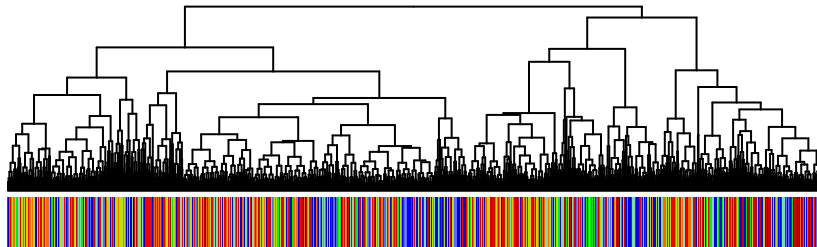


GSZ score

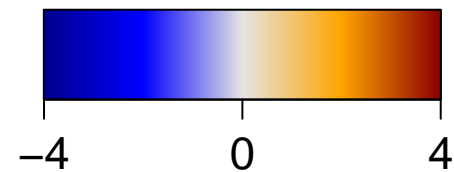
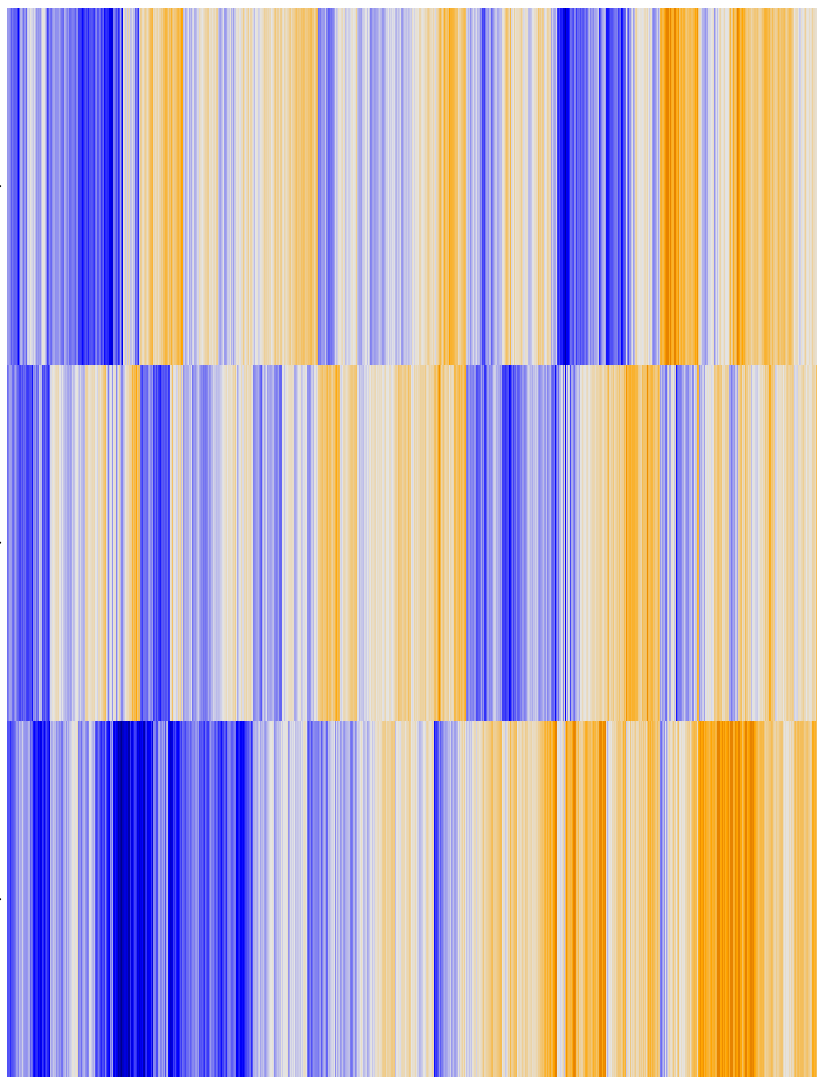
Category Aging



H HORVATH_aging_gen

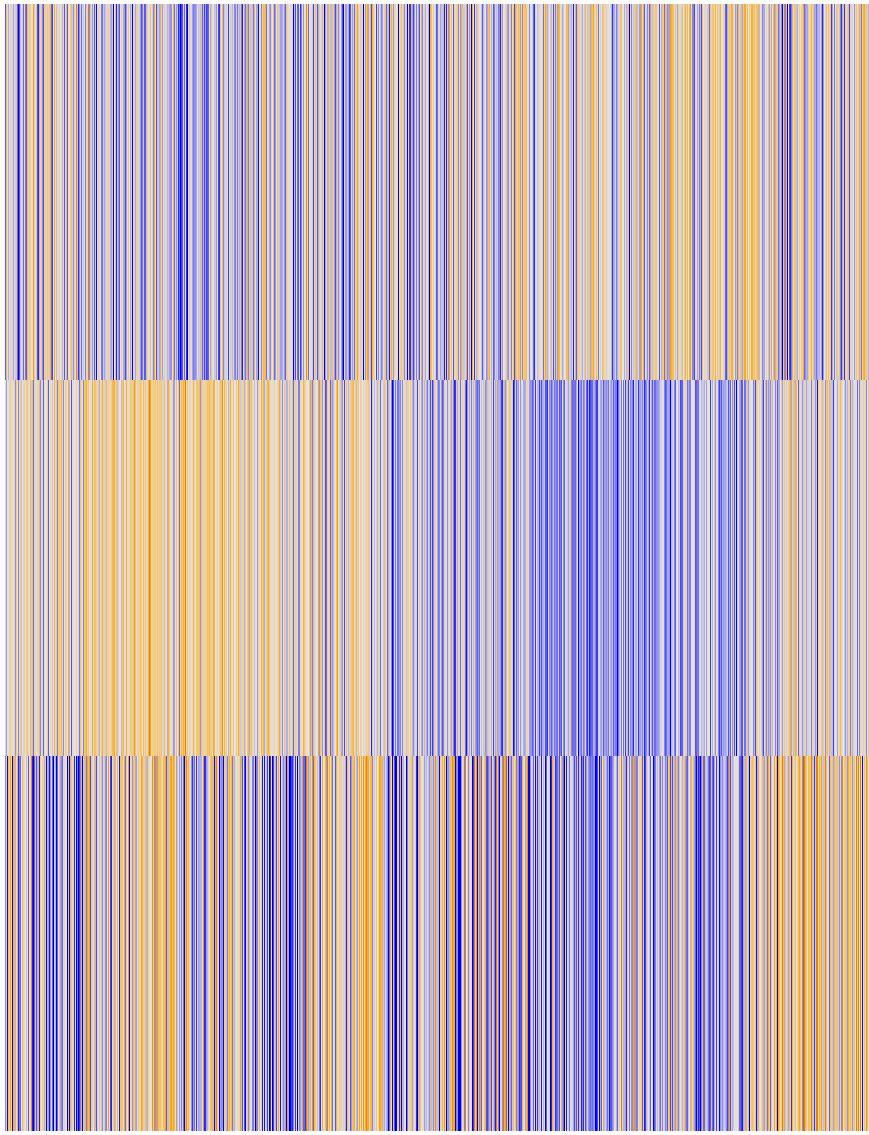
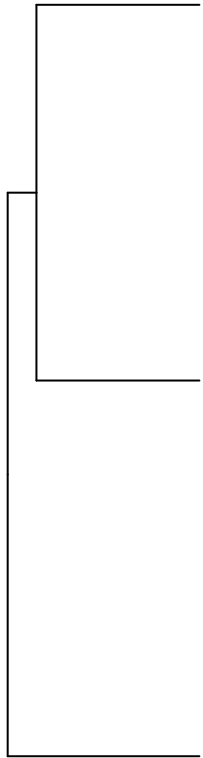
B TESCHENDORFF_ag

N HORVATH_aging_gen



GSZ score

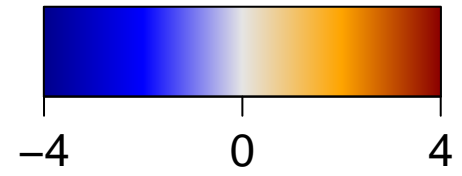
Category Aging



H HORVATH_aging_ge

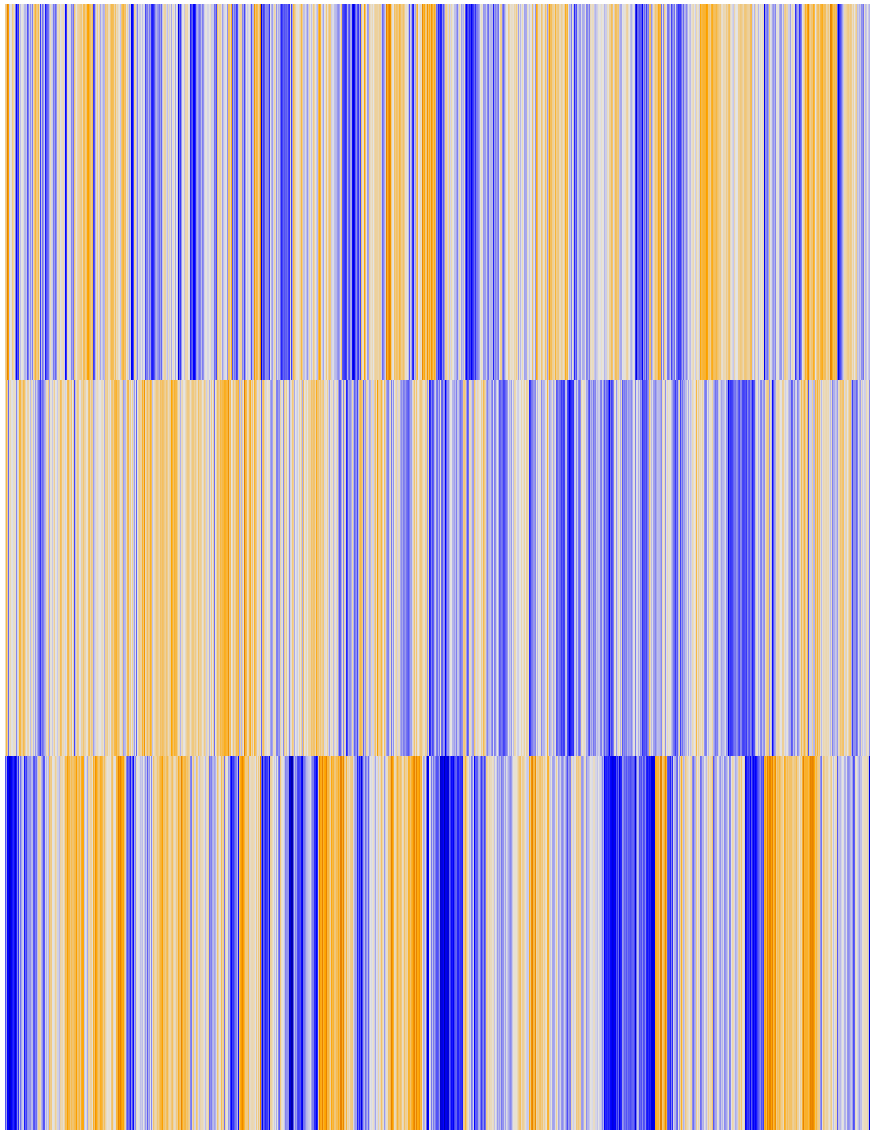
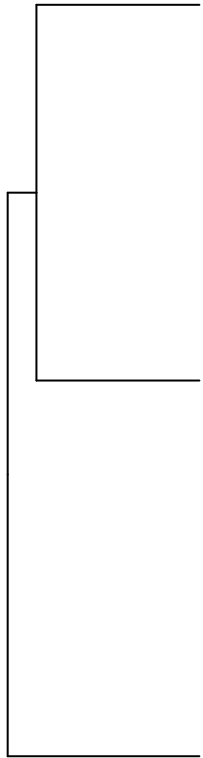
B TESCHENDORFF_a

N HORVATH_aging_ge



GSZ score

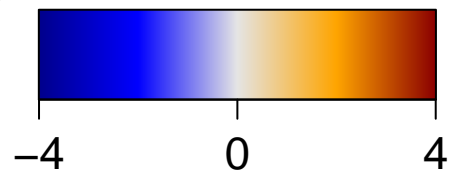
Category Aging



H HORVATH_aging_ge

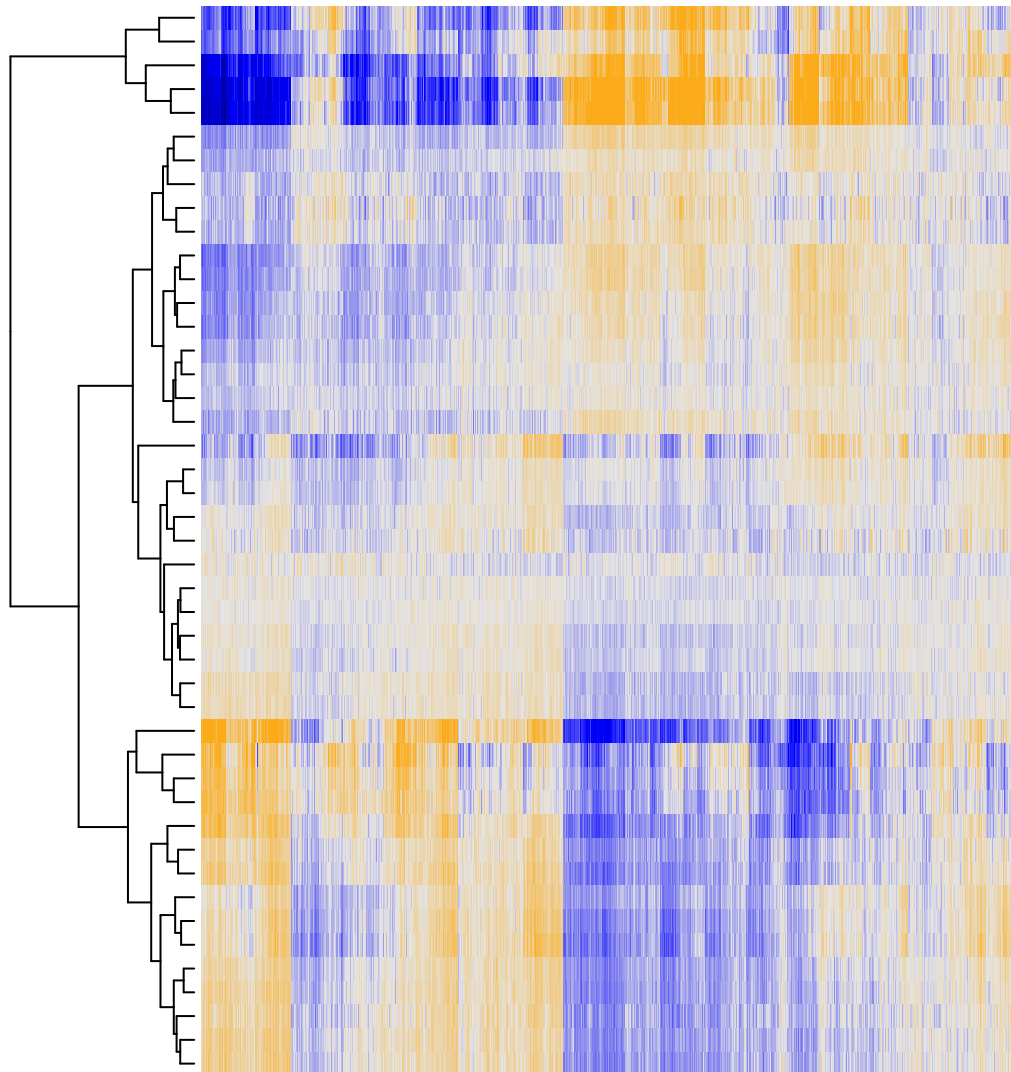
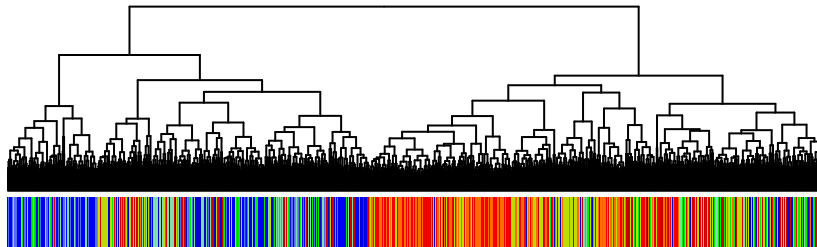
B TESCHENDORFF_a

N HORVATH_aging_ge

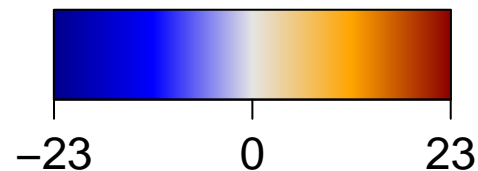


GSZ score

Category Brain

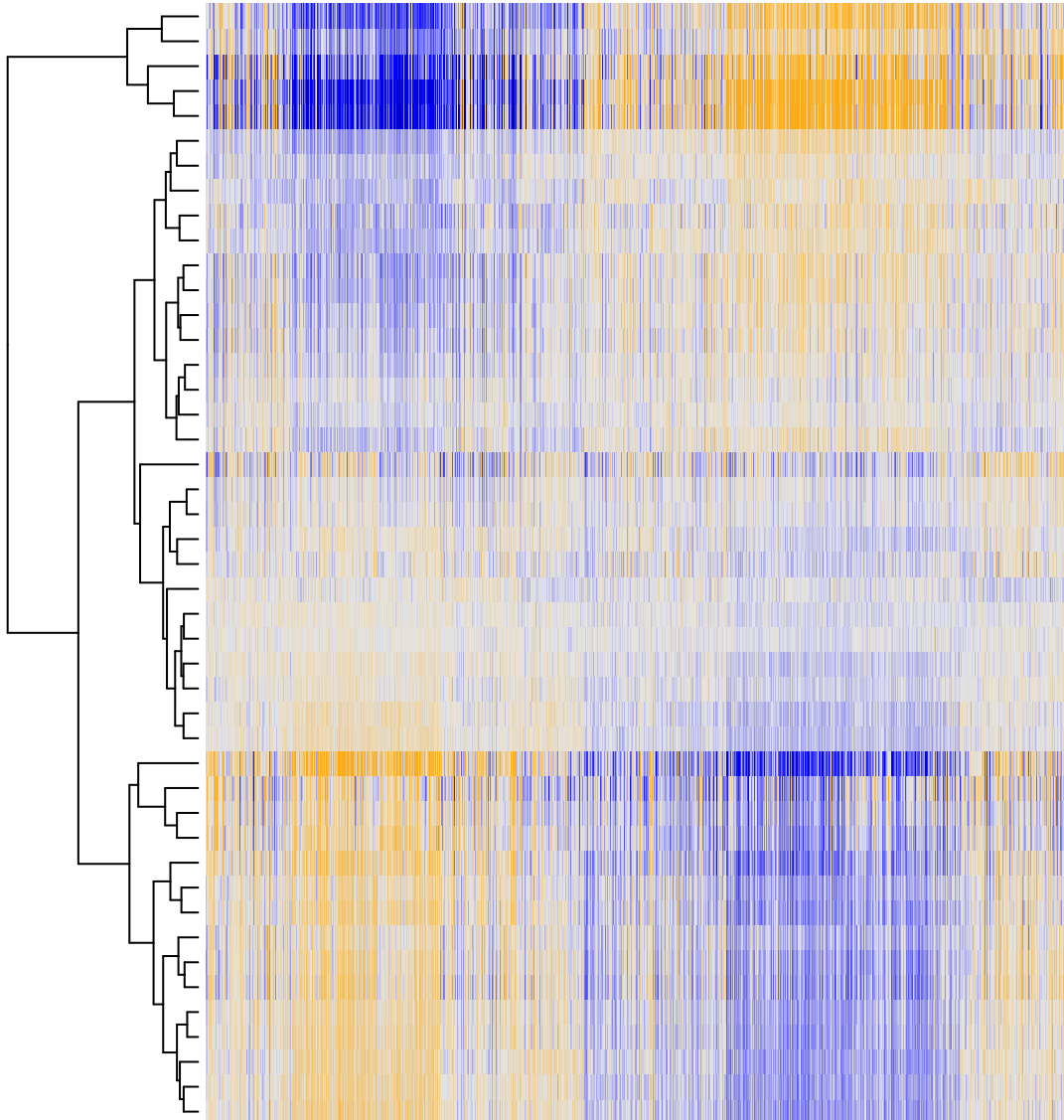


- E Overlap_fetal_midbrain_K9K27me3
- E Overlap_fetal_midbrain_Quies
- K Overlap_fetal_midbrain_ReprPCWk
- K Overlap_fetal_midbrain_ReprPC
- K Overlap_fetal_midbrain_HetRpts
- K Fetal_ZNF
- M Fetal_Het
- K Fetal_HetRpts
- J Overlap_fetal_midbrain_ZNF
- I Overlap_fetal_midbrain_Het
- K Fetal_EnhP
- K Fetal_EnhG
- K Fetal_K9K27me3
- K Fetal_Enh
- H Overlap_fetal_midbrain_Enh
- A Overlap_fetal_midbrain_EnhG
- K Mid_Frontal_Lobe_EnhP
- A Overlap_fetal_midbrain_EnhP
- L Fetal_TssP
- N Mid_Frontal_Lobe_Enh
- N Mid_Frontal_Lobe_EnhG
- L Fetal_Tx
- L Mid_Frontal_Lobe_Quies
- B Fetal_Quies
- A Fetal_ReprPC
- O Overlap_fetal_midbrain_Tx
- H Mid_Frontal_Lobe_Tx
- H Overlap_fetal_midbrain_TssP
- C Mid_Frontal_Lobe_TssA
- B Mid_Frontal_Lobe_TxTrans
- L Mid_Frontal_Lobe_ReprPC
- E Mid_Frontal_Lobe_ZNF
- E Mid_Frontal_Lobe_Het
- E Fetal_ReprPCWk
- E Mid_Frontal_Lobe_HetRpts
- L Mid_Frontal_Lobe_ReprPCWk
- L Mid_Frontal_Lobe_K9K27me3
- L Fetal_TssF
- L Fetal_TxTrans
- N Fetal_TssA
- H Overlap_fetal_midbrain_TssF
- N Overlap_fetal_midbrain_TxTrans
- C Mid_Frontal_Lobe_TssF
- N Overlap_fetal_midbrain_TssA
- N Mid_Frontal_Lobe_TssP

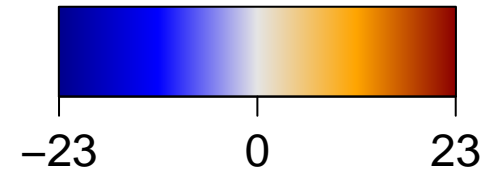


GSZ score

Category Brain

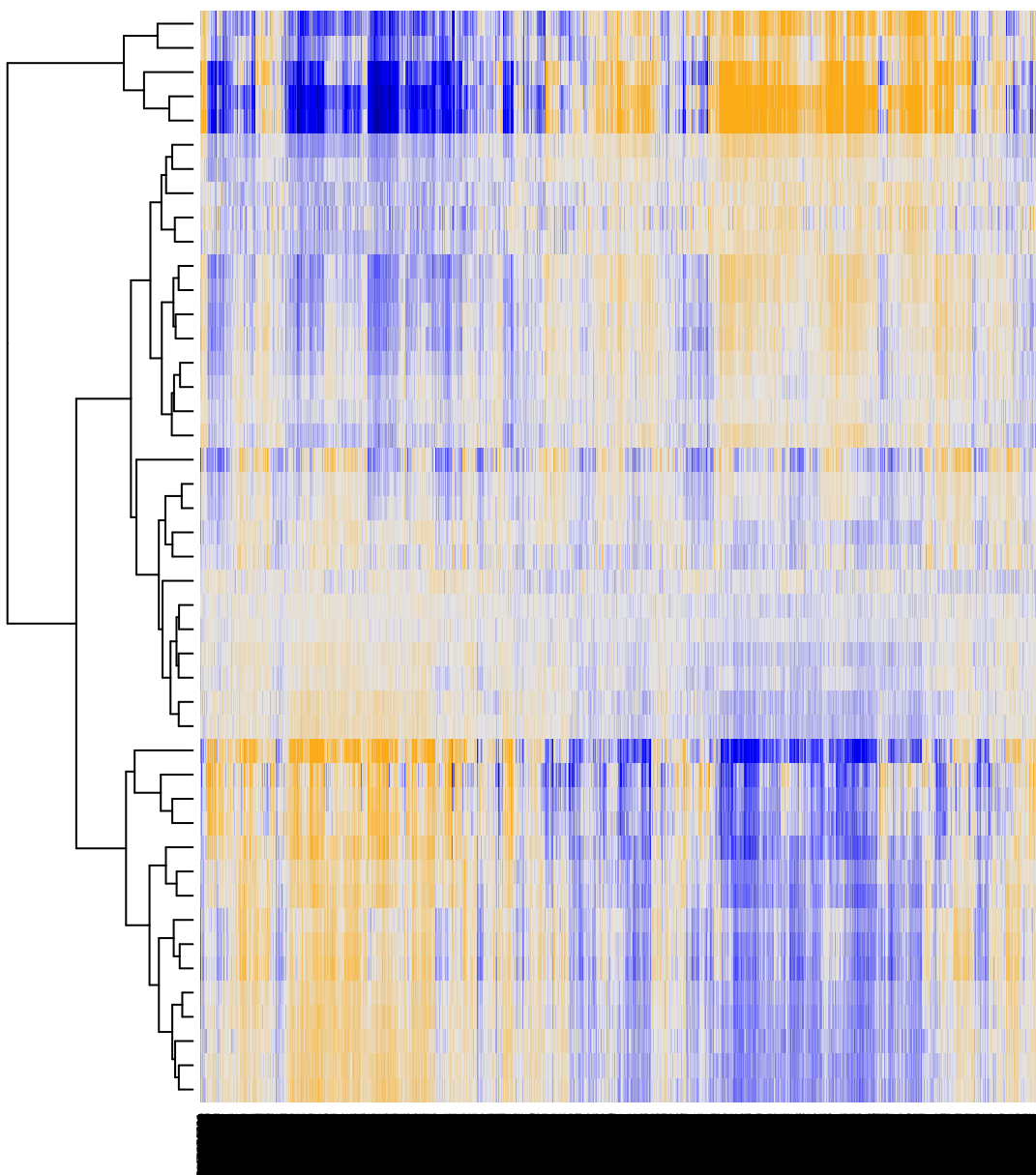


- E Overlap_fetal_midbrain_K9K27me3
- E Overlap_fetal_midbrain_Quies
- K Overlap_fetal_midbrain_ReprPCWk
- K Overlap_fetal_midbrain_ReprPC
- K Overlap_fetal_midbrain_HetRpts
- K Fetal_ZNF
- M Fetal_Het
- K Fetal_HetRpts
- J Overlap_fetal_midbrain_ZNF
- I Overlap_fetal_midbrain_Het
- K Fetal_EnhP
- K Fetal_EnhG
- K Fetal_K9K27me3
- K Fetal_Enh
- H Overlap_fetal_midbrain_Enh
- A Overlap_fetal_midbrain_EnhG
- K Mid_Frontal_Lobe_EnhP
- A Overlap_fetal_midbrain_EnhP
- L Fetal_TssP
- N Mid_Frontal_Lobe_Enh
- N Mid_Frontal_Lobe_EnhG
- L Fetal_Tx
- L Mid_Frontal_Lobe_Quies
- B Fetal_Quies
- A Fetal_ReprPC
- O Overlap_fetal_midbrain_Tx
- H Mid_Frontal_Lobe_Tx
- H Overlap_fetal_midbrain_TssP
- C Mid_Frontal_Lobe_TssA
- B Mid_Frontal_Lobe_TxTrans
- L Mid_Frontal_Lobe_ReprPC
- E Mid_Frontal_Lobe_ZNF
- E Mid_Frontal_Lobe_Het
- E Fetal_ReprPCWk
- E Mid_Frontal_Lobe_HetRpts
- L Mid_Frontal_Lobe_ReprPCWk
- L Mid_Frontal_Lobe_K9K27me3
- L Fetal_TssF
- L Fetal_TxTrans
- N Fetal_TssA
- H Overlap_fetal_midbrain_TssF
- N Overlap_fetal_midbrain_TxTrans
- C Mid_Frontal_Lobe_TssF
- N Overlap_fetal_midbrain_TssA
- N Mid_Frontal_Lobe_TssP

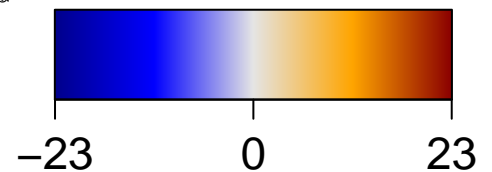


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Category Brain

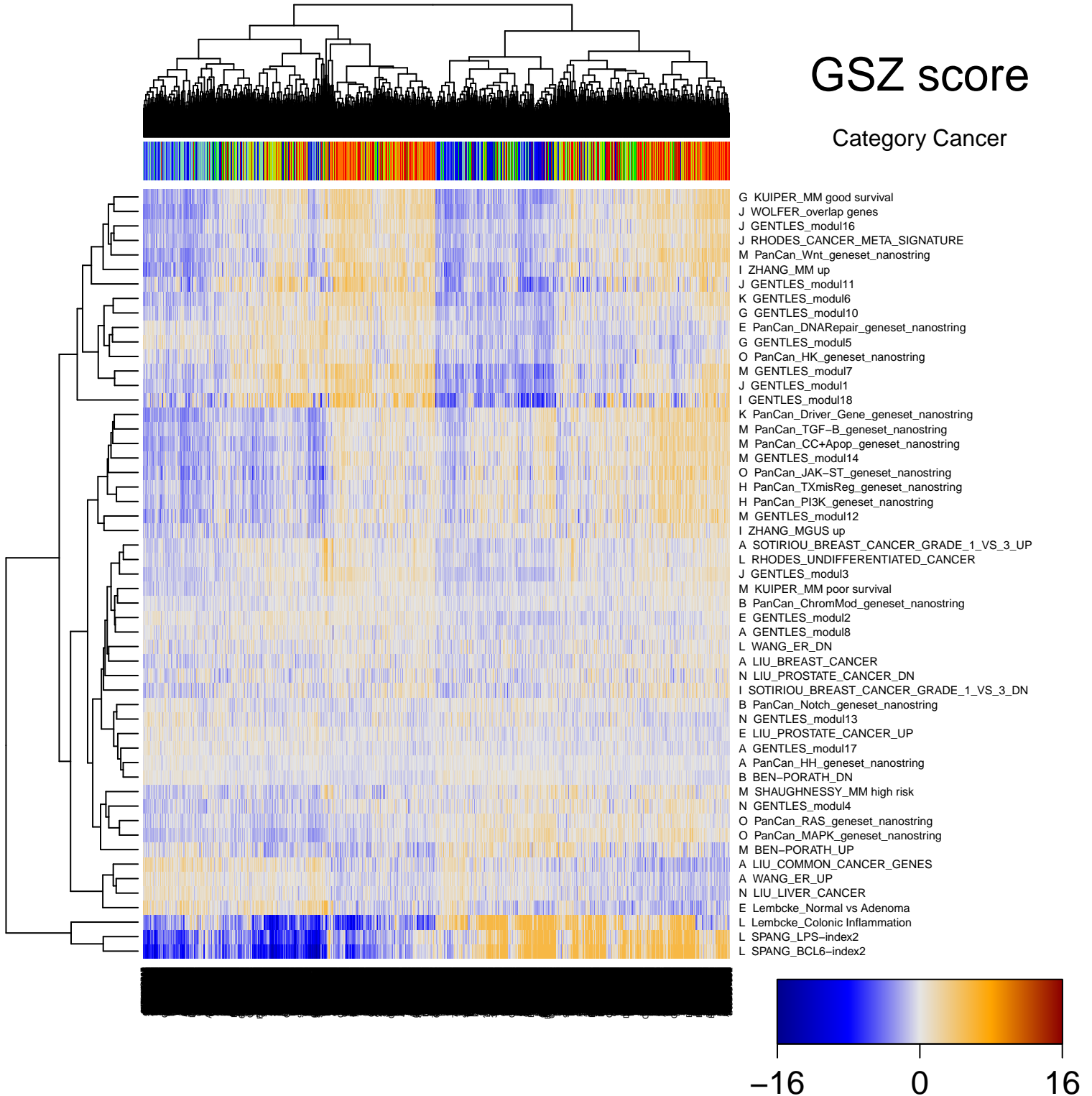


- E Overlap_fetal_midbrain_K9K27me3
- E Overlap_fetal_midbrain_Quies
- K Overlap_fetal_midbrain_ReprPCWk
- K Overlap_fetal_midbrain_ReprPC
- K Overlap_fetal_midbrain_HetRpts
- K Fetal_ZNF
- M Fetal_Het
- K Fetal_HetRpts
- J Overlap_fetal_midbrain_ZNF
- I Overlap_fetal_midbrain_Het
- K Fetal_EnhP
- K Fetal_EnhG
- K Fetal_K9K27me3
- K Fetal_Enh
- H Overlap_fetal_midbrain_Enh
- A Overlap_fetal_midbrain_EnhG
- K Mid_Frontal_Lobe_EnhP
- A Overlap_fetal_midbrain_EnhP
- L Fetal_TssP
- N Mid_Frontal_Lobe_Enh
- N Mid_Frontal_Lobe_EnhG
- L Fetal_Tx
- L Mid_Frontal_Lobe_Quies
- B Fetal_Quies
- A Fetal_ReprPC
- O Overlap_fetal_midbrain_Tx
- H Mid_Frontal_Lobe_Tx
- H Overlap_fetal_midbrain_TssP
- C Mid_Frontal_Lobe_TssA
- B Mid_Frontal_Lobe_TxTrans
- L Mid_Frontal_Lobe_ReprPC
- E Mid_Frontal_Lobe_ZNF
- E Mid_Frontal_Lobe_Het
- E Fetal_ReprPCWk
- E Mid_Frontal_Lobe_HetRpts
- L Mid_Frontal_Lobe_ReprPCWk
- L Mid_Frontal_Lobe_K9K27me3
- L Fetal_TssF
- L Fetal_TxTrans
- N Fetal_TssA
- H Overlap_fetal_midbrain_TssF
- N Overlap_fetal_midbrain_TxTrans
- C Mid_Frontal_Lobe_TssF
- N Overlap_fetal_midbrain_TssA
- N Mid_Frontal_Lobe_TssP



