Science Advances
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Supplementary Materials for

Assembly of catalytic complexes from randomized oligonucleotides

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Figure S1

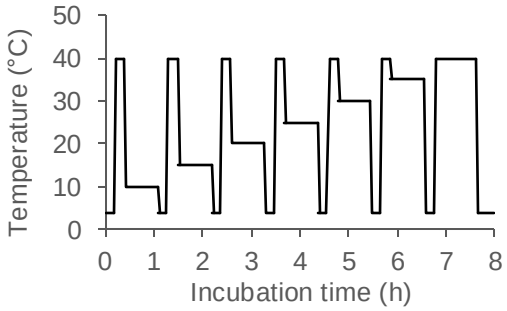


Figure S1. Temperature profile during the cTmp incubation in the selection. The incubation is composed of seven cycles each starting with a 10-minute denaturation at 40 °C , a 40-minute annealing / reaction at temperatures increasing from 10 °C to 40 °C, and a 10-minute reaction / stabilization stage at 4 °C. The samples were left at 4 °C for about another 8 hours before processing.

Figure S2

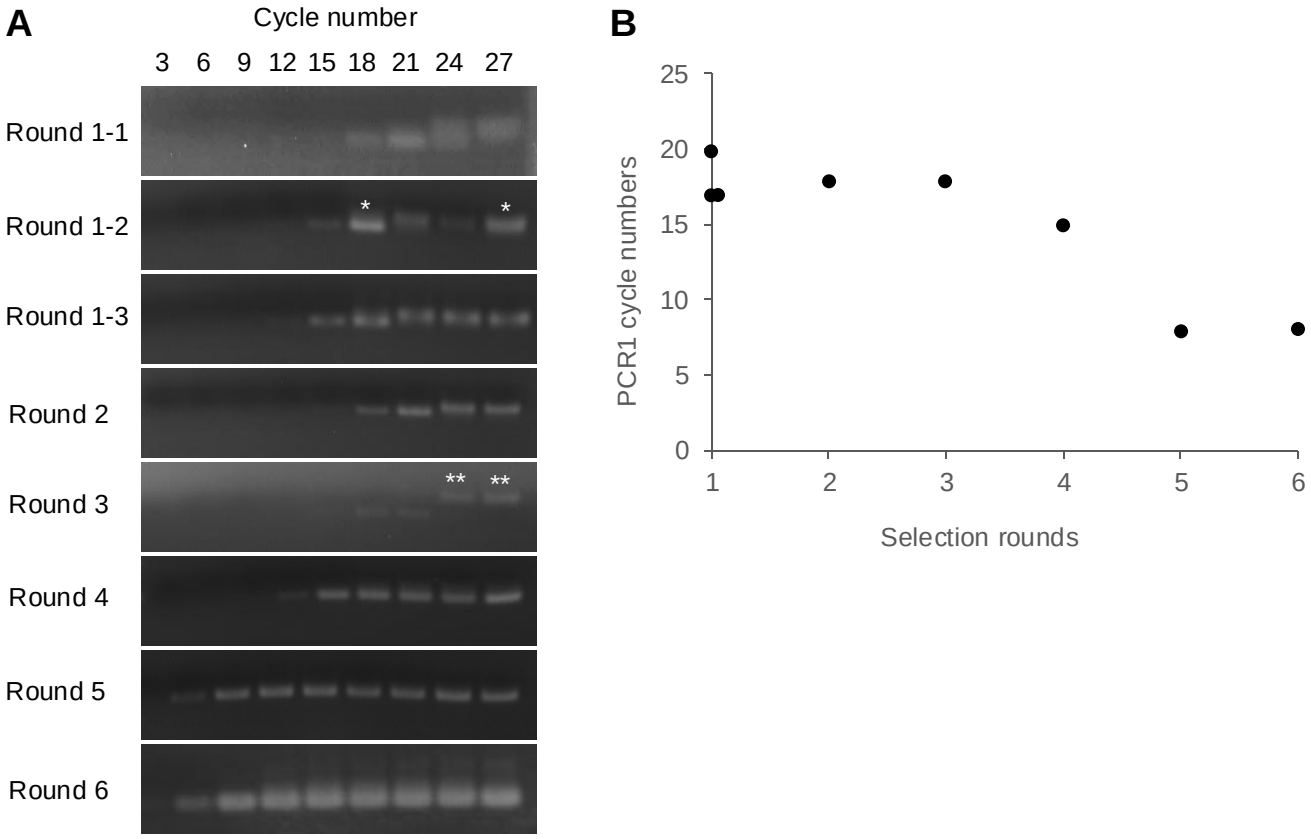


Figure S2. Enrichment of active sequences over the selection rounds, as judged by the number of PCR1 cycles. (A) PCR amplification of the reverse transcribed libraries recovered after the selection step. The first selection round was split into three groups for this PCR amplification, to help cover a large sequence space. *In selection round 1-2, accidentally about 30% more sample was loaded for PCR cycles 18 and 27. ** In selection round 3, PCR cycles 24 and 27 resulted in products of incorrect length, therefore 18 PCR cycles were chosen to avoid the takeover of incorrect products. **(B)** Graph showing the number of used PCR cycles as a function of the selection round.

Figure S3

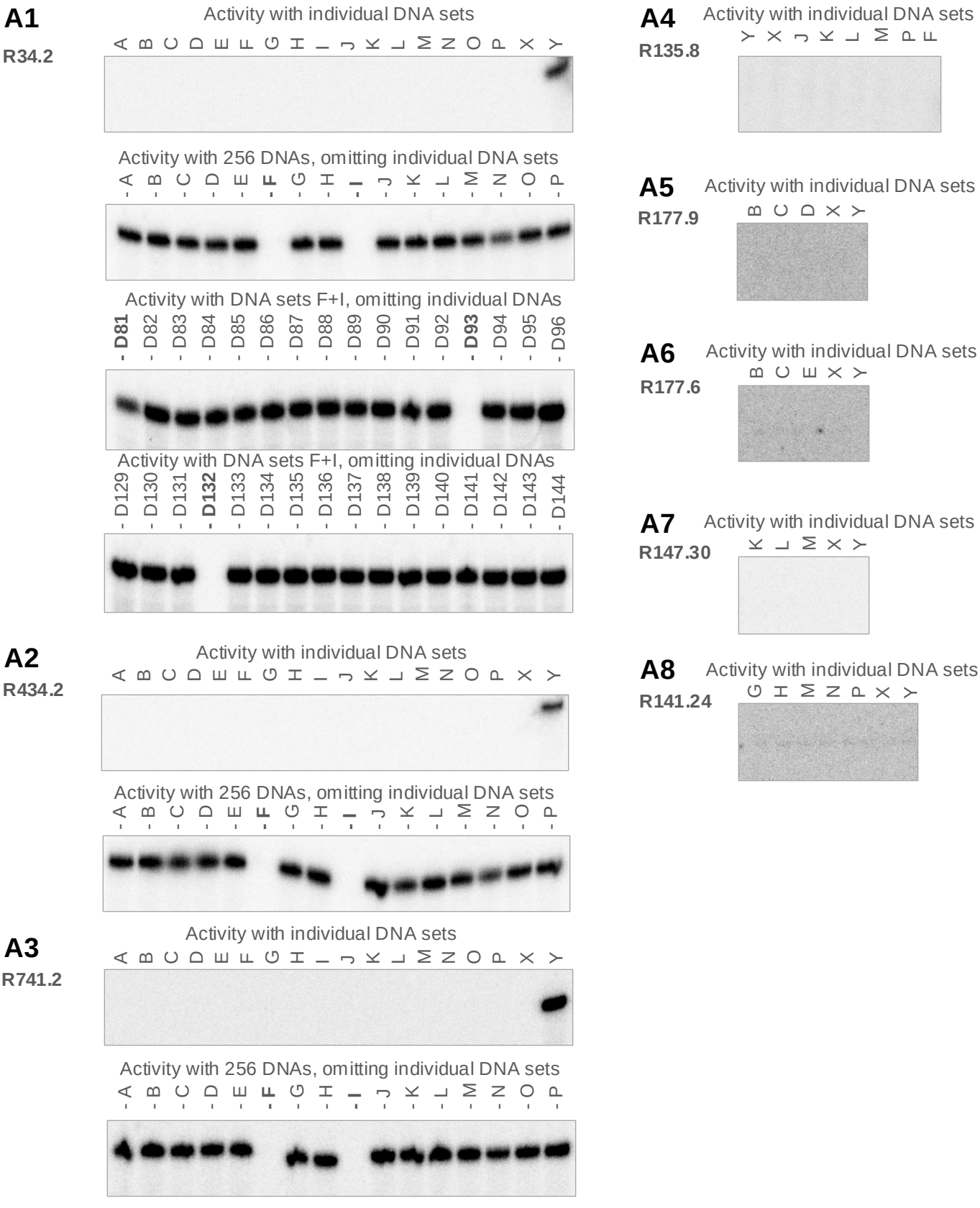
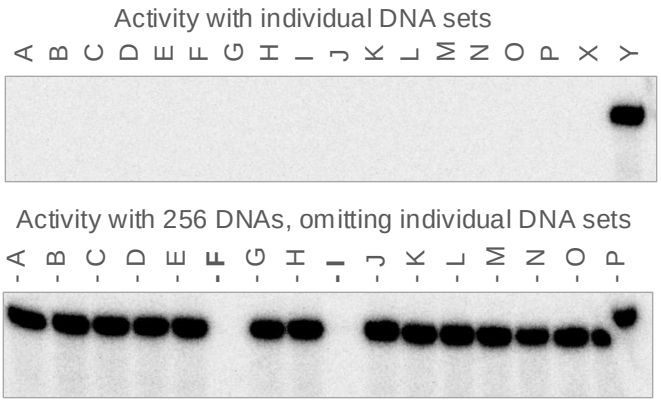

A1
R34.2
Activity with individual DNA sets
A B C D E F G H I J K L M N O P X Y
Activity with 256 DNAs, omitting individual DNA sets
-A -B -C -D -E -F -G -H -I -J -K -L -M -N -O -P
Activity with DNA sets F+I, omitting individual DNAs
-D81 -D82 -D83 -D84 -D85 -D86 -D87 -D88 -D89 -D90 -D91 -D92 -D93 -D94 -D95 -D96
Activity with DNA sets F+I, omitting individual DNAs
-D129 -D130 -D131 -D132 -D133 -D134 -D135 -D136 -D137 -D138 -D139 -D140 -D141 -D142 -D143 -D144
A2
R434.2
Activity with individual DNA sets
A B C D E F G H I J K L M N O P X Y
Activity with 256 DNAs, omitting individual DNA sets
-A -B -C -D -E -F -G -H -I -J -K -L -M -N -O -P
A3
R741.2
Activity with individual DNA sets
A B C D E F G H I J K L M N O P X Y
Activity with 256 DNAs, omitting individual DNA sets
-A -B -C -D -E -F -G -H -I -J -K -L -M -N -O -P
A4
R135.8
Activity with individual DNA sets
Y X J K L M P F
A5
R177.9
Activity with individual DNA sets
B C D X Y
A6
R177.6
Activity with individual DNA sets
B C E X Y
A7
R147.30
Activity with individual DNA sets
K L M X Y
A8
R141.24
Activity with individual DNA sets
G H M N P X Y

Figure S3 - continued

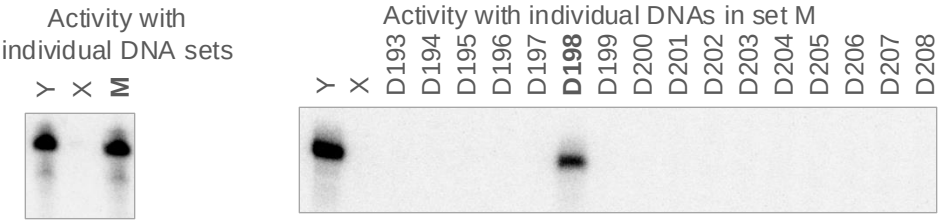
A9

R1869.2



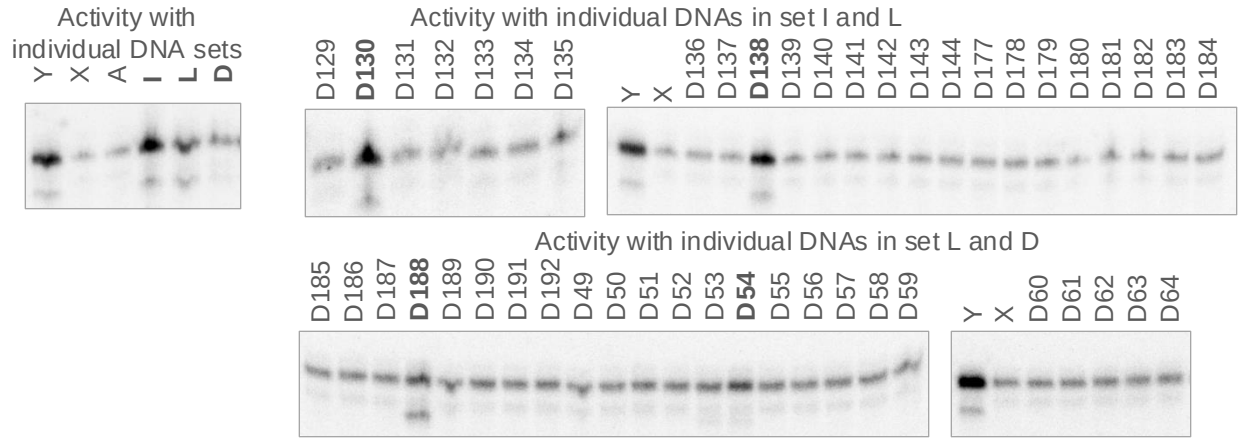
A10

R1943.2



A11

R118.7



A12

R47.2

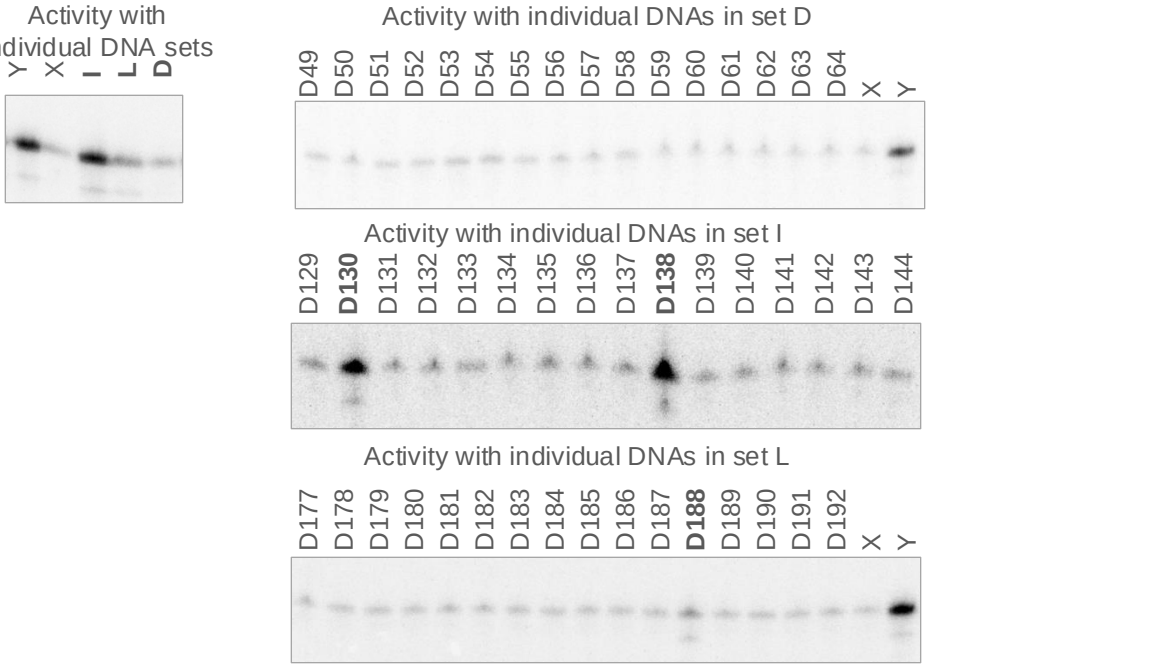


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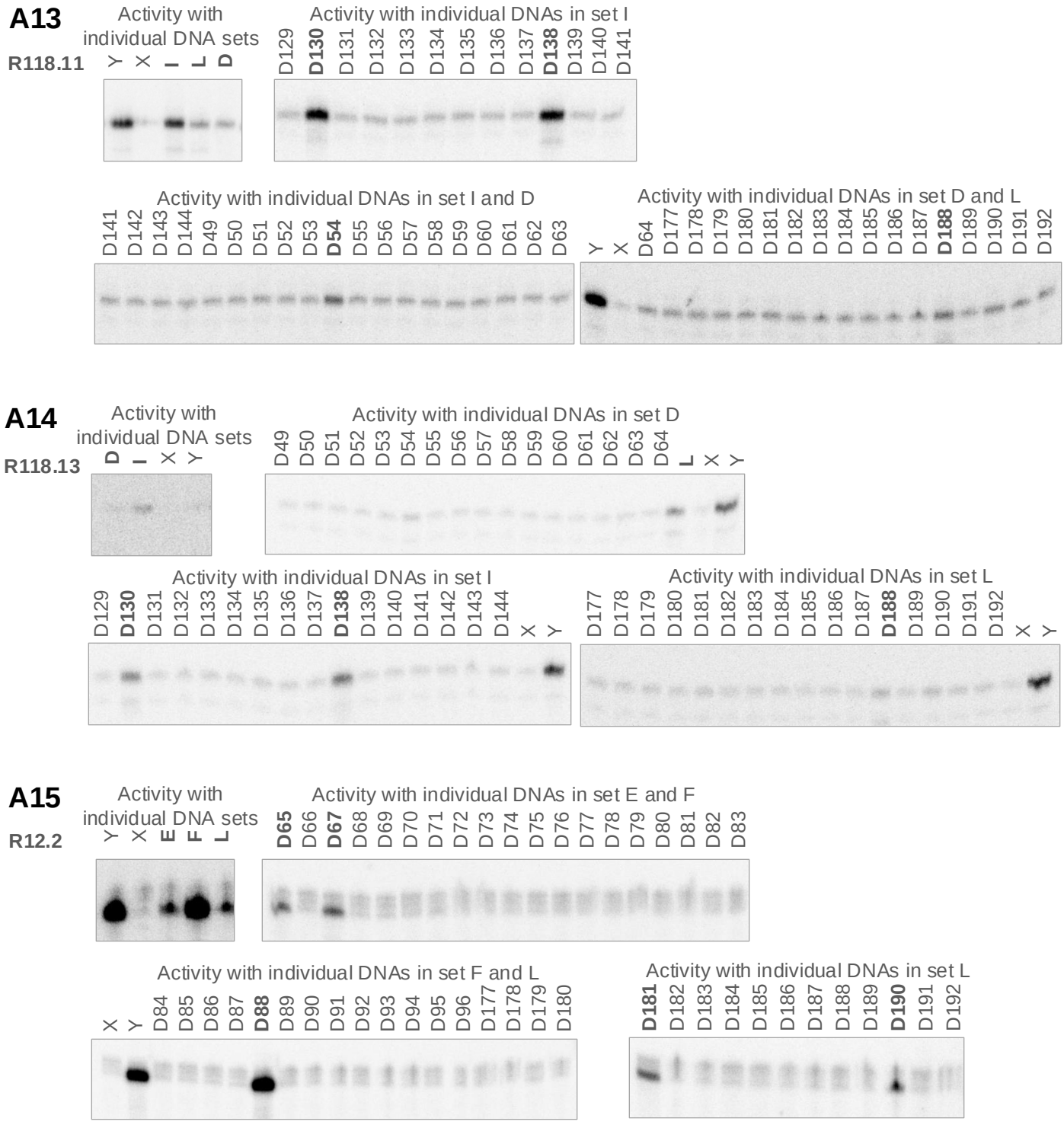


Figure S3 - continued

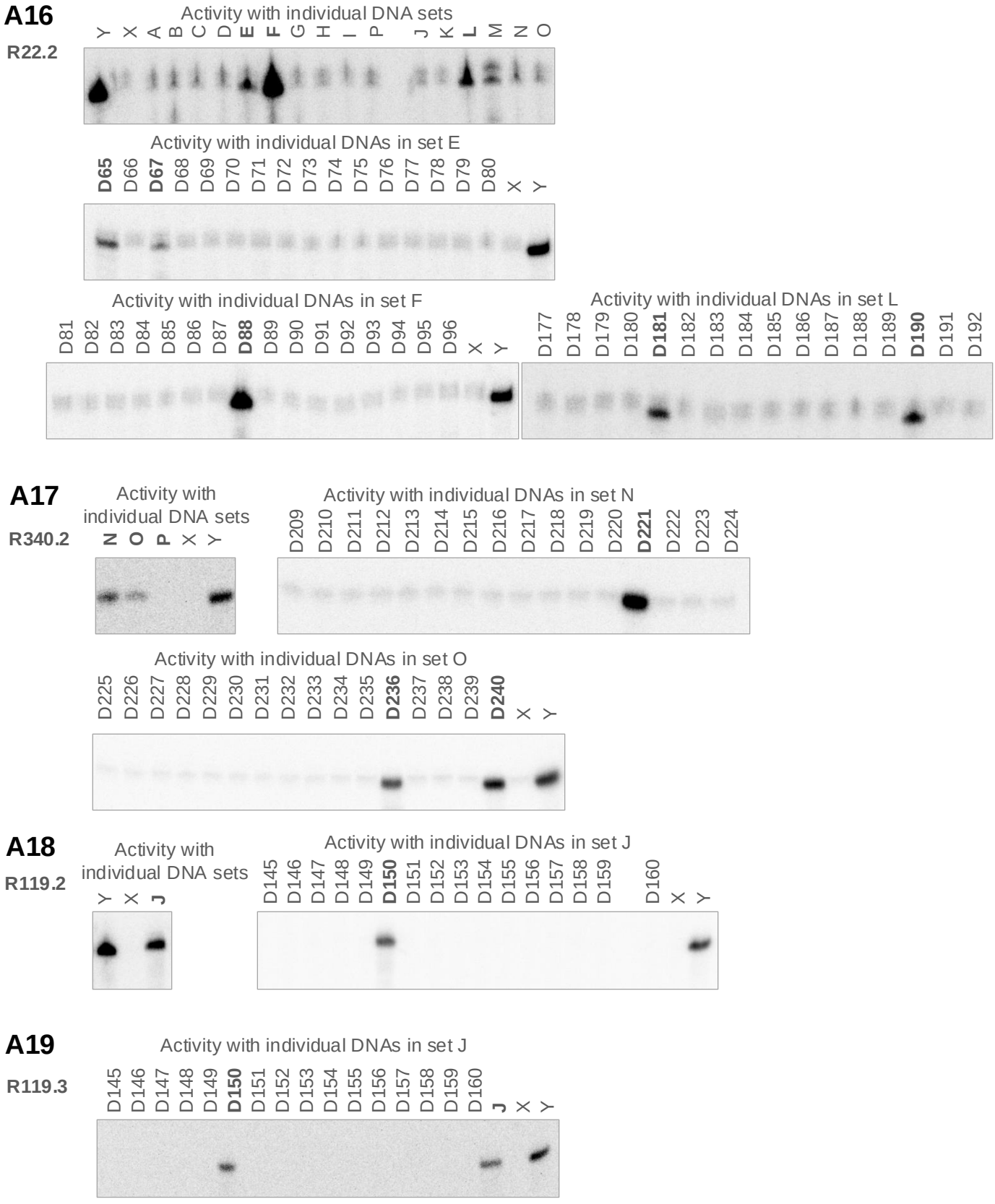


Figure S3 - continued

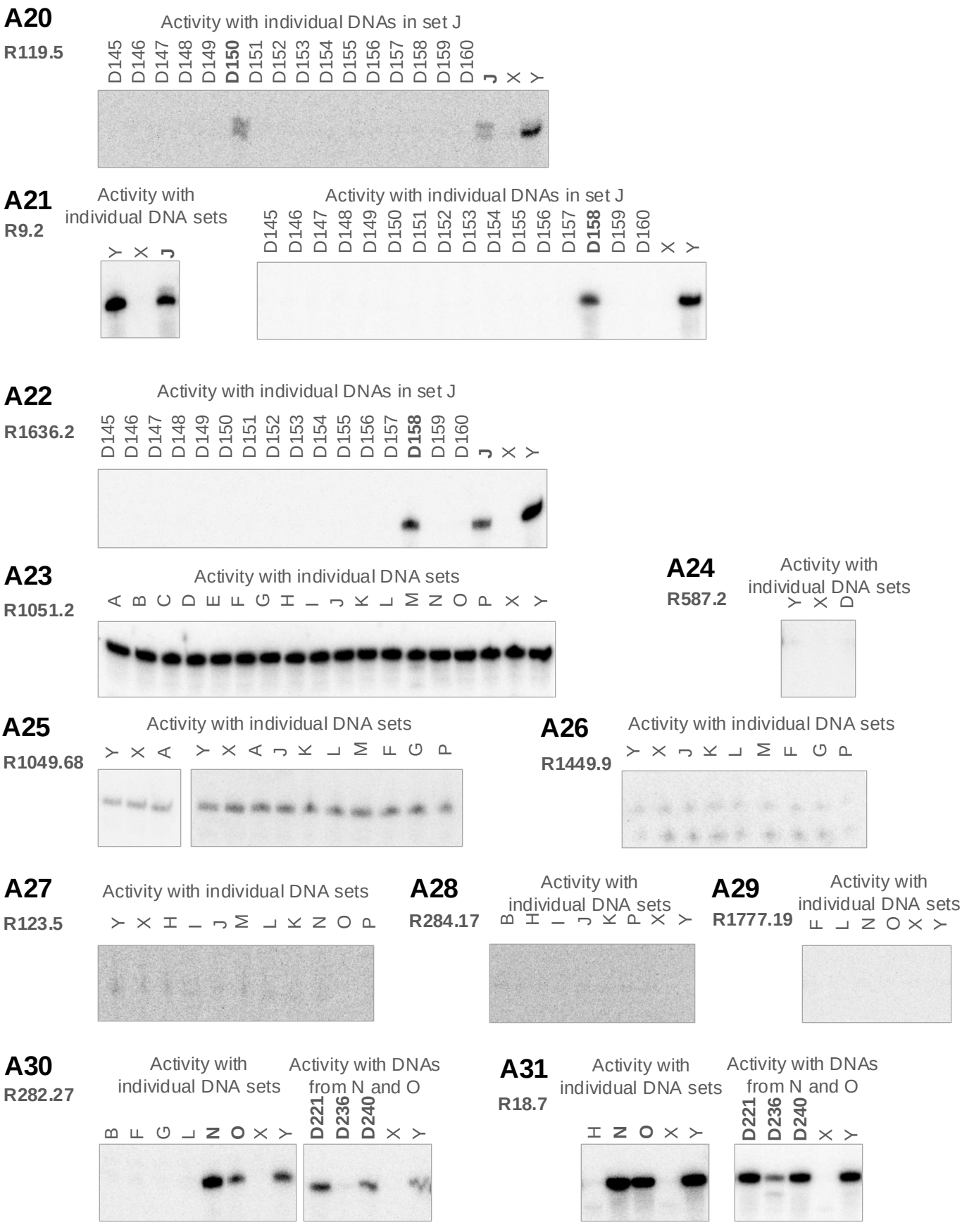
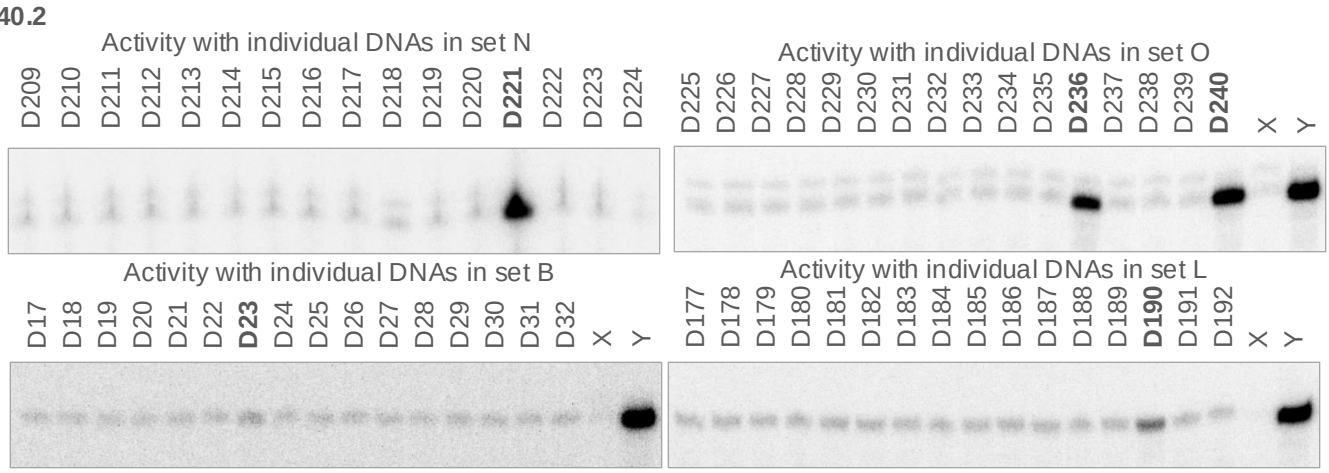


