Table S1. List of primers used in the study.

Construct	Abbreviation	Primer sequence (5' to 3')
p2300-NP	NP	**F:** GAGCTCATGGGTACCAACAAGCCAG **R:** GGATCCCTAGTCATCTGCACCTTCTGC
p2300-RdRp^{wt}	RdRp^{wt}	**F:** GAGAGGTCGCGAGCTCGGTACCATGACGACACCACCTCTCGTTATACC **R:** GCATGCCTGCAGGTCGACTCTAGATCAGAAATCGAACTTATGGTC
p2300-RdRp^{opt}	RdRp^{opt}	**F:** GAGAGGTCGCGAGCTCGGTACCATGACTACCCCTCCTCTTGTG **R:** GCATGCCTGCAGGTCGACTCTAGACTAGAAGTCGAACTTGTGATC
pCXSN-NSs	NSs	**F:** CTCGGTACCATGTCTTCAAGTGTTTATGAG **R:** GACTCTAGATTATTTTGATCCTGAAGCATATG
pBIN-NS3	NS3	**F:** CTCGGTACCATGAACGTGTTCACATCGTC **R:** AGTCTAGACTACAGCACAGCTGGAGAGC
pCXSN-NSvc4	NSvc4	**F:** CTCGGTACCATGGCTTTGTCTCGACTTTTG **R:** GACTCTAGACTACATGATGACAGAAACTTC
pCB301-HH-RNA1$_{(-)}$-RZ-NOS	RNA1$_{(-)}$	**F:** GGAATATCTTCCTATAGTCACACAAAGTCCAGAGGAAAACAAAATG **R:** GTGGAGATGCCATGCCGACCCACACATAGTCAGAGGAAAAAATAATTTTG
		F[a]**:** CAAAATTATTTTTTCCTCTGACTATGTGTGGGTCGGCATGGCATCTCCAC **R**[a]**:** CATTTTGTTTTCCTCTGGACTTTGTG TGACTATAGGAAGATATTCC
pCB301-HH-RNA2$_{(-)}$-RZ-NOS	RNA2$_{(-)}$	**F:** GGAATATCTTCCTATAGTCACACAAAGTCCTGGGTATATAAGCCAC **R:** GTGGAGATGCCATGCCGACCCACACAAAGTCTGGGTATAACTTCTTCG
		F[a]**:** GAAGAAGTTATACCCAGACTTTGTGTGGGTCGGCATGGCATCTCCAC **R**[a]**:** GTGGCTTATATACCCAGGACTTTGTGTGACTATAGGAAGATATTCC
pCB301-HH-RNA3$_{(-)}$-RZ-NOS	RNA3$_{(-)}$	**F:** CGAAACTATAGGAATATCTTCCTATAGTCACACAAAGTCCTGGGTAAAATAGTTAT **R:** GGTGGAGATGCCATGCCGACCCACACAAAGTCTGGGTAATAAAATTTTC
		F[a]**:** GAAAATTTTATTACCCAGACTTTGTGTGGGTCGGCATGGCATCTCCACC **R**[a]**:** GTTTCGGCCTTTCGGCCTCATCAGACACAAAGAGGCCTCTCCAAATGAAATG
pCB301-HH-RNA3$_{(+)}$-RZ-NOS	RNA3$_{(+)}$	**F:** CGAAACTATAGGAATATCTTCCTATAGTCACACAAAGTCTGGGTAATAAAATTTTC **R:** GAGGTGGAGATGCCATGCCGACCCACACAAAGTCCTGGGTAAAATAGTTATATTTTTAC
		F[a]**:** CTATTTTACCCAGGACTTTGTGTGGGTCGGCATGGCATCTCCACC **R**[a]**:** GAAAATTTTATTACCCAGACTTTGTGTGACTATAGGAAGATATTCCTATAGTTTCG
pCB301-HH-RNA4$_{(-)}$-RZ-NOS	RNA4$_{(-)}$	**F:** GGAATATCTTCCTATAGTCACACAAAGTCCAGGGCATTTGTACAACG **R:** GGTGGAGATGCCATGCCGACCCACACAAAGTCAGGGCATATCTTTTGAG
		F[a]**:** CTCAAAAGATATGCCCTGACTTTGTGTGGGTCGGCATGGCATCTCCACC **R**[a]**:** CGTTGTACAAATGCCCTGGACTTTGTGTGACTATAGGAAGATATTCC
pCB301-HH-RNA3$_{(-)eGFP}$-RZ-NOS	MR3$_{(-)eGFP}$	**F:** CCACAACTACTGATTTGTTCAGTTTACTTGTACAGCTCGTCCATGCCGAGA **R:** CATTCCTCCAGTACCTCTTGCTAGAATGGTGAGCAAGGGCGAGGAGCTGTTC
		F[a]**:** GAACAGCTCCTCGCCCTTGCTCACCATTCTAGCAAGAGGTACTGGAGGAATG **R**[a]**:** TCTCGGCATGGACGAGCTGTACAAGTAAACTGAACAAATCAGTAGTTGTGG
pCB301-HH-RNA3$_{(+)eGFP}$-RZ-NOS	MR3$_{(+)eGFP}$	**F:** CATTCCTCCAGTACCTCTTGCTAGAATGGTGAGCAAGGGCGAGGAGCTGTTC **R:** CCACAACTACTGATTTGTTCAGTTTACTTGTACAGCTCGTCCATGCCGAGA
		F[a]**:** TCTCGGCATGGACGAGCTGTACAAGTAAACTGAACAAATCAGTAGTTGTGG **R**[a]**:** GAACAGCTCCTCGCCCTTGCTCACCATTCTAGCAAGAGGTACTGGAGGAATG
pCB301-HH-RNA3$_{(-)mCherry\&eGFP}$-RZ-NOS	MR3$_{(-)mCherry\&eGFP}$	**F:** CAATACAATTCCGACATCATCTAAGTATGGTGAGCAAGGGCGAGGAGGATAAC **R:** TCTTTTCTTTTTTTCTTTTTCCTTTTATTTTTAAGATCTGTACAGCTCGTCCATGC
		F[a]**:**GCATGGACGAGCTGTACAGATCTTAAAAATAAAAGGAAAAAGAAAAAAAGAAAAG **R**[a]**:** GTTATCCTCCTCGCCCTTGCTCACCATACTTAGATGATGTCGGAATTGTATTG

