

Table S1. Nimaviral genomes used in this study.

Virus	Abbreviation	Accession	Length	GC%	CDS	Completeness
Marsupenaeus japonicus endogenous nimavirus	MjeNMV	LC738868.1	306,008	33	111	Complete
Melicertus latisulcatus majanivirus	MelaMJNV	LC738874.1	287,061	32	104	Complete
Metapenaeopsis lamellata majanivirus	MetlamMJNV	AP027153.1	267951	27	106	Complete
Penaeus monodon majanivirus A	PemoMJNVA	LC738870.1	294144	40	115	Complete
Penaeus monodon majanivirus B	PemoMJNVB	LC738871.1	360,489	35	114	Complete
Litopenaeus vannamei majanivirus	LvMJNV	LC738872.1	280452	35	119	Complete
Penaeus semisulcatus majanivirus	PeseMJNV	LC738873.1	291934	42	110	Complete
Metapenaeus ensis majanivirus	MeenMJNV	LC738876.1	292,272	29	101	Complete
Metapenaeus joyneri majanivirus	MejoMJNV	LC738878.1	401182	26	124	Complete
Trachysalambria curvirostris majanivirus	TrcuMJNV	LC738879.1	283150	28	101	Complete
Marsupenaeus japonicus pemonivirus	MjPMNV	AP027202.1	323944	48	102	Complete
Melicertus latisulcatus pemonivirus	MelaPMNV	LC738875.1	359647	48	109	Complete
Penaeus monodon endogenous nimavirus	PmeNMV	LC738869.1	300002	45	94	Complete
Penaeus semisulcatus pemonivirus	PesePMNV	AP027152.1	277334	43	102	Complete
Hemigrapsus takanoi nimavirus	HtNMV	LC738882.1	251731	47	111	Coding-complete
Trachysalambria curvirostris nimavirus	TrcuNMV	LC738880.1	331684	47	107	Complete
Sesarmops intermedium nimavirus	SiNMV	LC738884.1	267936	44	104	Complete
Chiromantes dehaani nimavirus	CdNMV	AP027155.1	285096	44	99	Complete
Metapenaeus ensis nimavirus	MeNMV	LC738877.1	341,283	44	117	Complete
Sicyonia whispovirus	SicyWSV	LC738881.1	347,493	54	89	Complete
Pasiphaea japonica whispovirus	PajaWSV	LC738885.1	276272	35	86	Complete
Chionoecetes opilio bacilliform virus	CoBV	LC741431.1	243979	40	105	Complete
White spot syndrome virus	WSSV	NC_003225.3	309286	41	177	Complete

Table S2. ANI matrix for closely related penaeid endogenous nimavirus MAGs (1).

ANI	MjeNMV	MlMJNV	PemoMJNVA	PeseMJNV	PemoMJNVB
MjeNMV	100%	97.50%	--	--	--
MlMJNV	97.50%	100%	--	--	--
PemoMJNVA	--	--	100%	92.89%	81.01%
PeseMJNV	--	--	92.89%	100%	80.63%
PemoMJNVB	--	--	81.01%	80.63%	100%

See Table S1 for the abbreviations of the virus names. --: ANI undetermined (too few matches to meet the threshold defined by ani.rb).

