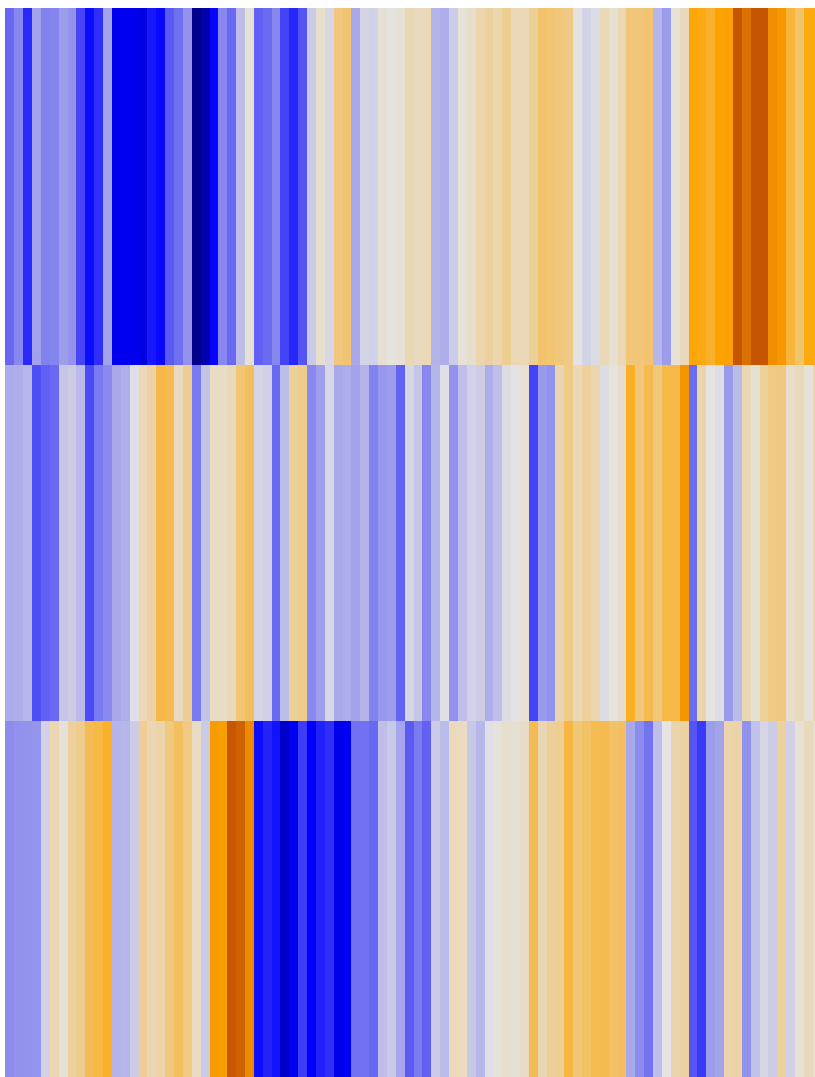
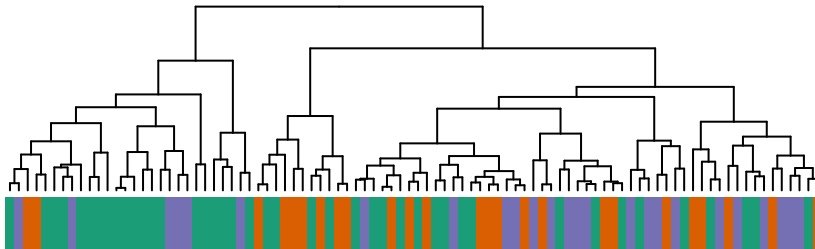


# GSZ score

Category Aging

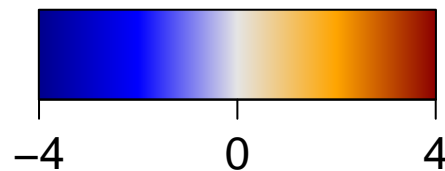


X HORVATH\_aging\_gen

K1 TESCHENDORFF\_a

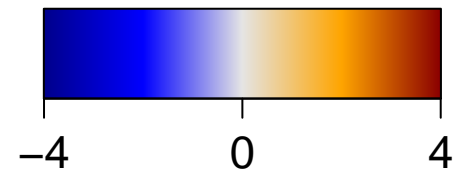
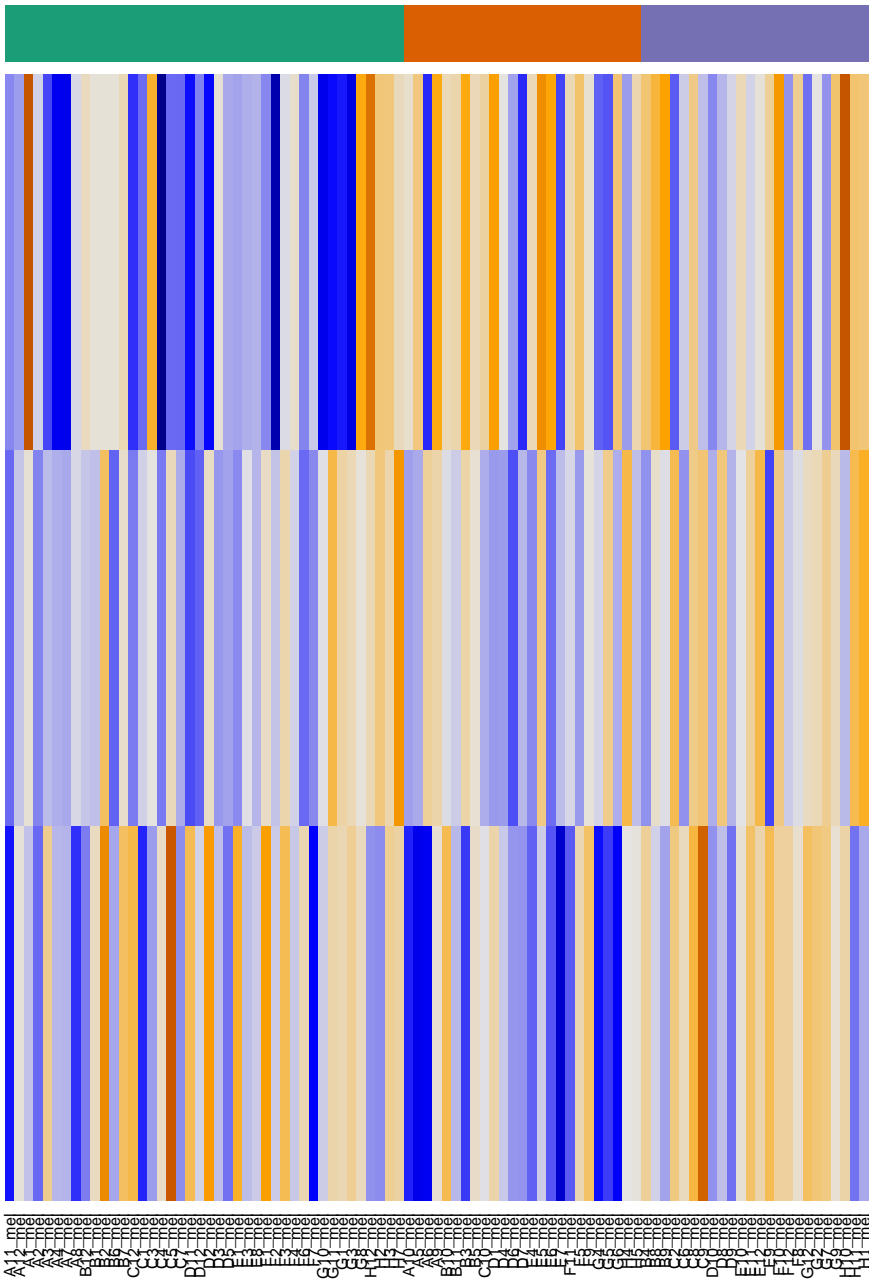
Q HORVATH\_aging\_gen

Sample IDs (e.g., S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S26, S27, S28, S29, S30, S31, S32, S33, S34, S35, S36, S37, S38, S39, S40, S41, S42, S43, S44, S45, S46, S47, S48, S49, S50, S51, S52, S53, S54, S55, S56, S57, S58, S59, S60, S61, S62, S63, S64, S65, S66, S67, S68, S69, S70, S71, S72, S73, S74, S75, S76, S77, S78, S79, S80, S81, S82, S83, S84, S85, S86, S87, S88, S89, S90, S91, S92, S93, S94, S95, S96, S97, S98, S99, S100)



# GSZ score

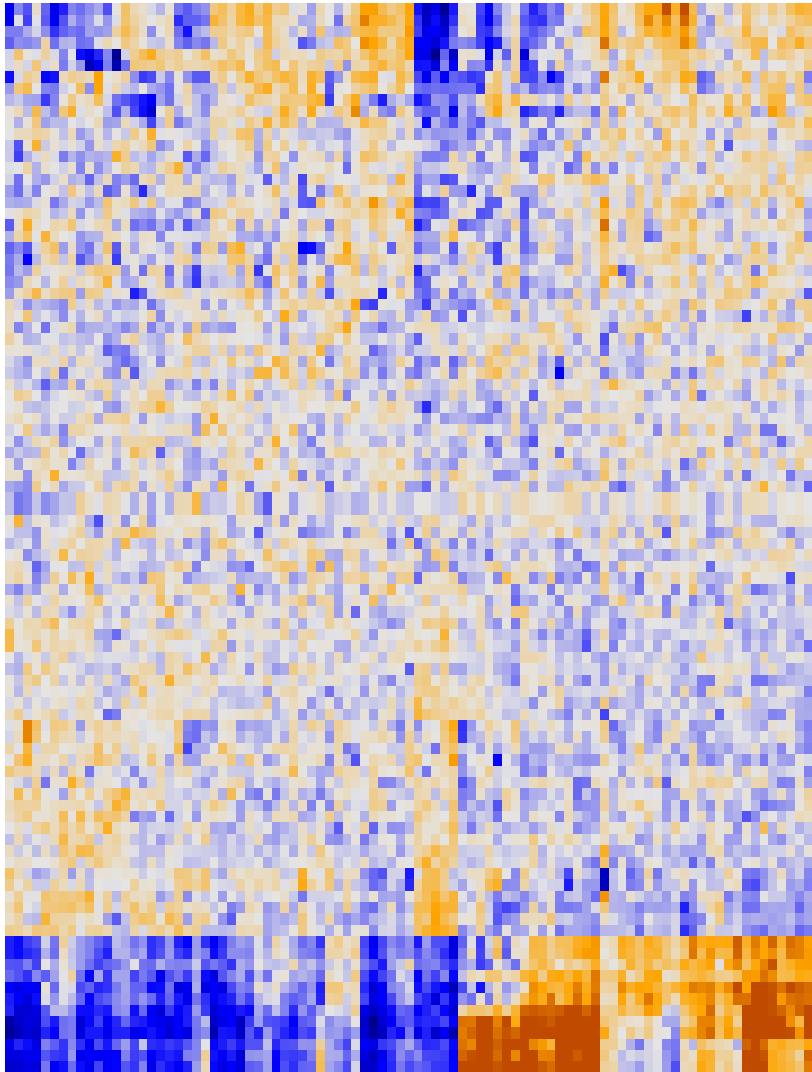
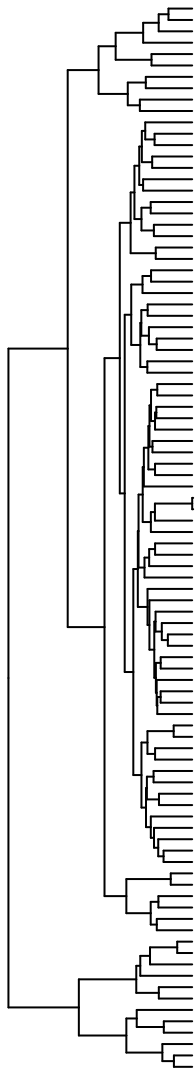
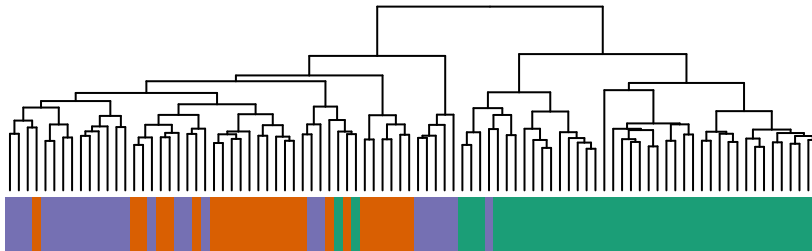
Category Aging





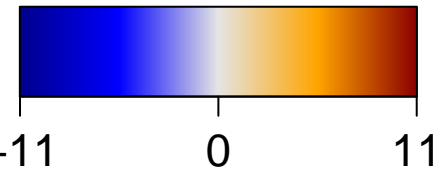
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Category BP



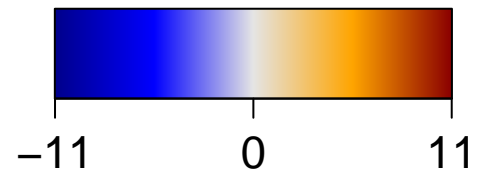
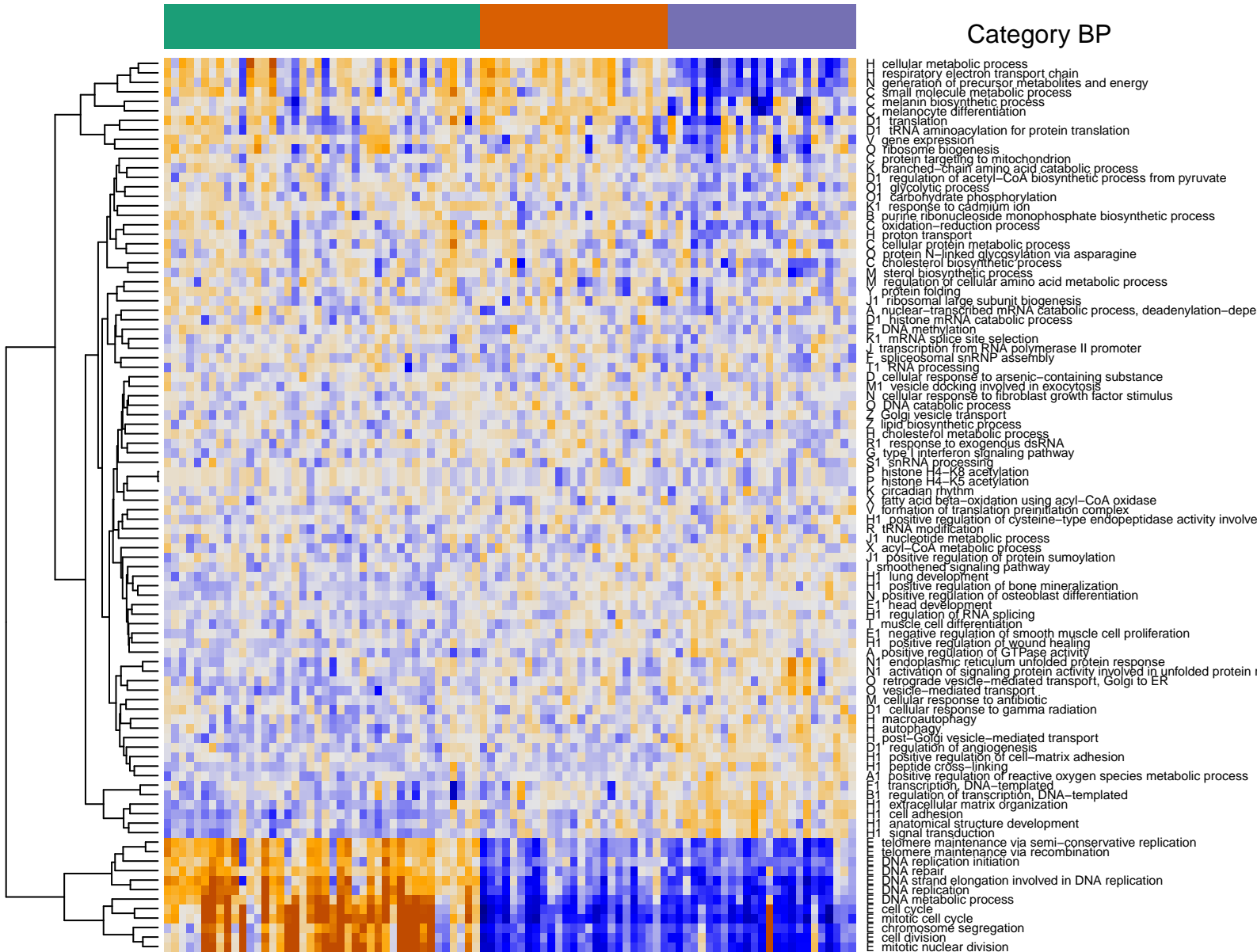
- cellular metabolic process
- respiratory electron transport chain
- generation of precursor metabolites and energy
- small molecule metabolic process
- melanin biosynthetic process
- melanocyte differentiation
- translation
- tRNA aminoacylation for protein translation
- gene expression
- ribosome biogenesis
- protein targeting to mitochondrion
- branched-chain amino acid catabolic process
- regulation of acetyl-CoA biosynthetic process from pyruvate
- glycolytic process
- carbohydrate phosphorylation
- response to cadmium ion
- purine ribonucleoside monophosphate biosynthetic process
- oxidation-reduction process
- cellular protein metabolic process
- protein N-linked glycosylation via asparagine
- cholesterol biosynthetic process
- sterol biosynthetic process
- regulation of cellular amino acid metabolic process
- protein folding
- ribosomal large subunit biogenesis
- nuclear-transcribed mRNA catabolic process, deadenylation-dependent
- histone mRNA catabolic process
- DNA methylation
- mRNA splice site selection
- transcription from RNA polymerase II promoter
- spliceosomal snRNP assembly
- mRNA processing
- cellular response to arsenic-containing substance
- vesicle docking involved in exocytosis
- cellular response to fibroblast growth factor stimulus
- DNA catabolic process
- Golgi vesicle transport
- lipid biosynthetic process
- cholesterol metabolic process
- response to exogenous dsRNA
- type I interferon signaling pathway
- snRNA processing
- histone H4-K8 acetylation
- histone H4-K8 acetylation
- circadian rhythm
- fatty acid beta-oxidation using acyl-CoA oxidase
- formation of translation preinitiation complex
- positive regulation of cysteine-type endopeptidase activity involved in
- tRNA modification
- nucleotide metabolic process
- acyl-CoA metabolic process
- positive regulation of protein sumoylation
- smoothed signaling pathway
- lung development
- positive regulation of bone mineralization
- head development
- regulation of RNA splicing
- muscle cell differentiation
- negative regulation of smooth muscle cell proliferation
- positive regulation of wound healing
- positive regulation of GTPase activity
- endoplasmic reticulum unfolded protein response
- activation of signaling protein activity involved in unfolded protein response
- retrograde vesicle-mediated transport, Golgi to ER
- vesicle-mediated transport
- cellular response to antibiotic
- cellular response to gamma radiation
- macroautophagy
- autophagy
- post-Golgi vesicle-mediated transport
- regulation of angiogenesis
- positive regulation of cell-matrix adhesion
- peptide cross-linking
- positive regulation of reactive oxygen species metabolic process
- transcription, DNA-templated
- regulation of transcription, DNA-templated
- extracellular matrix organization
- cell adhesion
- anatomical structure development
- signal transduction
- telomere maintenance via semi-conservative replication
- telomere maintenance via recombination
- DNA replication initiation
- DNA repair
- DNA strand elongation involved in DNA replication
- DNA replication
- DNA metabolic process
- cell cycle
- mitotic cell cycle
- chromosome segregation
- cell division
- mitotic nuclear division

Sample IDs: S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S26, S27, S28, S29, S30, S31, S32, S33, S34, S35, S36, S37, S38, S39, S40, S41, S42, S43, S44, S45, S46, S47, S48, S49, S50, S51, S52, S53, S54, S55, S56, S57, S58, S59, S60, S61, S62, S63, S64, S65, S66, S67, S68, S69, S70, S71, S72, S73, S74, S75, S76, S77, S78, S79, S80, S81, S82, S83, S84, S85, S86, S87, S88, S89, S90, S91, S92, S93, S94, S95, S96, S97, S98, S99, S100



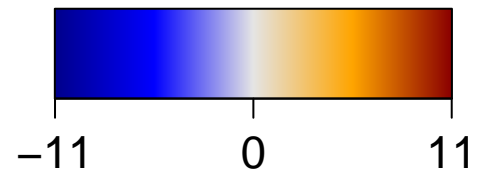
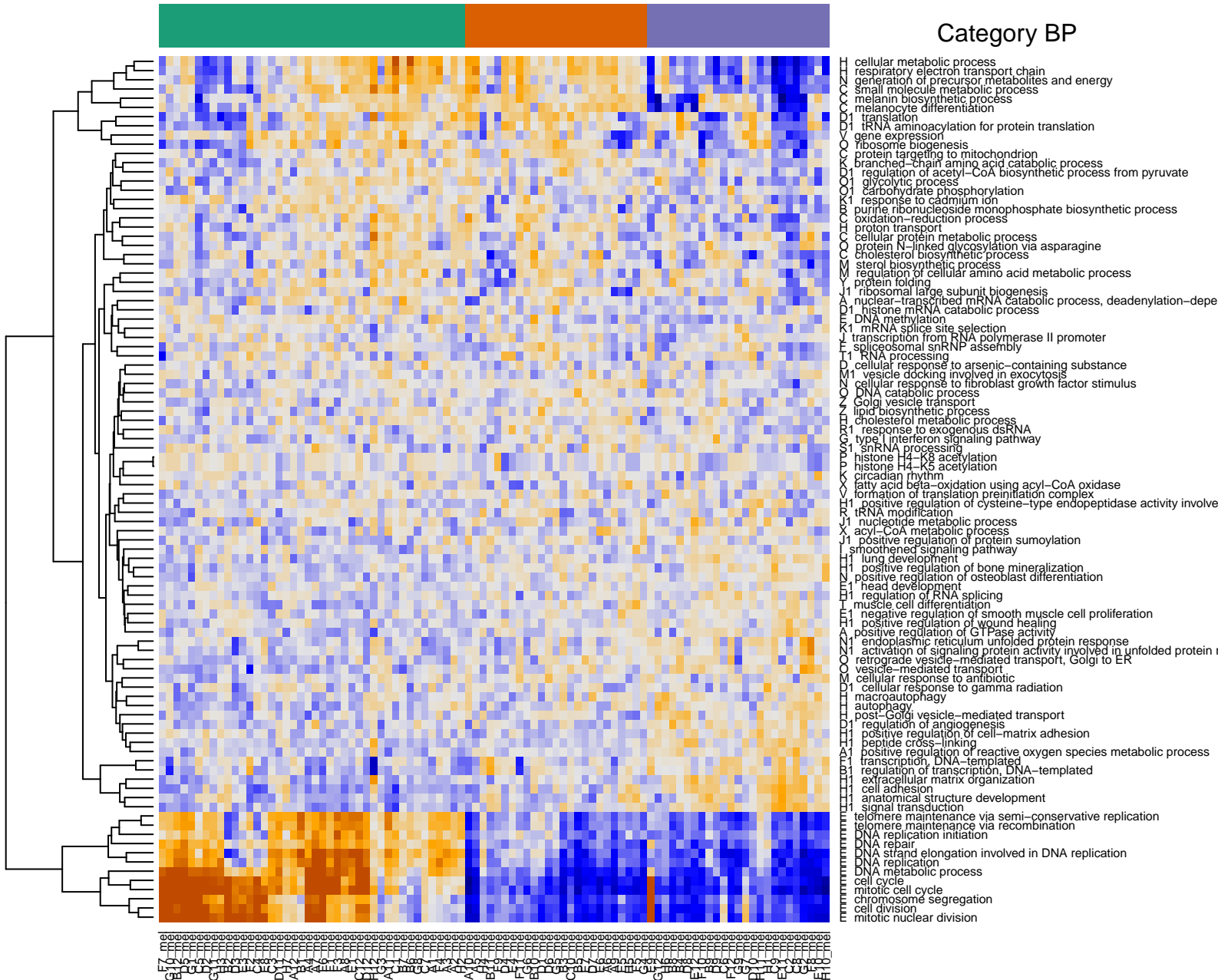
# GSZ score

Category BP



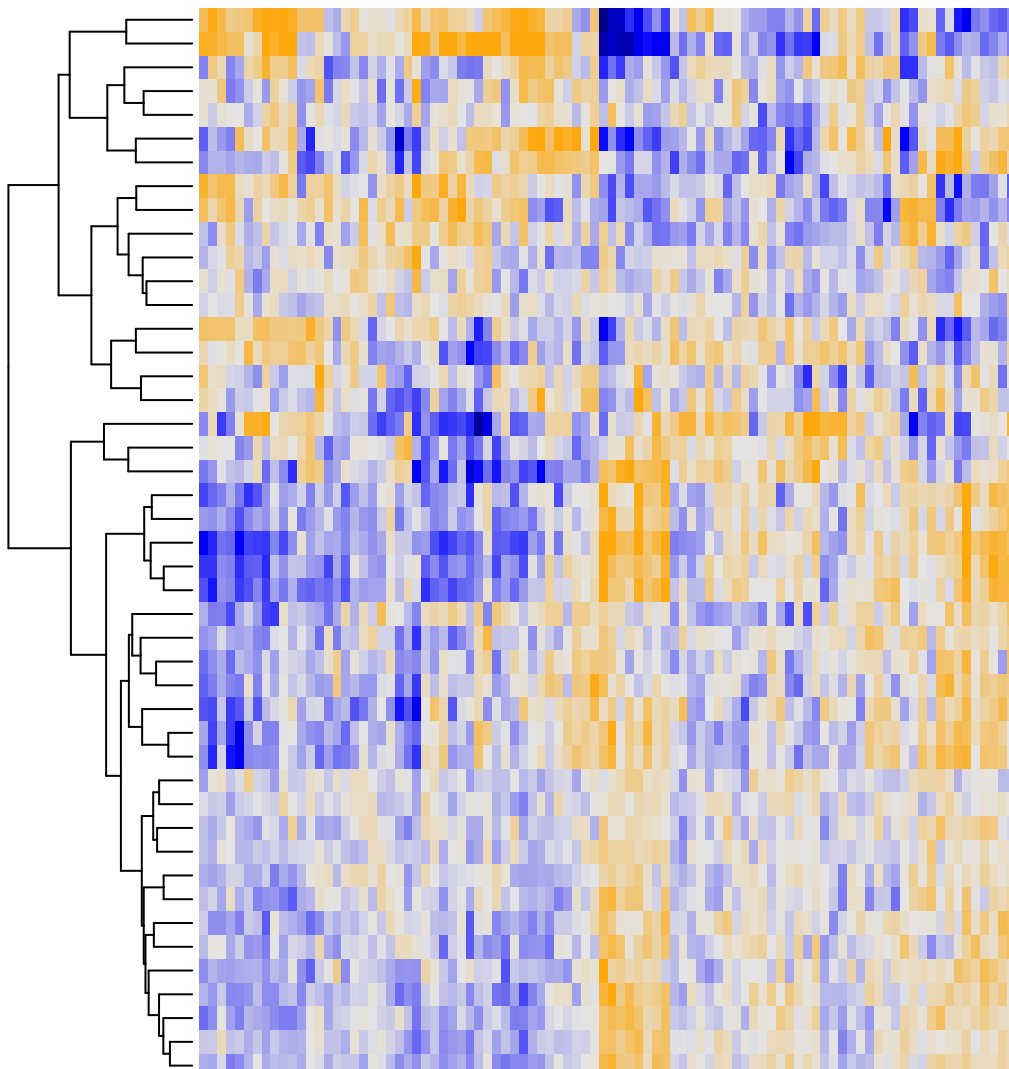
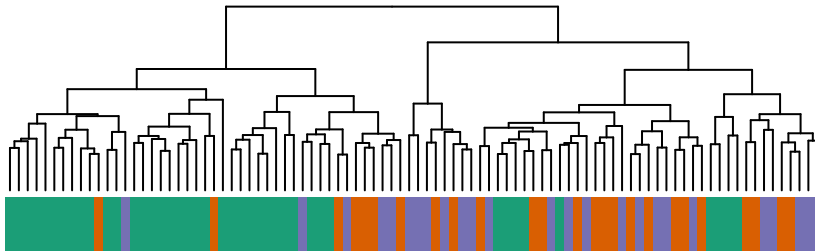
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Category BP

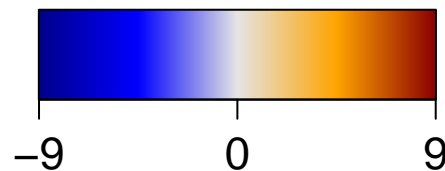
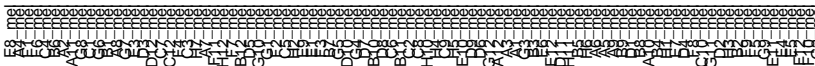


# GSZ score

Category Brain

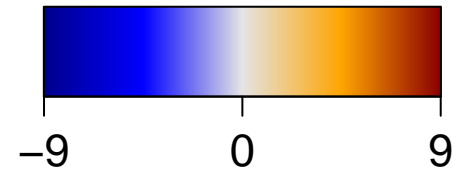
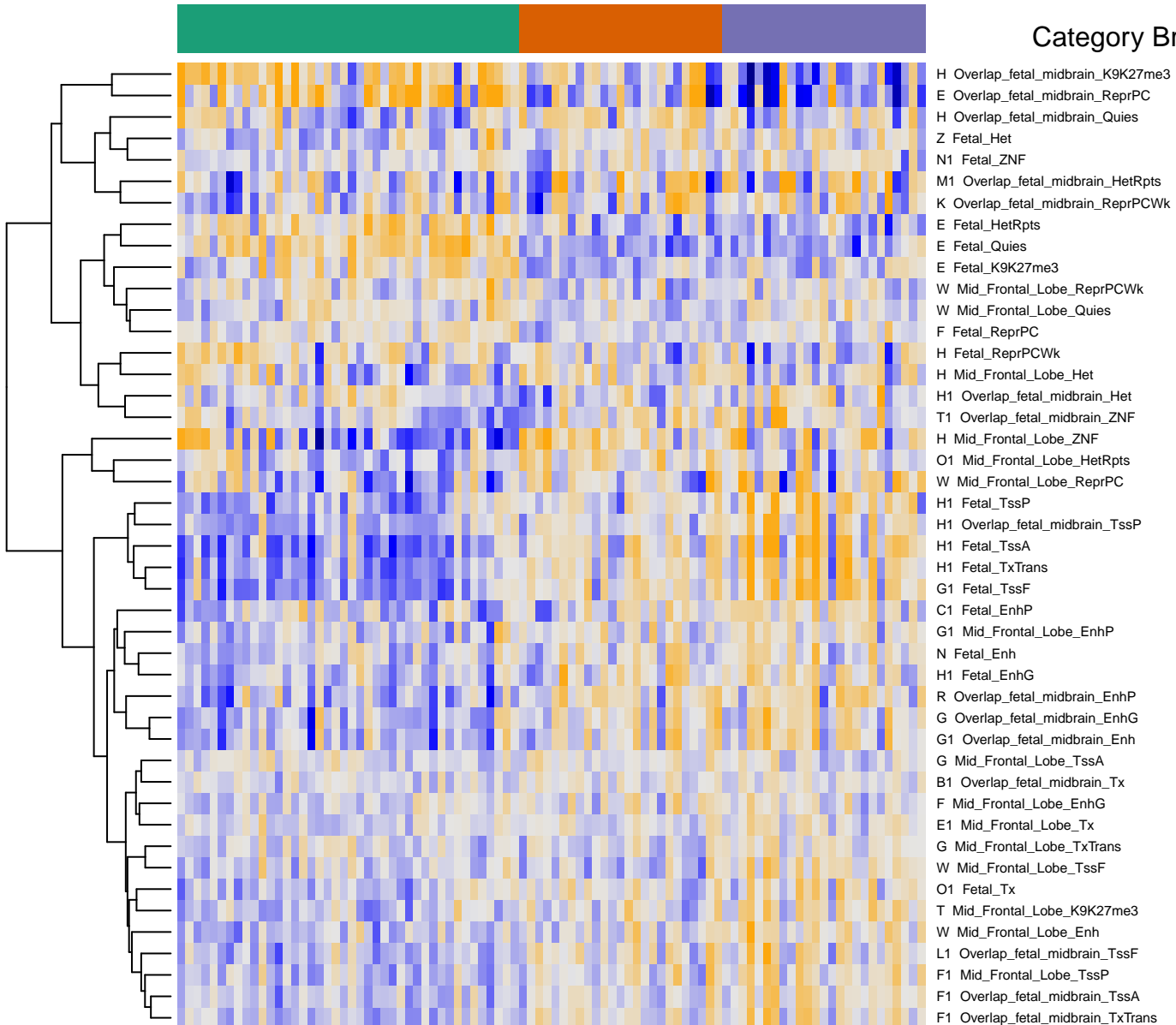


