

## Supplementary Information

**Figure S1.** DNA contents of gibel carps and diploid crucian carps measured by flow cytometry using chicken (G1) as the reference. The *x*-axis shows DNA content, and the *y*-axis is cell number. **(A)** exhibits DNA contents for chicken (G1), diploid crucian carp (G2) and gibel carp (G3); **(B–K)** show DNA contents of ten diploid crucian carps (G2) using chicken DNA content (G1) as the reference; **(L–U)** display DNA contents of ten gibel carps (G2) and chicken (G1). The mean DNA content of gibel carp population is 1.5 times that of the diploid crucian carps.

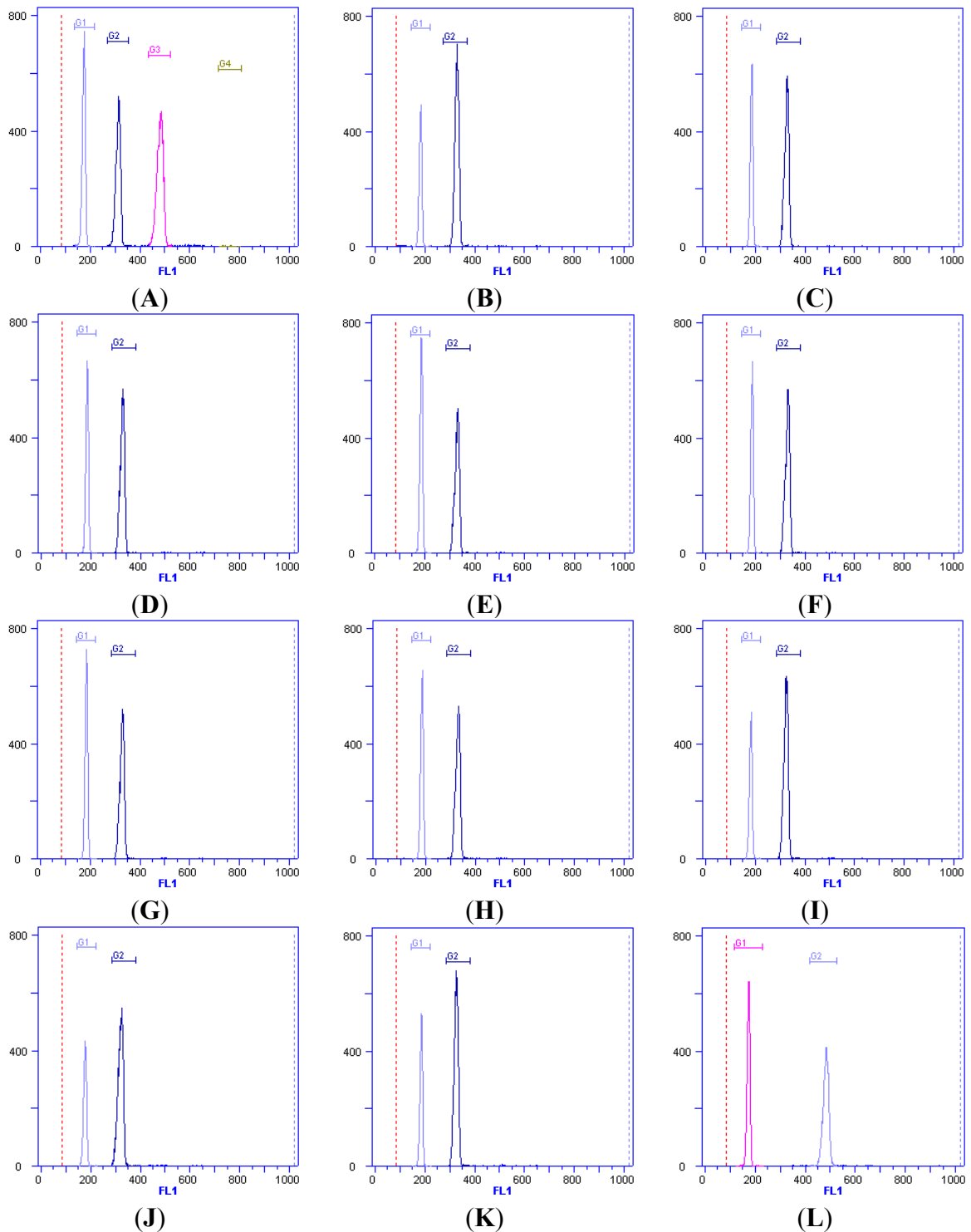


Figure S1. Cont.

