Chemokine *ccl33* is a key regulator of fish barbel development

by

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Abstract

Barbels are integumentary sense organ that can be found in fishes, reptiles and amphibians. Barbel structures are relatively simple, consisting of central rod of cartilage, nerve trunk, artery and taste bud. The cell types in barbels were highly conserved with that in human. So, the barbel provided a good system for studying angiogenesis, neural pathfinding, wound healing, scar formation and other key processes in vertebrate physiology. More than one century ago, people attempted to find the evolution and formation of the barbels. However, it is still unclear which genes regulate the barbel development, and the origin of the barbels.

Bottlenose catfish (*Ageneiosus Marmoratus*), a catfish species but lacking the sensory organ barbels, serves as an ideal model to determine the genomic basis for barbel development and its regeneration. Through comparative genome and transcriptome subtraction analysis, here I report a chemokine gene, *ccl33*, as a key regulator of barbel development and regeneration. The *ccl33* gene is present in fish with barbels but absent from fish without barbels. It has multiple copies in channel catfish, of which three copies, *ccl33.4*, *ccl33.6*, and *ccl33.7* were differentially expressed during barbel regeneration, in a fashion concordant with the timing of barbel regeneration. Knockout of *ccl33* genes in zebrafish resulted in various phenotypes including complete loss of barbels, reduced barbel sizes, curly barbels, and reduced body size and weak performance, suggesting that *ccl33* is a key regulator of barbel development, and may be important for normal development and immunological functions.

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List of Abbreviations

ccl33: CC motif chemokine ligand member 33

WT: wild type

FGF: fibroblast growth factor

MBP: Myelin basic protein

LINE: long interspersed elements

LTR: long terminal repeats

FDR: false discovery rate

FPKM: fragments per kilo-base million

GO: gene ontology

CRISPR: clustered regularly interspaced short palindromic repeats

Chapter 1 Introduction

Overview

Developmental biology is one of the fastest growing and most exciting fields in biology. Development can be found in regeneration, reproduction, morphogenesis and metamorphosis in the growth and differentiation of cells in the organisms. Regeneration of parts in free living animals is fascinating in developmental biology, since the discoveries have the potential to impact clinical outcomes of many diseases of organ damage, including heart failure, Alzheimer's disease, and diabetes. Different organisms have different regeneration ability. *Hydra* can regenerate any parts of the polyp from a small fragment (Bosch 2007). Planarian worms can regenerate both head and tail (Reddien and Alvarado 2004). Amphibians and fish can regenerate complex tissues much more effectively than other vertebrate (LeClair and Topczewski 2010). While, mammals have limited regenerative abilities (Gurtner et al. 2008). Distal regeneration of appendages can be found in various organisms, such as legs of cricket *Gryllus bimaculatus* (Nakamura et al. 2007), limbs of amphibians (Simon and Tanaka 2013), fins and barbel of zebrafish (LeClair and Topczewski 2010; Grotek et al. 2013). Zebrafish have emerged as a central model system for studying regeneration, due to their ability to regenerate myriad tissues such as heart, lesioned brain, retina, spinal cord, fins and barbels (LeClair and Topczewski 2010; Gemberling et al. 2013). Identifying the genetic bases of development and regeneration will provide insight into the explanation of variance of regeneration ability.

Evolution of fish barbel

Barbels are integumentary sense organ that can be found in fishes (**Error! Reference source not found.**), reptiles and amphibians. Barbel structures are relatively simple, consisting of central rod of cartilage, nerve trunk, artery and taste bud. More than a century age, Pollard (Pollard 1894; Pollard 1895) attempted to demonstrate morphological similarities of skeletal structures and nerves, in barbels of silurid fishes, that could traced back to a Myxine-type ancestral form. This view implied that barbels of fishes are homologues of the oral cirri of Amphioxus - the cirrhostomial theory (Fox 1999). However, the anatomical analysis revealed that the cartilages associated with catfish mandibular barbels are a de novo formation, that is not homologous or even similar to any other structure present in other teleosteans, fishes or animals (Diogo and Chardon 2000). Many cypriniforms and almost all siluroids have barbels. However, the barbels of cypriniforms and siluroids appear to have evolved independently (Fink and Fink 1981). The general consensus is that barbels have originated independently a number of times in different groups of fishes (Fink and Fink 1981). They may be derived or apomorphic in some cases, or in others may be primitive, originating *sui generis* (Fox 1999). However, within a teleost order such as the Siluriformes, barbel origin and development, number and location, could provide evidence of interfamilial or species relationships (Howes 1991). Discover the genetic background of barbel development will be helpful to answer the questions about barbel evolution.

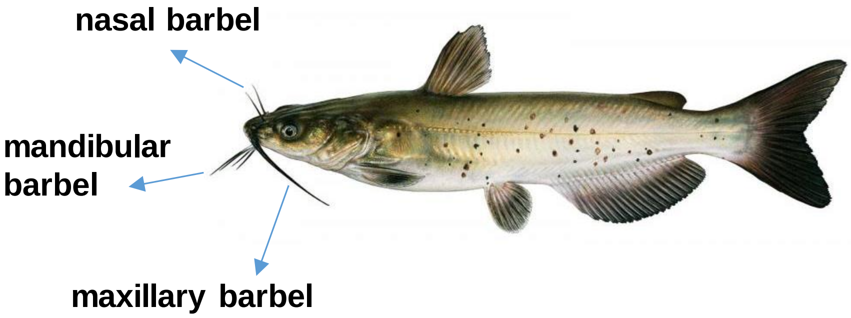


Figure 1 Channel catfish and its barbels.

The genes regulate barbel development

The cell types in barbels include skin cells, neural-crest derived pigment cells, circulatory vessels, taste buds and sensory nerves, which are highly conserved with human (LeClair and Topczewski 2010). So, the barbel could be a useful system for studying angiogenesis, neural pathfinding, wound healing, scar formation and other key processes in vertebrate physiology (LeClair and Topczewski 2010). The barbel can be regenerated in catfish (Goss 1956; Whitear 1990; Park et al. 2012), and zebrafish (LeClair and Topczewski 2010). After a proximal amputation in which more than 85% of the maxillary zebrafish barbel was removed, the appendage regenerated within 2-3 weeks (LeClair and Topczewski 2010). Understanding the gene regulation of barbel regeneration at the molecular level may be helpful to explain or augment the limited regenerative capacity of other species, including human own. Many fibroblast growth factor (FGF) and wingless (Wnt) pathway members are expressed during early barbel regeneration of zebrafish (Duszynski 2011). Myelin basic protein (mbp) are expressed in normal and regenerating adult barbels of zebrafish, indicating activity in both maintenance and repair (Moore et al. 2012). Although it was demonstrated that the regenerative abilities of barbels and the dependence of regeneration upon nerve supply (Kamrin and Singer 1955), it is still unknown how the nerve supply affect barbel development, what genes control barbel regeneration, what regulatory networks control the gene expression, and how these networks act in the barbel (Duszynski et al. 2013).

Bottlenose catfish is valuable for barbel related studies

Catfish is one of the most diverse vertebrate order. As of 2007, there were about 36 extant catfish families, and about 3,093 extant catfish species have been described (Ferraris 2007). One of the most visible characteristics of most catfish species is the presence of barbels.

However, *Ageneiosus* and *Tympanopleura* are distinct from other catfish in lacking mandibular barbels (Figure 2), having the maxillary barbels greatly reduced in size (Figure 3), and lying in a groove at the corner of the mouth above the upper lip (Birindelli 2014). The barbel-less feature of *Ageneiosus* and *Tympanopleura* could be valuable for comparative genomic studies, which can reveal unique mechanisms that may be restricted to certain clades, species, or cell lineages. Investigating the molecular similarities and differences among organs within those species, may reveal certain molecular regulators that will be widely used. In this study, we sequenced the genome of bottlenose catfish (*Ageneiosus marmoratus*), conducted barbel regeneration experiment of channel catfish, and sequenced the transcriptome of channel catfish barbel tissue. By using a comparative genomics pipeline (Figure 4), we are trying to identify the genes regulate barbel development of fish though comparative genomics analysis.

Figure 2 General morphology of bottlenose catfish.

Figure 3 The ossified maxillary barbel of bottlenose catfish.

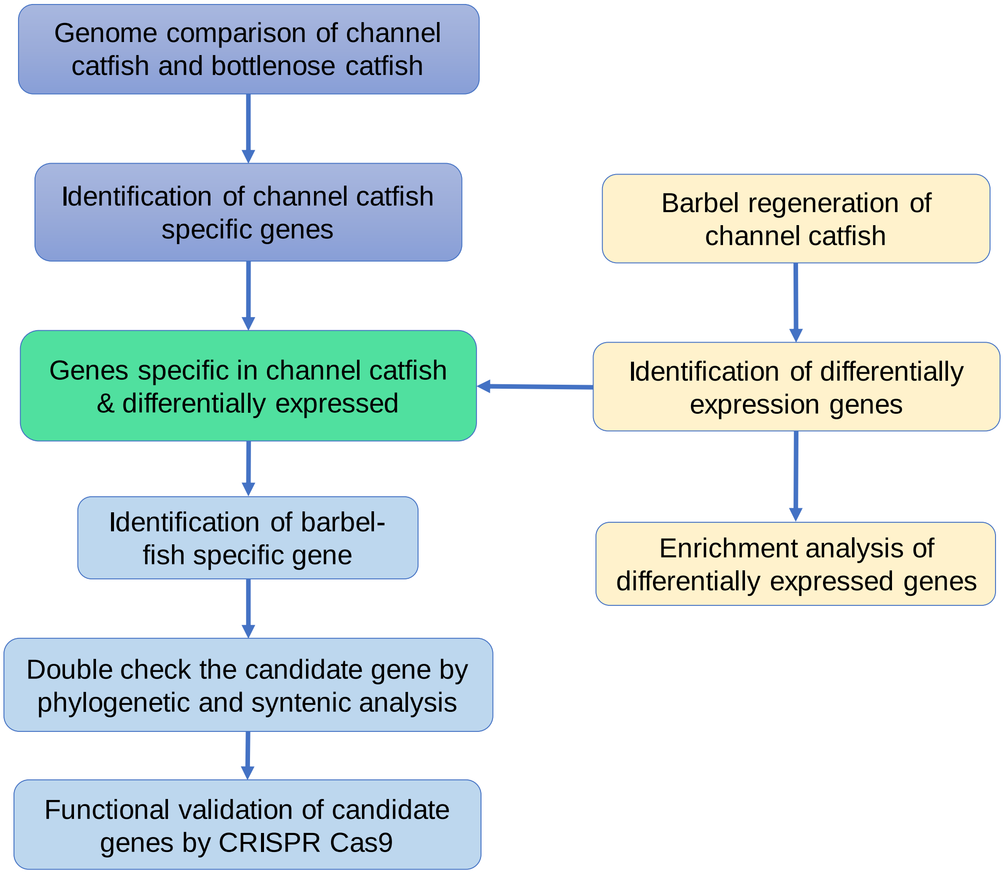


Figure 4 Schematic illustration of the comparative genomics pipeline.

Chapter 2 Sequencing, assembly and annotation of the bottlenose catfish genome sequences

Introduction

Teleost fish exhibit an amazing level of biodiversity affecting their morphology, ecology and behavior as well as many other aspects of their biology, which makes fish extremely attractive for the study of many biological questions, particularly of those related to evolution and development (Volff 2005). The developmental biology has been driven by advances in DNA sequencing technologies. More and more fish genomes are available including zebrafish *Danio rerio* (Howe et al. 2013), fugu *Takifugu rubripes* (Kai et al. 2011), tetraodon *Tetraodon nigroviridis* (Jaillon et al. 2004), stickleback *Gasterosteus aculeatus* (Jones et al. 2012), tilapia *Oreochromis niloticus* (Guyon et al. 2012), spotted gar *Lepisosteus oculatus* (Braasch et al. 2016), mekaka *Oryzias latipes* (Kasahara et al. 2007), cavefish *Astyanax mexicanus* (McGaugh et al. 2014), platyfish *Xiphophorus maculatus* (Schartl et al. 2013), Atlantic salmon *Salmo salar* (Lien et al. 2016) and channel catfish *Ictalurus punctatus* (Liu et al. 2016). As the first step of comparative analysis of barbel development, we sequenced, assembled and annotated the genome of bottlenose catfish *Ageneiosus marmoratus*.

Materials and methods

DNA extraction and genome sequencing of bottlenose catfish

The bottlenose catfish was bought from an online ornamental shop. After arriving, the fish was anaesthetized with MS-222 (Sigma-Alodrich). The blood was draw from the fish by using 1 ml syringe, and stored in cell lysis solution for DNA extraction. Genomic DNA was extracted by using standard protocols. In general, the blood sample stored in cell lysis solution was incubated at 58^{o}C overnight before extraction. The blood sample was lysed in cell lysis solution containing proteinase K. The protein in the solution was eliminated by adding protein precipitation solution. DNA was precipitated by isopropanol and collected by brief centrifugation. The collected DNA was washed twice with 70% ethanol, then air-dried and re-suspended in TE buffer. The quantity and purity of the DNA was measured by Nanodrop (Thermo Scientific, Wilmington, DE).

The collected genomic DNA was send to Genomics Services Lab at HudsonAlpha (Huntsville, AL) for sequencing. One paired end library with insert size of 220 bp, and two mate pair libraries with insert size of 3-5 kb and 7-10 kb respectively were prepared. The three libraries were sequenced on Illumina HiSeq 2500 instrument. The read length of pair end and mate pair libraries were 125bp and 100bp respectively.

Genome assembly, gene prediction, and annotation of the bottlenose catfish

The quality of the raw reads was checked by using FastQC (Andrews 2010). Based on the results of FastQC, the adapters, primers and low quality bases in the reads were trimmed by using cutadapt (Martin 2011). The trimmed high quality reads were put into ALLPATHS (MacCallum et al. 2009) pipeline to *de novo* assembly the bottlenose catfish genome. The assembled contigs and the reads from the two mate pair libraries were used in the scaffolding process in SSPACE (Boetzer et al. 2011). After scaffolding, five rounds of gap filling processes were performed to fill the gaps by using GapFiller (Boetzer and Pirovano 2012).

After gap filling, *de novo* repeat family identification and modeling were performed to construct custom repeat library by using RepeatModeler (Smit and Hubley 2010). The repetitive elements, including low-complexity sequences and interspersed repeats in the scaffolds were masked by aligning with the constructed custom repeat library using RepeatMasker (Smit et al. 2015). The masked scaffolds were input into AUGUSTUS (Stanke et al. 2004) to predict the genes. The predicted genes were annotated by blast UniProt (Consortium 2015) and NCBI non-redundant (nr) database.

Repetitive element analysis

The derived repetitive sequences in bottlenose catfish genome were searched against curated libraries and repetitive DNA sequence database Repbase (Bao et al. 2015) and Dfam (Wheeler et al. 2013) derived from RepeatMasker package. All the sequences were further queried and searched against the NCBI Nucleotide collection database (nt) using blastn to get deeper annotations (E-value $<10^{-5}$). The average number of substitutions per sites (K) for each LINE fragment were calculated. The K was calculated based on the Jukes-Cantor formula: $K=-300/4\times \mathrm{Ln}(1-D\times 4/300)$, the D represents the proportion of each LINE fragment differ from the consensus sequences (Chinwalla et al. 2002).

Results and discussion

In total, three DNA libraries were prepared and sequenced. The pair end library generated 498.45 million raw reads (read length 125 bp), the two mate pair libraries produced 586.69 and 590.97 million raw reads (read length 100 bp) respectively. Raw read data are archived at the NCBI Sequence Read Archive (SRA). After trimming, 455.09 million reads in the pair end library, 412.61 and 412.78 million reads in the mate pair libraries were kept and further assembled. The final genome assembly was 1.02 Gb, with 16,063 scaffolds and scaffold N50 of 223.14 kb (Table 1). The GC content of bottlenose catfish genome was 39.01%.

A set of 24,960 amino acid sequences were predicted by *ab initio* gene prediction of bottlenose catfish genome. After annotation, 23,367 protein coding genes were identified. The total number of protein coding genes in bottlenose catfish is similar with that of channel catfish (23,218, NCBI annotation).

Table 1 Assembly and annotation of the bottlenose catfish (*Ageneiosus marmoratus*) genome sequences.

Genome sequencing	Paired reads (125 bp/read)	498.5M (62.2X)
	Mate paired reads (library 1, 100 bp/read)	586.7M (58.7X)
	Mate paired reads (library 2, 100 bp/read)	591.0M (59.1X)
	Total reads	1,676.2M (180X)
Genome assembly	Total length of genome assembly	1,023 Mb
	GC Content	39.01%
	Number of scaffolds	16,063
	N50	223,139
	Average scaffold size	64,122

Genome annotation	Number of predicted genes	23,367
	Interspersed repeats	238.38 Mb (23.14%)
	Satellites	0.84 Mb (0.08%)
	Simple repeats	23.74 Mb (2.30%)
	Low complexity	2.11 Mb (0.20%)

A total of 264.79 Mb (25.71% of genome size) repetitive elements including interspersed repeats, microsatellites and simple repeats were identified from bottlenose catfish (Table 1). Among all the repetitive elements, Class II transposons were the most abundant elements making up 20.2% of the genome, and TC1 was the most abundant Class II transposable elements, representing 15.3% of the genome. Class I transposons, which include three major families: long interspersed elements (LINEs), long terminal repeats (LTRs) and short interspersed elements (SINEs), made up 8.0% of the genome. Interestingly, the LINEs in the bottlenose catfish genome had a significantly lower average number of substitutions per sites (K) of 17.57 than that in channel catfish of 13.75. Therefore, the lower K of LINEs implied that most the LINEs in the bottlenose catfish genome have much younger insertion time or less active in evolution (Figure 5).

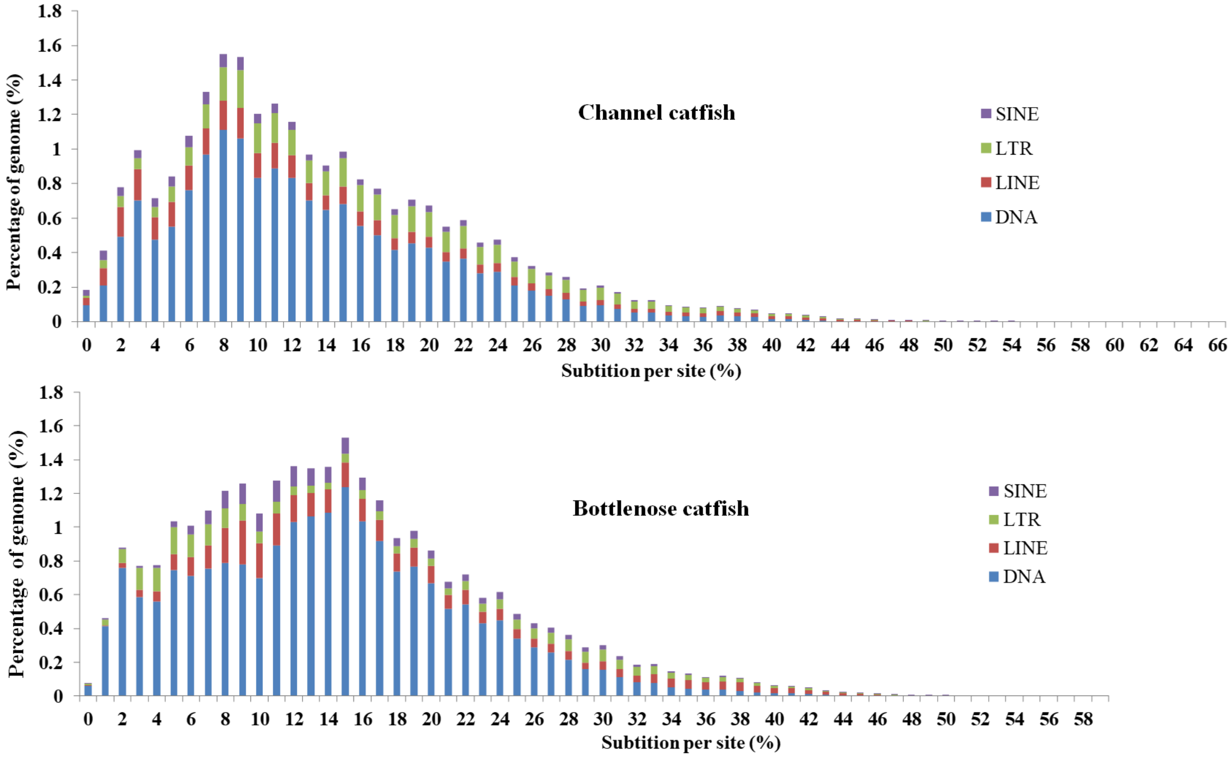


Figure 5 Comparison of repetitive elements from bottlenose catfish and channel catfish genome

Chapter 3 Genome comparison of bottlenose catfish and channel catfish

Introduction

In comparative genomics, whole genomes are compared to study basic biological similarities and differences as well as evolutionary relationships between organisms. The major principle of comparative genomics is that common features of two organisms will often be encoded within the DNA that is evolutionarily conserved between them (Hardison 2003). Genome comparison have become a powerful tool for development and evolution related studies. Through comparison of scaled and scale-less catfish, we identified the candidate genes regulate scale formation in teleost (Liu et al. 2016). By contrast of cavefish *Astyanax mexicanus* genome to other teleost genomes, the candidate genes for eye loss were identified (McGaugh et al. 2014). Comparative genomic analysis identifies higher protein and nucleotide evolutionary rates in seahorse *Hippocampus comes* compared with other teleost fish genomes (Lin et al. 2016). Comparative genomics is now a standard component of the analysis of every new genome sequence. The publication of channel catfish genome (Liu et al. 2016) makes it possible for the genome comparison of channel catfish and bottlenose catfish.

