

## Supplementary data:

**Supplementary Table S1 – Virus species and sequences identifiers used for phylogenetic tree construction**

<b>Virus</b>	<b>Abbreviation</b>	<b>Genus:</b>	<b>Reference</b>
Bombyx mori latent virus	BmLV	<i>Maculavirus</i>	AB624361.1
Bombyx mori latent virus	BmLV	<i>Maculavirus</i>	AB186123.1
Bombyx mori latent virus	BmLV	<i>Maculavirus</i>	KJ433990.1
grapevine fleck virus	GFkV	<i>Maculavirus</i>	NP_542612.1
grapevine red globe virus	GRGV	<i>Maculavirus</i>	YP_009268923.1
bee macula-like virus 2	BeeMLV2	<i>Maculavirus</i>	YP_009551952.1
turnip yellow mosaic virus	TYMV	<i>Tymovirus</i>	NP_663297.1
eggplant mosaic virus	EMV	<i>Tymovirus</i>	NP_040968.1
anagryis vein yellowing virus	AVYV	<i>Tymovirus</i>	YP_002308578.1
oat blue dwarf virus	OBDV	<i>Marafivirus</i>	NP_044447.1
maize rayado fino virus	MRFV	<i>Marafivirus</i>	NP_115454.2
citrus sudden death-associated virus	CSDaV	<i>Marafivirus</i>	YP_224218.1
potato virus x	PVX	<i>Potexvirus</i>	YP_002332929.1

**Supplementary Table S2 – Composition of *Helicoverpa* artificial diet**

<b>Component:</b>	<b>Weight (g):</b>	<b>Brand:</b>
Wheat Germ	72	Merck
Casein	33	Merck
Sugar	29.3	Generic
Brewer's Yeast	14.3	Generic
Wesson's salt	9.4	MP Biomedicals
Sorbic acid	1.5	Merck
4-hydroxybenzoic acid	0.93	Merck
linseed oil	1.87	MP Biomedicals
Bactoagar	18.8	BD
Vanderzant vitamin mix	1.0	Merck
Streptomycin sulphate	1.1	Merck
L-ascorbic acid	4.4	Merck
Methyl Paraben	2	Merck
cholesterol	0.5	Merck
water	To 1 liter	

Supplementary Table S3 – List of PCR primers

Purpose	Species	Gene (GenBank or RefSeq)	Strand	Sequence	Reference
qPCR	<i>Bombyx mori</i> <i>latent virus</i>	<i>coat protein</i> (de novo)	Forward	TTGACCTTTGTTGGACTACTGCTG	1
			Reverse	GTGGTTGGTGTATGGAATCGG	
		<i>replicase</i> (de novo)	Forward	CGTCCCTCCCAACTGTTTGT	
			Reverse	CTCCATTTTCTTCCGTTCCA	
	<i>Trichoplusia ni</i>	<i>ribosomal protein S18</i> (XM_026882096.1)	Forward	GCTCTGTATCGCCGTAACCA	2
			Reverse	TGCCGTTTCGAACACAAGAC	
		<i><math>\alpha</math>-tubulin</i> (XM_026877842.1)	Forward	TTACCGAGTTCCAGACCAAC	
			Reverse	AAGCAGGCGTTGGTGATCTC	
		<i>18S</i> (KY514086)	Forward	TGAGAAACGGCTACCACATCC	3
			Reverse	GATTACGAGGCCTCGTAAGAG	
		<i>argonaute-2</i> (XM_026877347.1)	Forward	GACTGCGCGTCGTATAAACC	4
			Reverse	TGACATTGCCGTCCCTCAAA	
		<i>siwi</i> (XM_026876665.1)	Forward	CGGCTCCAATGGTTGACCTA	2
			Reverse	TGTTAGCAGCCAGGAATGCA	
		<i>dicer-2</i> (XM_026878152.1)	Forward	CGGTGACTTGCAGACTGTCT	4
			Reverse	TTCCTGGCTGTTGCGGTAT	
	<i>Helicoverpa armigera</i>	<i>elongation factor 1<math>\alpha</math></i> (XM_021329970.2)	Forward	GAAGTCAAGTCCGTGGAGATG	5
			Reverse	GACCTGTGCTGTGAAGTCG	
		<i>ribosomal protein L27</i> (XM_021344525.2)	Forward	ACAGGTATCCCCGCAAAGTGC	5
			Reverse	GTCCTTGGCGCTGAAGTTCTC	
		<i><math>\alpha</math>-tubulin</i> (XM_021329536.2)	Forward	CGCCCTCAACGTCGATCTAA	
			Reverse	CCAGAGGGAAGTGGATACGC	

		<i>argonaute-2</i> (XM_049840284.1)	<b>Forward</b>	CGCTCTGCCGAGGAAGATAT	
			<b>Reverse</b>	CACCTGAGCGAACTGTCCTT	
		<i>siwi</i> (XM_049840316.1)	<b>Forward</b>	GATCGTGCTGTGCCTACTCA	
			<b>Reverse</b>	AGGTATTTCCACTCGCCACG	
		<i>dicer-2</i> (XM_049847753.1)	<b>Forward</b>	GTCGTTGATCACCCAATGCG	6
			<b>Reverse</b>	TTTTCCTTCGGGCAGACCTC	
Interspecies qPCR	<i>Helicoverpa armigera</i> & <i>Trichoplusia ni</i>	<i>elongation factor 1a</i> (XM_021329970.2 and XM_026883053.1)	<b>Forward</b>	TCAACCACCCCGGTCAAATC	
			<b>Reverse</b>	TGATTTCTGGCGAACTTGCAG	
		<i>heat shock protein 90</i> (XM_021341131.2 and XM_026875446.1)	<b>Forward</b>	ATCCCGCATGAAGGAGAACC	
			<b>Reverse</b>	CTCATCAATGGGCTCGGTCA	
		<i>glyceraldehyde-3-phosphate dehydrogenase</i> (JF417983.1 and XM_026892236.1)	<b>Forward</b>	GTACGACAACGAGTTCGGCT	
			<b>Reverse</b>	TGGTCTGGATGTACTTGATGAGA	
Cloning	<i>Trichoplusia ni</i>	<i>argonaute-2</i> (XM_026877347.1)	<b>Forward</b>	TCAAGGCTGGTCGTCAGTTC	
			<b>Reverse</b>	ATTGCCCTCTGAAACTCCG	
	<i>Bombyx mori latent virus</i>	Genome construct 1 (de novo)	<b>Forward</b>	CGATCAACAAAGTCAGCTTGTCC	
			<b>Reverse</b>	TTGGCGAGATTATCCCAGGC	
		Genome construct 2 (de novo)	<b>Forward</b>	GCTGGTGTACTCTCTCGAAGG	
			<b>Reverse</b>	CTCAGGGTCGCAACATTGG	
		Genome construct 3 (de novo)	<b>Forward</b>	CTTCCCCGATTCAAGCAACT	
			<b>Reverse</b>	TTTCCCAGGTTGAGACTCGC	
		Genome construct 4 (de novo)	<b>Forward</b>	GTGCAGCTCATTACATTACTGG	
			<b>Reverse</b>	AGAGGTGTCATTAGCAGGTAGTGG	
		Genome construct 5 (de novo)	<b>Forward</b>	TACTCTCGTCGCCACAACCTC	
			<b>Reverse</b>	ACAGCAGTGTACCGCCAGTC	

		Genome construct 6 (de novo)	<b>Forward</b>	ACCTCCAGTCTTCAGCCATCC	
			<b>Reverse</b>	AGTGGTGATGTCGTA CTCTCGCT	
		Genome construct 7 (de novo)	<b>Forward</b>	TCATGTCTGCAATGACTATACTGC	
			<b>Reverse</b>	TTGGCTAGACAGAACAAACGC	
		Genome construct 8 (de novo)	<b>Forward</b>	TTACAGCGAGTACGACATCACC	
			<b>Reverse</b>	GCGAACTCCTTCTAGTACGGC	
		Genome construct 9 (de novo)	<b>Forward</b>	CATTCCGTCCTTGGTCAATGC	
			<b>Reverse</b>	AGAGCGCGATGAACTAACAACC	
	Colony PCR	<i>Trichoplusia ni</i>	<b>Forward</b>	GCTCAAGGTGGTAGCCAGTT	
			<b>Reverse</b>	ACAAGCAGTTCAGATGCGGA	
		<i>Bombyx mori</i> <i>latent virus</i>	<b>Forward</b>	GTAAACGACGGCCAG	
			<b>Reverse</b>	CAGGAAACAGCTATGAC	

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**Supplementary Table S4 – BioProjects from which SRA experiments were used for the identification of BmLV prevalence**

<b>Species</b>	<b>Tissue / cell line</b>	<b>Project</b>	<b>Viruses identified</b>
<i>H. armigera</i>	Whole body	PRJNA261330	HaSNPV, HaIV
“	Adult gonads	PRJNA613606	N/A
<i>B. mori</i>	Whole body	PRJNA339876	BmNPV
“	“	PRJNA431156	N/A
“	“	PRJNA119935	BmIV
“	Eggs	PRJNA377550	N/A
“	“	PRJNA336361	N/A
“	Midgut	PRJEB7502	BmCPV
“	Hemolymph	PRJNA209084	BmIV
“	Silk Gland	PRJNA119935	BmIV
“	Ovary	PRJDB5508	N/A
“	<i>Bm</i> N4	PRJDB2257	<b>BmLV</b> , SfR
“	“	PRJDB4053	<b>BmLV</b>
“	“	PRJDB5376	<b>BmLV</b> , BmIV
“	“	PRJDB2929	<b>BmLV</b> , SfR
“	“	PRJNA383127	<b>BmLV</b> , SfR
“	“	PRJNA419912	<b>BmLV</b> , BmIV, SfRV, OpMNPV
“	“	PRJNA251635	<b>BmLV</b> , SfRV, BmIV
“	“	PRJNA251557	<b>BmLV</b>
“	“	PRJNA239665	<b>BmLV</b>
“	“	PRJNA284571	<b>BmLV</b> , SfRV
“	“	PRJNA632342	<b>BmLV</b> , TnTED
“	“	PRJDB5927	<b>BmLV</b> , SfRV, BmIV
“	“	PRJDB5142	<b>BmLV</b> , SfRV
“	“	PRJDB10429	<b>BmLV</b> , SfRV, BmIV
“	<i>Bm</i> -VF	PRJDB5144	<b>BmLV</b> , BmIV
<i>S. frugiperda</i>	Gonads + soma	PRJNA386859	TnTED
“	Whole body	PRJNA432886	OsEV, SeIV, SfRV
“	<i>Sf</i> -9	PRJNA523298	AcMNPV, PnPV, SfRV
<i>H. melpomene</i>	Whole body	PRJNA386859	HeIV
<i>P. xylostella</i>	Gonads	PRJNA386859	N/A

“	“	PRJNA421581	N/A
<i>T. ni</i>	Hi5 cells	PRJNA336361	FHV, BBV
“	“	PRJNA789788	<b>BmLV</b> , FHV
“	Gonads + soma	PRJNA336361	TnTED
<i>O. furnacalis</i>	“	PRJNA438858	N/A
<i>G. mellonella</i>	“	PRJNA510393	N/A
<i>P. Xuthus</i>	“	PRJNA445942	CTV

Abbreviation	Virus name
AcMNPV	Autographa californica multiple nucleopolyhedrovirus
BBV	Black Beetle Virus
BmCPV	Bombyx mori cytoplasmic polyhedrosis virus
BmIV	Bombyx mori iflavirus
BmNPV	Bombyx mori nucleopolyhedrovirus
CTV	citrus tristeza virus
FHV	Flock House Virus
GRLDaV	Grapevine roditis leaf discoloration-associated virus
HaIV	Helicoverpa armigera iflavirus
HaSNPV	Helicoverpa armigera single nucleopolyhedrovirus
HeIV	Heliconius erato iflavirus
OpMNPV	Orgyia pseudotsugata multiple nucleopolyhedrovirus
OsEV	Oryza sativa endornavirus
PnPV	Perida nuda picorna-like virus
SeIV	Spodoptera exigua iflavirus
SfRV	Spodoptera frugiperda Rhabdovirus
TaBV	Taro bacilliform virus
TnTED	Trichoplusia ni Transposable Element D virus
WSSV	White Spot Syndrome Virus

