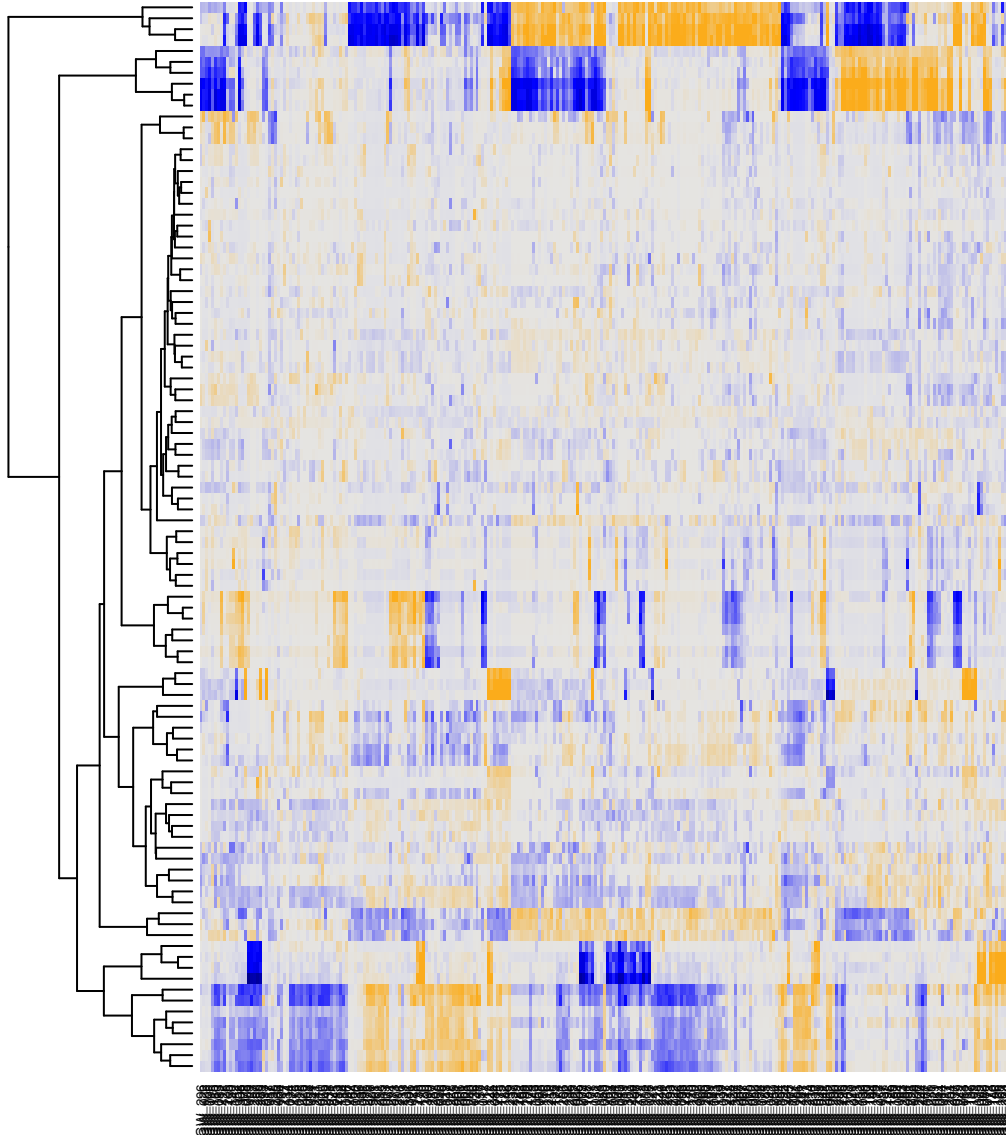
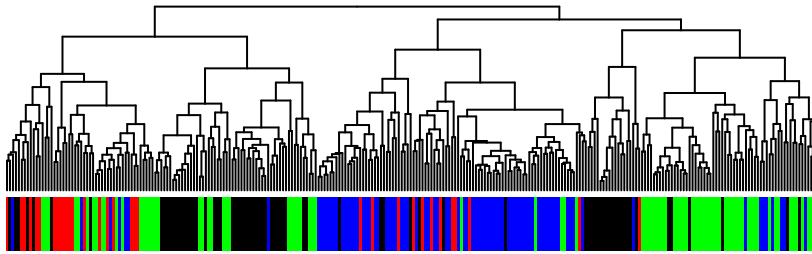
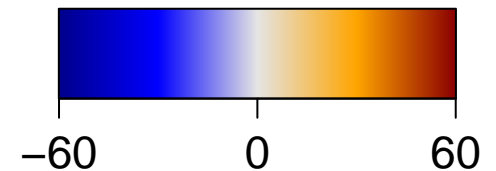


GSZ score

BP

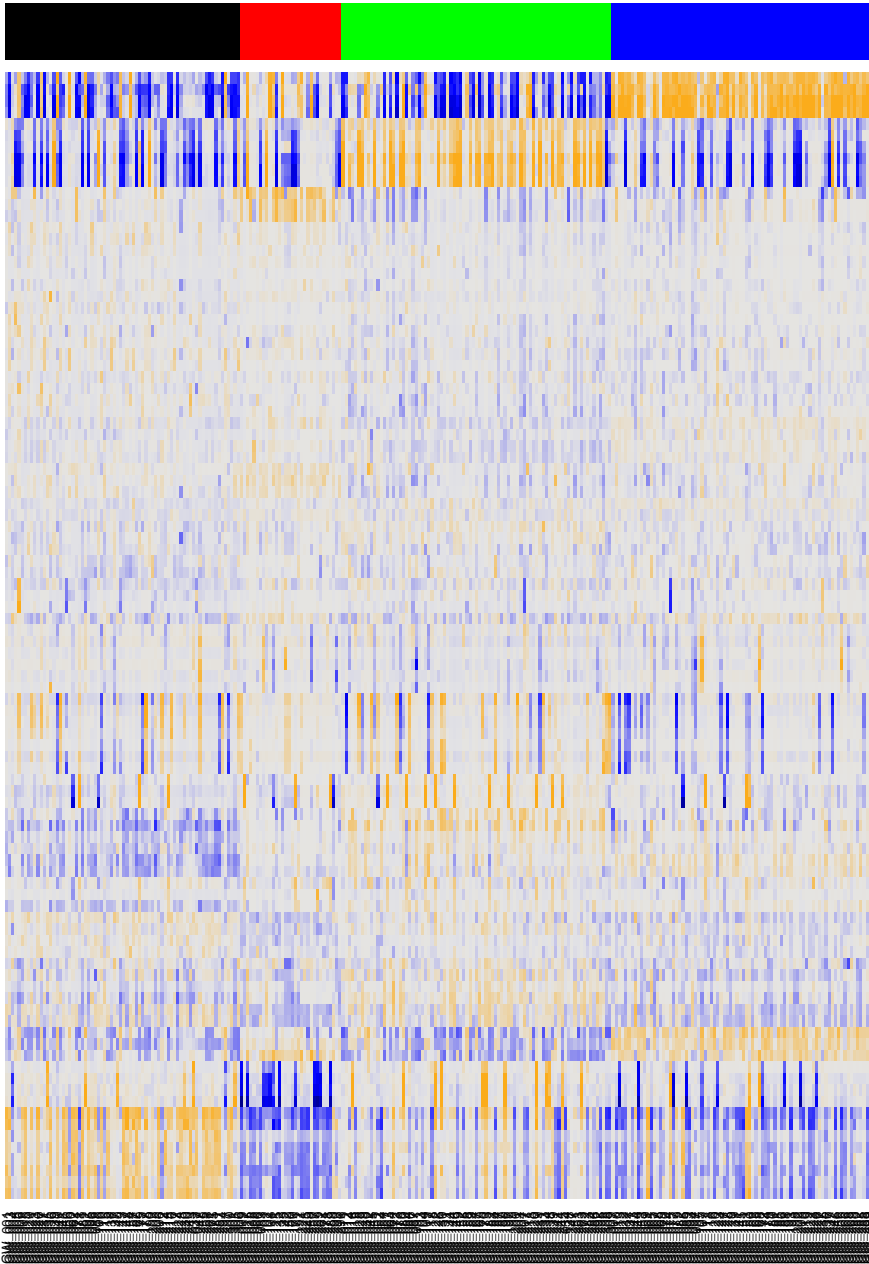


- peptide cross-linking
- epidermis development
- keratinocyte differentiation
- keratinization
- cell adhesion
- cellular response to amino acid stimulus
- collagen fibril organization
- extracellular matrix organization
- collagen catabolic process
- extracellular matrix disassembly
- regulation of blood vessel size
- glutathione metabolic process
- glutathione derivative biosynthetic process
- retinal ganglion cell axon guidance
- developmental pigmentation
- pancreas development
- dorsal/ventral axis specification
- positive regulation of macroautophagy
- urogenital system development
- peripheral nervous system development
- embryonic camera-type eye development
- neurotransmitter biosynthetic process
- mRNA catabolic process
- negative regulation of neurogenesis
- thymus development
- positive regulation of histone H3-K4 methylation
- iron ion transport
- negative regulation of multicellular organism growth
- epoxygenase P450 pathway
- drug metabolic process
- digestion
- glycogen biosynthetic process
- sodium ion transmembrane transport
- sensory perception of taste
- feeding behavior
- anatomical structure formation involved in morphogenesis
- biotin metabolic process
- calcium-dependent cell-cell adhesion
- biological process
- cell migration involved in sprouting angiogenesis
- negative regulation of JUN kinase activity
- negative regulation of epithelial to mesenchymal transition
- cellular response to lithium ion
- white fat cell differentiation
- response to cAMP
- response to corticosterone
- response to light stimulus
- retinoic acid metabolic process
- mRNA processing
- translation
- mitochondrial electron transport, NADH to ubiquinone
- respiratory electron transport chain
- viral transcription
- mitochondrial ATP synthesis coupled proton transport
- mitotic cell cycle
- DNA replication
- DNA strand elongation involved in DNA replication
- telomere maintenance via semi-conservative replication
- mitotic metaphase plate congression
- mitosis
- spindle organization
- cardiac muscle tissue morphogenesis
- muscle contraction
- muscle filament sliding
- cellular response to zinc ion
- epithelium assembly
- keratinocyte proliferation
- morphogenesis of an epithelium
- intermediate filament cytoskeleton organization
- response to zinc ion
- creatine metabolic process
- actomyosin structure organization
- skeletal muscle tissue regeneration
- complement activation
- positive regulation of interleukin-1 beta secretion
- positive regulation of cholesterol efflux
- sterol metabolic process
- positive regulation of cell death
- negative regulation of blood coagulation
- negative regulation of hormone secretion
- positive regulation of vascular endothelial growth factor production
- chemotaxis
- neutrophil chemotaxis
- negative regulation of peptidase activity
- epithelial cell differentiation
- cellular aldehyde metabolic process
- positive regulation of T cell mediated cytotoxicity
- deletive response to virus
- negative regulation of viral genome replication
- type I interferon signaling pathway
- immune response
- antigen processing and presentation
- B cell receptor signaling pathway
- positive regulation of neutrophil chemotaxis
- hematopoietic cell chemotaxis
- regulation of immune response
- antigen processing and presentation of exogenous peptide antigen via MHC class II
- T cell costimulation

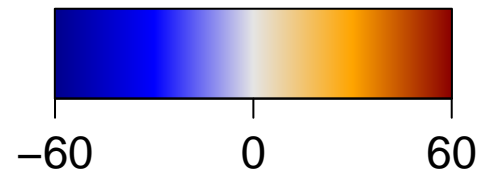


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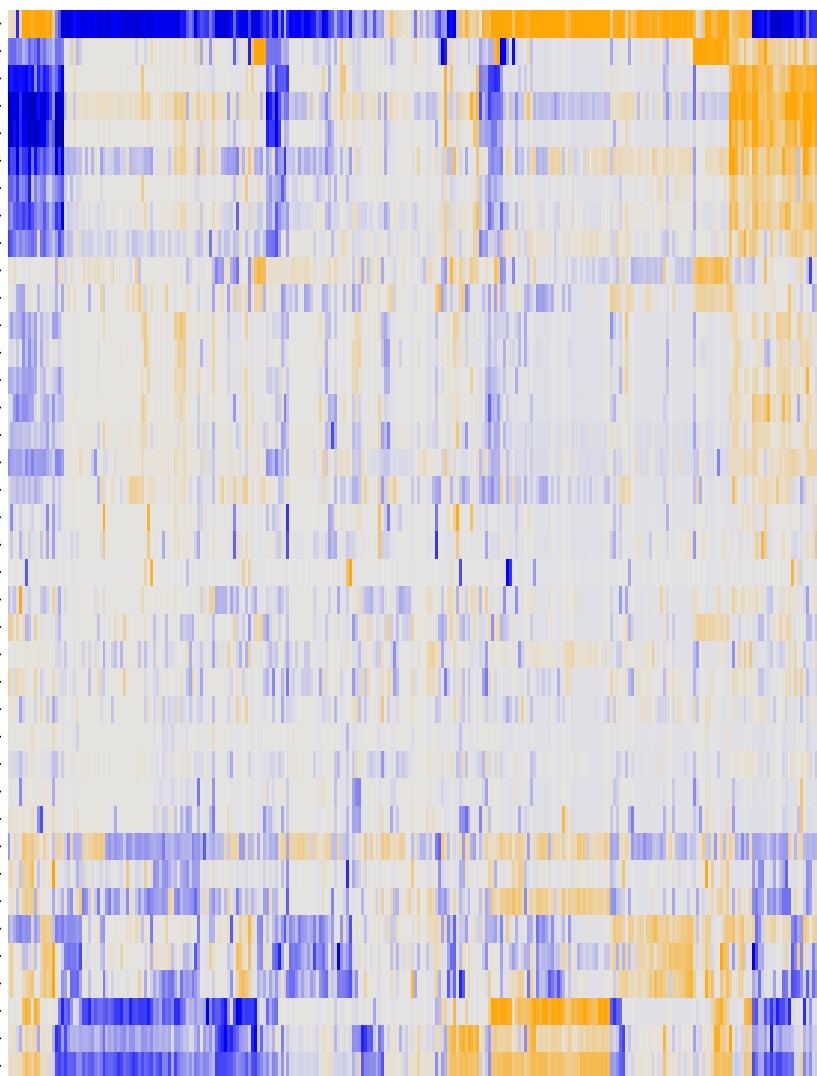
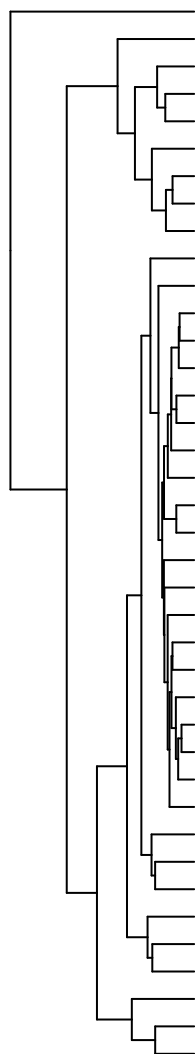
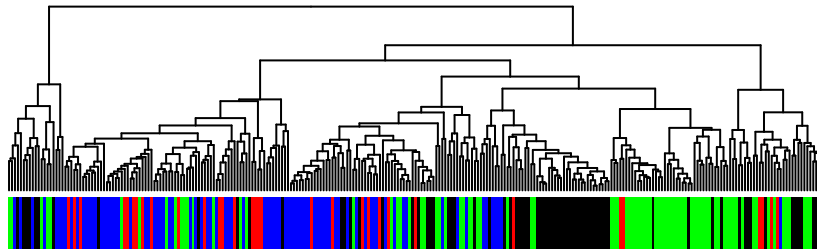


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extracellular matrix organization
collagen catabolic process
extracellular matrix disassembly
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glutathione derivative biosynthetic process
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developmental pigmentation
pancreas development
dorsal/ventral axis specification
positive regulation of macroautophagy
urogenital system development
peripheral nervous system development
embryonic camera-type eye development
neurotransmitter biosynthetic process
mRNA catabolic process
negative regulation of neurogenesis
thymus development
positive regulation of histone H3-K4 methylation
iron ion transport
negative regulation of multicellular organism growth
epoxyeicosanoid pathway
drug metabolic process
digestion
glycogen biosynthetic process
sodium ion transmembrane transport
sensory perception of taste
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regulation of immune response
antigen processing and presentation of exogenous peptide antigen
T cell costimulation

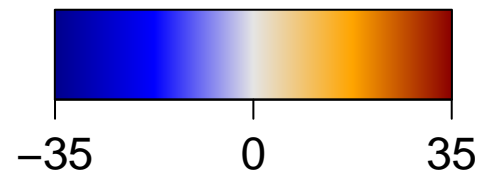


GSZ score

Cancer

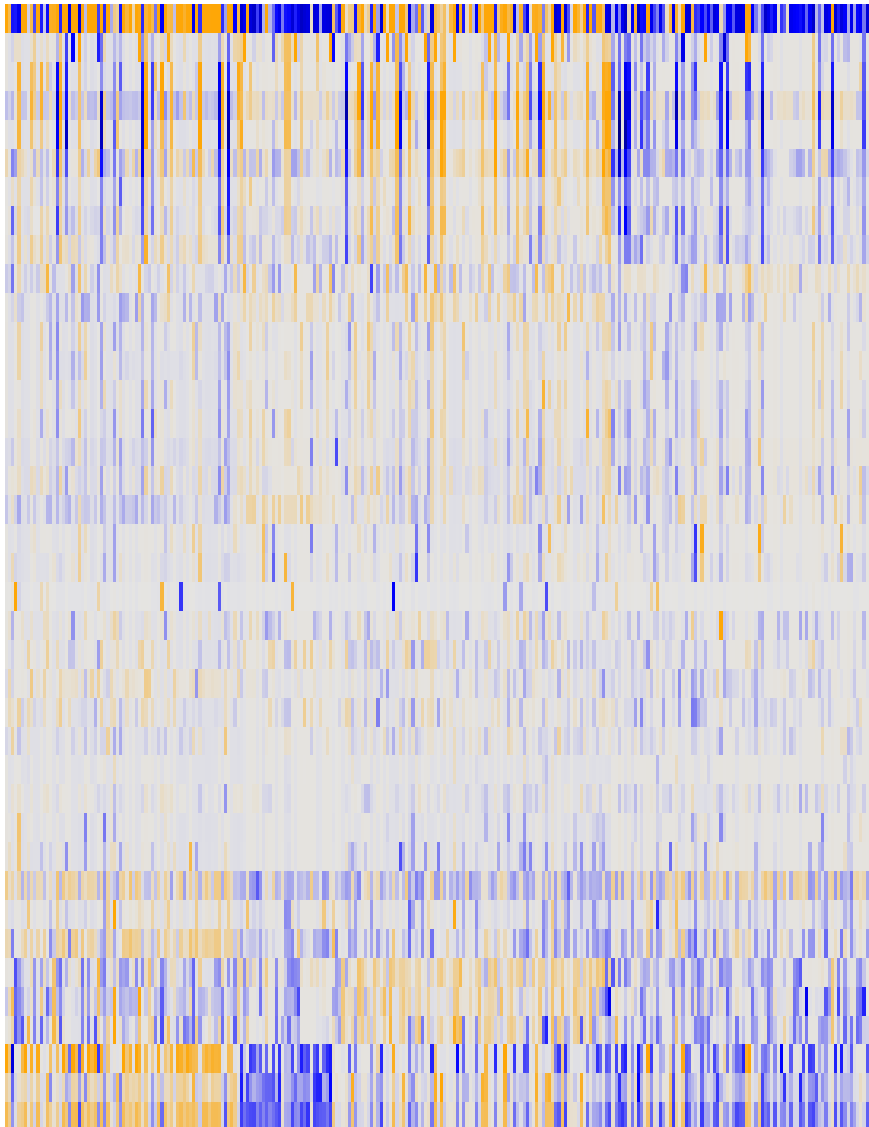
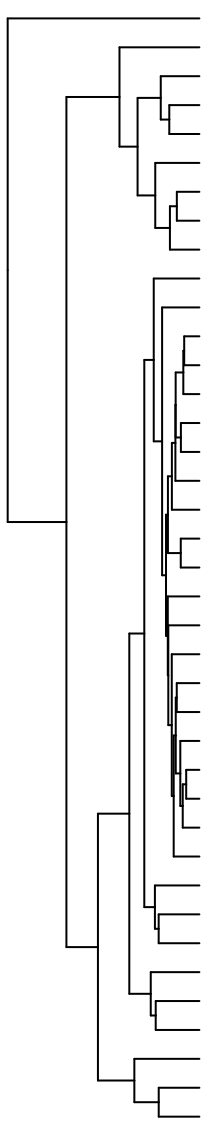


- G Lembcke_Colonc Inflammation
- K BEN-PORATH_UP
- K WOLFER_overlap genes
- K Lembcke_Normal vs Adenoma
- K SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
- K RHODES_UNDIFFERENTIATED_CANCER
- K GENTLES_modul3
- K SHAUGHNESSY_MM high risk
- K KUIPER_MM good survival
- N WANG_ER_DN
- L GENTLES_modul16
- M GENTLES_modul1
- M GENTLES_modul7
- M GENTLES_modul2
- K GENTLES_modul6
- R ZHANG_MM up
- K KUIPER_MM poor survival
- K GENTLES_modul4
- R GENTLES_modul5
- R GENTLES_modul10
- P GENTLES_modul8
- K LIU_COMMON_CANCER_GENES
- A LIU_LIVER_CANCER
- B GENTLES_modul12
- B LIU_BREAST_CANCER
- I LIU_PROSTATE_CANCER_UP
- I BEN-PORATH_DN
- J WANG_ER_UP
- E GENTLES_modul14
- I SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
- L GENTLES_modul11
- I GENTLES_modul13
- G ZHANG_MGUS up
- K RHODES_CANCER_META_SIGNATURE
- A LIU_PROSTATE_CANCER_DN
- I GENTLES_modul17
- G GENTLES_modul18
- F SPANG_LPS-index2
- G SPANG_BCL6-index2

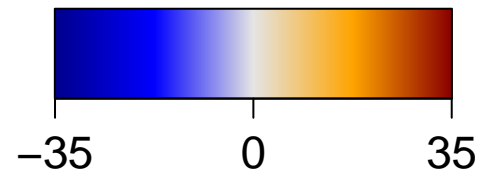


GSZ score

Cancer

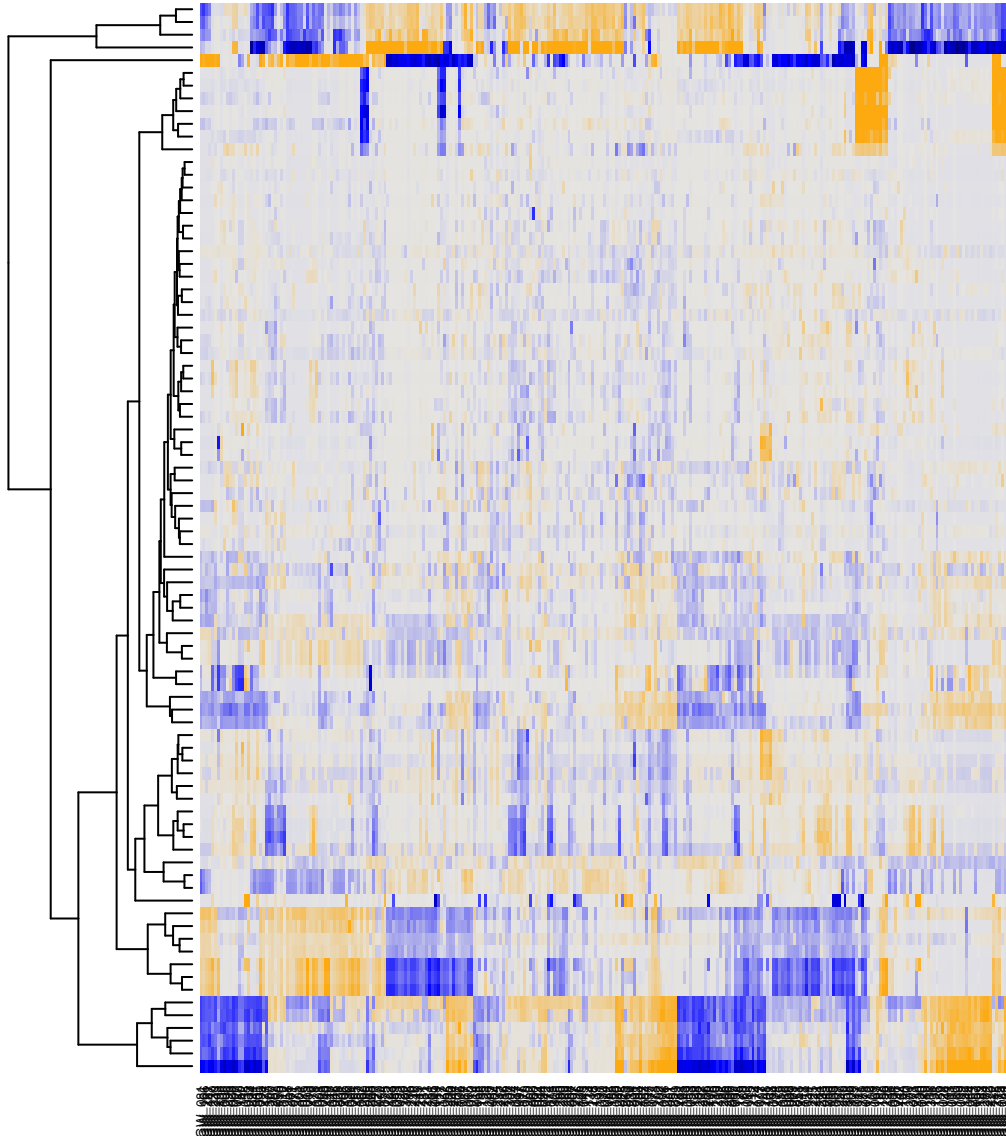
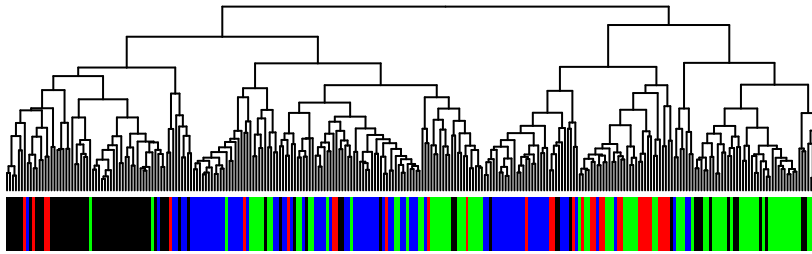


- G Lembcke_Colonc Inflammation
- K BEN-PORATH_UP
- K WOLFER_overlap genes
- K Lembcke_Normal vs Adenoma
- K SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
- K RHODES_UNDIFFERENTIATED_CANCER
- K GENTLES_modul3
- K SHAUGHNESSY_MM high risk
- K KUIPER_MM good survival
- N WANG_ER_DN
- L GENTLES_modul16
- M GENTLES_modul1
- M GENTLES_modul7
- M GENTLES_modul2
- K GENTLES_modul6
- R ZHANG_MM up
- K KUIPER_MM poor survival
- K GENTLES_modul4
- R GENTLES_modul5
- R GENTLES_modul10
- P GENTLES_modul8
- K LIU_COMMON_CANCER_GENES
- A LIU_LIVER_CANCER
- B GENTLES_modul12
- B LIU_BREAST_CANCER
- I LIU_PROSTATE_CANCER_UP
- I BEN-PORATH_DN
- J WANG_ER_UP
- E GENTLES_modul14
- I SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
- L GENTLES_modul11
- I GENTLES_modul13
- G ZHANG_MGUS up
- K RHODES_CANCER_META_SIGNATURE
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- I GENTLES_modul17
- G GENTLES_modul18
- F SPANG_LPS-index2
- G SPANG_BCL6-index2

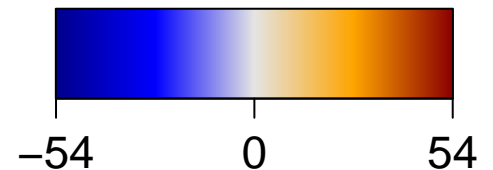


GSZ score

CC

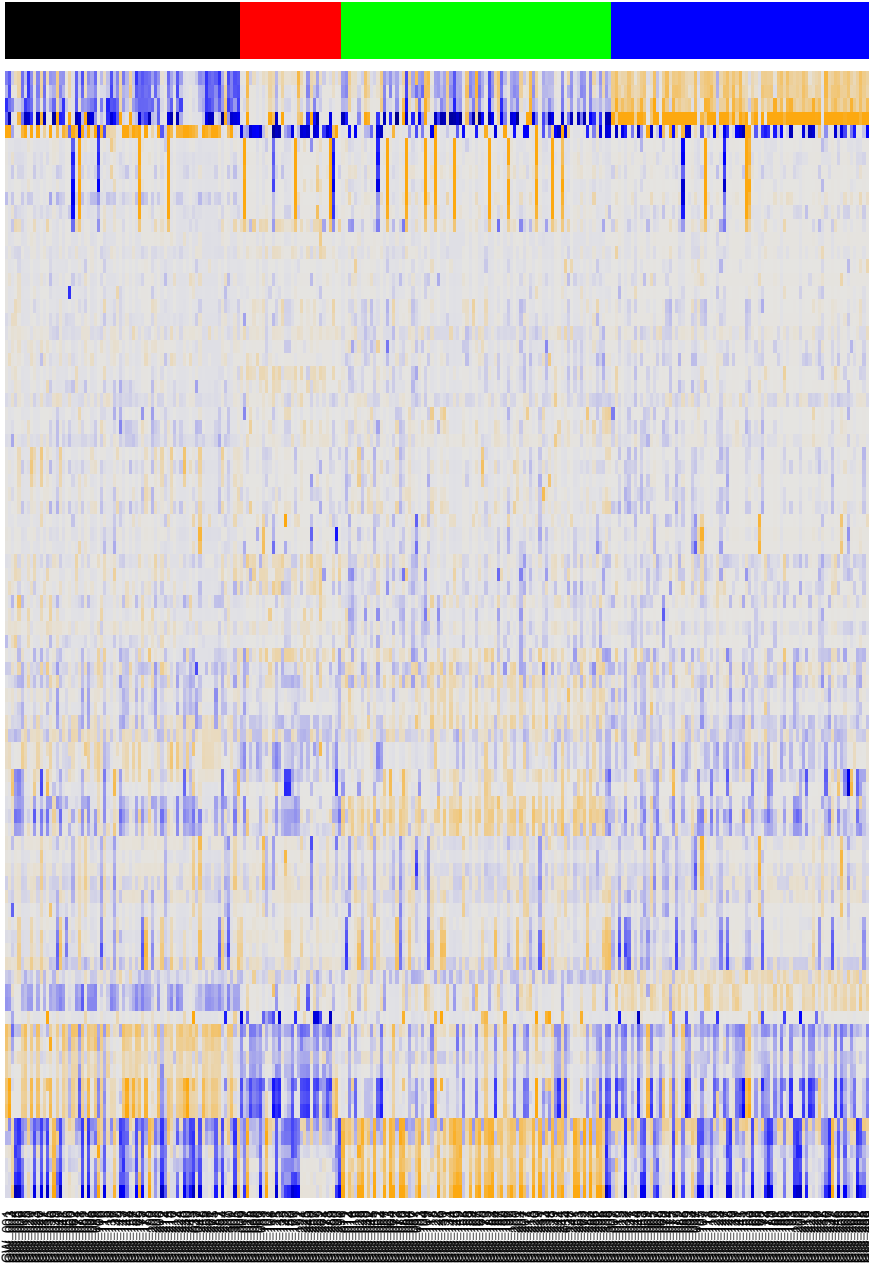


- O intermediate filament
- O keratin filament
- O desmosome
- O cornified envelope
- CC MHC class II protein complex
- CC muscle myosin complex
- CC sarcomere
- N M band
- N myosin filament
- N contractile fiber
- N I band
- N costamere
- A axoneme
- J motile cilium
- O XY body
- M small ribosomal subunit
- F dendrite cytoplasm
- R inclusion body
- R aggresome
- CC cellular_component
- B polysome
- B heterochromatin
- K excitatory synapse
- D COPI vesicle coat
- K intermediate filament cytoskeleton
- K zona pellucida receptor complex
- P microtubule plus-end
- P melanosome
- K lateral element
- K synaptonemal complex
- K Fanconi anaemia nuclear complex
- K nuclear periphery
- K male germ cell nucleus
- D mitochondrial respiratory chain
- R cytosolic large ribosomal subunit
- R mitochondrial proton-transporting ATP synthase complex
- R transport vesicle
- I dystrophin-associated glycoprotein complex
- A axolemma
- L chloride channel complex
- A photoreceptor outer segment membrane
- A tight junction
- A apical junction complex
- L membrane-bounded vesicle
- O microvillus membrane
- A secretory granule
- L filopodium
- L filopodium membrane
- L integrin complex
- O anchored to plasma membrane
- O high-density lipoprotein particle
- O very-low-density lipoprotein particle
- L endocytic vesicle lumen
- L hemoglobin complex
- L lamellipodium membrane
- L extracellular vesicular exosome
- L platelet alpha granule lumen
- R ribosome
- R mitochondrial respiratory chain complex I
- R mitochondrial inner membrane
- R mitochondrion
- K nucleolus
- M mitochondrial small ribosomal subunit
- K spindle microtubule
- K condensed chromosome kinetochore
- K chromosome, centromeric region
- K nucleoplasm
- O anchored to membrane
- O gap junction
- O connexon complex
- O MHC class I protein complex
- CC external side of plasma membrane
- CC T cell receptor complex
- CC integral to plasma membrane
- CC phagocytic cup
- CC integral to luminal side of endoplasmic reticulum membrane
- CC transport vesicle membrane
- CC clathrin-coated endocytic vesicle membrane
- L extracellular region
- L extracellular space
- L collagen
- L basement membrane
- L proteinaceous extracellular matrix
- L extracellular matrix

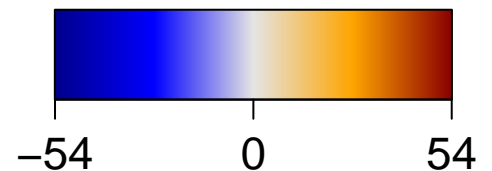


GSZ score

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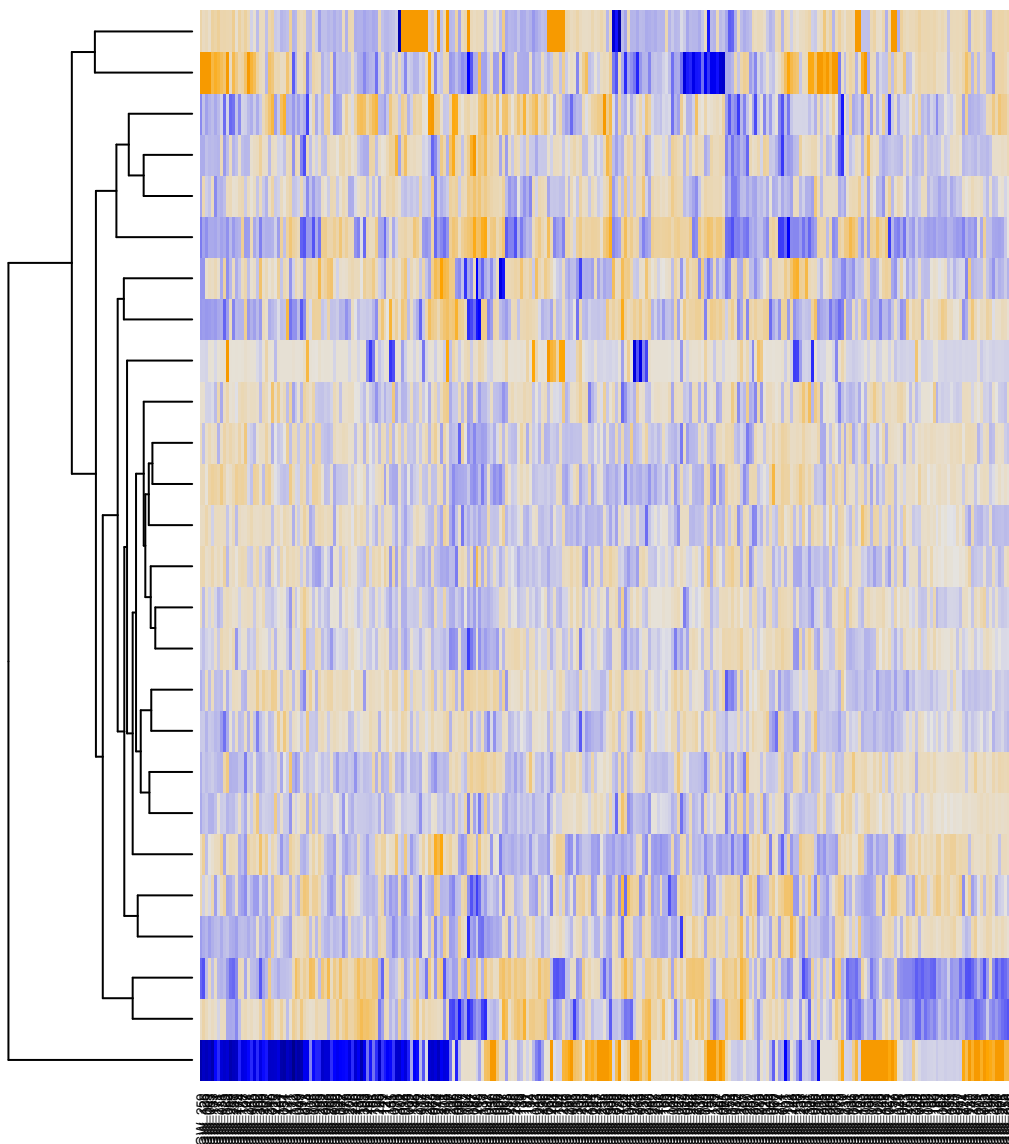
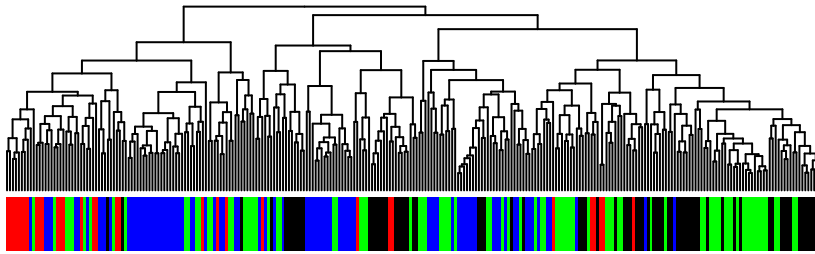


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- N contractile fiber
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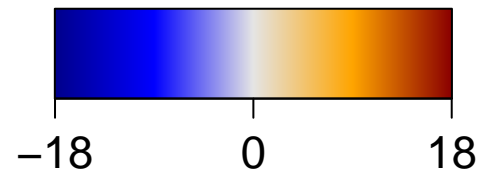


GSZ score

Chr

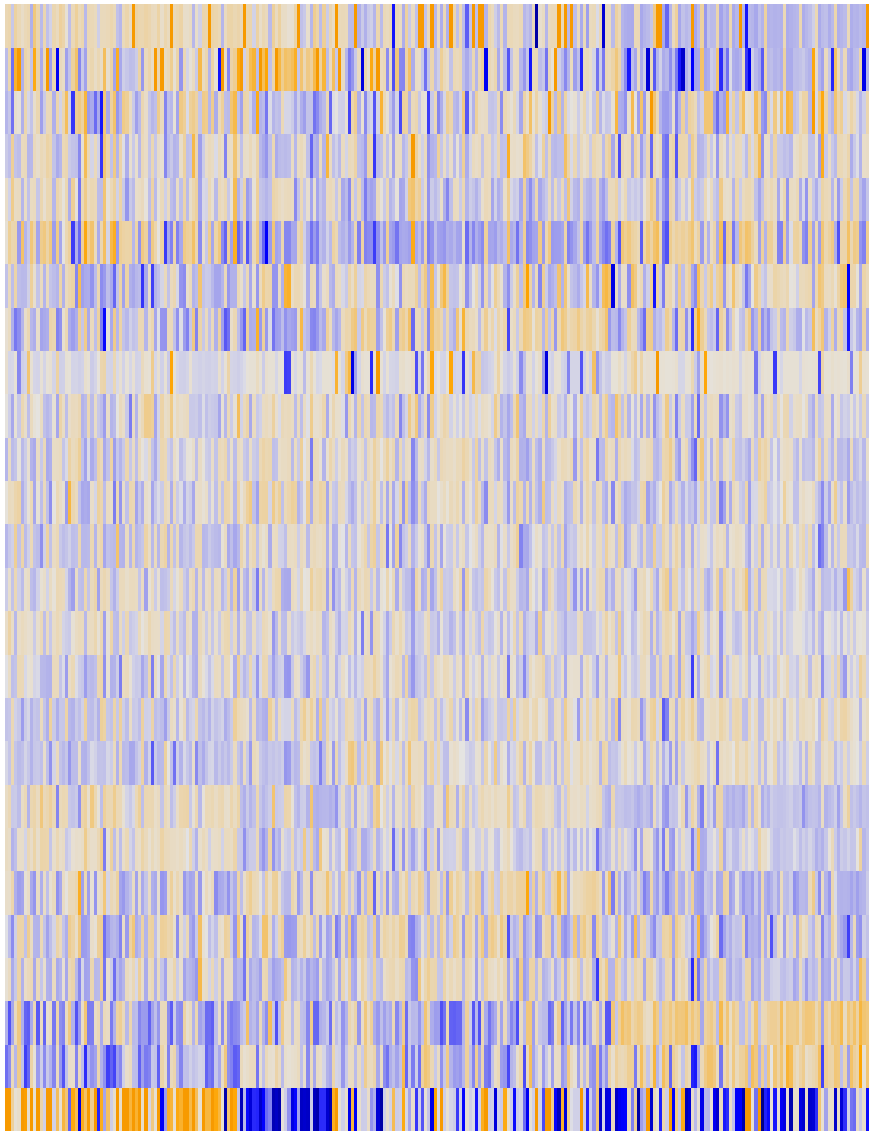
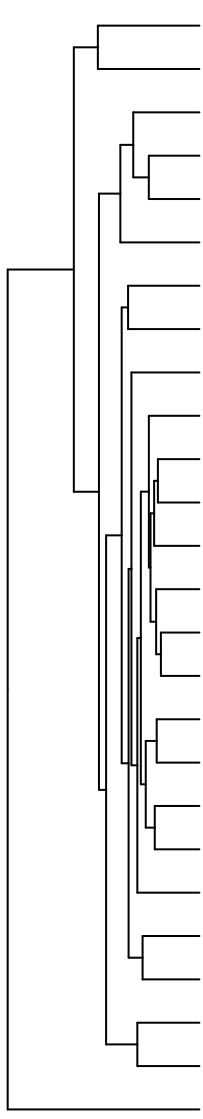


Q Chr X
K Chr 3
C Chr HSCHR6_MHC_DBB
M Chr 16
J Chr 17
C Chr 19
K Chr 8
R Chr 11
A Chr Y
K Chr 12
R Chr 6
K Chr 2
K Chr 15
J Chr 9
B Chr 10
R Chr 13
C Chr 20
I Chr 14
G Chr 22
E Chr 21
L Chr 7
R Chr 4
L Chr 5
O Chr 1
O Chr 18
F Chr HSCHR6_MHC_QBL

