

Supplementary Tables

Table S1. The statistics of sequenced reads in three Scatophagidae species.

Libraries	Data size (Gb)					
	<i>Sc. argus</i>		<i>Sc. tetracanthus</i>		<i>Se. multifasciata</i>	
	Female*	Male	Female	Male	Female	Male
Illumina	55.81	36.1	47.41	47.64	33.89	32.67
Hi-C	69.50	64.09	78.63	65.42	68.94	80.09
PaiBio	69.52	39.93	42.65	43.16	54.87	55.8

*:The data were cited from our previous report (Huang, et al., 2021)

Table S2. The statistics of chromosome length distribution based on Hi-C clustered contigs.

<i>Sc. argus</i>						
Chr	Female*		HapX		Male	
	Contig Number	Size (bp)	Contig Number	Size (bp)	Contig Number	Size (bp)
1	8	30379288	7	30051248	8	30161504
2	16	29376297	10	28626015	6	28790675
3	13	28520610	8	28517508	7	28366738
4	3	28002303	5	28346178	6	28442954
5	13	27658022	7	28236059	10	27508990
6	6	27367725	10	27315133	6	27303035
7	3	27141783	7	27140457	4	27045683
8	4	26699536	8	26562693	11	26543189
9	11	25481562	7	26720291	7	26556397
10	8	24788153	3	24770542	4	24869661
11	1	24704845	6	24786529	4	24727372
12	9	24687116	6	24616127	6	24290294
13	3	24604546	3	24601191	3	24581826
14	11	23867469	3	23597477	6	23692831
15	8	23639815	8	23340135	8	23278978
16	14	23283707	7	22711982	7	22537548
17	11	22750745	7	22663180	6	22576886
18	4	21485133	13	21387353	5	21399184
19	5	20887377	8	20882713	6	20916778
20	5	220853581	4	20726106	3	20810233
21	1	19600000	6	20446575	10	20173274
22	10	19103589	4	18406976	4	18410507
23	10	13426317	6	13018111	8	13018783
24	8	12567426	5	16206350	4	16308899

*:The data were cited from our previous report (Huang, et al., 2021)

Table S2. The statistics of chromosome length distribution based on Hi-C clustered contigs.

<i>Sc. tetracanthus</i>						
Chr	Female		Male			
	Contig Number	Size (bp)	HapX Contig Number	Size (bp)	HapY Contig Number	Size (bp)
1	4	30498112	6	29926500	7	52592521
2	2	28646431	3	28395265	6	30226692
3	3	28854961	1	28161899	6	28346819
4	1	28159124	1	27916072	2	28305453
5	1	27179642	11	26659880	2	27002161
6	1	27147947	7	26583116	2	26900500
7	1	27147947	6	26391500	3	26811953
8	1	26946907	4	26389380	3	26703899
9	5	26795458	3	25872182	2	26560996
10	3	24699241	2	24530500	1	24578533
11	1	24900363	3	24303120	2	24264500
12	3	24272214	1	24216120	5	23855721
13	1	24687926	3	23392928	2	23214500
14	2	23705858	3	23197439	4	23180659
15	2	23474445	8	22942500	4	22465453
16	1	23294229	6	22461500	3	22269339
17	1	23525964	4	22214318	2	21244920
18	2	21680115	4	21247500	7	20752533
19	2	21174368	9	20656880	2	20482667
20	1	21005355	2	20409500	6	19709798
21	2	21367498	5	19469214	1	18343000
22	1	18685932	4	18441632	7	16337953
23	2	14474561	3	16380186	4	13220453
24	3	17736155	3	13550814		

Table S2. The statistics of chromosome length distribution based on Hi-C clustered contigs.

<i>Se. multifasciata</i>						
Chr	Female		Male			
	Contig Number	Size (bp)	HapX Contig Number	HapX Size (bp)	HapY Contig Number	HapY Size (bp)
1	2	29692505	6	30122928	5	29725480
2	1	28851185	6	28412933	5	28623035
3	5	27866660	8	27967596	7	28342772
4	2	27819357	5	27967596	5	27578951
5	4	27147285	7	26387738	8	26344883
6	2	26941737	1	26429796	3	27112155
7	1	27098469	4	26831791	4	27036203
8	1	26211168	6	26187421	6	26271488
9	4	26573324	7	26615395	8	26500835
10	1	23908065	4	23956439	7	24139126
11	2	24102970	5	24275166	6	24014268
12	2	24080870	6	21397277	7	23990699
13	1	24730931	4	24417441	2	24330172
14	2	23074413	8	23163959	4	22867856
15	1	22507114	4	22322654	7	22637909
16	1	21719387	4	21659426	5	21718828
17	2	22629958	3	22564656	4	22574736
18	1	20621588	4	20427344	4	20459639
19	1	20446087	4	20434245	1	20378059
20	1	20921293	4	20620433	5	20874665
21	1	19088292	2	19343131	2	18710503
22	1	17221544	2	17154712	4	17182434
23	3	12268241	5	12421076	3	12249462
24	3	16734433	5	16714691	3	15984955

Table S3. Assessment of three Scatophagidae species genome completeness by BUSCO.

Type	<i>Sc. argus</i>					
	Female*		Male			
	Number	Percent (%)	HapX		HapY	
			Number	Percent (%)	Number	Percent (%)
Complete BUSCOs	3252	97.0	3279	97.7	3274	97.6
Complete and single-copy BUSCOs	3161	94.3	3264	97.3	3258	97.1
Complete and duplicated BUSCOs	91	2.7	15	0.4	16	0.5
Fragmented BUSCOs	33	1.0	25	0.7	28	0.8
Missing BUSCOs	69	2.1	50	1.5	52	1.6

*:The data were cited from our previous report (Huang, et al., 2021)

Table S3. Assessment of three Scatophagidae species genome completeness by BUSCO.

Type	<i>Sc. tetracanthus</i>					
	Female		Male			
	Number	Percent (%)	HapX		HapY	
			Number	Percent (%)	Number	Percent (%)
Complete BUSCOs	3307	98.6	3304	98.5	3284	97.9
Complete and single-copy BUSCOs	3294	98.2	3290	98.1	3263	97.3
Complete and duplicated BUSCOs	13	0.4	14	0.4	20	0.6
Fragmented BUSCOs	20	0.6	28	0.8	27	0.8
Missing BUSCOs	27	0.8	41	1.2	35	1

Table S3. Assessment of three Scatophagidae species genome completeness by BUSCO.

Type	<i>Se. multifasciata</i>					
	Female		Male			
	Number	Percent (%)	HapX		HapY	
			Number	Percent (%)	Number	Percent (%)
Complete BUSCOs	3294	98.2	3280	97.8	3274	97.6
Complete and single-copy BUSCOs	3277	97.7	3262	97.3	3257	97.1
Complete and duplicated BUSCOs	17	0.5	18	0.5	17	0.5
Fragmented BUSCOs	27	0.8	23	0.7	21	0.6
Missing BUSCOs	34	1	51	1.5	44	1.3

Table S4. The statistics of three Scatophagidae species gene sets compared with other species.

Specie		Number	Average gene length (bp)	Average CDS length (bp)	Average exon per gene	Average exon length (bp)	Average intron length (bp)
<i>Sc. argus</i>	Female*	22188	16605.7	1795.44	10.83	303.39	1322.36
	Male	22170	16545.92	1794.53	10.83	304.04	1317.48
<i>Sc. tetracanthus</i>	Female	22264	15878.39	1767.96	10.72	298.23	1281.74
	Male	22326	15831.54	1765.15	10.74	296.83	1276.76
<i>Se. multifasciata</i>	Female	21869	15441.11	1772.75	10.82	295.93	1221.85
	Male	21971	15462.52	1773.73	10.8	296.51	1225.33
<i>S. aurata</i>		39254	8413.6	1212.69	6.42	188.79	1327.71
<i>L. crocea</i>		37234	8654.27	1219.33	6.64	183.58	1317.77
<i>A. latus</i>		38585	8679.58	1245.58	6.56	189.76	1336.08
<i>N. albiflora</i>		24347	6653.61	945.21	5	189.23	1428.85
<i>C. lucidus</i>		38062	8115.74	1197.5	6.03	198.48	1374.5
<i>O. niloticus</i>		40243	7993.35	1179.04	6.19	190.42	1312.51
<i>D. rerio</i>		35746	8001.36	1110.38	6.11	181.82	1349.34
<i>O. latipes</i>		34898	8318.74	1227.59	6.66	184.36	1253.14

*:The data were cited from our previous report (Huang, et al., 2021)

Table S5. The statistics of genome re-sequencing from female and male.

<i>Sc. argus</i>						
Sample	Clean_bases (Gb)	Average_sequen cing_depth(x)	Coverage (%)	Coverage_at_ least_4X(%)	Coverage_at_ least_10X(%)	Coverage_at_ least_20X(%)
F1	5.36	9.12	98.65	93.1	42.6	1.13
F2	5.29	8.97	99	92.73	40.96	1.09
F3	5.57	9.46	99.09	94.11	46.16	1.35
F4	4.71	8.01	98.82	90.08	30.91	0.63
F5	5.23	8.89	98.99	92.67	40.22	1.02
F6	4.98	8.48	98.96	91.85	35.76	0.72
F7	4.42	7.51	98.82	88.43	25.33	0.44
F8	5.29	9	98.95	93.01	41.53	1.01
F9	4.88	8.29	98.91	91.11	33.96	0.66
F10	4.62	7.84	98.87	89.67	28.85	0.54
F11	5.55	9.42	99.06	93.83	45.94	1.3
F12	5.08	8.62	99.05	92.21	37.24	0.85
F13	5.18	8.8	99.06	92.8	39.28	0.87
F14	5.29	8.98	98.83	92.58	40.77	1.15
F15	4.99	8.46	98.98	91.6	35.57	0.79
F16	4.68	7.96	98.68	89.83	30.12	0.58
F17	5.38	9.11	98.88	91.92	42.21	1.62
F18	5.49	9.33	99.11	93.75	44.71	1.26
F19	5.36	9.12	99.06	93.16	42.59	1.17
F20	5.93	10.09	99.18	94.91	52.19	2.06
F21	4.73	8.02	98.87	89.57	31	0.74
F22	4.36	7.42	98.81	87.71	24.61	0.43
F23	4.47	7.59	98.74	88.34	26.44	0.47
F24	4.46	7.58	98.69	86.5	26.63	0.78
F25	4.50	7.64	98.49	84.72	28.44	0.86
F26	4.45	7.57	98.87	88.67	25.9	0.43
F27	4.32	7.37	98.83	87.35	24.71	0.37
F28	4.31	7.35	98.89	87.75	24.31	0.33
F29	4.54	7.72	98.94	89	28.23	0.49
F30	4.61	7.84	98.94	89.67	29.14	0.51
M1	5.08	8.6	99.01	91.61	37.02	0.91
M2	5.08	8.29	98.92	90.25	33.59	0.9
M3	4.92	8.32	98.94	90.4	34.05	0.86
M4	4.85	8.22	98.96	90.38	32.85	0.7
M5	4.70	7.94	98.85	89.45	30.22	0.58
M6	5.04	8.55	98.97	90.97	36.51	0.98
M7	4.52	7.68	98.8	88.46	27.5	0.52
M8	4.53	7.71	98.63	88.48	27.83	0.5
M9	4.81	8.18	98.97	90.64	32.62	0.62

Table S5. The statistics of genome re-sequencing from female and male.

<i>Sc. argus</i>						
Sample	Clean_bases (Gb)	Average_sequen cing_depth(x)	Coverage (%)	Coverage_at_ least_4X(%)	Coverage_at_ least_10X(%)	Coverage_at_ least_20X(%)
M10	4.43	7.51	98.83	88	25.44	0.45
M11	4.93	8.3	98.7	89.24	34.21	1.03
M12	5.02	8.53	99.04	91.6	36.02	0.89
M13	5.05	8.57	98.81	90.85	36.81	0.98
M14	4.51	7.68	98.89	88.77	27.18	0.54
M15	4.45	7.58	98.75	88.25	26.01	0.54
M16	4.55	7.65	98.88	88.76	26.99	0.47
M17	4.32	7.35	98.69	87.01	24.15	0.43
M18	4.59	7.81	98.91	89.35	28.68	0.5
M19	4.99	8.48	98.97	91.57	35.76	0.78
M20	5.38	9.15	98.99	93.12	42.97	1.2
M21	5.01	8.51	98.9	91.71	36.06	0.82
M22	5.08	8.64	98.99	92.28	37.59	0.8
M23	5.01	8.51	98.99	91.86	36	0.76
M24	4.52	7.68	98.7	88.9	27.28	0.48
M25	5.25	8.94	98.88	92.73	40.94	0.96
M26	5.44	9.24	99.07	93.55	43.73	1.28
M27	5.10	8.68	99.04	92.41	37.73	0.84
M28	4.99	8.47	99	91.72	35.57	0.77
M29	5.04	8.58	98.98	92.02	36.78	0.84
M30	5.33	9.02	99.05	92.91	41.41	1.15

Table S5. The statistics of genome re-sequencing from female and male.