**Supplementary Table S5 - Accession number and origin of SRA and TSA archives used for genome assembly. RPM values indicate the prevalence of BmLV derived reads per million total reads.**

Project:	SRA:	Lab/Institute	Country	Year	Cells	RPM
<b>sRNA archives:</b>						
PRJDB5144	DRR068690	GALS, U Tokyo	Japan	2018	<i>BmVF</i>	1328
“	DRR068691	“	Japan	2018	<i>BmVF</i>	2829
PRJDB10429	DRR241076	GALS, U Tokyo	Japan	2020	<i>BmN4</i>	2252
PRJDB2257	DRR006265	Ins. Gen, U Tokyo	Japan	2014	<i>BmN4</i>	1796
PRJDB4053	DRR039989	IMCB, U Tokyo	Japan	2016	<i>BmN4</i>	1083
PRJDB5376	DRR079253	Ins. Gen, U Tokyo	Japan	2018	<i>BmN4</i>	1277
PRJNA419912	SRR6324419-24	Siomi, U Tokyo	Japan	2017	<i>BmN4</i>	2295
PRJNA632342	SRR11781560+61	Siomi, U Tokyo	Japan	2020	<i>BmN4</i>	5043
PRJNA383127	SRR5458683	Comp Med Center, Thomas Jefferson U	USA	2017	<i>BmN4</i>	7430
PRJDB2929	DRR023337+40	Biomed. C.S. Med. Cen.	USA	2014	<i>BmN4</i>	6889
PRJNA239665	SRR1333837+38	Mol. Bio., U Geneva	Switzerland	2014	<i>BmN4</i>	7687
PRJNA789788	SRR17258733	Mol. Dev. Phys., KU Leuven	Belgium	2021	<i>BmN4</i>	5956
“	SRR17258732	Mol. Dev. Phys., KU Leuven	Belgium	2021	Hi5	574
“	SRR24542361	Mol. Dev. Phys., KU Leuven	Belgium	2021	Hi5	4529
<b>TSA archives:</b>						
PRJDB3935	DRR035925	Ins. Gen, U Tokyo	Japan	2018	<i>BmVF</i>	
PRJNA554660	SRR9685281	IMB Mainz	Germany	2019	<i>BmN4</i>	



Supplementary Table S6 – Sanger sequencing results

IOZCAS- <i>Ha-1 argonaute 2</i> - partial transcript
CCCGTCGACCTGGGTTCTGGATATGAAATGTGGACGGGACTGTTTCAGTCTGCCATTTTACAAACAAATCGTTTATTAATATCGATGTGGCCACAAAGGTTTTCCTAAAGCTCAGAGTATGATTGATTGTCTTGTAAGAGACTTCAACTTGGACCCTTATCGTCCTA TAGATAACCCAGAGGGGAGGAGACAAATTTGCAACATTTGTCAAGGGGCTCAAGGTGGTAGCCAGTTTAGTTGGTAAACACGGCGACGGCCGGACATAAACCGCGAGTTCGTATGTAACGGGTAGTTGGACCTCCGGACAAGCTCACATTCCTATCACTGAGTCGGA TGGCCGCTCTCGCAAGCTCACTGTCGCTGAATACTTTGCCAAGGAAAGCAATATAGACTGAAATATCCGCATCTGAACCTGCTTGTGGGTGGGTCCCGTGAAAAGATGCATTACTTCCCAATGGAACCTCTCAATGTTTCCCTATGGACAGCCTTTAGCAAGACAACT AAATGAAATGCAAGTCTCAAAAATGGTGAAGGAAGCGGCAACACCGCCTGATGAGCGTTTGGCTAAAAATTAAGAAGTTATTTCAAATATGCAGTACTCCAGAATAAAGATTTCGAAGCAGTTTGGACTGGAGATTTCGACAAATCTACACGGTCCAGGCCAAA ATTTTAGATCCACCCGTTTGGAAAGTTGGAAATGCAAAAGTTACTCCAGGAAGGGCCAATGGCAGGCTAATCGCCTCTTGAAGGCGGAAGCACTCCAGTCATGGGGTCTCATCGCCGTCGATACAGACCCGAGAAATCGATTATGACAGCATGATTTCAGTGATTAT CAGCACCCGGCAATCAGTTGGGCATGAATGTTTCCAAACCAAAGTTGCTTAATCTTGGCGCTAGAATGACGTCACTCCACGGCATTCTGATGAATGCTTACAAAGATGTGAGATTCTGTTTCGTGATCGTCTCTGCTAGGGGACGGGATGATTATCACAAGGTAAAGCA AATGGCCGAACGTGAAGTTGGCATTCTGACACAATGCAATTCGAGAGATGACTGCGCGTCGTATAAACAGATGACAGCCAAGAACATCTTACTCAAGGTGAACCTCAAACTGATGGGTGTTAACCAAGCGATTGAACACAACACATTGCCAAAGTGTGTGAGGGAC GGCAATGTCATGTCGCGCTGACGTCACTCATCCATCGCAAGTACGTACAGTCAAATGTTTCCAGTATTGACGCGGTAAACGGCTCCATCGATCCGCGATGCTATGATGATAACATTCGAACCTCAGCTCAGCGTGCAGACACCTAAGAAAGAGATGATTGTGGAGTTGCAAGA TATGATGTTTCGATCACCTCAAGGTGTACAAGGATCGCAACAACCTCCCTGCCAAAGAAGA
Bombyx mori latent virus (extracted from Hi5 cells)
GAATGGCTTTCACCAATTTAGTCGACACTCTCGCCAACACCATCCACCGAGACGCCATAACGGCTCCTCTAGTGGAAACGGCCATCAGCAATTTCCGTCACAAGCTTCAACTTTACCCATATCAGGTAAATCCAAAGCTCATCCCAATTGCTCAATCAACTCGGAATAGGAGTCACTCCTATGGCACTTCACTCATCTCTA TGCCGCTCATAAGGCCATAGAAACTTACCTCTGTTTGAACATTGGAATCATCTTGGCAGAGTCCCTTCTACGGTAATGTATATGAAACCTGAAAAATTTCAAAACTTCAGCAATTAACCCCAAACCTTTGCTTCCTCATTAACCTTCAGGCCACACCCAAAGGACATTACTCGGTACCCCGTTAGCAACCTCATCTGTGTC GAAACTGAAGTAGCGTTTCATGCACGACGCTCTCATGTTTCATACACCCCTTCCCAAATTTTAGGCCCTTTTCAAGGACTCCCTTCCATGACCTCACTCTATTGTTCTCTTATAGTCCCTGCCGAAGCCGCTTATGGAAGTGCTTCACTTTCCTGATCTCTACAGCTATACAATTAAGATGATCAGCTGGTGTACTCTCTCGAA GGAAATGCTACCGGCAATTACACTCAACCTCTCTGTTCTTTGGATTGGCTCCGCGCTCAGGTATTTCATAGGCGACCTTCATCTATCTGTCACTTTACTGGAATCCTTGTTTCCGTCATTCCATCTAATCACTCGAGTTCCTCAACCTCCCCCTCTCGCGGAACATGATTCTTAACCTCTCCAGCTTCCGTTCTCTA ATCCAGAAGGATTGAACCTGCCGATCAAAATCAGACTCTGTGCCAATCGAAGTTTACAATTTCTTTGTTTACTTATGTTTCGAGCGGTTTCGACGCTTCCGGTCACTGATCTCTCCGGATTTCGTAGGAGCGCAACGTCAAAACCGAGAATTCATGGGTCAATCTCAGCTGGGTAATCTCAGCTGGGTAATCTCGAACTCATACCTTTAGATGGCTGCCCACTCAITTTGGACTTC GTGCTCGGCCCGCCCTTCTTAGAGTATGGTTTCTGCTATAACTCATACAAGCTTTTATCACTCTGGATCGTGGTACATTTGCGTTTCGATATCAGTTATCACACTGGTTCCTTCTCACCATCCCAATTTCTCACCATCTTTCCCTTATCAGCTGTGTTATCGAACTCATACCTTTAGATGGCTGCCCACTCAITTTGGACTTC ACAAACCTTGCCCTCTTTGATTACAGAGCCTTCGCTAGCACTTACGGCGCTACCTCACCAACTCACCAGAGTTCGCCACTTCAATCTTTTCTATTAATCATTTATTACAGCTTTTGGCAAGTCATTGCAAAAAATTTCTCACCATCTCTTAGTCATTGCAACCAATCTGCTGCTTCCAGCAAAATCTGCTCTCTCATTTGCTGTGTCTCCACTTCT ACAACGAAGGTGGCTCTTGCTTGGTTTGTCTGCCCTCACTGGCATTGGGCCATTACCATCTCCGCGGTGGCAACTCACTCAAGAAAAAGTCCGATGCTTATCTCTCTTATTTCACCCGGATCCCTGGAGACTCACCAATTCGAACATCTAATGTGATGGCTATTCTCATTTCTTCCCGATTACAGCACTCGACTCC TTCACCGTCTACACAACCGTCCCTGACCCCATGTTATCGAACAACCCCTGCTAACGTCTCAAAACGTCACTCGTTTCCAAACGAGCTACCTACACCGGCTCATCTCGAGACACCCCAAGCCCAAGTAAACAAGAGATAAAATCCGGTGAGACTCTTGCCACCGGCTTCCAAATGTTGCGACCTGAGCGGCC TCGGAAGCCTCGAAACAGACGCGCCTCTACTCTTTAAGTTCCGATCCAAGTGTCTATGGGCCATCTCCCTCATAAAGAACTTTTGGCATTTTATCTCCGATCACGAGTGCAATGTTTAAATCGTAAGCACTCAATGTTTCAACGCTTCTTCCCGGATCAGCCTGTCTTGTGTTGCTTTTGCTCAAGCTCA AATTTACCCCTCAGCAAGTATGGGCTCACTTTGCACCCCTTTCCCTGATTCCCTTCTCGATGGTCCCTTAGAACGCTCTCAAGGCTCAAGCTCAGAACACCTCGAAGCTCTCGCTGGAGTTTGAATATCACGTCTCTTATCGCCATGGCGAACATGTCAACACCATAGGCCCGGATGAGCAGCACCATGCTCCGCTTAT TTACACTGGTGATGGATCATAGGTCAATGGGCTGCCGACGAATCCCTCTTCCCCCCCTTTCTCCTATTCAGAGCTTCGGCAAAACCCCTCAATTCATTGCTCAACAGCTATTCCGTTTAGAGACTCTCACGGCAATCTCCTACCAATTTCGACAAGTTTCAAGTACAAGCTCTGAAGCCAGGGCAAAAAATTTGG CCTCAAAATGAAAAATGAGACTGATGGAGTTATACAATCTAGCTCCGAGCGGCATCATCAGACCCCACTTTTTCACAACGCTTGACCAAGAGCGGACTTCGCCCAACAAGTTTCGCTGCGAGCTATTTCACATTAATCTGAGTTTCTGGTTGTGGGAAAACTTCCCTGTCACTCAGCTCCTCAAAACCAAAGCATTTAA AAGCCAGTACAGAGTCGCGCTCCCAACCCGAGTTGCGTACCGAATGGAAGACCACATGAAACTCCCTGTAGCGACGTTTGGCGAGTCTCAACCTGGGAAACCTCTCTCATGAAATCAGCACCCGCTTGGTTATCGACGAAGGTACAAAAATGGCTCGAGGTTTCTCGGATCTAGCTCTCTAGCTGATCCAGCCAT CCAATTTGTCATCTCTCTCGGAGACCATGCCAAACCGTCTATTCTCCGTCAATCCGGACTCTTCAATATCTGTCTGATTCCGGAAGTCGAACATCTTAAACCGTATCTGATTTTACTGTCTCTGGACCCACCGACTTCCTCTCGCTAGCTGATTTCTGCGGCTTCGACTACGAACCCCTCAAGAAGGTTTATCGGA CGTCGAGACATCCACAAAACTTATTCCCATATTAACATCAAGTCAGCAGACGGCGCGAGTCTGTGCCGATACAGGCCATCGAGCGTCACTTTTGTCTCTCAAGGTTCAACTTCCAGGCTCTGCCCCAAATCTCATCGACTCCAATGTGGCTCTGTCCACGTTTCTGCTACTCTGTCGCCACAACCTCGTTCCCG TTCCTGGAGTCATTTTACGGGAAACCATCGAATGTTTCCAATCAAGACCTGGTACGGCGCACTCTTCGAGGCTATGCTCAATGACCAACCTTCAACTCTCTCAACATATTGCTAATGAACCTTGGAGGATGGAACCTATTACATCACCGATCAAGAAACGAAAGACCATCTCTGTTGGCGGGTCTTATGACTTTTCAGCT TCCGAAAGCCACCAAAAAAGACATCACCGAATGACCAACTTTAAATTCGATCAGCTCATATCAGGGCTCTCGCCCTGCTATCTGCCAAACCACTACCTGCTAATGACACCTCTGACATAATAATTTTGCACCTGAACCTTTTGACCTCCAGTCTTCAGCCATCCCGAGACTTGACACTCATCATATCCAGAAACTCGTGC TCCTCTCCATTTTGATATTTCTTCTCTCTCCCTACCAAAAGTGGACATTAGTAGTGTGAATCTACAGACACCCGCATAGAACTGTTTATCCCGGCTGCGACTACAAAACTGTGGCGAGCTTAATGATGGATCCCGGGGACCCGACTCCCTTGAATCCGGCAACAGGGGGAGTCTCCAATCAATTTCCATGGGTGCTGTC TCCCTTATGAGAATGGCGCCCAAAACCTCAGCGTTATAGCACCCAAACATGACTCGAAAAATGACCCGACTTTACTTTGGGCTCCATAGCCAAAAAGACTCCGTTTTCGACCCTCTTCTCTCTTACAGACTTTCTCTCTGACGAAGTCTTGGCACATTTCTGTTTTCATCTCTATGTGCGAGCTATAAACGACATCCCA ATCATAAAGTTCTCTTTAGCCCGACCTTTTCGTTGAATGTATCAATCTTAATGAGTACTCACAGCTTTTCAACAAGACTCAAGCTGTCAATCCAAAGCGCAACATCGTTCCGGATCCCGACTGGCGGTACACTGCTGTCCGATATTTTCAAAACCTCAGCATAAAAATCAACGAAGGCTCAATTTTCGGCCCTTGGAAAGC ATGCCAGACATTAGCTCTGATGCAATGATGCCATTGTCTTAATTTTGGCCGATCAAGAAAAATCAGCGAATTTTCGACAGTAAGAATCGTCTCCCACTTGTTTTGGTATGGAAGGCCAAACTCAATACGATCTCTCGGGTTGCTCTGTCCTCACTGAAACCATACAAAATTCATGTCTGCAATGACTATATCGCTTTG ACCAATCTCAGCATGGTGAGGCGTGTGTTTGGAAACGGAAGAAAAATGGAGCGGCTTTCATTTCCATCTCATCTTATAGACTTCCATTGCTACATCAAAACCAACATTAACAAGTCAATTTGGACCTCTGACCTGCTATGCGGCTCACCGCGAGCCGGGACATTATGACGACAAACACGGATTACAAATATGCGGCTCAATTACAG CGAGTACGACATCAACCTCAACTGTCTTGTCTCAGGTGATGATCTTTAGTATACACCTCACTCTGCTCACCCGATTTGGGACGCGGTTTCTCCTCCTCTTCTCACACTTCAACATAAAGAGTTTGTGCAAAACGGGTCTCTCTGCGGCTATTTACTTGGGACGCGCCGGAGCAATTTAGCTGCTCCCTGCTTACTCGC TAAACTTTGTGTAGCTTACGACGACGAAACCTTTCTGACAAAAATAGCGCTTACTCTCAGTGAGTTTGTGTAGGCCACTCTCTCGCGGACGCTTCTCGGACTCTCTGCGCAGATCAAGTAATTTTACAGAGCGGCTCTTTTGAATTTCTTTGCGGTGAAATTTTAAAGGAACAAAACTCGCCCTCAAAATAGGGGAAG TGCCGAACATCTTTGTCAGAAAATGCTTTCCCTCGGTTTCTCTGGTTATCACACCCCTTATAGCTCTCTTGGATAGGACGCCCGCGCTACGTTTATAGCCCGCACTCGTTTGCAGCCCTCTTCTGATAGAGGTTTGTGCAACTAGATTTCGTATGACCTATTCATGGAAGAAATTTGCGCTTTAGTCG CTTCTGGCGCTTGGGCATTTCCGCTTGTGCTATGCTTCTCTTCCAAACCCGCTCAACTGATCACCCGCTTCGCGGTCATAGGATATGCAACCTTTCGCTAGCTCTGACAGGTTGTCTGTGTCAGCAACCGCTCCGCGGCTCTCCCTGGGACGATCTCCCTGGGACGATCTCTCAACGTTTGTATCAT CCCTTTTCAACGCTGTACTTCGATCTTACTGGCACGGAACCAAAATCGAACAGTGTCACTGTGCAATCACTACGAACGCTCTCCCTATCATCAAAAGGCTACCGGACGCGTATCTTGTCATCTTGAAGCTGTGCTTTTCCCTCCGCGCTAGCTCAAAATACCACTGACAGTGTGACTGTGCTGAGC TCACAGTTGAAGGAGTCAATGTGTGGGCAACCTTCACTCCGCTCGCTATTACTTTGGCGCTCGCCCTTCACTCCGATCCCTCGGATCTCGGTCAGACCCGATCACTCAACCCGATCACTCAACCAACCCAGACTTAACATCAATTTCCATATCCCTGACGCGGTACGAGAAGGTT CGCGCGGGGTTAAAGCTCCGTTGTGTCATCAGAGGCTCATCAGCGTATCTCACCCCTCGCTCACTGGGATGGCTGAAGGGGTTTCTCTCCCTTATTTTCAAGTGAATGATGTATCAACAAGCTTCGCGCTTATTAGTGCGTATCTCCAGCATCTCCAGCATCTTCGCTCCCTCTCTCAACTCACCCCTCATTTGAAGAGCTGTTATGG CCACAAACCAAGCATCTACGACTATAAAGTCAAAATCGCGGATAATGATTAGTAACTCAATGAACCTGCGGACGCTGATCTTCTGATCTTCTTAACTCTCCCTCGATACCCGATTTGATGACACAACATCATGACGGTTCGTAAGAACACAAAACTGCT TCTTCTCTGCTCATCTATTCAAGCTTCTCTCCCTTCTCCGAGATCTACCGCAGTTGATAGATCTCGCCATGTTTCTTCGACTCTTGGAGTTTACGTAAAAATCTTAATCCCTTATCTTCCAGATTGGGTTGTTAGTTTCAATCCGCTCT

