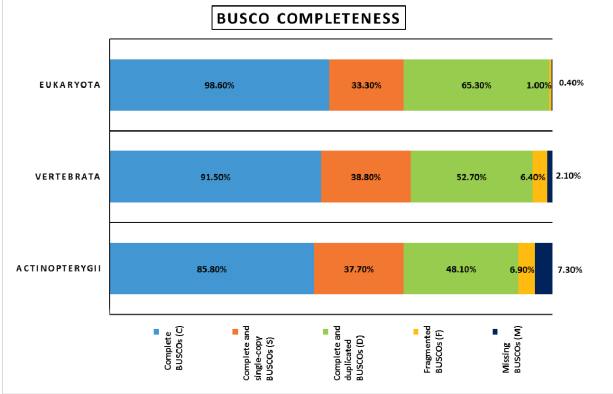
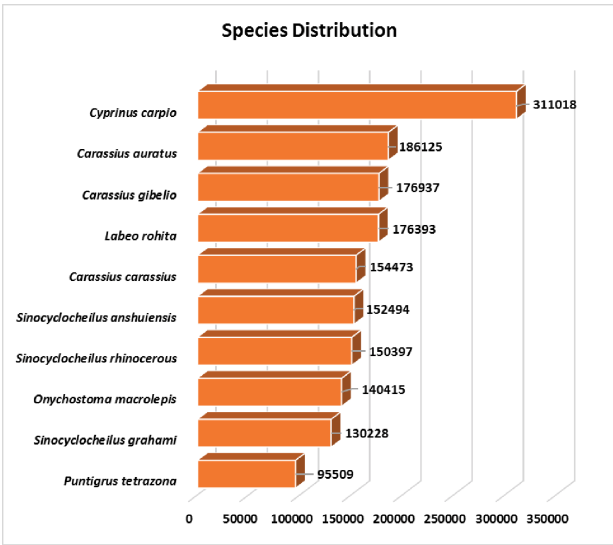


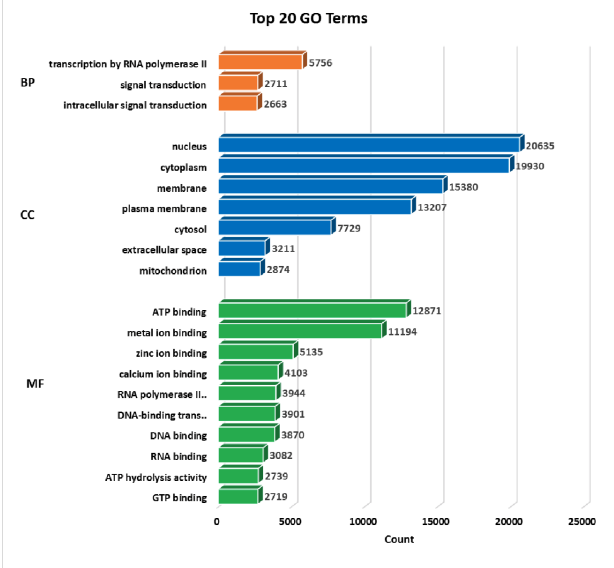
Supplementary Fig. 1. Length distribution of transcriptome of kidney tissue of *Cyprinus carpio*



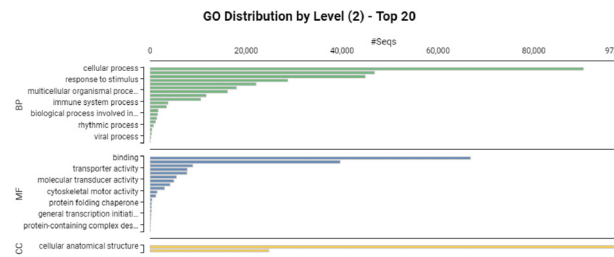
Supplementary Fig. 2. BUSCO result of *Cyprinus carpio* kidney transcriptome