pCB301-HH-RNA3$_{(-)eGFP\Delta NS3}$-RZ-NOS	MR3$_{(-)eGFP\Delta NS3}$	**F:** AAATAAAAGGAAAAAGAAAAAAAGAAAAGAAAACAAATAATC **R:** GGTGGAGATGCCATGCCGACCCACACAAAGTCTGGGTAATAAAATTTTC **F**[a]**:** GAAAATTTTATTACCCAGACTTTGTGTGGGTCGGCATGGCATCTCCACC **R**[a]**:** TTTTCTTTTTCCTTTTATTTACTTAGATGATGTCGGAATTGTATTG
pCB301-HH-RNA3$_{(-)eGFP\&NS3stop}$-RZ-NOS	MR3$_{(-)eGFP\&NS3stop}$	**F:** CAATTCCGACATCATCTAAGTATGTAAGTGTTCACATCGTCTG **R:** GGTGGAGATGCCATGCCGACCCACACAAAGTCTGGGTAATAAAATTTTC **F**[a]**:** GAAAATTTTATTACCCAGACTTTGTGTGGGTCGGCATGGCATCTCCACC **R**[a]**:** GACGATGTGAACACTTACATACTTAGATGATGTCGGAATTG
pCB301-HH-RNA3$_{(-)eGFPMut1}$-RZ-NOS	MR3$_{(-)eGFPMut1}$	**F:** CAATACAATTCCGACATCATCTAAGTAAATTTGACAATAGG **R:** TCTTTTCTTTTTTTCTTTTTCCTTTTATTTCTACAGCACAGCTGGAGAGC **F**[a]**:** GCTCTCCAGCTGTGCTGTAGAAATAAA AGGAAAAAGAAAAAAAGAAAAGA **R**[a]**:** ACTTAGATGATGTCGGAATTGTATTGTATAGTAAAAATA
pCB301-HH-RNA3$_{(-)eGFPMut2}$-RZ-NOS	MR3$_{(-)eGFPMut2}$	**F:** CAATACAATTCCGACATCATCTAAGTTTCTTCACTGAAGTGAAGCC **R:** TCTTTTCTTTTTTTCTTTTTCCTTTTATTTGACAGGCTTTCCATCATGGTCAG **F**[a]**:** AAATAAAAGGAAAAAGAAAAAAAGAAAAGAAAACAAATAATC **R**[a]**:** GGCTTCACTTCAGTGAAGAAACTTAGATGATGTCGGAATTGTATTG
pCB301-HH-RNA3$_{(-)eGFPMut3}$-RZ-NOS	MR3$_{(-)eGFPMut3}$	**F:** CAATACAATTCCGACATCATCTAAGTATTGATGAGCATCAG **R:** TCTTTTCTTTTTTTCTTTTTCCTTTTATTTTTTCACATAAGAGGATGACATC **F**[a]**:** AAATAAAAGGAAAAAGAAAAAAAGAAAAGAAAACAAATAATC **R**[a]**:** ACTTAGATGATGTCGGAATTGTATTGTATAGTAAAAATA
pCB301-HH-RNA3$_{(-)eGFPMut4}$-RZ-NOS	MR3$_{(-)eGFPMut4}$	**F:** CAATACAATTCCGACATCATCTAAGTATGAACGTGTTCAC **R:** TCTTTTCTTTTTTTCTTTTTCCTTTTATTTGGAGGGGTGCC **F**[a]**:** AAATAAAAGGAAAAAGAAAAAAAGAAAAGAAAACAAATAATC **R**[a]**:** ACTTAGATGATGTCGGAATTGTATTGTATAGTAAAAATA
pCB301-HH-RNA1$_{(-)eGFP}$-RZ-NOS	MR1$_{(-)eGFP}$	**F:** GTCCCTTTGTTGAAGAGGACTTCTTACTTGTACAGCTCGTCCATGCCGAGA **R:**GATTTTGTTTTCCACAAAAGAATTGAAGGATGGTGAGCAAGGGCGAGGAGCTGTTC **F**[a]**:** GAACAGCTCCTCGCCCTTGCTCACCATCCTTCAATTCTTTTGTGGAAAACAAAATC **R**[a]**:** TCTCGGCATGGACGAGCTGTACAAGTAAGAAGTCCTCTTCAACAAAGGGAC
pCB301-HH-RNA2$_{(-)eGFP}$-RZ-NOS	MR2$_{(-)eGFP}$	**F:** CATACATGAATGAACCTATTGGCTTACTTGTACAGCTCGTCCATGCCGAGA **R:** GTCTGGGTATAACTTCTTCGAAGATGGTGAGCAAGGGCGAGGAGCTGTTC **F**[a]**:** GAACAGCTCCTCGCCCTTGCTCACCATCTTCGAAGAAGTTATACCCAGAC **R**[a]**:** TCTCGGCATGGACGAGCTGTACAAGTAAGCCAATAGGTTCATTCATGTATG
pCB301-HH-RNA4$_{(-)eGFP}$-RZ-NOS	MR4$_{(-)eGFP}$	**F:** CATACTCCGGAACTGGTTATCTCACTTACTTGTACAGCTCGTCCATGCCGAGA **R:** GATTAAGCTAATATATACTTTAATTATGGTGAGCAAGGGCGAGGAGCTGTTC **F**[a]**:** GAACAGCTCCTCGCCCTTGCTCACCATAATTAAAGTATATATTAGCTTAATC **R**[a]**:** TCTCGGCATGGACGAGCTGTACAAGTAAGTGAGATAACCAGTTCCGGAGTATG
pGEM-eGFP	-	**F:** ATGGTGAGCAAGGGCGAGGAGCTGTTC **R:** TTACTTGTACAGCTCGTCCATGCCGAGA
pGEM-anti-eGFP	-	**F:** TTACTTGTACAGCTCGTCCATGCCGAGA **R:** ATGGTGAGCAAGGGCGAGGAGCTGTTC
pGEM-NS3	-	**F:** CATGGCGGCCGCGGGAATTCGATTATGAACGTGTTCACATCGTC **R:** CAGGCGGCCGCGAATTCACTAGTGATCTACAGCACAGCTGGAGAGC
pGEM-antiNS3	-	**F:** CATGGCGGCCGCGGGAATTCGATTCTACAGCACAGCTGGAGAGC **R:** CAGGCGGCCGCGAATTCACTAGTGATATGAACGTGTTCACATCGTC

