Family-wise cluster performance of Rfam

RNA family	F-measure	Recall	Precision	Family Size	Recalled Size	Cluster Size
5S_rRNA	0.99	0.98	1	139	136	136
5_8S_rRNA	0.89	0.8	1	30	24	24
6S	1	1	1	5	5	5
7SK	1	1	1	1	1	1
AMV_RNA1_SL	0.4	1	0.25	1	1	4
Alfamo_CPB	1	1	1	3	3	3
Alpha_RBS	0.75	0.6	1	5	3	3
Antizyme_FSE	1	1	1	3	3	3
ApoB_5_CRE	1	1	1	2	2	2
BLV_package	1	1	1	1	1	1
BTE	1	1	1	5	5	5
BaMV_CRE	0.5	1	0.33	1	1	3
C0299	0.67	1	0.5	1	1	2
C0343	1	1	1	1	1	1
C0465	0.5	1	0.33	1	1	3
C0719	1	1	1	1	1	1
CAESAR	0.67	0.5	1	4	2	2
CTV_rep_sig	1	1	1	1	1	1
Cardiovirus_CRE	1	1	1	6	6	6
Cobalamin	0.7	0.54	1	151	82	82
CopA	0.5	0.5	0.5	2	1	2
Corona_FSE	0.44	0.33	0.67	6	2	3
Corona_SL-III	1	1	1	1	1	1
Corona_package	1	1	1	2	2	2
Corona_pk3	0.86	0.75	1	4	3	3
CsrB	0.89	1	0.8	4	4	5
CsrC	0.4	0.5	0.33	2	1	3
Dengue_CRE	0.5	1	0.33	1	1	3
DicF	0.57	0.5	0.67	4	2	3
DnaX	1	1	1	2	2	2
DsrA	0.75	1	0.6	3	3	5
E2	0.86	0.75	1	4	3	3
E3	0.33	0.2	1	5	1	1
EAV_LTH	1	1	1	1	1	1
Entero_5_CRE	0.02	1	0.01	1	1	108
Entero_CRE	0.84	1	0.73	8	8	11
Entero_OriR	1	1	1	1	1	1
FIE3	0.5	0.33	1	3	1	1
FinP	0.67	1	0.5	1	1	2
Flavi_pk3	0.8	1	0.67	2	2	3
G-CSF_SLDE	0.5	1	0.33	1	1	3
GAIT	1	1	1	1	1	1
GadY	0.5	1	0.33	1	1	3
Gammaretro_CES	0.5	1	0.33	1	1	3
GcvB	0.67	0.67	0.67	3	2	3
HACA_sno_Snake	1	1	1	3	3	3
HCV_SLIV	1	1	1	8	8	8
HCV_SLVII	0.89	0.8	1	5	4	4
HCV_X3	0.8	1	0.67	2	2	3
HDV_ribozyme	0.8	1	0.67	2	2	3

Family-wise cluster performance of Rfam

HIV_FE	0.8	0.67	1	3	2	2
HIV_GSL3	0.86	1	0.75	3	3	4
HIV_PBS	0.67	1	0.5	1	1	2
HLE	0.5	1	0.33	1	1	3
Hairpin	0.67	0.67	0.67	3	2	3
Hammerhead_1	0.86	0.75	1	24	18	18
Hammerhead_3	0.38	0.23	1	13	3	3
HepC_CRE	1	1	1	1	1	1
HgcC	0.33	0.2	1	5	1	1
HgcE	0.8	1	0.67	2	2	3
HgcF	0.67	1	0.5	1	1	2
HgcG	0.5	0.33	1	3	1	1
Histone3	0.84	0.73	1	55	40	40
Hsp90_CRE	1	1	1	1	1	1
IBV_D-RNA	1	1	1	1	1	1
IFN_gamma	1	1	1	1	1	1
IRE	1	1	1	13	13	13
IRES_APC	0.86	0.75	1	4	3	3
IRES_Bag1	0.5	1	0.33	1	1	3
IRES_Bip	1	1	1	1	1	1
IRES_Cripavirus	1	1	1	7	7	7
IRES_Cx32	0.5	0.33	1	3	1	1
IRES_Cx43	0.75	0.6	1	5	3	3
IRES_EBNA	0.6	0.43	1	7	3	3
IRES_FGF1	0.8	1	0.67	2	2	3
IRES_HCV	0.46	0.75	0.33	4	3	9
IRES_HIF1	1	1	1	2	2	2
IRES_Hsp70	0.86	0.75	1	4	3	3
IRES_IGF2	1	1	1	1	1	1
IRES_Kv1.4	1	1	1	2	2	2
IRES_L-myc	1	1	1	1	1	1
IRES_Pesti	0.8	1	0.67	6	6	9
IRES_Picorna	0.4	0.5	0.33	2	1	3
IRES_Tobamo	1	1	1	1	1	1
IRES_VEGF_A	1	1	1	1	1	1
IRES_c-myc	0.67	1	0.5	1	1	2
IRES_mnt	1	1	1	1	1	1
IRES_n-myc	0.67	0.5	1	2	1	1
IS061	1	1	1	2	2	2
IS102	0.67	1	0.5	1	1	2
IS1222_FSE	1	1	1	1	1	1
IS128	1	1	1	1	1	1
Intron_gpI	0.56	0.39	1	23	9	9
Intron_gpII	0.81	0.7	0.98	79	55	56
JEV_hairpin	0.5	0.33	1	3	1	1
K10_TLS	1	1	1	1	1	1
K_chan_RES	0.92	0.85	1	20	17	17
Lysine	1	1	1	43	43	43
MPMV_package	0.67	0.5	1	2	1	1
MicC	0.8	1	0.67	2	2	3
MicF	0.5	0.33	1	3	1	1

