

Supplementary Tables and Figures

DNA gains and losses in gigantic genomes do not track differences in transposable element-host silencing interactions

Jie Wang^{1,*}, Guangpu Zhang¹, Cheng Sun², Liming Chang¹, Yingyong Wang³, Xin Yang⁴,
Guiying Chen⁵, Michael W. Itgen^{6,7}, Ava Haley⁶, Jiaxing Tang^{1,5,*}, Rachel Lockridge Mueller^{6,*}

* Correspondence:

Jie Wang, wangjie@cib.ac.cn

Jiaxing Tang, 773830970@qq.com

Rachel Lockridge Mueller, rlm@colostate.edu

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Table S1 Samples and data used in this study

Species	Tissue	Code	Sex	Mass: g	STL#: cm	Collection date	Collection sites	Source	Genomic sequencing		RNA quality				mRNA sequencing		small RNA sequencing	
									Raw reads	Accession code ¹	OD260/280	OD260/230	28S/18S	RIN	Raw reads	Accession code ²	Raw reads	Accession code ³
<i>Ranodon sibiricus</i>	Testis#1	WQ07	♂	16.83	17.252	2017.8.22.	Wenquan	wild			1.77	2.75	1.7	9.6	37,888,360	CRR610084	19,717,749	CRR610091
	Testis#2	WQ08	♂	19.79	18.192	2017.8.22.	County,	wild			1.73	0.95	1.1	8.9	35,386,396	CRR610085	21,815,001	CRR610092
	Testis#3	WQ10	♂	12.02	16.441	2017.8.22.	Xinjiang	wild			2.00	3.22	1.7	9.4	34,854,594	CRR610086	16,177,680	CRR610093
	Testis#4	WQ05	♂	20.48	15.591	2017.8.22.	Uygur	captive			1.70	2.13	1.7	9.3	31,732,246	CRR610083	19,005,099	CRR610090
	Ovary#1	WQ03	♀	32.85	21.001	2017.8.22.	Autonomous Region	captive	11,960,858	CRR609958	1.96	0.68	1.1	9.3	38,466,202	CRR610080	17,965,762	CRR610088
	Ovary#2	WQ02	♀	28.61	20.804	2017.8.22.		captive			1.64	0.49	1.5	9.6	40,660,732	CRR610079	15,836,634	CRR610087
	Ovary#3	WQ04	♀	35.37	20.437	2017.8.22.		captive			1.64	0.22	0.8	8.7	39,418,784	CRR610081	14,063,357	CRR610089
	Ovary#4	WQ06	♀	23.57	18.149	2017.8.22.		captive			1.66	0.15	0.1	7.7 ⁴	39,229,748	CRR610082		
<i>Tylototriton verrucosus</i>	Testis#1	HS02	♂	13.0	14.1	2017.7.8.	Husa	Wild			1.99	2.31	1.6	9.3	32,691,262	CRR649922	16,585,370	CRR649930
	Testis#2	HS04	♂	13.2	15.0	2017.7.8.	County,	Wild			1.94	2.42	1.7	9.2	32,973,554	CRR649923	17,619,593	CRR649931
	Testis#3	HS05	♂	13.0	15.2	2017.7.8.	Yunnan	Wild			1.99	2.01	1.7	9.6	42,699,602	CRR649924	17,707,096	CRR649932
	Testis#4	HS07	♂	20.2	15.4	2017.7.8.	province	Wild			2.02	2.32	1.6	9.3	35,485,366	CRR649925	16,278,837	CRR649933
	Ovary#1	HS08	♀	25.8	17.5	2017.7.8.		Wild			1.58	0.25	0.6	6.5	39,101,474	CRR649918	31,842,294	CRR649926
	Ovary#2	HS09	♀	34.3	20.2	2017.7.8.		Wild	12,129,476	CRR649917	1.84	0.97	1.1	8.5	39,718,882	CRR649919	18,122,932	CRR649927
	Ovary#3	HS11	♀	25.0	18.6	2017.7.8.		Wild			1.79	0.73	0.9	7.8	38,441,274	CRR649920	17,009,880	CRR649928
	Ovary#4	HS12	♀	20.1	16.7	2017.7.8.		Wild			1.61	0.29	0.6	7.8	40,016,632	CRR649921	35,999,752	CRR649929
<i>Pachytriton brevipes</i>	Testis#1	NF01	♂	9.8	13.1	2017.7.9.	Nanfeng	wild			2.00	2.22	1.1	9.4	38,735,632	CRR649888	17,289,840	CRR649896
	Testis#2	NF14	♂	31.5	20.0	2017.7.9.	County,	wild			1.91	2.32	1.4	9.8	37,515,790	CRR649889	18,259,136	CRR649897
	Testis#3	NF16	♂	29.3	18.6	2017.7.9.	Jiangxi	wild			2.0	2.18	1.4	9.7	35,913,846	CRR649890	19,728,618	CRR649898

	Testis#4	NF18	♂	15.9	15.4	2017.7.9.	Province	wild			1.95	2.27	1.3	9.7	41,001,140	CRR649891	18,206,032	CRR649899
	Ovary#1	NF08	♀	17.0	15.3	2017.7.9.		wild			1.58	0.35	0.9	8.5	32,094,588	CRR649884	32,733,395	CRR649892
	Ovary#2	NF09	♀	16.5	15.8	2017.7.9.		wild			1.95	1.45	1.5	8.3	34,827,584	CRR649885	18,218,210	CRR649893
	Ovary#3	NF20	♀	22.3	18.3	2017.7.9.		wild			1.99	1.41	1.0	8.7	33,516,658	CRR649886	17,778,912	CRR649894
	Ovary#4	NF21	♀	21.7	17.4	2017.7.9.		wild	15,505,860	CRR650566	1.95	2.22	1.5	8.3	40,024,958	CRR649887	18,167,875	CRR649895
<i>Cynops orientalis</i>	Testis#1	CO16	♂	1.2	6.9	2017.10.17.	Kecheng	wild			1.50	0.33	1.2	8.3	41,446,178	CRR649563	17,538,653	CRR649571
	Testis#2	CO17	♂	1.2	6.0	2017.10.17.	District,	wild			1.54	0.95	1.0	8.1	33,512,742	CRR649564	19,588,629	CRR649572
	Testis#3	QZ01	♂	1.8	6.3	2017.7.4.	Quzhou	wild			1.67	1.88	0.7	7.6	32,573,566	CRR649565	15,203,225	CRR649573
	Testis#4	QZ04	♂	2.0	6.7	2017.7.4.	City,	wild			1.96	1.93	0.7	8.1	41,743,244	CRR649566	18,690,834	CRR649574
	Ovary#1	CO12	♀	2.1	7.6	2017.10.17.	Zhejiang Province	wild			1.86	1.68	0.8	8.5	34,189,104	CRR649559	16,659,083	CRR649567
	Ovary#2	CO13	♀	2.0	8.1	2017.10.17.		wild			1.90	1.95	0.6	6.7	34,644,206	CRR649560	18,525,552	CRR649568
	Ovary#3	CO14	♀	1.6	7.5	2017.10.17.		wild			1.90	1.83	0.5	7.4	54,097,378	CRR649561	15,023,175	CRR649569
	Ovary#4	QZ09	♀	3.2	7.6	2017.7.4.		wild	33,153,950	CRR649558	1.81	0.62	0.5	8.3	36,944,040	CRR649562	16,661,516	CRR649570
<i>Andrias davidianus</i>	Testis#1	LY06	♂		74.0	2017.8.10.	Lueyang County, Shaanxi Province	captive			1.86	1.84	1.2	8.6	29,719,324	CRR638172	16,008,097	CRR638180
	Testis#2	LY07	♂		86.0	2017.8.10.		captive			1.87	1.77	2.3	8.2	34,960,348	CRR638173	17,458,603	CRR638181
	Testis#3	LY08	♂		87.5	2017.8.10.		captive			2.04	1.09	0.9	7.2	53,487,888	CRR638174	19,122,025	CRR638182
	Testis#4	LY09	♂		89.5	2017.8.10.		captive			1.88	1.56	1.2	8.7	33,144,322	CRR638175	20,191,827	CRR638183
	Ovary#1	LY01	♀		71.5	2017.8.10.		captive	24,305,964	CRR638167	1.00	0.23	1.5	8.2	31,801,468	CRR638168	17,631,197	CRR638176
	Ovary#2	LY03	♀		79.0	2017.8.10.		captive			1.97	2.25	0.9	7.0	32,312,166	CRR638169	18,539,178	CRR638177
	Ovary#3	LY04	♀		71.0	2017.8.10.		captive			1.99	2.40	0.9	7.5	34,674,288	CRR638170	16,260,101	CRR638178
	Ovary#4	LY05	♀		75.0	2017.8.10.		captive			1.96	2.44	0.8	7.3	37,821,156	CRR638171	18,605,559	CRR638179
<i>Paramesotriton honkongensis</i>	Testis#1	HK03	♂	7.5	12.0	2017.12.8.	Shenzhen	wild			1.82	0.68	1.2	9.0	41,780,356	CRR649905	16,326,142	
	Testis#2	HK04	♂	7.4	11.5	2017.12.8.	City,	wild			1.82	0.98	0.9	8.3	39,777,108	CRR649906	18,469,923	CRR649914
	Testis#3	HK05	♂	8.6	12.0	2017.12.8.	Guangdong	wild			1.68	0.68	1.0	8.2	39,191,664	CRR649907	16,805,777	CRR649915

	Testis#4	HK06	♂	9.4	11.5	2017.12.8.	Province	wild				1.80	1.06	0.9	8.5	41,074,192	CRR649908	18,347,342	CRR649916
	Ovary#1	HK08	♀	10.6	14.0	2017.12.8.		wild				1.51	0.21	0.4	5.9	37,576,072	CRR649901	9,308,482	CRR649909
	Ovary#2	HK09	♀	8.2	11.5	2017.12.8.		wild				1.49	0.15	0.5	7.4	38,208,494	CRR649902	15,027,311	CRR649910
	Ovary#3	HK10	♀	10.6	12.5	2017.12.8.		wild				1.38	0.17	0.4	7.0	42,629,786	CRR649903	21,879,203	CRR649911
	Ovary#4	HK11	♀	10.3	12.0	2017.12.8.		wild	16,943,516	CRR649900		1.58	0.22	0.9	8.3	35,881,698	CRR649904	18,743,046	CRR649912

STL: Snout-tail-length, length from the snout to the end of tail.

