nucleic acid phosphodiester bond hydrolysis

Color Key

−10 5

Value

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
UTP10	2	0	2	0	0	0	1	2
YCL075W	1	0	2	0	0	0	1	2
SSU72	1	0	1	1	0	1	1	1
CSL4	1	−1	1	1	0	0	2	3
RAD27	0	0	0	−1	0	0	1	2
DOM34	0	0	0	0	0	1	0	3
RNH1	0	−2	0	1	0	0	0	2
SAS10	0	−1	1	0	1	2	2	2
MEI4	0	−1	0	−1	0	2	1	1
SEN34	0	−2	0	0	0	1	1	2
YBL055C	1	−1	−1	−1	0	2	2	2
NGL3	1	−1	2	−1	2	2	1	1
YGL085W	1	−1	1	0	0	2	0	0
FCF1	0	−1	1	0	0	2	1	1
EBS1	0	−3	1	−2	0	2	0	4
RNT1	0	0	0	0	1	0	4	2
RPL17B	0	0	0	−2	1	0	4	3
POL2	2	0	2	−1	1	1	4	3
RPP1	0	1	1	0	1	−1	3	4
RRP46	0	−1	1	0	3	−1	4	2
RLP24	0	−2	2	0	4	0	2	2
RRP6	0	−2	0	−1	2	1	2	2
SPP1	−1	−3	1	−1	2	0	1	2
DIS3	1	−2	2	−2	1	1	3	5
RRP36	1	−1	1	−1	1	2	2	5
UTP14	1	0	1	−1	0	1	3	5
PWP2	1	−2	2	−2	0	1	1	5
KRI1	1	0	2	0	0	0	2	6
UTP23	1	1	1	−1	0	1	1	6
RRP42	0	0	2	−3	0	0	2	6
NOP58	2	1	2	−1	1	0	2	3
RAD14	2	0	1	−1	0	0	2	2
RAT1	1	1	1	1	0	−1	1	3
SAE2	2	1	2	0	−1	1	0	4
REC104	0	1	1	0	0	−1	1	1
PNO1	1	0	1	0	0	−1	1	1
TDP1	1	0	1	0	0	0	0	1
REX2	1	0	1	−1	0	0	0	1
UTP20	0	0	1	0	−1	0	1	2
MKT1	0	0	1	0	0	0	1	−1
PSO2	0	0	1	0	0	0	1	0
NOP14	0	1	1	0	0	−1	0	0
NPP1	0	0	1	0	0	0	0	0
RPR2	1	0	1	0	0	0	2	0
RPL37B	[0]	0	[0]	0	[0]	0	[0]	0
TFP1	[0]	0	[0]	0	[0]	0	[0]	0
MOT2	[0]	0	[0]	0	[0]	0	[0]	0
RNA15	[0]	0	[0]	0	[0]	0	[0]	0
RAD6	[0]	0	[0]	0	[0]	0	[0]	0
MRE11	[0]	0	[0]	0	[0]	0	[0]	0
PFS2	[0]	0	[0]	0	[0]	0	[0]	0
NOT5	[0]	0	[0]	0	[0]	0	[0]	0
KRR1	1	−1	2	0	0	0	1	1
LAS1	0	1	1	1	1	−1	1	−1
HNT3	0	1	1	1	1	0	0	−1
REV3	0	0	1	0	1	0	0	0
NGL1	0	0	0	0	1	1	0	0
REX4	−1	−1	1	0	1	0	0	1
NTG1	0	−1	1	−1	0	0	0	0
TRM2	0	−1	0	0	0	−1	0	1
RAD1	0	1	0	0	0	1	1	1
PAP2	0	1	−1	0	1	0	1	0
YSH1	0	1	0	1	0	0	1	0
YOR166C	0	1	−1	0	0	0	1	0
EXO1	0	1	0	0	0	−1	1	0
IRE1	0	1	−1	1	−1	−1	0	−1
RNY1	0	0	0	0	0	0	0	−1
PCH2	0	0	0	0	0	0	−1	0
APN2	0	0	0	0	0	1	0	0
NGL2	0	0	−1	1	1	0	0	0
DDP1	−1	0	−1	0	0	0	0	0
FIP1	1	1	2	0	0	0	0	0
RRP5	1	1	2	0	0	0	−1	0
APN1	1	0	1	0	0	0	0	1
SLX1	1	1	1	0	−1	−1	−1	0
RNH70	0	0	1	0	1	1	−1	1
POP7	0	−1	0	1	0	0	1	0
CDC7	0	−2	1	0	−1	1	0	0
EST1	0	−1	0	0	0	1	−1	0
RNH203	0	0	0	0	−1	1	0	−1
SPO11	1	−1	0	0	1	1	2	0
NTG2	0	0	−1	1	1	1	2	−1
REC102	0	−1	1	0	1	1	1	−2
REC114	0	−1	2	−1	2	0	3	1
SMC2	0	−1	1	−2	1	0	2	0
POP8	−1	0	1	0	2	−1	2	0
PTA1	2	1	3	0	−1	−2	4	−4
POL3	1	1	2	−1	−2	−1	1	−3
POP4	1	−2	1	0	0	0	3	−3
YCG1	0	1	−2	0	0	−2	4	0
LRP1	0	1	−2	1	1	−2	3	−2
MRPL3	−1	1	−2	1	0	−2	3	0
RNA14	0	2	0	1	0	−4	1	−2
YMR262W	0	1	−2	0	−1	−2	2	−1
RNH202	0	2	−1	0	0	−2	0	0
SEN54	2	1	3	0	1	−2	3	3
DCP1	3	2	3	0	0	−4	4	1
POP5	0	1	1	1	0	−3	5	−1
RCL1	1	1	2	−1	1	−3	4	−2
CFT1	1	2	3	−2	0	−3	2	3
DIP2	1	2	1	0	0	−3	2	3