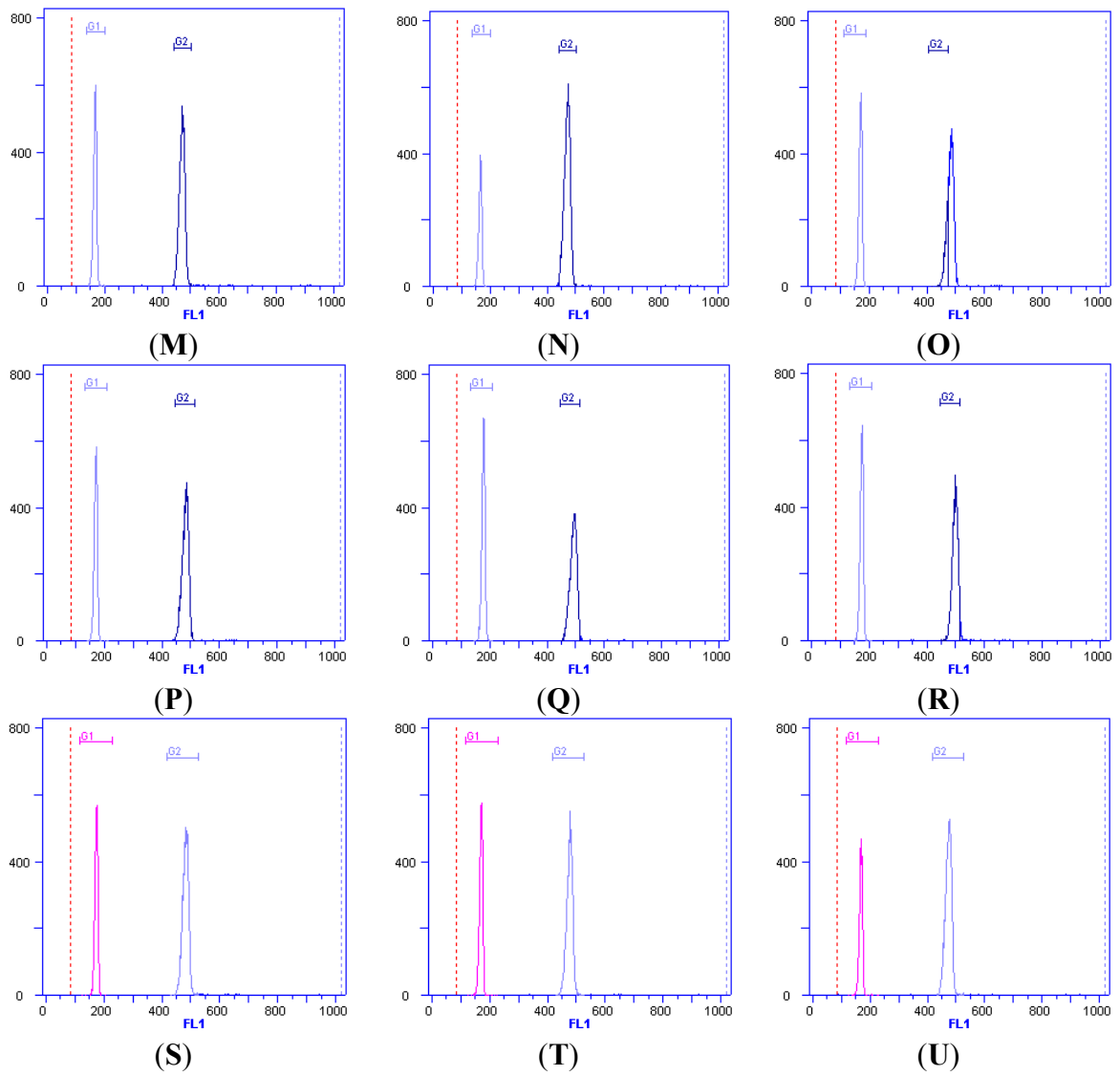
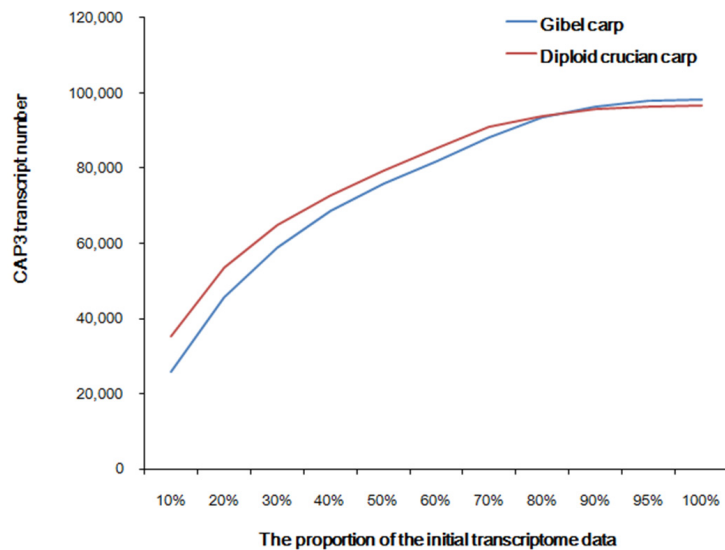
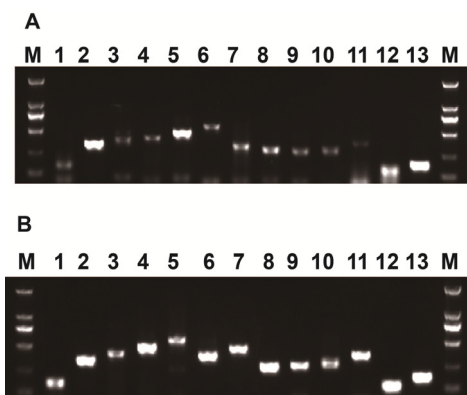


