

Dataset S1. Supplementary sequence information.

(A) Primers for cloning of PVS ORFs and probes for sRNA blot hybridization analysis
(B) Consensus sequences of *de novo* reconstructed viral genomes from the field potato samples ALYU-75 (cv. Zeren, non-transformed), ALYU-76 (cv. Zeren, transgenic line #119) and ALYU-79 (cv. Kormilitsa, transgenic line #103) and the reference sequence of the S-25K-AS RNAi transgene expression cassette (CaMV 35S promoter-PVS 25K ORF sense-*Ricinus communis* catalase gene *cat1* intron I-PVS 25K ORF antisense-NOS terminator)
(C) Multiple alignments of PVS and PVM 25K and CP coding sequences

Dataset S1A. Primers for cloning of PVS ORFs and probes for sRNA blot hybridization analysis.

Primers:

#302	5'-cgtatctagaatgccgcccaaacccggatcc-3'	XbaI
#304	5'-cgtaagatcttcattggtgatcgattacgggt-3'	BglII
#303	5'-cgtaccgggatgccgcccaaacccggatcc-3'	SmaI
#305	5'-cgtagtcgactcattggtgatcgattacgggt-3'	SalI
#306	5'-cgtaggatccttagcgcggtgtaagtgg-3'	NcoI
#308	5'-cgtaggatccatgaggatatttgatagctt-3'	BamHI
#307	5'-cgtagagctcatgaggatatttgatagctt-3'	SacI
#309	5'-cgtagtcgacttagcgcggtgtaagtgg-3'	SalI
intAS	5'-agtcgctatgtaatatatttgccccaataacc-3'	

Probes:

PVS_25K_s	5'-atatatggatgtgtttttgcaa-3'
miR160_as	5'-tgccatacaggagccaggca-3'

Dataset S1B. Consensus sequences of *de novo* reconstructed viral genomes from the field potato samples ALYU-75 (cv. Zeren, non-transformed), ALYU-76 (cv. Zeren, transgenic line #119) and ALYU-79 (cv. Kormilitsa, transgenic line #103) and the reference sequence of the S-25K-AS RNAi transgene expression cassette (CaMV 35S promoter-PVS 25K ORF sense-*Ricinus communis* catalase gene *cat1* intron I-PVS 25K ORF antisense-NOS terminator)

>PVS_ALYU-75_ON583978
TAAACACTCCGAAAAATATTGACTTAAACAAACGCGACAGTTCAAGCAAATTACTTAACATGGCACTTACTTACAGAAGTCCAATCGAGGAAGTGTTAACTACTAGAGCCTAATGCT
CAGTCCCTtaTTTCTAACGTCGCCACCAGCAGCTTTCAAGAGAGTGAGAAGGATAAATTCGCCTGGTTTTGCTACCATGTGTCGGCTAGCGCCAAGGAACACCTTAGTAGAGCAGGAAT
TACCTAAGCCCTTACTCGGGTATCCCTATCTCACCCGGTGTGCAAGACATTTGGAATAATACCTACTGTACAAAGTCTTACCACCACTTGTAAATAACACCTTTTACTTTGTAGGAATA
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TCAATTTAGGTGCGCAGTTGGGTAAATGAGTTTCTTCAGGATGTAATAAAGGGTGAAGGAATTTATCGGGAACAGTTGGCCATGGTTTTCAAACTTTTGACATCTGCGCGAGTGTGCAC
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>PVY ALYU-75 ON583979

RNAi V5_25K_cassette13.8
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GAATCCTGTTGCCGCTTGGCATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTTATGATTAGAGT
CCCGCAATTATACATTTAATACGCGATAGAAAACAAATATAGCGCGCAAACTAGGATAAATATCGCGCGCGGTGTCATCTATGTTACTAGATCGGGAATTC

Dataset S1C. Multiple alignments of PVS and PVM 25K and CP coding sequences.

