

Predicting Sex-Related Transcripts in the Chinese Giant Salamander (*Andrias davidianus*): A Transcriptomics Study, Selection Gender for Preservation, Breeding and Reintroduction

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Table S1. Sequencing data statistics of *Andrias davidianus* with three males and three females.

BMK-ID	Read number	Base number	GC content	% ≥ Q30
M-1	26,600,554	7,421,353,584	48.34%	91.53%
M-2	25,047,421	6,991,726,842	48.85%	91.63%
M-3	28,141,691	7,863,982,016	50.34%	90.76%
F-1	29,290,482	8,187,093,220	49.61%	92.08%
F-2	28,217,103	7,878,956,132	48.66%	92.24%
F-3	31,917,900	8,917,228,336	50.07%	91.98%

Table S2. *De novo* Assembly of *Andrias davidianus* transcript and unigenes.

Length Range	Transcript	Unigene
200–300	25,073(20.18%)	22,110(27.07%)
300–500	19,928(16.04%)	14,191(17.38%)
500–1000	27,181(21.88%)	17,724(21.70%)
1000–2000	23,338(18.78%)	13,284(16.27%)
2000+	28,719(23.12%)	14,362(17.59%)
Total Number	124,239	81,671
Total Length	177,584,245	96,226,355
N50 Length	2,722	2,341
Mean Length	1429.38	1178.22

Table S3. Statistics table of sequencing data of *Andrias davidianus*.

BMK-ID	Clean reads	Mapped reads	Mapped ratio
M-1	26,600,554	21,071,532	79.21%
M-2	25,047,421	20,260,614	80.89%
M-3	28,141,691	20,857,954	74.12%
F-1	29,290,482	24,611,936	84.03%
F-2	28,217,103	22,914,688	81.21%
F-3	31,917,900	26,756,456	83.83%

Table S4. GO terms of biological process of differentially expressed genes (DEGs) in the gonadal tissue of *Andrias davidianus* with two sexes.

GO ID	Term	Annotated genes	Significant genes	Expected value	p-value
GO:0006412	Translation	346	139	150.64	5.50E-05
GO:0048703	embryonic viscerocranium morphogenesis	15	14	6.53	6.90E-05
GO:0030509	BMP signaling pathway	36	27	15.67	0.00011
GO:0019432	triglyceride biosynthetic process	7	7	3.05	0.00064
GO:0051225	spindle assembly	17	14	7.4	0.00097
GO:0034502	protein localization to chromosome	9	9	3.92	0.00107
GO:0006470	protein dephosphorylation	71	40	30.91	0.00164
GO:0044786	cell cycle DNA replication	7	7	3.05	0.00251
GO:0001934	positive regulation of protein phosphorylation	130	65	56.6	0.00296
GO:0007062	sister chromatid cohesion	12	10	5.22	0.00318
GO:0007184	SMAD protein import into nucleus	5	5	2.18	0.00351
GO:0048752	semicircular canal morphogenesis	6	6	2.61	0.00421
GO:0051216	cartilage development	61	39	26.56	0.00428
GO:0006029	proteoglycan metabolic process	23	17	10.01	0.00588
GO:0050686	negative regulation of mRNA processing	11	8	4.79	0.00608
GO:0000070	mitotic sister chromatid segregation	14	11	6.1	0.00654
GO:0006265	DNA topological change	5	5	2.18	0.00658
GO:0035195	gene silencing by miRNA	11	8	4.79	0.0078
GO:0043085	positive regulation of catalytic activity	217	113	94.48	0.00878
GO:0009154	purine ribonucleotide catabolic process	306	137	133.23	0.00882
GO:0007338	single fertilization	16	11	6.97	0.0091
GO:0007265	Ras protein signal transduction	134	75	58.34	0.00916
GO:0048705	skeletal system morphogenesis	76	50	33.09	0.00948
GO:0010453	regulation of cell fate commitment	10	7	4.35	0.00979
GO:0006817	phosphate ion transport	5	5	2.18	0.00983

Table S5. GO terms of cellular component of differentially expressed genes (DEGs) in the gonadal tissue of *Andrias davidianus* with two sexes.

GO ID	Term	Annotated genes	Significant genes	Expected value	p-value
GO:0005840	ribosome	206	90	91.8	0.0002
GO:0022625	cytosolic large ribosomal subunit	53	21	23.62	0.0014
GO:0022627	cytosolic small ribosomal subunit	38	16	16.93	0.0036
GO:0032133	chromosome passenger complex	5	5	2.23	0.0073

Table S6. GO terms of molecular function of differentially expressed genes (DEGs) in the gonadal tissue of *Andrias davidianus* with two sexes.

GO ID	Term	Annotated genes	Significant genes	Expected value	p-value
GO:0005543	phospholipid binding	172	98	74	0.0008
GO:0005160	transforming growth factor beta receptor binding	6	6	2.58	0.0031
GO:0003677	DNA binding	633	296	272.35	0.0049
GO:0004721	phosphoprotein phosphatase activity	97	44	41.73	0.0052
GO:0008378	galactosyltransferase activity	6	6	2.58	0.0053
GO:0003729	mRNA binding	27	17	11.62	0.0053
GO:0003916	DNA topoisomerase activity	5	5	2.15	0.006
GO:0051920	peroxiredoxin activity	8	6	3.44	0.0063
GO:0008375	acetylglucosaminyltransferase activity	16	12	6.88	0.0065
GO:0043168	anion binding	1384	620	595.47	0.0075
GO:0097367	carbohydrate derivative binding	1134	491	487.91	0.0075
GO:0036094	small molecule binding	1479	661	636.35	0.0083
GO:0003876	AMP deaminase activity	3	3	1.29	0.0089
GO:1901677	phosphate transmembrane transporter activity	10	8	4.3	0.0091
GO:0008138	protein tyrosine/serine/threonine phosphatase activity	27	18	11.62	0.0098