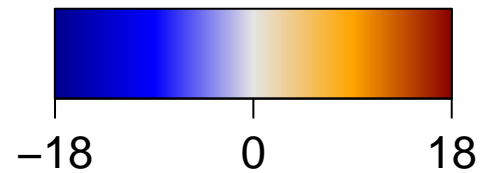


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Chr

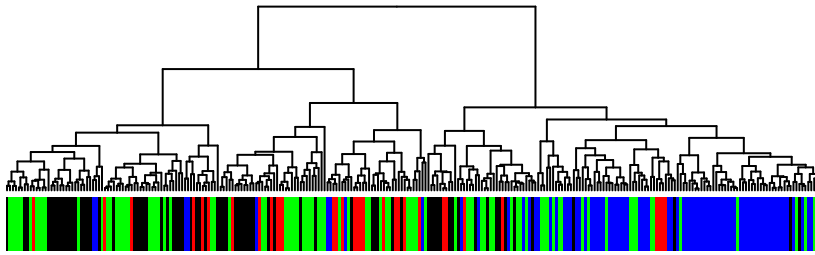


Q Chr X
K Chr 3
C Chr HSCR6_MHC_DBB
M Chr 16
J Chr 17
C Chr 19
K Chr 8
R Chr 11
A Chr Y
K Chr 12
R Chr 6
K Chr 2
K Chr 15
J Chr 9
B Chr 10
R Chr 13
C Chr 20
I Chr 14
G Chr 22
E Chr 21
L Chr 7
R Chr 4
L Chr 5
O Chr 1
O Chr 18
F Chr HSCR6_MHC_QBL



GSZ score

Disease



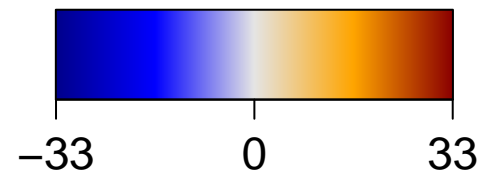
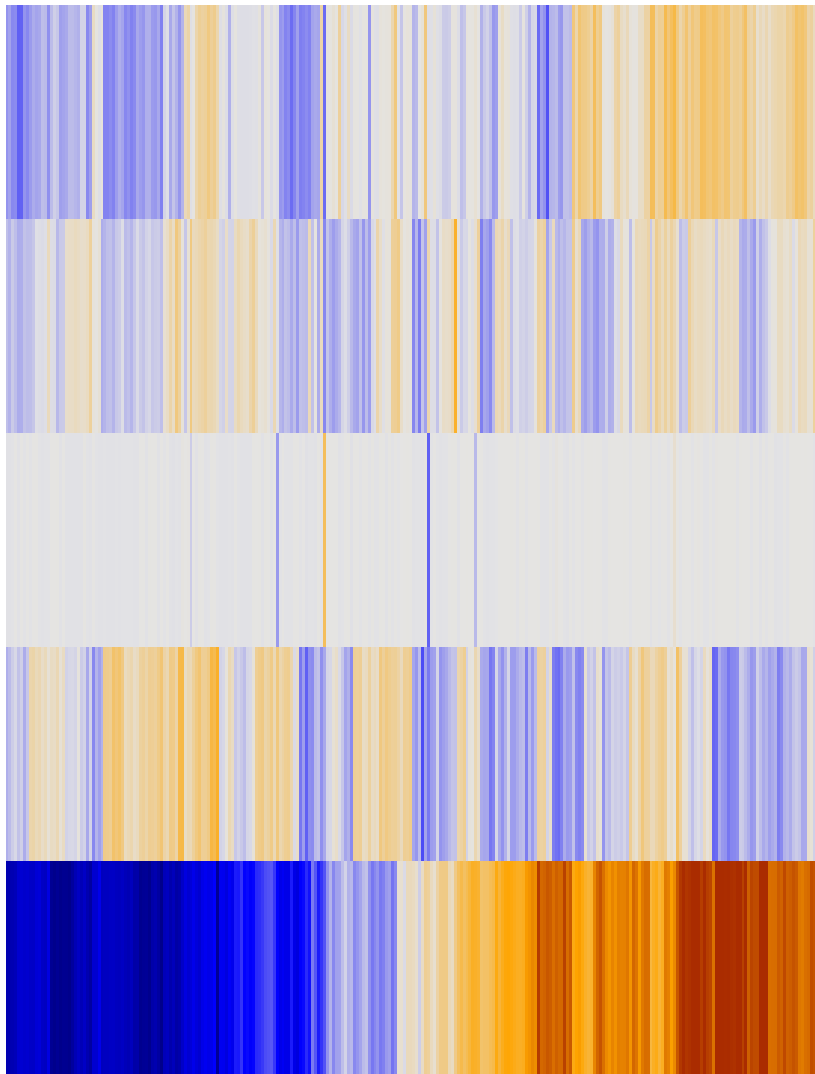
A BCHETNIA_EBM up

O BCHETNIA_EBM-DM up

A BCHETNIA_EBM down

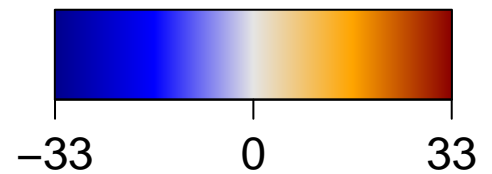
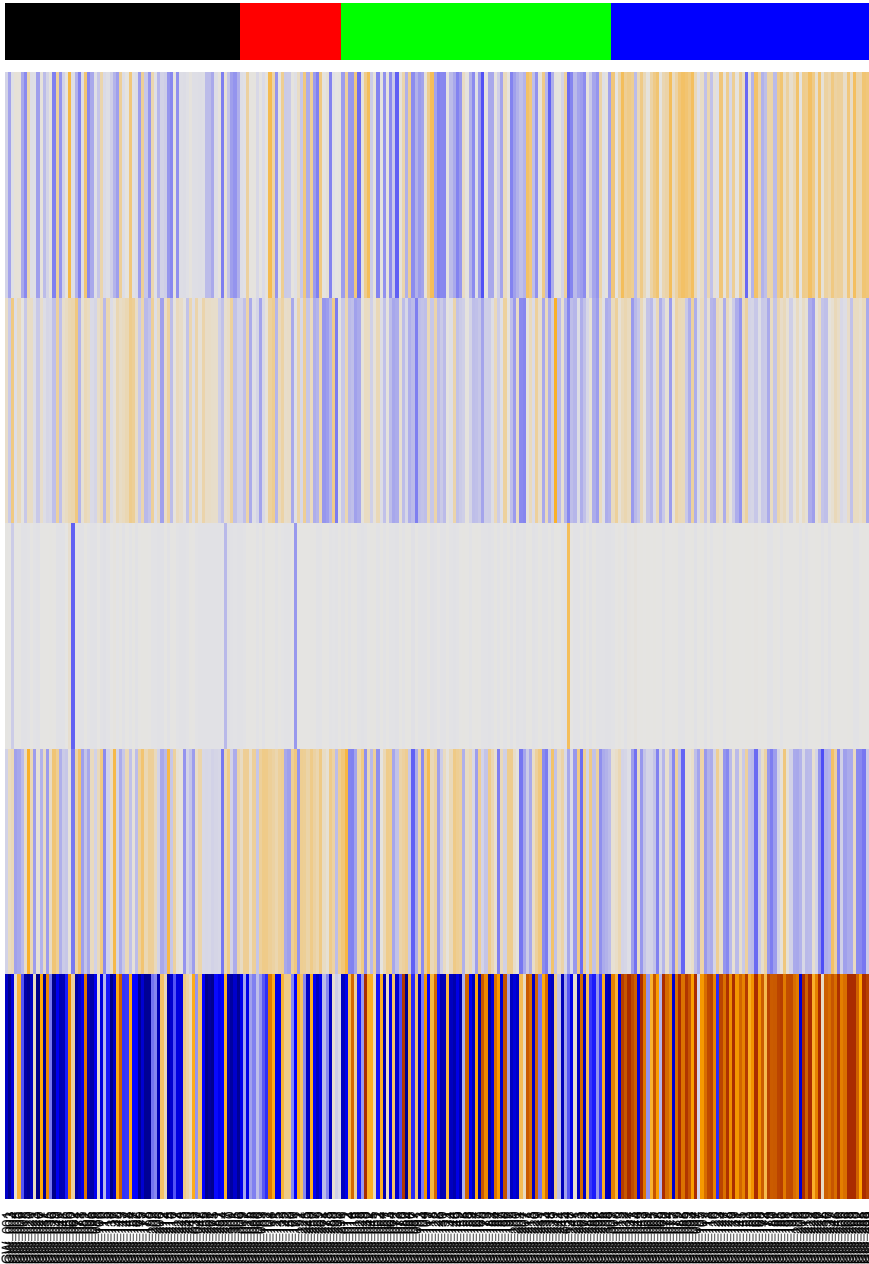
A GUDJ_psoriasis down

O GUDJ_psoriasis up



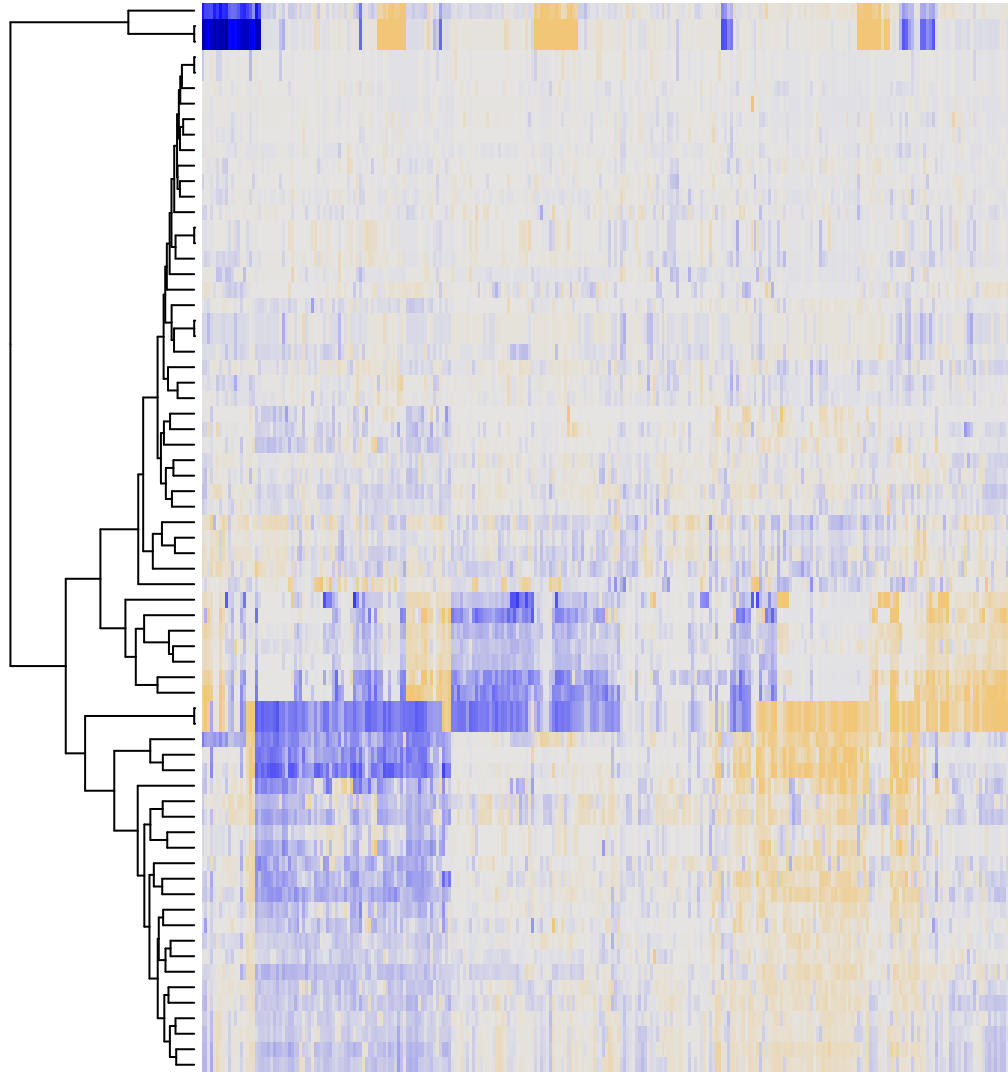
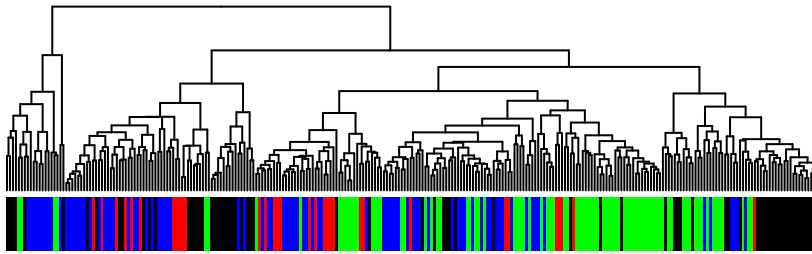
GSZ score

Disease

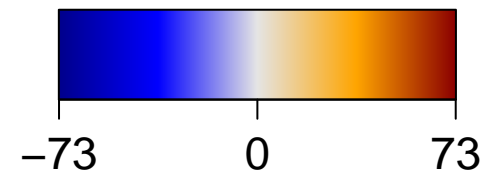


GSZ score

Glio

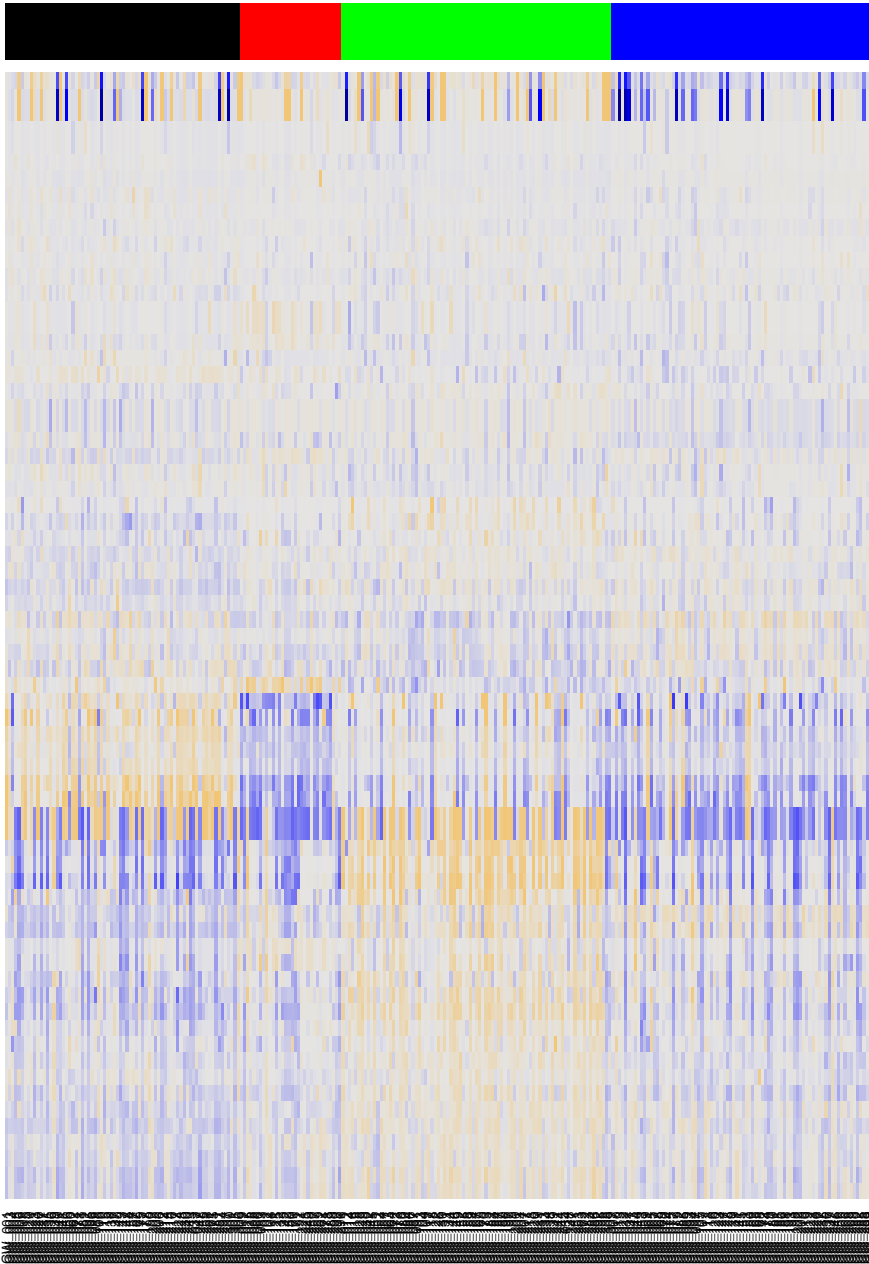


K developing astrocytes
K wilscher_GBM_Verhaak-PNmut_expression_C_down
K wilscher_GBM_Verhaak-CL_expression_C_up
M wilscher_GBM_Verhaak-PNmut_expression_I_up
M wilscher_GBM_Verhaak-PNwt_expression_I_up
A VERHAAK_PN_Brain
A wilscher_GBM_Verhaak-PNmut_expression_G_down
B WIRTH_PN subtype
B wilscher_GBM_LTSmut_proteomics-A_UP
E GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
A KIM amplified & overexpressed in LTS
R wilscher_GBM_LTSmut_proteomics-B_UP
M GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
O Phillips PN up vs MES & Prolif
Q wilscher_GBM_Verhaak-MES_expression_M_down
Q wilscher_GBM_Verhaak-CL_expression_M_down
K wilscher_GBM_proteomics_wtOnly_SpotH
C wilscher_GBM_Verhaak-PNwt_expression_J_up
H wilscher_GBM_STSwt_proteomics-L_UP
L wilscher_GBM_LTSwt_proteomics-C_UP
E wilscher_GBM_Verhaak-MES_expression_D_down
E wilscher_GBM_Verhaak-CL_expression_D_up
F Up
J mature astrocytes
R Stuehler_Proteins_up_in_STS
R wilscher_GBM_proteomics_wtOnly_SpotG
L wilscher_GBM_Verhaak-PNwt_expression_N_down
L VERHAAK_MES subtype
L Christensen_hypermethylated_in_ependymoma
L in vivo astrocytes vs. cultured astroglia
L Barbus_GBM_STS_vs_LTS
A Christensen_hypermethylated_in_primary_glioblastoma
K Martinez_Glio_hypermeth
O VERHAAK_Brain
I OL vs. OPC
I OL vs. MOG-OL
A wilscher_GBM_LTSwt_proteomics-G_UP
G neurons_glio
F Donson-immune cell intra signaling-associated with LTS in HGA
G Donson-cytotoxic effectors-associated with LTS in HGA
G Donson-innate immunity-associated with LTS in HGA
G Donson-Misc immune function-associated with LTS in HGA
G Donson-adaptive-immunity-associated with LTS in HGA
G Donson-chemokines/cytokines-associated with LTS in HGA
G Donson-migration tethering and rolling-associated with LTS in HGA
L wilscher_GBM_Verhaak-MES_expression_B_up
L wilscher_GBM_Verhaak-CL_expression_B_up
L cultured astroglia vs. in vivo astrocytes
L Phillips MES up vs Prolif & PN
L Colman_survival_associated
L Martinez_Glio_hypometh
L Christensen_hypermethylated_in_secondary_glioblastoma
L Christensen_hypermethylated_in_primary_glioblastoma
L Christensen_hypermethylated_in_grade2_astrocytoma
L Christensen_hypermethylated_in_grade2_oligodendroglioma
L KIM_epithelial-mesenchymal-transition related genes_decreased expr
L Christensen_hypermethylated_in_ependymoma
L GIEZELT_GBM_WT_up_VS_mut
L KIM deleted & downregulated in LTS
L Colman_survival_robust
L OPC
L VERHAAK_CL subtype
L wilscher_GBM_proteomics_wtOnly_SpotB
L wilscher_GBM_proteomics_wtOnly_SpotC
P Noushmehr_Pron_GCIMP_hypermeth_DN
L Christensen_hypermethylated_in_grade2_astrocytoma
L Christensen_hypermethylated_in_secondary_glioblastoma
L Christensen_hypermethylated_in_grade2_oligoastrocytoma
L laffaire_hypermeth_LGG_control

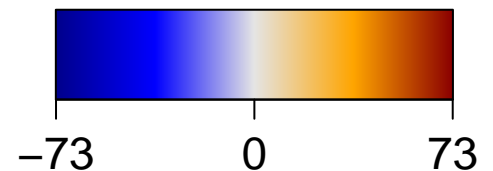


GSZ score

Glio

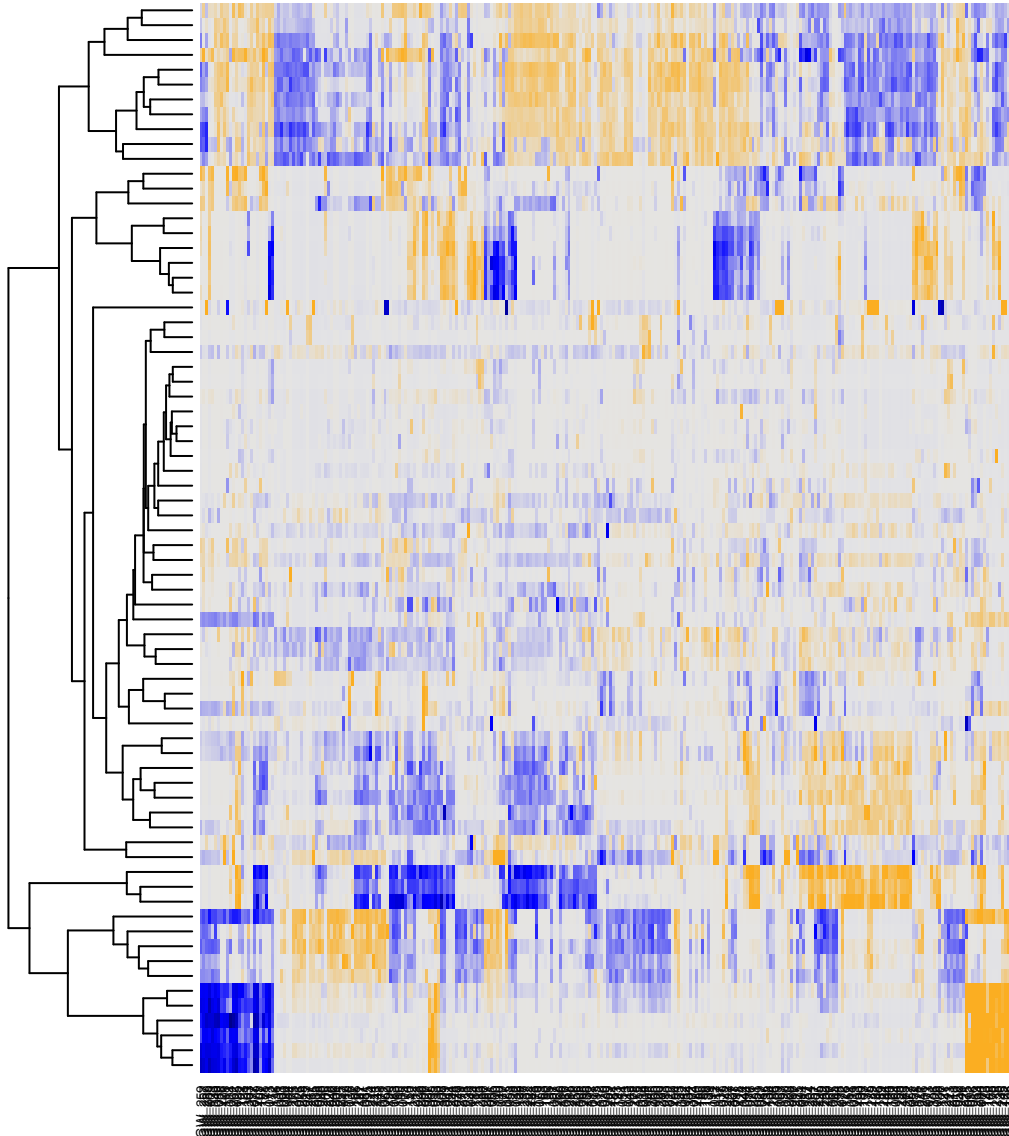
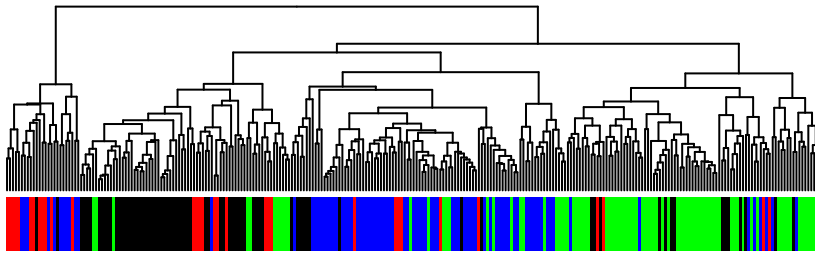


K developing astrocytes
K wilscher_GBM_Verhaak-PNmut_expression_C_down
K wilscher_GBM_Verhaak-CL_expression_C_up
M wilscher_GBM_Verhaak-PNmut_expression_I_up
M wilscher_GBM_Verhaak-PNwt_expression_I_up
A VERHAAK_PN_Brain
A wilscher_GBM_Verhaak-PNmut_expression_G_down
B WIRTH_PN subtype
B wilscher_GBM_LTSmut_proteomics-A_UP
E GIEZELT_GBM_MGMTmethyl_down_VS_nonmethyl
A KIM amplified & overexpressed in LTS
R wilscher_GBM_LTSmut_proteomics-B_UP
M GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
O Phillips PN up vs MES & Prolif
Q wilscher_GBM_Verhaak-MES_expression_M_down
Q wilscher_GBM_Verhaak-CL_expression_M_down
K wilscher_GBM_proteomics_wtOnly_SpotH
C wilscher_GBM_Verhaak-PNwt_expression_J_up
H wilscher_GBM_STSwt_proteomics-L_UP
L wilscher_GBM_LTSwt_proteomics-C_UP
E wilscher_GBM_Verhaak-MES_expression_D_down
E wilscher_GBM_Verhaak-CL_expression_D_up
F Up
J mature astrocytes
R Stuehler_Proteins_up_in_STS
R wilscher_GBM_proteomics_wtOnly_SpotG
L wilscher_GBM_Verhaak-PNwt_expression_N_down
L VERHAAK_MES subtype
L Christensen_hypermethylated_in_ependymoma
L in vivo astrocytes vs. cultured astroglia
L Barbus_GBM_STS_vs_LTS
A Christensen_hypermethylated_in_primary_glioblastoma
K Martinez_Glio_hypermeth
O VERHAAK_Brain
I OL vs. OPC
I OL vs. MOG-OL
A wilscher_GBM_LTSwt_proteomics-G_UP
G neurons_glio
F Donson-immune cell intra signaling-associated with LTS in HGA
G Donson-cytotoxic effectors-associated with LTS in HGA
G Donson-innate immunity-associated with LTS in HGA
G Donson-Misc immune function-associated with LTS in HGA
G Donson-adaptive immunity-associated with LTS in HGA
G Donson-chemokines/cytokines-associated with LTS in HGA
G Donson-migration tethering and rolling-associated with LTS in HGA
L wilscher_GBM_Verhaak-MES_expression_B_up
L wilscher_GBM_Verhaak-CL_expression_B_up
L cultured astroglia vs. in vivo astrocytes
L Phillips MES up vs Prolif & PN
L Colman_survival_associated
L Martinez_Glio_hypometh
L Christensen_hypomethylated_in_secondary_glioblastoma
L Christensen_hypomethylated_in_primary_glioblastoma
L Christensen_hypomethylated_in_grade2_astrocytoma
L Christensen_hypomethylated_in_grade2_oligodendroglioma
L KIM_epithelial-mesenchymal-transition related genes_decreased
L Christensen_hypomethylated_in_ependymoma
L GIEZELT_GBM_WT_up_VS_mut
L KIM deleted & downregulated in LTS
L Colman_survival_robust
L OPC
L VERHAAK_CL subtype
L wilscher_GBM_proteomics_wtOnly_SpotB
L wilscher_GBM_proteomics_wtOnly_SpotC
P Noushmehr_Pron_GCIMP_hypermeth_DN
L Christensen_hypermethylated_in_grade2_astrocytoma
L Christensen_hypermethylated_in_secondary_glioblastoma
L Christensen_hypermethylated_in_grade2_oligoastrocytoma
L laffaire_hypermeth_LGG_vs_control

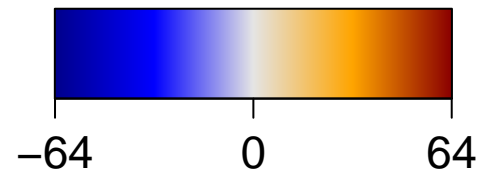


GSZ score

GSEA C2

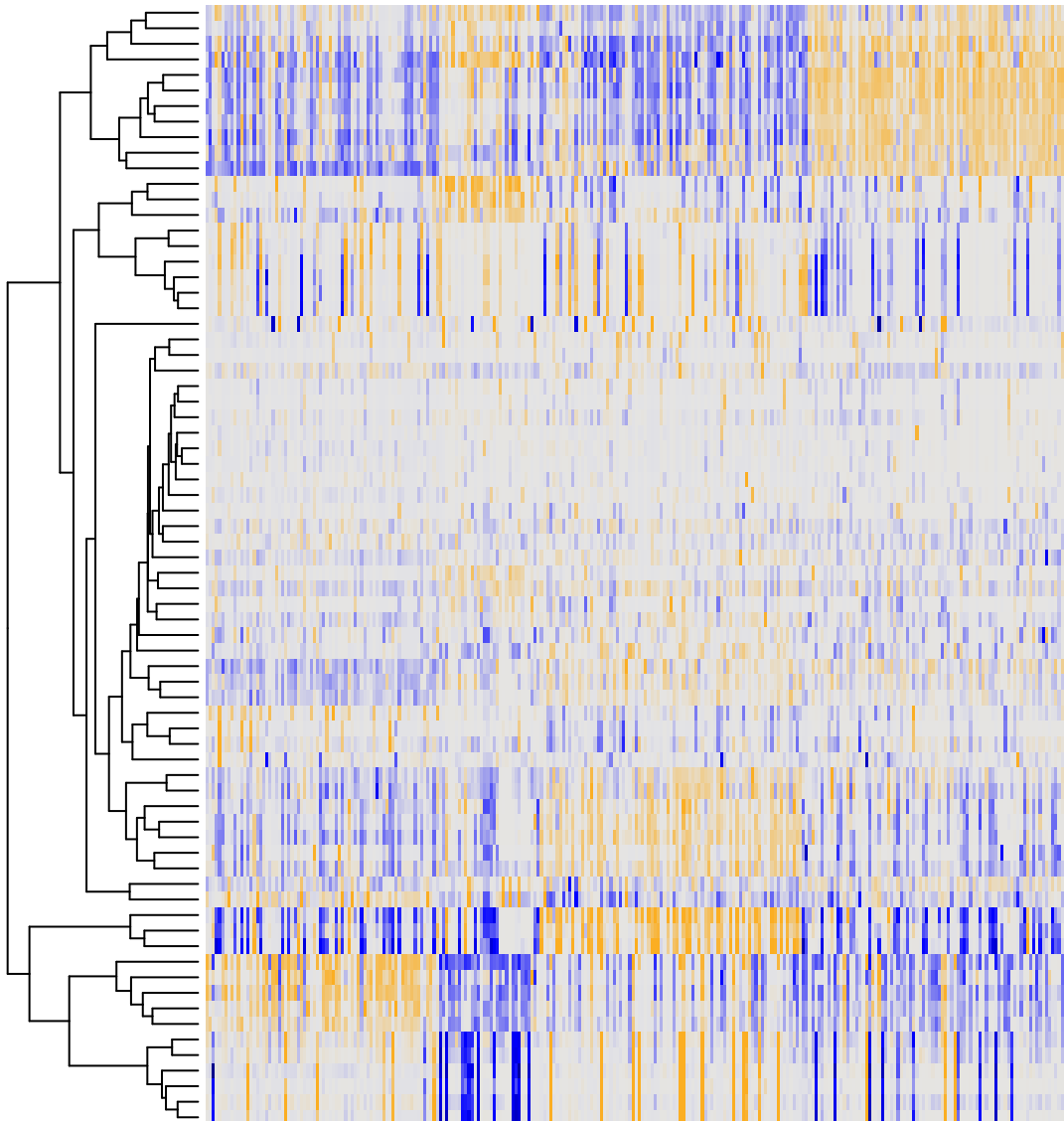


O RICKMAN_HEAD_AND_NECK_CANCER_E
O KEGG_LINOLEIC_ACID_METABOLISM
O CROMER_TUMORIGENESIS_DN
O LIU_CDX2_TARGETS_DN
O HINATA_NFKB_TARGETS_KERATINOCYTE_DN
O WANG_BARRETTES_ESOPHAGUS_DN
O WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
O SENGUPTA_NASOPHARYNGEAL_CARINOMA_DN
O ONDER_CDH1_TARGETS_3_DN
O AUJLA_IL22_AND_IL17A_SIGNALING
O HUPER_BREAST_BASAL_VS_LUMINAL_UP
K MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
K KEGG_GLUTATHIONE_METABOLISM
L FREDERICK_PRKCI_TARGETS
K SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
K KALMA_E2F1_TARGETS
K EGUCHI_CELL_CYCLE_RB1_TARGETS
K FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
K CRONQUIST_IL6_DEPRIVATION_DN
K FARMER_BREAST_CANCER_CLUSTER_2
N RICKMAN_HEAD_AND_NECK_CANCER_F
Q RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
Q WEBER_METHYLATED_ICP_IN_SPERM_DN
Q ABE_VEGFA_TARGETS_30MIN
M GALT_TP53_TARGETS_APOPTOTIC_DN
M WEBER_METHYLATED_LCP_IN_SPERM_DN
M WONG_MITOCHONDRIA_GENE_MODULE
P SCHEIDEREIT_IKK_INTERACTING_PROTEINS
R BIOCARTA_HIF_PATHWAY
R ZHAN_MULTIPLE_MYELOMA_MS_DN
C GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
P ZAIDI_OSTEOBLAST_TRANSCRIPTION_FACTORS
R REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA_CELL
L WANG_BARRETTES_ESOPHAGUS_UP
P REACTOME_ENDOGENOUS_STEROLS
L VERRECCHIA_RESPONSE_TO_TGFB1_C6
K MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_13
L MAHADEVAN_IMATINIB_RESISTANCE_UP
C KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
L WEINMANN_ADAPTATION_TO_HYPOXIA_DN
L BIOCARTA_AHSP_PATHWAY
F ZHU_CMV_24_HR_UP
O SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
O YE_METASTATIC_LIVER_CANCER
O WALLACE_PROSTATE_CANCER_DN
B RICKMAN_HEAD_AND_NECK_CANCER_A
A SMID_BREAST_CANCER_ERBB2_DN
F HUPER_BREAST_BASAL_VS_LUMINAL_DN
B CHASSOT_SKIN_WOUND
F BUDHU_LIVER_CANCER_METASTASIS_DN
L SEIKE_LUNG_CANCER_POOR_SURVIVAL
L AGARWAL_AKT_PATHWAY_TARGETS
L WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
L BEGUM_TARGETS_OF_PAX3_FOXP1_FUSION_DN
L KONDO_HYPOXIA
L TSUNODA_CISPLATIN_RESISTANCE_UP
O FERRARI_RESPONSE_TO_FENRETINIDE_DN
A RICKMAN_HEAD_AND_NECK_CANCER_D
L CROMER_TUMORIGENESIS_UP
L ONDER_CDH1_TARGETS_2_UP
L FARMER_BREAST_CANCER_CLUSTER_5
G FARMER_BREAST_CANCER_CLUSTER_1
G WONG_ENDOMETRIAL_CANCER_LATE
G BIOCARTA_TCYTOTOXIC_PATHWAY
G MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
G LIU_THYROID_CANCER_CLUSTER_4
F UROSEVIC_RESPONSE_TO_IMIQIMOD
F GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
F MOSERLE_IFNA_RESPONSE
F BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
F ZHANG_INTERFERON_RESPONSE
F BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX

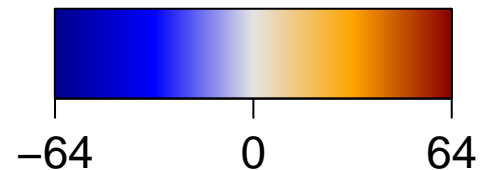


GSZ score

GSEA C2

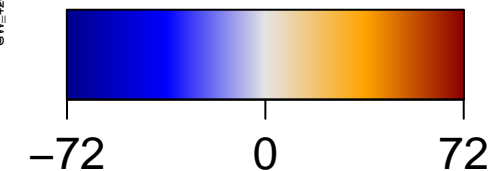
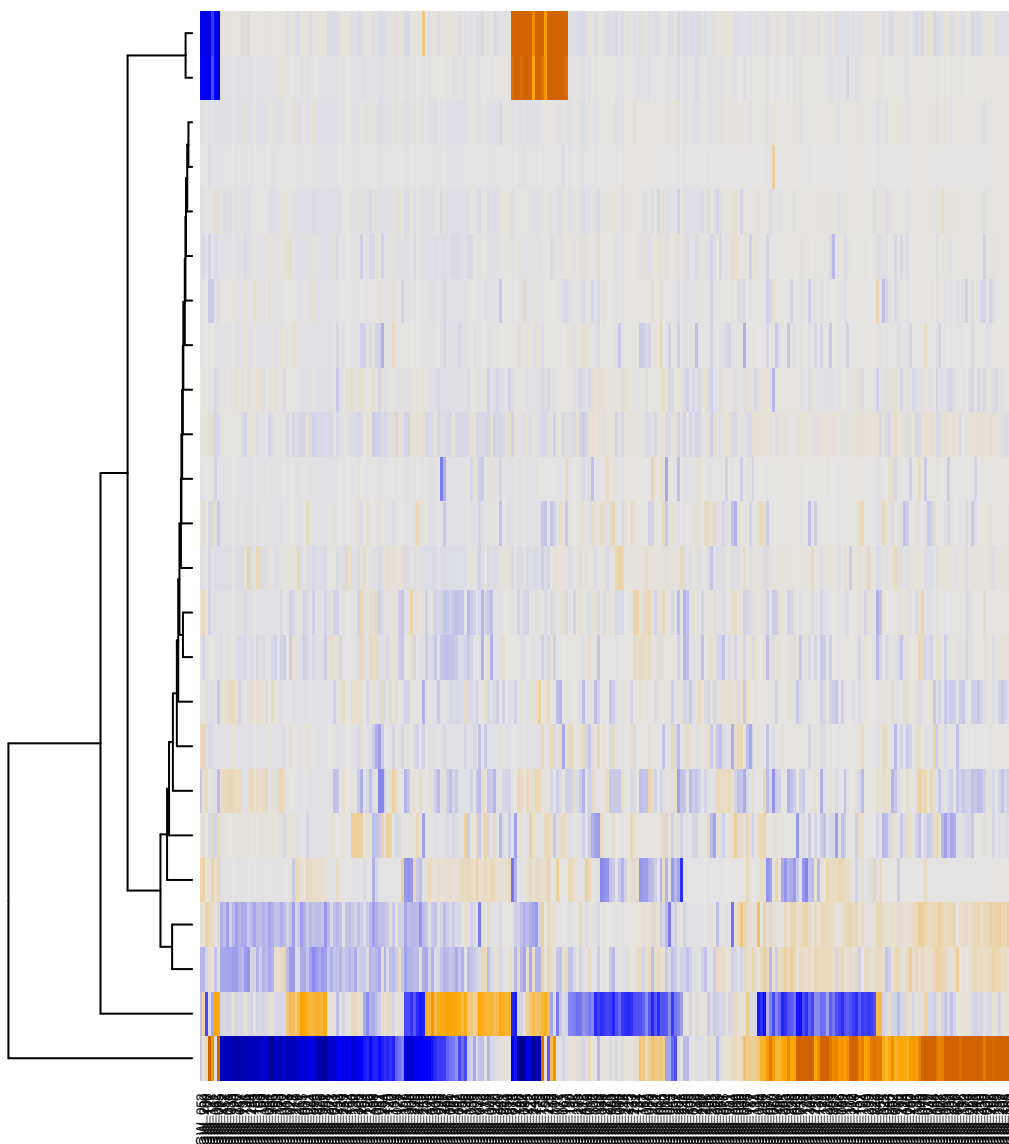
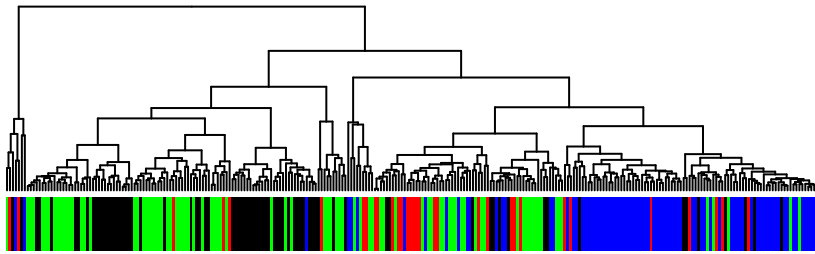