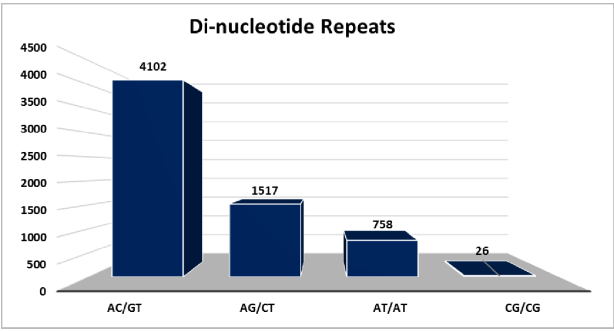
Supplementary Fig. 3. Top 10 species distribution of transcriptome of *Cyprinus carpio* kidney



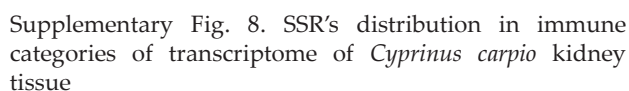
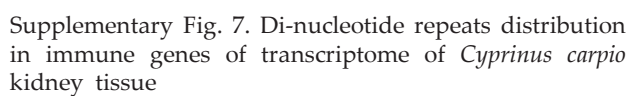
Supplementary Fig. 4. Top 20 Gene Ontology terms of transcriptome of *Cyprinus carpio* kidney



Supplementary Fig. 5. Level 2 Gene Ontology distribution in transcriptome of *Cyprinus carpio* kidney



Supplementary Fig. 6. Di-nucleotide repeats distribution in transcriptome of *Cyprinus carpio* kidney tissue

[illegible]

Supplementary Table 2. Length statistics of kidney tissue transcriptome of *Cyprinus carpio*

LENGTH STATISTICS AND COMPOSITION:	
Number of sequences	133419
Total length (nt)	103037913
Longest sequence (nt)	23272
Shortest sequence (nt)	4
Mean sequence length (nt)	772
Median sequence length (nt)	492
N50 sequence length (nt)	1194
L50 sequence count	24081
Number of sequences > 1K (nt)	31531 (23.6% of total number)
Number of sequences > 10K (nt)	81 (0.1% of total number)
Base composition (%)	A: 26.64 T: 21.73 G: 26.53 C: 25.10 N: 0.00
GC-content (%)	51.63

Supplementary Table 3. Completeness assessment of assembled transcriptome of *Cyprinus carpio* kidney tissue

Completeness Assessment	Eukaryote		Vertebrata		Actinopterygii	
Complete BUSCOs (C)	295	97.40%	2302	89.00%	3849	84.00%
Complete and single-copy BUSCOs (S)	86	28.40%	786	30.40%	1353	29.50%
Complete and duplicated BUSCOs (D)	209	69.00%	1516	58.60%	2496	54.50%
Fragmented BUSCOs (F)	5	1.70%	188	7.30%	364	7.90%
Missing BUSCOs (M)	3	0.90%	96	3.70%	371	8.10%
Total BUSCO groups searched	303		2586		4584	

Supplementary Table 4. Gene Ontology (GO) distribution by Level (2) of *Cyprinus carpio* kidney tissue transcriptome.

GO Distribution by Level (2)	GO-term	Seqs
Biological process		
GO:0009987	Cellular process	90334
GO:0065007	Biological regulation	46776
GO:0050789	Regulation of biological process	44827
GO:0050896	Response to stimulus	28626
GO:0051179	Localization	22043
GO:0032502	Developmental process	17947
GO:0032501	Multicellular organismal process	16130
GO:0048518	Positive regulation of biological process	11641
GO:0048519	Negative regulation of biological process	10495
GO:0002376	Immune system process	3707
GO:0042592	Homeostatic process	3402
GO:0040011	Locomotion	1653
GO:0044419	Biological process involved in interspecies interaction between organisms	1537
GO:0022414	Reproductive process	1332
GO:0040007	Growth	1077
GO:0048511	Rhythmic process	655
GO:0098754	Detoxification	339
GO:0043473	Pigmentation	262
GO:0016032	Viral process	144
GO:0051703	Biological process involved in intraspecies interaction between organisms	13
Molecular function		
GO:0005488	Binding	66757
GO:0003824	Catalytic activity	39572
GO:0098772	Molecular function regulator activity	8828
GO:0005215	Transporter activity	7693
GO:0140110	Transcription regulator activity	7614
GO:0140657	ATP-dependent activity	5460
GO:0060089	Molecular transducer activity	4878
GO:0060090	Molecular adaptor activity	4142
GO:0005198	Structural molecule activity	2971
GO:0003774	Cytoskeletal motor activity	1428
GO:0045182	Translation regulator activity	1138
GO:0140104	Molecular carrier activity	354
GO:0044183	Protein folding chaperone	283
GO:0038024	Cargo receptor activity	258
GO:0016209	Antioxidant activity	236
GO:0140223	General transcription initiation factor activity	177
GO:0009055	Electron transfer activity	119
GO:0141047	Molecular tag activity	54
GO:0140776	Protein-containing complex destabilizing activity	33
GO:0045735	Nutrient reservoir activity	24
Cellular component		
GO:0110165	Cellular anatomical structure	97292
GO:0032991	Protein-containing complex	24676