Materials and methods

Phylogenomic analyses

Phylogenomic analyses were based on protein coding sequence alignments. We obtained 372 single orthologue sequences from 13 representative species (Elephant shark *Callorhinchus* *milii*, human *Homo sapiens*, mouse *Mus musculus*, chicken *Gallus gallus*, lizard *Anolis carolinensis*, frog *Xenopus tropicalis*, zebrafish *Danio rerio*, bottlenose catfish *Ageneiosus marmoratus*, channel catfish *Ictalurus punctatus*, blind cave fish *Astyanax mexicanus*, pufferfish *Takifugu rubripes*, medaka *Oryzias latipes*, spotted gar *Lepisosteus oculatus*) by aligning with MAFFT v7.310 (Yamada et al. 2016). The alignments were combined in a super matrix with FASconCAT v1.0 (Kück and Meusemann 2010) and input into GBlocks v0.91b (Talavera and Castresana 2007) to exclude possible misaligned regions. Phylogenetic reconstruction was carried out in RAxML v8.2.10 (Stamatakis 2014) with the JTT+F+Γ4 model. Another round of phylogenetic reconstruction was performed using ExaBayes v1.5 (Aberer et al. 2014). Two independent runs were considered converged with the asdsf is below 0.05. The posterior consensus tree was obtained with exclusion of the first 2,000 trees as burn-in and sampling every 500 generations from both chains. Node support was evaluated with 100 bootstrap replicates (BS) for RAxML and posterior probability (PP) for ExaBayes. To explore further the robustness of any given node of the reconstructed phylogeny, we calculated the internode certainty (IC) of each node and the extended IC (ICA). IC and ICA metrics were developed to inform the certainty of a phylogeny's internode based on a given set of individual gene trees. IC is calculated based on the most prevalent conflicting bipartition at the trees set, while for calculating ICA all prevalent conflicting bipartitions are considered. The IC calculation was conducted on the JTT+F+Γ4 phylogeny using the individual genes phylogenies as the tree dataset to quantify incongruence. Individual gene phylogenies were estimated in RAxML using the same model as the one used in the main phylogeny. The 225 individual gene alignments that included sequence information for all 13 species were included in the calculation of IC values in RAxML.

Comparative analysis of gene contents in bottlenose catfish and channel catfish.

The available of channel catfish genome (Liu et al. 2016) makes it possible to conduct comparative genomics between channel catfish and bottlenose catfish. The pipeline described in Liu et al. (2016) was used and made some modification. The orthologs and orthogroups between bottlenose catfish and channel catfish were generated by using OrthoFinder (Emms and Kelly 2015). To obtain the species-specific genes, BLASTP was performed in which genes not included in the orthogroups were queried against the genes in the orthogroups within the same species, with a maximal e-value of 1e-10. A reciprocal BLASTP with maximal e-value of 1e-5 was used to query genes with no hits from previous steps (Liu et al. 2016). The genes with no hits to any orthologs were considered as species specific genes.

Results and discussion

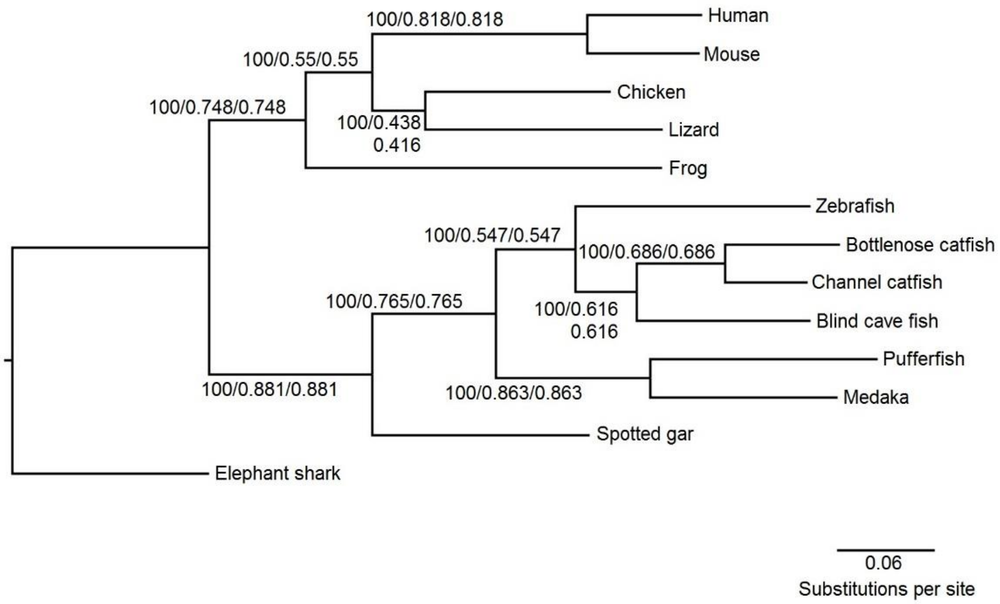


Figure 6 Phylogeny inferred from 225 conserved genes.

Bottlenose catfish and channel catfish both belong to the order Siluriformes and are the most closely related among the fish with sequenced genomes (Figure 6), but they have a sharp contrast with barbels: Channel catfish have 4 pairs of barbels, while bottlenose only have one pair of ossified maxillary barbels that are very short in size. This makes them a good natural model for understanding the genomic basis for barbel development. We first compared the gene contents of the bottlenose genome and the channel catfish genome (Liu et al. 2016) to determine what genes may have been lost in the bottlenose catfish genome. A total of 1,730 genes were identified to be present in the channel catfish genome, but absent from the bottlenose catfish genome (Appendix Table 1); conversely, 2,362 genes were found in the bottlenose catfish genome, but absent from the channel catfish genome.

Chapter 4 Differentially expressed genes during barbel regeneration in channel catfish

Introduction

The number of genes missing from the bottlenose catfish genome is still too large to provide insights into the candidate genes for barbel development. We reasoned that genes important for barbel development should perhaps be differentially expressed during barbel regeneration, and the genes that satisfy the following two conditions could be more likely involved in barbel development: 1) The gene(s) are present in fish with barbels but may be missing or mutated in fish without barbels; and 2) The gene(s) should be differentially expressed during barbel regeneration. In this section, we conducted barbel regeneration of channel catfish. After the amputation of the barbel, we collected barbel tissue from channel catfish. We are trying to identify the genes regulate barbel regeneration.

Materials and methods

Barbel regeneration experiment of channel catfish

The channel catfish barbel regeneration trial was conducted at E.W. Shell Fisheries Center, North Auburn Unit, Alabama. A total of 175 healthy channel catfish of two years old were randomly selected. To document the regeneration of channel catfish barbel tissue, we surgically removed the left side maxillary barbel at 11 time points (0h, 3h, 6h, 12h, 24h, 48h, 72d, 7d, 14d, 21d, 28d) and observed the progress of the regeneration. On the day of surgery, individual fish was lightly anesthetized in system water containing 0.015% buffered tricaine. Sterile fine forceps were used to elevate the maxillary barbel tissue. At the beginning of the experiment (0h), 1/3 of the left side maxillary barbel of the 175 channel catfish were amputated. The right side barbels were kept as control. At each of the following 10 time points, 15 fish individuals were randomly picked out, and another 1/3 of the left side maxillary barbel was amputated (Figure 7). After the surgery, the fish were restocked in the tank and feed twice daily. The amputated barbel tissue from 15 individuals was randomly stored in three 1.5 ml tubes, and was considered as three replicates. All the barbel tissue samples were stored in dry ice temporarily before moved into -80^{o}C refrigerator.

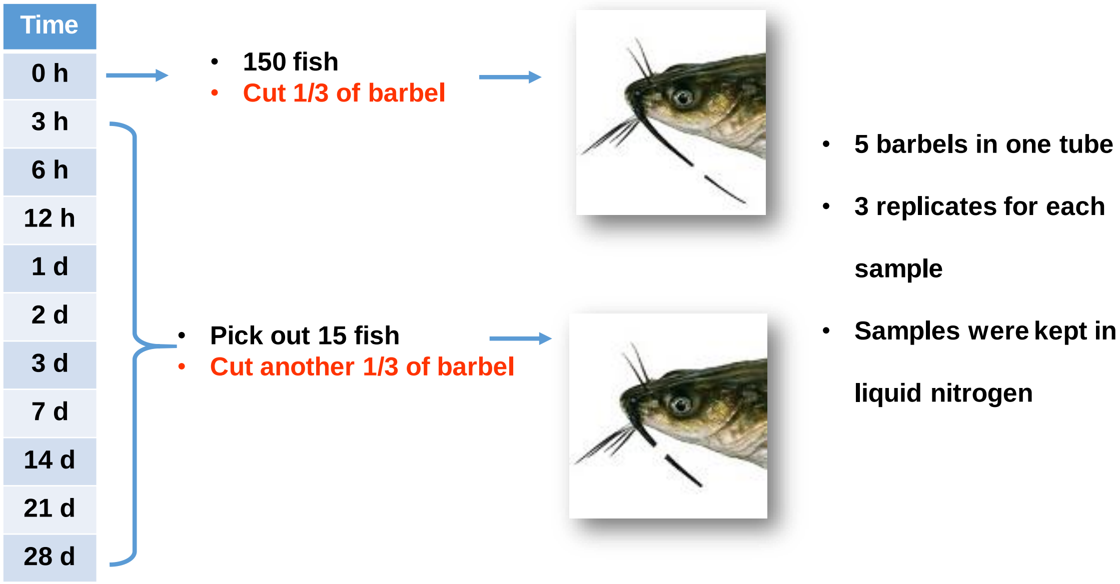


Figure 7 Barbel regeneration experiment design.

Total RNA was extracted from the collected barbel tissue by using the RNeasy Plus Kit (Qiagen, Valencia, CA). The collected RNA samples were send to Genomics Services Lab at HudsonAlpha (Huntsville, AL) for sequencing. Poly A RNA-seq libraries were prepared for

RNA sequencing. After KAPA quantitation and dilution, the libraries were sequenced on Illumina HiSeq 2000 instrument.

Identification of differentially expressed genes during channel catfish barbel regeneration

TopHat and Cufflinks pipeline was used to identify differentially expressed genes during channel catfish barbel regeneration (Trapnell et al. 2012). In general, the adapters, low quality sequences and short sequences (<30 bp) in the raw RNA-Seq reads were trimmed by using Trimmomatic (Bolger et al. 2014). After trimming, the survived high quality reads were aligned to the channel catfish fish genome by using TopHat (Trapnell et al. 2009). The aligned RNA-Seq reads and channel catfish transcript annotation file downloaded from NCBI were input into Cufflinks to detect the differentially expressed genes. The differential expression analysis was compared at gene level. At each time point, the expression value of each gene (FPKM) were compared with that of the control. The q value (FDR-adjusted p-value) of the test was calculated. Only the genes fulfill certain criteria (statistically significant, q value < 0.05, $|\text{fold change}| > 2$) were considered as differentially expressed genes.

Enrichment analysis

Enrichment analysis of differentially expressed genes at each time point were performed by using PANTHER classification system (Mi et al. 2013). Due to the relative less information of gene ontology annotation for channel catfish, the zebrafish background was selected for further analysis. The orthologs of channel catfish genes in zebrafish were identified by aligning the channel catfish genes to the zebrafish genome. The identified zebrafish gene ID and zebrafish genome background were selected to perform the enrichment analysis.

Results and discussion

Barbel regeneration of channel catfish after amputation

After amputation, the channel catfish barbel could be regenerated (Figure 8). After amputation of the maxillary barbels, the blastema covering over the amputation site was visible three days after amputation. Then the tissues began to accumulate in one side of the barbel. The barbels then were gradually regenerated, and one month later, approximately half of the amputated barbel was regenerated. The average length of regenerated barbel at certain time point can be found in Figure 9.

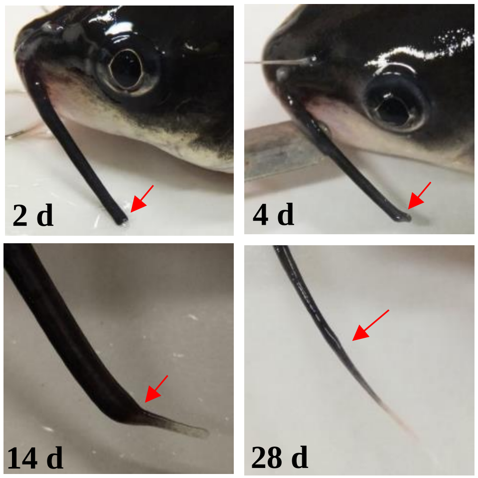


Figure 8 Morphology of the channel catfish barbel during regeneration.

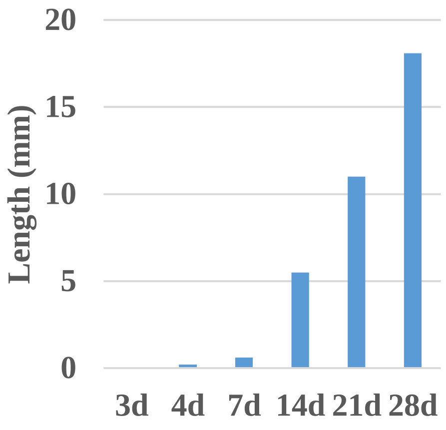


Figure 9 The length of the regenerated barbel at each time point.

Sequencing of RNA samples from channel catfish barbel

The RNA in the collected barbel tissue was isolated. Based on the regenerated barbel length at each time point, six RNA samples (0d, 1d, 2d, 3d, 7d, 14d) were sequenced on Illumina Hiseq 2500 platform. A total of 431.85 million raw reads were generated, and 406.99 million of high quality reads were kept after trimming of low quality sequences. Raw reads data are archived at the NCBI Sequence Read Archive (SRA).

Genes differentially expressed during barbel regeneration of channel catfish

The differentially expressed genes during barbel regeneration were identified by comparing the gene expression value (FPKM) at each point after amputation with control (0d). Gene expression profiles were determined during the first two weeks during barbel regeneration. RNA-Seq was conducted for samples collected immediately after amputation, and at day 1, day 2, day 3, day 7, and day 14 after amputation. RNA-Seq reads were mapped to the channel catfish reference genome sequence to determine differentially expressed genes. The largest number of differentially expressed genes was observed on day 1 after barbel amputation, with 2,723 differentially expressed genes. This was probably due to the induction of a large number of wound-response genes after amputation of the barbels. The number of differentially expressed genes at 2d was drastically decreased, with only 1,212 genes being differentially expressed. Similarly, the number of differentially expressed genes on 3d, 7d, and 14d were 1,013, 1,593, and 1,442 genes, respectively. When all the differentially expressed genes at various time points were combined, a total of 4,068 genes were identified to be differentially expressed during barbel regeneration at least at one time point.

Enrichment analysis of differentially expressed genes during barbel regeneration of channel catfish

Enrichment analysis of differentially expressed genes at each time point after amputation were conducted. The GO terms that most significantly enriched during barbel regeneration were listed in Table 2. One day after amputation, the most significant enriched GO terms were “cellular respiration” and “wound healing”. Two days later, they were shift to “organism development” and “single-organism developmental process”. Three days later, they became to be “anatomical structure development” and “embryonic organ development”. Seven days and 14 days after amputation, the most significant GO term were “cell adhesion” and “biological adhesion”. The most enriched GO terms were consistent with the observed characterizations during barbel regeneration.

Table 2 GO terms that significantly enriched during barbel regeneration of channel catfish.

Time point	GO biological process	Fold Enrichment	P value
1d	GO:0045333 cellular respiration	3.59	0.003
	GO:0042060 wound healing	2.57	0.03
	GO:0009611 response to wounding	2.51	0.01
2d	GO:0032502 developmental process	1.49	0.0006
	GO:0007275 multicellular organism development	1.49	0.003
	GO:0044767 single-organism developmental process	1.48	0.001
3d	GO:0048856 anatomical structure development	2.04	0.005
	GO:0048568 embryonic organ development	1.79	0.001
7d	GO:0007155 cell adhesion	2.21	0.026
	GO:0022610 biological adhesion	2.2	0.028
	GO:0032502 developmental process	1.36	0.037
14d	GO:0007155 cell adhesion	2.64	0.00019
	GO:0022610 biological adhesion	2.63	0.0002
	GO:0044699 single-organism process	1.22	0.007

Chapter 5 Chemokine *ccl33* as a candidate gene for barbel development

Introduction

In the previous sections, we have identified the genes present in the channel catfish genome but absent in the bottlenose catfish genome, as well as the genes differentially expressed during barbel regeneration. In this section, we are trying to narrow down the gene list for barbel development. The anatomical analysis revealed that the cartilages associated with catfish mandibular barbels are a *de novo* formation, that is not homologous or even similar to any other structure present in other fishes or animals (Diogo and Chardon 2000). This makes us to hypothesis that certain genes unique in catfish with barbels control the barbel development. To test this hypothesis, certain genes should present in channel catfish, absent in bottlenose catfish and differentially expressed during barbel development. Furthermore, the available genomes of other fish species with barbels or without barbels could also provide some clues for the identification of candidate gene for barbel development.

Materials and methods

Phylogenetic analysis of chemokine ligand genes

Phylogenetic analysis was conducted by using chemokine ligand genes from fish and some representative species including channel catfish, bottlenose catfish, zebrafish (*Danio rerio*), Atlantic salmon (*Salmo salar*), tilapia (*Oreochromis niloticus*), amazon molly (*Poecilia formosa*), spotted gar (*Lepisosteus oculatus*), medaka (*Oryzias latipes*), platyfish (*Xiphophorus* *maculatus*), cave fish (*Astyanax mexicanus*), fugu (*Takifugu rubripes*), stickleback (*Gasterosteus aculeatus*), tetraodon (*Tetraodon nigroviridis*), coelacanth (*Latimeria chalumnae*), lamprey (*Petromyzon marinus*), elephant shark (*Callorhinchus milii*), human (*Homo sapiens*), mouse (*Mus musculus*), cattle (*Bos taurus*), Xenopus (*Xenopus tropicalis*) and chicken (*Gallus gallus*). Multiple amino acid sequences were aligned by ClustalW (Thompson et al. 2002). The phylogenetic analysis was conducted using MEGA 6 (Tamura et al. 2013) with the maximum likelihood method and Jones-Taylor-Thornton (JTT) model. The bootstrap with 1000 replications was performed to evaluate the phylogenetic tree.

Syntenic analysis

Syntenic analysis was conducted to provide additional evidence for identity of genes. Genomic region contains the candidate gene was retrieved from channel catfish genome in NCBI, and zebrafish genome in Ensembl database. The localization of candidate genes in zebrafish and channel catfish was compared.

Results and discussion

Chemokine *ccl33* as a candidate gene for barbel development

To narrow down the list of genes potentially involved in the regulation of babel development, the 1,730 genes present in the channel catfish genome but absent in bottlenose catfish genome were compared with the 4,068 genes that were differentially expressed during regeneration. A set of 268 genes was identified to be present in the channel catfish genome and absent from the bottlenose catfish genome, and differentially expressed during barbel regeneration (Appendix Table 2). These 268 genes are potential candidates important for barbel development. We further reasoned that if these genes are indeed essential for barbel development, they should be present in fish with barbels such as channel catfish and zebrafish, and could be missing from fish without barbels. An analysis of gene contents from 13 fish genomes present in Ensembl databases was conducted (Figure 10), with two species, channel catfish and zebrafish, representing fish with barbels, and 11 species (fugu, tetraodon, stickleback, tilapia, spotted gar, mekaka, cavefish, amazon molly, platyfish, Atlantic salmon, and of course the bottlenose catfish) representing fish without barbels in the Ensembl database was examined. Such gene content analysis led to the identification of only one gene (GI: 108268439) was identified to be present in channel catfish and zebrafish, but absent in all the fish without barbels, and was differentially expressed in barbel regeneration. This gene was annotated as C-C motif chemokine 5-like gene at NCBI, but a recent comprehensive study of chemokine gene family re-annotated this gene as chemokine C-C motif ligand 33.7 (*ccl33.7*) (Fu et al. 2017). As such, the chemokine *ccl33* is likely a candidate gene important for the regulation of barbel development and regeneration.

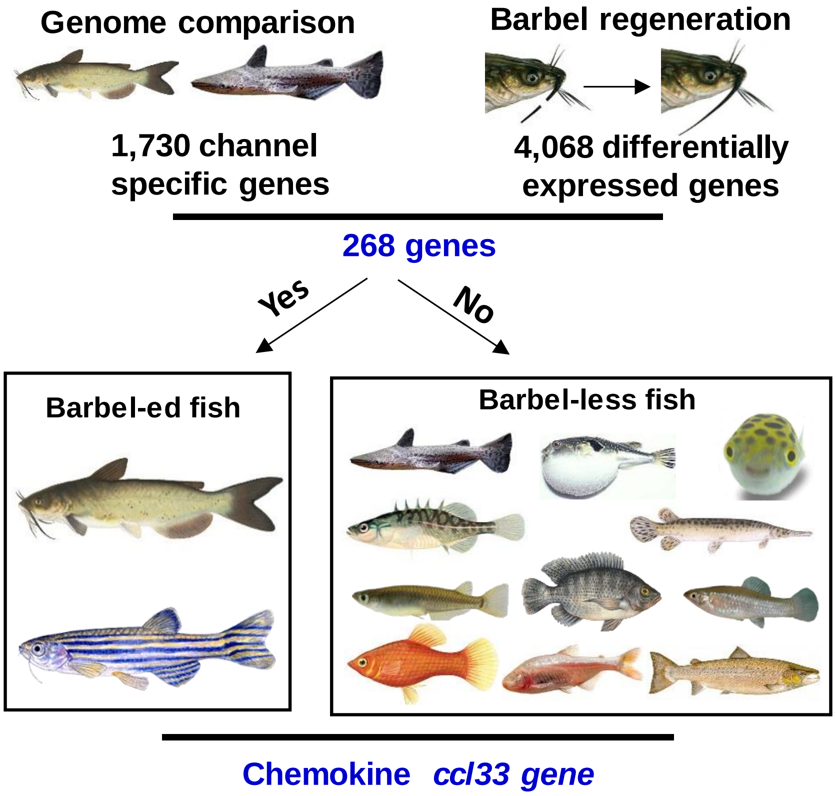


Figure 10 Chemokine *ccl33* was identified in barbel-ed fish, absent in barbel-less fish, and was differentially expressed during barbel regeneration.

Chemokines in different species

The importance of chemokine gene for barbel development make it necessary to compare chemokines in different species. The copy number of chemokine ligand including C-X-C motif and C-C motif genes were retrieved from Ensembl and NCBI database, and listed in Figure 11. The chemokine ligand genes have been reported in channel catfish (Fu et al. 2016; Fu et al. 2017). Compared with teleost fish, ancient lineage, cartilaginous fish, mammalian, amphibian, and avian, channel catfish have 81 copies of chemokine ligand genes, which is the highest. Zebrafish contains 75 copies of chemokine ligand genes, which is the second highest. In contrast, the copy number of chemokine genes in fish without barbels varies from 12 to 45. A total of 15 chemokine ligand genes were identified in bottlenose catfish, which was similar with fish without barbels. Ancient lineage species including lamprey and coelacanth contain 1 and 9 copies of chemokine ligand genes. Elephant shark contains 17 copies of chemokine ligand genes. Mammalian contains about 40 copies of chemokine ligand genes. Frog and chicken contain 13 and 11 chemokine ligand genes respectively (Figure 11).

