

**Supplementary Table 1. Sequence and functionality information for all sdRNAs.**

Listed in the table are the 50-nt target sequences containing the flanking regions and the corresponding sdRNA efficacy values, obtained in the functional screenings.

**Supplementary Table 2. Sequence and modification pattern of sdRNA in Figure 6.** The demonstrated sequences differ only in the chemical modification of position 14 in the antisense strand.

**Supplementary Figure 1. Characterization of datasets.** (A) The distribution of GC content of the siRNA-targeting region of 356 sdRNAs targeting 17 genes. (B) The distribution of the GC content of the siRNA-targeting regions of 2385 siRNAs, the efficacy of which is depicted in C. (C) The efficacy of 2385 siRNAs evaluated using an eCFP-eYFP dual reporter assay. Data from Huesken et al., 2005. Functionality cutoffs indicated.

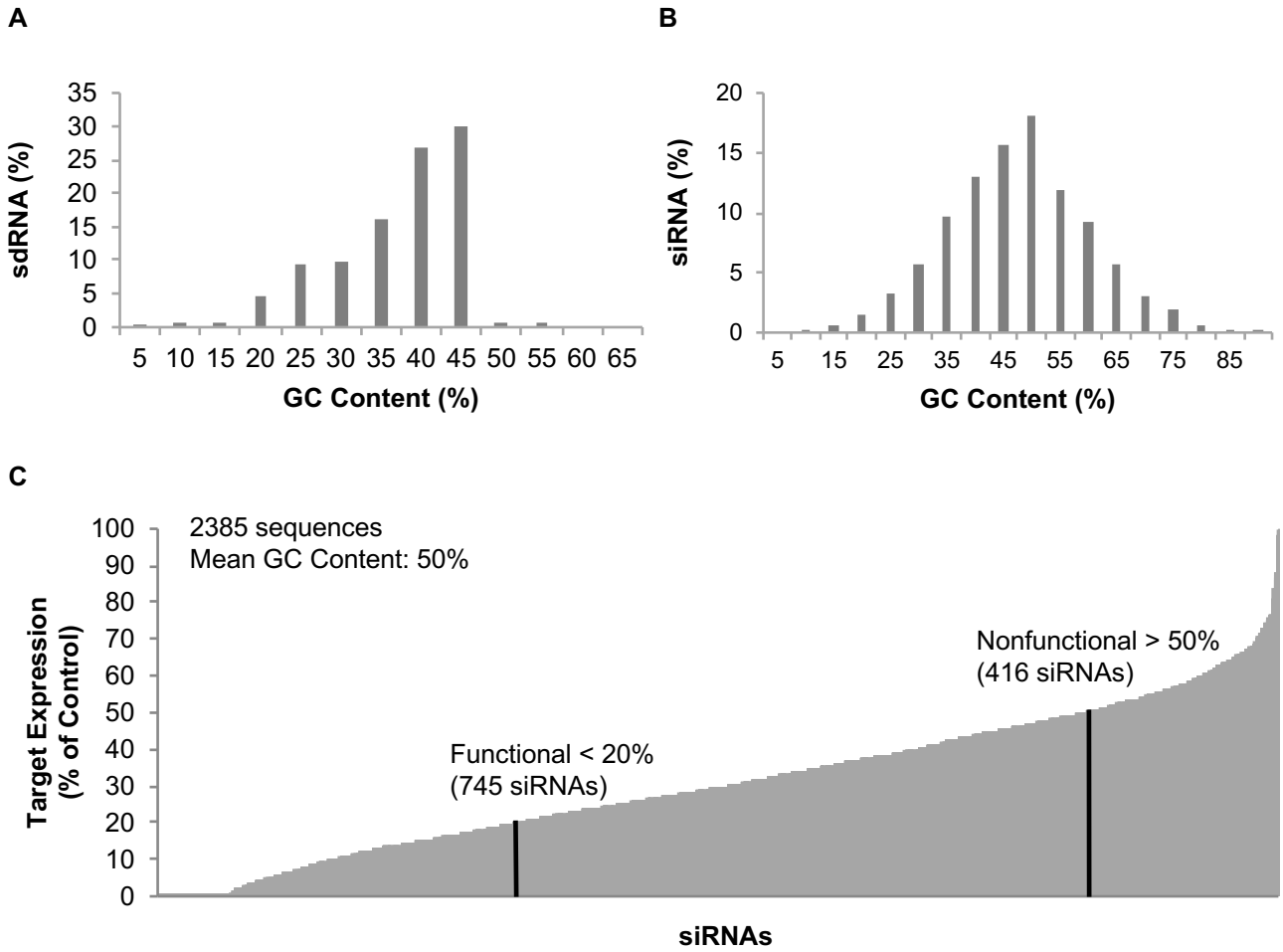
**Supplementary Figure 2. Algorithm performance visualized as ROC curves.**

Using linear regression analysis (R 3.4.1), the scoring algorithm was generated for positional preference matrices shown in Figure 2A. Black line shows performance of the control algorithm (see Methods). Area under the curve (AUC) for each curve is indicated.

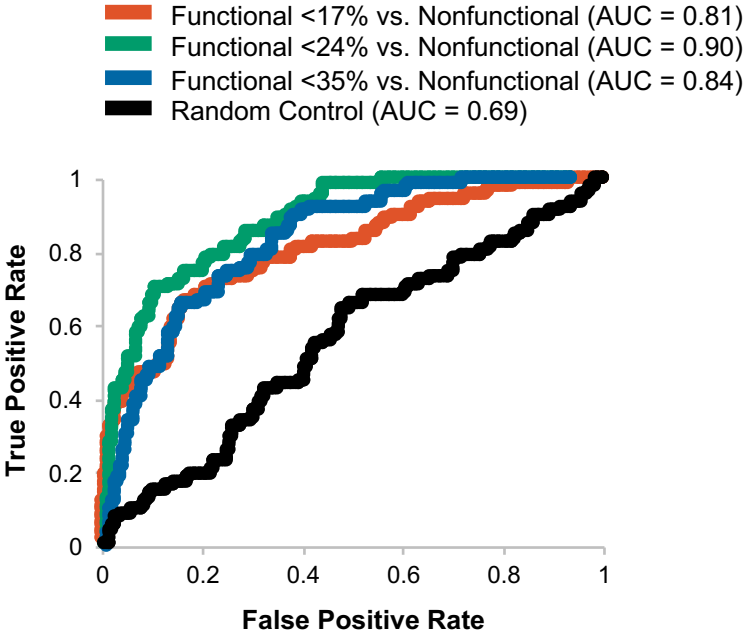
**Supplementary Figure 3. 2'-O-methyl modification at position 14 of the antisense strand negatively modulates sdRNA efficacy.**

(A) The frequency of 2'-O-methyl modification per position of the antisense strand in functional (defined as < 24% gene expression remaining) sdRNAs. (B) The frequency of 2'-O-methyl modification per position of the antisense strand in non-functional (defined as > 44% gene expression remaining) sdRNAs. (C, D) The efficacy of sdRNA targeting MAP4K4 with and without 2'-O-methyl modification in position 14 of the antisense strand (qPCR, 72 hours, n=3, SD, one-way ANOVA  $p < 0.05$ ). Different chemical modification patterns used in C and D, but within the graphs, only the position 14 modification differs.

