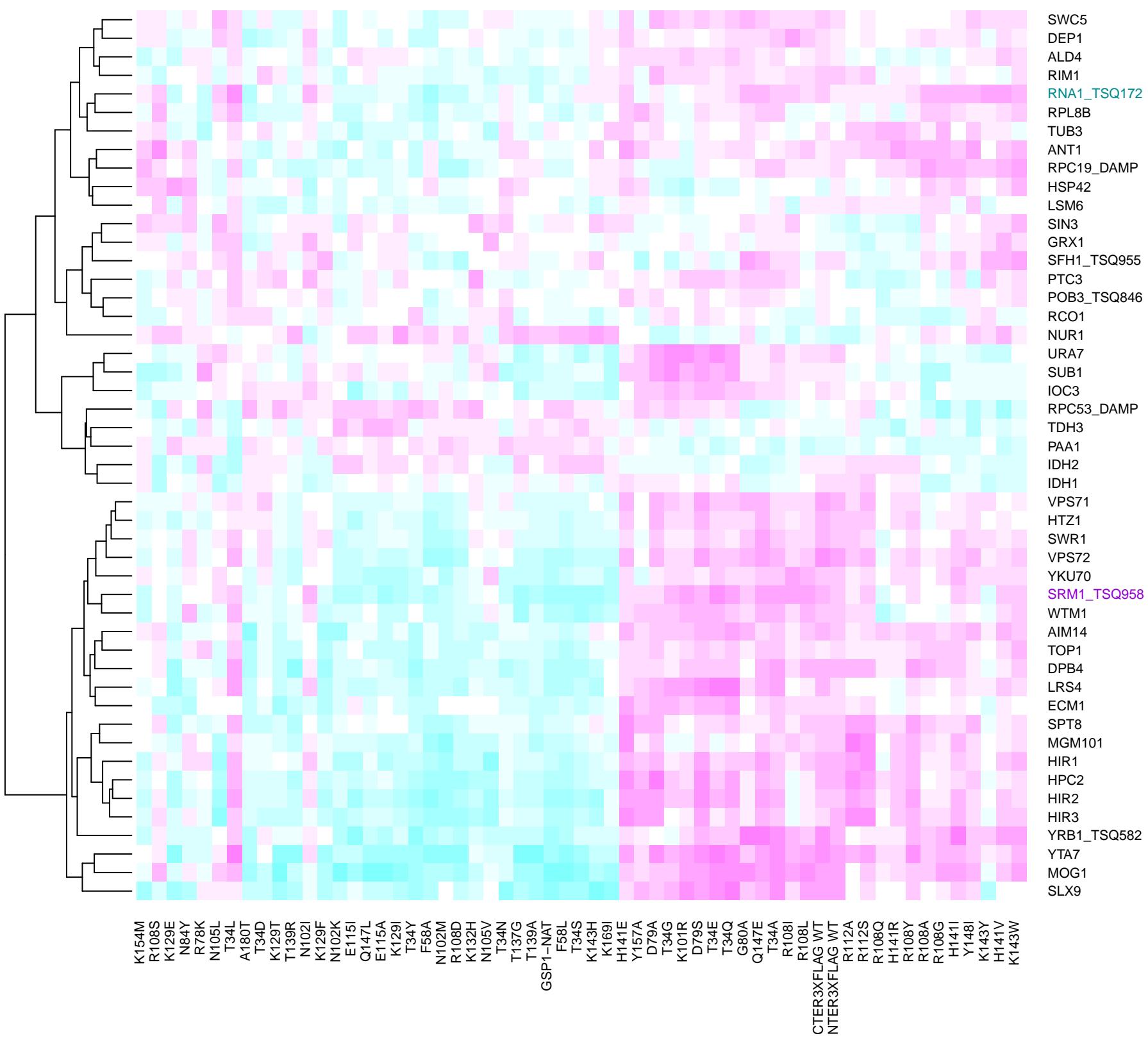


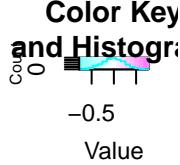
transcription factor activity, protein binding



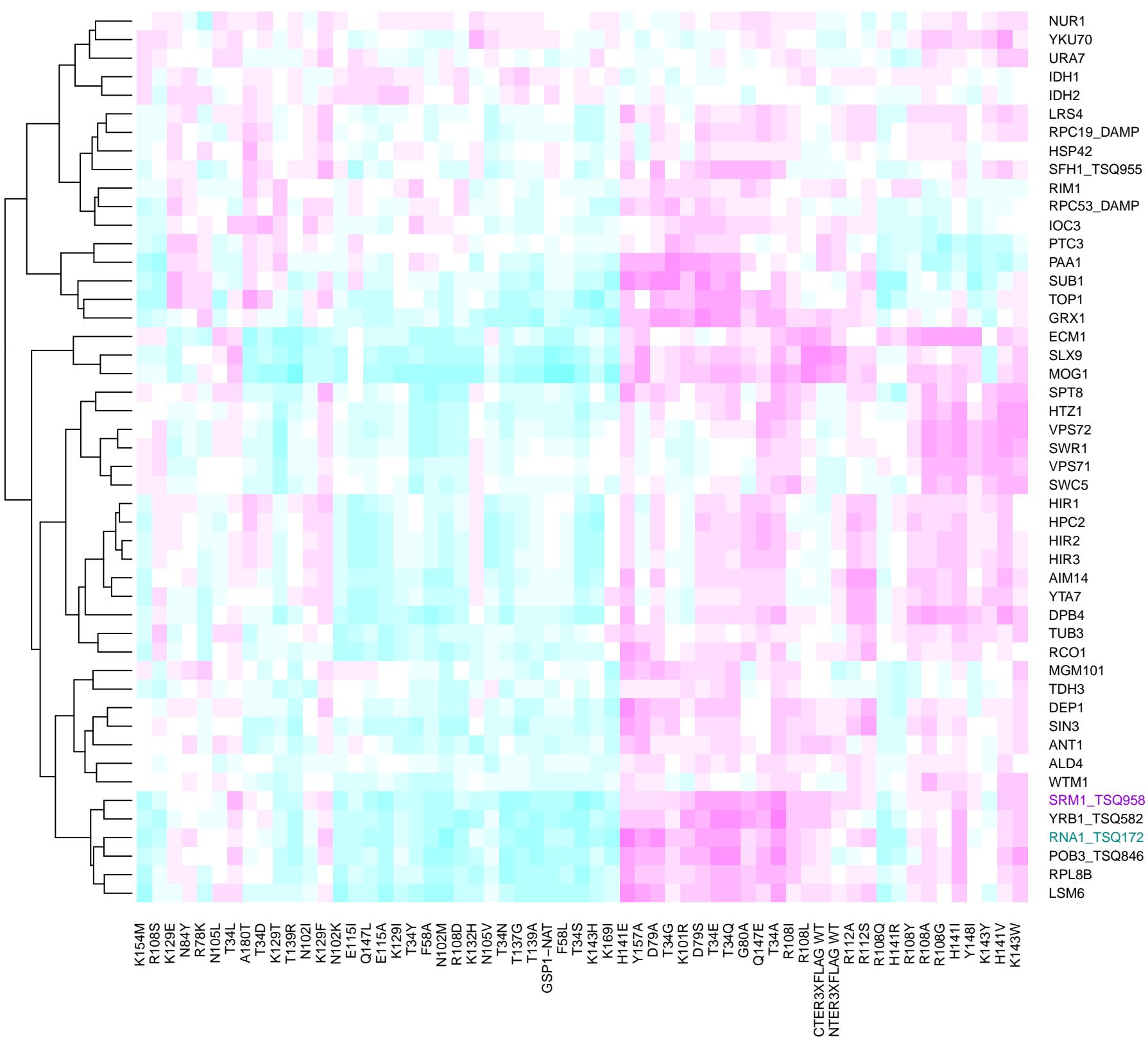


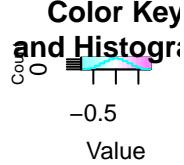
organelle fission_GO_30_5



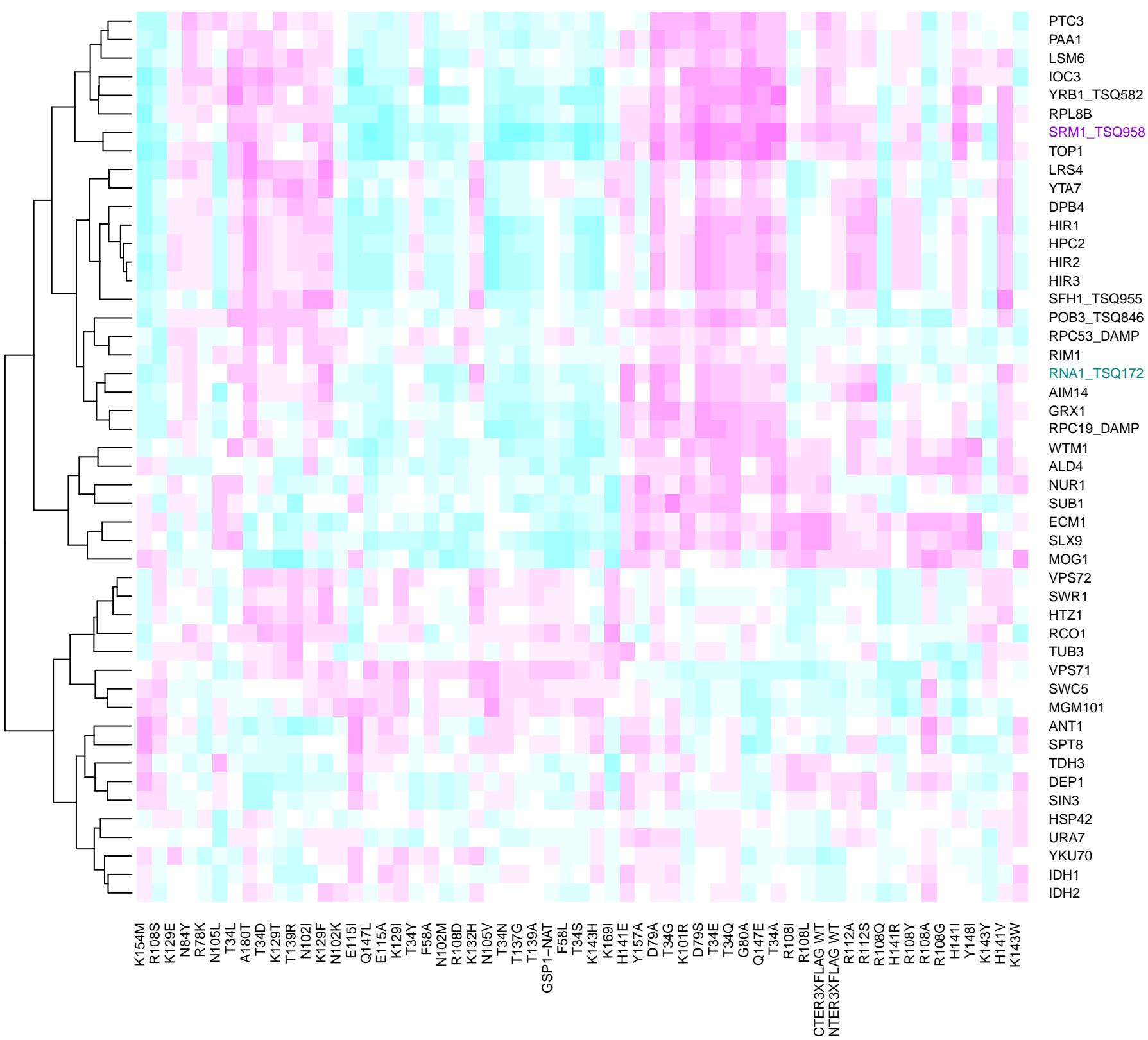


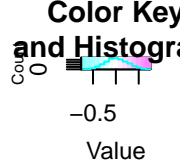
transcription factor activity, protein binding_GO_30_1



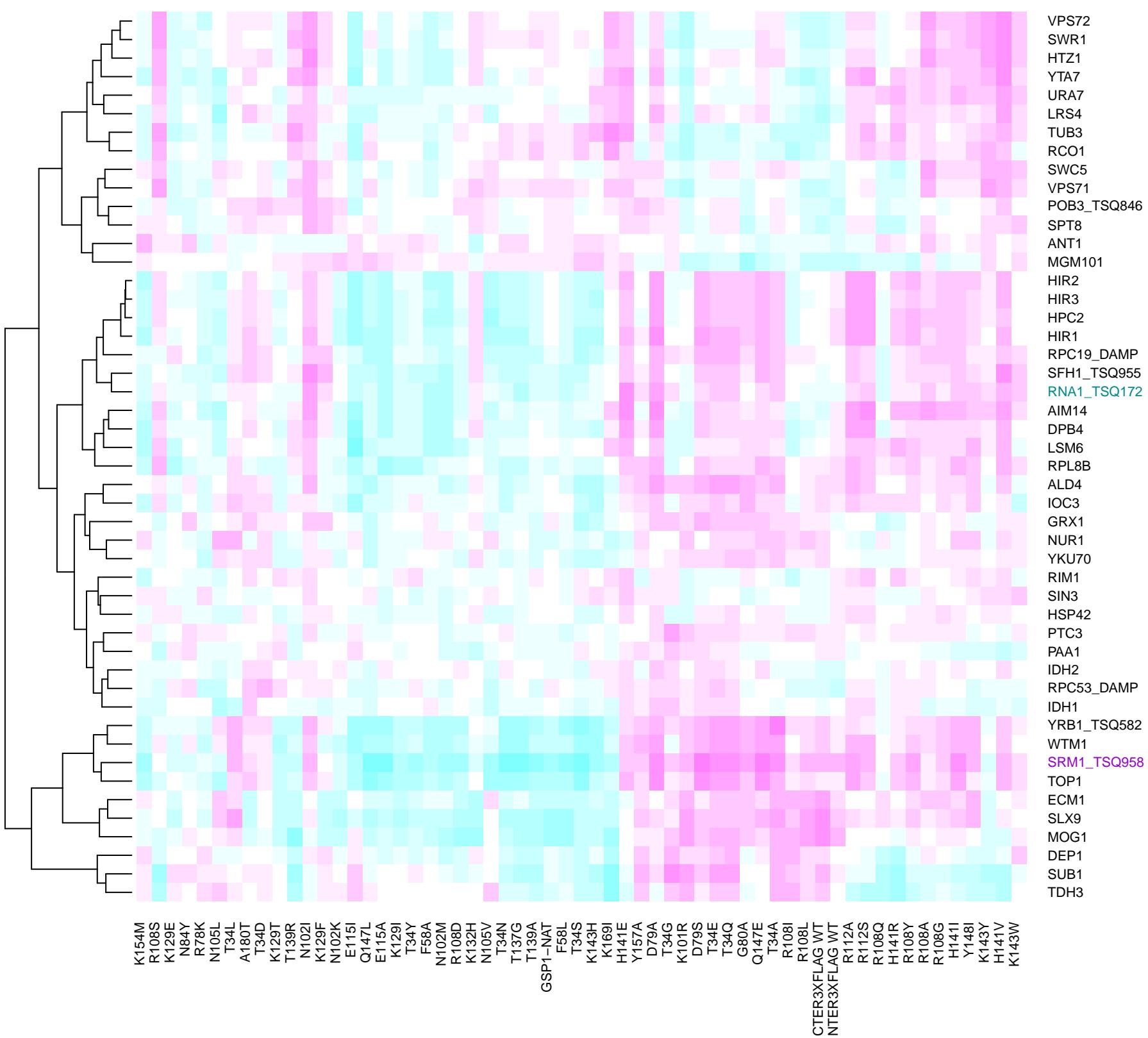


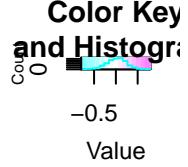
transcription from RNA polymerase II promoter_GO_30_2



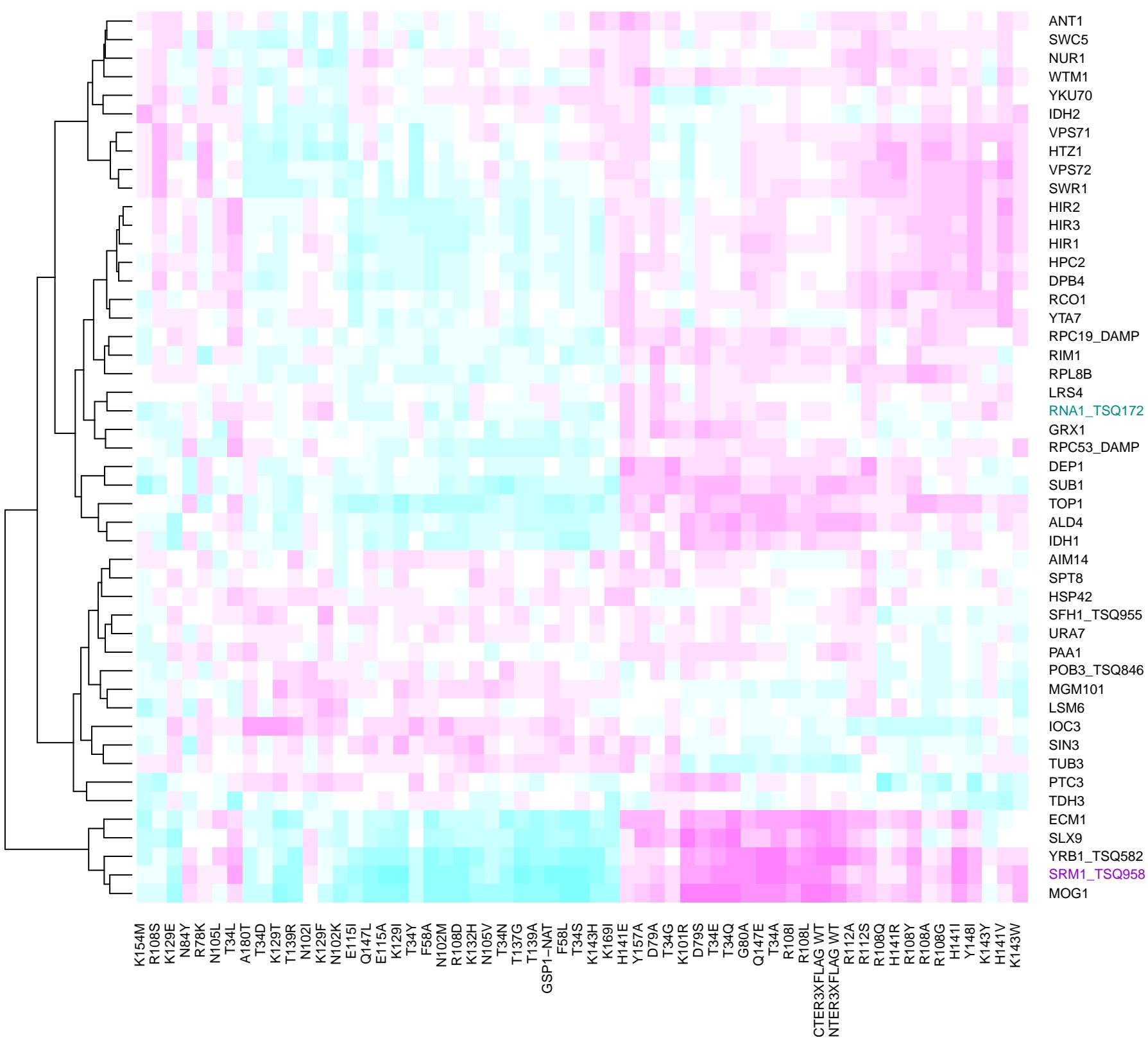


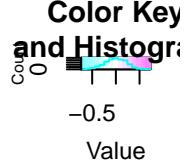
transcription_GO_30_4



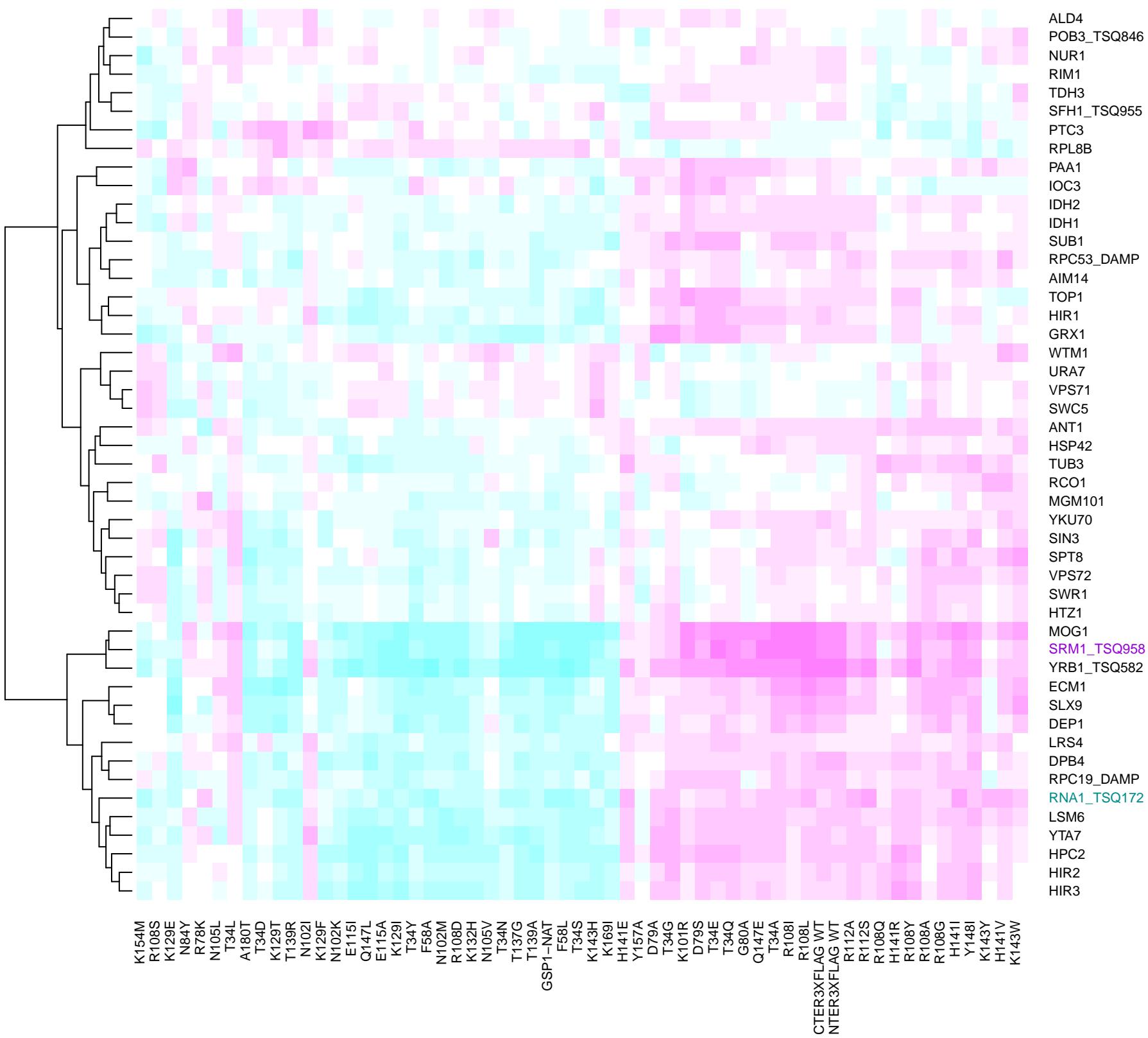


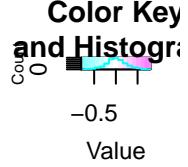
Golgi and ER_GO_30_12



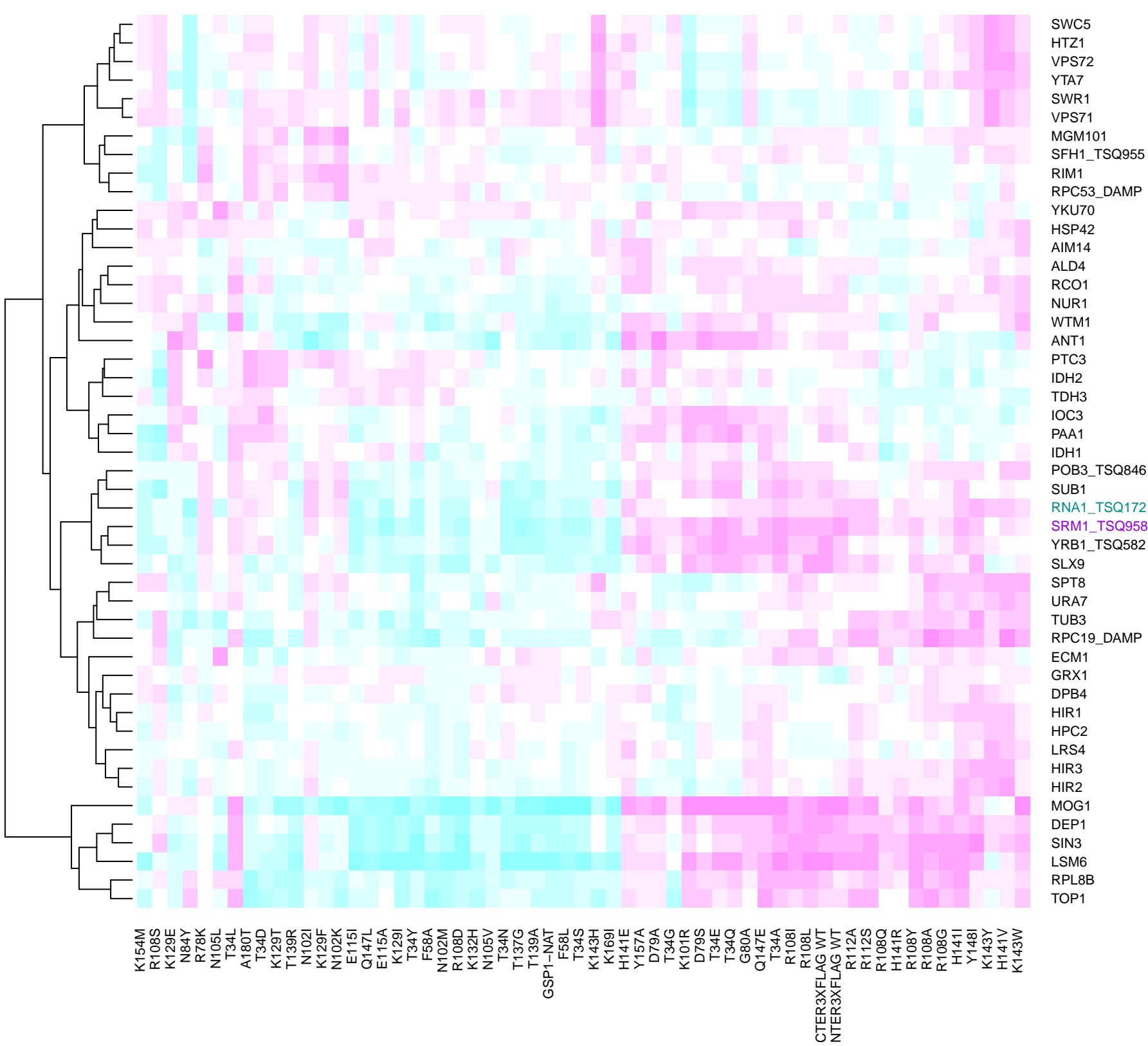


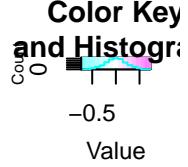
metabolic_GO_30_3



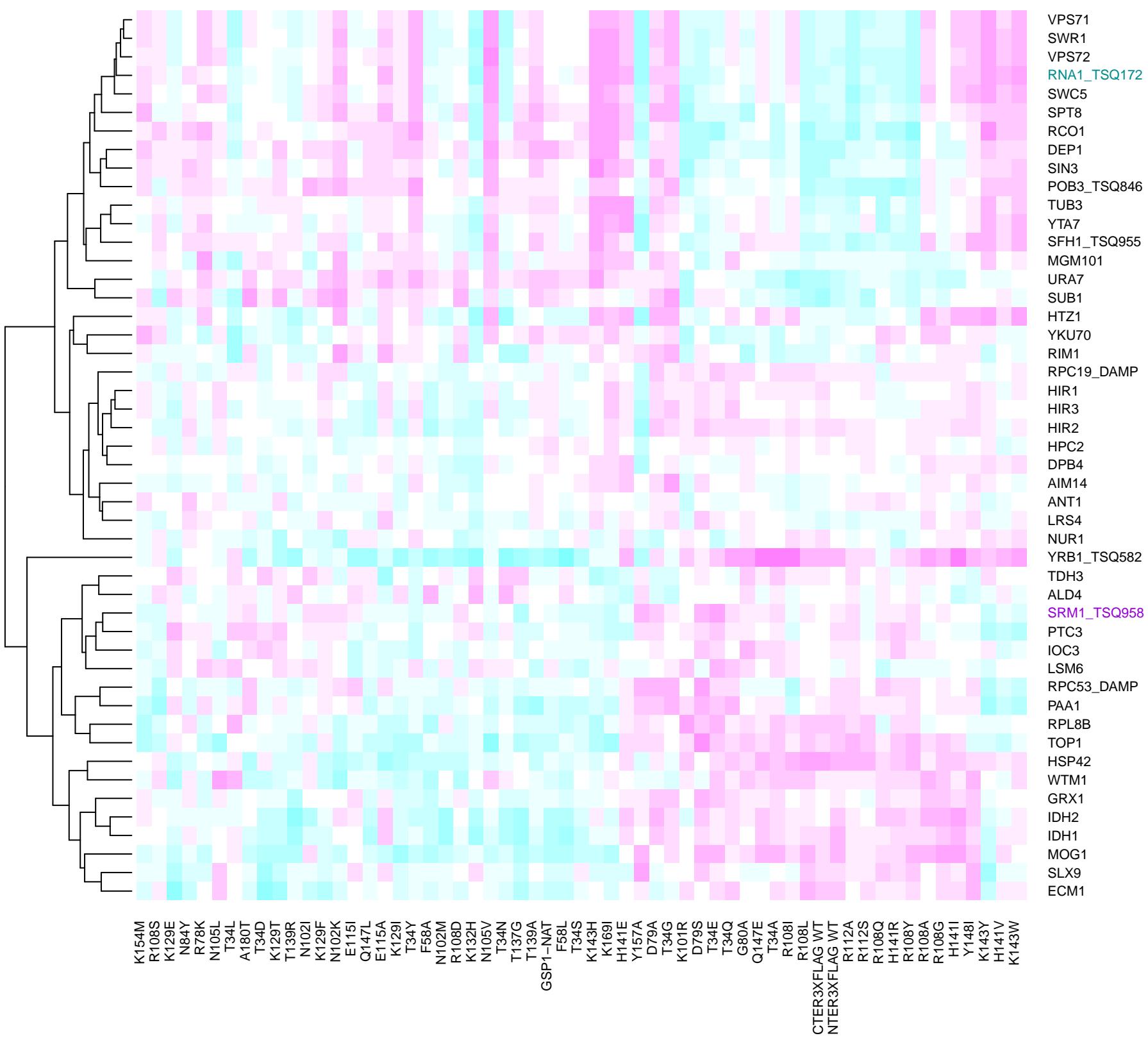


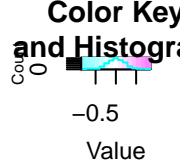
ribosomes and translation_GO_30_6



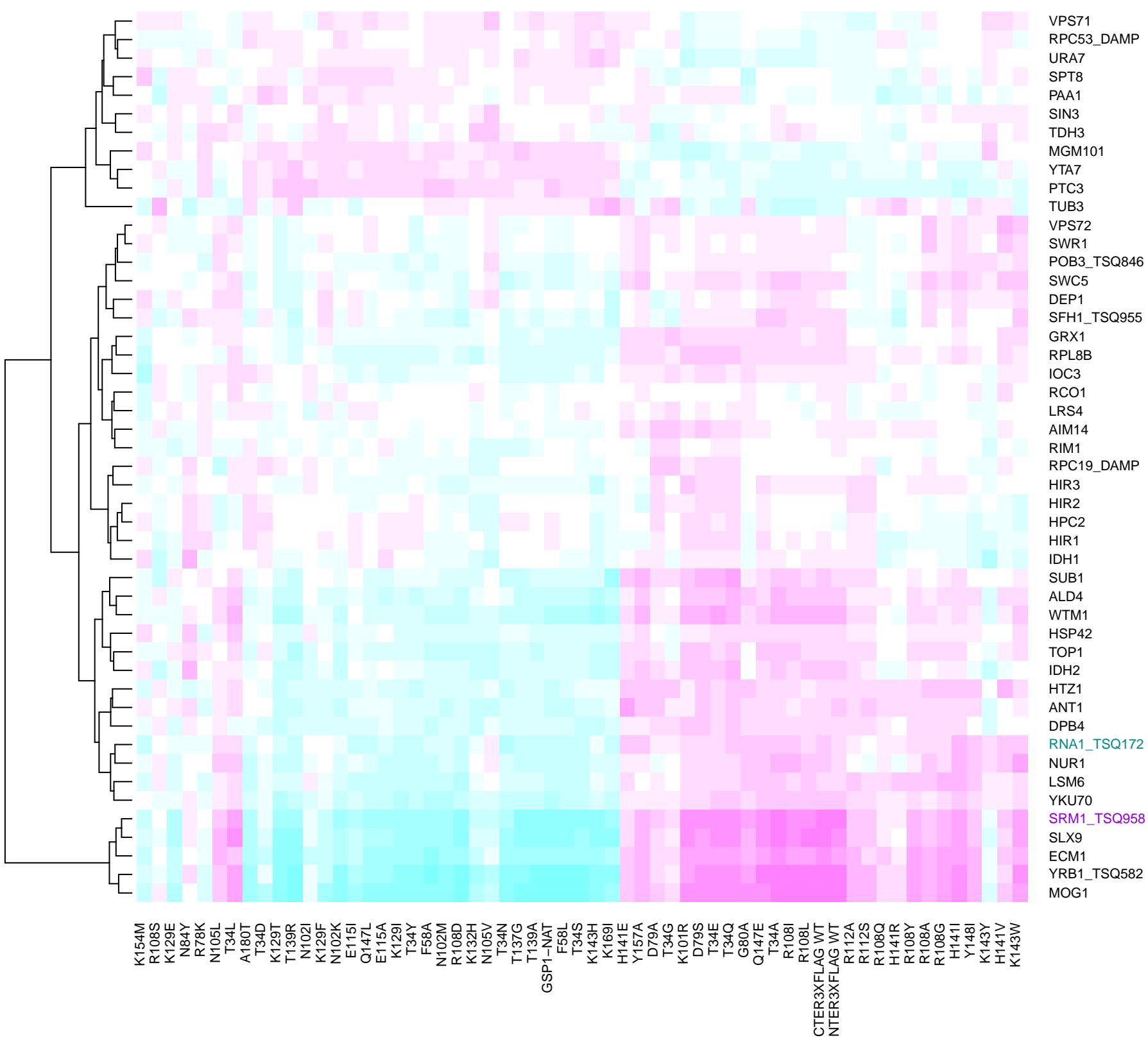


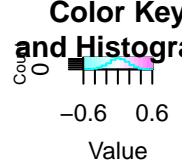
mitochondria and respiration_GO_30_14



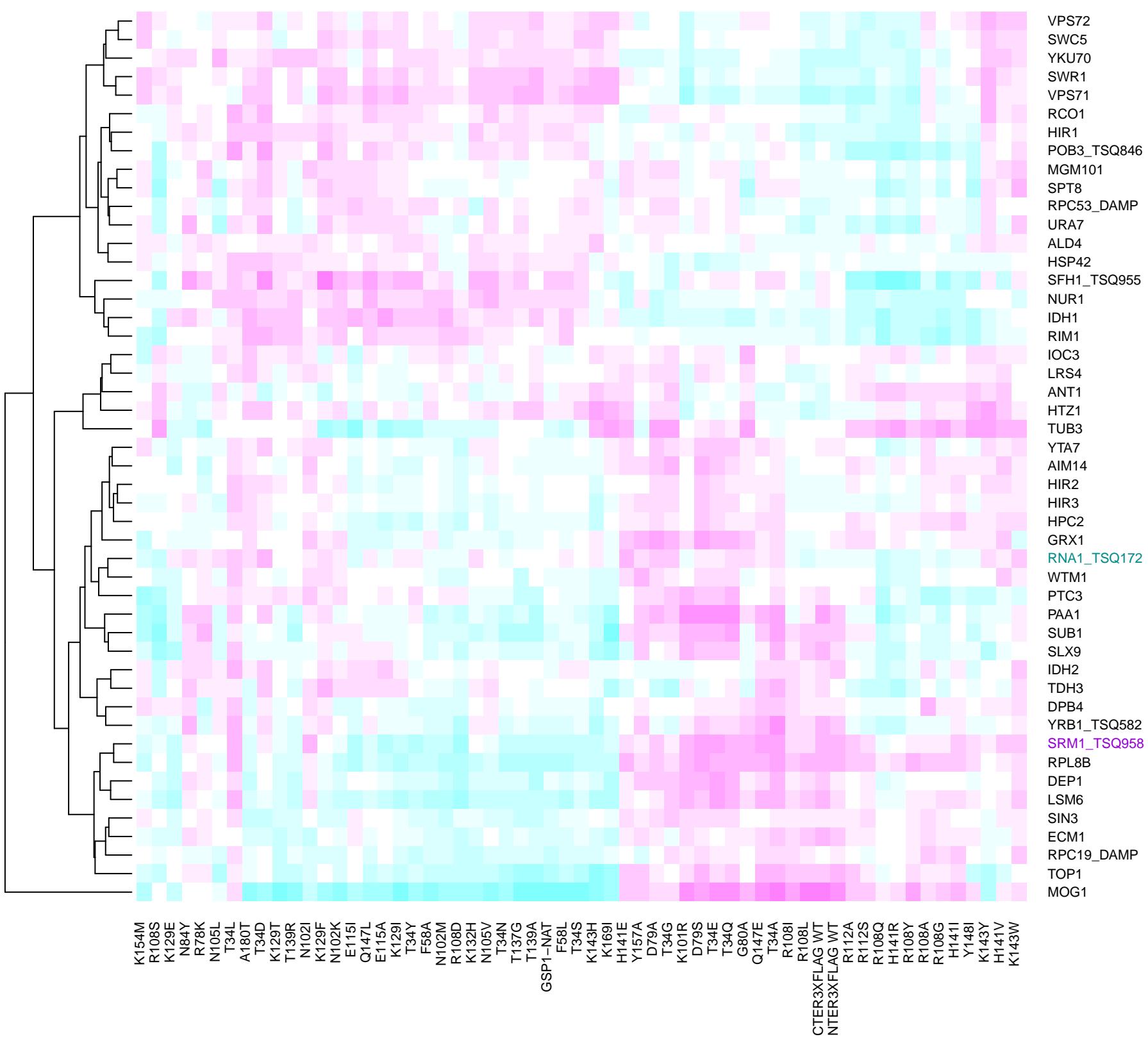


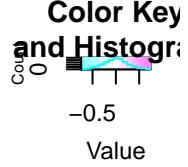
mitochondrion_GO_30_1



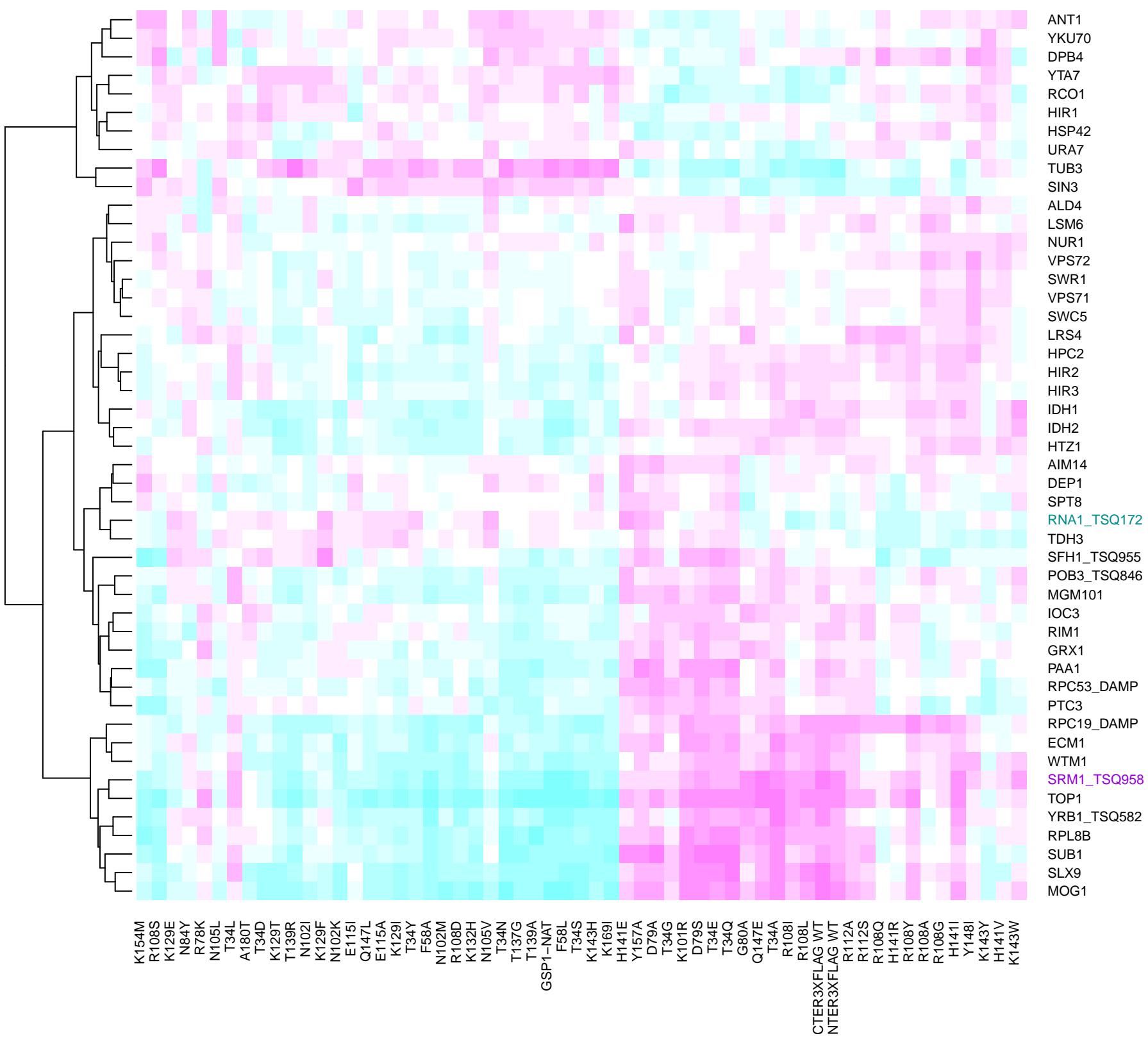


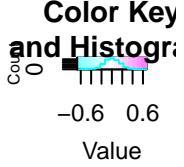
mitochondria and respiration_GO_30_1



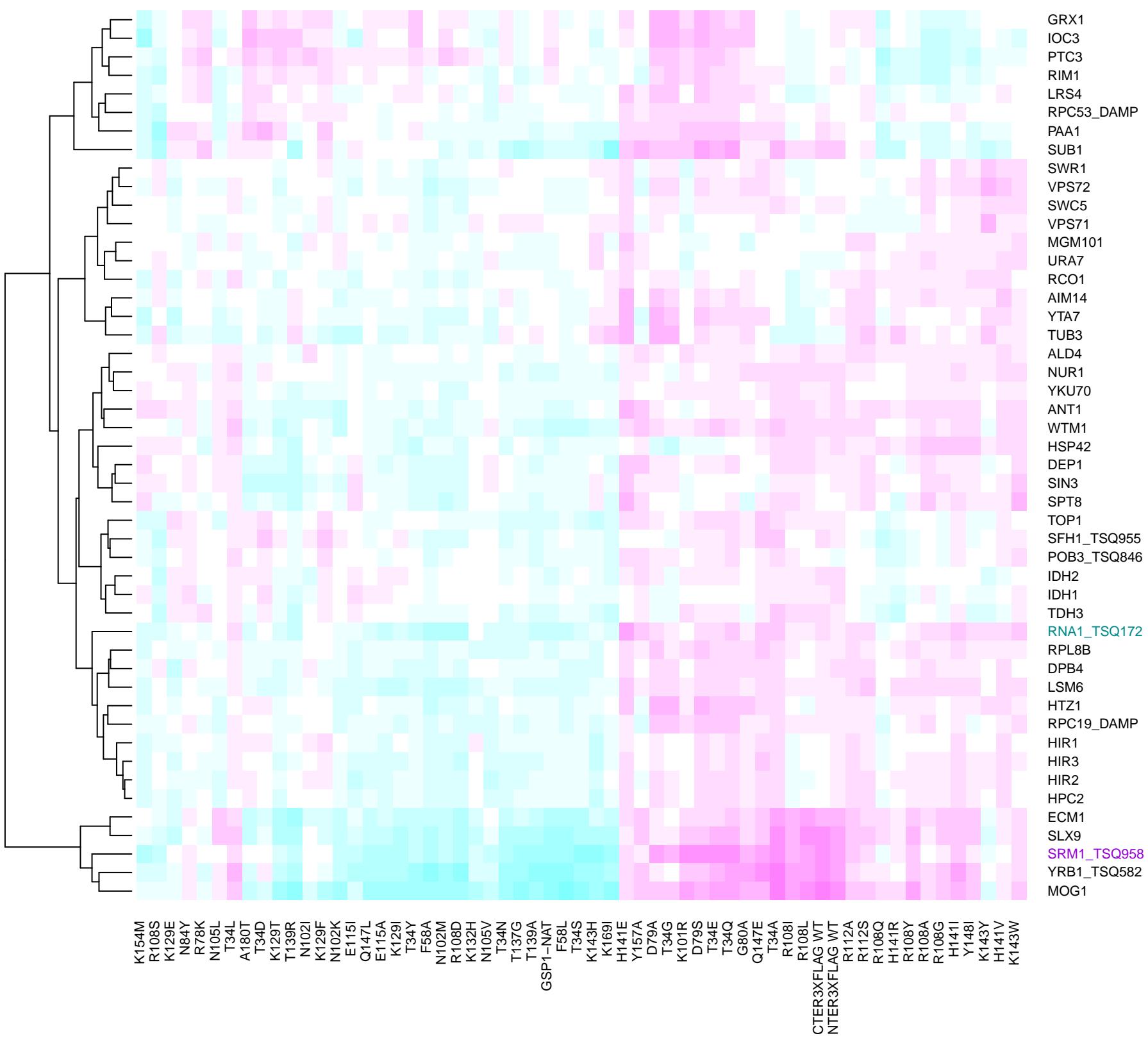


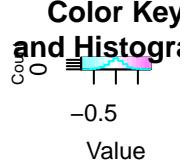
regulation of transport_GO_30_2



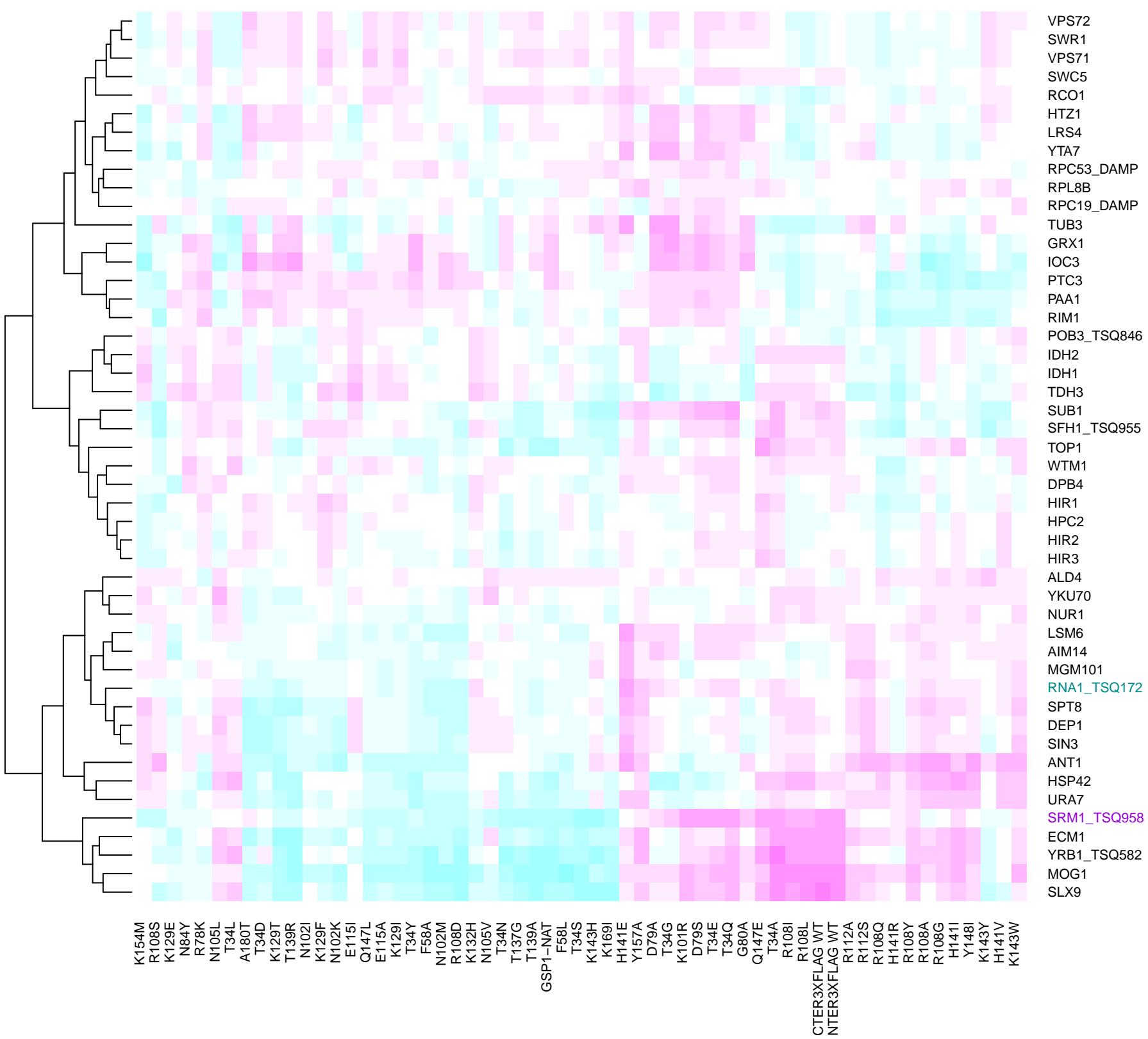


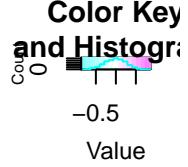
cell cycle



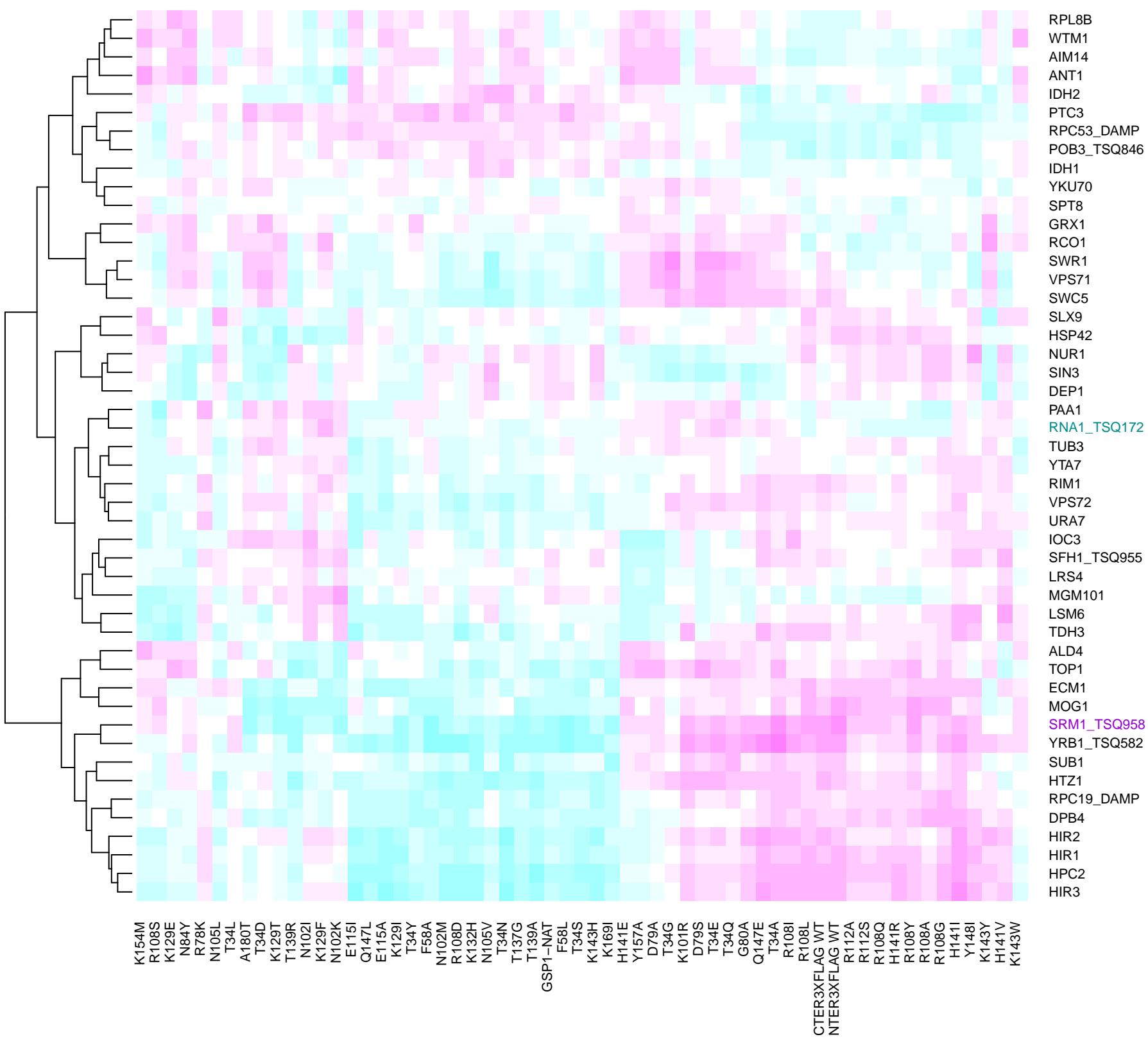


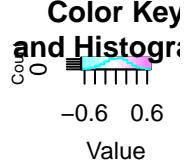
regulation of cell cycle_GO_30_1



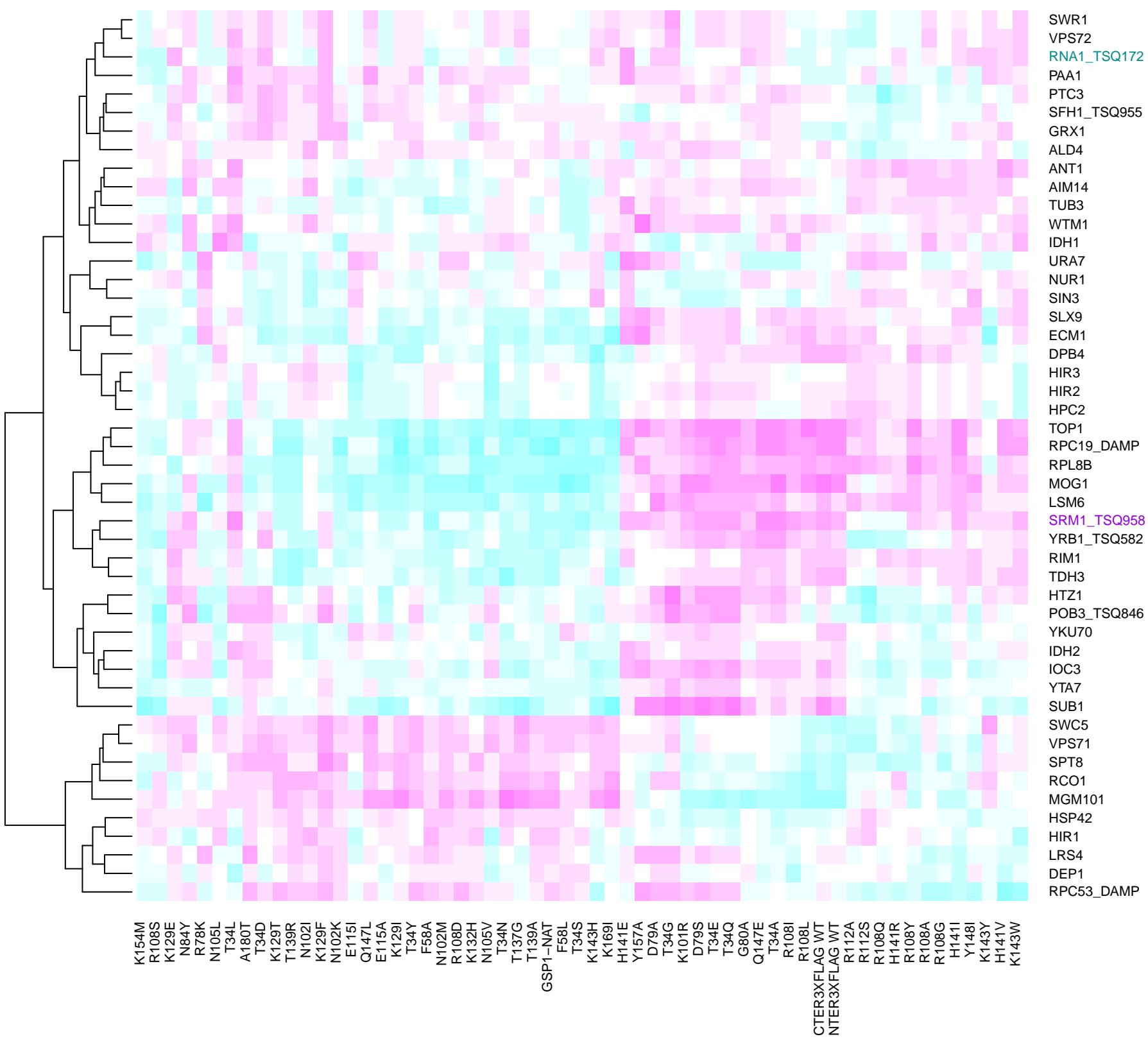


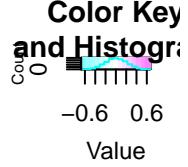
protein targeting_GO_30_4



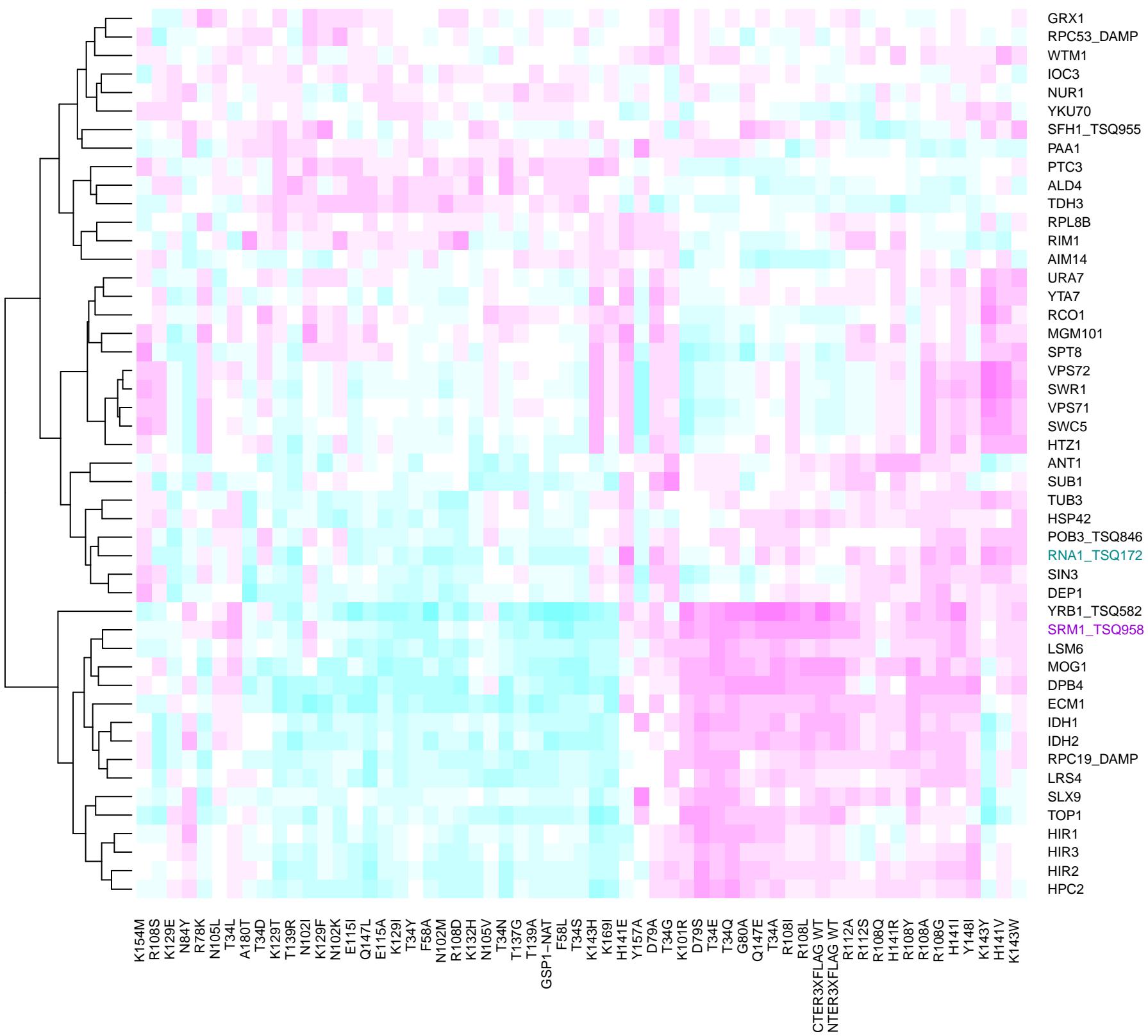


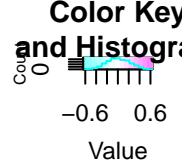
vacuoles_GO_30_7



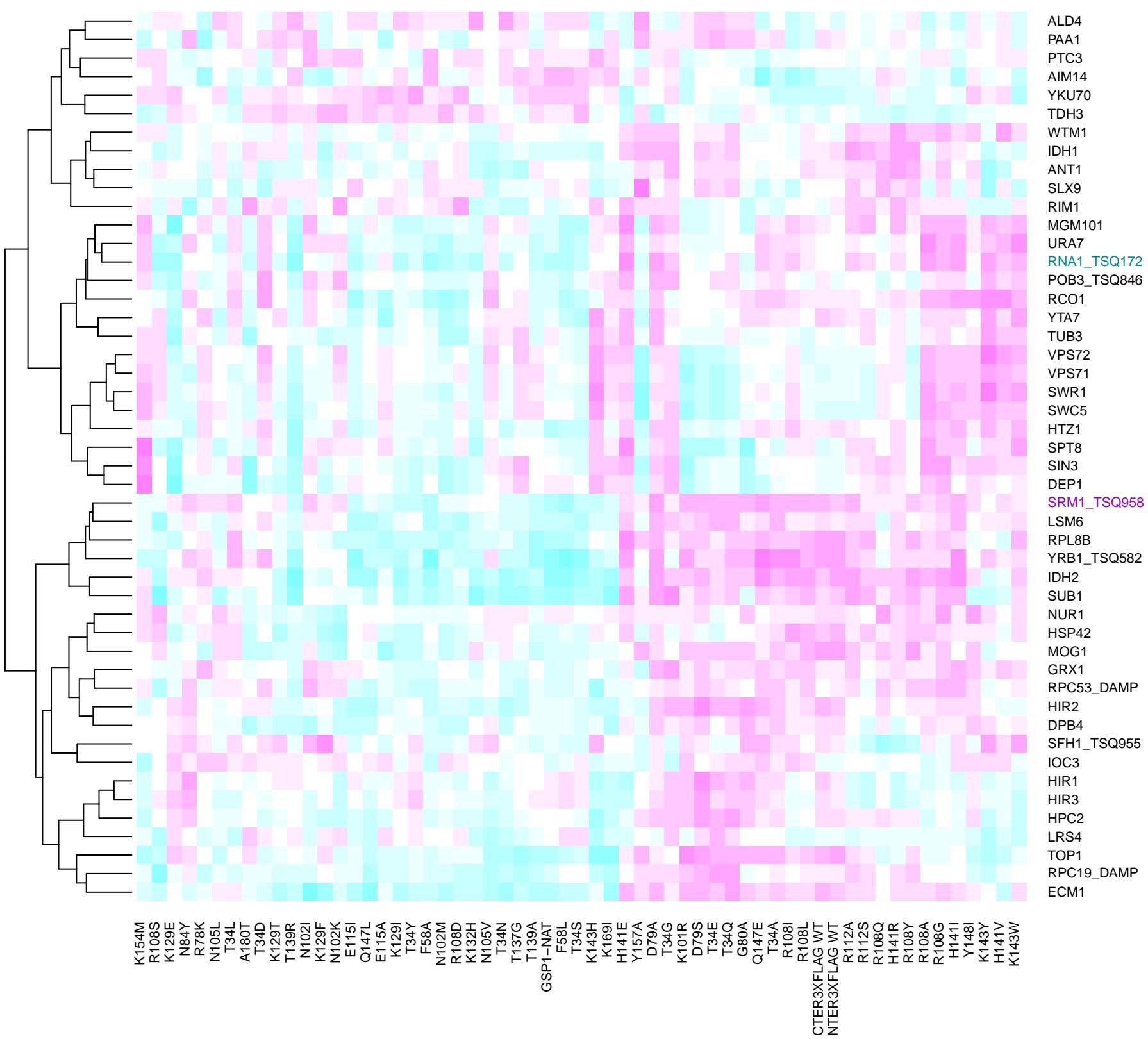


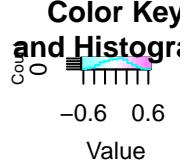
cellular respiration



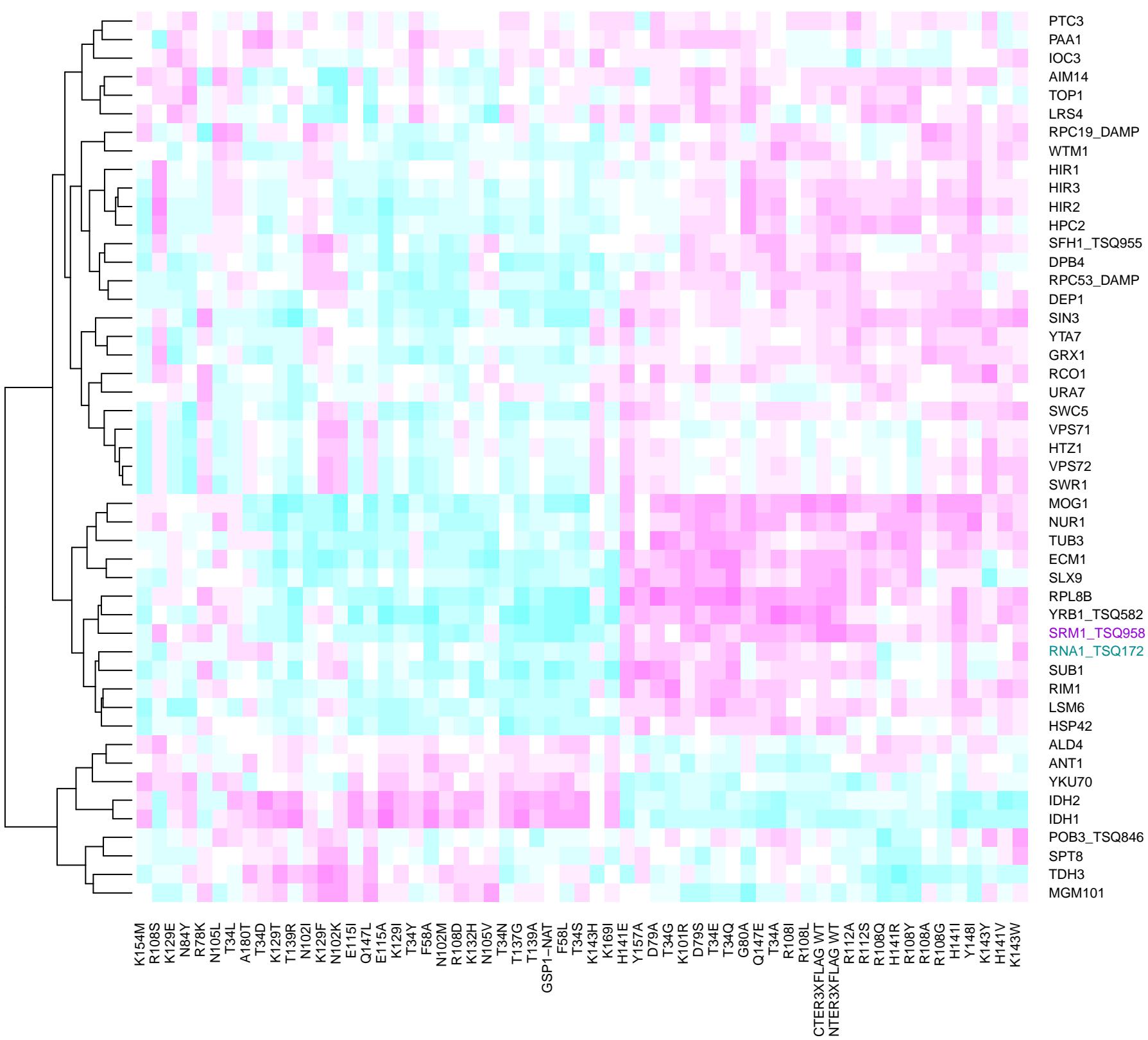


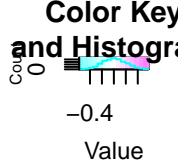
cellular respiration_GO_30_1



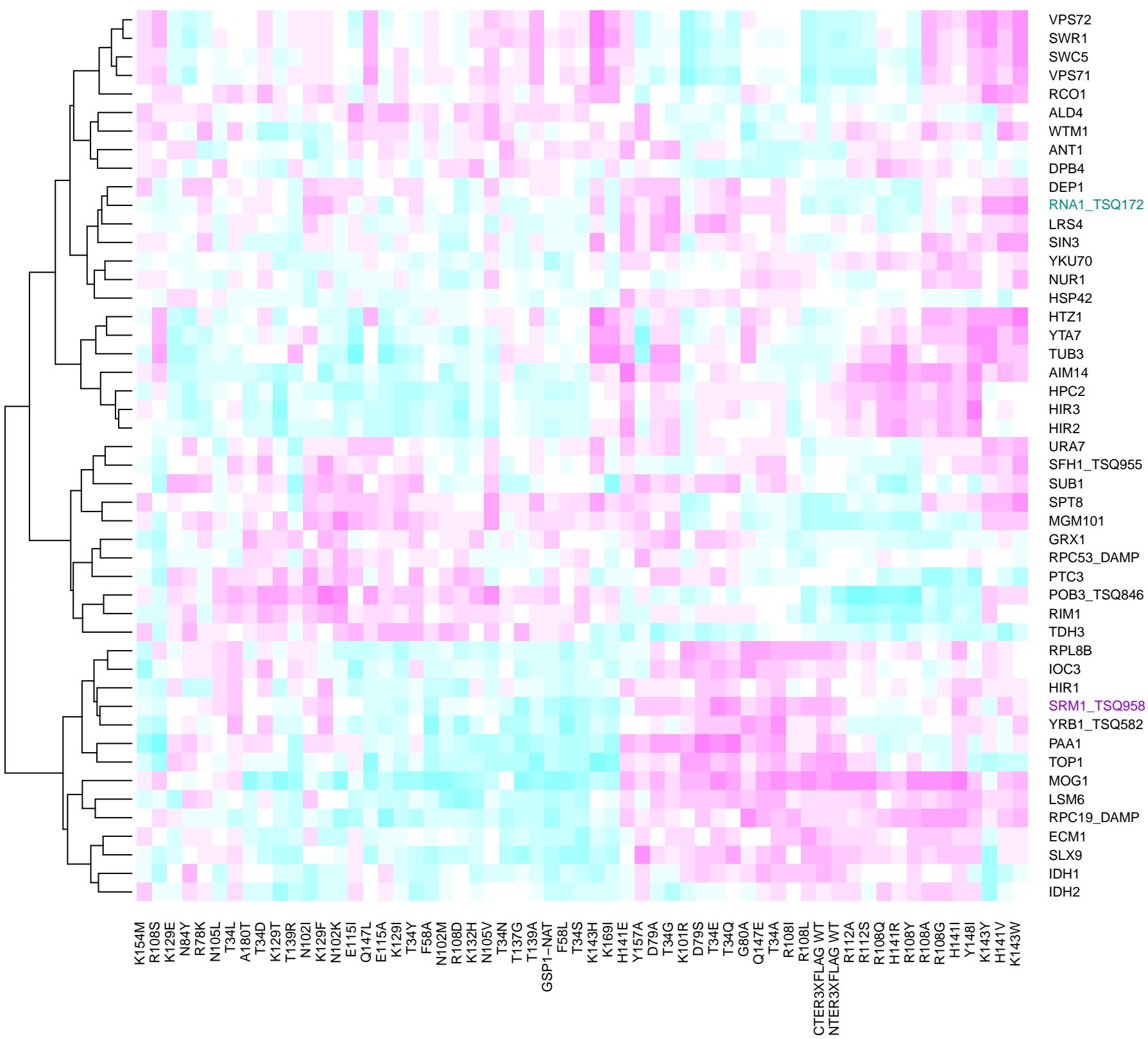


metabolic_GO_30_8

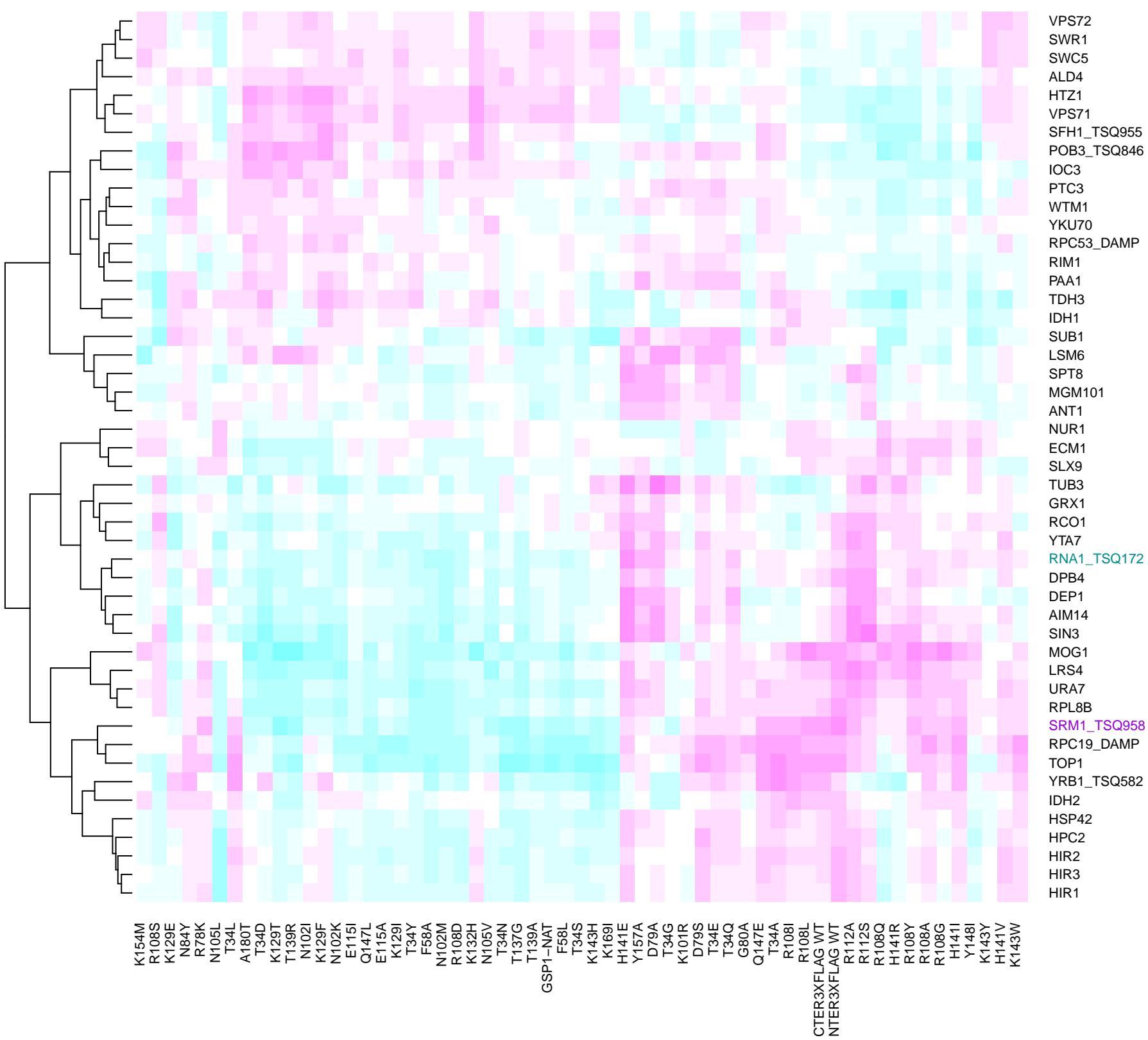
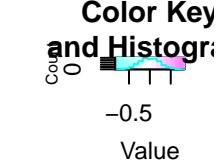


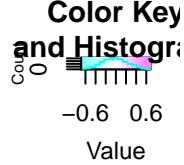


response to oxidative stress_GO_30_1

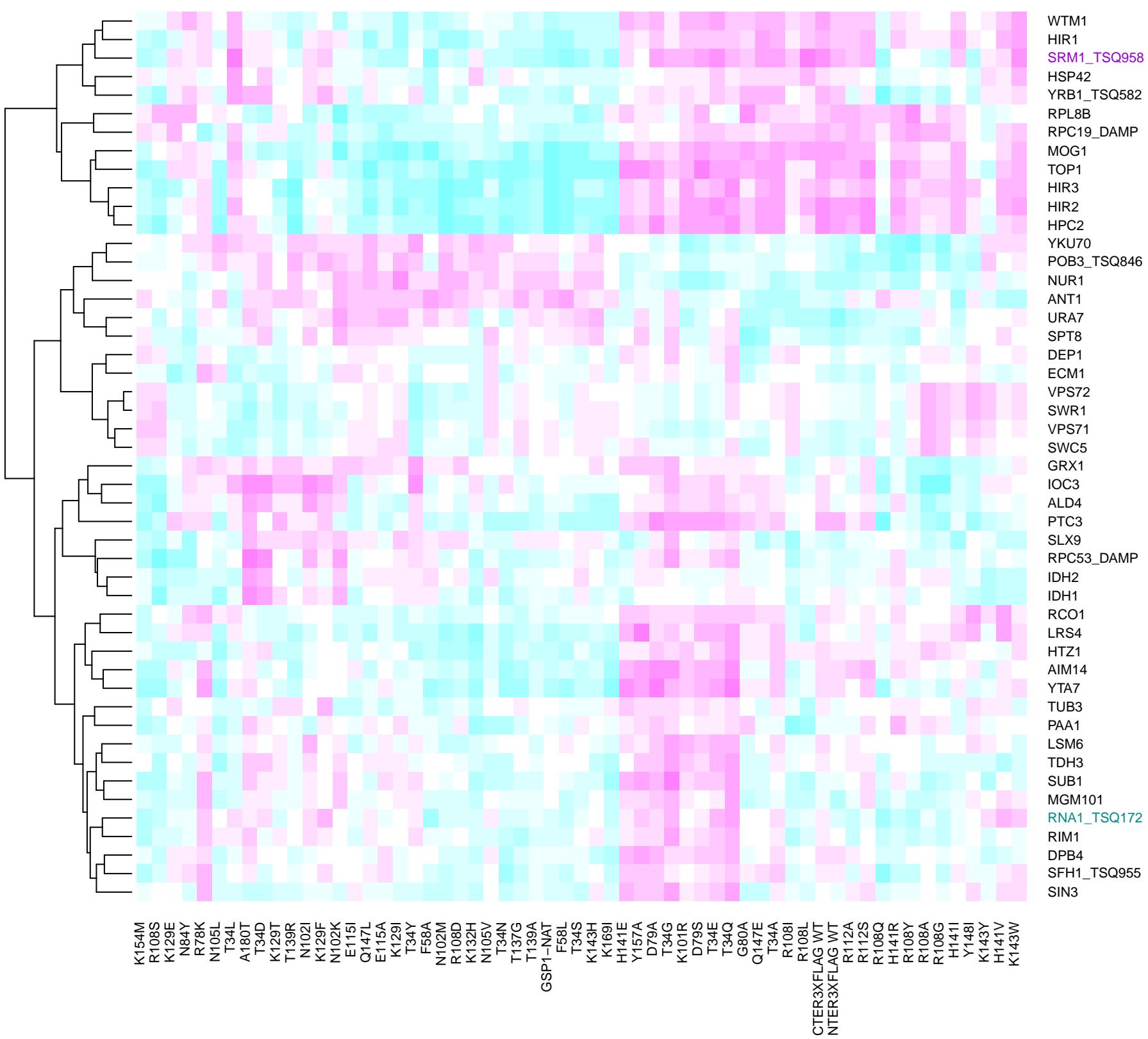


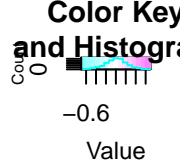
transcription and mRNA processing_GO_30_3



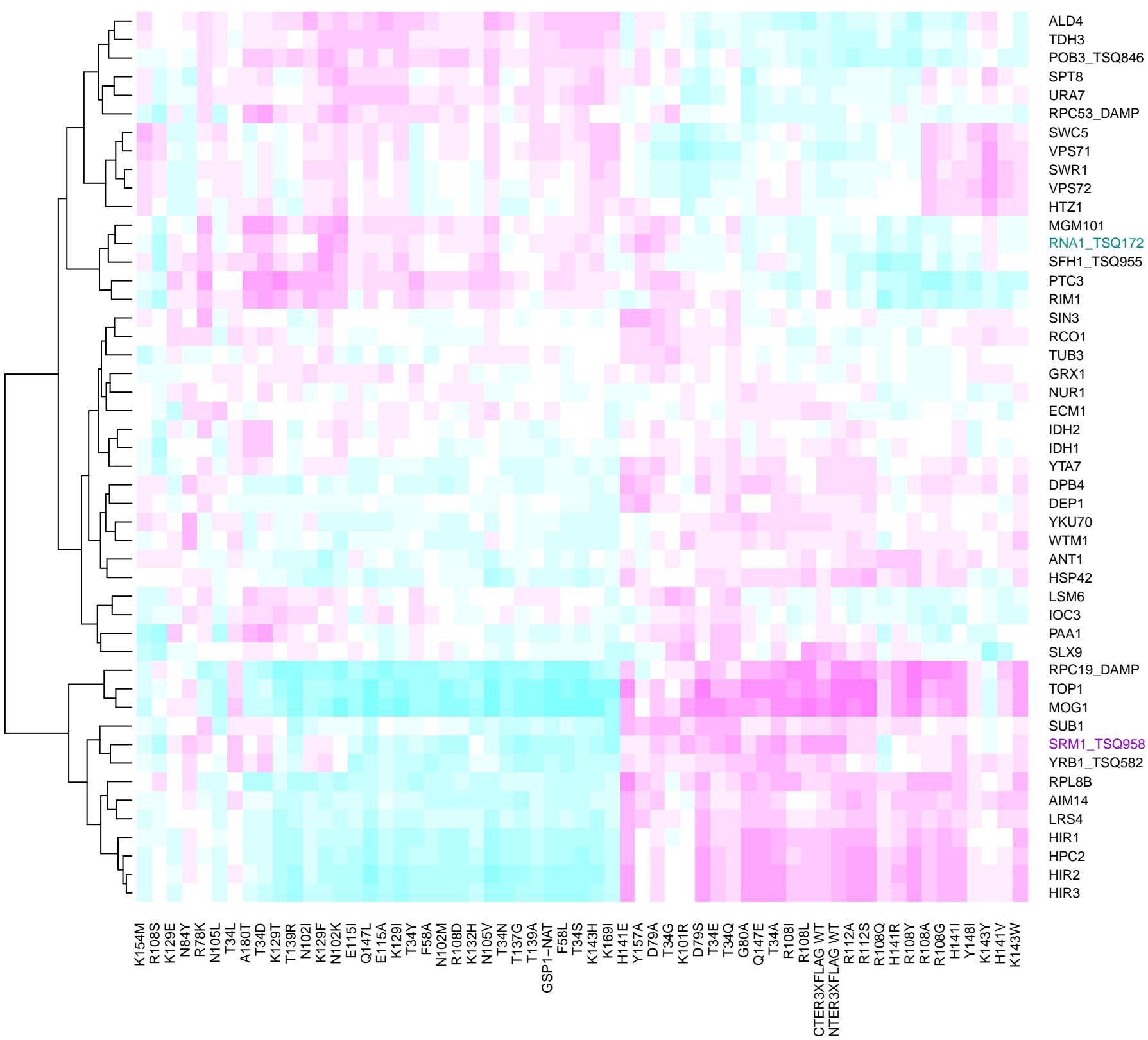


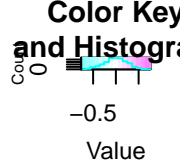
ribosome_GO_30_5



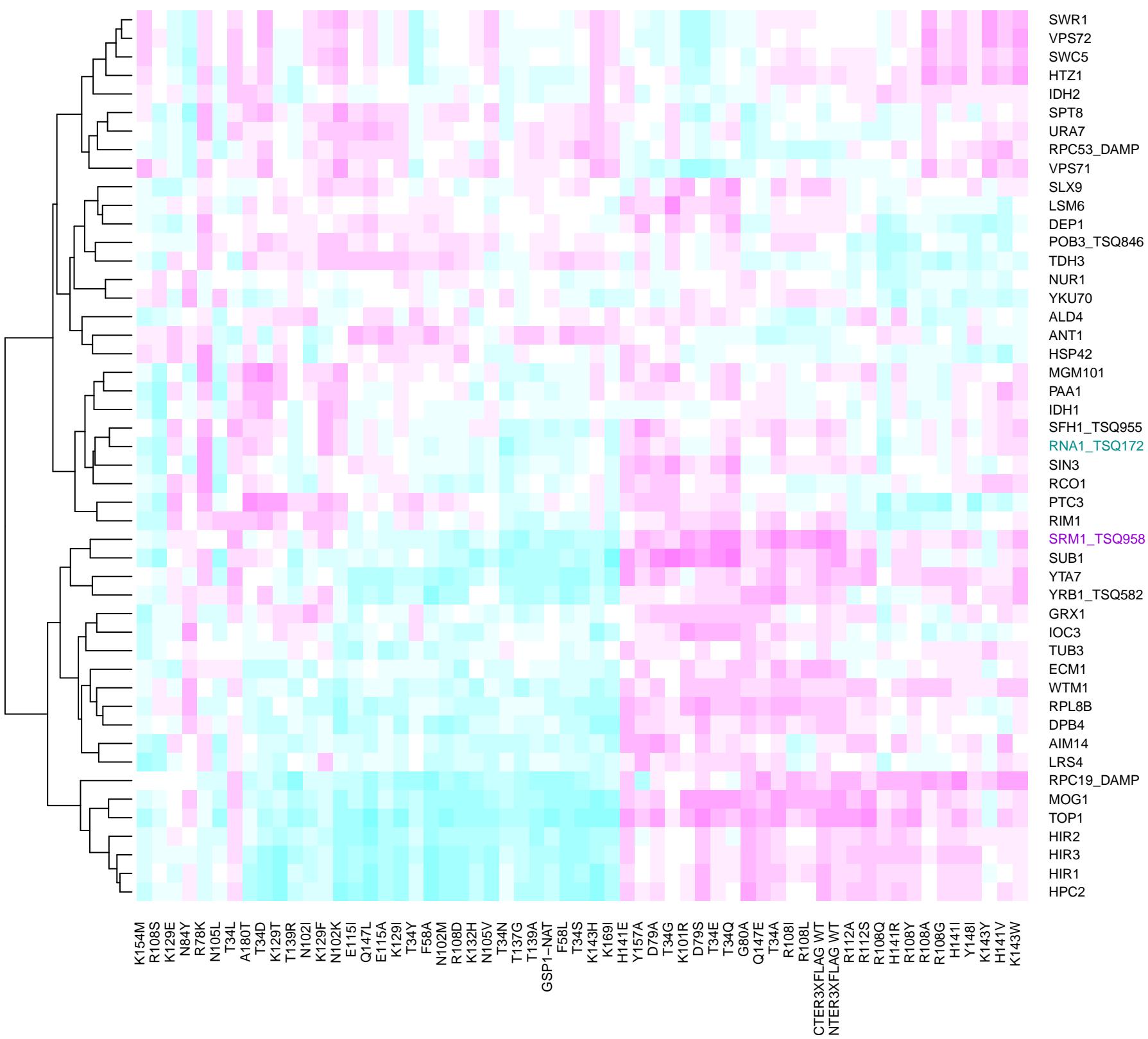


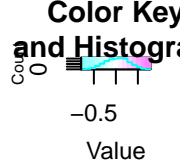
structural constituent of ribosome



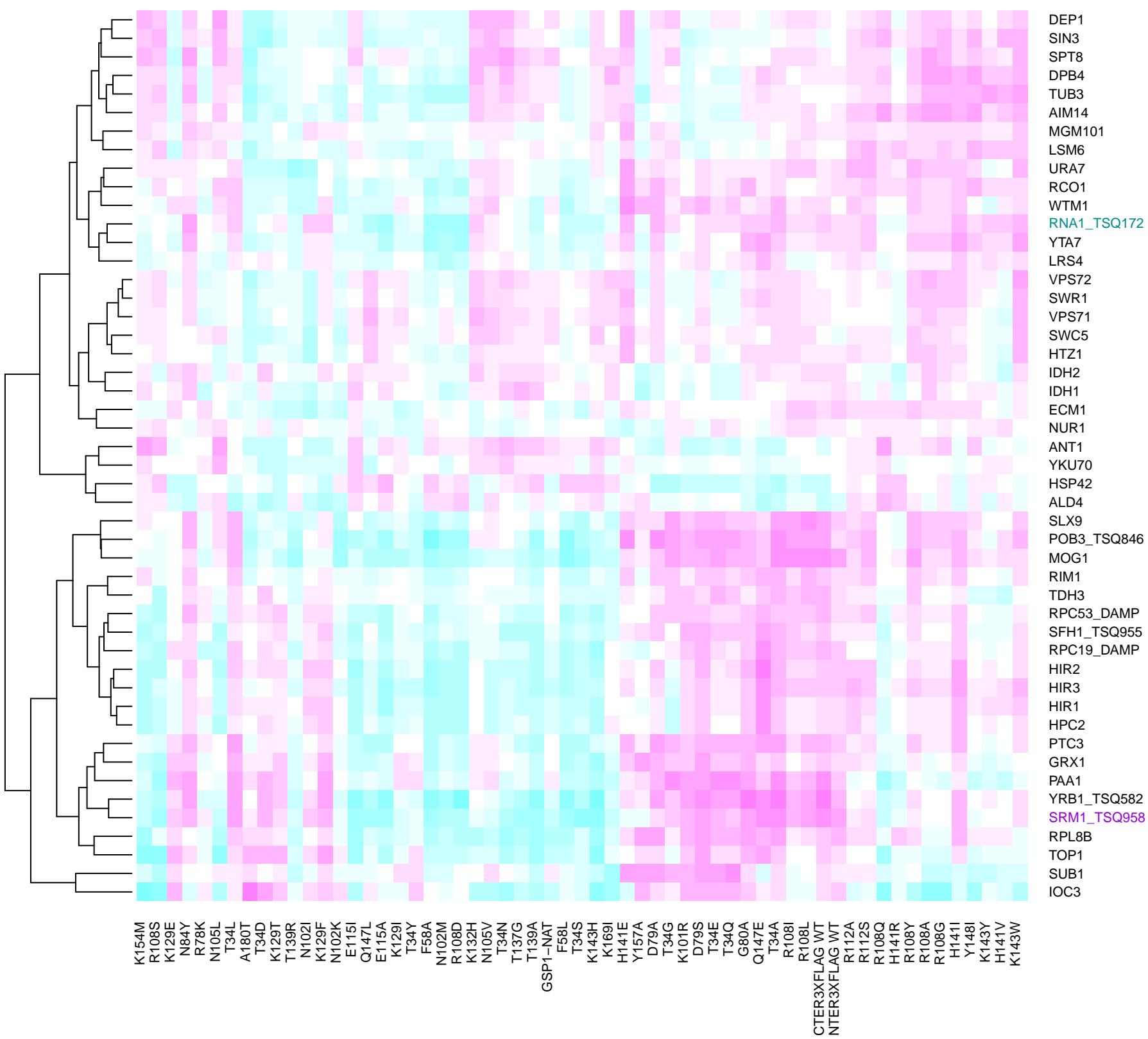


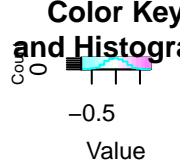
structural constituent of ribosome_GO_30_2