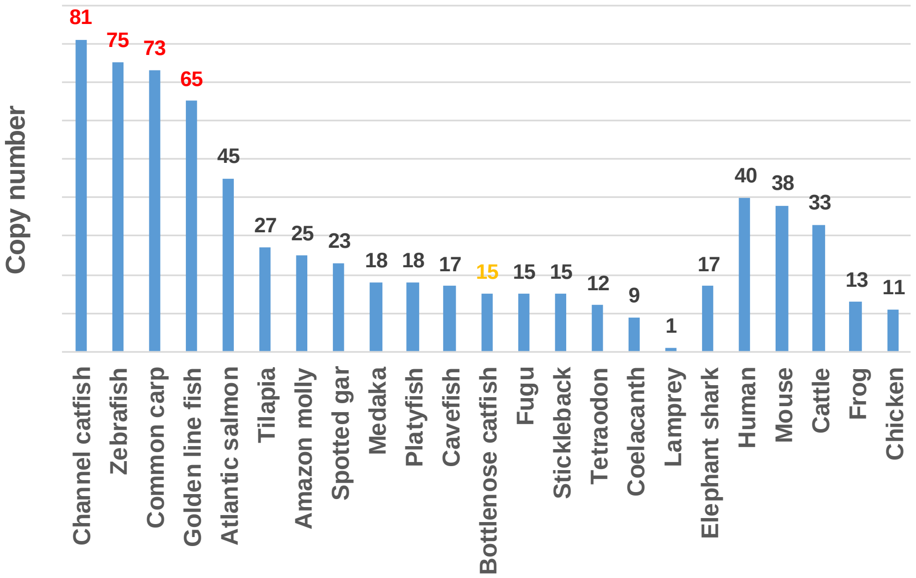


Figure 11 Copy number of chemokine ligand genes (C-C and C-X-C motif) in various species.

Phylogenetic and syntenic analysis of *ccl33*

The chemokine *ccl33* was identified as the candidate gene barbel development, making it necessary to further determine its identity and status in various fish species. Chemokines are a group of small, secreted molecules that signal through G protein-coupled receptors to promote cell survival and proliferation and to provide directional guidance to migrating cells (Wang and

Knaut 2014). They are divided into CC, CXC, CX_3C and XC according to the arrangements of the first two cysteine residues (Bachelerie et al. 2014). The gene *ccl33* is a member of the CC subfamily (Fu et al. 2016; Fu et al. 2017). Phylogenetic analysis confirmed the identity of *ccl33* (Figure 12). Analysis of *ccl33* and its copy numbers strongly supported the notion that its presence and absence in fish genomes are correlated with the presence or absence of barbels.

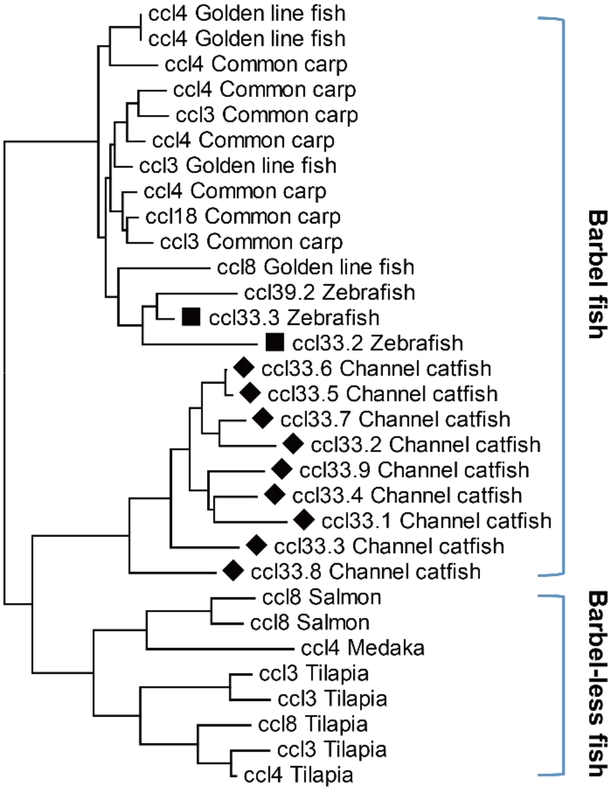


Figure 12 Phylogenetic analysis identified a clade contains *ccl33*.

However, in our analysis of gene contents, the assumption is that the genome sequences were complete. We further conducted syntenic analysis with fish species whose genome sequences are available to confirm that fish with barbels harbor *ccl33* while fish withour barbels lacks *ccl33* gene in their genomes. In the channel catfish genome, a total of nine copies of *ccl33* was identified. The conserved syntenic regions were then identified from fish with barbels, zebrafish, common carp, and golden line fish, and *ccl33* gene(s) were identified in the conserved syntenic regions (Figure 13). In contrast, *ccl33* gene was not found in the conserved syntenic regions of Atlantic salmon, Half-smooth tongue sole, swamp eel, nile tilapia, Japanese medaka, Asian bonytongue, and spotted gar, all fish without barbels. The syntenic analyses provided additional evidence that *ccl33* indeed was present in fish barbels but missing from fish without barbels. A related chemokine, *ccl39*, was found in the conserved syntenic regions of all fish under study, with or without barbels. As detailed below, only duplicated copies of *ccl33*, *ccl33.4*, *ccl33.6* and *ccl33.7* were differentially expressed, while the adjacent *ccl39* was not differentially expressed during barbel regeneration.

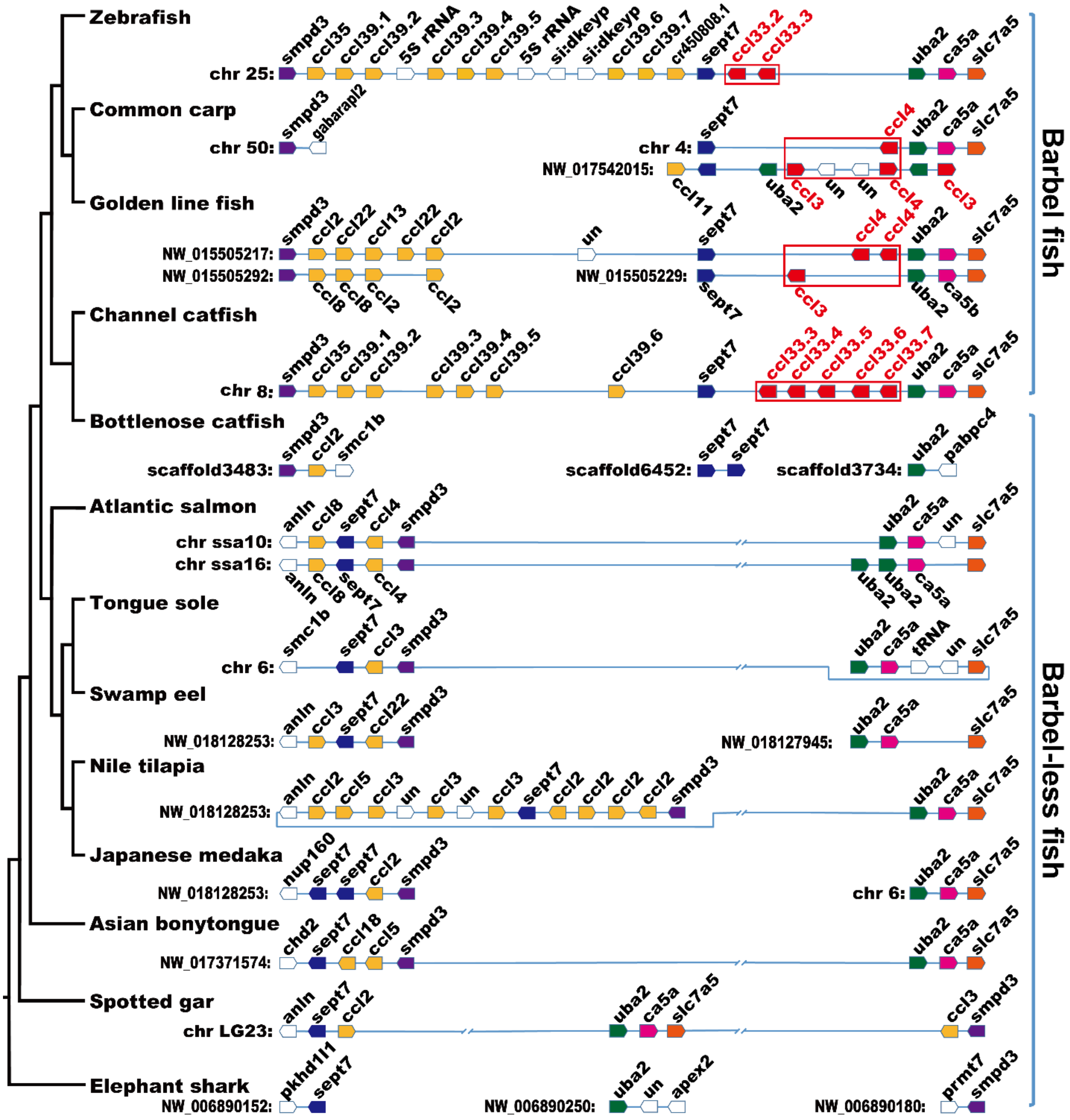


Figure 13 Syntenic analysis of the genomic region that contain *ccl33*.

Expression of *ccl33* genes

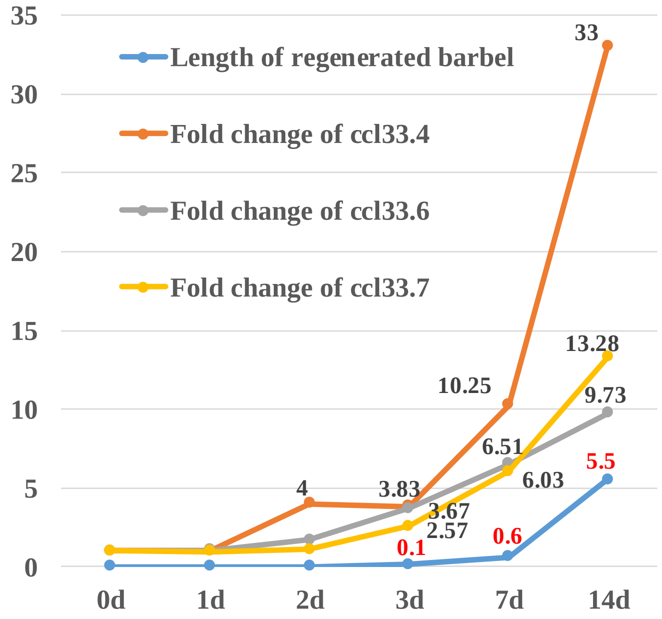


Figure 14 The expression of chemokine ligand *ccl33* genes were associated with the channel catfish barbel regeneration.

Of all the nine *ccl33* genes in channel catfish, three, *ccl33.4*, *ccl33.6*, and *ccl33.7*, were differentially expressed during barbel regeneration. Their enhanced expression during barbel regeneration was approximately synchronized with barbel regeneration (Figure 14). At the beginning of barbel regeneration, their expression was low; significantly increased expression started at day 3, and then drastically increased after one week during barbel regeneration, especially with *ccl33.4*. Interestingly, the increase in regenerated barbel lengths was well correlated with increased expression of the *ccl33* genes (Figure 14). Correlated expression of the *ccl33.4*, *ccl33.6*, and *ccl33.7* with barbel regeneration provided additional evidence for its involvement in the regulation of barbel development.

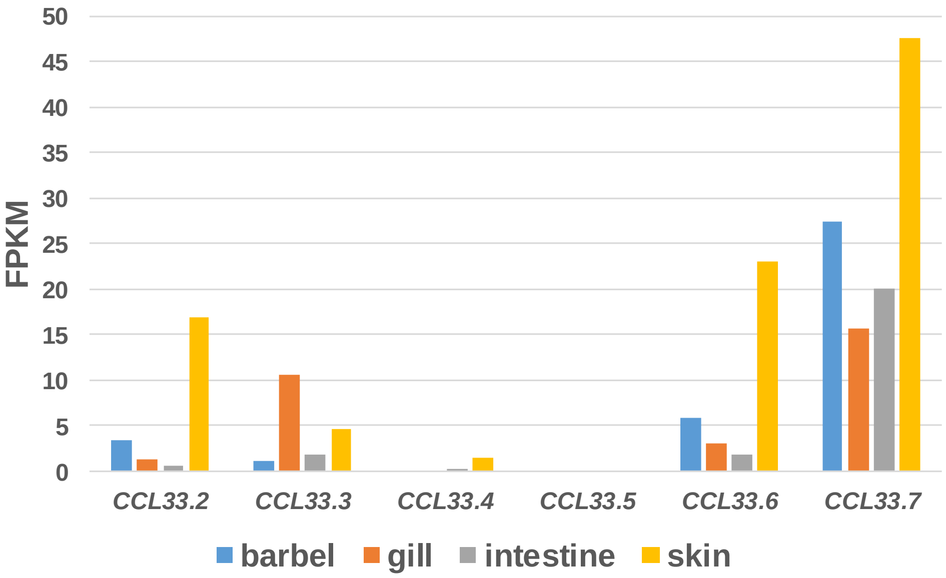


Figure 15 Expression of chemokine *ccl33* in different tissues.

The expression of *ccl33* was also determined through meta-analysis of RNA-Seq datasets from various tissues of channel catfish. Of the nine copies of the channel catfish *ccl33*, six copies were mapped to the channel catfish genome. Their expression value (FPKM) are listed in Figure 15. The highest expression value of all the copies of chemokine *ccl33* was identified in the skin, followed by the barbel, except for *ccl33.3*. The *ccl33.5* was not expressed in all the four tissues. The *ccl33.4* presented a low expression value in all the four tissues. The *ccl33* genes showed different expression pattern in different tissues. Generally, the high expression value of *ccl33* in skin and barbel may suggested its roles of in sensory and immunity.

Chapter 6 Chemokine *ccl33* knockout in zebrafish

Introduction

The CRISPR system is a microbial adaptive immune system that uses RNA guided nuclease to cleave foreign genetic elements that protects bacteria and archaea from invading viruses and plasmid (Deveau et al. 2010; Bhaya et al. 2011; Makarova et al. 2011; Chang et al. 2013). Three major types of CRISRP (types I-III) have been categorized based on locus organization and conservation (Makarova et al. 2011), each system comprise a cluster of Cas genes, noncoding RNAs and distinctive array of repetitive elements (direct repeats). These repeats are interspaced by short variable sequences derived from exogenous DNA targets known as protospacers, and together they constitute the CRISPR RNA (crRNA) array (Makarova et al. 2011). Within the DNA target, each protospacer is always associated with a protospacer adjacent motif (PAM), which can vary depending on the specific CRISPR system (Ran et al. 2013). The type II CRISPR system is one of the best characterized (Gasiunas et al. 2012; Jinek et al. 2012), which consists of the nuclease Cas9, the crRNA array that encodes the guide RNAs and a required auxiliary trans-activating crRNA (tracrRNA) that facilitates the processing of the crRNA array into discrete units. Each crRNA unit then contains a 20-nt guide sequence and a partial direct repeat, where the former direct Cas9 to a 20-bp DNA target. The crRNA and tracrRNA can be fused together to create a chimeric, single-guide RNA (Ran et al. 2013). Cas9 can thus be re-directed toward almost any target of interest in immediate vicinity of the PAM sequence by altering the 20-nt guide sequence within the sgRNA. Cas9 promotes genome editing by stimulating a double-strand break (DSB) at target locus. Upon cleavage by Cas9, the target locus typically undergoes the NHEJ and HDR. In the absence of a repair template, DSBs are religated by the NHEJ process, which leaves scars in the form of insertion/deletion mutation, which can lead to frameshift and premature stop codons.

CRISPR system is a powerful research tool that enables targeted gene editing in a wide variety of animals. CRISPR Cas9 system has been successfully utilized in many animals for the gene function analysis, such as nematode (*Caenorhabditis elegans*) (Friedland et al. 2013; Ward 2015), fruit fly (*Drosophila*) (Gratz et al. 2013), frog (*Xenopus tropicalis*) (Nakayama et al. 2013), zebrafish (Chang et al. 2013; Hwang et al. 2013), mice (Wang et al. 2013; Wu et al. 2015) and human cells (Cong et al. 2013; Mali et al. 2013). CRISPR Cas9 has been widely used for the validation of candidate genes. Functional analysis, using CRISPR Cas9 proved that *hox* genes are indispensable for the development of the wrists and digits of tetrapods (Nakamura et al. 2016). It was demonstrate that retinoic acid is critical in establishing asymmetric pigmentation and, via cross-talk with thyroid hormones, in modulating eye migration by using CRISPR Cas9 system (Shao et al. 2016). Knockout of *tbx4* in zebrafish using CRISPR Cas9 showed a ‘pelvic fin-loss’ phenotype similar to that of seahorses, which proved that *tbx4* is a regulator of hindlimb development (Lin et al. 2016).

Through the comparative analysis in the previous sections, we have proved the candidacy of chemokine *ccl33* for barbel development. In this section, we are trying to validate the function of *ccl33* by gene knock out using CRISPR Cas9 system.

Materials and methods

Designing of CRISPR targets and sgRNA preparation

To knock out *ccl33.2* and *ccl33.3* in zebrafish, we followed a high throughput targeted mutagenesis pipeline using CRISPR Cas9 technology (Varshney et al. 2015). We used a cloning-free method to generate sgRNA templates. Briefly, to generate sgRNA templates, an oligo consisting of the T7 promoter, 18 to 20 nucleotide target sequences (Table 3), and 20 nucleotide sequence that overlapped to a generic sgRNA template was designed. The targeting oligo was annealed with an 80 nuleotide chimeric sgRNA core sequence. The annealed oligos were then filled in using Accuzyme polymerase (Bioline). The quality of the assembled oligos was checked on a 2.5% agarose gel. Approximately 8ul of gRNA template was then used to transcribe RNA by in vitro transcription using the HiScribe T7 High Yield RNA Synthesis kit (New England BioLabs) according to the manufacturer’s instructions. The sgRNAs were purified by passage through a Microspin S-200 HR Column (GE Healthcare). The Cas9 protein was bought online directly (PNA Bio).

Table 3 Sequences of the genomic target sites of zebrafish *ccl33* genes.

Target gene	Strand	Target sequence
ccl33.2	-	CCGCCCTGCCCATGGATGTCC
ccl33.2	-	CCCTTGCCCCTGCCACCACCG
ccl33.2	-	CCACGAGAGCCAAAACCACCA
ccl33.3	-	CCCGAACCCTGTTGCTTCAAT
ccl33.3	-	CCAATCCCAGCCAACAAAGTA
ccl33.3	+	TTCACGCTGTGCTGTTAAAGG

Embryo injections

All animal husbandry procedures were performed according to approved animal protocols. All injections were performed in the wild-type strain EK. Approximately 2 nL total volume of Cas9 RNA and sgRNAs were co-injected into one-cell stage embryos at a concentration of 30pg of sgRNA with about 150 pg Cas9 protein. Then embryos were moved into 1L glass beakers containing E3 zebrafish medium and incubated at 28°C until hatch. Dead embryos were moved and water was changed daily.

Genotyping

Injected fish were grown to adulthood and screened for CRISPR induced mutations. The mutagenesis were analyzed by using T7 endonuclease I (T7E1) assay (Jao et al. 2013). Genomic DNA was extracted from muscle tissue. A short stretch of genomic region flanking the target site was PCR amplified from the genomic DNA (Table 4). PCR amplification consisted of a 2-min denaturing step at 94 °C, followed by 35 cycles of 30 s at 94 °C, 30 s at 57 °C, and 30 s at 72 °C. The PCR amplicons were purified using QIAquick PCR Purification kit (Qiagen). A total of 200 ng of the purified PCR amplicon was denatured and slowly reannealed to facilitate heteroduplex formation. The reannealing procedure consisted of a 5-min denaturing step at 95 °C, followed by cooling to 85 °C at -2 °C per second and further to 25 °C at -0.1 °C per second. The reannealed amplicon was then digested with 10 units of T7 endonuclease I (New England Biolabs) at 37 °C for 90 min. The reaction was stopped by adding 1 μL of 0.5MEDTA. Half of the sample was resolved by electrophoresis through a 2–2.5% agarose gel and visualized by ethidium bromide staining. The band intensity was quantified using Quantity One software (Bio-Rad).

Table 4 Sequences of the PCR primers for amplifying the target regions.

Target gene	Oligo Name	Sequence 5' to 3'	Length
ccl33.2	*ccl33.2* Primer3 F	AGCTCAATTTTCTCCGGGCT	20
ccl33.2	*ccl33.2* Primer3 R	TGACAGCAGAACTTACGGCCA	21
ccl33.3	*ccl33.3* Primer1 F	CCCGAACCCTGTTGCTTCAA	20
ccl33.3	*ccl33.3* Primer1 R	ATGCACACATTCAAATGACATCAG	24

Results and discussion

As the knockout system in channel catfish was not well developed, we used zebrafish knockout to test the roles of *ccl33* for barbel development. In zebrafish, two *ccl33* genes exist, *ccl33.2* and *ccl33.3*. The *ccl33.2* and *ccl33.3* in zebrafish was knocked out by using CRISPR-Cas9 system. We targeted three regions each of *ccl33.2* and *ccl33.3*. After injection of gRNA and Cas9 protein, the morphology of zebrafish embryo and larvae were continuously observed and recorded. Barbel blastema bud in the wild type zebrafish was observed 28 days after hatch (Figure 16), similar to previous reports (Hansen et al. 2002; LeClair and Topczewski 2010). We terminated the experiments 56 days after hatch as they became sexually mature and began to breed.

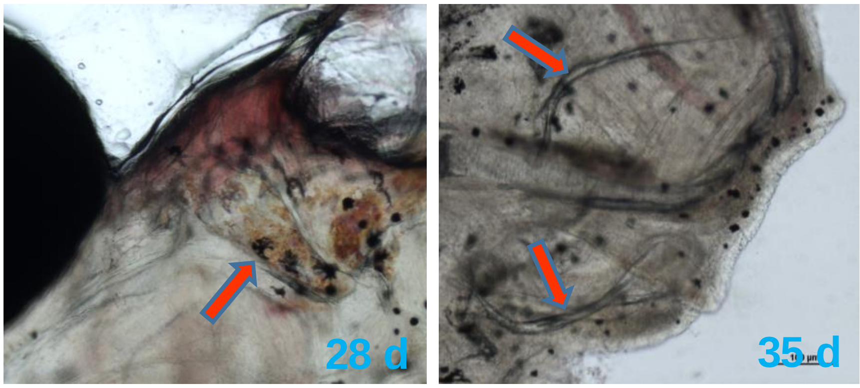


Figure 16 Early barbel morphology from control group.