PVS vs PVM

25K ORF

PVS MK442089.1	GTATGAGGATGTTT	AGTGTAT	CGGATGTTTGATAGCTTAGGTAATCAGCTTAGT	GTA
PVM HM854296.1	ATTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM AJ437481.1	GTTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM JN835299.1	GTTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM AY311394.1	GTTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM AY311395.1	GTTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM MH558036.1	ATTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM MH558037.1	ATTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM D14449.2	ATTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM NC_001361.2	ATTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM JX678982.1	ATTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM EU604672.1	GTTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM MW582794.1	GTTTGAAGTGCTTTAATTA	---	GTG-----	TAGCTTAGGTATT--GCT--ATTGTA
PVM MT114149.1	CTTTGAAGTACTTT	GATTGGT	AGTG-----	TAGCTTAGGTAGT--GCT--ATTGTA
PVM MG356508.1	GTTTGAAGTGCTTTAGATA	---	AGA-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM MG356509.1	GTTTGAAGTGCTTTAGATA	---	AGA-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM MF133527.1	GTTTGAAGTGCTTTAGATA	---	AGG-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM MF133530.1	GTTTGAAGTGCTTTAGATA	---	AGG-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM MW307264.1	GTTTCGAGTGCTTTAAAG	GA	GAGG-----	TAGCTTAGGTAGT--GCT--GTAGAT
PVM MF133528.1	GTTTGAAGTGCTTTAAATA	---	GG-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM MF133529.1	GTTTGAAGTGCTTTAAATA	---	GG-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM KY364848.1	ATTTGAAGTGCTTTAAATA	---	GG-----	TAGCTTAGGTAGT--GCT--ATTAGGT
PVM MT114148.1	GTTTGAAGTGCTTTAGATA	---	GG-----	TAGCTTAGGTAGT--GCT--ATAGGT
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PVS MK442089.1	TTGAATA--TATGGATGTGTTTTTGCA	ATT	TTGAATAAATA	AAGTTGAGCGTGTA
PVM HM854296.1	TYGAATATTTATGGAYGTGAT	CTAGATTGTTGTGTATAAATACAAGTTTGAGCG	CTTAAA	
PVM AJ437481.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAA			
PVM JN835299.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAAA			
PVM AY311394.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAA			
PVM AY311395.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAAA			
PVM MH558036.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGCATAA	G	TACAAGTTTGAGCGTTTAAA	
PVM MH558037.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGCATAA	G	ACAAGTTTGAGCGTTTAAA	
PVM D14449.2	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAA			
PVM NC_001361.2	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAA			
PVM JX678982.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTTTAA			
PVM EU604672.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGTCTAAG			
PVM MW582794.1	TTGAATATTTATGGATGTGATTGTAGATTGTTGTGTATAAATACAAGTTTGAGCGCTTAA			
PVM MT114149.1	TTGAATATTTATGGATGTACTTGTAGATTTATTCATAA	GTAAAGTTTGAGCGTTTGAA		
PVM MG356508.1	TTGAATATTTATGGATGTGTTGTAGAA	TTGTTGTGTAAGTATAAAGTTTGAACGTTTGCA		
PVM MG356509.1	TTGAATATTTATGGATGTGTTGTAGAA	TTGTTGTGTAAGTATAAAGTTTGAACGTTTGCA		
PVM MF133527.1	TTGAATATTTATGGATGTGTTGTAGAA	TTGTTGTGTAAGTATAAAGTTTGAACGTTTGCA		
PVM MF133530.1	TTGAATATTTATGGATGTGTTGTAGAA	TTGTTGTGTAAGTATAAATTTGAACGTTTGCA		
PVM MW307264.1	TTGAATATTTATGGACGTACTTGTAGAA	TTATTGTATAAATAAAGTTTGAGCGTTTGCA		
PVM MF133528.1	TTGAATATTTATGGATGTGTTGTAGAA	TTGTTGTGTAAGTATAAAGTTTGAACGTTTGCA		
PVM MF133529.1	TTGAATATTTATGGATGTGTTGTAGAA	TTGTTGTGTAAGTATAAAGTTTGAACGTTTGCA		
PVM KY364848.1	TTGAATATTTATGGATGTAGT	CTGAGAGTTGTTGTATAAATACAAGTTTGAACGTTTGCA		
PVM MT114148.1	TTGAATATTTATGGATGTGTTGTAGAA	CTGTTGTGTAAGTATAAAGTTTGAACGTTTGCA		
	* *****	*****	*****	*****

GCAAATTTGCTGGTTTGGACGAGTACACACTCTGTTGACTGAAGTGC---CTCCG---G
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[illegible][illegible]

[illegible]

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 AACCCCTGGGCAAAGTTGTGTTTCAGAGGAGGAAGTGGGTTGCTTCTGAGATCACAG
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 AACCAGAAGCGTGGTGTGATTTTCAGGAAAGTGGGTTGCTTCTAAGAGCATATA
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[illegible][illegible][illegible]