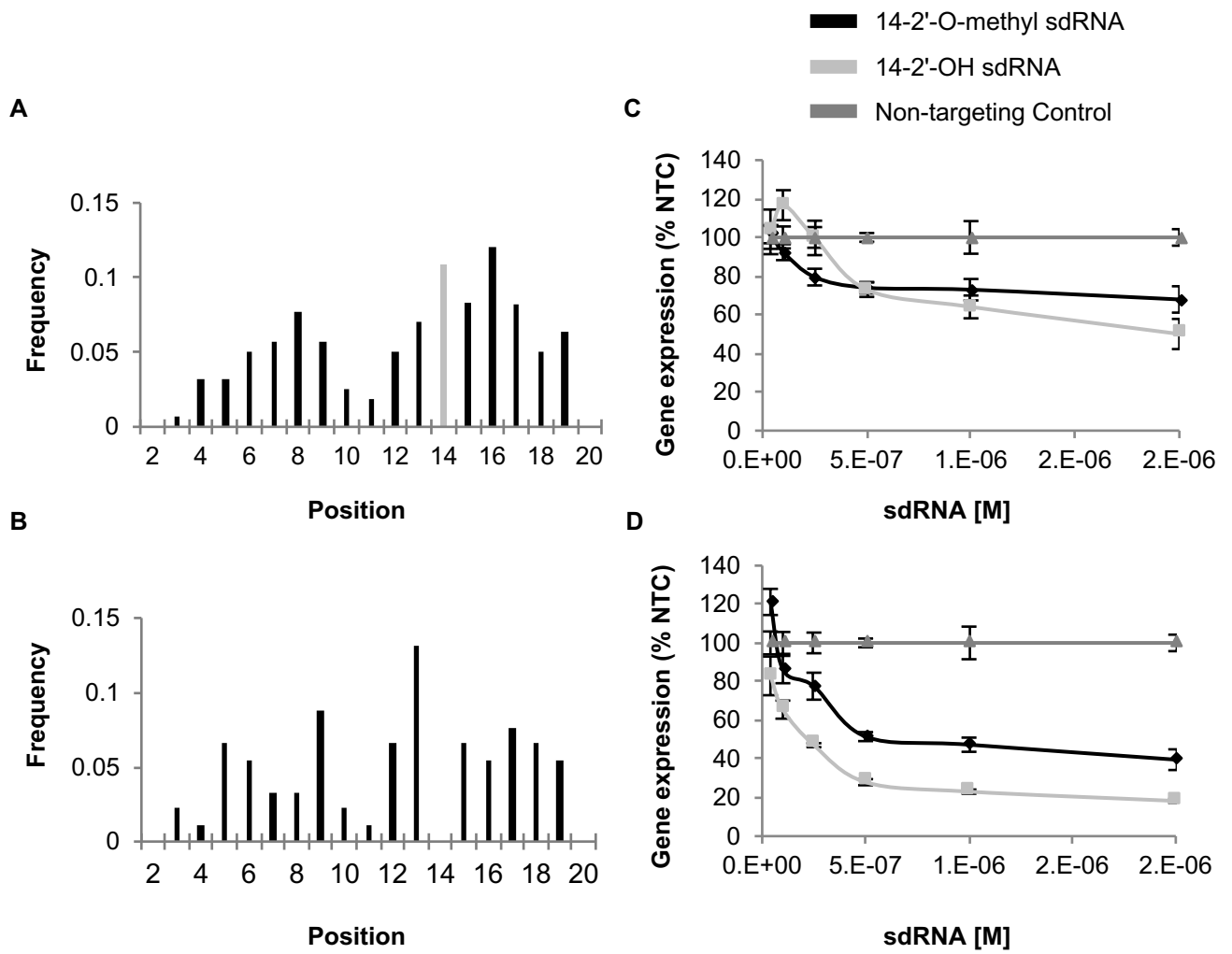
# Supplementary Figure 1



Supplementary Figure 2



Supplementary Figure 3



## Table of Contents

Supplementary Table 1  
Supplementary Table 2

S2-S10  
S11

**Supplementary Table 1.** Sequence and functionality information for all sdRNAs.

ID	5' Region - <b>siRNA Targeting Region</b> - 3' Region <sup>1</sup>	Target Expression (% of Control)	Standard Deviation <sup>2</sup>
1000	UUUCCUUGGCUUUUAUG <b>CACAUUAAACAGAUGUGAAU</b> UUCGUUUAAACUG	17.10	1.85
1001	AAGAAAUCUCGGAUUGAUC <b>UAAUGAAGGUUUUAAGCAUU</b> UCCACAGCCA	6.50	0.69
1002	CAAGCACAUUGGAAGAUG <b>CUUUUGUUUUGUGAGGUAAU</b> AAACAUGUGAGGAU	3.49	0.25
1003	AUUUGUGGUUAUACUG <b>UUGGCAUGUAUCUACUUGAG</b> CUAUUACUUCAGCC	4.61	0.37
1004	AAUGUACUGAAAUUAA <b>AGGAGGAAGAUAAACAAAAU</b> UUAACAAUGCUGA	5.07	0.08
1005	GUUUUUGUGUAUUUG <b>UUAUUGGUUUGAAUUA</b> AAACACUAUUGGCAGUGU	5.70	0.31
1006	CCUGGCAACUGAGA <b>ACAAAGCAACAAGCAACUGAAU</b> CUCAUUUCUUCAGC	5.79	0.43
1007	AUUCUAGGCGAUCG <b>CGUGCUCGAUGAGUUAGA</b> AACUUUGAGCAAGUUA	7.81	1.39
1008	UAUUGAAUUCGGAAC <b>UGUCCUUCUUGGCUUUUAUG</b> CACAUUAAACAGAU	8.21	0.31
1009	AAUCCAGAACUAGUG <b>AAAUUAAGGAAAGAAUACU</b> UAUGAAUUCAAGACC	8.45	0.65
1010	UGUCCUUUCUUGG <b>CUUUUAUGCACA</b> UUA <b>AAACAGAUGUGAAU</b> UUCGUUUA	8.69	0.37
1011	CAUCAUCA <b>AAGAGAU</b> CGU <b>UAGCAGAAACAAAAGG</b> AGAUUCAAGAGGAUG	8.93	0.53
1012	UUA <b>AUGUAUAGAUUUGA</b> AG <b>AAGAGCUGUUUCUG</b> AGGAGCCUUCAGGAUUA	10.31	0.93
1013	GCUUGCUCUUGUCA <b>UCUCUUUGAUUAU</b> UCCUG <b>AAGGUGCAACA</b> AUCAUU	10.33	0.46
1014	AAGGGAUCCCCU <b>UCCUGUGGUUCUAUU</b> AU <b>UUUAAUUA</b> AAUUAUAAUUAUUAAU	10.40	0.34
1015	CGAUGAGUUAGA <b>AGACUUUGAGCAAGU</b> UACUGUGAGUAUGUAAUACGCA	10.97	3.08
1016	GCUGCCAAGAGUGC <b>UCGAGAUUUGGACCUAAG</b> AGACGGACCUGGACCCCC	11.28	0.30
1017	CAGGAAGCAAGUUU <b>UUCUGUCAGGAAACA</b> AUGUUGGCUUCUGUUGACCU	11.68	0.75
1018	AGGCGCUAUGUA <b>UUUUAUUUAGCUACC</b> UGU <b>AAAGAAU</b> CACCUGGAUUA	11.74	0.51
1019	AUUGAAUUCGGAAC <b>UGUCCUUCUUGGCUUU</b> AUGCACA <b>UUAACAGA</b> UG	11.97	0.85
1020	GAAGAU <b>CACCCUCCU</b> U <b>AAAUUUUCCGCAUU</b> ACAUGAGCGAGCACUUGC	12.73	1.17
1021	UAAUUCUAGGCGAUC <b>GCAUU</b> AUG <b>UCAGAAUU</b> AAAAAAAAUUCUUUAACUUA	12.86	1.66
1022	GUA <b>AUACGCACUGAC</b> CCA <b>UAUGUCCACCCAU</b> UGAUGUGAUUUUUAGCAU	13.07	2.91
1023	CACAUGGAAGAUGC <b>UUUGUUUUGUGAGGUAAU</b> AAACAUGUGAGGAUGAAA	13.07	4.16
1024	GAAGAGCUGUUUC <b>UGAGGAGCCUUCAGGAU</b> UACAAGAUUCAAGUGCGCU	13.28	0.83
1025	UUGUACAGAAU <b>UUUCUAUUGAAUUCGGAAC</b> UGUCCU <b>UUCUUGGCU</b> UUA	13.50	1.77
1026	GACAAGGGAUCCCC <b>UCCUGUGGUUCUAUU</b> AU <b>UUUAAUUA</b> AAUUA	13.57	1.63
1027	UCGGAACUGUCCU <b>UUCUUGGCUUU</b> AUGCACA <b>UUAACAGA</b> UGUGAAUUAU	13.92	1.26
1028	GGAACUGUCCU <b>UUCUUGGCUUU</b> AUGCACA <b>UUAACAGA</b> UGUGAAUUAUUC	13.93	0.88
1029	GCAUUGCCC <b>UCAACGACCACUUUGUCAAGC</b> UCAUU <b>UCCUGGUAUGACA</b> AC	14.39	0.01
1030	UAUCCAACA <b>AUUAUCGCUUGUAUUACCGAGU</b> AAUGAUCUUAUUAAACAA	14.51	1.74
1031	GGUGACA <b>UCAAGUAGAGUUCU</b> UCCACA <b>AAACAGAACA</b> AGAUGCUCAAAAA	14.64	0.17
1032	UUUAA <b>CUCAAU</b> UUU <b>UCCAUGAAAUGCAACA</b> CAUGUAUAAU <b>UUUUUA</b>	14.85	0.53
1033	CCCUCAACGACCACU <b>UUGUCAAGCUC</b> AUU <b>UCCUGGUAUGACA</b> ACGAAUUU	14.87	1.03
1034	AAUGUCCGUUCGGU <b>UGGAGAGCUAUGAAACGAU</b> AUGGGCUGAAUACAA	15.13	0.50
1035	GGGCU <b>GCUUUUAA</b> CU <b>UGGUA</b> AAAGUGGAU <b>AUUGUUGCCA</b> UCAUGACCCC	15.22	0.15
1036	CCACCAU <b>AUGAAUUGUACAGAAU</b> AUU <b>UCUAUUGAAU</b> UCGGAACUGUCCUU	15.34	0.89
1037	GAUAACCGGGAGAU <b>AGUGAUGAAGUACA</b> UCCA <b>UUAUAAGCUGUCGCAGAG</b>	15.41	1.14
1038	GAGGCGAACUGUGUG <b>AGAGGUCCUAUGAU</b> UAUGUCCGGUUAUGUAAAC	16.06	1.80