**Supplementary Table S7 – Amino acid difference matrix of the replicase polyprotein between newly assembled and reference BmLV genomes. Cells are shaded from high (dark) to low (light) percentage difference. The reference BmLV genome and the genome of the BmLV variant employed in this research are written in bold.**

% Different AAs	DRR068691	SRR6324419-24	SRR11781560-1	SRR24542361	SRR17258732 (this paper)	KJ433990	AB186123.1	AB624361.1 (reference)	DRR241076	DRR035925	DRR068690	SRR1333837-38	SRR17258733	DRR079253	DRR039989	DRR023337+40	SRR5458683	SRR9685281	DRR006265
DRR068691	0	3.15	3.03	3.32	3.66	2.17	2.46	3.66	3.49	3.32	3.2	2.35	2.35	2.35	2.46	2.46	2.4	2.4	2.4
SRR6324419-24	3.15	0	1.26	4.41	4.75	3.78	3.43	4.98	4.86	4.69	4.58	3.49	3.43	3.43	3.55	3.55	3.49	3.49	3.49
SRR11781560-1	3.03	1.26	0	4.41	4.75	3.83	3.49	4.86	4.75	4.58	4.46	3.55	3.49	3.49	3.49	3.6	3.55	3.55	3.55
SRR24542361	3.32	4.41	4.41	0	0.69	2.75	2.75	4.29	4.23	3.89	3.89	2.69	2.63	2.63	2.75	2.75	2.69	2.69	2.69
<b>SRR17258732 (this paper)</b>	3.66	4.75	4.75	0.69	0	3.15	3.32	4.69	4.63	4.29	4.29	3.2	3.15	3.15	3.26	3.26	3.2	3.2	3.2
KJ433990	2.17	3.78	3.83	2.75	3.15	0	1.43	2.86	2.97	2.57	2.46	1.66	1.6	1.6	1.83	1.72	1.66	1.66	1.66
AB186123.1	2.46	3.43	3.49	2.75	3.32	1.43	0	2.8	2.86	2.52	2.4	1.77	1.72	1.72	1.89	1.83	1.77	1.77	1.77
<b>AB624361.1 (reference)</b>	3.66	4.98	4.86	4.29	4.69	2.86	2.8	0	2.69	2.12	2	3.26	3.2	3.21	3.26	3.32	3.26	3.26	3.26
DRR241076	3.49	4.86	4.75	4.23	4.63	2.97	2.86	2.69	0	1.6	1.49	2.97	2.92	2.92	2.92	3.03	2.97	2.97	2.97
DRR035925	3.32	4.69	4.58	3.89	4.29	2.57	2.52	2.12	1.6	0	0.11	2.92	2.86	2.86	2.92	2.97	2.92	2.92	2.92
DRR068690	3.2	4.58	4.46	3.89	4.29	2.46	2.4	2	1.49	0.11	0	2.8	2.75	2.75	2.8	2.86	2.8	2.8	2.8
SRR1333837-38	2.35	3.49	3.55	2.69	3.2	1.66	1.77	3.26	2.97	2.92	2.8	0	0.06	0.06	0.29	0.17	0.11	0.11	0.11
SRR17258733	2.35	3.43	3.49	2.63	3.15	1.6	1.72	3.2	2.92	2.86	2.75	0.06	0	0	0.23	0.11	0.06	0.06	0.06
DRR079253	2.35	3.43	3.49	2.63	3.15	1.6	1.72	3.21	2.92	2.86	2.75	0.06	0	0	0.23	0.11	0.06	0.06	0.06
DRR039989	2.46	3.55	3.49	2.75	3.26	1.83	1.89	3.26	2.92	2.92	2.8	0.29	0.23	0.23	0	0.23	0.17	0.17	0.17
DRR023337+40	2.46	3.55	3.6	2.75	3.26	1.72	1.83	3.32	3.03	2.97	2.86	0.17	0.11	0.11	0.23	0	0.06	0.06	0.06
SRR5458683	2.4	3.49	3.55	2.69	3.2	1.66	1.77	3.26	2.97	2.92	2.8	0.11	0.06	0.06	0.17	0.06	0	0	0
SRR9685281	2.4	3.49	3.55	2.69	3.2	1.66	1.77	3.26	2.97	2.92	2.8	0.11	0.06	0.06	0.17	0.06	0	0	0
DRR006265	2.4	3.49	3.55	2.69	3.2	1.66	1.77	3.26	2.97	2.92	2.8	0.11	0.06	0.06	0.17	0.06	0	0	0

**Supplementary Table S8 – Raw Ct values for amplicons of housekeeping genes or viral genes in infected IOZCAS-*Ha*-I cells.**