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PVS
25K ORF

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MF496659.1 -----GTGATAGGAGAGTTTGACAGCTTAGGTAATCAGCTTAGTAGTATTGA--AT
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MF375506.1 -----GTGATAGGAGATGTTTGATAGCTTAGGTAATCAGCTTAGTAGTATTGA--AT
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AJ863510.1 -----GTGATAGGAGATGTTTGATAGCTTAGGTAATCAGCTTAGTAGTATTGA--AT
D00461.1 -----GTGATAGGAGAGTTTGACAGCTTAGGTAATCAGCTTAGTAGTATTGAATAT
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MF496659.1 ATAAGGCTGCAGCTTTTCAGTGCTTAACTAGGCACACTAAGAGCTTACTCATATTGTGCC
MF418028.1 ATAAGGCCCGCCGCTTTCAGTGCTTAACGAGGCACACCAAGAGCTTGCTCATACTGTGCC
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MK563994.1 ATAAGGCCCGCCGCTTTCAGTGCTTAACGAGGCACACCAAGAGCTTGCTCATACTGTGCC
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* *

MF4180

TGAAGCACCTTTAGGTTACAGGTAAGAGTTCGAAGAACTGTCCCACAGAGAAATGCC
TGAACACCTTTAGGTTACAGGTAAGAGCTCGAATATACAGTCTCACAGCAAGA**ATGCC**
TGAACACCTTTAGGTTACAGGTAAGAGCTCGAATATACAGTCTCACAGCAAGAATGCC
* * * * *

[illegible]

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[illegible]

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KR152654.1 GATGAGGAGGAA^{CC}CAGAGA^{ACC}CATACTCGCGATTTTCAATCGATGAGTTGTTCAAGAT
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MF418032.1 GATGAGGAGGAATCCGGAA^{AA}CCCTACTC^{AC}GATTCTCGATCGATGAGCTGTTCAA^{AA}T
MF496659.1 GATGAGGAGGAA^{CC}CGGAGA^{ACC}CATACTCGCGATTTTC^{AT}CGA^{CG}GAGTTGTTCAAGAT
MF418028.1 GATGAGGAGGAATCCGGAA^{AA}CCATACTCTCGATTCTCAATTGACGAGCTGTTCAA^{AA}T
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MK563994.1 GATGAGAAGGAATCCGGAA^{AA}CCATACTCTCGATTCTCAATTGACGAGCTGTTCAA^{AA}T
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KU896946.1 GATGAGAAGGAATCCGGAA^{AA}CCATACTCTCGATTCTCAATTGACGAGCTGTTCAA^{AA}T
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MF418035.1 GGA^{TA}TC^{CG}GT^{TC}AGTGTCCAAT^{TA}ACATGGC^{AA}TA^{TA}CTGAGCAG^{AT}GGC^{TA}CAAT^{TA}CTGC
MF418032.1 GGAAAT^{TC}CGGT^{TC}AGTGTCCAAC^{AA}CAATGGCGAA^{TA}CTGAGCAG^{AT}GGC^{TA}CA^{TA}CTGC
MF496659.1 GGATAT^{TC}CGAT^{TC}GGTGTCCAAT^{TA}ACATGGCGAA^{CT}GAGCAAA^{AT}GGC^{TA}CA^{TA}CTGC
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MK442089.1 ^{GG}AAAT^{TC}CGAT^{TC}GGTGTCCAAC^{AA}CAATGGCGAA^{CA}CTGAGCAAA^{AT}GGC^{TA}CA^{TA}CTGC
AJ863510.1 GGAAAT^{TC}CGAT^{TC}GGTGTCCAAC^{AA}CAATGGCGAA^{CA}CTGAGCAAA^{AT}GGC^{TA}CA^{TA}CTGC
D00461.1 GGAAAT^{TC}CGAT^{TC}GGTGTCCAAC^{AA}CAATGGCGAA^{CA}CTGAGCAAA^{AT}GGC^{TA}CA^{TA}CTGC