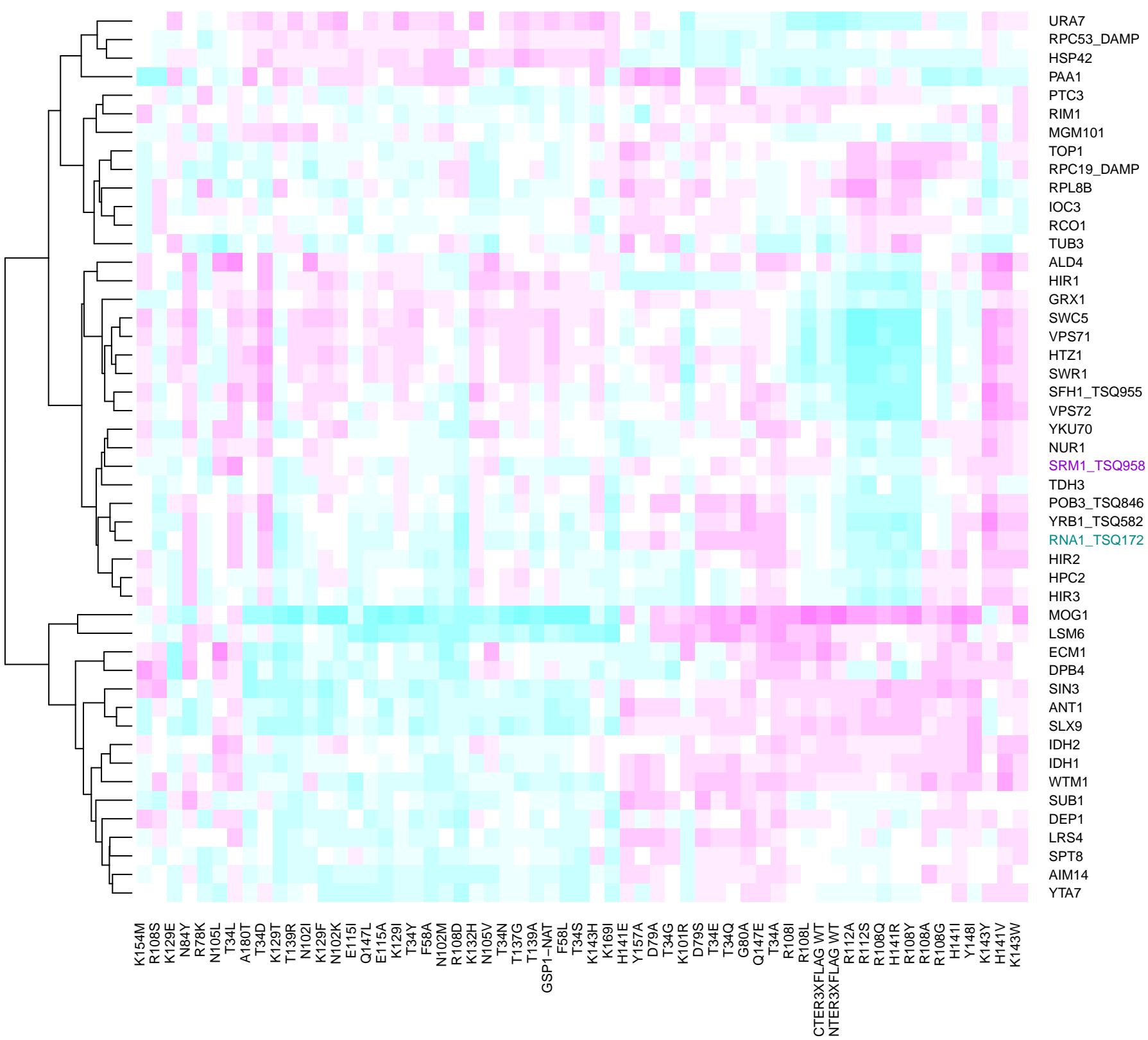


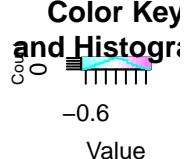
budding_GO_30_11



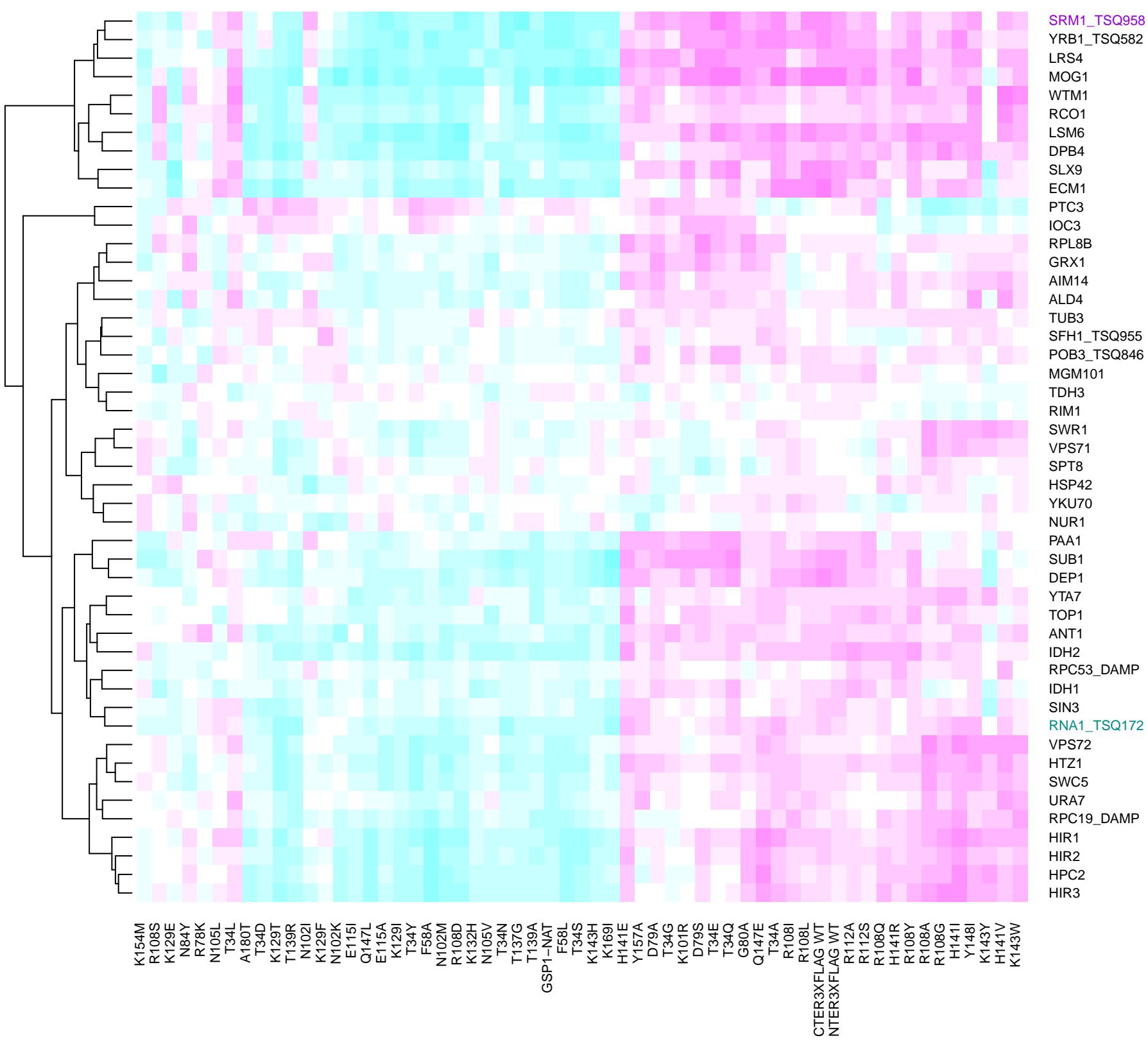


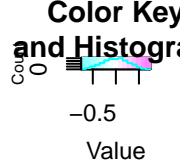
nucleolus_GO_30_1



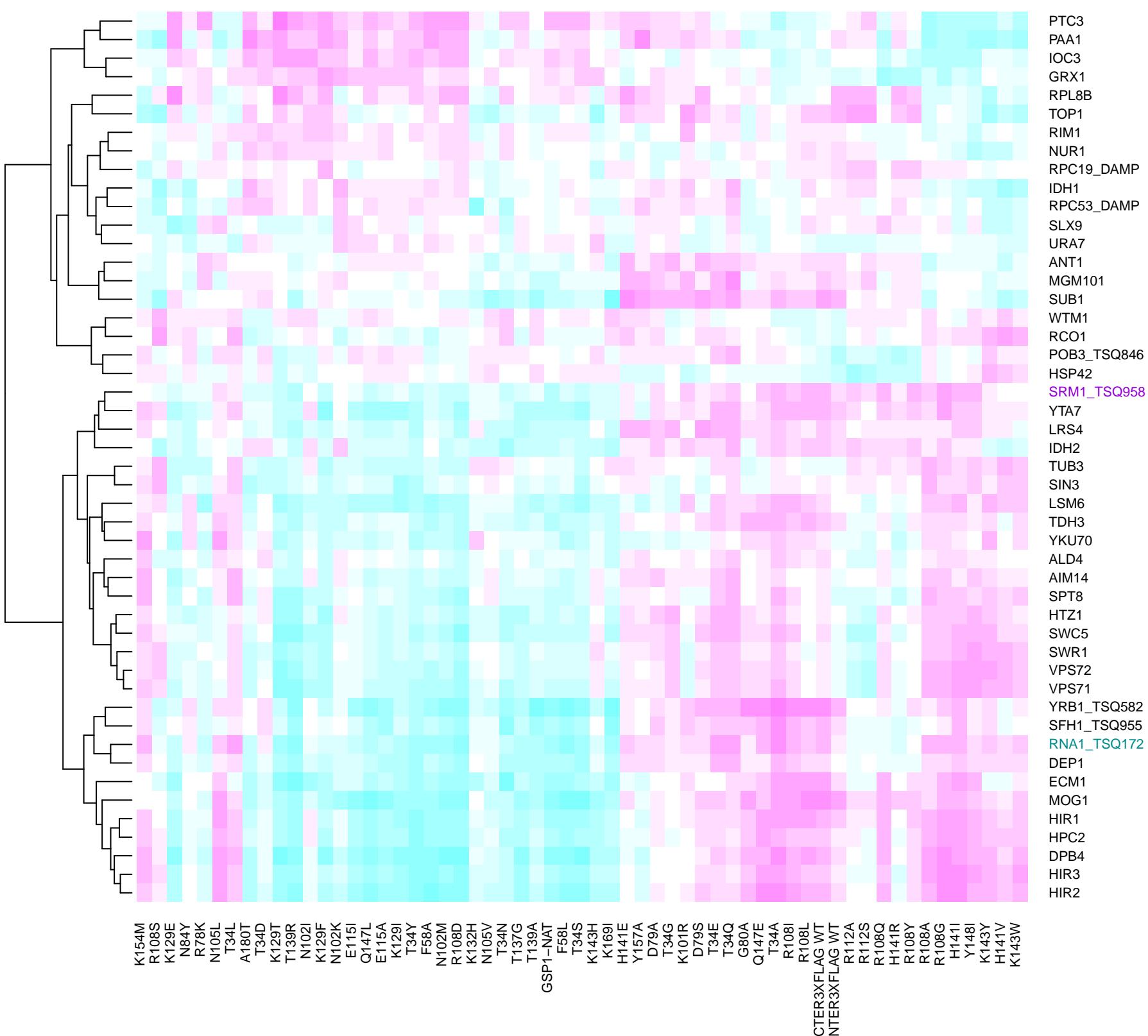


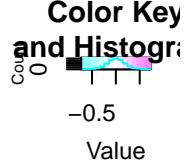
ribosome_GO_30_2



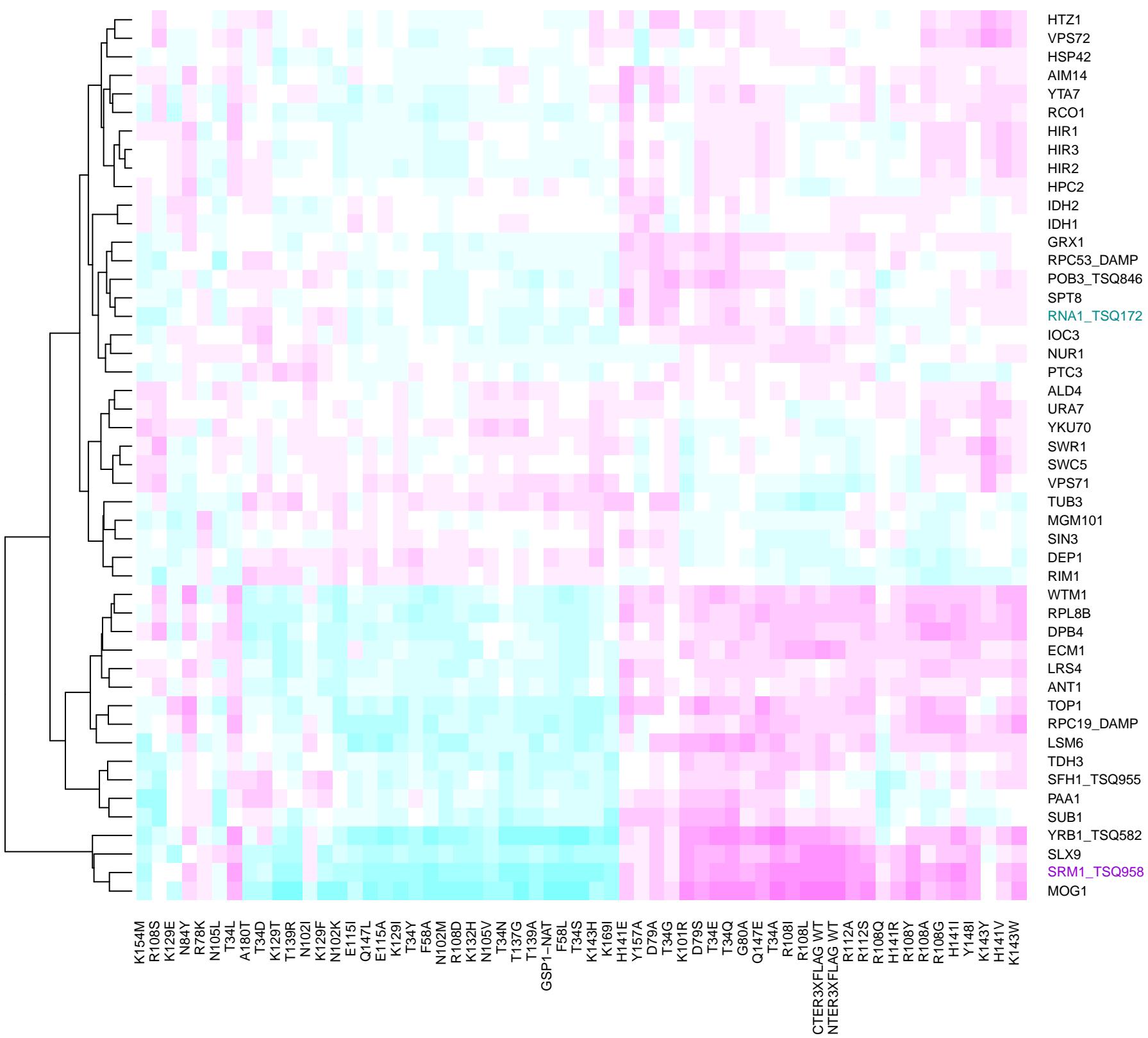


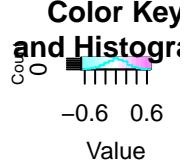
ribosomes and translation_GO_30_8



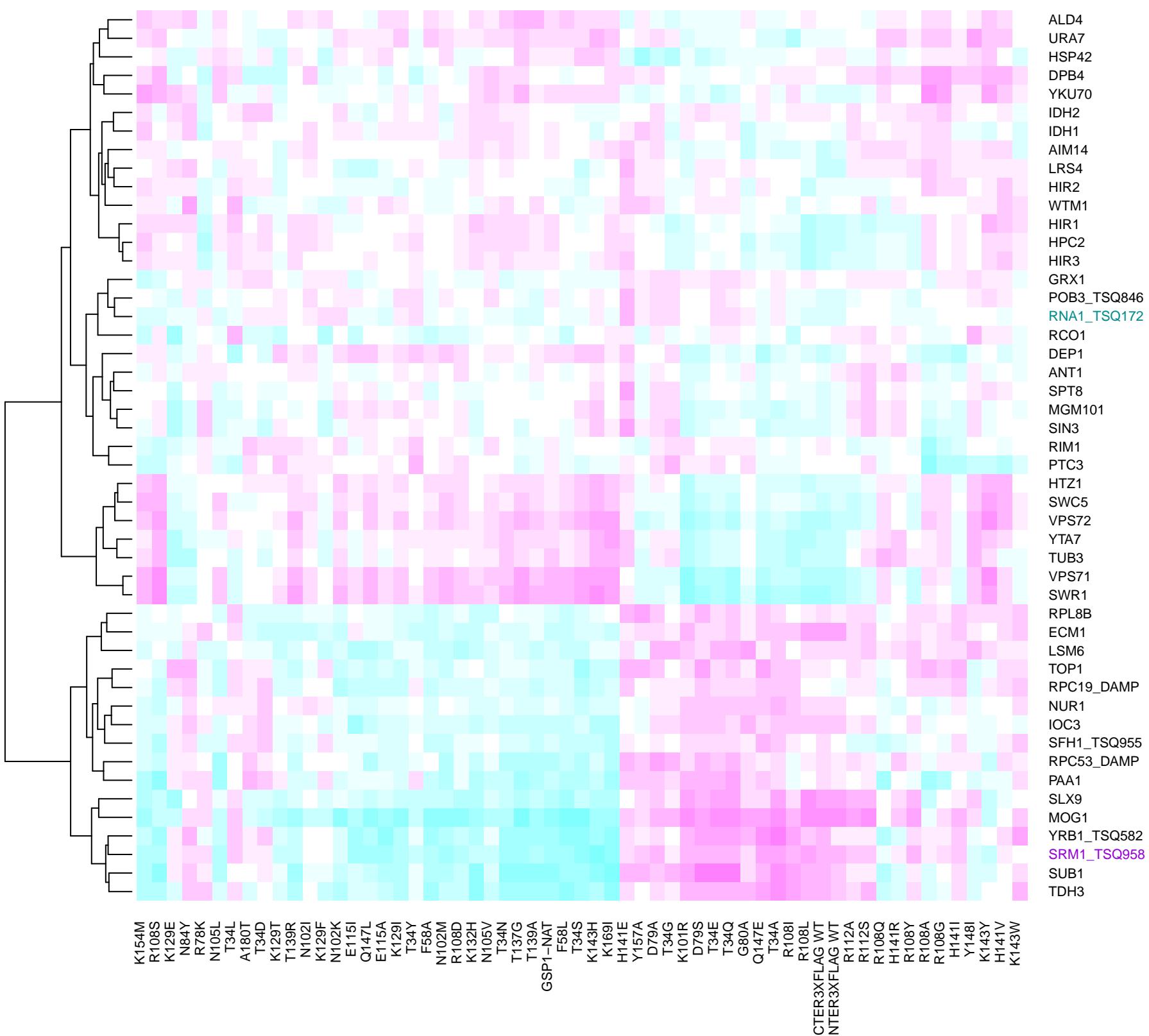


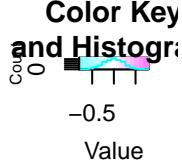
mRNA binding





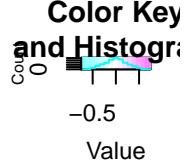
mRNA binding_GO_30_1



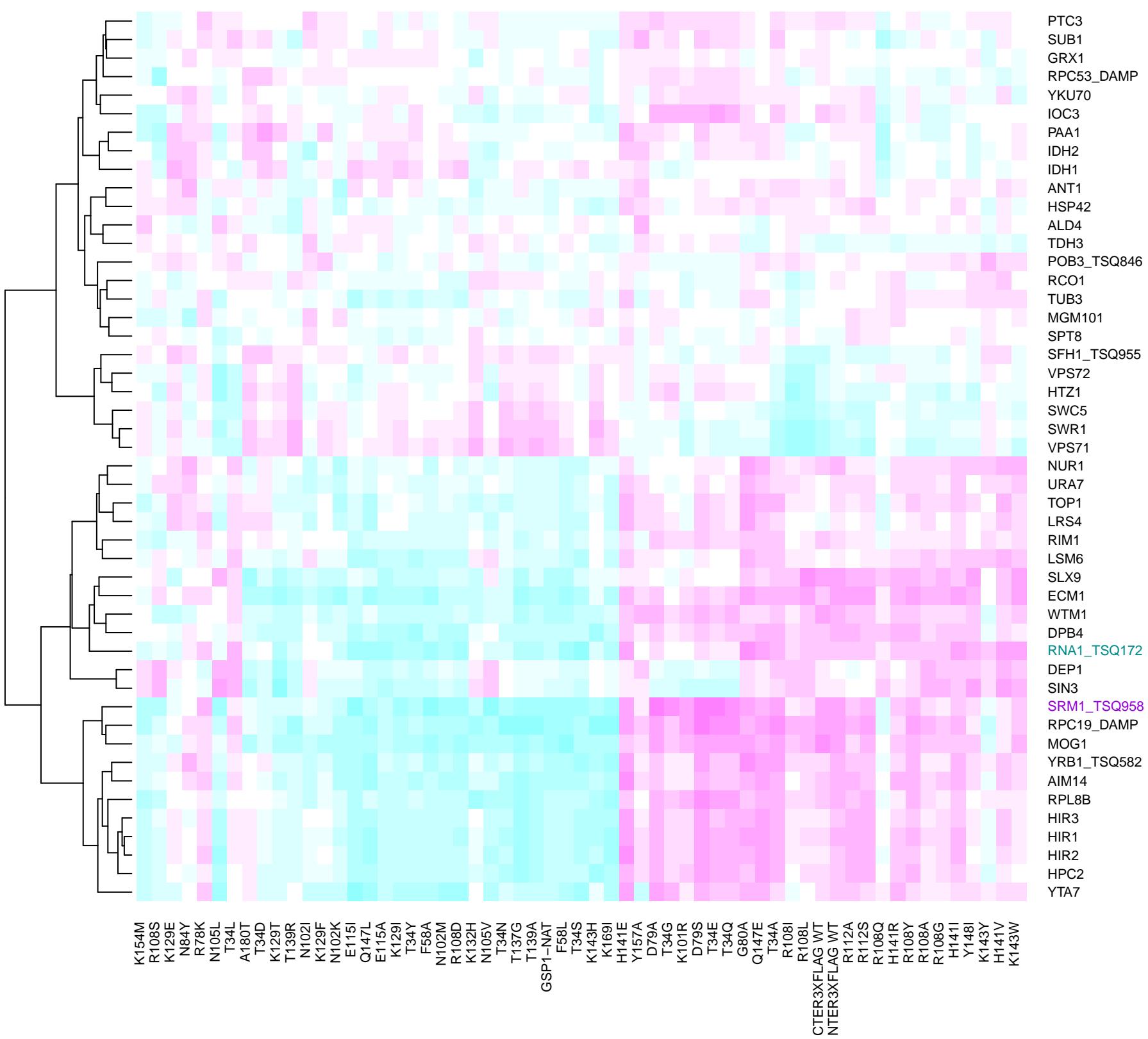


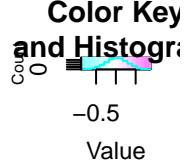
transcription and mRNA processing_GO_30_9



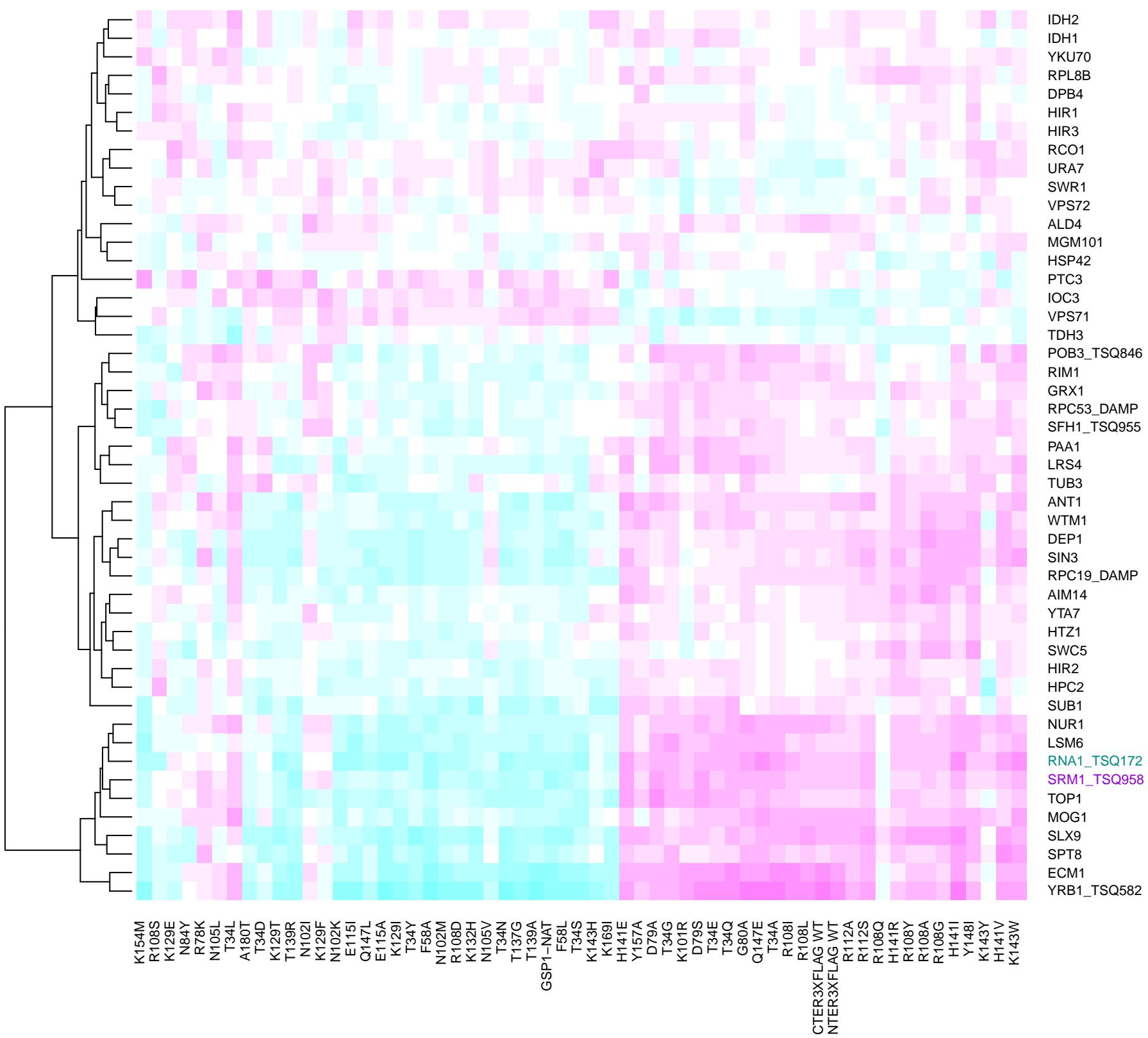


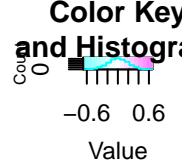
budding_GO_30_7



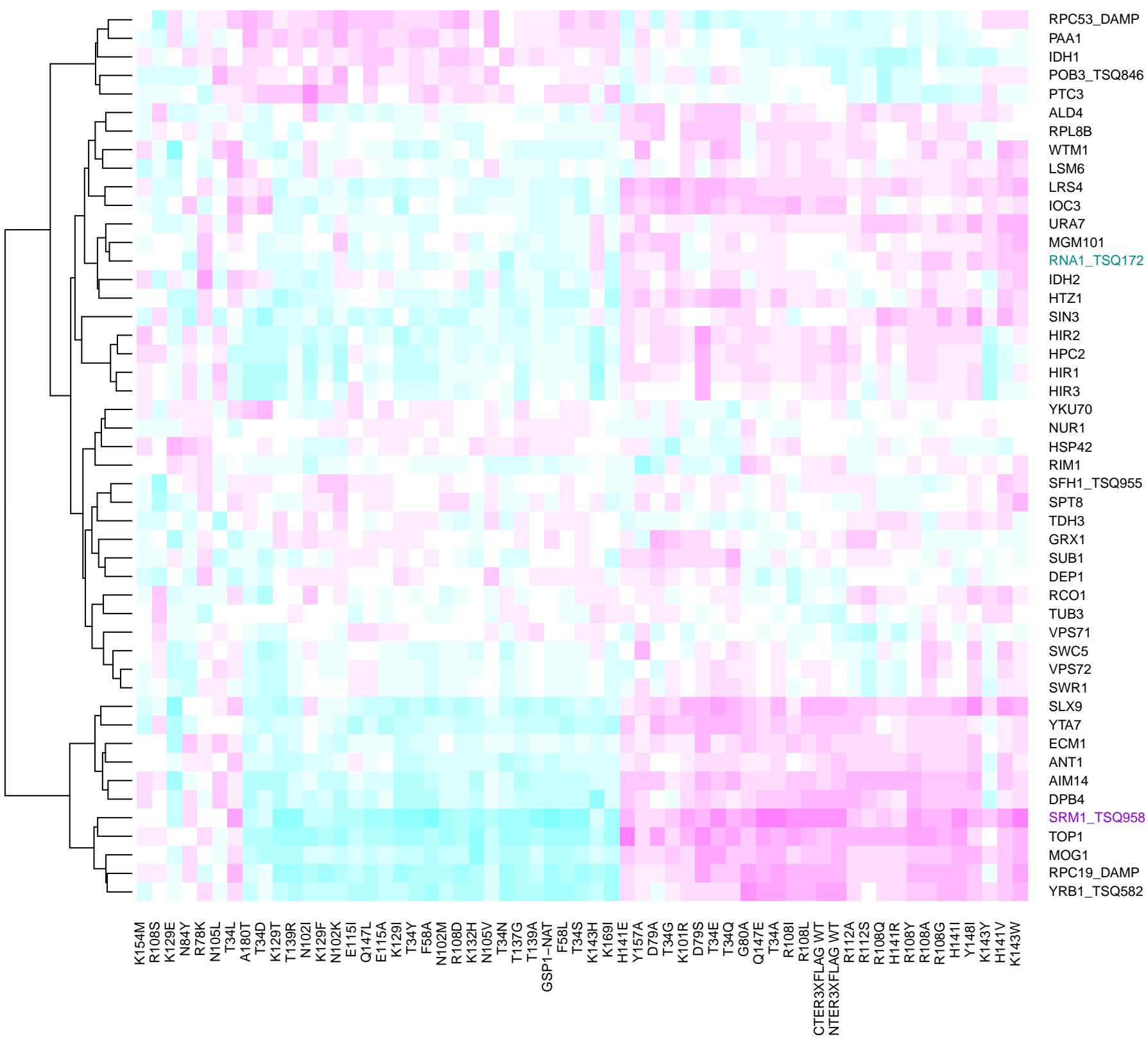


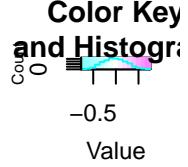
lipid metabolic process_GO_30_6



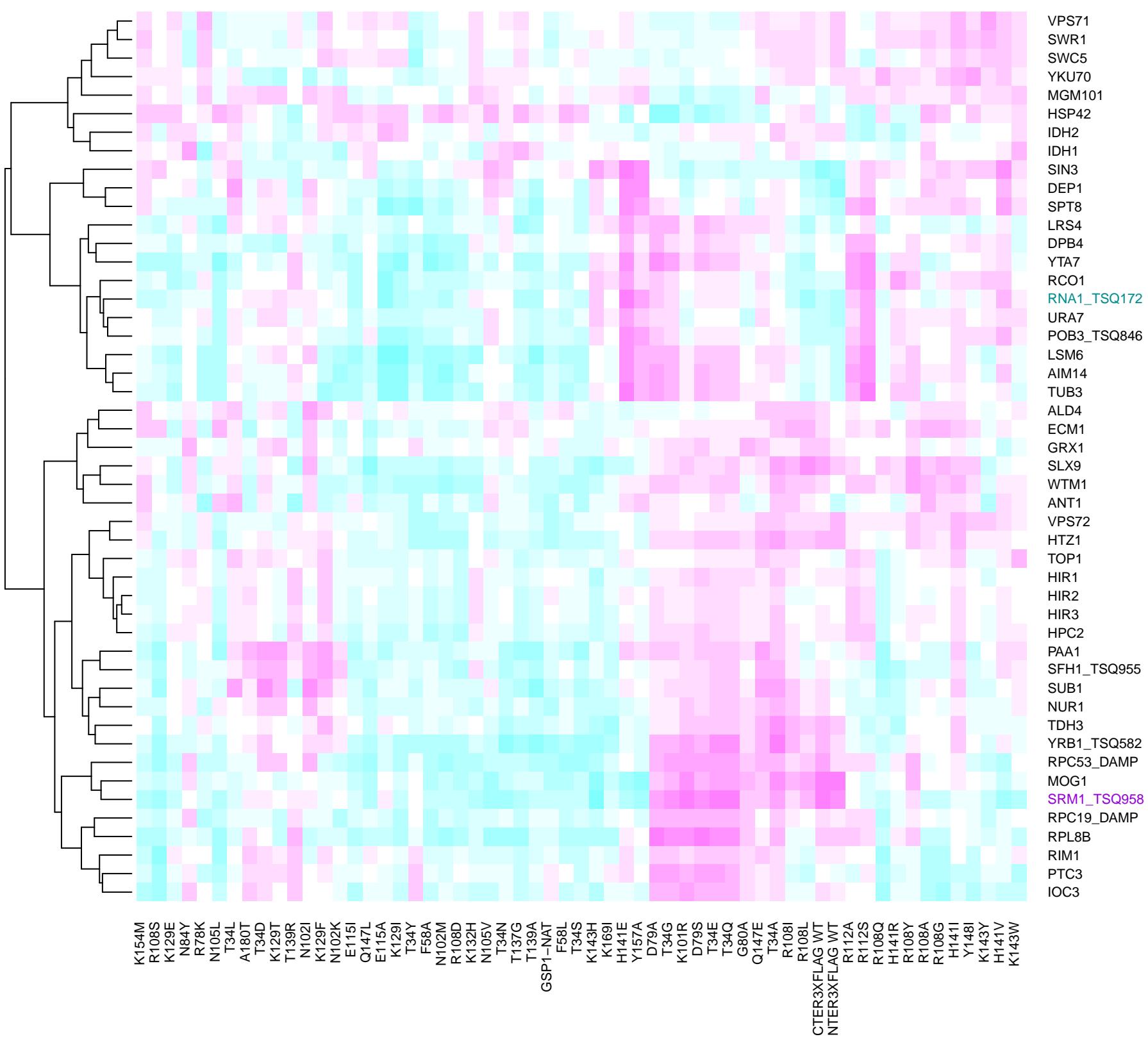


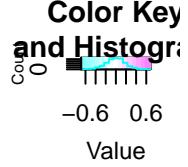
vacuole_GO_30_2



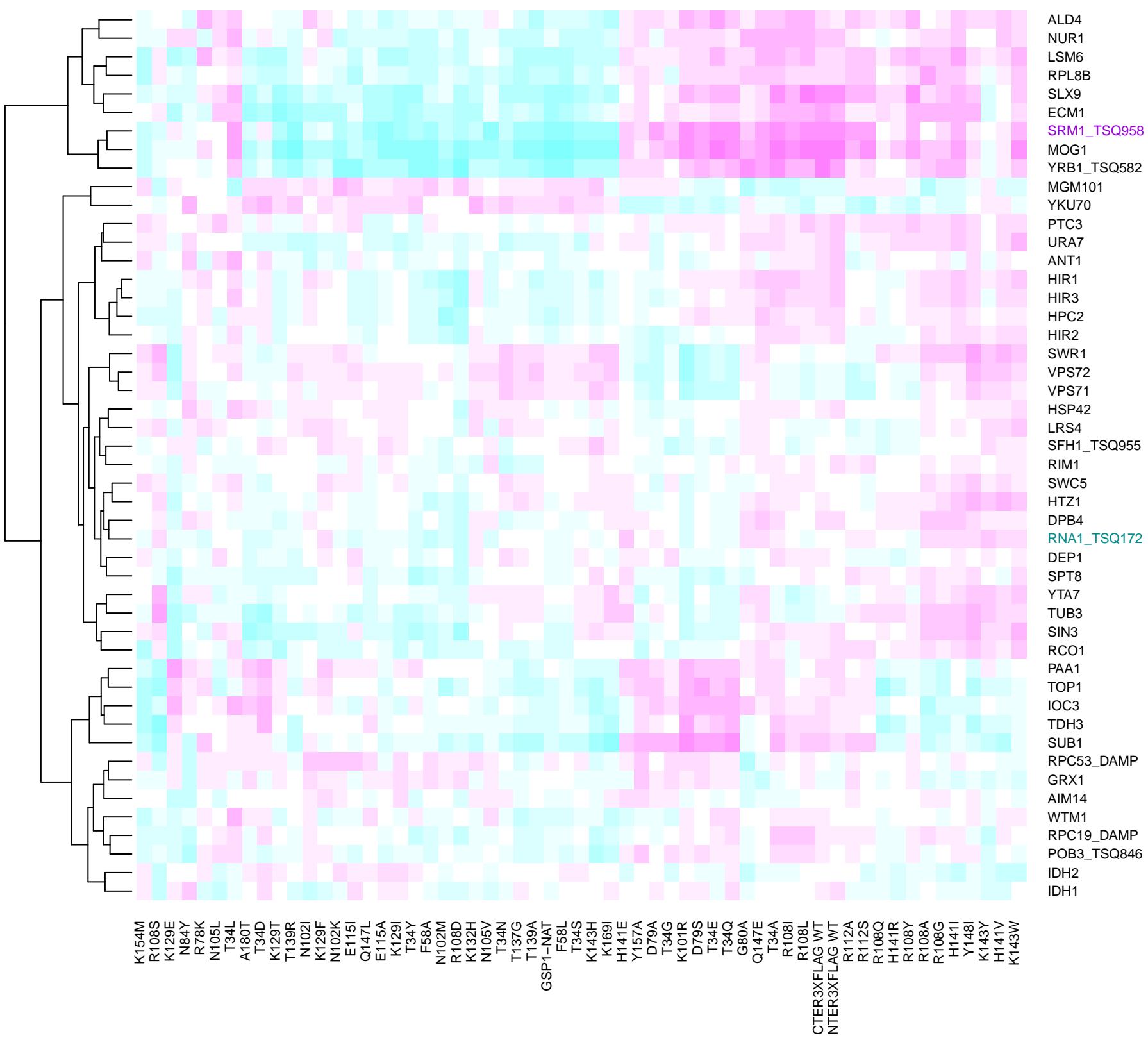


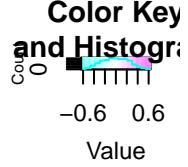
cell cycle_GO_30_8



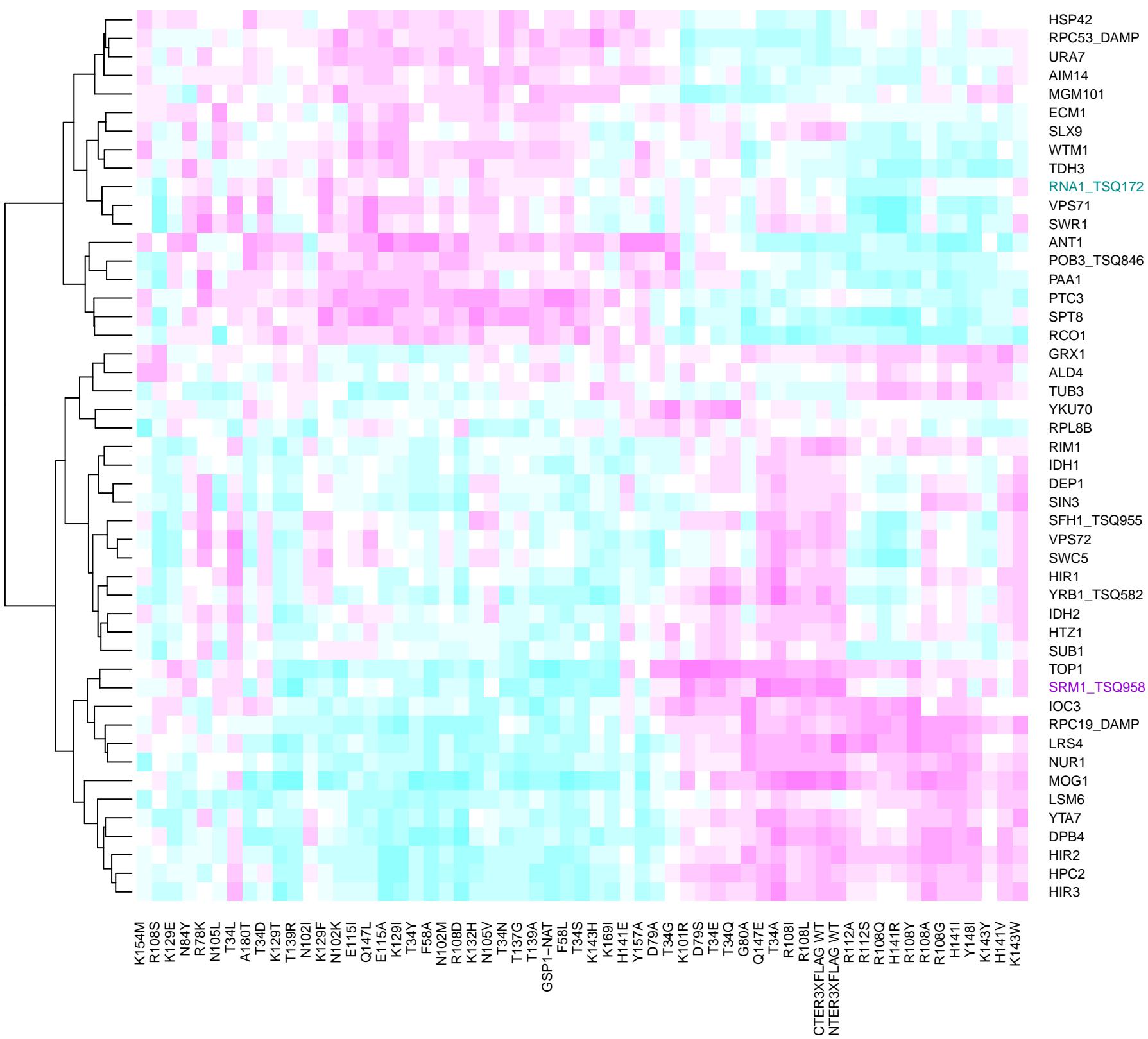


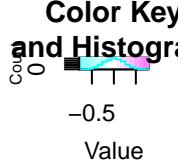
cell cycle_GO_30_5



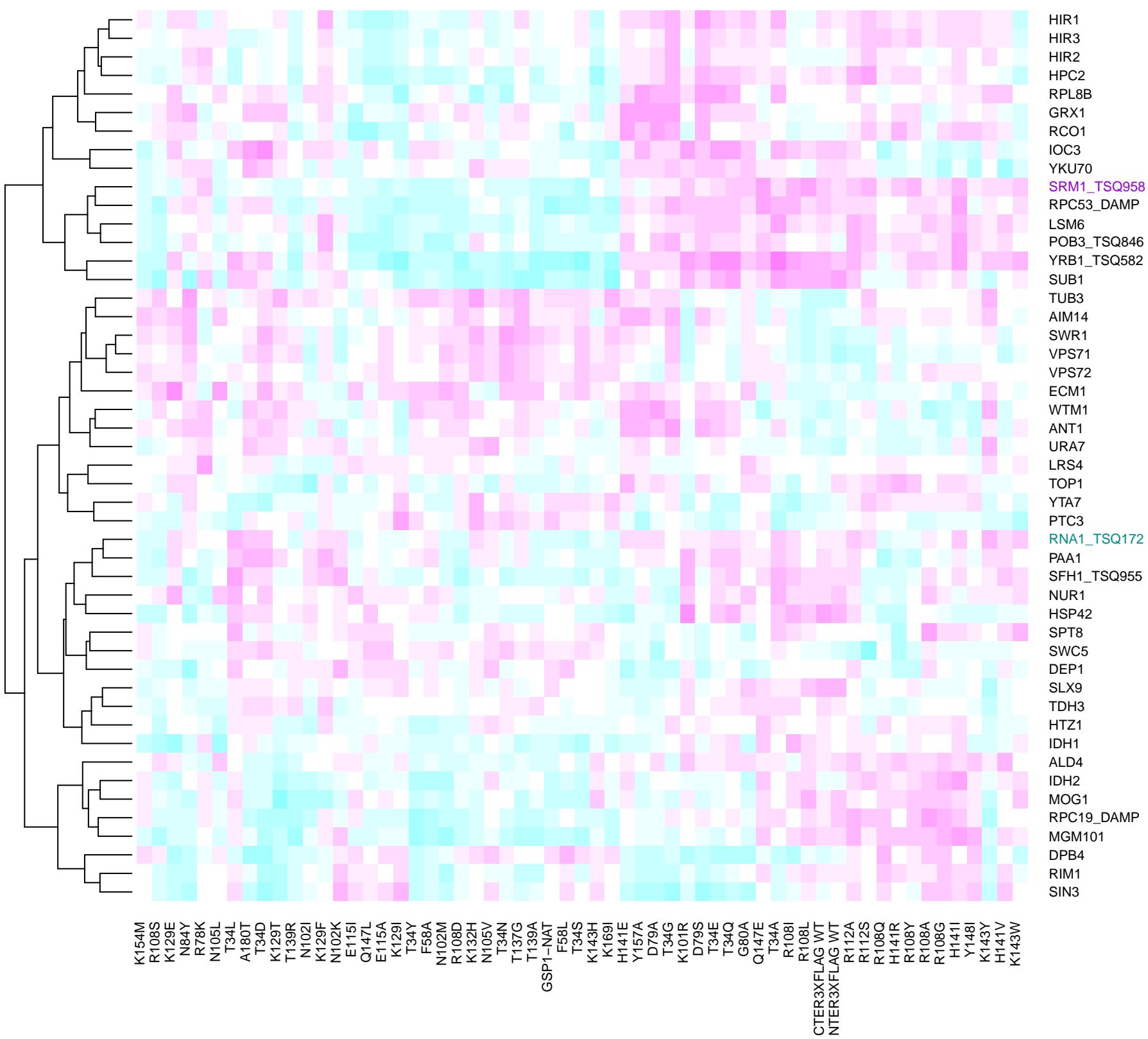


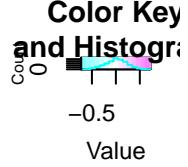
membrane fusion_GO_30_1



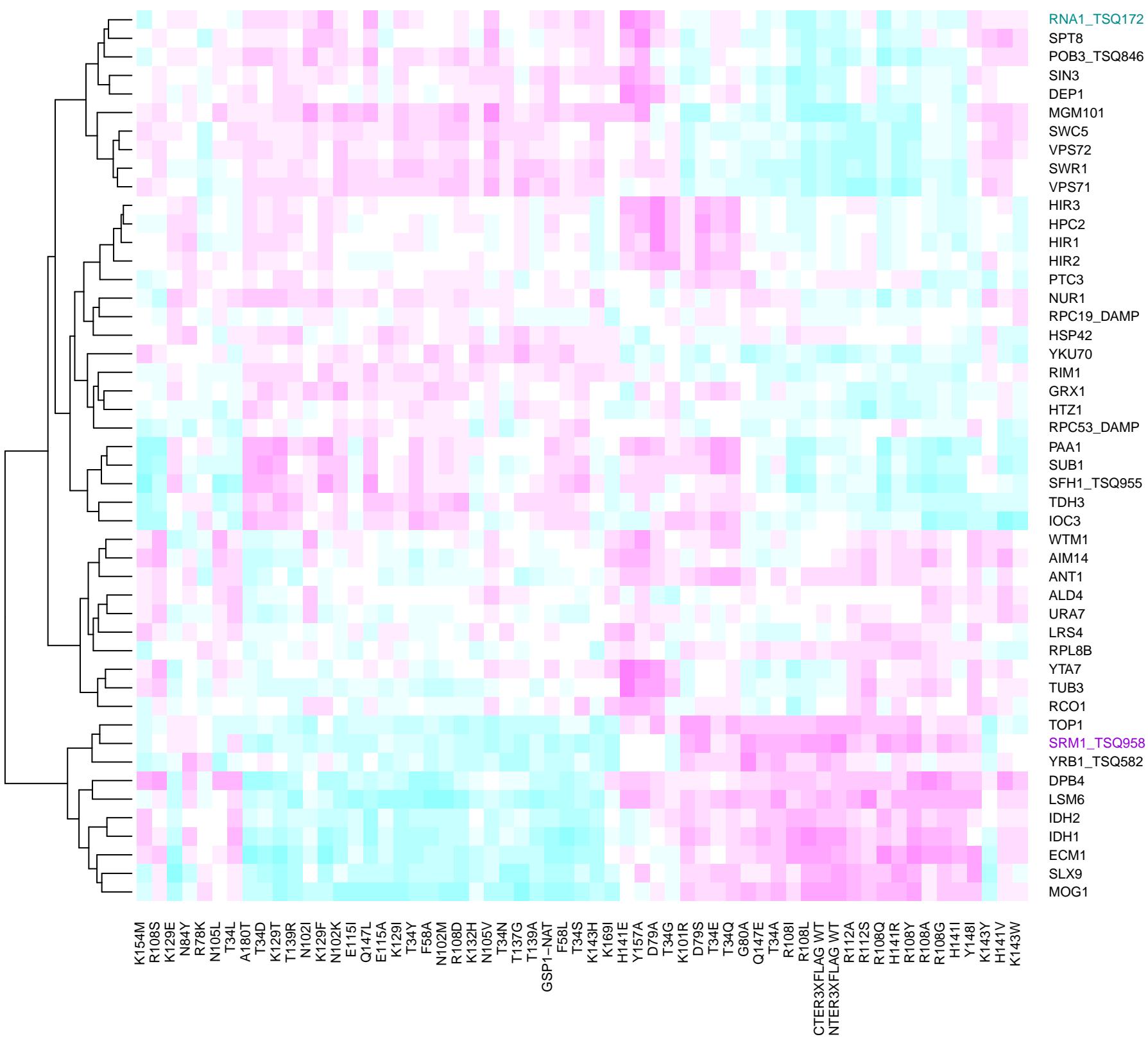


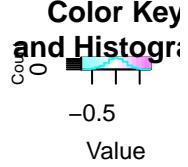
vacuole_GO_30_7



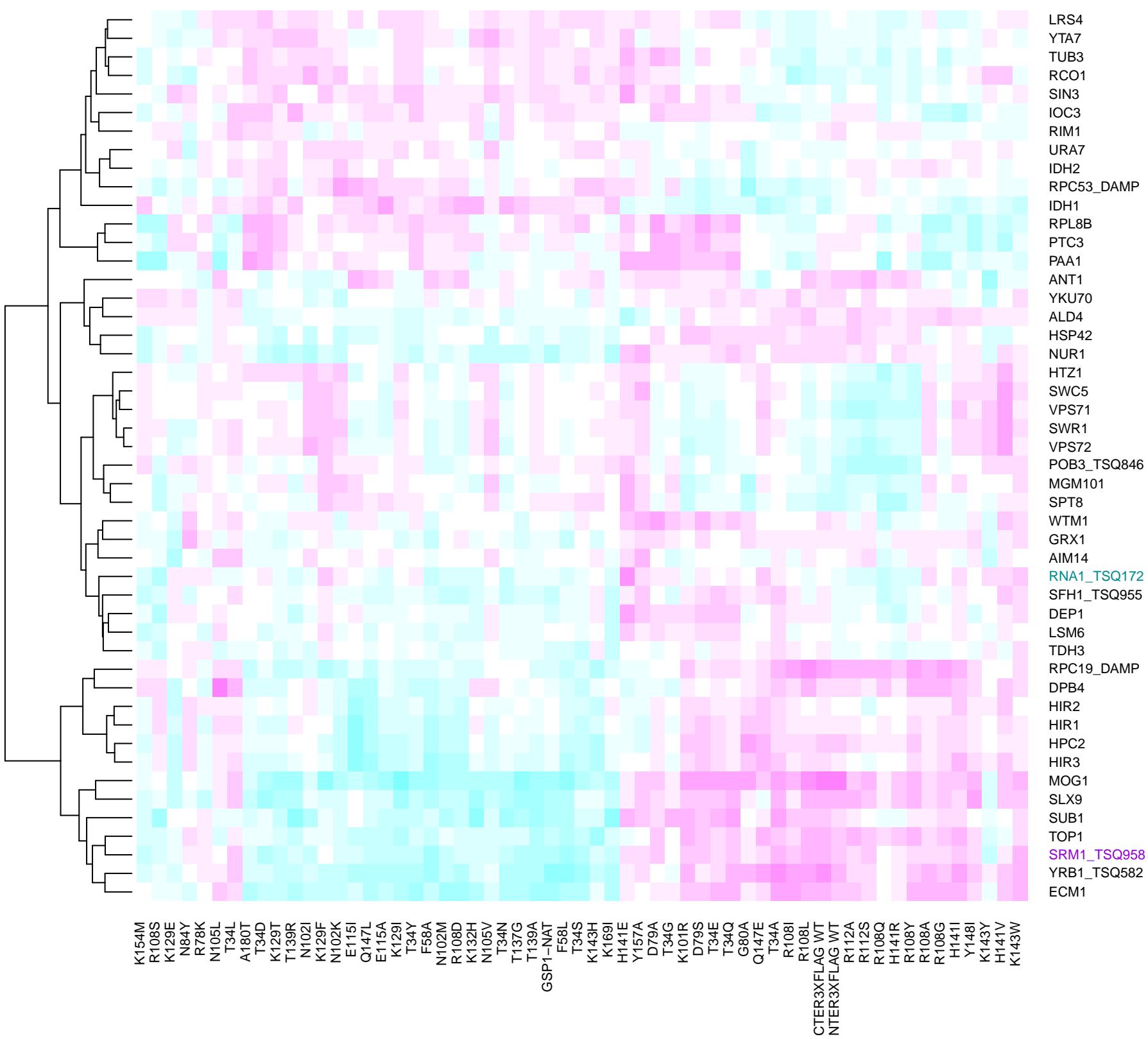


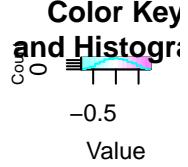
transcription from RNA polymerase II promoter_GO_30_5



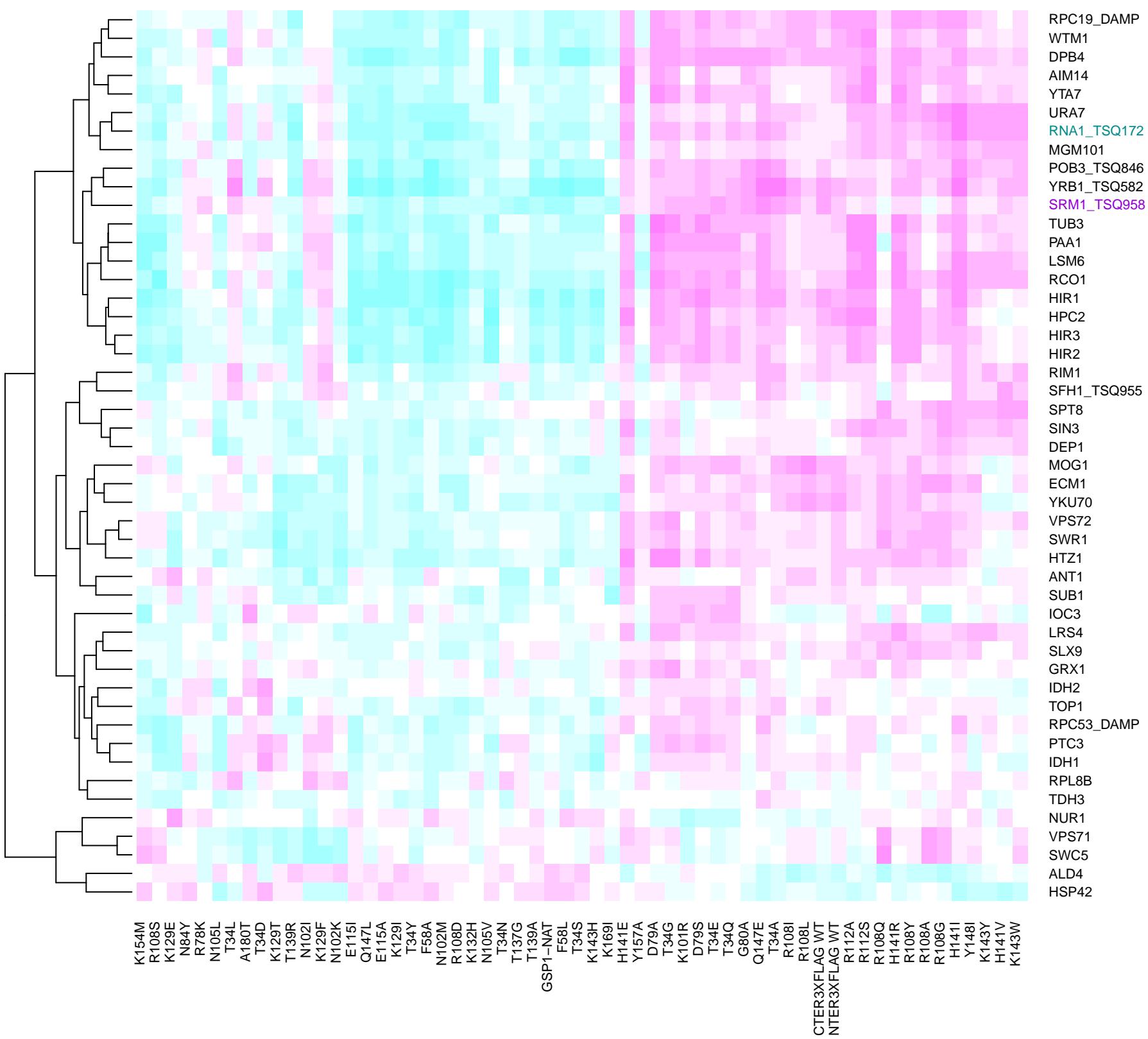


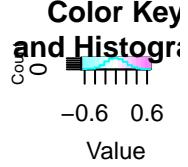
carbohydrate metabolic process_GO_30_1



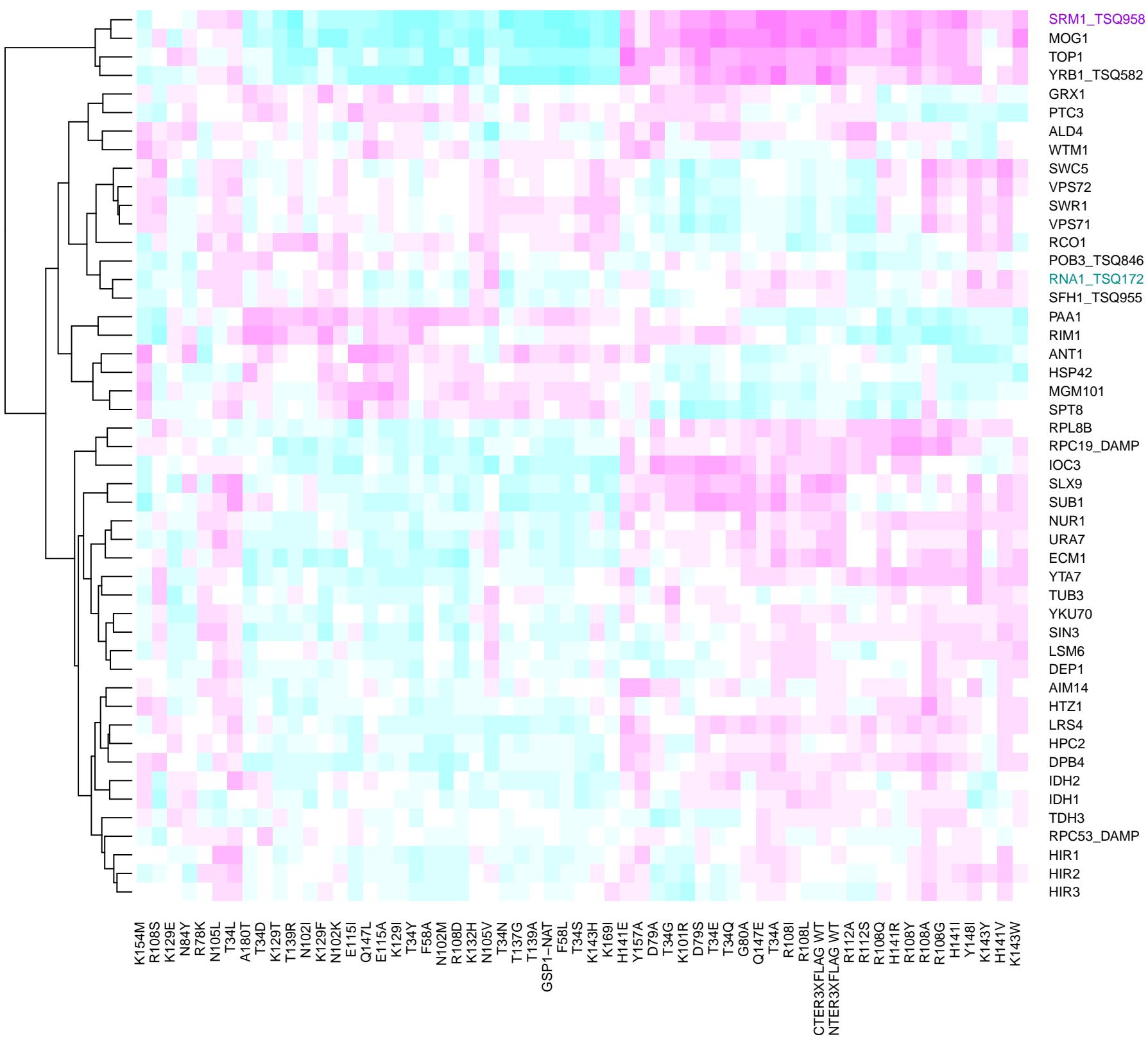


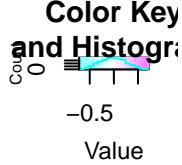
metabolic_GO_30_10



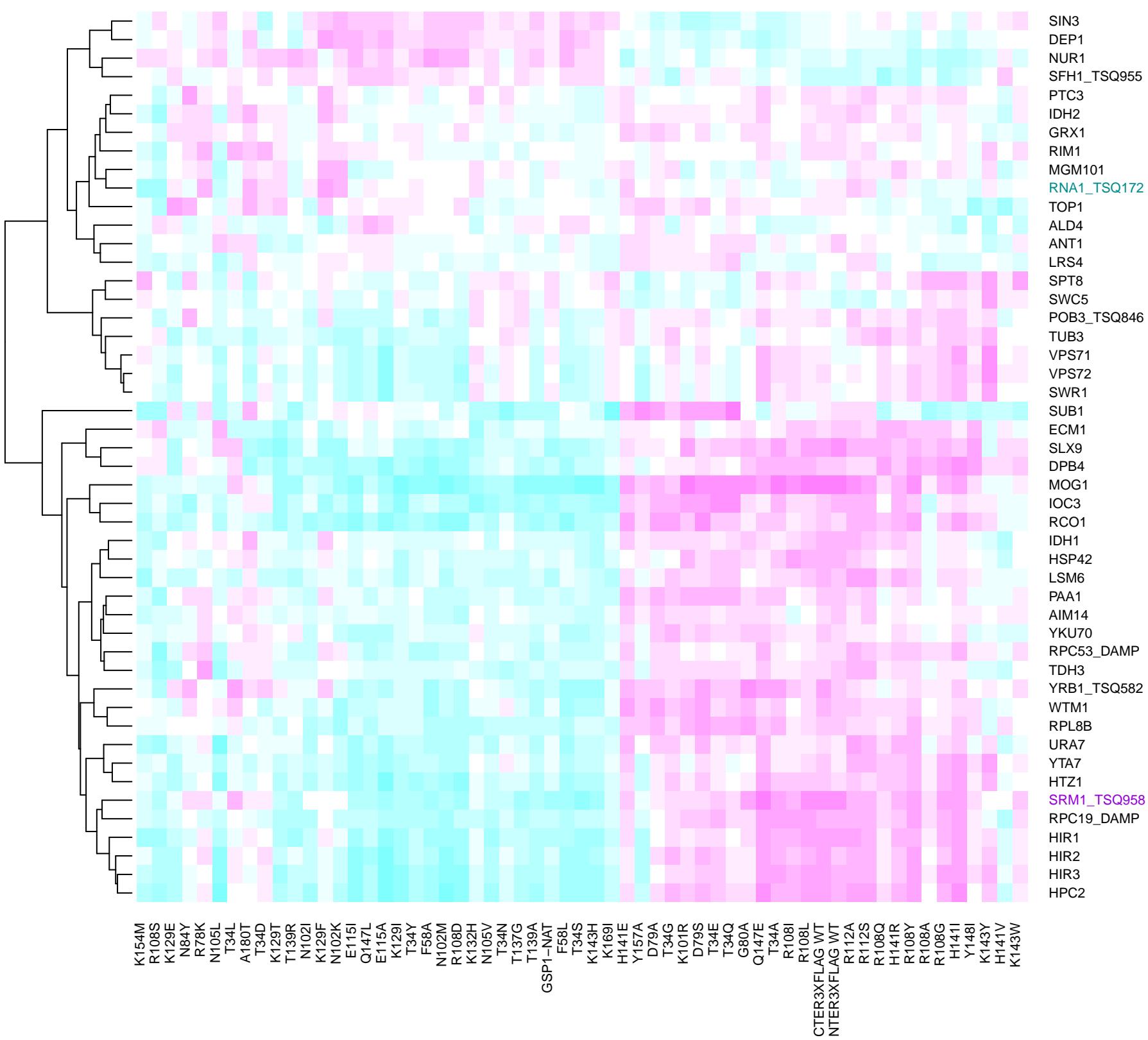


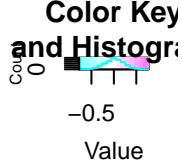
vacuoles_GO_30_2



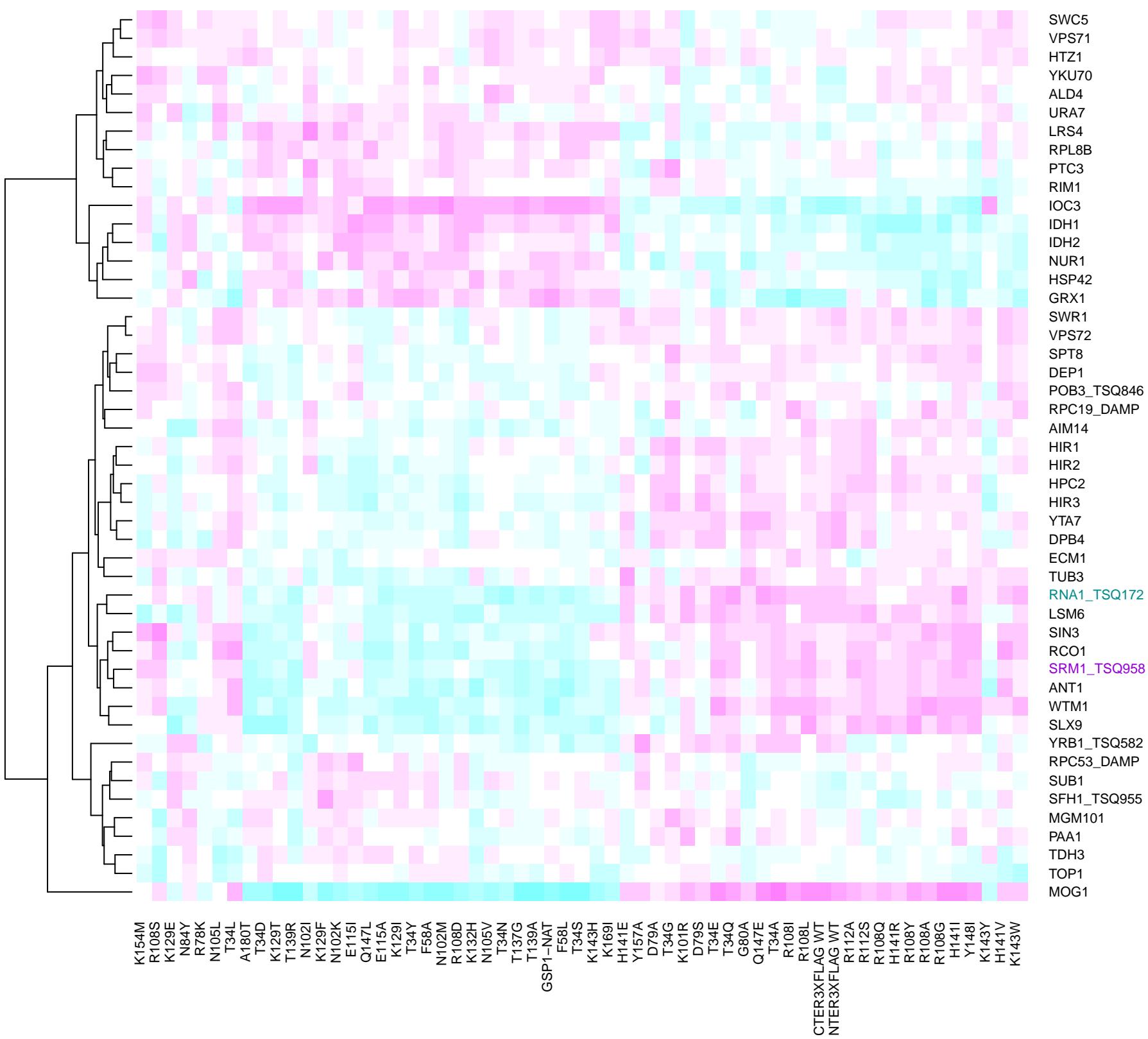


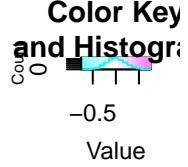
cell wall organization or biogenesis_GO_30_3



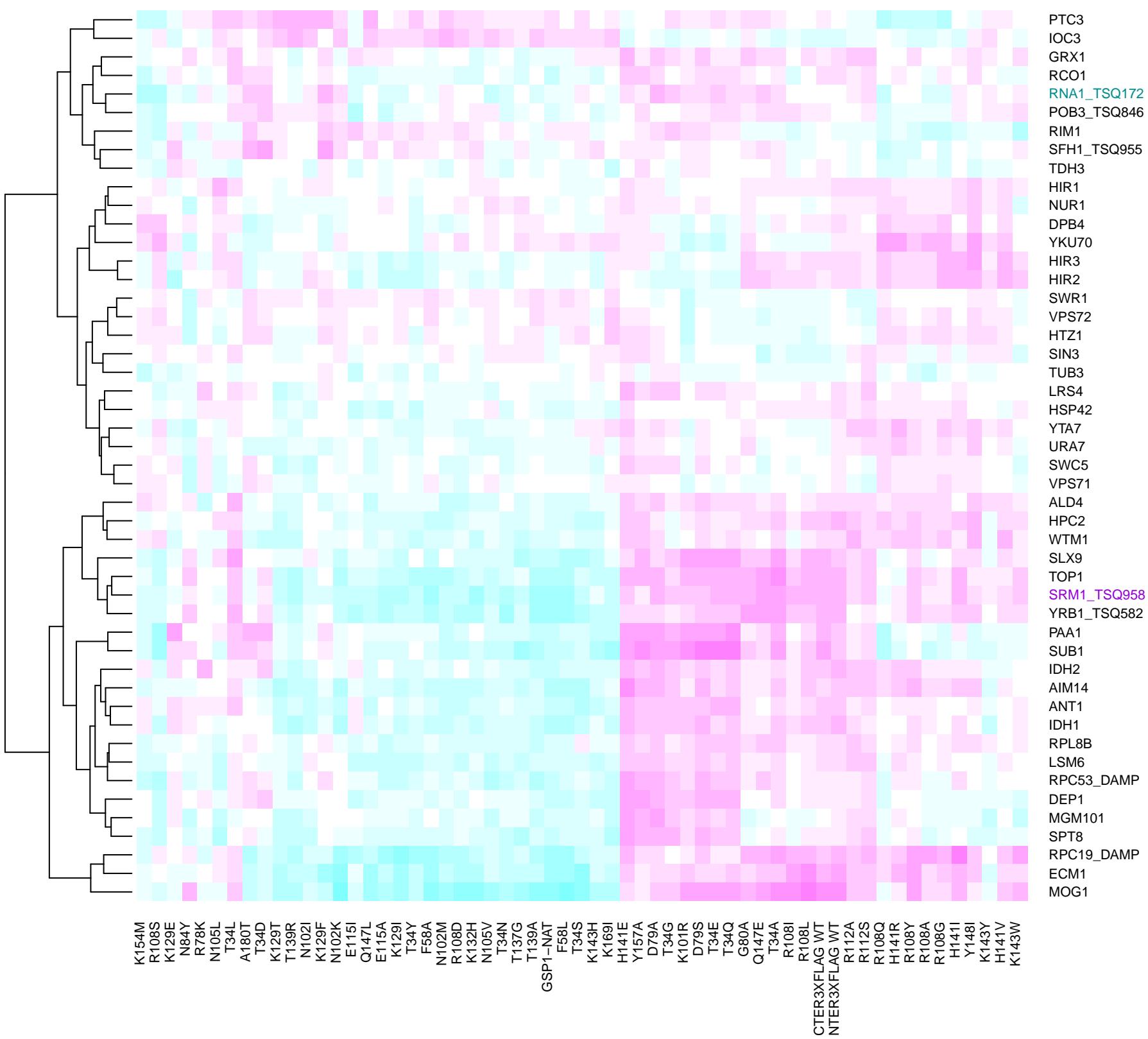


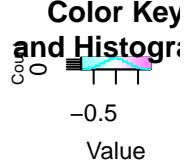
cell wall organization or biogenesis_GO_30_4



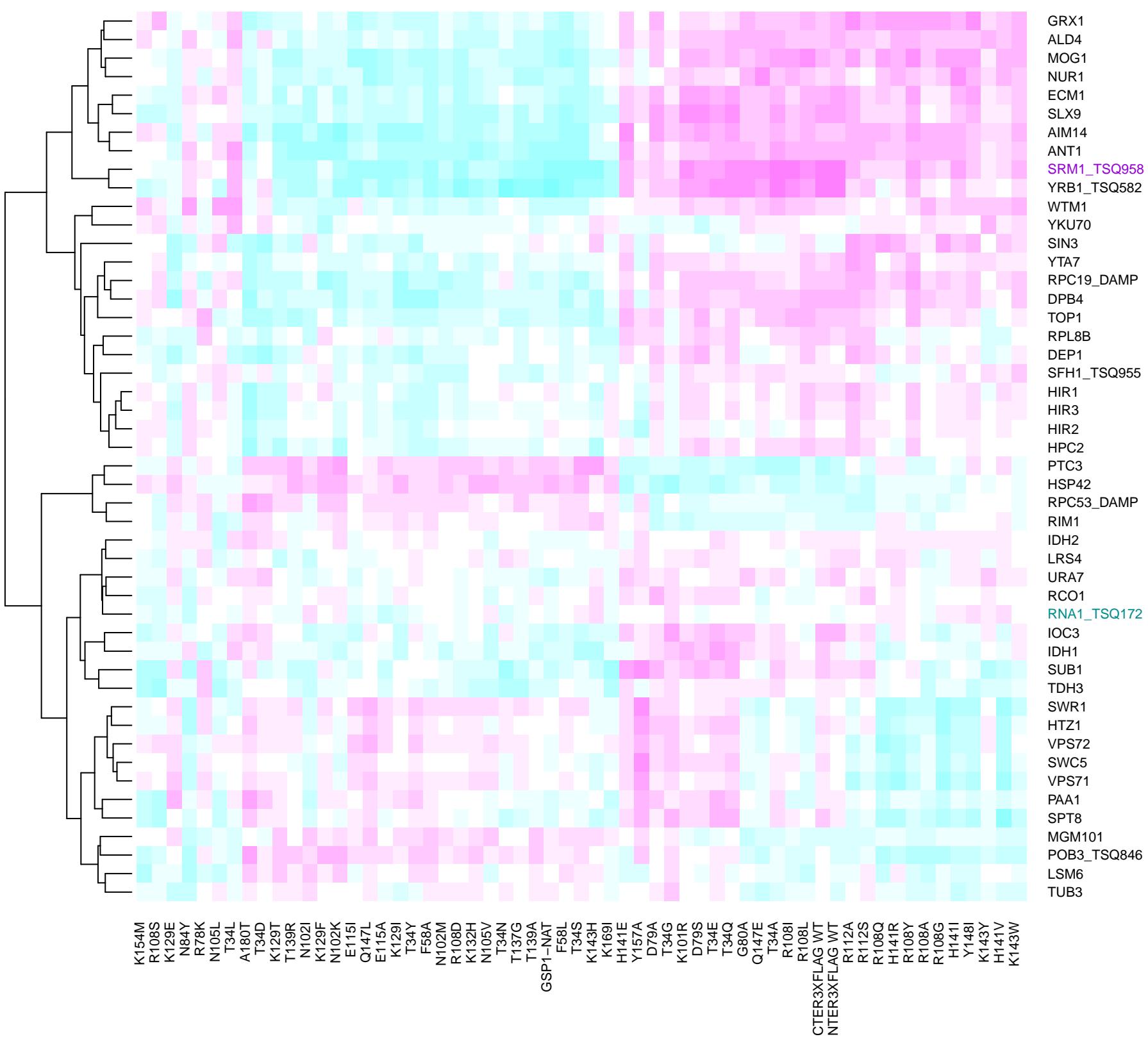


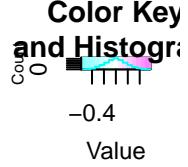
endomembrane system_GO_30_9



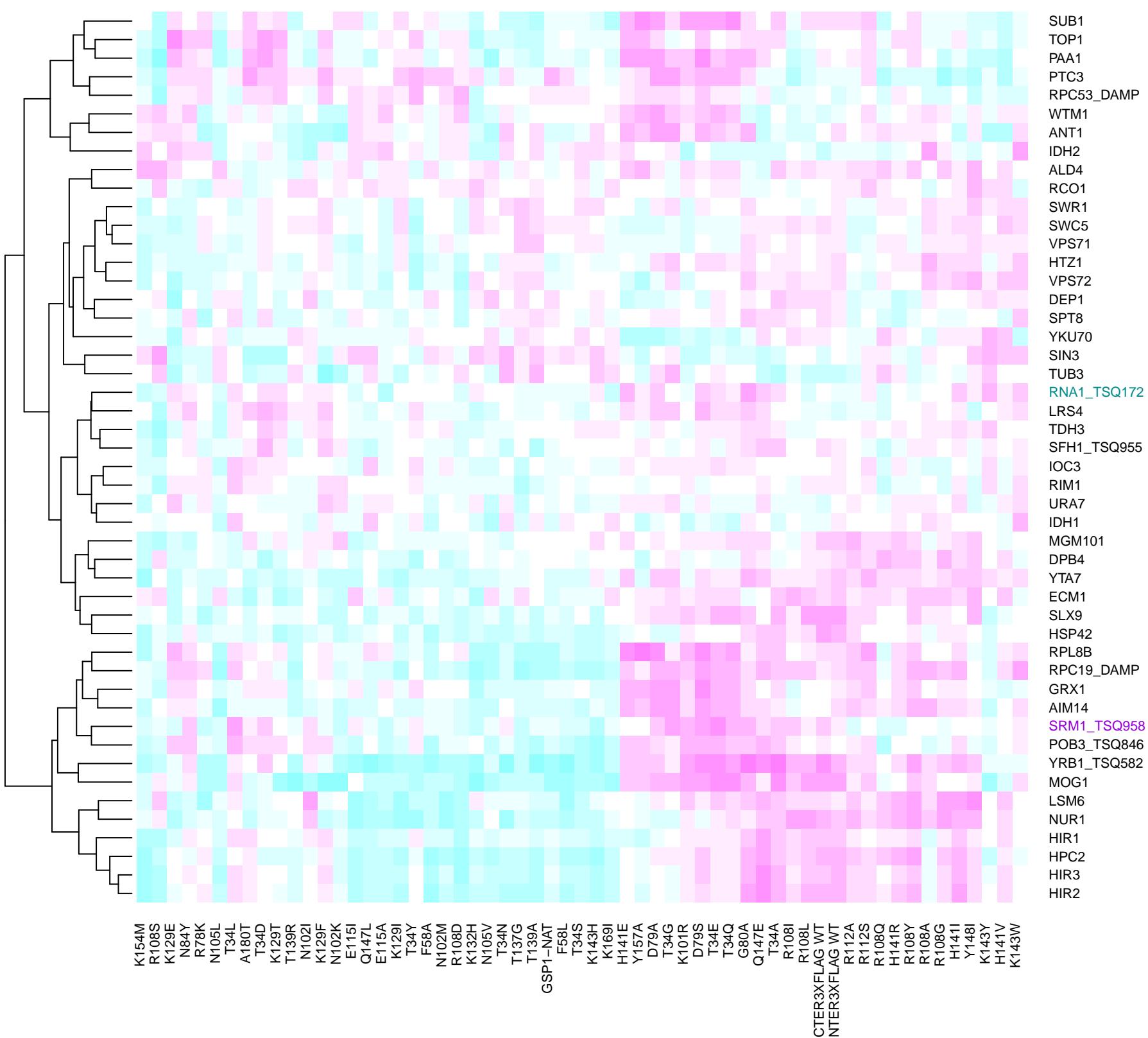


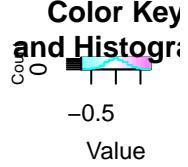
Golgi apparatus_GO_30_3



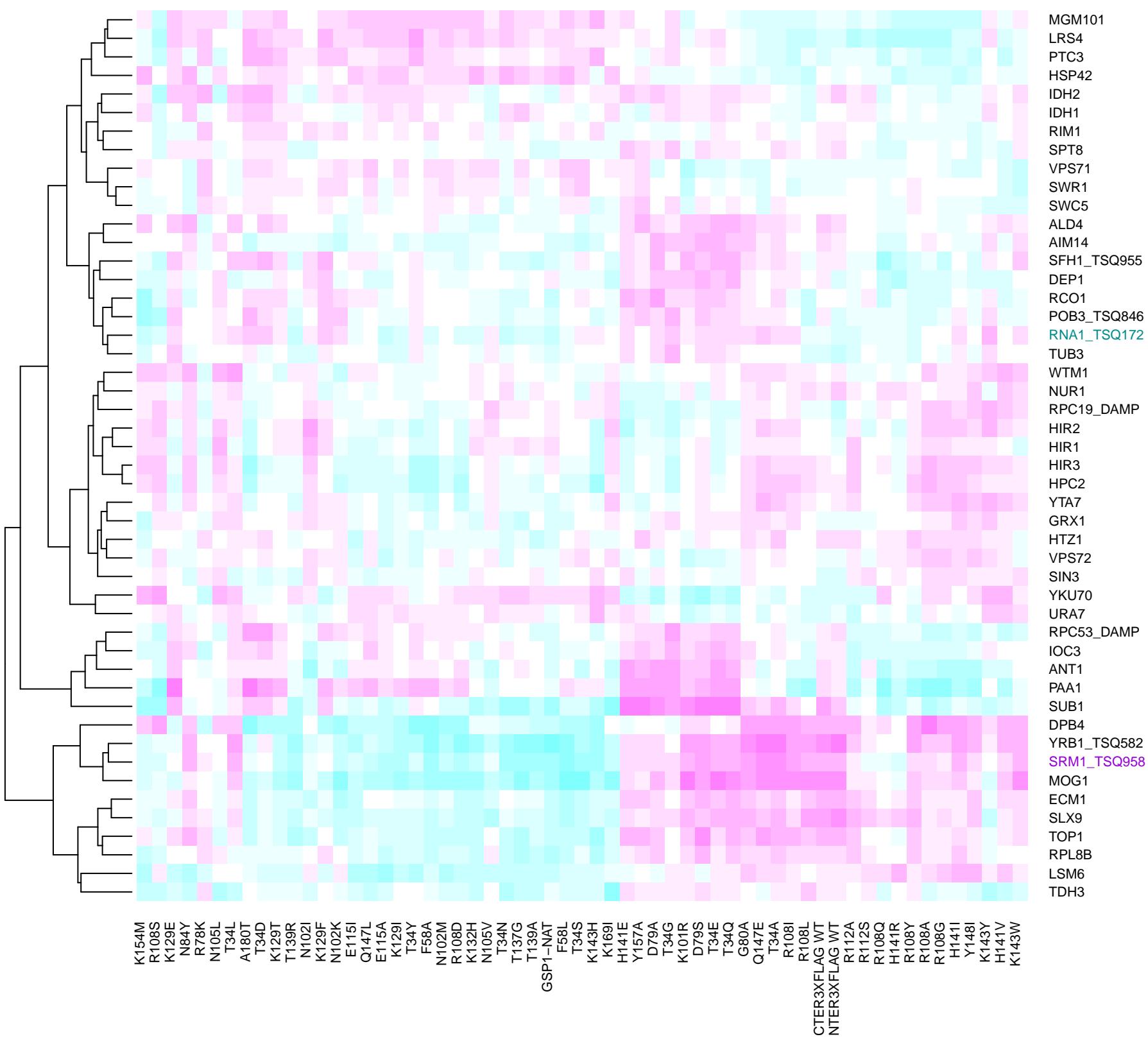


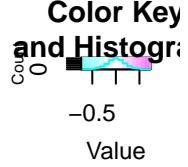
cytoskeleton and microtubules_GO_30_3



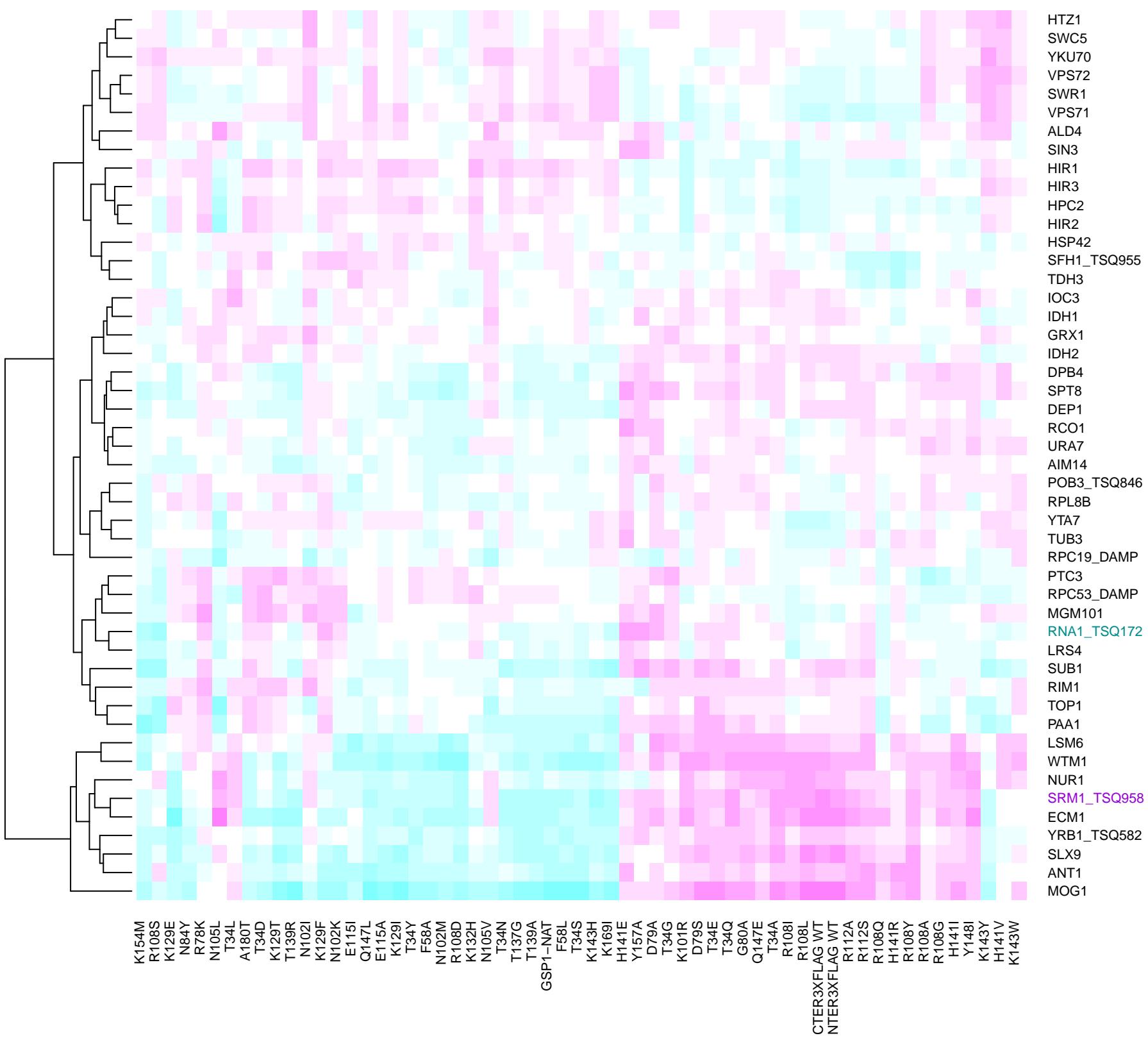


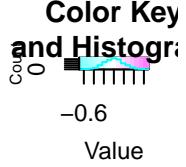
Golgi_GO_30_4



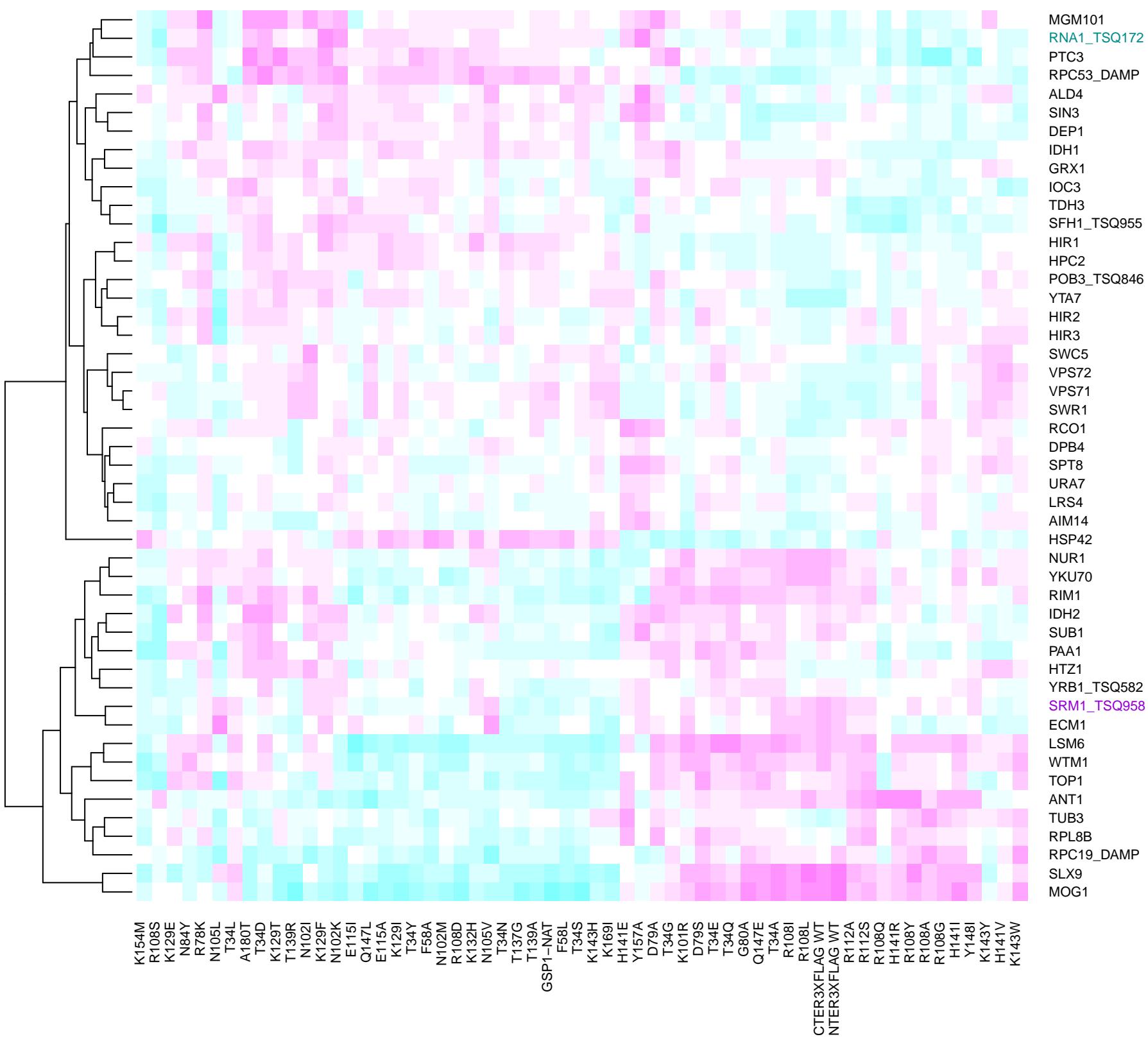


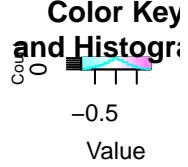
ribosomal small subunit biogenesis



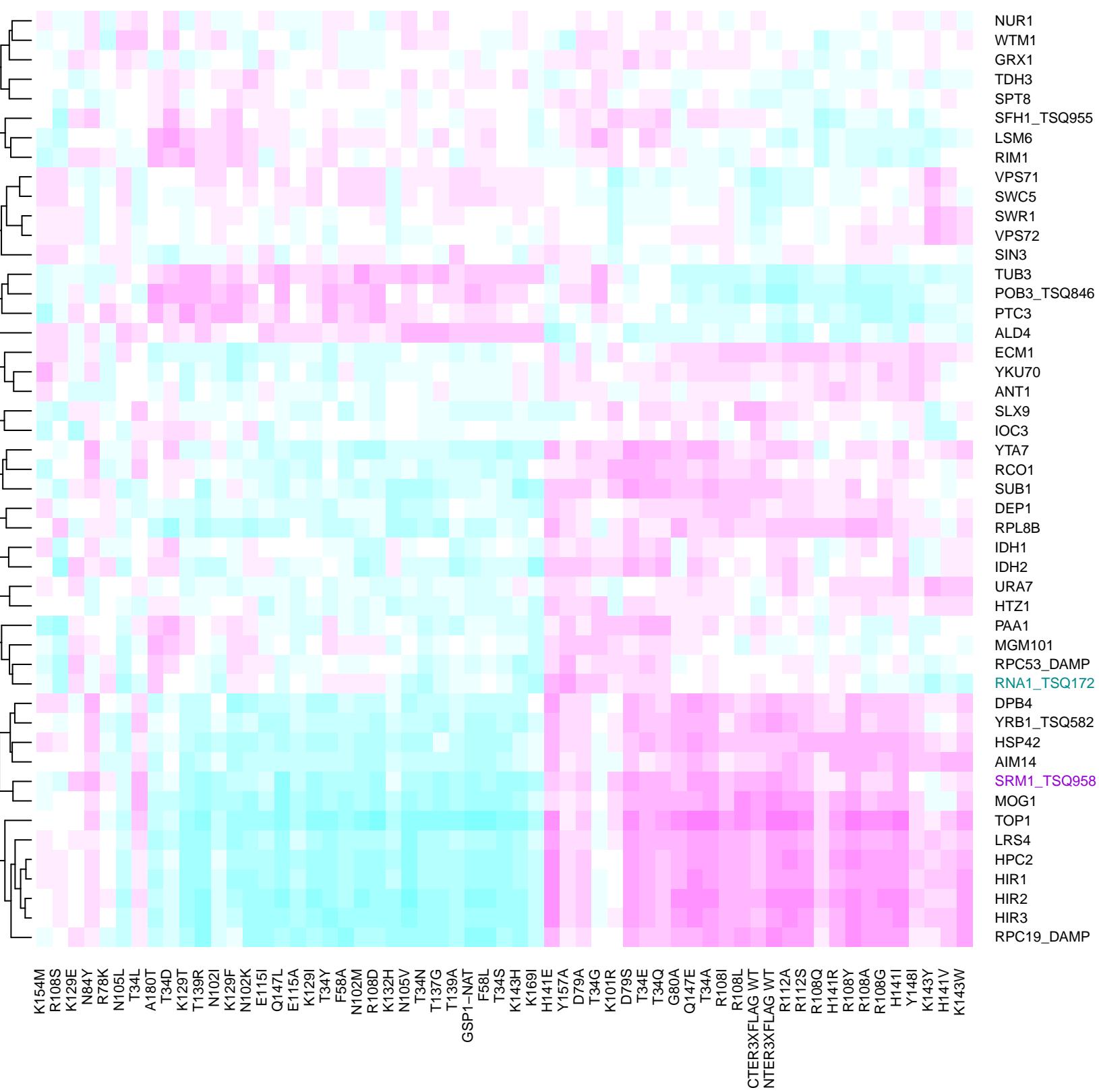


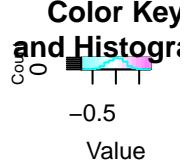
ribosomal small subunit biogenesis_GO_30_1