MPE1	0	1	1	−2	0	−3	3	4
DBR1	0	2	1	0	1	−2	2	1
TOM1	0	2	−1	−2	2	−3	3	2
DNA2	3	1	3	0	−1	−1	1	1
RAD10	2	1	2	0	−1	0	0	−1
TRZ1	1	1	2	1	0	−3	2	0
NOB1	1	1	1	1	0	−3	2	1
POP1	1	1	2	0	0	−3	2	0
ENP1	1	1	2	1	0	−4	0	0
YLR132C	0	2	1	0	0	−3	1	−1
RRP43	1	1	2	−1	−1	−4	1	0
POP6	0	1	1	0	2	−4	0	0
YGR251W	1	1	2	0	0	−3	1	1
MTR4	1	1	2	0	−1	−3	0	1
UTP13	1	1	0	0	−2	−4	1	2
YEN1	0	1	0	0	0	−1	0	1
ROK1	0	1	0	0	0	−2	−1	2
NOP9	1	1	1	0	0	−2	1	1
SNM1	0	1	0	0	0	−2	0	0
SSD1	0	1	0	0	0	−2	0	1
YTH1	0	1	0	0	−1	−3	0	1
EDC3	0	1	0	0	0	−3	0	0
CCR4	0	1	[0]	0	−1	−3	[0]	0
POL1	2	1	2	0	−2	−1	−2	1
GRC3	2	1	2	1	−1	−3	−1	−1
RAD2	2	1	1	1	−1	−1	−1	0
CDC36	0	1	1	0	−1	0	0	−1
RLP7	0	1	1	0	0	−2	−1	−1
NPP2	0	0	1	0	0	−1	0	−1
REX3	0	0	0	0	−1	−1	−1	0
REC102	1	1	1	1	−2	−2	−1	0
NUC1	0	1	[0]	0	−2	−1	[0]	0
SLX4	0	1	1	0	−2	−1	−1	−1
DIN7	1	1	0	1	−1	−1	−1	−1
YDR370C	0	1	1	1	−1	−2	−2	−1
YCS4	0	2	1	0	−2	−5	−1	−2
SEN2	1	1	1	1	−1	−4	−2	−1
CFT2	1	1	1	0	−1	−4	−1	−1
TSR1	1	1	1	0	−2	−4	−1	−2
NHP2	−1	0	−1	1	4	0	5	−1
RPS0A	−3	−2	0	1	7	0	3	−2
RPL37A	0	1	0	0	4	−1	4	−3
RPS18B	−1	1	−1	1	3	−2	4	−3
RPL37B	0	1	0	1	3	−1	3	−3
RPS21A	−1	−1	−2	0	2	−1	4	−4
DBP3	−2	−1	−3	5	4	−1	5	−3
RPS18A	−3	2	−3	2	5	−3	5	−5
SEN15	1	−3	2	−4	1	3	2	9
POP2	0	−1	1	−4	1	2	1	6
YNR024W	0	0	2	−6	2	−1	3	8
YCL074W	0	−1	2	−4	1	0	4	3
RNH201	1	−2	1	−4	0	2	4	3
ESF2	1	1	2	−4	1	−3	3	9
PCF11	2	1	3	−4	0	−4	4	6
MRD1	−1	1	0	−2	4	−1	2	6
RPM2	0	1	2	−3	2	−2	2	5
TRL1	1	−2	3	−2	2	2	2	13
RPC11	0	−6	2	−3	2	1	1	11
RPB9	−1	−1	−3	−9	6	2	6	7
RRS1	1	−1	1	−14	0	2	4	9
MMS4	0	−6	−1	−10	1	4	1	6
MCM21	−1	−6	0	−1	3	8	1	2
NOC4	−2	−8	−2	−1	3	7	1	7
PAN3	0	−6	0	−1	2	5	3	1
YER077C	0	−4	−2	−1	2	4	3	0
PAN2	1	−4	−1	1	−1	3	2	1
RPS21B	0	−4	1	1	0	3	0	0
MUS81	0	−7	−1	0	1	3	0	1
SWD3	0	−6	0	0	0	0	−1	1
RPS27B	−2	−4	−3	0	7	2	6	2
MCM21	1	−1	−5	−1	0	1	4	0
CCE1	−3	−1	−3	−3	2	0	3	3
MMS4	0	−6	−9	−4	1	4	6	5
MTR3	−7	2	−11	−2	8	−4	13	−15
BUD23	−2	0	−11	14	9	−2	8	0
KEM1	−4	4	−12	9	6	−6	7	2
POP3	1	1	−6	10	0	−2	8	−6
HRP1	1	−1	−5	8	1	0	9	−7
RPA12	−1	2	−2	3	2	−5	5	−8
BUD21	−4	−1	−8	−2	9	−2	12	0
RPS0B	−5	1	−5	1	8	−3	7	−3
PET309	−11	2	−8	−3	5	0	6	−3
YGR150C	−5	2	−9	−5	2	−1	6	3
SUV3	−3	1	−12	−1	3	0	5	−1
MIP1	−6	2	−15	−1	3	0	6	−1
MSU1	−8	−1	−13	−1	5	1	6	−2
MRPL15	−9	1	−13	1	4	0	0	10
LOC1	−19	3	[0]	0	11	−1	[0]	0
CCR4	−12	6	−21	9	5	−6	7	2
RAI1	−14	4	−16	7	10	−5	8	−2
DEM1	−12	3	−19	2	6	−3	7	0
BRE1	0	−10	0	−1	1	19	1	1
POL32	0	−9	0	−14	1	19	1	14
DDC1	0	−7	1	−27	0	14	0	6
DDC1	1	−1	1	−24	−2	6	−2	6
POP2	−1	−5	−3	−32	3	0	6	28
RAD50	0	−9	0	−40	1	14	1	32
RAD17	1	−8	2	−34	1	14	2	23
XRS2	−1	−9	−1	−39	1	13	2	21