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MF418035.1 TGA^{CA}T^TGCAGGACTTGGAGT^{TC}CT^{TA}CA^{TA}GAGCATGTTGCC^{TC}GGAGTCATA^{TA}TGAAGGT^{GG}T
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MN095414.1 AGATAT^TGCCGGGCTCGGTGT^{TC}CCACTGAGCATGTTGCT^{TC}GGCGTCATACTGAAGGT^{CG}T
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MF418031.1 GGACAT^{TC}CGTGGACTTGGG^{TC}GTCCCACTGA^{TA}CA^{TA}GTTGCAGGTGTCATACTGA^{AA}GTGGT
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KC430335.1 TGACAT^{TC}CGTGGACTTGGG^{TC}GTCCCACTGA^{TA}CA^{TA}GTTGCAGG^{TC}GTATACTGA^{AA}GTGGT
MF418033.1 TGACAT^{TC}CGTGGACTTGGG^{TC}GTCCCACTGA^{TA}CA^{TA}GTTGCAGG^{TC}GTATACTGA^{AA}GTGGT
MW331321.1 TGACAT^{TC}CGTGGGCTTGGG^{TC}GTCCCACTGA^{TA}CA^{TA}TGTTGCAGGAGTTACTGA^{AA}GTGGT
LC375227.1 TGACAT^{TC}CGTGGACTTGGG^{TC}GTCCCACTGA^{TA}CA^{TA}TGTTGCAGG^{TC}GTATACTGA^{AA}GTGGT
MF375506.1 TGACAT^{TC}CGTGGACTTGGG^{TC}GTCCCACTGA^{TA}CA^{TA}GTTGCAGG^{TC}GTATACTGA^{AA}GTG^TT
MK442089.1 ^{TG}ATAT^{TC}CGTGGGCT^{TC}GGG^{TC}GTCCCACTGA^{TA}CA^{TA}GTTGCAGG^{TC}GTATACTGA^{AA}GTGGT
AJ863510.1 ^{GG}ATAT^TGCAGGGCT^{TC}GGCGTCCCA^{TA}CAGCATGTGCG^{TC}GGG^{TC}TTATACTGAAGGT^{CG}T
D00461.1 ^{GG}ATAT^TGCAGGGCT^{TC}GGCGTCCCA^{TA}CAGCATGTGCG^{TC}GGG^{TC}TTATACTGAAGGT^{CG}T

MF418029.1 GATCATGTGTGCAAGCGTGAGCAGTTCTGTGTATCTGGATCCAGCTGGAAACGTTGAATT
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MF418035.1 GATTATGTGTGCAAGCGTGAGCAGCTCGGTGTATCTGGATCCAGCTGGAAACGTTGAGTT
MF418032.1 GATCATGTGCGCGAGTGTGAGTAGCTCTGTCTACCTAGACCCCTGCTGGAACTGTTGAGTT
MF496659.1 GATAATGTGCGCAAGTGTGAGCAGTTCTGTCTACTTTGGATCCCGCAGGAACGTTGAGTT
MF418028.1 GATCATGTGCGCGAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGAACGTTGAGTT
MH282867.1 GATTATGTGTGCGAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGAACGTTGAGTT
MK563994.1 GATTATGTGTGCGAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGAACGTTGAGTT
JQ647830.1 AATCATGTGCGCAAGCGTGAGTAGTTCTGTCTACTAGACCCCTGCAGGAACGTTGAGTT
MN095414.1 GATCATGTGCGCAAGCGTAAGCAGTTCTGTCTACTAGACCCCTGCAGGAACGTTGAGTT
KU058657.1 GATCATGTGCGCAAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGGACTGTTGAATT
KU896946.1 GATCATGTGCGCAAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGGACTGTTGAGTT
MF033144.1 GATCATGTGCGCAAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGAACGTTGAGTT
MF418030.1 GATCATGTGTGCAAGCGTGAGTAGCTCTGTCTATCTAGATCCAGCAGGGACTGTGAGTT
MF418031.1 GATCATGTGTGCAAGCGTGAGTAGCTCTGTCTATCTAGATCCAGCAGGGACTGTGAGTT
KP089978.1 GATCATGTGTGCAAGCGTGAGTAGCTCTGTCTATCTAGATCCAGCGGGACTGTAGAGTT
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LC375227.1 GATCATGTGTGCAAGCGTGAGTAGTTCAGTTATCTAGATCCAGCAGGGACTGTGAGTT
MF375506.1 GATCATGTGTGCAAGTGTGAGTAGCTCTGTCTATCTAGATCCAGCTGGGACTGTGAGTT
MK442089.1 GATCATGTGTGCAAGCGTGAGTAGCTCTGTCTATCTAGATCCAGCAGGGACTGTGAGTT
AJ863510.1 AATTATGTGCGCAAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGGACTGTTGAGTT
D00461.1 AATTATGTGCGCAAGCGTGAGCAGTTCTGTCTACTAGACCCCTGCAGGGACTGTTGAGTT