Family-wise cluster performance of Rfam

OxyS	1	1	1	2	2	2
PVX_3	1	1	1	1	1	1
Parecho_CRE	0.4	0.33	0.5	3	1	2
Phage_pRNA	1	1	1	1	1	1
Plasmid_R1162	0.86	0.75	1	4	3	3
Plasmid_RNAIII	0.8	1	0.67	2	2	3
Pospi_RY	0.8	0.67	1	3	2	2
Pox_AX_element	1	1	1	1	1	1
PrfA	0.5	0.33	1	3	1	1
PrrB_RsmZ	1	1	1	4	4	4
PrrF	0.8	0.67	1	3	2	2
Purine	1	1	1	34	34	34
QUAD	1	1	1	5	5	5
QaRNA	0.67	0.5	1	4	2	2
Qrr	0.8	1	0.67	2	2	3
REN-SRE	0.8	0.67	1	3	2	2
RFN	0.97	0.97	0.97	31	30	31
RNA-OUT	0.8	1	0.67	2	2	3
RNAI	0.29	0.2	0.5	5	1	2
RNAIII	1	1	1	1	1	1
RNaseP_arch	0.61	0.44	1	25	11	11
RNaseP_bact_a	0.98	0.98	0.98	149	146	149
RNaseP_bact_b	1	1	1	15	15	15
RNaseP_nuc	0.45	0.29	1	38	11	11
RNase_MRP	0.56	0.39	1	18	7	7
ROSE	0.5	0.5	0.5	2	1	2
RRE	0.67	1	0.5	1	1	2
RSV_PBS	0.5	1	0.33	1	1	3
RbcL_stabil	1	1	1	1	1	1
Retro_dr1	1	1	1	1	1	1
Retroviral_psi	0.67	1	0.5	1	1	2
Rhino_CRE	0.73	0.57	1	7	4	4
Rota_CRE	1	1	1	1	1	1
RprA	0.8	1	0.67	2	2	3
RsmY	1	1	1	3	3	3
RtT	0.71	0.71	0.71	7	5	7
Rubella_3	0.5	1	0.33	1	1	3
RybB	1	1	1	3	3	3
RydC	1	1	1	2	2	2
RyeB	0.29	1	0.17	1	1	6
RyeE	0.67	1	0.5	2	2	4
RyhB	1	1	1	8	8	8
S-element	1	1	1	8	8	8
S15	0.73	0.57	1	7	4	4
SECIS	0.46	0.3	1	44	13	13
SL1	0.67	0.5	1	2	1	1
SL2	1	1	1	5	5	5
SRP_bact	0.98	0.98	0.98	47	46	47
SRP_euk_arch	0.97	0.95	1	39	37	37
SSU_rRNA_5	0.89	0.8	1	69	55	55
SVLPA	1	1	1	3	3	3