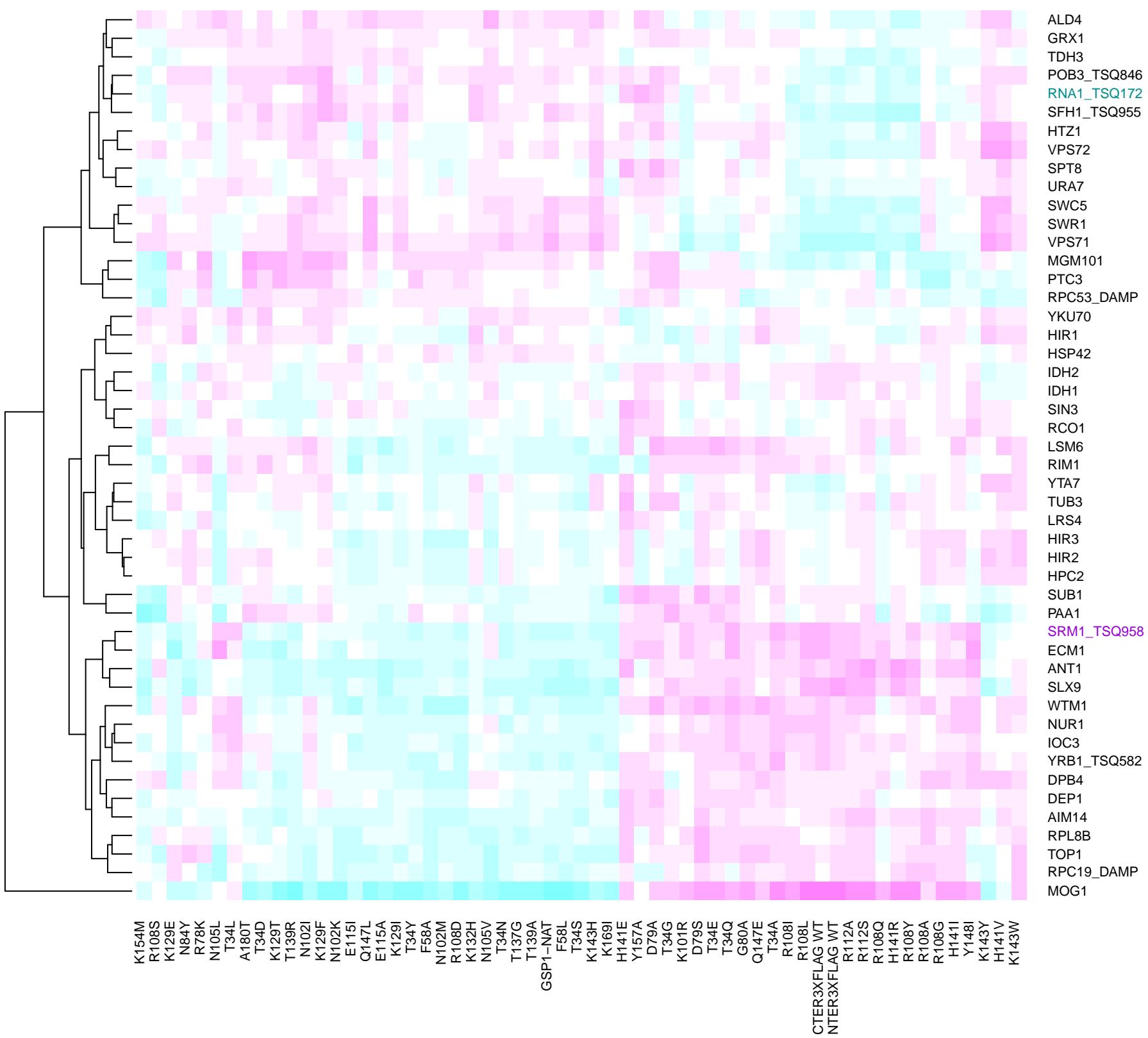


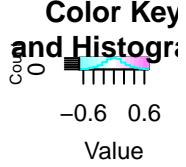
ribosomes and translation_GO_30_5



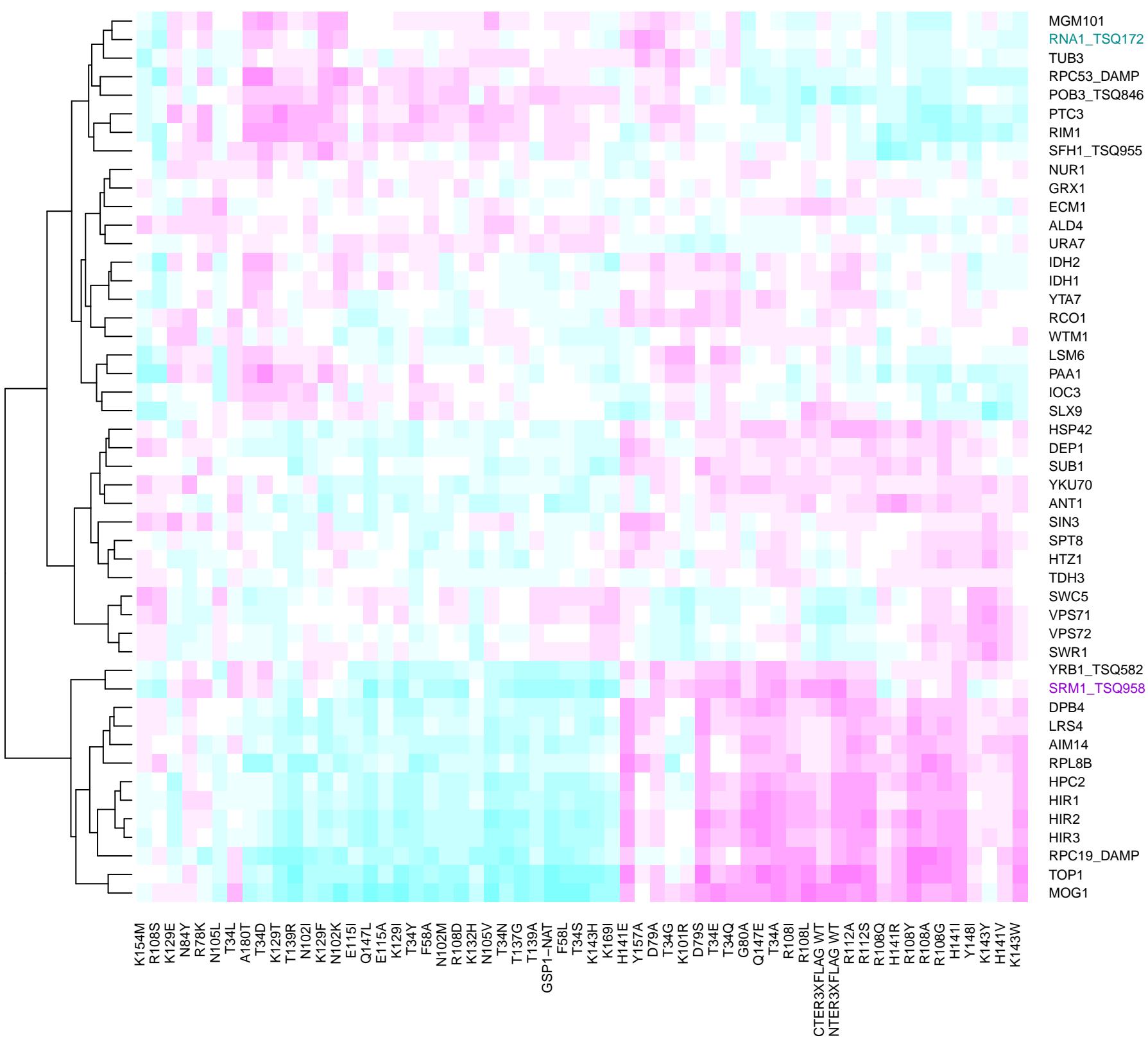


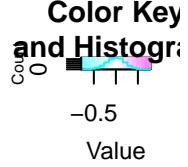
rRNA processing_GO_30_1



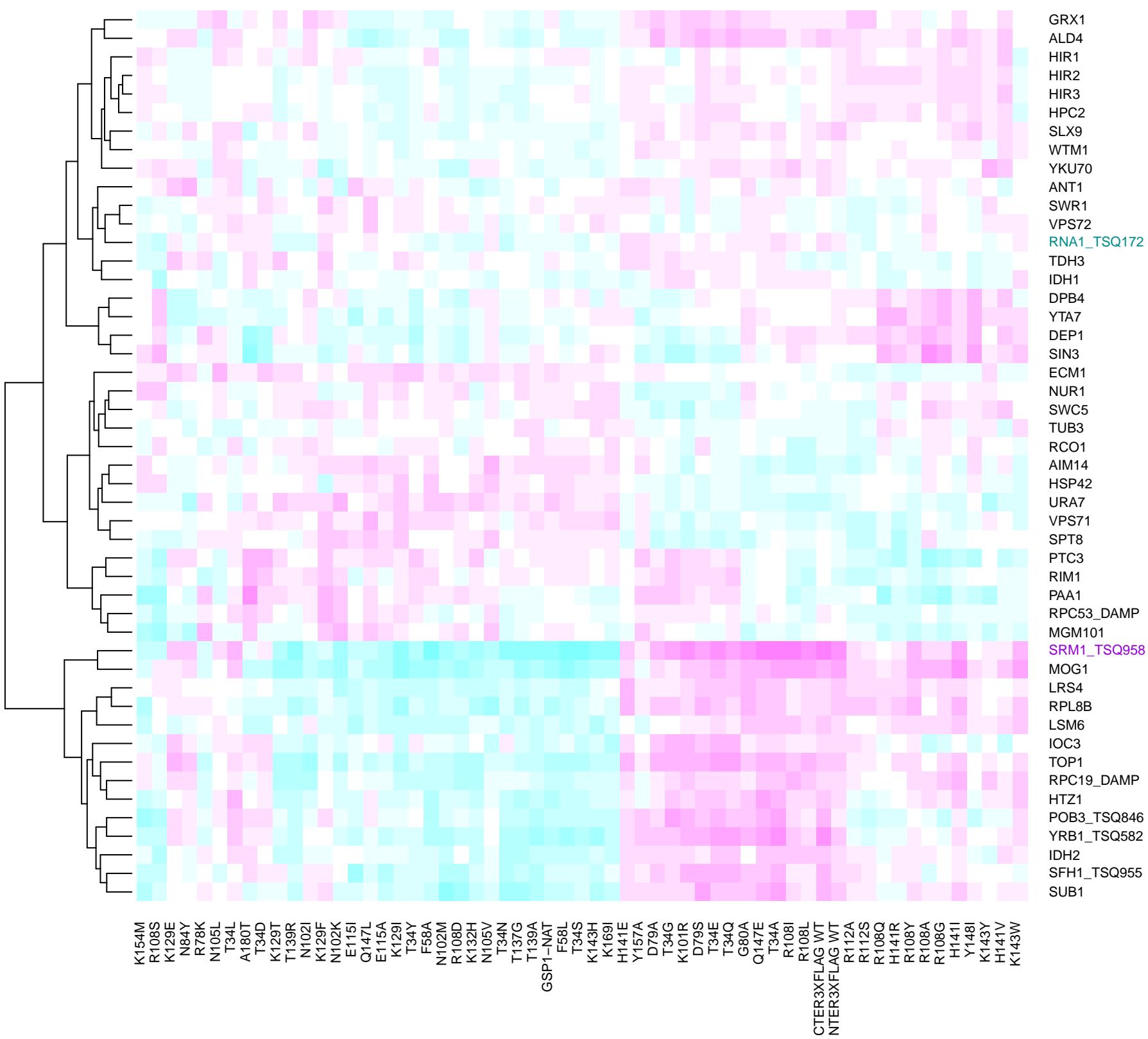


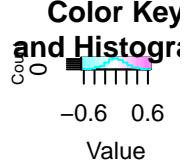
structural constituent of ribosome_GO_30_1



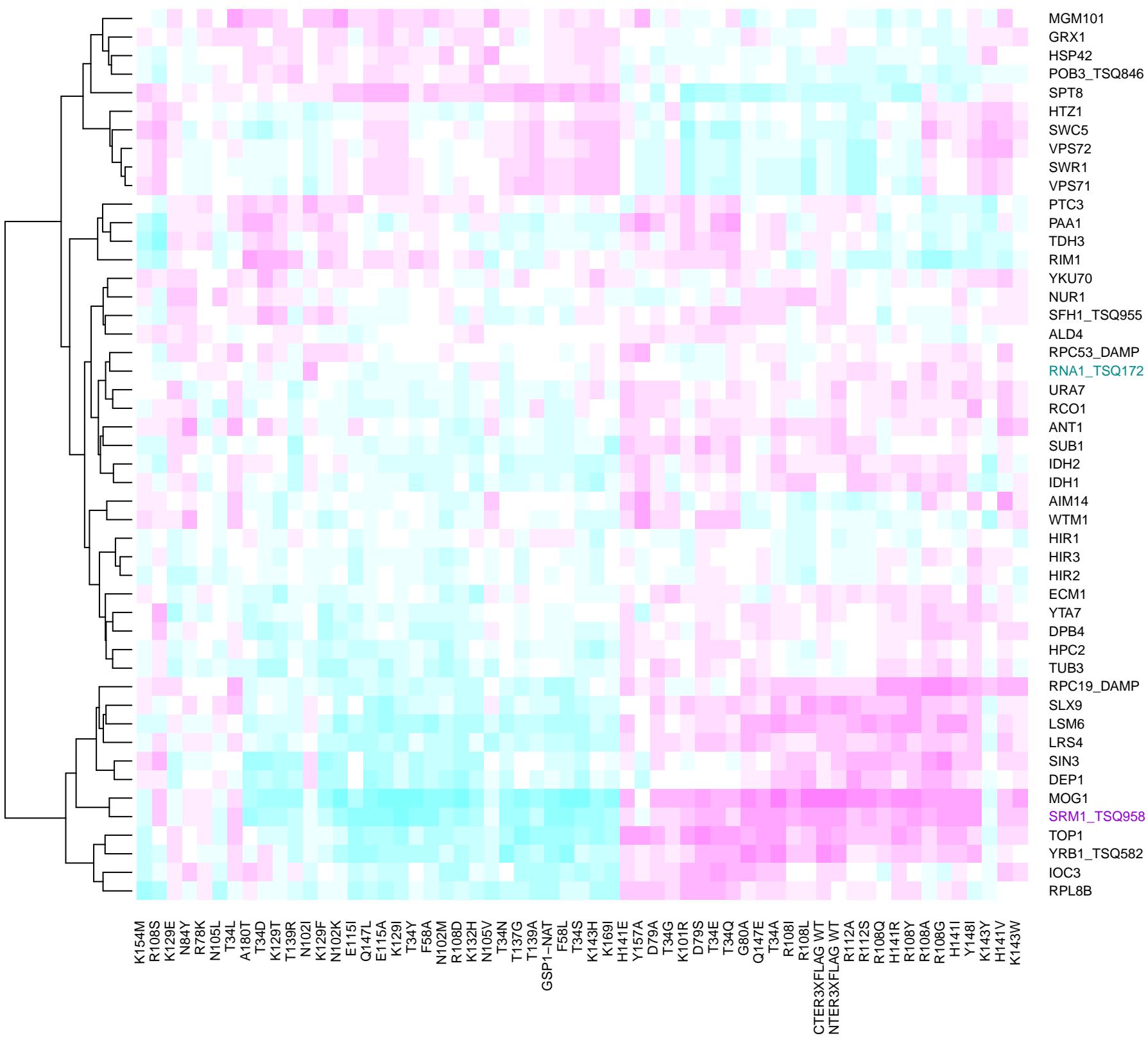


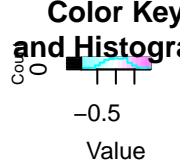
vacuole organization_GO_30_1



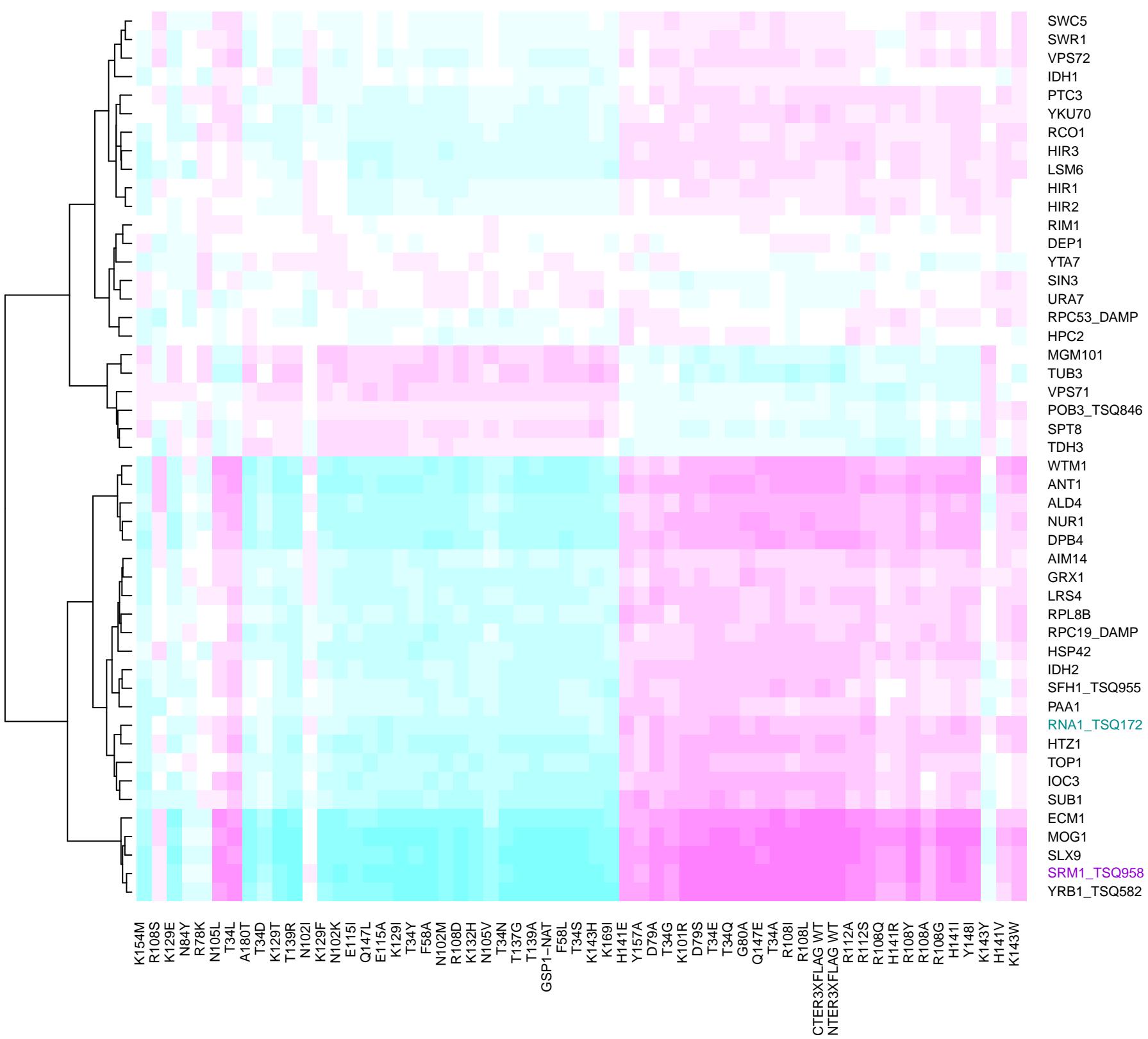


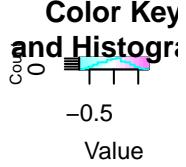
vacuole_GO_30_1



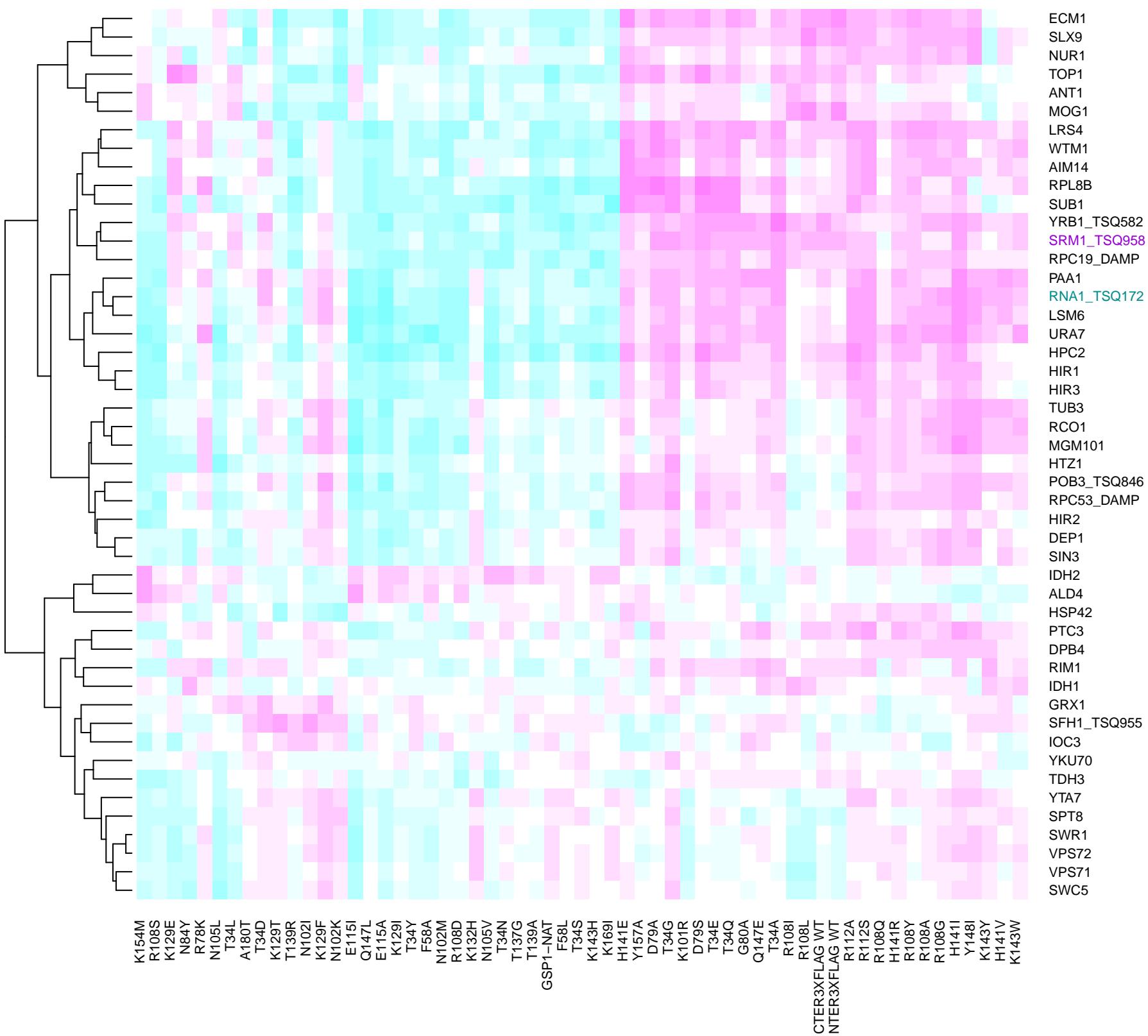


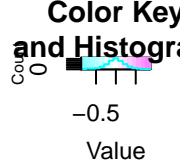
endomembrane system_GO_30_1



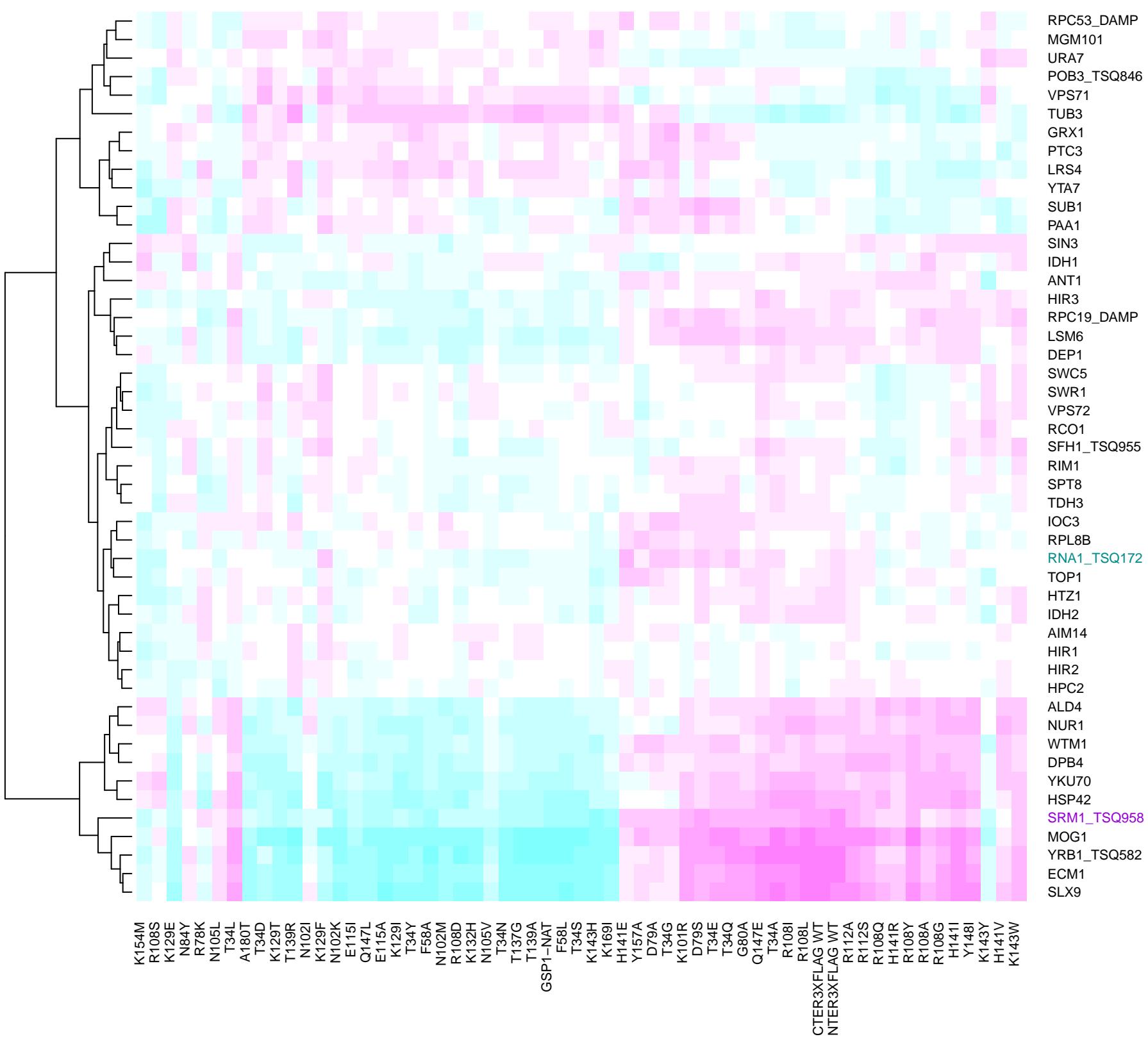


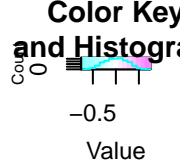
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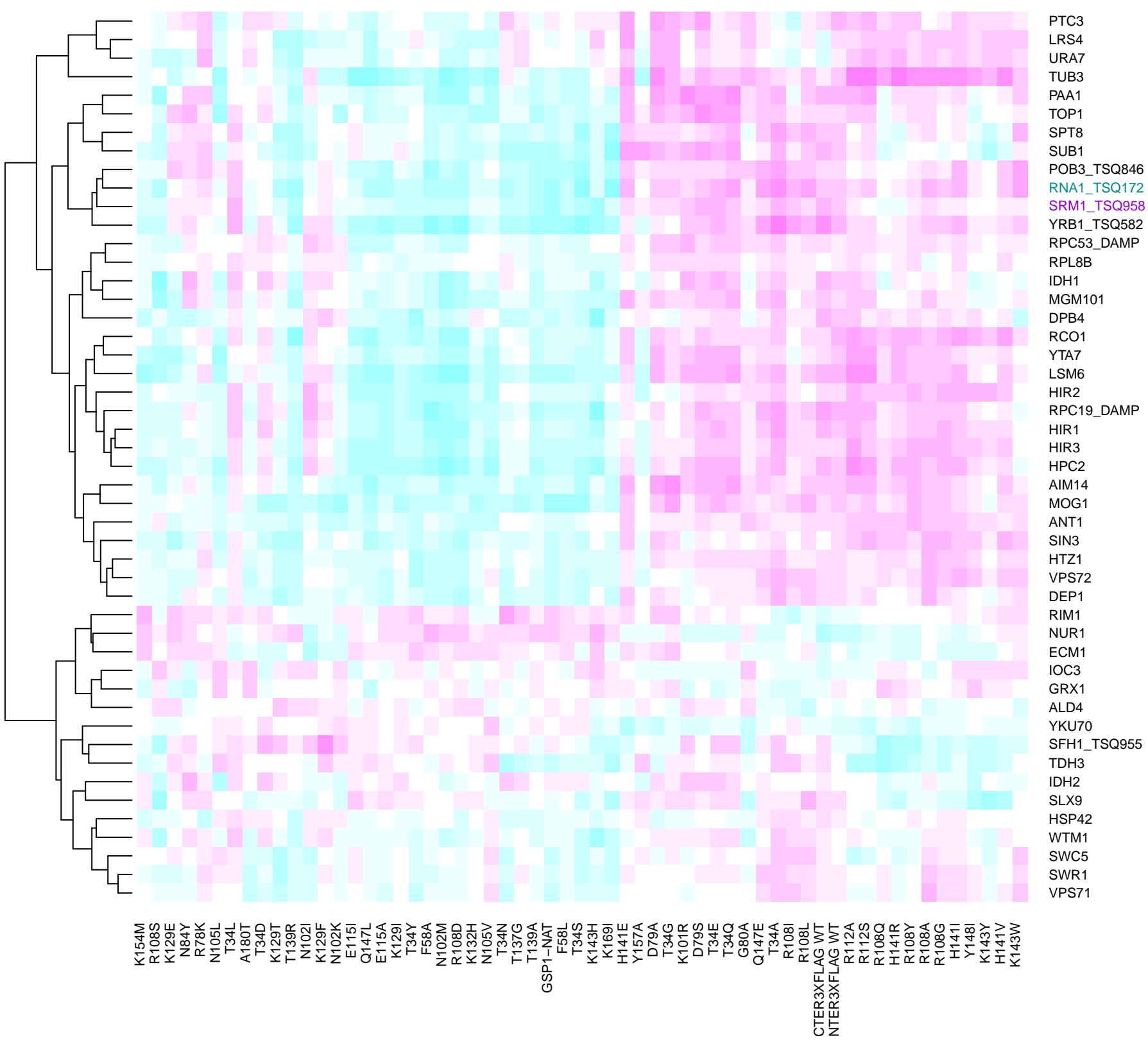


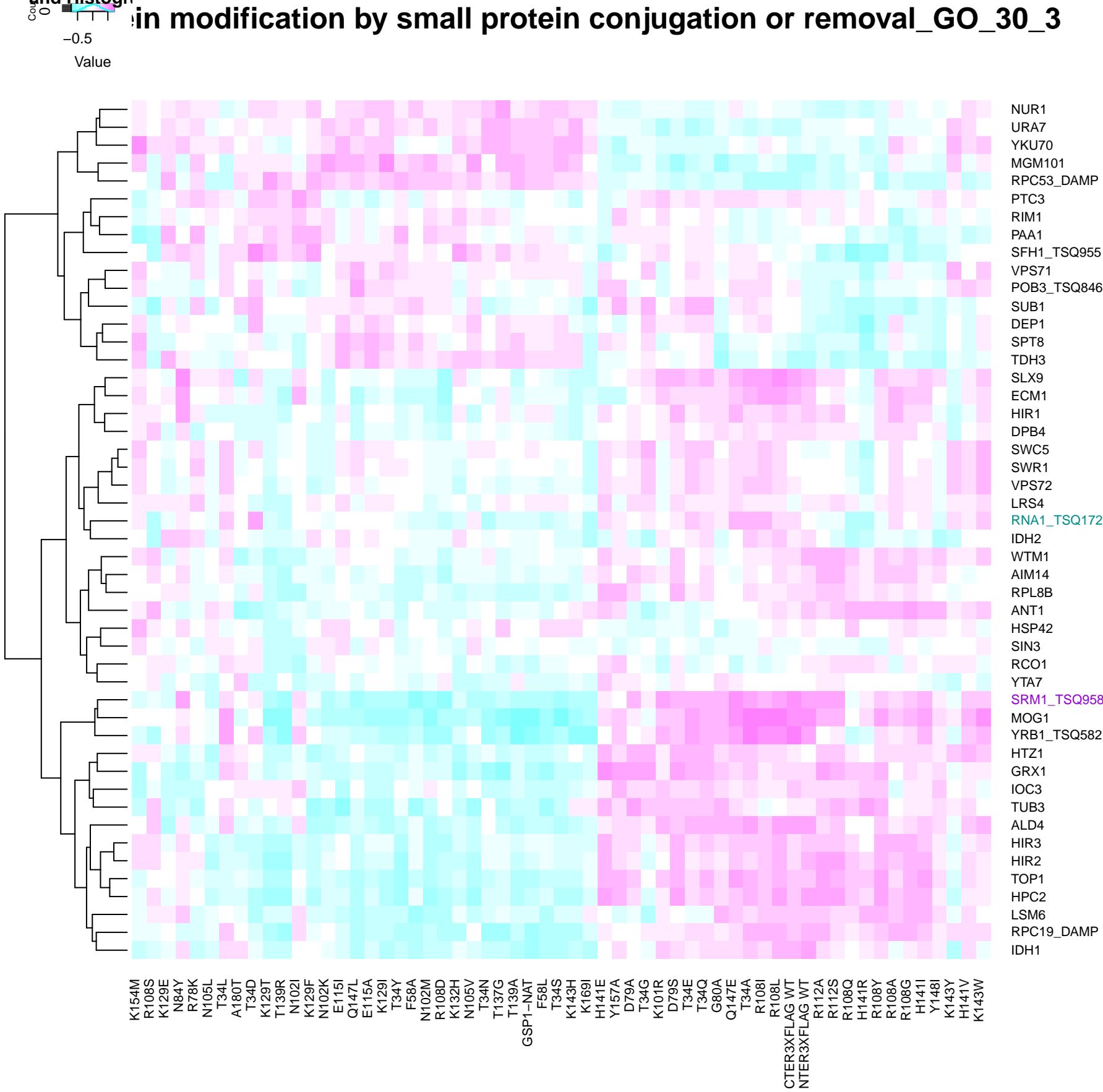
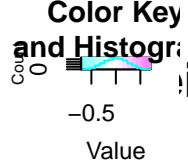
cytoskeleton organization_GO_30_1

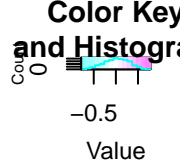




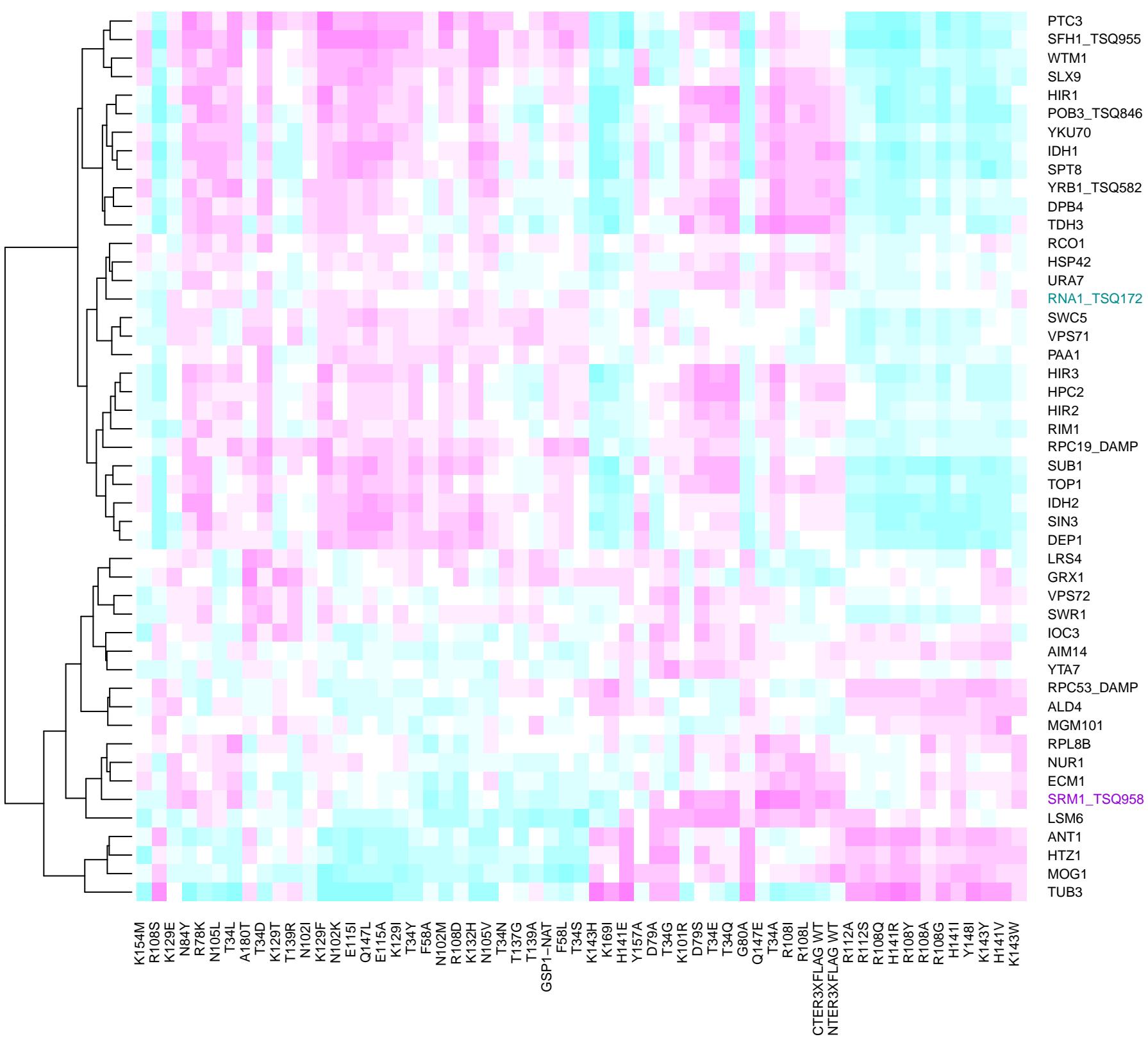
lipid metabolic process_GO_30_1

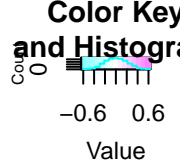




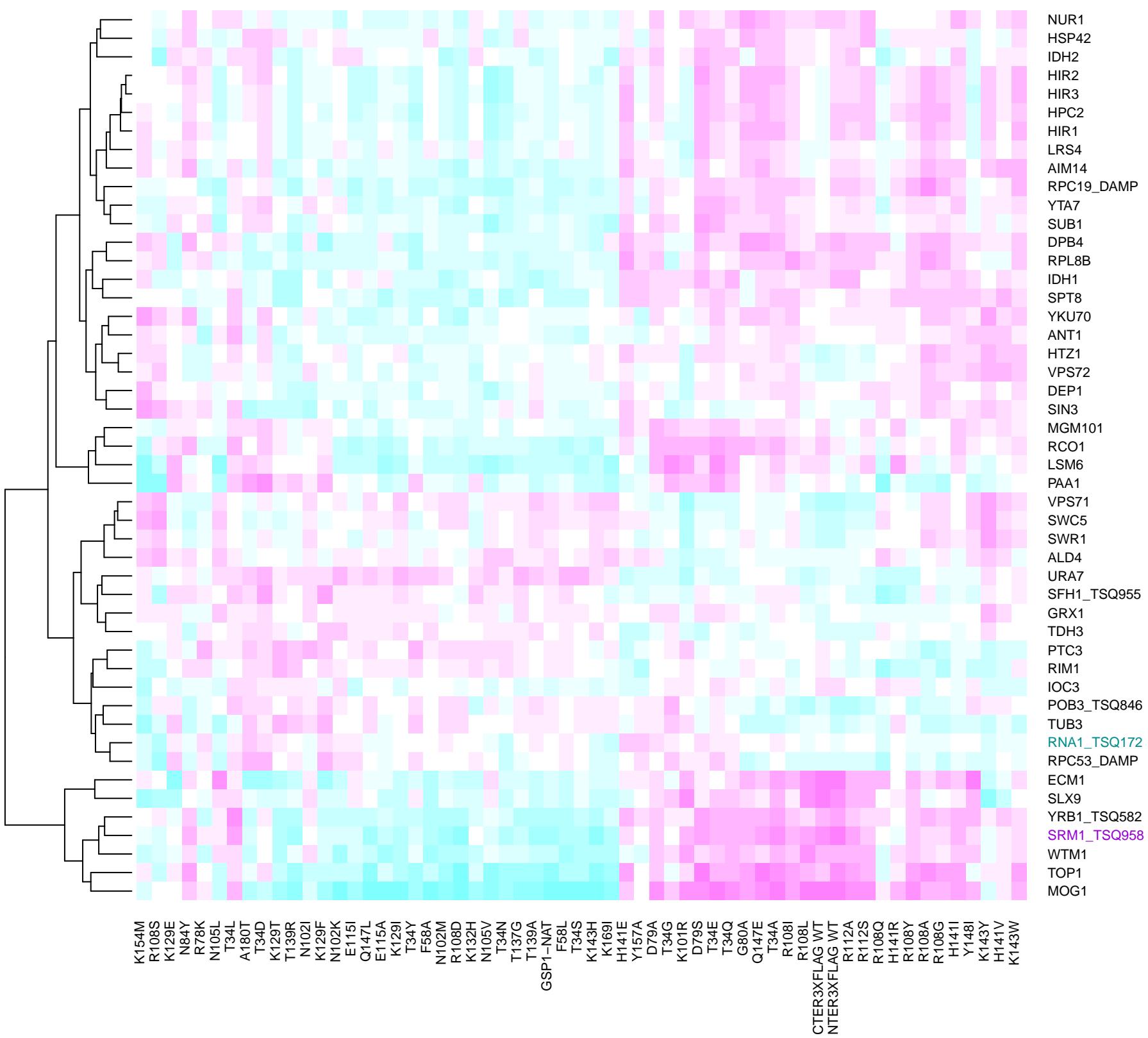


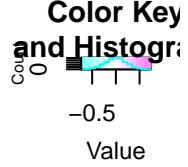
budding_GO_30_10



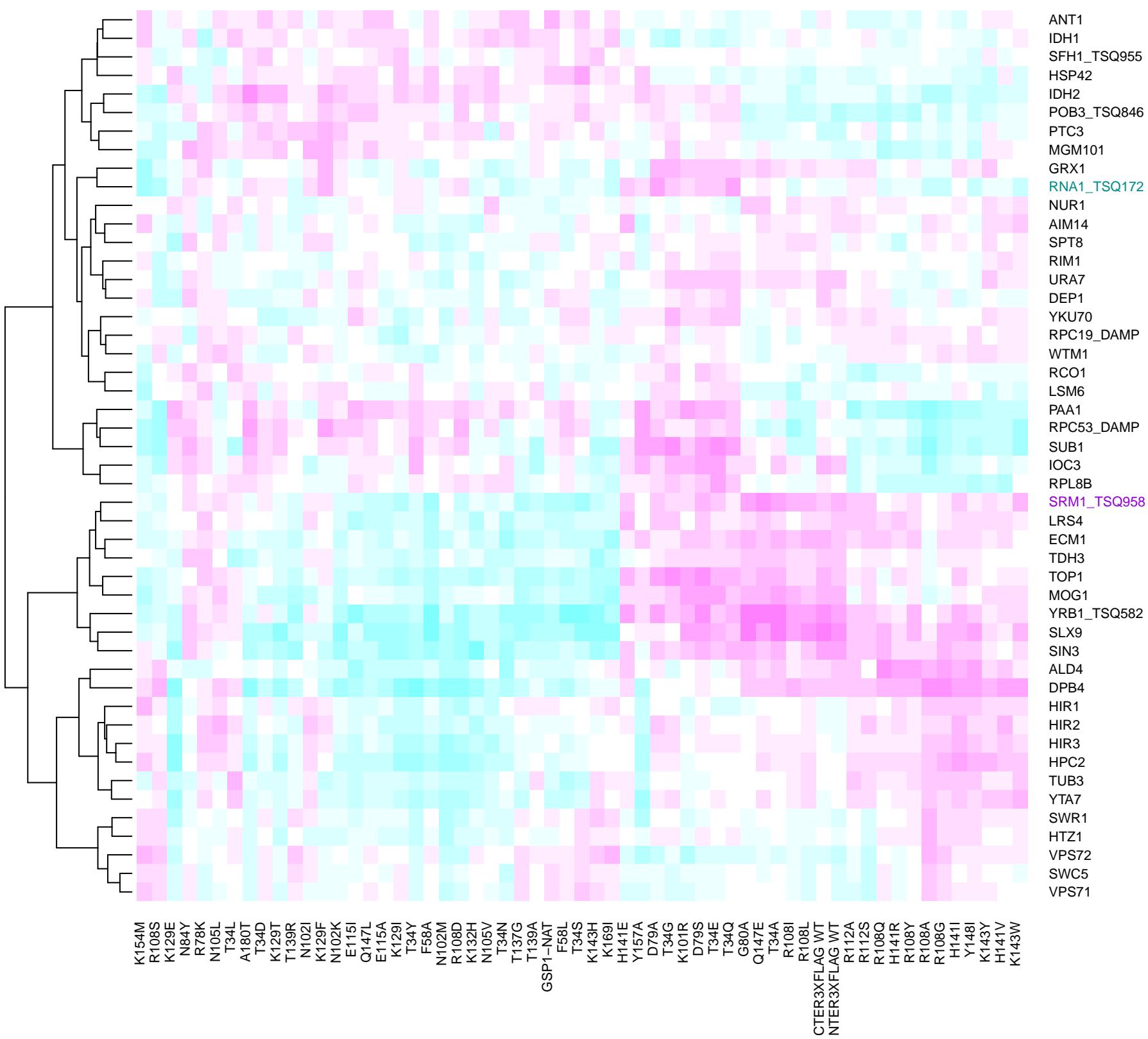


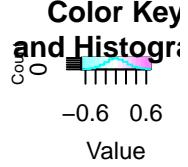
ribosome_GO_30_1



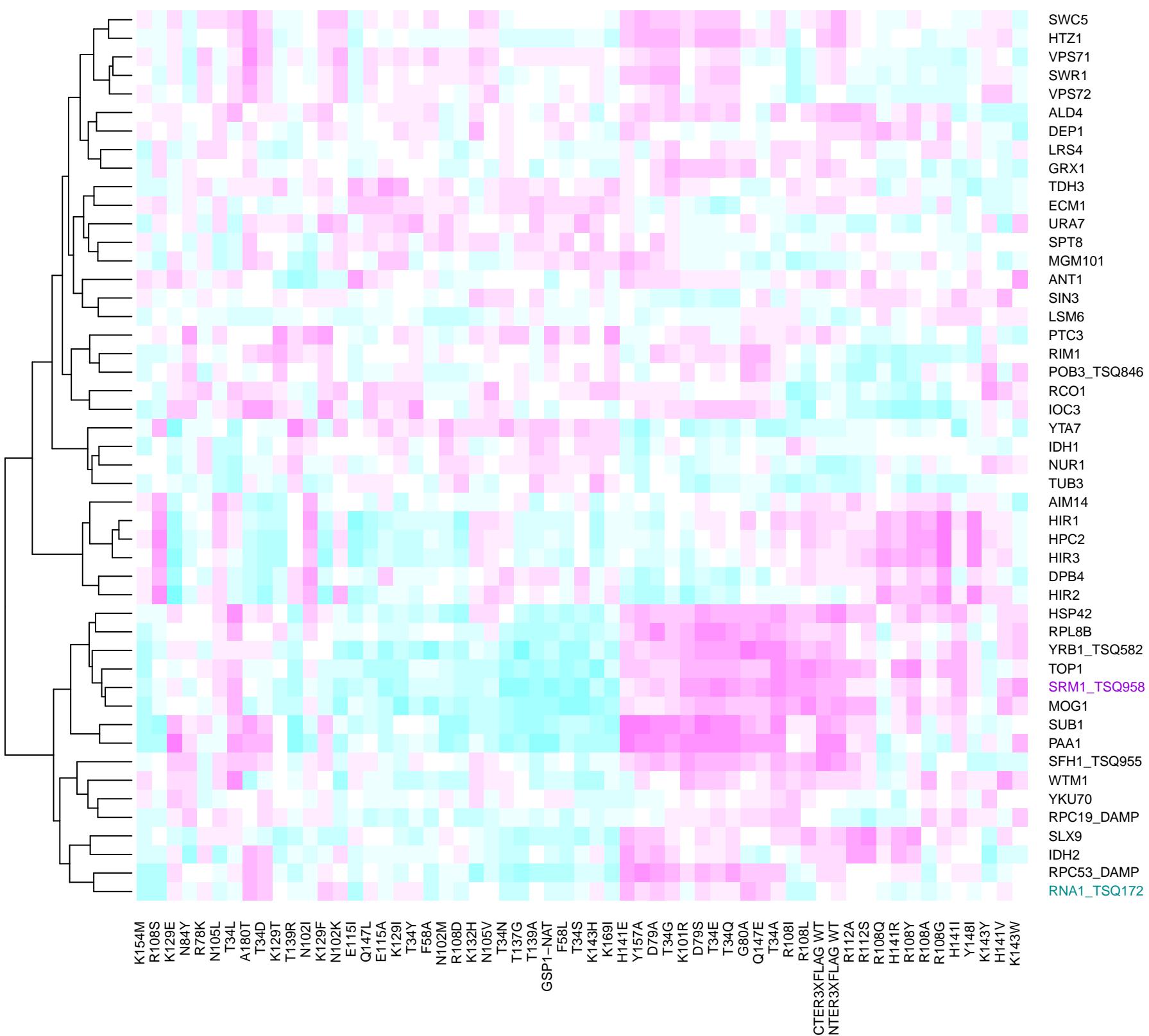


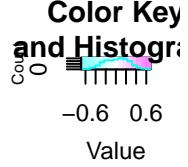
Golgi and ER_GO_30_17



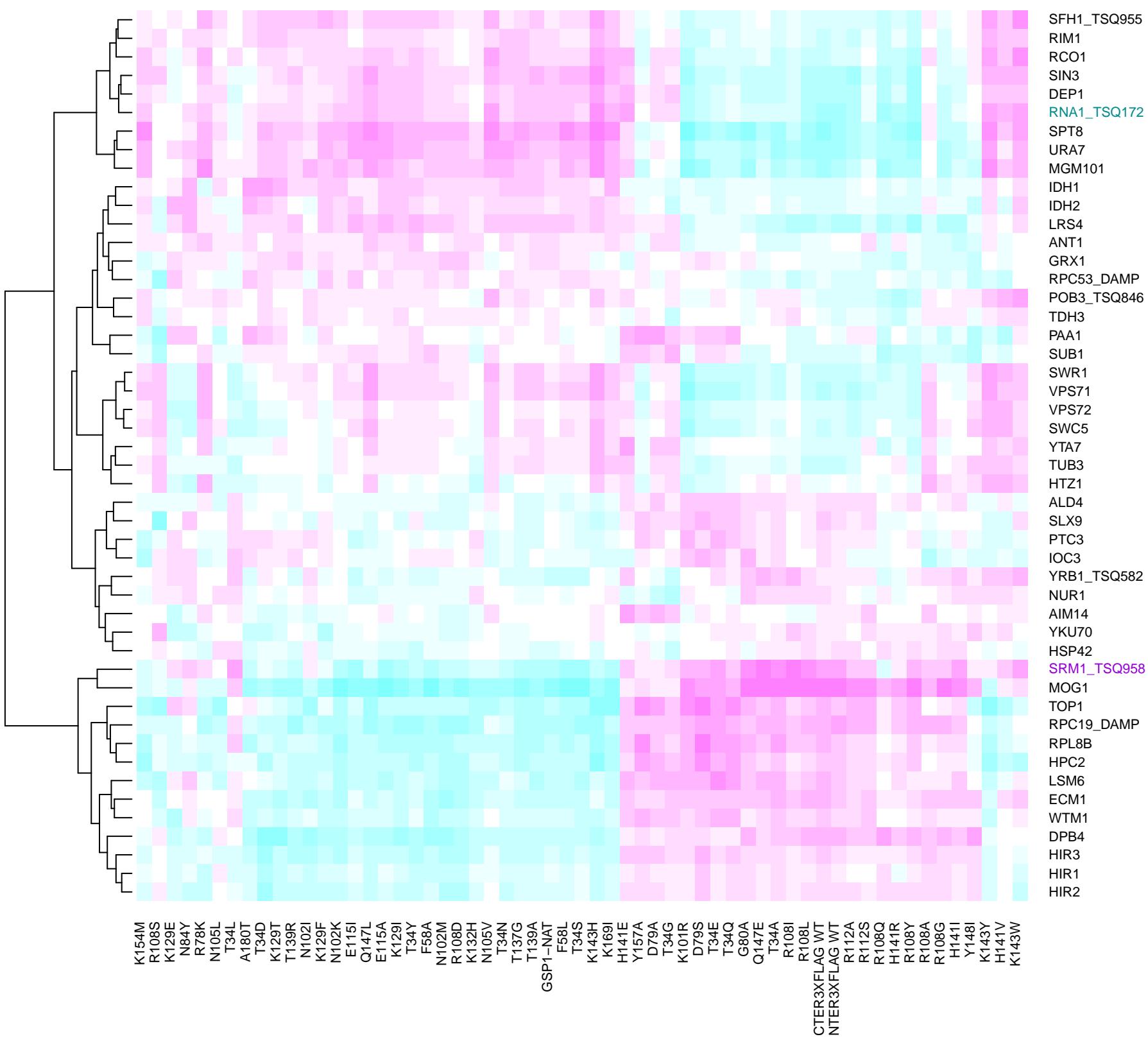


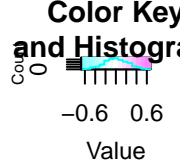
lipids_GO_30_7



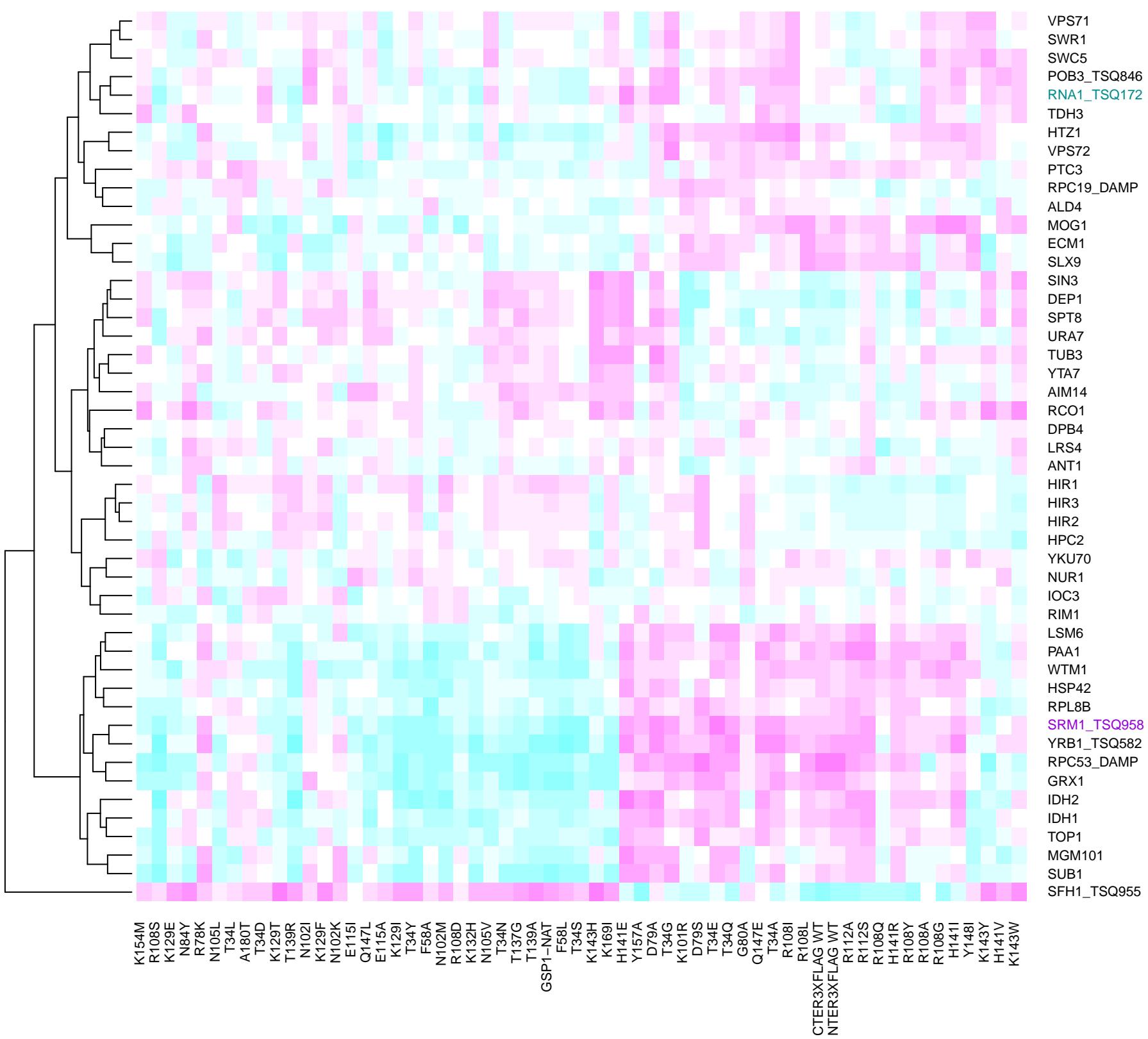


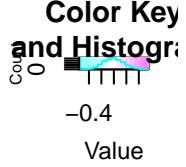
mitochondrial envelope_GO_30_3



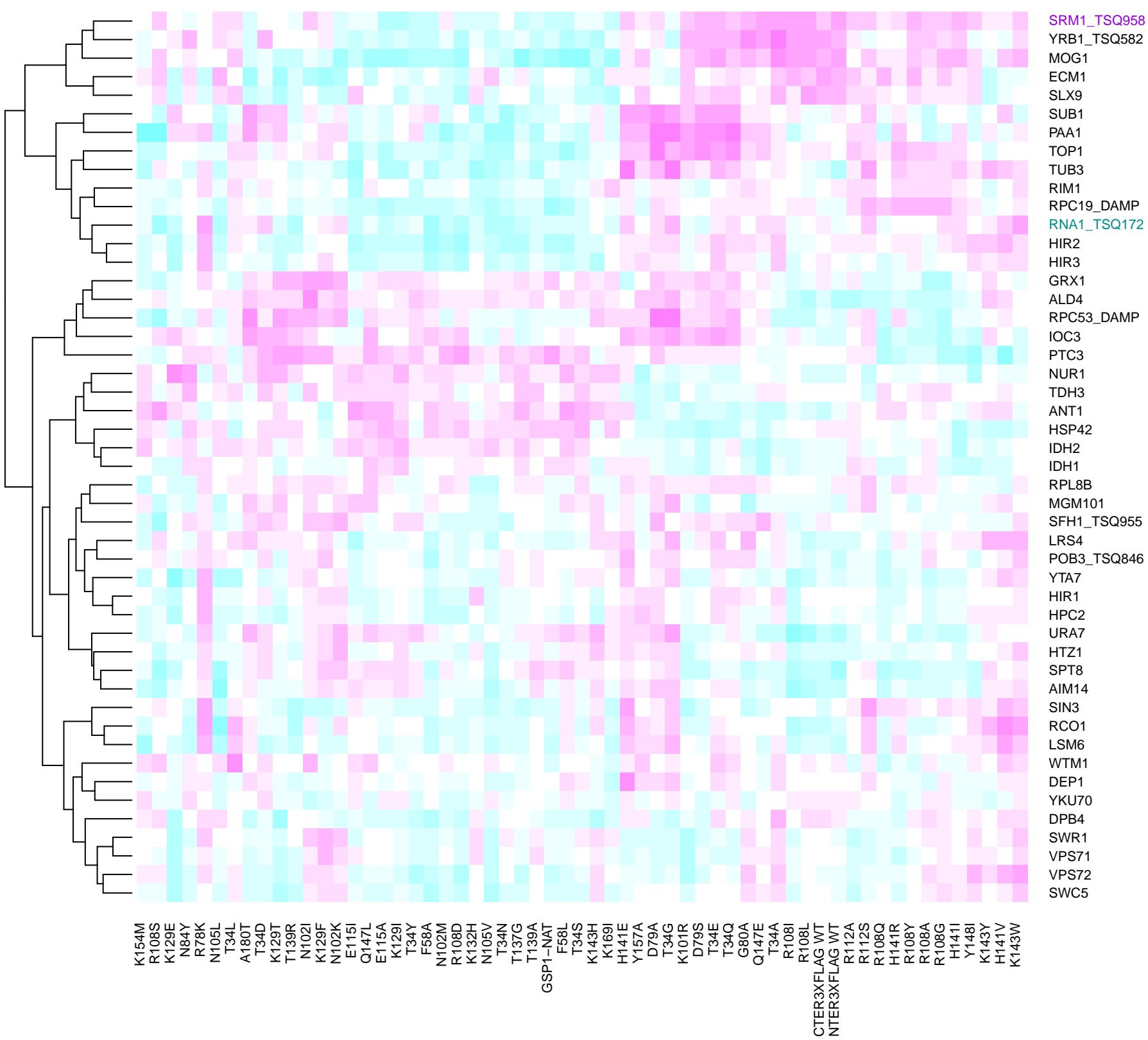


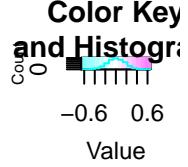
mitochondrion_GO_30_12



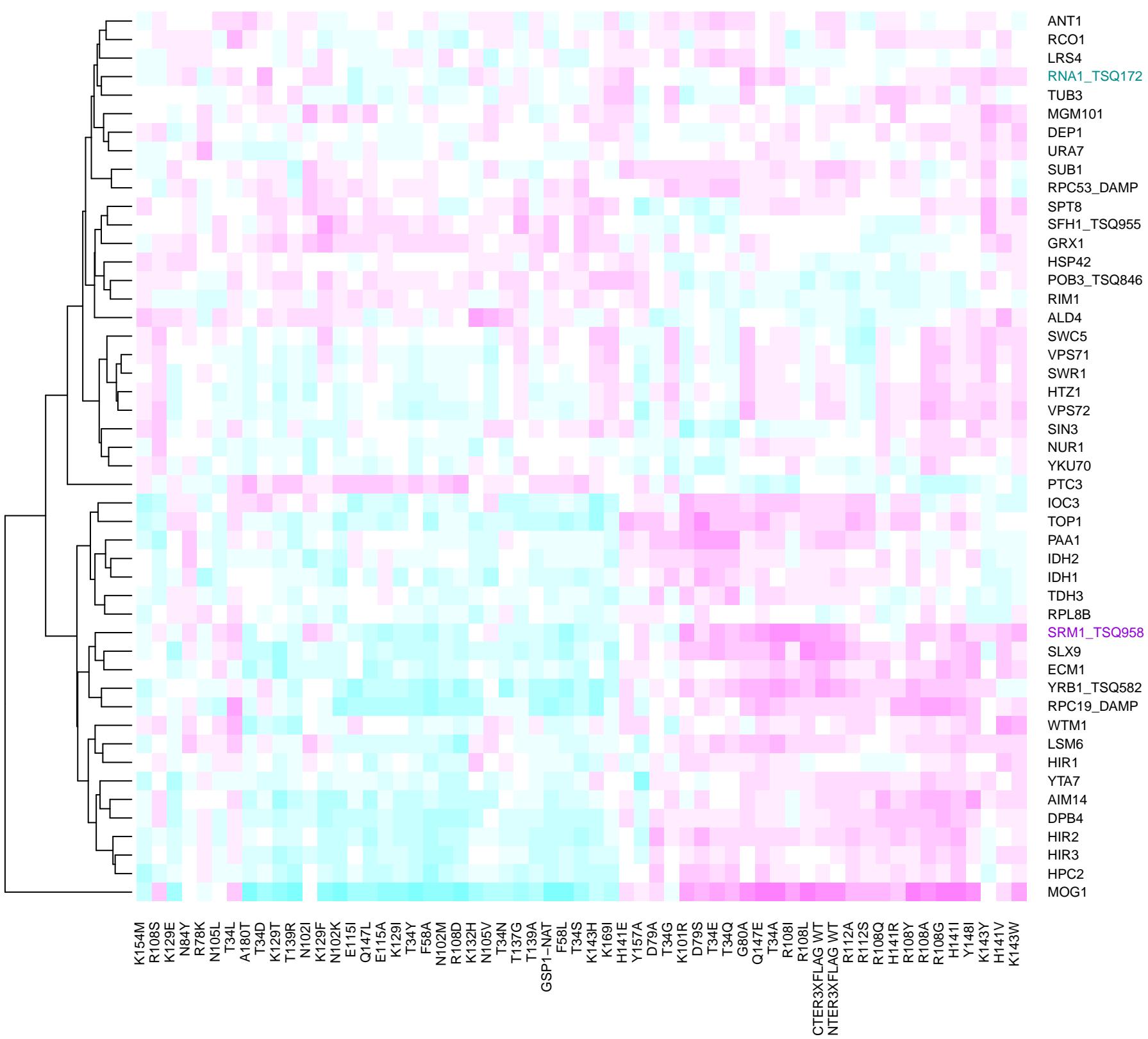


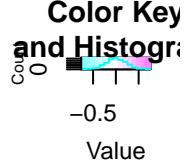
cofactor metabolic process_GO_30_2



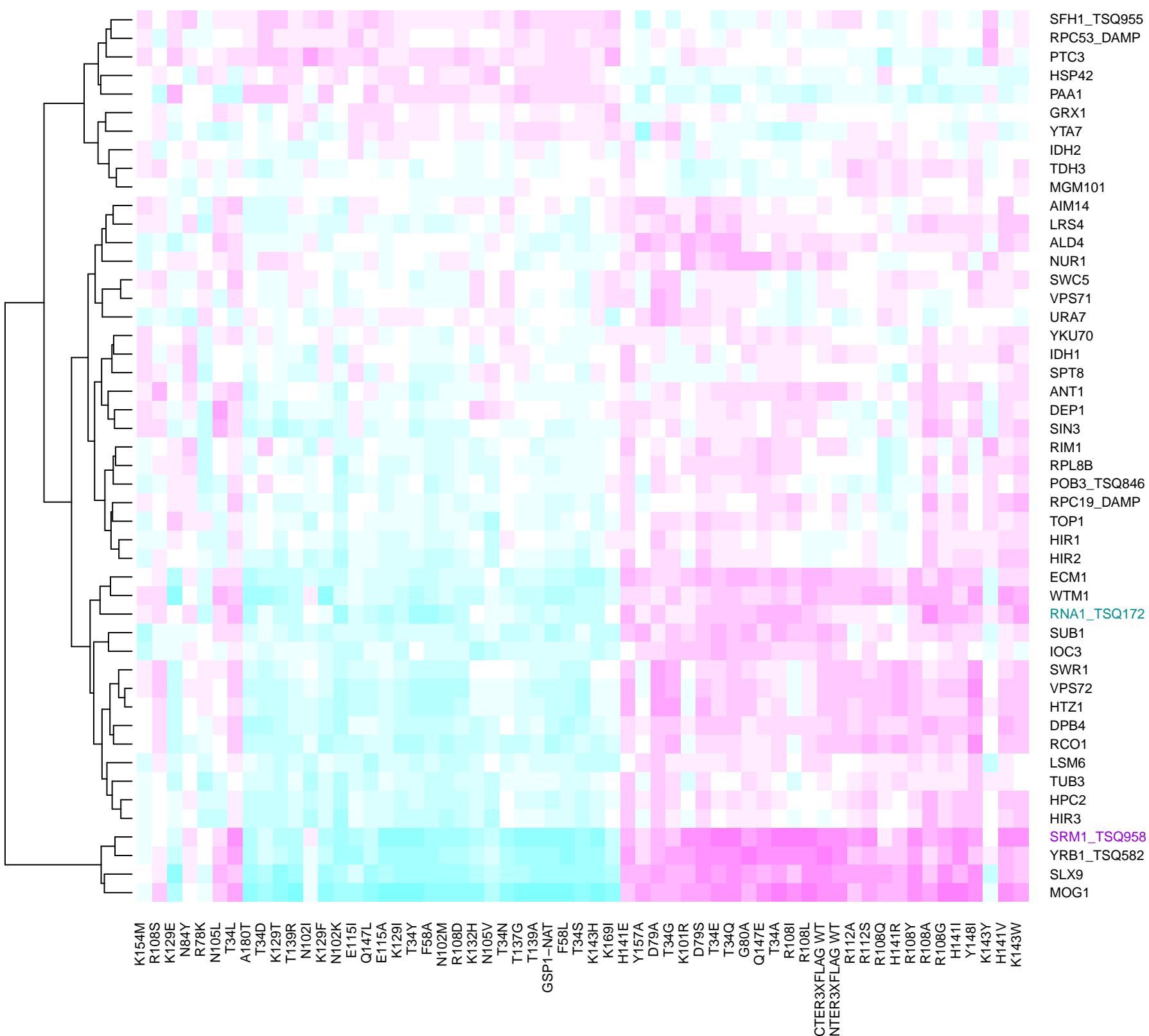


mitochondria and respiration_GO_30_2





meiotic cell cycle_GO_30_4



Color Key
and Histogram

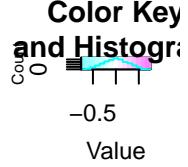
Value

leobase-containing small molecule metabolic process_GO_30_1

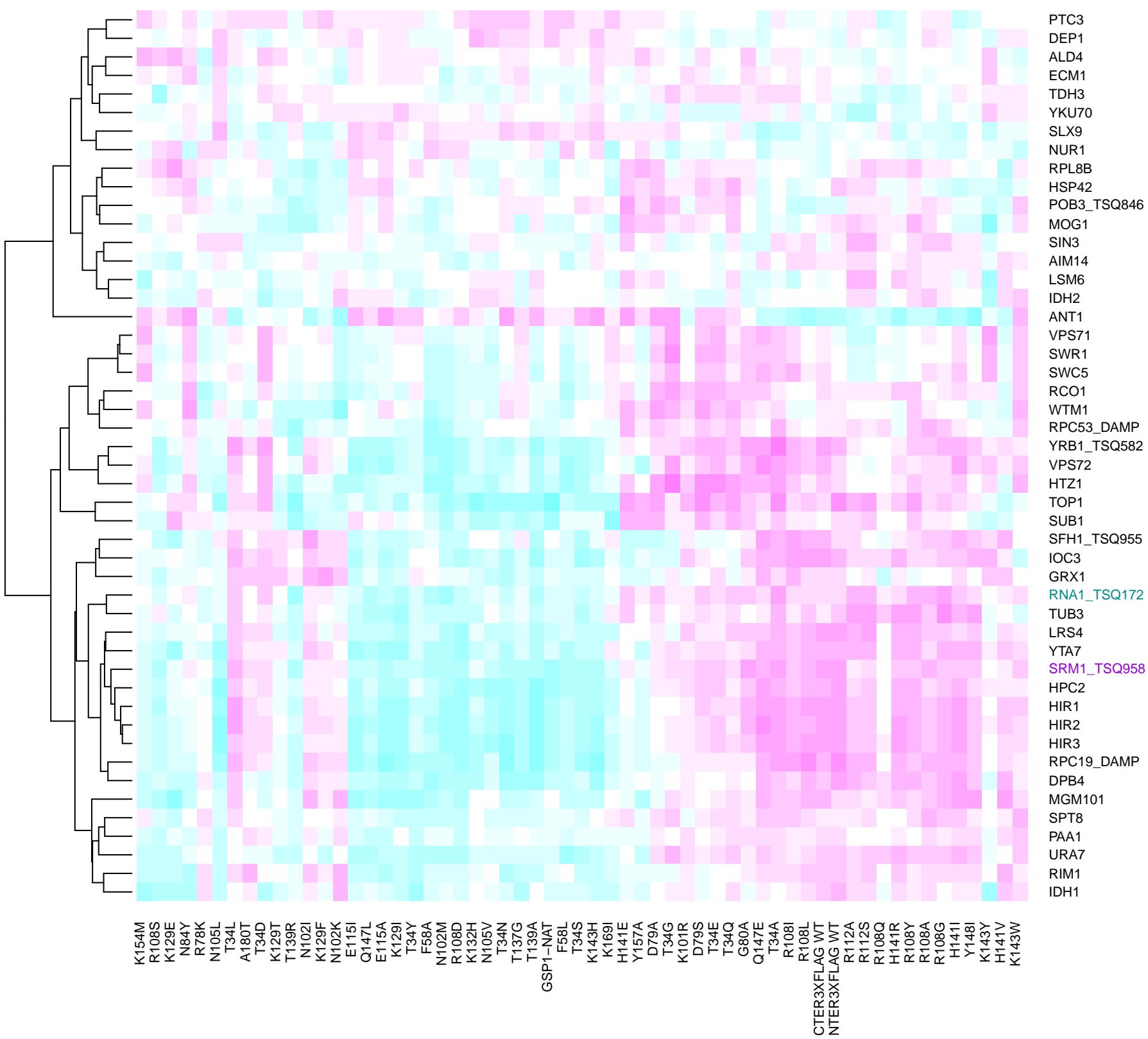
- GRX1
- IDH2
- IOC3
- PTC3
- POB3_TSQ846
- RPC53_DAMP
- RIM1
- SPT8
- MGM101
- IDH1
- HSP42
- ANT1
- ALD4
- NUR1
- YKU70
- VPS72
- SWR1
- VPS71
- HTZ1
- SWC5
- YTA7
- AIM14
- SIN3
- TUB3
- RCO1
- PAA1
- TDH3
- SUB1
- SRM1_TSQ958**
- WTM1
- HIR1
- HIR2
- HIR3
- HPC2
- TOP1
- DPB4
- RPC19_DAMP
- ECM1
- SLX9
- SFH1_TSQ955
- RNA1_TSQ172**
- DEP1
- URA7
- RPL8B
- LSM6
- LRS4
- YRB1_TSQ582
- MOG1

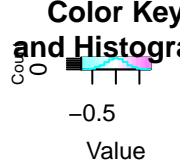
K154M
R108S
K129E
N84Y
R78K
N105L
T34L
A180T
T34D
K129T
T139R
N102I
K129F
N102K
E115I
Q147L
E115A
K29I
T34Y
F58A
N102M
R108D
K132H
N105V
T34N
T137G
T139A
GSP1-NAT
F58L
T34S
K143H
K169I
H141E
Y157A
D79A
T34G
K101R
D79S
T34E
T34Q
G80A
Q147E
T34A
R108I
R108L
CTER3XFLAG WT
NTER3XFLAG WT
R112A
R112S
R108Q
H141R
R108Y
R108A
R108G
H141I
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K143Y
H141V
K143W