<i>Sc. tetracanthus</i>						
Sample	Clean_bases (Gb)	Average_sequen cing_depth(x)	Coverage (%)	Coverage_at_ least_4X(%)	Coverage_at_ least_10X(%)	Coverage_at_ least_20X(%)
F1	20.84	35.64	99.59	99.2	98.17	93.58
F2	15.66	26.8	99.55	98.98	97.09	84.43
F3	20.11	34.39	99.59	99.2	98.1	91.73
F4	14.06	24.05	99.61	99.01	96.53	74.05
F5	14.19	24.28	99.52	98.91	96.53	76.97
F6	14.35	24.56	99.49	98.85	96.46	77.74
F7	15.23	26.08	99.54	98.96	96.92	82.63
F8	16.12	27.58	99.54	98.98	97.08	85.7
F9	14.99	25.65	99.54	98.95	96.49	76.82
F10	17.45	29.85	99.58	99.1	97.43	84.43
F11	15.4	26.36	99.53	98.99	97.06	81.56
F12	12.46	21.32	99.59	98.71	90.77	52.33
F13	11.83	20.22	99.5	96.43	76.38	42.48
F14	13.29	22.75	99.53	98.85	95.66	66.5
F15	15.71	26.89	99.59	99.09	97.15	79.45
F16	12.05	20.63	99.49	98.65	92.96	54.39
F17	15.75	26.94	99.58	99.05	97.1	78.35
F18	17.01	29.12	99.58	99.09	97.39	84.61
F19	14.52	24.87	99.58	98.95	95.87	71.66
F20	14.6	24.97	99.59	98.62	90.35	61.24
F21	13.73	23.49	99.53	98.87	96.26	73.78
F22	15.9	27.06	99.53	98.95	96.96	84.42
F23	11.36	19.44	99.46	98.58	94.14	49.74
F24	10.03	17.15	99.63	99.02	93.65	30.85
F25	9.79	16.73	99.61	98.95	92.93	27.82
F26	12.93	22.11	99.66	99.25	97.47	66.85
F27	13.66	23.35	99.68	99.28	97.81	73.91
F28	12.23	20.92	99.67	99.23	96.97	59.31
F29	12.41	21.21	99.68	99.27	97.16	61.35
F30	13.77	23.54	99.7	99.31	97.84	75.07
M1	14.39	24.61	99.6	99.04	96.28	71.06
M2	12.99	22.22	99.52	98.84	95.81	67.21
M3	14.08	24.09	99.55	98.95	96.48	75.92
M4	11.85	20.29	99.55	98.76	93.46	50.67
M5	23.3	39.87	99.61	99.29	98.44	95.24
M6	13.56	23.19	99.49	98.76	95.9	71.69
M7	12.38	21.21	99.58	98.84	93.18	56.03
M8	13.32	22.8	99.54	98.94	96.31	69.84
M9	10.36	17.71	99.5	98.54	89.65	36.81

Table S5. The statistics of genome re-sequencing from female and male.*Sc. tetracanthus*

Sample	Clean_bases (Gb)	Average_sequen cing_depth(x)	Coverage (%)	Coverage_at_ least_4X(%)	Coverage_at_ least_10X(%)	Coverage_at_ least_20X(%)
M10	12.88	22.04	99.49	98.72	95.54	66.73
M11	15.51	26.54	99.56	99.05	97.27	83.78
M12	15.45	26.44	99.58	99.05	97.16	82.91
M13	14.58	24.95	99.58	98.65	92.23	66.3
M14	13.37	22.88	99.53	98.88	96.02	70.79
M15	18.37	31.42	99.57	99.12	97.75	91.22
M16	13.8	23.61	99.56	98.98	96.55	73.51
M17	13.66	23.36	99.6	98.5	88.21	53.35
M18	16.25	27.82	99.57	99.06	97.18	81.82
M19	14.58	24.93	99.58	99.03	96.33	71.58
M20	13.39	22.9	99.65	98.78	89.89	53.57
M21	14.81	25.36	99.6	99.07	96.89	78.01
M22	16.88	28.89	99.58	99.07	96.79	82.56
M23	12.41	21.24	99.52	98.79	95.37	61.93
M24	15.98	27.32	99.57	99.07	97.3	85.57
M25	21.41	36.64	99.62	99.28	98.32	94.59
M26	15.7	26.83	99.87	99.64	98.6	85.14
M27	13.16	22.5	99.64	99.21	97.46	69.32
M28	12.77	21.83	99.67	99.26	97.39	65.25
M29	10.14	17.33	99.6	98.99	93.55	32.06
M30	9.52	16.27	99.61	98.92	91.76	24.18

Table S5. The statistics of genome re-sequencing from female and male.

<i>Se. multifasciata</i>						
Sample	Clean_bases (Gb)	Average_sequen cing_depth(x)	Coverage (%)	Coverage_at_ least_4X(%)	Coverage_at_ least_10X(%)	Coverage_at_ least_20X(%)
F1	4.79	8.38	98.55	90.83	35.04	0.85
F2	5.82	10.24	98.87	93.88	54.1	2.72
F3	5.78	10.1	98.89	94.34	53.08	2.12
F4	5.73	10.03	98.85	94.21	52.79	2.01
F5	4.89	8.57	98.65	91.59	37.21	0.94
F6	6.62	11.6	98.98	95.57	65.69	5.16
F7	5.93	10.4	98.81	94.39	56.12	2.53
F8	5.99	10.48	98.89	94.69	56.77	2.56
F9	5.97	10.46	98.88	94.65	56.97	2.51
F10	5.78	10.13	98.84	94.29	53.77	2.17
F11	5.57	9.75	98.75	93.6	49.85	1.75
F12	5.59	9.77	98.94	93.99	49.84	1.76
F13	5.35	9.38	98.67	92.9	46.11	1.42
F14	5.59	9.79	98.46	93.18	50.3	1.87
F15	4.82	8.42	98.53	90.35	35.33	1.11
F16	4.71	8.28	98.25	88.48	34.91	1.06
F17	4.9	8.58	98.43	89.43	37.45	1.43
F18	5.45	9.56	98.56	92.92	47.78	1.71
F19	5.91	10.35	98.85	93.99	55	2.89
F20	6.06	10.61	98.73	93.42	55.51	4.72
F21	5.83	10.19	98.67	93.45	53.78	2.65
F22	5.44	9.54	98.71	92.78	47.37	1.78
F23	4.78	8.38	98.47	90.67	35.28	0.86
F24	5.61	9.83	98.52	91.45	48.91	3.52
F25	5.23	9.16	98.75	92.66	43.73	1.27
F26	4.75	8.33	98.53	90.27	34.58	0.94
F27	5.26	9.21	98.66	92.77	43.92	1.34
F28	5.29	9.27	98.76	92.96	44.87	1.35
F29	5.67	9.93	98.82	93.99	51.45	1.92
F30	5.27	9.23	98.62	92.54	44.63	1.31
M1	7.06	12.35	98.96	95.28	67.3	9.89
M2	6.3	11.05	98.82	94.51	60.64	4.46
M3	5.82	10.2	98.66	93.5	54.12	2.54
M4	5.79	10	99.11	93.6	50.71	2.9
M5	5.48	9.6	98.62	91.69	45.7	3.1
M6	5.24	9.18	98.65	91.98	43.75	1.47
M7	6.26	10.9	98.95	94.62	58.71	4.71
M8	5.77	10.08	98.74	93.58	52.48	2.66
M9	6.08	10.6	98.86	94.47	57.45	3.21

Table S5. The statistics of genome re-sequencing from female and male.***Se. multifasciata***

Sample	Clean_bases (Gb)	Average_sequen cing_depth(x)	Coverage (%)	Coverage_at_ least_4X(%)	Coverage_at_ least_10X(%)	Coverage_at_ least_20X(%)
M10	6.56	11.45	99.06	95.55	64.55	4.93
M11	5.93	10.33	99.01	94.47	55.38	2.59
M12	6.15	10.77	98.68	94.26	59.19	3.4
M13	5.83	10.21	98.85	94.07	54.34	2.5
M14	6.16	10.75	98.94	94.74	58.78	3.49
M15	5.9	10.29	98.95	94.27	54.67	2.69
M16	6.53	11.42	98.99	94.23	59.41	8.17
M17	6.47	11.31	98.91	94.91	62.07	5.33
M18	6.35	11.11	99.04	95.13	61.18	4.57
M19	4.81	8.4	98.56	89.41	35.73	1.12
M20	4.59	8.03	98.49	88.31	31.6	1.03
M21	4.86	8.49	98.53	89.43	36.19	1.48
M22	4.87	8.51	98.59	89.53	36.1	1.6
M23	5.07	8.88	98.56	91.3	40.99	1.19
M24	4.57	8.01	98.52	89.35	31.55	0.69
M25	6.43	11.27	98.87	94.12	60.1	6.75
M26	6.17	10.82	98.86	94.66	59.59	3.51
M27	6.01	10.53	98.74	93.82	55.54	3.99
M28	6.21	10.88	98.83	94.32	58.6	4.41
M29	5.77	10.11	98.7	93.45	53	2.57
M30	6.35	11.11	98.58	94.09	60.19	5.28

Table S6. The statistics of SNP calling.

Sample	SNP num	<i>Sc. argus</i> (Female genome as reference genome)					
		Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
F1	2457548	1515499	903157	1560745	0.64	896803	0.36
F2	2351832	1450871	864059	1443736	0.61	908096	0.39
F3	2469236	1523058	906990	1570006	0.64	899230	0.36
F4	2422859	1494404	889979	1512689	0.62	910170	0.38
F5	2425415	1495165	891733	1535044	0.63	890371	0.37
F6	2429757	1499245	891935	1524495	0.63	905262	0.37
F7	2410879	1486848	885628	1498606	0.62	912273	0.38
F8	2365696	1458543	869133	1451741	0.61	913955	0.39
F9	2389403	1474706	876174	1462405	0.61	926998	0.39
F10	2466281	1521670	905510	1560318	0.63	905963	0.37
F11	2443376	1507298	897557	1536756	0.63	906620	0.37
F12	2425354	1496771	890234	1521727	0.63	903627	0.37
F13	2477873	1528100	910120	1581796	0.64	896077	0.36
F14	2366038	1458895	869232	1445322	0.61	920716	0.39
F15	2338620	1441790	859659	1440007	0.62	898613	0.38
F16	2354422	1451117	866177	1440983	0.61	913439	0.39
F17	2326776	1433345	857136	1412662	0.61	914114	0.39
F18	2287199	1407432	843770	1383449	0.6	903750	0.4
F19	2365770	1457689	870658	1460513	0.62	905257	0.38
F20	2452835	1512930	900609	1556920	0.63	895915	0.37
F21	2376969	1466092	873199	1476870	0.62	900099	0.38
F22	2425881	1497018	889982	1516781	0.63	909100	0.37
F23	2165440	1335123	796049	1421817	0.66	743623	0.34
F24	2144169	1320263	789701	1466453	0.68	677716	0.32
F25	2408136	1485208	884952	1506912	0.63	901224	0.37
F26	2156597	1328982	792939	1470777	0.68	685820	0.32
F27	2178671	1342606	800844	1453402	0.67	725269	0.33
F28	2364337	1458487	868736	1448462	0.61	915875	0.39
F29	2447928	1509948	899090	1547599	0.63	900329	0.37
F30	2391448	1474208	879527	1482249	0.62	909199	0.38
M1	2414166	1489564	886528	1510642	0.63	903524	0.37
M2	2351239	1448783	865281	1447802	0.62	903437	0.38
M3	2349880	1448646	863950	1452621	0.62	897259	0.38
M4	2393019	1476050	879101	1522424	0.64	870595	0.36
M5	2320308	1429956	853507	1421586	0.61	898722	0.39
M6	2322611	1432979	852359	1404192	0.6	918419	0.4
M7	2401484	1481448	881748	1508362	0.63	893122	0.37
M8	2401143	1480677	882424	1486417	0.62	914726	0.38
M9	2353355	1450009	865961	1431900	0.61	921455	0.39
M10	2355931	1453999	864567	1442820	0.61	913111	0.39
M11	2372043	1462349	872098	1475168	0.62	896875	0.38

Table S6. The statistics of SNP calling.