1039	GAGGCGCUAUGUAUUAUUUAUAGCUACCUGUUAAGAAUCACCUGGAUU	16.13	0.93
1040	ACAAGGGAUCCCCCUUCCUGUGGUUCUAUUUAUUUAUUAAUUAA	16.75	0.85
1041	CUGUCCUUUCCUUGGCCUUUAUGCACAUAUAACAGAUGUGAAUUAUCGUUU	16.86	0.94
1042	CUUUAAACUUACUAAAAACACUAUCCAACAUAUAUCGCUUGUAUUACCGA	17.17	1.96
1043	UGAAUUGUACAGAAUUAUUUCUAUUGAAUUCGGAACUGUCCUUCCUUGGC	17.31	1.96
1044	UGUCAUCUCUUUGAUUAUUAUCCUGAAGGUGCAACAUAUUUGAAAAGGC	17.84	0.55
1045	CAUUGACCUCAACUACAUGGUUUACAUGUCCAAUAUGAUUCCACCCAUG	18.06	1.04
1046	CGUCAUGGGUGUGAACCAUGAGAAGUAUGACAACAGCCUCAAGAUCAUCA	18.09	1.81
1047	AAUGUUUACUACACUCGGAUUAUUUGAUUUGGAAUUCGAGUCGUCUUA	18.13	1.38
1048	UUUCGAGUCGUCUUAUUGUAUAGAUUUGAAGAAGAGCUGUUUCUGAGGAG	18.16	0.62
1049	ACGACCACUUUGUCAAGCUCUAUUCCUGGUAUGACAACGAAUUUGGCUAC	18.18	0.74
1050	UGUCCACCCAUUGAUUGUGAUUAUUUAGCAUUUUGAAAGUUGUUGAAACAG	18.27	2.27
1051	GAUUGACAAAUACGAUUUAUCUAAUUUACACGAAUUGCUUCUGGUGGCG	18.28	0.31
1052	CAGGAAAACAAUGUUGGCCUUCUGUUGACCUUUAUUGAUUGUCUGAACAC	18.73	2.42
1053	UCACCAGGGCUGCUUUUAACUCUGGUAAGUGGAUUAUUGUUGCCAUCAAU	18.93	1.50
1054	UGGAUUUCGAGUCGUCUUAUUGUAUAGAUUUGAAGAAGAGCUGUUUCUGA	19.12	0.85
1055	CAUUCAAAUGAAAAUAUUUUUAGCACUGACUGAAGAACUCUUGGGACAA	19.32	2.88
1056	UCCCUCAGCCAUUGCCUGUGUGUGGUGACAUAAGUAGAGUUCUUCAC	19.51	0.50
1057	UGACCUCAACUACAUGGUUUACAUGUCCAAUAUGAUUCCACCCAUGGCA	19.52	1.00
1058	AAGUUAUUUUUAUGCCUUUAUUUCUUAACAAAUGUAUGAUUACAUCA	19.66	0.44
1059	AUGAUGUAGUAAGGUUUUUGGAUUCAAAGCAUAAAACCAUUACAAGUA	19.68	6.62
1060	UGUACAGAAUUAUUUCUAUUGAAUUCGGAACUGUCCUUUCCUUGGCUUAU	19.87	2.37
1061	GGAGCCGCACCUUGUCAUGUACCAUCAUAAGUACCCUGUGCUCAACCA	19.89	1.42
1062	GCUGGUGACAUUUGUGGUUAUACUGUUGGCAUGUAUCUACUUGAGCUAUU	19.99	1.75
1063	UUCGAGAGAAGAAAUCUCGGAUUGAUCUAAUGAAGGUUUUAAGCAUUU	20.16	1.98
1064	CCUCCCCUCAACCCACCAUAUGAAUUGUACAGAAUAUUUCUAUUGAAU	20.37	0.60
1065	GUGGAAAUGGAAGUCUUUGUGAUCAGGAAUUCGAUAGCAUUUGUAGUAU	20.44	1.53
1066	GUAUGAGACGUUUUAUAGCCGAAUUGAUCUUUCAAGUUAUUUUUAUGCC	20.57	0.74
1067	CAUGUUCGUAUGGGUGUGAACCAUGAGAAGUAUGACAACAGCCUCAAGA	20.58	1.11
1068	GGUGAAGGUCGGAGUCAACGGAUUUGGUCGUUUGGGCGCCUGGUCACCA	20.66	2.89
1069	UUGACAAGGAUGGAUGGCUACAUCUGGAGACAUAAGCUUACUGGGACGAA	21.29	1.03
1070	GACAAUACGAUUUAUCUAAUUUACACGAAUUGCUUCUGGUGGCGCUCC	21.44	2.36
1071	UAUAUAUUAUUUAUUUGAUAGUAUUGUGCAUAGAGCCACGUAUGUUUUU	21.57	0.38
1072	AUUGUACAGAAUUAUUUCUAUUGAAUUCGGAACUGUCCUUUCCUUGGCUUU	21.63	2.94
1073	GAACCGCUGGAGAGCAACUGCAUAAGGCUAUGAAGAGAUACGCCUGGUU	22.24	0.87
1074	UAGGGAGCCGCACCUUGUCAUGUACCAUCAUAAGUACCCUGUGCUCAA	22.55	0.80
1075	UAUUGCUAUGGGAUUUCUGCGAGAAAGACUUGAAGGUGUAUACAGGAACA	22.68	0.23
1076	GAUAUUUGAUUUGUGGAUUUCGAGUCGUCUUAUUGUAUAGAUUUGAAGAA	22.93	0.88
1077	GGUGUAUACAGGAACAUAUUGAUGAUGUAAGGUUUUUUGGAUUCAAA	23.15	1.04
1078	CAACUACAUGGUUUACAUGUCCAAUAUGAUUCCACCCAUGGCAAAUUC	23.17	2.31
1079	AAAGCACUCUGAUUGACAAUACGAUUUAUCUAAUUUACACGAAUUGCU	23.18	1.25
1080	UGAUAAACAGCGUGGGGUGCUCUCAAUGACUCAACACGCCUCAUCCUCU	23.32	1.44