CTER3XFLAG WT
NTER3XFLAG WT

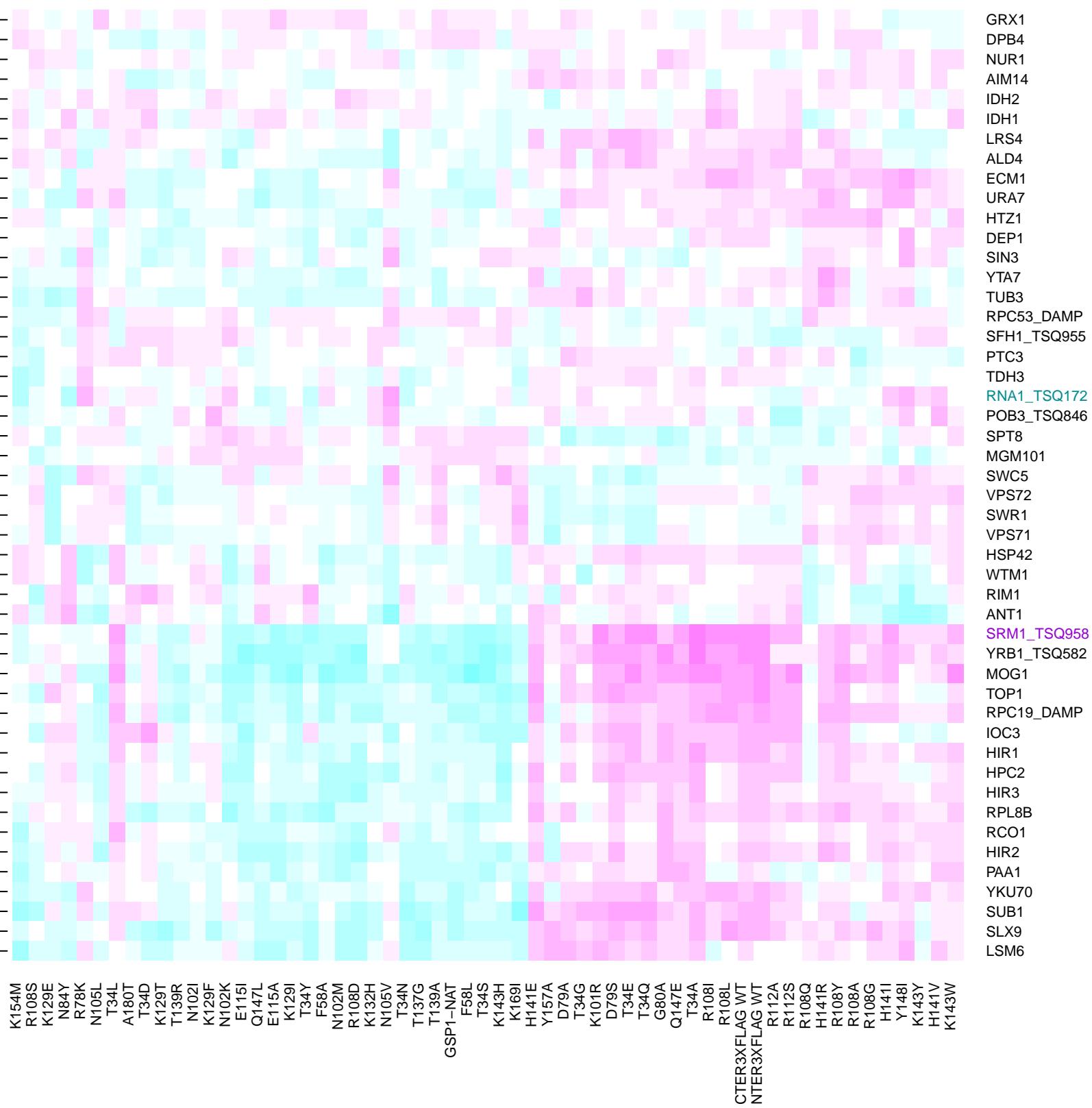


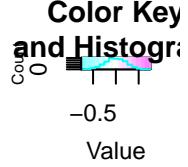
Golgi_GO_30_2



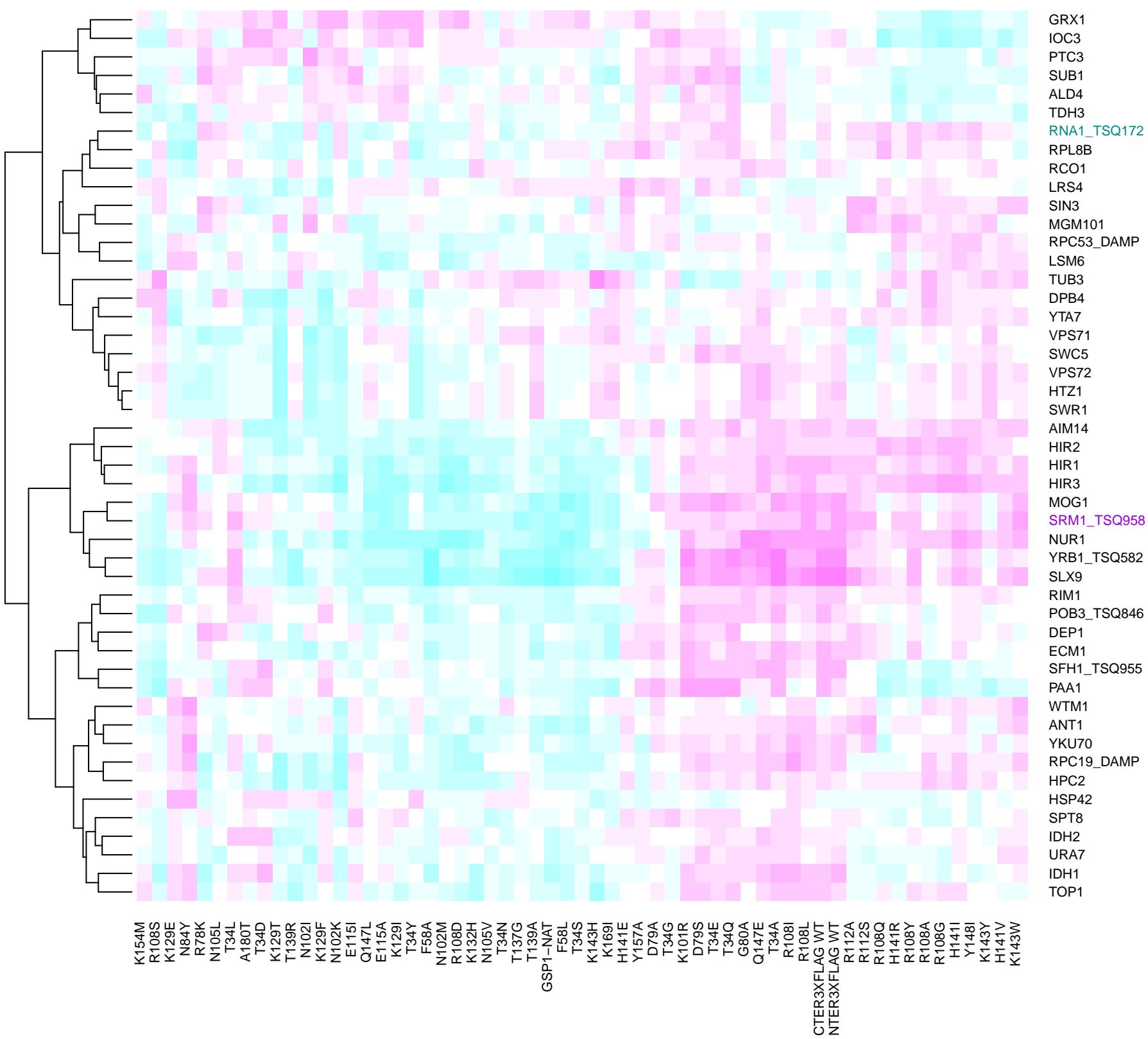


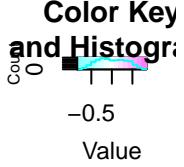
vacuole_GO_30_5



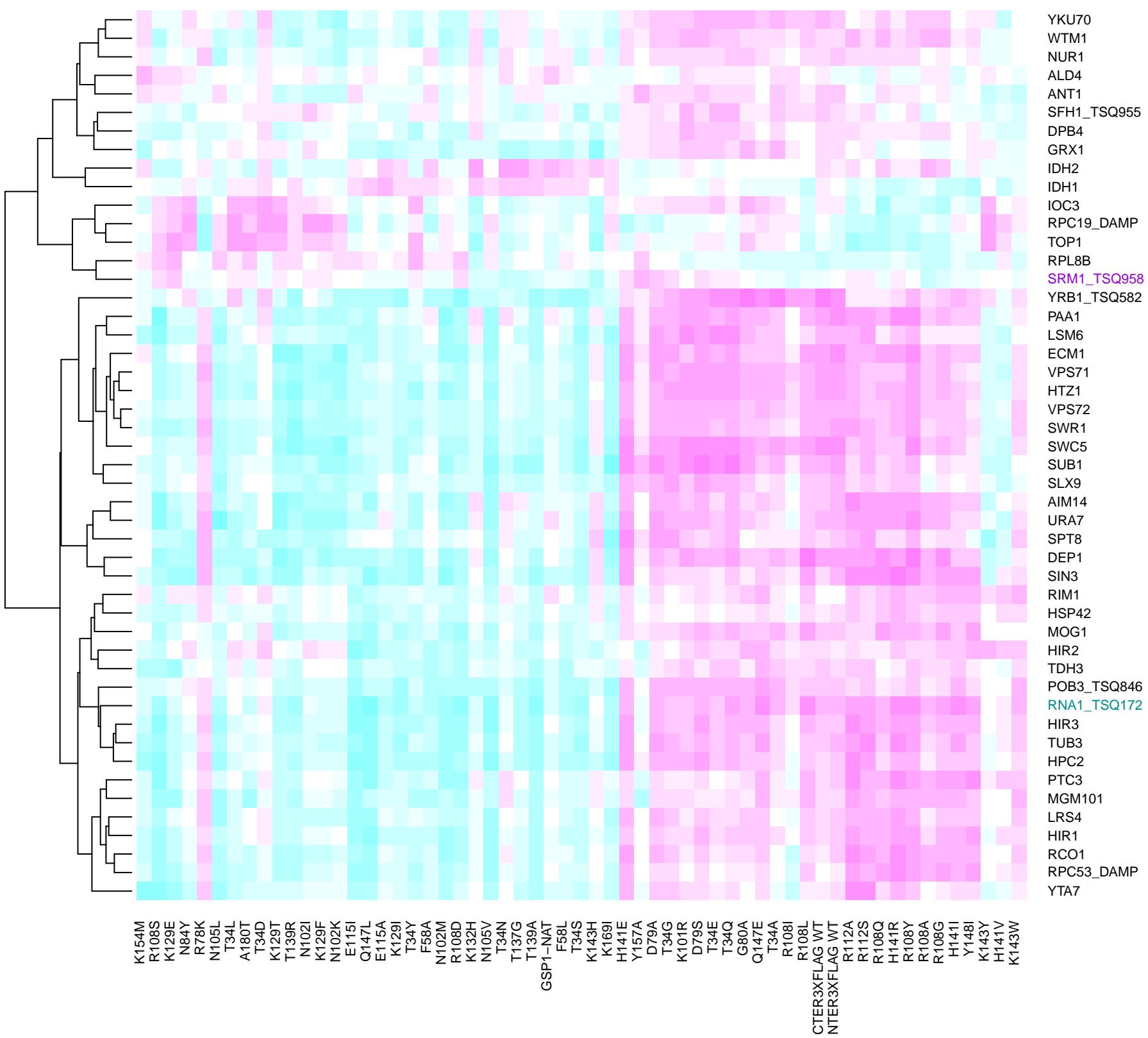


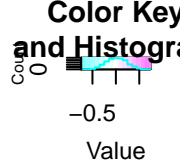
cellular bud_GO_30_2



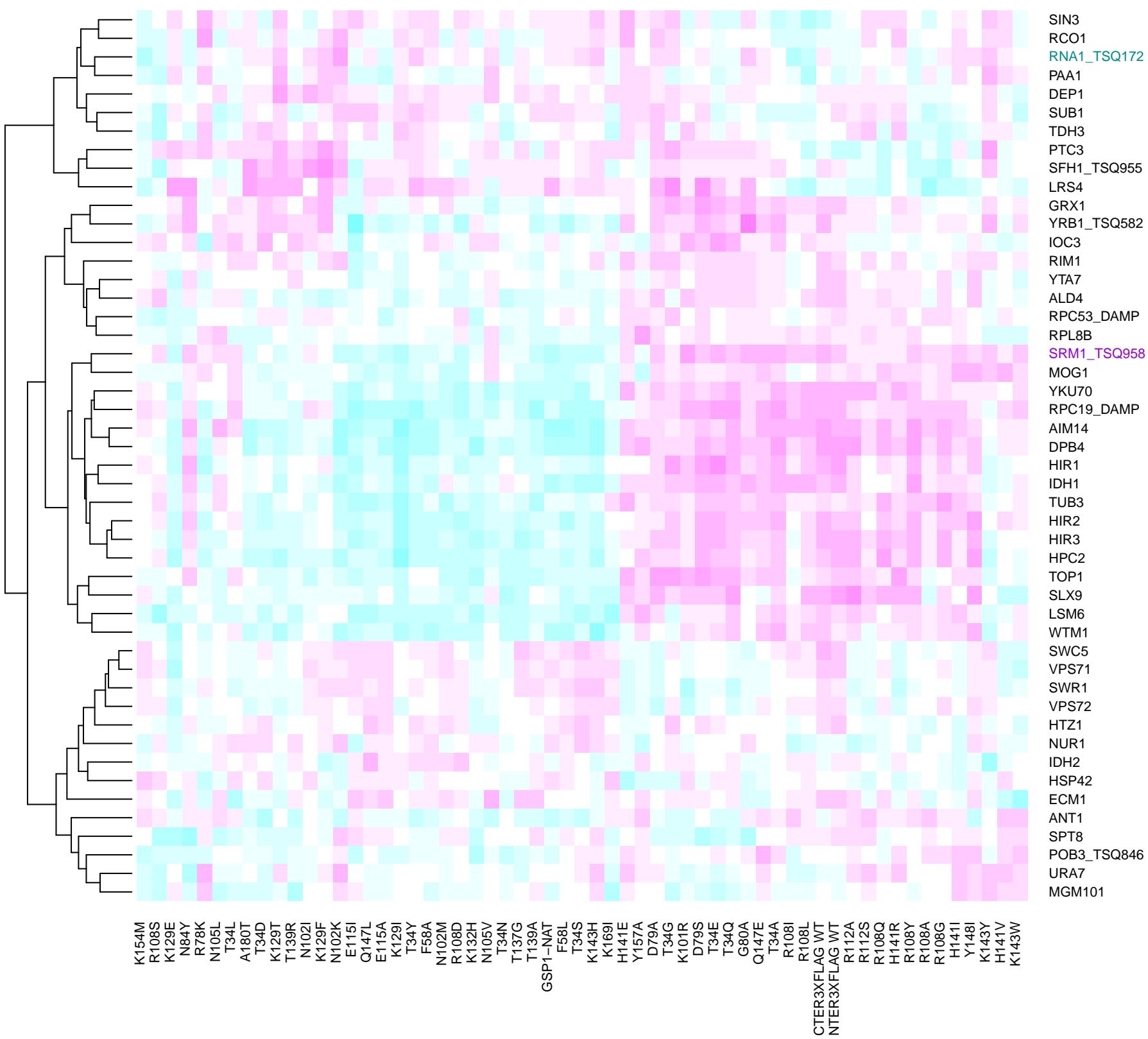


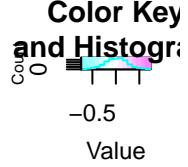
Golgi and ER_GO_30_13



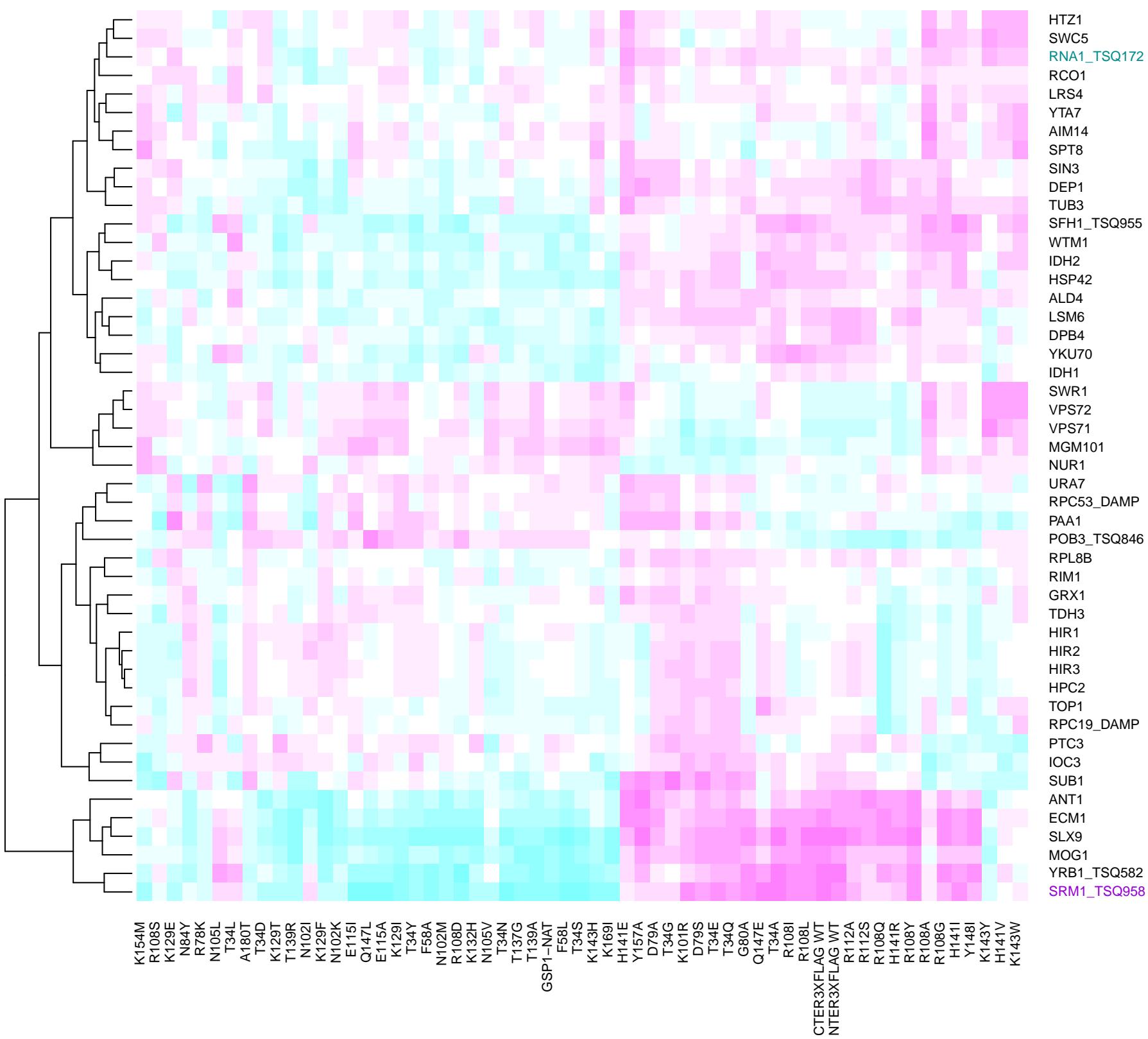


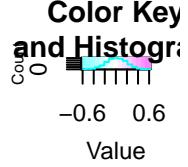
Golgi and ER_GO_30_18



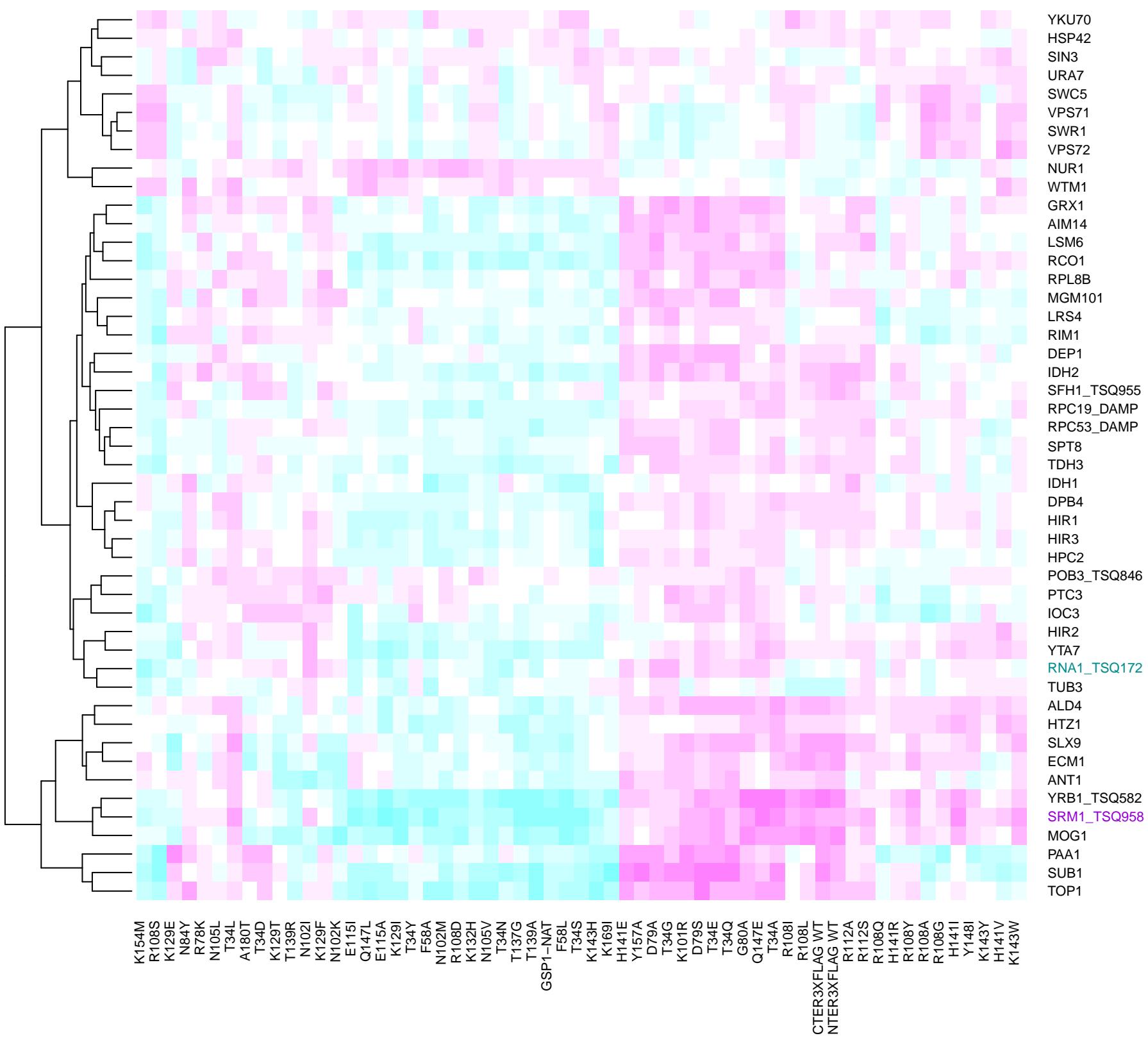


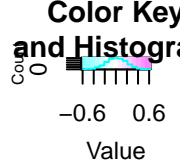
peptidyl-amino acid modification_GO_30_2



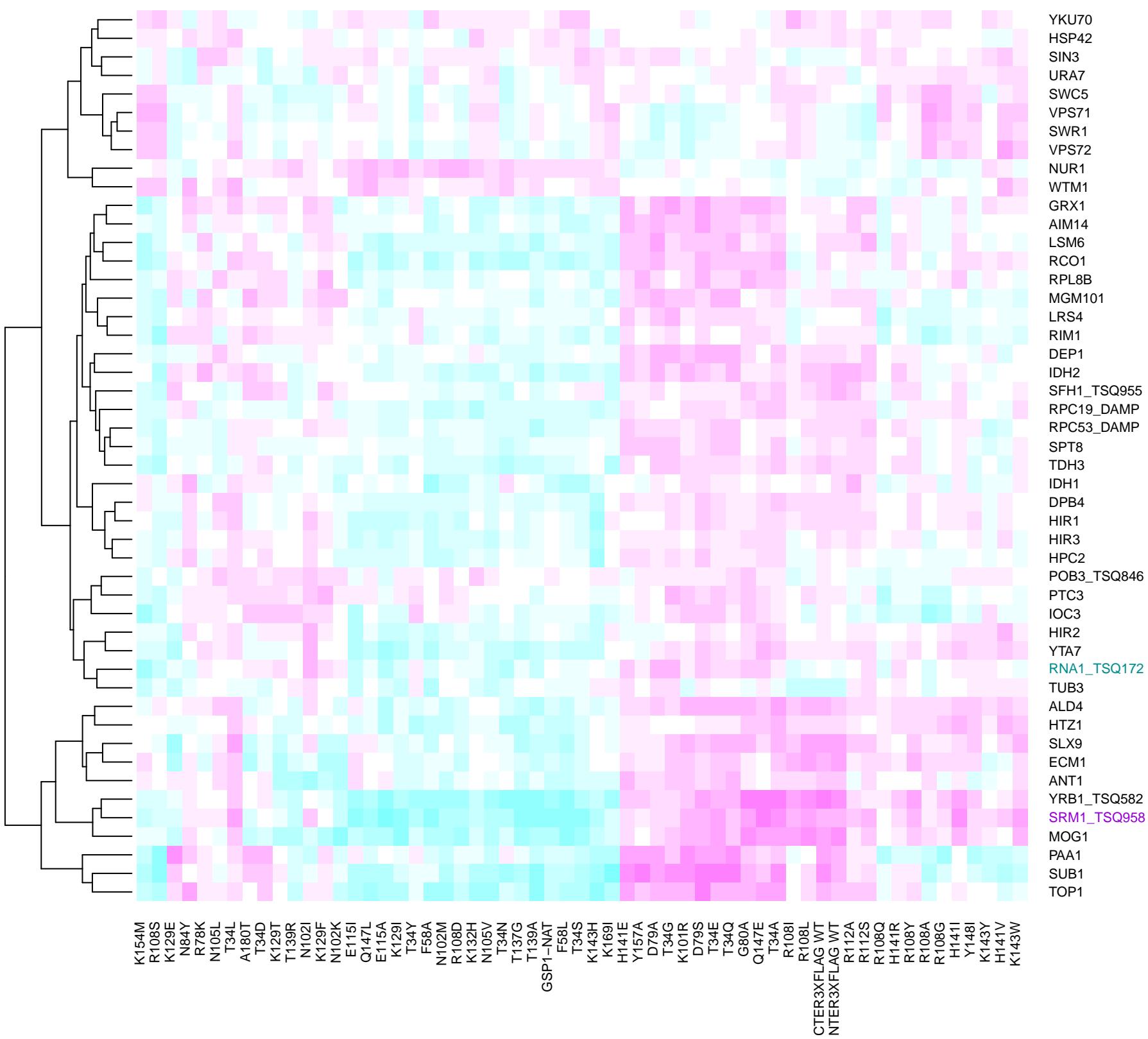


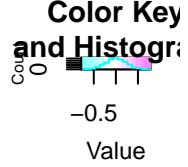
endoplasmic reticulum_GO_30_1



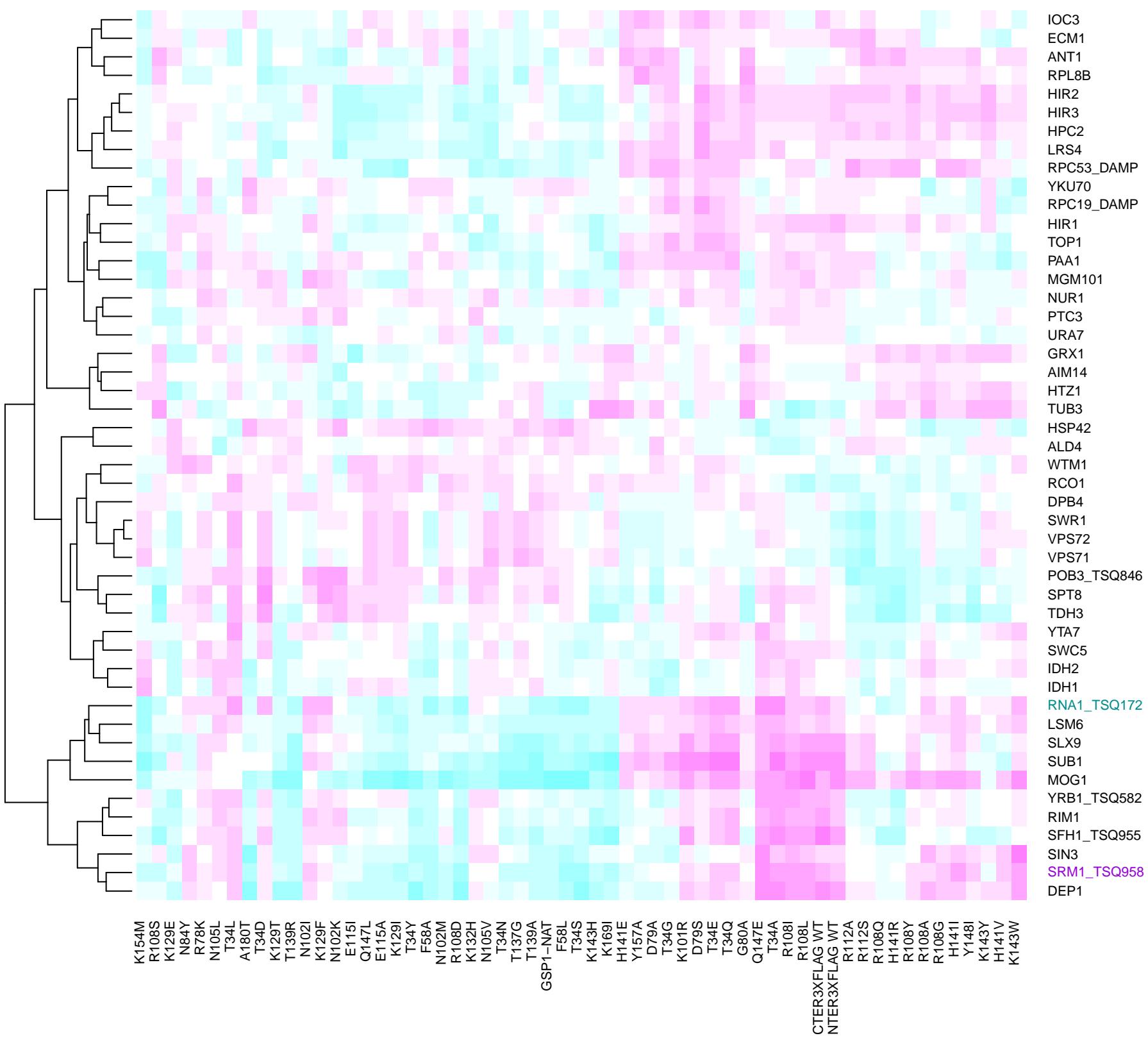


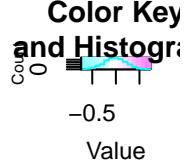
ER_GO_30_1



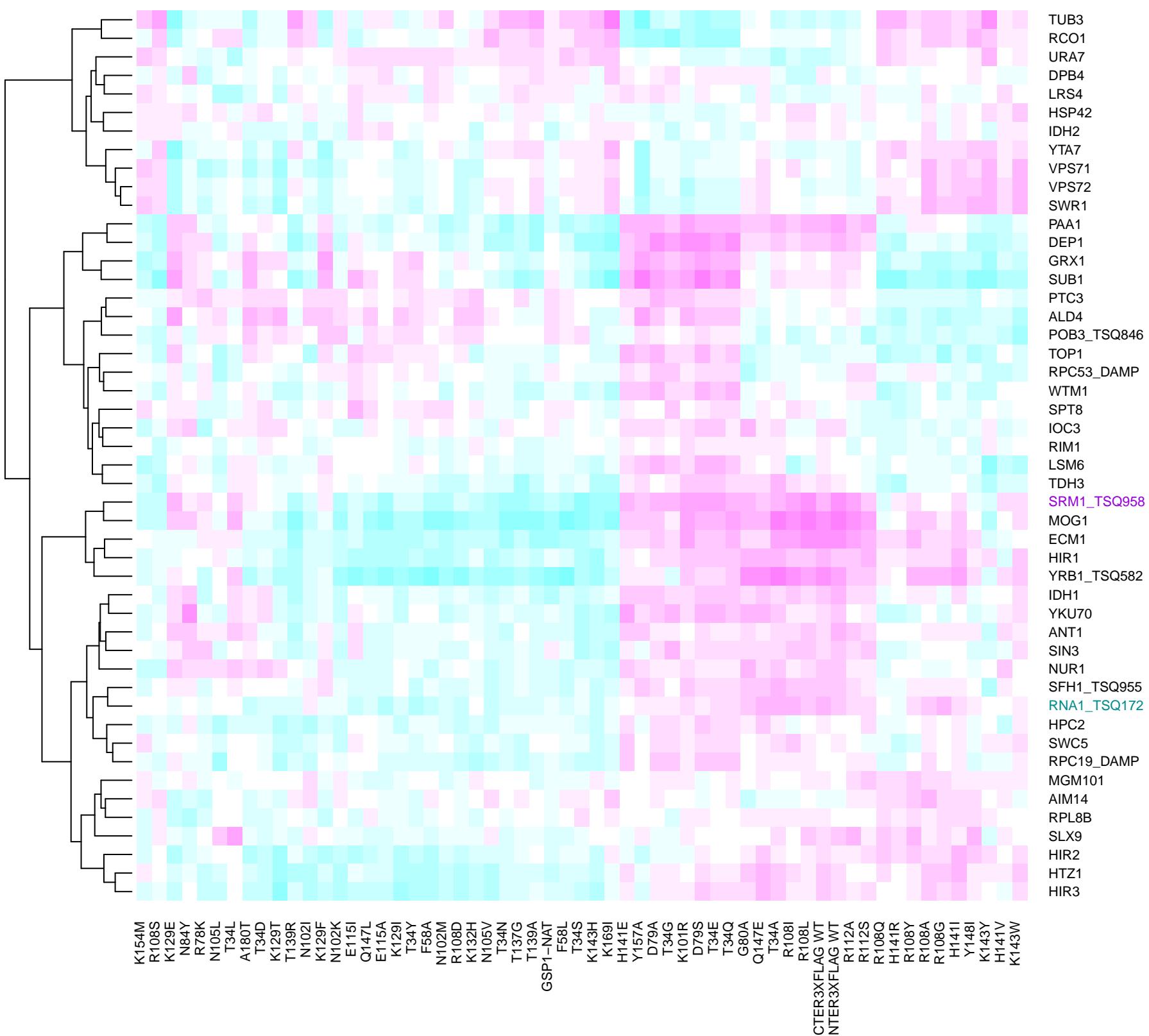


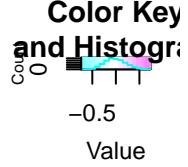
vacuole_GO_30_8



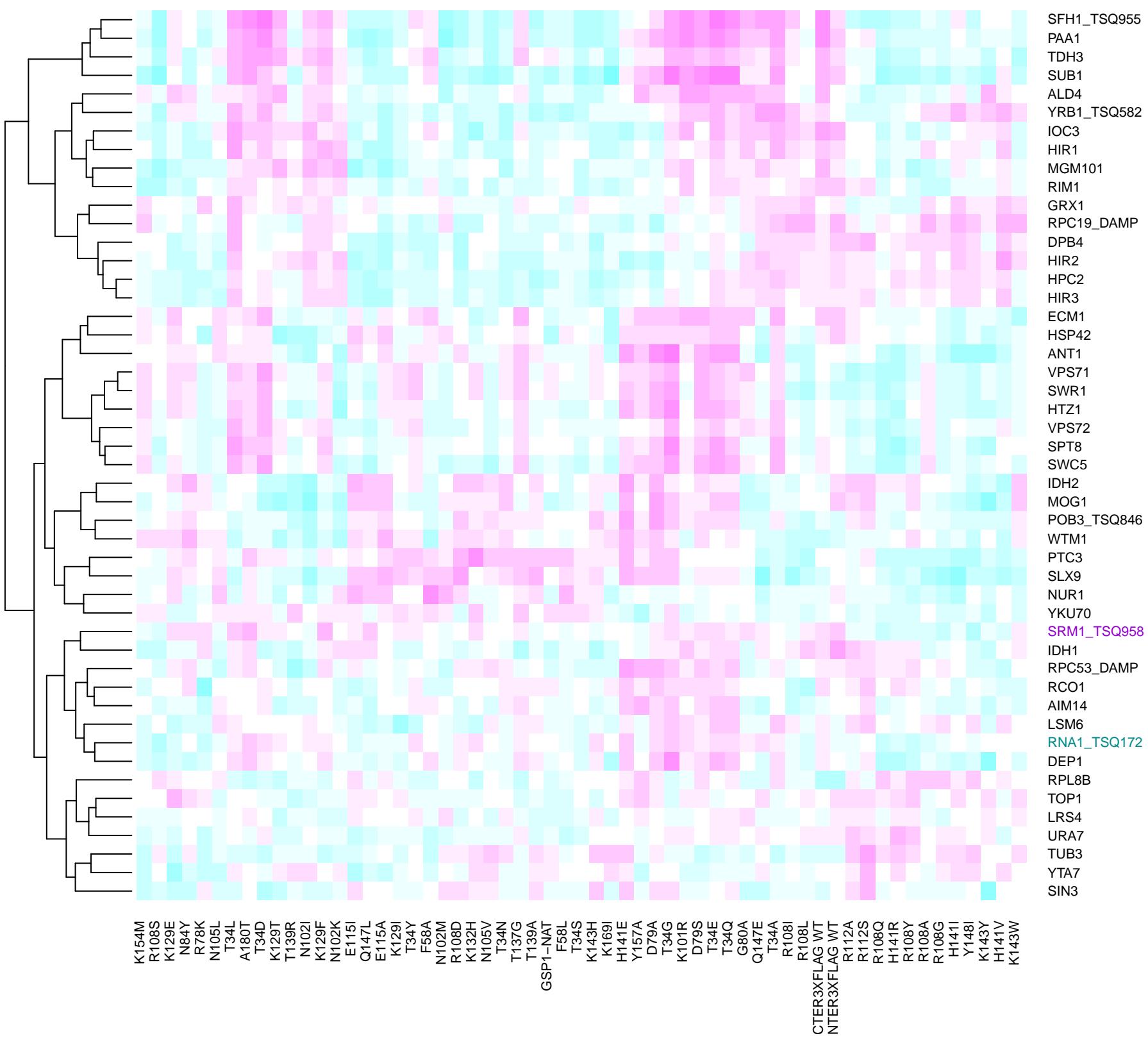


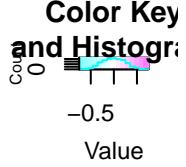
mitotic cell cycle_GO_30_3



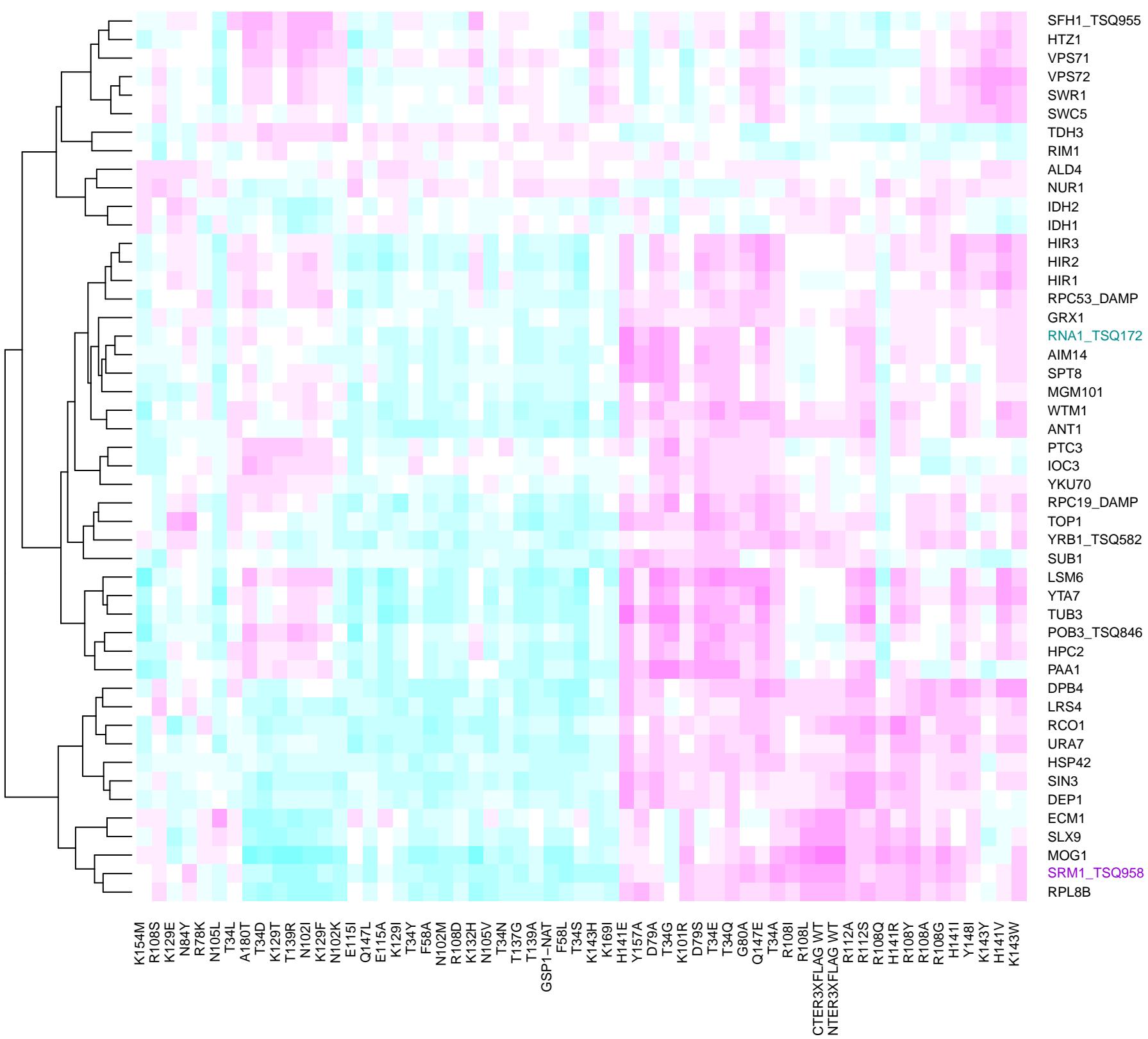


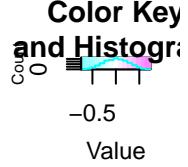
Golgi apparatus_GO_30_2



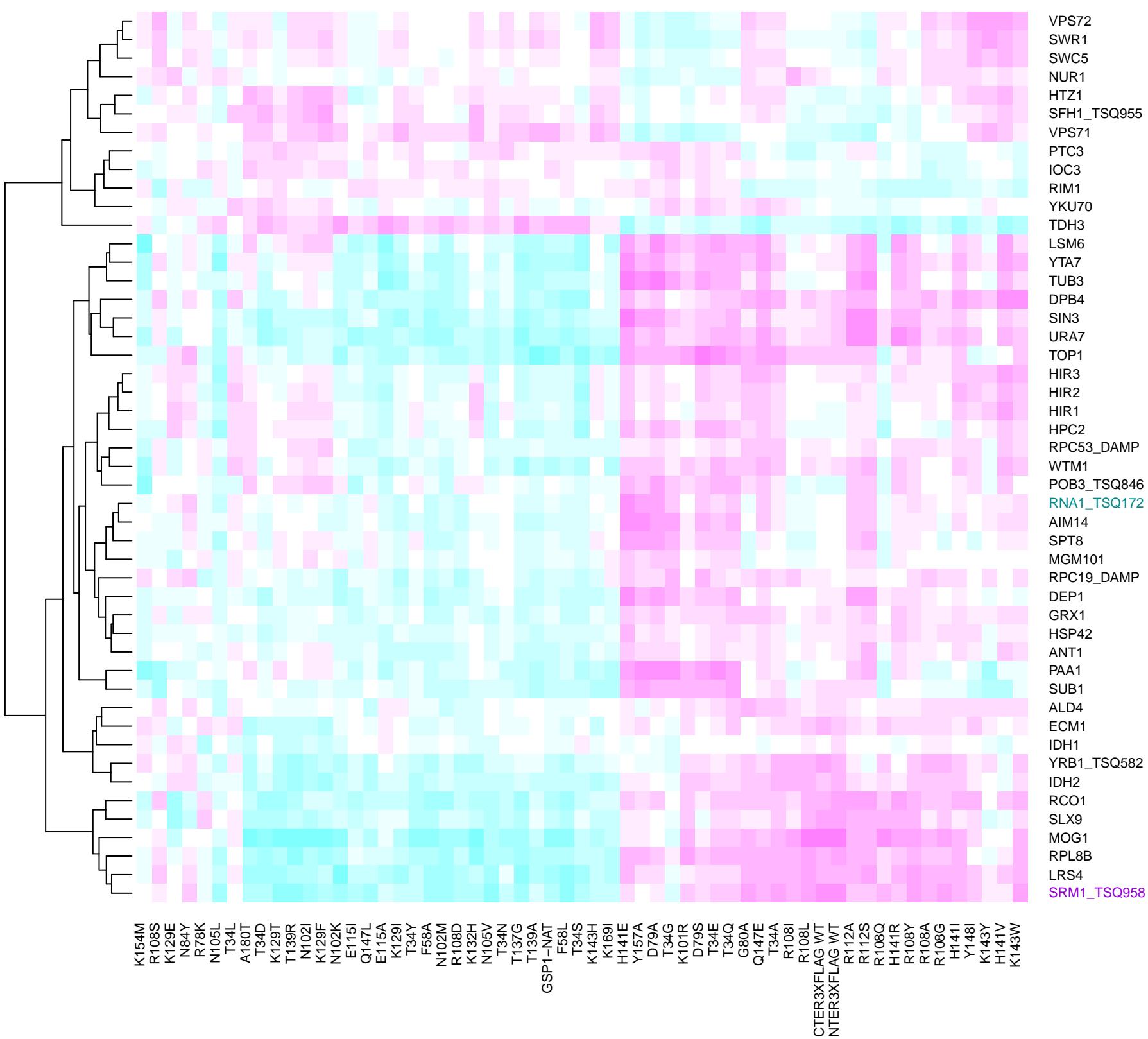


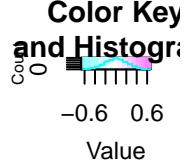
RNA splicing



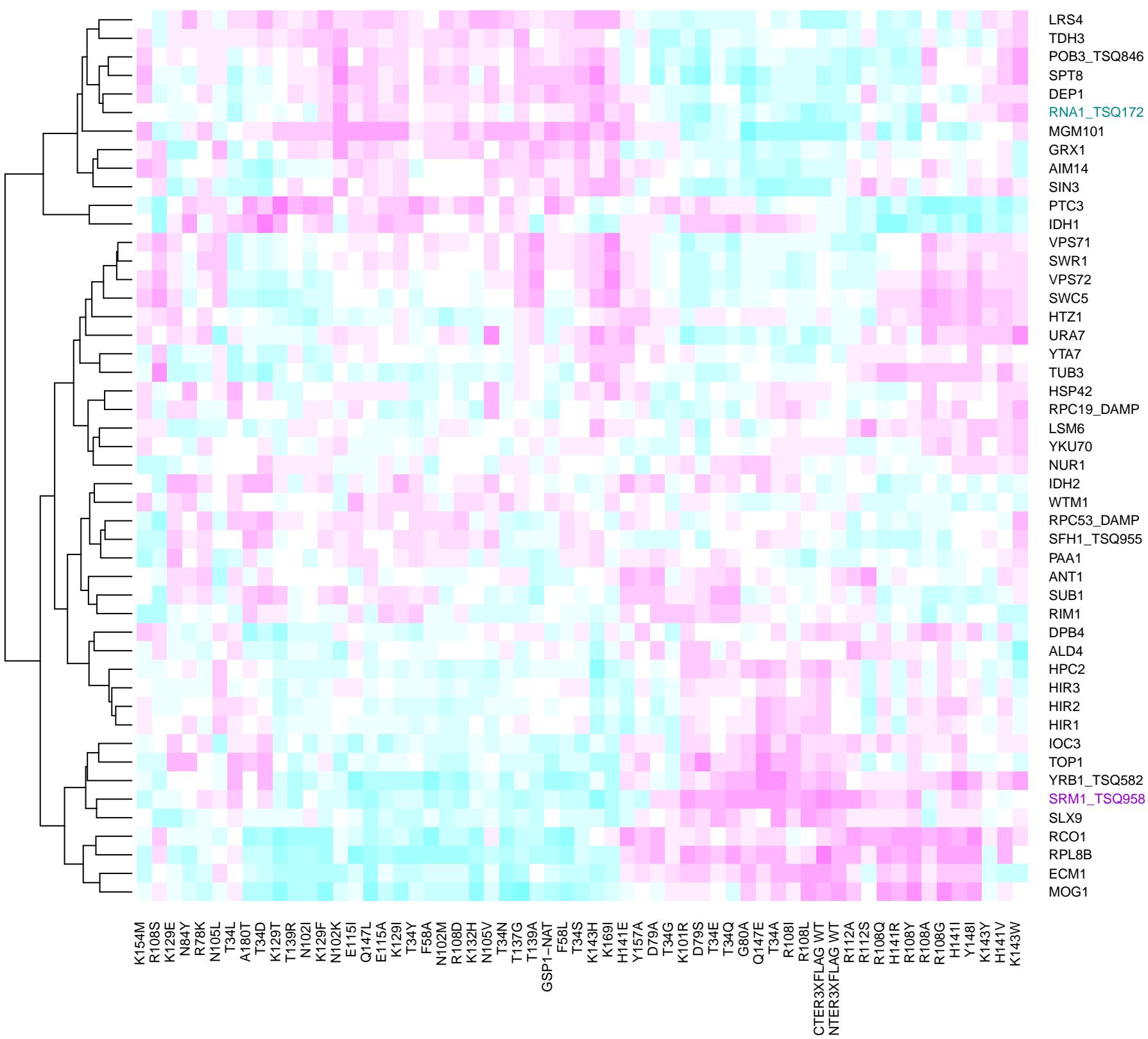


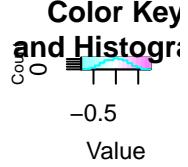
RNA splicing_GO_30_1



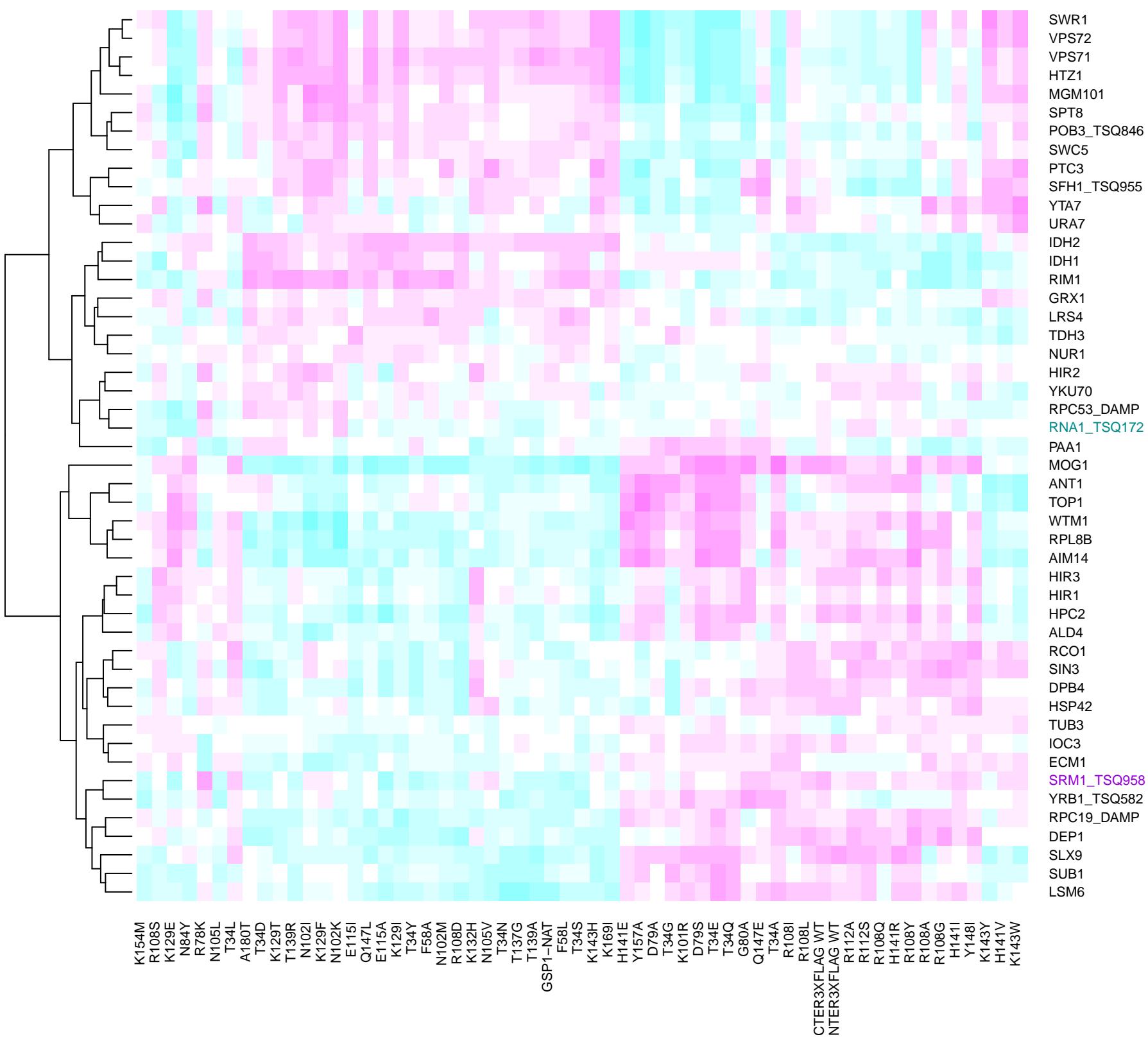


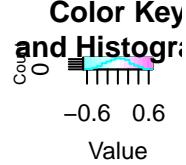
ion transport_GO_30_3



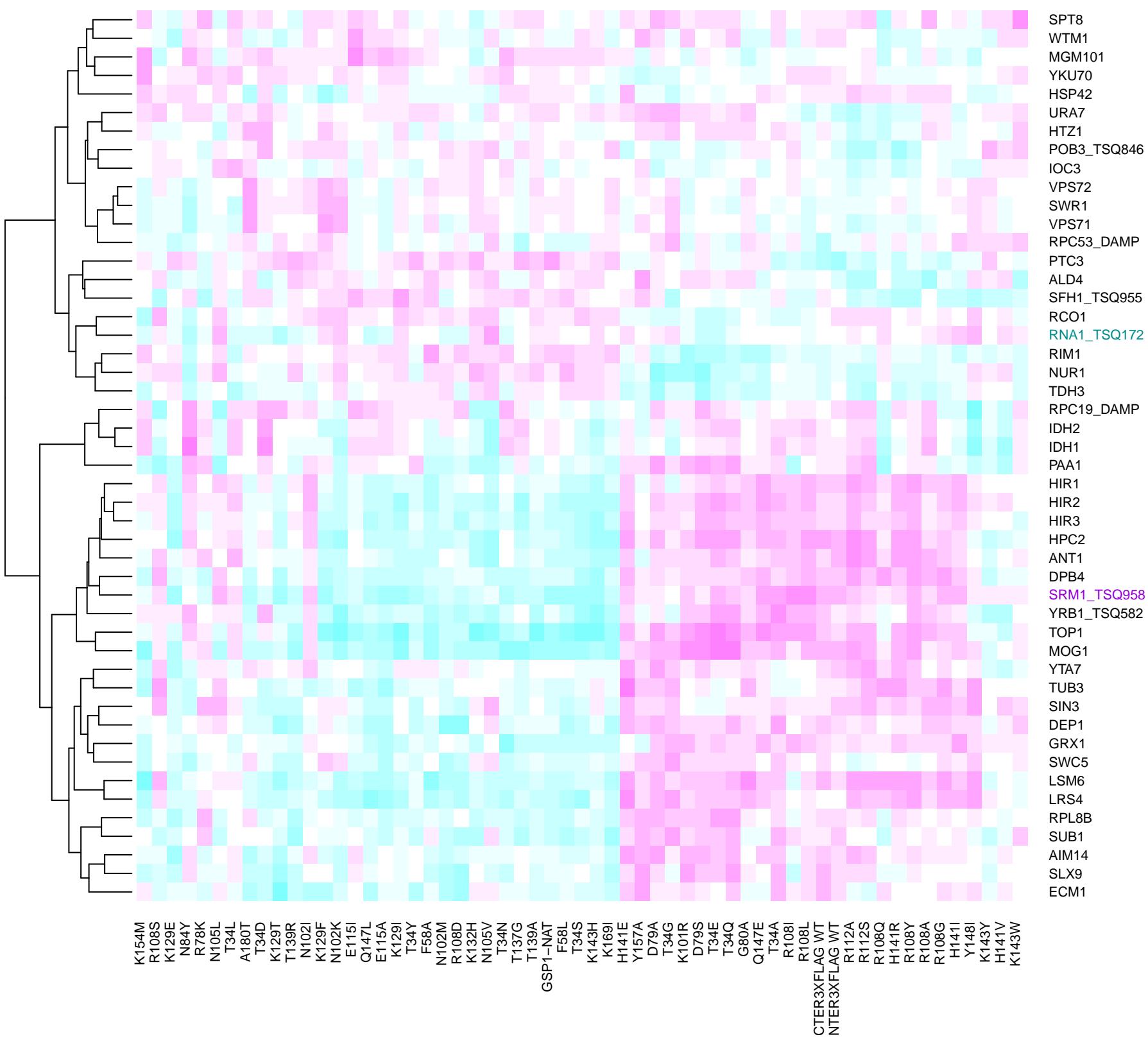


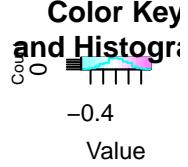
mitochondrial envelope_GO_30_4



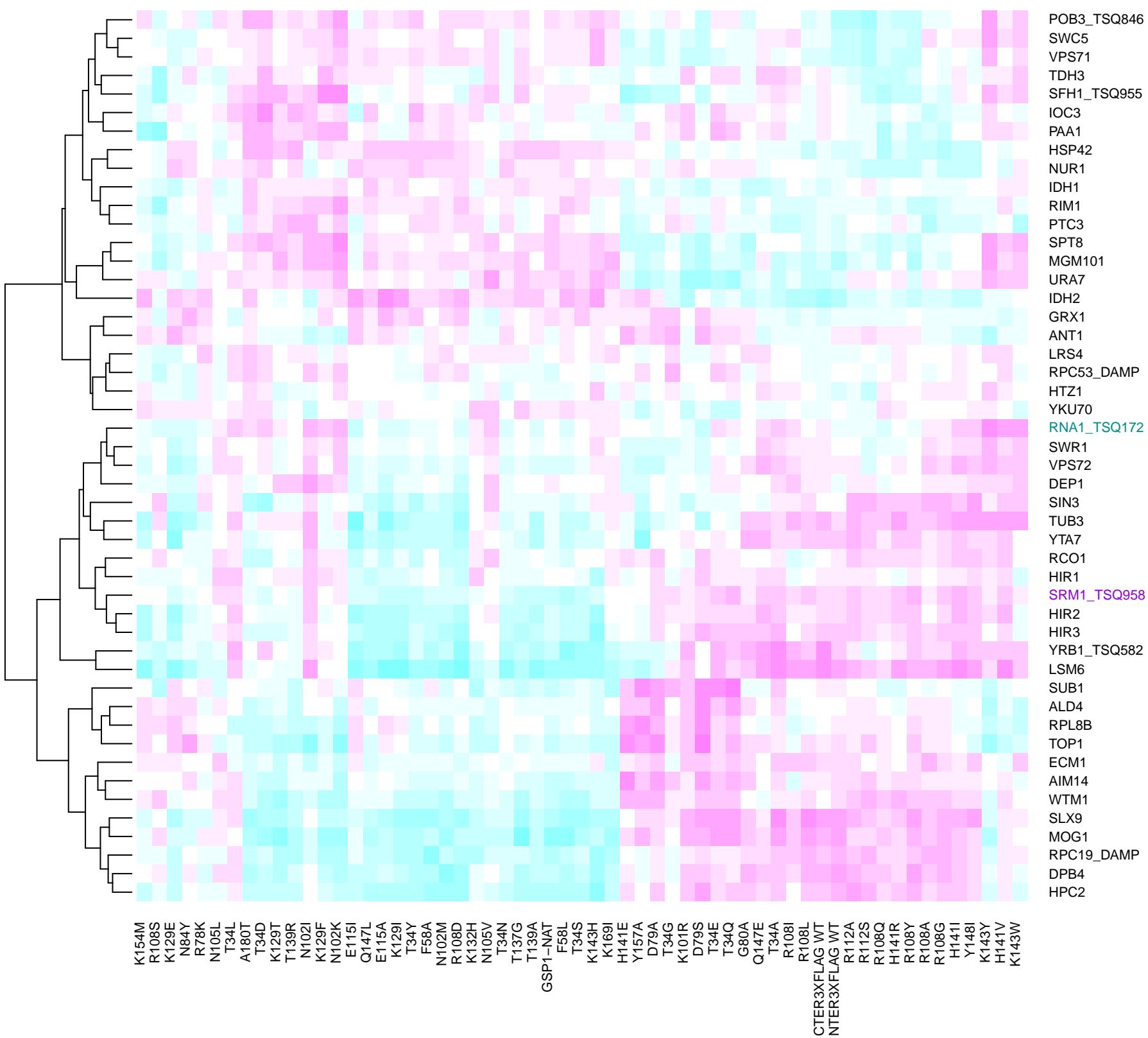


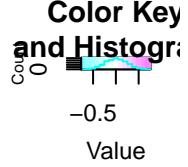
monocarboxylic acid metabolic process_GO_30_2



