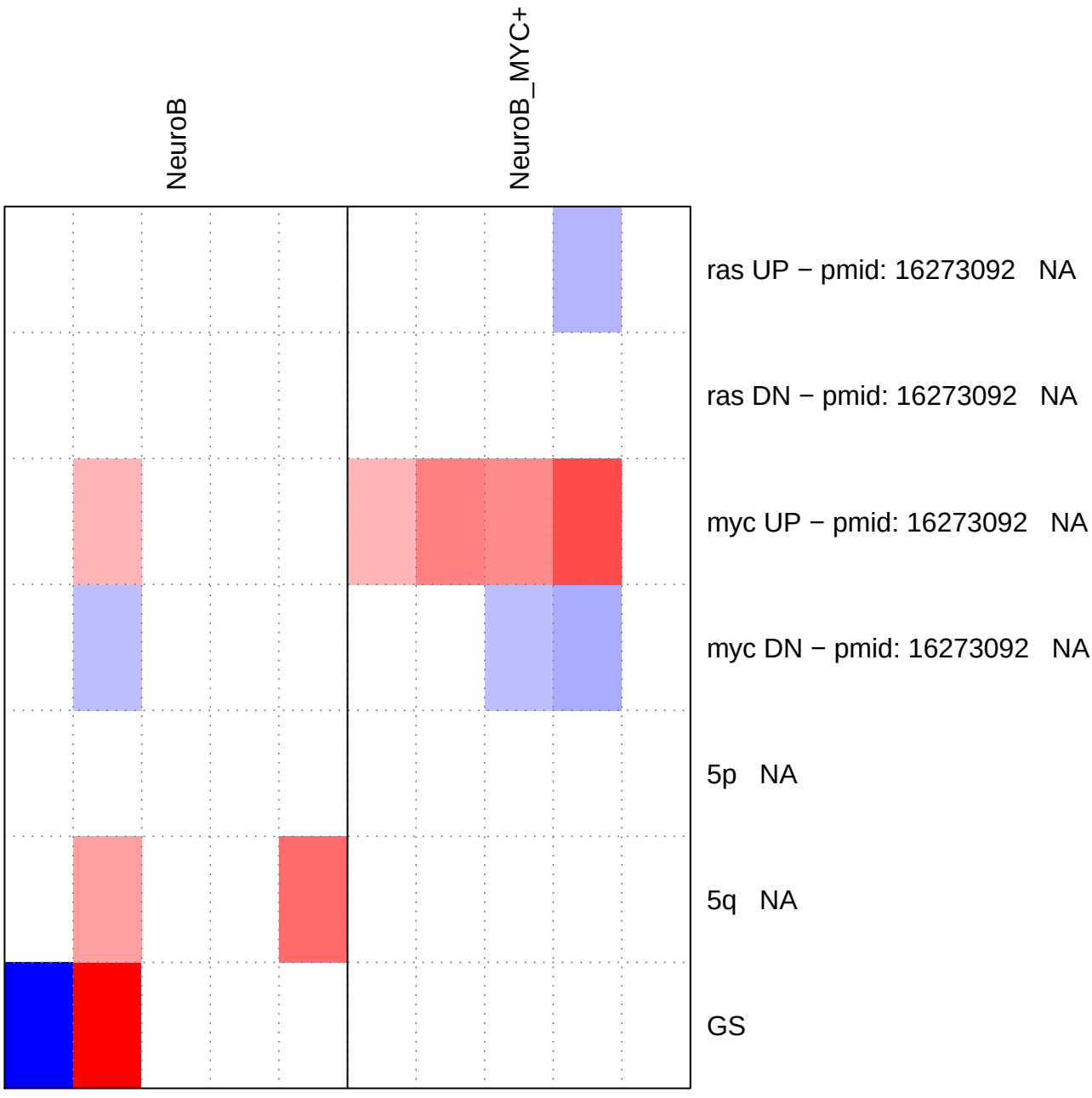
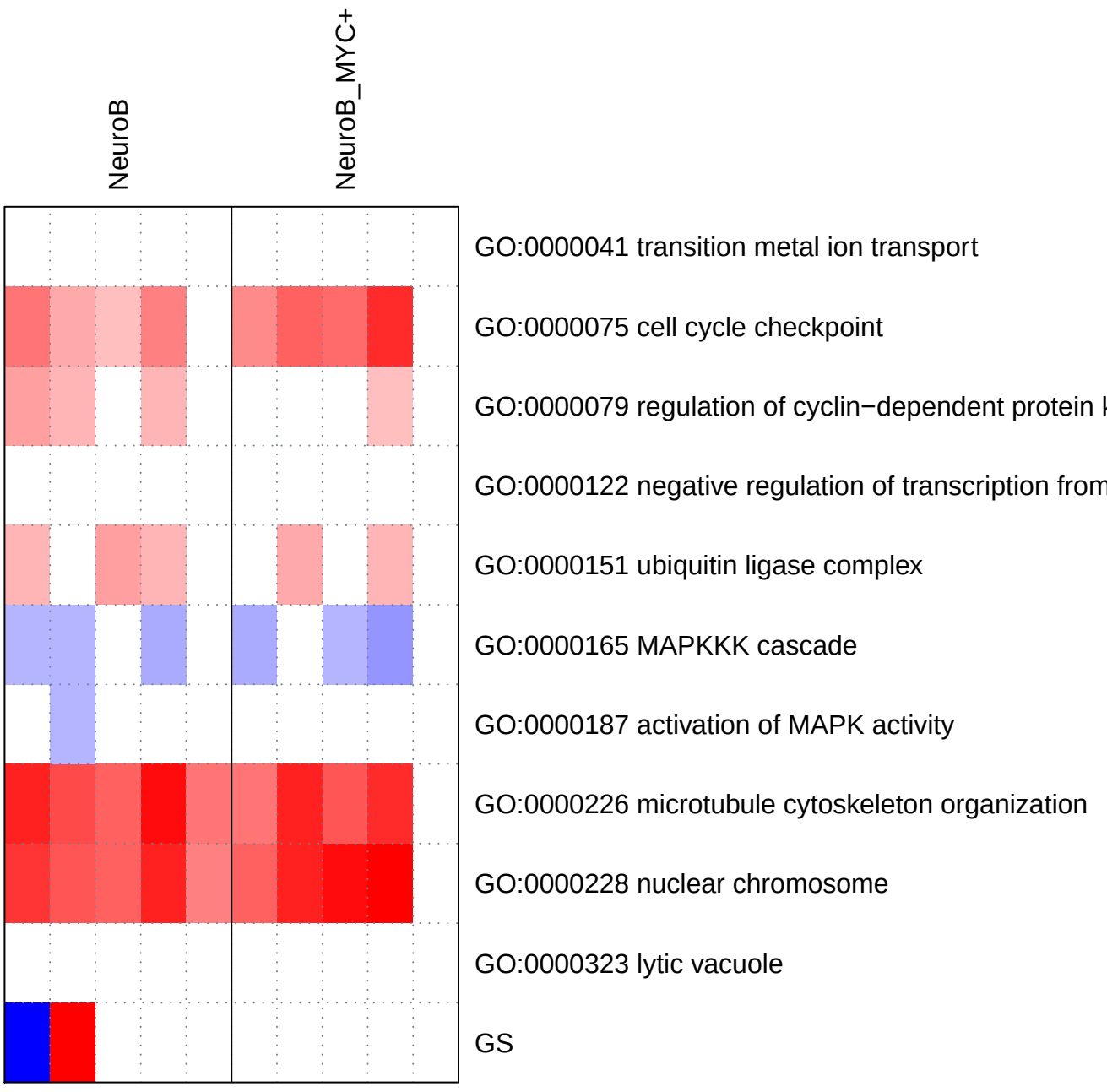
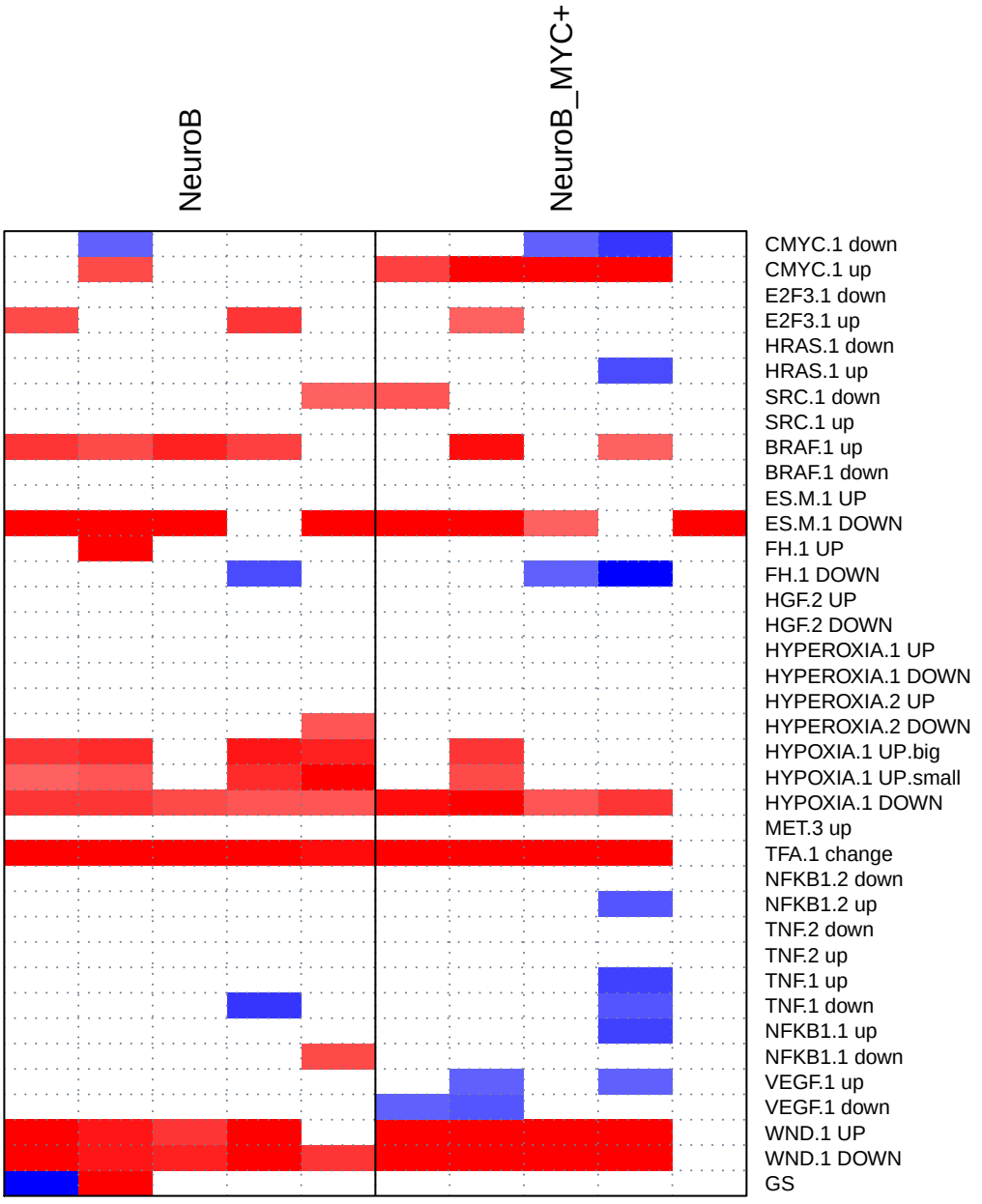
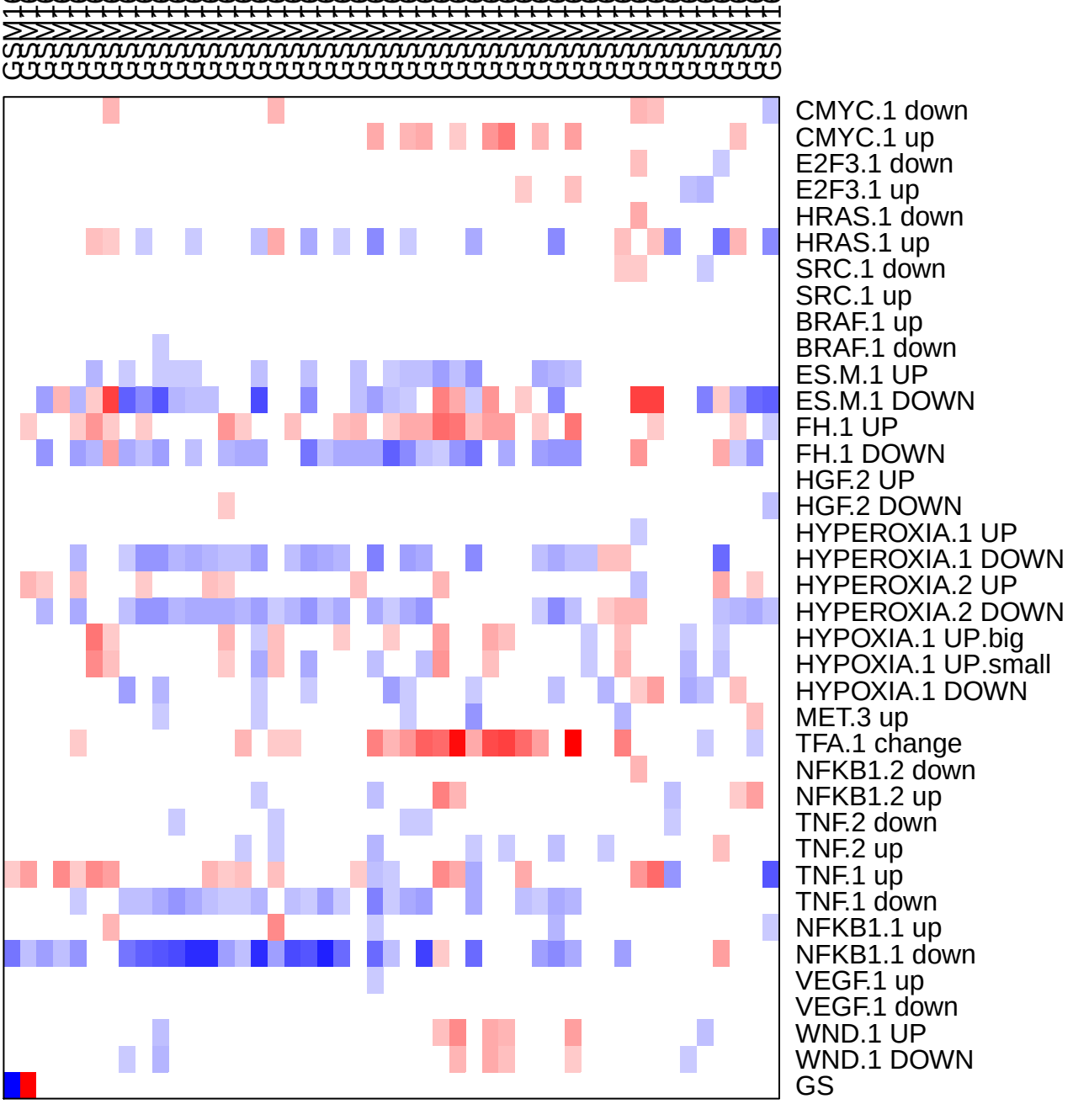
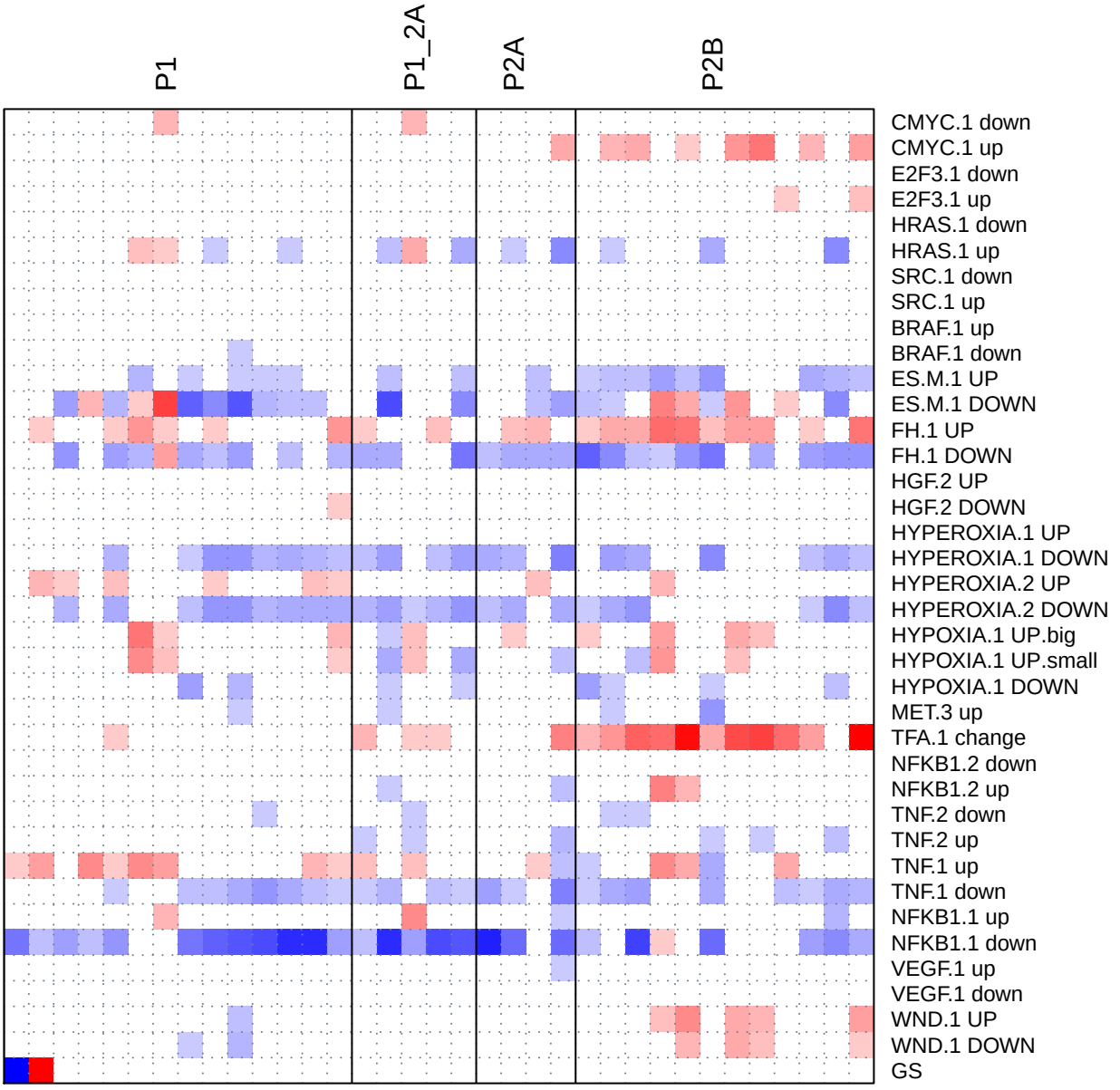
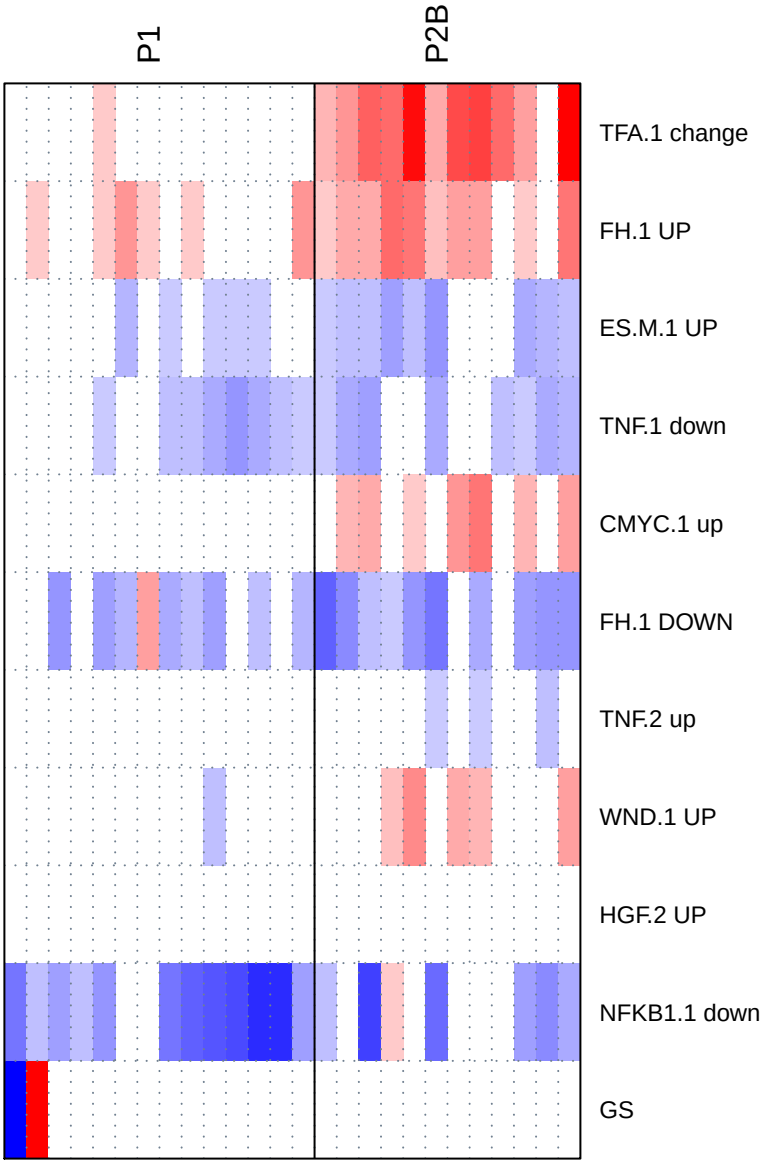

NeuroB
NeuroB_MYC+
ras UP − pmid: 16273092 NA
ras DN − pmid: 16273092 NA
myc UP − pmid: 16273092 NA
myc DN − pmid: 16273092 NA
5p NA
5q NA
GS

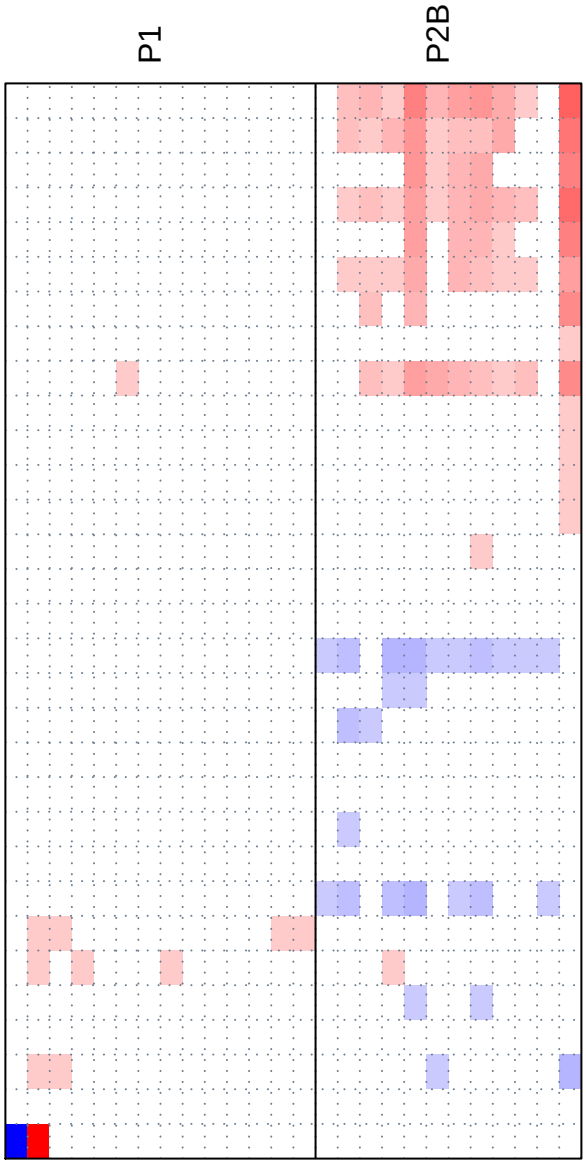

NeuroB
NeuroB_MYC+
GO:0000041 transition metal ion transport