[a] Forward and reverse primers were used to amplified the linearized pCB301 vectors by PCR.

Table S2. The predicted intron splicing sites of wild-type RdRp gene.

Position (bp)						
40	1233	2741	4107	5500	6655	7576
114	1258	2747	4113	5550	6678	7614
121	1275	2806	4195	5607	6682	7633
235	1293	2865	4246	5737	6708	7664
268	1313	2983	4378	5771	6750	7683
271	1369	3088	4558	5784	6817	7684
298	1385	3171	4567	5887	6829	7698
361	1536	3183	4612	5931	6930	7699
477	1558	3204	4624	6055	6944	7774
647	1654	3281	4662	6076	6948	7825
686	1675	3289	4692	6099	6961	7898
771	1767	3319	4738	6139	6972	7953
829	1806	3390	4783	6160	6998	7959
855	1861	3458	4801	6163	7034	8068
857	1887	3589	4869	6180	7179	8096
1015	1944	3640	4970	6228	7255	8113
1018	1965	3706	5023	6255	7307	8134
1033	1977	3712	5124	6360	7352	8187
1068	2114	3784	5180	6364	7457	8317
1087	2233	3791	5215	6399	7458	8346
1131	2353	3828	5250	6412	7482	8513
1132	2365	3940	5251	6426	7486	8573
1163	2385	3984	5277	6469	7509	8595
1164	2398	4014	5292	6476	7517	8648
1171	2437	4066	5386	6510	7546	8682
1176	2568	4090	5440	6555	7552	8704
1180	2709	4106	5498	6576	7568	

The putative 188 intron splicing sites (ISSs) of wild-type RdRp gene sequence were predicted by Alternative Splice Site Predictor (ASSP) (http://wangcomputing.com/assp/).

Table S3. Optimized RdRp gene sequence used in the study.