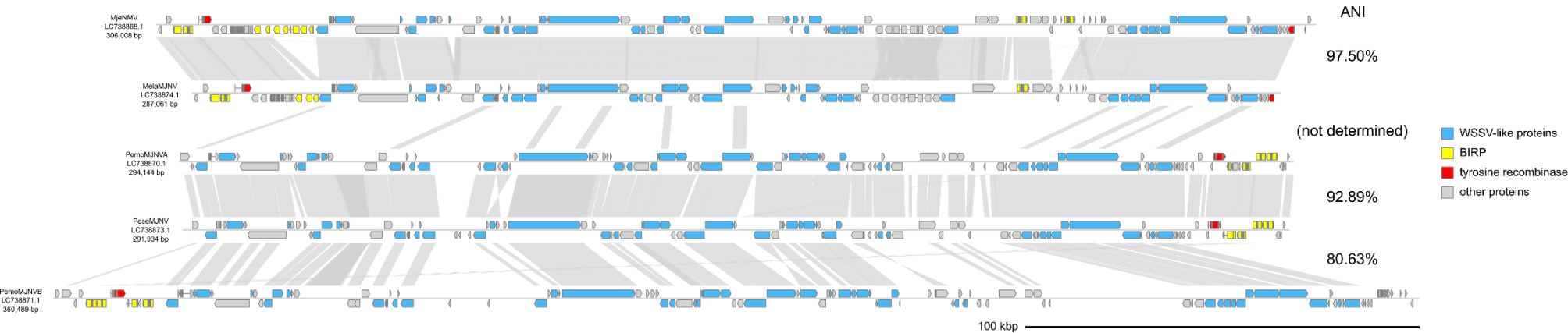


Figure S1. Genome diagrams of closely related penaeid endogenous nimavirus MAGs (1). Arrows indicate predicted genes and their transcriptional orientations. Gray ribbons indicate pairwise BLASTN hits (e-value :1–e20, bitscore: 1000, identity: 70%). See Table S1 for the abbreviations of the virus names.

Table S3. ANI matrix for closely related penaeid endogenous nimavirus MAGs (2).

ANI	PmeNMV	PesePMNV	MjPMNV	MlPMNV
PmeNMV	100%	81.34%	75.75%	--
PesePMNV	81.34%	100%	--	--
MjPMNV	75.75%	--	100%	96.29%
MlPMNV	--	--	96.29%	100%

See Table S1 for the abbreviations of the virus names. --: ANI undetermined (too few matches to meet the threshold defined by ani.rb).

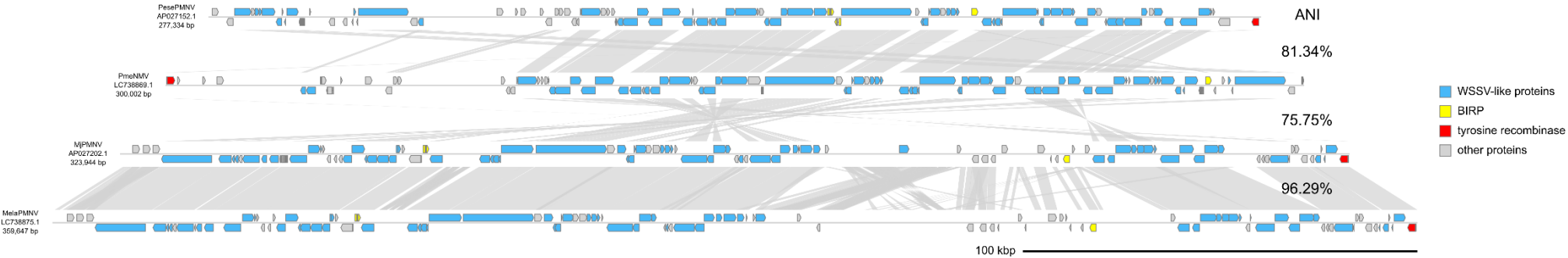


Figure S2. Genome diagrams of closely related penaeid endogenous nimavirus MAGs (2).

Arrows indicate predicted genes and their transcriptional orientations. Gray ribbons indicate pairwise BLASTN hits (e-value :1–e20, bitscore: 1000, identity: 70%). See Table S1 for the abbreviations of the virus names.

Table S4. ANI matrix for closely related sesarmid endogenous nimavirus MAGs.

ANI	SiNMV	CdNMV
SiNMV	100%	95.11%
CdNMV	95.11%	100%

See Table S1 for the abbreviations of the virus names.

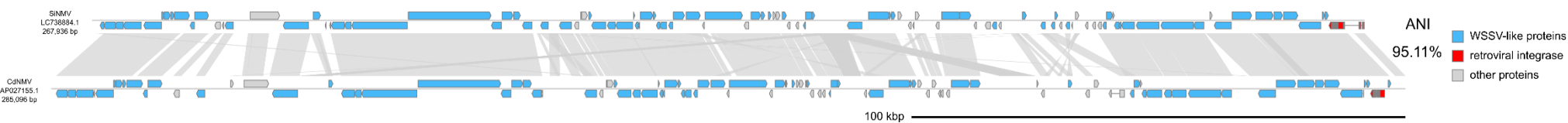


Figure S4. Genome diagrams of closely related sesarmid endogenous nimavirus MAGs.

Arrows indicate predicted genes and their transcriptional orientations. Gray ribbons indicate pairwise BLASTN hits (e-value :1–e20, bitscore: 1000, identity: 70%). See Table S1 for the abbreviations of the virus names.