

Table S1. Quality of the RNA

Sample name	28s/18s	RIN	Concentration (ng/μl)	260/230	260/280
Control Head kidney 1	1.53	9.2	852.84	2.31	2.07
Control Head kidney 2	0.90	7.8	955.81	2.19	2.06
Control Head kidney 3	1.48	9.3	299.9	2.24	2.05
3 dpi Head kidney 1	1.12	8.7	280.09	1.29	2.07
3 dpi Head kidney 2	0.65	6.8	847.86	2.1	2.09
3 dpi Head kidney 3	0.91	8.2	227.22	1.67	2.08
10 dpi Head kidney 1	1.11	8.7	229.25	1.79	2.02
10 dpi Head kidney 2	1.36	9	225.24	1.51	2.06
10 dpi Head kidney 3	0.50	5.4	1083.98	2.33	2.00
Control Spleen 1	0.94	7.6	356.49	1.52	2.03
Control Spleen 2	1.66	8.6	366.55	2.16	2.05
Control Spleen 3	1.08	8.7	286.33	2.05	2.05
3 dpi Spleen 1	1.42	9.2	521.28	1.98	2.08
3 dpi Spleen 2	1.67	9.5	339.04	1.56	2.04
3 dpi Spleen 3	1.62	9	470.4	2.33	1.95
10 dpi Spleen 1	1.01	6.8	875.61	2.31	2.05
10 dpi Spleen 2	0.81	6.7	687.89	2.27	2.05
10 dpi Spleen 3	1.30	8.7	639.58	1.91	2.06
Control Liver 1	1.18	8.6	346.84	1.52	2.03
Control Liver 2	1.7	7.6	356.49	2.16	2.05
Control Liver 3	1.32	10	912.41	2.05	2.05
3 dpi Liver 1	0.56	7.3	927.85	1.46	2.08
3 dpi Liver 2	1.62	9.6	586.1	1.85	2.09
3 dpi Liver 3	1.65	9.5	466.16	2.09	1.99
10 dpi Liver 1	1.13	8.7	780.28	2.23	2.06
10 dpi Liver 2	1.04	7.4	1351.75	2.33	2.05
10 dpi Liver 3	1.81	9.8	522.96	1.96	2.08

Table S2. Primers used in this study

Gene name (<i>Gene symbol</i>) (Trinity ID)	Nucleotide sequence (5'-3')	Efficiency (%)	Amplicon size (bp)
complement component 6 (<i>c6</i>) (DN137_c0_g1_i25)	F: CTGTCACCCCTCCACAGAGT	98.8	100
	R: GTTGCATGTCAGCGTTGAGT		
C-X-C motif chemokine receptor 3 (LOC117745182 / <i>cxcr3</i>)	F: AGAGTTCACCTGTGGGGGTTG	93.9	106
(DN2498_c0_g1_i8)	R: GACTGCACCTGGTGACCTTT		
galectin-3-binding protein (LOC117735282/ <i>igals3bp</i>) (DN1760_c1_g1_i3)	F: GTGCCTCAGAACGGTCTCTC	96	114
	R: GGCCATGTTGTCCTTGAAGT		
glutathione S-transferase alpha 4 (<i>gsta4.1</i>)	F: CCTATGGTGGAATGGATGG	92.9	108
(DN1192_c0_g1_i2)	R: CATGACCCGGTCTTTGAGAT		
hepcidin anti-microbial peptide b (LOC117728128 / <i>hampb</i>) (DN2492_c0_g1_i7)	F: CGTCGTGCTCACCTTCATTT	91.9	95
	R: CTGGGTTGTCAACGCTCAT		
interleukin 1 receptor type 2 (LOC117750249/ <i>il1r2</i>) (DN49226_c0_g1_i2)	F: CTCATTGATGAGCGGCAGTA	92.5	111
	R: GGGGTCAGAGGTCACAGAGA		
interleukin 8b (<i>il8b</i>) alias C-X-C motif chemokine ligand 8b (<i>cxc18b</i>)	F: GTCTGAGAAGCCTGGGAGTG	87.4	138
(DN2906_c0_g1_i1)	R: TCAGAGTGGCAATGATCTCG		

BPI fold-containing family C- like (<i>bpifcl</i>) (DN1675_c0_g2_i3)	F: GTTTCCCGGACTTCTGATGA	95.7	130
	R: GGTACCATTGTGGTTGGATGG		
pentraxin 3 (<i>ptx3a</i>)	F: GCCTCAAACCCAGAGATCAG	90	105
(DN6917_c2_g1_i1)	R: GTCGGGAAGTTTGCATTTGT		
ras-related protein ORAB-1 (LOC117743939/ <i>orab1</i>) (DN1973_c0_g3_i2)	F: ACAGGAGATCGACCGCTATG	92.4	117
	R: GAGTCTGCGAACTCCTTTGC		
serum amyloid A 5 (LOC117728776/ <i>saa5</i>) (DN17527_c0_g1_i1)	F: AGAGTGGGTGCAGGAAAGAA	92.1	116
	R: GAAGTCCTGGTGGCCTGTAA		
suppressor of cytokine signaling 3 (<i>socs3a</i>) (DN488_c0_g1_i2)	F: CATGCCTCAGAGCAAAGTGA	93.7	104
	R: AGCTGCAGGAGAGAGGTCTG		
TNF receptor superfamily member 9 (LOC117733297/ <i>tnfrsf9</i>) (DN2095_c0_g3_i4)	F: AGGAGAAGAAAAGCCGATCC	94.4	115
	R: CTCGTGGAAACTGCACTCAA		
toll-like receptor 5a (LOC117727165/ <i>tlr5a</i>) (DN8688_c0_g1_i1)	F: TGGACGAGTTTCAGCAGTTG	92.9	129

Table S3. Trimming and mapping statistics.