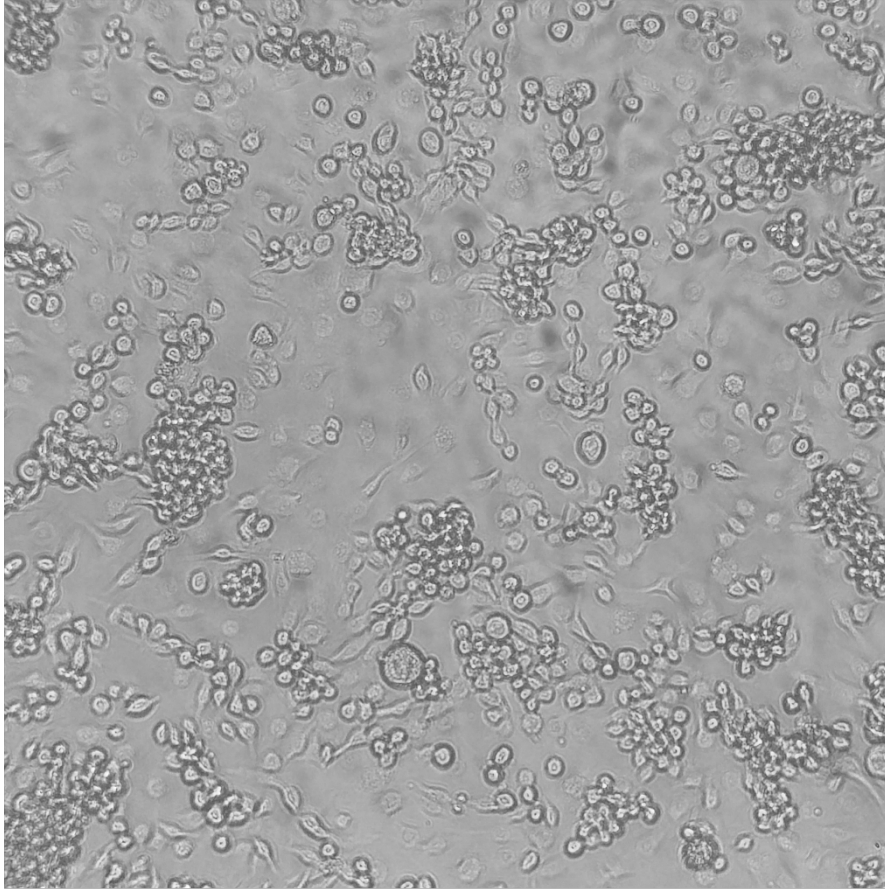
Ct values (average of 2 wells) for HKG and viral amplicons of infected samples					
Timepoint	Replicate	<i>α-Tub</i>	<i>RPS18</i>	<i>rep</i>	<i>cp</i>
Day 4	1	16.294	21.857	11.743	7.524
	2	16.321	21.935	11.976	7.413
	3	16.125	21.724	11.903	7.627
	4	16.219	21.807	11.975	7.445
Day 5	1	16.090	21.917	11.604	7.614
	2	16.401	22.112	12.020	7.786
	3	16.061	21.778	11.454	7.370
	4	16.072	21.901	11.660	7.550

Ct values (average of 2 wells) for HKGs of infected samples (replicate 1 of each timepoint)			
Timepoint	<i>α-Tub</i>	<i>RPS18</i>	<i>18S</i>
T0	17.196	23.251	7.394
4h	17.622	23.022	7.574
Day 1	15.948	21.72	6.566
Day 2	15.44	21.534	6.196
Day 3	16.13	21.959	5.961
Day 4	16.414	21.991	6.098

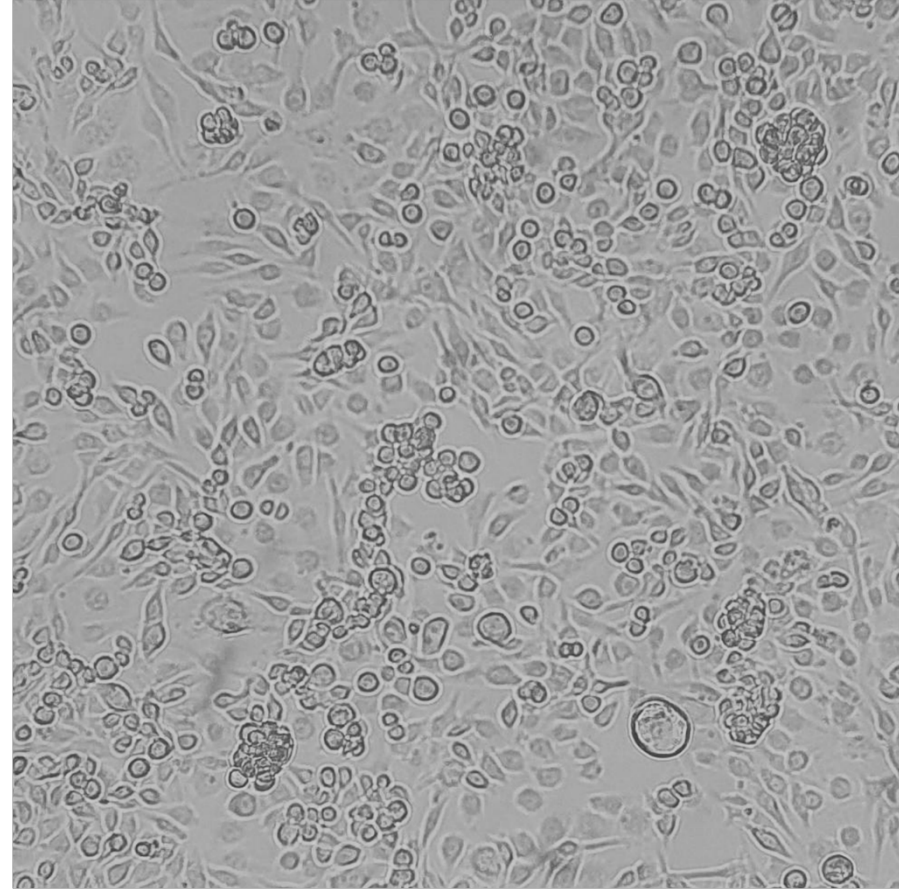
**Supplementary Table S9 - Number of subjects at risk during *H. armigera* infection experiment.**

<b>Day of event</b>	<b>Mock infected</b>	<b>BmLV infected</b>
0	94	96
1	94	96
2	82	83
3	70	70
6	58	58
8		46
12		45
14	45	44
15	40	41
16	39	39
17	38	38
18	37	35
19	34	34
20	27	25
21	21	21
22	15	18
23	11	16
24	8	12
25	6	9
26		4
27	5	
28	3	2
29	2	1
30	1	

2018

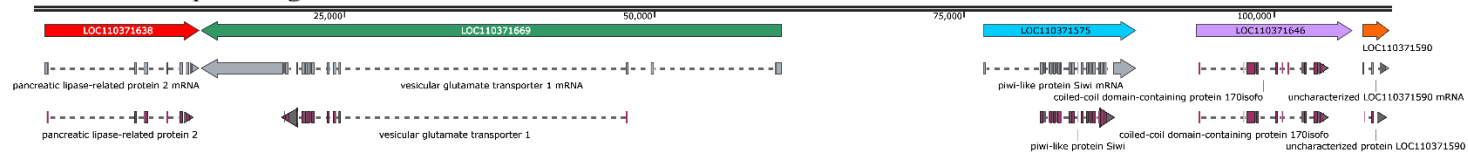


2022

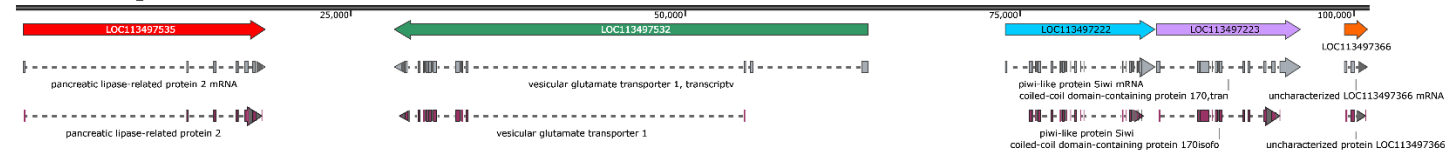


**Supplementary Figure S1 - Photomicrograph (100x magnification) of IOZCAS-*Ha-I* cells upon arrival in our lab in May 2018 (left) and IOZCAS-*Ha-I* cells on day 4 after the mock infection used for this study in 2022 (right). The form of the cells varies from spherical to spindle-shaped.**

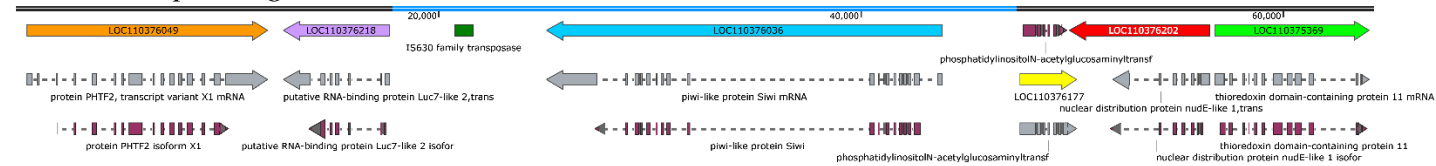
### A - *Helicoverpa armigera*



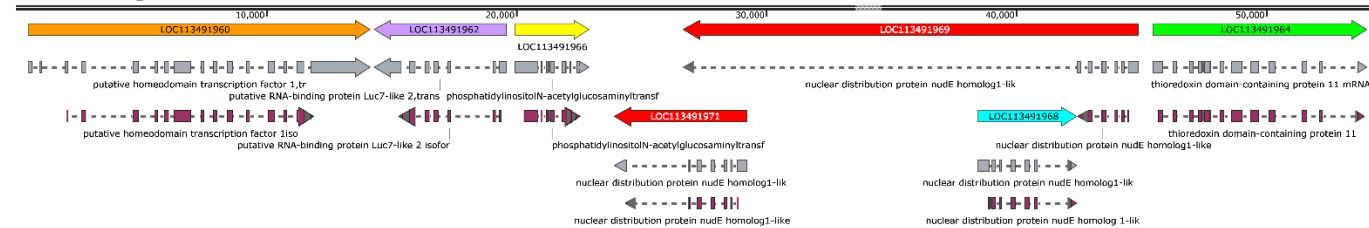
### B - *Trichoplusia ni*



### C - *Helicoverpa armigera*



### D - *Trichoplusia ni*

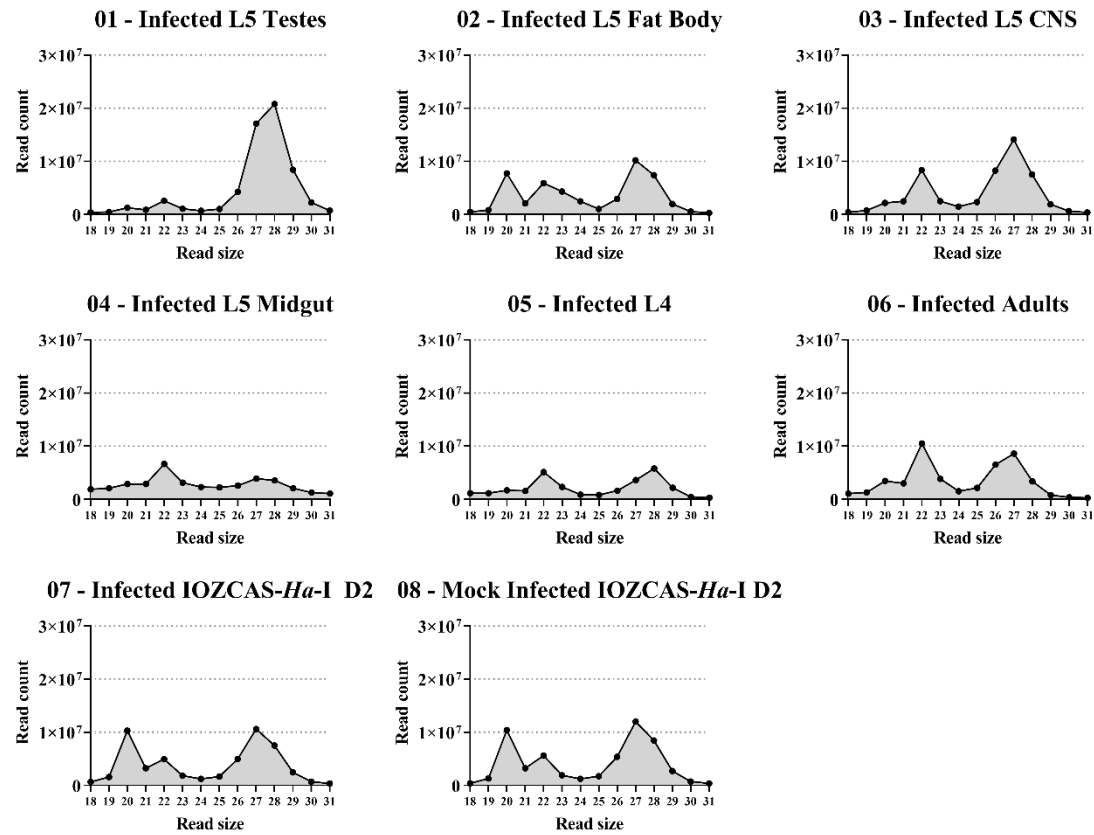


**Supplementary Figure S2 - Genomic loci of two *siwi* genes (blue arrow) in *Helicoverpa armigera* (A) (Chromosome 12, NC\_064787.1) and (C) (Chromosome 17, C\_064792.1), with the corresponding genomic loci in *Trichoplusia ni* (B) (Chromosome 9, NC\_039486.1) and (D)(Chromosome 3, NC\_039480.1), respectively. For simplicity, only one transcript variant and protein isoform are represented for each gene. The presumptive *H. armigera* transposed DNA sequence of figure C is indicated in blue. Data sourced from the National Center for Biotechnology Information.**