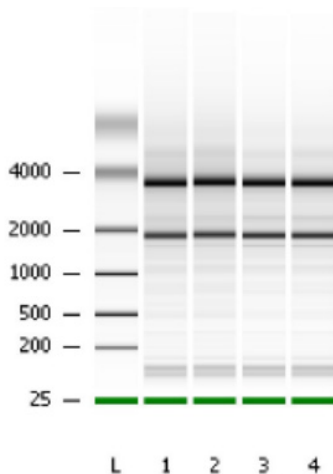
Figure S2. Saturation analysis for transcriptome coverage. Saturation curves for two species representing expected gene coverage rates. Curves were constructed for two fish.



**Figure S3.** (A) 1–12: Gibel carp conserved genes; 13: common carp  $\beta$ -actin; M: DL2000 DNA marker; (B) 1–12: Diploid crucian carp conserved genes; 13: common carp  $\beta$ -actin; M: DL2000 DNA marker.



**Figure S4.** Gel electrophoresis with Bioanalyzer 2100. L: ladder; 1: pooled tissues of triploid gibel carp; 2: pooled tissues of diploid crucian carp; 3: gonad of triploid gibel carp; 4: gonad of diploid crucian carp.



**Figure S5.** Amplification plots of beta-actin in the 1:10 dilution test. (A) 1:10 serial dilution series of cDNA from the pooled tissues of triploid gibel carp; (B) 1:10 serial dilution series of cDNA from the pooled tissues of diploid gibel carp; (C) 1:10 serial dilution series of cDNA from the gonad of triploid gibel carp; (D) 1:10 serial dilution series of cDNA from the gonad of diploid gibel carp.

