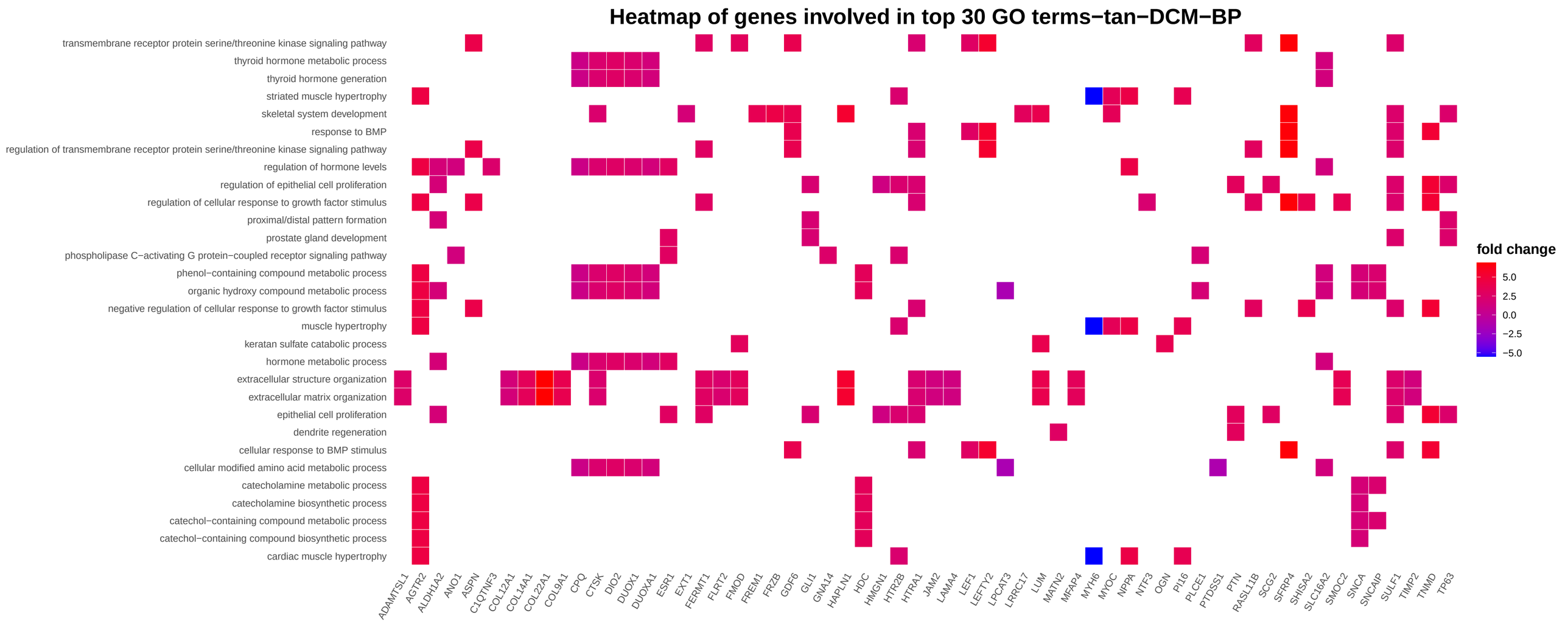
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thyroid hormone metabolic process
thyroid hormone generation
striated muscle hypertrophy
skeletal system development
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regulation of hormone levels
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regulation of cellular response to growth factor stimulus
proximal/distal pattern formation
prostate gland development
phospholipase C−activating G protein−coupled receptor signaling pathway
phenol−containing compound metabolic process
organic hydroxy compound metabolic process
negative regulation of cellular response to growth factor stimulus
muscle hypertrophy
keratan sulfate catabolic process
hormone metabolic process
extracellular structure organization
extracellular matrix organization
epithelial cell proliferation
dendrite regeneration
cellular response to BMP stimulus
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catecholamine metabolic process
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catechol−containing compound metabolic process
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cardiac muscle hypertrophy
ADAMTSL1
AGTR2
ALDH1A2
ANO1
ASPN
C1QTNF3
COL12A1
COL14A1
COL22A1
COL9A1
CPQ
CTSK
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FRZB
GDF6
GLI1
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HTR2B
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JAM2
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LEF1
LEFTY2
LPCAT3
LRRC17
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NTF3
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PI16
PLCE1
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PTN
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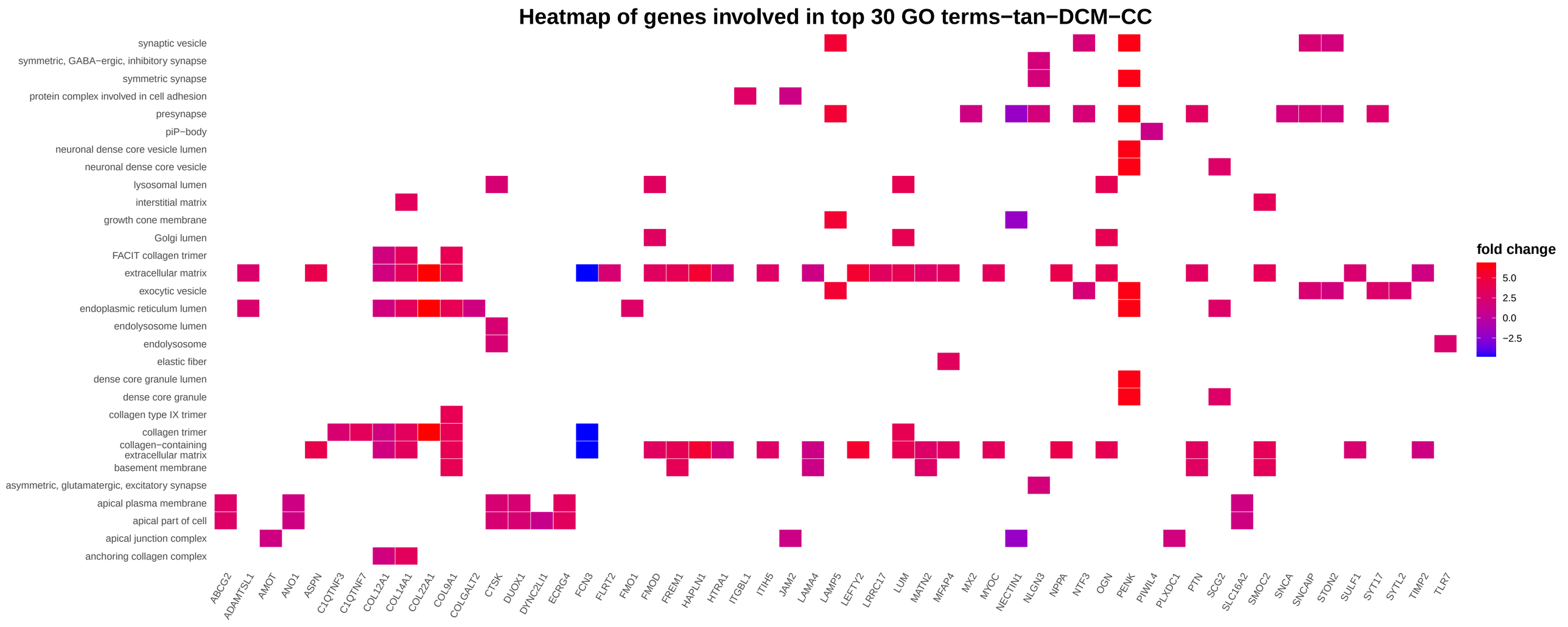
Heatmap of genes involved in top 30 GO terms−tan−DCM−CC
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symmetric, GABA−ergic, inhibitory synapse
symmetric synapse
protein complex involved in cell adhesion
presynapse
piP−body
neuronal dense core vesicle lumen
neuronal dense core vesicle
lysosomal lumen
interstitial matrix
growth cone membrane
Golgi lumen
FACIT collagen trimer
extracellular matrix
exocytic vesicle
endoplasmic reticulum lumen
endolysosome lumen
endolysosome
elastic fiber
dense core granule lumen
dense core granule
collagen type IX trimer
collagen trimer
collagen−containing extracellular matrix
basement membrane
asymmetric, glutamatergic, excitatory synapse
apical plasma membrane
apical part of cell
apical junction complex
anchoring collagen complex
ABCG2
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C1QTNF3
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COL14A1
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DYNC2LI1
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HTRA1
ITGBL1
ITIH5
JAM2
LAMA4
LAMP5
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NECTIN1
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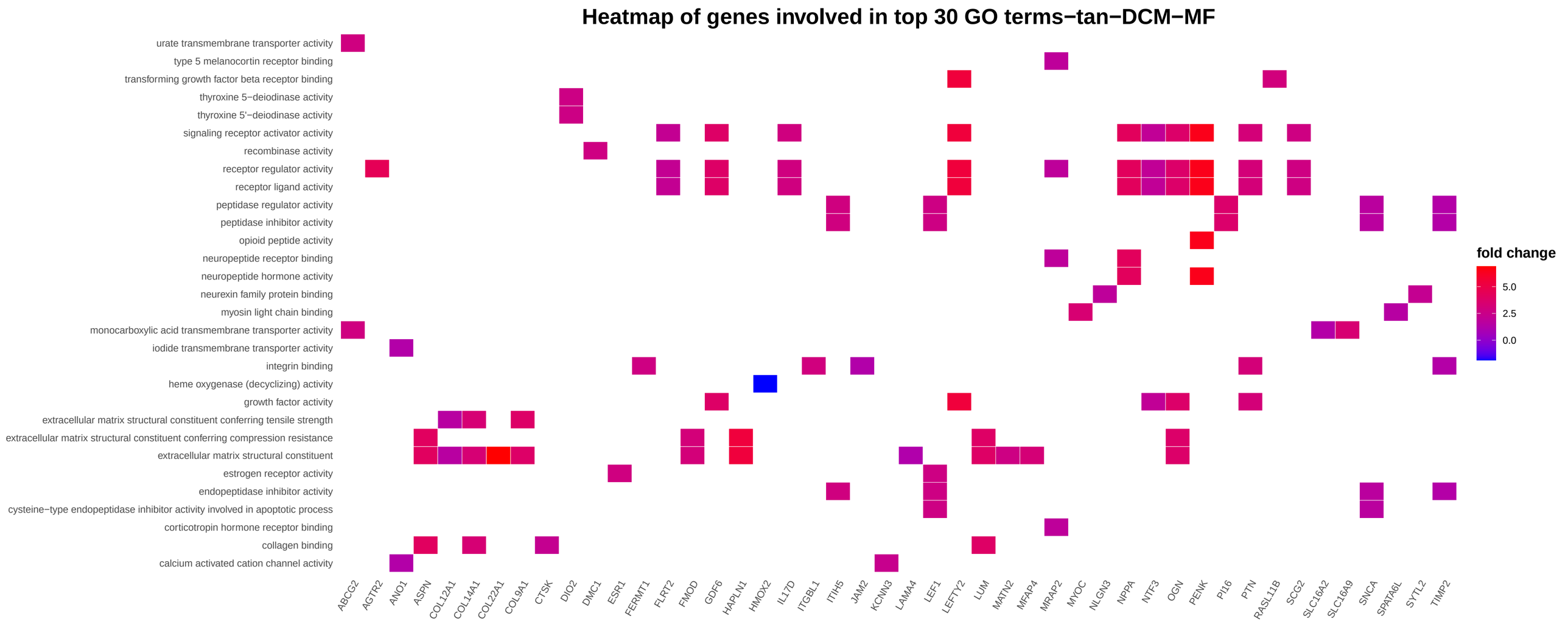
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iodide transmembrane transporter activity
integrin binding
heme oxygenase (decyclizing) activity
growth factor activity
extracellular matrix structural constituent conferring tensile strength
extracellular matrix structural constituent conferring compression resistance
extracellular matrix structural constituent
estrogen receptor activity
endopeptidase inhibitor activity
cysteine−type endopeptidase inhibitor activity involved in apoptotic process
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collagen binding
calcium activated cation channel activity
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AGTR2
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IL17D
ITGBL1
ITIH5
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LAMA4
LEF1
LEFTY2
LUM
MATN2
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MYOC
NLGN3
NPPA
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PI16
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RASL11B
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SLC16A9
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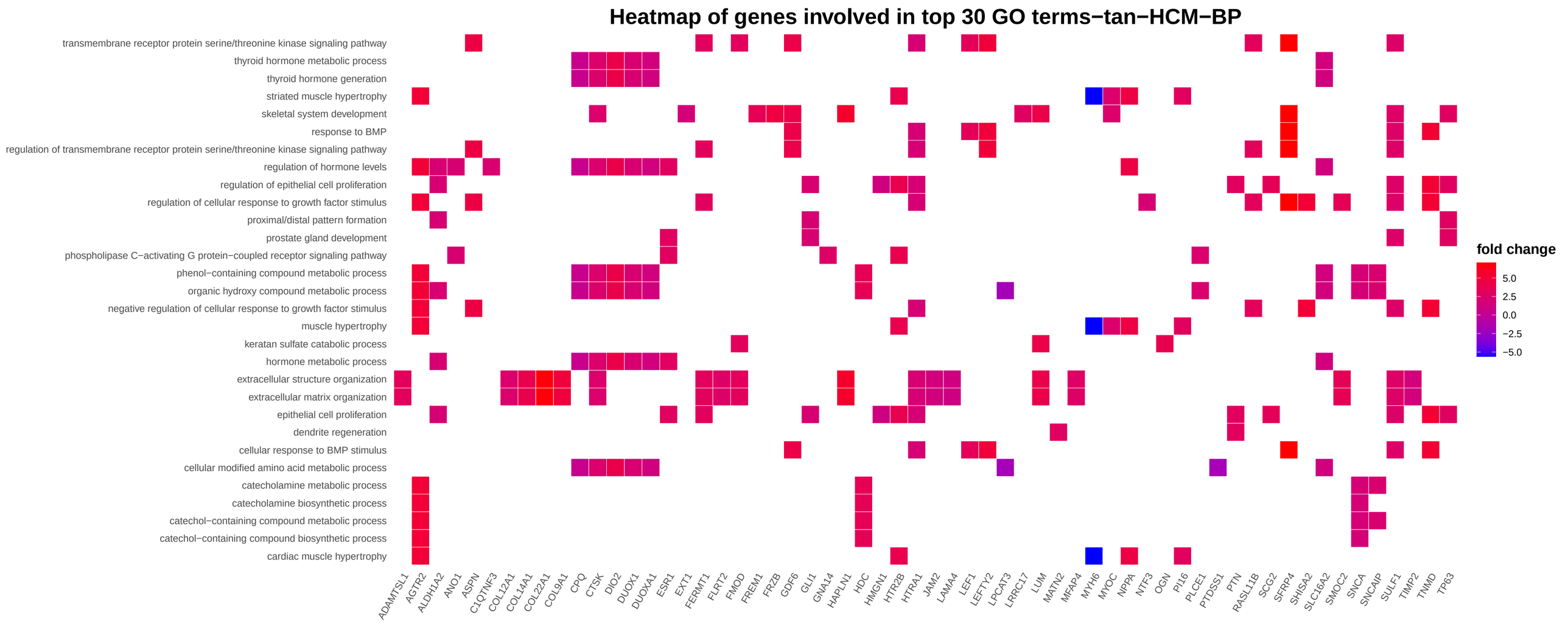
Heatmap of genes involved in top 30 GO terms−tan−DCM−ALL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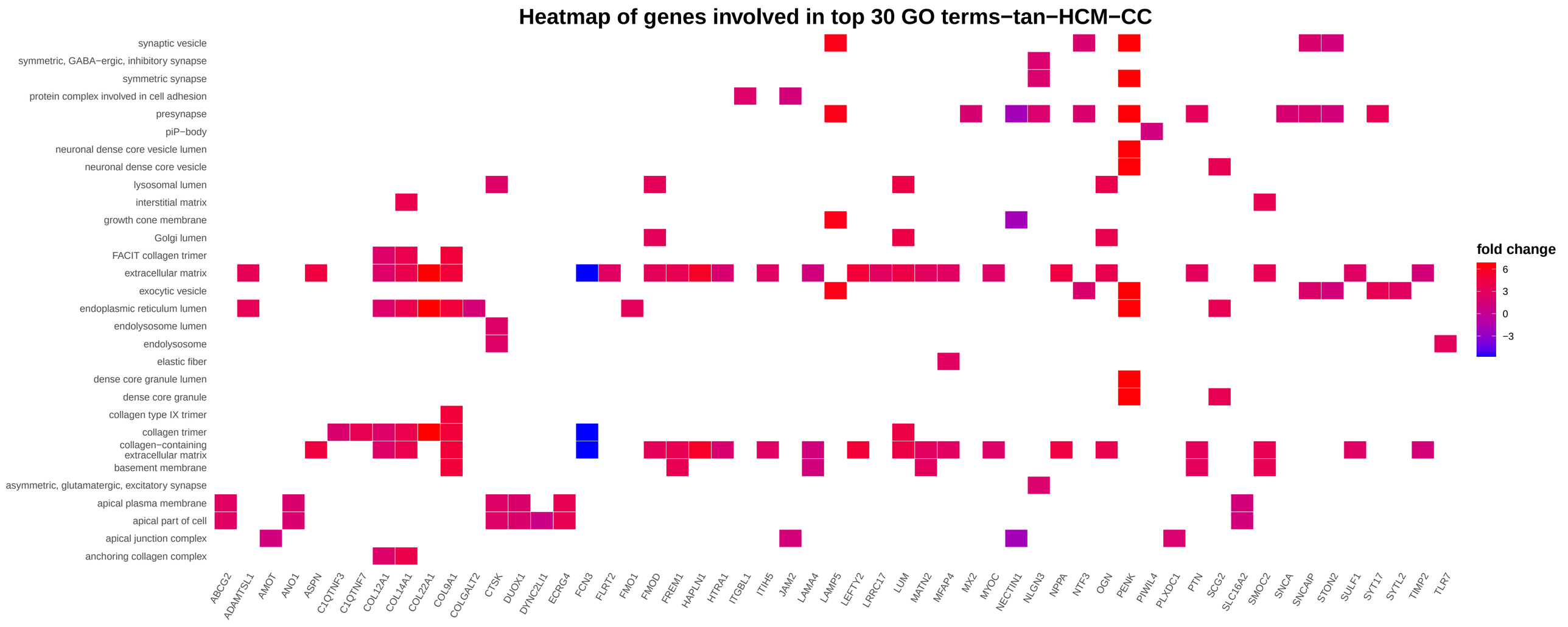
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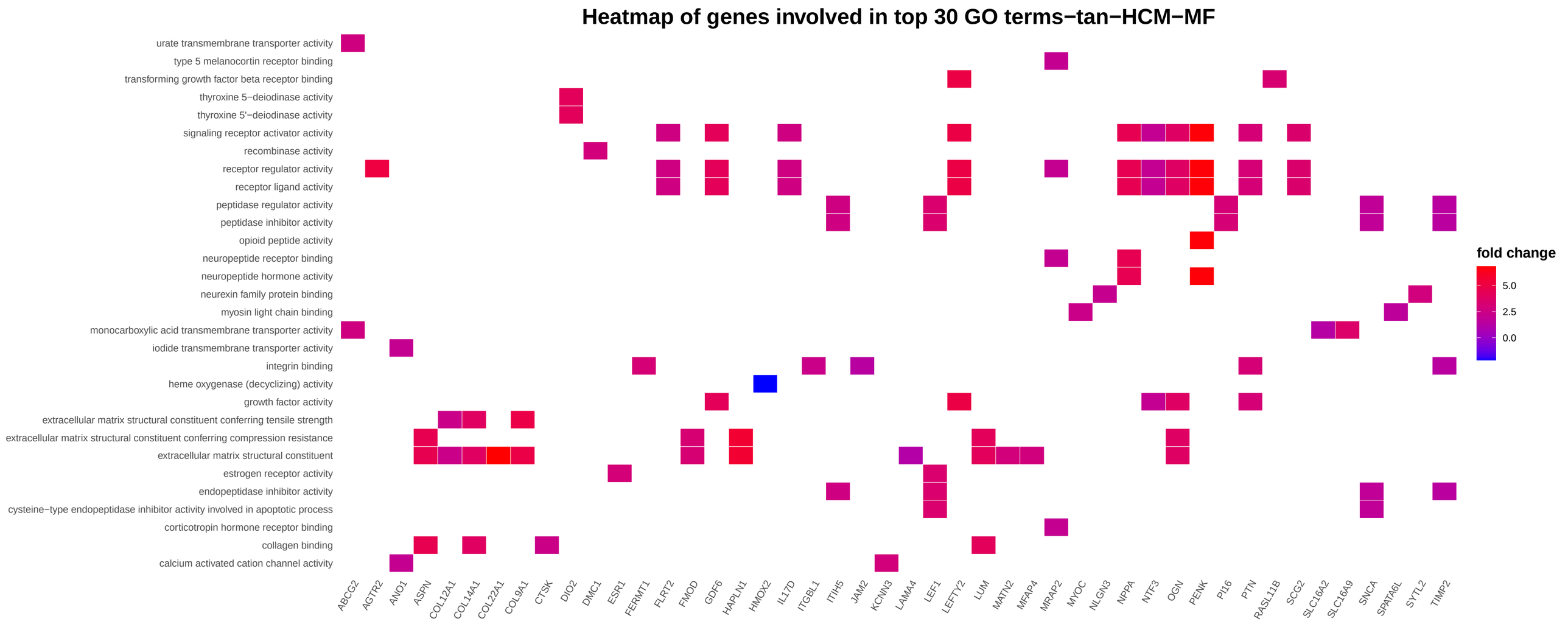
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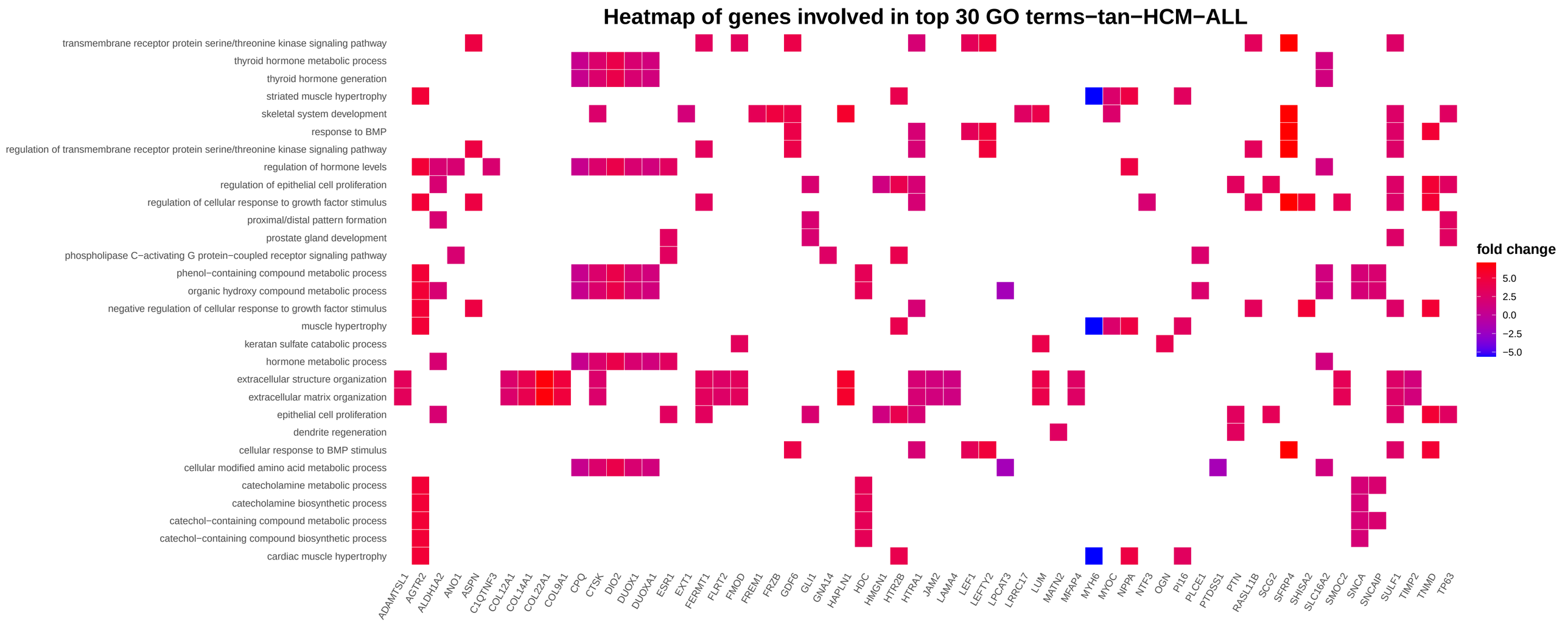
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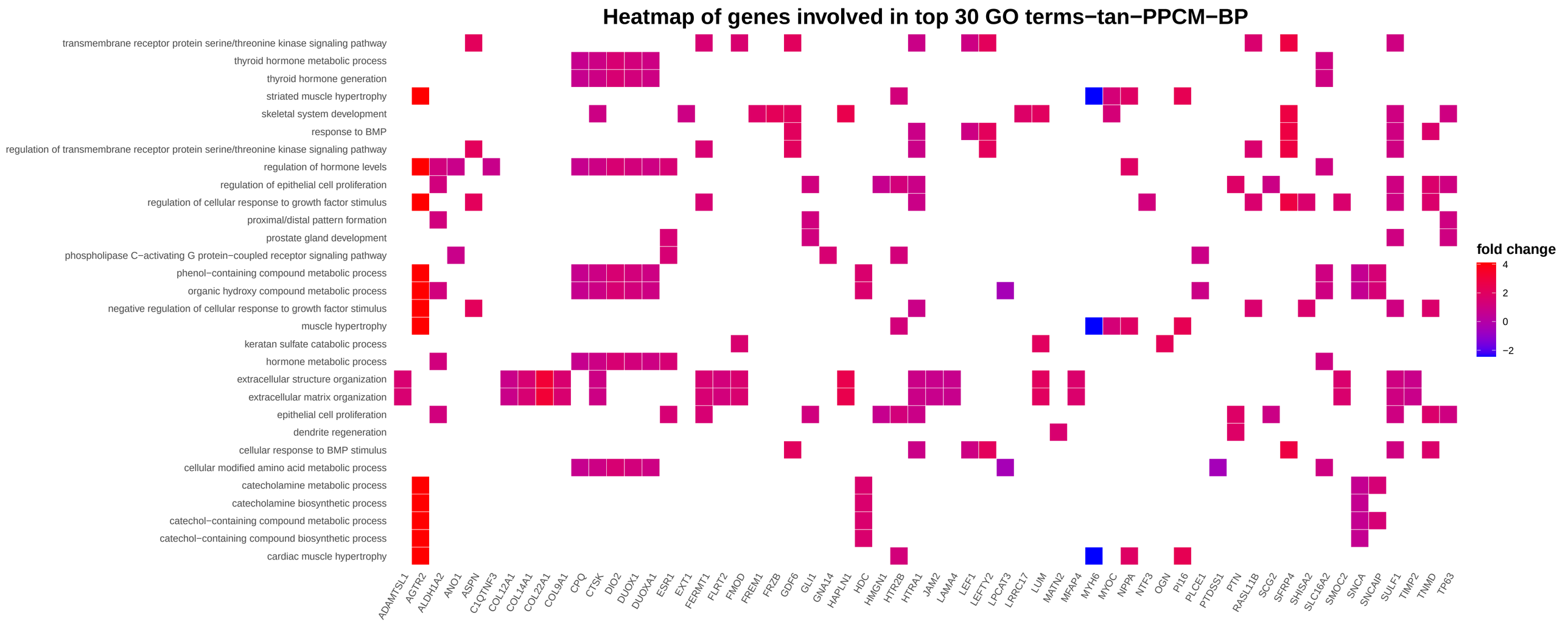
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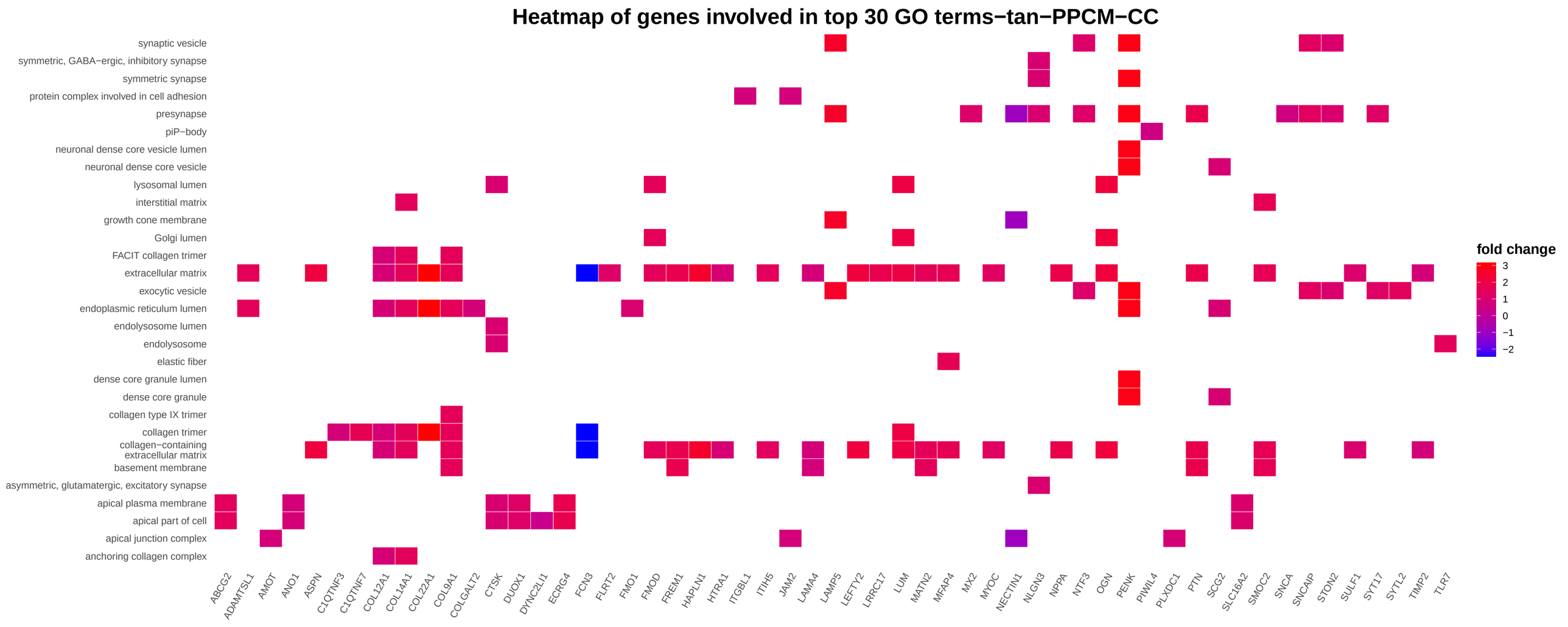
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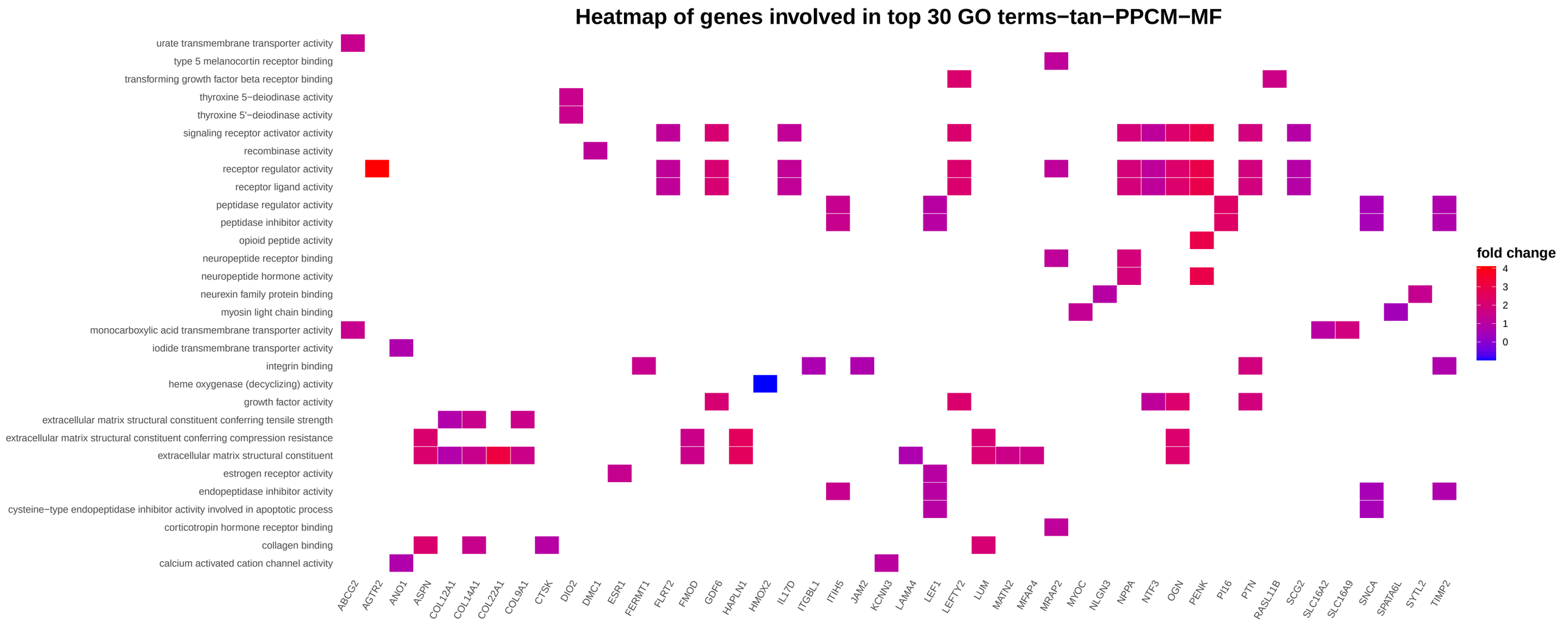
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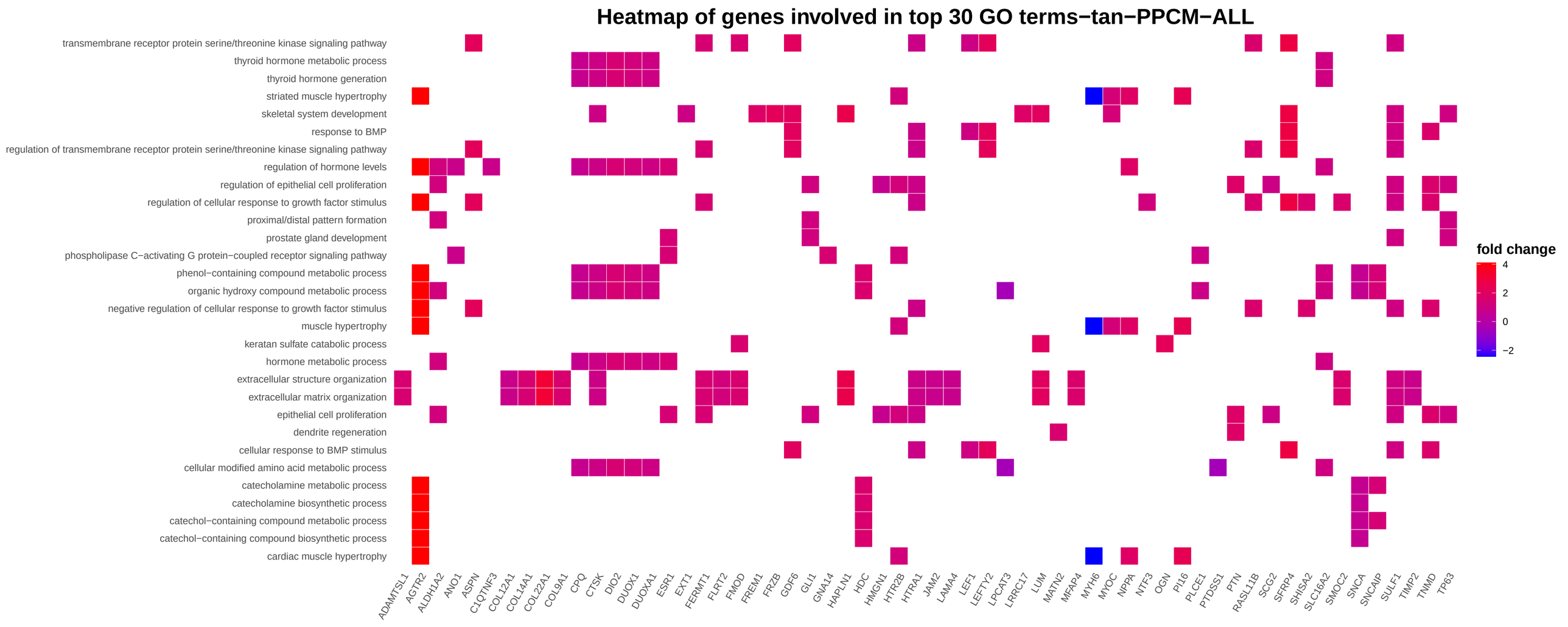
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Heatmap of genes involved in top 30 GO terms−darkred−DCM−BP
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T cell receptor signaling pathway
T cell differentiation in thymus
T cell differentiation
T cell activation
regulation of T cell differentiation
regulation of T cell activation
regulation of lymphocyte differentiation
regulation of lymphocyte activation
regulation of leukocyte cell−cell adhesion
regulation of leukocyte activation
regulation of cell−cell adhesion
positive T cell selection
positive regulation of T cell activation
positive regulation of lymphocyte activation
positive regulation of leukocyte cell−cell adhesion
positive regulation of leukocyte activation
positive regulation of cell adhesion
positive regulation of cell activation
positive regulation of cell−cell adhesion
lymphocyte differentiation
leukocyte differentiation
leukocyte cell−cell adhesion
immune response−regulating signaling pathway
immune response−regulating cell surface receptor signaling pathway
immune response−activating signal transduction
immune response−activating cell surface receptor signaling pathway
antigen receptor−mediated signaling pathway
adaptive immune response
activation of immune response
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BST1
CAMK4
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
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ITGAL
LCK
PRF1
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RUNX3
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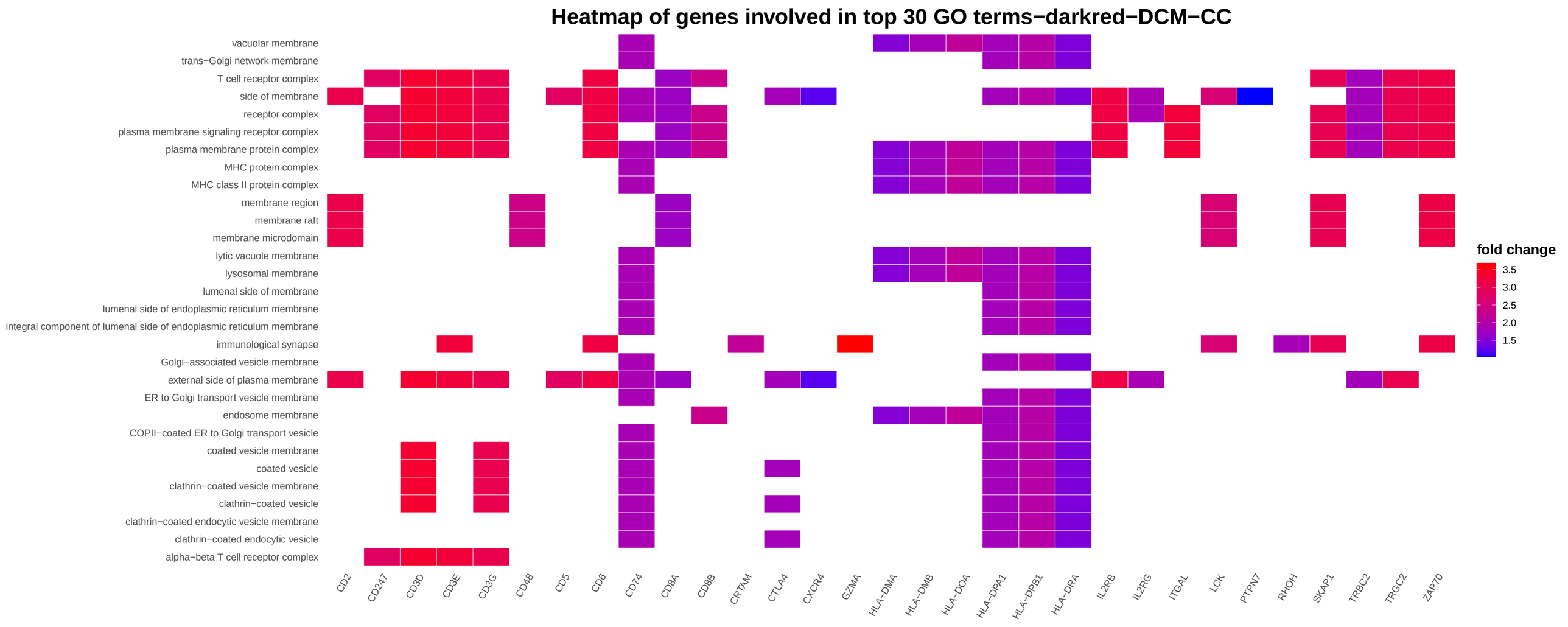
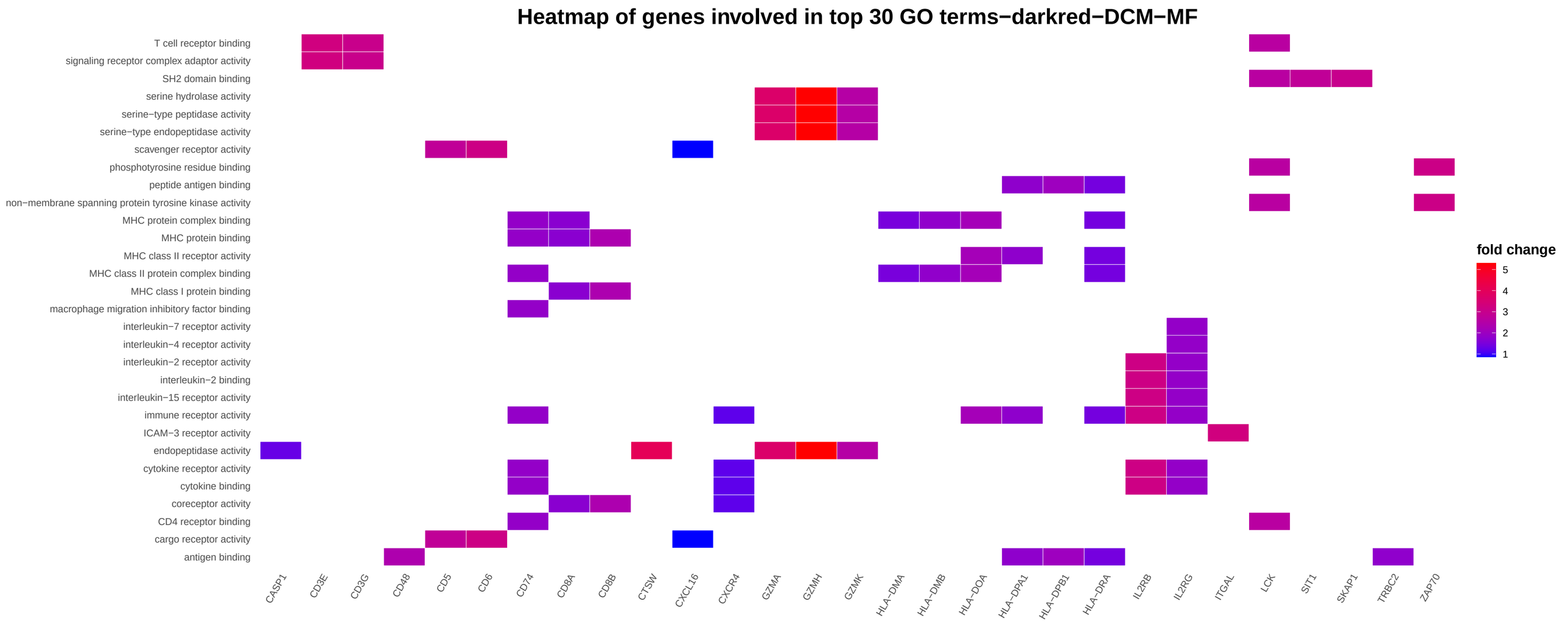
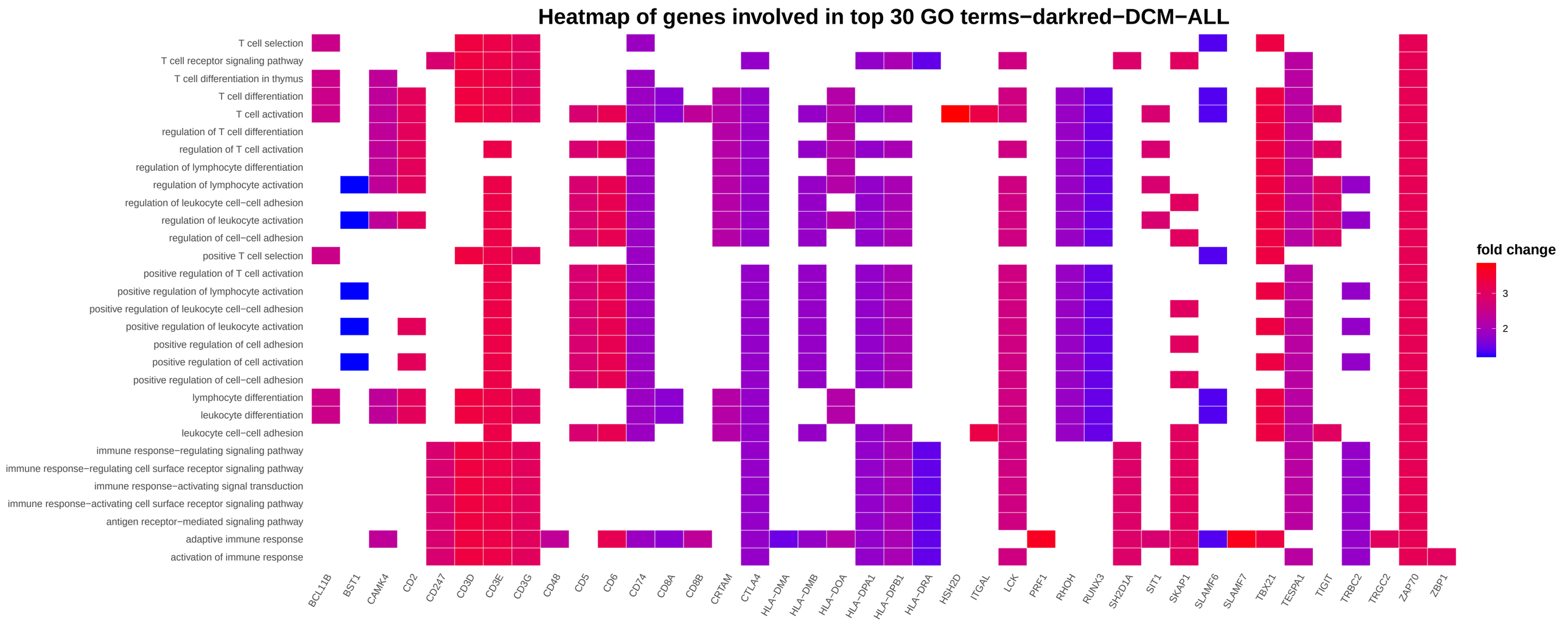
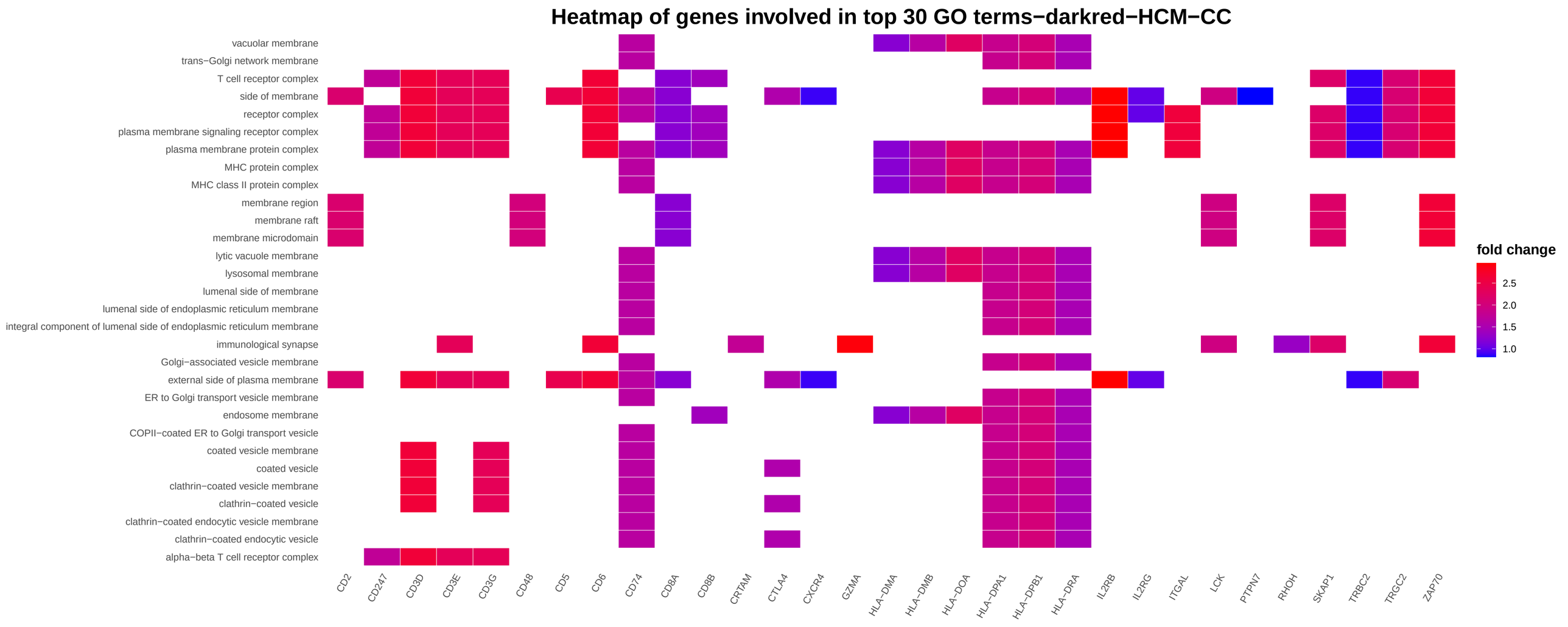
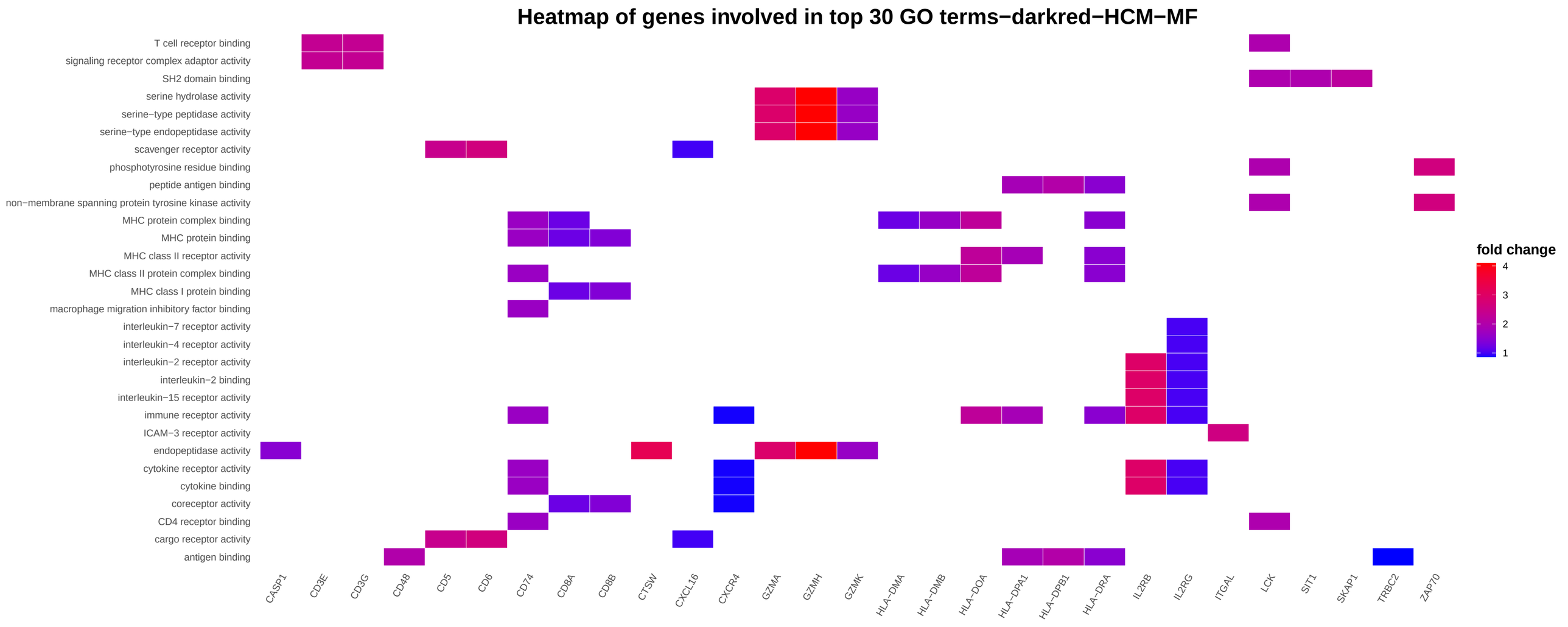