1081	GGGACAAGGGAUCCCCUCCUGUGGUUCUAUUUAUUUAUUAAUUAUUAAU	23.38	1.76
1082	UUUCUGAGGAGCCUUCAGGAUUACAAGAUUCAAGUGCGCUGCUGGGUGCC	23.55	1.56
1083	UACGAUAACCGGGAGAUAGUGAUGAAGUACAUCCAUUUAAGCUGUCGCA	23.57	1.38
1084	UCAUUUCCUGGUUUGACAACGAAUUUGGCUACAGCAACAGGGUGGUGGAC	23.69	0.65
1085	CAUGGGUGUGAACCAUGAGAAGUAUGACAACAGCCUCAAGAUAUCAGCA	23.72	2.67
1086	CUUUUAACUCUGGUAAAGUGGGAUUAUGUUGCCAUCAAUGACCCCUUCAUU	23.74	1.12
1087	UCAACGACCACUUUGUCAAGCUCAUUCCUGGUUUGACAACGAAUUUGGC	23.82	1.66
1088	AGGGAUCCCCUCCUGUGGUUCUAUUUAUUUAUUAAUUAUUAAUUAUUAAUUA	23.90	0.93
1089	CUUCGCCAAAAGCACUCUGAUUGACA AAUACGAUUUAUCUAAUUUACACG	23.91	0.48
1090	CCAGGGCUGCUUUUAACUCUGGUAAAGUGGGAUUAUGUUGCCAUCAAUAGAC	23.91	1.62
1091	ACCACCAGCCCAGCAAGAGCACAAGAGGAAGAGAGACCCUCACUGCU	24.57	2.65
1092	GCUGGGCAAAGAAGUCCUACGGAGUACCUAGAAAAUUAGUACAAAGCA	24.63	4.19
1093	ACAAAAAUGAUUCUUGACA AAAGCAAACAAGACAAGGCCAACCGAUACUU	24.84	1.49
1094	GAAGGUGAAGGUCGGAGUCAACGGAUUUGGUCGUUUGGGCGCCUGGUCA	25.13	1.71
1095	GAAUUGUACAGAAUAUUUCUAUUGAAUUCGGAACUGUCCUUUCCUUGGCU	25.405	1.82
1096	UCAAGCUCAUUUCUGGUUUGACAACGAAUUUGGCUACAGCAACAGGGUG	26.66	0.44
1097	UAUAAAGUCCUUGAUUCUGUGUGGGUUC AAACACAUUUCAAAGCUUCAGG	26.79	0.52
1098	CAAUCAUCCAAAAAUAUUUAUCAUGGAUUCUAAAACGGAUUACCAGGGA	26.85	2.21
1099	CUAUGAAACGAUAUGGGCUGAAUACA AAUCACAGAAUCGUCGUAUGCAGU	26.93	1.38
1100	GGAUGCAGCAUUUAUGAUGUGGGUCAAGGAAUUAAGUUAGGGAAUGGCACA	27.73	1.07
1101	UUGCUUUUAAUUAAAUGGUCUUGUUAGAAAACAAGCUUUUUUGUAUUGG	27.86	4.32
1102	GCCUAGGGAGCCGCACCUUGUCAUGUACCAUCAAUAAAGUACCCUGUGCU	27.91	2.12
1103	CGUGAGUCCCAUCCCAACUCCUUGAUGAAGAAGAUCACCCUCCUUAUU	28.07	1.36
1104	CUCAAGACCCUUCGUUCUUAACCACGUUCUUGAAAUCAGGGUCCCCAA	28.47	0.14
1105	GGGUGUGAACCAUGAGAAGUAUGACAACAGCCUCAAGAUAUCAGCAAUG	28.58	0.86
1106	UGUUGGUGGAUGAGCAAGAGACCUUGCUUAUUAGAAACAAGUUUAAACU	28.61	3.52
1107	UUAACUCUGGUAAAGUGGGAUUAUGUUGCCAUCAAUAGACCCCUUCAUUGAC	29.2	0.42
1108	CGAUAAACCGGGAGAUAGUGAUGAAGUACAUCCAUUUAAGCUGUCGCAGA	29.30	1.61
1109	GAAACAGGAAGCAAGUUUUUCUGUCAGGAAAACAUGUUGGCUUCUGUUG	29.38	1.65
1110	UGCCAUCAAUAGACCCCUUCAUUGACCUCAACUACAUGGUUUACAUGUUC	29.41	0.76
1111	GUCUGACAACCUCUUGGUGAACCUUAGUACCUAAAAGGAAAUCUCACCCC	29.63	0.65
1112	GGGGAGGAGGAUGGGGAGUAGGACAUAACAGCUUAGAUUUUAAGGUUUUU	29.76	3.76
1113	UUUCCUGGUUUGACAACGAAUUUGGCUACAGCAACAGGGUGGUGGACCUC	29.81	1.07
1114	AUCCAUCACGGUUUUGGAAUGUUUACUACACUCGGAUUAUUUGAUUGUG	30.00	1.74
1115	GGUGCCCACACUAUUUAGCUUCUUCGCUAAGAGCACUCUCAUCGACAAGU	30.22	7.81
1116	CCUCAACUACAUGGUUUAUCAUGUCCAUAUUGAUUCCACCCAUGGCAAAU	31.13	0.62
1117	GUUUCUGUGCAGCAUCAAUUCAGGCGUCCUGAAAAUAGACAGCACC AUCC	31.19	0.49
1118	AACCUGCCAAAUAUGAUGACAUCAAGAAGGUGGUGAAGCAGGGCUGCGGAG	31.49	5.80
1119	GAGCAAGUUACUGUGAGUAUGUAAUACGCACUGACCCAUAUGUCCACCCA	31.53	2.10
1120	AUUCUAGGCGAUCGCACGUUAUUGCAGAAAUCAAAUAGAUUCAACAUAGA	31.55	3.50
1121	CUUCAUUGACCUCAACUACAUGGUUUACAUGUUCCAAUAUGAUUCCACCC	31.58	1.41
1122	UAACCGGGAGAUAGUGAUGAAGUACAUCCAUUUAAGCUGUCGCAGAGGG	32.00	3.63