Figure S3 - continued

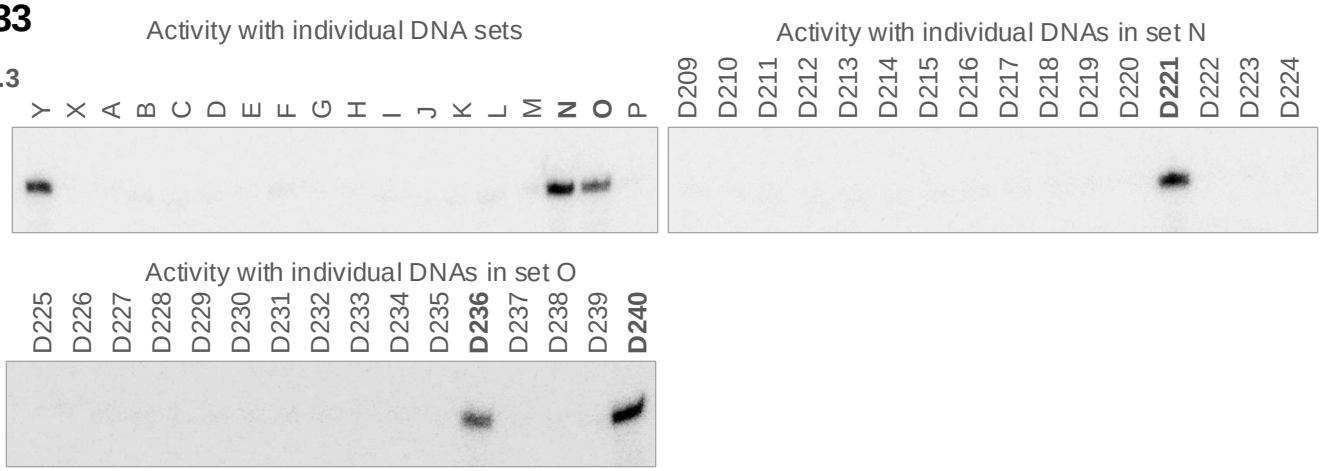
A32

R140.2



A33

R0.3



A34

R110.4

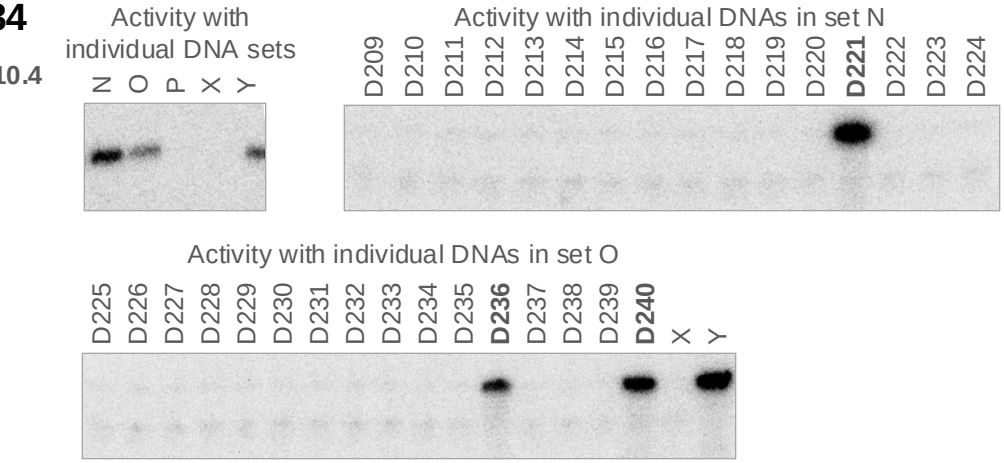


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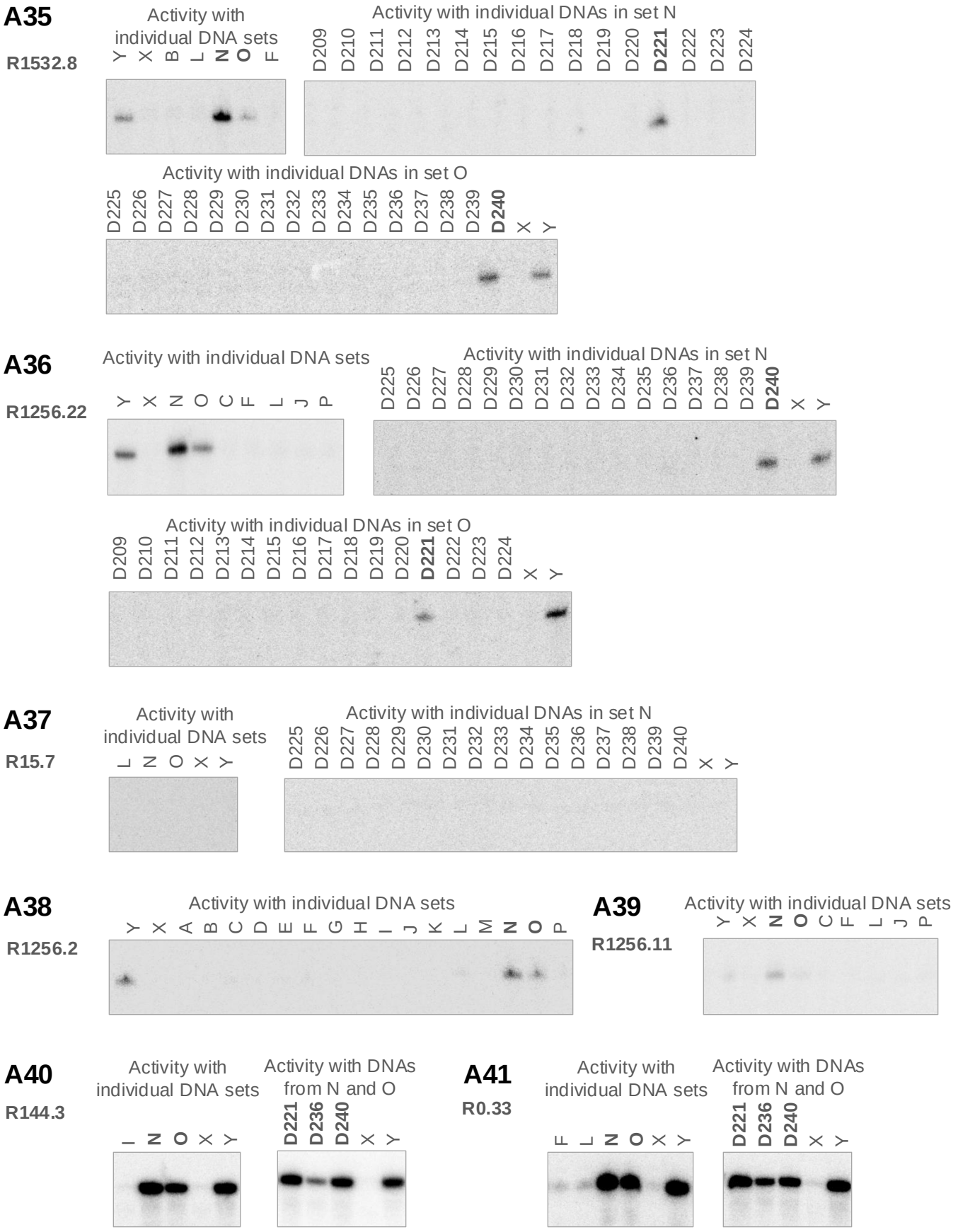


Figure S3 - continued

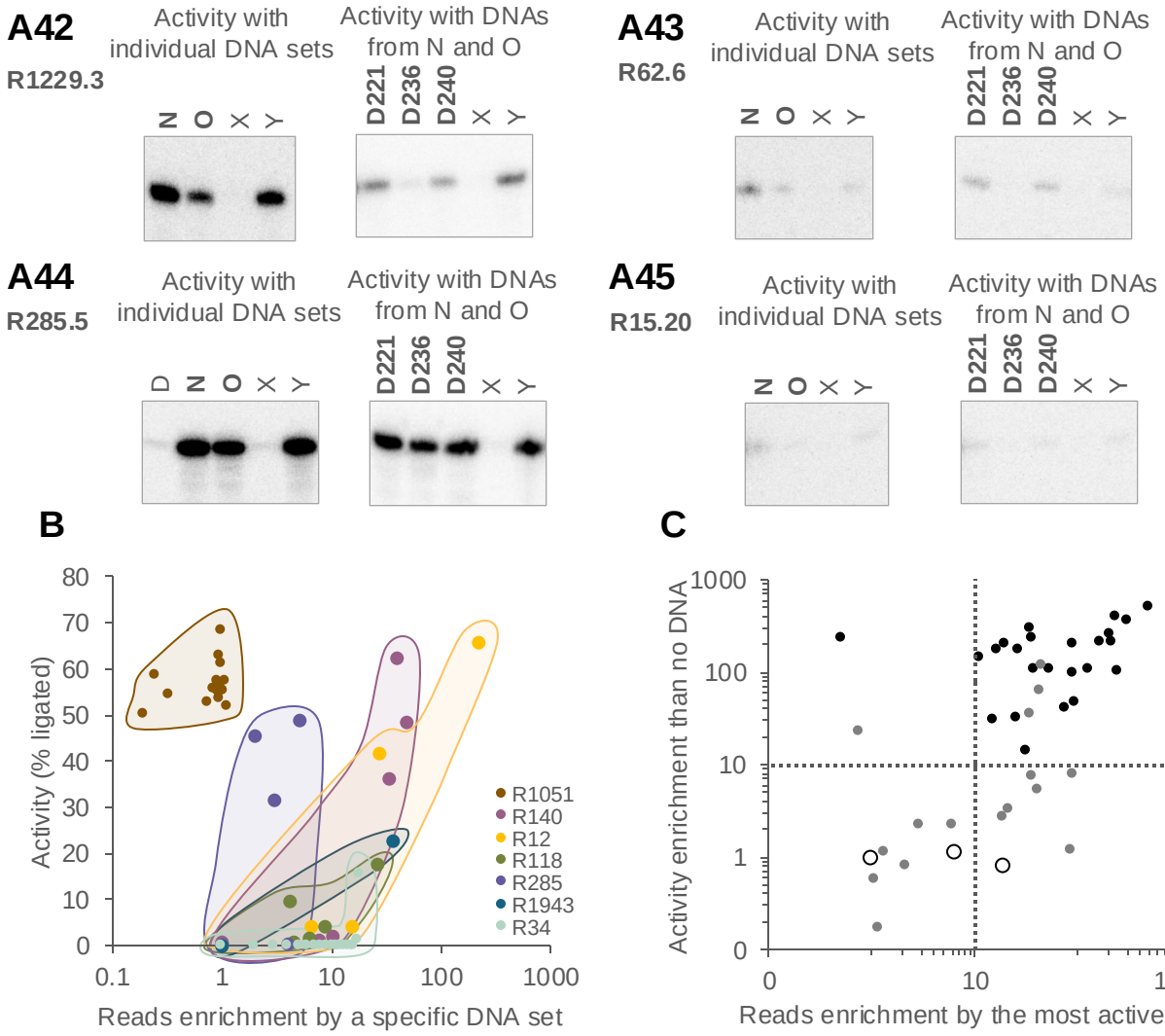


Figure S3. Biochemical assays that identified DNA cofactors required for activity by specific RNA sequences. (A1-A45) The two-step assays on 45 RNAs (45 panels) to identify DNA cofactors that can mediate RNA activity. The letters represent 16 DNA sets A-P, X represents No DNA, Y represents 256 DNAs. The name of the RNA sequence is given under each sub-panel label (e.g. R285.5 for sub-panel A44). **(B)** Correlation between biochemical activity and reads enrichment of seven RNAs with different DNA sets. The brown group (R1051) illustrated the distribution pattern of an RNA that does not require DNA for activity. The teal group (R34) illustrated the distribution pattern of an RNA that requires two different DNA sets for activity. The other groups illustrated the distribution pattern of RNAs that require one or more alternative DNA sets for activity. **(C)** Correlation between read enhancement in HTS analysis due to the presence of DNAs and the biochemical activity in the presence of each RNA's favorite DNA set. Black circles: more than 5% biochemical activity; gray circles: less than 5% biochemical activity; empty circles: RNAs didn't require DNA for activity.

Figure S4

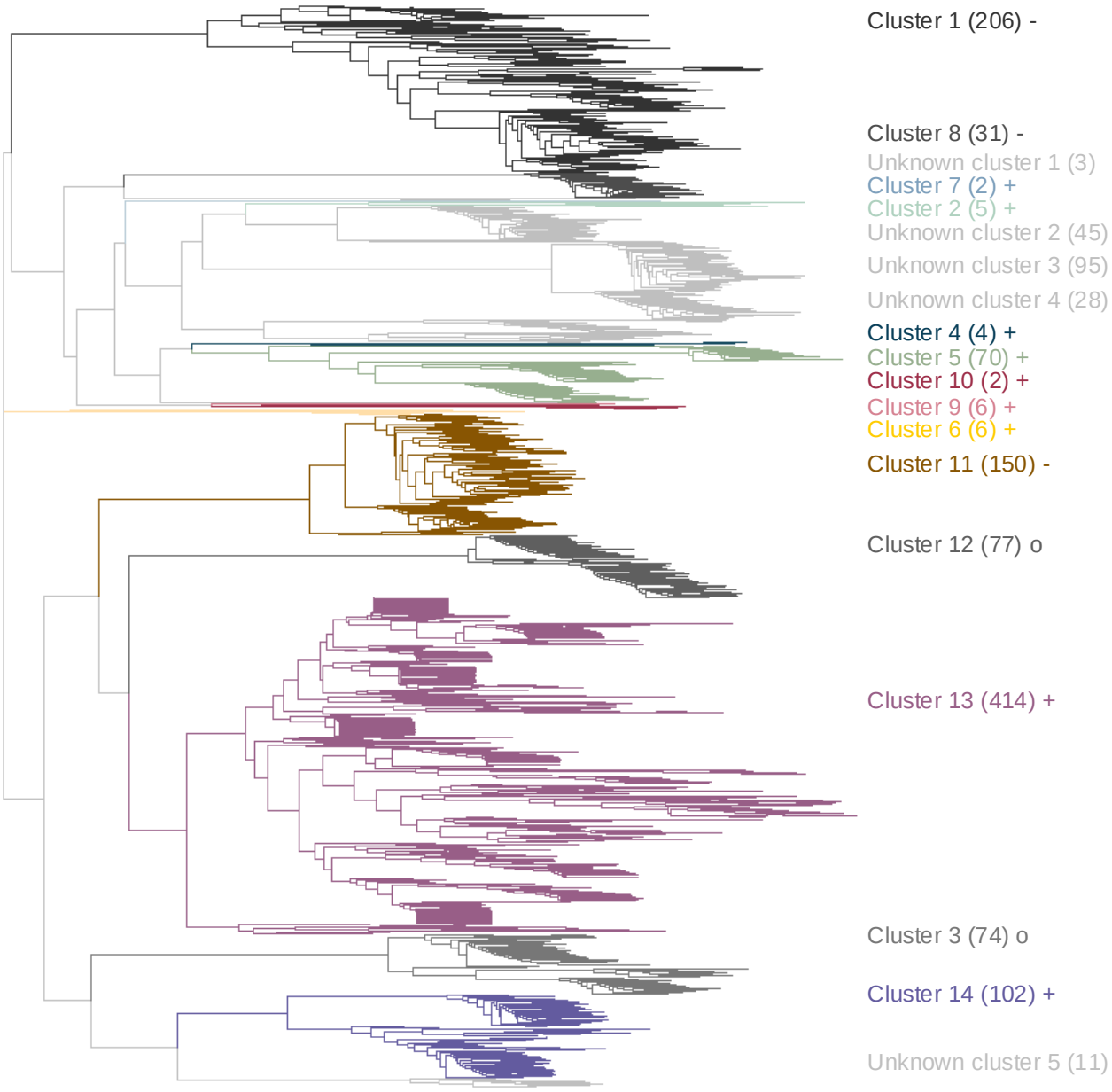


Figure S4: Sequence similarity and cluster assignment of the 1,331 RNA sequences that had at least 500 reads in selection round 6. Left: Phylogenetic tree alignment of the 1,331 sequences with clusters in different colors. Right: Names of the clusters, with the number of its identified RNA sequences in parentheses. The requirement of DNAs for activity was consistent within each cluster for all tested RNAs. RNAs from clusters 2, 4, 5, 6, 7, 9, 10, 13, 14 (611 sequences; annotated '+') depended on DNAs for activity. The RNA from cluster 11 (150 sequences) did not require DNA for activity (annotated '-'). RNAs from clusters 1, 8, 3, 12 (388 sequences) had no detectable activity (<0.1% ligated; annotated 'o'). RNAs from five clusters (182 sequences; shown in light gray) were not sampled in biochemical assays.

The estimate of DNA requirement for the total number of 1,331 RNA sequences assumes that DNA cofactor use is consistent across the entire phylogenetic tree. The estimate calculates an upper limit, a lower limit, and a 'most likely' value. The upper limit assumes that cluster 11 (150 sequences) is the only cluster not requiring DNA cofactors, corresponding to 89% of the 1,331 selected RNAs. The lower limit assumes that clusters 2, 4, 5, 6, 7, 9, 10, 13, 14 (611 sequences) are the only clusters requiring DNA cofactors, corresponding to 46% of the 1,331 selected RNAs. The 'most likely' estimate assumes that on average, all clusters behave like the RNAs in the biochemically characterized clusters that gave RNA activity data (761 sequences), with 611 DNA-dependent and 150 DNA-independent RNA sequences, corresponding to 80% of the 1,331 selected RNAs.

Figure S5

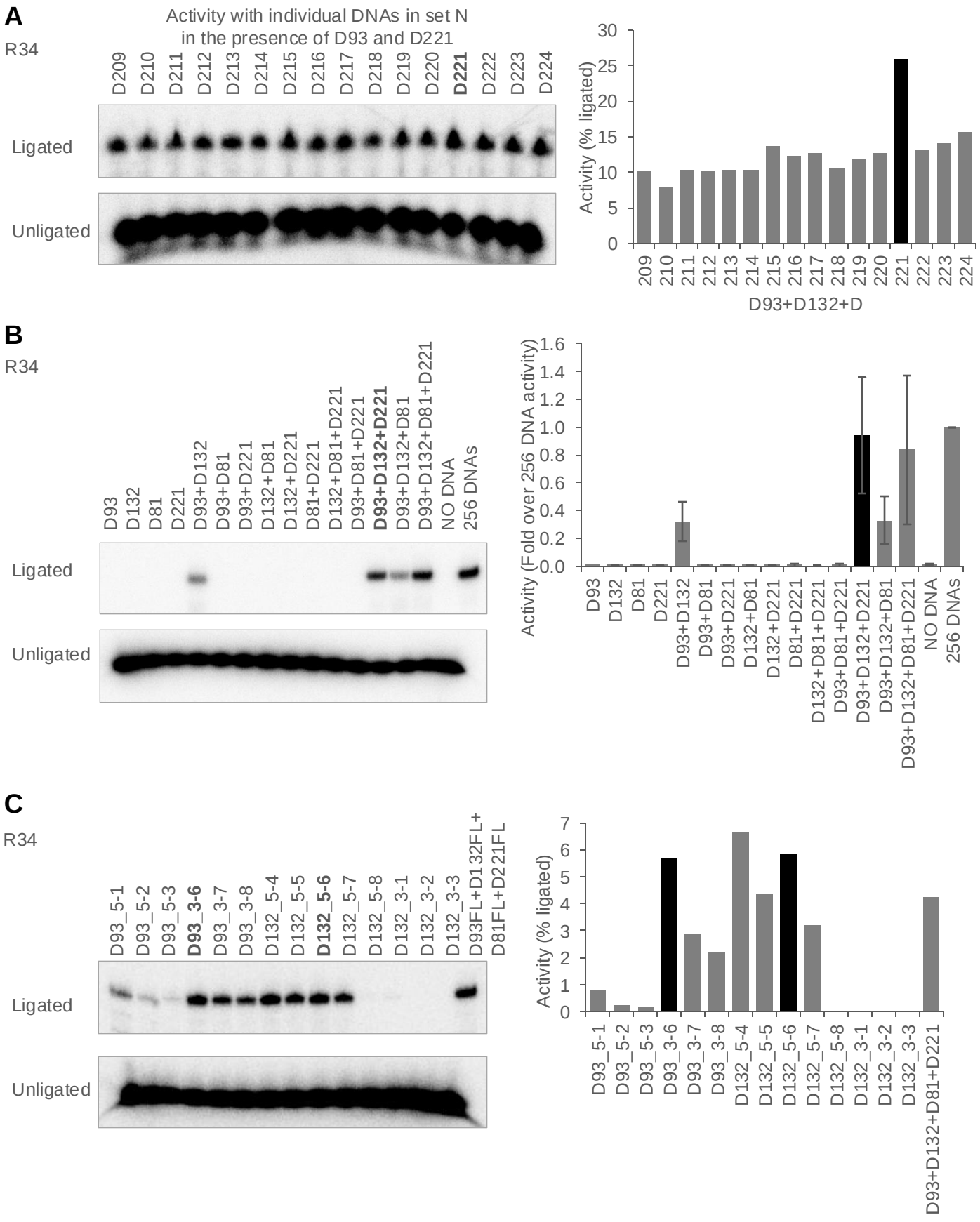

A
R34
Activity with individual DNAs in set N
in the presence of D93 and D221
D209
D210
D211
D212
D213
D214
D215
D216
D217
D218
D219
D220
D221
D222
D223
D224
Ligated
Unligated
Activity (% ligated)
D93+D132+D
B
R34
D93
D132
D81
D221
D93+D132
D93+D81
D93+D221
D132+D81
D132+D221
D81+D221
D132+D81+D221
D93+D81+D221
D93+D132+D221
D93+D132+D81
D93+D132+D81+D221
NO DNA
256 DNAs
Ligated
Unligated
Activity (Fold over 256 DNA activity)
C
R34
D93_5-1
D93_5-2
D93_5-3
D93_3-6
D93_3-7
D93_3-8
D132_5-4
D132_5-5
D132_5-6
D132_5-7
D132_5-8
D132_3-1
D132_3-2
D132_3-3
D93FL+D132FL+
D81FL+D221FL
Ligated
Unligated
Activity (% ligated)
D93+D132+D81+D221

Figure S5 - continued

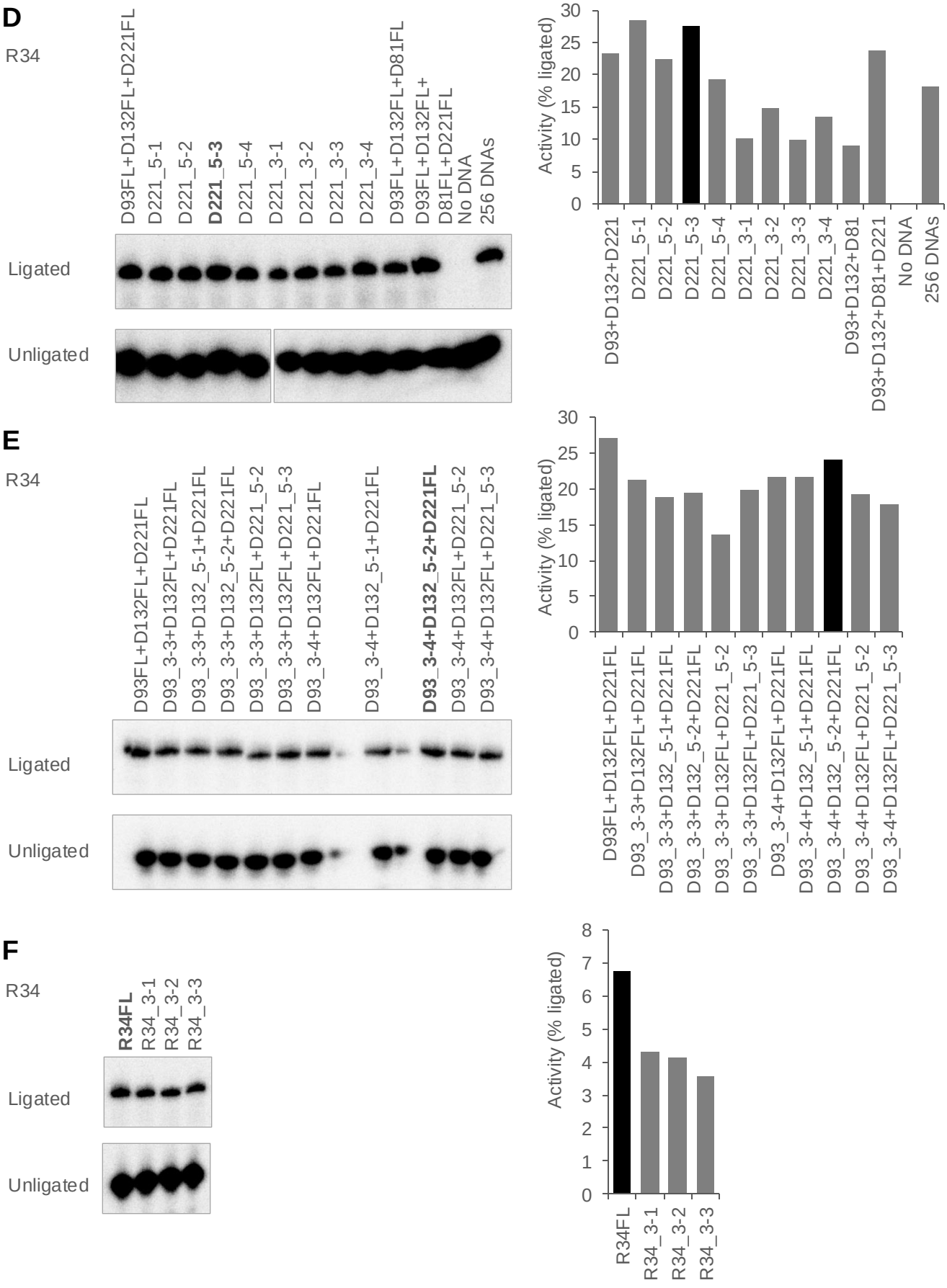


Figure S5 - continued

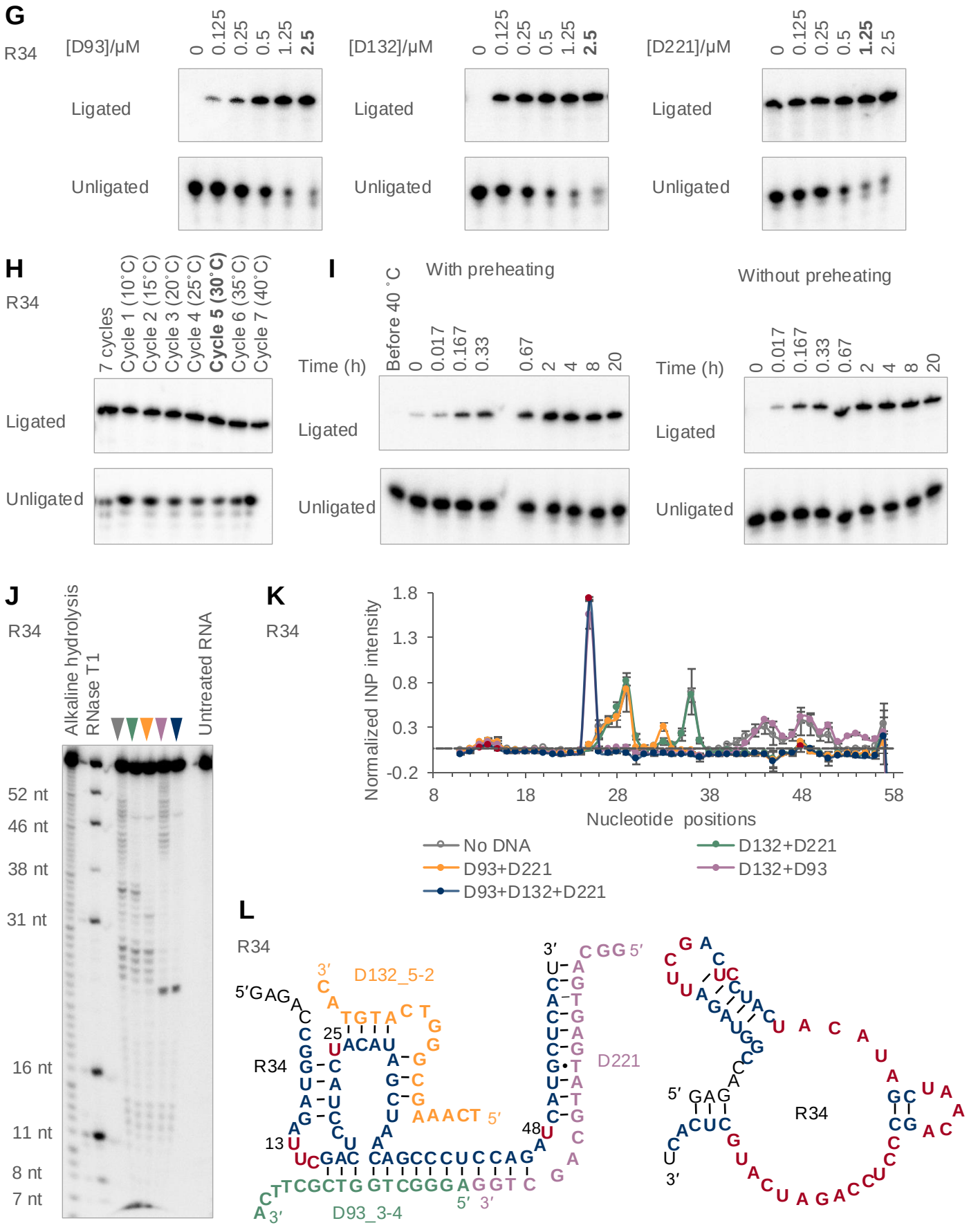


Figure S5 - continued

Figure S5. Characterization of complex R34, D93, D132 and D221. (A) Quantitatively identify the DNA cofactors from set N that can increase R34 activity in the presence of D93, D132 and D81. D221 led to about 2-fold increase of the activity. **(B)** The RNA activity with all possible combinations with D93, D132, D81 and D221. Histogram to the right of the gel showed the quantification data. The maximum activity was mediated by DNA D93, D132 and D221. **(C) and (D)** Truncation of D93, D132 and D221 at both 5′ and 3′ ends. Each DNA was truncated in the presence of the other two DNAs in full length. **(E)** The activity was tested with all three DNAs truncated, and the truncation of each DNA was slightly adjusted to maintain the activity. **(F)** Truncation of R34 at 3′ end. The assays were performed in the presence of three truncated DNAs. **(G)** Titration of each DNA cofactor up to 2.5 μM in the presence of the other two cofactors in excess amount (1.75 μM). The quantification plot is shown main figure 4. **(H)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown the main figure 4. **(I)** The kinetics of the complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantified histogram is shown the main figure 4. **(J)** In-line probing of the complex. The R34 was incubated with alkaline hydrolysis buffer, RNase T1, triphosphorylation buffer without DNA, triphoshorylation buffer with every two DNAs and all three DNAs (the five colors indicate different DNA components as shown in K). **(K)** The quantification of the in-line probing. The intensity of each band was normalized to the untreated RNA lane. The critical value of intensity indicating flexible and constrained nucleotides is 0.06. The gray line with empty circles indicated the structure without DNA; the green line with filled circles indicated the structure of D93; the pink line and filled circles indicated the structure of D221; the orange line with filled circles indicated the structure of D132; the blue and red filled circles indicated the constrained nucleotides and flexible nucleotides respectively in the presence of three DNAs. **(L)** The secondary structure models of R34 D93 D132 D221 complex and only the R34. The colors of nucleotides corresponded with the quantification plot.