O RICKMAN_HEAD_AND_NECK_CANCER_E
O KEGG_LINOLEIC_ACID_METABOLISM
O CROMER_TUMORIGENESIS_DN
O LIU_CD_X2_TARGETS_DN
O HINATA_NFKB_TARGETS_KERATINOCYTE_DN
O WANG_BARRETTES_ESOPHAGUS_DN
O WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER
O SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
O ONDER_CDH1_TARGETS_3_DN
O AUJLA_IL22_AND_IL17A_SIGNALING
O HUPER_BREAST_BASAL_VS_LUMINAL_UP
K MCCOLLUM_GELDANAMYCIN_RESISTANCE_DN
K KEGG_GLUTATHIONE_METABOLISM
L FREDERICK_PRKCI_TARGETS
K SLEBOS_HEAD_AND_NECK_CANCER_WITH_HPV_UP
K KALMA_E2F1_TARGETS
K EGUCHI_CELL_CYCLE_RB1_TARGETS
K FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
K CROONQUIST_IL6_DEPRIVATION_DN
K FARMER_BREAST_CANCER_CLUSTER_2
N RICKMAN_HEAD_AND_NECK_CANCER_F
Q RAY_TARGETS_OF_P210_BCR_ABL_FUSION_UP
Q WEBER_METHYLATED_ICP_IN_SPERM_DN
Q ABE_VEGFA_TARGETS_30MIN
M GALI_TP53_TARGETS_APOPTOTIC_DN
M WEBER_METHYLATED_LCP_IN_SPERM_DN
M WONG_MITOCHONDRIA_GENE_MODULE
P SCHEIDEREIT_IKK_INTERACTING_PROTEINS
R BIOCARTE_HIF_PATHWAY
R ZHAN_MULTIPLE_MYELOMA_MS_DN
C GRASEMANN_RETINOBLASTOMA_WITH_6P_AMPLIFICATION
P ZAIDI_OSTEOLAST_TRANSCRIPTION_FACTORS
R REACTOME_REGULATION_OF_GENE_EXPRESSION_IN_BETA
L WANG_BARRETTES_ESOPHAGUS_UP
P REACTOME_ENDOGENOUS_STEROLS
L VERRECCHIA_RESPONSE_TO_TGFB1_C6
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L MAHADEVAN_IMATINIB_RESISTANCE_UP
C KUROKAWA_LIVER_CANCER_EARLY_RECURRENCE_UP
L WEINMANN_ADAPTATION_TO_HYPOXIA_DN
L BIOCARTE_AHSP_PATHWAY
F ZHU_CMV_24_HR_UP
O SMID_BREAST_CANCER_RELAPSE_IN_PLEURA_UP
O YE_METASTATIC_LIVER_CANCER
O WALLACE_PROSTATE_CANCER_DN
B RICKMAN_HEAD_AND_NECK_CANCER_A
A SMID_BREAST_CANCER_ERBB2_DN
F HUPER_BREAST_BASAL_VS_LUMINAL_DN
B CHASSOT_SKIN_WOUND
F BUDHU_LIVER_CANCER_METASTASIS_DN
L SEIKE_LUNG_CANCER_POOR_SURVIVAL
L AGARWAL_AKT_PATHWAY_TARGETS
L WANG_ESOPHAGUS_CANCER_PROGRESSION_UP
L BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
L KONDO_HYPOXIA
L TSUNODA_CISPLATIN_RESISTANCE_UP
O FERRARI_RESPONSE_TO_FENRETINIDE_DN
A RICKMAN_HEAD_AND_NECK_CANCER_D
L CROMER_TUMORIGENESIS_UP
L ONDER_CDH1_TARGETS_2_UP
L FARMER_BREAST_CANCER_CLUSTER_5
G FARMER_BREAST_CANCER_CLUSTER_1
G WONG_ENDOMETRIAL_CANCER_LATE
G BIOCARTE_TCYTOTOXIC_PATHWAY
G MILICIC_FAMILIAL_ADENOMATOUS_POLYPOSIS_DN
G LUI_THYROID_CANCER_CLUSTER_4
F UROSEVIC_RESPONSE_TO_IMIQIMOD
F GRANDVAUX_IFN_RESPONSE_NOT_VIA_IRF3
F MOSERLE_IFNA_RESPONSE
F BENNETT_SYSTEMIC_LUPUS_ERYTHEMATOSUS
F ZHANG_INTERFERON_RESPONSE
F BOWIE_RESPONSE_TO_EXTRACELLULAR_MATRIX



GSZ score

H.Tiss

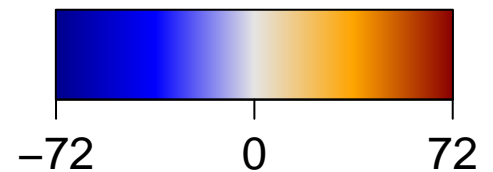


GSZ score

H.Tiss

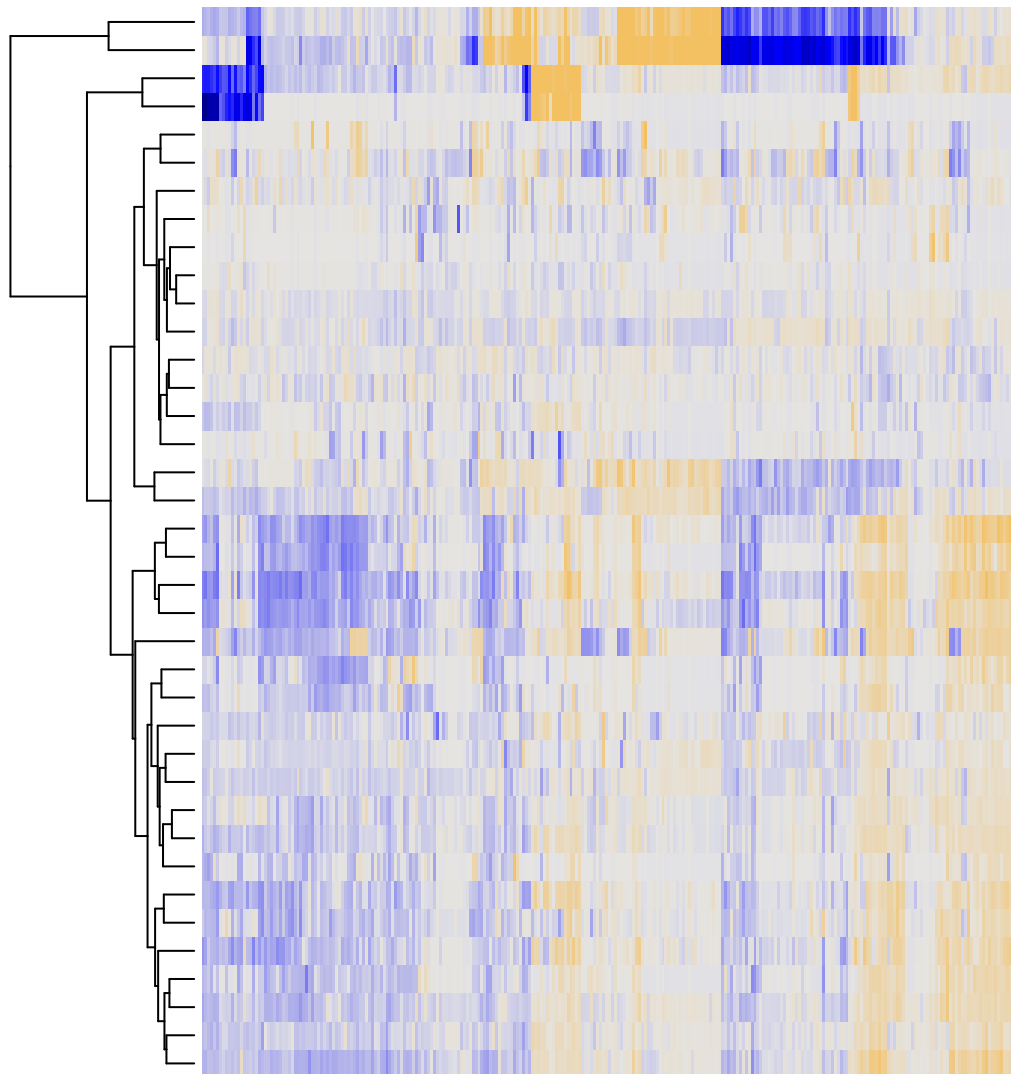
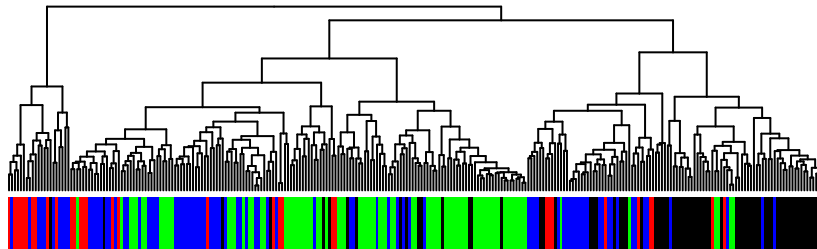


N WIRTH_Muscle
N WIRTH_Hippocampus
P WIRTH_Homeostasis
A WIRTH_Pituitary gland
P WIRTH_Liver
I WIRTH_Pancreas
P WIRTH_Thyroid gland
I WIRTH_Globus pallidus
L WIRTH_Placenta
A WIRTH_Nervous System
M WIRTH_B-cells
K WIRTH_Telencephalon
Q WIRTH_Testis
I WIRTH_Thalamus
O WIRTH_Thymus
L WIRTH_Cortex cerebri
K WIRTH_Cerebellum
I WIRTH_Sec. lymphoid organs
F WIRTH_Lymphocytes
G WIRTH_Bone marrow
O WIRTH_Tonsil
O WIRTH_Prim. lymphoid organs
G WIRTH_Immune system
O WIRTH_Mucosa

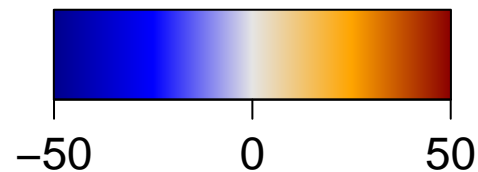


GSZ score

Lymphoma

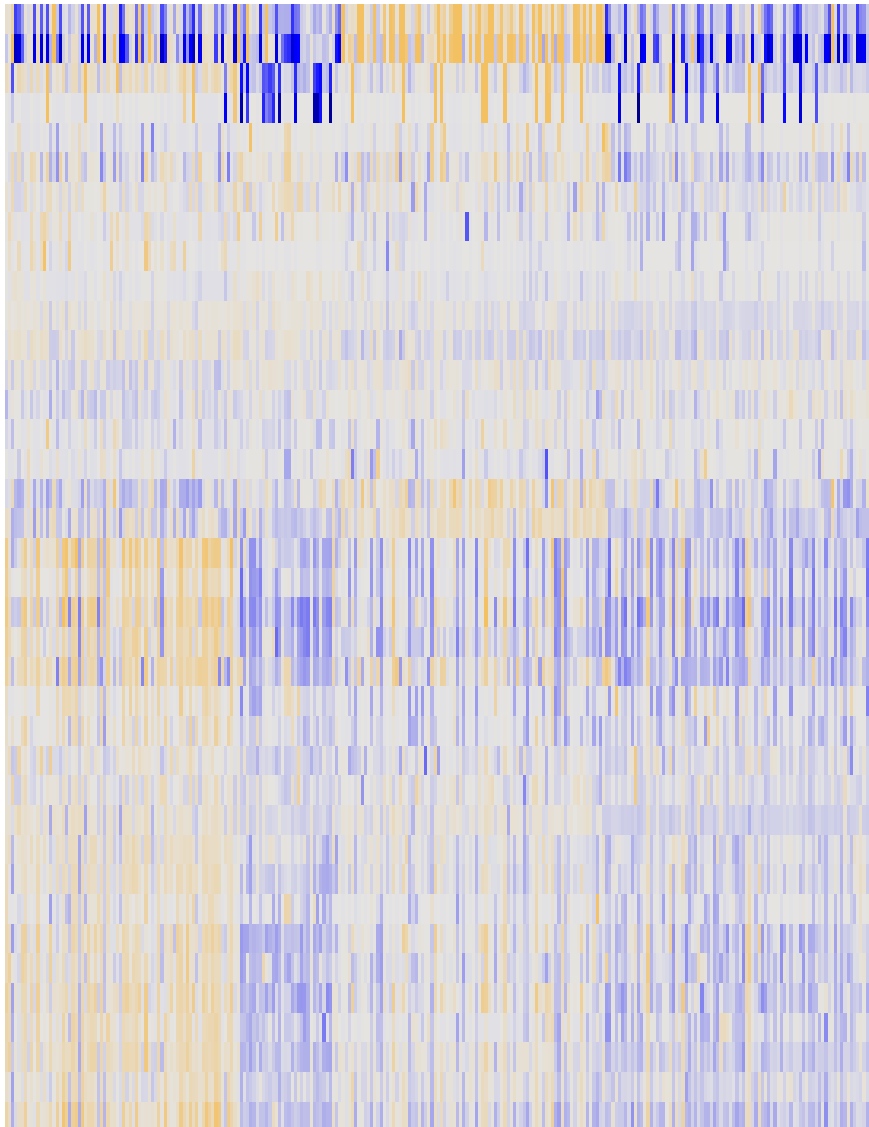
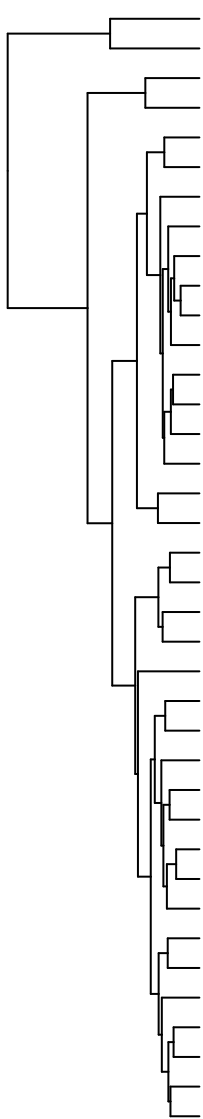


- L ROSOLOWSKI_green total
- L LENZ_Stromal signature 1
- F SPANG_IL21 DN
- F DAVE_MHCCII BL DN
- K DAVE_c-myc BL UP
- K ROSOLOWSKI_blue total
- G DAVE_BL UP
- B BENTINK_mBL UP
- B MASCQUE_mBL UP
- J DAVE_BL Inter
- B SPANG_IL21 UP
- B SPANG_BCR UP
- O ZHANG_DLBCl mutated
- I SPANG_BAFF 9hrs UP
- I DAVE_BL DN
- D ROSOLOWSKI_red UP
- L LENZ_Stromal signature 2
- L ROSOLOWSKI_green UP
- G WRIGHT_ABC UP
- H MASCQUE_ABC UP
- G DAVE_Immune response 1
- G WRIGHT_GCB UP
- K DAVE_BL-vs-DLBCL
- G WRIGHT_custom ABC-DLBCL UP
- I WRIGHT_custom GCB-DLBCL UP
- F DAVE_Immune response 2
- G MASCQUE_GCB UP
- G SPANG_BCR DN
- E SPANG_BAFF 9hrs DN
- G SPANG_LPS 6hrs DN
- G MASCQUE_mBL DOWN
- F ROSOLOWSKI_blue DOWN
- R ROSOLOWSKI_red total
- G DAVE_NFKB BL DN
- G BENTINK_mBL DOWN
- G SPANG_CD40 6hrs DN
- G SPANG_LPS 6hrs UP
- G SPANG_CD40 6hrs UP

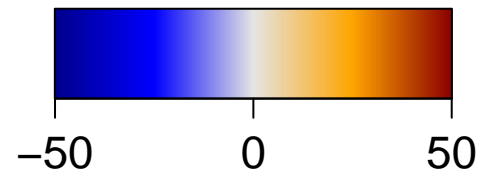


GSZ score

Lymphoma

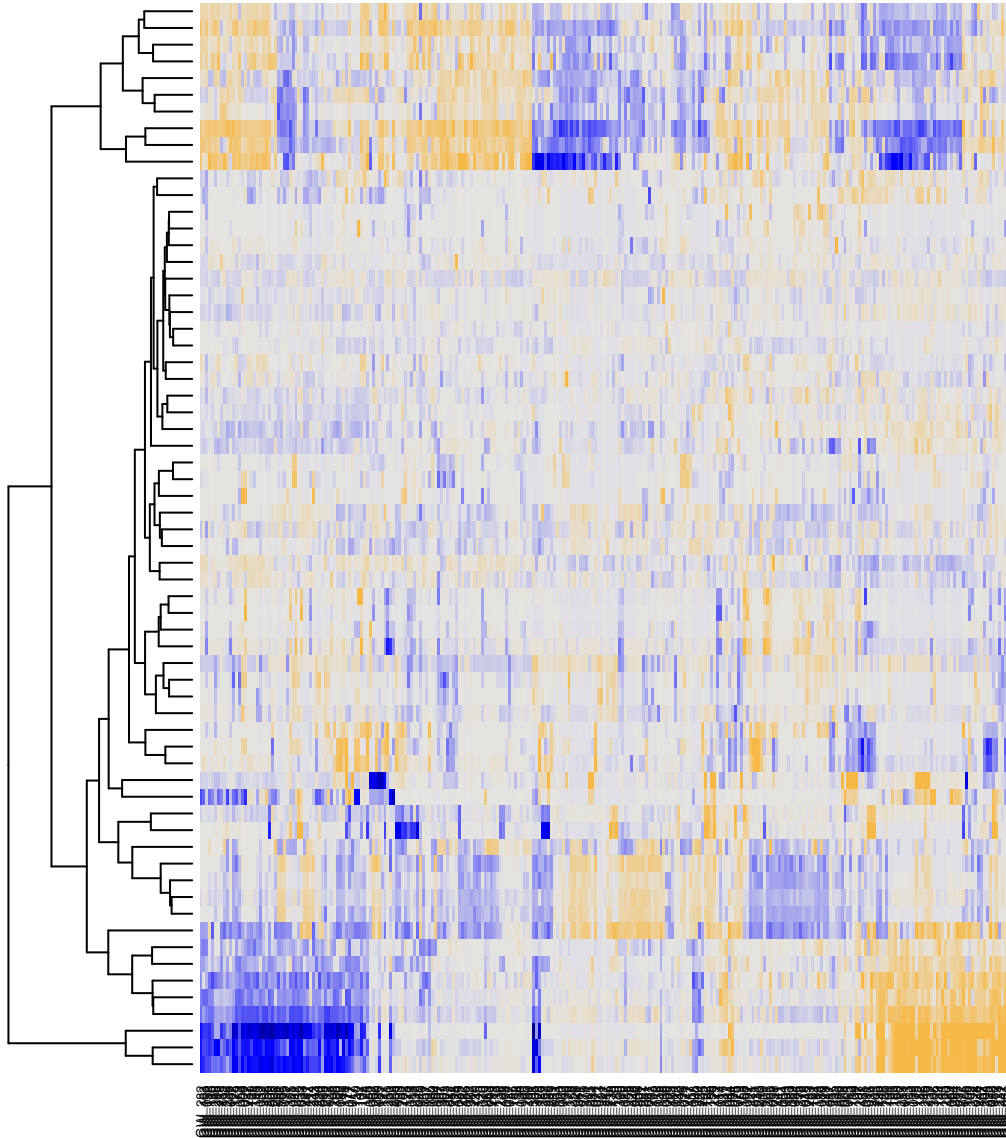
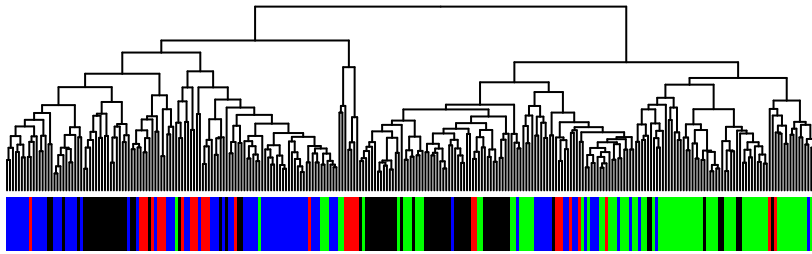


- L ROSOLOWSKI_green total
- L LENZ_Stromal signature 1
- F SPANG_IL21 DN
- F DAVE_MHCCII BL DN
- K DAVE_c-myc BL UP
- K ROSOLOWSKI_blue total
- G DAVE_BL UP
- B BENTINK_mBL UP
- B MASCQUE_mBL UP
- J DAVE_BL Inter
- B SPANG_IL21 UP
- B SPANG_BCR UP
- O ZHANG_DLCL mutated
- I SPANG_BAFF 9hrs UP
- I DAVE_BL_DN
- D ROSOLOWSKI_red UP
- L LENZ_Stromal signature 2
- L ROSOLOWSKI_green UP
- G WRIGHT_ABC UP
- H MASCQUE_ABC UP
- G DAVE_Immune response 1
- G WRIGHT_GCB UP
- K DAVE_BL-vs-DLBCL
- G WRIGHT_custom ABC-DLBCL UP
- I WRIGHT_custom GCB-DLBCL UP
- F DAVE_Immune response 2
- G MASCQUE_GCB UP
- G SPANG_BCR DN
- E SPANG_BAFF 9hrs DN
- G SPANG_LPS 6hrs DN
- G MASCQUE_mBL DOWN
- F ROSOLOWSKI_blue DOWN
- R ROSOLOWSKI_red total
- G DAVE_NFkB BL DN
- G BENTINK_mBL DOWN
- G SPANG_CD40 6hrs DN
- G SPANG_LPS 6hrs UP
- G SPANG_CD40 6hrs UP

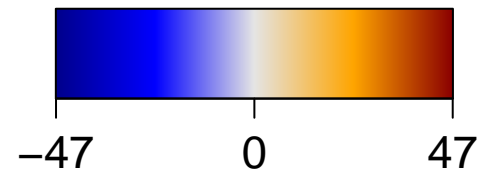


GSZ score

MF

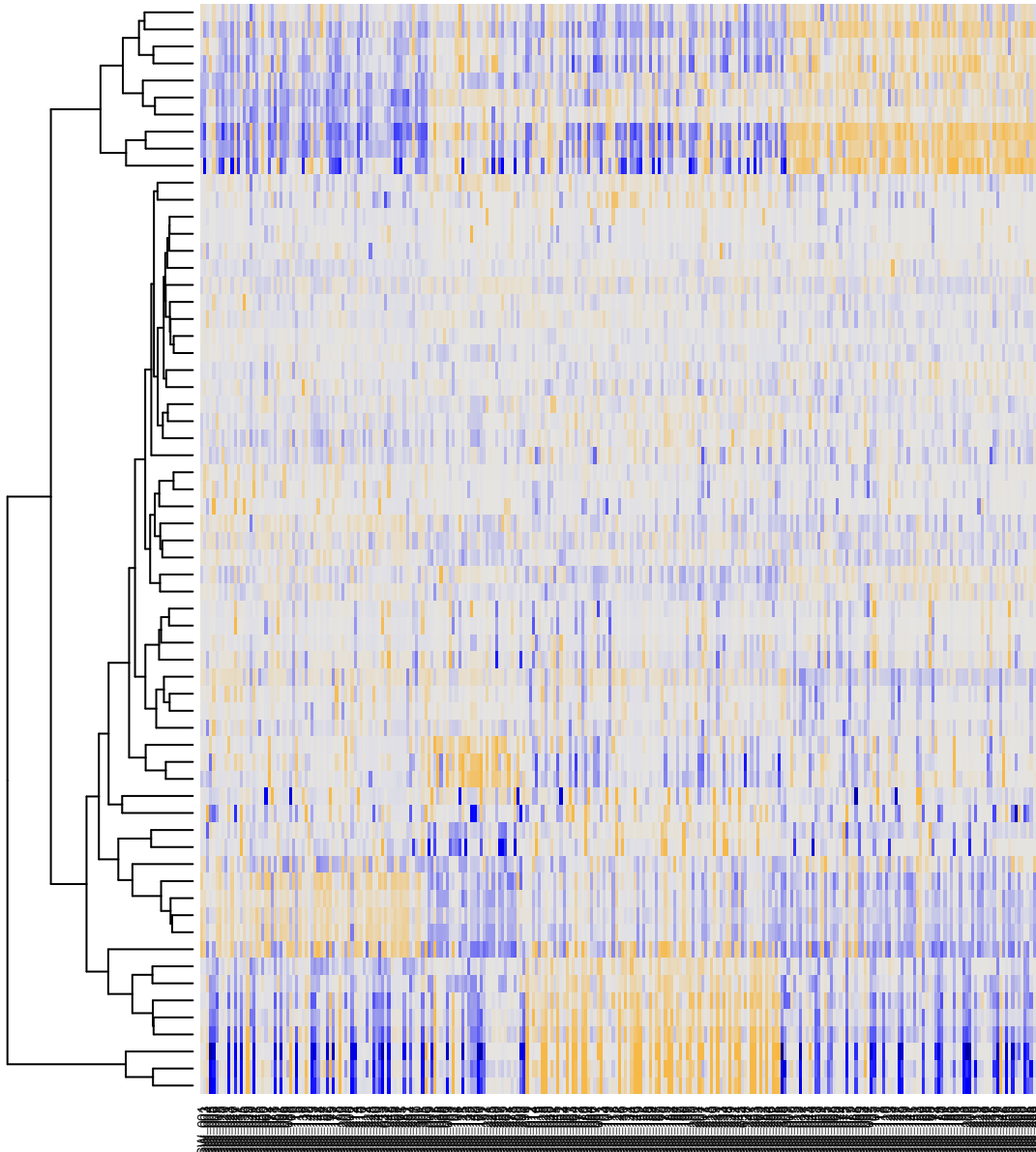


- P channel activity
- O serine-type endopeptidase activity
- O retinol binding
- O retinol dehydrogenase activity
- O interleukin-1 receptor binding
- O structural constituent of cytoskeleton
- O gap junction channel activity
- O structural molecule activity
- O serine-type endopeptidase inhibitor activity
- O RAGE receptor binding
- L heparan sulfate proteoglycan binding
- L actin-dependent ATPase activity
- P death receptor binding
- R oxidoreductase activity, acting on NAD(P)H
- P ephrin receptor activity
- O zinc ion transmembrane transporter activity
- Q molecular_function
- I E-box binding
- A frizzled binding
- J insulin receptor substrate binding
- G lipopolysaccharide binding
- M monosaccharide binding
- B acetylglucosaminyltransferase activity
- L G-protein coupled receptor binding
- I low-density lipoprotein receptor activity
- C substrate-specific transmembrane transporter activity
- I metallocarboxypeptidase activity
- B RNA polymerase II transcription coactivator activity
- B enhancer sequence-specific DNA binding
- P GABA-A receptor activity
- G coreceptor activity
- P virus receptor activity
- E low-density lipoprotein particle receptor binding
- O sodium channel activity
- R lysophospholipase activity
- R NADH dehydrogenase (ubiquinone) activity
- M NADH dehydrogenase activity
- R rRNA binding
- R structural constituent of ribosome
- K ATP binding
- K DNA helicase activity
- K nucleocytoplasmic transporter activity
- K double-stranded DNA binding
- M neuropeptide hormone activity
- K glutathione binding
- K glutathione transferase activity
- N structural constituent of muscle
- L oxygen transporter activity
- F double-stranded RNA binding
- F peptide antigen binding
- G fatty acid binding
- G antigen binding
- G cytokine binding
- G transmembrane signaling receptor activity
- G Rac GTPase activator activity
- G chemokine activity
- L L-ascorbic acid binding
- L metalloendopeptidase inhibitor activity
- L fibronectin binding
- L metalloendopeptidase activity
- L integrin binding
- L platelet-derived growth factor binding
- L extracellular matrix binding
- L extracellular matrix structural constituent

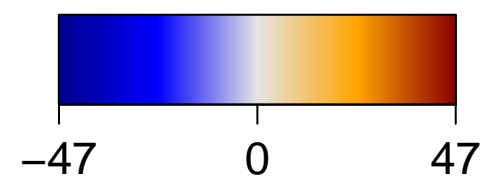


GSZ score

MF

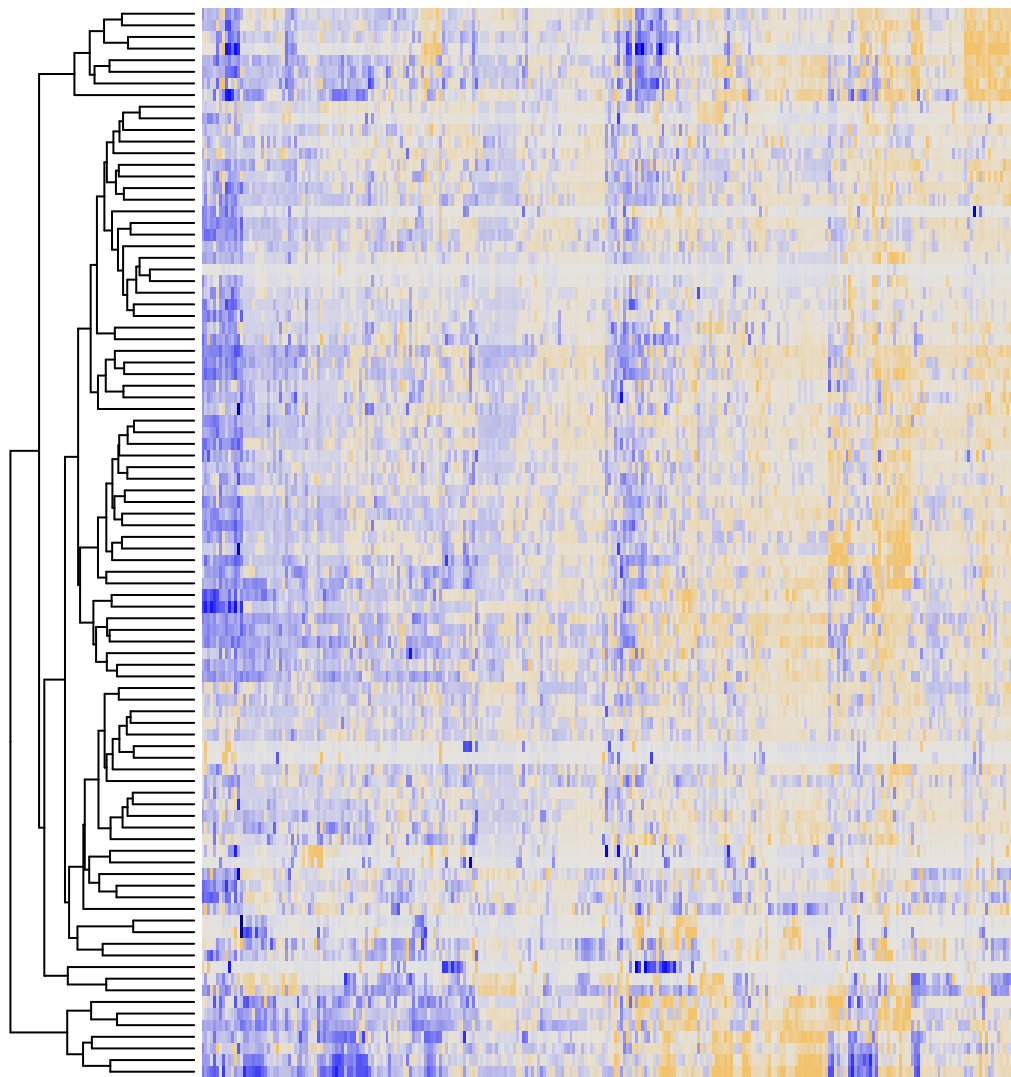
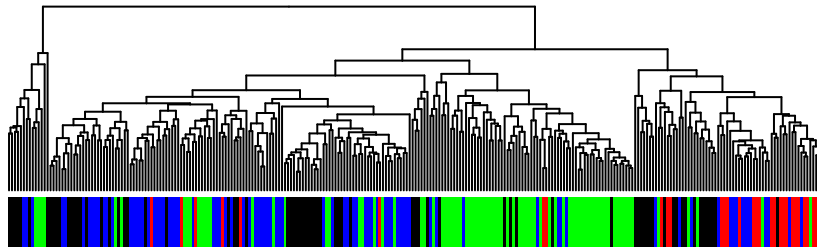


- P channel activity
- O serine-type endopeptidase activity
- O retinol binding
- O retinol dehydrogenase activity
- O interleukin-1 receptor binding
- O structural constituent of cytoskeleton
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- L actin-dependent ATPase activity
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- I E-box binding
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- J insulin receptor substrate binding
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- K ATP binding
- K DNA helicase activity
- K nucleocytoplasmic transporter activity
- K double-stranded DNA binding
- M neuropeptide hormone activity
- K glutathione binding
- K glutathione transferase activity
- N structural constituent of muscle
- L oxygen transporter activity
- F double-stranded RNA binding
- F peptide antigen binding
- G fatty acid binding
- G antigen binding
- G cytokine binding
- G transmembrane signaling receptor activity
- G Rac GTPase activator activity
- G chemokine activity
- L L-ascorbic acid binding
- L metalloendopeptidase inhibitor activity
- L fibronectin binding
- L metalloendopeptidase activity
- L integrin binding
- L platelet-derived growth factor binding
- L extracellular matrix binding
- L extracellular matrix structural constituent

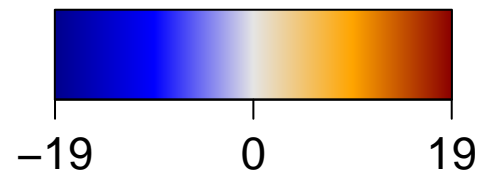


GSZ score

miRNA 3UTR

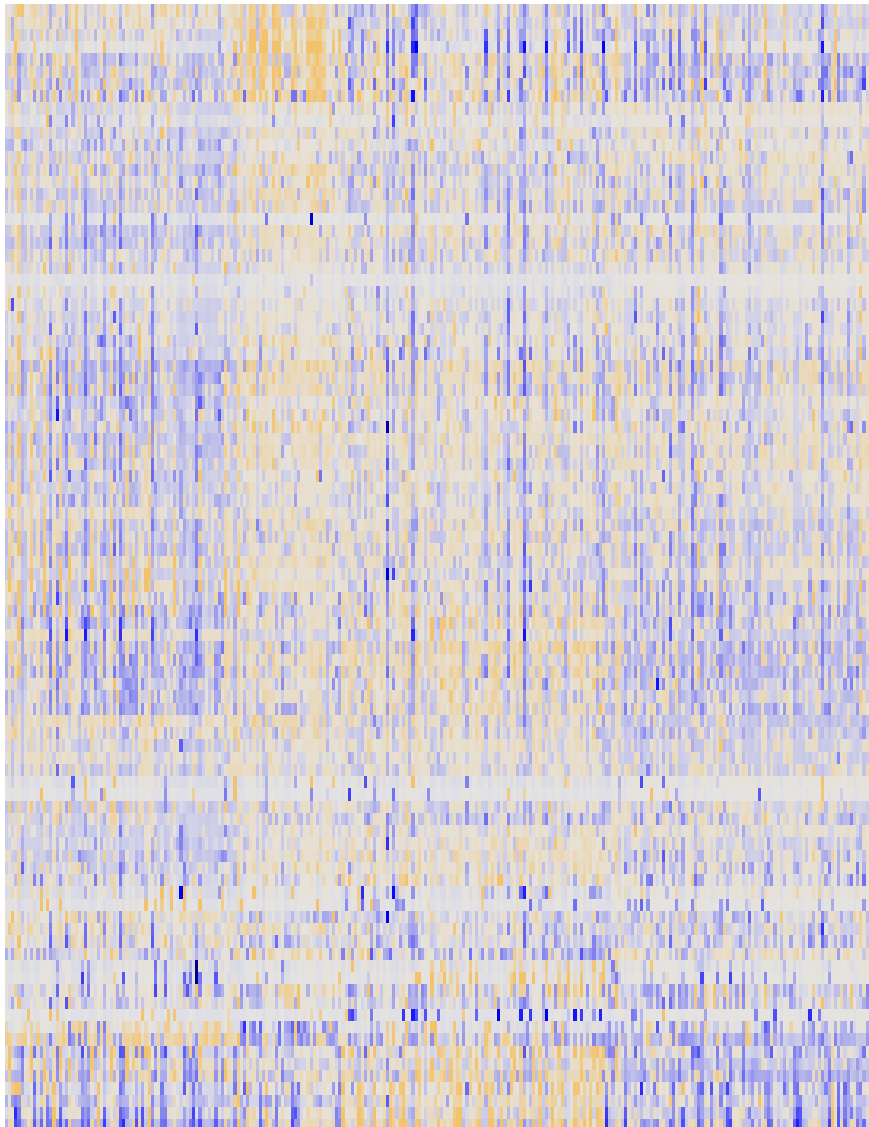
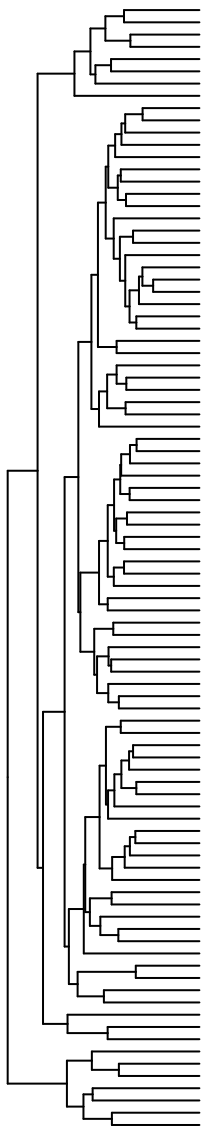


ACCA-509
GCAC-18A-18B
GCCTG-512-5P
TAGCA-450
TAGCA-9
AAAG-511
AGGG-328
GTTCA-380-5P
GTTCA-393
CTAC-325
CTCT-520A-525
GTTCT-342
ACAG-10A-10B
GTGG-297-211
ATGG-302C
GTGG-369-5P
GTTA-292
GTTA-292
AAGC-520F
CAGT-134
AGTG-521
AGTC-345
ATCT-31
CTCT-368
CTCT-528C-518F-526A
CACG-302A
ATCT-493
TGGC-519C-519B-519A
TGGC-30A-301-130B
ACAT-190
GATC-488
GTTG-302B
CTTG-30A-3P-30E-3P
TGCA-148A-152-148B
GATA-489-5P
TCCA-516-5P
AGCC-515-3P
AGCG-7-3P
AGCG-330
ACTG-27A-27B
ACAT-1-206
GTTT-373
TGCT-378
GACT-212-132
CTGG-150
CTGG-57
GTAC-901
ACTG-139
GTAC-30A-5P-30C-30D-30B-30E-5P
GTAC-17-5P-20A-106A-106B-20B-519D
CAGT-200B-200C-429
GGCC-193A-193B
GTGG-26A-26B
CTCA-125B-125A
GGCC-332
GGCC-332
CAGC-485-5P
CTTG-214
GTGG-184
GAGC-371
GAGC-371
AATG-136
AAG-422B-422A
GCCA-324-3P
GTAC-384
TGCA-99A-100-99B
TGCA-99A-517C
CGGT-220
GATA-409-5P
TACA-182
GTAG-189
GGA1-171
TGCA-503
GTCT-503
TGG-1910
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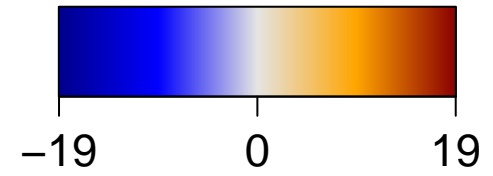


GSZ score

miRNA 3UTR

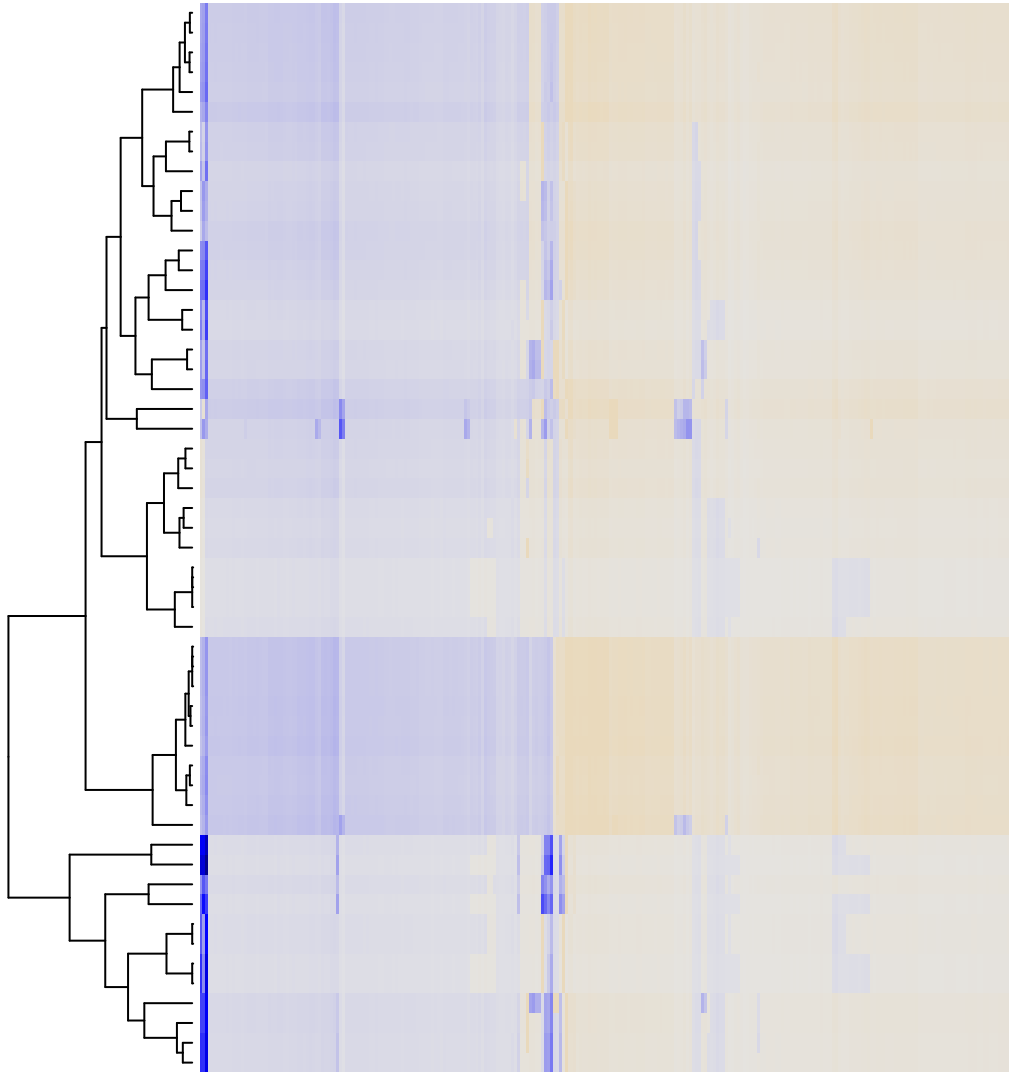
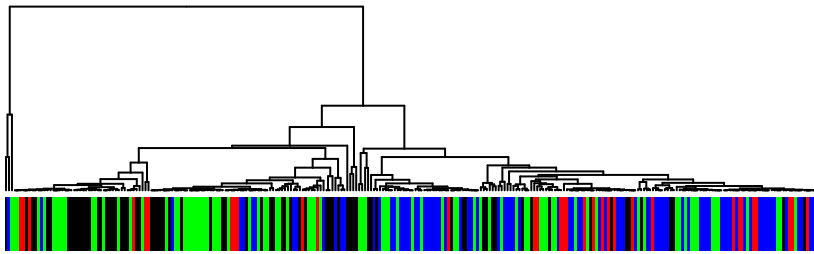


ACCA-509
GCAC-18A--18B
CCTG-512-5P
GAG-450
TAG-9
AAAG-511
AGGG-328
GTC-389 5P
CTAC-325
CTCT-520A--525
GTCT-379
ACAG-10A--10B
GTGG-197
AAAG-204
ATG-302C
GTCC-369-5P
ACCA-522
CAIT-203
CAG-549F
CAG-549
AGTG-521
AACG-451
AGTC-345
CTCT-368
CTCT-526C--518F--526A
CAGC-302A
GTG-393
TGCA-519C--519B--519A
TTGC-130A--301--130B
ACAT-190
TTC-486
GTTA-302B
ACTG-30A-3P--30E-3P
TGCA-148A--152--148B
ATA-446
ATA-299-5P
TCCA-516-5P
AGGC-515-3P
ACTG-17-3P
ACTG-27A--27B
ACAT-1--206
ACT-373
AGCT-28
AGCT-212--132
TTGG-150
CTTT-527
GTAC-101
ACTG-30A-5P--30C--30D--30B--30E-5P
GCAC-17-5P--20A--106A--106B--20B--519D
CAGT-200B--200C--429
GGCC-193A--193B
TAG-26A--26B
GTGC-25--32--92--363--367
CTCA-125B--125A
GCTC-338
GCTC-338
CAGC-485-5P
CCTG-214
TCCG-184
GGCC-371
GAGC-337
AATG-136
CCAG-490
GAG-422B--422A
GAG-324-3P
CIAG-384
TACG-99A--100--99B
TGCA-517A--517C
GGT-220
GGTA-409-5P
AACT-223
TAG-182
GTAG-182
GGAT-127
TCCA-213
TTCC-503
ATGC-110
CGTC-208
AGCA-155
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GAT-153
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AGTC-151
AGCA-516-3P
ACTA-196A--196B
TTGT-29A--29B--29C