ATGACTACCCCTCCTCTTGTGATTCCTCTTCATGTGCACGGTAGGTCTTACGAGCTTCTTGCTGGTTACCATGAGGTGGACTG
GCAAGAGATTGAGGAACTGGAAGAGACTGATGTGAGAGGTGATGGCTTCTGCCTGTACCACTCTATCCTTTACTCTATGGGC
CTGAGCAAAGAGAACTCTAGGACCACCGAGTTCATGATCAAGCTGAGGTCTAACCCTGCTATCTGCCAGCTGGATCAAGAG
ATGCAGCTGTCTCTTATGAAGCAGCTGGACCCGAACGATTCTTCTGCTTGGGGTGAAGATATCGCCATCGGCTTCATGGCTAT
CATCCTGCGGATCAAGATTATCGCCTACCAGACCGTGGATGGCAAGCTGTTCAAGACTATCTACGGTGCCGAGTTCGAGAGC
ACCATCAGGATTAGGAACTACGGCAACTACCACTTCAAGAGCCTCGAGACTGATTTCGACCACAAGGTGAAGCTCCGGTCC
AAGATTGAAGAGTTCCTTCGGATGCCTGTTGAGGACTGCGAGTCTATTTCTCTGTGGCACGCTTCTGTGTACAAGCCGATCG
TGTCTGATTCTCTGAGCGGCCACAAGAGCTTCAGCAATGTGGATGAGCTGATCGGCAGCATCATCAGCAGCATGTACAAGAT
CATGGACAACGGCGATCAGTGCTTCCTGTGGTCTGCTATGAGAATGATCGCTCGGCCTTCTGAGAAGCTTTACGCTCTTGCT
GTGTTCCTGGGCTTCAACCTGAAGTTCTACCATGTGAGAAAGCGGGCAGAGAAGCTTACCGCTAAGTTGGAGTCTGATCAC
ACCAACCTGGGTGTGAAGCTTATCGAGGTTTACGAGGTGTCAGAGCCTACTAGGTCTACTTGGGTTTTGAAGCCTGGTGGCT
CTCGGATTACTGAGACTAGGAACTTCGTGATCGAAGAGATCATCGATAACCGGCGGAGCCTTGAGTCTCTGTTCGTGTCATC
TTCTAACTACCCTGCCGAGCTGTGCTCTCAGAAGCTTTCTGCTATCAAGGACCGGATCGCTCTGATGTTCGGCTTTATTAACA
GGACCCCTGAGAACAGCGGTCGTGAGCTTTACATCAACACCTACTACCTGAAGCGGATCCTCCAGGTGGACAGAAATGTGA
TCAGGGACTCTCTTAGGTCACAGCCTGCTGTGGGTATGATCCAGATTATTAGGCTGCCTACCGCTTTCGGCACTTACAATCCT
GAGGTTGGGACCCTTTTGCTTGCTCAGACTGGTCTTATCTACAGGCTTGGTACTACTACCCGGGTGCAGATGGAAGTTAGAA
GGTCCCCATCTGTGATCAGCCGGTCACACAAGATCACTAGCTTCCCCGAGACTCAGAAGCACAACAACAACCTGTACGACT
ACGCTCCGAGGACTCAAGAGACTTTCTACCATCCTAACGCCGAGATCTACGAGGCTGTGGATGTTAAGACCCCTTCCGTGAT
TACCGAGATCGTCGACAACCACATCGTGATTAAGCTGAACACCGACGACAAAGGCTGGTCCGTGAGCGATTCTATCAAGCA
GGATTTCGTGTACCGGAAGCGGCTGATGGACGCTAAGAATATTGTGCACGACTTCGTGTTCGACATCCTGTCTACCGAGACT
GACAAGTCCTTCAAGGGTGCTGATCTGAGCATCGGCGGTATCTCTGATAACTGGTCCCCTGACGTGATCATCAGCCGTGAAT