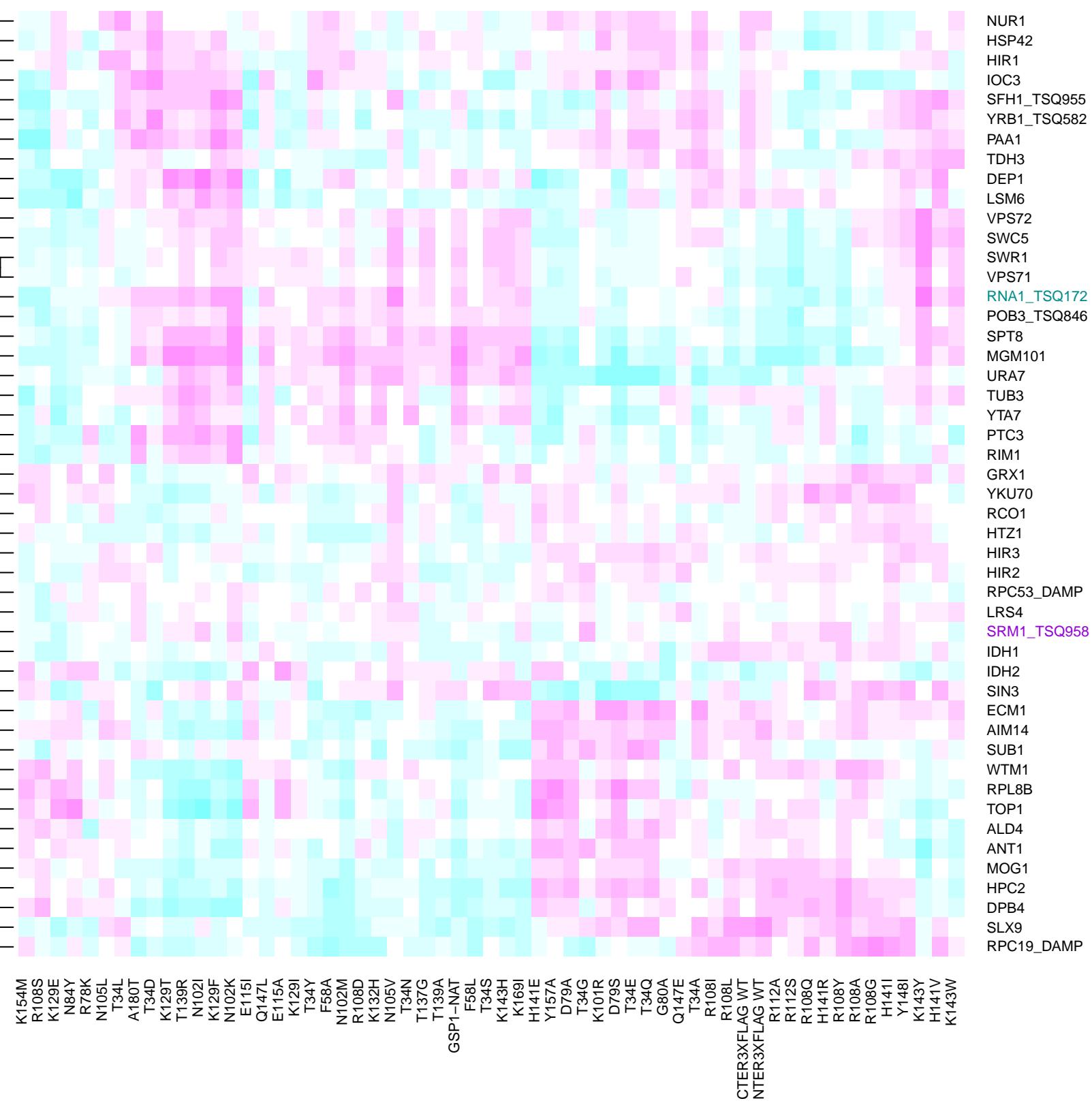


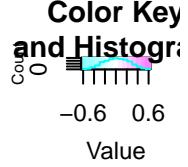
cellular ion homeostasis



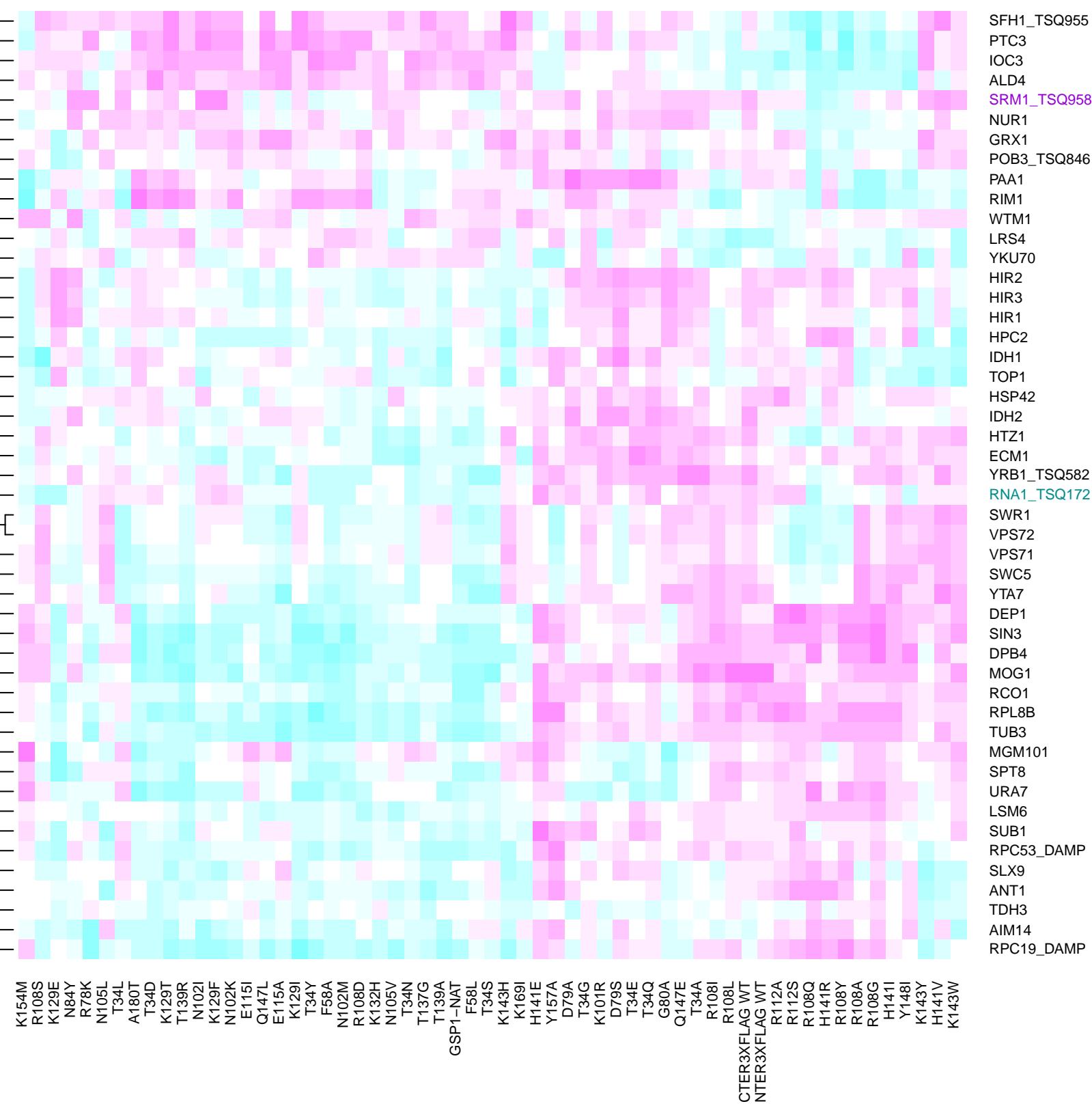


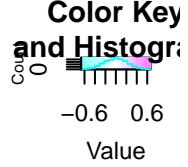
cellular ion homeostasis_GO_30_2



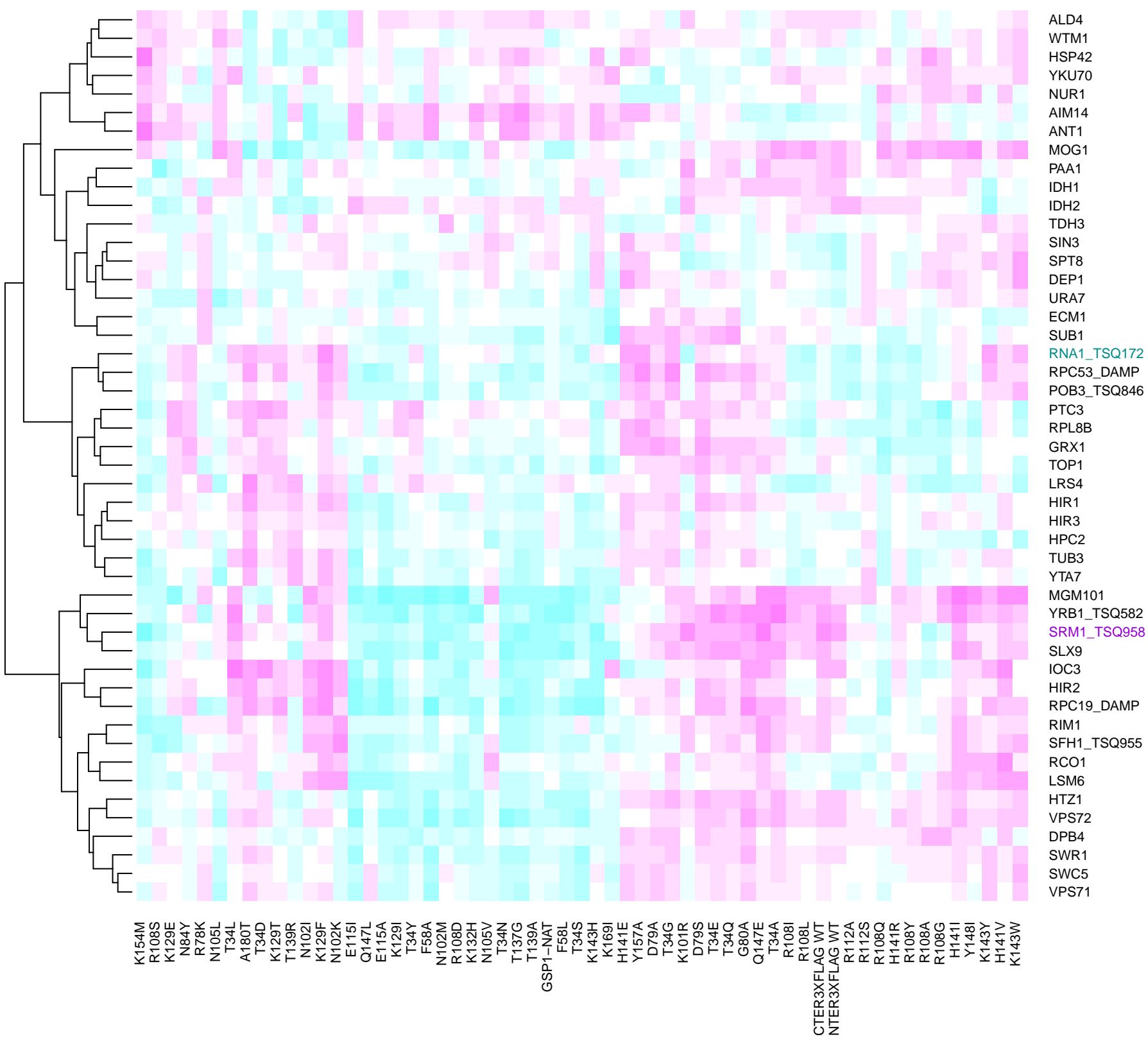


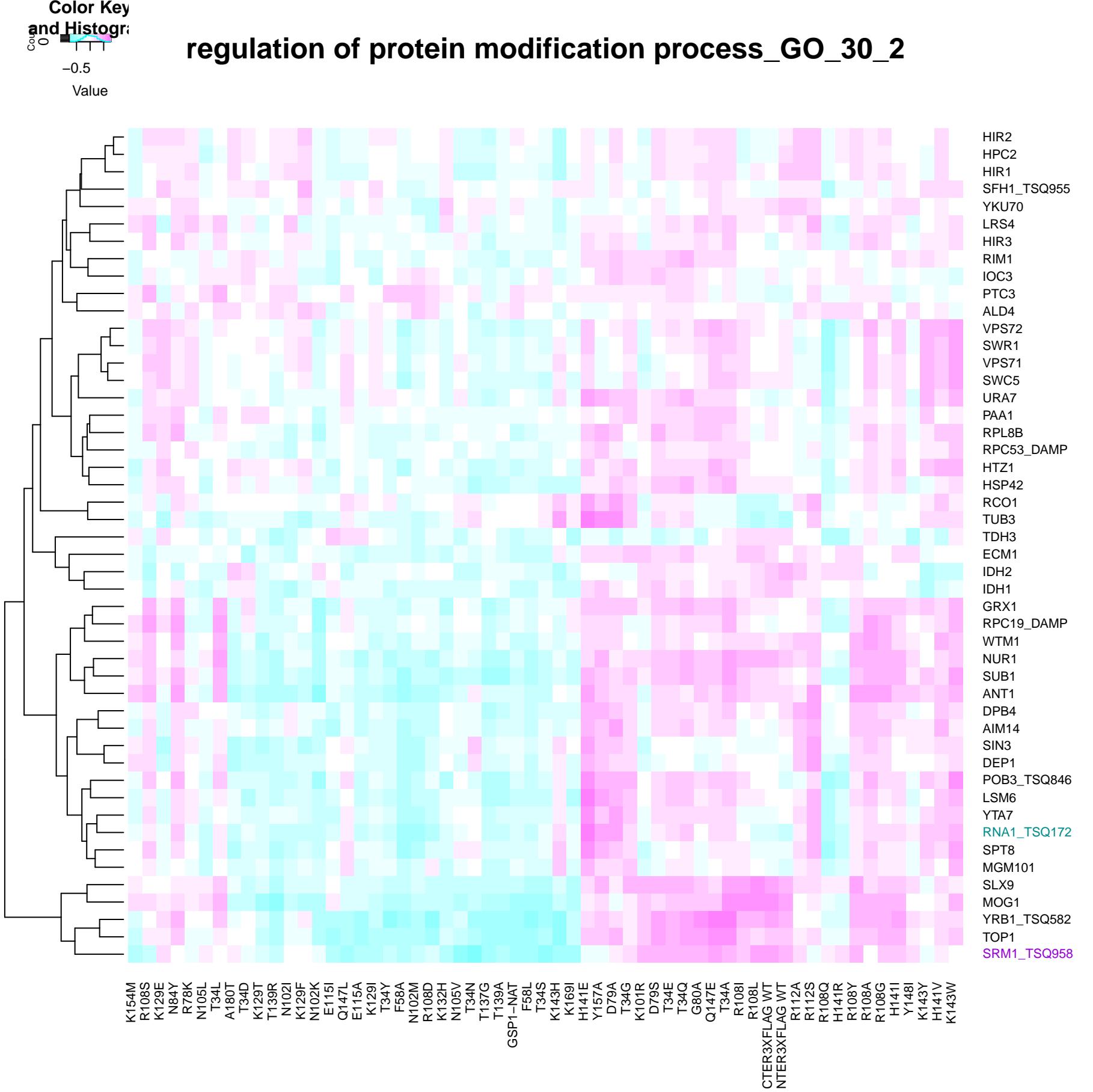
mitochondrion_GO_30_11

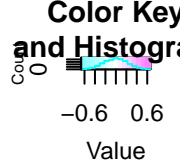




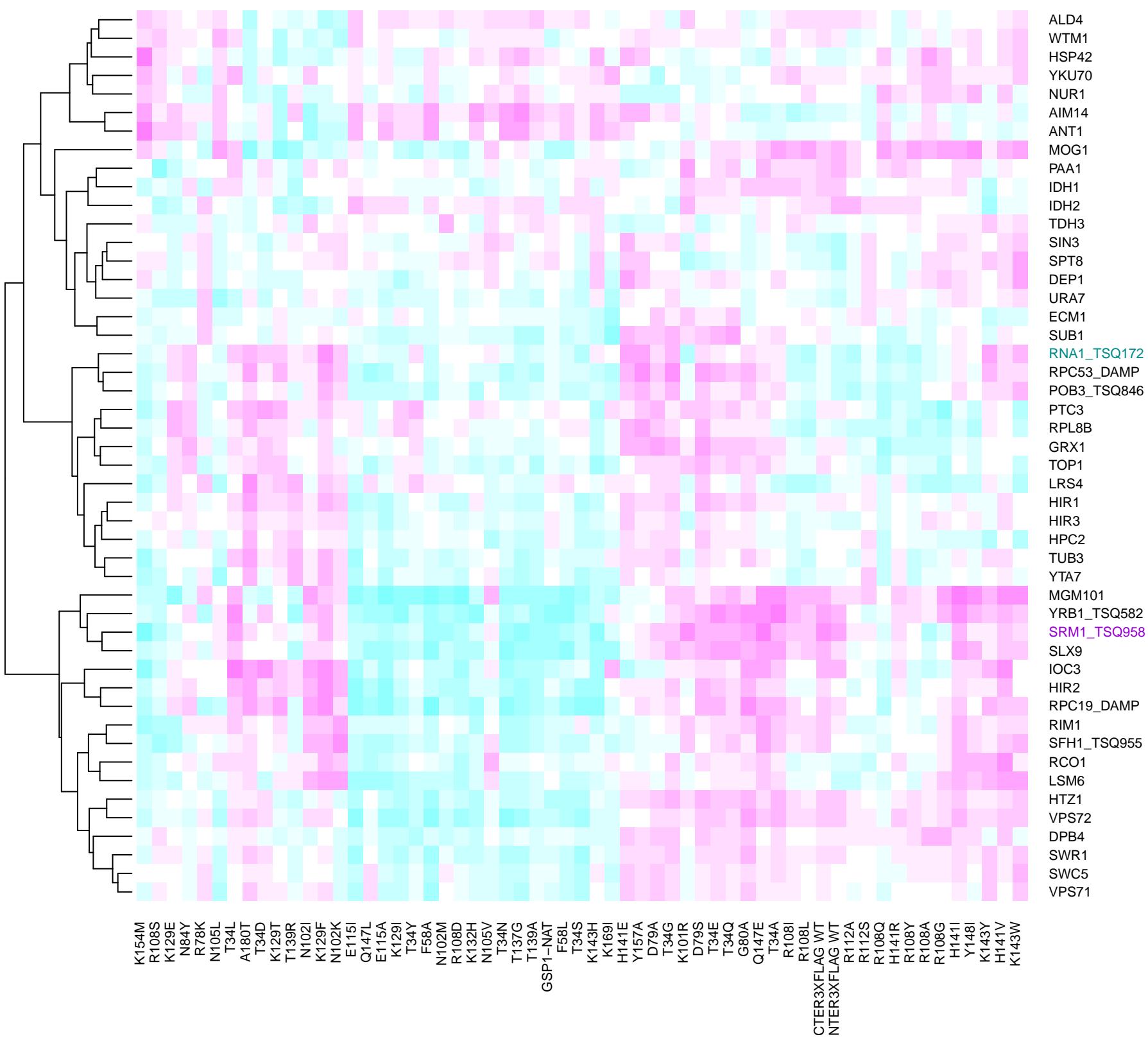
endoplasmic reticulum_GO_30_4

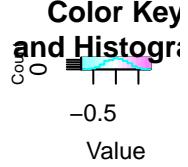




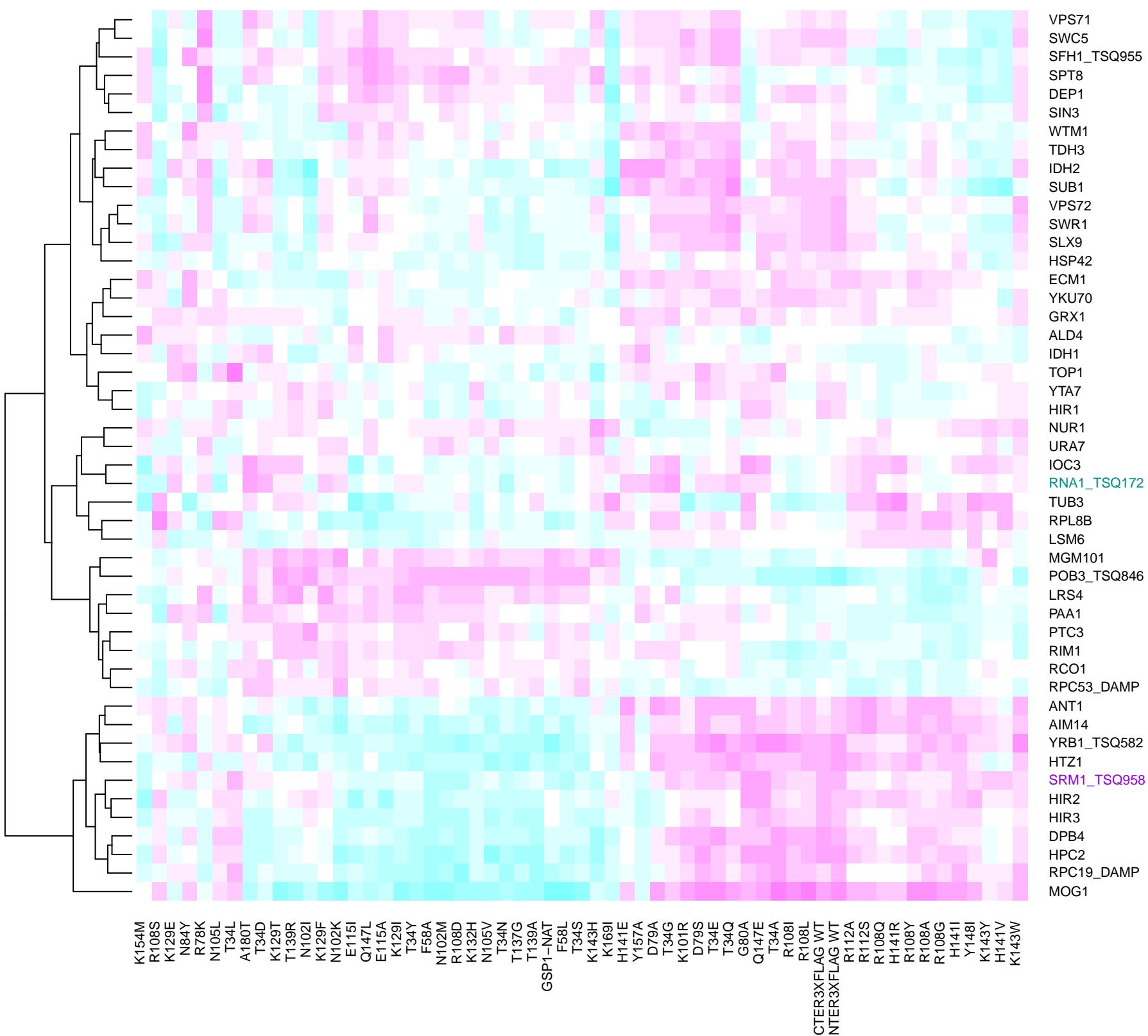


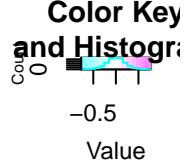
ER_GO_30_4



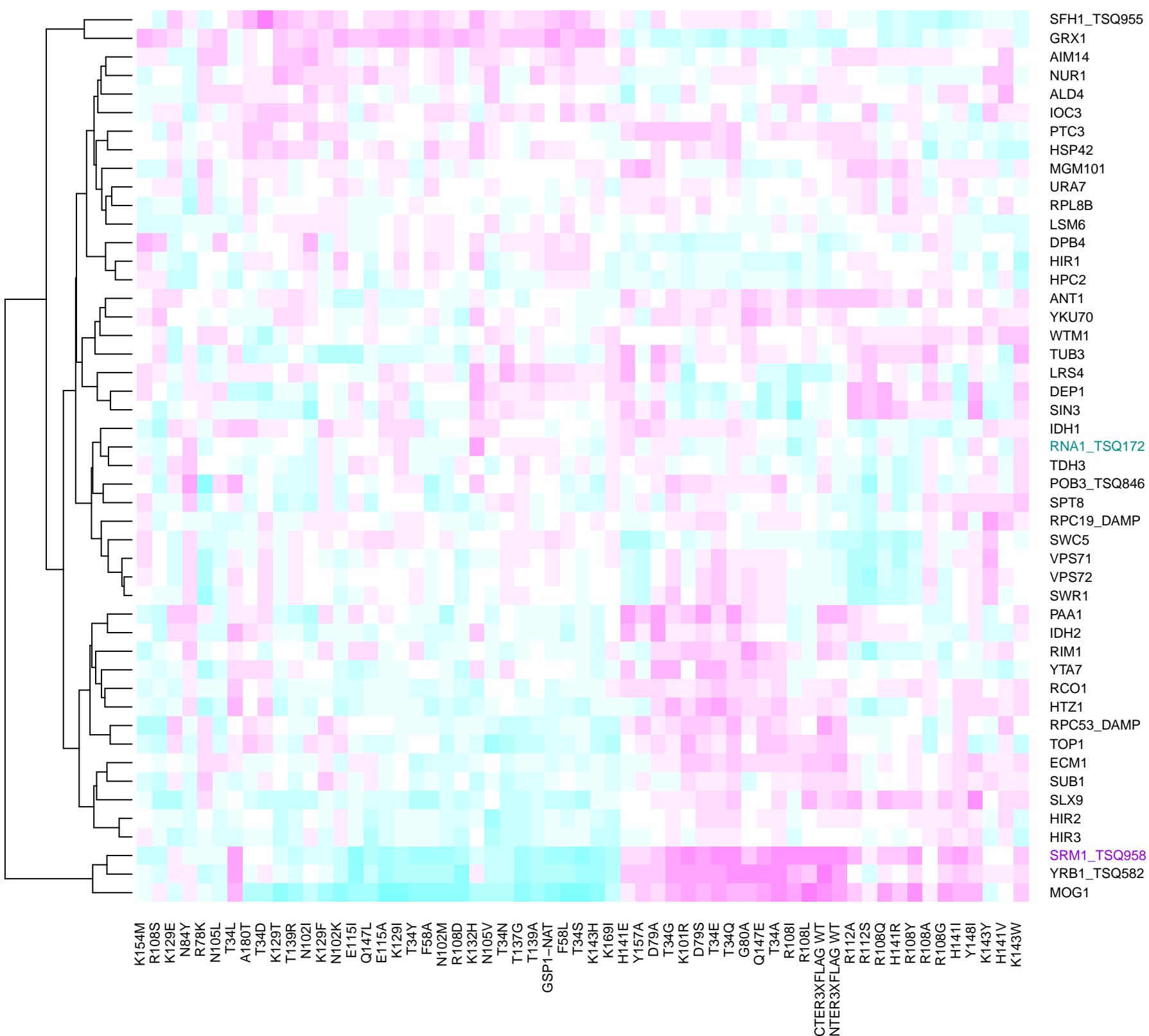


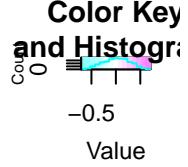
peroxisomes_GO_30_2



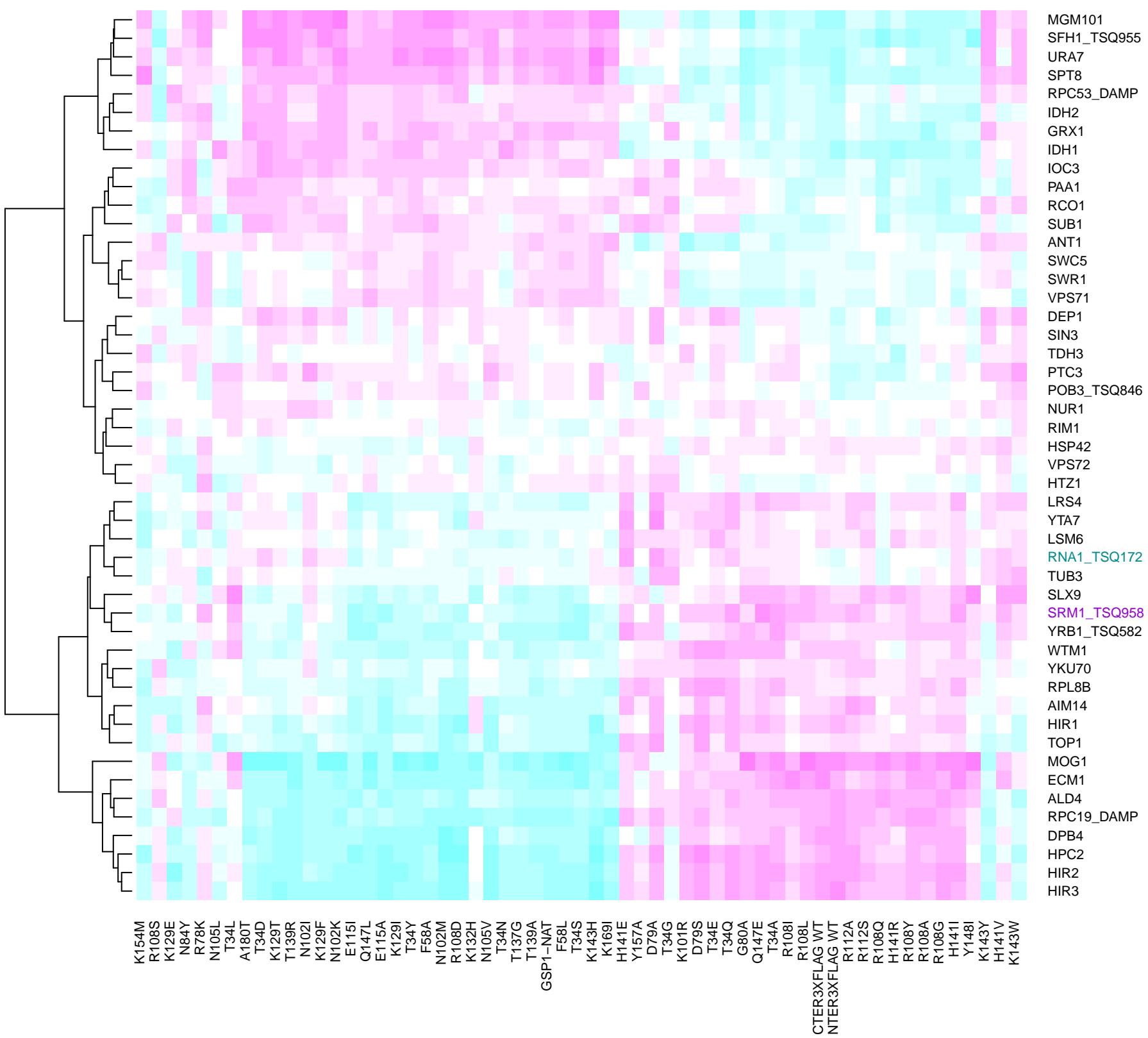


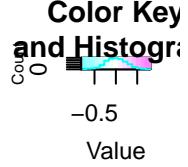
sporulation_GO_30_3



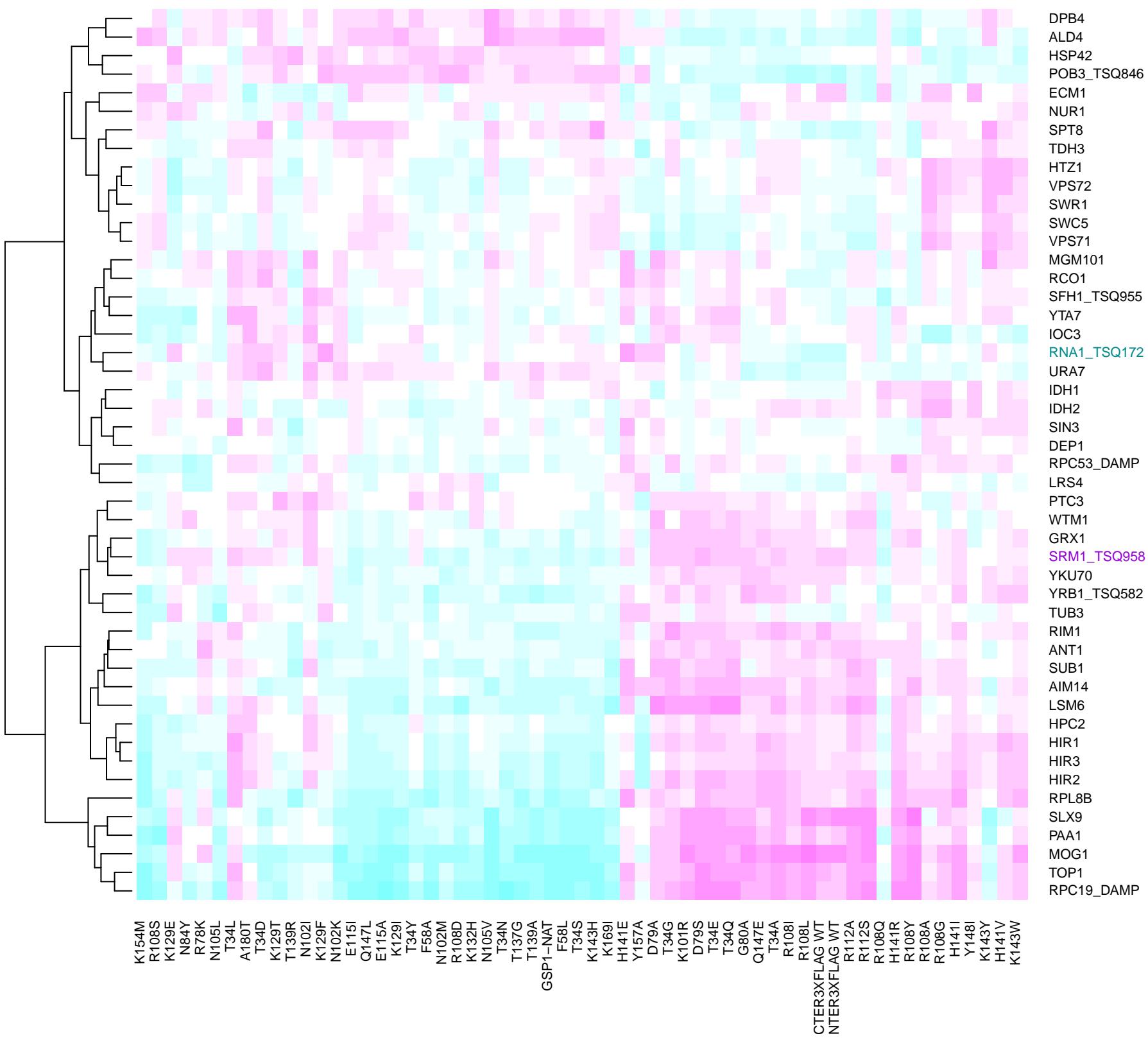


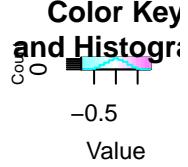
mitochondrion_GO_30_9



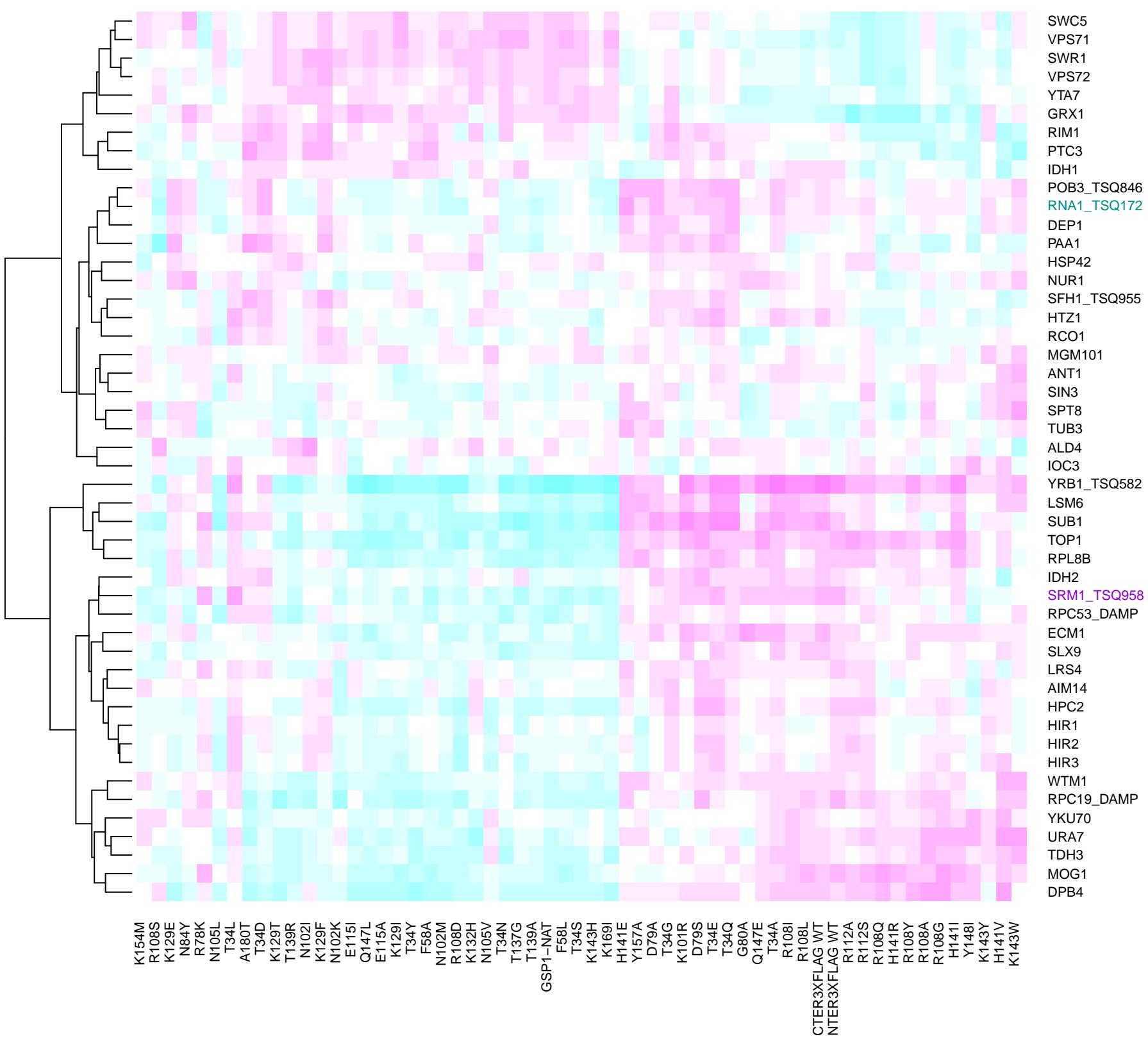


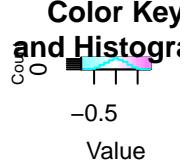
ribosomes and translation_GO_30_7



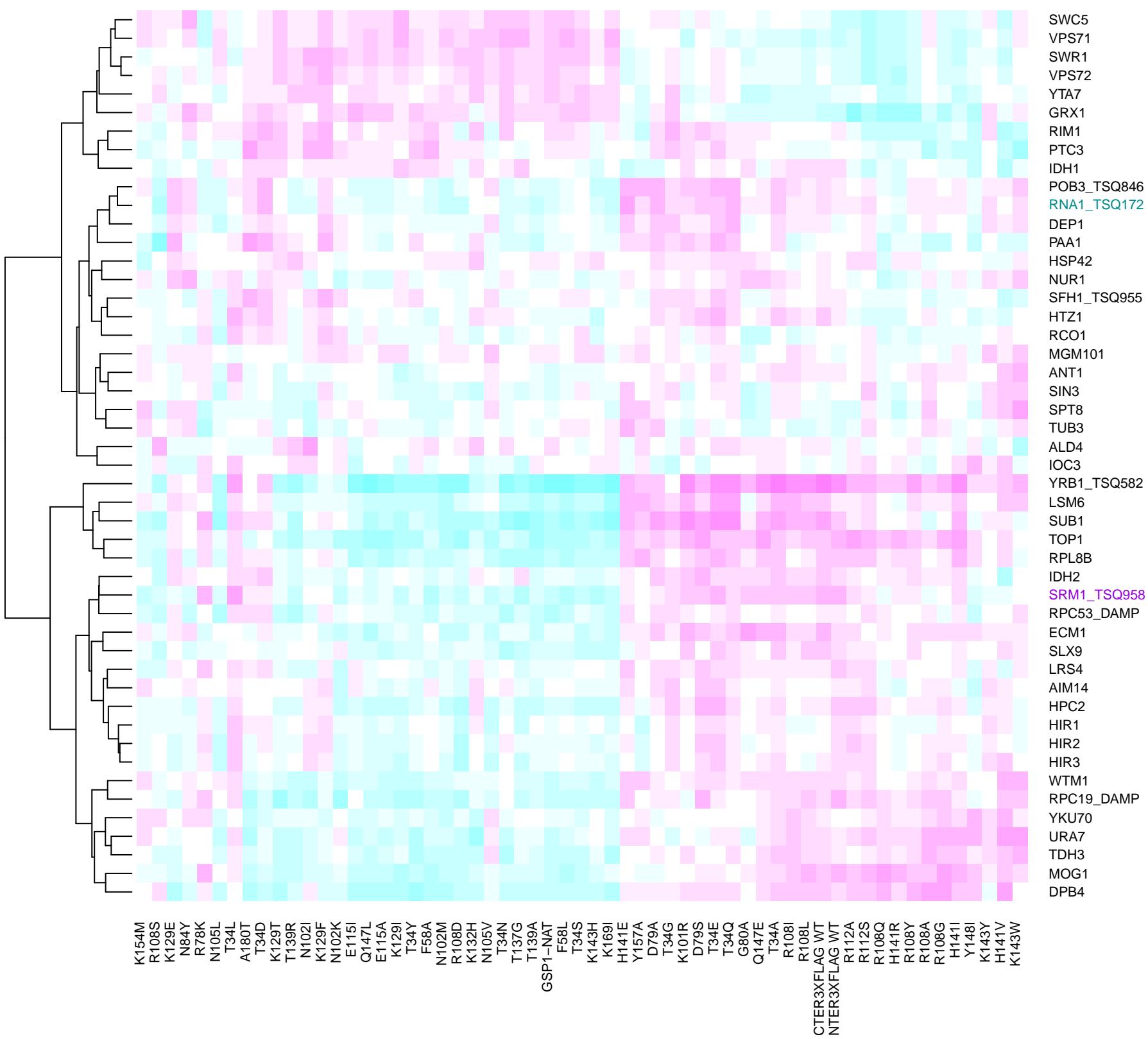


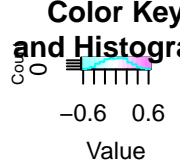
endoplasmic reticulum_GO_30_10



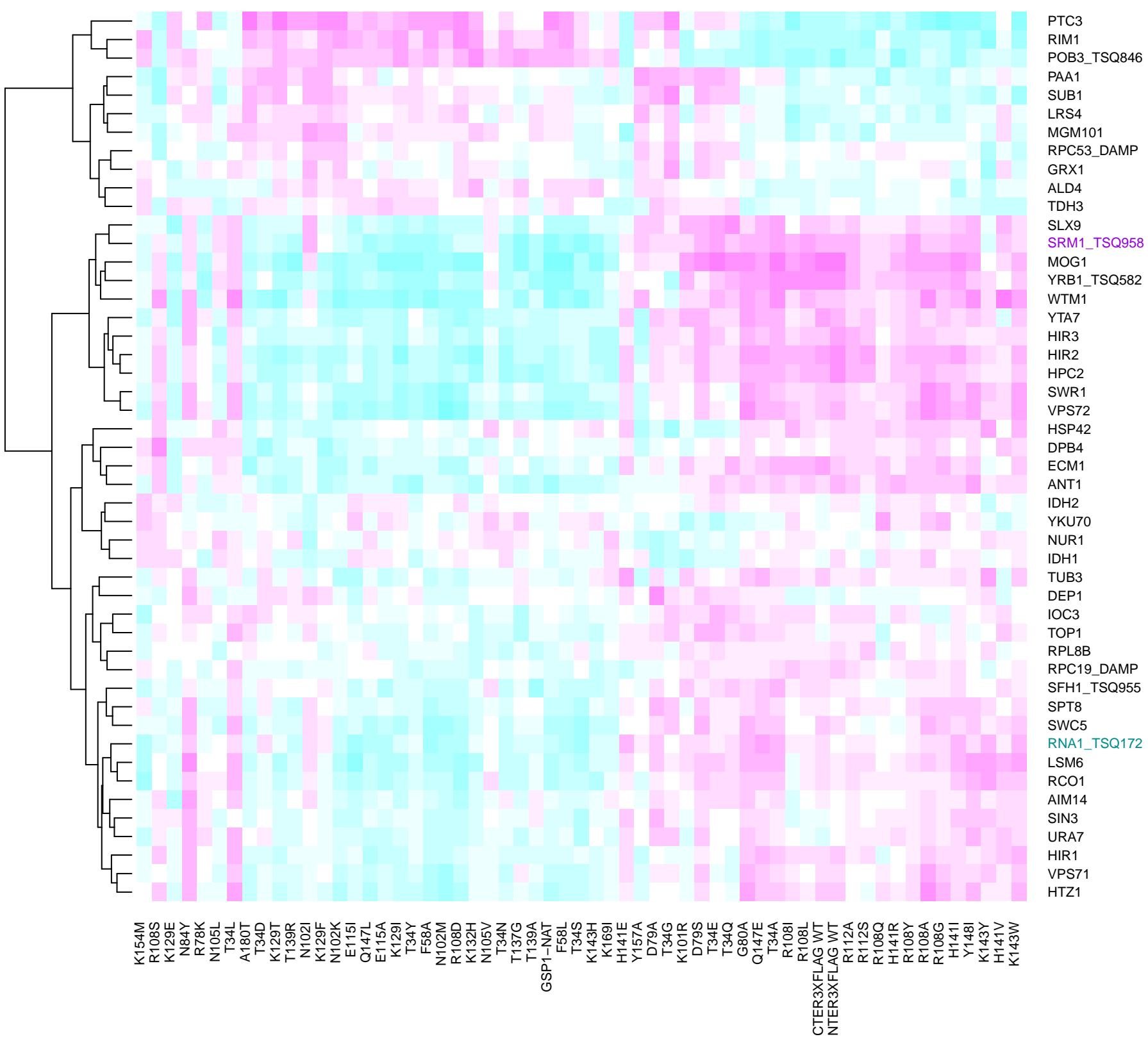


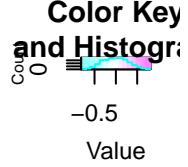
ER_GO_30_10



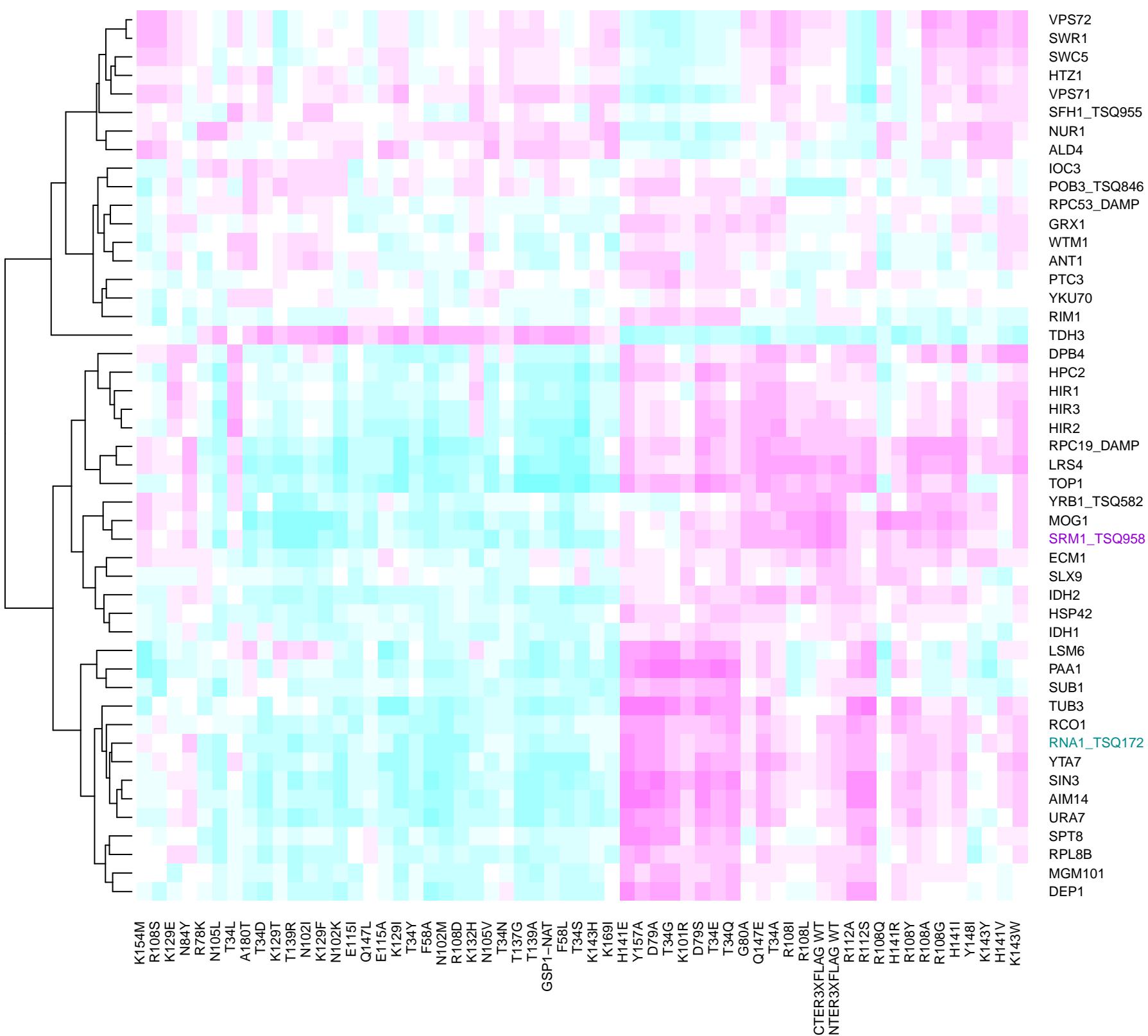


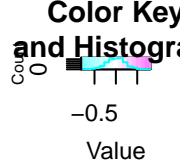
mitochondrion_GO_30_7



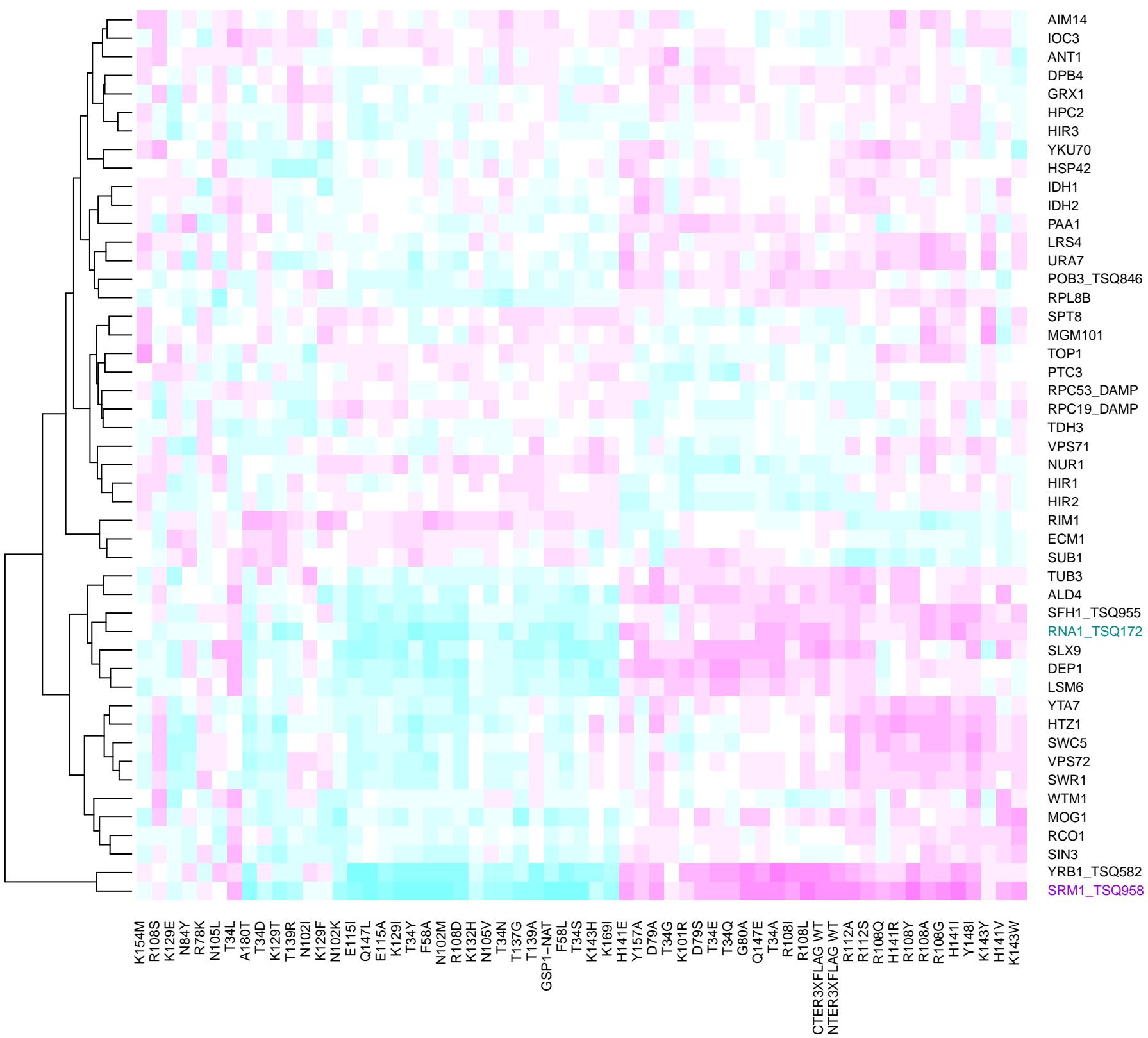


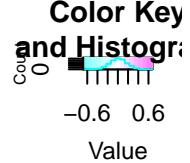
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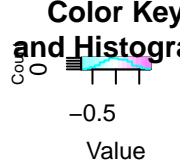
mitochondria and respiration_GO_30_15



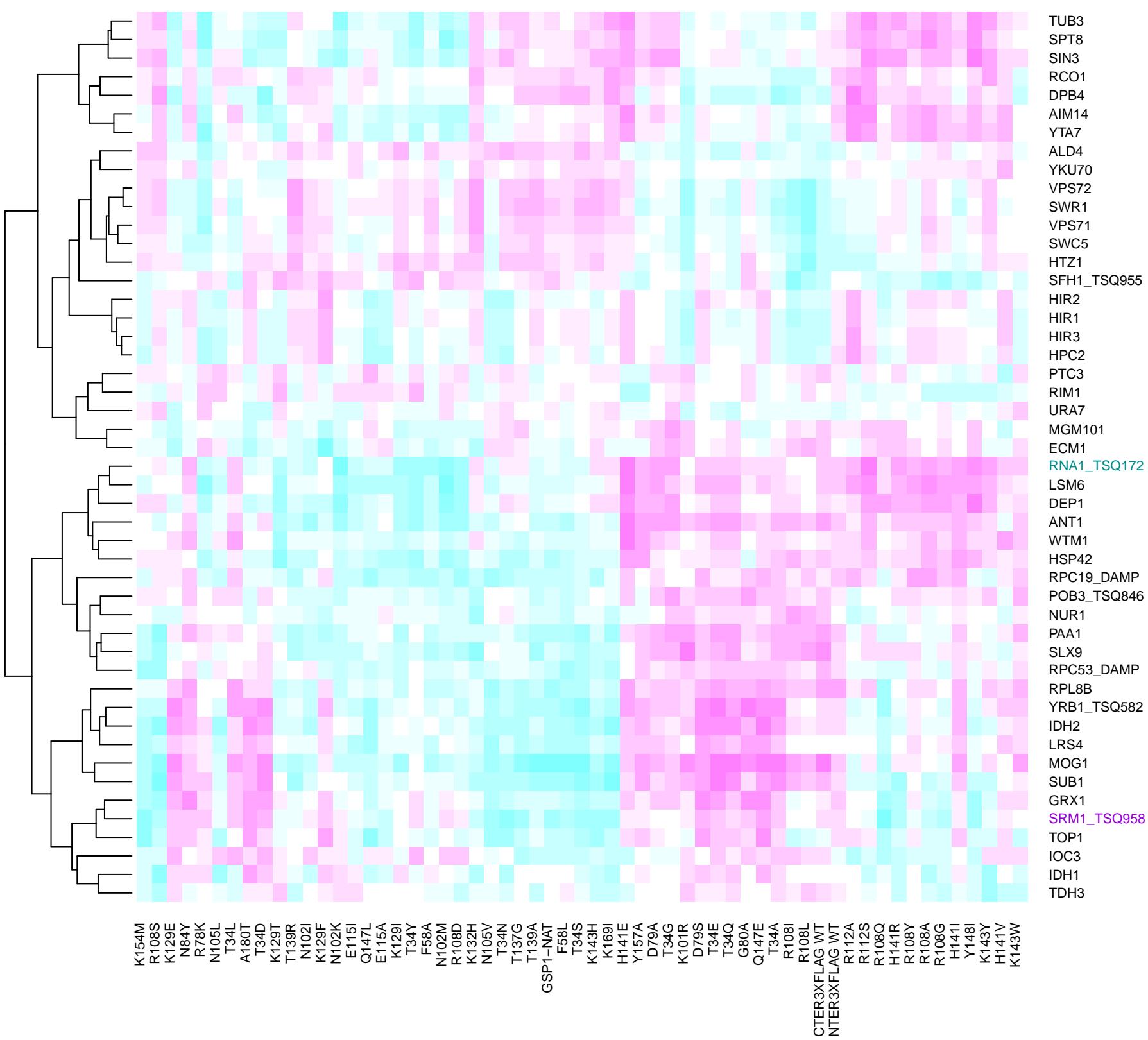


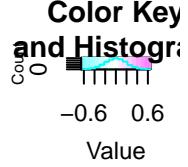
cell cycle_GO_30_3



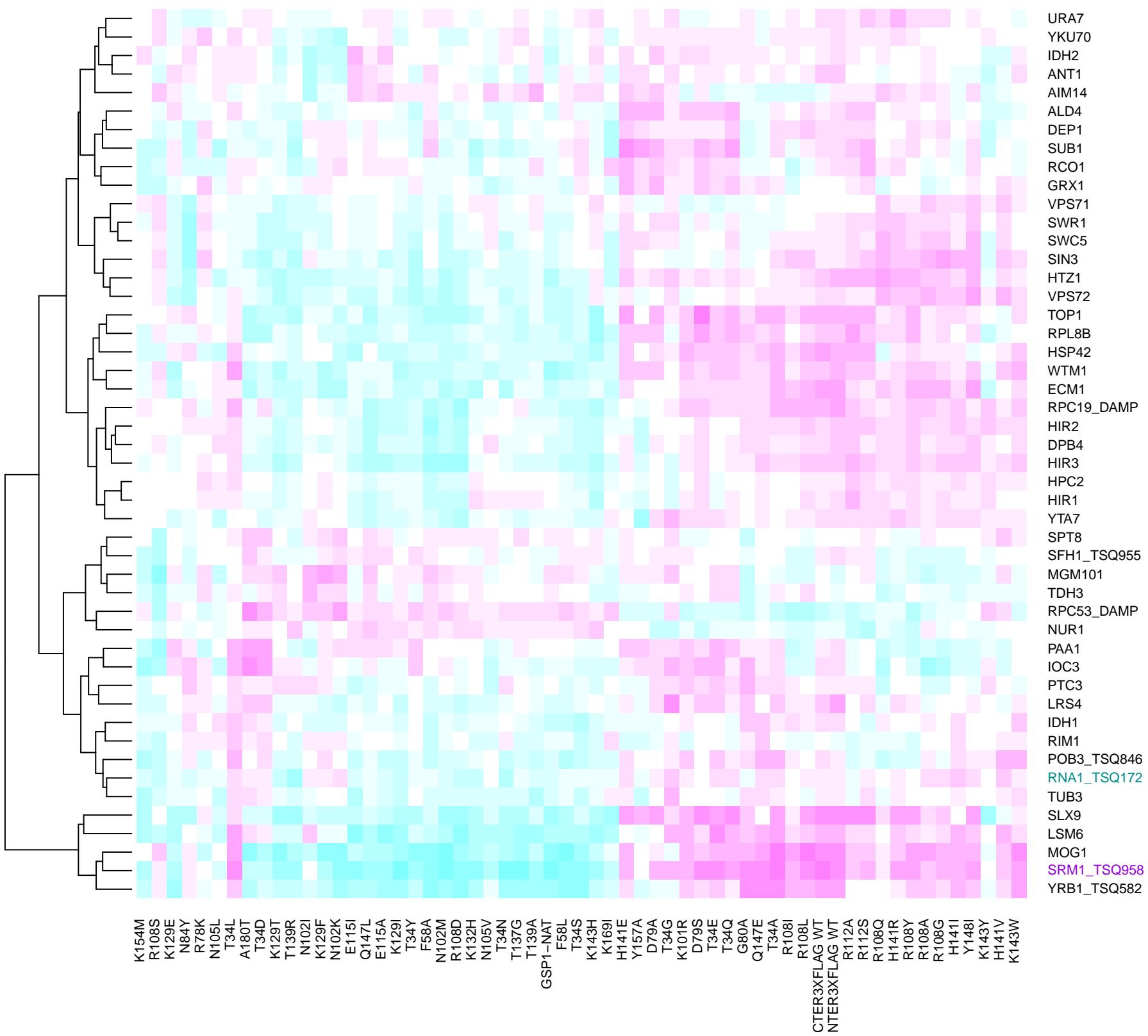


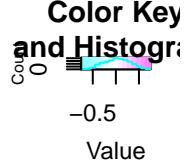
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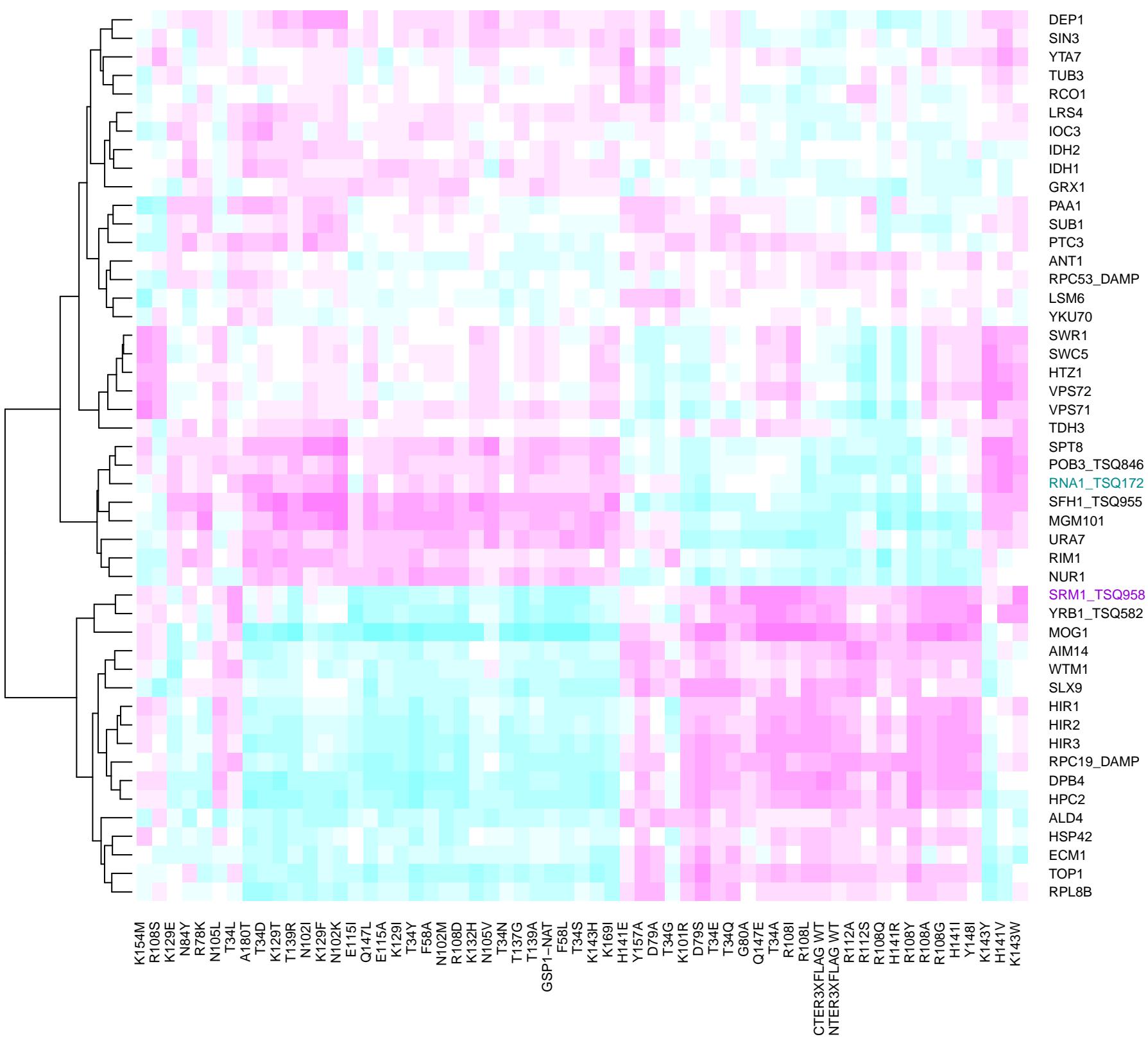


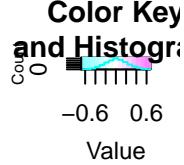
ion transport_GO_30_2





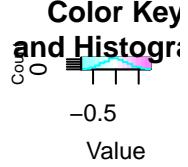
transmembrane transport_GO_30_4



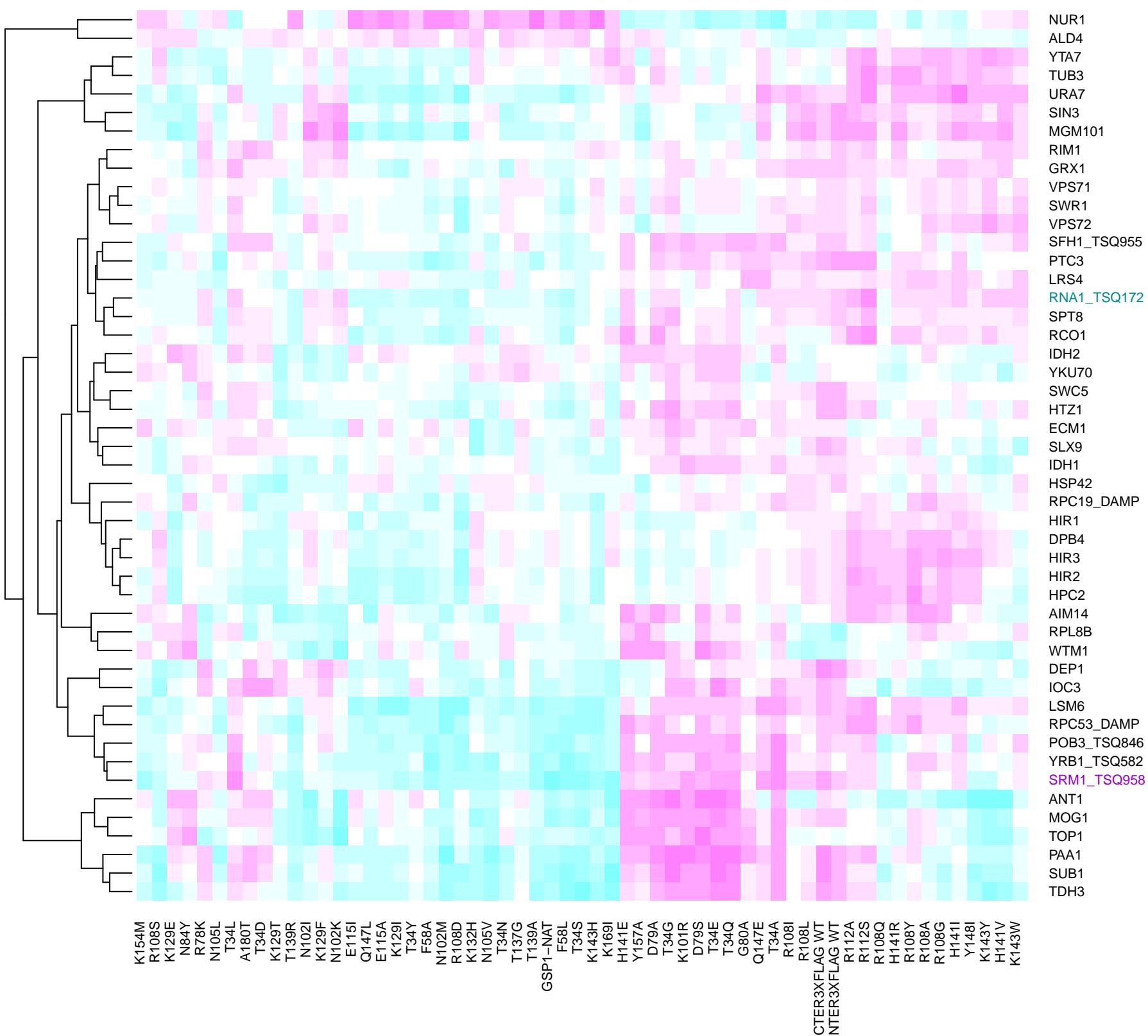


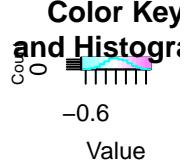
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mitochondrion_GO_30_13

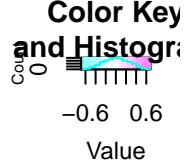




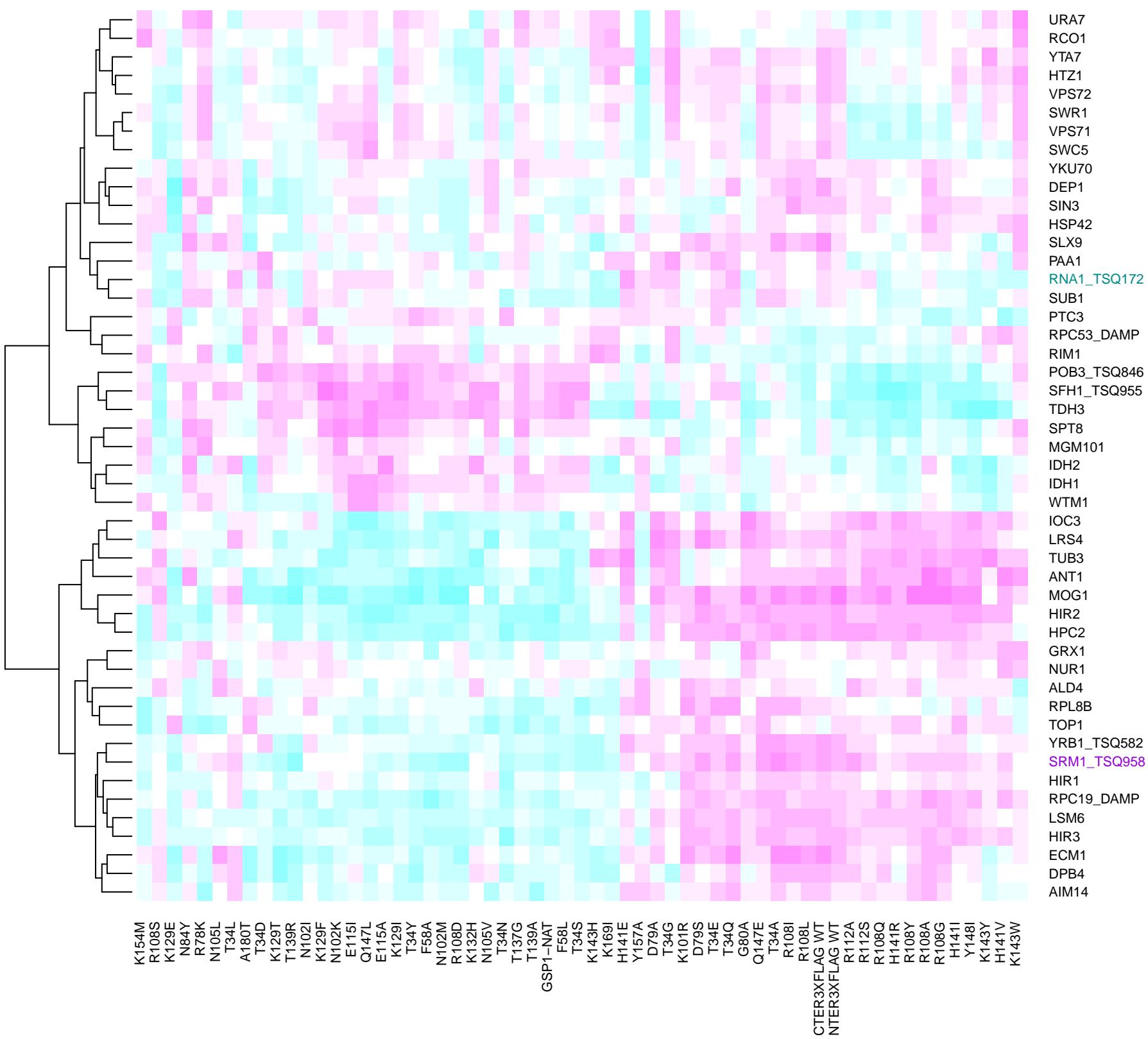
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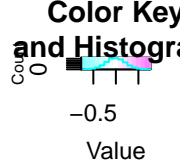


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PAA1
GRX1
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ALD4
HTZ1
LRS4
SWR1
VPS72
PTC3
RIM1
YRB1_TSQ582
RNA1_TSQ172
IDH2
WTM1
RPL8B
TOP1
RPC19_DAMP
SLX9
SPT8
RCO1
DPB4
HIR1
HPC2
HIR3
HIR2
TUB3
SRM1_TSQ958
POB3_TSQ846
YTA7
LSM6
MOG1
YKU70
ECM1
SUB1
RPC53_DAMP
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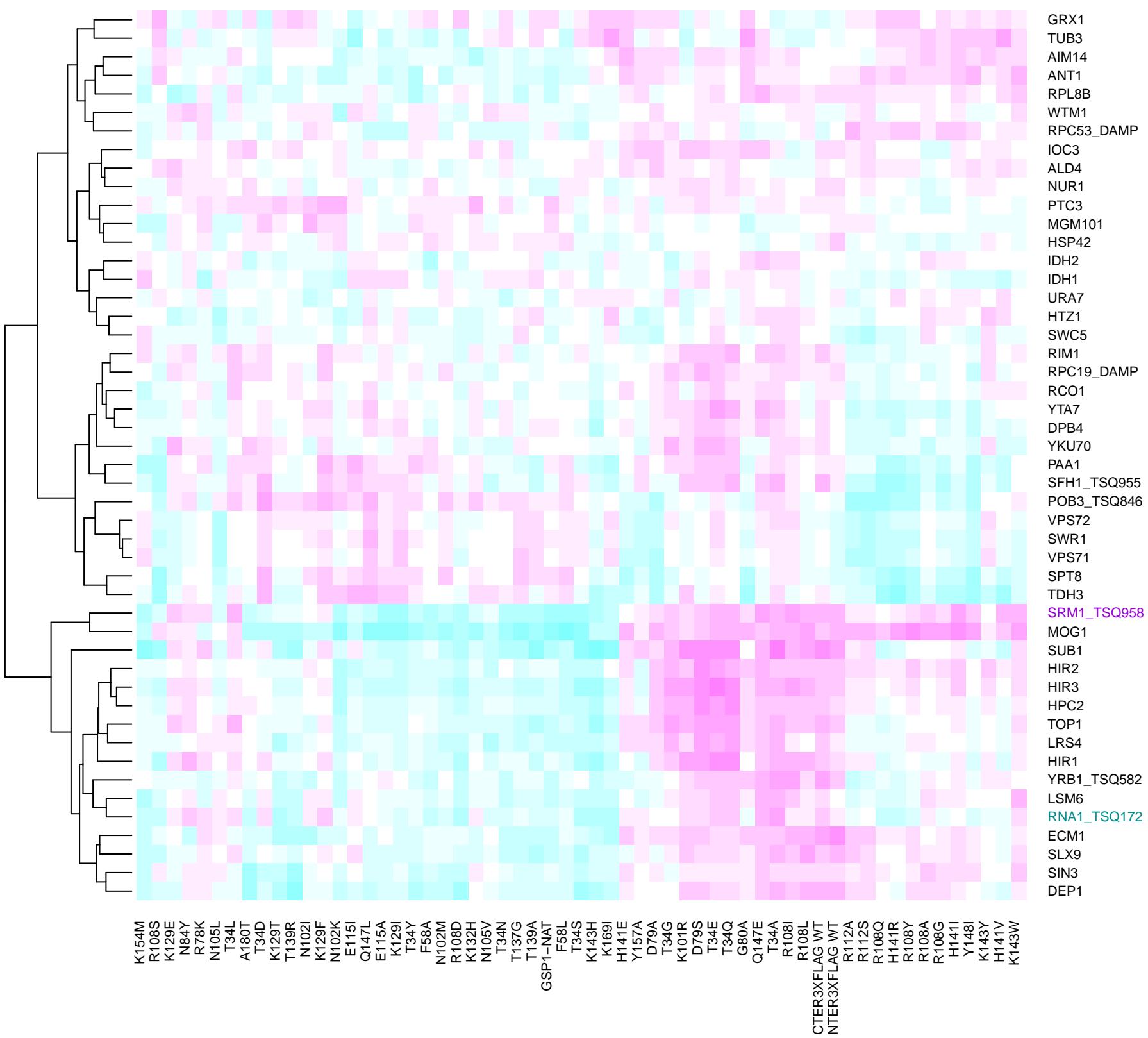


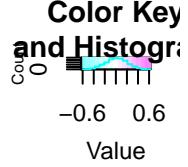
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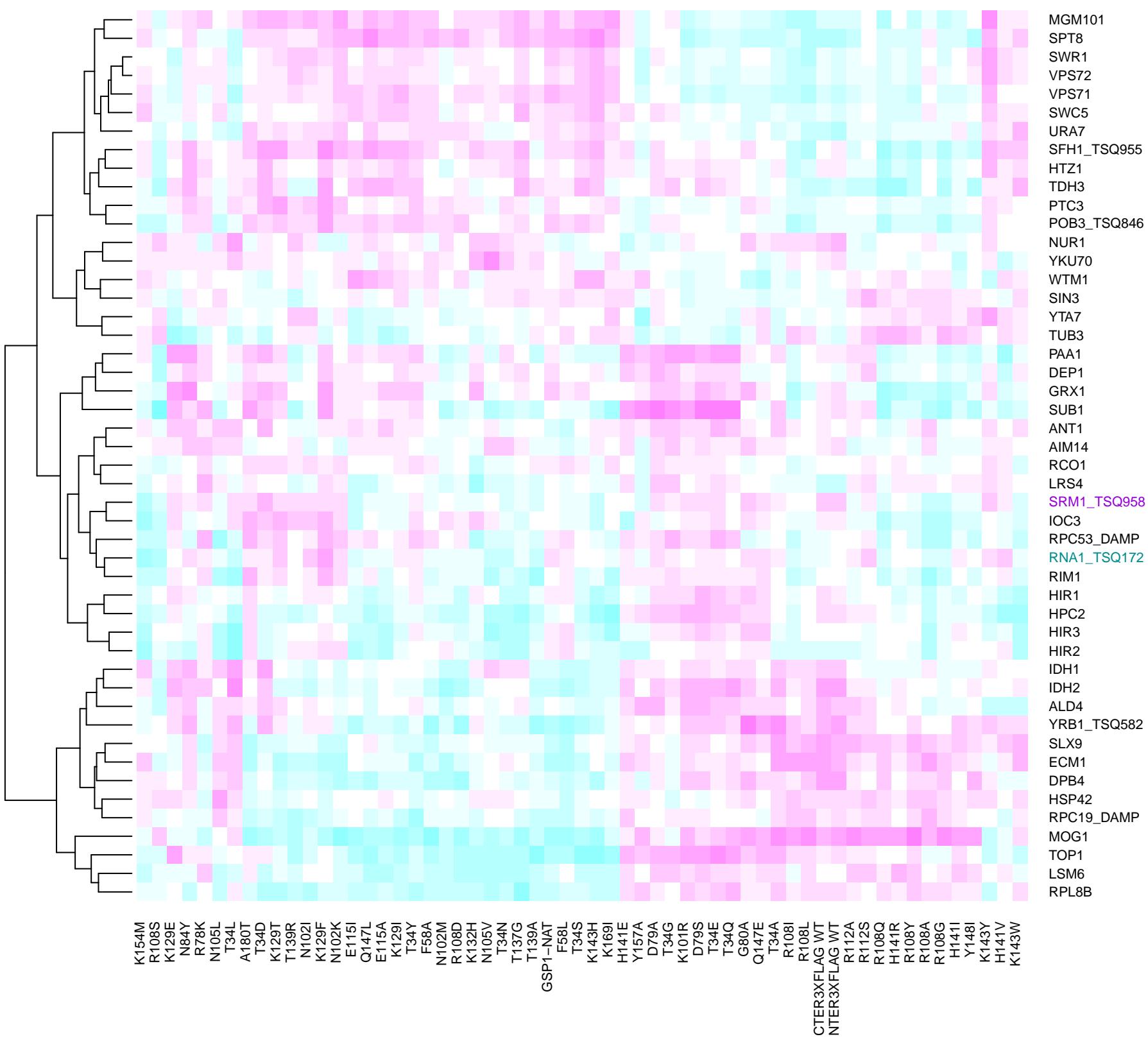


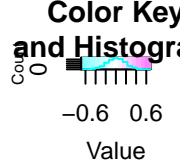
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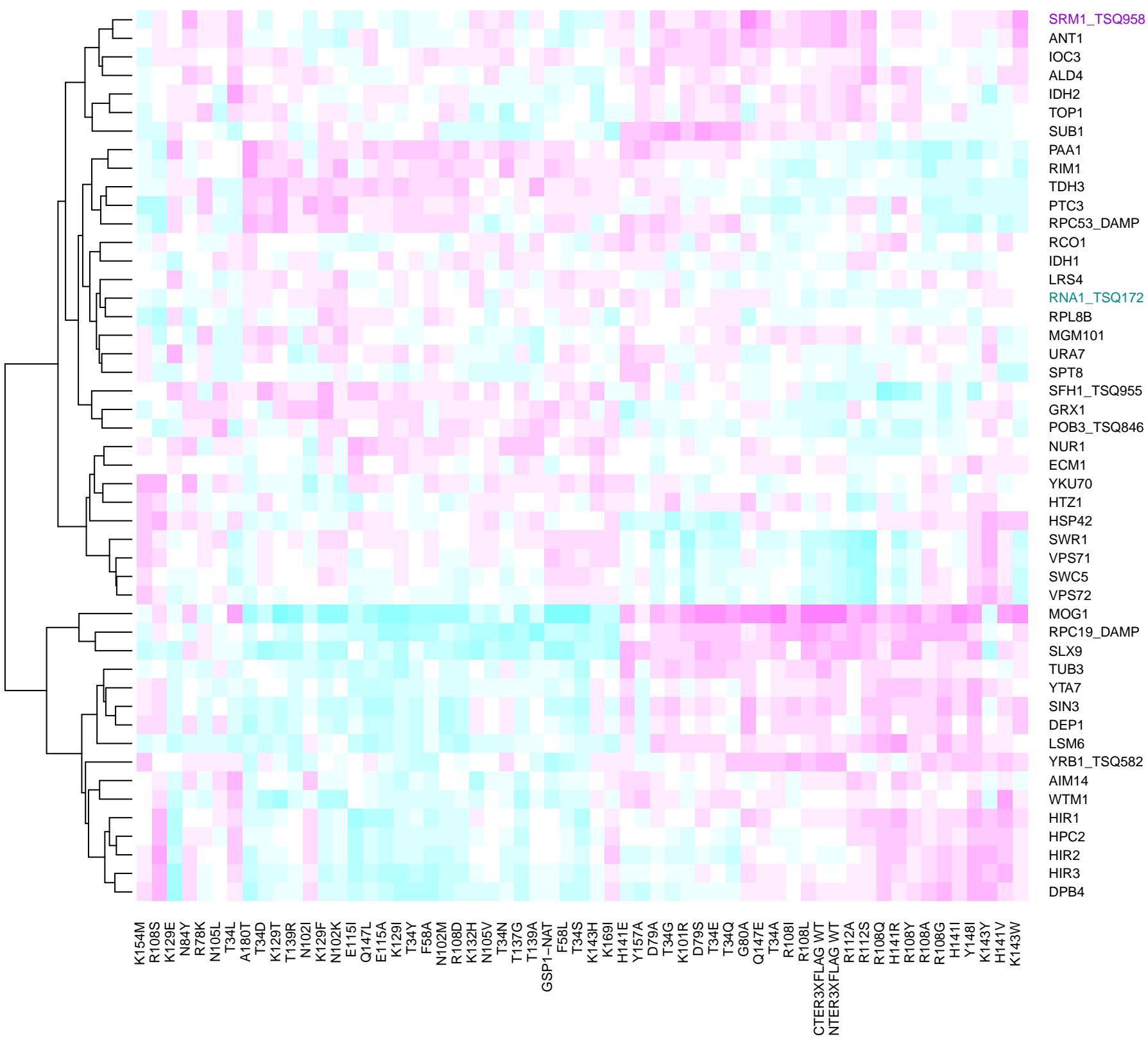


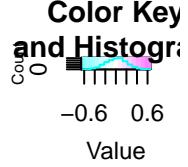
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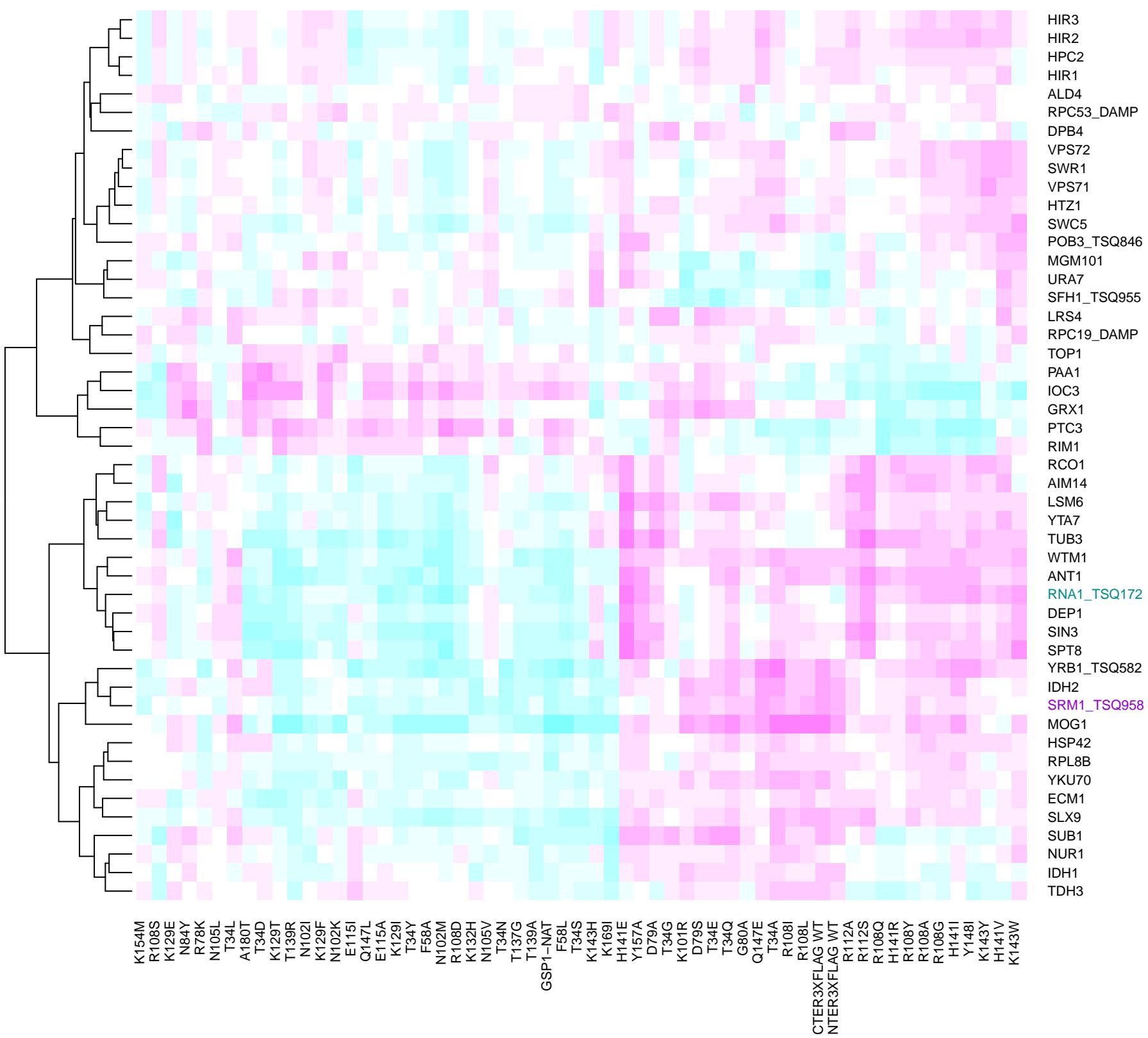


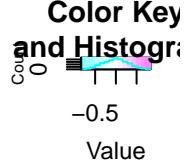
transferase activity, transferring glycosyl groups_GO_30_1



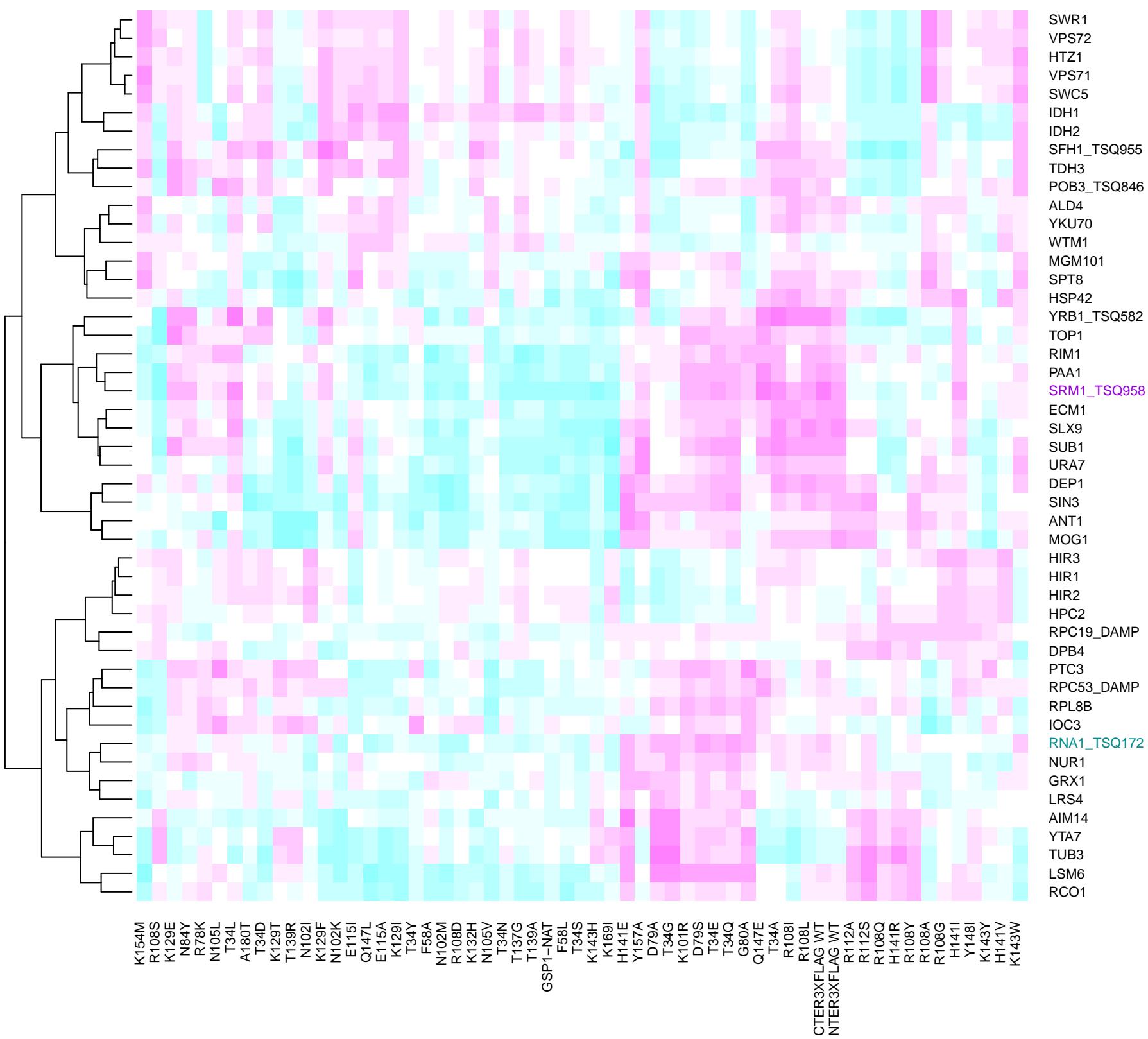


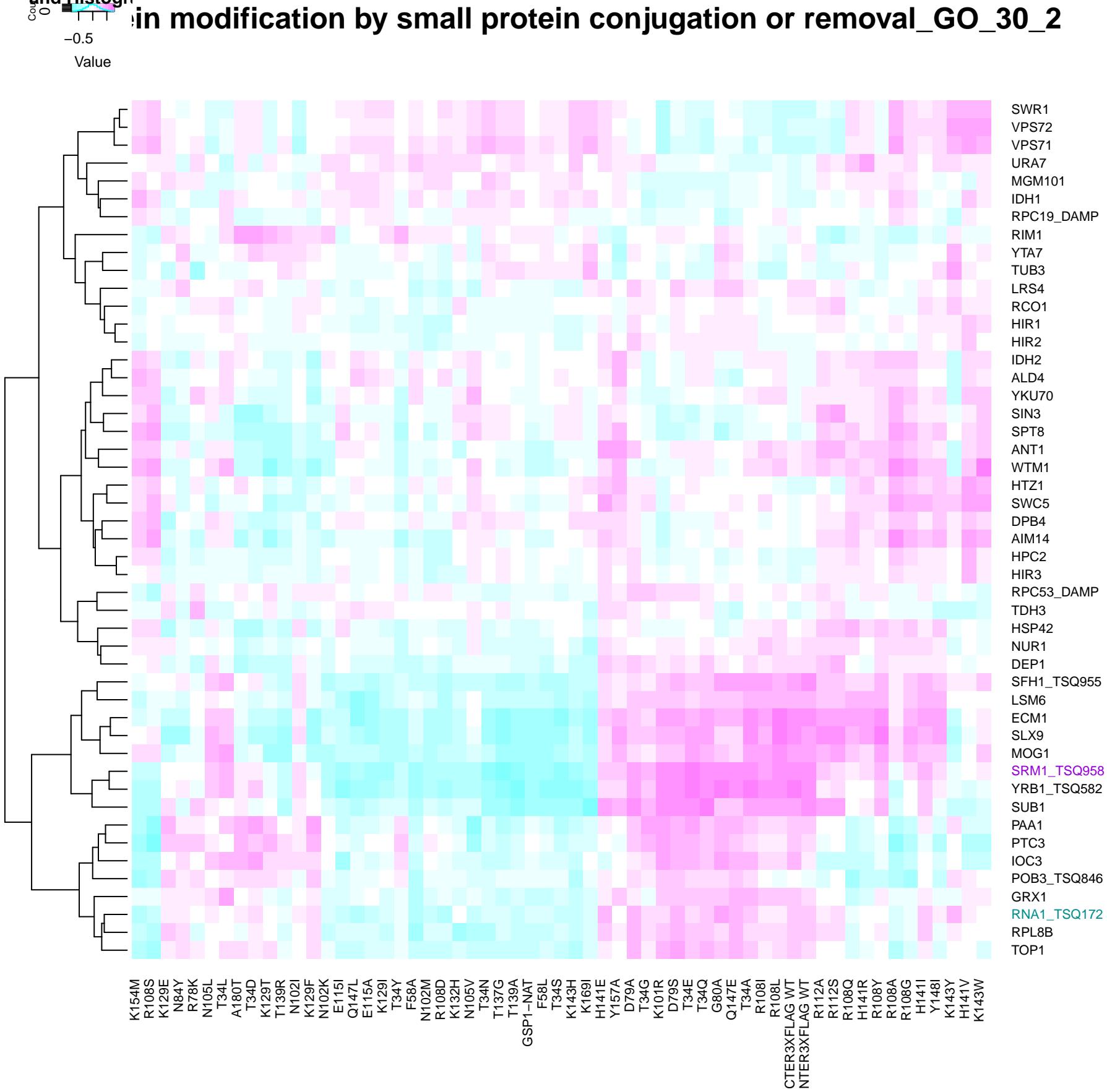
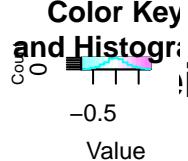
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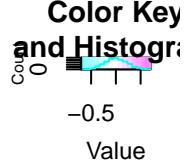




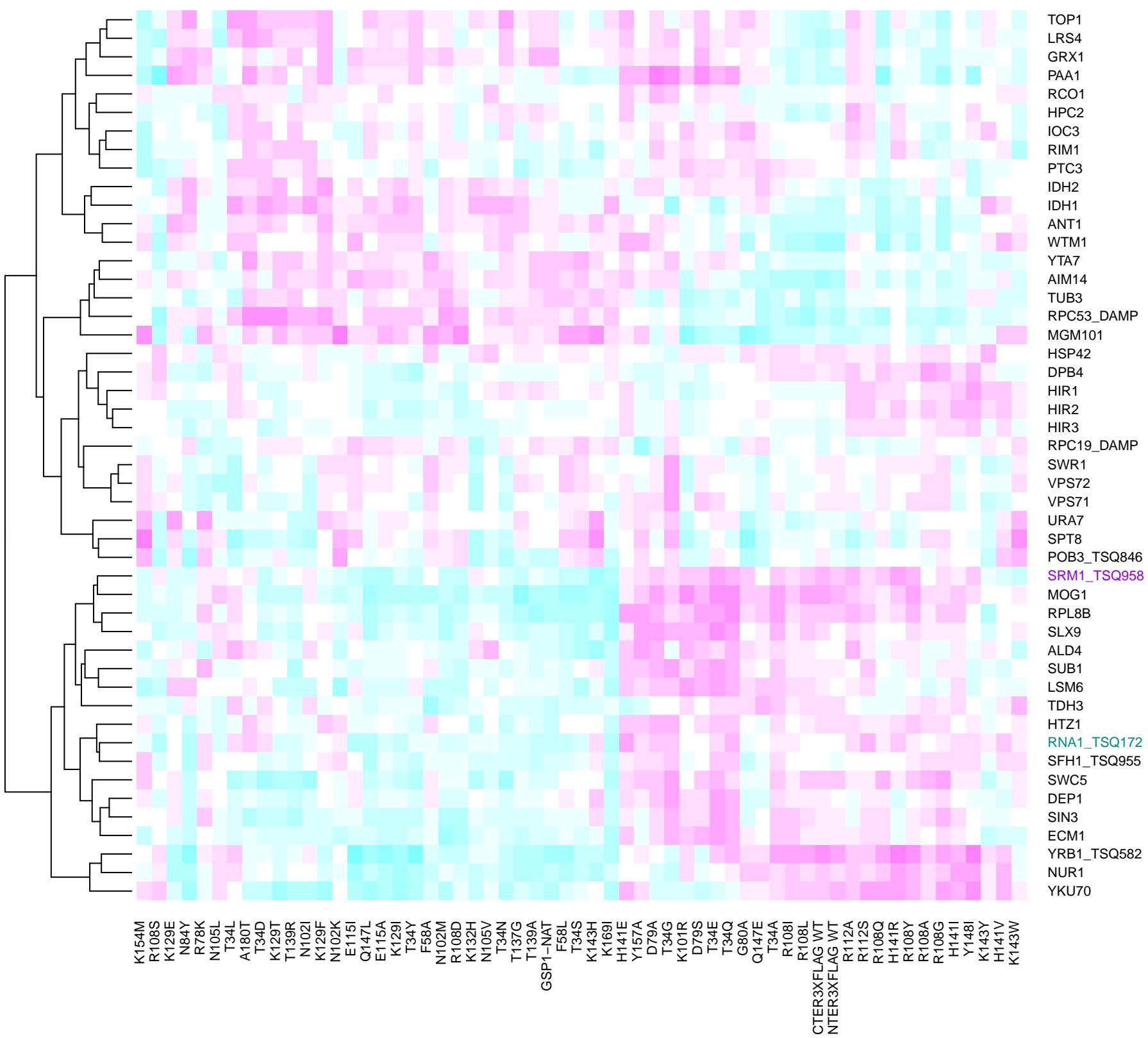
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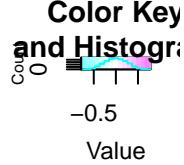




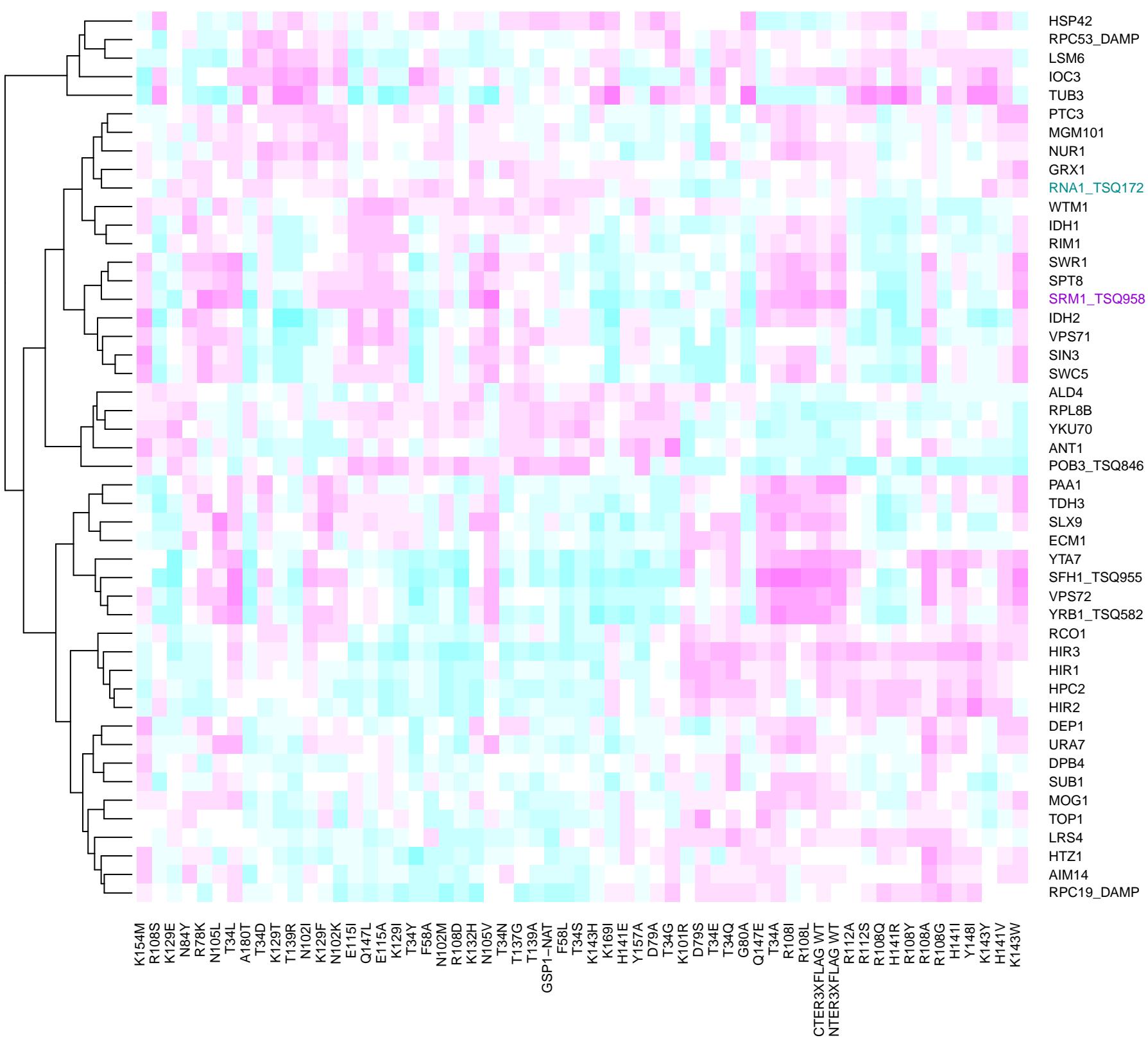


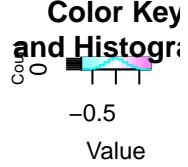
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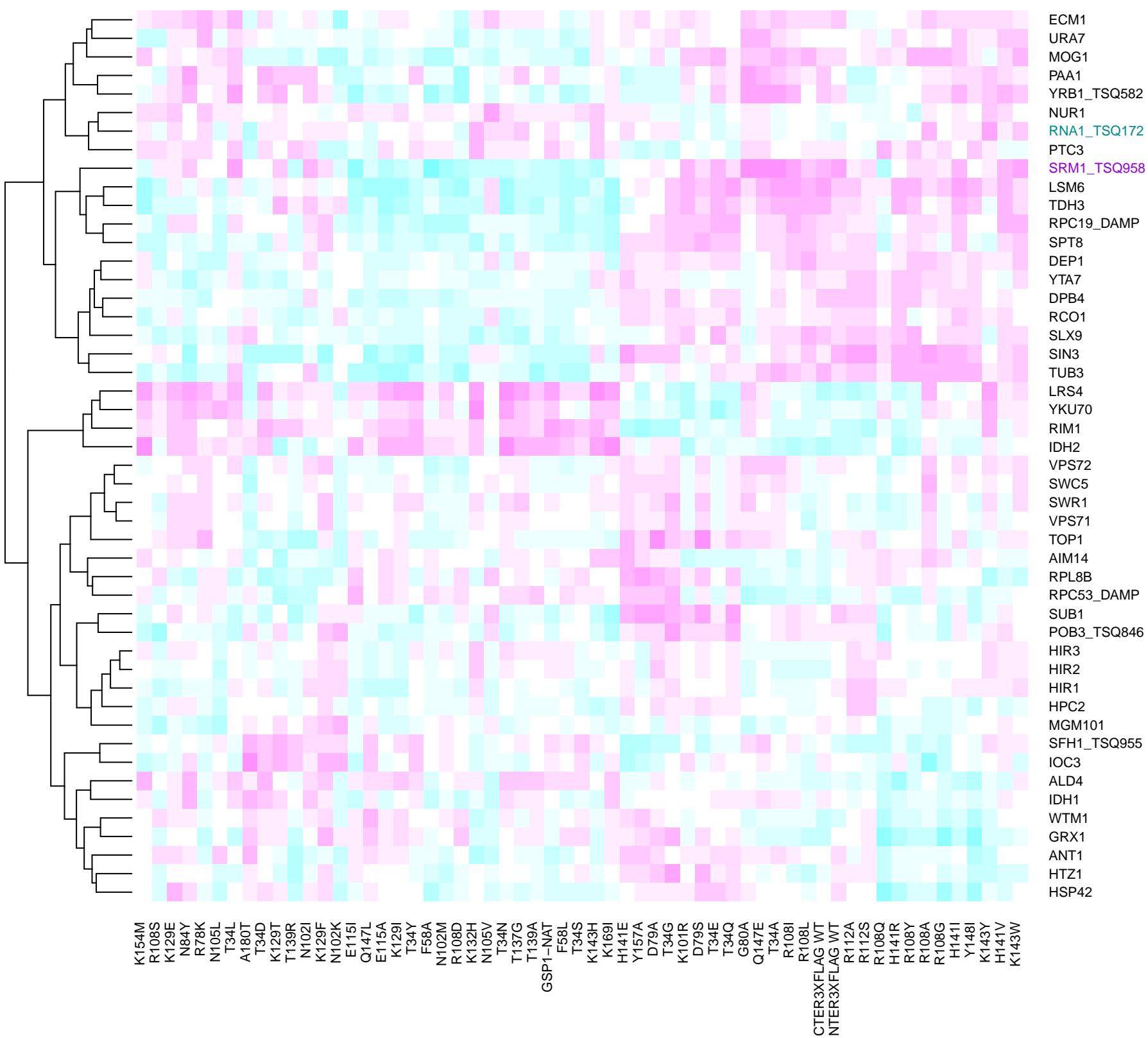


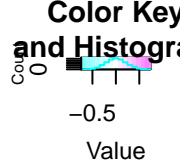
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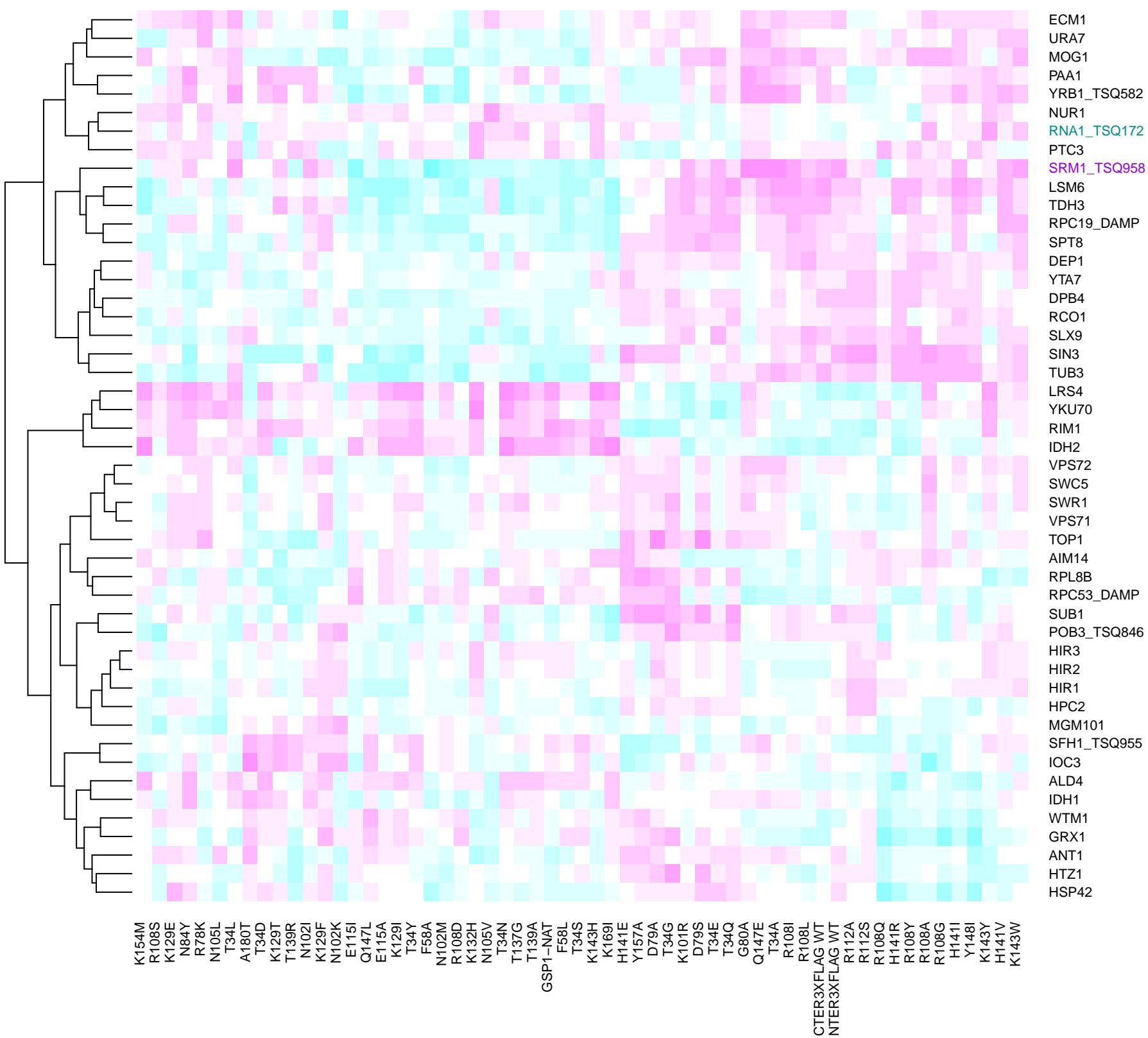


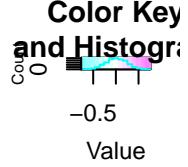
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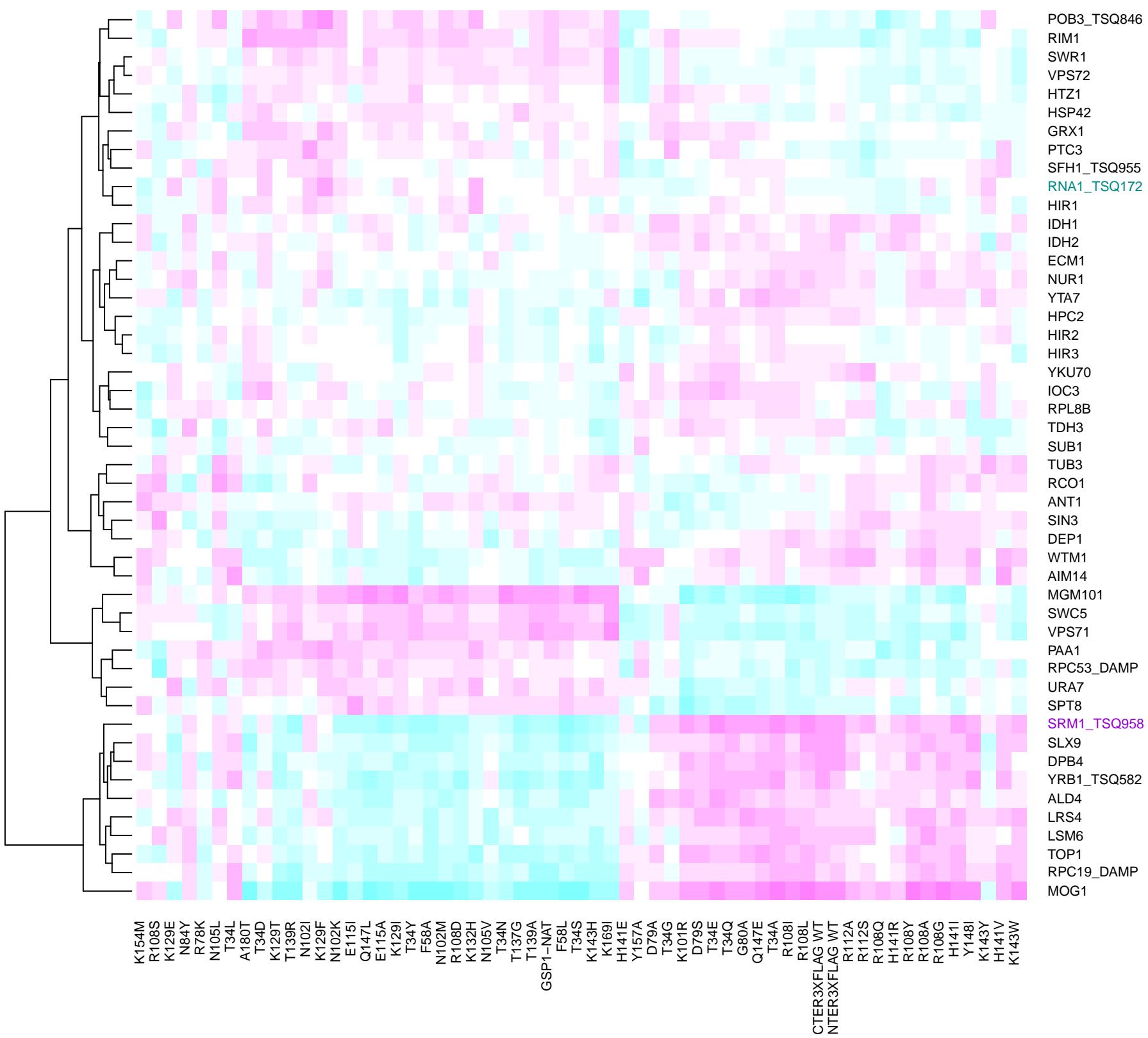


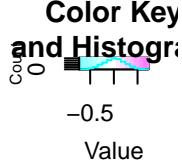
ER_GO_30_7



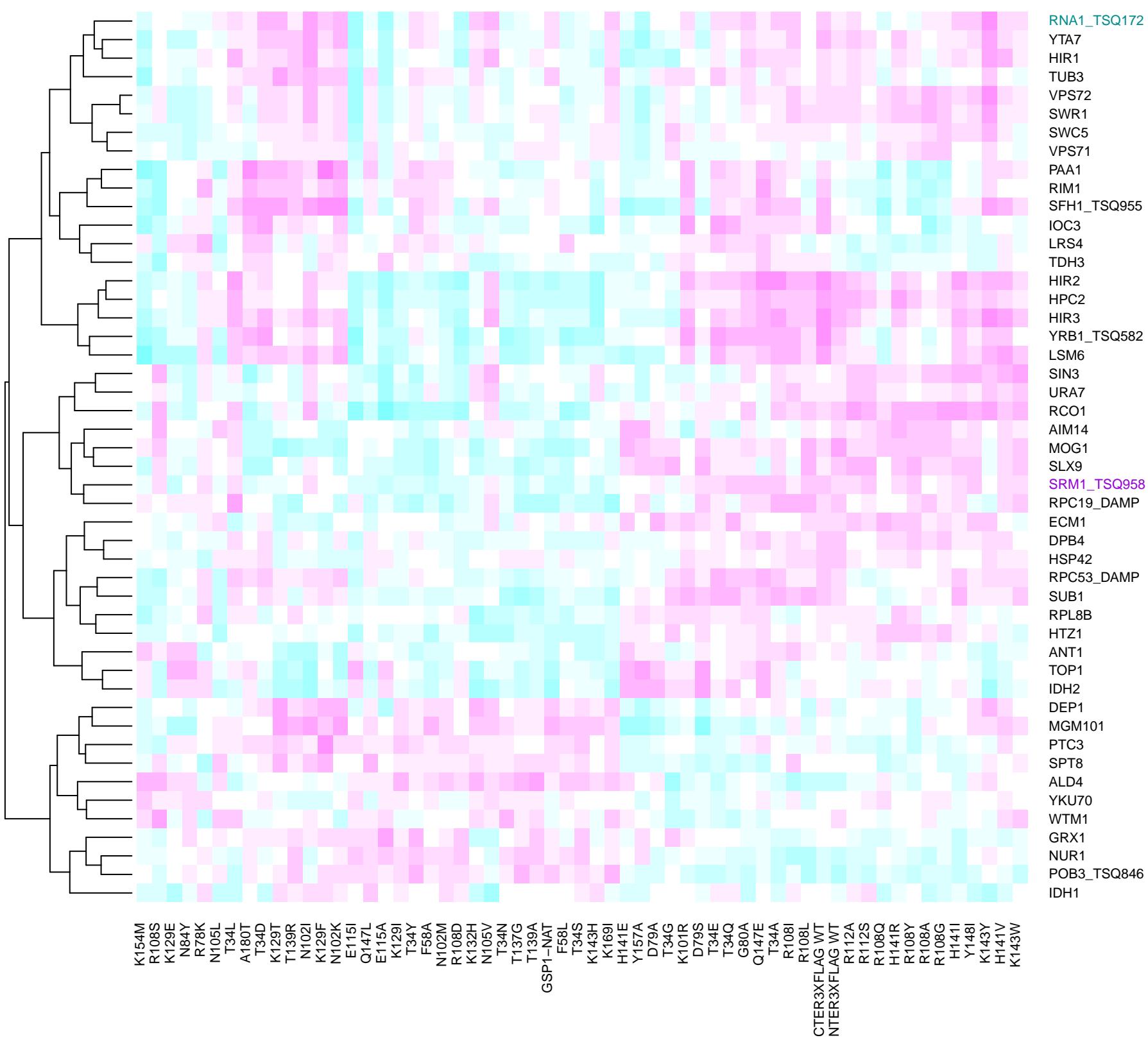


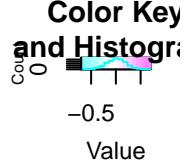
ion transport_GO_30_4



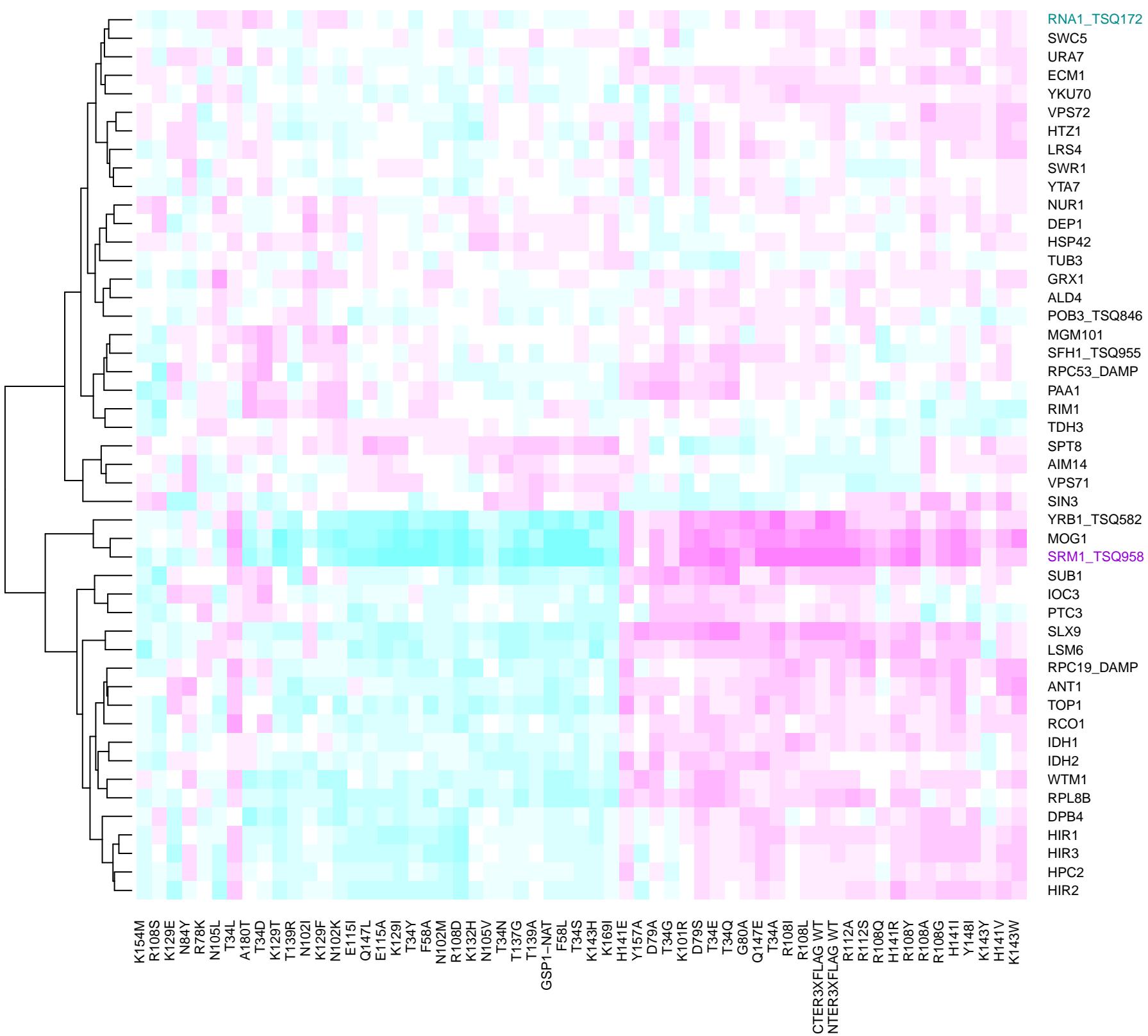


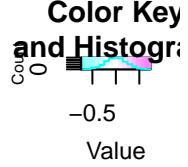
transmembrane transporter activity_GO_30_4