GO:0000075 cell cycle checkpoint
GO:0000079 regulation of cyclin−dependent protein k
GO:0000122 negative regulation of transcription from
GO:0000151 ubiquitin ligase complex
GO:0000165 MAPKKK cascade
GO:0000187 activation of MAPK activity
GO:0000226 microtubule cytoskeleton organization
GO:0000228 nuclear chromosome
GO:0000323 lytic vacuole
GS


NeuroB
NeuroB_MYC+
CMYC.1 down
CMYC.1 up
E2F3.1 down
E2F3.1 up
HRAS.1 down
HRAS.1 up
SRC.1 down
SRC.1 up
BRAF.1 up
BRAF.1 down
ES.M.1 UP
ES.M.1 DOWN
FH.1 UP
FH.1 DOWN
HGF.2 UP
HGF.2 DOWN
HYPEROXIA.1 UP
HYPEROXIA.1 DOWN
HYPEROXIA.2 UP
HYPEROXIA.2 DOWN
HYPOXIA.1 UP.big
HYPOXIA.1 UP.small
HYPOXIA.1 DOWN
MET.3 up
TFA.1 change
NFKB1.2 down
NFKB1.2 up
TNF.2 down
TNF.2 up
TNF.1 up
TNF.1 down
NFKB1.1 up
NFKB1.1 down
VEGF.1 up
VEGF.1 down
WND.1 UP
WND.1 DOWN
GS


CMYC.1 down
CMYC.1 up
E2F3.1 down
E2F3.1 up
HRAS.1 down
HRAS.1 up
SRC.1 down
SRC.1 up
BRAF.1 up
BRAF.1 down
ES.M.1 UP
ES.M.1 DOWN
FH.1 UP
FH.1 DOWN
HGF.2 UP
HGF.2 DOWN
HYPEROXIA.1 UP