MF418029.1 CCCCCTGGTGCAGTTCCCTTAGATTCCATCATCGCAATCATGAAAATCGCGCGGGGCT
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MF418032.1 CCCCCTGGGCGGTTCCCTTGGATTCTAATATTGCCATATGAAAATCGAGCAGGGTT
MF496659.1 CTCTCTCTGGGCGAGTCCCTTGGATTCCATATTGCCATCATGAAGAATCGCGCAGGGTT
MF418028.1 CCCCCTGGAGCAGTCCCTTGGATTCCATATTGCAATCATGAAAATCGTGTGGACT
MH282867.1 CCCCCTGGGCGAGTCCCTTGGATTCCATATTGCAATCATGAAAATCGTGTGGACT
MK563994.1 CTCCACTGGGCGAGTCCCTTGGATTCCATATTGCAATCATGAAAATCGTGTGGACT
JQ647830.1 CCCCCTGGAGCAGTCCCTTGGATTCCATATTGCAATCATGAAAATCGTGTGGACT
MN095414.1 CCCCCTGGAGCAGTCCCTTGGACTCCATATTGCAATCATGAAAATCGTGTGGACT
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KU896946.1 CCCCCTGGAGCGGTTCCCTTGGACTCCATATTGCAATCATGAAAATCGTGTGGACT
MF033144.1 CCCCCTGGGCGAGTCCCTTGGACTCCATATTGCAATCATGAAAATCGTGTGGACT
MF418030.1 CCCCACGGGCGAGTGCCTTGGACTCGATCATTGCAATCATGAAGAATCGCGCGGGATT
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MF418033.1 CTCCACGGGCGAGTGCCTTGGACTCGATCATTGCAATCATGAAGAATCGCGCGGGATT
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LC375227.1 CCCCACGGGCGAGTGCCTTGGACTCGATCATTGCAATCATGAAGAATCGCGCGGGATT
MF375506.1 CCCCACGGGCGAGTGCCTTGGACTCGATCATTGCAATCATGAAGAATCGCGCGGGATT
MK442089.1 CCCCACGGGCGAGTGCCTTGGACTCAGTCCATCATTGCAATCATGAAGAATCGCGCGGGATT
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D00461.1 CCTACTGGGCGAGTGCCTAGTGGATTCCATATTGCAATCATGAAAACCGTGTGGGTT

MF418029.1 GAGGAAGGTGTGTAGGTTATATGCTCCAGTCGTTTGAATTACATGCTCGTACAGAACAG
KR152654.1 AAGGAAGGTGTGTAGGTTGTATGCTCCAGTCGTCGGAATTACATGCTCGTCAAAATAG
MF418035.1 AAGGAAGGTGTGTAGGTTGTATGCTCCAGTCGTCGGAATTACATGCTCGTCAAAATAG
MF418032.1 GAGGAAGGTGTGTAGGTTGTATGCTCCAGTTGTTTGGAACTACATGCTTGTTCAGAACAG
MF496659.1 GAGGAAGGTGTGTAGGTTGTATGCTCCAGTTGTTTGGAACTATATGCTTGTTCAGAAATAG
MF418028.1 GAGGAAGGTGTGCAGGCTGTATGCTCCGTCGCTCTGGAATTACATGCTCGTTCAGAACAG
MH282867.1 GAGGAAGGTGTGCAGGCTGTATGCTCCGTCGCTCTGGAATTACATGCTCGTTCAGAACAG
MK563994.1 GAGGAAGGTGTGCAGGCTGTATGCTCCGTCGCTCTGGAATTACATGCTCGTTACAGAACAG
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LC375227.1 GAGGAAGGTGTGCAGGCTGTATGCTCCAGTCGTTGGAATTACATGCTAGTTCAGAAATAG
MF375506.1 GAGGAAGGTGTGCAGGCTGTATGCTCCAGTTGTTTGGAAATTACATGCTAGTTCAGAAATAG
MK442089.1 GAGGAAGGTGTGTAGGTTGTATGCTCCGTCGCTTGAATTATATGCTTGTTCAGAAATAG
AJ863510.1 GAGGAAGGTGTGTAGGTTGTATGCTCCGTCGCTTGAATTATATGCTTGTTCAGAAATAG
D00461.1 GAGGAAGGTGTGTAGGTTGTATGCTCCGTCGCTTGAATTATATGCTTGTTCAGAAATAG