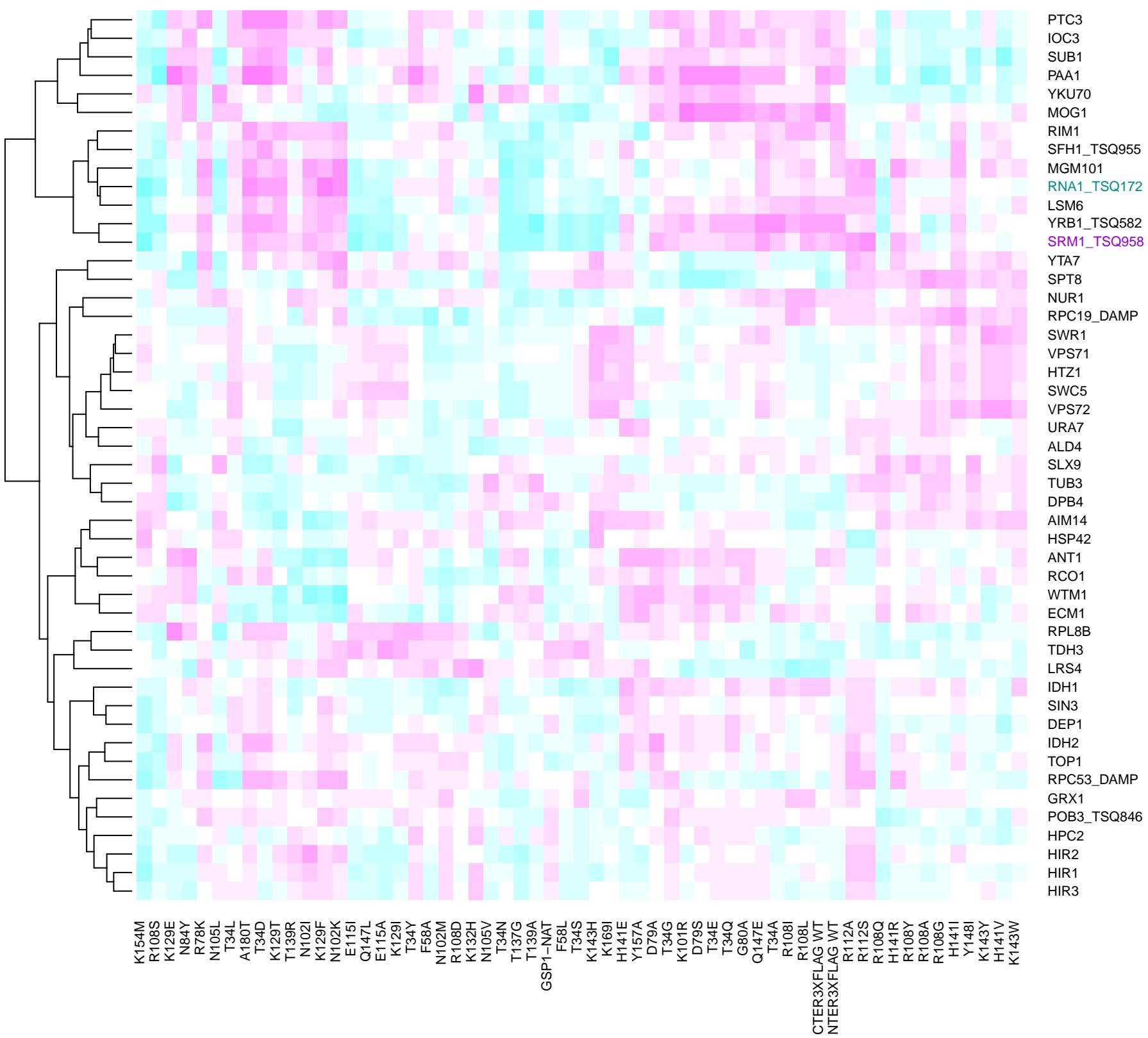


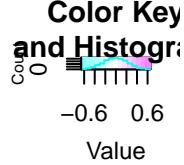
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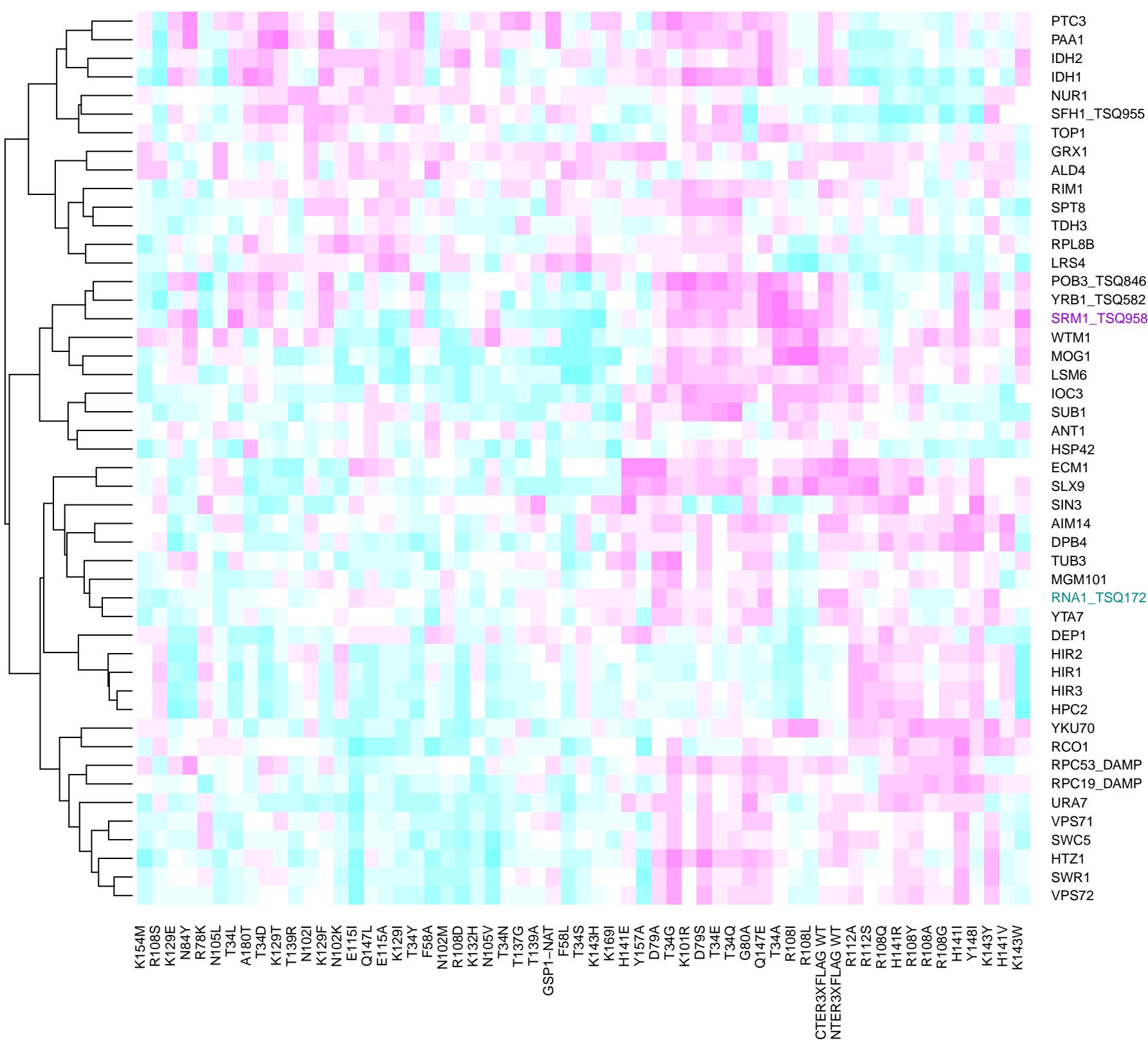


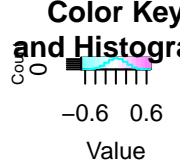
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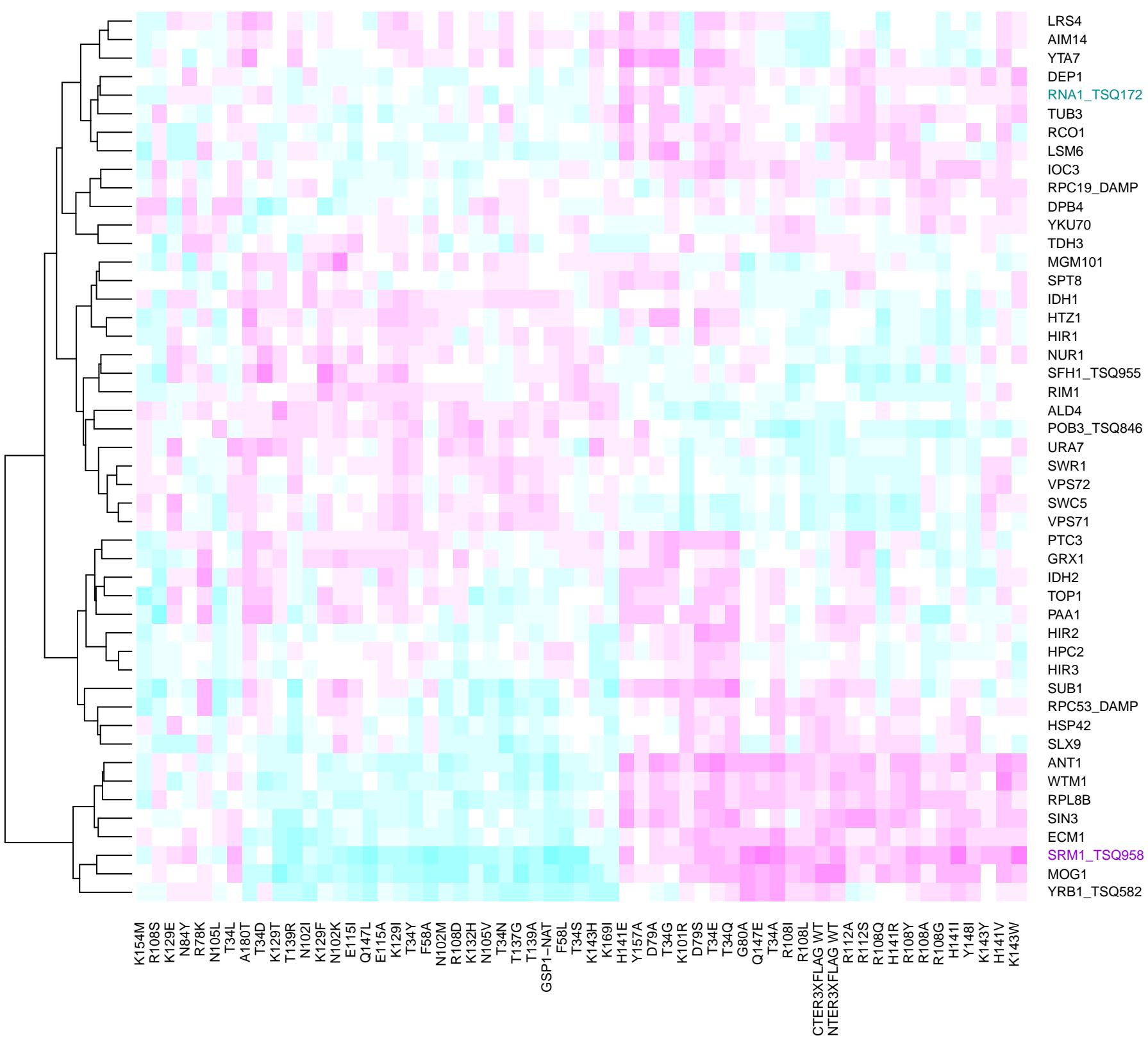


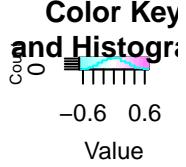
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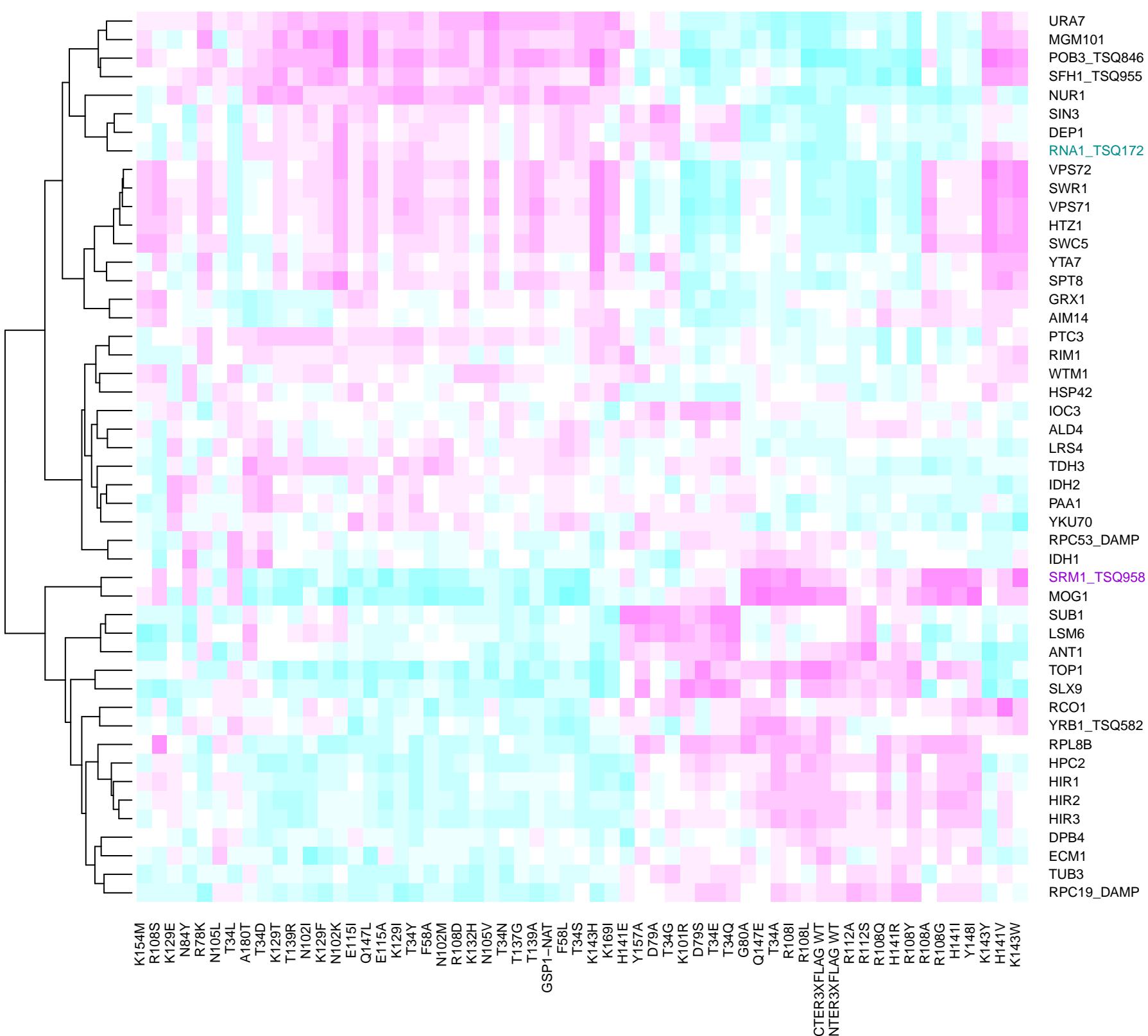


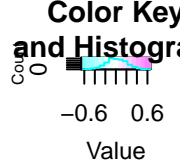
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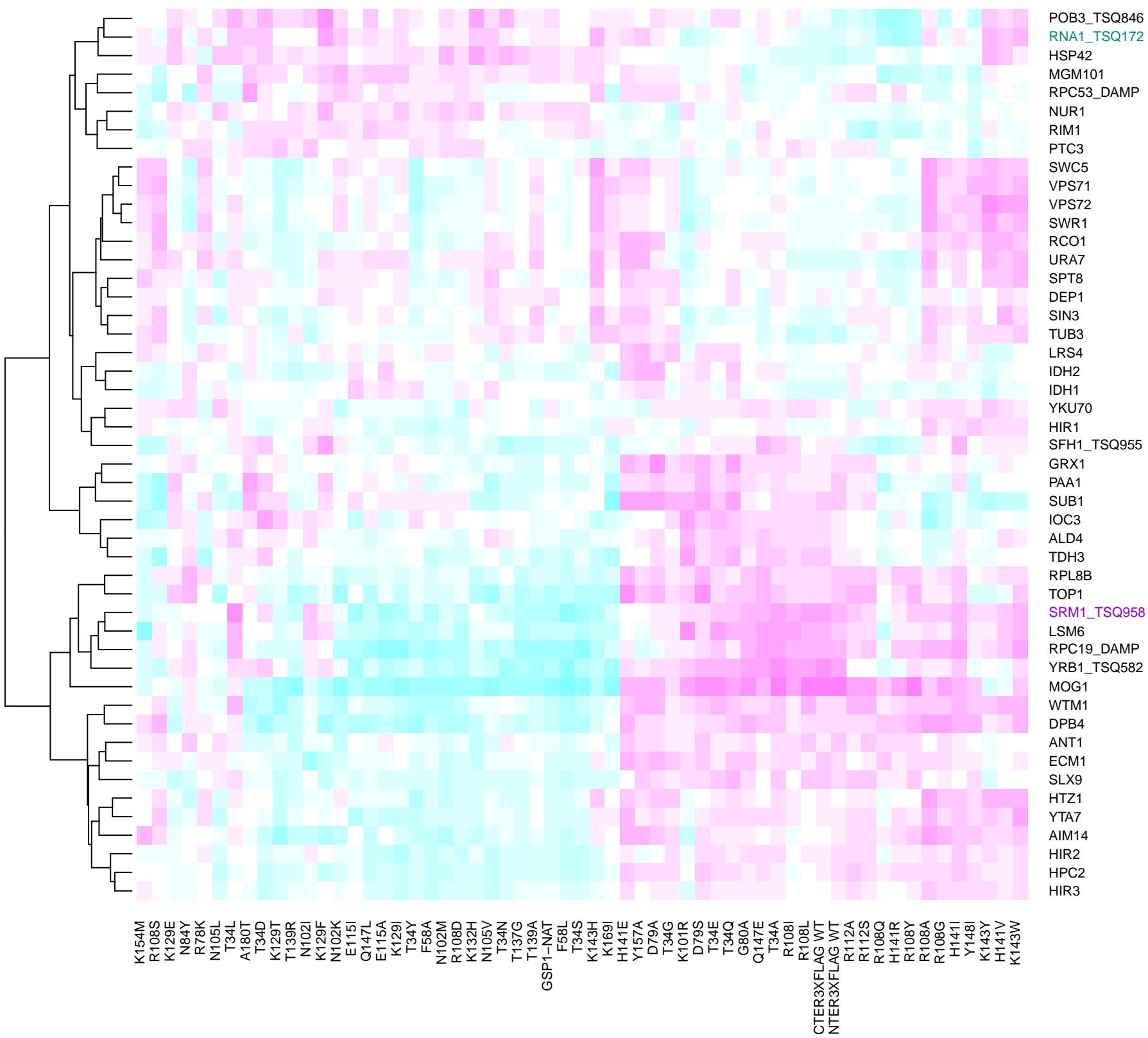


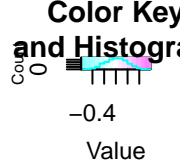
transmembrane transporter activity_GO_30_5



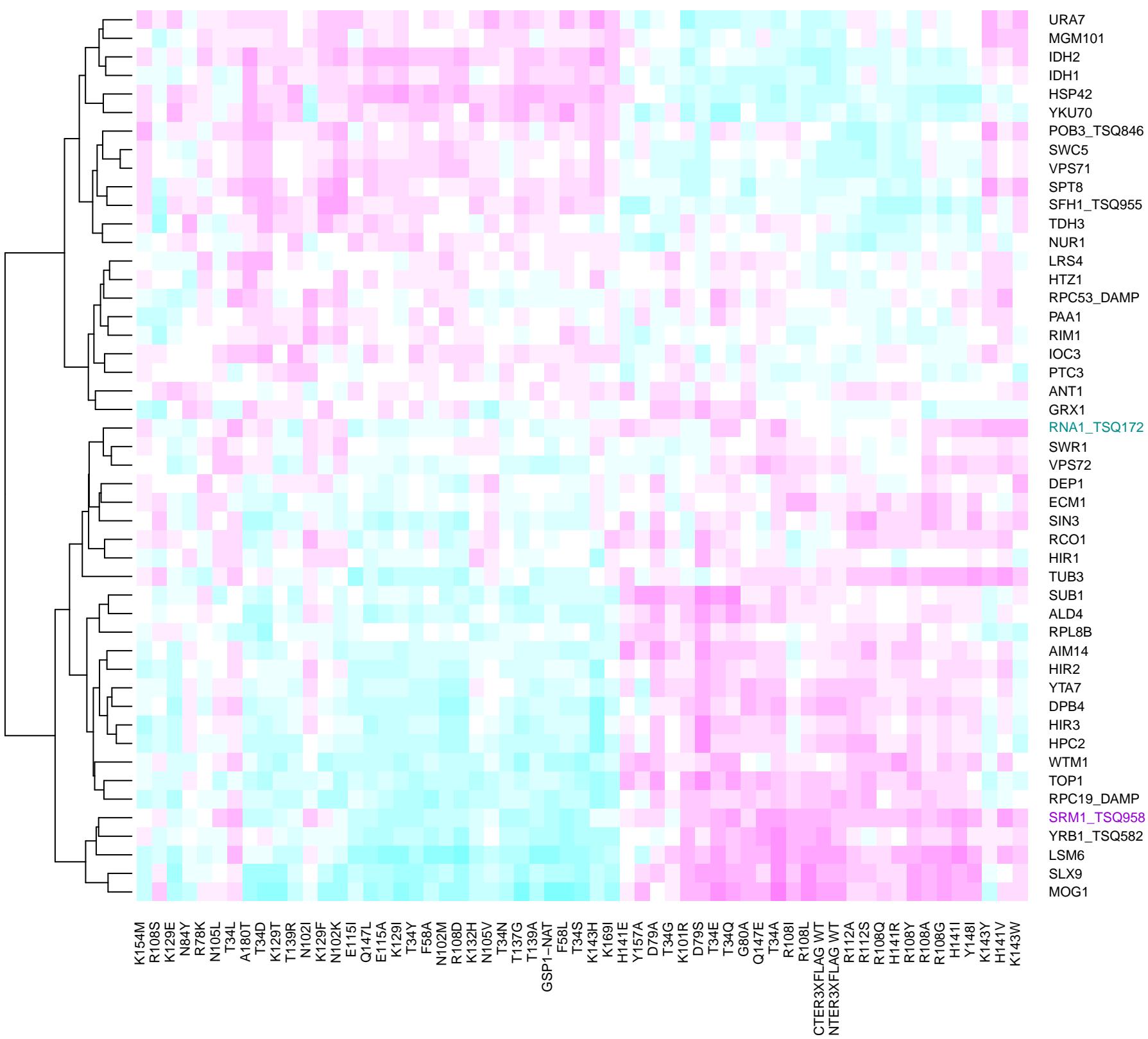


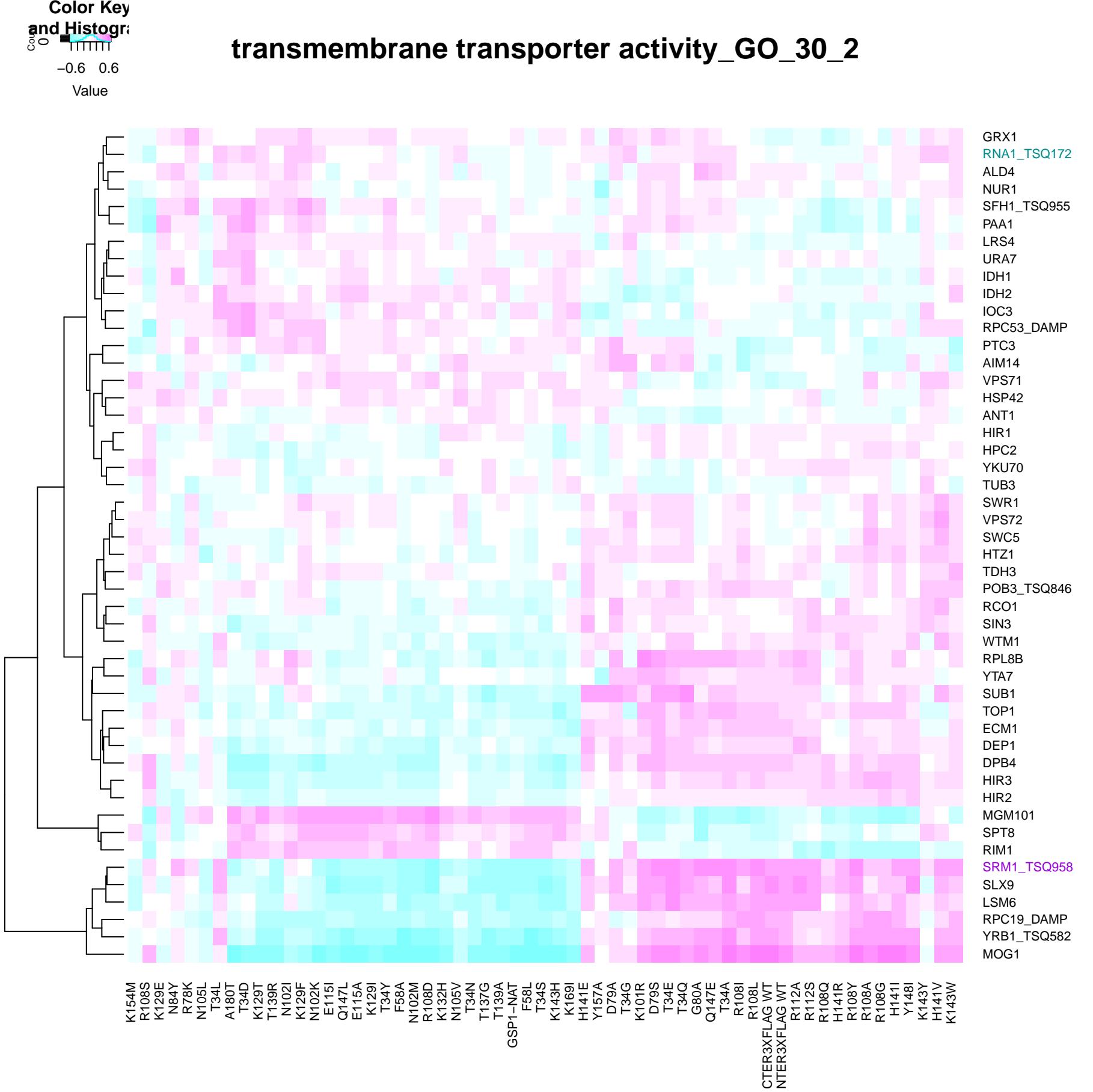
regulation of translation

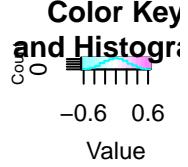




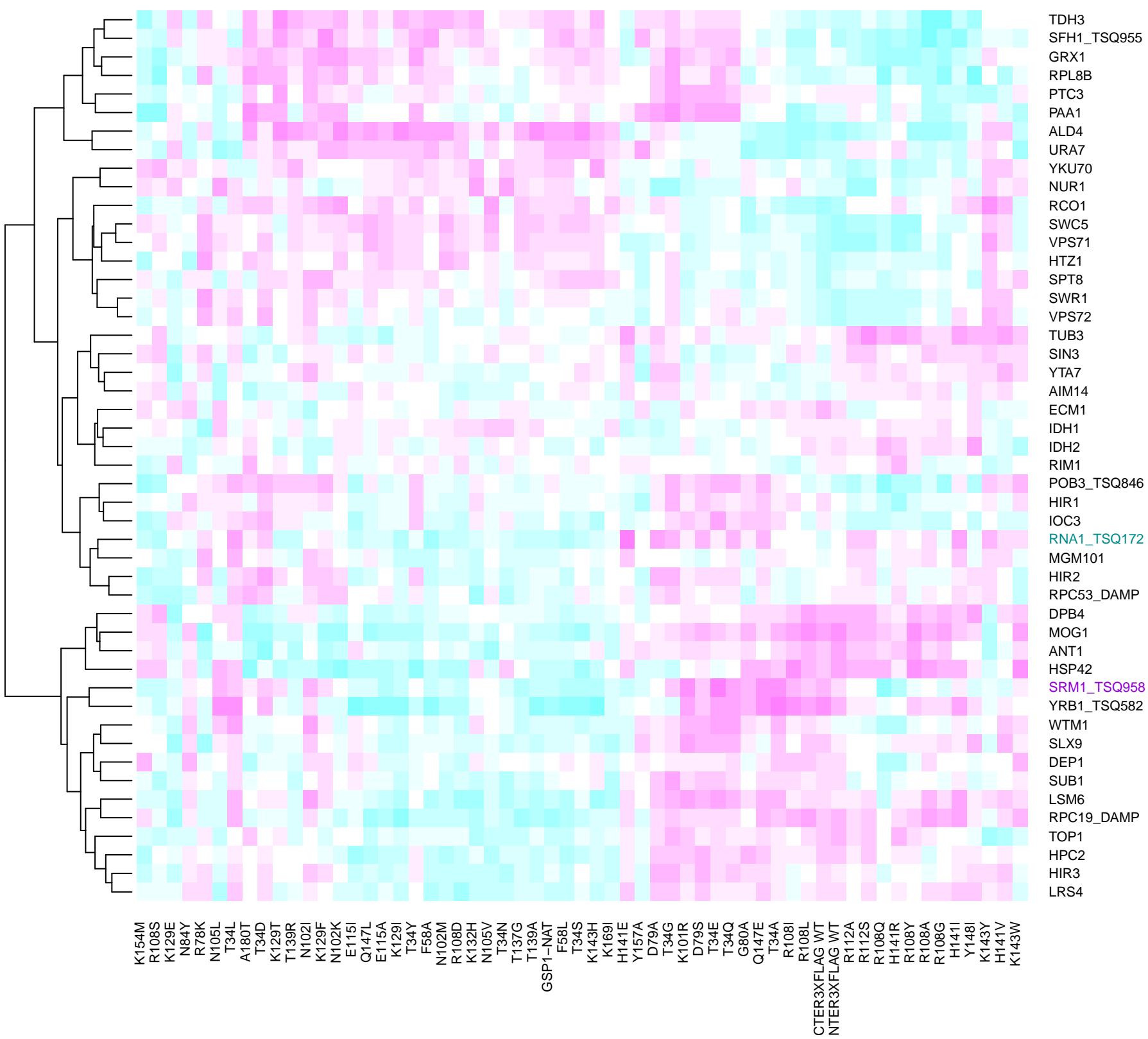
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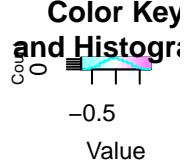




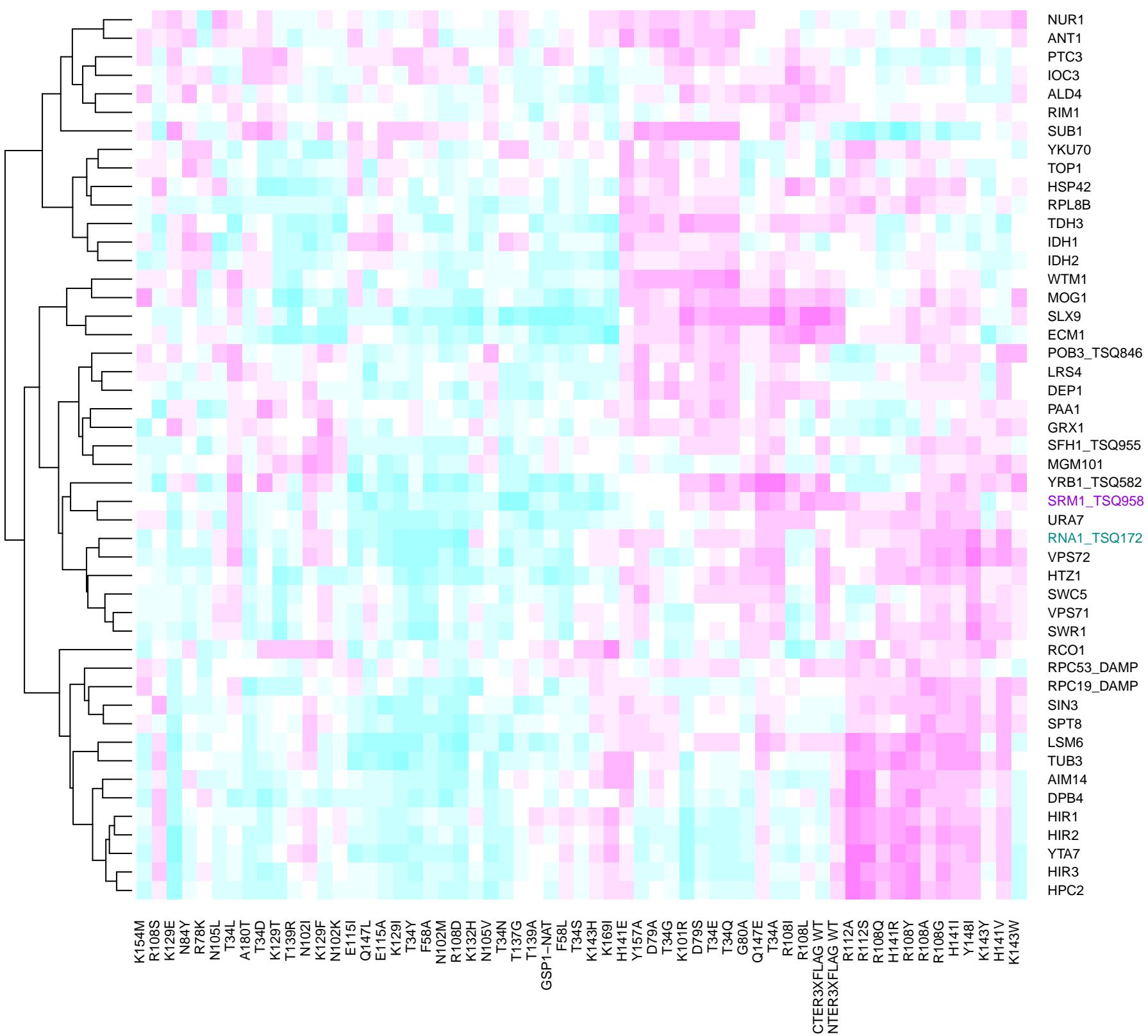


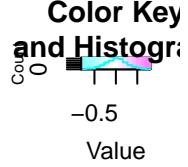
generation of precursor metabolites and energy_GO_30_2



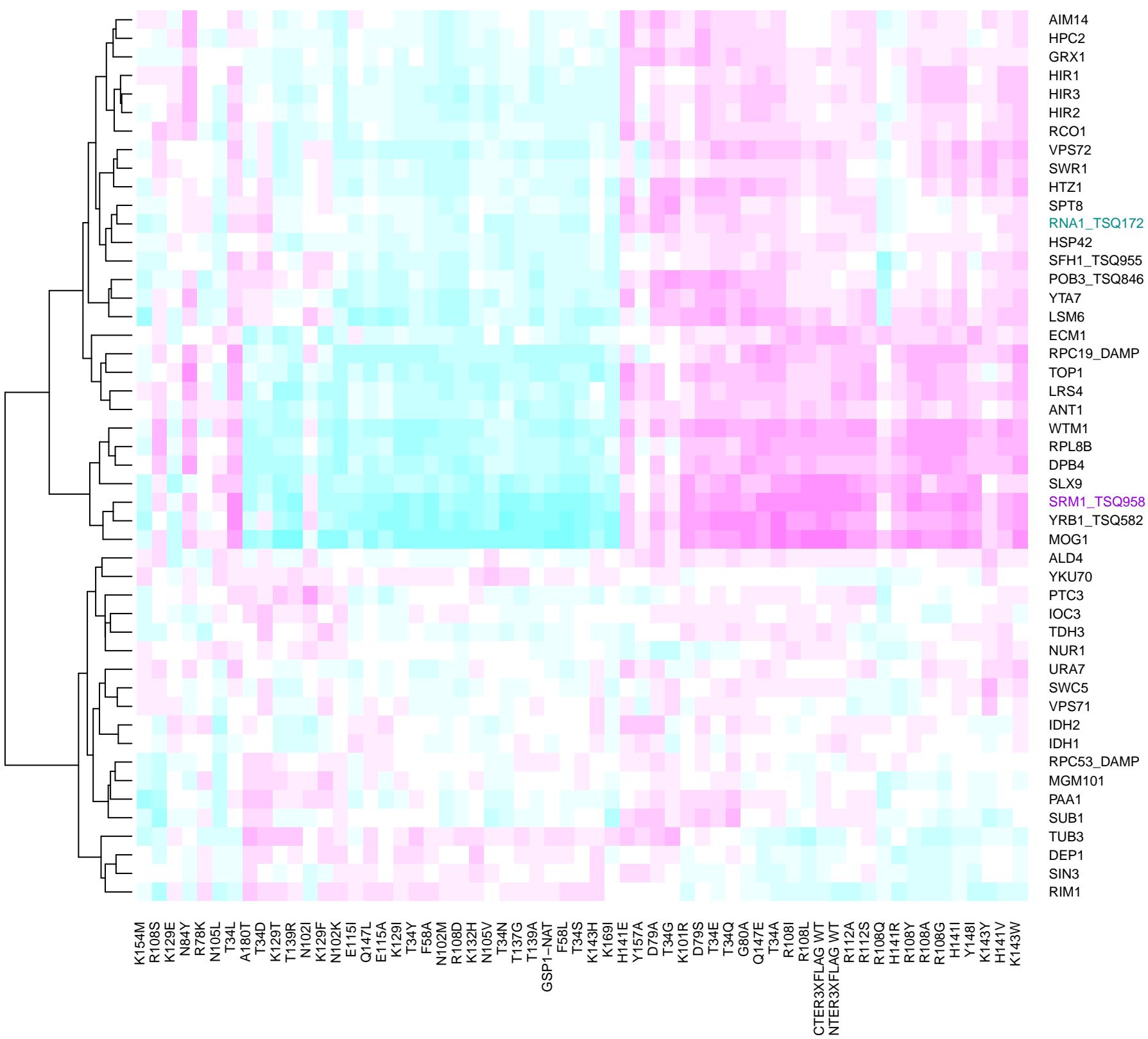


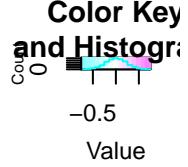
nucleic acid binding transcription factor activity_GO_30_3



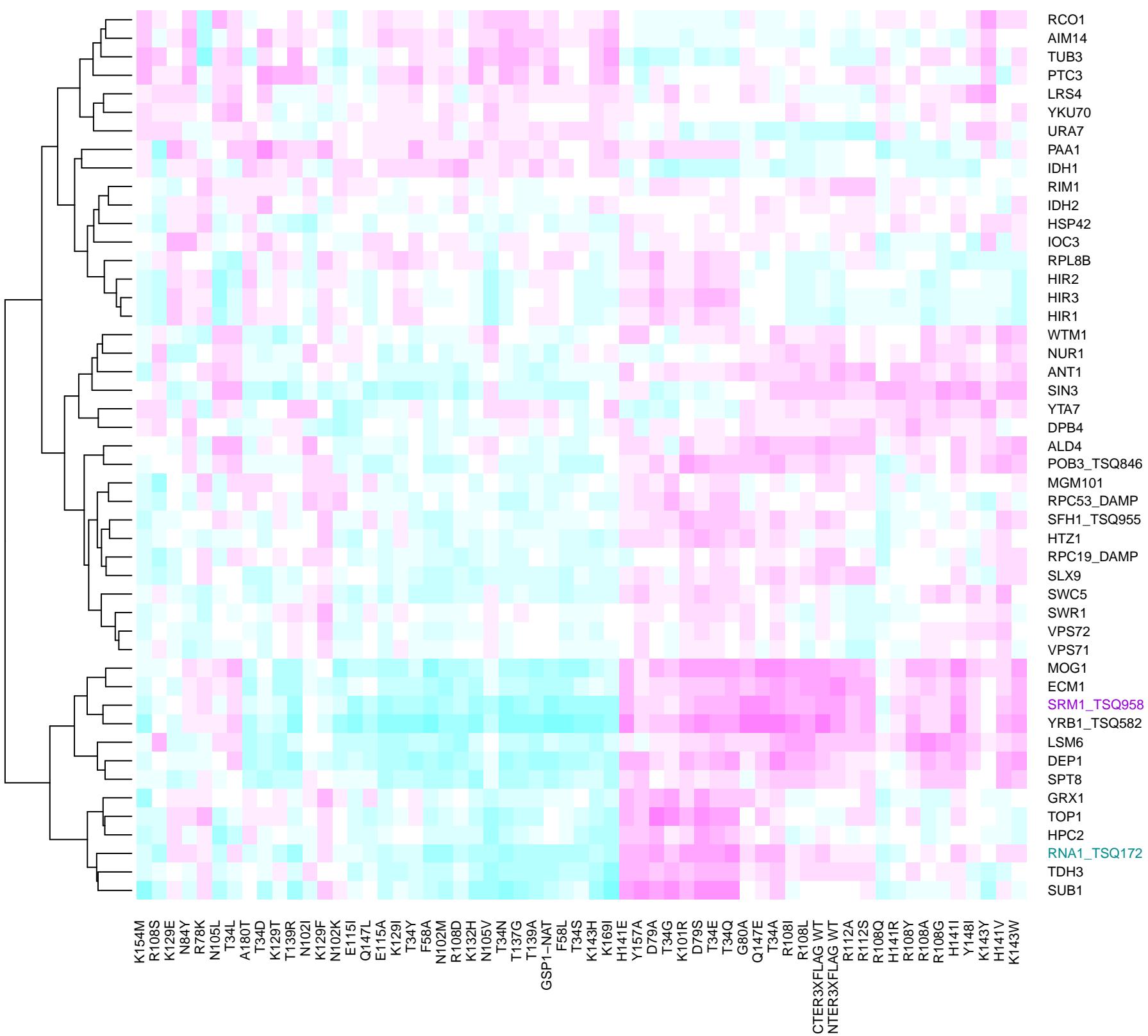


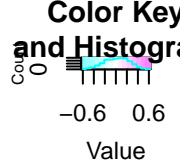
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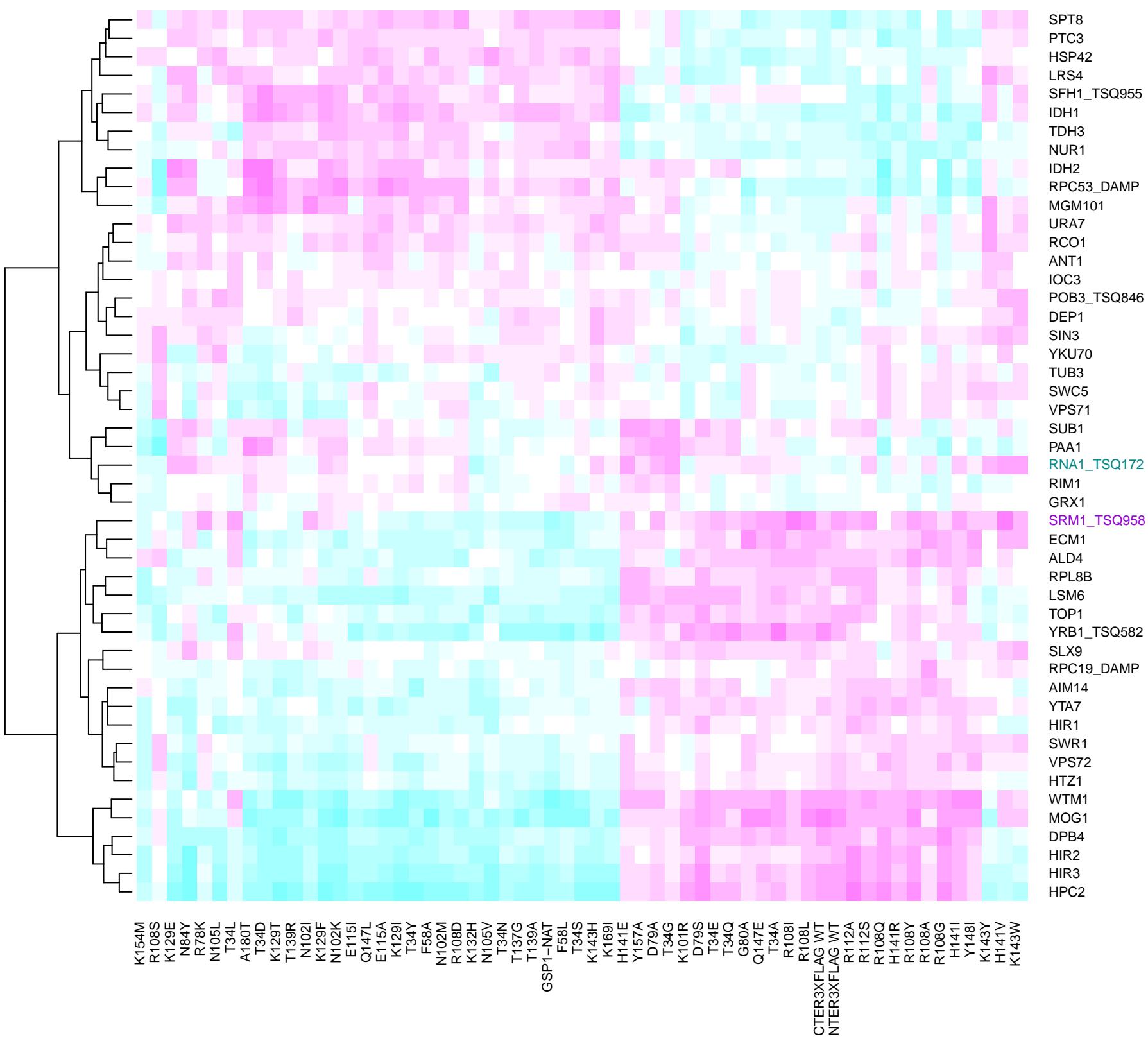


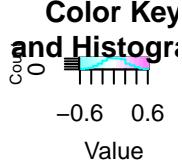
lipids_GO_30_5



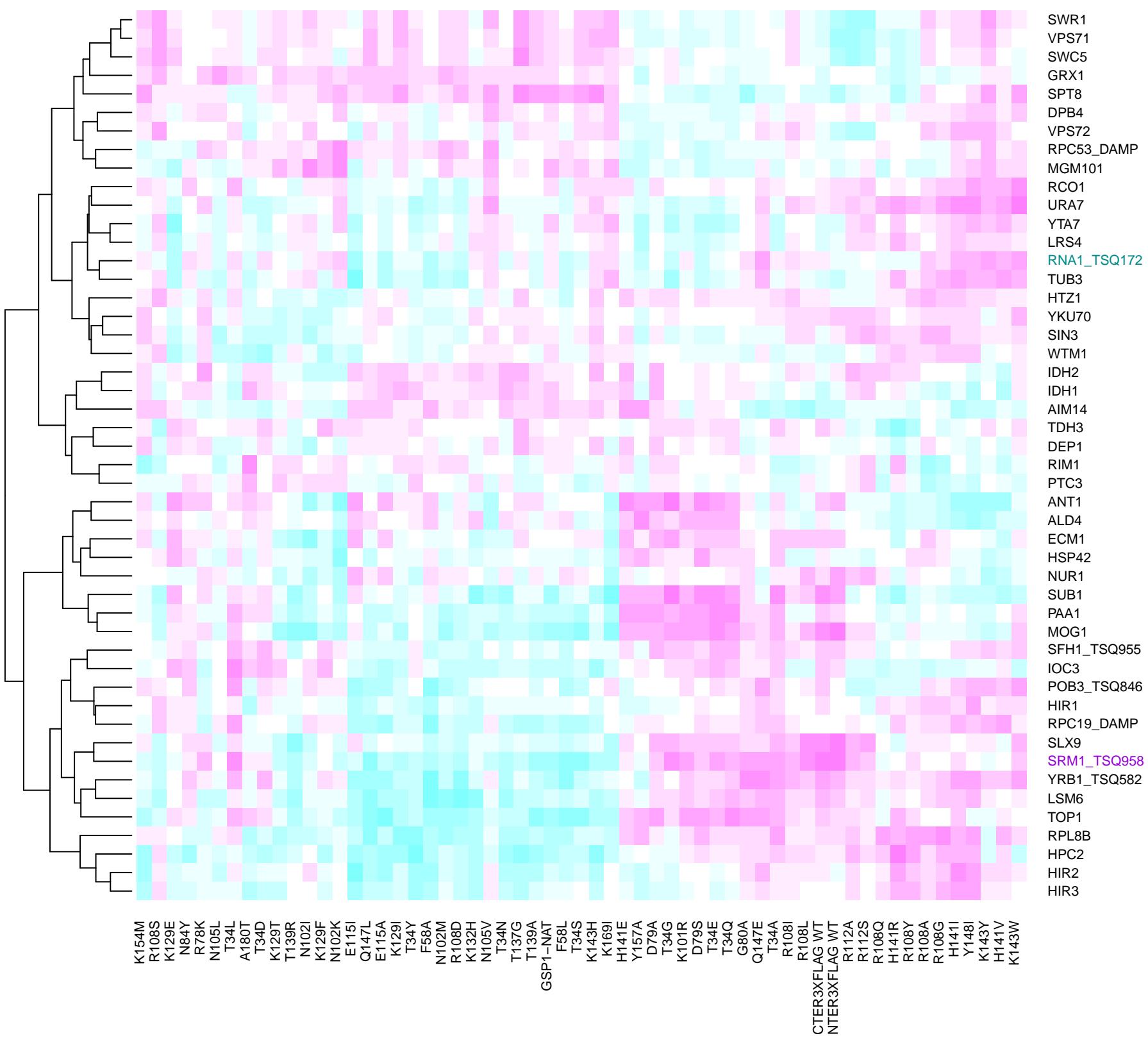


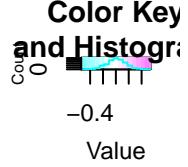
mitochondrion organization_GO_30_4



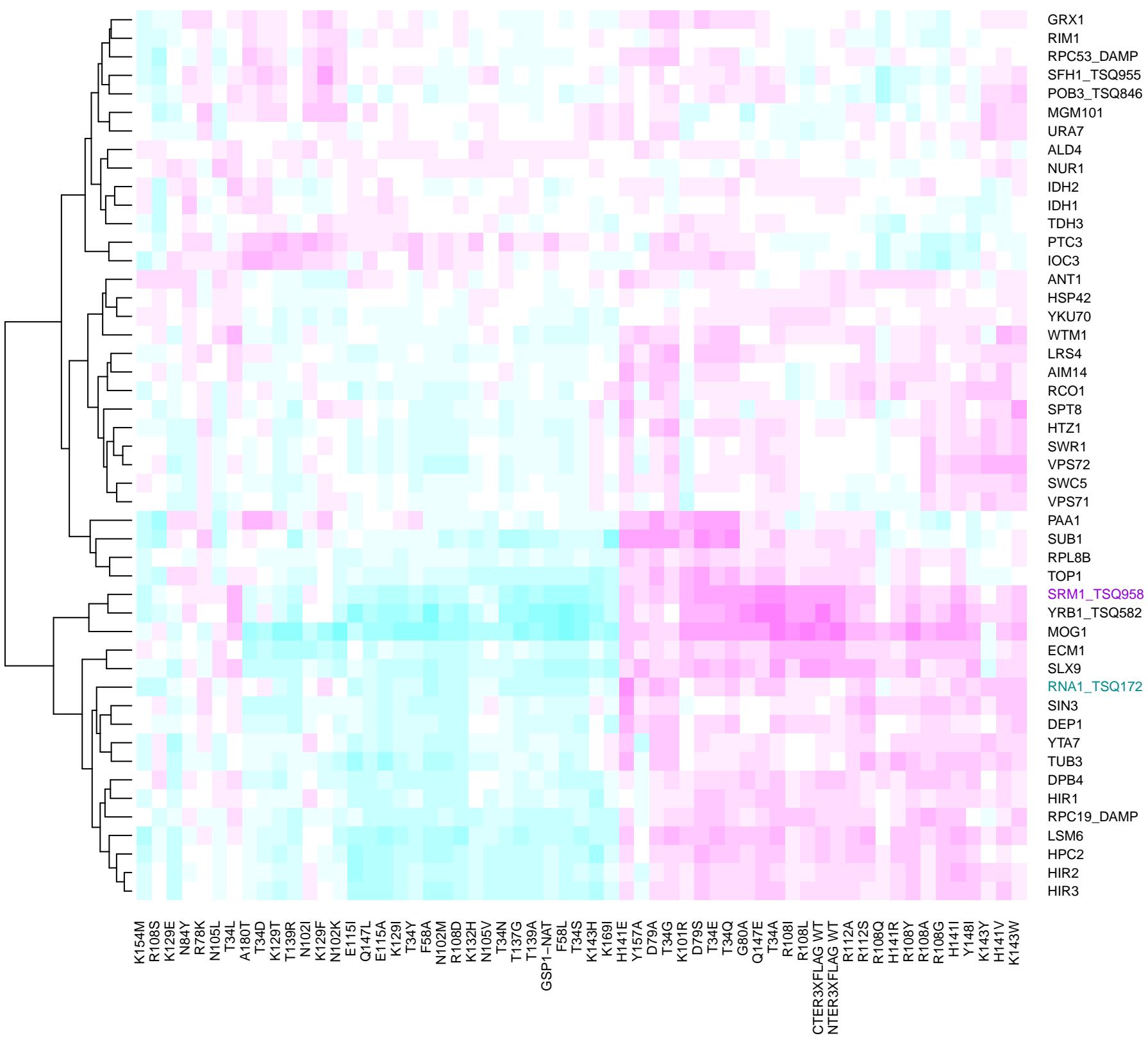


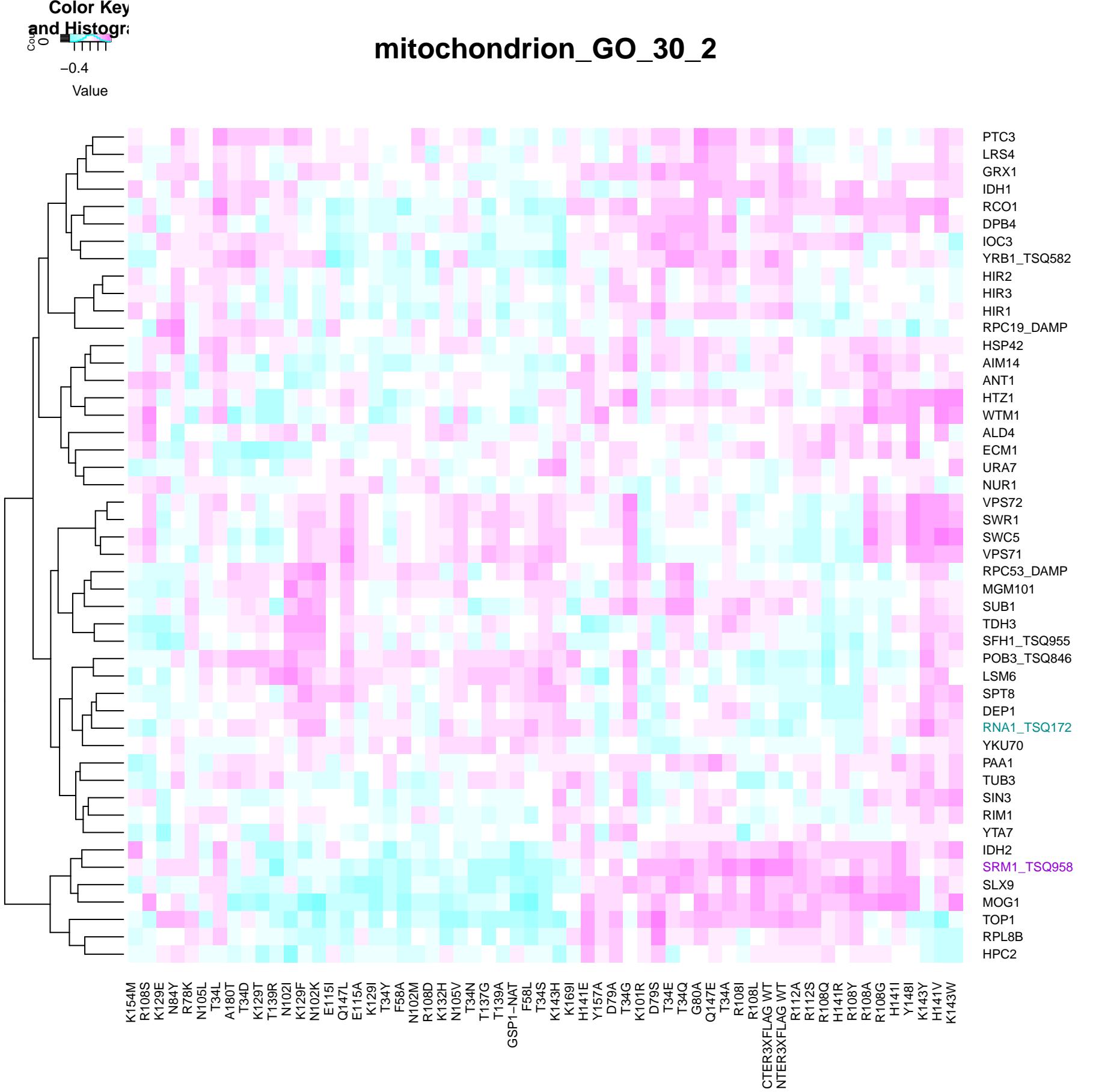
transmembrane transporter activity_GO_30_3

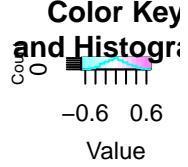




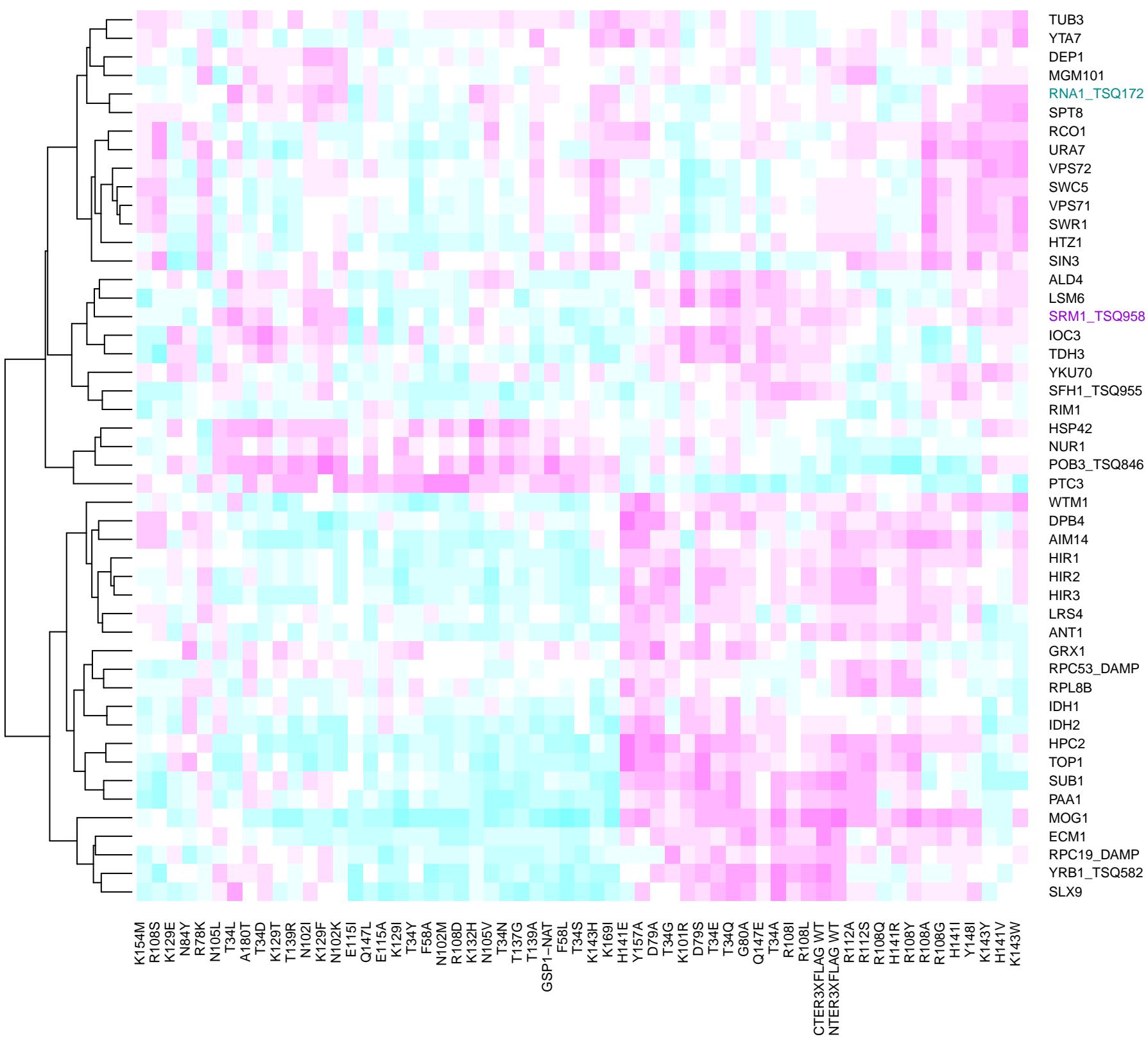
metabolic

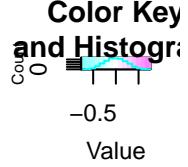




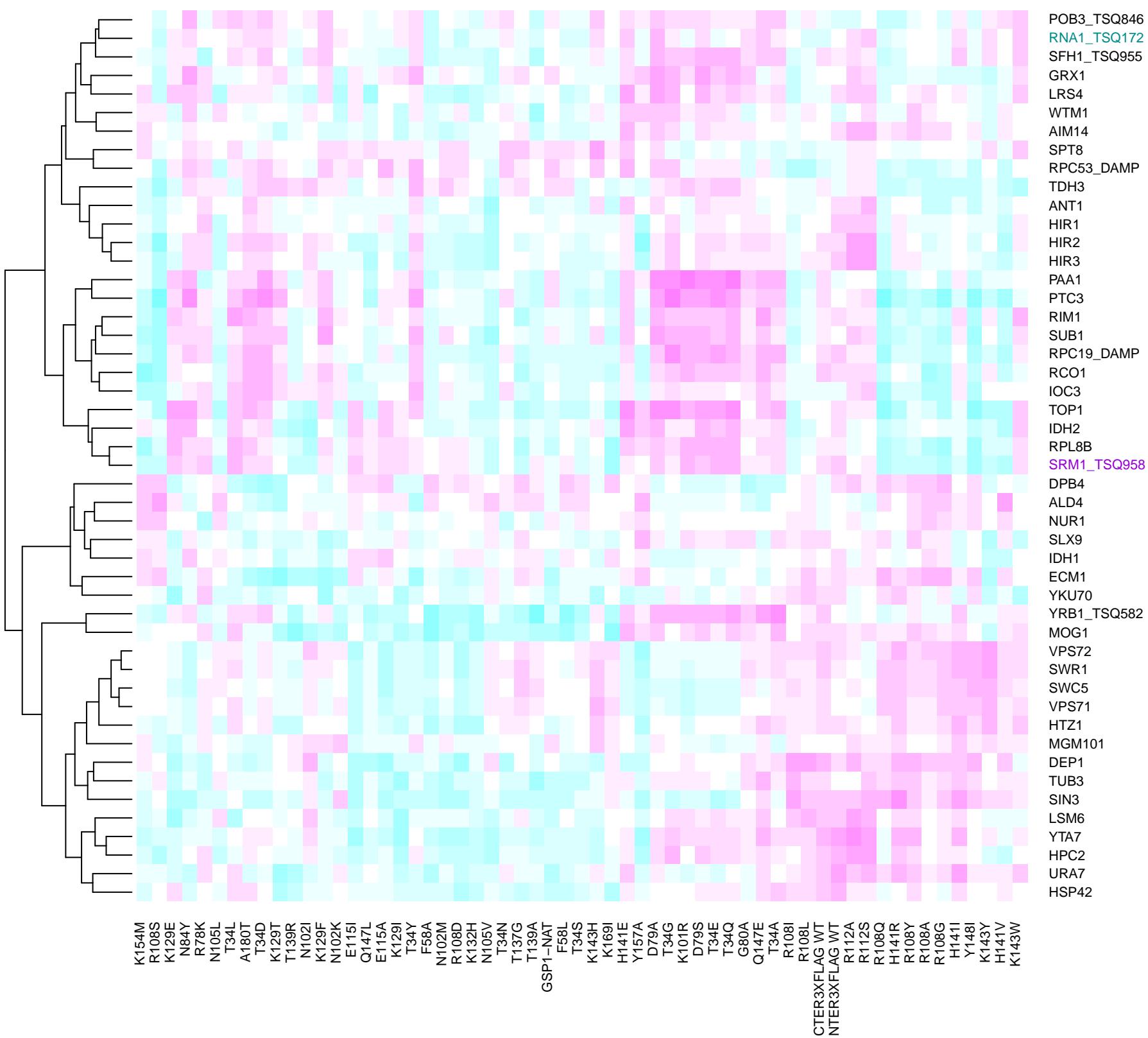


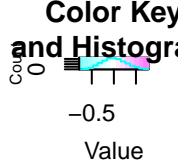
regulation of translation_GO_30_1



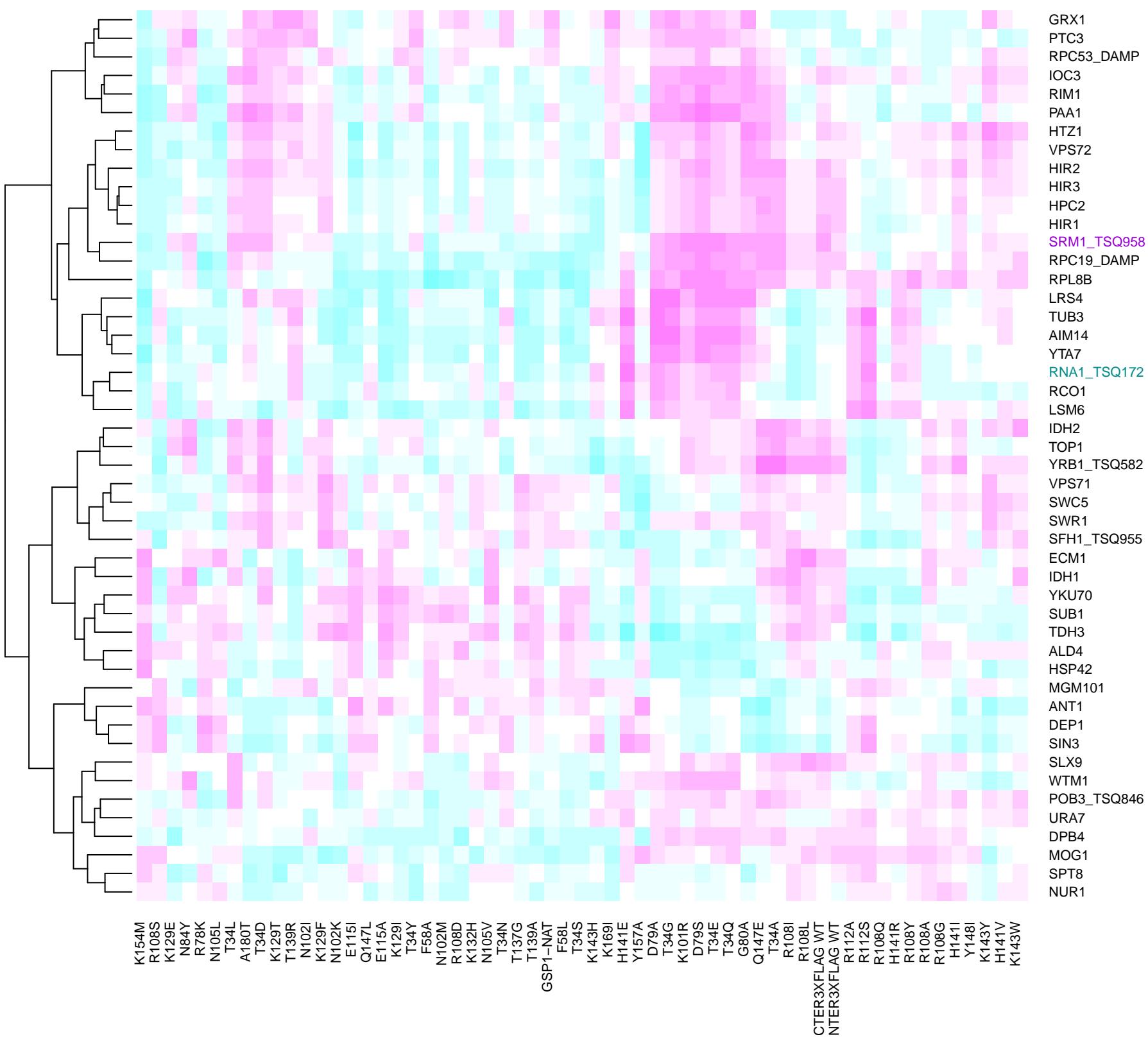


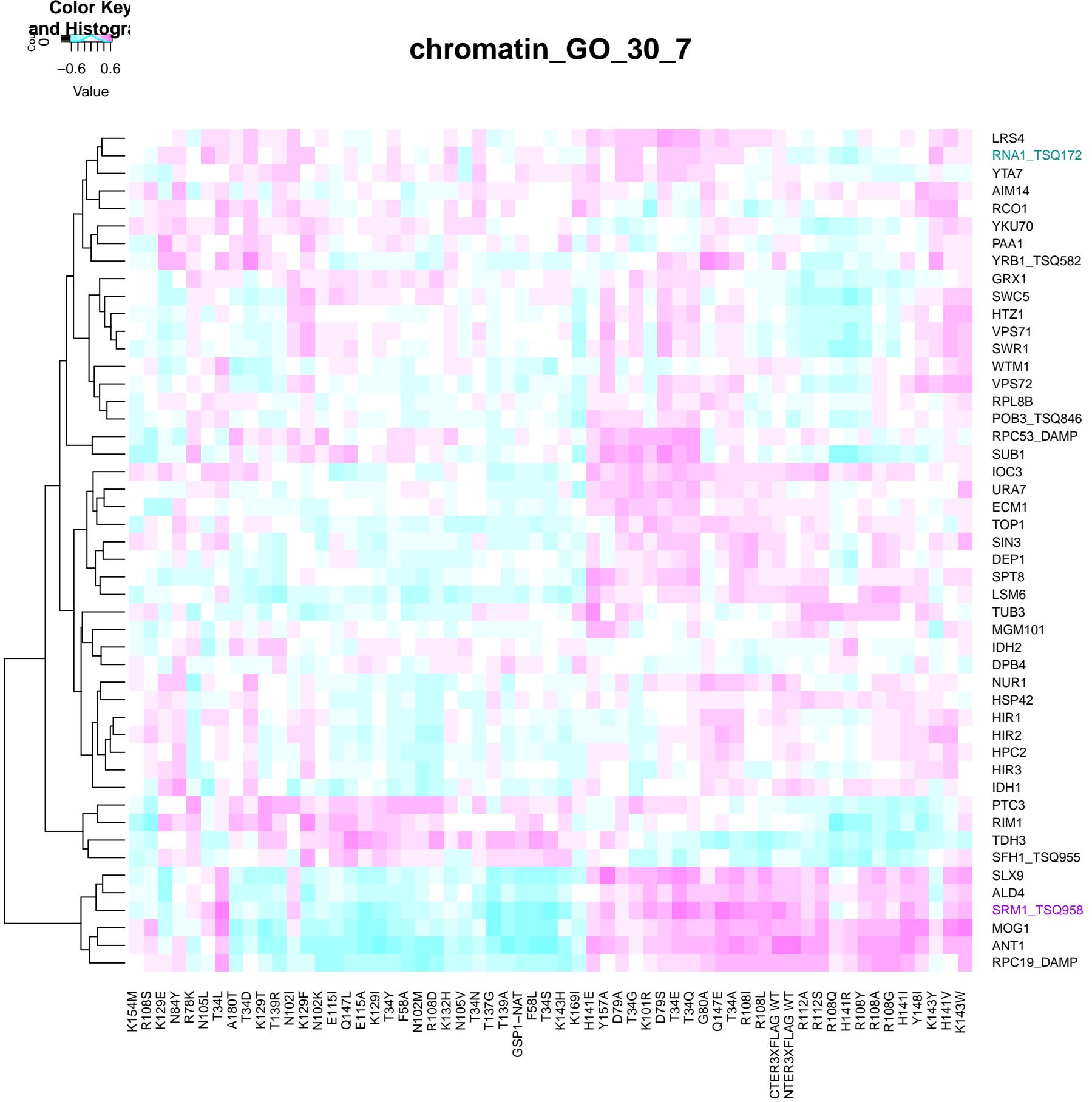
response to osmotic stress_GO_30_2

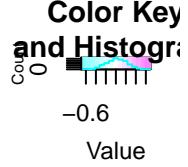




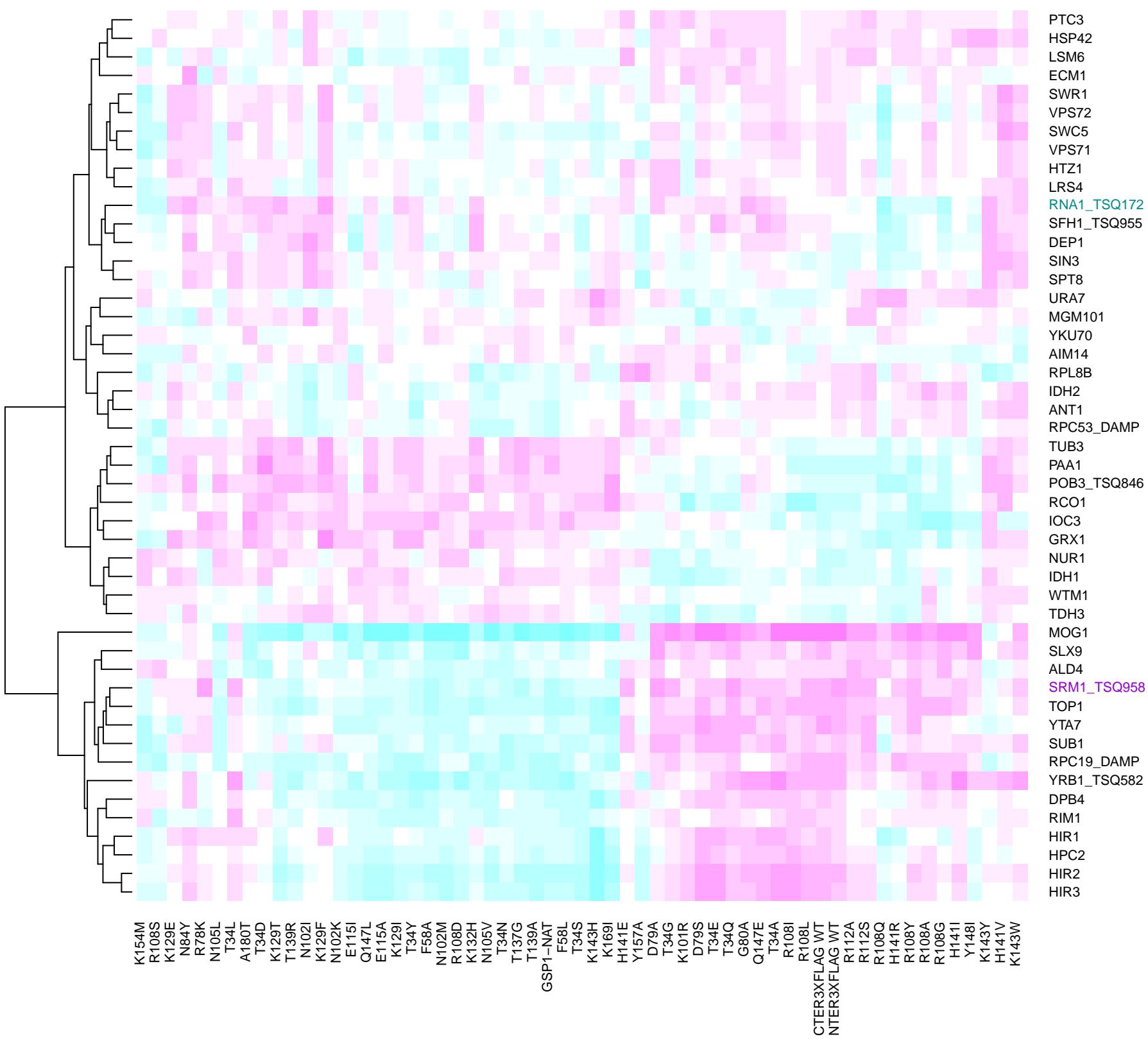
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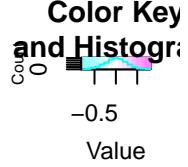




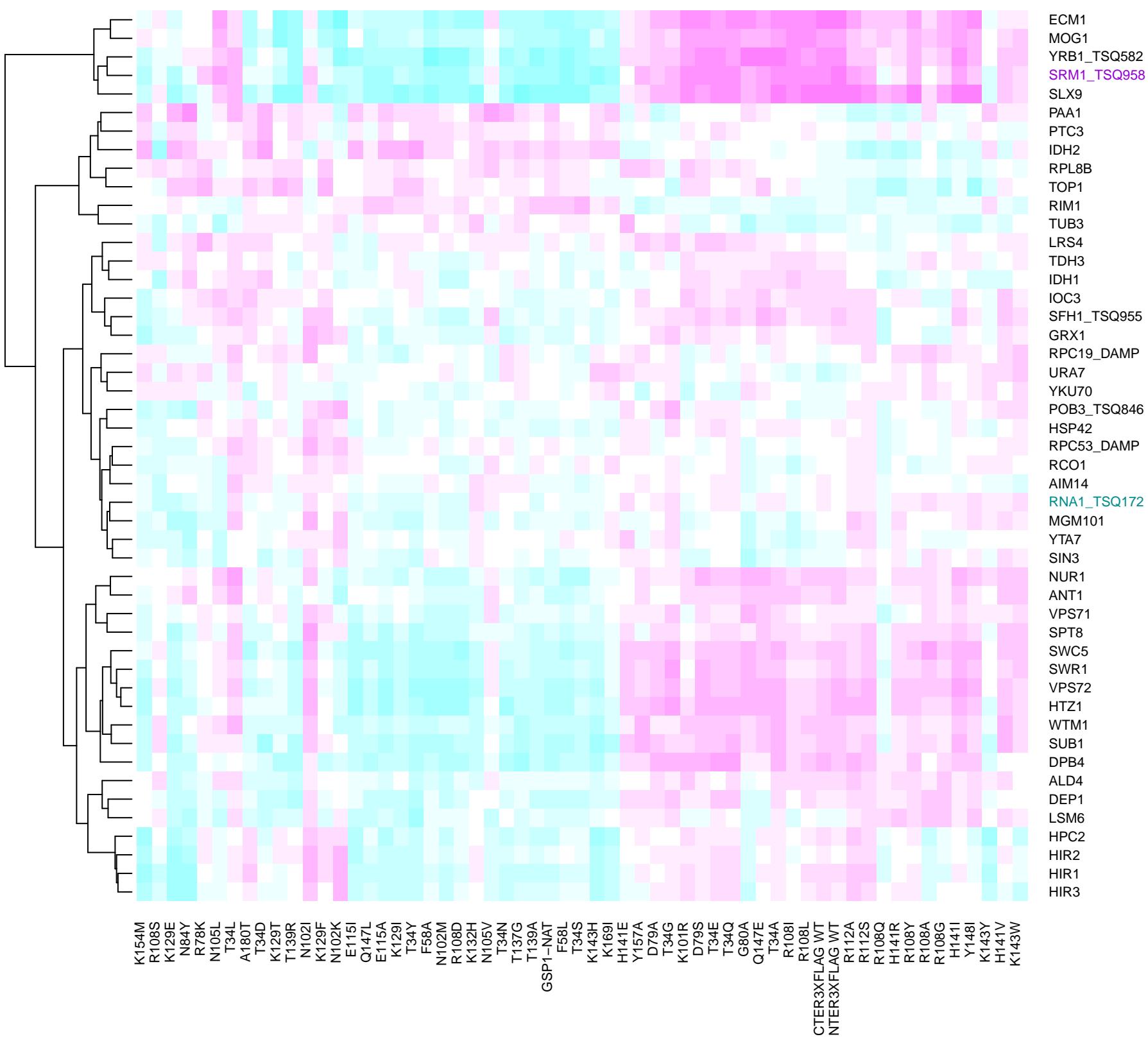


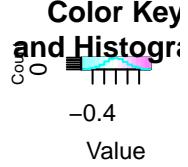
mitochondria and respiration_GO_30_9



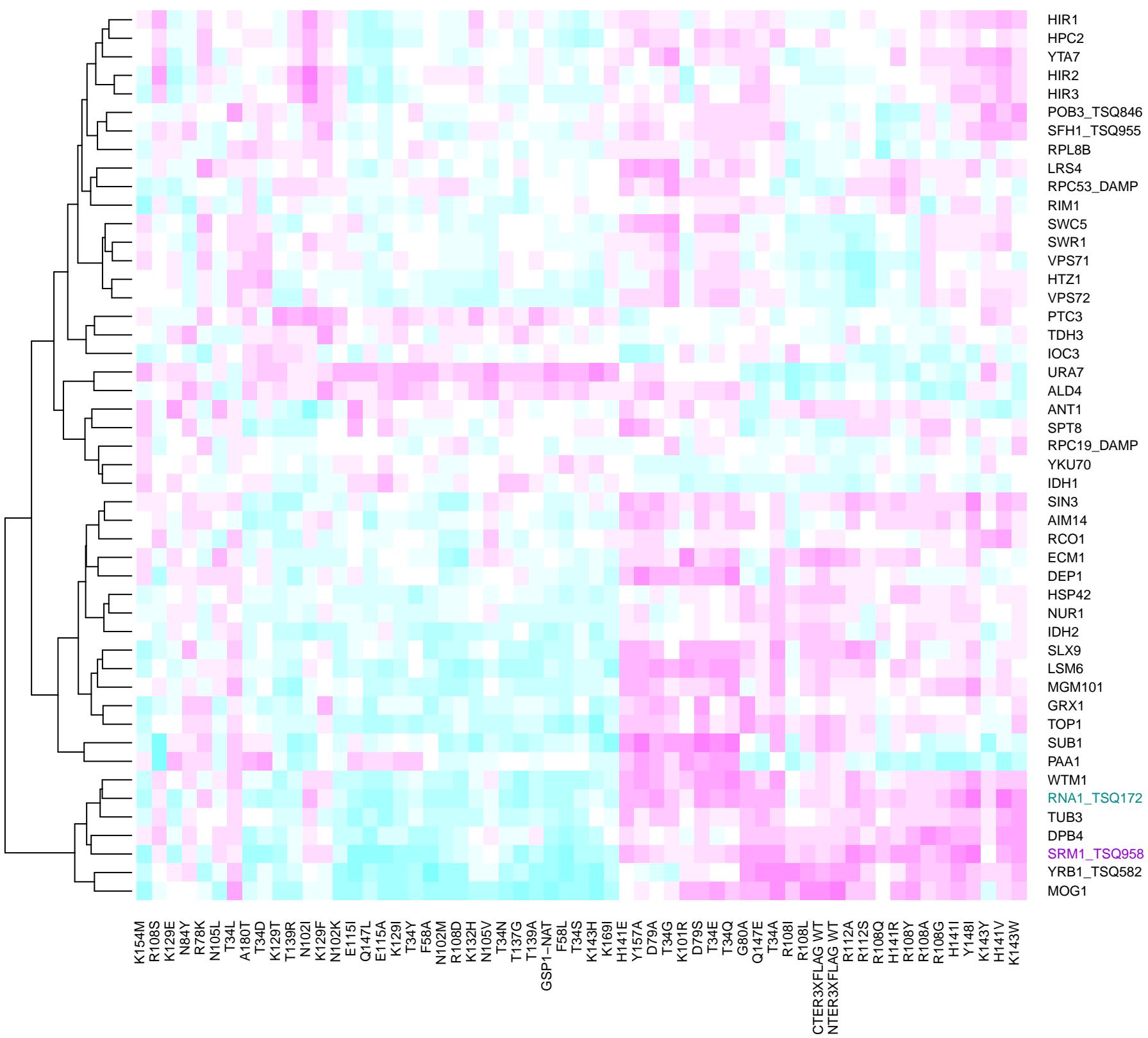


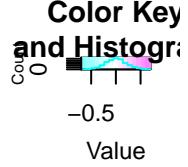
Golgi and ER_GO_30_11



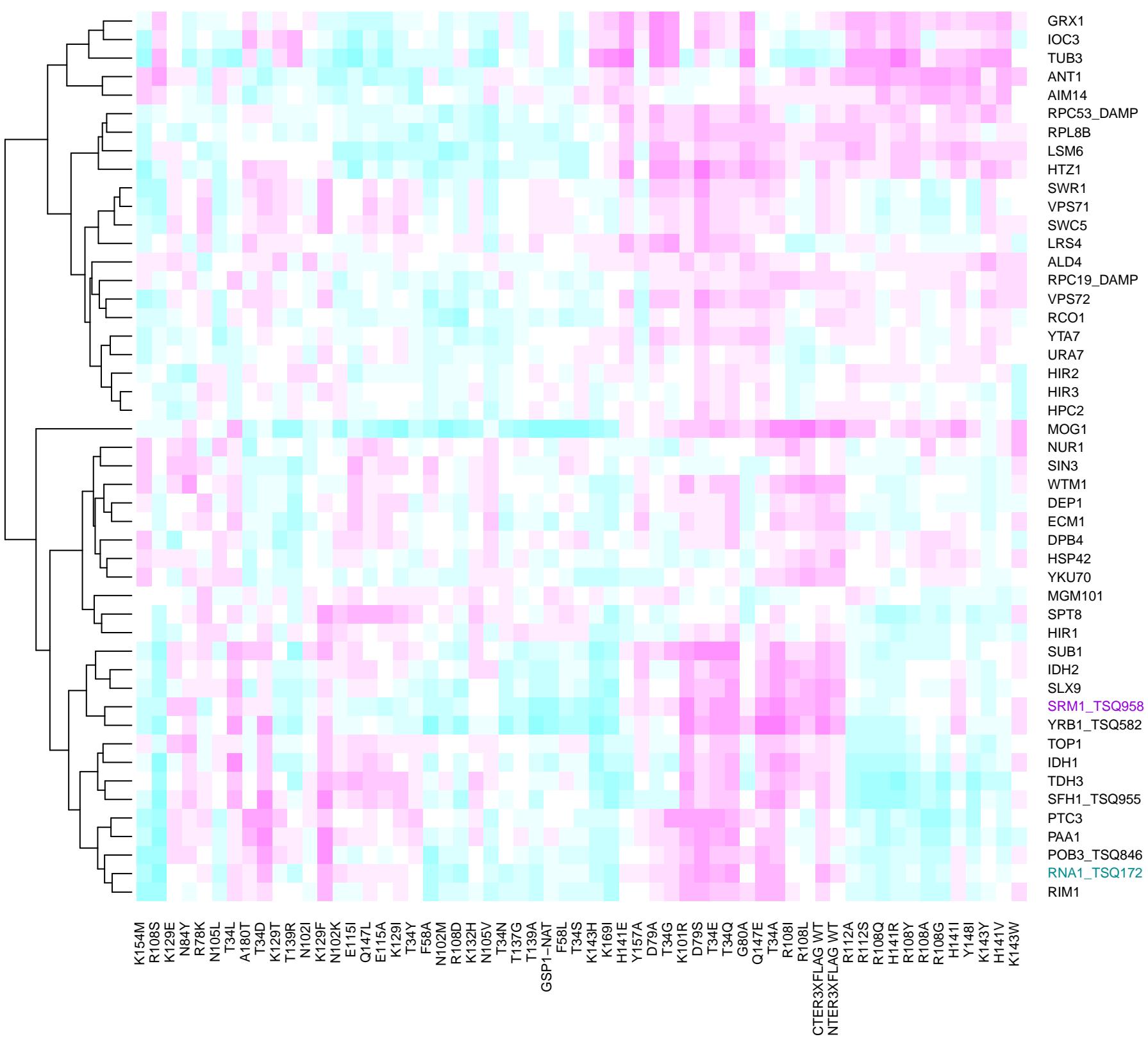


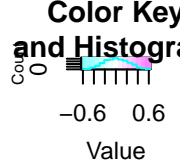
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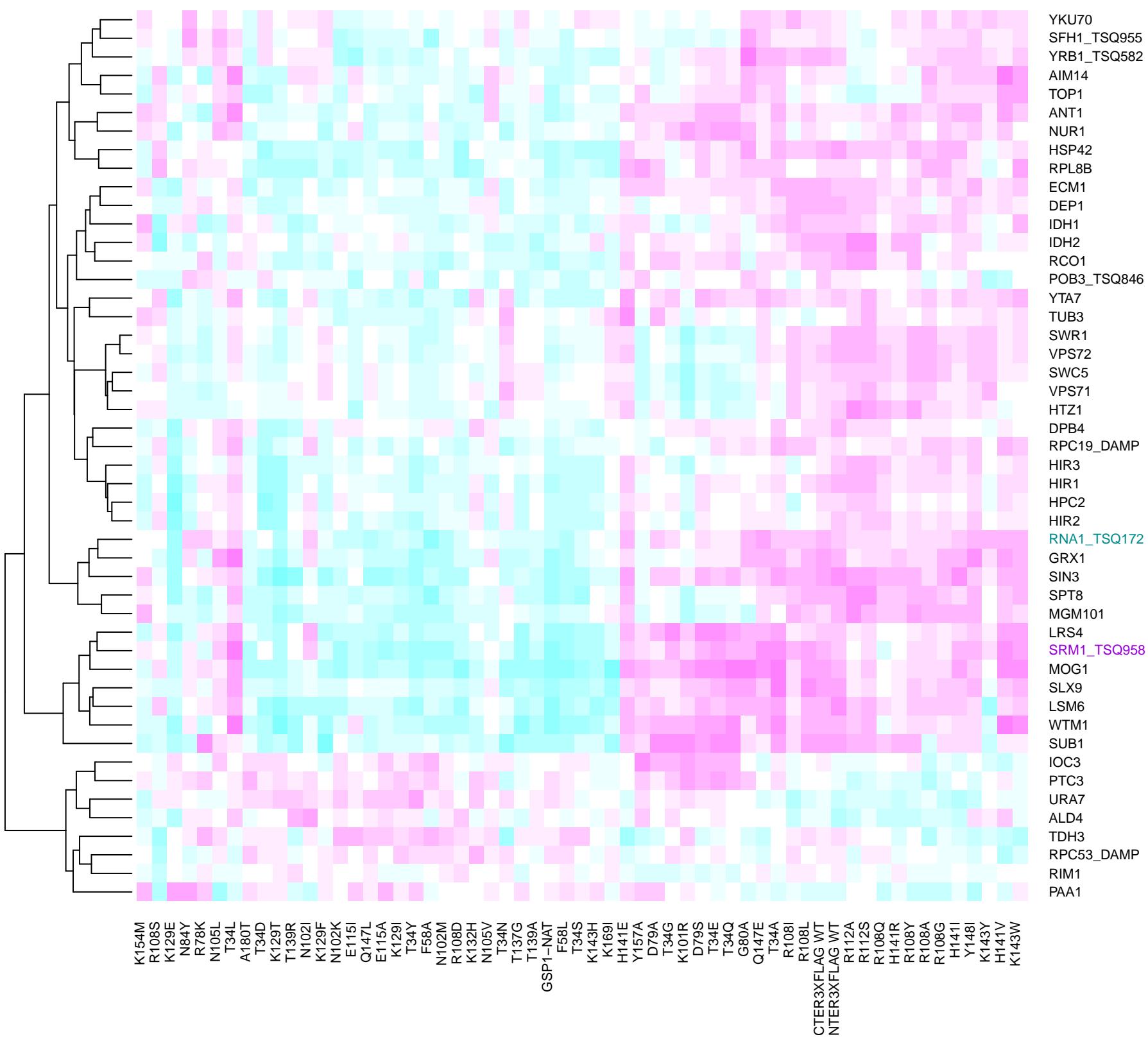