<i>Sc. argus</i> (Female genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
M12	2354359	1451457	865659	1469212	0.62	885147	0.38
M13	2331628	1437994	857114	1420883	0.61	910745	0.39
M14	2363046	1457665	867763	1465800	0.62	897246	0.38
M15	2411499	1486675	886891	1504406	0.62	907093	0.38
M16	2453639	1512605	902008	1551867	0.63	901772	0.37
M17	2401403	1479750	883432	1495022	0.62	906381	0.38
M18	2413975	1488100	887579	1506728	0.62	907247	0.38
M19	2427303	1497568	891597	1532300	0.63	895003	0.37
M20	2337092	1441652	858802	1448204	0.62	888888	0.38
M21	2376113	1465810	872364	1483198	0.62	892915	0.38
M22	2425338	1496159	890481	1544451	0.64	880887	0.36
M23	2448468	1509980	899626	1562938	0.64	885530	0.36
M24	2421795	1493513	890023	1529332	0.63	892463	0.37
M25	2414663	1489666	887010	1512785	0.63	901878	0.37
M26	2406972	1484607	884008	1515164	0.63	891808	0.37
M27	2437994	1504056	894939	1530457	0.63	907537	0.37
M28	2378058	1466263	874063	1479628	0.62	898430	0.38
M29	2367006	1460225	869495	1460867	0.62	906139	0.38
M30	2387415	1471147	878687	1487281	0.62	900134	0.38

Table S6. The statistics of SNP calling.

<i>Sc. argus</i> (HapY genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
F1	2637911	1615964	984016	1709082	0.65	928829	0.35
F2	2460619	1507619	918793	1553703	0.63	906916	0.37
F3	2667569	1633266	996664	1723124	0.65	944445	0.35
F4	2580250	1580343	963164	1649094	0.64	931156	0.36
F5	2591729	1586700	968083	1670631	0.64	921098	0.36
F6	2602222	1594669	970168	1668846	0.64	933376	0.36
F7	2557406	1566150	955010	1631819	0.64	925587	0.36
F8	2484956	1521734	927299	1568487	0.63	916469	0.37
F9	2547095	1561922	948257	1610020	0.63	937075	0.37
F10	2660741	1630347	992617	1711893	0.64	948848	0.36
F11	2629484	1611009	981111	1683651	0.64	945833	0.36
F12	2592260	1588928	966359	1661837	0.64	930423	0.36
F13	2693502	1649034	1005331	1747314	0.65	946188	0.35
F14	2473698	1513804	924437	1556969	0.63	916729	0.37
F15	2397166	1466827	896823	1520882	0.63	876284	0.37
F16	2421727	1481892	906024	1525032	0.63	896695	0.37
F17	2368405	1445684	889461	1485644	0.63	882761	0.37
F18	2317046	1411635	873013	1456946	0.63	860100	0.37
F19	2430290	1486149	909790	1540781	0.63	889509	0.37
F20	2663203	1631023	994139	1714215	0.64	948988	0.36
F21	2492952	1527043	930725	1590870	0.64	902082	0.36
F22	2597996	1592402	968466	1658603	0.64	939393	0.36
F23	2187066	1338311	817820	1495946	0.68	691120	0.32
F24	2176747	1330292	815711	1529139	0.7	647608	0.3
F25	2555124	1564666	954660	1635925	0.64	919199	0.36
F26	2258251	1380921	845286	1568080	0.69	690171	0.31
F27	2317614	1417428	866959	1557756	0.67	759858	0.33
F28	2446526	1497594	914928	1546880	0.63	899646	0.37
F29	2625172	1608098	980130	1687594	0.64	937578	0.36
F30	2528132	1547387	944916	1605470	0.64	922662	0.36
M1	2544108	1558165	949863	1632103	0.64	912005	0.36
M2	2426548	1484118	908427	1538801	0.63	887747	0.37
M3	2421321	1481548	905549	1544915	0.64	876406	0.36
M4	2499362	1530158	934215	1629540	0.65	869822	0.35
M5	2391104	1462350	895043	1516810	0.63	874294	0.37
M6	2417854	1481745	901237	1523745	0.63	894109	0.37
M7	2533760	1551302	946228	1629807	0.64	903953	0.36
M8	2542410	1556175	949656	1614719	0.64	927691	0.36
M9	2429172	1486117	909265	1525921	0.63	903251	0.37
M10	2427226	1487238	905875	1533103	0.63	894123	0.37
M11	2479051	1516611	927074	1590843	0.64	888208	0.36

Table S6. The statistics of SNP calling.

<i>Sc. argus</i> (HapY genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
M12	2424922	1484976	906114	1562584	0.64	862338	0.36
M13	2383995	1458664	892209	1497829	0.63	886166	0.37
M14	2444081	1495836	913520	1568486	0.64	875595	0.36
M15	2551445	1561554	953970	1630953	0.64	920492	0.36
M16	2634528	1612582	984055	1697103	0.64	937425	0.36
M17	2545377	1557472	951753	1627654	0.64	917723	0.36
M18	2573665	1575960	961880	1642595	0.64	931070	0.36
M19	2575513	1577679	961539	1664316	0.65	911197	0.35
M20	2426431	1485925	906410	1555079	0.64	871352	0.36
M21	2491516	1525651	930097	1599380	0.64	892136	0.36
M22	2596141	1590195	968695	1686656	0.65	909485	0.35
M23	2639029	1617205	984070	1716702	0.65	922327	0.35
M24	2570095	1574407	959248	1661349	0.65	908746	0.35
M25	2556264	1565805	954304	1647539	0.64	908725	0.36
M26	2558897	1567401	955037	1652378	0.65	906519	0.35
M27	2616638	1603594	975410	1677140	0.64	939498	0.36
M28	2481827	1518703	928019	1586626	0.64	895201	0.36
M29	2464374	1509339	920932	1563325	0.63	901049	0.37
M30	2507318	1533605	938369	1607021	0.64	900297	0.36

Table S6. The statistics of SNP calling.

<i>Sc. tetracanthus</i> (Female genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
F1	831900	511485	314321	558648	0.67	273252	0.33
F2	836177	514787	315629	563737	0.67	272440	0.33
F3	828378	509319	312724	560024	0.68	268354	0.32
F4	1062034	655012	400785	932797	0.88	129237	0.12
F5	826784	508904	312410	553798	0.67	272986	0.33
F6	830231	511088	313684	555585	0.67	274646	0.33
F7	827957	509681	312419	553323	0.67	274634	0.33
F8	830491	511223	313639	559497	0.67	270994	0.33
F9	826521	509047	311738	546896	0.66	279625	0.34
F10	827258	509347	311794	559895	0.68	267363	0.32
F11	824797	507542	311453	551445	0.67	273352	0.33
F12	823422	507156	310608	555665	0.67	267757	0.33
F13	784803	485191	294266	520993	0.66	263810	0.34
F14	822488	506687	310097	553062	0.67	269426	0.33
F15	832697	513052	313770	559017	0.67	273680	0.33
F16	819372	504515	309288	543031	0.66	276341	0.34
F17	830857	511465	313569	558805	0.67	272052	0.33
F18	828386	508965	313492	556309	0.67	272077	0.33
F19	829995	511158	313141	556648	0.67	273347	0.33
F20	824073	507621	310746	556623	0.68	267450	0.32
F21	827596	509356	312557	553123	0.67	274473	0.33
F22	825027	508082	311206	548129	0.66	276898	0.34
F23	823214	507295	310640	549033	0.67	274181	0.33
F24	837831	515220	316920	565329	0.67	272502	0.33
F25	822069	505151	311144	552999	0.67	269070	0.33
F26	822460	504781	311222	551726	0.67	270734	0.33
F27	825054	506632	311967	555001	0.67	270053	0.33
F28	837880	514931	316803	564079	0.67	273801	0.33
F29	847753	520753	320736	575106	0.68	272647	0.32
F30	846883	520338	320266	571743	0.68	275140	0.32
M1	841415	518162	317550	570965	0.68	270450	0.32
M2	835129	514253	315481	567487	0.68	267642	0.32
M3	833127	512198	315147	563974	0.68	269153	0.32
M4	836063	515203	315518	556449	0.67	279614	0.33
M5	852453	524279	321751	577219	0.68	275234	0.32
M6	838475	516572	316416	570934	0.68	267541	0.32
M7	833952	513737	314574	565419	0.68	268533	0.32
M8	844754	520237	318836	568823	0.67	275931	0.33
M9	829600	511994	312284	562518	0.68	267082	0.32
M10	836312	514219	316703	565045	0.68	271267	0.32
M11	847438	520937	320701	575314	0.68	272124	0.32

Table S6. The statistics of SNP calling.

<i>Sc. tetracanthus</i> (Female genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
M12	842796	518568	318441	572881	0.68	269915	0.32
M13	832665	513474	313299	559569	0.67	273096	0.33
M14	836832	515255	315988	569404	0.68	267428	0.32
M15	846601	520709	319956	576162	0.68	270439	0.32
M16	843529	518631	319107	570318	0.68	273211	0.32
M17	833664	514436	313587	556595	0.67	277069	0.33
M18	845595	519912	319701	570511	0.67	275084	0.33
M19	844713	519906	319073	570626	0.68	274087	0.32
M20	835934	515565	314667	562231	0.67	273703	0.33
M21	840818	516930	317981	566463	0.67	274355	0.33
M22	843737	519289	318573	570778	0.68	272959	0.32
M23	837481	515796	316308	564719	0.67	272762	0.33
M24	843580	519057	318779	570145	0.68	273435	0.32
M25	729610	448334	275609	574189	0.79	155421	0.21
M26	851953	522813	322836	572798	0.67	279155	0.33
M27	553210	339241	208477	552604	1	606	0
M28	843466	518401	318744	568514	0.67	274952	0.33
M29	829531	510072	313526	553936	0.67	275595	0.33
M30	837862	515558	316693	568354	0.68	269508	0.32

Table S6. The statistics of SNP calling.

<i>Sc. tetracanthus</i> (HapY genome as reference genome)								
Sample	SNP num	Transition	Transversion	Ts/Tv	Heter num	Heter ratio	Hom num	Hom ratio
F1	857338	527021	324169	1.63	564488	0.66	292850	0.34
F2	849686	523113	320986	1.63	568251	0.67	281435	0.33
F3	851296	523678	321398	1.63	565889	0.66	285407	0.34
F4	1080575	666673	407663	1.64	938943	0.87	141632	0.13
F5	846804	521687	319609	1.63	555368	0.66	291436	0.34
F6	850385	523758	320995	1.63	560957	0.66	289428	0.34
F7	845778	520803	319247	1.63	557163	0.66	288615	0.34
F8	853741	525588	322561	1.63	563600	0.66	290141	0.34
F9	840424	517891	316999	1.63	551555	0.66	288869	0.34
F10	852745	525288	321562	1.63	566358	0.66	286387	0.34
F11	836890	514721	316538	1.63	557604	0.67	279286	0.33
F12	846314	521552	319214	1.63	562901	0.67	283413	0.33
F13	805819	498405	302023	1.65	527957	0.66	277862	0.34
F14	849395	523084	320885	1.63	558032	0.66	291363	0.34
F15	848152	522375	319833	1.63	562537	0.66	285615	0.34
F16	838222	515939	316682	1.63	547992	0.65	290230	0.35
F17	852597	524875	321862	1.63	566510	0.66	286087	0.34
F18	847978	521715	320517	1.63	561923	0.66	286055	0.34
F19	847691	521980	320202	1.63	562329	0.66	285362	0.34
F20	846787	521788	319350	1.63	563892	0.67	282895	0.33
F21	840289	517215	317635	1.63	556222	0.66	284067	0.34
F22	840564	517969	317191	1.63	554364	0.66	286200	0.34
F23	845386	520946	319233	1.63	554043	0.66	291343	0.34
F24	837457	515396	316403	1.63	568904	0.68	268553	0.32
F25	845537	520062	319694	1.63	556273	0.66	289264	0.34
F26	853743	524659	322819	1.63	558900	0.65	294843	0.35
F27	850623	522705	321534	1.63	560155	0.66	290468	0.34
F28	851350	523002	322211	1.62	569852	0.67	281498	0.33
F29	838840	515382	317288	1.62	578659	0.69	260181	0.31
F30	842596	517981	318200	1.63	576981	0.68	265615	0.32
M1	838725	516340	316794	1.63	575431	0.69	263294	0.31
M2	840672	517848	317435	1.63	571353	0.68	269319	0.32
M3	838393	515950	316877	1.63	568547	0.68	269846	0.32
M4	828264	510581	312422	1.63	560893	0.68	267371	0.32
M5	847814	521303	320206	1.63	581017	0.69	266797	0.31
M6	841287	518626	317327	1.63	576595	0.69	264692	0.31
M7	834702	514400	314640	1.63	569474	0.68	265228	0.32
M8	838653	516681	316461	1.63	572809	0.68	265844	0.32
M9	832034	513688	313101	1.64	567886	0.68	264148	0.32
M10	832979	512754	314777	1.63	568250	0.68	264729	0.32
M11	851030	523371	321760	1.63	581062	0.68	269968	0.32

Table S6. The statistics of SNP calling.