HYPEROXIA.1 DOWN
HYPEROXIA.2 UP
HYPEROXIA.2 DOWN
HYPOXIA.1 UP.big
HYPOXIA.1 UP.small
HYPOXIA.1 DOWN
MET.3 up
TFA.1 change
NFKB1.2 down
NFKB1.2 up
TNF.2 down
TNF.2 up
TNF.1 up
TNF.1 down
NFKB1.1 up
NFKB1.1 down
VEGF.1 up
VEGF.1 down
WND.1 UP
WND.1 DOWN
GS


P1
P1_2A
P2A
P2B
CMYC.1 down
CMYC.1 up
E2F3.1 down
E2F3.1 up
HRAS.1 down
HRAS.1 up
SRC.1 down
SRC.1 up
BRAF.1 up
BRAF.1 down
ES.M.1 UP
ES.M.1 DOWN
FH.1 UP
FH.1 DOWN
HGF.2 UP
HGF.2 DOWN
HYPEROXIA.1 UP
HYPEROXIA.1 DOWN
HYPEROXIA.2 UP
HYPEROXIA.2 DOWN
HYPOXIA.1 UP.big
HYPOXIA.1 UP.small
HYPOXIA.1 DOWN
MET.3 up
TFA.1 change
NFKB1.2 down
NFKB1.2 up
TNF.2 down
TNF.2 up
TNF.1 up
TNF.1 down
NFKB1.1 up
NFKB1.1 down
VEGF.1 up
VEGF.1 down
WND.1 UP
WND.1 DOWN
GS


P1
P2B
TFA.1 change
FH.1 UP
ES.M.1 UP
TNF.1 down
CMYC.1 up
FH.1 DOWN
TNF.2 up
WND.1 UP
HGF.2 UP
NFKB1.1 down
GS



GO:0000775 chromosome, centromeric region
GO:0007059 chromosome segregation
GO:0005819 spindle
GO:0000793 condensed chromosome
GO:0000776 kinetochore
GO:0007346 regulation of mitotic cell cycle
GO:0000226 microtubule cytoskeleton organization
GO:0034399 nuclear periphery
GO:0000075 cell cycle checkpoint
GO:0010564 regulation of cell cycle process
GO:0007126 meiosis
GO:0051321 meiotic cell cycle
GO:0051327 M phase of meiotic cell cycle
GO:0016763 transferase activity, transferring pentosyl groups
GO:0000079 regulation of cyclin−dependent protein kinase activity
GO:0060249 anatomical structure homeostasis
GO:0001822 kidney development
GO:0044463 cell projection part
GO:0007369 gastrulation
GO:0032990 cell part morphogenesis
GO:0048858 cell projection morphogenesis
GO:0008237 metallopeptidase activity
GO:0048592 eye morphogenesis
GO:0001655 urogenital system development
GO:0005319 lipid transporter activity
GO:0051047 positive regulation of secretion
GO:0007423 sensory organ development
GO:0043010 camera−type eye development
GO:0004553 hydrolase activity, hydrolyzing O−glycosyl compounds
GO:0001654 eye development
GS