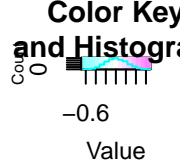
mitotic cell cycle_GO_30_1



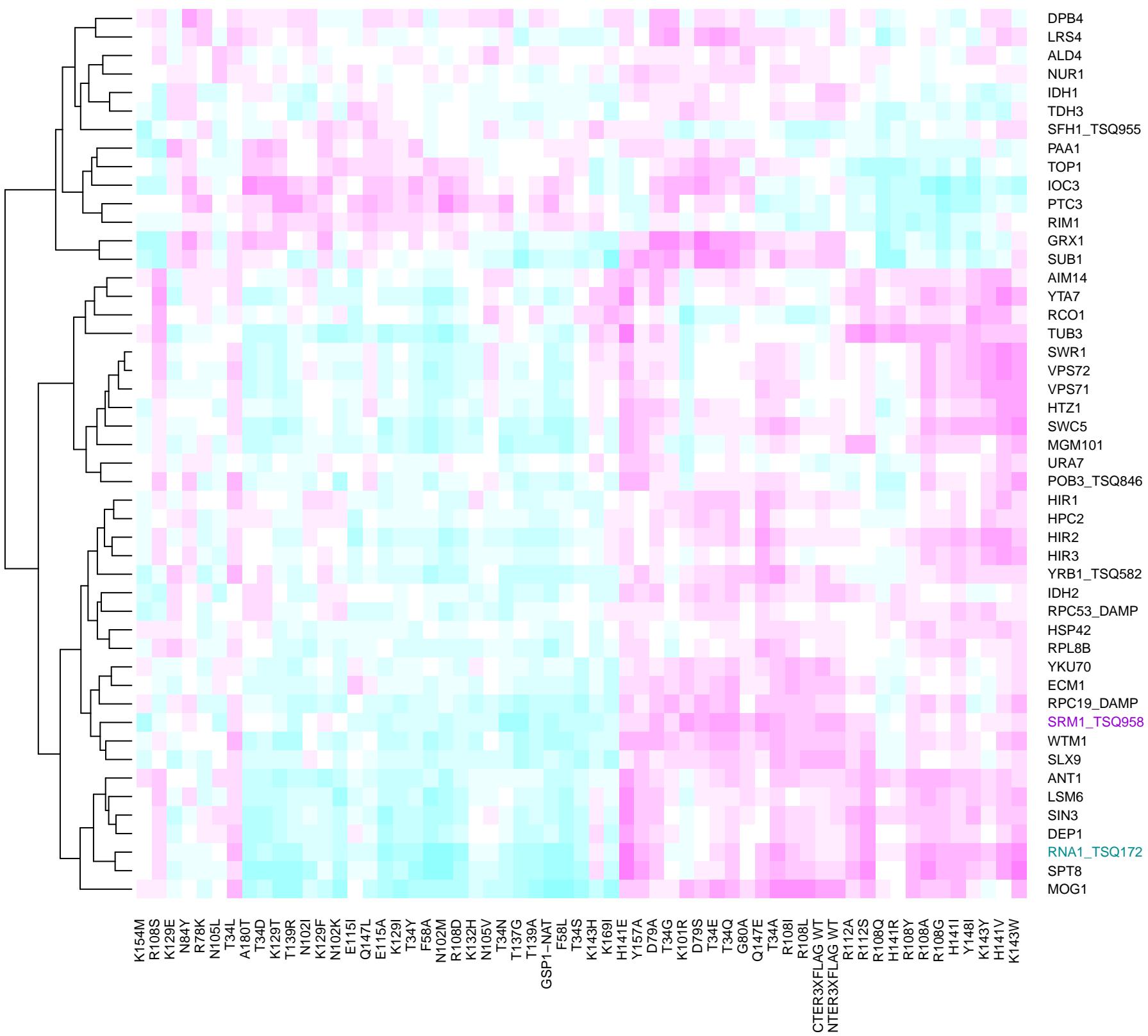


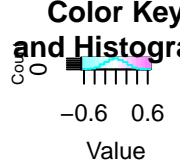
regulation of cell cycle_GO_30_3



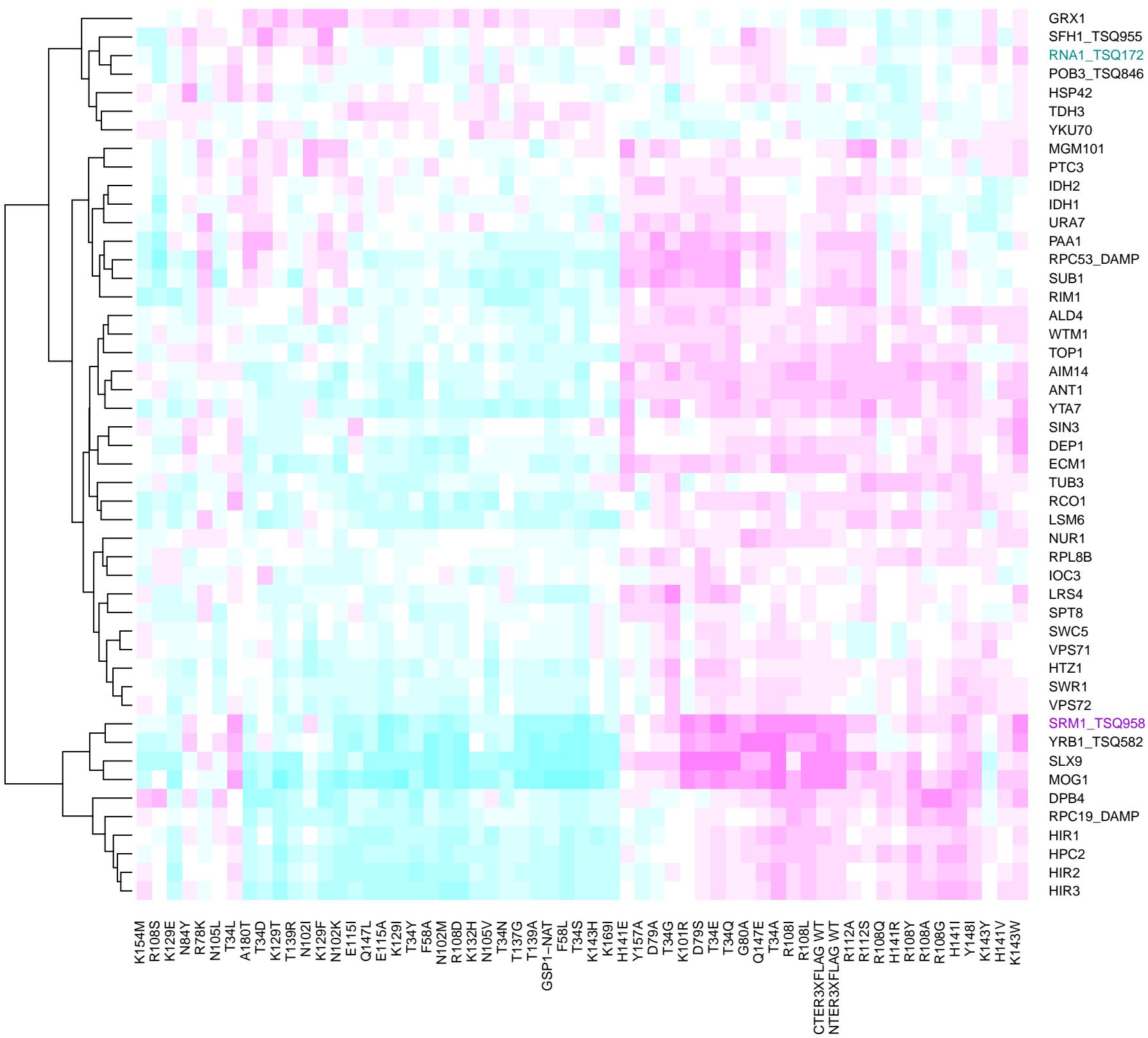


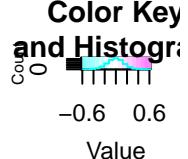
regulation of DNA metabolic process



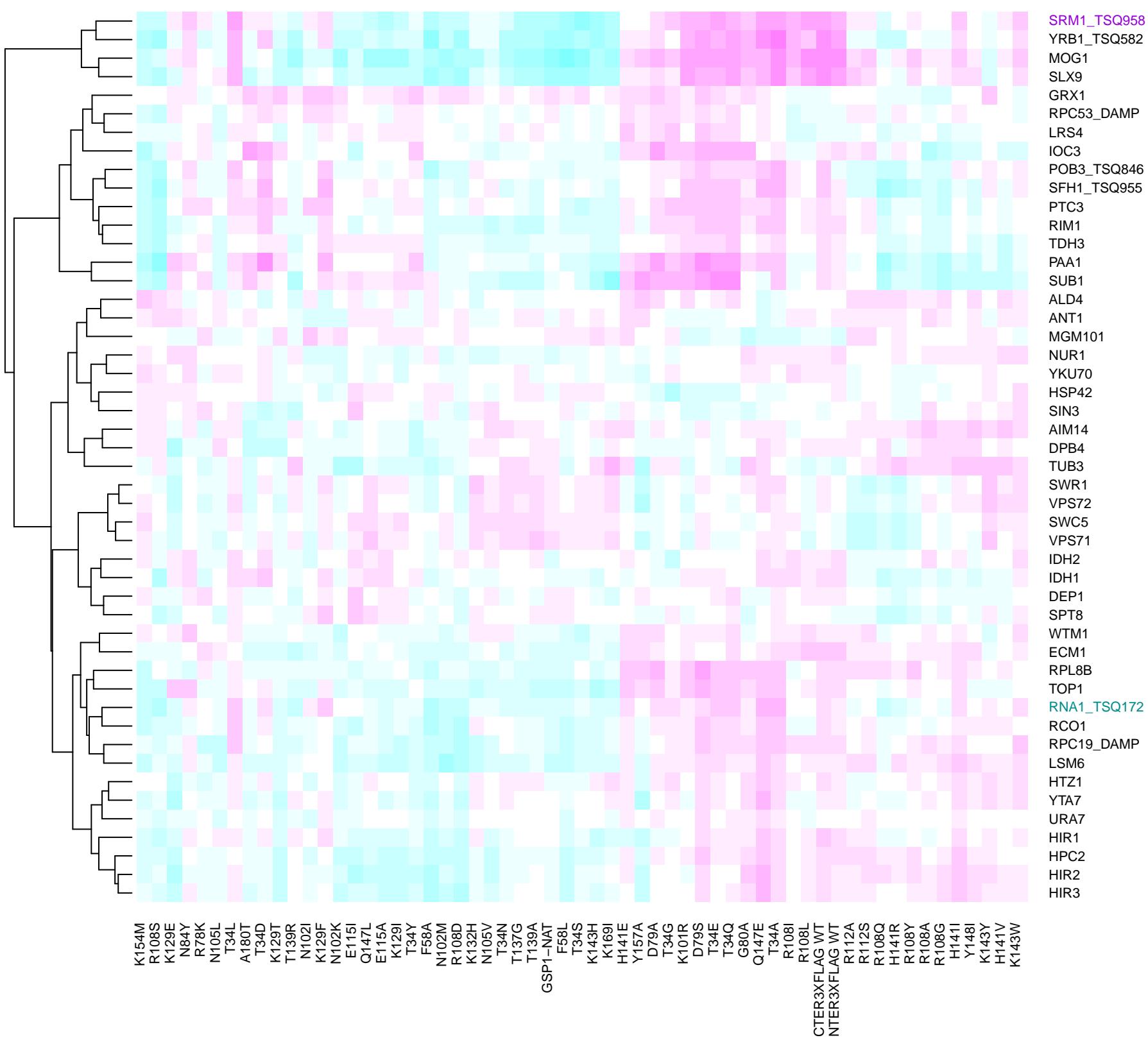


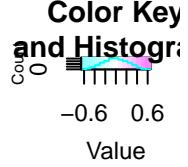
budding_GO_30_1



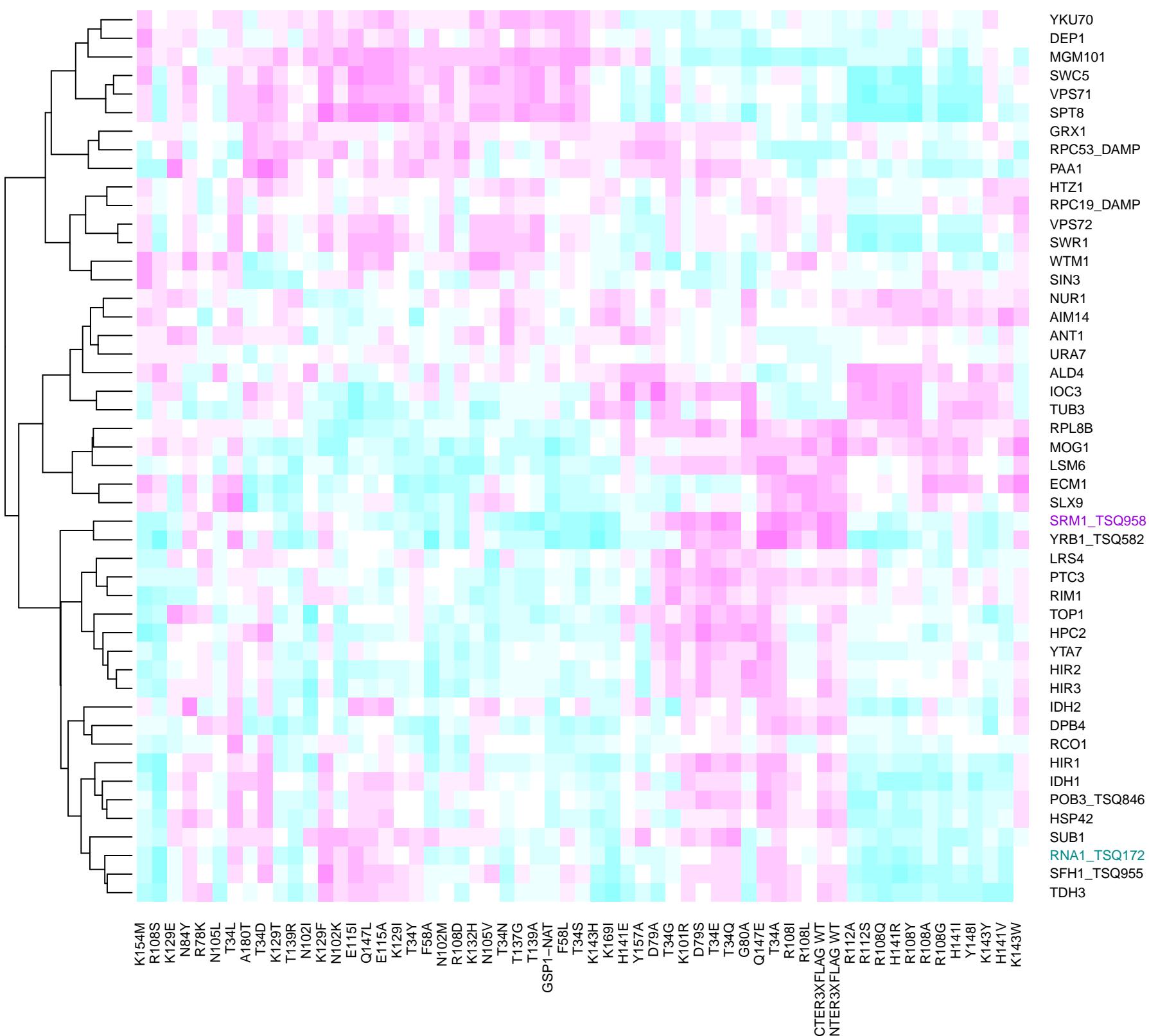


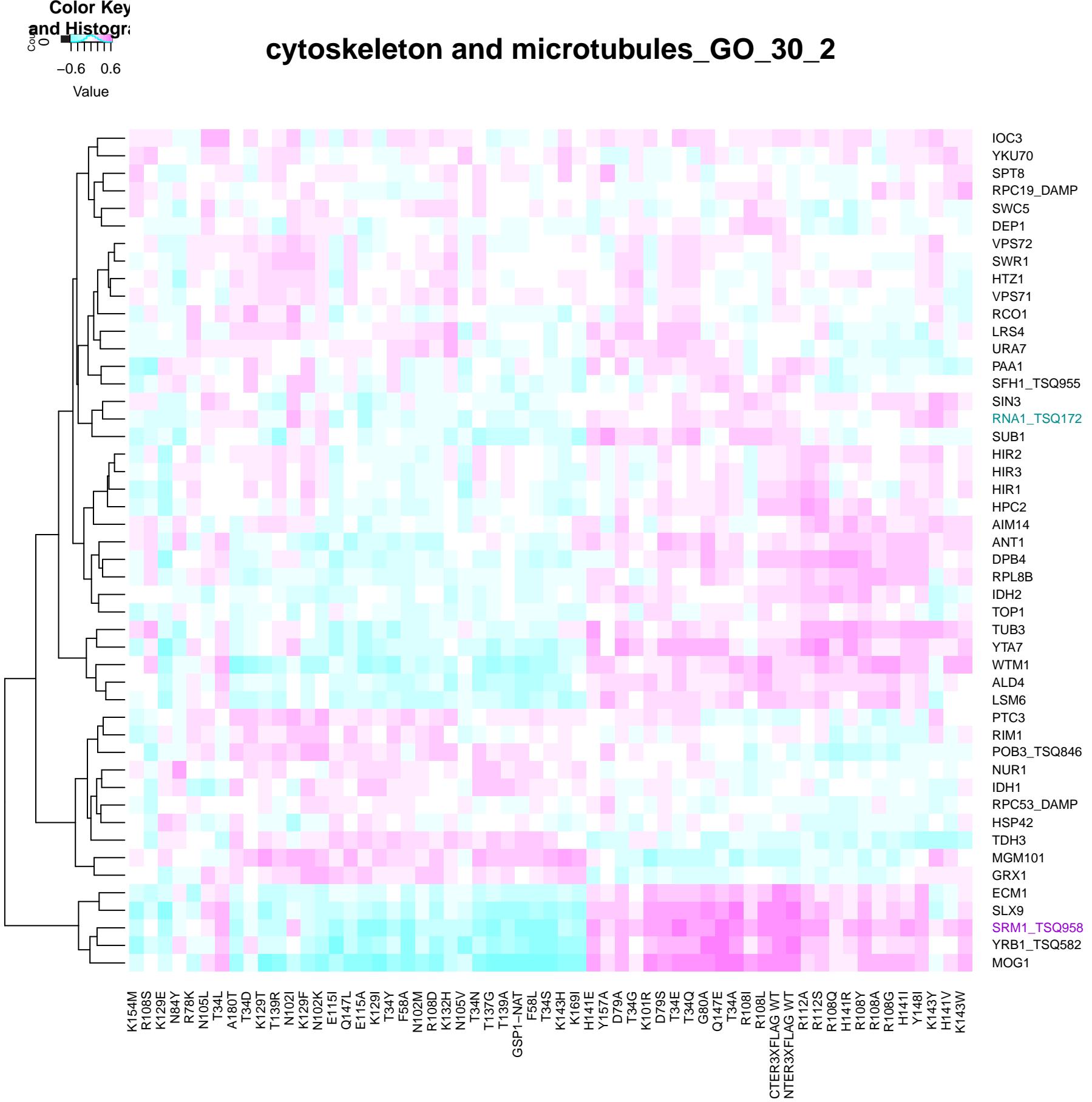
cellular bud

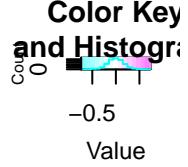




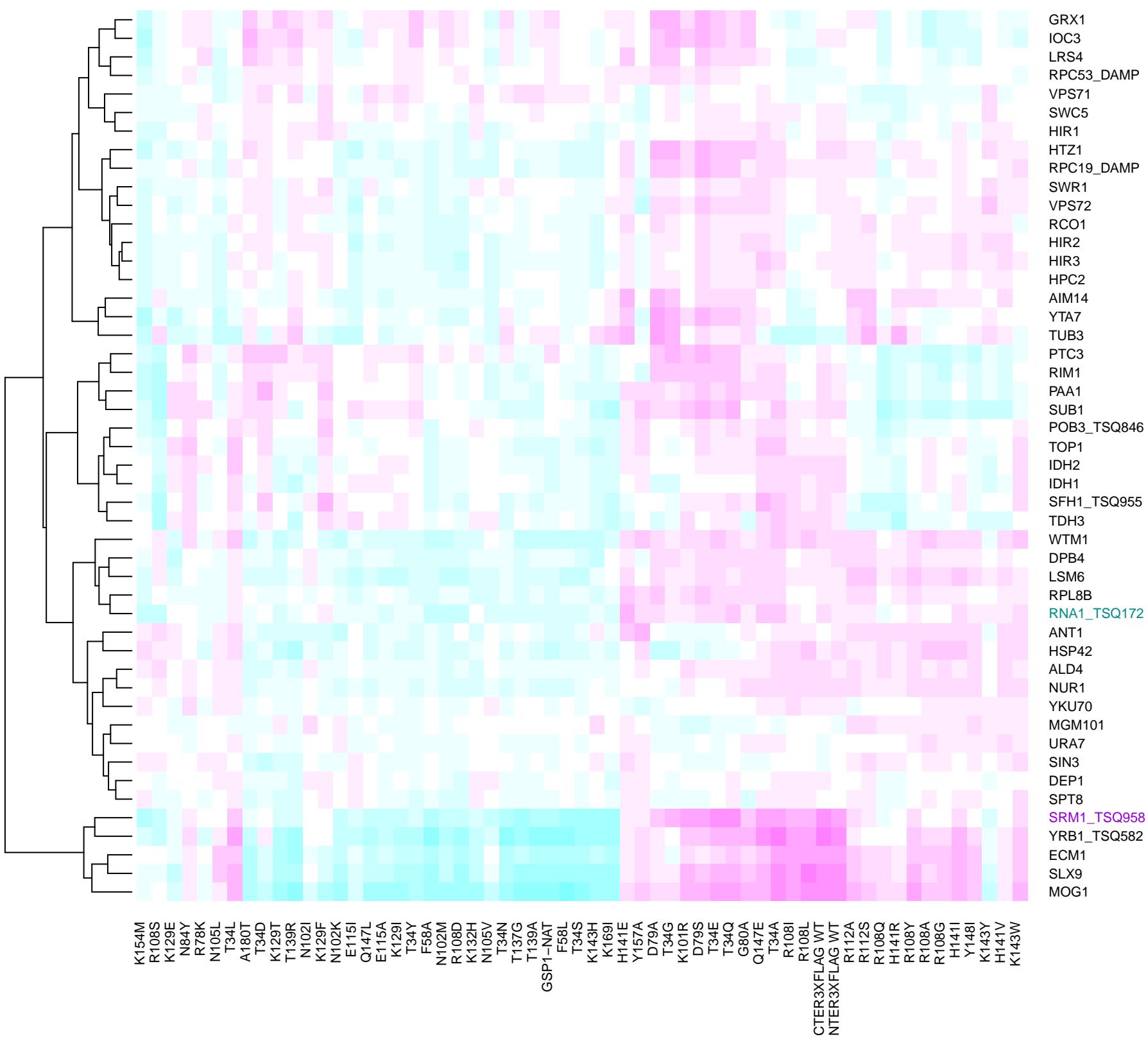
cellular bud_GO_30_3

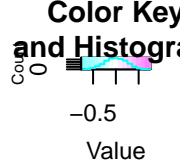




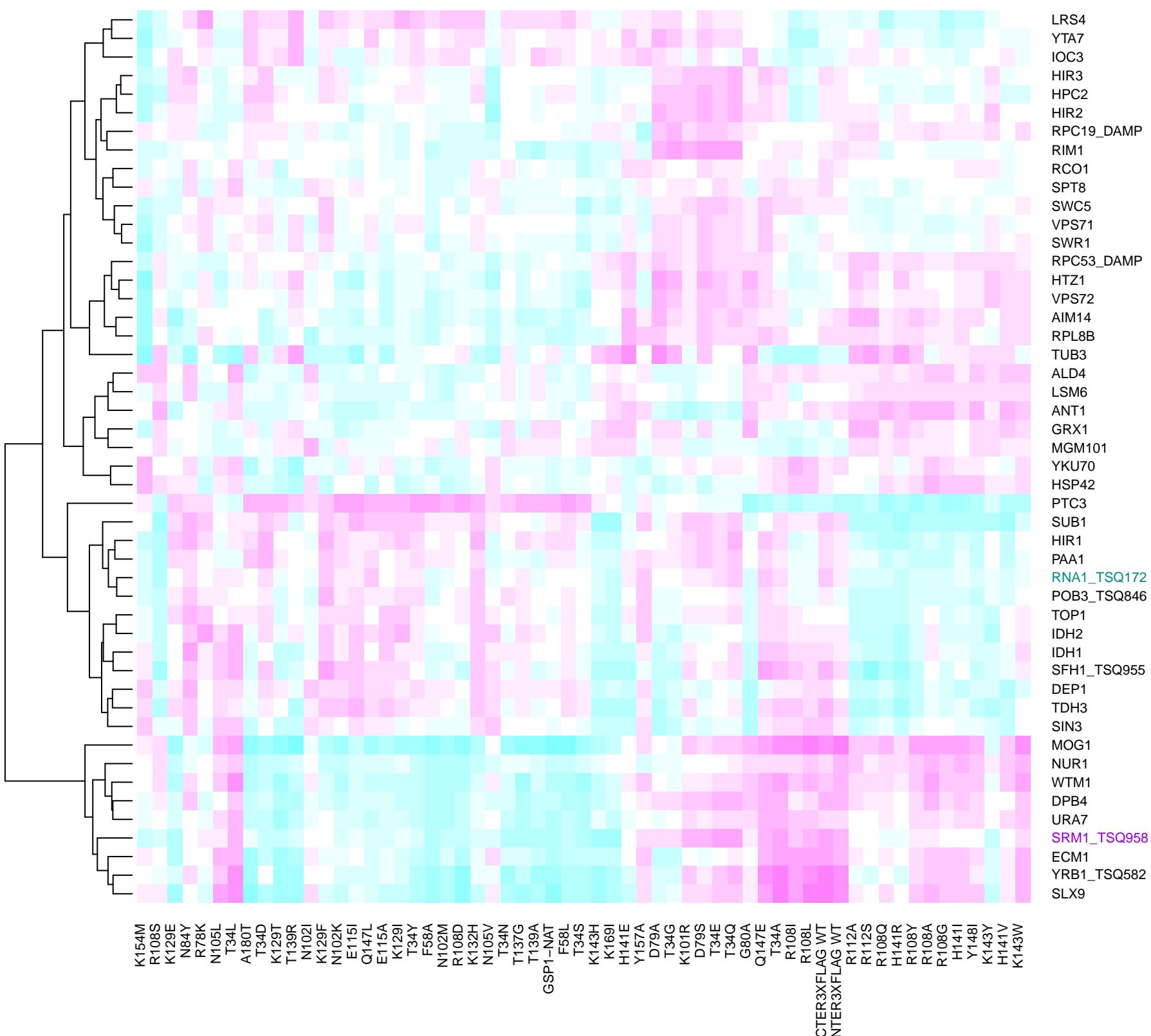


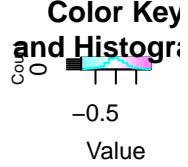
cytoskeleton and microtubules



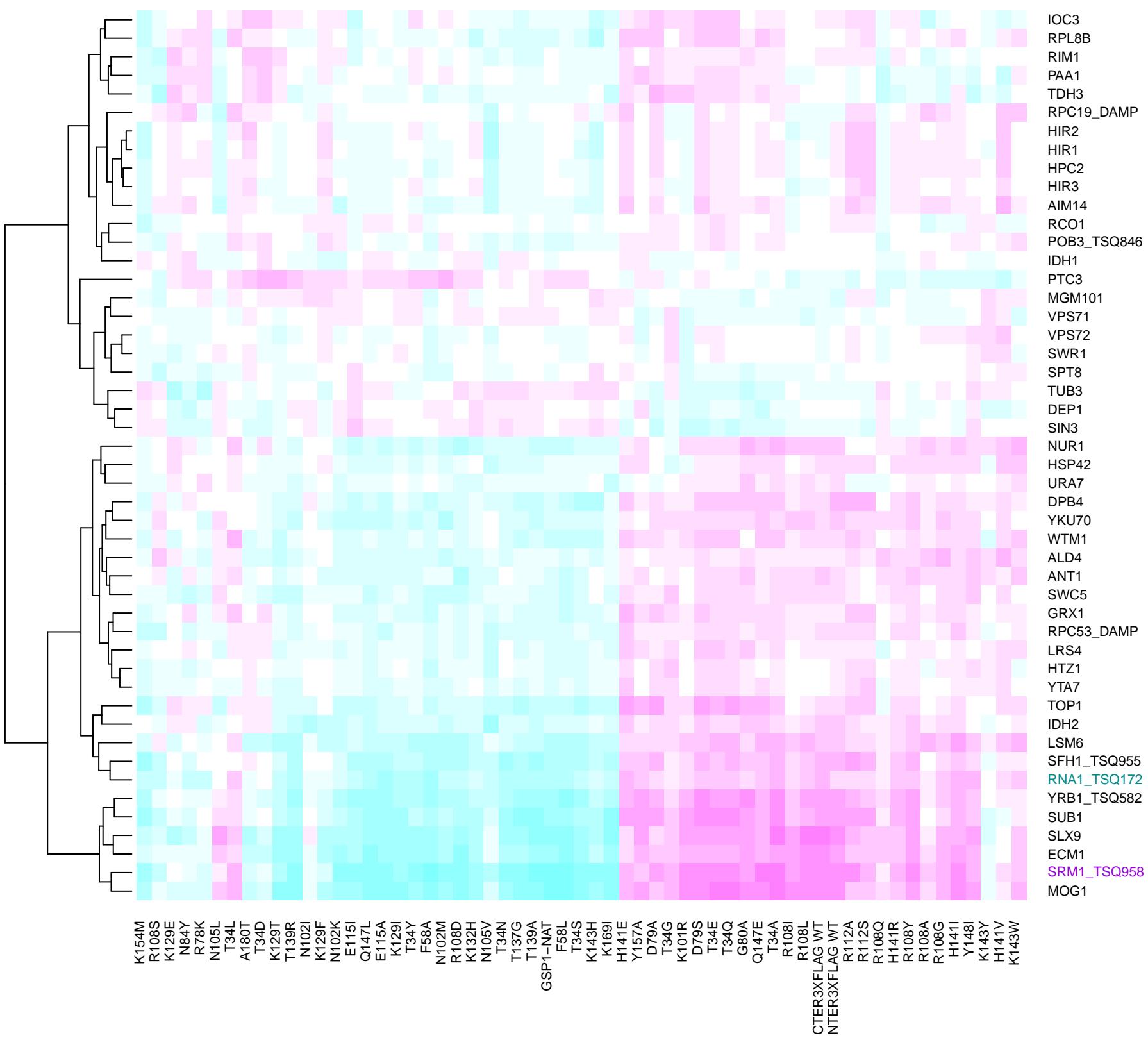


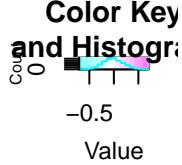
microtubule organizing center



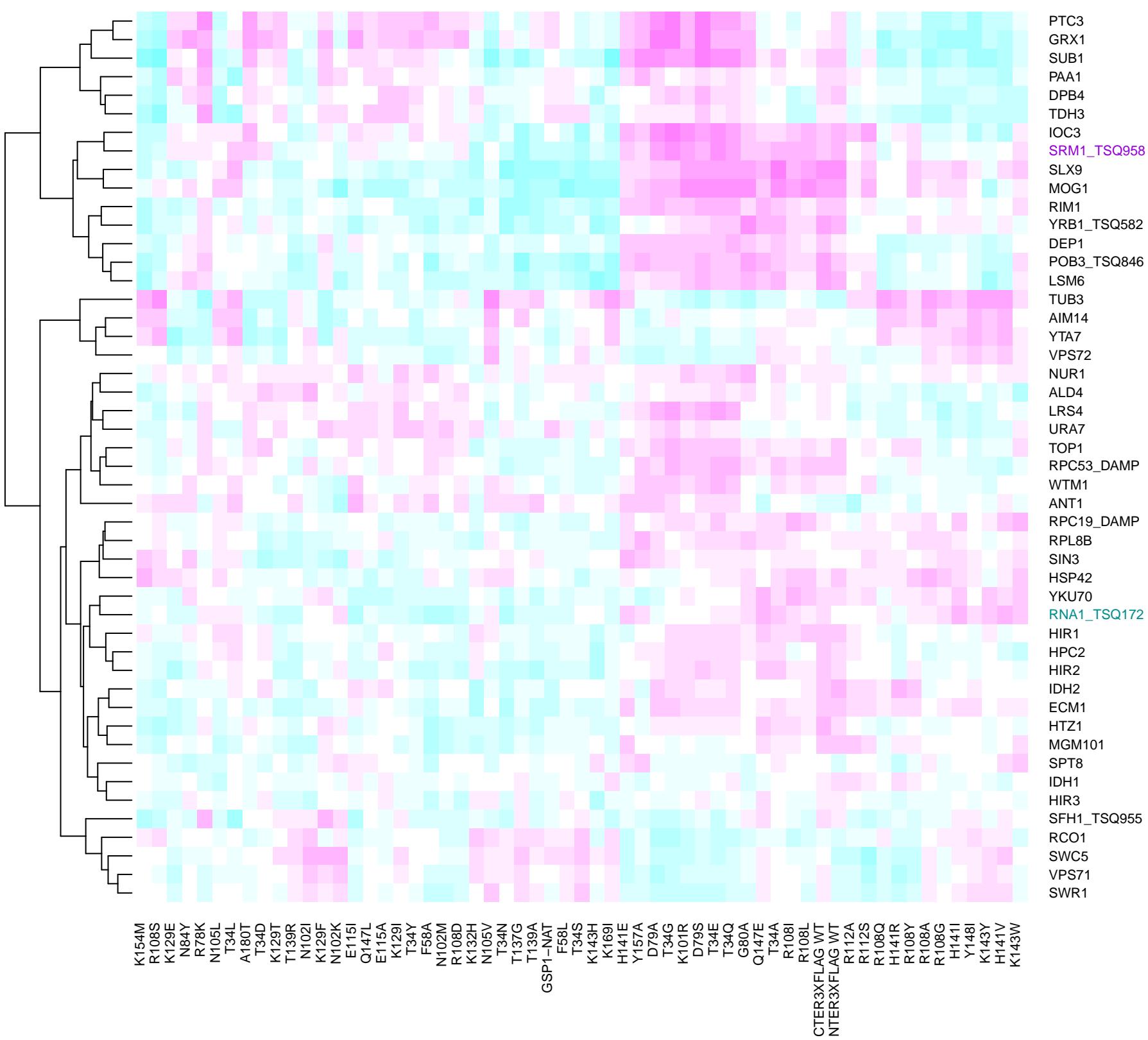


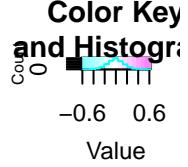
mitotic cell cycle_GO_30_2





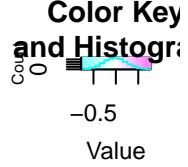
regulation of organelle organization_GO_30_2



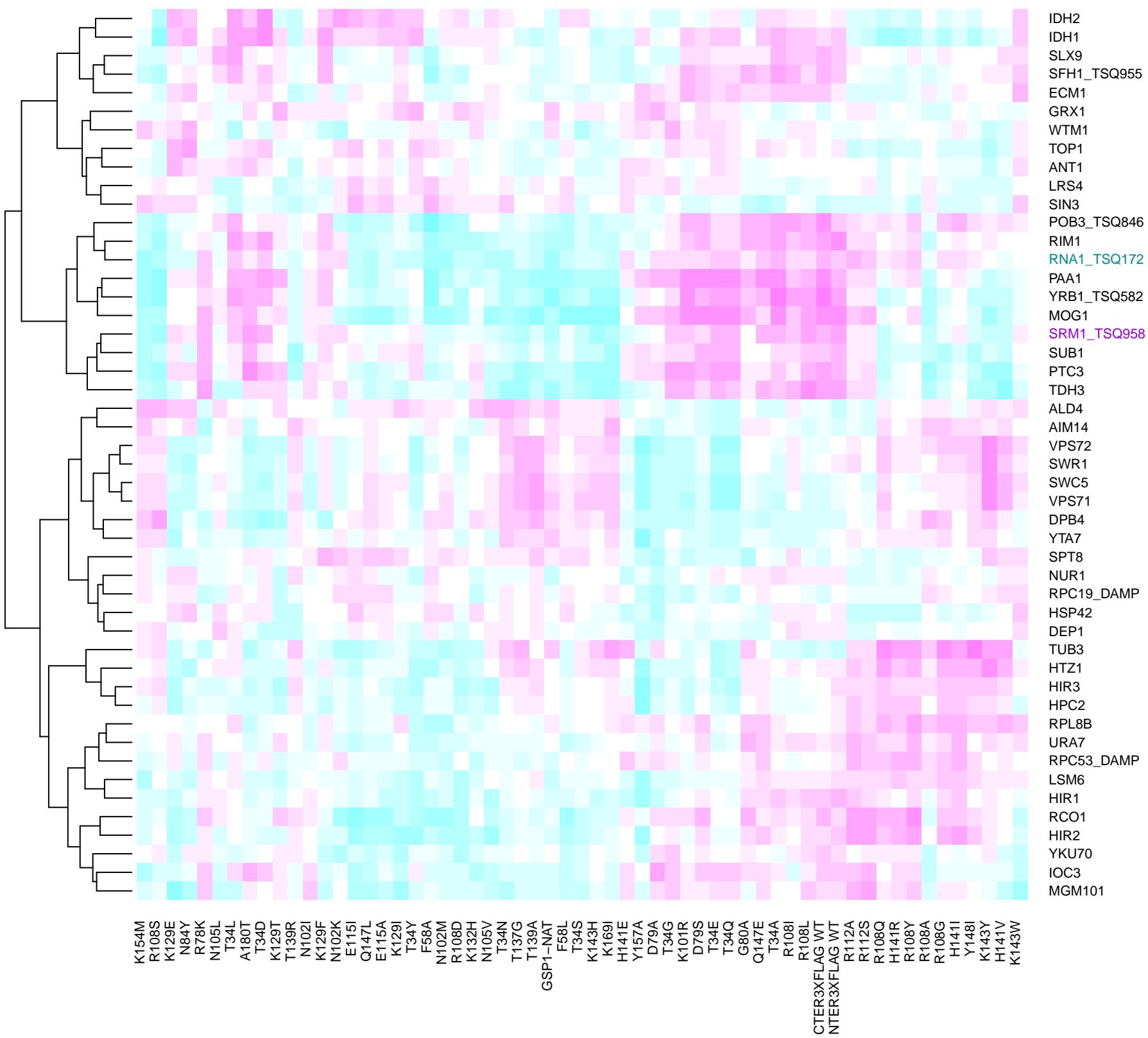


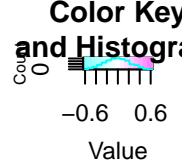
site of polarized growth



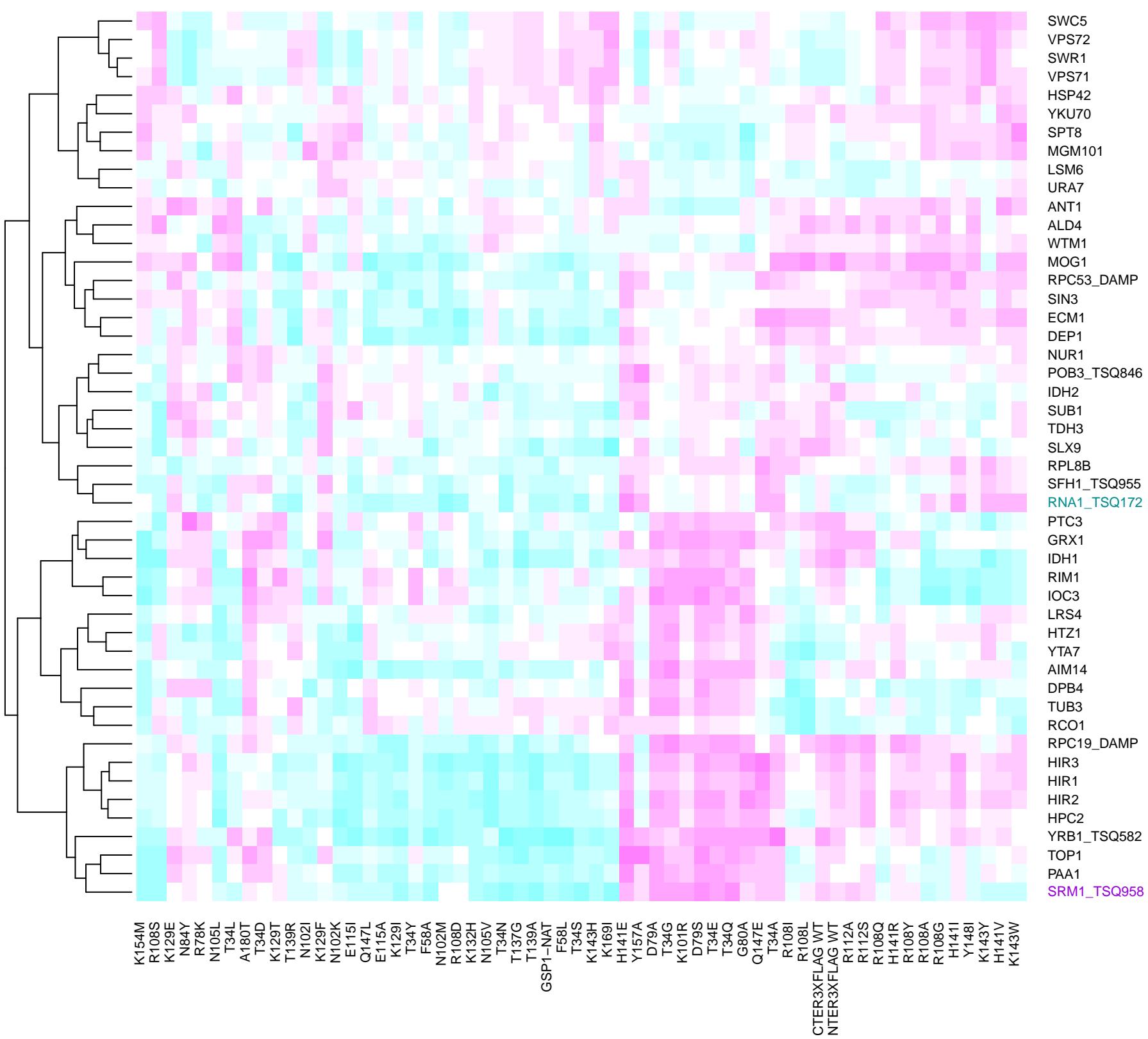


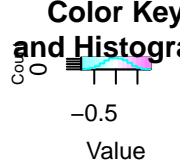
site of polarized growth_GO_30_4



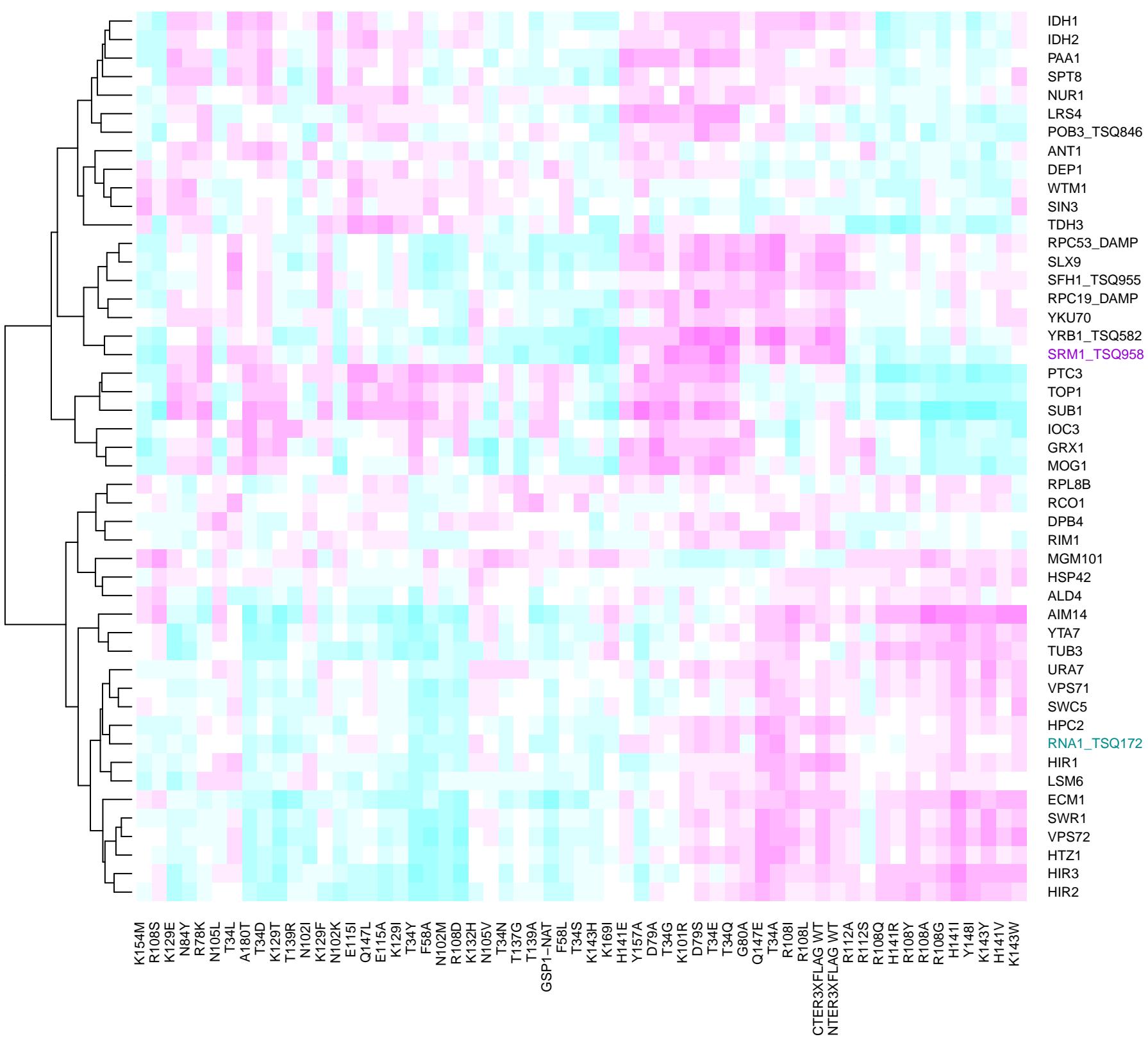


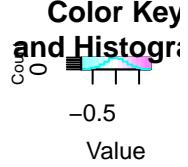
budding_GO_30_9



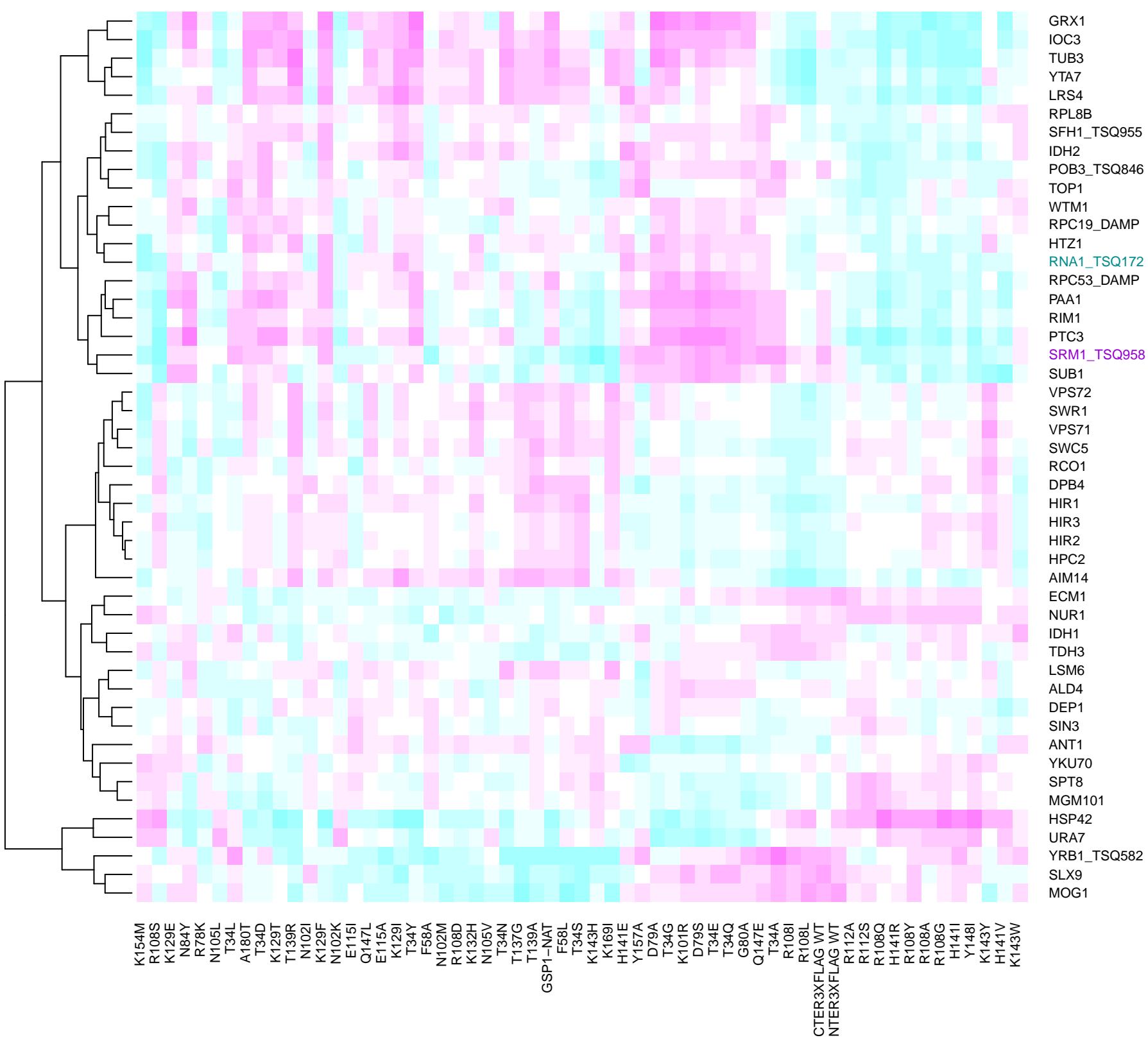


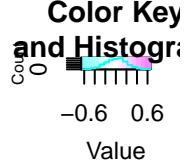
cell cycle_GO_30_11



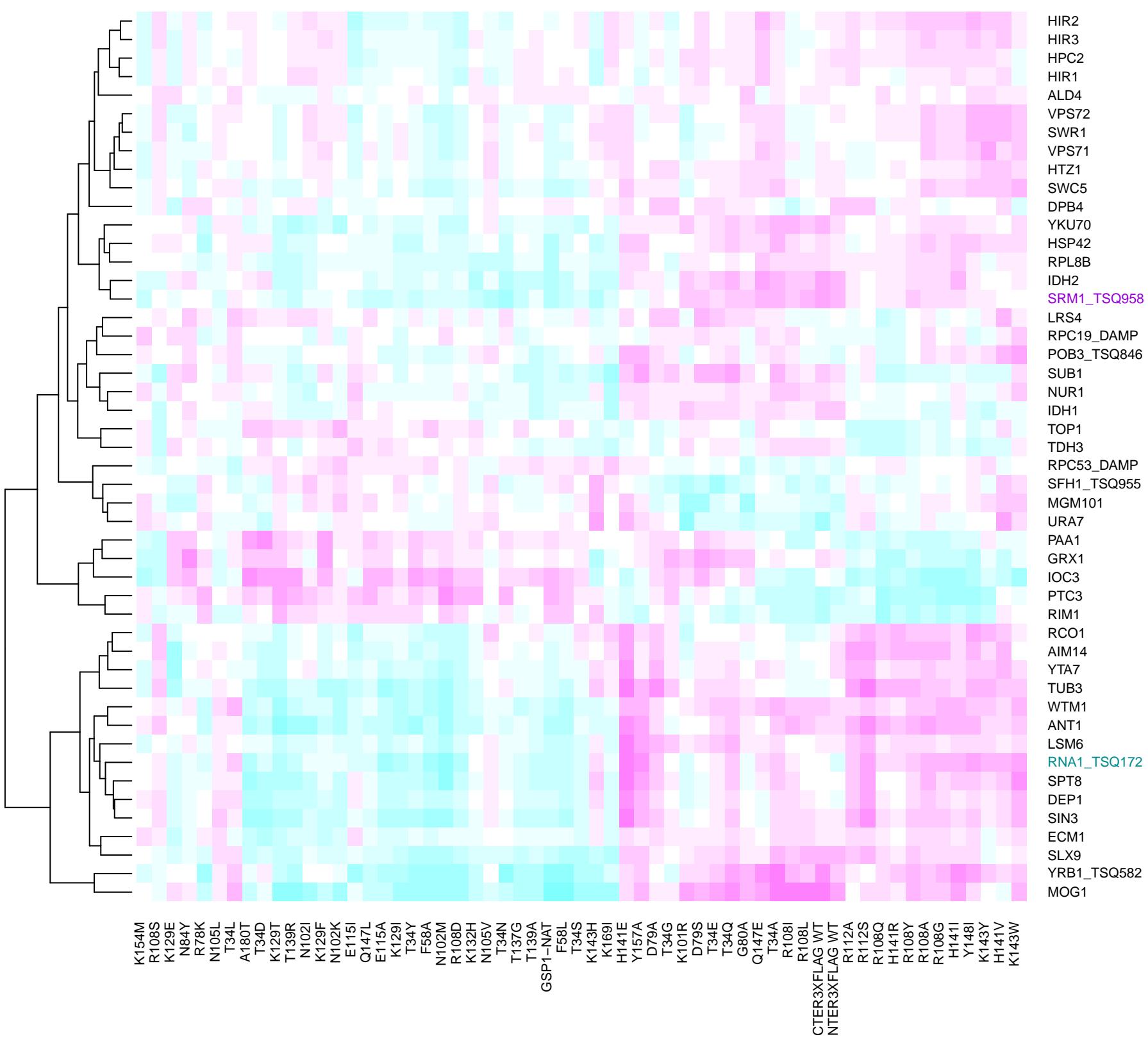


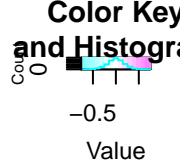
cytoskeleton and microtubules_GO_30_1



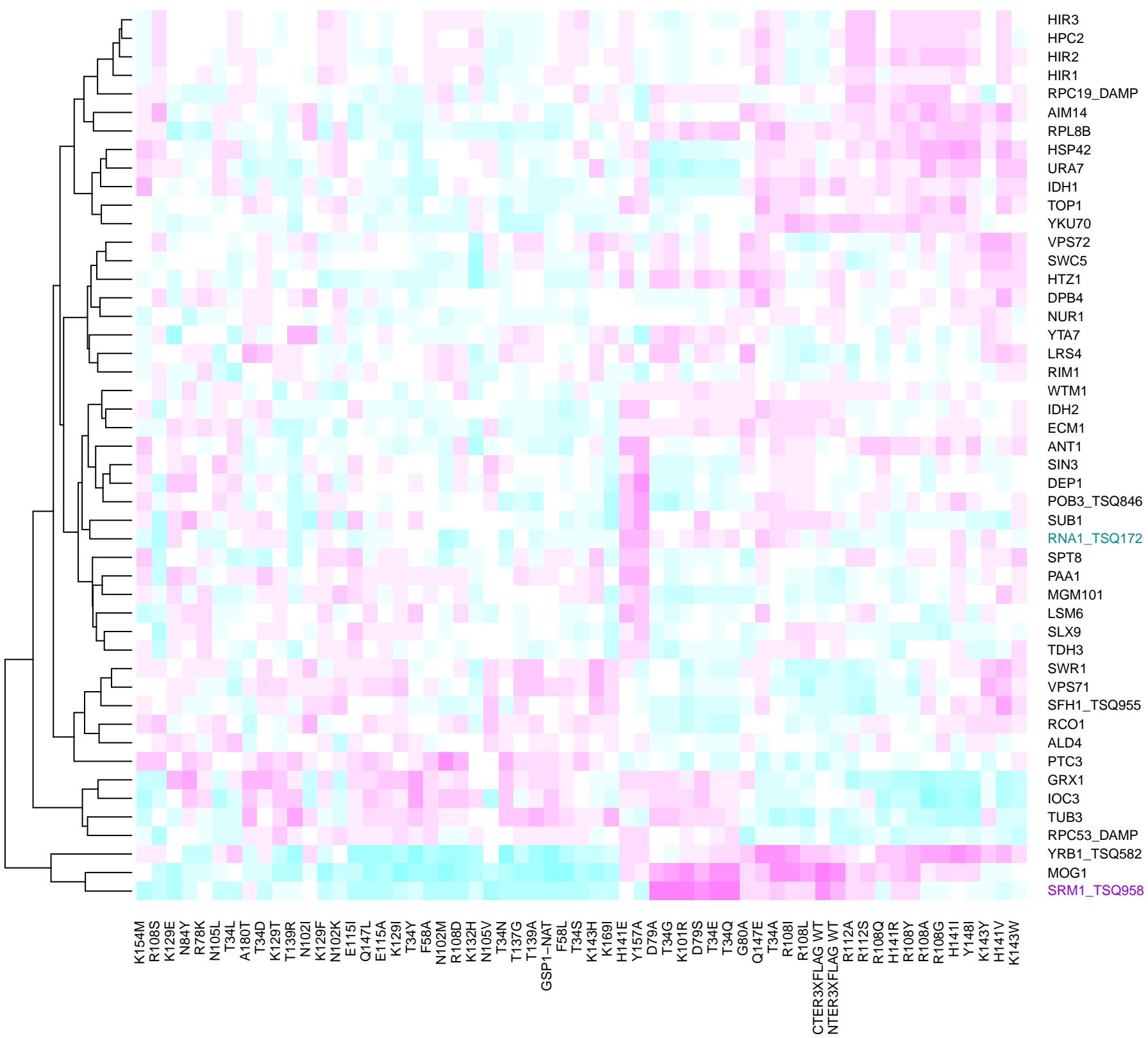


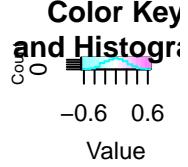
DNA replication_GO_30_1



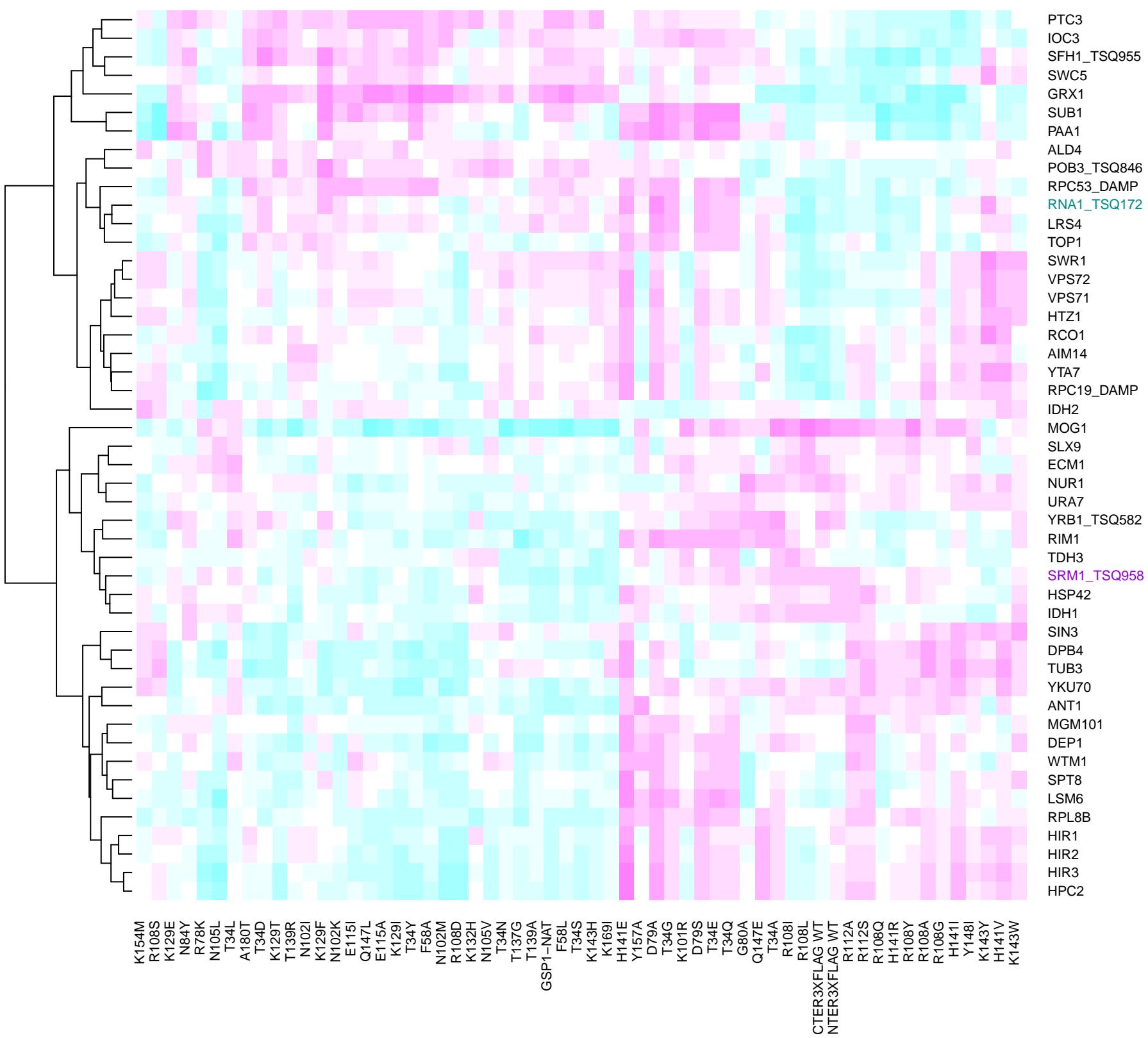


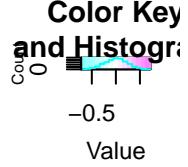
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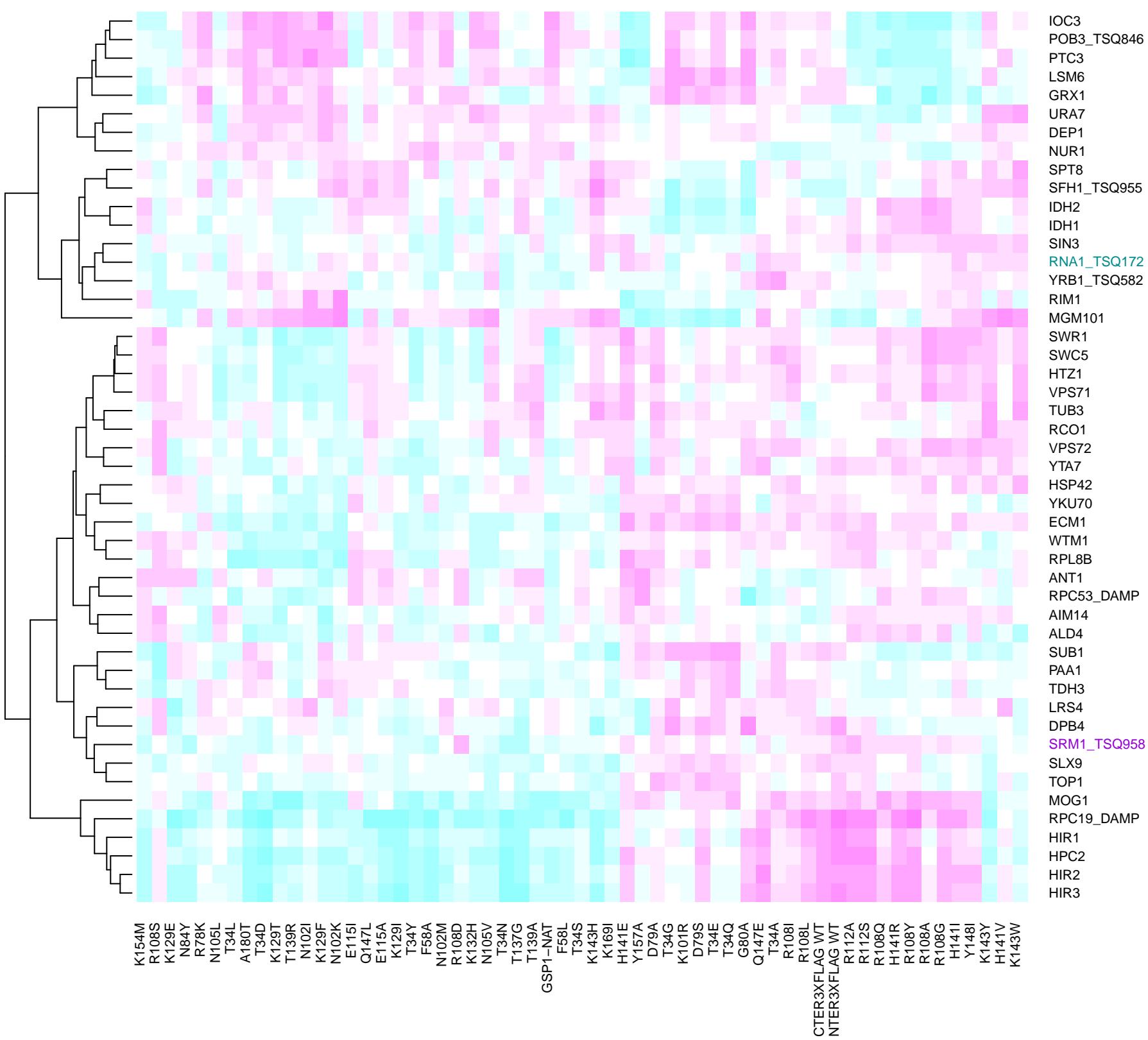


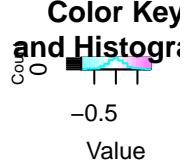
cytoskeleton and microtubules_GO_30_4



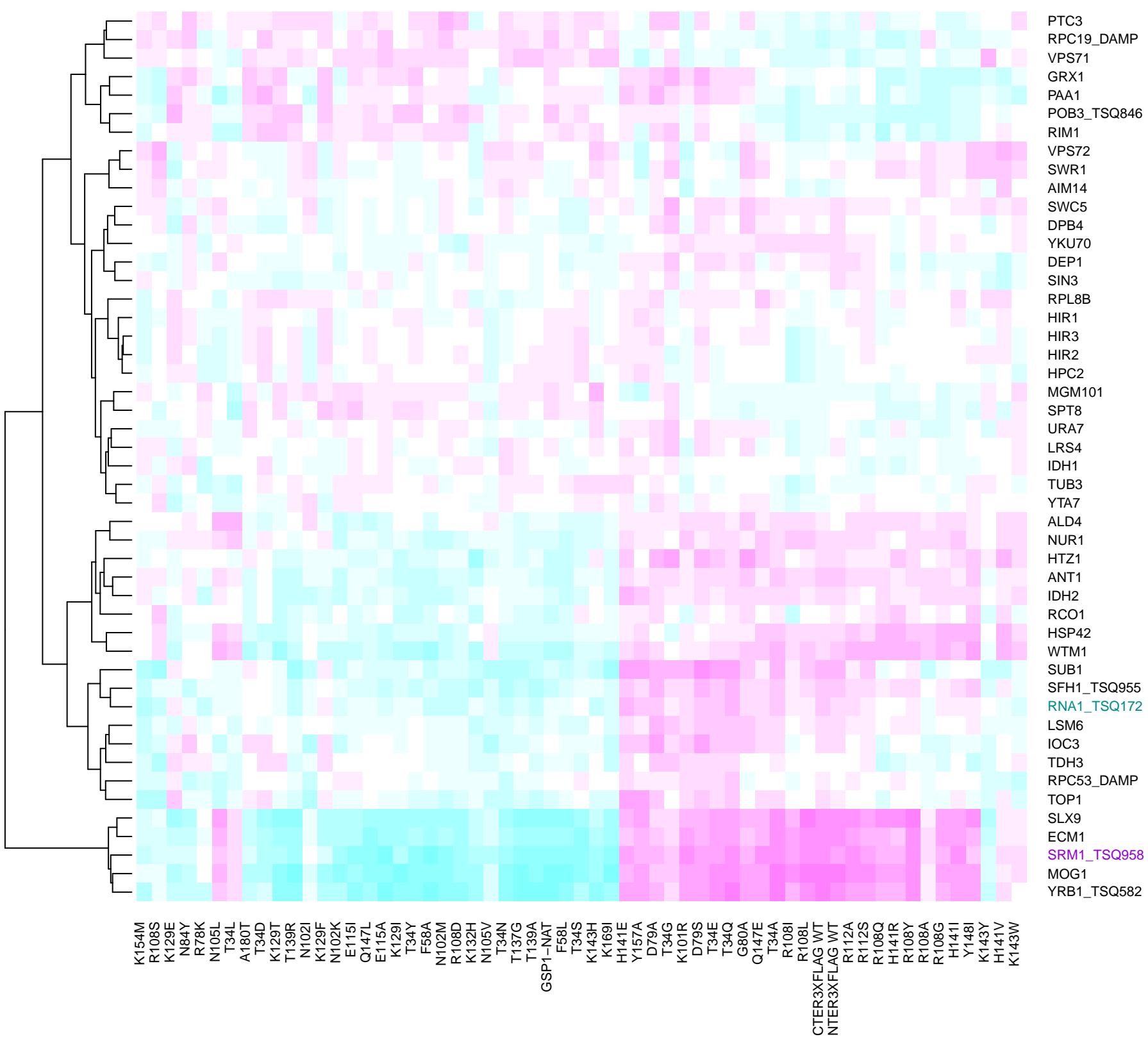


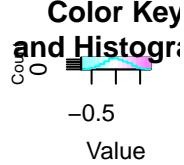
metabolic_GO_30_12



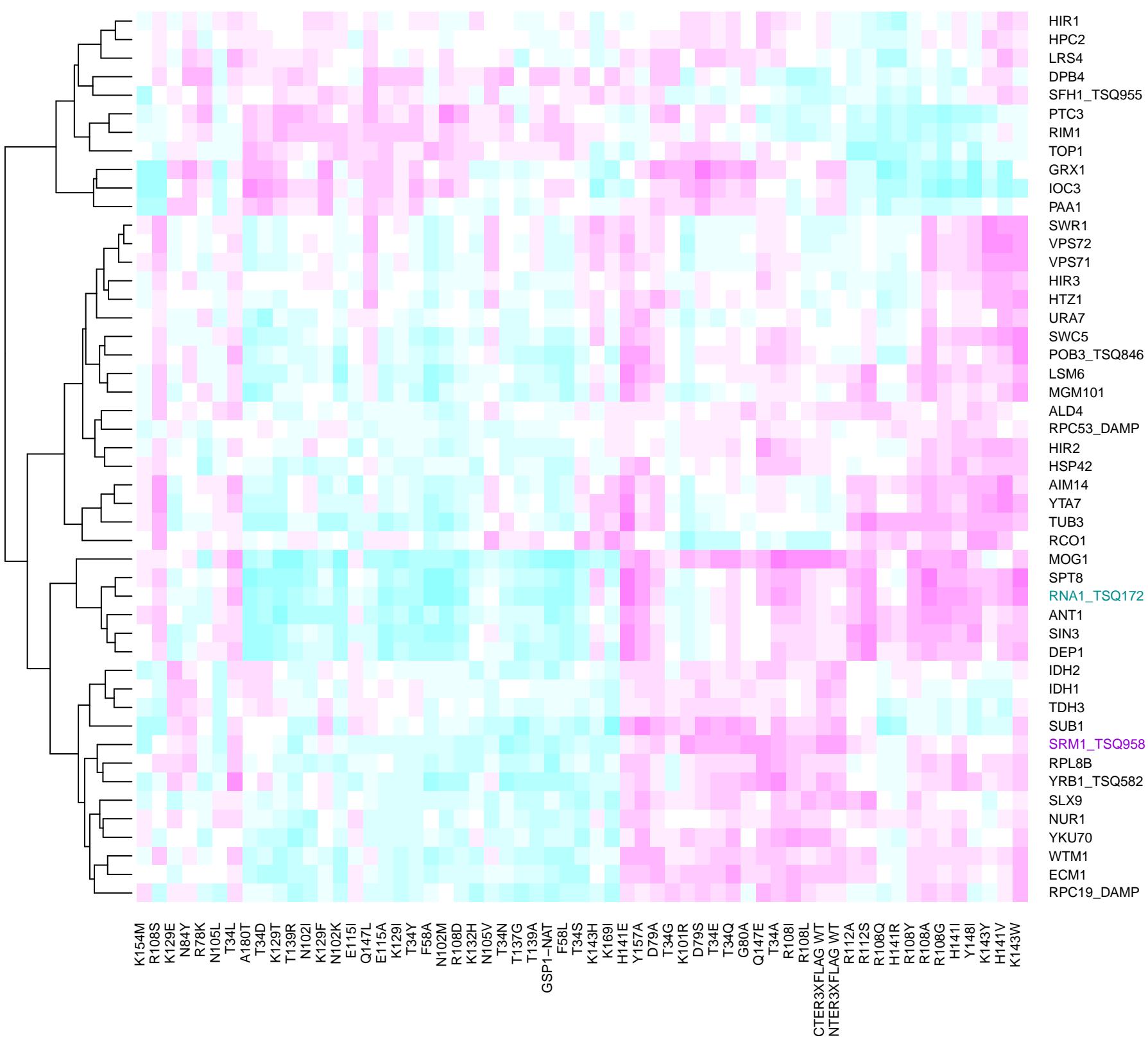


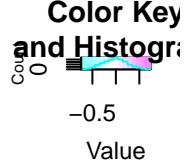
organelle fission_GO_30_2



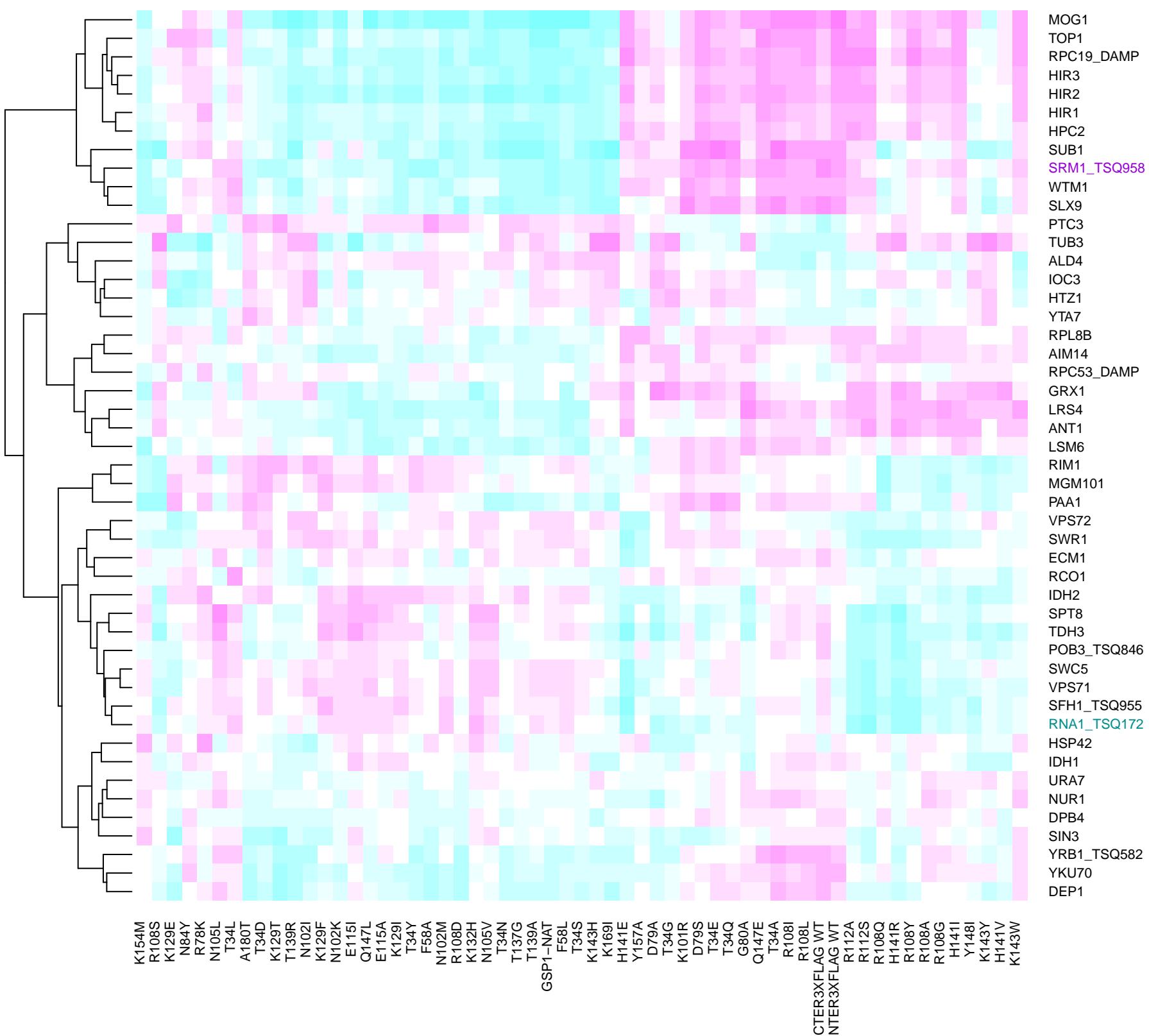


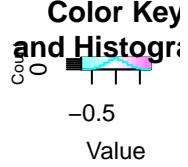
regulation of DNA metabolic process_GO_30_1



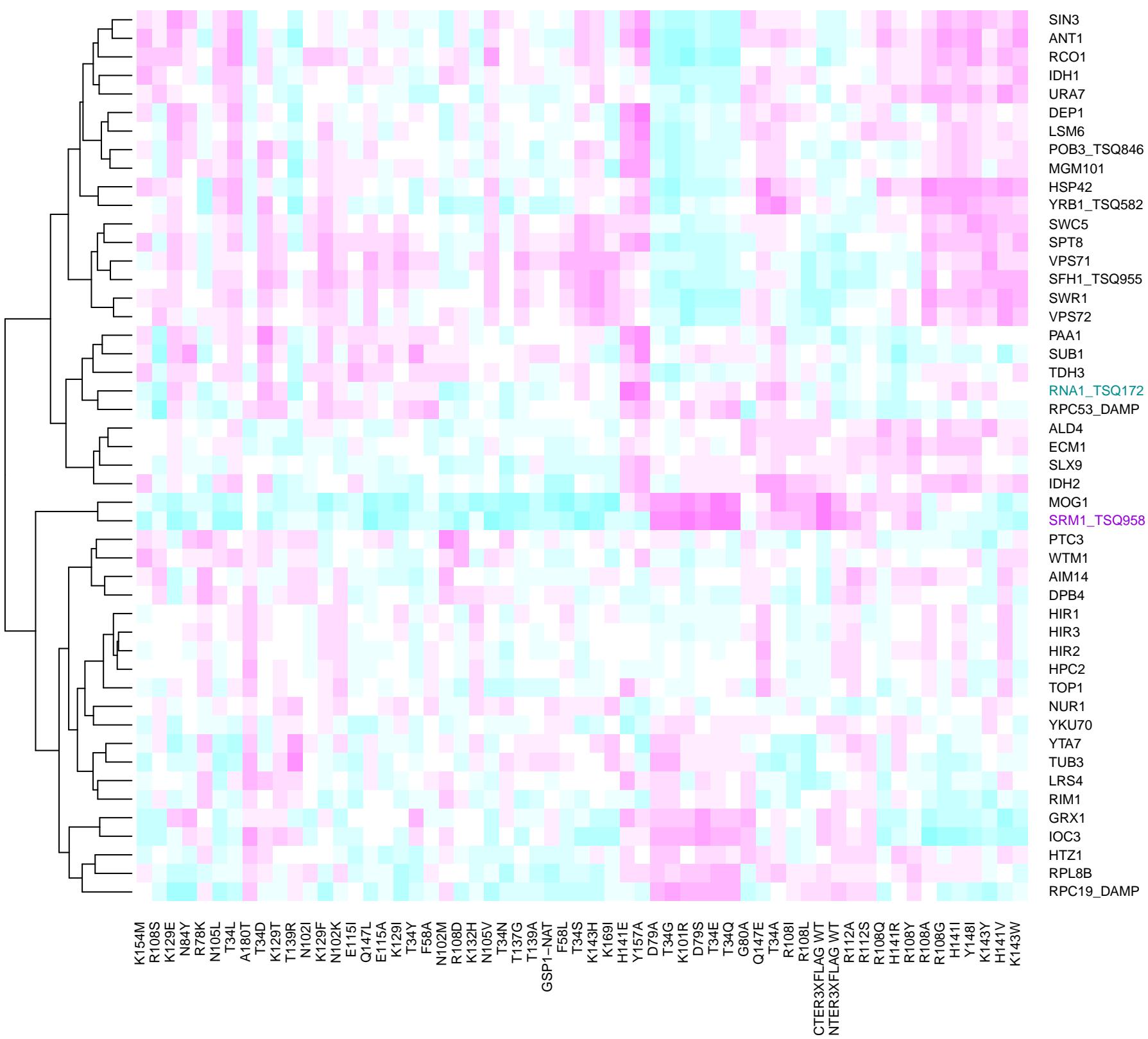


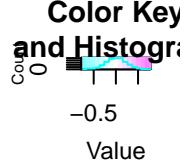
organelle assembly_GO_30_2





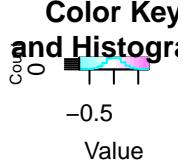
budding_GO_30_5



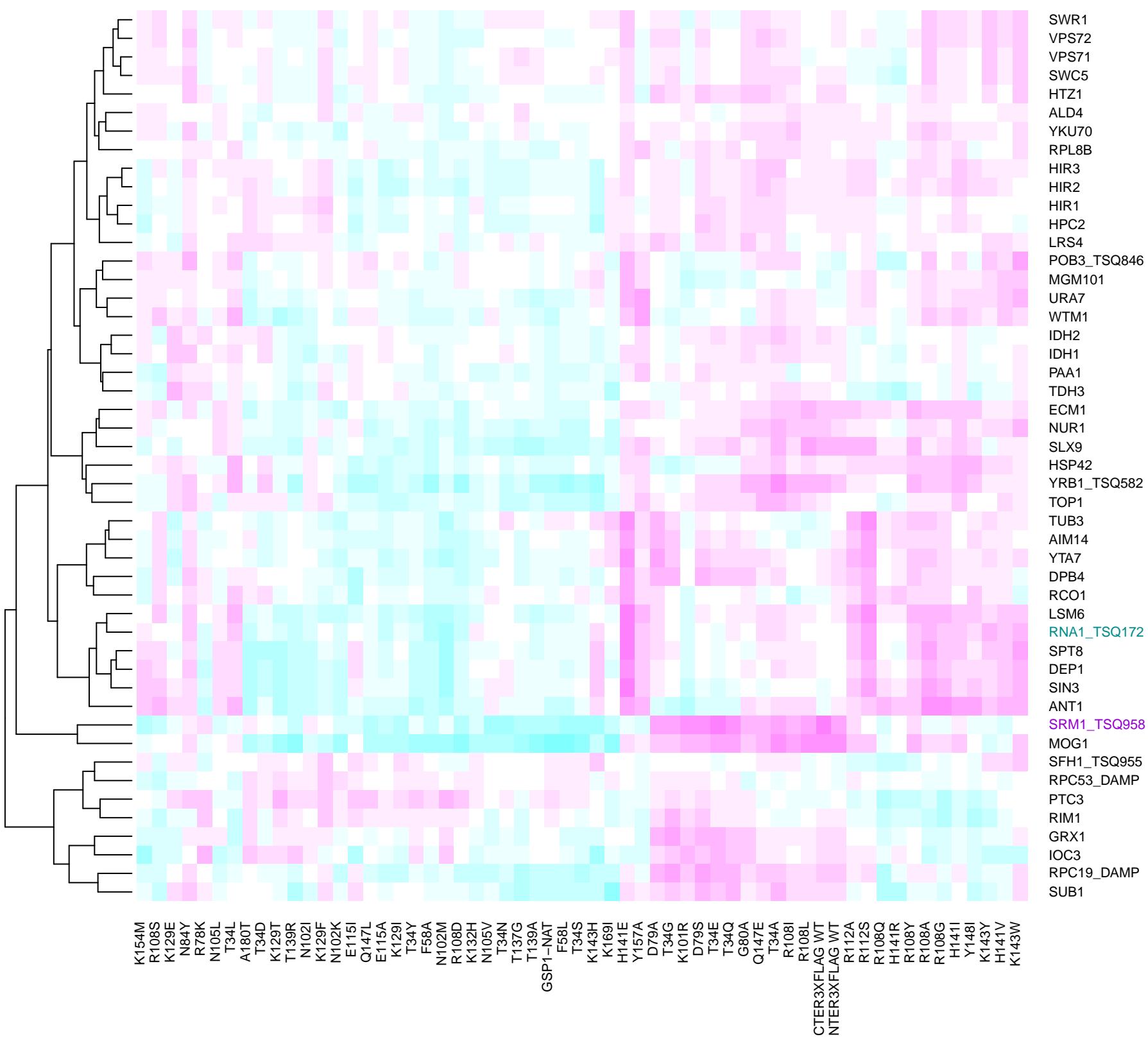


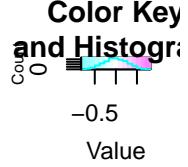
cell cycle_GO_30_1



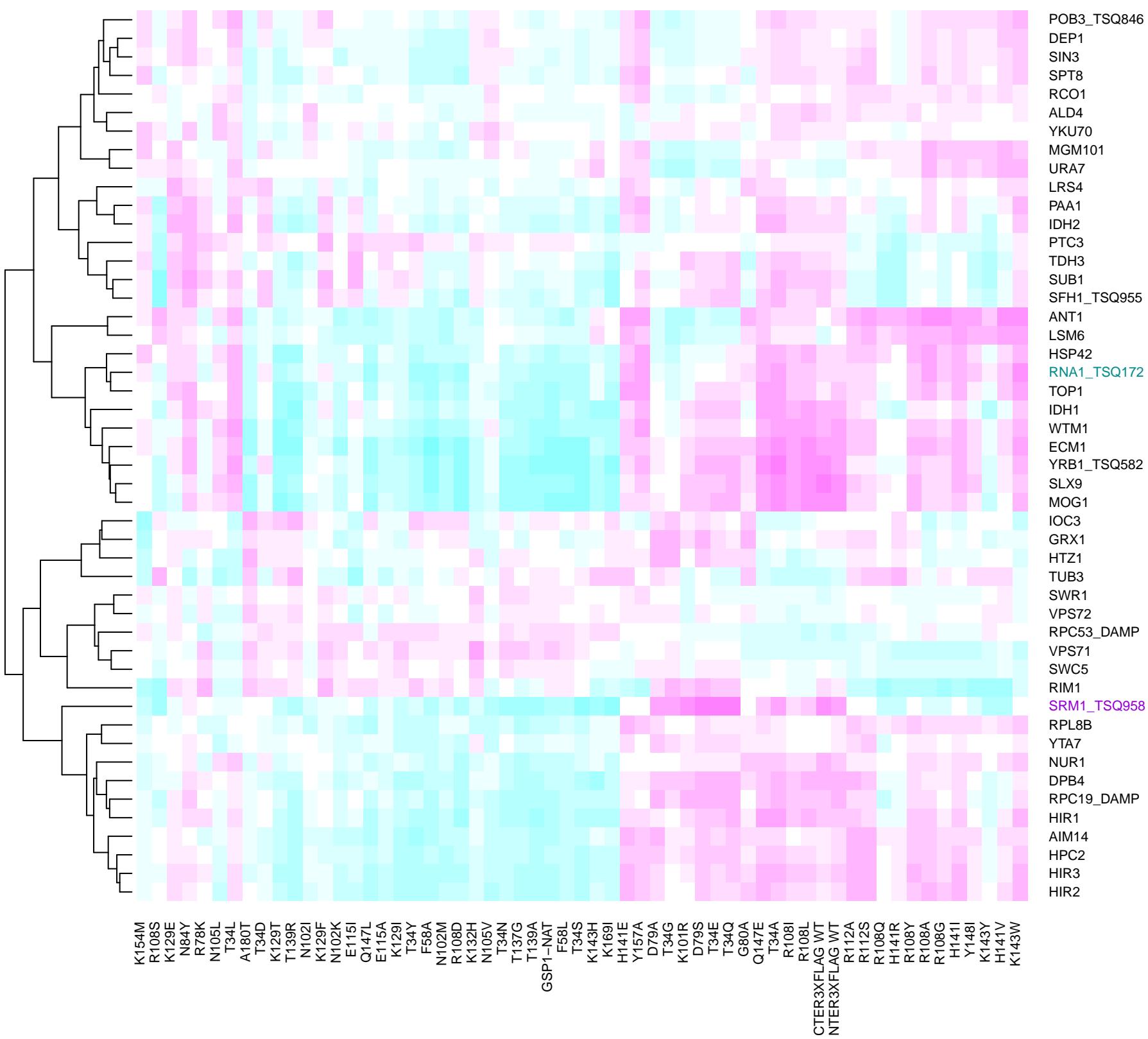


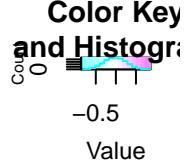
cellular response to DNA damage stimulus_GO_30_1