Figure S6

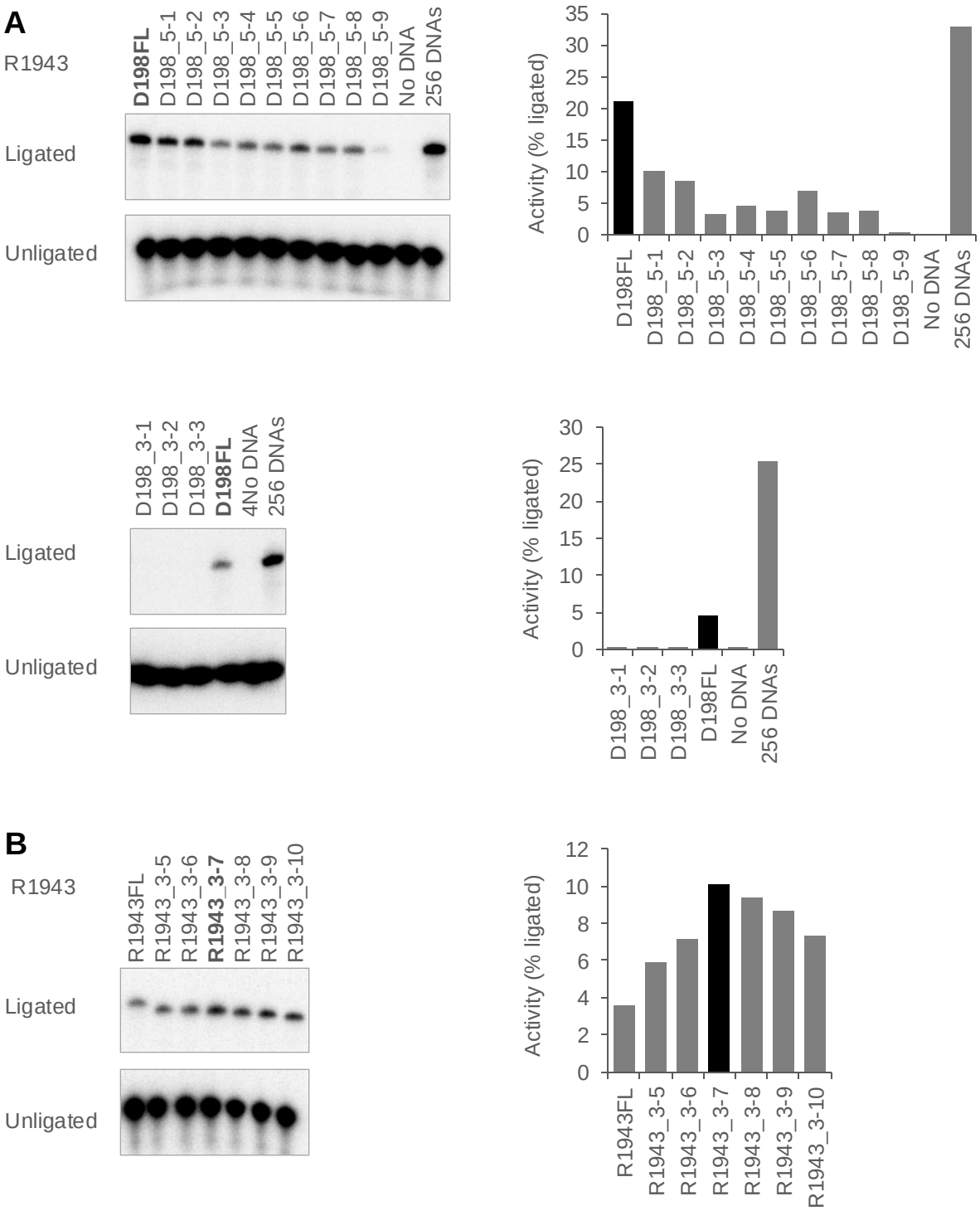

A
R1943
D198FL
D198_5-1
D198_5-2
D198_5-3
D198_5-4
D198_5-5
D198_5-6
D198_5-7
D198_5-8
D198_5-9
No DNA
256 DNAs
Ligated
Unligated
Activity (% ligated)
D198_3-1
D198_3-2
D198_3-3
D198FL
4No DNA
256 DNAs
B
R1943
R1943FL
R1943_3-5
R1943_3-6
R1943_3-7
R1943_3-8
R1943_3-9
R1943_3-10

Figure S6 - continued

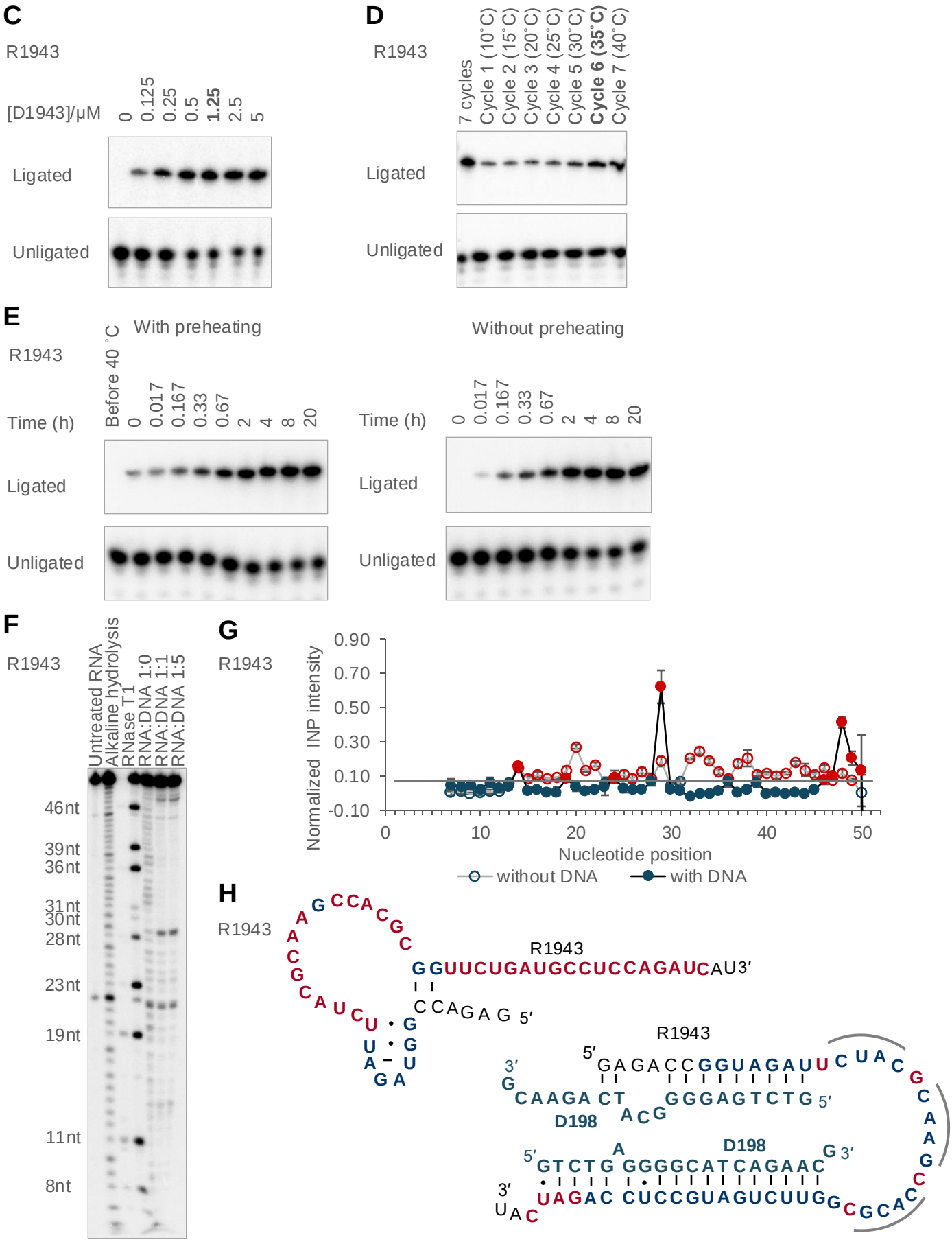


Figure S6 - continued

Figure S6. Characterization of complex R1943 and D198. (A) Truncation of D198 at both 5′ and 3′ ends. The activity of this complex fluctuated within replicates of different D198 truncations, so the D198 was kept full length. **(B)** Truncation of R1943 at the 3′ end. 7 nucleotides were truncated in the following assays. **(C)** Titration of D198 up to 5 μM. The quantification and fitting curve is shown the main figure 5. **(D)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown the main figure 5. **(E)** The kinetic analysis of this complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantified histogram is shown in main figure 5. **(F)** In-line probing of the complex. R1943 was incubated in water, alkaline hydrolysis buffer, RNase T1, Tmp reaction buffer without DNA, and Tmp reaction buffer with different amount of D198 respectively. **(G)** Quantification of the in-line probing data. The intensity of each band was normalized to the untreated RNA and the critical value of intensity indicating flexible or constrained nucleotides is 0.07. The gray line with empty circles indicated the structure without DNA; the black line with filled circles indicated the structure in presence of DNA; the blue and red circles indicated the constrained nucleotides and flexible nucleotides respectively. **(K)** The secondary structure models of complex R1943 D198 and R1943 self structure. The colors of nucleotides corresponded with the quantification plot.

Figure S7

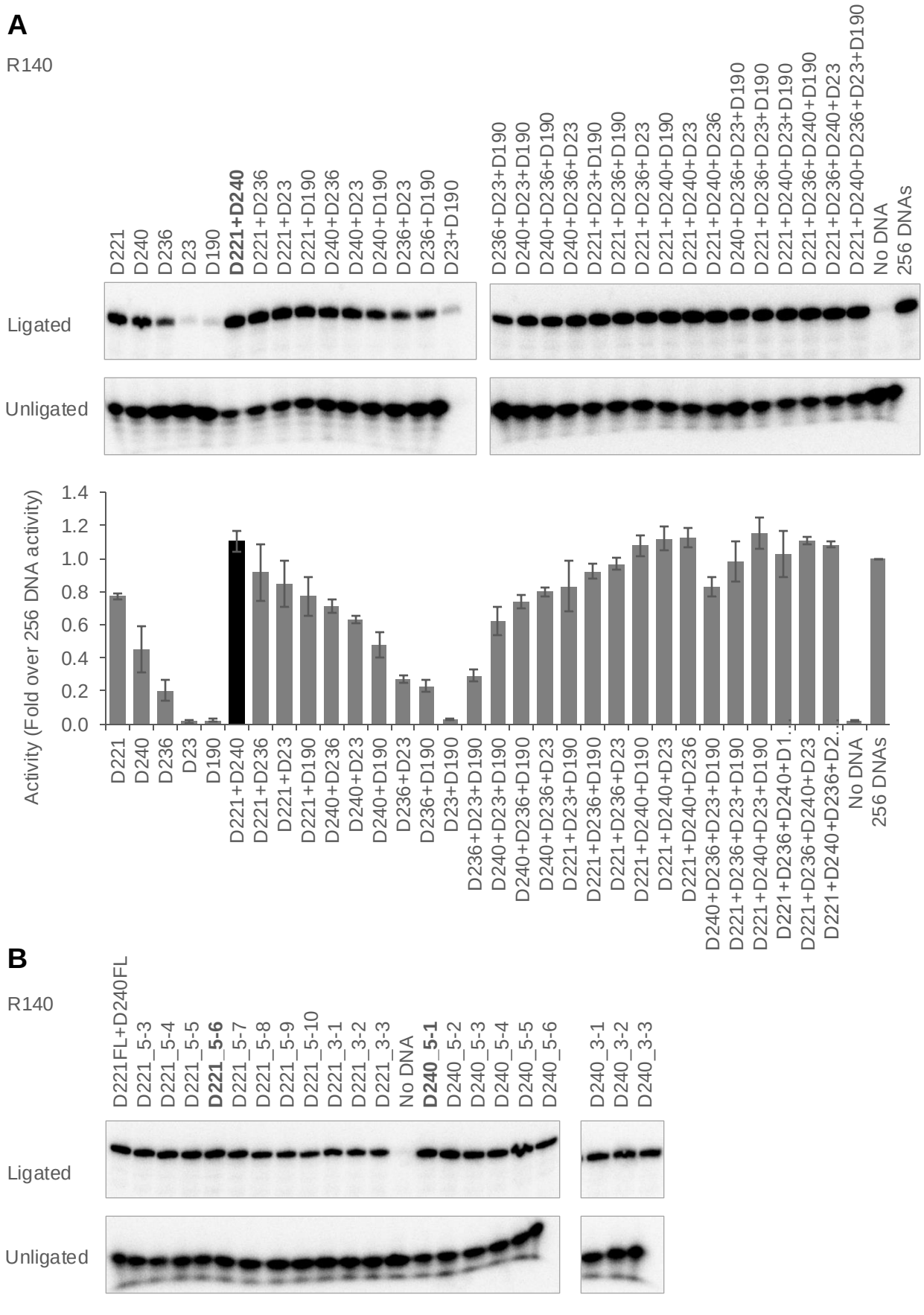
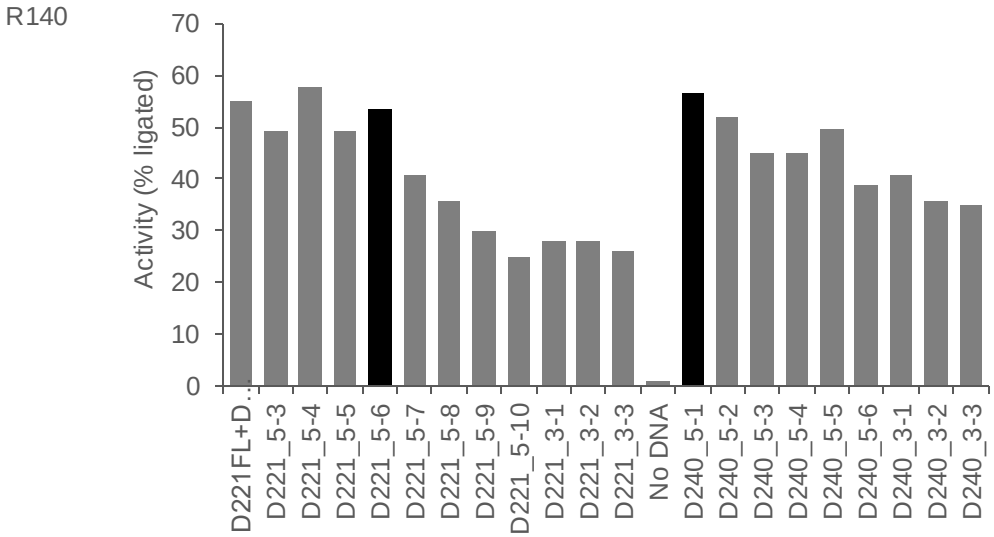
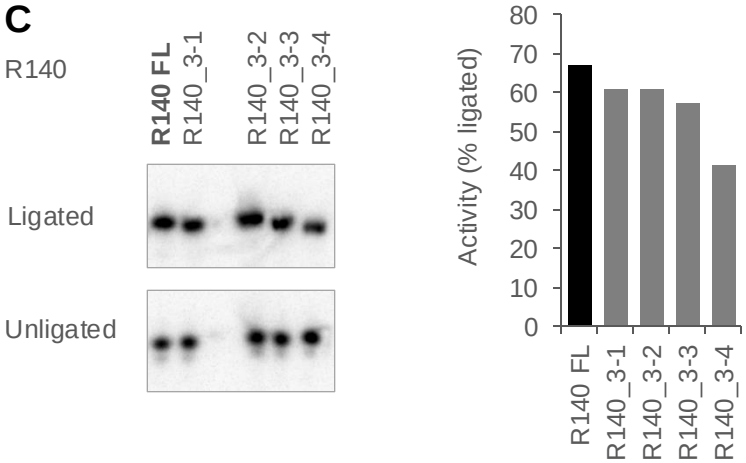

A
R140
D221
D240
D236
D23
D190
D221+D240
D221+D236
D221+D23
D221+D190
D240+D236
D240+D23
D240+D190
D236+D23
D236+D190
D23+D190
D236+D23+D190
D240+D23+D190
D240+D236+D190
D240+D236+D23
D240+D236+D23
D221+D23+D190
D221+D236+D190
D221+D236+D23
D221+D240+D190
D221+D240+D23
D221+D240+D236
D240+D236+D23+D190
D221+D236+D23+D190
D221+D240+D23+D190
D221+D236+D240+D190
D221+D236+D240+D23
D221+D240+D236+D23+D190
No DNA
256 DNAs
Ligated
Unligated
Activity (Fold over 256 DNA activity)
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
B
R140
D221FL+D240FL
D221_5-3
D221_5-4
D221_5-5
D221_5-6
D221_5-7
D221_5-8
D221_5-9
D221_5-10
D221_3-1
D221_3-2
D221_3-3
No DNA
D240_5-1
D240_5-2
D240_5-3
D240_5-4
D240_5-5
D240_5-6
D240_3-1
D240_3-2
D240_3-3
Ligated
Unligated

Figure S7 - continued

B - continued



C



D

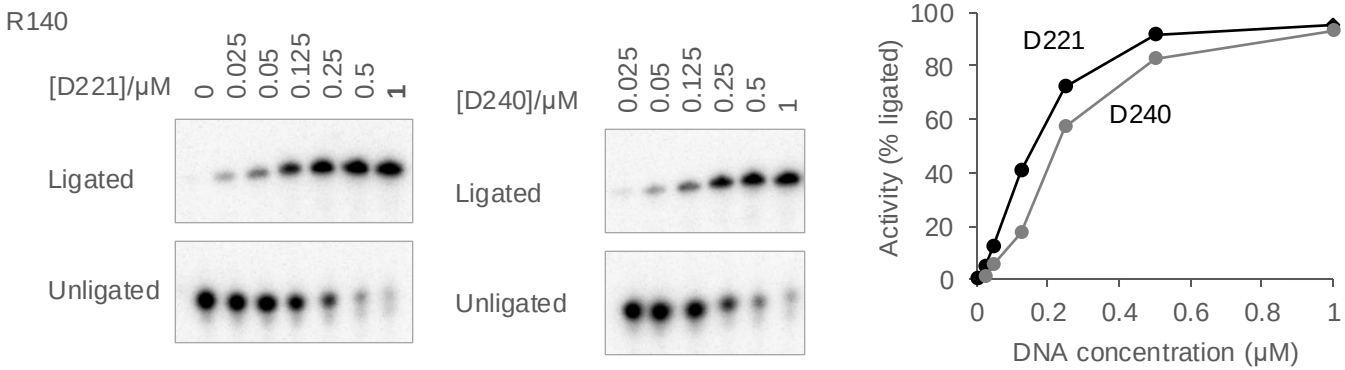


Figure S7 - continued

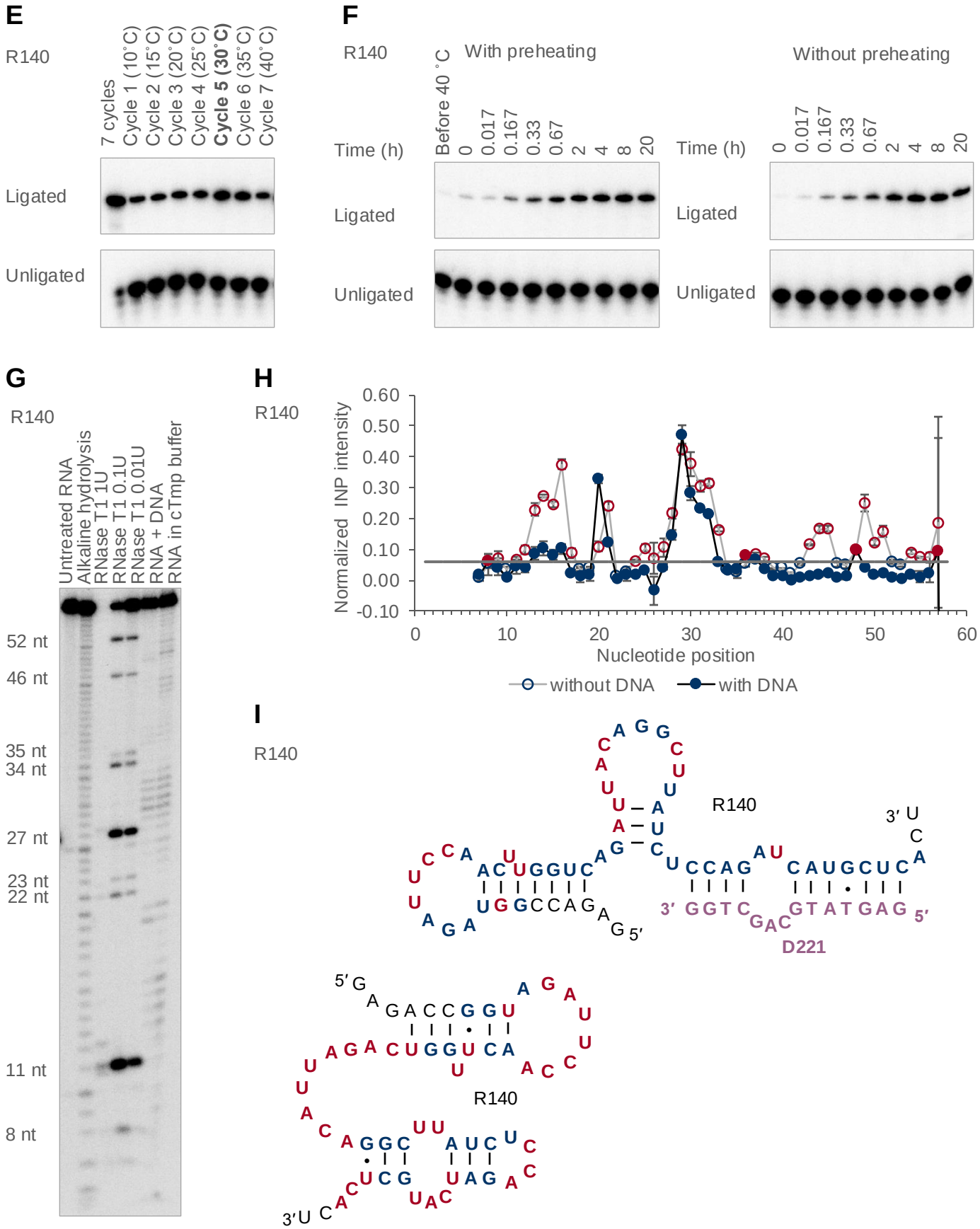


Figure S7 - continued

Figure S7. Characterization of complex R140 and D221. (A) Identification of the minimal group of DNAs that can mediate maximum activity. The RNA activity with all possible combinations of D221, D236, D240, D23 and D190. D221 and D240 together mediated the maximum activity. **(B)** Truncation of D221 and D240. D221 was truncated 6 nucleotides at 3′ end and D240 was truncated 1 nucleotide at 5′ end. **(C)** Truncation assay of R140 in the presence of truncated D221 and D236. R140 was kept full length for constantly high activity. **(D)** Titration of each DNA cofactor up to 1 μM in the absence of the other cofactor. The curve plot showed the individual effect of each DNA cofactor. The diamond point in the plot showed the best condition (1 μM D221_5-6) used in the following assays. The fitting curve of D221 is in main figure 7. **(E)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown the main figure 7. **(F)** The kinetic analysis of the complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantification histogram is shown the main figure 6. **(G)** In-line probing analysis. R140 was incubated with water, alkaline hydrolysis buffer, RNase T1, Tmp reaction buffer with D221 and without DNA. **(H)** The quantification of the in-line probing data. The intensity of each band was normalized to the untreated RNA and the critical value of intensity indicating flexible or constrained nucleotides is 0.06. The gray line with empty circles indicated the structure without DNA; the black line with filled circles indicated the structure in the presence of DNA; the blue and red circles indicated constrained and flexible nucleotides respectively. **(I)** The secondary structure models of complex R140 D221 and R140 self structure. The colors of nucleotides corresponded with the quantification plot.

Figure S8

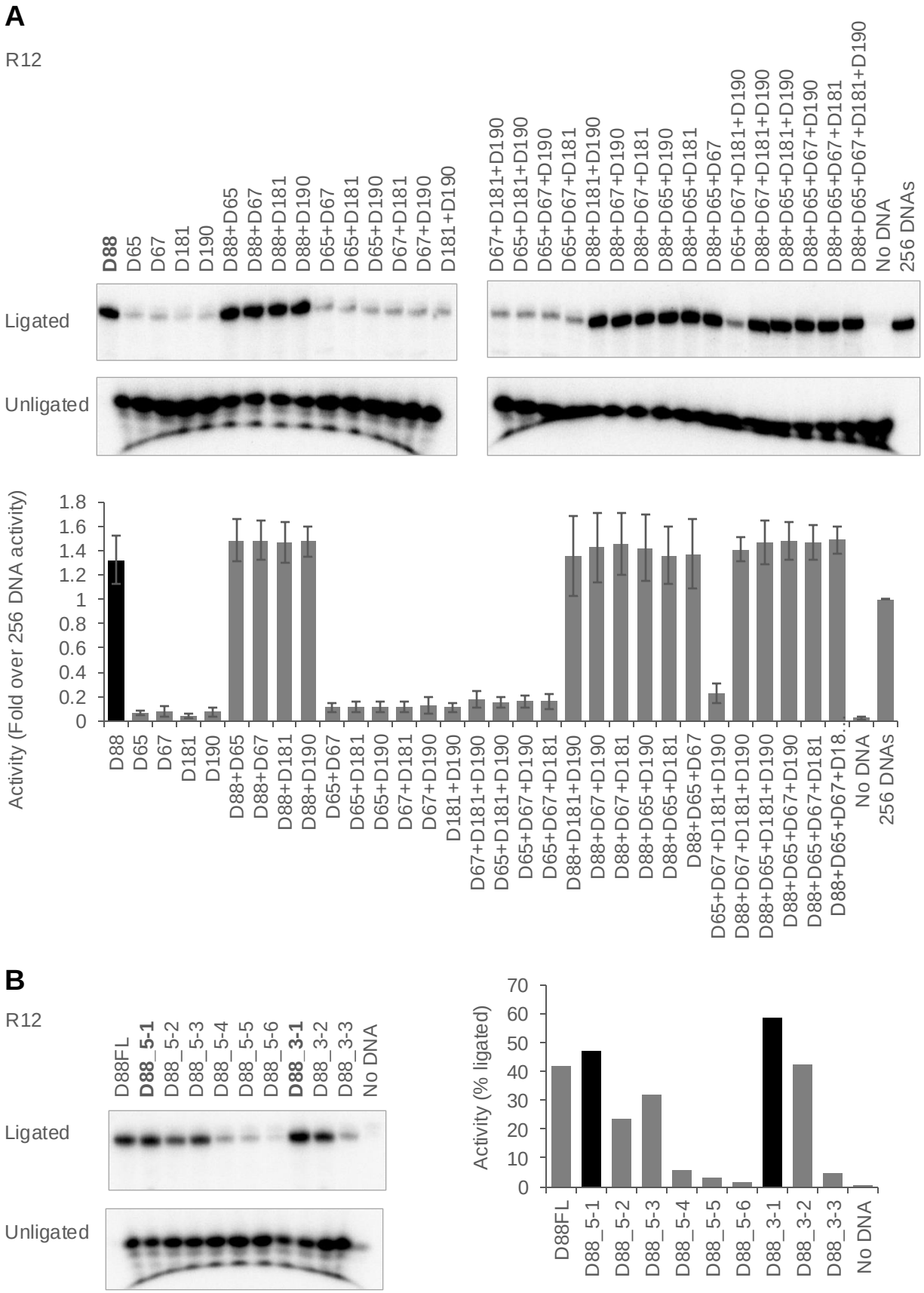

A
R12
D88
D65
D67
D181
D190
D88+D65
D88+D67
D88+D181
D88+D190
D65+D67
D65+D181
D65+D190
D67+D181
D67+D190
D181+D190
D67+D181+D190
D65+D181+D190
D65+D67+D190
D65+D67+D181
D88+D181+D190
D88+D67+D190
D88+D67+D181
D88+D65+D190
D88+D65+D181
D88+D65+D67
D65+D67+D181+D190
D88+D67+D181+D190
D88+D65+D181+D190
D88+D65+D67+D190
D88+D65+D67+D181
D88+D65+D67+D181+D190
No DNA
256 DNAs
Ligated
Unligated
Activity (Fold over 256 DNA activity)
1.8
1.6
1.4
1.2
1
0.8
0.6
0.4
0.2
0
B
R12
D88FL
D88_5-1
D88_5-2
D88_5-3
D88_5-4
D88_5-5
D88_5-6
D88_3-1
D88_3-2
D88_3-3
No DNA
Ligated
Unligated
Activity (% ligated)
70
60
50
40
30
20
10
0

Figure S8 - continued

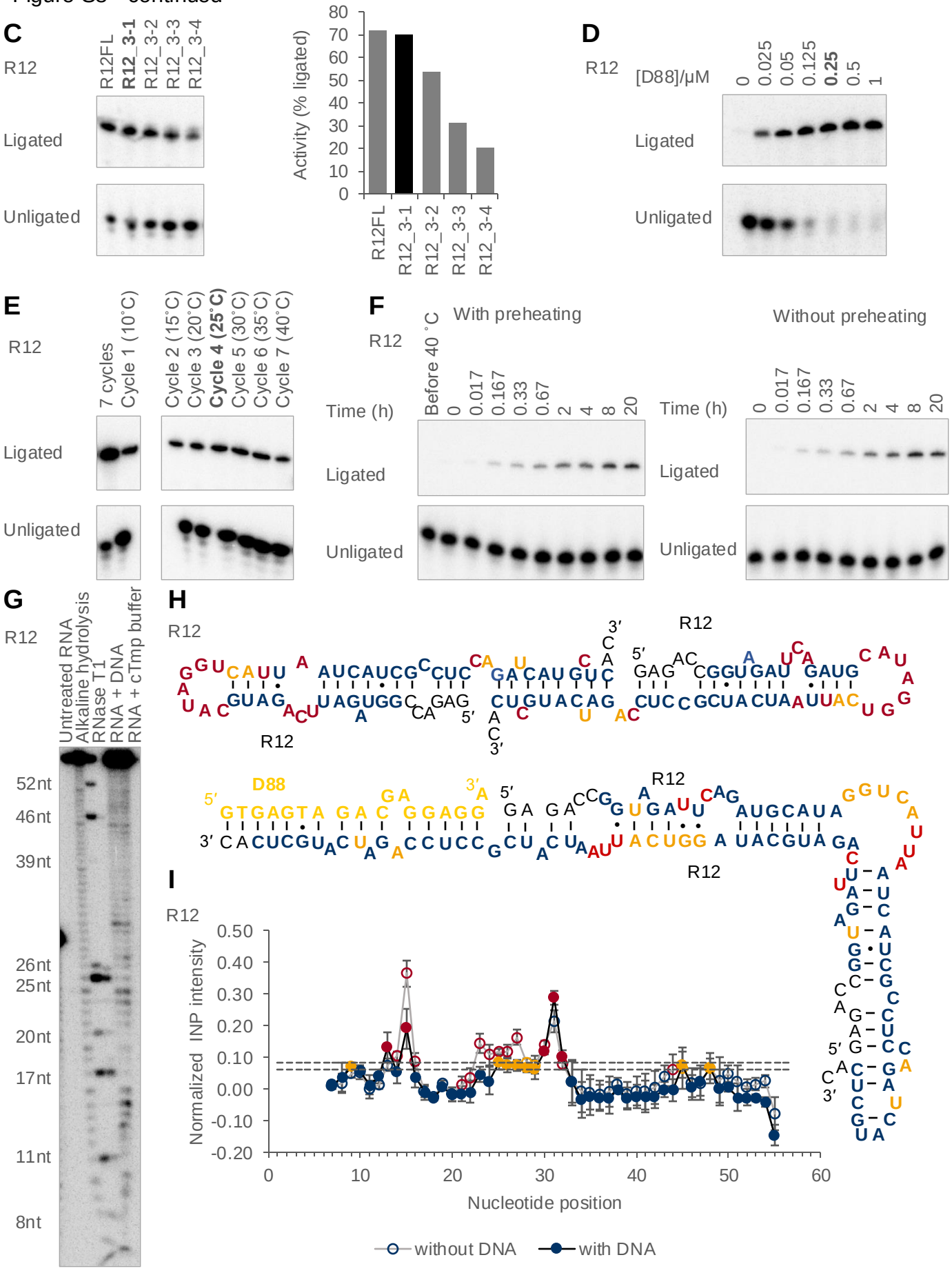


Figure S8 - continued

Figure S8. Characterization of complex R12 and D88. (A) Identification of the minimal group of DNAs that can mediate highest activity. The RNA activity with all possible combinations of D88, D65, D67, D181 and D190. D88 mediated the maximum activity. **(B)** Truncation of D88 at both 5′ and 3′ ends. One nucleotide was truncated from both ends. **(C)** Truncation of R12 at 3′ end in the present of truncated D88. R12 was truncated 1 nucleotide at 3′ end. **(D)** Titration of D88 up to 1 μM. The fitting curve is shown in main figure 7. **(E)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown the main figure 8. **(F)** The kinetic analysis of the complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantification histogram is shown the main figure 8. **(G)** In-line probing analysis of the complex. R12 was incubated with water, alkaline hydrolysis buffer, RNase T1, Tmp reaction buffer with D88 and without DNA. **(H)** The secondary structure models of complex R12 D88 and R12 self structure. Since the binding curve indicated one D88 activating two molecules of R12 (figure 8), a structure with two R12 and one D88 was proposed. The R12 sequence was also highly self complementary that could form a dimer structure stabilized by a long duplex. The colors of nucleotides corresponded with the quantification plot I. **(I)** The quantification of the in-line probing data. The intensity of each band was normalized to the untreated RNA. This data was interpreted as a mixture of two possible structures at each nucleotide position. In the presence of D88, two critical values 0.0610 and 0.0846 separated the nucleotide positions into constrained (blue), mixed structures (yellow) and flexible (red) nucleotides. In the absence of DNA, R12 molecules could form the same structure as with DNA, or fold into a different new structure (shown in I). Therefore, the structure without DNA was determined by the difference from the RNA/DNA complex. The positions showed significant decrease (difference larger than the standard deviation) were regarded as constrained (blue); the positions showed significant increase were regarded as flexible (red); those positions with insignificant difference were regarded as the same status as the structure with DNA. The gray line with empty circles indicated the structure without DNA; the black line with filled circles indicated the structure in the presence of DNA.