Several phenotypes were observed as compared to the wild type fish created at the same time. The major phenotypes observed from the knockout fish included smaller body size (Figure 17), curved barbels (Figure 18), barbels of reduced lengths, and complete loss of barbels (Figure 19). Genotyping analysis revealed that the target region of most of the mutated individuals were edited (Figure 20). Apparently, the multiple phenotypes after knockout of *ccl33* genes, suggesting pleiotropic effect of *ccl33* knockout. These results suggest that *ccl33* is a key regulator of barbel development. In addition, it may have many other functions related to growth and development in general.

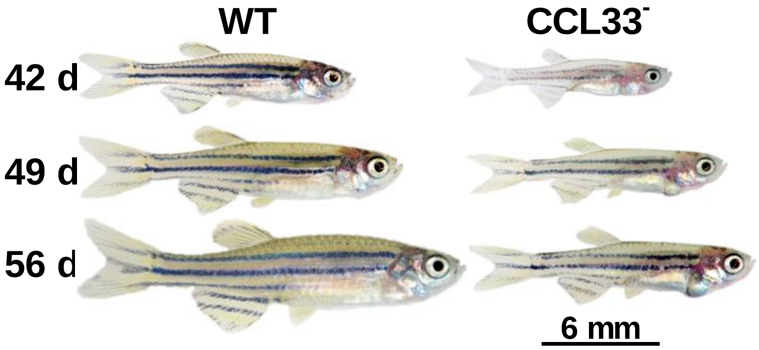


Figure 17 General morphology of wild type and *ccl33* mutation zebrafish.

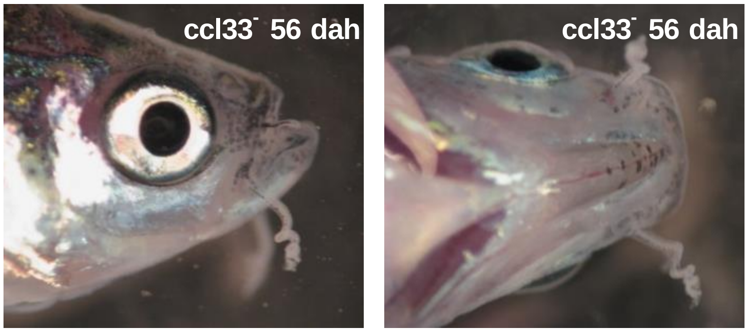


Figure 18 Curly barbels were observed from *ccl33* mutation zebrafish.

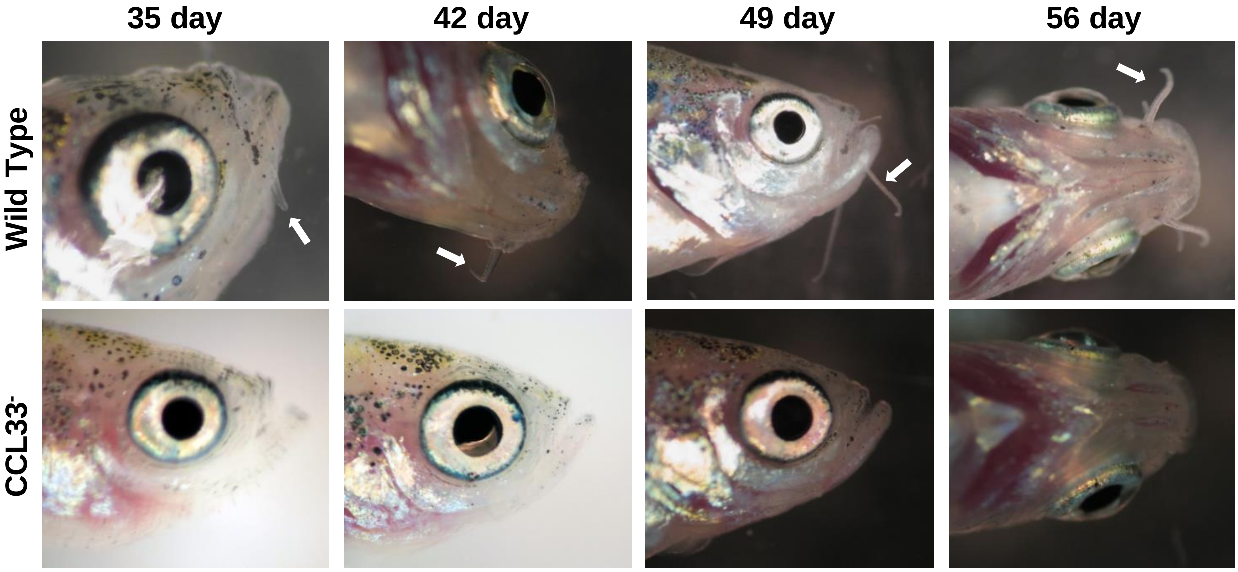
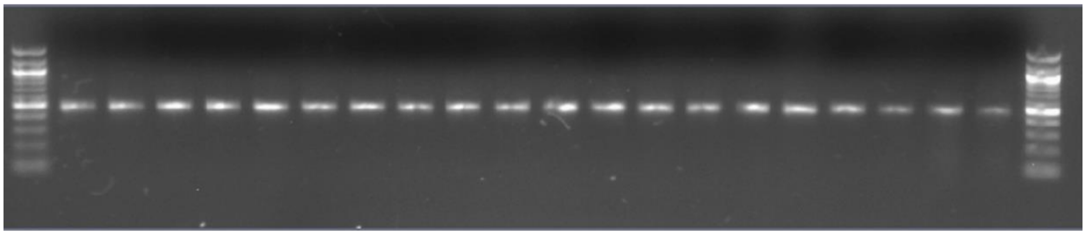
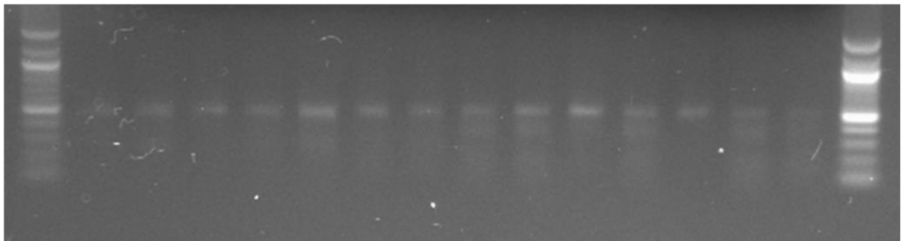


Figure 19 Barbel features of wild type and *ccl33* mutation zebrafish.



Before T7E1 treat



After T7E1 treat

Figure 20 Genotyping of the mutated zebrafish.

The primary functions of homeostatic chemokines in development include organogenesis, which was defined as the processes that lead to the formation of an organ or limb (Zlotnik et al. 2011). Homeostatic chemokines have an important role in several organogenesis steps, including direct the migration of a committed stem cell to the site where an organ is going to develop (Doitsidou et al. 2002; Knaut et al. 2003), promote angiogenesis (Cui et al. 2011), maintain stem cells in a niche site until they are needed to produce progeny cells (Steinberg and Silva 2010), provide a framework or cellular organization to produce the organ (Valentin et al. 2007; Mahabaleshwar et al. 2008), and direct proliferative effects on cells (Ehtesham et al. 2009). The function of several chemokine and its receptors in directing organogenesis or regeneration have been well studied in zebrafish. For example, Cxcl12, also known as stromal cell derived factor 1 (Sdf1), is the guidance cue for the lateral line primordium in zebrafish (Perlin and Talbot 2007). The *cxcl12a* and *cxcr4* were essential for heart regeneration in zebrafish (Itou et al. 2012). Cxcr4 guides gonadal stem cells to their proper site in the developing embryo (Raz and Mahabaleshwar 2009). Cxcr4 is also involved, along with Cxcr7, in modulating the development of the central nervous system (CNS) (Dambly-Chaudiere et al. 2007; Thelen and Thelen 2008). Pathways activated by members of the CXC family of chemokines play important roles in the mechanisms of liver repair and regeneration through their effects on hepatocytes (Van Sweringen et al. 2011). The CXC chemokines regulate the hepatic proliferative response and subsequent liver regeneration (Wilson et al. 2015). In spite of these rich knowledge of the involvement of chemokines or their receptors in organogenesis, no information was available for the function of *ccl33*. In this work, for the first time, we identified *ccl33* as a candidate gene for barbel development in teleost fish. Its correlated expression during barbel regeneration, and its knockout provided strong support for its candidacy as a key regulator of barbel development. In addition, its broad effects on growth and development suggested that *ccl33* may have important functions for normal development and growth of zebrafish. Although its knockout was not lethal, the knockout fish were all small and weak in performance, suggesting additional roles of *ccl33* beyond controlling barbel development. It is possible that the loss of barbels or reduced size, or modified architecture of barbels may have a secondary effect on growth because of the roles of barbels in sensing the food, and thereby the effects on feeding. The *ccl33* knockout could have other effects such as reduced immunity against infections. This research therefore opens a new venue for increased research for the functions of chemokines in development, as well as in defense response against infectious agents.

Summary

A barbel on a fish is a slender, whisker-like sensory organ near the mouth that can be found in many fish species, such as catfish, common carp, goatfish, hagfish, sturgeon, zebrafish, and some species of shark like the sawshark. Barbels house the taste buds, olfactory sensors and tactual sensors, and are used to search for food in murky water. Barbels help the catfish to adapt to the benthic environment. As an organ, barbel may play important roles during fish evolution, adaption, and provide a useful model for developmental related studies.

Bottlenose catfish is unique in Siluriformes for its absence of barbels. Its close phylogenetic relationship with channel catfish (with prominent barbels) offered an ideal natural model to determine the genomic basis of barbel development. Subtractive comparative genome analysis, when coupled to transcriptome analysis of differentially expressed genes, was proven to be very effective for the identification of genes of structural significance (Liu et al. 2016). In this study, we extended the subtractive comparative genome analysis to include a large number of fish species sharing the phenotypes. Comparison of the genes within the genomes of fish with barbels with those without barbels, along with the differentially expressed genes during barbel regeneration, allowed us to identify a single candidate gene, *ccl33,* for barbel development. The *ccl33* genes, their expression patterns, synchronized expression with barbel regeneration, and their knockout provided strong evidence that *ccl33* is a key regulator of barbel development. A spectrum of phenotype variations including partial and complete loss of barbels, formation of curly barbels, reduced growth was observed in the knockout zebrafish, suggesting that *ccl33* may have many different functions for normal growth and development, as well as barbel development. The fact that the same gene was lost in many barbel-less fish belonging to a broad range of phelogenies suggested that the mechanism of barbel development may have been

conserved across teleost fish species, a group representing over 50% of all vertebrates. Future studies are needed to determine the specific molecular mechanisms of *ccl33* function during barbel development, and growth and development in general.

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Appendix Table 1 Genes present in channel catfish, absent in bottlenose catfish

Gene ID	Locus	Protein product	Length
108255763	LOC108255763	XP_017307450.1	2337
108256026	carnmt1	XP_017307985.1	418
108256526	polr1d	XP_017308970.1	172
108257874	atraid	XP_017311470.1	230
108259733	LOC108259733	XP_017314930.1	219
108262226	LOC108262226	XP_017318301.1	186
108262879	LOC108262879	XP_017318723.1	329
108264799	LOC108264799	XP_017322162.1	383
108264825	LOC108264825	XP_017322217.1	689
108265132	c1h8orf59	XP_017322758.1	98
108268648	fanca	XP_017329197.1	1141
108270530	LOC108270530	XP_017332816.1	228
108271080	LOC108271080	XP_017333819.1	342
108272891	LOC108272891	XP_017337204.1	300
108273999	ccser2	XP_017339238.1	791
108274164	bricd5	XP_017339608.1	228
108275464	mdp1	XP_017341794.1	160
100304470	b2m	NP_001187001.1	116
100304887	cript	NP_001232877.1	101
100305060	LOC100305060	NP_001187223.1	78
108259533	LOC108259533	XP_017314605.1	211
108260286	LOC108260286	XP_017315915.1	1346
108264443	LOC108264443	XP_017321459.1	449
108265414	tgoln2	XP_017323183.1	307
108266931	LOC108266931	XP_017326252.1	197
108270925	LOC108270925	XP_017333435.1	193
108271021	LOC108271021	XP_017333665.1	119
108278302	LOC108278302	XP_017347058.1	180
108280891	LOC108280891	XP_017351876.1	90
804877	ATP6	NP_612130.1	227
804880	ND1	NP_612125.1	324
100304584	LOC100304584	NP_001187095.1	105
100528356	brk1	NP_001187555.1	75
108255519	LOC108255519	XP_017307008.1	110
108256275	hcrt	XP_017308436.1	126
108257472	edn1	XP_017310769.1	195
108259812	cchcr1	XP_017315017.1	692
108260858	LOC108260858	XP_017316999.1	231
108261098	LOC108261098	XP_017317468.1	226
108263206	borcs7	XP_017319270.1	103
108263260	LOC108263260	XP_017319384.1	100

108265761	clps	XP_017323916.1	136
108266496	LOC108266496	XP_017325497.1	114
108267632	LOC108267632	XP_017327393.1	139
108268185	LOC108268185	XP_017328487.1	215
108268439	LOC108268439	XP_017328905.1	78
108269115	LOC108269115	XP_017330184.1	86
108269806	mrps5	XP_017331332.1	400
108271223	cep19	XP_017334118.1	160
108271379	slc39a3	XP_017334439.1	315
108273111	ten1	XP_017337625.1	126
108276417	LOC108276417	XP_017343554.1	241
108276694	prr11	XP_017344007.1	299
108278804	LOC108278804	XP_017347903.1	365
108280026	LOC108280026	XP_017350293.1	305
108280749	LOC108280749	XP_017351609.1	510
804878	ND3	NP_612132.1	116
804882	ND4	NP_612134.1	460
804885	COX3	NP_612131.1	261
804886	ND6	NP_612136.1	171
100304587	LOC100304587	NP_001187096.1	92
100304595	LOC100304595	XP_017306663.1	119
100528255	cck	NP_001187454.1	123
100528304	ebag9	NP_001187503.1	212
100528339	dal1b	NP_001187538.1	102
100528727	arpc4	NP_001187926.1	168
100529001	psmf1	NP_001188200.1	270
108254817	LOC108254817	XP_017305644.1	239
108255518	LOC108255518	XP_017307006.1	112
108255701	LOC108255701	XP_017307331.1	108
108256245	LOC108256245	XP_017308375.1	111
108256436	pkia	XP_017308799.1	85
108257443	LOC108257443	XP_017310711.1	645
108257542	ociad2	XP_017310896.1	160
108258002	LOC108258002	XP_017311708.1	177
108258663	LOC108258663	XP_017312951.1	107
108259248	LOC108259248	XP_017314029.1	227
108259575	pex11a	XP_017314657.1	246
108260035	LOC108260035	XP_017315449.1	270
108260899	LOC108260899	XP_017317094.1	264
108262451	LOC108262451	XP_017318391.1	224
108263381	pdss2	XP_017319591.1	381
108264196	LOC108264196	XP_017321018.1	231
108264363	tsnaxip1	XP_017321304.1	548
108264506	c4h15orf48	XP_017321604.1	87

108264531	LOC108264531	XP_017321623.1	152
108265590	epgn	XP_017323600.1	153
108266135	LOC108266135	XP_017324656.1	268
108266359	LOC108266359	XP_017325014.1	332
108266750	tex30	XP_017325928.1	265
108266945	LOC108266945	XP_017326272.1	224
108267969	LOC108267969	XP_017328071.1	407
108268228	ssx2ip	XP_017328565.1	501
108268874	LOC108268874	XP_017329676.1	222
108268928	LOC108268928	XP_017329784.1	177
108269592	mtfr1l	XP_017331025.1	303
108270531	tmem44	XP_017332820.1	454
108270589	LOC108270589	XP_017332908.1	463
108271423	LOC108271423	XP_017334509.1	222
108272514	smdt1	XP_017336449.1	97
108273408	mrpl58	XP_017338087.1	198
108274023	c13h10orf128	XP_017339285.1	91
108274089	LOC108274089	XP_017339438.1	264
108274225	LOC108274225	XP_017339729.1	394
108274412	smim22	XP_017340039.1	81
108274670	LOC108274670	XP_017340388.1	112
108275545	haus8	XP_017341915.1	364
108278494	LOC108278494	XP_017347401.1	142
108279884	ccdc167	XP_017349960.1	100
108280886	LOC108280886	XP_017351869.1	171
108280991	LOC108280991	XP_017351996.1	222
108281088	LOC108281088	XP_017352141.1	130
804875	COX2	NP_612128.1	230
804876	ATP8	NP_612129.1	55
804879	ND5	NP_612135.1	607
804881	ND4L	NP_612133.1	98
804883	ND2	NP_612126.1	348
100304478	LOC100304478	NP_001187006.1	60
100305002	LOC100305002	NP_001187171.1	184
100415908	LOC100415908	NP_001187260.1	223
100528072	cf125	NP_001187271.1	129
100528215	emc4	NP_001187414.1	187
100528363	gins3	NP_001187562.1	211
100528404	rabif	NP_001187603.1	133
100528408	tesc	NP_001187607.1	123
100528430	anapc13	NP_001187629.1	74
100528515	vps28	NP_001187714.1	223
100528592	spcs1	NP_001187791.1	101
100528639	skp1	NP_001187838.1	163

100528677	pdcd5	NP_001187876.1	126
100528681	cops9	NP_001187880.1	57
100528704	mzt1	NP_001187903.1	75
100528768	lyrm5	NP_001187967.1	85
100528801	mrps14	NP_001188000.1	133
100528912	ndufb4	NP_001188111.1	127
100528986	znrd1	NP_001188185.1	133
108254720	LOC108254720	XP_017305459.1	209
108254755	arv1	XP_017305523.1	241
108255397	batf	XP_017306830.1	124
108255480	ascc2	XP_017306909.1	763
108255648	LOC108255648	XP_017307240.1	232
108255681	LOC108255681	XP_017307300.1	204
108256237	azi2	XP_017308361.1	353
108256239	cmc1	XP_017308367.1	107
108256594	LOC108256594	XP_017309125.1	83
108256728	LOC108256728	XP_017309381.1	157
108257072	LOC108257072	XP_017309972.1	267
108257184	cap2	XP_017310199.1	389
108257214	LOC108257214	XP_017310313.1	408
108257382	LOC108257382	XP_017310602.1	132
108257495	tomm7	XP_017310796.1	55
108258433	LOC108258433	XP_017312537.1	378
108258502	pld6	XP_017312671.1	243
108258651	LOC108258651	XP_017312925.1	186
108258791	cytl1	XP_017313201.1	192
108259146	agrp	XP_017313858.1	143
108259227	cklf	XP_017313985.1	143
108259252	LOC108259252	XP_017314032.1	210
108259526	LOC108259526	XP_017314593.1	249
108259529	fam207a	XP_017314596.1	237
108259534	LOC108259534	XP_017314606.1	211
108260421	LOC108260421	XP_017316197.1	151
108260508	LOC108260508	XP_017316354.1	170
108260511	slc9b2	XP_017316357.1	533
108261049	LOC108261049	XP_017317354.1	163
108261625	LOC108261625	XP_017317933.1	130
108262792	LOC108262792	XP_017318612.1	416
108262793	LOC108262793	XP_017318613.1	259
108263202	apopt1	XP_017319259.1	198
108263248	LOC108263248	XP_017319364.1	111
108263386	kmo	XP_017319604.1	473
108263832	LOC108263832	XP_017320489.1	112
108263890	LOC108263890	XP_017320565.1	108

108263973	LOC108263973	XP_017320709.1	410
108264385	kiaa0513	XP_017321347.1	421
108264547	nutf2	XP_017321659.1	127
108265078	LOC108265078	XP_017322663.1	263
108265287	stap2	XP_017322931.1	415
108265611	c5h9orf116	XP_017323639.1	141
108265844	LOC108265844	XP_017324081.1	209
108266094	LOC108266094	XP_017324579.1	243
108266430	LOC108266430	XP_017325223.1	258
108266545	LOC108266545	XP_017325499.1	218
108266662	dcaf17	XP_017325779.1	529
108266787	c6h21orf62	XP_017326002.1	214
108266789	LOC108266789	XP_017326011.1	132
108267124	c7h22orf39	XP_017326584.1	108
108267188	LOC108267188	XP_017326670.1	101
108267255	LOC108267255	XP_017326735.1	124
108267286	LOC108267286	XP_017326792.1	224
108267350	LOC108267350	XP_017326880.1	203
108267429	LOC108267429	XP_017326988.1	129
108267455	pex19	XP_017327016.1	282
108267567	LOC108267567	XP_017327250.1	124
108267962	c7h4orf48	XP_017328062.1	86
108268115	LOC108268115	XP_017328326.1	97
108268327	ltbr	XP_017328717.1	353
108268437	LOC108268437	XP_017328903.1	595
108268603	ndufc1	XP_017329138.1	69
108268660	LOC108268660	XP_017329227.1	363
108268687	LOC108268687	XP_017329271.1	241
108268882	tmsb15b	XP_017329693.1	46
108268918	LOC108268918	XP_017329751.1	115
108269344	LOC108269344	XP_017330655.1	78
108269355	LOC108269355	XP_017330676.1	204
108269361	c8h12orf73	XP_017330683.1	64
108269490	tmem229b	XP_017330904.1	185
108270120	LOC108270120	XP_017331955.1	127
108270394	crls1	XP_017332524.1	378
108270478	cfl2	XP_017332713.1	166
108270539	c1h16orf91	XP_017332839.1	155
108270745	LOC108270745	XP_017333119.1	925
108270746	LOC108270746	XP_017333120.1	921
108270874	timm13	XP_017333325.1	95
108271006	LOC108271006	XP_017333637.1	491
108271096	elp4	XP_017333857.1	389
108271220	serf2	XP_017334114.1	59