Supplementary Table 5. KEGG Orthology (KO) count of *Cyprinus carpio* kidney tissue transcriptome

Level I	Level II	Count
Cellular Processes		1446
	Cell growth and death	424
	Cell motility	337
	Cellular community - eukaryotes	376
	Cellular community - prokaryotes	7
	Transport and catabolism	641
Environmental Information Processing		1474
	Membrane transport	37
	Signal transduction	1230
	Signaling molecules and interaction	423
Genetic Information Processing		1165
	Chromosome	126
	Folding, sorting and degradation	378
	Information processing in viruses	79
	Replication and repair	159
	Transcription	165
	Translation	328
Metabolism		1136
	Amino acid metabolism	228
	Biosynthesis of other secondary metabolites	28
	Carbohydrate metabolism	229
	Energy metabolism	151
	Glycan biosynthesis and metabolism	176
	Lipid metabolism	242
	Metabolism of cofactors and vitamins	184
	Metabolism of other amino acids	73
	Metabolism of terpenoids and polyketides	29
	Nucleotide metabolism	106
	Xenobiotics biodegradation and metabolism	62
Organismal Systems		1778
	Aging	103
	Circulatory system	159
	Development and regeneration	242
	Digestive system	282
	Endocrine system	609
	Environmental adaptation	242
	Excretory system	93
	Immune system	630
	Nervous system	352
	Sensory system	101

Supplementary Table 6. Total Simple Sequence Repeats (SSRs) identified in *Cyprinus carpio* Kidney tissue transcriptome

Total number of sequences examined	38891
Total size of examined sequences (bp)	63562618
Total number of identified SSRs	19154
Number of SSR containing sequences	13049
Number of sequences containing more than 1 SSR	4259
Number of SSRs present in compound formation	2083
Mono nucleotide	9742
Di nucleotide	6403
Tri nucleotide	2536
Tetra nucleotide	390
Penta nucleotide	25
Hexa nucleotide	3
Septa nucleotide	3
Octa nucleotide	18
Nona nucleotide	24
Deca nucleotide	10

Supplementary Table 7. Total SSR frequency identified in *Cyprinus carpio* Kidney tissue transcriptome

