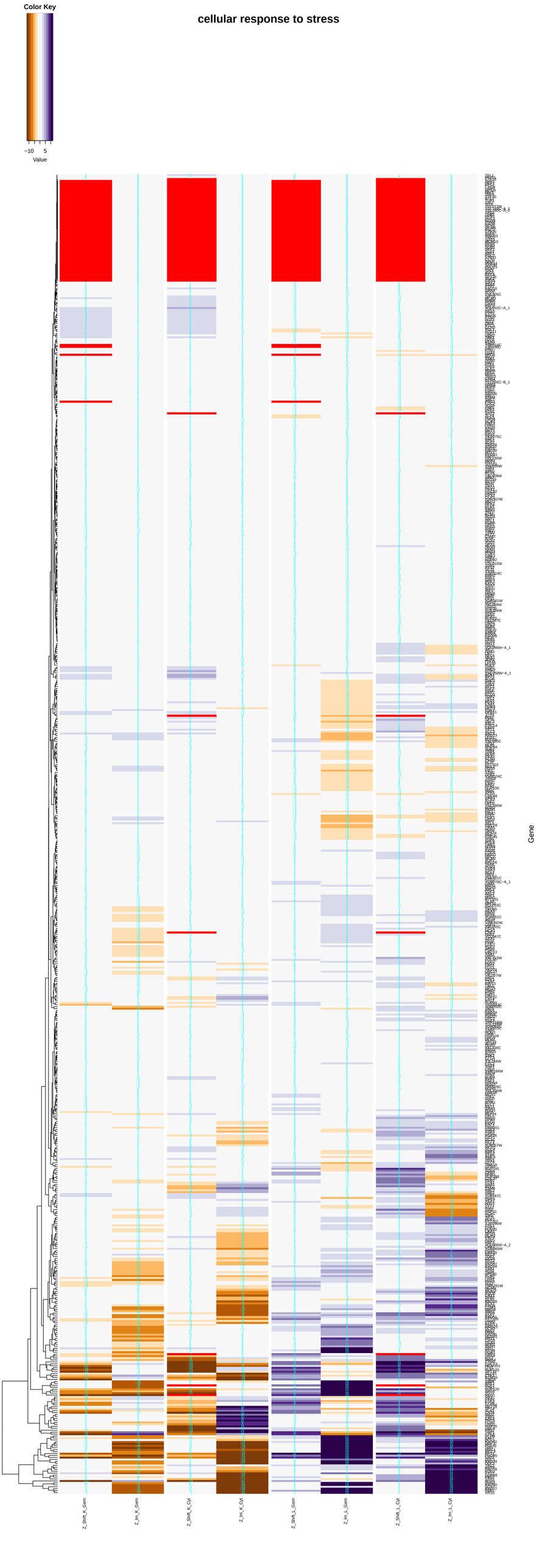
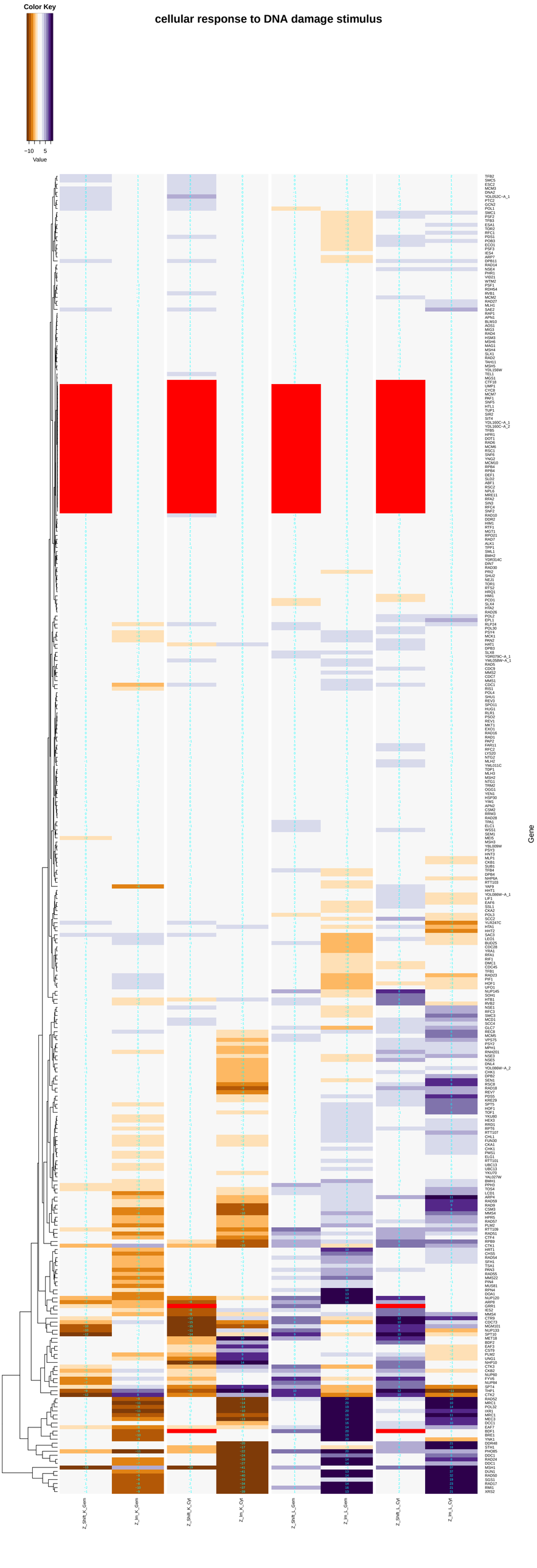
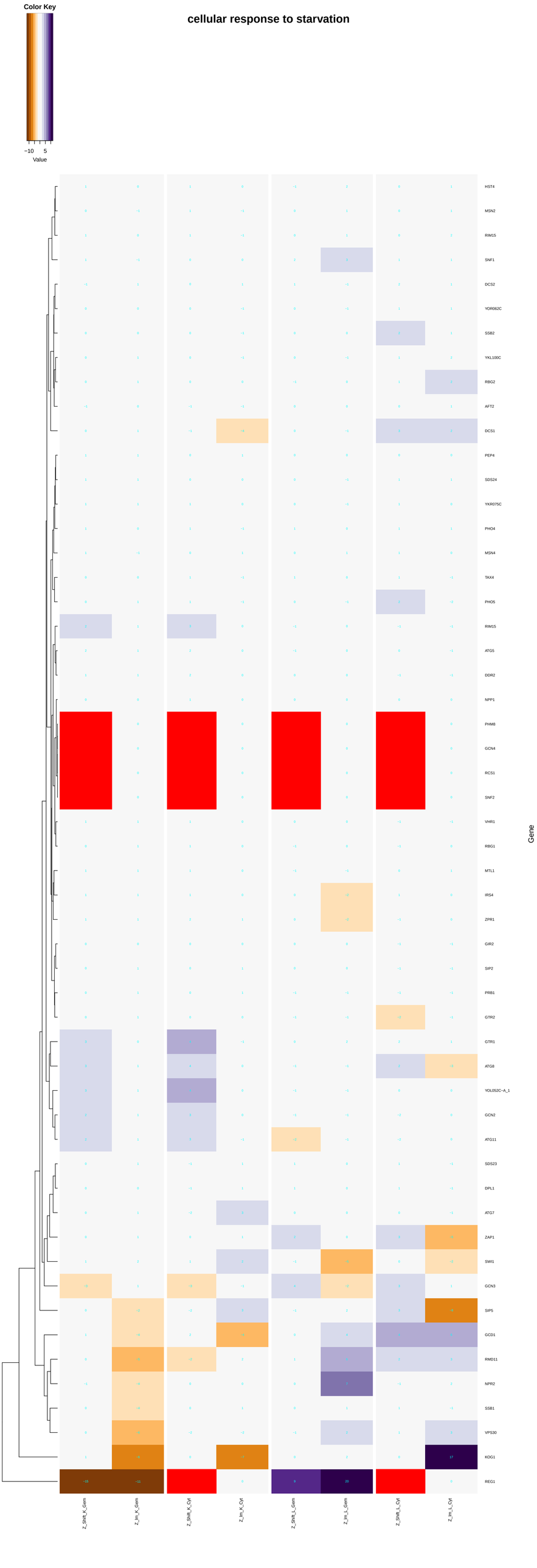
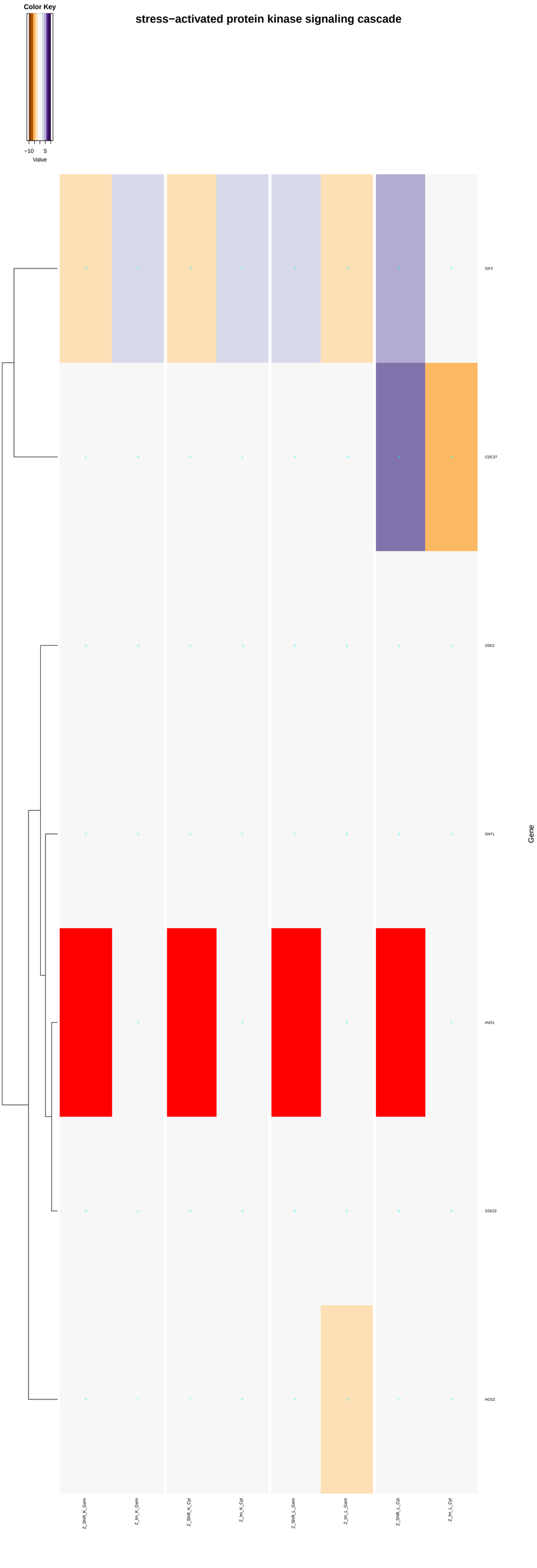

Color Key
−10
5
Value
cellular response to stress
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
cellular response to DNA damage stimulus
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
cellular response to starvation
HST4
MSN2
RIM15
SNF1
DCS2
YOR062C
SSB2
YKL100C
RBG2
AFT2
DCS1
PEP4
SDS24
YKR075C
PHO4
MSN4
TAX4
PHO5
RIM15
ATG5
DDR2
NPP1
PHM8
GCN4
RCS1
SNF2
YHR1
RBG1
MTL1
IRS4
ZPR1
GIR2
SIP2
PRB1
GTR2
GTR1
ATG8
YOL052C−A_1
GCN2
ATG11
SDS23
DPL1
ATG7
ZAP1
SWI1
GCN3
SIP5
GCD1
RMD11
NPR2
SSB1
VPS30
KOG1
REG1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
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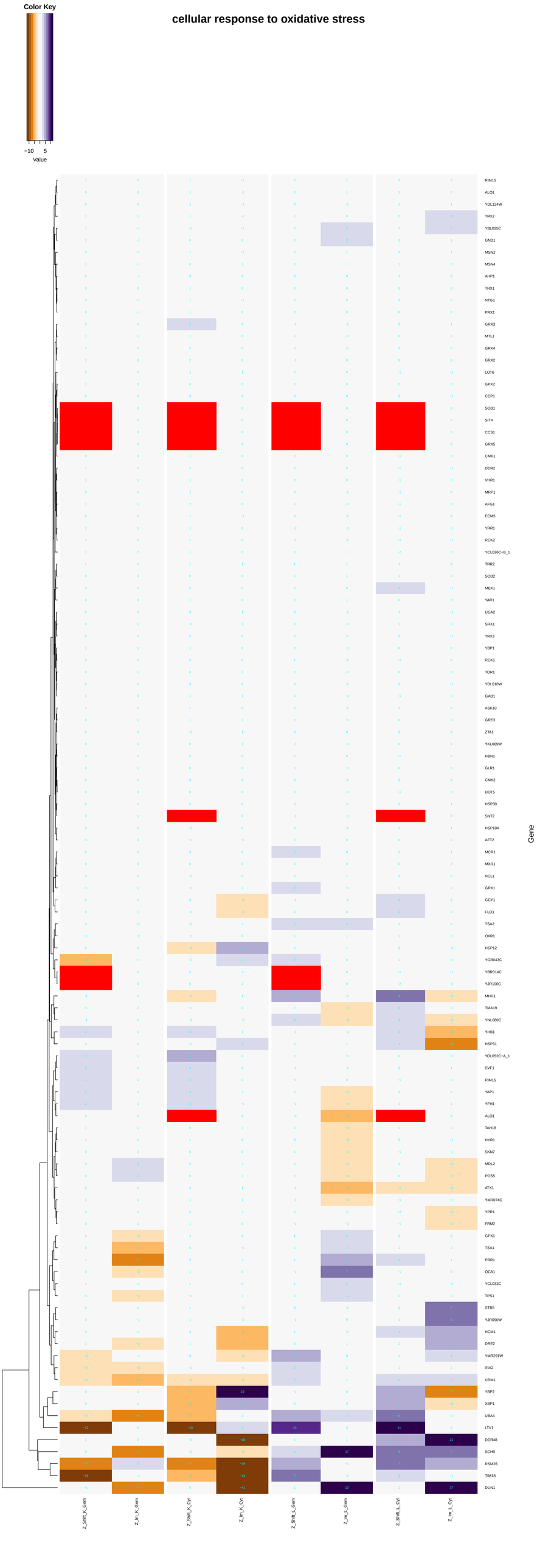
Value
stress−activated protein kinase signaling cascade
SIF2
CDC37
SSK2
SNT1
AVO1
SSK22
HOS2
Gene
Z_Shlt_K_Gem
Z_In_K_Gem
Z_Shlt_K_Cyt
Z_In_K_Cyt
Z_Shlt_L_Gem
Z_In_L_Gem
Z_Shlt_L_Cyt
Z_In_L_Cyt


Color Key
−10
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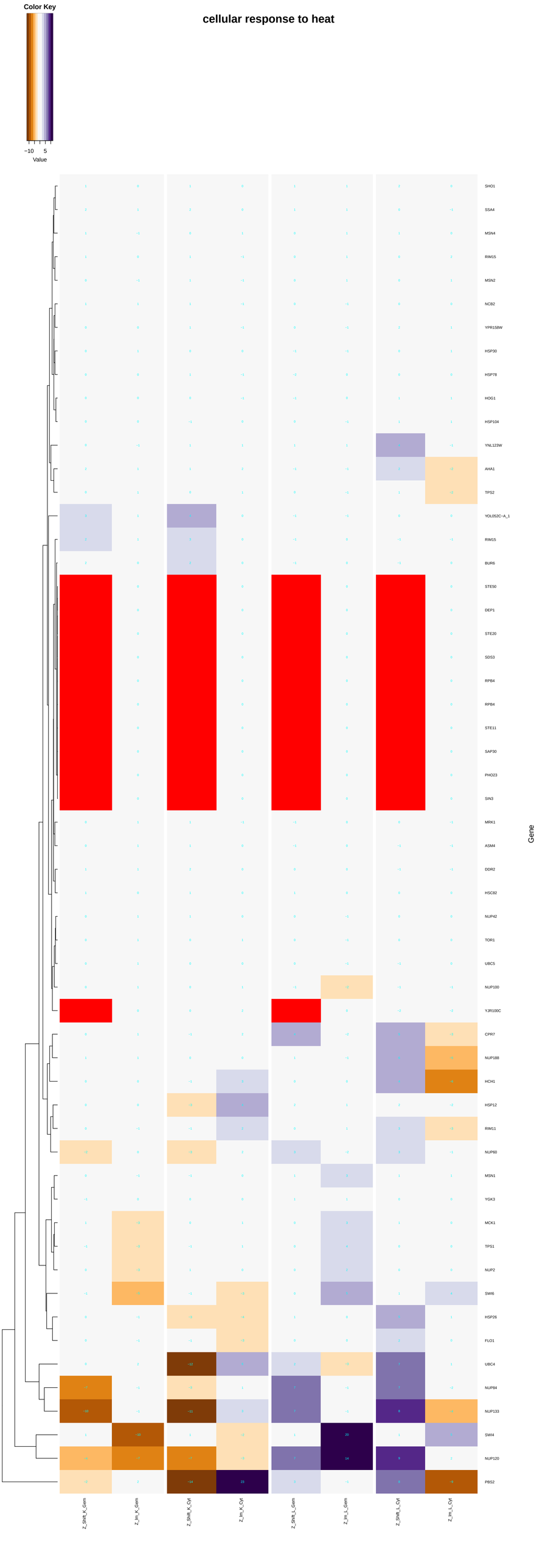
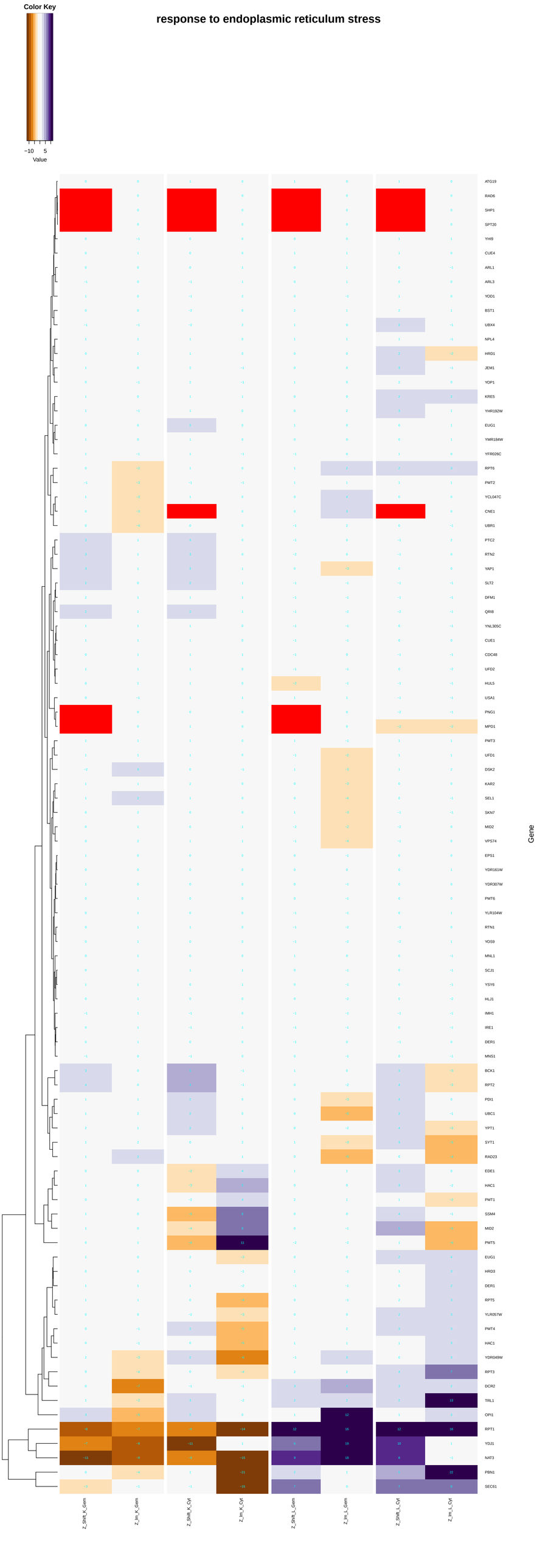
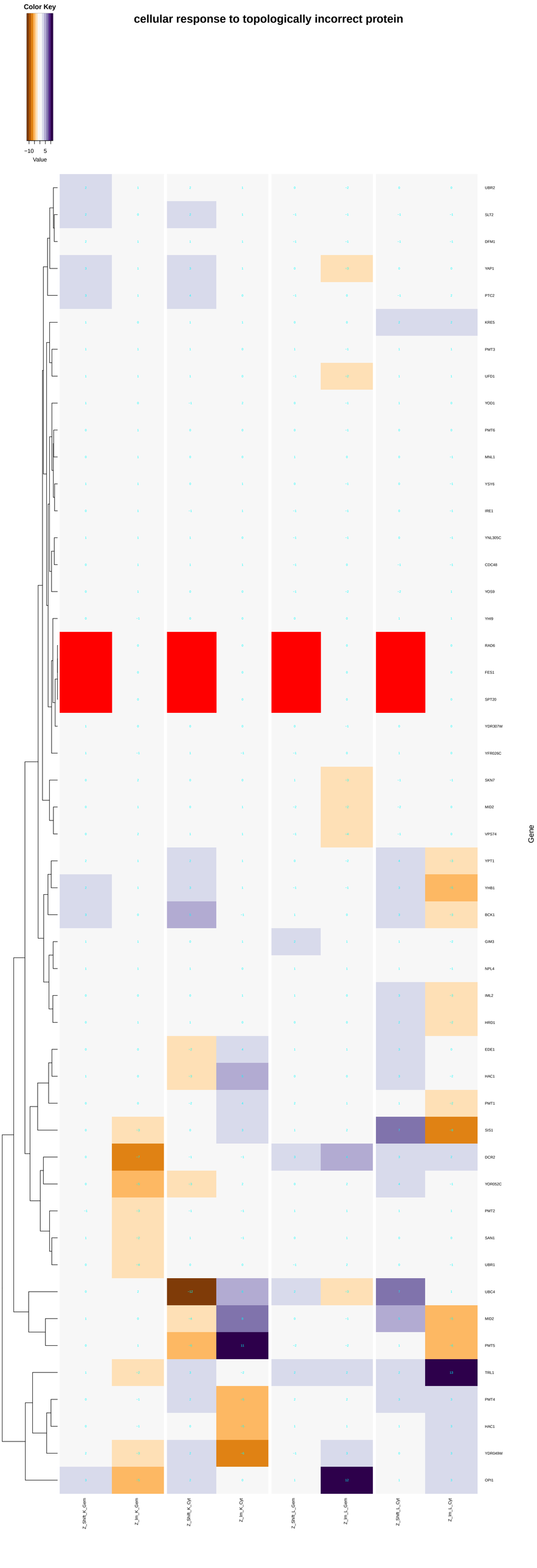
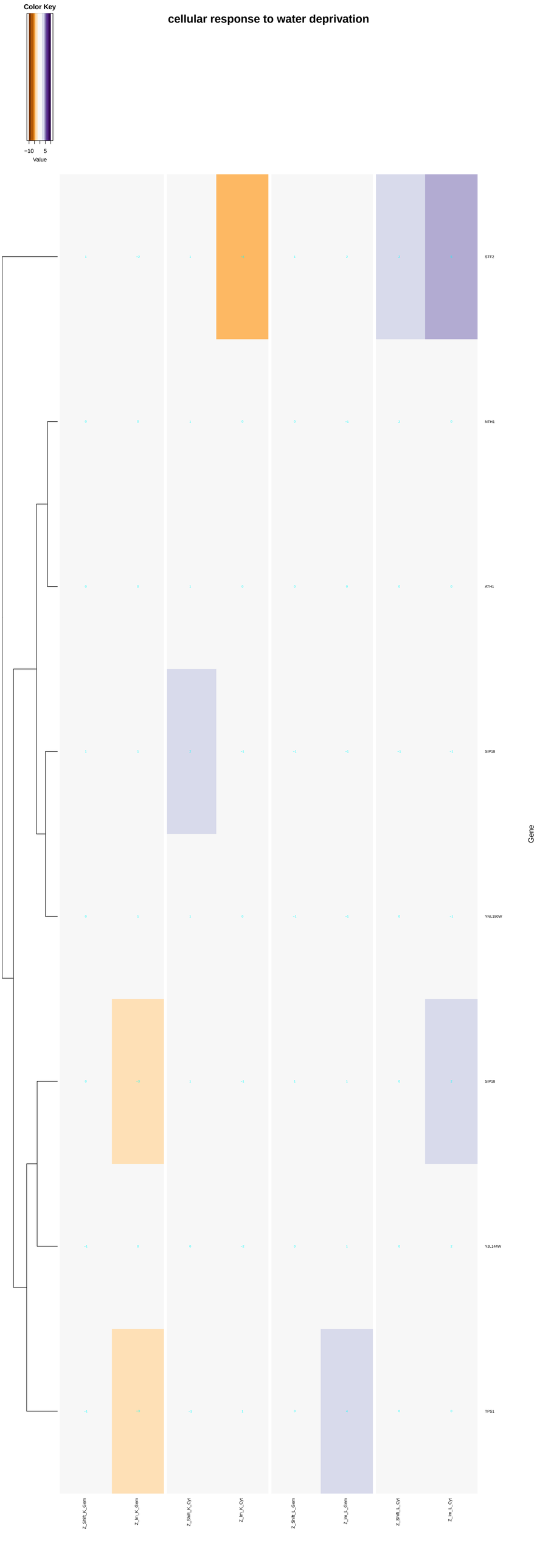
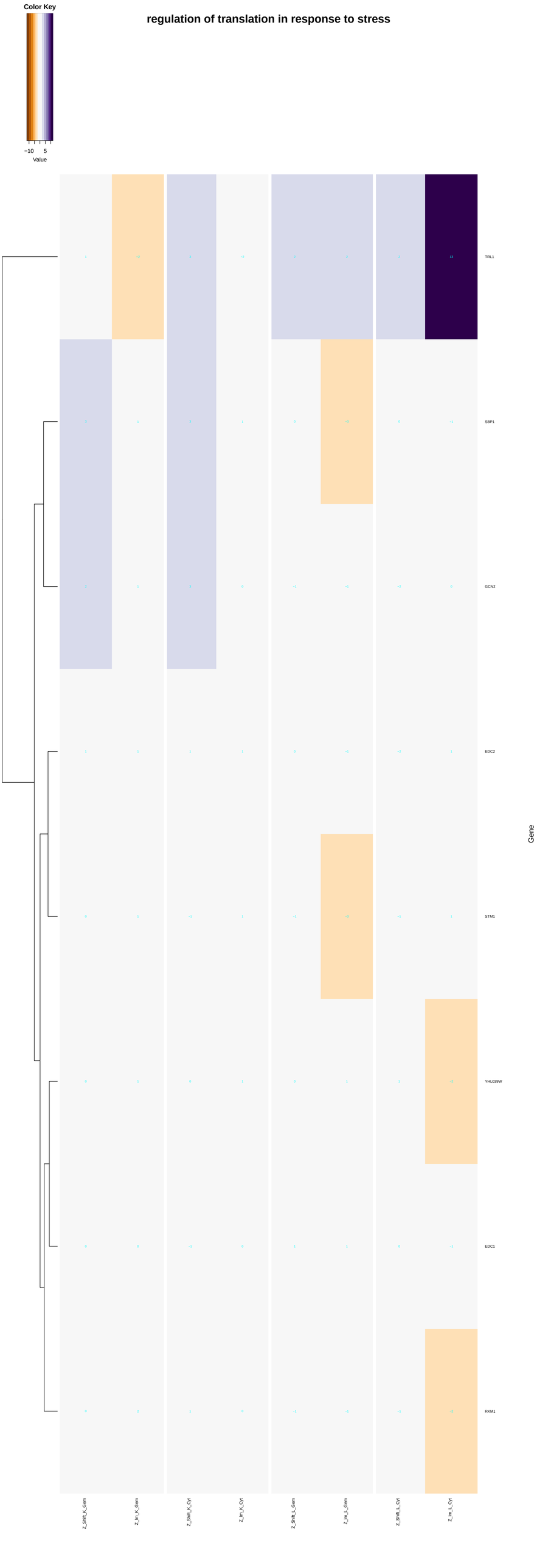
Value
cellular response to oxidative stress
RIM15
ALO1
YDL124W
TRX2
YBL055C
GND1
MSN2
MSN4
AHP1
TRX1
NTG1
PRX1
GRX3
MTL1
GRX4
GRX2
LOT6
GPX2
CCP1
SOD1
SIT4
CCS1
GRX5
CMK1
DDR2
YHR1
MRP1
AFG1
ECM5
YRR1
RCK2
YCL026C−B_1
TRR2
SOD2
MEK1
YAR1
UGA2
SRX1
TRX3
YBP1
RCK1
TOR1
YDL010W
GAD1
ASK10
GRE3
ZTA1
YKL069W
HBN1
GLR1
CMK2
DOT5
HSP30
SNT2
HSP104
AFT2
MCR1
MXR1
NCL1
GRX1
GCY1
FLO1
TSA2
OXR1
HSP12
YGR043C
YBR014C
YJR100C
MHR1
TMA19
YNL080C
YHB1
HSP31
YOL052C−A_1
SVF1
RIM15
YAP1
YFH1
ALO1
TAH18
HYR1
SKN7
MDL2
POS5
ATX1
YMR074C
YPR1
FRM2
GPX1
TSA1
PRR1
OCA1
YCL033C
TPS1
STB5
YJR096W
HCM1
DRE2
YMR291W
IRA2
URM1
YBP2
XBP1
UBA4
LTV1
DDR48
SCH9
RSM26
TIM18
DUN1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

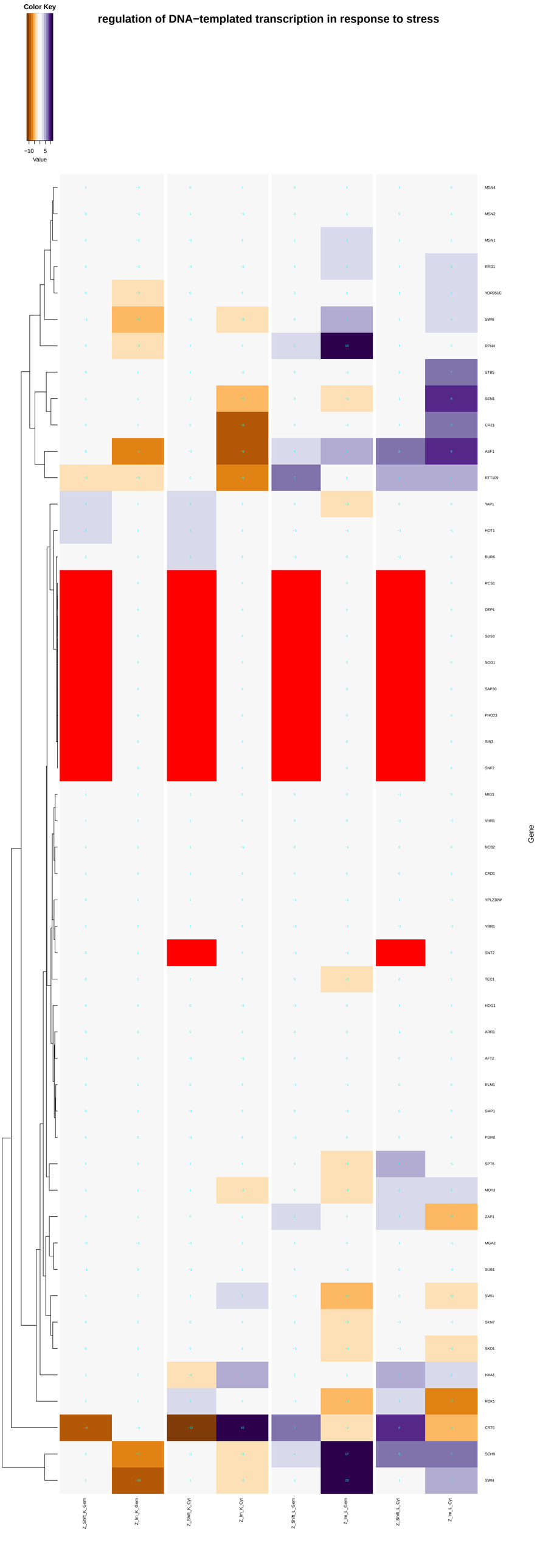

Color Key
−10
5
Value
cellular response to heat
SHO1
SSA4
MSN4
RIM15
MSN2
NCB2
YPR158W
HSP30
HSP78
HOG1
HSP104
YNL123W
AHA1
TPS2
YOL052C−A_1
RIM15
BUR6
STE50
DEP1
STE20
SDS3
RPB4
RPB4
STE11
SAP30
PHO23
SIN3
MRK1
ASM4
DDR2
HSC82
NUP42
TOR1
UBC5
NUP100
YJR100C
CPR7
NUP188
HCH1
HSP12
RIM11
NUP60
MSN1
YGK3
MCK1
TPS1
NUP2
SWI6
HSP26
FLO1
UBC4
NUP84
NUP133
SWI4
NUP120
PBS2
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

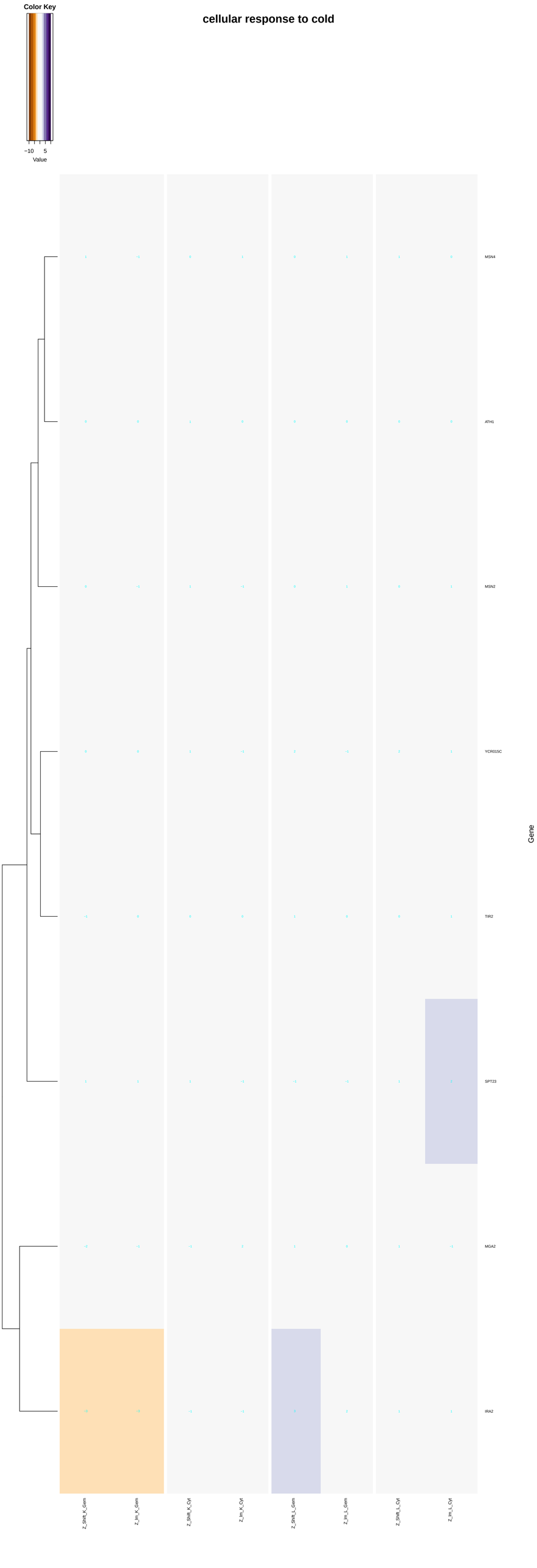

Color Key
−10
5
Value
response to endoplasmic reticulum stress
Gene
ATG19
RAD6
SHP1
SPT20
YHI9
CUE4
ARL1
ARL3
YOD1
BST1
UBX4
NPL4
HRD1
JEM1
YOP1
KRE5
YHR192W
EUG1
YMR184W
YFR026C
RPT6
PMT2
YCL047C
CNE1
UBR1
PTC2
RTN2
YAP1
SLT2
DFM1
QRI8
YNL305C
CUE1
CDC48
UFD2
HUL5
USA1
PNG1
MPD1
PMT3
UFD1
DSK2
KAR2
SEL1
SKN7
MID2
VPS74
EPS1
YDR161W
YDR307W
PMT6
YLR104W
RTN1
YOS9
MNL1
SCJ1
YSY6
HLJ1
IMH1
IRE1
DER1
MNS1
BCK1
RPT2
PDI1
UBC1
YPT1
SYT1
RAD23
EDE1
HAC1
PMT1
SSM4
MID2
PMT5
EUG1
HRD3
DER1
RPT5
YLR057W
PMT4
HAC1
YDR049W
RPT3
DCR2
TRL1
OPI1
RPT1
YDJ1
NAT3
PBN1
SEC61
Z_Shit_K_Gem
Z_Im_K_Gem
Z_Shit_K_Cyt
Z_Im_K_Cyt
Z_Shit_L_Gem
Z_Im_L_Gem
Z_Shit_L_Cyt
Z_Im_L_Cyt

