Supporting Information

Title: Pseudogenization of *Mc1r* gene associated with transcriptional changes related to melanogensis explains leucistic phenotypes in *Oreonectes* cavefish (Cypriniformes, Nemacheilidae)

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Short running title: Leucistic *Oreonectes* cavefish

Supplementary Table S1. List of the species used in this study, with GenBank accession numbers of mitochondrial genes.

Family	Species name	Accession number
Outgroups		
Cobitidae	*Cobitis sinensis*	AY526868.1
	Misgurnusan guillicaudatus	KM186181.1
Balitoridae	*Jinshaia sinensis*	JX155733.1
	Sinogastromyzon sichangensis	KF711948.1
Ingroups		
Nemacheilidae	*Aborichthys elongatus*	NC_031582.1
	Acanthocobitis botia	NC_033958.1
	Barbatula barbatula	KP715096.1
	Barbatula nuda	NC_022858.1
	Barbatula toni	KM405199.1
	Schistura balteata	AB242172.1
	Schistura longa	KT213583.1
	Schistura corica	NC_031640.1
	Schistura geisleri	NC_029437.1
	Schistura pridii	NC_031638.1
	Schistura jarutanini	NC_031584.1
	Schistura scaturigina	NC_031378.1
	Schistura sikmaiensis	NC_034746.1
	Schistura notostigma	NC_031585.1
	Triplophysa aliensis	KT213584.1
	Triplophysa lixianensis	NC_030521.1
	Triplophysa stenura	NC_032692.1
	Triplophysa brevicauda	KT213588.1
	Triplophysa nujiangensa	KT213598.1
	Triplophysa stewartia	KT213605.1
	Triplophysa tibetana	KM212178.1
	Triplophysa microps	KT213595.1
	Triplophysa chondrostoma	KT213589.1
	Triplophysa markehenensis	KT213594.1
	Triplophysa stoliczkai	NC_017890.1
	Triplophysa leptosoma	KT213593.1
	Triplophysa xichangensis	KT224366.1
	Triplophysa moquensis	KT213597.1
	Triplophysa dorsalis	KT241024.1
	Triplophysa strauchii	KP297875.1
	Triplophysa ulacholica	KT259194.1
	Triplophysa tenuis	KT224363.1
	Triplophysa scleropter	KT213602.1
	Triplophysa dalaica	KT213590.1
	Triplophysa wuweiensis	KT224365.1
	Triplophysa anterodorsalis	NC_024597.1
	Triplophysa bleekeri	JX135578.1
	Triplophysa hsutschouensis	KT213592.1
	Triplophysa orientalis	NC_030505.1
	Triplophysa venusta	KT008666.1
	Triplophysa brevibarba	KY971608.1
	Triplophysa pappenheimi	KY419201.1
	Triplophysa robusta	KM396312.1
	Triplophysa pseudoscleroptera	KU587513.1

	Triplophysa pseudostenura	KT213601.1
	Triplophysa siluroides	NC_024611.1
	Triplophysa xiangxiensis	KT751089.1
	Triplophysa rosa	NC_019587.1
	Homatula potanini	NC_025321.1
	Homatula variegatus	NC_020095.1
	Oreonectes platycephalus	NC_031579
	Lefua costata	KT943751.1
	Lefua nikkonis	AP011300.1

* The newly generated data are underlined.

Supplementary Table S2. Comparison of De Novo Transcriptome Assemblies of *O. shuilongensis* and other fishes.

Species	*Oreonectes shuilongensis*	*Amphiprion Percula*	*Fundulus heteroclitus*	*Hucho taimen*	*Salmo Salar*
Contig Number	99,305	88,074	180,658	242,069	36,505
N50 Length	3,571	1,969	1,189	10.60	2,464
BUSCO completeness	89.60%	70.00%	70.25%	55.77%	79.00%
Complete single-copy BUSCOs	43.85%	-	42.20%	29.87%	42.00%
Complete duplicated BUSCOs	45.75%	-	28.05%	25.90%	37.00%
Fragmented BUSCOs	5.24%	15.40%	7.45%	18.93%	10.00%
Missing BUSCOs	5.26%	14.60%	22.30%	25.30%	10.00%
Reference	This study	Maytin et al. 2018	Rana et al. 2016	Tong et al. 2017	Carruthers et al. 2018