108271274	nr2c2ap	XP_017334228.1	141
108271425	tax1bp3	XP_017334514.1	125
108271519	snrpc	XP_017334632.1	159
108271554	LOC108271554	XP_017334684.1	223
108272082	LOC108272082	XP_017335732.1	75
108272167	LOC108272167	XP_017335903.1	76
108272348	cks1b	XP_017336199.1	79
108272510	ccdc134	XP_017336446.1	229
108272602	atp5e	XP_017336584.1	51
108272615	pex11b	XP_017336601.1	252
108272622	dctn3	XP_017336621.1	185
108272639	LOC108272639	XP_017336661.1	218
108272745	LOC108272745	XP_017336922.1	363
108272856	hn1	XP_017337160.1	139
108273013	LOC108273013	XP_017337460.1	239
108273081	LOC108273081	XP_017337557.1	173
108273140	LOC108273140	XP_017337676.1	158
108273612	LOC108273612	XP_017338452.1	127
108273994	tomm22	XP_017339229.1	133
108274251	LOC108274251	XP_017339791.1	425
108274303	nt5m	XP_017339890.1	230
108274403	c2h8orf82	XP_017340011.1	213
108274852	LOC108274852	XP_017340775.1	247
108274856	LOC108274856	XP_017340782.1	231
108274859	LOC108274859	XP_017340785.1	226
108274881	LOC108274881	XP_017340817.1	128
108275268	lrrc61	XP_017341463.1	281
108275426	LOC108275426	XP_017341728.1	129
108275551	LOC108275551	XP_017341922.1	326
108275692	LOC108275692	XP_017342101.1	432
108276169	cenpw	XP_017343137.1	75
108276560	lyrm7	XP_017343819.1	104
108276725	LOC108276725	XP_017344082.1	114
108276884	LOC108276884	XP_017344430.1	125
108276957	LOC108276957	XP_017344627.1	271
108276972	LOC108276972	XP_017344667.1	113
108277089	LOC108277089	XP_017344948.1	87
108277678	LOC108277678	XP_017345975.1	916
108277757	LOC108277757	XP_017346142.1	281
108278384	spcs2	XP_017347223.1	219
108278455	LOC108278455	XP_017347336.1	202
108278465	LOC108278465	XP_017347351.1	209
108278988	slc31a2	XP_017348330.1	138
108279232	c18h5orf15	XP_017348793.1	290

108279644	orc5	XP_017349462.1	445
108279850	LOC108279850	XP_017349874.1	222
108280490	LOC108280490	XP_017351002.1	55
108280668	mbp	XP_017351437.1	133
108280775	LOC108280775	XP_017351656.1	290
108280863	twsg1	XP_017351823.1	223
108280907	mrpl34	XP_017351897.1	115
804884	COX1	NP_612127.1	516
804887	CYTB	NP_612137.1	379
100304479	cga	NP_001187007.1	116
100304514	LOC100304514	NP_001187029.1	550
100304516	rplp1	NP_001187031.1	113
100304521	rpl6	XP_017323447.1	262
100304529	rpl13	NP_001187042.1	211
100304531	rpl14	NP_001187043.1	141
100304533	rpl18	NP_001187045.1	188
100304534	rpl18a	NP_001187046.1	176
100304543	rpl29	NP_001187054.1	64
100304549	LOC100304549	NP_001187060.1	106
100304550	rpl37	NP_001187061.1	97
100304551	rpl37a	NP_001187062.1	92
100304552	rpl38	NP_001187063.1	70
100304554	rpl41	NP_001187065.1	25
100304557	rps3	NP_001187068.1	245
100304558	rps4x	NP_001187069.1	263
100304561	rps7	NP_001187072.1	194
100304566	rps14	NP_001187077.1	151
100304569	LOC100304569	NP_001187080.1	134
100304579	rps29	NP_001187090.1	56
100304588	LOC100304588	XP_017326447.1	137
100304589	LOC100304589	NP_001187098.1	87
100304604	ifn	NP_001187107.1	162
100304621	LOC100304621	XP_017313766.1	173
100304622	gcg	NP_001187117.1	120
100304630	LOC100304630	XP_017330182.1	81
100304631	LOC100304631	XP_017326449.1	117
100304644	LOC100304644	NP_001187134.1	94
100304692	LOC100304692	NP_001187144.1	81
100304698	LOC100304698	XP_017350431.1	298
100304709	LOC100304709	NP_001232870.1	44
100304735	eif1b	NP_001232871.1	113
100304756	gss	XP_017342234.1	477
100304809	ddost	XP_017342350.1	466
100304934	sssca1	XP_017345580.1	257

100304967	LOC100304967	XP_017307935.1	269
100304977	LOC100304977	NP_001187154.1	520
100304978	LOC100304978	XP_017329493.1	471
100304979	LOC100304979	NP_001187156.1	412
100304990	cd59	NP_001187161.1	119
100304994	cd79a	NP_001187165.1	227
100305023	cd247	NP_001187191.1	153
100305027	sst2	XP_017351534.1	105
100305047	rpl10a	NP_001187211.1	216
100305053	rpl39	NP_001187217.1	51
100305055	rps11	NP_001187218.1	159
100305056	rps16	NP_001187219.1	149
100329224	LOC100329224	NP_001187244.1	108
100379165	il11	XP_017336316.1	221
100526711	nat9	XP_017339780.1	218
100526712	fam50a	XP_017343230.1	323
100528083	gstk1	XP_017340493.1	213
100528089	scnm1	XP_017342376.1	253
100528105	bbs5	NP_001187304.1	320
100528129	sc5d	NP_001187328.1	281
100528135	naa38	NP_001187334.1	103
100528157	pigf	NP_001187356.1	219
100528158	rdm1	NP_001187357.1	280
100528161	s39a9	NP_001187360.1	306
100528168	c5h9orf64	NP_001187367.1	339
100528172	wdr77	NP_001187371.1	322
100528176	hdhd3	XP_017334553.1	243
100528187	mtch2	NP_001187386.1	300
100528206	cmc4	NP_001187405.1	71
100528212	va0e1	NP_001187411.1	81
100528228	atox1	NP_001187427.1	67
100528240	ska2	XP_017343725.1	230
100528243	med20	NP_001187442.1	212
100528245	mrpl10	NP_001187444.1	255
100528253	eif3k	NP_001187452.1	219
100528257	elp6	NP_001187456.1	268
100528262	fmc1	NP_001187461.1	110
100528272	rbx1	NP_001187471.1	108
100528301	mustn1	NP_001187500.1	78
100528302	ost4	NP_001187501.1	37
100528303	smim7	XP_017332752.1	104
100528337	trappc4	NP_001187536.1	219
100528343	ufm1	NP_001187542.1	90
100528355	lamtor5	NP_001187554.1	91

100528360	cwc15	NP_001187559.1	231
100528364	f162b	NP_001187563.1	155
100528378	wdr83os	NP_001187577.1	106
100528379	nhej1	NP_001187578.1	319
100528382	htatip2	NP_001187581.1	248
100528395	anfc1	XP_017318884.1	132
100528401	creld2	NP_001187600.1	289
100528407	c28hxorf56	NP_001187606.1	224
100528414	rpe	XP_017324522.1	183
100528437	psmg4	NP_001187636.1	126
100528457	taf7l	XP_017328782.1	362
100528458	snrpd2	NP_001187657.1	118
100528459	ptpmt1	XP_017313779.1	185
100528467	col	NP_001187666.1	113
100528469	ndufaf4	NP_001187668.1	174
100528479	c24h1orf109	NP_001187678.1	202
100528497	tm14c	NP_001187696.1	107
100528498	tac1	XP_017336125.1	107
100528507	mrps24	NP_001187706.1	171
100528508	eapp	NP_001187707.1	310
100528513	polr2l	NP_001187712.1	67
100528516	polr2j	NP_001187715.1	117
100528517	mycbp	NP_001187716.1	103
100528518	cp080	NP_001187717.1	193
100528525	mnd1	NP_001187724.1	205
100528530	mrpl51	NP_001187729.1	129
100528536	guc2a	NP_001187735.1	108
100528538	pop5	NP_001187737.1	167
100528548	cnot9	NP_001187747.1	297
100528550	pop7	NP_001187749.1	151
100528557	nop10	NP_001187756.1	64
100528558	pttg	NP_001187757.1	188
100528560	tmem258	NP_001187759.1	79
100528576	mrpl32	NP_001187775.1	175
100528578	med8	NP_001187777.1	266
100528590	mcrip2	NP_001187789.1	144
100528602	supt4h1	NP_001187801.1	117
100528603	smn1	NP_001187802.1	315
100528607	pmm2	NP_001187806.1	250
100528615	ndufa2	XP_017347290.1	100
100528619	zfand1	NP_001187818.1	270
100528620	med11	XP_017343742.1	140
100528627	tmem141	NP_001187826.1	128
100528632	rnf7	NP_001187831.1	111

100528641	ysmu	NP_001187840.1	268
100528642	cdc26	NP_001187841.1	86
100528646	siva1	NP_001187845.1	173
100528647	snrpe	NP_001187846.1	92
100528653	hddc3	NP_001187852.1	179
100528660	hikeshi	NP_001187859.1	197
100528668	hsbp1	XP_017320578.1	76
100528675	oxnad1	NP_001187874.1	299
100528683	chchd7	XP_017326470.1	87
100528688	tango2	XP_017306670.1	274
100528690	meig1	XP_017349154.1	92
100528702	spaca9	XP_017306675.1	210
100528707	ccdc58	NP_001187906.1	143
100528715	taz	NP_001187914.1	262
100528719	apip	NP_001187918.1	240
100528724	pir	NP_001187923.1	291
100528728	pomp	NP_001187927.1	142
100528732	anapc11	NP_001187931.1	88
100528735	bola2	NP_001187934.1	86
100528747	pam16	NP_001187946.1	138
100528764	ndufs5	XP_017309438.1	106
100528771	rpa3	NP_001187970.1	122
100528777	ndufb2	NP_001187976.1	100
100528778	mrpl33	NP_001187977.1	65
100528790	c8h4orf47	NP_001187989.1	313
100528791	mcts1	XP_017328794.1	181
100528792	ndufa13	NP_001187991.1	144
100528793	cb064	NP_001187992.1	75
100528795	psmg3	NP_001187994.1	120
100528829	ntpcr	NP_001188028.1	197
100528831	aida	XP_017338596.1	303
100528850	hspb11	NP_001188049.1	133
100528856	pex3	NP_001188055.1	366
100528857	tmem82	NP_001188056.1	339
100528862	stpg1	XP_017340046.1	326
100528867	c18h11orf70	NP_001188066.1	236
100528870	nup35	NP_001188069.1	310
100528895	gtf2h5	XP_017310853.1	71
100528896	minos1	NP_001188095.1	76
100528925	wbscr22	NP_001188124.1	282
100528934	atpaf1	XP_017332765.1	286
100528948	tomm5	NP_001188147.1	51
100528956	c10h19orf25	XP_017332776.1	104
100528959	alg13	NP_001188158.1	164

100528971	lsm2	NP_001188170.1	95
100528981	ccdc124	NP_001188180.1	214
100528983	nosip	XP_017338737.1	258
100528988	crym	XP_017338059.1	337
100529003	gatad1	NP_001188202.1	244
100529008	rangrf	NP_001188207.1	182
100529009	sptssa	NP_001188208.1	68
100529011	aspdh	NP_001188210.1	278
100529014	cq072	XP_017338829.1	255
100529017	dap3	NP_001188216.1	401
100529027	ndufaf2	NP_001188226.1	161
100529048	glrx	NP_001188247.1	106
100529049	bcas2	XP_017322329.1	208
101154653	mxra8	XP_017343117.1	445
108254697	mfap2	XP_017305432.1	142
108254699	atad3a	XP_017305435.1	660
108254725	LOC108254725	XP_017305467.1	562
108254727	LOC108254727	XP_017305478.1	1040
108254774	LOC108254774	XP_017305564.1	196
108254791	LOC108254791	XP_017305600.1	89
108254805	tmem167b	XP_017305612.1	74
108254814	LOC108254814	XP_017305638.1	123
108254893	ift52	XP_017305820.1	436
108254896	LOC108254896	XP_017305824.1	207
108254934	chchd4	XP_017305921.1	151
108254936	c21h1orf50	XP_017305925.1	189
108254962	LOC108254962	XP_017305995.1	284
108254989	fam213b	XP_017306033.1	176
108254990	LOC108254990	XP_017306034.1	125
108254996	LOC108254996	XP_017306041.1	146
108255031	ghrh	XP_017306121.1	163
108255055	LOC108255055	XP_017306185.1	1006
108255058	shisa5	XP_017306191.1	237
108255082	rpp14	XP_017306230.1	170
108255096	traip	XP_017306253.1	455
108255119	svbp	XP_017306296.1	66
108255122	LOC108255122	XP_017306301.1	203
108255135	c21h6orf89	XP_017306337.1	282
108255139	LOC108255139	XP_017306343.1	169
108255147	ccdc51	XP_017306352.1	416
108255149	tma7	XP_017306355.1	64
108255216	timm17a	XP_017306477.1	166
108255220	LOC108255220	XP_017306486.1	714
108255228	LOC108255228	XP_017306532.1	147

108255235	LOC108255235	XP_017306540.1	369
108255243	coil	XP_017306556.1	659
108255267	LOC108255267	XP_017306591.1	310
108255287	c21h1orf116	XP_017306640.1	390
108255299	pdrg1	XP_017306661.1	132
108255335	zc3h14	XP_017306735.1	657
108255369	LOC108255369	XP_017306787.1	349
108255377	LOC108255377	XP_017306803.1	299
108255378	LOC108255378	XP_017306805.1	295
108255387	LOC108255387	XP_017306816.1	175
108255407	lrrc43	XP_017306835.1	582
108255432	mvk	XP_017306861.1	399
108255462	LOC108255462	XP_017306888.1	90
108255481	LOC108255481	XP_017306911.1	81
108255492	arsk	XP_017306939.1	449
108255512	sdf2l1	XP_017306997.1	167
108255545	gtf2h2c	XP_017307048.1	274
108255569	ccdc125	XP_017307116.1	471
108255592	gatc	XP_017307164.1	215
108255639	stpg2	XP_017307223.1	555
108255757	LOC108255757	XP_017307436.1	172
108255767	ccdc180	XP_017307454.1	1461
108255780	LOC108255780	XP_017307475.1	103
108255781	LOC108255781	XP_017307476.1	101
108255808	arl6ip4	XP_017307546.1	253
108255874	c22h2orf81	XP_017307686.1	220
108255880	emb	XP_017307704.1	279
108255899	c22h9orf135	XP_017307738.1	189
108255906	psmd9	XP_017307757.1	213
108255927	naaa	XP_017307788.1	365
108255932	c22h12orf49	XP_017307797.1	199
108255941	ccdc60	XP_017307816.1	561
108255954	LOC108255954	XP_017307846.1	186
108255955	acad10	XP_017307848.1	586
108256047	tmem116	XP_017308025.1	358
108256051	ndufs4	XP_017308033.1	208
108256053	coq5	XP_017308036.1	326
108256075	sra1	XP_017308081.1	230
108256082	cmtm7	XP_017308109.1	165
108256097	commd3	XP_017308136.1	195
108256100	LOC108256100	XP_017308140.1	122
108256113	evc	XP_017308177.1	823
108256129	LOC108256129	XP_017308183.1	305
108256135	LOC108256135	XP_017308191.1	157

108256187	LOC108256187	XP_017308278.1	252
108256193	bola1	XP_017308293.1	150
108256195	apoa2	XP_017308295.1	133
108256218	eef1e1	XP_017308336.1	173
108256258	LOC108256258	XP_017308395.1	322
108256264	gpatch3	XP_017308407.1	514
108256291	ubxn11	XP_017308456.1	472
108256306	LOC108256306	XP_017308488.1	162
108256311	LOC108256311	XP_017308506.1	199
108256382	LOC108256382	XP_017308673.1	214
108256418	LOC108256418	XP_017308760.1	249
108256435	zc2hc1a	XP_017308798.1	296
108256447	yae1d1	XP_017308830.1	221
108256495	mcmdc2	XP_017308914.1	673
108256572	LOC108256572	XP_017309088.1	206
108256623	ropn1l	XP_017309172.1	215
108256628	dap	XP_017309178.1	106
108256635	otos	XP_017309188.1	90
108256676	acot9	XP_017309270.1	419
108256685	LOC108256685	XP_017309298.1	217
108256722	hmgn2	XP_017309368.1	77
108256723	LOC108256723	XP_017309370.1	372
108256762	shfm1	XP_017309457.1	70
108256765	LOC108256765	XP_017309460.1	209
108256780	mgmt	XP_017309478.1	181
108256787	mrpl53	XP_017309490.1	107
108256811	LOC108256811	XP_017309524.1	159
108256834	LOC108256834	XP_017309546.1	188
108256835	LOC108256835	XP_017309547.1	188
108256837	LOC108256837	XP_017309549.1	172
108256863	LOC108256863	XP_017309575.1	225
108256890	mrpl12	XP_017309630.1	194
108256894	vwa3a	XP_017309634.1	1145
108256922	snrpd1	XP_017309693.1	119
108256952	LOC108256952	XP_017309753.1	211
108256955	nkain1	XP_017309760.1	212
108256969	syce1	XP_017309777.1	205
108256972	LOC108256972	XP_017309794.1	152
108256989	lyrm2	XP_017309831.1	88
108257029	cap1	XP_017309902.1	469
108257046	LOC108257046	XP_017309935.1	428
108257066	LOC108257066	XP_017309962.1	193
108257098	rmi2	XP_017310004.1	146
108257119	pet100	XP_017310061.1	78

108257163	batf3	XP_017310155.1	113
108257166	pithd1	XP_017310168.1	210
108257169	wdyhv1	XP_017310173.1	188
108257170	LOC108257170	XP_017310176.1	83
108257185	aunip	XP_017310200.1	413
108257189	LOC108257189	XP_017310214.1	593
108257244	snx8	XP_017310333.1	520
108257259	LOC108257259	XP_017310371.1	217
108257301	mrpl9	XP_017310438.1	247
108257309	polr2k	XP_017310458.1	63
108257344	LOC108257344	XP_017310513.1	219
108257350	rbm48	XP_017310525.1	367
108257358	gfer	XP_017310540.1	179
108257365	LOC108257365	XP_017310553.1	478
108257386	bud31	XP_017310608.1	144
108257403	LOC108257403	XP_017310634.1	126
108257415	jtb	XP_017310659.1	150
108257427	LOC108257427	XP_017310671.1	73
108257430	LOC108257430	XP_017310678.1	339
108257509	spaca6	XP_017311013.1	310
108257527	LOC108257527	XP_017310880.1	285
108257534	LOC108257534	XP_017310886.1	181
108257571	nkain2	XP_017310941.1	206
108257612	LOC108257612	XP_017311006.1	218
108257636	LOC108257636	XP_017311042.1	257
108257650	c25h2orf70	XP_017311055.1	159
108257670	LOC108257670	XP_017311089.1	687
108257682	cgrrf1	XP_017311107.1	249
108257760	LOC108257760	XP_017311258.1	720
108257781	fgfr1op	XP_017311303.1	468
108257807	LOC108257807	XP_017311356.1	247
108257816	pcsk9	XP_017311375.1	667
108257832	LOC108257832	XP_017311393.1	109
108257834	LOC108257834	XP_017311397.1	79
108257842	LOC108257842	XP_017311419.1	202
108257849	c25h14orf2	XP_017311428.1	54
108257867	tmem244	XP_017311461.1	174
108257882	pln	XP_017311492.1	52
108257908	aasdh	XP_017311543.1	1157
108257921	nmu	XP_017311564.1	156
108257923	lexm	XP_017311566.1	337
108257959	LOC108257959	XP_017311629.1	666
108257970	aven	XP_017311646.1	342
108257986	LOC108257986	XP_017311678.1	92

108257996	ttc32	XP_017311695.1	189
108258021	LOC108258021	XP_017311744.1	146
108258054	cebpzos	XP_017311809.1	129
108258098	dnaaf5	XP_017311966.1	834
108258106	pfas	XP_017311977.1	1317
108258115	LOC108258115	XP_017312002.1	242
108258116	saysd1	XP_017311999.1	164
108258128	c25h12orf57	XP_017312026.1	122
108258156	LOC108258156	XP_017312095.1	296
108258157	katnbl1	XP_017312100.1	246
108258242	thegl	XP_017312264.1	240
108258312	cenpk	XP_017312347.1	272
108258329	cyyr1	XP_017312374.1	157
108258353	fastkd2	XP_017312413.1	641
108258406	brat1	XP_017312506.1	560
108258418	mycbpap	XP_017312516.1	836
108258440	LOC108258440	XP_017312563.1	444
108258448	knop1	XP_017312582.1	370
108258451	LOC108258451	XP_017312586.1	366
108258468	ndufb7	XP_017312617.1	121
108258469	c26h19orf53	XP_017312618.1	102
108258509	spp2	XP_017312686.1	187
108258514	smim13	XP_017312693.1	88
108258548	LOC108258548	XP_017312736.1	205
108258585	nthl1	XP_017312785.1	486
108258597	tmco3	XP_017312805.1	672
108258632	LOC108258632	XP_017312886.1	658
108258635	pcnp	XP_017312889.1	157
108258639	LOC108258639	XP_017312898.1	365
108258647	LOC108258647	XP_017312912.1	190
108258669	ndufab1	XP_017312958.1	153
108258673	pibf1	XP_017312962.1	666
108258685	LOC108258685	XP_017312976.1	293
108258694	sugt1	XP_017312997.1	325
108258709	LOC108258709	XP_017313029.1	105
108258723	b3gntl1	XP_017313051.1	558
108258728	gtf3c1	XP_017313057.1	2027
108258771	thumpd1	XP_017313161.1	415
108258818	LOC108258818	XP_017313252.1	167
108258880	LOC108258880	XP_017313343.1	124
108258903	LOC108258903	XP_017313388.1	536
108258907	LOC108258907	XP_017313395.1	1377
108258909	c26hxorf38	XP_017313402.1	310
108258993	tmsb4x	XP_017313580.1	43

108259008	ubac2	XP_017313601.1	342
108259068	rnf175	XP_017313702.1	301
108259078	c26h1orf100	XP_017313733.1	137
108259079	obfc1	XP_017313738.1	316
108259081	LOC108259081	XP_017313745.1	330
108259085	LOC108259085	XP_017313746.1	236
108259140	LOC108259140	XP_017313853.1	463
108259167	LOC108259167	XP_017313919.1	208
108259176	LOC108259176	XP_017313895.1	702
108259225	bean1	XP_017313982.1	197
108259236	cnep1r1	XP_017314006.1	125
108259247	LOC108259247	XP_017314025.1	272
108259250	LOC108259250	XP_017314030.1	227
108259251	LOC108259251	XP_017314031.1	218
108259274	LOC108259274	XP_017314085.1	252
108259323	mcee	XP_017314193.1	175
108259366	hypk	XP_017314279.1	127
108259434	LOC108259434	XP_017314441.1	312
108259442	tmem186	XP_017314451.1	224
108259472	muc15	XP_017314477.1	347
108259531	LOC108259531	XP_017314609.1	266
108259535	LOC108259535	XP_017314608.1	195
108259542	LOC108259542	XP_017314619.1	131
108259605	LOC108259605	XP_017314715.1	231
108259607	LOC108259607	XP_017314717.1	199
108259617	LOC108259617	XP_017314735.1	190
108259684	fam96b	XP_017314833.1	159
108259693	cdca5	XP_017314865.1	262
108259696	pigw	XP_017314873.1	491
108259741	LOC108259741	XP_017314949.1	370
108259751	spag8	XP_017314967.1	189
108259753	LOC108259753	XP_017314969.1	224
108259760	LOC108259760	XP_017314975.1	121
108259773	lrwd1	XP_017314987.1	806
108259817	igbp1	XP_017315025.1	349
108259819	fam76b	XP_017315027.1	312
108259820	LOC108259820	XP_017315029.1	290
108259838	las1l	XP_017315044.1	573
108259872	cenpv	XP_017315124.1	154
108259903	LOC108259903	XP_017315187.1	355
108259909	vma21	XP_017315195.1	104
108259925	LOC108259925	XP_017315227.1	747
108259938	LOC108259938	XP_017315250.1	154
108259939	LOC108259939	XP_017315251.1	80