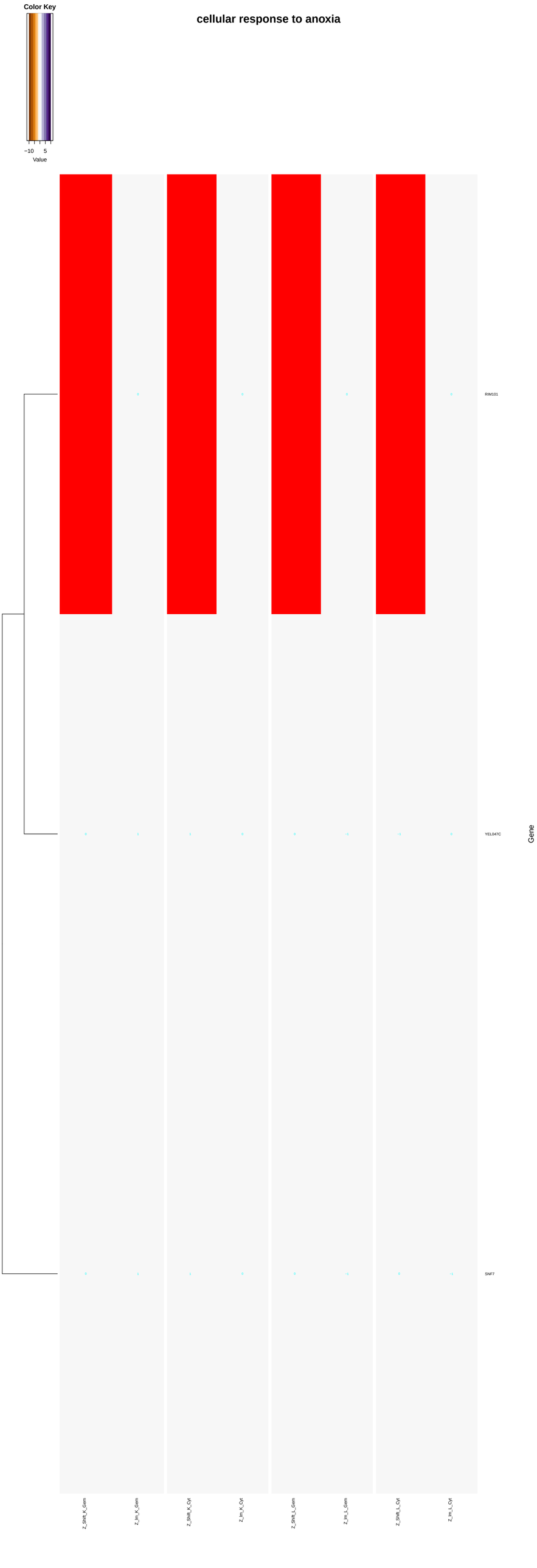

Color Key
−10
5
Value
cellular response to topologically incorrect protein
UBR2
SLT2
DFM1
YAP1
PTC2
KRE5
PMT3
UFD1
YOD1
PMT6
MNL1
YSY6
IRE1
YNL305C
CDC48
YOS9
YHI9
RAD6
FES1
SPT20
YDR307W
YFR026C
SKN7
MID2
VPS74
YPT1
YHB1
BCK1
GIM3
NPL4
IML2
HRD1
EDE1
HAC1
PMT1
SIS1
DCR2
YDR052C
PMT2
SAN1
UBR1
UBC4
MID2
PMT5
TRL1
PMT4
HAC1
YDR049W
OPI1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

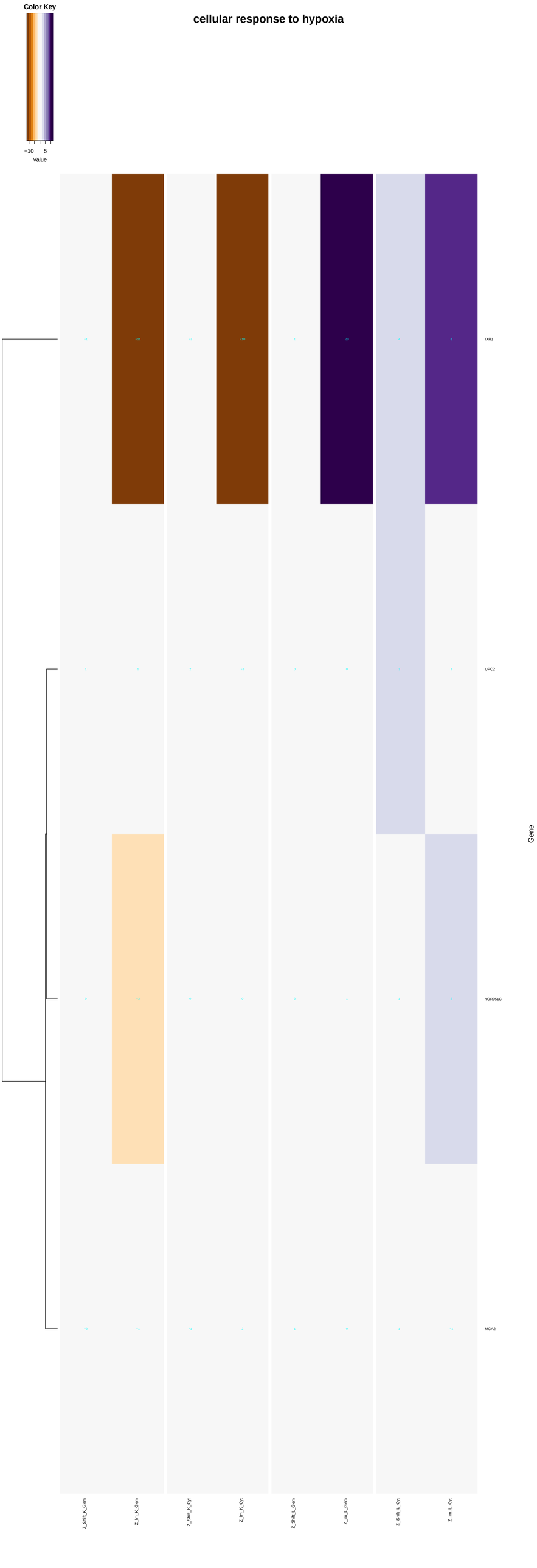

Color Key
−10
5
Value
cellular response to water deprivation
STF2
NTH1
ATH1
SIP18
YNL190W
SIP18
YJL144W
TPS1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

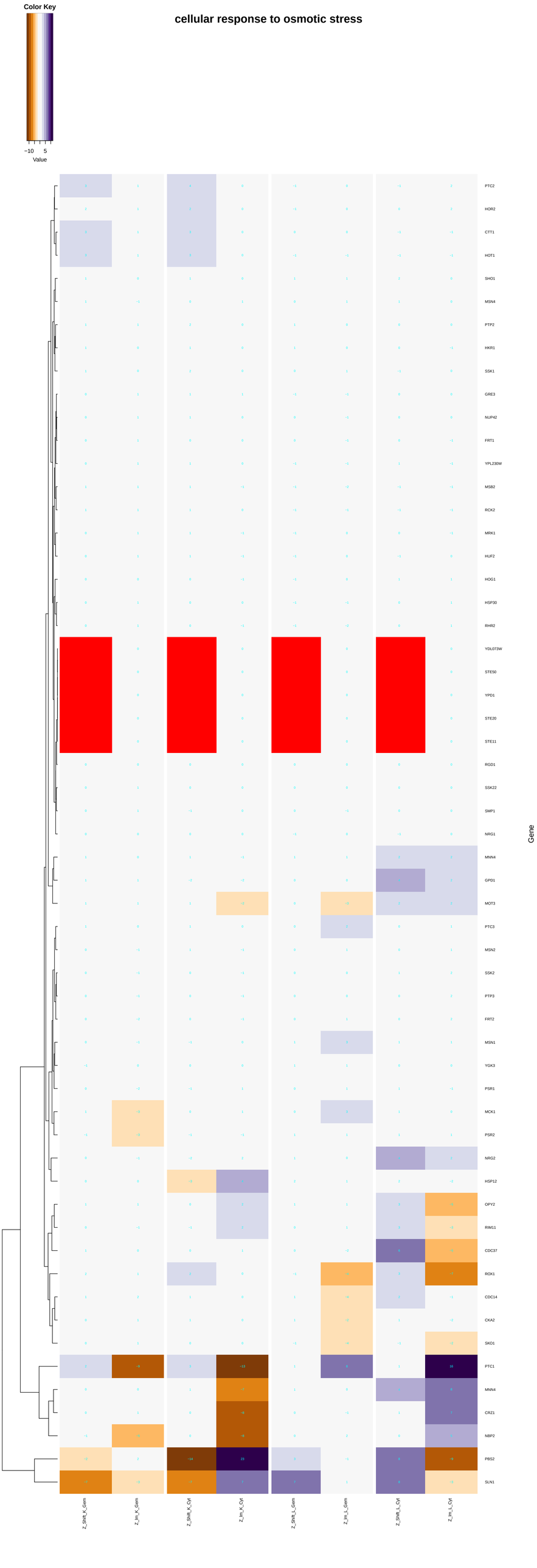

Color Key
−10
5
Value
regulation of translation in response to stress
TRL1
SBP1
GCN2
EDC2
STM1
YHL039W
EDC1
RKM1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

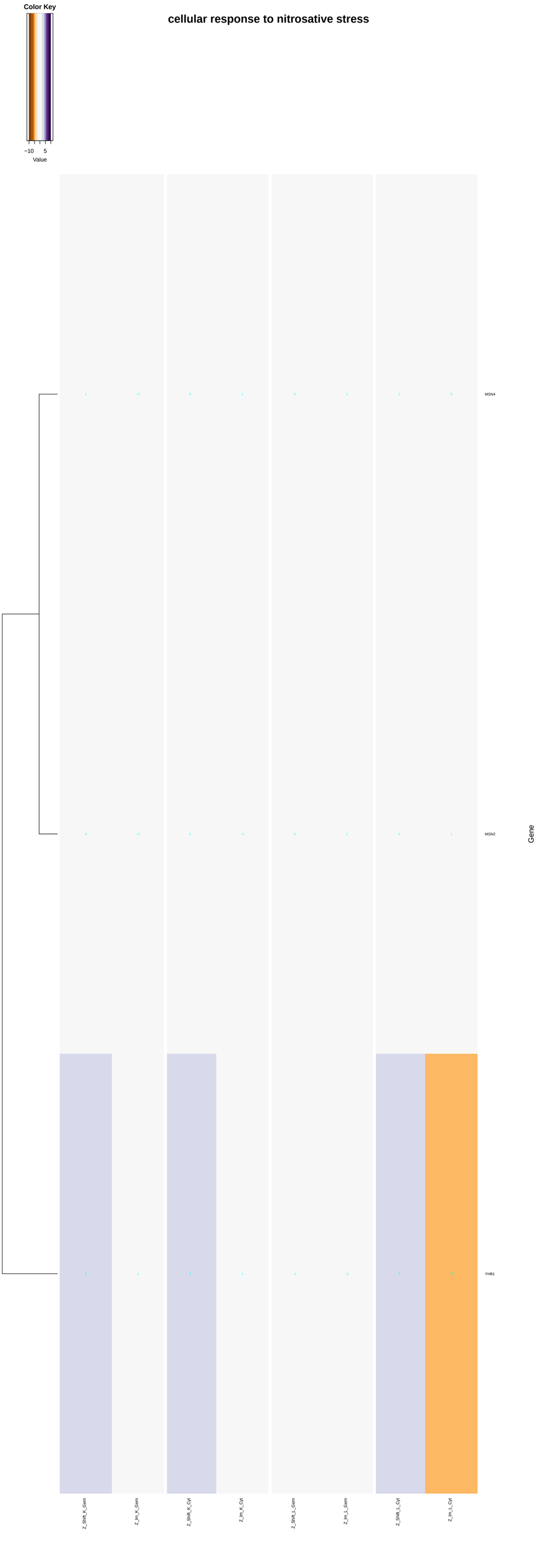

Color Key
−10
5
Value
regulation of DNA−templated transcription in response to stress
MSN4
MSN2
MSN1
RRD1
YOR051C
SWI6
RPN4
STB5
SEN1
CRZ1
ASF1
RTT109
YAP1
HOT1
BUR6
RCS1
DEP1
SDS3
SOD1
SAP30
PHO23
SIN3
SNF2
MIG3
YHR1
NCB2
CAD1
YPL230W
YRR1
SNT2
TEC1
HOG1
ARR1
AFT2
RLM1
SMP1
PDR8
SPT6
MOT3
ZAP1
MGA2
SUB1
SWI1
SKN7
SKO1
HAA1
ROX1
CST6
SCH9
SWI4
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

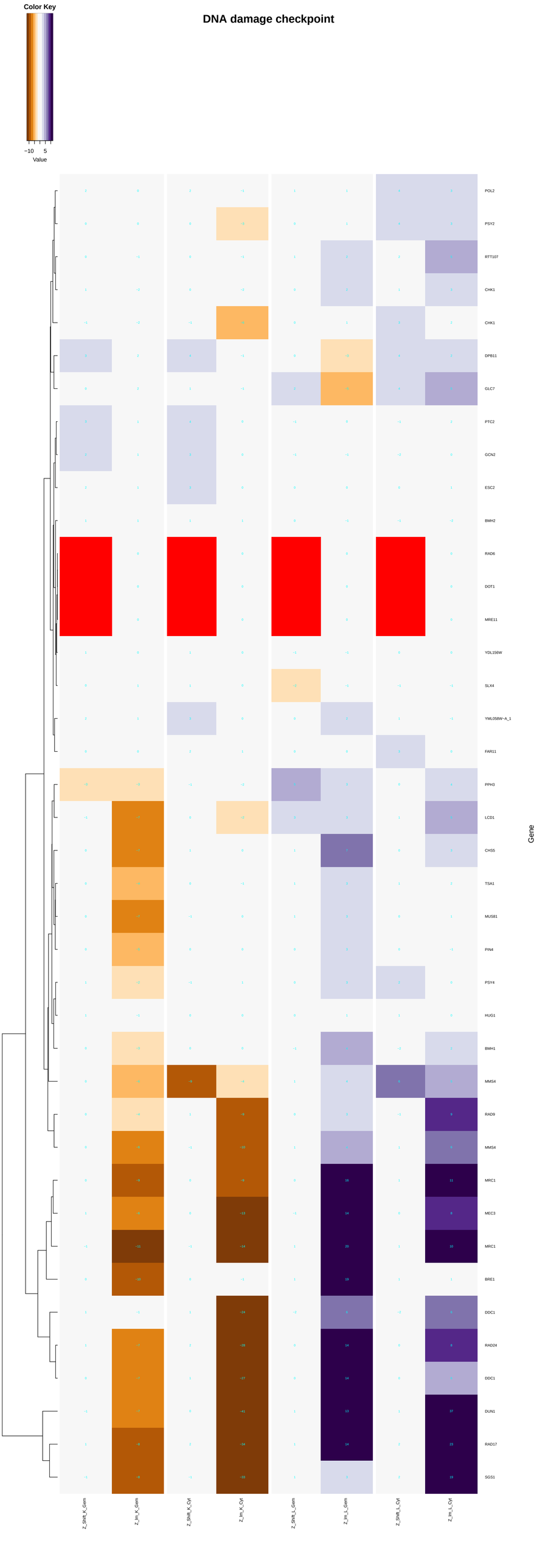

Color Key
−10
5
Value
cellular response to cold
MSN4
ATH1
MSN2
YCR015C
TIR2
SPT23
MGA2
IRA2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

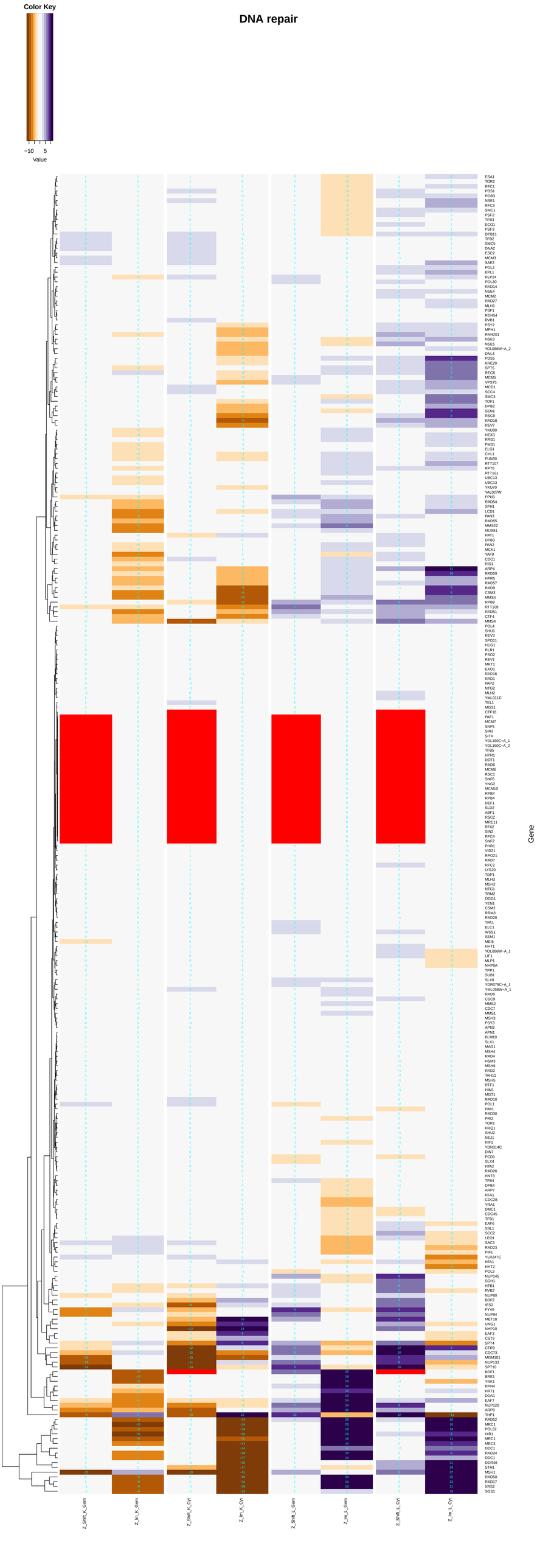

Color Key
−10
5
Value
cellular response to anoxia
RIM101
YEL047C
SNF7
Gene
Z_Shft_K_Germ
Z_Im_K_Germ
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Germ
Z_Im_L_Germ
Z_Shft_L_Cyt
Z_Im_L_Cyt

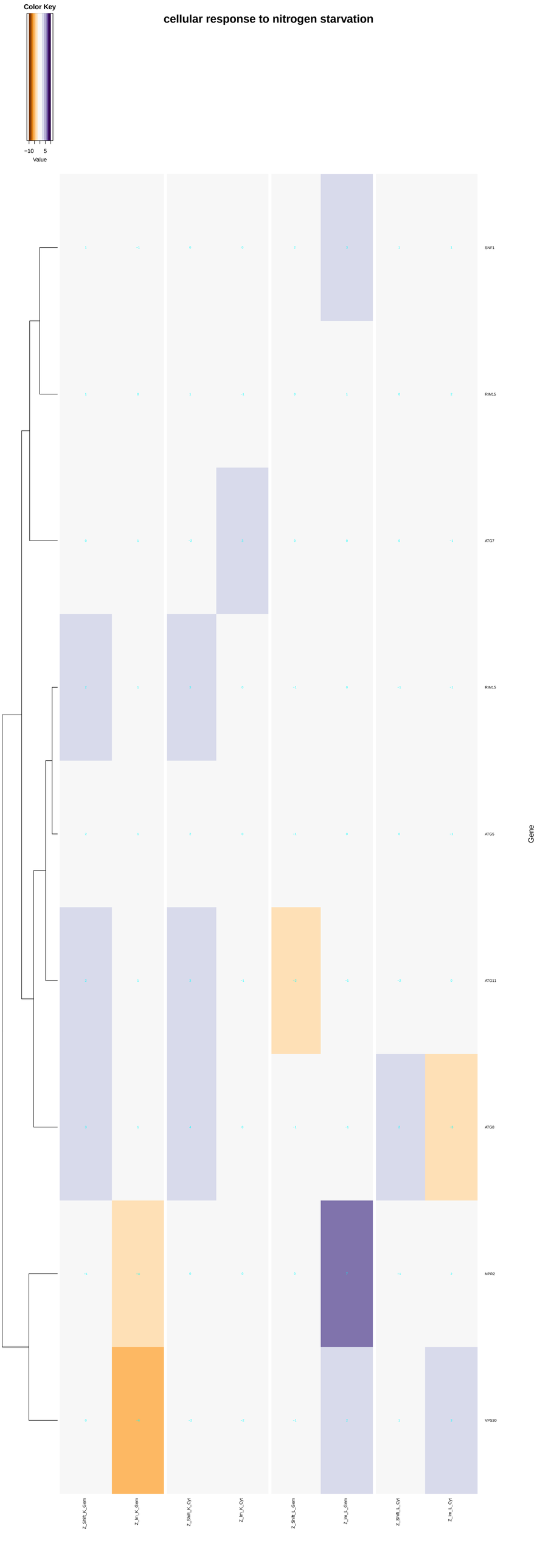

Color Key
−10
5
Value
cellular response to hypoxia
−1
−11
−2
−10
1
20
4
8
IXR1
1
1
2
−1
0
0
3
1
UPC2
0
−3
0
0
2
1
1
2
YOR051C
−2
−1
−1
2
1
0
1
−1
MGA2
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt
Gene


Color Key
−10
5
Value
cellular response to osmotic stress
PTC2
HOR2
CTT1
HOT1
SHO1
MSN4
PTP2
HKR1
SSK1
GRE3
NUP42
FRT1
YPL230W
MSB2
RCK2
MRK1
HUF2
HOG1
HSP30
RHR2
YDL073W
STE50
YPD1
STE20
STE11
RGD1
SSK22
SMP1
NRG1
MNN4
GPD1
MOT3
PTC3
MSN2
SSK2
PTP3
FRT2
MSN1
YGK3
PSR1
MCK1
PSR2
NRG2
HSP12
OPY2
RIM11
CDC37
ROX1
CDC14
CKA2
SKO1
PTC1
MNN4
CRZ1
NBP2
PBS2
SLN1
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt
Gene


Color Key
−10
5
Value
cellular response to nitrosative stress
MSN4
MSN2
YHB1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
DNA damage checkpoint
POL2
PSY2
RTT107
CHK1
CHK1
DPB11
GLC7
PTC2
GCN2
ESC2
BMH2
RAD6
DOT1
MRE11
YDL156W
SLX4
YML058W−A_1
FAR11
PPH3
LCD1
CHS5
TSA1
MUS81
PIN4
PSY4
HUG1
BMH1
MMS4
RAD9
MMS4
MRC1
MEC3
MRC1
BRE1
DDC1
RAD24
DDC1
DUN1
RAD17
SGS1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
DNA repair
Gene
ESA1
TOR2
RFC1
PDS1
POB3
NSE1
RFC3
SMC1
PSF2
TFB1
ECO1
PSF3
DPB11
TFB2
SMC5
DNA2
ESC2
MCM3
SAE2
POL2
EPL1
RLP24
POL30
RAD14
NSE4
MCM2
RAD27
MLH1
PSF1
RDH54
RVB1
PSY2
MPH1
RNH201
NSE3
NSE5
YDL086W−A_2
DNL4
PDS5
KRE29
SPT5
REC8
MCM5
VPS75
MCD1
SCC4
SMC3
TOF1
DPB2
SEN1
RSC8
RAD18
REV7
YKU80
HEX3
RRD1
PMS1
ELG1
CHL1
FUN30
RTT107
RPT5
RTT101
UBC13
UBC13
YKU70
YAL027W
PPH3
RAD54
SFH1
LCD1
PAN3
RAD55
MMS22
MUS81
HAT1
DPB3
PAN2
MCK1
YAF9
CDC1
RIS1
ARP4
RAD59
HPR5
RAD57
SUV3
CSM3
MMS4
RPB9
RTT109
RAD51
CTF4
MMS4
POL4
SHU1
REV3
SPO11
HUG1
RLR1
PSO2
REV1
MKT1
EXO1
RAD16
RAD1
PAP2
NTG2
MLH2
YML011C
TEL1
MGS1
CTF18
PAF1
MCM7
SNF5
SIR2
SIT4
YDL160C−A_1
YDL160C−A_2
TFB5
HPR1
DOT1
RAD6
MCM6
RSC1
SNF6
YNG2
MCM10
RPB4
RPB4
DEF1
SLD2
ABF1
RSC2
MRE11
RFA2
SIN3
RFC4
SNF2
PHR1
VID21
RPO21
RAD27
RFC2
LYS20
TDP1
MLH3
MSH2
NTG1
TRM2
OGG1
YEN1
CSM2
RRM3
RAD28
TPA1
ELC1
WSS1
SEM1
MEI5
HHT1
YDL086W−A_1
LIF1
MLP1
NHP6A
TPP1
SUB1
SLX8
YDR079C−A_1
YML086W−A_1
RAD5
CDC9
MMS2
CDC7
MMS1
MSH3
PSY3
APN2
APN1
BLM10
SLX1
MAG1
MSH4
RAD4
HSM3
MSH6
RAD2
TAH11
MSH5
RTF1
HIM1
MGT1
RAD10
POL1
HIM1
RAD30
PRI2
TOR1
HRQ1
SHU2
NEJ1
RIF1
YDR314C
DIN7
PCD1
SLX4
HTA2
RAD26
HNT1
TFB4
DPB4
ARP7
RFA1
CDC28
YRA1
DMC1
CDC45
TFB1
EAF6
SSL1
SCC2
LEO1
SAC3
RAD23
PIF1
YLR247C
HTA1
HHT2
POL5
NUP145
SOH1
HTB1
RVB2
NUP60
BDF2
IES2
FYV6
NUP84
MET18
UNG1
NHP10
EAF3
CST9
CTR1
CTR9
CDC73
MGM101
NUP133
SPT10
BDF1
BRE1
YNK1
RPN4
HRT1
DOA1
EAF7
NUP120
ARP8
THP1
RAD52
MRC1
POL32
IXR1
MRC1
MEC3
DDC1
RAD24
DDC1
DDR48
STH1
MSH1
RAD50
RAD17
XRS2
SGS1
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
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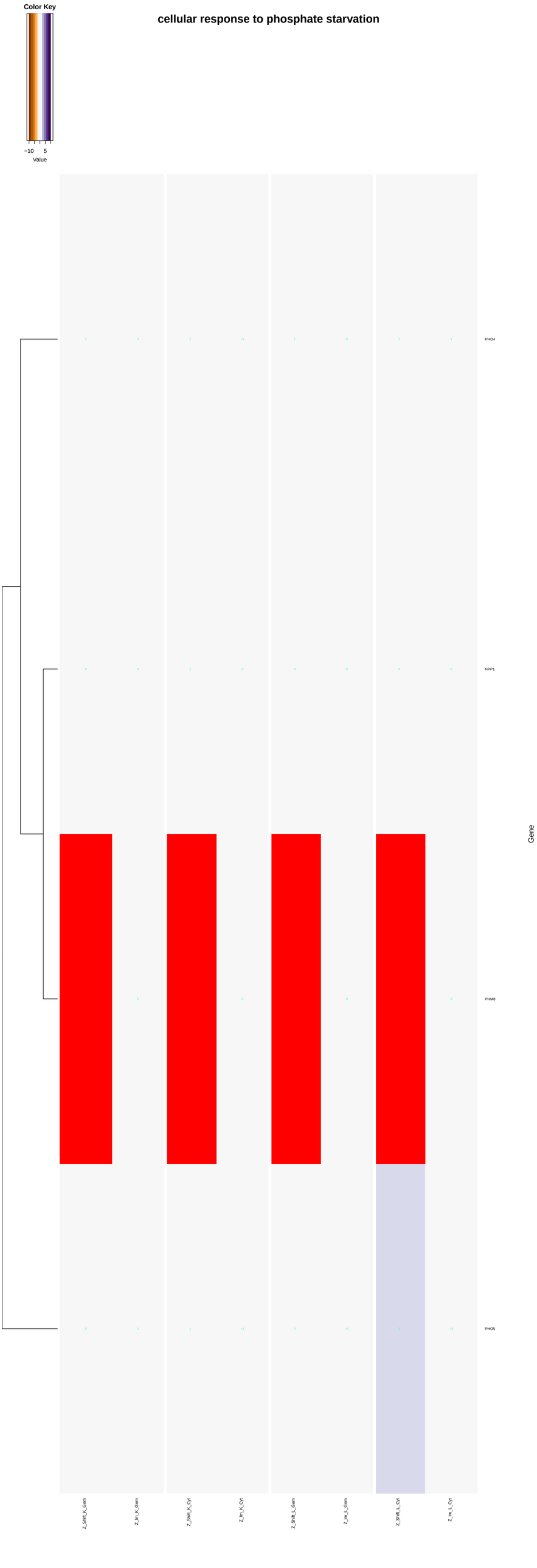
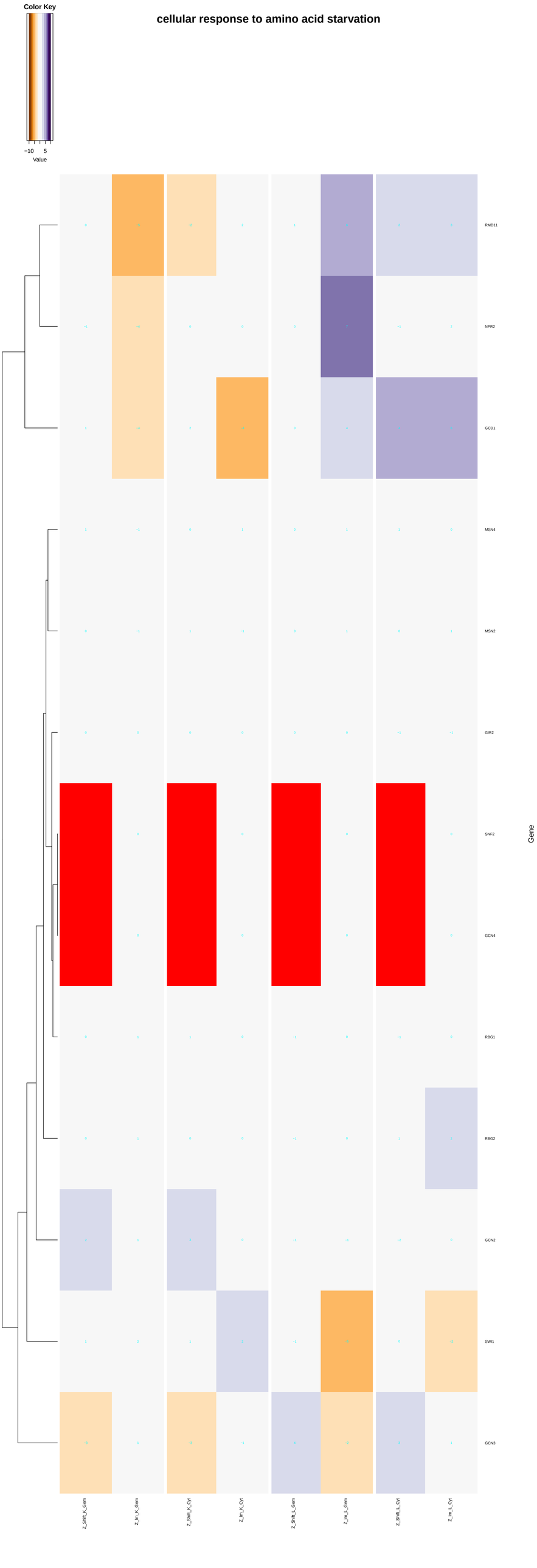
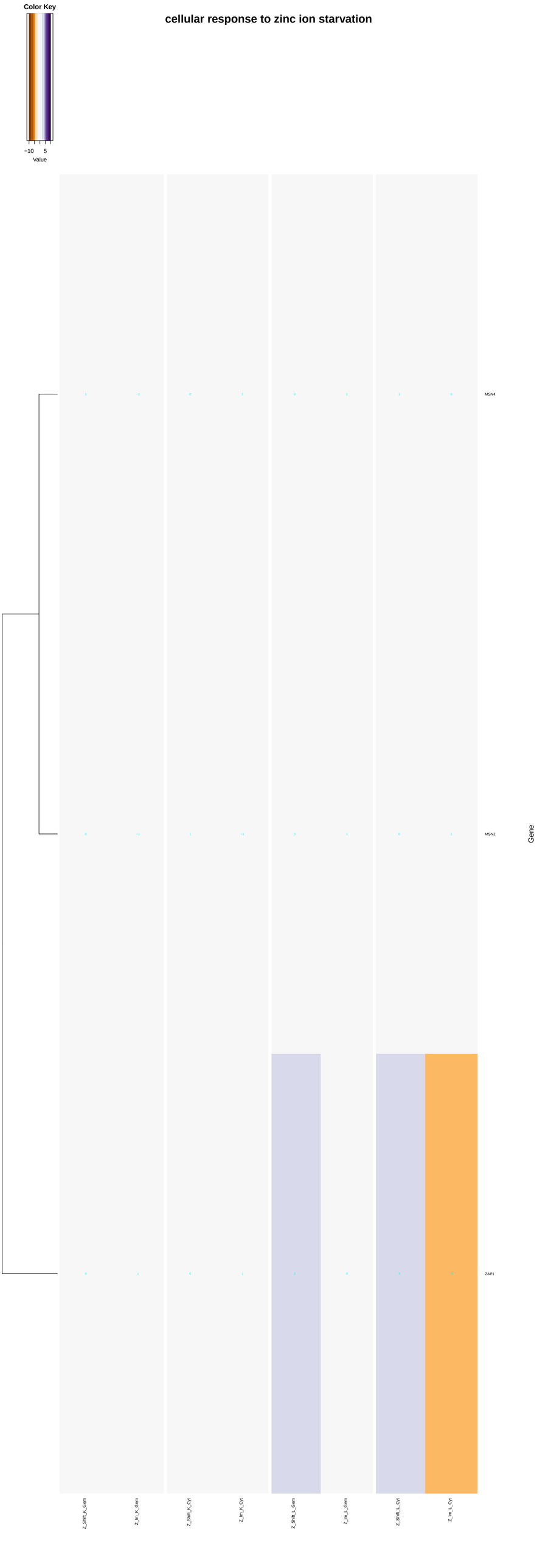
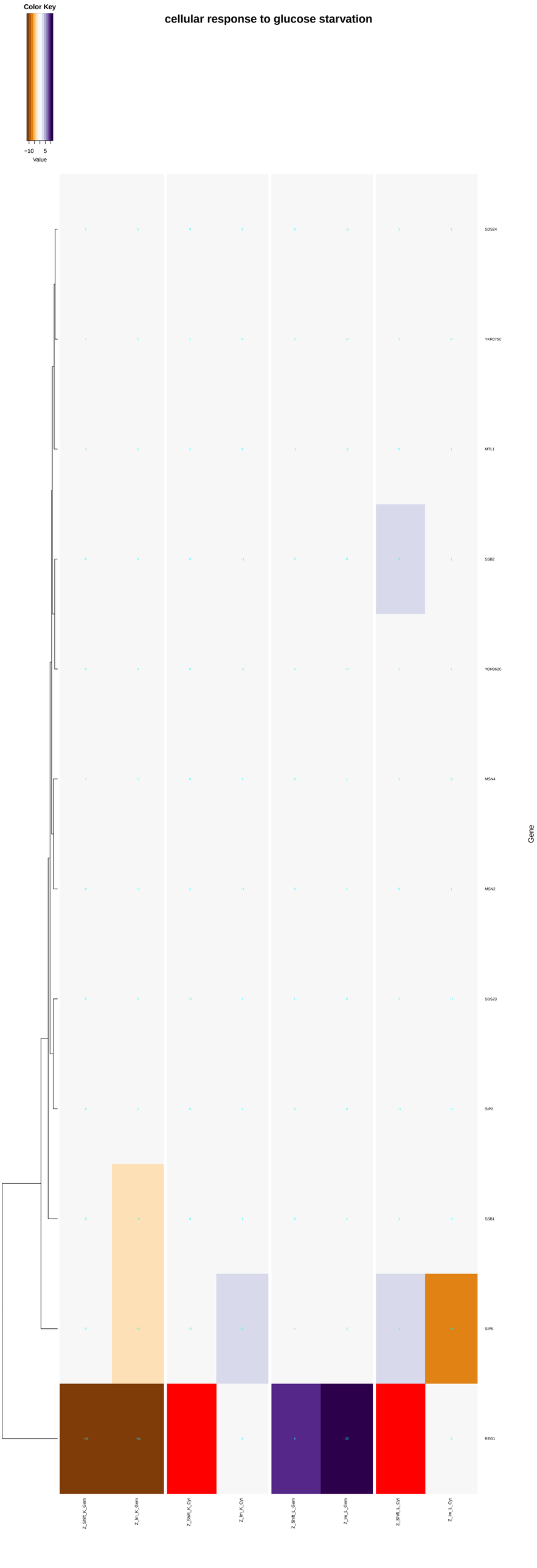
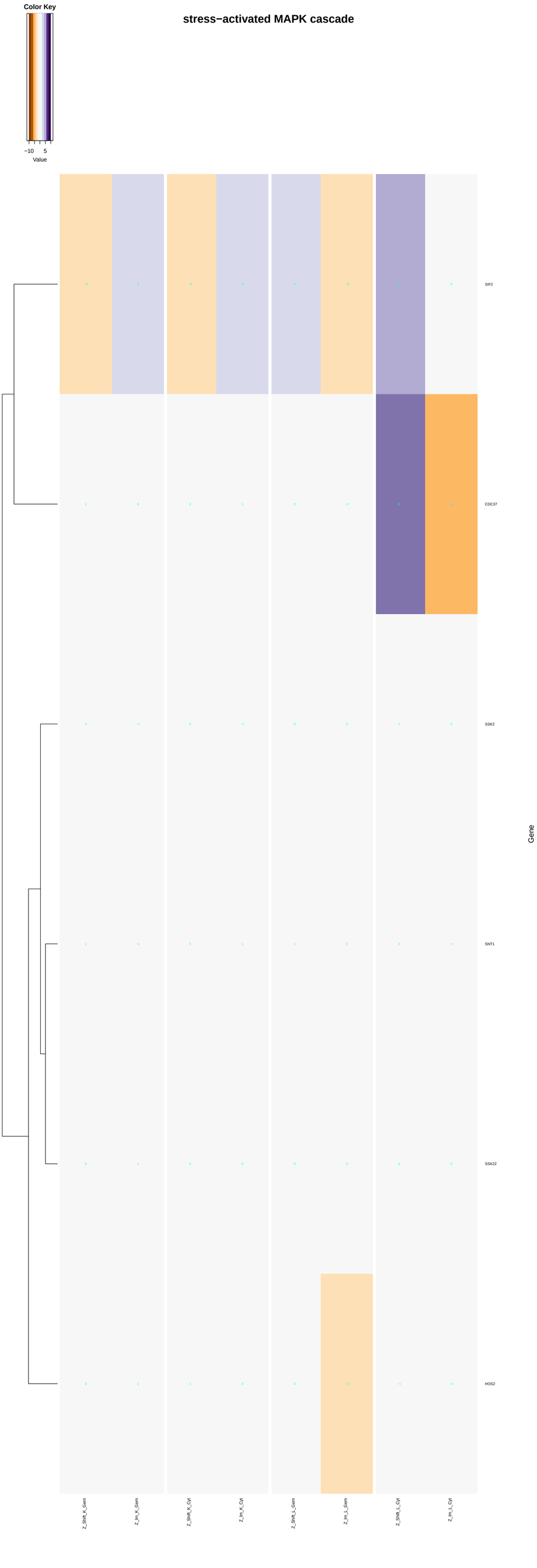
Value
cellular response to nitrogen starvation
SNF1
RIM15
ATG7
RIM15
ATG5
ATG11
ATG8
NPR2
VPS30
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