Heatmap of genes involved in top 30 GO terms−darkred−DCM−CC
vacuolar membrane
trans−Golgi network membrane
T cell receptor complex
side of membrane
receptor complex
plasma membrane signaling receptor complex
plasma membrane protein complex
MHC protein complex
MHC class II protein complex
membrane region
membrane raft
membrane microdomain
lytic vacuole membrane
lysosomal membrane
lumenal side of membrane
lumenal side of endoplasmic reticulum membrane
integral component of lumenal side of endoplasmic reticulum membrane
immunological synapse
Golgi−associated vesicle membrane
external side of plasma membrane
ER to Golgi transport vesicle membrane
endosome membrane
COPII−coated ER to Golgi transport vesicle
coated vesicle membrane
coated vesicle
clathrin−coated vesicle membrane
clathrin−coated vesicle
clathrin−coated endocytic vesicle membrane
clathrin−coated endocytic vesicle
alpha−beta T cell receptor complex
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
CXCR4
GZMA
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
IL2RB
IL2RG
ITGAL
LCK
PTPN7
RHOH
SKAP1
TRBC2
TRGC2
ZAP70
fold change
3.5
3.0
2.5
2.0
1.5


Heatmap of genes involved in top 30 GO terms−darkred−DCM−MF
T cell receptor binding
signaling receptor complex adaptor activity
SH2 domain binding
serine hydrolase activity
serine−type peptidase activity
serine−type endopeptidase activity
scavenger receptor activity
phosphotyrosine residue binding
peptide antigen binding
non−membrane spanning protein tyrosine kinase activity
MHC protein complex binding
MHC protein binding
MHC class II receptor activity
MHC class II protein complex binding
MHC class I protein binding
macrophage migration inhibitory factor binding
interleukin−7 receptor activity
interleukin−4 receptor activity
interleukin−2 receptor activity
interleukin−2 binding
interleukin−15 receptor activity
immune receptor activity
ICAM−3 receptor activity
endopeptidase activity
cytokine receptor activity
cytokine binding
coreceptor activity
CD4 receptor binding
cargo receptor activity
antigen binding
CASP1
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CTSW
CXCL16
CXCR4
GZMA
GZMH
GZMK
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
IL2RB
IL2RG
ITGAL
LCK
SIT1
SKAP1
TRBC2
ZAP70
fold change
5
4
3
2
1


Heatmap of genes involved in top 30 GO terms−darkred−DCM−ALL
T cell selection
T cell receptor signaling pathway
T cell differentiation in thymus
T cell differentiation
T cell activation
regulation of T cell differentiation
regulation of T cell activation
regulation of lymphocyte differentiation
regulation of lymphocyte activation
regulation of leukocyte cell−cell adhesion
regulation of leukocyte activation
regulation of cell−cell adhesion
positive T cell selection
positive regulation of T cell activation
positive regulation of lymphocyte activation
positive regulation of leukocyte cell−cell adhesion
positive regulation of leukocyte activation
positive regulation of cell adhesion
positive regulation of cell activation
positive regulation of cell−cell adhesion
lymphocyte differentiation
leukocyte differentiation
leukocyte cell−cell adhesion
immune response−regulating signaling pathway
immune response−regulating cell surface receptor signaling pathway
immune response−activating signal transduction
immune response−activating cell surface receptor signaling pathway
antigen receptor−mediated signaling pathway
adaptive immune response
activation of immune response
BCL11B
BST1
CAMK4
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
HSH2D
ITGAL
LCK
PRF1
RHOH
RUNX3
SH2D1A
SIT1
SKAP1
SLAMF6
SLAMF7
TBX21
TESPA1
TIGIT
TRBC2
TRGC2
ZAP70
ZBP1
fold change
3
2


Heatmap of genes involved in top 30 GO terms−darkred−HCM−BP
T cell selection
T cell receptor signaling pathway
T cell differentiation in thymus
T cell differentiation
T cell activation
regulation of T cell differentiation
regulation of T cell activation
regulation of lymphocyte differentiation
regulation of lymphocyte activation
regulation of leukocyte cell−cell adhesion
regulation of leukocyte activation
regulation of cell−cell adhesion
positive T cell selection
positive regulation of T cell activation
positive regulation of lymphocyte activation
positive regulation of leukocyte cell−cell adhesion
positive regulation of leukocyte activation
positive regulation of cell adhesion
positive regulation of cell activation
positive regulation of cell−cell adhesion
lymphocyte differentiation
leukocyte differentiation
leukocyte cell−cell adhesion
immune response−regulating signaling pathway
immune response−regulating cell surface receptor signaling pathway
immune response−activating signal transduction
immune response−activating cell surface receptor signaling pathway
antigen receptor−mediated signaling pathway
adaptive immune response
activation of immune response
BCL11B
BST1
CAMK4
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
HSH2D
ITGAL
LCK
PRF1
RHOH
RUNX3
SH2D1A
SIT1
SKAP1
SLAMF6
SLAMF7
TBX21
TESPA1
TIGIT
TRBC2
TRGC2
ZAP70
ZBP1
fold change
3
2
1


Heatmap of genes involved in top 30 GO terms−darkred−HCM−CC
vacuolar membrane
trans−Golgi network membrane
T cell receptor complex
side of membrane
receptor complex
plasma membrane signaling receptor complex
plasma membrane protein complex
MHC protein complex
MHC class II protein complex
membrane region
membrane raft
membrane microdomain
lytic vacuole membrane
lysosomal membrane
lumenal side of membrane
lumenal side of endoplasmic reticulum membrane
integral component of lumenal side of endoplasmic reticulum membrane
immunological synapse
Golgi−associated vesicle membrane
external side of plasma membrane
ER to Golgi transport vesicle membrane
endosome membrane
COPII−coated ER to Golgi transport vesicle
coated vesicle membrane
coated vesicle
clathrin−coated vesicle membrane
clathrin−coated vesicle
clathrin−coated endocytic vesicle membrane
clathrin−coated endocytic vesicle
alpha−beta T cell receptor complex
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
CXCR4
GZMA
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
IL2RB
IL2RG
ITGAL
LCK
PTPN7
RHOH
SKAP1
TRBC2
TRGC2
ZAP70
fold change
2.5
2.0
1.5
1.0


Heatmap of genes involved in top 30 GO terms−darkred−HCM−MF
T cell receptor binding
signaling receptor complex adaptor activity
SH2 domain binding
serine hydrolase activity
serine−type peptidase activity
serine−type endopeptidase activity
scavenger receptor activity
phosphotyrosine residue binding
peptide antigen binding
non−membrane spanning protein tyrosine kinase activity
MHC protein complex binding
MHC protein binding
MHC class II receptor activity
MHC class II protein complex binding
MHC class I protein binding
macrophage migration inhibitory factor binding
interleukin−7 receptor activity
interleukin−4 receptor activity
interleukin−2 receptor activity
interleukin−2 binding
interleukin−15 receptor activity
immune receptor activity
ICAM−3 receptor activity
endopeptidase activity
cytokine receptor activity
cytokine binding
coreceptor activity
CD4 receptor binding
cargo receptor activity
antigen binding
CASP1
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CTSW
CXCL16
CXCR4
GZMA
GZMH
GZMK
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
IL2RB
IL2RG
ITGAL
LCK
SIT1
SKAP1
TRBC2
ZAP70
fold change
4
3
2
1


Heatmap of genes involved in top 30 GO terms−darkred−HCM−ALL
T cell selection
T cell receptor signaling pathway
T cell differentiation in thymus
T cell differentiation
T cell activation
regulation of T cell differentiation
regulation of T cell activation
regulation of lymphocyte differentiation
regulation of lymphocyte activation
regulation of leukocyte cell−cell adhesion
regulation of leukocyte activation
regulation of cell−cell adhesion
positive T cell selection
positive regulation of T cell activation
positive regulation of lymphocyte activation
positive regulation of leukocyte cell−cell adhesion
positive regulation of leukocyte activation
positive regulation of cell adhesion
positive regulation of cell activation
positive regulation of cell−cell adhesion
lymphocyte differentiation
leukocyte differentiation
leukocyte cell−cell adhesion
immune response−regulating signaling pathway
immune response−regulating cell surface receptor signaling pathway
immune response−activating signal transduction
immune response−activating cell surface receptor signaling pathway
antigen receptor−mediated signaling pathway
adaptive immune response
activation of immune response
BCL11B
BST1
CAMK4
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
HSH2D
ITGAL
LCK
PRF1
RHOH
RUNX3
SH2D1A
SIT1
SKAP1
SLAMF6
SLAMF7
TBX21
TESPA1
TIGIT
TRBC2
TRGC2
ZAP70
ZBP1
fold change
3
2
1


Heatmap of genes involved in top 30 GO terms−darkred−PPCM−BP
T cell selection
T cell receptor signaling pathway
T cell differentiation in thymus
T cell differentiation
T cell activation
regulation of T cell differentiation
regulation of T cell activation
regulation of lymphocyte differentiation
regulation of lymphocyte activation
regulation of leukocyte cell−cell adhesion
regulation of leukocyte activation
regulation of cell−cell adhesion
positive T cell selection
positive regulation of T cell activation
positive regulation of lymphocyte activation
positive regulation of leukocyte cell−cell adhesion
positive regulation of leukocyte activation
positive regulation of cell adhesion
positive regulation of cell activation
positive regulation of cell−cell adhesion
lymphocyte differentiation
leukocyte differentiation
leukocyte cell−cell adhesion
immune response−regulating signaling pathway
immune response−regulating cell surface receptor signaling pathway
immune response−activating signal transduction
immune response−activating cell surface receptor signaling pathway
antigen receptor−mediated signaling pathway
adaptive immune response
activation of immune response
BCL11B
BST1
CAMK4
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
HSH2D
ITGAL
LCK
PRF1
RHOH
RUNX3
SH2D1A
SIT1
SKAP1
SLAMF6
SLAMF7
TBX21
TESPA1
TIGIT
TRBC2
TRGC2
ZAP70
ZBP1
fold change
2.0
1.5
1.0
0.5


Heatmap of genes involved in top 30 GO terms−darkred−PPCM−CC
vacuolar membrane
trans−Golgi network membrane
T cell receptor complex
side of membrane
receptor complex
plasma membrane signaling receptor complex
plasma membrane protein complex
MHC protein complex
MHC class II protein complex
membrane region
membrane raft
membrane microdomain
lytic vacuole membrane
lysosomal membrane
lumenal side of membrane
lumenal side of endoplasmic reticulum membrane
integral component of lumenal side of endoplasmic reticulum membrane
immunological synapse
Golgi−associated vesicle membrane
external side of plasma membrane
ER to Golgi transport vesicle membrane
endosome membrane
COPII−coated ER to Golgi transport vesicle
coated vesicle membrane
coated vesicle
clathrin−coated vesicle membrane
clathrin−coated vesicle
clathrin−coated endocytic vesicle membrane
clathrin−coated endocytic vesicle
alpha−beta T cell receptor complex
CD2
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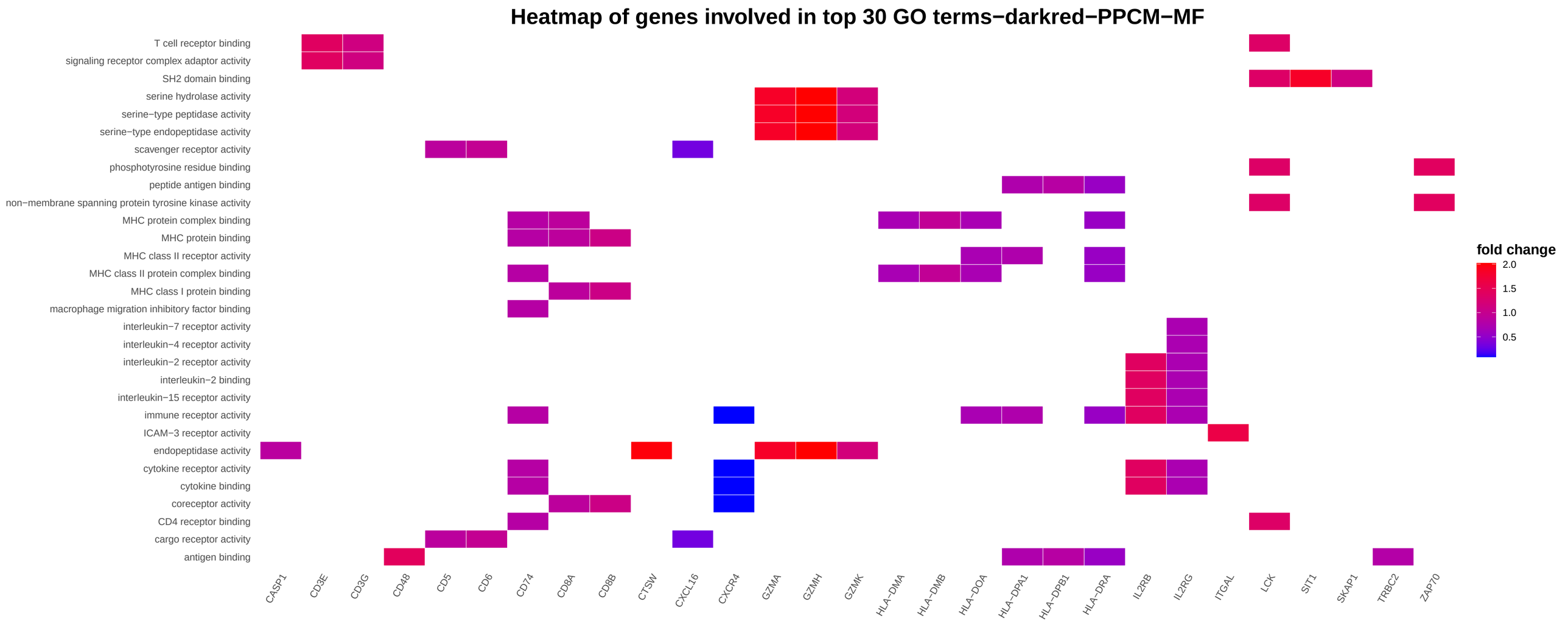
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
CXCR4
GZMA
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
IL2RB
IL2RG
ITGAL
LCK
PTPN7
RHOH
SKAP1
TRBC2
TRGC2
ZAP70
fold change
1.5
1.0
0.5