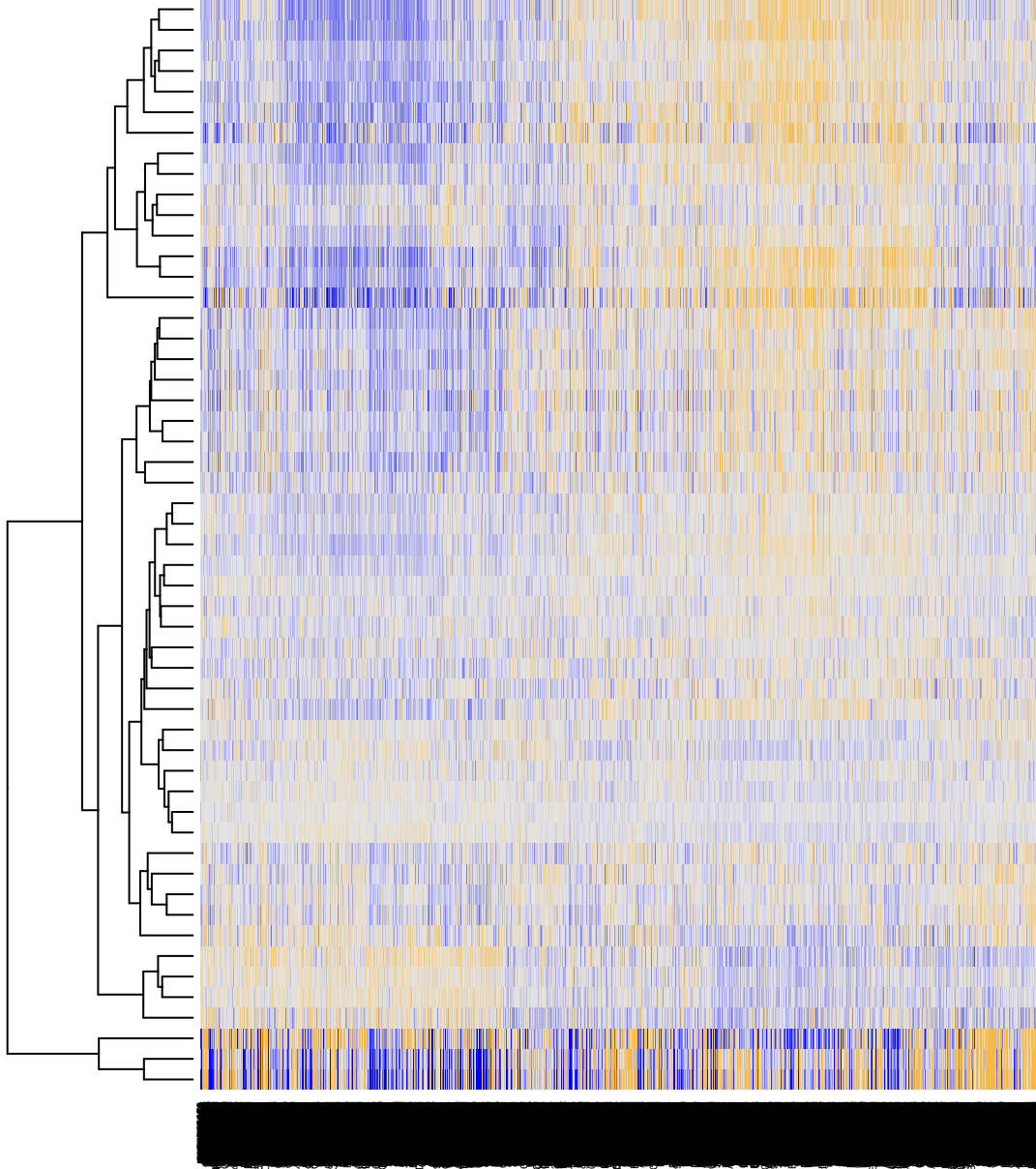
GSZ score

Category Cancer

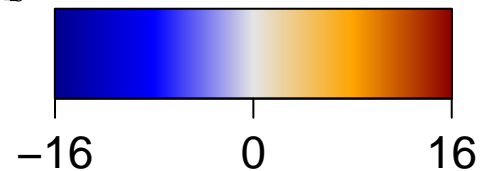


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Category Cancer

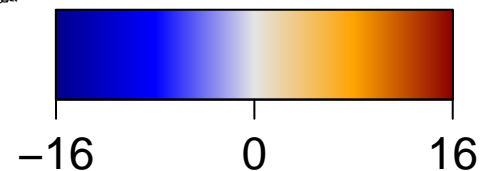
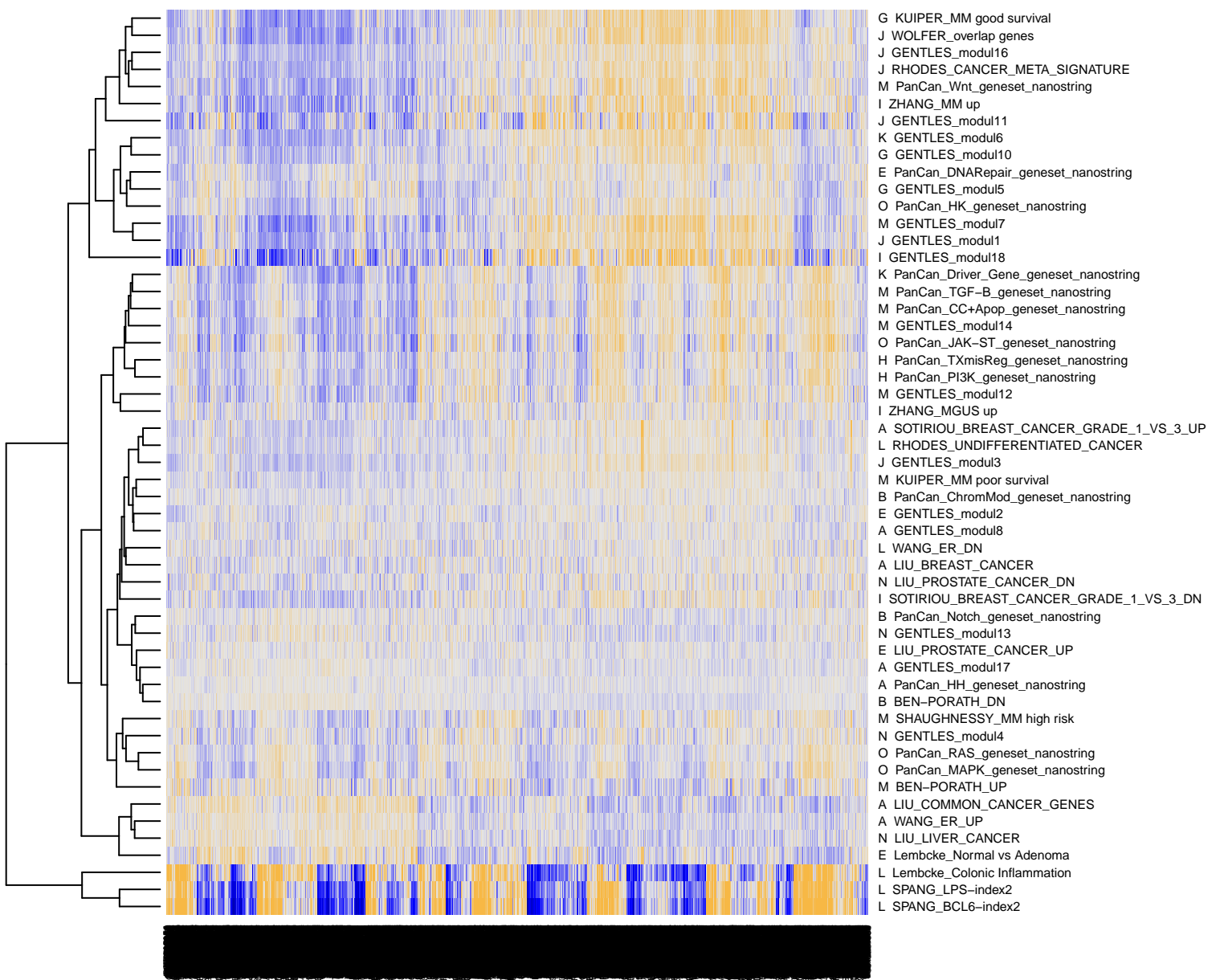


G KUIPER_MM good survival
J WOLFER_overlap genes
J GENTLES_modul16
J RHODES_CANCER_META_SIGNATURE
M PanCan_Wnt_geneset_nanostring
I ZHANG_MM up
J GENTLES_modul11
K GENTLES_modul6
G GENTLES_modul10
E PanCan_DNARepair_geneset_nanostring
G GENTLES_modul5
O PanCan_HK_geneset_nanostring
M GENTLES_modul7
J GENTLES_modul1
I GENTLES_modul18
K PanCan_Driver_Gene_geneset_nanostring
M PanCan_TGF-B_geneset_nanostring
M PanCan_CC+Apop_geneset_nanostring
M GENTLES_modul14
O PanCan_JAK-ST_geneset_nanostring
H PanCan_TXmisReg_geneset_nanostring
H PanCan_PI3K_geneset_nanostring
M GENTLES_modul12
I ZHANG_MGUS up
A SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
L RHODES_UNDIFFERENTIATED_CANCER
J GENTLES_modul3
M KUIPER_MM poor survival
B PanCan_ChromMod_geneset_nanostring
E GENTLES_modul2
A GENTLES_modul8
L WANG_ER_DN
A LIU_BREAST_CANCER
N LIU_PROSTATE_CANCER_DN
I SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
B PanCan_Notch_geneset_nanostring
N GENTLES_modul13
E LIU_PROSTATE_CANCER_UP
A GENTLES_modul17
A PanCan_HH_geneset_nanostring
B BEN-PORATH_DN
M SHAUGHNESSY_MM high risk
N GENTLES_modul4
O PanCan_RAS_geneset_nanostring
O PanCan_MAPK_geneset_nanostring
M BEN-PORATH_UP
A LIU_COMMON_CANCER_GENES
A WANG_ER_UP
N LIU_LIVER_CANCER
E Lembcke_Normal vs Adenoma
L Lembcke_Colonc Inflammation
L SPANG_LPS-index2
L SPANG_BCL6-index2



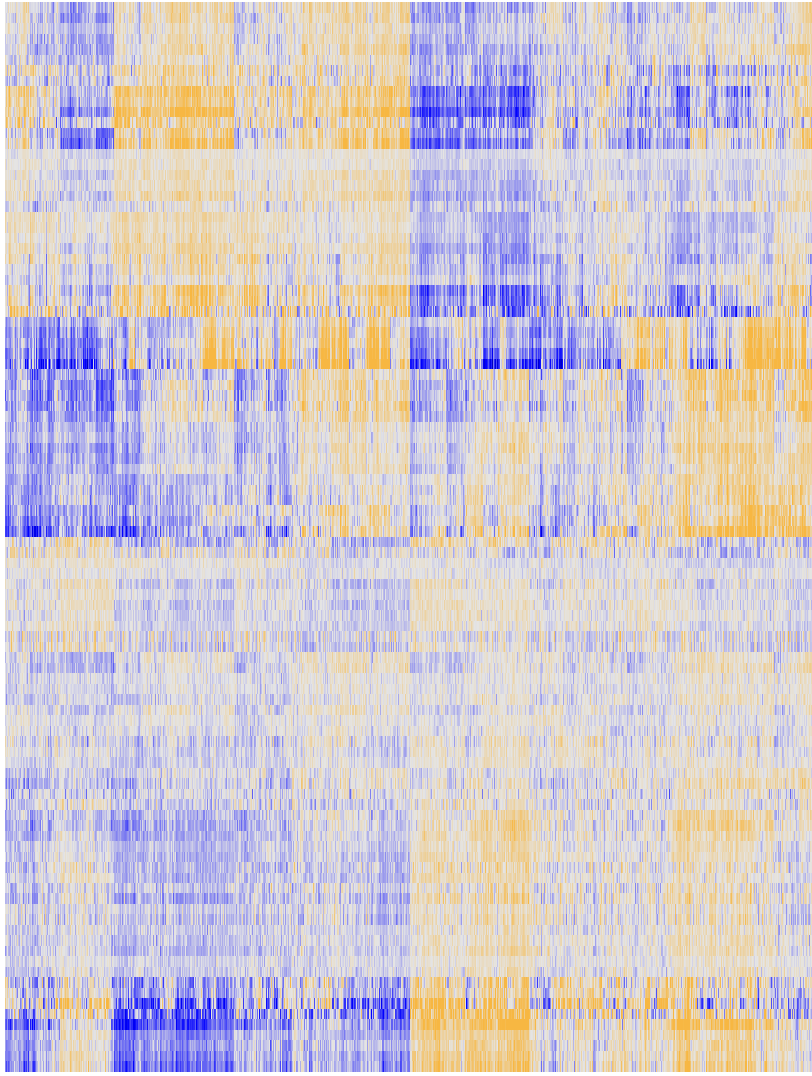
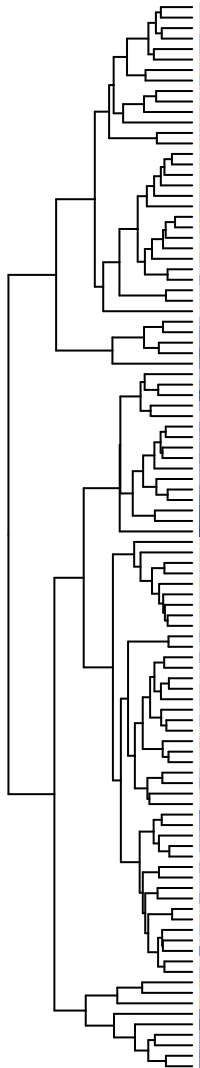
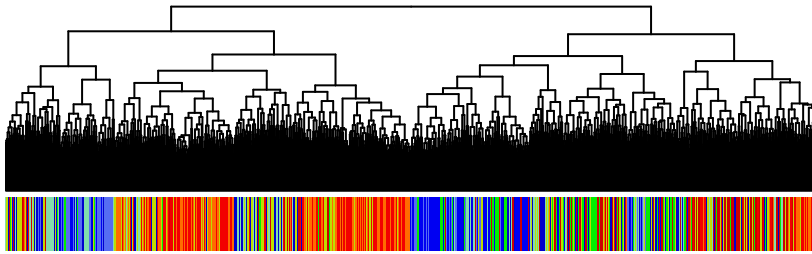
GSZ score

Category Cancer

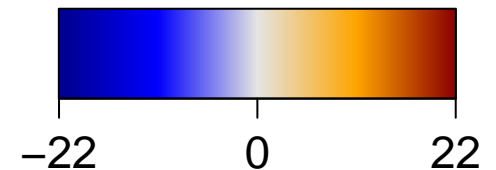


GSZ score

Category CC

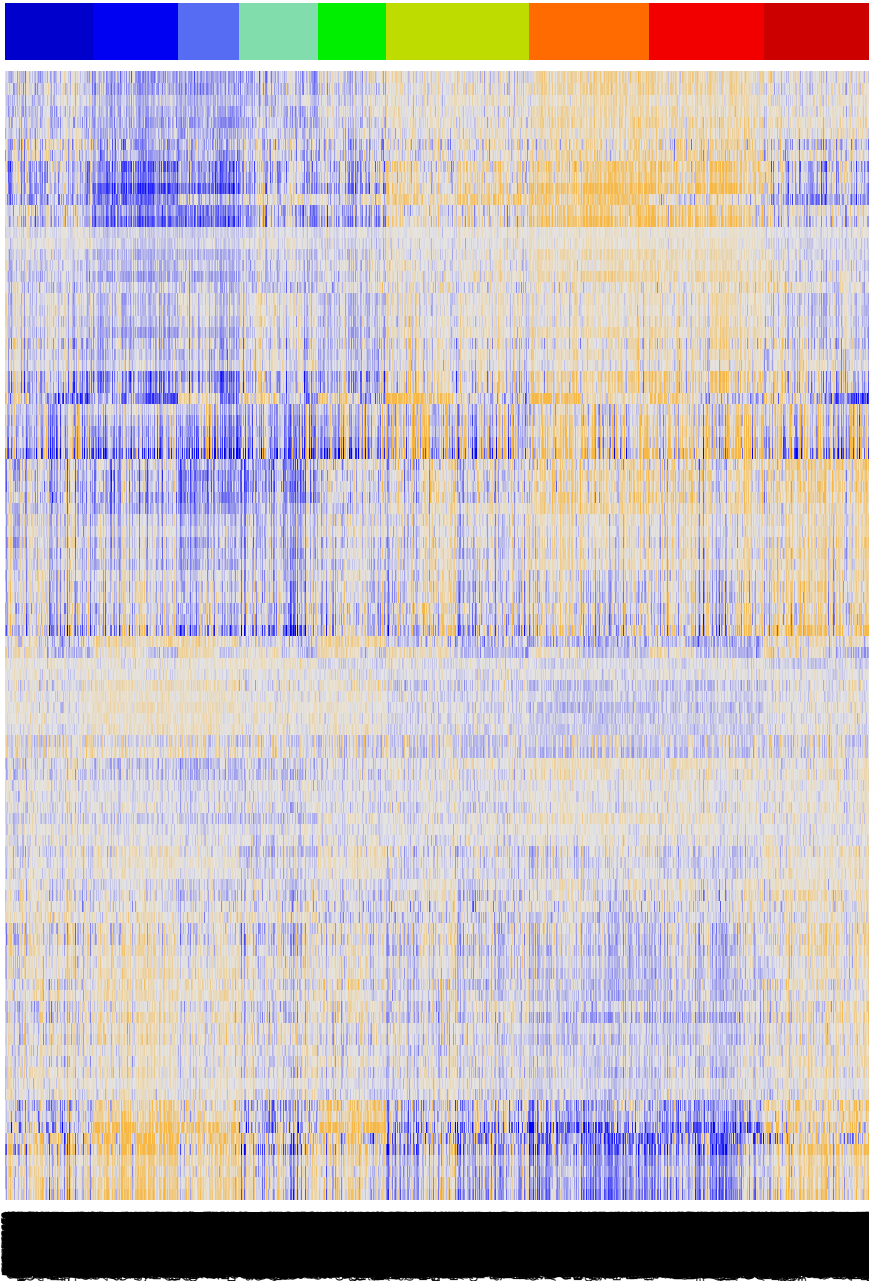


- intracellular ribonucleoprotein complex
- nuclear speck
- cytoplasmic ribonucleoprotein granule
- COP-coated vesicle
- myelin sheath
- external side of plasma membrane
- T cell receptor complex
- immunological synapse
- cytosolic large ribosomal subunit
- ribosome
- nucleolus
- small ribosomal subunit
- nucleus
- nucleoplasm
- pericentriolar material
- chromosome
- Ada2/Gcn5/Ada3 transcription activator complex
- mitochondrial outer membrane translocase complex
- eukaryotic translation initiation factor 3 complex
- extracellular matrix
- small-subunit processome
- SUS preribosome
- mitochondrial large ribosomal subunit
- preribosome, large subunit precursor
- mitochondrial respiratory chain complex I
- proteasome complex
- proteasome core complex
- mitochondrion
- mitochondrial inner membrane
- cytosolic small ribosomal subunit
- endocytic vesicle membrane
- clathrin-coated endocytic vesicle membrane
- ER to Golgi transport vesicle membrane
- luminal component of luminal side of endoplasmic reticulum membrane
- MHC class II protein complex
- focal adhesion
- cytosol
- membrane
- cell-cell adherens junction
- phagocytic vesicle
- trans-Golgi network
- Golgi apparatus
- intracellular membrane-bounded organelle
- endoplasmic reticulum membrane
- cell surface
- lysosome
- lysosomal lumen
- lysosomal membrane
- lysosomal membrane
- extracellular exosome
- Glc complex
- polyosome
- cytosolic ribosome
- aggresome
- apical dendrite
- keratin filament
- endomembrane system
- filamentous actin
- stereocilium bundle
- microvillus filament
- M band
- protein phosphatase type 1 complex
- transport vesicle
- cleavage furrow
- recycling endosome membrane
- endoplasmic reticulum-Golgi intermediate compartment
- ubiquitin ligase complex
- Cul-1-Rbx ubiquitin ligase complex
- protein-DNA complex
- inclusion body
- postynapse
- rough endoplasmic reticulum
- phagocytic cup
- vesicle
- microvillus membrane
- uropod
- mast cell granule
- phagocytic vesicle membrane
- early endosome
- autophagosome membrane
- autophagosome
- secretory granule
- anchored component of membrane
- platelet alpha granule
- platelet alpha granule lumen
- nuclear nucleosome
- nucleosome
- stress fiber
- heterotrimeric G-protein complex
- pseudopodium
- cell
- lipid particle
- platelet alpha granule membrane
- blood microparticle
- cortical cytoskeleton
- specific granule
- plasma membrane
- integral component of plasma membrane
- integral component of membrane
- extracellular region
- extracellular space

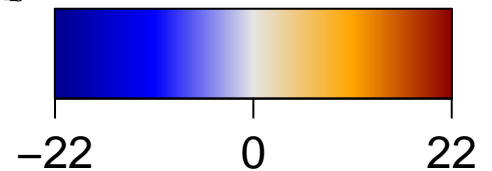


GSZ score

Category CC

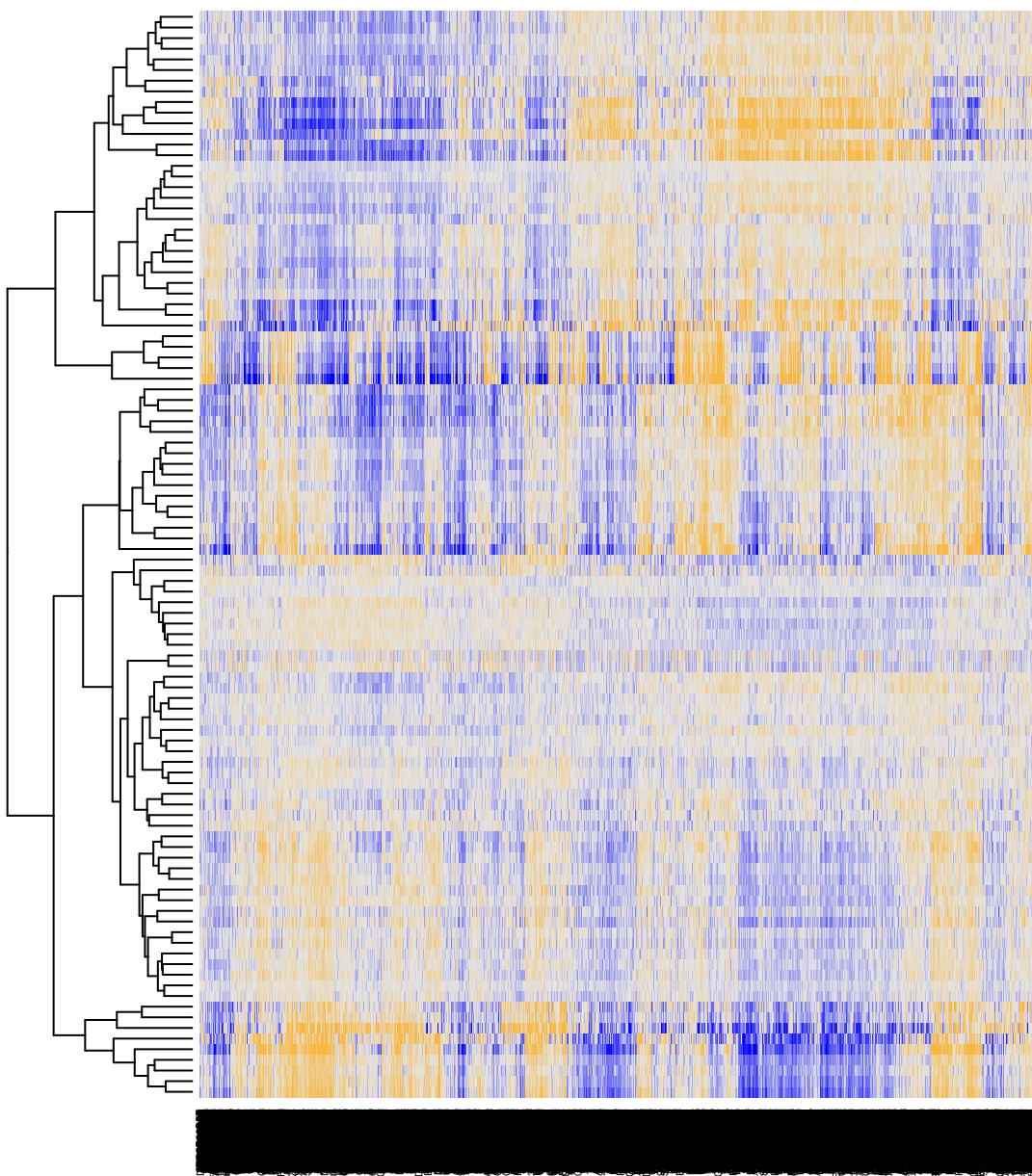


intracellular ribonucleoprotein complex
nuclear speck
cytoplasmic ribonucleoprotein granule
COPII-coated vesicle
myelin sheath
external side of plasma membrane
T cell receptor complex
immunological synapse
cytosolic large ribosomal subunit
ribosome
nucleolus
small ribosomal subunit
nucleus
nucleoplasm
pericentriolar material
chromosome
RNA polymerase II/Ada3 transcription activator complex
mitochondrial outer membrane translocase complex
eukaryotic translation initiation factor 3 complex
extracellular matrix
small-subunit processome
90S preribosome
mitochondrial large ribosomal subunit
preribosome, large subunit precursor
mitochondrial respiratory chain complex I
proteasome complex
proteasome core complex
mitochondrion
mitochondrial inner membrane
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focal adhesion
cytoplasm
cytosol
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phagocytic vesicle
trans-Golgi network
Golgi spherule
intracellular membrane-bounded organelle
endoplasmic reticulum membrane
cell surface
lysosome
lysosomal lumen
late endosome membrane
lysosomal membrane
extracellular exosome
TORC2 complex
polyome
cytosolic ribosome
aggresome
apical dendrite
keratin filament
endomembrane system
filamentous actin
stereocilium bundle
myosin filament
M band
protein phosphatase type 1 complex
transport vesicle
cleavage furrow
recycling endosome membrane
endoplasmic reticulum-Golgi intermediate compartment
ubiquitin ligase complex
Golgi-Ringo ubiquitin ligase complex
protein-DNA complex
inclusion body
postsynapse
rough endoplasmic reticulum
phagocytic cup
vesicle
microvillus membrane
uropod
mast cell granule
phagocytic vesicle membrane
early endosome
autophagosome membrane
autophagosome
secretory granule
anchored component of membrane
platelet alpha granule
platelet alpha granule lumen
nuclear nucleosome
nucleosome
stress fiber
heterotrimeric G-protein complex
pseudopodium
cell
lipid particle
platelet alpha granule membrane
blood microparticle
cortical cytoskeleton
specific granule
plasma membrane
integral component of plasma membrane
integral component of membrane
extracellular region
extracellular space

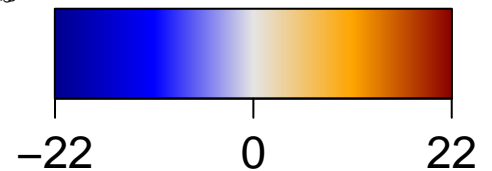


GSZ score

Category CC

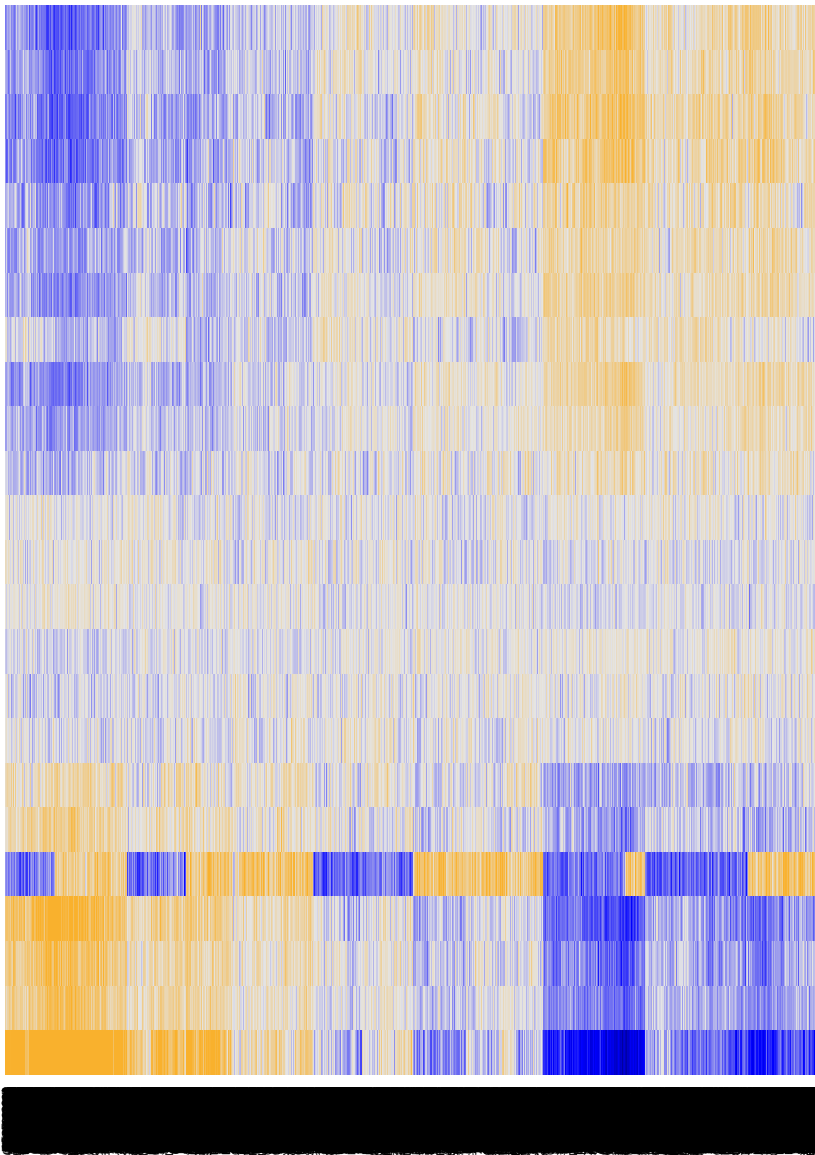
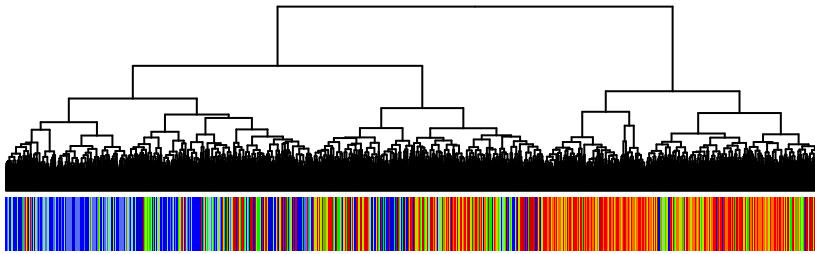


- intracellular ribonucleoprotein complex
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- COPII-coated vesicle
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- external side of plasma membrane
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- extracellular exosome
- TORC2 complex
- polyome
- cytosolic ribosome
- aggresome
- apical dendrite
- keratin filament
- endomembrane system
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- stereocilium bundle
- myosin filament
- M-band
- protein phosphatase type 1 complex
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- ubiquitin ligase complex
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- pseudopodium
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- lipid particle
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- blood microparticle
- cortical cytoskeleton
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- integral component of membrane
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- extracellular space

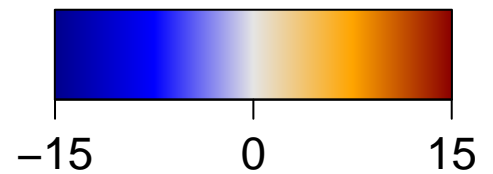


GSZ score

Category Chr

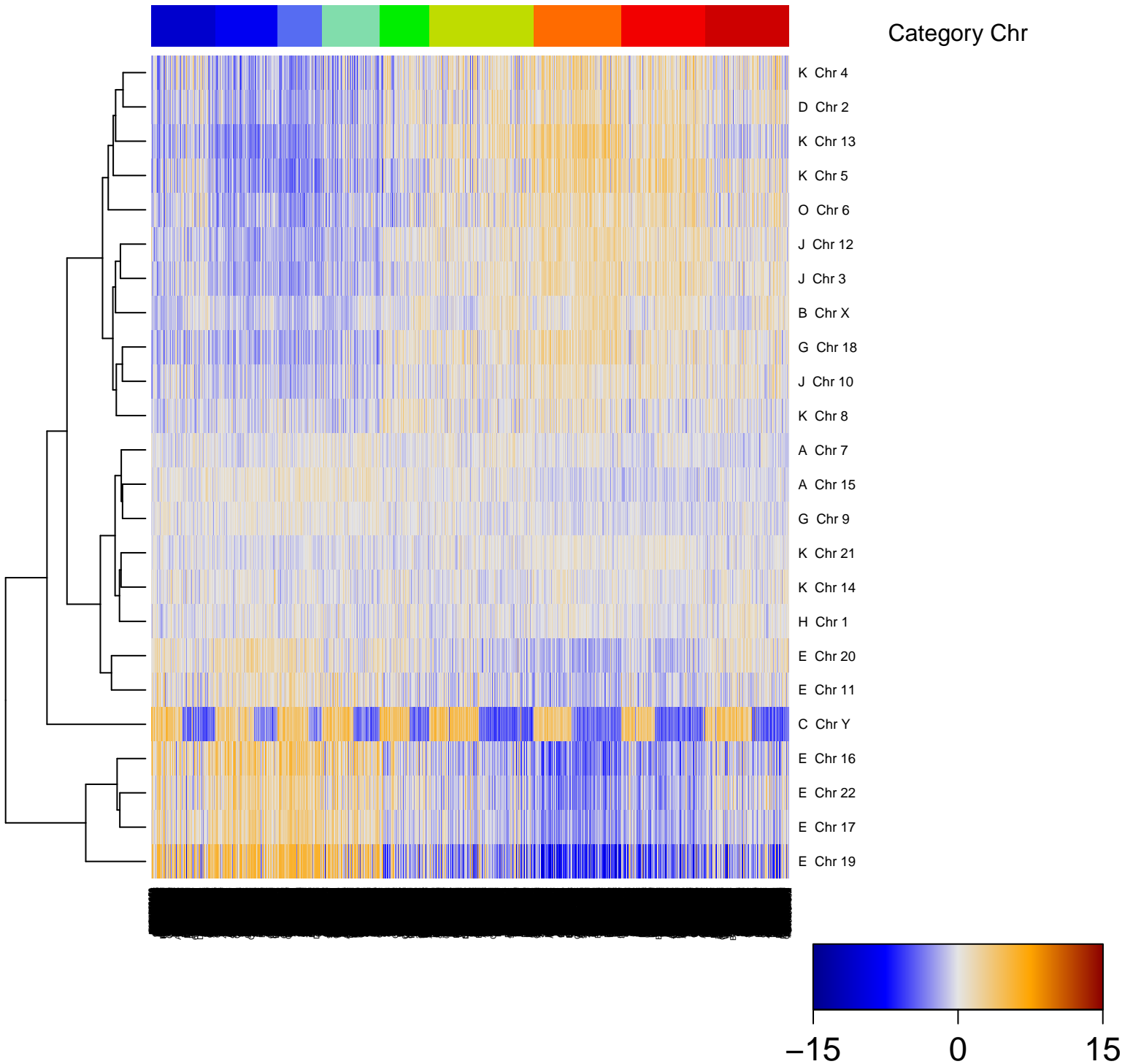


K Chr 4
D Chr 2
K Chr 13
K Chr 5
O Chr 6
J Chr 12
J Chr 3
B Chr X
G Chr 18
J Chr 10
K Chr 8
A Chr 7
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E Chr 20
E Chr 11
C Chr Y
E Chr 16
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E Chr 17
E Chr 19