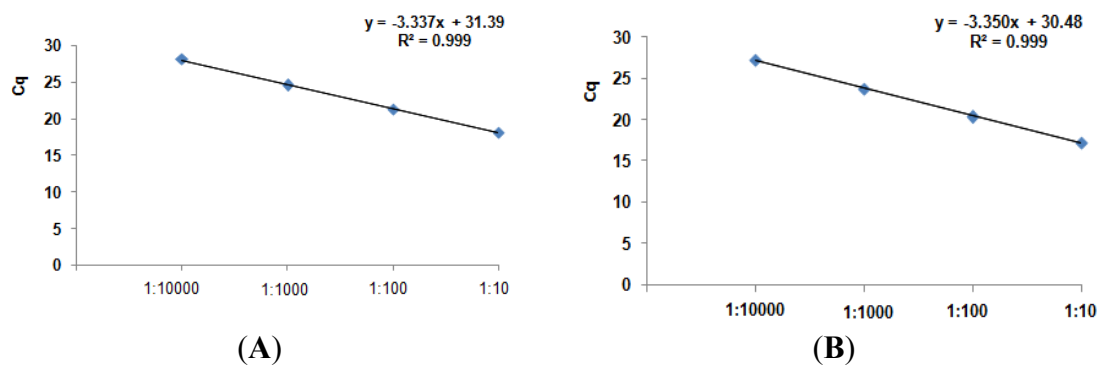


Figure S5. Cont.

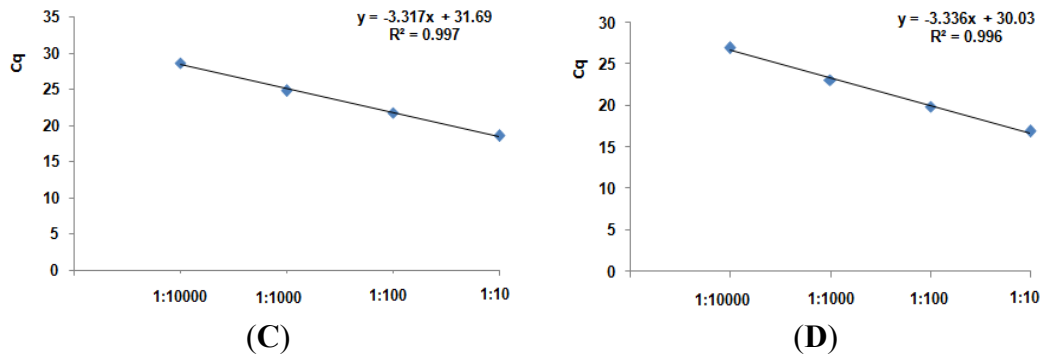


Table S1. Summary of microsatellites identified from the transcriptomes.

Type	Number	
	<i>Gibel Carp</i>	Diploid Crucian Carp
Di-nucleotide repeats	2141	2229
Tri-nucleotide repeats	1641	1754
Tetra-nucleotide repeats	155	158
Penta-nucleotide repeats	8	3
Hexa-nucleotide repeats	8	9
Total number of identified SSRs	3953	4153
Number of transcripts containing SSRs	3258	3382

Table S2. The level of tri-allelic heterozygosity estimated by microsatellite genotyping in individuals.

Loci	<i>Gibel Carp</i> Transcript	Sample									
		1	2	3	4	5	6	7	8	9	10
1 <sup>S</sup>	000000377	2 %	2	1 <sup>※</sup>	2	2	2	2	2	3	2
2	000002772	2	2	3 <sup>#</sup>	2	2	2	2	1	3	2
3	000003185	1	1	3	1	1	2	2	2	1	2
4	000003195	N &	1	2	3	3	2	3	2	2	3
5	000006001	2	2	3	1	3	2	2	2	3	3
6	000003781	1	1	1	1	1	1	1	1	1	1
7	000003916	2	2	1	2	1	1	1	2	2	1
8	000003932	1	1	1	1	1	1	1	1	1	1
9	000001091	2	3	3	1	3	3	3	3	2	N
10	000001234	1	2	2	2	2	1	2	2	2	1
11	000001414	1	2	2	3	3	3	2	3	3	2
12	000004045	N	N	N	1	1	N	N	N	1	N
13	000004497	2	2	1	2	2	2	2	2	2	3
14	000005660	N	2	3	3	3	2	3	3	N	N
15	000006377	2	2	2	3	N	2	2	1	2	1
16	000006392	2	1	2	2	2	2	2	3	2	2
17	000007745	2	1	N	1	1	1	1	2	3	2
18	000033229	3	3	1	2	2	N	2	3	N	N

※ 1 represents homozygous sites; % 2 represents di-allelic polymorphism; # 3 represents tri-allelic polymorphic sites; & N represents no amplification; <sup>S</sup> the information of the eighteen loci was showed in Table S4 (Supplementary Information).