CTGATCCACAGTACGAGGACATTGTGGTGTACGAGTTCACTACCAGGTCCACCGAGTCTATCGAGTCTCTTCTGAGATCCGT
CGAGGTGAAGTCCCTGAGATACAAAGAGGCTATCCAAGAGAGGGCTATCACCCTGAAGAAGAGGATCAGCTACTACACCAT
CTGCGTGAGCCTTGATGCTGTGGCTACCAACCTTCTTTCTCTGCCTGCTGATGTGTGCAGAGAGCTTATCATTAGGCTCAGGG
TTGCCAACCAGGTGAAGATTCAGCTGGCTGACAACGACATCAACCTGGATTCTGCTACCCTTCTGGCTCCTGACATCTACCG
TATCAAAGAGATGTTCCGAGAGAGCTTCCCGAACAACAAGTTCATTCACCCGATCACCAAAGAAATGTACGAGCACTTCGT
GAACCCCATGATCAGCGGCGAGAAGGATTATGTGGCTAACCTCAAGTCCATCATCGACAAAGAGACTAGGGACGAGCAGCG
GAAGAACCTCGAGTCTTTGAAGGTTGTGGACGGGAAGAAGTACACCGAGAGGAAGGCTGAAACTGCCCTGAATGAGATGT
CTCAGGCTGAGGAACACTACCGGTCTTACTTCGAGAACGACAACTTCCGGTCTACCTTGAAGGCTCCTGTTCAGCTGCCTCT
GATCATCCCTGATGTGTCCTCTCAGGACAACCAGTTCAGCAACAAAGAGCTGAGCGACCGGATCCGTAAGAAGCCTATTGAT
CACCCCATCTACAACATCTGGGACCAAGCTGTGAACAAGCGGAACTGCTCTATTGCTCTTGGTCACCTGGATGAGTTGGAGA
TCTCTATGCTTGAGGGCCAAGTGGCCAAGAAGGTGGAAGAGTCTTACAAGAAGGACCGGTCACAGTACAACAGGACCACC
TTGCTTACCAACATGAAGGAAGATATCTACCTGGCCGAGAGGGGCATCAATGCTAAGAAGAGGCTTGAGGAACCGGACGTC
AAGTTCTACAGGGATCAAAGCAAGCGGCCTTTCCATCCTTTCGTGTCAGAGACAAGGGACATCGAGCAGTTCACTCAGAAA
GAATGCCTCGAGCTGAACGAAGAGTCTGGTCACTGCTCTCTCATCAACGTCGAGGATCTTGTGCTGTCTGCTCTTGAGCTTC
ACGAGGTTGGAGATTTGGAGCACCTGTGGAACAACATCAAGGCCCACTCTAAGACCAAGTTCGCTCTGTACGCCAAGTTCA
TCTCTGATCTTGCTACCGAGCTGGCCATCTCTCTGTCTCAGAATTGCAAAGAGGACACCTACGTCGTCAAGAAGCTGAGGGA
CTTCTCTTGCTACGTGCTGATCAAGCCTGTGAACCTGAAGAGTAACGTGTTCTTCTCCCTGTACATCCCGTCCAACATCTACA
AGTCTCACAACACTACCTTCAAGACCCTGATCGGCTCTCCTGAGTCTGGTTACATGACCGATTTCGTGAGCGCCAACGTGAG
CAAGCTTGTGAATTGGGTTAGATGCGAGGCTATGATGCTGGCCCAAAGAGGATTTTGGAGAGAGTTCTACGCTGTCGCCCCT
TCTATCGAAGAACAGGATGGTATGGCTGAGCCAGAGTCTGTTTGCCAGATGATGTCTTGGACCCTTCTGATCCTGCTGAACG
ATAAGCACCAGCTTGAAGAGATGATCACCGTGTCCAGATTCGTCCACATGGAAGGCTTCGTTACTTTCCCTGCTTGGCCTAA
GCCGTACAAGATGTTCGACAAGCTGTCTGTGACTCCGAGGTCTAGACTTGAGTGCCTTGTGATCAAGCGGCTCATCATGCTG