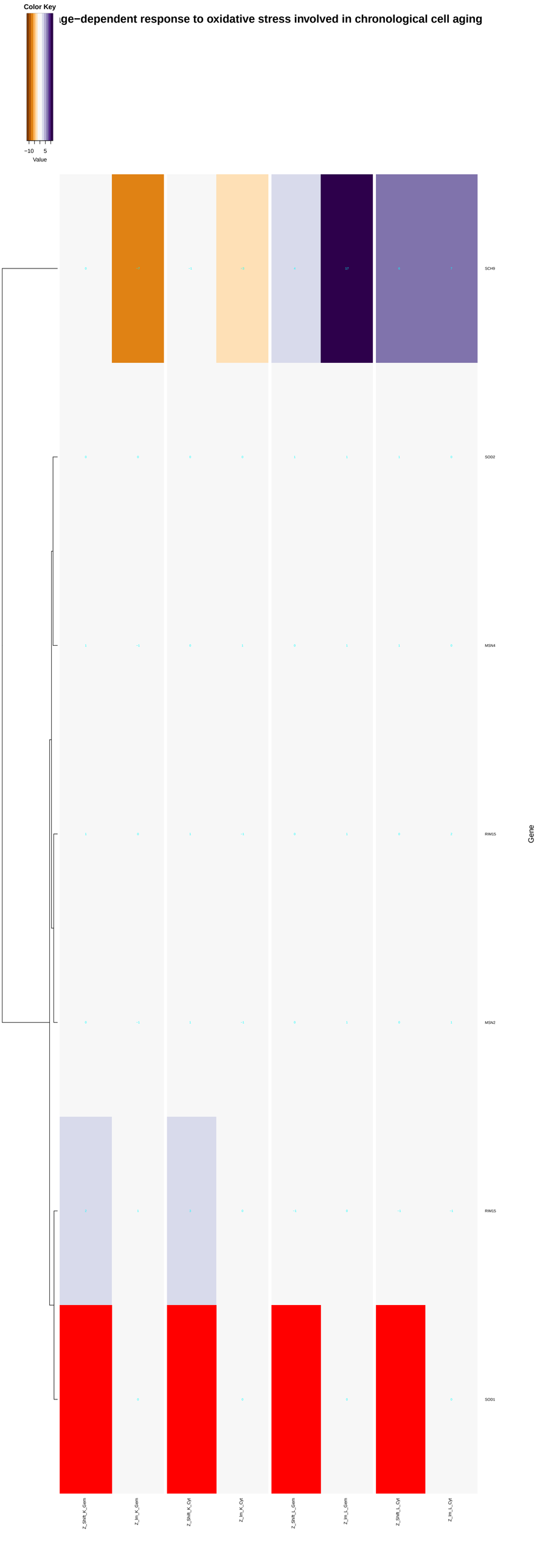

Color Key
−10
5
Value
cellular response to phosphate starvation
PHO4
NPP1
PHM8
PHO5
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

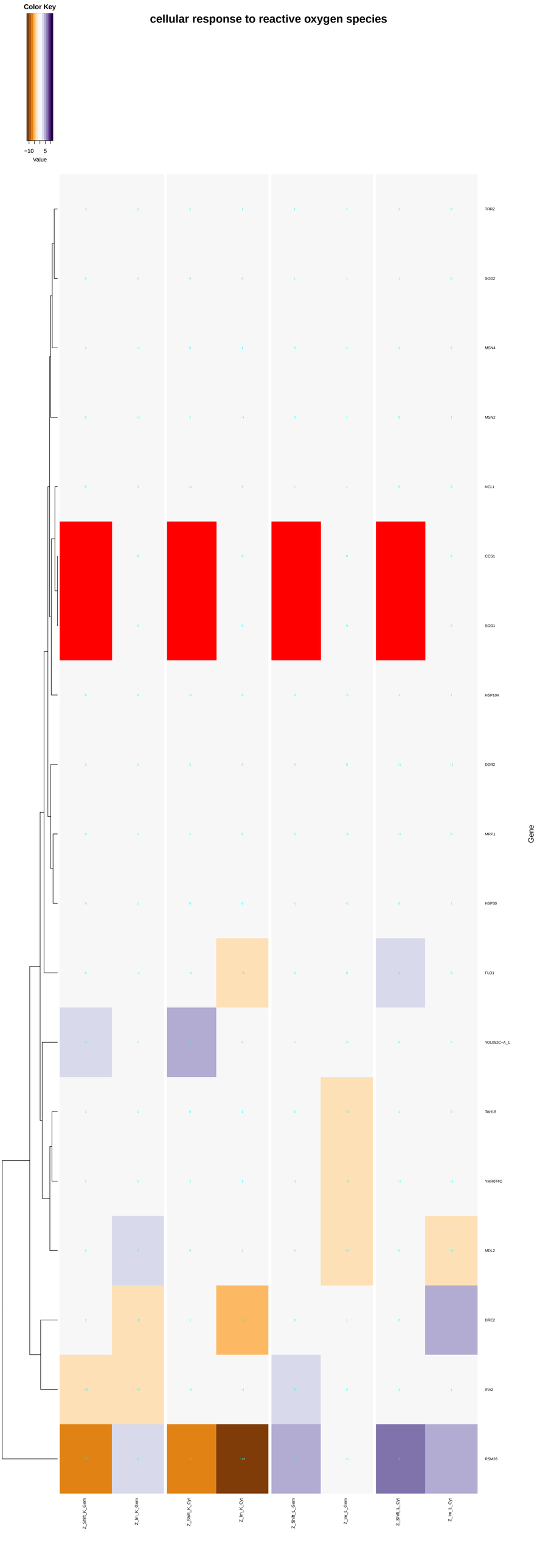

Color Key
−10
5
Value
cellular response to amino acid starvation
RMD11
NPR2
GCD1
MSN4
MSN2
GIR2
SNF2
GCN4
RBG1
RBG2
GCN2
SWI1
GCN3
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

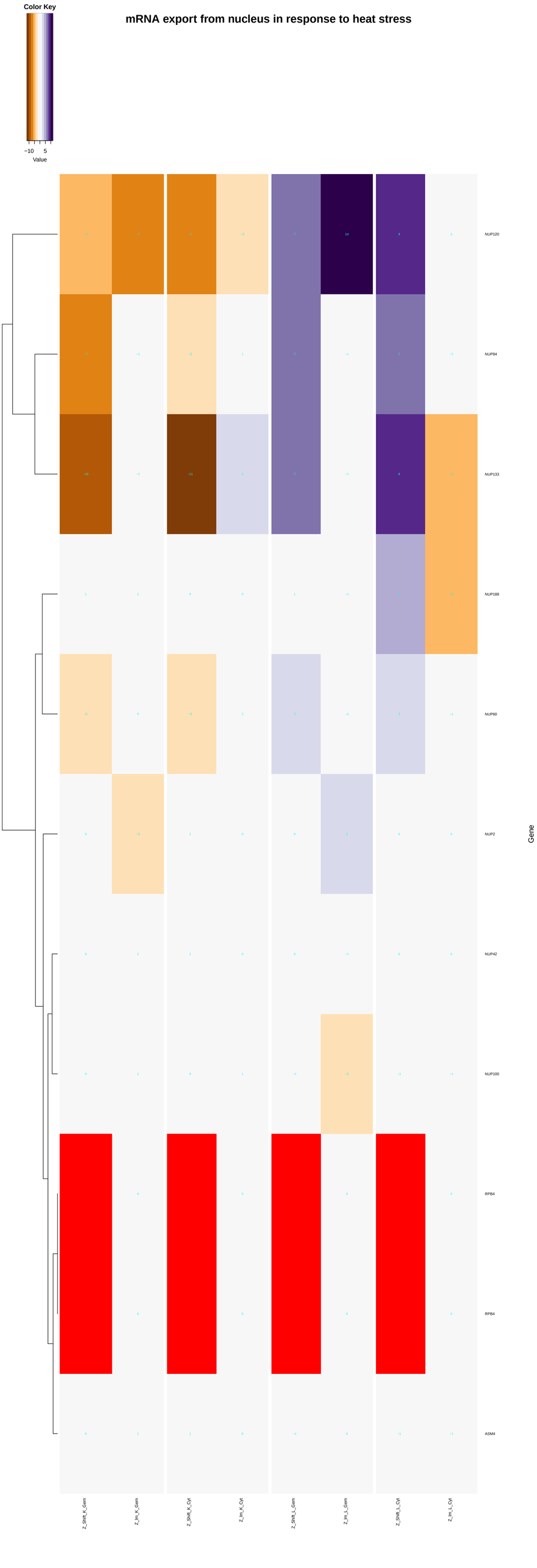

Color Key
−10
5
Value
cellular response to zinc ion starvation
1
−1
0
1
0
1
1
0
MSN4
0
−1
1
−1
0
1
0
1
MSN2
Gene
0
1
0
1
2
0
3
3
ZAP1
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

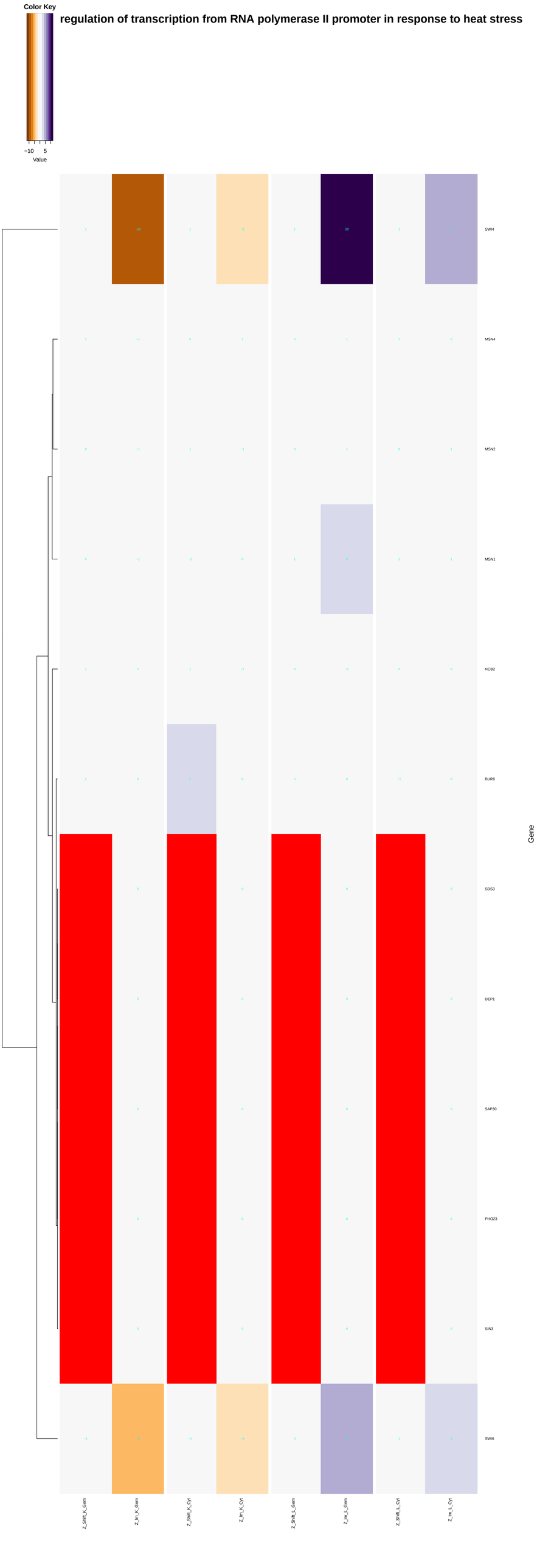

Color Key
−10
5
Value
cellular response to glucose starvation
SDS24
YKR075C
MTL1
SSB2
YOR062C
MSN4
MSN2
SDS23
SIP2
SSB1
SIP5
REG1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

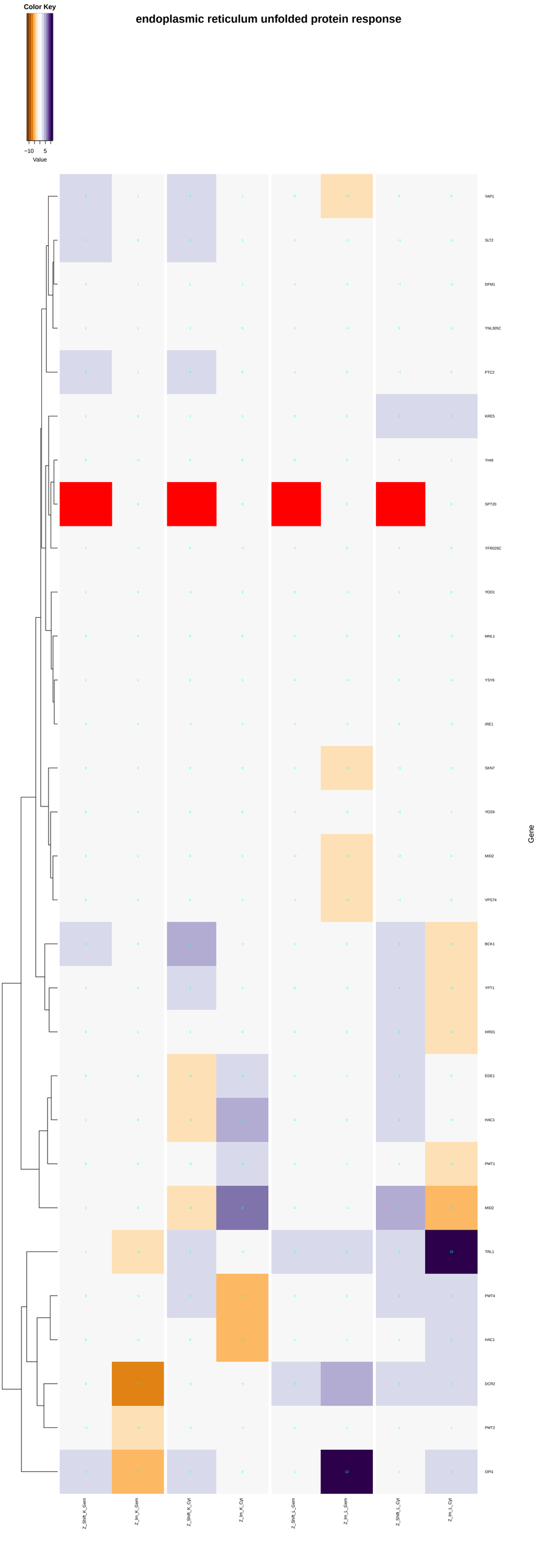

Color Key
−10
5
Value
stress−activated MAPK cascade
−3
3
−3
4
3
−3
0
0
SIF2
1
0
0
1
0
−2
8
−8
CDC37
0
−1
0
−1
0
0
1
2
SSK2
1
−1
0
1
1
0
0
−1
SNT1
0
1
0
0
0
0
0
0
SSK22
0
1
1
0
0
−9
−1
−2
HOS2
Z_Shlt_K_Gem
Z_In_K_Gem
Z_Shlt_K_Cyt
Z_In_K_Cyt
Z_Shlt_L_Gem
Z_In_L_Gem
Z_Shlt_L_Cyt
Z_In_L_Cyt
Gene

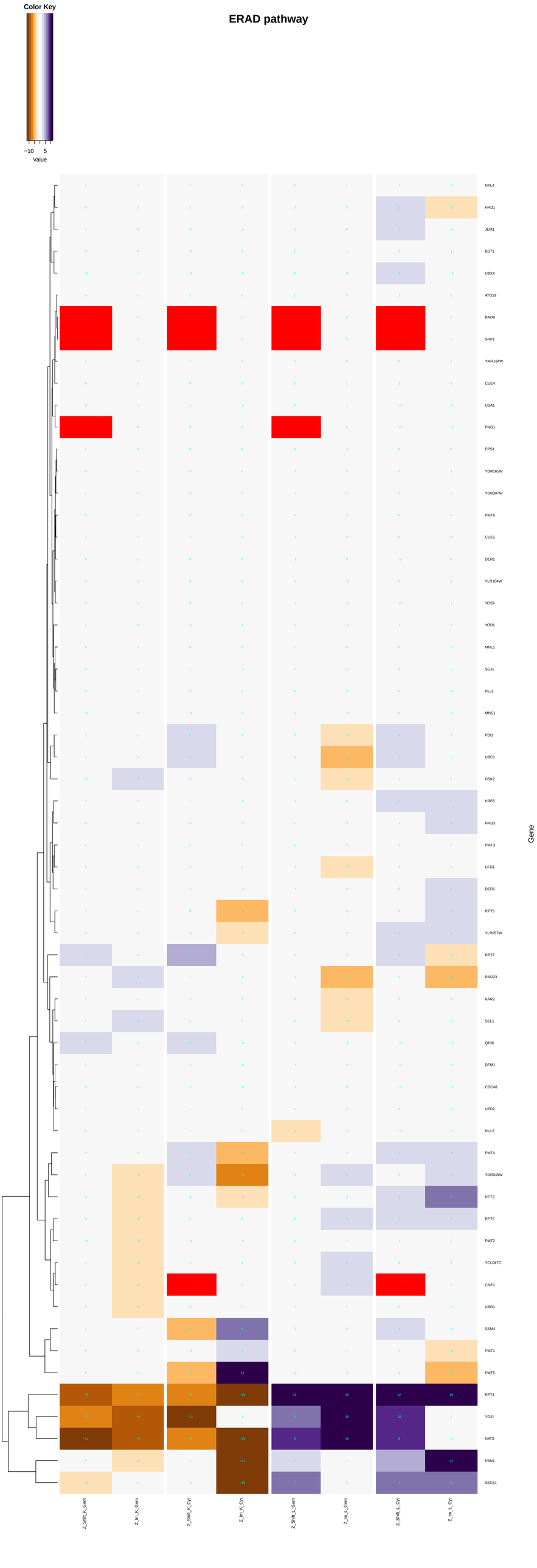

Color Key
−10
5
Value
ge−dependent response to oxidative stress involved in chronological cell aging
0 −7 −1 −3 4 17 8 7
SCH9
0 0 0 0 1 1 1 0
SOD2
1 −1 0 1 0 1 1 0
MSN4
1 0 1 −1 0 1 0 2
RIM15
0 −1 1 −1 0 1 0 1
MSN2
2 1 3 0 −1 0 −1 −1
RIM15
0 0 0 0 0 0 0 0
SOD1
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt
Gene

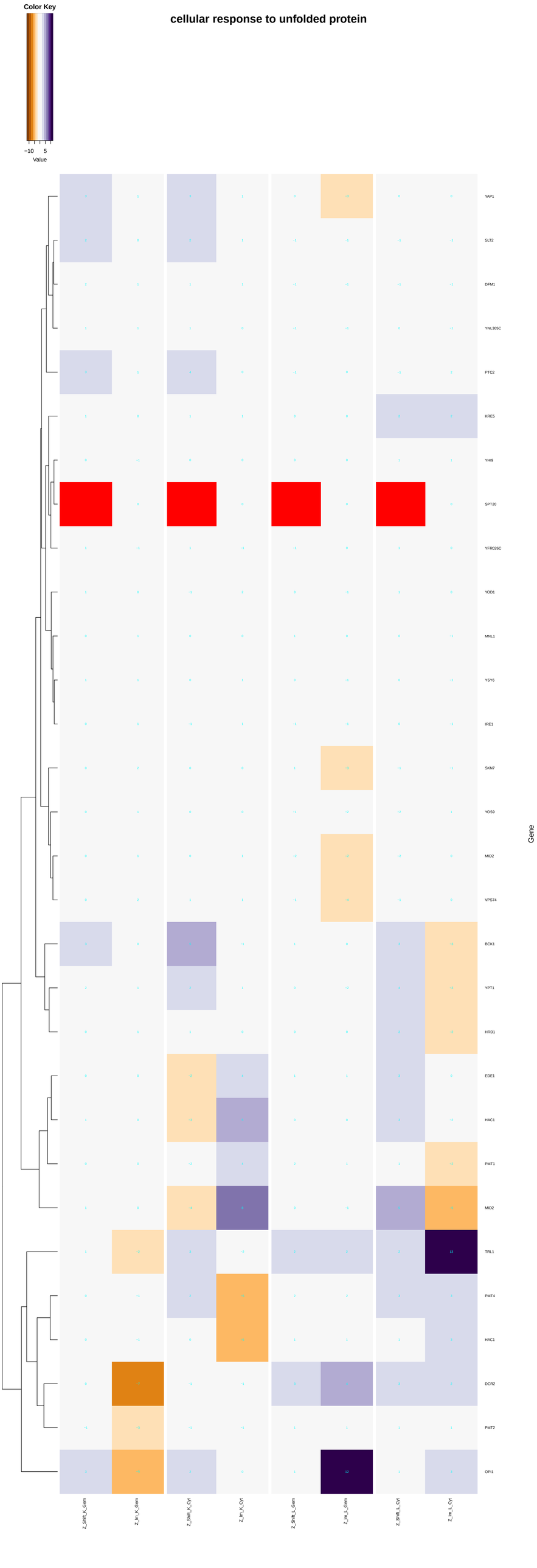

Color Key
−10
5
Value
cellular response to reactive oxygen species
TRR2
SOD2
MSN4
MSN2
NCL1
CCS1
SOD1
HSP104
DDR2
MRP1
HSP30
FLO1
YOL052C−A_1
TAH18
YMR074C
MDL2
DRE2
IRA2
RSM26
Gene
Z_Shft_K_Germ
Z_Im_K_Germ
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Germ
Z_Im_L_Germ
Z_Shft_L_Cyt
Z_Im_L_Cyt

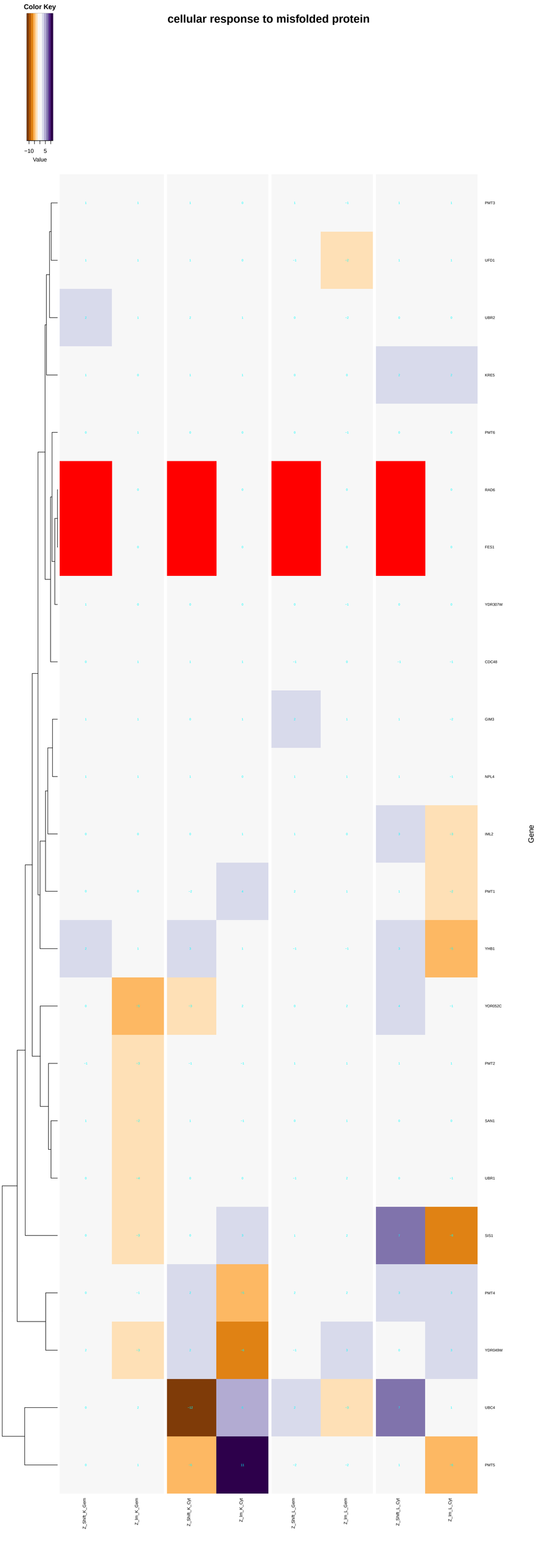

Color Key
−10
5
Value
mRNA export from nucleus in response to heat stress
NUP120
NUP84
NUP133
NUP188
NUP60
NUP2
NUP42
NUP100
RPB4
RPB4
ASM4
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

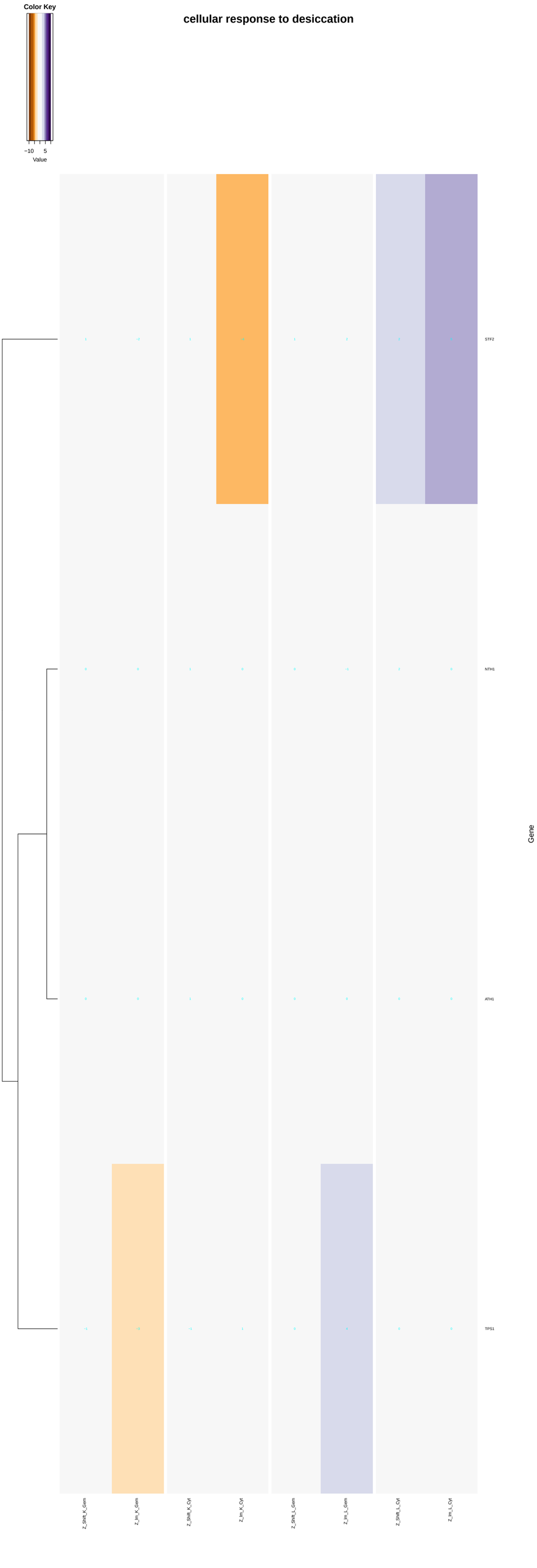

Color Key
−10
5
Value
regulation of transcription from RNA polymerase II promoter in response to heat stress
SWI4
MSN4
MSN2
MSN1
NCB2
BUR6
SDS3
DEP1
SAP30
PHO23
SIN3
SWI6
Gene
Z_Shift_K_Gem
Z_In_K_Gem
Z_Shift_K_Cyt
Z_In_K_Cyt
Z_Shift_L_Gem
Z_In_L_Gem
Z_Shift_L_Cyt
Z_In_L_Cyt

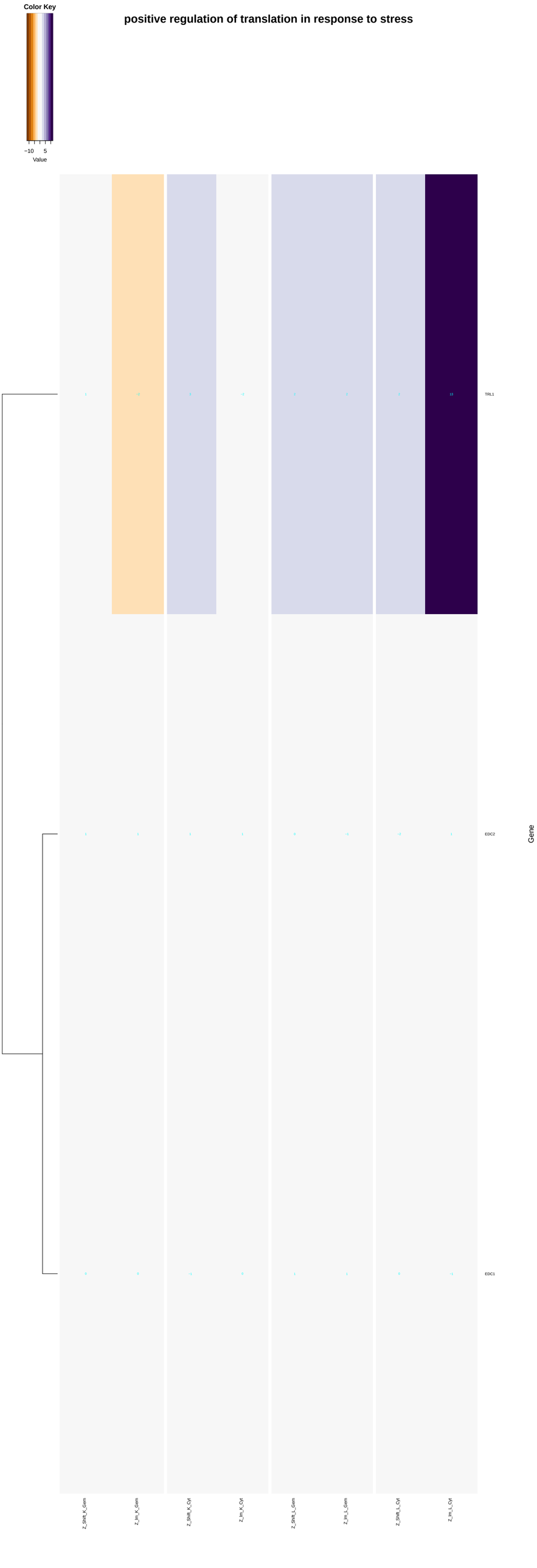

Color Key
−10
5
Value
endoplasmic reticulum unfolded protein response
YAP1
SLT2
DFM1
YNL305C
PTC2
KRE5
YHI9
SPT20
YFR026C
YOD1
MNL1
YSY6
IRE1
SKN7
YOS9
MID2
YPS74
BCK1
YPT1
HRD1
EDE1
HAC1
PMT1
MID2
TRL1
PMT4
HAC1
DCR2
PMT2
OPI1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

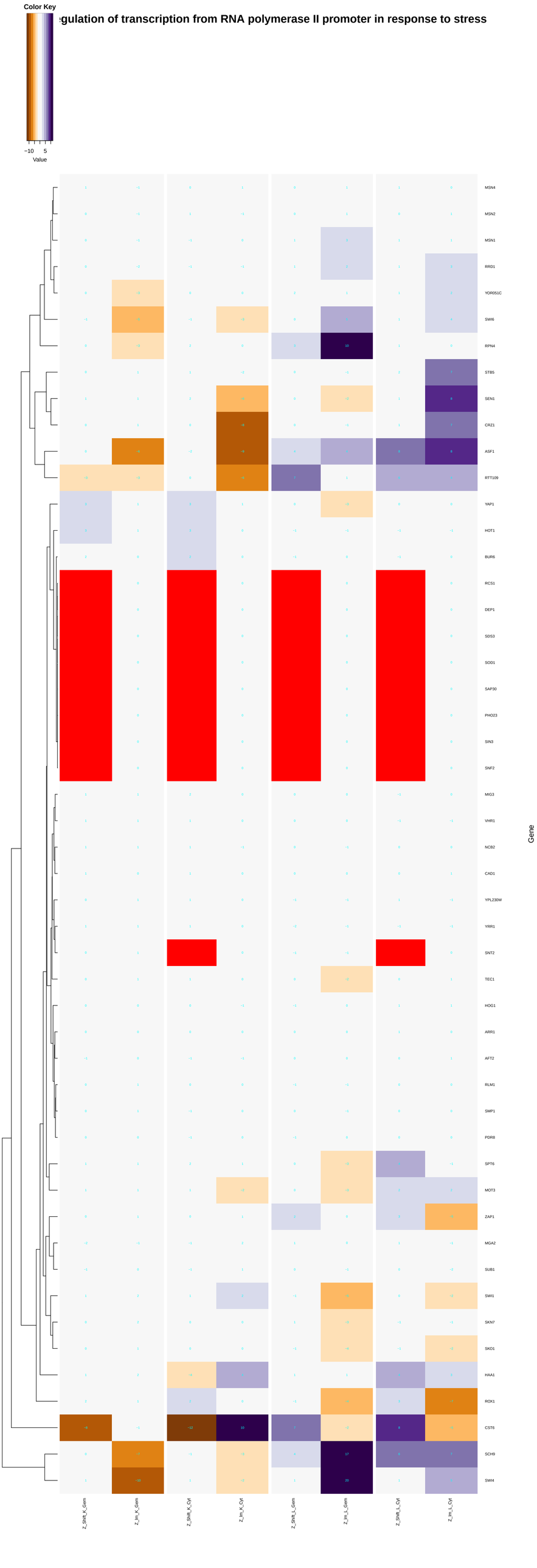

Color Key
−10
5
Value
ERAD pathway
Gene
NPL4
HRD1
JEM1
BST1
UBX4
ATG19
RAD6
SHP1
YMR184W
CUE4
USA1
PNG1
EPS1
YDR161W
YDR307W
PMT6
CUE1
DER1
YLR104W
YOS9
YOD1
MNL1
SCJ1
HLJ1
MNS1
PDI1
UBC1
DSK2
KRE5
HRD3
PMT3
UFD1
DER1
RPT5
YLR057W
RPT2
RAD23
KAR2
SEL1
QRI8
DFM1
CDC48
UFD2
HUL5
PMT4
YDR049W
RPT3
RPT6
PMT2
YCL047C
CNE1
UBR1
SSM4
PMT1
PMT5
RPT1
YDJ1
NAT3
PBN1
SEC61
Z_Shlt_K_Gem
Z_In_K_Gem
Z_Shlt_K_Cyt
Z_In_K_Cyt
Z_Shlt_L_Gem
Z_In_L_Gem
Z_Shlt_L_Cyt
Z_In_L_Cyt