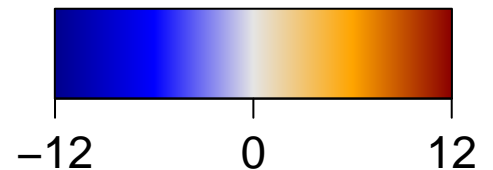


GSZ score

miRNA Disease

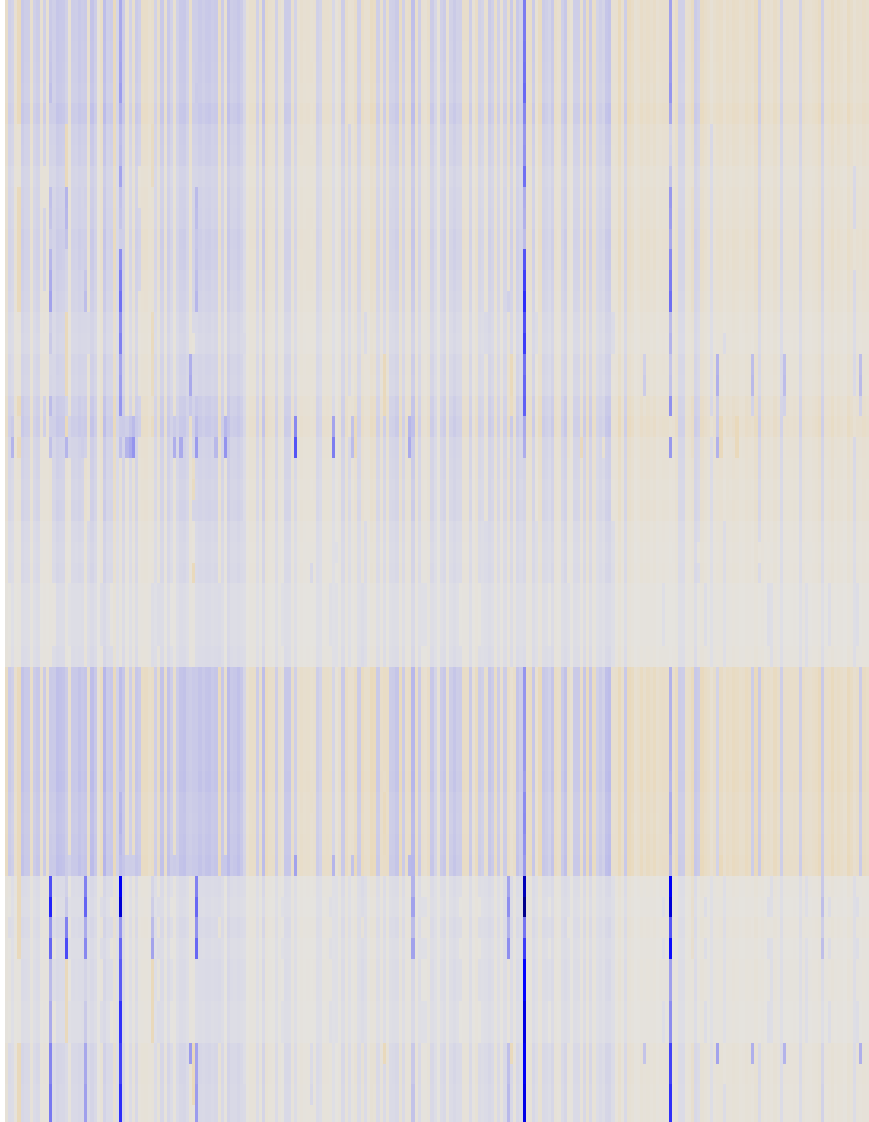
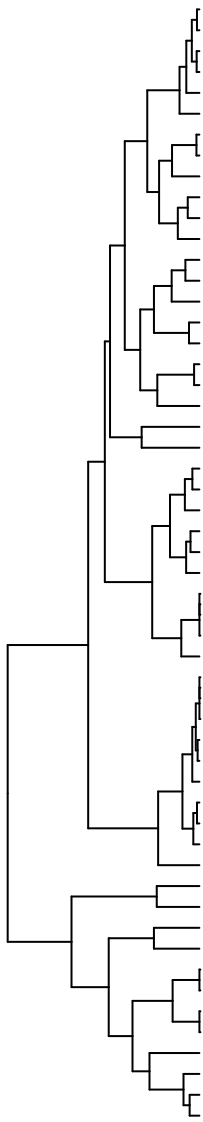


- A Muscular
- A Hepatocellular carcinoma
- A Glioblastoma multiforme, somatic
- A Gastrointestinal
- A Multiple myeloma
- A Colorectal cancer
- A Cervical cancer, somatic
- A Medulloblastoma
- A Immunological
- A Alzheimer disease, susceptibility to
- A Neuroblastoma
- A Myopathy, nemaline, 3
- A Gastric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

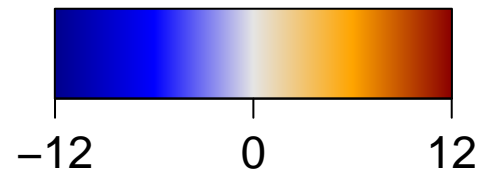


GSZ score

miRNA Disease

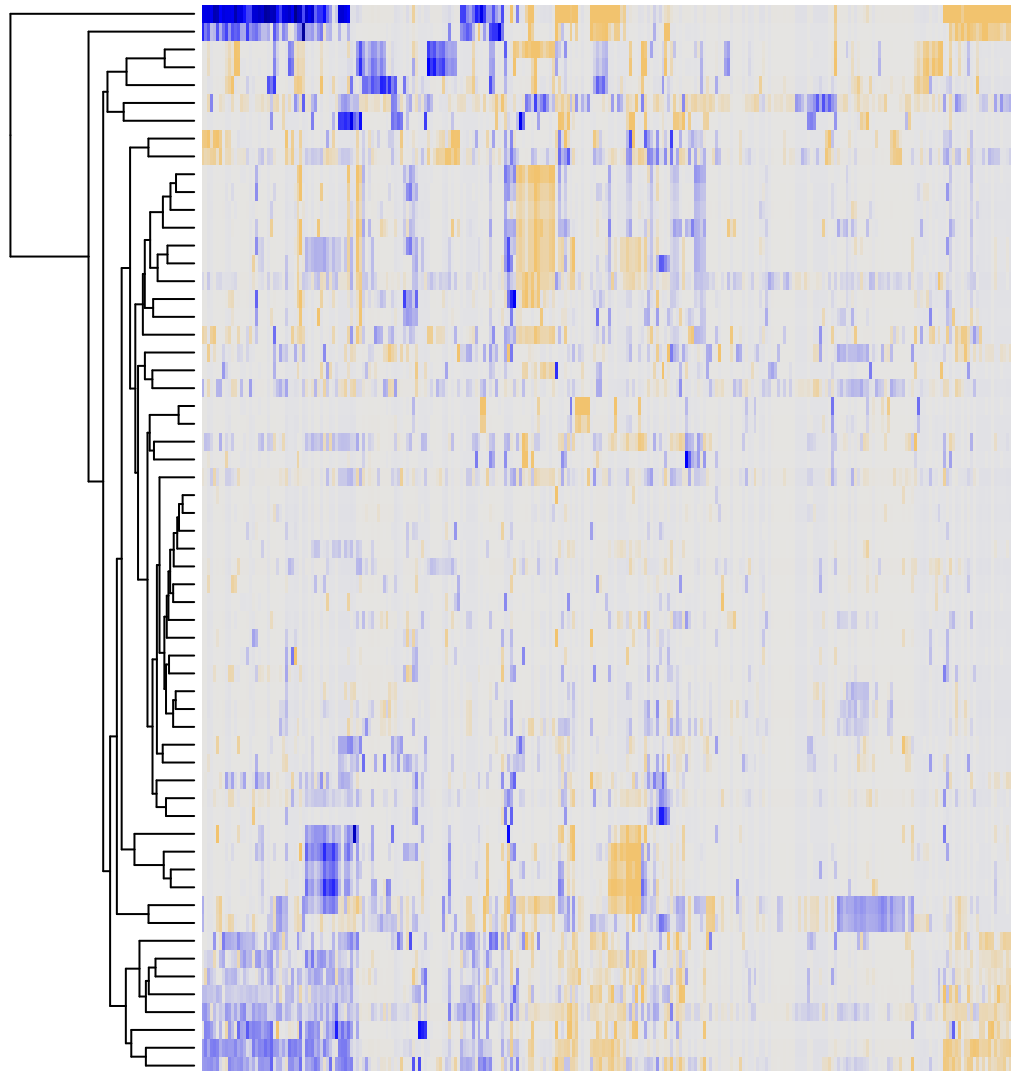
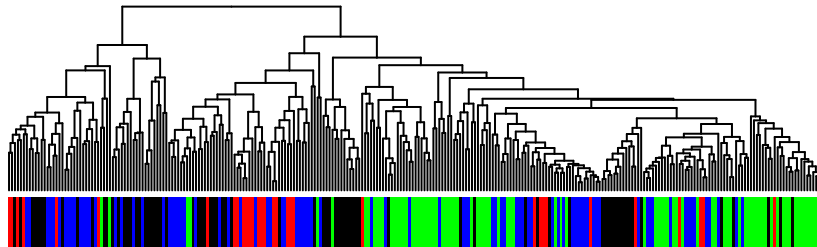


- A Muscular
- A Hepatocellular carcinoma
- A Glioblastoma multiforme, somatic
- A Gastrointestinal
- A Multiple myeloma
- A Colorectal cancer
- A Cervical cancer, somatic
- A Medulloblastoma
- A Immunological
- A Alzheimer disease, susceptibility to
- A Neuroblastoma
- A Myopathy, nemaline, 3
- A Gastric cancer
- A Bladder cancer
- A Esophageal cancer
- A Psoriasis, susceptibility to
- A Autism, susceptibility to
- A Non-Hodgkin lymphoma, somatic
- A Hodgkin lymphoma
- A Cardiomyopathy, dilated
- A Stroke, susceptibility to
- A Melanoma, cutaneous malignant, 2
- A Myelofibrosis, idiopathic
- A Parkinson disease
- A Systemic lupus erythematosus (SLE)
- A Supravalvar aortic stenosis
- A Multiple sclerosis, susceptibility to
- A Pigmented adrenocortical disease, primary isolated
- A Cardiovascular
- A Adenomas, multiple colorectal
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- A Squamous cell carcinoma, head and neck
- A Pancreatic cancer
- A Hematological
- A Cancer
- A Prostate cancer
- A Breast cancer
- A Ovarian cancer
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- A Leukemia
- A Lung cancer
- A Thyroid carcinoma, papillary
- A Polycythemia vera
- A Thyroid carcinoma, follicular
- A Cardiomyopathy, idiopathic dilated
- A Dermatitis, atopic
- A Systemic lupus erythematosus, susceptibility
- A Myocardial infarction, susceptibility to
- A Pituitary adenoma
- A Miyoshi myopathy
- A Muscular dystrophy
- A Duchenne muscular dystrophy
- A Gastroesophageal reflux

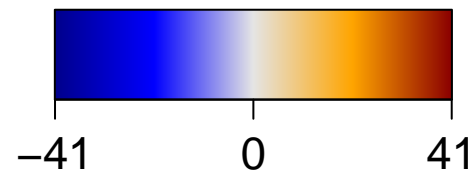


GSZ score

miRNA target

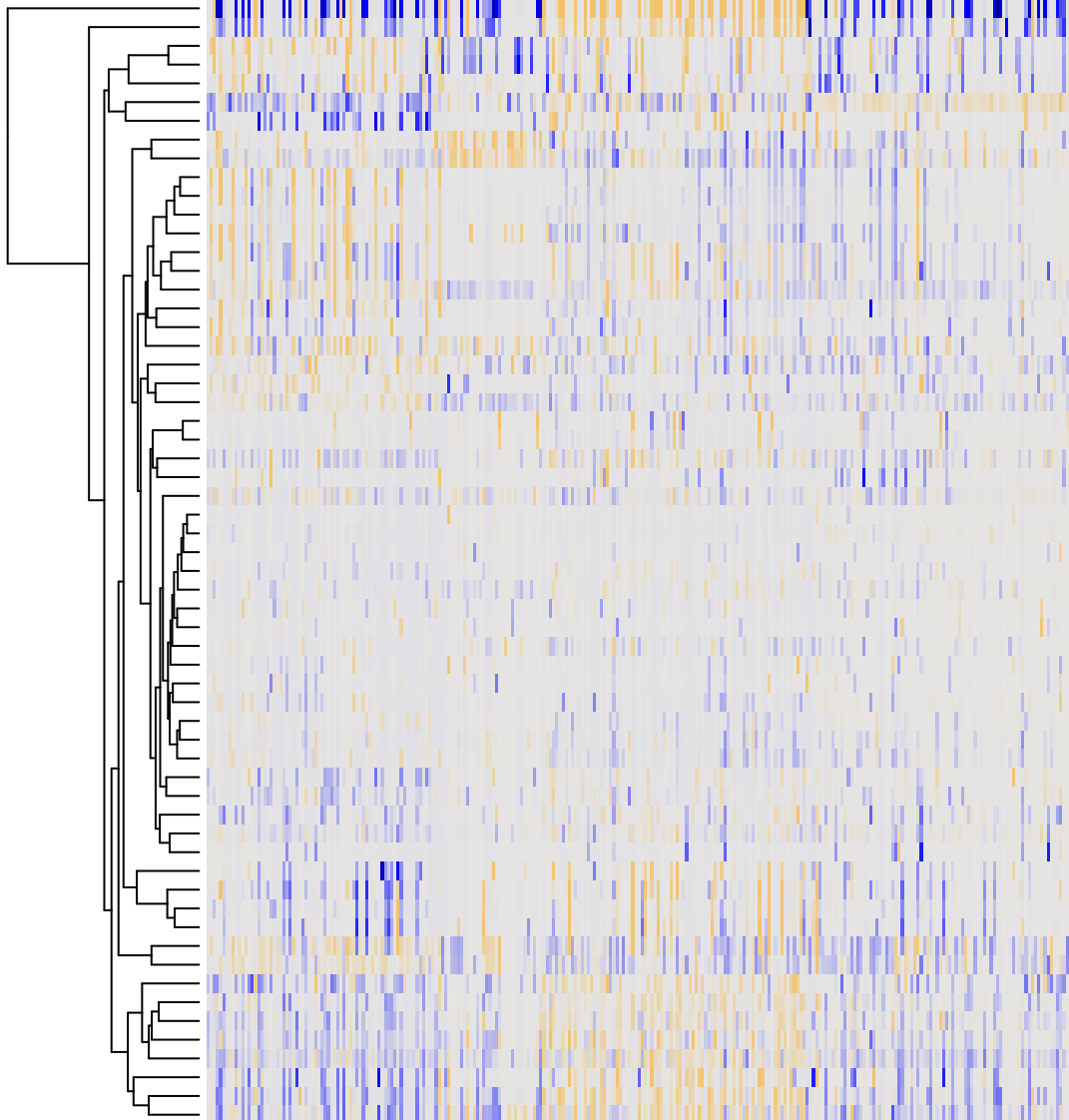


L miR-29c
L miR-18
F miR-148a
F miR-152
K miR-24
O miR-196a
O miR-199a*
K miR-127
L miR-145
B miR-153
B miR-34c
B miR-15b
A miR-204
B miR-34b
E let-7c
B miR-34a
B miR-101
A miR-223
N miR-320
I miR-205
H miR-193a
G miR-155
A miR-107
A miR-181a
L miR-126
A miR-129
O miR-1
P miR-128b
A miR-210
R miR-19a
L miR-29a
P miR-17
M miR-27a
R miR-375
A miR-133a
P miR-7
R miR-659
O miR-125a
A miR-93
I miR-146a
I miR-221
P miR-206
C miR-122
L miR-197
E miR-125b
E miR-98
P miR-124a
L miR-195
L miR-20a
L miR-16-1
B miR-15a
E miR-26a
L miR-346
L miR-143
L miR-200c
L miR-9
L miR-21
L miR-101b
L miR-29b
I miR-222

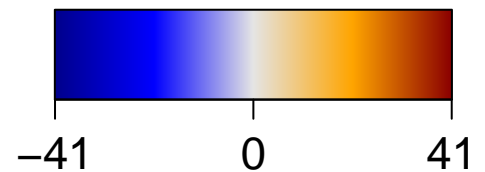


GSZ score

miRNA target

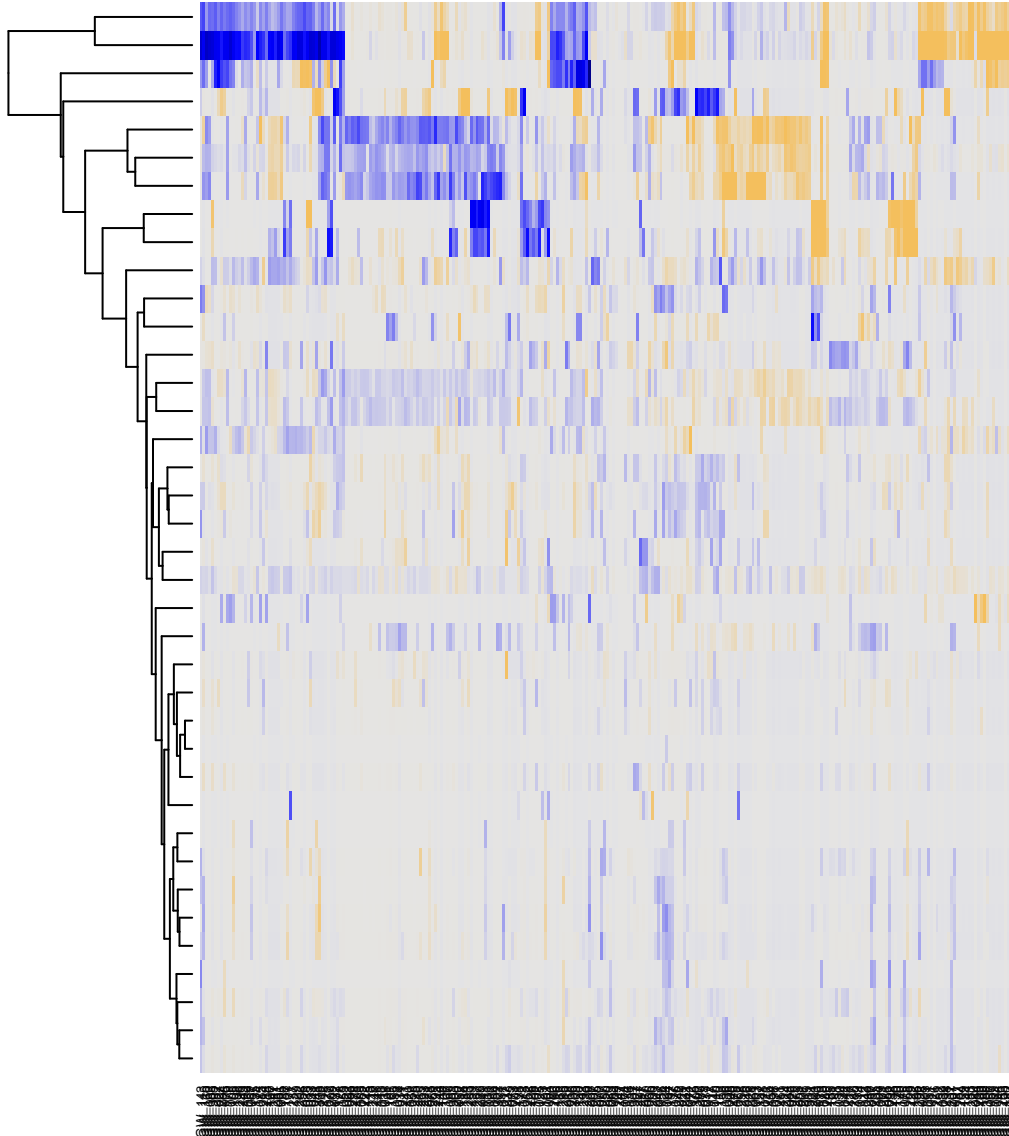
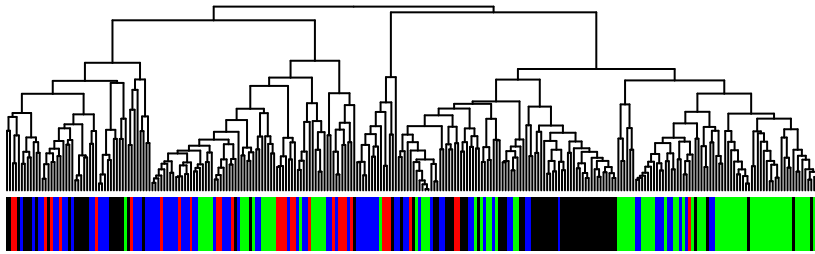


- L miR-29c
- L miR-18
- F miR-148a
- F miR-152
- K miR-24
- O miR-196a
- O miR-199a*
- K miR-127
- L miR-145
- B miR-153
- B miR-34c
- B miR-15b
- A miR-204
- B miR-34b
- E let-7c
- B miR-34a
- B miR-101
- A miR-223
- N miR-320
- I miR-205
- H miR-193a
- G miR-155
- A miR-107
- A miR-181a
- L miR-126
- A miR-129
- O miR-1
- P miR-128b
- A miR-210
- R miR-19a
- L miR-29a
- P miR-17
- M miR-27a
- R miR-375
- A miR-133a
- P miR-7
- R miR-659
- O miR-125a
- A miR-93
- I miR-146a
- I miR-221
- P miR-206
- C miR-122
- L miR-197
- E miR-125b
- E miR-98
- P miR-124a
- L miR-195
- L miR-20a
- L miR-16-1
- B miR-15a
- E miR-26a
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- L miR-9
- L miR-21
- L miR-101b
- L miR-29b
- I miR-222

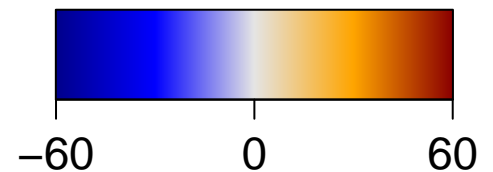


GSZ score

MMML CGS

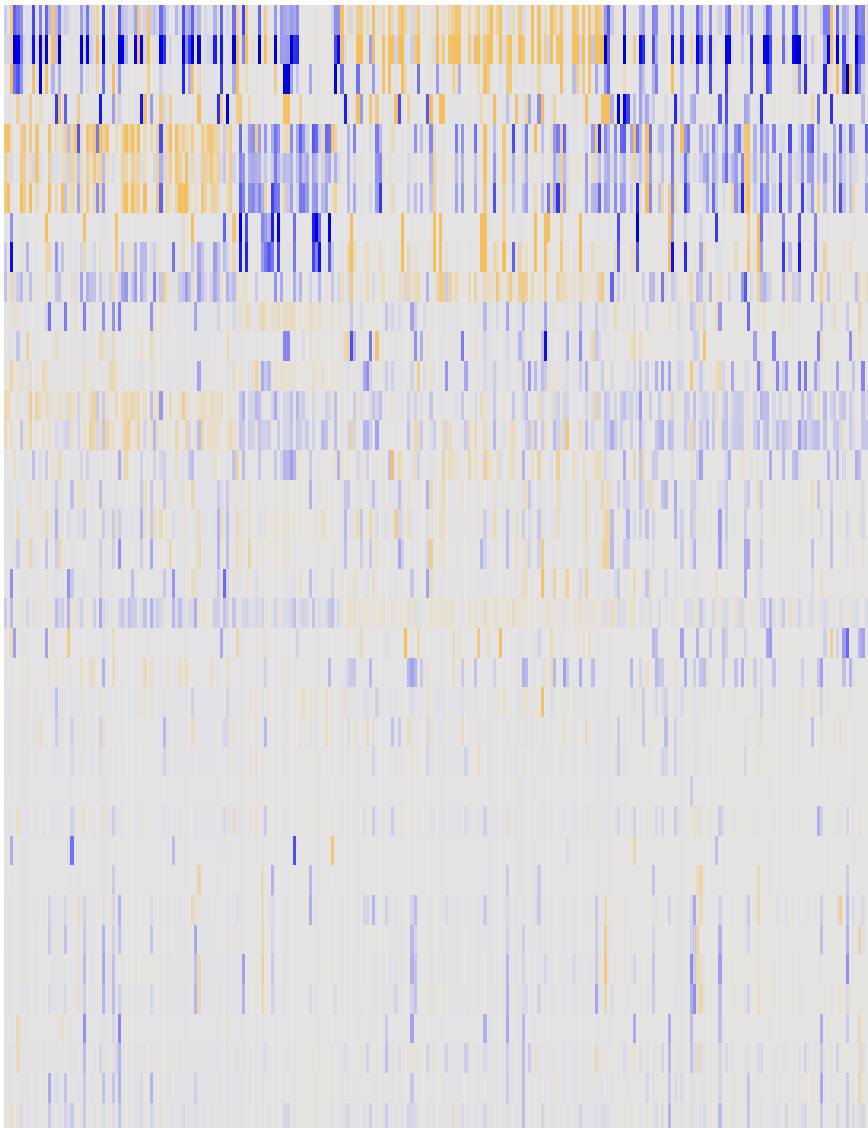
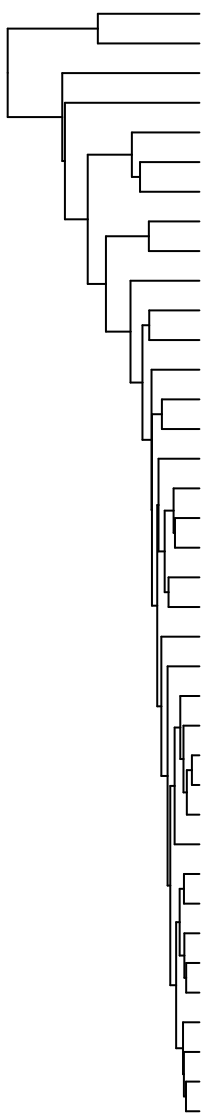


L MACIEJ_MMML 31
L MACIEJ_MMML 1
L MACIEJ_MMML 23
K MACIEJ_MMML 4
G MACIEJ_MMML 2
H MACIEJ_MMML 6
G MACIEJ_MMML 7
F MACIEJ_MMML 27
F MACIEJ_MMML 47
L MACIEJ_MMML 13
R MACIEJ_MMML 50
E MACIEJ_MMML 5
J MACIEJ_MMML 8
G MACIEJ_MMML 20
J MACIEJ_MMML 44
D MACIEJ_MMML 40
K MACIEJ_MMML 15
K MACIEJ_MMML 19
K MACIEJ_MMML 41
P MACIEJ_MMML 9
G MACIEJ_MMML 3
A MACIEJ_MMML 46
I MACIEJ_MMML 32
A MACIEJ_MMML 26
M MACIEJ_MMML 29
A MACIEJ_MMML 14
A MACIEJ_MMML 35
C MACIEJ_MMML 24
A MACIEJ_MMML 43
R MACIEJ_MMML 17
R MACIEJ_MMML 48
R MACIEJ_MMML 28
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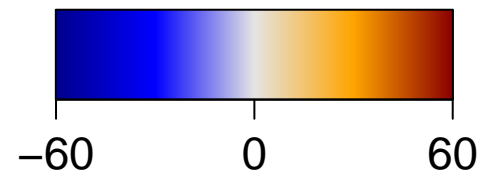


GSZ score

MMML CGS

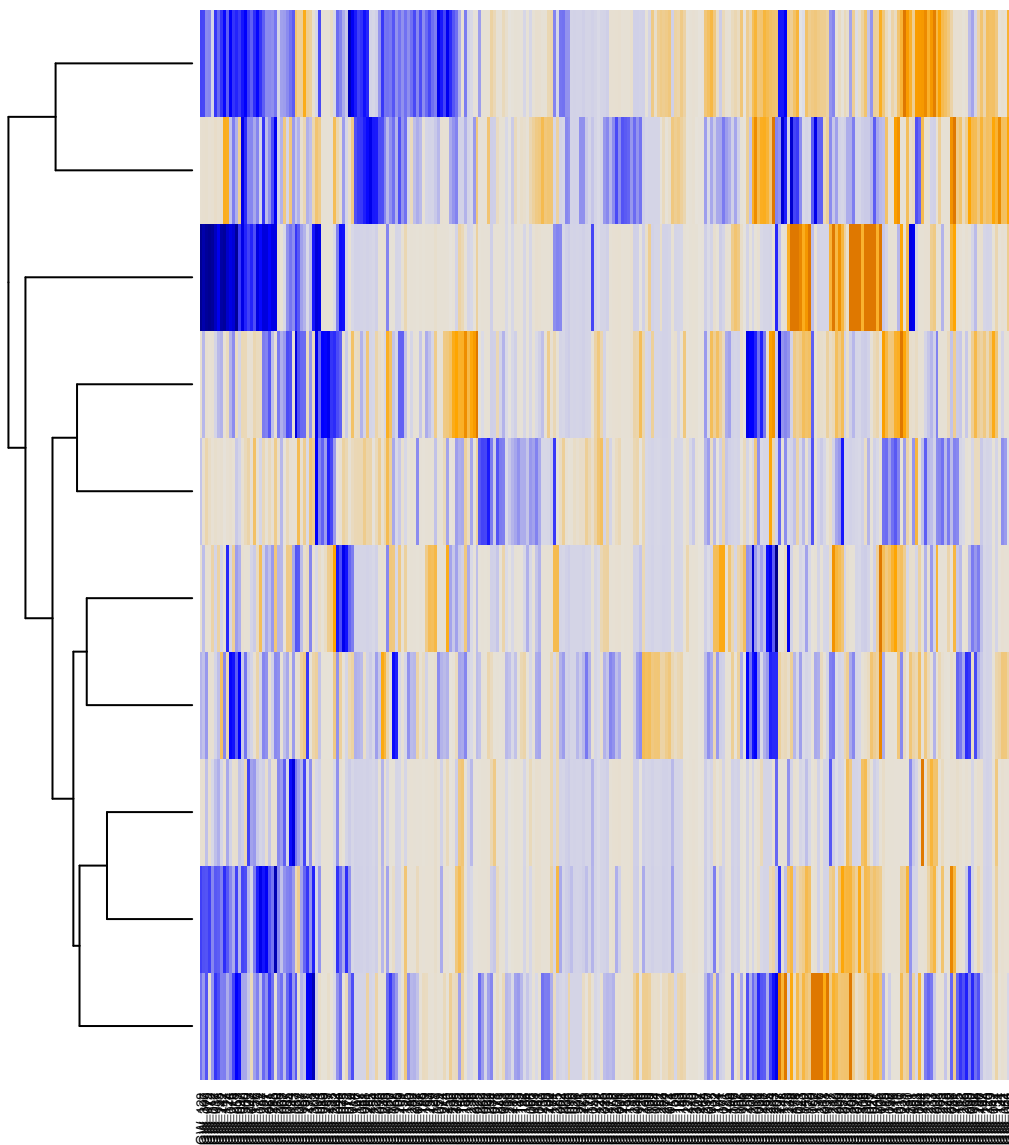
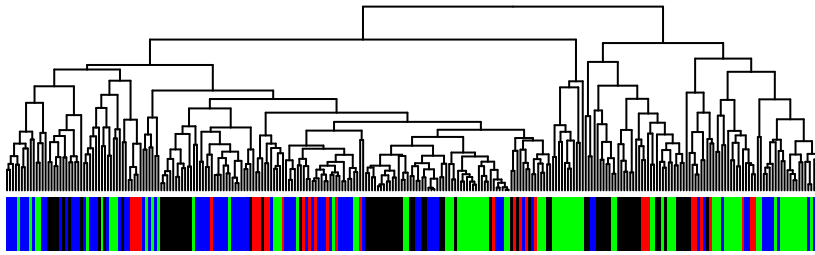


L MACIEJ_MMML 31
L MACIEJ_MMML 1
L MACIEJ_MMML 23
K MACIEJ_MMML 4
G MACIEJ_MMML 2
H MACIEJ_MMML 6
G MACIEJ_MMML 7
F MACIEJ_MMML 27
F MACIEJ_MMML 47
L MACIEJ_MMML 13
R MACIEJ_MMML 50
E MACIEJ_MMML 5
J MACIEJ_MMML 8
G MACIEJ_MMML 20
J MACIEJ_MMML 44
D MACIEJ_MMML 40
K MACIEJ_MMML 15
K MACIEJ_MMML 19
K MACIEJ_MMML 41
P MACIEJ_MMML 9
G MACIEJ_MMML 3
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I MACIEJ_MMML 32
A MACIEJ_MMML 26
M MACIEJ_MMML 29
A MACIEJ_MMML 14
A MACIEJ_MMML 35
C MACIEJ_MMML 24
A MACIEJ_MMML 43
R MACIEJ_MMML 17
R MACIEJ_MMML 48
R MACIEJ_MMML 28
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A MACIEJ_MMML 38
J MACIEJ_MMML 16
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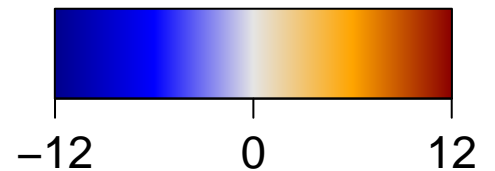


GSZ score

Pathw Act

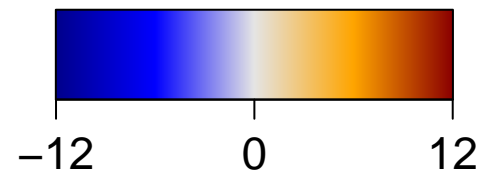
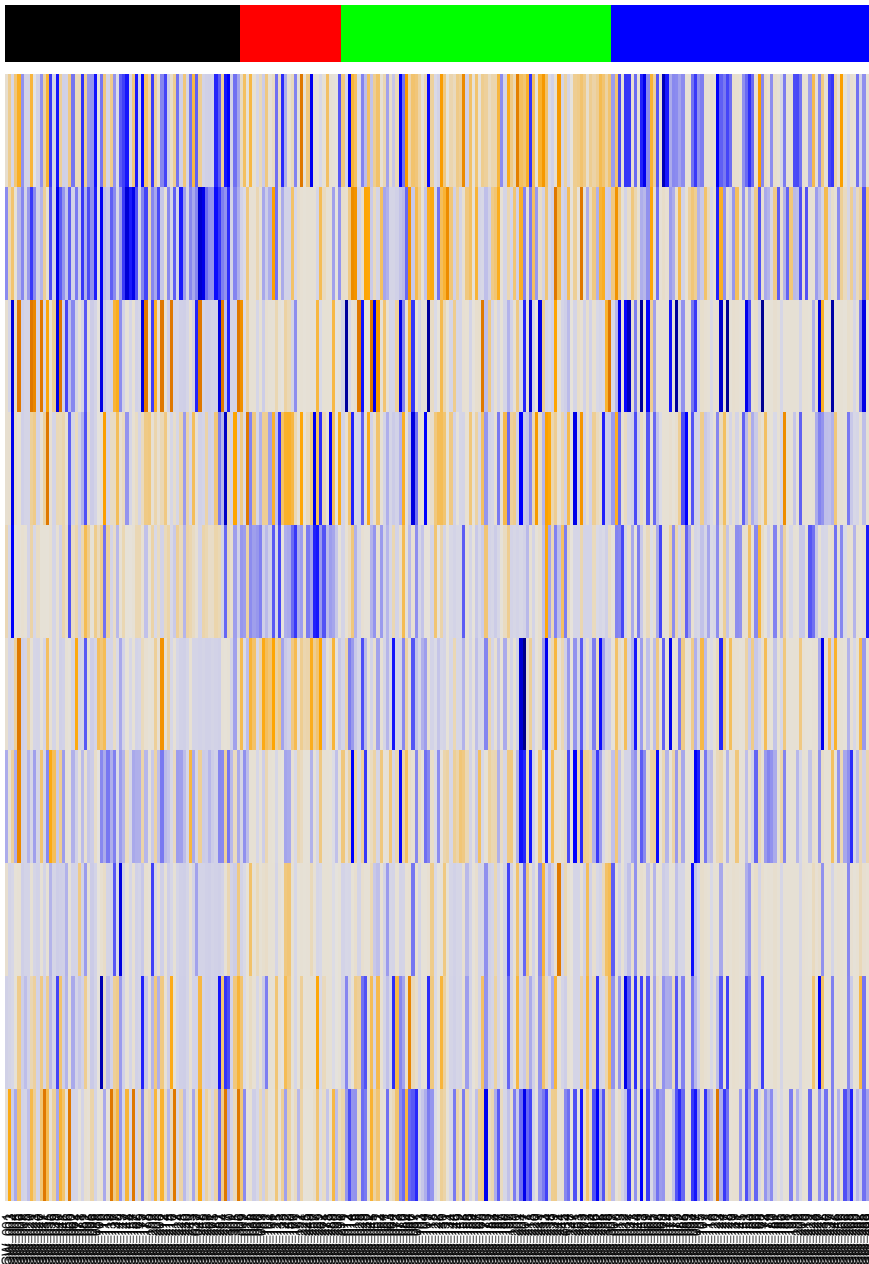


K BENTINK_myc.1
L GUSTAFSON_PI3K_DN
K GUSTAFSON_PI3K_UP
F BENTINK_src.10
F BENTINK_ras.4
O BENTINK_e2f3.1
L BENTINK_ras.1
R BENTINK_src.2
K BENTINK_ras.6
K BENTINK_e2f3.2



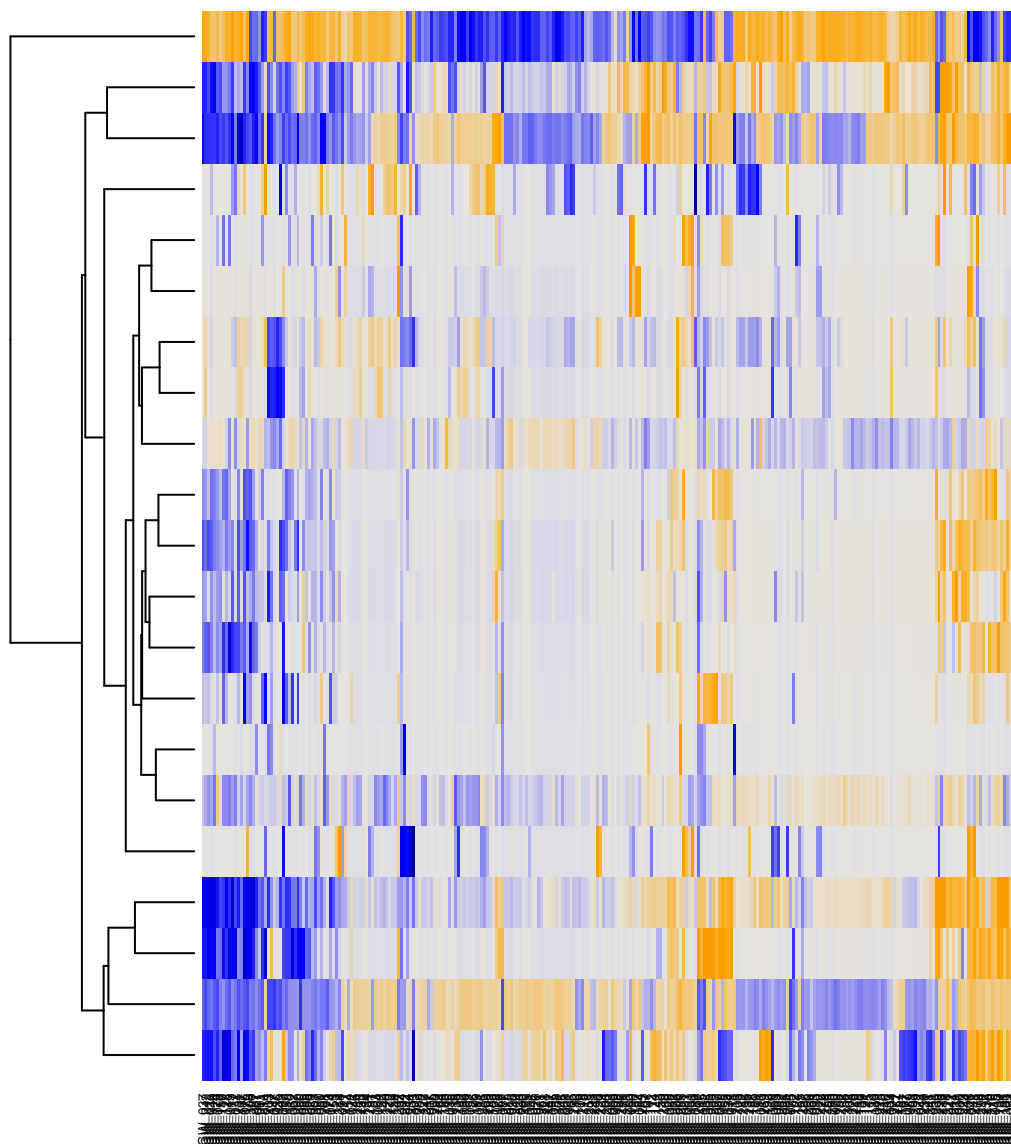
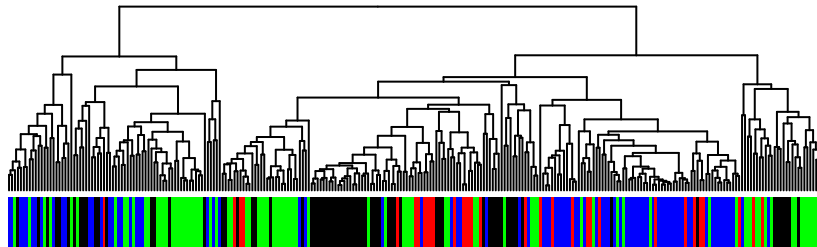
GSZ score