ATGAAGCACTACAGCGAGAACCCGATCAAGTTTATGATCGAGGACGAGAAGAAGAAGTGGTTCGGCTTCAAGAATATGTTC

CTGCTGGACTGCAACGGCAAGCTCGCTGATCTTTCTGATCAGGACCAGATGCTGAACCTGTTCTACCTGGGTTACCTGAAGA

ACAAGGACGAAGAGGTCGAGGATAACGGTATGGGTCAGCTTCTGACCAAGATCCTGGGATTCGAGTCAGCTATGCCTAAGA

CCAGGGATTTCCTGGGCATGAAGGATCCTGAGTACGGCACCATTAAGAAGCACGAGTTCTCCATCAGCTACGTGAAGGATCT

GTGCGACAAGTTCCTGGACAGGCTGAAGAAAACCCACGGCATTAAGGACCCTATTACCTACCTGGGCGACAAGATCGCTAA

GTTCTTGAGCACCCAGTTCATCGAGACTATGGCTAGCCTGAAGGCCAGCTCTAACTTCAGCGAGGATTACTACCTGTACACC

CCTTCTAGGCGGCTCAAGAATCAAGAACAGAGCCGGTCTAAGCACGTGATCGATGCTGGTGGTAACATCAGCGCTTCAGTG

AAGGGTAAGCTGTACCACAGGTCTAAGGTGATCGAGAAGCTCACTACCCTGATCAAGGATGAGACTCCGGGCAAAGAACTG

AAGATCGTGGTGGATCTTCTGCCGAAGGCTATGGAAGTGCTGAACAAGAACGAGTGCATGCATATCTGCATCTTCAAGAAGA

ACCAGCACGGCGGTCTGCGAGAGATCTATGTGCTTAACATCTTCGAGCGGATCATGCAAAAGACCGTCGAGGACTTCAGCA

GGGCTATTCTTGAGTGTTGCCCGTCTGAGACTATGACCTCTCCAAAGAACAAGTTTCGGATCCCCGAGCTGCACAACATGGA

AGCTAGAAAGACCCTCAAGAATGAGTATATGACCATCAGCACCAGCGACGACGCCTCTAAGTGGAATCAGGGACATTACGT

GTCAAAGTTTATGTGCATGCTCCTGAGGCTGACCCCGACTTACTACCATGGTTTTTGGTTCAGGCTCTGCAGCTGTGGCACC

ACAAGAAGATTTTCTTGGGAGATCAGCTGCTGCAGCTTTTCAACCAGAACGCCATGCTTAACACCATGGACACCACCTTGAT

GAAGGTGTTCCAGGCTTACAAGGGCGAGATTCAGGTTCCATGGATGAAGGCTGGCCGTAGCTATATCGAAACCGAGACAGG

TATGATGCAGGGCATTCTGCACTACACCTCTTCTCTGTTCCACGCCATTTTTCTGGACCAGCTTGCTGAAGAGTGCCGGCGTG

ATATCAACCGGGCTATTAAGACCATCAACAACAAAGAAAACGAGAAGGTGAGCTGCATCGTGAACAATATGGAAAGCTCCG

ACGACAGCAGCTTCATCATCTCTATCCCGAACTTCAAAGAGAATGAGGCTGCCCAGCTTTACCTTCTGTGCGTGGTGAATAG

CTGGTTTCGGAAGAAAGAGAAGCTCGGCACCTACCTCGGTATCTACAAGAGCCCTAAGTCTACCACTCAGACCCTGTTCGT

GATGGAATTCAACAGCGAGTTTTTCTTCTCCGGCGACGTGCACAGGCCTACTTTTAGATGGGTTAACGCTGCTGTGCTCATCG

GCGAGCAAGAAACCCTTTCTGGCATTCAAGAGGAACTGAGCAACACCCTCAAGGACGTTATCGAAGGTGGTGGAACCTAC