Family-wise cluster performance of Rfam

S_box	0.88	0.79	1	53	42	42
Spi-1	1	1	1	2	2	2
Spot_42	0.67	0.5	1	2	1	1
SraB	0.8	1	0.67	2	2	3
SraC_RyeA	0.67	0.5	1	6	3	3
SraD	0.8	1	0.67	2	2	3
SraE_RygA_RygB	1	1	1	3	3	3
SraG	0.86	0.75	1	4	3	3
SraH	0.8	1	0.67	2	2	3
SraJ	1	1	1	1	1	1
SscA	1	1	1	2	2	2
T-box	0.71	0.55	1	40	22	22
TAR	0.86	0.75	1	4	3	3
TCV_H5	0.67	1	0.5	1	1	2
TCV_Pr	0.67	0.5	1	2	1	1
THI	0.71	0.56	0.99	192	107	108
Telomerase-cil	0.62	0.44	1	9	4	4
Telomerase-vert	0.67	0.67	0.67	3	2	3
Thr_leader	0.55	0.43	0.75	7	3	4
Toga_5_CRE	0.91	0.83	1	6	5	5
Tombus_3_III	0.8	0.67	1	3	2	2
Tombus_3_IV	1	1	1	1	1	1
Tombus_5	0.92	0.86	1	7	6	6
Tymo_tRNA-like	0.96	1	0.93	13	13	14
U1	0.94	0.89	1	18	16	16
U101	1	1	1	1	1	1
U102	0.5	1	0.33	1	1	3
U103	0.5	1	0.33	1	1	3
U12	0.8	0.67	1	3	2	2
U14	0.44	0.29	1	7	2	2
U15	0.62	0.44	1	9	4	4
U16	1	1	1	3	3	3
U17	0.29	0.17	1	6	1	1
U18	0.57	0.4	1	10	4	4
U19	0.5	0.5	0.5	2	1	2
U1A_PIE	1	1	1	3	3	3
U2	1	1	1	18	18	18
U20	0.5	1	0.33	1	1	3
U21	0.67	0.5	1	4	2	2
U22	0.67	0.5	1	2	1	1
U23	0.4	0.25	1	4	1	1
U24	0.44	0.29	1	7	2	2
U25	0.86	0.75	1	4	3	3
U26	0.33	0.33	0.33	3	1	3
U27	0.5	0.33	1	6	2	2
U28	0.8	0.67	1	3	2	2
U29	0.4	0.25	1	4	1	1
U3	0.7	0.54	1	13	7	7
U30	0.67	0.5	1	2	1	1
U31	0.86	0.75	1	4	3	3
U32	1	1	1	2	2	2

U33	0.67	1	0.5	1	1	2
U34	0.57	0.4	1	5	2	2
U35	0.57	0.4	1	5	2	2
U36	0.4	0.25	1	12	3	3
U37	1	1	1	3	3	3
U38	0.5	0.33	1	3	1	1
U39	0.5	1	0.33	1	1	3
U4	0.9	0.82	1	11	9	9
U40	0.57	0.4	1	5	2	2
U42	0.75	0.6	1	5	3	3
U43	0.75	0.6	1	5	3	3
U44	0.8	1	0.67	2	2	3
U45	0.4	0.25	1	4	1	1
U47	0.67	0.5	1	2	1	1
U48	1	1	1	2	2	2
U49	0.5	0.33	1	3	1	1
U5	0.81	0.68	1	22	15	15
U50	0.67	0.67	0.67	3	2	3
U51	0.67	0.5	1	2	1	1
U52	1	1	1	2	2	2
U53	1	1	1	2	2	2
U54	0.6	0.43	1	7	3	3
U56	0.57	0.5	0.67	4	2	3
U57	0.8	0.67	1	3	2	2
U58	0.8	1	0.67	2	2	3
U59	0.8	0.67	1	3	2	2
U6	0.96	0.92	1	12	11	11
U60	0.5	0.33	1	3	1	1
U61	0.5	1	0.33	1	1	3
U62	0.5	0.5	0.5	2	1	2
U63	0.4	0.5	0.33	2	1	3
U64	1	1	1	2	2	2
U65	0.4	0.5	0.33	2	1	3
U66	0.05	1	0.02	1	1	42
U67	1	1	1	2	2	2
U68	0.33	1	0.2	1	1	5
U69	0.09	1	0.05	2	2	42
U7	0.92	0.86	1	7	6	6
U70	0.33	0.33	0.33	3	1	3
U71	0.36	0.25	0.67	8	2	3
U72	0.67	0.67	0.67	3	2	3
U73	0.86	1	0.75	3	3	4
U79	0.67	0.5	1	2	1	1
U8	0.86	0.75	1	4	3	3
U81	1	1	1	1	1	1
U82	0.5	0.5	0.5	2	1	2
U83	0.67	0.5	1	2	1	1
U87	0.67	0.5	1	2	1	1
U88	1	1	1	2	2	2
U91	1	1	1	3	3	3
U92	0.25	1	0.14	1	1	7

