

Table S1: Data of the principal component analysis with the Varimax rotation method. Correlations higher than 0.5 are in bold.

		Component	
		1	2
Gene	<i>rdrp</i>	-0.028	0.687
	<i>cp</i>	-0.053	0.659
	<i>mx</i>	0.946	-0.068
	<i>mda5</i>	0.924	0.199
	<i>hsp70</i>	0.933	0.106
	<i>il1b</i>	0.414	0.511
	<i>il8</i>	0.261	0.58
	<i>nccrp1</i>	0.750	0.405
	<i>hamp</i>	0.289	-0.67
	<i>nkl</i>	0.874	-0.253
	<i>prf</i>	0.901	-0.254
	<i>gzma</i>	0.901	0.194
	<i>gzmb</i>	0.964	-0.055
Survival		-0.746	-0.535

Table S2: Primers used for real-time PCR analysis.

Gene name	Gene abbreviation	Accession number	Primer sequence (5' → 3')
Nodavirus RNA-dependent polymerase	<i>rdrp</i>	AF319555	GTGTCCGGAGAGGTTAAGGATG CTTGAATTGATCAACGGTGAACA
Nodavirus coat protein	<i>cp</i>	D38636	CAACTGACAACGATCACACCTTC CAATCGAACACTCCAGCGACA
Elongation factor 1 alpha	<i>ef1a</i>	AF184170	CTTCAACGCTCAGGTCATCAT GCACAGCGAAACGACCAAGGGGA
Interferon-induced protein Mx	<i>mx</i>	FJ490556 FJ490555 FJ652200	AAGAGGAGGACGAGGAGGAG CATCCCAGATCCTGGTCAGT
Melanoma differentiation-associated protein 5	<i>mda5</i>	HS988207	CATCGAGATCATCGAGGACA CCAGATGTCGCTCTTGAAGG
Interleukin 1 beta	<i>il1b</i>	AJ277166	GGGCTGAACAACAGCACTCTC TTAACACTCTCCACCCTCCA
Interleukin 8	<i>il8</i>	AM765841	GCCACTCTGAAGAGGACAGG TTTGTTGTCTTTGGTCGAA
Heat-shock protein 70	<i>hsp70</i>	EU805481	AATGTTCTGCGCATCATCAA GCCTCCACCAAGATCAAAGA
Non-specific cytotoxic cell receptor protein 1	<i>nccrp1</i>	AY651258	ACTTCCTGCACCGACTCAAG TAGGAGCTGGTTTTGGTTGG
Granzyme A	<i>gzma</i>	MK568066	GCTGCTCGGAGTCACTTCTT GGATCCAGGTGAGCTGCTTT
Granzyme B	<i>gzmb</i>	AM957224	GAAACAAAGGAACGGGTCAA GAGCTGTCCATCTTTTGCTTG
Perforin	<i>prf</i>	AM950868	CAGACCATGAGGGGAACACT TGGAACCATGCAACACCTTA
NK-lysin	<i>nkl</i>	MN240490	CGCACCTCGGAGAACTGATT TCCACGTCGCTTCGGTAAAA
Hepcidin	<i>hamp</i>	CB184616	GCCATCGTGCTCACCTTTAT CTGTTGCCATACCCCATCTT