**Table S3.** Specific primers to amplify the assembled transcripts.

Loci	<i>Gibel Carp</i> Transcript	<i>Diploid Crucian</i> <i>Carp</i> Transcript	Forward Primer	Reverse Primer
1	000006377	fed000000971	AGATGCTTGAACCTGAGAACCCTG	AGGCAAGGCACTATAACAACG
2	000014179	fed000005970	ATTCAGAGCGAGGGAGC	CCTGGAGCAAATAACAAC
3	000016617	fed0000064895	ATAGTGGCACGTATAGGCA	AACACCGAACACGAGAAT
4	000016230	fed000002177	GGGTCAGAGTCAGTGGTGT	GCTCCTCAGAGTGGTGCA
5	000000055	fed000012838	ACAGCCCACAGCAGAGCA	CACCAGCAGCCTGAAGAT
6	000037964	fed000052155	TACTTCATGCCATGCTCC	AACCTCGACGATCTCAAA
7	000003195	fed000017309	TGCCACATTATATGCGGAC	GGAGGAGAATGGGATACAGG
8	000003633	fed000011424	CCATGTTGGTTGTGAGGCAT	TGGGCTTGTGACAGATACG
9	000003916	fed000049725	GAGCTATGGGACAAACTG	TCTGACTTTGCGGTTGGATG
10	000001234	fed000012474	CCGCTAATGAACATCGTG	TCCTCCGTCTGTAATCCC
11	000004497	fed000051313	CGATTCCCTGATGAACAAGC	CATTCTCAGACAAGGCGACA
12	000005660	fed000060066	AGAGCAGAGCCAGTGGAGCA	AGTTCAGGGTCGGCGGAGTA
13 *	M24113.1	M24113.1	TGCAAAGCCGGATTGCTGG	AGTTGGTGACAATACCGTGC

\* common carp beta-actin.

**Table S4.** Specific genotyping primers in gibel carps to estimate the level of tri-allelic polymorphism.

Loci	<i>Gibel Carp</i> Transcript	Forward Primer	Reverse Primer
1	00000377	CCCACCCTCAGAATGTTT	CTTCTCCATTTCACTGCGTC
2	000002772	GCTGATTGGCTCTGGTCTGT	TCCCAGGGCTTCTGATGTT
3	000003185	TCTAGGTCTACAGGGAATGG	AGACGGTAGATGAACTCCCT
4	000003195	TGCCACATTATATGCGGAC	GGAGGAGAATGGGATACAGG
5	000006001	GCGTTGGGAATCAGAAGAG	AATCCGAACACGAGTCCACG
6	000003781	CCTGAGGCAGCATGTGATT	GTACTCCGTCTCATCCGCAT
7	000003916	GAGCTATGGGACAAACTG	TCTGACTTTGCGGTTGGATG
8	000003932	ACCACAGCCCAGCACATTCT	TCAGCCGTAACGCAACCT
9	000001091	ACCCTCGAGCTGGATTAT	CGCACACGCACATTTAGTCA
10	000001234	CCGCTAATGAACATCGTG	TCCTCCGTCTGTAATCCC
11	000001414	GACTCGCAGCAGTTGGTT	CATTGGGATGGAGGAAGA
12	000004045	TTGAGCACAGAGGCTGGTTC	GGGCTGCTACTGAAGACATACA
13	000004497	CGATTCCCTGATGAACAAGC	CATTCTCAGACAAGGCGACA
14	000005660	AGAGCAGAGCCAGTGGAGCA	AGTTCAGGGTCGGCGGAGTA
15	000006377	AGATGCTTGAACCTGAGAACCCTG	AGGCAAGGCACTATAACAACG
16	000006392	ACTGGATGGAGTGGGTGCTT	GGTTTGTGGTGTCAAAGGGT
17	000007745	TAACCGTGCACCCGTGATA	AATATCGCCTTCAGCCCACA
18	000033229	GTTACAGCGGAAATCAAGC	CCAGCAGAGCATTCCATACG