108259940	LOC108259940	XP_017315252.1	78
108259966	c28h11orf1	XP_017315314.1	168
108259982	znf653	XP_017315381.1	544
108259990	LOC108259990	XP_017315359.1	175
108259991	LOC108259991	XP_017315363.1	177
108259992	LOC108259992	XP_017315364.1	78
108260003	alkbh6	XP_017315390.1	234
108260037	LOC108260037	XP_017315450.1	95
108260049	ssna1	XP_017315475.1	118
108260077	LOC108260077	XP_017315523.1	143
108260082	surf4	XP_017315527.1	269
108260085	tmem248	XP_017315532.1	315
108260112	LOC108260112	XP_017315588.1	335
108260130	LOC108260130	XP_017315692.1	323
108260135	kiaa0141	XP_017315665.1	485
108260174	LOC108260174	XP_017315736.1	289
108260178	LOC108260178	XP_017315741.1	258
108260186	spag7	XP_017315755.1	228
108260191	LOC108260191	XP_017315768.1	203
108260199	LOC108260199	XP_017315780.1	170
108260225	alkbh7	XP_017315802.1	250
108260245	LOC108260245	XP_017315837.1	139
108260247	LOC108260247	XP_017315882.1	104
108260262	hsf5	XP_017315870.1	349
108260266	ptcd2	XP_017315880.1	383
108260267	ttc33	XP_017315884.1	262
108260287	LOC108260287	XP_017315918.1	59
108260299	prkrip1	XP_017315949.1	189
108260306	LOC108260306	XP_017315966.1	307
108260307	LOC108260307	XP_017316009.1	957
108260360	aif1l	XP_017316091.1	148
108260394	rogdi	XP_017316154.1	300
108260397	LOC108260397	XP_017316153.1	169
108260453	dpm2	XP_017316255.1	83
108260455	ccdc15	XP_017316258.1	483
108260475	tsen54	XP_017316300.1	496
108260515	LOC108260515	XP_017316370.1	291
108260518	LOC108260518	XP_017316374.1	322
108260523	LOC108260523	XP_017316399.1	238
108260524	LOC108260524	XP_017316400.1	238
108260525	LOC108260525	XP_017316401.1	226
108260529	LOC108260529	XP_017316404.1	97
108260543	LOC108260543	XP_017316415.1	270
108260555	smim18	XP_017316430.1	126

108260576	LOC108260576	XP_017316449.1	559
108260589	LOC108260589	XP_017316464.1	645
108260594	LOC108260594	XP_017316473.1	276
108260595	LOC108260595	XP_017316476.1	295
108260596	LOC108260596	XP_017316480.1	237
108260598	LOC108260598	XP_017316485.1	873
108260607	LOC108260607	XP_017316512.1	511
108260672	LOC108260672	XP_017316597.1	224
108260679	LOC108260679	XP_017316606.1	91
108260684	gne	XP_017316613.1	737
108260685	LOC108260685	XP_017316616.1	674
108260695	c29h4orf33	XP_017316633.1	197
108260699	LOC108260699	XP_017316636.1	218
108260701	LOC108260701	XP_017316639.1	224
108260722	smim14	XP_017316683.1	103
108260727	LOC108260727	XP_017316700.1	170
108260731	c2h1orf131	XP_017316709.1	255
108260732	clhc1	XP_017316708.1	587
108260777	asah1	XP_017316818.1	393
108260828	memo1	XP_017316937.1	295
108260846	cfap97	XP_017316982.1	489
108260849	ociad1	XP_017316987.1	231
108260857	LOC108260857	XP_017316995.1	232
108260867	LOC108260867	XP_017317017.1	105
108260901	LOC108260901	XP_017317095.1	275
108260909	apela	XP_017317109.1	54
108260910	LOC108260910	XP_017317113.1	169
108260935	LOC108260935	XP_017317156.1	120
108260956	cfap36	XP_017317193.1	364
108260961	natd1	XP_017317205.1	110
108261080	fbxo47	XP_017317430.1	228
108261105	LOC108261105	XP_017317475.1	160
108261133	cops8	XP_017317496.1	191
108261138	LOC108261138	XP_017317508.1	361
108261139	LOC108261139	XP_017317509.1	328
108261140	LOC108261140	XP_017317512.1	321
108261202	LOC108261202	XP_017317572.1	99
108261206	LOC108261206	XP_017317588.1	205
108261220	LOC108261220	XP_017317634.1	192
108261238	LOC108261238	XP_017317619.1	274
108261275	LOC108261275	XP_017317672.1	119
108261285	LOC108261285	XP_017317680.1	240
108261332	LOC108261332	XP_017317728.1	122
108261389	LOC108261389	XP_017317773.1	287

108261405	LOC108261405	XP_017317784.1	285
108261432	LOC108261432	XP_017317816.1	219
108261485	LOC108261485	XP_017317843.1	226
108261486	LOC108261486	XP_017317845.1	203
108261511	LOC108261511	XP_017317859.1	83
108261543	LOC108261543	XP_017317882.1	323
108261591	LOC108261591	XP_017317914.1	307
108261642	LOC108261642	XP_017317951.1	101
108261655	LOC108261655	XP_017317962.1	180
108261657	LOC108261657	XP_017317963.1	209
108261661	LOC108261661	XP_017317972.1	271
108261695	LOC108261695	XP_017317996.1	219
108261706	LOC108261706	XP_017318007.1	296
108261723	LOC108261723	XP_017318019.1	95
108261749	LOC108261749	XP_017318040.1	226
108261754	c1h8orf88	XP_017318099.1	125
108261769	LOC108261769	XP_017318052.1	446
108261801	LOC108261801	XP_017318066.1	178
108261817	LOC108261817	XP_017318072.1	161
108261820	LOC108261820	XP_017318074.1	231
108261826	LOC108261826	XP_017318078.1	122
108261863	LOC108261863	XP_017318117.1	137
108262000	LOC108262000	XP_017318188.1	241
108262034	LOC108262034	XP_017318209.1	169
108262041	LOC108262041	XP_017318214.1	151
108262248	LOC108262248	XP_017318307.1	462
108262276	LOC108262276	XP_017318316.1	91
108262318	LOC108262318	XP_017318337.1	172
108262356	LOC108262356	XP_017318352.1	255
108262380	LOC108262380	XP_017318362.1	96
108262473	LOC108262473	XP_017318405.1	252
108262561	LOC108262561	XP_017318440.1	211
108262581	lect2	XP_017318445.1	158
108262582	LOC108262582	XP_017318447.1	124
108262588	LOC108262588	XP_017318449.1	262
108262600	LOC108262600	XP_017318457.1	288
108262645	LOC108262645	XP_017318476.1	284
108262656	LOC108262656	XP_017318482.1	85
108262726	LOC108262726	XP_017318516.1	294
108262746	LOC108262746	XP_017318532.1	147
108262768	LOC108262768	XP_017318560.1	1409
108262770	LOC108262770	XP_017318578.1	257
108262779	LOC108262779	XP_017318597.1	633
108262785	LOC108262785	XP_017318604.1	474

108262798	LOC108262798	XP_017318627.1	189
108262802	LOC108262802	XP_017318633.1	201
108262803	LOC108262803	XP_017318634.1	161
108262805	pold4	XP_017318636.1	112
108262869	tmem72	XP_017318714.1	207
108262878	LOC108262878	XP_017318722.1	574
108262883	LOC108262883	XP_017318726.1	223
108262889	LOC108262889	XP_017318731.1	136
108262892	LOC108262892	XP_017318734.1	317
108262894	sprn	XP_017318735.1	137
108262926	LOC108262926	XP_017318764.1	413
108262965	LOC108262965	XP_017318815.1	264
108262977	LOC108262977	XP_017318821.1	158
108262984	nusap1	XP_017318830.1	446
108263026	LOC108263026	XP_017318894.1	137
108263033	c3h6orf118	XP_017318923.1	387
108263058	LOC108263058	XP_017318968.1	196
108263074	LOC108263074	XP_017319005.1	125
108263086	trmt5	XP_017319020.1	491
108263118	LOC108263118	XP_017319089.1	195
108263125	LOC108263125	XP_017319105.1	132
108263132	tmem14a	XP_017319114.1	99
108263138	LOC108263138	XP_017319123.1	127
108263158	c3h7orf72	XP_017319166.1	382
108263195	LOC108263195	XP_017319244.1	253
108263201	LOC108263201	XP_017319263.1	110
108263212	rsrp1	XP_017319281.1	319
108263232	LOC108263232	XP_017319341.1	106
108263240	mavs	XP_017319351.1	703
108263281	atp5s	XP_017319424.1	174
108263348	spef1	XP_017319533.1	232
108263353	sdhaf4	XP_017319548.1	111
108263360	tmem134	XP_017319560.1	206
108263364	supv3l1	XP_017319565.1	764
108263367	LOC108263367	XP_017319588.1	297
108263388	LOC108263388	XP_017319609.1	287
108263411	b3galnt2	XP_017319649.1	375
108263412	cacul1	XP_017319651.1	315
108263423	pyroxd2	XP_017319674.1	613
108263433	commd8	XP_017319691.1	198
108263516	zcchc24	XP_017319887.1	238
108263520	malsu1	XP_017319894.1	237
108263525	LOC108263525	XP_017319907.1	152
108263584	ap5s1	XP_017320039.1	202

108263629	spcs3	XP_017320140.1	180
108263633	LOC108263633	XP_017320151.1	145
108263697	LOC108263697	XP_017320238.1	253
108263725	urb2	XP_017320285.1	1522
108263733	srgn	XP_017320300.1	148
108263754	LOC108263754	XP_017320354.1	91
108263759	tmem254	XP_017320362.1	124
108263773	spag5	XP_017320395.1	1673
108263776	uso1	XP_017320401.1	963
108263827	LOC108263827	XP_017320482.1	605
108263836	LOC108263836	XP_017320500.1	200
108263844	pus3	XP_017320531.1	403
108263892	LOC108263892	XP_017320595.1	66
108263893	il34	XP_017320597.1	211
108263954	LOC108263954	XP_017320675.1	213
108263963	LOC108263963	XP_017320691.1	269
108263999	LOC108263999	XP_017320756.1	237
108264008	treh	XP_017320782.1	494
108264013	LOC108264013	XP_017320798.1	414
108264015	LOC108264015	XP_017320801.1	314
108264030	LOC108264030	XP_017320810.1	807
108264043	LOC108264043	XP_017320838.1	124
108264051	LOC108264051	XP_017320847.1	701
108264064	lrriq1	XP_017320859.1	1667
108264074	LOC108264074	XP_017320867.1	246
108264080	LOC108264080	XP_017320872.1	309
108264144	c4h15orf65	XP_017320937.1	126
108264161	bbs10	XP_017320968.1	594
108264169	LOC108264169	XP_017320982.1	357
108264185	LOC108264185	XP_017321006.1	229
108264190	ndufa3	XP_017321015.1	123
108264194	LOC108264194	XP_017321016.1	138
108264211	LOC108264211	XP_017321034.1	144
108264219	nts	XP_017321039.1	157
108264233	LOC108264233	XP_017321056.1	118
108264237	cenpn	XP_017321062.1	313
108264238	cmc2	XP_017321063.1	78
108264245	gins2	XP_017321080.1	186
108264257	LOC108264257	XP_017321092.1	151
108264300	LOC108264300	XP_017321199.1	199
108264329	LOC108264329	XP_017321260.1	195
108264395	pex16	XP_017321360.1	339
108264412	cetp	XP_017321397.1	496
108264425	clasrp	XP_017321415.1	637

108264437	pigb	XP_017321446.1	531
108264448	tsr3	XP_017321483.1	298
108264460	c4h15orf61	XP_017321502.1	156
108264496	dtwd1	XP_017321582.1	324
108264498	LOC108264498	XP_017321589.1	212
108264501	LOC108264501	XP_017321593.1	202
108264504	bloc1s6	XP_017321601.1	163
108264507	fam103a1	XP_017321606.1	82
108264508	cdc42se2	XP_017321607.1	75
108264532	LOC108264532	XP_017321624.1	112
108264533	LOC108264533	XP_017321625.1	112
108264555	LOC108264555	XP_017321671.1	101
108264585	LOC108264585	XP_017321723.1	186
108264601	bcl2l13	XP_017321774.1	603
108264602	LOC108264602	XP_017321778.1	199
108264645	reln	XP_017321864.1	3479
108264646	LOC108264646	XP_017321865.1	204
108264685	LOC108264685	XP_017321935.1	148
108264699	LOC108264699	XP_017321948.1	348
108264700	LOC108264700	XP_017321955.1	188
108264701	LOC108264701	XP_017321956.1	278
108264702	LOC108264702	XP_017321957.1	251
108264703	LOC108264703	XP_017321959.1	203
108264781	trabd	XP_017322130.1	359
108264797	LOC108264797	XP_017322159.1	1448
108264813	siae	XP_017322201.1	538
108264830	LOC108264830	XP_017322227.1	171
108264832	LOC108264832	XP_017322230.1	183
108264899	anapc5	XP_017322365.1	762
108264909	tmem241	XP_017322401.1	271
108264910	hps4	XP_017322388.1	532
108264913	LOC108264913	XP_017322399.1	424
108264926	c5h12orf43	XP_017322424.1	242
108264931	LOC108264931	XP_017322428.1	225
108264934	LOC108264934	XP_017322432.1	219
108264941	LOC108264941	XP_017322439.1	109
108265008	LOC108265008	XP_017322550.1	280
108265034	nppa	XP_017322593.1	131
108265041	exosc10	XP_017322612.1	900
108265067	LOC108265067	XP_017322645.1	251
108265075	c5h6orf226	XP_017322659.1	147
108265095	LOC108265095	XP_017322697.1	324
108265099	LOC108265099	XP_017322700.1	301
108265117	izumo1	XP_017322730.1	376

108265131	lrriq3	XP_017322753.1	595
108265146	oxct1	XP_017322772.1	509
108265149	LOC108265149	XP_017322774.1	234
108265200	c5h1orf228	XP_017322816.1	358
108265226	LOC108265226	XP_017322837.1	236
108265261	LOC108265261	XP_017322890.1	186
108265300	LOC108265300	XP_017322961.1	726
108265304	gins4	XP_017322969.1	225
108265306	LOC108265306	XP_017322993.1	625
108265323	sap30bp	XP_017323003.1	304
108265342	LOC108265342	XP_017323047.1	482
108265350	LOC108265350	XP_017323076.1	472
108265359	LOC108265359	XP_017323096.1	459
108265372	mrps36	XP_017323112.1	180
108265397	chmp7	XP_017323157.1	443
108265418	lrif1	XP_017323192.1	917
108265449	stkld1	XP_017323263.1	523
108265464	ndufb11	XP_017323294.1	149
108265476	renbp	XP_017323315.1	402
108265477	LOC108265477	XP_017323320.1	185
108265490	apoc1	XP_017323353.1	87
108265518	gucd1	XP_017323413.1	226
108265560	LOC108265560	XP_017323532.1	183
108265563	prok1	XP_017323540.1	105
108265568	LOC108265568	XP_017323546.1	255
108265571	pold2	XP_017323551.1	467
108265585	LOC108265585	XP_017323593.1	423
108265586	LOC108265586	XP_017323595.1	379
108265588	c5h5orf51	XP_017323597.1	279
108265593	tmco1	XP_017323609.1	188
108265624	LOC108265624	XP_017323664.1	107
108265640	LOC108265640	XP_017323682.1	130
108265669	timm17b	XP_017323731.1	172
108265681	LOC108265681	XP_017323753.1	212
108265734	gnrh1	XP_017323861.1	104
108265776	tmem252	XP_017323950.1	178
108265832	LOC108265832	XP_017324062.1	286
108265860	LOC108265860	XP_017324133.1	189
108265906	fance	XP_017324237.1	509
108265952	LOC108265952	XP_017324329.1	77
108265953	LOC108265953	XP_017324330.1	247
108265975	gkap1	XP_017324369.1	347
108265979	LOC108265979	XP_017324377.1	531
108265986	LOC108265986	XP_017324386.1	197

108266019	dmap1	XP_017324444.1	463
108266026	LOC108266026	XP_017324497.1	158
108266038	LOC108266038	XP_017324473.1	424
108266044	ocstamp	XP_017324487.1	575
108266124	LOC108266124	XP_017324636.1	281
108266151	ndp	XP_017324677.1	138
108266154	LOC108266154	XP_017324681.1	206
108266253	LOC108266253	XP_017324831.1	253
108266266	ccdc89	XP_017324846.1	354
108266275	LOC108266275	XP_017324848.1	201
108266276	LOC108266276	XP_017324851.1	180
108266320	LOC108266320	XP_017324920.1	166
108266442	LOC108266442	XP_017325283.1	717
108266448	LOC108266448	XP_017325267.1	235
108266464	LOC108266464	XP_017325306.1	203
108266484	LOC108266484	XP_017325361.1	675
108266515	LOC108266515	XP_017325429.1	125
108266526	gtdc1	XP_017325449.1	409
108266537	LOC108266537	XP_017325475.1	63
108266547	LOC108266547	XP_017325506.1	123
108266550	LOC108266550	XP_017325508.1	245
108266569	LOC108266569	XP_017325546.1	511
108266593	dnajc15	XP_017325615.1	150
108266691	cmss1	XP_017325829.1	290
108266707	LOC108266707	XP_017325857.1	222
108266719	LOC108266719	XP_017325873.1	245
108266728	serp2	XP_017325886.1	65
108266731	LOC108266731	XP_017325891.1	108
108266781	il11	XP_017325999.1	195
108266784	cd302	XP_017326000.1	247
108266918	nms	XP_017326239.1	138
108266939	LOC108266939	XP_017326266.1	236
108266940	LOC108266940	XP_017326267.1	311
108266946	LOC108266946	XP_017326274.1	207
108267013	lmln	XP_017326374.1	655
108267040	LOC108267040	XP_017326417.1	323
108267042	LOC108267042	XP_017326422.1	192
108267095	LOC108267095	XP_017326553.1	214
108267131	LOC108267131	XP_017326595.1	91
108267133	LOC108267133	XP_017326596.1	90
108267154	LOC108267154	XP_017326631.1	341
108267168	LOC108267168	XP_017326645.1	331
108267181	LOC108267181	XP_017326661.1	95
108267189	LOC108267189	XP_017326671.1	239

108267198	LOC108267198	XP_017326688.1	391
108267209	LOC108267209	XP_017326702.1	366
108267224	LOC108267224	XP_017326707.1	223
108267263	LOC108267263	XP_017326742.1	195
108267271	LOC108267271	XP_017326753.1	371
108267281	LOC108267281	XP_017326782.1	323
108267283	LOC108267283	XP_017326784.1	272
108267285	LOC108267285	XP_017326787.1	263
108267289	LOC108267289	XP_017326797.1	264
108267346	LOC108267346	XP_017326878.1	242
108267376	LOC108267376	XP_017326900.1	85
108267378	LOC108267378	XP_017326897.1	353
108267379	LOC108267379	XP_017326898.1	351
108267380	LOC108267380	XP_017326899.1	310
108267390	ccdc24	XP_017326907.1	400
108267398	LOC108267398	XP_017326926.1	502
108267413	LOC108267413	XP_017326948.1	351
108267415	fam159a	XP_017326949.1	158
108267416	tmem88	XP_017326950.1	218
108267444	sec62	XP_017326999.1	393
108267488	LOC108267488	XP_017327074.1	165
108267509	mettl17	XP_017327107.1	459
108267516	LOC108267516	XP_017327122.1	2010
108267528	LOC108267528	XP_017327165.1	169
108267537	majin	XP_017327173.1	253
108267540	batf2	XP_017327178.1	165
108267541	gpha2	XP_017327179.1	135
108267547	aadat	XP_017327204.1	342
108267564	LOC108267564	XP_017327248.1	207
108267588	zzz3	XP_017327315.1	872
108267619	c7h1orf123	XP_017327359.1	160
108267658	serp1	XP_017327437.1	65
108267692	LOC108267692	XP_017327515.1	168
108267693	rwdd4	XP_017327521.1	186
108267714	LOC108267714	XP_017327548.1	124
108267721	LOC108267721	XP_017327558.1	189
108267727	tkfc	XP_017327575.1	616
108267746	LOC108267746	XP_017327616.1	101
108267766	snapc2	XP_017327666.1	409
108267767	LOC108267767	XP_017327667.1	321
108267771	LOC108267771	XP_017327675.1	293
108267833	LOC108267833	XP_017327773.1	189
108267856	nol7	XP_017327813.1	211
108267873	elp5	XP_017327847.1	297