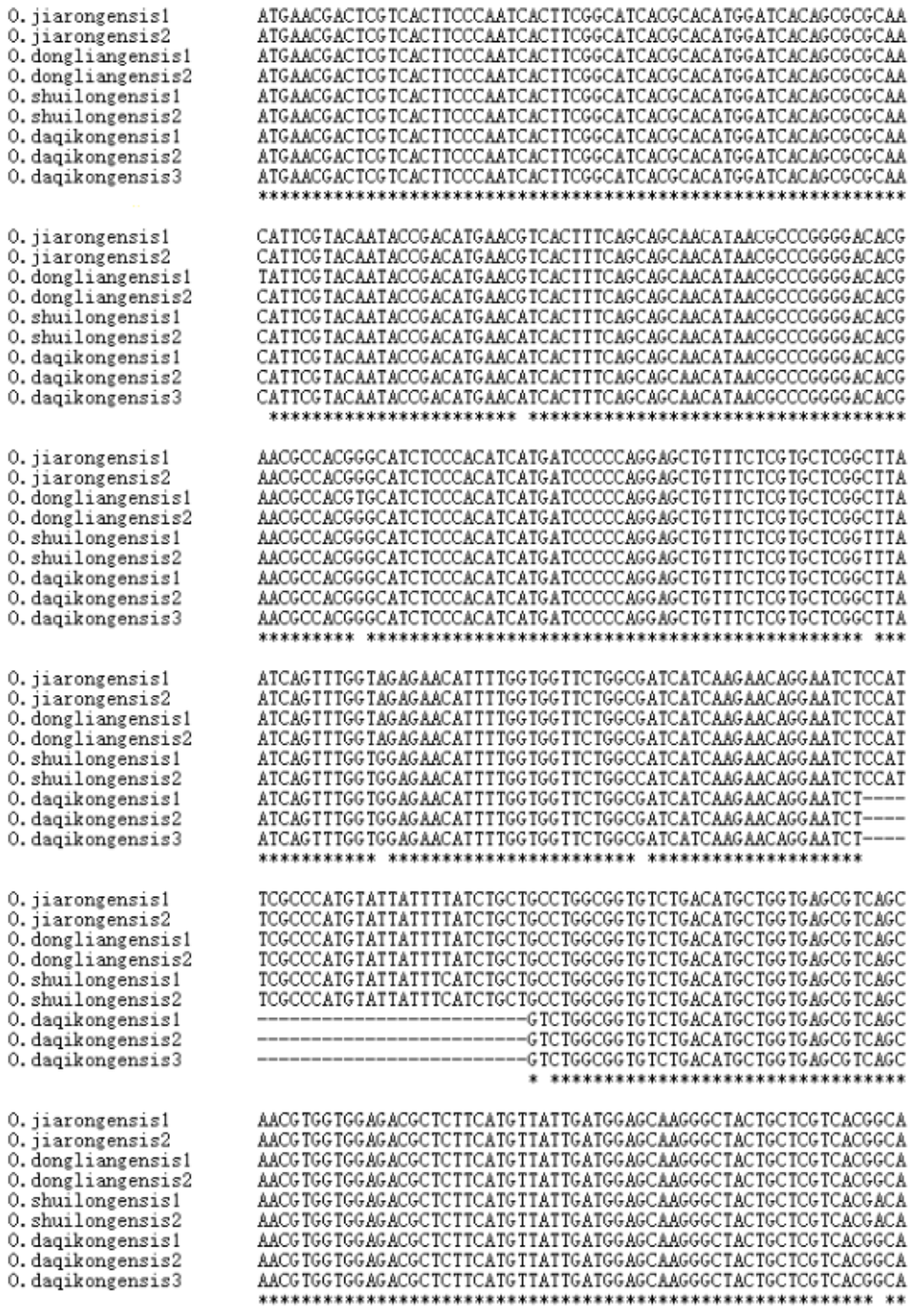
Maytin AK, Davies SW, Smith GE, Mullen SP and Buston PM (2018) *De novo* Transcriptome Assembly of the Clown Anemonefish (Amphiprion percula): A New Resource to Study the Evolution of Fish Color. Front. Mar. Sci. 5:284.