Repeats	3	4	5	6	7	8	9	10	>10	total	frq
A/T	-	-	-	-	-	-	-	2761	6867	9628	50.27
C/G	-	-	-	-	-	-	-	47	67	114	0.60
Total Mono nucleotide	9742	50.86									
AC/GT	-	-	-	940	553	392	303	246	1668	4102	21.42
AG/CT	-	-	-	621	265	147	77	61	346	1517	7.92
AT/AT	-	-	-	269	163	88	42	35	161	758	3.96
CG/CG	-	-	-	19	5	2			0	26	0.14
Total Di nucleotide	6403	33.43									
ATC/ATG	-	-	242	114	75	41	13	13	11	509	2.66
AGG/CCT	-	-	259	138	43	36			0	476	2.49
AGC/CTG	-	-	285	90	59	25	4		2	465	2.43
AAT/ATT	-	-	199	85	89	27			0	400	2.09
AAG/CTT	-	-	149	67	45	21			0	282	1.47
AAC/GTT	-	-	140	38	26	14			0	218	1.14
ACC/GGT	-	-	74	19	7				0	100	0.52
CCG/CGG	-	-	39	16	1	3			0	59	0.31
ACT/AGT	-	-	11	4	1				0	16	0.08
ACG/CGT	-	-	9	2					0	11	0.06
Total Tri nucleotide	2536	13.24									
AAAC/GTTT	-	-	44	11					0	55	0.29
AAAG/CTTT	-	-	29	10					0	39	0.20
AAAT/ATTT	-	-	41	18					0	59	0.31
AACC/GGTT	-	-		1					0	1	0.01
AACT/AGTT	-	-	1		2	1			1	5	0.03
AAGG/CCTT	-	-	1	1					0	2	0.01
AATC/ATTG	-	-	1	4	1				2	8	0.04
AATG/ATTC	-	-	2	7	1		1	1	0	12	0.06
AATT/AATT	-	-	3						0	3	0.02
ACAG/CTGT	-	-	6	9	3				2	20	0.10
ACAT/ATGT	-	-	7	4		2			1	14	0.07
ACCT/AGGT	-	-	1						0	1	0.01
ACGC/CGTG	-	-	2	2					0	4	0.02
ACGG/CCGT	-	-	1						0	1	0.01
ACTC/AGTG	-	-	7	22		3			0	32	0.17
ACTG/AGTC	-	-	1						0	1	0.01
AGAT/ATCT	-	-	34	25	10	6	5	7	35	122	0.64
AGGC/CCTG	-	-	1						0	1	0.01
AGGG/CCCT	-	-	1						0	1	0.01
ATCC/ATGG	-	-	3	4		1			1	9	0.05
Total Tetra nucleotide	390	2.04									
AAAAC/GTTTT	-	-	2						0	2	0.01
AAAAG/CTTTT	-	-	2						0	2	0.01
AAAAT/ATTTT	-	-	2						0	2	0.01
AAACT/AGTTT	-	-	1			1			0	2	0.01
AACAC/GTGTT	-	-	1						0	1	0.01
AACAG/CTGTT	-	-					1		0	1	0.01
AACCG/CGGTT	-	-	1						0	1	0.01
AAGAC/CTTGT	-	-	1						0	1	0.01
AAGAG/CTCTT	-	-	1						0	1	0.01
AAGTC/ACTTG	-	-	1						0	1	0.01
AATAG/ATTCT	-	-	1	1			1		1	4	0.02
AATCT/AGATT	-	-	2						1	3	0.02
ACCTC/AGGTG	-	-	1						0	1	0.0

ACGAG/CGTCT	-	-	1						0	1	0.01
ACGCG/CGCGT	-	-	1						0	1	0.01
AGATG/ATCTC	-	-	1						0	1	0.01