URL for data download:

Genome, transcriptome, and small RNA data of *Ranodon sibiricus* (CRA008892, CRA008899, CRA008900);

<https://ngdc.cncb.ac.cn/gsa/browse/CRA008892> (genome data)

<https://ngdc.cncb.ac.cn/gsa/browse/CRA008899> (transcriptome data)

<https://ngdc.cncb.ac.cn/gsa/browse/CRA008900> (small RNA data)

Genome, transcriptome, and small RNA data of *Andrias davidianus* (CRA009444):

<https://ngdc.cncb.ac.cn/gsa/browse/CRA009444>

Genome, transcriptome, and small RNA data of *Cynops orientalis* (CRA009736);

<https://ngdc.cncb.ac.cn/gsa/browse/CRA009736>

Genome, transcriptome, and small RNA data of *Pachytriton brevipes* (CRA009747);

<https://ngdc.cncb.ac.cn/gsa/browse/CRA009747>

Genome, transcriptome, and small RNA data of *Paramesotriton hongkongensis* (CRA009748);

<https://ngdc.cncb.ac.cn/gsa/browse/CRA009748>

Genome, transcriptome, and small RNA data of *Tylosotriton verrucosus* (CRA009749);

<https://ngdc.cncb.ac.cn/gsa/browse/CRA009749>

Table S2 Steps for the genomic assembly and the estimation of sequencing depth

Steps	Types	<i>Ranodon sibiricus</i>	<i>Tylototriton verrucosus</i>	<i>Pachytriton brevipes</i>	<i>Cynops orientalis</i>	<i>Andrias davidianus</i>	<i>Paramesotriton honkongensi</i>
		WQ03	HS09	NF21	QZ09	LY01	HK11
	Raw reads	11,960,858	12,129,476	15,505,860	33,153,950	24,305,964	16,943,516
Trimmomatic	Clean reads	11,168,678	11,080,362	14,218,520	30,343,958	22,113,929	14,752,452
	N50 of clean reads	250	246	250	245	243	250
	Sum length of clean reads	2,314,096,923	2,403,712,090	3,195,482,437	6,506,579,244	4,634,122,878	3,222,403,582
Sequencing	Genome size [#]	21,300,000,000	23,961,000,000	38,924,400,000	43,325,400,000	48,900,000,000	49,878,000,000
Depth	Depth	0.11 X	0.10 X	0.08 X	0.15 X	0.09 X	0.06 X
Merged by Pear	No. of merged pair-reads	3,783,512	9,518,030	9,870,941	25,315,531	18,112,904	10,935,902
	Unassembled forward/reverse reads	1,500,762	3,661,719	2,165,798	8,922,442	6,256,605	2,750,468
	N50 of reads	388	250	362	250	249	250
	Sum length of reads	1,997,175,501	2,267,438,309	2,787,991,555	6,029,429,512	4,256,895,753	2,911,584,397
Assembled by dipSpades	No. of contigs	478,991	166,335	649,430	662,111	276,974	634,076
	Sum length of contigs	249,425,929	95,192,733	360,507,191	429,174,065	161,443,731	368,170,024
	Min length of contigs	128	128	128	130	128	128
	N50 of contigs	447	536	475	626	540	516
	Max length of contigs	25,462	16,789	20,021	18,448	28,984	26,186

[#] Data from Gregory 2024. Animal genome size database. <http://www.genomesize.com>.

Table S3.1 Classification of repeat contigs (modified from Wicker 2007) and summary of repeats detected in the genome of *Ranodon sibiricus* (Wang et al., 2023)

Order	Superfamily	Percent of Genome ^a	Genomic Contigs (100% Identical)	Genomic Contigs (95% Identical)	Genomic Contigs (80% Identical)	Average Genomic Contig Length (100% identical) (bp)	Longest Genomic Contig (bp)	Transcriptome contigs (80% Identical)	Average Expression Level in females (TPM)	Average Expression Level in males (TPM)
Class I - Retrotransposons - Autonomous										
LTR	<i>Gypsy</i>	3.85-6.50	5,985	5,464	3,835	548	7,587	2,057	827	3,024
	<i>ERV</i>	0.41-0.43	417	398	267	542	11,567	321	392	694
	<i>Copia</i>	0.10-0.25	23	21	19	592	1,353	27	31	26
	<i>Bel-Pao</i>	0.05	12	7	2	575	766	-	-	-
	<i>Retrovirus</i>	-	3	2	2	1,375	1,719	10	1	10
	Unknown LTR	-	4	4	4	469	955	-	-	-
DIRS	<i>DIRS</i>	4.44-5.95	8,087	7,821	3,844	379	4,266	4,844	5,427	11,962
PLE	<i>Penelope</i>	0.09-0.12	482	462	376	407	3,208	460	123	352
LINE	<i>Jockey</i>	9.69-12.12	25,276	23,361	13,287	426	3,625	11,622	6,206	15,535
	<i>L1</i>	5.04-6.62	10,189	8,997	5,941	672	6,546	8,241	2,954	7,610
	<i>RTE</i>	0.12-0.24	227	201	137	676	4,540	399	130	360
	<i>I</i>	0.09-0.17	32	25	10	905	3,858	48	42	125
	<i>R2</i>	-						1	-	1
	Unknown LINE	0.39-1.89	90	77	72	1,393	5,881	1	-	-
Class I - Retrotransposons - Non-autonomous										
SINE	<i>5S</i>	0.23-0.18	57	41	15	773	1,783	4	5	1
	<i>7SL</i>	-	43	41	15	243	450	2	1	-
	<i>tRNA</i>	-	22	22	22	273	403	-	-	-
	Unknown SINE	0.45-3.42	365	348	338	377	695	219	2,901	2,471
Retrotransposon Derivatives	TRIM	3.80-9.76	748	631	465	588	2,619	492	1,651	5,847
	LARD	0.15-0.73	45	37	35	2,834	8,148	153	515	2,643

Class II DNA transposons Subclass 1										
TIR	<i>PIF-Harbinger</i>	2.98-4.22	1,164	1,014	434	411	5,169	416	575	1,359
	<i>hAT</i>	1.15-1.12	177	135	55	869	5,706	35	83	26
	<i>Tc1-Mariner</i>	0.18-0.63	73	40	24	1025	3,781	20	58	87
	<i>PiggyBac</i>	0.05-0.08	9	8	6	1,087	1,956	6	21	15
	<i>MuDR</i>	0	3	3	3	266	417	13	4	10
	<i>CACTA</i>	0	2	2	2	645	846	3	2	1
	<i>Academ</i>	-						11	5	8
	<i>Ginger</i>	-						4	10	6
	<i>ISL2EU</i>	-						1	18	16
	<i>P</i>	-						1	1	1
	Unknown TIR	0.33-1.46	22	20	19	754	2,174	-	-	-
Transposon Derivatives	MITE	0.56-4.07	357	346	321	258	1,942	137	465	1,188
Class II - DNA Transposons - Subclass 2										
Maverick	<i>Maverick</i>	0.05	258	228	65	583	6,090	123	44	762
Helitron	<i>Helitron</i>	0.18-0.48	49	38	19	939	6,551	13	2	10
Total		34.38-60.54	54,221	49,794	29,634	489	11,567	29,684	22,494	42,200

^aThe first and second numbers were estimated including and excluding unknown repeats, respectively, from the repeat library.

Table S3.2 Classification of repeat contigs (modified from Wicker 2007) and summary of repeats detected in the genome of *Tylototriton*

verrucosus

Order	Superfamily	Percent of Genome ^a	Genome Contigs (100% identical)	genome contigs (95% identical)	genome contigs (80% identical)	Average genome contig length (100% identical)	Longest genomic contig	transcriptome contigs (80% identical)	Average Expression Level in females (TPM)	Average Expression Level in males (TPM)
Class I Retrotransposon-Autonomous										
LTR	<i>Gypsy</i>	7.83-14.06	2,736	2,463	1,629	523	7,664	4614	5978	24646
	<i>ERV</i>	1.55-2.03	746	568	307	493	3,198	824	1255	11480
	<i>Copia</i>	0	1	1	1	214	214	87	416	0
	<i>Retrovirus</i>	0.71-0.90	38	20	6	1,082	5,401	48	406	1631
	Unknown LTR	0.01-0.02	4	4	4	443	584	1	3	0
DIRS	<i>DIRS</i>	2.07-2.80	2,352	2,223	1,330	465	5,232	5369	5524	48717
PLE	<i>Penelope</i>	0.13-0.14	344	343	309	314	2,161	1392	1082	3604
LINE	<i>Jockey</i>	2.13-2.45	1,350	1,173	694	460	3,173	2350	3038	16417
	<i>L1</i>	2.79-3.03	4,998	4,584	2,897	692	4,057	7016	5210	22665
	<i>RTE</i>	0.15-0.16	197	177	158	691	2,640	1082	736	3523
	<i>I</i>	0	1	1	1	122	122	15	32	54
	<i>R2</i>	0	2	2	2	1,072	1,419	2	0	9
	Unknown LINE	0.09-0.15	7	6	5	978	1,392	-	-	-
Class I Retrotransposon Non-autonomous										
SINE	<i>5S</i>	0.04	1	1	1	851	851	2	4	70
	<i>7SL</i>	0.01	25	24	11	218	360	3	107	80
	Unknown SINE	0.36-1.00	80	67	60	380	4,309	84	259	2096
Retrotransposon derivative	TRIM	1.99-3.22	108	72	54	635	1,666	132	4749	10838
	LARD	0.08-0.18	11	9	9	2,223.90	3,099	17	146	112

unknown Class I	unknown Class I	0	2	2	2	585	952	-	-	-
Class II DNA transposons Subclass 1										
TIR	<i>PIF-Harbinger</i>	5.04-12.52	467	328	90	552	4,467	240	2095	6541
	<i>PiggyBac</i>	0.14-0.18	21	16	6	895	2,323	19	57	562
	<i>Novosib</i>	0.12-0.45	29	28	23	356	833			
	<i>hAT</i>	0.06-0.13	44	41	36	479	2,144	105	1487	1295
	<i>Tc1-Mariner</i>	0	22	22	22	413	1,153	15	232	68
	<i>Academ</i>	0	8	8	6	590	2,287	20	52	304
	<i>MuDR</i>	0	4	4	3	326	534	12	65	54
	<i>Ginger</i>	0	2	2	2	421	705	14	65	203
	<i>Sola</i>	0	2	1	1	224	231	-	-	-
	<i>P</i>	0	1	1	1	299	299	-	-	-
	<i>Kolobok</i>	-	-	-	-	-	-	7	3098	981
	<i>CACTA</i>	-	-	-	-	-	-	5	8	25
	<i>Zisupton</i>	-	-	-	-	-	-	3	0	4
	Unknown TIR	0.1-0.11	181	179	140	402	1,207	-	-	-
Crypton	Crypton	0.1-0.11	21	21	19	1,770	5,955	1	3	1
Transposon derivative	MITE	0.4-2.96	122	114	104	234	2,679	53	369	2805
Class II DNA transposon Subclass 2										
Maverick	<i>Maverick</i>	0.14	73	55	22	771	5,661	77	158	2244
Helitron	<i>Helitron</i>	0.03	15	14	7	383	935	32	4	107
unknown Class II		0	2	2	2	379	516	-	-	-
Total		26.07-46.82	14,006	12,576	7,964	18,712	77,324	23,641	36,638	161,136

^aThe first and second numbers were estimated including and excluding unknown repeats, respectively, from the repeat library.