<i>Sc. tetracanthus</i> (HapY genome as reference genome)								
Sample	SNP num	Transition	Transversion	Ts/Tv	Heter num	Heter ratio	Hom num	Hom ratio
M12	844548	519671	319077	1.63	577435	0.68	267113	0.32
M13	831863	512783	313298	1.64	566422	0.68	265441	0.32
M14	834747	514325	315012	1.63	571866	0.69	262881	0.31
M15	842505	518502	318199	1.63	581807	0.69	260698	0.31
M16	837561	515401	316562	1.63	572783	0.68	264778	0.32
M17	830627	512956	311997	1.64	562765	0.68	267862	0.32
M18	840760	517416	317424	1.63	573959	0.68	266801	0.32
M19	843831	519462	318610	1.63	576070	0.68	267761	0.32
M20	831749	512856	313205	1.64	567177	0.68	264572	0.32
M21	835416	514087	315573	1.63	570716	0.68	264700	0.32
M22	840656	517416	317416	1.63	575289	0.68	265367	0.32
M23	836110	515224	315662	1.63	568651	0.68	267459	0.32
M24	842774	518471	318611	1.63	573526	0.68	269248	0.32
M25	843699	518987	318494	1.63	580603	0.69	263096	0.31
M26	569316	348621	215256	1.62	568808	1	508	0
M27	854373	525100	322970	1.63	563179	0.66	291194	0.34
M28	840647	516650	317753	1.63	572944	0.68	267703	0.32
M29	844579	519666	318938	1.63	560045	0.66	284534	0.34
M30	841527	517845	318066	1.63	572813	0.68	268714	0.32

Table S6. The statistics of SNP calling.

<i>Se. multifasciata</i> (Female genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
F1	2384400	1497940	857631	1624744	0.68	759656	0.32
F2	2322919	1456592	836704	1740230	0.75	582689	0.25
F3	2386975	1499494	858104	1589172	0.67	797803	0.33
F4	2384338	1497985	857998	1745260	0.73	639078	0.27
F5	2085117	1307240	751462	1549384	0.74	535733	0.26
F6	2045851	1283211	735602	1537422	0.75	508429	0.25
F7	2543295	1596617	914118	1669907	0.66	873388	0.34
F8	2059503	1290843	740573	1600176	0.78	459327	0.22
F9	2430897	1526778	874450	1728071	0.71	702826	0.29
F10	2464313	1544880	888359	1565317	0.64	898996	0.36
F11	2407928	1511988	865472	1564382	0.65	843546	0.35
F12	2595806	1630312	933233	1738592	0.67	857214	0.33
F13	2356508	1480420	847077	1603904	0.68	752604	0.32
F14	2488284	1560313	896319	1751526	0.7	736758	0.3
F15	2467181	1549182	887697	1722985	0.7	744196	0.3
F16	2444226	1534108	878982	1669366	0.68	774860	0.32
F17	2201852	1381068	791144	1652819	0.75	549033	0.25
F18	2644973	1659481	951596	1775762	0.67	869211	0.33
F19	2414952	1513668	869335	1719716	0.71	695236	0.29
F20	1612544	1010794	577033	1594011	0.99	18533	0.01
F21	1850896	1161216	663990	1133780	0.61	717116	0.39
F22	2413621	1518562	866495	1579182	0.65	834439	0.35
F23	2258526	1421772	809256	1362599	0.6	895927	0.4
F24	2145061	1346885	771023	1443266	0.67	701795	0.33
F25	2456275	1541612	883203	1435874	0.58	1020401	0.42
F26	2440560	1530263	879670	1684803	0.69	755757	0.31
F27	2506350	1571415	904341	1677611	0.67	828739	0.33
F28	2028532	1270907	730494	1586421	0.78	442111	0.22
F29	2417242	1517884	869886	1671625	0.69	745617	0.31
F30	2384343	1491420	863011	1371488	0.58	1012855	0.42
M1	2348810	1471041	847440	1752630	0.75	596180	0.25
M2	2026042	1267736	729887	1392417	0.69	633625	0.31
M3	2020335	1267166	728119	1492586	0.74	527749	0.26
M4	2544262	1592663	920419	1651488	0.65	892774	0.35
M5	2600996	1631026	937451	1760733	0.68	840263	0.32
M6	2392550	1500056	862841	1726573	0.72	665977	0.28
M7	2041428	1278343	735021	1585542	0.78	455886	0.22
M8	2075434	1301262	746881	1569031	0.76	506403	0.24
M9	1965946	1230700	708330	1305323	0.66	660623	0.34
M10	2464559	1545465	888948	1713996	0.7	750563	0.3
M11	2416960	1517533	870305	1674491	0.69	742469	0.31

Table S6. The statistics of SNP calling.

<i>Se. multifasciata</i> (Female genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
M12	1811776	1132157	653689	1375019	0.76	436757	0.24
M13	2024751	1267332	730699	1396491	0.69	628260	0.31
M14	2391276	1499554	863174	1658917	0.69	732359	0.31
M15	2391325	1497852	861644	1645706	0.69	745619	0.31
M16	2483301	1556848	894560	1670293	0.67	813008	0.33
M17	2477268	1553123	891910	1709234	0.69	768034	0.31
M18	2498045	1564174	900319	1739180	0.7	758865	0.3
M19	2479104	1553981	893228	1679969	0.68	799135	0.32
M20	2474816	1550054	893206	1734413	0.7	740403	0.3
M21	2481527	1555864	893949	1691618	0.68	789909	0.32
M22	2547544	1597003	917841	1703237	0.67	844307	0.33
M23	2531023	1583498	914076	1719708	0.68	811315	0.32
M24	2516958	1576895	907892	1773770	0.7	743188	0.3
M25	2516919	1576700	907566	1716175	0.68	800744	0.32
M26	2312640	1450182	833342	1488047	0.64	824593	0.36
M27	2273877	1424191	823041	1437827	0.63	836050	0.37
M28	2359686	1478664	851947	1533113	0.65	826573	0.35
M29	2375789	1487440	859818	1553421	0.65	822368	0.35
M30	2109207	1324072	758917	1500879	0.71	608328	0.29

Table S6. The statistics of SNP calling.

<i>Se. multifasciata</i> (HapY genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
F1	2484669	1559514	896237	1638829	0.66	845840	0.34
F2	2429245	1520818	877486	1579060	0.65	850185	0.35
F3	2365724	1482367	852034	1573398	0.67	792326	0.33
F4	2554510	1602194	919933	1752028	0.69	802482	0.31
F5	2366857	1484990	852672	1617054	0.68	749803	0.32
F6	2615912	1638772	944502	1768951	0.68	846961	0.32
F7	2611308	1638015	942390	1737240	0.67	874068	0.33
F8	2486792	1558842	896465	1683424	0.68	803368	0.32
F9	2431989	1524585	875814	1674354	0.69	757635	0.31
F10	2647399	1659780	953559	1790256	0.68	857143	0.32
F11	2600201	1629470	938651	1739992	0.67	860209	0.33
F12	2553379	1601089	921821	1757399	0.69	795980	0.31
F13	2419301	1518550	872482	1621828	0.67	797473	0.33
F14	2337100	1464370	842251	1157777	0.5	1179323	0.5
F15	2347205	1474250	844511	1591064	0.68	756141	0.32
F16	2241347	1408169	804649	1387114	0.62	854233	0.38
F17	2215789	1388675	799246	1476215	0.67	739574	0.33
F18	2449983	1536232	881879	1454262	0.59	995721	0.41
F19	2458300	1538530	889069	1702069	0.69	756231	0.31
F20	2527469	1582678	913757	1696405	0.67	831064	0.33
F21	2467199	1545455	892310	1608289	0.65	858910	0.35
F22	2492327	1563633	899015	1685353	0.68	806974	0.32
F23	2495382	1566008	899658	1602878	0.64	892504	0.36
F24	2322535	1451875	840945	1388158	0.6	934377	0.4
F25	2564732	1610026	925388	1764116	0.69	800616	0.31
F26	2358207	1478535	852895	1563167	0.66	795040	0.34
F27	2447662	1534587	883728	1559539	0.64	888123	0.36
F28	2571963	1612694	926740	1679768	0.65	892195	0.35
F29	2458425	1541305	887268	1627724	0.66	830701	0.34
F30	2566634	1611086	925264	1737838	0.68	828796	0.32
M1	2609373	1633255	944680	1775116	0.68	834257	0.32
M2	2615783	1638765	945972	1732252	0.66	883531	0.34
M3	2552915	1601789	921596	1695424	0.66	857491	0.34
M4	2310484	1444684	836474	1427176	0.62	883308	0.38
M5	2403924	1504376	871259	1428305	0.59	975619	0.41
M6	2465217	1544896	891503	1679244	0.68	785973	0.32
M7	2454100	1536432	885814	1670211	0.68	783889	0.32
M8	2603533	1630496	941023	1694802	0.65	908731	0.35
M9	2585939	1619821	933707	1728556	0.67	857383	0.33
M10	2493683	1559303	900834	1763476	0.71	730207	0.29
M11	2414000	1510852	871605	1700764	0.7	713236	0.3

Table S6. The statistics of SNP calling.

<i>Se. multifasciata</i> (HapY genome as reference genome)							
Sample	SNP num	Transition	Transversion	Heter num	Heter ratio	Hom num	Hom ratio
M12	2437390	1525980	880664	1416823	0.58	1020567	0.42
M13	2564122	1604912	927046	1757164	0.69	806958	0.31
M14	2580877	1616325	932719	1717115	0.67	863762	0.33
M15	2585243	1619553	933198	1729511	0.67	855732	0.33
M16	2401296	1500478	867742	1744732	0.73	656564	0.27
M17	2678224	1676654	968774	1804090	0.67	874134	0.33
M18	2414857	1510617	872130	1736609	0.72	678248	0.28
M19	2329422	1458898	841154	1526659	0.66	802763	0.34
M20	2239247	1400812	812129	1460180	0.65	779067	0.35
M21	2370949	1483063	858999	1554082	0.66	816867	0.34
M22	2345591	1467394	849612	1579043	0.67	766548	0.33
M23	2345167	1470931	847196	1518829	0.65	826338	0.35
M24	2256842	1415196	814610	1519096	0.67	737746	0.33
M25	2458927	1537802	890488	1675065	0.68	783862	0.32
M26	2587391	1621075	932942	1779641	0.69	807750	0.31
M27	2458999	1539588	889451	1615588	0.66	843411	0.34
M28	2578544	1615895	932007	1747851	0.68	830693	0.32
M29	2404069	1506603	867903	1596058	0.66	808011	0.34
M30	2426004	1518422	876661	1336862	0.55	1089142	0.45

Table S7. Summary of the SNP-based high-density genetic map of *Sc. argus*

Linkage group	Number of markers	Genetic length (cM)	Marker interval (cM)	Maximum gap (cM)
LG1	316	87.78	0.28	3.2
LG2	254	91.2	0.36	5.03
LG3	252	82.83	0.33	2.18
LG4	137	59.96	0.44	2.56
LG5	193	60.89	0.32	1.74
LG6	218	92.66	0.43	2.91
LG7	285	95.06	0.33	2.12
LG8	260	92.34	0.36	5.52
LG9	295	85.88	0.29	3.81
LG10	276	89.44	0.32	4.38
LG11	278	95.13	0.34	2.44
LG12	291	127.09	0.44	4.89
LG13	202	117.17	0.58	5.71
LG14	236	88.52	0.38	2.91
LG15	305	73.94	0.24	1.46
LG16	232	92.51	0.4	7.27
LG17	231	101.8	0.44	5.33
LG18	327	112.81	0.34	9.09
LG19	216	89.17	0.41	1.76
LG20	351	105.94	0.3	2.28
LG21	310	85.41	0.28	1.95
LG22	238	97.44	0.41	2.57
LG23	150	78.19	0.52	5.38
LG24	340	88.48	0.26	1.52
Maximum	351	127.09	0.58	9.09
Minimum	137	59.96	0.24	1.46
Total	6193	2191.65	8.79	87.99
Average	258	91.32	0.35	3.67

*:The data were cited from our previous report (Yang, et al., 2020)

Table S8. The similarity of corresponding chromosomes or region in the female and male genomes of three Scatophagidae species

Chr	<i>Sc. argus</i>	<i>Sc. tetracanthus</i>	<i>Se. multifasciata</i>
Chr1	99.45	99.82	99.43
Chr2	99.32	99.83	99.44
Chr3	99.42	99.81	99.56
Chr4	99.40	99.76	99.44
Chr5	99.42	99.82	99.44
Chr6	99.45	99.83	99.41
Chr7	99.44	99.84	99.18
Chr8	99.46	99.84	99.44
Chr9	99.47	99.84	99.44
Chr10	99.43	99.84	99.45
Chr11	99.46	99.82	99.48
Chr12	99.36	99.82	99.44
Chr13	99.45	99.76	99.53
Chr14	99.43	99.83	99.49
Chr15	99.40	99.82	99.56
Chr16	99.42	99.79	99.49
Chr17	99.42	99.81	99.71
Chr18	99.40	99.82	99.50
Chr19	99.29	99.83	99.47
Chr20	99.42	99.84	99.60
Chr21	99.43	99.81	99.46
Chr22	99.40	99.80	99.46
Chr23	99.28	99.82	99.60
Chr24	99.20	99.79	99.40
Average	99.40	99.82	99.48
Genome	99.47	99.89	99.51
SDR	98.17	99.64	99.46
<i>dmrt1Y</i> +/-200kb	97.94	99.00	99.47
<i>dmrt1Y</i> +/-100kb	97.89	99.42	98.65