Family-wise cluster performance of Rfam

U93	1	1	1	1	1	1
U95	0.67	0.5	1	2	1	1
U98	0.67	0.5	1	2	1	1
U99	0.5	1	0.33	1	1	3
UPSK	1	1	1	4	4	4
UnaL2	0.89	0.8	1	49	39	39
VA	0.75	0.6	1	5	3	3
Vault	0.86	0.75	1	8	6	6
Vimentin3	0.67	0.5	1	4	2	2
Y	0.55	0.38	1	8	3	3
ctRNA_p42d	0.4	0.25	1	12	3	3
ctRNA_pGA1	0.6	0.75	0.5	4	3	6
ctRNA_pND324	0.88	0.78	1	9	7	7
ctRNA_pT181	0.91	0.83	1	6	5	5
gcvT	0.33	0.2	1	102	20	20
glmS	0.82	0.69	1	13	9	9
hspAT_ROSE	0.67	1	0.5	1	1	2
let-7	0.57	0.4	1	10	4	4
lin-4	0.33	0.2	1	5	1	1
mir-1	0.34	1	0.21	5	5	24
mir-10	0.45	0.7	0.33	10	7	21
mir-101	0.4	0.5	0.33	2	1	3
mir-103	0.67	1	0.5	3	3	6
mir-124	0.2	0.5	0.13	6	3	24
mir-129	0.12	1	0.07	4	4	61
mir-130	0.08	0.5	0.04	2	1	24
mir-133	0.29	0.25	0.33	4	1	3
mir-135	0.09	1	0.05	3	3	61
mir-148	0.18	0.25	0.14	4	1	7
mir-15	0.09	1	0.05	3	3	61
mir-156	0.22	0.14	0.5	7	1	2
mir-16	0.4	0.5	0.33	2	1	3
mir-160	0.29	0.17	1	6	1	1
mir-166	0.53	0.36	1	11	4	4
mir-17	0.33	0.33	0.33	3	1	3
mir-172	0.55	1	0.38	8	8	21
mir-181	0.6	1	0.43	3	3	7
mir-19	0.5	0.33	1	3	1	1
mir-192	0.8	1	0.67	2	2	3
mir-194	0.33	0.25	0.5	4	1	2
mir-196	0.22	0.25	0.2	8	2	10
mir-199	0.2	0.33	0.14	3	1	7
mir-2	0.22	0.13	1	8	1	1
mir-218	0.31	0.67	0.2	3	2	10
mir-219	0.25	1	0.14	3	3	21
mir-24	0.67	0.5	1	2	1	1
mir-26	0.24	0.75	0.14	4	3	21
mir-29	0.4	0.5	0.33	2	1	3
mir-30	1	1	1	2	2	2
mir-34	0.09	0.75	0.05	4	3	61
mir-395	0.26	0.28	0.24	18	5	21

Family-wise cluster performance of Rfam

mir-399	0.36	0.5	0.29	12	6	21
mir-46	0.29	0.25	0.33	4	1	3
mir-6	0.22	0.33	0.17	3	1	6
mir-7	0.18	1	0.1	6	6	61
mir-8	0.25	0.2	0.33	5	1	3
mir-9	0.5	1	0.33	3	3	9
mir-92	0.8	0.67	1	3	2	2
mir-BART1	0.5	1	0.33	1	1	3
mir-BART2	0.5	0.33	1	3	1	1
mir-BHRF1-1	0.2	1	0.11	1	1	9
mir-BHRF1-2	0.46	0.75	0.33	4	3	9
mir-BHRF1-3	0.5	1	0.33	1	1	3
msr	0.44	0.29	1	7	2	2
nos_TCE	0.8	1	0.67	2	2	3
p27_CRE	1	1	1	1	1	1
rne5	0.75	0.6	1	5	3	3
rydB	1	1	1	1	1	1
ryfA	0.8	1	0.67	2	2	3
s2m	1	1	1	10	10	10
sar	0.57	1	0.4	2	2	5
satBaMV_CRE	1	1	1	1	1	1
snoACA1	0.4	0.5	0.33	2	1	3
snoACA10	0.5	1	0.33	1	1	3
snoACA11	0.4	0.5	0.33	2	1	3
snoACA12	0.67	0.5	1	2	1	1
snoACA13	0.05	1	0.02	1	1	42
snoACA14	0.05	1	0.02	1	1	42
snoACA15	0.5	0.33	1	3	1	1
snoACA18	1	1	1	2	2	2
snoACA19	0.67	0.5	1	2	1	1
snoACA2	0.6	0.5	0.75	6	3	4
snoACA20	0.5	0.5	0.5	2	1	2
snoACA21	0.05	1	0.02	1	1	42
snoACA22	0.5	1	0.33	1	1	3
snoACA24	1	1	1	1	1	1
snoACA25	0.33	0.33	0.33	3	1	3
snoACA26	0.05	1	0.02	1	1	42
snoACA27	0.67	0.5	1	2	1	1
snoACA28	0.67	0.5	1	2	1	1
snoACA29	0.2	0.33	0.14	3	1	7
snoACA30	0.5	0.5	0.5	2	1	2
snoACA32	0.5	0.33	1	3	1	1
snoACA33	0.33	0.33	0.33	3	1	3
snoACA38	0.05	1	0.02	1	1	42
snoACA4	0.89	0.8	1	5	4	4
snoACA41	0.33	0.33	0.33	3	1	3
snoACA42	0.5	0.33	1	3	1	1
snoACA43	0.67	0.75	0.6	4	3	5
snoACA44	0.4	0.5	0.33	2	1	3
snoACA45	0.25	1	0.14	1	1	7
snoACA46	0.09	1	0.05	2	2	42