Table S3.3 Classification of repeat contigs (modified from Wicker 2007) and summary of repeats detected in the genome of *Pachytriton brevipes*

Order	Superfamily	Percent of Genome ^a	Genomic Contigs (100% Identical)	Genomic Contigs (95% Identical)	Genomic Contigs (80% Identical)	Average Genomic Contig Length (100% identical)	Longest Genomic Contig	Transcriptome contigs (80% Identical)	Average Expression Level in females (TPM)	Average Expression Level in males (TPM)
Class I - Retrotransposons - Autonomous										
LTR	<i>Gypsy</i>	5.10-7.83	14,331	12,967	7,721	474.9	6,483	2534	3314	14381
	<i>ERV</i>	2.25-2.74	4,241	2,778	873	431.1	10,078	578	1782	11090
	<i>Copia</i>	0.17-0.38	22	22	20	541.5	5,265	1	0	76
	<i>Retrovirus</i>	0.76-0.95	40	31	18	1,086	3,261	64	166	1855
	Unknown LTR	0.23-0.49	13	13	12	515.8	2,296	2	3	2
DIRS	<i>DIRS</i>	3.41-4.89	10,137	9,447	5,011	428.2	7,363	3099	3409	40461
PLE	<i>Penelope</i>	0.78-1.44	3,127	3,075	2,384	337	6,401	688	376	1647
	<i>Jockey</i>	4.57-6.47	11,590	10,610	5,571	474.6	3,601	2519	2535	15714
LINE	<i>L1</i>	4.10-6.24	20,570	19,481	13,743	515	3,696	6489	3477	16085
	<i>RTE</i>	0.55-0.77	1,444	1,303	899	653.1	3,521	670	433	1309
	<i>I</i>	0	4	4	3	191.8	261	6	0	8
	<i>R2</i>	0	2	2	2	912.5	1,482	2	62	273
	Unknown LINE	0.07-1.19	5	5	5	1,076	3,385	-	-	-
Class I - Retrotransposons - Non-autonomous										
SINE	<i>5S</i>	0	7	7	5	124.3	151	3	18	144
	<i>7SL</i>	0.05-0.06	79	72	35	246.7	678	2	14	20
	Unknown SINE	0.42-1.22	175	171	134	198.2	615	27	100	637
Retrotransposon Derivatives	TRIM	9.38-11.4	216	198	152	710.4	4,327	187	2585	12485
	LARD	0.89-1.69	36	36	35	2,364	7,468	131	329	3100
unknown Class I		0.02-0.03	19	18	16	383.6	1,237	7	1	5

Class II - DNA Transposons - Subclass 1										
TIR	<i>PIF-Harbinger</i>	1.43-1.89	571	463	172	341	4,168	92	1542	1172
	<i>hAT</i>	0.34-0.40	196	145	76	511.9	3,366	81	2968	1541
	<i>Novosib</i>	0.12-0.19	77	76	61	308.1	1,729	-	-	-
	<i>MuDR</i>	0.06	30	28	18	480.9	3,449	22	17	163
	<i>PiggyBac</i>	0.05	32	31	10	477.3	1,617	11	239	187
	<i>Tc1-Mariner</i>	0	12	12	12	282.8	406	2	127	18
	<i>Sola</i>	0	5	5	5	338.2	783	-	-	-
	<i>Academ</i>	0	5	5	5	422.6	550	12	9	68
	<i>Ginger</i>	0	1	1	1	1,554	1,554	7	99	101
	<i>Kolobok</i>	-	-	-	-	-	-	5	4170	1619
	<i>CACTA</i>	-	-	-	-	-	-	1	0	2
	<i>Zator</i>	-	-	-	-	-	-	1	0	1
	Unknown TIR	0.25-0.51	617	614	544	399.5	3,538	-	-	-
Crypton	Crypton	0.43-0.45	142	128	105	1625	2,931	3	1	12
Transposon Derivatives	MITE	0.44-1.52	399	385	387	188.2	704	60	340	971
Class II - DNA Transposons - Subclass 2										
Maverick	<i>Maverick</i>	0.06	149	111	31	502.7	3,875	27	67	633
Helitron	<i>Helitron</i>	0.51-0.66	162	126	55	528.6	4,613	69	81	393
unknown Class II		0	1	1	1	267	267	1	32	4
Total		36.44-53.58	68,457	62,371	38,122	19,892	105,119	17,403	28,296	126,177

^aThe first and second numbers were estimated including and excluding unknown repeats, respectively, from the repeat library.

Table S3.4 Classification of repeat contigs (modified from Wicker 2007) and summary of repeats detected in the genome of *Cynops orientalis*

Order	Superfamily	Percent of Genome ^a	Genomic Contigs (100% Identical)	Genomic Contigs (95% Identical)	Genomic Contigs (80% Identical)	Average Genomic Contig Length (100% identical)	Longest Genomic Contig	Transcriptome contigs (80% Identical)	Expression Level in females (TPM)	Expression Level in males (TPM)
Class I Retrotransposon-Autonomous										
LTR	<i>Gypsy</i>	6.67-10.56	11,859	11,377	6,530	513.8	6,918	5568	4845	16979
	<i>ERV</i>	1.33-2.04	1,120	1,030	502	504.3	9,189	868	668	6594
	<i>Copia</i>	0.05-0.08	39	37	32	320.1	2,791	2	0	3
	<i>Retrovirus</i>	0.67-0.76	56	37	16	1362.9	3,039	70	126	885
	Unknown LTR	0.40-0.49	3	2	2	619.3	1,087	1	0	10
DIRS	<i>DIRS</i>	3.85-4.89	9,941	9,660	4,682	446.6	7,546	5033	4342	38368
PLE	<i>Penelope</i>	0.44-0.54	2,102	2,099	1,635	280.3	5,686	2249	1429	4574
	<i>Jockey</i>	4.30-5.48	11,475	10,802	5,183	483.4	3,359	4426	3417	20134
LINE	<i>L1</i>	5.33-6.05	28,897	27,360	17,278	571	3,696	13797	6087	30695
	<i>RTE</i>	0.47-0.54	1,337	1,131	760	800.7	3,261	1390	867	2770
	<i>I</i>	0	1	1	1	232	232	9	33	17
	<i>R2</i>	0	2	2	1	1,439.50	2,547	5	187	73
	Unknown LINE	0.04-0.09	9	9	9	832.8	1,830	5	5	4
Class I Retrotransposon Non-autonomous										
SINE	<i>5S</i>	0	10	10	7	120.1	153	-	-	-
	<i>7SL</i>	0	9	9	9	264.5	378	4	55	39
	Unknown SINE	0.33-1.09	171	164	123	223.1	1,695	58	236	723
Retrotransposon derivative	TRIM	4.7-8.37	344	217	183	710.3	4,455	297	3524	13636
	LARD	0.49-1.45	58	54	52	2424.8	7,089	186	539	1475
unknown Class I		0.01	33	31	29	308.8	1,084	19	2	42

Class II DNA transposon Subclass 1										
TIR	<i>PIF-Harbinger</i>	2.02-2.96	645	507	177	447.5	5,785	145	331	837
	<i>hAT</i>	0.57-0.66	119	93	69	746.9	6,593	113	1596	721
	<i>PiggyBac</i>	0.05-0.06	31	26	7	712.5	2,861	16	273	125
	<i>MuDR</i>	0.02-0.04	18	18	15	298.2	630	23	6	62
	<i>Novosib</i>	0.02-0.03	33	32	29	291.8	959	-	-	-
	<i>Tc1-Mariner</i>	0	11	11	11	351.5	765	7	127	16
	<i>Academ</i>	0	6	6	6	393.8	785	12	17	35
	<i>Ginger</i>	0	1	1	1	1,554	1,554	12	24	34
	<i>Sola</i>	0	1	1	1	250	250	-	-	-
	<i>Kolobok</i>	-	-	-	-	-	-	8	3978	801
	<i>ISL2EU</i>	-	-	-	-	-	-	1	49	2
	<i>CACTA</i>	-	-	-	-	-	-	3	2	6
	<i>Zator</i>	-	-	-	-	-	-	2	0	3
	<i>Zisupton</i>	-	-	-	-	-	-	1	0	0
	Unknown TIR	0.19-0.29	1,091	1,090	900	358	2,054	-	-	-
Crypton	<i>Crypton</i>	0.49-0.54	143	135	106	1,799.70	4,658	6	0	11
Transposon derivative	MITE	0.75-3.01	435	428	407	196	982	92	363	1268
Class II DNA transposon Subclass 2										
Maverick	<i>Maverick</i>	0.07-0.08	118	106	42	572.7	3,187	37	69	684
Helitron	<i>Helitron</i>	0.44-0.69	105	85	46	739.7	4,280	69	78	249
unknown Class II		0	4	4	4	199.3	372	-	-	-
Total		33.7-50.8	60,296	66,575	38,854	21,634	102,052	34,534	33,275	141,875

^aThe first and second numbers were estimated including and excluding unknown repeats, respectively, from the repeat library.

Table S3.5 Classification of repeat contigs (modified from Wicker 2007) and summary of repeats detected in the genome of *Andrias davidianus*

Order	Superfamily	Percent of Genome ^a	Genomic Contigs (100% Identical)	Genomic Contigs (95% Identical)	Genomic Contigs (80% Identical)	Average Genomic Contig Length (100% identical)	Longest Genomic Contig	Transcriptome contigs (80% Identical)	Expression Level in females (TPM)	Expression Level in males (TPM)
Class I - Retrotransposons – Autonomous										
LTR	<i>Gypsy</i>	14.43 -23.37	9,757	9,092	5,360	466.6	7,584	2467	4,209	16,675
	<i>ERV</i>	0.45-0.58	353	347	262	501.6	6,764	324	409	1,974
	<i>Retrovirus</i>	0.01	2	2	2	1334.5	2,490	20	23	57
	<i>Copia</i>	0	4	4	4	524	628	75	284	3
	Unknown LTR	0	3	3	3	167	244	1	0	3
DIRS	<i>DIRS</i>	3.10-4.94	4,836	4,746	2,103	384.5	4,348	3679	57,717	69,660
PLE	<i>Penelope</i>	0.51-1.27	1,491	1,478	1,213	342	5,891	1318	2,458	4,377
LINE	<i>Jockey</i>	4.57-5.83	8,867	8,579	5,193	371.4	3,674	4978	15,839	26,889
	<i>L1</i>	3.27-3.95	5,162	4,989	3,359	443.1	6,610	4664	4,049	17,989
	<i>RTE</i>	0.09-0.32	70	69	57	482	5,365	144	218	514
	<i>I</i>	0	7	7	6	474.3	1,253	17	32	68
	<i>R2</i>	0	2	2	2	527	816	28	414	197
	Unknown LINE	0.03-0.04	2	2	2	852	864	-	-	-
Class I - Retrotransposons - Non-autonomous										
SINE	<i>5S</i>	0	1	1	1	128	128	1	4	81
	<i>7SL</i>	0.01	40	39	20	296.4	727	11	49	174
	Unknown SINE	0.31-0.94	99	98	93	239.2	649	74	303	893
Retrotransposon Derivatives	TRIM	4.46-6.19	138	112	65	672.9	5,511	1505.18	1,505	5,651
	LARD	0.34-1.57	20	20	20	3084.5	7,373	109	369	1,608

Unknown class I		0-0.02	7	5	4	191.7	325	12	23	23
Class II - DNA Transposons - Subclass 1										
TIR	<i>PIF-Harbinger</i>	0.89-1.42	413	380	132	318.2	3,892	129	322	709
	<i>hAT</i>	0.33-0.44	81	71	45	337.6	1,134	80	630	625
	<i>Tc1-Mariner</i>	0.10-0.11	50	35	22	296.1	688	40	424	254
	<i>Novosib</i>	0.01-0.04	18	18	17	268.8	372	-	-	-
	<i>PiggyBac</i>	0.01	7	7	5	467.6	1,333	8	23	43
	<i>Academ</i>	0.01	6	6	5	520.3	910	7	36	133
	<i>MuDR</i>	0	1	1	1	471	471	16	78	39
	<i>Ginger</i>	0	1	1	1	538	538	2	6	2
	<i>P</i>	0	1	1	1	305	305	-	-	-
	<i>Kolobok</i>	-	-	-	-	-	-	5	2056	1186
	<i>CACTA</i>	-	-	-	-	-	-	2	3	0
	Unknown TIR	0.37-0.63	112	110	78	424.3	2,576	-	-	-
Crypton	<i>Crypton</i>	0.21-0.25	29	29	23	1,513.40	2,216	-	-	-
Transposon Derivatives	MITE	0.63-4.26	228	227	218	195	1,158	91	2121	3243
Class II - DNA Transposons - Subclass 2										
Maverick	<i>Maverick</i>	0.16-0.26	159	148	89	553.7	3,829	67	470	586
Helitron	<i>Helitron</i>	0.06-0.08	16	15	11	522.9	2,362	11	8	4,894
unknown Class II		0.01-0.01	17	8	6	190.8	403	1	-	-
Total		34.37-56.56	32,000	30,652	18,423	18,702	83,794	18,381	94,082	158,550

^aThe first and second numbers were estimated including and excluding unknown repeats, respectively, from the repeat library.