Rana SB, Zadlock FJ IV, Zhang Z, Murphy WR, Bentivegna CS (2016) Comparison of *De Novo* Transcriptome Assemblers and k-mer Strategies Using the Killifish, *Fundulus heteroclitus*. PLoS ONE 11(4): e0153104.

Tong GX, Xu W, Zhang YQ, Zhang QY, Yin JS, Kuang YY (2018) *De novo* assembly and characterization of the Hucho taimen transcriptome. Ecol Evol. 8:1271 – 1285.

Carruthers M, Yurchenko AA, Augley JJ, Adams CE, Herzyk P, Elmer KR (2018) *De novo* transcriptome assembly, annotation and comparison of four ecological and evolutionary model salmonid fish species. BMC Genomics. 19: 32.

Supplementary Fig. S1. Coding sequences of *Mc1r* genes of *O. daqikongensis*, *O. jiarongensis*, *O. dongliangensis* and *O. shuilongensis*. Asterisks denote fully conserved sites.



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O.jiarongensis2         AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAGCTGCAGCTCGGTCGTGTCC
O.dongliangensis1       AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAGCTGCAGCTCGGTCGTGTCC
O.dongliangensis2       AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAACTGCAGCTCGGTCGTGTCC
O.shuilongensis1        AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAACTGCAGCTCGGTCGTGTCC
O.shuilongensis2        AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAACTGCAGCTCGGTCGTGTCC
O.daqikongensis1        AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAACTGCAGCTCGGTCGTGTCC
O.daqikongensis2        AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAACTGCAGCTCGGTCGTGTCC
O.daqikongensis3        AAGATGTTACAGCACCTGGACAACGTGATCGACATCATGAACTGCAGCTCGGTCGTGTCC
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O.jiarongensis1         TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
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O.dongliangensis1       TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
O.dongliangensis2       TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
O.shuilongensis1        TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
O.shuilongensis2        TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
O.daqikongensis1        TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
O.daqikongensis2        TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
O.daqikongensis3        TCGCTGTCGTTCCTGTGCACCATCGCGGCGGACCGCTACATCACCATCTTTTACGCGCTT
                        ************************************************************