Total Penta nucleotide	25	0.13									
ACACAG/CTGTGT	-	-	1						0	1	0.01
ACCAGC/CTGGTG	-	-				1			0	1	0.01
AGGATC/ATCCTG	-	-		1					0	1	0.01
Total Hexa nucleotide	3	0.02									
AAGCAGG/CCTGCTT	-	2							0	2	0.01
AAGGGGT/ACCCCTT	-	1							0	1	0.01
Total Septa nucleotide	3	0.02									
AAAAAAAC/GTTTTTTT	2								0	2	0.01
AAAAAAAG/CTTTTTTT	2								0	2	0.01
AAAAAAAT/ATTTTTTT	1								0	1	0.01
AAAACAAC/GTTGTTTT	1								0	1	0.01
AAAATGAC/ATTTTGTC	1								0	1	0.01
AAAATTCT/AATTTTAG	1								0	1	0.01
AAAGAGAG/CTCTCTTT	1								0	1	0.01
AAAGAGAT/ATCTCTTT	1								0	1	0.01
AAGAGAGG/CCTCTCTT	1								0	1	0.01
ACACACTC/AGTGTGTG	3								0	3	0.02
ACAGAGAG/CTCTCTGT	1								0	1	0.01
AGAGAGGG/CCCTCTCT	2								0	2	0.01
AGAGGAGG/CCTCCTCT	1								0	1	0.01
Total Octa nucleotide	18	0.09									
AAAAAAAAT/ATTTTTTTT	1								0	1	0.01
AAAAATAAG/ATTTTTCTT	1								0	1	0.01
AACCACTAC/AGTGGTTGT	1								0	1	0.01
AACGGGGCC/CCCCGTTGG	1								0	1	0.01
AAGAGGATG/ATCCTCTTC	1								0	1	0.01
AAGTGGAGG/ACTTCCTCC	1								0	1	0.01
AATGCCTGG/AGGCATTCC	3								0	3	0.02
AATGGAGTG/ACTCCATTC	1								0	1	0.01
AATGTGCTC/ACATTGAGC	1								0	1	0.01
AATTACTAT/AATTATAGT	1								0	1	0.01
ACCATCACG/ATGGTCGTG	1								0	1	0.01
ACCATGATG/ATCATGGTC	1								0	1	0.01
ACCCGCTCC/AGCGGGTGG	1								0	1	0.01
ACCCGTCTC/ACGGGTGAG	2								0	2	0.01
ACCGGGAGC/CCCGGTGCT	1								0	1	0.01
ACCTCCGTG/ACGGAGGTC	1								0	1	0.01
ACCTCCTCG/AGGAGGTCG	1								0	1	0.01
AGGAGGATG/ATCCTCCTC	1								0	1	0.01
AGGAGGCGC/CCTCCTGCG	1								0	1	0.01
AGGAGGGCG/CCCTCCTCG	2								0	2	0.01
Total Nona nucleotide	24	0.13									
AAAAAAAAT/ATTTTTTTTT	1								0	1	0.01
AAAAGAAGAG/CTCTTCTTT	2								0	2	0.01
AACCAGAACT/AGTTCTGGTT		1							0	1	0.01
AATCAATTCT/AATTGATTAG	2								0	2	0.01
ACACACACAG/CTGTGTGTGT	1								0	1	0.01
ACACACACTC/AGTGTGTGTG	2								0	2	0.01
AGCGGCGCGG/CCGCGCCGCT	1								0	1	0.01
Total Deca nucleotide	10	0.05									
Total	51	4	1613	2542	1349	810	448	3171	9166	19154	