Table S3.6 Classification of repeat contigs (modified from Wicker 2007) and summary of repeats detected in the genome of *Paramesotriton honkongensis*

Order	Superfamily	Percent of Genome ^a	Genomic Contigs (100% Identical)	Genomic Contigs (95% Identical)	Genomic Contigs (80% Identical)	Average Genomic Contig Length (100% identical)	Longest Genomic Contig	Transcriptome contigs (80% Identical)	Expression Level in females (TPM)	Expression Level in males (TPM)
Class I - Retrotransposons - Autonomous										
LTR	<i>Gypsy</i>	7.27-10.28	12,700	12,251	8,347	473	11,581	6,431	8,420	25,662
	<i>ERV</i>	3.17-4.69	2,227	1,958	994	512	12,607	1,008	4,091	15,182
	<i>Copia</i>	0.05-0.08	6	6	6	372	1,409	31	72	119
	<i>Retrovirus</i>	1.19-1.59	70	50	18	1,186.00	3,158	92	997	3,135
	Unknown LTR	0.14-0.71	11	11	11	1,378	6,092	4	3	9
DIRS	<i>DIRS</i>	2.97-3.79	7,501	7,335	4,481	434	7,171	6,359	22,104	80,955
PLE	<i>Penelope</i>	1.12-1.32	4,343	4,328	3,397	313.9	5,670	3,570	2,654	9,016
LINE	<i>Jockey</i>	3.71-4.38	9,514	9,000	5,195	488	3,542	6,352	9,650	29,090
	<i>L1</i>	4.06-4.56	16,670	16,090	12,100	511	7,355	19,197	14,948	52,747
	<i>RTE</i>	0.66-0.79	1,450	1,284	943	715	4,583	1,867	1,572	4,879
	<i>I</i>	0	4	4	4	235	291	21	9	47
	<i>R2</i>	0.02	7	6	1	827	4,100	3	14	64
	Unknown LINE	0.06-0.46	7	5	5	715	4,583	3	2	2
Class I - Retrotransposons - Non-autonomous										
SINE	<i>5S</i>	0.01-0.02	11	9	3	413	1,735	-	-	-
	<i>7SL</i>	0.01	29	29	14	221.5	444	4	1	23
	Unknown SINE	0.21-1.04	169	166	132	214	1,071	39	508	1778
Retrotransposon Derivatives	TRIM	5.35-7.77	296	206	155	805	4,354	291	8,332	17,011
	LARD	0.66-1.85	67	64	61	2,277.00	6,205	190	875	2,219
unknown Class I		0-0.01	19	19	19	291	949			

Class II - DNA Transposons - Subclass 1										
TIR	<i>PIF-Harbinger</i>	2.09-3.19	524	430	167	523	12,770	133	767	1545
	<i>hAT</i>	0.63-0.98	187	150	100	851	6,459	93	1,690	1,050
	<i>Novosib</i>	0.09-0.13	72	71	65	287	957	-	-	-
	<i>PiggyBac</i>	0.08-0.09	46	42	16	561	2,768	14	162	236
	<i>MuDR</i>	0.05-0.06	22	22	15	375	1,418	28	36	132
	<i>Tc1-Mariner</i>	0	17	17	17	376	1,153	5	141	28
	<i>Academ</i>	0	17	17	17	401	1,332	19	35	47
	<i>Ginger</i>	0	8	8	6	419	1,554	10	161	43
	<i>P</i>	0	571	473	184	526	12,770	-	-	-
	<i>CACTA</i>	-	-	-	-	-	-	16	29	52
	<i>Kolobok</i>	-	-	-	-	-	-	9	3,941	1,624
	<i>Zator</i>	-	-	-	-	-	-	1	2	10
	Unknown TIR	0.18-0.28	490	488	425	342	1,922	-	-	-
Crypton	<i>Crypton</i>	0.50-0.53	137	128	95	1,729	3,078	10	17	9
Transposon Derivatives	MITE	0.54-1.88	381	378	371	178	727	100	356	1,053
Class II - DNA Transposons - Subclass 2										
Maverick	<i>Maverick</i>	0.09-0.10	127	119	51	625	3,188	39	136	1,098
<i>Helitron</i>	<i>Helitron</i>	1.63-2.33	237	174	64	899	10,888	104	221	890
unknown Class II		0.47-1.44	4	3	3	442	528	-	-	-
Total		37.01-54.38	57,371	54,869	37,299	20,913	136,140	46,043	81,946	249,755

^aThe first and second numbers were estimated including and excluding unknown repeats, respectively, from the repeat library.

Table S4 Shannon diversity index (SI) and Gini-Simpson diversity index (GS) summarizing the TE communities of 84 vertebrate species with different genome size (GS). The six focal salamander species are in bold and red

Type	Chinese name	English name	Latin name	Family	GS	SI	GSI
Bony Fishes	菊黄东方鲀	yellowbelly pufferfish	<i>Takifugu flavidus</i>	Tetraodontidae	0.38	2.01	0.83
Bony Fishes	红鳍东方鲀	fugu	<i>Takifugu rubripes</i>	Tetraodontidae	0.38	1.95	0.81
Bony Fishes	半滑舌鳎	Chinese tongue sole	<i>Cynoglossus semilaevis</i>	Cynoglossidae	0.47	1.56	0.69
Bony Fishes	莱茵河杜父鱼	Rhine sculpin	<i>Cottus rhenanus</i>	Cottidae	0.56	1.92	0.80
Bony Fishes	太平洋蓝鳍金枪鱼	North Pacific bluefin tuna	<i>Thunnus orientalis</i>	Scombridae	0.83	1.83	0.78
Bony Fishes	白鲟	white sturgeon	<i>Acipenser transmontanus</i>	Acipenseridae	0.86	2.06	0.85
Bony Fishes	雀鳝	Alligator gar	<i>Atractosteus spatula</i>	Lepisosteidae	1.10	1.99	0.82
Bony Fishes	鲤	common carp	<i>Cyprinus carpio</i>	Cyprinidae	1.68	2.15	0.87
Bony Fishes	斑马鱼	zebrafish	<i>Danio rerio</i>	Cyprinidae	1.70	2.11	0.85
Bony Fishes	金线鲃	Golden line barbel	<i>Sinocyclocheilus grahami</i>	Cyprinidae	1.75	2.09	0.86
Bony Fishes	俄罗斯鲟鱼	Russian sturgeon	<i>Acipenser gueldenstaedtii</i>	Acipenseridae	2.40	2.11	0.86
Bony Fishes	大马哈鱼	Dog salmon	<i>Oncorhynchus keta</i>	Salmonidae	2.60	1.70	0.75
Bony Fishes	大西洋鲑鱼	Atlantic salmon	<i>Salmo salar</i>	Salmoninae	3.00	1.79	0.77
Lobe-finned fish	腔棘鱼	African coelacanth	<i>Latimeria chalumnae</i>	Latimeriidae	2.74	1.90	0.81
Cartilaginous fish	大白鲨	white shark	<i>Carcharodon carcharias</i>	Alopiidae	4.63	1.53	0.66
Cartilaginous fish	点纹斑竹鲨	brown banded bamboo shark	<i>Chiloscyllium punctatum</i>	Hemiscylliidae	4.70	1.31	0.58
Cartilaginous fish	云纹猫鲨	cloudy catshark	<i>Scyliorhinus torazame</i>	Scyliorhinidae	6.70	1.74	0.77
Lobe-finned fish	非洲肺鱼	African lungfish	<i>Protopterus annectens</i>	Protopteridae	40.00	1.63	0.72
Lobe-finned fish	澳大利亚肺鱼	Australian lungfish	<i>Neoceratodus forsteri</i>	Ceratodontidae	43.00	1.45	0.69
Frogs	华丽穴居蛙	Ornate burrowing frog	<i>Platyplectrum ornatum</i>	Myobatrachidae	1.06	2.15	0.87
Frogs	热带爪蟾	western clawed frog	<i>Xenopus tropicalis</i>	Pipidae	1.50	2.12	0.86
Frogs	高山倭蛙	Tibetan frog	<i>Nanorana parkeri</i>	Dicroglossidae	2.30	2.14	0.86
Frogs	非洲爪蟾	African clawed frog	<i>Xenopus laevis</i>	Pipidae	2.70	2.06	0.85

Frogs	黑蹼树蛙	Black-webbed Treefrog	<i>Rhacophorus kio</i>	Rhacophoridae	2.70	1.95	0.83
Frogs	宝兴树蛙	Sichuan whipping frog	<i>Zhangixalus dugritei</i>	Rhacophoridae	3.40	2.04	0.85
Frogs	雷山髭蟾	Leishan moustache toad	<i>Leptobrachium leishanense</i>	Megophryidae	3.50	2.00	0.84
Frogs	中华大蟾蜍	Asiatic toad	<i>Bufo gargarizans</i>	Bufonidae	5.40	1.96	0.82
Frogs	美洲牛蛙	American bullfrog	<i>Lithobates catesbeianus</i>	Ranidae	6.30	2.09	0.86
Frogs	箭毒蛙	strawberry poison arrow frog	<i>Oophaga pumilio</i>	Dendrobatidae	6.76	1.90	0.81
Salamanders	山暗蝾螈	Allegheny mountain dusky salamander	<i>Desmognathus ochrophaeus</i>	Plethodontidae	15.00	1.61	0.71
Salamanders	新疆北鲵	Central Asian Salamander	<i>Ranodon sibiricus</i>	Hynobiidae	21.30	1.81	0.80
Salamanders	棕黑疣螈	Longchuan Crocodile Newt	<i>Tylototriton verrucosus</i>	Salamandridae	24.00	1.88	0.80
Salamanders	黑腹细长蝾螈	Black-bellied slender salamander	<i>Batrachoseps nigriventris</i>	Plethodontidae	25.00	2.18	0.86
Salamanders	墨西哥钝口螈	axolotl	<i>Ambystoma mexicanum</i>	Ambystomatidae	32.00	1.98	0.83
Salamanders	黑斑肥螈	Spotted paddle-tail newt	<i>Pachytriton brevipes</i>	Salamandridae	38.90	2.07	0.85
Salamanders	东方蝾螈	Chinese Fire belly Newt	<i>Cynops orientalis</i>	Salamandridae	43.30	2.09	0.86
Salamanders	斑点黑蝾螈	speckled black salamander	<i>Aneides flavipunctatus</i>	Plethodontidae	44.00	1.96	0.78
Salamanders	大鲵	Chinese giant salamander	<i>Andrias davidianus</i>	Cryptobranchidae	48.90	1.92	0.81
Salamanders	香港蝾螈	Hong Kong Warty Newt	<i>Paramesotriton hongkongensis</i>	Salamandridae	49.90	2.16	0.87
Salamanders	美国隐鳃鲵	Hellbender	<i>Cryptobranchus alleganiensis</i>	Cryptobranchidae	55.00	2.02	0.84
Non-avian reptiles	响尾蛇	prairie rattlesnake	<i>Crotalus viridis</i>	Viperidae	1.30	1.98	0.82
Non-avian reptiles	束带蛇	Common garter snake	<i>Thamnophis sirtalis</i>	Colubridae	1.42	2.04	0.84
Non-avian reptiles	蚺	Burmese python	<i>Python bivittatus</i>	Pythonidae	1.44	1.95	0.81
Non-avian reptiles	绿蜥蜴	green anole	<i>Anolis carolinensis</i>	Dactyloidae	1.70	2.13	0.86
Non-avian reptiles	玉米蛇	Red corn snake	<i>Pantherophis guttatus</i>	Colubridae	1.73	1.99	0.82
Non-avian reptiles	印度眼镜蛇	India cobra	<i>Naja naja</i>	Elapidae	1.79	1.81	0.76
Non-avian reptiles	温泉蛇	hot-spring snake	<i>Thermophis baileyi</i>	Colubridae	1.85	2.02	0.83
Non-avian reptiles	环形海蛇	blue-banded sea snake	<i>Hydrophis cyanocinctus</i>	Elapidae	2.02	1.81	0.76
Non-avian reptiles	平颏海蛇	Shaw's sea snake	<i>Hydrophis curtus</i>	Elapidae	2.03	2.05	0.85
Non-avian reptiles	扬子鳄	Chinese alligator	<i>Alligator sinensis</i>	Alligatoridae	2.10	1.84	0.80