1123	AACCGGGAGAUAGUGAUGAAGUACAUCCAUUUAAGCUGUCGCAGAGGGG	32.01	4.81
1124	UCAACCCACCAUAUGAAUUGUACAGAAUUAUUCUAUUGAAUUCGGAACU	32.21	1.45
1125	CCCAGCCAAACCCUGUCUGACAACCUCUUGGUGAACCUUAGUACCUAAAA	32.21	1.40
1126	GGGCUGGCAUUGCCCUCAACGACCACUUUGUCAAGCUCAUUUCCUGGUAU	32.22	2.13
1127	UUGCGCCCGCGAACGACAUUUUAUAUGAACGUGAAUUGCUCACAGUAUG	32.23	0.64
1128	UCGAAAUGUCCGUUCGGUUGGCAGAAGCUAUGAAACGAUAUGGGCUGAAU	32.38	0.48
1129	GCUAUCCAGCUAUUUUUUAUUUGUUUGUCAUUUGGGGGAAUUCAUCUCU	32.58	0.80
1130	GCUGCAAAGAUCUCAACGUGCAAAGAAGCUACCGAUCAUACAAAAGA	32.62	5.83
1131	CUUUCACGAUUGAAGUAUUUAUUCUUGCUCAGUAACGGUCUUUAUUACAAA	32.94	1.72
1132	UCUAUAUAAAGUCCUUGAUUCUGUGGGUUCAAACACAUUUCAAAGCUU	33.28	1.56
1133	UGAAGAGAUACGCCUGGUUCCUGGAACAAUUGCUUUUACAGAUGCACAU	33.79	1.79
1134	GGCCAAGGUCAUCCAUGACAACUUUGGUAUCGUGGAAGGACUCAUGACCA	33.81	1.72
1135	CGGAUAUUUGAUUUGUGGAAUUCGAGUCGUCUUAUGUAUAGAUUUGAAG	34.21	0.50
1136	GUUCGUCAUGGGUGUGAACCAUGAGAAGUAUGACAACAGCCUCAAGAUCA	34.64	1.16
1137	GUCUAGAAAAACCGCCAAAUUGAUGACAUCAAGAAGGUGGUGAAGCAG	34.94	4.70
1138	ACAUCAAAGUAGAGUUCUUCACAAACAGAACAAGAUGCUCAAAAAGGAC	35.01	1.47
1139	GUGUAUUUGUUAUUGGUUUGAAUAUAACACUAUAUGGCAGUGUCUUUCC	35.08	3.22
1140	CUUAAACAAUUGUAUGAUUACAUCAAGGCUUCAAAAAUACUCACAUGGCU	35.22	1.09
1141	CCUUCGAUAGGGACAAGACA AUUGCACUGAUCAUGAACUCCUCUGGAUCU	35.30	2.01
1142	CAAUGACCCCUUCAUUGACCUCAACUACAUGGUUUACAUGUUCCAAUAUG	35.31	1.52
1143	CUGGAACAAUUGC UUUUACAGAUGCACAUUUCGAGGUGGACAUCACUUC	35.47	2.02
1144	ACCCUGGGAGCUCUCCUUGGAACCAUUCUGAAAUUAUUUAAAGGGGUU	35.59	3.88
1145	CAGGCACAGCCCCACCACAGGACUCAUGUCUCAUUGCCACAGUGAGCCC	35.77	2.23
1146	ACCCUGGCCAAGGUCAUCCAUGACAACUUUGGUAUCGUGGAAGGACUCA	35.82	1.03
1147	ACUUUGUCAAGCUCAUUUCUGGUAUGACAACGAAUUUGGCUACAGCAAC	35.85	1.18
1148	GGAUACUGCGAUUUUAAGUGUUGUUCCAUUCACGGUUUUGGAAUGU	35.96	1.91
1149	GUGAUGAAGUACAUCCAUUUAAGCUGUCGCAGAGGGGCUACGAGUGGGA	36.08	1.84
1150	UGUGAACCAUGAGAAGUAUGACAACAGCCUCAAGAUCAUCAGCAAUGCCU	36.31	0.17
1151	UUGUCAAGCUCAUUUCUGGUAUGACAACGAAUUUGGCUACAGCAACAGG	36.70	1.28
1152	UGUGAGGGAUGUUUGGGAGAUGUAAGAAUUGUUCUUGCAGUUAAGGGUUA	36.72	1.60
1153	ACUCUCGGACGAGUUUCUGUGCAGCAUCAAAUCAGGCGUCCUGAAAAUUG	36.83	1.17
1154	UGAGCUCAAAGACCCUUCGUUCUUAACCACGUUCUUGAAAUCAGGGUCC	36.88	2.39
1155	UCAAGUUAUUUUUAUGCCUUUAUUUCUUAACAAUUGUAUGAUUACAU	36.95	0.53
1156	UUAUUGCUAUGGGAAUUCUGCAGAAAGACUUGAAGGUGUAUACAGGAAC	37.28	1.65
1157	CCCUGACAAAAAUUGAUCUUGACAAGCAAACAAGACAAGGCCAACCGA	37.40	3.23
1158	GGAAGCGACCAACGCCUUGAUUGACAAGGAUGGAUGGCUACAUCUGGAG	37.96	2.68
1159	UCUGGGAUCAAGCUAUCUAUAUAAGUCCUUGAUUCUGUGUGGGUUCAA	37.98	1.72
1160	AGCACCCUGGCCAAGGUCAUCCAUGACAACUUUGGUAUCGUGGAAGGAC	38.40	2.18
1161	UUGUUAGAAAACAAAGCUUUUUUGUAUUGGUUAAACUCGAGUGGUGAUUG	38.52	1.96
1162	GUUAAGGGUUAGUUUACAAUCAGCCACAUUCUAGGUAGGGGCCACUUCA	38.60	5.11
1163	CAUCUCUUGUAUAUGAUGAUCUGGAUCCACCAAGACUUGUUUUAUGCUC	38.66	1.58
1164	UCACAUUCUAUUCUGAAAUUCGAGAACUAGUGAAAUUAAGGAAAGAAUA	38.80	2.04

1165	GCUGAGAACGGGAAGCUUGUCAUCAUGGAAAUCCCAUCACCAUCUCCA	38.86	1.51
1166	GGUACGAUAACCGGGAGAUAGUGAUGAAGUACAUCCAUUAUAAGCUGUCG	38.93	2.99
1167	UAUUGUUUUCAGGGGGCCUAUGGCUAAAUCAAAUUAACCUACCCCGCAUA	38.93	1.60
1168	UUGCCCUCAACGACCACUUUGUCAAGCUCAUUUCUGGUAUGACAACGAA	38.95	1.79
1169	ACAUUUCGAGGUGGACAUCACUUCGUGAGUACUUCGAAAUGUCCGUUC	39.11	1.37
1170	CGAGGUGGACAUCACUUACGCUGAGUACUUCGAAAUGUCCGUUCGGUUGG	39.23	0.54
1171	GACAACAUCGCCUGUGGAUGACUGAGUACCUGAACCGGCACCUGCACAC	39.33	1.19
1172	CAUCACGGUUUUGGAAUGUUUACUACACUCGGAUUUUUGAUUUGGGAUU	39.39	1.77
1173	AUUUGAUUUGUGGAUUUCGAGUCGUCUUAUUGUAUAGAUUUGAAGAAGAG	39.57	1.31
1174	CAUAUGAAUUGUACAGAAUUAUUUCUAUUGAAUUCGGAACUGUCCUUUCCU	39.61	1.39
1175	AAAAGAGAUCGUGGAUUACGUCGCCAGUCAAGUAACAACCGCGAAAAAGU	39.63	1.58
1176	CUGUUGACCUUUAAAUGAUUGUCUGAACACAUAACUCGAGUGGUGAUUG	39.73	4.47
1177	ACUUAGACUUGACCUAUUUUAUCCAAAUAUUUAUUGCUAUGGGAUUUCU	39.74	1.82
1178	GAUUCAAAGCAUAAAACCAUUACAAGAUUAACAUCUAUGUGCUGAGAG	40.00	2.34
1179	CUUAGCACCCUGGCCAAGGUCAUCCAUGACAACUUUGGUAUCGUGGAAG	40.44	1.75
1180	AGGACUCUCUUUUUCCUCUUCUGGUAGUUGUAUUGACCACUCCCAUAAG	40.73	1.68
1181	UCAACAUAGACUACAUUCAGAUUGGAGGAAAGGAAACCGUUCUGACCCA	40.73	3.61
1182	GGUGAAGCUAAUCUGGAAAUGGAGGAACCAGAAGAAUCAUUGAACACUCU	40.74	1.41
1183	ACCCCUAACAGUGCCAGAAUAAGGCAUUUCUCUAUUGUUUUCAGGGGGCC	40.74	0.97
1184	GUCAUCCAUGACAACUUUGGUAUCGUGGAAGGACUCAUGACCACAGUCCA	40.92	2.90
1185	UGUUUUCAGGGGGCCUAUGGCUAAAUCAAAUUAACCUACCCCGCAUAGGG	41.15	2.41
1186	GUUGCGCGGAGGAGUUGUGUUUGUGGACGAAGUACCGAAAGGUCUUACCG	41.16	0.81
1187	CUCUAACUUCAAGGCCAUUUCUGUGAAAUGCUGGCAUUUGCACCUACCU	41.22	1.58
1188	AGCUCAUUUCUGGUAUGACAACGAAUUUGGCUACAGCAACAGGGUGGUG	41.32	1.46
1189	UCUGAUUGACAAUACGAUUUAUCUAAUUUACACGAAUUGCUUCUGGUG	42.12	1.67
1190	GGACUCUCUUUUUCCUCUUCUGGUAGUUGUAUUGACCACUCCCAUAAGG	42.19	1.33
1191	CCCUUCAUUGACCUCAACUACAUGGUUUACAUGUUCCAAUAUGAUUCCA	42.47	1.17
1192	CUUCUUCGCCAAAAGCACUCUGAUUGACAAAUACGAUUUAUCUAAUUUAC	42.74	1.67
1193	UCCUAUGAUUAUGUCCGGUUAUGUAAACAUCGGAAGCGACCAACGCCU	43.01	1.29
1194	UUAGCAUUUUGAAAGUUGUUGAAACAGGAAGCAAGUUUUUCUGUCAGGAA	43.26	2.02
1195	UCAAGACCCUUCGUUCUUUAACCACGUUCUUGAAAUCAGGGUCCCAAC	43.39	2.43
1196	UAGAAAACCGCCAAUAUGAUGACAUCAAGAAGGUGGUGAAGCAGGCG	43.74	2.74
1197	GUUCUUCGAGUUAAGGGUJAGUUUACAUCAGCCACAUUCUAGGUAGGGG	43.74	2.99
1198	GAACCAUGAGAAGUAUGACAACAGCCUCAAGAUCUAGCAAUGCCUCCU	43.81	1.54
1199	UUAGCACUGACUGAAGAACUCUUGGGACAAGGAUAUAUUUUUAAAUCA	44.10	1.17
1200	AGUGGCAUCUGUUUUGUAGGCUACAAGAACUAUCGGUACCGUGCUGGCUU	44.34	1.44
1201	GUGCGUCAGAAGCACCCAGGACUCCAUUUGCUUUUGUCCCGGGGCUCCAC	44.38	3.12
1202	CAUCAUUGACCCCUUCAUUGACCUCAACUACAUGGUUUACAUGUUCCAAU	44.56	0.59
1203	CCUGCCGUCUAGAAAAACCGGCCAAAUAUGAUGACAUCAAGAAGGUGGUG	44.79	3.17
1204	GAGCUGUUUCUGAGGAGCCUUCAGGAUUACAAGAUUCAAGUGCGCUGCU	44.84	3.30
1205	UGUUUGGAGAUGUAAGAAAUGUUCUUGCAGUUAAGGGUJAGUUUACAUAU	45.29	5.74
1206	UGACCCCUUCAUUGACCUCAACUACAUGGUUUACAUGUUCCAAUAUGAUU	45.54	1.84