Pathw Act

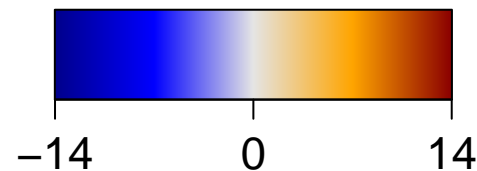


GSZ score

TF

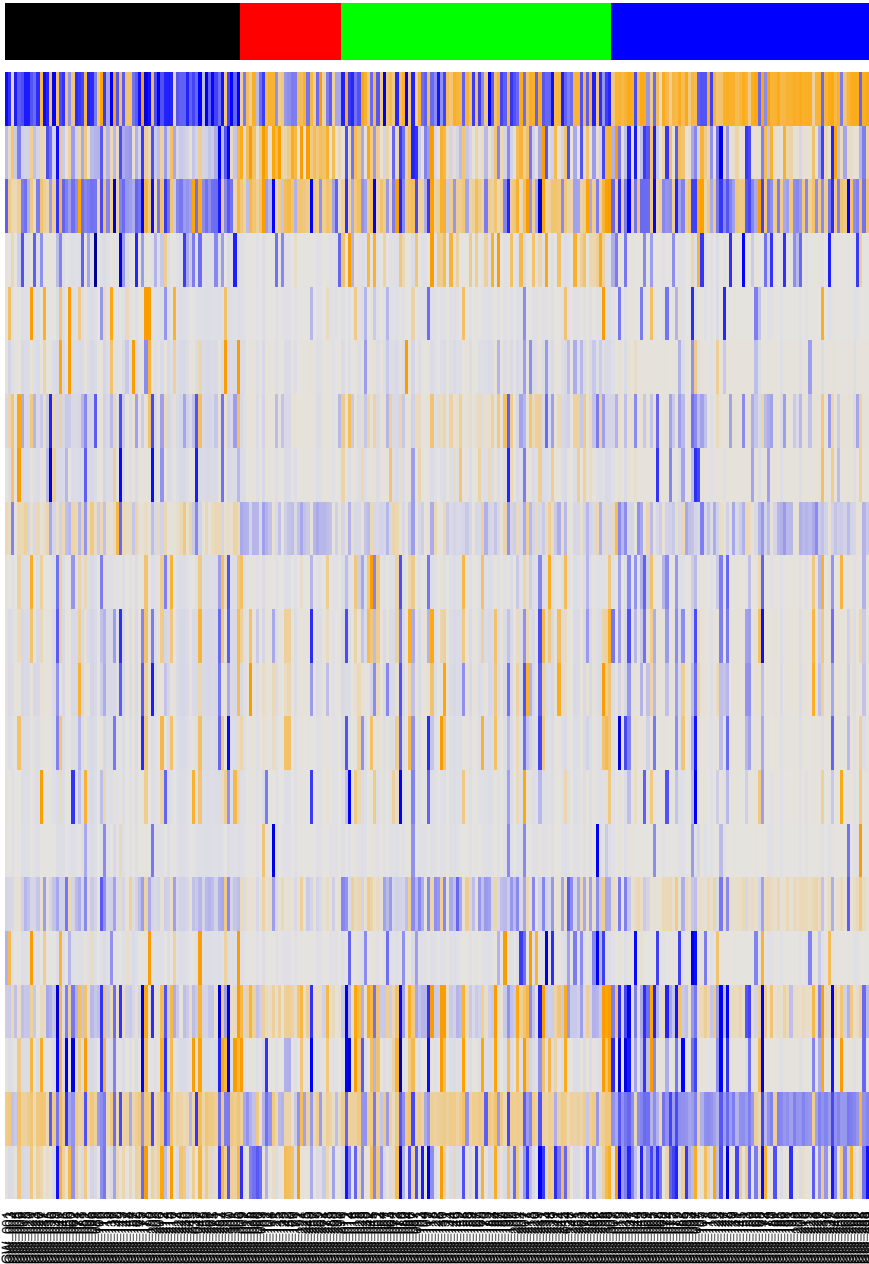


- O HEBENSTREIT_low expression TF
- K MYC_Metabolism UP
- R KIM_MYC targets
- L MYC_ECM cell adhesion DOWN
- B MYC_Chromatin_modification UP
- B MYC_TFs
- B MYC_Targets DOWN
- A MYC_TF and cofactors
- F NOWICK_TF
- M MYC_DNA replication UP
- K MYC_DNA repair UP
- R MYC_RNA processing binding UP
- R MYC_Apoptosis UP
- M MYC_Tumor supressor genes UP
- R MYC_Signal transduction UP
- E MYC_Protein synthesis degradation UP
- B MYC_Cell cycle DOWN
- K MYC_Targets UP
- M MYC_Cell growth and proliferation UP
- K HEBENSTREIT_high expression TF
- K MYC_Cell cycle UP



GSZ score

TF



-14

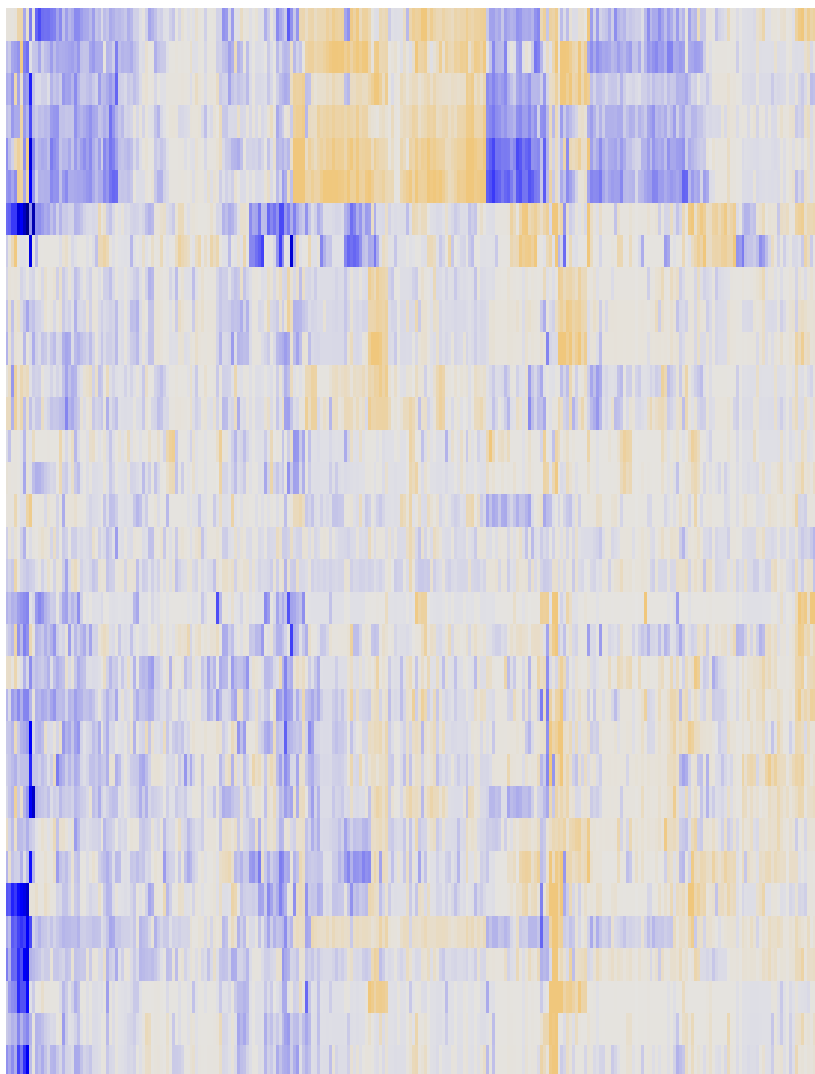
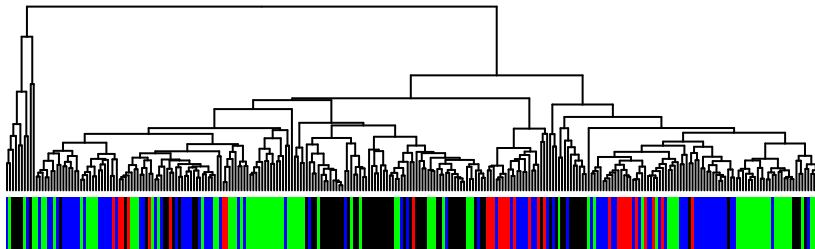
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14

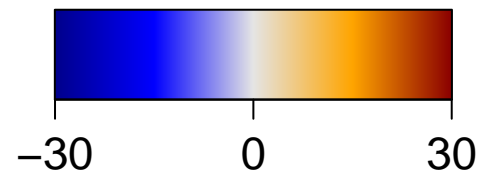
- O HEBENSTREIT_low expression TF
- K MYC_Metabolism UP
- R KIM_MYC targets
- L MYC_ECM cell adhesion DOWN
- B MYC_Chromatin_modification UP
- B MYC_TFs
- B MYC_Targets DOWN
- A MYC_TF and cofactors
- F NOWICK_TF
- M MYC_DNA replication UP
- K MYC_DNA repair UP
- R MYC_RNA processing binding UP
- R MYC_Apoptosis UP
- M MYC_Tumor suppressor genes UP
- R MYC_Signal transduction UP
- E MYC_Protein synthesis degradation UP
- B MYC_Cell cycle DOWN
- K MYC_Targets UP
- M MYC_Cell growth and proliferation UP
- K HEBENSTREIT_high expression TF
- K MYC_Cell cycle UP

GSZ score

TF Tissue

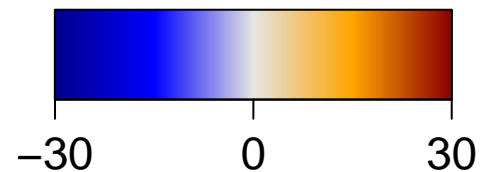
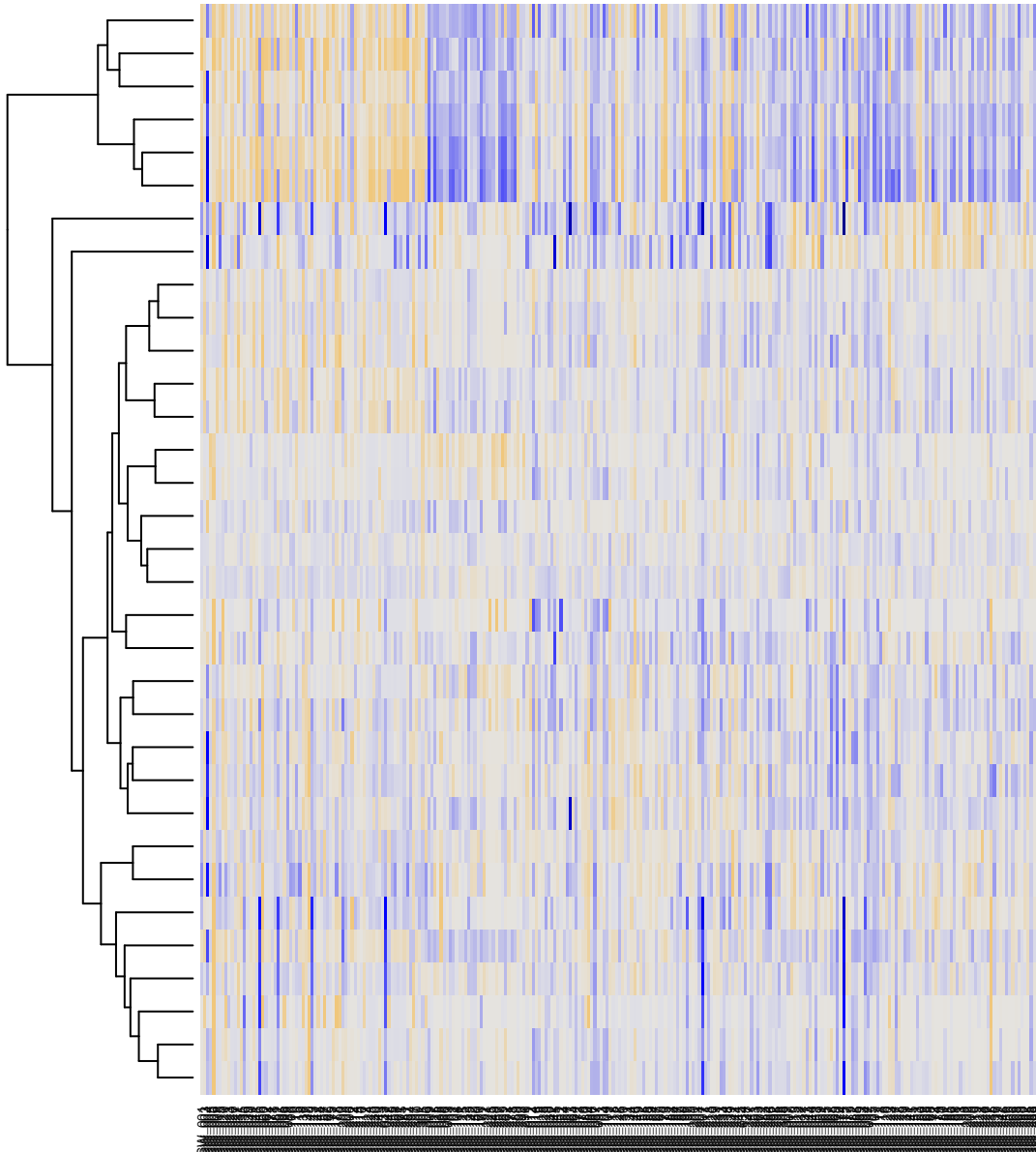


- A VAQUERIZAS_Salivary gland
- G VAQUERIZAS_Bone marrow
- B VAQUERIZAS_Thymus
- F VAQUERIZAS_Whole blood
- F VAQUERIZAS_Tonsil
- F VAQUERIZAS_Lymph node
- O VAQUERIZAS_Trachea
- O VAQUERIZAS_Tongue
- A VAQUERIZAS_Spinal cord
- B VAQUERIZAS_Whole brain
- B VAQUERIZAS_Fetal brain
- H VAQUERIZAS_Fetal liver
- H VAQUERIZAS_Liver
- K VAQUERIZAS_Skeletal.muscle.psoas
- A VAQUERIZAS_Ovary
- F VAQUERIZAS_Heart
- C VAQUERIZAS_Testis
- C VAQUERIZAS_General
- A VAQUERIZAS_Appendix
- I VAQUERIZAS_Pituitary
- J VAQUERIZAS_Fetal thyroid
- A VAQUERIZAS_Prostate
- H VAQUERIZAS_Fetal lung
- I VAQUERIZAS_Uterus
- E VAQUERIZAS_Smooth muscle
- O VAQUERIZAS_Placenta
- O VAQUERIZAS_Skin
- O VAQUERIZAS_Pancreas
- H VAQUERIZAS_Lung
- I VAQUERIZAS_Thyroid
- B VAQUERIZAS_Kidney
- A VAQUERIZAS_Adrenal gland
- I VAQUERIZAS_Adrenal cortex



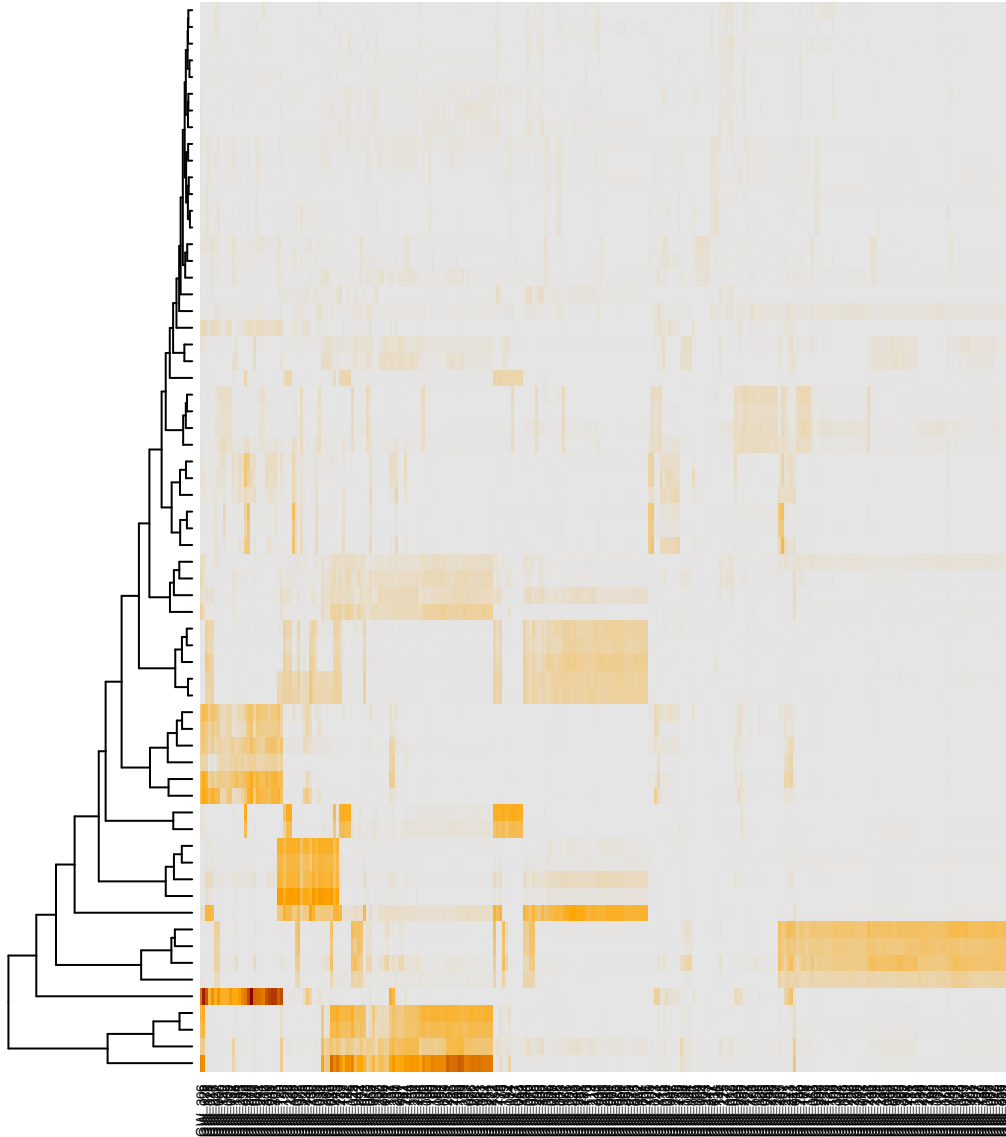
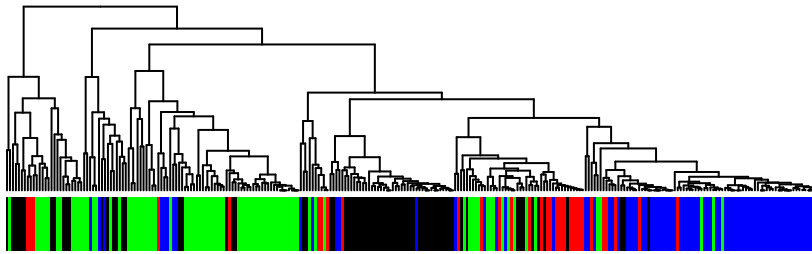
GSZ score

TF Tissue

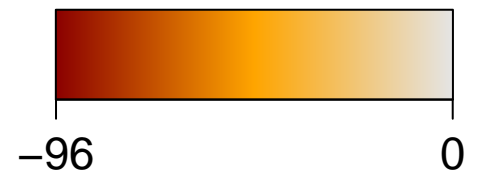


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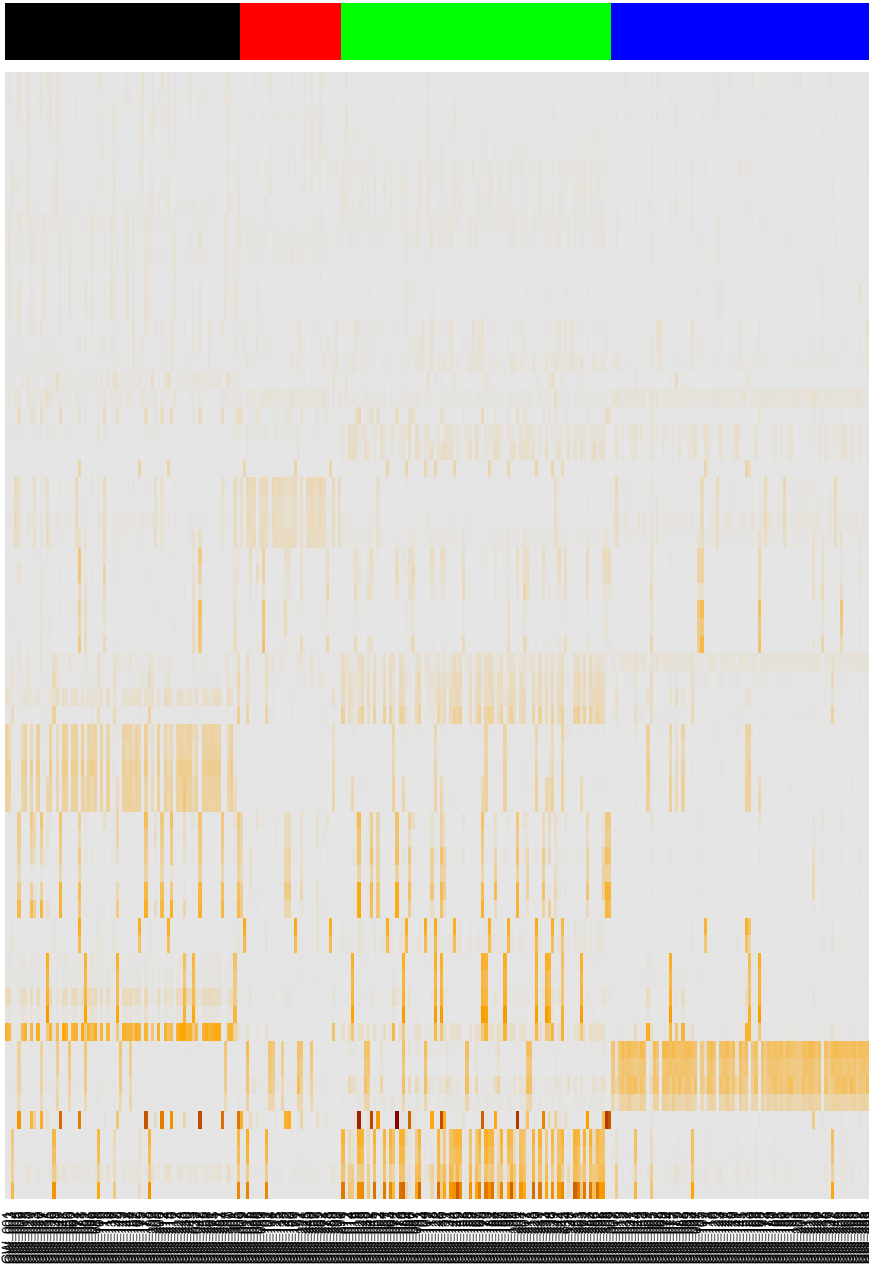


- A drug metabolic process
- A epoxigenase P450 pathway
- I calcium-independent cell-cell adhesion
- A negative regulation of epithelial to mesenchymal transition
- A urogenital system development
- A somitogenesis
- A iron ion transport
- I cellular response to thyroid hormone stimulus
- B positive regulation of transcription from RNA polymerase II promoter
- B negative regulation of neuron differentiation
- B thymus development
- B cilium morphogenesis
- B transcription, DNA-templated
- B regulation of transcription, DNA-dependent
- Q spermatogenesis
- Q biological_process
- L cell differentiation
- I complement activation
- P oxidation-reduction process
- K DNA recombination
- O skin development
- L hemidesmosome assembly
- N cardiac muscle contraction
- K glutathione metabolic process
- K glutathione derivative biosynthetic process
- K xenobiotic metabolic process
- R small molecule metabolic process
- R viral process
- R gene expression
- M rRNA processing
- R respiratory electron transport chain
- R cellular metabolic process
- R translation
- L proteolysis
- L negative regulation of cell proliferation
- L blood coagulation
- L angiogenesis
- G cell surface receptor signaling pathway
- T T cell receptor signaling pathway
- G T cell costimulation
- G antigen processing and presentation
- G regulation of immune response
- K DNA repair
- K DNA strand elongation involved in DNA replication
- K G1/S transition of mitotic cell cycle
- K spindle organization
- K mitosis
- K DNA replication
- N muscle filament sliding
- N muscle contraction
- F defense response to virus
- F response to virus
- F cytokine-mediated signaling pathway
- F type I interferon signaling pathway
- G immune response
- O keratinocyte differentiation
- O keratinization
- O epidermis development
- O peptide cross-linking
- K mitotic cell cycle
- L extracellular matrix disassembly
- L collagen catabolic process
- L cell adhesion
- L extracellular matrix organization

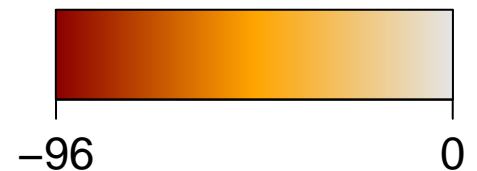


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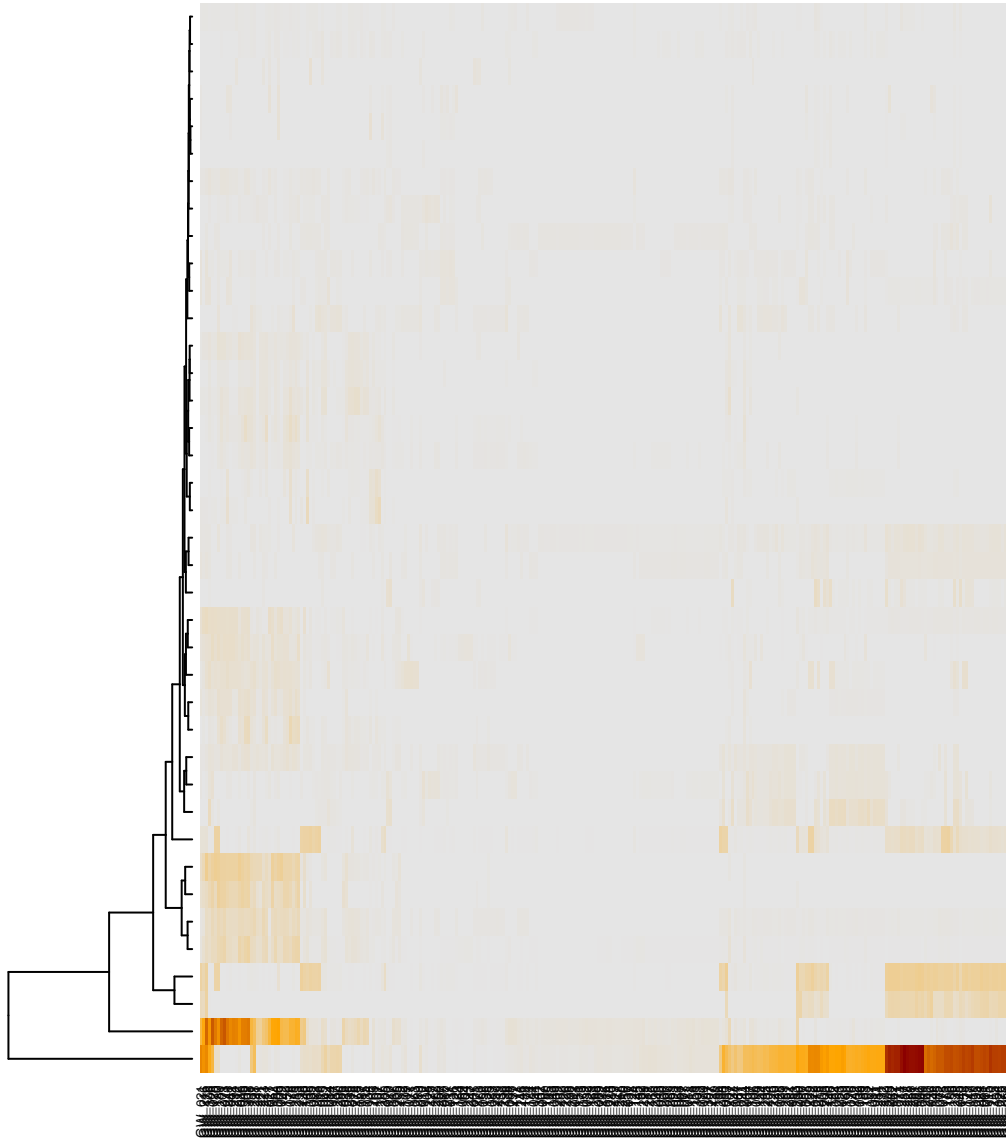
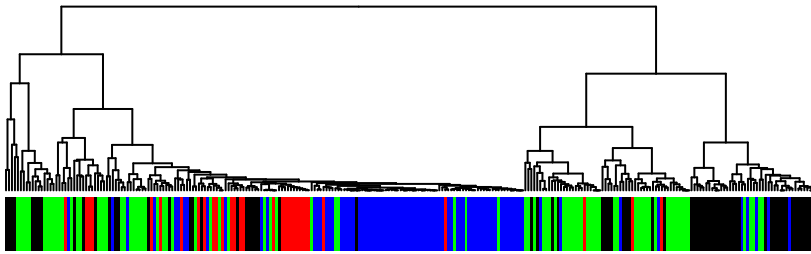


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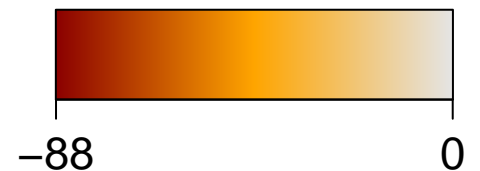


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Cancer

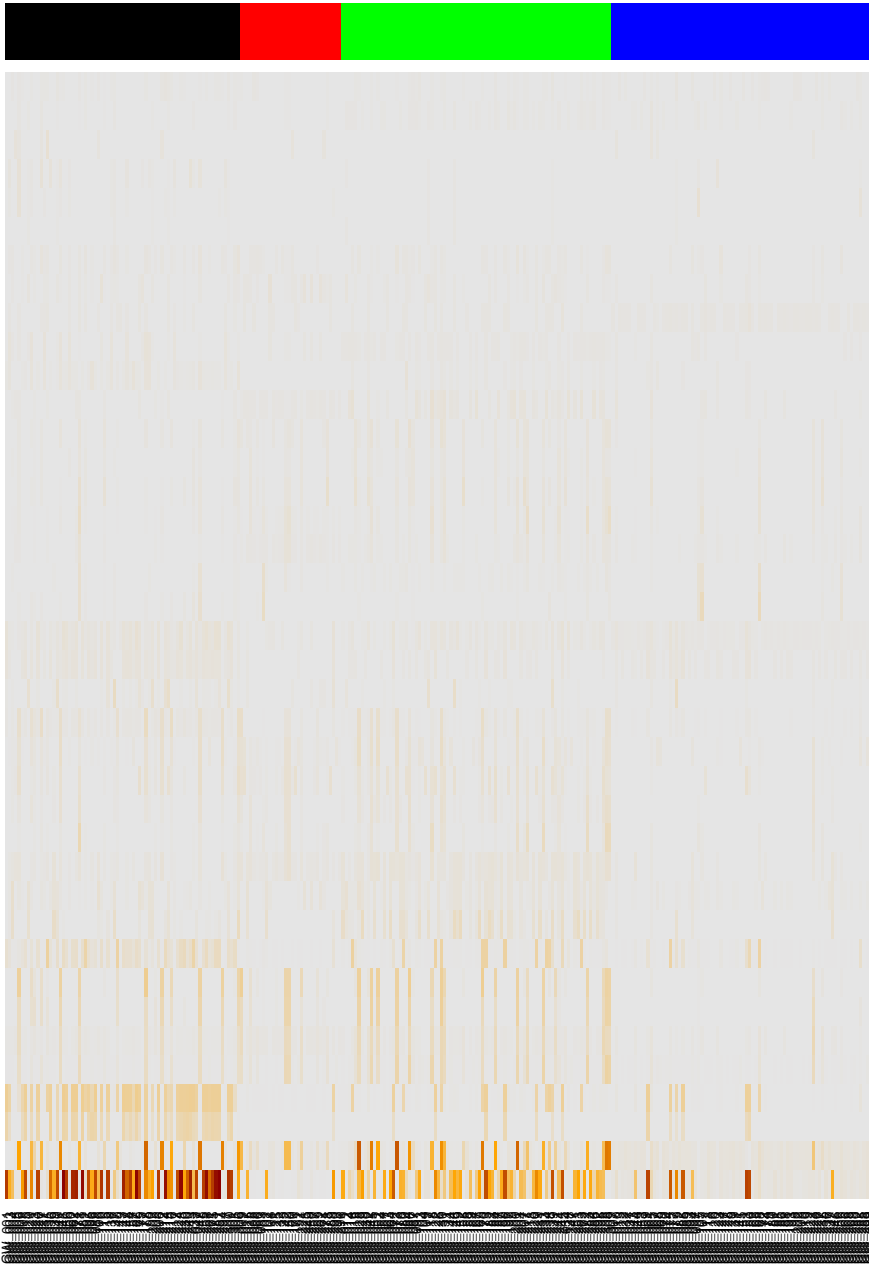


J WANG_ER_UP
I LIU_PROSTATE_CANCER_UP
P GENTLES_modul8
I SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_DN
E GENTLES_modul14
I BEN-PORATH_DN
K LIU_COMMON_CANCER_GENES
A LIU_LIVER_CANCER
N WANG_ER_DN
B LIU_BREAST_CANCER
B GENTLES_modul12
L GENTLES_modul16
M GENTLES_modul2
M GENTLES_modul7
M GENTLES_modul1
R ZHANG_MM up
K GENTLES_modul4
R GENTLES_modul10
R GENTLES_modul5
L GENTLES_modul11
G ZHANG_MGUS up
I GENTLES_modul13
K KUIPER_MM good survival
K KUIPER_MM poor survival
K BEN-PORATH_UP
K GENTLES_modul3
K GENTLES_modul6
K RHODES_CANCER_META_SIGNATURE
A LIU_PROSTATE_CANCER_DN
I GENTLES_modul17
F SPANG_LPS-index2
K SOTIRIOU_BREAST_CANCER_GRADE_1_VS_3_UP
K WOLFER_overlap genes
K RHODES_UNDIFFERENTIATED_CANCER
K SHAUGHNESSY_MM high risk
G SPANG_BCL6-index2
G GENTLES_modul18
K Lembcke_Normal vs Adenoma
G Lembcke_Coloniac Inflammation

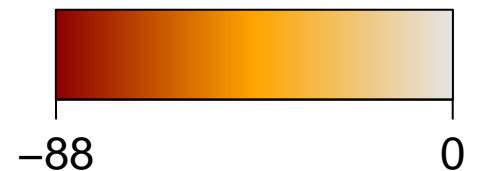


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Cancer

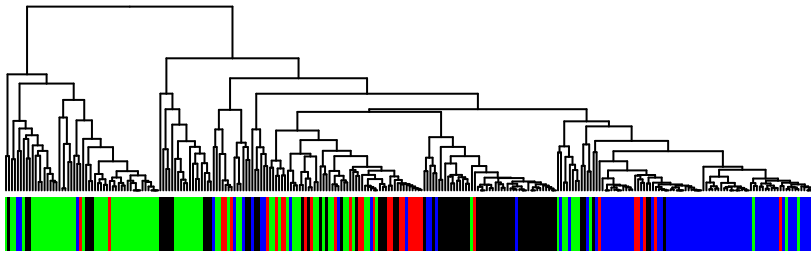


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A LIU_LIVER_CANCER
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B GENTLES_modul12
L GENTLES_modul16
M GENTLES_modul2
M GENTLES_modul7
M GENTLES_modul1
R ZHANG_MM up
K GENTLES_modul4
R GENTLES_modul10
R GENTLES_modul5
L GENTLES_modul11
G ZHANG_MGUS up
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K SHAUGHNESSY_MM high risk
G SPANG_BCL6-index2
G GENTLES_modul18
K Lembcke_Normal vs Adenoma
G Lembcke_Colonic Inflammation

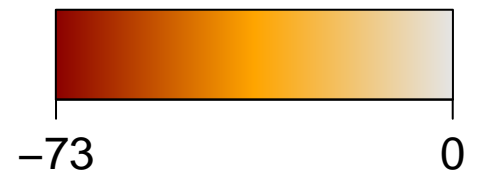


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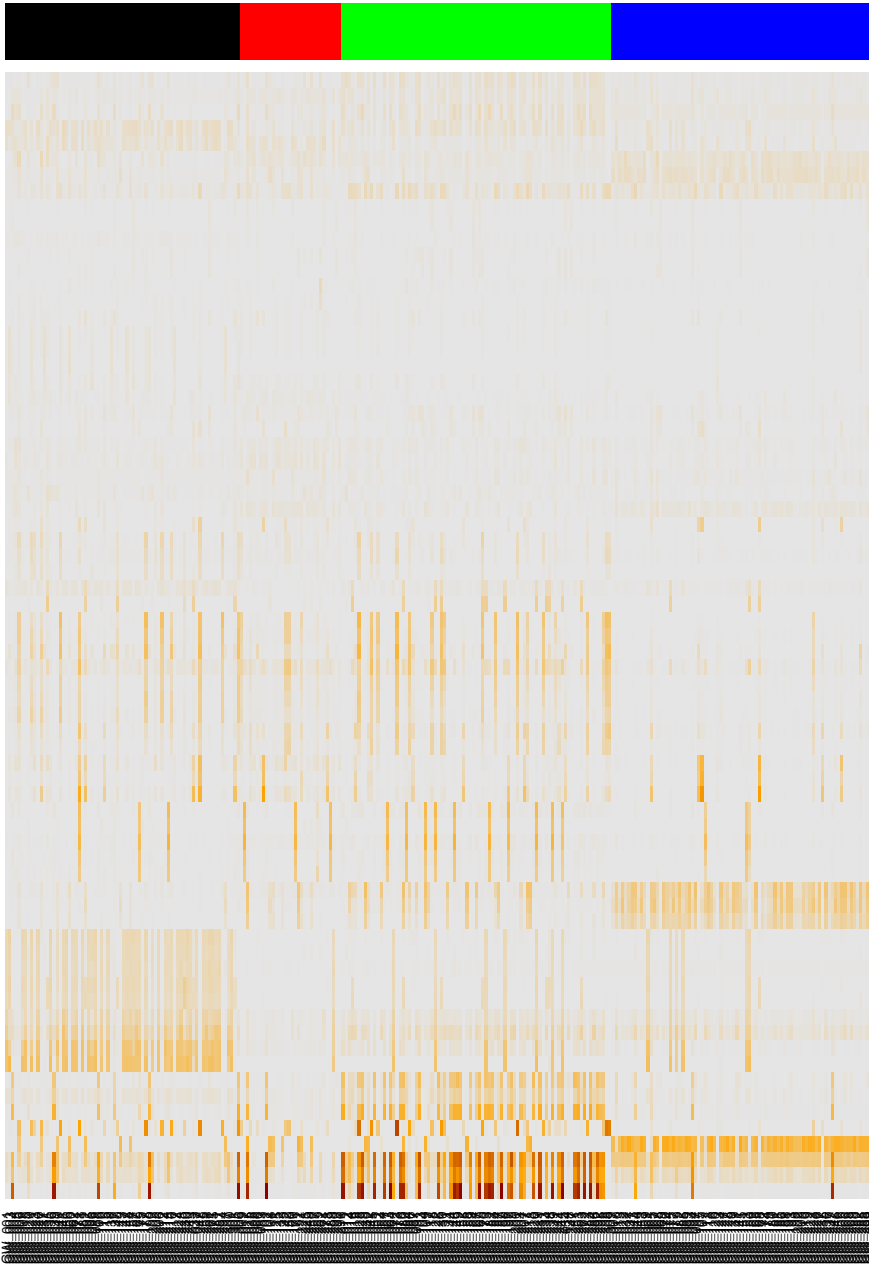


- A secretory granule
- L endoplasmic reticulum
- L Golgi lumen
- L membrane
- P integral to membrane
- O apical plasma membrane
- O anchored to membrane
- K cytoplasm
- P presynaptic membrane
- A photoreceptor disc membrane
- P receptor complex
- Q axonemal dynein complex
- Q XY body
- B cilium
- A axoneme
- R oligosaccharyltransferase complex
- B SWI/SNF complex
- B npBAF complex
- B nBAF complex
- B PRC1 complex
- D peroxisome
- Q cellular_component
- D mitochondrial respiratory chain
- K mitochondrial outer membrane
- K mitochondrial envelope
- P endosome
- A tight junction
- O lateral plasma membrane
- R mitochondrial respiratory chain complex I
- K chromosome
- K chromatin
- K lateral element
- F phagocytic vesicle membrane
- F MHC class I protein complex
- K chromosome, centromeric region
- K condensed chromosome kinetochore
- K nucleus
- K cytosol
- K kinetochore
- K spindle pole
- K centrosome
- K nucleolus
- K nuclear pore
- R mitochondrial inner membrane
- R ribosome
- R mitochondrion
- N myofibril
- N myosin filament
- N Z disc
- N sarcomere
- N I band
- O intermediate filament
- O desmosome
- O keratin filament
- G clathrin-coated endocytic vesicle membrane
- G transport vesicle membrane
- G trans-Golgi network membrane
- G integral to luminal side of endoplasmic reticulum membrane
- F ER to Golgi transport vesicle membrane
- G integral to plasma membrane
- G plasma membrane
- G external side of plasma membrane
- G MHC class II protein complex
- L basement membrane
- L cell surface
- L proteinaceous extracellular matrix
- K nucleoplasm
- O cornified envelope
- L extracellular region
- L extracellular space
- L extracellular matrix

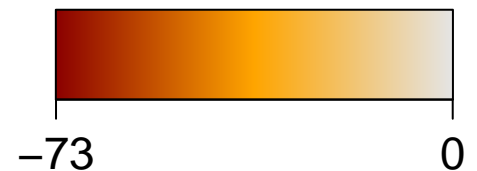


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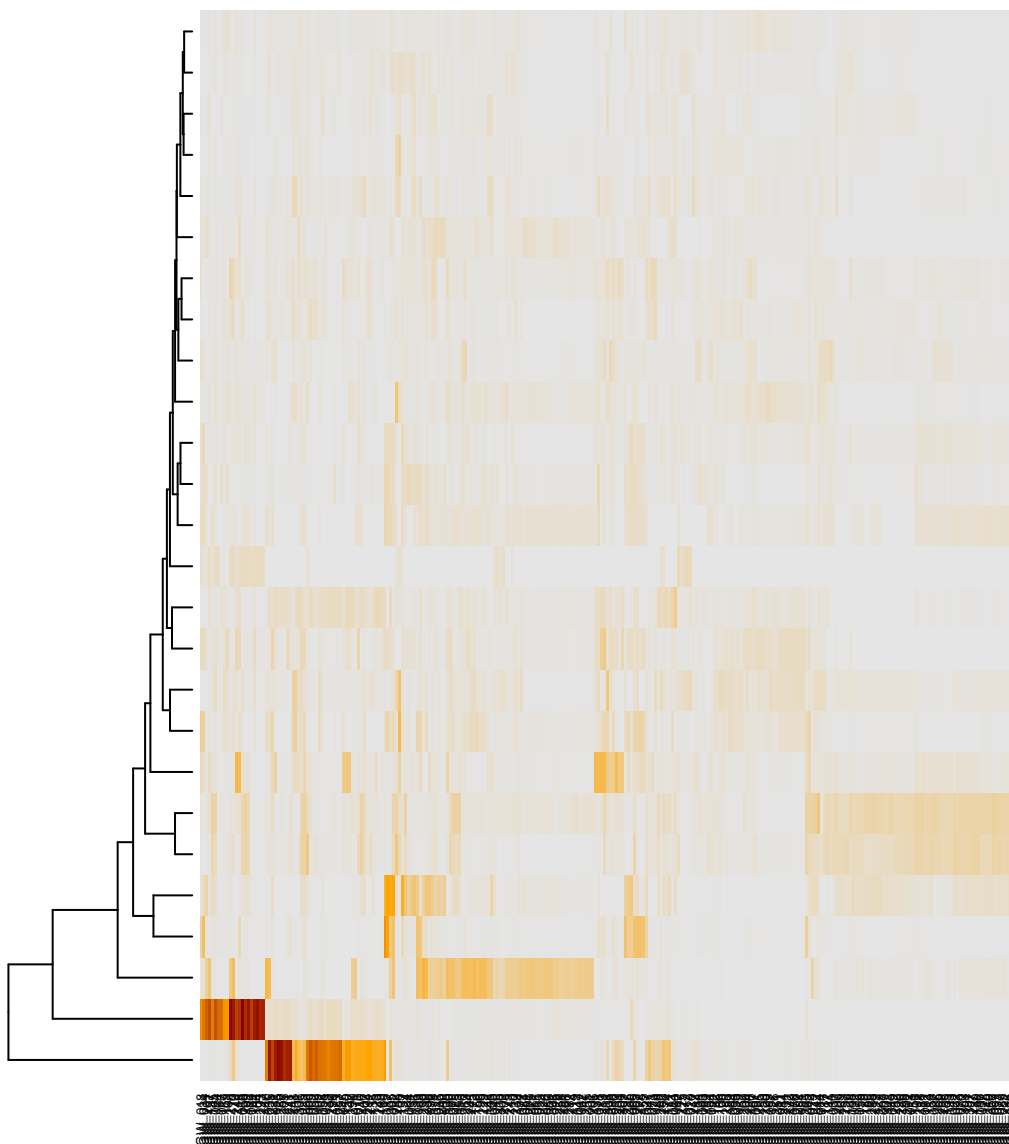
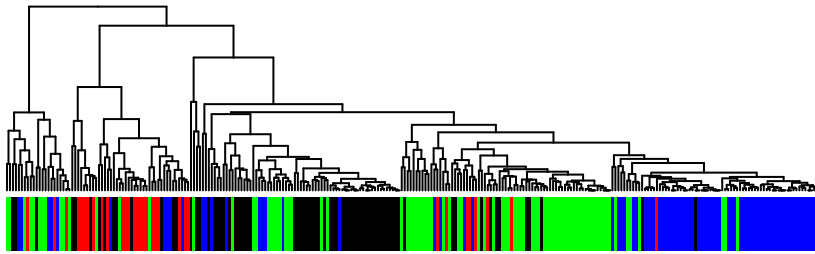