Non-avian reptiles	鳄鱼	Siamese Crocodile	<i>Crocodylus siamensis</i>	Crocodylinae	2.10	1.81	0.79
Non-avian reptiles	乌龟	three-keeled pond turtle	<i>Mauremys reevesii</i>	Geoemydidae	2.20	1.95	0.82
Non-avian reptiles	鳄蜥	crocodile lizard	<i>Shinisaurus crocodilurus</i>	Shinisauridae	2.20	1.79	0.76
Non-avian reptiles	悬崖壁蜥	Cape cliff lizard	<i>Hemicordylus capensis</i>	Cordylidae	2.30	1.73	0.75
Non-avian reptiles	三趾箱龟	Three-toed box turtle	<i>Terrapene carolina</i>	Emydidae	4.18	1.96	0.83
Non-avian reptiles	大蜥蜴	tuatara	<i>Sphenodon punctatus</i>	Sphenodontidae	5.00	1.69	0.71
Birds	环颈雉	Ring-necked pheasant	<i>Phasianus colchicus</i>	Phasianidae	0.90	0.89	0.43
Birds	鸡	chicken	<i>Gallus gallus</i>	Phasianidae	1.10	0.89	0.45
Birds	鸭	duck	<i>Anas anas</i>	Anatidae	1.10	0.60	0.26
Birds	双领鸨	killdeer	<i>Charadrius vociferus</i>	Charadriidae	1.20	0.62	0.33
Birds	绒毛啄木鸟	Downy woodpecker	<i>Dryobates pubescens</i>	Picidae	1.20	0.36	0.16
Birds	白尾鸫	White-tailed Tropicbird	<i>Phaethon lepturus</i>	Phaethontidae	1.20	0.73	0.42
Birds	红冠鹦鹉	Red-crested Turaco	<i>Tauraco erythrolophus</i>	Musophagidae	1.20	0.72	0.40
Birds	斑马雀	zebra finch	<i>Taeniopygia guttata</i>	Estrildidae	1.20	0.84	0.53
Birds	纹腹鹰	Sharp-shinned hawk	<i>Accipiter striatus</i>	Accipitridae	1.55	1.03	0.57
Birds	美洲角雕	harpy eagle	<i>Harpia harpyja</i>	Accipitridae	1.58	1.01	0.44
Birds	亚马逊白头鹦鹉	Cuban parrot	<i>Amazona leucocephala</i>	Psittacidae	1.65	0.75	0.58
Birds	小凤头鹦鹉	Little corella	<i>Cacatua sanguinea</i>	Psittacidae	1.71	0.74	0.39
Birds	欧亚雕鸮	Eurasian eagle owl	<i>Bubo bubo</i>	Strigidae	2.03	0.90	0.48
Birds	鸵鸟	South African ostrich	<i>Struthio australis</i>	Struthionidae	2.16	0.75	0.28
Mammals	鸭嘴兽	platypus	<i>Ornithorhynchus anatinus</i>	Ornithorhynchidae	1.99	0.96	0.55
Mammals	针鼹	short-beaked echidna	<i>Tachyglossus aculeatus</i>	Tachyglossidae	2.20	0.96	0.55
Mammals	大熊猫	giant panda	<i>Ailuropoda melanoleuca</i>	Ursidae	2.20	1.56	0.74
Mammals	大蝙蝠	large flying fox	<i>Pteropus vampyrus</i>	Pteropodidae	2.20	1.44	0.64
Mammals	狗	dog	<i>Canis lupus familiaris</i>	Canidae	2.39	1.15	0.56
Mammals	猪	pig	<i>Sus scrofa</i>	Suidae	2.50	1.44	0.70
Mammals	小袋鼠	Quokka	<i>Setonix brachyurus</i>	Macropodidae	2.50	1.58	0.76

Mammals	小鼠	house mouse	<i>Mus musculus</i>	Muridae	2.70	1.24	0.65
Mammals	鲸	northern bottlenose whale	<i>Hyperoodon ampullatus</i>	Ziphiidae	2.80	1.01	0.45
Mammals	人	human	<i>Homo sapiens</i>	Hominidae	3.00	1.68	0.77
Mammals	考拉	Koala	<i>Phascolarctos cinereus</i>	Phascolarctidae	3.20	1.55	0.72
Mammals	亚洲象	Asian elephant	<i>Elephas maximus</i>	Elephantidae	3.20	1.52	0.72
Mammals	象鼩	Cape elephant shrew	<i>Elephantulus edwardii</i>	Macroscelididae	4.20	1.15	0.58
Mammals	金毛鼹	Cape golden mole	<i>Chrysochloris asiatica</i>	Chrysochloridae	4.70	1.37	0.71

Table S5 Relationship between the abundance and expression of TE superfamilies in males and females of six salamander species

Species	Relationship between abundance (bp, x) of TE superfamilies in the genome and their expression (y) in the gonads					
	Equation of relationship		Comparison of correlation between sex			
	Testis	Ovary	<i>t</i> (Slope)	<i>P</i> (Slope)	<i>t</i> (Intercept)	<i>P</i> (Intercept)
RS	$\log(y) = \mathbf{0.6555} \log(x) \mathbf{-2.2045}$	$\log(y) = \mathbf{0.7215} \log(x) \mathbf{-3.0247}$	0.1227	0.9032	-0.8655	0.3941
TV	$\log(y) = 0.9734 \log(x) -4.2162$	$\log(y) = 1.0496 \log(x) -5.4483$	0.2029	0.8409	-2.2149	0.0361
PB	$\log(y) = 1.0671 \log(x) -5.4918$	$\log(y) = 0.9395 \log(x) -5.0998$	-0.2754	0.7850	-1.7232	0.0955
CO	$\log(y) = \mathbf{1.3530} \log(x) \mathbf{-8.1203}$	$\log(y) = 1.0665 \log(x) \mathbf{-6.3788}$	-0.6398	0.5271	-1.3564	0.1851
AD	$\log(y) = 0.7841 \log(x) -3.0878$	$\log(y) = 0.8658 \log(x) -4.1511$	0.4360	0.6664	-2.4164	0.0230
PH	$\log(y) = 1.1394 \log(x) -5.9990$	$\log(y) = \mathbf{1.1321} \log(x) -6.3466$	-0.0170	0.9866	-1.2679	0.2135

Analysis of covariance	Comparison of slopes for males across species		Comparison of slopes for females across species	
	Heterogeneity of slopes	intercept	Heterogeneity of slopes	intercept
<i>F</i>	0.739	28.822	0.284	37.323
<i>P</i>	0.596	< 0.001	0.921	< 0.001

RS, *Ranodon sibiricus*; TV, *Tylototriton verrucosus*; PB, *Pachytriton brevipes*; CO, *Cynops orientalis*; AD, *Andrias davidianus*; PH, *Paramesotriton hongkongensis*

Table S6 The 10 most highly expressed TE superfamilies in the six salamander species

species	Top 10 expressed superfamilies in females	Average expression in Females (TPM)	Top 10 expressed superfamilies in males	Average expression in males (TPM)
<i>R. sibiricus</i>	LINE/Jockey	6206	LINE/Jockey	15535
<i>R. sibiricus</i>	DIRS/DIRS	5427	DIRS/DIRS	11962
<i>R. sibiricus</i>	LINE/L1	2954	LINE/L1	7610
<i>R. sibiricus</i>	LTR/Gypsy	827	LTR/Gypsy	3024
<i>R. sibiricus</i>	TIR/Harbinger	575	TIR/Harbinger	1359
<i>R. sibiricus</i>	LTR/ERV	392	Maverick/Maverick	762
<i>R. sibiricus</i>	LINE/RTE	130	LTR/ERV	694
<i>R. sibiricus</i>	PLE/Penelope	123	LINE/RTE	360
<i>R. sibiricus</i>	TIR/hAT	83	PLE/Penelope	352
<i>R. sibiricus</i>	TIR/Mariner	58	LINE/I	125
<i>T. verrucosus</i>	LTR/Gypsy	1495	DIRS/DIRS	12179
<i>T. verrucosus</i>	DIRS/DIRS	1381	LTR/Gypsy	6162
<i>T. verrucosus</i>	LINE/L1	1302	LINE/L1	5666
<i>T. verrucosus</i>	LINE/Jockey	759	LINE/Jockey	4104
<i>T. verrucosus</i>	TIR/Harbinger	524	LTR/ERV	2870
<i>T. verrucosus</i>	TIR/hAT	372	TIR/Harbinger	1635
<i>T. verrucosus</i>	LTR/ERV	314	PLE/Penelope	901
<i>T. verrucosus</i>	PLE/Penelope	270	LINE/RTE	881
<i>T. verrucosus</i>	LINE/RTE	184	Maverick/Maverick	561
<i>T. verrucosus</i>	LTR/Retrovirus	101	LTR/Retrovirus	408
<i>P. brevipes</i>	LINE/L1	869	DIRS/DIRS	10115
<i>P. brevipes</i>	DIRS/DIRS	852	LINE/L1	4021

<i>P. brevipes</i>	LTR/Gypsy	828	LINE/Jockey	3928
<i>P. brevipes</i>	TIR/hAT	742	LTR/Gypsy	3595
<i>P. brevipes</i>	LINE/Jockey	634	LTR/ERV	2773
<i>P. brevipes</i>	LTR/ERV	445	LTR/Retrovirus	464
<i>P. brevipes</i>	TIR/Harbinger	386	PLE/Penelope	412
<i>P. brevipes</i>	LINE/RTE	108	TIR/hAT	385
<i>P. brevipes</i>	PLE/Penelope	94	LINE/RTE	327
<i>P. brevipes</i>	TIR/PiggyBac	60	TIR/Harbinger	293
<i>C. orientalis</i>	LINE/L1	1522	DIRS/DIRS	9592
<i>C. orientalis</i>	LTR/Gypsy	1211	LINE/L1	7674
<i>C. orientalis</i>	DIRS/DIRS	1085	LINE/Jockey	5033
<i>C. orientalis</i>	LINE/Jockey	854	LTR/Gypsy	4245
<i>C. orientalis</i>	TIR/hAT	399	LTR/ERV	1649
<i>C. orientalis</i>	PLE/Penelope	357	PLE/Penelope	1143
<i>C. orientalis</i>	LINE/RTE	217	LINE/RTE	692
<i>C. orientalis</i>	LTR/ERV	167	LTR/Retrovirus	221
<i>C. orientalis</i>	TIR/Harbinger	83	TIR/Harbinger	209
<i>C. orientalis</i>	TIR/PiggyBac	68	TIR/hAT	180
<i>A. davidianus</i>	DIRS/DIRS	14429	DIRS/DIRS	17415
<i>A. davidianus</i>	LINE/Jockey	3960	LINE/Jockey	6722
<i>A. davidianus</i>	LTR/Gypsy	1052	LINE/L1	4497
<i>A. davidianus</i>	LINE/L1	1012	LTR/Gypsy	4169
<i>A. davidianus</i>	PLE/Penelope	615	Helitron/Helitron	1223
<i>A. davidianus</i>	TIR/hAT	157	PLE/Penelope	1094
<i>A. davidianus</i>	Maverick/Maverick	117	LTR/ERV	493
<i>A. davidianus</i>	TIR/Mariner	106	TIR/Harbinger	177
<i>A. davidianus</i>	LTR/ERV	102	TIR/hAT	156