Figure S9

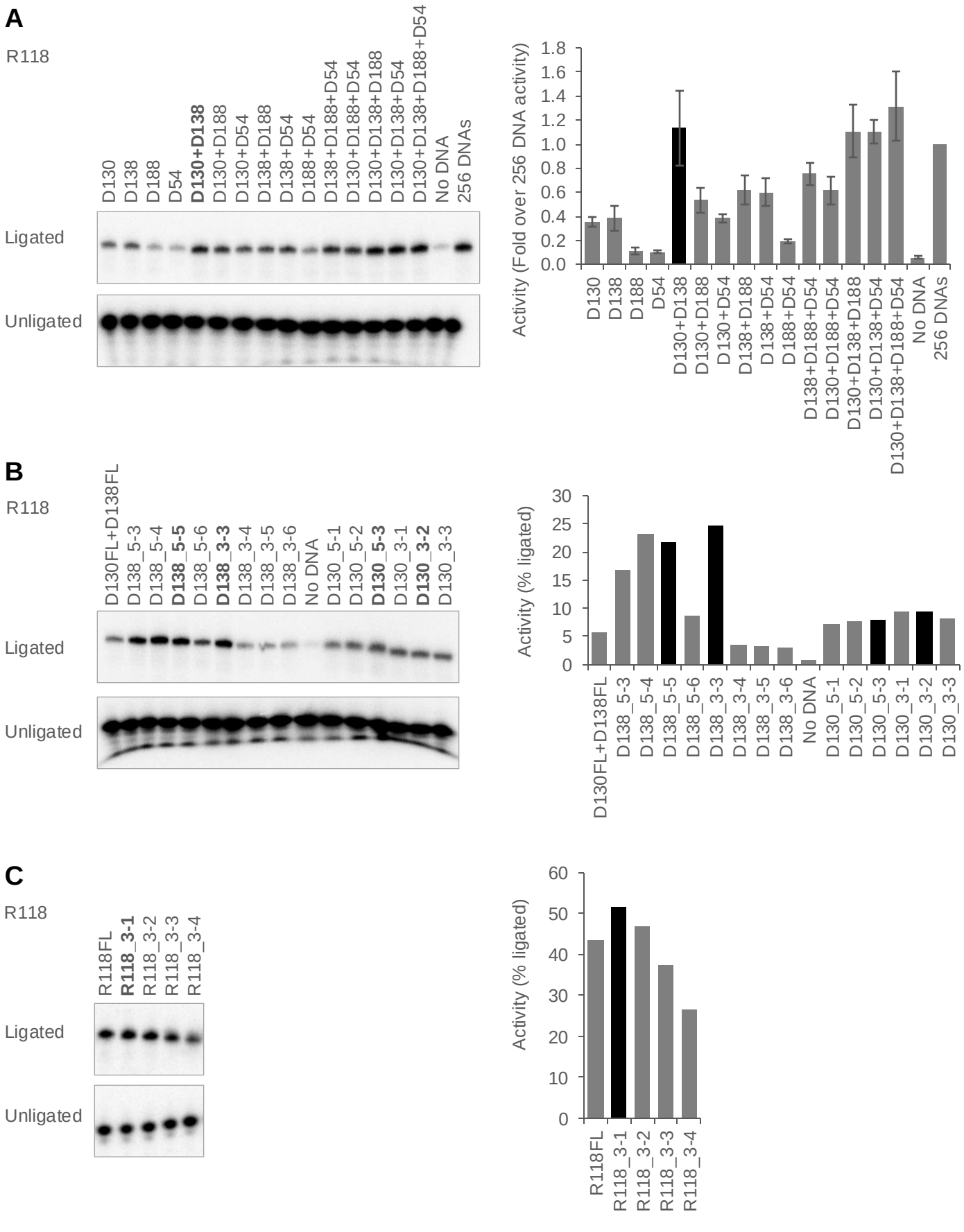

A
R118
D130
D138
D188
D54
D130+D138
D130+D188
D130+D54
D138+D188
D138+D54
D188+D54
D138+D188+D54
D130+D188+D54
D130+D138+D188
D130+D138+D54
D130+D138+D188+D54
No DNA
256 DNAs
Ligated
Unligated
Activity (Fold over 256 DNA activity)
1.8
1.6
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
B
R118
D130FL+D138FL
D138_5-3
D138_5-4
D138_5-5
D138_5-6
D138_3-3
D138_3-4
D138_3-5
D138_3-6
No DNA
D130_5-1
D130_5-2
D130_5-3
D130_3-1
D130_3-2
D130_3-3
Ligated
Unligated
Activity (% ligated)
30
25
20
15
10
5
0
C
R118
R118FL
R118_3-1
R118_3-2
R118_3-3
R118_3-4
Ligated
Unligated
Activity (% ligated)
60
50
40
30
20
10
0

Figure S9 - continued

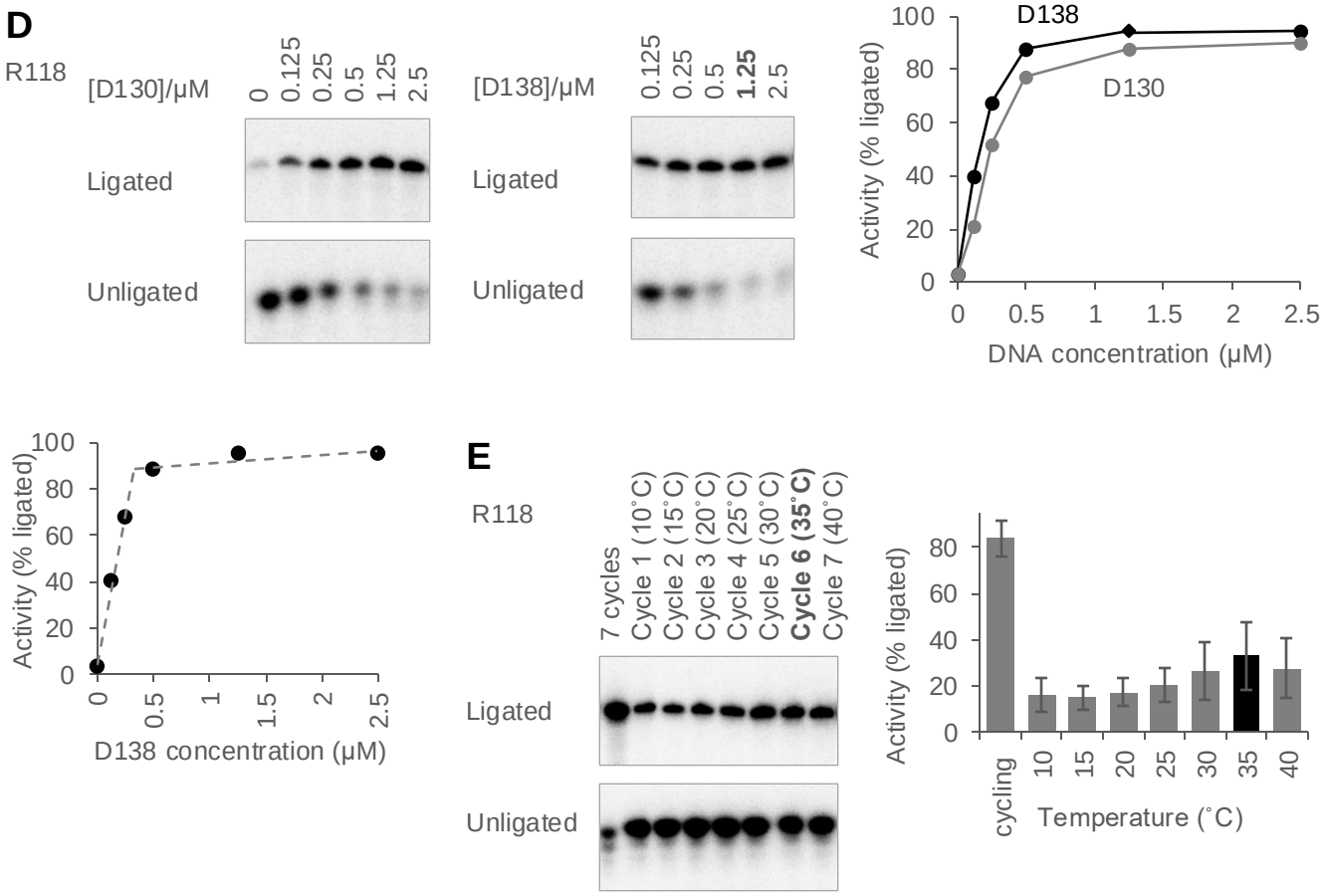


Figure S9 - continued

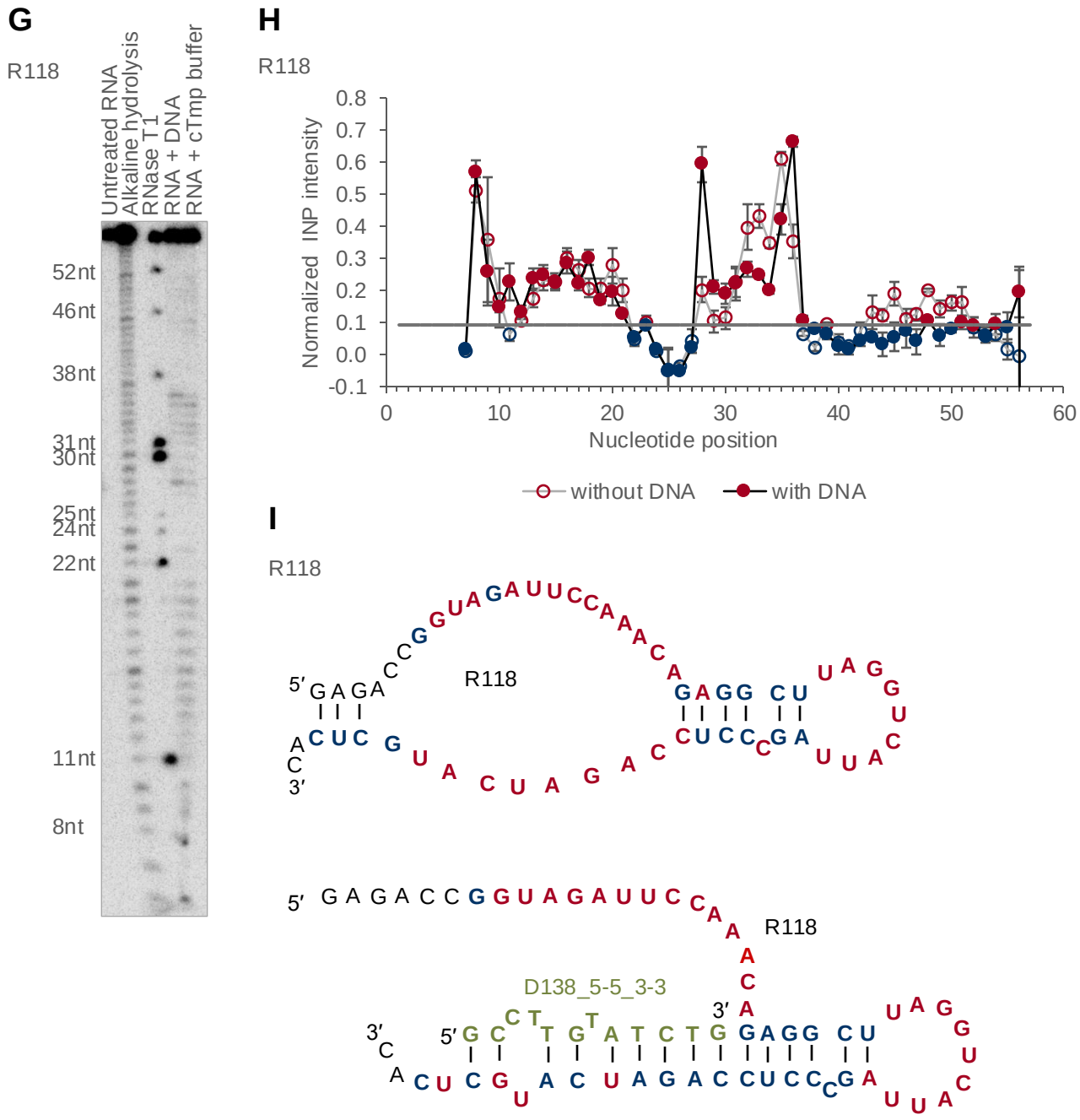


Figure S9 - continued

Figure S9. Characterization of complex R118 and D138. (A) Identification of the minimal group of DNAs that can mediate highest activity. The RNA activity with all possible combinations of D130, D138, D188 and D54. D130 and D138 together mediated the maximum activity **(B)** Truncation of D130 and D138 at 5′ and 3′ end individually with the other one in full length. D130 was truncated 3 nucleotides at 5′ end and 2 nucleotides at 3′ end. D138 was truncated by 5 and 3 nucleotides at 5′ and 3′ ends respectively. **(C)** Truncation of R118 in the presence of the two truncated DNAs. R118 was truncated by 1 nucleotide at 3′ end. **(D)** Titration of each DNA cofactor up to 2.5 μM in the absence of the other cofactor. The quantification plot showed the individual effect of each DNA cofactor. The diamond in the plot showed the optimum cofactor concentration (1.5 μM of D138) and was used in the following assays. The fitting curve of the more efficient cofactor D138 is shown below. Dashed lines show the linear fit of the unsaturated phase and the saturated phase, with an intercept at 328 nM D138. **(E)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown to the right. **(F)** The kinetics of the complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantification histogram is shown below. The kinetics were 0.012 /min (with preheating) and 0.011 /min (without preheating). **(G)** In-line probing analysis of the complex. R118 was incubated with water, alkaline hydrolysis buffer, RNase T1, Tmp reaction buffer with D138 and without DNA. **(H)** The quantification of the in-line probing data. The intensity of each band was normalized to the untreated RNA and the critical value of intensity indicating flexible and constrained nucleotides is 0.09. The gray line with empty circles indicated the structure without DNA; the black line with filled circles indicated the structure in the presence of DNA; the blue and red circles indicated constrained nucleotides and flexible nucleotides respectively. **(I)** The secondary structure models of the complex R118 D138 and R118 self structure. The colors of nucleotides corresponded with the quantification plot.

Figure S10

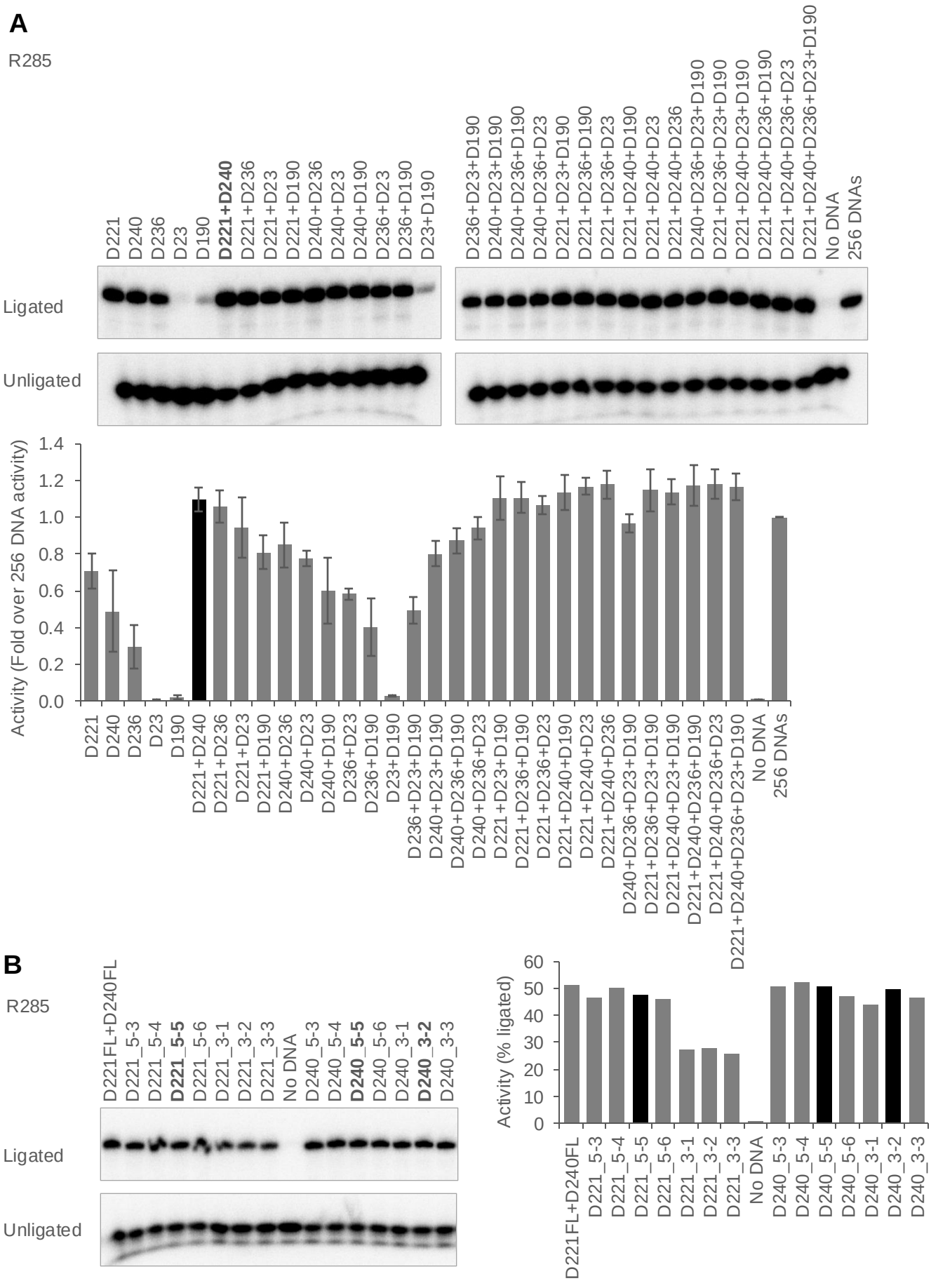

A
R285
D221
D240
D236
D23
D190
D221+D240
D221+D236
D221+D23
D221+D190
D240+D236
D240+D23
D240+D190
D236+D23
D236+D190
D23+D190
D236+D23+D190
D240+D23+D190
D240+D236+D190
D240+D236+D23
D221+D240+D190
D221+D240+D23
D221+D236+D190
D221+D236+D23
D221+D240+D236
D240+D236+D23+D190
D221+D236+D23+D190
D221+D240+D23+D190
D221+D240+D236+D190
D221+D240+D236+D23
D221+D240+D236+D23+D190
No DNA
256 DNAs
Ligated
Unligated
Activity (Fold over 256 DNA activity)
0.0
0.2
0.4
0.6
0.8
1.0
1.2
1.4
B
R285
D221FL+D240FL
D221_5-3
D221_5-4
D221_5-5
D221_5-6
D221_3-1
D221_3-2
D221_3-3
No DNA
D240_5-3
D240_5-4
D240_5-5
D240_5-6
D240_3-1
D240_3-2
D240_3-3
Ligated
Unligated
Activity (% ligated)
0
10
20
30
40
50
60

Figure S10 - continued

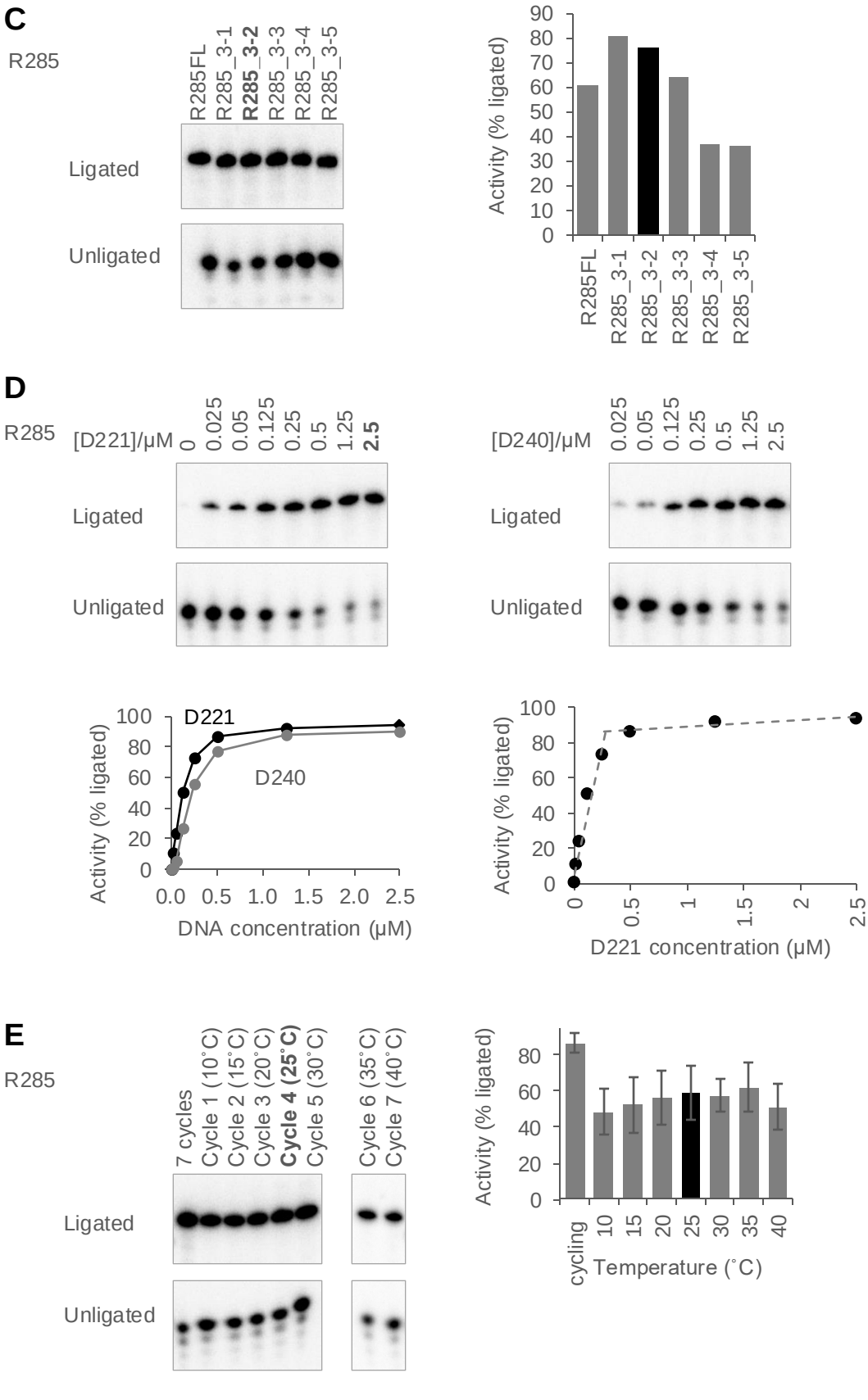


Figure S10 - continued

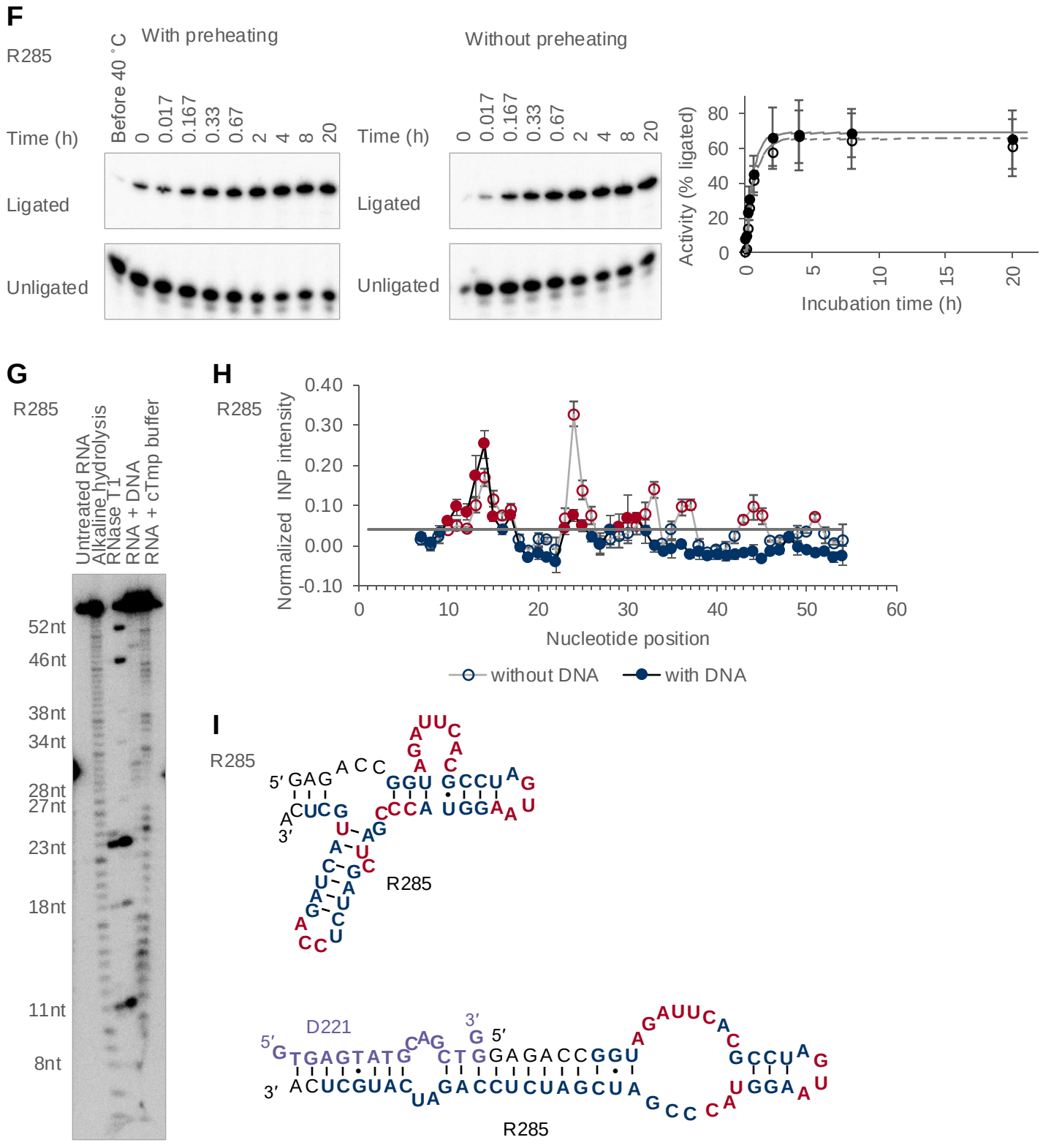


Figure S10 - continued

Figure S10. Characterization of complex R285 and D221. (A) Identification of the minimal group of DNAs that can mediate highest activity. The RNA activity with all possible combinations of D221, D236, D240, D23 and D190. D221 and D240 together mediated the maximum activity. **(B)** Truncation of D221 and D240 at both 5′ and 3′ ends with the other DNA in full length. D221 was truncated by 5 nucleotides at 5′ end. D240 was truncated by 5 and 2 nucleotides at 5′ and 3′ ends respectively. **(C)** Truncation of R285 at 3′ end in the presence of the two truncated DNAs. R285 was truncated by 2 nucleotides at 3′ end. **(D)** Titration of each DNA cofactor up to 2.5 μM in the absence of the other cofactor. The quantification plot showed the individual effect of each DNA cofactor. The diamond in the plot showed the optimum cofactor concentration (2.5 μM of D221) and was used in the following assays. The fitting curve of the more efficient cofactor D221 is shown to the right. Dashed lines show the linear fit of the unsaturated phase and the saturated phase, with an intercept at 280 nM D221. **(E)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown to the right. **(F)** The kinetic analysis of the complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantification histogram is shown below. The kinetics were 0.030 /min (with preheating) and 0.023 /min (without preheating). **(G)** In-line probing analysis of the complex. R285 was incubated with water, alkaline hydrolysis, RNase T1, Tmp buffer with D221 and with no DNA. **(H)** The quantification of the in-line probing data. The intensity of each band was normalized to the untreated RNA and the critical value of intensity indicating flexible and constrained nucleotides is 0.04. The gray line with empty circles indicated the structure without DNA; the black line with filled circles indicated the structure in the presence of DNA; the blue and red circles indicated constrained nucleotides and flexible nucleotides respectively. **(I)** The secondary structure models of the complex R285 D221 and R285 self structure. The colors of nucleotides corresponded with the quantification plot.

Figure S11

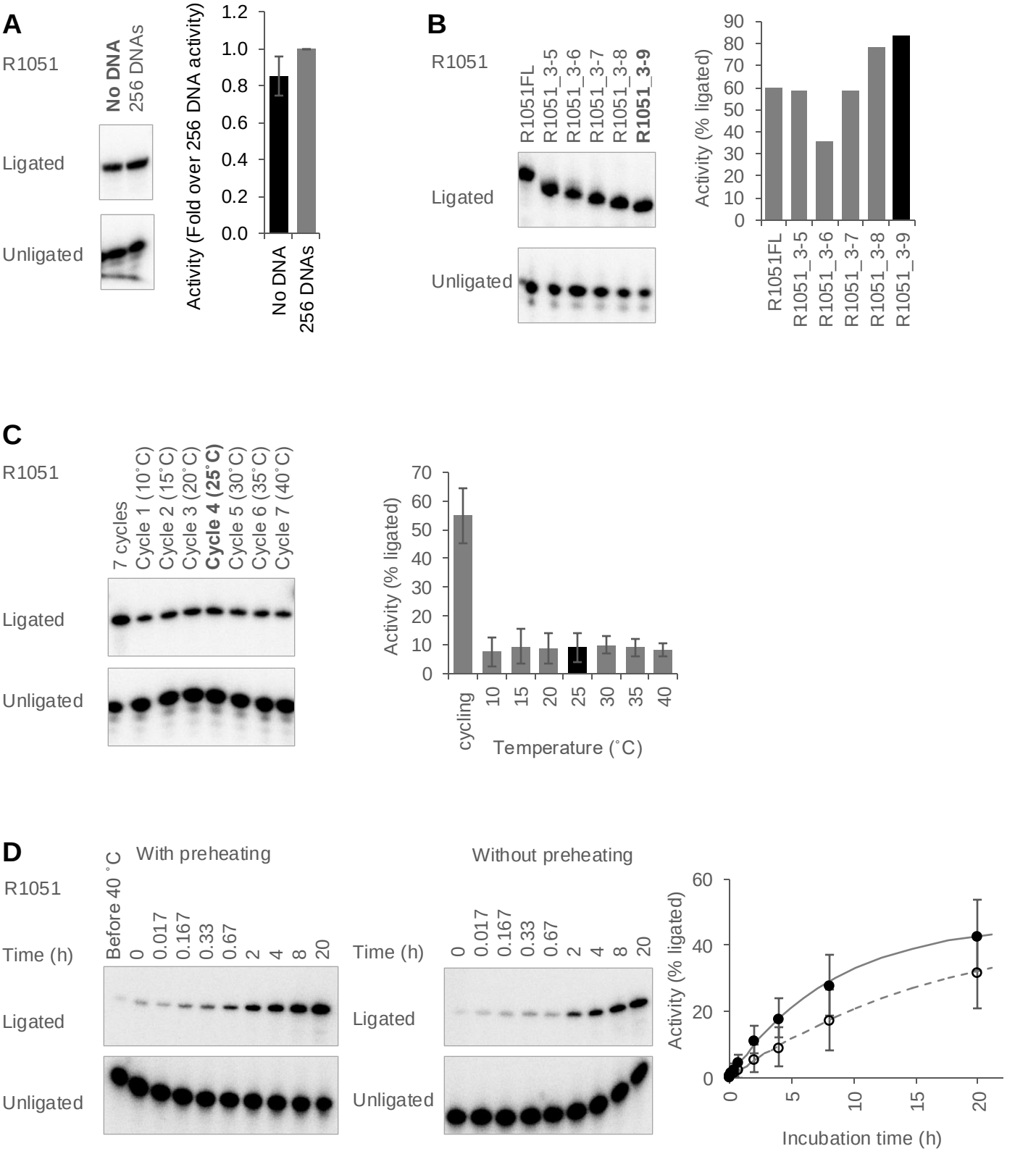

A
R1051
No DNA
256 DNAs
Ligated
Unligated
Activity (Fold over 256 DNA activity)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
No DNA
256 DNAs
B
R1051
R1051FL
R1051_3-5
R1051_3-6
R1051_3-7
R1051_3-8
R1051_3-9
Ligated
Unligated
Activity (% ligated)
90
80
70
60
50
40
30
20
10
0
C
R1051
7 cycles
Cycle 1 (10˚C)
Cycle 2 (15˚C)
Cycle 3 (20˚C)
Cycle 4 (25˚C)
Cycle 5 (30˚C)
Cycle 6 (35˚C)
Cycle 7 (40˚C)
Ligated
Unligated
Activity (% ligated)
70
60
50
40
30
20
10
0
cycling
10
15
20
25
30
35
40
Temperature (˚C)
D
R1051
With preheating
Before 40 ˚C
Time (h)
0
0.017
0.167
0.33
0.67
2
4
8
20
Ligated
Unligated
Without preheating
Time (h)
0
0.017
0.167
0.33
0.67
2
4
8
20
Ligated
Unligated
Activity (% ligated)
60
40
20
0
0
5
10
15
20
Incubation time (h)

Figure S11 - continued

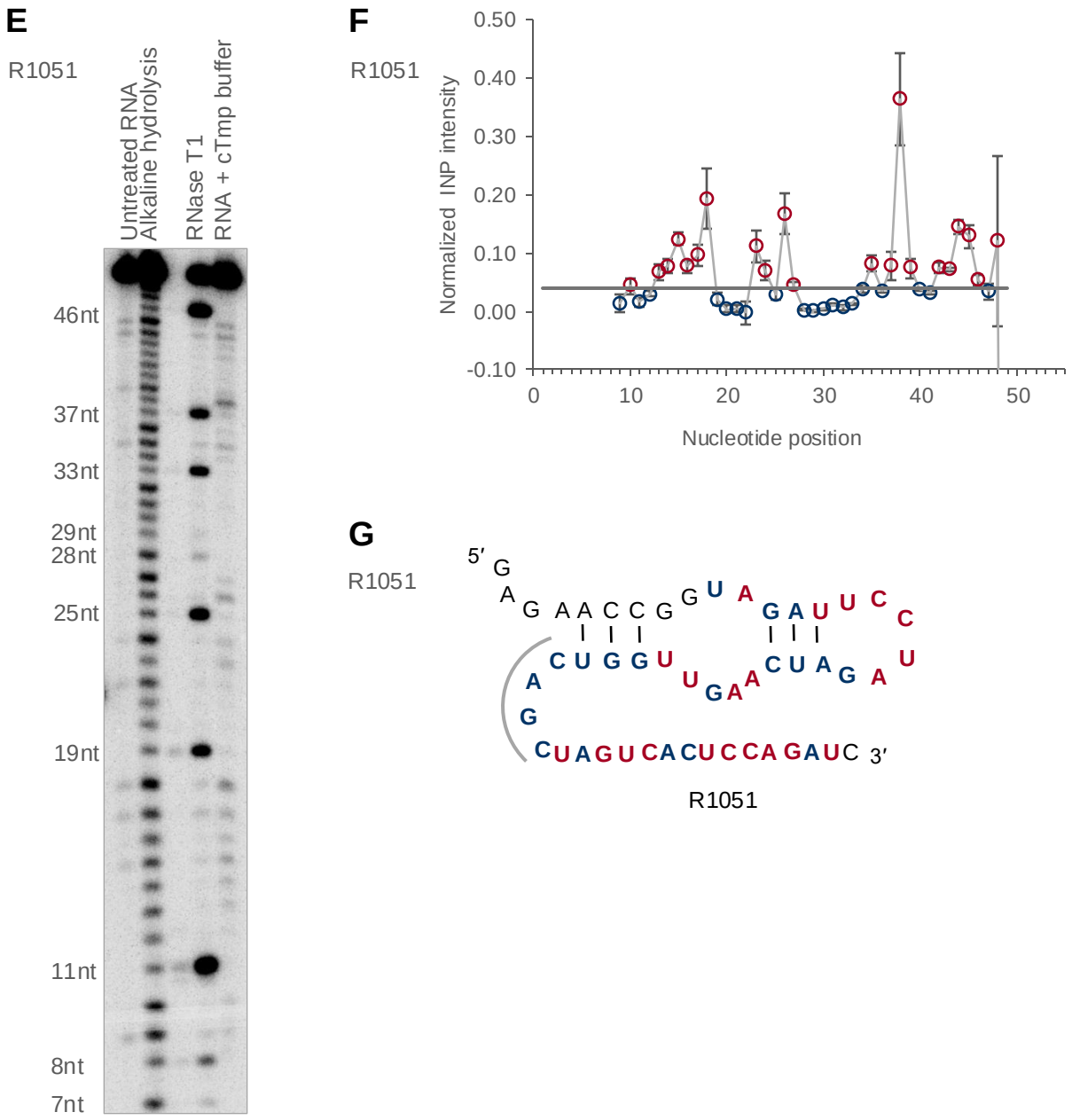


Figure S11 - continued

Figure S11. Characterization of ribozyme R1051. (A) R1051 activity with and without DNA cofactors. No DNA is necessary for the maximum activity. **(B)** Truncation of R1051 at 3′ end. R1051 showed maximum activity after truncated by 9 nucleotides at 3′ end and was consistent in two replicates. **(C)** Optimization of the reaction temperature. The truncated complex was tested with the seven-cycle temperature profile and each individual cycle (figure S1). The quantification histogram is shown to the right. **(D)** The kinetics of the complex under the optimum temperature, with and without preheating (40˚C/ 10 min). The quantification histogram is shown below. The kinetics were 0.002 /min (with preheating) and 0.001 /min (without preheating). **(E)** In-line probing analysis of R1051. R1051 was incubated with water, alkaline hydrolysis, RNase T1, and Tmp reaction buffer. **(F)** The quantification of the in-line probing data. The intensity of each band was normalized to the untreated RNA and the critical value of intensity indicating flexible and constrained nucleotides is 0.04. The blue and red circles indicated constrained nucleotides and flexible nucleotides respectively. **(G)** The secondary structure model of R1051. The colors of nucleotides corresponded with the quantification plot. The gray curve indicates unknown protection of the nucleotides.