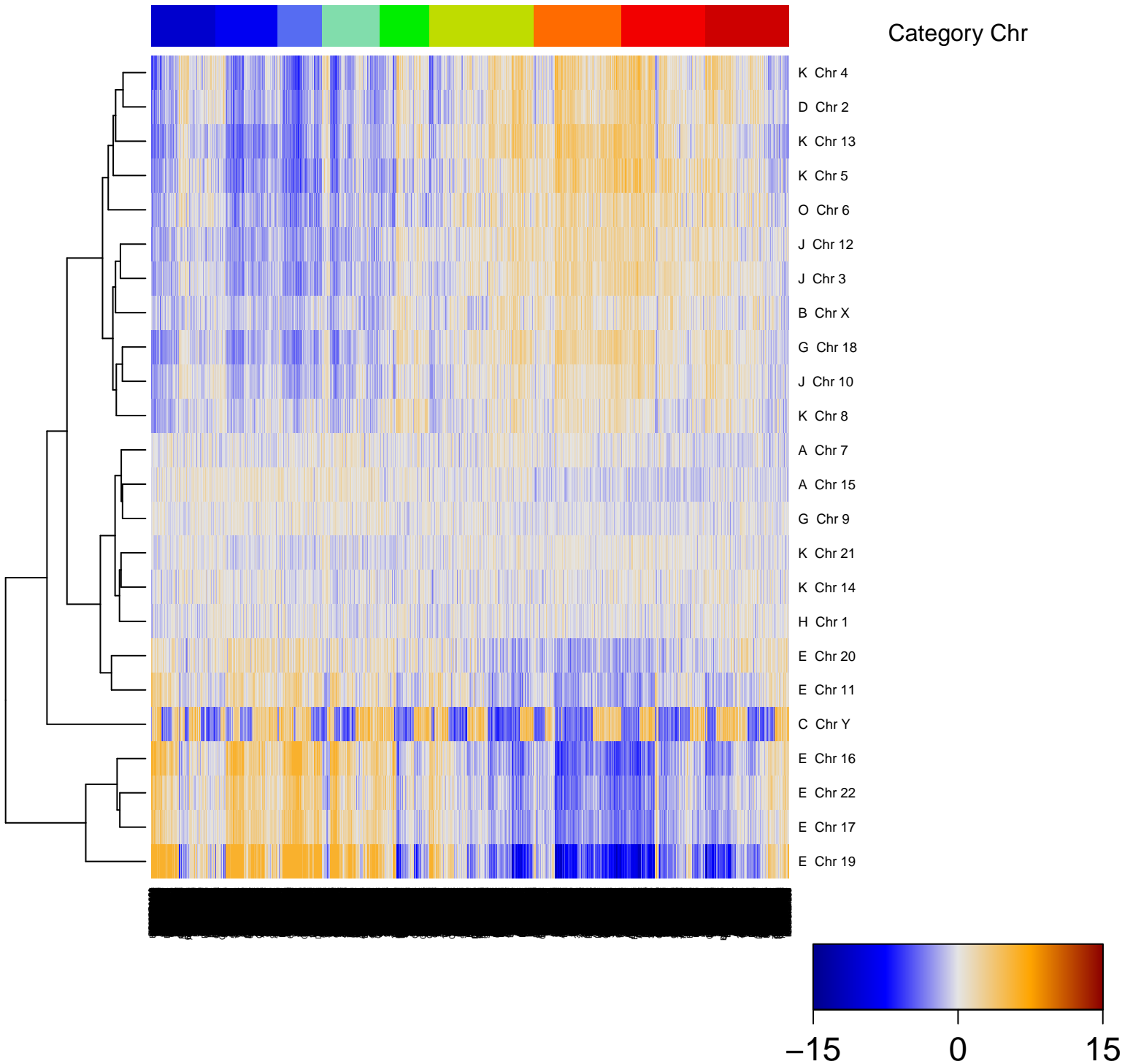
GSZ score

Category Chr



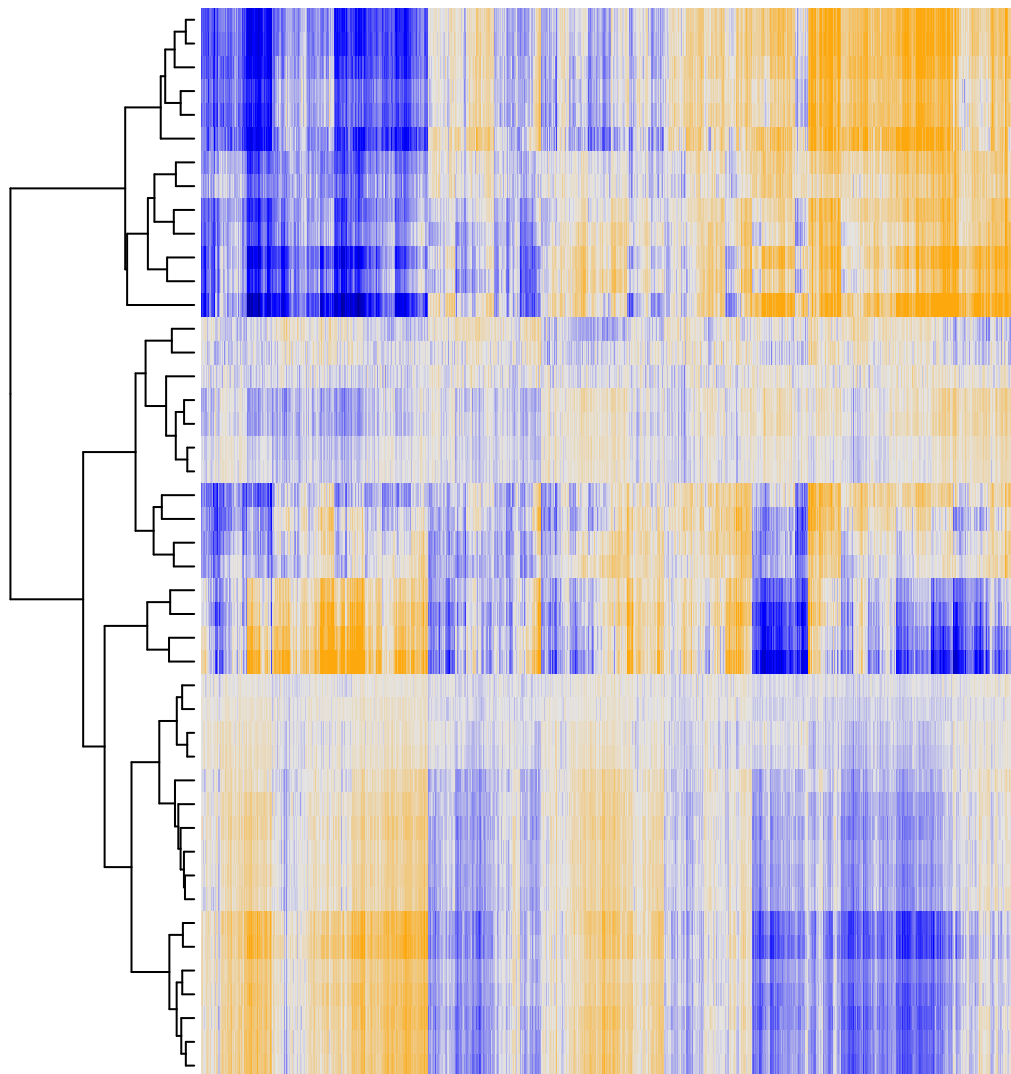
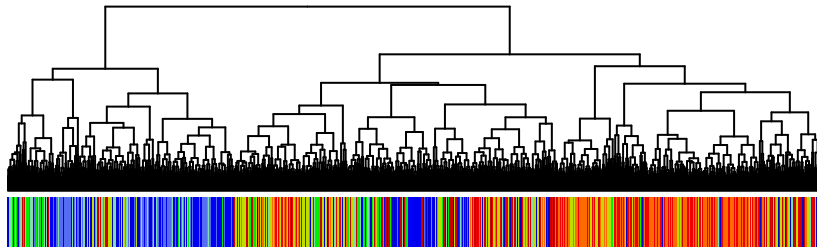
GSZ score

Category Chr

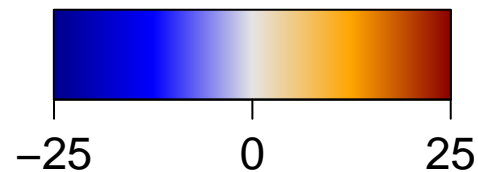


GSZ score

Category Chromatin states

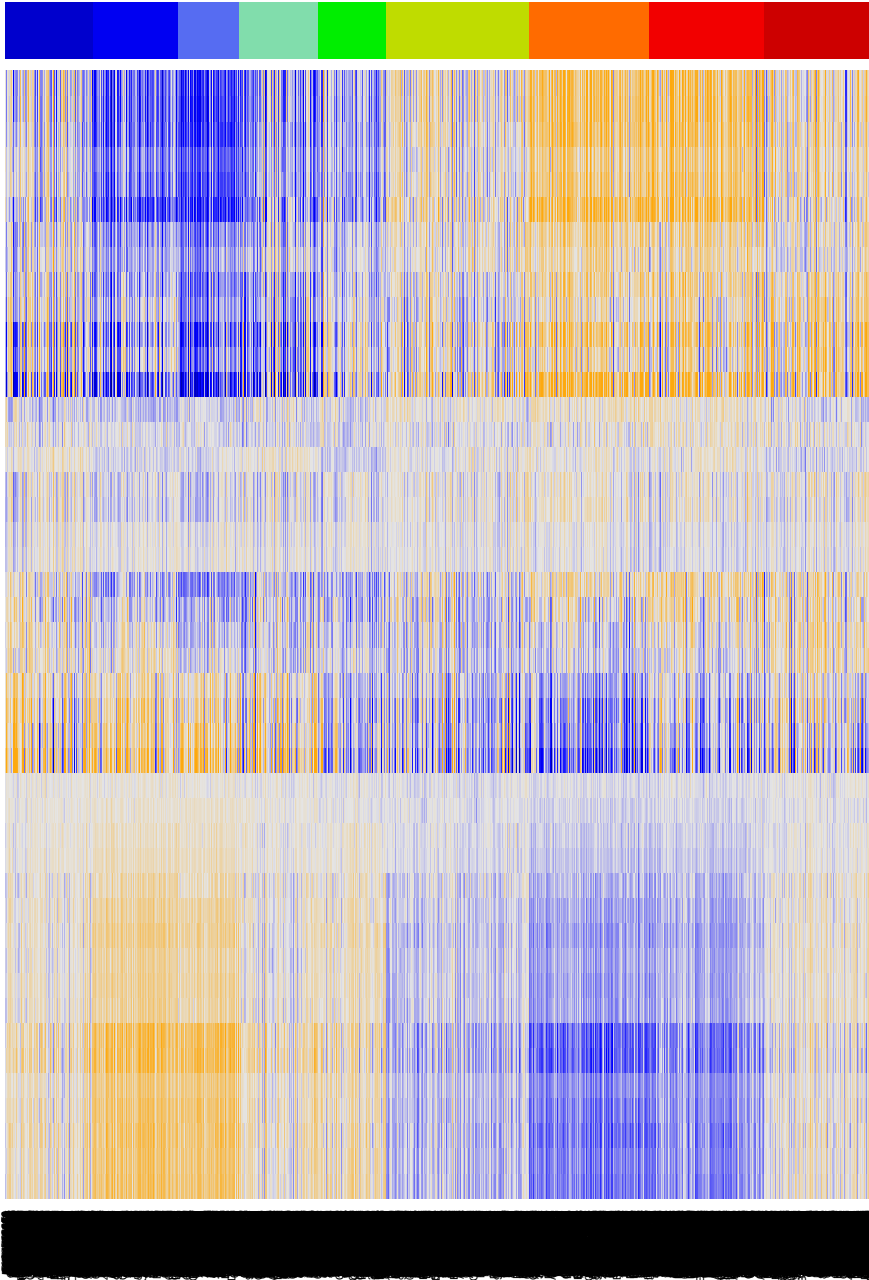


- K 5_Tx_Melanocytes
- K 5_Tx_Fibroblasts
- E 2_TssA_Fibroblasts
- E 2_TssA_Neural_Progenitor
- E 2_TssA_Melanocytes
- K 5_Tx_Neural_Progenitor
- K 14_ZNF_Neural_Progenitor
- K 14_ZNF_Melanocytes
- K 15_Quies_Neural_Progenitor
- K 7_Enh_Melanocytes
- K 15_Quies_Melanocytes
- K 7_Enh_Fibroblasts
- K 15_Quies_Fibroblasts
- G 4_TxTrans_Neural_Progenitor
- C 6_EnhG_Neural_Progenitor
- A 14_ZNF_Fibroblasts
- O 13_HetRpts_Neural_Progenitor
- O 12_Het_Neural_Progenitor
- H 13_HetRpts_Melanocytes
- H 12_Het_Melanocytes
- E 3_TssF_Melanocytes
- E 6_EnhG_Melanocytes
- E 3_TssF_Fibroblasts
- E 7_Enh_Neural_Progenitor
- E 3_TssF_Neural_Progenitor
- E 6_EnhG_Fibroblasts
- E 4_TxTrans_Melanocytes
- E 4_TxTrans_Fibroblasts
- O 11_K9K27me3_Neural_Progenitor
- H 11_K9K27me3_Fibroblasts
- H 13_HetRpts_Fibroblasts
- H 12_Het_Fibroblasts
- N 9_ReprPCWk_Neural_Progenitor
- H 11_K9K27me3_Melanocytes
- H 1_TssP_Melanocytes
- N 8_EnhP_Neural_Progenitor
- H 10_ReprPC_Neural_Progenitor
- H 1_TssP_Neural_Progenitor
- H 10_ReprPC_Fibroblasts
- H 8_EnhP_Fibroblasts
- H 8_EnhP_Melanocytes
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- H 10_ReprPC_Melanocytes
- H 9_ReprPCWk_Melanocytes

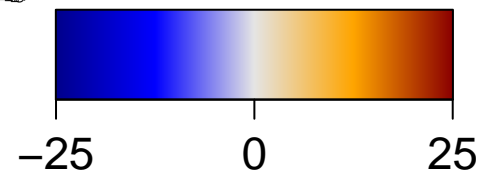


GSZ score

Category Chromatin states

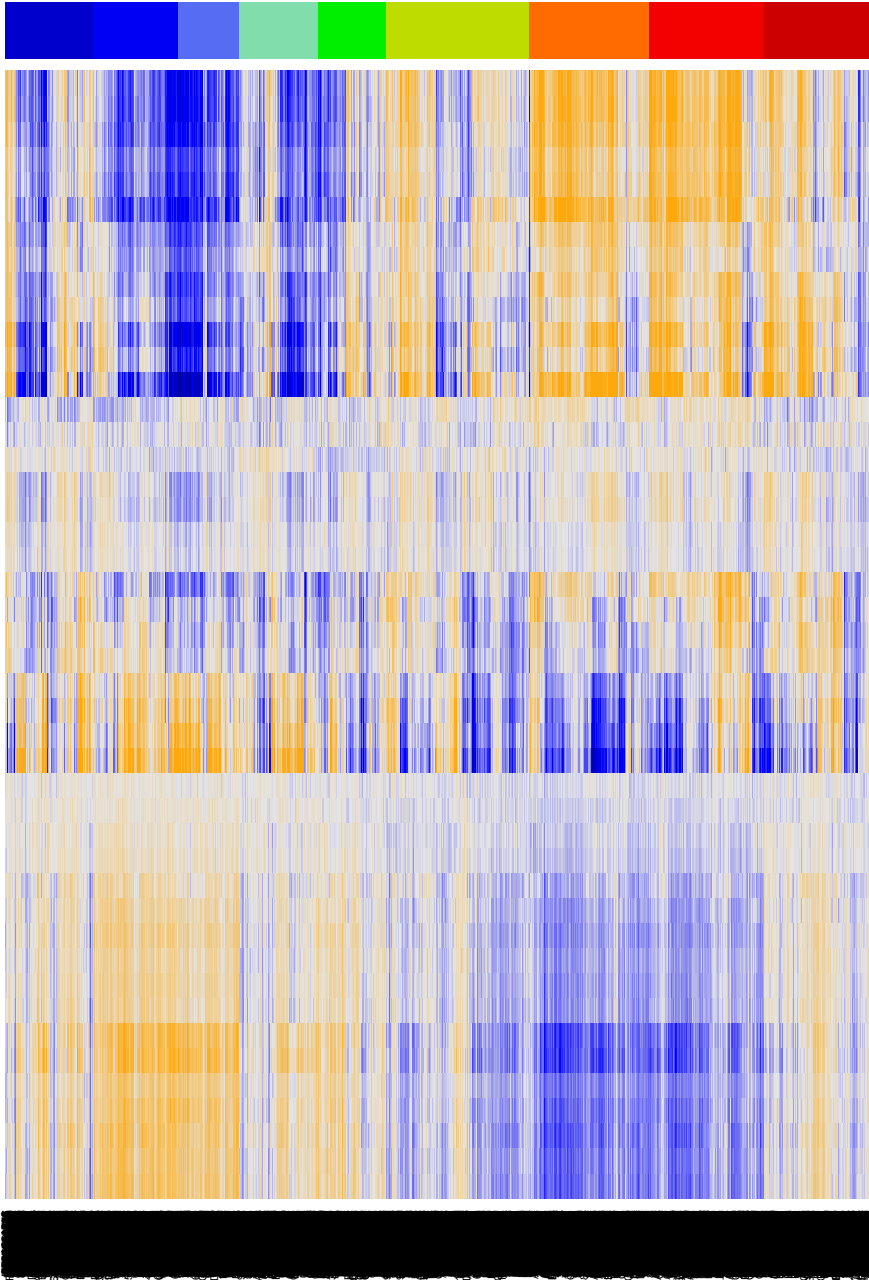


K 5_Tx_Melanocytes
K 5_Tx_Fibroblasts
E 2_TssA_Fibroblasts
E 2_TssA_Neural_Progenitor
E 2_TssA_Melanocytes
K 5_Tx_Neural_Progenitor
K 14_ZNF_Neural_Progenitor
K 14_ZNF_Melanocytes
K 15_Quies_Neural_Progenitor
K 7_Enh_Melanocytes
K 15_Quies_Melanocytes
K 7_Enh_Fibroblasts
K 15_Quies_Fibroblasts
G 4_TxTrans_Neural_Progenitor
C 6_EnhG_Neural_Progenitor
A 14_ZNF_Fibroblasts
O 13_HetRpts_Neural_Progenitor
O 12_Het_Neural_Progenitor
H 13_HetRpts_Melanocytes
H 12_Het_Melanocytes
E 3_TssF_Melanocytes
E 6_EnhG_Melanocytes
E 3_TssF_Fibroblasts
E 7_Enh_Neural_Progenitor
E 3_TssF_Neural_Progenitor
E 6_EnhG_Fibroblasts
E 4_TxTrans_Melanocytes
E 4_TxTrans_Fibroblasts
O 11_K9K27me3_Neural_Progenitor
H 11_K9K27me3_Fibroblasts
H 13_HetRpts_Fibroblasts
H 12_Het_Fibroblasts
N 9_ReprPCWk_Neural_Progenitor
H 11_K9K27me3_Melanocytes
H 1_TssP_Melanocytes
N 8_EnhP_Neural_Progenitor
H 10_ReprPC_Neural_Progenitor
H 1_TssP_Neural_Progenitor
H 10_ReprPC_Fibroblasts
H 8_EnhP_Fibroblasts
H 8_EnhP_Melanocytes
H 1_TssP_Fibroblasts
H 9_ReprPCWk_Fibroblasts
H 10_ReprPC_Melanocytes
H 9_ReprPCWk_Melanocytes

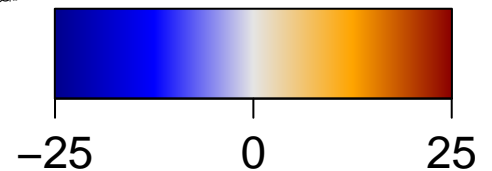


GSZ score

Category Chromatin states

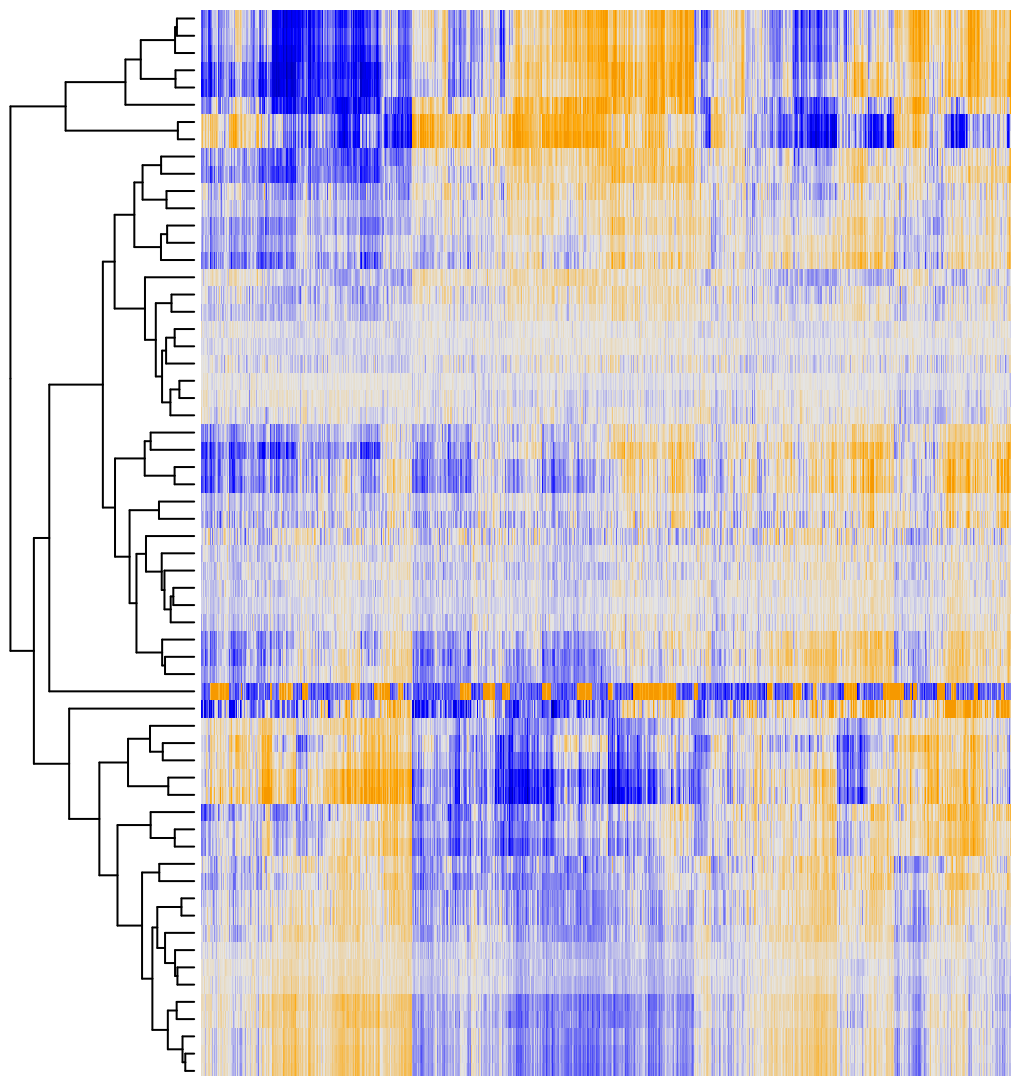
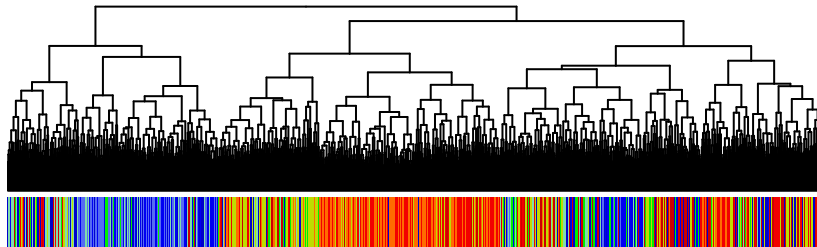


K 5_Tx_Melanocytes
K 5_Tx_Fibroblasts
E 2_TssA_Fibroblasts
E 2_TssA_Neural_Progenitor
E 2_TssA_Melanocytes
K 5_Tx_Neural_Progenitor
K 14_ZNF_Neural_Progenitor
K 14_ZNF_Melanocytes
K 15_Quies_Neural_Progenitor
K 7_Enh_Melanocytes
K 15_Quies_Melanocytes
K 7_Enh_Fibroblasts
K 15_Quies_Fibroblasts
G 4_TxTrans_Neural_Progenitor
C 6_EnhG_Neural_Progenitor
A 14_ZNF_Fibroblasts
O 13_HetRpts_Neural_Progenitor
O 12_Het_Neural_Progenitor
H 13_HetRpts_Melanocytes
H 12_Het_Melanocytes
E 3_TssF_Melanocytes
E 6_EnhG_Melanocytes
E 3_TssF_Fibroblasts
E 7_Enh_Neural_Progenitor
E 3_TssF_Neural_Progenitor
E 6_EnhG_Fibroblasts
E 4_TxTrans_Melanocytes
E 4_TxTrans_Fibroblasts
O 11_K9K27me3_Neural_Progenitor
H 11_K9K27me3_Fibroblasts
H 13_HetRpts_Fibroblasts
H 12_Het_Fibroblasts
N 9_ReprPCWk_Neural_Progenitor
H 11_K9K27me3_Melanocytes
H 1_TssP_Melanocytes
N 8_EnhP_Neural_Progenitor
H 10_ReprPC_Neural_Progenitor
H 1_TssP_Neural_Progenitor
H 10_ReprPC_Fibroblasts
H 8_EnhP_Fibroblasts
H 8_EnhP_Melanocytes
H 1_TssP_Fibroblasts
H 9_ReprPCWk_Fibroblasts
H 10_ReprPC_Melanocytes
H 9_ReprPCWk_Melanocytes

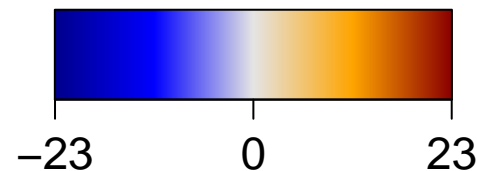


GSZ score

Category Colon Cancer

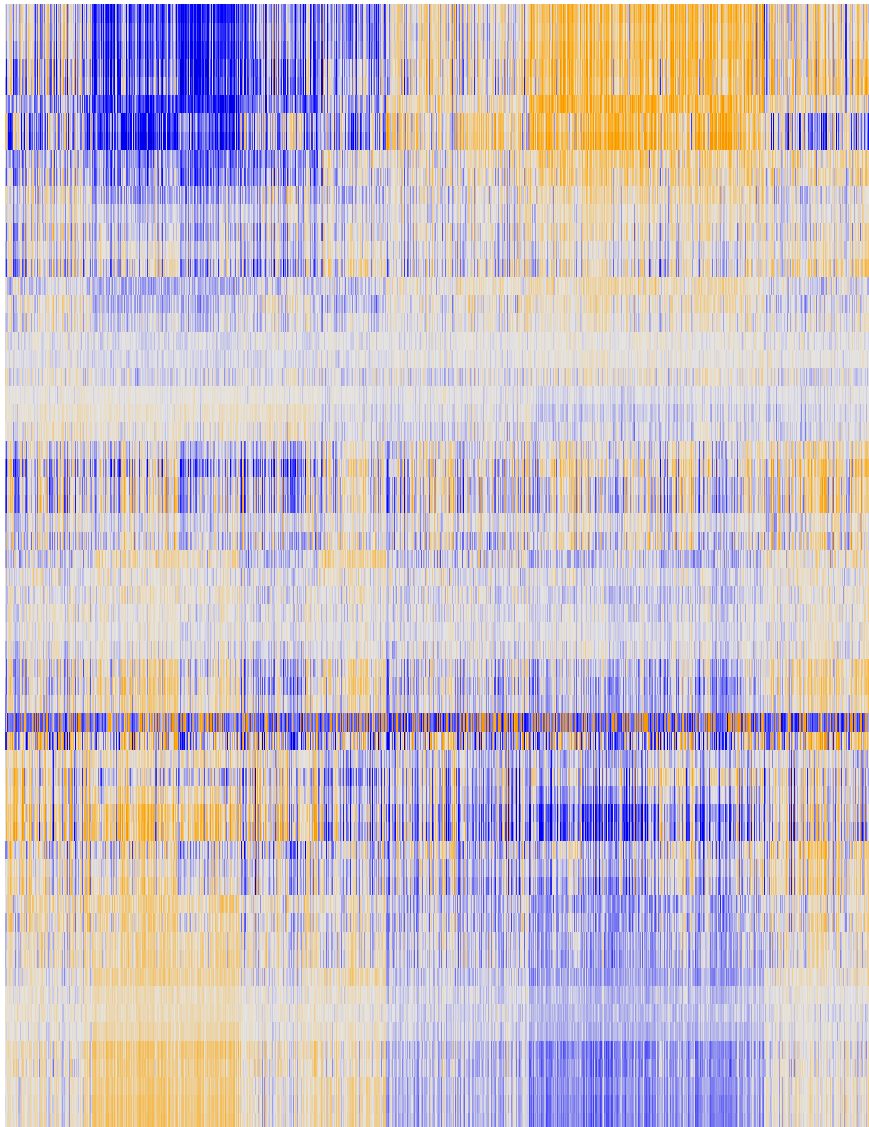
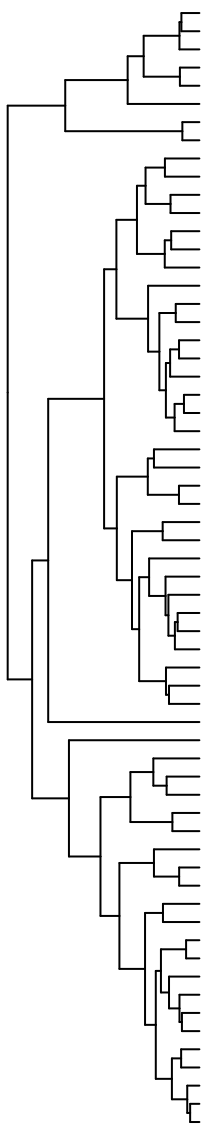


E TssA_Colon
E Tx_Colon
K TxWk_Colon
K Quies3_Colon
K TssWk_Colon
K LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending_colon_
I Pentrack_CRC_TCGA_corr_R_normal_DN
J Pentrack_CRC_TCGA_group.over_C_normal_DN
N LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending_colon_
K TssD1_Colon
K LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_transvers
K LaPointe_mucosa-position_kmeans_O_transverse_colon_UP_
K LaPointe_mucosa-position_kmeans_D_transverse_colon_UP_
M LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
N Quies1_Colon
J Kosinski_lower-crypt-long-list
A ZNF_Colon
O Het_Colon
H Kaneda_CIMP-group1
A Hewish_dMMR-secondary-mutations_Transcriptional_regulation
N Marisa_CRC-cluster-c
D TCGA_Mutated-in-CRC_mismatch-repair-genes
D Hewish_dMMR-secondary-mutations_DNA-repair
A LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending_colon_
L Marisa_CRC-cluster-a
K LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum_colon_
L Pentrack_CRC_TCGA_group.over_B_msi-h_UP
L Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
L TCGA-CRC_less-aggressive-disease-markers
L Marisa_CRC-cluster-g
N Marisa_CRC-C6
N Budinska_E_Mixed_UP
O Pentrack_CRC_TCGA_group.over_A_normal_UP
A Budinska_D_Mesenchymal_DOWN
M Hewish_dMMR-secondary-mutations_Apoptosis
A Hewish_dMMR-secondary-mutations_Cell-motility
N EnhWk2_Colon
C Pentrack_CRC_TCGA_corr_C_normal_UP
O Kosinski_top-crypt-long-list
A Juehling_HNPCC-mutated-in-6-to-8
L Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
E TxEnhG2_Colon
E TssF_Colon
E TssD2_Colon
E EnhA_Colon
E TxEnhG1_Colon
E LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending_colon_
E EnhWk1_Colon
E Enh_Colon
A LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse_colon_
O LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecum co
L Ang_CRC_Hypomethylated
L Ang_CRC-CIMPH-vs-L_hypo
B Lembcke_TCGA-expr_kmeans_L_CIMP.H_UP_Cluster4_DN
C Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
D Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
B Lembcke_TCGA-expr_kmeans_M_CIMP.H_DN
N EnhP_Colon
C Lembcke_TCGA-expr_kmeans_H_CIMP.H_UP_Cluster3_DN
N ReprPCWk_Colon
N TssP_Colon
N ReprPC_Colon

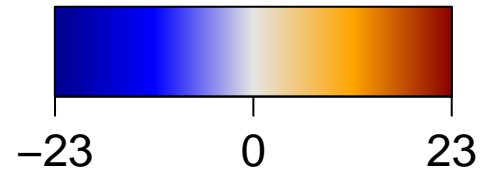


GSZ score

Category Colon Cancer

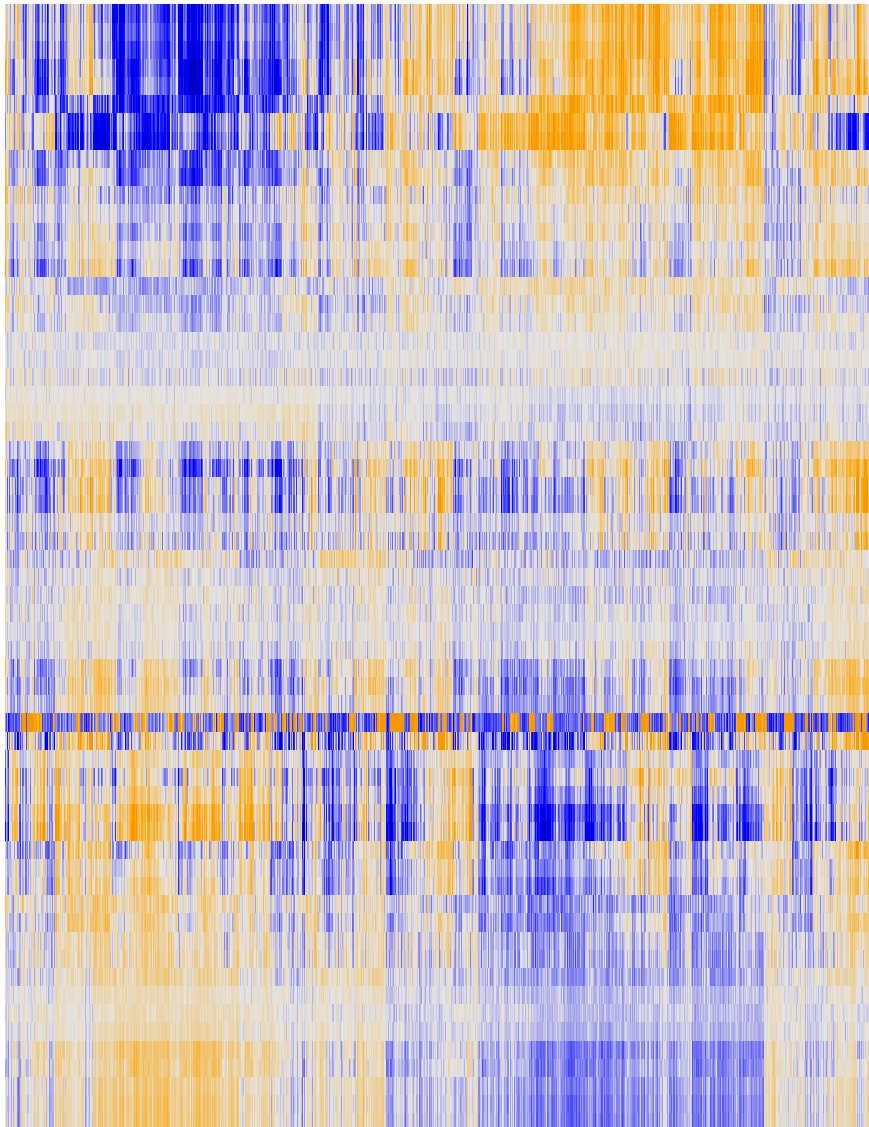
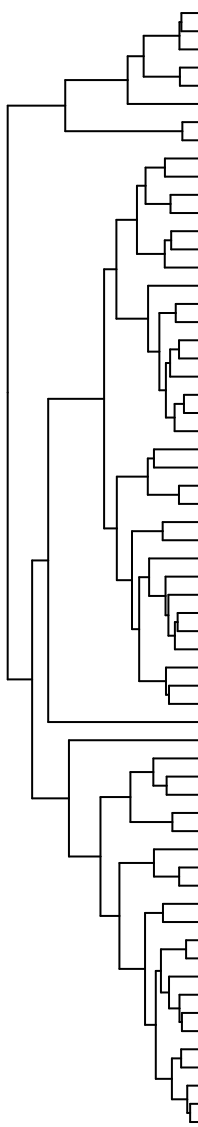


- E TssA_Colon
- E Tx_Colon
- K TxWk_Colon
- K Quies3_Colon
- K TssWk_Colon
- K LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending co
- I Pentrack_CRC_TCGA_corr_R_normal_DN
- J Pentrack_CRC_TCGA_group.over_C_normal_DN
- N LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending co
- K TssD1_Colon
- K LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_trans
- K LaPointe_mucosa-position_kmeans_O_transverse_colon_UP_
- K LaPointe_mucosa-position_kmeans_D_transverse_colon_UP_
- M LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
- N Quies1_Colon
- J Kosinski_lower-crypt-long-list
- A ZNF_Colon
- O Het_Colon
- H Kaneda_CIMP-group1
- A Hewish_dMMR-secondary-mutations_Transcriptional_regulation
- N Marisa_CRC-cluster-c
- D TCGA_Mutated-in-CRC_mismatch-repair-genes
- D Hewish_dMMR-secondary-mutations_DNA-repair
- A LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending co
- L Marisa_CRC-cluster-a
- K LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum co
- L Pentrack_CRC_TCGA_group.over_B_msi-h_UP
- L Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
- L TCGA-CRC_less-aggressive-disease-markers
- L Marisa_CRC-cluster-g
- N Marisa_CRC-C6
- N Budinska_E_Mixed_UP
- O Pentrack_CRC_TCGA_group.over_A_normal_UP
- A Budinska_D_Mesenchymal_DOWN
- M Hewish_dMMR-secondary-mutations_Apoptosis
- A Hewish_dMMR-secondary-mutations_Cell-motility
- N EnhWk2_Colon
- C Pentrack_CRC_TCGA_corr_C_normal_UP
- O Kosinski_top-crypt-long-list
- A Juehling_HNPCC-mutated-in-6-to-8
- L Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
- E TxEnhG2_Colon
- E TssF_Colon
- E TssD2_Colon
- E EnhA_Colon
- E TxEnhG1_Colon
- E LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending co
- E EnhWk1_Colon
- E Enh_Colon
- A LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse co
- O LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecu
- L Ang_CRC_Hypomethylated
- L Ang_CRC-CIMPH-vs-L_hypo
- B Lembcke_TCGA-expr_kmeans_L_CIMP.H_UP_Cluster4_DN
- C Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
- D Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
- B Lembcke_TCGA-expr_kmeans_M_CIMP.H_DN
- N EnhP_Colon
- C Lembcke_TCGA-expr_kmeans_H_CIMP.H_UP_Cluster3_DN
- N ReprPCWk_Colon
- N TssP_Colon
- N ReprPC_Colon