<i>A. davidianus</i>	TIR/Harbinger	80	Maverick/Maverick	147
<i>P. hongkongensis</i>	DIRS/DIRS	5526	DIRS/DIRS	20239
<i>P. hongkongensis</i>	LINE/L1	3737	LINE/L1	13187
<i>P. hongkongensis</i>	LINE/Jockey	2412	LINE/Jockey	7272
<i>P. hongkongensis</i>	LTR/Gypsy	2105	LTR/Gypsy	6415
<i>P. hongkongensis</i>	LTR/ERV	1023	LTR/ERV	3795
<i>P. hongkongensis</i>	PLE/Penelope	664	PLE/Penelope	2254
<i>P. hongkongensis</i>	TIR/hAT	423	LINE/RTE	1220
<i>P. hongkongensis</i>	LINE/RTE	393	LTR/Retrovirus	784
<i>P. hongkongensis</i>	LTR/Retrovirus	249	TIR/Harbinger	386
<i>P. hongkongensis</i>	TIR/Harbinger	192	Maverick/Maverick	274

Table S7 The clean small RNAs and putative piRNAs in each salamander sample

species	sex	sample	clean_18-40 nt	Total putative piRNAs (25-30 nt)	Unique putative piRNA (25-30 nt)	Total piRNA (25-30)/total clean (18-40 nt)	Average Total piRNA (25-30 nt) / total clean (18-40 nt)	Unique piRNA /total piRNAs (25-30 nt)	Normalized uniq piRNA (per 10M small RNAs 18-40 nt in length)	Normalized unique piRNAs mapping to TEs
<i>Ranodon sibiricus</i>	female	WQ02	11,604,083	4,868,129	496,496	42.0%		10.2%	427,863	97,510
	female	WQ03	13,591,993	5,581,827	779,671	41.1%	37%	14.0%	573,625	154,936
	female	WQ04	6,896,722	2,003,438	266,851	29.0%		13.3%	386,924	71,349
	male	WQ05	16,935,126	13,288,223	470,649	78.5%		3.5%	277,913	42,826
	male	WQ07	16,496,516	9,374,629	986,996	56.8%	60%	10.5%	598,306	140,662
	male	WQ08	18,341,802	9,814,338	905,599	53.5%		9.2%	493,735	101,660
	male	WQ10	13,082,664	6,940,705	774,833	53.1%		11.2%	592,259	138,529
<i>Tylototriton verrucosus</i>	female	HS08	10,838,684	6,590,103	395,443	60.8%		6.0%	364,844	98,070
	female	HS09	14,332,777	6,818,958	904,658	47.6%	53%	13.3%	631,181	206,017
	female	HS11	9,689,432	4,312,095	496,054	44.5%		11.5%	511,954	159,218
	female	HS12	12,501,636	7,527,884	417,748	60.2%		5.5%	334,155	92,093
	male	HS02	13,921,523	3,858,594	839,636	27.7%		21.8%	603,121	176,292
	male	HS04	15,021,365	5,336,718	1,091,850	35.5%	33%	20.5%	726,865	217,841
	male	HS05	14,815,435	5,445,816	1,007,806	36.8%		18.5%	680,241	211,419
	male	HS07	11,682,213	3,650,348	756,193	31.2%		20.7%	647,303	198,528
<i>Pachytriton brevipes</i>	female	NF08	10,245,368	3,469,373	354,227	33.9%		10.2%	345,744	47,263
	female	NF09	14,267,591	6,234,115	921,343	43.7%	46%	14.8%	645,759	89,890
	female	NF20	14,800,637	8,157,582	1,015,889	55.1%		12.5%	686,382	98,564
	female	NF21	14,697,533	7,341,309	974,122	49.9%		13.3%	662,779	97,362
	male	NF01	14,346,946	6,047,212	1,020,091	42.1%	44%	16.9%	711,016	117,460
	male	NF14	16,313,396	7,178,965	1,166,880	44.0%		16.3%	715,289	116,807

	male	NF16	17,477,879	7,790,731	1,241,258	44.6%	15.9%	710,188	113,914
	male	NF18	16,367,997	7,599,481	1,142,246	46.4%	15.0%	697,853	108,656
<i>Cynops orientalis</i>	female	CO12	14,482,941	7,682,291	951,754	53.0%	12.4%	657,155	123,282
	female	CO13	12,185,835	5,083,594	723,200	41.7%	14.2%	593,476	93,710
	female	CO14	5,146,586	1,704,233	293,067	33.1%	17.2%	569,440	84,505
	female	QZ09	10,100,463	4,939,582	684,507	48.9%	13.9%	677,699	103,417
	male	CO16	11,142,943	2,926,582	561,094	26.3%	19.2%	503,542	72,258
	male	CO17	13,176,247	4,998,264	670,222	37.9%	13.4%	508,659	80,877
	male	QZ01	9,725,994	4,175,352	589,702	42.9%	14.1%	606,315	116,716
	male	QZ04	15,768,386	7,463,655	1,057,250	47.3%	14.2%	670,487	123,101
<i>Andrias davidianus</i>	female	LY01	9,035,740	3,683,819	730,110	40.8%	19.8%	808,025	161,605
	female	LY03	13,542,759	4,628,997	782,411	34.2%	16.9%	577,734	157,548
	female	LY04	8,088,094	2,798,328	487,252	34.6%	17.4%	602,431	162,355
	female	LY05	14,577,753	6,223,416	969,496	42.7%	15.6%	665,052	185,283
	male	LY06	7,339,454	1,018,559	187,174	13.9%	18.4%	255,024	51,107
	male	LY07	6,929,866	240,388	48,312	3.5%	20.1%	69,716	12,786
	male	LY08	10,126,404	2,313,631	421,496	22.8%	18.2%	416,235	90,032
	male	LY09	11,471,238	3,440,088	829,412	30.0%	24.1%	723,036	148,005
<i>Paramesotriton honkongensis</i>	male	HK03	12,200,956	4,848,719	671,892	39.7%	13.9%	550,688	109,477
	male	HK04	14,084,143	6,242,456	894,350	44.3%	14.3%	635,005	136,018
	male	HK05	11,872,338	3,769,704	614,821	31.8%	16.3%	517,860	103,468
	male	HK06	13,394,295	5,533,221	687,128	41.3%	12.4%	513,000	98,650

Table S8 Relationship between the expression of TE superfamilies and piRNAs mapping to TE superfamilies

Species	Relationship between expression (TPM, x) of TE superfamilies and the piRNAs mapped to TE superfamilies (y)					
	Equation of relationship		Comparison of correlation between sex			
	Testis	Ovary	<i>t</i> (Slope)	<i>P</i> (Slope)	<i>t</i> (Intercept)	<i>P</i> (Intercept)
RS	$\log(y) = 0.6235 \log(x) + 2.4754$	$\log(y) = 0.6508 \log(x) + 2.4353$	0.1015	0.9197	0.0872	0.9310
TV	$\log(y) = 0.6241 \log(x) + 2.7548$	$\log(y) = 0.6296 \log(x) + 2.7359$	0.0244	0.9806	-0.0204	0.9838
PB	$\log(y) = 0.8638 \log(x) + 1.9357$	$\log(y) = 0.5894 \log(x) + 3.0540$	-1.1419	0.2590	1.6104	0.1137
CO	$\log(y) = 0.9118 \log(x) + 1.8017$	$\log(y) = 0.5867 \log(x) + 3.0809$	-1.6060	0.1144	2.2127	0.0314
AD	$\log(y) = 0.8454 \log(x) + 1.9993$	$\log(y) = 0.8853 \log(x) + 1.8208$	0.1749	0.8620	-0.3010	0.7649
PH	$\log(y) = 0.8939 \log(x) + 1.5568$					

Analysis of covariance	Comparison of slopes for males across species		Comparison of slopes for females across species	
	Heterogeneity of slopes	intercept	Heterogeneity of slopes	intercept
<i>F</i>	0.818	168.825	0.356	153.621
<i>P</i>	0.539	< 0.001	0.84	< 0.001

RS, *Ranodon sibiricus*; TV, *Tylototriton verrucosus*; PB, *Pachytriton brevipes*; CO, *Cynops orientalis*; AD, *Andrias davidianus*; PH, *Paramesotriton hongkongensis*

Table S9 Results of the *de novo* transcriptome assembly

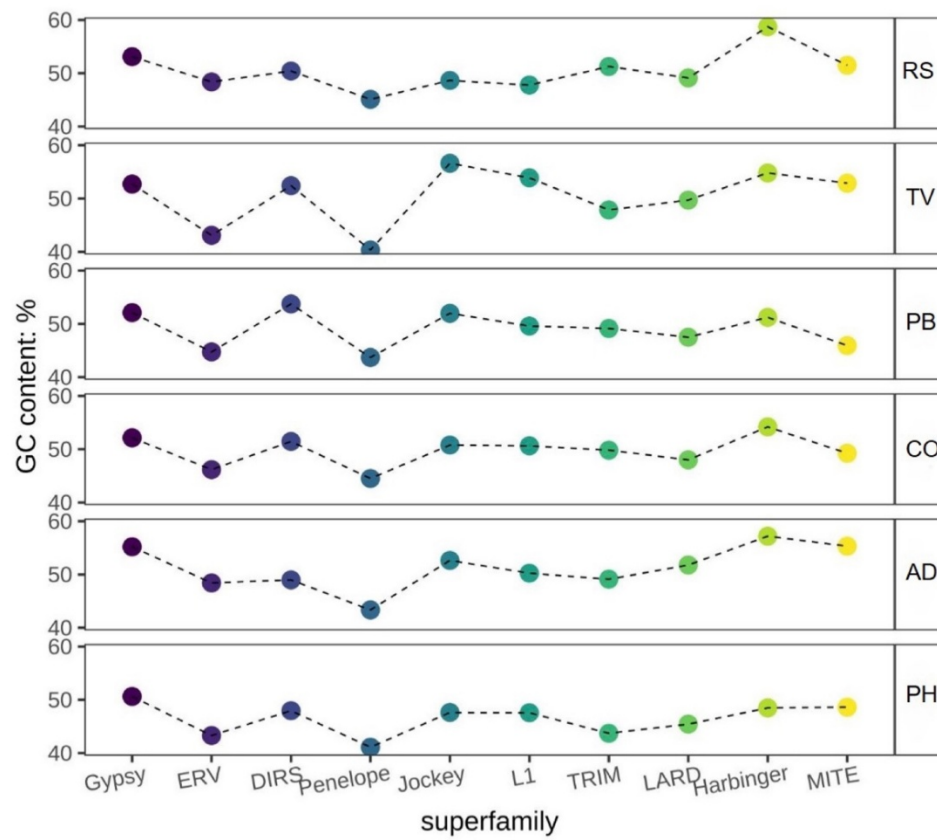
Species	Number of transcript	Sum length	Min length	Average length	Max length	N50 of transcripts
<i>Ranodon sibiricus</i>	573,681	473,363,550	183	825	28,590	1,874
<i>Tylototriton verrucosus</i>	614,818	544,285,339	175	885	24,708	2,205
<i>Pachytriton brevipes</i>	597,551	531,263,346	180	889	39,116	2,099
<i>Cynops orientalis</i>	598,805	514,032,901	182	858	25,106	2,093
<i>Andrias davidianus</i>	452,395	401,061,354	174	887	27,377	2,099
<i>Paramesotriton hongkongensis</i>	690,114	531,632,536	168	770	28,364	1,927

Table S10 The number of retained small RNA molecules after each processing step.