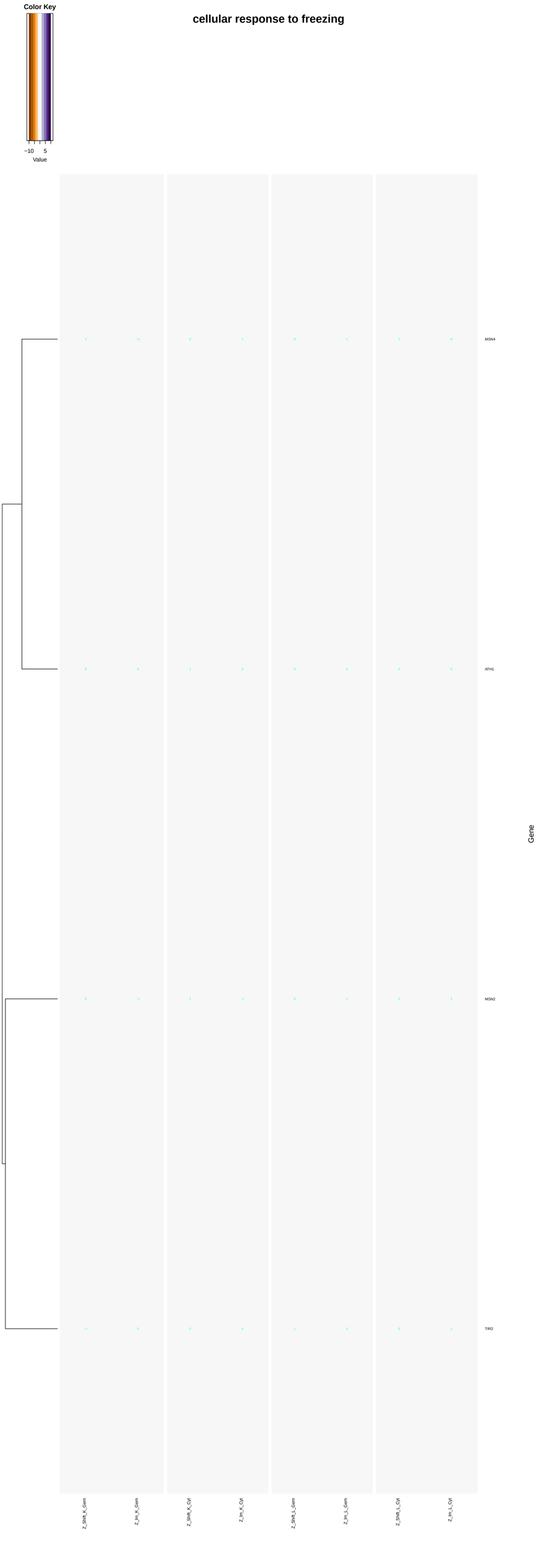

Color Key
−10
5
Value
cellular response to unfolded protein
YAP1
SLT2
DFM1
YNL305C
PTC2
KRE5
YHI9
SPT20
YFR026C
YOD1
MNL1
YSY6
IRE1
SKN7
YOS9
MID2
VPS74
BCK1
YPT1
HRD1
EDE1
HAC1
PMT1
MID2
TRL1
PMT4
HAC1
DCR2
PMT2
OPI1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

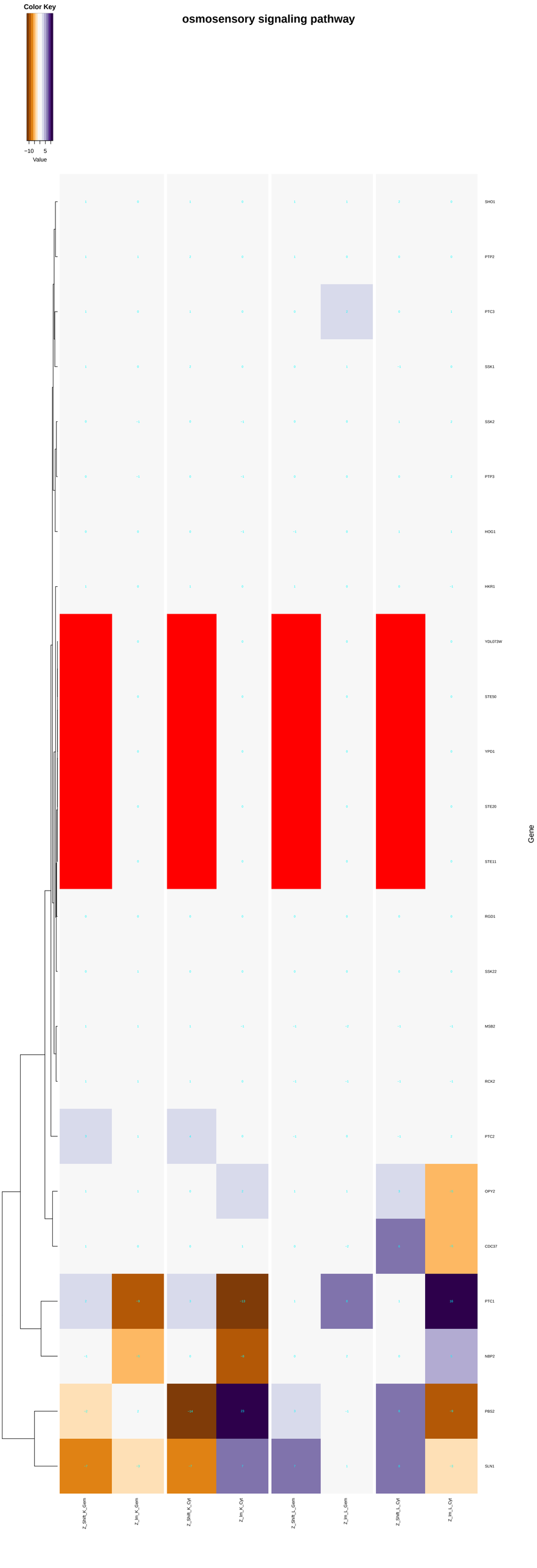

Color Key
−10
5
Value
cellular response to misfolded protein
PMT3
UFD1
UBR2
KRE5
PMT6
RAD6
FES1
YDR307W
CDC48
GIM3
NPL4
IML2
PMT1
YHB1
YOR052C
PMT2
SAN1
UBR1
SIS1
PMT4
YDR049W
UBC4
PMT5
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

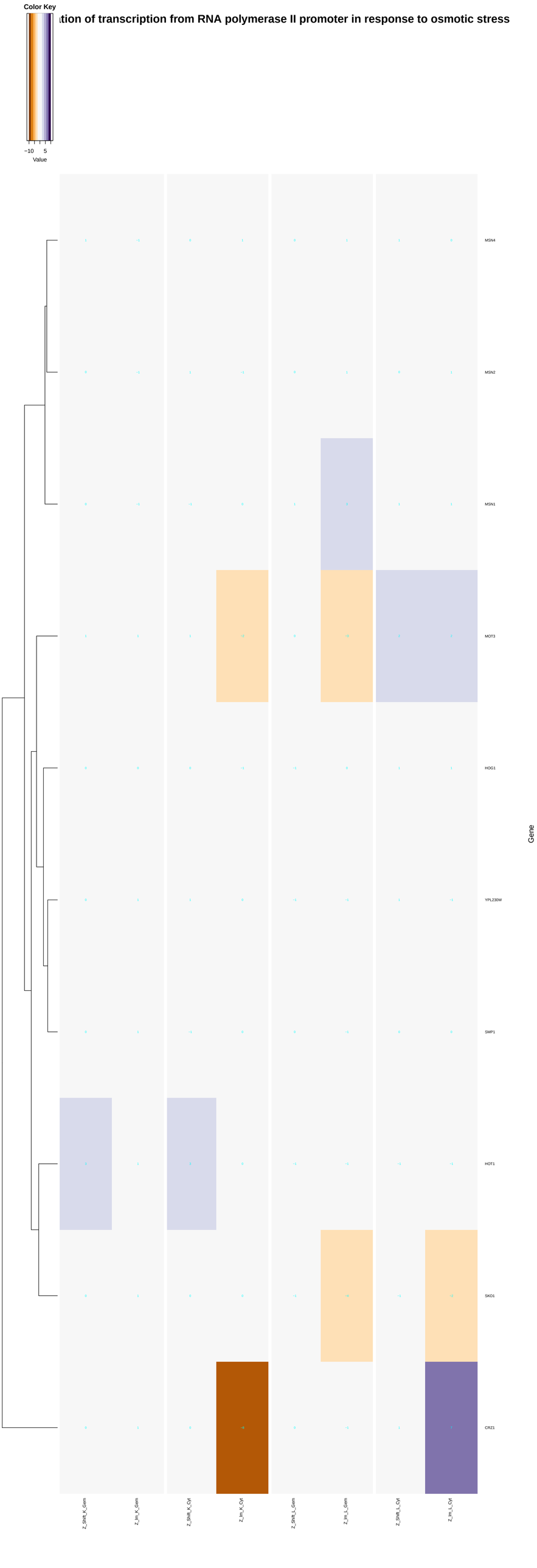

Color Key
−10
5
Value
cellular response to desiccation
STF2
NTH1
ATH1
TPS1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

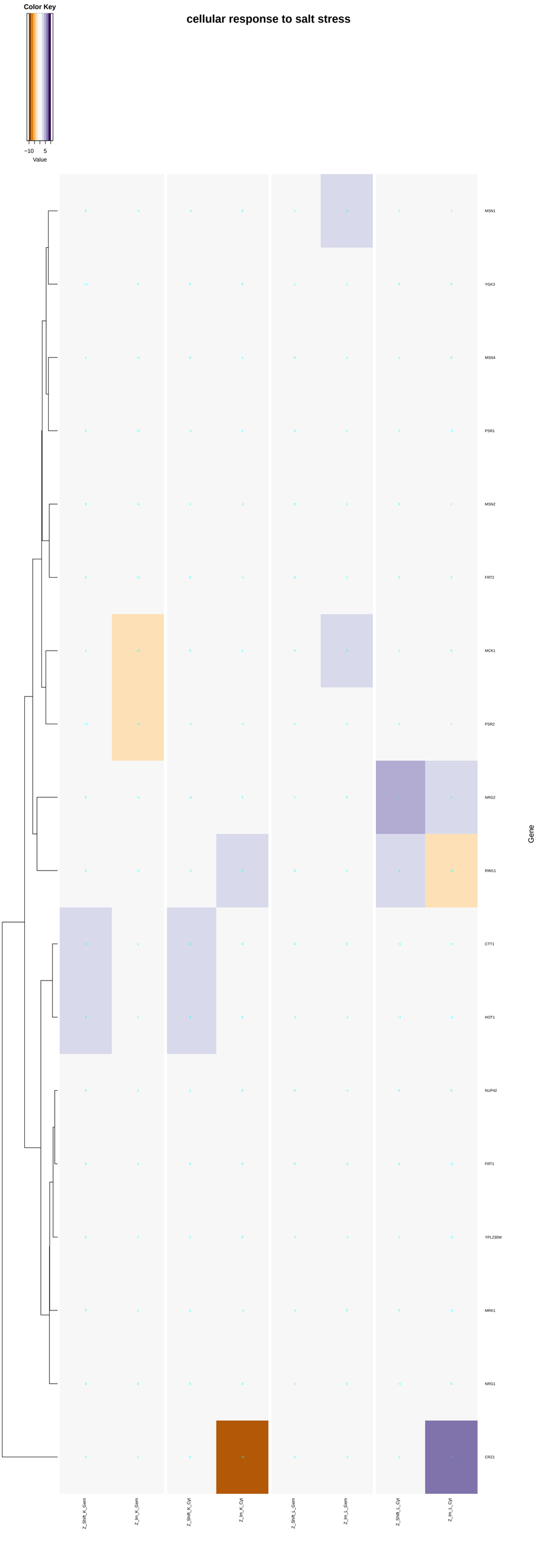

Color Key
−10
5
Value
positive regulation of translation in response to stress
1
−2
3
−2
2
2
2
13
TRL1
1
1
1
1
0
−1
−2
1
EDC2
0
0
−1
0
1
1
0
−1
EDC1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

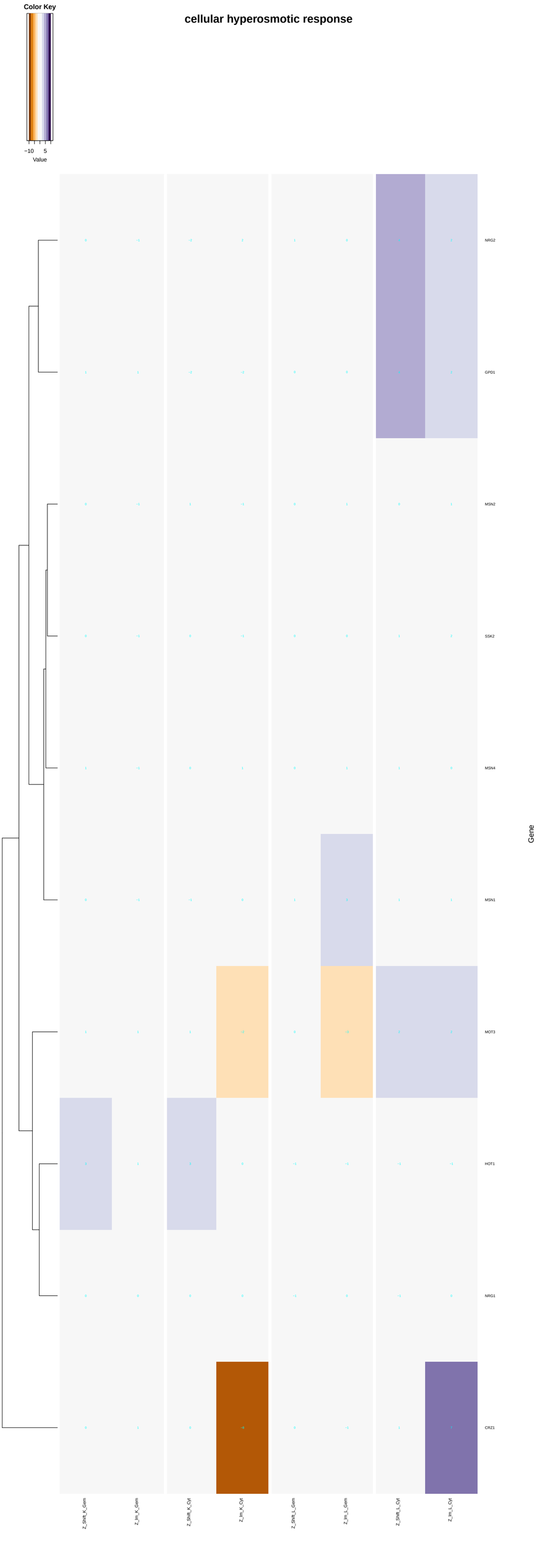

Color Key
−10
5
Value
gulation of transcription from RNA polymerase II promoter in response to stress
MSN4
MSN2
MSN1
RRD1
YOR051C
SWI6
RPN4
STB5
SEN1
CRZ1
ASF1
RTT109
YAP1
HOT1
BUR6
RCS1
DEP1
SDS3
SOD1
SAP30
PHO23
SIN3
SNF2
MIG3
YHR1
NCB2
CAD1
YPL230W
YRR1
SNT2
TEC1
HOG1
ARR1
AFT2
RLM1
SMP1
PDR8
SPT6
MOT3
ZAP1
MGA2
SUB1
SWI1
SKN7
SKO1
HAA1
ROX1
CST6
SCH9
SWI4
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

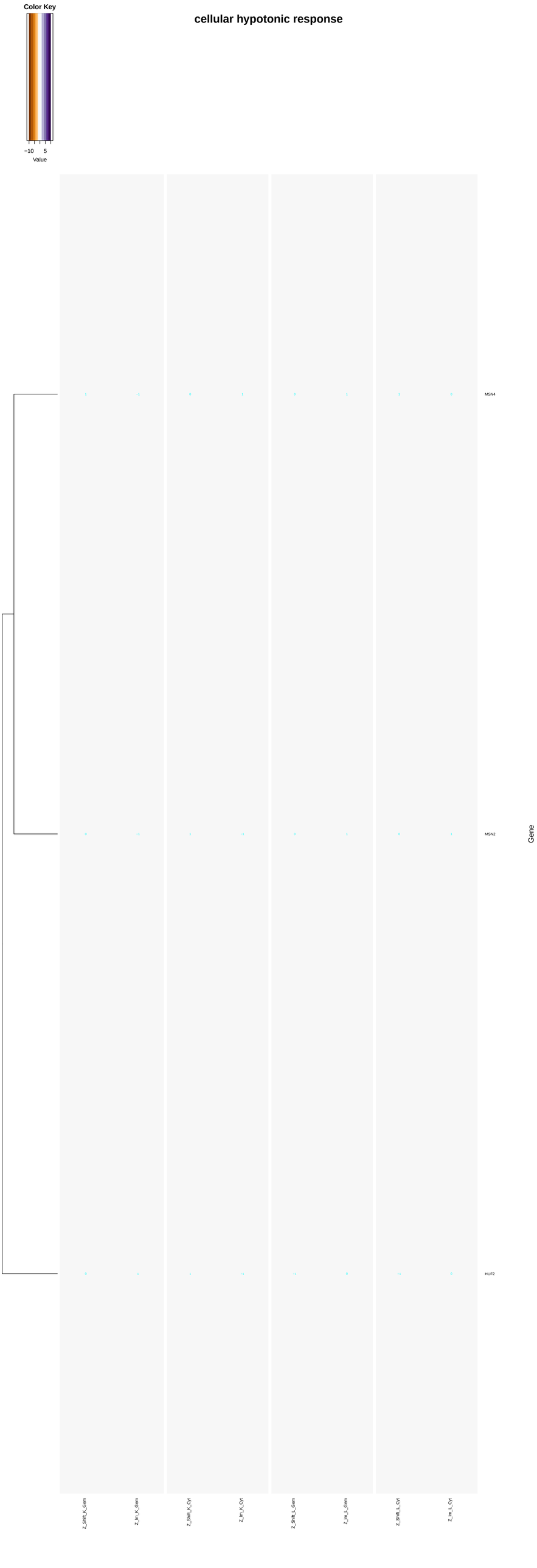

Color Key
−10
5
Value
cellular response to freezing
MSN4
ATH1
MSN2
TIR2
Gene
Z_Shft_K_Germ
Z_Im_K_Germ
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Germ
Z_Im_L_Germ
Z_Shft_L_Cyt
Z_Im_L_Cyt

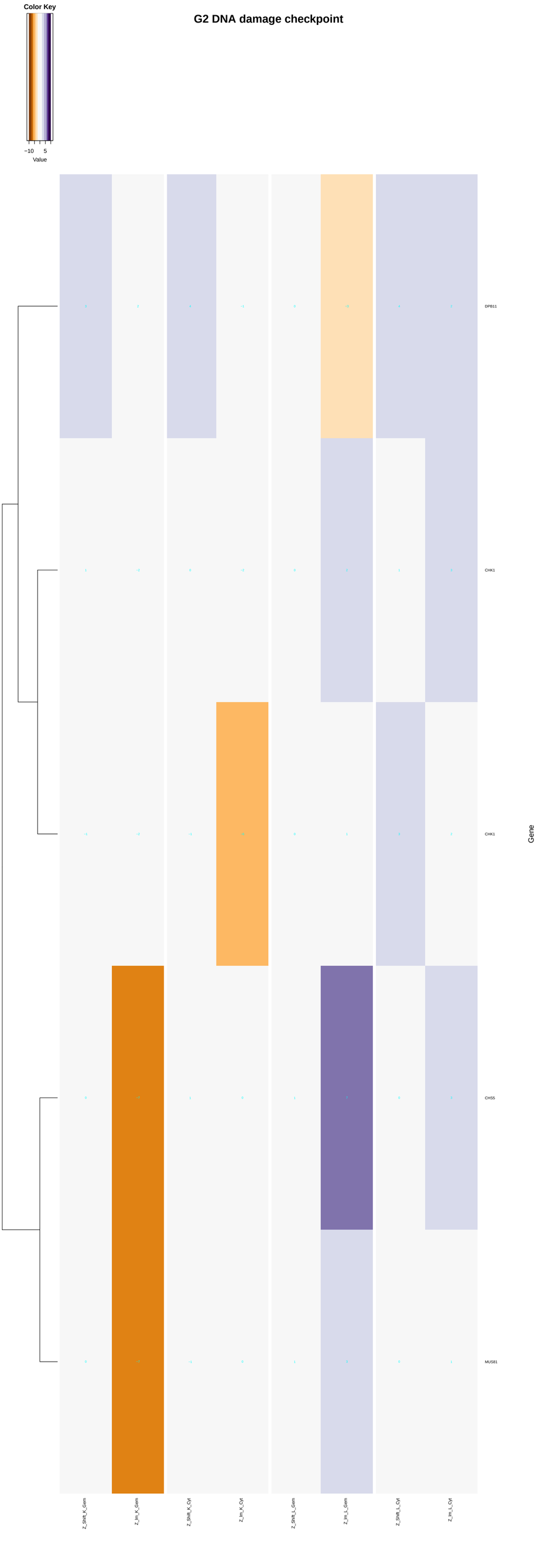

Color Key
−10
5
Value
osmosensory signaling pathway
SHO1
PTP2
PTC3
SSK1
SSK2
PTP3
HOG1
HKR1
YDL073W
STE50
YPD1
STE20
STE11
RGD1
SSK22
MSB2
RCK2
PTC2
OPY2
CDC37
PTC1
NBP2
PBS2
SLN1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

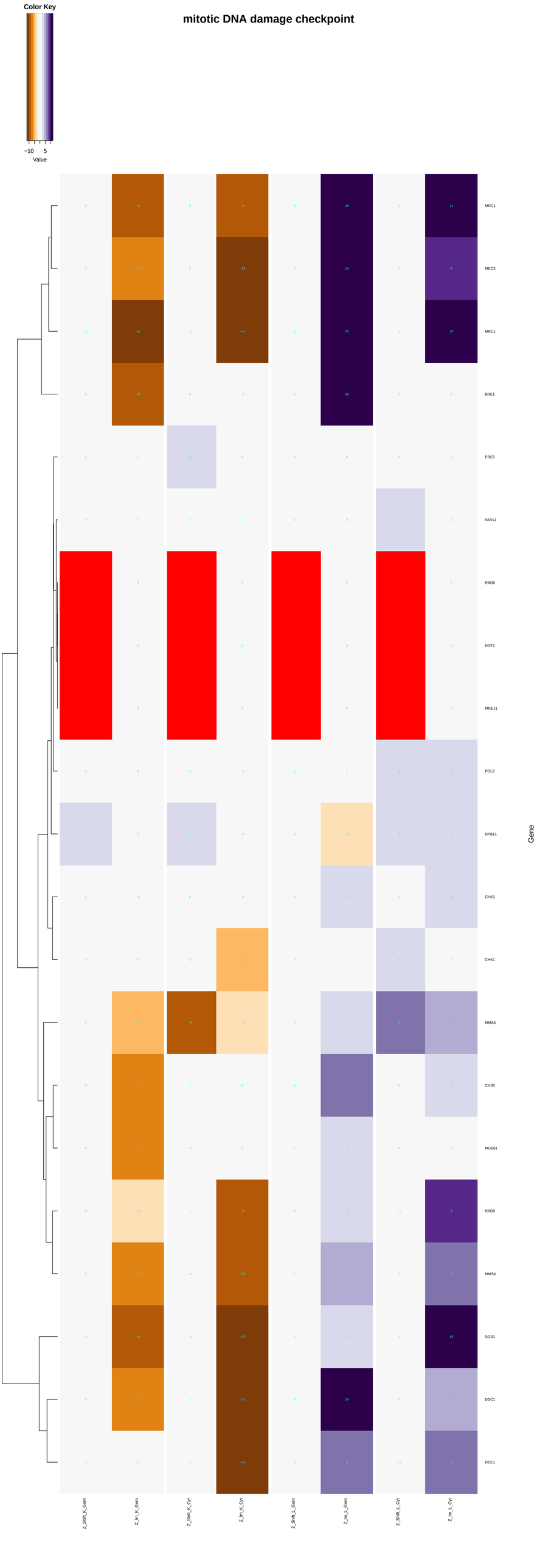

Color Key
−10
5
Value
tion of transcription from RNA polymerase II promoter in response to osmotic stress
MSN4
MSN2
MSN1
MOT3
HOG1
YPL230W
SMP1
HOT1
SKO1
CRZ1
Gene
Z_Shift_K_Gem
Z_In_K_Gem
Z_Shift_K_Cyt
Z_In_K_Cyt
Z_Shift_L_Gem
Z_In_L_Gem
Z_Shift_L_Cyt
Z_In_L_Cyt

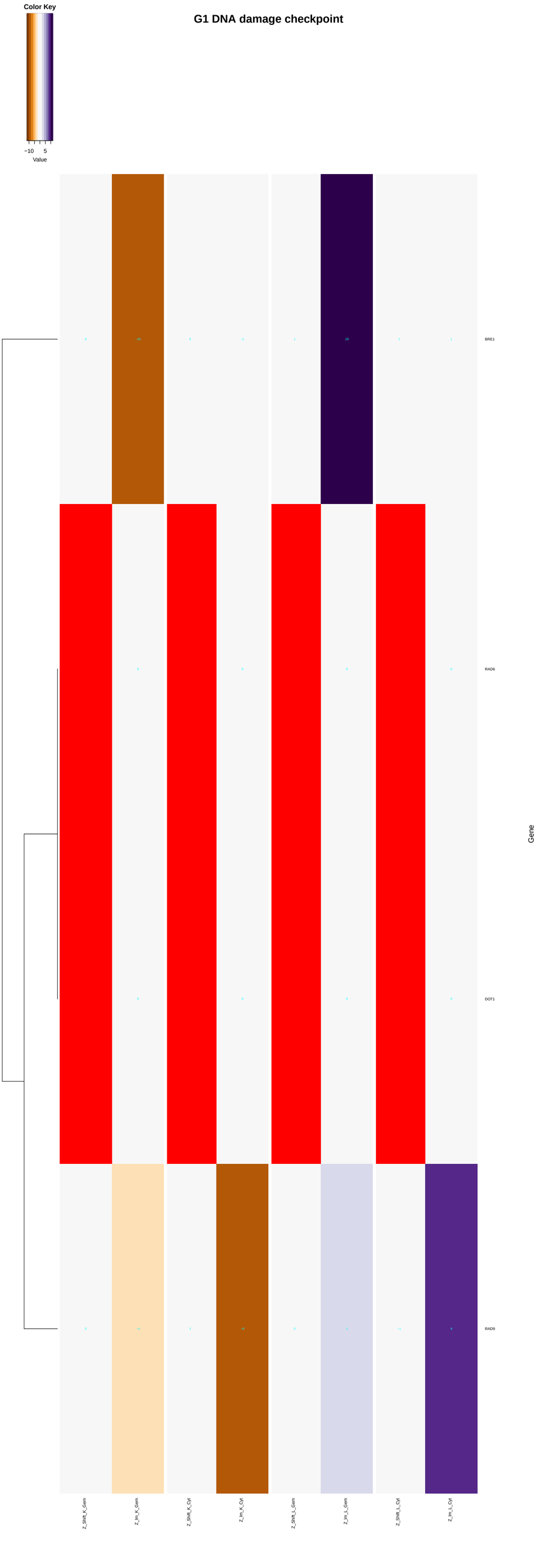

Color Key
−10
5
Value
cellular response to salt stress
MSN1
YGK3
MSN4
PSR1
MSN2
FRT2
MCK1
PSR2
NRG2
RIM11
CTT1
HOT1
NUP42
FRT1
YPL230W
MRK1
NRG1
CRZ1
Gene
Z_Shift_K_Gem
Z_Im_K_Gem
Z_Shift_K_Cyt
Z_Im_K_Cyt
Z_Shift_L_Gem
Z_Im_L_Gem
Z_Shift_L_Cyt
Z_Im_L_Cyt

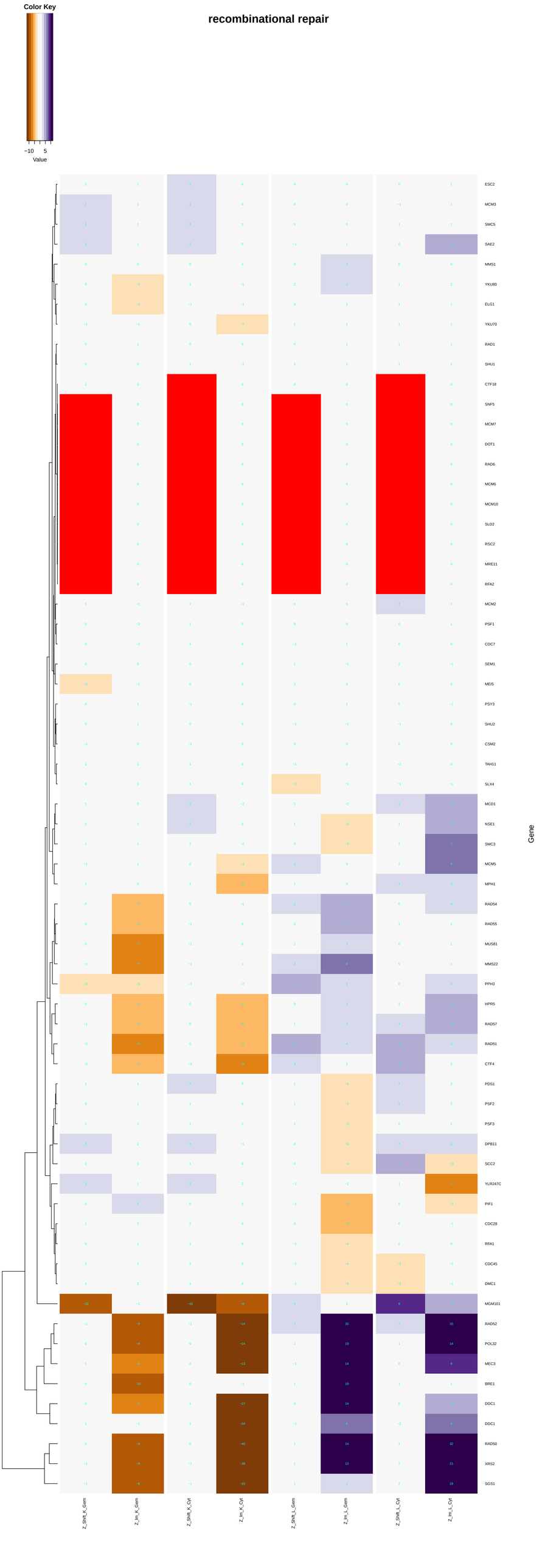

Color Key
−10
5
Value
cellular hyperosmotic response
NRG2
GPD1
MSN2
SSK2
MSN4
MSN1
MOT3
HOT1
NRG1
CRZ1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

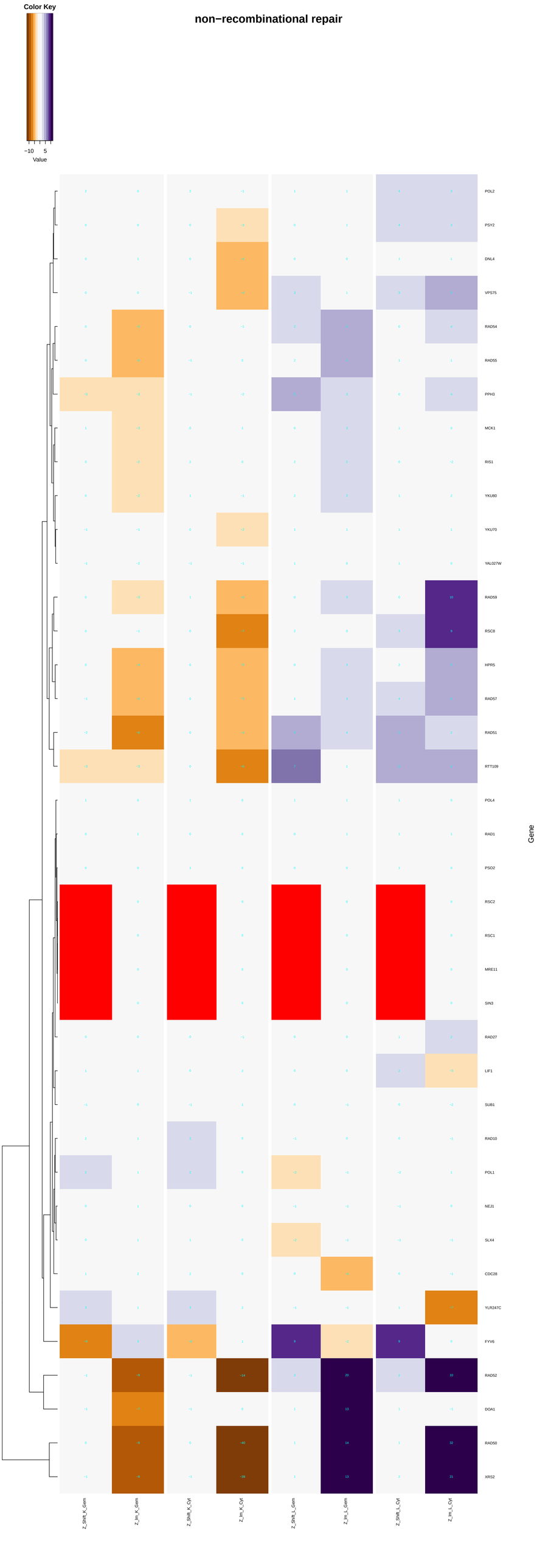

Color Key
−10
5
Value
cellular hypotonic response
MSN4
MSN2
HUF2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

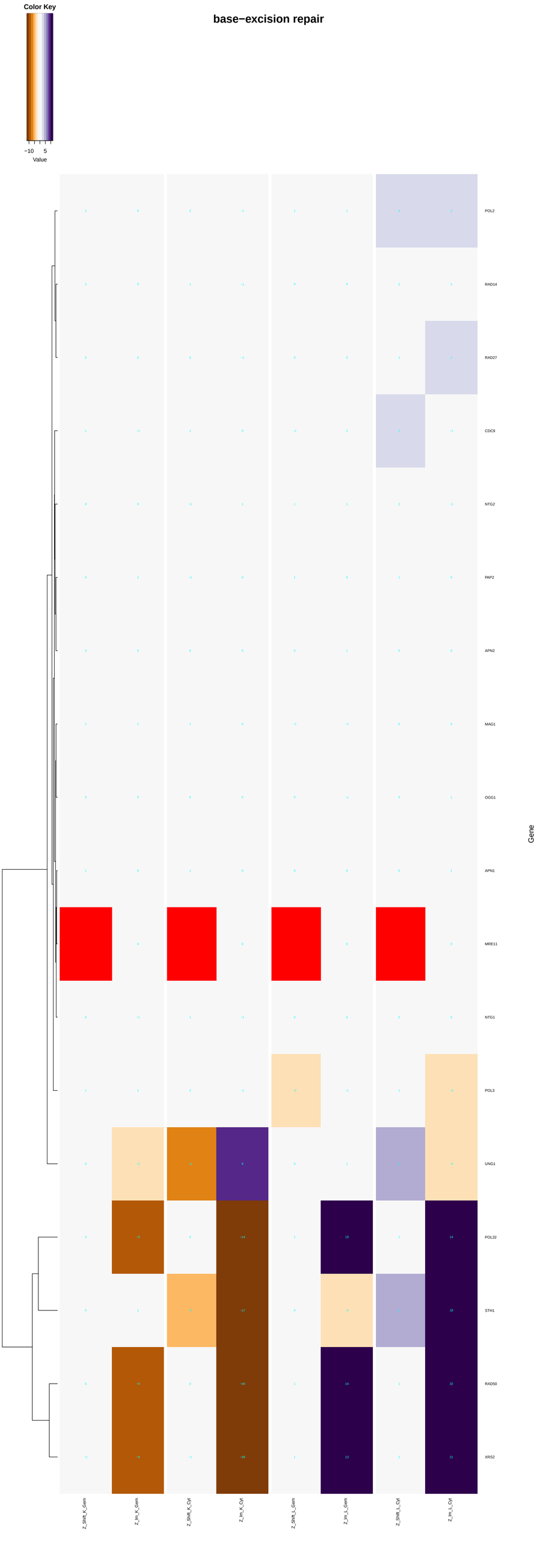

Color Key
−10
5
Value
G2 DNA damage checkpoint
3
2
4
−1
0
−3
4
2
DPB11
1
−2
0
−2
0
2
1
3
CHK1
−1
−2
−1
−6
0
1
3
2
CHK1
0
−4
1
0
1
3
0
3
CHS5
0
−4
−1
0
1
3
0
1
MUS81
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt
Gene

