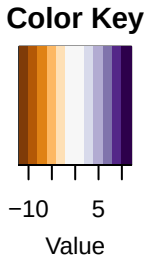
cleavage involved in rRNA processing



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
RAT1	1	1	1	1	0	−1	1	3
CSL4	1	−1	1	1	0	0	2	3
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
REX2	1	0	1	−1	0	0	0	1
SAS10	0	−1	1	0	1	2	2	2
FCF1	0	−1	1	0	0	2	1	1
RRP46	0	−1	1	0	3	−1	4	2
RPL17B	0	0	0	−2	1	0	4	3
RRP6	0	−2	0	−1	2	1	2	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
RPS21B	0	−4	1	1	0	3	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
RRP5	1	1	2	0	0	0	−1	0
RNH70	0	0	1	0	1	1	−1	1
NOP14	0	1	1	0	0	−1	0	0
RLP7	0	1	1	0	0	−2	−1	−1
REX3	0	0	0	0	−1	−1	−1	0
YGR251W	1	1	2	0	0	−3	1	1
NOB1	1	1	1	1	0	−3	2	1
MTR4	1	1	2	0	−1	−3	0	1
ENP1	1	1	2	1	0	−4	0	0
RRP43	1	1	2	−1	−1	−4	1	0
GRC3	2	1	2	1	−1	−3	−1	−1
TSR1	1	1	1	0	−2	−4	−1	−2
DIP2	1	2	1	0	0	−3	2	3
UTP13	1	1	0	0	−2	−4	1	2
TOM1	0	2	−1	−2	2	−3	3	2
RCL1	1	1	2	−1	1	−3	4	−2
NHP2	−1	0	−1	1	4	0	5	−1
RPS0A	−3	−2	0	1	7	0	3	−2
RPS27B	−2	−4	−3	0	7	2	6	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
LRP1	0	1	−2	1	1	−2	3	−2
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
ESF2	1	1	2	−4	1	−3	3	9
YNR024W	0	0	2	−6	2	−1	3	8
MRD1	−1	1	0	−2	4	−1	2	6
RRS1	1	−1	1	−14	0	2	4	9
NOC4	−2	−8	−2	−1	3	7	1	7
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
MTR3	−7	2	−11	−2	8	−4	13	−15
LOC1	−19	3	[0]	0	11	−1	[0]	0
RAI1	−14	4	−16	7	10	−5	8	−2