DNA catabolic process, endonucleolytic

Color Key

−10 5

Value

	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	
SAE2	2	1	2	0	−1	1	0	4	SAE2
YBL055C	1	−1	−1	−1	0	2	2	2	YBL055C
SPO11	1	−1	0	0	1	1	2	0	SPO11
NUC1	0	1	0	0	−2	−1	0	0	NUC1

Gene

Color Key

−10 5

Value

deadenylation−independent decapping of nuclear−transcribed mRNA

	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
DCP1	3	2	3	0	0	−4	4	1
CDC36	0	1	1	0	−1	0	0	−1
NOT5	0	0	0	0	0	0	0	0
MOT2	0	0	0	0	0	0	0	0
EDC3	0	1	0	0	0	−3	0	0
RAI1	−14	4	−16	7	10	−5	8	−2

Gene

Color Key

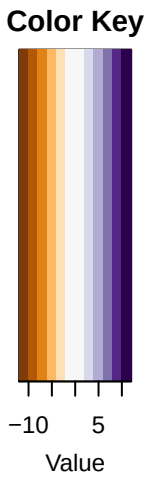
−10 5

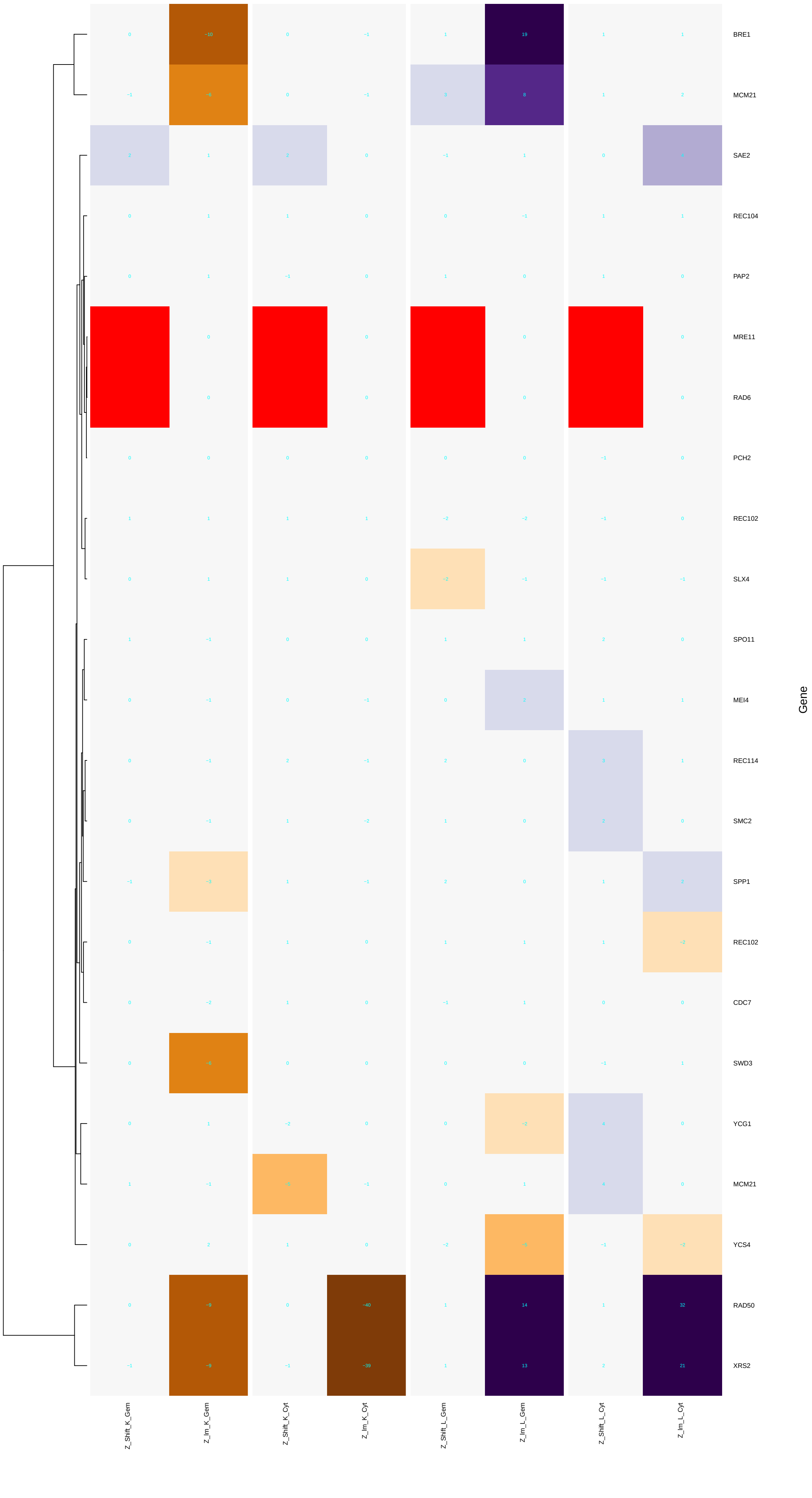
Value

nucleotide−excision repair, DNA incision

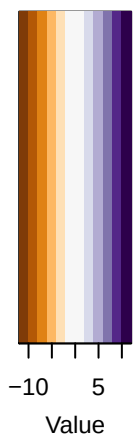
	Z_Shift_K_Gem	Z_Im_K_Gem	Z_Shift_K_Cyt	Z_Im_K_Cyt	Z_Shift_L_Gem	Z_Im_L_Gem	Z_Shift_L_Cyt	Z_Im_L_Cyt	Gene
RAD14	2	0	1	−1	0	0	2	2	
RAD1	0	1	0	0	0	1	1	1	
NTG1	0	−1	1	−1	0	0	0	0	
RAD10	2	1	2	0	−1	0	0	−1	
RAD2	2	1	1	1	−1	−1	−1	0	
NTG2	0	0	−1	1	1	1	2	−1	