**Supplementary Figure S3 – Sequence alignment (from AA 1 to 600) of *H. armigera* SIWI proteins XP\_049696273.1 (upper row) and XP\_049699728.1 (lower row). Conserved domains predicted with the NCBI conserved domain search tool. Dots represent identical AAs. No mutations are present in the C-terminal region omitted from the figure.**

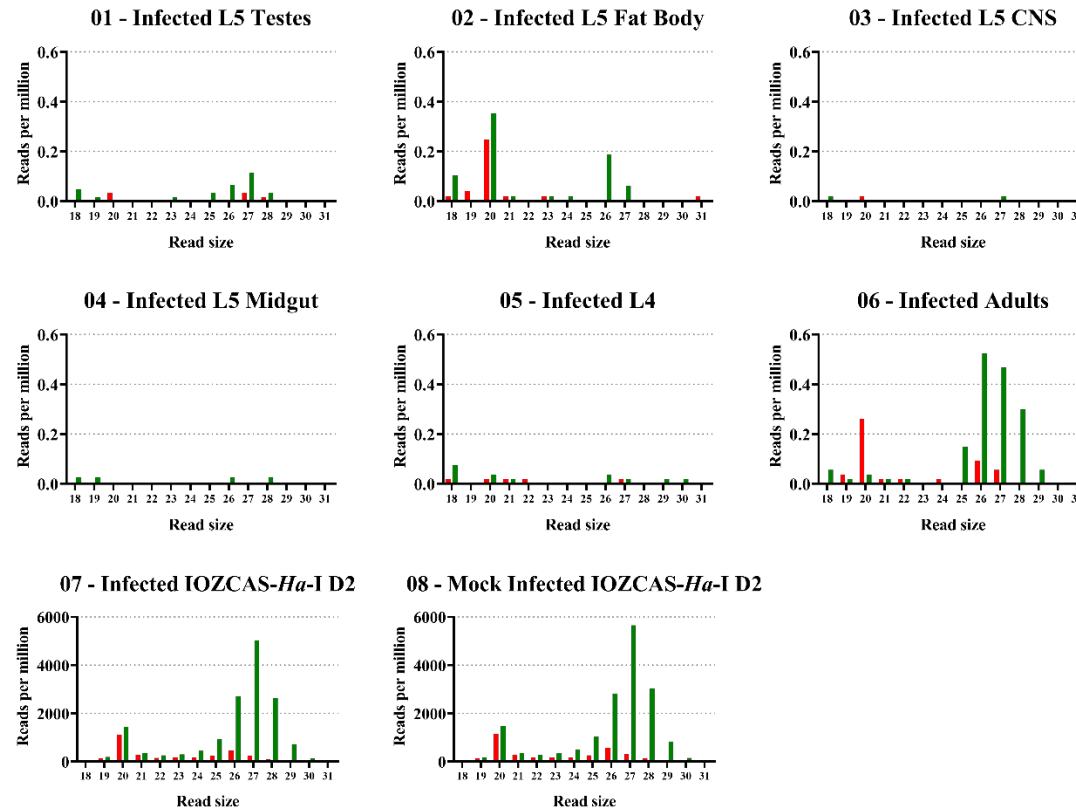
### Size distribution of total library reads



Supplementary Figure S4 – Size distribution of the total sRNA reads in the curated libraries for each sample.

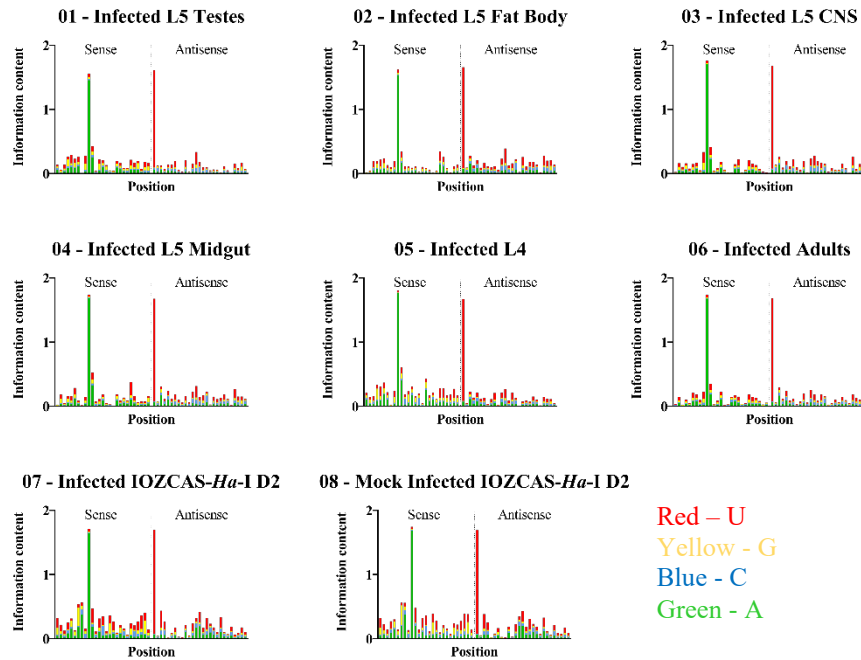


### Reads mapping to *Trichoplusia ni* PiggyBac transposon

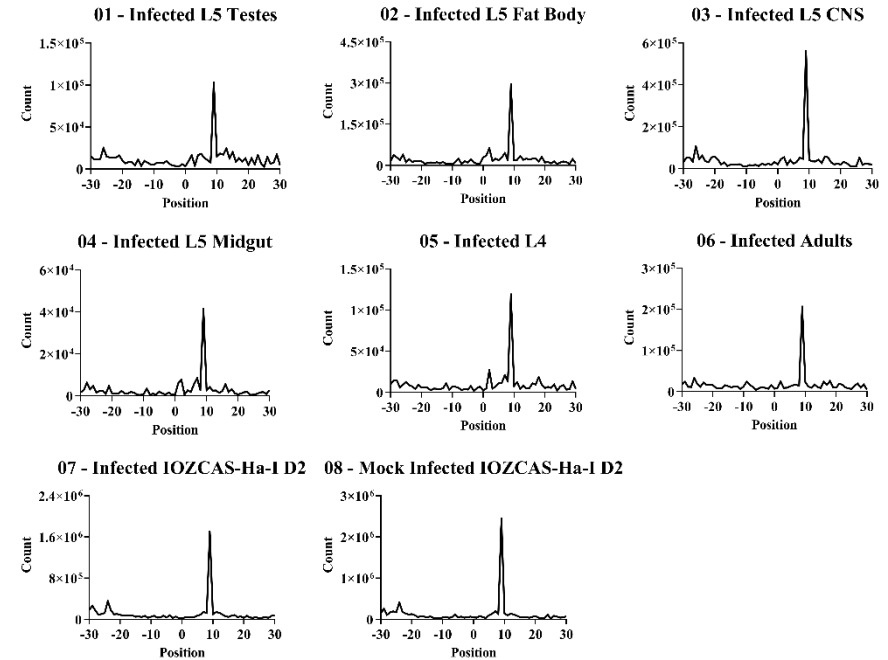


**Supplementary Figure S5 - Analysis of sRNAs mapping onto the *Trichoplusia ni* PiggyBac transposon (GenBank: DQ340395.1) sampled from *H. armigera* animals (samples 01 to 06) and *Trichoplusia* cells (samples 07 and 08). Tissues were dissected on day 6 after infection, whole larvae were collected on day 2 after infection, whole adults were collected on day 1 of the adult stage, and the cells were collected on day 2 after (mock) infection. The frequency of sRNAs mapping onto the PiggyBac sequence is expressed in reads per million and divided by the read size (from 18 to 31 nt).**