- H Overlap\_fetal\_midbrain\_K9K27me3
- E Overlap\_fetal\_midbrain\_ReprPC
- H Overlap\_fetal\_midbrain\_Quies
- Z Fetal\_Het
- N1 Fetal\_ZNF
- M1 Overlap\_fetal\_midbrain\_HetRpts
- K Overlap\_fetal\_midbrain\_ReprPCWk
- E Fetal\_HetRpts
- E Fetal\_Quies
- E Fetal\_K9K27me3
- W Mid\_Frontal\_Lobe\_ReprPCWk
- W Mid\_Frontal\_Lobe\_Quies
- F Fetal\_ReprPC
- H Fetal\_ReprPCWk
- H Mid\_Frontal\_Lobe\_Het
- H1 Overlap\_fetal\_midbrain\_Het
- T1 Overlap\_fetal\_midbrain\_ZNF
- H Mid\_Frontal\_Lobe\_ZNF
- O1 Mid\_Frontal\_Lobe\_HetRpts
- W Mid\_Frontal\_Lobe\_ReprPC
- H1 Fetal\_TssP
- H1 Overlap\_fetal\_midbrain\_TssP
- H1 Fetal\_TssA
- H1 Fetal\_TxTrans
- G1 Fetal\_TssF
- C1 Fetal\_EnhP
- G1 Mid\_Frontal\_Lobe\_EnhP
- N Fetal\_Enh
- H1 Fetal\_EnhG
- R Overlap\_fetal\_midbrain\_EnhP
- G Overlap\_fetal\_midbrain\_EnhG
- G1 Overlap\_fetal\_midbrain\_Enh
- G Mid\_Frontal\_Lobe\_TssA
- B1 Overlap\_fetal\_midbrain\_Tx
- F Mid\_Frontal\_Lobe\_EnhG
- E1 Mid\_Frontal\_Lobe\_Tx
- G Mid\_Frontal\_Lobe\_TxTrans
- W Mid\_Frontal\_Lobe\_TssF
- O1 Fetal\_Tx
- T Mid\_Frontal\_Lobe\_K9K27me3
- W Mid\_Frontal\_Lobe\_Enh
- L1 Overlap\_fetal\_midbrain\_TssF
- F1 Mid\_Frontal\_Lobe\_TssP
- F1 Overlap\_fetal\_midbrain\_TssA
- F1 Overlap\_fetal\_midbrain\_TxTrans



# GSZ score

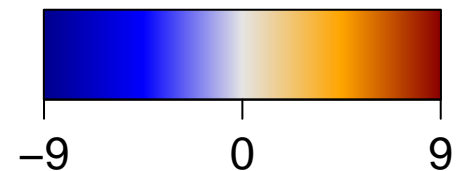
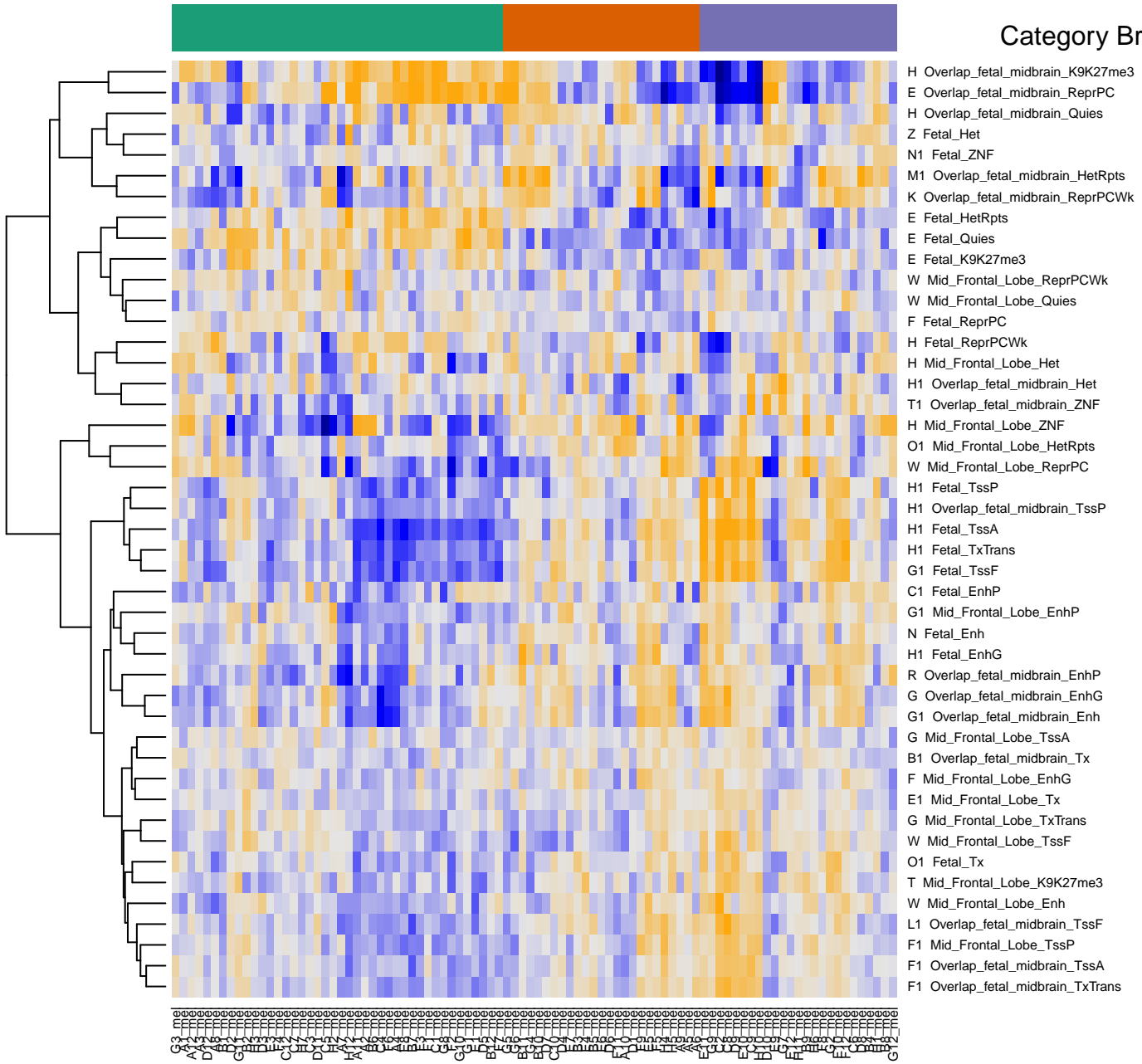
Category Brain





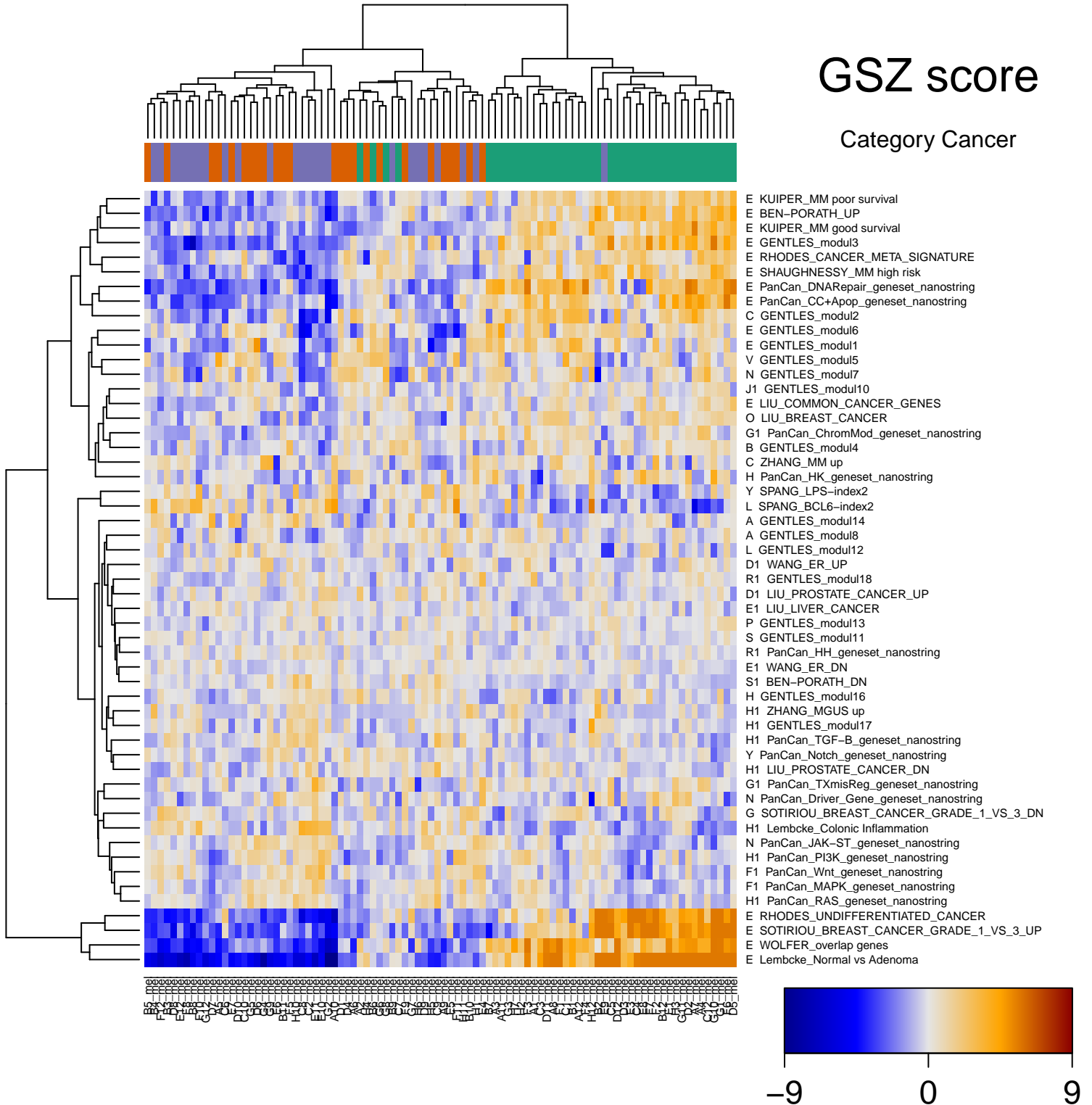
# GSZ score

Category Brain



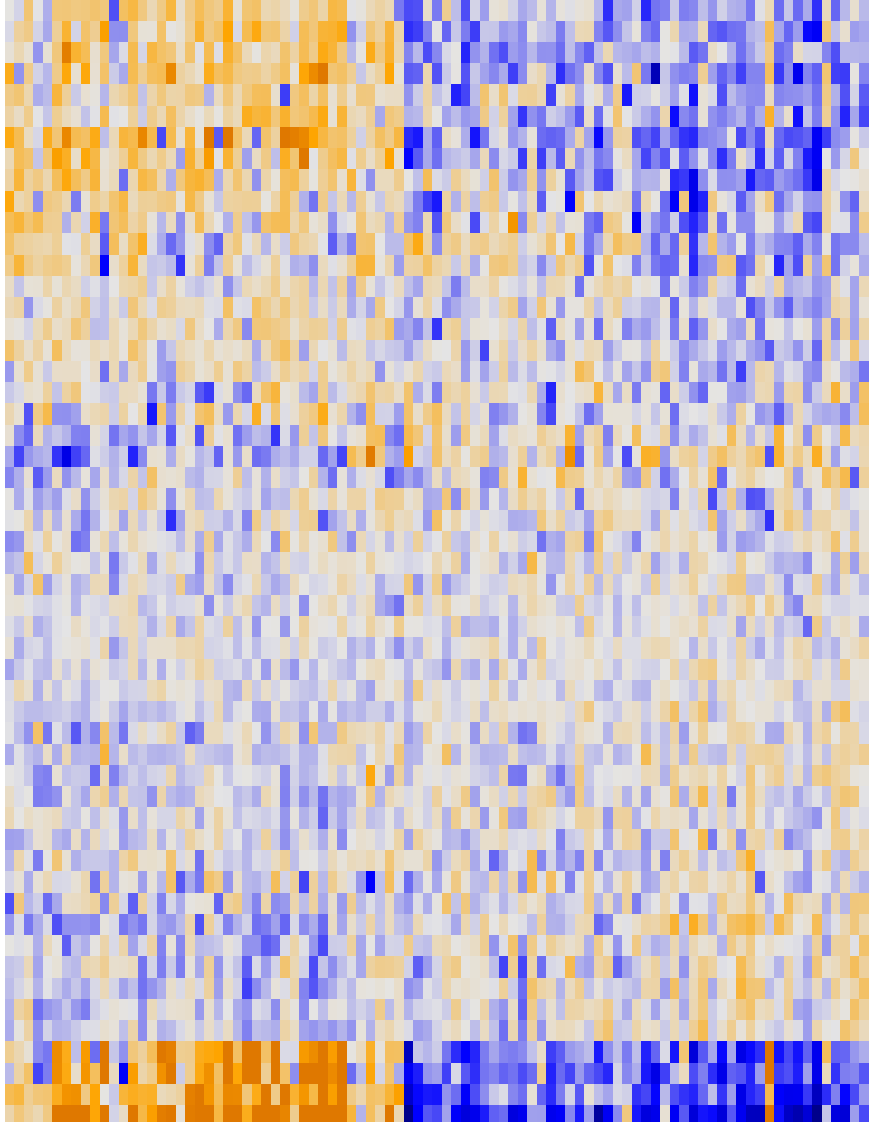
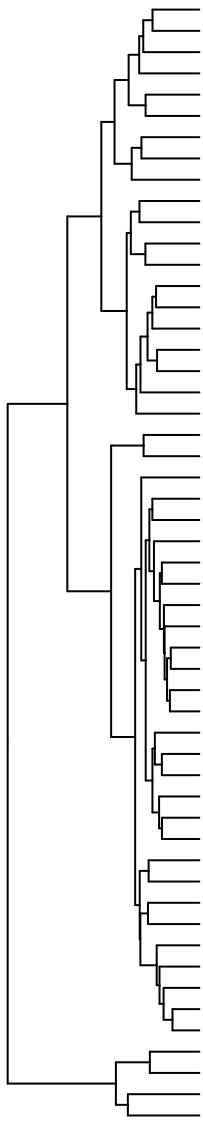
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Category Cancer

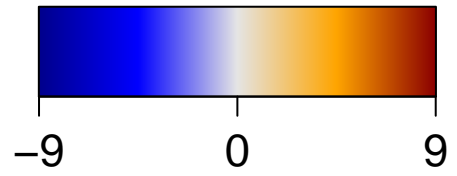


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Category Cancer

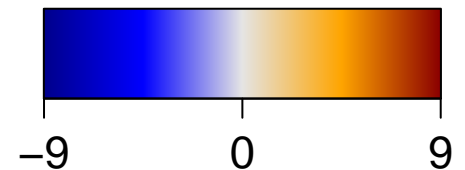
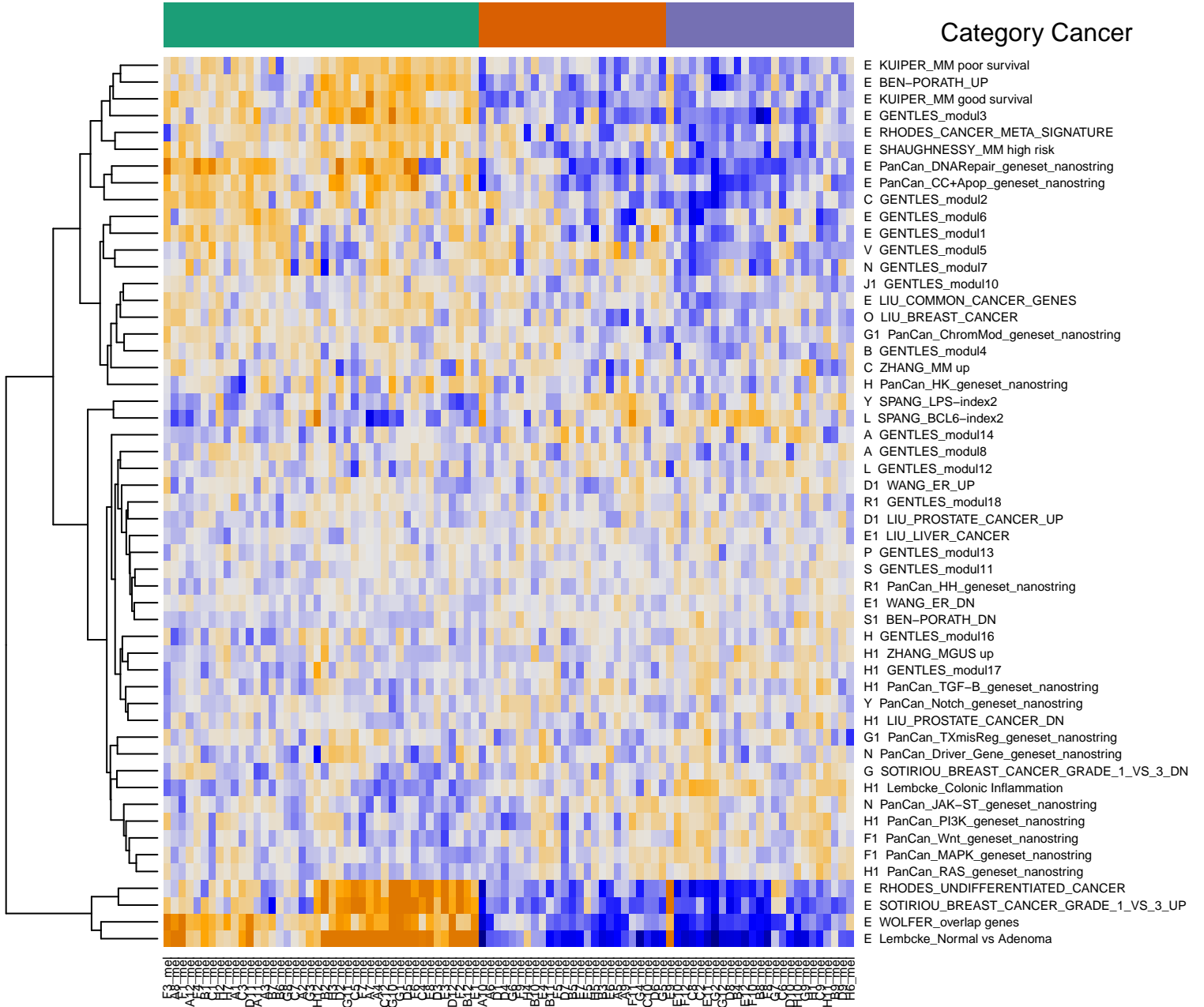


- E KUIPER\_MM poor survival
- E BEN-PORATH\_UP
- E KUIPER\_MM good survival
- E GENTLES\_modul3
- E RHODES\_CANCER\_META\_SIGNATURE
- E SHAUGHNESSY\_MM high risk
- E PanCan\_DNARepair\_geneset\_nanostring
- E PanCan\_CC+Apop\_geneset\_nanostring
- C GENTLES\_modul2
- E GENTLES\_modul6
- E GENTLES\_modul1
- V GENTLES\_modul5
- N GENTLES\_modul7
- J1 GENTLES\_modul10
- E LIU\_COMMON\_CANCER\_GENES
- O LIU\_BREAST\_CANCER
- G1 PanCan\_ChromMod\_geneset\_nanostring
- B GENTLES\_modul4
- C ZHANG\_MM up
- H PanCan\_HK\_geneset\_nanostring
- Y SPANG\_LPS-index2
- L SPANG\_BCL6-index2
- A GENTLES\_modul14
- A GENTLES\_modul8
- L GENTLES\_modul12
- D1 WANG\_ER\_UP
- R1 GENTLES\_modul18
- D1 LIU\_PROSTATE\_CANCER\_UP
- E1 LIU\_LIVER\_CANCER
- P GENTLES\_modul13
- S GENTLES\_modul11
- R1 PanCan\_HH\_geneset\_nanostring
- E1 WANG\_ER\_DN
- S1 BEN-PORATH\_DN
- H GENTLES\_modul16
- H1 ZHANG\_MGUS up
- H1 GENTLES\_modul17
- H1 PanCan\_TGF-B\_geneset\_nanostring
- Y PanCan\_Notch\_geneset\_nanostring
- H1 LIU\_PROSTATE\_CANCER\_DN
- G1 PanCan\_TXmisReg\_geneset\_nanostring
- N PanCan\_Driver\_Gene\_geneset\_nanostring
- G SOTIRIOU\_BREAST\_CANCER\_GRADE\_1\_VS\_3\_DN
- H1 Lembcke\_Colonc Inflammation
- N PanCan\_JAK-ST\_geneset\_nanostring
- H1 PanCan\_PI3K\_geneset\_nanostring
- F1 PanCan\_Wnt\_geneset\_nanostring
- F1 PanCan\_MAPK\_geneset\_nanostring
- H1 PanCan\_RAS\_geneset\_nanostring
- E RHODES\_UNDIFFERENTIATED\_CANCER
- E SOTIRIOU\_BREAST\_CANCER\_GRADE\_1\_VS\_3\_UP
- E WOLFER\_overlap genes
- E Lembcke\_Normal vs Adenoma



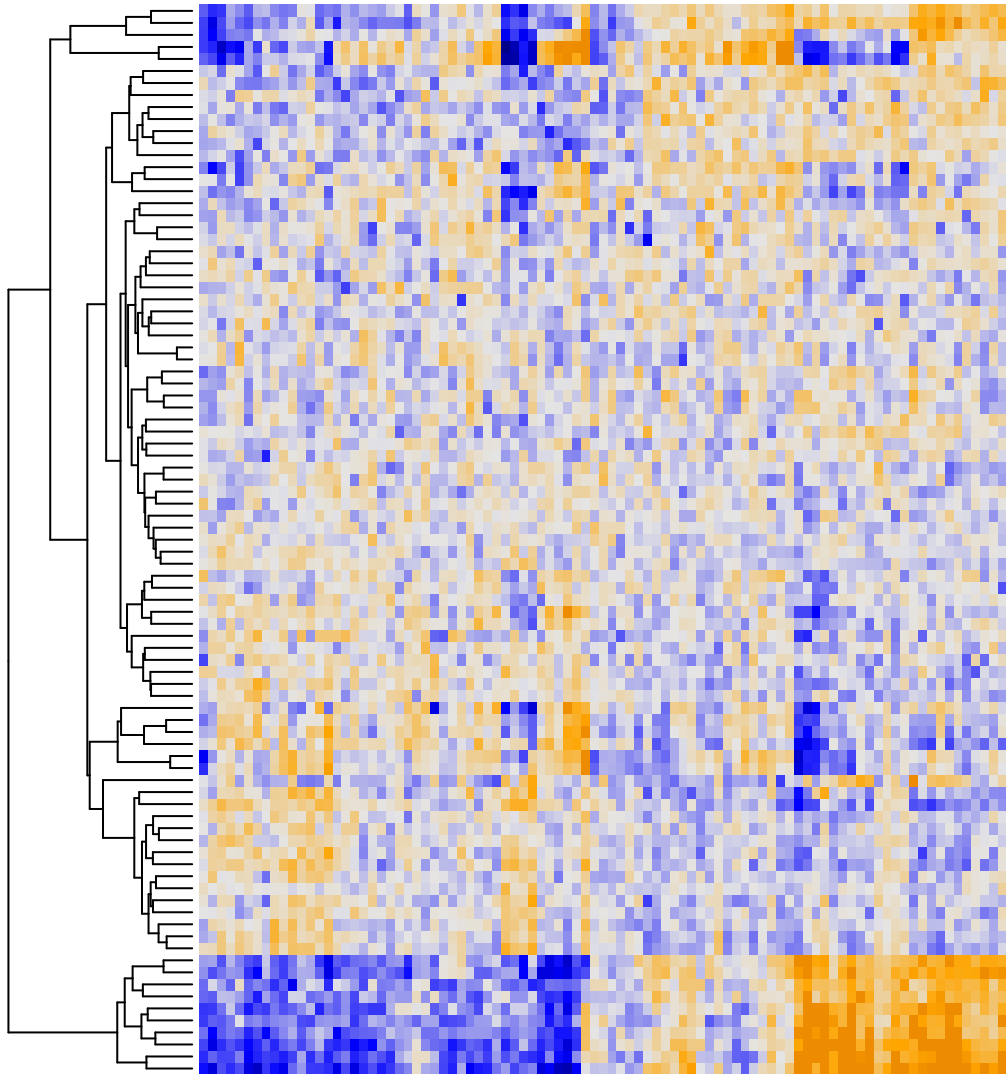
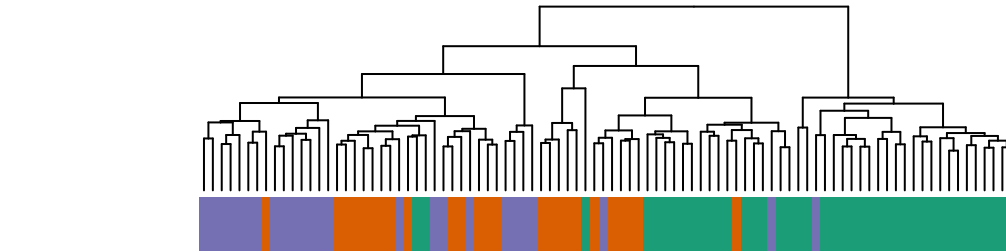
# GSZ score

Category Cancer

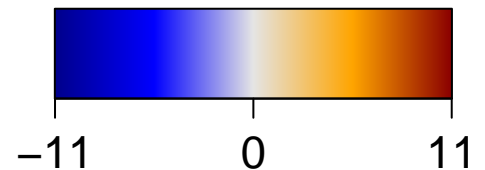


# GSZ score

Category CC

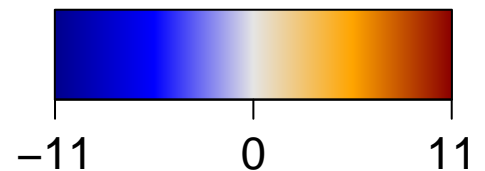
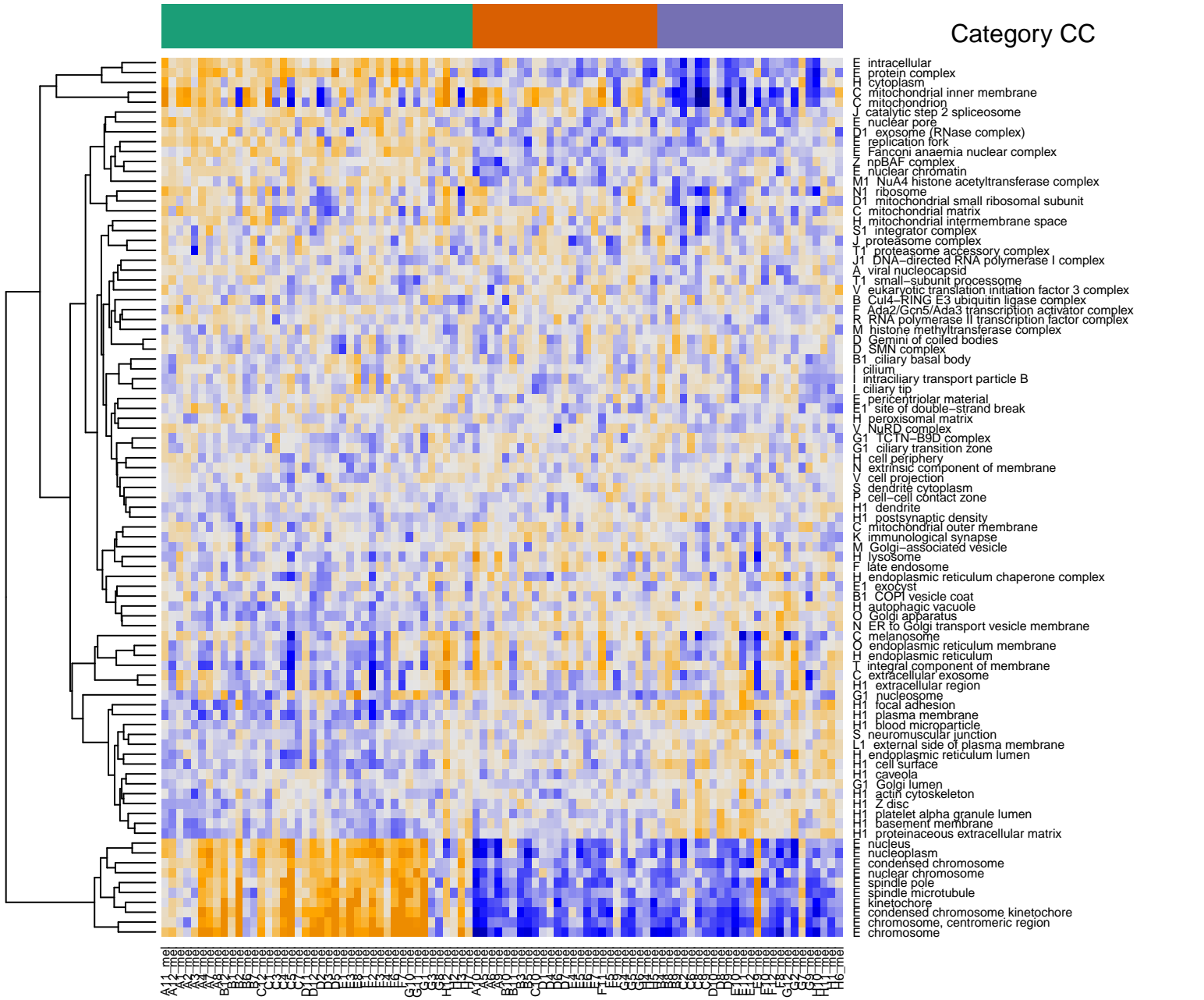


- intracellular protein complex
- cytoplasm
- mitochondrial inner membrane
- mitochondrion
- catalytic step 2 spliceosome
- nuclear pore
- exosome (RNase complex)
- replication fork
- Fanconi anaemia nuclear complex
- npBAF complex
- nuclear chromatin
- NUA4 histone acetyltransferase complex
- ribosome
- mitochondrial small ribosomal subunit
- mitochondrial matrix
- mitochondrial intermembrane space
- integrator complex
- proteasome complex
- proteasome accessory complex
- DNA-directed RNA polymerase I complex
- viral nucleocapsid
- small-subunit processome
- eukaryotic translation initiation factor 3 complex
- Cul4-RING E3 ubiquitin ligase complex
- Ara2/Cen5/Ara3 transcription activator complex
- RNA polymerase II transcription factor complex
- histone methyltransferase complex
- Gemini of coiled bodies
- SMN complex
- ciliary basal body
- cilium
- intraciliary transport particle B
- ciliary tip
- pericentriolar material
- site of double-strand break
- peroxisomal matrix
- NurD complex
- LC1N-BSD complex
- ciliary transition zone
- cell periphery
- extrinsic component of membrane
- cell projector
- dendrite cytoplasm
- cell-cell contact zone
- dendrite
- postsynaptic density
- mitochondrial outer membrane
- immunological synapse
- Golgi-associated vesicle
- lysosome
- late endosome
- endoplasmic reticulum chaperone complex
- exocyst
- COPI vesicle coat
- autophagic vacuole
- Golgi apparatus
- ER to Golgi transport vesicle membrane
- melanosome
- endoplasmic reticulum membrane
- endoplasmic reticulum
- integral component of membrane
- extracellular exosome
- extracellular region
- nucleosome
- focal adhesion
- plasma membrane
- blood microparticle
- neuromuscular junction
- external side of plasma membrane
- endoplasmic reticulum lumen
- cell surface
- caveola
- Golgi lumen
- actin cytoskeleton
- z disc
- platelet alpha granule lumen
- basement membrane
- proteinaceous extracellular matrix
- nucleus
- nucleoplasm
- condensed chromosome
- nuclear chromosome
- spindle pole
- spindle microtubule
- kinetochore
- condensed chromosome kinetochore
- chromosome, centromeric region
- chromosome