exonucleolytic trimming involved in rRNA processing

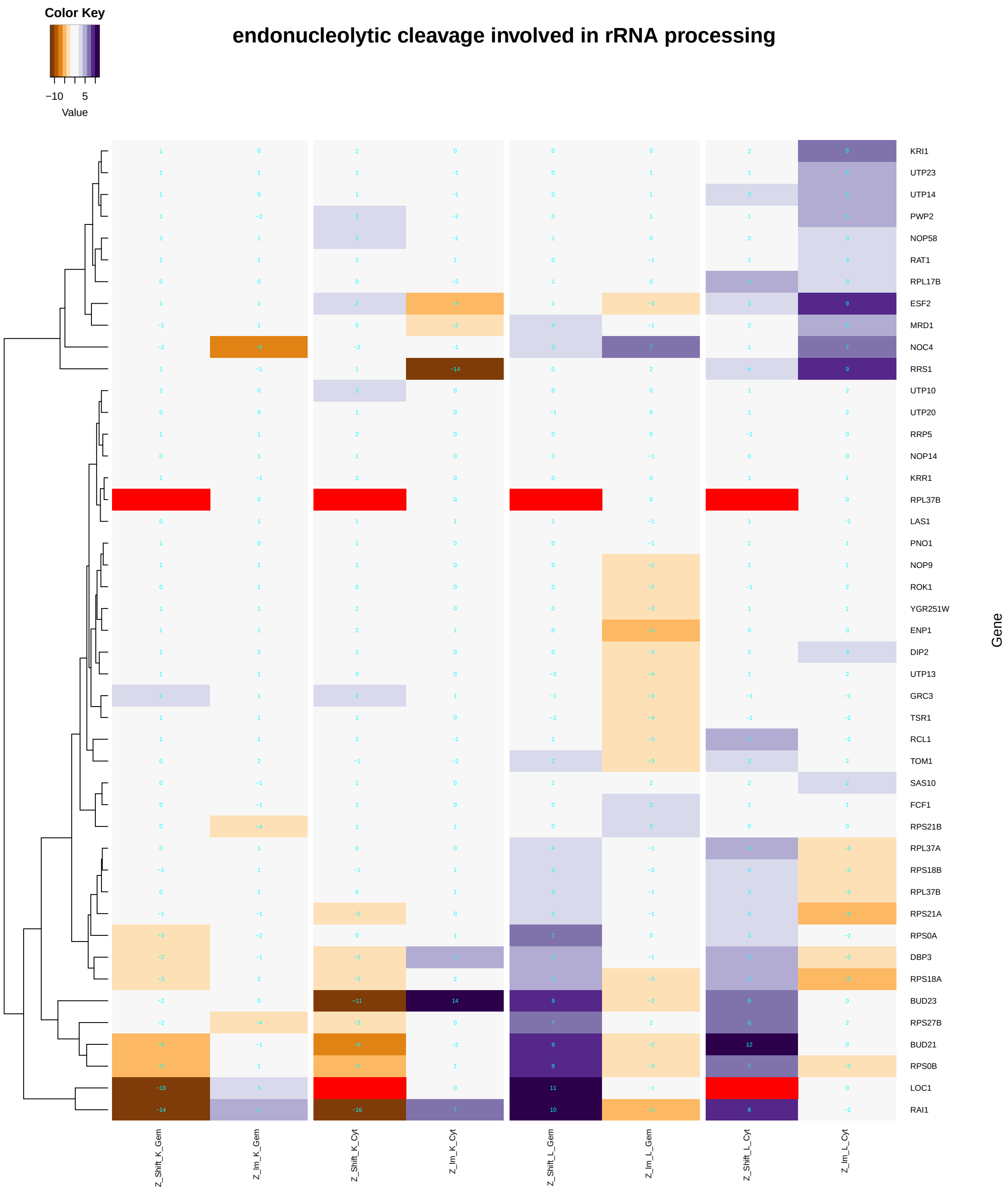
Color Key

−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
DIS3	1	−2	2	−2	1	1	3	5
RRP42	0	0	2	−3	0	0	2	5
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

endonucleolytic cleavage involved in rRNA processing



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_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
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	[off]	0	[off]	0	[off]	0	[off]	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	[off]	0	11	−1	[off]	0
RAI1	−14	4	−16	7	10	−5	8	−2

Gene

Color Key

−10 5

Value

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

	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
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	6
PWP2	1	−2	2	−2	0	1	1	6
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
RPL17B	0	0	0	−2	1	0	4	3
TOM1	0	2	−1	−2	2	−3	3	2
LAS1	0	1	1	1	1	−1	1	−1
RPL37B	0	0	0	0	0	0	0	0
GRC3	2	1	2	1	−1	−3	−1	−1
RPL37A	0	1	0	0	4	−1	4	−3
RPL37B	0	1	0	1	3	−1	3	−3
RAI1	−14	4	−16	7	10	−5	8	−2

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
RPS0A	−3	−2	0	1	7	0	3	−2
RPS21A	−1	−1	−2	0	2	−1	4	−4
RPS21B	0	−4	1	1	0	3	0	0
TSR1	1	1	1	0	−2	−4	−1	−2

Gene

Color Key

−10 5

Value

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

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
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		0	11	−1		0

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
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
DIP2	1	2	1	0	0	−3	2	3
UTP13	1	1	0	0	−2	−4	1	2
YGR251W	1	1	2	0	0	−3	1	1
NOP9	1	1	1	0	0	−2	1	1
ROK1	0	1	0	0	0	−2	−1	2
TOM1	0	2	−1	−2	2	−3	3	2
RCL1	1	1	2	−1	1	−3	4	−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
LOC1	−19	3		0	11	−1		0

Gene