snoACA47	0.8	1	0.67	2	2	3
snoACA5	0.33	0.33	0.33	3	1	3
snoACA50	0.05	1	0.02	1	1	42
snoACA51	0.4	0.5	0.33	2	1	3
snoACA52	0.4	0.5	0.33	2	1	3
snoACA54	0.5	1	0.33	1	1	3
snoACA55	0.5	1	0.33	1	1	3
snoACA56	0.5	1	0.33	1	1	3
snoACA58	0.33	0.33	0.33	3	1	3
snoACA61	0.4	0.5	0.33	2	1	3
snoACA7	1	1	1	2	2	2
snoACA8	1	1	1	1	1	1
snoACA9	0.05	1	0.02	1	1	42
snoF1_F2	1	1	1	1	1	1
snoHBII-52	0.67	0.67	0.67	3	2	3
snoHBII-85	0.5	0.33	1	3	1	1
snoJ26	1	1	1	1	1	1
snoJ33	0.67	0.5	1	2	1	1
snoM1	1	1	1	2	2	2
snoMBI-1	0.67	1	0.5	1	1	2
snoMBI-161	0.67	0.5	1	2	1	1
snoMBI-28	0.44	1	0.29	2	2	7
snoMBI-87	0.4	0.5	0.33	2	1	3
snoMBII-202	1	1	1	2	2	2
snoPyro_CD	0.43	0.27	1	22	6	6
snoR1	0.67	0.5	1	4	2	2
snoR105_108	0.8	1	0.67	2	2	3
snoR11	0.67	0.5	1	2	1	1
snoR12	0.44	0.33	0.67	6	2	3
snoR16	1	1	1	4	4	4
snoR160	0.6	0.43	1	7	3	3
snoR20	0.67	0.5	1	2	1	1
snoR21	0.4	0.5	0.33	2	1	3
snoR24	0.67	0.67	0.67	3	2	3
snoR28	1	1	1	1	1	1
snoR30	0.67	0.5	1	2	1	1
snoR31_Z110_Z27	0.5	0.33	1	3	1	1
snoR32_R81	1	1	1	2	2	2
snoR38	0.36	0.25	0.67	8	2	3
snoR39	0.67	0.5	1	2	1	1
snoR41	0.5	0.33	1	3	1	1
snoR43	0.8	1	0.67	2	2	3
snoR44_J54	0.5	0.33	1	3	1	1
snoR53	0.5	1	0.33	1	1	3
snoR60	0.67	0.67	0.67	3	2	3
snoR639	0.25	1	0.14	1	1	7
snoR64	1	1	1	1	1	1
snoR66	0.67	0.5	1	2	1	1
snoR71	1	1	1	1	1	1
snoR72	0.5	1	0.33	1	1	3
snoR79	1	1	1	1	1	1