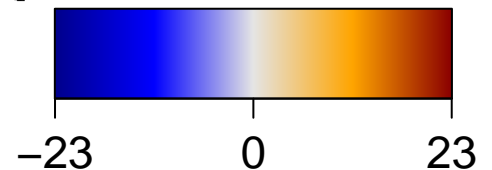


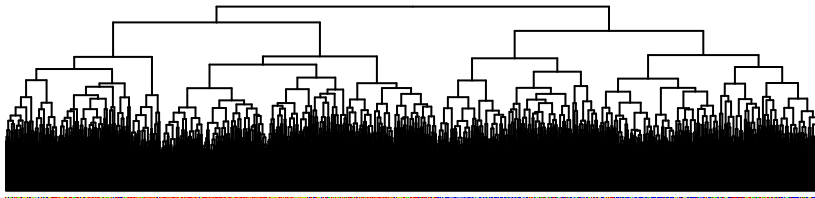
GSZ score

Category Colon Cancer



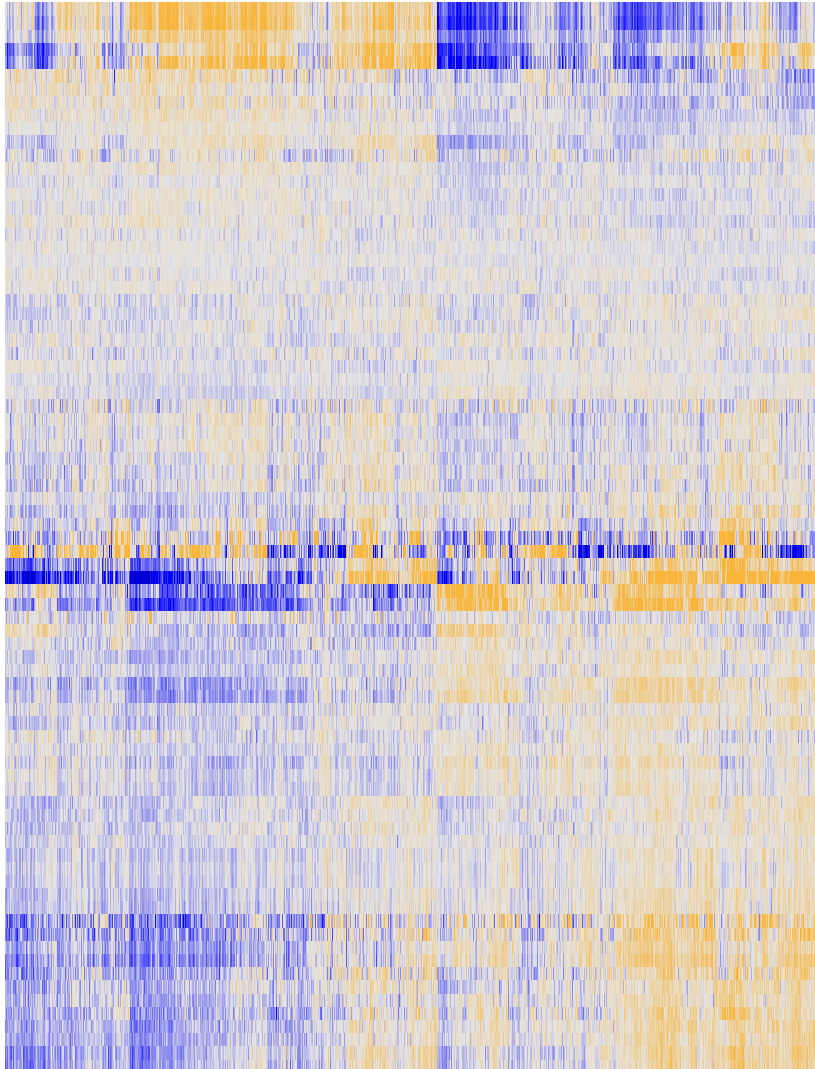
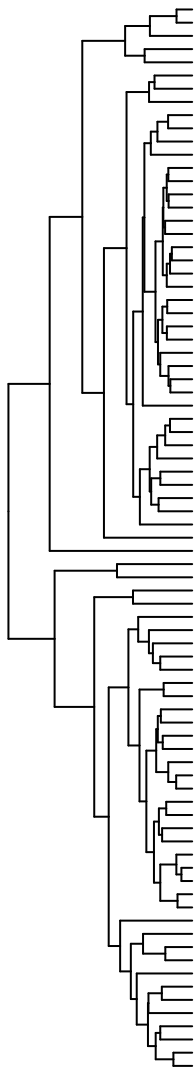
- E TssA_Colon
- E Tx_Colon
- K TxWk_Colon
- K Quies3_Colon
- K TssWk_Colon
- K LaPointe_mucosa-position_kmeans_N_cecum_colon_ascending co
- I Pentrack_CRC_TCGA_corr_R_normal_DN
- J Pentrack_CRC_TCGA_group.over_C_normal_DN
- N LaPointe_mucosa-position_kmeans_H_cecum_colon_ascending co
- K TssD1_Colon
- K LaPointe_mucosa-position_kmeans_E_transverse_colon_UP_trans
- K LaPointe_mucosa-position_kmeans_O_transverse_colon_UP_
- K LaPointe_mucosa-position_kmeans_D_transverse_colon_UP_
- M LaPointe_mucosa-position_kmeans_A_ascending_colon_UP_
- N Quies1_Colon
- J Kosinski_lower-crypt-long-list
- A ZNF_Colon
- O Het_Colon
- H Kaneda_CIMP-group1
- A Hewish_dMMR-secondary-mutations_Transcriptional_regulation
- N Marisa_CRC-cluster-c
- D TCGA_Mutated-in-CRC_mismatch-repair-genes
- D Hewish_dMMR-secondary-mutations_DNA-repair
- A LaPointe_mucosa-position_kmeans_C_cecum_colon_ascending co
- L Marisa_CRC-cluster-a
- K LaPointe_mucosa-position_kmeans_L_transverse_colon_cecum co
- L Pentrack_CRC_TCGA_group.over_B_msi-h_UP
- L Pentrack_CRC_TCGA_corr_J_msi-h_UP_mss_DN
- L TCGA-CRC_less-agressive-disease-markers
- L Marisa_CRC-cluster-g
- N Marisa_CRC-C6
- N Budinska_E_Mixed_UP
- O Pentrack_CRC_TCGA_group.over_A_normal_UP
- A Budinska_D_Mesenchymal_DOWN
- M Hewish_dMMR-secondary-mutations_Apoptosis
- A Hewish_dMMR-secondary-mutations_Cell-motility
- N EnhWk2_Colon
- C Pentrack_CRC_TCGA_corr_C_normal_UP
- O Kosinski_top-crypt-long-list
- A Juehling_HNPCC-mutated-in-6-to-8
- L Lembcke_TCGA-expr_kmeans_E_CIMP.H_UP_Cluster4_DN
- E TxEnhG2_Colon
- E TssF_Colon
- E TssD2_Colon
- E EnhA_Colon
- E TxEnhG1_Colon
- E LaPointe_mucosa-position_kmeans_J_cecum_colon_ascending co
- E EnhWk1_Colon
- E Enh_Colon
- A LaPointe_mucosa-position_kmeans_F_cecum_colon_transverse co
- O LaPointe_mucosa-position_kmeans_K_transverse_colon_UP_cecu
- L Ang_CRC_Hypomethylated
- L Ang_CRC-CIMPH-vs-L_hypo
- B Lembcke_TCGA-expr_kmeans_L_CIMP.H_UP_Cluster4_DN
- C Lembcke_TCGA_meth_kmeans_B_Cluster4_DN
- D Lembcke_TCGA_meth_kmeans_J_CIMP.H_DN
- B Lembcke_TCGA-expr_kmeans_M_CIMP.H_DN
- N EnhP_Colon
- C Lembcke_TCGA-expr_kmeans_H_CIMP.H_UP_Cluster3_DN
- N ReprPCWk_Colon
- N TssP_Colon
- N ReprPC_Colon



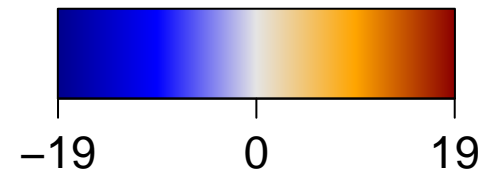


GSZ score

Category Glio

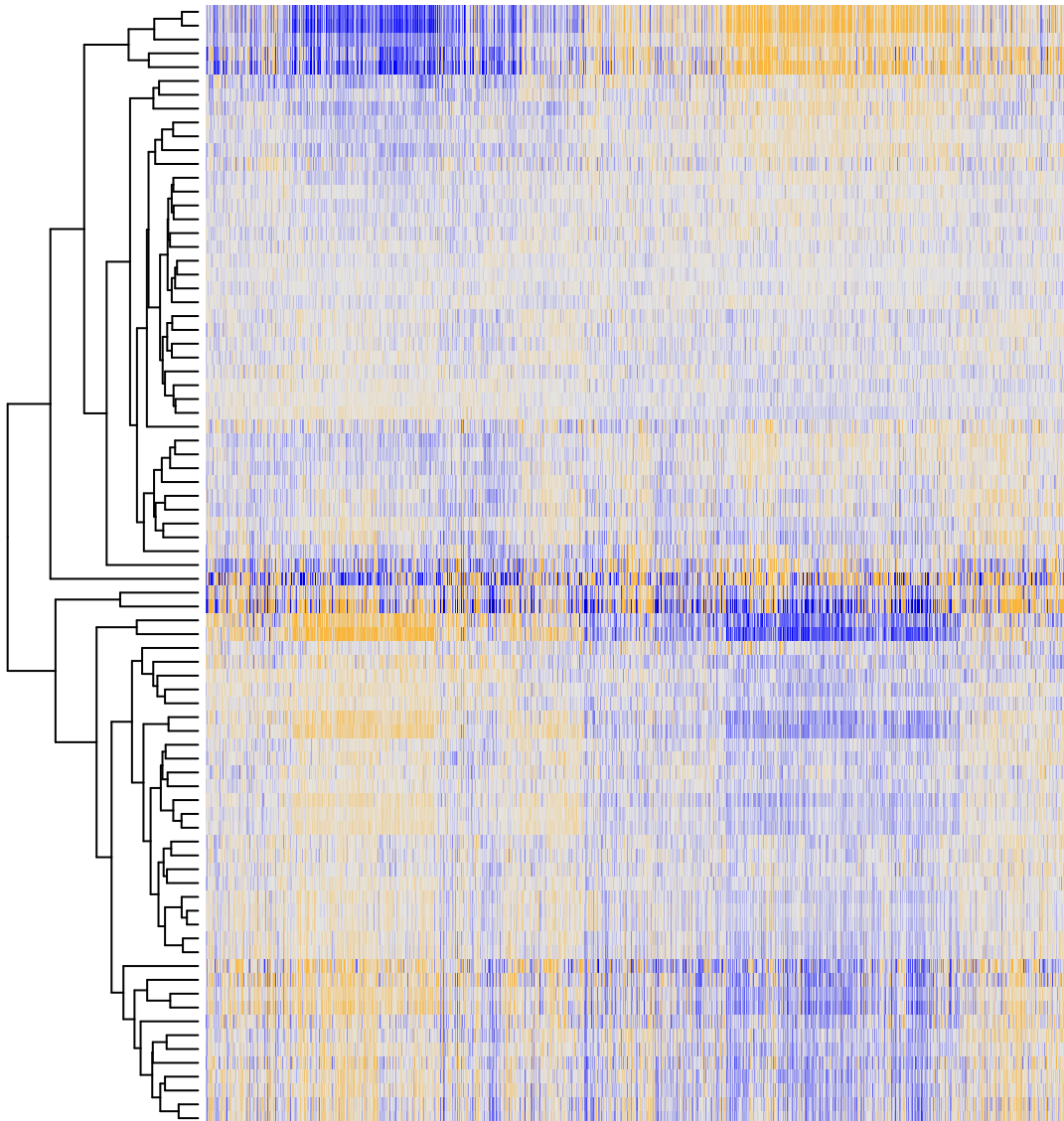


- K Hopp Sturm_GBM_Epi3_no_zentr.6_fetus_UP
- K Hopp Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
- K Sturm_GBM_Meth_overexpression_E_G34_UP
- M Up
- M WILLSCHER_GBM_Verhaak-PNwt & CL_up
- C Stuehler_Proteins_up_in_STS
- C Down_b
- D Donson-adaptive-immunity-associated with LTS in HGA
- D WILLSCHER_GBM_Verhaak-PNwt & MES_up
- A WILLSCHER_GBM_LTSmut_proteomics-A_UP
- O Vishal_subnetwork signature of survival in GBM
- H Donson-chemokine/cytokine-receptors-associated with LTS in HGA
- A Sturm_GBM_Meth_overexpression_G_IDH_UP
- N VERHAAK_CL subtype
- J Weller_LGG_A_vs_O_DOWN
- K Phillips Prolif up vs PN & MES
- K Sturm_GBM_Meth_overexpression_H_K27_UP
- Barbus_GBM_STS_vs_LTS
- NO GIEZELT_GBM_STS_down_VS_LTS
- A WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (L)
- N OL vs OPC
- G WILLSCHER_GBM_LTSmut_proteomics-E_UP
- K WILLSCHER_GBM_proteomics_wtOnly_SpotH
- bbp VERHAAK_PN subtype
- J Goveais_LGG_EPL_subclass
- BB Mukasa_UP_in_Oligodendrogloma_with_1intact
- A Noushmehr_Pron_GCIMP_hypermeth_DN
- A GIEZELT_GBM_STS_up_VS_LTS
- B Hopp Sturm_GBM_Epi3_F_RTKII_UP_adult_fetus_K27_DN
- A WILLSCHER_GBM_Verhaak-PNmut_up (M)
- J Donson-migration_tethering_and_rolling-associated with LTS in HGA
- N WILLSCHER_GBM_proteomics_wtOnly_Differencelist
- K WILLSCHER_GBM_proteomics_wtOnly_SpotG
- K WILLSCHER_GBM_STSwt_proteomics-O_UP
- D Weller_LGG_gradell-vs-III_DOWN
- N WILLSCHER_GBM_proteomics_wtOnly_SpotB
- N WILLSCHER_GBM_proteomics_wtOnly_SpotC
- C Colman_survival_robust
- L Colman_survival_associated
- L Donson-Misc immune function-associated with LTS in HGA
- L Donson-immune cell intra signaling-associated with LTS in HGA
- H Donson-cytotoxic effectors-associated with LTS in HGA
- H Donson-innate immunity-associated with LTS in HGA
- L WILLSCHER_GBM_Verhaak-CL & MES_up
- EE WILLSCHER_GBM_Verhaak-PNwt_up
- H Hopp Sturm_GBM_Epi3_no_zentr.2_adult_UP_G34_DN
- A WILLSCHER_GBM_Verhaak-CL_up (C)
- F GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
- Donson-chemokines/cytokines-associated with LTS in HGA
- B Sturm_GBM_Meth_overexpression_I_RTKI_PDGFR_A_UP
- G Sturm_GBM_Meth_overexpression_F_IDH_UP
- O Sturm_GBM_Meth_overexpression_B_adult_UP
- C Hopp Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
- N Mukasa_UP_in_GBM
- N OL vs MOG-OL
- M VERHAAK_Brain
- N Phillips MES up vs Prolif & PN
- C Down_a
- C Weller_LGG_gradell-vs-III_UP
- C WIRTH_Normal Brain
- H Hopp Sturm_GBM_Epi3_E_G34_UP
- N Sturm_GBM_Meth_overexpression_D_G34_UP
- N mature astrocytes
- H Hopp Sturm_GBM_Epi3_C_IDH_UP
- Christensen_hypomethylated_in_grade2_astrocytoma
- bbp Christensen_hypomethylated_in_grade3_oligoastrocytoma
- bbp Christensen_hypomethylated_in_grade2_oligodendrogloma
- BB KIM prognostic signature LTS_STS
- BB KIM deleted & downregulated in LTS
- N WILLSCHER_GBM_LTSwt_proteomics-G_UP
- L Martinez_Glio_hypometh
- A Christensen_hypomethylated_in_secondary_glioblastoma
- L Christensen_hypomethylated_in_primary_glioblastoma
- M WILLSCHER_GBM_STSwt_proteomics-L_UP
- N Shaw_down_in_1p19q
- C Shaw_responders_down_in_oligo_glioma
- N Hopp Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
- GIEZELT_GBM_WT_up_VS_mut
- N Christensen_hypermethylated_in_grade3_oligoastrocytoma
- L Weller_LGG_1p19qDel-vs-intact_DOWN
- L Weller_LGG_A_vs_O_UP

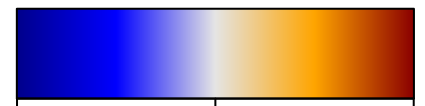


GSZ score

Category Glio



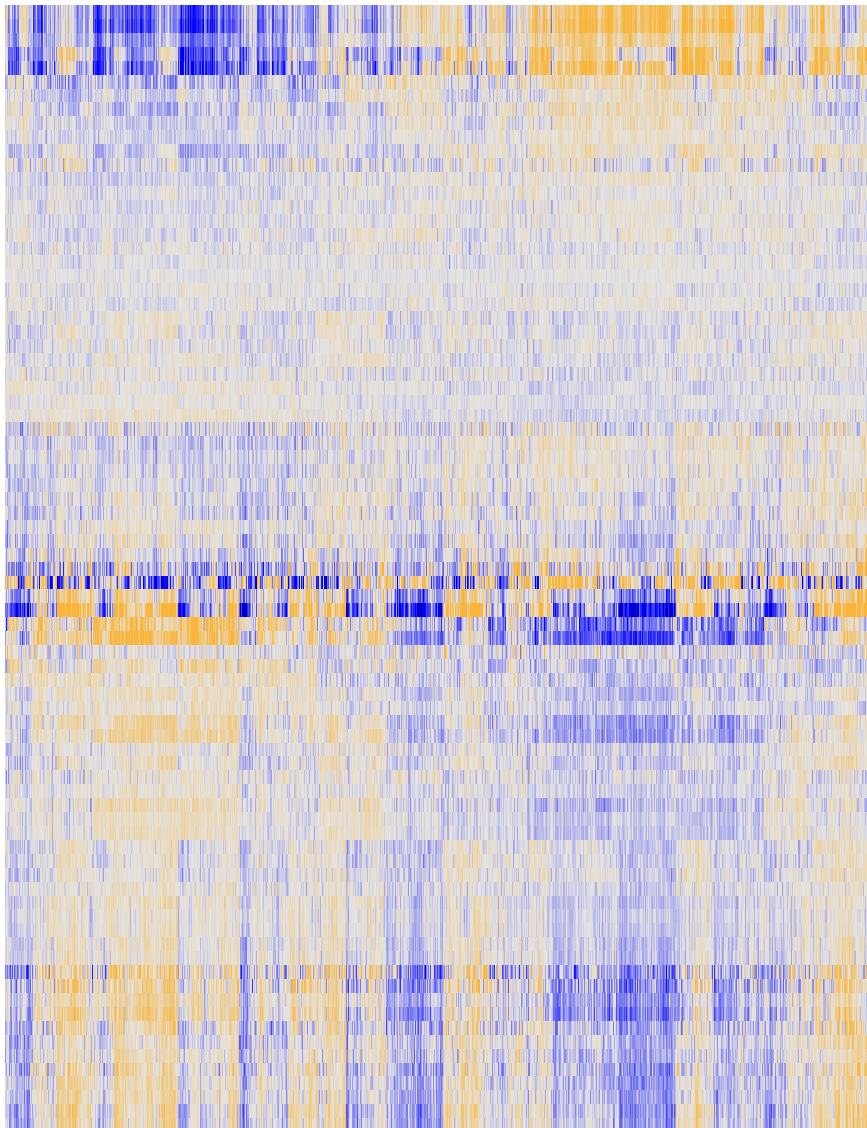
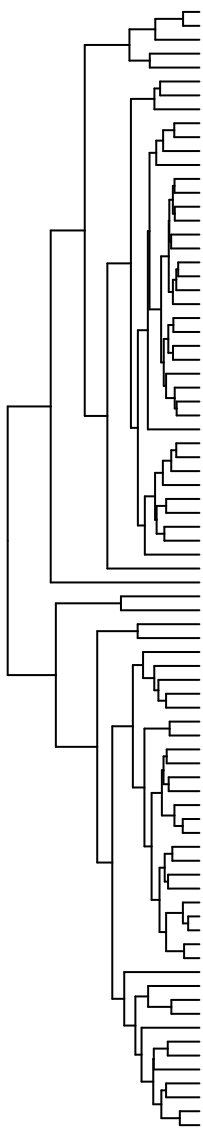
K Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
K Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
K Sturm_GBM_Meth_overexpression_E_G34_UP
M Up
M WILLSCHER_GBM_Verhaak-PNwt & CL_up
G Stuehler_Proteins_up_in_STS
C Down_b
I Donson-adaptive-immunity-associated with LTS in HGA
D WILLSCHER_GBM_Verhaak-PNwt & MES_up
A WILLSCHER_GBM_LTsmut_proteomics-A_UP
O Vishal_subnetwork_signature_of_survival_in_GBM
H Donson-chemokine/cytokine-receptors-associated with LTS in HGA
A Sturm_GBM_Meth_overexpression_G_IDH_UP
N VERHAAK_CL_subtype
J Weller_LGG_A_vs_O_DOWN
K Phillips_Prolif_up_vs_PN & MES
K Sturm_GBM_Meth_overexpression_H_K27_UP
O Barbus_GBM_STS_vs_LTS
E GIEZELT_GBM_STS_down_VS_LTS
A WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (L)
N OL_vs_OPC
G WILLSCHER_GBM_LTsmut_proteomics-E_UP
K WILLSCHER_GBM_proteomics_wtOnly_SpotH
B VERHAAK_PN_subtype
B Gorovets_LGG_EPL_subclass
B Mukasa_UP_in_Oligodendroglioma_with_1intact
A Noushmehr_Pron_GCIMP_hypermeth_DN
A GIEZELT_GBM_STS_up_VS_LTS
B Hopp_Sturm_GBM_Epi3_F_RTK_II_UP_adult_fetus_K27_DN
A WILLSCHER_GBM_Verhaak-PNmut_up (M)
J Donson-migration_tethering_and_rolling-associated with LTS in HGA
N WILLSCHER_GBM_proteomics_wtOnly_Differencelist
K WILLSCHER_GBM_proteomics_wtOnly_SpotG
K WILLSCHER_GBM_STSwt_proteomics-O_UP
D Weller_LGG_gradell-vs-III_DOWN
N WILLSCHER_GBM_proteomics_wtOnly_SpotB
N WILLSCHER_GBM_proteomics_wtOnly_SpotC
C Colman_survival_robust
C Colman_survival_associated
L Donson-Misc immune function-associated with LTS in HGA
L Donson-immune cell intra signaling-associated with LTS in HGA
H Donson-cytotoxic effectors-associated with LTS in HGA
L Donson-innate immunity-associated with LTS in HGA
L WILLSCHER_GBM_Verhaak-CL & MES_up
E WILLSCHER_GBM_Verhaak-PNwt_up
H Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
A WILLSCHER_GBM_Verhaak-CL_up (C)
E GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
L Donson-chemokines/cytokines-associated with LTS in HGA
B Sturm_GBM_Meth_overexpression_I_RTK_I 'PDGFRA'_UP
G Sturm_GBM_Meth_overexpression_F_IDH_UP
O Sturm_GBM_Meth_overexpression_B_adult_UP
C Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
N Mukasa_UP_in_GBM
N OL_vs_MOG-OL
M VERHAAK_Brain
N Phillips_MES_up_vs_Prolif & PN
C Down_a
C Weller_LGG_gradell-vs-III_UP
C WIRTH_Normal_Brain
H Hopp_Sturm_GBM_Epi3_E_G34_UP
N Sturm_GBM_Meth_overexpression_D_G34_UP
N mature_astrocytes
H Hopp_Sturm_GBM_Epi3_C_IDH_UP
B Christensen_hypomethylated_in_grade2_astrocytoma
B Christensen_hypomethylated_in_grade3_oligoastrocytoma
B Christensen_hypomethylated_in_grade2_oligodendroglioma
B KIM_prognostic_signature_LTS_vs_STS
B KIM_deleted & downregulated in LTS
N WILLSCHER_GBM_LTSwt_proteomics-G_UP
A Martinez_Glio_hypometh
A Christensen_hypomethylated_in_secondary_glioblastoma
L Christensen_hypomethylated_in_primary_glioblastoma
M WILLSCHER_GBM_STSwt_proteomics-L_UP
N Shaw_down_in_1p19q
C Shaw_responders_down_in_oligo_glioma
N Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
L GIEZELT_GBM_WT_up_VS_mut
N Christensen_hypermethylated_in_grade3_oligoastrocytoma
L Weller_LGG_1p19qDel-vs-intact_DOWN
L Weller_LGG_A_vs_O_UP



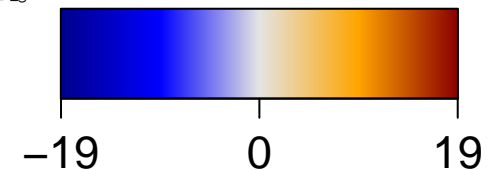
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GSZ score

Category Glio

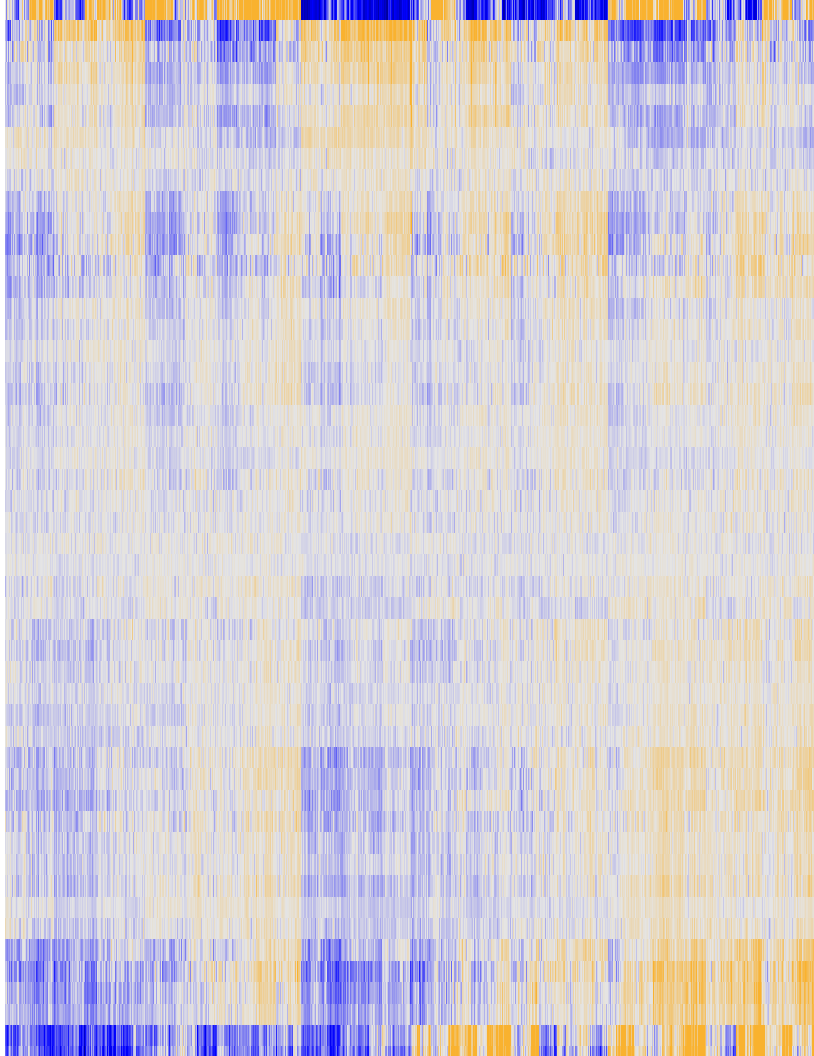
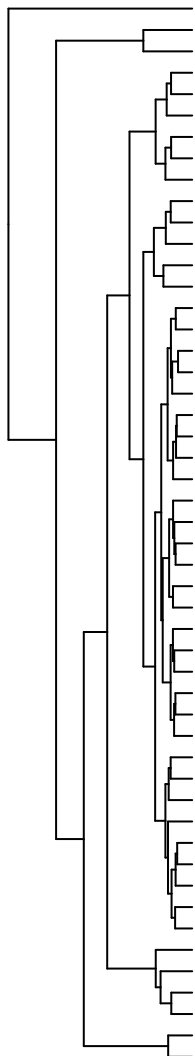
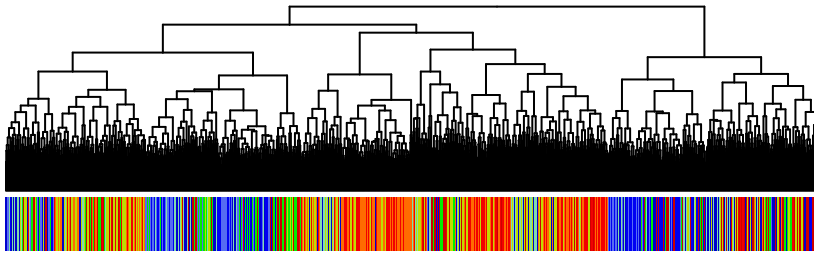


- K Hopp_Sturm_GBM_Epi3_no_zentr_6_fetus_UP
- K Hopp_Sturm_GBM_Epi3_E1_fetus_UP_fetus_DN
- K Sturm_GBM_Meth_overexpression_E_G34_UP
- M Up
- G WILLSCHER_GBM_Verhaak-PNwt & CL_up
- C Stuehler_Proteins_up_in_STS
- G Down_b
- I Donson-adaptive-immunity-associated with LTS in HGA
- D WILLSCHER_GBM_Verhaak-PNwt & MES_up
- A WILLSCHER_GBM_LTSmut_proteomics-A_UP
- O Vishal_subnetwork_signature_of_survival_in_GBM
- H Donson-chemokine/cytokine-receptors-associated with LTS in HGA
- A Sturm_GBM_Meth_overexpression_G_IDH_UP
- N VERHAAK_CL_subtype
- J Weller_LGG_A_vs_O_DOWN
- K Phillips_Prolif_up_vs_PN & MES
- K Sturm_GBM_Meth_overexpression_H_K27_UP
- O Barbus_GBM_STS_vs_LTS
- E GIEZELT_GBM_STS_down_VS_LTS
- A WILLSCHER_GBM_Verhaak-PN (mut&wt)_up (L)
- N OL_vs_OPC
- G WILLSCHER_GBM_LTSmut_proteomics-E_UP
- K WILLSCHER_GBM_proteomics_wtOnly_SpotH
- B VERHAAK_PN_subtype
- B Gorovets_LGG_EPL_subclass
- B Mukasa_UP_in_Oligodendroglioma_with_1intact
- A Noushmehr_Pron_GCIMP_hypermeth_DN
- A GIEZELT_GBM_STS_up_VS_LTS
- B Hopp_Sturm_GBM_Epi3_F_RTK_II_UP_adult_fetus_K27_DN
- A WILLSCHER_GBM_Verhaak-PNmut_up (M)
- J Donson-migration_tethering_and_rolling-associated with LTS in HGA
- N WILLSCHER_GBM_proteomics_wtOnly_Differencelist
- K WILLSCHER_GBM_proteomics_wtOnly_SpotG
- K WILLSCHER_GBM_STSwt_proteomics-O_UP
- D Weller_LGG_gradell-vs-III_DOWN
- N WILLSCHER_GBM_proteomics_wtOnly_SpotB
- N WILLSCHER_GBM_proteomics_wtOnly_SpotC
- C Colman_survival_robust
- C Colman_survival_associated
- L Donson-Misc immune function-associated with LTS in HGA
- L Donson-immune_cell_intra_signaling-associated with LTS in HGA
- H Donson-cytotoxic effectors-associated with LTS in HGA
- L Donson-innate immunity-associated with LTS in HGA
- L WILLSCHER_GBM_Verhaak-CL & MES_up
- E WILLSCHER_GBM_Verhaak-PNwt_up
- H Hopp_Sturm_GBM_Epi3_no_zentr_2_adult_UP_G34_DN
- A WILLSCHER_GBM_Verhaak-CL_up (C)
- E GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
- L Donson-chemokines/cytokines-associated with LTS in HGA
- B Sturm_GBM_Meth_overexpression_I_RTK_I_'PDGFRA'_UP
- G Sturm_GBM_Meth_overexpression_F_IDH_UP
- O Sturm_GBM_Meth_overexpression_B_adult_UP
- C Hopp_Sturm_GBM_Epi3_A_adult_fetus_UP_G34_DN
- N Mukasa_UP_in_GBM
- N OL_vs_MOG-OL
- M VERHAAK_Brain
- N Phillips_MES_up_vs_Prolif & PN
- C Down_a
- C Weller_LGG_gradell-vs-III_UP
- C WIRTH_Normal_Brain
- H Hopp_Sturm_GBM_Epi3_E_G34_UP
- N Sturm_GBM_Meth_overexpression_D_G34_UP
- N mature_astrocytes
- H Hopp_Sturm_GBM_Epi3_C_IDH_UP
- B Christensen_hypomethylated_in_grade2_astrocytoma
- B Christensen_hypomethylated_in_grade3_oligoastrocytoma
- B Christensen_hypomethylated_in_grade2_oligodendroglioma
- B KIM_prognostic_signature_LTS_vs_STS
- B KIM_deleted & downregulated in LTS
- N WILLSCHER_GBM_LTSwt_proteomics-G_UP
- A Martinez_Glio_hypometh
- A Christensen_hypomethylated_in_secondary_glioblastoma
- L Christensen_hypomethylated_in_primary_glioblastoma
- M WILLSCHER_GBM_STSwt_proteomics-L_UP
- N Shaw_down_in_1p19q
- C Shaw_responders_down_in_oligo_glioma
- N Hopp_Sturm_GBM_Epi3_D_adult_fetus_IDH_UP
- E GIEZELT_GBM_WT_up_VS_mut
- N Christensen_hypermethylated_in_grade3_oligoastrocytoma
- C Weller_LGG_1p19qDel-vs-intact_DOWN
- L Weller_LGG_A_vs_O_UP