1207	GUUUGGGAGAUGUAAGAAAUGUUCUUGCAGUUAAGGGUUAGUUUACAAUC	45.58	4.45
1208	CUGUUGGUGGAUGAGCAAGAGACCUUGC UU AUUAGAAACAAAGUUUAAAC	45.63	2.95
1209	CCUACCCCGCAUAGGGGCGUGGACUCUACAAUAGAACUUCACCCAAGGGG	45.96	1.93
1210	GAUUCCACCCAUGGC AAAU UCCAUGGCACCGUCAAGGCUGAGAACGGGAA	46.07	3.31
1211	AAAAACCUGCCAAAU AUGAUGACAUCAAGAAGGUGGUGAAGCAGGCGUCG	46.18	9.84
1212	GUGAACUGGGGGAGGAUUGUGGGCCUUCUUUGAGUUCGGUGGGGUGAUGUG	46.19	1.14
1213	GCCGUCUAGAAAAACCUGCCAAAU AUGAUGACAUCAAGAAGGUGGUGAAG	46.33	4.34
1214	UUUUAACUCAAUUUUCCAUGAAAAUGCAACAACAUGUAUAAU AUUUUU	46.48	0.76
1215	GGGAGGAGGAUGGGGAGUAGGACAUACCAGCUUAGAUUUUUAAGGUUUUUA	46.51	4.49
1216	CGCCAAAAGCACUCUGAUUGACAAAUACGAUUUAUCUAAUUUACACGAAA	47.07	1.32
1217	AAUGAAGGU AUUU AAGCAUUUCCACAGCCAUUGAUUGAAUGCCGCAAUCU	47.47	6.28
1218	CCACCCAUUGAUGUGAU AUUUUAGCAUUUUGAAAGUUGUUGAAACAGGAA	47.70	3.03
1219	UAUUAAACAAUCAAAACUCUUUCACUGUUUUAUAAAAAUUUUGCUUUUAA	47.96	0.41
1220	AAGGCUGAGAACGGGAAGCUUGUCAUCA AUGGAAAUCCCAUCACCAUCUU	48.27	5.06
1221	UAGUGAUGAAGUACA UCCA UUAU AAGCUGUCGCAGAGGGGCUACGAGUGG	48.45	1.24
1222	GGUGAACUGGGGGAGGAUUGUGGGCCUUCUUUGAGUUCGGUGGGGUGAUGU	48.60	1.45
1223	GU AUUACCGAGUAAUGAUCUUAUUAACAAUCAAAACUCUUUCACUGUUUU	48.84	4.54
1224	GUUUUUGGU AUUGAUUGUAGUGUGUGUCCUACCAUCUCUAAUAGACAUAA	48.96	2.06
1225	GAAGAAGCAAUUGGAUGCUUCUUUCCACGAUUGAAGUAUUUACUUGCUCU	49.08	1.31
1226	GCCUGACUCAGACUGACA UUCUCCACUUCUUGUUC CCCACUGACAGCCUC	49.24	0.86
1227	GGUGUGAGCAGUGUCAGAGUGUGGUAAGCCUGAU AUCGUGUUUUUCGGU	49.42	1.70
1228	CCUGGGAGCUCUCCUUGGAACCAUUCUGAAA UUAUUUAAAGGGGUUGG	49.51	1.59
1229	CCCUGUUGGUCGGUGGGUUGGUAGUUUCUACAGUUGGGCAGCUGGUUAGG	49.68	0.97
1230	UCGGCCCAGCCUCCUGGUGGAGAAGAUCAAUCU AUUUGCCAUGUUUGGCA	49.75	1.67
1231	UCCACAGCCAUUGAUUGAAUGCCGCAAUCU AUACAACAUGUCUAAAAUU	49.77	6.92
1232	ACCACUUUGUCAAGCUC AUUUCUGGUAUGACAACGAAUUGGCUACAGC	49.95	2.49
1233	GCGGAGGAGUUGUGUUUGUGGACGAAGUACCGAAAGGUCUUACCGGAAAA	50.27	1.37
1234	AGGGUCAACAUCUUUUACA UUCUGCAAGCACAUCUGCAUUUUCACCCAC	50.33	2.74
1235	UGAGCAGACGGAGUAUGCCACCAUUGUCUUUCUAGCGGAAUGGGCACCU	50.48	2.75
1236	CAAGGUCAUCAUGACAACU UUGGUAUCGUGGAAGGACUCAUGACCACAG	50.52	3.88
1237	UGGAUGAGCAAGAGACCUUGC UU AUUAGAAACAAAGUUUAAACUGGUGAU	51.16	2.08
1238	UUCUGACCCAUCAUAAGUUUGAAGAAGCAAUUGGAUGCUUCUUCCACGA	51.25	1.95
1239	GAUGGAGGAAAGGAAACCUGUUCUGACCCAUCAUAAGUUUGAAGAAGCAA	51.33	4.05
1240	AUUGUUUUUCAGGGGGCCU AUGGC UAAAUC AAAUUAACCUACCCCGCAUAG	51.33	1.68
1241	GAUUUUUUAUGGGGAAGUAAGGACCAGAGAUAAAAAGGGAGUAACU AUUC	51.43	2.24
1242	CUGCUUUUAACUCUGGUA AAGUGGAU AUUGUUGCCAUCA AUGACCCCUUC	51.56	4.64
1243	ACUCUGGUAAAGUGGAU AUUGUUGCCAUCA AUGACCCCUUCAUUGACCUC	52.10	0.62
1244	CCUGGU AUGACAACGAAU UUGGCUACAGCAACAGGGUGGUGGACCUCAUG	52.27	1.36
1245	ACUCCCAGGUGUGAGCAGUGUCAGAGUGUGGUA AAGCCUGAU AUCGUGUU	52.37	2.80
1246	UCUUAACAAAUGUAUGAUUACAUCAAGGCUUCAAAAAUACUCACAUGGC	52.41	4.28
1247	CCCCUUC CUGUGGUUCU AUUUAU AUUUA AUUUA AUUUA AUUUAUGAGAGC	52.74	4.62
1248	CCCCUCAGCCGUGCCUGUGUUCUCUGUGGACUAUGGGGAGCUGGAUUUCC	52.96	1.46