Family-wise cluster performance of Rfam

snoR86	0.67	0.5	1	2	1	1
snoR9	1	1	1	3	3	3
snoR98	1	1	1	3	3	3
snoR9_plant	1	1	1	2	2	2
snoTBR17	1	1	1	2	2	2
snoTBR5	0.67	0.67	0.67	3	2	3
snoTBR7	0.8	0.67	1	3	2	2
snoU12-22	1	1	1	3	3	3
snoU2-30	0.5	1	0.33	1	1	3
snoU2_19	0.5	1	0.33	1	1	3
snoU6-53	0.8	0.67	1	3	2	2
snoZ1	1	1	1	2	2	2
snoZ101	1	1	1	1	1	1
snoZ102_R77	1	1	1	2	2	2
snoZ103	0.57	0.4	1	5	2	2
snoZ105	1	1	1	4	4	4
snoZ107_R87	0.8	1	0.67	2	2	3
snoZ112	1	1	1	1	1	1
snoZ118	0.67	0.5	1	2	1	1
snoZ119	0.67	1	0.5	1	1	2
snoZ12	0.8	1	0.67	2	2	3
snoZ122	0.67	0.5	1	2	1	1
snoZ13_snr52	0.5	0.33	1	3	1	1
snoZ152	0.5	0.33	1	3	1	1
snoZ155	0.67	0.5	1	2	1	1
snoZ157	0.44	0.33	0.67	6	2	3
snoZ159	0.75	0.6	1	5	3	3
snoZ161_228	0.33	0.33	0.33	3	1	3
snoZ162	1	1	1	1	1	1
snoZ163	0.5	1	0.33	1	1	3
snoZ165	1	1	1	1	1	1
snoZ168	1	1	1	1	1	1
snoZ169	0.8	1	0.67	2	2	3
snoZ17	0.4	0.5	0.33	2	1	3
snoZ173	0.5	1	0.33	1	1	3
snoZ175	0.5	1	0.33	1	1	3
snoZ177	0.5	1	0.33	1	1	3
snoZ178	1	1	1	1	1	1
snoZ18	1	1	1	2	2	2
snoZ182	1	1	1	1	1	1
snoZ185	0.4	0.5	0.33	2	1	3
snoZ188	1	1	1	2	2	2
snoZ194	0.5	1	0.33	1	1	3
snoZ195	0.67	1	0.5	1	1	2
snoZ196	0.86	0.75	1	4	3	3
snoZ199	1	1	1	1	1	1
snoZ200	0.5	1	0.33	1	1	3
snoZ206	1	1	1	1	1	1
snoZ221	1	1	1	1	1	1
snoZ223	0.4	0.5	0.33	2	1	3
snoZ242	1	1	1	1	1	1

Family-wise cluster performance of Rfam

snoZ247	1	1	1	1	1	1
snoZ248	1	1	1	1	1	1
snoZ256	1	1	1	2	2	2
snoZ266	1	1	1	1	1	1
snoZ267	0.67	0.67	0.67	3	2	3
snoZ268	0.67	0.5	1	2	1	1
snoZ278	1	1	1	1	1	1
snoZ279	0.5	1	0.33	1	1	3
snoZ30	1	1	1	1	1	1
snoZ37	0.8	0.67	1	6	4	4
snoZ39	0.8	1	0.67	2	2	3
snoZ40	0.5	1	0.33	1	1	3
snoZ43	0.8	1	0.67	2	2	3
snoZ50	0.5	0.33	1	3	1	1
snoZ6	1	1	1	1	1	1
snoZ7	1	1	1	1	1	1
sno_14q_I_II	0.33	0.2	1	25	5	5
snosnR48	0.75	0.75	0.75	4	3	4
snosnR54	0.89	0.8	1	5	4	4
snosnR55	0.5	0.33	1	6	2	2
snosnR57	0.57	0.4	1	5	2	2
snosnR60_Z15	0.3	0.18	1	17	3	3
snosnR61	1	1	1	7	7	7
snosnR64	1	1	1	4	4	4
snosnR66	0.4	0.25	1	4	1	1
snosnR69	0.67	0.67	0.67	3	2	3
snosnR71	0.91	1	0.83	5	5	6
sroB	1	1	1	4	4	4
sroC	0.4	0.5	0.33	2	1	3
sroD	1	1	1	1	1	1
sroE	0.5	1	0.33	1	1	3
sroH	1	1	1	1	1	1
t44	0.86	0.75	1	4	3	3
tRNA	0.88	0.78	1	661	517	518
tke1	0.67	1	0.5	1	1	2
tmRNA	0.66	0.49	1	61	30	30
traJ_5	0.4	0.5	0.33	2	1	3
ydaO-yuaA	0.78	0.64	1	28	18	18
ykkC-yxkD	0.93	0.87	1	15	13	13
ykoK	0.98	0.96	1	26	25	25
yybP-ykoY	0.54	0.37	1	57	21	21