Table S9. The statistics of annotated genes in SD region of *Sc. argus*

Chr	Gene	Start	End
Chr4 of HapY	<i>adamts3</i>	25323205	25439951
Chr4 of HapY	<i>snf212</i>	25492529	25546149
Chr4 of HapY	<i>dmrt2</i>	25620935	25628948
Chr4 of HapY	<i>dmrt3</i>	25635797	25637750
Chr4 of HapY	<i>dmrt1Y</i>	25643756	25679098
Chr4 of HapY	<i>cfap157</i>	25680915	25686662
Chr4 of HapY	<i>kank1</i>	25686834	25754441
Chr4 of HapY	<i>fbp1</i>	25755634	25761166
Chr4 of HapY	<i>ctsl</i>	25773951	25778866
Chr4 of HapY	<i>dapk1</i>	25784595	25869451
Chr4 of HapY	<i>zbed1</i>	25865310	25873642
Chr4 of HapY	<i>atp8b2</i>	25877830	25915556
Chr4 of HapY	<i>trim35</i>	25924530	25926999
Chr4 of HapY	<i>cnnm4</i>	25929022	25967806
Chr4 of HapY	<i>il1b</i>	25972171	25975066
Chr4 of HapY	<i>ckap2l</i>	25976750	25985531
Chr4 of HapY	<i>loc104923460</i>	25989391	25993715
Chr4 of HapY	<i>loc119221051</i>	26000455	26006342
Chr4 of HapY	<i>purb</i>	26017161	26020796
Chr4 of HapY	<i>h2afv</i>	26020804	26026685
Chr4 of HapY	<i>hs3st1</i>	26031610	26054200

Table S10. The statistics of annotated genes in SD region of *Sc. tetracanthus*

Chr	Gene	Start	End
Chr1 of HapY	<i>tomm20</i>	16815752	16817950
Chr1 of HapY	<i>arid4b</i>	16818690	16857062
Chr1 of HapY	<i>ggpps</i>	16857337	16869278
Chr1 of HapY	<i>b3galnt2</i>	16876084	16884938
Chr1 of HapY	<i>gng4</i>	16889995	16898296
Chr1 of HapY	<i>lyst</i>	16900439	16945619
Chr1 of HapY	<i>nid1</i>	16957810	16971259
Chr1 of HapY	<i>gpr137b</i>	16974917	16980331
Chr1 of HapY	<i>egln1</i>	16980421	17001265
Chr1 of HapY	<i>tsnax</i>	17003589	17009979
Chr1 of HapY	<i>disc1</i>	17011656	17013904
Chr1 of HapY	<i>sipal12</i>	17017879	17061769
Chr1 of HapY	<i>map10</i>	17098179	17177733
Chr1 of HapY	<i>ntpcr</i>	17178500	17181187
Chr1 of HapY	<i>sptbn5</i>	17181823	17185059
Chr1 of HapY	<i>npas4</i>	17190140	17219007
Chr1 of HapY	<i>tmem121</i>	17250034	17266191
Chr1 of HapY	<i>pacs1</i>	17343406	17344923
Chr1 of HapY	<i>mrpl2</i>	17406398	17448413
Chr1 of HapY	<i>klc1</i>	17451079	17453731
Chr1 of HapY	<i>ptk7</i>	17455662	17477103
Chr1 of HapY	<i>srf</i>	17479078	17551440
Chr1 of HapY	<i>fam160b1</i>	17552651	17570609
Chr1 of HapY	<i>ablim1</i>	17574296	17582675
Chr1 of HapY	<i>trim11</i>	17583381	17622736
Chr1 of HapY	<i>habp2</i>	17624097	17625360
Chr1 of HapY	<i>trim25</i>	17626805	17633347
Chr1 of HapY	<i>aldh18a1</i>	17633472	17635637
Chr1 of HapY	<i>ate1</i>	17636498	17643456
Chr1 of HapY	<i>fgfr2</i>	17643549	17692136
Chr1 of HapY	<i>wdr11</i>	17718271	17757535
Chr1 of HapY	<i>plpp4</i>	17797022	17802776
Chr1 of HapY	<i>cdh23</i>	17825823	17863664
Chr1 of HapY	<i>EIF3L</i>	17893624	17936910
Chr1 of HapY	<i>SMOC2</i>	17963845	18102648
Chr1 of HapY	<i>DACT2</i>	18104461	18109771
Chr1 of HapY	<i>LRIFIP2</i>	18110933	18132644
Chr1 of HapY	<i>MLH1</i>	18158301	18163016
Chr1 of HapY	<i>FAM83HA</i>	18181127	18201600
Chr1 of HapY	<i>ADTRP</i>	18201859	18207753
Chr1 of HapY	<i>HERC4</i>	18214667	18223844
Chr1 of HapY	<i>COX5B</i>	18224984	18228732

Table S10. The statistics of annotated genes in SD region of *Sc. tetracanthus*

Chr	Gene	Start	End
Chr1 of HapY	<i>dnajc12</i>	18231471	18242000
Chr1 of HapY	<i>sirt1</i>	18339984	18345405
Chr1 of HapY	<i>cacul1</i>	18346341	18366069
Chr1 of HapY	<i>mypn</i>	18366071	18378243
Chr1 of HapY	<i>pkd2l1</i>	18379627	18392361
Chr1 of HapY	<i>tial1</i>	18392267	18395030
Chr1 of HapY	<i>bag3</i>	18397757	18406606
Chr1 of HapY	<i>inpp5f</i>	18411986	18412633
Chr1 of HapY	<i>mcmbp</i>	18413073	18420414
Chr1 of HapY	<i>sec23ip</i>	18422081	18452846
Chr1 of HapY	<i>csgalnact2</i>	18467250	18478059
Chr1 of HapY	<i>ret</i>	18500985	18518207
Chr1 of HapY	<i>hgsnat</i>	18558541	18574195
Chr1 of HapY	<i>pcdb1</i>	18656073	18660907
Chr1 of HapY	<i>sgpl1</i>	18663377	18672927
Chr1 of HapY	<i>neurog3</i>	18674426	18676890
Chr1 of HapY	<i>pdlim1</i>	18677947	18681589
Chr1 of HapY	<i>sh3d5</i>	18682143	18690252
Chr1 of HapY	<i>pik3ap1</i>	18690478	18701180
Chr1 of HapY	<i>fam204a</i>	18703208	18708796
Chr1 of HapY	<i>rab11fip2</i>	18708977	18717155
Chr1 of HapY	<i>emx2</i>	18723511	18730200
Chr1 of HapY	<i>elf3a</i>	18742003	18757177
Chr1 of HapY	<i>fam45a</i>	18770253	18778842
Chr1 of HapY	<i>sfxn4</i>	18779635	18801670
Chr1 of HapY	<i>prdx3</i>	18805012	18809227
Chr1 of HapY	<i>tm9sf3</i>	18809610	18816981
Chr1 of HapY	<i>abhd12</i>	18819426	18825415
Chr1 of HapY	<i>mocos</i>	18825208	18829136
Chr1 of HapY	<i>pcbp3</i>	18853932	18856452
Chr1 of HapY	<i>vwc2</i>	18860058	18891898
Chr1 of HapY	<i>ikzf1</i>	18910172	18916680
Chr1 of HapY	<i>fign1l</i>	18960959	18968628
Chr1 of HapY	<i>ttl</i>	18968796	18982358
Chr1 of HapY	<i>polr1b</i>	18983528	19009106
Chr1 of HapY	<i>nanp</i>	19010616	19033793
Chr1 of HapY	<i>cyp1b1</i>	19034555	19069307
Chr1 of HapY	<i>rmdn2</i>	19074813	19096031
Chr1 of HapY	<i>cdc42ep3</i>	19111044	19116593
Chr1 of HapY	<i>opn3</i>	19116067	19137897
Chr1 of HapY	<i>kmo</i>	19141690	19208564
Chr1 of HapY	<i>ide</i>	19241351	19263575

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Chr	Gene	Start	End
Chr1 of HapY	<i>march5</i>	19268168	19272439
Chr1 of HapY	<i>cpeb3</i>	19301266	19302375
Chr1 of HapY	<i>btaf1</i>	19303826	19304897
Chr1 of HapY	<i>ccnj</i>	19307866	19343809
Chr1 of HapY	<i>znf518a</i>	19356594	19492461
Chr1 of HapY	<i>blnk</i>	19507551	19509040
Chr1 of HapY	<i>hs3st1a</i>	19528185	19562675
Chr1 of HapY	<i>vent1</i>	19611925	19656682
Chr1 of HapY	<i>pv.1</i>	19685159	19705230
Chr1 of HapY	<i>kndc1</i>	19734199	19736381
Chr1 of HapY	<i>adgral</i>	19739413	19869387
Chr1 of HapY	<i>gabrp</i>	19873496	19903767
Chr1 of HapY	<i>cfap46</i>	19905817	19909873
Chr1 of HapY	<i>valopa</i>	19910814	19917018
Chr1 of HapY	<i>nkx6-2</i>	19918057	19985169
Chr1 of HapY	<i>inpp5a</i>	19985332	19994235
Chr1 of HapY	<i>pwwp2b</i>	19998225	20009652
Chr1 of HapY	<i>lrrc27</i>	20033549	20050487
Chr1 of HapY	<i>stk32c</i>	20051708	20058732
Chr1 of HapY	<i>plac9</i>	20059954	20074173
Chr1 of HapY	<i>srr</i>	20095873	20098827
Chr1 of HapY	<i>tmem254</i>	20099614	20103064
Chr1 of HapY	<i>otx5</i>	20104733	20148142
Chr1 of HapY	<i>rhoq</i>	20153971	20197196
Chr1 of HapY	<i>socs5</i>	20202197	20205161
Chr1 of HapY	<i>prop1</i>	20206601	20230270
Chr1 of HapY	<i>mcf2d</i>	20233429	20236779
Chr1 of HapY	<i>ttc7a</i>	20237329	20329027
Chr1 of HapY	<i>muc4</i>	20331673	20335333
Chr1 of HapY	<i>epcam</i>	20553697	20556378
Chr1 of HapY	<i>plekhh2</i>	20557088	20560198
Chr1 of HapY	<i>thada</i>	20561816	20566451
Chr1 of HapY	<i>zfp36l2</i>	20568183	20582679
Chr1 of HapY	<i>hcar2</i>	20583727	20598511
Chr1 of HapY	<i>haao</i>	20608978	20612937
Chr1 of HapY	<i>papolg</i>	20613239	20623448
Chr1 of HapY	<i>rel</i>	20625058	20649721
Chr1 of HapY	<i>pex13</i>	20653994	20656146
Chr1 of HapY	<i>sanbr</i>	20659743	20670970
Chr1 of HapY	<i>xpo1</i>	20673018	20680492
Chr1 of HapY	<i>loc102297702</i>	20680830	20686111
Chr1 of HapY	<i>rnfl22</i>	20756620	20838110

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Chr	Gene	Start	End
Chr1 of HapY	<i>pcgf6</i>	20840233	20883928
Chr1 of HapY	<i>ina</i>	20884160	20905295
Chr1 of HapY	<i>sertad2</i>	20906384	20917710
Chr1 of HapY	<i>slc1a4</i>	20922557	20925869
Chr1 of HapY	<i>smap1</i>	20946304	20953271
Chr1 of HapY	<i>b3gat2</i>	20956327	21044890
Chr1 of HapY	<i>ogfr11</i>	21055214	21057245
Chr1 of HapY	<i>asrg11</i>	21057393	21106079
Chr1 of HapY	<i>rims1</i>	21296534	21342941
Chr1 of HapY	<i>bcl11a</i>	21382882	21398208
Chr1 of HapY	<i>fanc1</i>	21613813	21623723
Chr1 of HapY	<i>vrk2</i>	21659554	21686815
Chr1 of HapY	<i>loc108881720</i>	21686765	21707652
Chr1 of HapY	<i>ccdc85a</i>	21769893	21775360
Chr1 of HapY	<i>hebp2</i>	21842879	21878817
Chr1 of HapY	<i>slc24a3</i>	21883112	21885680
Chr1 of HapY	<i>rin2</i>	21949127	21986924
Chr1 of HapY	<i>loc104933667</i>	21990457	22032027
Chr1 of HapY	<i>ncapd3</i>	22036320	22039637
Chr1 of HapY	<i>calhm2</i>	22041243	22061191
Chr1 of HapY	<i>tubb4b</i>	22061414	22066648
Chr1 of HapY	<i>vps8</i>	22073234	22076360
Chr1 of HapY	<i>zic3</i>	22077838	22120965
Chr1 of HapY	<i>pcca</i>	22123052	22131325
Chr1 of HapY	<i>tm9sf2</i>	22169583	22189067
Chr1 of HapY	<i>piezo1</i>	22257613	22264742
Chr1 of HapY	<i>cdt1</i>	22264956	22270101
Chr1 of HapY	<i>aprt</i>	22272606	22278270
Chr1 of HapY	<i>tk2</i>	22277585	22288800
Chr1 of HapY	<i>tubb6</i>	22289255	22313496
Chr1 of HapY	<i>nvl</i>	22313523	22322523
Chr1 of HapY	<i>degsl</i>	22327675	22336974
Chr1 of HapY	<i>fbxo28</i>	22338636	22349608
Chr1 of HapY	<i>polr1c</i>	22354487	22361947
Chr1 of HapY	<i>gprin2</i>	22365428	22389316
Chr1 of HapY	<i>ndst2</i>	22393750	22428244
Chr1 of HapY	<i>zswim8</i>	22433969	22455565
Chr1 of HapY	<i>prss12</i>	22460624	22465826
Chr1 of HapY	<i>chchd1</i>	22481525	22498454
Chr1 of HapY	<i>rap1gds1</i>	22504980	22526149
Chr1 of HapY	<i>galm</i>	22532966	22571240
Chr1 of HapY	<i>hnrnp11</i>	22579460	22592489

