

Table. S1. Sequence information for primers used in this study.

Gene	GenBank accession no.	Primer Sequence (5'-> 3')
IHNV-G	NC_001652.1	F: CACGGAAACAACACCACCATTA R: AACAGCAAGGAGGAGAACAAGG
<i>EF1a</i>	NM_001124339.1	F: CAACGATATCCGTCGTGGCA R: ACAGCGAAACGACCAAGAGG
<i>β-actin</i>	XM_036973727.1	F: CCGCGACCTCACAGACTACC R: GTGCCCATCTCCTGCTCAAA
<i>mx1</i>	XM_021567440.1	F: GATGCTGCACCTCAAGTCCTACTA R: CGGATCACCATGGGAATCTGA
<i>ddx58</i>	XM_036973405.1	F: CAGAGGTACTACAGGAAATGG R: TTACTGGTCTTCAAGCAATG
<i>dhx58</i>	XM_036940961.1	F: AGTTTGGCACGCAGGAGTA R: CAAGCAGGAAGAAGTCGGT
<i>stat1</i>	XM_021579196.2	F: CTCATCCCCTGGACCAAGTT R: TTATTGTAGCCCTCCACCCA
<i>ifih1</i>	NM_001195179.1	F: CAGTGGAGATGACGATGGG R: ACTTGGCGTTCTTGTGCTT
<i>tlr3</i>	NM_001124578.1	F: GGGAAATCTGACACGGCTCAA R: GGAGACTCATCAAACCCGCA
<i>c3</i>	XM_036947707.1	F: AGAAGGTGGGAGGGGGATAC R: ACTTGGTGACTGATGCCCTG
<i>il6</i>	CCV01624.1	F: ATTTTCATCGTTCTCACAGC R: ACTACCTCAGCAACCTTCA
<i>cath1</i>	NM_001124480.1	F: CTGGAGGCAAGCAACAAC R: CCCCCAAGACGAGAGACA
<i>vig1</i>	NM_001124253.1	F: CAGGCCAGGTGAAGACTAGTAA R: GCTGCAAAGATGCACTGGAG
<i>saa5</i>	XM_021586448.2	F: CGAGGACATGAGGACTCAGC R: TGTTTGGATTGTGGTCCTTTCA
<i>mx2</i>	NM_001124751.1	F: AGGGAGTTGGAAAGGGTTACCT R: CCAGACGCTGACTGGCAATA
<i>gig2e</i>	XM_036944105.1	F: GGAATGCAGAACCATGTGGC R: TTTTCCTGTGCCTTCGCAGA
<i>ccl19a.1</i>	XM_036936451.1	F: ACGTCTGCTACCAGGTGACT R: CCCCTAACCTGAGGCTGGTA
<i>cd209</i>	NM_001124633.1	F: GCCGTGTGACCACATCTACA R: AACCGAGTTCAGTTCCCAGT
<i>legumain</i>	XM_036955355.1	F: CGGGCGATAACCACGAGAAT R: GTCTACTCGGACCCCTCCTT
<i>stat1b</i>	XM_021579195.2	F: CGCAACTACAAGGTGATGGC R: CGATGGGGCAAGACTACCAAT

Table. S2. Summary of sequencing and assembly statistics for the transcriptome data.

Sample	Raw Reads Number	Clean Reads Number	Clean Reads Rate(%)	Q20 rate(%)	Q30 rate(%)	GC content	Total mapped
Control 1	49371190	44388328	89.9	96.97	93.04	48.8	40099894 (90.34%)
Control 2	46036276	41676344	90.52	96.85	92.81	49.16	37561300 (90.13%)
Control 3	48273392	43388684	89.88	96.63	92.47	48.69	39029723 (89.95%)
4 dpi_1	52559076	47391380	90.16	96.57	92.25	48.05	42040879 (88.71%)
4 dpi_2	54021116	48408900	89.61	96.93	92.99	48.78	43713489 (90.30%)
4 dpi_3	44734772	39769710	88.9	97.07	93.21	47.53	35662480 (89.67%)
14 dpi_1	50206686	45734156	91.09	97.43	93.73	48.81	41857943 (91.52%)
14 dpi_2	50728900	45820868	90.32	96.96	92.93	48.64	41299349 (90.13%)
14 dpi_3	45721264	41230876	90.17	96.99	92.9	48.72	37243327 (90.33%)

Table. S3. The statistical results of Anosim and Permanova.

	Anosim		Permanova	
	R-value	P-value	Pseudo-F	P-value
Control-4 dpi	0.661111	0.001	6.028944	0.003
Control-14 dpi	0.747093	0.001	8.636558	0.001
4 dpi-14 dpi	0.312016	0.003	1.887767	0.014
All	0.579937	0.001	5.28605	0.001

Table. S6. Significant differences of different taxa determined by non-parametric analysis using the Kruskal-Wallis test followed by Mann-Whitney test.

Level	Taxa	Kruskal-Wallis (p value)	Mann-Whitney test	
			4 dpi vs Con	14 dpi vs Con
Phylum	Proteobacteria	0.0002	**	***
	Actinobacteria	0.0037	*	**
	Firmicutes	0.2594	ns	ns
	Bacteroidetes	0.1412	ns	ns
	Cyanobacteria	0.8694	ns	ns
	Verrucomicrobia	0.2201	ns	ns
	Acidobacteria	0.8470	ns	ns
	[Thermi]	0.0193	ns	ns
	Thermotogae	0.5587	ns	ns
	Fusobacteria	0.5261	ns	ns
Order	Actinomycetales	0.0037	*	**
	Rickettsiales	0.0001	**	***
	Vibrionales	0.0151	ns	*
	Pseudomonadales	0.1494	ns	ns
	Oceanospirillales	0.1842	ns	ns
	Lactobacillales	0.4429	ns	ns
	Burkholderiales	0.5099	ns	ns
	Flavobacteriales	0.0481	ns	ns
	Bacillales	0.5689	ns	ns
	Clostridiales	0.0430	ns	*
Genus	<i>Rhodococcus</i>	0.0123	*	*
	<i>Vibrio</i>	0.0085	ns	*
	<i>Halomonas</i>	0.1530	ns	ns
	<i>Acinetobacter</i>	0.0008	ns	*
	<i>Streptococcus</i>	0.9989	ns	ns
	<i>Pseudoalteromonas</i>	0.0579	ns	*
	<i>Paracoccus</i>	0.3679	ns	ns
	<i>Corynebacterium</i>	0.8013	ns	ns
	<i>Salinivibrio</i>	0.7175	ns	ns
	<i>Flavobacterium</i>	0.0105	ns	*
	<i>Lactobacillus</i>	0.2505	ns	ns
	<i>Bacillus</i>	0.2889	ns	ns
	<i>Arthrobacter</i>	0.1346	ns	ns
	<i>Brevibacterium</i>	0.0842	ns	ns
	<i>Uruburuella</i>	0.0045	ns	**
	<i>Aeromonas</i>	0.7487	ns	ns
	<i>Acidovorax</i>	0.3359	ns	ns
	<i>Bacteroides</i>	0.0573	ns	*
	<i>Rubritalea</i>	0.4835	ns	ns
	<i>Chryseobacterium</i>	0.0011	ns	*