meiotic DNA double−strand break formation





RNA phosphodiester bond hydrolysis



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

nucleotide−excision repair, DNA incision, 5'−to lesion

	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	Gene
	0	0	−1	1	1	1	2	−1	NTG2
	0	1	0	0	0	1	1	1	RAD1
	0	−1	1	−1	0	0	0	0	NTG1
	2	1	2	0	−1	0	0	−1	RAD10

Color Key

−10 5

Value

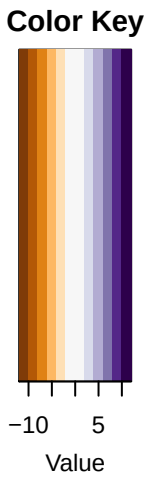
tic DNA double−strand break formation involved in reciprocal meiotic recombination

−1	−6	0	−1	3	8	1	2	MCM21
1	−1	−5	−1	0	1	4	0	MCM21
0	1	1	0	−2	−1	−1	−1	SLX4

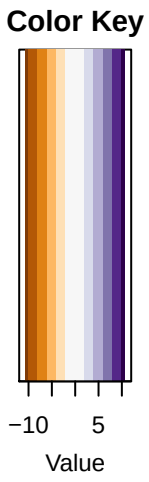
Gene

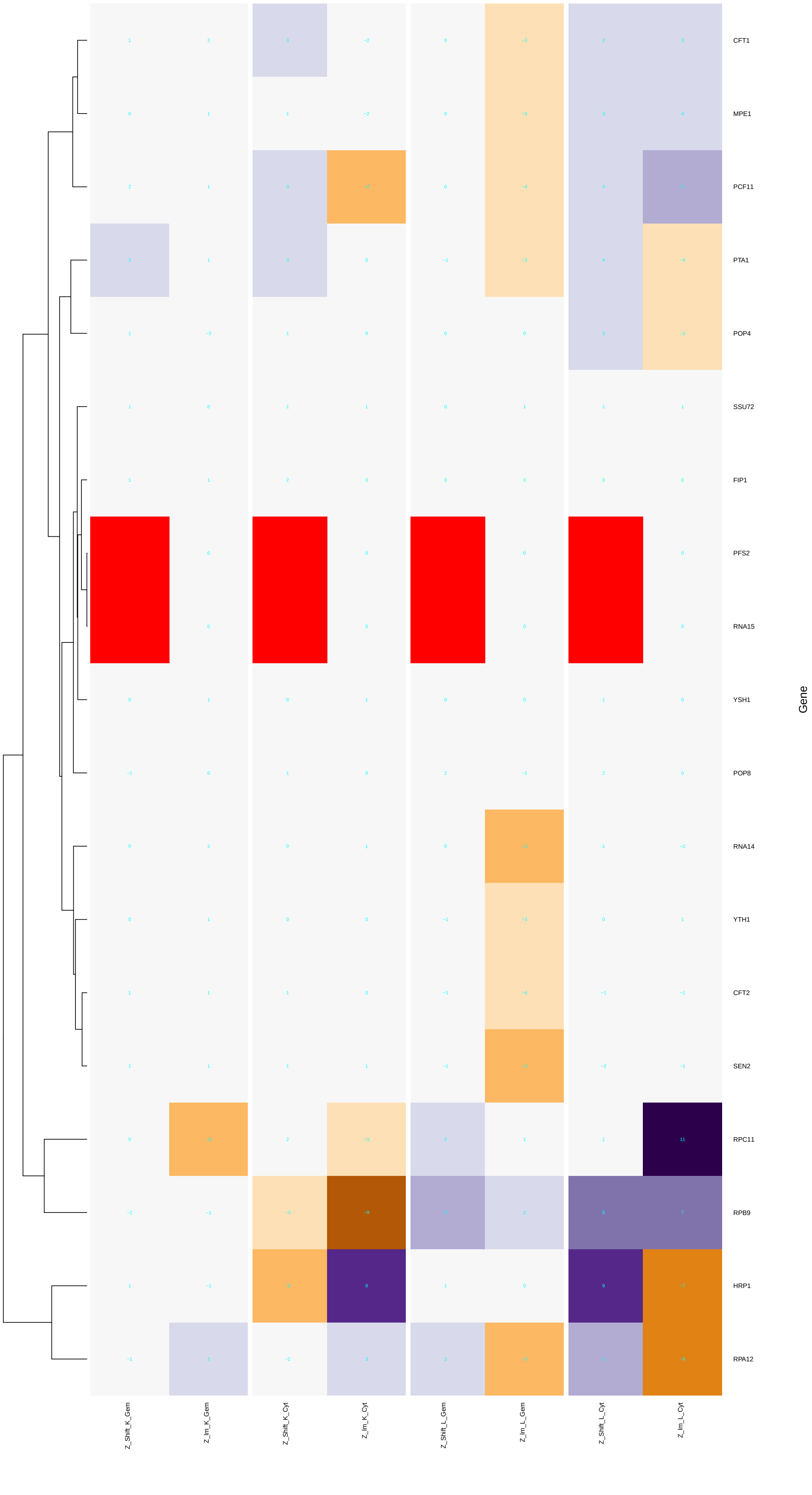
Z_Shift_K_Gem
Z_Im_K_Gem
Z_Shift_K_Cyt
Z_Im_K_Cyt
Z_Shift_L_Gem
Z_Im_L_Gem
Z_Shift_L_Cyt
Z_Im_L_Cyt