108267897	LOC108267897	XP_017327885.1	257
108267901	smim20	XP_017327891.1	68
108267947	LOC108267947	XP_017328036.1	285
108267949	LOC108267949	XP_017328039.1	1316
108267960	poln	XP_017328059.1	1192
108267971	rgp1	XP_017328073.1	386
108267988	LOC108267988	XP_017328099.1	91
108268026	LOC108268026	XP_017328153.1	240
108268037	naa40	XP_017328168.1	238
108268044	wrnip1	XP_017328193.1	511
108268072	mettl12	XP_017328248.1	215
108268101	LOC108268101	XP_017328293.1	413
108268114	LOC108268114	XP_017328323.1	99
108268196	mblac1	XP_017328500.1	218
108268244	LOC108268244	XP_017328602.1	584
108268283	LOC108268283	XP_017328636.1	309
108268284	LOC108268284	XP_017328639.1	249
108268302	LOC108268302	XP_017328674.1	95
108268303	LOC108268303	XP_017328676.1	101
108268304	LOC108268304	XP_017328678.1	95
108268310	LOC108268310	XP_017328690.1	526
108268323	LOC108268323	XP_017328708.1	213
108268332	cd27	XP_017328761.1	235
108268342	haus6	XP_017328742.1	792
108268344	kiaa0040	XP_017328749.1	111
108268384	emg1	XP_017328774.1	238
108268388	cenpi	XP_017328814.1	721
108268409	pyurf	XP_017328852.1	111
108268412	m6pr	XP_017328869.1	268
108268432	fam185a	XP_017328889.1	366
108268441	LOC108268441	XP_017328911.1	1057
108268449	LOC108268449	XP_017328925.1	188
108268450	LOC108268450	XP_017328929.1	181
108268454	LOC108268454	XP_017328933.1	99
108268456	ecm1	XP_017328944.1	669
108268463	LOC108268463	XP_017328953.1	349
108268479	LOC108268479	XP_017328988.1	335
108268486	syce3	XP_017328995.1	94
108268490	LOC108268490	XP_017328999.1	424
108268498	LOC108268498	XP_017329011.1	271
108268500	LOC108268500	XP_017329013.1	197
108268505	c8hxorf65	XP_017329021.1	104
108268532	LOC108268532	XP_017329044.1	362
108268533	slc30a9	XP_017329045.1	1135

108268536	rep15	XP_017329049.1	224
108268543	LOC108268543	XP_017329053.1	100
108268582	c8h5orf45	XP_017329107.1	376
108268585	LOC108268585	XP_017329111.1	243
108268592	tmem231	XP_017329124.1	309
108268626	cenpu	XP_017329170.1	428
108268651	znf276	XP_017329208.1	414
108268662	LOC108268662	XP_017329223.1	221
108268663	LOC108268663	XP_017329225.1	118
108268671	slbp	XP_017329239.1	295
108268715	zgrf1	XP_017329327.1	545
108268795	nup62	XP_017329480.1	512
108268819	LOC108268819	XP_017329532.1	130
108268848	LOC108268848	XP_017329602.1	574
108268865	LOC108268865	XP_017329658.1	272
108268900	LOC108268900	XP_017329725.1	448
108268938	nxt2	XP_017329800.1	143
108268953	LOC108268953	XP_017329827.1	118
108268958	LOC108268958	XP_017329853.1	795
108268966	ubl3	XP_017329876.1	118
108268984	LOC108268984	XP_017329916.1	473
108268995	coq9	XP_017329950.1	333
108269003	borcs5	XP_017329960.1	195
108269101	LOC108269101	XP_017330157.1	318
108269114	LOC108269114	XP_017330183.1	85
108269120	LOC108269120	XP_017330191.1	282
108269176	LOC108269176	XP_017330307.1	245
108269185	LOC108269185	XP_017330322.1	156
108269188	fibp	XP_017330340.1	357
108269237	ndufa1	XP_017330468.1	70
108269238	cfl1	XP_017330469.1	165
108269272	fam149a	XP_017330522.1	655
108269287	efcab6	XP_017330552.1	1478
108269326	LOC108269326	XP_017330629.1	347
108269346	rnf4	XP_017330657.1	191
108269357	LOC108269357	XP_017330674.1	391
108269364	LOC108269364	XP_017330687.1	187
108269379	mmgt1	XP_017330712.1	130
108269405	spata4	XP_017330744.1	230
108269408	glod5	XP_017330752.1	160
108269432	jdp2	XP_017330797.1	170
108269435	g2e3	XP_017330800.1	652
108269445	LOC108269445	XP_017330825.1	260
108269449	spata7	XP_017330834.1	410

108269538	LOC108269538	XP_017330973.1	914
108269545	LOC108269545	XP_017330982.1	380
108269546	c9h2orf71	XP_017330979.1	1131
108269553	mrps15	XP_017330993.1	260
108269556	LOC108269556	XP_017330992.1	1129
108269564	LOC108269564	XP_017331003.1	211
108269573	LOC108269573	XP_017331011.1	480
108269574	LOC108269574	XP_017331012.1	214
108269637	srp14	XP_017331100.1	110
108269750	kiaa0586	XP_017331217.1	1588
108269761	ecd	XP_017331237.1	639
108269771	tmem206	XP_017331259.1	350
108269838	LOC108269838	XP_017331403.1	151
108269857	LOC108269857	XP_017331439.1	221
108269858	LOC108269858	XP_017331440.1	195
108269863	LOC108269863	XP_017331449.1	304
108269946	tex36	XP_017331608.1	196
108270035	LOC108270035	XP_017331764.1	466
108270064	iah1	XP_017331846.1	250
108270131	c9h14orf1	XP_017331983.1	143
108270148	bre	XP_017332021.1	386
108270179	cenpo	XP_017332083.1	282
108270183	fam149b1	XP_017332087.1	610
108270209	c9h8orf74	XP_017332135.1	279
108270291	kiaa1841	XP_017332307.1	705
108270326	slc39a9	XP_017332387.1	305
108270334	erich1	XP_017332400.1	308
108270385	nubpl	XP_017332506.1	328
108270427	LOC108270427	XP_017332609.1	699
108270430	LOC108270430	XP_017332613.1	191
108270459	lin52	XP_017332679.1	112
108270467	fam181a	XP_017332692.1	291
108270468	LOC108270468	XP_017332694.1	151
108270512	pex11g	XP_017332787.1	218
108270515	LOC108270515	XP_017332796.1	204
108270527	axdnd1	XP_017332811.1	1042
108270528	c1h7orf50	XP_017332817.1	279
108270544	LOC108270544	XP_017332843.1	303
108270569	pdzk1ip1	XP_017332885.1	109
108270606	tmem204	XP_017332952.1	219
108270612	ogfod1	XP_017332928.1	540
108270622	LOC108270622	XP_017332938.1	848
108270629	ankub1	XP_017332943.1	637
108270633	spata1	XP_017332948.1	390

108270659	LOC108270659	XP_017332973.1	206
108270682	mrpl21	XP_017332998.1	206
108270721	LOC108270721	XP_017333063.1	536
108270750	tp53inp1	XP_017333134.1	242
108270760	lyrm1	XP_017333275.1	122
108270813	LOC108270813	XP_017333245.1	371
108270820	rsph3	XP_017333258.1	328
108270827	LOC108270827	XP_017333268.1	229
108270830	c1h8orf37	XP_017333284.1	208
108270841	c10h19orf60	XP_017333295.1	157
108270843	fam174a	XP_017333296.1	129
108270897	LOC108270897	XP_017333386.1	651
108270906	LOC108270906	XP_017333404.1	127
108270910	ist1	XP_017333413.1	342
108270958	mrpl54	XP_017333510.1	139
108271009	tradd	XP_017333645.1	294
108271026	LOC108271026	XP_017333685.1	133
108271030	afmid	XP_017333706.1	293
108271033	ppp1r2	XP_017333711.1	204
108271034	LOC108271034	XP_017333713.1	395
108271047	vimp	XP_017333731.1	189
108271049	mecr	XP_017333748.1	344
108271079	LOC108271079	XP_017333817.1	469
108271133	dnajc19	XP_017333934.1	116
108271157	prune1	XP_017334001.1	429
108271173	impact	XP_017334024.1	322
108271184	mydgf	XP_017334042.1	178
108271190	LOC108271190	XP_017334054.1	289
108271194	LOC108271194	XP_017334058.1	221
108271213	LOC108271213	XP_017334100.1	112
108271221	pigx	XP_017334116.1	215
108271222	LOC108271222	XP_017334120.1	230
108271237	lins1	XP_017334154.1	662
108271246	LOC108271246	XP_017334171.1	1368
108271266	c10h19orf70	XP_017334212.1	111
108271272	tmem221	XP_017334223.1	273
108271275	borcs8	XP_017334230.1	128
108271285	r3hdm4	XP_017334247.1	254
108271332	nadsyn1	XP_017334345.1	701
108271362	LOC108271362	XP_017334427.1	77
108271369	c1h9orf152	XP_017334440.1	224
108271373	fbxo22	XP_017334431.1	389
108271386	LOC108271386	XP_017334449.1	154
108271399	bola3	XP_017334473.1	105

108271413	c10h1orf53	XP_017334492.1	158
108271431	mrps11	XP_017334520.1	202
108271500	LOC108271500	XP_017334602.1	201
108271505	LOC108271505	XP_017334614.1	259
108271521	LOC108271521	XP_017334637.1	617
108271526	manbal	XP_017334643.1	87
108271565	LOC108271565	XP_017334707.1	919
108271582	rsg1	XP_017334731.1	250
108271588	LOC108271588	XP_017334740.1	853
108271659	ssb	XP_017334864.1	407
108271660	LOC108271660	XP_017334866.1	313
108271708	LOC108271708	XP_017334922.1	90
108271721	LOC108271721	XP_017334924.1	124
108271730	trub2	XP_017334930.1	350
108271731	LOC108271731	XP_017334932.1	157
108271797	LOC108271797	XP_017335063.1	127
108271804	blcap	XP_017335073.1	87
108271811	ccdc174	XP_017335082.1	474
108271834	LOC108271834	XP_017335152.1	144
108271867	LOC108271867	XP_017335235.1	168
108271895	nprl2	XP_017335313.1	379
108271903	mrpl47	XP_017335326.1	251
108271970	ddi2	XP_017335457.1	426
108272020	nubp2	XP_017335618.1	270
108272024	pxmp4	XP_017335579.1	210
108272045	LOC108272045	XP_017335630.1	111
108272056	tomm6	XP_017335657.1	71
108272058	LOC108272058	XP_017335663.1	283
108272076	LOC108272076	XP_017335728.1	81
108272088	c11h1orf146	XP_017335739.1	175
108272129	lrrc41	XP_017335822.1	584
108272150	LOC108272150	XP_017335866.1	238
108272178	sycp1	XP_017335927.1	954
108272267	LOC108272267	XP_017336069.1	114
108272277	c11h1orf159	XP_017336084.1	192
108272321	mrpl36	XP_017336148.1	116
108272336	ube3d	XP_017336175.1	392
108272338	LOC108272338	XP_017336173.1	168
108272359	rps19bp1	XP_017336220.1	150
108272378	dtd1	XP_017336253.1	257
108272400	zglp1	XP_017336283.1	537
108272404	c12h17orf67	XP_017336299.1	85
108272416	LOC108272416	XP_017336321.1	86
108272422	LOC108272422	XP_017336327.1	579

108272442	LOC108272442	XP_017336348.1	111
108272482	mei1	XP_017336392.1	1292
108272509	nol12	XP_017336445.1	234
108272515	polr2f	XP_017336450.1	121
108272526	stx8	XP_017336462.1	236
108272547	pigv	XP_017336530.1	486
108272548	fopnl	XP_017336504.1	121
108272558	LOC108272558	XP_017336524.1	204
108272565	LOC108272565	XP_017336532.1	118
108272599	LOC108272599	XP_017336578.1	211
108272621	s100a14	XP_017336616.1	104
108272626	LOC108272626	XP_017336622.1	260
108272632	LOC108272632	XP_017336641.1	90
108272697	c12h6orf136	XP_017336800.1	415
108272718	zdbf2	XP_017336858.1	871
108272728	LOC108272728	XP_017336879.1	275
108272746	LOC108272746	XP_017336925.1	248
108272747	LOC108272747	XP_017336926.1	212
108272753	ppp1r11	XP_017336941.1	123
108272758	endov	XP_017336952.1	250
108272761	sdha	XP_017336956.1	662
108272796	c12h5orf49	XP_017337035.1	136
108272805	LOC108272805	XP_017337090.1	472
108272811	fbf1	XP_017337070.1	1137
108272837	LOC108272837	XP_017337122.1	345
108272843	rtbdn	XP_017337130.1	263
108272846	pmm1	XP_017337135.1	259
108272847	LOC108272847	XP_017337136.1	216
108272854	LOC108272854	XP_017337156.1	150
108272857	LOC108272857	XP_017337161.1	132
108272880	gtf2h4	XP_017337174.1	467
108272884	pdss1	XP_017337193.1	422
108272889	LOC108272889	XP_017337203.1	364
108272892	LOC108272892	XP_017337206.1	250
108272972	LOC108272972	XP_017337368.1	3158
108273004	jmjd8	XP_017337429.1	261
108273007	hspbp1	XP_017337448.1	326
108273027	tmem220	XP_017337487.1	167
108273100	catip	XP_017337611.1	368
108273138	LOC108273138	XP_017337668.1	142
108273139	LOC108273139	XP_017337671.1	345
108273197	ssr2	XP_017337788.1	185
108273218	LOC108273218	XP_017337834.1	165
108273235	dph3	XP_017337868.1	85

108273240	csnk2b	XP_017337877.1	215
108273242	nudt15	XP_017337881.1	162
108273279	arl6ip6	XP_017337929.1	183
108273299	triqk	XP_017337949.1	84
108273303	wbp4	XP_017337956.1	369
108273407	LOC108273407	XP_017338083.1	602
108273421	tnfrsf17	XP_017338113.1	186
108273470	fads6	XP_017338193.1	355
108273531	cd84	XP_017338293.1	632
108273532	LOC108273532	XP_017338295.1	255
108273533	LOC108273533	XP_017338296.1	327
108273539	LOC108273539	XP_017338302.1	214
108273543	LOC108273543	XP_017338304.1	219
108273551	LOC108273551	XP_017338314.1	150
108273621	pstk	XP_017338466.1	298
108273634	LOC108273634	XP_017338475.1	69
108273640	LOC108273640	XP_017338488.1	903
108273643	nif3l1	XP_017338492.1	413
108273677	LOC108273677	XP_017338571.1	326
108273694	LOC108273694	XP_017338585.1	241
108273715	cep131	XP_017338627.1	1095
108273736	zcchc4	XP_017338684.1	482
108273764	amz2	XP_017338764.1	352
108273775	LOC108273775	XP_017338787.1	133
108273793	LOC108273793	XP_017338810.1	122
108273794	c13h17orf89	XP_017338811.1	70
108273805	ghdc	XP_017338850.1	627
108273871	armc7	XP_017338998.1	198
108273878	lsm5	XP_017339009.1	91
108273919	mettl9	XP_017339098.1	323
108273920	LOC108273920	XP_017339103.1	326
108273936	LOC108273936	XP_017339127.1	332
108273940	c13h10orf2	XP_017339130.1	736
108274003	mto1	XP_017339245.1	660
108274006	LOC108274006	XP_017339251.1	414
108274049	tmem128	XP_017339338.1	165
108274088	LOC108274088	XP_017339436.1	362
108274099	anapc16	XP_017339456.1	109
108274101	LOC108274101	XP_017339469.1	132
108274118	cby1	XP_017339507.1	125
108274124	LOC108274124	XP_017339516.1	266
108274132	LOC108274132	XP_017339533.1	213
108274154	stra13	XP_017339585.1	81
108274158	igsf6	XP_017339599.1	252

108274169	uros	XP_017339630.1	263
108274171	c13h17orf62	XP_017339636.1	211
108274181	LOC108274181	XP_017339652.1	101
108274182	cntd1	XP_017339655.1	227
108274237	slamf7	XP_017339755.1	333
108274239	LOC108274239	XP_017339766.1	110
108274317	LOC108274317	XP_017339904.1	119
108274323	rsl1d1	XP_017339916.1	378
108274332	LOC108274332	XP_017339931.1	426
108274357	atpaf2	XP_017339977.1	288
108274373	adprm	XP_017340008.1	324
108274421	LOC108274421	XP_017340070.1	385
108274437	LOC108274437	XP_017340103.1	377
108274465	LOC108274465	XP_017340142.1	145
108274489	LOC108274489	XP_017340213.1	494
108274543	LOC108274543	XP_017340246.1	382
108274556	mansc4	XP_017340260.1	455
108274570	LOC108274570	XP_017340272.1	253
108274594	LOC108274594	XP_017340295.1	145
108274600	LOC108274600	XP_017340300.1	281
108274660	c14h5orf24	XP_017340376.1	203
108274663	LOC108274663	XP_017340380.1	195
108274703	pgghg	XP_017340465.1	699
108274729	nfatc2ip	XP_017340516.1	325
108274730	LOC108274730	XP_017340517.1	210
108274805	msto1	XP_017340682.1	589
108274815	LOC108274815	XP_017340704.1	132
108274833	LOC108274833	XP_017340746.1	317
108274844	LOC108274844	XP_017340765.1	278
108274851	LOC108274851	XP_017340774.1	254
108274880	LOC108274880	XP_017340816.1	132
108274911	LOC108274911	XP_017340854.1	97
108274930	nrg4	XP_017340843.1	97
108274964	LOC108274964	XP_017340920.1	356
108274971	LOC108274971	XP_017340934.1	136
108274994	rfwd3	XP_017340989.1	698
108275006	LOC108275006	XP_017341021.1	298
108275008	snupn	XP_017341026.1	363
108275034	LOC108275034	XP_017341076.1	173
108275085	LOC108275085	XP_017341189.1	222
108275124	LOC108275124	XP_017341218.1	262
108275137	fbxl22	XP_017341238.1	227
108275153	LOC108275153	XP_017341260.1	259
108275158	LOC108275158	XP_017341265.1	230

108275160	LOC108275160	XP_017341266.1	1148
108275170	pdcd2l	XP_017341285.1	352
108275196	jmjd6	XP_017341324.1	140
108275210	lrrc56	XP_017341346.1	629
108275351	LOC108275351	XP_017341616.1	234
108275371	dctn4	XP_017341640.1	467
108275393	LOC108275393	XP_017341663.1	719
108275413	fam96a	XP_017341695.1	157
108275422	LOC108275422	XP_017341716.1	245
108275461	LOC108275461	XP_017341784.1	299
108275481	epm2a	XP_017341821.1	323
108275523	LOC108275523	XP_017341878.1	166
108275566	LOC108275566	XP_017341953.1	474
108275567	lkaaear1	XP_017341956.1	144
108275572	irak1bp1	XP_017341961.1	249
108275574	ubxn10	XP_017341965.1	222
108275597	LOC108275597	XP_017341990.1	340
108275606	LOC108275606	XP_017342001.1	1102
108275610	LOC108275610	XP_017342005.1	367
108275615	LOC108275615	XP_017342009.1	548
108275642	LOC108275642	XP_017342036.1	555
108275660	LOC108275660	XP_017342078.1	148
108275665	LOC108275665	XP_017342075.1	289
108275681	LOC108275681	XP_017342084.1	183
108275682	LOC108275682	XP_017342086.1	122
108275702	LOC108275702	XP_017342115.1	273
108275703	LOC108275703	XP_017342117.1	206
108275704	trappc1	XP_017342118.1	145
108275706	LOC108275706	XP_017342121.1	100
108275707	LOC108275707	XP_017342122.1	66
108275752	LOC108275752	XP_017342185.1	167
108275757	LOC108275757	XP_017342195.1	447
108275758	LOC108275758	XP_017342196.1	445
108275760	LOC108275760	XP_017342203.1	221
108275801	c15h20orf24	XP_017342288.1	128
108275809	LOC108275809	XP_017342298.1	275
108275817	kti12	XP_017342313.1	275
108275827	LOC108275827	XP_017342333.1	79
108275830	LOC108275830	XP_017342336.1	297
108275832	LOC108275832	XP_017342338.1	605
108275833	plekhm2	XP_017342343.1	938
108275920	LOC108275920	XP_017342544.1	286
108275937	slc35c2	XP_017342591.1	354
108275956	LOC108275956	XP_017342623.1	168

108275963	LOC108275963	XP_017342641.1	108
108275973	LOC108275973	XP_017342672.1	228
108276081	LOC108276081	XP_017342914.1	201
108276082	LOC108276082	XP_017342915.1	158
108276104	LOC108276104	XP_017342966.1	770
108276126	gpr157	XP_017343012.1	336
108276133	smim4	XP_017343022.1	81
108276175	aurkaip1	XP_017343118.1	209
108276194	ccdc103	XP_017343151.1	244
108276198	LOC108276198	XP_017343154.1	99
108276253	dnajc22	XP_017343255.1	340
108276266	ctc1	XP_017343276.1	1260
108276292	LOC108276292	XP_017343345.1	172
108276302	LOC108276302	XP_017343366.1	175
108276309	oard1	XP_017343377.1	155
108276342	LOC108276342	XP_017343433.1	396
108276355	LOC108276355	XP_017343456.1	253
108276400	hmgn3	XP_017343533.1	96
108276434	LOC108276434	XP_017343592.1	174
108276471	LOC108276471	XP_017343659.1	376
108276476	haus7	XP_017343667.1	411
108276528	LOC108276528	XP_017343763.1	627
108276534	LOC108276534	XP_017343774.1	210
108276535	ier3ip1	XP_017343776.1	82
108276537	setd9	XP_017343779.1	259
108276556	dcps	XP_017343808.1	323
108276590	LOC108276590	XP_017343905.1	102
108276593	c16h5orf63	XP_017343869.1	123
108276612	phf24	XP_017343903.1	416
108276651	LOC108276651	XP_017343949.1	236
108276652	sertm1	XP_017343950.1	123
108276653	LOC108276653	XP_017343951.1	249
108276691	rhbdd2	XP_017344003.1	376
108276721	ccdc62	XP_017344067.1	523
108276734	snx24	XP_017344098.1	172
108276745	srek1ip1	XP_017344136.1	158
108276751	LOC108276751	XP_017344146.1	84
108276768	LOC108276768	XP_017344177.1	240
108276771	LOC108276771	XP_017344185.1	150
108276776	crebzf	XP_017344205.1	271
108276778	ift46	XP_017344209.1	351
108276779	LOC108276779	XP_017344213.1	248
108276807	htatsf1	XP_017344282.1	459
108276825	lcn2	XP_017344320.1	203

