

## Supplemental Tables

**Table S1 Sequences of primers used for quantitative real-time PCR.**

Gene		Sequence (5'- 3')
C2	Forward	GCATATTCACACAGAGAGTCAGAGG
	Reverse	AGTCACATCAGTGGGCTGTTTAG
CCL2	Forward	TGCTGTCTCCTGCCTCAACTC
	Reverse	TGGACTTGCCTGTTGTAACCT
CCR7	Forward	TCGTTGTCCAAAACAGGACTATGT
	Reverse	TGCTGTGGTGGCTGTGTT
CD8A	Forward	TCTGGTGATTCTGGTGTATGC
	Reverse	TGTGGTTCTGTCCCTCTTACTTC
CSF3	Forward	CAGATGATGATGAGCTCACTGG
	Reverse	TTTCGCACAGAGGTTGAGG
CXCR4	Forward	CAGCCACACACCCACATAGA
	Reverse	AACAGCCAAGCCACAAGAAAG
HMBS	Forward	CTCTACAAACGGACAAGAGC
	Reverse	GATCTTACTGGCCGTGAC
IL10	Forward	GAACAACATCTGGAGTTTACCTG
	Reverse	TGTCCTCGGTTTGGTTATGG
IL12A	Forward	ACGAAACTGCTATCAAGTCC
	Reverse	AGGAGTGCTTCTTCTTGATG

**Table S2. Summary of sequencing reads after filtering**

Sample	Clean reads	Clean Bases	Q20 (%)	Q30 (%)	GC (%)
PBS_head kidney	32.5 M	9.7 G	97.7	93.6	49.7
SI_head kidney	35.1 M	10.5 G	97.7	93.6	49.8
PBS_spleen	39.6 M	11.9 G	97.6	93.4	50.0
SI_spleen	34.4 M	10.3 G	97.6	93.2	49.2

Clean data are read counts filtered from raw data; clean bases: base number of raw data after filtering, (number of clean reads) × (sequence length). Q20: percentage of bases whose Q Phred values are greater than 20, (number of bases with Q Phred value > 20) / (Number of total bases) ×100; Q30: percentage of bases whose Q Phred values are greater than 30, (number of bases with Q Phred value > 30) / (number of total bases) ×100; GC: percentage of G and C bases out of the number of total bases, (G&C base number) / (Total base number) ×100. PBS, phosphate-buffered saline; SI, *Streptococcus iniae*.

**Table S3 Length distribution and quality matrix of *de novo* assembled unigenes**

Sample	Min Length	Mean Length	Median Length	Max Length	N50	N90	Total Unigene
Kidney_Unigene	301	1567	848	25024	2781	590	37655
Spleen_Unigene	301	1574	858	23999	2804	594	39965

N50 and N90: weighted median statistics at which 50% and 90%, respectively, of the total length are contained in transcripts that are greater than or equal to this value.