GCTCTTACCTTCATTGTGCAGGTTGCCCAGGCAATGATCCACTACAGAATGCTCGGTTCCAGCGCTTCTTCTGTTTGGCCTGC

TTACGAGACTCTGCTGAAGAACTCTTACGATCCTGCTCTGGGCTTCTTCCTGATGGATAATCCTAAGTGCGCTGGTCTGCTGG

GGTTCAATTACAACGTTTGGATTGCCTGCACCACCACTCCTCTTGGTGAGAAGTACCACGAGATGATCCAAGAGGAAATGAA

GGCAGAGTCCCAGTCTCTGAAGTCTGTTACCGAGGACACCATTAACACCGGTCTTGTGTCTCGGACCACCATGGTTGGTTTC

GGCAACAAGAAACGGTGGATGAAGCTCATGACCACTCTCAACCTTAGCGCTGACGTGTACGAGAAGATCGAGGAAGAACC

GCGGGTCTACTTTTTCCATGCTGCTACTGCTGAGCAGATCATCCAGAAAATCGCTATCAAGATGAAGTCACCGGGCGTGATCC

AGAGCCTTTCTAAGGGTAATATGCTCGCCCGGAAGATCGCCTCTTCAGTGTTCTTCATTAGCCGGCACATCGTGTTCACCATG

AGCGCTTATTACGATGCTGACCCTGAGACACGGAAAACCAGCCTGCTTAAAGAGCTAATCAACAGCTCTAAGATCCCGCAG

AGGCACGATTACTTGCAAGAGCCACATACTCTCAAGCCGACCAAGGTTGAAGTTGACGAGGATAGCTGGGAGTTCAAGAGC

GCAAAAGAGGAATGCATCCGGGTTCTCAAGCAGCGGATTAAGATTCACACTGGCCGGGAAGAGAGATCCATCTCCTTGCTT

TTTGAGAACATGGCCAAGAGCATGATCGGTAGGTGCACCGATCAGTACGATGTGAGGGAAAACGTGTCCATTCTTGCTTGCG

CCCTGAAGATGAACTACTCCATCTTTAAGAAGGACGCTGCCCCGAACAGATACCTGTTGGATGAGAAGAACCTGGTGTACCC

GCTGATCGGTAAAGAGGTTAGCGTCTACGTCAAGAGCGACAAGGTGCACATTGAGATCTCCGAGAAGAAAGAACGGCTGA

GCACCAAGTTGTTCAACATCGATAAGATGAAGGATATCGAGGAAACCCTGTCTCTGCTGTTCCCAAGCTACGGTGATTACCT

GAGCCTGAAAGAGACAATCGACCAGGTCACATTCCAGAGCGCTATCCACAAGGTTAACGAGAGAAGGCGTGTTAGGGCTG

ATGTGCATCTTACTGGTACAGAGGGCTTCTCCAAGCTGCCTATGTATACTGCTGCTGTGTGGGCCTGGTTCGACGTTAAGACT

ATTCCTGCTCACGACAGCATCTACCGGACCATTTGGAAGGTGTACAAAGAGCAGTACTCCTGGCTGAGCGATACCCTGAAAG

AAACCGTTGAGAAGGGGCCTTTCAAGACCGTTCAGGGCGTTGTGAACTTCATCTCTAGAGCTGGTGTGCGGTCTAGGGTTG

TGCATTTGGTTGGTTCTTTCGGCAAGAACGTGCGGGGTTCTATTAACCTGGTGACCGCCATCAAGGACAACTTCTCTAACGG

GCTTGTGTTCAAGGGCAACATTTTCGATATCAAGGCCAAAAAGACCCGTGAGAGCCTGGACAACTACCTGTCTATCTGCACC

ACACTTAGCCAGGCTCCTATCACCAAGCACGACAAGAACCAGATCCTGCGGTCACTTTTCGTTAGCGGTCCTCGGATTCAGT

ACGTGAGTTCTCAGTTTGGCTCTAGGCGGAACCGGATGTCTATTCTTCAAGAGGTTGTGGCTGACGACCCTACTCTTCATTG