Heatmap of genes involved in top 30 GO terms−darkred−PPCM−MF
T cell receptor binding
signaling receptor complex adaptor activity
SH2 domain binding
serine hydrolase activity
serine−type peptidase activity
serine−type endopeptidase activity
scavenger receptor activity
phosphotyrosine residue binding
peptide antigen binding
non−membrane spanning protein tyrosine kinase activity
MHC protein complex binding
MHC protein binding
MHC class II receptor activity
MHC class II protein complex binding
MHC class I protein binding
macrophage migration inhibitory factor binding
interleukin−7 receptor activity
interleukin−4 receptor activity
interleukin−2 receptor activity
interleukin−2 binding
interleukin−15 receptor activity
immune receptor activity
ICAM−3 receptor activity
endopeptidase activity
cytokine receptor activity
cytokine binding
coreceptor activity
CD4 receptor binding
cargo receptor activity
antigen binding
CASP1
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CTSW
CXCL16
CXCR4
GZMA
GZMH
GZMK
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
IL2RB
IL2RG
ITGAL
LCK
SIT1
SKAP1
TRBC2
ZAP70
fold change
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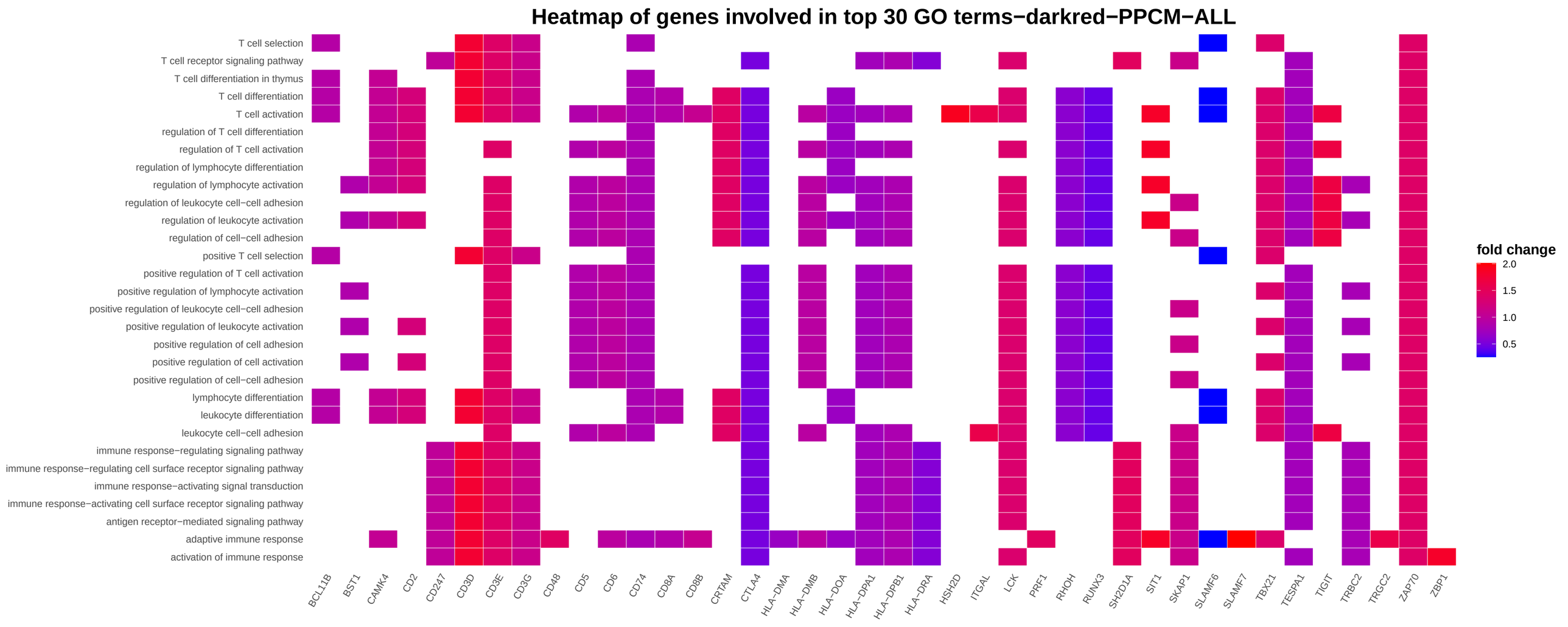
1.5
1.0
0.5


Heatmap of genes involved in top 30 GO terms−darkred−PPCM−ALL
T cell selection
T cell receptor signaling pathway
T cell differentiation in thymus
T cell differentiation
T cell activation
regulation of T cell differentiation
regulation of T cell activation
regulation of lymphocyte differentiation
regulation of lymphocyte activation
regulation of leukocyte cell−cell adhesion
regulation of leukocyte activation
regulation of cell−cell adhesion
positive T cell selection
positive regulation of T cell activation
positive regulation of lymphocyte activation
positive regulation of leukocyte cell−cell adhesion
positive regulation of leukocyte activation
positive regulation of cell adhesion
positive regulation of cell activation
positive regulation of cell−cell adhesion
lymphocyte differentiation
leukocyte differentiation
leukocyte cell−cell adhesion
immune response−regulating signaling pathway
immune response−regulating cell surface receptor signaling pathway
immune response−activating signal transduction
immune response−activating cell surface receptor signaling pathway
antigen receptor−mediated signaling pathway
adaptive immune response
activation of immune response
BCL11B
BST1
CAMK4
CD2
CD247
CD3D
CD3E
CD3G
CD48
CD5
CD6
CD74
CD8A
CD8B
CRTAM
CTLA4
HLA−DMA
HLA−DMB
HLA−DOA
HLA−DPA1
HLA−DPB1
HLA−DRA
HSH2D
ITGAL
LCK
PRF1
RHOH
RUNX3
SH2D1A
SIT1
SKAP1
SLAMF6
SLAMF7
TBX21
TESPA1
TIGIT
TRBC2
TRGC2
ZAP70
ZBP1
fold change
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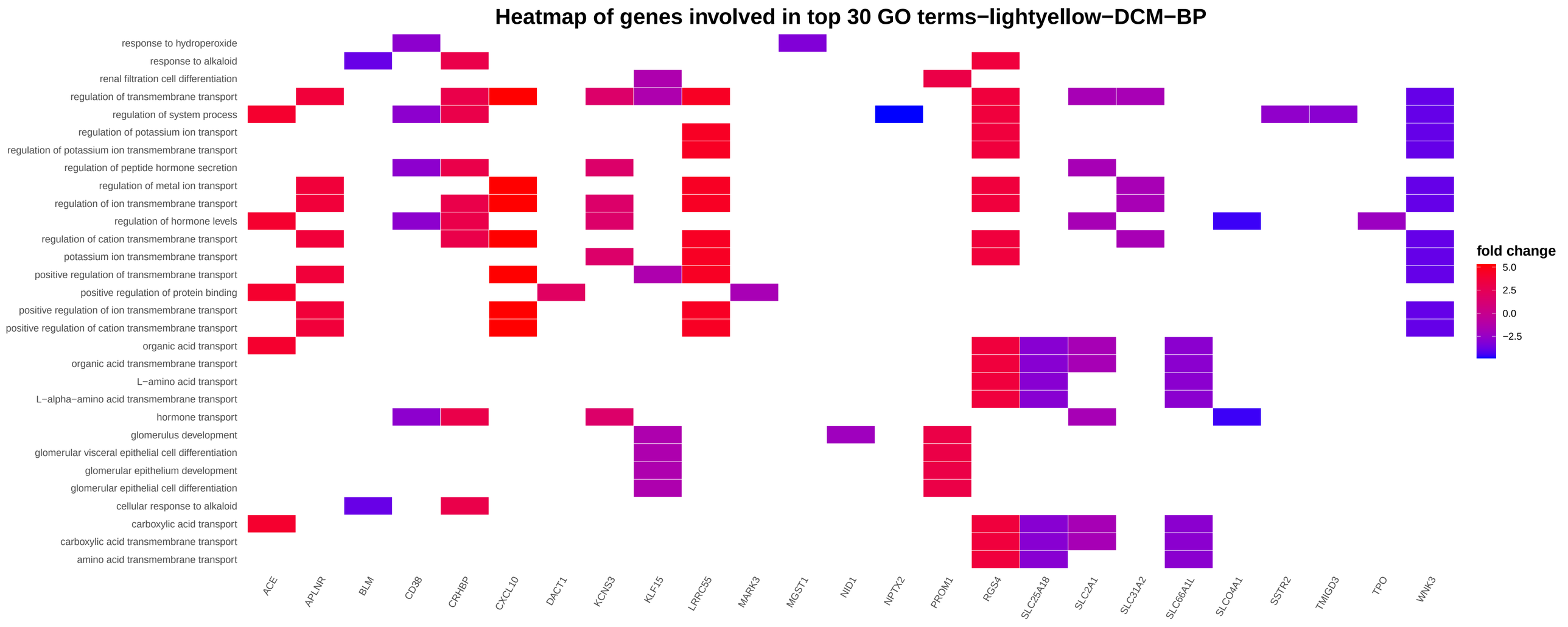
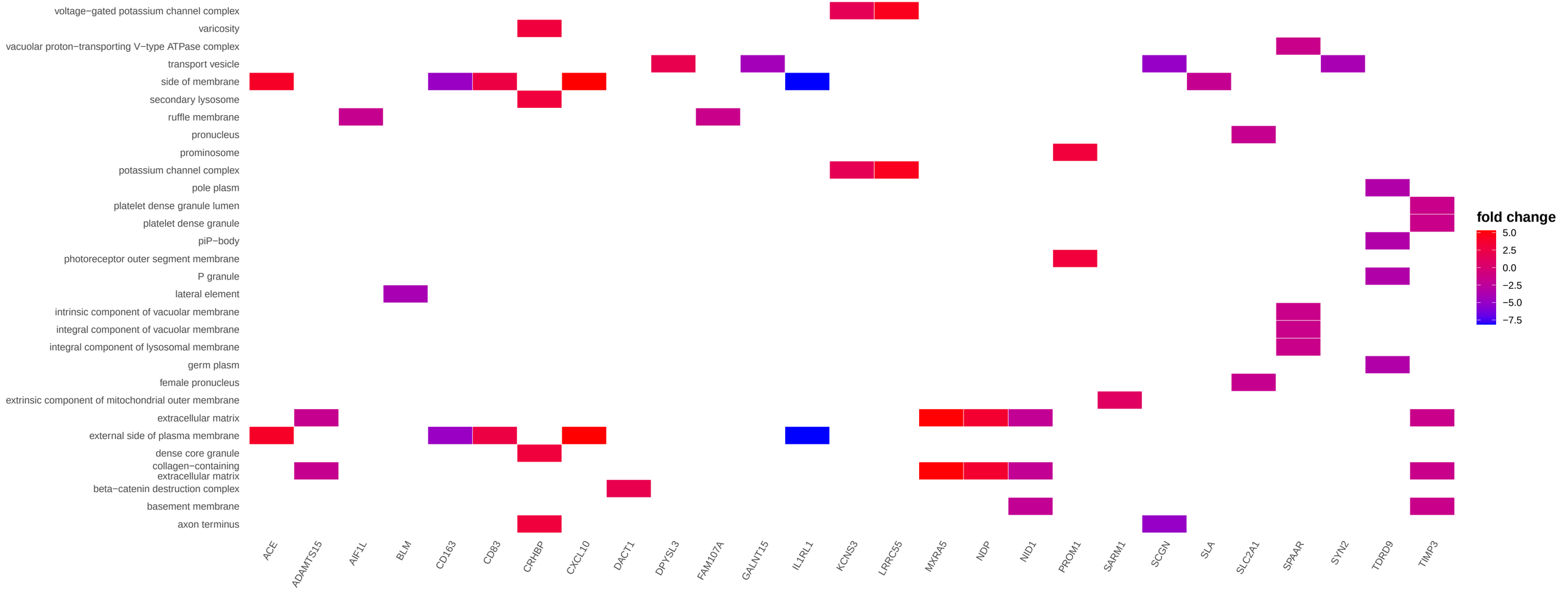
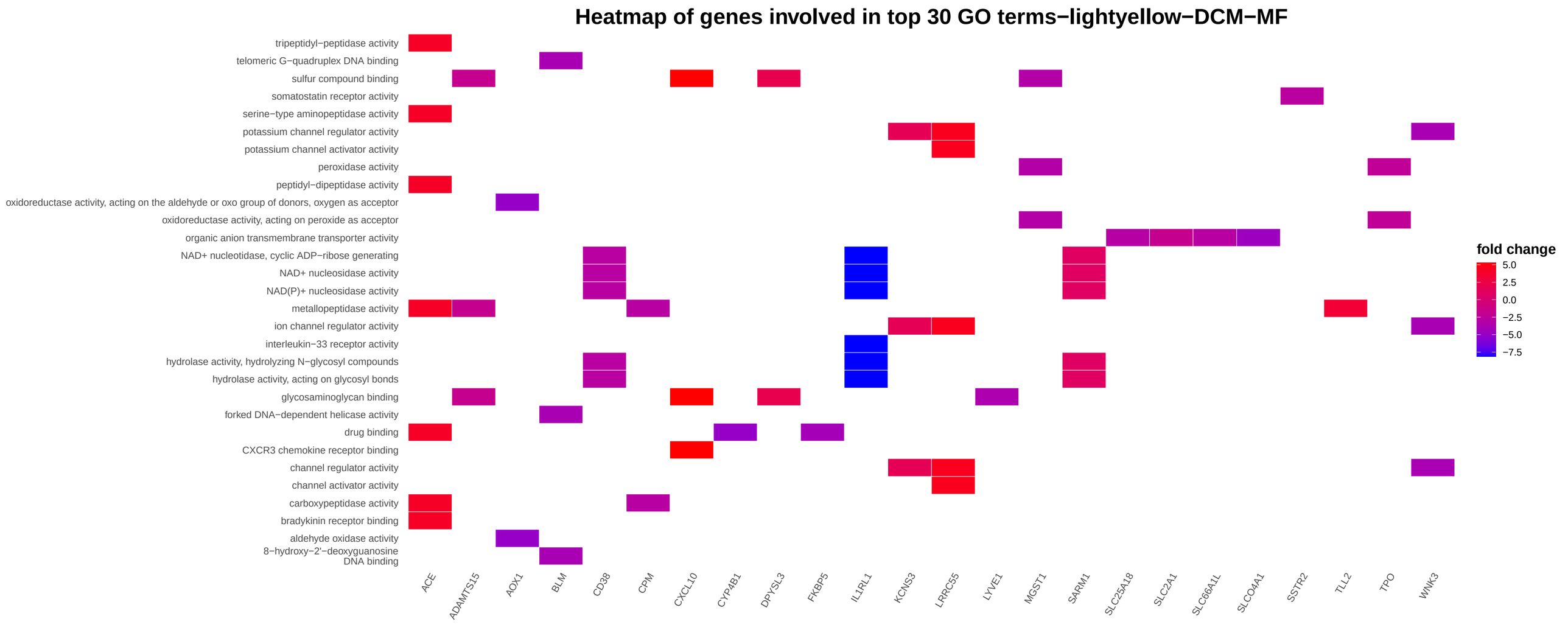
1.5
1.0
0.5


Heatmap of genes involved in top 30 GO terms−lightyellow−DCM−BP
response to hydroperoxide
response to alkaloid
renal filtration cell differentiation
regulation of transmembrane transport
regulation of system process
regulation of potassium ion transport
regulation of potassium ion transmembrane transport
regulation of peptide hormone secretion
regulation of metal ion transport
regulation of ion transmembrane transport
regulation of hormone levels
regulation of cation transmembrane transport
potassium ion transmembrane transport
positive regulation of transmembrane transport
positive regulation of protein binding
positive regulation of ion transmembrane transport
positive regulation of cation transmembrane transport
organic acid transport
organic acid transmembrane transport
L−amino acid transport
L−alpha−amino acid transmembrane transport
hormone transport
glomerulus development
glomerular visceral epithelial cell differentiation
glomerular epithelium development
glomerular epithelial cell differentiation
cellular response to alkaloid
carboxylic acid transport
carboxylic acid transmembrane transport
amino acid transmembrane transport
ACE
APLNR
BLM
CD38
CRHBP
CXCL10
DACT1
KCNS3
KLF15
LRRC55
MARK3
MGST1
NID1
NPTX2
PROM1
RGS4
SLC25A18
SLC2A1
SLC31A2
SLC66A1L
SLCO4A1
SSTR2
TMIGD3
TPO
WNK3
fold change
5.0
2.5
0.0
−2.5

Heatmap of genes involved in top 30 GO terms−lightyellow−DCM−CC




Heatmap of genes involved in top 30 GO terms−lightyellow−DCM−MF
tripeptidyl−peptidase activity
telomeric G−quadruplex DNA binding
sulfur compound binding
somatostatin receptor activity
serine−type aminopeptidase activity
potassium channel regulator activity
potassium channel activator activity
peroxidase activity
peptidyl−dipeptidase activity
oxidoreductase activity, acting on the aldehyde or oxo group of donors, oxygen as acceptor
oxidoreductase activity, acting on peroxide as acceptor
organic anion transmembrane transporter activity
NAD+ nucleotidase, cyclic ADP−ribose generating
NAD+ nucleosidase activity
NAD(P)+ nucleosidase activity
metallopeptidase activity
ion channel regulator activity
interleukin−33 receptor activity
hydrolase activity, hydrolyzing N−glycosyl compounds
hydrolase activity, acting on glycosyl bonds
glycosaminoglycan binding
forked DNA−dependent helicase activity
drug binding
CXCR3 chemokine receptor binding
channel regulator activity
channel activator activity
carboxypeptidase activity
bradykinin receptor binding
aldehyde oxidase activity
8−hydroxy−2'−deoxyguanosine DNA binding
ACE
ADAMTS15
AOX1
BLM
CD38
CPM
CXCL10
CYP4B1
DPYSL3
FKBP5
IL1RL1
KCNS3
LRRC55
LYVE1
MGST1
SARM1
SLC25A18
SLC2A1
SLC66A1L
SLCO4A1
SSTR2
TLL2
TPO
WNK3
fold change
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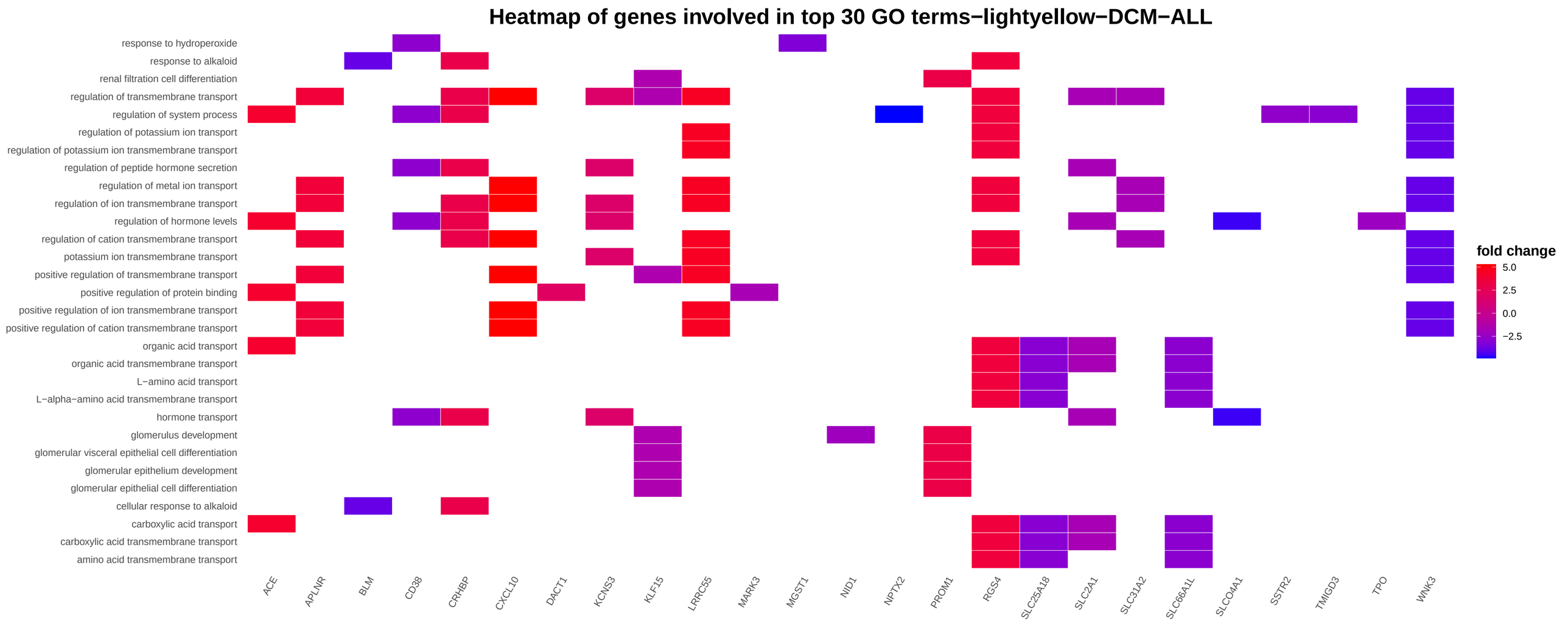
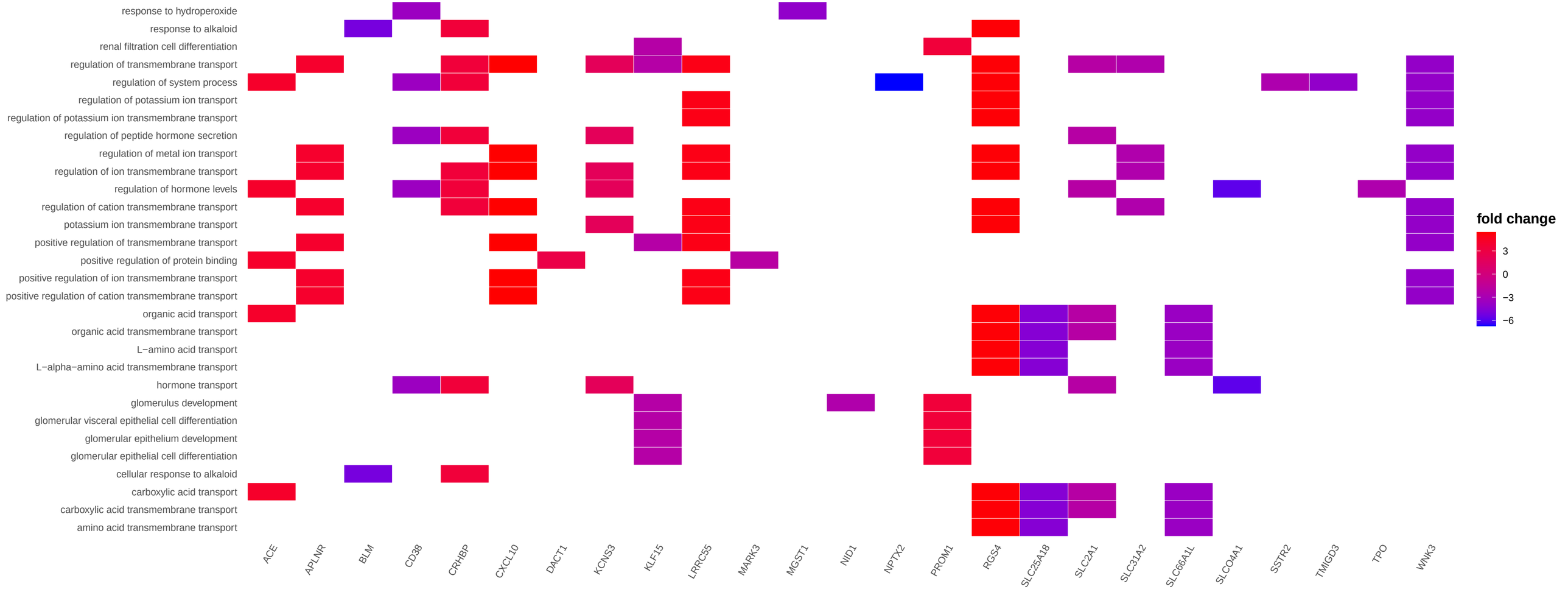
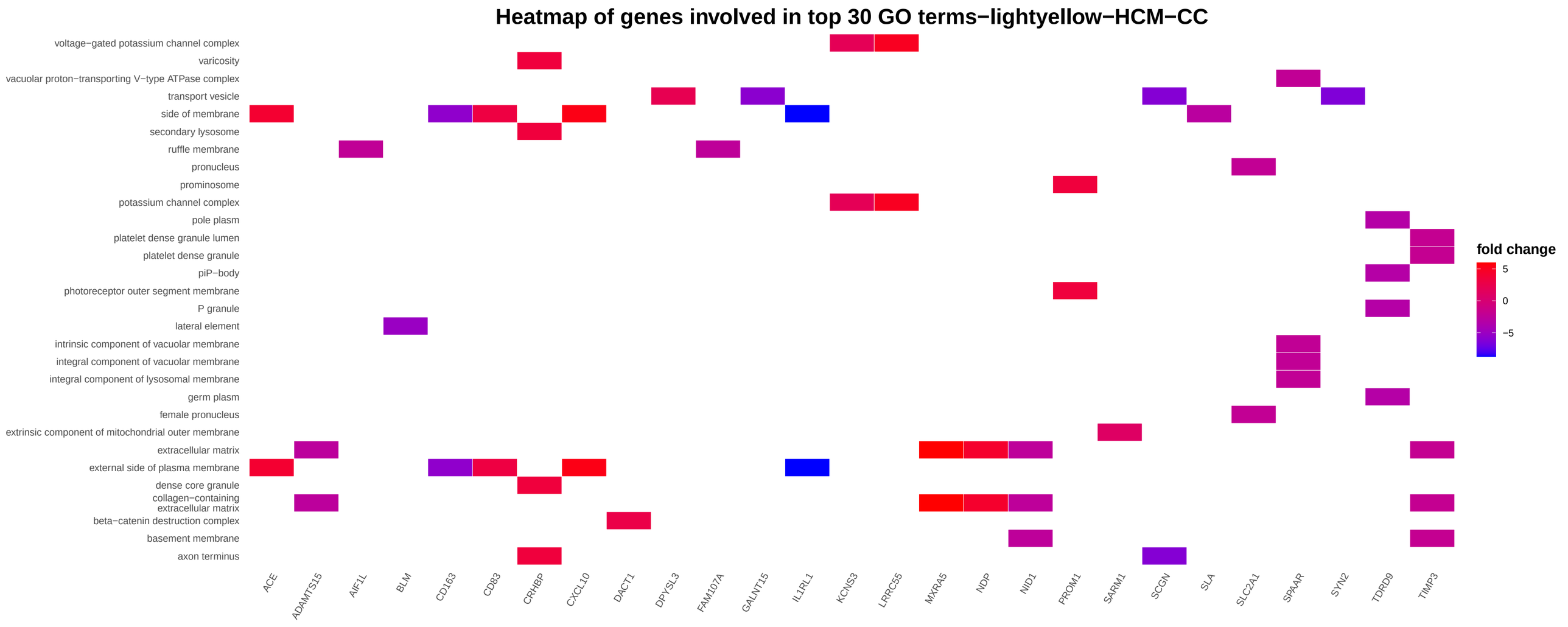
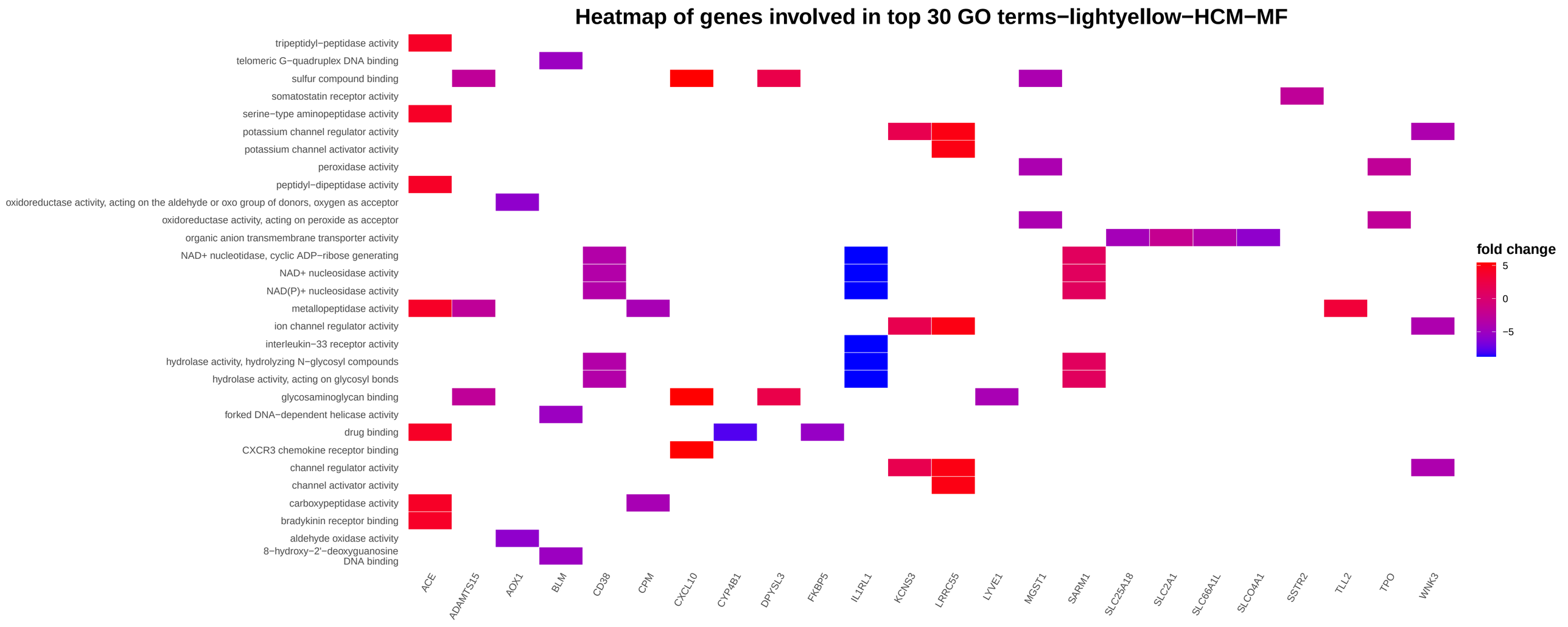
−7.5


Heatmap of genes involved in top 30 GO terms−lightyellow−DCM−ALL
response to hydroperoxide
response to alkaloid
renal filtration cell differentiation
regulation of transmembrane transport
regulation of system process
regulation of potassium ion transport
regulation of potassium ion transmembrane transport
regulation of peptide hormone secretion
regulation of metal ion transport
regulation of ion transmembrane transport
regulation of hormone levels
regulation of cation transmembrane transport
potassium ion transmembrane transport
positive regulation of transmembrane transport
positive regulation of protein binding
positive regulation of ion transmembrane transport
positive regulation of cation transmembrane transport
organic acid transport
organic acid transmembrane transport
L−amino acid transport
L−alpha−amino acid transmembrane transport
hormone transport
glomerulus development
glomerular visceral epithelial cell differentiation
glomerular epithelium development
glomerular epithelial cell differentiation
cellular response to alkaloid
carboxylic acid transport
carboxylic acid transmembrane transport
amino acid transmembrane transport
ACE
APLNR
BLM
CD38
CRHBP
CXCL10
DACT1
KCNS3
KLF15
LRRC55
MARK3
MGST1
NID1
NPTX2
PROM1
RGS4
SLC25A18
SLC2A1
SLC31A2
SLC66A1L
SLCO4A1
SSTR2
TMIGD3
TPO
WNK3
fold change
5.0
2.5
0.0
−2.5

Heatmap of genes involved in top 30 GO terms−lightyellow−HCM−BP




Heatmap of genes involved in top 30 GO terms−lightyellow−HCM−CC
voltage−gated potassium channel complex
varicosity
vacuolar proton−transporting V−type ATPase complex
transport vesicle
side of membrane
secondary lysosome
ruffle membrane
pronucleus
prominosome
potassium channel complex
pole plasm
platelet dense granule lumen
platelet dense granule
piP−body
photoreceptor outer segment membrane
P granule
lateral element
intrinsic component of vacuolar membrane
integral component of vacuolar membrane
integral component of lysosomal membrane
germ plasm
female pronucleus
extrinsic component of mitochondrial outer membrane
extracellular matrix
external side of plasma membrane
dense core granule
collagen−containing extracellular matrix
beta−catenin destruction complex
basement membrane
axon terminus
ACE
ADAMTS15
AIF1L
BLM
CD163
CD83
CRHBP
CXCL10
DACT1
DPYSL3
FAM107A
GALNT15
IL1RL1
KCNS3
LRRC55
MXRA5
NDP
NID1
PROM1
SARM1
SCGN
SLA
SLC2A1
SPAAR
SYN2
TDRD9
TIMP3
fold change
5
0
−5