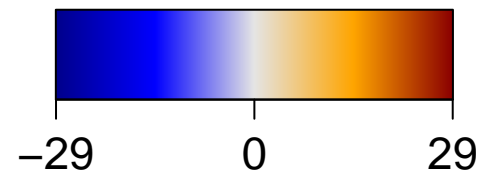


GSZ score

Category HM

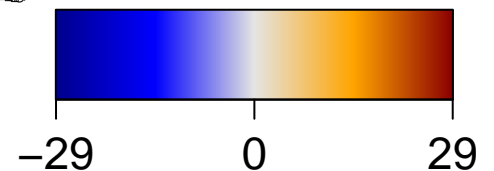
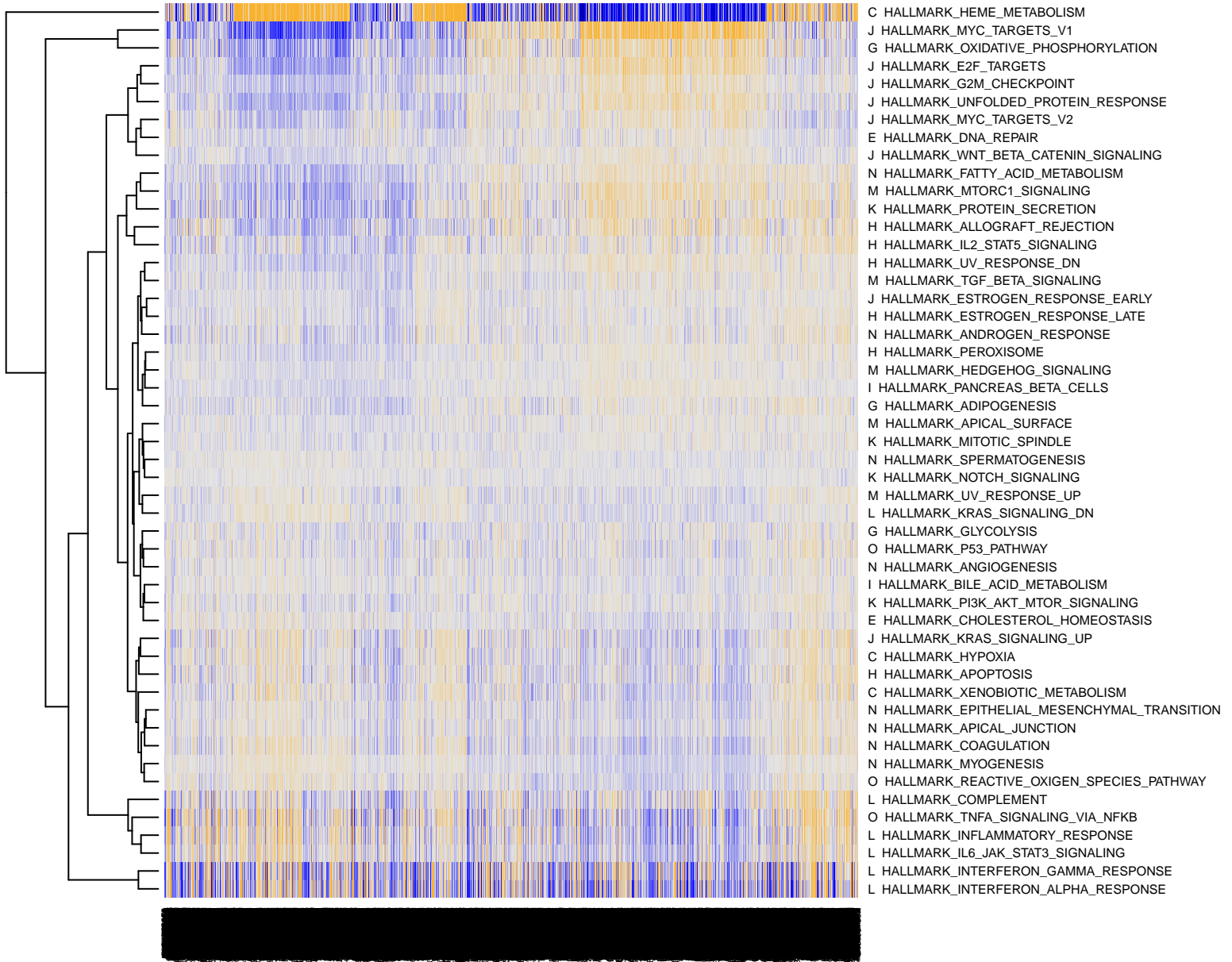


C HALLMARK_HEME_METABOLISM
J HALLMARK_MYC_TARGETS_V1
G HALLMARK_OXIDATIVE_PHOSPHORYLATION
J HALLMARK_E2F_TARGETS
J HALLMARK_G2M_CHECKPOINT
J HALLMARK_UNFOLDED_PROTEIN_RESPONSE
J HALLMARK_MYC_TARGETS_V2
E HALLMARK_DNA_REPAIR
J HALLMARK_WNT_BETA_CATENIN_SIGNALING
N HALLMARK_FATTY_ACID_METABOLISM
M HALLMARK_MTORC1_SIGNALING
K HALLMARK_PROTEIN_SECRETION
H HALLMARK_ALLOGRAFT_REJECTION
H HALLMARK_IL2_STAT5_SIGNALING
H HALLMARK_UV_RESPONSE_DN
M HALLMARK_TGF_BETA_SIGNALING
J HALLMARK_ESTROGEN_RESPONSE_EARLY
H HALLMARK_ESTROGEN_RESPONSE_LATE
N HALLMARK_ANDROGEN_RESPONSE
H HALLMARK_PEROXISOME
M HALLMARK_HEDGEHOG_SIGNALING
I HALLMARK_PANCREAS_BETA_CELLS
G HALLMARK_ADIPOGENESIS
M HALLMARK_APICAL_SURFACE
K HALLMARK_MITOTIC_SPINDLE
N HALLMARK_SPERMATOGENESIS
K HALLMARK_NOTCH_SIGNALING
M HALLMARK_UV_RESPONSE_UP
L HALLMARK_KRAS_SIGNALING_DN
G HALLMARK_GLYCOLYSIS
O HALLMARK_P53_PATHWAY
N HALLMARK_ANGIOGENESIS
I HALLMARK_BILE_ACID_METABOLISM
K HALLMARK_PI3K_AKT_MTOR_SIGNALING
E HALLMARK_CHOLESTEROL_HOMEOSTASIS
J HALLMARK_KRAS_SIGNALING_UP
C HALLMARK_HYPOXIA
H HALLMARK_APOPTOSIS
C HALLMARK_XENOBIOTIC_METABOLISM
N HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION
N HALLMARK_APICAL_JUNCTION
N HALLMARK_COAGULATION
N HALLMARK_MYOGENESIS
O HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY
L HALLMARK_COMPLEMENT
O HALLMARK_TNFA_SIGNALING_VIA_NFKB
L HALLMARK_INFLAMMATORY_RESPONSE
L HALLMARK_IL6_JAK_STAT3_SIGNALING
L HALLMARK_INTERFERON_GAMMA_RESPONSE
L HALLMARK_INTERFERON_ALPHA_RESPONSE



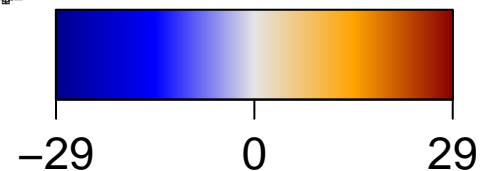
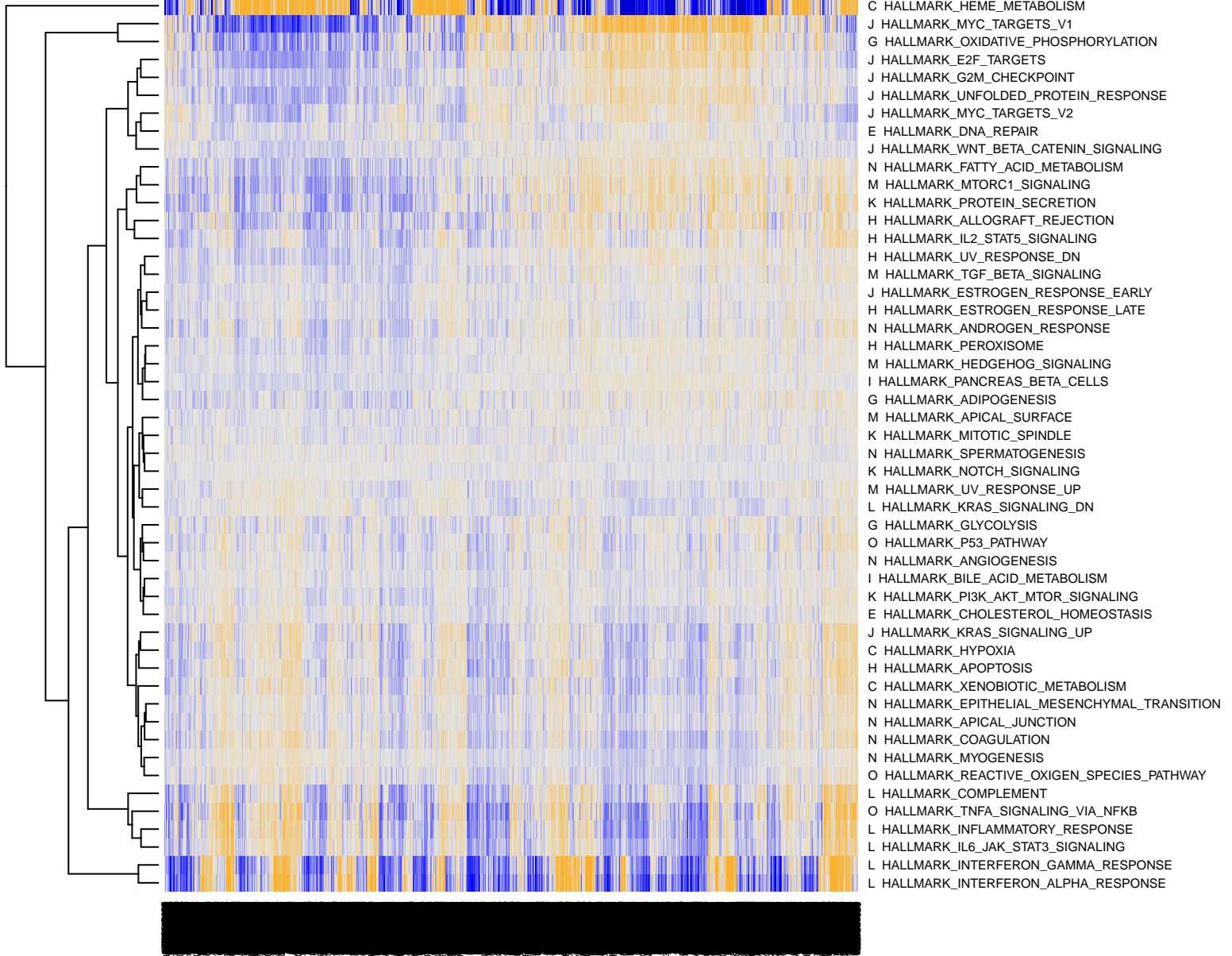
GSZ score

Category HM



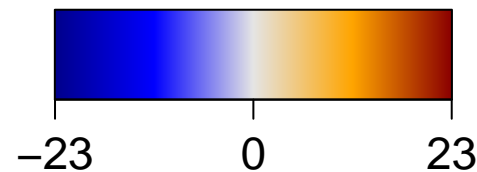
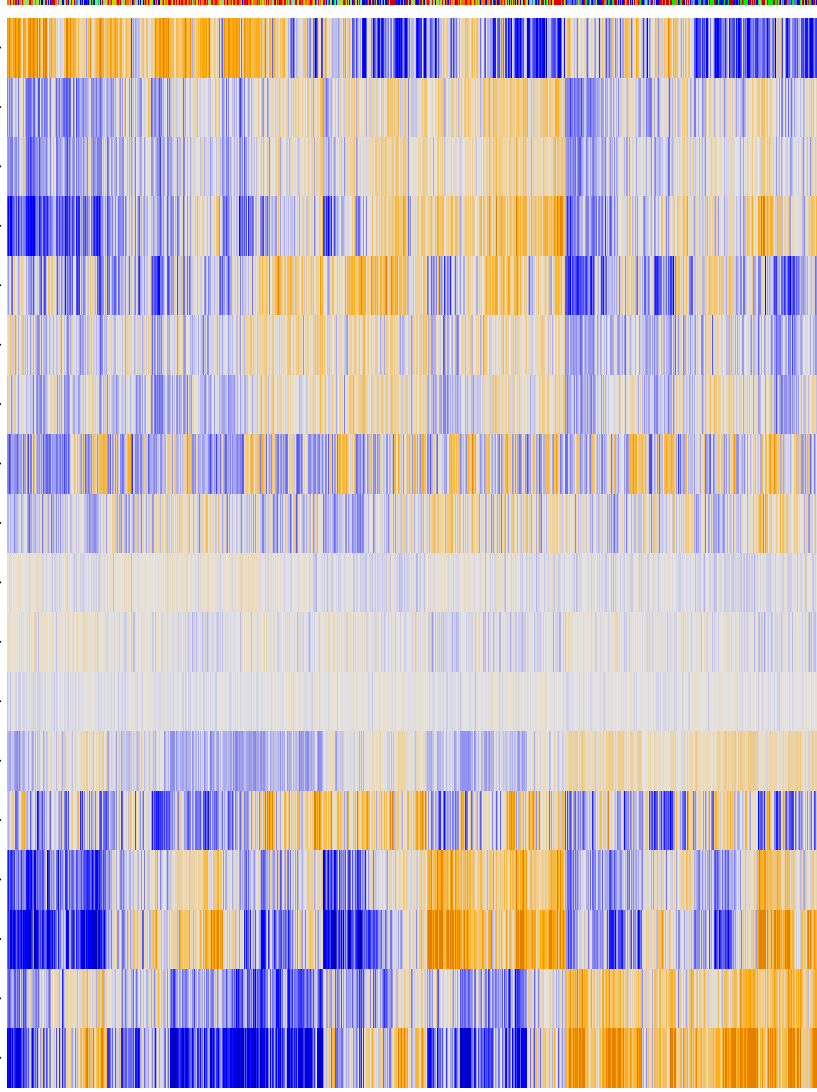
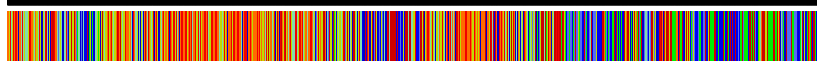
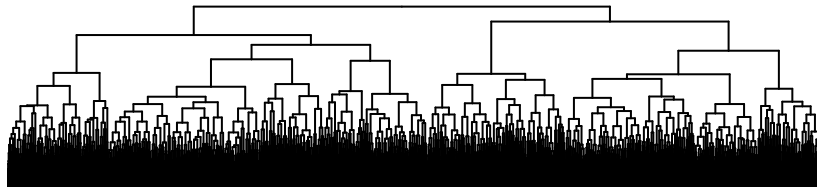
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Category HM



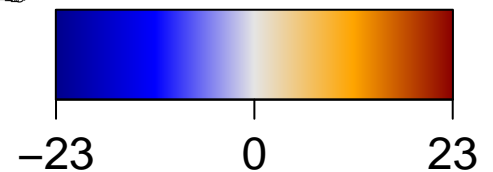
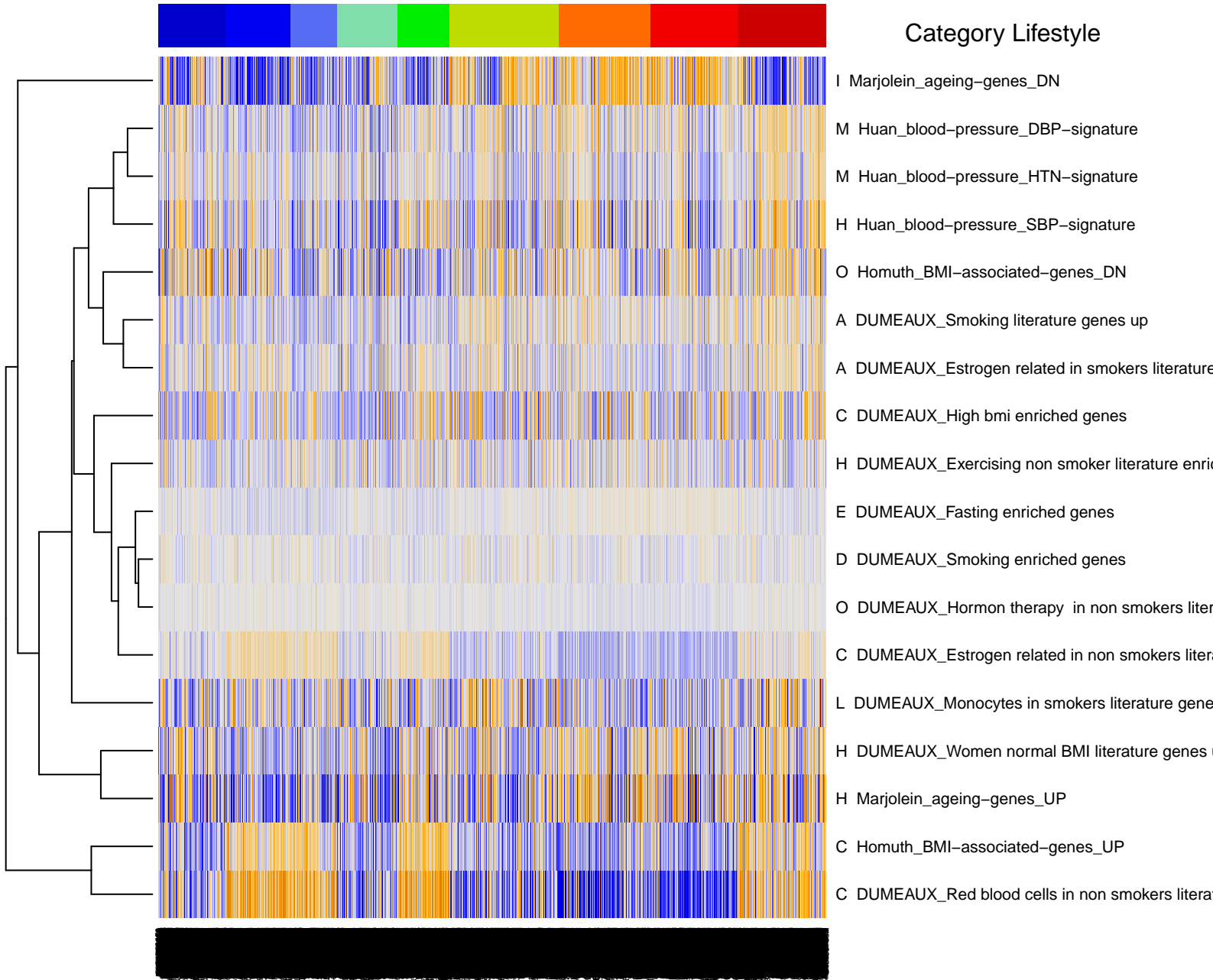
GSZ score

Category Lifestyle



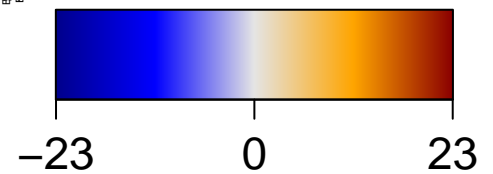
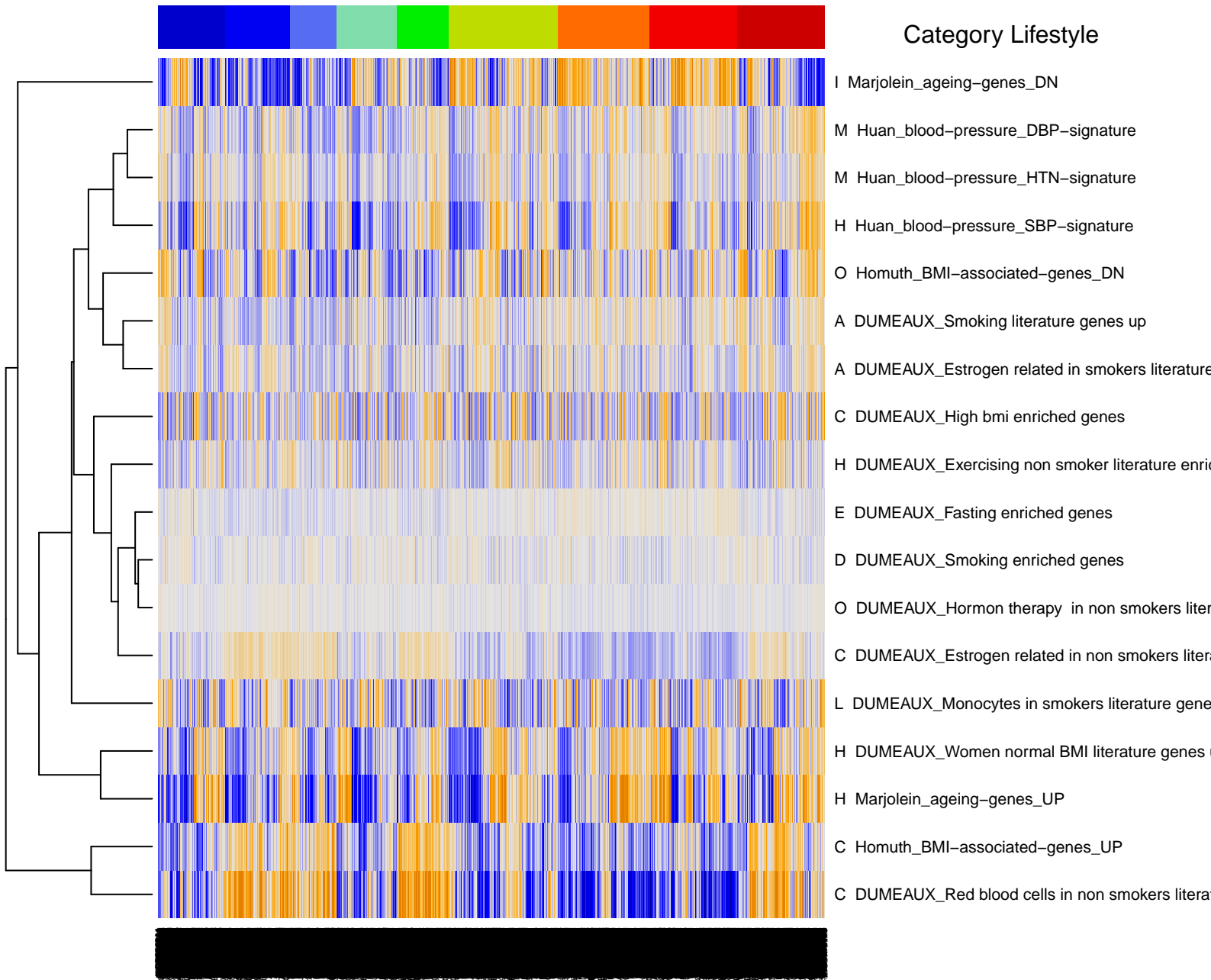
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Category Lifestyle



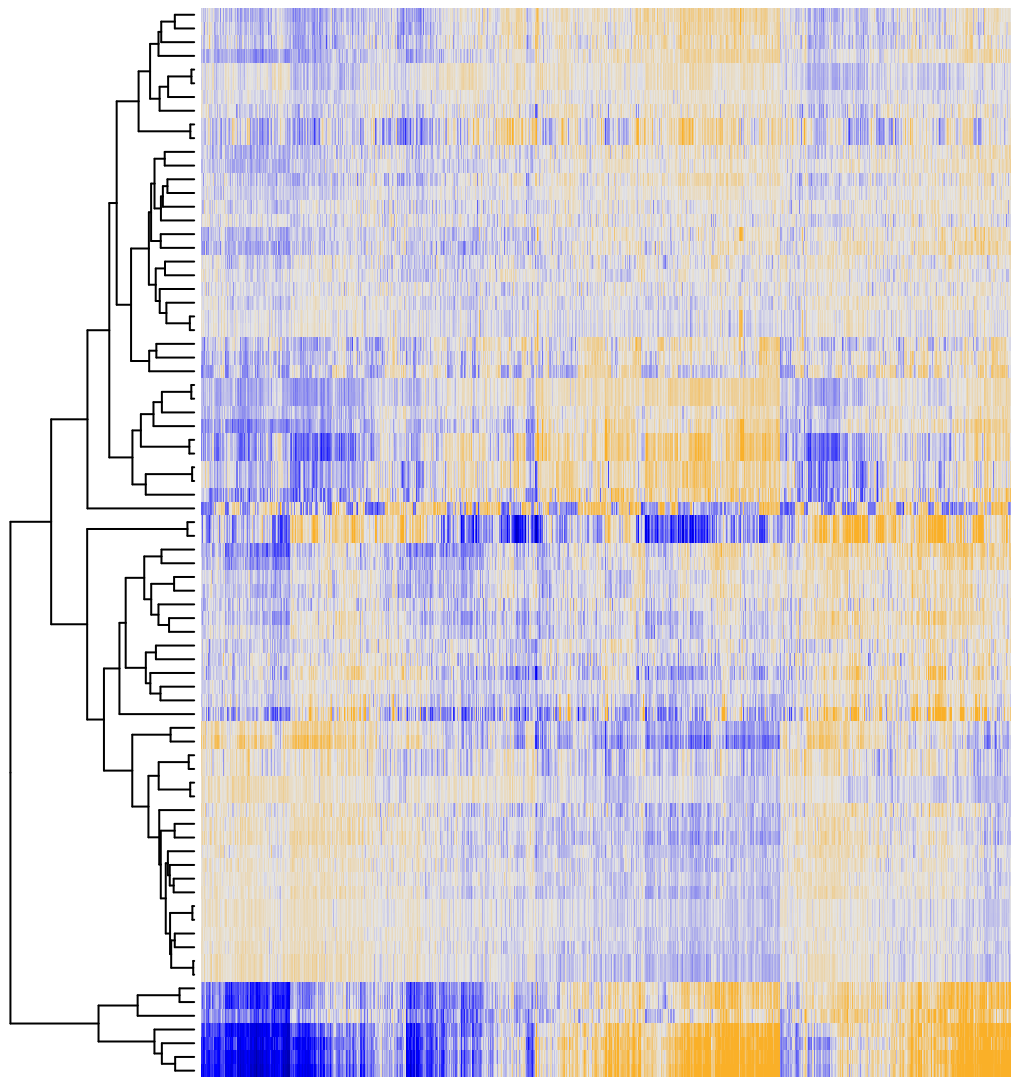
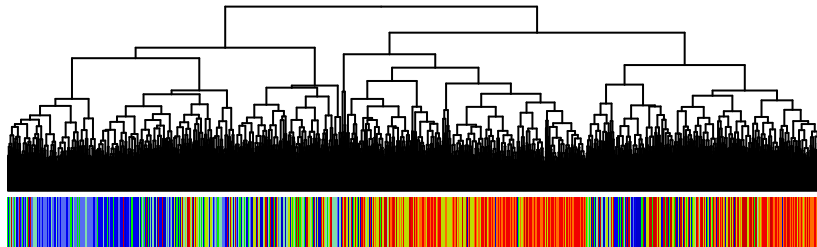
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Category Lifestyle

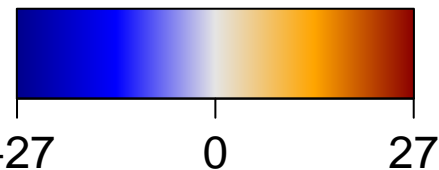


GSZ score

Category Lymphoma

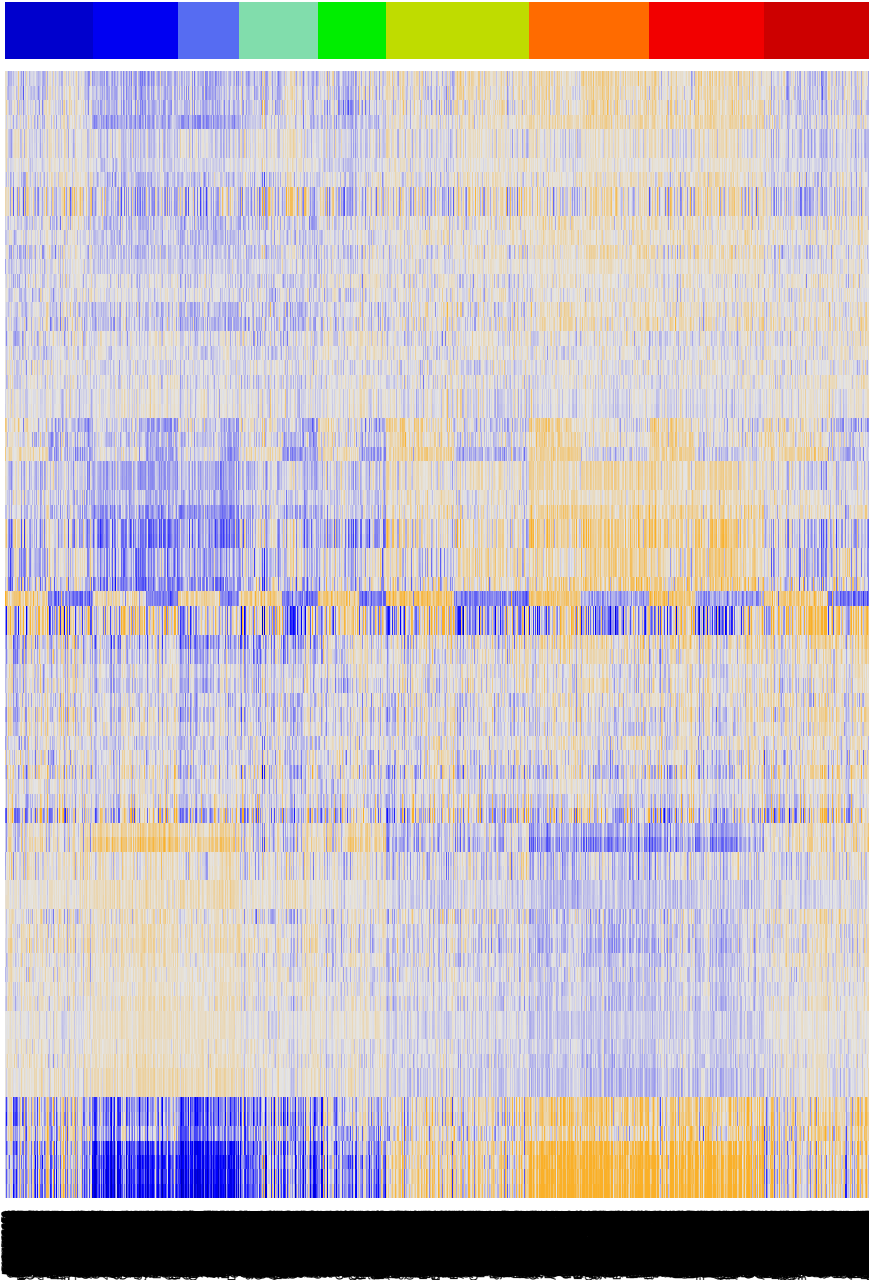


I Sha_BL_UP
I WIRTH_lymphoma937_spot A
I Monti_BCR_cluster
K SPANG_BCR_UP
G Hopp_June14_MMML937_tumors+controls_group.overexpression_B_ce
G WIRTH_lymphoma937_spot B
G Aukema_BCL2_UP_BCL6_DN
J DAVE_Immune_response_1
D Hopp_June14_MMML937_tumors+controls_group.overexpression_J_G
O WIRTH_lymphoma937_spot J
J WRIGHT_GCB_UP
J ROSOLOWSKI_green_UP
E WRIGHT_ABC_UP
L DAVE_NFkB_BL_DN
J MASCQUE_ABC_UP
L YAMANE_AICDA_targets_recruited
M TARTE_Plasma_cell_signature
M SPANG_CD40_6hrs_DN
N HOPP_Heterochrom
C SPANG_BAFF_9hrs_UP
L Shaknovich_ABC_hypo_meth
O Aukema_BCL2_DN_BCL6_UP
H Hopp_June14_MMML937_tumors+controls_group.overexpression_MM
H WIRTH_lymphoma937_spot MM
I Hopp_June14_MMML937_tumors+controls_group.overexpression_A_mB
I TARTE_B-cell_signature
J ROSOLOWSKI_red_total
J WIRTH_lymphoma937_spot C
H Hopp_June14_MMML937_tumors+controls_group.overexpression_C_ce
E CARO_OxPhos_in_DLBCL_UP
M TARTE_Plasma_blast_signature
E WIRTH_lymphoma937_spot D
H Hopp_June14_MMML937_tumors+controls_group.overexpression_D_ce
J Hopp_June14_MMML937_tumors+controls_group.overexpression_F_FL
J Care_Polarized_immune_response
E ROSOLOWSKI_red_UP
L Hopp_June14_MMML937_tumors+controls_group.overexpression_E_G
L WIRTH_lymphoma937_spot E
M SPANG_BCR_DN
N HOPP_Repetitive
L SPANG_LPS_6hrs_UP
L SPANG_CD40_6hrs_UP
M MASCQUE_mBL_DOWN
M Sha_DLBCL_UP
M BENTINK_mBL_DOWN
H Care_Extended_T-cell
A DAVE_MHCCII_BL_DN
L Monti_Host_response_cluster
L DAVE_Immune_response_2
L ROSOLOWSKI_blue_DOWN
L SPANG_IL21_DN
N HOPP_Poised_promoter
N HOPP_Repressed
O WIRTH_lymphoma937_spot H
O Hopp_June14_MMML937_tumors+controls_group.overexpression_H_G
A Hopp_June14_MMML937_tumors+controls_group.overexpression_I_MM
A WIRTH_lymphoma937_spot I
L TARTE_Mature_plasma_cell_signature
N Subero_T-ALL_hypo_meth
K Subero_T-ALL_hypo_meth
N LENZ_Stromal_signature_1
E Subero_B-ALL_hypo_meth
O Care_GCB_UP
L Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
G Hopp_June14_MMML937_tumors+controls_group.overexpression_IM_n
G WIRTH_lymphoma937_spot IM
N Subero_INT_hypo_meth
O Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
B Hopp_June14_MMML937_tumors+controls_group.overexpression_G_to
B WIRTH_lymphoma937_spot G
K HOPP_Weak_txn
K HOPP_Weak_enhancer
M HOPP_Strong_enhancer
K HOPP_Weak_promoter
K HOPP_Weak_promoter
K HOPP_Txn_transition
K HOPP_Active_promoter
K HOPP_Txn_elongation