### A Sequence logo of 27nt sense and antisense reads mapping onto TEs

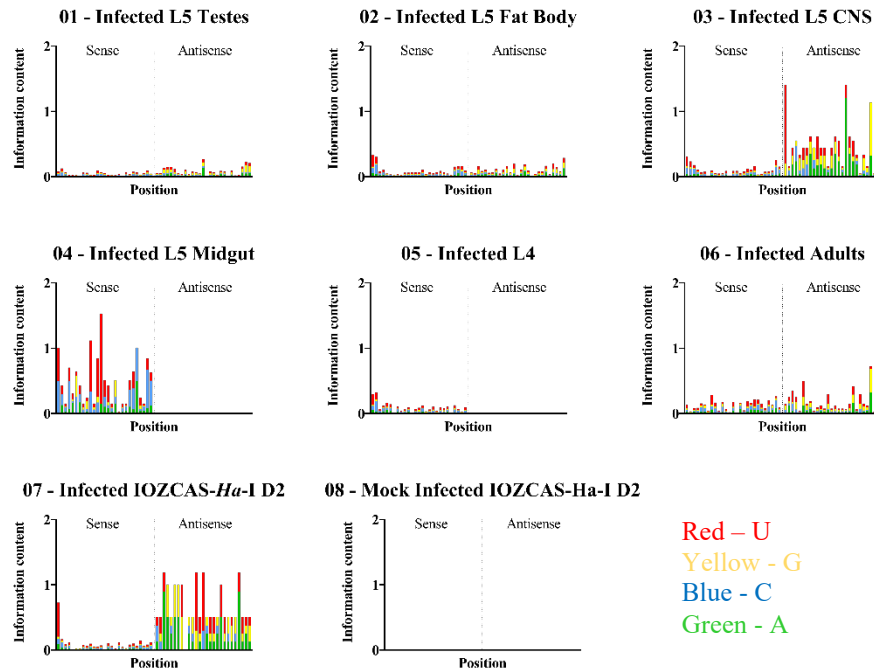


### B Distance plot of 27 nt reads mapping onto TEs

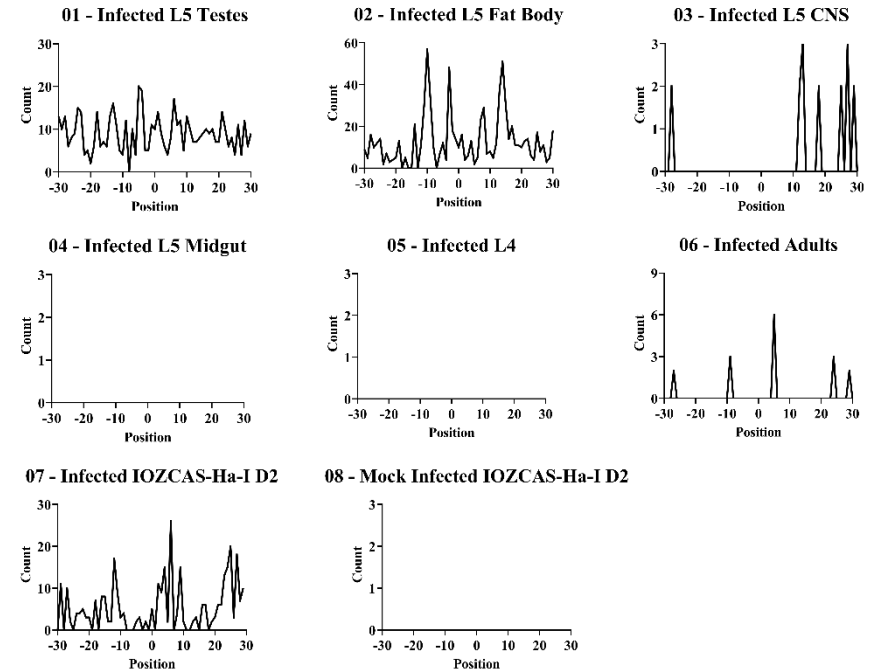


**Supplementary Figure S6 – Secondary piRNA biogenesis pathway fingerprint analysis for reads mapping onto transposable elements.** Tissues were dissected on day 6 after infection, whole larvae were collected on day 2 after infection, whole adults were collected on day 1 of the adult stage, and the cells were collected on day 2 after (mock) infection. (A) Nucleotide biases of 27 nt sized reads mapping onto transposable elements. Reads from *H. armigera* samples (01 till 06) were mapped onto the *HaRT1* sequence (GenBank: EU016079.1), reads from *Trichoplusia* samples (07 and 08) were mapped onto a PiggyBac transposon sequence (GenBank: DQ340395.1). For all samples, sense reads display a strong bias for an adenine on the 10<sup>th</sup> position whereas antisense reads have a strong bias towards an uracil on the 1<sup>st</sup> position. Information content (Y-axis) calculated according to the formula of Schneider and Stephens (1990). (B) Read distance plot of 27 nt reads mapping onto the same TEs. For all samples, a clear peak is seen at a distance of 9 nucleotides.

## A Sequence logo of 27 nt sense and antisense reads mapping onto BmLV



## B Distance plot of 27 nt reads mapping onto BmLV



**Supplementary Figure S7 - Secondary piRNA biogenesis pathway fingerprint analysis for reads mapping onto BmLV. Tissues were dissected on day 6 after infection, whole larvae were collected on day 2 after infection, whole adults were collected on day 1 of the adult stage, and the cells were collected on day 2 after (mock) infection. (A) Nucleotide biases of 27 nt sized reads mapping onto BmLV. No 1U or 10A nucleotide biases are found except for antisense reads from CNS where a 1U bias is present. Information content calculated according to the formula of Schneider and Stephens (1990). (B) Read distance plot of 27 nt reads mapping onto BmLV. No clear 9 nt distance peak is present in any sample.**

**Supplementary text S1 – Multiple sequence alignment of replicase polypeptides assembled from publicly available SRA datasets. Sequences aligned with MEGA7 (version 7.0.26) and then visualized with MView (version 1.63). Amino acids are colored according to their identity.**

	cov	pid	1	80
1 DRR068690	100.0%	100.0%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
2 DRR068691	100.0%	96.8%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
3 DRR006265	100.0%	97.2%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
4 DRR039989	99.9%	97.1%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
5 DRR079253	99.9%	97.2%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
6 SRR6324419-24	100.0%	95.4%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
7 SRR11781560-1	100.0%	95.5%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
8 SRR5458683	100.0%	97.2%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
9 DRR023337+40	100.0%	97.1%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
10 SRR1333837-38	100.0%	97.2%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
11 DRR241076	100.0%	98.5%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
12 SRR17258733	100.0%	97.3%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
13 SRR24542361	100.0%	96.1%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
14 SRR17258732	100.0%	95.7%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
15 SRR9685281	100.0%	97.2%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
16 DRR035925	100.0%	99.9%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
17 AB186123.1	99.9%	97.5%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
18 KJ433990	100.0%	97.5%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
19 AB624361.1	100.0%	97.3%	MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
consensus/100%			MAFTNLVDTLANIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
consensus/90%			MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
consensus/80%			MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
consensus/70%			MAFTNLVDTLANTIHRDAITAPLVETAINNFRHKQLYPYQVNSKLIPLLNLGIGVTSYGTSPHFHAAHKAETHLLFE	
	cov	pid	81	160
1 DRR068690	100.0%	100.0%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
2 DRR068691	100.0%	96.8%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
3 DRR006265	100.0%	97.2%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
4 DRR039989	99.9%	97.1%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
5 DRR079253	99.9%	97.2%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
6 SRR6324419-24	100.0%	95.4%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
7 SRR11781560-1	100.0%	95.5%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
8 SRR5458683	100.0%	97.2%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
9 DRR023337+40	100.0%	97.1%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
10 SRR1333837-38	100.0%	97.2%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
11 DRR241076	100.0%	98.5%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
12 SRR17258733	100.0%	97.3%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
13 SRR24542361	100.0%	96.1%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	
14 SRR17258732	100.0%	95.7%	HWNHLLARVPSTVMYMKPEKFQKLQQLNENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAALMEITPSQILGLFKDS	

15	SRR9685281	100.0%	97.2%	HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
16	DRR035925	100.0%	99.9%	HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
17	AB186123.1	99.9%	97.5%	HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
18	KJ433990	100.0%	97.5%	HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
19	AB624361.1	100.0%	97.3%	HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
	consensus/100%			HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
	consensus/90%			HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
	consensus/80%			HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
	consensus/70%			HWNNLARVPSTVMYMKKEKFQKLQQTENFASLINFRHTPKDITRYPVSNPHPVETEVAFMHDAIMFITPSQILGLFKDS
		cov	pid	261
1	DRR068690	100.0%	100.0%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
2	DRR068691	100.0%	96.8%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
3	DRR006265	100.0%	97.2%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
4	DRR039989	99.9%	97.1%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
5	DRR079253	99.9%	97.2%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
6	SRR6324419-24	100.0%	95.4%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
7	SRR11781560-1	100.0%	95.5%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
8	SRR5458683	100.0%	97.2%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
9	DRR023337+40	100.0%	97.1%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
10	SRR1333837-38	100.0%	97.2%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
11	DRR241076	100.0%	98.5%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
12	SRR17258733	100.0%	97.3%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
13	SRR24542361	100.0%	96.1%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
14	SRR17258732	100.0%	95.7%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
15	SRR9685281	100.0%	97.2%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYSLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
16	DRR035925	100.0%	99.9%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
17	AB186123.1	99.9%	97.5%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
18	KJ433990	100.0%	97.5%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
19	AB624361.1	100.0%	97.3%	PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYTLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
	consensus/100%			PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYOLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
	consensus/90%			PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYOLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
	consensus/80%			PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYOLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
	consensus/70%			PSMTSLYCSLIVPAEAAAGVPSLFPDLYSYTIKDDQLVYOLEGNATGNYTQPLRSIDWLRRSGISSGDLHLSVTLLSFV
		cov	pid	241
1	DRR068690	100.0%	100.0%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
2	DRR068691	100.0%	96.8%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
3	DRR006265	100.0%	97.2%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
4	DRR039989	99.9%	97.1%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
5	DRR079253	99.9%	97.2%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
6	SRR6324419-24	100.0%	95.4%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
7	SRR11781560-1	100.0%	95.5%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH
8	SRR5458683	100.0%	97.2%	SVHSLIITRVPPPPSCHEVFLTPPASLLPNPEGIEELPIKSRLVPTDEVYNSLFTYVRAVRTLRVTDESGFVRTQORQKEH

9	DRR023337+40	100.0%	97.1%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYDSLFITYVRAVRTLRVTDPSGFVTRORQKEH
10	SRR1333837-38	100.0%	97.2%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYDSLFITYVRAVRTLRVTDPSGFVTRORQKEH
11	DRR241076	100.0%	98.5%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
12	SRR17258733	100.0%	97.3%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYDSLFITYVRAVRTLRVTDPSGFVTRORQKEH
13	SRR24542361	100.0%	96.1%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
14	SRR17258732	100.0%	95.7%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
15	SRR9685281	100.0%	97.2%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYDSLFITYVRAVRTLRVTDPSGFVTRORQKEH
16	DRR035925	100.0%	99.9%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
17	AB186123.1	99.9%	97.5%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
18	KJ433990	100.0%	97.5%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
19	AB624361.1	100.0%	97.3%	SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
	consensus/100%			SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
	consensus/90%			SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
	consensus/80%			SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH
	consensus/70%			SVHSLLI TRVPQPPPSCEHVFLTPPASLLNPEGLELPISKRLVPTEVYNSLFITYVRAVRTLRVTDPSGFVTRORQKEH

	cov	pid	321	.	:	.	.	4	400
1	DRR068690	100.0%	100.0%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
2	DRR068691	100.0%	96.8%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIMRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
3	DRR006265	100.0%	97.2%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
4	DRR039989	99.9%	97.1%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
5	DRR079253	99.9%	97.2%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
6	SRR6324419-24	100.0%	95.4%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIMRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
7	SRR11781560-1	100.0%	95.5%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIMRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
8	SRR5458683	100.0%	97.2%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
9	DRR023337+40	100.0%	97.1%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
10	SRR1333837-38	100.0%	97.2%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
11	DRR241076	100.0%	98.5%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
12	SRR17258733	100.0%	97.3%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
13	SRR24542361	100.0%	96.1%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYNSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
14	SRR17258732	100.0%	95.7%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYNSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
15	SRR9685281	100.0%	97.2%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
16	DRR035925	100.0%	99.9%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
17	AB186123.1	99.9%	97.5%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
18	KJ433990	100.0%	97.5%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
19	AB624361.1	100.0%	97.3%	SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
	consensus/100%			SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIMRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
	consensus/90%			SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIMRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
	consensus/80%			SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					
	consensus/70%			SWVQSSAWDNLANFALLTCSARPSLEYGFCYSSYKLLSIWIVRTLRSISAYHTGSLTIPILHHLSPYQLCYRTHTFRWL					

	cov	pid	401	.	:	.	.	480
1	DRR068690	100.0%	100.0%	PTHLDHFHKTLP SLIHRFA SITGRYLTNSPEFPSTSTFSINHLLQPECKSLQKFPHSLVIOENPTSFIVRCSTLLERRWL				
2	DRR068691	100.0%	96.8%	PTHLDHFHKTLP SLIHRFA SITGRYLTNSPEFPSTSTFSINHLLQPECKSLQKFPHSLVIRENPASFIVRCSTLLORRWL				