Heatmap of genes involved in top 30 GO terms−lightyellow−HCM−MF
tripeptidyl−peptidase activity
telomeric G−quadruplex DNA binding
sulfur compound binding
somatostatin receptor activity
serine−type aminopeptidase activity
potassium channel regulator activity
potassium channel activator activity
peroxidase activity
peptidyl−dipeptidase activity
oxidoreductase activity, acting on the aldehyde or oxo group of donors, oxygen as acceptor
oxidoreductase activity, acting on peroxide as acceptor
organic anion transmembrane transporter activity
NAD+ nucleotidase, cyclic ADP−ribose generating
NAD+ nucleosidase activity
NAD(P)+ nucleosidase activity
metallopeptidase activity
ion channel regulator activity
interleukin−33 receptor activity
hydrolase activity, hydrolyzing N−glycosyl compounds
hydrolase activity, acting on glycosyl bonds
glycosaminoglycan binding
forked DNA−dependent helicase activity
drug binding
CXCR3 chemokine receptor binding
channel regulator activity
channel activator activity
carboxypeptidase activity
bradykinin receptor binding
aldehyde oxidase activity
8−hydroxy−2'−deoxyguanosine DNA binding
ACE
ADAMTS15
AOX1
BLM
CD38
CPM
CXCL10
CYP4B1
DPYSL3
FKBP5
IL1RL1
KCNS3
LRRC55
LYVE1
MGST1
SARM1
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SLCO4A1
SSTR2
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TPO
WNK3
fold change
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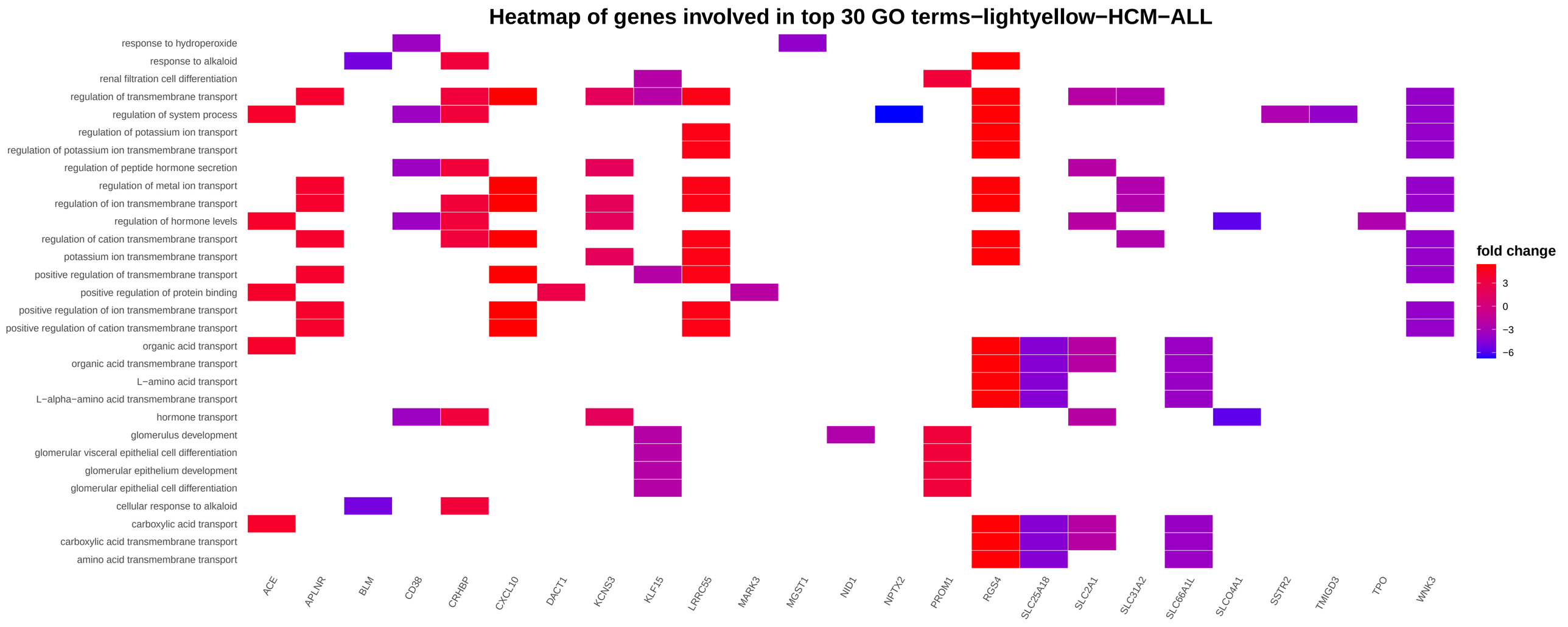
Heatmap of genes involved in top 30 GO terms−lightyellow−HCM−ALL
response to hydroperoxide
response to alkaloid
renal filtration cell differentiation
regulation of transmembrane transport
regulation of system process
regulation of potassium ion transport
regulation of potassium ion transmembrane transport
regulation of peptide hormone secretion
regulation of metal ion transport
regulation of ion transmembrane transport
regulation of hormone levels
regulation of cation transmembrane transport
potassium ion transmembrane transport
positive regulation of transmembrane transport
positive regulation of protein binding
positive regulation of ion transmembrane transport
positive regulation of cation transmembrane transport
organic acid transport
organic acid transmembrane transport
L−amino acid transport
L−alpha−amino acid transmembrane transport
hormone transport
glomerulus development
glomerular visceral epithelial cell differentiation
glomerular epithelium development
glomerular epithelial cell differentiation
cellular response to alkaloid
carboxylic acid transport
carboxylic acid transmembrane transport
amino acid transmembrane transport
ACE
APLNR
BLM
CD38
CRHBP
CXCL10
DACT1
KCNS3
KLF15
LRRC55
MARK3
MGST1
NID1
NPTX2
PROM1
RGS4
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SLC2A1
SLC31A2
SLC66A1L
SLCO4A1
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TPO
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fold change
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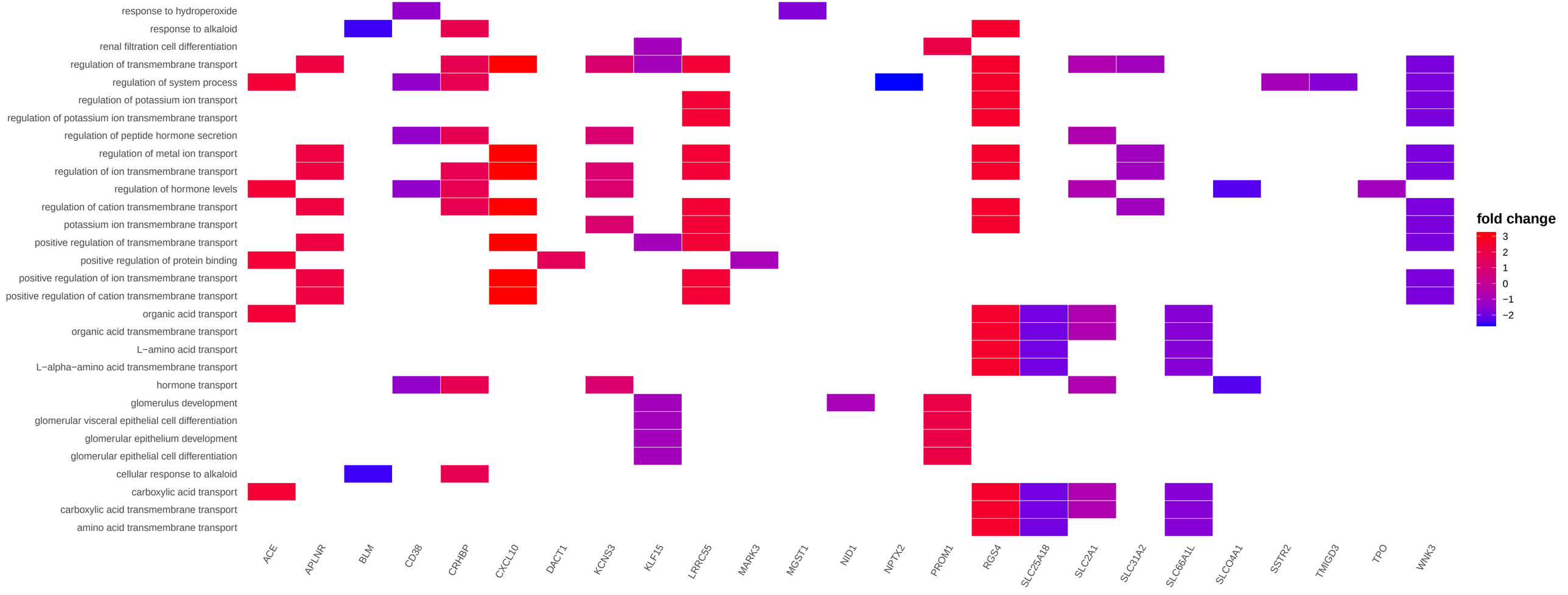
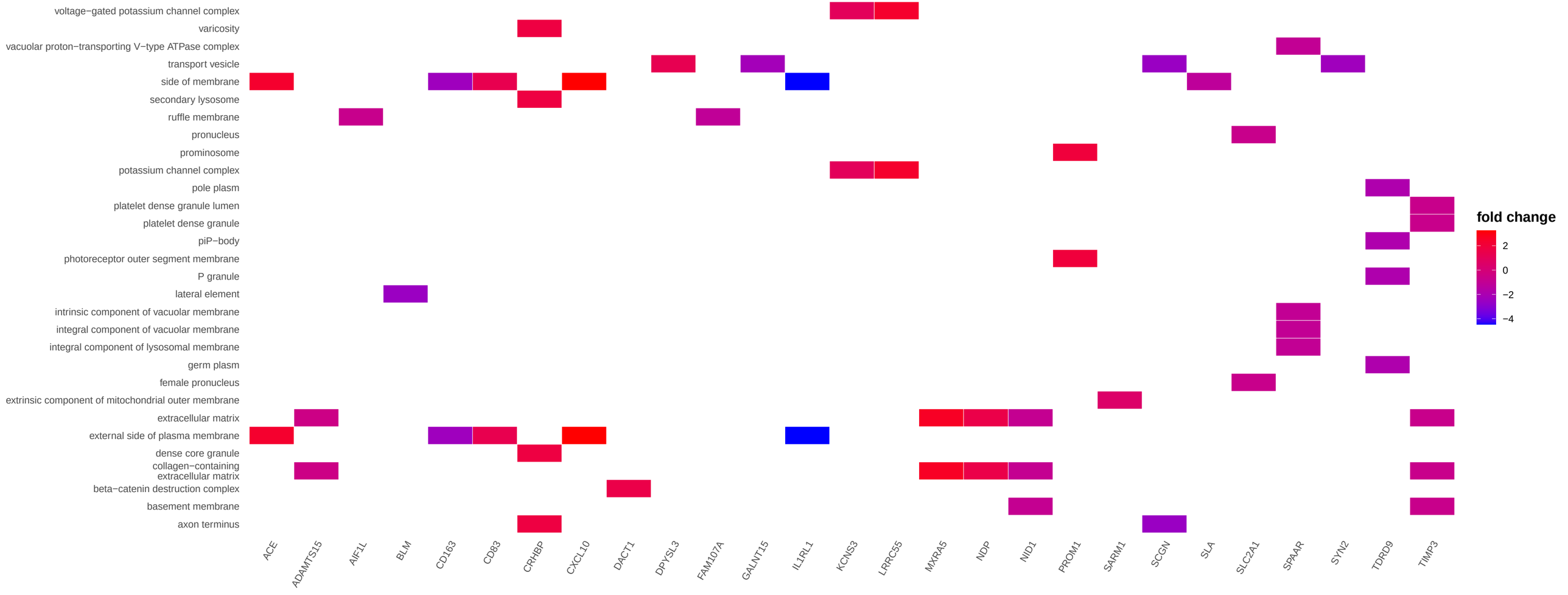
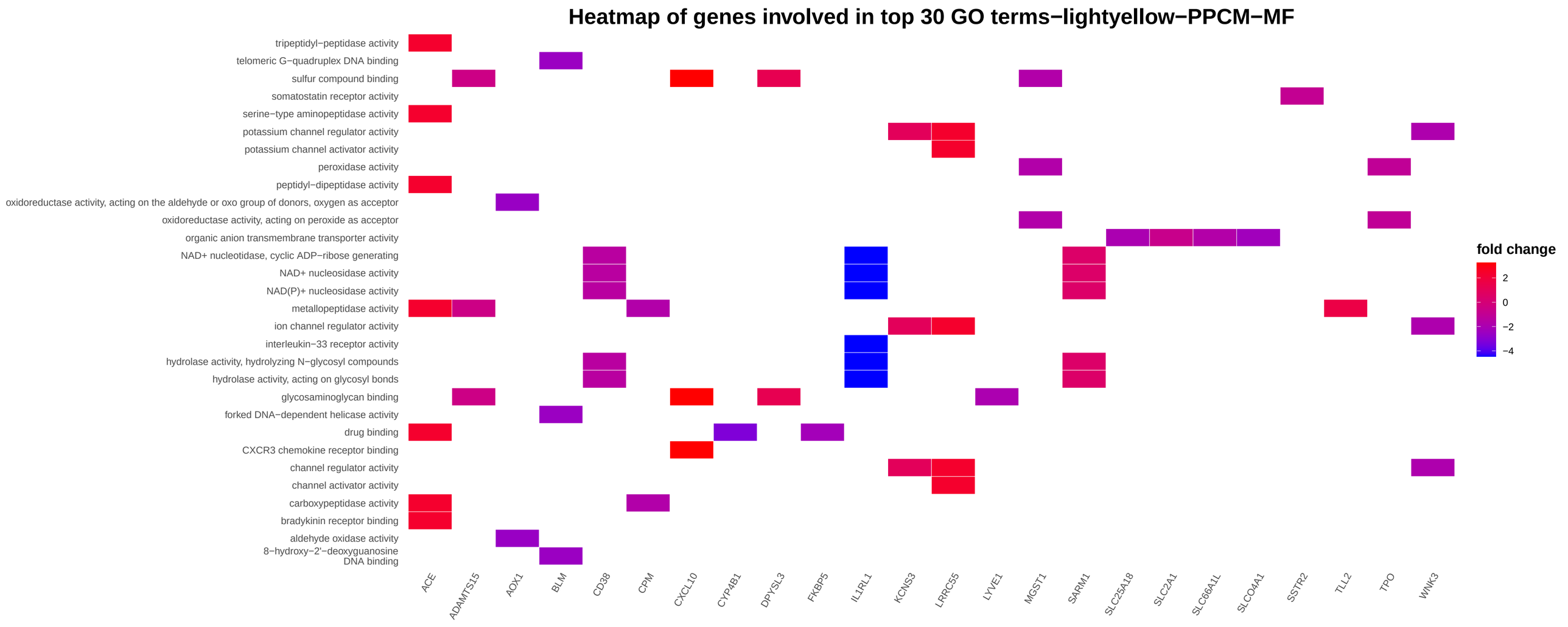
−6

Heatmap of genes involved in top 30 GO terms−lightyellow−PPCM−BP



Heatmap of genes involved in top 30 GO terms−lightyellow−PPCM−CC




Heatmap of genes involved in top 30 GO terms−lightyellow−PPCM−MF
tripeptidyl−peptidase activity
telomeric G−quadruplex DNA binding
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somatostatin receptor activity
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LRRC55
LYVE1
MGST1
SARM1
SLC25A18
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SLCO4A1
SSTR2
TLL2
TPO
WNK3
fold change
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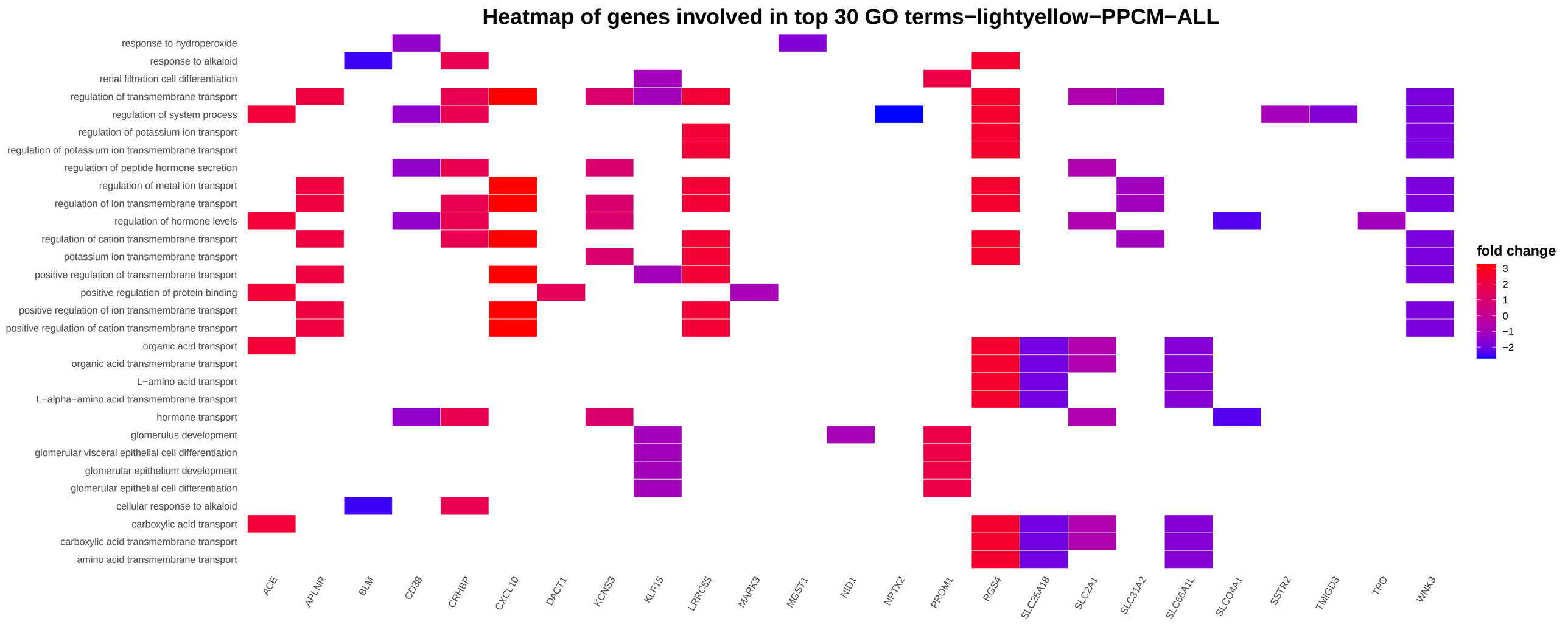
−2
−4


Heatmap of genes involved in top 30 GO terms−lightyellow−PPCM−ALL
response to hydroperoxide
response to alkaloid
renal filtration cell differentiation
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regulation of system process
regulation of potassium ion transport
regulation of potassium ion transmembrane transport
regulation of peptide hormone secretion
regulation of metal ion transport
regulation of ion transmembrane transport
regulation of hormone levels
regulation of cation transmembrane transport
potassium ion transmembrane transport
positive regulation of transmembrane transport
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positive regulation of ion transmembrane transport
positive regulation of cation transmembrane transport
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carboxylic acid transport
carboxylic acid transmembrane transport
amino acid transmembrane transport
ACE
APLNR
BLM
CD38
CRHBP
CXCL10
DACT1
KCNS3
KLF15
LRRC55
MARK3
MGST1
NID1
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PROM1
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SLC2A1
SLC31A2
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fold change
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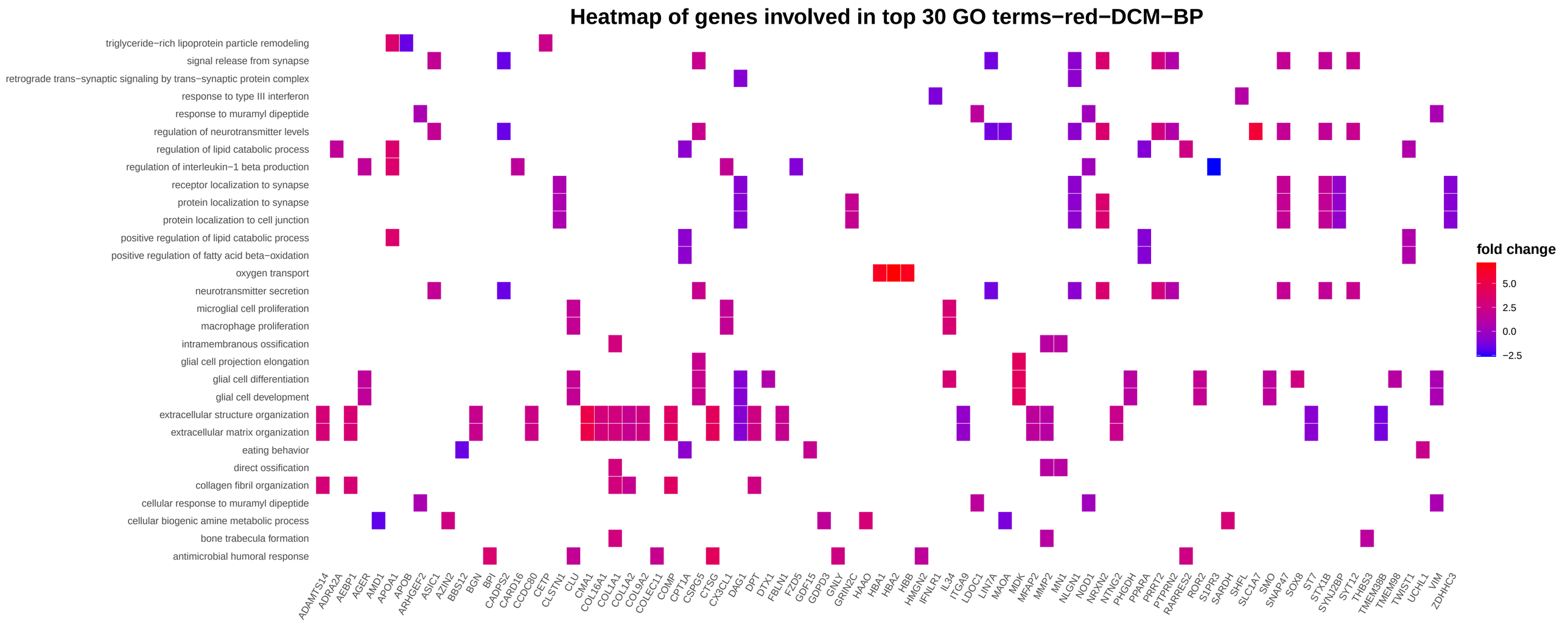
−2


Heatmap of genes involved in top 30 GO terms−red−DCM−BP
triglyceride−rich lipoprotein particle remodeling
signal release from synapse
retrograde trans−synaptic signaling by trans−synaptic protein complex
response to type III interferon
response to muramyl dipeptide
regulation of neurotransmitter levels
regulation of lipid catabolic process
regulation of interleukin−1 beta production
receptor localization to synapse
protein localization to synapse
protein localization to cell junction
positive regulation of lipid catabolic process
positive regulation of fatty acid beta−oxidation
oxygen transport
neurotransmitter secretion
microglial cell proliferation
macrophage proliferation
intramembranous ossification
glial cell projection elongation
glial cell differentiation
glial cell development
extracellular structure organization
extracellular matrix organization
eating behavior
direct ossification
collagen fibril organization
cellular response to muramyl dipeptide
cellular biogenic amine metabolic process
bone trabecula formation
antimicrobial humoral response
ADAMTS14
ADRA2A
AEBP1
AGER
AMD1
APOA1
APOB
ARHGEF2
ASIC1
AZIN2
BBS12
BGN
BPI
CADPS2
CARD16
CCDC80
CETP
CLSTN1
CLU
CMA1
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COL1A1
COL1A2
COL9A2
COLEC11
COMP
CPT1A
CSPG5
CTSG
CX3CL1
DAG1
DPT
DTX1
FBLN1
FZD5
GDF15
GDPD3
GNLY
GRIN2C
HAAO
HBA1
HBA2
HBB
HMGN2
IFNLR1
IL34
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LINTA
MAOA
MDK
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MMP2
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NOD1
NRXN2
NTNG2
PHGDH
PPARA
PRRT2
PTPRN2
RARRES2
ROR2
S1PR3
SARDH
SHFL
SLC1A7
SMO
SNAP47
SOX8
ST7
STX1B
SYNJ2BP
SYT12
THBS3
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TWIST1
UCHL1
VIM
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fold change
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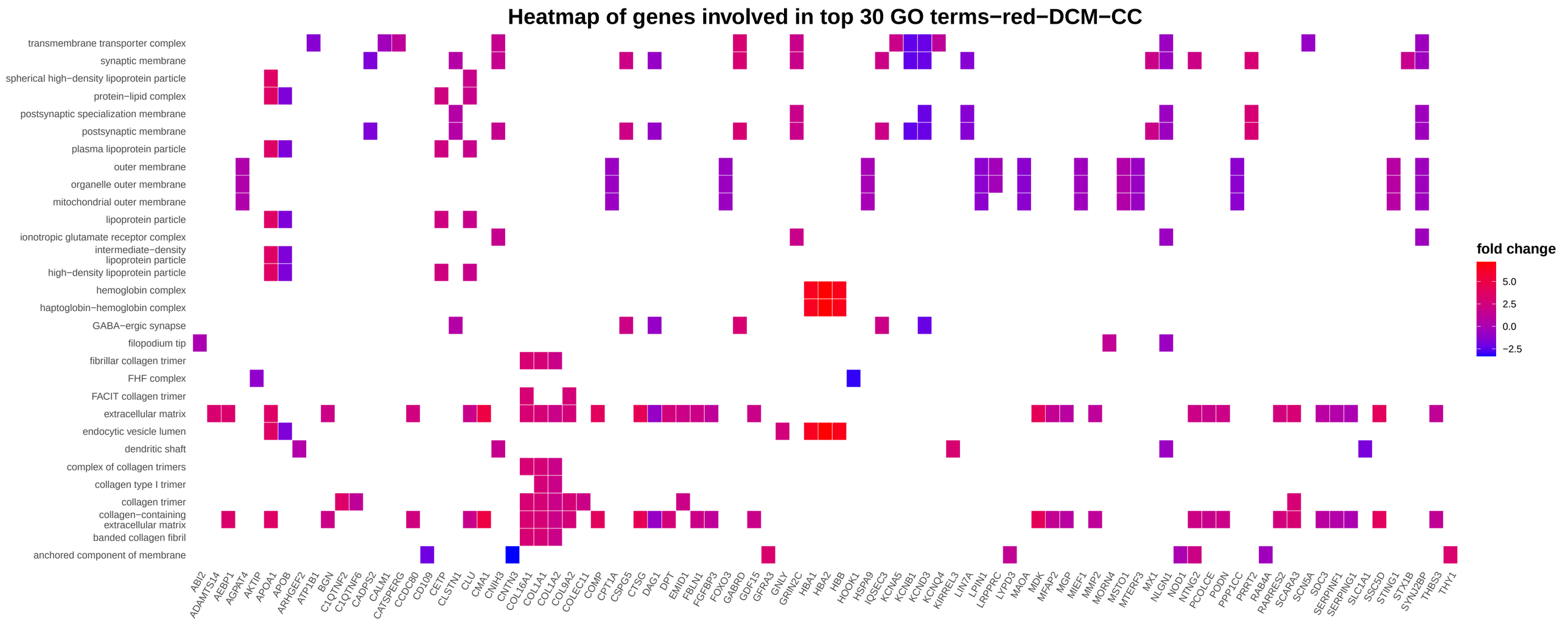
Heatmap of genes involved in top 30 GO terms−red−DCM−CC
transmembrane transporter complex
synaptic membrane
spherical high−density lipoprotein particle
protein−lipid complex
postsynaptic specialization membrane
postsynaptic membrane
plasma lipoprotein particle
outer membrane
organelle outer membrane
mitochondrial outer membrane
lipoprotein particle
ionotropic glutamate receptor complex
intermediate−density lipoprotein particle
high−density lipoprotein particle
hemoglobin complex
haptoglobin−hemoglobin complex
GABA−ergic synapse
filopodium tip
fibrillar collagen trimer
FHF complex
FACIT collagen trimer
extracellular matrix
endocytic vesicle lumen
dendritic shaft
complex of collagen trimers
collagen type I trimer
collagen trimer
collagen−containing extracellular matrix
banded collagen fibril
anchored component of membrane
ABI2
ADAMTS14
AEBP1
AGPAT4
AKTIP
APOA1
APOB
ARHGEF2
ATP1B1
BGN
C1QTNF2
C1QTNF6
CADPS2
CALM1
CATSPERG
CCDC80
CD109
CETP
CLSTN1
CLU
CMA1
CNIH3
CNTN3
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COL1A1
COL1A2
COL9A2
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CTSG
DAG1
DPT
EMID1
FBLN1
FGFBP3
FOXO3
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GFRA3
GNLY
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HBA2
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HOOK1
HSPA9
IQSEC3
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KCND3
KCNQ4
KIRREL3
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LYPD3
MAOA
MDK
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MIEF1
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MORN4
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MTERF3
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NOD1
NTNG2
PCOLCE
PODN
PPP1CC
PRRT2
RAB4A
RARRES2
SCARA3
SCN5A
SDC3
SERPINF1
SERPING1
SLC1A1
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STX1B
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THBS3
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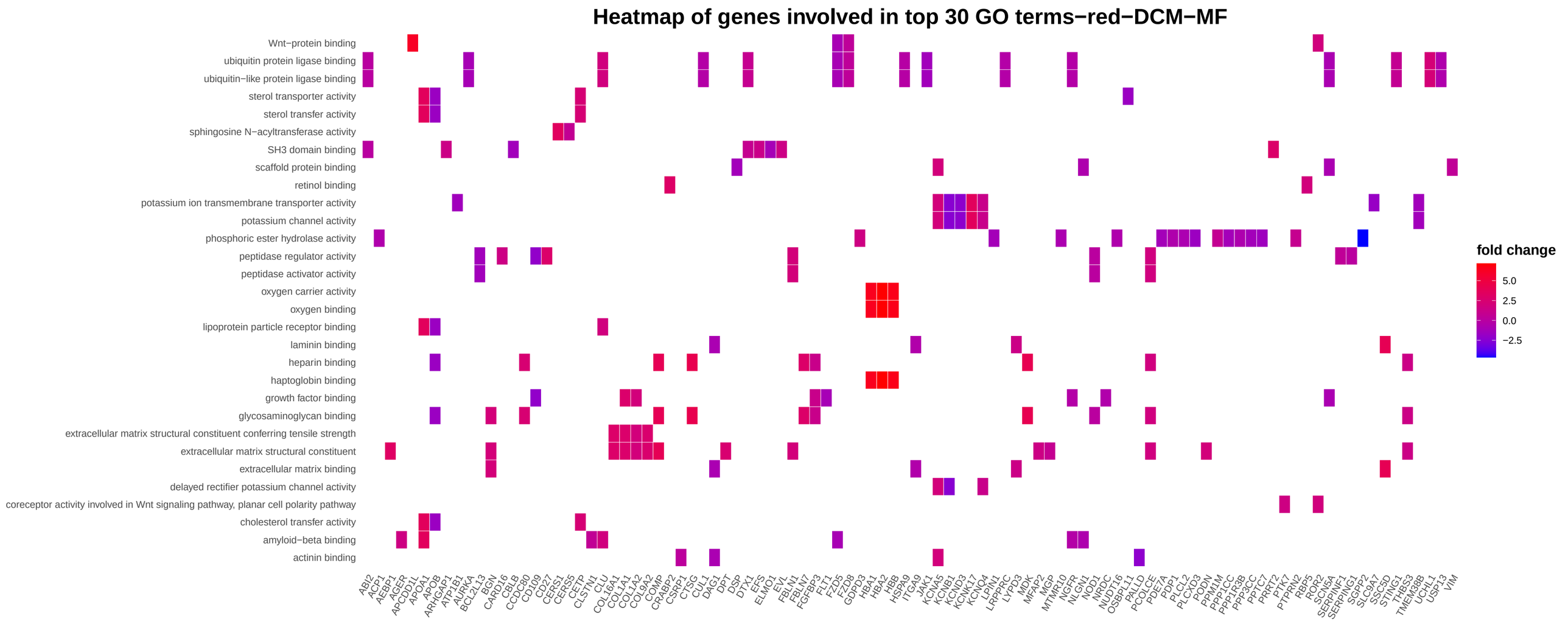
−2.5