**Table S5.** Purity Ratios (*A260/A280*) of four RNA samples.

Sample	<i>A260/A280</i>
pooled tissues of triploid gibel carp	2.010
pooled tissues of diploid crucian carp	2.128
gonad of triploid gibel carp	2.039
gonad of diploid crucian carp	2.079

**Table S6.** RIN values of four RNA samples.

Sample	RIN
pooled tissues of triploid gibel carp	7.8
pooled tissues of diploid crucian carp	7.8
gonad of triploid gibel carp	8
gonad of diploid crucian carp	8

**Table S7.** Specific RT-qPCR primers of twenty DEGs to validate their expression differences.

Function	Gene Symbol	Forward Primer	Reverse Primer
Immune response	<i>lect2l</i>	GGACGACCGCAGAGAAGATA	GCGGTTACTTGAGTTCAC
	<i>cbn14</i>	TAACCCTCCCAAGCAAGACA	AGTAGGTGTCCACTGAAGGT
	<i>c5</i>	TGCCCTTGTTTTTCATGTGG	TGGTTCGTGGAGAGCAGATT
	<i>c7</i>	ATGTCCTGGAGAACAGCCA	TCAGGGTCTCACAGCTTTT
	<i>vtnb</i>	ACGGAGAAAGAAGACCAGGG	GTCATCCGGGTCATAGCTCA
	<i>tesca</i>	CGCAACTTTTCTGGGACGAA	TAGTCACTGTAGAGCTGCCG
	<i>c8b</i>	CTTTGGCGTTTTCTGCTCCT	GTCCTTCTTCAGACCACCCA
Junction proteins	<i>cx32.3</i>	GGCAGTCCCCATCTCTCAT	TGGGTTAGATAGCTGCCGAG
	<i>sid4</i>	GCTTCTCTCTGCTTTCCTGC	AGTGATGGTCAGGACAGCTC
	<i>itga6b</i>	CTCGTTGGCATGACTGACTG	CAGCTTGTTCCGGTTTCTCCC
Transferases	<i>vtna</i>	CTTTGCCATTCTGCTCACA	CTCAGCCCATCGGTCATAGT
	<i>tat</i>	CACACGGATTGGATGGGTTG	GCCATCAGCGTGTGTGTGTA
	<i>cetp</i>	AGTCAAGTCATGCCAGCTCT	CTCCTCCATCTCAGTGGGTC
Binding proteins	<i>fabp11a</i>	ATCCCAGGTCTGTTTCTGCA	ACCTGATCGTGTGTGTGGAT
	<i>rbp2b</i>	AGATTGCAGCCCACCTTACT	CCCAGGTCACCAGAGTCTTT
Ubiquitin related proteins	<i>ube3a</i>	AACTCTACATTGGGCGACA	GAAACGGCCTCTGGTTCATC
Transporters	<i>Tnp1</i>	TCACCTCGCAGTCTTCATCA	GCTCTGAATCGACCCCTCAA
	<i>TMEM87A</i>	AGAAGGAGGGTTGCAGTGAA	TTGGCAGGTGGATGATTTGC
	<i>accn2</i>	TCCGTAGCGTGTGAAGATCA	CACTTGGTAGAGGAGAGCGT
Signaling Proteins	<i>IQGAP1</i>	TCGAACAGCTTCATCACTGC	GAAATCGAGGATCTGCAGCC
	<i>srp54</i>	TTTGCCAAACCAACAACCCT	GGGCGGAAGAAGATGGTTTT
	<i>Pcsk6</i>	ATCCCACCACCTCTCCTTTG	GACCTGCGTTCTGAATGTG
	<i>Map4k4</i>	ATATAAGCGACGGAGGTGGG	ATGCAGTGGATGTGGACTCA
	<i>smarcb1a</i>	CCAGTCTGGCCTGTAGTCAA	ACGGTCATCCCAAGCTTTTG
Fish-egg lectin-like precursor	<i>fel</i>	ATGTGAGCTTTGACCTGGGA	GTCACCTTGAGGCTTCGGTC