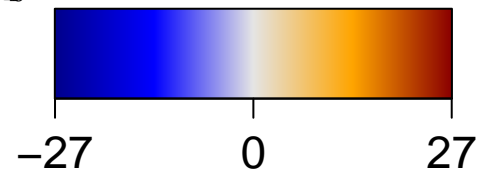


GSZ score

Category Lymphoma

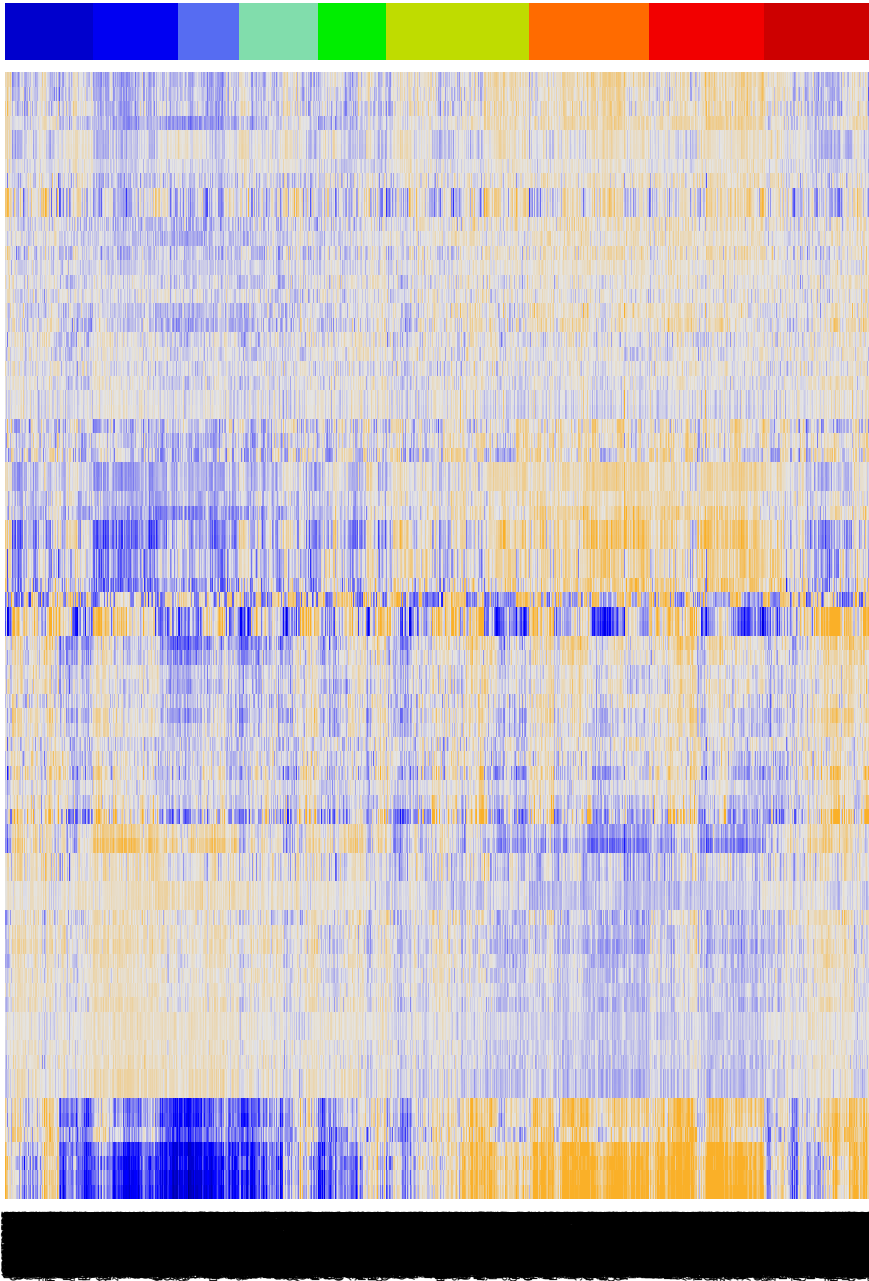


- I Sha_BL UP
- I WIRTH_lymphoma937_spot A
- I Monti_BCR_cluster
- K SPANG_BCR UP
- G Hopp_June14_MMML937_tumors+controls_group.overexpression_
- G WIRTH_lymphoma937_spot B
- G Aukema_BCL2 UP_BCL6 DN
- J DAVE_Immune response 1
- D Hopp_June14_MMML937_tumors+controls_group.overexpression_
- O WIRTH_lymphoma937_spot J
- J WRIGHT_GCB UP
- J ROSOLOWSKI_green UP
- E WRIGHT_ABC UP
- L DAVE_NFkB BL DN
- J MASCQUE_ABC UP
- L YAMANE_AICDA_targets_recruited
- M TARTE_Plasma cell signature
- M SPANG_CD40 6hrs DN
- N HOPP_Heterochrom
- C SPANG_BAFF 9hrs UP
- L Shaknovich_ABC_hypo_meth
- O Aukema_BCL2 DN_BCL6 UP
- H Hopp_June14_MMML937_tumors+controls_group.overexpression_
- H WIRTH_lymphoma937_spot MM
- I Hopp_June14_MMML937_tumors+controls_group.overexpression_A
- I TARTE_B-cell signature
- J ROSOLOWSKI_red total
- E WIRTH_lymphoma937_spot C
- E Hopp_June14_MMML937_tumors+controls_group.overexpression_
- E CARE_OxPhos_in_DLBCL_UP
- M TARTE_PlasmaBlast signature
- E WIRTH_lymphoma937_spot D
- E Hopp_June14_MMML937_tumors+controls_group.overexpression_
- J WIRTH_lymphoma937_spot F
- J Hopp_June14_MMML937_tumors+controls_group.overexpression_f
- J Care_Polarized immune response
- E ROSOLOWSKI_red UP
- L Hopp_June14_MMML937_tumors+controls_group.overexpression_
- L WIRTH_lymphoma937_spot E
- M SPANG_BCR DN
- N HOPP_Repetitive
- L SPANG_LFS 6hrs UP
- L SPANG_CD40 6hrs UP
- M MASCQUE_mBL DOWN
- M Sha_DLBCL UP
- M BENTINK_mBL DOWN
- H Care_Extended T-cell
- A DAVE_MHCCII BL DN
- L Monti_Host_response_cluster
- L DAVE_Immune response 2
- L ROSOLOWSKI_blue DOWN
- L SPANG_IL21 DN
- N HOPP_Poised_promoter
- N HOPP_Repressed
- O WIRTH_lymphoma937_spot H
- O Hopp_June14_MMML937_tumors+controls_group.overexpression_
- A Hopp_June14_MMML937_tumors+controls_group.overexpression_
- A WIRTH_lymphoma937_spot I
- L TARTE_Mature plasma cell signature
- N Subero_T-ALL_hypo_meth
- E Subero_T-PLL_hypo_meth
- N LENZ_Stromal signature 1
- E Subero_B-ALL_hypo_meth
- O Care_GCB UP
- L Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
- G Hopp_June14_MMML937_tumors+controls_group.overexpression_
- G WIRTH_lymphoma937_spot IM
- G Subero_INT_hypo_meth
- O Hopp_Lymphoma_Epi1_with_zentr_iv_B.cell_MM_UP
- B Hopp_June14_MMML937_tumors+controls_group.overexpression_
- B WIRTH_lymphoma937_spot G
- K HOPP_Weak_txn
- K HOPP_Weak_enhancer
- M HOPP_Strong_enhancer
- K HOPP_Weak_promoter
- K HOPP_Txn_transition
- K HOPP_Active_promoter
- K HOPP_Txn_elongation

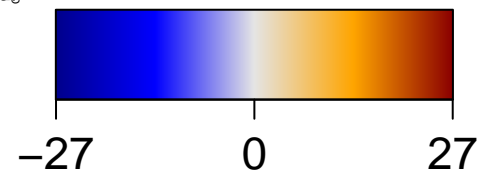


GSZ score

Category Lymphoma

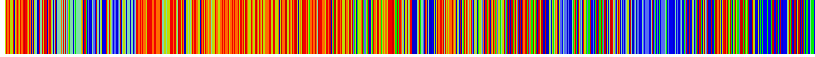
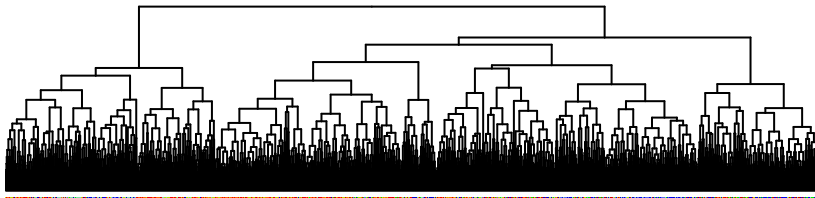


I Sha_BL UP
I WIRTH_lymphoma937_spot A
I Monti_BCR_cluster
K SPANG_BCR UP
G Hopp_June14_MMML937_tumors+controls_group.overexpression_
G WIRTH_lymphoma937_spot B
G Aukema_BCL2 UP_BCL6 DN
J DAVE_Immune_response_1
D Hopp_June14_MMML937_tumors+controls_group.overexpression_
O WIRTH_lymphoma937_spot J
J WRIGHT_GCB UP
J ROSOLOWSKI_green UP
E WRIGHT_ABC UP
L DAVE_NFKB BL DN
J MASCQUE_ABC UP
L YAMANE_AICDA_targets_recruited
M TARTE_Plasma_cell_signature
M SPANG_CD40_6hrs DN
N HOPP_Heterochrom
C SPANG_BAFF_9hrs UP
L Shaknovich_ABC_hypo_meth
O Aukema_BCL2 DN_BCL6 UP
H Hopp_June14_MMML937_tumors+controls_group.overexpression_
H WIRTH_lymphoma937_spot MM
I Hopp_June14_MMML937_tumors+controls_group.overexpression_A
I TARTE_B-cell_signature
J ROSOLOWSKI_red_total
E WIRTH_lymphoma937_spot C
E Hopp_June14_MMML937_tumors+controls_group.overexpression_
E CARE_OxPhos_in_DLBCL_UP
M TARTE_PlasmaBlast_signature
E WIRTH_lymphoma937_spot D
E Hopp_June14_MMML937_tumors+controls_group.overexpression_
J WIRTH_lymphoma937_spot F
J Hopp_June14_MMML937_tumors+controls_group.overexpression_
J Care_Polarized_immune_response
E ROSOLOWSKI_red UP
L Hopp_June14_MMML937_tumors+controls_group.overexpression_
L WIRTH_lymphoma937_spot E
M SPANG_BCR DN
N HOPP_Repetitive
L SPANG_LFS_6hrs UP
L SPANG_CD40_6hrs UP
M MASCQUE_mBL DOWN
M Sha_DLBCL UP
M BENTINK_mBL DOWN
H Care_Extended_T-cell
A DAVE_MHCC11 BL DN
L Monti_Host_response_cluster
L DAVE_Immune_response_2
L ROSOLOWSKI_blue DOWN
L SPANG_IL21 DN
N HOPP_Poised_promoter
N HOPP_Repressed
O WIRTH_lymphoma937_spot H
O Hopp_June14_MMML937_tumors+controls_group.overexpression_
A Hopp_June14_MMML937_tumors+controls_group.overexpression_
A WIRTH_lymphoma937_spot I
L TARTE_Mature_plasma_cell_signature
N Subero_T-ALL_hypo_meth
E Subero_T-PLL_hypo_meth
N LENZ_Stromal_signature_1
E Subero_B-ALL_hypo_meth
O Care_GCB UP
L Hopp_Lymphoma_Epi1_with_zentr_iii_B.cell_GCB_UP
G Hopp_June14_MMML937_tumors+controls_group.overexpression_
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G Subero_INT_hypo_meth
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B Hopp_June14_MMML937_tumors+controls_group.overexpression_
B WIRTH_lymphoma937_spot G
K HOPP_Weak_txn
K HOPP_Weak_enhancer
M HOPP_Strong_enhancer
K HOPP_Weak_promoter
K HOPP_Txn_transition
K HOPP_Active_promoter
K HOPP_Txn_elongation



GSZ score

Category Melanoma



H Hugo_melanoma-all-LEF1_UP

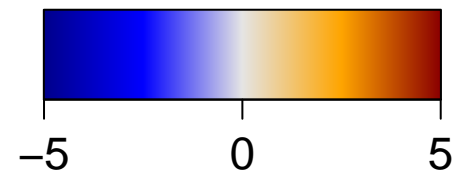
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A Hugo_melanoma-BRAFmut-LEF1

H Hugo_melanoma-all-MET_DN

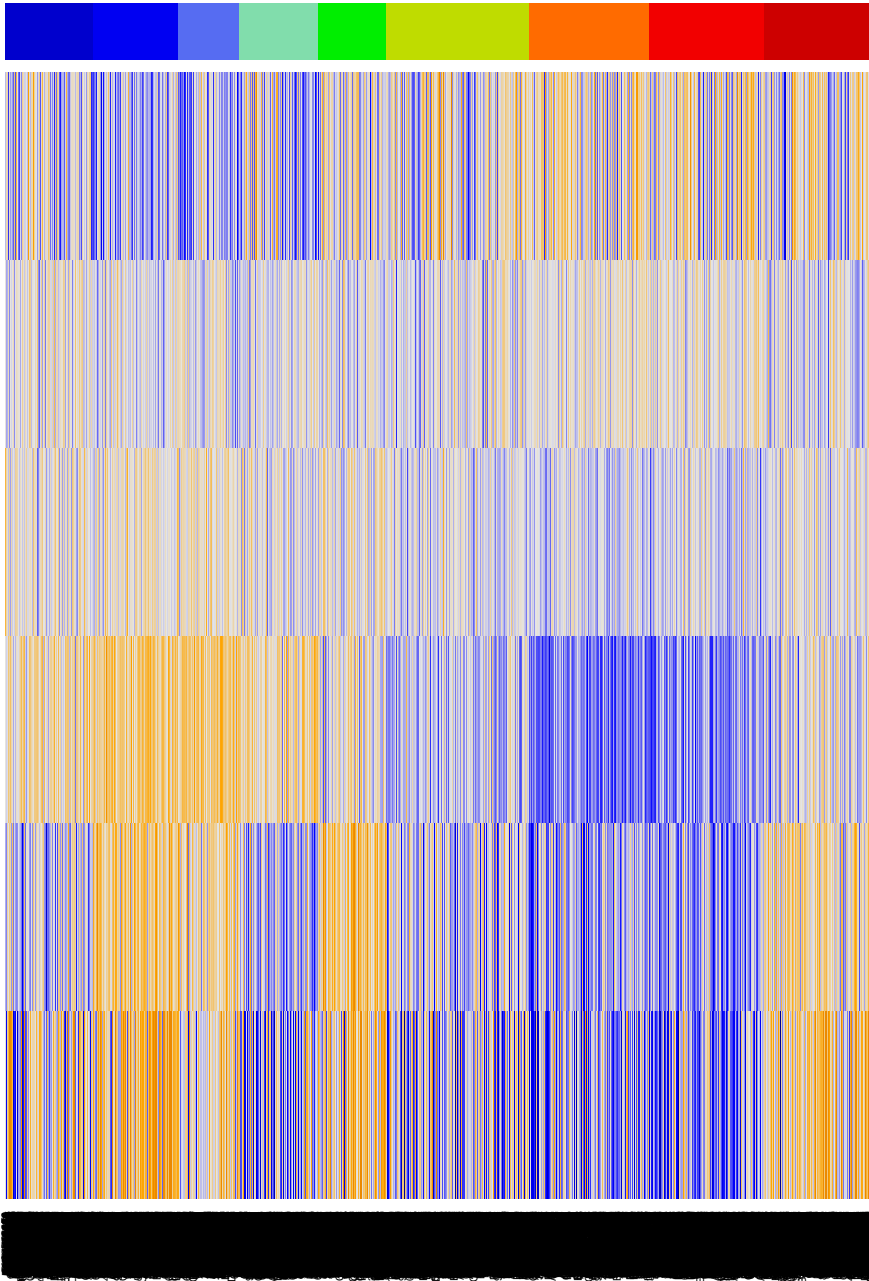
M Hugo_melanoma-all-MET_UP

G Hugo_melanoma-BRAFmut-MET



GSZ score

Category Melanoma



H Hugo_melanoma-all-LEF1_UP

A Hugo_melanoma-BRAFmut-ME

A Hugo_melanoma-BRAFmut-LE

H Hugo_melanoma-all-MET_DN

M Hugo_melanoma-all-MET_UP

G Hugo_melanoma-BRAFmut-ME

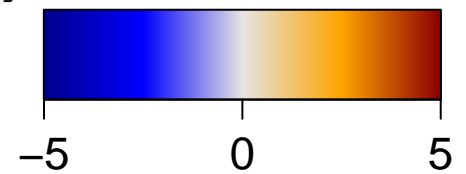
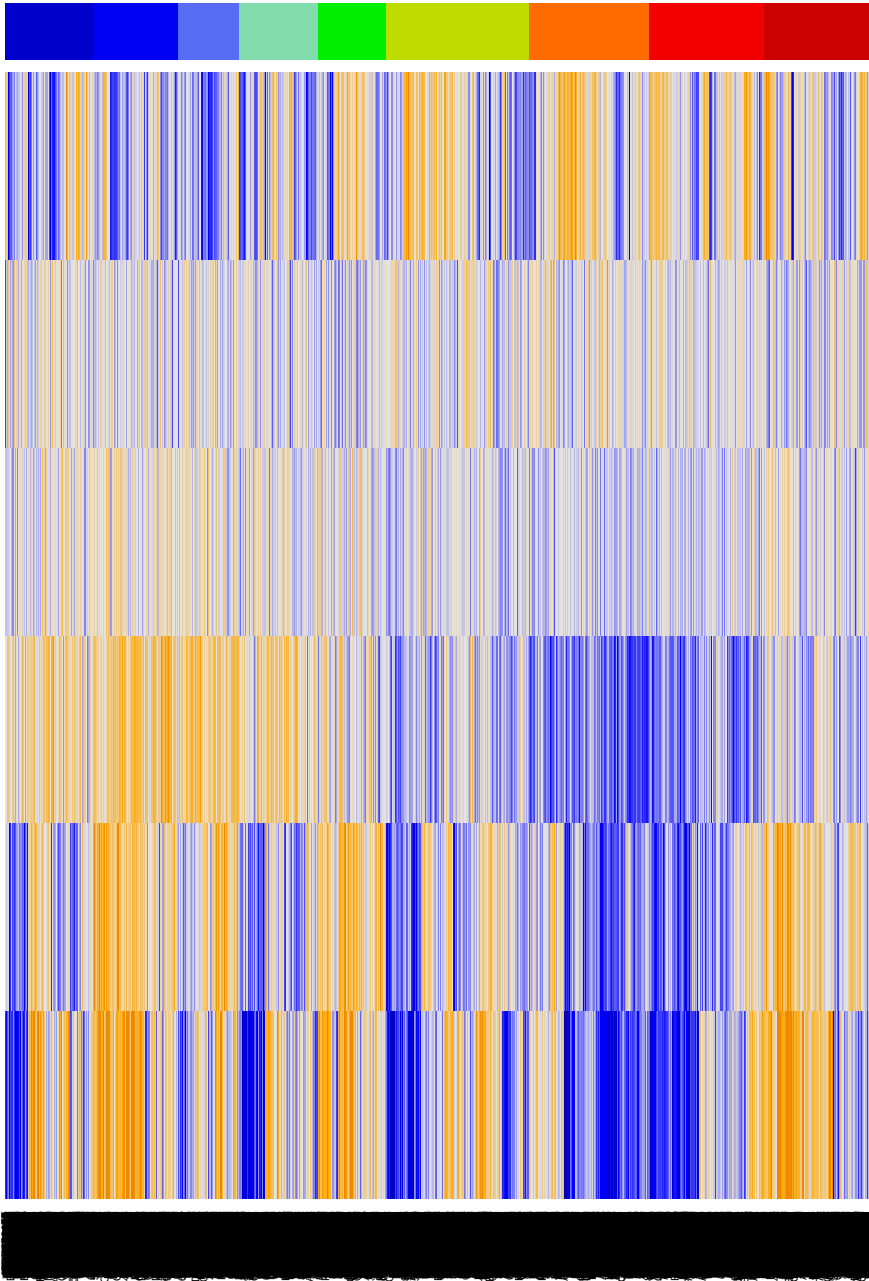
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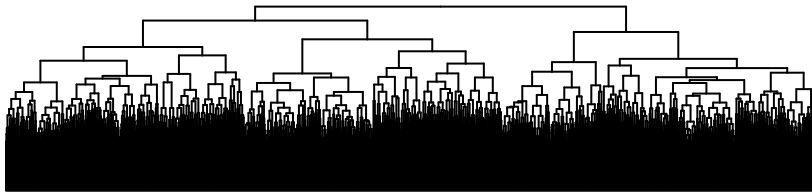
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GSZ score

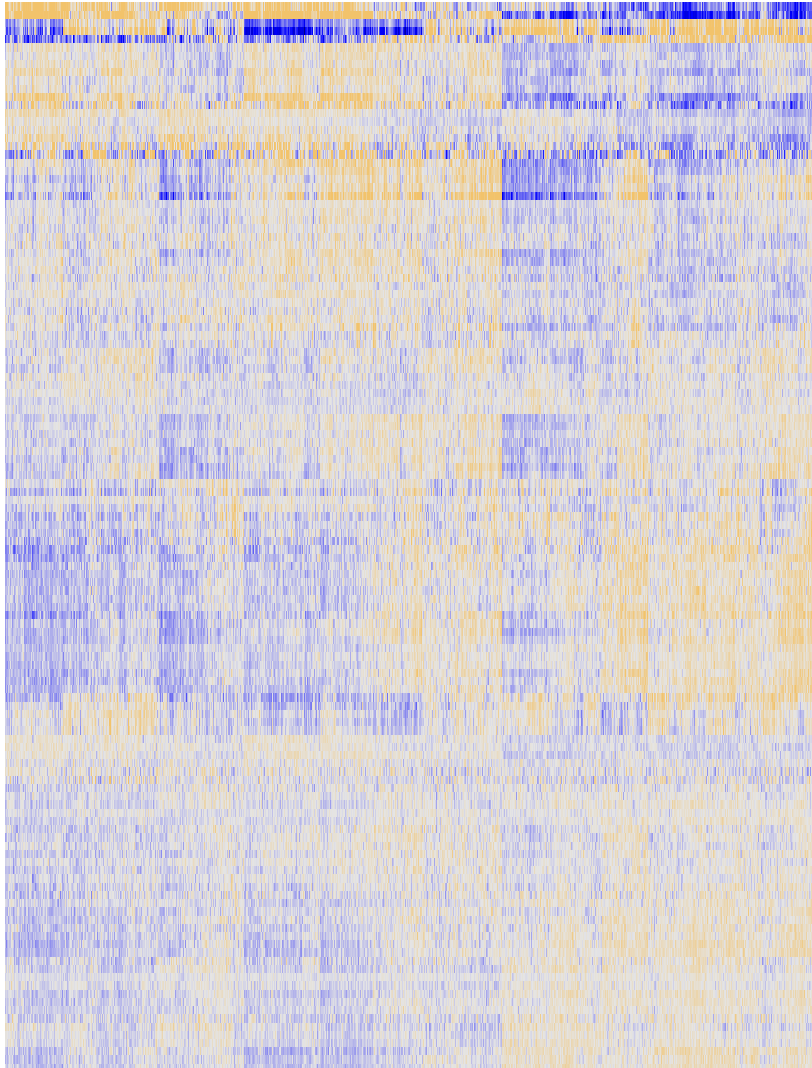
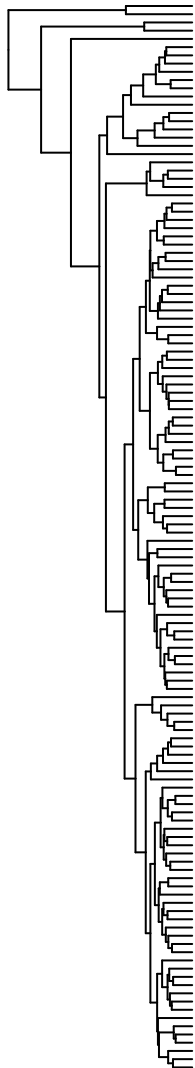
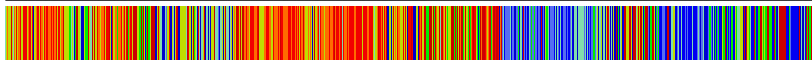
Category Melanoma



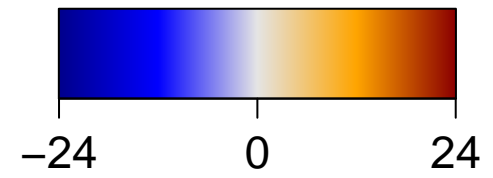


GSZ score

Category MF

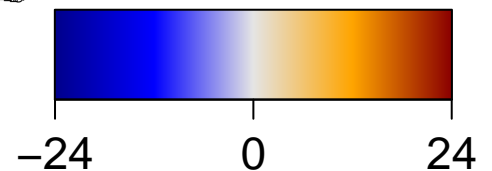
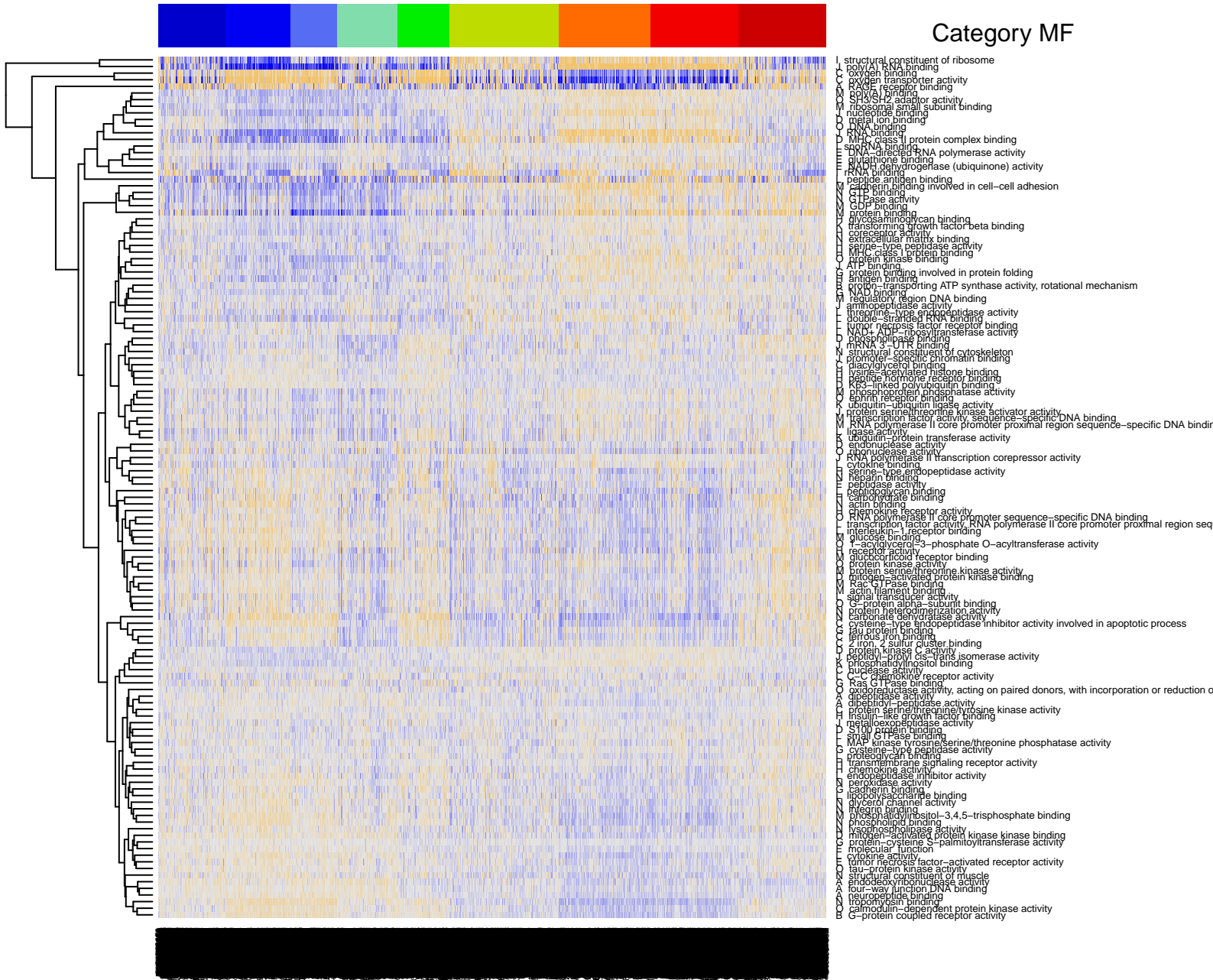


- 1 structural constituent of ribosome
- 107A RNA binding
- 108 cytoskeleton binding
- 109 oxygen transporter activity
- 110 RNA receptor binding
- 111 RNA binding
- 112 ribosomal small subunit binding
- 113 nucleotide binding
- 114 RNA binding
- 115 RNA class I protein complex binding
- 116 RNA directed RNA polymerase activity
- 117 RNA dehydrogenase (ubiquinone) activity
- 118 peptide antigen binding
- 119 cell-cell contact involved in cell-cell adhesion
- 120 DNA binding
- 121 GDP binding
- 122 protein binding
- 123 glycosaminoglycan binding
- 124 transforming growth factor beta binding
- 125 coreceptor activity
- 126 extracellular matrix binding
- 127 serine-type peptidase activity
- 128 RNA class I protein binding
- 129 protein kinase binding
- 130 protein binding involved in protein folding
- 131 ribonucleoprotein complex binding
- 132 ATP binding
- 133 regulatory region DNA binding
- 134 serine-type endopeptidase activity
- 135 double-stranded RNA binding
- 136 RNA polymerase II core promoter proximal region sequence-specific DNA binding
- 137 RNA polymerase II core promoter proximal region sequence-specific DNA binding
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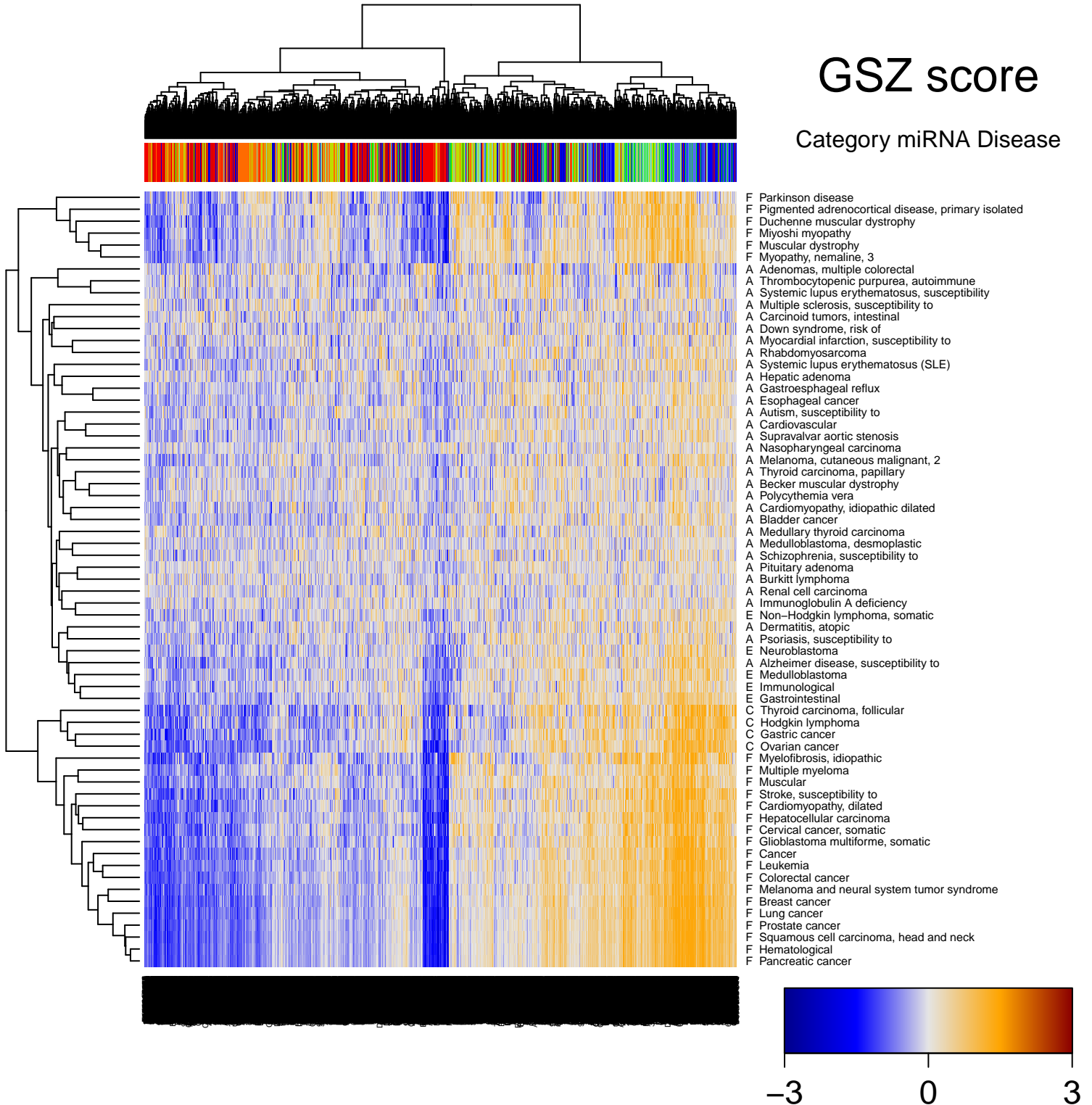
GSZ score

Category MF



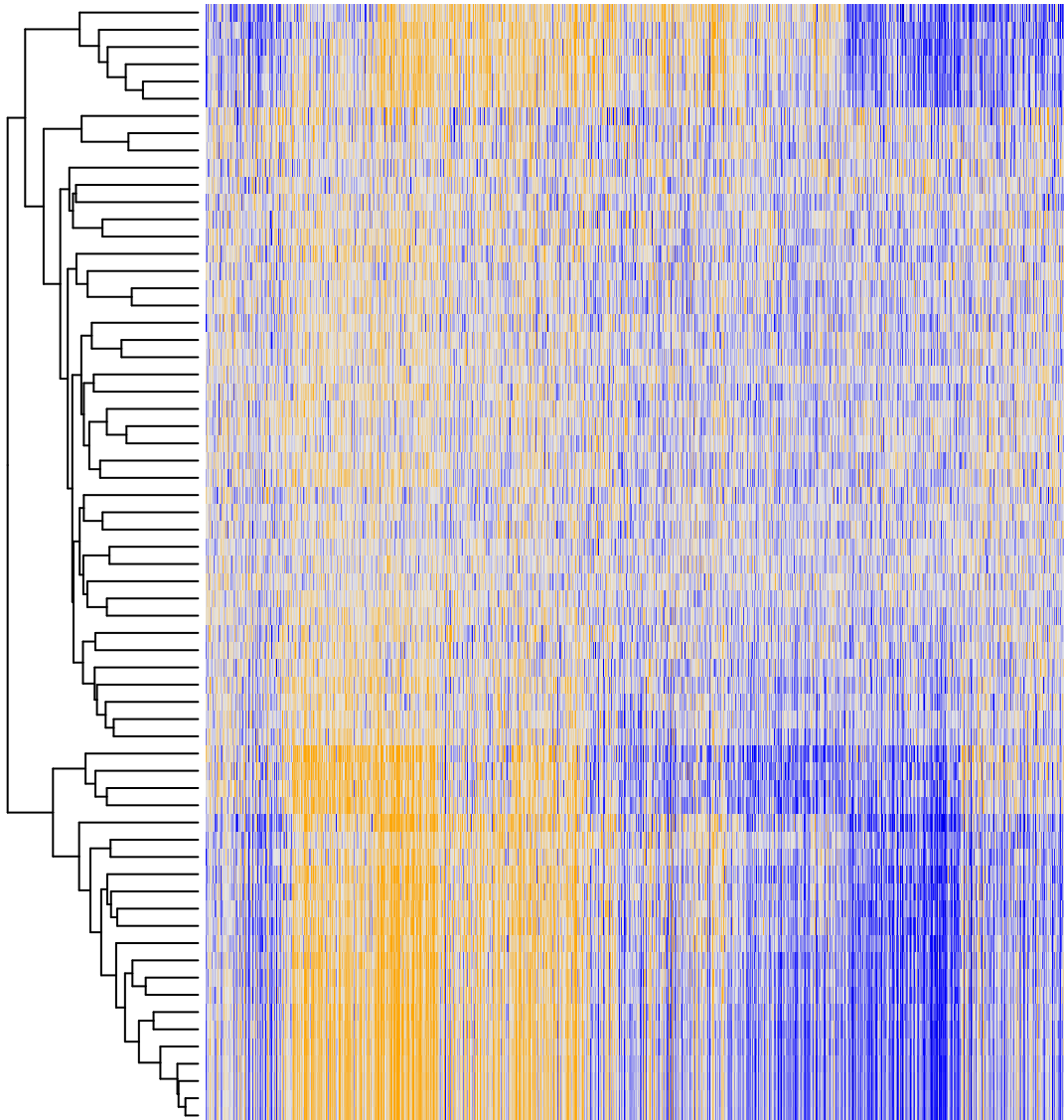
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Category miRNA Disease