1249	UGUGUGUGAGAGGUCCUAUGAUUAUGUCCGGUUAUGUAAACAAUCCGGAA	53.06	1.50
1250	CUGCCAAUAUGAUGACAUCAAGAAGGUGGUGAAGCAGGCGUCGGAGGGC	53.20	4.69
1251	GGGGCCUCUAACCACCAUAGCCUCUAACCACCAUAGCCUCUAACCACCAU	53.48	1.54
1252	AGAGUGCAUUGUGAGGGUUAUGAAUAAUGUACAUCUGGCCUUGAAACC	53.59	2.67
1253	UUACAAAGUAUJAGAACCUIUAAGAAGUUAUGAACUCGAGUGGUGAUUG	54.25	5.24
1254	AUUGCAGAAAUCAAAUAGAUUCAACAUAGACUACAUIUCCAGAUGGAGGAA	54.27	3.99
1255	GAUUUCGAGUCGUCUUAUUGUAUAGAUUUGAAGAAGAGCUGUUUCUGAGG	55.31	5.77
1256	AGGUGGCAUGGAUUUUGACUCCAAGAAGGCUUACAGGGACGUGGCCUGGC	55.36	3.47
1257	UCAUGAACUCCUCUGGAUCUACUGGUCUGCCUAAAGGUGUCGCUCUGCCU	55.99	0.00
1258	GAUAGUGAUGAAGUACAUCAUCCAUAUAAGCUGUCGCAGAGGGGCUACGAGU	56.01	0.15
1259	CCUGGCCAAGGUCAUCAUGACAACUUGGUAUCGUGGAAGGACUCAUGA	56.25	2.65
1260	CCUUAUUUAUUUCCGCAAUUAUAGAGCGAGCACUUGCUGAAGGCAGGUG	56.90	5.78
1261	CUGAAUACAAAUCACAGAAUCGUCGUUAGCAGUGAAAACUCUCUCAAUU	56.90	0.93
1262	CAAAACCCCUAACAGUGCCAGAAUAAGGCAUUUCUCUAUUGUUUUCAGGG	56.94	0.61
1263	GUGGAUGAGCAAGAGACCUUGCUIUAUUGAAACAAGUUUAAACUGGUGA	57.03	7.00
1264	CGAACGACAUUUUAUUAUGAACGUGAAUUGCUCACAGUAUGGGCAUUUCG	57.08	3.29
1265	ACUCGACGCAAGAAAAUCAGAGAGAUCCUCAUAAAGGCCAAGAAGGGCG	57.43	3.55
1266	UGACAUCAAAGUAGAGUUCUCCACAAACAGAACAAGAUGCUCAAAAAGG	57.87	1.08
1267	GAGGGUUAUUGAAAUAUUGUACAUCUGGCCUUGAAACCACCUUUUAUUAC	58.46	2.03
1268	AGAGGUCCUAUGAUUAUGUCCGGUUAUGUAAACAAUCCGGAAGCGACCAA	59.61	1.64
1269	GAAUACAAAUCACAGAAUCGUCGUUAGCAGUGAAAACUCUCUCAAUUUCU	59.82	0.61
1270	CCAUGAGAAGUAUGACAACAGCCUCAAGAUCUAGCAAUGCCUCCUGCA	61.07	5.80
1271	UCGUUAGCAGUGAAAACUCUCUCAAUUCUUUAUGCCGGUGUUGGGCGCG	61.43	1.71
1272	AGUGAUGAAGUACAUCAUCCAUAUAAGCUGUCGCAGAGGGGCUACGAGUGGG	61.94	2.53
1273	GUGAGAGGUCCUAUGAUUAUGUCCGGUUAUGUAAACAAUCCGGAAGCGAC	61.97	1.73
1274	AAUAAAACAAAAAAAUUUUACCAAAGAGAAAUUUGUUUUUAUUUAUUU	62.59	3.71
1275	UAUGAAACGAUAUGGGCUGAAUACAAAUCACAGAAUCGUCGUUAGCAGUG	63.05	1.90
1276	UGGAGAGGCAGAGAUGGACUCCUGAGGAAUUUAUUCACCCAGACCCUGG	63.35	1.34
1277	AGAAGUAUGACAACAGCCUCAAGAUCUAGCAAUGCCUCCUGCACCACC	63.51	3.76
1278	CAAGGAUAUGGGCUCACUGAGACUACAUCAGCUAUUCUGAUUACACCCGA	64.03	1.48
1279	GGGGUGAACUGGGGGAGGAUUGUGGCCUUCUUUGAGUUCGGUGGGGUGAU	64.40	0.62
1280	CUUCCUGGCCUUUGGCUUUGUCUCAUCACCUUCAGCUGCCACUUCUAUG	64.40	1.86
1281	UGUGAGCAGUGUCAGAGUGUGGUAAAGCCUGAUUUCGUGUUUUUCGGUGA	64.76	0.77
1282	UUGUUUUCAGGGGGCCUAUGGCUAAAUCAAAUUAACCUACCCCGCAUAGG	64.81	0.22
1283	GGAGCUAUUCUUGCGCAGCUUGCAAGACUUAUAGAUUCAUUCUGCCCUGC	65.06	7.75
1284	CCGGGAGAUAGUGAUGAAGUACAUCAUCCAUAUAAGCUGUCGCAGAGGGGCU	65.16	5.14
1285	GGGAUGCAGCAUUAUGAUGUGGGUCAAGGAAUUAAGUUAGGGAAUGGCAC	65.23	6.27
1286	CUUUUACAGAUGCACAUUUCGAGGUGGACAUCACUUAACGCUGAGUACUUC	65.24	1.42
1287	AUCGGCCCAGCCUCCUGGUGGAGAAGAUCAAUCUAUUUGCCAUGUUUGGC	65.52	5.43
1288	UGAUGAAGUACAUCAUCCAUAUAAGCUGUCGCAGAGGGGCUACGAGUGGGAU	65.62	1.88
1289	CAAAGACCCUUCGUUCUUUAACCACGUUCUUGAAAUCAGGGUCCCAACU	65.82	1.18
1290	UUUUGGAAUGUUUACUACACUCGGAUUUUGAUUUGUGGAUUUCGAGUCG	66.08	5.94