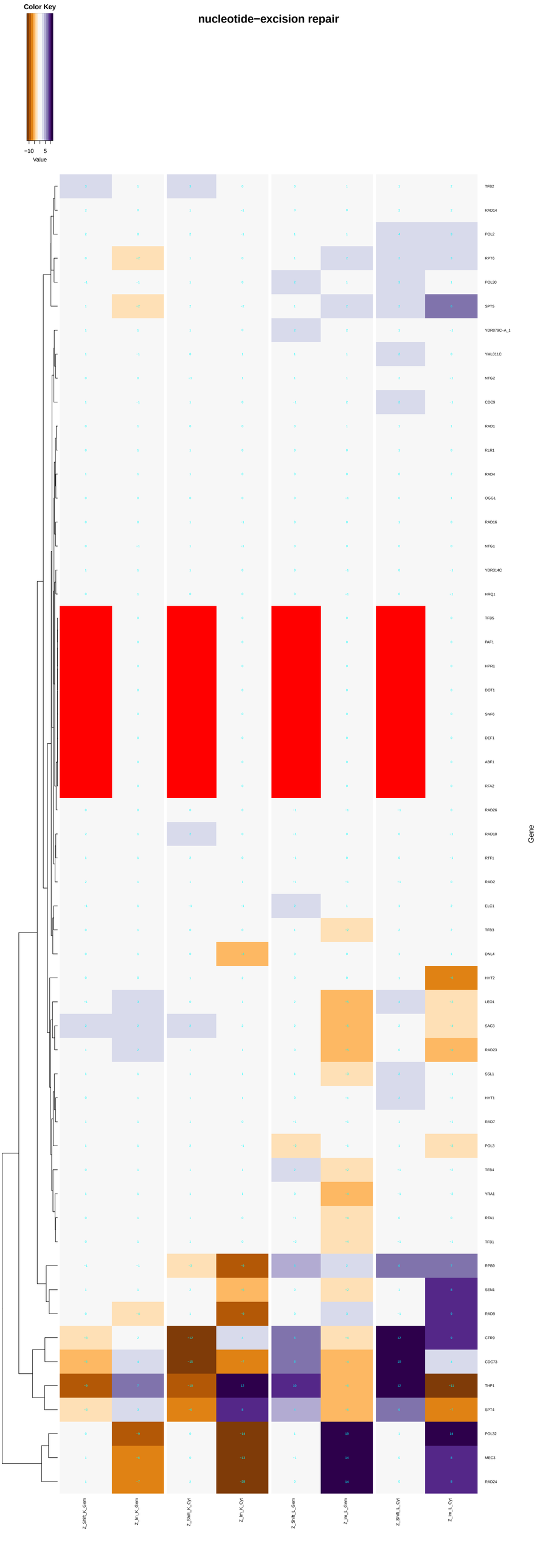

Color Key
−10
5
Value
mitotic DNA damage checkpoint
MRC1
MEC3
MRC1
BRE1
ESC2
FAR11
RAD6
DOT1
MRE11
POL2
DPB11
CHK1
CHK1
MMS4
CHS5
MUS81
RAD9
MMS4
SGS1
DDC1
DDC1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

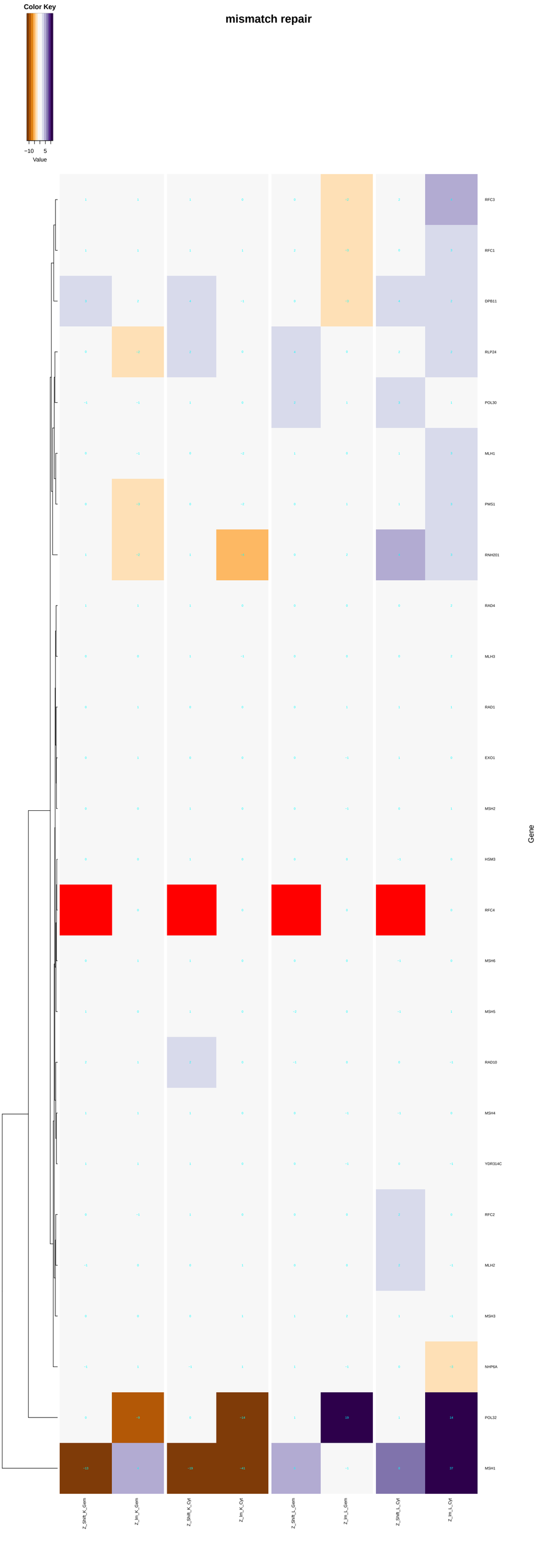

Color Key
−10
5
Value
G1 DNA damage checkpoint
0
−10
0
−1
1
10
1
1
BRE1
0
0
0
0
RAD6
0
0
0
0
DOT1
0
−4
1
−8
0
3
−1
9
RAD9
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt
Gene

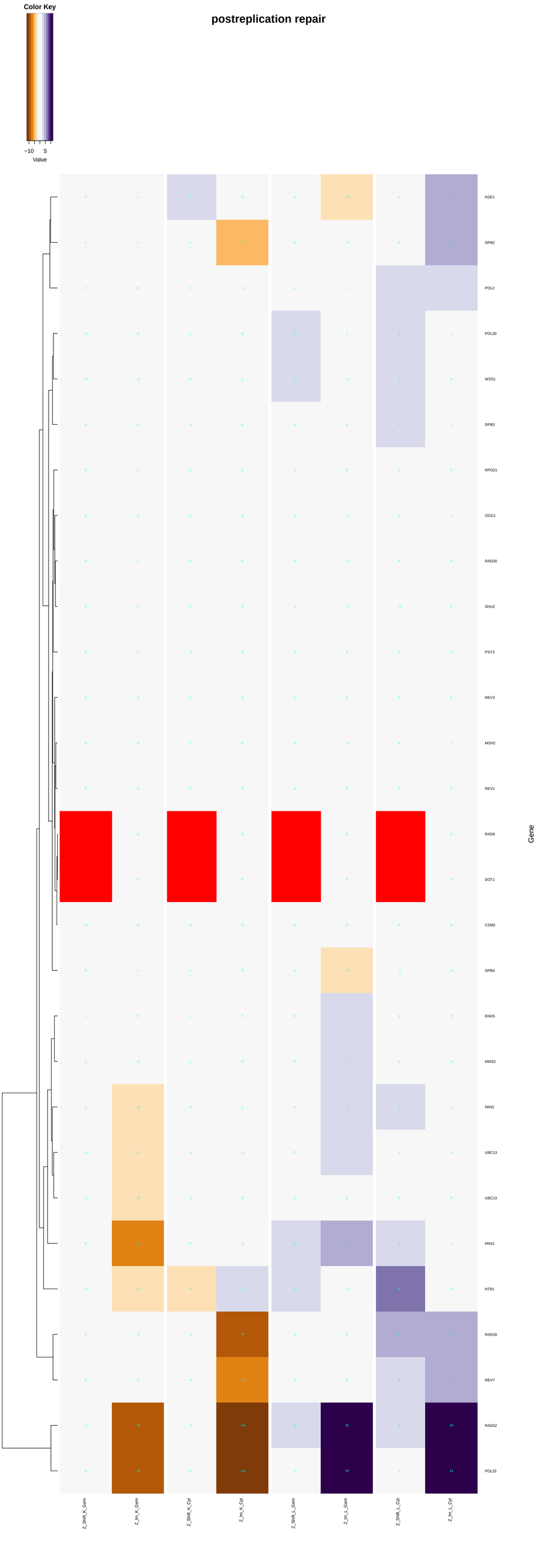

Color Key
−10
5
Value
recombinational repair
Gene
ESC2
MCM3
SMC5
SAE2
MMS1
YKU80
ELG1
YKU70
RAD1
SHU1
CTF18
SNF5
MCM7
DOT1
RAD6
MCM6
MCM10
SLD2
RSC2
MRE11
RFA2
MCM2
PSF1
CDC7
SEM1
MEI5
PSY3
SHU2
CSM2
TAH11
SLX4
MCD1
NSE1
SMC3
MCM5
MPH1
RAD54
RAD55
MUS81
MMS22
PPH3
HPR5
RAD57
RAD51
CTF4
PDS1
PSF2
PSF3
DPB11
SCC2
YLR247C
PIF1
CDC28
RFA1
CDC45
DMC1
MGM101
RAD52
POL32
MEC3
BRE1
DDC1
DDC1
RAD50
XRS2
SGS1
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt

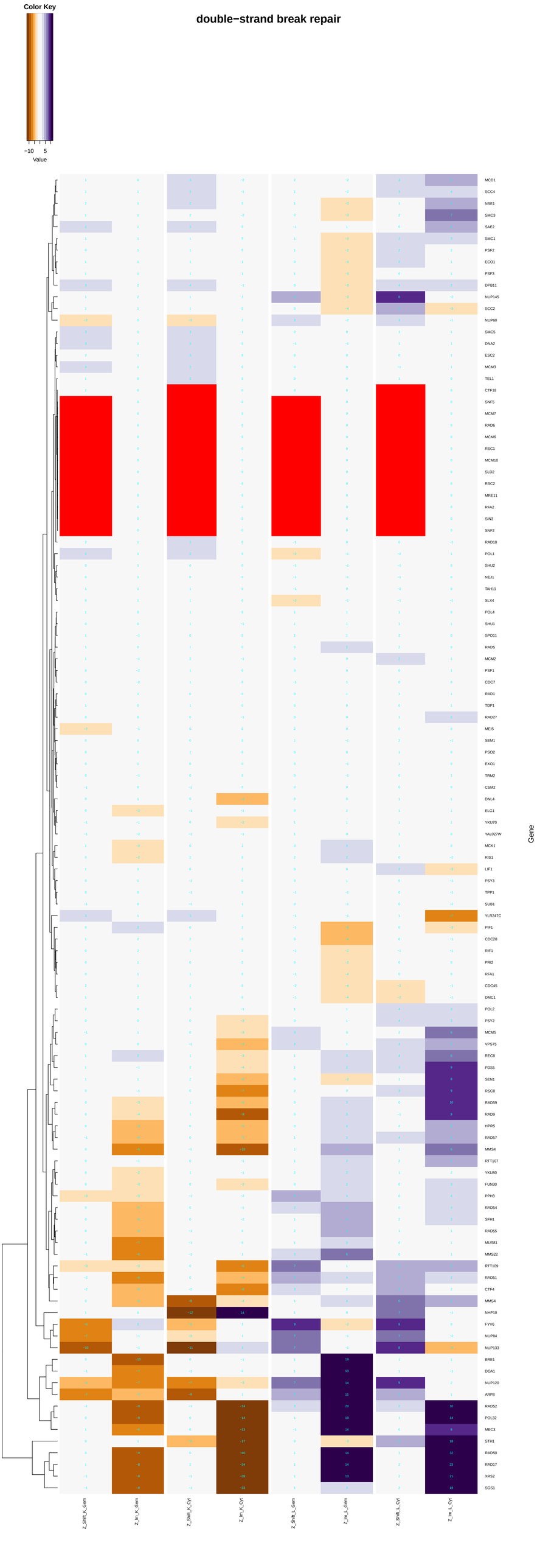

Color Key
−10
5
Value
non−recombinational repair
POL2
PSY2
DNL4
VPS75
RAD54
RAD55
PPH3
MCK1
RIS1
YKU80
YKU70
YAL027W
RAD59
RSC8
HPR5
RAD57
RAD51
RTT109
POL4
RAD1
PSO2
RSC2
RSC1
MRE11
SIN3
RAD27
LIF1
SUB1
RAD10
POL1
NEJ1
SLX4
CDC28
YLR247C
FYV6
RAD52
DOA1
RAD50
XRS2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

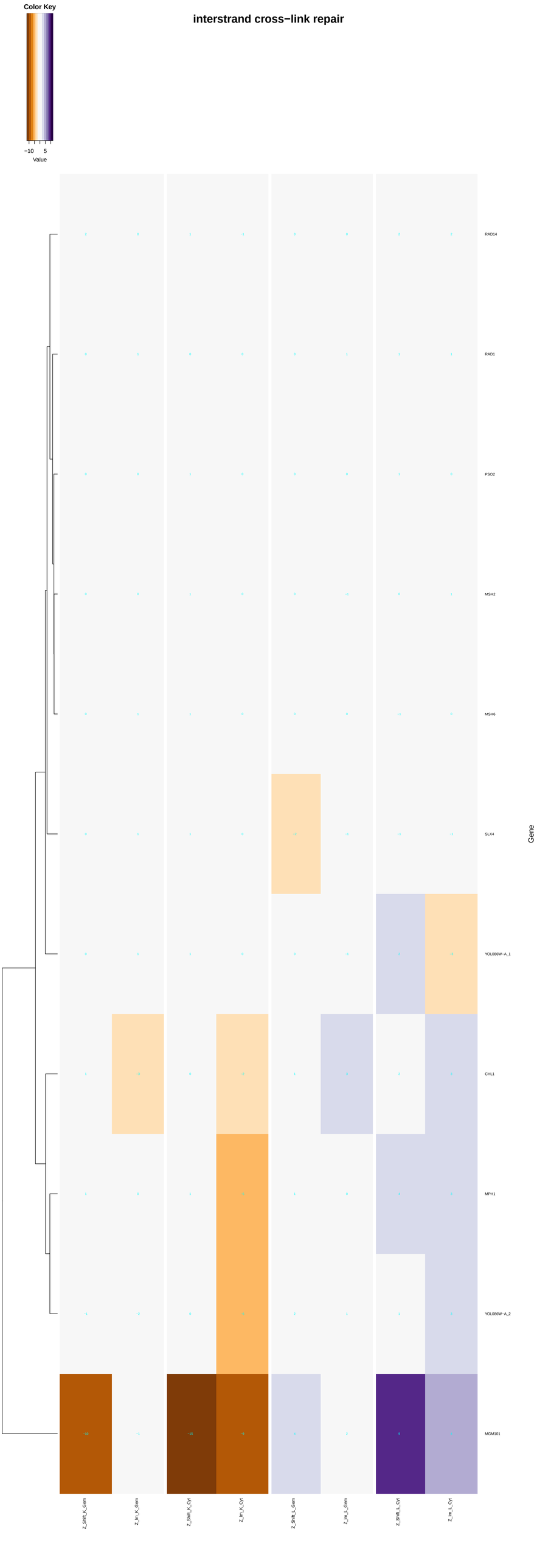

Color Key
−10
5
Value
base−excision repair
POL2
RAD14
RAD27
CDC9
NTG2
PAP2
APN2
MAG1
OGG1
APN1
MRE11
NTG1
POL3
UNG1
POL32
STH1
RAD50
XRS2
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

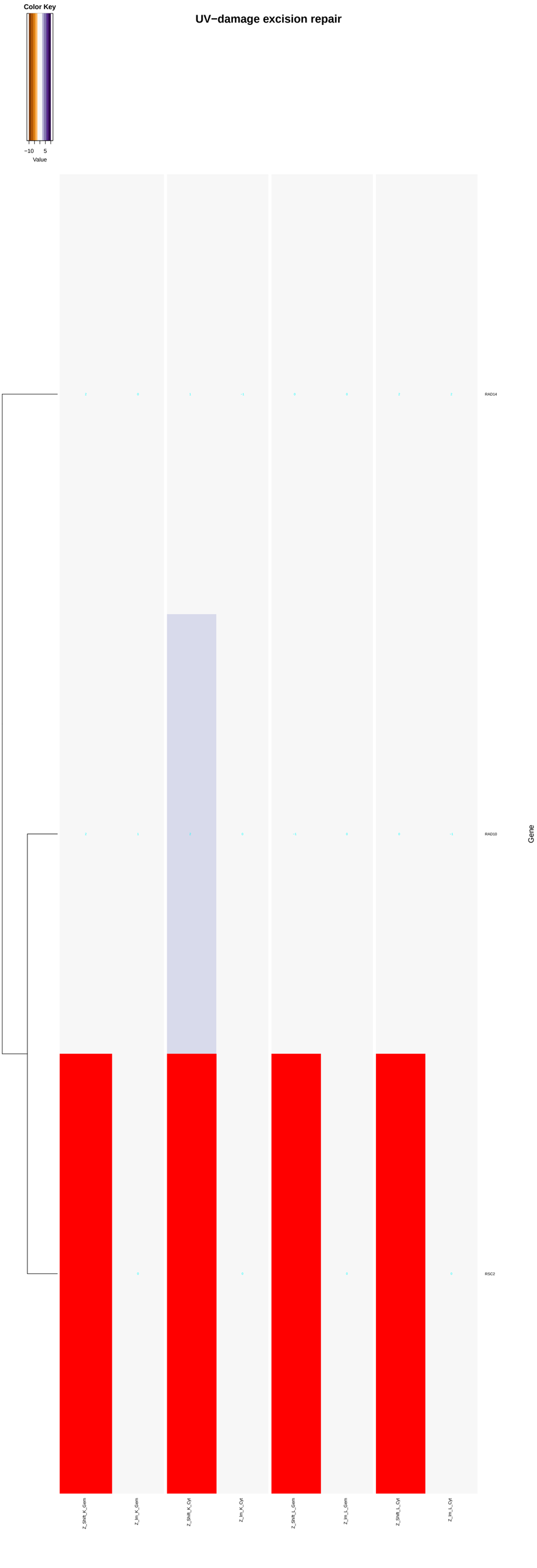

Color Key
−10
5
Value
nucleotide−excision repair
TFB2
RAD14
POL2
RPT6
POL30
SPT5
YDR079C−A_1
YML011C
NTG2
CDC9
RAD1
RLR1
RAD4
OGG1
RAD16
NTG1
YDR314C
HRQ1
TFB5
PAF1
HPR1
DOT1
SNF6
DEF1
ABF1
RFA2
RAD26
RAD10
RTF1
RAD2
ELC1
TFB3
DNL4
HHT2
LEO1
SAC3
RAD23
SSL1
HHT1
RAD7
POL3
TFB4
YRA1
RFA1
TFB1
RPB9
SEN1
RAD9
CTR9
CDC73
THP1
SPT4
POL32
MEC3
RAD24
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

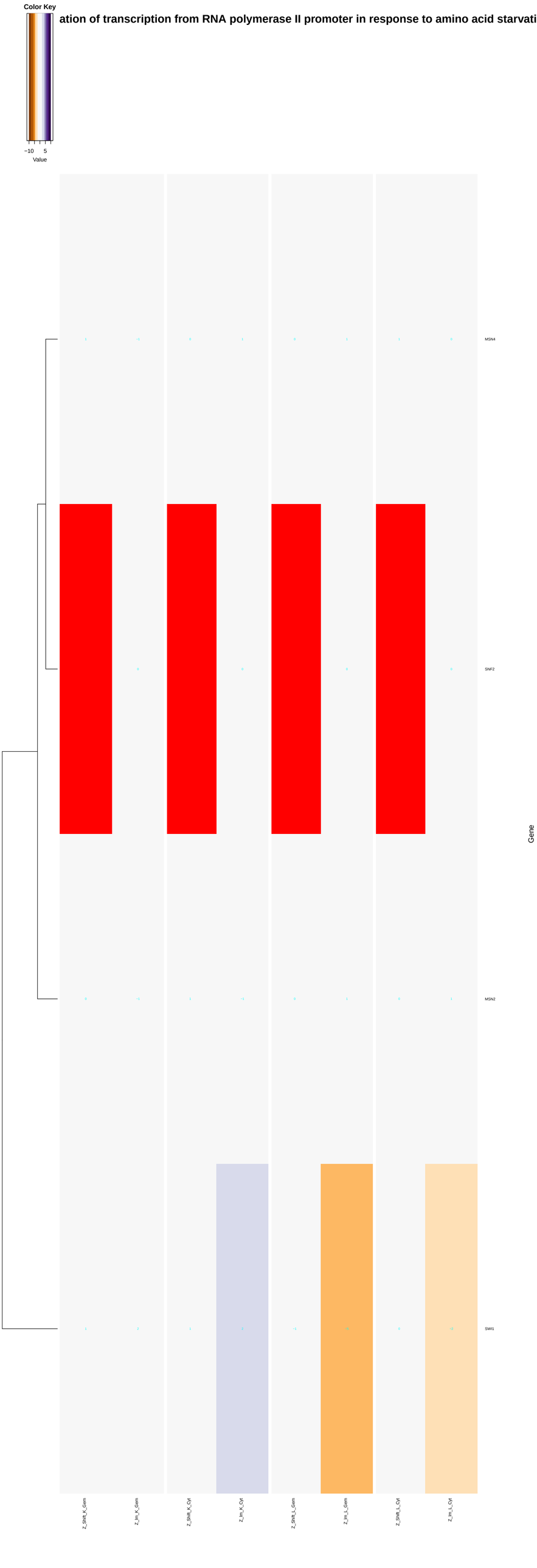

Color Key
−10
5
Value
mismatch repair
RFC3
RFC1
DPB11
RLP24
POL30
MLH1
PMS1
RNH201
RAD4
MLH3
RAD1
EXO1
MSH2
HSM3
RFC4
MSH6
MSH5
RAD10
MSH4
YDR314C
RFC2
MLH2
MSH3
NHP6A
POL32
MSH1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

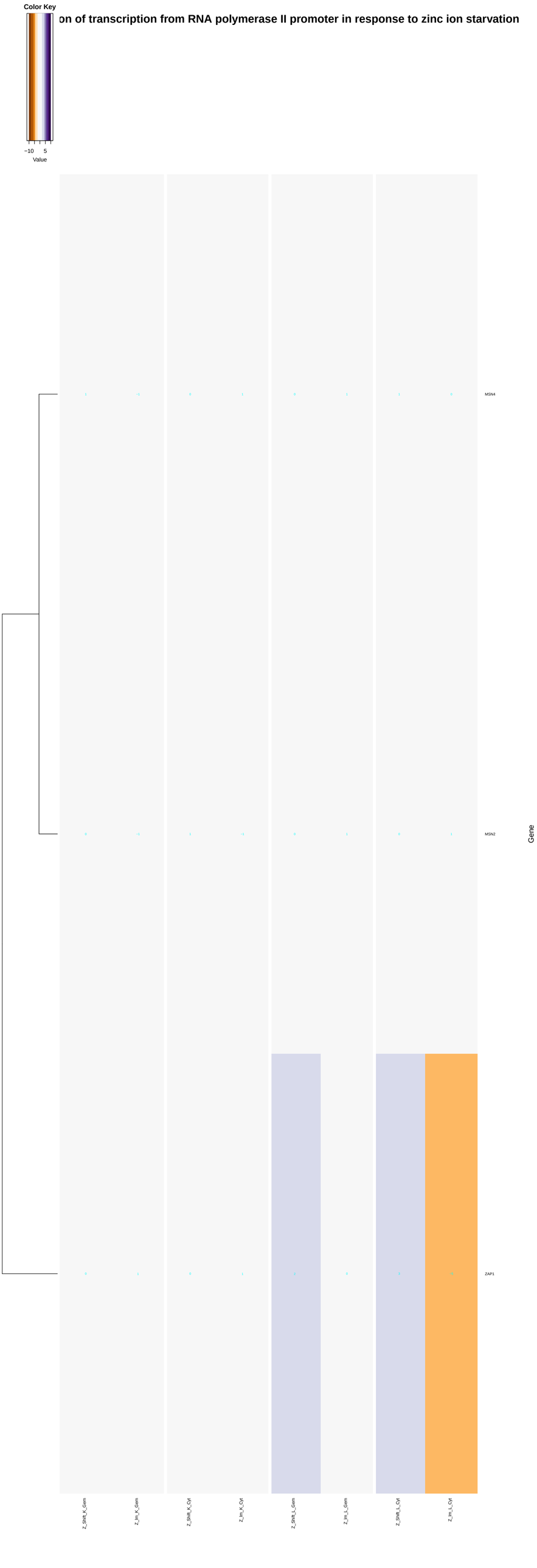

Color Key
−10
5
Value
postreplication repair
NSE1
DPB2
POL2
POL30
WSS1
DPB3
RPO21
OGG1
RAD30
SHU2
PSY3
REV3
MSH2
REV1
RAD6
DOT1
CSM2
DPB4
RAD5
MMS2
PAN2
UBC13
UBC13
PAN3
HTB1
RAD18
REV7
RAD52
POL32
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

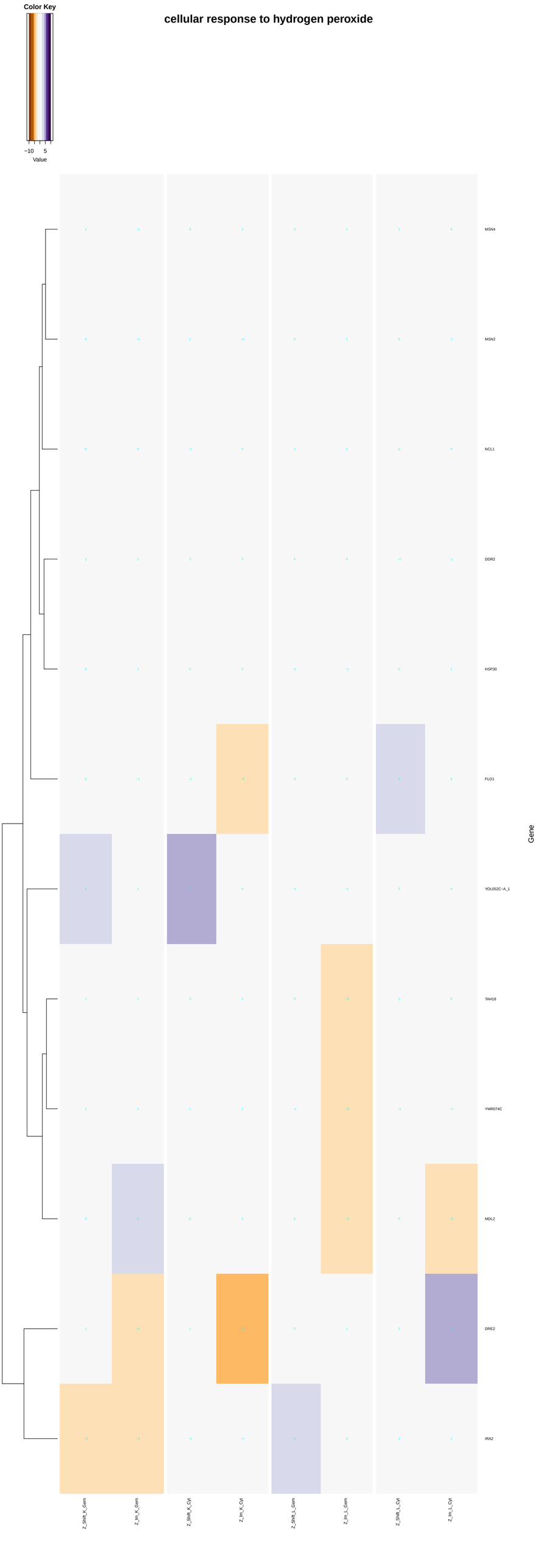

Color Key
−10
5
Value
double−strand break repair
Gene
MCD1
SCC4
NSE1
SMC3
SAE2
SMC1
PSF2
ECO1
PSF3
DPB11
NUP145
SCC2
NUP60
SMC5
DNA2
ESC2
MCM3
TEL1
CTF18
SNF5
MCM7
RAD6
MCM6
RSC1
MCM10
SLD2
RSC2
MRE11
RFA2
SIN3
SNF2
RAD10
POL1
SHU2
NEJ1
TAH11
SLX4
POL4
SHU1
SPO11
RAD5
MCM2
PSF1
CDC7
RAD1
TDP1
RAD27
MEI5
SEM1
PSO2
EXO1
TRM2
CSM2
DNL4
ELG1
YKU70
YAL027W
MCK1
RIS1
LIF1
PSY3
TPP1
SUB1
YLR247C
PIF1
CDC28
RIF1
PRI2
RFA1
CDC45
DMC1
POL2
PSY2
MCM5
VPS75
REC8
PDS5
SEN1
RSC8
RAD59
RAD9
HPR5
RAD57
MMS4
RTT107
YKU80
FUN30
PPH3
RAD54
SFH1
RAD55
MUS81
MMS22
RTT109
RAD51
CTF4
MMS4
NHP10
FYV6
NUP84
NUP133
BRE1
DOA1
NUP120
ARP8
RAD52
POL32
MEC3
STH1
RAD50
RAD17
XRS2
SGS1
Z_Shh_K_Gem
Z_Im_K_Gem
Z_Shh_K_Cyt
Z_Im_K_Cyt
Z_Shh_L_Gem
Z_Im_L_Gem
Z_Shh_L_Cyt
Z_Im_L_Cyt

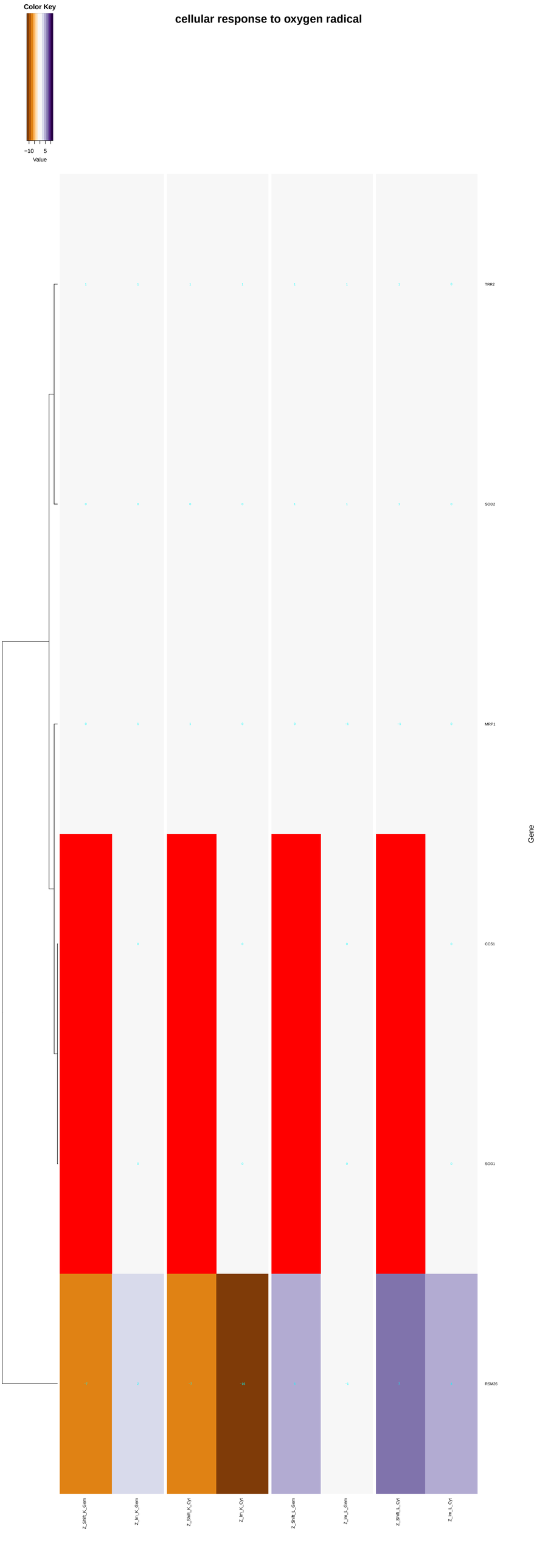

Color Key
−10
5
Value
interstrand cross−link repair
RAD14
RAD1
PSO2
MSH2
MSH6
SLX4
YOL086W−A_1
CHL1
MPH1
YOL086W−A_2
MGM101
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

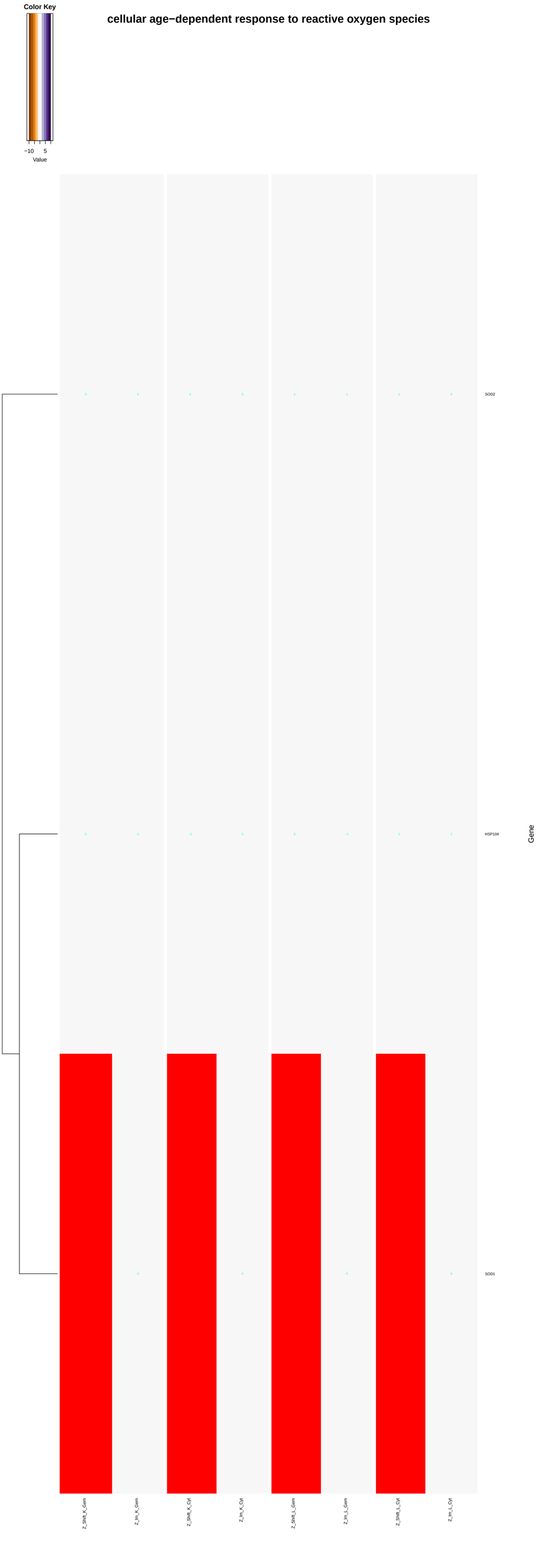

Color Key
−10
5
Value
UV−damage excision repair
RAD14
RAD10
RSC2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

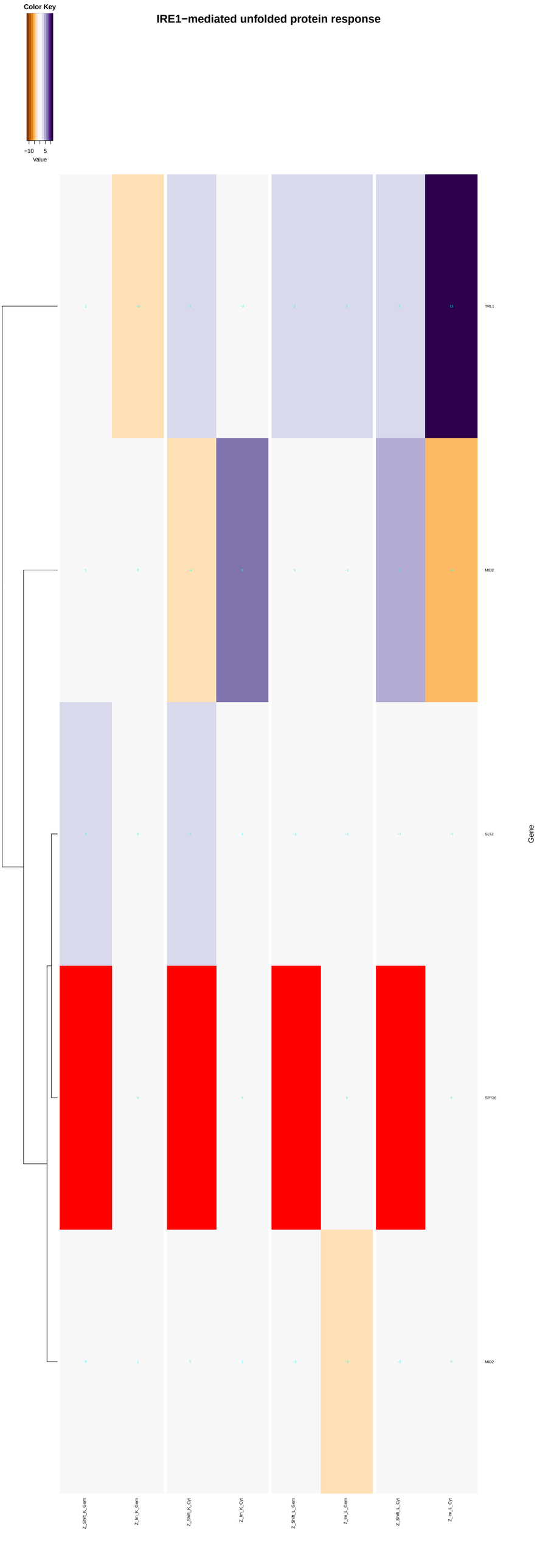

Color Key
−10
5
Value
ation of transcription from RNA polymerase II promoter in response to amino acid starvati
MSN4
SNF2
MSN2
SWI1
Gene
Z_Shift_K_Germ
Z_Im_K_Germ
Z_Shift_K_Cyt
Z_Im_K_Cyt
Z_Shift_L_Germ
Z_Im_L_Germ
Z_Shift_L_Cyt
Z_Im_L_Cyt