Experimental conditions	Number of reads before trim	Number of reads after trim	Percentage trimmed (%)	Number of mapped reads	% of mapped reads
HK1 control	90,833,894	89,460,642	98.49	88,772,934	99.23127
HK2 control	82,357,896	81,214,335	98.61	80,651,238	99.30665
HK3 control	95,840,032	94,471,719	98.57	93,794,340	99.28298
HK1 3 dpi	85,364,678	84,249,691	98.69	83,689,892	99.33555
HK2 3 dpi	69,166,462	68,321,181	98.78	67,915,962	99.40689
HK3 3 dpi	83,210,266	82,006,542	98.55	81,417,744	99.28201
HK1 10 dpi	74,687,068	73,641,866	98.6	80,640,940	109.5042
HK2 10 dpi	75,696,762	74,572,712	98.52	73,123,686	98.0569
HK3 10 dpi	83,134,430	81,500,846	98.04	74,020,234	90.82143
LV1 control	75,238,962	74,186,108	98.6	73,667,016	99.30028
LV2 control	82,613,962	81,592,390	98.76	81,097,032	99.39289
LV3 control	89,149,382	87,873,344	98.57	87,249,434	99.28999
LV1 3 dpi	73,482,382	72,624,442	98.83	72,205,844	99.42361
LV2 3 dpi	76,781,706	75,902,586	98.86	75,475,798	99.43772
LV3 3 dpi	78,365,294	77,336,892	98.69	76,810,090	99.31882
LV1 10 dpi	66,590,420	65,684,895	98.64	73,681,162	112.1737
LV2 10 dpi	84,053,066	82,945,239	98.68	72,873,446	87.8573
LV3 10 dpi	72,837,270	71,790,152	98.56	69,948,408	97.43455
SL1 control	82,894,516	81,638,490	98.48	81,023,884	99.24716
SL2 control	85,830,500	84,711,276	98.7	84,168,702	99.3595
SL3 control	80,510,892	79,352,845	98.56	78,781,698	99.28024
SL1 3 dpi	67,505,126	66,241,078	98.13	65,565,504	98.98013
SL2 3 dpi	95,481,322	94,028,713	98.48	93,300,368	99.2254
SL3 3 dpi	79,665,640	78,523,117	98.57	77,967,908	99.29294
SL1 10 dpi	75,150,950	74,159,068	98.68	65,230,402	87.96012
SL2 10 dpi	74,330,220	73,364,626	98.7	82,383,274	112.2929

SL3_10 dpi	71,265,916	70,388,130	98.77	71,286,900	101.2769
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Table S4. Trinity statistics

Total trinity transcripts	403204
Total trinity genes	270150
Percent GC	45.99
Contig N10	9165
Contig N20	6690
Contig N30	5231
Contig N40	4164
Contig N50	3235
Median contig length	497
Average contig	1296.15
Total assembled bases	522614427

Table S5. Alignment statistics

Sample name	Aligned concordantly exactly 1 time	Aligned concordantly >1 times	Overall alignment rate (%)
Control Head kidney 1	6056815 (14%)	33309331 (76.98%)	97.92
Control Head kidney 2	5561239 (14.17%)	30303899 (77.21%)	97.99
Control Head kidney 3	5823611 (12.66%)	36266811 (78.81%)	98.2
3 dpi Head kidney 1	5995555 (14.67%)	31412470 (76.87%)	97.79

3 dpi Head kidney 2	4668466 (14.02%)	26009476 (78.11%)	98.16
3 dpi Head kidney 3	5534685 (13.99%)	30610945 (77.4%)	97.93
10 dpi Head kidney 1	6204518 (15.73%)	28809529 (73.06%)	96.6
10 dpi Head kidney 2	4851800 (13.56%)	27816099 (77.73%)	97.66
10 dpi Head kidney 3	4818814 (13.3%)	28270093 (78.02%)	98.01
Control Spleen 1	4935796 (13.74%)	27895313 (77.64%)	97.95
Control Spleen 2	4769616 (11.99%)	31464709 (79.13%)	98.33
Control Spleen 3	5384352 (12.62%)	33497395 (78.51%)	98.1
3 dpi Spleen 1	5420901 (15.39%)	26700202 (75.8%)	97.82
3 dpi Spleen 2	5093933 (13.8%)	28863984 (78.17%)	98.12
3 dpi Spleen 3	5421149 (14.45%)	28750313 (76.62%)	97.88
10 dpi Spleen 1	5355795 (14.93%)	27159109 (75.71%)	97.73
10 dpi Spleen 2	5198840 (14.71%)	26876759 (76.07%)	97.81
10 dpi Spleen 3	5145686 (15.11%)	25916830 (76.1%)	97.83
Control Liver 1	4775243 (12.14%)	31337959 (79.64%)	98.18
Control Liver 2	5060475 (12.24%)	33095542 (80.03%)	98.29
Control Liver 3	3988922 (10.35%)	31537686 (81.8%)	98.49
3 dpi Liver 1	3499716 (10.92%)	25588309 (79.87%)	97.92
3 dpi Liver 2	4756240 (10.41%)	37275425 (81.56%)	98.44
3 dpi Liver 3	5063196 (10.72%)	38469695 (81.42%)	98.67
10 dpi Liver 1	3473492 (10.91%)	25995568 (81.64%)	98.55
10 dpi Liver 2	4197048 (10.44%)	33072408 (82.25%)	98.52
10 dpi Liver 3	3454200 (9.93%)	28709153 (82.54%)	98.5