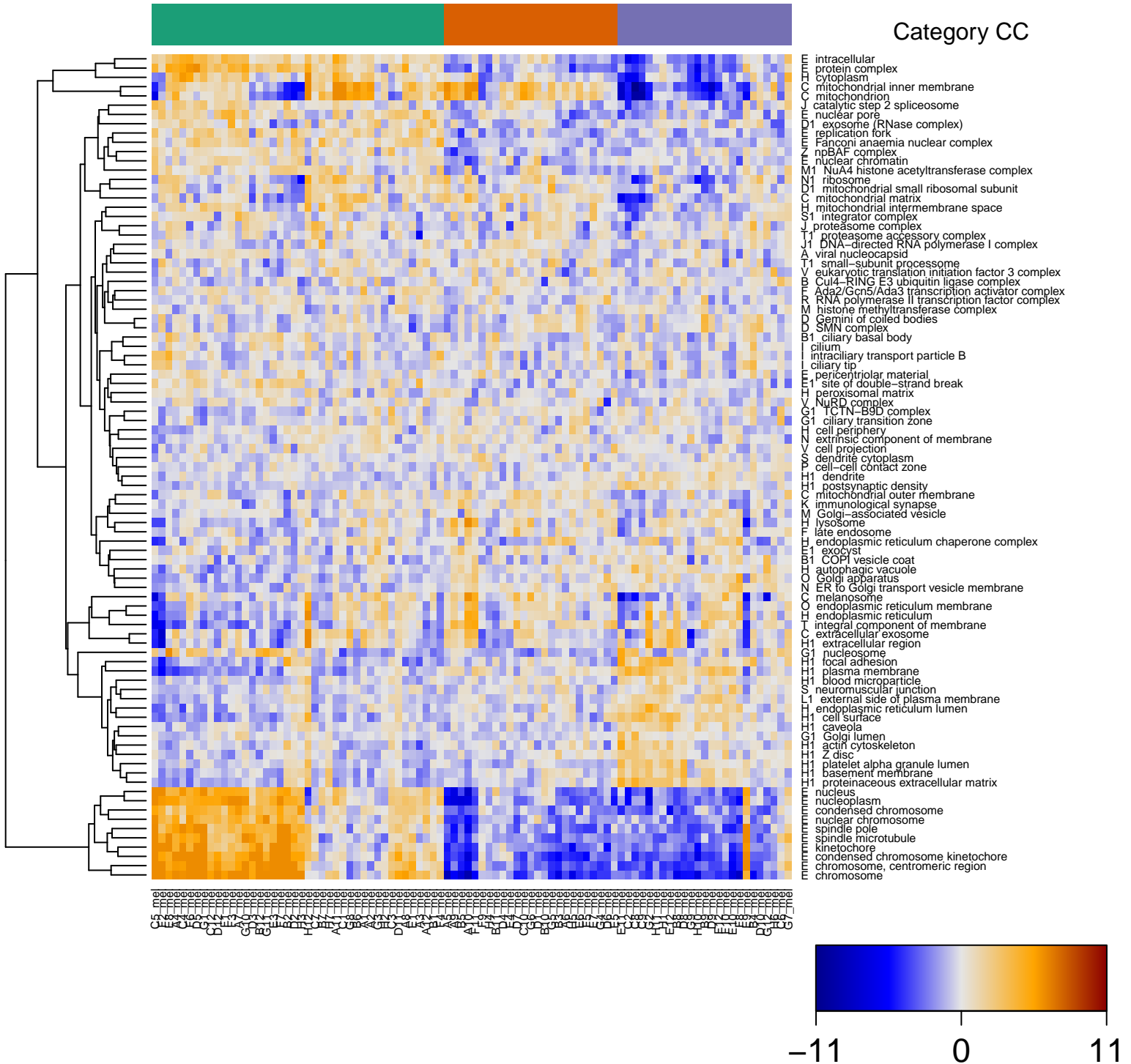
# GSZ score

Category CC



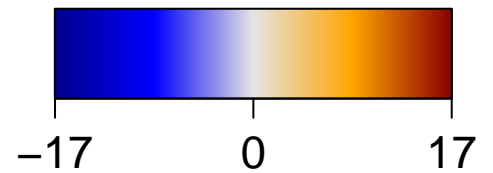
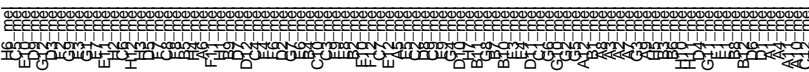
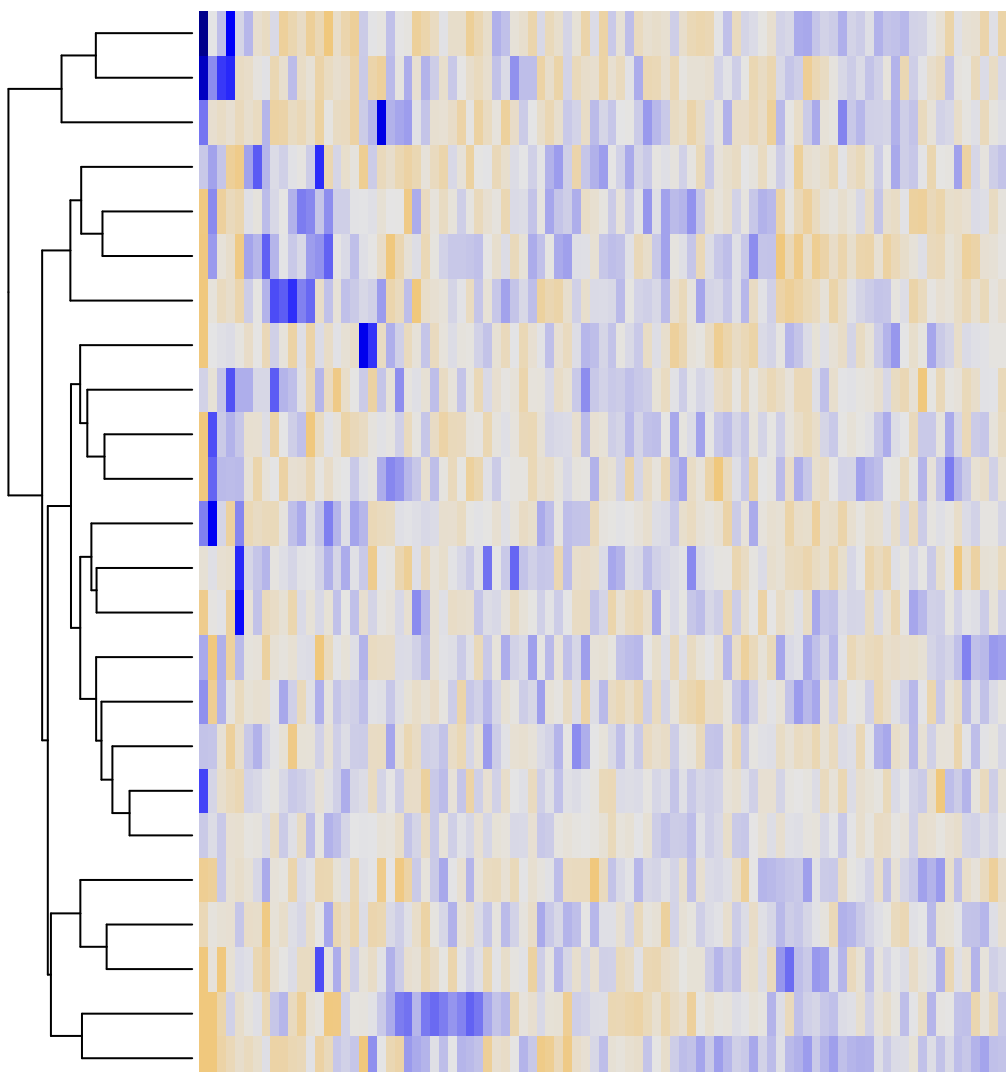
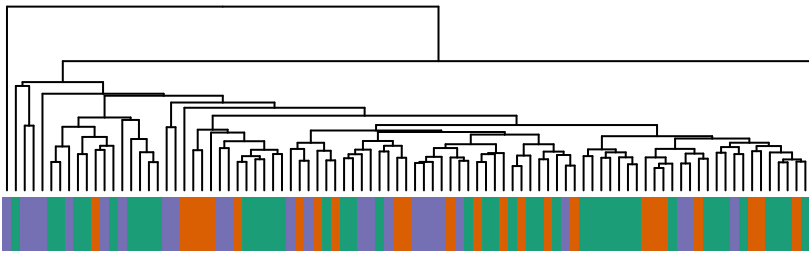
# GSZ score

Category CC



# GSZ score

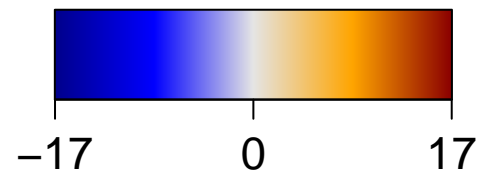
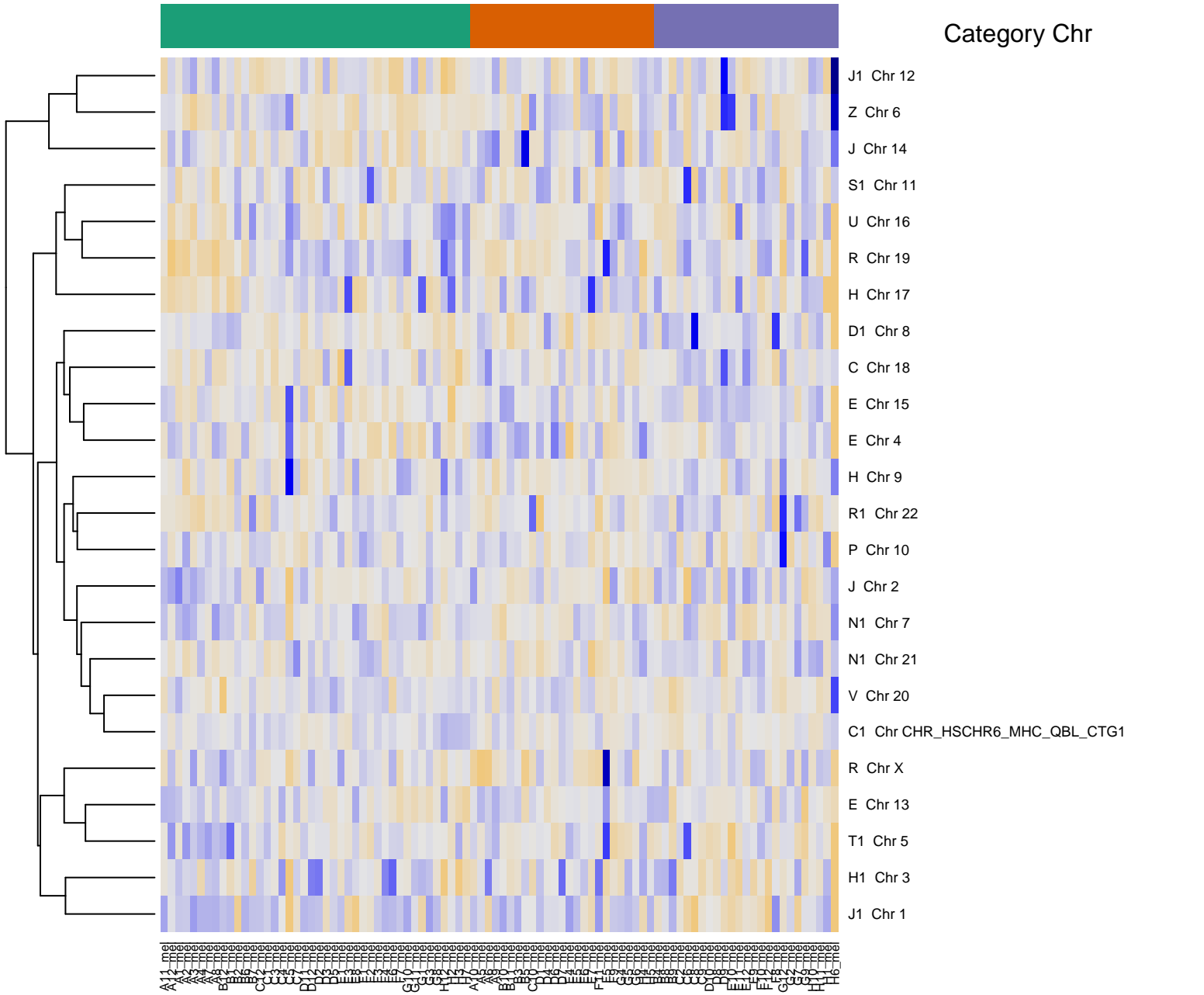
Category Chr





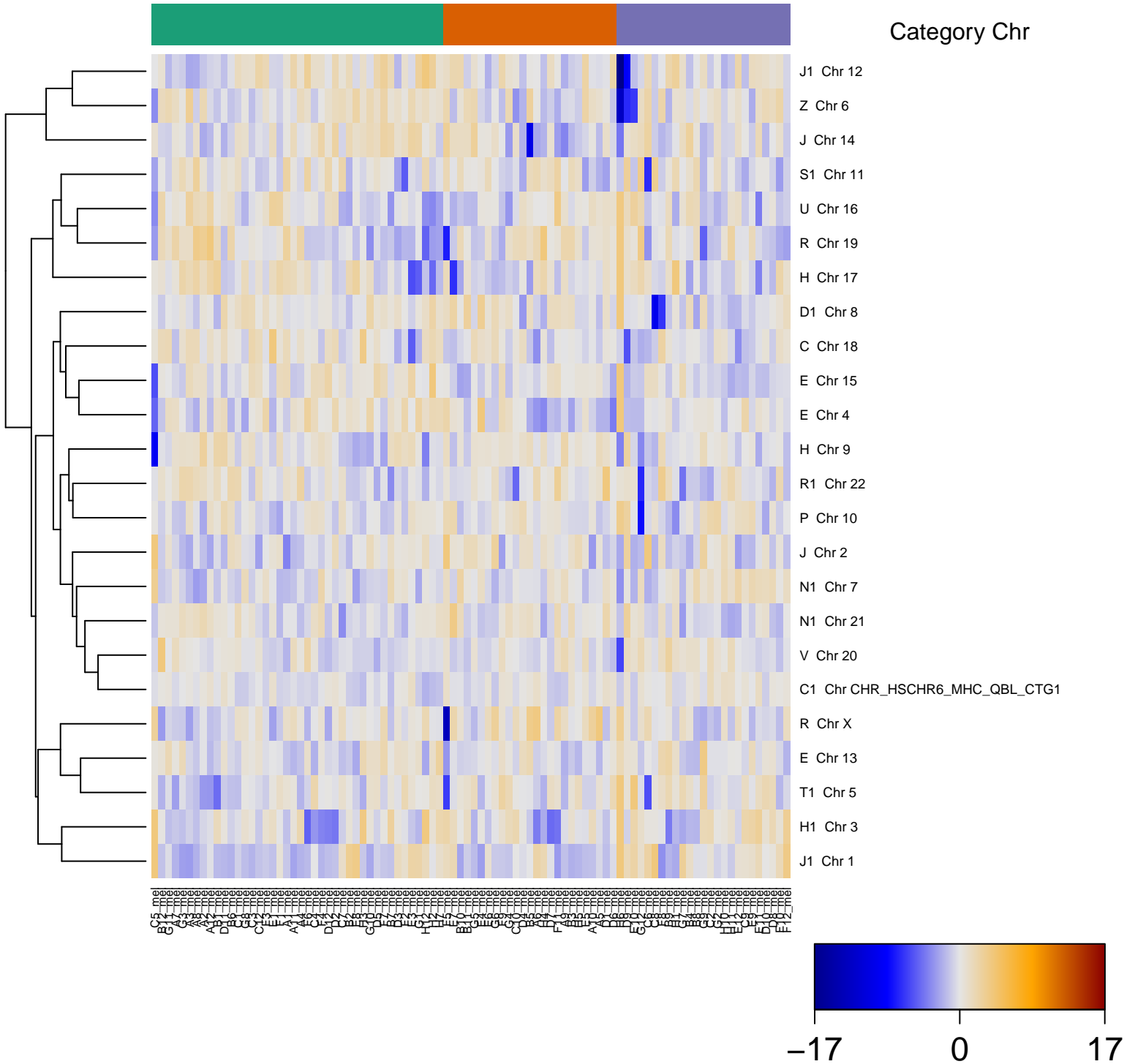
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Category Chr



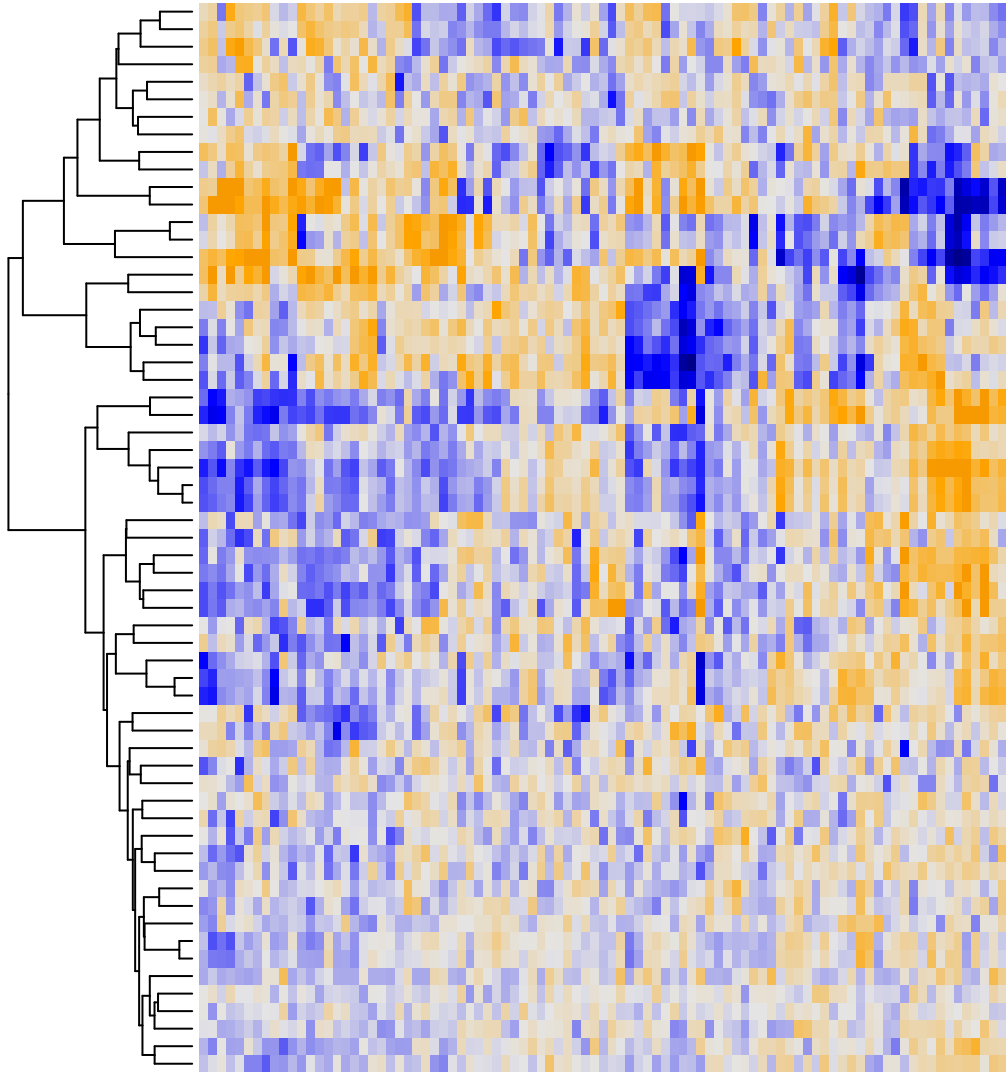
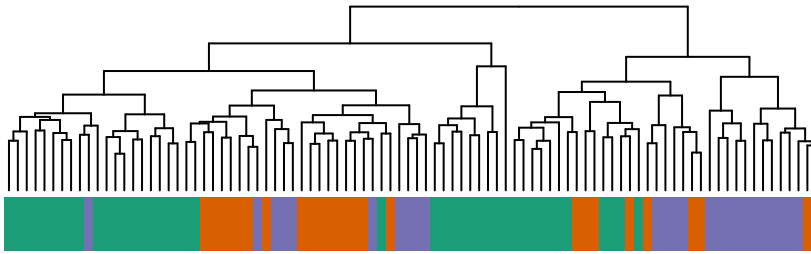
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Category Chr

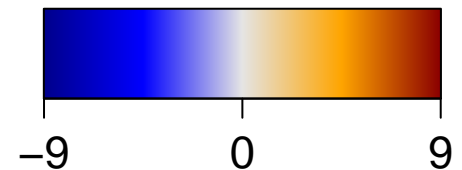
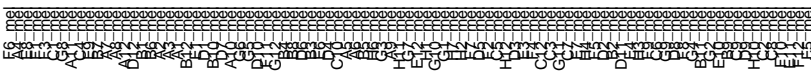


# GSZ score

Category Colon Cancer

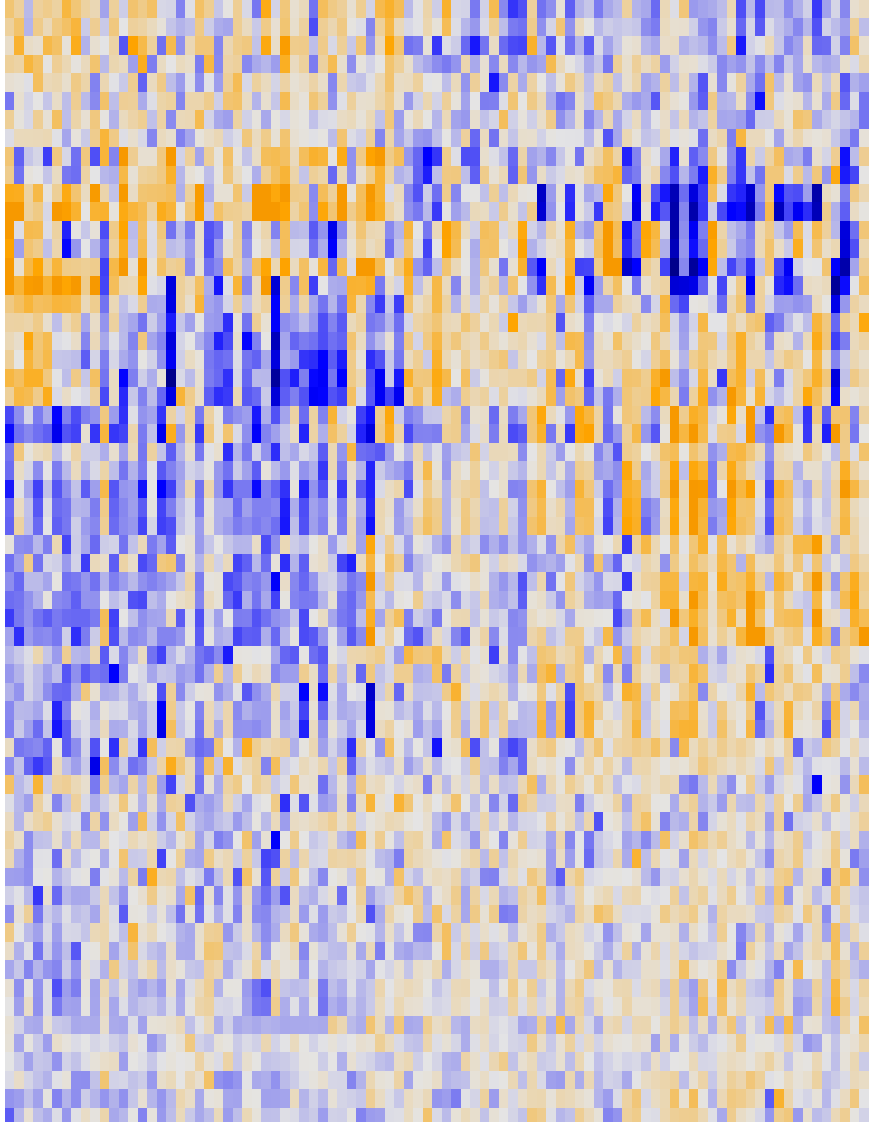
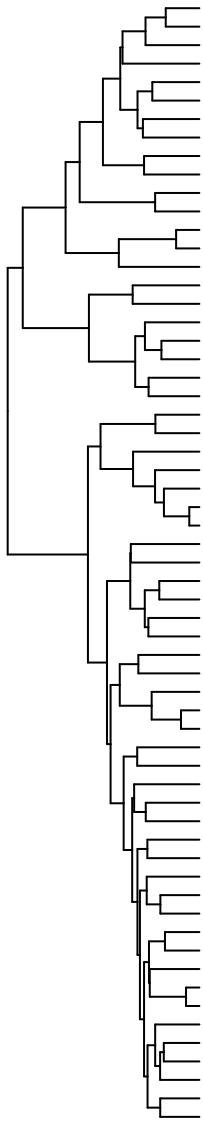


- E Boland\_CRC-MMR-system
- E TCGA\_Mutated-in-CRC\_mismatch-repair-genes
- E Hewish\_dMMR-secondary-mutations\_DNA-repair
- H Hewish\_dMMR-secondary-mutations\_Damage\_signaling
- T Juehling-MSI-enriched-in-6
- E KIM\_MSI-in-EC
- S1 Marisa\_CRC-cluster-e
- R Juehling\_HNPCC-mutated-in-6-to-8
- H1 TssWk\_Colon
- Q1 Quies3\_Colon
- E Pentrack\_CRC\_TCGA\_corr\_R\_normal\_DN
- E Pentrack\_CRC\_TCGA\_group.over\_C\_normal\_DN
- I1 Tx\_Colon
- I1 TxWk\_Colon
- H TssA\_Colon
- H TssF\_Colon
- H TssD2\_Colon
- H TxEnhG2\_Colon
- H Enh\_Colon
- N1 EnhWk1\_Colon
- N1 TxEnhG1\_Colon
- H EnhA\_Colon
- K EnhWk2\_Colon
- H1 Quies1\_Colon
- P1 Lembcke\_TCGA-expr\_kmeans\_H\_CIMP.H\_UP\_Cluster3\_DN
- F1 EnhP\_Colon
- F1 TssP\_Colon
- F1 ReprPCWk\_Colon
- F1 ReprPC\_Colon
- H1 Pentrack\_CRC\_TCGA\_corr\_U\_msi-h\_UP
- M1 Budinska\_D\_Mesenchymal\_UP
- H1 Pentrack\_CRC\_TCGA\_group.over\_B\_msi-h\_UP
- H1 Pentrack\_CRC\_TCGA\_corr\_J\_msi-h\_UP\_mss\_DN
- H1 Marisa\_CRC-cluster-b
- H1 Marisa\_CRC-cluster-a
- K Lembcke\_TCGA-expr\_kmeans\_N\_CIMP.H\_DN
- H1 Pentrack\_CRC\_TCGA\_corr\_C\_normal\_UP
- R ZNF\_Colon
- S HetRpts\_Colon
- R Het\_Colon
- K Budinska\_C\_CIMP-H-like\_UP
- H1 Hewish\_dMMR-secondary-mutations\_Cell-motility
- H Hewish\_dMMR-secondary-mutations\_Transcriptional\_regulation
- J Pentrack\_CRC\_TCGA\_corr\_N\_msi-h\_DN
- P1 Marisa\_CRC-C2
- J KIM\_MSI-in-CRC
- T KIM\_CRC-MSI-regulated\_DN
- Q1 Juehling-MSI-enriched-in-8-to-9
- T Hewish\_dMMR-secondary-mutations\_Signal\_transduction
- N Juehling\_HNPCC-mutated-in-5
- N TCGA\_Mutated-in-CRC\_hypermutated
- N Vilar\_hypermutated-in-CRC
- O1 Pentrack\_CRC\_TCGA\_corr\_H\_mss\_UP\_msi-h\_DN
- H1 Vilar\_non-hypermutated-in-CRC
- H1 TCGA\_Mutated-in-CRC\_non-hypermutated
- H1 Budinska\_A\_Surface\_crypt-like\_DOWN
- F1 Hewish\_dMMR-secondary-mutations\_Immune\_surveillance
- S Pentrack\_CRC\_TCGA\_corr\_S\_normal\_DN
- H1 Ang\_CRC-CIMP-vs-L\_hyper
- U Lembcke\_TCGA-expr\_kmeans\_E\_CIMP.H\_UP\_Cluster4\_DN
- G Lembcke\_TCGA-expr\_kmeans\_M\_CIMP.H\_DN

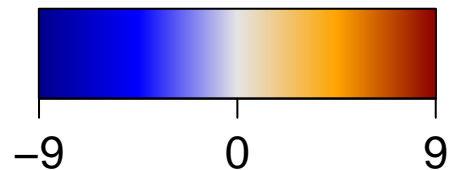
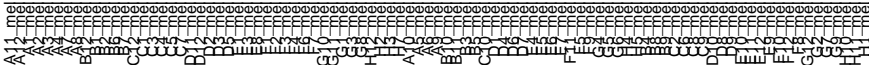


# GSZ score

Category Colon Cancer

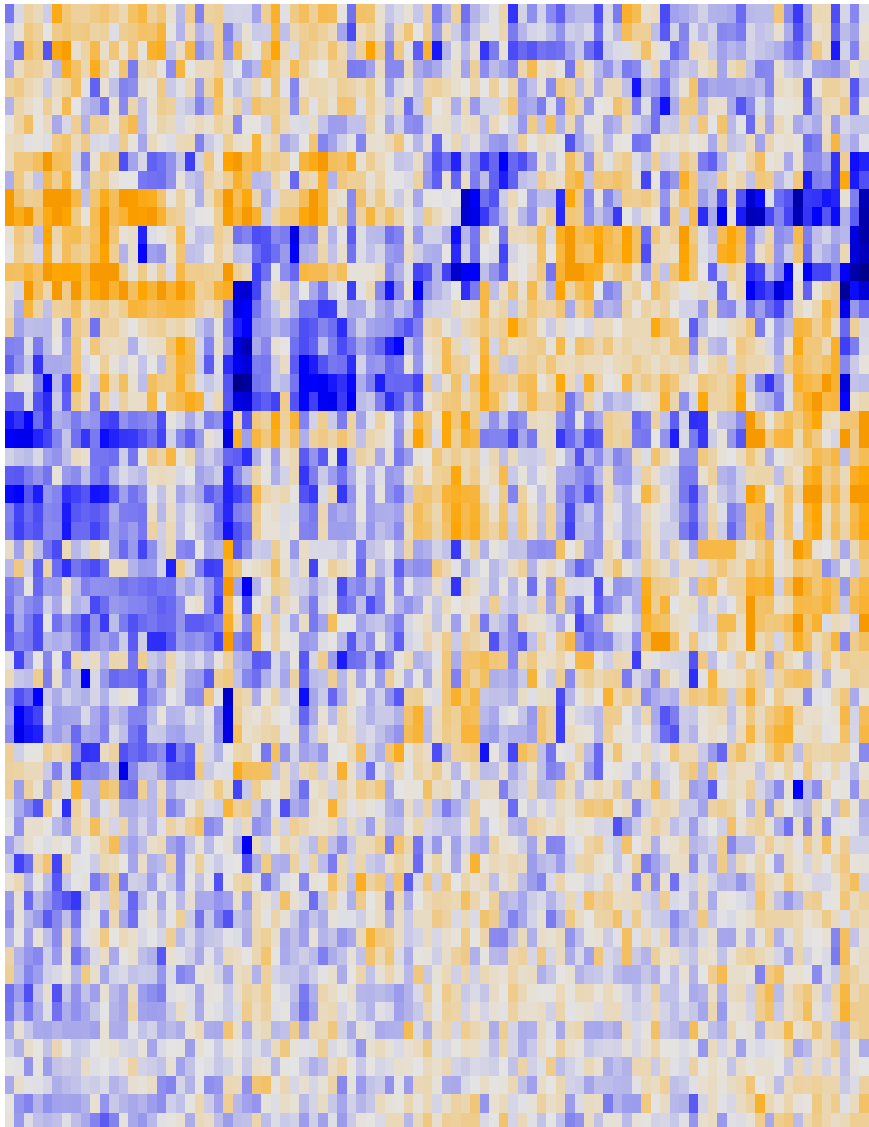
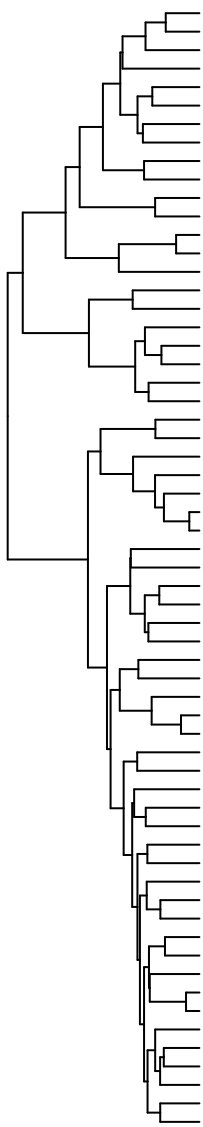


- E Boland\_CRC-MMR-system
- E TCGA\_Mutated-in-CRC\_mismatch-repair-genes
- E Hewish\_dMMR-secondary-mutations\_DNA-repair
- H Hewish\_dMMR-secondary-mutations\_Damage\_signaling
- T Juehling-MSI-enriched-in-6
- E KIM\_MSI-in-EC
- S1 Marisa\_CRC-cluster-e
- R Juehling\_HNPCC-mutated-in-6-to-8
- H1 TssWk\_Colon
- Q1 Quies3\_Colon
- E Pentrack\_CRC\_TCGA\_corr\_R\_normal\_DN
- E Pentrack\_CRC\_TCGA\_group.over\_C\_normal\_DN
- I1 Tx\_Colon
- I1 TxWk\_Colon
- H TssA\_Colon
- H TssF\_Colon
- H TssD2\_Colon
- H TxEnhG2\_Colon
- H Enh\_Colon
- N1 EnhWk1\_Colon
- N1 TxEnhG1\_Colon
- H EnhA\_Colon
- K EnhWk2\_Colon
- H1 Quies1\_Colon
- P1 Lembcke\_TCGA-expr\_kmeans\_H\_CIMP.H\_UP\_Cluster3\_DN
- F1 EnhP\_Colon
- F1 TssP\_Colon
- F1 ReprPCWk\_Colon
- F1 ReprPC\_Colon
- H1 Pentrack\_CRC\_TCGA\_corr\_U\_msi-h\_UP
- M1 Budinska\_D\_Mesenchymal\_UP
- H1 Pentrack\_CRC\_TCGA\_group.over\_B\_msi-h\_UP
- H1 Pentrack\_CRC\_TCGA\_corr\_J\_msi-h\_UP\_mss\_DN
- H1 Marisa\_CRC-cluster-b
- H1 Marisa\_CRC-cluster-a
- K Lembcke\_TCGA-expr\_kmeans\_N\_CIMP.H\_DN
- H1 Pentrack\_CRC\_TCGA\_corr\_C\_normal\_UP
- R ZNF\_Colon
- S HetRpts\_Colon
- R Het\_Colon
- K Budinska\_C\_CIMP-H-like\_UP
- H1 Hewish\_dMMR-secondary-mutations\_Cell-motility
- H Hewish\_dMMR-secondary-mutations\_Transcriptional\_regulation
- J Pentrack\_CRC\_TCGA\_corr\_N\_msi-h\_DN
- P1 Marisa\_CRC-C2
- J KIM\_MSI-in-CRC
- T KIM\_CRC-MSI-regulated\_DN
- Q1 Juehling-MSI-enriched-in-8-to-9
- T Hewish\_dMMR-secondary-mutations\_Signal\_transduction
- N Juehling\_HNPCC-mutated-in-5
- N TCGA\_Mutated-in-CRC\_hypermutated
- N Vilar\_hypermutated-in-CRC
- O1 Pentrack\_CRC\_TCGA\_corr\_H\_mss\_UP\_msi-h\_DN
- H1 Vilar\_non-hypermutated-in-CRC
- H1 TCGA\_Mutated-in-CRC\_non-hypermutated
- H1 Budinska\_A\_Surface crypt-like\_DOWN
- F1 Hewish\_dMMR-secondary-mutations\_Immune\_surveillance
- S Pentrack\_CRC\_TCGA\_corr\_S\_normal\_DN
- H1 Ang\_CRC-CIMPH-vs-L\_hyper
- U Lembcke\_TCGA-expr\_kmeans\_E\_CIMP.H\_UP\_Cluster4\_DN
- G Lembcke\_TCGA-expr\_kmeans\_M\_CIMP.H\_DN