Heatmap of genes involved in top 30 GO terms−red−DCM−MF
Wnt−protein binding
ubiquitin protein ligase binding
ubiquitin−like protein ligase binding
sterol transporter activity
sterol transfer activity
sphingosine N−acyltransferase activity
SH3 domain binding
scaffold protein binding
retinol binding
potassium ion transmembrane transporter activity
potassium channel activity
phosphoric ester hydrolase activity
peptidase regulator activity
peptidase activator activity
oxygen carrier activity
oxygen binding
lipoprotein particle receptor binding
laminin binding
heparin binding
haptoglobin binding
growth factor binding
glycosaminoglycan binding
extracellular matrix structural constituent conferring tensile strength
extracellular matrix structural constituent
extracellular matrix binding
delayed rectifier potassium channel activity
coreceptor activity involved in Wnt signaling pathway, planar cell polarity pathway
cholesterol transfer activity
amyloid−beta binding
actinin binding
ABI2
ACP1
AEBP1
AGER
APCDD1L
APOA1
APOB
ARHGAP1
ATP1B1
AURKA
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CERS5
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PPP3CC
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ROR2
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SGPP2
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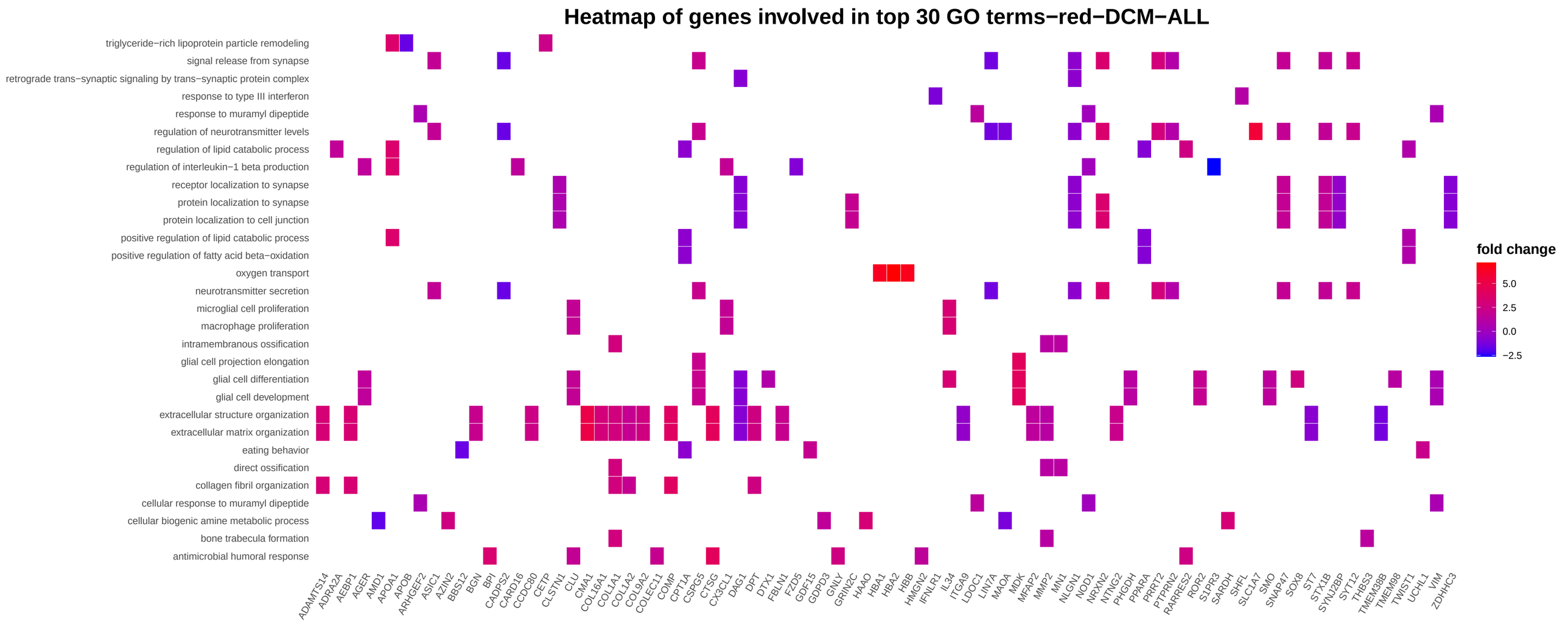
Heatmap of genes involved in top 30 GO terms−red−DCM−ALL
triglyceride−rich lipoprotein particle remodeling
signal release from synapse
retrograde trans−synaptic signaling by trans−synaptic protein complex
response to type III interferon
response to muramyl dipeptide
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regulation of interleukin−1 beta production
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protein localization to synapse
protein localization to cell junction
positive regulation of lipid catabolic process
positive regulation of fatty acid beta−oxidation
oxygen transport
neurotransmitter secretion
microglial cell proliferation
macrophage proliferation
intramembranous ossification
glial cell projection elongation
glial cell differentiation
glial cell development
extracellular structure organization
extracellular matrix organization
eating behavior
direct ossification
collagen fibril organization
cellular response to muramyl dipeptide
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bone trabecula formation
antimicrobial humoral response
ADAMTS14
ADRA2A
AEBP1
AGER
AMD1
APOA1
APOB
ARHGEF2
ASIC1
AZIN2
BBS12
BGN
BPI
CADPS2
CARD16
CCDC80
CETP
CLSTN1
CLU
CMA1
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COL1A1
COL1A2
COL9A2
COLEC11
COMP
CPT1A
CSPG5
CTSG
CX3CL1
DAG1
DPT
DTX1
FBLN1
FZD5
GDF15
GDPD3
GNLY
GRIN2C
HAAO
HBA1
HBA2
HBB
HMGN2
IFNLR1
IL34
ITGA9
LDOC1
LINTA
MAOA
MDK
MFAP2
MMP2
MN1
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NOD1
NRXN2
NTNG2
PHGDH
PPARA
PRRT2
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RARRES2
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S1PR3
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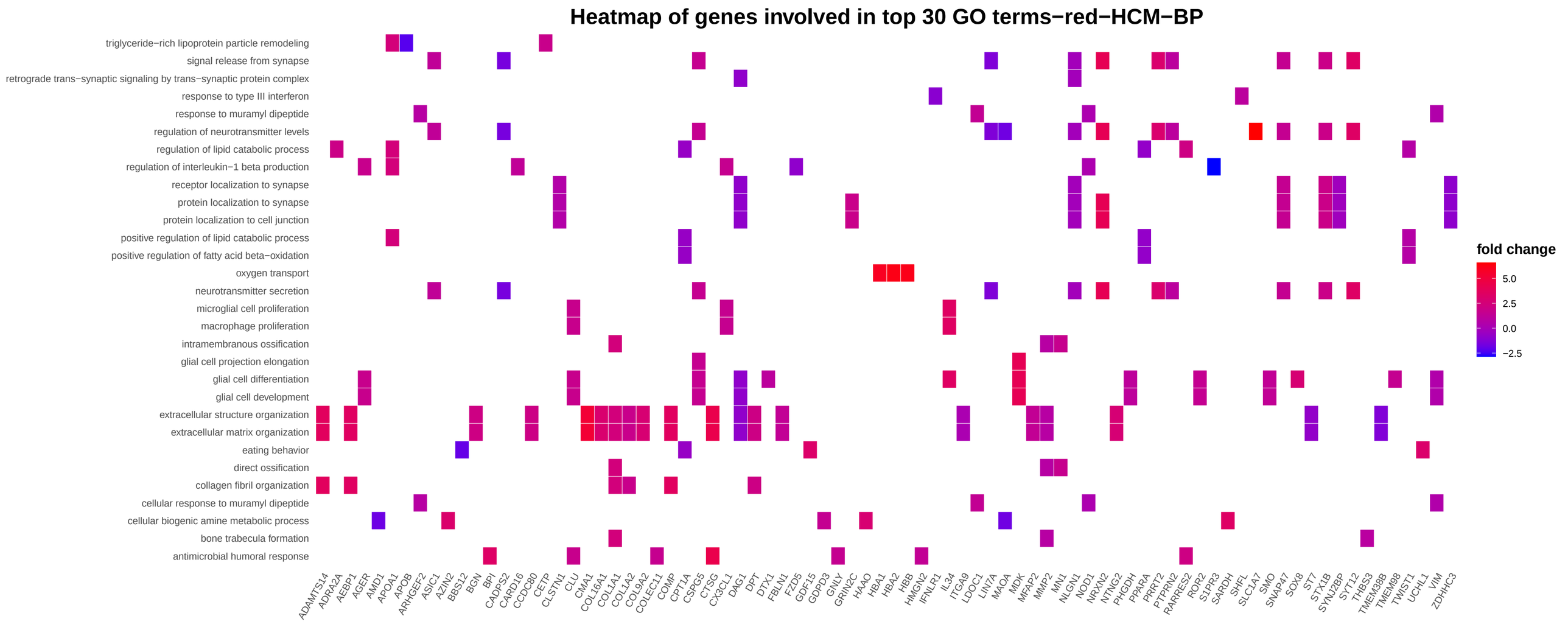
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GDPD3
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HBA1
HBA2
HBB
HMGN2
IFNLR1
IL34
ITGA9
LDOC1
LIN7A
MAOA
MDK
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MMP2
MN1
NLGN1
NOD1
NRXN2
NTNG2
PHGDH
PPARA
PRRT2
PTPRN2
RARRES2
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SARDH
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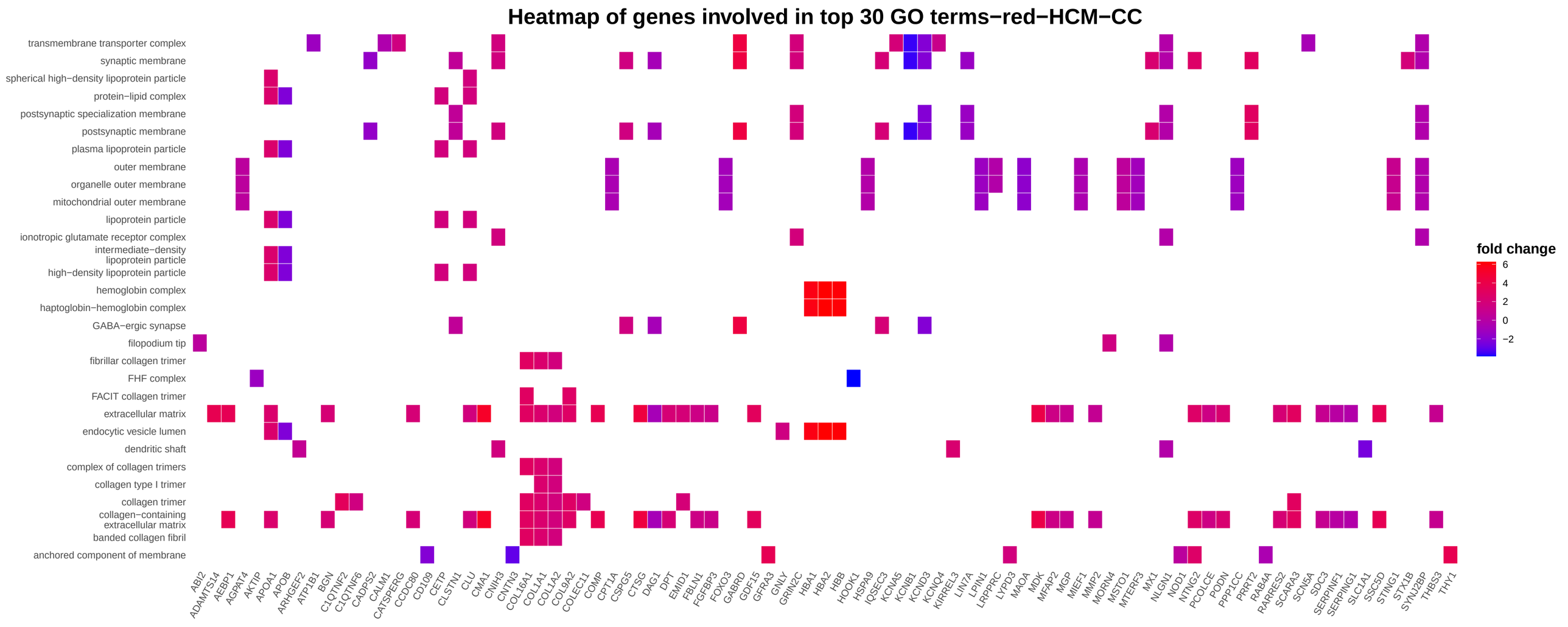
Heatmap of genes involved in top 30 GO terms−red−HCM−CC
transmembrane transporter complex
synaptic membrane
spherical high−density lipoprotein particle
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postsynaptic specialization membrane
postsynaptic membrane
plasma lipoprotein particle
outer membrane
organelle outer membrane
mitochondrial outer membrane
lipoprotein particle
ionotropic glutamate receptor complex
intermediate−density lipoprotein particle
high−density lipoprotein particle
hemoglobin complex
haptoglobin−hemoglobin complex
GABA−ergic synapse
filopodium tip
fibrillar collagen trimer
FHF complex
FACIT collagen trimer
extracellular matrix
endocytic vesicle lumen
dendritic shaft
complex of collagen trimers
collagen type I trimer
collagen trimer
collagen−containing extracellular matrix
banded collagen fibril
anchored component of membrane
ABI2
ADAMTS14
AEBP1
AGPAT4
AKTIP
APOA1
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ARHGEF2
ATP1B1
BGN
C1QTNF2
C1QTNF6
CADPS2
CALM1
CATSPERG
CCDC80
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CNIH3
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COL9A2
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COMP
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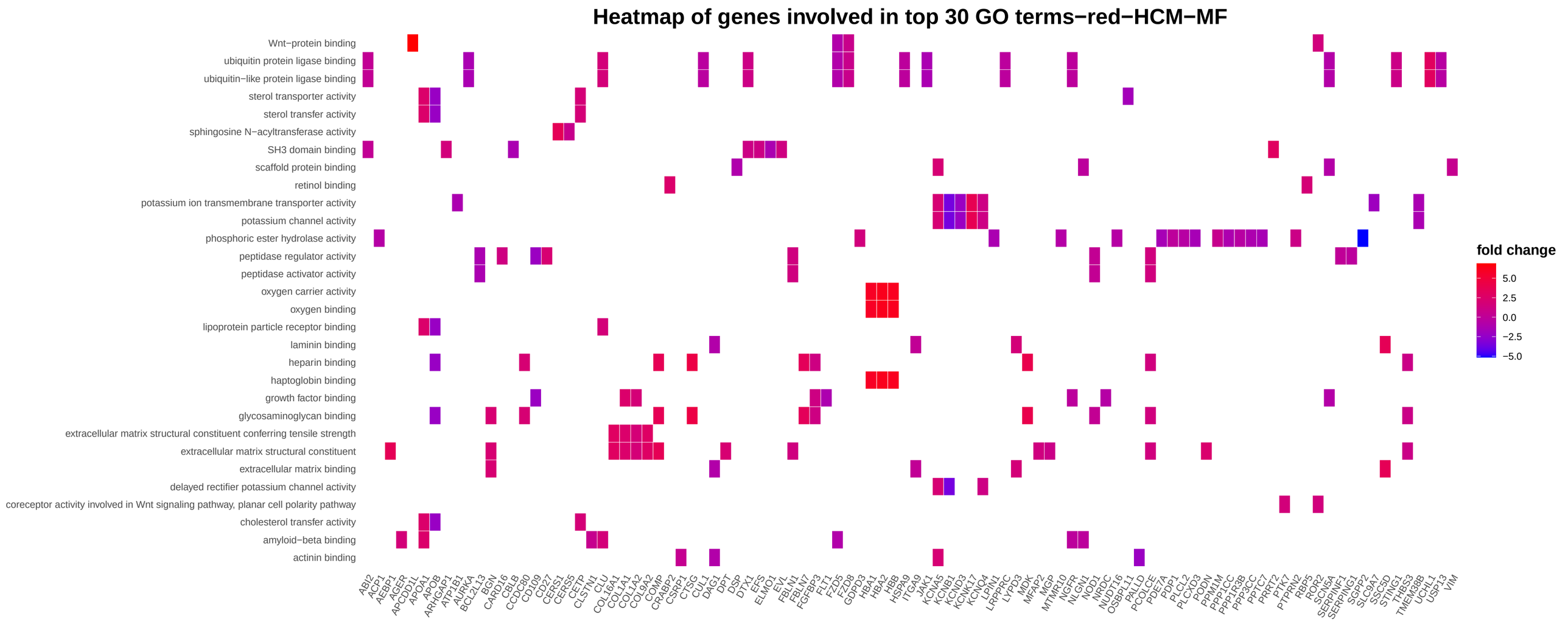
Heatmap of genes involved in top 30 GO terms−red−HCM−MF
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ubiquitin−like protein ligase binding
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sterol transfer activity
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scaffold protein binding
retinol binding
potassium ion transmembrane transporter activity
potassium channel activity
phosphoric ester hydrolase activity
peptidase regulator activity
peptidase activator activity
oxygen carrier activity
oxygen binding
lipoprotein particle receptor binding
laminin binding
heparin binding
haptoglobin binding
growth factor binding
glycosaminoglycan binding
extracellular matrix structural constituent conferring tensile strength
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amyloid−beta binding
actinin binding
ABI2
ACP1
AEBP1
AGER
APCDD1L
APOA1
APOB
ARHGAP1
ATP1B1
AURKA
BCL2L13
BGN
CARD16
CBLB
CCDC80
CD109
CD27
CERS1
CERS5
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CLU
COL16A1
COL1A1
COL1A2
COL9A2
COMP
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CSRP1
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CUL1
DAG1
DPT
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DTYX1
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EVL
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FLT1
FZD5
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GUPD3
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HBB
HSPA9
ITGA9
JAK1
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MTMR10
NGFR
NLGN1
NOD1
NRDC
NUDT16
OSBPL11
PALLD
PCOLCE
PDE7A
PDP1
PLCL2
PLCXD3
PODN
PPM1M
PPP1CC
PPP1R3B
PPP3CC
PPTC7
PRRT2
PTK7
PTPRN2
RBP5
ROR2
SCN5A
SERPINF1
SERPING1
SGPP2
SLC9A7
SSC5D
STING1
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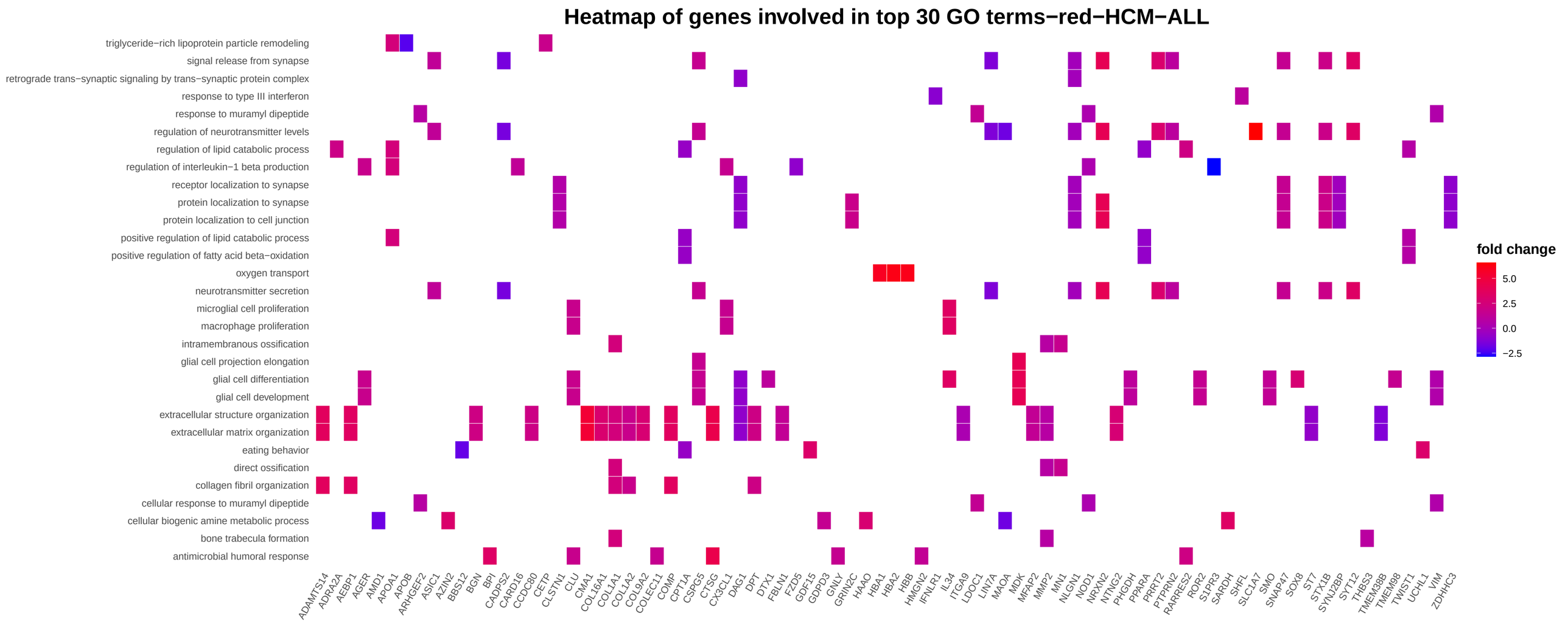
Heatmap of genes involved in top 30 GO terms−red−HCM−ALL
triglyceride−rich lipoprotein particle remodeling
signal release from synapse
retrograde trans−synaptic signaling by trans−synaptic protein complex
response to type III interferon
response to muramyl dipeptide
regulation of neurotransmitter levels
regulation of lipid catabolic process
regulation of interleukin−1 beta production
receptor localization to synapse
protein localization to synapse
protein localization to cell junction
positive regulation of lipid catabolic process
positive regulation of fatty acid beta−oxidation
oxygen transport
neurotransmitter secretion
microglial cell proliferation
macrophage proliferation
intramembranous ossification
glial cell projection elongation
glial cell differentiation
glial cell development
extracellular structure organization
extracellular matrix organization
eating behavior
direct ossification
collagen fibril organization
cellular response to muramyl dipeptide
cellular biogenic amine metabolic process
bone trabecula formation
antimicrobial humoral response
ADAMTS14
ADRA2A
AEBP1
AGER
AMD1
APOA1
APOB
ARHGEF2
ASIC1
AZIN2
BBS12
BGN
BPI
CADPS2
CARD16
CCDC80
CETP
CLSTN1
CLU
CMA1
COL16A1
COL1A1
COL1A2
COL9A2
COLEC11
COMP
CPT1A
CSPG5
CTSG
CX3CL1
DAG1
DPT
DTX1
FBLN1
FZD5
GDF15
GDPD3
GNLY
GRIN2C
HAAO
HBA1
HBA2
HBB
HMGN2
IFNLR1
IL34
ITGA9
LDOC1
LIN7A
MAOA
MDK
MFAP2
MMP2
MN1
NLGN1
NOD1
NRXN2
NTNG2
PHGDH
PPARA
PRRT2
PTPRN2
RARRES2
ROR2
S1PR3
SARDH
SHFL
SLC1A7
SMO
SNAP47
SOX8
ST7
STX1B
SYNJ2BP
SYT12
THBS3
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TWIST1
UCHL1
VIM
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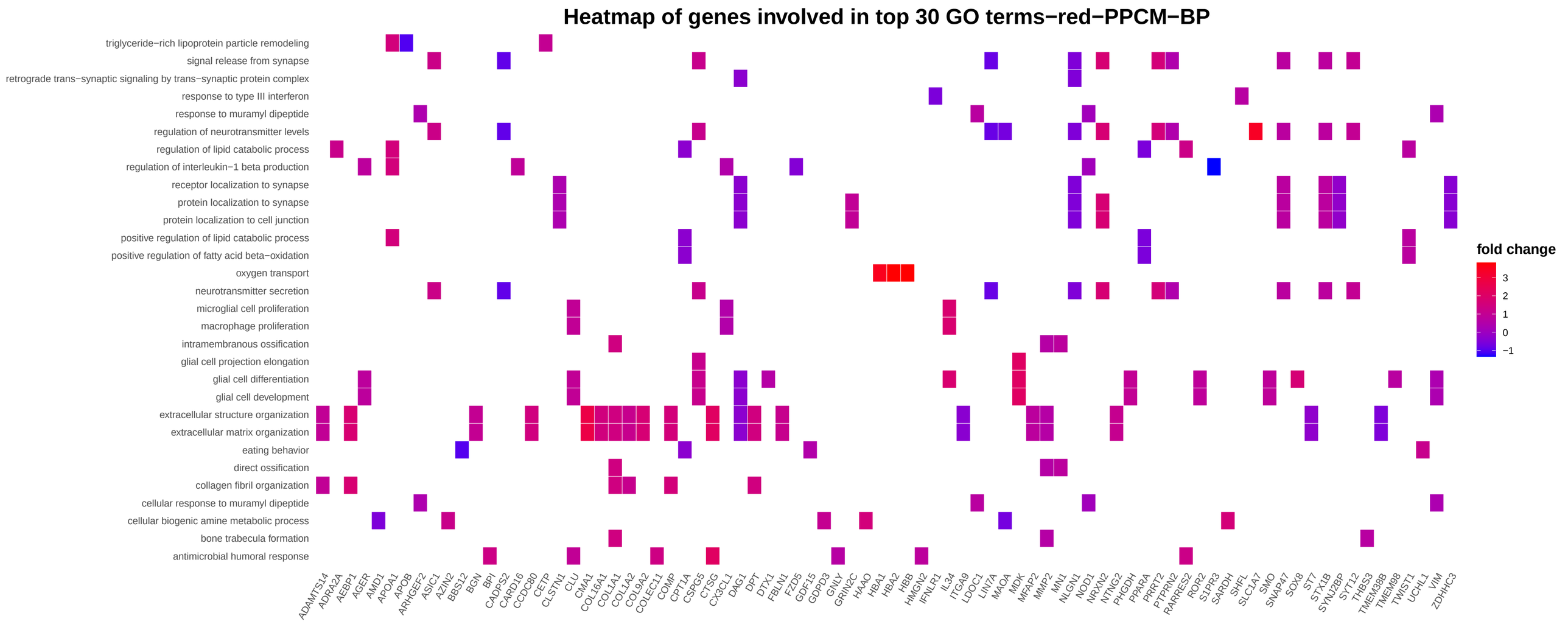
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CARD16
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CLSTN1
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CMA1
COL16A1
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ITGA9
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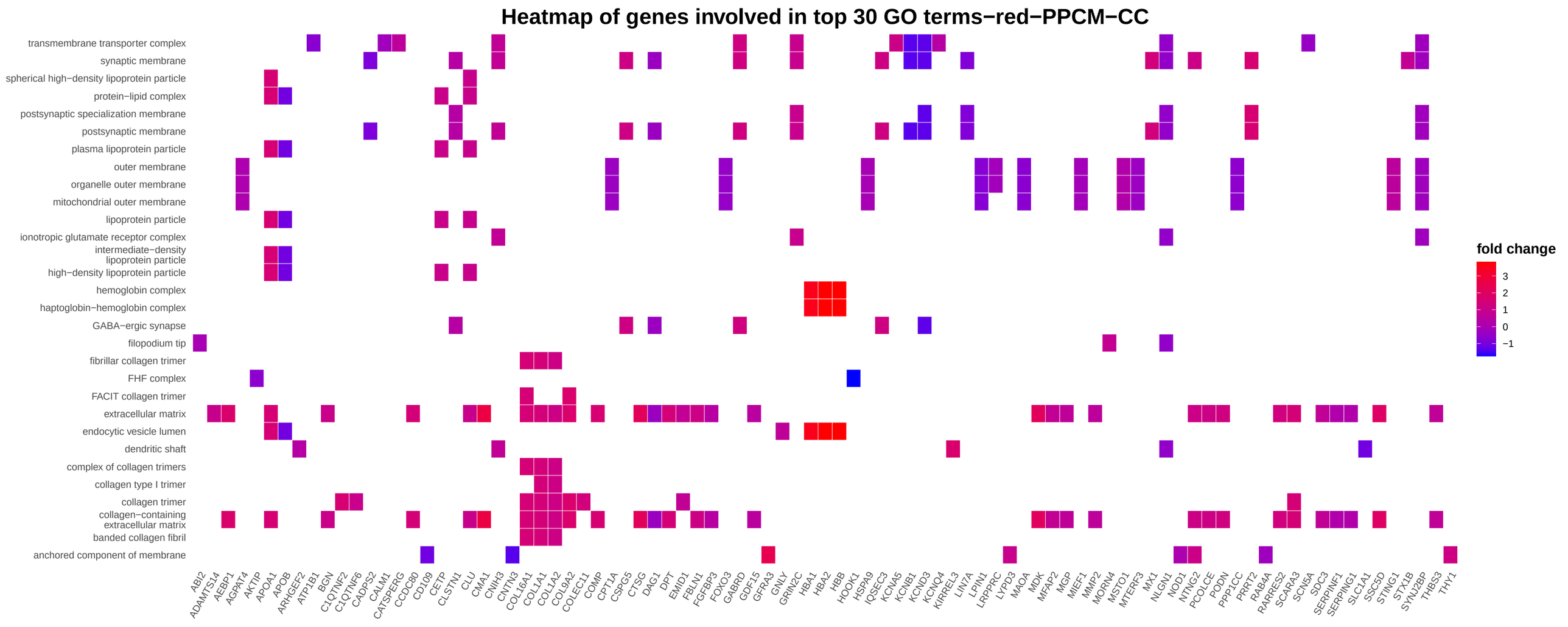
Heatmap of genes involved in top 30 GO terms−red−PPCM−CC
transmembrane transporter complex
synaptic membrane
spherical high−density lipoprotein particle
protein−lipid complex
postsynaptic specialization membrane
postsynaptic membrane
plasma lipoprotein particle
outer membrane
organelle outer membrane
mitochondrial outer membrane
lipoprotein particle
ionotropic glutamate receptor complex
intermediate−density lipoprotein particle
high−density lipoprotein particle
hemoglobin complex
haptoglobin−hemoglobin complex
GABA−ergic synapse
filopodium tip
fibrillar collagen trimer
FHF complex
FACIT collagen trimer
extracellular matrix
endocytic vesicle lumen
dendritic shaft
complex of collagen trimers
collagen type I trimer
collagen trimer
collagen−containing extracellular matrix
banded collagen fibril
anchored component of membrane
ABI2
ADAMTS14
AEBP1
AGPAT4
AKTIP
APOA1
APOB
ARHGEF2
ATP1B1
BGN
C1QTNF2
C1QTNF6
CADPS2
CALM1
CATSPERG
CCDC80
CD109
CETP
CLSTN1
CLU
CMA1
CNIH3
CNTN3
COL16A1
COL1A1
COL1A2
COL9A2
COLEC11
COMP
CPT1A
CSPG5
CTSG
DAG1
DPT
EMID1
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FOXO3
GABRD
GDF15
GFRA3
GNLY
GRIN2C
HBA1
HBA2
HBB
HOOK1
HSPA9
IQSEC3
KCNA5
KCNB1
KCND3
KCNQ4
KIRREL3
LIN7A
LPIN1
LRPPRC
LYPD3
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MFAP2
MGP
MIEF1
MMP2
MORN4
MSTO1
MTERF3
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NOD1
NTNG2
PCOLCE
PODN
PPP1CC
PRRT2
RAB4A
RARRES2
SCARA3
SCN5A
SDC3
SERPINF1
SERPING1
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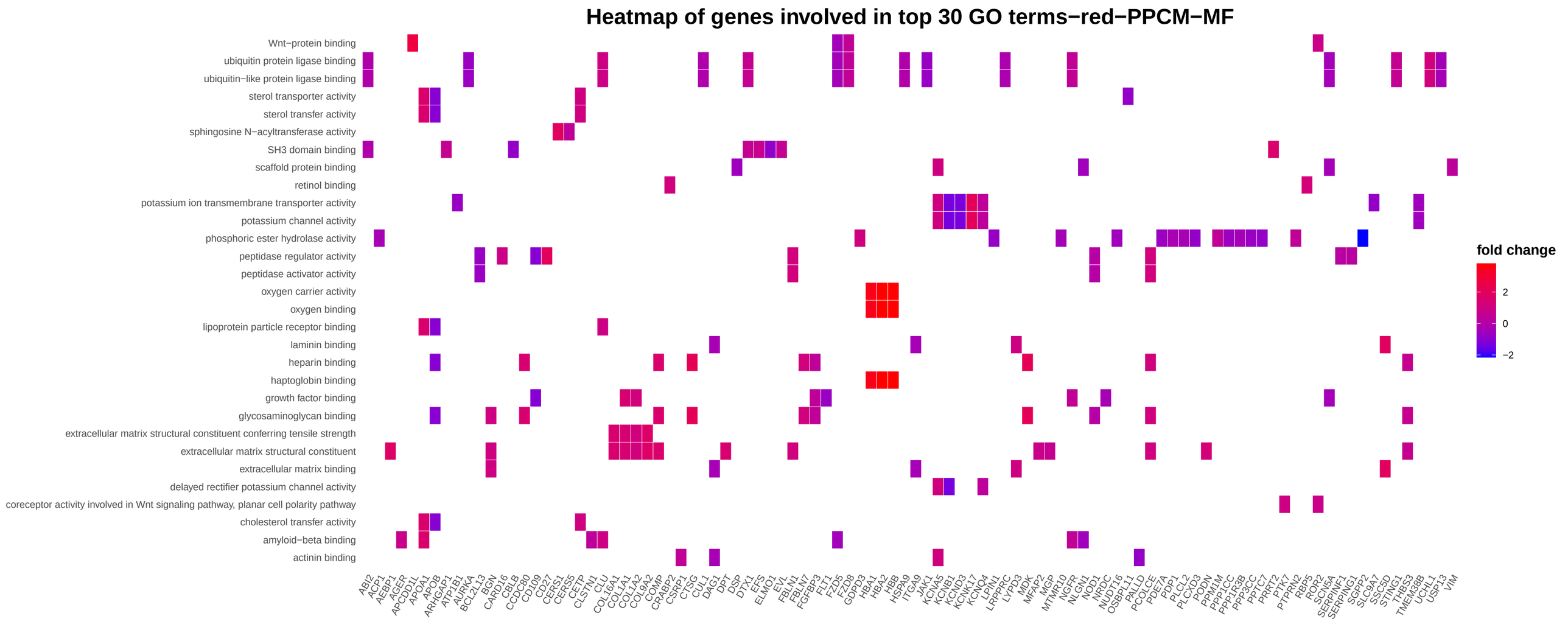
Heatmap of genes involved in top 30 GO terms−red−PPCM−MF
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ubiquitin protein ligase binding
ubiquitin−like protein ligase binding
sterol transporter activity
sterol transfer activity
sphingosine N−acyltransferase activity
SH3 domain binding
scaffold protein binding
retinol binding
potassium ion transmembrane transporter activity
potassium channel activity
phosphoric ester hydrolase activity
peptidase regulator activity
peptidase activator activity
oxygen carrier activity
oxygen binding
lipoprotein particle receptor binding
laminin binding
heparin binding
haptoglobin binding
growth factor binding
glycosaminoglycan binding
extracellular matrix structural constituent conferring tensile strength
extracellular matrix structural constituent
extracellular matrix binding
delayed rectifier potassium channel activity
coreceptor activity involved in Wnt signaling pathway, planar cell polarity pathway
cholesterol transfer activity
amyloid−beta binding
actinin binding
ABI2
ACP1
AEBP1
AGER
APCDD1L
APOA1
APOB
ARHGAP1
ATP1B1
AURKA
BCL2L13
BGN
CARD16
CBLB
CCDC80
CD109
CD27
CERS1
CERS5
CETP
CLSTN1
CLU
COL16A1
COL1A1
COL1A2
COL9A2
COMP
CRABP2
CSRP1
CTSG
CUL1
DAG1
DPT
DSP
DTYX1
EFS
ELMO1
EVL
FBLN1
FBLN7
FGFBP3
FLT1
FZD5
FZD8
GUPD3
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HBA2
HBB
HSPA9
ITGA9
JAK1
KCNA5
KCNB1
KCND3
KCNK17
KCNQ4
LPIN1
LRPPRC
LYPD3
MDK
MFAP2
MGP
MTMR10
NGFR
NLGN1
NOD1
NRDC
NUDT16
OSBPL11
PALLD
PCOLCE
PDE7A
PDP1
PLCL2
PLCXD3
PODN
PPM1M
PPP1CC
PPP1R3B
PPP3CC
PPTC7
PRRT2
PTK7
PTPRN2
RBP5
ROR2
SCN5A
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SERPING1
SGPP2
SLC9A7
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UCHL1
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VIM
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Heatmap of genes involved in top 30 GO terms−red−PPCM−ALL
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AZIN2
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BPI
CADPS2
CARD16
CCDC80
CETP
CLSTN1
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CMA1
COL16A1
COL1A1
COL1A2
COL9A2
COLEC11
COMP
CPT1A
CSPG5
CTSG
CX3CL1
DAG1
DPT
DTX1
FBLN1
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IFNLR1