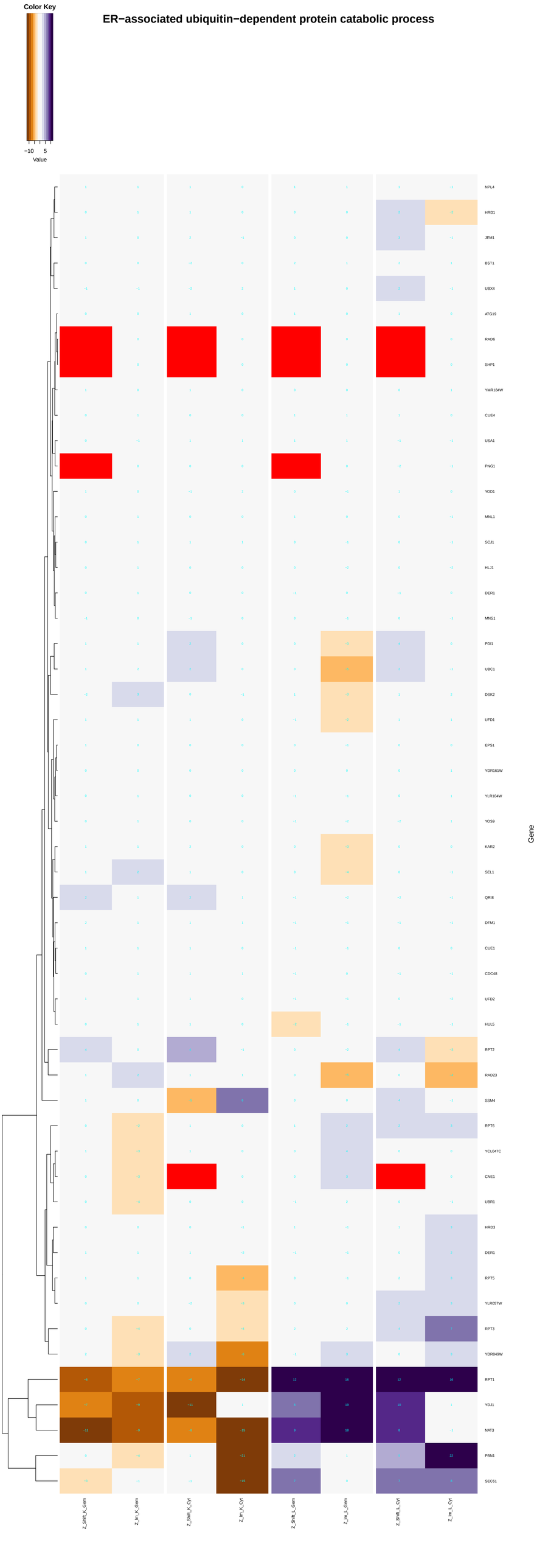

Color Key
−10
5
Value
on of transcription from RNA polymerase II promoter in response to zinc ion starvation
1
−1
0
1
0
1
1
0
MSN4
0
−1
1
−1
0
1
0
1
MSN2
Gene
0
1
0
1
2
0
3
3
ZAP1
Z_Shift_K_Germ
Z_Im_K_Germ
Z_Shift_K_Cyt
Z_Im_K_Cyt
Z_Shift_L_Germ
Z_Im_L_Germ
Z_Shift_L_Cyt
Z_Im_L_Cyt

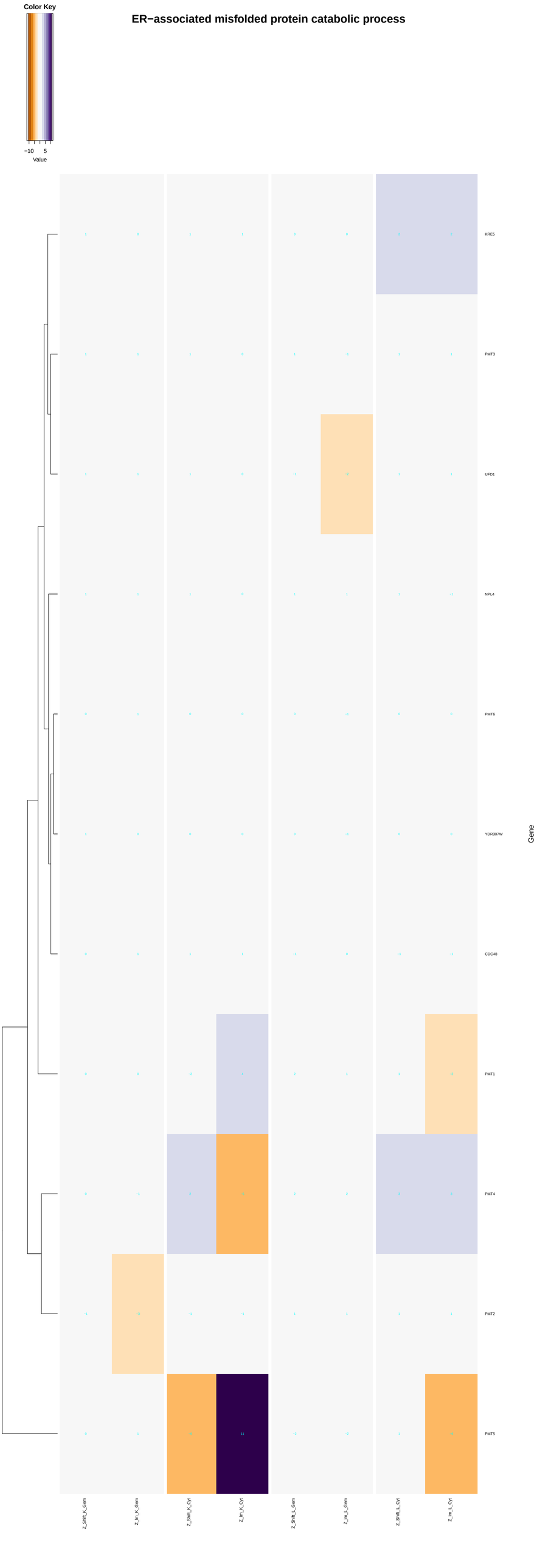

Color Key
−10
5
Value
cellular response to hydrogen peroxide
MSN4
MSN2
NCL1
DDR2
HSP30
FLO1
YOL052C−A_1
TAH18
YMR074C
MDL2
DRE2
IRA2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

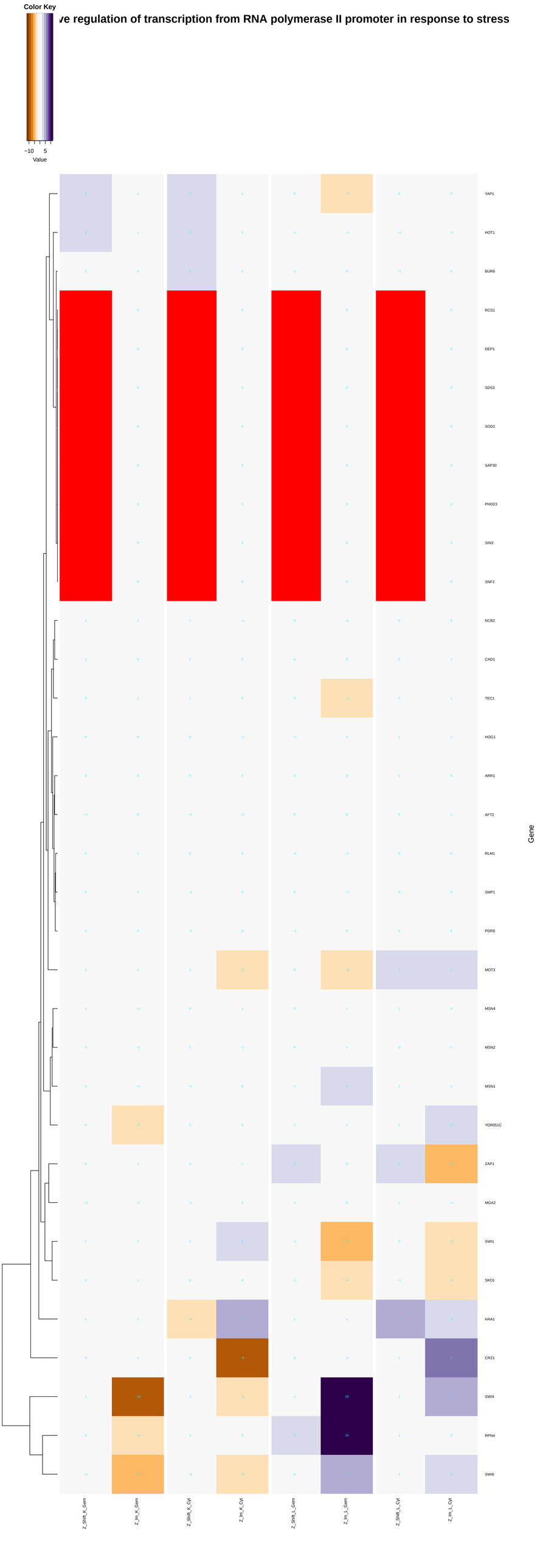

Color Key
−10
5
Value
cellular response to oxygen radical
TRR2
SOD2
MRP1
CCS1
SOD1
RSM26
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt

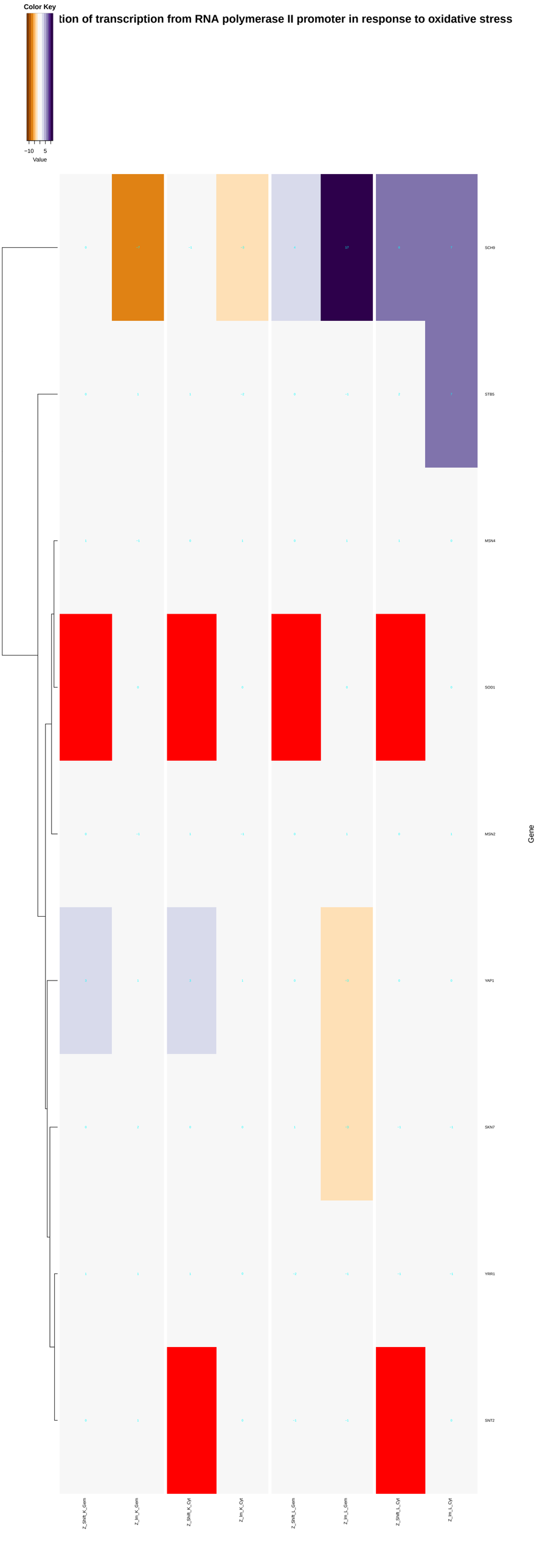

Color Key
−10
5
Value
cellular age−dependent response to reactive oxygen species
0
0
0
0
1
1
1
0
SOD2
0
0
−1
0
0
−1
1
1
HSP104
0
0
0
0
SOD1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

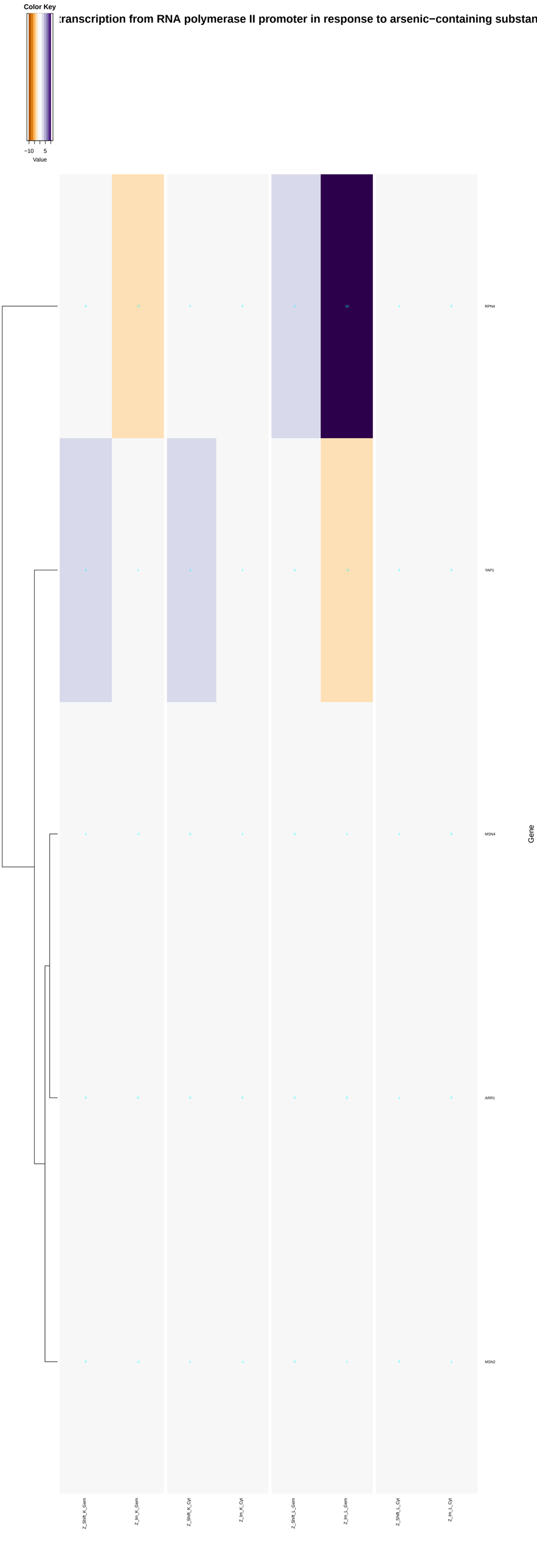

Color Key
−10
5
Value
IRE1−mediated unfolded protein response
1
−2
3
−2
2
2
2
13
TRL1
1
0
−4
8
0
−1
7
10
MID2
2
0
2
1
−1
−1
−1
−1
SLT2
0
0
0
0
0
SPT20
0
1
0
1
−2
−2
−2
0
MID2
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
ER−associated ubiquitin−dependent protein catabolic process
NPL4
HRD1
JEM1
BST1
UBX4
ATG19
RAD6
SHP1
YMR184W
CUE4
USA1
PNG1
YOD1
MNL1
SCJ1
HLJ1
DER1
MNS1
PDI1
UBC1
DSK2
UFD1
EPS1
YDR161W
YLR104W
YOS9
KAR2
SEL1
QRI8
DFM1
CUE1
CDC48
UFD2
HUL5
RPT2
RAD23
SSM4
RPT6
YCL047C
CNE1
UBR1
HRD3
DER1
RPT5
YLR057W
RPT3
YDR049W
RPT1
YDJ1
NAT3
PBN1
SEC61
Gene
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
ER−associated misfolded protein catabolic process
KRE5
PMT3
UFD1
NPL4
PMT6
YDR307W
CDC48
PMT1
PMT4
PMT2
PMT5
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
ve regulation of transcription from RNA polymerase II promoter in response to stress
YAP1
HOT1
BUR6
RCS1
DEP1
SDS3
SOD1
SAP30
PHO23
SIN3
SNF2
NCB2
CAD1
TEC1
HOG1
ARR1
AFT2
RLM1
SMP1
PDR8
MOT3
MSN4
MSN2
MSN1
YOR051C
ZAP1
MGA2
SWI1
SKO1
HAA1
CRZ1
SWI4
RPN4
SWI6
Gene
Z_Shift_K_Gem
Z_In_K_Gem
Z_Shift_K_Cyt
Z_In_K_Cyt
Z_Shift_L_Gem
Z_In_L_Gem
Z_Shift_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
tion of transcription from RNA polymerase II promoter in response to oxidative stress
SCH9
STB5
MSN4
SOD1
MSN2
YAP1
SKN7
YRR1
SNT2
Gene
Z_Shift_K_Gem
Z_Im_K_Gem
Z_Shift_K_Cyt
Z_Im_K_Cyt
Z_Shift_L_Gem
Z_Im_L_Gem
Z_Shift_L_Cyt
Z_Im_L_Cyt


Color Key
−10
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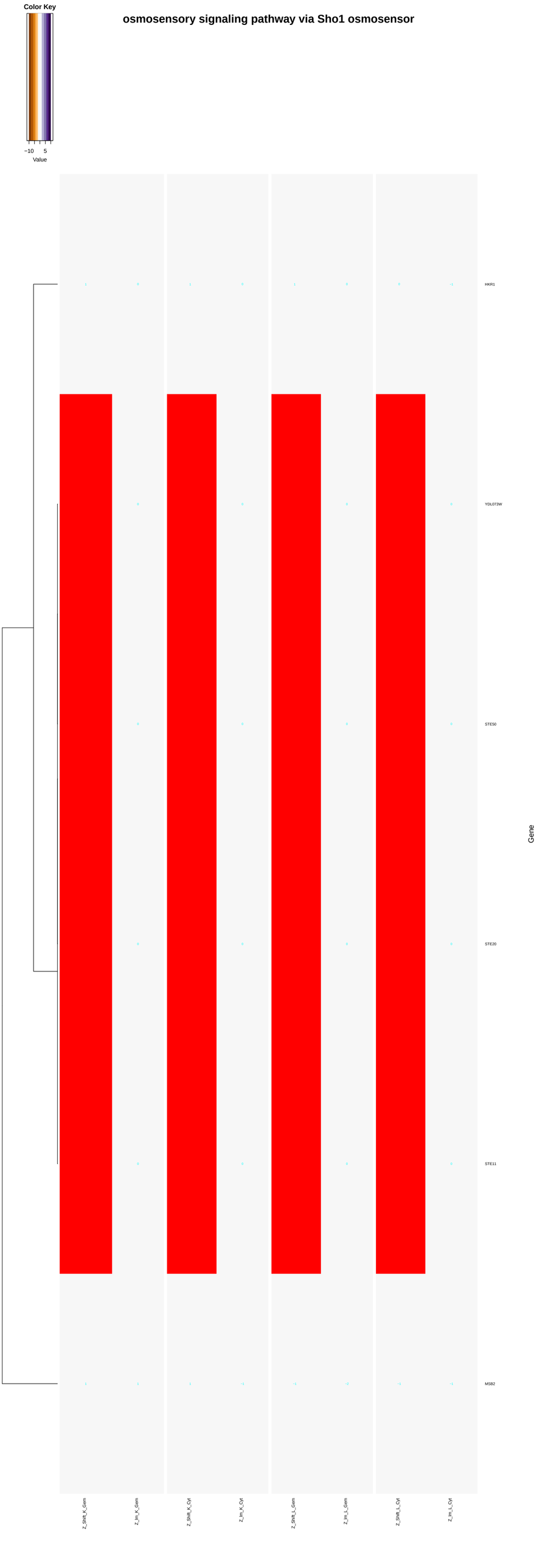
Value
transcription from RNA polymerase II promoter in response to arsenic−containing substan
0
−3
2
0
3
10
1
0
RPN4
3
1
3
1
0
−3
0
0
YAP1
1
−1
0
1
0
1
1
0
MSN4
0
0
0
0
0
0
1
0
ARR1
0
−1
1
−1
0
1
0
1
MSN2
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt
Gene


Color Key
−10
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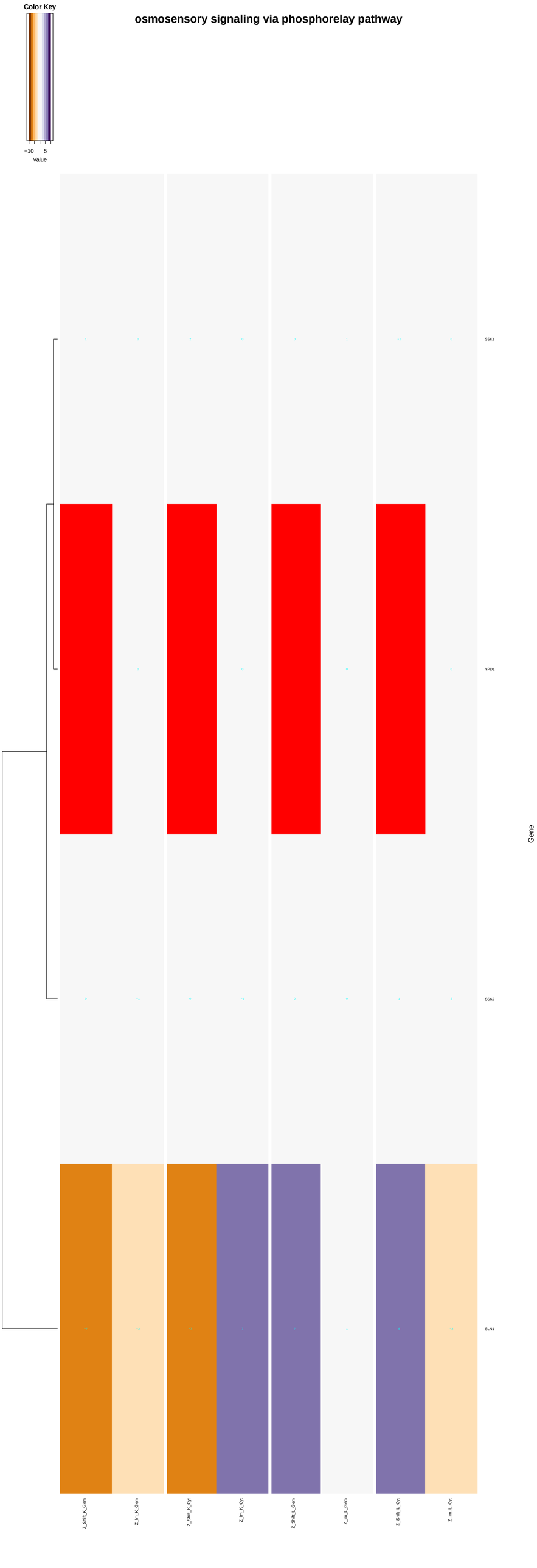
Value
osmosensory signaling pathway via Sho1 osmosensor
HKR1
YDL073W
STE50
STE20
STE11
MSB2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt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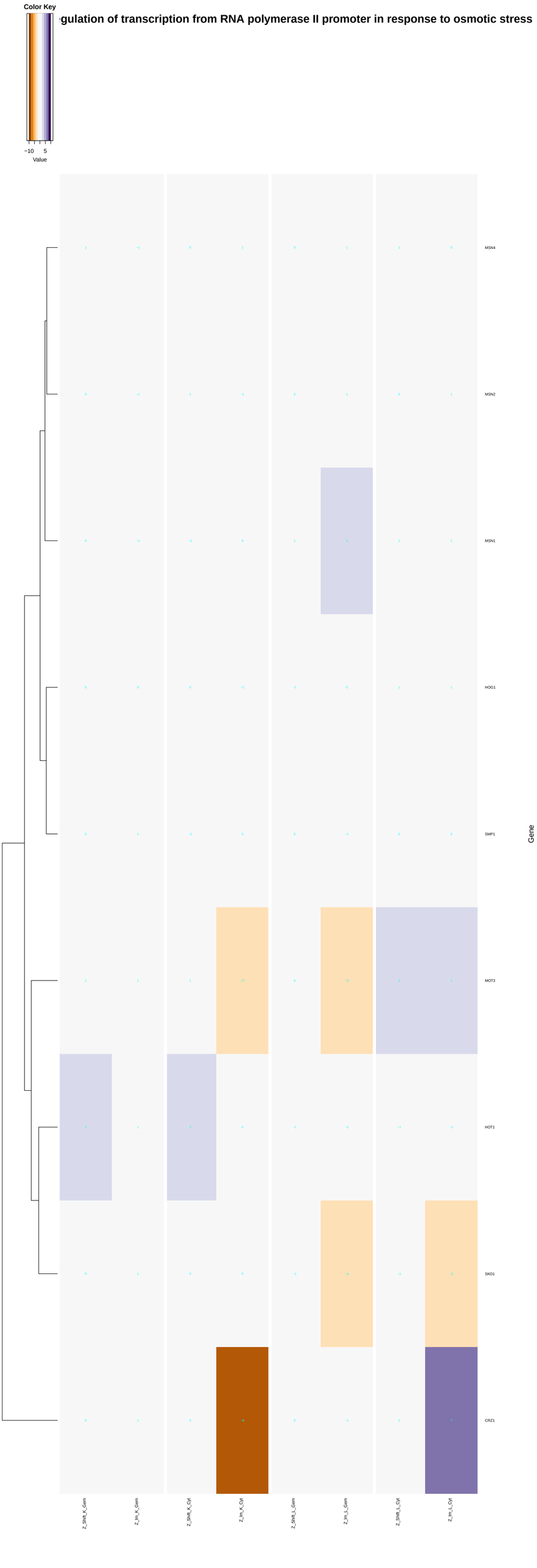
Value
osmosensory signaling via phosphorelay pathway
SSK1
YPD1
SSK2
SLN1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt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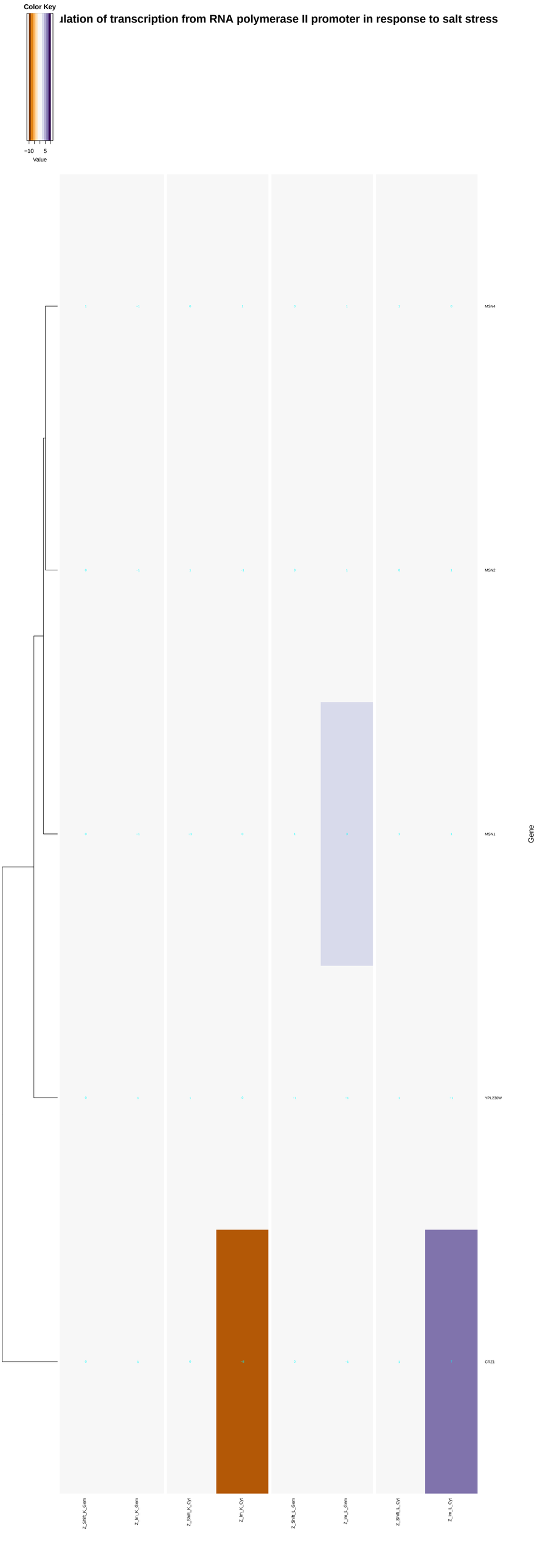
Value
gulation of transcription from RNA polymerase II promoter in response to osmotic stress
MSN4
MSN2
MSN1
HOG1
SMP1
MOT3
HOT1
SKO1
CRZ1
Gene
Z_Shift_K_Gem
Z_In_K_Gem
Z_Shift_K_Cyt
Z_In_K_Cyt
Z_Shift_L_Gem
Z_In_L_Gem
Z_Shift_L_Cyt
Z_In_L_Cyt