Figure S12

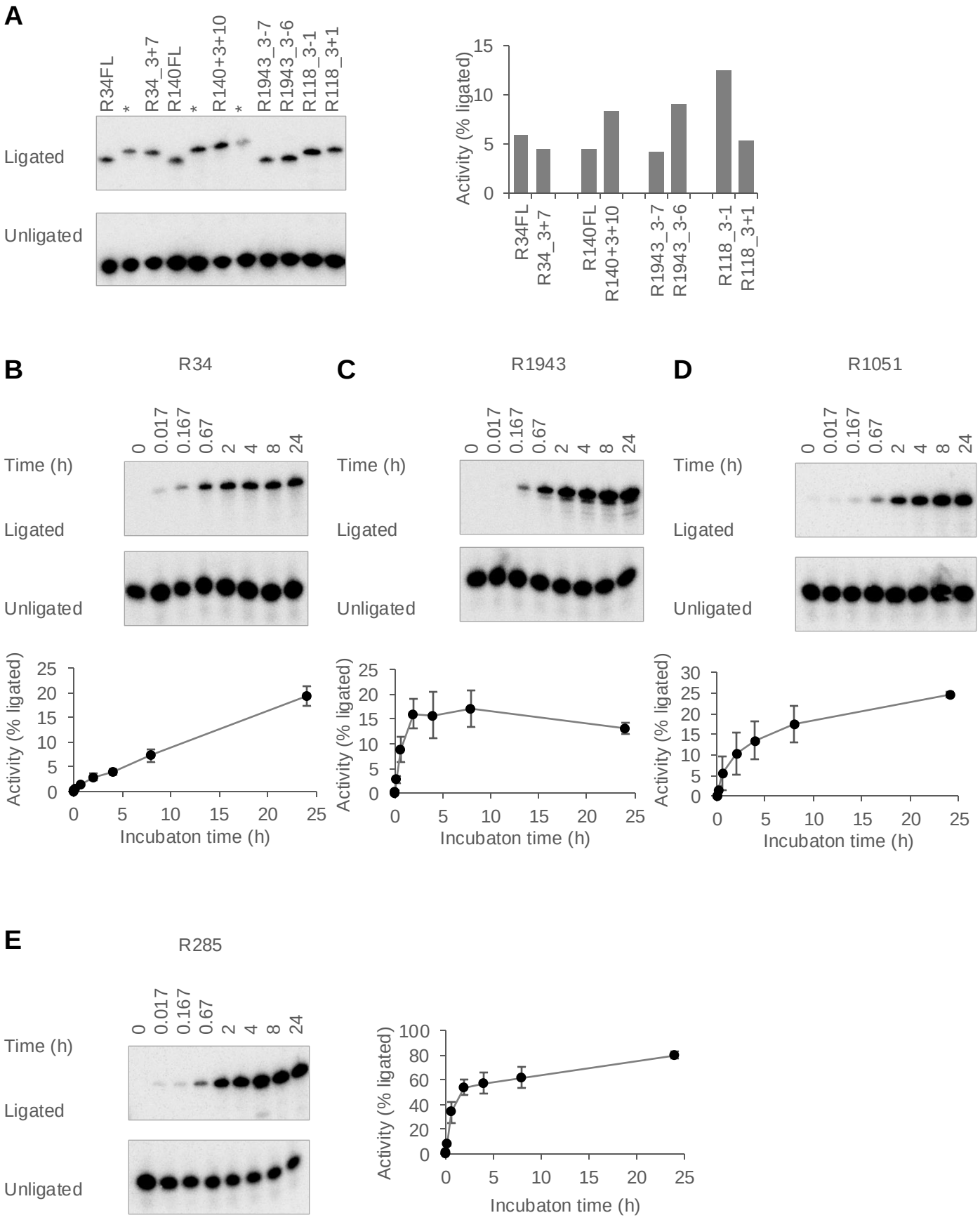

A
R34FL
*
R34_3+7
R140FL
*
R140+3+10
*
R1943_3-7
R1943_3-6
R118_3-1
R118_3+1
Ligated
Unligated
Activity (% ligated)
R34FL
R34_3+7
R140FL
R140+3+10
R1943_3-7
R1943_3-6
R118_3-1
R118_3+1
B
R34
C
R1943
D
R1051
Time (h)
0
0.017
0.167
0.67
2
4
8
24
Ligated
Unligated
Activity (% ligated)
Incubaton time (h)
E
R285

Figure S12 - continued

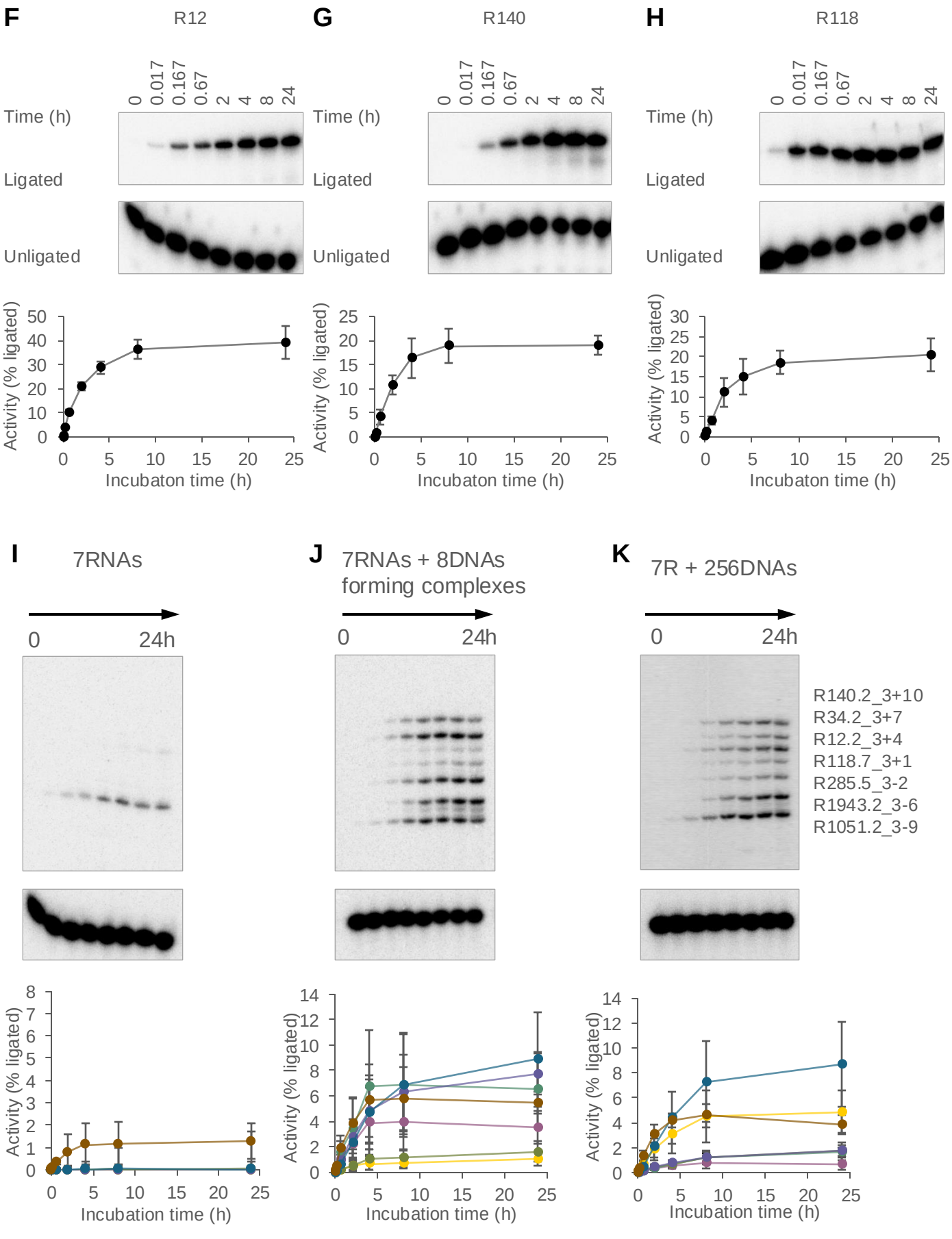


Figure S12 - continued

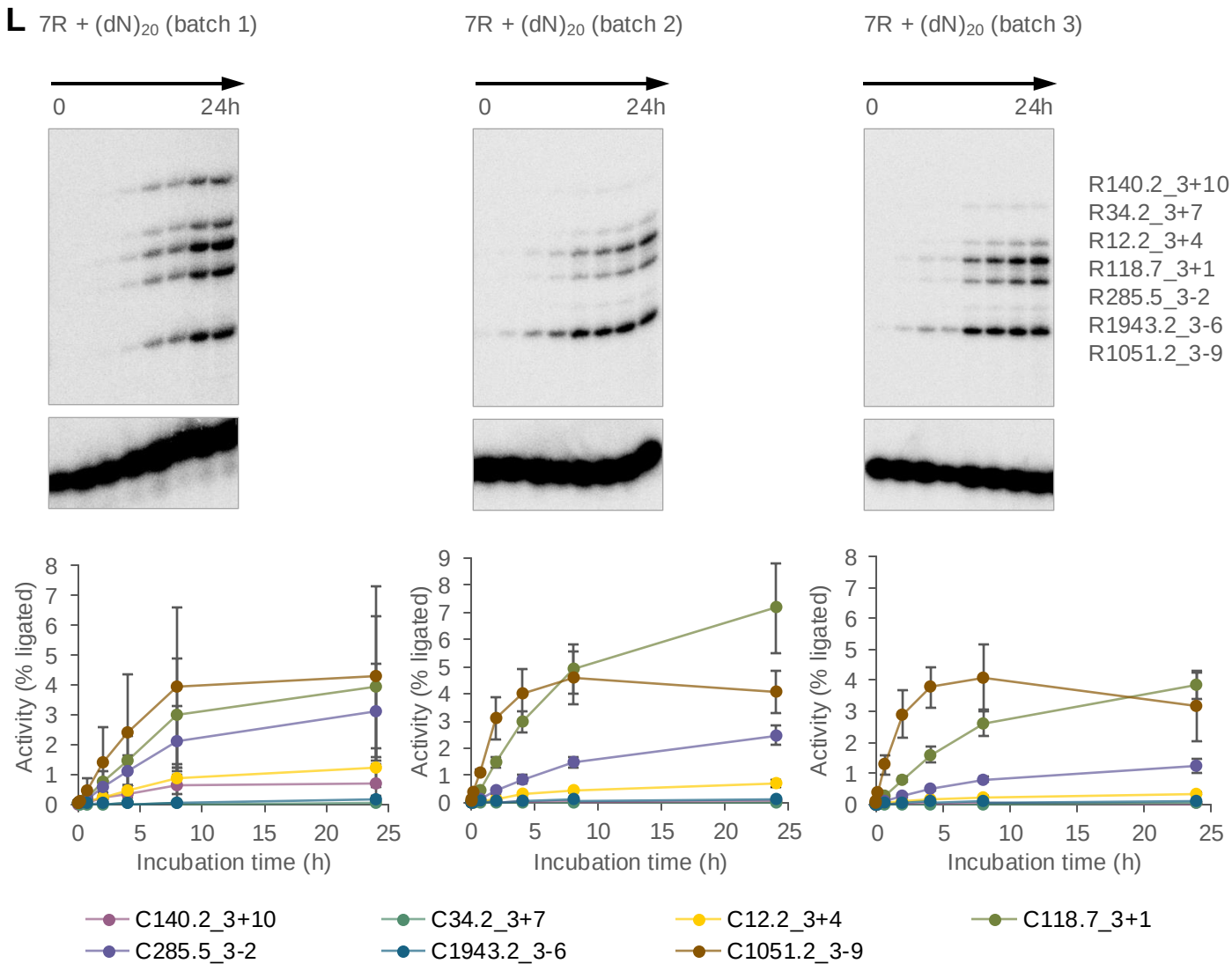


Figure S12. Analysis of RNA activity with randomized DNA cofactors. (A) Activity of elongated RNAs. * Other constructs that had lower activity than the chosen ones. **(B-H)** Kinetics of each individual complex under 30 ˚C. **(I)** The activity of seven RNAs under 30 ˚C without DNA. Only R1051 showed weak activity. **(J)** Six RNA/DNA complex and one ribozyme R1051 activity in one pot reaction. **(K)** Activity of the seven RNAs with 256 library DNAs. **(L)** Activity of the seven RNAs in the presence of three different preps of randomized DNA 20-mers. Histograms showed the quantified activity of the corresponding gel above.

Figure S13

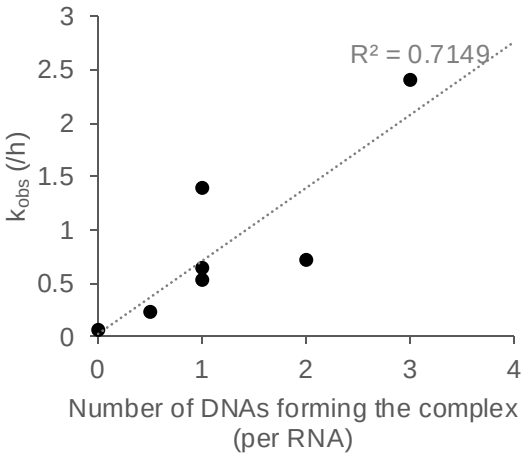


Figure S13. Correlation between reaction kinetics and the number of DNA cofactors in the seven complexes/ ribozyme. Each of the symbols represents one of the seven biochemically characterized RNAs, and the complexes formed by them. The data are taken from the fits to reaction kinetics in figures 4C, 5C, 6C and 7C. The dashed line is a least-squares fit to the data, with a coefficient of determination r^2=0.71.

Figure S14

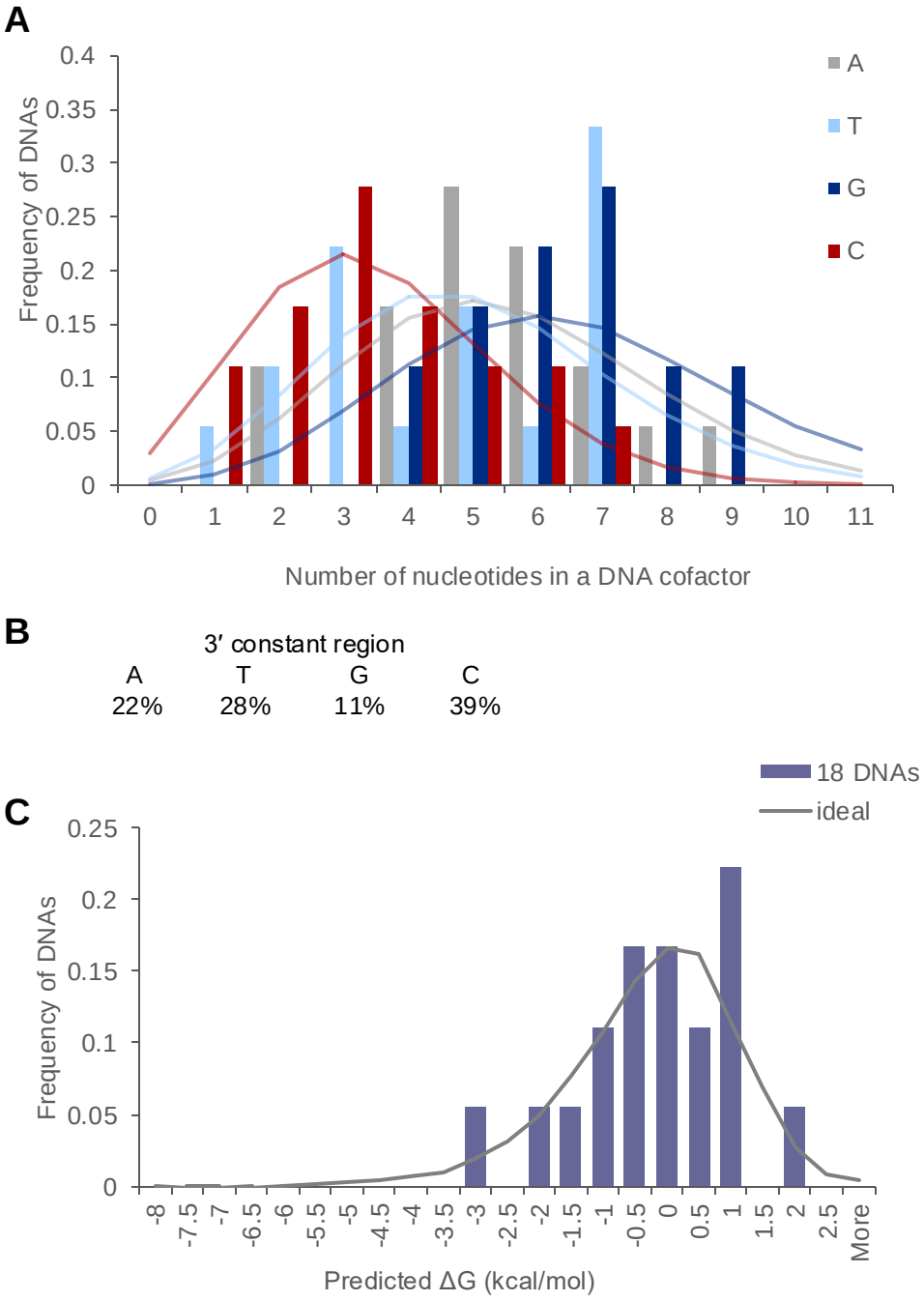


Figure S14. Nucleotide bias and self-structure tendency of 18 DNA cofactors that mediated activity. (A) Distribution of four nucleotides content. Gray, light blue, dark blue and dark red represent A, T, G and C respectively. The lines indicate the Poisson distribution of the corresponding nucleotides, with average nucleotide numbers A = 5.5, T = 5, G = 6.5, C = 3.5. **(B)** The nucleotide composition in the 3′ constant region of the RNA pool. **(C)** The distribution of the ΔG values predicted by DNA mfold.

Table S1

Set A	D1	ATGCTTTTATGTCAGCGCTT	Set C	D33	AGGAAGTTATATCTATTAGA
	D2	GACAGCAAATGCTTGTAGGG		D34	TTTACGACGTGTTCGGGAAC
	D3	AATTCCACTCATTCCTCCTA		D35	TAACAATTAGCTGACTCCTT
	D4	CTATTTAACCCTTGGACAAC		D36	AAAATGGACTCGTGTCATGT
	D5	ACTCAAGATAGAATACAGTT		D37	CGTCTGCGGTAGTTTGCGGT
	D6	ATCAATTAGTACTTCGGGTG		D38	GAACACCAGTCGGTCGGTCA
	D7	GACTCTACAGTCTGCCTAGC		D39	GGTTTAGTTACGAAAGATCA
	D8	GACGGCATCCCGCGTCTAGC		D40	CGGAAAGGGACCGCGTTCTT
	D9	AGAACCCTTAAAGAGGTGGT		D41	TACGCCCTGGTACGTCAGGA
	D10	TTGTGGGACGACTCGATACG		D42	AGGGGCTATTATAGCCCCAT
	D11	TTAACAGTCCGACAACAACG		D43	ACTTATGTGCGCGGCCCAAG
	D12	TATTCCACACACCTAAGAAG		D44	GGAAATCAGTCCTGGACTCA
	D13	GTCGGCCTGACAGGGCAAAA		D45	CTGTTCATACCAACGGTGGG
	D14	TGGACGATAACTGCCCACCT		D46	GTGGAGAAATGACGGTGAAT
	D15	GAACCTCTACCACCTGGAGT		D47	GCGCTGTTATTTCCAAGTGT
	D16	CCTGAGCAAGCGCTCATACG		D48	TGATCATCCAATACATGTAT
Set B	D17	CCAGCCCGCGGTAGTATCGT	Set D	D49	GTCTAGCTGTAACCAAGGGG
	D18	ATACGACGCCAATATTAAAA		D50	CGCCATATGATGGGGGCGAA
	D19	ATTTATCTCAATGGCGTCGC		D51	CTCCGAGGGAAACTTGCATT
	D20	CCCTCGGCGTCCCGGCGCCC		D52	CACCTACGATTGCCCAGGAT
	D21	GCAGAACCGCAGTTTTAAGA		D53	TGTGGTCTGCGGAATGTCCC
	D22	TAACGCGGTAAGAACTGTGT		D54	AATAGGCTTCGTGTATACTG
	D23	GGTGACTTTGCGATCCCCGG		D55	CCGGGTTGGACTAGGCTTGA
	D24	ACCACTCCAAGCACCAATAA		D56	GAGAGAGCTTAACACCTATT
	D25	ATAATCACGGCCCCATGCAG		D57	TCGCTCCCCATCGCACTTGT
	D26	GACCAGCCTTTTCGGCCACG		D58	ACAATTGGTCGTCCATTGTT
	D27	ATTTTCCCCGATTTCTACTT		D59	CTCCCGGACGGAGGAAAGTG
	D28	CGCTACACACTGATGGTACG		D60	GTTTCGCAAACCGAAGTAAG
	D29	TGGGGCGTGGTAATCATAAT		D61	CTAGCCATGACAATTATTAA
	D30	GTCTAGGGTTTACAACAGGA		D62	CTAAGTAGGGCAGTAAGGCT
	D31	TACGATGCCACGCCCCAATA		D63	AAACCCTCCCGCCCAATTTC
	D32	TATCTAACAATCTGGGTTCT		D64	GCCCGGCACTGGCTCTCTAT

Table S1 - continued

Set E	D65	TTGCTAATGTATTCGGAGAG	Set G	D97	CTAGTGATTGCGGGACTATC
	D66	CGTCCCCCGACGACGATCGT		D98	GATCTTCAACCGAAAATCCT
	D67	CAAAGCGAGGAGGACTATAG		D99	AAGAGTGACCCTCAGAATAT
	D68	TTAATTCTGTCACGGGCAAA		D100	TTACAGCGCACTTACGCGCC
	D69	GTTGCCATCATAGGCAGCAA		D101	CACGGAACGAATCGTTTCGT
	D70	AGACAGACTCAGCTATTTCA		D102	AACCTACAATCCTGGATAGA
	D71	TAGTGATTGAGAGTGATACA		D103	TGAACTACCAGGGCTTTGGA
	D72	CTTGATAAACTCGCGATGGA		D104	GGGTCCTCTAGTCGCTCATT
	D73	TATAACCAGCTAACGGCCAT		D105	TTTATTGTCCTCAATCACCG
	D74	ATTTGCGTAAGATGTGGCTG		D106	TGAAGGGATTCAATTTCATT
	D75	GATACTACGAAGTATACCTG		D107	GAATGCATGACACAGCATAG
	D76	TGGGTAAGCAACAGAGCGTA		D108	TGAAGATCTTGTACATTTCA
	D77	TGCCCTATTAGCTTTCGCAC		D109	GTAATACAATGTTCCAAATT
	D78	GAAGGCCCGTCCGCATTACG		D110	CAAGATTCTACCTGCAATAT
	D79	GGATACCACACAAACTTGTA		D111	ACCTTAATAGGCTGAAAGCA
	D80	TTCTCGTAAAATAAGGGCCA		D112	AGTAGTAGCCCAGCTGATTA
Set F	D81	ACTGCCTGTCCAGGGTCTAC	Set H	D113	GGCGACAGCAATTTTTCACA
	D82	AGGACTGCTGTATTTCTCAA		D114	CATTTAACACATATGGTCAC
	D83	ATTAGTTATCATATCATCTC		D115	ACGCCACTCAATGTTCGGGG
	D84	CTTATAGGGGGTCTTACACC		D116	TTAAGGTTCCCGGGTTCCCT
	D85	TTCCTAAATCCACGGTACAC		D117	ACTTAGATACAAAGGCCAAC
	D86	CACCGTCCCCCAAGTTTGCT		D118	CGTAAACACACATAACCTAT
	D87	GTCCGATTCCGCTATTTAGC		D119	CCTCTTCCCCGTTGGGATGA
	D88	AGTGAGTAGACGAGGAGGAT		D120	CATCTTTTCAGCCTTTCGAA
	D89	AAGGTACAGCAGGGCAATGC		D121	CTATGCTACGCTATGTTCAG
	D90	GTAATTCTCGGGTCTCGGCT		D122	TGGGGTGAAAGGTCGTCCTT
	D91	TCATAATGTTGCTCCTACAT		D123	CACTCAGACGCACGAACACG
	D92	TCTAAGTTCTGTTATGTAAT		D124	CCTGACGGGCAAAATTTCTC
	D93	AGGGCTGGTCGCTTCAATAT		D125	CAGCCACCAGTACGCGGGTT
	D94	CAGGCCCTTGGCTTGACAGC		D126	GAAGGCTACTAAGAGCCGGT
	D95	CCCGTCGGCGCGCTGTGACG		D127	TTGACTGTTATGCGTTACAG
	D96	GTCTCGAGGAGGGATTTAAA		D128	AGGCAGCAGAGATGCCCCGC

Table S1 - continued

Set I	D129	GCGCAAAGTAACCAGCCAAG	Set K	D161	ACTAGGCTTATTGAGGCGCT
	D130	GATCCTGATCTGATATATAG		D162	AAAAAGCAATGTCGCGATAT
	D131	TGACCGGCCTGCCTAGGCAG		D163	TTTTTGCGGCTGTGGACAAA
	D132	ATTCAAAGCGGGTCATGTAC		D164	TTGGAGCCACCGGGCGGTAG
	D133	AGTGCTCTGAAGTGAAAATT		D165	CAGTCACCAGTTGATTCTCA
	D134	GGTACGACTAATAGGGTCAC		D166	TCGACACCCTGCCGGAAATC
	D135	ACTAAGTCGGGTCTGCTCAG		D167	CACTAACGGGTGATGTCCGT
	D136	AGATTGGCCCTAAAAGAAGG		D168	TCTTTCAATCAGCCGCTGCA
	D137	ACCTACTTGTACGCCTAGCA		D169	GGGATTCCGAAAGCAAACAA
	D138	GAGGCGCCTTGTATCTGTTC		D170	AGGGCATGCATTGATTCTAC
	D139	GGTCAGCGAAGACGTTAACC		D171	TAACACATAACGTTCTAAAT
	D140	CTTTTTCATTTCAACGATAG		D172	CTTGCATTTAGTTCTATGTT
	D141	ATAATAGAAATATGCTATCA		D173	GTCTCCTGGATAAATATATA
	D142	AATTGGCCGGATCGAGCGCC		D174	CGAGCCTCGATGATTCCGAA
	D143	TTGTTAGTAACACATAACCG		D175	CCTTATGCATTAAATTCGTC
	D144	ATAGGGCCAAAACGGTTCTA		D176	AGAACTCAGAAGCCCCCTCA
Set J	D145	ATTTGATATCCACCCGCACC	Set L	D177	TTGCTTCGTCAGATGGTGTG
	D146	GCCCAAGTCGTGCACAACTG		D178	TATCAAGGACGCTGCGCTTC
	D147	GCGTTTCCTTACATAACTGT		D179	AGCCATAGAACACTTTTTAG
	D148	ATCCCTCGGTGAATTACATG		D180	TAGACTTAGAGGATACAGTG
	D149	GCCGTTTCCGTACCCAATAA		D181	TTGCATGTAACATTGAGGTA
	D150	ACGGGTCCAAGGAGCCAGGT		D182	TAGATCACCCTGTGCTCGCG
	D151	GCTCTGCGGAGTTAAGAATA		D183	TCCGAATGTCCAATTGGCTA
	D152	TGACGCGTCATGCTGTGTCG		D184	GATTTCCAACAGGATCCCAG
	D153	TACTTTGGCAGACTACGGTT		D185	GTCTATCACTGCTTCCATTG
	D154	GCGGCGTTGTCGTCCGGTTG		D186	TACTTCCCTCTGAAGCACGT
	D155	CCGGGAGTGGCCCGCAGACT		D187	CTCGTACTGTCGGCCATTGA
	D156	ACTTCACATGGTGTAGTGCG		D188	GATCTGAAATTGATGAAAAC
	D157	GTAAGTCTGTTGCAAACGTA		D189	GGGCCCATACCAGCATCCCT
	D158	GGCAAACCGATCCGGGGCAC		D190	GGACATGATTGGAAGCCAAG
	D159	TGTTGGGCTAGTCTACGGCA		D191	TCATGCAGTTTTCCCTACAC
	D160	ACATCCAGTCTGCATATTCG		D192	GAGTGTACATTCGGTTAAGA

Table S1 - continued

Set M	D193	CCACATCCCAAGGAGGACTA	Set O	D225	CATCCCAAACAAGGGTGACT
	D194	CTGTATTAACTACTCACGGG		D226	TCAACCCGCCGGACATCGTG
	D195	CACGTCGTTTCTGTTGCATC		D227	TCTGCGACTAGCTCGCGCTC
	D196	CATAAGCTGTCAGCGTACAA		D228	GGCCTCATGGACAGTTGGAG
	D197	GAATTTTTACACAGCGCGAA		D229	AACCCGCCTAATGTGATTGC
	D198	GTCTGAGGGGCATCAGAACG		D230	TAGGAAGCCTCTGGTCCGCG
	D199	AAGAGTGGCGCCGCCACCGG		D231	AATTAAGTAGAGCTGCATAA
	D200	AGGCTTTCCGCACCCCCTTT		D232	GTCGGGCAGCCAACGCATAC
	D201	CCGCGCGTCTCAAGTGACCA		D233	AAACAAGCGAATAGGATCAA
	D202	AGGGGTAGTCTAGCGGACCT		D234	CAGCCCACTGTCACGATGAG
	D203	TCCCTTAGCGTAGAGTTCTT		D235	TCCGGCGCTAAGACGTGATA
	D204	TTCGCGCTCGGAGTATAGGC		D236	GCGAACTGCACGATCTGGCG
	D205	ATGATTAGGAATTAGGTTCG		D237	TACTTGAAGAATTTGGCCAG
	D206	TATTGTTCAATGGTGTCCCG		D238	ACATGGGATCTTTATCTAAA
	D207	CGTTAGCCGGGTTATGTCCA		D239	ACGTAATGCACATAGACAGT
	D208	GGCTCTATGGACCGACGTCA		D240	TTAGAGTGGCATAAATTTGG
Set N	D209	GAGCAACAGTAGCTAGGCAC	Set P	D241	GCTAGATACCCCCTCTCAGG
	D210	CCCGGATAGTTCGGGGCCCC		D242	GGAGGCTCGGTATCTCTTTC
	D211	CATGCCCCCGTTCTGCGGTC		D243	GTGTCAATGGTTTCCCATAT
	D212	TCAGAGTGAAGACTTCCCCA		D244	AAGTCCTCCTAGCAGAGGCC
	D213	TGGCATCAGCGCTAAGTACG		D245	TGCGCGTCTCGACAGTCCAG
	D214	GGATCTAATTCTCGTGACCG		D246	GATCGTGGTAAGTTACGCAT
	D215	ATATCTGATGTTGCCTCGCA		D247	ATGCCTTTACTCTGACGTTC
	D216	AAGTGGCGGTTGACTTTTTT		D248	TATTCACGCTTTAATGCACT
	D217	ACAGTTCTTAGGCAGAGGAT		D249	CGAGGTACTAATCAGGCATT
	D218	TTTACTTGATAACACCAGTC		D250	CAACTGTATGCTAGAGACCC
	D219	TCTATCACATTTCCATGAGC		D251	AGATCAATGCTCGCCAGTGC
	D220	CTTATGCTTCCCGTCCCGCA		D252	GCGAAATTACAGGATTAGTA
	D221	GGCAGTGAGTATGCAGCTGG		D253	ACAATAATTACGTCAAGCGT
	D222	GCACGAACATGGGTACCATG		D254	GCCTATGGGGCGAGGTGTTA
	D223	CCAGGAATATCATAGAATTT		D255	ACGTAAGTCATGGGGAATTA
	D224	GGGTGACCGGGTAATTAGCT		D256	TCAGATAGGGATACTGGGCA

Table S1. Sequences of the 256 library DNAs.