IL34
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LDOC1
LIN7A
MAOA
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MFAP2
MMP2
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NOD1
NRXN2
NTNG2
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PRRT2
PTPRN2
RARRES2
ROR2
S1PR3
SARDH
SHFL
SLC1A7
SMO
SNAP47
SOX8
ST7
STX1B
SYNJ2BP
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THBS3
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UCHL1
VIM
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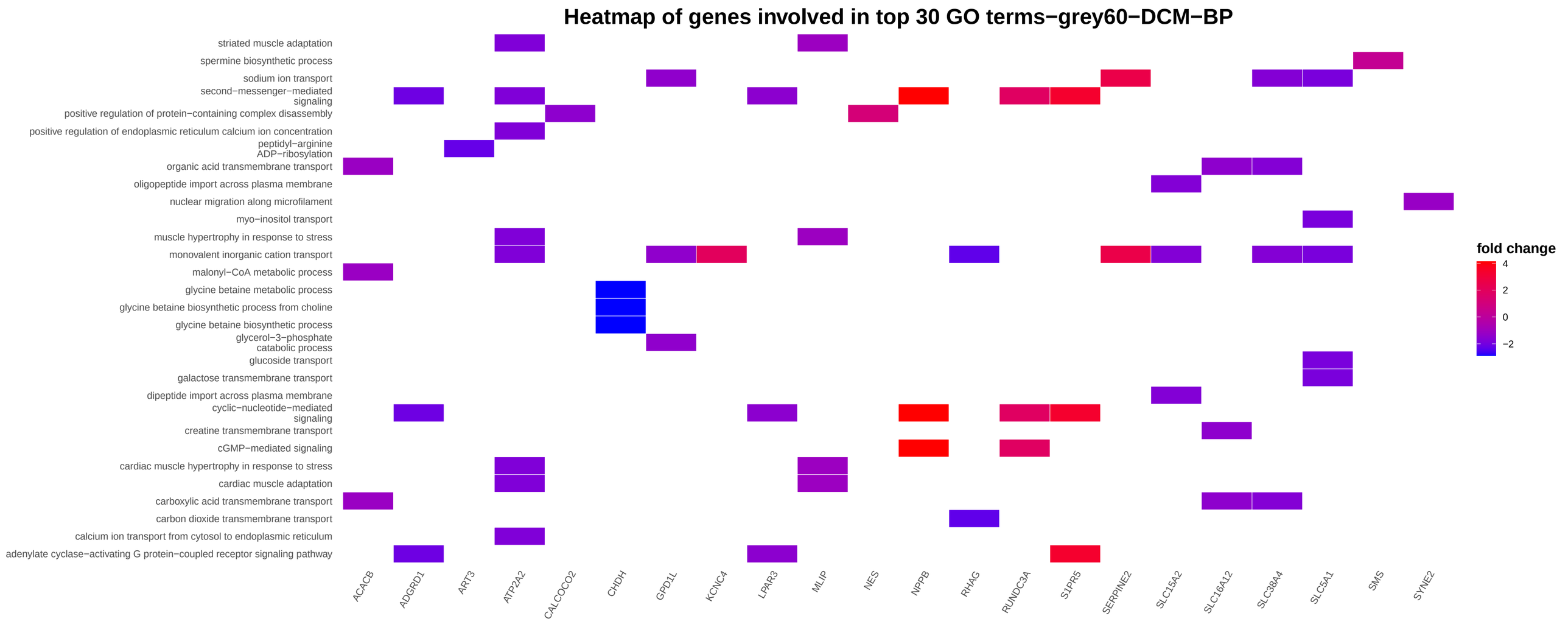
Heatmap of genes involved in top 30 GO terms−grey60−DCM−BP
striated muscle adaptation
spermine biosynthetic process
sodium ion transport
second−messenger−mediated signaling
positive regulation of protein−containing complex disassembly
positive regulation of endoplasmic reticulum calcium ion concentration
peptidyl−arginine ADP−ribosylation
organic acid transmembrane transport
oligopeptide import across plasma membrane
nuclear migration along microfilament
myo−inositol transport
muscle hypertrophy in response to stress
monovalent inorganic cation transport
malonyl−CoA metabolic process
glycine betaine metabolic process
glycine betaine biosynthetic process from choline
glycine betaine biosynthetic process
glycerol−3−phosphate catabolic process
glucoside transport
galactose transmembrane transport
dipeptide import across plasma membrane
cyclic−nucleotide−mediated signaling
creatine transmembrane transport
cGMP−mediated signaling
cardiac muscle hypertrophy in response to stress
cardiac muscle adaptation
carboxylic acid transmembrane transport
carbon dioxide transmembrane transport
calcium ion transport from cytosol to endoplasmic reticulum
adenylate cyclase−activating G protein−coupled receptor signaling pathway
ACACB
ADGRD1
ART3
ATP2A2
CALCOCO2
CHDH
GPD1L
KCNC4
LPAR3
MLIP
NES
NPPB
RHAG
RUNDC3A
SIPR5
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fold change
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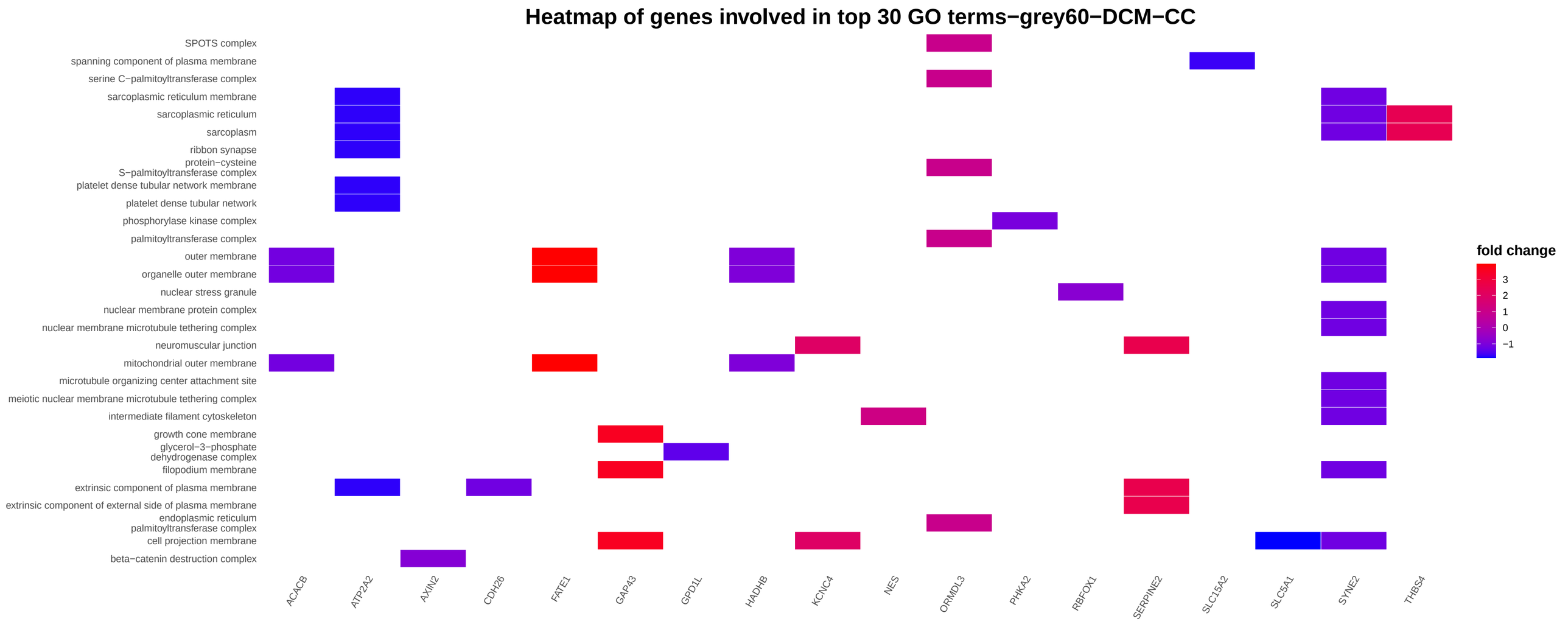
Heatmap of genes involved in top 30 GO terms−grey60−DCM−CC
SPOTS complex
spanning component of plasma membrane
serine C−palmitoyltransferase complex
sarcoplasmic reticulum membrane
sarcoplasmic reticulum
sarcoplasm
ribbon synapse
protein−cysteine S−palmitoyltransferase complex
platelet dense tubular network membrane
platelet dense tubular network
phosphorylase kinase complex
palmitoyltransferase complex
outer membrane
organelle outer membrane
nuclear stress granule
nuclear membrane protein complex
nuclear membrane microtubule tethering complex
neuromuscular junction
mitochondrial outer membrane
microtubule organizing center attachment site
meiotic nuclear membrane microtubule tethering complex
intermediate filament cytoskeleton
growth cone membrane
glycerol−3−phosphate dehydrogenase complex
filopodium membrane
extrinsic component of plasma membrane
extrinsic component of external side of plasma membrane
endoplasmic reticulum palmitoyltransferase complex
cell projection membrane
beta−catenin destruction complex
ACACB
ATP2A2
AXIN2
CDH26
FATE1
GAP43
GPD1L
HADHB
KCNC4
NES
ORMDL3
PHKA2
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SLC5A1
SYNE2
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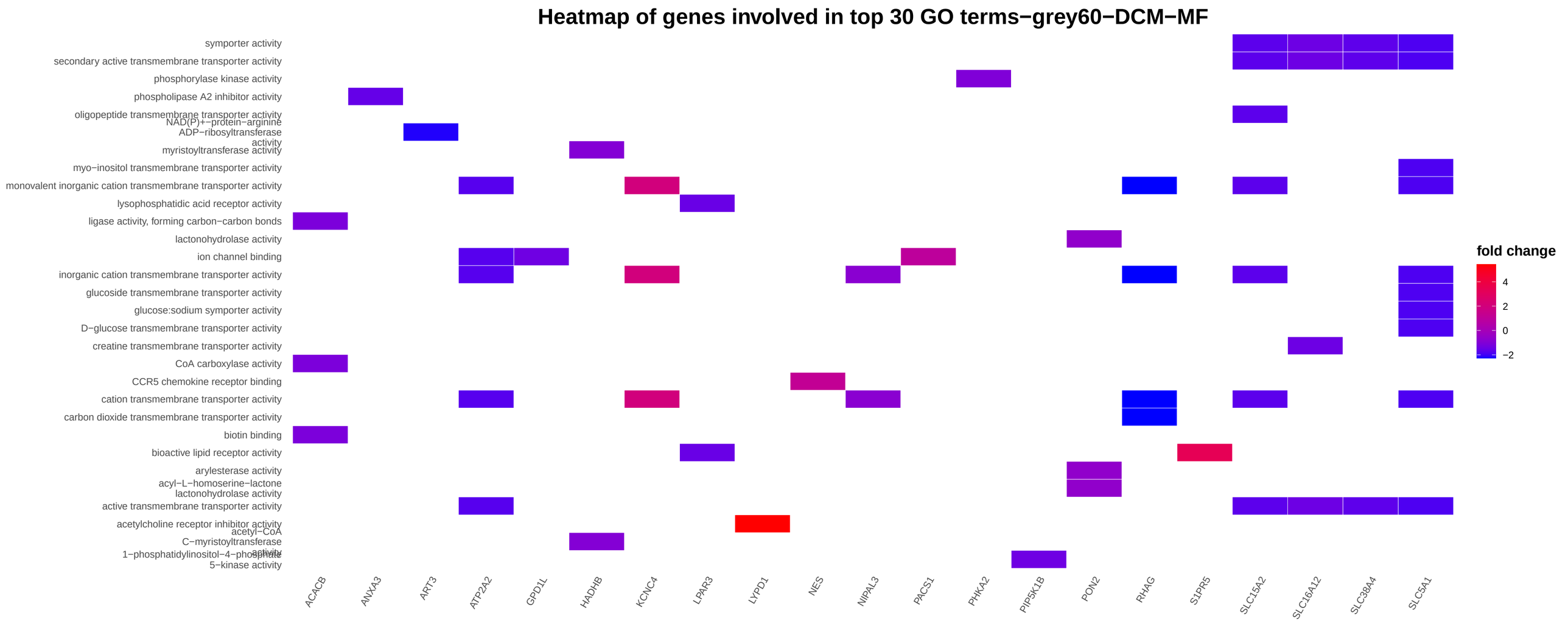
Heatmap of genes involved in top 30 GO terms−grey60−DCM−MF
symporter activity
secondary active transmembrane transporter activity
phosphorylase kinase activity
phospholipase A2 inhibitor activity
oligopeptide transmembrane transporter activity
NAD(P)+−protein−arginine ADP−ribosyltransferase activity
myristoyltransferase activity
myo−inositol transmembrane transporter activity
monovalent inorganic cation transmembrane transporter activity
lysophosphatidic acid receptor activity
ligase activity, forming carbon−carbon bonds
lactonohydrolase activity
ion channel binding
inorganic cation transmembrane transporter activity
glucoside transmembrane transporter activity
glucose:sodium symporter activity
D−glucose transmembrane transporter activity
creatine transmembrane transporter activity
CoA carboxylase activity
CCR5 chemokine receptor binding
cation transmembrane transporter activity
carbon dioxide transmembrane transporter activity
biotin binding
bioactive lipid receptor activity
arylesterase activity
acyl−L−homoserine−lactone lactonohydrolase activity
active transmembrane transporter activity
acetylcholine receptor inhibitor activity
acetyl−CoA C−myristoyltransferase activity
1−phosphatidylinositol−4−phosphate 5−kinase activity
ACACB
ANXA3
ART3
ATP2A2
GPD1L
HADHB
KCNC4
LPAR3
LYPD1
NES
NIPAL3
PACS1
PHKA2
PIP5K1B
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RHAG
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SLC5A1
fold change
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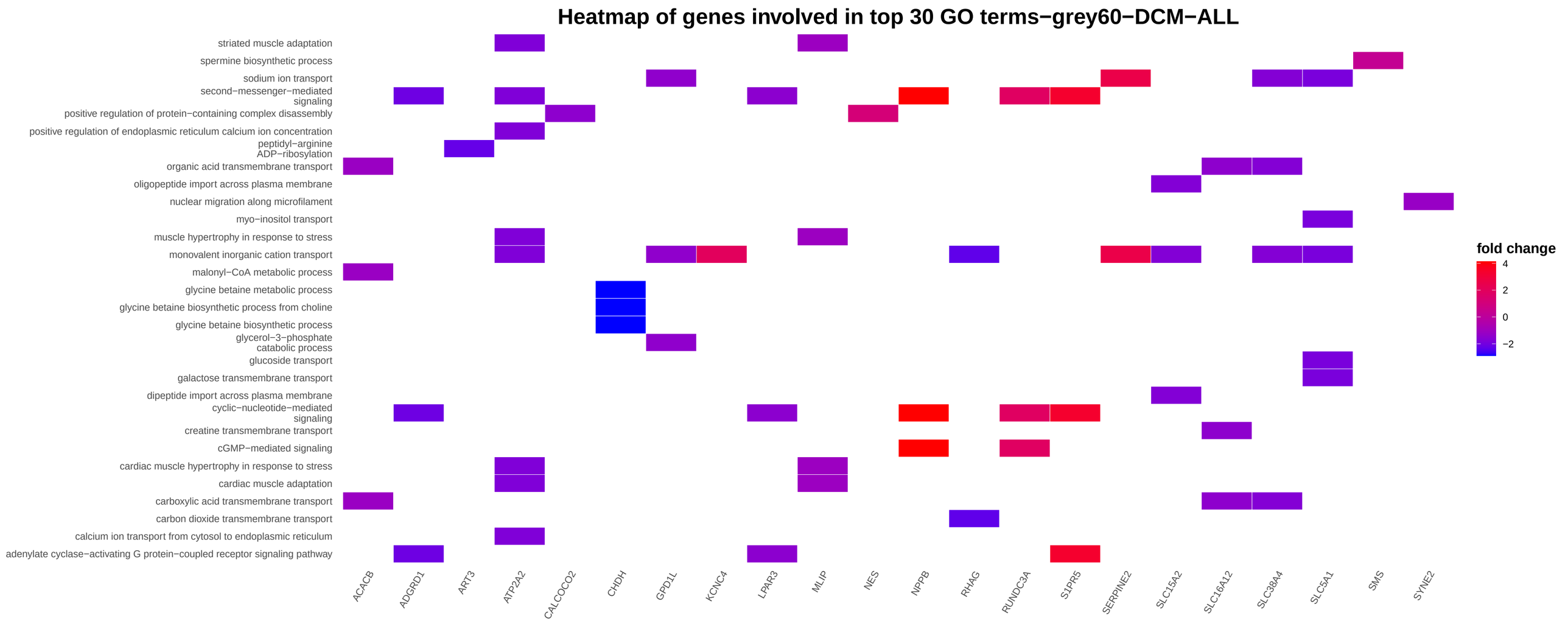
−2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glycerol−3−phosphate catabolic process
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galactose transmembrane transport
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RHAG
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S1PR5
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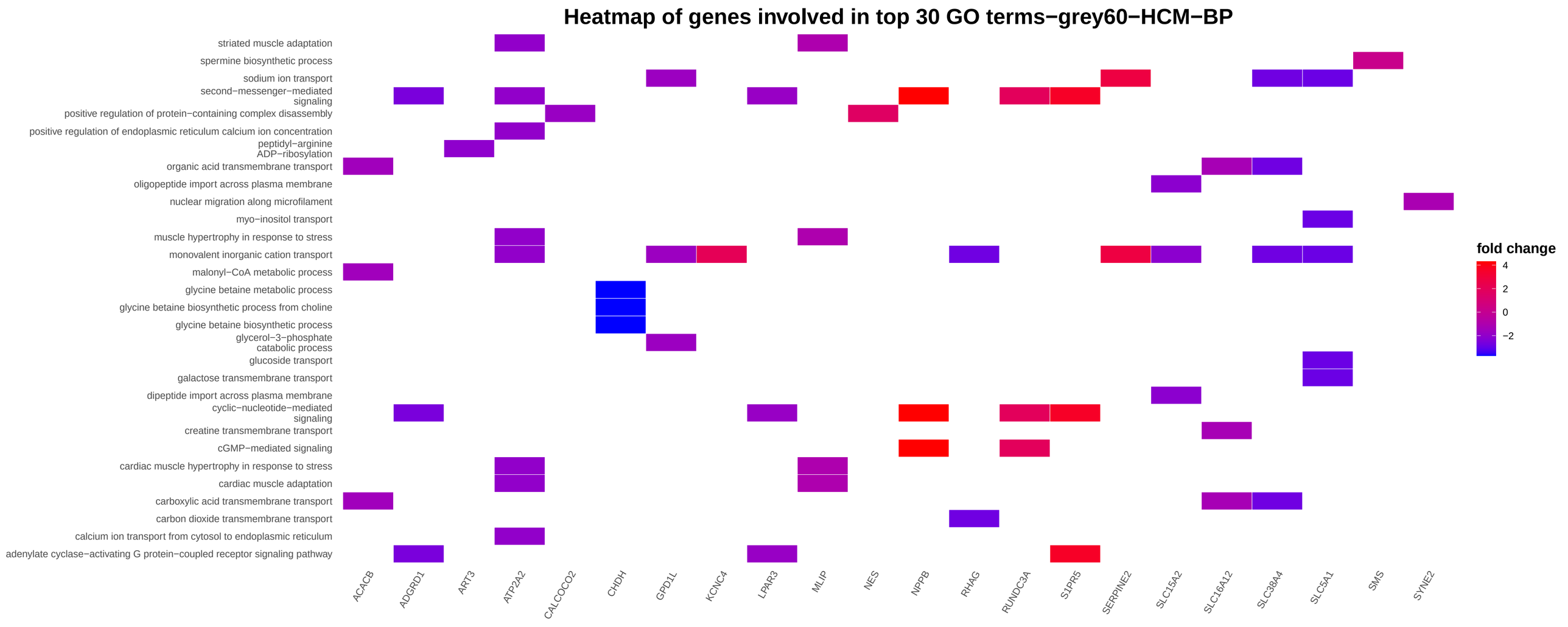
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myo−inositol transport
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malonyl−CoA metabolic process
glycine betaine metabolic process
glycine betaine biosynthetic process from choline
glycine betaine biosynthetic process
glycerol−3−phosphate catabolic process
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galactose transmembrane transport
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GPD1L
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LPAR3
MLIP
NES
NPPB
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SIPR5
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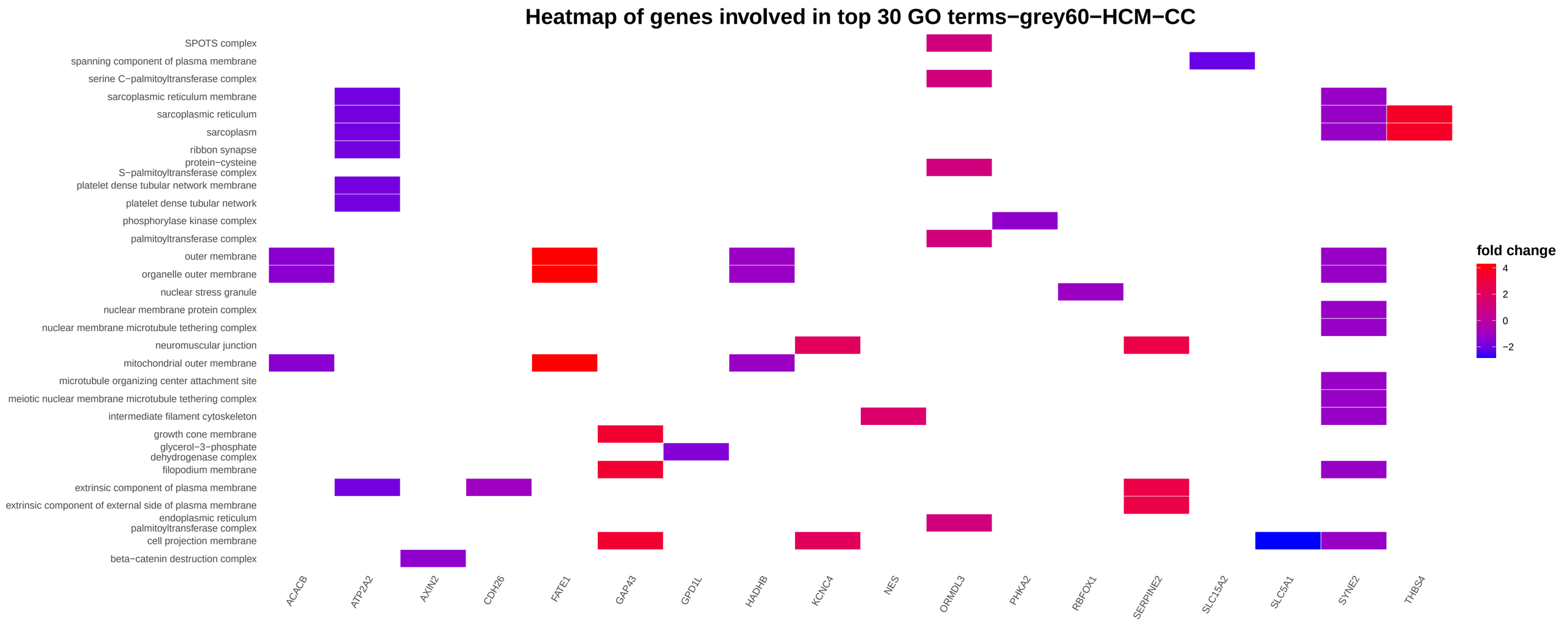
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platelet dense tubular network membrane
platelet dense tubular network
phosphorylase kinase complex
palmitoyltransferase complex
outer membrane
organelle outer membrane
nuclear stress granule
nuclear membrane protein complex
nuclear membrane microtubule tethering complex
neuromuscular junction
mitochondrial outer membrane
microtubule organizing center attachment site
meiotic nuclear membrane microtubule tethering complex
intermediate filament cytoskeleton
growth cone membrane
glycerol−3−phosphate dehydrogenase complex
filopodium membrane
extrinsic component of plasma membrane
extrinsic component of external side of plasma membrane
endoplasmic reticulum palmitoyltransferase complex
cell projection membrane
beta−catenin destruction complex
ACACB
ATP2A2
AXIN2
CDH26
FATE1
GAP43
GPD1L
HADHB
KCNC4
NES
ORMDL3
PHKA2
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SLC15A2
SLC5A1
SYNE2
THBS4
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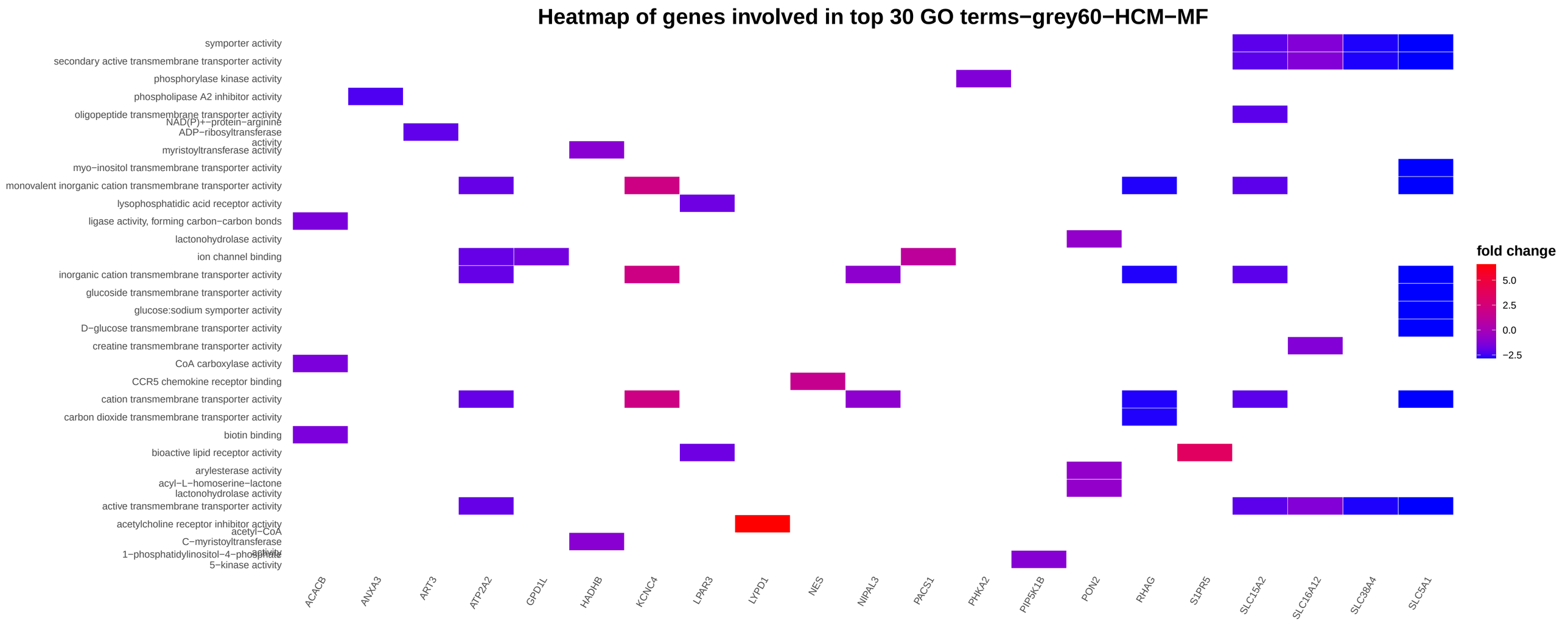
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myo−inositol transmembrane transporter activity
monovalent inorganic cation transmembrane transporter activity
lysophosphatidic acid receptor activity
ligase activity, forming carbon−carbon bonds
lactonohydrolase activity
ion channel binding
inorganic cation transmembrane transporter activity
glucoside transmembrane transporter activity
glucose:sodium symporter activity
D−glucose transmembrane transporter activity
creatine transmembrane transporter activity
CoA carboxylase activity
CCR5 chemokine receptor binding
cation transmembrane transporter activity
carbon dioxide transmembrane transporter activity
biotin binding
bioactive lipid receptor activity
arylesterase activity
acyl−L−homoserine−lactone lactonohydrolase activity
active transmembrane transporter activity
acetylcholine receptor inhibitor activity
acetyl−CoA C−myristoyltransferase activity
1−phosphatidylinositol−4−phosphate 5−kinase activity
ACACB
ANXA3
ART3
ATP2A2
GPD1L
HADHB
KCNC4
LPAR3
LYPD1
NES
NIPAL3
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PIP5K1B
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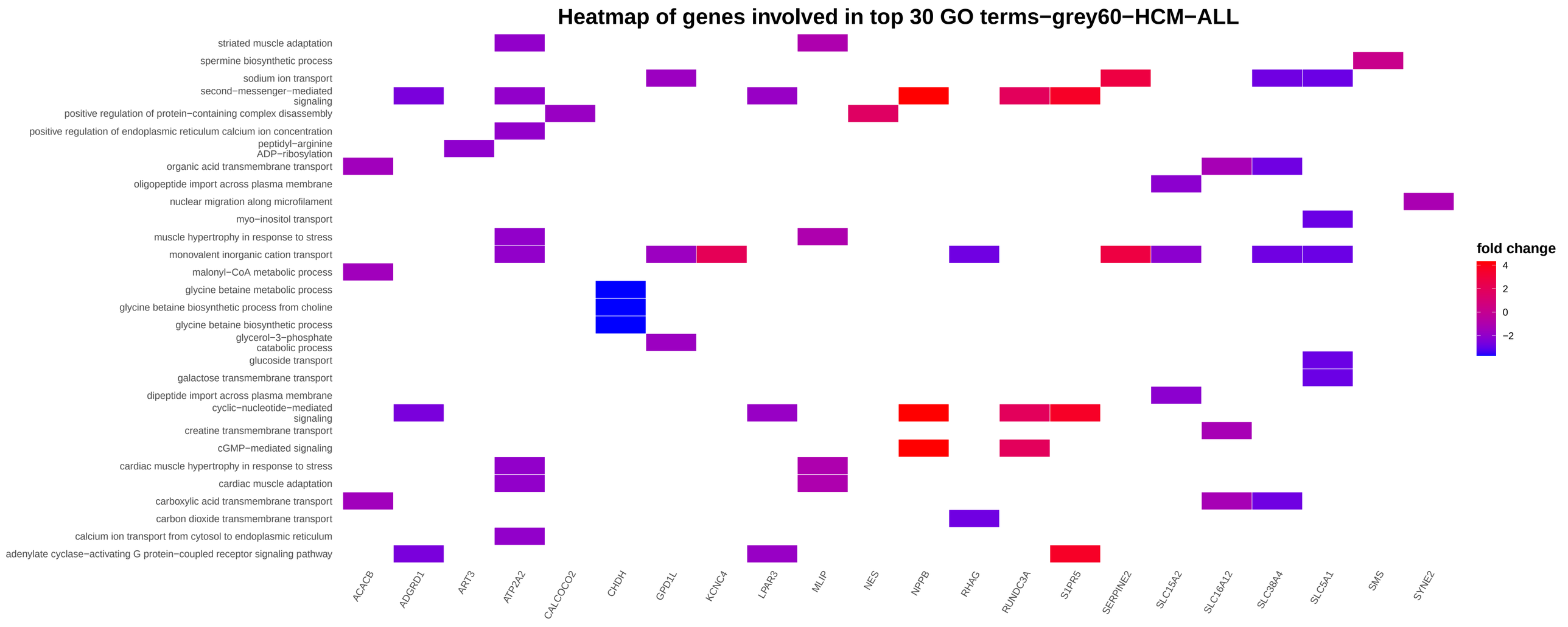
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second−messenger−mediated signaling
positive regulation of protein−containing complex disassembly
positive regulation of endoplasmic reticulum calcium ion concentration
peptidyl−arginine ADP−ribosylation
organic acid transmembrane transport
oligopeptide import across plasma membrane
nuclear migration along microfilament
myo−inositol transport
muscle hypertrophy in response to stress
monovalent inorganic cation transport
malonyl−CoA metabolic process
glycine betaine metabolic process
glycine betaine biosynthetic process from choline
glycine betaine biosynthetic process
glycerol−3−phosphate catabolic process
glucoside transport
galactose transmembrane transport
dipeptide import across plasma membrane
cyclic−nucleotide−mediated signaling
creatine transmembrane transport
cGMP−mediated signaling
cardiac muscle hypertrophy in response to stress
cardiac muscle adaptation
carboxylic acid transmembrane transport
carbon dioxide transmembrane transport
calcium ion transport from cytosol to endoplasmic reticulum
adenylate cyclase−activating G protein−coupled receptor signaling pathway
ACACB
ADGRD1
ART3
ATP2A2
CALCOCO2
CHDH
GPD1L
KCNC4
LPAR3
MLIP
NES
NPPB
RHAG
RUNDC3A
SIPR5
SERPINE2
SLC15A2
SLC16A12
SLC38A4
SLC5A1
SMS
SYNE2
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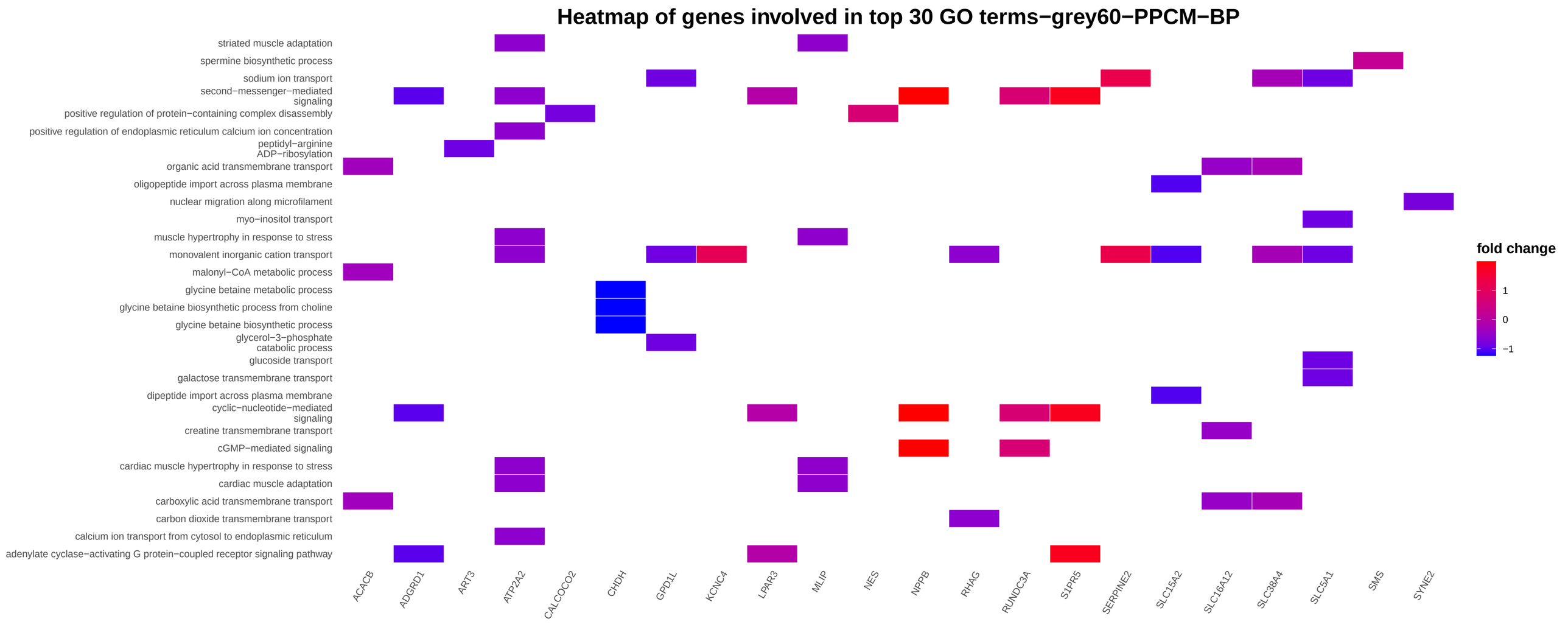
Heatmap of genes involved in top 30 GO terms−grey60−PPCM−BP
striated muscle adaptation
spermine biosynthetic process
sodium ion transport
second−messenger−mediated signaling
positive regulation of protein−containing complex disassembly
positive regulation of endoplasmic reticulum calcium ion concentration
peptidyl−arginine ADP−ribosylation
organic acid transmembrane transport
oligopeptide import across plasma membrane
nuclear migration along microfilament
myo−inositol transport
muscle hypertrophy in response to stress
monovalent inorganic cation transport
malonyl−CoA metabolic process
glycine betaine metabolic process
glycine betaine biosynthetic process from choline
glycine betaine biosynthetic process
glycerol−3−phosphate catabolic process
glucoside transport
galactose transmembrane transport
dipeptide import across plasma membrane
cyclic−nucleotide−mediated signaling
creatine transmembrane transport
cGMP−mediated signaling
cardiac muscle hypertrophy in response to stress
cardiac muscle adaptation
carboxylic acid transmembrane transport
carbon dioxide transmembrane transport
calcium ion transport from cytosol to endoplasmic reticulum
adenylate cyclase−activating G protein−coupled receptor signaling pathway
ACACB
ADGRD1
ART3
ATP2A2
CALCOCO2
CHDH
GPD1L
KCNC4
LPAR3
MLIP
NES
NPPB
RHAG
RUNDC3A
S1PR5
SERPINE2
SLC15A2
SLC16A12
SLC38A4
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SMS
SYNE2
fold change
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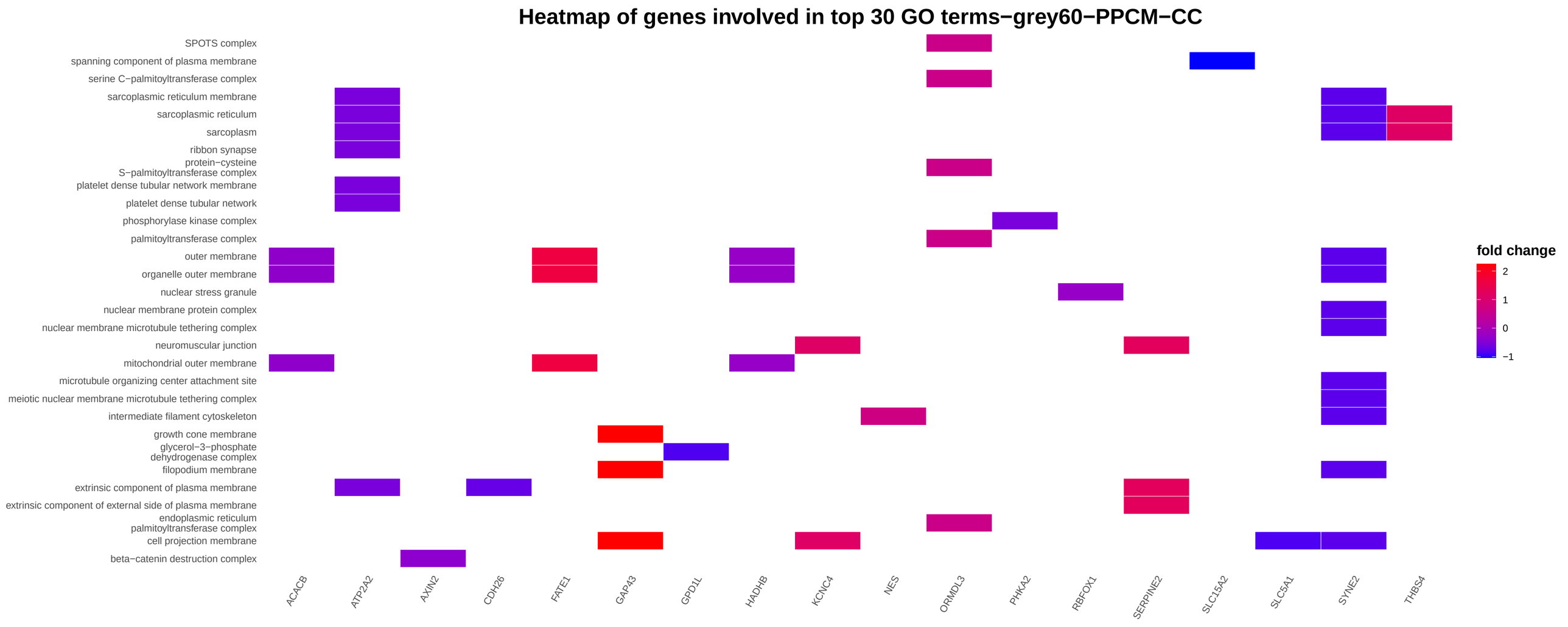
Heatmap of genes involved in top 30 GO terms−grey60−PPCM−CC
SPOTS complex
spanning component of plasma membrane
serine C−palmitoyltransferase complex
sarcoplasmic reticulum membrane
sarcoplasmic reticulum
sarcoplasm
ribbon synapse
protein−cysteine S−palmitoyltransferase complex
platelet dense tubular network membrane
platelet dense tubular network
phosphorylase kinase complex
palmitoyltransferase complex
outer membrane
organelle outer membrane
nuclear stress granule
nuclear membrane protein complex
nuclear membrane microtubule tethering complex
neuromuscular junction
mitochondrial outer membrane
microtubule organizing center attachment site
meiotic nuclear membrane microtubule tethering complex
intermediate filament cytoskeleton
growth cone membrane
glycerol−3−phosphate dehydrogenase complex
filopodium membrane
extrinsic component of plasma membrane
extrinsic component of external side of plasma membrane
endoplasmic reticulum palmitoyltransferase complex
cell projection membrane
beta−catenin destruction complex
ACACB
ATP2A2
AXIN2
CDH26
FATE1
GAP43
GPD1L
HADHB
KCNC4
NES
ORMDL3
PHKA2
RBFOX1
SERPINE2
SLC15A2
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SYNE2
THBS4
fold change
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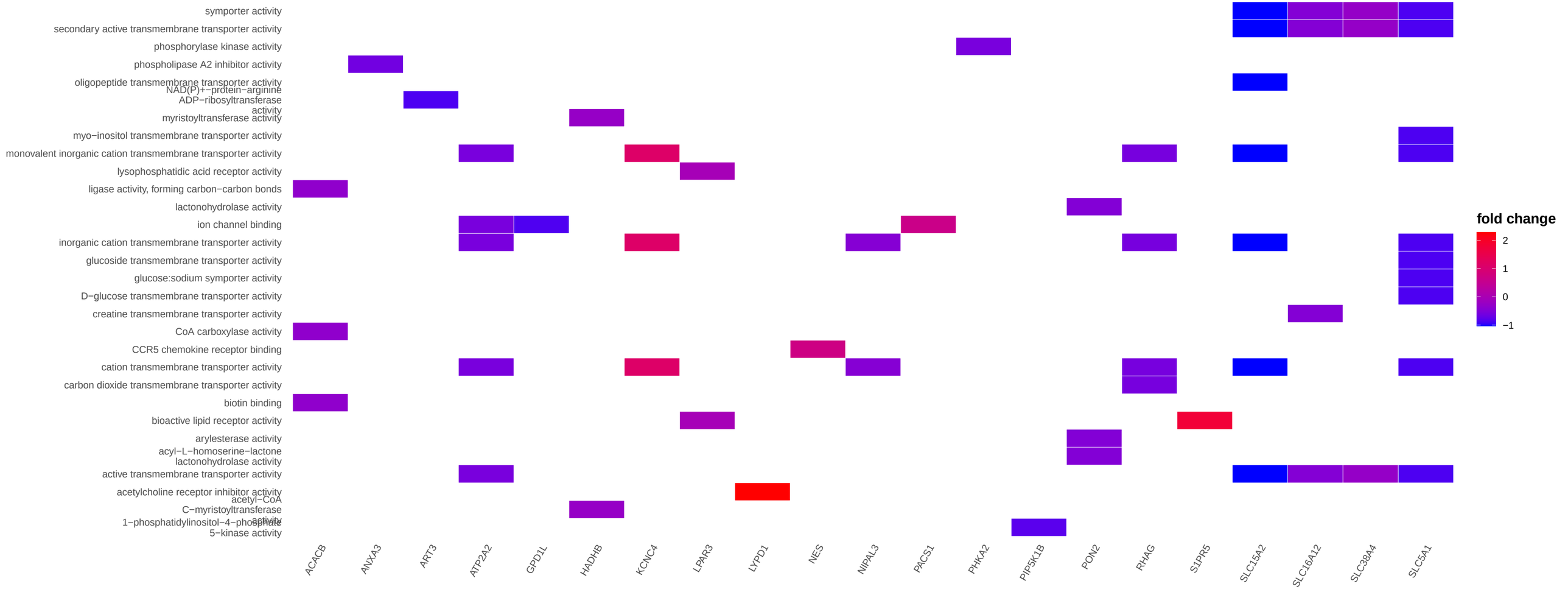
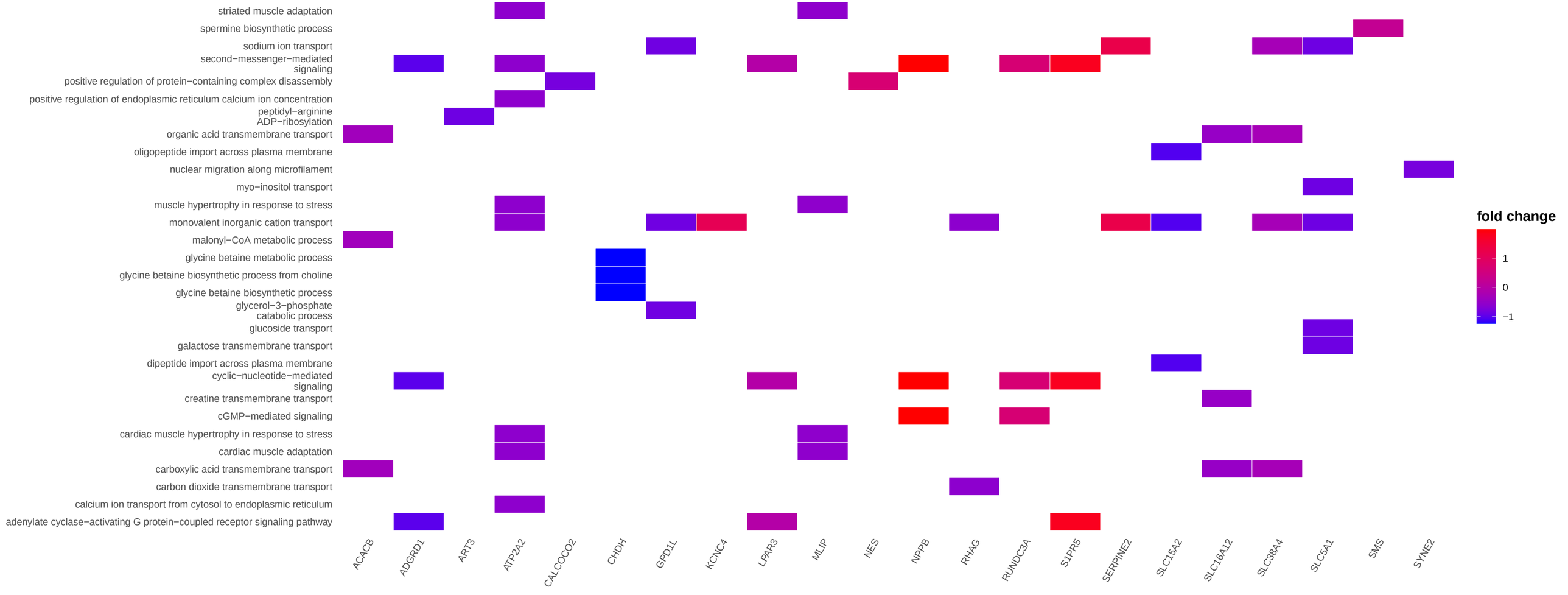
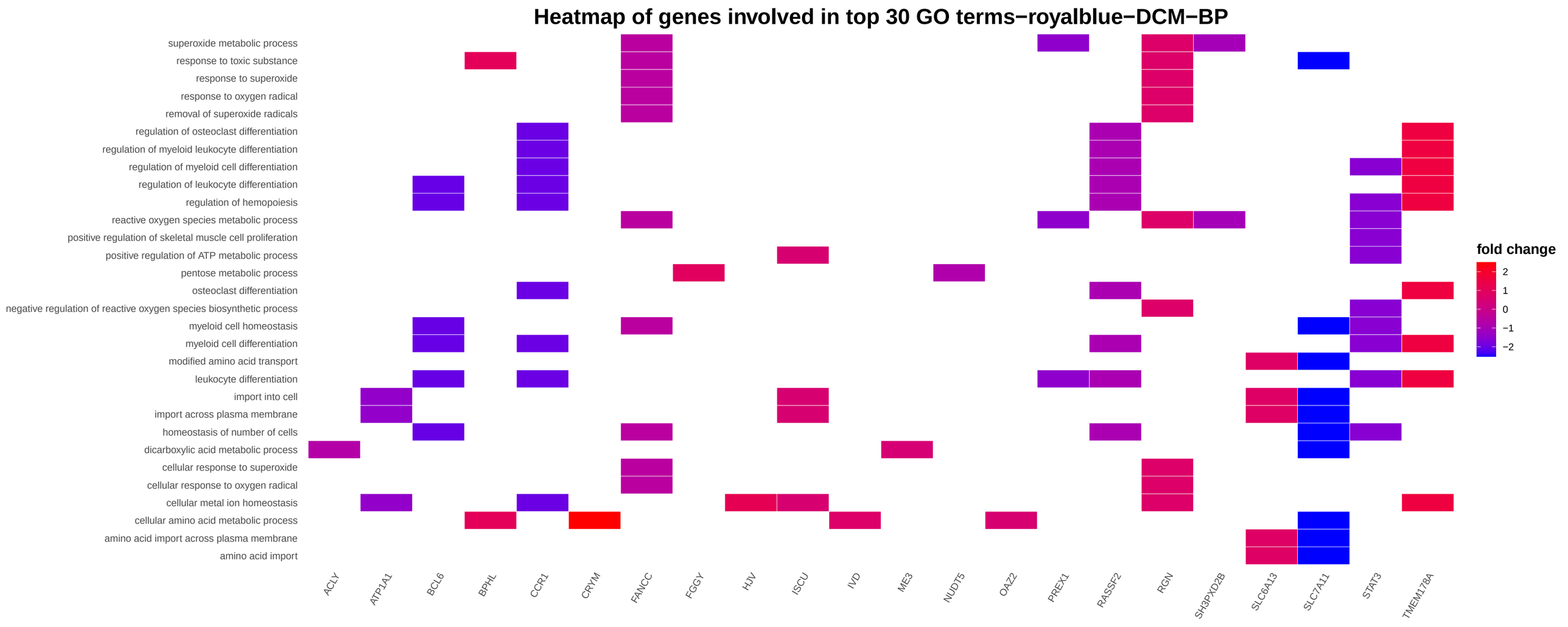
−1