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Chr	Gene	Start	End
Chr1 of HapY	<i>ctu2</i>	22593350	22603688
Chr1 of HapY	<i>mf166</i>	22619928	22626804
Chr1 of HapY	<i>snai2</i>	22627258	22635020
Chr1 of HapY	<i>cyp17a1</i>	22636029	22640702
Chr1 of HapY	<i>borcs7</i>	22642826	22661239
Chr1 of HapY	<i>nt5c2</i>	22666346	22669411
Chr1 of HapY	<i>loc124063885</i>	22674699	22680753
Chr1 of HapY	<i>wbp11</i>	22695013	22740899
Chr1 of HapY	<i>fbxw4</i>	22751462	22758492
Chr1 of HapY	<i>fgf8</i>	22785628	22810540
Chr1 of HapY	<i>slc2a9</i>	22815380	22815787
Chr1 of HapY	<i>lbx1</i>	22891349	22906566
Chr1 of HapY	<i>tlx1</i>	22909374	22919613
Chr1 of HapY	<i>hells</i>	22922054	22932189
Chr1 of HapY	<i>rab1a</i>	22932357	22935128
Chr1 of HapY	<i>cep68</i>	22937132	22943007
Chr1 of HapY	<i>sdhgf4</i>	22962251	22995823
Chr1 of HapY	<i>calhm3</i>	23006816	23021880
Chr1 of HapY	<i>loc109629162</i>	23028142	23140937
Chr1 of HapY	<i>prkg2a</i>	23264872	23276410
Chr1 of HapY	<i>coll3a1</i>	23276855	23356910
Chr1 of HapY	<i>h2afy2</i>	23365534	23388955
Chr1 of HapY	<i>gbf1</i>	23397209	23413343
Chr1 of HapY	<i>pitx3</i>	23419377	23472204
Chr1 of HapY	<i>pnliprp1</i>	23482947	23484916
Chr1 of HapY	<i>hspa12a</i>	23498031	23513757
Chr1 of HapY	<i>loc124053561</i>	23525041	23567653
Chr1 of HapY	<i>eno4</i>	23568582	23615303
Chr1 of HapY	<i>shtn1</i>	23644060	23649724
Chr1 of HapY	<i>atp6v1b2</i>	23669833	23693371
Chr1 of HapY	<i>vax1</i>	23712699	23716334
Chr1 of HapY	<i>pla2g4f</i>	23717012	23731501
Chr1 of HapY	<i>kcnk18</i>	23742031	23772344
Chr1 of HapY	<i>slc18a2</i>	23777534	23828842
Chr1 of HapY	<i>pdzd8</i>	23829566	23844423
Chr1 of HapY	<i>edaradd</i>	23858704	23866360
Chr1 of HapY	<i>loc104929388</i>	23876184	23897423
Chr1 of HapY	<i>exo1</i>	23904044	23913511
Chr1 of HapY	<i>yipf4</i>	23937811	24084535
Chr1 of HapY	<i>birc6</i>	24107342	24359764
Chr1 of HapY	<i>ltbp1</i>	24383778	24492146
Chr1 of HapY	<i>ttc27</i>	24597874	24617964

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Chr	Gene	Start	End
Chr1 of HapY	<i>fam98a</i>	24632358	24633160
Chr1 of HapY	<i>loc115596078</i>	24647765	24671746
Chr1 of HapY	<i>cdh1</i>	24730398	24733448
Chr1 of HapY	<i>cd53</i>	24787527	24792509
Chr1 of HapY	<i>sub1</i>	24808775	24812919
Chr1 of HapY	<i>loc112139785</i>	24812993	24819168
Chr1 of HapY	<i>npr3</i>	24869329	24870019
Chr1 of HapY	<i>pdzd2</i>	24919833	24980699
Chr1 of HapY	<i>golp3</i>	24993674	25008302
Chr1 of HapY	<i>dtx3</i>	25081845	25106792
Chr1 of HapY	<i>isl1</i>	25109253	25118411
Chr1 of HapY	<i>pgbd2</i>	25118234	25125793
Chr1 of HapY	<i>ccdc125</i>	25207663	25208137
Chr1 of HapY	<i>rad17</i>	25232730	25242207
Chr1 of HapY	<i>ak6</i>	25394252	25402321
Chr1 of HapY	<i>ydjc</i>	25455400	25464299
Chr1 of HapY	<i>ube2l3</i>	25546564	25588519
Chr1 of HapY	<i>pias2</i>	25589064	25606771
Chr1 of HapY	<i>arid3a</i>	25606967	25621887
Chr1 of HapY	<i>tesk1</i>	25632513	25658725
Chr1 of HapY	<i>b3galt2</i>	25664759	25678638
Chr1 of HapY	<i>tnc</i>	25704871	25739765
Chr1 of HapY	<i>traf2</i>	25754495	25779993
Chr1 of HapY	<i>rabl6</i>	25851500	25903186
Chr1 of HapY	<i>imp4</i>	25908892	25912050
Chr1 of HapY	<i>araf</i>	26081661	26104639
Chr1 of HapY	<i>orf2</i>	26108985	26113593
Chr1 of HapY	<i>pnpla7</i>	26113649	26141643
Chr1 of HapY	<i>mrpl41</i>	26141649	26147175
Chr1 of HapY	<i>dph7</i>	26148652	26179246
Chr1 of HapY	<i>sh3glb2</i>	26179608	26181407
Chr1 of HapY	<i>lta</i>	26181359	26191871
Chr1 of HapY	<i>megf9</i>	26195858	26225634
Chr1 of HapY	<i>ppp6c</i>	26236162	26240988
Chr1 of HapY	<i>golgal</i>	26241704	26273547
Chr1 of HapY	<i>rpl35</i>	26274383	26281871
Chr1 of HapY	<i>loc119891964</i>	26283466	26303331
Chr1 of HapY	<i>olfml2a</i>	26303544	26306912
Chr1 of HapY	<i>nr6a1</i>	26307512	26311938
Chr1 of HapY	<i>nr5a1</i>	26313373	26319161
Chr1 of HapY	<i>adgrd2</i>	26350098	26373031
Chr1 of HapY	<i>lhx2</i>	26410488	26455292

Table S10. The statistics of annotated genes in SD region of *Sc. tetracanthus*

Chr	Gene	Start	End
Chr1 of HapY	<i>crb2</i>	26479517	26498331
Chr1 of HapY	<i>fpgs</i>	26500370	26537145
Chr1 of HapY	<i>bcl2l16</i>	26604326	26663744
Chr1 of HapY	<i>loc101061694</i>	26687007	26697807
Chr1 of HapY	<i>glipr2</i>	26734677	26757257
Chr1 of HapY	<i>nrde2</i>	26781422	26785688
Chr1 of HapY	<i>trim35</i>	26806160	26832608
Chr1 of HapY	<i>hs3st1b</i>	26842928	26852261
Chr1 of HapY	<i>h2afv</i>	26861406	26865298
Chr1 of HapY	<i>purb</i>	26866972	26870082
Chr1 of HapY	<i>loc104923460</i>	26881908	26887662
Chr1 of HapY	<i>ckap2l</i>	26893075	26893621
Chr1 of HapY	<i>il1b</i>	26903084	26913658
Chr1 of HapY	<i>cnnm4</i>	26929443	26954734
Chr1 of HapY	<i>atp8b2</i>	26957970	26961072
Chr1 of HapY	<i>dapk1</i>	26961365	26964902
Chr1 of HapY	<i>ctsl</i>	26978987	26984191
Chr1 of HapY	<i>fbp2</i>	26987295	26996247
Chr1 of HapY	<i>fbp1</i>	26997273	27000202
Chr1 of HapY	<i>kank1</i>	27005544	27049051
Chr1 of HapY	<i>cfap157</i>	27051546	27061193
Chr1 of HapY	<i>dmrt1Y</i>	27062138	27101459
Chr1 of HapY	<i>dmrt3</i>	27104673	27172902
Chr1 of HapY	<i>dmrt2</i>	27179376	27184971
Chr1 of HapY	<i>snf2l2</i>	27186162	27195901
Chr1 of HapY	<i>pol</i>	27268475	27294748
Chr1 of HapY	<i>adamts3</i>	27302964	27306314
Chr1 of HapY	<i>npffr2</i>	27312795	27318283
Chr1 of HapY	<i>slc4a4</i>	27387013	27430744
Chr1 of HapY	<i>rufy3</i>	27460312	27461439
Chr1 of HapY	<i>grsfl</i>	27487023	27605813
Chr1 of HapY	<i>trim16</i>	27631599	27640106
Chr1 of HapY	<i>mapk1</i>	27670368	27732235
Chr1 of HapY	<i>ypell</i>	27736399	27756114
Chr1 of HapY	<i>ppil2</i>	27756904	27762312
Chr1 of HapY	<i>slc39a14</i>	27765482	27770738
Chr1 of HapY	<i>ascc2</i>	27772888	27800584
Chr1 of HapY	<i>rnf215</i>	27803676	27834672
Chr1 of HapY	<i>sec14l2</i>	27838272	27844627
Chr1 of HapY	<i>unc13b</i>	27851061	27885701
Chr1 of HapY	<i>loc124057552</i>	27887273	27913422
Chr1 of HapY	<i>rusc2</i>	27914122	27923183

Table S10. The statistics of annotated genes in SD region of *Sc. tetracanthus*

Chr	Gene	Start	End
Chr1 of HapY	<i>sh3bgrl</i>	27923215	27930199
Chr1 of HapY	<i>ccl19</i>	27932344	27946258
Chr1 of HapY	<i>wdfy3</i>	27947873	28100816
Chr1 of HapY	<i>cds1</i>	28096640	28103044
Chr1 of HapY	<i>tmem175</i>	28112403	28148734
Chr1 of HapY	<i>zscan20</i>	28150833	28154255
Chr1 of HapY	<i>rasgef1b</i>	28158524	28159991
Chr1 of HapY	<i>prkg2b</i>	28165191	28180071
Chr1 of HapY	<i>bmp3</i>	28170775	28262119
Chr1 of HapY	<i>cunh4orf22</i>	28263708	28292144
Chr1 of HapY	<i>fgf5</i>	28292136	28298411
Chr1 of HapY	<i>prdm8</i>	28306643	28307650
Chr1 of HapY	<i>antxr2</i>	28324946	28327187
Chr1 of HapY	<i>paqr3</i>	28360042	28374448
Chr1 of HapY	<i>bmp2k</i>	28405814	28409350
Chr1 of HapY	<i>fras1</i>	28413218	28443477
Chr1 of HapY	<i>mrpl1</i>	28448542	28476902
Chr1 of HapY	<i>cnot6l</i>	28477225	28485356
Chr1 of HapY	<i>fam102a</i>	28487642	28557753
Chr1 of HapY	<i>slc25a25a</i>	28564106	28575382
Chr1 of HapY	<i>zdhhc12</i>	28575413	28575649
Chr1 of HapY	<i>pkn2</i>	28592708	28598973
Chr1 of HapY	<i>odf2</i>	28632076	28705491
Chr1 of HapY	<i>gle1</i>	28690749	28711230
Chr1 of HapY	<i>ptges2</i>	29517678	29522949
Chr1 of HapY	<i>ralgds</i>	29537561	29563872
Chr1 of HapY	<i>smarcb1</i>	29564687	29571521
Chr1 of HapY	<i>sh2d3c</i>	29580488	29582853
Chr1 of HapY	<i>strbp</i>	29586387	29594130
Chr1 of HapY	<i>gpr21</i>	29606092	29613264
Chr1 of HapY	<i>p2rx7</i>	29615009	29618766
Chr1 of HapY	<i>gstt3</i>	29620019	29621325
Chr1 of HapY	<i>loc100708255</i>	29625344	29626608
Chr1 of HapY	<i>mmp11</i>	29656144	29667901
Chr1 of HapY	<i>loc100692885</i>	29672153	29681449
Chr1 of HapY	<i>loc102079727</i>	29707355	29710751
Chr1 of HapY	<i>tor2a</i>	29714648	29721952
Chr1 of HapY	<i>ptrh1</i>	29722496	29735891
Chr1 of HapY	<i>loc124057810</i>	29737982	29756127
Chr1 of HapY	<i>loc124057819</i>	29757812	29768102
Chr1 of HapY	<i>fam163b</i>	29768900	29773974
Chr1 of HapY	<i>adamts12</i>	29775712	29794181