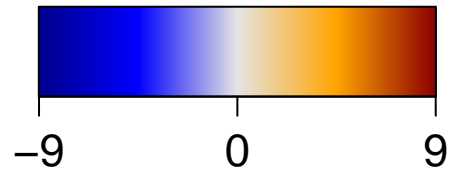


# GSZ score

Category Colon Cancer

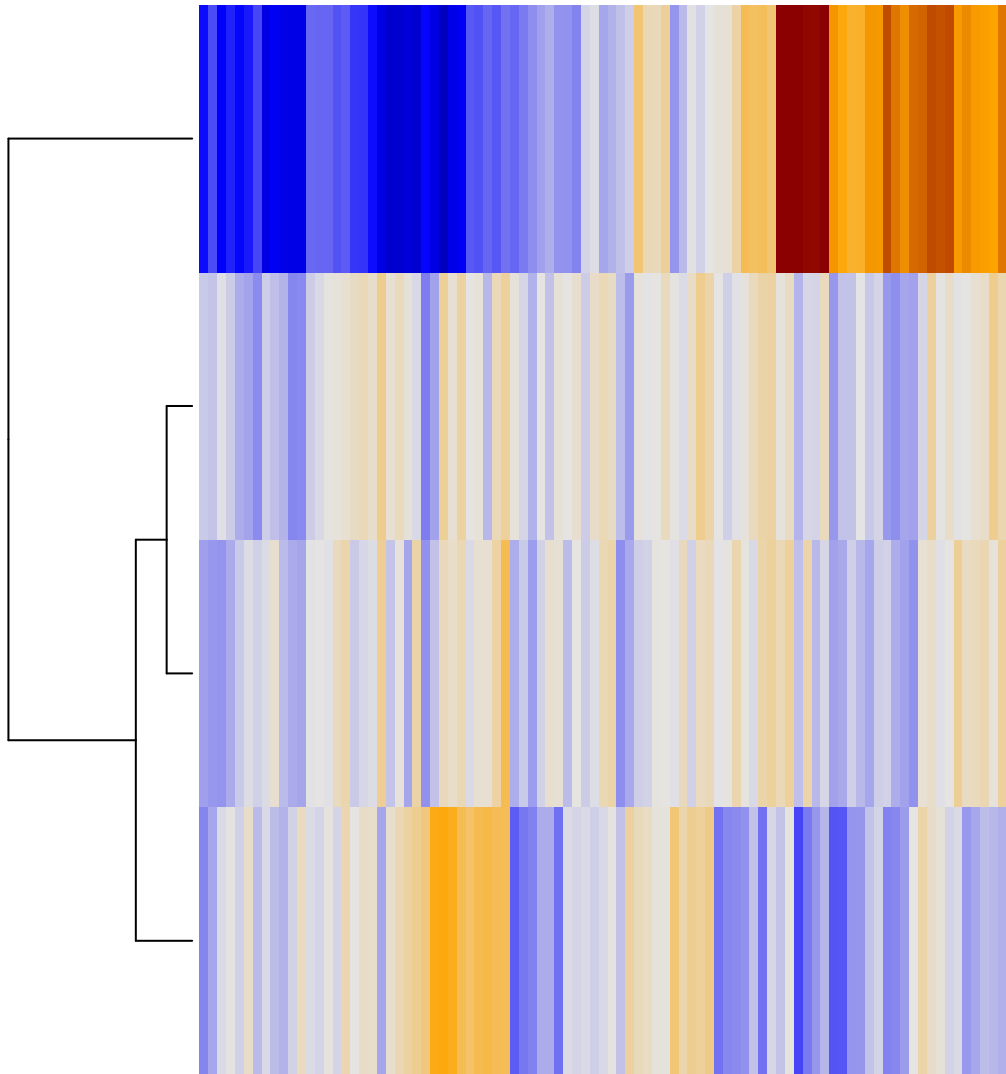
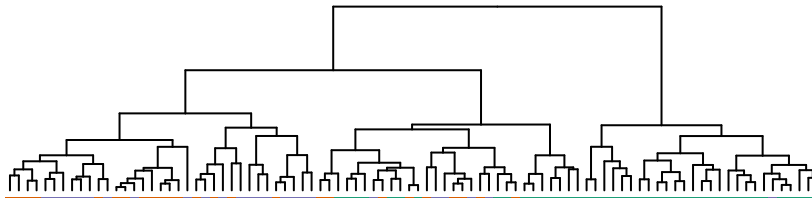


- E Boland\_CRC-MMR-system
- E TCGA\_Mutated-in-CRC\_mismatch-repair-genes
- E Hewish\_dMMR-secondary-mutations\_DNA-repair
- H Hewish\_dMMR-secondary-mutations\_Damage\_signaling
- T Juehling-MSI-enriched-in-6
- E KIM\_MSI-in-EC
- S1 Marisa\_CRC-cluster-e
- R Juehling\_HNPCC-mutated-in-6-to-8
- H1 TssWk\_Colon
- Q1 Quies3\_Colon
- E Pentrack\_CRC\_TCGA\_corr\_R\_normal\_DN
- E Pentrack\_CRC\_TCGA\_group.over\_C\_normal\_DN
- I1 Tx\_Colon
- I1 TxWk\_Colon
- H TssA\_Colon
- H TssF\_Colon
- H TssD2\_Colon
- H TxEnhG2\_Colon
- H Enh\_Colon
- N1 EnhWk1\_Colon
- N1 TxEnhG1\_Colon
- H EnhA\_Colon
- K EnhWk2\_Colon
- H1 Quies1\_Colon
- P1 Lembcke\_TCGA-expr\_kmeans\_H\_CIMP.H\_UP\_Cluster3\_DN
- F1 EnhP\_Colon
- F1 TssP\_Colon
- F1 ReprPCWk\_Colon
- F1 ReprPC\_Colon
- H1 Pentrack\_CRC\_TCGA\_corr\_U\_msi-h\_UP
- M1 Budinska\_D\_Mesenchymal\_UP
- H1 Pentrack\_CRC\_TCGA\_group.over\_B\_msi-h\_UP
- H1 Pentrack\_CRC\_TCGA\_corr\_J\_msi-h\_UP\_mss\_DN
- H1 Marisa\_CRC-cluster-b
- H1 Marisa\_CRC-cluster-a
- K Lembcke\_TCGA-expr\_kmeans\_N\_CIMP.H\_DN
- H1 Pentrack\_CRC\_TCGA\_corr\_C\_normal\_UP
- R ZNF\_Colon
- S HetRpts\_Colon
- R Het\_Colon
- K Budinska\_C\_CIMP-H-like\_UP
- H1 Hewish\_dMMR-secondary-mutations\_Cell-motility
- H Hewish\_dMMR-secondary-mutations\_Transcriptional\_regulation
- J Pentrack\_CRC\_TCGA\_corr\_N\_msi-h\_DN
- P1 Marisa\_CRC-C2
- J KIM\_MSI-in-CRC
- T KIM\_CRC-MSI-regulated\_DN
- Q1 Juehling-MSI-enriched-in-8-to-9
- T Hewish\_dMMR-secondary-mutations\_Signal\_transduction
- N Juehling\_HNPCC-mutated-in-5
- N TCGA\_Mutated-in-CRC\_hypermutated
- N Vilar\_hypermutated-in-CRC
- O1 Pentrack\_CRC\_TCGA\_corr\_H\_mss\_UP\_msi-h\_DN
- H1 Vilar\_non-hypermutated-in-CRC
- H1 TCGA\_Mutated-in-CRC\_non-hypermutated
- H1 Budinska\_A\_Surface\_crypt-like\_DOWN
- F1 Hewish\_dMMR-secondary-mutations\_Immune\_surveillance
- S Pentrack\_CRC\_TCGA\_corr\_S\_normal\_DN
- H1 Ang\_CRC-CIMPH-vs-L\_hyper
- U Lembcke\_TCGA-expr\_kmeans\_E\_CIMP.H\_UP\_Cluster4\_DN
- G Lembcke\_TCGA-expr\_kmeans\_M\_CIMP.H\_DN



# GSZ score

Category Disease



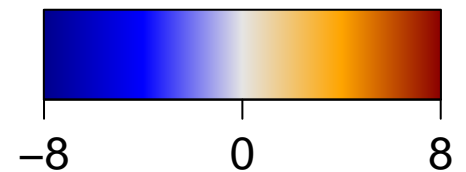
E GUDJ\_psoriasis up

L1 BCHETNIA\_EBM-DM up

L1 BCHETNIA\_EBM up

H1 GUDJ\_psoriasis down

Small text labels at the bottom of the heatmap, likely representing gene identifiers or symbols, such as GUDJ, BCHETNIA, and EBM.



# GSZ score

Category Disease

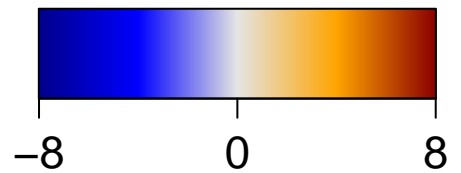


E GUDJ\_psoriasis up

L1 BCHETNIA\_EBM-DM u

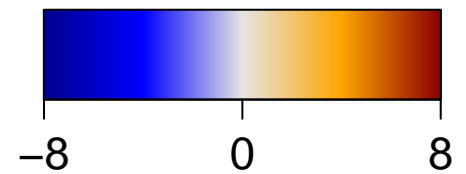
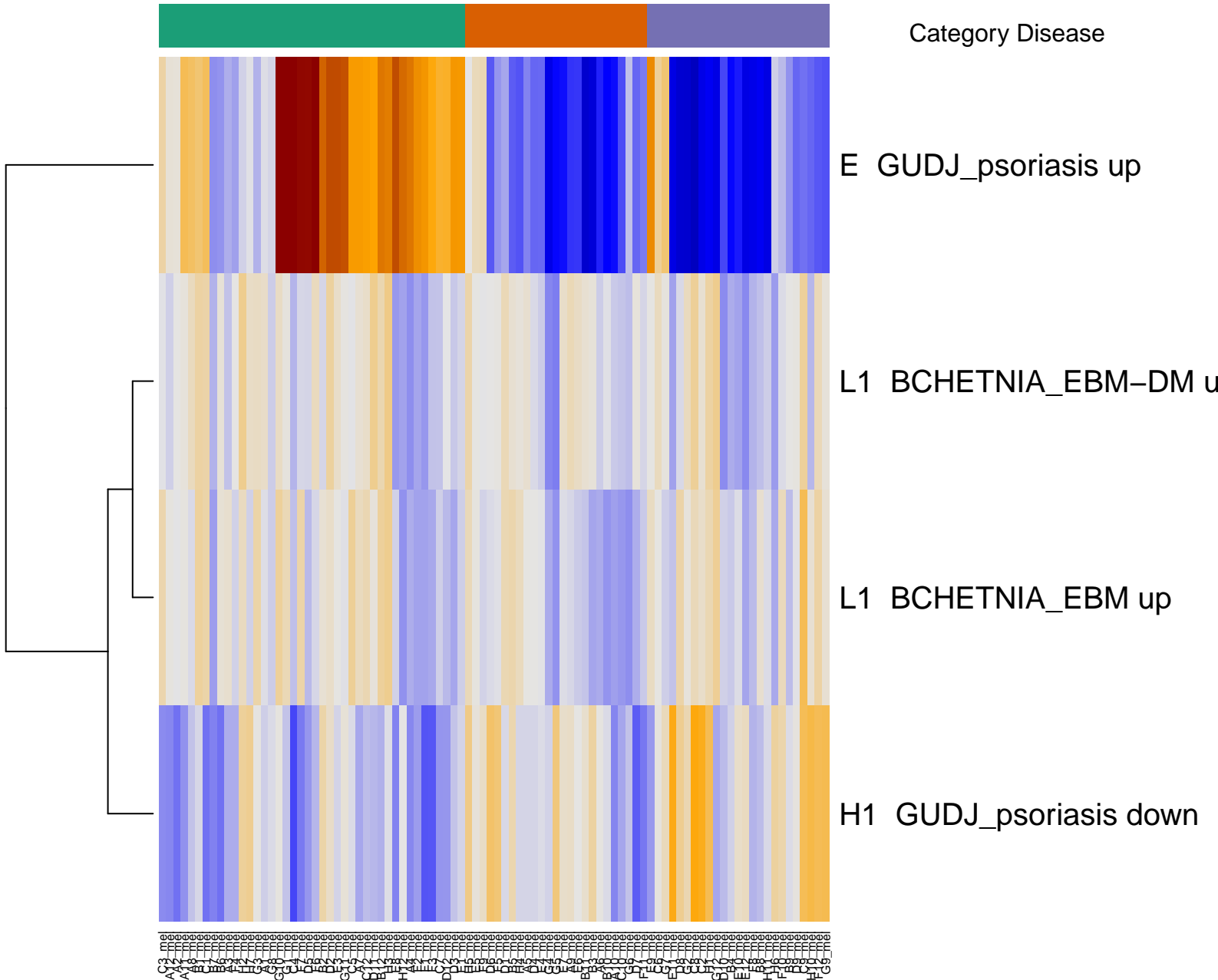
L1 BCHETNIA\_EBM up

H1 GUDJ\_psoriasis down



# GSZ score

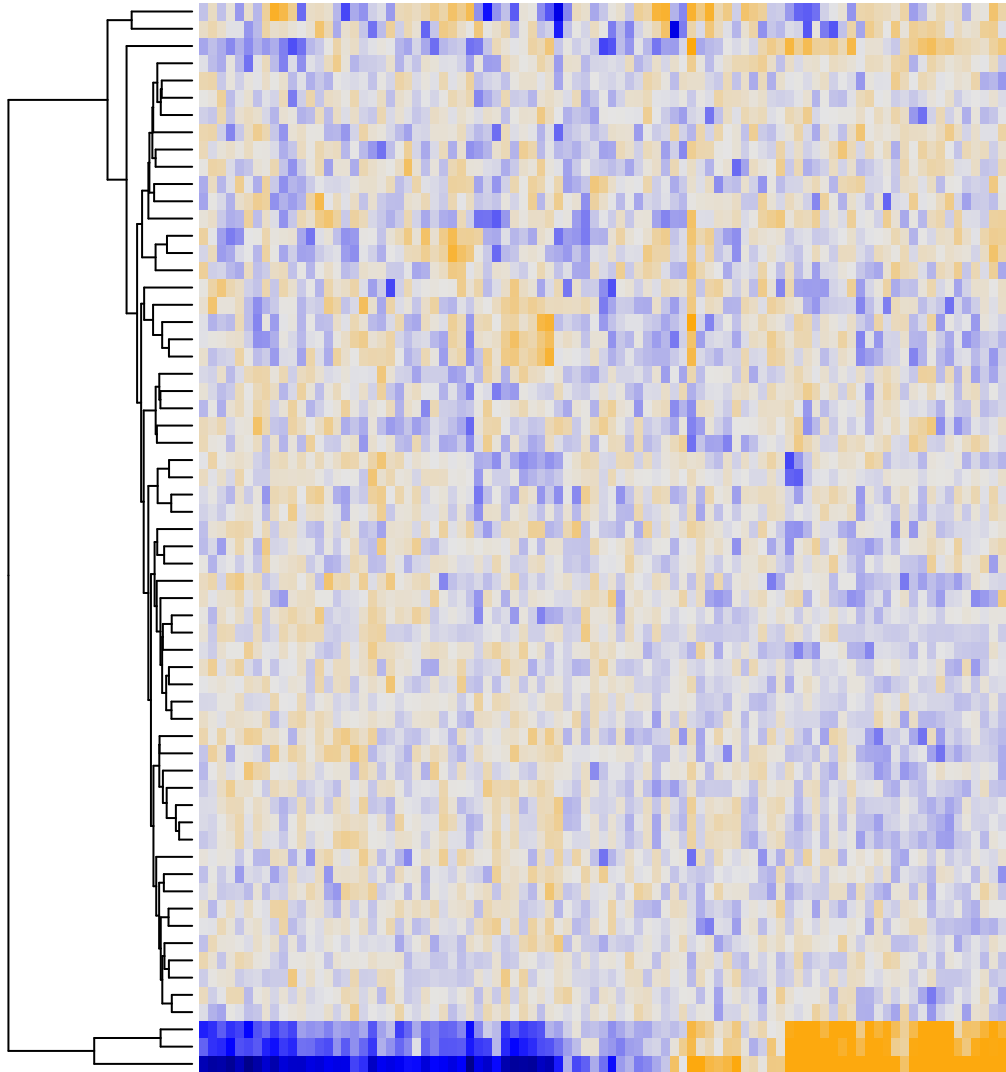
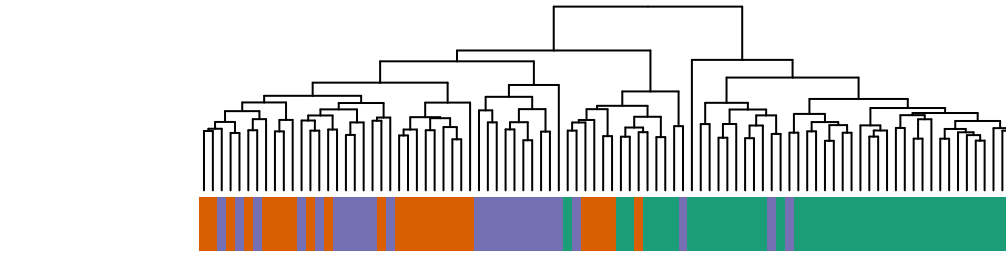
Category Disease



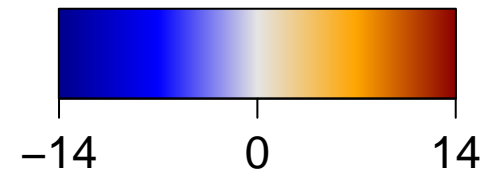
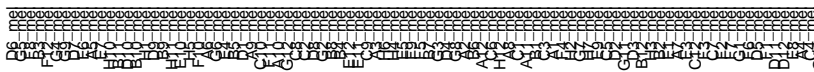


# GSZ score

Category Glio

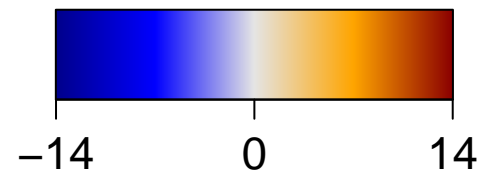
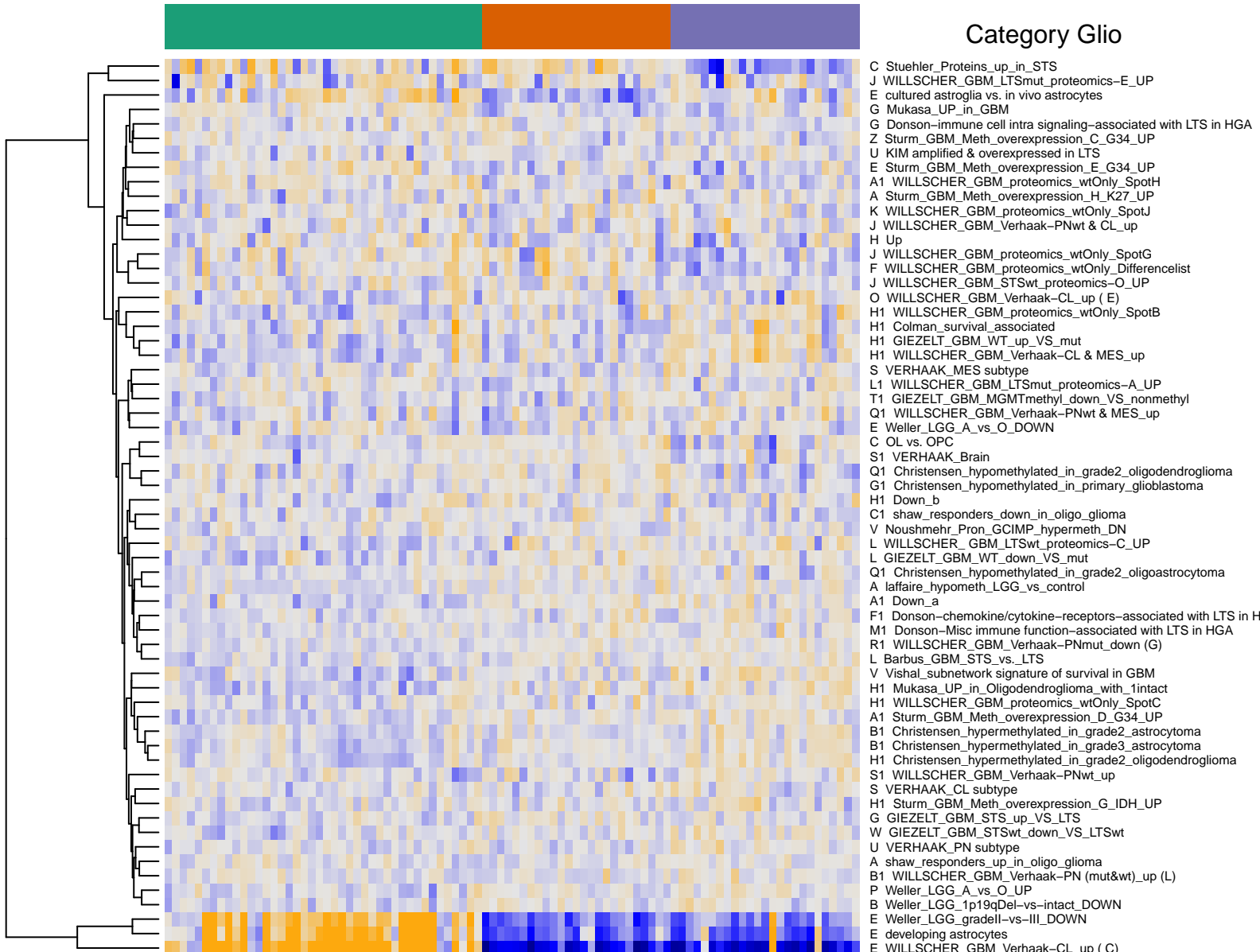


- C Stuehler\_Proteins\_up\_in\_STS
- J WILLSCHER\_GBM\_LTSmut\_proteomics-E\_UP
- E cultured astroglia vs. in vivo astrocytes
- G Mukasa\_UP\_in\_GBM
- G Donson-immune cell intra signaling-associated with LTS in HGA
- Z Sturm\_GBM\_Meth\_overexpression\_C\_G34\_UP
- U KIM amplified & overexpressed in LTS
- E Sturm\_GBM\_Meth\_overexpression\_E\_G34\_UP
- A1 WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotH
- A Sturm\_GBM\_Meth\_overexpression\_H\_K27\_UP
- K WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotJ
- J WILLSCHER\_GBM\_Verhaak-PNwt & CL\_up
- H Up
- J WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotG
- F WILLSCHER\_GBM\_proteomics\_wtOnly\_Differencelist
- J WILLSCHER\_GBM\_STSwt\_proteomics-O\_UP
- O WILLSCHER\_GBM\_Verhaak-CL\_up (E)
- H1 WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotB
- H1 Colman\_survival\_associated
- H1 GIEZELT\_GBM\_WT\_up\_VS\_mut
- H1 WILLSCHER\_GBM\_Verhaak-CL & MES\_up
- S VERHAAK\_MES subtype
- L1 WILLSCHER\_GBM\_LTSmut\_proteomics-A\_UP
- T1 GIEZELT\_GBM\_MGMTmethyl\_down\_VS\_nonmethyl
- Q1 WILLSCHER\_GBM\_Verhaak-PNwt & MES\_up
- E Weller\_LGG\_A\_vs\_O\_DOWN
- C OL vs. OPC
- S1 VERHAAK\_Brain
- Q1 Christensen\_hypomethylated\_in\_grade2\_oligodendroglioma
- G1 Christensen\_hypomethylated\_in\_primary\_glioblastoma
- H1 Down\_b
- C1 shaw\_responders\_down\_in\_oligo\_glioma
- V Noushmehr\_Pron\_GCIMP\_hypermeth\_DN
- L WILLSCHER\_GBM\_LTSwt\_proteomics-C\_UP
- L GIEZELT\_GBM\_WT\_down\_VS\_mut
- Q1 Christensen\_hypomethylated\_in\_grade2\_oligoastrocytoma
- A laffaire\_hypometh\_LGG\_vs\_control
- A1 Down\_a
- F1 Donson-chemokine/cytokine-receptors-associated with LTS in HGA
- M1 Donson-Misc immune function-associated with LTS in HGA
- R1 WILLSCHER\_GBM\_Verhaak-PNmut\_down (G)
- L Barbus\_GBM\_STS\_vs\_LTS
- V Vishal\_subnetwork signature of survival in GBM
- H1 Mukasa\_UP\_in\_Oligodendroglioma\_with\_1intact
- H1 WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotC
- A1 Sturm\_GBM\_Meth\_overexpression\_D\_G34\_UP
- B1 Christensen\_hypermethylated\_in\_grade2\_astrocytoma
- B1 Christensen\_hypermethylated\_in\_grade3\_astrocytoma
- H1 Christensen\_hypermethylated\_in\_grade2\_oligodendroglioma
- S1 WILLSCHER\_GBM\_Verhaak-PNwt\_up
- S VERHAAK\_CL subtype
- H1 Sturm\_GBM\_Meth\_overexpression\_G\_IDH\_UP
- G GIEZELT\_GBM\_STS\_up\_VS\_LTS
- W GIEZELT\_GBM\_STSwt\_down\_VS\_LTSwt
- U VERHAAK\_PN subtype
- A shaw\_responders\_up\_in\_oligo\_glioma
- B1 WILLSCHER\_GBM\_Verhaak-PN (mut&wt)\_up (L)
- P Weller\_LGG\_A\_vs\_O\_UP
- B Weller\_LGG\_1p19qDel-vs-intact\_DOWN
- E Weller\_LGG\_gradell-vs-III\_DOWN
- E developing astrocytes
- E WILLSCHER\_GBM\_Verhaak-CL\_up (C)



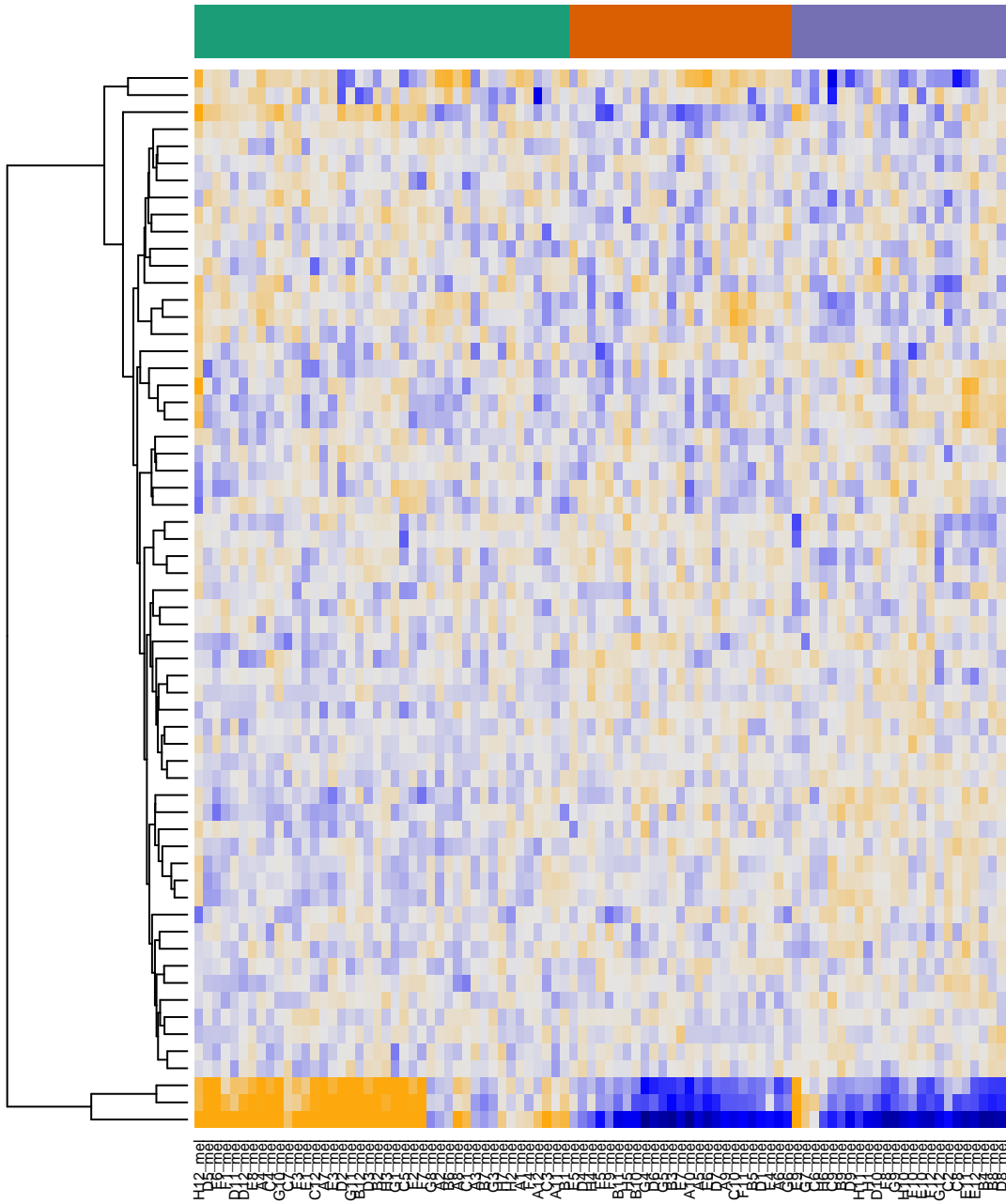
# GSZ score

Category Glio

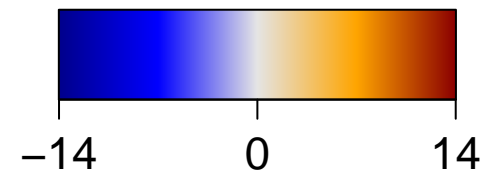


# GSZ score

Category Glio



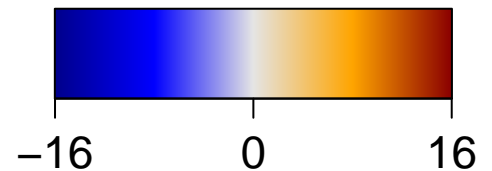
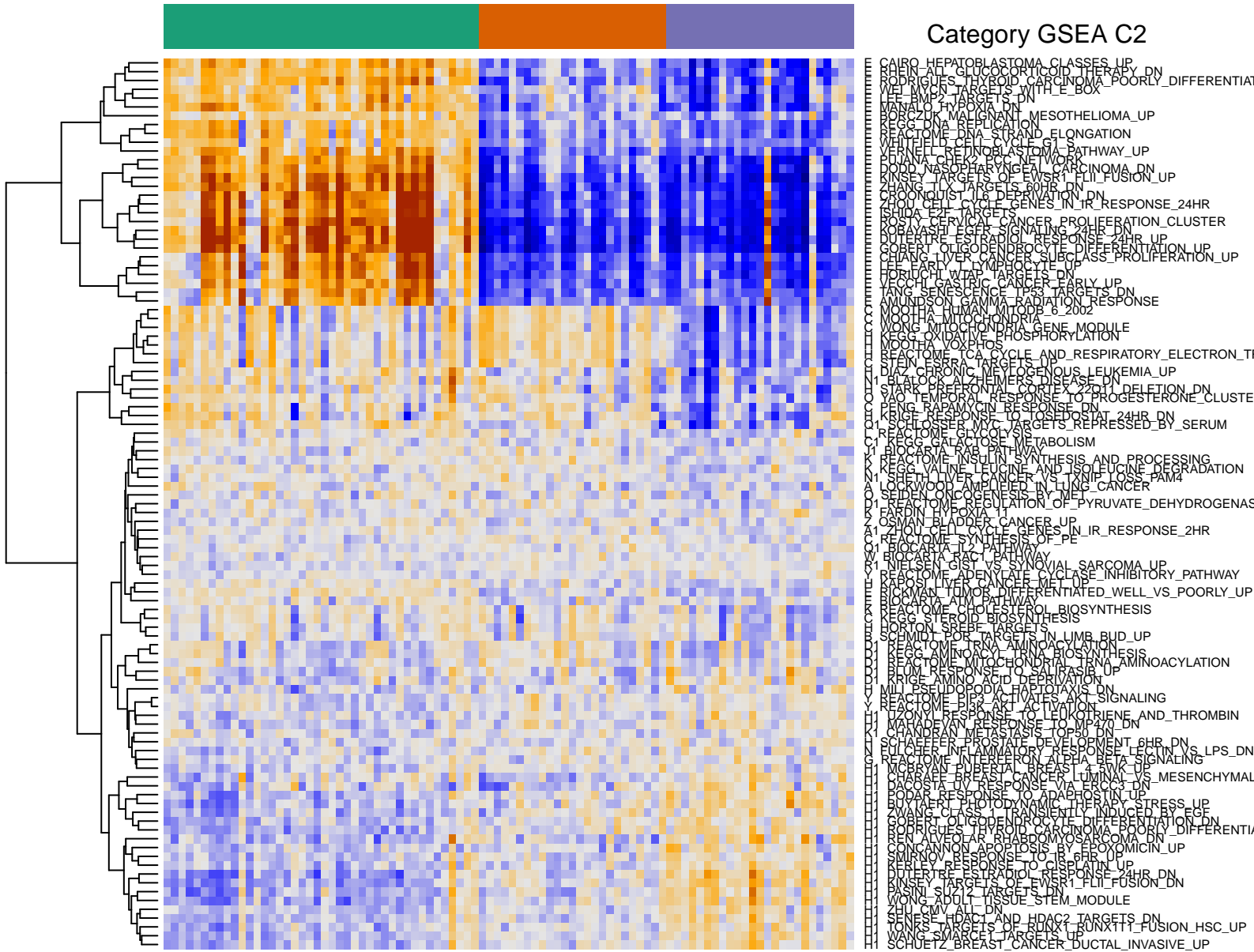
C Stuehler\_Proteins\_up\_in\_STS  
J WILLSCHER\_GBM\_LTSmut\_proteomics-E\_UP  
E cultured astroglia vs. in vivo astrocytes  
G Mukasa\_UP\_in\_GBM  
G Donson-immune cell intra signaling-associated with LTS in HGA  
Z Sturm\_GBM\_Meth\_overexpression\_C\_G34\_UP  
U KIM amplified & overexpressed in LTS  
E Sturm\_GBM\_Meth\_overexpression\_E\_G34\_UP  
A1 WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotH  
A Sturm\_GBM\_Meth\_overexpression\_H\_K27\_UP  
K WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotJ  
J WILLSCHER\_GBM\_Verhaak-PNwt & CL\_up  
H Up  
J WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotG  
F WILLSCHER\_GBM\_proteomics\_wtOnly\_Differencelist  
J WILLSCHER\_GBM\_STSwt\_proteomics-O\_UP  
O WILLSCHER\_GBM\_Verhaak-CL\_up ( E)  
H1 WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotB  
H1 Colman\_survival\_associated  
H1 GIEZELT\_GBM\_WT\_up\_VS\_mut  
H1 WILLSCHER\_GBM\_Verhaak-CL & MES\_up  
S VERHAAK\_MES subtype  
L1 WILLSCHER\_GBM\_LTSmut\_proteomics-A\_UP  
T1 GIEZELT\_GBM\_MGMTmethyl\_down\_VS\_nonmethyl  
Q1 WILLSCHER\_GBM\_Verhaak-PNwt & MES\_up  
E Weller\_LGG\_A\_vs\_O\_DOWN  
C OL vs. OPC  
S1 VERHAAK\_Brain  
Q1 Christensen\_hypomethylated\_in\_grade2\_oligodendroglioma  
G1 Christensen\_hypomethylated\_in\_primary\_glioblastoma  
H1 Down\_b  
C1 shaw\_responders\_down\_in\_oligo\_glioma  
V Noushmehr\_Pron\_GCIMP\_hypermeth\_DN  
L WILLSCHER\_GBM\_LTSwt\_proteomics-C\_UP  
L GIEZELT\_GBM\_WT\_down\_VS\_mut  
Q1 Christensen\_hypomethylated\_in\_grade2\_oligoastrocytoma  
A laffaire\_hypometh\_LGG\_vs\_control  
A1 Down\_a  
F1 Donson-chemokine/cytokine-receptors-associated with LTS in H  
M1 Donson-Misc immune function-associated with LTS in HGA  
R1 WILLSCHER\_GBM\_Verhaak-PNmut\_down (G)  
L Barbus\_GBM\_STS\_vs\_LTS  
V Vishal\_subnetwork signature of survival in GBM  
H1 Mukasa\_UP\_in\_Oligodendroglioma\_with\_1intact  
H1 WILLSCHER\_GBM\_proteomics\_wtOnly\_SpotC  
A1 Sturm\_GBM\_Meth\_overexpression\_D\_G34\_UP  
B1 Christensen\_hypermethylated\_in\_grade2\_astrocytoma  
B1 Christensen\_hypermethylated\_in\_grade3\_astrocytoma  
H1 Christensen\_hypermethylated\_in\_grade2\_oligodendroglioma  
S1 WILLSCHER\_GBM\_Verhaak-PNwt\_up  
S VERHAAK\_CL subtype  
H1 Sturm\_GBM\_Meth\_overexpression\_G\_IDH\_UP  
G GIEZELT\_GBM\_STS\_up\_VS\_LTS  
W GIEZELT\_GBM\_STSwt\_down\_VS\_LTSwt  
U VERHAAK\_PN subtype  
A shaw\_responders\_up\_in\_oligo\_glioma  
B1 WILLSCHER\_GBM\_Verhaak-PN (mut&wt)\_up (L)  
P Weller\_LGG\_A\_vs\_O\_UP  
B Weller\_LGG\_1p19qDel-vs-intact\_DOWN  
E Weller\_LGG\_gradell-vs-III\_DOWN  
E developing astrocytes  
E WILLSCHER\_GBM\_Verhaak-CL\_up ( C)