Heatmap of genes involved in top 30 GO terms−grey60−PPCM−MF



Heatmap of genes involved in top 30 GO terms−grey60−PPCM−ALL




Heatmap of genes involved in top 30 GO terms−royalblue−DCM−BP
superoxide metabolic process
response to toxic substance
response to superoxide
response to oxygen radical
removal of superoxide radicals
regulation of osteoclast differentiation
regulation of myeloid leukocyte differentiation
regulation of myeloid cell differentiation
regulation of leukocyte differentiation
regulation of hemopoiesis
reactive oxygen species metabolic process
positive regulation of skeletal muscle cell proliferation
positive regulation of ATP metabolic process
pentose metabolic process
osteoclast differentiation
negative regulation of reactive oxygen species biosynthetic process
myeloid cell homeostasis
myeloid cell differentiation
modified amino acid transport
leukocyte differentiation
import into cell
import across plasma membrane
homeostasis of number of cells
dicarboxylic acid metabolic process
cellular response to superoxide
cellular response to oxygen radical
cellular metal ion homeostasis
cellular amino acid metabolic process
amino acid import across plasma membrane
amino acid import
ACLY
ATP1A1
BCL6
BPHL
CCR1
CRYM
FANCC
FGGY
HJV
ISCU
IVD
ME3
NUDT5
OAZ2
PREX1
RASSF2
RGN
SH3PXD2B
SLC6A13
SLC7A11
STAT3
TMEM178A
fold change
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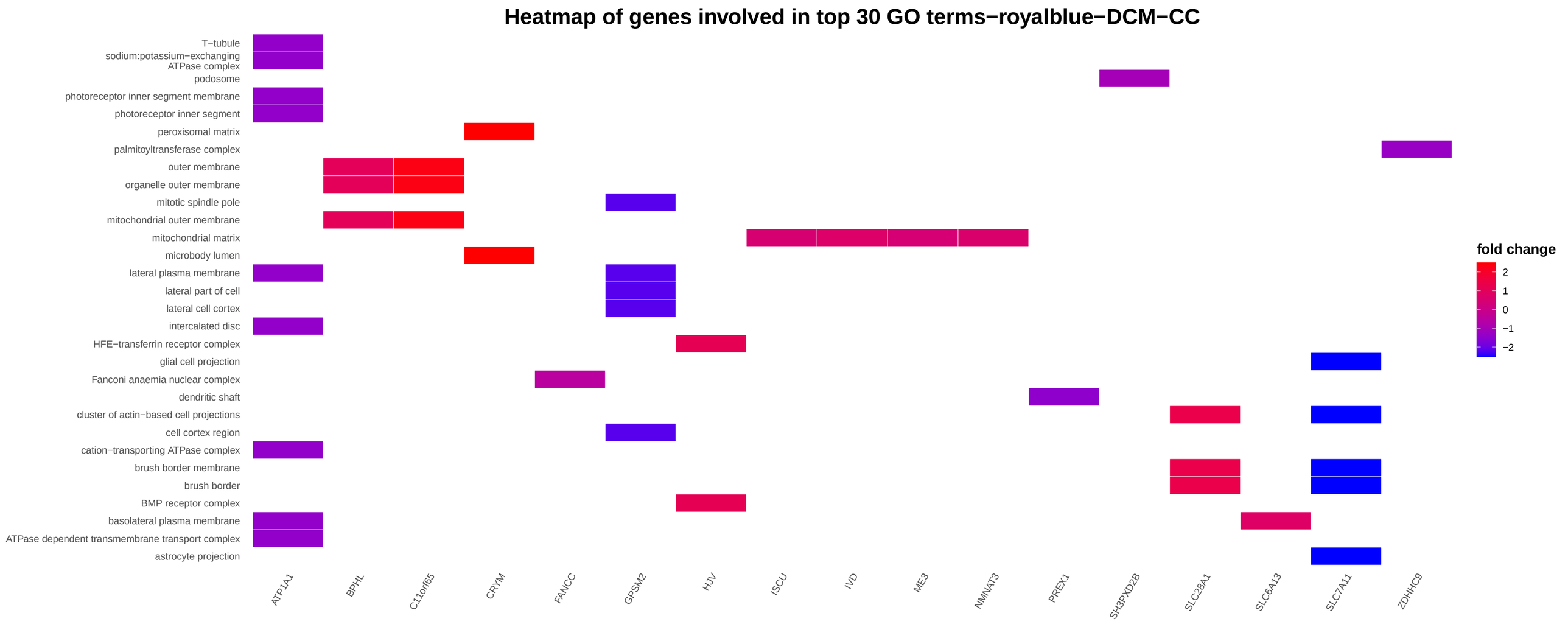
−1
−2


Heatmap of genes involved in top 30 GO terms−royalblue−DCM−CC
T−tubule
sodium:potassium−exchanging ATPase complex
podosome
photoreceptor inner segment membrane
photoreceptor inner segment
peroxisomal matrix
palmitoyltransferase complex
outer membrane
organelle outer membrane
mitotic spindle pole
mitochondrial outer membrane
mitochondrial matrix
microbody lumen
lateral plasma membrane
lateral part of cell
lateral cell cortex
intercalated disc
HFE−transferrin receptor complex
glial cell projection
Fanconi anaemia nuclear complex
dendritic shaft
cluster of actin−based cell projections
cell cortex region
cation−transporting ATPase complex
brush border membrane
brush border
BMP receptor complex
basolateral plasma membrane
ATPase dependent transmembrane transport complex
astrocyte projection
ATP1A1
BPHL
C11orf65
CRYM
FANCC
GPSM2
HJV
ISCU
IVD
ME3
NMNAT3
PREX1
SH3PXD2B
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SLC7A11
ZDHHC9
fold change
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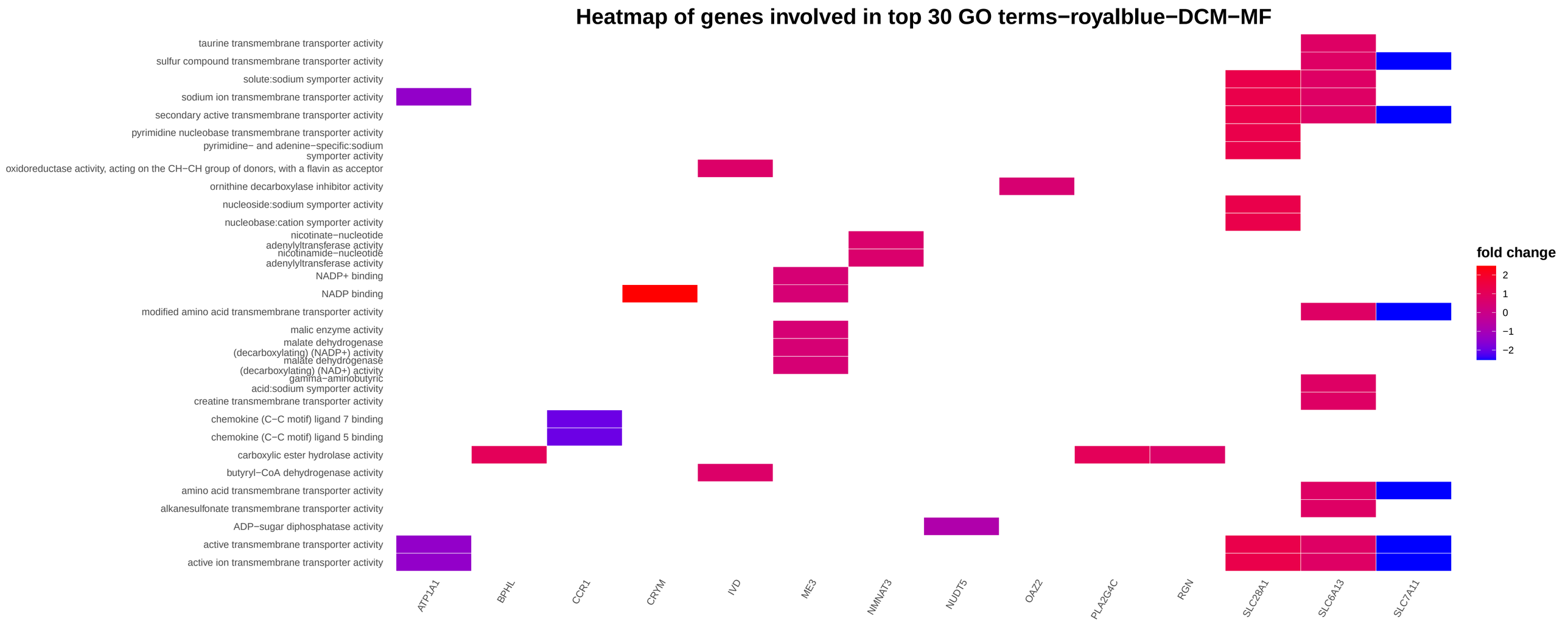
Heatmap of genes involved in top 30 GO terms−royalblue−DCM−MF
taurine transmembrane transporter activity
sulfur compound transmembrane transporter activity
solute:sodium symporter activity
sodium ion transmembrane transporter activity
secondary active transmembrane transporter activity
pyrimidine nucleobase transmembrane transporter activity
pyrimidine− and adenine−specific:sodium symporter activity
oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as acceptor
ornithine decarboxylase inhibitor activity
nucleoside:sodium symporter activity
nucleobase:cation symporter activity
nicotinate−nucleotide adenylyltransferase activity
nicotinamide−nucleotide adenylyltransferase activity
NADP+ binding
NADP binding
modified amino acid transmembrane transporter activity
malic enzyme activity
malate dehydrogenase (decarboxylating) (NADP+) activity
malate dehydrogenase (decarboxylating) (NAD+) activity
gamma−aminobutyric acid:sodium symporter activity
creatine transmembrane transporter activity
chemokine (C−C motif) ligand 7 binding
chemokine (C−C motif) ligand 5 binding
carboxylic ester hydrolase activity
butyryl−CoA dehydrogenase activity
amino acid transmembrane transporter activity
alkanesulfonate transmembrane transporter activity
ADP−sugar diphosphatase activity
active transmembrane transporter activity
active ion transmembrane transporter activity
ATP1A1
BPHL
CCR1
CRYM
IVD
ME3
NMNAT3
NUDT5
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SLC7A11
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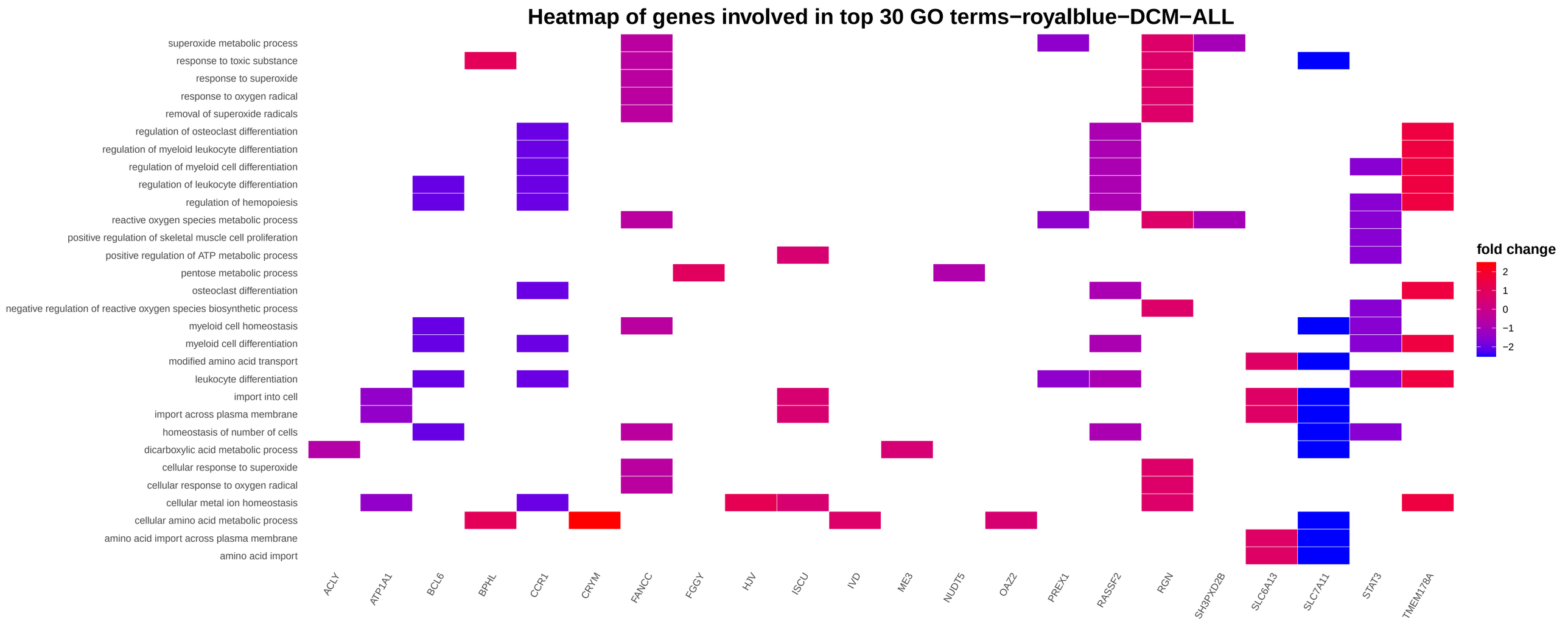
Heatmap of genes involved in top 30 GO terms−royalblue−DCM−ALL
superoxide metabolic process
response to toxic substance
response to superoxide
response to oxygen radical
removal of superoxide radicals
regulation of osteoclast differentiation
regulation of myeloid leukocyte differentiation
regulation of myeloid cell differentiation
regulation of leukocyte differentiation
regulation of hemopoiesis
reactive oxygen species metabolic process
positive regulation of skeletal muscle cell proliferation
positive regulation of ATP metabolic process
pentose metabolic process
osteoclast differentiation
negative regulation of reactive oxygen species biosynthetic process
myeloid cell homeostasis
myeloid cell differentiation
modified amino acid transport
leukocyte differentiation
import into cell
import across plasma membrane
homeostasis of number of cells
dicarboxylic acid metabolic process
cellular response to superoxide
cellular response to oxygen radical
cellular metal ion homeostasis
cellular amino acid metabolic process
amino acid import across plasma membrane
amino acid import
ACLY
ATP1A1
BCL6
BPHL
CCR1
CRYM
FANCC
FGGY
HJV
ISCU
IVD
ME3
NUDT5
OAZ2
PREX1
RASSF2
RGN
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SLC7A11
STAT3
TMEM178A
fold change
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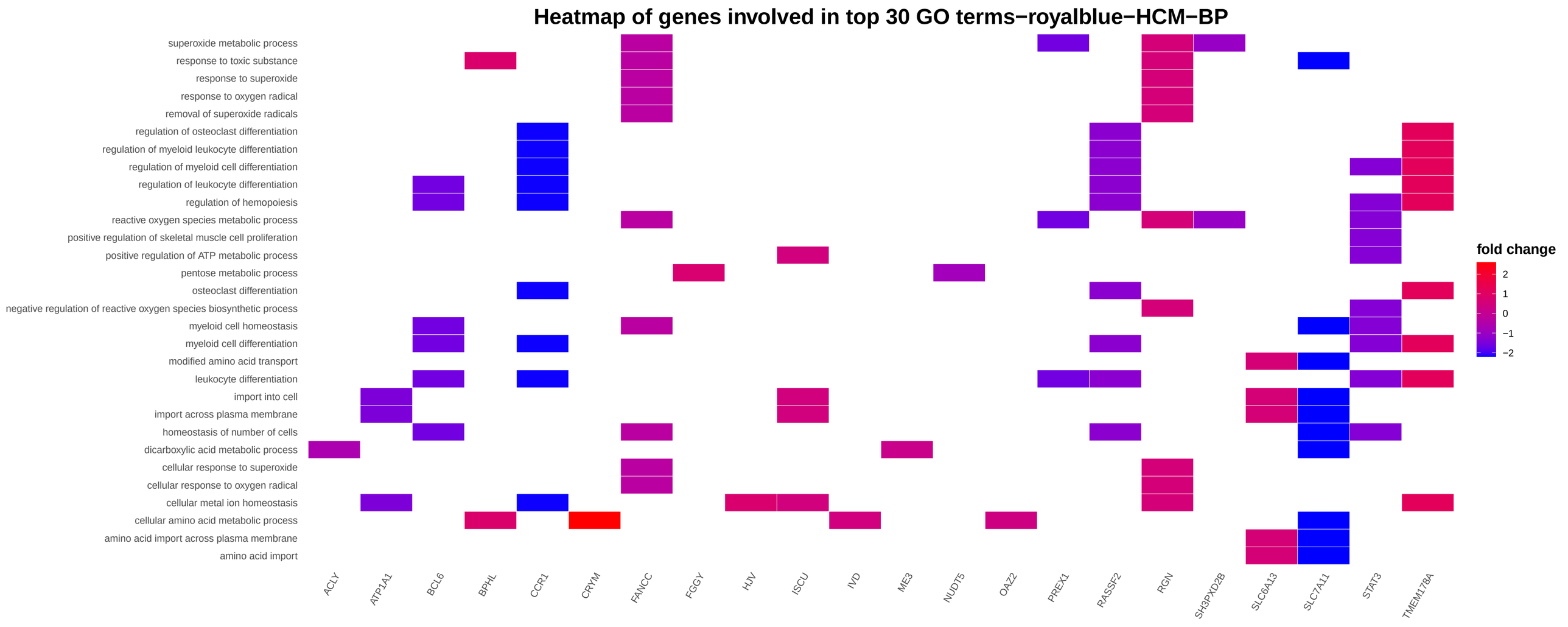
−2