Supplementary Table 8. Total SSRs identified under unique immune related genes from Kidney tissue transcriptome of *Cyprinus carpio*

Total number of sequences examined	1294
Total size of examined sequences (bp)	2112063
Total number of identified SSRs	605
Number of SSR containing sequences	449
Number of sequences containing more than 1 SSR	115
Number of SSRs present in compound formation	59
Mono nucleotide	307
Di nucleotide	212
Tri nucleotide	74
Tetra nucleotide	12

Supplementary Table 9. SSRs identified under immune related genes in Kidney tissue transcriptome of *Cyprinus carpio*

Innate Immune genes	Gene name	Sequence desc.	SSR type raw	size raw	SSR raw	Position
Chemokine	LOC109100617	chemokine XC receptor 1-like	p2	16	(CA)8	3'UTR
	CCL-C5A	chemokine CCL-C5a-like protein	p2	12	(TG)6	3'UTR
	LOC109106102	chemokine-like receptor 1	p2	22	(TG)11	3'UTR
Complement system	c1qtnf4	complement C1q tumor necrosis factor-related protein 4	p2	12	(GA)6	5'UTR
	C5-2	complement component C5-2	p2	24	(TG)12	5'UTR
	A1cf	PREDICTED: APOBEC1 complementation factor-like	p3	15	(TTG)5	5'UTR
Costimulatory molecule	LOC109076170	complement system-related protein C1qR-1	p3	21	(TTG)7	3'UTR
	LOC109058010	T-cell surface glycoprotein CD3 zeta chain-like	p2	18	(AC)9	5'UTR
	LOC109088766	cdc42 effector protein 2-like	p2	12	(TA)6	3'UTR
Cytokine	LOC109049851	T-cell surface glycoprotein CD4-like	p2	24	(TG)12	3'UTR
	cdc42se2	CDC42 small effector protein 2	p2	14	(GT)7	3'UTR
	LOC132142960	T-cell surface glycoprotein CD3 zeta chain-like isoform X1	p2	22	(AC)11	3'UTR
	LOC132142960	T-cell surface glycoprotein CD3 zeta chain-like isoform X1	p2	24	(CA)12	5'UTR
	LOC109058010	T-cell surface glycoprotein CD3 zeta chain-like	p2	14	(TG)7	5'UTR
	LOC122136444	CD9 antigen-like isoform X1	p2	22	(CT)11	3'UTR
	LOC109079512	T-cell surface glycoprotein CD3 epsilon chain-like	p2	28	(TG)14	3'UTR
	cd276	CD276 antigen isoform X1	p2	24	(CA)12	5'UTR
	LOC109054117	CD276 antigen isoform X3	p2	24	(CA)12	5'UTR
	LOC109054500	CD209 antigen-like protein D	p3	18	(TTA)6	5'UTR
	tnip2	TNFAIP3-interacting protein 2	p2	18	(GT)9	3'UTR
	LOC113055050	suppressor of cytokine signaling 7-like isoform X2	p2	24	(AT)12	3'UTR
	socs7	PREDICTED: suppressor of cytokine signaling 7	p2	24	(AT)12	3'UTR
	LOC113055050	PREDICTED: suppressor of cytokine signaling 7-like isoform X2	p2	24	(AT)12	3'UTR
	dock2	dedicator of cytokinesis 2	p2	20	(TG)10	5'UTR
	dock3	dedicator of cytokinesis protein 3 isoform X1, partial	p2	14	(AC)7	5'UTR
	dock4b	dedicator of cytokinesis protein 4b isoform X1, partial	p2	16	(CA)8	3'UTR
	DOCK4	Dedicator of cytokinesis protein 4	p2	16	(CA)8	3'UTR
	LOC109104913	cytokine receptor-like factor 1 isoform X1	p2	24	(TG)12	3'UTR
	LOC109111375	cytokine receptor-like factor 1 isoform X2	p2	24	(TG)12	5'UTR
	si:ch211-202h22.7	lipopolysaccharide-induced tumor necrosis factor-alpha factor homolog	p2	36	(AC)18	3'UTR
	LOC109110284	dedicator of cytokinesis protein 7-like isoform X2	p2	12	(TG)6	3'UTR
	LOC109063179	TNF receptor-associated factor 2	p2	12	(AT)6	5'UTR
	LOC109095670	dedicator of cytokinesis 9-like protein	p2	24	(GT)12	5'UTR
	LOC109098971	tumor necrosis factor receptor superfamily member 9-like isoform X2	p2	14	(GT)7	5'UTR
	LOC109102414	TNFAIP3-interacting protein 1-like isoform X1	p2	20	(AT)10	3'UTR
	LOC109082862	tumor necrosis factor receptor superfamily member 19-like	p2	22	(GT)11	3'UTR