108276831	swi5	XP_017344328.1	138
108276852	dexi	XP_017344374.1	89
108276856	mocs2	XP_017344379.1	86
108276870	nubp1	XP_017344407.1	326
108276896	wdr74	XP_017344466.1	404
108276919	acer3	XP_017344520.1	230
108276925	bri3	XP_017344535.1	135
108276953	LOC108276953	XP_017344611.1	365
108276954	LOC108276954	XP_017344615.1	296
108276955	LOC108276955	XP_017344617.1	287
108276956	LOC108276956	XP_017344623.1	271
108276990	morn5	XP_017344712.1	183
108276991	rbm18	XP_017344713.1	189
108277062	mrpl48	XP_017344860.1	257
108277066	tiprl	XP_017344868.1	225
108277077	rnasek	XP_017344886.1	101
108277099	LOC108277099	XP_017344969.1	261
108277109	tmem135	XP_017344982.1	463
108277116	LOC108277116	XP_017344993.1	1220
108277174	LOC108277174	XP_017345150.1	393
108277202	abhd18	XP_017345207.1	435
108277208	LOC108277208	XP_017345234.1	129
108277210	ripply3	XP_017345218.1	127
108277298	hirip3	XP_017345391.1	576
108277311	brf2	XP_017345409.1	401
108277312	LOC108277312	XP_017345410.1	388
108277329	zcchc9	XP_017345453.1	292
108277351	timm10b	XP_017345491.1	188
108277380	urm1	XP_017345552.1	101
108277426	mrps23	XP_017345656.1	190
108277433	parl	XP_017345675.1	358
108277470	LOC108277470	XP_017345743.1	390
108277487	LOC108277487	XP_017345780.1	251
108277501	LOC108277501	XP_017345807.1	149
108277510	lyrm9	XP_017345821.1	94
108277513	LOC108277513	XP_017345825.1	780
108277523	gap43	XP_017345837.1	222
108277527	fam181b	XP_017345841.1	322
108277556	LOC108277556	XP_017345867.1	244
108277586	lrrc72	XP_017345892.1	260
108277607	LOC108277607	XP_017345909.1	449
108277654	LOC108277654	XP_017345945.1	246
108277656	sln	XP_017345947.1	32
108277673	psenen	XP_017345967.1	101

108277677	mettl16	XP_017345972.1	506
108277679	LOC108277679	XP_017345977.1	909
108277709	vmp1	XP_017346028.1	406
108277730	LOC108277730	XP_017346078.1	236
108277785	tex12	XP_017346181.1	157
108277787	sdhd	XP_017346194.1	155
108277805	rffl	XP_017346225.1	349
108277806	mkks	XP_017346231.1	506
108277841	LOC108277841	XP_017346308.1	310
108277928	lamtor1	XP_017346475.1	159
108278005	LOC108278005	XP_017346606.1	329
108278066	LOC108278066	XP_017346700.1	273
108278141	znf414	XP_017346821.1	322
108278146	LOC108278146	XP_017346829.1	203
108278149	thap4	XP_017346834.1	176
108278189	nudt8	XP_017346876.1	328
108278221	med29	XP_017346922.1	182
108278229	tp53i13	XP_017346932.1	498
108278243	LOC108278243	XP_017346950.1	224
108278261	LOC108278261	XP_017346976.1	560
108278282	kiaa0753	XP_017347020.1	856
108278291	LOC108278291	XP_017347038.1	398
108278320	cd3g	XP_017347102.1	165
108278351	tex26	XP_017347167.1	281
108278357	LOC108278357	XP_017347175.1	341
108278360	LOC108278360	XP_017347185.1	95
108278379	apom	XP_017347210.1	186
108278390	colca2	XP_017347232.1	238
108278459	cdipt	XP_017347344.1	213
108278492	LOC108278492	XP_017347394.1	376
108278522	LOC108278522	XP_017347453.1	377
108278547	LOC108278547	XP_017347486.1	408
108278567	LOC108278567	XP_017347507.1	567
108278588	LOC108278588	XP_017347534.1	323
108278599	bhmg1	XP_017347539.1	479
108278638	LOC108278638	XP_017347586.1	225
108278668	elof1	XP_017347637.1	125
108278689	LOC108278689	XP_017347659.1	61
108278700	LOC108278700	XP_017347674.1	83
108278728	LOC108278728	XP_017347728.1	144
108278760	pigs	XP_017347807.1	564
108278771	prdx5	XP_017347825.1	185
108278818	arpc3	XP_017347929.1	178
108278861	LOC108278861	XP_017348002.1	286

108278864	ik	XP_017348012.1	544
108278895	LOC108278895	XP_017348088.1	179
108278918	ecscr	XP_017348142.1	131
108278938	cks2	XP_017348210.1	77
108278976	rnf121	XP_017348306.1	334
108278982	LOC108278982	XP_017348322.1	163
108279000	LOC108279000	XP_017348348.1	108
108279074	sart1	XP_017348517.1	778
108279103	ostm1	XP_017348568.1	294
108279148	gnrh2	XP_017348636.1	86
108279163	dolpp1	XP_017348668.1	238
108279178	LOC108279178	XP_017348697.1	219
108279196	mcrip1	XP_017348735.1	94
108279207	tmigd1	XP_017348747.1	263
108279211	LOC108279211	XP_017348754.1	256
108279226	LOC108279226	XP_017348784.1	92
108279231	LOC108279231	XP_017348792.1	78
108279234	LOC108279234	XP_017348795.1	184
108279242	taf1a	XP_017348811.1	429
108279254	zw10	XP_017348824.1	768
108279288	LOC108279288	XP_017348905.1	271
108279312	fech	XP_017348952.1	412
108279328	LOC108279328	XP_017348985.1	696
108279342	ddias	XP_017349010.1	644
108279354	ripply1	XP_017349040.1	152
108279367	xrra1	XP_017349072.1	558
108279396	LOC108279396	XP_017349126.1	97
108279446	mrps33	XP_017349191.1	106
108279450	LOC108279450	XP_017349198.1	156
108279454	LOC108279454	XP_017349203.1	369
108279460	c19h12orf75	XP_017349212.1	80
108279494	ccdc107	XP_017349285.1	315
108279518	ptrhd1	XP_017349317.1	127
108279552	atp6v1f	XP_017349376.1	119
108279572	LOC108279572	XP_017349381.1	507
108279594	LOC108279594	XP_017349401.1	344
108279608	LOC108279608	XP_017349416.1	208
108279616	LOC108279616	XP_017349420.1	140
108279620	LOC108279620	XP_017349423.1	282
108279621	LOC108279621	XP_017349426.1	176
108279633	spx	XP_017349443.1	112
108279678	iapp	XP_017349512.1	132
108279705	rhno1	XP_017349597.1	293
108279729	slc35e3	XP_017349642.1	260

108279730	llph	XP_017349645.1	178
108279790	LOC108279790	XP_017349766.1	76
108279802	alg12	XP_017349784.1	496
108279808	mest	XP_017349793.1	298
108279818	LOC108279818	XP_017349799.1	341
108279866	c19h11orf98	XP_017349919.1	116
108279867	mansc1	XP_017349921.1	458
108279898	cdpf1	XP_017350000.1	113
108280010	smkr1	XP_017350226.1	87
108280035	LOC108280035	XP_017350265.1	228
108280046	mrpl42	XP_017350283.1	150
108280048	ttll12	XP_017350287.1	620
108280054	lsm8	XP_017350294.1	96
108280084	ccdc42	XP_017350344.1	334
108280094	ssbp1	XP_017350360.1	146
108280096	LOC108280096	XP_017350362.1	79
108280105	LOC108280105	XP_017350396.1	204
108280128	tmem243	XP_017350378.1	139
108280143	mrps18a	XP_017350409.1	208
108280144	c19h12orf40	XP_017350413.1	611
108280224	LOC108280224	XP_017350549.1	268
108280245	LOC108280245	XP_017350580.1	247
108280283	hhla1	XP_017350622.1	429
108280321	LOC108280321	XP_017350678.1	195
108280322	LOC108280322	XP_017350679.1	194
108280326	LOC108280326	XP_017350681.1	260
108280350	LOC108280350	XP_017350740.1	367
108280351	LOC108280351	XP_017350743.1	267
108280363	LOC108280363	XP_017350755.1	135
108280381	tstd3	XP_017350785.1	156
108280382	LOC108280382	XP_017350786.1	81
108280406	pih1d3	XP_017350834.1	239
108280437	adhfe1	XP_017350884.1	443
108280468	rpap2	XP_017350945.1	608
108280484	LOC108280484	XP_017350999.1	315
108280493	LOC108280493	XP_017351012.1	323
108280507	pih1d1	XP_017351032.1	281
108280514	LOC108280514	XP_017351063.1	272
108280542	LOC108280542	XP_017351122.1	283
108280592	sptssb	XP_017351226.1	80
108280629	mre11a	XP_017351314.1	698
108280651	sugp1	XP_017351363.1	626
108280671	atp5sl	XP_017351447.1	257
108280678	LOC108280678	XP_017351462.1	308

108280687	LOC108280687	XP_017351482.1	92
108280738	pnisr	XP_017351582.1	753
108280817	ech1	XP_017351736.1	305
108280846	emc10	XP_017351788.1	253
108280854	kncn	XP_017351803.1	149
108280912	LOC108280912	XP_017351907.1	104
108280990	LOC108280990	XP_017351995.1	251
108281024	LOC108281024	XP_017352057.1	302
108281047	LOC108281047	XP_017352082.1	201
108281048	nek4	XP_017352083.1	310
108281053	npff	XP_017352088.1	117
108281058	LOC108281058	XP_017352093.1	813
108281064	LOC108281064	XP_017352099.1	218
108281068	LOC108281068	XP_017352103.1	185
108281094	LOC108281094	XP_017352153.1	172
108281103	asb17	XP_017352164.1	206
108281106	LOC108281106	XP_017352166.1	295

Appendix Table 2 Genes specific in channel catfish and were differentially expressed during barbel regeneration of channel catfish.

Gene ID	Name	Protein product	Length
804886	ND6	NP_612136.1	171
108263381	pdss2	XP_017319591.1	381
108266750	tex30	XP_017325928.1	265
108263386	kmo	XP_017319604.1	473
108270394	crls1	XP_017332524.1	378
108266931	LOC108266931	XP_017326252.1	197
100528215	emc4	NP_001187414.1	187
108255681	LOC108255681	XP_017307300.1	204
108263202	apopt1	XP_017319259.1	198
108257472	edn1	XP_017310769.1	195
108279850	LOC108279850	XP_017349874.1	222
108275545	haus8	XP_017341915.1	364
100528430	anapc13	NP_001187629.1	74
108272348	cks1b	XP_017336199.1	79
108276169	cenpw	XP_017343137.1	75
100528304	ebag9	NP_001187503.1	212
108266359	LOC108266359	XP_017325014.1	332
108268882	tmsb15b	XP_017329693.1	46
108257184	cap2	XP_017310199.1	389
108268648	fanca	XP_017329197.1	1141
108274164	bricd5	XP_017339608.1	228
100528677	pdcd5	NP_001187876.1	126
108271425	tax1bp3	XP_017334514.1	125
108262879	LOC108262879	XP_017318723.1	329
108270530	LOC108270530	XP_017332816.1	228
108280749	LOC108280749	XP_017351609.1	510
804882	ND4	NP_612134.1	460
108258791	cytl1	XP_017313201.1	192
108268228	ssx2ip	XP_017328565.1	501
108270589	LOC108270589	XP_017332908.1	463
100304887	cript	NP_001232877.1	101
100528363	gins3	NP_001187562.1	211
100528639	skp1	NP_001187838.1	163
108279644	orc5	XP_017349462.1	445
108264799	LOC108264799	XP_017322162.1	383
108270120	LOC108270120	XP_017331955.1	127
108274859	LOC108274859	XP_017340785.1	226
108265590	epgn	XP_017323600.1	153
108266789	LOC108266789	XP_017326011.1	132
108262226	LOC108262226	XP_017318301.1	186
108271379	slc39a3	XP_017334439.1	315

108273999	ccser2	XP_017339238.1	791
108271223	cep19	XP_017334118.1	160
100528704	mzt1	NP_001187903.1	75
108268687	LOC108268687	XP_017329271.1	241
108272622	dctn3	XP_017336621.1	185
108255763	LOC108255763	XP_017307450.1	2337
108271519	snrpc	XP_017334632.1	159
108261049	LOC108261049	XP_017317354.1	163
108270478	cfl2	XP_017332713.1	166
108255701	LOC108255701	XP_017307331.1	108
108271021	LOC108271021	XP_017333665.1	119
108274856	LOC108274856	XP_017340782.1	231
108259812	cchcr1	XP_017315017.1	692
108264363	tsnaxip1	XP_017321304.1	548
100304584	LOC100304584	NP_001187095.1	105
108280863	twsg1	XP_017351823.1	223
108257874	atraid	XP_017311470.1	230
108281088	LOC108281088	XP_017352141.1	130
108260511	slc9b2	XP_017316357.1	533
108268439	LOC108268439	XP_017328905.1	78
108272615	pex11b	XP_017336601.1	252
108256728	LOC108256728	XP_017309381.1	157
108266662	dcaf17	XP_017325779.1	529
108276694	prr11	XP_017344007.1	299
108256526	polr1d	XP_017308970.1	172
108268918	LOC108268918	XP_017329751.1	115
108259227	cklf	XP_017313985.1	143
108258502	pld6	XP_017312671.1	243
108256594	LOC108256594	XP_017309125.1	83
108273111	ten1	XP_017337625.1	126
108272082	LOC108272082	XP_017335732.1	75
108260508	LOC108260508	XP_017316354.1	170
108255648	LOC108255648	XP_017307240.1	232
108265132	c1h8orf59	XP_017322758.1	98
100304470	b2m	NP_001187001.1	116
100305060	LOC100305060	NP_001187223.1	78
100528356	brk1	NP_001187555.1	75
108255519	LOC108255519	XP_017307008.1	110
108260858	LOC108260858	XP_017316999.1	231
108261098	LOC108261098	XP_017317468.1	226
108269115	LOC108269115	XP_017330184.1	86
100304587	LOC100304587	NP_001187096.1	92
100304595	LOC100304595	XP_017306663.1	119
100528727	arpc4	NP_001187926.1	168

100529001	psmf1	NP_001188200.1	270
108254817	LOC108254817	XP_017305644.1	239
108255518	LOC108255518	XP_017307006.1	112
108256245	LOC108256245	XP_017308375.1	111
108264196	LOC108264196	XP_017321018.1	231
108264531	LOC108264531	XP_017321623.1	152
108266135	LOC108266135	XP_017324656.1	268
100415908	LOC100415908	NP_001187260.1	223
108255397	batf	XP_017306830.1	124
108256237	azi2	XP_017308361.1	353
108257382	LOC108257382	XP_017310602.1	132
108258651	LOC108258651	XP_017312925.1	186
108261625	LOC108261625	XP_017317933.1	130
108262793	LOC108262793	XP_017318613.1	259
108263248	LOC108263248	XP_017319364.1	111
108265287	stap2	XP_017322931.1	415
108267188	LOC108267188	XP_017326670.1	101
108268115	LOC108268115	XP_017328326.1	97
108268327	ltbr	XP_017328717.1	353
108269344	LOC108269344	XP_017330655.1	78
108271554	LOC108271554	XP_017334684.1	223
108272639	LOC108272639	XP_017336661.1	218
108273140	LOC108273140	XP_017337676.1	158
108275426	LOC108275426	XP_017341728.1	129
108277757	LOC108277757	XP_017346142.1	281
108280668	mbp	XP_017351437.1	133
108280775	LOC108280775	XP_017351656.1	290
100304478	LOC100304478	NP_001187006.1	60
100528404	rabif	NP_001187603.1	133
100528408	tesc	NP_001187607.1	123
100528986	znrd1	NP_001188185.1	133
108256239	cmc1	XP_017308367.1	107
108256026	carnmt1	XP_017307985.1	418
108264825	LOC108264825	XP_017322217.1	689
108275464	mdp1	XP_017341794.1	160
108256275	hcrt	XP_017308436.1	126
108265761	clps	XP_017323916.1	136
108266496	LOC108266496	XP_017325497.1	114
108269592	mtfr1l	XP_017331025.1	303
804876	ATP8	NP_612129.1	55
804879	ND5	NP_612135.1	607
804883	ND2	NP_612126.1	348
100528072	cf125	NP_001187271.1	129
100528912	ndufb4	NP_001188111.1	127

108254755	arv1	XP_017305523.1	241
108259146	agrp	XP_017313858.1	143
108263832	LOC108263832	XP_017320489.1	112
108263890	LOC108263890	XP_017320565.1	108
108267455	pex19	XP_017327016.1	282
108268603	ndufc1	XP_017329138.1	69
108272167	LOC108272167	XP_017335903.1	76
108272602	atp5e	XP_017336584.1	51
108274303	nt5m	XP_017339890.1	230
108276884	LOC108276884	XP_017344430.1	125
108280490	LOC108280490	XP_017351002.1	55
108257443	LOC108257443	XP_017310711.1	645
108274881	LOC108274881	XP_017340817.1	128
108280026	LOC108280026	XP_017350293.1	305
804878	ND3	NP_612132.1	116
108259575	pex11a	XP_017314657.1	246
100528592	spcs1	NP_001187791.1	101
108276972	LOC108276972	XP_017344667.1	113
108278384	spcs2	XP_017347223.1	219
100528255	cck	NP_001187454.1	123
108270925	LOC108270925	XP_017333435.1	193
108270874	timm13	XP_017333325.1	95
108280891	LOC108280891	XP_017351876.1	90
108255480	ascc2	XP_017306909.1	763
108267567	LOC108267567	XP_017327250.1	124
108271096	elp4	XP_017333857.1	389
108271274	nr2c2ap	XP_017334228.1	141
108269806	mrps5	XP_017331332.1	400
108258002	LOC108258002	XP_017311708.1	177
108273408	mrpl58	XP_017338087.1	198
100528801	mrps14	NP_001188000.1	133
108280907	mrpl34	XP_017351897.1	115
108265414	tgoln2	XP_017323183.1	307
804877	ATP6	NP_612130.1	227
804880	ND1	NP_612125.1	324
804885	COX3	NP_612131.1	261
108256436	pkia	XP_017308799.1	85
108264506	c4h15orf48	XP_017321604.1	87
108272514	smdt1	XP_017336449.1	97
108280886	LOC108280886	XP_017351869.1	171
804875	COX2	NP_612128.1	230
804881	ND4L	NP_612133.1	98
100528515	vps28	NP_001187714.1	223
108257495	tomm7	XP_017310796.1	55

108264547	nutf2	XP_017321659.1	127
108273994	tomm22	XP_017339229.1	133
108276560	lyrm7	XP_017343819.1	104
108277678	LOC108277678	XP_017345975.1	916
108278988	slc31a2	XP_017348330.1	138
108268928	LOC108268928	XP_017329784.1	177
108259733	LOC108259733	XP_017314930.1	219
108271080	LOC108271080	XP_017333819.1	342
108272891	LOC108272891	XP_017337204.1	300
108259533	LOC108259533	XP_017314605.1	211
108260286	LOC108260286	XP_017315915.1	1346
108264443	LOC108264443	XP_017321459.1	449
108278302	LOC108278302	XP_017347058.1	180
108263206	borcs7	XP_017319270.1	103
108263260	LOC108263260	XP_017319384.1	100
108267632	LOC108267632	XP_017327393.1	139
108268185	LOC108268185	XP_017328487.1	215
108276417	LOC108276417	XP_017343554.1	241
108278804	LOC108278804	XP_017347903.1	365
100528339	dal1b	NP_001187538.1	102
108257542	ociad2	XP_017310896.1	160
108258663	LOC108258663	XP_017312951.1	107
108259248	LOC108259248	XP_017314029.1	227
108260035	LOC108260035	XP_017315449.1	270
108260899	LOC108260899	XP_017317094.1	264
108262451	LOC108262451	XP_017318391.1	224
108266945	LOC108266945	XP_017326272.1	224
108267969	LOC108267969	XP_017328071.1	407
108268874	LOC108268874	XP_017329676.1	222
108270531	tmem44	XP_017332820.1	454
108271423	LOC108271423	XP_017334509.1	222
108274023	c13h10orf128	XP_017339285.1	91
108274089	LOC108274089	XP_017339438.1	264
108274225	LOC108274225	XP_017339729.1	394
108274412	smim22	XP_017340039.1	81
108274670	LOC108274670	XP_017340388.1	112
108278494	LOC108278494	XP_017347401.1	142
108279884	ccdc167	XP_017349960.1	100
108280991	LOC108280991	XP_017351996.1	222
100305002	LOC100305002	NP_001187171.1	184
100528681	cops9	NP_001187880.1	57
100528768	lyrm5	NP_001187967.1	85
108254720	LOC108254720	XP_017305459.1	209
108257072	LOC108257072	XP_017309972.1	267

108257214	LOC108257214	XP_017310313.1	408
108258433	LOC108258433	XP_017312537.1	378
108259252	LOC108259252	XP_017314032.1	210
108259526	LOC108259526	XP_017314593.1	249
108259529	fam207a	XP_017314596.1	237
108259534	LOC108259534	XP_017314606.1	211
108260421	LOC108260421	XP_017316197.1	151
108262792	LOC108262792	XP_017318612.1	416
108263973	LOC108263973	XP_017320709.1	410
108264385	kiaa0513	XP_017321347.1	421
108265078	LOC108265078	XP_017322663.1	263
108265611	c5h9orf116	XP_017323639.1	141
108265844	LOC108265844	XP_017324081.1	209
108266094	LOC108266094	XP_017324579.1	243
108266430	LOC108266430	XP_017325223.1	258
108266545	LOC108266545	XP_017325499.1	218
108266787	c6h21orf62	XP_017326002.1	214
108267124	c7h22orf39	XP_017326584.1	108
108267255	LOC108267255	XP_017326735.1	124
108267286	LOC108267286	XP_017326792.1	224
108267350	LOC108267350	XP_017326880.1	203
108267429	LOC108267429	XP_017326988.1	129
108267962	c7h4orf48	XP_017328062.1	86
108268437	LOC108268437	XP_017328903.1	595
108268660	LOC108268660	XP_017329227.1	363
108269355	LOC108269355	XP_017330676.1	204
108269361	c8h12orf73	XP_017330683.1	64
108269490	tmem229b	XP_017330904.1	185
108270539	c1h16orf91	XP_017332839.1	155
108270745	LOC108270745	XP_017333119.1	925
108270746	LOC108270746	XP_017333120.1	921
108271006	LOC108271006	XP_017333637.1	491
108271220	serf2	XP_017334114.1	59
108272510	ccdc134	XP_017336446.1	229
108272745	LOC108272745	XP_017336922.1	363
108272856	hn1	XP_017337160.1	139
108273013	LOC108273013	XP_017337460.1	239
108273081	LOC108273081	XP_017337557.1	173
108273612	LOC108273612	XP_017338452.1	127
108274251	LOC108274251	XP_017339791.1	425
108274403	c2h8orf82	XP_017340011.1	213
108274852	LOC108274852	XP_017340775.1	247
108275268	lrrc61	XP_017341463.1	281
108275551	LOC108275551	XP_017341922.1	326

108275692	LOC108275692	XP_017342101.1	432
108276725	LOC108276725	XP_017344082.1	114
108276957	LOC108276957	XP_017344627.1	271
108277089	LOC108277089	XP_017344948.1	87
108278455	LOC108278455	XP_017347336.1	202
108278465	LOC108278465	XP_017347351.1	209
108279232	c18h5orf15	XP_017348793.1	290