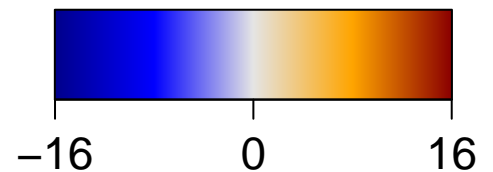
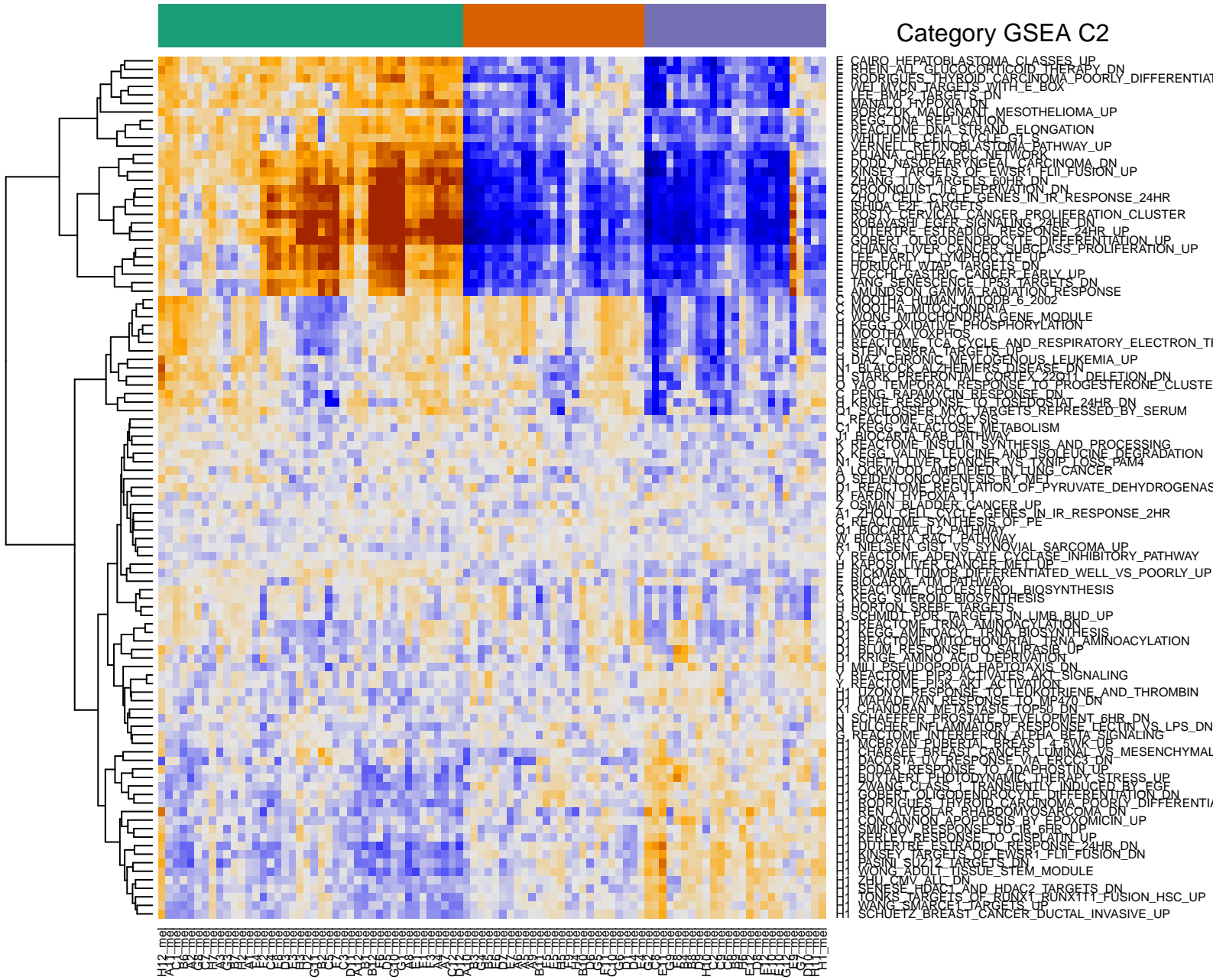
# GSZ score

Category GSEA C2



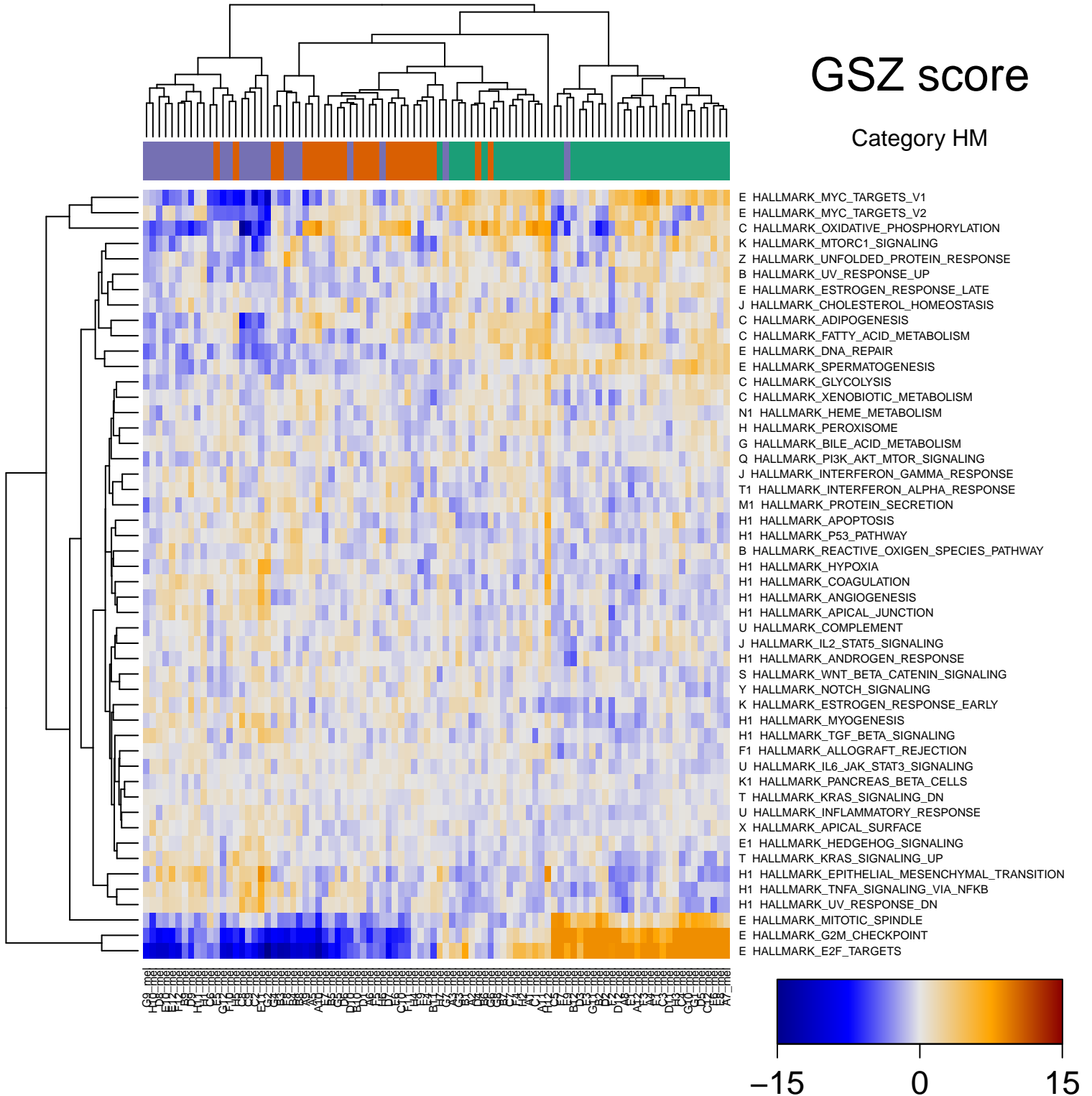
# GSZ score

Category GSEA C2



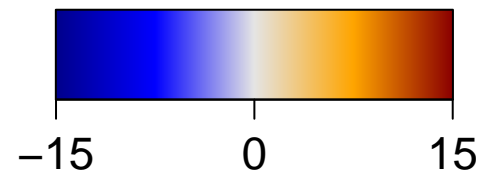
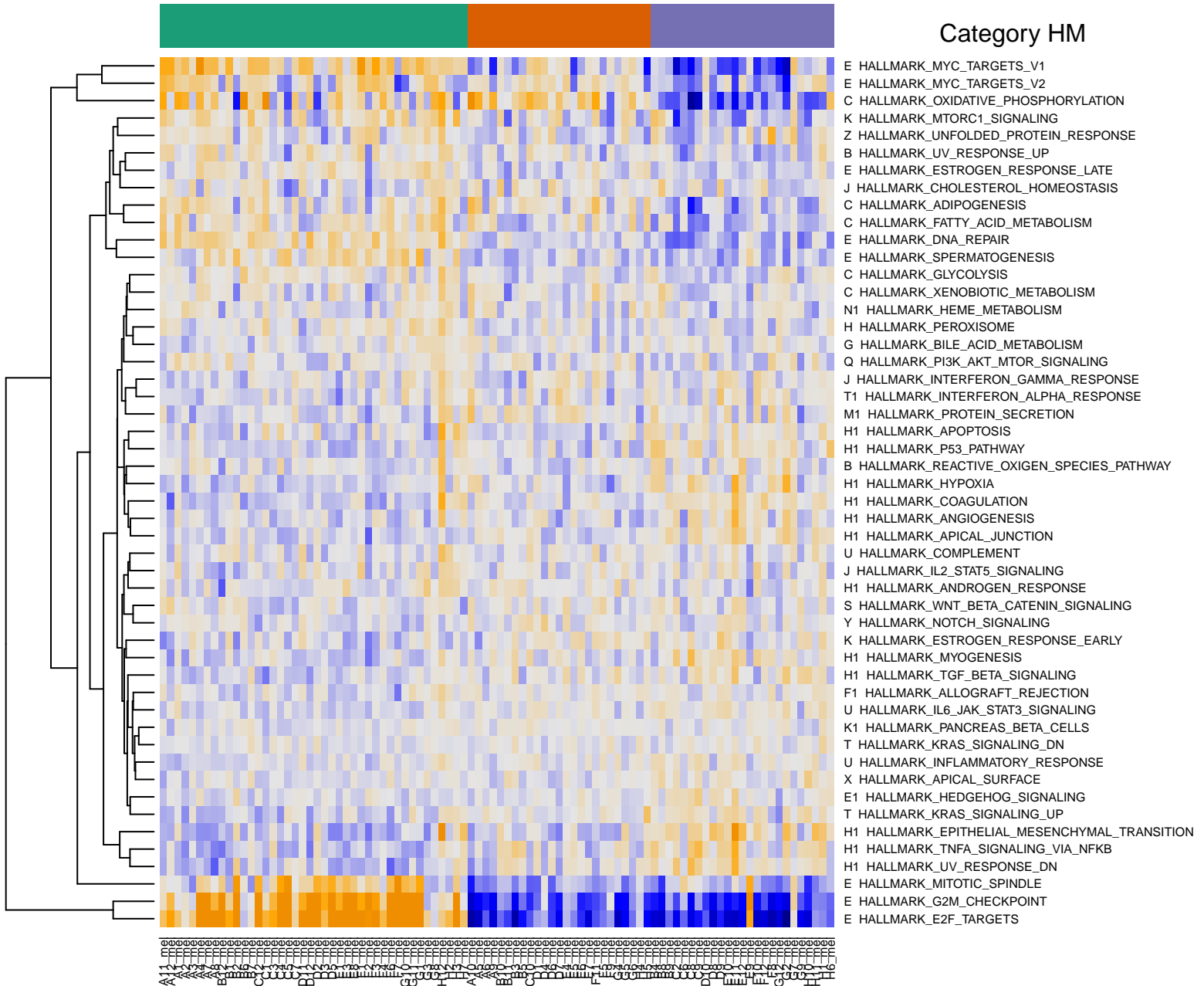
# GSZ score

Category HM



# GSZ score

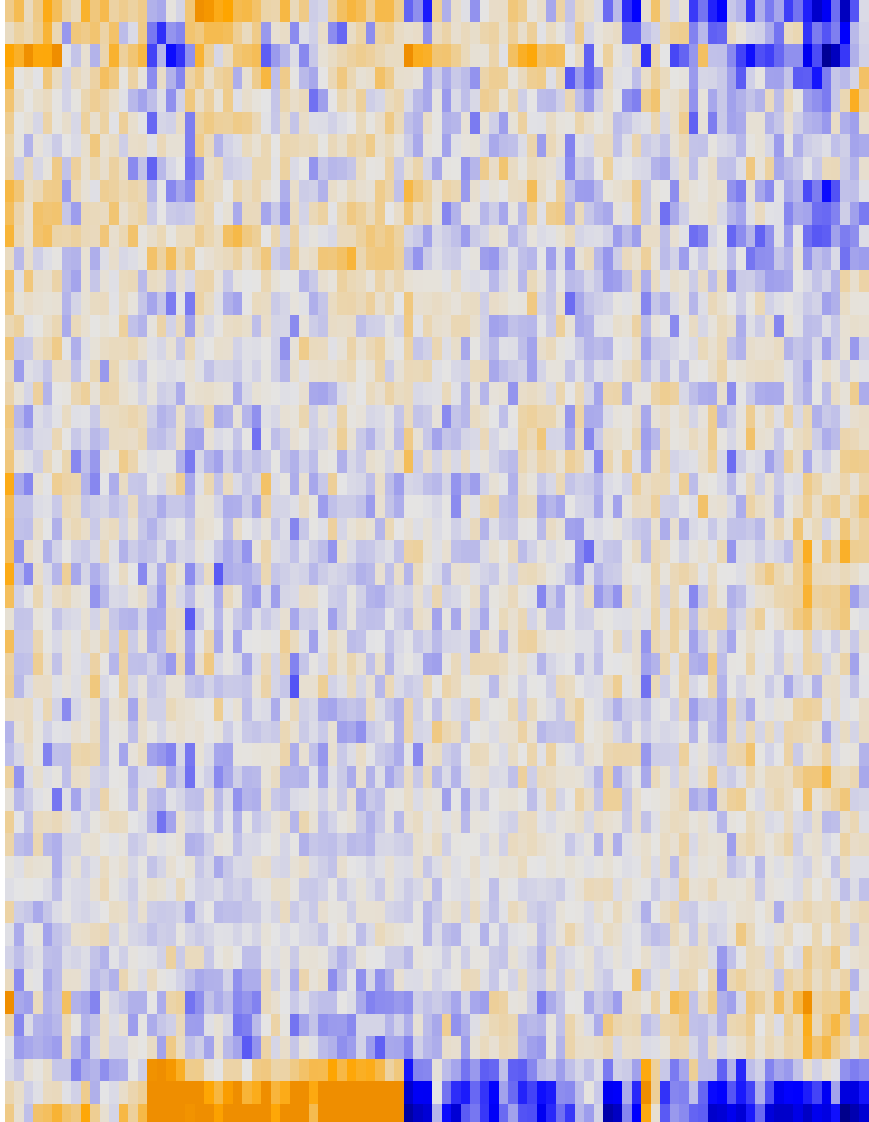
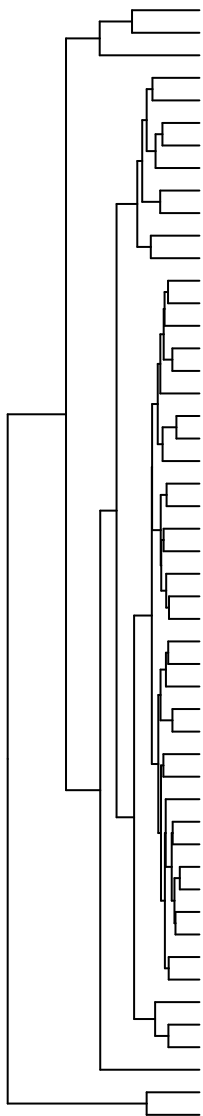
Category HM





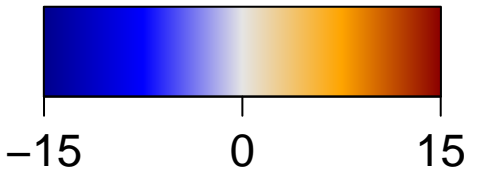
# GSZ score

Category HM



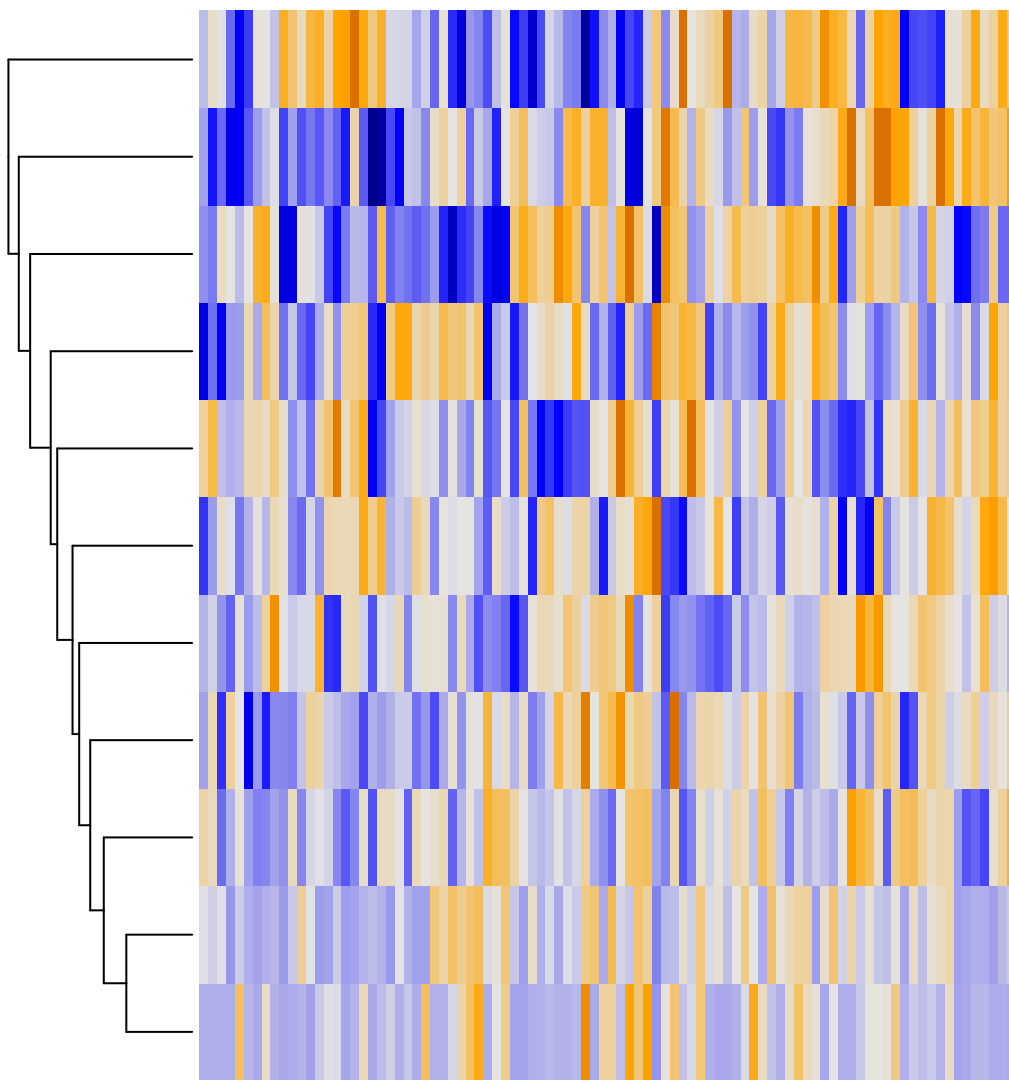
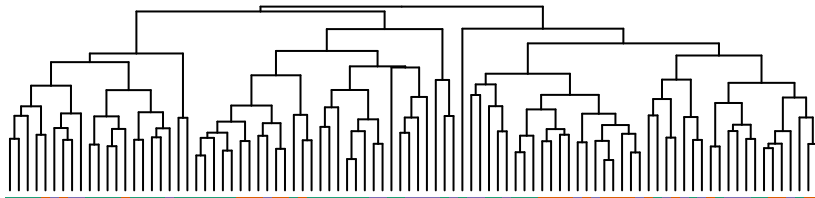
- E HALLMARK\_MYC\_TARGETS\_V1
- E HALLMARK\_MYC\_TARGETS\_V2
- C HALLMARK\_OXIDATIVE\_PHOSPHORYLATION
- K HALLMARK\_MTORC1\_SIGNALING
- Z HALLMARK\_UNFOLDED\_PROTEIN\_RESPONSE
- B HALLMARK\_UV\_RESPONSE\_UP
- E HALLMARK\_ESTROGEN\_RESPONSE\_LATE
- J HALLMARK\_CHOLESTEROL\_HOMEOSTASIS
- C HALLMARK\_ADIPOGENESIS
- C HALLMARK\_FATTY\_ACID\_METABOLISM
- E HALLMARK\_DNA\_REPAIR
- E HALLMARK\_SPERMATOGENESIS
- C HALLMARK\_GLYCOLYSIS
- C HALLMARK\_XENOBIOTIC\_METABOLISM
- N1 HALLMARK\_HEME\_METABOLISM
- H HALLMARK\_PEROXISOME
- G HALLMARK\_BILE\_ACID\_METABOLISM
- Q HALLMARK\_PI3K\_AKT\_MTOR\_SIGNALING
- J HALLMARK\_INTERFERON\_GAMMA\_RESPONSE
- T1 HALLMARK\_INTERFERON\_ALPHA\_RESPONSE
- M1 HALLMARK\_PROTEIN\_SECRETION
- H1 HALLMARK\_APOPTOSIS
- H1 HALLMARK\_P53\_PATHWAY
- B HALLMARK\_REACTIVE\_OXIGEN\_SPECIES\_PATHWAY
- H1 HALLMARK\_HYPOXIA
- H1 HALLMARK\_COAGULATION
- H1 HALLMARK\_ANGIOGENESIS
- H1 HALLMARK\_APICAL\_JUNCTION
- U HALLMARK\_COMPLEMENT
- J HALLMARK\_IL2\_STAT5\_SIGNALING
- H1 HALLMARK\_ANDROGEN\_RESPONSE
- S HALLMARK\_WNT\_BETA\_CATENIN\_SIGNALING
- Y HALLMARK\_NOTCH\_SIGNALING
- K HALLMARK\_ESTROGEN\_RESPONSE\_EARLY
- H1 HALLMARK\_MYOGENESIS
- H1 HALLMARK\_TGF\_BETA\_SIGNALING
- F1 HALLMARK\_ALLOGRAFT\_REJECTION
- U HALLMARK\_IL6\_JAK\_STAT3\_SIGNALING
- K1 HALLMARK\_PANCREAS\_BETA\_CELLS
- T HALLMARK\_KRAS\_SIGNALING\_DN
- U HALLMARK\_INFLAMMATORY\_RESPONSE
- X HALLMARK\_APICAL\_SURFACE
- E1 HALLMARK\_HEDGEHOG\_SIGNALING
- T HALLMARK\_KRAS\_SIGNALING\_UP
- H1 HALLMARK\_EPITHELIAL\_MESENCHYMAL\_TRANSITION
- H1 HALLMARK\_TNFA\_SIGNALING\_VIA\_NFKB
- H1 HALLMARK\_UV\_RESPONSE\_DN
- E HALLMARK\_MITOTIC\_SPINDLE
- E HALLMARK\_G2M\_CHECKPOINT
- E HALLMARK\_E2F\_TARGETS

Sample IDs: S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S26, S27, S28, S29, S30, S31, S32, S33, S34, S35, S36, S37, S38, S39, S40, S41, S42, S43, S44, S45, S46, S47, S48, S49, S50, S51, S52, S53, S54, S55, S56, S57, S58, S59, S60, S61, S62, S63, S64, S65, S66, S67, S68, S69, S70, S71, S72, S73, S74, S75, S76, S77, S78, S79, S80, S81, S82, S83, S84, S85, S86, S87, S88, S89, S90, S91, S92, S93, S94, S95, S96, S97, S98, S99, S100

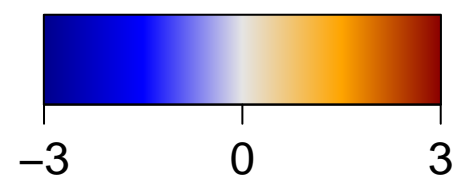


# GSZ score

Category Lifestyle

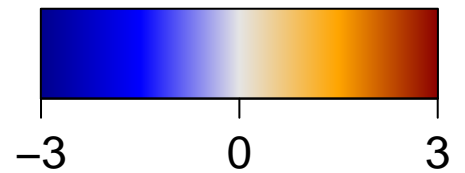
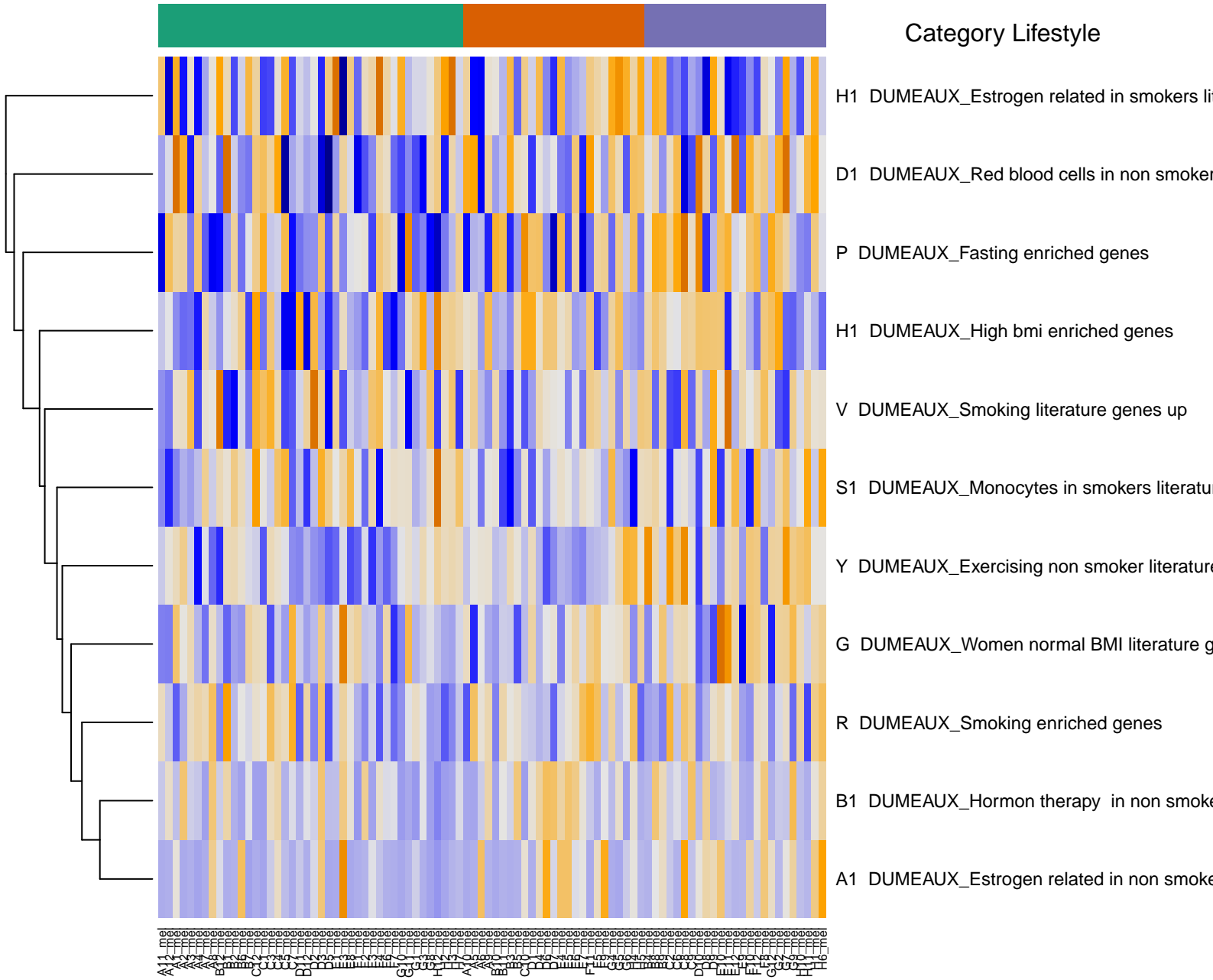


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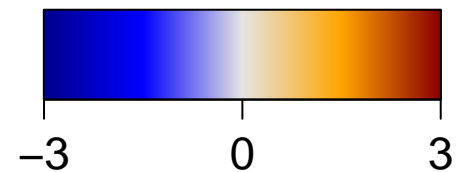
# GSZ score

Category Lifestyle



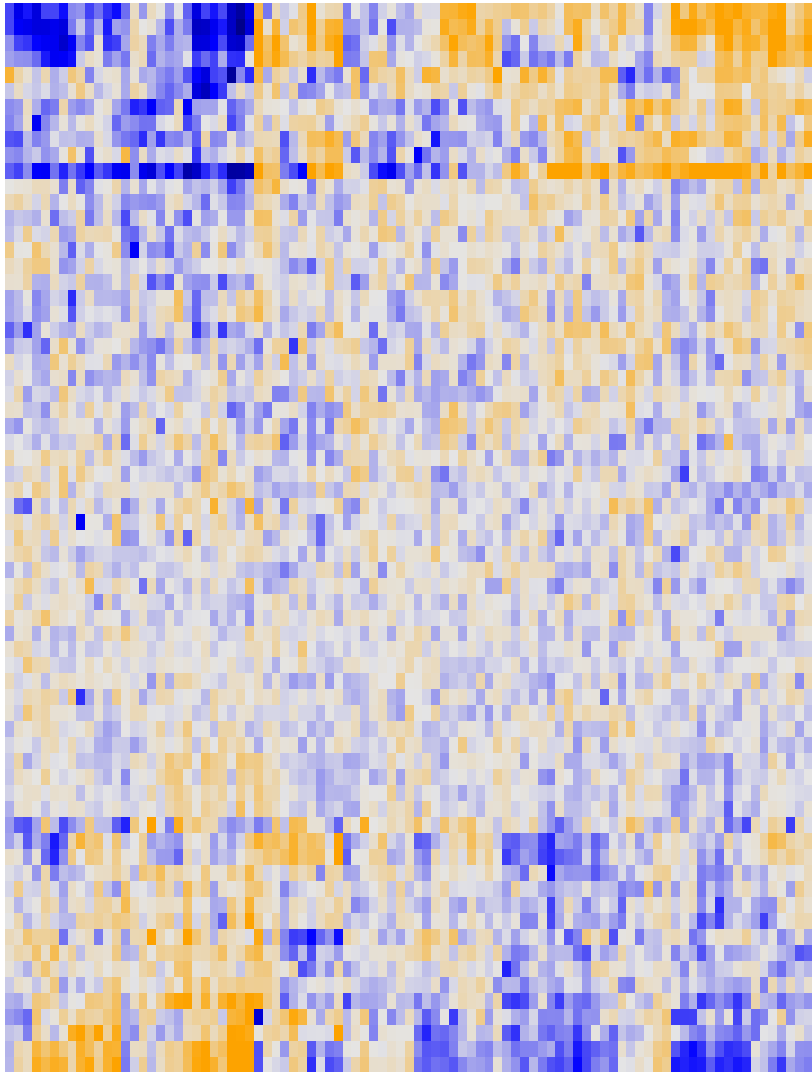
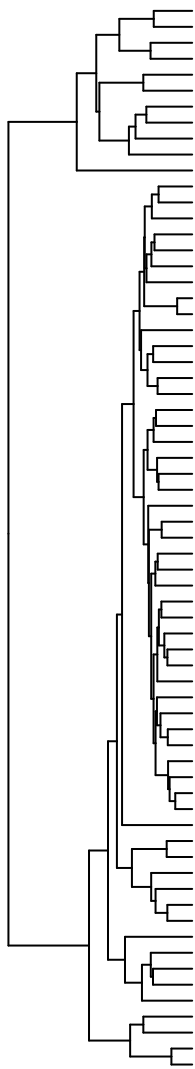
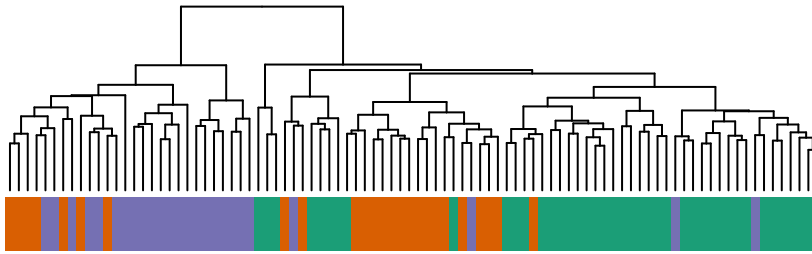
# GSZ score