cleavage involved in rRNA processing

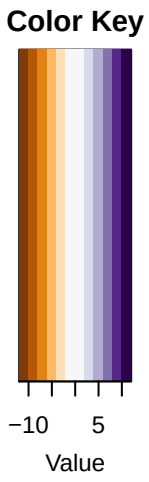


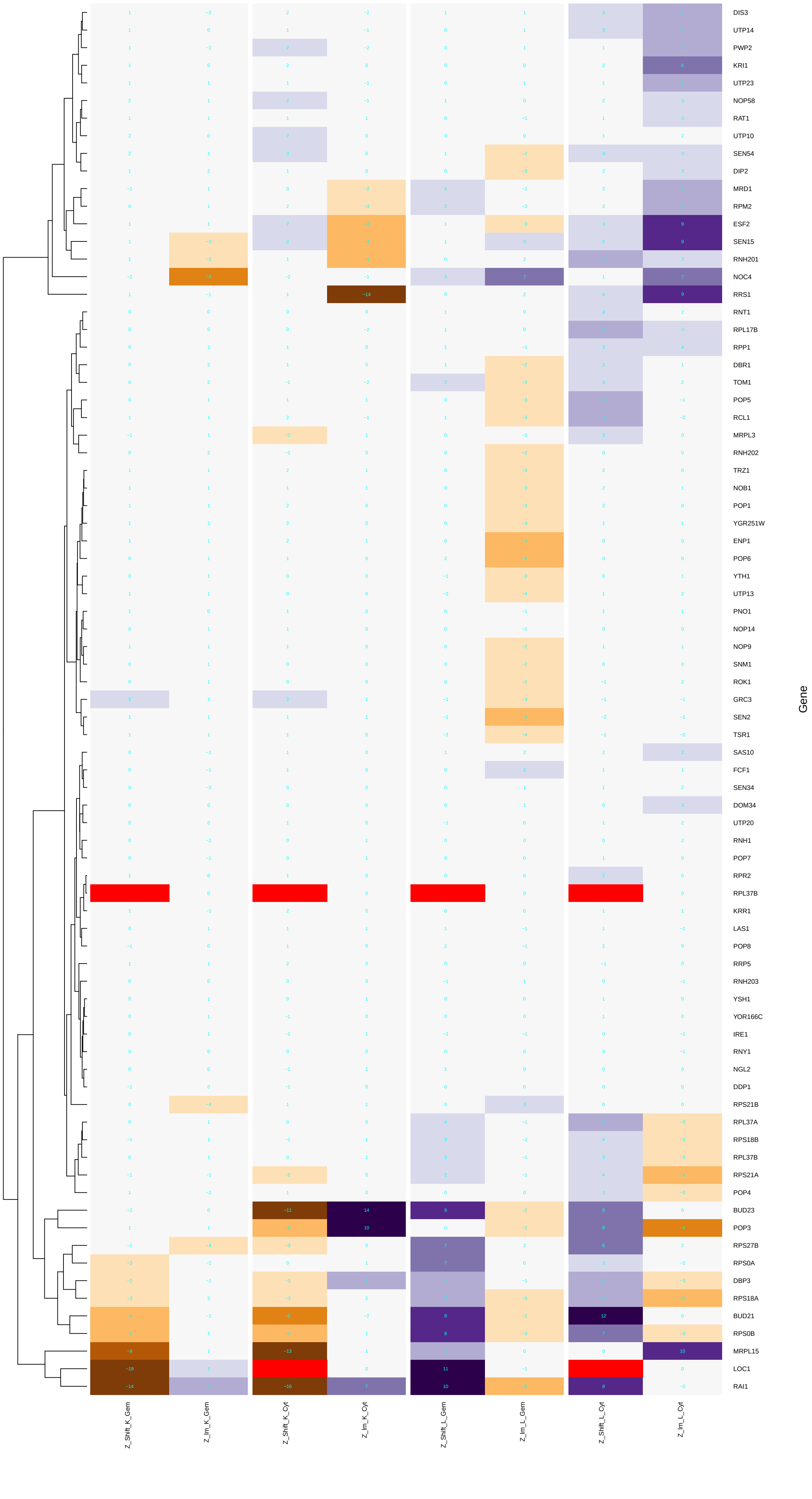
mRNA cleavage



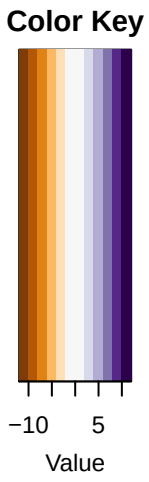


RNA phosphodiester bond hydrolysis, endonucleolytic



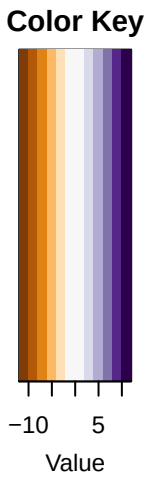


RNA phosphodiester bond hydrolysis, exonucleolytic



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
DIS3	1	−2	2	−2	1	1	3	5
RRP42	0	0	2	−3	0	0	2	6
POP2	0	−1	1	−4	1	2	1	6
YNR024W	0	0	2	−6	2	−1	3	8
PAN3	0	−6	0	−1	2	5	3	1
PAN2	1	−4	−1	1	−1	3	2	1
RRP46	0	−1	1	0	3	−1	4	2
RRP6	0	−2	0	−1	2	1	2	2
NGL3	1	−1	2	−1	2	2	1	1
RAT1	1	1	1	1	0	−1	1	3
CSL4	1	−1	1	1	0	0	2	3
RNH70	0	0	1	0	1	1	−1	1
REX2	1	0	1	−1	0	0	0	1
SSD1	0	1	0	0	0	−2	0	1
RLP7	0	1	1	0	0	−2	−1	−1
REX3	0	0	0	0	−1	−1	−1	0
RRP43	1	1	2	−1	−1	−4	1	0
YLR132C	0	2	1	0	0	−3	1	−1
MTR4	1	1	2	0	−1	−3	0	1
CCR4	0	1	[off-scale]	0	−1	−3	[off-scale]	0
LRP1	0	1	−2	1	1	−2	3	−2
KEM1	−4	4	−12	9	6	−6	7	2
CCR4	−12	6	−21	9	5	−6	7	2
MTR3	−7	2	−11	−2	8	−4	13	−15
SUV3	−3	1	−12	−1	3	0	5	−1
MSU1	−8	−1	−13	−1	5	1	6	−2
POP2	−1	−5	−3	−32	3	0	6	28

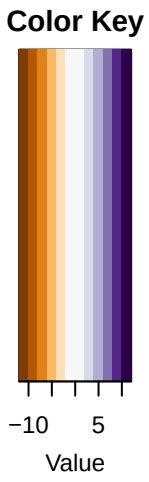
exonucleolytic trimming involved in rRNA processing



	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
DIS3	1	−2	2	−2	1	1	3	5
RRP42	0	0	2	−3	0	0	2	6
YNR024W	0	0	2	−6	2	−1	3	8
RRP46	0	−1	1	0	3	−1	4	2
RRP6	0	−2	0	−1	2	1	2	2
CSL4	1	−1	1	1	0	0	2	3
LRP1	0	1	−2	1	1	−2	3	−2
MTR4	1	1	2	0	−1	−3	0	1
RRP43	1	1	2	−1	−1	−4	1	0
RNH70	0	0	1	0	1	1	−1	1
REX2	1	0	1	−1	0	0	0	1
RLP7	0	1	1	0	0	−2	−1	−1
REX3	0	0	0	0	−1	−1	−1	0
MTR3	−7	2	−11	−2	8	−4	13	−15

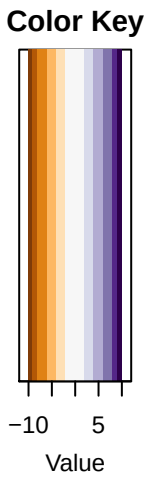
Gene