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P receptor complex
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L extracellular space
L extracellular matrix

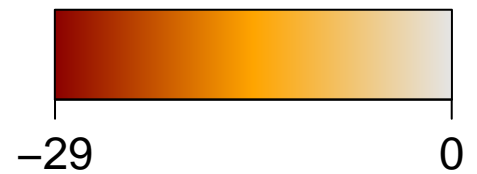


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Chr

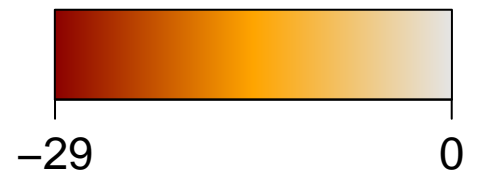


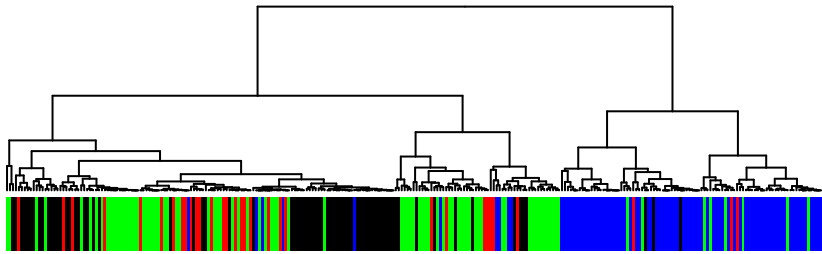
- J Chr 9
- E Chr 21
- B Chr 10
- R Chr 13
- R Chr 6
- G Chr 22
- K Chr 12
- K Chr 15
- I Chr 14
- L Chr 5
- C Chr 20
- J Chr 17
- C Chr HSCHR6_MHC_DBB
- A Chr Y
- K Chr 2
- L Chr 7
- R Chr 4
- R Chr 11
- K Chr 8
- O Chr 1
- O Chr 18
- C Chr 19
- M Chr 16
- F Chr HSCHR6_MHC_QBL
- Q Chr X
- K Chr 3



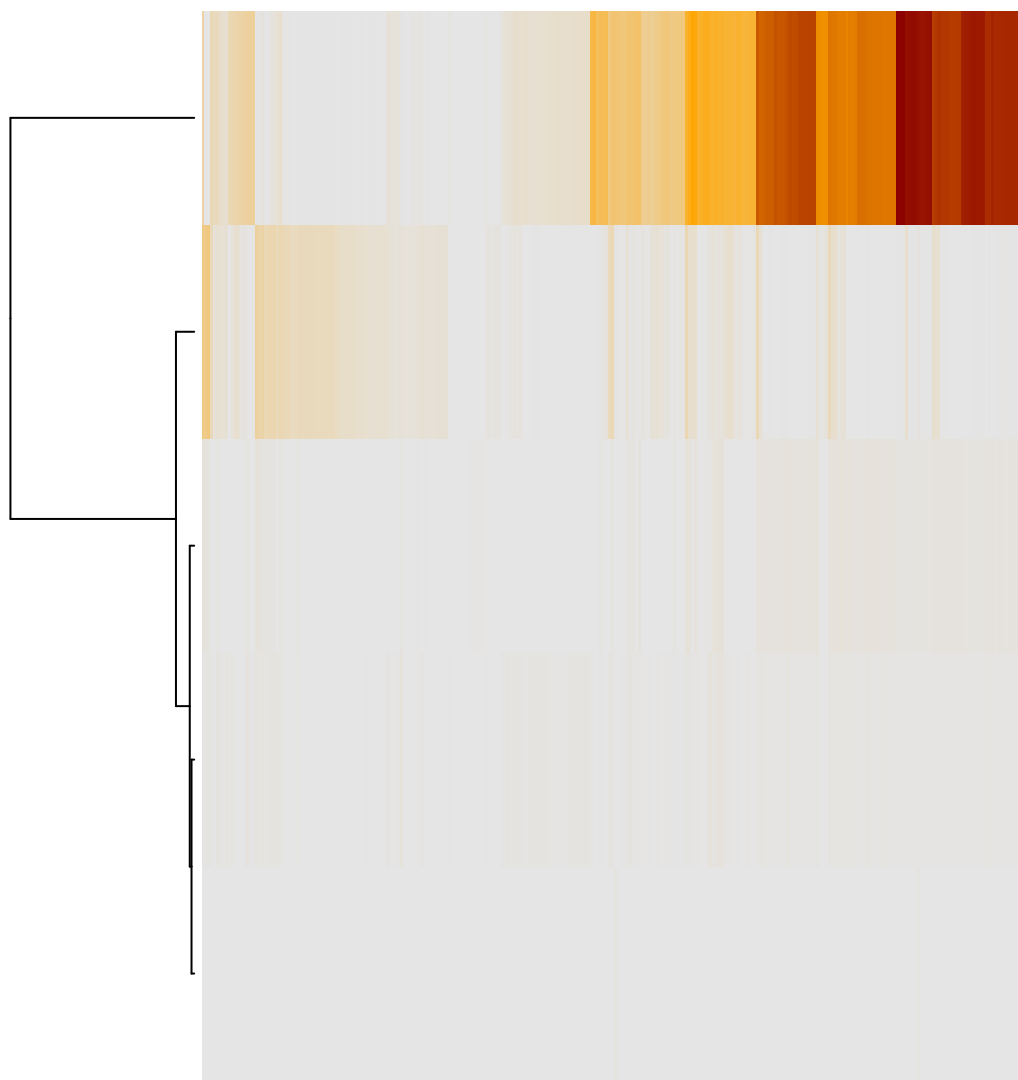
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Chr

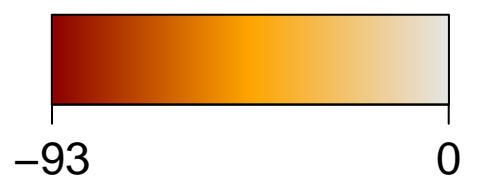




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Disease

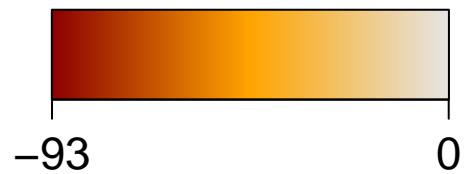
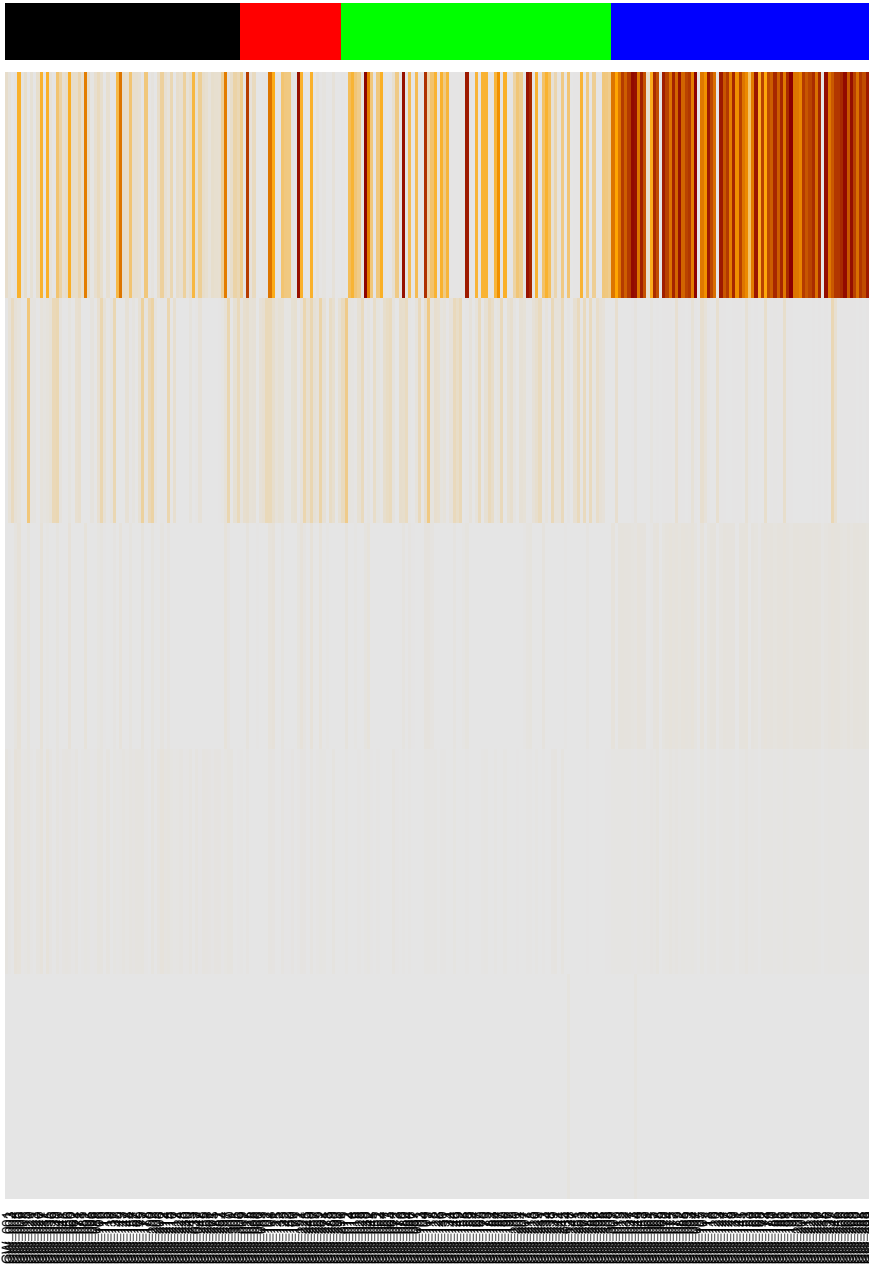


O GUDJ_psoriasis up
A GUDJ_psoriasis down
A BCHETNIA_EBM up
O BCHETNIA_EBM-DM up
A BCHETNIA_EBM down



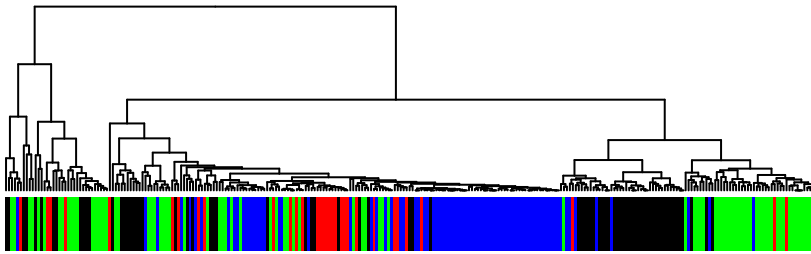
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Disease

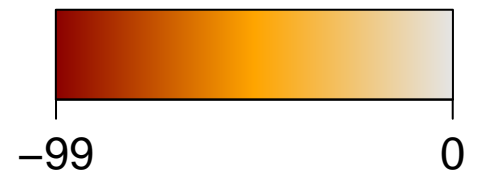


log(p.value)

Glio



- J mature astrocytes
- L in vivo astrocytes vs. cultured astroglia
- O VERHAAK_Brain
- K Martinez_Glio_hypermeth
- A Christensen_hypermethylated_in_primary_glioblastoma
- I OL vs. MOG- OL
- A willscher_GBM_LTSwt_proteomics-G_UP
- L KIM prognostic signature LTS vs. STS
- L KIM deleted & downregulated in LTS
- L Martinez_Glio_hypometh
- L KIM_epithelial-mesenchymal-transition related genes_decreased expression
- L VERHAAK_CL subtype
- L laffaire_hypermeth_LGG_vs_control
- L Christensen_hypermethylated_in_secondary_glioblastoma
- L Christensen_hypermethylated_in_grade3_astrocytoma
- P Noushmehr_Pron_GCIMP_hypermeth_DN
- L Christensen_hypomethylated_in_ependymoma
- L OPC
- Q willscher_GBM_Verhaak-MES_expression_M_down
- Q willscher_GBM_Verhaak-CL_expression_M_down
- Q willscher_GBM_Verhaak-PNmut_expression_M_up
- J willscher_GBM_Verhaak-MES_expression_H_up
- J willscher_GBM_Verhaak-CL_expression_H_down
- J willscher_GBM_Verhaak-PNwt_expression_H_up
- K willscher_GBM_proteomics_wtOnly_SpotH
- O Down_b
- L Vishal_subnetwork signature of survival in GBM
- L Barbus_GBM_STS_vs_LTS
- B WIRTH_PN subtype
- M GIEZELT_GBM_STS_up_VS_LTS
- R VERHAAK_NL subtype
- I GIEZELT_GBM_STS_down_VS_LTS
- E GIEZELT_GBM_STSwt_up_VS_LTSwt
- M GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
- I OL vs. OPC
- A astrocytes_glio
- E willscher_GBM_Verhaak-MES_expression_D_down
- E willscher_GBM_Verhaak-CL_expression_D_up
- E willscher_GBM_Verhaak-PNwt_expression_D_up
- R willscher_GBM_proteomics_wtOnly_Differencelist
- R willscher_GBM_proteomics_wtOnly_SpotG
- R Stuehler_Proteins_up_in_STS
- F Up
- C willscher_GBM_Verhaak-PNwt_expression_J_up
- L Christensen_hypermethylated_in_grade3_oligoastrocytoma
- L Christensen_hypermethylated_in_grade2_oligoastrocytoma
- L Christensen_hypermethylated_in_grade2_oligodendroglioma
- L Christensen_hypomethylated_in_primary_glioblastoma
- L Christensen_hypomethylated_in_secondary_glioblastoma
- A willscher_GBM_Verhaak-PNmut_expression_G_down
- G Donson-chemokines/cytokines-associated with LTS in HGA
- G Donson-cytotoxic effectors-associated with LTS in HGA
- G Donson-innate immunity-associated with LTS in HGA
- F Donson-immune cell intra signaling-associated with LTS in HGA
- L GIEZELT_GBM_WT_up_VS_mut
- L Colman_survival_associated
- L cultured astroglia vs. in vivo astrocytes
- K developing astrocytes
- L willscher_GBM_Verhaak-MES_expression_B_up
- L willscher_GBM_Verhaak-CL_expression_B_up
- L willscher_GBM_Verhaak-PNwt_expression_B_down
- K willscher_GBM_Verhaak-PNmut_expression_C_down
- K willscher_GBM_Verhaak-CL_expression_C_up

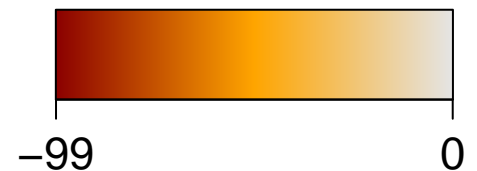


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Glio

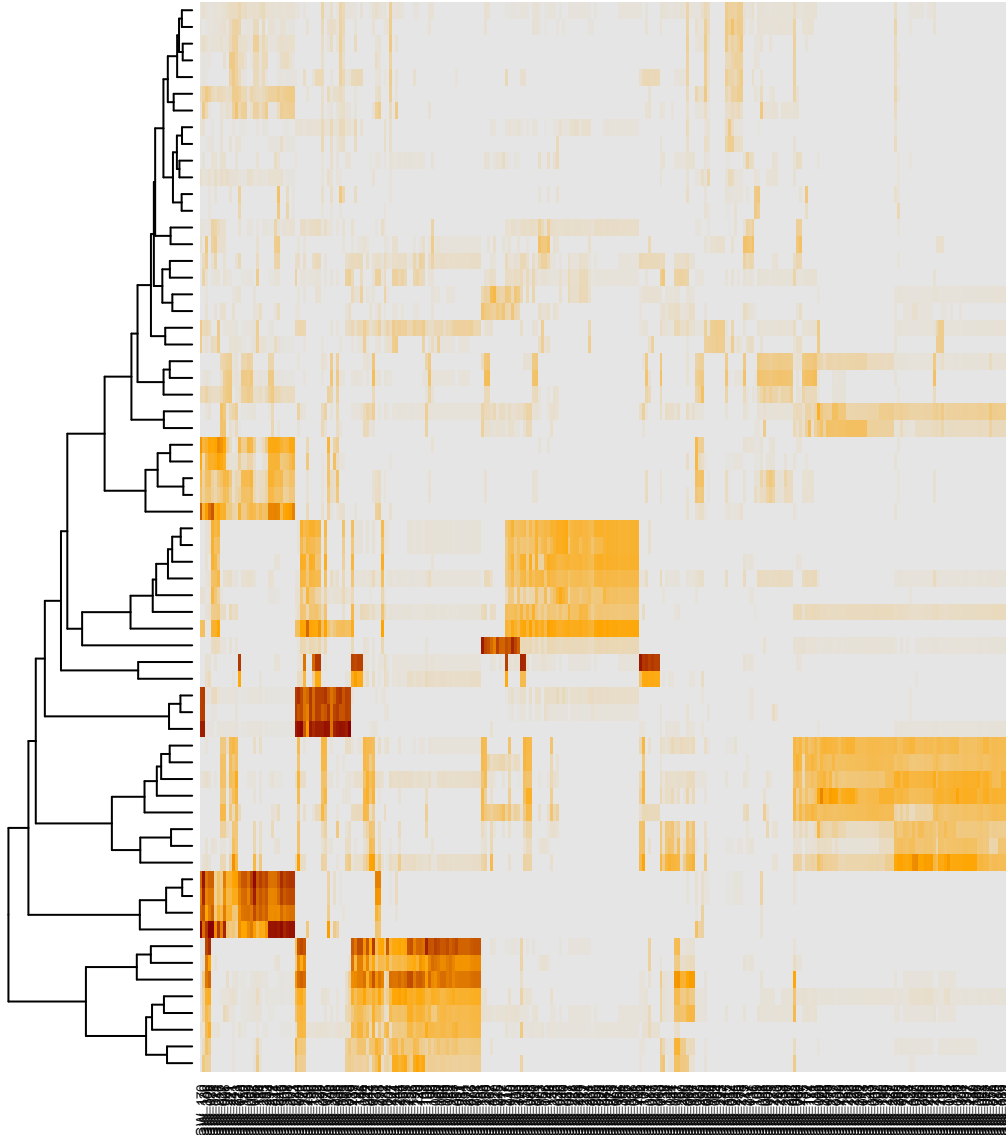
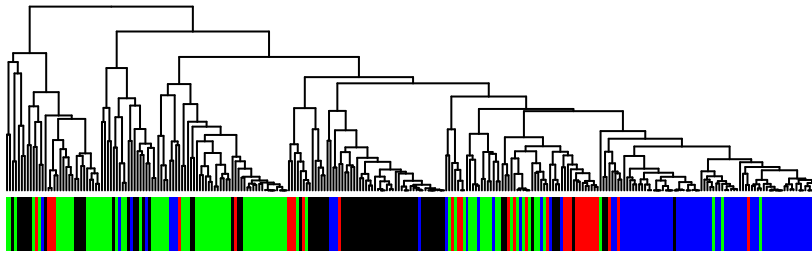


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E GIEZELT_GBM_STSwt_up_VS_LTSwt
M GIEZELT_GBM_MGMTmethyl_up_VS_nonmethyl
I OL vs. OPC
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E willscher_GBM_Verhaak-MES_expression_D_down
E willscher_GBM_Verhaak-CL_expression_D_up
E willscher_GBM_Verhaak-PNwt_expression_D_up
R willscher_GBM_proteomics_wtOnly_Differencelist
R willscher_GBM_proteomics_wtOnly_SpotG
R Stuehler_Proteins_up_in_STS
F Up
C willscher_GBM_Verhaak-PNwt_expression_J_up
L Christensen_hypermethylated_in_grade3_oligoastrocytoma
L Christensen_hypermethylated_in_grade2_oligoastrocytoma
L Christensen_hypermethylated_in_grade2_oligodendroglioma
L Christensen_hypomethylated_in_primary_glioblastoma
L Christensen_hypomethylated_in_secondary_glioblastoma
A willscher_GBM_Verhaak-PNmut_expression_G_down
G Donson-chemokines/cytokines-associated with LTS in HGA
G Donson-cytotoxic effectors-associated with LTS in HGA
G Donson-innate immunity-associated with LTS in HGA
F Donson-immune cell intra signaling-associated with LTS in HGA
L GIEZELT_GBM_WT_up_VS_mut
L Colman_survival_associated
L cultured astroglia vs. in vivo astrocytes
K developing astrocytes
L willscher_GBM_Verhaak-MES_expression_B_up
L willscher_GBM_Verhaak-CL_expression_B_up
L willscher_GBM_Verhaak-PNwt_expression_B_down
K willscher_GBM_Verhaak-PNmut_expression_C_down
K willscher_GBM_Verhaak-CL_expression_C_up

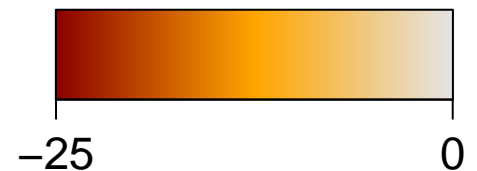


log(p.value)

GSEA C2



M KORKOLA_EMBRYONAL_CARCINOMA_UP
M LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
M REACTOME_HIV_LIFE_CYCLE
M XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
M REACTOME_GLYCOLYSIS
K WONG_EMBRYONIC_STEM_CELL_CORE
K SCHUHMACHER_MYC_TARGETS_UP
I REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL_SURVIVAL
C CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
P MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
E REACTOME_G2_M_TRANSITION
R REACTOME_FORMATION_OF_ATP_BY_CHEMOSMOTIC_COUPLING
R SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN
B GOLUB_ALL_VS_AML_UP
B RICKMAN_HEAD_AND_NECK_CANCER_A
L DAVICIONI_PAX_FOXP1_SIGNATURE_IN_ARMS_DN
L ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
I SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
A POOLA_INVASIVE_BREAST_CANCER_DN
L MAHADEVAN_IMATINIB_RESISTANCE_UP
Q MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
K KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P450
K KEGG_Glutathione_Metabolism
K VANTVEER_BREAST_CANCER_METASTASIS_DN
O LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
O KEGG_LINOLEIC_ACID_METABOLISM
K KALMA_E2F1_TARGETS
K KEGG_DNA_REPLICATION
K PUJANA_BRCA_CENTERED_NETWORK
K PUJANA_XPRSS_INT_NETWORK
K CHANG_CYCLING_GENES
G BIOCARTE_TCYTOTOXIC_PATHWAY
G BIOCARTE_THELPER_PATHWAY
G SU_THYMUS
G FINAK_BREAST_CANCER_SDPD_SIGNATURE
G BIOCARTE_NO2IL12_PATHWAY
G ZHAN_MULTIPLE_MYELOMA_DN
G FARMER_BREAST_CANCER_CLUSTER_1
A RICKMAN_HEAD_AND_NECK_CANCER_D
N RICKMAN_HEAD_AND_NECK_CANCER_F
N REACTOME_STRIATED_MUSCLE_CONTRACTION
F ZHANG_INTERFERON_RESPONSE
F EINAV_INTERFERON_SIGNATURE_IN_CANCER
F MOSERLE_IFNA_RESPONSE
O HINATA_NFKB_TARGETS_KERATINOCYTE_DN
O SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN
O ONDER_CDH1_TARGETS_3_DN
O WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCER_DN
O CROMER_TUMORIGENESIS_DN
O AIGNER_ZEB1_TARGETS
O RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATELY_DIFFERENTIATED
O HUPER_BREAST_BASAL_VS_LUMINAL_UP
K FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
K FINETTI_BREAST_CANCER_KINOME_RED
K FARMER_BREAST_CANCER_CLUSTER_2
K EGUCHI_CELL_CYCLE_RB1_TARGETS
L FARMER_BREAST_CANCER_CLUSTER_5
L ONDER_CDH1_TARGETS_2_UP
L CROMER_TUMORIGENESIS_UP
L ONDER_CDH1_SIGNALING_VIA_CTNNB1
L LEE_LIVER_CANCER_HEPATOBLAST
L TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_NORM
L BEGUM_TARGETS_OF_PAX3_FOXP1_FUSION_DN
L MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH

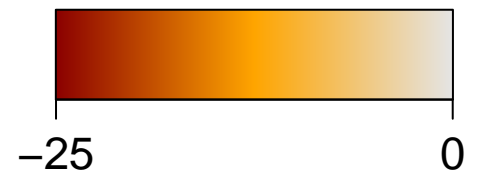


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GSEA C2

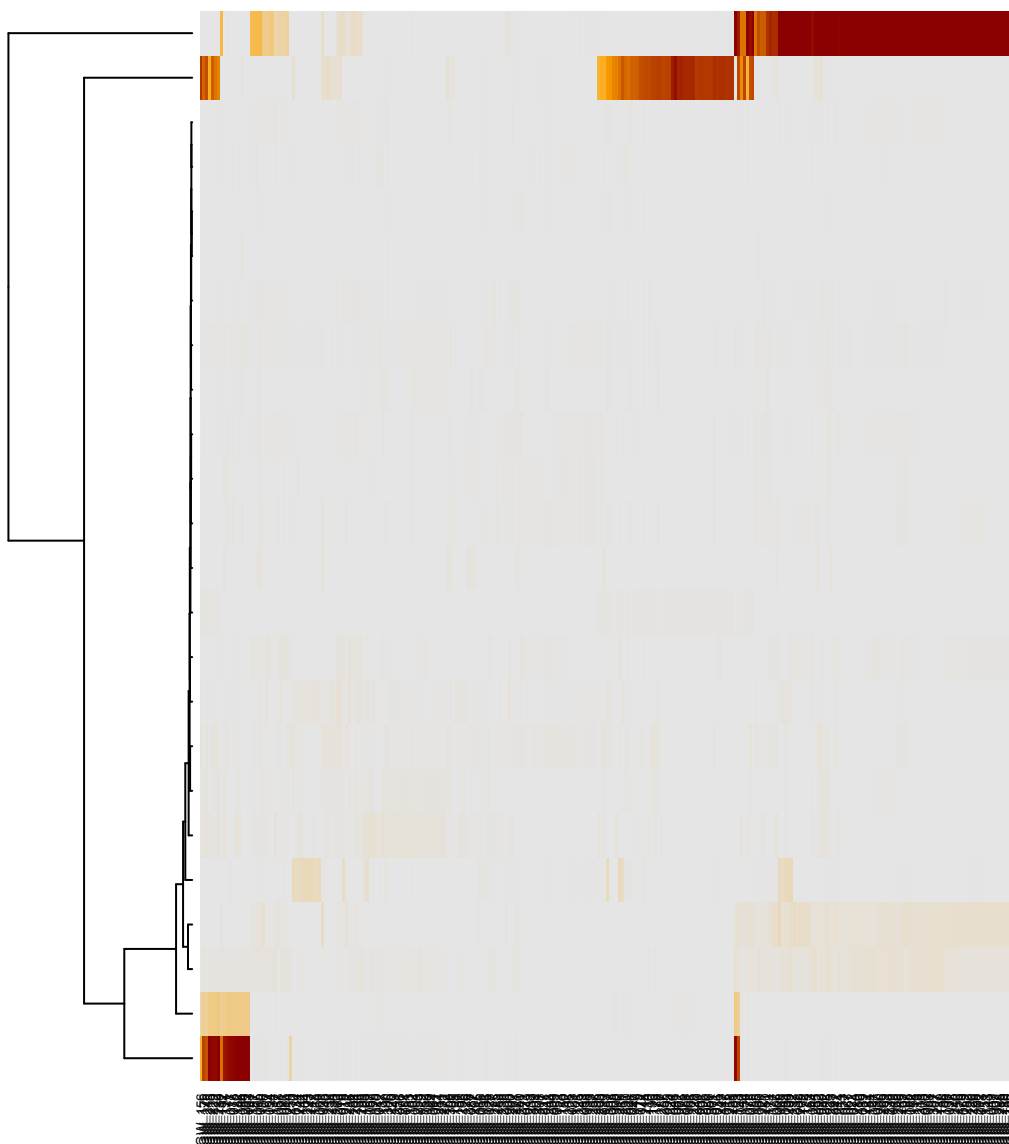
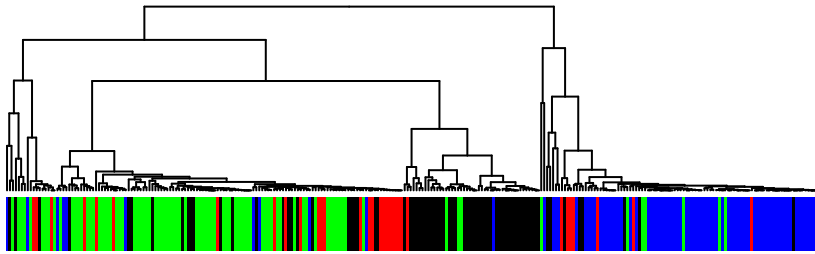


M KORKOLA_EMBRYONAL_CARCINOMA_UP
M LOCKWOOD_AMPLIFIED_IN_LUNG_CANCER
M REACTOME_HIV_LIFE_CYCLE
M XU_RESPONSE_TO_TRETINOIN_AND_NSC682994_DN
M REACTOME_GLYCOLYSIS
K WONG_EMBRYONIC_STEM_CELL_CORE
K SCHUHMACHER_MYC_TARGETS_UP
I REACTOME_NEF_MEDIATES_DOWN_MODULATION_OF_CELL
C CREIGHTON_AKT1_SIGNALING_VIA_MTOR_UP
P MEINHOLD_OVARIAN_CANCER_LOW_GRADE_UP
E REACTOME_G2_M_TRANSITION
R REACTOME_FORMATION_OF_ATP_BY_CHEMIOSMOTIC_COU
R SAKAI_TUMOR_INFILTRATING_MONOCYTES_DN
B GOLUB_ALL_VS_AML_UP
B RICKMAN_HEAD_AND_NECK_CANCER_A
L DAVICIONI_PAX_FOXO1_SIGNATURE_IN_ARMS_DN
L ABRAHAM_ALPC_VS_MULTIPLE_MYELOMA_UP
I SMID_BREAST_CANCER_RELAPSE_IN_LUNG_DN
A POOLA_INVASIVE_BREAST_CANCER_DN
L MAHADEVAN_IMATINIB_RESISTANCE_UP
Q MATTIOLI_MULTIPLE_MYELOMA_SUBGROUPS
K KEGG_METABOLISM_OF_XENOBIOTICS_BY_CYTOCHROME_P
K KEGG_GLUTATHIONE_METABOLISM
K VANTVEER_BREAST_CANCER_METASTASIS_DN
O LIN_SILENCED_BY_TUMOR_MICROENVIRONMENT
O KEGG_LINOLEIC_ACID_METABOLISM
K KALMA_E2F1_TARGETS
K KEGG_DNA_REPLICATION
K PUJANA_BRCA_CENTERED_NETWORK
K PUJANA_XPRSS_INT_NETWORK
K CHANG_CYCLING_GENES
G BIOCARTA_TCYTOTOXIC_PATHWAY
G BIOCARTA_THELPER_PATHWAY
G SU_THYMUS
G FINAK_BREAST_CANCER_SDPP_SIGNATURE
G BIOCARTA_NO2IL12_PATHWAY
G ZHAN_MULTIPLE_MYELOMA_DN
G FARMER_BREAST_CANCER_CLUSTER_1
A RICKMAN_HEAD_AND_NECK_CANCER_D
N RICKMAN_HEAD_AND_NECK_CANCER_F
N REACTOME_STRIATED_MUSCLE_CONTRACTION
F ZHANG_INTERFERON_RESPONSE
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O HINATA_NFKB_TARGETS_KERATINOCYTE_DN
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O ONDER_CDH1_TARGETS_3_DN
O WANG_BARRETTES_ESOPHAGUS_AND_ESOPHAGUS_CANCE
O CROMER_TUMORIGENESIS_DN
O AIGNER_ZEB1_TARGETS
O RICKMAN_TUMOR_DIFFERENTIATED_WELL_VS_MODERATEL
O HUPER_BREAST_BASAL_VS_LUMINAL_UP
K FINETTI_BREAST_CANCER_BASAL_VS_LUMINAL
K FINETTI_BREAST_CANCER_KINOME_RED
K FARMER_BREAST_CANCER_CLUSTER_2
K EGUCHI_CELL_CYCLE_RB1_TARGETS
L FARMER_BREAST_CANCER_CLUSTER_5
L ONDER_CDH1_TARGETS_2_UP
L CROMER_TUMORIGENESIS_UP
L ONDER_CDH1_SIGNALING_VIA_CTNNB1
L LEE_LIVER_CANCER_HEPATOBLAST
L TURASHVILI_BREAST_LOBULAR_CARCINOMA_VS_DUCTAL_N
L BEGUM_TARGETS_OF_PAX3_FOXO1_FUSION_DN
L MAHADEVAN_GIST_MORPHOLOGICAL_SWITCH

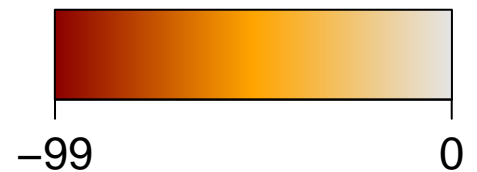


log(p.value)

H.Tiss



- O WIRTH_Mucosa
- G WIRTH_Immune system
- I WIRTH_Pancreas
- I WIRTH_Globus pallidus
- P WIRTH_Homeostasis
- A WIRTH_Pituitary gland
- P WIRTH_Liver
- A WIRTH_Nervous System
- P WIRTH_Thyroid gland
- I WIRTH_Thalamus
- K WIRTH_Telencephalon
- K WIRTH_Cerebellum
- M WIRTH_B-cells
- G WIRTH_Bone marrow
- O WIRTH_Thymus
- L WIRTH_Placenta
- F WIRTH_Lymphocytes
- L WIRTH_Cortex cerebri
- I WIRTH_Sec. lymphoid organs
- Q WIRTH_Testis
- O WIRTH_Tonsil
- O WIRTH_Prim. lymphoid organs
- N WIRTH_Hippocampus
- N WIRTH_Muscle

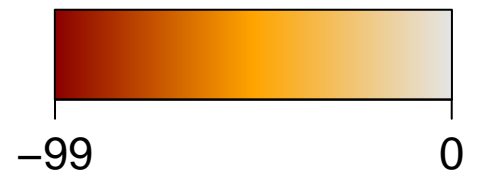


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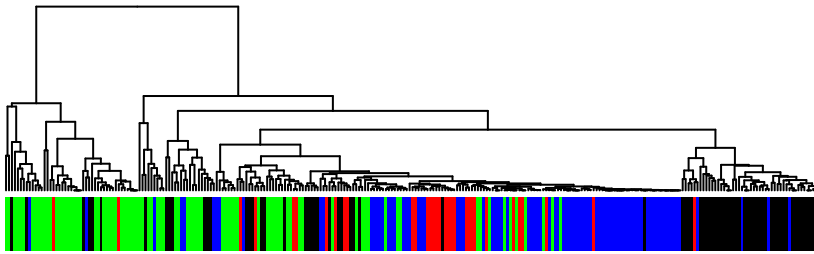


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- Q WIRTH_Testis
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- O WIRTH_Prim. lymphoid organs
- N WIRTH_Hippocampus
- N WIRTH_Muscle

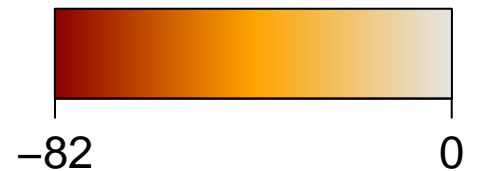


log(p.value)

Lymphoma



- G SPANG_LPS 6hrs DN
- G BENTINK_mBL DOWN
- G WRIGHT_GCB UP
- G SPANG_LPS 6hrs UP
- G SPANG_BCR DN
- G DAVE_NFkB BL DN
- F ROSOLOWSKI_blue DOWN
- R ROSOLOWSKI_red total
- H MASCQUE_ABC UP
- F DAVE_Immune response 2
- B SPANG_IL21 UP
- G DAVE_BL UP
- G MASCQUE_GCB UP
- I DAVE_BL_DN
- D ROSOLOWSKI_red UP
- J DAVE_BL Inter
- B BENTINK_mBL UP
- B MASCQUE_mBL UP
- I WRIGHT_custom GCB-DLBCL UP
- G MASCQUE_mBL DOWN
- G WRIGHT_custom ABC-DLBCL UP
- E SPANG_BAFF 9hrs DN
- O ZHANG_DLBCL mutated
- I SPANG_BAFF 9hrs UP
- L ROSOLOWSKI_green UP
- K ROSOLOWSKI_blue total
- K DAVE_c-myc BL UP
- B SPANG_BCR UP
- L LENZ_Stromal signature 2
- F DAVE_MHCCII BL DN
- G DAVE_Immune response 1
- G WRIGHT_ABC UP
- G SPANG_CD40 6hrs DN
- G SPANG_CD40 6hrs UP
- K DAVE_BL-vs-DLBCL
- L ROSOLOWSKI_green total
- F SPANG_IL21 DN
- L LENZ_Stromal signature 1

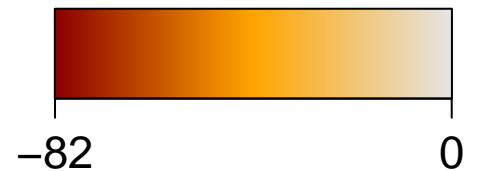


log(p.value)

Lymphoma

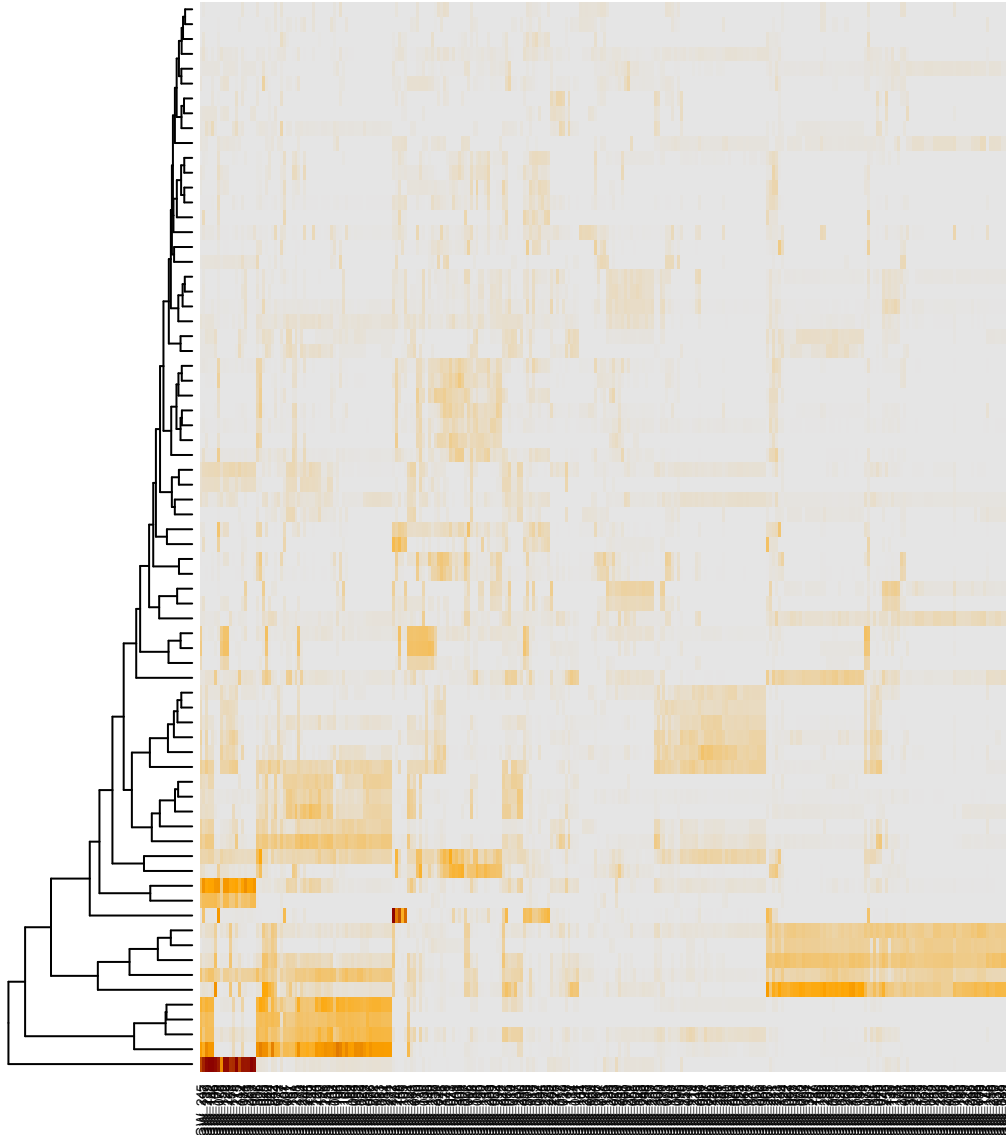
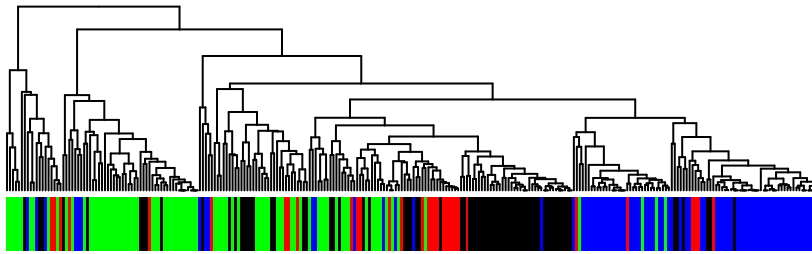