Category Lifestyle

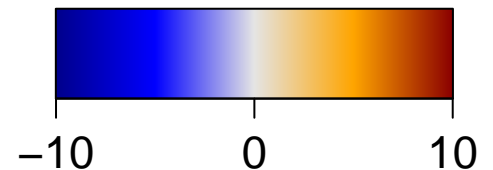
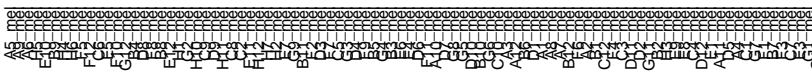


# GSZ score

Category Lymphoma

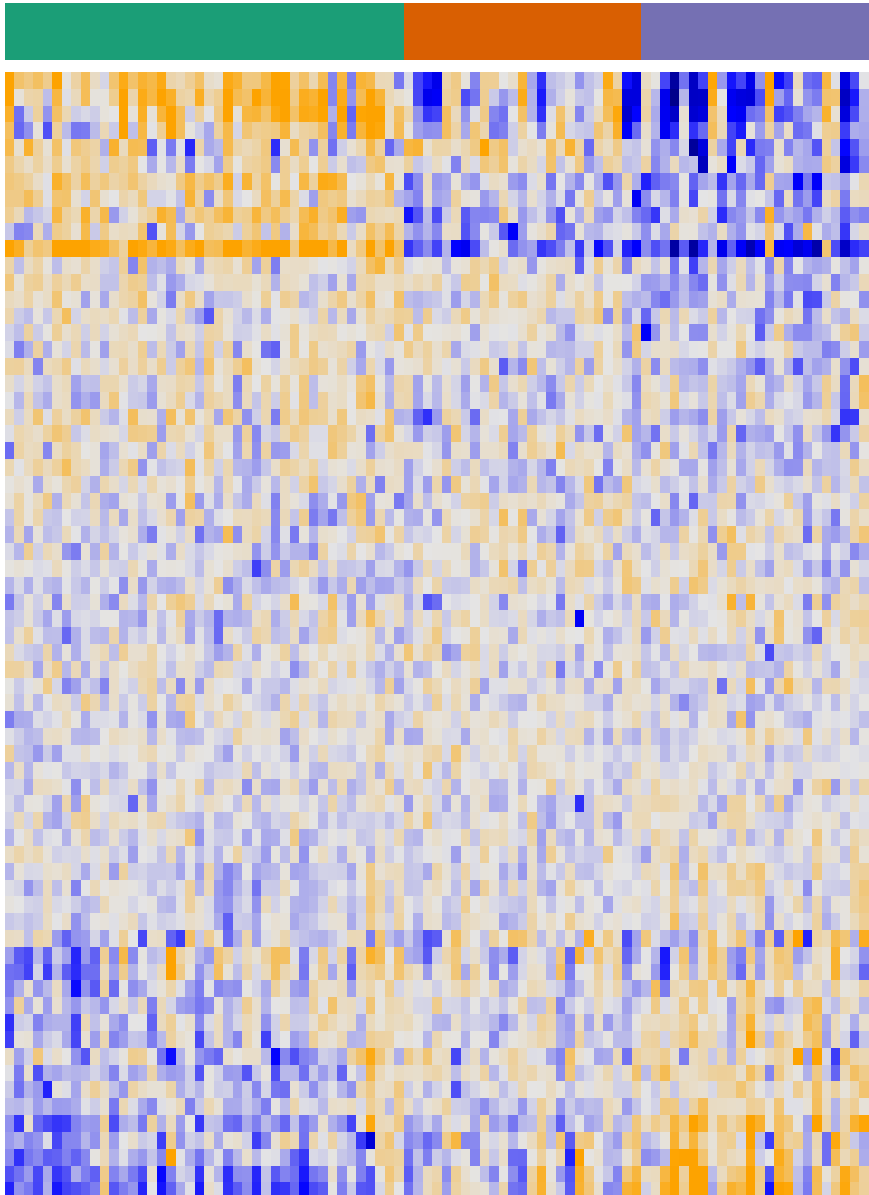


E HOPP\_Txn\_transition  
E HOPP\_Txn\_elongation  
E HOPP\_Active\_promoter  
J HOPP\_Weak\_promoter  
A CARO\_OxPhos\_in\_DLBCL\_UP  
J CARO\_OxPhos\_vs\_BCR\_UP  
E DAVE\_BL-vs-DLBCL  
A DAVE\_c-myc BL UP  
E ROSOLOWSKI\_blue total  
E SPANG\_BCR UP  
E TARTE\_Plasma blast signature  
H ROSOLOWSKI\_red total  
A ROSOLOWSKI\_red UP  
K Aukema\_BCL2 DN\_BCL6 UP  
N1 DAVE\_immune response 2  
L DAVE\_NFkB BL DN  
G TARTE\_B-cell signature  
J MASCQUE\_GCB UP  
H1 ROSOLOWSKI\_green UP  
H1 ROSOLOWSKI\_green total  
E HOPP\_Strong\_enhancer  
E MASCQUE\_mBL UP  
B BENTINK\_mBL UP  
P YAMANE\_AICDA\_targets\_recruited  
H DAVE\_BL Inter  
J1 SPANG\_CD40 6hrs DN  
J1 SPANG\_BAFF 9hrs DN  
G1 SPANG\_LPS 6hrs DN  
B1 WRIGHT\_custom ABC-DLBCL UP  
M ZHANG\_DLBCL mutated  
Y DAVE\_MHCCII BL DN  
S1 SPANG\_IL21 DN  
J1 BENTINK\_mBL DOWN  
K MASCQUE\_mBL DOWN  
U Subero\_MCL\_hyper\_meth  
S1 Subero\_MCL\_hypo\_meth  
L1 DAVE\_BL DN  
L1 WRIGHT\_GCB UP  
V MASCQUE\_ABC UP  
R1 Shaknovich\_ABC\_hyper\_meth  
U DAVE\_BL UP  
L Subero\_MM\_hypo\_meth  
E1 DAVE\_immune response 1  
F1 ROSOLOWSKI\_blue DOWN  
X Aukema\_BCL2 UP\_BCL6 DN  
B Subero\_T-PLL\_hypo\_meth  
B Subero\_B-ALL\_hypo\_meth  
H1 Subero\_MM\_hyper\_meth  
U Subero\_T-ALL\_hyper\_meth  
H1 Subero\_mBL\_hyper\_meth  
H1 Subero\_FL\_hyper\_meth  
L SPANG\_BCR DN  
H1 HOPP\_Weak\_enhancer  
H1 HOPP\_Weak\_txn  
H1 SPANG\_IL21 UP  
H1 SPANG\_BAFF 9hrs UP  
H1 SPANG\_LPS 6hrs UP  
H1 SPANG\_CD40 6hrs UP  
H TARTE\_Plasma cell signature  
H1 TARTE\_Mature plasma cell signature  
E1 Subero\_T-ALL\_hypo\_meth  
H1 LENZ\_Stromal signature 2  
H1 LENZ\_Stromal signature 1  
N HOPP\_Repetitive  
H1 HOPP\_Heterochrom  
H1 HOPP\_Poised\_promoter  
H1 HOPP\_Repressed

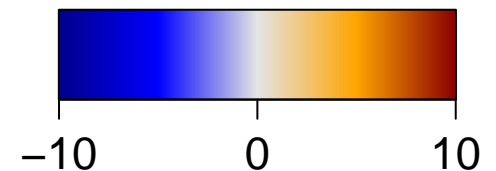


# GSZ score

Category Lymphoma

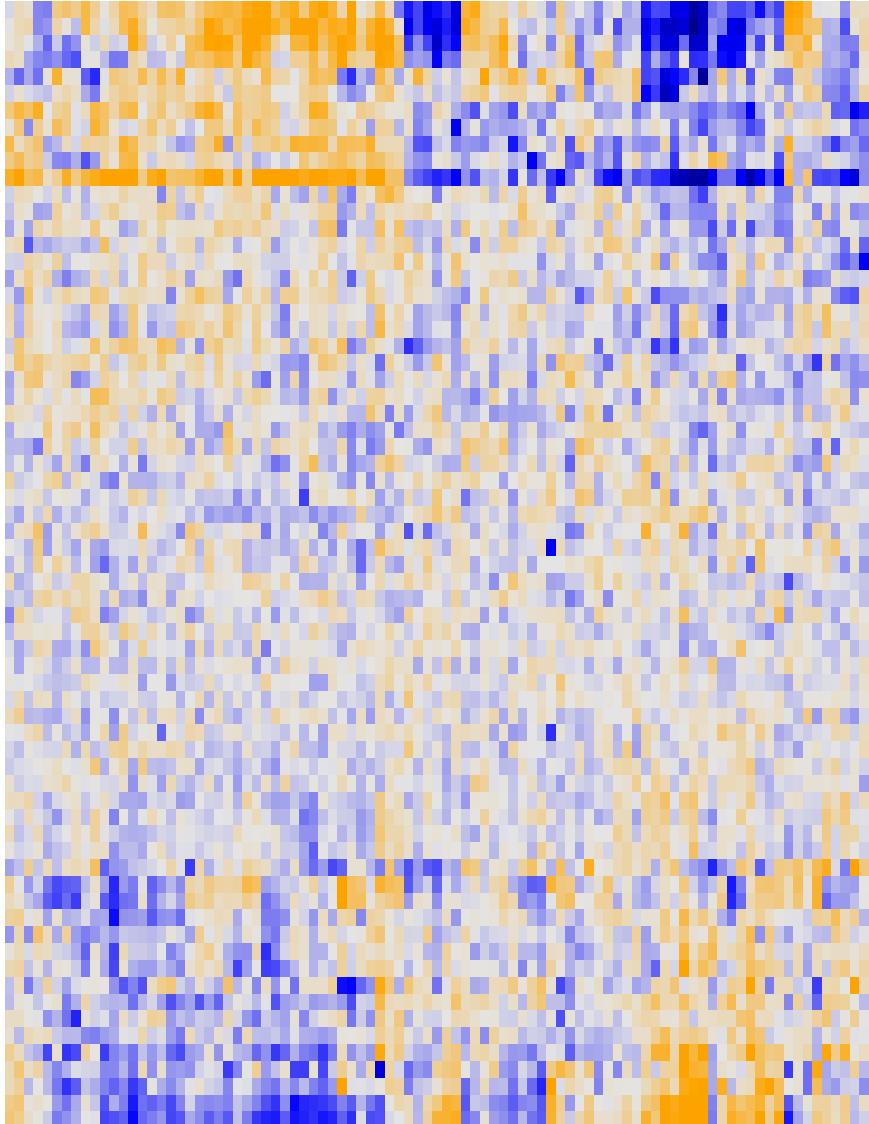
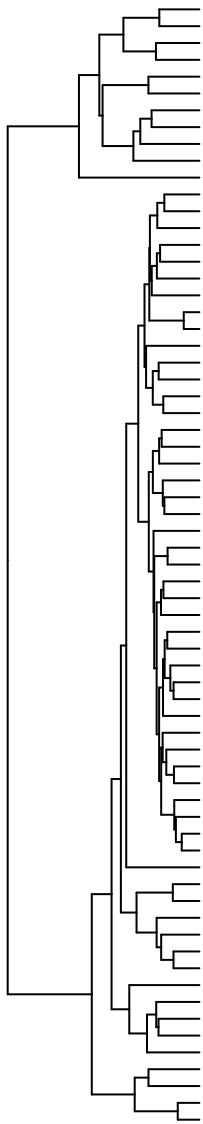


E HOPP\_Txn\_transition  
E HOPP\_Txn\_elongation  
E HOPP\_Active\_promoter  
J HOPP\_Weak\_promoter  
A CARO\_OxPhos\_in\_DLBCL\_UP  
J CARO\_OxPhos\_vs\_BCR\_UP  
E DAVE\_BL-vs-DLBCL  
A DAVE\_c-myc BL UP  
E ROSOLOWSKI\_blue total  
E SPANG\_BCR UP  
E TARTE\_Plasmablast signature  
H ROSOLOWSKI\_red total  
A ROSOLOWSKI\_red UP  
K Aukema\_BCL2 DN\_BCL6 UP  
N1 DAVE\_Immune response 2  
L DAVE\_NFkB BL DN  
G TARTE\_B-cell signature  
J MASCQUE\_GCB UP  
H1 ROSOLOWSKI\_green UP  
H1 ROSOLOWSKI\_green total  
E HOPP\_Strong\_enhancer  
E MASCQUE\_mBL UP  
B BENTINK\_mBL UP  
P YAMANE\_AICDA\_targets\_recruited  
H DAVE\_BL Inter  
J1 SPANG\_CD40 6hrs DN  
J1 SPANG\_BAFF 9hrs DN  
G1 SPANG\_LPS 6hrs DN  
B1 WRIGHT\_custom ABC-DLBCL UP  
M ZHANG\_DLBCL mutated  
Y DAVE\_MHCCII BL DN  
S1 SPANG\_IL21 DN  
J1 BENTINK\_mBL DOWN  
K MASCQUE\_mBL DOWN  
U Subero\_MCL\_hyper\_meth  
S1 Subero\_MCL\_hypo\_meth  
L1 DAVE\_BL DN  
L1 WRIGHT\_GCB UP  
V MASCQUE\_ABC UP  
R1 Shaknovich\_ABC\_hyper\_meth  
U DAVE\_BL UP  
L Subero\_MM\_hypo\_meth  
E1 DAVE\_Immune response 1  
F1 ROSOLOWSKI\_blue DOWN  
X Aukema\_BCL2 UP\_BCL6 DN  
B Subero\_T-PLL\_hypo\_meth  
B Subero\_B-ALL\_hypo\_meth  
H1 Subero\_MM\_hyper\_meth  
U Subero\_T-ALL\_hyper\_meth  
H1 Subero\_mBL\_hyper\_meth  
H1 Subero\_FL\_hyper\_meth  
L SPANG\_BCR DN  
H1 HOPP\_Weak\_enhancer  
H1 HOPP\_Weak\_txn  
H1 SPANG\_IL21 UP  
H1 SPANG\_BAFF 9hrs UP  
H1 SPANG\_LPS 6hrs UP  
H1 SPANG\_CD40 6hrs UP  
H TARTE\_Plasma cell signature  
H1 TARTE\_Mature plasma cell signature  
E1 Subero\_T-ALL\_hypo\_meth  
H1 LENZ\_Stromal signature 2  
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N HOPP\_Repetitive  
H1 HOPP\_Heterochrom  
H1 HOPP\_Poised\_promoter  
H1 HOPP\_Repressed

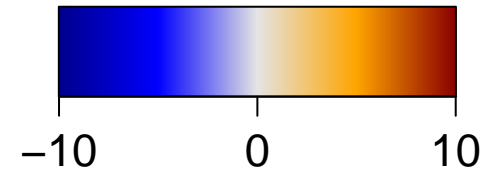
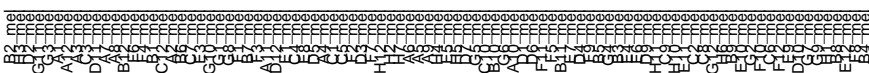


# GSZ score

Category Lymphoma

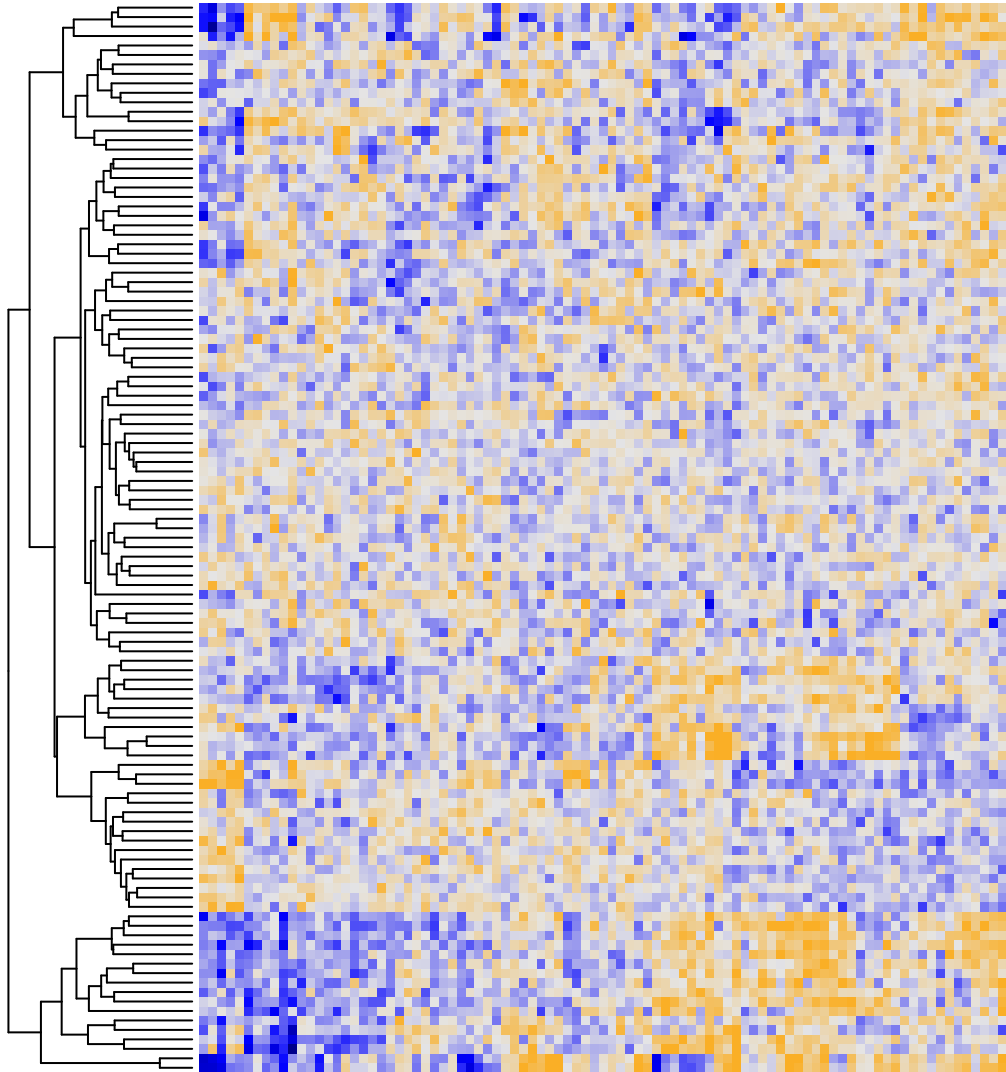
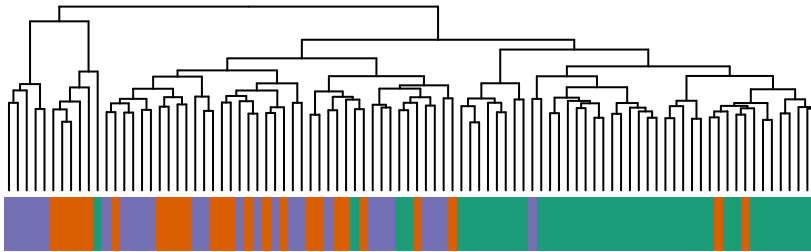


- E HOPP\_Txn\_transition
- E HOPP\_Txn\_elongation
- E HOPP\_Active\_promoter
- J HOPP\_Weak\_promoter
- A CARO\_OxPhos\_in\_DLBCL\_UP
- J CARO\_OxPhos\_vs\_BCR\_UP
- E DAVE\_BL-vs-DLBCL
- A DAVE\_c-myc BL UP
- E ROSOLOWSKI\_blue total
- E SPANG\_BCR UP
- E TARTE\_Plasmablast signature
- H ROSOLOWSKI\_red total
- A ROSOLOWSKI\_red UP
- K Aukema\_BCL2 DN\_BCL6 UP
- N1 DAVE\_Immune response 2
- L DAVE\_NFkB BL DN
- G TARTE\_B-cell signature
- J MASCQUE\_GCB UP
- H1 ROSOLOWSKI\_green UP
- H1 ROSOLOWSKI\_green total
- E HOPP\_Strong\_enhancer
- E MASCQUE\_mBL UP
- B BENTINK\_mBL UP
- P YAMANE\_AICDA\_targets\_recruited
- H DAVE\_BL Inter
- J1 SPANG\_CD40 6hrs DN
- J1 SPANG\_BAFF 9hrs DN
- G1 SPANG\_LPS 6hrs DN
- B1 WRIGHT\_custom ABC-DLBCL UP
- M ZHANG\_DLBCL mutated
- Y DAVE\_MHCCII BL DN
- S1 SPANG\_IL21 DN
- J1 BENTINK\_mBL DOWN
- K MASCQUE\_mBL DOWN
- U Subero\_MCL\_hyper\_meth
- S1 Subero\_MCL\_hypo\_meth
- L1 DAVE\_BL DN
- L1 WRIGHT\_GCB UP
- V MASCQUE\_ABC UP
- R1 Shaknovich\_ABC\_hyper\_meth
- U DAVE\_BL UP
- L Subero\_MM\_hypo\_meth
- E1 DAVE\_Immune response 1
- F1 ROSOLOWSKI\_blue DOWN
- X Aukema\_BCL2 UP\_BCL6 DN
- B Subero\_T-PLL\_hypo\_meth
- B Subero\_B-ALL\_hypo\_meth
- H1 Subero\_MM\_hyper\_meth
- U Subero\_T-ALL\_hyper\_meth
- H1 Subero\_mBL\_hyper\_meth
- H1 Subero\_FL\_hyper\_meth
- L SPANG\_BCR DN
- H1 HOPP\_Weak\_enhancer
- H1 HOPP\_Weak\_txn
- H1 SPANG\_IL21 UP
- H1 SPANG\_BAFF 9hrs UP
- H1 SPANG\_LPS 6hrs UP
- H1 SPANG\_CD40 6hrs UP
- H TARTE\_Plasma cell signature
- H1 TARTE\_Mature plasma cell signature
- E1 Subero\_T-ALL\_hypo\_meth
- H1 LENZ\_Stromal signature 2
- H1 LENZ\_Stromal signature 1
- N HOPP\_Repetitive
- H1 HOPP\_Heterochrom
- H1 HOPP\_Poised\_promoter
- H1 HOPP\_Repressed

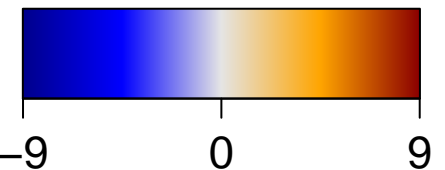
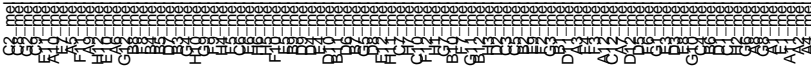


# GSZ score

Category MF



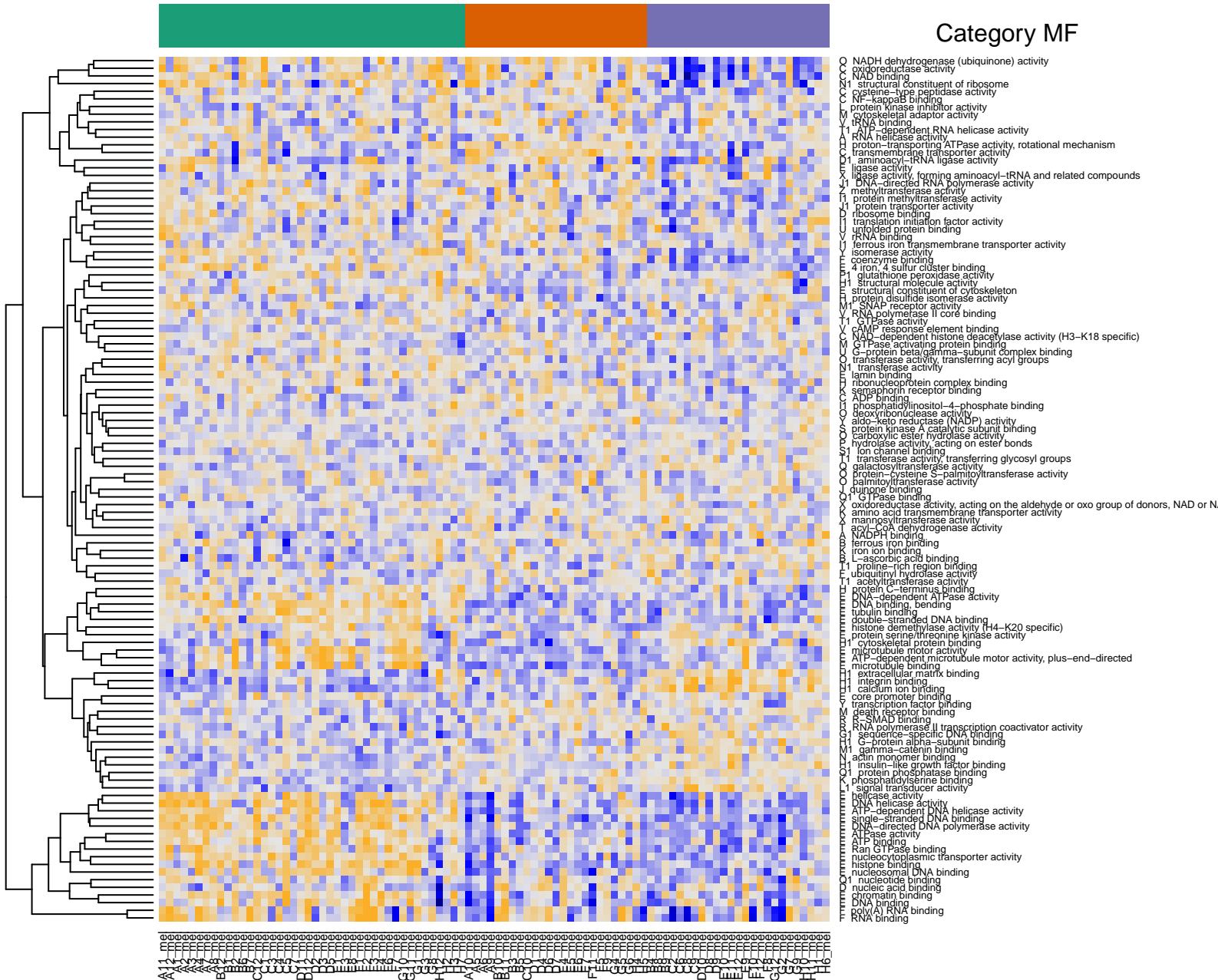
- NADH dehydrogenase (ubiquinone) activity
- oxidoreductase activity
- NAD binding
- structural constituent of ribosome
- cysteine-type peptidase activity
- NF-kappaB binding
- protein kinase inhibitor activity
- cytoskeletal adaptor activity
- RNA binding
- ATP-dependent RNA helicase activity
- RNA helicase activity
- proton-transporting ATPase activity, rotational mechanism
- transmembrane transporter activity
- anion-cation antiporter activity
- ligase activity
- protein-lysine forming aminoacyl-tRNA and related compounds
- DNA-directed RNA polymerase activity
- methyltransferase activity
- protein methyltransferase activity
- protein transporter activity
- ribosome binding
- translation initiation factor activity
- unfolded protein binding
- RNA binding
- ferrous iron transmembrane transporter activity
- isomerase activity
- coenzyme binding
- 4 iron 4 sulfur cluster binding
- glutathione peroxidase activity
- structural molecule activity
- protein disulfide isomerase activity
- ATP receptor activity
- RNA polymerase II core binding
- GTPase activity
- GTPase element binding
- NAD-dependent histone deacetylase activity (H3-K18 specific)
- G-Protein activating protein binding
- G-protein beta-gamma-subunit complex binding
- transferase activity, transferring acyl groups
- transferase activity
- lamin binding
- nucleosome-protein complex binding
- semaphorin receptor binding
- ADP binding
- phosphatidylinositol-4-phosphate binding
- deoxyribonuclease activity
- aldo-keto reductase (NADP) activity
- protein kinase A catalytic subunit binding
- carboxylic ester hydrolase activity
- hydrolyase activity, acting on ester bonds
- ion channel binding
- transferase activity, transferring glycosyl groups
- galactosyltransferase activity
- protein-cysteine S-palmitoyltransferase activity
- palmitoyltransferase activity
- diurone binding
- G-Protein binding
- oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP
- amino acid transmembrane transporter activity
- transaminase activity
- acyl-CoA dehydrogenase activity
- NADH binding
- ferrous iron binding
- iron ion binding
- ascorbic acid binding
- proline-rich region binding
- ubiquitinyl hydrolase activity
- acetyltransferase activity
- protein C-terminus binding
- DNA-dependent ATPase activity
- DNA binding, bending
- tubulin binding
- double-stranded DNA binding
- histone demethylase activity (H4-K20 specific)
- protein serine threonine kinase activity
- cytoskeletal protein binding
- microtubule motor activity
- ATP-dependent microtubule motor activity, plus-end-directed
- microtubule binding
- extracellular matrix binding
- integrin binding
- calcium ion binding
- core promoter binding
- transcription factor binding
- acidic amino acid binding
- SMAD binding
- RNA polymerase II transcription coactivator activity
- sequence-specific DNA binding
- G-protein alpha-subunit binding
- gamma-catenin binding
- actin monomer binding
- insulin-like growth factor binding
- protein phosphatase binding
- phosphatidylserine binding
- signal transducer activity
- helicase activity
- DNA helicase activity
- ATP-dependent DNA helicase activity
- single-stranded DNA binding
- single-directed DNA polymerase activity
- ATPase activity
- ATP binding
- Ran GTPase binding
- nucleocytoplasmic transporter activity
- histone binding
- nucleosomal DNA binding
- nucleotide binding
- nucleic acid binding
- chromatin binding
- DNA binding
- poly(A) RNA binding
- RNA binding