Species	Tissue	Samples name	RIN value of RNA	Clean reads (after FastX)	After adapter cut (18-40 nt)	After riboRNA fragments removed	After tRNA fragments removed	Clean molecules of 18-40 nt	Putative piRNAs (25-30 nt)	piRNAs mapped to TEs (25-30 nt)	Unique piRNAs (25-30 nt)	Normalized unique piRNA (10M, 18-40)	% unique piRNA mapped to TE transcript	ping pong occurrence (10 bp overlap)
<i>Ranodon sibiricus</i>	Testis#1	WQ07	9.6	18,628,420	18,387,280	1,393,269	497,495	16,496,516	9,374,629	1,621,347	986,996	598,306	23.51%	11,766
	Testis#2	WQ08	8.9	20,632,085	20,127,121	702,889	1,082,430	18,341,802	9,814,338	1,111,036	905,599	493,735	20.59%	8,230
	Testis#3	WQ10	9.4	15,341,619	15,148,223	1,731,806	333,753	13,082,664	6,940,705	1,189,737	774,833	592,259	23.39%	7,520
	Testis#4	WQ05	9.3	18,141,749	18,022,557	682,282	405,149	16935126	13,288,223	582,031	470,649	277,913	15.41%	3,398
	Ovary#1	WQ03	9.3	17,133,153	16,652,089	2,708,832	351,264	13,591,993	5,581,827	1,835,311	779,671	573,625	27.01%	10,287
	Ovary#2	WQ02	9.6	15,112,304	14,382,824	2,298,340	480,401	11604083	4,868,129	1,518,581	496,496	427,863	22.79%	2,735
	Ovary#3	WQ04	8.7	13,323,488	11,664,671	4,260,265	507,684	6896722	2,003,438	810,078	266,851	386,924	18.44%	1,678
<i>Tylototriton verrucosus</i>	Testis#1	HS02	9.3	15,812,676	15,593,182	551,836	1,119,823	13,921,523	3,858,594	1,093,581	839,636	603,121	29.23%	4,047
	Testis#2	HS04	9.2	16,818,923	16,603,246	475,376	1,106,505	15,021,365	5,336,718	1,558,405	1,091,850	726,865	29.97%	6,056
	Testis#3	HS05	9.6	16,893,170	16,721,870	277,675	1,628,760	14,815,435	5,445,816	1,688,611	1,007,806	680,241	31.08%	5,942
	Testis#4	HS07	9.3	15,502,396	15,246,506	445,413	3,118,880	11,682,213	3,650,348	1,088,187	756,193	647,303	30.67%	3,803
	Ovary#1	HS08	6.5	30,369,861	15,511,083	3,212,333	1,460,066	10,838,684	6,590,103	2,272,313	395,443	364,844	26.88%	2,216
	Ovary#2	HS09	8.5	17,236,506	16,690,699	1,520,090	837,832	14,332,777	6,818,958	2,553,943	904,658	631,181	32.64%	10,485
	Ovary#3	HS11	7.8	16,009,250	14,887,546	2,502,646	2,695,468	9,689,432	4,312,095	1,458,617	496,054	511,954	31.10%	3,859
	Ovary#4	HS12	7.8	34,354,037	16,987,985	3,450,516	1,035,833	12,501,636	7,527,884	2,725,514	417,748	334,155	27.56%	2,187
<i>Pachytriton brevipes</i>	Testis#1	NF01	9.4	16,480,564	16,288,267	420,115	1,521,206	14,346,946	6,047,212	975,057	1,020,091	711,016	16.52%	3,043
	Testis#2	NF14	9.8	17,411,312	17,244,483	538,568	392,519	16,313,396	7,178,965	1,151,729	1,166,880	715,289	16.33%	3,829
	Testis#3	NF16	9.7	18,801,974	18,559,761	727,164	354,718	17,477,879	7,790,731	1,198,551	1,241,258	710,188	16.04%	4,015
	Testis#4	NF18	9.7	17,318,113	17,116,842	345,509	403,336	16,367,997	7,599,481	1,070,642	1,142,246	697,853	15.57%	3,320
	Ovary#1	NF08	8.5	31,360,428	12,576,185	99,238	2,231,579	10,245,368	3,469,373	497,323	354,227	345,744	13.67%	689
	Ovary#2	NF09	8.3	16,735,557	16,200,399	1,187,120	745,688	14,267,591	6,234,115	890,850	921,343	645,759	13.92%	3,934
	Ovary#3	NF20	8.7	16,919,838	16,544,102	1,032,781	710,684	14,800,637	8,157,582	1,216,667	1,015,889	686,382	14.36%	4,844
	Ovary#4	NF21	8.3	17,317,850	16,958,860	1,749,003	512,324	14,697,533	7,341,309	1,123,775	974,122	662,779	14.69%	4,227

<i>Cynops orientalis</i>	Testis#1	CO16	8.3	16,241,320	15,527,596	667,498	3,717,155	11,142,943	2,926,582	381,623	561,094	503,542	14.35%	630
	Testis#2	CO17	8.1	18,577,955	16,985,684	1,780,592	2,028,845	13,176,247	4,998,264	830,554	670,222	508,659	15.90%	1,525
	Testis#3	QZ01	7.6	14,530,233	14,401,574	555,596	4,119,984	9,725,994	4,175,352	786,848	589,702	606,315	19.25%	1,706
	Testis#4	QZ04	8.1	17,831,129	17,552,203	880,748	903,069	15,768,386	7,463,655	1,405,890	1,057,250	670,487	18.36%	3,669
	Ovary#1	CO12	8.5	15,716,060	15,427,646	279,633	665,072	14,482,941	7,682,291	1,500,478	951,754	657,155	18.76%	5,606
	Ovary#2	CO13	6.7	17,546,503	17,220,001	251,580	4,782,586	12,185,835	5,083,594	717,686	723,200	593,476	15.79%	2,732
	Ovary#3	CO14	7.4	13,607,087	13,337,094	350,564	7,839,944	5,146,586	1,704,233	222,006	293,067	569,440	14.84%	544
	Ovary#4	QZ09	8.3	15,910,436	14,940,315	1,567,766	3,272,086	10,100,463	4,939,582	696,729	684,507	677,699	15.26%	2,214
<i>Andrias davidianus</i>	Testis#1	LY06	8.6	15,210,326	13,637,209	2,595,045	3,702,710	7,339,454	1,018,559	126,220	187,174	255,024	20.04%	723
	Testis#2	LY07	8.2	16,624,734	11,166,742	3,533,085	703,791	6,929,866	240,388	27,777	48,312	69,716	18.34%	96
	Testis#3	LY08	7.2	18,033,692	16,524,625	4,351,823	2,046,398	10,126,404	2,313,631	352,947	421,496	416,235	21.63%	2,609
	Testis#4	LY09	8.7	19,154,630	17,722,859	4,327,063	1,924,558	11,471,238	3,440,088	661,005	829,412	723,036	20.47%	4,707
	Ovary#1	LY01	8.2	17,702,705	14,359,441	3,357,714	1,965,987	9,035,740	3,683,819	739,659	730,110	808,025	20.00%	4,317
	Ovary#2	LY03	7.0	17,702,705	17,258,351	2,589,766	1,125,826	13,542,759	4,628,997	1,150,861	782,411	577,734	27.27%	7,168
	Ovary#3	LY04	7.5	17,702,705	14,713,470	1,477,203	5,148,173	8,088,094	2,798,328	722,970	487,252	602,431	26.95%	3,047
	Ovary#4	LY05	7.3	17,702,705	17,364,607	1,788,881	997,973	14,577,753	6,223,416	1,671,421	969,496	665,052	27.86%	10,004
<i>Paramesotriton honkongensis</i>	Testis#1	HK03	9.0	15,551,891	14,837,493	1,095,238	1,541,299	12,200,956	4,848,719	902,050	671,892	550,688	19.88%	1,628
	Testis#2	HK04	8.3	17,610,098	17,122,533	1,530,794	1,507,596	14,084,143	6,242,456	1,251,077	894,350	635,005	21.42%	2,475
	Testis#3	HK05	8.2	16,135,021	15,352,462	1,160,350	2,319,774	11,872,338	3,769,704	617,744	614,821	517,860	19.98%	1,536
	Testis#4	HK06	8.5	17,486,533	16,778,665	916,317	2,468,053	13,394,295	5,533,221	922,286	687,128	513,000	19.23%	1,628

Fig. S1 GC content of TE superfamilies across salamander species.



Species are arranged top to bottom by increasing genome size: RS, *Ranodon sibiricus*; PB, *Pachytriton brevipes*; CO, *Cynops orientalis*; AD, *Andrias davidianus*; PH, *Paramesotriton hongkongensis*.

Fig. S2 Volcano plots showing differential expression between males and females for individual TE contigs; positive fold change values indicate male-biased expression, and negative fold change values indicate female-biased expression. Four contigs from *A. davidianus* and two contigs from *P. brevipes* with extreme adjusted P-values were omitted for visual clarity.

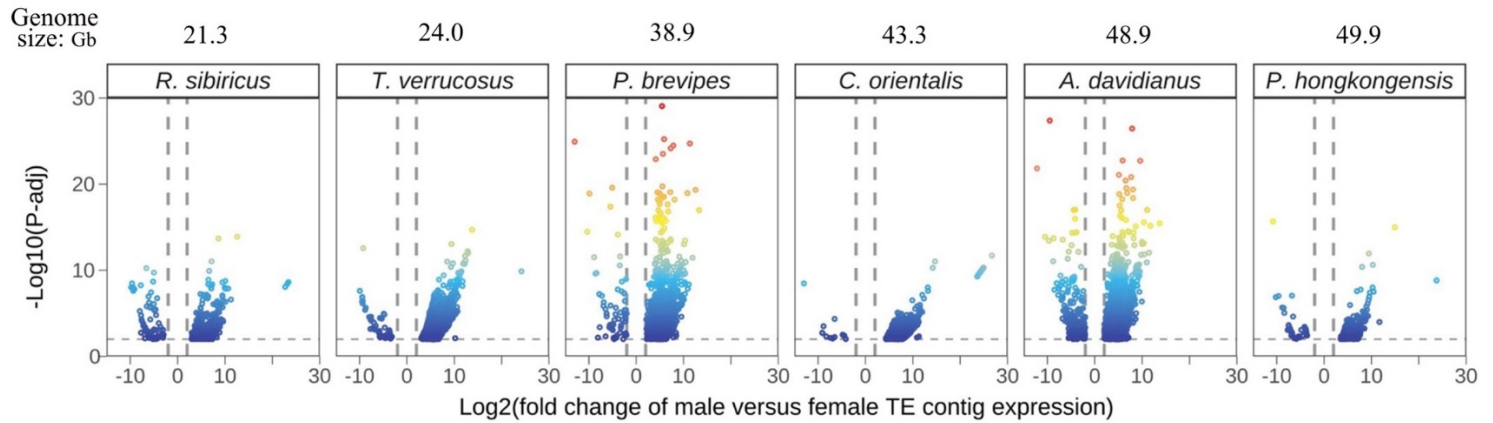
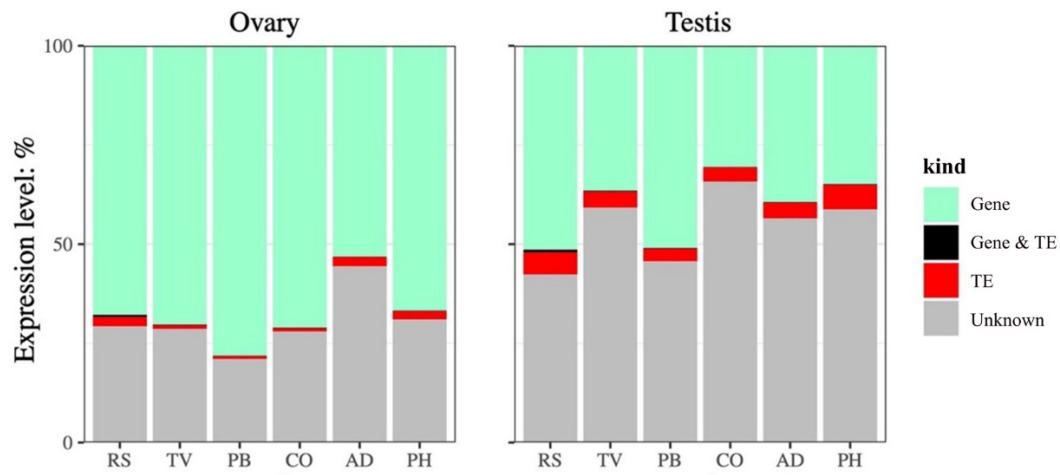


Fig. S3 Overall expression levels of genes and TEs in the ovary or testis of the six salamander species (% TPM)



Species are arranged left to right by increasing genome size: RS, *Ranodon sibiricus*; TV, *Tylototriton verrucosus*; PB, *Pachytriton brevipes*; CO, *Cynops orientalis*; AD, *Andrias davidianus*; PH, *Paramesotriton hongkongensis*

Fig. S4 Length distribution (A) and 5' U bias (B) of small RNA molecules in the gonads of individual male and female salamander samples.