endonucleolytic cleavage involved in rRNA processing



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
KRI1	1	0	2	0	0	0	2	6
UTP23	1	1	1	−1	0	1	1	6
UTP14	1	0	1	−1	0	1	3	5
PWP2	1	−2	2	−2	0	1	1	5
NOP58	2	1	2	−1	1	0	2	3
RAT1	1	1	1	1	0	−1	1	3
RPL17B	0	0	0	−2	1	0	4	3
ESF2	1	1	2	−4	1	−3	3	9
MRD1	−1	1	0	−2	4	−1	2	6
NOC4	−2	−8	−2	−1	3	7	1	7
RRS1	1	−1	1	−14	0	2	4	9
UTP10	2	0	2	0	0	0	1	2
UTP20	0	0	1	0	−1	0	1	2
RRP5	1	1	2	0	0	0	−1	0
NOP14	0	1	1	0	0	−1	0	0
KRR1	1	−1	2	0	0	0	1	1
RPL37B	[0]	0	[0]	0	[0]	0	[0]	0
LAS1	0	1	1	1	1	−1	1	−1
PNO1	1	0	1	0	0	−1	1	1
NOP9	1	1	1	0	0	−2	1	1
ROK1	0	1	0	0	0	−2	−1	2
YGR251W	1	1	2	0	0	−3	1	1
ENP1	1	1	2	1	0	−4	0	0
DIP2	1	2	1	0	0	−3	2	3
UTP13	1	1	0	0	−2	−4	1	2
GRC3	2	1	2	1	−1	−3	−1	−1
TSR1	1	1	1	0	−2	−4	−1	−2
RCL1	1	1	2	−1	1	−3	4	−2
TOM1	0	2	−1	−2	2	−3	3	2
SAS10	0	−1	1	0	1	2	2	2
FCF1	0	−1	1	0	0	2	1	1
RPS21B	0	−4	1	1	0	3	0	0
RPL37A	0	1	0	0	4	−1	4	−3
RPS18B	−1	1	−1	1	3	−2	4	−3
RPL37B	0	1	0	1	3	−1	3	−3
RPS21A	−1	−1	−2	0	2	−1	4	−4
RPS0A	−3	−2	0	1	7	0	3	−2
DBP3	−2	−1	−3	5	4	−1	5	−3
RPS18A	−3	2	−3	2	5	−3	5	−5
BUD23	−2	0	−11	14	9	−2	8	0
RPS27B	−2	−4	−3	0	7	2	6	2
BUD21	−4	−1	−8	−2	9	−2	12	0
RPS0B	−5	1	−5	1	8	−3	7	−3
LOC1	−19	3	[0]	0	11	−1	[0]	0
RAI1	−14	4	−16	7	10	−5	8	−2

mRNA cleavage involved in mRNA processing



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
CFT1	1	2	3	−2	0	−3	2	3
MPE1	0	1	1	−2	0	−3	3	4
PCF11	2	1	3	−4	0	−4	4	6
SSU72	1	0	1	1	0	1	1	1
FIP1	1	1	2	0	0	0	0	0
PFS2	0	0	0	0	0	0	0	0
RNA15	0	0	0	0	0	0	0	0
YSH1	0	1	0	1	0	0	1	0
PTA1	2	1	3	0	−1	−2	4	−4
YTH1	0	1	0	0	−1	−3	0	1
RNA14	0	2	0	1	0	−4	1	−2
CFT2	1	1	1	0	−1	−4	−1	−1
HRP1	1	−1	−5	8	1	0	9	−7