Color Key
−10
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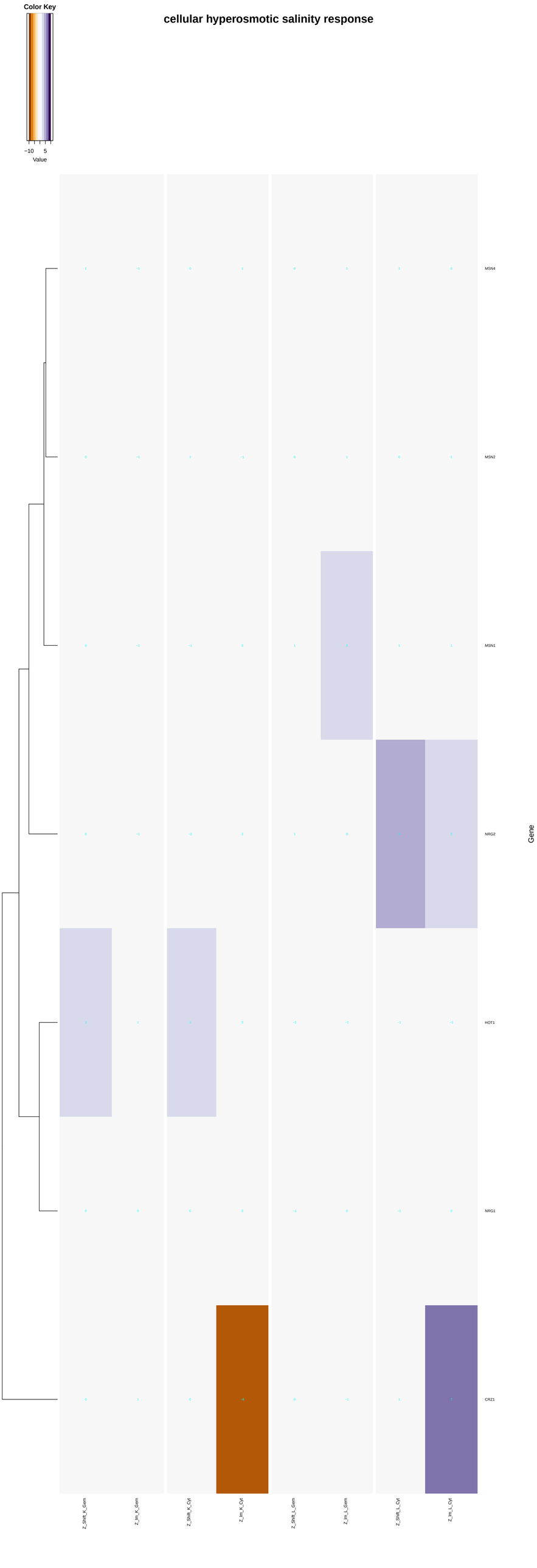
Value
ılation of transcription from RNA polymerase II promoter in response to salt stress
MSN4
MSN2
MSN1
YPL230W
CRZ1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
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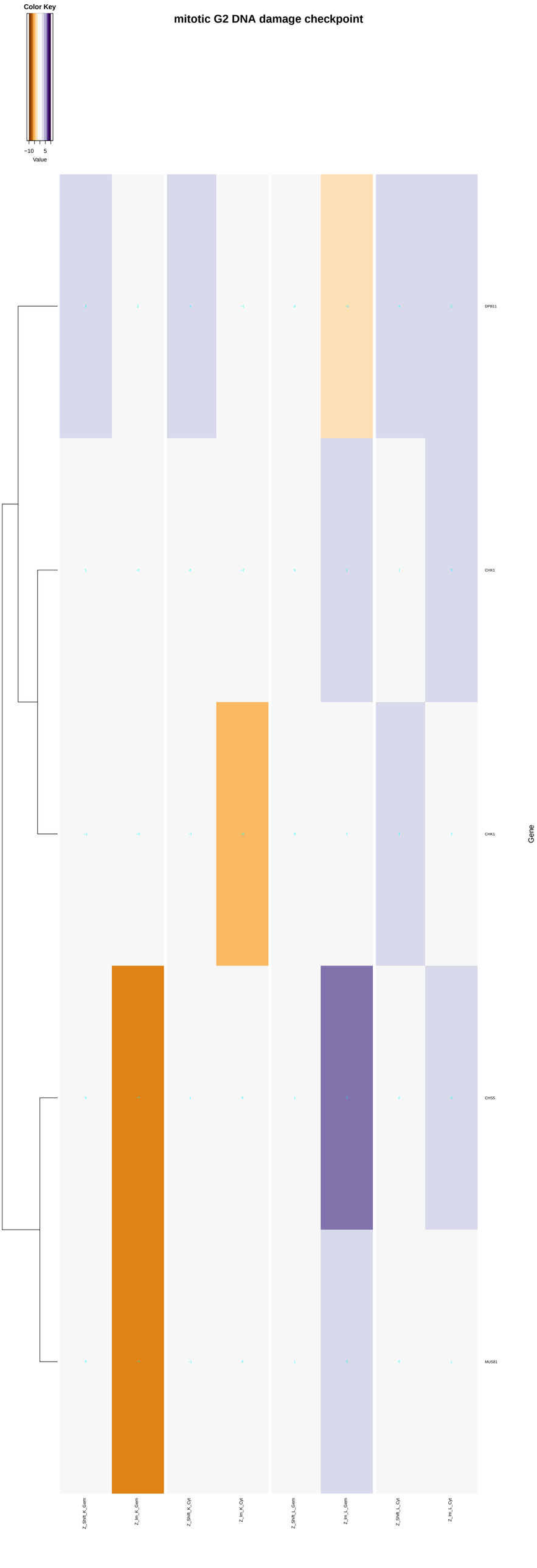
Value
cellular hyperosmotic salinity response
MSN4
MSN2
MSN1
NRG2
HOT1
NRG1
CRZ1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
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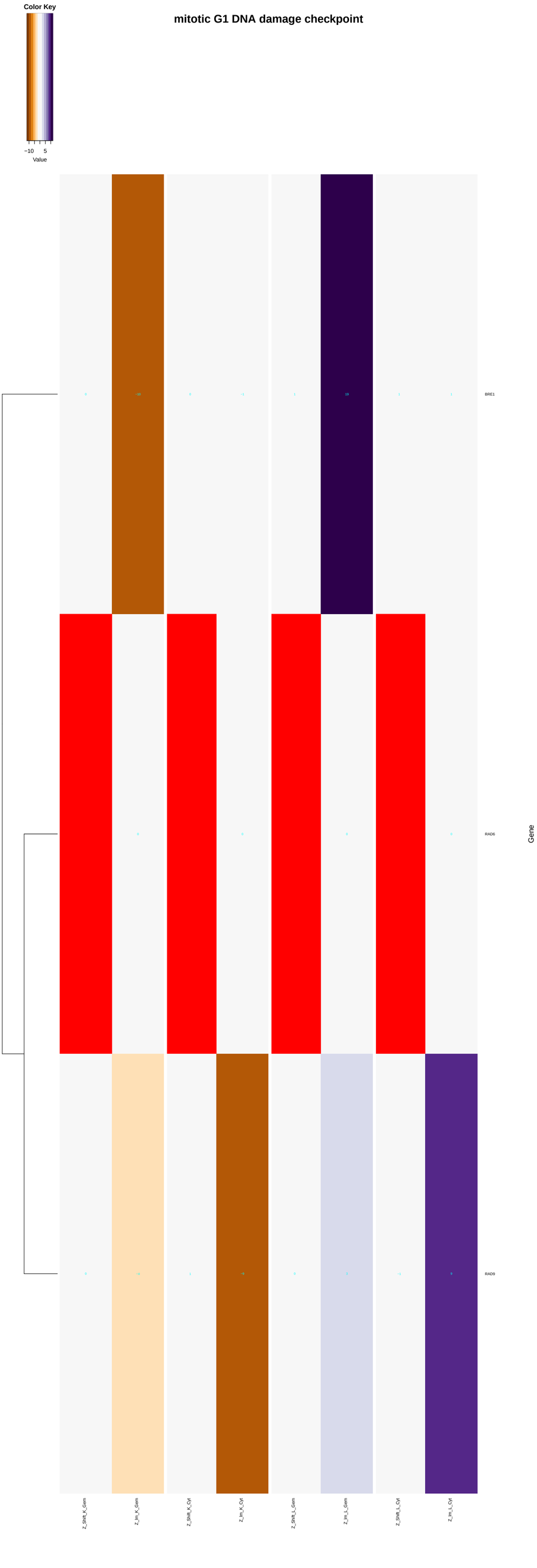
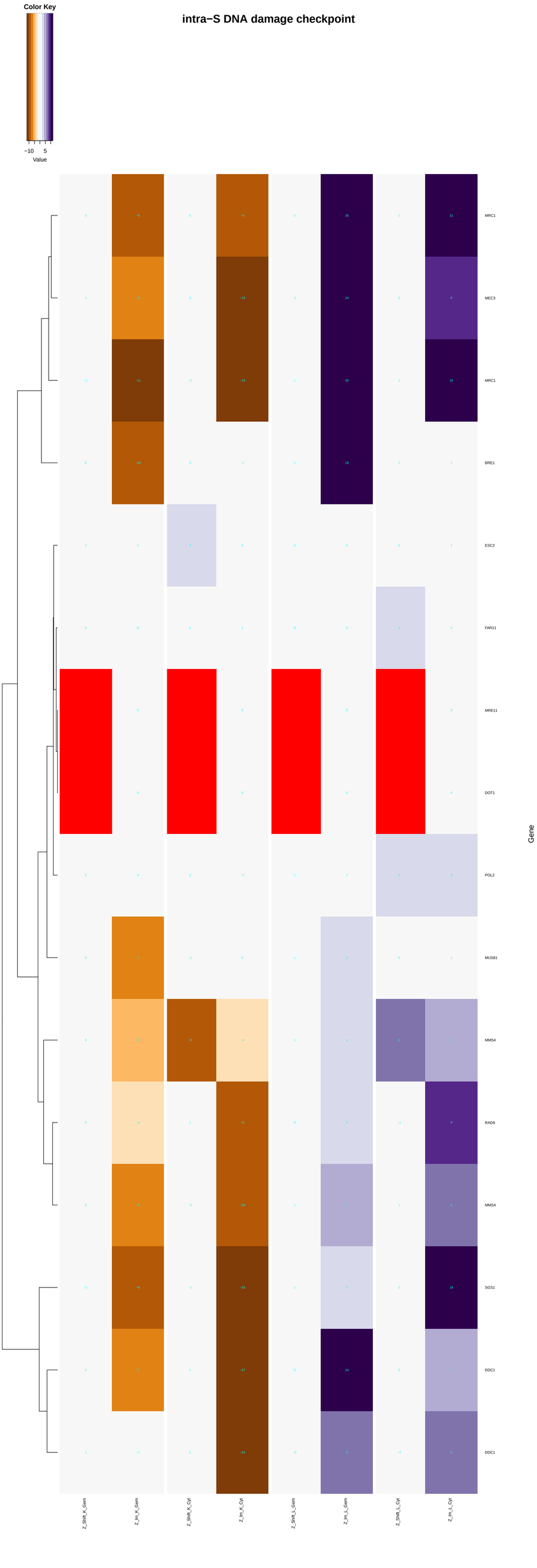
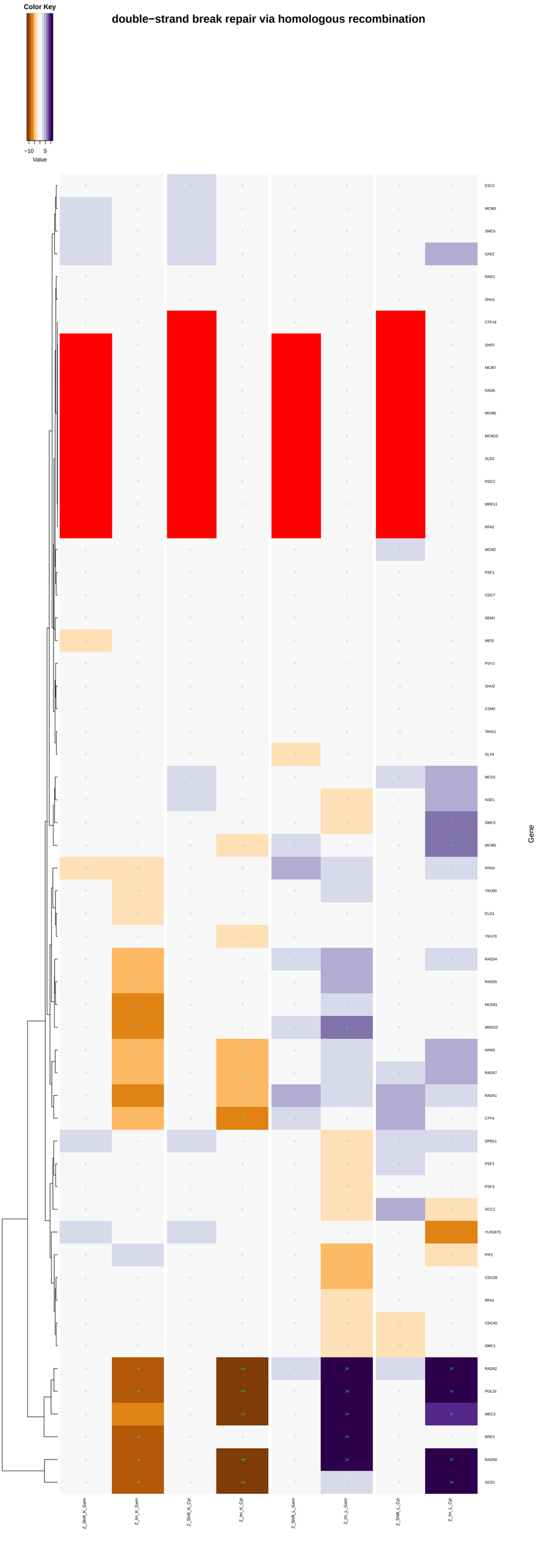
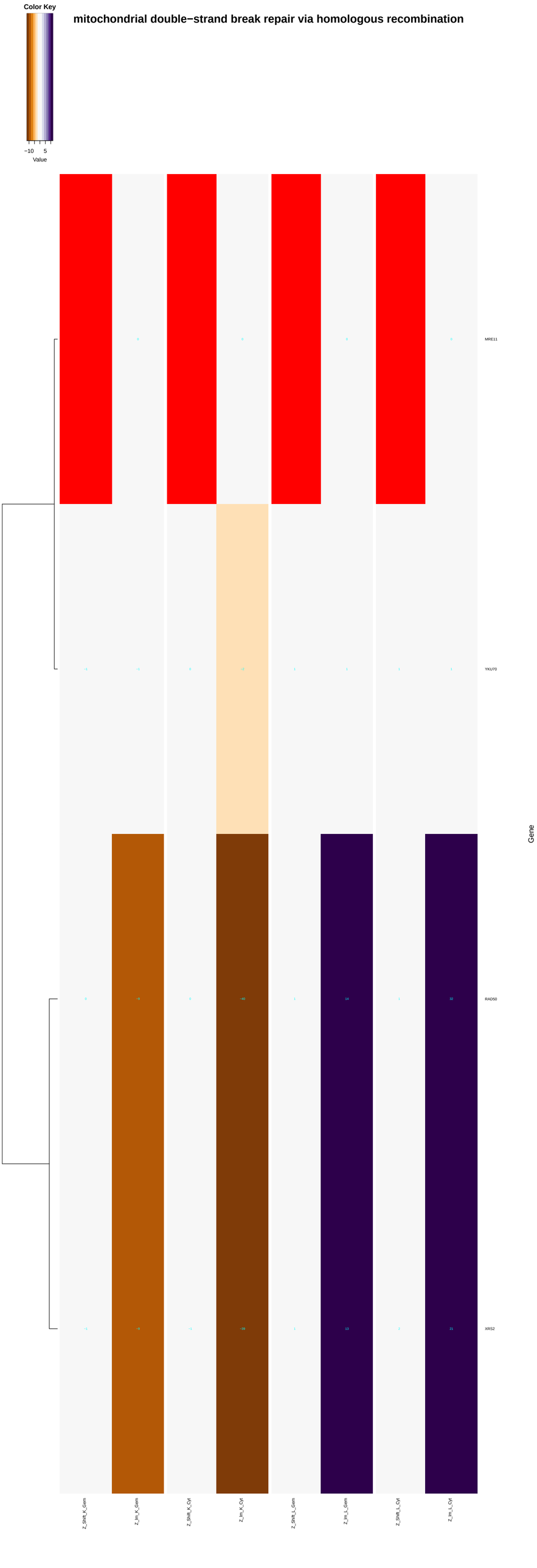
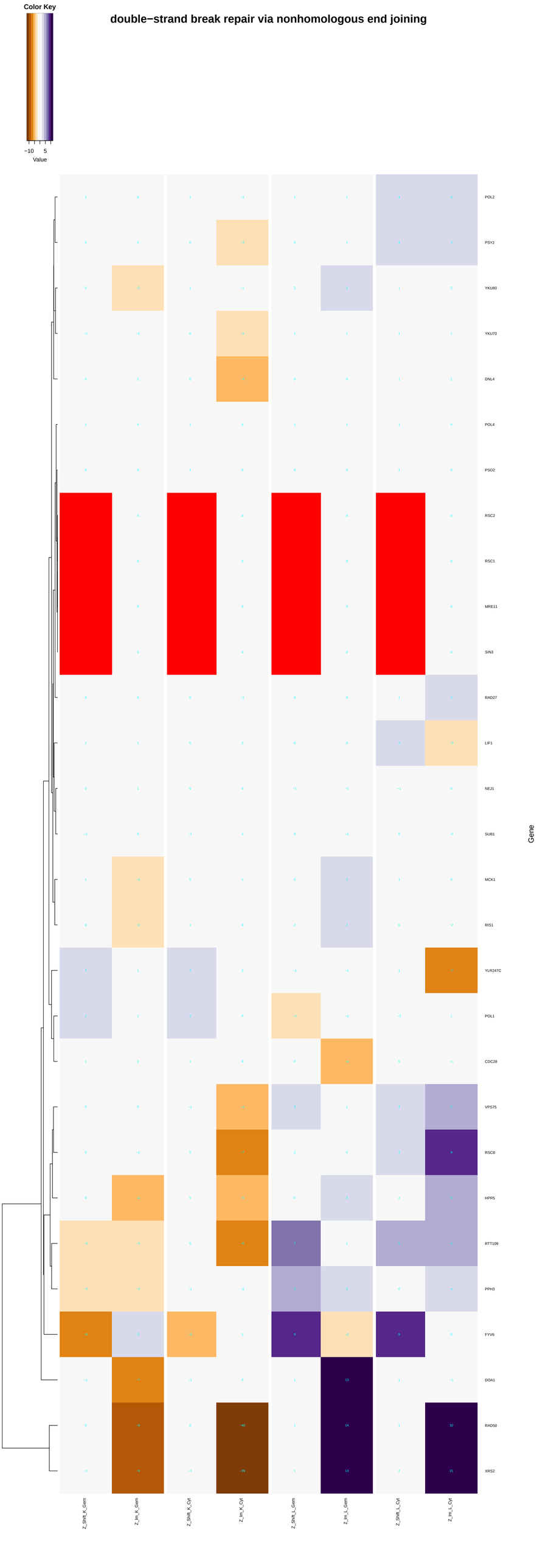
Value
mitotic G2 DNA damage checkpoint
3
2
4
−1
0
−3
4
2
DPB11
1
−2
0
−2
0
2
1
3
CHK1
−1
−2
−1
−6
0
1
3
2
CHK1
0
−4
1
0
1
3
0
3
CHS5
0
−4
−1
0
1
3
0
1
MUS81
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt
Gene

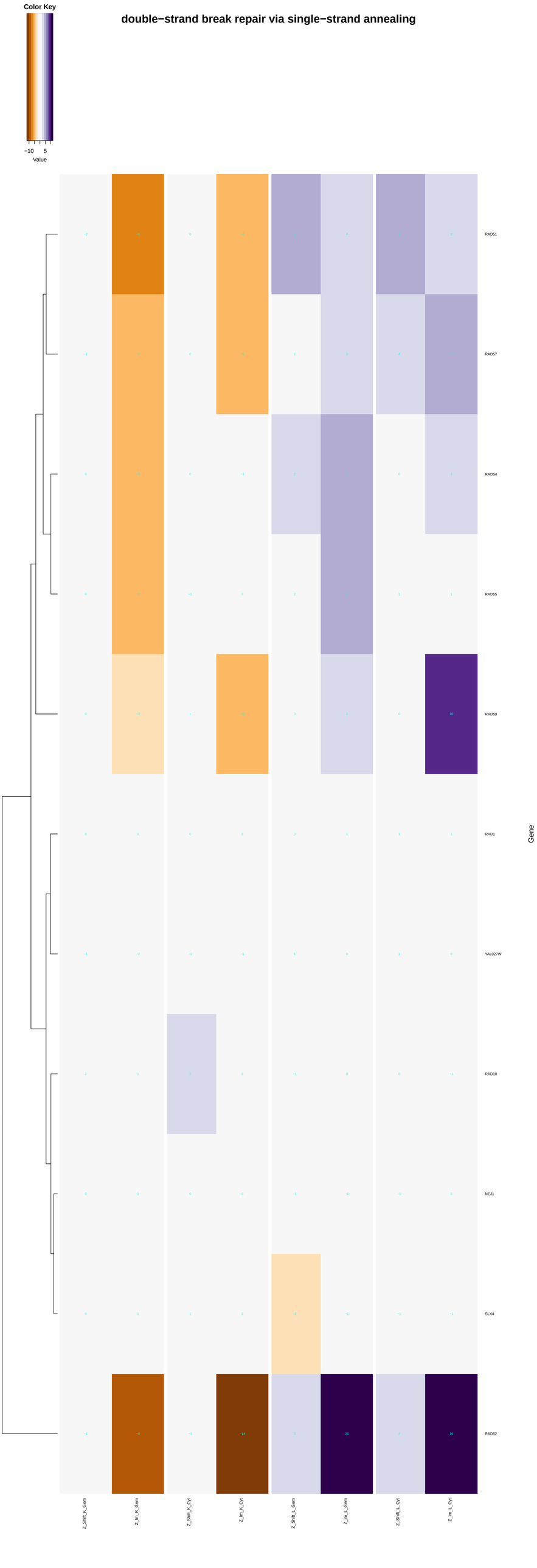

Color Key
−10
5
Value
mitotic G1 DNA damage checkpoint
0
−10
0
−1
1
19
1
1
BRE1
0
0
0
0
0
RAD6
0
−4
1
−9
0
3
−1
9
RAD9
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

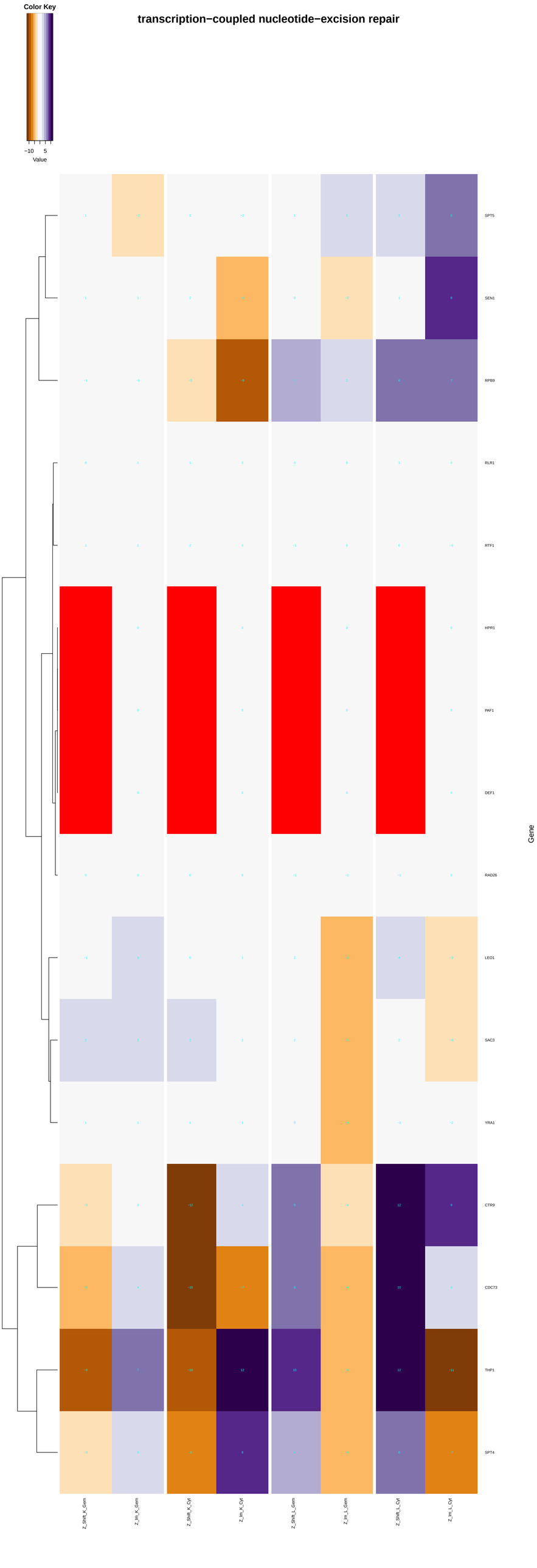

Color Key
−10
5
Value
intra−S DNA damage checkpoint
MRC1
MEC3
MRC1
BRE1
ESC2
FAR11
MRE11
DOT1
POL2
MUS81
MMS4
RAD9
MMS4
SGS1
DDC1
DDC1
Z_Shlt_K_Gem
Z_In_K_Gem
Z_Shlt_K_Cyt
Z_In_K_Cyt
Z_Shlt_L_Gem
Z_In_L_Gem
Z_Shlt_L_Cyt
Z_In_L_Cyt
Gene

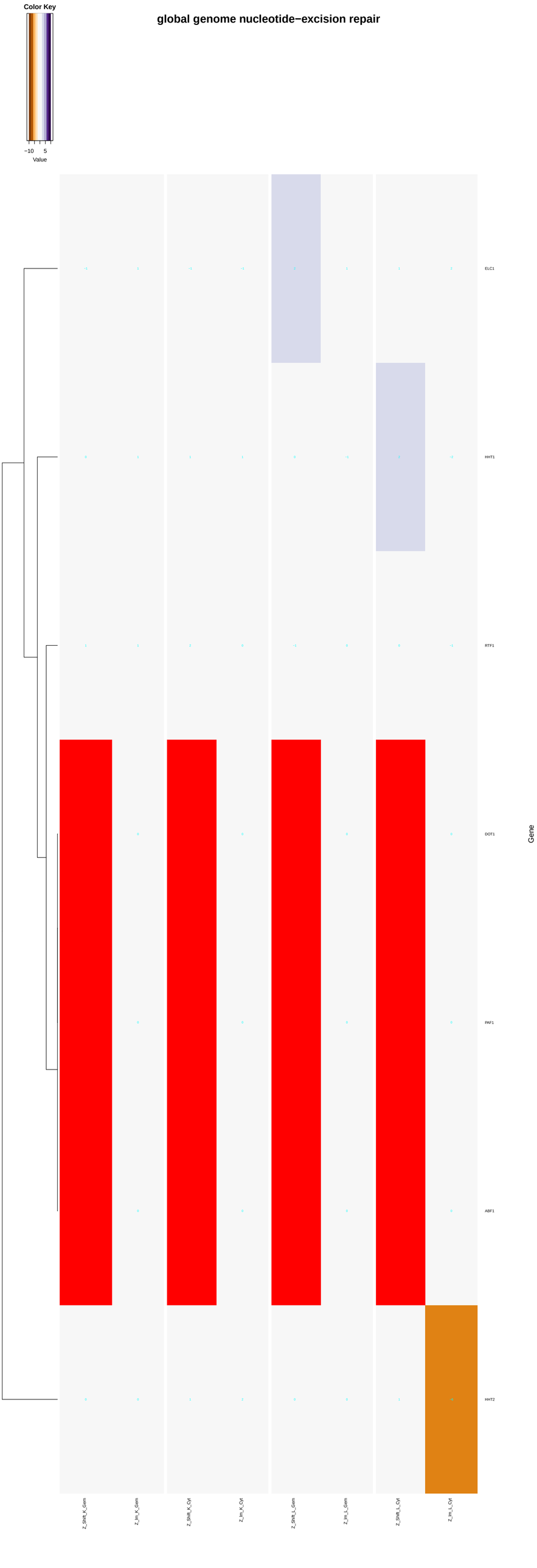

Color Key
−10
5
Value
double−strand break repair via homologous recombination
Gene
ESC2
MCM3
SMC5
SAE2
RAD1
SHU1
CTF18
SNF5
MCM7
RAD6
MCM6
MCM10
SLD2
RSC2
MRE11
RFA2
MCM2
PSF1
CDC7
SEM1
MEI5
PSY3
SHU2
CSM2
TAH11
SLX4
MCD1
NSE1
SMC3
MCM5
PPH3
YKU80
ELG1
YKU70
RAD54
RAD55
MUS81
MMS22
HPR5
RAD57
RAD51
CTF4
DPB11
PSF2
PSF3
SCC2
YLR247C
PIF1
CDC28
RFA1
CDC45
DMC1
RAD52
POL32
MEC3
BRE1
RAD50
SGS1
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt

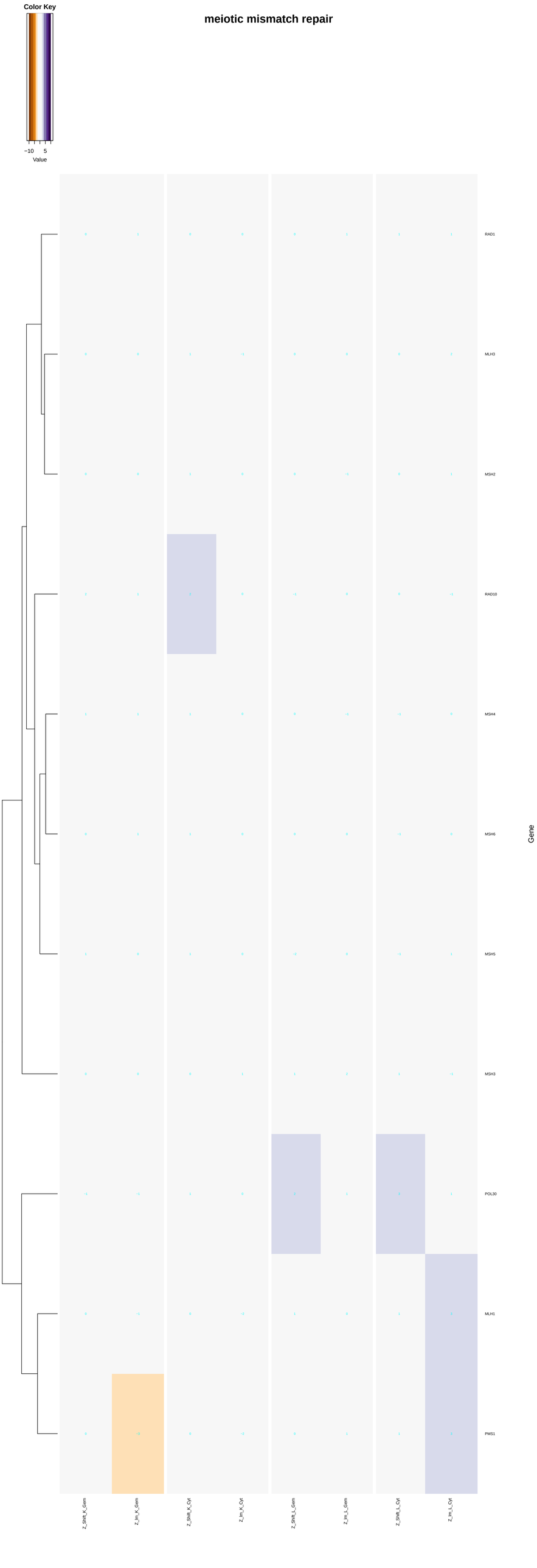

Color Key
−10
5
Value
mitochondrial double−strand break repair via homologous recombination
MRE11
YKU70
RAD50
XRS2
Gene
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
double−strand break repair via nonhomologous end joining
POL2
PSY2
YKU80
YKU70
DNL4
POL4
PSO2
RSC2
RSC1
MRE11
SIN3
RAD27
LIF1
NEJ1
SUB1
MCK1
RIS1
YLR247C
POL1
CDC28
VPS75
RSC8
HPR5
RTT109
PPH3
FYV6
DOA1
RAD50
XRS2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
double−strand break repair via single−strand annealing
RAD51
RAD57
RAD54
RAD55
RAD59
RAD1
YAL027W
RAD10
NEJ1
SLX4
RAD52
Gene
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
transcription−coupled nucleotide−excision repair
SPT5
SEN1
RPB9
RLR1
RTF1
HPR1
PAF1
DEF1
RAD26
LEO1
SAC3
YRA1
CTR9
CDC73
THP1
SPT4
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
global genome nucleotide−excision repair
ELC1
HHT1
RTF1
DOT1
PAF1
ABF1
HHT2
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
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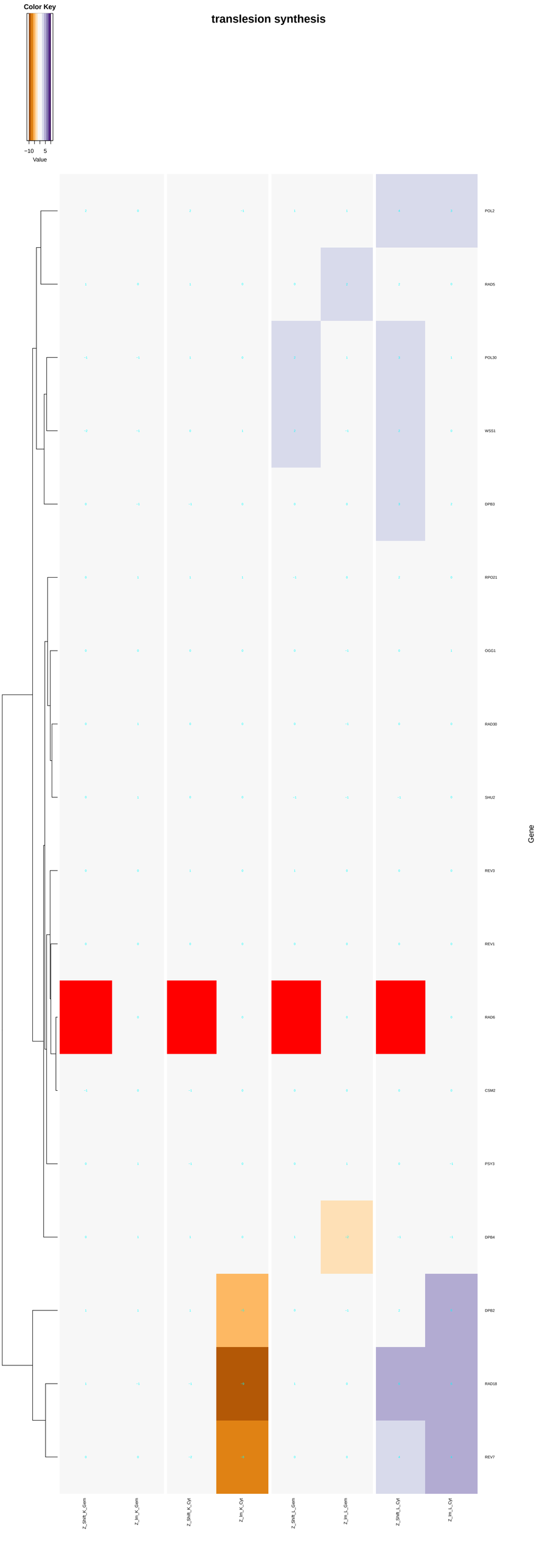
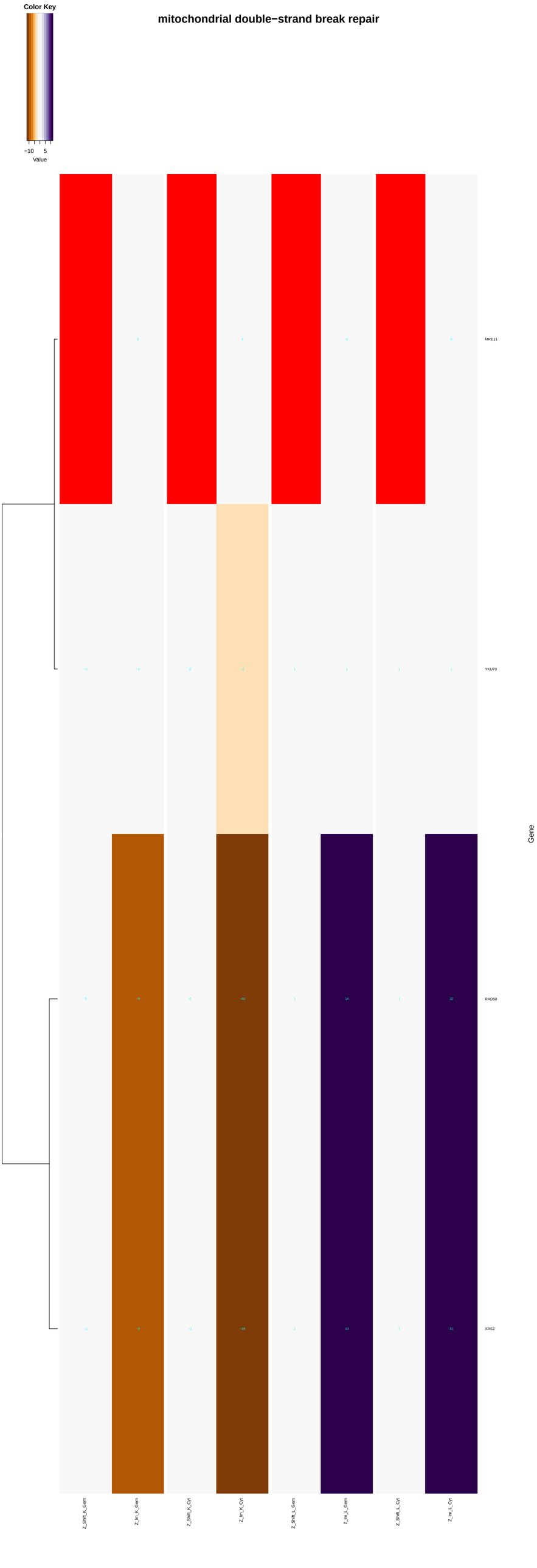
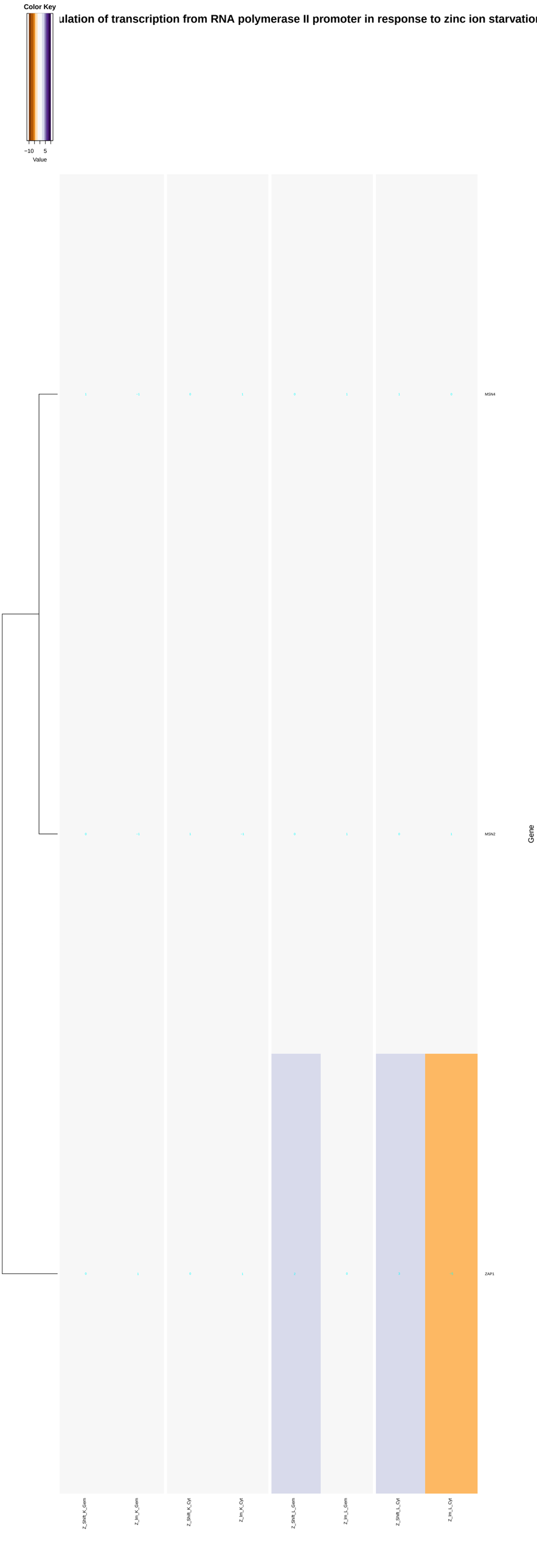
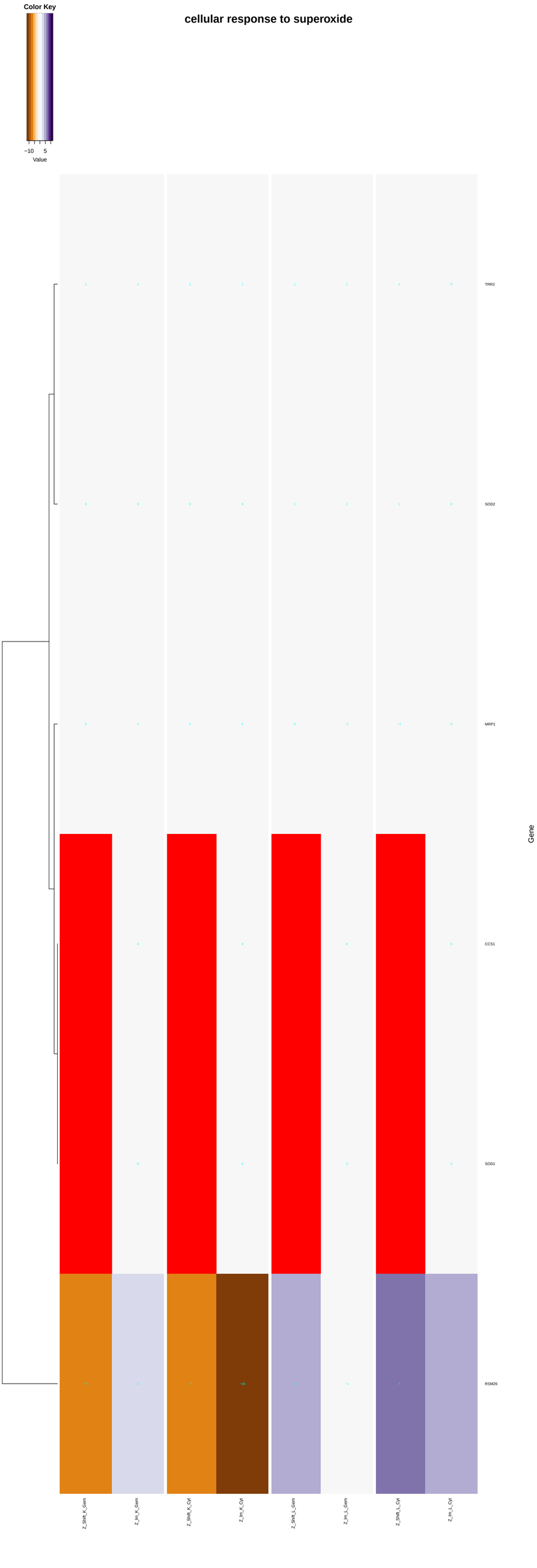
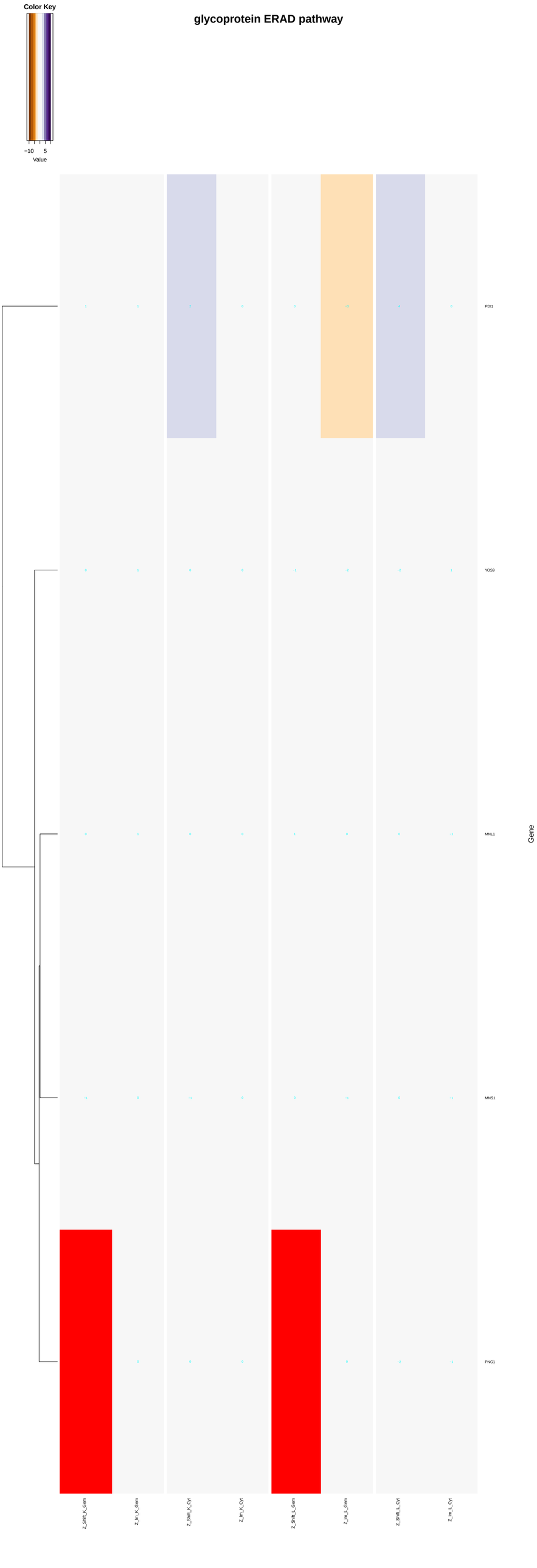
Value
meiotic mismatch repair
RAD1
MLH3
MSH2
RAD10
MSH4
MSH6
MSH5
MSH3
POL30
MLH1
PMS1
Gene
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt

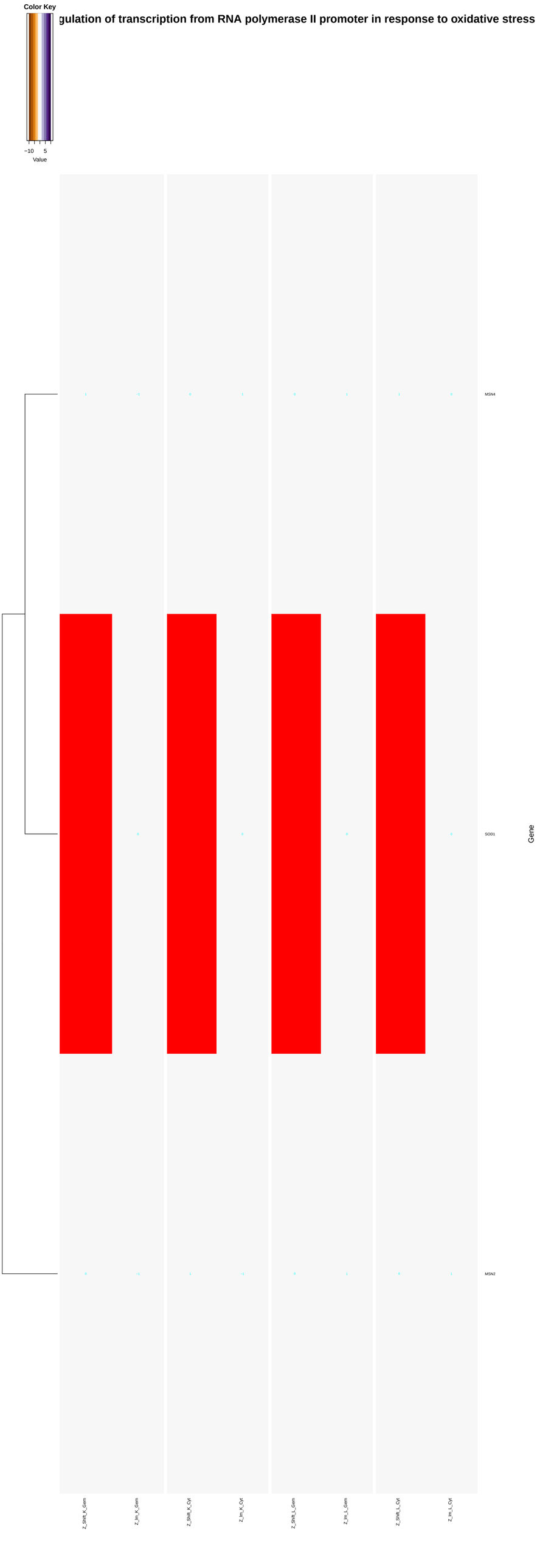

translesion synthesis
Color Key
−10
5
Value
POL2
RAD5
POL30
WSS1
DPB3
RPO21
OGG1
RAD30
SHU2
REV3
REV1
RAD6
CSM2
PSY3
DPB4
DPB2
RAD18
REV7
Gene
Z_Shlt_K_Gem
Z_In_K_Gem
Z_Shlt_K_Cyt
Z_In_K_Cyt
Z_Shlt_L_Gem
Z_In_L_Gem
Z_Shlt_L_Cyt
Z_In_L_Cyt

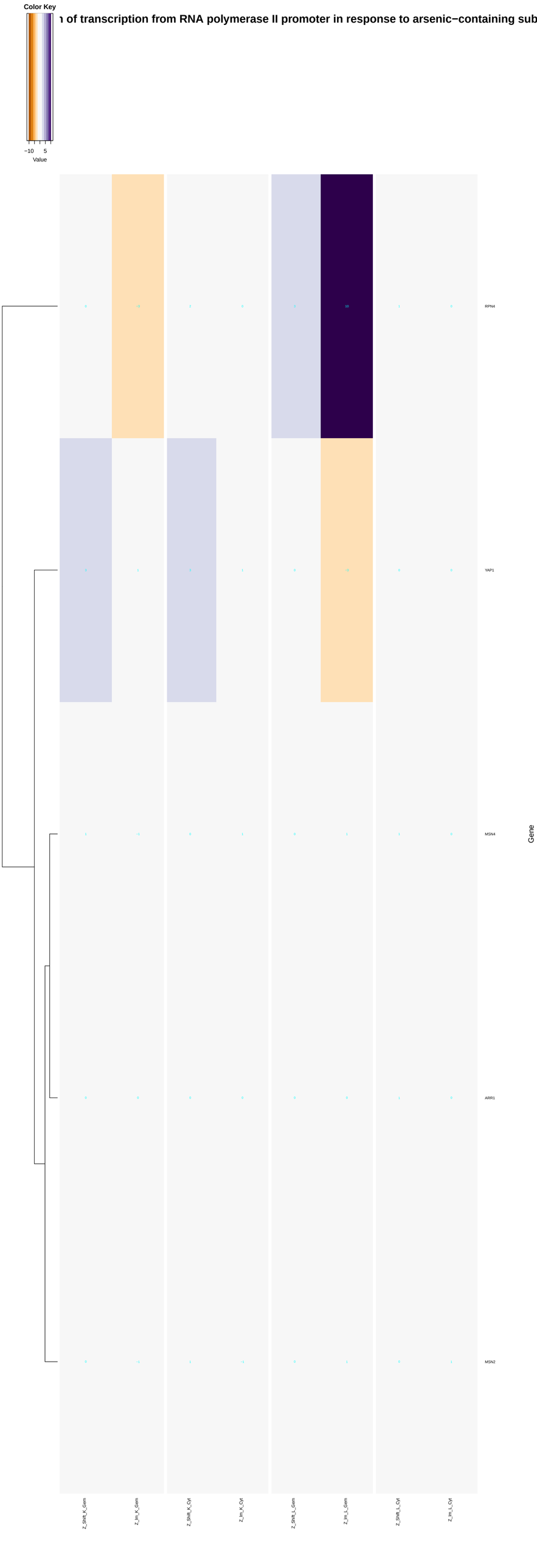

Color Key
−10
5
Value
mitochondrial double−strand break repair
MRE11
YKU70
RAD50
XRS2
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

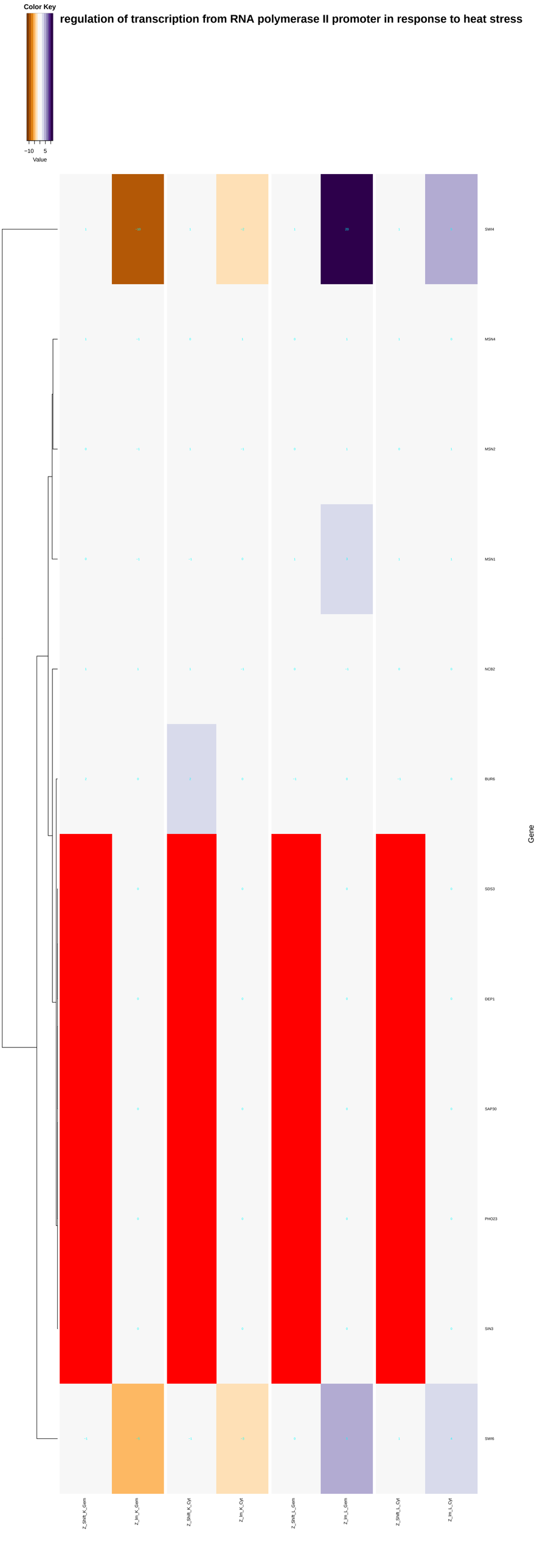

Color Key
−10
5
Value
ulation of transcription from RNA polymerase II promoter in response to zinc ion starvation
MSN4
MSN2
ZAP1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt

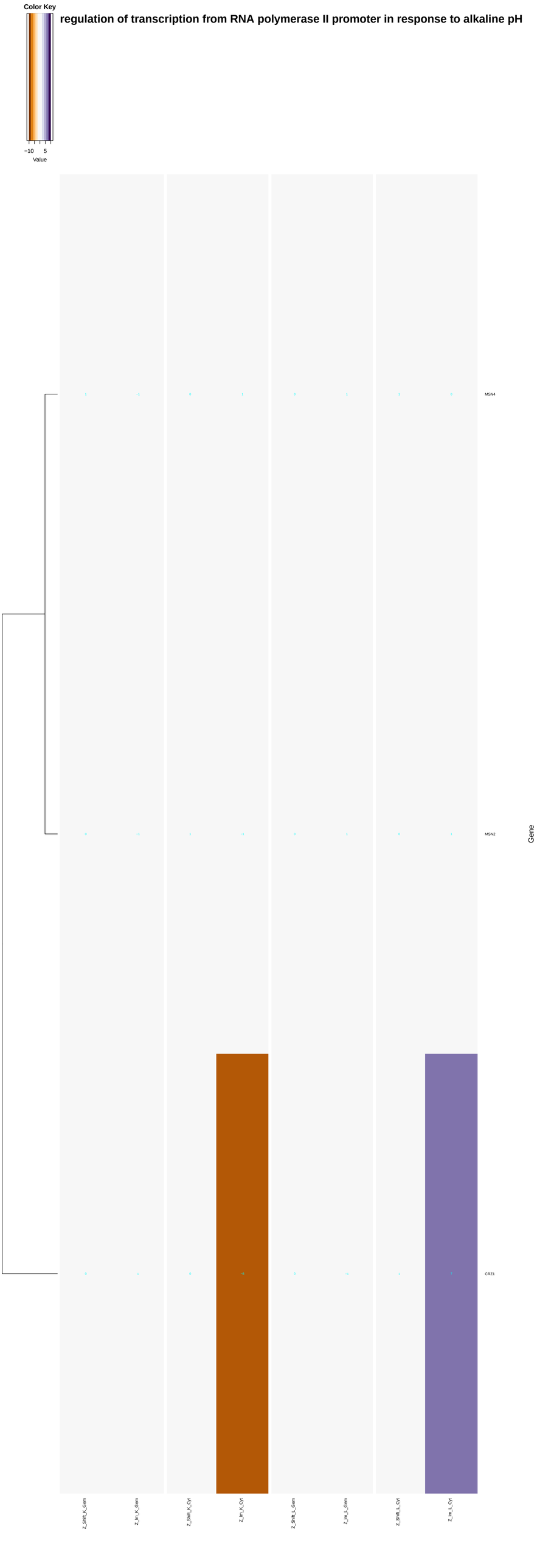

Color Key
−10
5
Value
cellular response to superoxide
TRR2
SOD2
MRP1
CCS1
SOD1
RSM26
Gene
Z_Shlt_K_Gem
Z_Im_K_Gem
Z_Shlt_K_Cyt
Z_Im_K_Cyt
Z_Shlt_L_Gem
Z_Im_L_Gem
Z_Shlt_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
glycoprotein ERAD pathway
1 1 2 0 0 3 4 0
0 1 0 0 −1 −2 −2 1
0 1 0 0 1 0 0 −1
−1 0 −1 0 0 −1 0 −1
0 0 0 0 −2 −1
PDI1
YOS9
MNL1
MNS1
PNG1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
gulation of transcription from RNA polymerase II promoter in response to oxidative stress
1
−1
0
1
0
1
1
0
MSN4
0
0
0
0
SOD1
0
−1
1
−1
0
1
0
1
MSN2
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
n of transcription from RNA polymerase II promoter in response to arsenic−containing sub
−10
5
Value
0
−3
2
0
3
10
1
0
RPN4
3
1
3
1
0
−3
0
0
YAP1
1
−1
0
1
0
1
1
0
MSN4
0
0
0
0
0
0
1
0
ARR1
0
−1
1
−1
0
1
0
1
MSN2
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt
Gene


Color Key
−10
5
Value
regulation of transcription from RNA polymerase II promoter in response to heat stress
SWI4
MSN4
MSN2
MSN1
NCB2
BUR6
SDS3
DEP1
SAP30
PHO23
SIN3
SWI6
Gene
Z_Shift_K_Gem
Z_In_K_Gem
Z_Shift_K_Cyt
Z_In_K_Cyt
Z_Shift_L_Gem
Z_In_L_Gem
Z_Shift_L_Cyt
Z_In_L_Cyt


Color Key
−10
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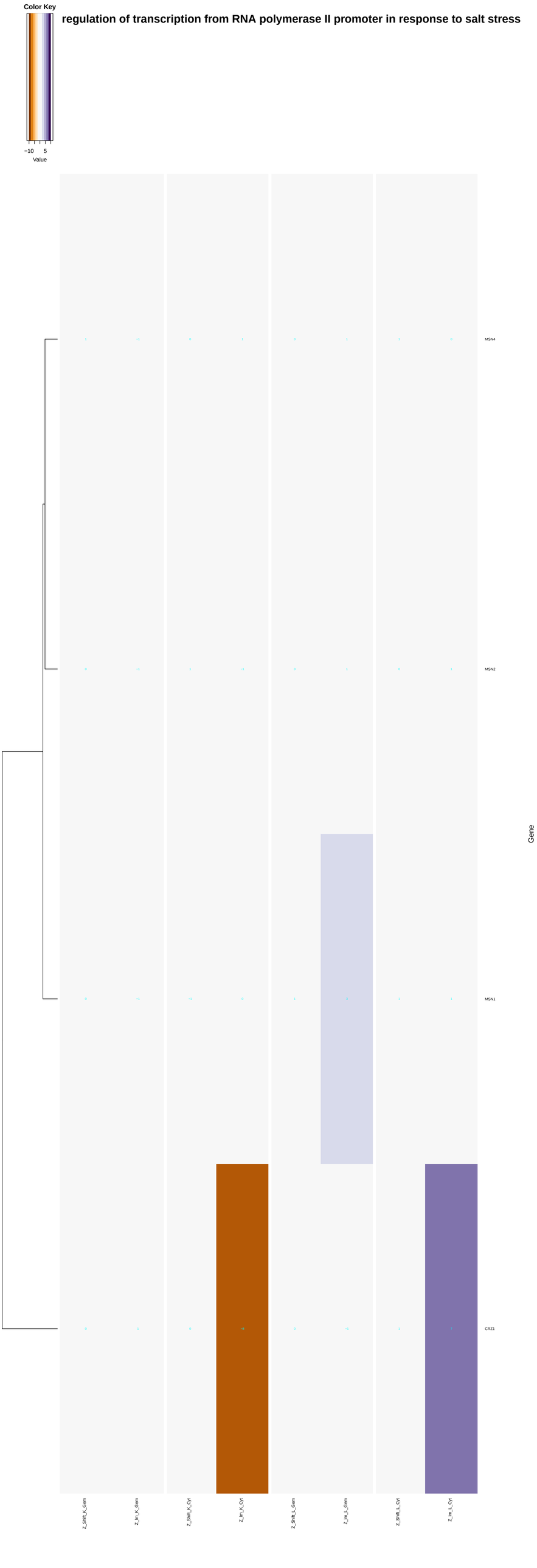
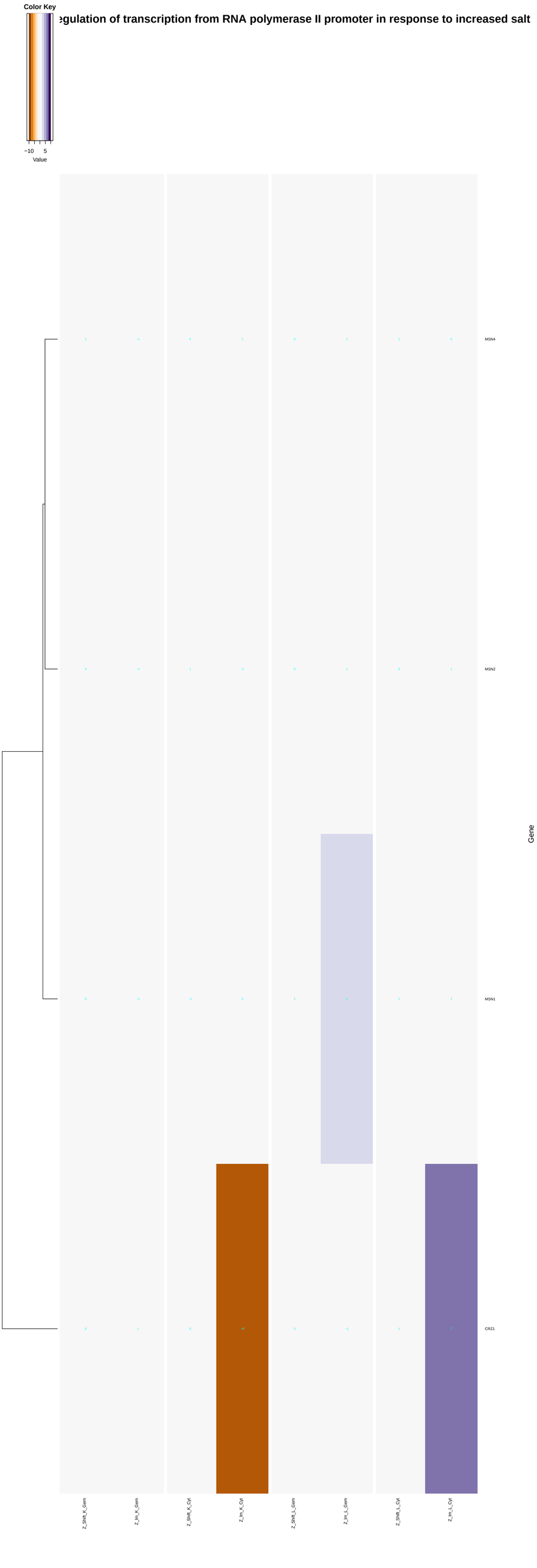
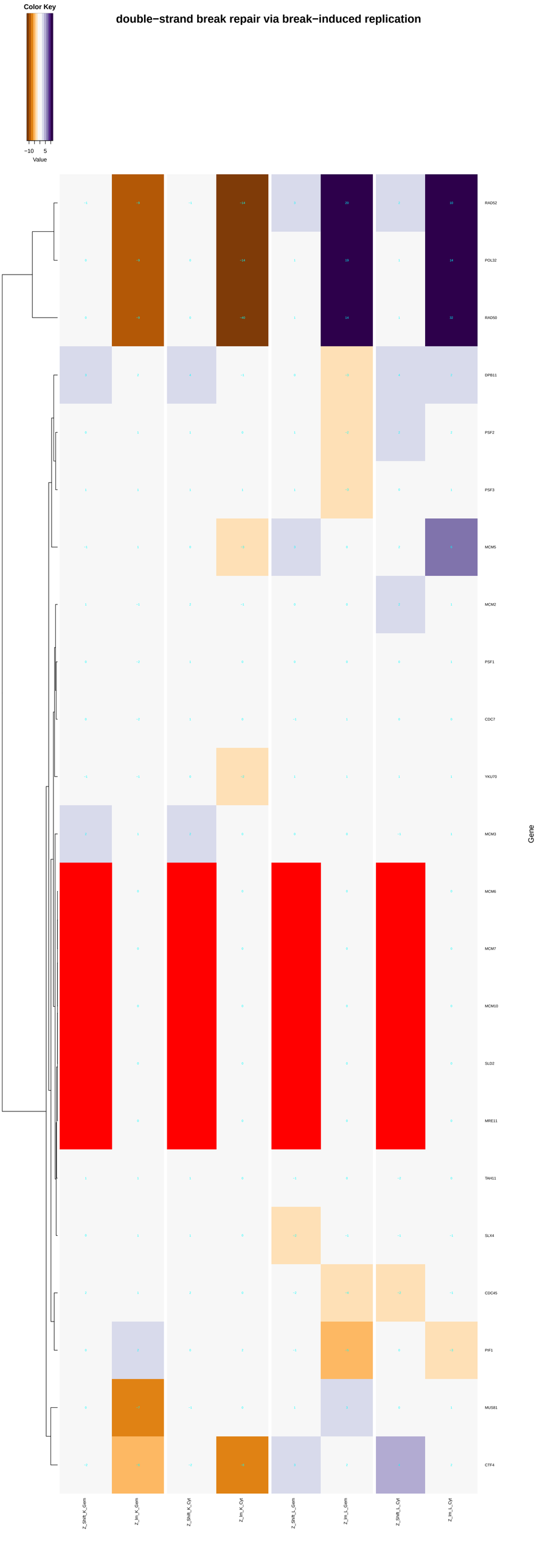
Value
regulation of transcription from RNA polymerase II promoter in response to alkaline pH
MSN4
MSN2
CRZ1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
regulation of transcription from RNA polymerase II promoter in response to salt stress
MSN4
MSN2
MSN1
CRZ1
Gene
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
MSN4
MSN2
MSN1
CRZ1
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
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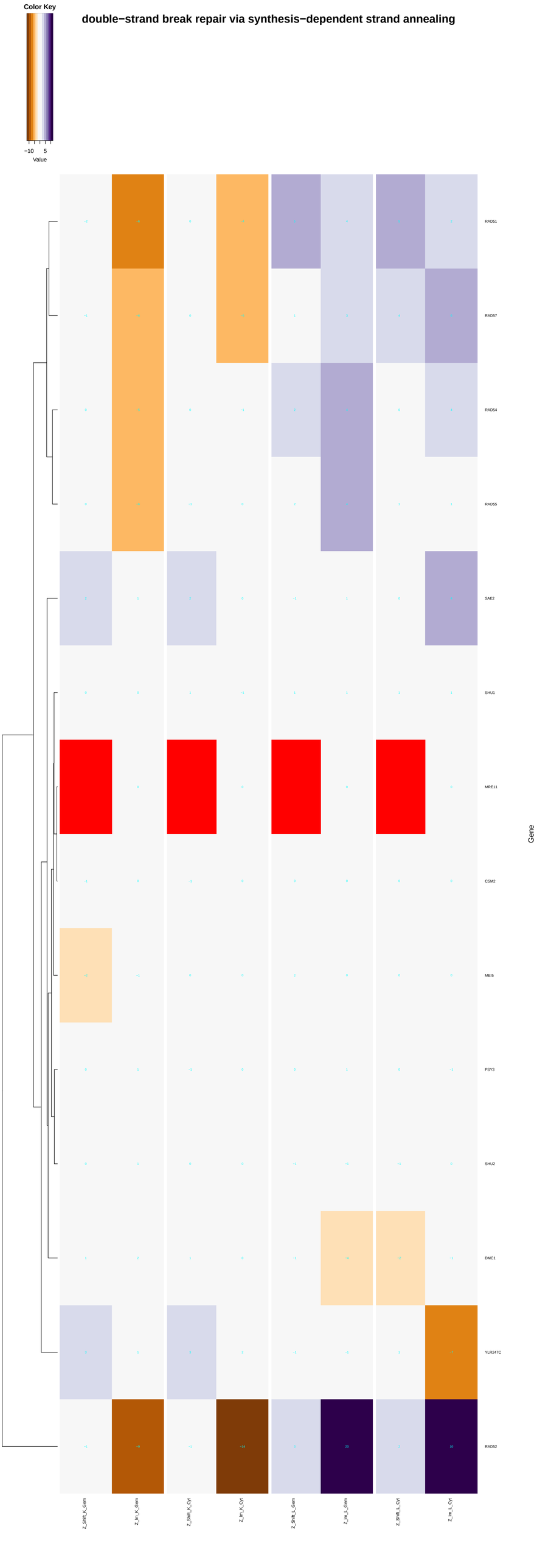
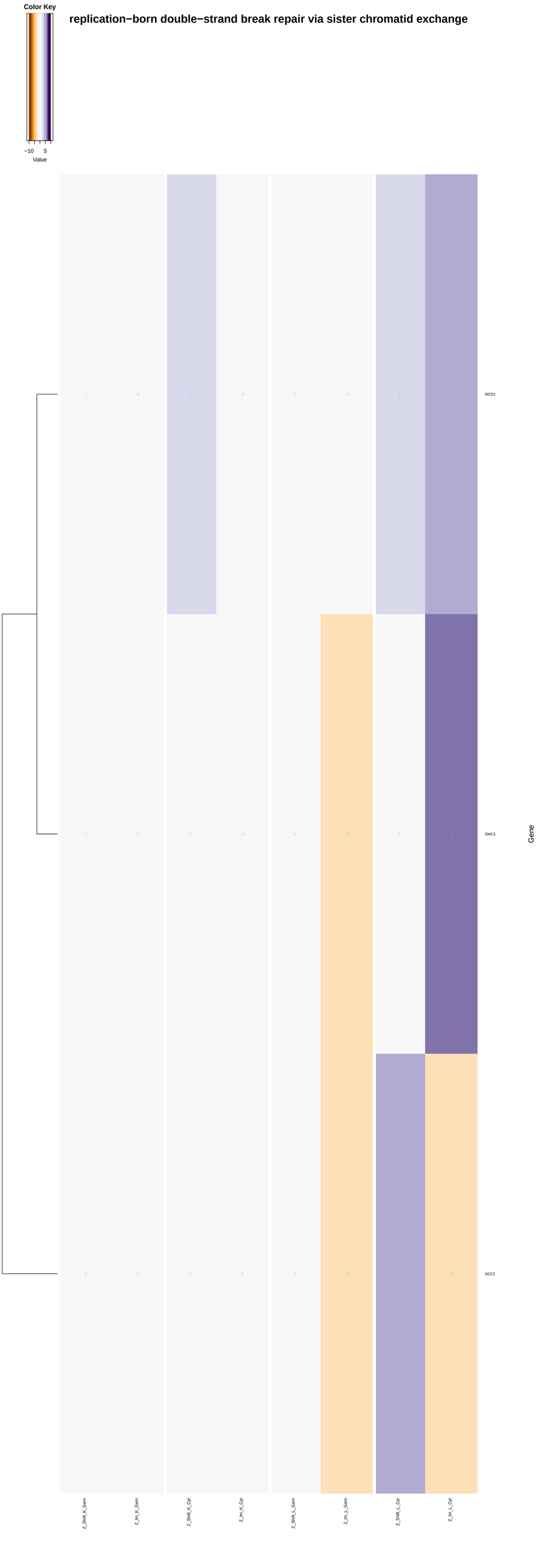
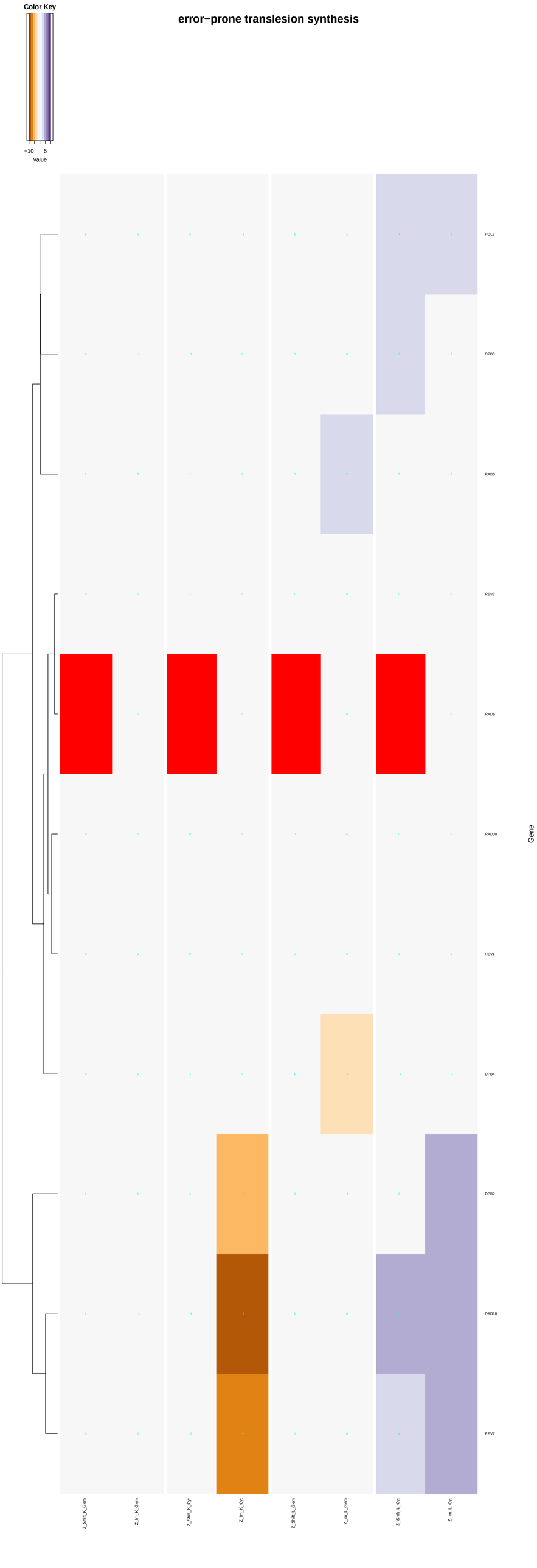
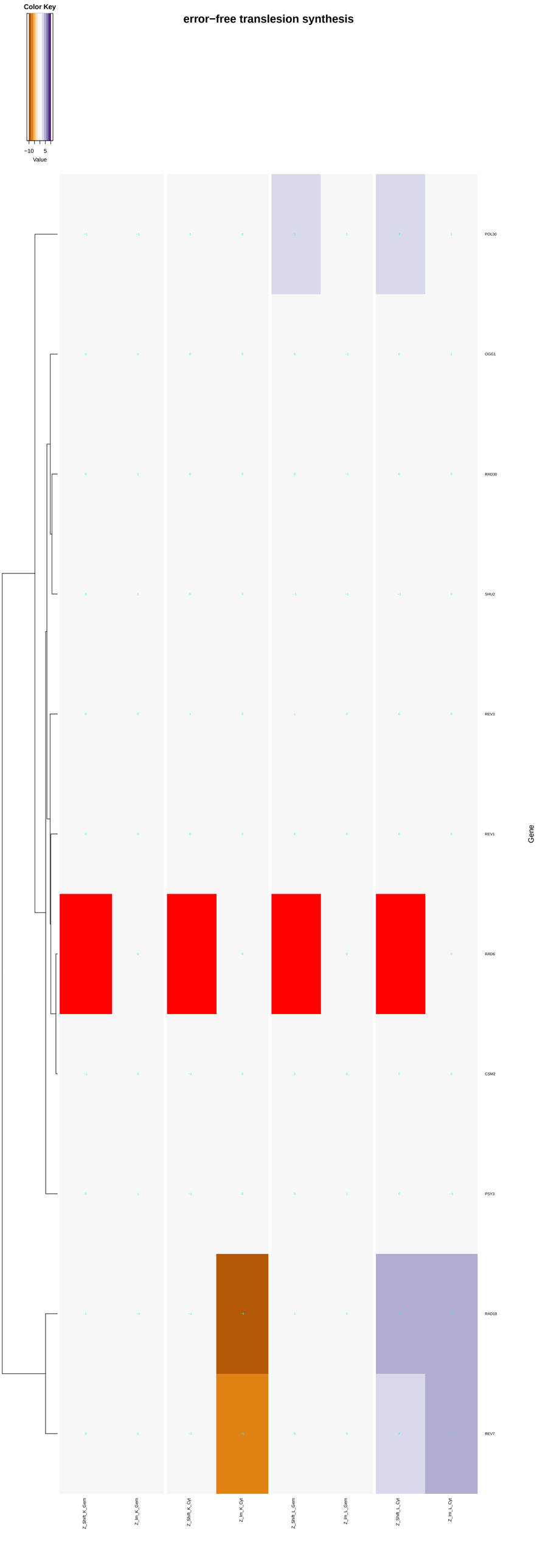
Value
double−strand break repair via break−induced replication
RAD52
POL32
RAD50
DPB11
PSF2
PSF3
MCM5
MCM2
PSF1
CDC7
YKU70
MCM3
MCM6
MCM7
MCM10
SLD2
MRE11
TAH11
SLX4
CDC45
PIF1
MUS81
CTF4
Gene
Z_Shift_K_Gem
Z_Im_K_Gem
Z_Shift_K_Cyt
Z_Im_K_Cyt
Z_Shift_L_Gem
Z_Im_L_Gem
Z_Shift_L_Cyt
Z_Im_L_Cyt


Color Key
−10
5
Value
double−strand break repair via synthesis−dependent strand annealing
RAD51
RAD57
RAD54
RAD55
SAE2
SHU1
MRE11
CSM2
MEI5
PSY3
SHU2
DMC1
YLR247C
RAD52
Gene
Z_Shlt_K_Gem
Z_In_K_Gem
Z_Shlt_K_Cyt
Z_In_K_Cyt
Z_Shlt_L_Gem
Z_In_L_Gem
Z_Shlt_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
replication−born double−strand break repair via sister chromatid exchange
1
0
3
−2
2
−2
3
3
MCD1
1
1
2
−2
0
−3
2
3
SMC3
1
1
1
0
0
−4
1
−3
SCC2
Z_Shft_K_Gem
Z_Im_K_Gem
Z_Shft_K_Cyt
Z_Im_K_Cyt
Z_Shft_L_Gem
Z_Im_L_Gem
Z_Shft_L_Cyt
Z_Im_L_Cyt
Gene


Color Key
−10
5
Value
error−prone translesion synthesis
POL2
DPB3
RAD5
REV3
RAD6
RAD30
REV1
DPB4
DPB2
RAD18
REV7
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt


Color Key
−10
5
Value
error−free translesion synthesis
POL30
OGG1
RAD30
SHU2
REV3
REV1
RAD6
CSM2
PSY3
RAD18
REV7
Gene
Z_Shft_K_Gem
Z_In_K_Gem
Z_Shft_K_Cyt
Z_In_K_Cyt
Z_Shft_L_Gem
Z_In_L_Gem
Z_Shft_L_Cyt
Z_In_L_Cyt