Interferon	tnfaip8l3	tumor necrosis factor alpha-induced protein 8-like protein 3	p2	32	(AG)16	5'UTR
	dock4	Dedicator of cytokinesis protein 4	p2	12	(TG)6	5'UTR
	LOC109097924	tumor necrosis factor alpha-induced protein 8-like protein 1 isoform X2	p3	15	(TTG)5	3'UTR
	LOC109065755	interferon regulatory factor 4-like	p2	16	(TG)8	3'UTR
	irf5	interferon regulatory factor 5	p2	12	(AC)6	5'UTR
	LOC109067118	interferon regulatory factor 6-like isoform X1	p2	12	(AC)6	5'UTR
	LOC109082506	interferon alpha/beta receptor 1a-like isoform X3	p2	22	(CA)11	3'UTR
	LOC109065507	interferon alpha/beta receptor 1b-like	p2	18	(AC)9	5'UTR
	prkra	interferon-inducible double-stranded RNA-dependent protein kinase activator A homolog isoform X3	p2	40	(GT)20	5'UTR
	LOC116332750	interferon-induced protein with tetratricopeptide repeats 5-like	p2	22	(AC)11	3'UTR
	LOC109085153	interferon-induced GTP-binding protein Mx2-like	p2	54	(GT)27	5'UTR
	prkra	interferon-inducible double-stranded RNA-dependent protein kinase activator A homolog isoform X2	p2	40	(GT)20	5'UTR
	LOC109111911	interferon gamma receptor 1-like	p2	32	(TC)16	3'UTR
	IRF-1	interferon regulatory factor 1	p2	18	(AT)9	3'UTR
	LOC109070803	interferon regulatory factor 7 isoform X1	p2	22	(CA)11	3'UTR
Lectin family members	isg20l2	PREDICTED: interferon-stimulated 20 kDa exonuclease-like 2	p3	18	(AAT)6	3'UTR
	LOC109078724	fucoslectin-like	p2	28	(GT)14	5'UTR
	LOC109072365	sialic acid-binding Ig-like lectin 14	p2	20	(AT)10	5'UTR
	LOC109083161	galectin-related protein-like	p2	24	(AC)12	5'UTR
	preb	prolactin regulatory element-binding protein	p2	12	(AT)6	3'UTR
NLR	LOC109112338	plectin isoform X13	p2	16	(GT)8	5'UTR
	LOC109078027	galectin-8-like isoform X1	p2	18	(AT)9	3'UTR
	LOC122139768	NACHT, LRR and PYD domains-containing protein 1a allele 5-like isoform X3	p2	32	(GT)16	5'UTR
	LOC122134236	NACHT, LRR and PYD domains-containing protein 12-like isoform X1	p2	14	(TA)7	5'UTR
	LOC109092179	PREDICTED: protein NLRC3-like isoform X3	p2	34	(AC)17	5'UTR
	LOC122137612	PREDICTED: NACHT, LRR and PYD domains-containing protein 6-like	p2	24	(TG)12	5'UTR
	nlr1	NLR family member X1 isoform X3	p2	24	(GT)12	5'UTR
	LOC109103209	NLR family member X1 isoform X1	p2	12	(TA)6	5'UTR
	LOC109053867	NACHT, LRR and PYD domains-containing protein 12 isoform X1	p2	22	(TA)11	3'UTR
	LOC109113594	PREDICTED: protein NLRC3-like isoform X1	p2	34	(AC)17	5'UTR
RLR	LOC109067147	probable ATP-dependent RNA helicase DHX58	p2	40	(GT)20	5'UTR
	DHX36	ATP-dependent DNA/RNA helicase DHX36	p2	24	(TG)12	5'UTR
	LOC109085958	retinoic acid-induced protein 2-like isoform X1	p2	22	(GA)11	5'UTR
	LOC109085957	retinoic acid-induced protein 2-like	p2	22	(GA)11	5'UTR
	LOC109076721	putative ATP-dependent RNA helicase DDX23	p2	16	(TA)8	5'UTR
	rarga	retinoic acid receptor gamma-2, partial	p2	20	(TC)10	5'UTR
	LOC109101281	retinoic acid receptor alpha-A-like isoform X2	p2	22	(AC)11	5'UTR
	LOC109057926	retinoic acid receptor alpha-like isoform X3	p2	24	(TG)12	5'UTR
	LOC109110237	PREDICTED: retinoic acid receptor gamma-A isoform X3	p2	12	(AC)6	3'UTR
	LOC109045792	probable ATP-dependent RNA helicase DDX31	p3	18	(TAA)6	3'UTR
TLR	LOC109045012	Toll-like receptor 8	p2	22	(GT)11	3'UTR
	LOC109067352	toll-like receptor 13	p2	24	(AT)12	3'UTR

Adaptive Immune genes

Immunoglobulin	LOC109070054	leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 3	p2	16	(TC)8	5'UTR
	LOC109098546	immunoglobulin superfamily member 21-like isoform X2	p2	24	(GA)12	5'UTR
	LOC109083627	leucine-rich repeats and immunoglobulin-like domains protein 1	p2	40	(GA)20	5'UTR
	LOC109100532	V-type immunoglobulin domain-containing suppressor of T-cell activation-like	p2	14	(AC)7	3'UTR
	LOC109079510	immunoglobulin superfamily DCC subclass member 4-like	p2	12	(TG)6	5'UTR
	LOC109095485	immunoglobulin-like domain-containing receptor 1	p2	20	(TG)10	3'UTR
	LOC109082378	leucine-rich repeat and immunoglobulin-like domain-containing nogo receptor-interacting protein 1 isoform X2	p2	14	(CA)7	3'UTR
	rbpja	recombination signal binding protein for immunoglobulin kappa J region a isoform X1	p3	24	(TAT)8	5'UTR
	LOC109094002	PREDICTED: high affinity immunoglobulin epsilon receptor subunit gamma-like	p4	24	(GTGA)6	5'UTR
	LOC109094694	interleukin-17 receptor C-like	p2	16	(AC)8	5'UTR
Interleukin	LOC109084617	Interleukin-1 receptor accessory protein-like 1-B	p2	24	(TG)12	3'UTR
	IL-6a	interleukin-6a	p2	20	(AC)10	3'UTR
	il7r	interleukin-7 receptor subunit alpha	p2	22	(TA)11	3'UTR