1291	CAGGACUCUCUUUUUCCUCUUCUGGUAGUUGUAAUGACCACUCCCAUAA	66.34	2.65
1292	AUUCUAGGCGAUCGCGUGGUUUCGAGAGAAGAAAUCUCGGAUUGAUCUA	66.54	1.82
1293	CUGCAGGCCUAGAGAAGUUUCAGGGAAGGUCAGAAGAGCUCCUGGCUGUG	66.97	7.95
1294	AUUUUUJGGCAAUCAAAUCAUUCGGAUACUGCGAUUUUAAGUGUUGUUC	67.14	3.64
1295	UCGUACAAGUGUCUGAAGGUGCUGGAGAACAUAUAAAAGCAAUGGGCAGGG	67.28	3.85
1296	UUUCAAGUUAUUUUUAUGCCUUUUUAUUUCUUAACCAAUGUAUGAUUAC	67.93	1.24
1297	GAGAUAGUGAUGAAGUACAUCCAUAUAAGCUGUCGCAGAGGGGCUACGA	68.37	0.61
1298	CAAGACCGACUACCAGGGCUUCCAAAGCAUGUACACCUUCGUGACUCCC	69.14	10.06
1299	UACUGCGAUUUUAAGUGUUGUCCAUCCAUCACGGUUUUGGAAUGUUUA	69.55	2.36
1300	CUGUGAAAUGCUGGCAUUUGCACCUACCUCACAGAGUGCAUUGUGAGGGU	69.84	7.32
1301	GAGUGGCAUCUGUUUUGUAGGCUACAAGAACUAUCGGUACCGUGCUGGCU	70.58	3.59
1302	CUCCGUGAGUGGCAUCUGUUUUGUAGGCUACAAGAACUAUCGGUACCGUG	70.93	5.02
1303	AGUGUUUAUUGUGUCAUUUGUCUUUGUCUAGGAGAGGACAGGACUCUCU	71.13	8.63
1304	GCUGGCAUUUGCACCUACCUCACAGAGUGCAUUGUGAGGGUUAUGAAU	71.63	2.22
1305	GGAACCGCUGGAGAGCAACUGCAUAAGGCUAUGAAGAGAUACGCCUGGU	72.28	0.62
1306	UACUUGCUCAGUAACGGUCUUUAUUACAAAGUAUUAGAACCUUUAAGAAG	73.01	4.02
1307	GGAGAUAGUGAUGAAGUACAUCCAUAUAAGCUGUCGCAGAGGGGCUACG	73.87	4.72
1308	AGUAUGACAACAGCCUCAAGAUAUCAGCAAUGCCUCCUGCACCACCAAC	73.88	3.17
1309	CGGGAGAUAGUGAUGAAGUACAUCCAUAUAAGCUGUCGCAGAGGGGCUA	74.29	7.70
1310	ACAAGCAACUGAAUCUCAUUUCUUCAGCUUGAAGAAGUGAUCUUGGCCAA	74.62	2.19
1311	CAUCGUUGACCGCCUGAAGUCUCUGAUUAAGUACAAGGCUAUCAGGUGG	75.04	1.22
1312	CCUCUUCUGGUAGUUGUAAUGACCACUCCAUAAAGGCUAUAACUGUUC	75.10	15.33
1313	AGGGUUAUGAAUAAUGUACAUCUGGCCUUGAAACCACCUUUUAUUACA	75.99	3.29
1314	CAAAGAGGCGAACUGUGUGUGAGAGGUCCUAUGAUUAUGUCCGGUUAUGU	76.65	3.10
1315	UGAUGUAGUAAGGUUUUUGGAUUCAAAGCAUAAAACCAUUACAAGAUU	78.21	1.45
1316	GAUAUGUGGAUUUCGAGUCGUCUUAUUGUAUAGAUUUGAAGAAGAGCUGU	79.54	2.99
1317	ACUGGGCACAGUGAUGAUGAGCCCAAGAGAAUCAAGAAGAGCAAGAUGAU	80.23	4.94
1318	AUGUCAGAAUUAAAAAUUCUUUAACUUAACUAAAAACACUAUCCAACAA	80.72	4.18
1319	GGGAUCCCCUUCUUGUGGUUCUAUUUAUUUAUUUAUUUAUUUAUUUAU	81.30	4.22
1320	UGUCUAGUCAUUUUAUAGUGCCCCACAUUCAAGAACCAGACAACAGGAU	81.58	4.64
1321	UAAAUUUUAUGCCUUUUUAUUUCUUAACAAAUGUAUGAUUACAUCAAGGC	82.26	1.01
1322	GGGAGAUAGUGAUGAAGUACAUCCAUAUAAGCUGUCGCAGAGGGGCUAC	82.74	5.35
1323	CAGAGGGUACAUGACUCUGUUCUCCAUCAAGAGCAACCACCCUGGGCUUC	83.10	11.76
1324	CGUCAUAGAAGAAUAGAUUAGAAACGUCCACAAGAGUAAGUGUGCUUUG	83.13	5.78
1325	UCUAUGUGCUGAGAGACAUUAUGACACCGCCAAAUUUAACUGCAGAGUUG	84.53	7.10
1326	GUCUAAAAUUUAAGGUUUUCAUUCAAAUGAAAAUUAUUUUUAGCACUGA	84.61	11.22
1327	CGUGAGUGGCAUCUGUUUUGUAGGCUACAAGAACUAUCGGUACCGUGCUG	84.82	5.63
1328	GCUCAACAUGGGGCCCGGGUUCCAAAGUUUGCAAAGUUGGGAGUCGAGGG	85.29	3.75
1329	CAUCGUGGACCGGCUGAAGAGCCUGAUCAAUAACAAGGGCUACCAGGUAG	85.59	10.39
1330	GCCGCAAUCUAUACAAACAUGUCUAAAAUUUAAGGUUUUCAUUCAAAUA	86.86	2.30
1331	CCUGCAGGCCUAGAGAAGUUUCAGGGAAGGUCAGAAGAGCUCCUGGCUGU	87.60	2.91
1332	UCACUGUUUUUAUAAAAAUUUUGCUUUUAUUAAAUGGUCUUGUUAGAAA	87.73	10.46

1333	CCUGUCCUGUGUCAUCAUCUUUGUCAUUGUGUACUAUGCCUUGAUGGCUG	87.81	10.74
1334	UGAACUGGGGGAGGAUUGUGGCCUUCUUUGAGUUCGGUGGGGUCAUGUGU	87.88	0.59
1335	UUGCUCAGUAACGGUCUUUUAUUAACAAGUAUUAGAACCUUUAAGAAGUUA	88.19	12.32
1336	UUUGUGCAUUUGGGGGGAAUUCAUCUCUCUUUAUAUAAAGUUGGAUGCG	88.20	4.50
1337	AUAGUGAUGAAGUACAUC <b>CAUUAUAAGCUGUCG</b> CAGAGGGGCUACGAGUG	90.70	1.38
1338	GGUGGAGAAGAUCAAUC <b>UAUUUGCCAUGUUUGGC</b> ACUGGCAUUGCCAUGA	91.39	9.76
1339	UGUCAUCAUCUUUGUCAUUGUGUACUAUGCCUUGAUGGCUGGAGUAGUCU	91.85	5.13
1340	AGUGAAAACUCUCUCAAUUCUUUAUGCCGGUGUUGGGCGCGUUAUUUAU	92.53	10.73
1341	GCGGUGGUGUUGUGUUCGUGGACGAGGUGCCUAAAGGACUGACCGGCAAG	94.38	8.92
1342	CCUGAAGUCUCUGAUUAAGUACA <b>AAAGGCUAUCAGG</b> UGGCUCCCGCUGAAU	94.69	1.53
1343	AUGAGGGCUGUUUGCCCUUUUCUGUGCCA <b>AAUGAGUG</b> CCCUUUUCUGGCAC	95.21	7.33
1344	CUUGGGACAAAGGAUAUAUUUUUAAAUCAUUAUGCUCGAGUGGUGAUUG	95.73	6.53
1345	AAAGAUCAUCAUCAUGGAUAGCAAGACCGACUACCAGGGCUUCCAAAGCA	96.63	16.25
1346	GAUGGACCUGUUGCGGGUUUGGCUUUUGACCUC <b>AAUGAACCCUCAGCUGA</b>	97.51	4.08
1347	CUUCGAGGAGGAGCUAUUCUUGCGCAGCUUGCAAGACUAUAAGAUUCAAU	101.21	4.07
1348	CAUUUGGGGGGAAUUCAUCUCUCUUUAUAUAAAGUUGGAUGCGGAACCC	102.25	4.03
1349	CAUCAGAGGGGUCAUGACUCUGUUC <b>CAUCAAGAGCAACC</b> ACCCUGGGC	103.05	1.77
1350	ACAUAUCGAGGUGGACA <b>UUACCUACGCCGAGUACU</b> UCGAGAUGAGCGUUC	106.40	15.37
1351	UUCGAGAUGAGCGUUCGGCUGGCAG <b>AAGCUAUGAAG</b> CGCUAUGGGCUGAA	109.21	8.64
1352	GCUCUCCUUGGAACCCAU <b>UCCUGAAAUAUUUAAAG</b> GGGUUGGCCGGGCU	109.88	8.13
1353	GAGCUCUCCUUGGAACCCAU <b>UCCUGAAAUAUUUAAAG</b> GGGUUGGCCGGG	113.42	1.88
1354	UCUCUCCAAAUUUUAAGGUGAAGUUAU <b>ACUUCACAAAAC</b> AGUAGAGGAG	116.70	8.50
1355	GCAGGCCUAGAGAAGU <b>UUCAGGGAAGGUCAGAAG</b> AGCUCCUGGCUGUGGU	119.88	2.99

<sup>1</sup> Shown are mRNA sequences containing 20-nucleotide target sites (in bold) and the flanking regions.

<sup>2</sup> N=3.

**Supplementary Table 2.** Sequence and modification pattern of sdRNAs in Figure 6.

Name	Sequence <sup>1,2</sup>
MAP4K3149 (14-2'-O-methyl)	P.mU.mA.mG.mA.fC.fU.fU.fC.fC.mA.mC#mA#mG# <b>mA</b> #mA#fC#fU#fC#fU
MAP4K3149 (14-2'-OH)	P.mU.mA.mG.mA.fC.fU.fU.fC.fC.mA.mC#mA#mG# <b>A</b> #mA#fC#fU#fC#fU

<sup>1</sup> m= 2'-O-methyl (2'-ribose modification), f= 2'-fluoro (2'-ribose modification), #= phosphorothioate (backbone modification), P= phosphate.

<sup>2</sup> Position 14 is shown in bold.