Heatmap of genes involved in top 30 GO terms−royalblue−HCM−BP
superoxide metabolic process
response to toxic substance
response to superoxide
response to oxygen radical
removal of superoxide radicals
regulation of osteoclast differentiation
regulation of myeloid leukocyte differentiation
regulation of myeloid cell differentiation
regulation of leukocyte differentiation
regulation of hemopoiesis
reactive oxygen species metabolic process
positive regulation of skeletal muscle cell proliferation
positive regulation of ATP metabolic process
pentose metabolic process
osteoclast differentiation
negative regulation of reactive oxygen species biosynthetic process
myeloid cell homeostasis
myeloid cell differentiation
modified amino acid transport
leukocyte differentiation
import into cell
import across plasma membrane
homeostasis of number of cells
dicarboxylic acid metabolic process
cellular response to superoxide
cellular response to oxygen radical
cellular metal ion homeostasis
cellular amino acid metabolic process
amino acid import across plasma membrane
amino acid import
ACLY
ATP1A1
BCL6
BPHL
CCR1
CRYM
FANCC
FGGY
HJV
ISCU
IVD
ME3
NUDT5
OAZ2
PREX1
RASSF2
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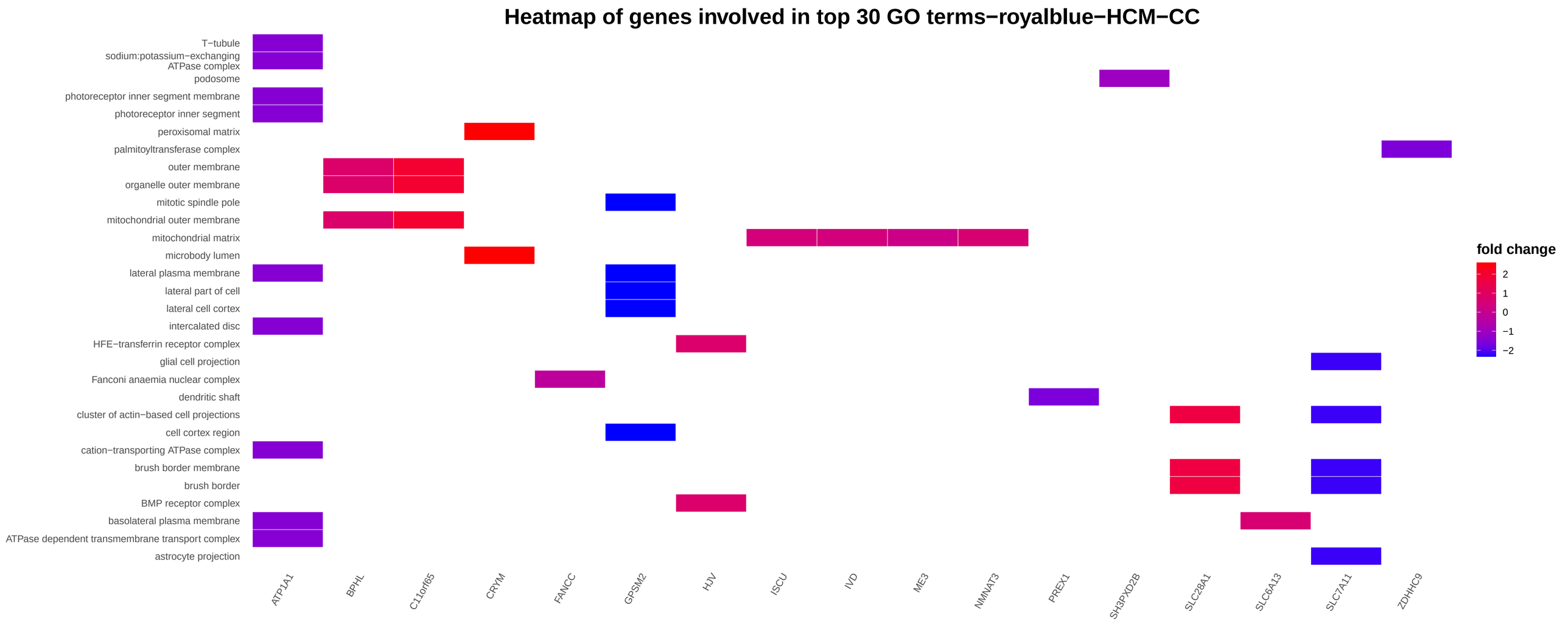
Heatmap of genes involved in top 30 GO terms−royalblue−HCM−CC
T−tubule
sodium:potassium−exchanging ATPase complex
podosome
photoreceptor inner segment membrane
photoreceptor inner segment
peroxisomal matrix
palmitoyltransferase complex
outer membrane
organelle outer membrane
mitotic spindle pole
mitochondrial outer membrane
mitochondrial matrix
microbody lumen
lateral plasma membrane
lateral part of cell
lateral cell cortex
intercalated disc
HFE−transferrin receptor complex
glial cell projection
Fanconi anaemia nuclear complex
dendritic shaft
cluster of actin−based cell projections
cell cortex region
cation−transporting ATPase complex
brush border membrane
brush border
BMP receptor complex
basolateral plasma membrane
ATPase dependent transmembrane transport complex
astrocyte projection
ATP1A1
BPHL
C11orf65
CRYM
FANCC
GPSM2
HJV
ISCU
IVD
ME3
NMNAT3
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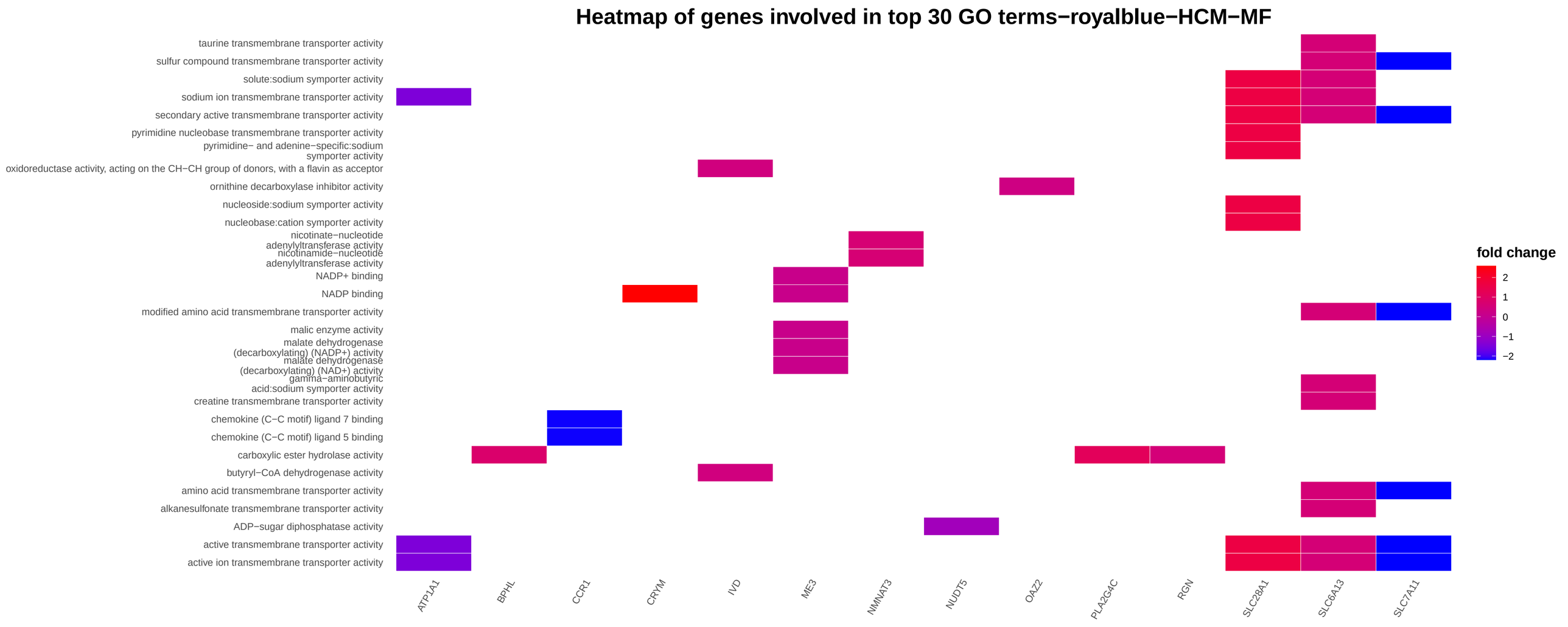
Heatmap of genes involved in top 30 GO terms−royalblue−HCM−MF
taurine transmembrane transporter activity
sulfur compound transmembrane transporter activity
solute:sodium symporter activity
sodium ion transmembrane transporter activity
secondary active transmembrane transporter activity
pyrimidine nucleobase transmembrane transporter activity
pyrimidine− and adenine−specific:sodium symporter activity
oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as acceptor
ornithine decarboxylase inhibitor activity
nucleoside:sodium symporter activity
nucleobase:cation symporter activity
nicotinate−nucleotide adenylyltransferase activity
nicotinamide−nucleotide adenylyltransferase activity
NADP+ binding
NADP binding
modified amino acid transmembrane transporter activity
malic enzyme activity
malate dehydrogenase (decarboxylating) (NADP+) activity
malate dehydrogenase (decarboxylating) (NAD+) activity
gamma−aminobutyric acid:sodium symporter activity
creatine transmembrane transporter activity
chemokine (C−C motif) ligand 7 binding
chemokine (C−C motif) ligand 5 binding
carboxylic ester hydrolase activity
butyryl−CoA dehydrogenase activity
amino acid transmembrane transporter activity
alkanesulfonate transmembrane transporter activity
ADP−sugar diphosphatase activity
active transmembrane transporter activity
active ion transmembrane transporter activity
ATP1A1
BPHL
CCR1
CRYM
IVD
ME3
NMNAT3
NUDT5
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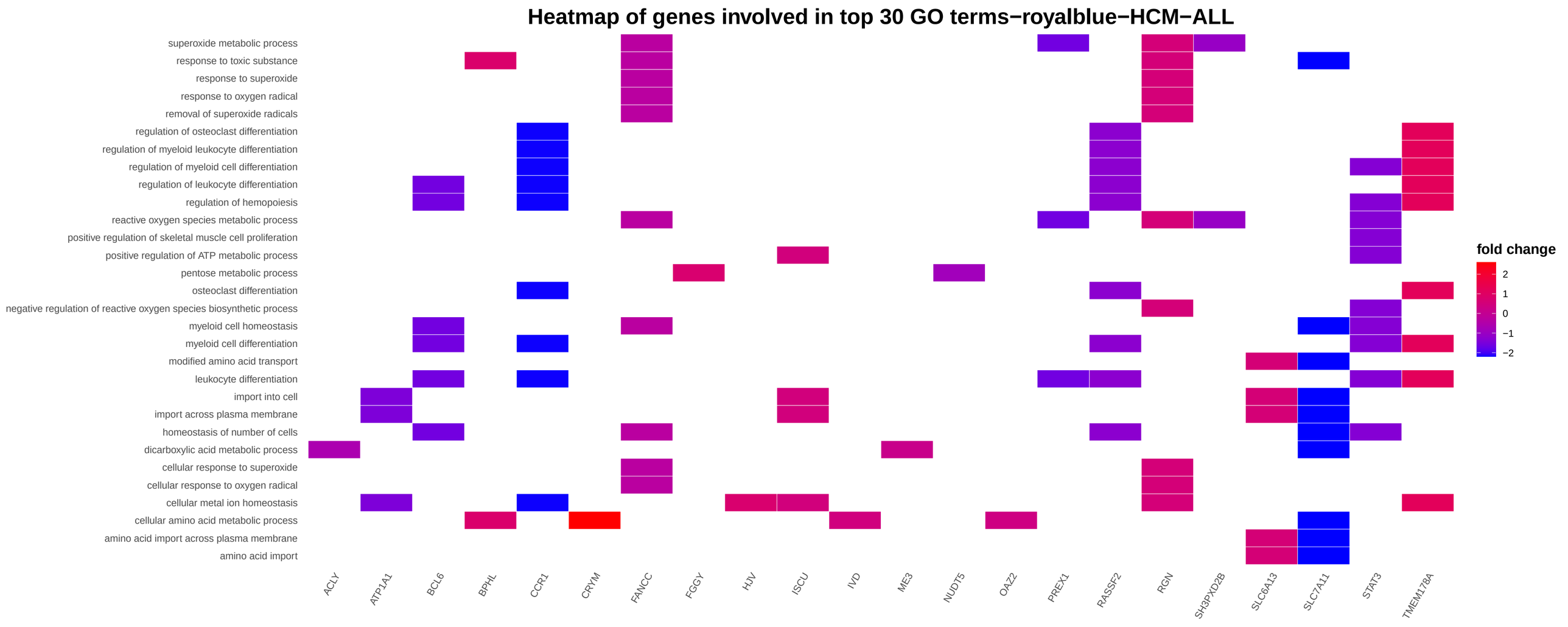
Heatmap of genes involved in top 30 GO terms−royalblue−HCM−ALL
superoxide metabolic process
response to toxic substance
response to superoxide
response to oxygen radical
removal of superoxide radicals
regulation of osteoclast differentiation
regulation of myeloid leukocyte differentiation
regulation of myeloid cell differentiation
regulation of leukocyte differentiation
regulation of hemopoiesis
reactive oxygen species metabolic process
positive regulation of skeletal muscle cell proliferation
positive regulation of ATP metabolic process
pentose metabolic process
osteoclast differentiation
negative regulation of reactive oxygen species biosynthetic process
myeloid cell homeostasis
myeloid cell differentiation
modified amino acid transport
leukocyte differentiation
import into cell
import across plasma membrane
homeostasis of number of cells
dicarboxylic acid metabolic process
cellular response to superoxide
cellular response to oxygen radical
cellular metal ion homeostasis
cellular amino acid metabolic process
amino acid import across plasma membrane
amino acid import
ACLY
ATP1A1
BCL6
BPHL
CCR1
CRYM
FANCC
FGGY
HJV
ISCU
IVD
ME3
NUDT5
OAZ2
PREX1
RASSF2
RGN
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STAT3
TMEM178A
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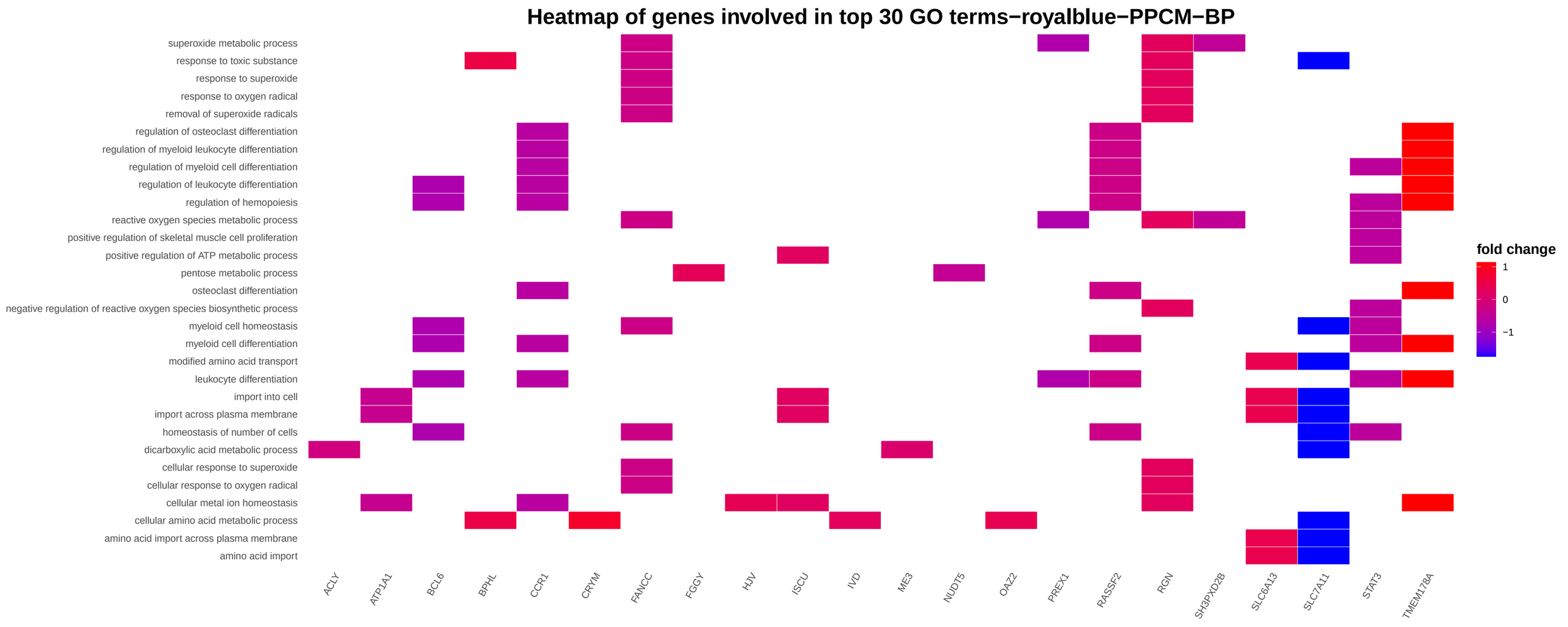
Heatmap of genes involved in top 30 GO terms−royalblue−PPCM−BP
superoxide metabolic process
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NUDT5
OAZ2
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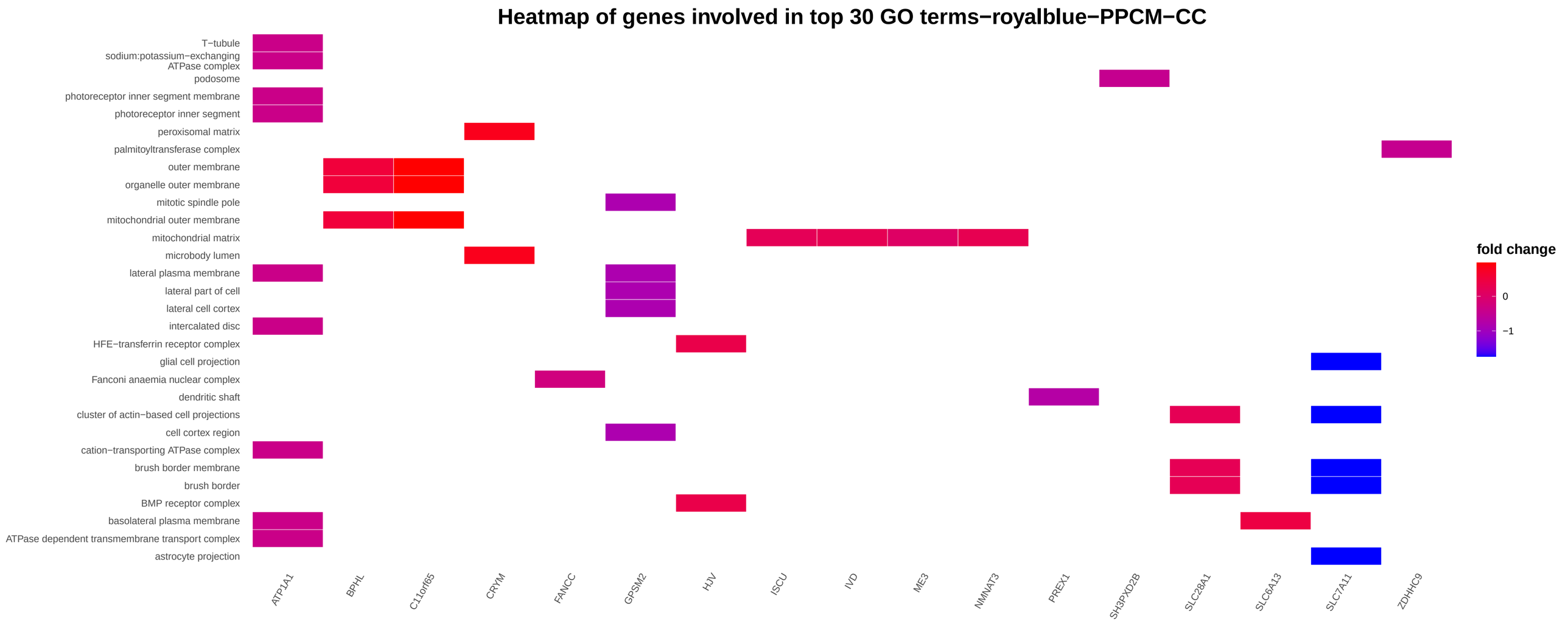
Heatmap of genes involved in top 30 GO terms−royalblue−PPCM−CC
T−tubule
sodium:potassium−exchanging ATPase complex
podosome
photoreceptor inner segment membrane
photoreceptor inner segment
peroxisomal matrix
palmitoyltransferase complex
outer membrane
organelle outer membrane
mitotic spindle pole
mitochondrial outer membrane
mitochondrial matrix
microbody lumen
lateral plasma membrane
lateral part of cell
lateral cell cortex
intercalated disc
HFE−transferrin receptor complex
glial cell projection
Fanconi anaemia nuclear complex
dendritic shaft
cluster of actin−based cell projections
cell cortex region
cation−transporting ATPase complex
brush border membrane
brush border
BMP receptor complex
basolateral plasma membrane
ATPase dependent transmembrane transport complex
astrocyte projection
ATP1A1
BPHL
C11orf65
CRYM
FANCC
GPSM2
HJV
ISCU
IVD
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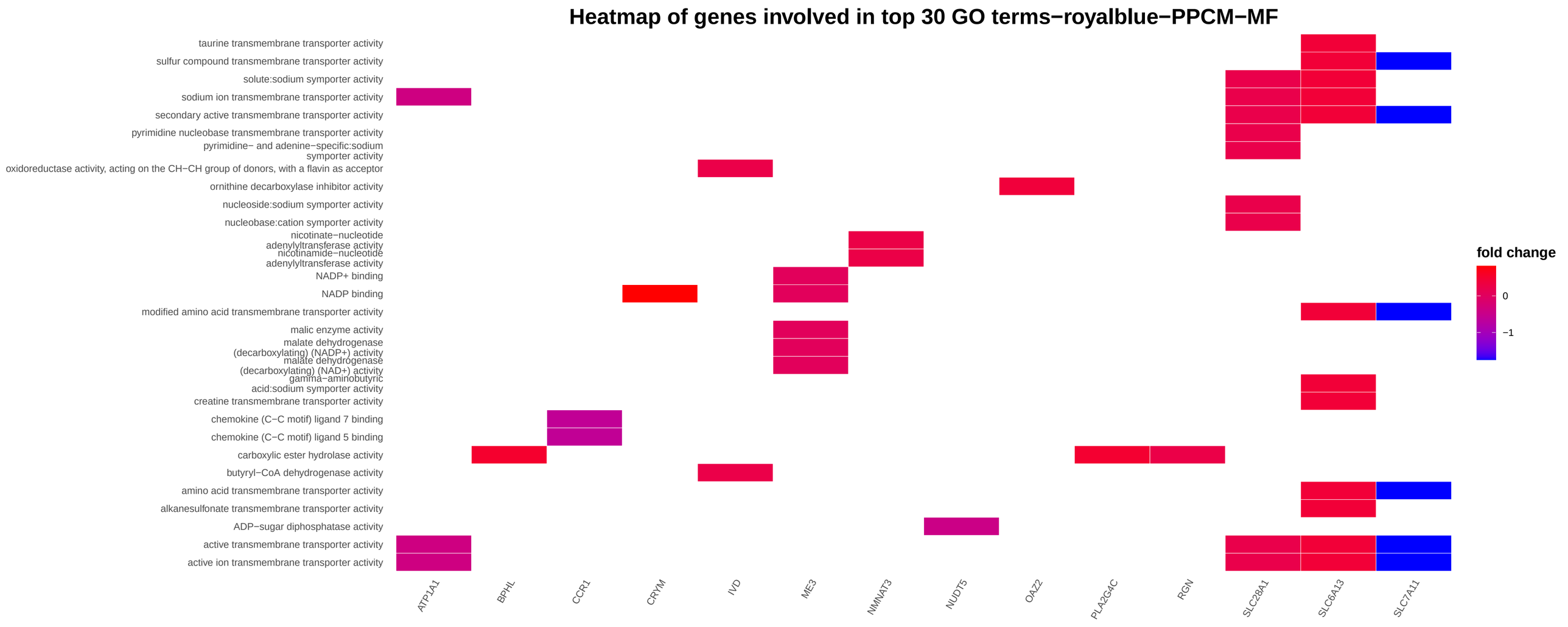
Heatmap of genes involved in top 30 GO terms−royalblue−PPCM−MF
taurine transmembrane transporter activity
sulfur compound transmembrane transporter activity
solute:sodium symporter activity
sodium ion transmembrane transporter activity
secondary active transmembrane transporter activity
pyrimidine nucleobase transmembrane transporter activity
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oxidoreductase activity, acting on the CH−CH group of donors, with a flavin as acceptor
ornithine decarboxylase inhibitor activity
nucleoside:sodium symporter activity
nucleobase:cation symporter activity
nicotinate−nucleotide adenylyltransferase activity
nicotinamide−nucleotide adenylyltransferase activity
NADP+ binding
NADP binding
modified amino acid transmembrane transporter activity
malic enzyme activity
malate dehydrogenase (decarboxylating) (NADP+) activity
malate dehydrogenase (decarboxylating) (NAD+) activity
gamma−aminobutyric acid:sodium symporter activity
creatine transmembrane transporter activity
chemokine (C−C motif) ligand 7 binding
chemokine (C−C motif) ligand 5 binding
carboxylic ester hydrolase activity
butyryl−CoA dehydrogenase activity
amino acid transmembrane transporter activity
alkanesulfonate transmembrane transporter activity
ADP−sugar diphosphatase activity
active transmembrane transporter activity
active ion transmembrane transporter activity
ATP1A1
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CCR1
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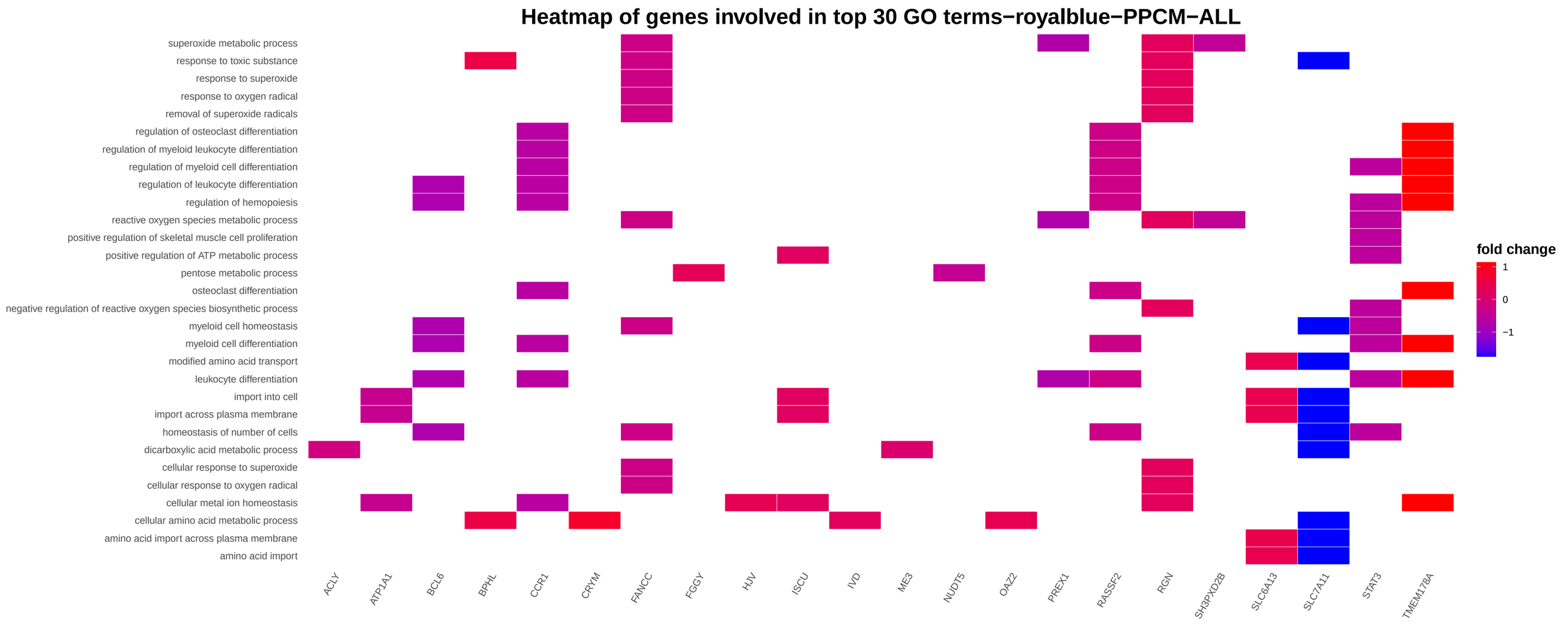
Heatmap of genes involved in top 30 GO terms−royalblue−PPCM−ALL
superoxide metabolic process
response to toxic substance
response to superoxide
response to oxygen radical
removal of superoxide radicals
regulation of osteoclast differentiation
regulation of myeloid leukocyte differentiation
regulation of myeloid cell differentiation
regulation of leukocyte differentiation
regulation of hemopoiesis
reactive oxygen species metabolic process
positive regulation of skeletal muscle cell proliferation
positive regulation of ATP metabolic process
pentose metabolic process
osteoclast differentiation
negative regulation of reactive oxygen species biosynthetic process
myeloid cell homeostasis
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modified amino acid transport
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import into cell
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homeostasis of number of cells
dicarboxylic acid metabolic process
cellular response to superoxide
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cellular metal ion homeostasis
cellular amino acid metabolic process
amino acid import across plasma membrane
amino acid import
ACLY
ATP1A1
BCL6
BPHL
CCR1
CRYM
FANCC
FGGY
HJV
ISCU
IVD
ME3
NUDT5
OAZ2
PREX1
RASSF2
RGN
SH3PXD2B
SLC6A13
SLC7A11
STAT3
TMEM178A
fold change
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