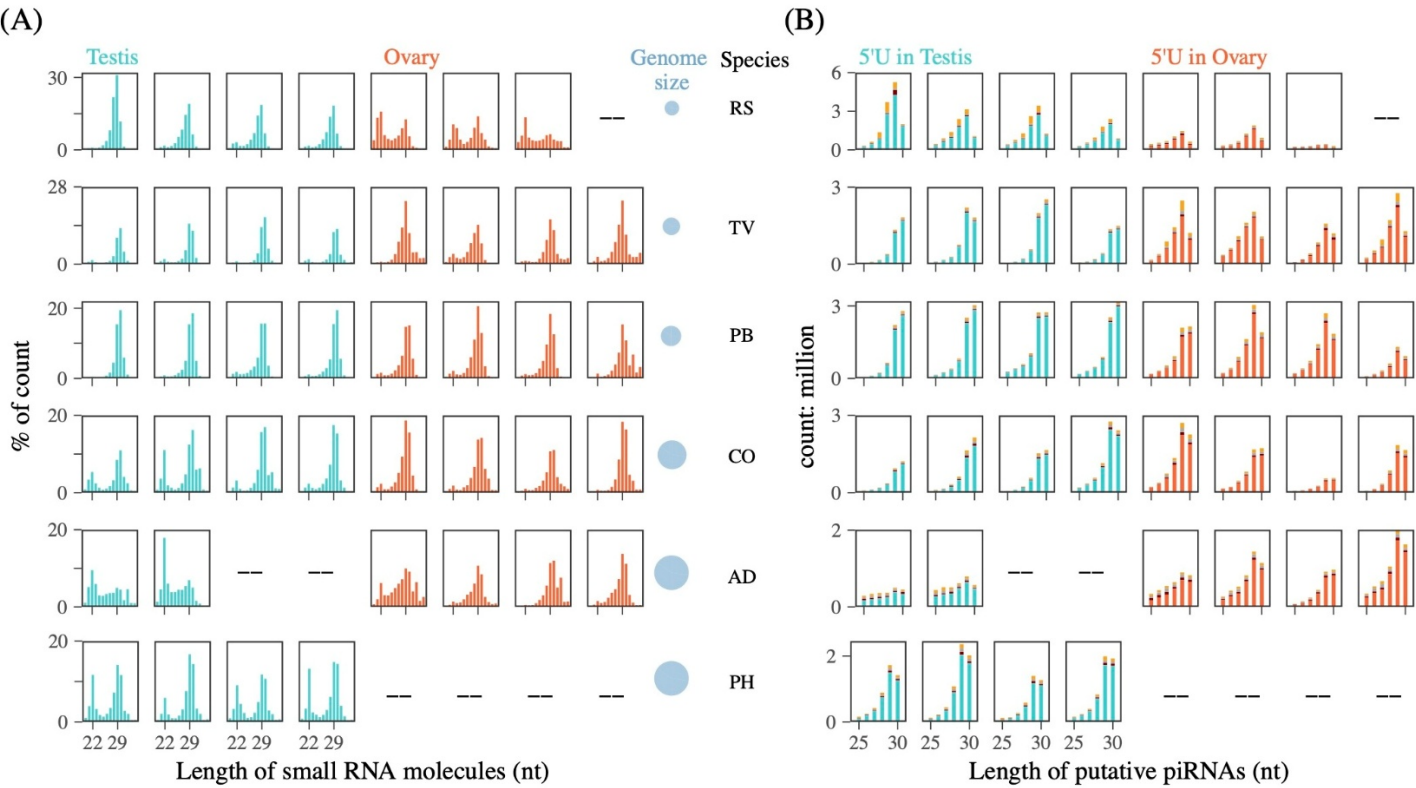
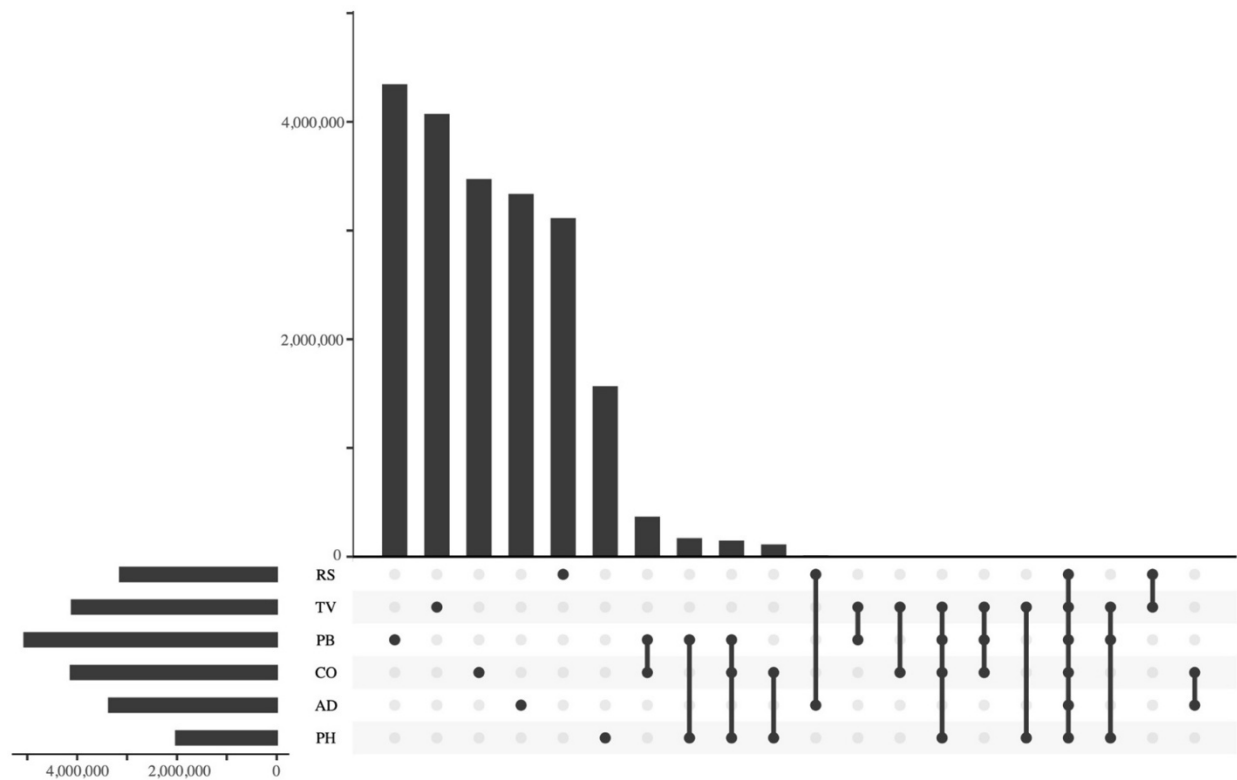


Fig. S5 Very few unique piRNAs are shared between salamander species



Species are arranged top to bottom by increasing genome size: RS, *Ranodon sibiricus*; TV, *Tylototriton verrucosus*; PB, *Pachytriton brevipes*; CO, *Cynops orientalis*; AD, *Andrias davidianus*; PH, *Paramesotriton hongkongensis*.

Vertical bars show the number of unique piRNAs in each species (columns 1-6, with a black dot indicating the species) or shared between two or more species (black dots and lines connecting them). Columns 11-20 include fewer than 111,314 unique piRNA sequences.

Fig. S6 The percentage of 5' - 5' overlap between pairs of sense and antisense piRNAs of different lengths in testes and ovaries. The high Z-score associated with the 10 nt overlap is a typical signature of ping-pong piRNA biogenesis.

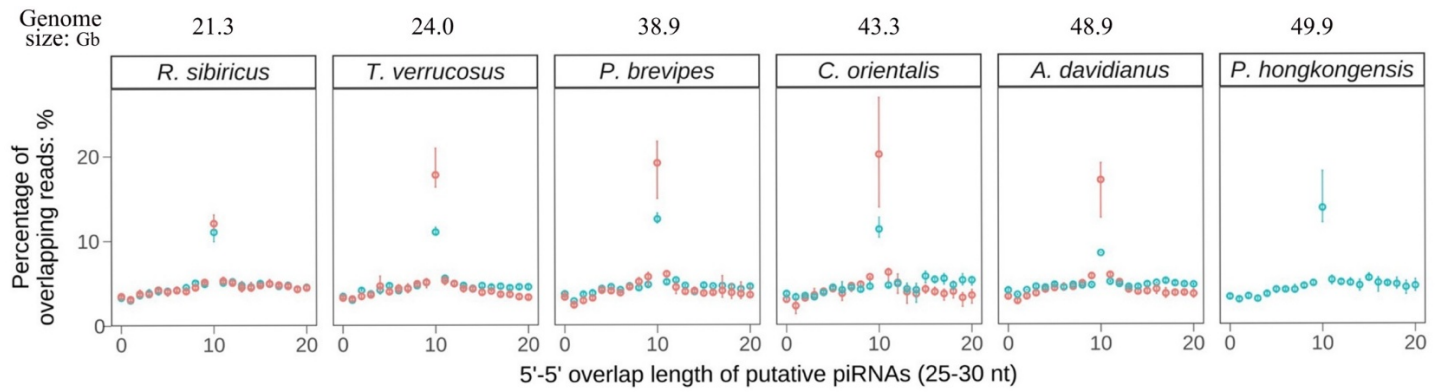
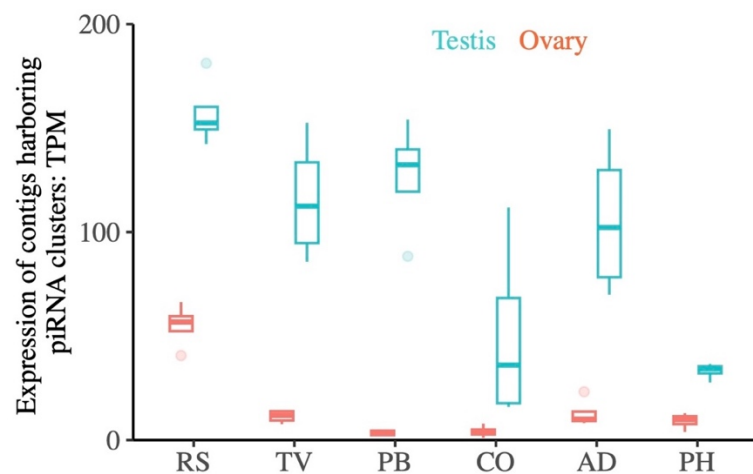


Fig. S7 The average expression levels of all putative piRNA clusters in each salamander species.



Species are arranged left to right by increasing genome size: RS, *Ranodon sibiricus*; TV, *Tylototriton verrucosus*; PB, *Pachytriton brivipes*; CO, *Cynops orientalis*; AD, *Andrias davidianus*; PH, *Paramesotriton hongkongensis*.