Table S2

Full length RNAs	
R34	GAGACCGGTAGATTCGACTCCTACTACATAGCTAACAGCCCTCCAGATCATGCTCACT
R1943	GAGACCGGTAGATTCTACGCAAGCCACGCGGTTCTGATGCCTCCAGATCATGCTCACT
R140	GAGACCGGTAGATTCCAACTTGGTCAGATTACAGGCTTATCTCCAGATCATGCTCACT
R12	GAGACCGGTAGATTCAGATGCATAGGTCATTAATCATCGCCTCCAGATCATGCTCACT
R118	GAGACCGGTAGATTCCAAACAGAGGCTTAGGTCATTAGCCCTCCAGATCATGCTCACT
R285	GAGACCGGTAGATTCACGCCTAGTAAGGTACCCGATCGATCTCCAGATCATGCTCACT
R1051	GAGACCGGTAGATTCCTAGATCAAGTTGGTCAGCTAGTCACTCCAGATCATGCTCACT
Reconstructed RNAs in the combinatory assays	
R34_3+7	GAGACCGGTAGATTCGACTCCTACTACATAGCTAACAGCCCTCCAGATCATGCTCACTAACTCAT
R1943_3-6	GAGACCGGTAGATTCTACGCAAGCCACGCGGTTCTGATGCCTCCAGATCATG
R140_3+10	GAGACCGGTAGATTCCAACTTGGTCAGATTACAGGCTTATCTCCAGATCATGCTCACTUCAGACAAUG
R12_3+4	GAGACCGGTAGATTCAGATGCATAGGTCATTAATCATCGCCTCCAGATCATGCTCACTACAC
R118_3+1	GAGACCGGTAGATTCCAAACAGAGGCTTAGGTCATTAGCCCTCCAGATCATGCTCACTA
R285_3-2	GAGACCGGTAGATTCACGCCTAGTAAGGTACCCGATCGATCTCCAGATCATGCTCA
R1051_3-9	GAGACCGGTAGATTCCTAGATCAAGTTGGTCAGCTAGTCACTCCAGATC

Table S2. Sequences of the 7 characterized RNAs and the reconstructed RNAs for one-pot assays

Table S3

RNA	N25 sequences
R118.30	AAAACAGAGGCTCAGGTCATAAGTC
R118.35	AAAACAGAGGCTTAGGTCATTAGTC
R49.9	AAAAGTGAGCAGTTCCCGGTCTGAT
R1532.18	AAAATTGGTCAGTTAACACGCTTAT
R1256.37	AAACTTAGTAAGGTACCCGGTCGAT
R6.3	AAACTTGGTCAGTTGTCAGGCTTAT
R282.14	AAAGCTGGTCAGTTAACACGCTTAT
R49.8	AAAGTAAGCAGTTCCCGGTCTGATC
R282.17	AAAGTCGGTCAGTTAACACGCTTAT
R1532.14	AAAGTTAGTCAGTTAACACGCTTAT
R282.26	AAAGTTGATCAGTTAACACGCTTAT
R636.9	AAAGTTGGCCAGTTAACACGCTTAT
R282.20	AAAGTTGGTAAGTTAACACGCTTAT
R2164.3	AAAGTTGGTCAAACATCACGCTCAT
R880.4	AAAGTTGGTCAAATCACACGCTCAT
R336.11	AAAGTTGGTCAAATTTCACGCTTAT
R266.3	AAAGTTGGTCAACTAGTCACACAAT
R116.3	AAAGTTGGTCAACTCACACGCTTAT
R116.4	AAAGTTGGTCAACTCTCACGCTTAT
R1395.6	AAAGTTGGTCAAGTTTCACACTTAT
R1395.3	AAAGTTGGTCAAGTTTCACGCTCAT
R1395.4	AAAGTTGGTCAAGTTTCACGCTTAT
R0.14	AAAGTTGGTCAATAGTCACGCTTAT
R2164.4	AAAGTTGGTCAATCGTCACGCTCAT
R110.3	AAAGTTGGTCAATGTTCACGCTTAT
R117.4	AAAGTTGGTCAATTAACACGCTTAT
R14.2	AAAGTTGGTCAATTAATCACACAAT
R0.6	AAAGTTGGTCAATTGTCACGCTTAT
R1395.7	AAAGTTGGTCAATTTACACGCTTAT
R13.4	AAAGTTGGTCAGATTTCACGCTTAT
R115.7	AAAGTTGGTCAGCCCACACGCTCAT
R115.2	AAAGTTGGTCAGCCCACACGCTTAT
R115.6	AAAGTTGGTCAGCCTACACGCTTAT
R1599.4	AAAGTTGGTCAGCTAACACGCTTAT
R1599.6	AAAGTTGGTCAGCTAACACTCTTAT
R1638.4	AAAGTTGGTCAGCTAATCACACAAT
R1335.9	AAAGTTGGTCAGCTAGTCACACAAT
R2.7	AAAGTTGGTCAGCTCACACACTTAT
R2.6	AAAGTTGGTCAGCTCACACGCTTAT
R202.2	AAAGTTGGTCAGCTCATCACTCAAT
R11.6	AAAGTTGGTCAGTAATCACGCTTAT
R13.10	AAAGTTGGTCAGTATTCACGCTCAT
R13.5	AAAGTTGGTCAGTCAACACGCTTAT
R1049.28	AAAGTTGGTCAGTCAGTCACACAAT
R13.2	AAAGTTGGTCAGTCTTCACGCTTAT
R1532.9	AAAGTTGGTCAGTTAACACACTTAT
R282.10	AAAGTTGGTCAGTTAACACGCCTAT
R1532.16	AAAGTTGGTCAGTTAACACGCTAAT
R18.4	AAAGTTGGTCAGTTAACACGCTCAT
R282.11	AAAGTTGGTCAGTTAACACGCTTAA
R1532.8	AAAGTTGGTCAGTTAACACGCTTAC
R1532.17	AAAGTTGGTCAGTTAACACGCTTAG
R1532.2	AAAGTTGGTCAGTTAACACGCTTAT
R282.21	AAAGTTGGTCAGTTAACACGCTTGT
R282.27	AAAGTTGGTCAGTTAACACGTTTAT
R282.18	AAAGTTGGTCAGTTAACACTCTTAT
R1532.15	AAAGTTGGTCAGTTAACATGCTTAT
R1532.10	AAAGTTGGTCAGTTAACGCGCTTAT
R282.29	AAAGTTGGTCAGTTAATACGCTTAT
R65.2	AAAGTTGGTCAGTTAATCACACAAT
R59.30	AAAGTTGGTCAGTTACTACGCTAAT
R105.20	AAAGTTGGTCAGTTAGCACGCTTAT
R1335.11	AAAGTTGGTCAGTTAGTCACACAAT
R13.6	AAAGTTGGTCAGTTATCACGCTTAT
R18.7	AAAGTTGGTCAGTTCACACGCTTAT
R282.15	AAAGTTGGTCAGTTGACACGCTTAT
R13.7	AAAGTTGGTCAGTTTTCACGCTCAT
R282.35	AAAGTTGGTCATTTAACACGCTTAT
R282.12	AAAGTTGGTCGGTTAACACGCTTAT
R282.28	AAAGTTGGTTAGTTAACACGCTTAT
R282.24	AAAGTTGTTCAGTTAACACGCTTAT
R282.23	AAAGTTTGTCAGTTAACACGCTTAT
R282.31	AAATTTGGTCAGTTAACACGCTTAT
R7.4	AACCTGAGCCTAACTAGTCAACGAT
R123.19	AACGGTTGCTACTGATCAGGCTATA
R1599.3	AACGTTGGTCAGCTTACACGCTTAT
R697.17	AACGTTGGTCAGTTAGTCACGCAAT
R13.3	AACGTTGGTCAGTTTTCACGCTTAT
R7.38	AAGAGCCTAACTAGTCAACGATCCT
R1256.15	AAGCCTAGTAAGGTACCCGGTCGAT
R1256.22	AAGCTCAGTAAGGTACCCGGTCGAT
R1256.36	AAGCTTAATAAGGTACCCGGTCGAT
R309.40	AAGCTTACTAAGGTACCCGGTCGAT
R15.12	AAGCTTAGAAAGGTACCCGATCTAT
R15.42	AAGCTTAGAAAGGTACCCGGTCGAT
R1228.4	AAGCTTAGCAAGGTACCCGGTCGAT
R1256.31	AAGCTTAGTAAAGTACCCGGTCGAT
R1256.30	AAGCTTAGTAAGATACCCGGTCGAT
R1256.44	AAGCTTAGTAAGCTACCCGGTCGAT
R1256.43	AAGCTTAGTAAGGAACCCGGTCGAT
R1256.12	AAGCTTAGTAAGGCACCCGGTCGAT
R1256.35	AAGCTTAGTAAGGTACACGGTCGAT
R1256.24	AAGCTTAGTAAGGTACCAGGTCGAT
R1256.8	AAGCTTAGTAAGGTACCCAGTCGAT
R1256.3	AAGCTTAGTAAGGTACCCGATCGAT
R1256.5	AAGCTTAGTAAGGTACCCGATCTAT
R1256.9	AAGCTTAGTAAGGTACCCGGCCGAT
R1256.25	AAGCTTAGTAAGGTACCCGGTAGAT
R1256.20	AAGCTTAGTAAGGTACCCGGTCAAT
R1256.21	AAGCTTAGTAAGGTACCCGGTCGAA
R1256.7	AAGCTTAGTAAGGTACCCGGTCGAC
R1256.45	AAGCTTAGTAAGGTACCCGGTCGAG
R1256.2	AAGCTTAGTAAGGTACCCGGTCGAT
R1256.16	AAGCTTAGTAAGGTACCCGGTCGGT
R1256.39	AAGCTTAGTAAGGTACCCGGTCTAT
R1256.28	AAGCTTAGTAAGGTACCCGGTTGAT
R1256.42	AAGCTTAGTAAGGTACCCTGTCGAT
R43.21	AAGCTTAGTAAGGTACCTGGTCGAT
R1256.27	AAGCTTAGTAAGGTACTCGGTCGAT
R1256.32	AAGCTTAGTAAGGTATCCGGTCGAT
R309.4	AAGCTTAGTAAGGTGCCCGGTCGAT
R1552.6	AAGCTTAGTAAGGTTCCCAGTCGAT
R1552.5	AAGCTTAGTAAGGTTCCCGGTCGAT
R1256.18	AAGCTTAGTAAGTTACCCGGTCGAT
R1256.29	AAGCTTAGTAATGTACCCGGTCGAT
R1256.11	AAGCTTAGTAGGGTACCCGGTCGAT
R1256.19	AAGCTTAGTGAGGTACCCGGTCGAT
R1256.34	AAGCTTATTAAGGTACCCGGTCGAT
R1256.17	AAGCTTGGTAAGGTACCCGGTCGAT
R420.2	AAGCTTGGTCAGTTAACAGCCTTAT
R2.17	AAGGCTGGTCAGCTCACACACTTAT
R2.25	AAGGTCGGTCAGCTCACACACTTAT
R1335.22	AAGGTTGGCCAGCTAGTCACACAAT
R2.14	AAGGTTGGCCAGCTCACACACTTAT
R1732.5	AAGGTTGGTCAAATAACACACTTAT
R1.10	AAGGTTGGTCAAATTTCACACTTAT
R14.4	AAGGTTGGTCAACTAATCACACAAT
R266.5	AAGGTTGGTCAACTAGTCACACAAT
R2.19	AAGGTTGGTCAACTCACACACTTAT
R172.3	AAGGTTGGTCAAGCATCACACTCAT
R172.2	AAGGTTGGTCAAGCGTCACACTTAT
R1.14	AAGGTTGGTCAAGTTTCACACTTAT
R117.3	AAGGTTGGTCAATTAACACACTCAT
R18.5	AAGGTTGGTCAATTAACACGCTCAT
R1732.2	AAGGTTGGTCAATTGTCACACTTAT
R0.23	AAGGTTGGTCAATTGTCACGCTTAT
R2164.2	AAGGTTGGTCAGACATCACGCTTAT
R306.2	AAGGTTGGTCAGATTGCACACTTAT
R2.13	AAGGTTGGTCAGCACACACACTTAT
R2.9	AAGGTTGGTCAGCCCACACACTTAT
R115.4	AAGGTTGGTCAGCCCACACGCTTAT
R144.3	AAGGTTGGTCAGCTAACACACTTAT
R1638.7	AAGGTTGGTCAGCTAATCACACAAT
R183.2	AAGGTTGGTCAGCTAATCACACTCT
R1335.18	AAGGTTGGTCAGCTAGCCACACAAT
R1335.20	AAGGTTGGTCAGCTAGTCACACAAC
R1335.2	AAGGTTGGTCAGCTAGTCACACAAT
R1335.21	AAGGTTGGTCAGCTAGTCACACAGT
R1335.19	AAGGTTGGTCAGCTAGTCACACGAT
R2.21	AAGGTTGGTCAGCTCACACACCTAT
R2.4	AAGGTTGGTCAGCTCACACACTCAT
R2.18	AAGGTTGGTCAGCTCACACACTTAA
R2.11	AAGGTTGGTCAGCTCACACACTTAC
R2.2	AAGGTTGGTCAGCTCACACACTTAT
R2.5	AAGGTTGGTCAGCTCACACGCTTAT
R2.12	AAGGTTGGTCAGCTCACGCACTTAT
R2.8	AAGGTTGGTCAGCTCGCACACTTAT
R2.10	AAGGTTGGTCAGCTTACACACTTAT
R2.23	AAGGTTGGTCAGCTTTCACACTTAT
R658.2	AAGGTTGGTCAGTACATCACACAAT
R282.4	AAGGTTGGTCAGTTAACACGCTTAT
R14.5	AAGGTTGGTCAGTTAATCACACAAT
R18.6	AAGGTTGGTCAGTTCACACACTTAT
R18.3	AAGGTTGGTCAGTTCACACGCTCAT
R18.2	AAGGTTGGTCAGTTCACACGCTTAT
R1732.3	AAGGTTGGTCAGTTTTCACACTTAT
R2.15	AAGGTTGGTCGGCTCACACACTTAT
R35.13	AAGTAAGACATCCGTAGGTATGATC
R177.12	AAGTAAGACATCCGTATACGTGATC
R147.20	AAGTTAGACATCCGTAGGCACGATC
R1049.77	AAGTTGGTCAGTTAATCACACACAT
R1256.38	AAGTTTAGTAAGGTACCCGGTCGAT
R1256.40	AATCTTAGTAAGGTACCCGGTCGAT
R306.3	AATGTTGGTCAGACTACACACTTAT
R1335.15	AATGTTGGTCAGCTAAGCACACAAT
R1335.14	AATGTTGGTCAGCTAGTCACACAAT
R227.2	AATGTTGGTCAGCTTACACACTTAT
R1335.12	AATGTTGGTCAGCTTATCACACAAT
R1335.5	AATGTTGGTCAGTTAGTCACACAAT
R1447.11	ACACGCTGGTCAGCTAATCACGTGC
R1447.9	ACACGTTGGTCAGCTAACCACGTGC
R1447.12	ACACGTTGGTCAGCTAATCACGTAT
R1447.7	ACACGTTGGTCAGCTAATCACGTGA
R1447.2	ACACGTTGGTCAGCTAATCACGTGC
R1447.3	ACACGTTGGTCAGCTAATCACGTGT
R1447.13	ACACGTTGGTCAGCTAATCGCGTGC
R1447.5	ACACGTTGGTCAGCTAGTCACGTGC
R15.27	ACACTTAGAAAGGTACCCGATCTAT
R41.2	ACAGCTGAAGATGTTAACCGGTCAG
R41.3	ACAGCTGAAGATGTTAGCCGGTCAG
R62.17	ACAGCTGGTCAGCTAACACTCTTAT
R62.22	ACAGTCGGTCAGCTAACACTCTTAT
R62.9	ACAGTTGGCCAGCTAACACTCTTAT
R205.4	ACAGTTGGTCAACTAACACTCTTAT
R205.3	ACAGTTGGTCAATGAACACTCTTAT
R205.6	ACAGTTGGTCAATGCACACTCTTAT
R205.5	ACAGTTGGTCAGCCAACACTCTTAT
R1599.8	ACAGTTGGTCAGCTAACACCCTTAT
R1599.14	ACAGTTGGTCAGCTAACACGCTTAT
R1599.11	ACAGTTGGTCAGCTAACACTCCTAT
R1599.7	ACAGTTGGTCAGCTAACACTCTCAT
R1599.13	ACAGTTGGTCAGCTAACACTCTTAA
R62.6	ACAGTTGGTCAGCTAACACTCTTAC
R1599.2	ACAGTTGGTCAGCTAACACTCTTAT
R1599.10	ACAGTTGGTCAGCTAACGCTCTTAT
R1638.3	ACAGTTGGTCAGCTAATCACACAAT
R62.8	ACAGTTGGTCAGCTAGCACTCTTAT
R62.20	ACAGTTGGTCAGCTGACACTCTTAT
R282.32	ACAGTTGGTCAGTTAACACGCTTAT
R191.5	ACAGTTGGTCAGTTAACACTCTTAT
R159.2	ACAGTTGGTCAGTTTTCACTCTTAT
R62.12	ACAGTTGGTCGGCTAACACTCTTAT
R5.28	ACATCGCGTGAGCTAAGCGGTCATC
R135.10	ACATCGCGTTAGCTAAGCGGTCATC
R283.2	ACCAGAGGCGTTCGGGTCATTAGTC
R284.3	ACCAGGTTGCTACTGATCAGGCTAA
R741.2	ACCATCCACTACATAGCTAACAGCC
R123.23	ACCCGGTTGCTACTGATCAGGCTAA
R15.43	ACCCTTAGAAAGGTACCCGATCTAT
R111.2	ACCCTTGGTCAAGTTTCAGGCTCAT
R119.5	ACCGGAGGTACGTGGAACTTGGACA
R119.2	ACCGGAGGTACGTGGAACTTGGACC
R119.4	ACCGGAGGTACGTGGAACTTGGACT
R284.22	ACCTAGTTGCTACTGATCAGGCTAA
R284.31	ACCTGATTGCTACTGATCAGGCTAA
R284.7	ACCTGGCTGCTACTGATCAGGCTAA
R284.13	ACCTGGTCGCTACTGATCAGGCTAA
R284.23	ACCTGGTTACTACTGATCAGGCTAA
R284.26	ACCTGGTTCCTACTGATCAGGCTAA
R284.14	ACCTGGTTGCCACTGATCAGGCTAA
R284.15	ACCTGGTTGCTACCGATCAGGCTAA
R284.28	ACCTGGTTGCTACTAATCAGGCTAA
R284.9	ACCTGGTTGCTACTGACCAGGCTAA
R284.27	ACCTGGTTGCTACTGATAAGGCTAA
R284.33	ACCTGGTTGCTACTGATCAAGCTAA
R284.30	ACCTGGTTGCTACTGATCAGACTAA
R284.18	ACCTGGTTGCTACTGATCAGGCCAA
R284.2	ACCTGGTTGCTACTGATCAGGCTAA
R284.4	ACCTGGTTGCTACTGATCAGGCTAG
R123.36	ACCTGGTTGCTACTGATCAGGCTAT
R284.10	ACCTGGTTGCTACTGATCAGGCTGA
R284.19	ACCTGGTTGCTACTGATCAGGCTTA
R284.29	ACCTGGTTGCTACTGATCAGGTTAA
R284.6	ACCTGGTTGCTACTGATCGGGCTAA
R284.16	ACCTGGTTGCTACTGATTAGGCTAA
R284.8	ACCTGGTTGCTACTGGTCAGGCTAA
R284.32	ACCTGGTTGCTATTGATCAGGCTAA
R284.11	ACCTGGTTGCTGCTGATCAGGCTAA
R284.25	ACCTGGTTGTTACTGATCAGGCTAA
R284.24	ACCTGGTTTCTACTGATCAGGCTAA
R745.2	ACCTTGGTCAATTAATCAGGCTAAT
R3.4	ACCTTGGTCAGCCAATCAGTCAAAT
R3.3	ACCTTGGTCAGCGAATCAGTCAAAT
R745.3	ACCTTGGTCAGTTAATCAGGCTAAT
R15.15	ACGCCTAGAAAGGTACCCGATCTAT
R285.5	ACGCCTAGTAAGGTACCCGATCGAT
R64.3	ACGCCTAGTAAGGTGCCCGATCGAT
R1447.10	ACGCGTTGGTCAGCTAATCACGTGC
R285.3	ACGCTAAGTAAGGTACCCGATCGAT
R15.30	ACGCTCAGAAAGGTACCCGATCTAT
R15.21	ACGCTTAAAAAGGTACCCGATCTAT
R15.36	ACGCTTAGAAAAGTACCCGATCTAT
R15.32	ACGCTTAGAAAGATACCCGATCTAT
R15.18	ACGCTTAGAAAGGAACCCGATCTAT
R15.19	ACGCTTAGAAAGGCACCCGATCTAT
R15.37	ACGCTTAGAAAGGTACACGATCTAT
R15.28	ACGCTTAGAAAGGTACCAGATCTAT
R15.29	ACGCTTAGAAAGGTACCCAATCTAT
R15.14	ACGCTTAGAAAGGTACCCGACCTAT
R15.24	ACGCTTAGAAAGGTACCCGATCAAT
R15.17	ACGCTTAGAAAGGTACCCGATCCAT
R15.3	ACGCTTAGAAAGGTACCCGATCGAT
R15.13	ACGCTTAGAAAGGTACCCGATCTAA
R15.6	ACGCTTAGAAAGGTACCCGATCTAC
R15.38	ACGCTTAGAAAGGTACCCGATCTAG
R15.2	ACGCTTAGAAAGGTACCCGATCTAT
R15.26	ACGCTTAGAAAGGTACCCGATCTGT
R15.20	ACGCTTAGAAAGGTACCCGATTTAT
R15.5	ACGCTTAGAAAGGTACCCGGTCGAT
R15.23	ACGCTTAGAAAGGTACCCGGTCTAT
R15.40	ACGCTTAGAAAGGTACCCTATCTAT
R15.25	ACGCTTAGAAAGGTACCTGATCTAT
R15.31	ACGCTTAGAAAGGTACTCGATCTAT
R15.33	ACGCTTAGAAAGGTATCCGATCTAT
R15.16	ACGCTTAGAAAGGTGCCCGATCTAT
R15.4	ACGCTTAGAAAGGTGCCCGGTCGAT
R15.39	ACGCTTAGAAAGTTACCCGATCTAT
R15.41	ACGCTTAGAAATGTACCCGATCTAT