Color Key

−10 5

Value

generate mature 3'−end of 5.8S rRNA from tricistronic rRNA transcript (SSU−rRNA, 5.8S rR

	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
DIS3	1	−2	2	−2	1	1	3	5
RRP42	0	0	2	−3	0	0	2	6
YNR024W	0	0	2	−6	2	−1	3	8
RRP46	0	−1	1	0	3	−1	4	2
RRP6	0	−2	0	−1	2	1	2	2
CSL4	1	−1	1	1	0	0	2	3
LRP1	0	1	−2	1	1	−2	3	−2
MTR4	1	1	2	0	−1	−3	0	1
RRP43	1	1	2	−1	−1	−4	1	0
RNH70	0	0	1	0	1	1	−1	1
REX2	1	0	1	−1	0	0	0	1
REX3	0	0	0	0	−1	−1	−1	0
MTR3	−7	2	−11	−2	8	−4	13	−15

Gene

Color Key

−10 5

Value

ucleolytic cleavage of tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)

	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
KRI1	1	0	2	0	0	0	2	6
UTP23	1	1	1	−1	0	1	1	6
UTP14	1	0	1	−1	0	1	3	5
PWP2	1	−2	2	−2	0	1	1	5
NOP58	2	1	2	−1	1	0	2	3
RAT1	1	1	1	1	0	−1	1	3
RPL17B	0	0	0	−2	1	0	4	3
ESF2	1	1	2	−4	1	−3	3	9
MRD1	−1	1	0	−2	4	−1	2	6
NOC4	−2	−8	−2	−1	3	7	1	7
RRS1	1	−1	1	−14	0	2	4	9
UTP10	2	0	2	0	0	0	1	2
UTP20	0	0	1	0	−1	0	1	2
RRP5	1	1	2	0	0	0	−1	0
NOP14	0	1	1	0	0	−1	0	0
KRR1	1	−1	2	0	0	0	1	1
RPL37B	[0]	0	[0]	0	[0]	0	[0]	0
LAS1	0	1	1	1	1	−1	1	−1
PNO1	1	0	1	0	0	−1	1	1
NOP9	1	1	1	0	0	−2	1	1
ROK1	0	1	0	0	0	−2	−1	2
YGR251W	1	1	2	0	0	−3	1	1
ENP1	1	1	2	1	0	−4	0	0
DIP2	1	2	1	0	0	−3	2	3
UTP13	1	1	0	0	−2	−4	1	2
GRC3	2	1	2	1	−1	−3	−1	−1
TSR1	1	1	1	0	−2	−4	−1	−2
RCL1	1	1	2	−1	1	−3	4	−2
TOM1	0	2	−1	−2	2	−3	3	2
SAS10	0	−1	1	0	1	2	2	2
FCF1	0	−1	1	0	0	2	1	1
RPS21B	0	−4	1	1	0	3	0	0
RPL37A	0	1	0	0	4	−1	4	−3
RPS18B	−1	1	−1	1	3	−2	4	−3
RPL37B	0	1	0	1	3	−1	3	−3
RPS21A	−1	−1	−2	0	2	−1	4	−4
RPS0A	−3	−2	0	1	7	0	3	−2
DBP3	−2	−1	−3	5	4	−1	5	−3
RPS18A	−3	2	−3	2	5	−3	5	−5
BUD23	−2	0	−11	14	9	−2	8	0
RPS27B	−2	−4	−3	0	7	2	6	2
BUD21	−4	−1	−8	−2	9	−2	12	0
RPS0B	−5	1	−5	1	8	−3	7	−3
LOC1	−19	3	[0]	0	11	−1	[0]	0
RAI1	−14	4	−16	7	10	−5	8	−2

Gene

Color Key

−10 5

Value

pre−mRNA cleavage required for polyadenylation

	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
CFT1	1	2	3	−2	0	−3	2	3
MPE1	0	1	1	−2	0	−3	3	4
PCF11	2	1	3	−4	0	−4	4	6
SSU72	1	0	1	1	0	1	1	1
FIP1	1	1	2	0	0	0	0	0
PFS2	0	0	0	0	0	0	0	0
RNA15	0	0	0	0	0	0	0	0
YSH1	0	1	0	1	0	0	1	0
PTA1	2	1	3	0	−1	−2	4	−4
YTH1	0	1	0	0	−1	−3	0	1
RNA14	0	2	0	1	0	−4	1	−2
CFT2	1	1	1	0	−1	−4	−1	−1
HRP1	1	−1	−5	8	1	0	9	−7

Gene

Color Key

−10 5

Value

arate SSU−rRNA from 5.8S rRNA and LSU−rRNA from tricistronic rRNA transcript (SSU−r