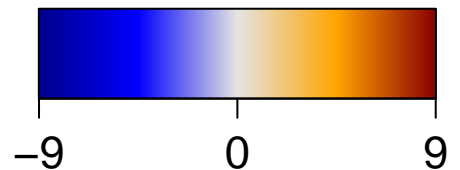


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Category MF

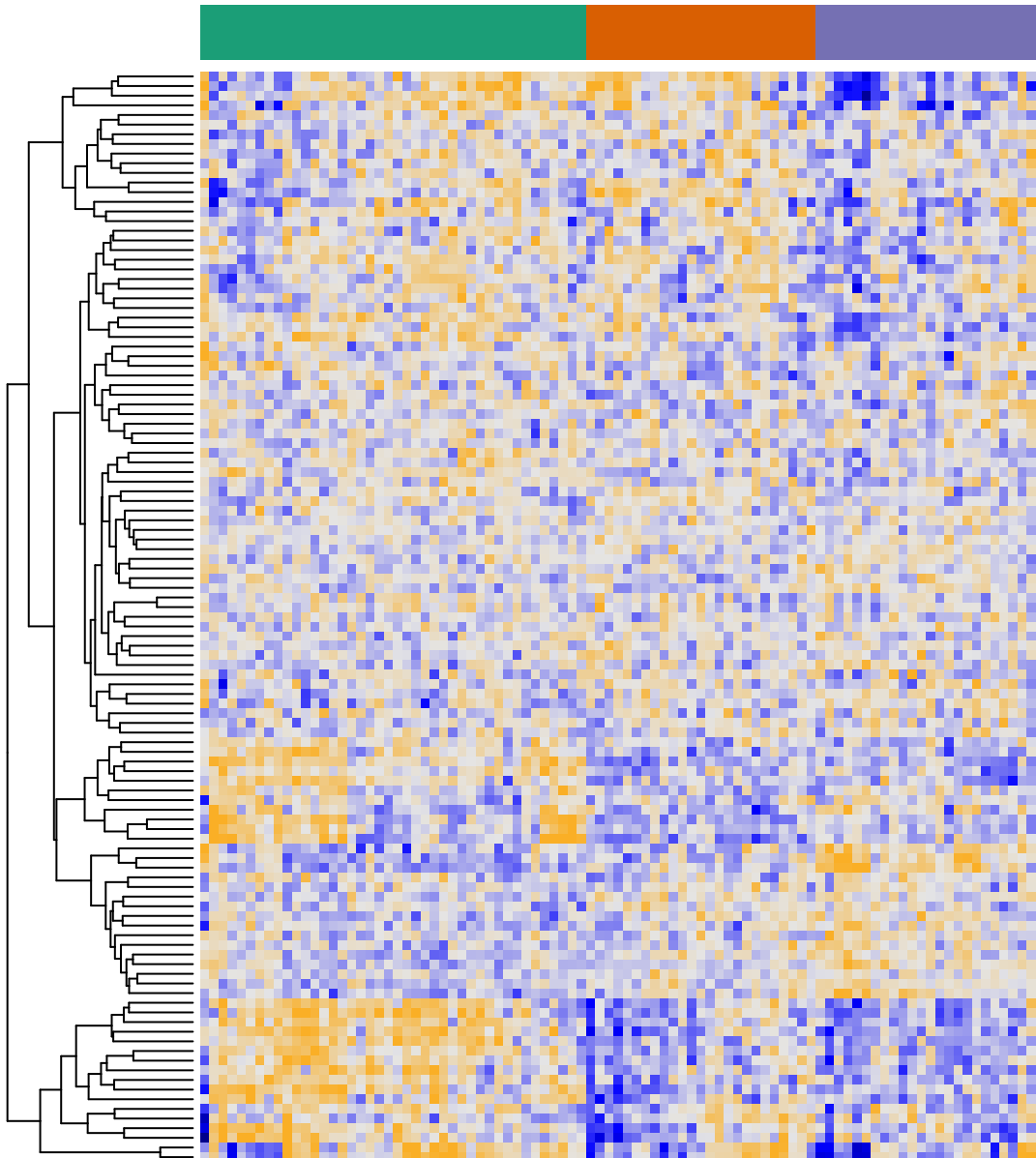


NADH dehydrogenase (ubiquinone) activity  
oxidoreductase activity  
NAD binding  
structural constituent of ribosome  
cysteine-type peptidase activity  
cysteine binding  
protein kinase inhibitor activity  
cytoskeletal adaptor activity  
tRNA binding  
RNA-dependent RNA helicase activity  
RNA helicase activity  
proton-transporting ATPase activity, rotational mechanism  
transmembrane transporter activity  
aminoacyl-tRNA ligase activity  
ligase activity  
base activity forming aminoacyl-tRNA and related compounds  
DNA-directed RNA polymerase activity  
methyltransferase activity  
protein methyltransferase activity  
protein transporter activity  
ribosome binding  
translation initiation factor activity  
unfolded protein binding  
tRNA binding  
ferrrous iron transmembrane transporter activity  
isomerase activity  
coenzyme binding  
4 iron-4 sulfur cluster binding  
glutathione peroxidase activity  
structural molecule activity  
structural constituent of cytoskeleton  
protein disulfide isomerase activity  
GAP receptor activity  
RNA polymerase II core binding  
GTPase activity  
cAMP response element binding  
NAD-dependent histone deacetylase activity (H3-K18 specific)  
G-Phase activating protein binding  
G-protein beta/gamma-subunit complex binding  
transferase activity, transferring acyl groups  
transferase activity  
lamin binding  
ribonucleoprotein complex binding  
semaphorin receptor binding  
ADP binding  
phosphatidylinositol-4-phosphate binding  
deoxyribonuclease activity  
aldo-keto reductase (NADP) activity  
protein kinase A catalytic subunit binding  
carboxylic ester hydrolase activity  
hydrolase activity, acting on ester bonds  
ion channel binding  
transferase activity, transferring glycosyl groups  
galactosyltransferase activity  
protein-cysteine S-palmitoyltransferase activity  
palmitoyltransferase activity  
guanine binding  
GTPase binding  
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP  
amino acid transmembrane transporter activity  
mannosyltransferase activity  
acyl-CoA dehydrogenase activity  
NADPH binding  
ferrrous iron binding  
iron ion binding  
L-ascorbic acid binding  
proline-rich region binding  
ubiquitinyl hydrolase activity  
acetyltransferase activity  
protein C-terminus binding  
DNA-dependent ATPase activity  
DNA binding, bending  
tubulin binding  
double-stranded DNA binding  
histone demethylase activity (H4-K20 specific)  
protein serine/threonine kinase activity  
cytoskeletal protein binding  
microtubule motor activity  
ATP-dependent microtubule motor activity, plus-end-directed  
microtubule binding  
extracellular matrix binding  
integrin binding  
calcium ion binding  
core promoter binding  
transcription factor binding  
death receptor binding  
p53/MAD binding  
RNA polymerase II transcription coactivator activity  
scutellin-specific DNA binding  
G-protein alpha-subunit binding  
gamma-catenin binding  
actin monomer binding  
insulin-like growth factor binding  
protein phosphatase binding  
phosphatidylserine binding  
signal transducer activity  
helicase activity  
DNA helicase activity  
ATP-dependent DNA helicase activity  
single-stranded DNA binding  
DNA-directed DNA polymerase activity  
ATPase activity  
ATP binding  
Ran GTPase binding  
nucleocytoplasmic transporter activity  
histone binding  
nucleosomal DNA binding  
nucleotide binding  
nucleic acid binding  
nucleic acid binding  
DNA binding  
poly(A) RNA binding  
RNA binding

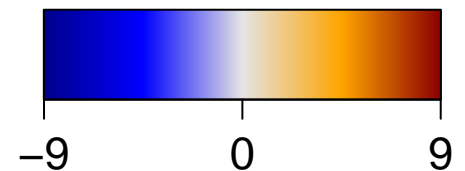


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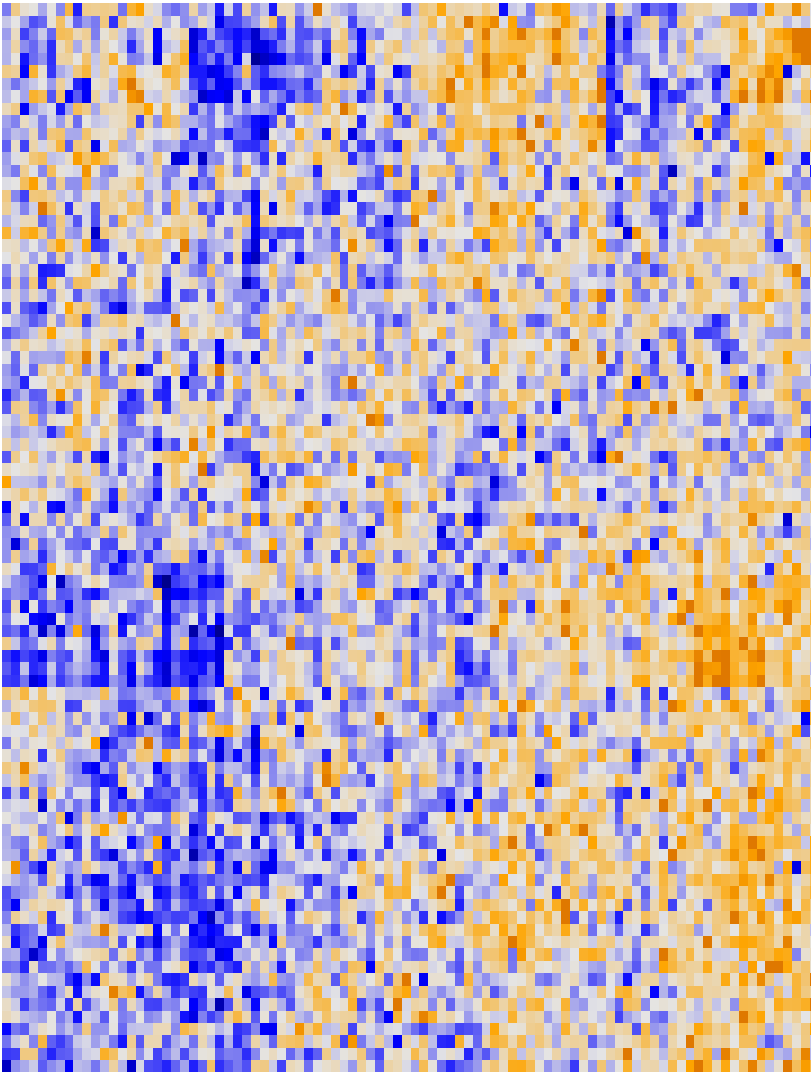
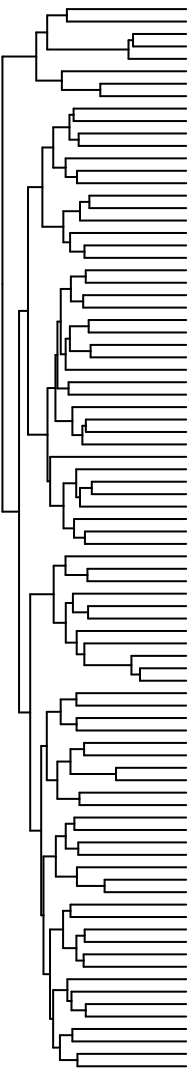
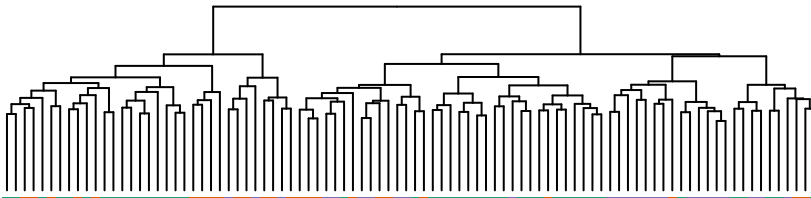


NADH dehydrogenase (ubiquinone) activity  
oxidoreductase activity  
NAD binding  
structural constituent of ribosome  
cysteine-type peptidase activity  
catalytic binding  
protein kinase inhibitor activity  
cytoskeletal adaptor activity  
tRNA binding  
RNA binding  
DNA-dependent RNA helicase activity  
RNA helicase activity  
proton-transporting ATPase activity, rotational mechanism  
transmembrane transporter activity  
aminoacyl-tRNA ligase activity  
ligase activity  
base activity forming aminoacyl-tRNA and related compounds  
DNA-directed RNA polymerase activity  
methyltransferase activity  
protein methyltransferase activity  
protein transporter activity  
ribosome binding  
translation initiation factor activity  
unfolded protein binding  
RNA binding  
ferrous iron transmembrane transporter activity  
isomerase activity  
coenzyme binding  
4 iron-4 sulfur cluster binding  
glutathione peroxidase activity  
structural molecule activity  
structural constituent of cytoskeleton  
protein disulfide isomerase activity  
cAMP response element binding  
RNA polymerase II core binding  
GTPase activity  
NAD-dependent histone deacetylase activity (H3-K18 specific)  
GTPase activating protein binding  
G-protein beta/gamma-subunit complex binding  
transferase activity, transferring acyl groups  
transferase activity  
lamin binding  
ribonucleoprotein complex binding  
semaphorin receptor binding  
ADP binding  
phosphatidylinositol-4-phosphate binding  
deoxyribonuclease activity  
aldo-keto reductase (NADP) activity  
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hydrolase activity, acting on ester bonds  
ion channel binding  
transferase activity, transferring glycosyl groups  
galactosyltransferase activity  
protein-cysteine S-palmitoyltransferase activity  
palmitoyltransferase activity  
guanine binding  
GTPase binding  
oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP  
amino acid transmembrane transporter activity  
mannosyltransferase activity  
acyl-CoA dehydrogenase activity  
NADPH binding  
ferrous iron binding  
iron ion binding  
L-ascorbic acid binding  
proline-rich region binding  
ubiquitinyl hydrolase activity  
acetyltransferase activity  
protein C-terminus binding  
DNA-dependent ATPase activity  
DNA binding, bending  
tubulin binding  
double-stranded DNA binding  
histone demethylase activity (H4-K20 specific)  
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cytoskeletal protein binding  
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ATP-dependent microtubule motor activity, plus-end-directed  
microtubule binding  
extracellular matrix binding  
integrin binding  
calcium ion binding  
core promoter binding  
transcription factor binding  
receptor binding  
cAMP binding  
RNA polymerase II transcription coactivator activity  
sequence-specific DNA binding  
G-protein alpha-subunit binding  
gamma-catenin binding  
actin monomer binding  
insulin-like growth factor binding  
protein phosphatase binding  
phosphatidylserine binding  
signal transducer activity  
helicase activity  
DNA helicase activity  
ATP-dependent DNA helicase activity  
single-stranded DNA binding  
DNA-directed DNA polymerase activity  
ATPase activity  
ATP binding  
Ran GTPase binding  
nucleocytoplasmic transporter activity  
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DNA binding  
poly(A) RNA binding  
RNA binding

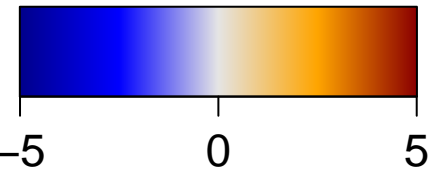


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Category miRNA target

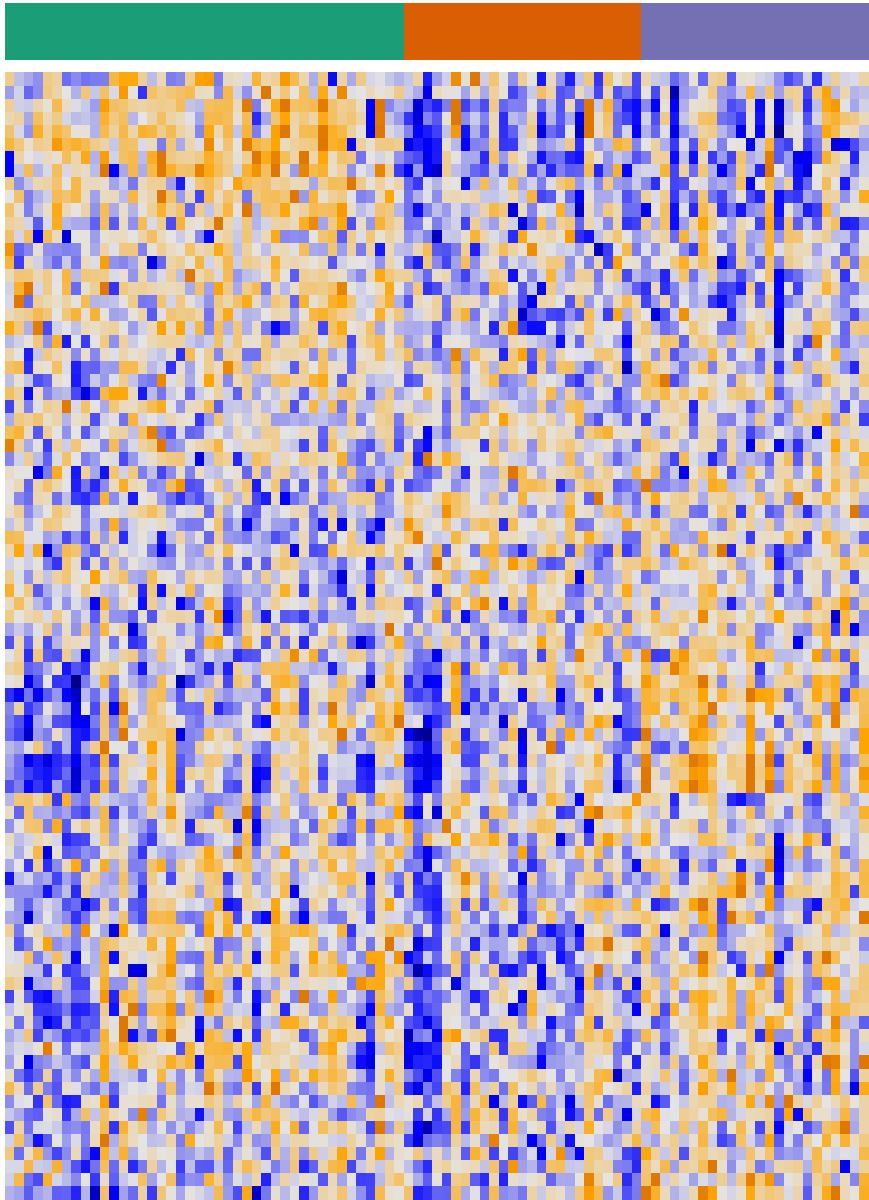


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- h1 hsa-miR-526b
- h1 hsa-miR-548i
- h1 hsa-miR-548h
- h1 hsa-miR-548d-5p
- h1 hsa-miR-708
- h1 hsa-miR-28-5p
- h1 hsa-miR-518f
- h1 hsa-miR-520a-5p
- h1 hsa-miR-323b-3p
- h1 hsa-miR-223
- h1 hsa-miR-1298
- h1 hsa-miR-457
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- h1 hsa-miR-127-5p
- h1 hsa-miR-191
- h1 hsa-miR-337-5p
- h1 hsa-miR-575
- h1 hsa-miR-592
- h1 hsa-miR-892a
- h1 hsa-miR-1178
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- h1 hsa-miR-937
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- h1 hsa-miR-508-5p
- h1 hsa-miR-940
- h1 hsa-miR-326
- h1 hsa-miR-299-5p
- h1 hsa-miR-596
- h1 hsa-miR-602
- h1 hsa-miR-191
- h1 hsa-miR-875-5p
- h1 hsa-miR-99b
- h1 hsa-miR-297
- h1 hsa-miR-576-3p
- h1 hsa-miR-429
- h1 hsa-miR-944
- h1 hsa-miR-548k
- h1 hsa-miR-18b
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- h1 hsa-miR-519d
- h1 hsa-miR-17
- h1 hsa-miR-342-5p
- h1 hsa-miR-9
- h1 hsa-miR-639
- h1 hsa-miR-22
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- h1 hsa-miR-492
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- h1 hsa-miR-199b-5p
- h1 hsa-miR-190b
- h1 hsa-miR-651
- h1 hsa-miR-626
- h1 hsa-miR-183
- h1 hsa-miR-206
- h1 hsa-miR-636
- h1 hsa-miR-373
- h1 hsa-miR-302c
- h1 hsa-miR-380
- h1 hsa-miR-656
- h1 hsa-miR-548d-3p
- h1 hsa-miR-548g
- h1 hsa-miR-493
- h1 hsa-miR-1248
- h1 hsa-miR-513a-5p
- h1 hsa-miR-1269
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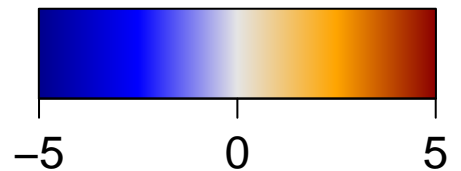


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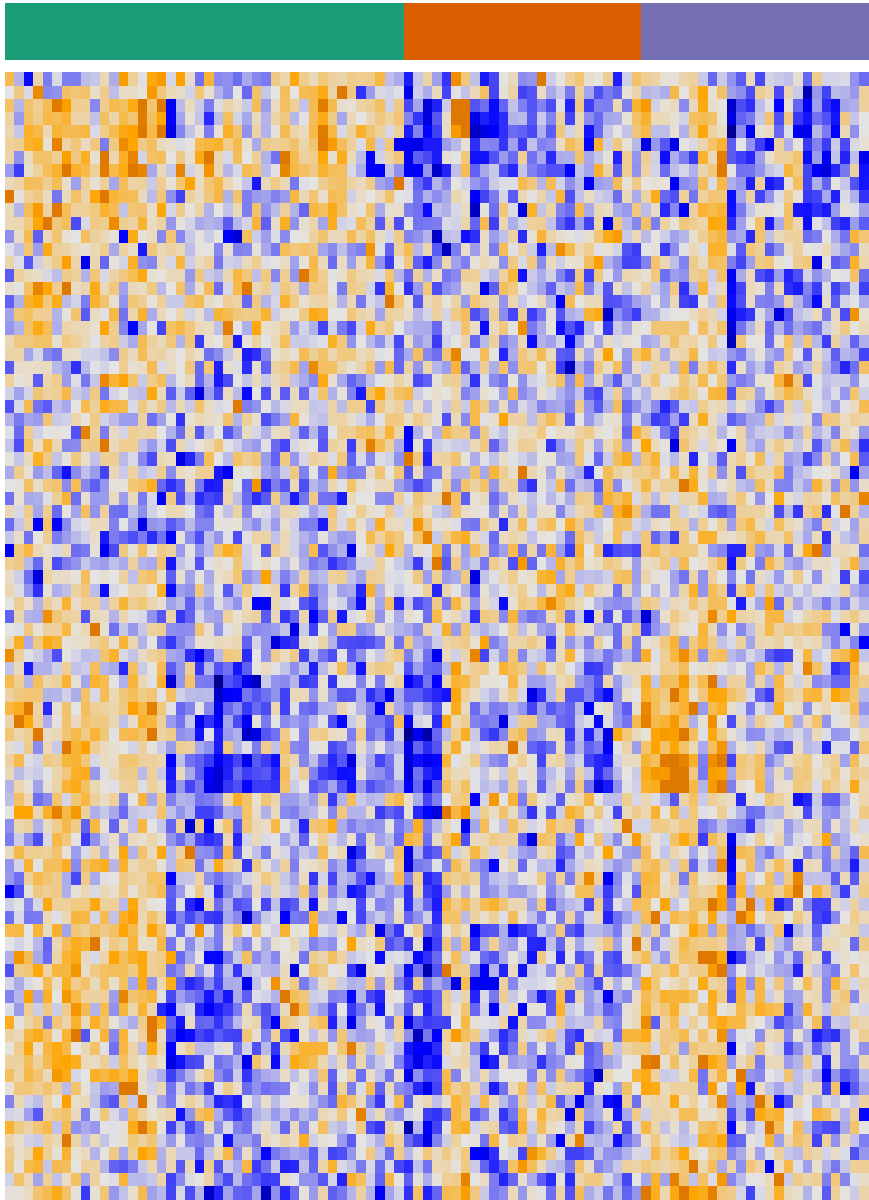


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M1 hsa-miR-520a-5p  
M1 hsa-miR-323b-5p  
N1 hsa-miR-223  
B1 hsa-miR-1298  
F1 hsa-miR-452\*  
J1 hsa-miR-1258  
H1 hsa-miR-518e  
N1 hsa-miR-127-5p  
R1 hsa-miR-191\*  
C1 hsa-miR-337-5p  
Y1 hsa-miR-575  
H1 hsa-miR-592  
S1 hsa-miR-892a  
N1 hsa-miR-1178  
S1 hsa-miR-1246  
L1 hsa-miR-942  
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N1 hsa-miR-937  
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J1 hsa-miR-548k  
H1 hsa-miR-18b  
H1 hsa-miR-20a  
Q1 hsa-miR-519d  
Q1 hsa-miR-17  
K1 hsa-miR-342-5p  
K1 hsa-miR-97  
B1 hsa-miR-639  
T1 hsa-miR-22  
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O1 hsa-miR-626  
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C1 hsa-miR-656  
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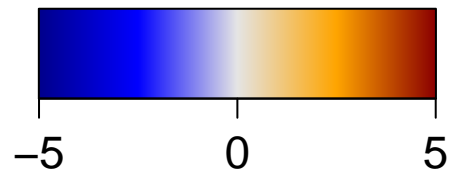


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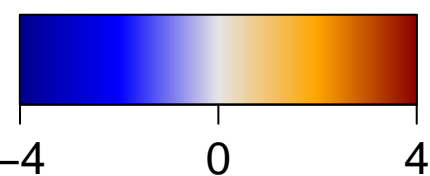
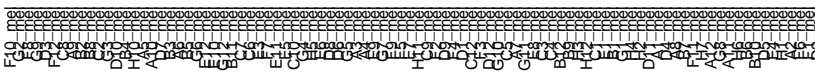
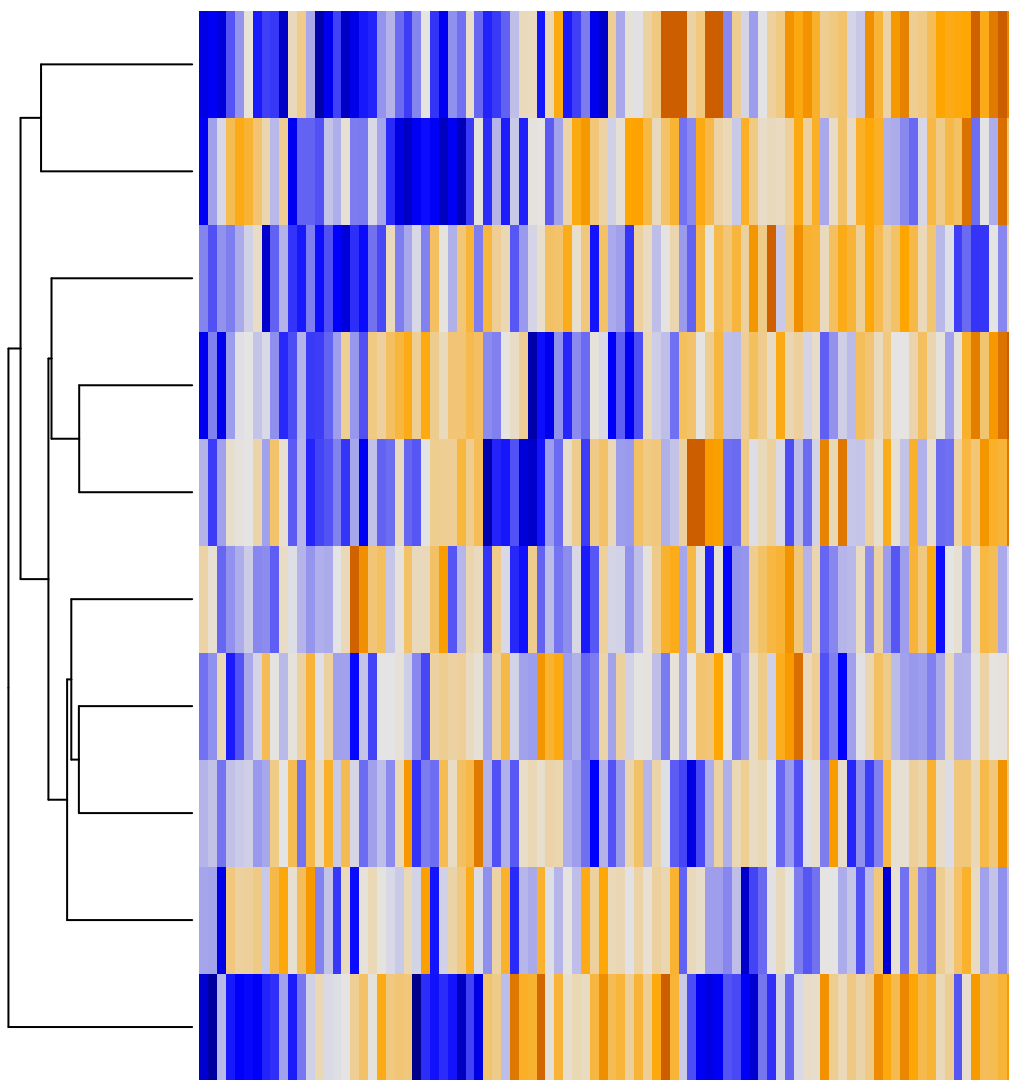
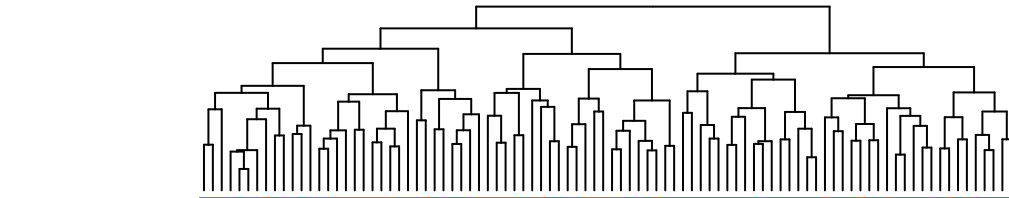


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H1 hsa-miR-526b  
R1 hsa-miR-548i  
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M1 hsa-miR-323b-5p  
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Y1 hsa-miR-151-5p  
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Y1 hsa-miR-596  
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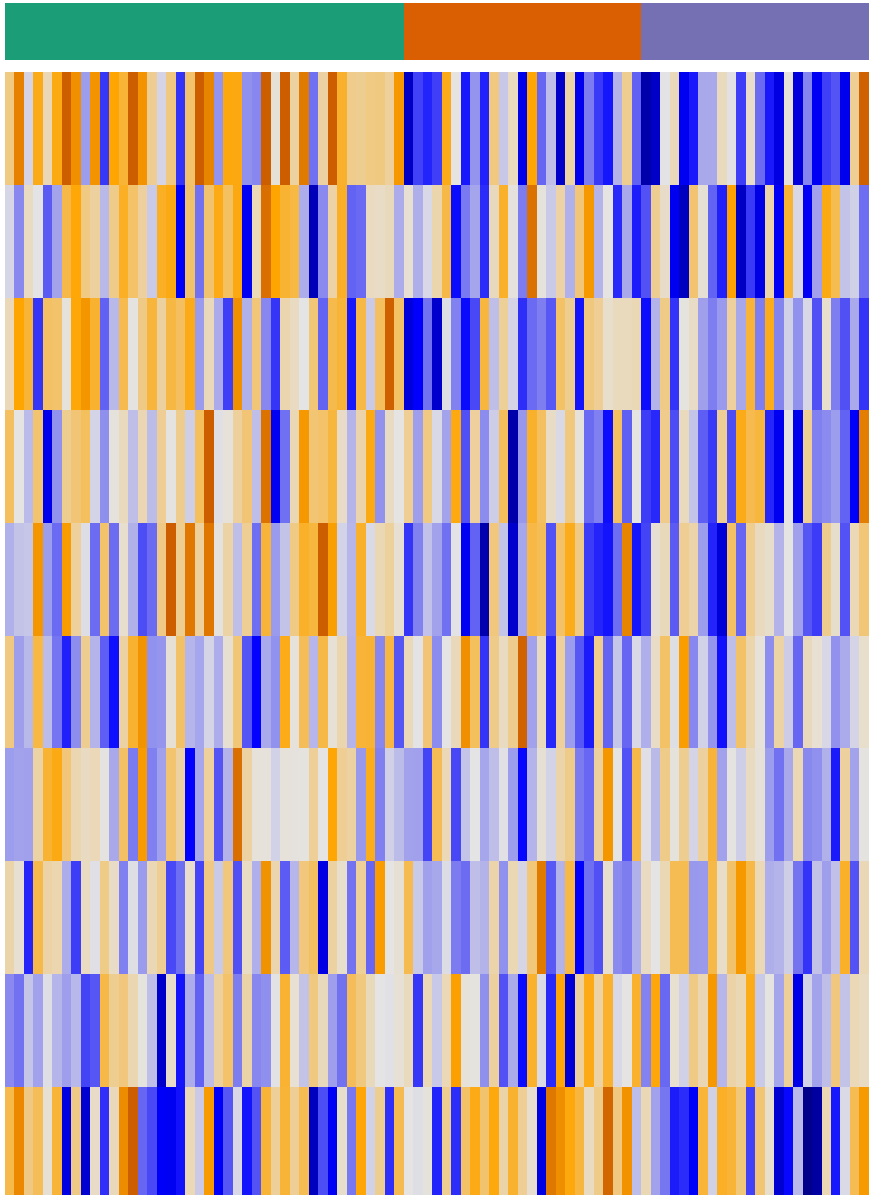
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Category Pathw Act

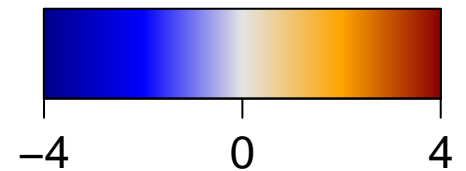


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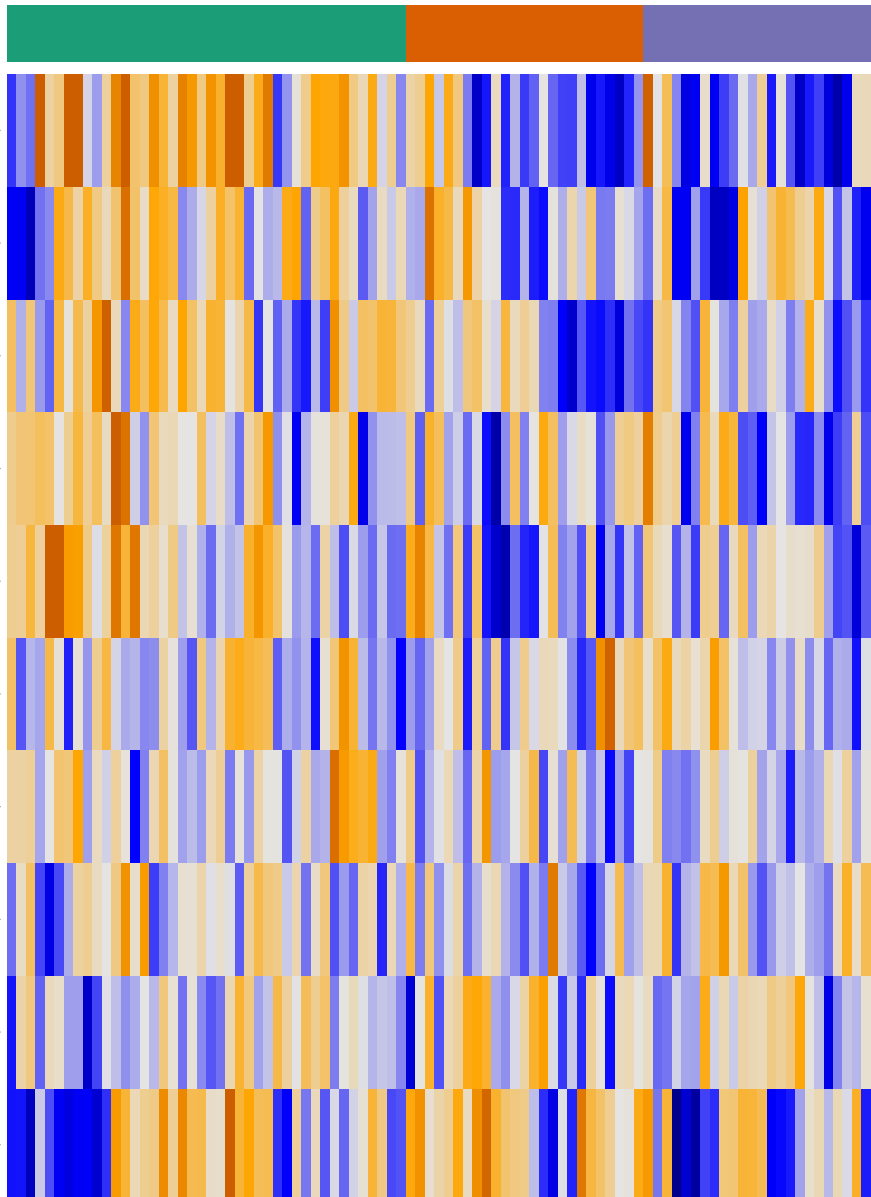