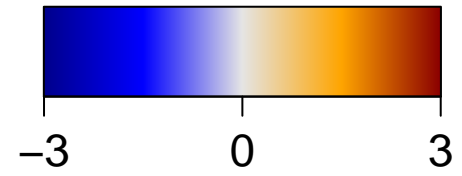


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Category miRNA Disease

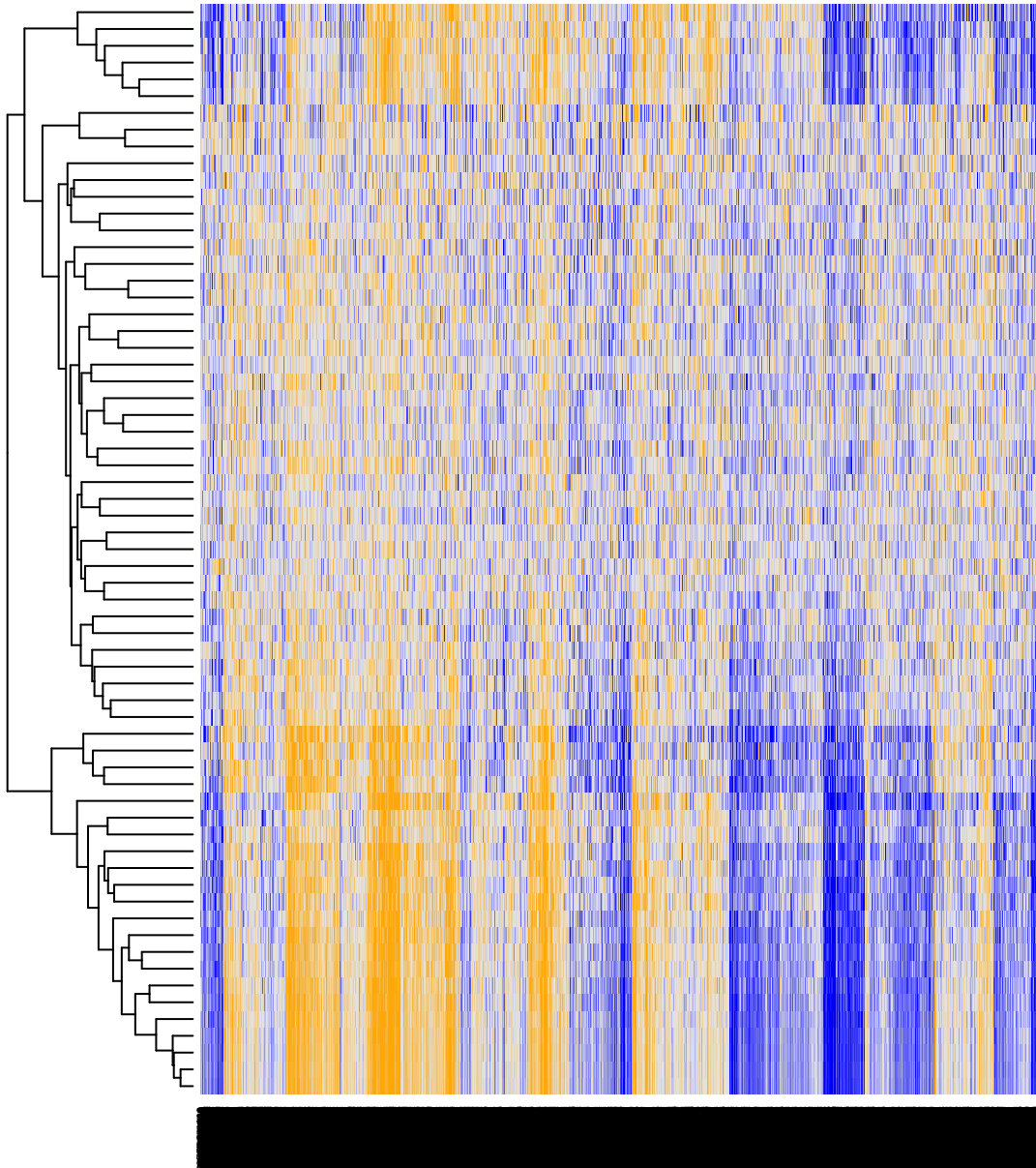


- F Parkinson disease
- F Pigmented adrenocortical disease, primary isolated
- F Duchenne muscular dystrophy
- F Miyoshi myopathy
- F Muscular dystrophy
- F Myopathy, nemaline, 3
- A Adenomas, multiple colorectal
- A Thrombocytopenic purpura, autoimmune
- A Systemic lupus erythematosus, susceptibility
- A Multiple sclerosis, susceptibility to
- A Carcinoid tumors, intestinal
- A Down syndrome, risk of
- A Myocardial infarction, susceptibility to
- A Rhabdomyosarcoma
- A Systemic lupus erythematosus (SLE)
- A Hepatic adenoma
- A Gastroesophageal reflux
- A Esophageal cancer
- A Autism, susceptibility to
- A Cardiovascular
- A Supravalvar aortic stenosis
- A Nasopharyngeal carcinoma
- A Melanoma, cutaneous malignant, 2
- A Thyroid carcinoma, papillary
- A Becker muscular dystrophy
- A Polycythemia vera
- A Cardiomyopathy, idiopathic dilated
- A Bladder cancer
- A Medullary thyroid carcinoma
- A Medulloblastoma, desmoplastic
- A Schizophrenia, susceptibility to
- A Pituitary adenoma
- A Burkitt lymphoma
- A Renal cell carcinoma
- A Immunoglobulin A deficiency
- E Non-Hodgkin lymphoma, somatic
- A Dermatitis, atopic
- A Psoriasis, susceptibility to
- E Neuroblastoma
- A Alzheimer disease, susceptibility to
- E Medulloblastoma
- E Immunological
- E Gastrointestinal
- C Thyroid carcinoma, follicular
- C Hodgkin lymphoma
- C Gastric cancer
- C Ovarian cancer
- F Myelofibrosis, idiopathic
- F Multiple myeloma
- F Muscular
- F Stroke, susceptibility to
- F Cardiomyopathy, dilated
- F Hepatocellular carcinoma
- F Cervical cancer, somatic
- F Glioblastoma multiforme, somatic
- F Cancer
- F Leukemia
- F Colorectal cancer
- F Melanoma and neural system tumor syndrome
- F Breast cancer
- F Lung cancer
- F Prostate cancer
- F Squamous cell carcinoma, head and neck
- F Hematological
- F Pancreatic cancer

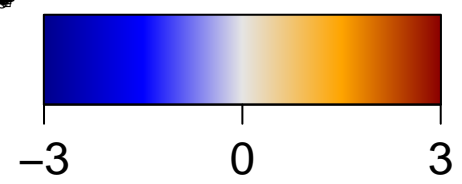


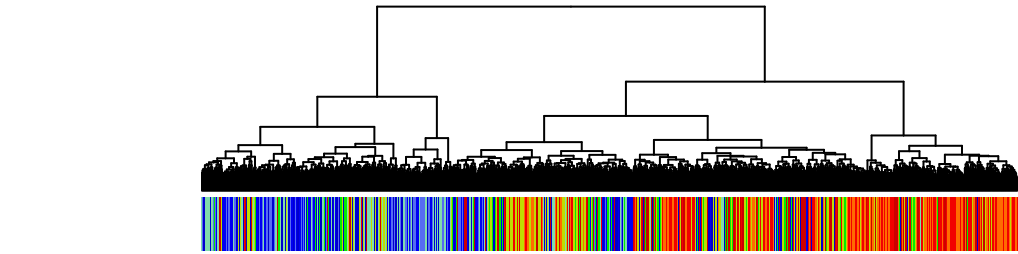
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Category miRNA Disease



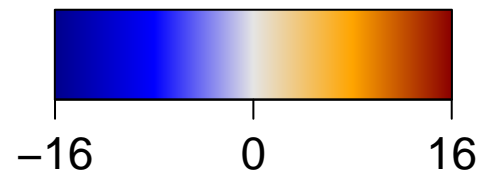
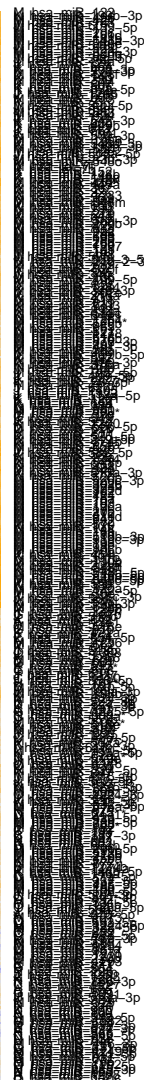
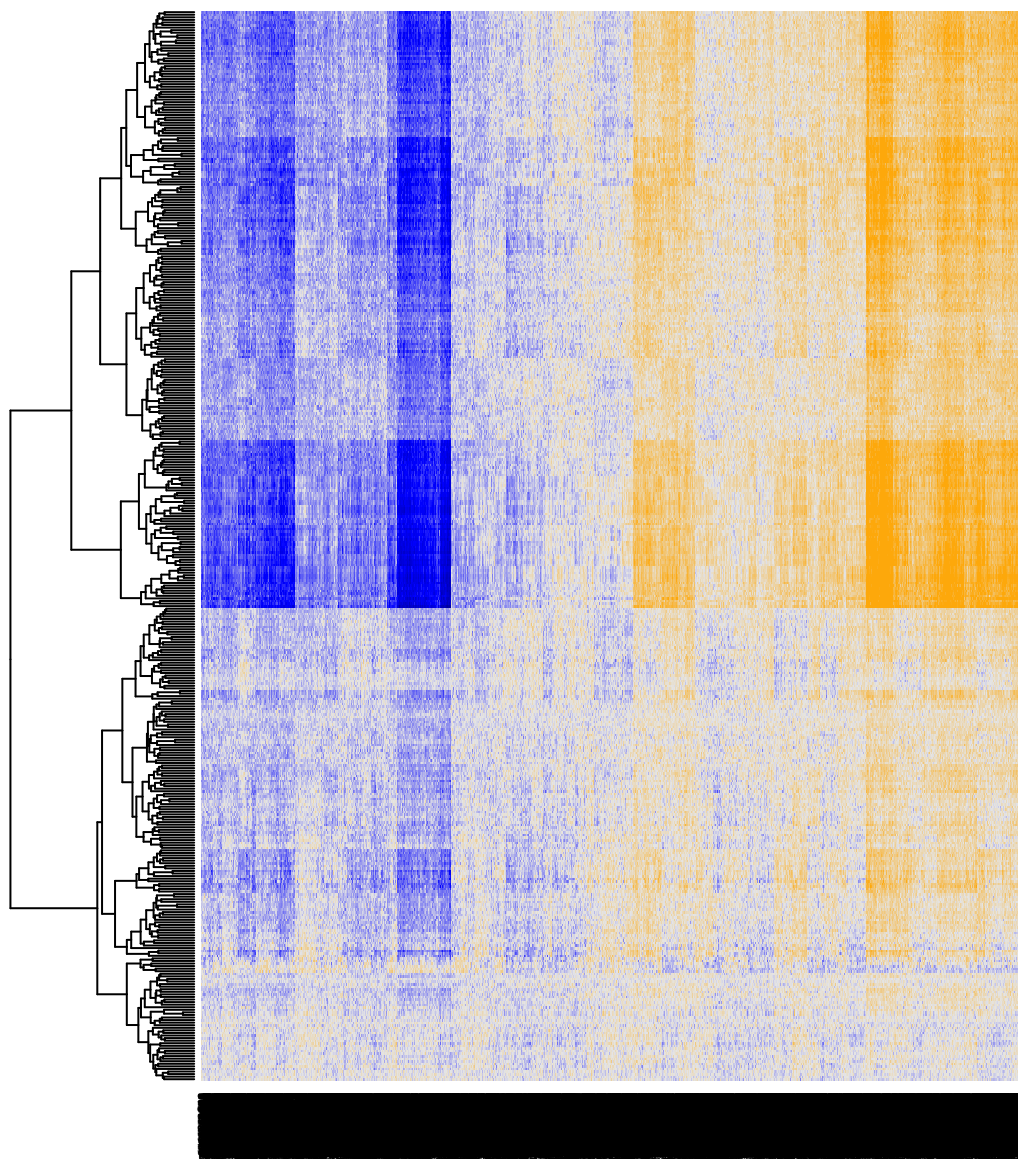
- F Parkinson disease
- F Pigmented adrenocortical disease, primary isolated
- F Duchenne muscular dystrophy
- F Miyoshi myopathy
- F Muscular dystrophy
- F Myopathy, nemaline, 3
- A Adenomas, multiple colorectal
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- A Becker muscular dystrophy
- A Polycythemia vera
- A Cardiomyopathy, idiopathic dilated
- A Bladder cancer
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- A Schizophrenia, susceptibility to
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- A Burkitt lymphoma
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- A Immunoglobulin A deficiency
- E Non-Hodgkin lymphoma, somatic
- A Dermatitis, atopic
- A Psoriasis, susceptibility to
- E Neuroblastoma
- A Alzheimer disease, susceptibility to
- E Medulloblastoma
- E Immunological
- E Gastrointestinal
- C Thyroid carcinoma, follicular
- C Hodgkin lymphoma
- C Gastric cancer
- C Ovarian cancer
- F Myelofibrosis, idiopathic
- F Multiple myeloma
- F Muscular
- F Stroke, susceptibility to
- F Cardiomyopathy, dilated
- F Hepatocellular carcinoma
- F Cervical cancer, somatic
- F Glioblastoma multiforme, somatic
- F Cancer
- F Leukemia
- F Colorectal cancer
- F Melanoma and neural system tumor syndrome
- F Breast cancer
- F Lung cancer
- F Prostate cancer
- F Squamous cell carcinoma, head and neck
- F Hematological
- F Pancreatic cancer





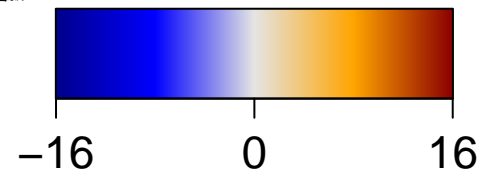
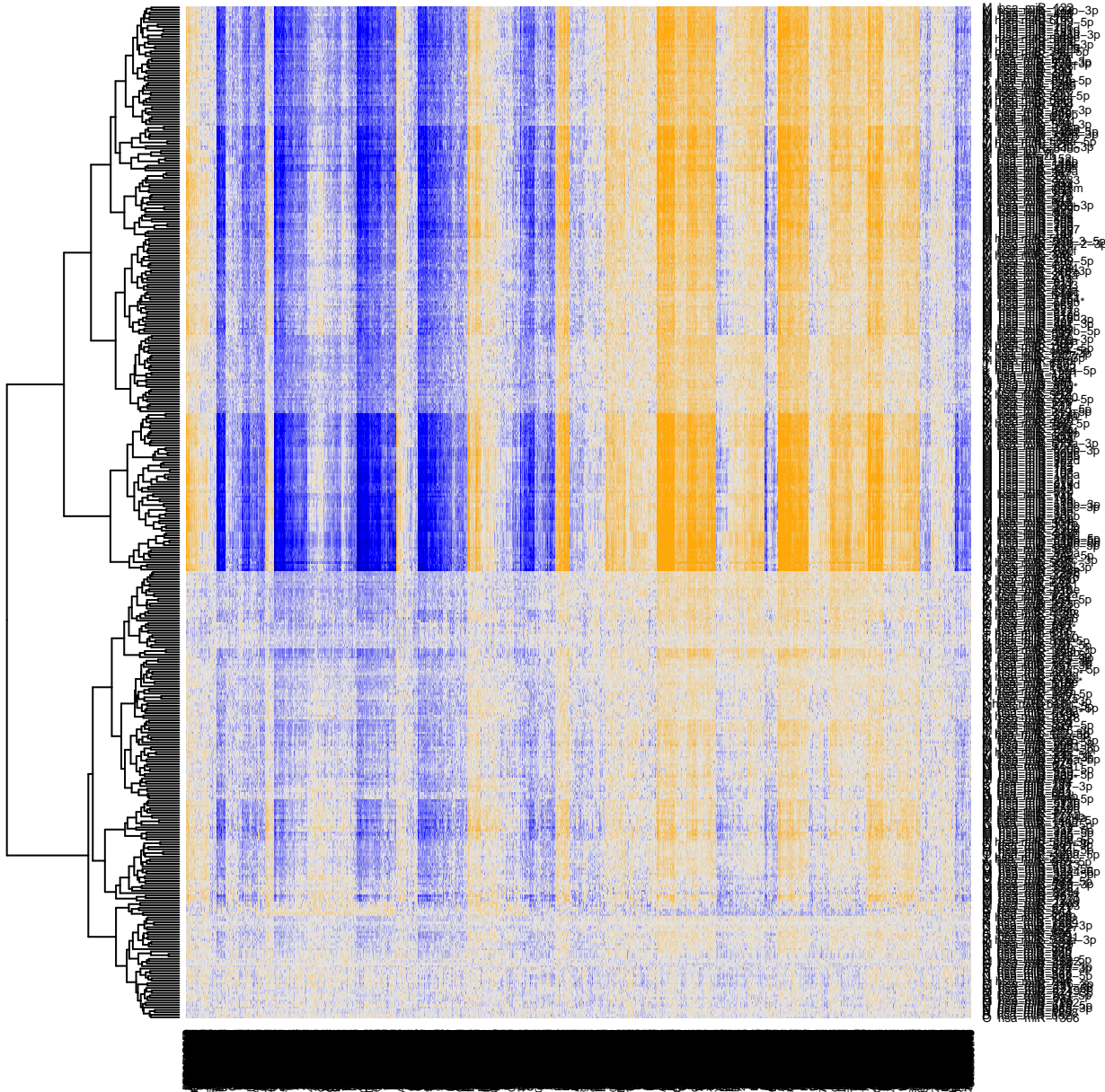
GSZ score

Category miRNA target



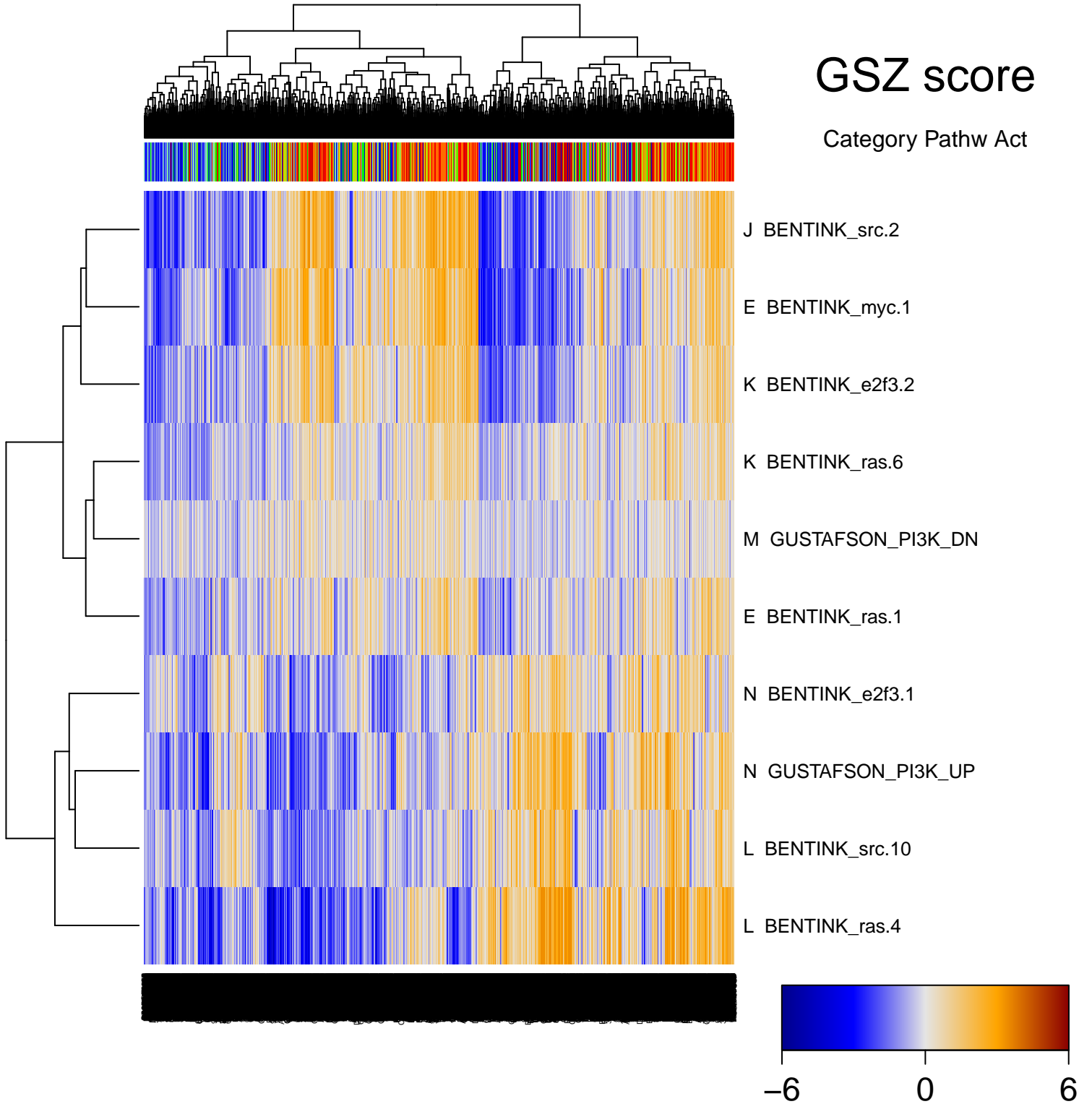
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Category miRNA target



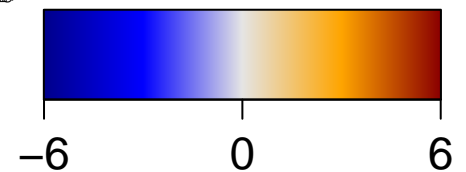
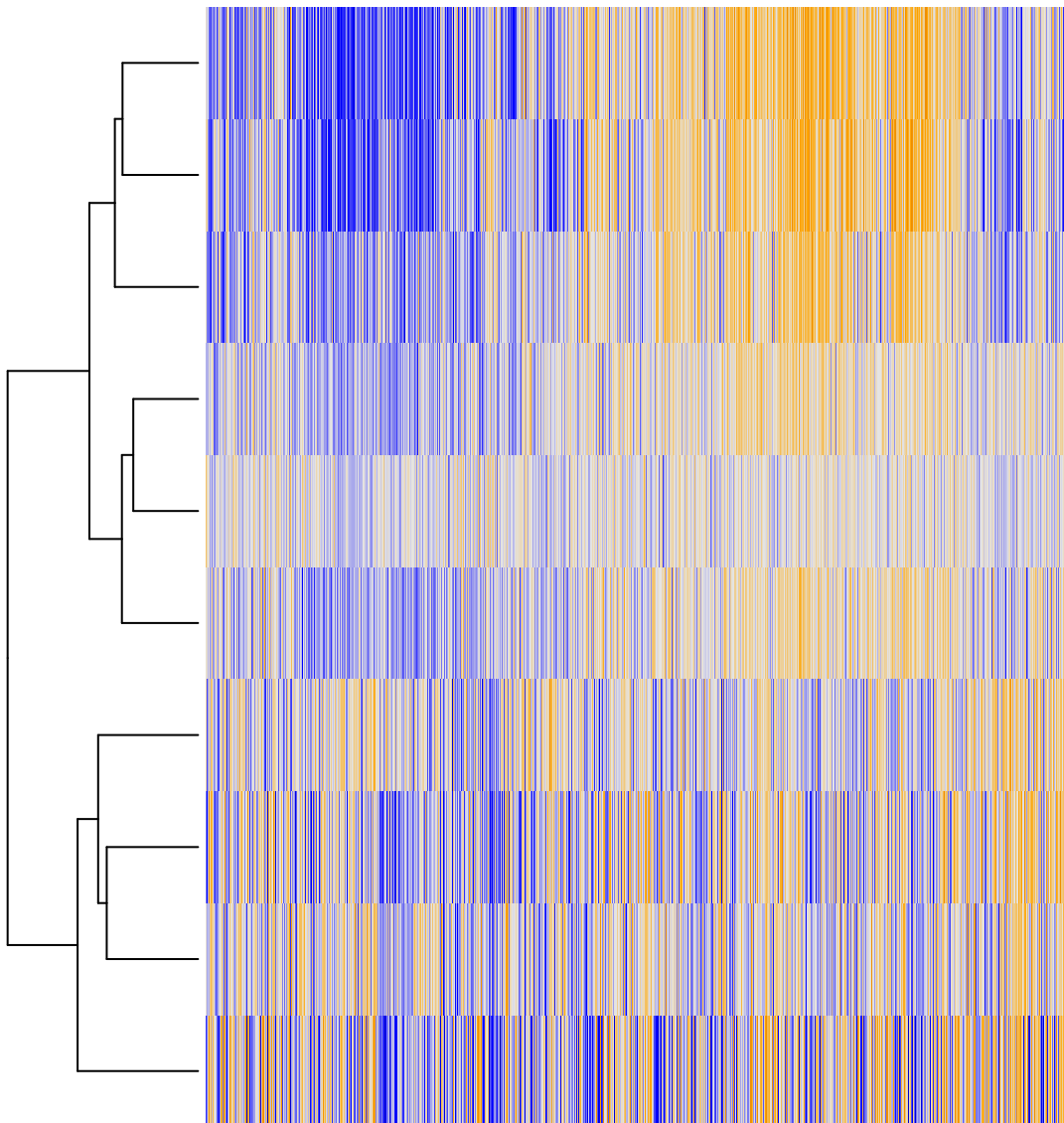
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Category Pathw Act



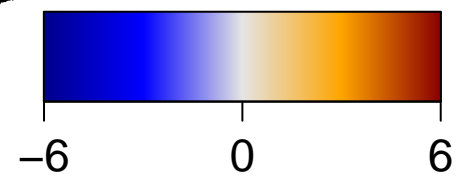
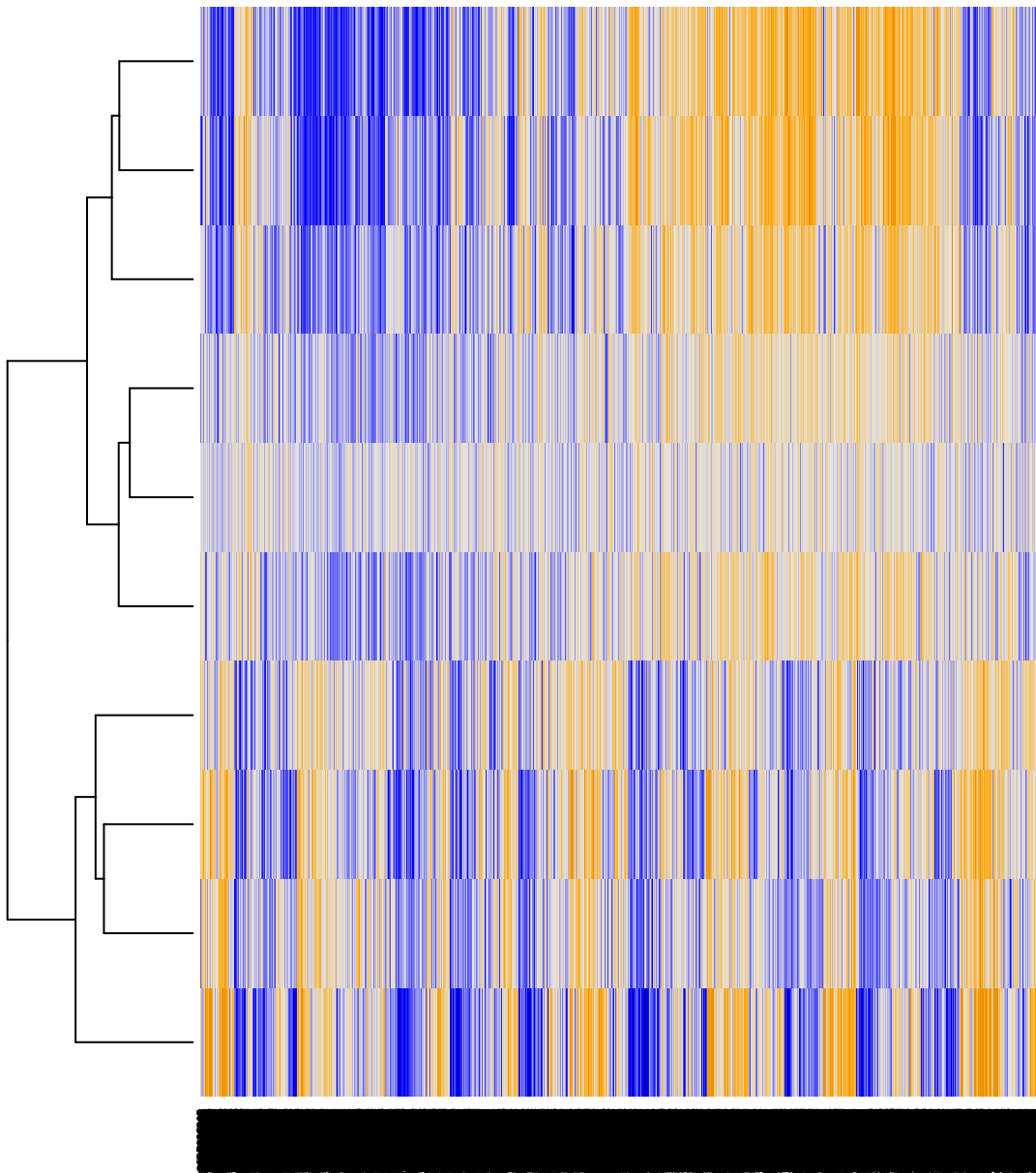
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Category Pathw Act



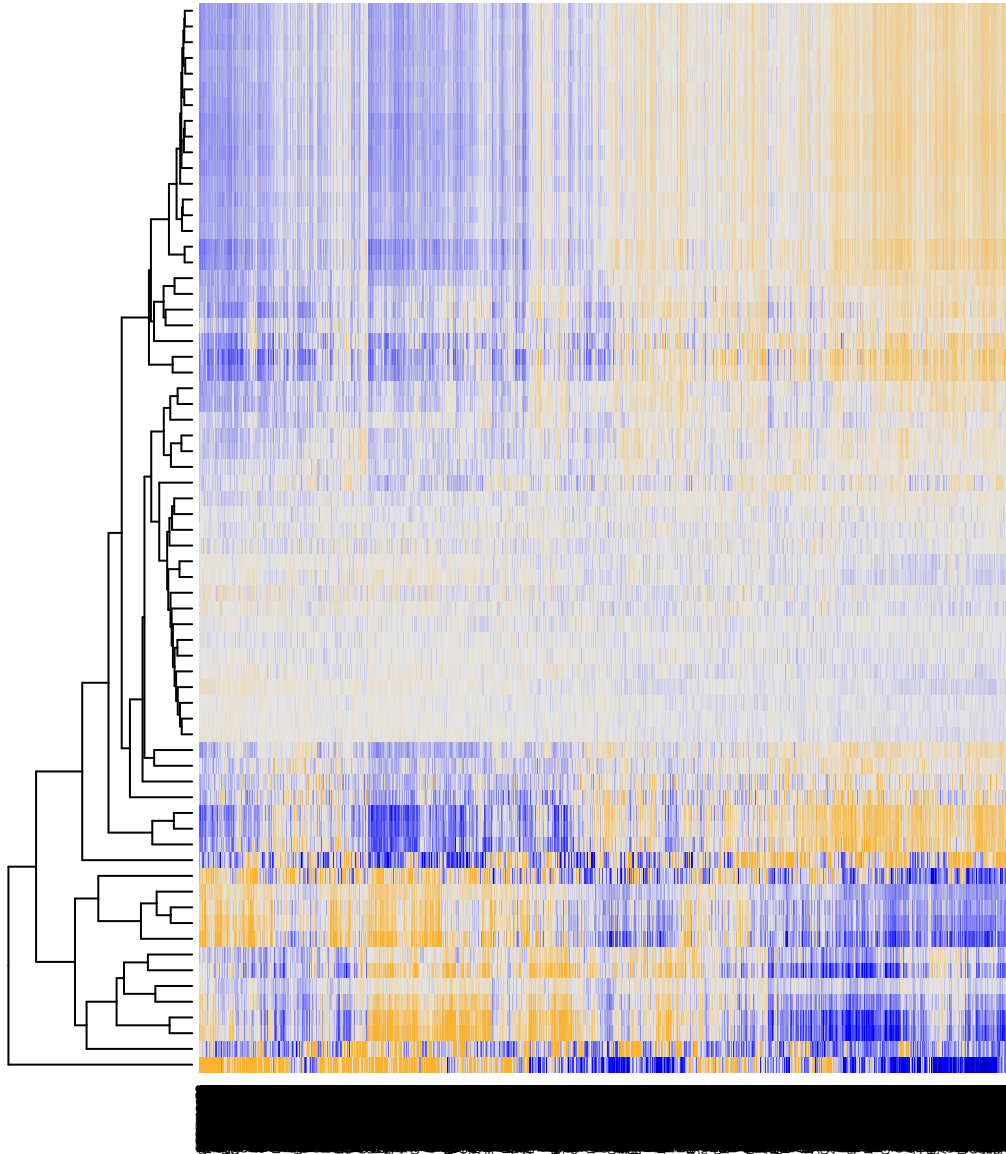
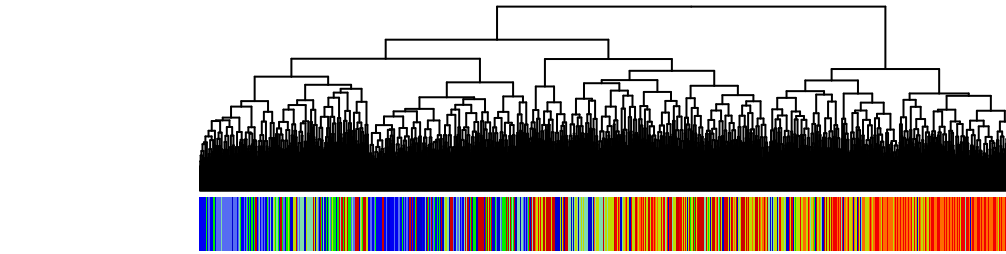
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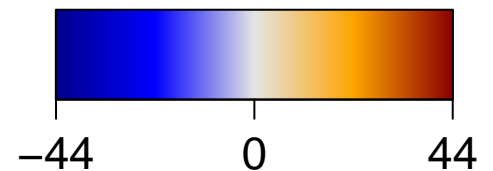


GSZ score

Category Reference Signatures

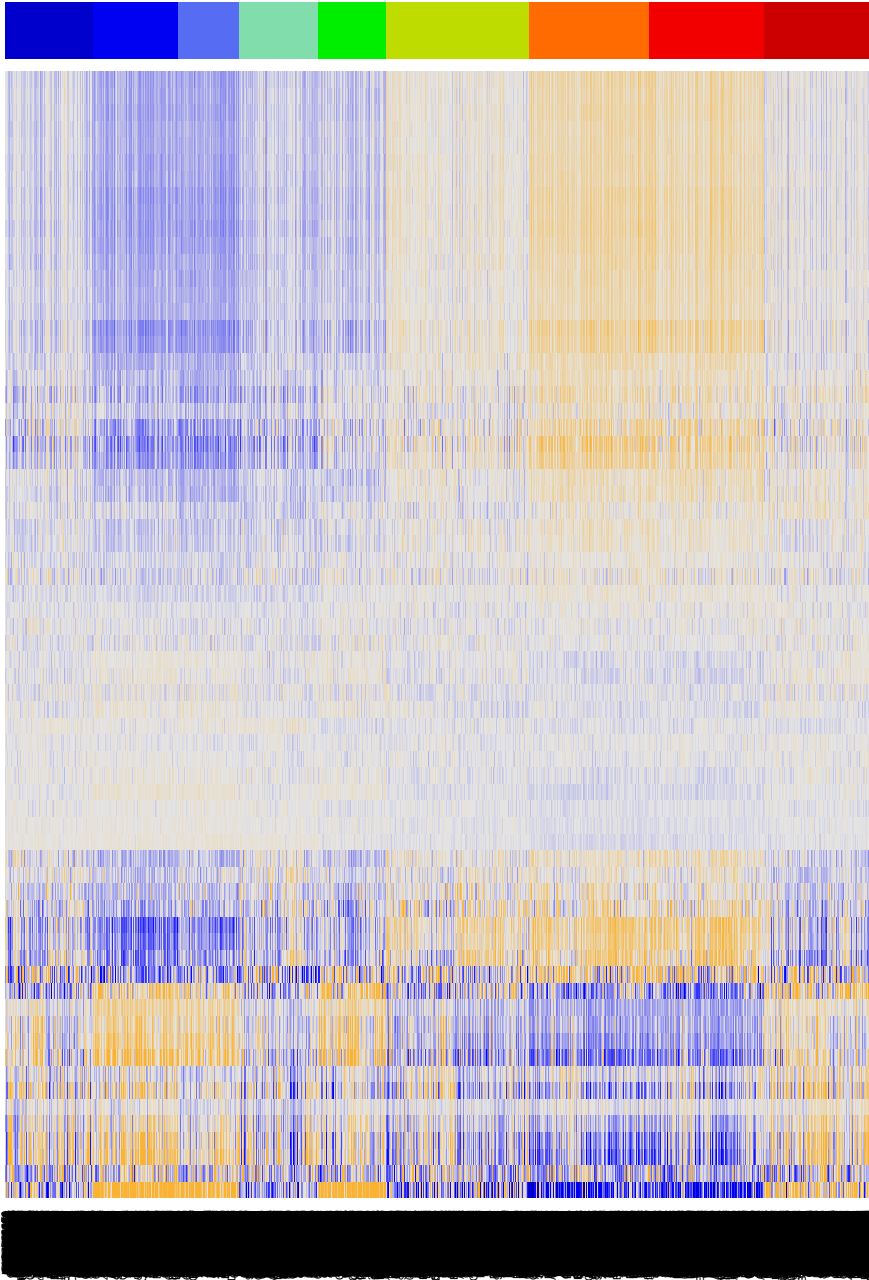


- J PROTEINATLAS_endometrium
- J PROTEINATLAS_gallbladder
- J PROTEINATLAS_cerebellum
- J PROTEINATLAS_salivary_gland
- J PROTEINATLAS_nasopharynx
- J PROTEINATLAS_seminal vesicle
- J PROTEINATLAS_kidney
- J PROTEINATLAS_adrenal_gland
- E PROTEINATLAS_stomach
- J PROTEINATLAS_testis
- J PROTEINATLAS_appendix
- J PROTEINATLAS_skin
- E PROTEINATLAS_placenta
- E PROTEINATLAS_colon
- J PROTEINATLAS_lateral ventricle
- J PROTEINATLAS_lymph node
- J PROTEINATLAS_tonsil
- K Chaussabel_1_8_Metabolism Biosynthesis
- K Chaussabel_3_6_Mitochondrial ribosomal proteins
- M Chaussabel_2_9_Cytoskeleton
- K Chaussabel_2_11_Replication
- H WIRTH_Immune system
- K Chaussabel_3_4_Protein phosphatases
- K Chaussabel_3_9_Kinases
- I PROTEINATLAS_spleen
- J PROTEINATLAS_lung
- J PROTEINATLAS_bone marrow
- L VAQUERIZAS_Lymph node_TF
- L VAQUERIZAS_Tonsil_TF
- L WIRTH_Lymphocytes
- H JONGENEEL_Peripheral Blood Lymphocytes
- I VAQUERIZAS_Thyroid_TF
- B JONGENEEL_Trachea
- L JONGENEEL_Spleen
- N WIRTH_Thyroid gland
- N JONGENEEL_Bladder
- N WIRTH_Sec_lymphoid organs
- C JONGENEEL_Fetal Brain
- C JONGENEEL_Thymus
- A Chaussabel_2_7_Unknown function
- H JONGENEEL_Uterus
- M WIRTH_B-cells
- O JONGENEEL_Lung
- N WIRTH_Nervous System
- L VAQUERIZAS_Heart_TF
- B WIRTH_Muscle
- B JONGENEEL_Colon
- E Chaussabel_3_7_Spliceosome
- K Chaussabel_3_8_Enzymes
- J Chaussabel_1_1_Plasma Cells
- I Chaussabel_1_3_B-cells
- I Chaussabel_1_7_MHC Ribosomal proteins
- I Chaussabel_2_4_Ribosomal proteins
- I Chaussabel_2_8_T-cells
- H Chaussabel_2_1_Cytotoxic cells
- N Chaussabel_1_2_Platelets
- C WIRTH_Prim_lymphoid organs
- C WIRTH_Bone marrow
- C JONGENEEL_Bone Marrow
- C Chaussabel_2_2_Neutrophils
- L Chaussabel_2_10_Immune related cell surface molecules
- L Chaussabel_1_5_Myeloid lineage
- M VAQUERIZAS_Whole blood_TF
- O Chaussabel_3_2_Inflammation I
- M Chaussabel_3_3_Inflammation II
- O Chaussabel_2_6_Myeloid lineage
- L Chaussabel_3_1_Interferon-inducible
- C Chaussabel_2_3_Erythrocytes