GCCAGATCAGGATACCAGCCAGAAGCAGCTTGAGGATAAGTTCAGGGAACTCGCCCACAAAGAGTTGCCTTTCTTGACCGA

GAAGGTTTTCCACGACCACCTCGAGAAGATTGAGCAGCTTATGAAAGAAAACACCCACCTCGGTGGCAGGGATGTTGATGC
TTCTAAGACTCCTTACGTGCTGGCTAGGGCTAACGATATTGAGATCCACTGCTACGAGCTTTGGCGTGAGTATGATGAAGATG
AGGACGAGGCTTACCAGGCATACTGTTCTGAAGTTGAGGCCGCTATGGACCAAGAAAAGCTGAACGCTCTGATCGAGAGGT
ATCACGTTGACCCTAAGGCCAACTGGATCCAAATGCTTATGAACGGCGAGATCGAGACTGTCGAAGAGTTGAACAAGCTGG
ACAAGGGCTTCGAGTCTCACAGGTTGGCTCTTGTTGAGAGGATTCGTGTGGGTAAGCTTGGCATTCTTGGCAGCTATACAAA
GTGCCAGCAGCGAATCGAGGAACTTGATGGTGAGGGTAACAAGACCCATAGGTACACCGGTGAAGGCATTTGGAGGGGCTC
ATTCGATGATTCTGACGTGTGCATCGTTGTGCAGGACCTGAAAAAGACCAGAGAAAGCTACCTCAAGTGCGTCGTGTTCTCC
AAGGTTTCCGATTACAAGGTTCTGATGGGCCACCTCAAGACTTGGTGCAGGGAACACCATATCAGCAACGATGAGTTCCCG
ACTTGTACCCAGAAAGAACTCCTGTCTTACGGCGTGACCAAGTCCTCTGTGCTGCTCTACAAGATGAACGGCATGAAGATGC
TGCGGAACATGGAAAAGGGCATCCCACTTTACTGGAACCCGAGCCTTTCAACAAGGTCCCAGACCTACATTAACTGGCTGG
CTGTGGACATCACCGATCACTCACTTAGGCTTAGGAATAGGACCGTCGAAAACGGCAGGGTTGTGAACCAGACTATTATGGT
GGTGCCGCTGTACAAGACTGACGTGCAGATATTCAAGACCTCTCCGGTTGATCTCGAGCAGGATGTTCAGAACGATAGGCTG
AAGCTTCTGTCAGTGACTAAGGCTGGTGAGCTTAGATGGCTGCAGGACTGGATAATGTGGCGGTCATCTGCTGTGGACGACC
TCAACATTCTGAATCAGGTCAGGCGTAACAAGGCTGCTAGGGATCATTTCAACGCCAAGCCGGAATTCAAGAAGTGGATCA
AAGAGCTTTGGGACTACGCCCTGGATACCACTCTGATTAACAAGAAAGTGTTCATCACTACCCAGGGCAGCGAGTCTCAGTC
TACTGTTTCAAGCGGCGATTCCGATTCTGCTGTTGCTCCTCTTACTGATGAGGCCGTGGATGAGATCCATGACCTGCTTGACA
AAGAATTGGAGAAGGGGACCCTGAAGCAGATTATCCACGATGCTACCATTGACGCCCAGCTGGACATTCCTGCTATTGAGTC
TTTCCTGGCCGAAGAAATGGAAGTGTTCAAGTCCAGCCTCGCTAAGTCTCACCCTCTGCTTTTGAACTACGTGCGGTACATG
ATTCAAGAGATCGGGGTGACCAACTTCCGTAGCCTGATCGATAGCTTCAATCAGAAGGACCCGCTCAAGTCCGTGTCCTTGT
CTATCATCGATCTGAAAGAGGTTTTCAAGTTCGTCTACCAGGACATCAACGACGCCTACTTCGTTAAGCAAGAGGAAGATCA
CAAGTTCGACTTCTAG