	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
KRI1	1	0	2	0	0	0	2	6
UTP23	1	1	1	−1	0	1	1	6
UTP14	1	0	1	−1	0	1	3	5
PWP2	1	−2	2	−2	0	1	1	5
NOP58	2	1	2	−1	1	0	2	3
ESF2	1	1	2	−4	1	−3	3	9
MRD1	−1	1	0	−2	4	−1	2	6
NOC4	−2	−8	−2	−1	3	7	1	7
RRS1	1	−1	1	−14	0	2	4	9
UTP10	2	0	2	0	0	0	1	2
KRR1	1	−1	2	0	0	0	1	1
UTP20	0	0	1	0	−1	0	1	2
RRP5	1	1	2	0	0	0	−1	0
NOP14	0	1	1	0	0	−1	0	0
SAS10	0	−1	1	0	1	2	2	2
FCF1	0	−1	1	0	0	2	1	1
RPS21B	0	−4	1	1	0	3	0	0
PNO1	1	0	1	0	0	−1	1	1
NOP9	1	1	1	0	0	−2	1	1
ROK1	0	1	0	0	0	−2	−1	2
YGR251W	1	1	2	0	0	−3	1	1
ENP1	1	1	2	1	0	−4	0	0
DIP2	1	2	1	0	0	−3	2	3
UTP13	1	1	0	0	−2	−4	1	2
RCL1	1	1	2	−1	1	−3	4	−2
TOM1	0	2	−1	−2	2	−3	3	2
RPS0A	−3	−2	0	1	7	0	3	−2
RPS18A	−3	2	−3	2	5	−3	5	−5
RPS18B	−1	1	−1	1	3	−2	4	−3
RPS21A	−1	−1	−2	0	2	−1	4	−4
BUD23	−2	0	−11	14	9	−2	8	0
BUD21	−4	−1	−8	−2	9	−2	12	0
RPS0B	−5	1	−5	1	8	−3	7	−3
LOC1	−19	3		0	11	−1		0

Gene

Color Key

−10 5

Value

ween 5.8S rRNA and LSU−rRNA of tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LS

	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	
RAT1	1	1	1	1	0	−1	1	3	RAT1
RPL17B	0	0	0	−2	1	0	4	3	RPL17B
TOM1	0	2	−1	−2	2	−3	3	2	TOM1
LAS1	0	1	1	1	1	−1	1	−1	LAS1
RPL37B	2	0	2	0	−1	−3	−1	−1	RPL37B
GRC3	2	1	2	1	−1	−3	−1	−1	GRC3
RPL37A	0	1	0	0	4	−1	4	−3	RPL37A
RPL37B	0	1	0	1	3	−1	3	−3	RPL37B
RAI1	−14	4	−16	7	10	−5	8	−2	RAI1

Gene

Color Key

−10 5

Value

c cleavage to generate mature 3'−end of SSU−rRNA from (SSU−rRNA, 5.8S rRNA, LSU−rRI

	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	
RPS0B	−5	1	−5	1	8	−3	7	−3	RPS0B
RPS0A	−3	−2	0	1	7	0	3	−2	RPS0A
RPS21A	−1	−1	−2	0	2	−1	4	−4	RPS21A
RPS21B	0	−4	1	1	0	3	0	0	RPS21B
TSR1	1	1	1	0	−2	−4	−1	−2	TSR1

Gene

Color Key

−10 5

Value

c cleavage to generate mature 5'−end of SSU−rRNA from (SSU−rRNA, 5.8S rRNA, LSU−rRI

	Z_Shift_K_Gem	Z_lm_K_Gem	Z_Shift_K_Cyt	Z_lm_K_Cyt	Z_Shift_L_Gem	Z_lm_L_Gem	Z_Shift_L_Cyt	Z_lm_L_Cyt
UTP14	1	0	1	−1	0	1	3	5
PWP2	1	−2	2	−2	0	1	1	5
UTP23	1	1	1	−1	0	1	1	6
NOP58	2	1	2	−1	1	0	2	3
UTP10	2	0	2	0	0	0	1	2
UTP20	0	0	1	0	−1	0	1	2
RRP5	1	1	2	0	0	0	−1	0
NOP14	0	1	1	0	0	−1	0	0
SAS10	0	−1	1	0	1	2	2	2
FCF1	0	−1	1	0	0	2	1	1
PNO1	1	0	1	0	0	−1	1	1
NOP9	1	1	1	0	0	−2	1	1
YGR251W	1	1	2	0	0	−3	1	1
ROK1	0	1	0	0	0	−2	−1	2
DIP2	1	2	1	0	0	−3	2	3
UTP13	1	1	0	0	−2	−4	1	2
RCL1	1	1	2	−1	1	−3	4	−2
TOM1	0	2	−1	−2	2	−3	3	2
ESF2	1	1	2	−4	1	−3	3	9
MRD1	−1	1	0	−2	4	−1	2	6
NOC4	−2	−8	−2	−1	3	7	1	7
BUD21	−4	−1	−8	−2	9	−2	12	0
LOC1	−19	3	−8	0	11	−1	−8	0

Gene

Color Key

−10 5

Value

lytic cleavage in 5'−ETS of tricistronic rRNA transcript (SSU−rRNA, 5.8S rRNA, LSU−rRNA)

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	Gene
1	0	1	−1	0	1	3	5	UTP14
1	−2	2	−2	0	1	1	5	PWP2
1	1	1	−1	0	1	1	6	UTP23
2	1	2	−1	1	0	2	3	NOP58
2	0	2	0	0	0	1	2	UTP10
0	0	1	0	−1	0	1	2	UTP20
1	1	2	0	0	0	−1	0	RRP5
0	1	1	0	0	−1	0	0	NOP14
0	−1	1	0	1	2	2	2	SAS10
0	−1	1	0	0	2	1	1	FCF1
1	2	1	0	0	−3	2	3	DIP2
1	1	0	0	−2	−4	1	2	UTP13
1	1	2	0	0	−3	1	1	YGR251W
1	1	1	0	0	−2	1	1	NOP9
0	1	0	0	0	−2	−1	2	ROK1
0	2	−1	−2	2	−3	3	2	TOM1
1	1	2	−1	1	−3	4	−2	RCL1
1	1	2	−4	1	−3	3	9	ESF2
−1	1	0	−2	4	−1	2	6	MRD1
−2	−8	−2	−1	3	7	1	7	NOC4
−19	3	[red]	0	11	−1	[red]	0	LOC1