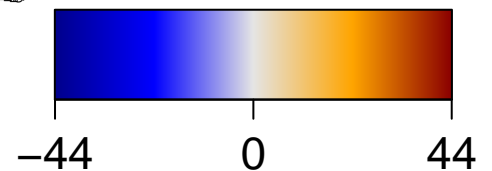


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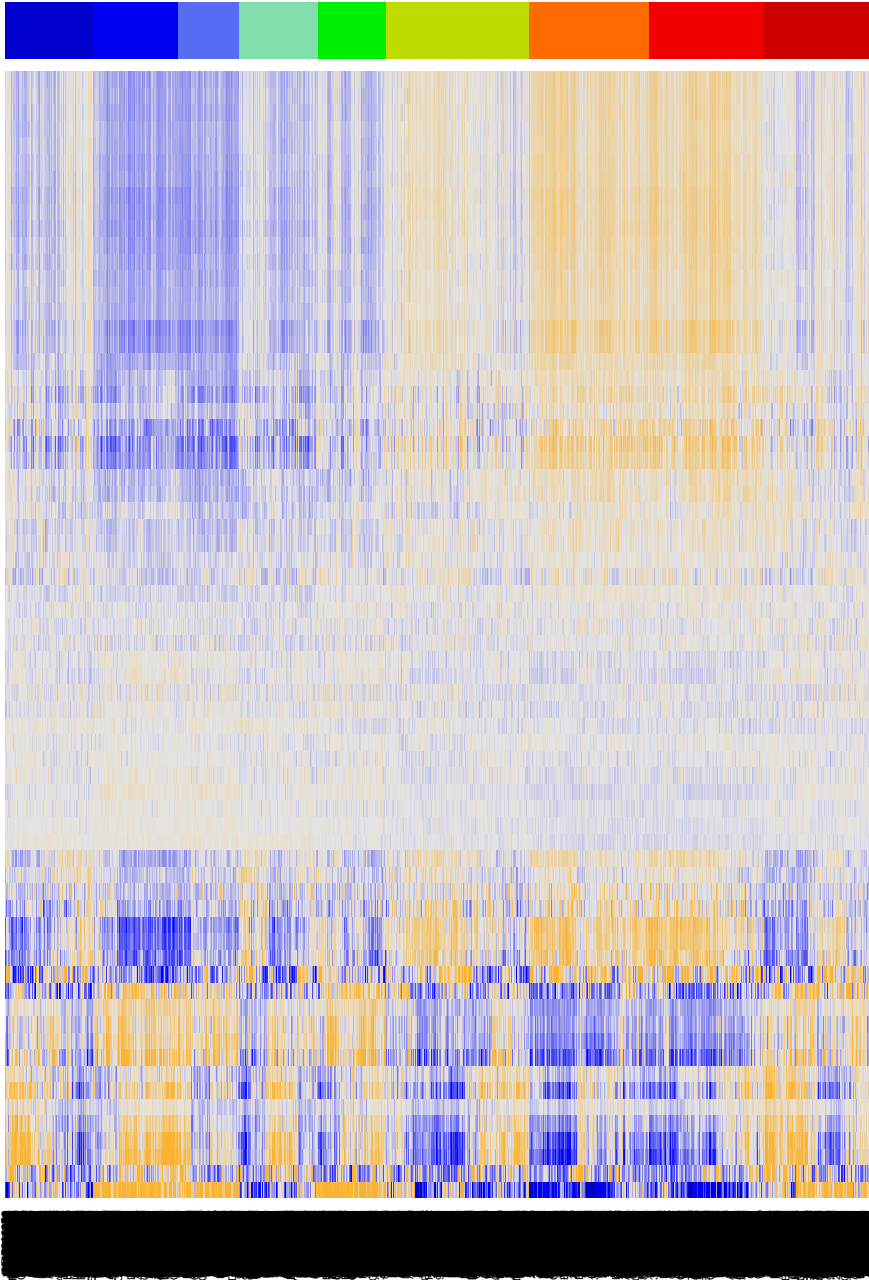


J PROTEINATLAS_endometrium
J PROTEINATLAS_gallbladder
J PROTEINATLAS_cerebellum
J PROTEINATLAS_salivary_gland
J PROTEINATLAS_nasopharynx
J PROTEINATLAS_seminal vesicle
J PROTEINATLAS_kidney
J PROTEINATLAS_adrenal_gland
E PROTEINATLAS_stomach
J PROTEINATLAS_testis
J PROTEINATLAS_appendix
J PROTEINATLAS_skin
E PROTEINATLAS_placenta
E PROTEINATLAS_colon
J PROTEINATLAS_lateral ventricle
J PROTEINATLAS_lymph node
J PROTEINATLAS_tonsil
K Chaussabel_1.8_Metabolism Biosynthesis
K Chaussabel_3.6_Mitochondrial ribosomal proteins
M Chaussabel_2.9_Cytoskeleton
K Chaussabel_2.11_Replication
H WIRTH_Immune system
K Chaussabel_3.4_Protein phosphatases
K Chaussabel_3.9_Kinases
I PROTEINATLAS_spleen
J PROTEINATLAS_lung
J PROTEINATLAS_bone marrow
L VAQUERIZAS_Lymph node_TF
L VAQUERIZAS_tonsil_TF
L WIRTH_Lymphocytes
H JONGENEEL_Peripheral Blood Lymphocytes
I VAQUERIZAS_Thyroid_TF
B JONGENEEL_Trachea
L JONGENEEL_Spleen
N WIRTH_Thyroid_gland
N JONGENEEL_Bladder
N WIRTH_Sec.lymphoid organs
C JONGENEEL_Fetal Brain
C JONGENEEL_Thymus
A Chaussabel_2.7_Unknown function
H JONGENEEL_Uterus
M WIRTH_B-cells
O JONGENEEL_Lung
N WIRTH_Nervous System
L VAQUERIZAS_Heart_TF
B WIRTH_Muscle
B JONGENEEL_Colon
E Chaussabel_3.7_Spliceosome
K Chaussabel_3.8_Enzymes
J Chaussabel_1.1_Plasma Cells
I Chaussabel_1.3_B-cells
I Chaussabel_1.7_MHC Ribosomal proteins
I Chaussabel_2.4_Ribosomal proteins
I Chaussabel_2.8_T-cells
H Chaussabel_2.1_Cytotoxic cells
N Chaussabel_1.2_Platelets
C WIRTH_Prim.lymphoid organs
C WIRTH_Bone marrow
C JONGENEEL_Bone Marrow
C Chaussabel_2.2_Neutrophils
L Chaussabel_2.10_Immune related cell surface molecules
L Chaussabel_1.5_Myeloid lineage
M VAQUERIZAS_Whole blood_TF
O Chaussabel_3.2_Inflammation I
M Chaussabel_3.3_Inflammation II
O Chaussabel_2.6_Myeloid lineage
L Chaussabel_3.1_Interferon-inducible
C Chaussabel_2.3_Erythrocytes

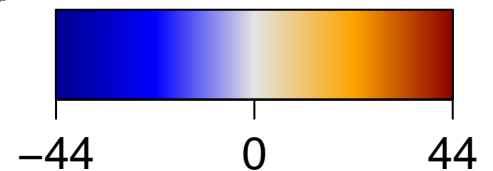


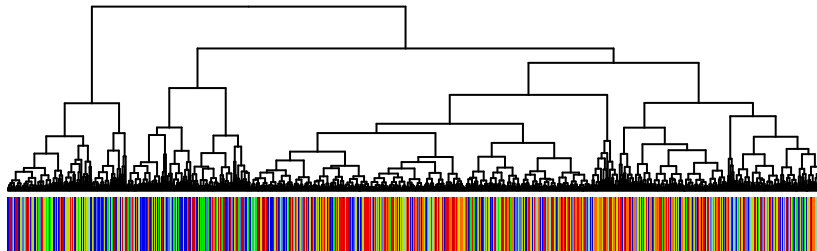
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Category Reference Signatures



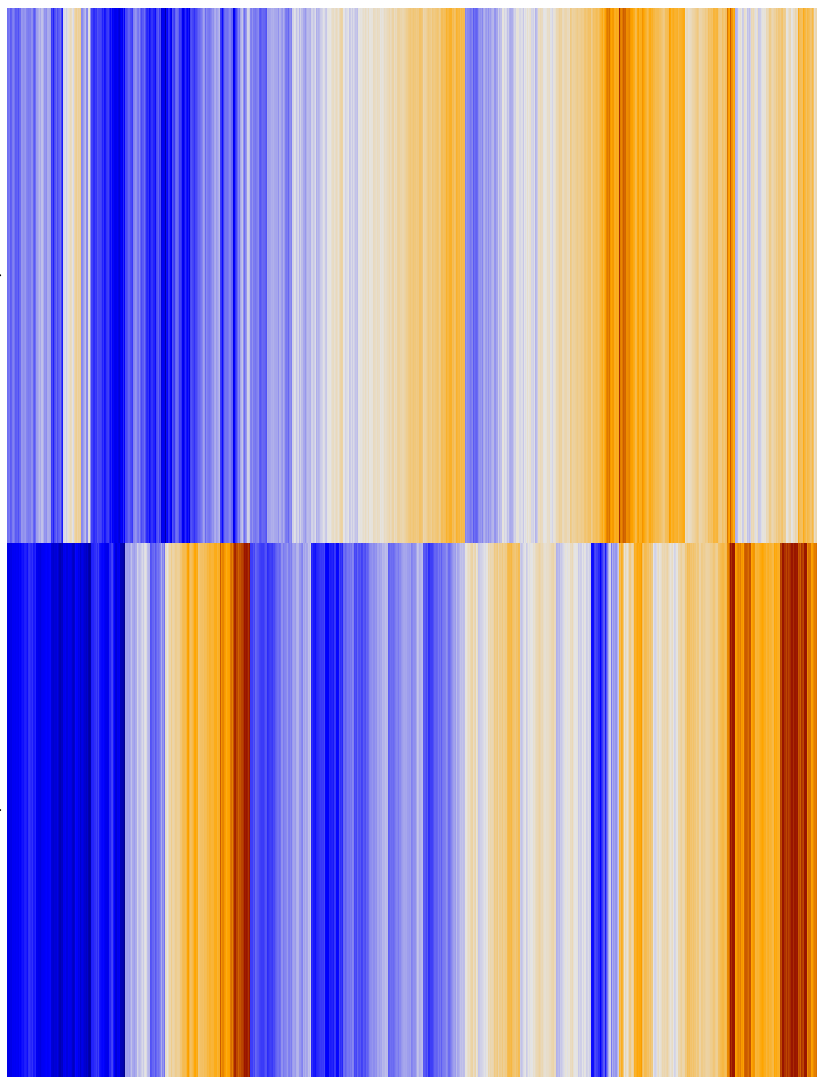
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J PROTEINATLAS_kidney
J PROTEINATLAS_adrenal_gland
E PROTEINATLAS_stomach
J PROTEINATLAS_testis
J PROTEINATLAS_appendix
J PROTEINATLAS_skin
E PROTEINATLAS_placenta
E PROTEINATLAS_colon
J PROTEINATLAS_lateral ventricle
J PROTEINATLAS_lymph node
J PROTEINATLAS_tonsil
K Chaussabel_1.8_Metabolism Biosynthesis
K Chaussabel_3.6_Mitochondrial ribosomal proteins
M Chaussabel_2.9_Cytoskeleton
K Chaussabel_2.11_Replication
H WIRTH_Immune system
K Chaussabel_3.4_Protein phosphatases
K Chaussabel_3.9_Kinases
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J PROTEINATLAS_lung
J PROTEINATLAS_bone marrow
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L VAQUERIZAS_tonsil_TF
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H JONGENEEL_Peripheral Blood Lymphocytes
I VAQUERIZAS_Thyroid_TF
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L JONGENEEL_Spleen
N WIRTH_Thyroid_gland
N JONGENEEL_Bladder
N WIRTH_Sec. lymphoid organs
C JONGENEEL_Fetal Brain
C JONGENEEL_Thymus
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M WIRTH_B-cells
O JONGENEEL_Lung
N WIRTH_Nervous System
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O Chaussabel_2.6_Myeloid lineage
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C Chaussabel_2.3_Erythrocytes





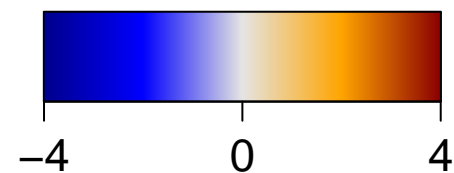
GSZ score

Category Telomeres



A Alternative le

C Nabetani_alt



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0

4

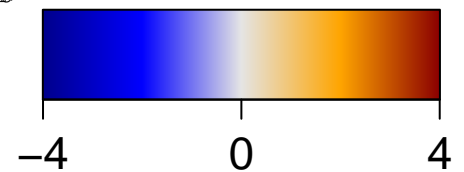
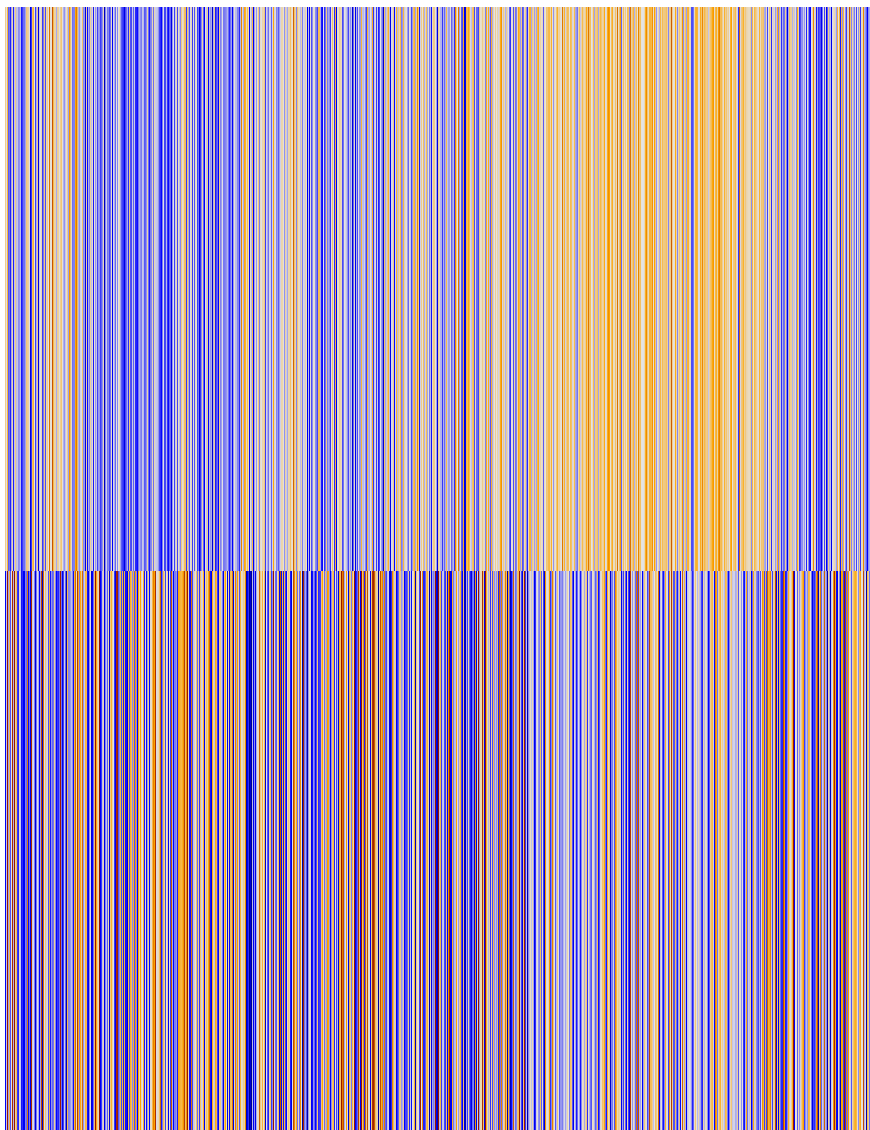
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Category Telomeres



A Alternative le

C Nabetani_al



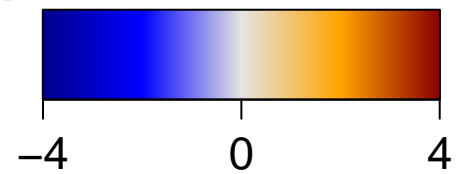
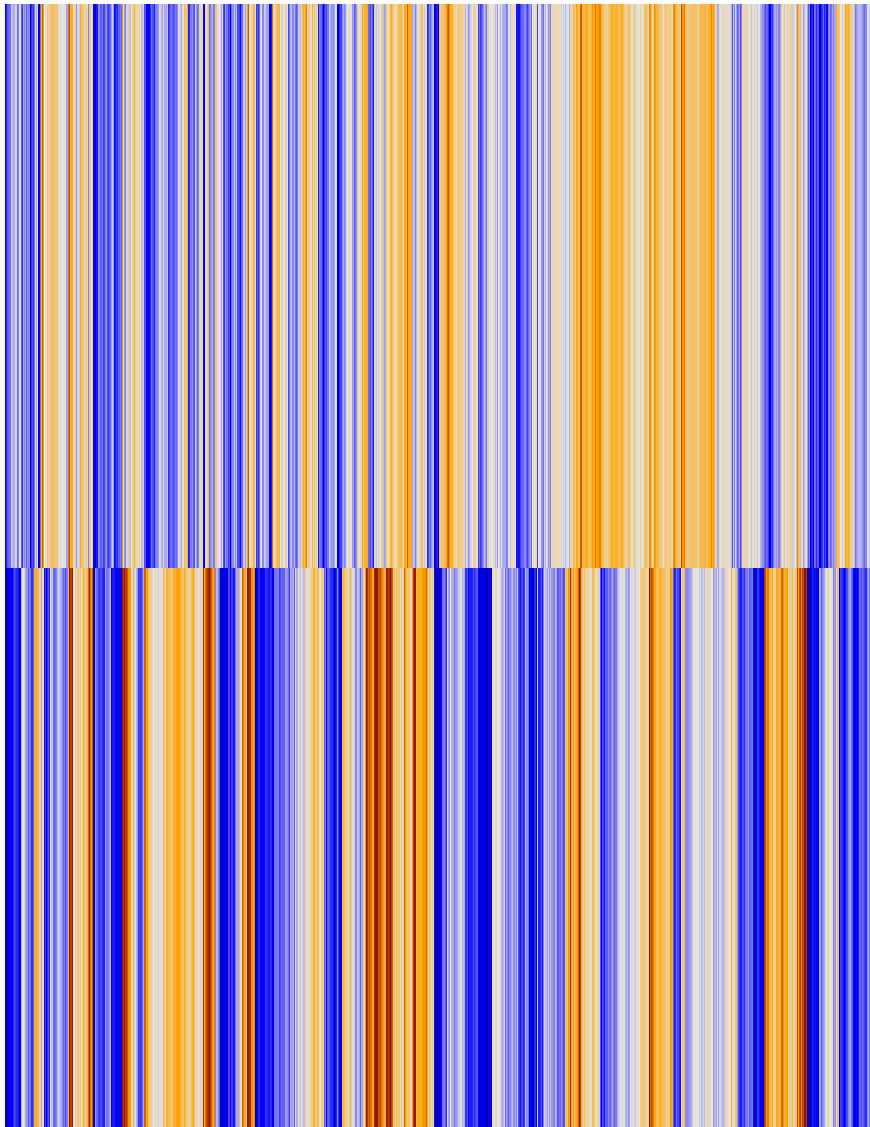
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Category Telomeres



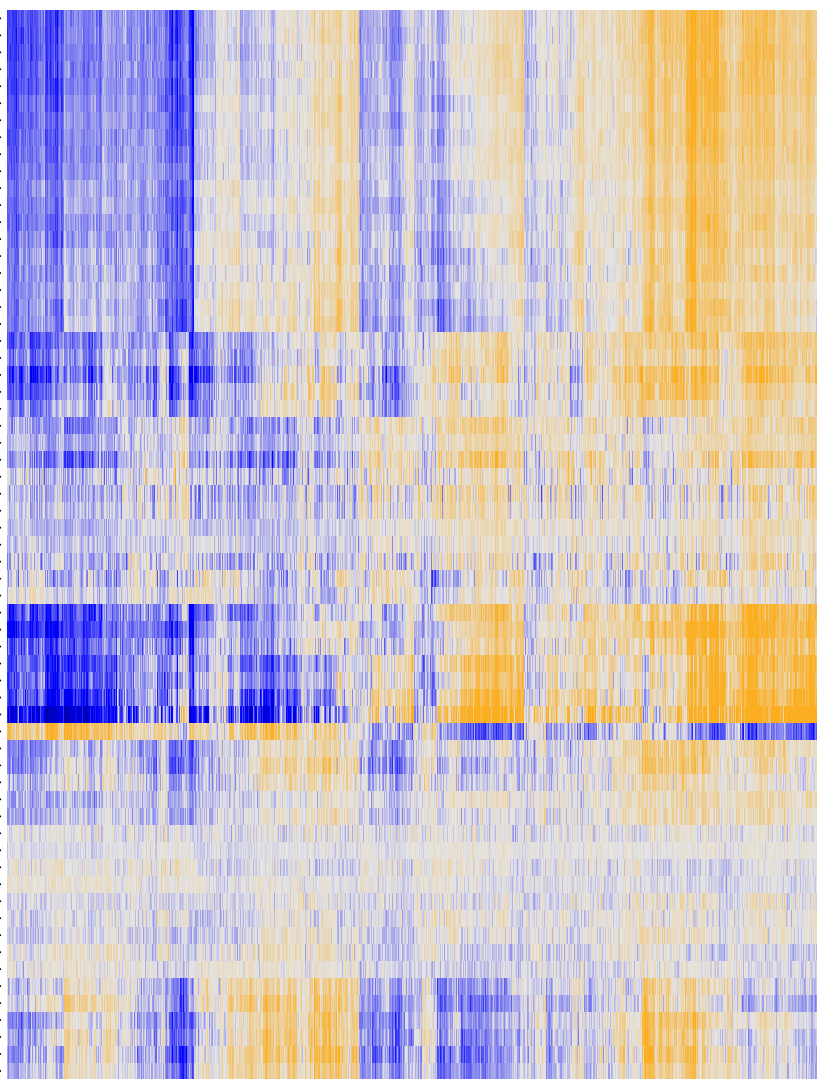
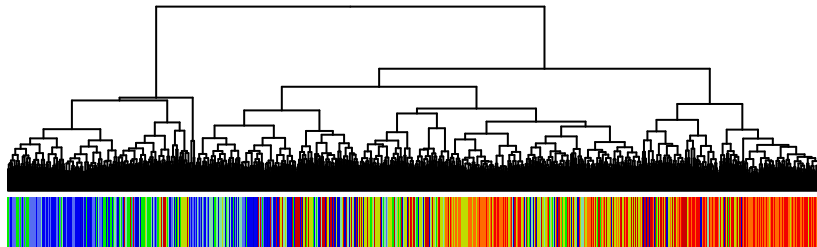
A Alternative le

C Nabetani_al

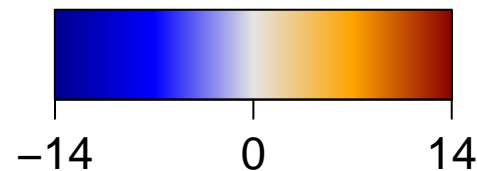


GSZ score

Category TF

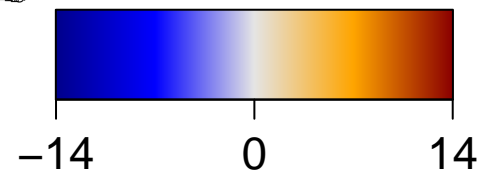
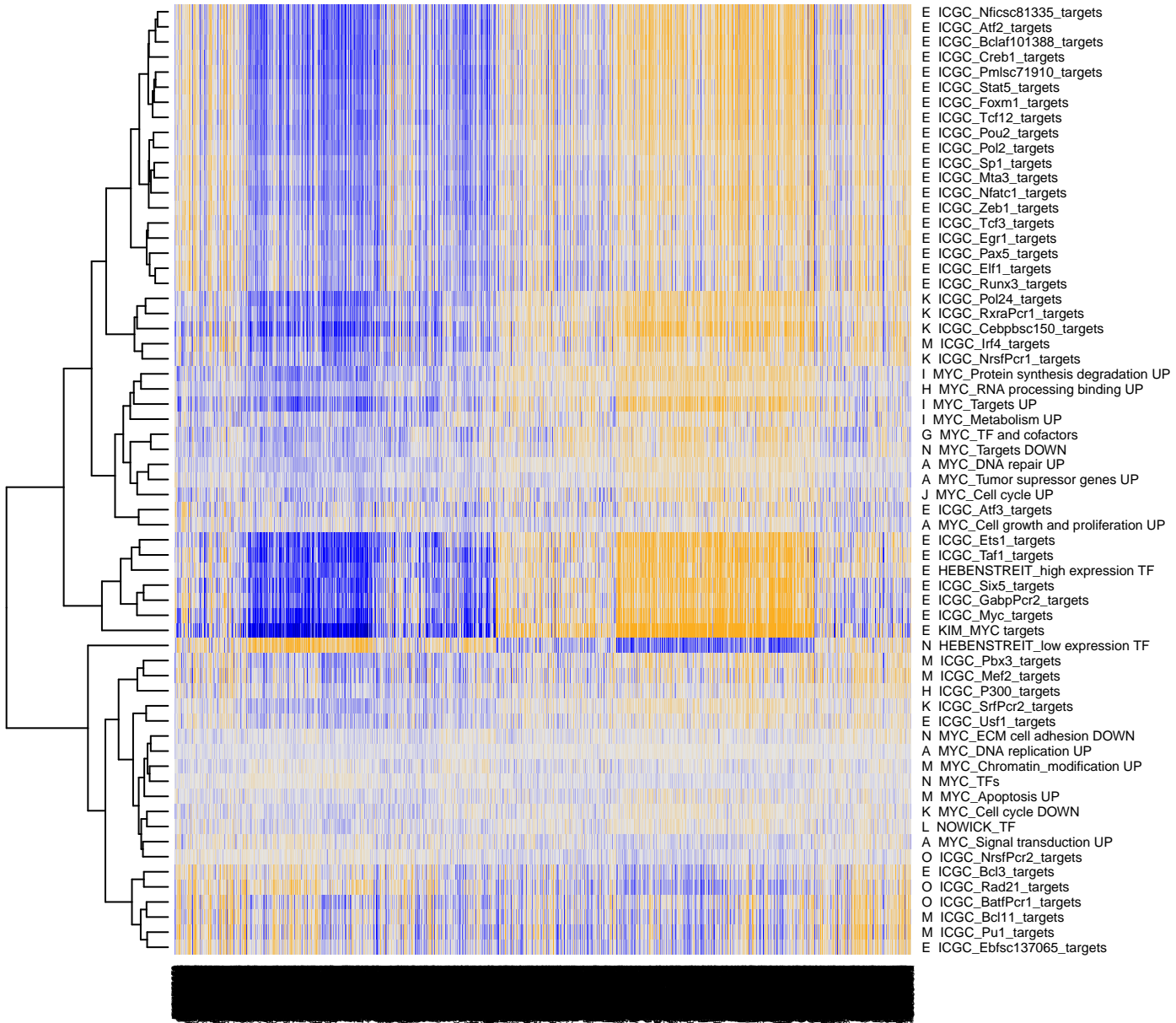


E ICGC_Nficsc81335_targets
E ICGC_Atf2_targets
E ICGC_Bclaf101388_targets
E ICGC_Creb1_targets
E ICGC_Pmlsc71910_targets
E ICGC_Stat5_targets
E ICGC_Foxm1_targets
E ICGC_Tcf12_targets
E ICGC_Pou2_targets
E ICGC_Pol2_targets
E ICGC_Sp1_targets
E ICGC_Mta3_targets
E ICGC_Nfatc1_targets
E ICGC_Zeb1_targets
E ICGC_Tcf3_targets
E ICGC_Egr1_targets
E ICGC_Pax5_targets
E ICGC_Elf1_targets
E ICGC_Runx3_targets
K ICGC_Pol24_targets
K ICGC_RxraPcr1_targets
K ICGC_Cebpsc150_targets
M ICGC_Irf4_targets
K ICGC_NrsfPcr1_targets
I MYC_Protein synthesis degradation UP
H MYC_RNA processing binding UP
I MYC_Targets UP
I MYC_Metabolism UP
G MYC_TF and cofactors
N MYC_Targets DOWN
A MYC_DNA repair UP
A MYC_Tumor suppressor genes UP
J MYC_Cell cycle UP
E ICGC_Atf3_targets
A MYC_Cell growth and proliferation UP
E ICGC_Ets1_targets
E ICGC_Taf1_targets
E HEBENSTREIT_high expression TF
E ICGC_Six5_targets
E ICGC_GabpPcr2_targets
E ICGC_Myc_targets
E KIM_MYC targets
N HEBENSTREIT_low expression TF
M ICGC_Pbx3_targets
M ICGC_Mef2_targets
H ICGC_P300_targets
K ICGC_SrfPcr2_targets
E ICGC_Usf1_targets
N MYC_ECM cell adhesion DOWN
A MYC_DNA replication UP
M MYC_Chromatin_modification UP
N MYC_TFs
M MYC_Apoptosis UP
K MYC_Cell cycle DOWN
L NOWICK_TF
A MYC_Signal transduction UP
O ICGC_NrsfPcr2_targets
E ICGC_Bcl3_targets
O ICGC_Rad21_targets
O ICGC_BatfPcr1_targets
M ICGC_Bcl11_targets
M ICGC_Pu1_targets
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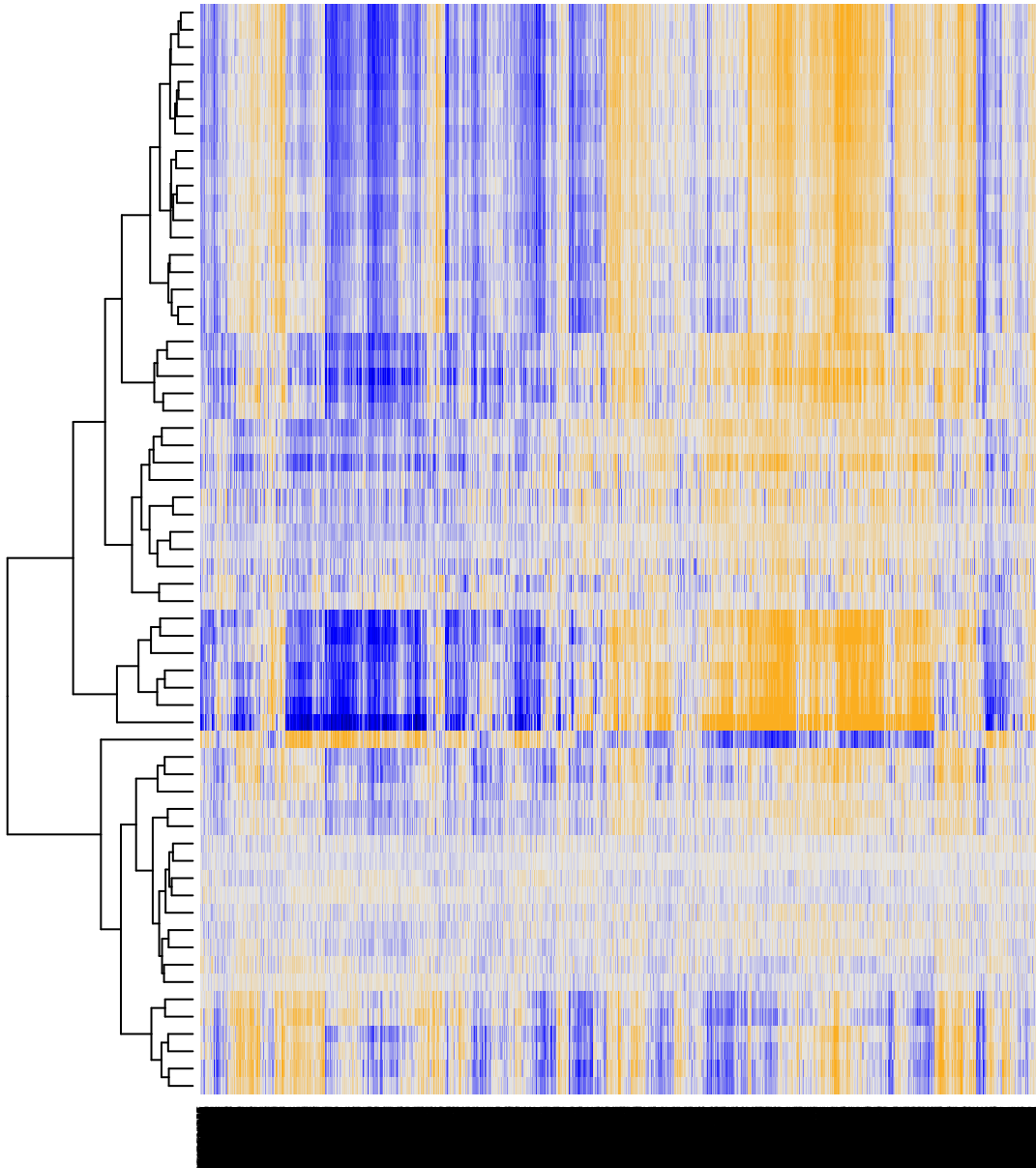
GSZ score

Category TF



GSZ score

Category TF



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- K ICGC_Cebpbc150_targets
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- K ICGC_NrsfPcr1_targets
- I MYC_Protein synthesis degradation UP
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- I MYC_Targets UP
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- E ICGC_Ebfsc137065_targets