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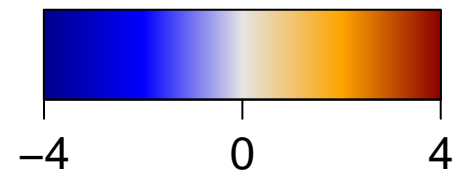


# GSZ score

Category Pathw Act



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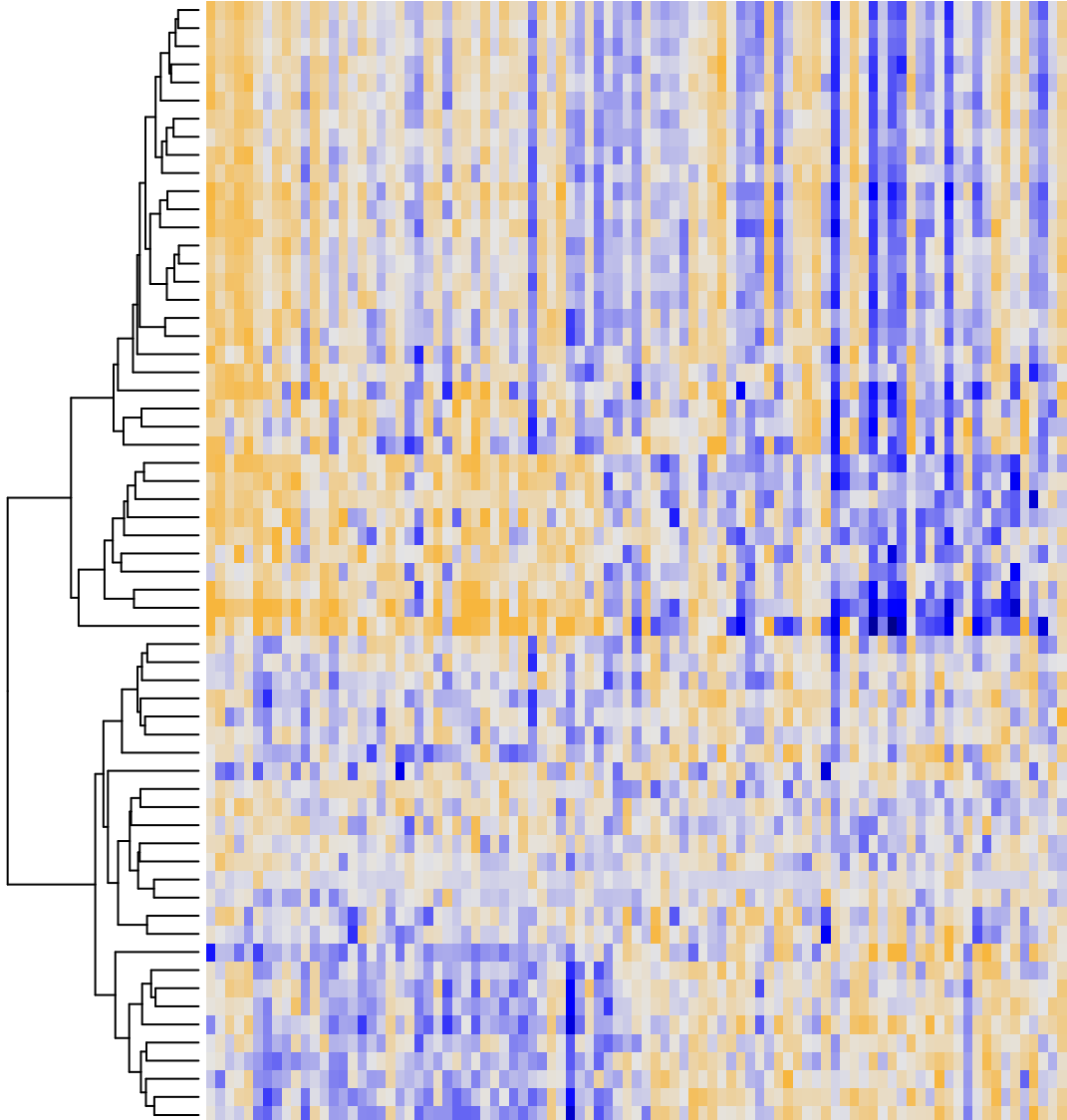




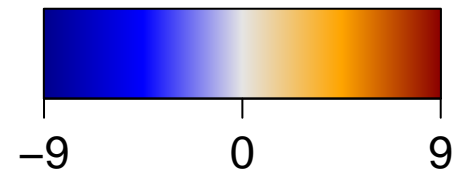


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Category TF

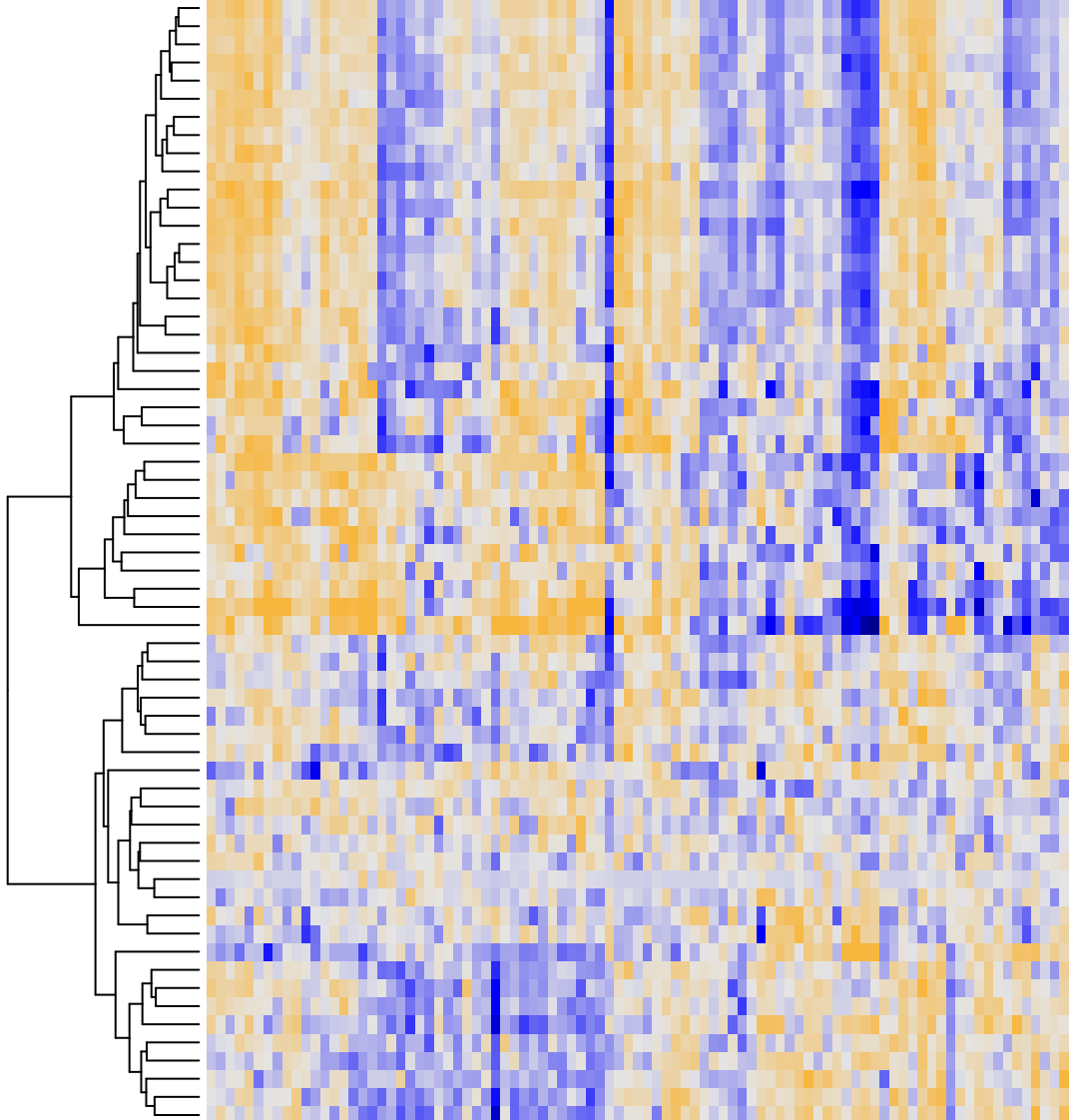


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- D ICGC\_Nfatc1\_targets
- E ICGC\_Sp1\_targets
- D ICGC\_Pol2\_targets
- D ICGC\_Tcf12\_targets
- C ICGC\_Zeb1\_targets
- E ICGC\_Taf1\_targets
- D ICGC\_Stat5\_targets
- E ICGC\_Creb1\_targets
- C ICGC\_Elf1\_targets
- H ICGC\_Runx3\_targets
- E ICGC\_Pou2\_targets
- E ICGC\_Nficsc81335\_targets
- C ICGC\_Egr1\_targets
- C ICGC\_Tcf3\_targets
- T1 ICGC\_SrfV0416101\_targets
- F ICGC\_Atf3\_targets
- F ICGC\_Myc\_targets
- E ICGC\_Ets1\_targets
- J1 ICGC\_Six5\_targets
- D ICGC\_GabpPcr2\_targets
- E MYC\_Cell growth and proliferation UP
- E MYC\_Cell cycle UP
- N MYC\_DNA replication UP
- E MYC\_DNA repair UP
- B MYC\_Metabolism UP
- J HEBENSTREIT\_high expression TF
- E MYC\_RNA processing binding UP
- A MYC\_Protein synthesis degradation UP
- E MYC\_Targets UP
- E KIM\_MYC targets
- D ICGC\_Cebpbpc150\_targets
- E ICGC\_RxraPcr1\_targets
- T1 ICGC\_NrstPcr1\_targets
- F ICGC\_Irf4\_targets
- Q1 ICGC\_SrfPcr2\_targets
- D ICGC\_Pbx3\_targets
- M1 ICGC\_Usf1\_targets
- J MYC\_ECM cell adhesion DOWN
- A MYC\_Chromatin\_modification UP
- E MYC\_Tumor suppressor genes UP
- T MYC\_Apoptosis UP
- A MYC\_Signal transduction UP
- A MYC\_TFs
- A MYC\_Cell cycle DOWN
- T1 NOWICK\_TF
- N MYC\_TF and cofactors
- C1 MYC\_Targets DOWN
- L1 HEBENSTREIT\_low expression TF
- S ICGC\_Pu1\_targets
- C ICGC\_Ebfsc137065\_targets
- H ICGC\_Bcl3\_targets
- S ICGC\_Rad21\_targets
- D ICGC\_Mef2\_targets
- Q ICGC\_P300\_targets
- E1 ICGC\_NrstPcr2\_targets
- K ICGC\_BatfPcr1\_targets
- K ICGC\_Bcl11\_targets

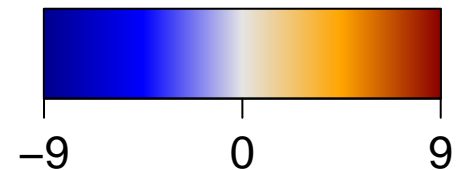


# GSZ score

Category TF

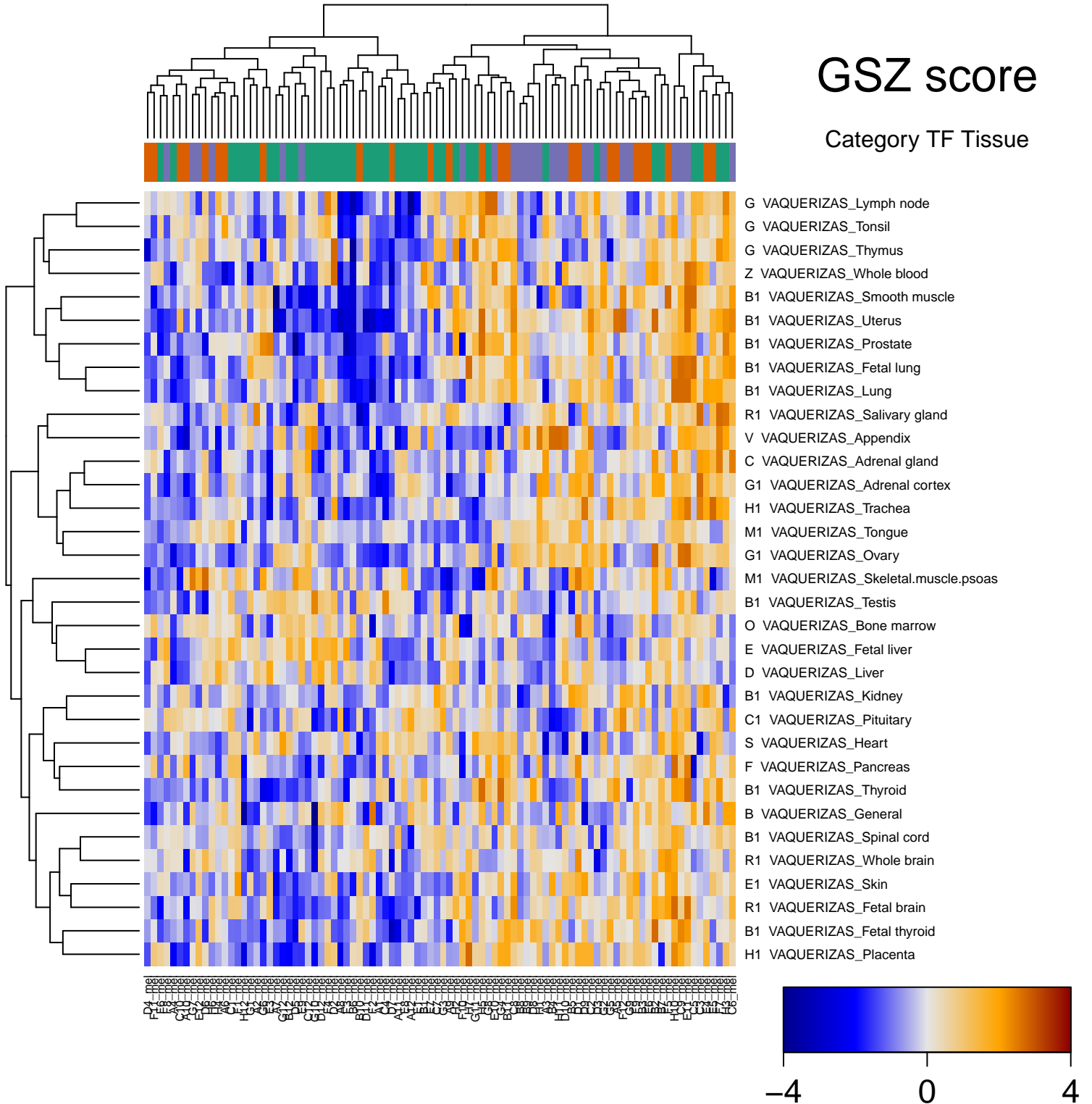


- E ICGC\_Pmlsc71910\_targets
- D ICGC\_Mta3\_targets
- E ICGC\_Foxm1\_targets
- D ICGC\_Bclaf101388\_targets
- E ICGC\_Atf2\_targets
- D ICGC\_Nfatc1\_targets
- E ICGC\_Sp1\_targets
- D ICGC\_Pol2\_targets
- D ICGC\_Tcf12\_targets
- C ICGC\_Zeb1\_targets
- E ICGC\_Taf1\_targets
- D ICGC\_Stat5\_targets
- E ICGC\_Creb1\_targets
- C ICGC\_Elf1\_targets
- H ICGC\_Runx3\_targets
- E ICGC\_Pou2\_targets
- E ICGC\_Nficsc81335\_targets
- C ICGC\_Egr1\_targets
- C ICGC\_Tcf3\_targets
- T1 ICGC\_SrfV0416101\_targets
- F ICGC\_Atf3\_targets
- F ICGC\_Myc\_targets
- E ICGC\_Ets1\_targets
- J1 ICGC\_Six5\_targets
- D ICGC\_GabpPcr2\_targets
- E MYC\_Cell growth and proliferation UP
- E MYC\_Cell cycle UP
- N MYC\_DNA replication UP
- E MYC\_DNA repair UP
- B MYC\_Metabolism UP
- J HEBENSTREIT\_high expression TF
- E MYC\_RNA processing binding UP
- A MYC\_Protein synthesis degradation UP
- E MYC\_Targets UP
- E KIM\_MYC targets
- D ICGC\_Cebpbpc150\_targets
- E ICGC\_RxraPcr1\_targets
- T1 ICGC\_NrstPcr1\_targets
- F ICGC\_Irf4\_targets
- Q1 ICGC\_SrfPcr2\_targets
- D ICGC\_Pbx3\_targets
- M1 ICGC\_Usf1\_targets
- J MYC\_ECM cell adhesion DOWN
- A MYC\_Chromatin\_modification UP
- E MYC\_Tumor suppressor genes UP
- T MYC\_Apoptosis UP
- A MYC\_Signal transduction UP
- A MYC\_TFs
- A MYC\_Cell cycle DOWN
- T1 NOWICK\_TF
- N MYC\_TF and cofactors
- C1 MYC\_Targets DOWN
- L1 HEBENSTREIT\_low expression TF
- S ICGC\_Pu1\_targets
- C ICGC\_Ebfsc137065\_targets
- H ICGC\_Bcl3\_targets
- S ICGC\_Rad21\_targets
- D ICGC\_Mef2\_targets
- Q ICGC\_P300\_targets
- E1 ICGC\_NrstPcr2\_targets
- K ICGC\_BatfPcr1\_targets
- K ICGC\_Bcl11\_targets



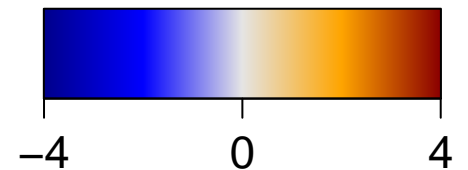
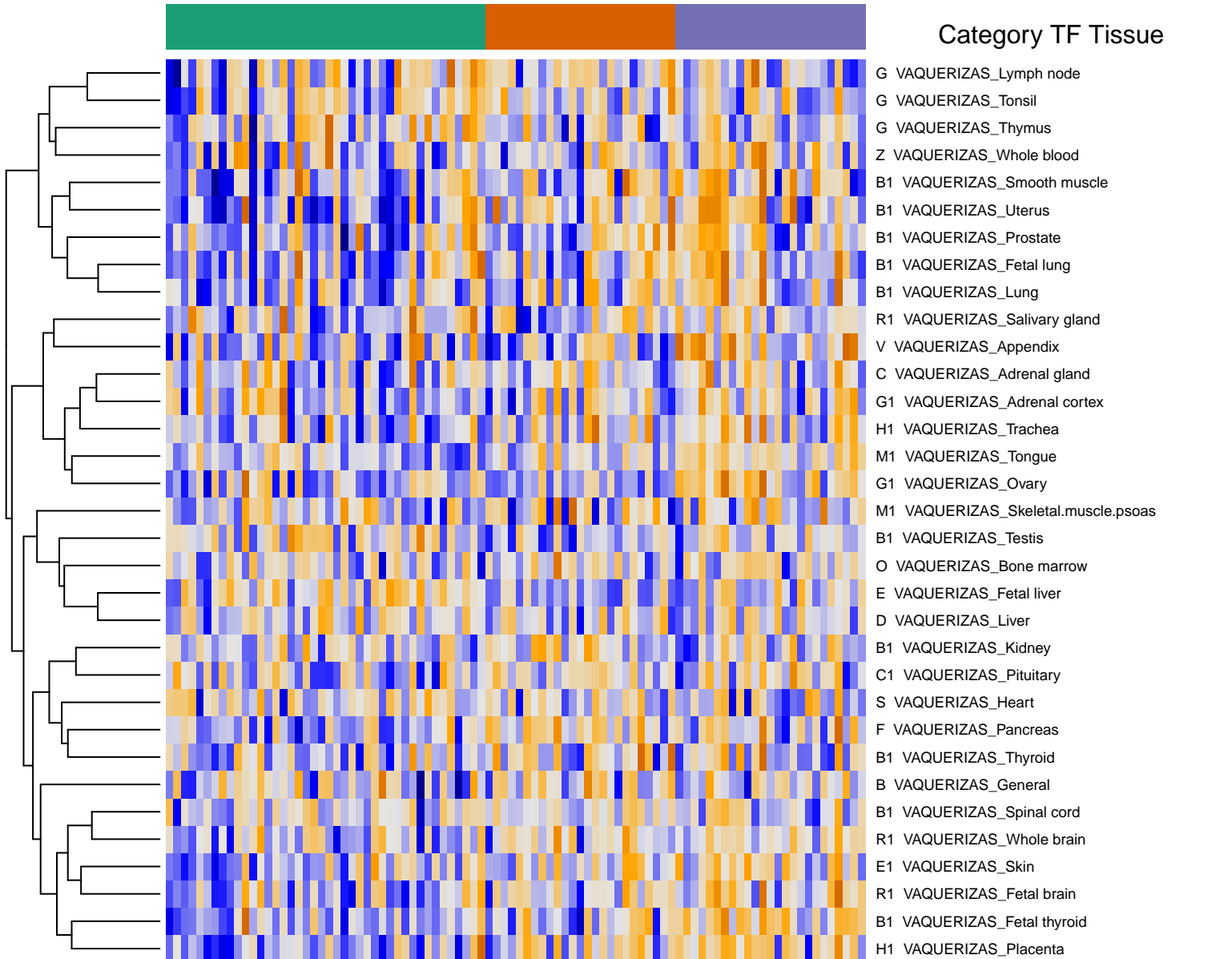
# GSZ score

Category TF Tissue



# GSZ score

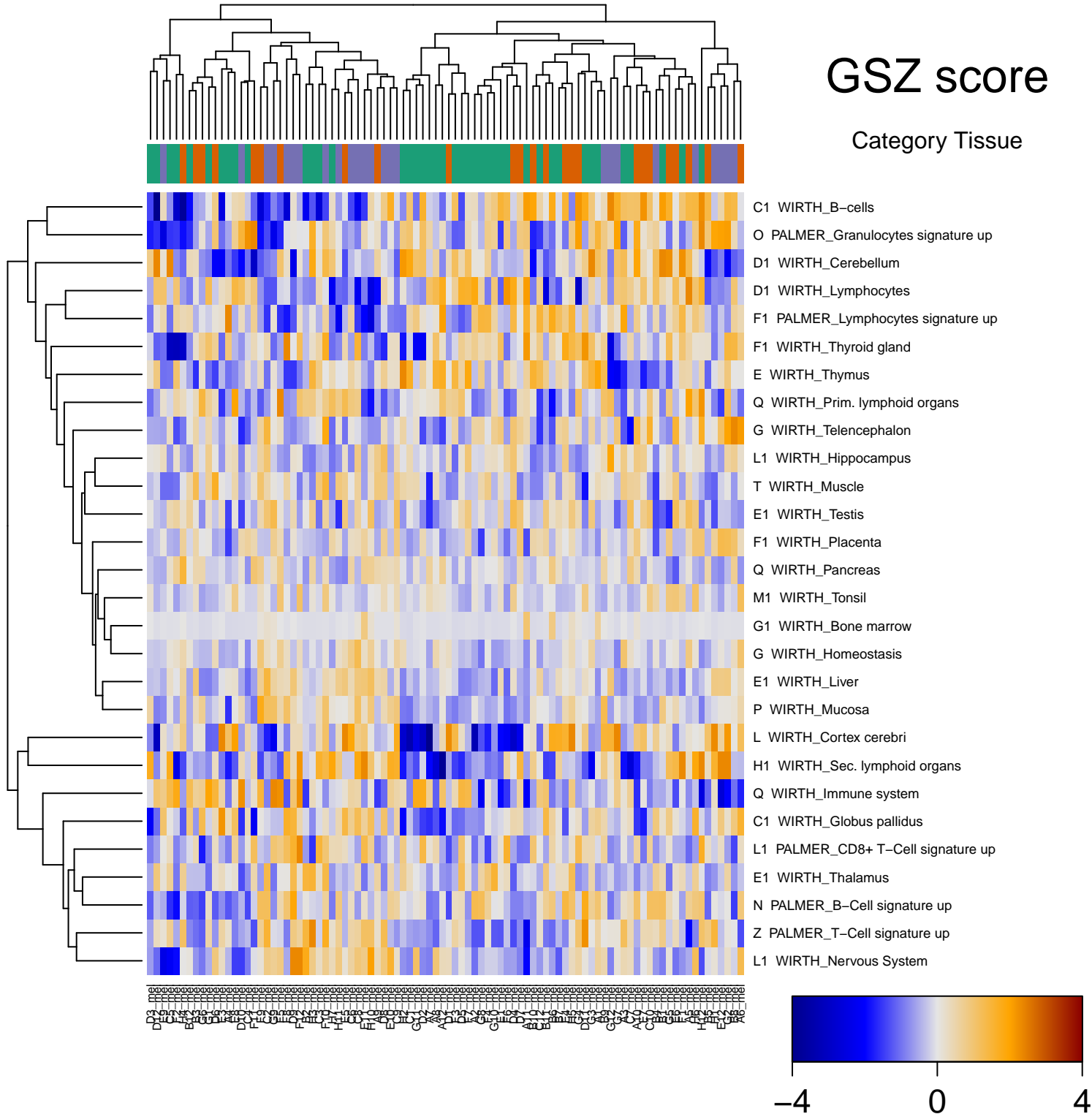
Category TF Tissue





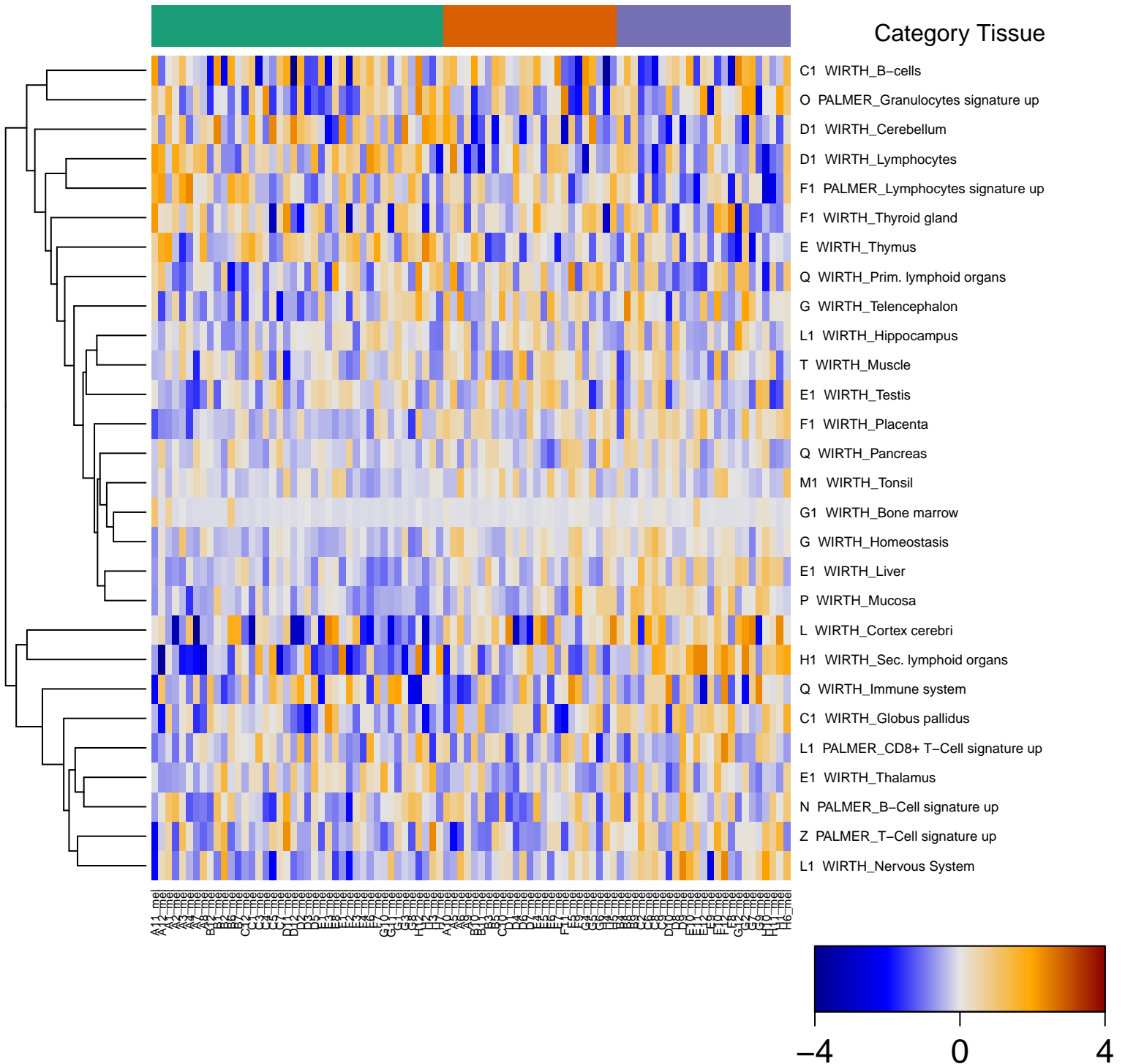
# GSZ score

Category Tissue



# GSZ score

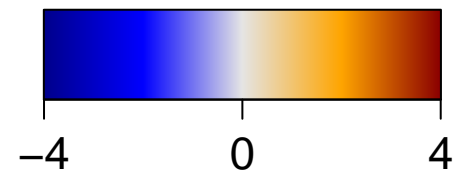
Category Tissue

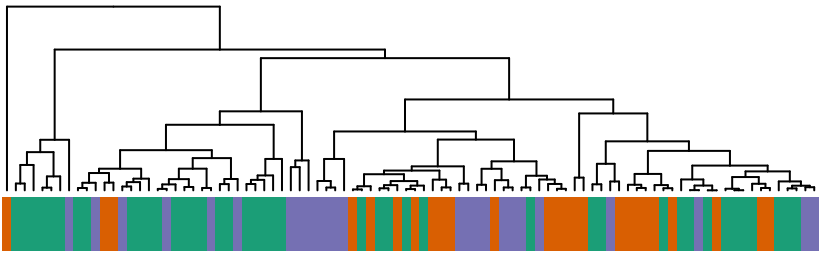




# GSZ score

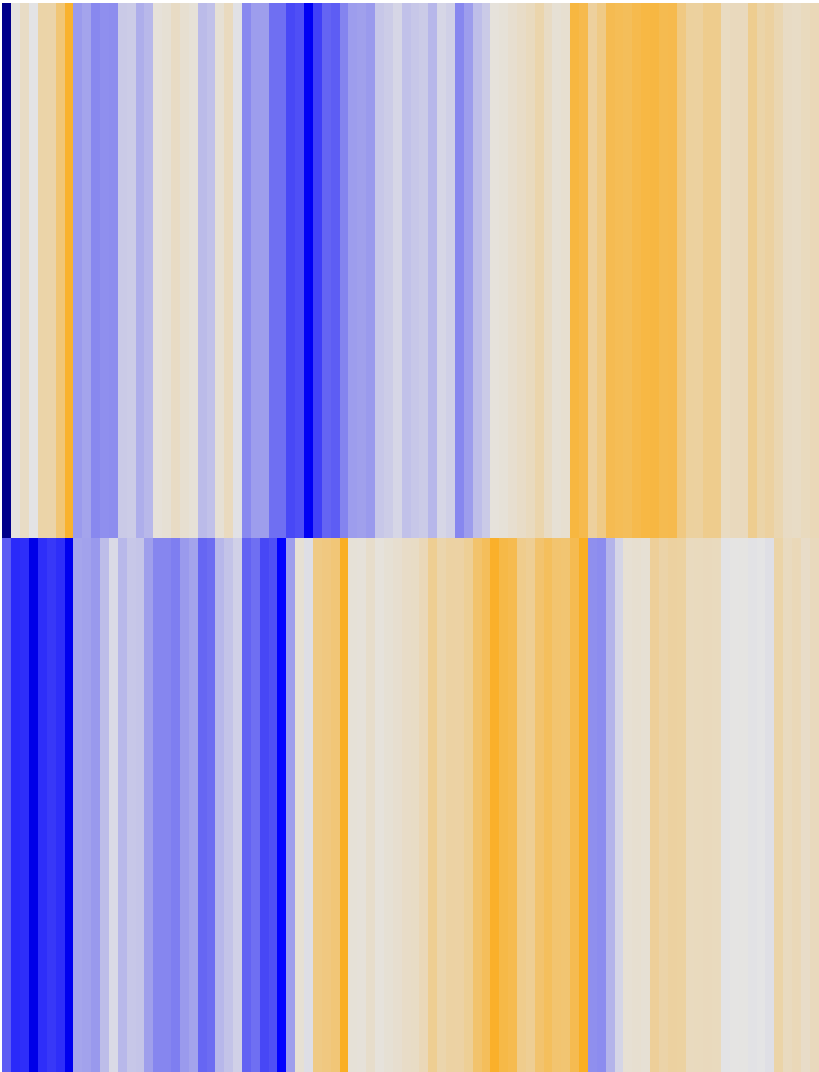
Category Tissue





GSZ score

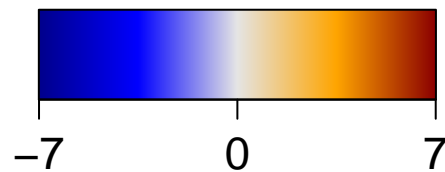
Category Toxic



G LU\_BPDE 1h

R LU\_BPDE 0.6

Small text labels at the bottom of the heatmap, likely representing individual sample identifiers or gene names.







# p-values (GSZ)