G SPANG_LPS 6hrs DN
G BENTINK_mBL DOWN
G WRIGHT_GCB UP
G SPANG_LPS 6hrs UP
G SPANG_BCR DN
G DAVE_NFkB BL DN
F ROSOLOWSKI_blue DOWN
R ROSOLOWSKI_red total
H MASCQUE_ABC UP
F DAVE_Immune response 2
B SPANG_IL21 UP
G DAVE_BL UP
G MASCQUE_GCB UP
I DAVE_BL_DN
D ROSOLOWSKI_red UP
J DAVE_BL Inter
B BENTINK_mBL UP
B MASCQUE_mBL UP
I WRIGHT_custom GCB-DLBCL UP
G MASCQUE_mBL DOWN
G WRIGHT_custom ABC-DLBCL UP
E SPANG_BAFF 9hrs DN
O ZHANG_DLBCL mutated
I SPANG_BAFF 9hrs UP
L ROSOLOWSKI_green UP
K ROSOLOWSKI_blue total
K DAVE_c-myc BL UP
B SPANG_BCR UP
L LENZ_Stromal signature 2
F DAVE_MHCCII BL DN
G DAVE_Immune response 1
G WRIGHT_ABC UP
G SPANG_CD40 6hrs DN
G SPANG_CD40 6hrs UP
K DAVE_BL-vs-DLBCL
L ROSOLOWSKI_green total
F SPANG_IL21 DN
L LENZ_Stromal signature 1

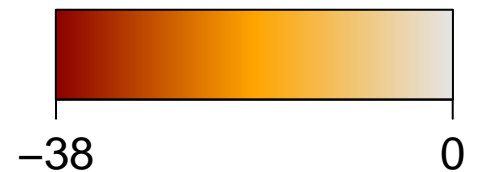


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MF

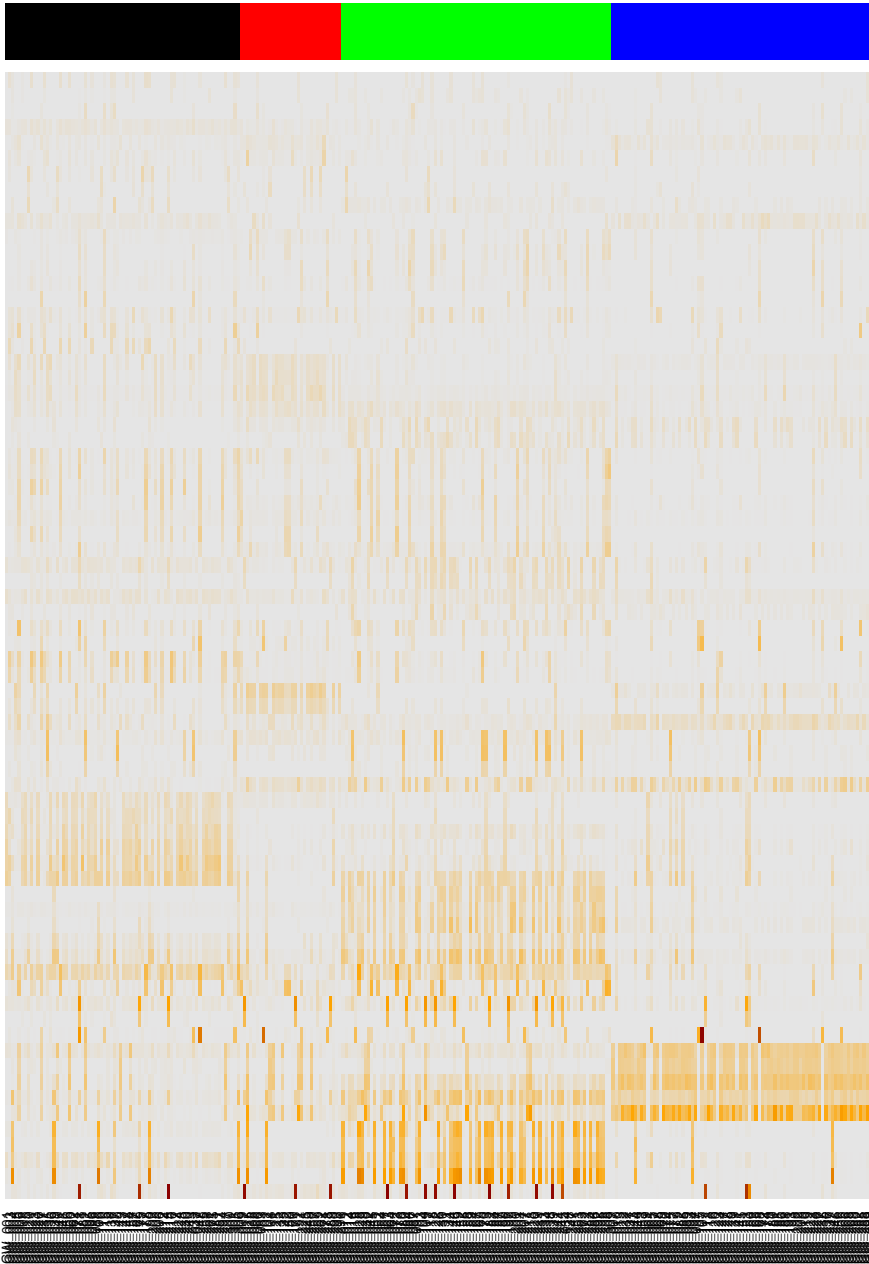


C histone acetyl-lysine binding
O retinoic acid receptor binding
C ribosome binding
M ubiquitin protein ligase binding
P cation-transporting ATPase activity
P ATPase activity, coupled to transmembrane movement of substances
A selenium binding
A calcium-dependent cysteine-type endopeptidase activity
I metalloproteinase activity
R lysophospholipase activity
M tRNA binding
K aminoacyl-tRNA ligase activity
M ribonucleoprotein complex binding
M methyltransferase activity
M NADH dehydrogenase activity
Q molecular_function
C nucleic acid binding
B RNA polymerase II transcription coactivator activity
K NAD binding
K oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP
P enzyme binding
K protein domain specific binding
O scaffold protein binding
L cadherin binding
K nucleotide binding
K single-stranded DNA binding
K DNA helicase activity
K microtubule motor activity
K protein serine/threonine kinase activity
K nucleocytoplasmic transporter activity
K unfolded protein binding
N actin filament binding
L actin-dependent ATPase activity
P virus receptor activity
L Notch binding
R RNA binding
R NADH dehydrogenase (ubiquinone) activity
B DNA binding
B chromatin binding
K glutathione transferase activity
K glutathione binding
P oxidoreductase activity
F double-stranded RNA binding
F peptide antigen binding
F NAD+ ADP-ribosyltransferase activity
O structural constituent of cytoskeleton
G coreceptor activity
G Rac GTPase activator activity
G receptor activity
G antigen binding
G transmembrane signaling receptor activity
G chemokine activity
L L-ascorbic acid binding
L growth factor activity
L fibronectin binding
L glycosaminoglycan binding
L heparin binding
L protein binding
K ATP binding
N actin binding
N titin binding
R structural constituent of ribosome
O serine-type endopeptidase activity
O RAGE receptor binding
O serine-type endopeptidase inhibitor activity
L calcium ion binding
O structural molecule activity
L extracellular matrix binding
L platelet-derived growth factor binding
L integrin binding
L extracellular matrix structural constituent
N structural constituent of muscle

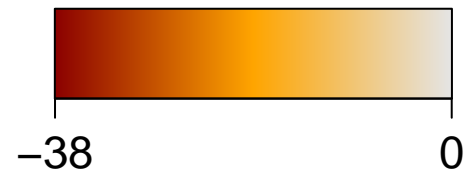


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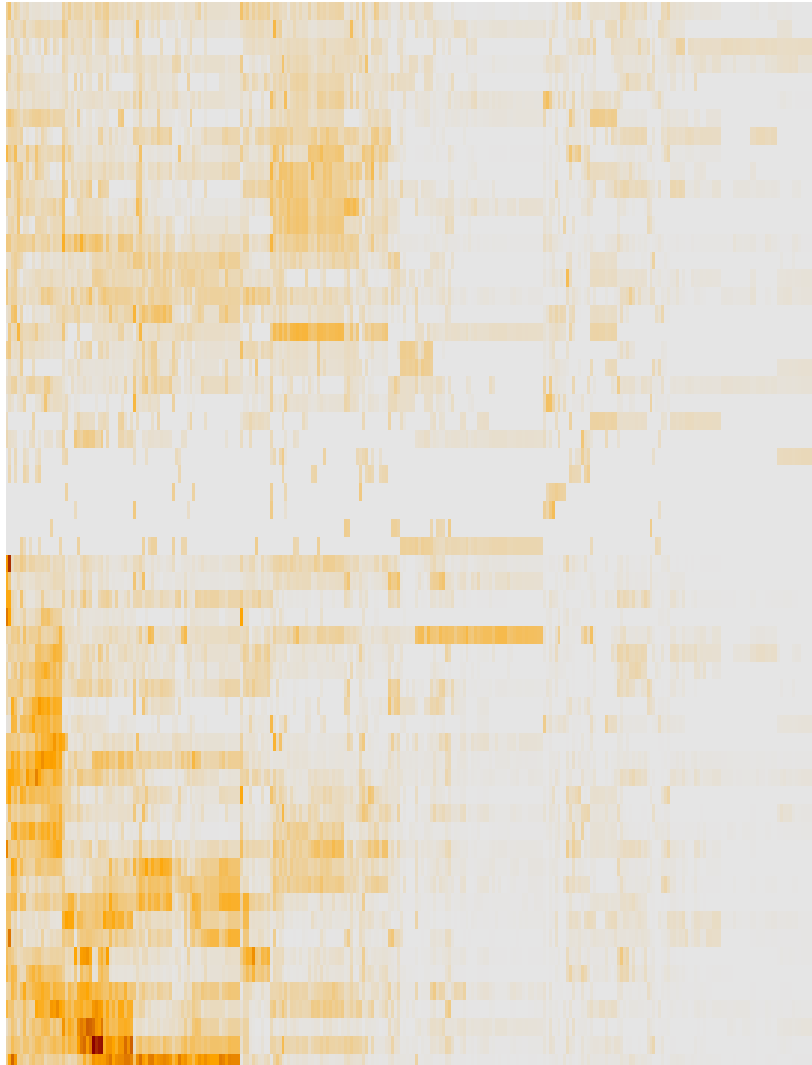
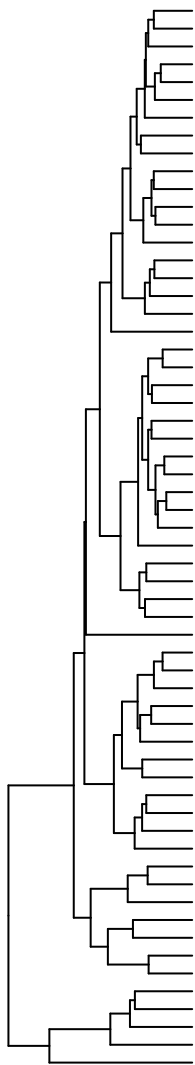
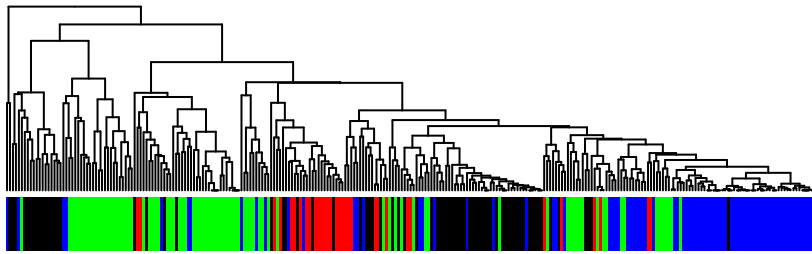


- C histone acetyl-lysine binding
- Q retinoic acid receptor binding
- C ribosome binding
- M ubiquitin protein ligase binding
- P cation-transporting ATPase activity
- P ATPase activity, coupled to transmembrane movement of substance
- A selenium binding
- A calcium-dependent cysteine-type endopeptidase activity
- I metalloprotease activity
- R lysophospholipase activity
- M tRNA binding
- K aminoacyl-tRNA ligase activity
- M ribonucleoprotein complex binding
- M methyltransferase activity
- M NADH dehydrogenase activity
- Q molecular_function
- C nucleic acid binding
- B RNA polymerase II transcription coactivator activity
- K NAD binding
- K oxidoreductase activity, acting on the CH-OH group of donors, NAD
- P enzyme binding
- K protein domain specific binding
- O scaffold protein binding
- L cadherin binding
- K nucleotide binding
- K single-stranded DNA binding
- K DNA helicase activity
- K microtubule motor activity
- K protein serine/threonine kinase activity
- K nucleocytoplasmic transporter activity
- K unfolded protein binding
- N actin filament binding
- L actin-dependent ATPase activity
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- L Notch binding
- R RNA binding
- R NADH dehydrogenase (ubiquinone) activity
- B DNA binding
- B chromatin binding
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- K glutathione binding
- P oxidoreductase activity
- F double-stranded RNA binding
- F peptide antigen binding
- F NAD+ ADP-ribosyltransferase activity
- O structural constituent of cytoskeleton
- G coreceptor activity
- G Rac GTPase activator activity
- G receptor activity
- G antigen binding
- G transmembrane signaling receptor activity
- L chemokine activity
- L L-ascorbic acid binding
- L growth factor activity
- L fibronectin binding
- L glycosaminoglycan binding
- L heparin binding
- L protein binding
- K ATP binding
- N actin binding
- N titin binding
- R structural constituent of ribosome
- O serine-type endopeptidase activity
- O RAGE receptor binding
- O serine-type endopeptidase inhibitor activity
- L calcium ion binding
- O structural molecule activity
- L extracellular matrix binding
- L platelet-derived growth factor binding
- L integrin binding
- L extracellular matrix structural constituent
- N structural constituent of muscle

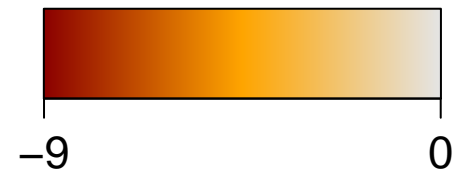


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miRNA 3UTR

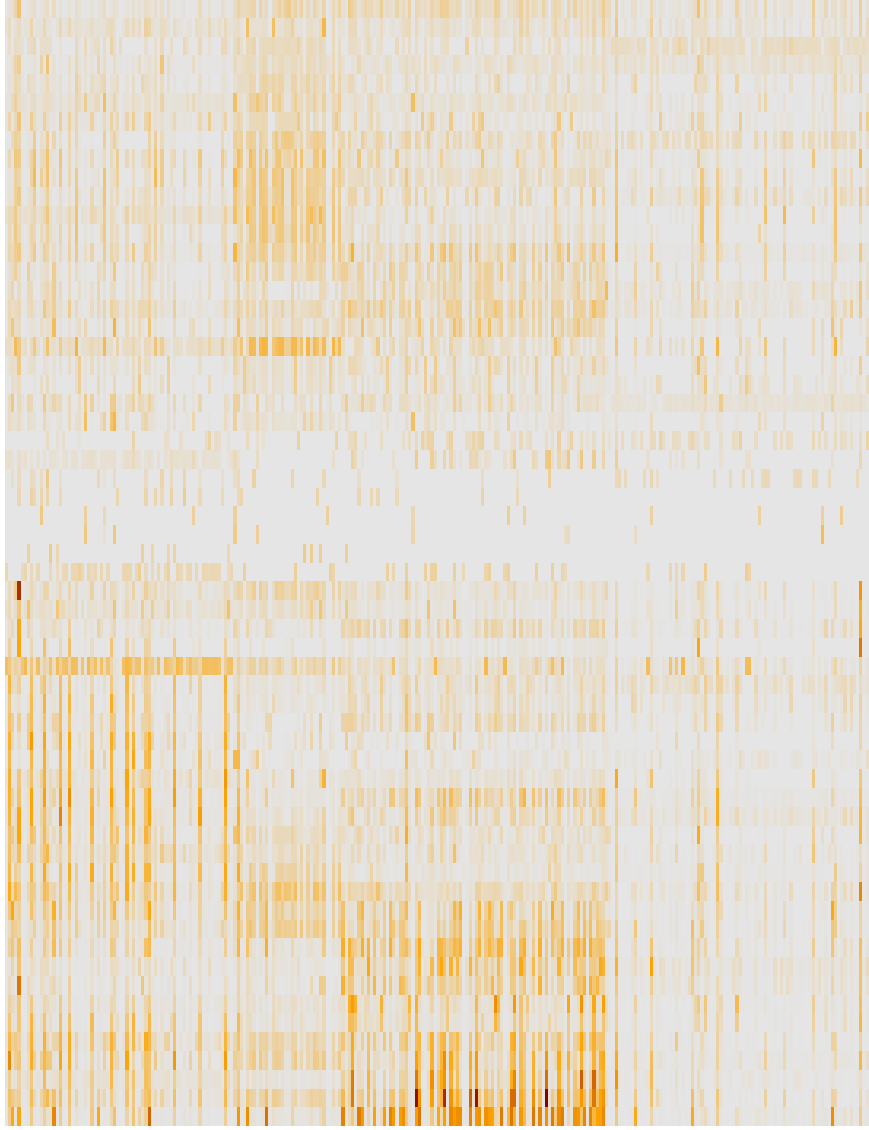
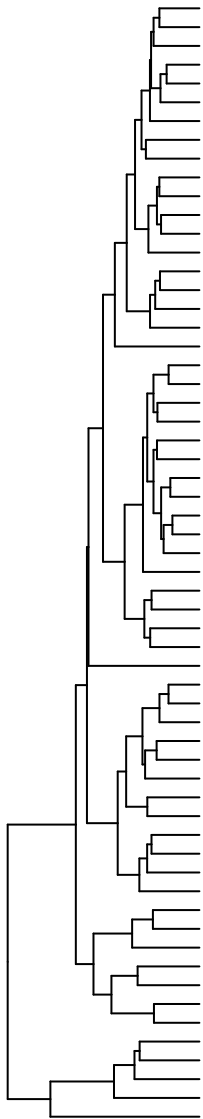


K ACCA-522
P TATC-488
H GTAG-189
E CTCT-520A--525
H GTCA-378
C CTCA-125B--125A
B AGTC-499
K GTTA-302B
E ATGT-302C
K AGGG-328
O ACAG-10A--10B
B GCAC-18A--18B
B GCTG-512-5P
L CACT-34A--34C--449
A ATAA-21
E TCTA-376A--376B
L TACT-26A--26B
L GGCA-324-3P
K GTCA-380-5P
E CTCT-526C--518F--526A
N GACA-339
J AATG-136
C GGGG-296
O GTCT-379
E GGTA-409-5P
P TGCA-517A--517C
K CGGT-220
M GGCG-371
C TCCG-184
A ACGC-210
N CGTC-208
A ACTT-142-5P
A AACT-223
E CTTT-524
E GTAT-154--487
G AGCA-155
B TCCA-516-5P
B GGTG-329
B GACA-219
B GCAA-502
B AGCT-28
P ATGT-221--222
B CTTT-527
B TTTG-19A--19B
E GACT-212--132
B AGCA-93--302A--302B--302C--302D--372--373--520E--520A--
B TTTT-373
E ATAC-144
B ATAC-202
L TAGC-9
L TGTT-30A-5P--30C--30D--30B--30E-5P
L GTAC-101
L TATT-374
E GCAC-17-5P--20A--106A--106B--20B--519D
B TGCA-519C--519B--519A
B GTGC-96
L TGCC-124A
L CTAT-153
L GTGC-506
L TGGT-29A--29B--29C

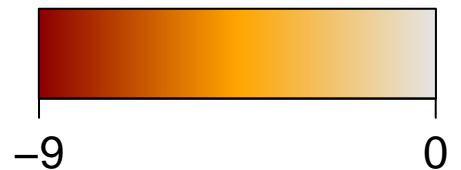


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miRNA 3UTR

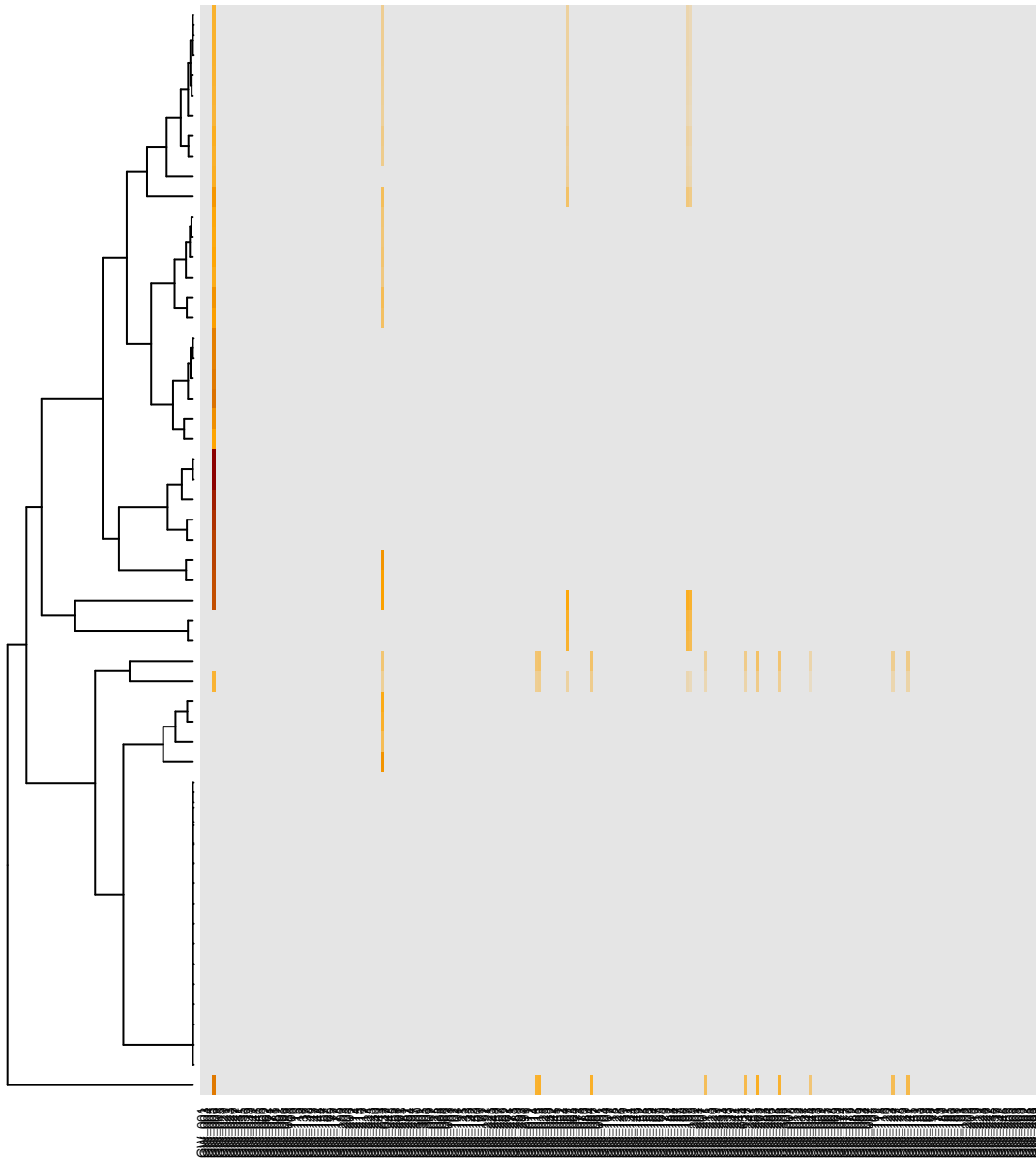


- K ACCA-522
- P TATC-488
- H GTAG-189
- E CTCT-520A--525
- H GTCA-378
- C CTCA-125B--125A
- B AGTC-499
- K GTTA-302B
- E ATGT-302C
- K AGGG-328
- O ACAG-10A--10B
- B GCAC-18A--18B
- B GCTG-512-5P
- L CACT-34A--34C--449
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- E TCTA-376A--376B
- L TACT-26A--26B
- L GGCA-324-3P
- K GTCA-380-5P
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- N GACA-339
- J AATG-136
- C GGGG-296
- O GTCT-379
- E GGTA-409-5P
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- K CGGT-220
- M GGCG-371
- C TCCG-184
- A ACGC-210
- N CGTC-208
- A ACTT-142-5P
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- E CTTT-524
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- B TCCA-516-5P
- B GGTG-329
- B GACA-219
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- B AGCT-28
- P ATGT-221--222
- B CTTT-527
- B TTTG-19A--19B
- E GACT-212--132
- B AGCA-93--302A--302B--302C--302D--372--373--520E--520F--520G--520H--520I--520J--520K--520L--520M--520N--520O--520P--520Q--520R--520S--520T--520U--520V--520W--520X--520Y--520Z
- B TTTT-373
- E ATAC-144
- B ATAC-202
- L TAGC-9
- L TGTT-30A-5P--30C--30D--30B--30E-5P
- L GTAC-101
- L TAIT-374
- E GCAC-17-5P--20A--106A--106B--20B--519D
- B TGCA-519C--519B--519A
- B GTGC-96
- L TGCC-124A
- L CTAT-153
- L GTGC-506
- L TGGT-29A--29B--29C

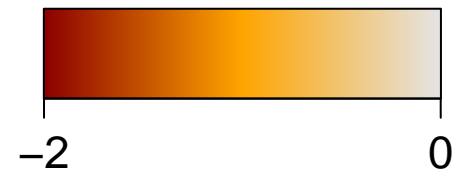


log(p.value)

miRNA Disease

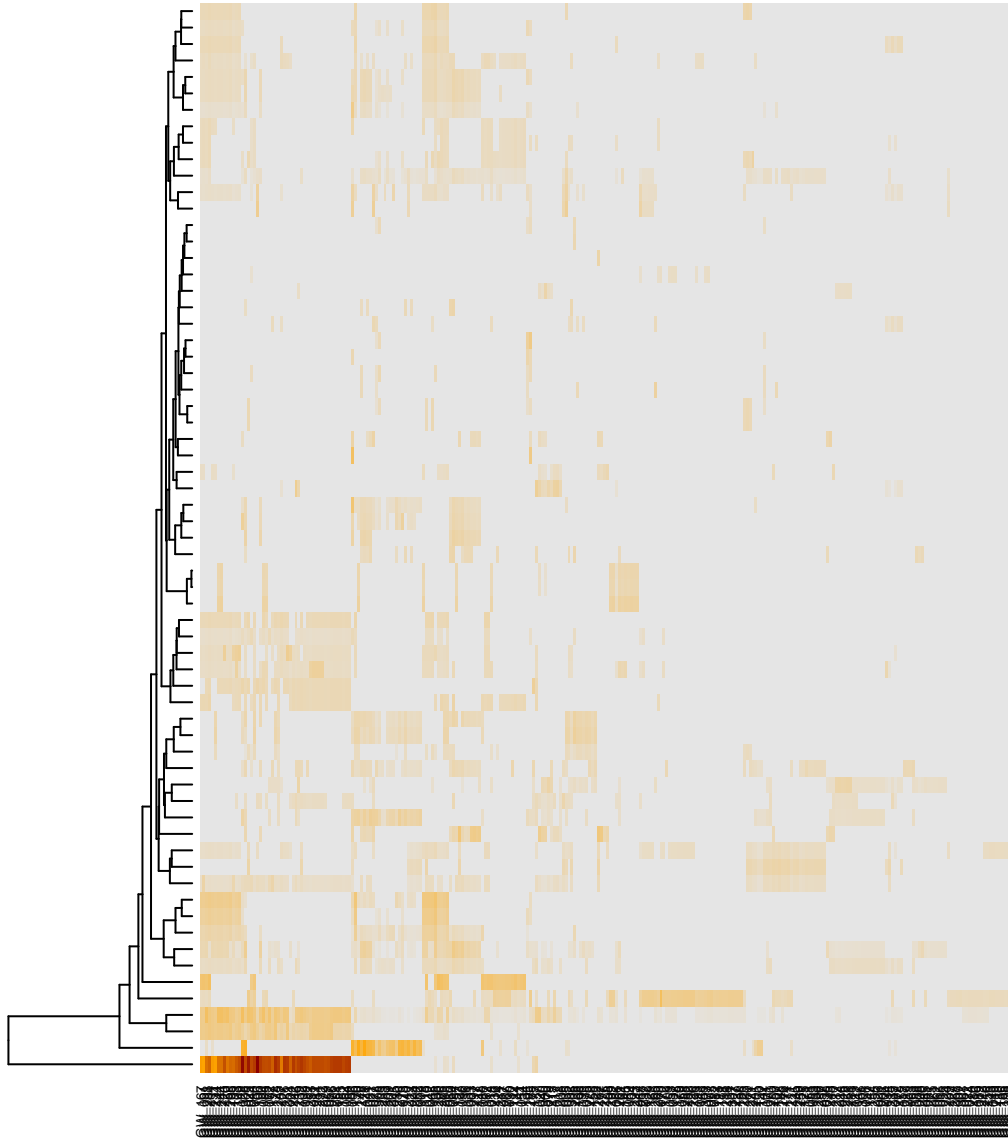
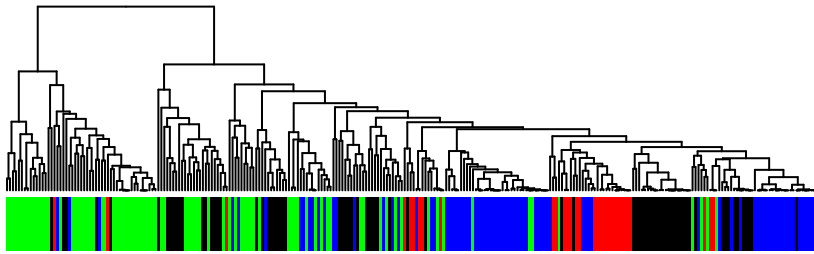


- A Squamous cell carcinoma, head and neck
- A Pancreatic cancer
- A Hematological
- A Prostate cancer
- A Cancer
- A Breast cancer
- A Melanoma and neural system tumor syndrome
- A Leukemia
- A Ovarian cancer
- A Cardiomyopathy, dilated
- A Hepatocellular carcinoma
- A Muscular
- A Glioblastoma multiforme,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

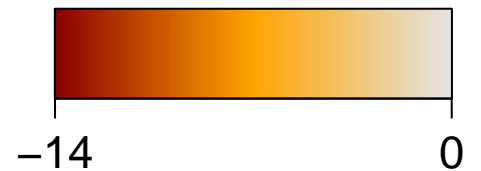


log(p.value)

miRNA target

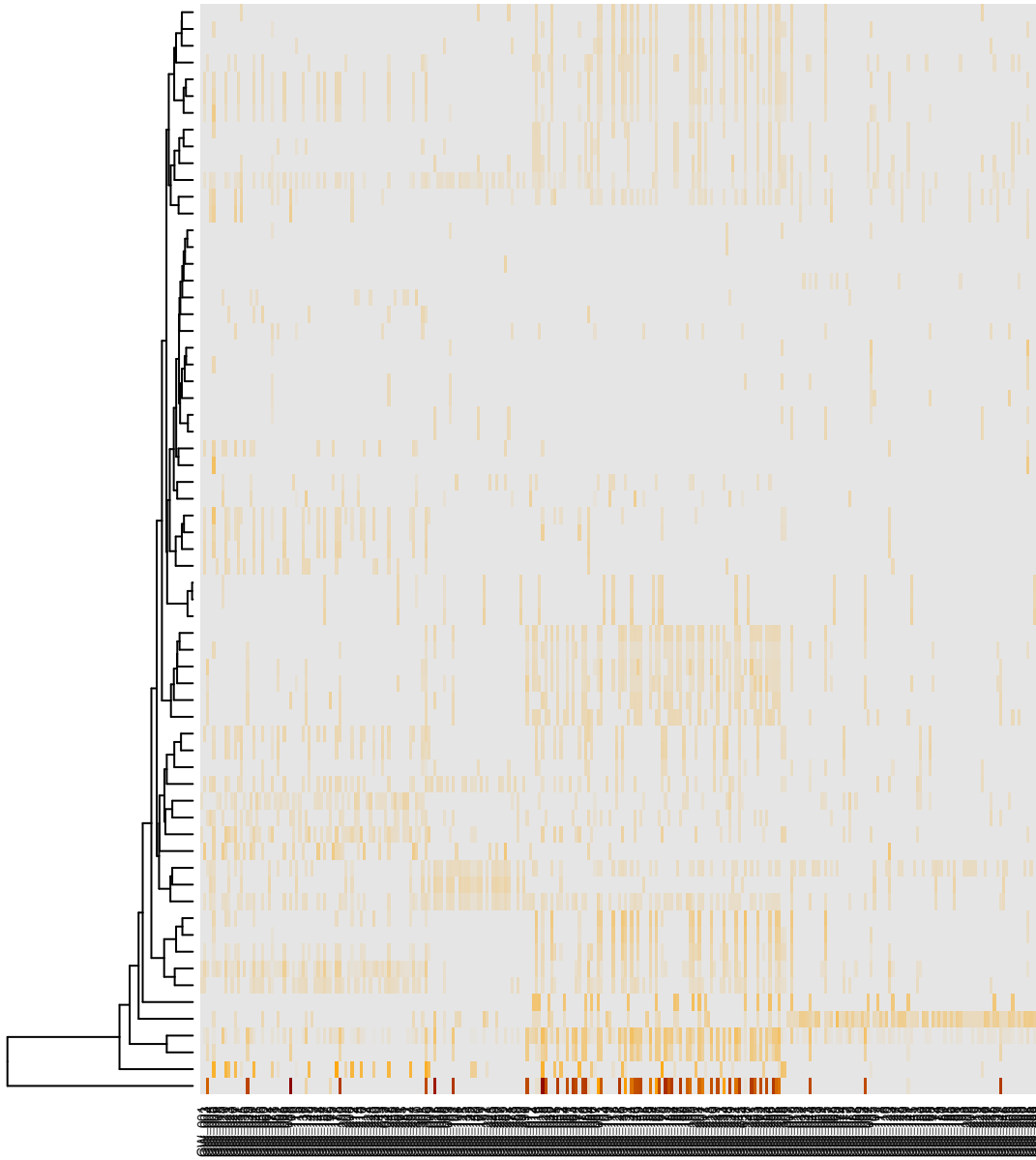


P miR-124a
E let-7g
L miR-16-1
L miR-126
E let-7c
B miR-34b
E let-7a
A miR-133b
C miR-122
P miR-206
O miR-1
E miR-125b
O miR-125a
R miR-19a
A miR-19b
A miR-433
A miR-210
A miR-93
A miR-129
M miR-27a
R miR-214
E miR-98
R miR-659
R miR-375
P miR-7
P miR-128b
A miR-223
A miR-373
A miR-133a
I miR-146a
B miR-101
B miR-34c
B miR-153
H miR-193a
A miR-181a
A miR-181b
A miR-107
L miR-101b
L miR-9
L miR-143
L miR-200c
L miR-18
L miR-346
F miR-148a
F miR-152
P miR-17
N miR-320
G miR-155
I miR-205
E miR-26a
A miR-204
L miR-145
K miR-127
I miR-222
L miR-195
L let-7b
L miR-16
B miR-34a
B miR-15a
O miR-199a*
O miR-196a
L miR-21
L miR-29b
K miR-24
L miR-29c

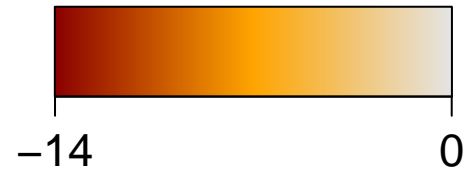


log(p.value)

miRNA target

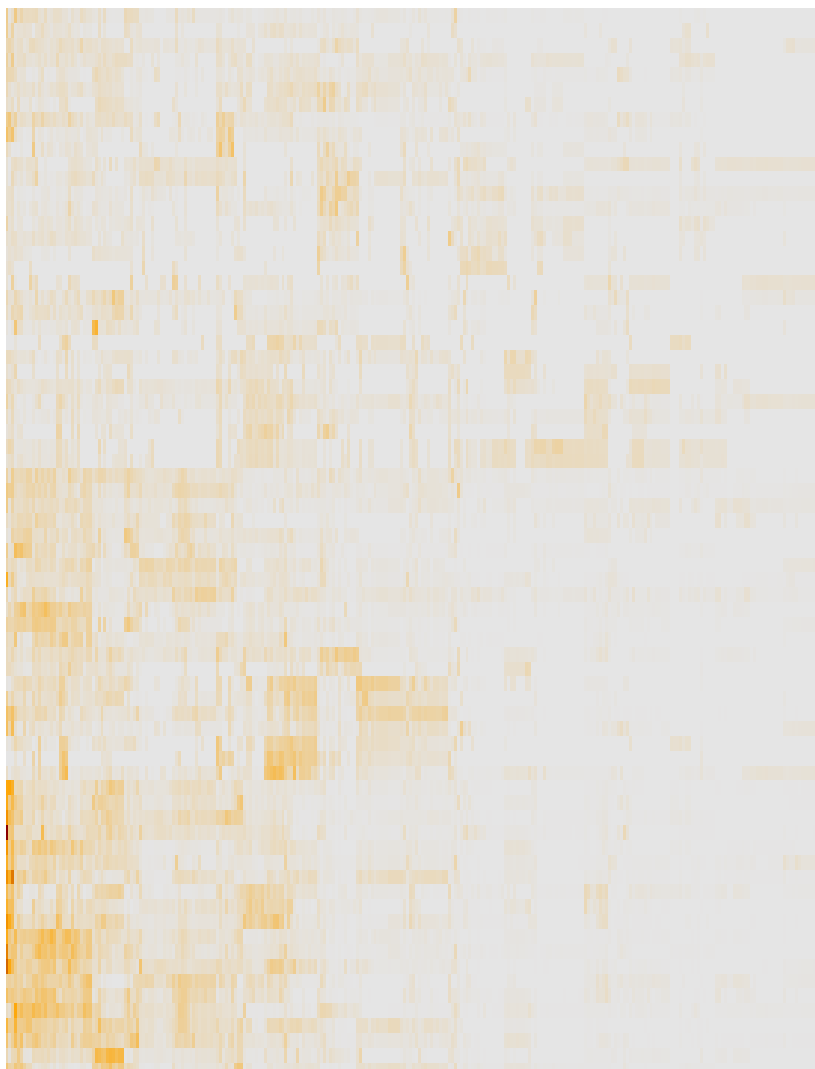
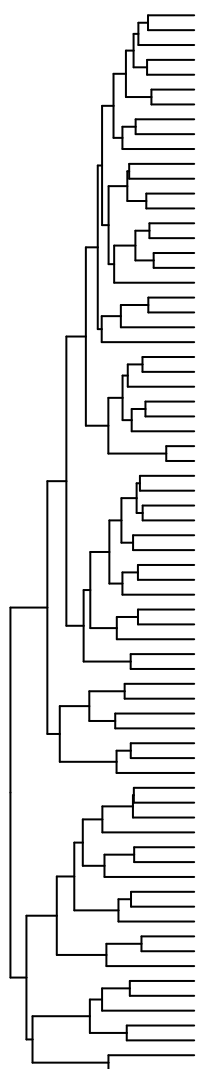
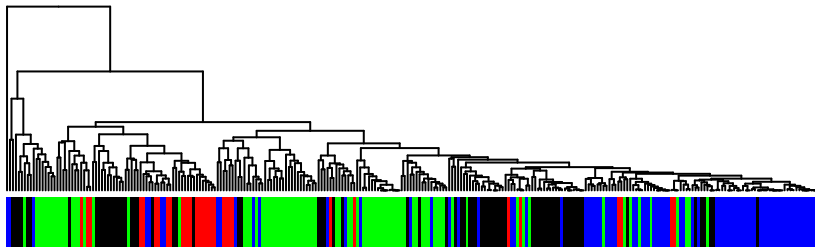


- P miR-124a
- E let-7g
- L miR-16-1
- L miR-126
- E let-7c
- B miR-34b
- E let-7a
- A miR-133b
- C miR-122
- P miR-206
- O miR-1
- E miR-125b
- O miR-125a
- R miR-19a
- A miR-19b
- A miR-433
- A miR-210
- A miR-93
- A miR-129
- M miR-27a
- R miR-214
- E miR-98
- R miR-659
- R miR-375
- P miR-7
- P miR-128b
- A miR-223
- A miR-373
- A miR-133a
- I miR-146a
- B miR-101
- B miR-34c
- B miR-153
- H miR-193a
- A miR-181a
- A miR-181b
- A miR-107
- L miR-101b
- L miR-9
- L miR-143
- L miR-200c
- L miR-18
- L miR-346
- F miR-148a
- F miR-152
- P miR-17
- N miR-320
- G miR-155
- I miR-205
- E miR-26a
- A miR-204
- L miR-145
- K miR-127
- I miR-222
- L miR-195
- L let-7b
- L miR-16
- B miR-34a
- B miR-15a
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- L miR-21
- L miR-29b
- K miR-24
- L miR-29c