3	DRR006265	100.0%	97.2%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
4	DRR039989	99.9%	97.1%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
5	DRR079253	99.9%	97.2%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
6	SRR6324419-24	100.0%	95.4%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSSQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
7	SRR11781560-1	100.0%	95.5%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
8	SRR5458683	100.0%	97.2%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
9	DRR023337+40	100.0%	97.1%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
10	SRR1333837-38	100.0%	97.2%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
11	DRR241076	100.0%	98.5%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
12	SRR17258733	100.0%	97.3%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
13	SRR24542361	100.0%	96.1%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
14	SRR17258732	100.0%	95.7%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
15	SRR9685281	100.0%	97.2%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQKRWL
16	DRR035925	100.0%	99.9%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
17	AB186123.1	99.9%	97.5%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
18	KJ433990	100.0%	97.5%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
19	AB624361.1	100.0%	97.3%	PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
	consensus/100%			PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
	consensus/90%			PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
	consensus/80%			PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
	consensus/70%			PTHLDHFHKTLP SLIHRAEASITGRYLTNSPEFPTSTFSINHLLQPEGKSLQKFPEHSLVIRPNPASFIIVRCSTLLQRRWL
		cov	pid	
			481	5
1	DRR068690	100.0%	100.0%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSAPSSPPSPDPPIVIEQPS
2	DRR068691	100.0%	96.8%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
3	DRR006265	100.0%	97.2%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
4	DRR039989	99.9%	97.1%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
5	DRR079253	99.9%	97.2%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
6	SRR6324419-24	100.0%	95.4%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
7	SRR11781560-1	100.0%	95.5%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
8	SRR5458683	100.0%	97.2%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
9	DRR023337+40	100.0%	97.1%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
10	SRR1333837-38	100.0%	97.2%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
11	DRR241076	100.0%	98.5%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSAPSSPPSPDPPIVIEQPS
12	SRR17258733	100.0%	97.3%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
13	SRR24542361	100.0%	96.1%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
14	SRR17258732	100.0%	95.7%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
15	SRR9685281	100.0%	97.2%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVTAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
16	DRR035925	100.0%	99.9%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSAPSSPPSPDPPIVIEQPS
17	AB186123.1	99.9%	97.5%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
18	KJ433990	100.0%	97.5%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSTPSSRPPSPDPPIVIEQPS
19	AB624361.1	100.0%	97.3%	LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSAPSSPPSPDPPIVIEQPS
	consensus/100%			LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSAPSSPPSPDPPIVIEQPS
	consensus/90%			LLGLSALTGVWYYHRRGNSPQEKSDAYLSYFHPDEWRLTIRTSNVMAIPHSFFEDSGYSAPSSPPSPDPPIVIEQPS

consensus/80%  
consensus/70%

LLGLSALTGVWAYYHRRUNSPQEKSDAYLSYFHPDEWRLTIRTSNVHAIPHSEFFDSGYSSPSPPSPPPSPPIVICOPS  
LLGLSALTGVWAYYHRRUNSPQEKSDAYLSYFHPDEWRLTIRTSNVHAIPHSEFFDSGYSTPSPPSPPPSPPIVICOPS

	cov	pid	561	6	640
1 DRR068690	100.0%	100.0%	SNVSKHHQVQNQAYLTPAHPETPPSPGKQEI	ESGETLATGFPNVATISGPSKASKDAPPTPLSSDETAHGPILPHKELF	
2 DRR068691	100.0%	96.8%	ANVSKHHQVQNQAHLTPAHSETPPSPTKQEI	IKSGETLATGFPNVATISGPSEASKDTPPTPLSSDETAHGPILPHKELF	
3 DRR006265	100.0%	97.2%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
4 DRR039989	99.9%	97.1%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
5 DRR079253	99.9%	97.2%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
6 SRR6324419-24	100.0%	95.4%	SDVSKHHQVQNQAYLTPAHPETPPSPTKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDSTA	HGPILPHKELF
7 SRR11781560-1	100.0%	95.5%	SDVSKHHQVQNQAYLTPAHPETPPSPTKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDSTA	HGPILPHKELF
8 SRR5458683	100.0%	97.2%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
9 DRR023337+40	100.0%	97.1%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
10 SRR1333837-38	100.0%	97.2%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
11 DRR241076	100.0%	98.5%	SNVSKHHQVQNQAYLTPAHPETPPCPSKQKIE	SGETLATGFPNVATISGPSEASKDAPPTPLSSDETAHGPILPHELF	
12 SRR17258733	100.0%	97.3%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
13 SRR24542361	100.0%	96.1%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDETAHGPILPHKELF	
14 SRR17258732	100.0%	95.7%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDETAHGPILPHKELF	
15 SRR9685281	100.0%	97.2%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLNSDETAHGPILPHKELF	
16 DRR035925	100.0%	99.9%	SNVSKHHQVQNQAYLTPAHPETPPSPGKQEI	ESGETLATGFPNVATISGPSKASKDAPPTPLSSDETAHGPILPHKELF	
17 AB186123.1	99.9%	97.5%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDETAHGPILPHKELF	
18 KJ433990	100.0%	97.5%	SNVSKHHQVQNQAHLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDETAHGPILPHKELF	
19 AB624361.1	100.0%	97.3%	SNVSKHHQVQNQAYLTPAHPETPPSPSKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSSDETAHGPILPHKELF	
consensus/100%			usVSKHHQVQNQAaLTPAHSETPPSPSKQcIc	SGETLATGFPNVATISGPSKASKDAPPTPLSSDSTA	HGPILPHELF
consensus/90%			ssVSKHHQVQNQAaLTPAHETPPSPSKQEIc	SGETLATGFPNVATISGPSKASKDAPPTPLSSDSTA	HGPILPHKELF
consensus/80%			SNVSKHHQVQNQAYLTPAHPETPPSPKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSDETAHGPILPHKELF	
consensus/70%			SNVSKHHQVQNQAYLTPAHPETPPSPKQEI	IKSGETLATGFPNVATISGPSEASKDAPPTPLSDETAHGPILPHKELF	

consensus/80%  
consensus/70%

GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL  
GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL

	cov	pid	641	7	720
1 DRR068690	100.0%	100.0%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
2 DRR068691	100.0%	96.8%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
3 DRR006265	100.0%	97.2%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
4 DRR039989	99.9%	97.1%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
5 DRR079253	99.9%	97.2%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
6 SRR6324419-24	100.0%	95.4%	GISSPDHECTFLQGRINVSKLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
7 SRR11781560-1	100.0%	95.5%	GISSPDHECTFLQVGRINVSKLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
8 SRR5458683	100.0%	97.2%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
9 DRR023337+40	100.0%	97.1%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
10 SRR1333837-38	100.0%	97.2%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
11 DRR241076	100.0%	98.5%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
12 SRR17258733	100.0%	97.3%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
13 SRR24542361	100.0%	96.1%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
14 SRR17258732	100.0%	95.7%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWAHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		
15 SRR9685281	100.0%	97.2%	GISSPDHECTFLNRKRINVSTLPFPAPCELLVAFQAASNSTPQRVWDHLCTLFDPSSLDGPLERSQCFSSSEHDEALAWSL		





10	SRR1333837-38	100.0%	97.2%	HEYKLCPRAKNLASNMKNETDGVIOSSLRTASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
11	DRR241076	100.0%	98.5%	HEYTLCKPRAKNLASNMKNETDGVIOSTLRTASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
12	SRR17258733	100.0%	97.3%	HEYKLCPRAKNLASNMKNETDGVIOSSLRTASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
13	SRR24542361	100.0%	96.1%	HEYKLCPRAKNLASNMKNETDGVIOSSLRAASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
14	SRR17258732	100.0%	95.7%	HEYKLCPRAKNLASNMKNETDGVIOSSLRAASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
15	SRR9685281	100.0%	97.2%	HEYKLCPRAKNLASNMKNETDGVIOSSLRTASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
16	DRR035925	100.0%	99.9%	HEYTLCKPRAKNLASNMKNETDGVIOSTLRTASSDPTFFHRLDQRA	DFPQVSVOLIHIAFGPGCGKTFPVTQLIKTKAF
17	AB186123.1	99.9%	97.5%	HEYKLCPRAK-IWPHENETDGVIOSSLRAASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
18	KJ433990	100.0%	97.5%	HEYKLCPRAKNLASNMKNETDGVIOSSLRAASSDPTFFHRLDQRA	DFAPRVSVOLIHITGFPGCGKTFPVTQLIKTKAF
19	AB624361.1	100.0%	97.3%	HEYTLCKPRAKNLASNMKNETDGVIOSTLRAASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
consensus/100%				HEYpLCPRAKl <sup>l</sup> hsph.NETDGVIOSSlRsASSDPTFFHRLDQRA	dh...pVSVOLIHIsGFPGCGKTFPVTQLIKTKuh
consensus/90%				HEYpLCPRAKNLASNM <sup>c</sup> NETDGVIOSSlRsASSDPTFFHRLDQRA	dh...QVSVOLIHIsGFPGCGKTFPVTQLIKTKuh
consensus/80%				HEYpLCPRAKNLASNMKNETDGVIOSSoLrsASSDPTFFHRLDQRA	DFsPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
consensus/70%				HEYKLCPRAKNLASNMKNETDGVIOSoLrsASSDPTFFHRLDQRA	DFAPQVSVOLIHITGFPGCGKTFPVTQLIKTKAF
cov				pid	881 . 9 . : . 960
1	DRR068690	100.0%	100.0%	KCQYRVAVPTTELSEWKDHMKLPSSSEVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
2	DRR068691	100.0%	96.8%	KCQYRVAVPTTELSEWKDHMKLPSSDVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
3	DRR006265	100.0%	97.2%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
4	DRR039989	99.9%	97.1%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
5	DRR079253	99.9%	97.2%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
6	SRR6324419-24	100.0%	95.4%	KEQYRVITVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
7	SRR11781560-1	100.0%	95.5%	KEQYRVITVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
8	SRR5458683	100.0%	97.2%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
9	DRR023337+40	100.0%	97.1%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
10	SRR1333837-38	100.0%	97.2%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
11	DRR241076	100.0%	98.5%	KCQYRVAVPTTELSEWKDHMKLPSSSEVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
12	SRR17258733	100.0%	97.3%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
13	SRR24542361	100.0%	96.1%	KSQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
14	SRR17258732	100.0%	95.7%	KSQYRVAVPTTELSEWKDHMKLPSSDVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
15	SRR9685281	100.0%	97.2%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
16	DRR035925	100.0%	99.9%	KCQYRVAVPTTELSEWKDHMKLPSSSEVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
17	AB186123.1	99.9%	97.5%	KCQYRVAVPTTELSEWKDHMKLPSSDAWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
18	KJ433990	100.0%	97.5%	KCQYRVAVPTTELSEWKDHMKLPSSDVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
19	AB624361.1	100.0%	97.3%	KCQYRVAVPTTELSEWKDHMKLPSSSEVWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
consensus/100%				KtQYRVsVPTTELSEWKDHMKLP <u>s</u> -sWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLslADPALQFVILLGDFCQT	
consensus/90%				KtQYRVsVPTTELSEWKDHMKLP <u>s</u> -sWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
consensus/80%				KtQYRVAVPTTELSEWKDHMKLPSS-sWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
consensus/70%				KCQYRVAVPTTELSEWKDHMKLPSSsWRVSTWETSLMKSAPVLVIDEVYKMERGFLDLALVADPALQFVILLGDFCQT	
cov				pid	961 . 0 . . 1040
1	DRR068690	100.0%	100.0%	VYSSVNPSSNYRLISEVEHLKPYRDFYCHWTHRLPRLARFFGVSTTNPOEGFICRRDNPHKSYPILTSSQQTARVCAG	
2	DRR068691	100.0%	96.8%	VYSSVNPSSNYRLISEVEHLKPYRDFYCHWTHRLPRLARFFGVSTTNPOEGFICRRDNPHKSYPILTSSQQTARVCAG	
3	DRR006265	100.0%	97.2%	VYSSVNPSSNYRLISEVEHLKPYRDFYCHWTHRLPRLARFFGVSTTNPOEGFICRRDNPHKSYPILTSSQQTARVCAG	