Table S10. The statistics of annotated genes in SD region of *Sc. tetracanthus*

Chr	Gene	Start	End
Chr1 of HapY	<i>ttc16</i>	29795825	29796719
Chr1 of HapY	<i>slc2a8</i>	29797445	29812242
Chr1 of HapY	<i>hira</i>	29815039	29865430
Chr1 of HapY	<i>il6st</i>	29866297	29892248
Chr1 of HapY	<i>nudt12</i>	29903140	29984296
Chr1 of HapY	<i>slc12a2l</i>	29992680	29996664
Chr1 of HapY	<i>gramd2b</i>	30051110	30078521
Chr1 of HapY	<i>znf608</i>	30079767	30086612
Chr1 of HapY	<i>cep120</i>	30095079	30115187
Chr1 of HapY	<i>ppic</i>	30120340	30125669
Chr1 of HapY	<i>snx2</i>	30135292	30166231
Chr1 of HapY	<i>mf214</i>	30183175	30184313
Chr1 of HapY	<i>sncaip</i>	30198457	30200090
Chr1 of HapY	<i>lox</i>	30211975	30216396
Chr1 of HapY	<i>ddr2</i>	30216935	30222642
Chr1 of HapY	<i>ier3</i>	30225253	30226937
Chr1 of HapY	<i>loc124057473</i>	30231612	30249042
Chr1 of HapY	<i>mf223</i>	30255802	30278363
Chr1 of HapY	<i>piwil2</i>	30318277	30328652
Chr1 of HapY	<i>htr7</i>	30361026	30443435
Chr1 of HapY	<i>atad1a</i>	30443629	30444387
Chr1 of HapY	<i>galnt9</i>	30565750	30830787
Chr1 of HapY	<i>fbrs1l</i>	30844105	30857693
Chr1 of HapY	<i>chfr</i>	30858426	30878518
Chr1 of HapY	<i>loc104921085</i>	30880918	30896336
Chr1 of HapY	<i>golga3</i>	30896467	30909860
Chr1 of HapY	<i>ankle2</i>	30909894	30914655
Chr1 of HapY	<i>pgam5</i>	30914572	30977061
Chr1 of HapY	<i>zdhhc8</i>	30979968	30985215
Chr1 of HapY	<i>ranbp1</i>	30985718	30992774
Chr1 of HapY	<i>trmt2a</i>	30993084	31002622
Chr1 of HapY	<i>dgcr8</i>	31003133	31021556
Chr1 of HapY	<i>tango2</i>	31095921	31220084
Chr1 of HapY	<i>arvcf</i>	31245738	31249034
Chr1 of HapY	<i>txnrd2</i>	31258637	31281921
Chr1 of HapY	<i>gnb1l</i>	31287196	31297085
Chr1 of HapY	<i>tbx1</i>	31304857	31323516

Table S11. The statistics of annotated genes in SD region of *Se. multifasciata*

Chr	Gene	Start	End
Chr18 of HapY genome	<i>sytl4</i>	7683305	7695855
Chr18 of HapY genome	<i>nt5c1a</i>	7697784	7705459
Chr18 of HapY genome	<i>rdh14</i>	7735376	7737155
Chr18 of HapY genome	<i>il6st</i>	7738590	7748733
Chr18 of HapY genome	<i>mggt</i>	7773714	7843237
Chr18 of HapY genome	<i>cnr1</i>	7865972	7869896
Chr18 of HapY genome	<i>akirin2</i>	7870881	7875383
Chr18 of HapY genome	<i>rars2</i>	7876005	7883700
Chr18 of HapY genome	<i>ypel5</i>	7886868	7889491
Chr18 of HapY genome	<i>sipa11l</i>	7904066	7969803
Chr18 of HapY genome	<i>rgs6</i>	7980491	7980935
Chr18 of HapY genome	<i>lama2</i>	8044176	8193864
Chr18 of HapY genome	<i>slc32a1</i>	8195372	8211126
Chr18 of HapY genome	<i>ptprk</i>	8234743	8337239
Chr18 of HapY genome	<i>dlgap2</i>	8345671	8349318
Chr18 of HapY genome	<i>specc1</i>	8355567	8430782
Chr18 of HapY genome	<i>grcc10</i>	8431104	8433556
Chr18 of HapY genome	<i>saysd1</i>	8433599	8434957
Chr18 of HapY genome	<i>bpnt1</i>	8434989	8438827
Chr18 of HapY genome	<i>ppp1c</i>	8437805	8444147
Chr18 of HapY genome	<i>plb1</i>	8444672	8453445
Chr18 of HapY genome	<i>rab15</i>	8483677	8493867
Chr18 of HapY genome	<i>fntb</i>	8494448	8508315
Chr18 of HapY genome	<i>max</i>	8508807	8517893
Chr18 of HapY genome	<i>srsf5</i>	8527708	8533784
Chr18 of HapY genome	<i>susd6</i>	8534552	8563679
Chr18 of HapY genome	<i>dmrt1Y</i>	8589812	8603778
Chr18 of HapY genome	<i>tcla</i>	8623819	8631129
Chr18 of HapY genome	<i>nrde2</i>	8640390	8647245
Chr18 of HapY genome	<i>acot22</i>	8649348	8653452
Chr18 of HapY genome	<i>gpr176</i>	8654392	8665276
Chr18 of HapY genome	<i>thbs1</i>	8714305	8725724
Chr18 of HapY genome	<i>katnbl</i>	8818888	8824396
Chr18 of HapY genome	<i>emc7</i>	8824995	8828958
Chr18 of HapY genome	<i>chrn5b</i>	8858928	8933605
Chr18 of HapY genome	<i>ld</i>	8948209	8965241
Chr18 of HapY genome	<i>grem1</i>	8965920	8966459
Chr18 of HapY genome	<i>scg5</i>	8966897	8970367
Chr18 of HapY genome	<i>arhgap11a</i>	8970663	8973220
Chr18 of HapY genome	<i>acta2</i>	8973321	8978206
Chr18 of HapY genome	<i>ak7</i>	8982394	8990487
Chr18 of HapY genome	<i>scara3</i>	9004488	9017257

Table S11. The statistics of annotated genes in SD region of *Se. multifasciata*

Chr	Gene	Start	End
Chr18 of HapY genome	<i>clu</i>	9023142	9031514
Chr18 of HapY genome	<i>reps1</i>	9032072	9048737
Chr18 of HapY genome	<i>abracl</i>	9050812	9055404
Chr18 of HapY genome	<i>heca</i>	9056424	9064576
Chr18 of HapY genome	<i>mtif3</i>	9062948	9068309
Chr18 of HapY genome	<i>spag5</i>	9072688	9078602
Chr18 of HapY genome	<i>nudt14</i>	9103297	9125988
Chr18 of HapY genome	<i>jag2</i>	9135696	9177426
Chr18 of HapY genome	<i>esr2</i>	9200385	9211629
Chr18 of HapY genome	<i>syne2</i>	9226454	9270041
Chr18 of HapY genome	<i>hadha</i>	9300398	9309515
Chr18 of HapY genome	<i>hadhb</i>	9309741	9316459
Chr18 of HapY genome	<i>loc119264033</i>	9375937	9379122
Chr18 of HapY genome	<i>tfap2d</i>	9403833	9419601
Chr18 of HapY genome	<i>tfap2b</i>	9427715	9438657
Chr18 of HapY genome	<i>lrp11</i>	9485471	9543878
Chr18 of HapY genome	<i>pcmt</i>	9544079	9550489
Chr18 of HapY genome	<i>lats1</i>	9554548	9563733
Chr18 of HapY genome	<i>rab10</i>	9560974	9576436
Chr18 of HapY genome	<i>kif3c</i>	9581145	9599843
Chr18 of HapY genome	<i>tlr5</i>	9600961	9603767
Chr18 of HapY genome	<i>dtmb</i>	9606479	9635226
Chr18 of HapY genome	<i>dnmt3a</i>	9636990	9656094
Chr18 of HapY genome	<i>sun1</i>	9673034	9682351
Chr18 of HapY genome	<i>dpysl5</i>	9685327	9704084
Chr18 of HapY genome	<i>mapre3</i>	9704784	9713657
Chr18 of HapY genome	<i>tmem214</i>	9714705	9727805
Chr18 of HapY genome	<i>gtf2h5</i>	9730236	9730594
Chr18 of HapY genome	<i>serac1</i>	9731551	9739007
Chr18 of HapY genome	<i>myct1</i>	9739231	9747223
Chr18 of HapY genome	<i>esr1</i>	9867668	9880243
Chr18 of HapY genome	<i>arnt1</i>	9881255	9885637
Chr18 of HapY genome	<i>zbtb2</i>	9888175	9897602
Chr18 of HapY genome	<i>akap12</i>	9897819	9910180
Chr18 of HapY genome	<i>methfd11</i>	9941038	9975576
Chr18 of HapY genome	<i>stx11</i>	9976391	9979807
Chr18 of HapY genome	<i>utrn</i>	9981230	9982132
Chr18 of HapY genome	<i>epm2a</i>	10183830	10190280
Chr18 of HapY genome	<i>aloxe3</i>	10191201	10202458
Chr18 of HapY genome	<i>fbxo30</i>	10228605	10237607
Chr18 of HapY genome	<i>grm1</i>	10237721	10268350
Chr18 of HapY genome	<i>rab32</i>	10269094	10282040

Table S11. The statistics of annotated genes in SD region of *Se. multifasciata*

Chr	Gene	Start	End
Chr18 of HapY genome	<i>adgb</i>	10283272	10318043
Chr18 of HapY genome	<i>stxbp5</i>	10327613	10411680
Chr18 of HapY genome	<i>sash1</i>	10477060	10626149

Table S12. The expression of sex determining region genes in different tissues of *Sc. argus*

Gene	Ovary- 1_fpk	Ovary- 2_fpk	Ovary- 3_fpk	Testis- 1_fpk	Testis- 2_fpk	Testis- 3_fpk
<i>adamts3</i>	0.12	0.06	0.18	0.76	0.73	1.38
<i>snf2l2</i>	0.00	0.06	0.04	5.86	0.00	5.12
<i>dmrt2</i>	0.13	0.00	0.07	0.44	0.14	1.60
<i>dmrt3</i>	0.00	0.00	0.00	2.40	0.17	1.64
<i>dmrt1Y</i>	0.00	0.01	0.00	5.27	15.06	6.97
<i>cfap157</i>	0.04	0.00	0.00	4.62	15.95	7.06
<i>kank1</i>	0.00	0.00	0.00	5.79	0.00	6.02
<i>fbp1</i>	6.83	7.33	15.19	6.07	0.38	8.16
<i>ctsl</i>	142.57	149.11	130.73	49.33	25.58	51.27
<i>dapk1</i>	2.41	2.46	3.62	4.85	9.60	3.95
<i>zbed1</i>	0.00	0.00	0.00	1.24	0.00	0.76
<i>atp8b2</i>	0.02	0.03	0.00	0.74	0.78	1.87
<i>trim35</i>	0.73	0.00	0.00	2.04	3.24	0.22
<i>cnnm4</i>	0.68	0.85	1.41	2.14	1.97	2.48
<i>il1b</i>	0.07	0.00	0.00	0.68	0.88	0.50
<i>ckap2l</i>	15.34	11.38	19.46	3.70	4.25	4.05
<i>loc104923460</i>	0.35	0.12	0.00	47.76	19.45	20.33
<i>loc119221051</i>	0.01	0.02	0.00	0.38	3.84	0.50
<i>purb</i>	3.19	4.64	2.52	20.15	24.86	19.79
<i>h2afv</i>	56.38	60.55	57.21	68.50	56.30	58.35
<i>hs3st1</i>	0.00	0.00	0.15	2.98	2.62	4.75