Table S3 - continued

RNA	N25 sequences	RNA	N25 sequences	RNA	N25 sequences
R15.8	ACGCTTAGAAGGGTACCCGATCTAT	R118.29	CAAACAGAGGCTTAGGTCGTTAGTC	R228.9	CAAGTTGGTCAGATTTCACGCCTAT
R15.7	ACGCTTAGAGAGGTACCCGATCTAT	R118.38	CAAACAGAGGCTTATGTCATTAGTC	R1291.17	CAAGTTGGTCAGATTTCACGCTCAT
R1256.13	ACGCTTAGGAAGGTACCCGATCTAT	R118.12	CAAACAGAGGCTTGGGTCATTAGTC	R228.10	CAAGTTGGTCAGATTTCACGCTTAA
R1256.41	ACGCTTAGTAAGGTACCCGATCGAT	R118.41	CAAACAGAGGTTCAGGTCATAAGTC	R228.3	CAAGTTGGTCAGATTTCACGCTTAC
R1256.26	ACGCTTAGTAAGGTACCCGATCTAT	R118.9	CAAACAGGGGCTCAGGTCATAAGTC	R228.2	CAAGTTGGTCAGATTTCACGCTTAT
R1256.6	ACGCTTAGTAAGGTACCCGGTCGAT	R118.14	CAAACAGGGGCTTAGGTCATTAGTC	R228.18	CAAGTTGGTCAGATTTCACGCTTGT
R1552.2	ACGCTTAGTAAGGTTCCCAGTCGAT	R118.36	CAAACATAGGCTCAGGTCATAAGTC	R228.21	CAAGTTGGTCAGATTTCATGCTTAT
R1552.4	ACGCTTAGTAAGGTTCCCGGTCGAT	R118.25	CAAACGGAGGCTCAGGTCATAAGTC	R228.8	CAAGTTGGTCAGATTTCGCGCTTAT
R15.22	ACGCTTGGAAAGGTACCCGATCTAT	R118.32	CAAACGGAGGCTTAGGTCATTAGTC	R115.3	CAAGTTGGTCAGCCCACACGCTTAT
R256.2	ACGCTTGGTCAACGCACAGCCTTAT	R7.31	CAAAGCCTAACTAGTCAACGATCCT	R1599.12	CAAGTTGGTCAGCTAACACTCTTAT
R94.3	ACGCTTGGTCAGCCAACAGCCTTAT	R49.4	CAAAGTGAGCAGTTCCCGGTCTGAT	R2.20	CAAGTTGGTCAGCTCACACACTTAT
R94.2	ACGCTTGGTCAGCTAACAGCCTTAT	R1049.81	CAAATTGGTCAGCTAATCATTCAAT	R1395.5	CAAGTTGGTCAGGTTTCACGCTTAT
R62.16	ACGGTTGGTCAGCTAACACTCTTAT	R24.2	CAACCAGAGGCGTCGGTCATTAGTC	R11.5	CAAGTTGGTCAGTAATCACGCTTAT
R1447.4	ACGTTGGTCAGCTAATCACTTAAAT	R140.2	CAACTTGGTCAGATTACAGGCTTAT	R11.2	CAAGTTGGTCAGTACTCACGCTTAT
R21.3	ACGTTGGTCAGTTAATCACTCATAT	R6.4	CAACTTGGTCAGTCATCAGGCTTAT	R13.8	CAAGTTGGTCAGTGTTCACGCTTAT
R15.35	ACGTTTAGAAAGGTACCCGATCTAT	R6.2	CAACTTGGTCAGTTATCAGGCTTAT	R1532.6	CAAGTTGGTCAGTTAACACGCTCAT
R15.34	ACTCTTAGAAAGGTACCCGATCTAT	R1049.45	CAAGATCAAGTTGGTCAGCTAGTCA	R1532.3	CAAGTTGGTCAGTTAACACGCTTAT
R1638.2	ACTGTTGGTCAACTAATCACACAAT	R118.11	CAAGCAGAGGCTCAGGTCATAAGTC	R14.7	CAAGTTGGTCAGTTAATCACACAAT
R144.2	ACTGTTGGTCAGCTAACACACTTAT	R118.15	CAAGCAGAGGCTTAGGTCATTAGTC	R0.4	CAAGTTGGTCAGTTGTCACGCTTAT
R1335.16	ACTGTTGGTCAGCTAATCACACAAT	R434.2	CAAGCCTACTACATAGCTAACAGCC	R13.11	CAAGTTGGTCAGTTTTCACGCTTAT
R284.17	ACTTGGTTGCTACTGATCAGGCTAA	R1395.18	CAAGCTGGTCAAGTTTCACGCTTAT	R1395.19	CAAGTTGGTCGAGTTTCACGCTTAT
R46.3	AGAACACCTGTTAGCTAAGCGGTCA	R110.11	CAAGCTGGTCAATGTTCACGCTTAT	R0.25	CAAGTTGGTCGATTGTCACGCTTAT
R31.2	AGACCTAACAGGTGATACATTTCTA	R0.21	CAAGCTGGTCAATTGTCACGCTTAT	R228.11	CAAGTTGGTCGGATTTCACGCTTAT
R1532.13	AGAGTTGGTCAGTTAACACGCTTAT	R228.12	CAAGCTGGTCAGATTTCACGCTTAT	R1395.33	CAAGTTGGTTAAGTTTCACGCTTAT
R12.3	AGATGCATAGGTCATTAATCATCAC	R49.5	CAAGGTGAGCAGTTCCCGGTCTGAT	R0.39	CAAGTTGGTTAATTGTCACGCTTAT
R12.2	AGATGCATAGGTCATTAATCATCGC	R123.38	CAAGGTTGCTACTGATCAGGCTATA	R228.20	CAAGTTGGTTAGATTTCACGCTTAT
R12.4	AGATGCATAGGTCATTAGTCATCGC	R1395.22	CAAGTCGGTCAAGTTTCACGCTTAT	R0.38	CAAGTTTGTCAATTGTCACGCTTAT
R180.21	AGATTAAGCATGTAGGTCAGGCCGG	R0.24	CAAGTCGGTCAATTGTCACGCTTAT	R228.24	CAAGTTTGTCAGATTTCACGCTTAT
R128.18	AGATTATAGCATGTAGGTCAGCCCG	R228.15	CAAGTCGGTCAGATTTCACGCTTAT	R143.4	CAATACGGTTAGCTAAGCGGTCCTC
R22.2	AGCTGCATAGGTCATTAACCAGCGC	R1395.26	CAAGTTAGTCAAGTTTCACGCTTAT	R47.2	CAATCAGAGGCATAGGTCATCAGTC
R1256.4	AGGCTTAGTAAGGTACCCGGTCGAT	R0.31	CAAGTTAGTCAATTGTCACGCTTAT	R1395.29	CAATTTGGTCAAGTTTCACGCTTAT
R2.16	AGGGTTGGTCAGCTCACACACTTAT	R228.19	CAAGTTAGTCAGATTTCACGCTTAT	R228.22	CAATTTGGTCAGATTTCACGCTTAT
R26.3	AGGTCTCTGGTCGACTAAAATTCGA	R1395.31	CAAGTTGATCAAGTTTCACGCTTAT	R143.3	CACAAAACGGTTAGCTAAGCGGTCC
R26.2	AGGTCTCTGGTCGACTAAAATTCGG	R228.23	CAAGTTGATCAGATTTCACGCTTAT	R258.3	CACACGCTGGTTAGCTAAGCGGTCA
R1229.3	AGGTTGGTCAGTCAATCACCCAATG	R108.3	CAAGTTGGCCAAGTTTCACGCTTAT	R258.2	CACACGCTGGTTAGCTAAGCGGTCC
R344.4	AGTAGAGGCCCGGTCACTAGATCGC	R110.6	CAAGTTGGCCAATGTTCACGCTTAT	R123.21	CACAGTTGCTACTGATCAGGCTATA
R141.18	AGTCGATGCCAGTTGGGTATCACAG	R0.20	CAAGTTGGCCAATTGTCACGCTTAT	R29.2	CACCTTGGTCAGCTTATCAGGCAAT
R147.24	AGTTAGACATCCGTAGGCTTGATTC	R228.6	CAAGTTGGCCAGATTTCACGCTTAT	R123.29	CACGATTGCTACTGATCAGGCTATA
R821.2	AGTTGCATAGGTCATCAATCAACGC	R1395.25	CAAGTTGGTAAAGTTTCACGCTTAT	R123.7	CACGGCTGCTACTGATCAGGCTATA
R1869.2	ATAACCTACTACATAGCTAACAGCC	R0.27	CAAGTTGGTAAATTGTCACGCTTAT	R123.17	CACGGTCGCTACTGATCAGGCTATA
R7.37	ATACTGAGCCTAACAAGTCAACGAT	R228.16	CAAGTTGGTAAGATTTCACGCTTAT	R123.24	CACGGTTACTACTGATCAGGCTATA
R14.3	ATAGATCAAGTTGGTCAATTAATCA	R336.8	CAAGTTGGTCAAACTTCACGCTTAT	R123.32	CACGGTTCCTACTGATCAGGCTATA
R1049.112	ATAGATCAAGTTGGTCAGCTAAACA	R116.2	CAAGTTGGTCAAATCACACGCTTAT	R123.16	CACGGTTGCCACTGATCAGGCTATA
R1049.25	ATAGATCAAGTTGGTCAGCTAGTCA	R336.13	CAAGTTGGTCAAATTCCACGCTTAT	R123.15	CACGGTTGCTACCGATCAGGCTATA
R1049.89	ATAGATCAAGTTGGTCAGCTTATCA	R1.5	CAAGTTGGTCAAATTTCACACTTAT	R123.22	CACGGTTGCTACTAATCAGGCTATA
R1049.82	ATAGATCAAGTTGGTCAGTTAGTCA	R1.3	CAAGTTGGTCAAATTTCACGCTTAT	R123.12	CACGGTTGCTACTGACCAGGCTATA
R9.2	ATATCGGTGGTACAACGGCGGTTTG	R222.7	CAAGTTGGTCAACGTTCACGCTTAT	R123.26	CACGGTTGCTACTGATAAGGCTATA
R284.20	ATCTGGTTGCTACTGATCAGGCTAA	R0.10	CAAGTTGGTCAACTGTCACGCTTAT	R123.34	CACGGTTGCTACTGATCAAGCTATA
R3.12	ATCTTGGCCAGCCAATCAGTCAAAT	R336.5	CAAGTTGGTCAAGCTTCACGCTTAT	R123.31	CACGGTTGCTACTGATCAGACTATA
R45.2	ATCTTGGTCAATTAATCAGTCAAAT	R0.16	CAAGTTGGTCAAGTCTCACGCTTAT	R123.20	CACGGTTGCTACTGATCAGGCCATA
R3.8	ATCTTGGTCAGCCAATCAGTCAAAC	R108.4	CAAGTTGGTCAAGTTCCACGCTTAT	R123.41	CACGGTTGCTACTGATCAGGCTAAA
R3.2	ATCTTGGTCAGCCAATCAGTCAAAT	R1.7	CAAGTTGGTCAAGTTTCACACTTAT	R123.3	CACGGTTGCTACTGATCAGGCTACA
R3.11	ATCTTGGTCAGCCAATCAGTCAAGT	R1395.15	CAAGTTGGTCAAGTTTCACGCCTAT	R123.5	CACGGTTGCTACTGATCAGGCTAGA
R3.7	ATCTTGGTCAGCCAATCAGTCAGAT	R1395.11	CAAGTTGGTCAAGTTTCACGCTCAT	R123.2	CACGGTTGCTACTGATCAGGCTATA
R3.6	ATCTTGGTCAGCCAATCAGTCATAT	R1395.17	CAAGTTGGTCAAGTTTCACGCTTAA	R123.47	CACGGTTGCTACTGATCAGGCTATC
R3.9	ATCTTGGTCAGCCAATCAGTCGAAT	R1395.8	CAAGTTGGTCAAGTTTCACGCTTAC	R123.13	CACGGTTGCTACTGATCAGGCTATG
R3.14	ATCTTGGTCAGCCAGTCAGTCAAAT	R1395.2	CAAGTTGGTCAAGTTTCACGCTTAT	R123.39	CACGGTTGCTACTGATCAGGCTATT
R3.5	ATCTTGGTCAGCTAATCAGTCAAAT	R1395.24	CAAGTTGGTCAAGTTTCACGCTTGT	R123.11	CACGGTTGCTACTGATCAGGCTGTA
R3.13	ATCTTGGTCAGTCAATCAGTCAAAT	R1395.30	CAAGTTGGTCAAGTTTCACGTTTAT	R123.46	CACGGTTGCTACTGATCAGGCTTTA
R3.10	ATCTTGGTCGGCCAATCAGTCAAAT	R108.5	CAAGTTGGTCAAGTTTCACTCTTAT	R123.33	CACGGTTGCTACTGATCAGGTTATA
R56.2	ATGCAGAGGCCAATGGTCATAAGTC	R1395.27	CAAGTTGGTCAAGTTTCATGCTTAT	R123.45	CACGGTTGCTACTGATCAGTCTATA
R64.2	ATGCCTAGTAAGGTGCCCGATCGAT	R1395.14	CAAGTTGGTCAAGTTTCGCGCTTAT	R123.43	CACGGTTGCTACTGATCATGCTATA
R15.9	ATGCTTAGAAAGGTACCCGATCTAT	R1395.32	CAAGTTGGTCAAGTTTTACGCTTAT	R123.8	CACGGTTGCTACTGATCGGGCTATA
R1256.33	ATGCTTAGTAAGGTACCCGGTCGAT	R0.29	CAAGTTGGTCAATATTCACGCTTAT	R123.44	CACGGTTGCTACTGATCTGGCTATA
R348.5	ATGTTGGTCAACGAGTCACTCAAAT	R2164.5	CAAGTTGGTCAATCGTCACGCTTAT	R123.18	CACGGTTGCTACTGATTAGGCTATA
R266.2	ATGTTGGTCAACTAGTCACTCAAAT	R0.5	CAAGTTGGTCAATGCTCACGCTTAT	R123.9	CACGGTTGCTACTGGTCAGGCTATA
R181.2	ATGTTGGTCAGCTAATCACACTCAT	R222.3	CAAGTTGGTCAATGTCCACGCTTAT	R123.37	CACGGTTGCTACTTATCAGGCTATA
R1049.109	ATGTTGGTCAGCTAATCACACTTAT	R110.5	CAAGTTGGTCAATGTTCACACTTAT	R123.30	CACGGTTGCTATTGATCAGGCTATA
R1049.34	ATGTTGGTCAGCTAATCACTCGTAT	R110.9	CAAGTTGGTCAATGTTCACGCCTAT	R123.14	CACGGTTGCTGCTGATCAGGCTATA
R1335.17	ATGTTGGTCAGCTAGTCACTCAAAT	R110.10	CAAGTTGGTCAATGTTCACGCTCAT	R123.27	CACGGTTGTTACTGATCAGGCTATA
R21.2	ATGTTGGTCAGTTAATCACTCAGAT	R222.10	CAAGTTGGTCAATGTTCACGCTTAA	R123.28	CACGGTTTCTACTGATCAGGCTATA
R118.13	CAAACAGAGGCCCAGGTCATAAGTC	R222.4	CAAGTTGGTCAATGTTCACGCTTAC	R1049.29	CACGTTGGTCAGCTAATCACGTCAT
R118.26	CAAACAGAGGCCTAGGTCATTAGTC	R0.3	CAAGTTGGTCAATGTTCACGCTTAT	R1777.23	CACGTTGGTCAGTAATCACGCTTAT
R118.39	CAAACAGAGGCTAAGGTCATAAGTC	R222.9	CAAGTTGGTCAATGTTCGCGCTTAT	R123.42	CACGTTTGCTACTGATCAGGCTATA
R118.10	CAAACAGAGGCTCAGGCCATAAGTC	R0.12	CAAGTTGGTCAATTATCACGCTTAT	R17.8	CACTCGGTTAGCTAAGCGGTCCTTG
R118.37	CAAACAGAGGCTCAGGTAATAAGTC	R0.33	CAAGTTGGTCAATTCTCACGCTTAT	R123.40	CACTGTTGCTACTGATCAGGCTATA
R118.40	CAAACAGAGGCTCAGGTCACAAGTC	R0.8	CAAGTTGGTCAATTGCCACGCTTAT	R7.36	CAGAACCTAACTAGTCAACGATCCT
R118.6	CAAACAGAGGCTCAGGTCATAAGCC	R0.37	CAAGTTGGTCAATTGTAACGCTTAT	R118.5	CAGACAGAGGCTCAGGTCATAAGTC
R118.21	CAAACAGAGGCTCAGGTCATAAGTA	R0.13	CAAGTTGGTCAATTGTCACACTTAT	R88.11	CAGACAGAGGCTTAGGTCATTAGTC
R118.2	CAAACAGAGGCTCAGGTCATAAGTC	R0.18	CAAGTTGGTCAATTGTCACGCCTAT	R7.42	CAGAGCATAACTAGTCAACGATCCT
R118.19	CAAACAGAGGCTCAGGTCATAAGTT	R0.19	CAAGTTGGTCAATTGTCACGCTCAT	R7.20	CAGAGCCCAACTAGTCAACGATCCT
R118.18	CAAACAGAGGCTCAGGTCATAGGTC	R0.17	CAAGTTGGTCAATTGTCACGCTTAA	R7.18	CAGAGCCTAACCAGTCAACGATCCT
R118.34	CAAACAGAGGCTCAGGTCATGAGTC	R0.11	CAAGTTGGTCAATTGTCACGCTTAC	R7.34	CAGAGCCTAACTAATCAACGATCCT
R118.8	CAAACAGAGGCTCAGGTCATTAGTC	R0.2	CAAGTTGGTCAATTGTCACGCTTAT	R7.12	CAGAGCCTAACTAGCCAACGATCCT
R118.20	CAAACAGAGGCTCAGGTCGTAAGTC	R0.28	CAAGTTGGTCAATTGTCACGCTTGT	R7.29	CAGAGCCTAACTAGTAAACGATCCT
R118.31	CAAACAGAGGCTCATGTCATAAGTC	R0.35	CAAGTTGGTCAATTGTCACGTTTAT	R7.28	CAGAGCCTAACTAGTCAACAATCCT
R118.4	CAAACAGAGGCTCGGGTCATAAGTC	R0.32	CAAGTTGGTCAATTGTCATGCTTAT	R7.44	CAGAGCCTAACTAGTCAACCATCCT
R118.16	CAAACAGAGGCTTAGGCCATTAGTC	R0.15	CAAGTTGGTCAATTGTCGCGCTTAT	R7.17	CAGAGCCTAACTAGTCAACGACCCT
R118.33	CAAACAGAGGCTTAGGTCACTAGTC	R0.34	CAAGTTGGTCAATTGTTACGCTTAT	R7.40	CAGAGCCTAACTAGTCAACGATACT
R118.28	CAAACAGAGGCTTAGGTCATAAGTC	R0.7	CAAGTTGGTCAATTTTCACGCTTAT	R7.7	CAGAGCCTAACTAGTCAACGATCAT
R47.3	CAAACAGAGGCTTAGGTCATCAGTC	R11.3	CAAGTTGGTCAGAAATCACGCTTAT	R7.5	CAGAGCCTAACTAGTCAACGATCCA
R118.7	CAAACAGAGGCTTAGGTCATTAGCC	R11.4	CAAGTTGGTCAGACTTCACGCTTAT	R7.3	CAGAGCCTAACTAGTCAACGATCCC
R118.27	CAAACAGAGGCTTAGGTCATTAGTA	R11.7	CAAGTTGGTCAGATCTCACGCTTAT	R7.9	CAGAGCCTAACTAGTCAACGATCCG
R118.3	CAAACAGAGGCTTAGGTCATTAGTC	R1688.3	CAAGTTGGTCAGATTACACGCTTAT	R7.2	CAGAGCCTAACTAGTCAACGATCCT
R118.23	CAAACAGAGGCTTAGGTCATTAGTT	R228.4	CAAGTTGGTCAGATTCCACGCTTAT	R7.8	CAGAGCCTAACTAGTCAACGATCTT
R88.31	CAAACAGAGGCTTAGGTCATTGGTC	R1.8	CAAGTTGGTCAGATTTCACACTTAT	R7.27	CAGAGCCTAACTAGTCAACGATTCT

Table S3 - continued

RNA	N25 sequences	RNA	N25 sequences	RNA	N25 sequences
R7.16	CAGAGCCTAACTAGTCAACGGTCCT	R1777.12	CCCGTTGGTCAGTAATCACGCCTAT	R44.37	CTAGATCAACTTGGTCAGCTAGTCA
R7.24	CAGAGCCTAACTAGTCAACTATCCT	R1777.6	CCCGTTGGTCAGTAATCACGCTCAT	R44.57	CTAGATCAAGATGGTCAGCTAGTCA
R7.26	CAGAGCCTAACTAGTCAATGATCCT	R1777.14	CCCGTTGGTCAGTAATCACGCTTAA	R1049.75	CTAGATCAAGCTGGTCAGCTAAACA
R7.14	CAGAGCCTAACTAGTCAGCGATCCT	R1777.5	CCCGTTGGTCAGTAATCACGCTTAC	R970.2	CTAGATCAAGCTGGTCAGCTAGTCA
R7.15	CAGAGCCTAACTAGTCGACGATCCT	R1777.2	CCCGTTGGTCAGTAATCACGCTTAT	R970.4	CTAGATCAAGCTGGTCAGTTAGTCA
R7.19	CAGAGCCTAACTGGTCAACGATCCT	R1777.25	CCCGTTGGTCAGTAATCACGCTTGT	R37.77	CTAGATCAAGGTGGTCAGCTAGTCA
R7.33	CAGAGCCTAATTAGTCAACGATCCT	R1777.15	CCCGTTGGTCAGTAATCGCGCTTAT	R1049.86	CTAGATCAAGTCGGTCAGCTAAACA
R7.11	CAGAGCCTAGCTAGTCAACGATCCT	R1777.4	CCCGTTGGTCAGTAGTCACGCTTAT	R1335.4	CTAGATCAAGTCGGTCAGCTAGTCA
R7.21	CAGAGCCTGACTAGTCAACGATCCT	R1777.18	CCCGTTGGTCAGTGATCACGCTTAT	R1049.52	CTAGATCAAGTCGGTCAGTTAGTCA
R7.35	CAGAGCTTAACTAGTCAACGATCCT	R1777.3	CCCGTTGGTCAGTTAACACGCTTAT	R1049.93	CTAGATCAAGTTAGTCAGCTAAACA
R7.32	CAGAGTCTAACTAGTCAACGATCCT	R1777.11	CCCGTTGGTCGGTAATCACGCTTAT	R1049.17	CTAGATCAAGTTAGTCAGCTAGTCA
R7.43	CAGATCCTAACTAGTCAACGATCCT	R284.21	CCCTGGTTGCTACTGATCAGGCTAA	R44.48	CTAGATCAAGTTCGTCAGCTAGTCA
R1256.23	CAGCTTAGTAAGGTACCCGGTCGAT	R1777.19	CCCTTTGGTCAGTAATCACGCTTAT	R1049.96	CTAGATCAAGTTGATCAGCTAAACA
R1.22	CAGGCTGGTCAAATTTCACACTTAT	R7.30	CCGAGCCTAACTAGTCAACGATCCT	R1049.19	CTAGATCAAGTTGATCAGCTAGTCA
R7.10	CAGGGCCTAACTAGTCAACGATCCT	R465.2	CCGCATGAATAAGGTACCCGGTCAG	R1049.66	CTAGATCAAGTTGATCAGTTAGTCA
R1.26	CAGGTCGGTCAAATTTCACACTTAT	R15.10	CCGCTTAGAAAGGTACCCGATCTAT	R1049.40	CTAGATCAAGTTGCTCAGCTAGTCA
R1.19	CAGGTTGGCCAAATTTCACACTTAT	R456.2	CCGTCTCCAGTCGACTAAAATTCGG	R1049.104	CTAGATCAAGTTGCTCAGTTAGTCA
R1.20	CAGGTTGGTCAAAATTCACACTTAT	R105.4	CCTAGATCAAGTTGGTCAGTTAACA	R1049.39	CTAGATCAAGTTGGACAGCTAGTCA
R1.6	CAGGTTGGTCAAACTTCACACTTAT	R8.2	CCTCTTGGTCAGATAATCAGACAAT	R1049.113	CTAGATCAAGTTGGACAGTTAGTCA
R1.15	CAGGTTGGTCAAATCTCACACTTAT	R8.4	CCTCTTGGTCAGCTTATCAGACAAT	R1049.61	CTAGATCAAGTTGGCCAGCTAAACA
R1.25	CAGGTTGGTCAAATTACACACTTAT	R8.5	CCTCTTGGTCAGTTCATCAGACAAT	R167.2	CTAGATCAAGTTGGCCAGCTAGTCA
R1.16	CAGGTTGGTCAAATTCCACACTTAT	R8.3	CCTCTTGGTCAGTTTATCAGACAAT	R105.8	CTAGATCAAGTTGGCCAGTTAGTCA
R1.24	CAGGTTGGTCAAATTTCACACCTAT	R1017.2	CCTGATGGTCAGTTTATCTCACAAT	R1049.64	CTAGATCAAGTTGGGCAGCTAGTCA
R1.12	CAGGTTGGTCAAATTTCACACTCAT	R338.2	CCTGGAACCCGCGGGTCGGTCATAA	R1049.91	CTAGATCAAGTTGGTAAGCTAAACA
R1.13	CAGGTTGGTCAAATTTCACACTTAC	R338.3	CCTGGAACCCGTGGGTCGGTCATAA	R1049.16	CTAGATCAAGTTGGTAAGCTAGTCA
R1.2	CAGGTTGGTCAAATTTCACACTTAT	R338.4	CCTGGAGCCCGCGGGTCGGTCATAA	R1049.90	CTAGATCAAGTTGGTCAACTAAACA
R1.4	CAGGTTGGTCAAATTTCACGCTTAT	R122.2	CCTGTTGGTCAGCGCACACACTCAT	R1049.8	CTAGATCAAGTTGGTCAACTAGTCA
R1.18	CAGGTTGGTCAAATTTCGCACTTAT	R1777.24	CCTGTTGGTCAGTAATCACGCTTAT	R37.91	CTAGATCAAGTTGGTCAATTTGTCA
R40.3	CAGGTTGGTCAACAATCACACTTAT	R581.2	CCTTAGGGTAAGCTAAGCGGTCATC	R1049.26	CTAGATCAAGTTGGTCACCTAGTCA
R40.2	CAGGTTGGTCAACCCTCACACTTAT	R143.8	CCTTTTACGGTTAGCTAAGCGGTCC	R1049.102	CTAGATCAAGTTGGTCACTTAGTCA
R1.17	CAGGTTGGTCAAGTTTCACACTTAT	R118.17	CGAACAGAGGCTCAGGTCATAAGTC	R1049.42	CTAGATCAAGTTGGTCAGATAGTCA
R1395.10	CAGGTTGGTCAAGTTTCACGCTTAT	R88.22	CGAACAGAGGCTTAGGTCATTAGTC	R1049.47	CTAGATCAAGTTGGTCAGCAAGTCA
R1060.2	CAGGTTGGTCAATCACTACACTTAT	R1051.11	CGAGATCAAGTTGGTCAGCTAGTCA	R1049.65	CTAGATCAAGTTGGTCAGCCAAACA
R1060.3	CAGGTTGGTCAATCGCTACACTTAT	R7.41	CGAGCCTAACTAGTCAACGATACTT	R1049.10	CTAGATCAAGTTGGTCAGCCAGTCA
R110.4	CAGGTTGGTCAATGTTCACGCTTAT	R1395.20	CGAGTTGGTCAAGTTTCACGCTTAT	R1049.88	CTAGATCAAGTTGGTCAGCGAGTCA
R117.2	CAGGTTGGTCAATTAACACACTTAT	R110.12	CGAGTTGGTCAATGTTCACGCTTAT	R1049.3	CTAGATCAAGTTGGTCAGCTAAACA
R0.26	CAGGTTGGTCAATTGTCACACTTAT	R0.22	CGAGTTGGTCAATTGTCACGCTTAT	R1049.67	CTAGATCAAGTTGGTCAGCTAAACG
R0.9	CAGGTTGGTCAATTGTCACGCTTAT	R228.14	CGAGTTGGTCAGATTTCACGCTTAT	R1049.79	CTAGATCAAGTTGGTCAGCTAAACT
R1.11	CAGGTTGGTCAGATTTCACACTTAT	R383.2	CGATGGTCAACTAATCTCTTAGAAT	R1049.98	CTAGATCAAGTTGGTCAGCTAAATA
R1.9	CAGGTTGGTCAGATTTCACGCTTAT	R128.47	CGATTATAGCATGTAGGTCAGCCCG	R1049.106	CTAGATCAAGTTGGTCAGCTAACCA
R1335.13	CAGGTTGGTCAGCTAGTCACACAAT	R845.6	CGCAACTTAGGTTAGCTAAGCGGTC	R1049.33	CTAGATCAAGTTGGTCAGCTAAGCA
R2.3	CAGGTTGGTCAGCTCACACACTTAT	R293.3	CGCATGAATATAGGCACTCGGTCAG	R1049.4	CTAGATCAAGTTGGTCAGCTAATCA
R35.5	CAGTAAGACATCCGTAGGTATGATC	R293.2	CGCATGAATATAGGTACTCGGTCAG	R1049.27	CTAGATCAAGTTGGTCAGCTACTCA
R177.6	CAGTAAGACATCCGTATACGTGATC	R250.12	CGCATGAATTAGGCAACTCGGTCAG	R1050.86	CTAGATCAAGTTGGTCAGCTAGAAA
R558.2	CAGTCTCAGGGTACGTAGTTTGGCC	R250.11	CGCATGAGCTAGGCAACTCGGTCAG	R1049.31	CTAGATCAAGTTGGTCAGCTAGACA
R147.5	CAGTTAGACATCCGTAGGCACGATC	R250.13	CGCATGAGTCAGGCAACTCGGTCAG	R1449.3	CTAGATCAAGTTGGTCAGCTAGCCA
R10.4	CAGTTGGTCAGCCAATCACAGGGGG	R250.6	CGCATGAGTTAGGCAACCCGGTCAG	R971.10	CTAGATCAAGTTGGTCAGCTAGGCA
R1050.83	CAGTTGGTCAGCTAAACACTCGGAG	R250.10	CGCATGAGTTAGGCAACTCGGCCAG	R971.11	CTAGATCAAGTTGGTCAGCTAGGCT
R10.3	CAGTTGGTCAGTCAATCACAGGGGA	R250.4	CGCATGAGTTAGGCAACTCGGTCAA	R1049.15	CTAGATCAAGTTGGTCAGCTAGTAA
R10.2	CAGTTGGTCAGTCAATCACAGGGGG	R250.2	CGCATGAGTTAGGCAACTCGGTCAG	R1051.2	CTAGATCAAGTTGGTCAGCTAGTCA
R1314.2	CAGTTGGTCAGTTAATCACAGAGGC	R250.15	CGCATGAGTTAGGCAACTCGGTCAT	R1049.30	CTAGATCAAGTTGGTCAGCTAGTCC
R10.5	CAGTTGGTCAGTTAATCACAGGGGG	R250.9	CGCATGAGTTAGGCAACTCGGTCGG	R1049.5	CTAGATCAAGTTGGTCAGCTAGTCG
R447.2	CAGTTGGTCAGTTAATCACTCGTTT	R250.8	CGCATGAGTTAGGCAGCTCGGTCAG	R1049.14	CTAGATCAAGTTGGTCAGCTAGTCT
R7.22	CATAGCCTAACTAGTCAACGATCCT	R250.5	CGCATGAGTTAGGCGACTCGGTCAG	R1049.46	CTAGATCAAGTTGGTCAGCTAGTGA
R106.4	CATATTGGTTAGCTAAGCGGTCATC	R250.3	CGCATGAGTTAGGTAACTCGGTCAG	R1049.18	CTAGATCAAGTTGGTCAGCTAGTTA
R123.10	CATGGTTGCTACTGATCAGGCTATA	R250.14	CGCATGAGTTGGGCAACTCGGTCAG	R1049.21	CTAGATCAAGTTGGTCAGCTATTCA
R959.2	CATTCGGTTAGCTAAGCGGTCCTTG	R250.7	CGCATGGGTTAGGCAACTCGGTCAG	R1049.101	CTAGATCAAGTTGGTCAGCTCATCA
R88.34	CCAACAGAGGCTTAGGTCATTAGTC	R106.7	CGCATTGGTTAGCTAAGCGGTCATC	R1049.62	CTAGATCAAGTTGGTCAGCTCGTCA
R146.3	CCAAGCGGTTAGCTAAGCGGTCATC	R123.4	CGCGGTTGCTACTGATCAGGCTATA	R1049.80	CTAGATCAAGTTGGTCAGCTGAACA
R1447.8	CCACGTTGGTCAGCTAATCACGTGC	R340.2	CGGACGTAGAAAGGTTTATTAAGTT	R1049.11	CTAGATCAAGTTGGTCAGCTGGTCA
R48.2	CCACTTGGTCAGTTAACAGTCTTAT	R7.13	CGGAGCCTAACTAGTCAACGATCCT	R1049.35	CTAGATCAAGTTGGTCAGCTTGTCA
R1049.72	CCAGATCAAGTTGGTCAGCTAAACA	R1.21	CGGGTTGGTCAAATTTCACACTTAT	R1049.74	CTAGATCAAGTTGGTCAGGTAGTCA
R1051.3	CCAGATCAAGTTGGTCAGCTAGTCA	R106.5	CGTACTGGTTAGCTAAGCGGTCATC	R1049.38	CTAGATCAAGTTGGTCAGTCAGTCA
R105.14	CCAGATCAAGTTGGTCAGTTAGTCA	R845.5	CGTATAGGTTAGCTAAGCGGTCATA	R1049.78	CTAGATCAAGTTGGTCAGTTAAACA
R19.5	CCAGCATGAACATGTAACCGGTCAG	R106.14	CGTATCGGTTAGCTAAGCGGTCATC	R1049.32	CTAGATCAAGTTGGTCAGTTAATCA
R19.3	CCAGCATGAATATGTAACCAGTCAG	R106.12	CGTATTGGCTAGCTAAGCGGTCATC	R1049.84	CTAGATCAAGTTGGTCAGTTACTCA
R19.2	CCAGCATGAATATGTAACCGGTCAG	R106.20	CGTATTGGTCAGCTAAGCGGTCATC	R1049.43	CTAGATCAAGTTGGTCAGTTAGCCA
R19.4	CCAGCATGAATATGTAATCGGTCAG	R106.17	CGTATTGGTTAGCCAAGCGGTCATC	R105.19	CTAGATCAAGTTGGTCAGTTAGTAA
R19.6	CCAGCATGAATATGTAGCCGGTCAG	R106.19	CGTATTGGTTAGCTAAGCAGTCATC	R1049.2	CTAGATCAAGTTGGTCAGTTAGTCA
R19.7	CCAGCATGAGTATGTAACCGGTCAG	R106.10	CGTATTGGTTAGCTAAGCGGCCATC	R1049.99	CTAGATCAAGTTGGTCAGTTAGTCC
R249.2	CCAGTTGGTCAAAGTACACTCTTAT	R106.3	CGTATTGGTTAGCTAAGCGGTCACC	R1049.41	CTAGATCAAGTTGGTCAGTTAGTCG
R20.2	CCAGTTGGTCAAATGTCACTCTTAT	R106.15	CGTATTGGTTAGCTAAGCGGTCAGC	R1049.56	CTAGATCAAGTTGGTCAGTTAGTCT
R205.2	CCAGTTGGTCAACTAACACTCTTAT	R106.9	CGTATTGGTTAGCTAAGCGGTCATA	R1049.63	CTAGATCAAGTTGGTCAGTTAGTTA
R108.2	CCAGTTGGTCAAGTTTCACTCTTAT	R106.2	CGTATTGGTTAGCTAAGCGGTCATC	R1049.70	CTAGATCAAGTTGGTCAGTTATTCA
R1599.5	CCAGTTGGTCAGCTAACACTCTTAT	R106.6	CGTATTGGTTAGCTAAGCGGTCATT	R1049.48	CTAGATCAAGTTGGTCAGTTGGTCA
R1777.22	CCAGTTGGTCAGTAATCACGCTTAT	R106.8	CGTATTGGTTAGCTAAGCGGTCGTC	R1049.105	CTAGATCAAGTTGGTCAGTTTGTCA
R191.2	CCAGTTGGTCAGTAATCACTCTTAT	R106.18	CGTATTGGTTAGCTGAGCGGTCATC	R1049.111	CTAGATCAAGTTGGTCATCTAAACA
R135.18	CCATCGCGTTAGCTAAGCGGTCATC	R106.13	CGTATTGGTTGGCTAAGCGGTCATC	R1049.23	CTAGATCAAGTTGGTCATCTAGTCA
R223.2	CCATTGGTCAGCCATATCATGCAAT	R106.16	CGTGTTGGTTAGCTAAGCGGTCATC	R1049.68	CTAGATCAAGTTGGTCATTTAGTCA
R124.2	CCCATTGGTCAGCCAATCATGCAAT	R1049.100	CTAAATCAAGTTGGTCAGCTAAACA	R1049.50	CTAGATCAAGTTGGTCCGCTAGTCA
R1777.13	CCCGCTGGTCAGTAATCACGCTTAT	R1049.20	CTAAATCAAGTTGGTCAGCTAGTCA	R1049.60	CTAGATCAAGTTGGTCGGCTAAACA
R123.35	CCCGGTTGCTACTGATCAGGCTATA	R146.5	CTAAGCGGTTAGCTAAGCGGTCACC	R1049.7	CTAGATCAAGTTGGTCGGCTAGTCA
R1777.17	CCCGTCGGTCAGTAATCACGCTTAT	R146.2	CTAAGCGGTTAGCTAAGCGGTCATC	R1049.36	CTAGATCAAGTTGGTCTGCTAGTCA
R1777.10	CCCGTTGGCCAGTAATCACGCTTAT	R146.4	CTAAGTGGTTAGCTAAGCGGTCATC	R1049.110	CTAGATCAAGTTGGTCTGTTAGTCA
R1777.21	CCCGTTGGTAAGTAATCACGCTTAT	R1449.9	CTACATCAAGTTGGTCAGCTAGTCA	R1052.55	CTAGATCAAGTTGGTGAGCTAGTCA
R110.2	CCCGTTGGTCAAAATTCACGCTTAT	R266.6	CTACATCAAGTTGGTCAGTTAGTCA	R1049.94	CTAGATCAAGTTGGTTAGCTAAACA
R452.2	CCCGTTGGTCAAATGCTACGCTCAT	R1812.4	CTAGAACAAGTTGGTCAGCTAGTCA	R1049.83	CTAGATCAAGTTGTTCAGTTAGTCA
R108.6	CCCGTTGGTCAAGTTTCACGCTTAT	R1049.69	CTAGACCAAGTTGGTCAGCTAAACA	R1049.95	CTAGATCAAGTTTGTCAGCTAAACA
R110.7	CCCGTTGGTCAATAATCACGCTTAT	R1812.2	CTAGACCAAGTTGGTCAGCTAGTCA	R970.3	CTAGATCAAGTTTGTCAGCTAGTCA
R0.30	CCCGTTGGTCAATTGTCACGCTTAT	R1812.3	CTAGACCAAGTTGGTCAGTTAGTCA	R1049.103	CTAGATCAATTTGGTCAGCTAAACA
R1291.14	CCCGTTGGTCAGATTTCACGCTTAT	R1812.9	CTAGAGCAAGTTGGTCAGCTAGTCA	R44.18	CTAGATCAATTTGGTCAGCTAGTCA
R1777.7	CCCGTTGGTCAGCAATCACGCTTAT	R7.6	CTAGAGCCTAACTAGTCAAACGATC	R1049.71	CTAGATCACGTTGGTCAGCTAGTCA
R1777.8	CCCGTTGGTCAGGCATCACGCTCAT	R1049.107	CTAGATAAAGTTGGTCAGCTAAACA	R1049.59	CTAGATCACGTTGGTCAGCTCATCA
R1777.20	CCCGTTGGTCAGTAAACACGCTTAT	R1049.22	CTAGATAAAGTTGGTCAGCTAGTCA	R1049.58	CTAGATCAGGTTGGTCAGCTAAACA
R1777.9	CCCGTTGGTCAGTAACCACGCTTAT	R1049.108	CTAGATCAAATTGGTCAGCTAAACA	R1049.9	CTAGATCAGGTTGGTCAGCTAGTCA
R1777.16	CCCGTTGGTCAGTAATCACACTTAT	R1049.24	CTAGATCAAATTGGTCAGCTAGTCA	R44.44	CTAGATCAGGTTGGTCAGTTAGTCA