4	DRR039989	99.9%	97.1%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
5	DRR079253	99.9%	97.2%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
6	SRR6324419-24	100.0%	95.4%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
7	SRR11781560-1	100.0%	95.5%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
8	SRR5458683	100.0%	97.2%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
9	DRR023337+40	100.0%	97.1%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
10	SRR1333837-38	100.0%	97.2%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
11	DRR241076	100.0%	98.5%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
12	SRR17258733	100.0%	97.3%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
13	SRR24542361	100.0%	96.1%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CLWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
14	SRR17258732	100.0%	95.7%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CLWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
15	SRR9685281	100.0%	97.2%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
16	DRR035925	100.0%	99.9%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
17	AB186123.1	99.9%	97.5%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
18	KJ433990	100.0%	97.5%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
19	AB624361.1	100.0%	97.3%	VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
	consensus/100%			VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
	consensus/90%			VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
	consensus/80%			VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG
	consensus/70%			VYSSVNE	DSSNYRLI	SEVEHLKPYRDFY	CHWTHRLE	RLARFFGVSTTN	PQEGFIC	RRDNPHKSY	PILTSSQQT	ARVCAG

		cov	pid	1041	:	.	.	.	.	1	.	1120	
1	DRR068690	100.0%	100.0%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
2	DRR068691	100.0%	96.8%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
3	DRR006265	100.0%	97.2%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
4	DRR039989	99.9%	97.1%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
5	DRR079253	99.9%	97.2%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
6	SRR6324419-24	100.0%	95.4%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
7	SRR11781560-1	100.0%	95.5%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
8	SRR5458683	100.0%	97.2%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
9	DRR023337+40	100.0%	97.1%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
10	SRR1333837-38	100.0%	97.2%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
11	DRR241076	100.0%	98.5%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
12	SRR17258733	100.0%	97.3%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
13	SRR24542361	100.0%	96.1%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
14	SRR17258732	100.0%	95.7%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
15	SRR9685281	100.0%	97.2%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
16	DRR035925	100.0%	99.9%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
17	AB186123.1	99.9%	97.5%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
18	KJ433990	100.0%	97.5%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	DFLNT
19	AB624361.1	100.0%	97.3%	TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	NFLNT
	consensus/100%			TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
	consensus/90%			TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT
	consensus/80%			TGHRALTE	CSSQGSTF	QAPAQIF	VDSNVASV	HVSATLVAT	TRSRS	GVIFTGNHRL	FQSRPGTAPL	FEAMLNDQPF	SFLNT

consensus/70%			TGHRALTECSSQGSTFQAPAQIFVDSNVASVHVSATLVATTTRSRSGVIFTGNHRLFQSRPGTAPLFEAMLNDQPFSELNT
	cov	pid 1121	2 1200
1	100.0%	100.0%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPPPNANDTSDVIIIFAELEFD
2	100.0%	96.8%	FANELGGMELIASPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDVIIIFAELEFD
3	100.0%	97.2%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
4	99.9%	97.1%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDVIIIFAELEFD
5	99.9%	97.2%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
6	100.0%	95.4%	FANELRGMEPITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSASAKPLPANDASDIIITFAELEFD
7	100.0%	95.5%	FANELRGMEPITSPIKERKTIILRGGSYDFSAYRRKLPKHHRTNFKFDPAHIRAPRSASAKPLPANDTSDVIIIFAELEFD
8	100.0%	97.2%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
9	100.0%	97.1%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
10	100.0%	97.2%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
11	100.0%	98.5%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDVIIIFAELEFD
12	100.0%	97.3%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
13	100.0%	96.1%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSHQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
14	100.0%	95.7%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSHQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
15	100.0%	97.2%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
16	100.0%	99.9%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPPPNANDTSDVIIIFAELEFD
17	99.9%	97.5%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
18	100.0%	97.5%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIIIFAELEFD
19	100.0%	97.3%	FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDVIIIFAELEFD
consensus/100%			FANELGMEIISSPIKERKTIILRGGSYDFSAAaRph...HHRhTNFKFDPAHhRAPHss.AKP.PANDSSDIIIfAELEFD
consensus/90%			FANELGMEIITSPIKERKTIILRGGSYDFSAAaRsaop+HHRMTNFKFDPAHhRAPRss.AKP.PANDTSDIIIfAELEFD
consensus/80%			FANELGGMELITSPIKERKTIILRGGSYDFSAAaRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIfAELEFD
consensus/70%			FANELGGMELITSPIKERKTIILRGGSYDFSAYRSYQKRHHMTNFKFDPAHIRAPRSTSAKPLPANDTSDIIIfAELEFD
	cov	pid 1201	1280
1	100.0%	100.0%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKADISGAEPDTSIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
2	100.0%	96.8%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
3	100.0%	97.2%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
4	99.9%	97.1%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
5	99.9%	97.2%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
6	100.0%	95.4%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
7	100.0%	95.5%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
8	100.0%	97.2%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
9	100.0%	97.1%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
10	100.0%	97.2%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
11	100.0%	98.5%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKADISGAEPDTSIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
12	100.0%	97.3%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
13	100.0%	96.1%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVESTDTAIEPVYPGCDYKTVAALMMDPRDEDSLEIRHNGEFSN
14	100.0%	95.7%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVESTDTAIEPVYPGCDYKTVAALMMDPRDEDSLEIRHNGEFSN
15	100.0%	97.2%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKVDISSVEPTDTAIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN
16	100.0%	99.9%	LQSSAIFRLDTHHLPETRRPLHFDIPSSLPTKADISGAEPDTSIEPVYPGCDYKTVAALMMEPRDEDSLEIRHNGEFSN



17	AB186123.1	99.9%	97.5%	LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKVDISSAEPDTDAIEPVYPGCDYKIVAALMMEPRDEDSLEIRHGEFSN
18	KJ433990	100.0%	97.5%	LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKVDISSVEPTDTAIEPVYPGCDYKIVAALMMEPRDEDSLEIRHGEFSN
19	AB624361.1	100.0%	97.3%	LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKVDISSAEPDTDSIEPVYPGCDYKIVAALMMEPRDEDSLEIRHGEFSN
	consensus/100%			LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKSDISSSESTDTAIEPVYPGCDYKIVAALMM-PRSEDSLEIRHGEFSN
	consensus/90%			LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKSDISSSESTDTAIEPVYPGCDYKIVAALMM-PRDEDSLEIRHGEFSN
	consensus/80%			LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKVDISSSEPTDTAIEPVYPGCDYKIVAALMMEPRDEDSLEIRHGEFSN
	consensus/70%			LQSSAIFRLDTHHLPETRRPLHFDIFSSLPTKVDISSVEPTDTAIEPVYPGCDYKIVAALMMEPRDEDSLEIRHGEFSN
		cov	pid 1281	. 3 . . . . :
1	DRR068690	100.0%	100.0%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
2	DRR068691	100.0%	96.8%	QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
3	DRR006265	100.0%	97.2%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
4	DRR039989	99.9%	97.1%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
5	DRR079253	99.9%	97.2%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
6	SRR6324419-24	100.0%	95.4%	QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
7	SRR11781560-1	100.0%	95.5%	QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
8	SRR5458683	100.0%	97.2%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
9	DRR023337+40	100.0%	97.1%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
10	SRR1333837-38	100.0%	97.2%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
11	DRR241076	100.0%	98.5%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
12	SRR17258733	100.0%	97.3%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
13	SRR24542361	100.0%	96.1%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
14	SRR17258732	100.0%	95.7%	QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
15	SRR9685281	100.0%	97.2%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
16	DRR035925	100.0%	99.9%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
17	AB186123.1	99.9%	97.5%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
18	KJ433990	100.0%	97.5%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
19	AB624361.1	100.0%	97.3%	QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
	consensus/100%			QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
	consensus/90%			QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
	consensus/80%			QFPWVDLEFYENGAQTLSVIAPKHDSKNDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
	consensus/70%			QFPWVDLEFYENGAQTLSVIAPKHDSKYDPTLLSASIAKRLRFRPSELFYRLSPSDEVLGTFLLFSSLCRAYKRHPNHKVVF
		cov	pid 1361	. . . 4 . . . . 1440
1	DRR068690	100.0%	100.0%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
2	DRR068691	100.0%	96.8%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
3	DRR006265	100.0%	97.2%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
4	DRR039989	99.9%	97.1%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
5	DRR079253	99.9%	97.2%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
6	SRR6324419-24	100.0%	95.4%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
7	SRR11781560-1	100.0%	95.5%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
8	SRR5458683	100.0%	97.2%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
9	DRR023337+40	100.0%	97.1%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI
10	SRR1333837-38	100.0%	97.2%	QPDLFVEICINLNEYSQISNKTQAVIQANANRSDPDWRYTAVRIEAKTQHKINEGSI FGPWKACQTLALMMDAIVLIFGPI

11	DRR241076	100.0%	98.5%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFAKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
12	SRR17258733	100.0%	97.3%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
13	SRR24542361	100.0%	96.1%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
14	SRR17258732	100.0%	95.7%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
15	SRR9685281	100.0%	97.2%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
16	DRR035925	100.0%	99.9%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFAKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
17	AB186123.1	99.9%	97.5%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
18	KJ433990	100.0%	97.5%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
19	AB624361.1	100.0%	97.3%	QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFAKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
	consensus/100%			QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFUKT	QHKINEGS	IFGPWK	ACQTLALM	HDSIVL	IFGPI
	consensus/90%			QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFUKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
	consensus/80%			QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFUKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
	consensus/70%			QPDLFVE	CINLNEYS	QISNKTQ	AVIQANANR	SDPDWRYT	AVRIFSKT	QHKINEGS	IFGPWK	ACQTLALM	HDAIVL	IFGPI
		cov	pid	1441	:	.	.	.	.	.	5	.	.	1520
1	DRR068690	100.0%	100.0%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
2	DRR068691	100.0%	96.8%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
3	DRR006265	100.0%	97.2%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
4	DRR039989	99.9%	97.1%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
5	DRR079253	99.9%	97.2%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
6	SRR6324419-24	100.0%	95.4%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
7	SRR11781560-1	100.0%	95.5%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
8	SRR5458683	100.0%	97.2%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
9	DRR023337+40	100.0%	97.1%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
10	SRR1333837-38	100.0%	97.2%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
11	DRR241076	100.0%	98.5%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
12	SRR17258733	100.0%	97.3%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
13	SRR24542361	100.0%	96.1%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
14	SRR17258732	100.0%	95.7%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
15	SRR9685281	100.0%	97.2%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
16	DRR035925	100.0%	99.9%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
17	AB186123.1	99.9%	97.5%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
18	KJ433990	100.0%	97.5%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
19	AB624361.1	100.0%	97.3%	KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
	consensus/100%			KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
	consensus/90%			KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
	consensus/80%			KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
	consensus/70%			KKYQR	VFDSKDR	PPNLFV	YGGQTPYD	LSRFAS	SHLKPLQ	IHVCNDY	SAFDQ	SOHCE	AVVLER	KKMERLS
		cov	pid	1521	:	.	.	.	.	.	.	.	.	1600
1	DRR068690	100.0%	100.0%	IKTNI	TSQFGL	PTCMRL	TGEPG	TYDDNT	DYNI	AVIYSEY	DITTQ	TFEV	SGD	SLVSPPP
2	DRR068691	100.0%	96.8%	IKTNI	TSQFGL	PTCMRL	TGEPG	TYDDNT	DYNI	AVIYSEY	DITTQ	TFEV	SGD	SLVSPPP
3	DRR006265	100.0%	97.2%	IKTNI	TSQFGL	PTCMRL	TGEPG	TYDDNT	DYNI	AVIYSEY	DITTQ	TFEV	SGD	SLVSPPP
4	DRR039989	99.9%	97.1%	IKTNI	TSQFGL	PTCMRL	TGEPG	TYDDNT	DYNI	AVIYSEY	DITTQ	TFEV	SGD	SLVSPPP



		cov	pid	1681	.	7	.	.	.	:	] 1760
1	DRR068690	100.0%	100.0%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
2	DRR068691	100.0%	96.8%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
3	DRR006265	100.0%	97.2%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
4	DRR039989	99.9%	97.1%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
5	DRR079253	99.9%	97.2%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
6	SRR6324419-24	100.0%	95.4%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
7	SRR11781560-1	100.0%	95.5%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
8	SRR5458683	100.0%	97.2%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
9	DRR023337+40	100.0%	97.1%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
10	SRR1333837-38	100.0%	97.2%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
11	DRR241076	100.0%	98.5%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
12	SRR17258733	100.0%	97.3%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
13	SRR24542361	100.0%	96.1%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
14	SRR17258732	100.0%	95.7%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
15	SRR9685281	100.0%	97.2%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
16	DRR035925	100.0%	99.9%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
17	AB186123.1	99.9%	97.5%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
18	KJ433990	100.0%	97.5%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
19	AB624361.1	100.0%	97.3%	SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
	consensus/100%			SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
	consensus/90%			SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
	consensus/80%			SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							
	consensus/70%			SKEQKLALKIGEVPEHLCQTMLSLGFSWLSRPLYALLDRTARLRLLARTRFAPLFSDFSVEGVLIQIDF-----							