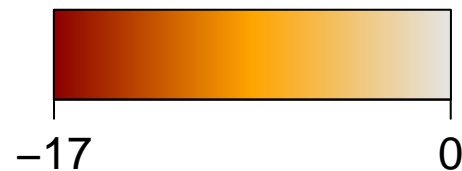


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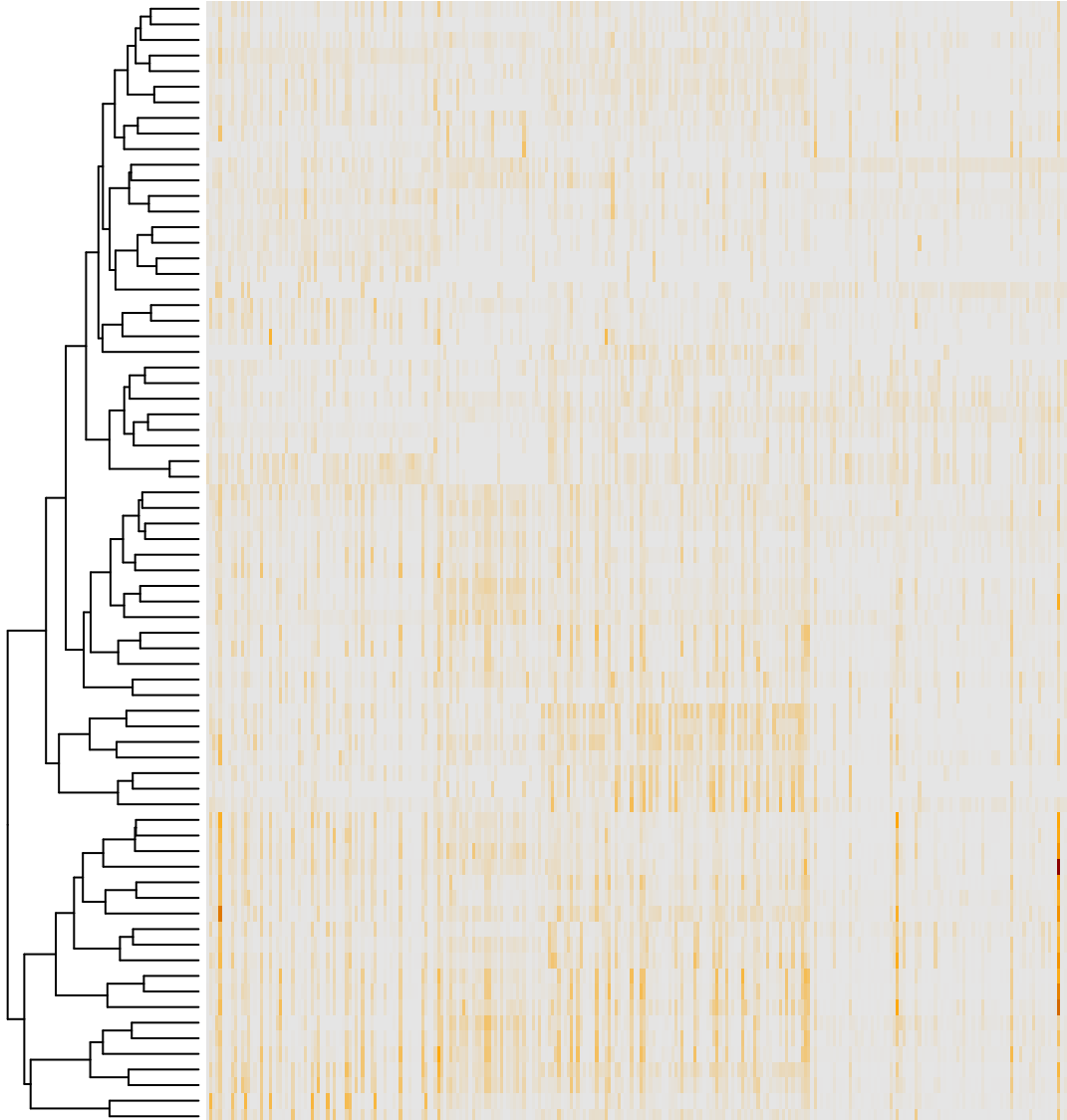
miRNA target starBase



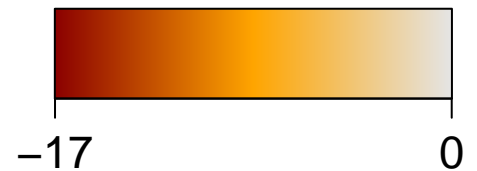
K hsa-miR-125a-3p
E hsa-miR-519e*
E hsa-miR-504
G hsa-miR-628-5p
E hsa-miR-491-3p
C hsa-miR-571
C hsa-miR-296-5p
P hsa-miR-509-3p
E hsa-miR-302b*
P hsa-miR-127-3p
A hsa-miR-564
M hsa-miR-874
M hsa-miR-939
C hsa-miR-125a-5p
E hsa-miR-517*
E hsa-miR-1226
I hsa-miR-1228
I hsa-miR-639
O hsa-miR-1298
K hsa-miR-1305
B hsa-miR-524-3p
C hsa-miR-1237
N hsa-miR-566
O hsa-miR-484
J hsa-miR-933
B hsa-miR-450a
O hsa-miR-1290
J hsa-miR-370
C hsa-miR-602
G hsa-miR-551a
E hsa-miR-551b
K hsa-miR-520a-5p
E hsa-miR-520f
R hsa-miR-629-3p
K hsa-miR-518d-3p
K hsa-miR-345
K hsa-miR-625
K hsa-miR-518b
K hsa-miR-641
K hsa-miR-506
K hsa-miR-496
K hsa-miR-210
K hsa-miR-297
M hsa-miR-378
M hsa-miR-593
L hsa-miR-1224-3p
L hsa-miR-485-3p
L hsa-let-7f
L hsa-miR-1259
L hsa-miR-483-3p
L hsa-miR-1249
L hsa-miR-220c
E hsa-miR-301b
R hsa-miR-548m
P hsa-miR-633
R hsa-miR-1244
E hsa-miR-548l
E hsa-miR-382
E hsa-let-7b
E hsa-miR-105
E hsa-miR-16
E hsa-miR-20a
K hsa-miR-186
K hsa-miR-548d-5p
K hsa-miR-590-3p
K hsa-miR-886
K hsa-miR-582-5p
K hsa-miR-28-5p
E hsa-miR-548c-3p
K hsa-miR-181b
B hsa-miR-188-5p
B hsa-miR-380



log(p.value)
miRNA target starBase

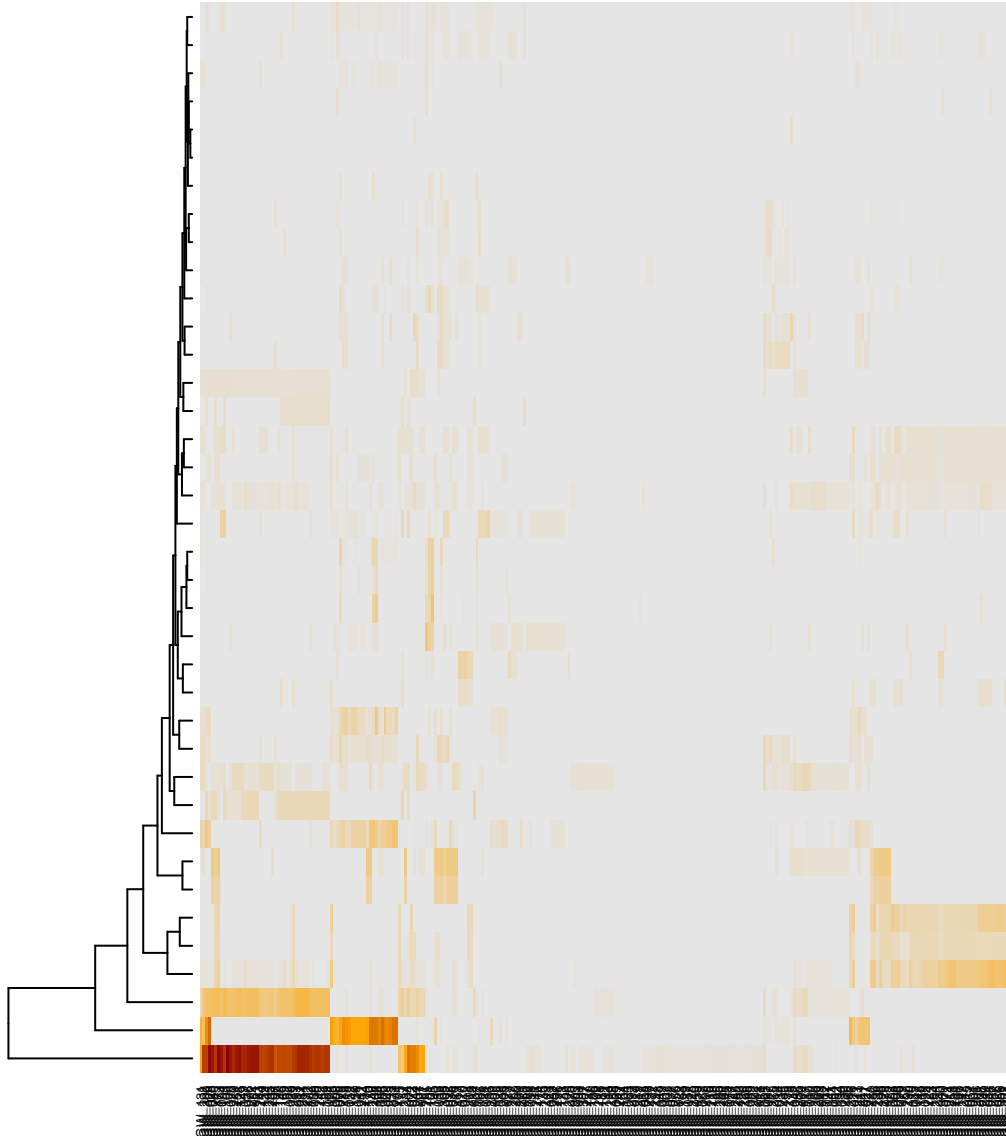
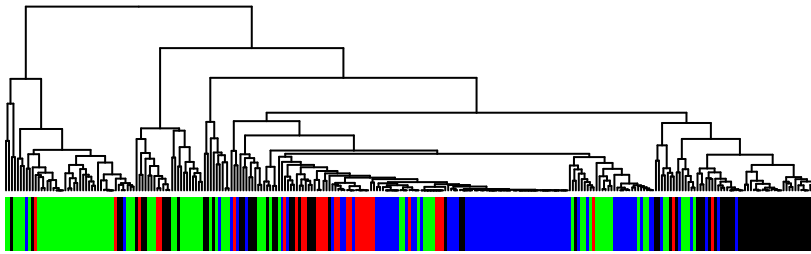


K hsa-miR-125a-3p
E hsa-miR-519e*
E hsa-miR-504
G hsa-miR-628-5p
E hsa-miR-491-3p
C hsa-miR-571
C hsa-miR-296-5p
P hsa-miR-509-3p
E hsa-miR-302b*
P hsa-miR-127-3p
A hsa-miR-564
M hsa-miR-874
M hsa-miR-939
C hsa-miR-125a-5p
E hsa-miR-517*
E hsa-miR-1226
I hsa-miR-1228
I hsa-miR-639
O hsa-miR-1298
K hsa-miR-1305
B hsa-miR-524-3p
C hsa-miR-1237
N hsa-miR-566
O hsa-miR-484
J hsa-miR-933
B hsa-miR-450a
O hsa-miR-1290
J hsa-miR-370
C hsa-miR-602
G hsa-miR-551a
E hsa-miR-551b
K hsa-miR-520a-5p
E hsa-miR-520f
R hsa-miR-628-3p
K hsa-miR-518d-3p
K hsa-miR-345
K hsa-miR-625
K hsa-miR-518b
K hsa-miR-641
K hsa-miR-506
K hsa-miR-496
K hsa-miR-210
K hsa-miR-297
M hsa-miR-378
M hsa-miR-593
L hsa-miR-1224-3p
L hsa-miR-485-3p
L hsa-let-7f
L hsa-miR-1259
L hsa-miR-483-3p
L hsa-miR-1249
L hsa-miR-220c
E hsa-miR-301b
R hsa-miR-548m
P hsa-miR-633
R hsa-miR-1244
E hsa-miR-548l
E hsa-miR-382
E hsa-let-7b
B hsa-miR-105
E hsa-miR-16
E hsa-miR-20a
K hsa-miR-186
K hsa-miR-548d-5p
K hsa-miR-590-3p
K hsa-miR-888
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E hsa-miR-548c-3p
K hsa-miR-181b
B hsa-miR-188-5p
B hsa-miR-380

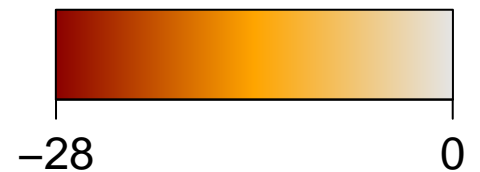


log(p.value)

MMML CGS

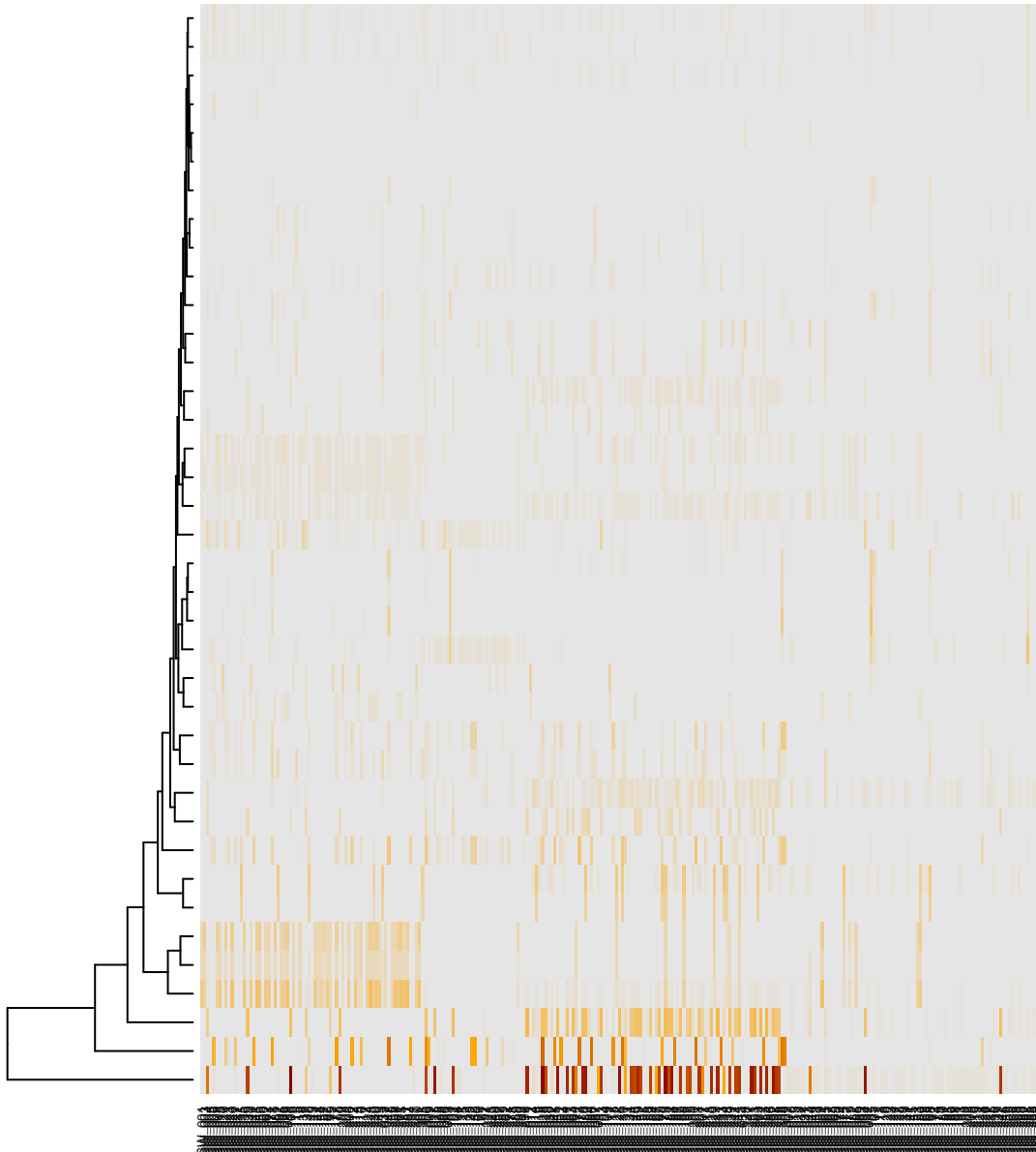


J MACIEJ_MMML 16
A MACIEJ_MMML 30
R MACIEJ_MMML 10
A MACIEJ_MMML 38
A MACIEJ_MMML 43
A MACIEJ_MMML 35
R MACIEJ_MMML 17
C MACIEJ_MMML 24
A MACIEJ_MMML 14
A MACIEJ_MMML 26
R MACIEJ_MMML 48
P MACIEJ_MMML 9
M MACIEJ_MMML 29
D MACIEJ_MMML 40
A MACIEJ_MMML 46
J MACIEJ_MMML 44
G MACIEJ_MMML 20
G MACIEJ_MMML 3
J MACIEJ_MMML 8
R MACIEJ_MMML 22
R MACIEJ_MMML 28
R MACIEJ_MMML 49
R MACIEJ_MMML 50
E MACIEJ_MMML 5
I MACIEJ_MMML 32
K MACIEJ_MMML 41
K MACIEJ_MMML 15
L MACIEJ_MMML 13
L MACIEJ_MMML 23
K MACIEJ_MMML 19
F MACIEJ_MMML 47
F MACIEJ_MMML 27
G MACIEJ_MMML 7
G MACIEJ_MMML 2
H MACIEJ_MMML 6
L MACIEJ_MMML 31
K MACIEJ_MMML 4
L MACIEJ_MMML 1

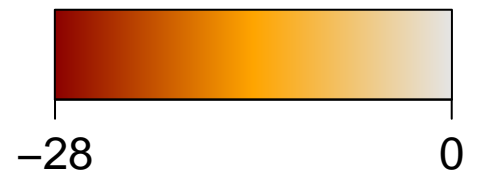


log(p.value)

MMML CGS

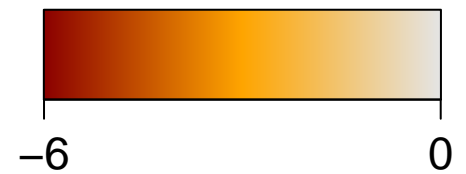
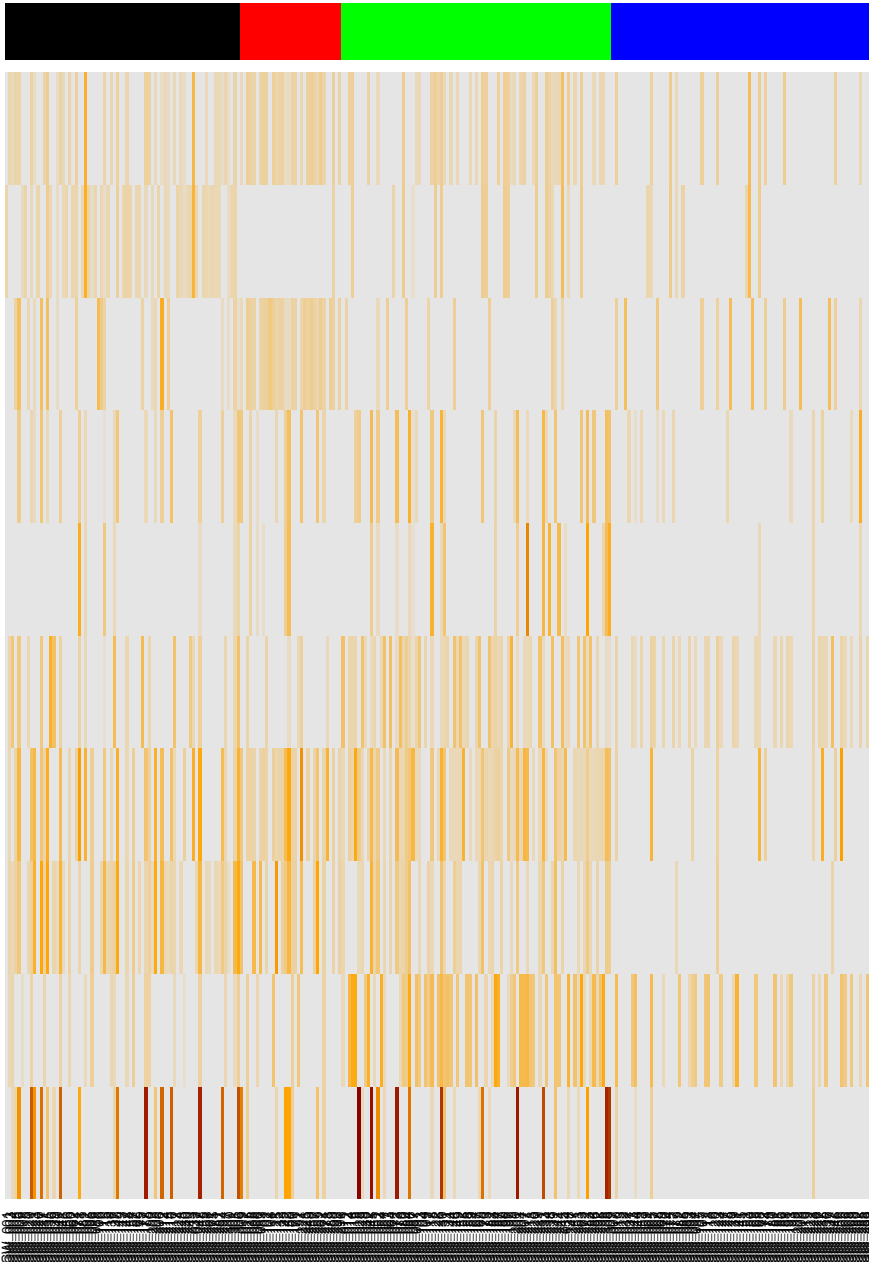


J MACIEJ_MMML 16
A MACIEJ_MMML 30
R MACIEJ_MMML 10
A MACIEJ_MMML 38
A MACIEJ_MMML 43
A MACIEJ_MMML 35
R MACIEJ_MMML 17
C MACIEJ_MMML 24
A MACIEJ_MMML 14
A MACIEJ_MMML 26
R MACIEJ_MMML 48
P MACIEJ_MMML 9
M MACIEJ_MMML 29
D MACIEJ_MMML 40
A MACIEJ_MMML 46
J MACIEJ_MMML 44
G MACIEJ_MMML 20
G MACIEJ_MMML 3
J MACIEJ_MMML 8
R MACIEJ_MMML 22
R MACIEJ_MMML 28
R MACIEJ_MMML 49
R MACIEJ_MMML 50
E MACIEJ_MMML 5
I MACIEJ_MMML 32
K MACIEJ_MMML 41
K MACIEJ_MMML 15
L MACIEJ_MMML 13
L MACIEJ_MMML 23
K MACIEJ_MMML 19
F MACIEJ_MMML 47
F MACIEJ_MMML 27
G MACIEJ_MMML 7
G MACIEJ_MMML 2
H MACIEJ_MMML 6
L MACIEJ_MMML 31
K MACIEJ_MMML 4
L MACIEJ_MMML 1



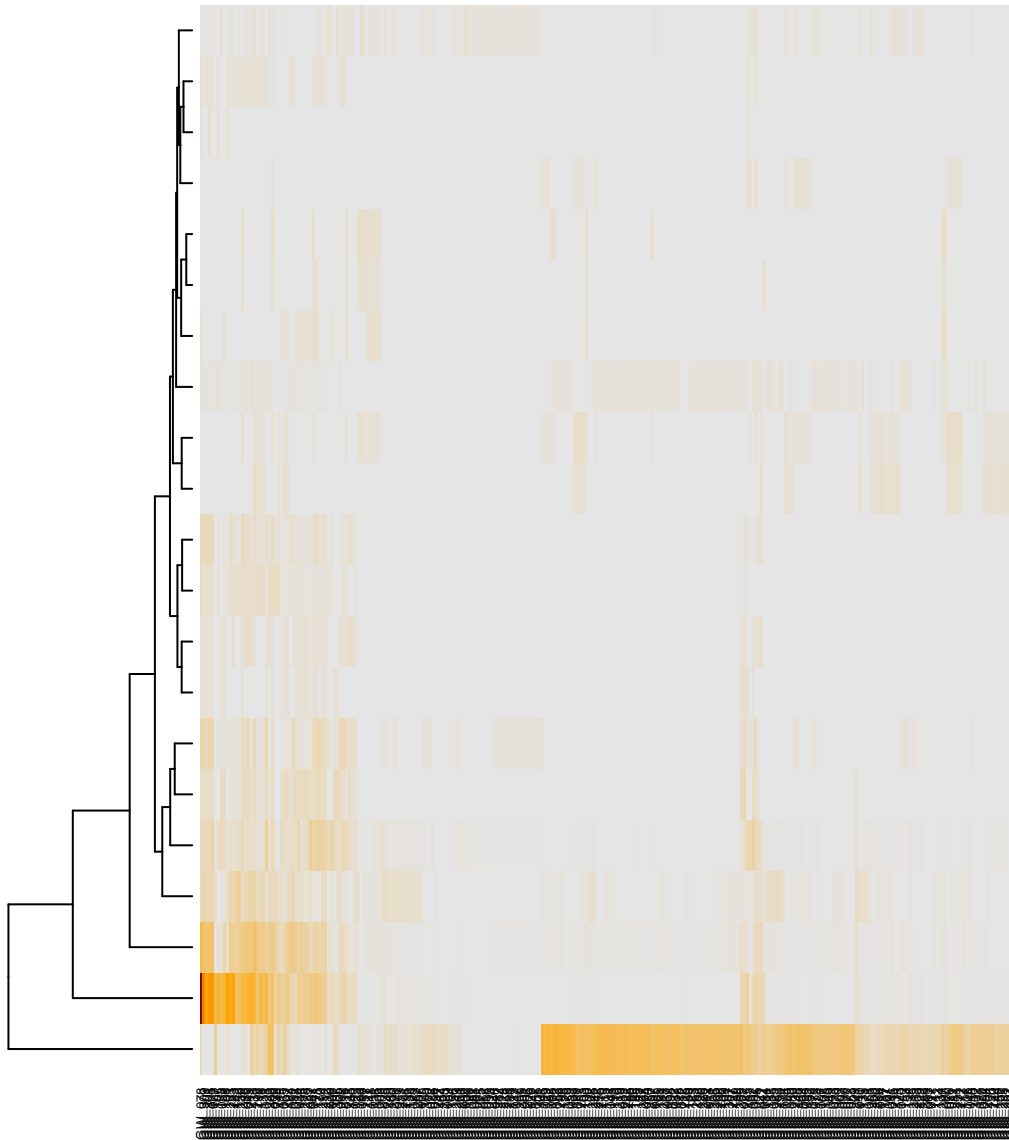
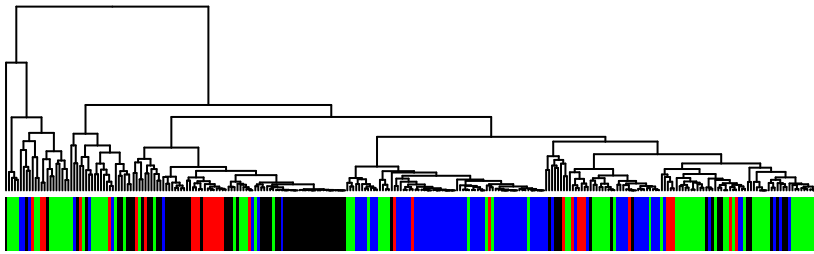
log(p.value)

Pathw Act

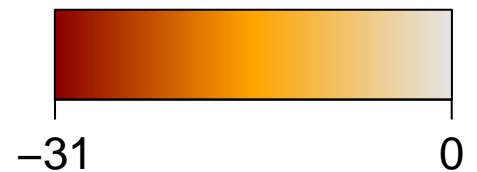


log(p.value)

TF

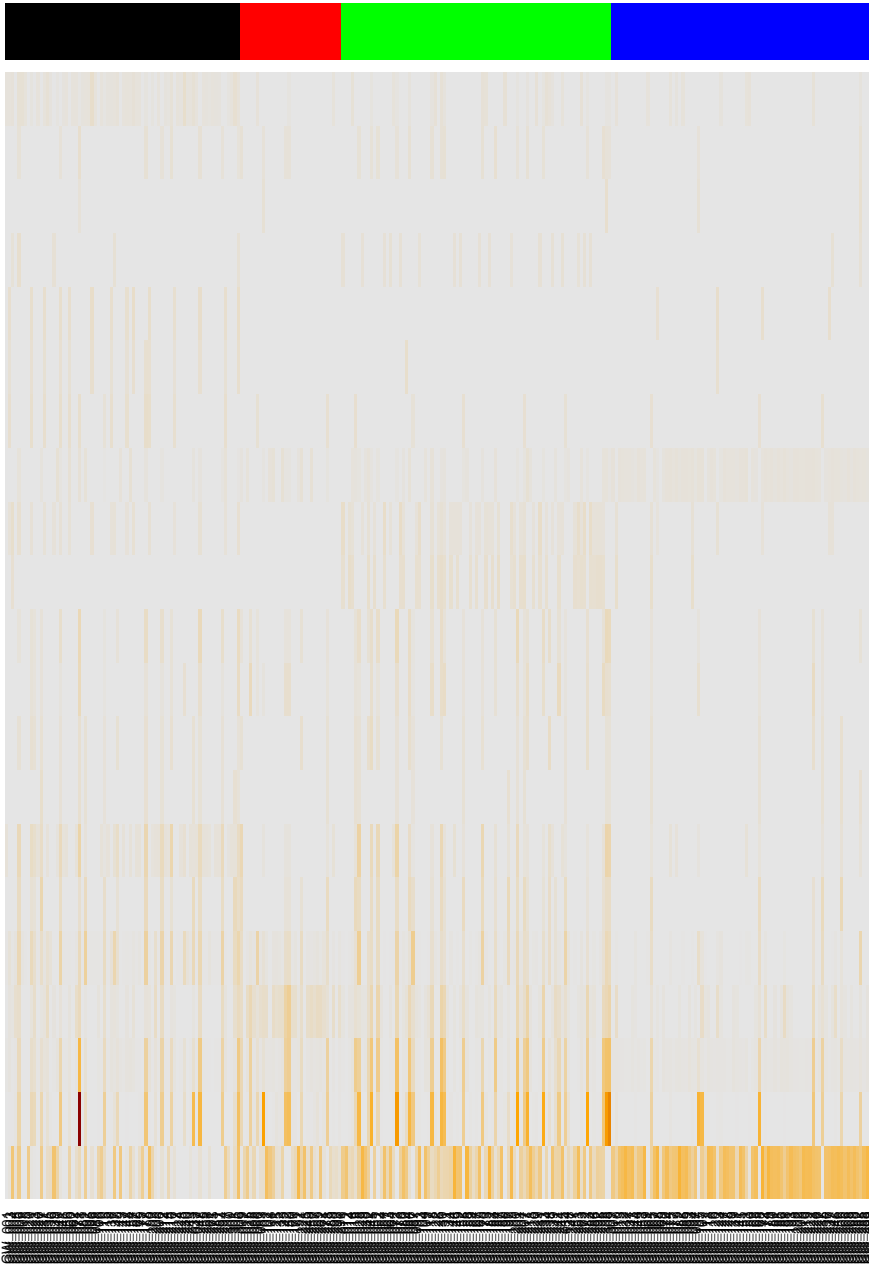


- F NOWICK_TF
- R MYC_Apoptosis UP
- R MYC_Signal transduction UP
- A MYC_TF and cofactors
- B MYC_Cell cycle DOWN
- B MYC_TFs
- B MYC_Chromatin_modification UP
- E MYC_Protein synthesis degradation UP
- B MYC_Targets DOWN
- L MYC_ECM cell adhesion DOWN
- K MYC_DNA repair UP
- R MYC_RNA processing binding UP
- M MYC_DNA replication UP
- M MYC_Tumor supressor genes UP
- K MYC_Cell cycle UP
- M MYC_Cell growth and proliferation UP
- K HEBENSTREIT_high expression TF
- K MYC_Metabolism UP
- K MYC_Targets UP
- R KIM_MYC targets
- O HEBENSTREIT_low expression TF

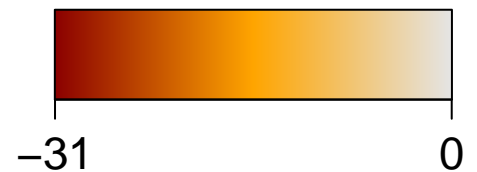


log(p.value)

TF

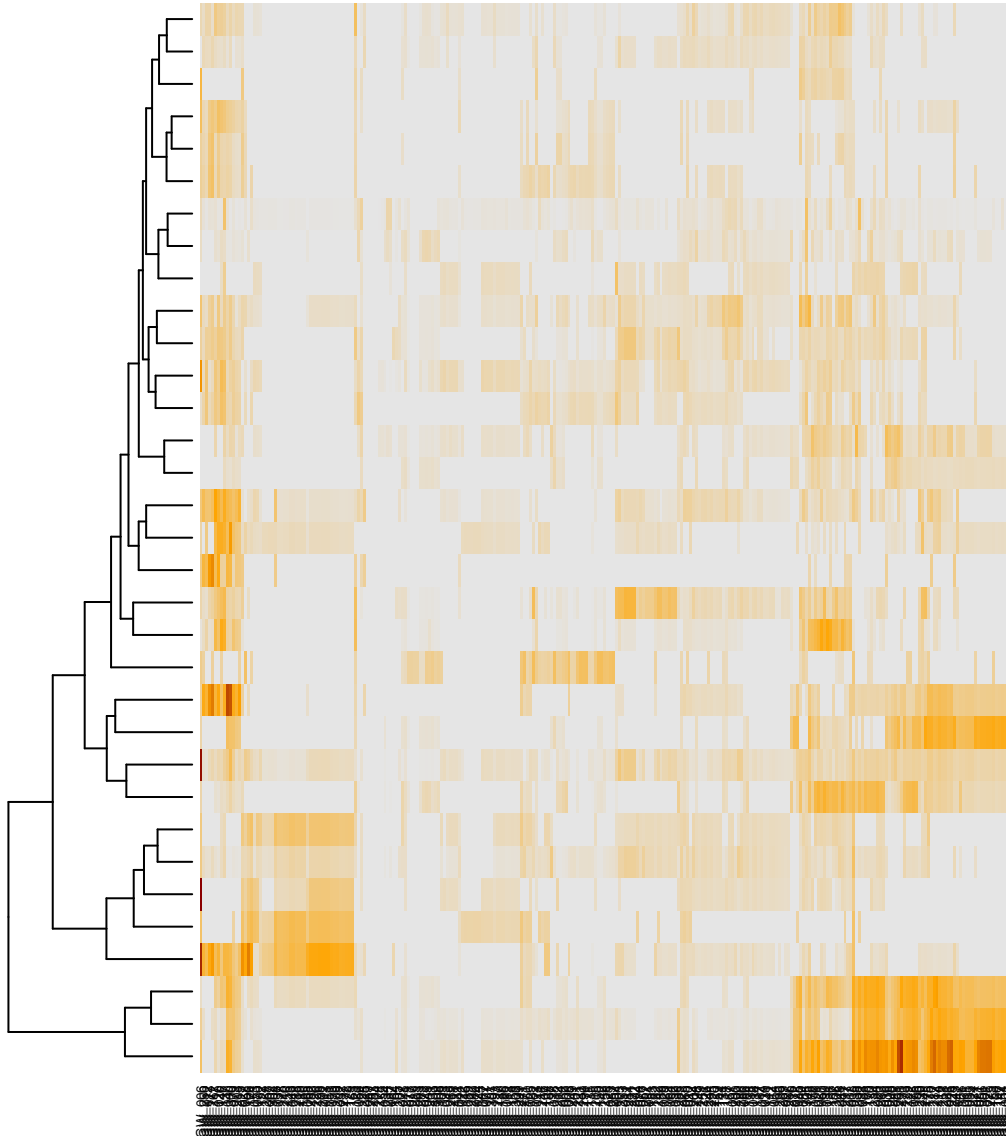
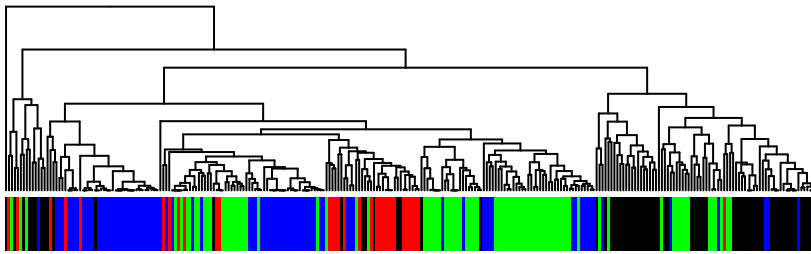


- F NOWICK_TF
- R MYC_Apoptosis UP
- R MYC_Signal transduction UP
- A MYC_TF and cofactors
- B MYC_Cell cycle DOWN
- B MYC_TFs
- B MYC_Chromatin_modification UP
- E MYC_Protein synthesis degradation UP
- B MYC_Targets DOWN
- L MYC_ECM cell adhesion DOWN
- K MYC_DNA repair UP
- R MYC_RNA processing binding UP
- M MYC_DNA replication UP
- M MYC_Tumor suppressor genes UP
- K MYC_Cell cycle UP
- M MYC_Cell growth and proliferation UP
- K HEBENSTREIT_high expression TF
- K MYC_Metabolism UP
- K MYC_Targets UP
- R KIM_MYC targets
- O HEBENSTREIT_low expression TF

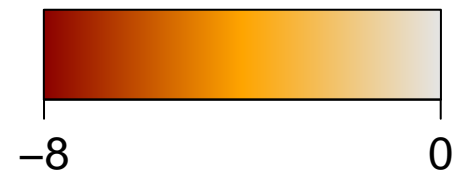


log(p.value)

TF Tissue

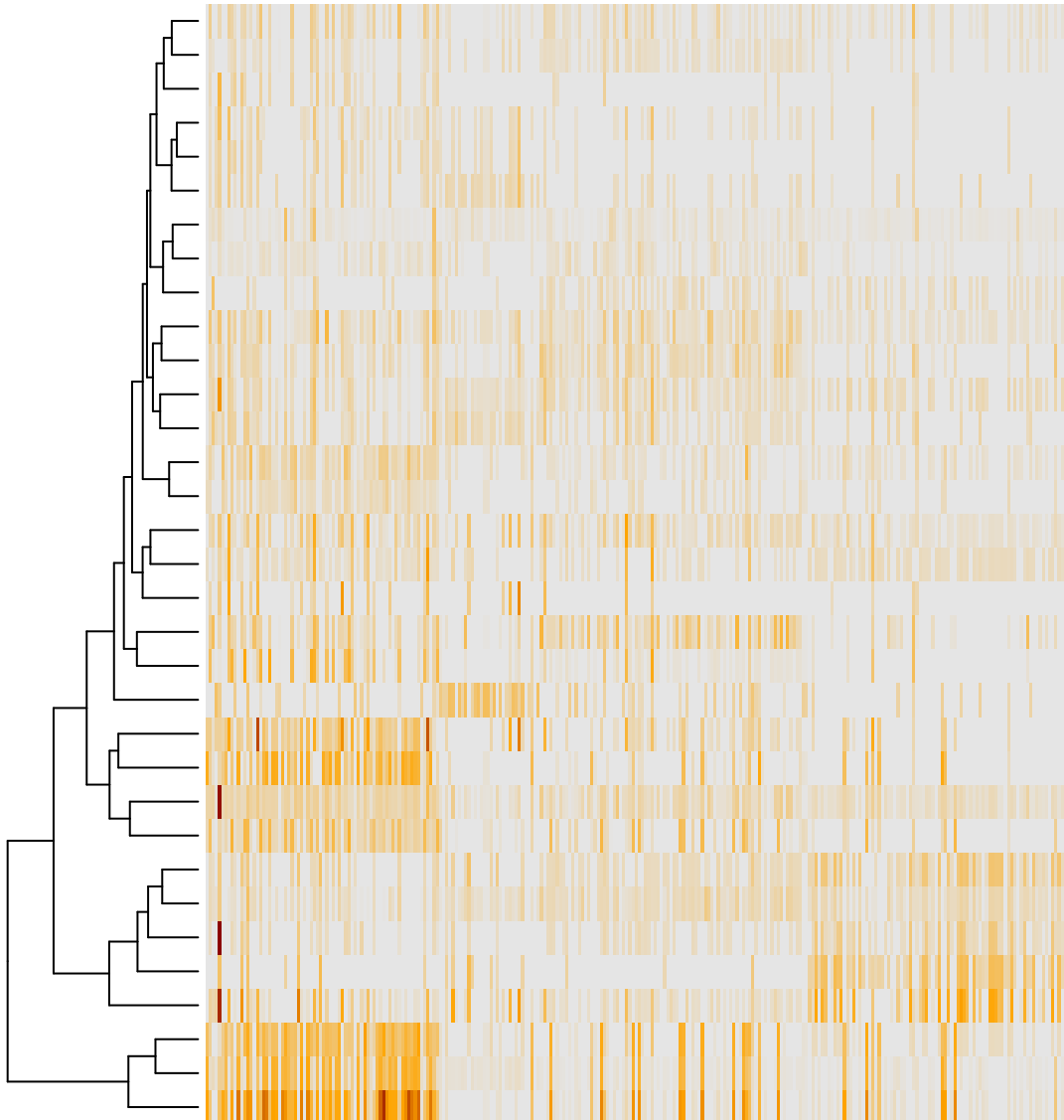


B VAQUERIZAS_Whole brain
A VAQUERIZAS_Spinal cord
B VAQUERIZAS_Kidney
I VAQUERIZAS_Adrenal cortex
A VAQUERIZAS_Adrenal gland
A VAQUERIZAS_Ovary
C VAQUERIZAS_General
C VAQUERIZAS_Testis
F VAQUERIZAS_Heart
H VAQUERIZAS_Fetal lung
E VAQUERIZAS_Smooth muscle
I VAQUERIZAS_Thyroid
J VAQUERIZAS_Fetal thyroid
H VAQUERIZAS_Liver
H VAQUERIZAS_Fetal liver
A VAQUERIZAS_Prostate
I VAQUERIZAS_Pituitary
A VAQUERIZAS_Appendix
I VAQUERIZAS_Uterus
B VAQUERIZAS_Fetal brain
K VAQUERIZAS_Skeletal.muscle.psoas
A VAQUERIZAS_Salivary gland
G VAQUERIZAS_Bone marrow
H VAQUERIZAS_Lung
B VAQUERIZAS_Thymus
O VAQUERIZAS_Skin
O VAQUERIZAS_Placenta
O VAQUERIZAS_Pancreas
O VAQUERIZAS_Tongue
O VAQUERIZAS_Trachea
F VAQUERIZAS_Tonsil
F VAQUERIZAS_Whole blood
F VAQUERIZAS_Lymph node

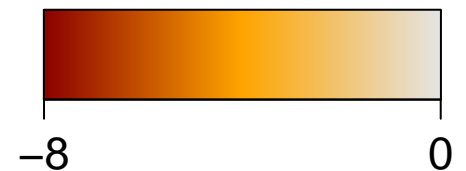


log(p.value)

TF Tissue



- B VAQUERIZAS_Whole brain
- A VAQUERIZAS_Spinal cord
- B VAQUERIZAS_Kidney
- I VAQUERIZAS_Adrenal cortex
- A VAQUERIZAS_Adrenal gland
- A VAQUERIZAS_Ovary
- C VAQUERIZAS_General
- C VAQUERIZAS_Testis
- F VAQUERIZAS_Heart
- H VAQUERIZAS_Fetal lung
- E VAQUERIZAS_Smooth muscle
- I VAQUERIZAS_Thyroid
- J VAQUERIZAS_Fetal thyroid
- H VAQUERIZAS_Liver
- H VAQUERIZAS_Fetal liver
- A VAQUERIZAS_Prostate
- I VAQUERIZAS_Pituitary
- A VAQUERIZAS_Appendix
- I VAQUERIZAS_Uterus
- B VAQUERIZAS_Fetal brain
- K VAQUERIZAS_Skeletal.muscle.psoas
- A VAQUERIZAS_Salivary gland
- G VAQUERIZAS_Bone marrow
- H VAQUERIZAS_Lung
- B VAQUERIZAS_Thymus
- O VAQUERIZAS_Skin
- O VAQUERIZAS_Placenta
- O VAQUERIZAS_Pancreas
- O VAQUERIZAS_Tongue
- O VAQUERIZAS_Trachea
- F VAQUERIZAS_Tonsil
- F VAQUERIZAS_Whole blood
- F VAQUERIZAS_Lymph node



p-value (Fisher)