Table S3 - continued

RNA	N25 sequences	RNA	N25 sequences	RNA	N25 sequences
R1335.8	CTAGATCATGTTGGTCAGCTAGTCA	R317.3	GCACTTCATCGTTAGCTAAGCGGTC	R180.37	GGATTAAGCATGTAGGTCAGGCCGC
R1049.49	CTAGATCCAGTTGGTCAGCTAGTCA	R391.2	GCACTTGGTCAGCTCATCAGTCGCA	R180.2	GGATTAAGCATGTAGGTCAGGCCGG
R1049.76	CTAGATCGAGTTGGTCAGCTAAACA	R1599.9	GCAGTTGGTCAGCTAACACTCTTAT	R180.27	GGATTAAGCATGTAGGTCAGGCCGT
R1049.13	CTAGATCGAGTTGGTCAGCTAGTCA	R135.23	GCATAGCGTTAGCTAAGCGGTCATC	R180.18	GGATTAAGCATGTAGGTCAGGCTGG
R37.44	CTAGATCTAGTTGGTCAGCTAGTCA	R5.30	GCATCACGTGAGCTAAGCGGTCATC	R180.16	GGATTAAGCATGTAGGTCAGGTCGG
R37.96	CTAGATGAAGTTGGTCAGCTAGTCA	R1138.4	GCATCACGTTAGCTAAGCGGTCATC	R180.4	GGATTAAGCATGTAGGTCAGTCCGG
R1049.97	CTAGATTAAGTTGGTCAGCTAAACA	R135.26	GCATCCCGTTAGCTAAGCGGTCATC	R180.8	GGATTAAGCATGTAGGTCGGGCCGG
R37.22	CTAGATTAAGTTGGTCAGCTAGTCA	R28.5	GCATCGAGTTAGCTAAGCGGTCATC	R180.20	GGATTAAGCATGTAGGTTAGGCCGG
R65.3	CTAGATTAAGTTGGTCAGTTAGTCA	R135.17	GCATCGCATTAGCTAAGCGGTCATC	R180.39	GGATTAAGCATGTAGTTCAGGCCGG
R1049.85	CTAGCTCAAGTTGGTCAGCTAGTCA	R135.27	GCATCGCCTTAGCTAAGCGGTCATC	R180.26	GGATTAAGCATGTATGTTCAGGCCGG
R1049.54	CTAGGTCAAGTTGGTCAGCTAAACA	R5.27	GCATCGCGCGAGCTAAGCGGTCATC	R180.10	GGATTAAGCATGTGGGTCAGGCCGG
R1049.6	CTAGGTCAAGTTGGTCAGCTAGTCA	R5.13	GCATCGCGTAAGCTAAGCGGTCATC	R180.28	GGATTAAGCATTTAGGTCAGGCCGG
R37.42	CTAGGTCAAGTTGGTCAGTTAGTCA	R5.9	GCATCGCGTCAGCTAAGCGGTCATC	R180.13	GGATTAAGCGTGTAGGTCAGGCCGG
R1049.51	CTAGTTCAAGTTGGTCAGCTAGTCA	R5.36	GCATCGCGTGAACTAAGCGGTCATC	R180.34	GGATTAAGTATGTAGGTCAGGCCGG
R114.2	CTAGTTGGTCAACCCACACACTCAT	R5.34	GCATCGCGTGAGCCAAGCGGTCATC	R180.38	GGATTAATCATGTAGGTCAGGCCGG
R114.3	CTAGTTGGTCAACTAACACACTCAT	R5.31	GCATCGCGTGAGCTAAGCAGTCATC	R128.5	GGATTACAGCATGTAGGTCAGCCCG
R563.3	CTAGTTGGTCAATCAACACACTTAT	R5.23	GCATCGCGTGAGCTAAGCGGCCATC	R180.6	GGATTAGGCATGTAGGTCAGGCCGG
R563.2	CTAGTTGGTCAATCATCACACTCAT	R5.33	GCATCGCGTGAGCTAAGCGGTAATC	R128.23	GGATTATAACATGTAGGTCAGCCCG
R204.3	CTAGTTGGTCAATTTACACACTTAT	R5.18	GCATCGCGTGAGCTAAGCGGTCACC	R128.42	GGATTATACCATGTAGGTCAGCCCG
R463.3	CTAGTTGGTCAGAATACACACTCAT	R5.22	GCATCGCGTGAGCTAAGCGGTCATA	R128.54	GGATTATAGAATGTAGGTCAGCCCG
R114.4	CTAGTTGGTCAGCCCACACACTCAT	R5.2	GCATCGCGTGAGCTAAGCGGTCATC	R128.57	GGATTATAGCAAGTAGGTCAGCCCG
R204.2	CTAGTTGGTCAGCTTTCACACTTAT	R5.16	GCATCGCGTGAGCTAAGCGGTCATT	R128.11	GGATTATAGCACGTAGGTCAGCCCG
R463.4	CTAGTTGGTCAGTATTCACACTCAT	R5.24	GCATCGCGTGAGCTAAGCGGTCGTC	R128.58	GGATTATAGCAGGTAGGTCAGCCCG
R463.2	CTAGTTGGTCAGTATTCACACTTAT	R5.35	GCATCGCGTGAGCTAAGCGGTTATC	R128.24	GGATTATAGCATATAGGTCAGCCCG
R143.6	CTATACGGTTAGCTAAGCGGTCCCC	R5.32	GCATCGCGTGAGCTAAGTGGTCATC	R128.45	GGATTATAGCATCTAGGTCAGCCCG
R143.5	CTATACGGTTAGCTAAGCGGTCCTA	R5.15	GCATCGCGTGAGCTAGGCGGTCATC	R128.46	GGATTATAGCATGAAGGTCAGCCCG
R143.2	CTATACGGTTAGCTAAGCGGTCCTC	R5.29	GCATCGCGTGAGCTGAGCGGTCATC	R128.15	GGATTATAGCATGCAGGTCAGCCCG
R143.7	CTATACGGTTAGCTAAGCGGTCCTG	R5.21	GCATCGCGTGGGCTAAGCGGTCATC	R128.27	GGATTATAGCATGTAAGTCAGCCCG
R1049.92	CTATATCAAGTTGGTCAGCTAAACA	R5.11	GCATCGCGTTAACTAAGCGGTCATC	R128.31	GGATTATAGCATGTAGATCAGCCCG
R1449.5	CTATATCAAGTTGGTCAGCTAGTCA	R5.17	GCATCGCGTTACCTAAGCGGTCATC	R128.48	GGATTATAGCATGTAGCTCAGCCCG
R106.11	CTCATATTGGTTAGCTAAGCGGTCC	R5.10	GCATCGCGTTAGCCAAGCGGTCATC	R128.43	GGATTATAGCATGTAGGACAGCCCG
R1049.57	CTCGATCAAGTTGGTCAGCTAGTCA	R1138.10	GCATCGCGTTAGCTAAACGGTCATC	R128.6	GGATTATAGCATGTAGGCCAGCCCG
R123.25	CTCGGTTGCTACTGATCAGGCTATA	R1138.14	GCATCGCGTTAGCTAAGAGGTCATC	R128.26	GGATTATAGCATGTAGGTAAGCCCG
R38.4	CTGAAAGGTTAGCTAAGCGGTCACC	R1138.6	GCATCGCGTTAGCTAAGCAGTCATC	R128.30	GGATTATAGCATGTAGGTCAACCCG
R7.23	CTGAGCCTAACTAGTCAACGATCCT	R1138.9	GCATCGCGTTAGCTAAGCGATCATC	R128.32	GGATTATAGCATGTAGGTCACCCCG
R38.2	CTGATAGGTTAGCTAAGCGGTCATC	R135.36	GCATCGCGTTAGCTAAGCGGACATC	R128.52	GGATTATAGCATGTAGGTCAGACCG
R56.4	CTGCAGAGGCCAATGGTCATAAGTC	R1138.2	GCATCGCGTTAGCTAAGCGGCCATC	R128.40	GGATTATAGCATGTAGGTCAGCACG
R1049.73	CTGGATCAAGTTGGTCAGCTAAACA	R1138.7	GCATCGCGTTAGCTAAGCGGTAATC	R128.19	GGATTATAGCATGTAGGTCAGCCAG
R1049.12	CTGGATCAAGTTGGTCAGCTAGTCA	R135.32	GCATCGCGTTAGCTAAGCGGTCAAC	R128.3	GGATTATAGCATGTAGGTCAGCCCA
R105.15	CTGGATCAAGTTGGTCAGTTAGTCA	R299.4	GCATCGCGTTAGCTAAGCGGTCACC	R128.29	GGATTATAGCATGTAGGTCAGCCCC
R297.2	CTGTATGGGTTAGCTAAGCGGTCGG	R299.5	GCATCGCGTTAGCTAAGCGGTCAGC	R128.2	GGATTATAGCATGTAGGTCAGCCCG
R457.2	CTTCGAAGGTTAGCTAAGCGGTCGG	R299.3	GCATCGCGTTAGCTAAGCGGTCATA	R128.12	GGATTATAGCATGTAGGTCAGCCCT
R1049.37	CTTGATCAAGTTGGTCAGCTAGTCA	R299.2	GCATCGCGTTAGCTAAGCGGTCATC	R128.55	GGATTATAGCATGTAGGTCAGCCGG
R105.36	CTTGATCAAGTTGGTCAGTTAGTCA	R299.6	GCATCGCGTTAGCTAAGCGGTCATG	R128.20	GGATTATAGCATGTAGGTCAGCCTG
R38.3	CTTTTAGGTTAGCTAAGCGGTCATC	R135.3	GCATCGCGTTAGCTAAGCGGTCATT	R128.28	GGATTATAGCATGTAGGTCAGCTCG
R46.2	GAAAACCTCGTTAGCTAAGCGGTCA	R1138.13	GCATCGCGTTAGCTAAGCGGTCCTC	R128.10	GGATTATAGCATGTAGGTCAGTCCG
R66.2	GAAAACTTCGTTAGCTAAGCGGTCC	R1138.3	GCATCGCGTTAGCTAAGCGGTCGTC	R128.37	GGATTATAGCATGTAGGTCATCCCG
R1532.12	GAAGTTGGTCAGTTAACACGCTTAT	R135.33	GCATCGCGTTAGCTAAGCGGTCTTC	R128.7	GGATTATAGCATGTAGGTCGGCCCG
R66.3	GAATAACTTCGTTAGCTAAGCGGTC	R1138.5	GCATCGCGTTAGCTAAGCGGTTATC	R128.22	GGATTATAGCATGTAGGTTAGCCCG
R615.2	GAATACTCGTTAGCTAAGCGGTCAC	R135.34	GCATCGCGTTAGCTAAGCGTTCATC	R128.41	GGATTATAGCATGTAGTTCAGCCCG
R615.4	GAATACTCGTTAGCTAAGCGGTCAT	R1138.11	GCATCGCGTTAGCTAAGCTGTCATC	R128.33	GGATTATAGCATGTATGTCAGCCCG
R135.37	GAATCGCGTTAGCTAAGCGGTCATC	R1138.8	GCATCGCGTTAGCTAAGTGGTCATC	R128.13	GGATTATAGCATGTGGGTCAGCCCG
R46.4	GAATCTCGTTAGCTAAGCGGTCATA	R135.24	GCATCGCGTTAGCTAATCGGTCATC	R128.50	GGATTATAGCATGTTGGTCAGCCCG
R66.4	GAATCTCTTCGTTAGCTAAGCGGTC	R595.2	GCATCGCGTTAGCTAGGCGGTCATC	R128.36	GGATTATAGCATTTAGGTCAGCCCG
R180.32	GAATTAAGCATGTAGGTCAGGCCGG	R595.5	GCATCGCGTTAGCTATGCGGTCATC	R128.8	GGATTATAGCGTGTAGGTCAGCCCG
R128.34	GAATTATAGCATGTAGGTCAGCCCG	R135.11	GCATCGCGTTAGCTGAGCGGTCATC	R128.53	GGATTATAGCTTGTAGGTCAGCCCG
R16.11	GACAACCCGTTAGCTAAGCGGTCAG	R5.12	GCATCGCGTTAGTTAAGCGGTCATC	R128.16	GGATTATAGTATGTAGGTCAGCCCG
R16.4	GACAACTCGTTAGCTAAGCGGTCAA	R5.14	GCATCGCGTTATCTAAGCGGTCATC	R128.39	GGATTATATCATGTAGGTCAGCCCG
R16.9	GACAACTCGTTAGCTAAGCGGTCAC	R5.7	GCATCGCGTTGGCTAAGCGGTCATC	R128.51	GGATTATCGCATGTAGGTCAGCCCG
R16.2	GACAACTCGTTAGCTAAGCGGTCAG	R135.8	GCATCGCTTTAGCTAAGCGGTCATC	R180.30	GGATTATGCATGTAGGTCAGGCCGG
R16.8	GACAACTCGTTAGCTAAGCGGTCAT	R135.16	GCATCGTGTTAGCTAAGCGGTCATC	R128.4	GGATTATGGCATGTAGGTCAGCCCG
R16.3	GACAACTCGTTAGCTAAGCGGTCGG	R135.22	GCATCTCGTTAGCTAAGCGGTCATC	R128.35	GGATTATTGCATGTAGGTCAGCCCG
R1094	GACAACTCGTTAGCTAGGCGGTCAG	R135.35	GCATGGCGTTAGCTAAGCGGTCATC	R180.19	GGATTGAGCATGTAGGTCAGGCCGG
R468.2	GACAAGTTCGTTAGCTAAGCGGCCA	R128.49	GCATTATAGCATGTAGGTCAGCCCG	R128.17	GGATTGTAGCATGTAGGTCAGCCCG
R1094.2	GACAATTCGTTAGCTAGGCGGTCAG	R5.5	GCATTGCGTGAGCTAAGCGGTCATC	R128.56	GGATTTTAGCATGTAGGTCAGCCCG
R587.2	GACACTTATGCGGTCAGCCTTACTG	R135.2	GCATTGCGTTAGCTAAGCGGTCATC	R344.3	GGCAGAGGCCCGGTCACTAGATCGC
R236.4	GACCTGTATCGTTAGCTAAGCGGTC	R50.3	GCATTTTGCGTTAGCTAAGCGGCCA	R476.2	GGCATCAACGTTAGCTAAGCGGTCA
R16.7	GACGACTCGTTAGCTAAGCGGTCAG	R50.2	GCATTTTGCGTTAGCTAAGCGGCCC	R476.4	GGCATCAACGTTAGCTAAGCGGTCC
R1138.12	GACGATATGCGTTAGCTAAGCGGCC	R137.2	GCCGCGTGGTACGTGGACTTGGACC	R476.3	GGCATCAACGTTAGCTAAGCGGTCG
R1187.6	GACTATATCGTTAGCTAAGCGGTAC	R119.3	GCCGGAGGTACGTGGAACTTGGACC	R30.2	GGCATGAGTTACGACAATCGGTCAG
R34.2	GACTCCTACTACATAGCTAACAGCC	R135.25	GCCTCGCGTTAGCTAAGCGGTCATC	R30.3	GGCATGAGTTACGACAGTCGGTCAG
R1187.3	GAGAATATCGTTAGCTAAGCGTGTC	R284.5	GCCTGGTTGCTACTGATCAGGCTAA	R17.4	GGCCACACCGTTAGCTAAGCGGTCC
R317.5	GAGATCATCGTTAGCTAAGCGGTCG	R15.11	GCGCTTAGAAAGGTACCCGATCTAT	R141.7	GGCCGATGCCAGTTGGGTATCACAG
R7.39	GAGCCTAACTAGTCAAACGATTCTT	R5.26	GCGTCGCGTGAGCTAAGCGGTCATC	R199.5	GGCCTCCGTTAGCTATGCGGTATCC
R1256.14	GAGCTTAGTAAGGTACCCGGTCGAT	R135.4	GCGTCGCGTTAGCTAAGCGGTCATC	R199.4	GGCTTCCGTTAGCTATGCGGTATCA
R2.22	GAGGTTGGTCAGCTCACACACTTAT	R135.31	GCTTCGCGTTAGCTAAGCGGTCATC	R199.2	GGCTTCCGTTAGCTATGCGGTATCC
R470.2	GAGTATCGTTAGCTAGGCGGTCATC	R600.3	GGAATTCACGTTAGCTAGGCGGTCA	R199.3	GGCTTCCGTTAGCTATGCGGTATCT
R16.10	GATAACTCGTTAGCTAAGCGGTCAG	R600.2	GGAATTCACGTTAGCTAGGCGGTCC	R199.6	GGCTTCCGTTAGCTATGCGGTGTCC
R344.8	GATAGAGGCCCGGTCACTAGATCGC	R180.14	GGACTAAGCATGTAGGTCAGGCCGG	R16.5	GGGGCCACTCGTTAGCTAAGCGGTC
R1094.3	GATATATTCGTTAGCTAGGCGTGTC	R128.14	GGACTATAGCATGTAGGTCAGCCCG	R180.9	GGGTTAAGCATGTAGGTCAGGCCGG
R1119.2	GATCAGTCGTTAGCTAAGCGGTCAC	R180.29	GGATCAAGCATGTAGGTCAGGCCGG	R128.9	GGGTTATAGCATGTAGGTCAGCCCG
R1119.4	GATCAGTCGTTAGCTAAGCGGTCAT	R128.21	GGATCATAGCATGTAGGTCAGCCCG	R344.16	GGTAGAGGCCCAGTCACTAGATCGC
R317.7	GATCCATCGTTAGCTAAGCGGTCGT	R180.25	GGATTAAACATGTAGGTCAGGCCGG	R344.7	GGTAGAGGCCCGGCCACTAGATCGC
R236.3	GATCTGTATCGTTAGCTAAGCGGCC	R128.44	GGATTAAAGCATGTAGGTCAGCCCG	R344.15	GGTAGAGGCCCGGTCACTAGACCGC
R236.2	GATCTGTATCGTTAGCTAAGCGGTC	R180.12	GGATTAAGCACGTAGGTCAGGCCGG	R344.10	GGTAGAGGCCCGGTCACTAGATCGA
R388.2	GATGTTGGTCAGCCAATCACACTCC	R180.24	GGATTAAGCATATAGGTCAGGCCGG	R344.2	GGTAGAGGCCCGGTCACTAGATCGC
R317.4	GATTCATCGTTAGCTAAGCGGTCAT	R180.11	GGATTAAGCATGCAGGTCAGGCCGG	R344.9	GGTAGAGGCCCGGTCACTAGATCGT
R317.6	GATTCATCGTTAGCTAAGCGGTCGA	R180.23	GGATTAAGCATGTAAGTCAGGCCGG	R344.17	GGTAGAGGCCCGGTCACTAGATTGC
R317.2	GATTCATCGTTAGCTAAGCGGTCGT	R180.31	GGATTAAGCATGTAGATCAGGCCGG	R344.5	GGTAGAGGCCCGGTCACTAGGTCGC
R5.20	GCAACGCGTGAGCTAAGCGGTCATC	R180.7	GGATTAAGCATGTAGGCCAGGCCGG	R344.12	GGTAGAGGCCCGGTCACTGGATCGC
R135.30	GCAACGCGTTAGCTAAGCGGTCATC	R180.22	GGATTAAGCATGTAGGTAAGCCGG	R344.13	GGTAGAGGCCCGGTCGCTAGATCGC
R1119.3	GCAATTAGTCGTTAGCTAAGCGGTC	R180.33	GGATTAAGCATGTAGGTCAAGCCGG	R141.20	GGTAGATGCCAGTTGGGTATCACAG
R321.9	GCACATACGTTAGCTAAGCGGTCGG	R180.5	GGATTAAGCATGTAGGTCAGACCGG	R344.6	GGTAGGGGCCCGGTCACTAGATCGC
R5.25	GCACCGCGTGAGCTAAGCGGTCATC	R180.15	GGATTAAGCATGTAGGTCAGCCCGG	R141.14	GGTCAATGCCAGTTGGGTATCACAG
R135.6	GCACCGCGTTAGCTAAGCGGTCATC	R180.17	GGATTAAGCATGTAGGTCAGGCCAG	R17.11	GGTCACACCGTTAGCTAAGCGGCCC
R1447.6	GCACGTTGGTCAGCTAATCACGTGC	R180.3	GGATTAAGCATGTAGGTCAGGCCGA	R17.3	GGTCACACCGTTAGCTAAGCGGTCA

Table S3 - continued

RNA	N25 sequences	RNA	N25 sequences
R17.2	GGTCACACCGTTAGCTAAGCGGTCC	R177.4	TAGAAAGACATCCGTATGCGTGCTC
R17.5	GGTCACACCGTTAGCTAAGCGGTCT	R7.25	TAGAGCCTAACTAGTCAACGATCCT
R17.9	GGTCACACCGTTAGCTAGGCGGTCC	R147.39	TAGATAGACATCCGTAGGCACGATC
R17.7	GGTCACGCCGTTAGCTAAGCGGTCC	R37.32	TAGATCAAGTTGGTCAACTATGTCA
R17.10	GGTCATACCGTTAGCTAAGCGGTCC	R1050.53	TAGATCAAGTTGGTCAGCTAAATCA
R141.13	GGTCGACGCCAGTTGGGTATCACAG	R1049.44	TAGATCAAGTTGGTCAGCTTCATCA
R141.24	GGTCGATACCAGTTGGGTATCACAG	R35.9	TAGCAAGACATCCGTAGGTATGATC
R141.10	GGTCGATGCCAGCTGGGTATCACAG	R177.9	TAGCAAGACATCCGTATACGTGATC
R141.16	GGTCGATGCCAGTCGGGTATCACAG	R147.9	TAGCTAGACATCCGTAGGCACGATC
R141.25	GGTCGATGCCAGTTAGGTATCACAG	R1228.3	TAGCTTAGCAAGGAACCCGATCGAT
R141.26	GGTCGATGCCAGTTGAGTATCACAG	R1256.46	TAGCTTAGTAAGGTACCCGGTCGAT
R141.27	GGTCGATGCCAGTTGGATATCACAG	R1229.2	TAGCTTGGTCAGTCAATCAGCCAAT
R141.12	GGTCGATGCCAGTTGGGCATCACAG	R35.20	TAGTAAGACACCCGTAGGTATGATC
R141.5	GGTCGATGCCAGTTGGGTACCACAG	R35.19	TAGTAAGACATCCGCAGGTATGATC
R141.3	GGTCGATGCCAGTTGGGTATCACAA	R35.21	TAGTAAGACATCCGTAAGTATGATC
R141.30	GGTCGATGCCAGTTGGGTATCACAC	R177.13	TAGTAAGACATCCGTACACGTGATC
R141.2	GGTCGATGCCAGTTGGGTATCACAG	R147.13	TAGTAAGACATCCGTAGGCACGATC
R141.15	GGTCGATGCCAGTTGGGTATCACAT	R35.11	TAGTAAGACATCCGTAGGTACGATC
R141.4	GGTCGATGCCAGTTGGGTATCACGG	R35.7	TAGTAAGACATCCGTAGGTATGACC
R141.17	GGTCGATGCCAGTTGGGTATCATAG	R35.6	TAGTAAGACATCCGTAGGTATGATA
R141.8	GGTCGATGCCAGTTGGGTATCGCAG	R35.2	TAGTAAGACATCCGTAGGTATGATC
R141.32	GGTCGATGCCAGTTGGGTATTACAG	R35.3	TAGTAAGACATCCGTAGGTATGATT
R141.6	GGTCGATGCCAGTTGGGTGTCACAG	R35.4	TAGTAAGACATCCGTAGGTATGGTC
R141.23	GGTCGATGCCAGTTTGGTATCACAG	R35.8	TAGTAAGACATCCGTAGGTGTGATC
R141.31	GGTCGATGCCATTTGGGTATCACAG	R177.8	TAGTAAGACATCCGTATACGTGACC
R141.9	GGTCGATGCCGGTTGGGTATCACAG	R177.10	TAGTAAGACATCCGTATACGTGATA
R141.29	GGTCGATGCTAGTTGGGTATCACAG	R177.2	TAGTAAGACATCCGTATACGTGATC
R141.28	GGTCGATGTCAGTTGGGTATCACAG	R177.7	TAGTAAGACATCCGTATACGTGATT
R141.22	GGTCGATTCCAGTTGGGTATCACAG	R177.5	TAGTAAGACATCCGTATACGTGGTC
R17.6	GGTCGCACCGTTAGCTAAGCGGTCC	R177.3	TAGTAAGACATCCGTATGCGTGATC
R141.11	GGTCGGTGCCAGTTGGGTATCACAG	R35.17	TAGTAAGACATCCGTGGGTATGATC
R141.19	GGTCTATGCCAGTTGGGTATCACAG	R35.14	TAGTAAGACATCCTTAGGTATGATC
R344.14	GGTGGAGGCCCGGTCACTAGATCGC	R35.18	TAGTAAGACGTCCGTAGGTATGATC
R141.21	GGTTGATGCCAGTTGGGTATCACAG	R35.10	TAGTAAGGCATCCGTAGGTATGATC
R237.3	GTACACACGTTAGCTAAGCGGTCGG	R177.11	TAGTAAGGCATCCGTATACGTGATC
R321.16	GTACATACGTCAGCTAAGCGGTCGG	R35.12	TAGTAGGACATCCGTAGGTATGATC
R321.14	GTACATACGTTAGCCAAGCGGTCGG	R147.4	TAGTCAGACATCCGTAGGCACGATC
R321.12	GTACATACGTTAGCTAAGCGGCCGG	R35.22	TAGTGAGACATCCGTAGGTATGATC
R321.3	GTACATACGTTAGCTAAGCGGTCAG	R147.37	TAGTTAAACATCCGTAGGCACGATC
R321.4	GTACATACGTTAGCTAAGCGGTCGA	R147.15	TAGTTAGACACCCGTAGGCACGATC
R321.6	GTACATACGTTAGCTAAGCGGTCGC	R147.40	TAGTTAGACATACGTAGGCACGATC
R321.2	GTACATACGTTAGCTAAGCGGTCGG	R147.33	TAGTTAGACATCAGTAGGCACGATC
R321.11	GTACATACGTTAGCTAAGCGGTCGT	R147.25	TAGTTAGACATCCATAGGCACGATC
R321.15	GTACATACGTTAGCTAAGCGGTTGG	R147.23	TAGTTAGACATCCGCAGGCACGATC
R321.13	GTACATACGTTAGCTGAGCGGTCGG	R147.16	TAGTTAGACATCCGTAAGCACGATC
R321.10	GTACATACGTTGGCTAAGCGGTCGG	R147.21	TAGTTAGACATCCGTAGACACGATC
R321.8	GTACATGCGTTAGCTAAGCGGTCGG	R147.27	TAGTTAGACATCCGTAGGCACAATC
R39.4	GTACATTACGTTAGCTAAGCGGTCA	R147.7	TAGTTAGACATCCGTAGGCACGACC
R39.2	GTACATTACGTTAGCTAAGCGGTCC	R147.6	TAGTTAGACATCCGTAGGCACGATA
R237.4	GTACGACACGTTAGCTAAGCGGTCA	R147.2	TAGTTAGACATCCGTAGGCACGATC
R237.2	GTACGACACGTTAGCTAAGCGGTCC	R147.3	TAGTTAGACATCCGTAGGCACGATT
R39.5	GTACTTACGTTAGCTAAGCGGTCGG	R147.11	TAGTTAGACATCCGTAGGCACGGTC
R1049.53	GTAGATCAAGTTGGTCAGCTAGTCA	R147.34	TAGTTAGACATCCGTAGGCACTATC
R321.7	GTATATACGTTAGCTAAGCGGTCGG	R147.28	TAGTTAGACATCCGTAGGCATGATC
R1187.7	GTATATCGTTAGCTAAGCGGTCATA	R147.8	TAGTTAGACATCCGTAGGCGCGATC
R1187.4	GTATATCGTTAGCTAAGCGGTCATC	R147.14	TAGTTAGACATCCGTAGGTACGATC
R1187.2	GTATATCGTTAGCTAAGCGGTCATG	R35.15	TAGTTAGACATCCGTAGGTATGATC
R1187.5	GTATATCGTTAGCTAAGCGGTCGTG	R147.38	TAGTTAGACATCCGTAGTCACGATC
R135.14	GTATCGCGTTAGCTAAGCGGTCATC	R147.36	TAGTTAGACATCCGTATGCACGATC
R180.36	GTATTAAGCATGTAGGTCAGGCCGG	R147.17	TAGTTAGACATCCGTGGGCACGATC
R128.38	GTATTATAGCATGTAGGTCAGCCCG	R147.22	TAGTTAGACATCCTTAGGCACGATC
R612.3	GTCAATGCGACTAAGCGGTCCTTGA	R147.26	TAGTTAGACATCTGTAGGCACGATC
R612.2	GTCAATGCGACTAAGCGGTCCTTGG	R147.31	TAGTTAGACATTCGTAGGCACGATC
R615.3	GTCATACTCGTTAGCTAAGCGGTCC	R147.12	TAGTTAGACGTCCGTAGGCACGATC
R23.2	GTCTATAGCCTAAAGCCGACAGGTC	R147.29	TAGTTAGATATCCGTAGGCACGATC
R135.28	GTGAAAAGCGTTAGCTAAGCGGTCA	R147.10	TAGTTAGGCATCCGTAGGCACGATC
R321.5	GTGCATACGTTAGCTAAGCGGTCGG	R147.18	TAGTTGGACATCCGTAGGCACGATC
R135.9	GTGTCAAAGCGTTAGCTAAGCGGTC	R225.2	TAGTTTAGACATCCGTAGGCATCAT
R344.11	GTTAGAGGCCCGGTCACTAGATCGC	R225.3	TAGTTTAGACATCCGTAGGCATTAT
R1636.2	GTTCCGGTGGTACAACGGCGGTTTG	R489.2	TATCTTGGTCAGTTAATCAGACAAT
R118.24	TAAACAGAGGCTCAGGTCATAAGTC	R1335.7	TATGTTGGTCAACTAGTCACACAAT
R118.22	TAAACAGAGGCTTAGGTCATTAGTC	R147.30	TATTTAGACATCCGTAGGCACGATC
R49.7	TAAAGTGAACAGTTCCCGGTCTGAT	R135.19	TCATCGCGTTAGCTAAGCGGTCATC
R49.11	TAAAGTGAGCAGTCCCCGGTCTGAT	R28.2	TCCTCGAGTTAGCTAAGCGGTCATC
R49.10	TAAAGTGAGCAGTTCCCGGCCTGAT	R28.4	TCCTCGTGAGTTAGCTAAGCGGTCA
R49.12	TAAAGTGAGCAGTTCCCGGTCTGAC	R36.2	TCCTTGGTCAGCTAATCAGACGAAT
R49.2	TAAAGTGAGCAGTTCCCGGTCTGAT	R180.35	TGATTAAGCATGTAGGTCAGGCCGG
R49.6	TAAAGTGGGCAGTTCCCGGTCTGAT	R128.25	TGATTATAGCATGTAGGTCAGCCCG
R49.3	TAAGGTGAGCAGTTCCCGGTCTGAT	R1228.2	TGGCTTAGTAAGGAACCCGATCGAT
R1395.28	TAAGTTGGTCAAGTTTCACGCTTAT	R35.16	TGGTAAGACATCCGTAGGTATGATC
R0.36	TAAGTTGGTCAATTGTCACGCTTAT	R147.19	TGGTTAGACATCCGTAGGCACGATC
R376.36	TAAGTTGGTCAGATTTCACGCTTAT	R1049.87	TTAGATCAAGTTGGTCAGCTAAACA
R1050.87	TAAGTTGGTCAGCTAAACACGCAAT	R1051.5	TTAGATCAAGTTGGTCAGCTAGTCA
R147.35	TAATTAGACATCCGTAGGCACGATC	R1049.55	TTAGATCAAGTTGGTCAGTTAGTCA
R1211.3	TACAAGAGCCTCGCTAGTCAACGAT	R147.32	TTAGTTAGACATCCGTAGGCATAAT
R1211.2	TACAAGAGCCTTGCTAGTCAACGAT	R56.3	TTGCAGAGGCCAATGGTCATAAGTC
R1943.2	TACGCAAGCCACGCGGTTCTGATGC	R349.4	TTGCCTAGTAAGGAACCCGGTCGAT
R1943.3	TACGCAAGCCACGTGGTTCTGATGC	R1.27	CAGGTTGGTCAAATTTCACACTTAA
R406.2	TACGGCATGTAAACGGACCGGTCAG	R4.7	ATGCTTAGTAAGGTTCCCAGTCGAT
R123.6	TACGGTTGCTACTGATCAGGCTATA		

Table S3. Sequences of the 1,331 RNA sequences that had at least 500 reads in selection round 6.