O.jiarongensis1         CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
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O.dongliangensis1       CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
O.dongliangensis2       CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
O.shuilongensis1        CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
O.shuilongensis2        CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
O.daqikongensis1        CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
O.daqikongensis2        CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
O.daqikongensis3        CGCTACCACAGCATCATGACCACGAGACGCGCCGTGGCCATCATCGCGGTGGTTTGGCTT
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O.jiarongensis1         ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.jiarongensis2         ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.dongliangensis1       ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.dongliangensis2       ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.shuilongensis1        ACGAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.shuilongensis2        ACGAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.daqikongensis1        ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.daqikongensis2        ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
O.daqikongensis3        ACAAGCATCACCTCCAGCTCTTTGTTTATCGTGTACCACACGAACAAAGCGGTCATCGCG
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O.jiarongensis1         TGTCTCGTCACGTTTTTTGGCGTGACGCTTGTGTTCACGGCGGTCCTGTACCTGCACATG
O.jiarongensis2         TGTCTCGTCACGTTTTTTGGCGTGACGCTTGTGTTCACGGCGGTCCTGTACCTGCACATG
O.dongliangensis1       TGTCTCGTCACGTTTTTTGGCGTGACGCTTGTGTTCACGGCGGTCCTGTACCTGCACATG
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O.daqikongensis1        TGTCTCGTCGCGTTTTTTGGCGTGACGCTTGTGTTCACAGCGGTCATGTACCTGCACATG
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O.daqikongensis3        TGTCTCGTCGCGTTTTTTGGCGTGACGCTTGTGTTCACAGCGGTCATGTACCTGCACATG
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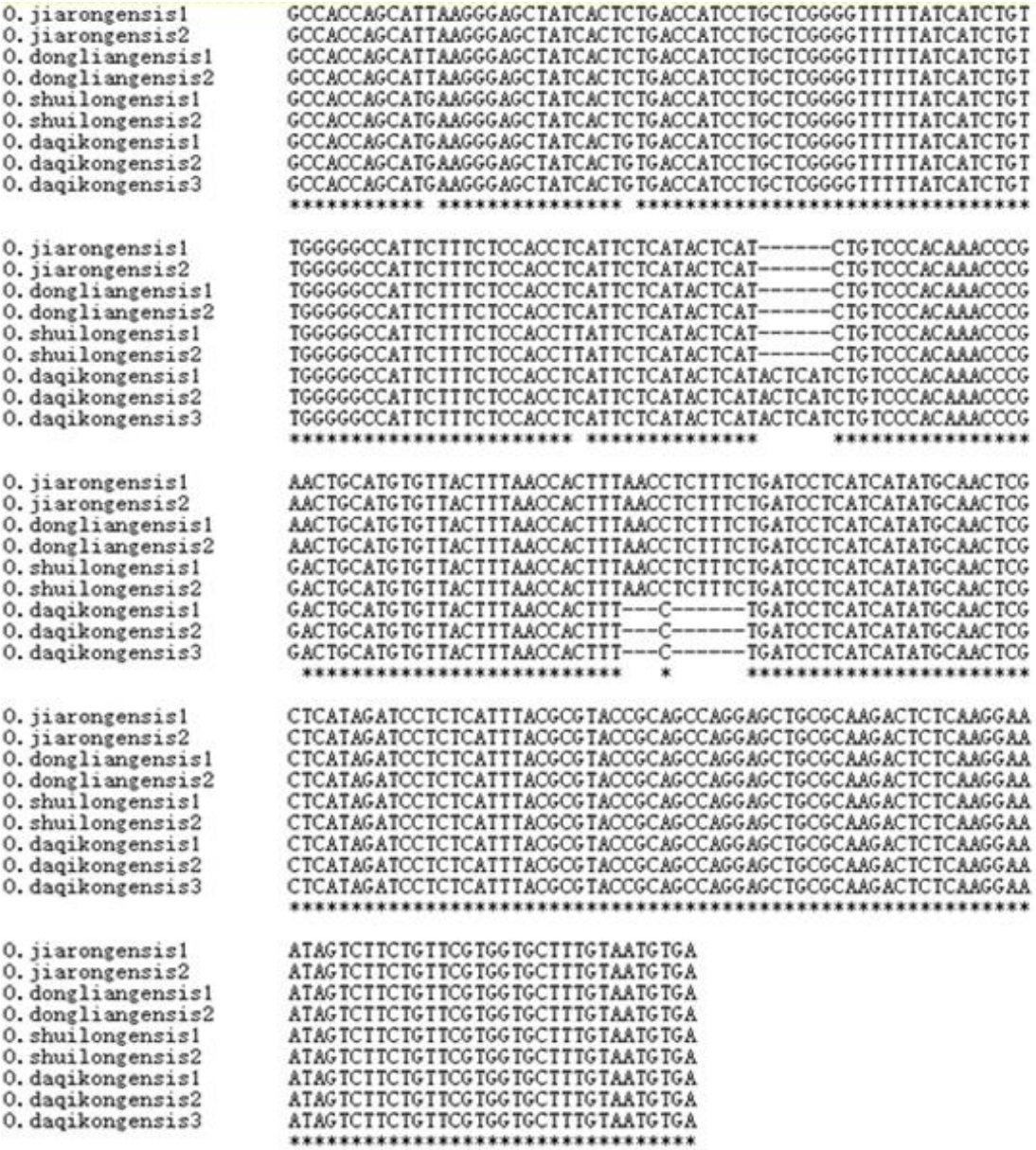
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Supplementary Fig. S2. BUSCO assessment of *O. shuilongensis* transcriptome assembly.