MF418029.1 GCCACCCTCAGACTGGCAGGCTATGGGCTTTCAATGGGCTGCTTCGCTTGGCCGCTTTGGA
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MF418035.1 GCCACCATCAGACTGGCAGGCTATGGGTTTCAATGGAAAGCTCGCTTCGCCGCTTTTGA
MF418032.1 ACCCCCTCAGACTGGCAAGCCTATGGGTTTCAATGGAATGCACGTTTCGCCGCTTTTGA
MF496659.1 GCCCCCTTCTGATTGGCAGGCTATGGGTTTCAATGGAATGCACGTTTCGCCGCTTTTGA
MF418028.1 GCCCCCTTCGGATTGGCAGGCAATGGGTTTCAATGGAATGCACGCTTCGCCGCTTTTGA
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MF375506.1 GCCACCTTCGATTGGCAGGCTATGGGTTTCAATGGAAAGCAGCTTCGCCGCTTTTGA
MK442089.1 GCCACCTTCGGATTGGCAGGCTATGGGTTTCAATGGAAAGCAGCTTCGCCGCTTTTGA
AJ863510.1 GCCACCTTCGATTGGCAGGCTATGGGTTTCAATGGAAAGCAGCTTCGCCGCTTTTGA
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MF418035.1 CACATTGATTATGTGACTAACGGCGCGGCTATCAACCCGGTCCGAGGGGCTATCCGAAG
MF418032.1 CACATTGACTATGTGACTAACGGTGCAGCAATCCAGCCTGTAGAGGGGCTATCCGTAG
MF496659.1 CACATTGATTATGTGACTAATGGTGCAGGATCCACCCCGTAGAGGGGCTATCCGTAG
MF418028.1 CACATTGATTATGTGACTAACGGCGCGGATCCAGCCAGTGAGGGGCTATCCGTAG
MH282867.1 CACATTGATTATGTGACTAACGGCGCGGATCCAGCCAGTGAGGGGCTATCCGTAG
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JQ647830.1 CACATTGATTATGTGACTAACGGCGCGGATCCAGCCTGTGAGGGGCTATCCGTAG
MN095414.1 CACATTGATTATGTGACTAACGGCGCGGATCCAGCCTGTGAGGGGCTATCCGTAG
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KU896946.1 CACATTGATTATGTGACTAACGGCGCGGATCCAGCCTGTGAGGGGCTATCCGTAG
MF033144.1 CACATTGATTATGTGACTAACGGCGCGGATCCAGCCTGTGAGGGGCTATCCGTAG
MF418030.1 CACATTGATTATGTGACTAATGGGCTGCAATCCACCCCGTAGAGGGGCTATCCGAAG
MF418031.1 CACATTGATTATGTGACTAATGGGCTGCAATCCACCCCGTAGAGGGGCTATCCGAAG
KP089978.1 CACATTGATTATGTGACTAATGACGCTGCAATCCAGCCCGTAGAGGGGCTATCCGAAG
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MF418032.1 GCCCACTCCTGAGGAGACAAATAGCTCATAATGCGCACAAAGCATGGCTTTGATAAGTC
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MF418031.1 GCCCTACACCAAGGAAACAATAGCTCACAATGCCACAAGAGATGGCAATTGATAAGTC
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LC375227.1 GCCCAGCCTGAGGAAACAATAGCTCACAATGCCACAAGAGATGGCAATTGATAAGTC
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MK442089.1 GCCCACCTCCGAGGAAACAATAGCTCACAATGCCACAAGAGATGGCAATTGATAAGTC
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KP089978.1 GAACAGAAATGAGCGATTGGCCAACACTAATGTTGAGTACACTGGAGGATGCTTGGCGC
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AJ863510.1 GAACAGAAATGAAAGGTTGGCTAACACCAACGTTGAGTACTGGGGCATGCTGGTGC
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MF418032.1 TGAGATTGTGCGCAACCATCGGAATGCGATAAACCAATGAAGCGGAGCGTTAGAAATG
MF496659.1 TGAGATTGTGCGCAACCATCGGAATGCAATTAACCAATGAAAGCGGAGCGTTAGAAATG
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MF418030.1 TGAGATTGTGCGCAATCACCAGCAATGCATTAACCAATGAAGGCAGACCGTTTAGCCATG
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D00461.1 TGAGATTGTGCGTAATCATCGGAATGCAATTAACCAATGAAAGCGGAGCGTTAGAAATG
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