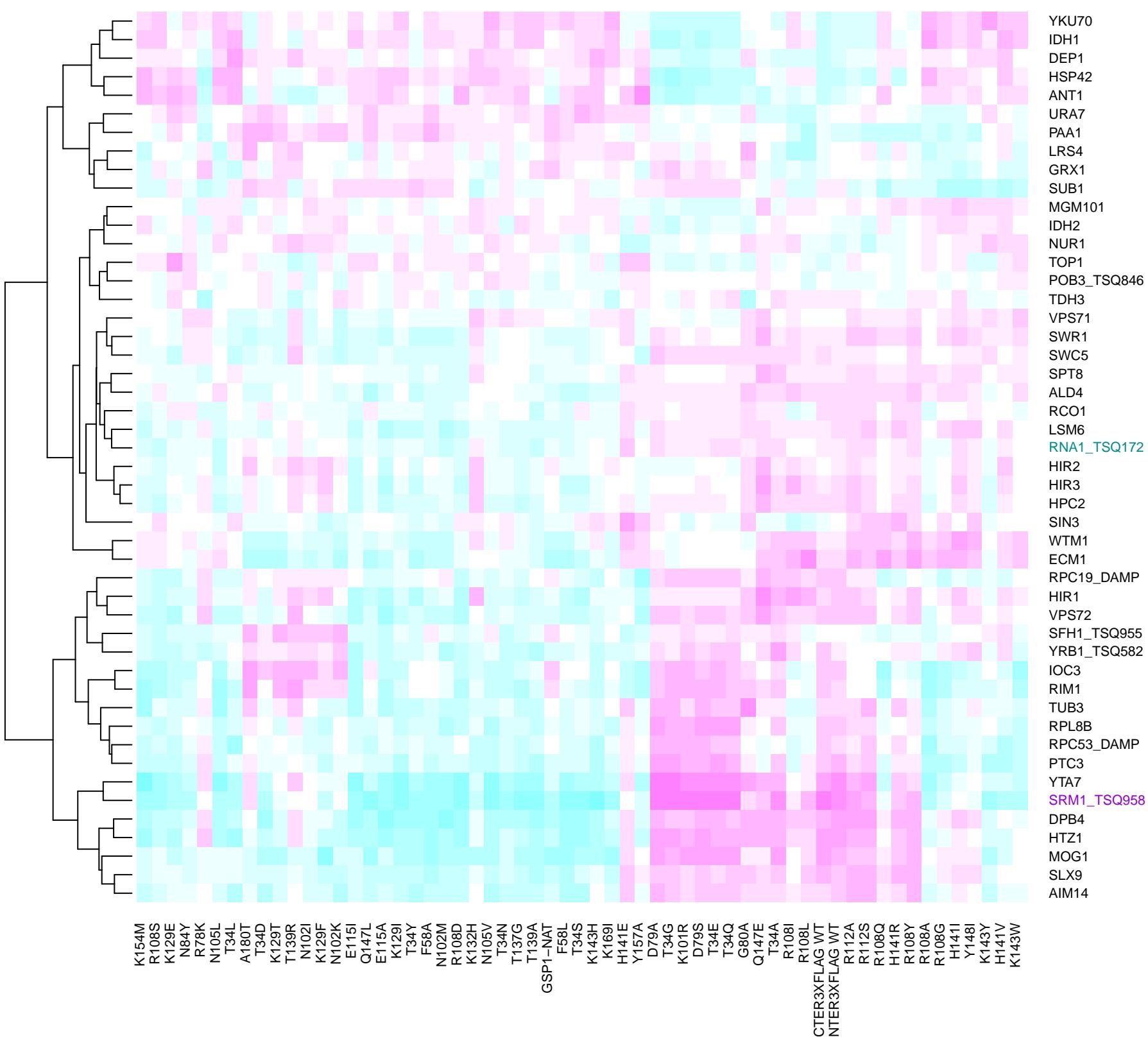


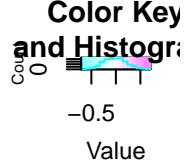
chromosome segregation_GO_30_2



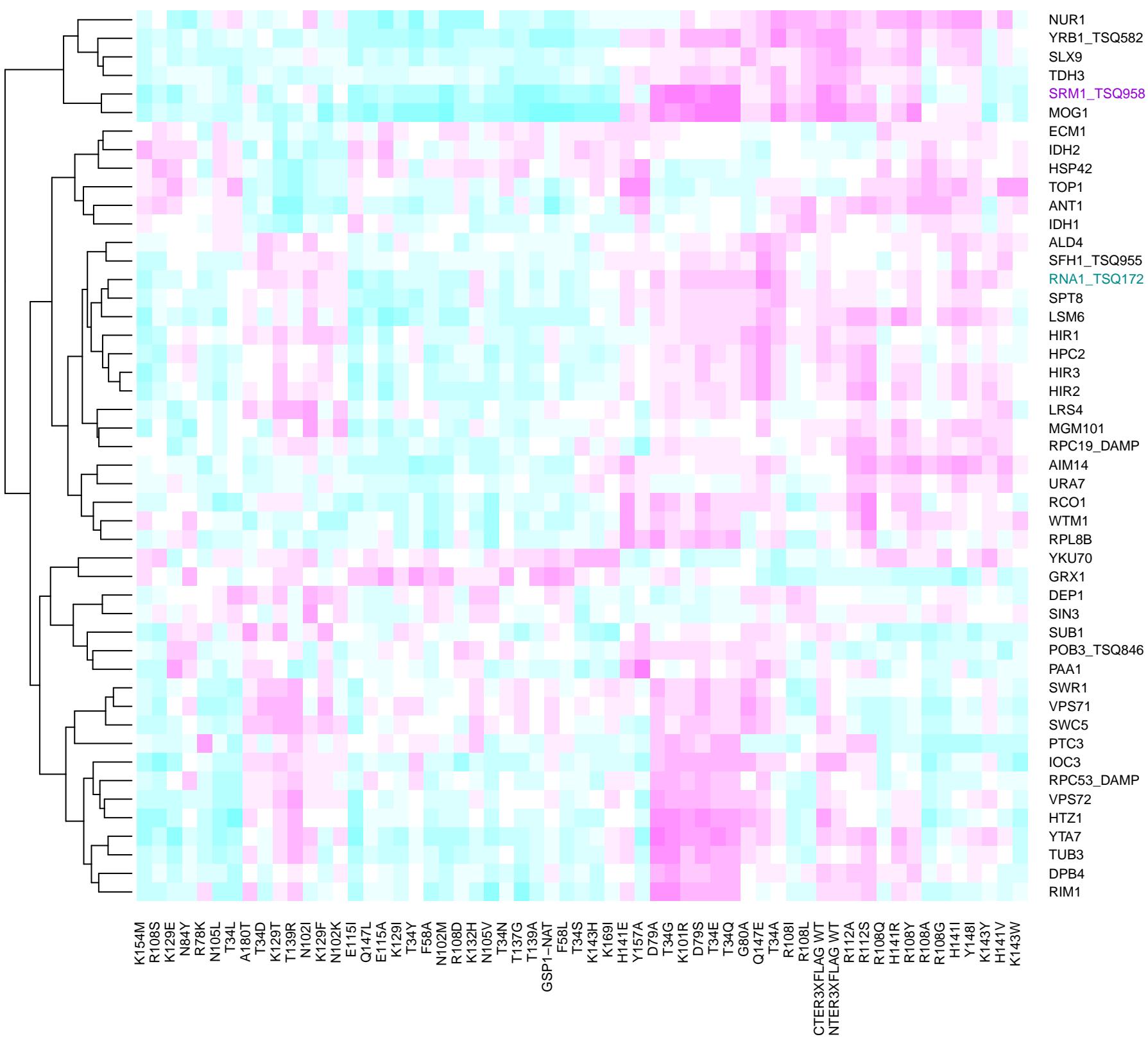


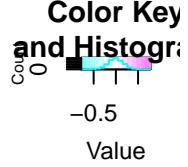
cytoskeleton and microtubules_GO_30_6



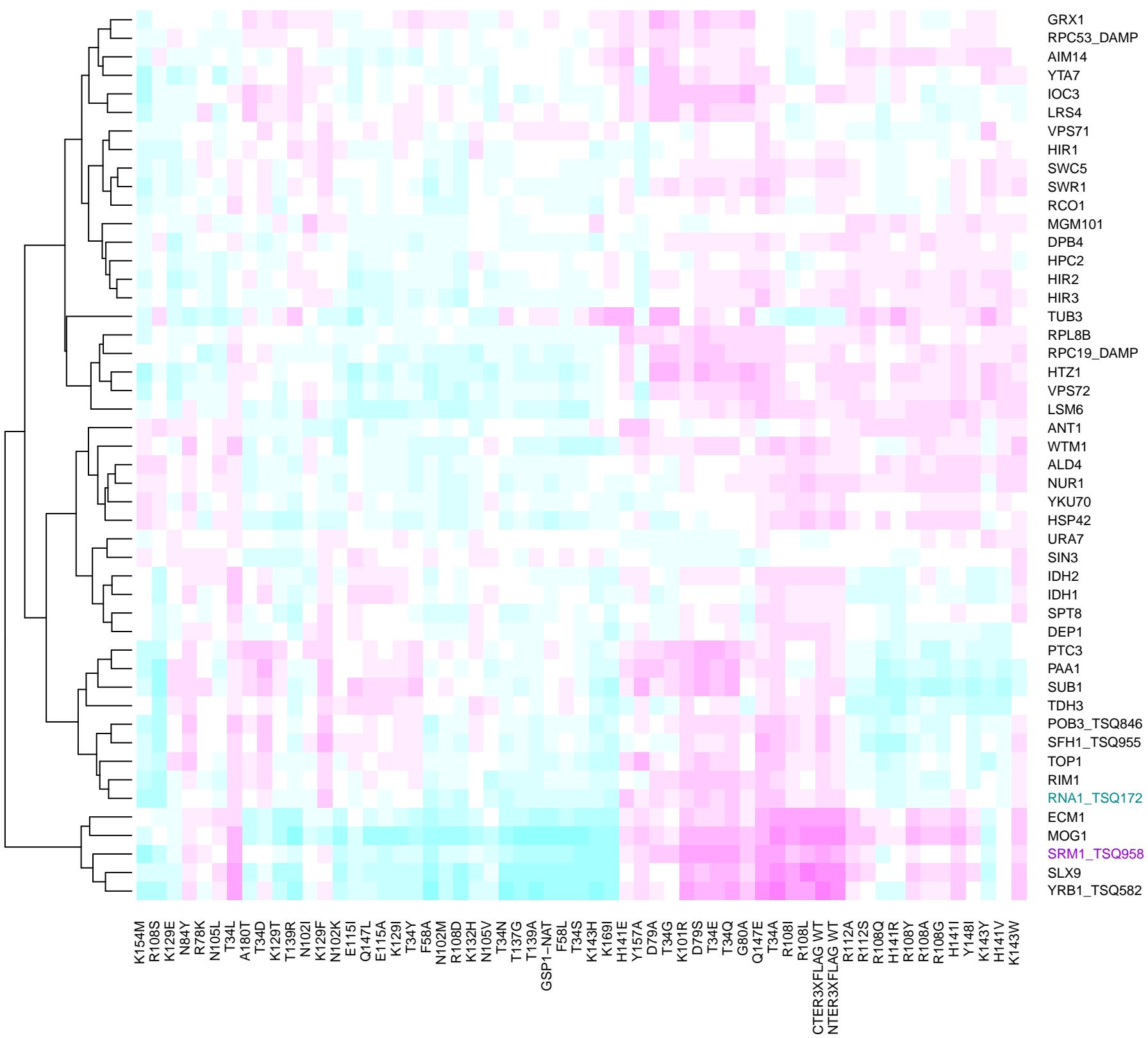


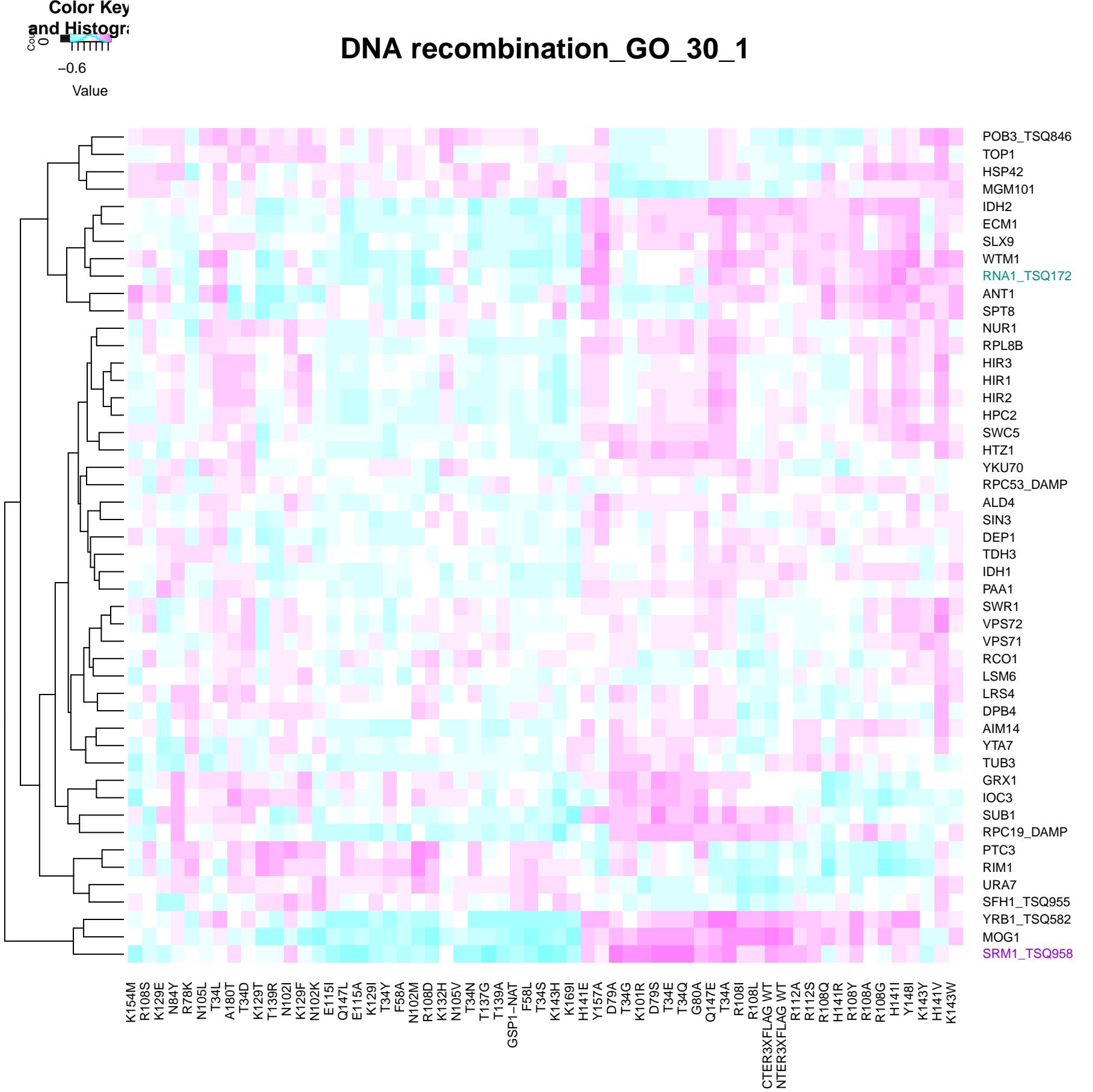
cytoskeleton_GO_30_2

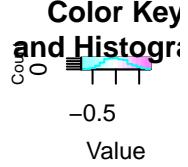




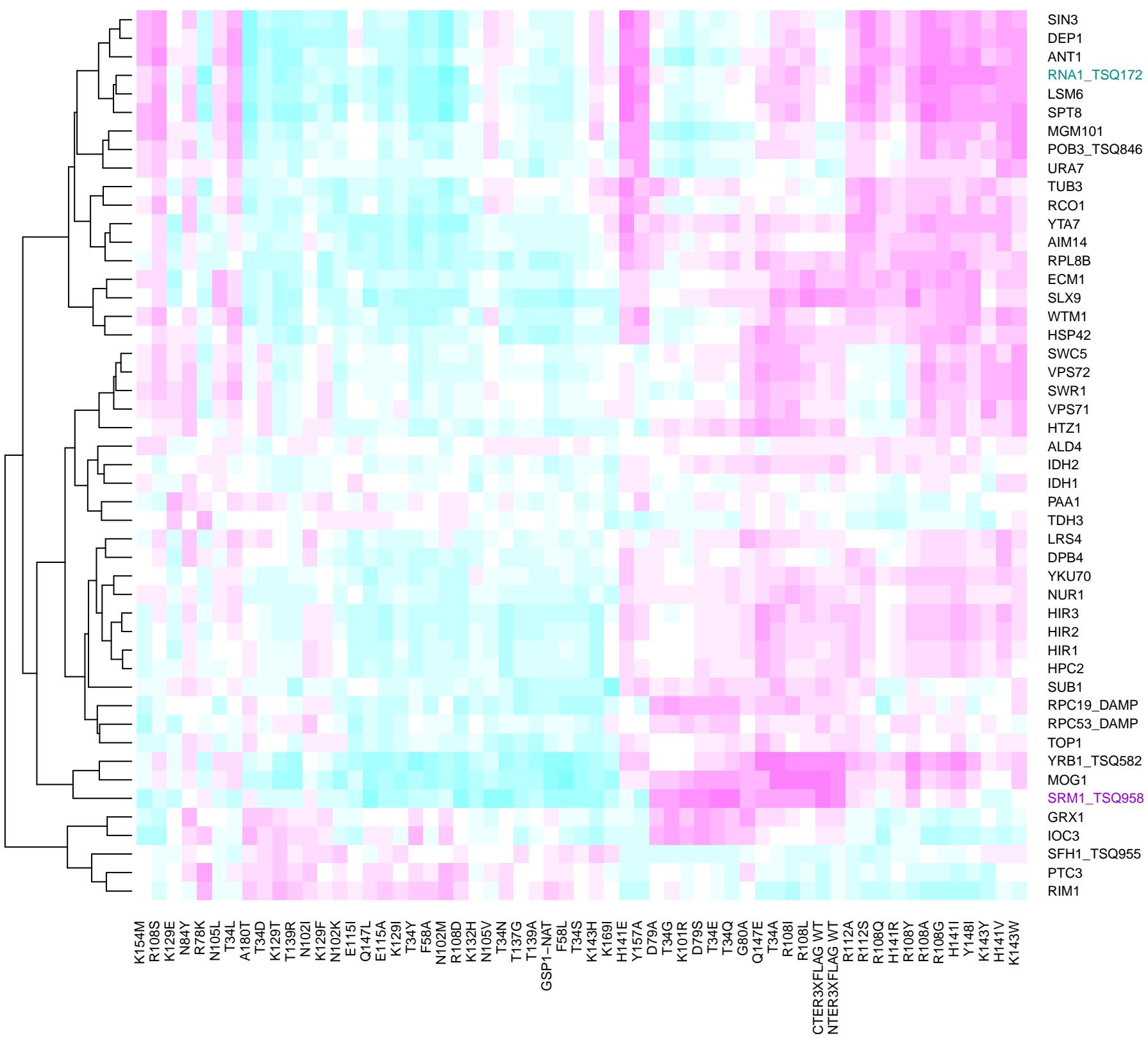
cytoskeleton organization

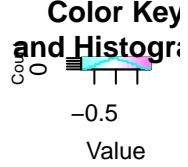




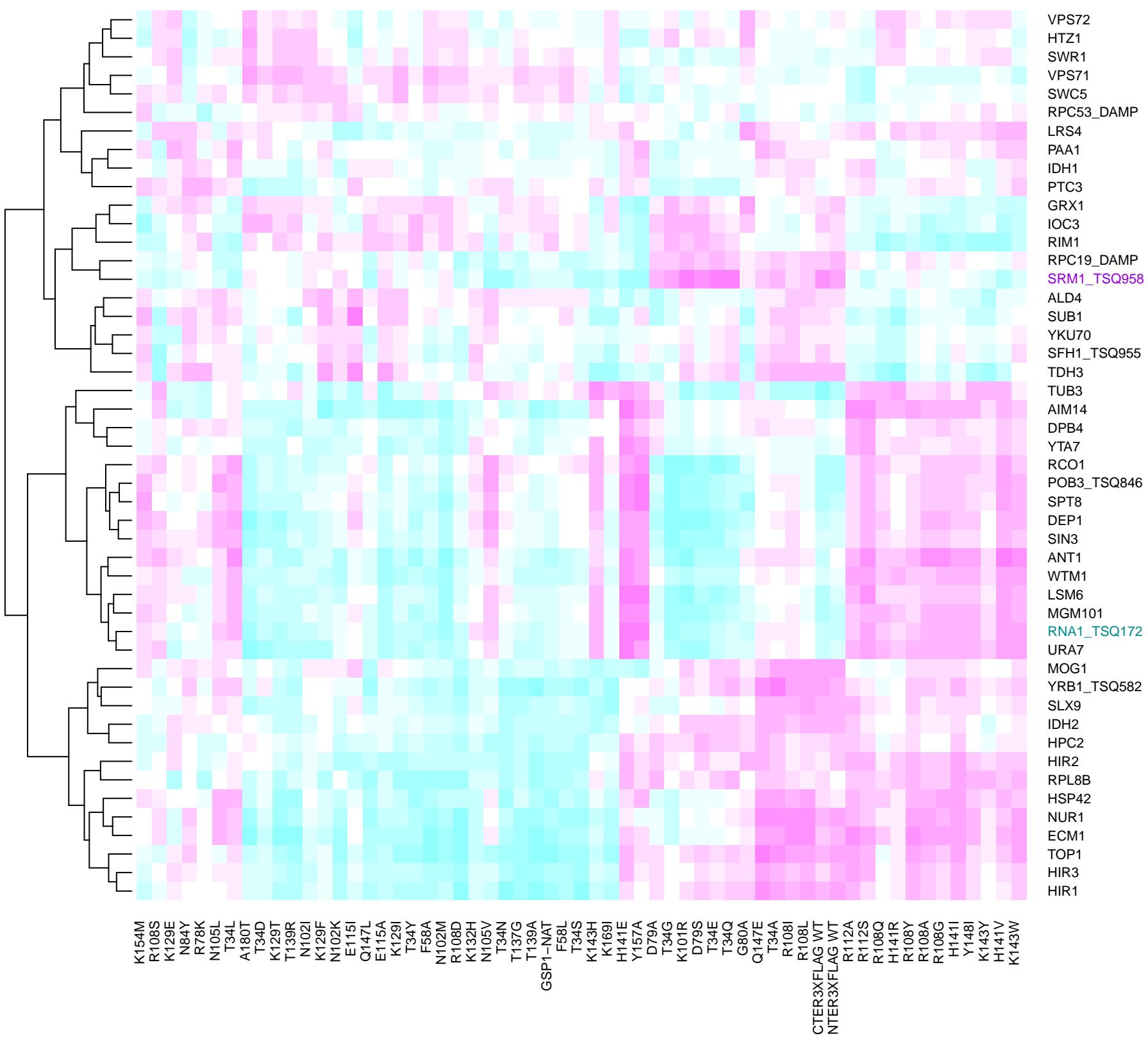


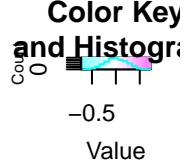
DNA repair_GO_30_1



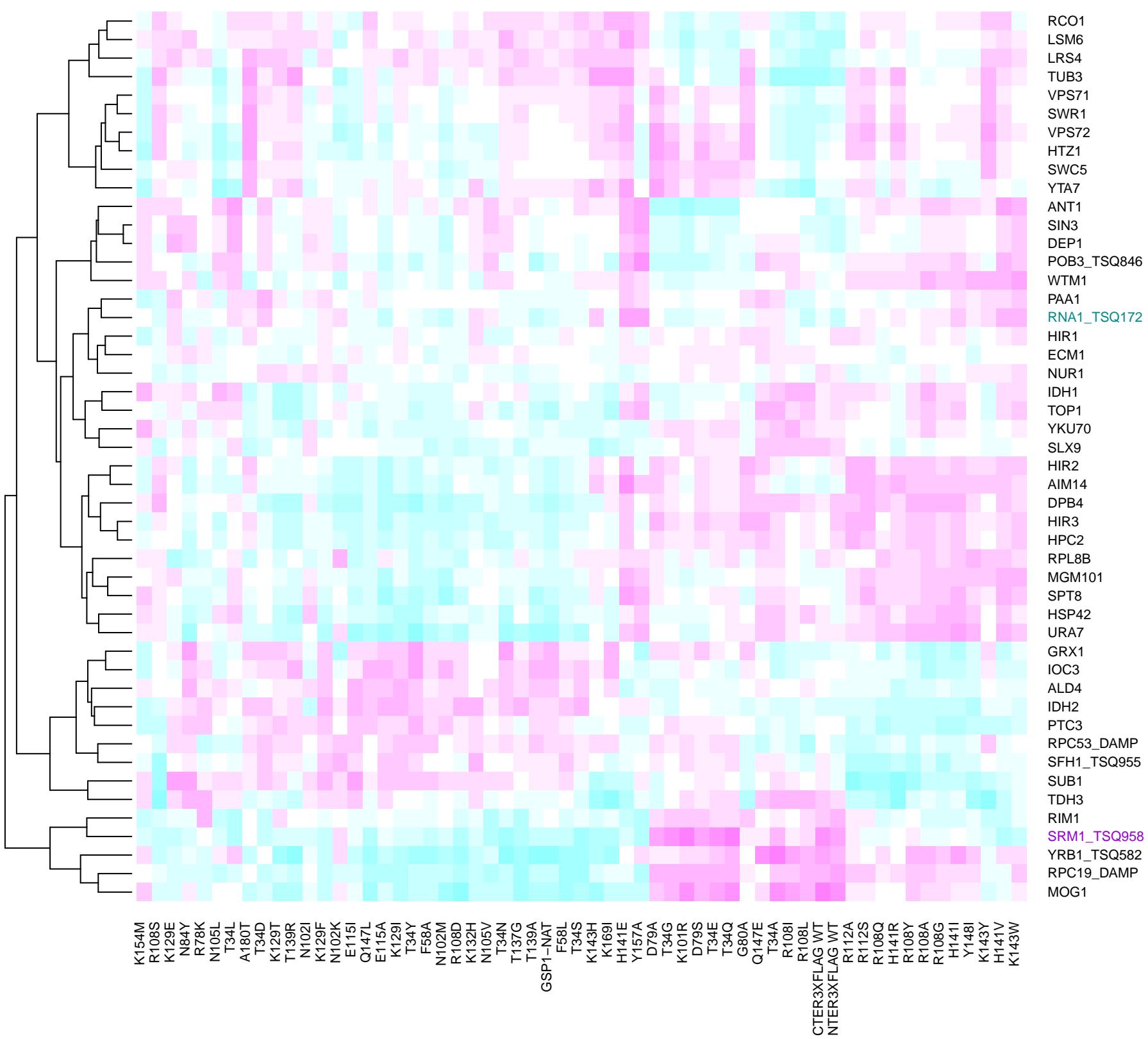


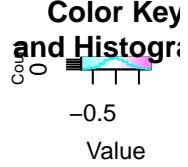
mitotic cell cycle_GO_30_5



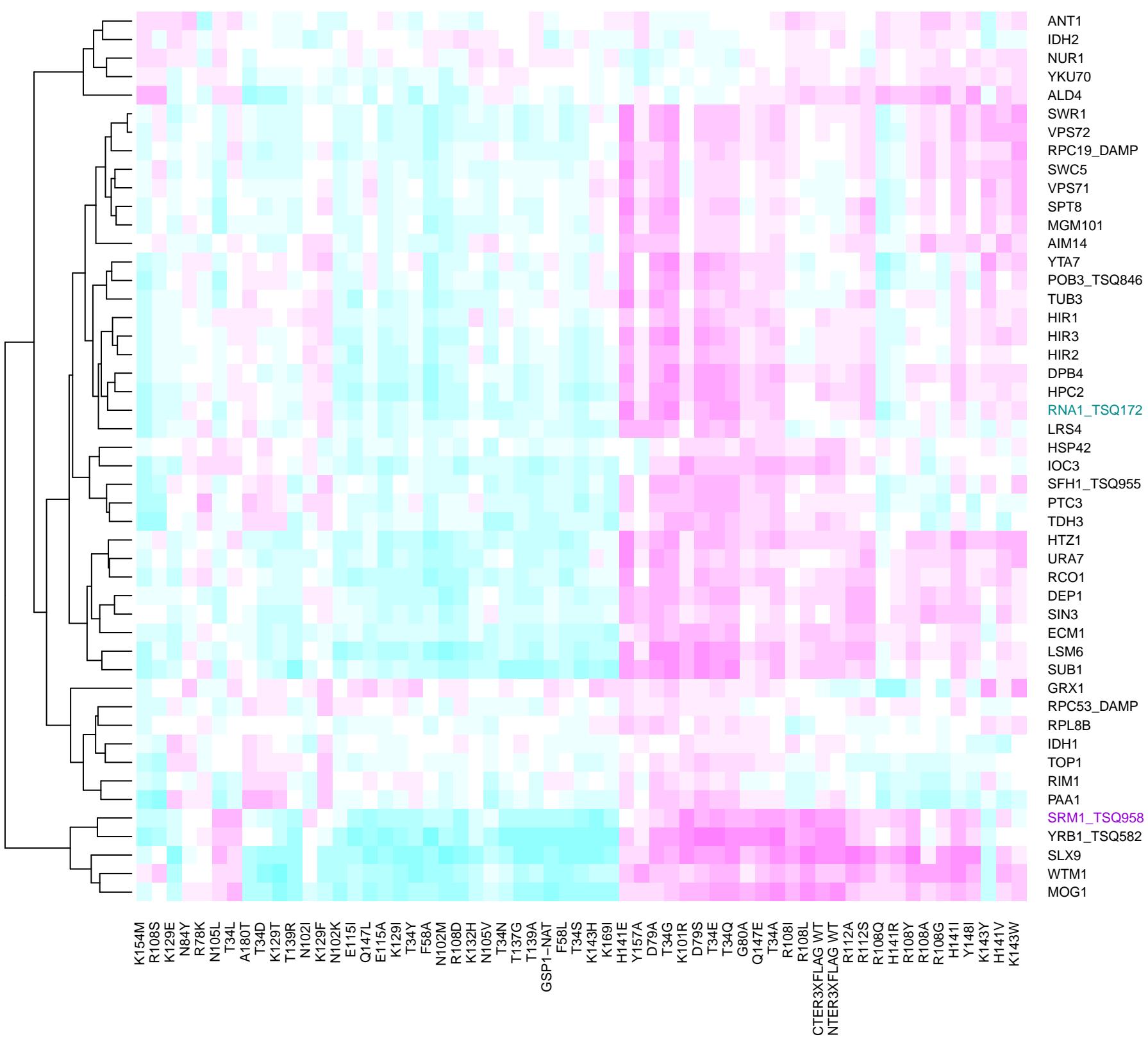


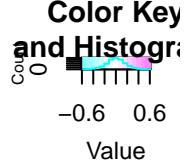
organelle fission_GO_30_1



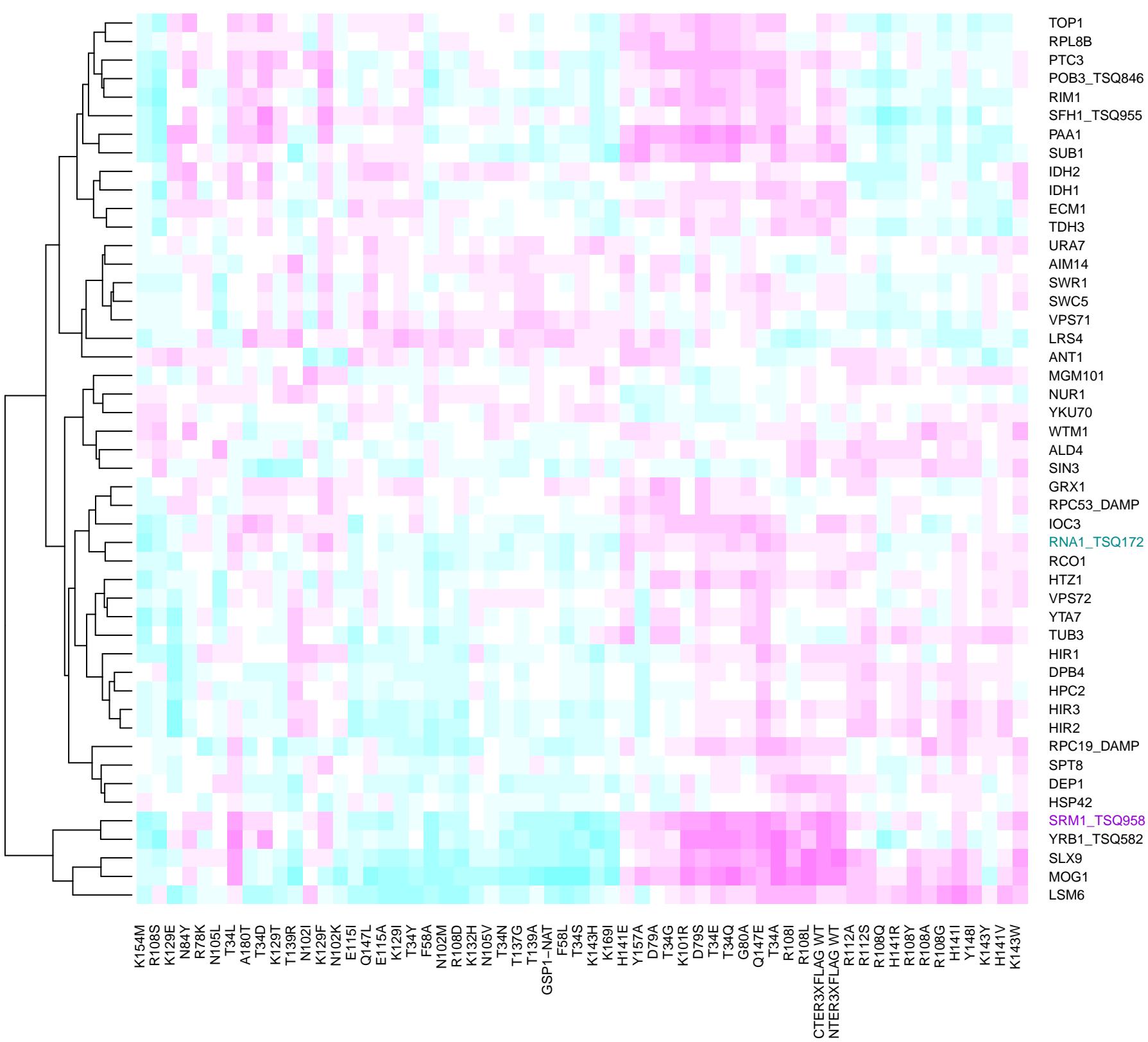


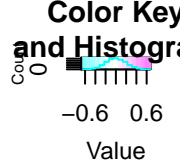
budding_GO_30_2



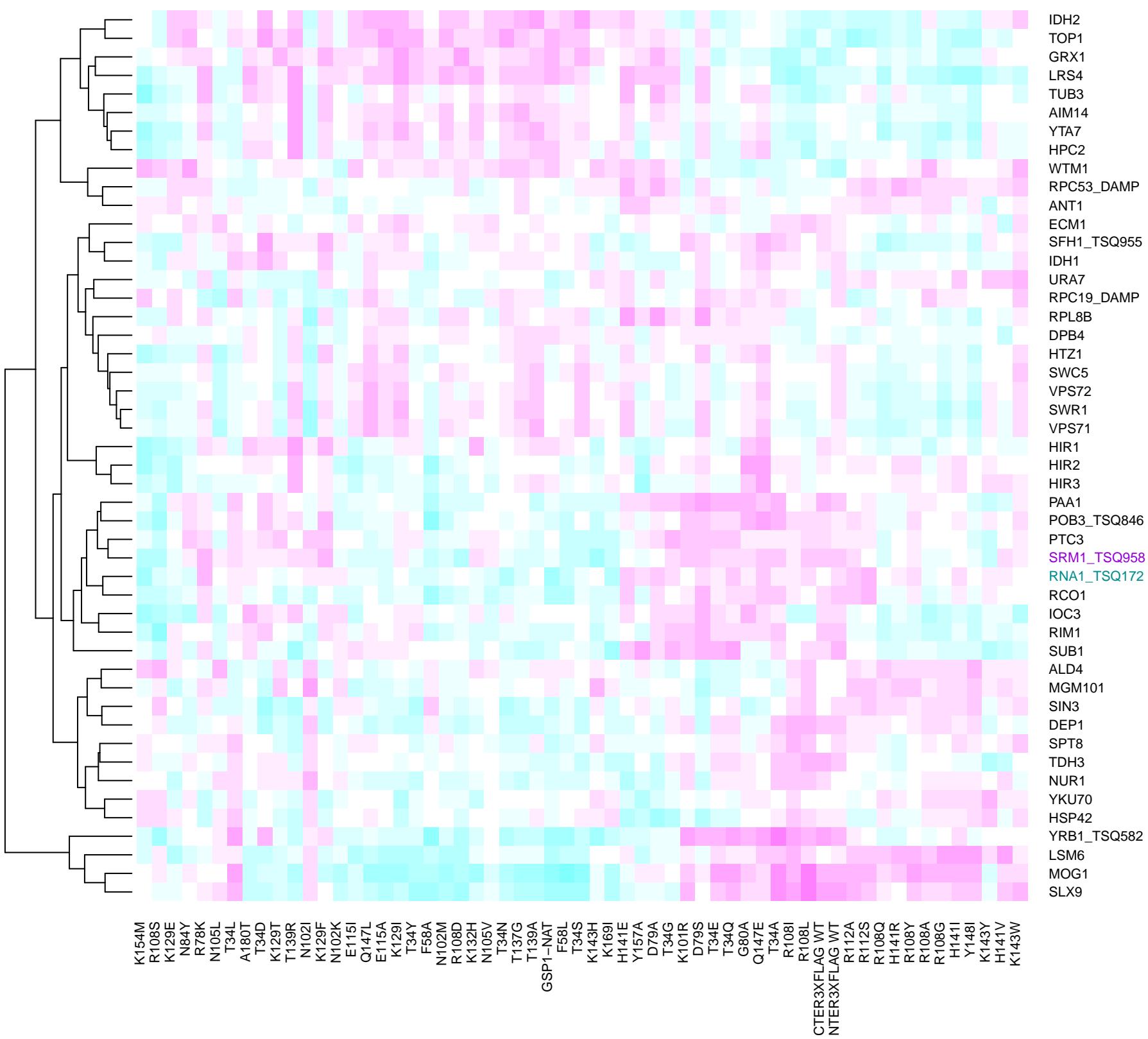


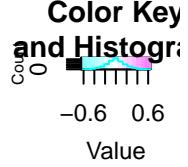
cell cortex



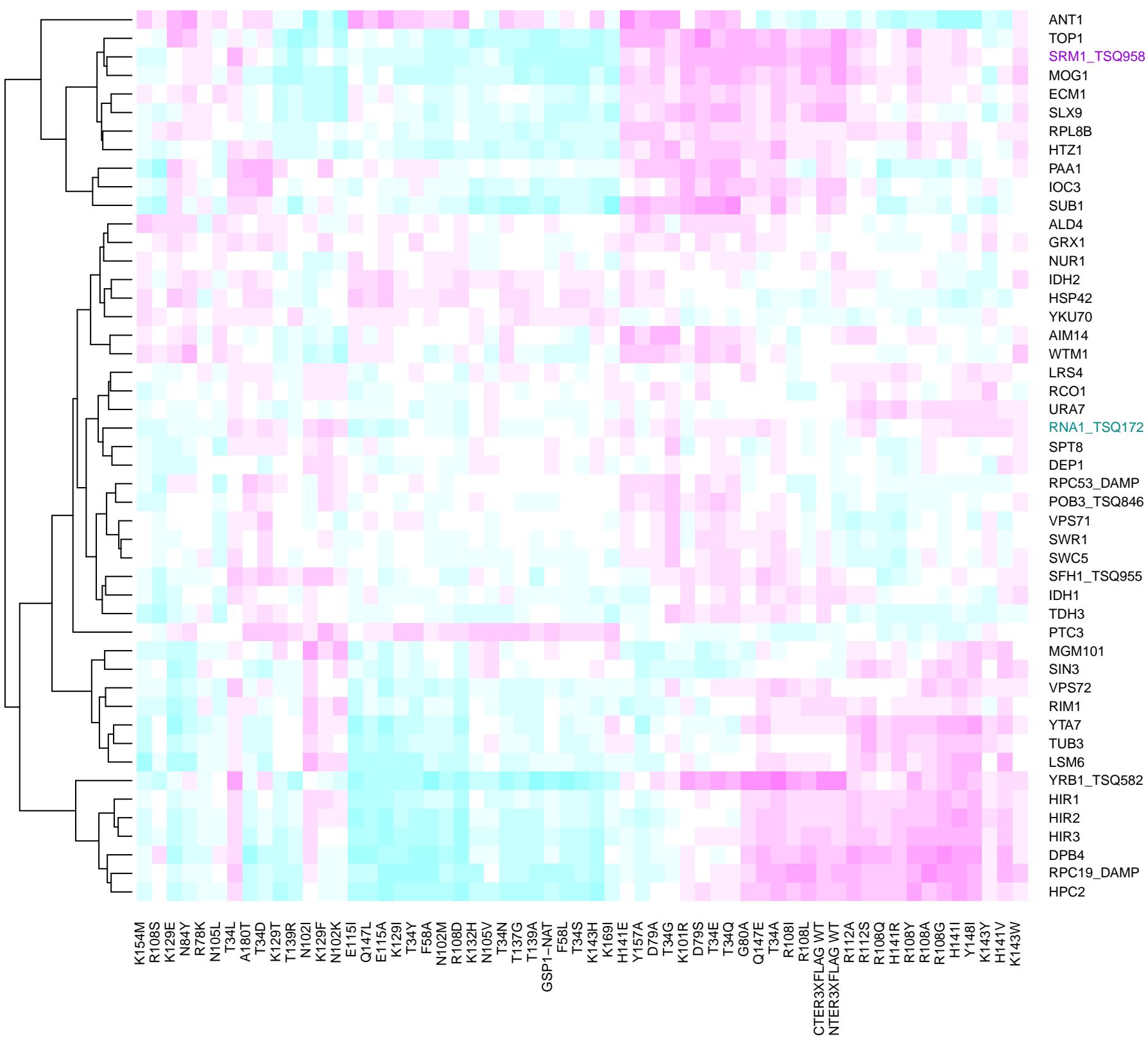


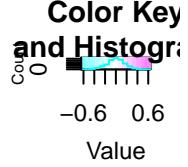
cell cortex_GO_30_1



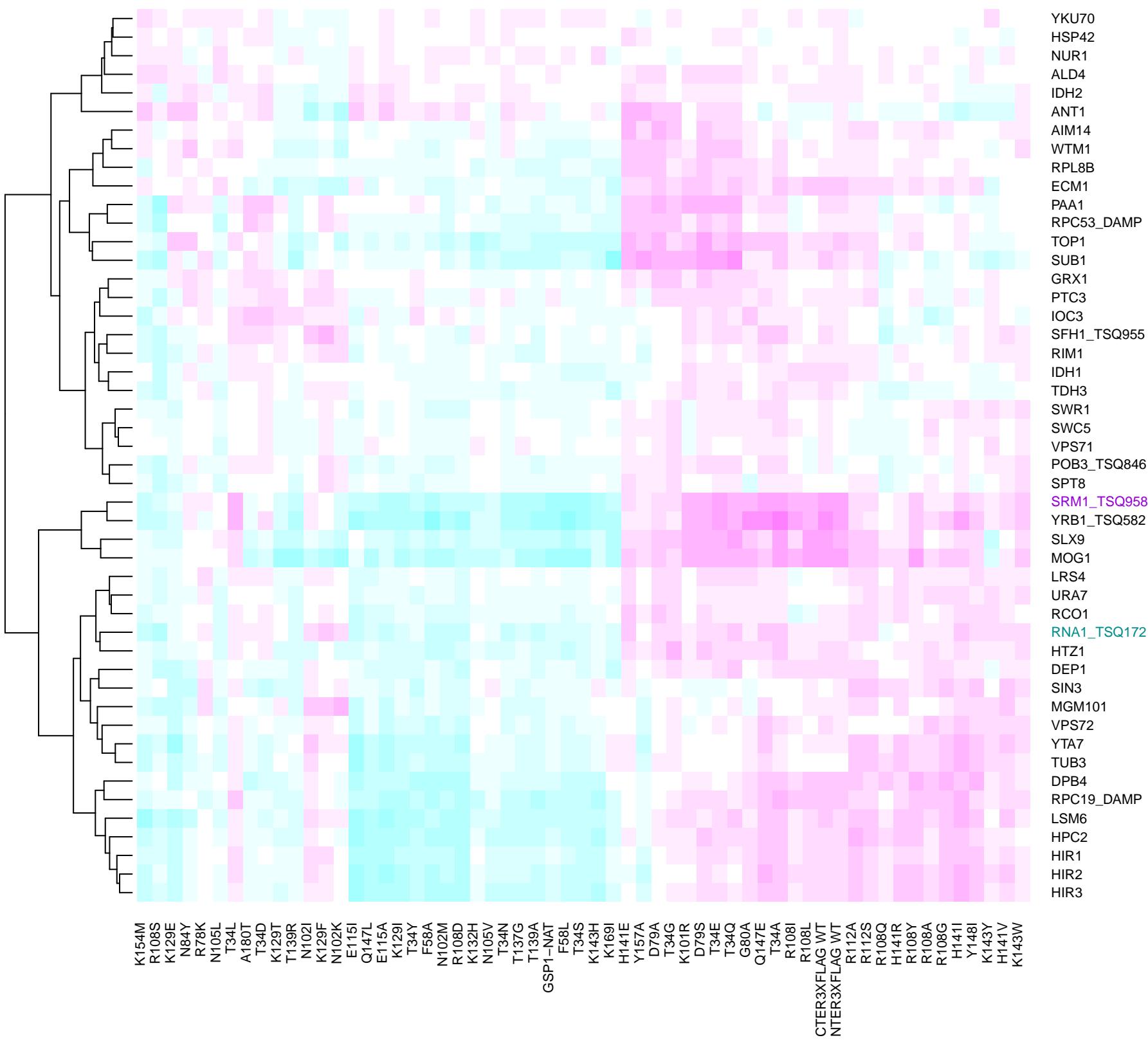


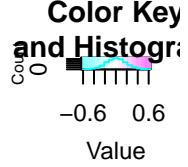
Golgi



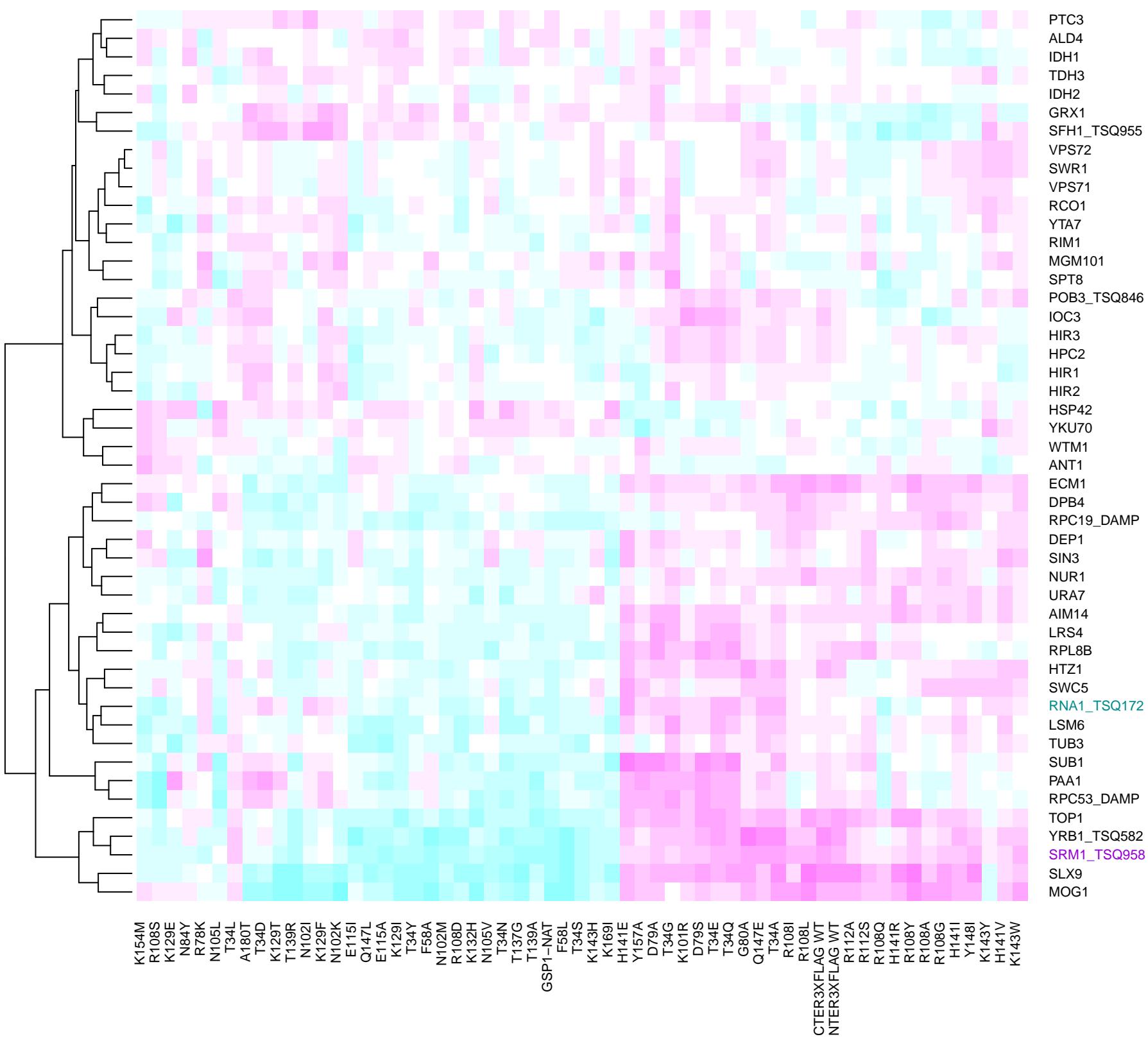


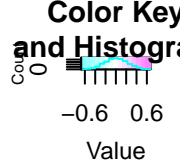
Golgi and ER



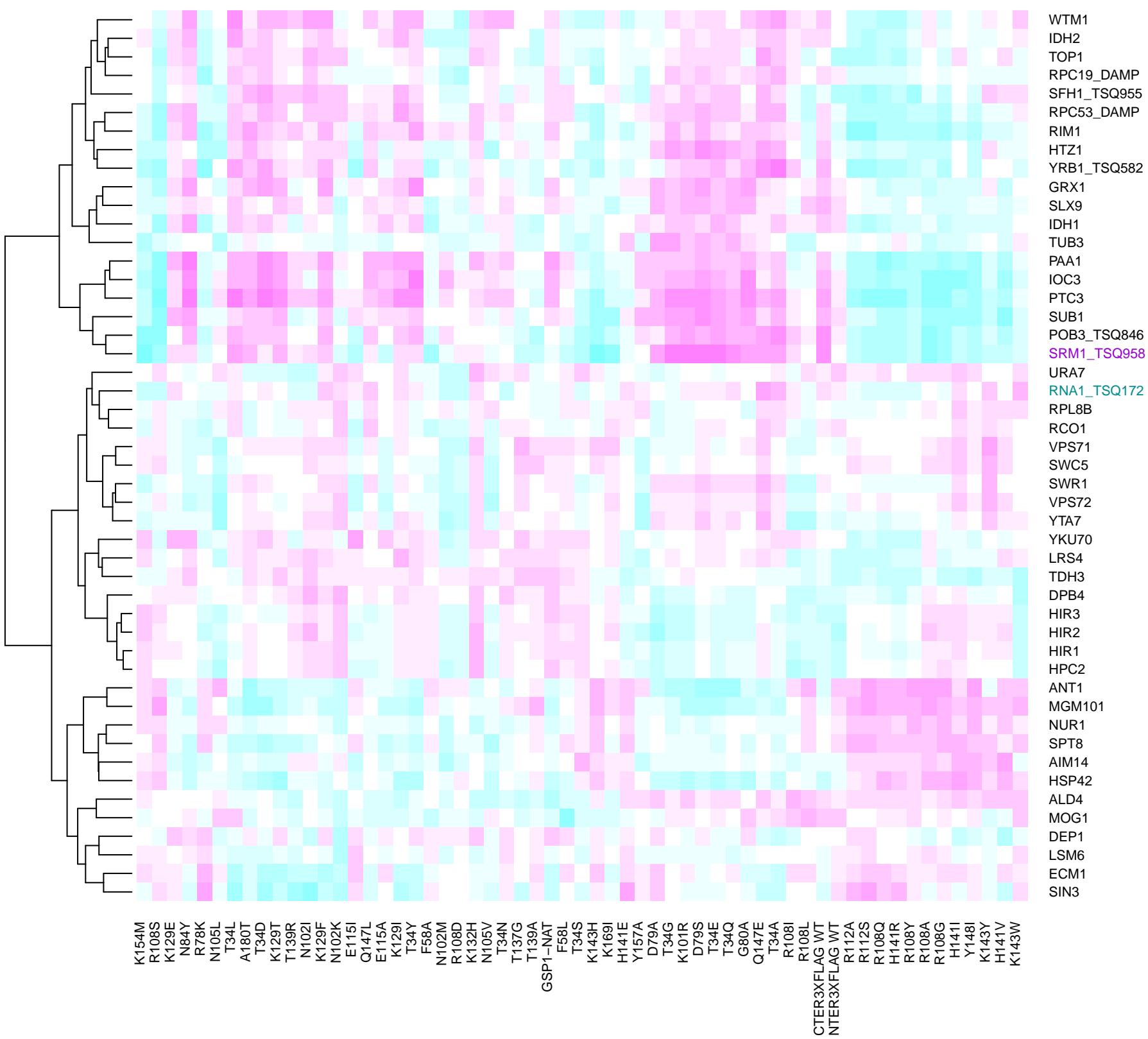


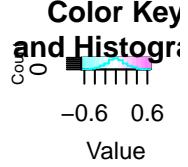
Golgi and ER_GO_30_2



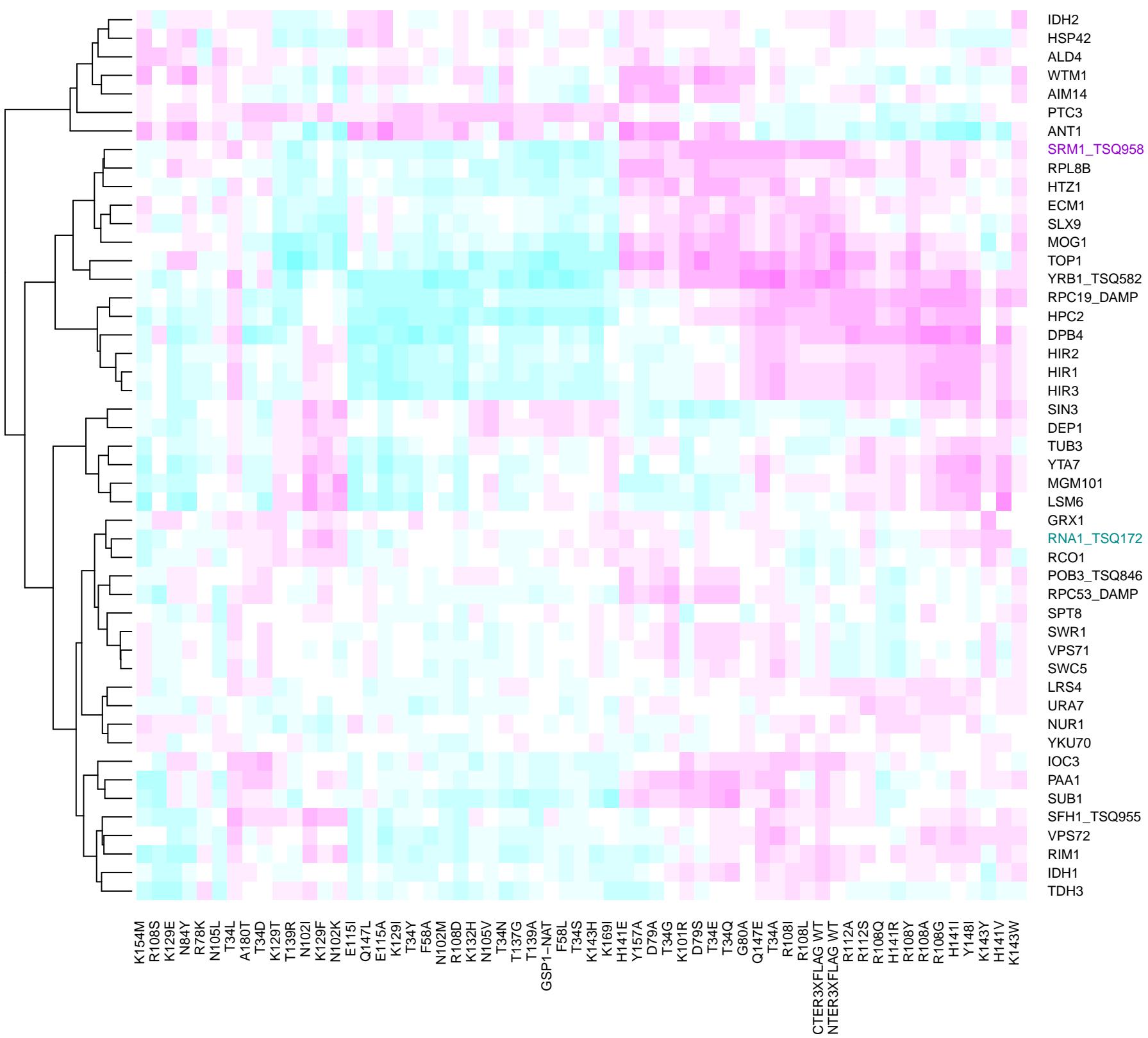


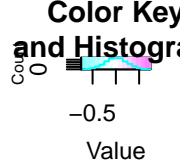
cytoskeleton organization_GO_30_3



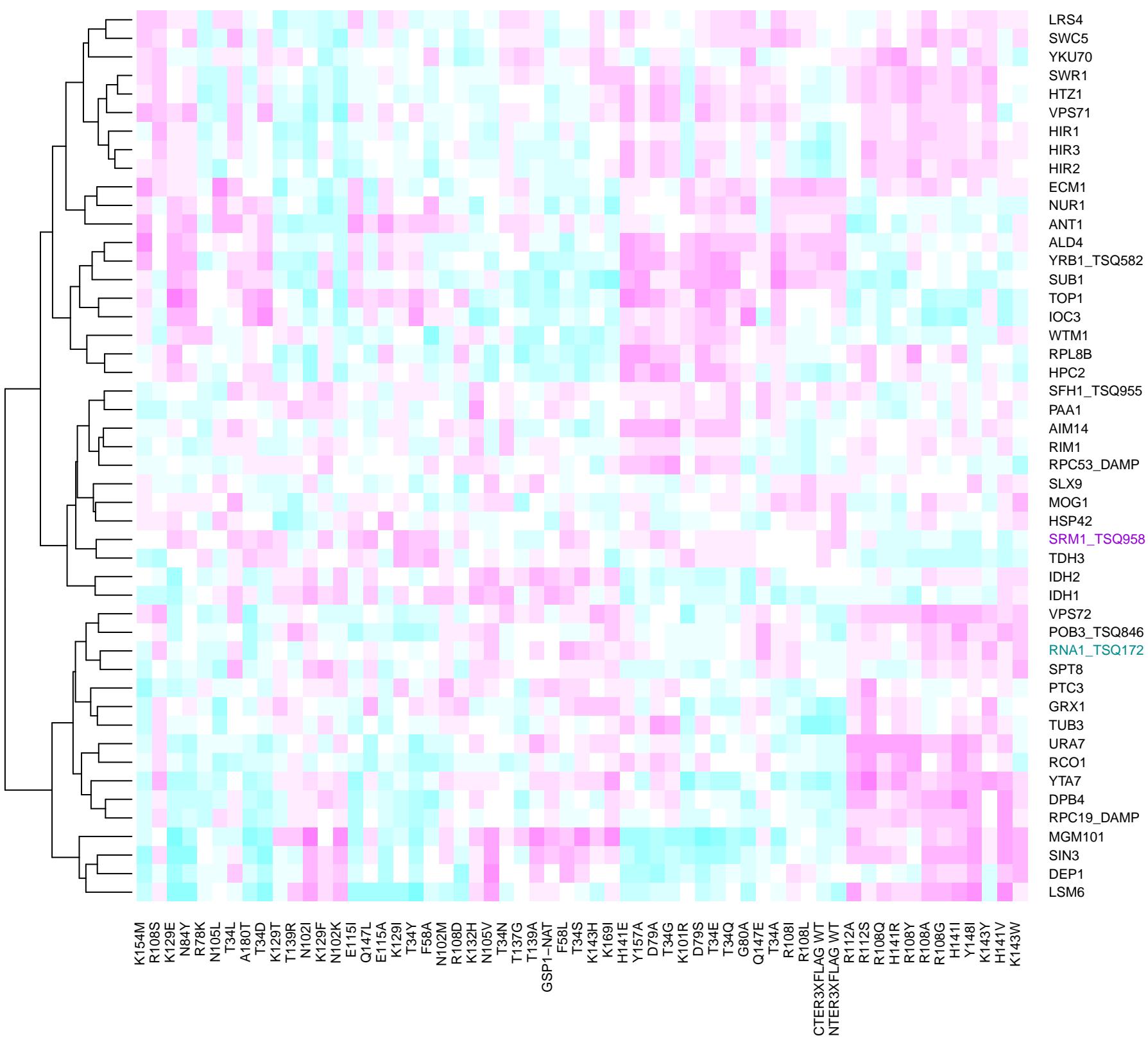


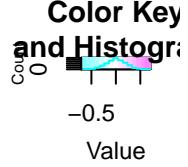
Golgi vesicle transport



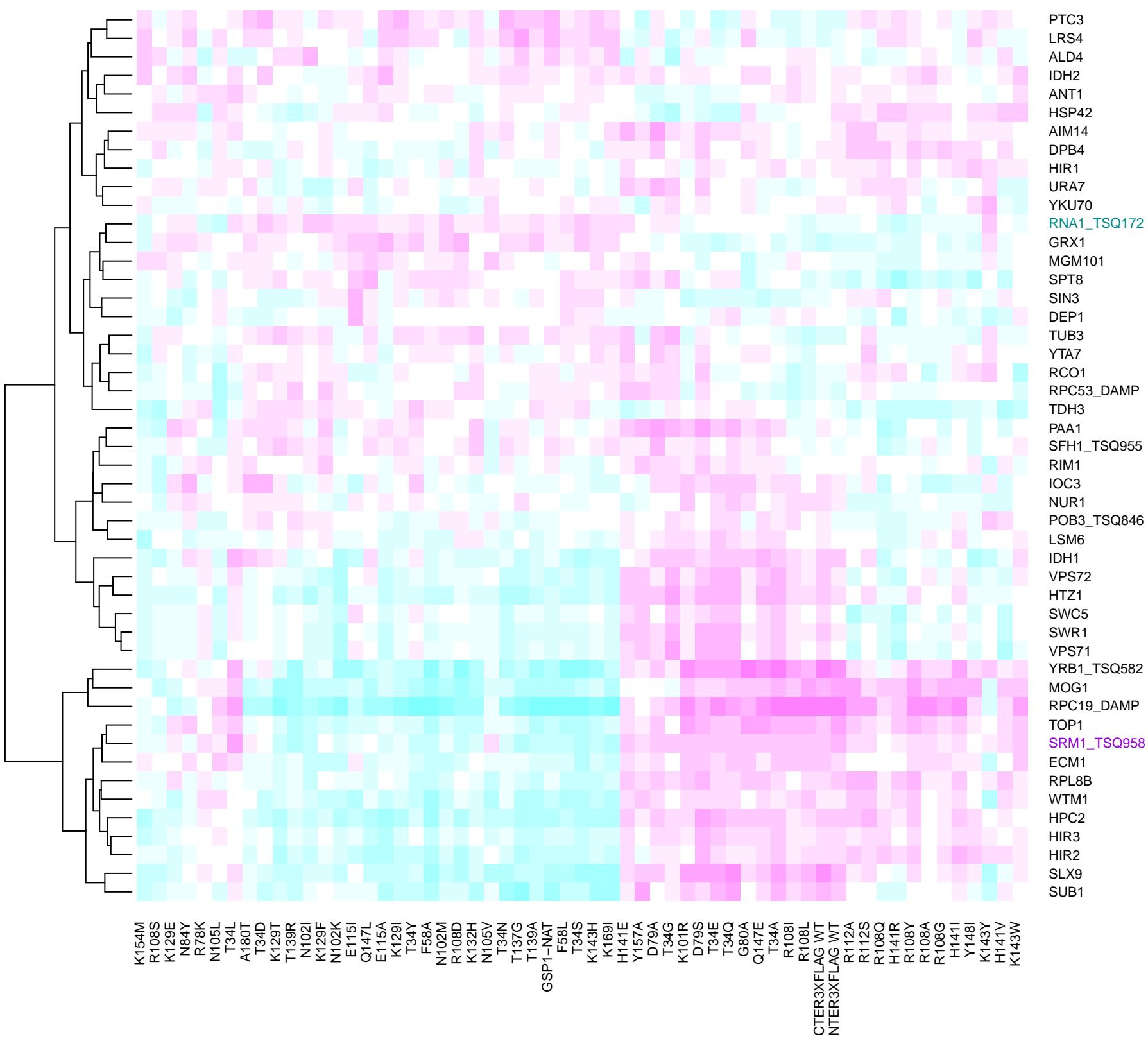


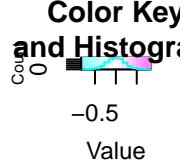
Golgi vesicle transport_GO_30_2



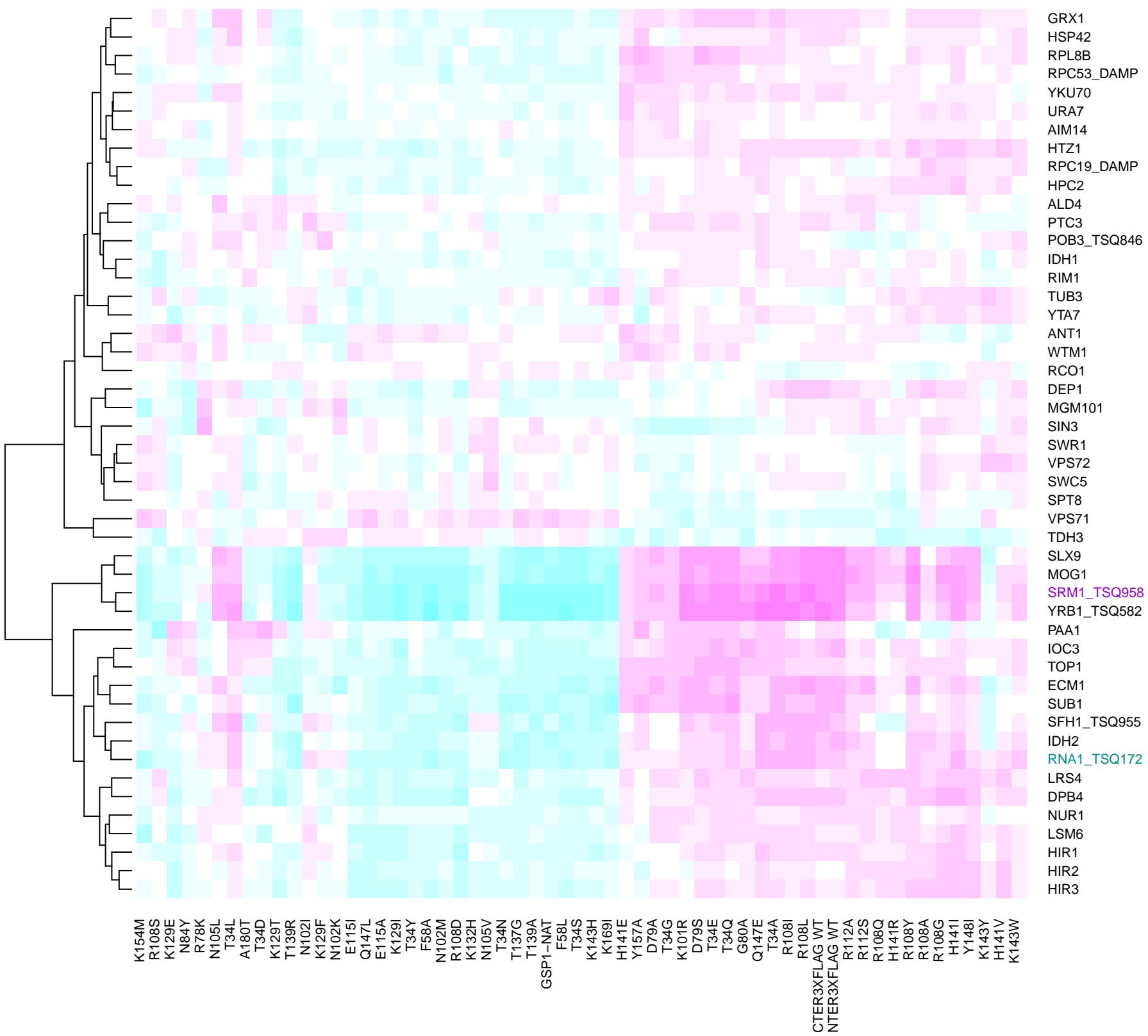


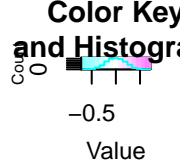
Golgi_GO_30_1



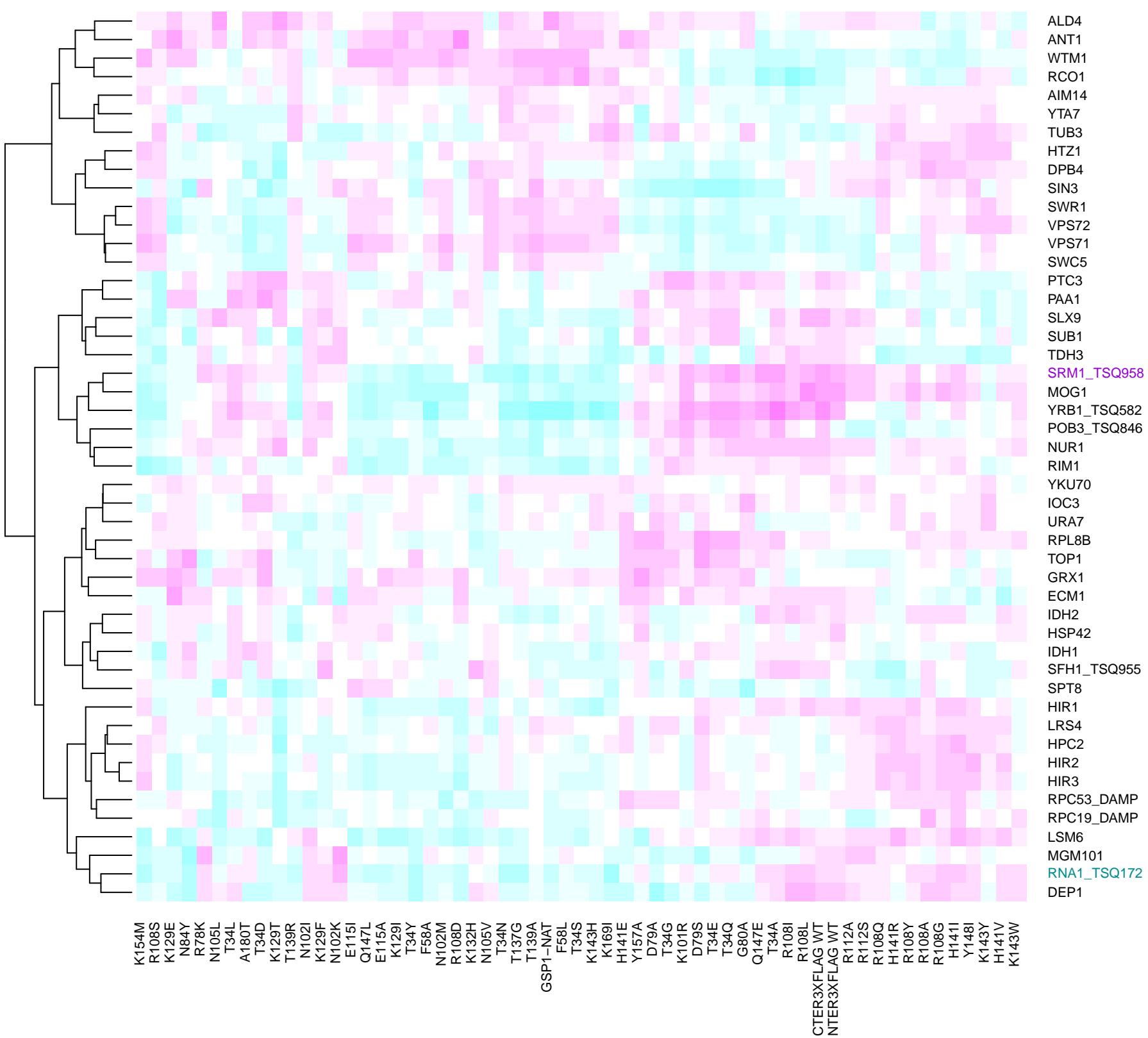


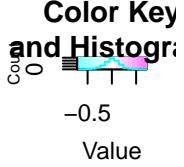
lipid binding



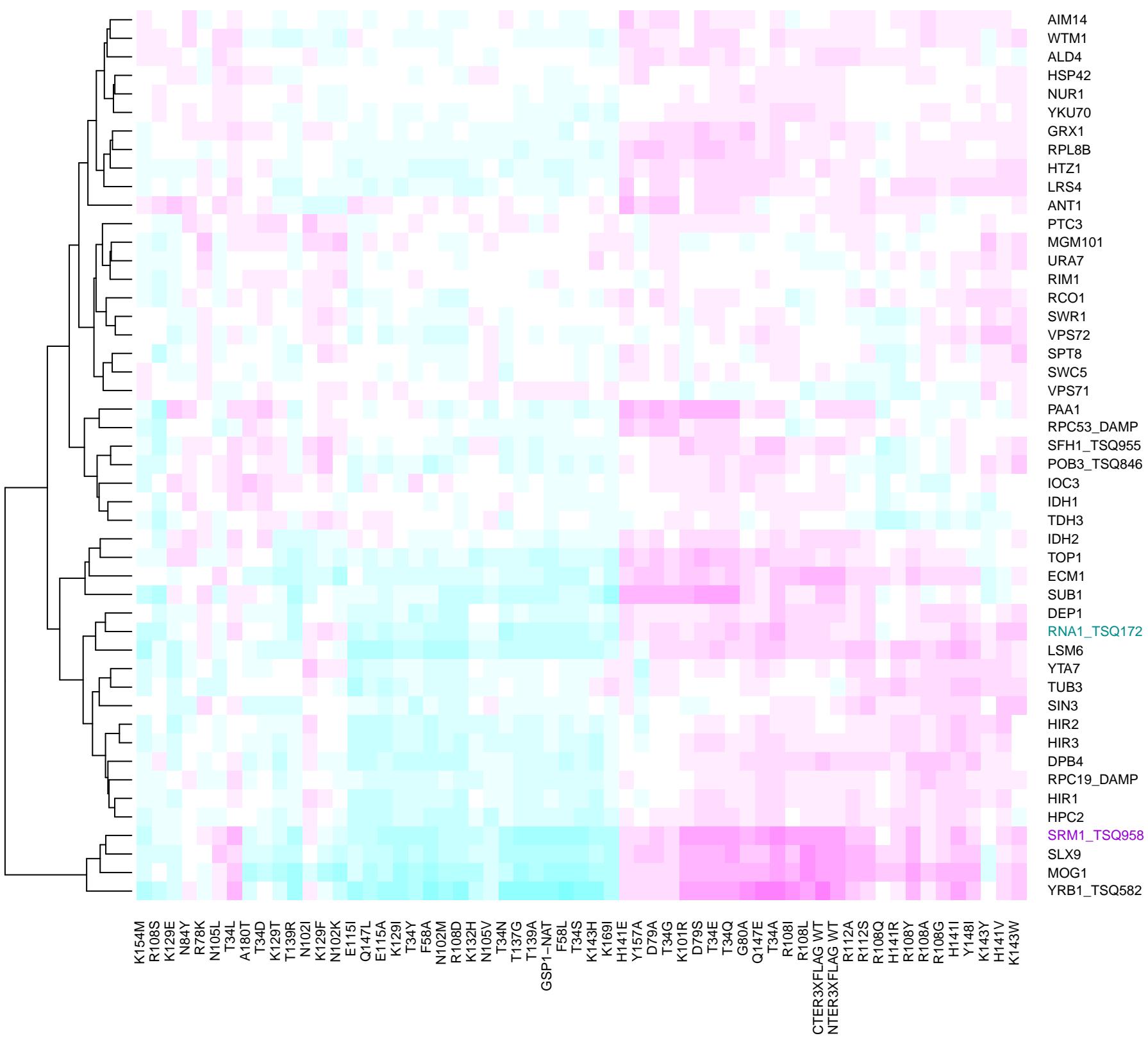


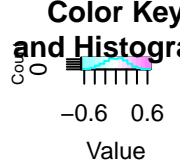
lipid binding_GO_30_1



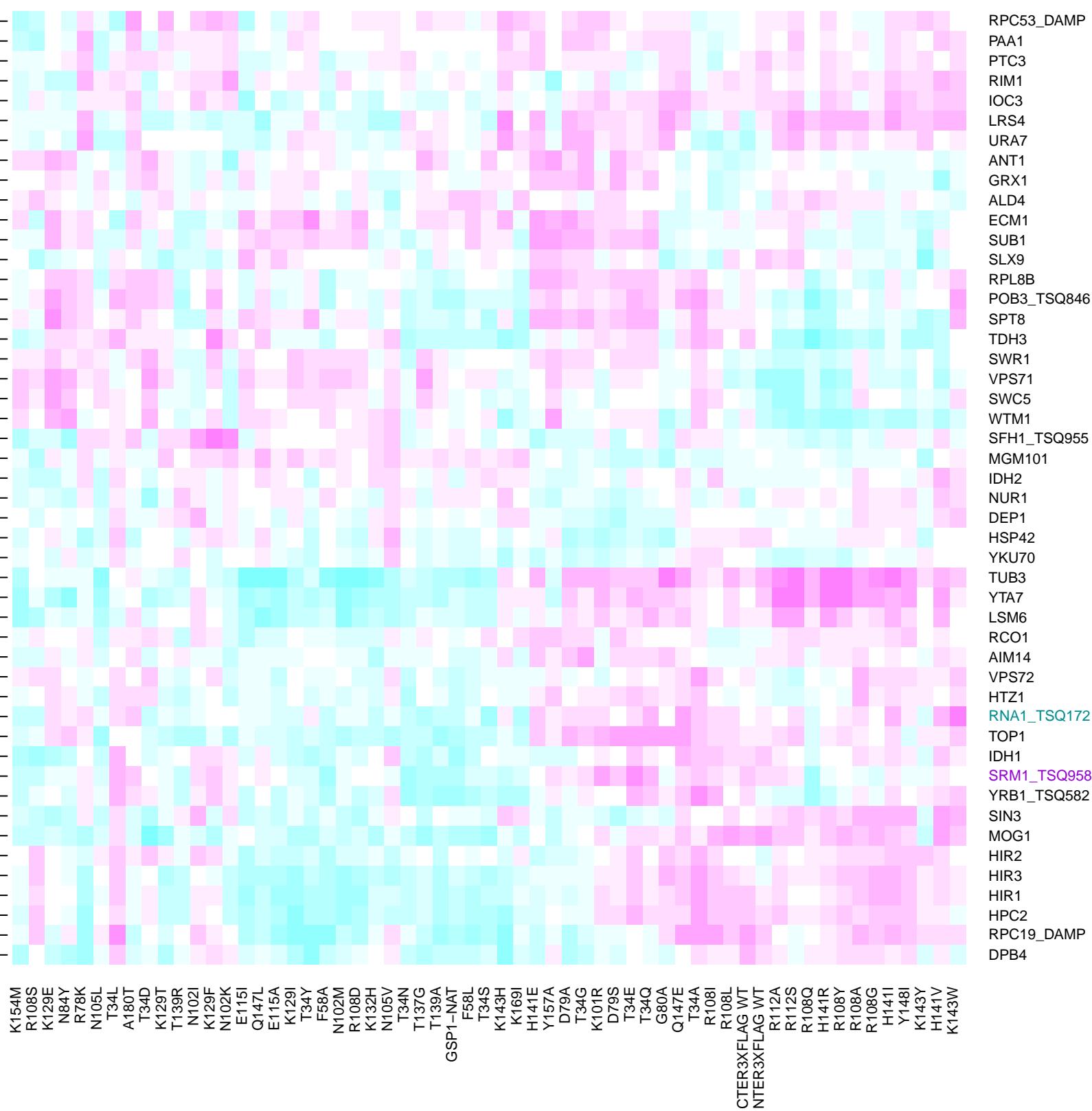


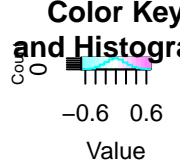
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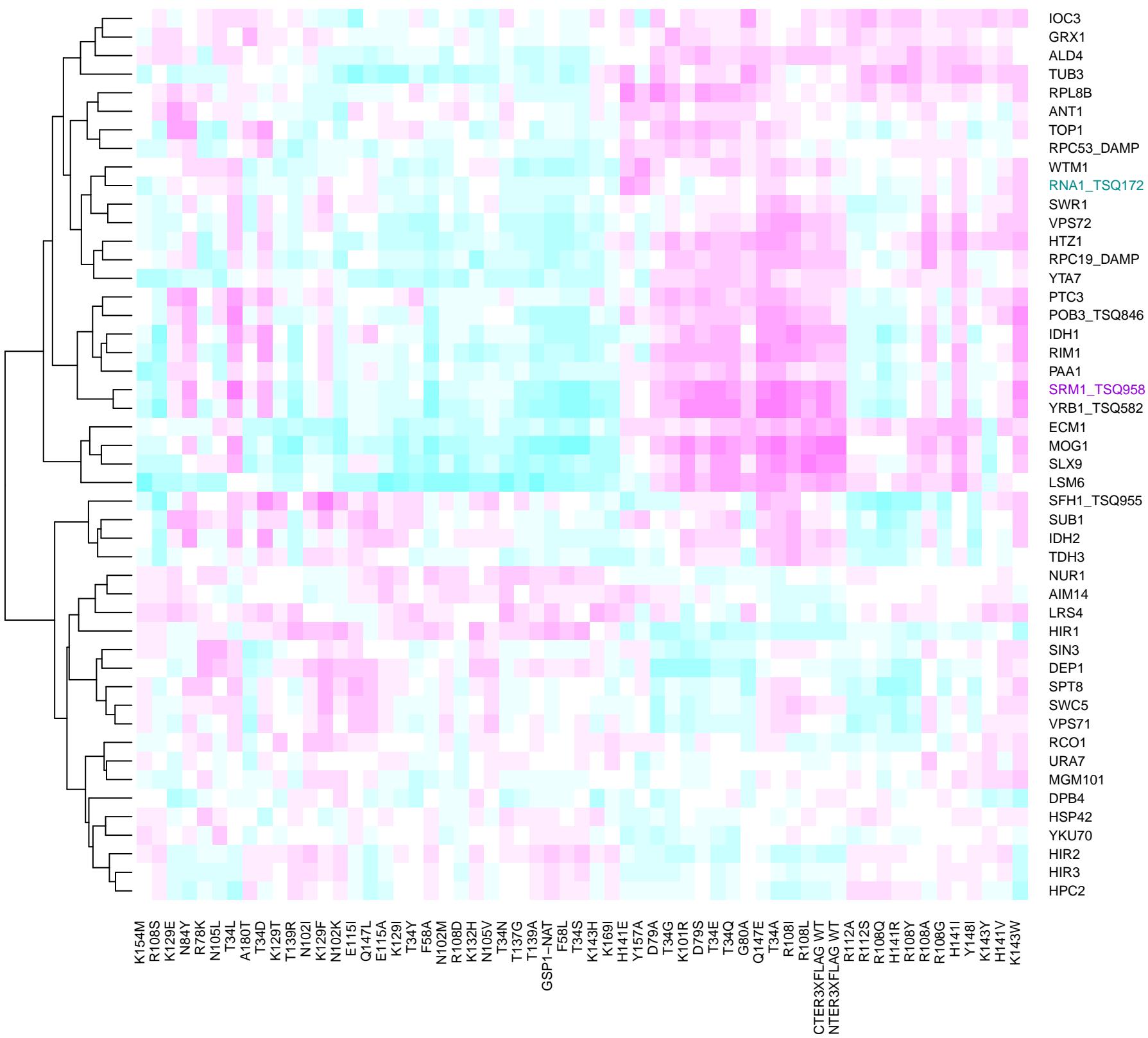


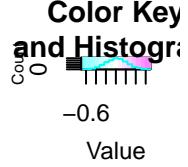
lipids_GO_30_4



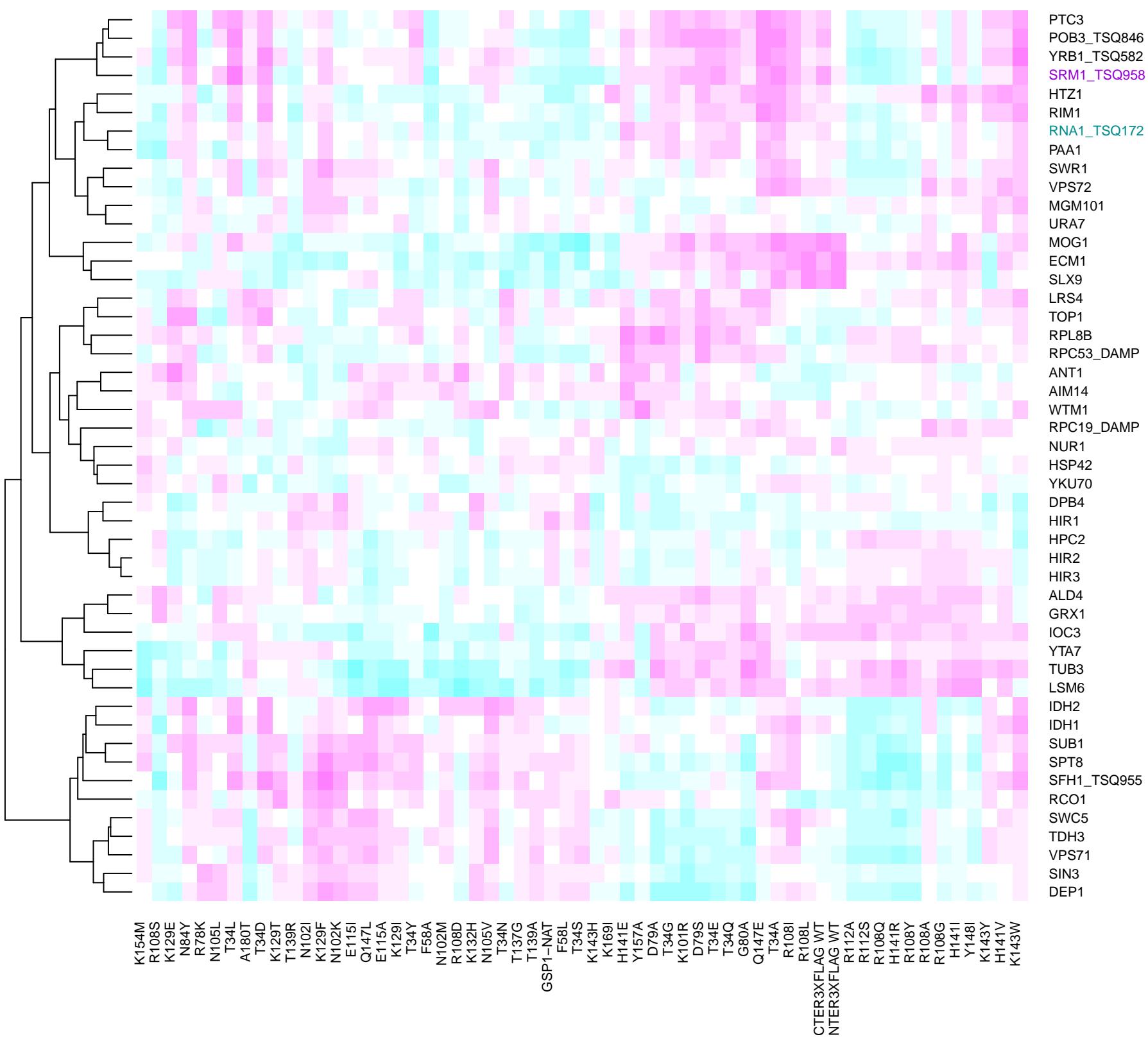


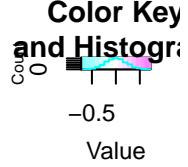
organelle inheritance





organelle inheritance_GO_30_1





site of polarized growth_GO_30_3