Table S12. The expression of sex determining region genes in different tissues of *Sc. argus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>adamts3</i>	1.51	1.08	5.77	5.59
<i>snf2l2</i>	6.86	7.34	16.78	17.56
<i>dmrt2</i>	0.00	0.00	0.00	0.00
<i>dmrt3</i>	0.00	0.00	0.26	0.19
<i>dmrt1</i>	0.00	0.00	0.00	0.00
<i>cfap157</i>	0.03	0.10	1.52	1.48
<i>kank1</i>	92.78	54.88	27.13	19.01
<i>fbp1</i>	2.34	2.90	1.49	0.51
<i>ctsl</i>	72.98	89.62	47.42	44.93
<i>dapk1</i>	0.52	0.82	13.50	9.96
<i>zbed1</i>	0.00	0.51	0.57	0.09
<i>atp8b2</i>	1.61	2.42	2.20	2.04
<i>trim35</i>	0.24	0.24	0.00	0.20
<i>cnnm4</i>	1.00	0.87	4.98	7.83
<i>il1b</i>	0.10	0.09	0.05	0.62
<i>ckap2l</i>	0.04	0.12	0.22	0.39
<i>loc104923460</i>	0.40	0.92	9.50	20.69
<i>loc119221051</i>	0.08	0.21	0.04	0.06
<i>purb</i>	2.73	3.19	17.28	17.54
<i>h2afv</i>	8.92	7.77	32.07	35.47
<i>hs3st1</i>	1.98	3.73	1.95	5.28

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1_fpkm	Ovary- 2_fpkm	Ovary- 3_fpkm	Testis- 1_fpkm	Testis- 2_fpkm	Testis- 3_fpkm
<i>tomm20</i>	3.99	4.60	2.29	7.49	10.42	4.90
<i>arid4b</i>	0.23	0.33	0.37	13.56	11.67	12.14
<i>ggpps</i>	50.96	42.69	41.80	11.19	9.94	10.53
<i>b3galnt2</i>	1.74	1.62	2.91	7.60	5.80	7.57
<i>gng4</i>	0.00	0.00	0.00	0.84	1.17	0.76
<i>lyst</i>	0.23	0.15	0.24	9.15	5.98	10.72
<i>nid1</i>	0.50	0.48	0.22	9.97	6.84	8.31
<i>gpr137b</i>	2.79	2.69	3.92	4.64	5.24	4.68
<i>egln1</i>	59.50	54.79	47.15	28.36	28.30	27.19
<i>tsnax</i>	56.15	54.11	40.49	44.08	45.35	37.18
<i>disc1</i>	0.02	0.00	0.00	1.77	1.21	1.58
<i>sipal12</i>	0.24	0.15	0.24	6.44	5.05	6.09
<i>map10</i>	0.84	1.76	0.70	8.95	14.86	9.52
<i>ntpcr</i>	36.64	37.46	34.44	29.55	33.68	23.31
<i>sptbn5</i>	0.73	0.42	0.34	12.27	9.40	10.87
<i>npas4</i>	0.00	0.00	0.00	1.14	0.99	0.98
<i>tmem121</i>	0.00	0.00	0.00	0.00	0.04	0.03
<i>pacs1</i>	0.58	0.36	0.59	23.20	18.74	24.62
<i>mrpl2</i>	206.94	161.62	130.06	34.44	31.41	29.82
<i>klc1</i>	9.65	7.82	12.37	15.78	14.46	14.51
<i>ptk7</i>	2.12	2.02	2.83	7.15	5.11	5.33
<i>sf</i>	8.73	10.08	10.31	6.65	5.74	6.54
<i>fam160b1</i>	8.22	8.71	6.80	12.43	15.02	10.60
<i>ablim1</i>	0.00	0.05	0.11	3.27	3.71	3.26
<i>trim11</i>	0.00	0.00	0.00	0.14	0.07	0.17
<i>habp2</i>	0.00	0.00	0.00	0.12	0.09	0.07
<i>trim25</i>	0.00	0.00	0.00	0.34	0.37	0.13
<i>aldh18a1</i>	7.56	7.73	9.48	29.25	18.71	27.45
<i>ate1</i>	10.58	11.44	12.33	9.09	9.86	8.60
<i>fgfr2</i>	0.10	0.17	0.13	6.24	4.93	6.17
<i>wdr11</i>	0.94	0.60	1.28	11.07	9.65	9.41
<i>plpp4</i>	1.90	1.88	2.54	2.35	2.20	1.42
<i>cdh23</i>	2.55	1.77	2.05	3.73	2.20	3.14
<i>EIF3L</i>	196.21	171.22	168.07	59.26	44.00	52.44
<i>smoc2</i>	0.13	0.06	0.05	1.76	1.25	1.44
<i>dact2</i>	0.08	0.26	0.10	5.88	4.94	5.74
<i>lrrfip2</i>	17.68	18.56	22.22	100.27	136.36	124.88
<i>mlh1</i>	21.28	20.51	26.21	12.94	10.24	8.11
<i>fam83ha</i>	0.04	0.19	0.12	5.56	6.84	4.18

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>adtrp</i>	0.00	0.00	0.00	4.48	7.56	4.41
<i>herc4</i>	9.12	8.62	13.40	70.63	88.00	76.00
<i>cox5b</i>	1.32	1.11	0.49	24.03	20.82	15.65
<i>dnajc12</i>	0.74	0.90	0.67	4.43	8.29	3.17
<i>sirt1</i>	23.24	22.18	25.85	12.18	11.33	11.72
<i>cacul1</i>	0.62	1.18	0.85	5.89	6.99	4.53
<i>mypn</i>	0.09	0.24	0.13	1.45	1.44	1.46
<i>pkd2l1</i>	29.72	51.09	20.89	0.32	0.45	0.33
<i>tial1</i>	4.31	6.04	4.28	11.67	16.17	9.14
<i>bag3</i>	0.38	0.70	0.73	18.46	23.77	24.92
<i>inpp5f</i>	0.06	0.04	0.09	4.47	4.31	3.88
<i>mcm6p</i>	102.80	94.10	119.79	36.08	25.69	34.18
<i>sec23ip</i>	9.66	9.19	12.07	8.60	7.11	6.17
<i>csgalnact2</i>	6.30	7.10	5.72	18.38	15.73	18.95
<i>ret</i>	0.05	0.00	0.06	6.35	5.81	4.65
<i>hgsnat</i>	0.61	0.44	0.07	0.07	0.15	0.15
<i>pcdb1</i>	65.79	77.31	62.16	3.82	2.50	2.62
<i>sgpl1</i>	3.60	3.47	4.95	25.04	19.43	19.96
<i>neurog3</i>	0.00	0.00	0.00	0.29	0.11	0.16
<i>pdlim1</i>	139.28	134.04	128.81	13.74	15.04	13.55
<i>sh3d5</i>	0.06	0.05	0.06	7.16	7.25	5.09
<i>pik3ap1</i>	0.39	0.29	0.48	19.66	24.98	18.70
<i>fam204a</i>	11.58	14.65	8.59	17.14	32.57	13.76
<i>rab11fip2</i>	0.15	0.07	0.12	4.82	4.67	3.74
<i>emx2</i>	0.24	0.47	0.38	4.41	3.78	3.13
<i>EIF3A</i>	81.98	81.51	125.76	106.06	85.68	101.16
<i>fam45a</i>	2.09	2.68	2.29	6.19	7.69	5.74
<i>sfxn4</i>	12.23	16.31	12.40	3.15	6.80	3.86
<i>prdx3</i>	131.32	116.10	139.35	62.22	55.53	58.90
<i>tm9sf3</i>	2.51	2.42	2.08	32.30	49.04	36.14
<i>abhd12</i>	2.95	2.51	3.92	2.83	4.60	2.75
<i>mocos</i>	0.09	0.19	0.10	7.72	7.01	6.18
<i>pcbp3</i>	0.00	0.05	0.00	0.62	0.37	0.40
<i>vwc2</i>	0.05	0.05	0.09	2.44	1.27	2.53
<i>ikzf1</i>	0.00	0.04	0.03	3.25	2.11	2.33
<i>fign1l</i>	172.31	159.26	224.08	16.16	15.20	14.37
<i>ttl</i>	0.65	0.64	0.56	3.82	4.75	3.02
<i>polr1b</i>	42.96	33.97	45.73	15.74	12.02	15.01
<i>nanp</i>	38.07	40.53	29.67	4.69	3.29	3.81
<i>cyp11b1</i>	0.03	0.00	0.07	0.78	0.56	1.35
<i>rmdn2</i>	0.44	0.60	0.53	1.65	1.01	1.11

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>cdc42ep3</i>	0.28	0.17	0.12	16.86	12.43	9.88
<i>opn3</i>	0.12	0.07	0.17	2.82	2.98	1.94
<i>kmo</i>	0.40	0.58	0.36	3.47	4.29	3.73
<i>ide</i>	2.80	3.26	3.75	48.88	73.59	56.52
<i>march5</i>	18.74	17.95	26.13	13.87	11.35	13.91
<i>cpeb3</i>	0.20	0.24	0.30	4.55	2.96	3.82
<i>btafl1</i>	6.76	7.57	10.80	22.16	18.58	27.73
<i>ccnj</i>	98.69	84.75	88.18	8.30	6.16	8.33
<i>znf518a</i>	0.35	0.39	0.25	6.68	8.80	6.07
<i>blnk</i>	0.02	0.04	0.10	1.23	2.53	0.81
<i>hs3st1a</i>	0.00	0.00	0.00	1.90	2.23	1.47
<i>vent1</i>	0.00	0.00	0.00	0.54	1.18	0.36
<i>pv.1</i>	0.87	0.75	0.39	0.33	0.29	0.66
<i>kndc1</i>	0.03	0.05	0.02	3.48	2.75	2.69
<i>adgral</i>	3.32	2.37	2.63	7.81	5.09	7.61
<i>gabbrp</i>	0.00	0.00	0.00	0.82	0.90	0.65
<i>cfap46</i>	0.32	0.13	0.49	24.68	28.11	29.55
<i>valopa</i>	0.00	0.00	0.00	2.09	1.66	1.67
<i>nkx6-2</i>	0.29	0.50	0.67	2.11	1.70	1.50
<i>inpp5a</i>	0.82	1.83	1.76	7.20	6.57	6.16
<i>pwwp2b</i>	7.94	11.87	15.88	8.77	8.68	7.79
<i>lrrc27</i>	1.79	1.88	1.17	31.11	71.06	35.31
<i>stk32c</i>	0.15	0.10	0.02	4.23	4.85	3.36
<i>plac9</i>	0.29	0.65	0.38	1.32	1.46	0.80
<i>srr</i>	0.00	0.00	0.00	0.03	0.17	0.03
<i>tmem254</i>	54.58	48.97	43.77	6.27	9.74	5.48
<i>otx5</i>	0.00	0.08	0.00	0.49	0.00	0.00
<i>rhoq</i>	0.02	0.09	0.12	2.13	3.04	2.03
<i>socs5</i>	2.43	1.76	2.92	13.63	12.33	15.36
<i>prop1</i>	0.00	0.00	0.00	0.63	0.49	0.30
<i>mcfcd2</i>	47.18	47.97	30.98	5.25	7.11	3.88
<i>ttc7a</i>	0.02	0.04	0.06	3.13	2.55	1.98
<i>muc4</i>	0.03	0.05	0.02	0.72	0.98	1.06
<i>epcam</i>	436.24	451.51	532.23	47.61	45.93	41.19
<i>plekhh2</i>	0.27	0.22	0.18	9.39	6.31	8.39
<i>thada</i>	11.60	9.28	17.01	7.47	5.35	6.73
<i>zfp36l2</i>	2.38	2.30	3.25	13.90	9.63	10.18
<i>hcar2</i>	0.00	0.00	0.00	0.06	0.07	0.00
<i>haao</i>	0.04	0.00	0.00	0.25	0.51	0.43
<i>papolg</i>	2.48	3.14	3.17	14.37	16.20	11.88
<i>rel</i>	0.18	0.13	0.40	15.10	15.25	15.29

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>pex13</i>	51.85	52.68	70.41	20.83	21.62	18.86
<i>sanbr</i>	0.24	0.43	0.43	24.19	24.20	22.26
<i>xpol</i>	5.50	5.51	10.20	29.13	28.19	27.73
<i>loc102297702</i>	1.58	2.79	2.51	113.25	251.85	150.37
<i>mf122</i>	0.10	0.16	0.12	2.89	3.21	2.44
<i>pcgf6</i>	10.42	8.54	6.25	13.39	18.17	12.98
<i>ina</i>	0.17	1.44	0.76	7.90	4.91	5.99
<i>sertad2</i>	0.00	0.05	0.04	3.57	2.63	2.65
<i>slc1a4</i>	0.00	0.00	0.00	0.09	0.15	0.11
<i>smap1</i>	5.07	7.12	4.57	20.80	12.56	22.79
<i>b3gat2</i>	1.11	0.51	0.40	1.49	1.70	2.34
<i>ogfrl1</i>	0.08	0.07	0.05	12.18	19.38	11.78
<i>asrgl1</i>	20.85	16.01	20.33	13.94	9.02	14.77
<i>rims1</i>	0.29	0.30	0.27	19.73	18.11	19.29
<i>bcl11a</i>	0.02	0.03	0.00	2.16	1.07	1.37
<i>fanc1</i>	12.09	13.22	13.77	17.93	20.48	15.51
<i>vrk2</i>	4.00	3.89	3.25	15.70	17.61	12.74
<i>loc108881720</i>	0.00	0.00	0.12	5.99	8.82	5.55
<i>ccdc85a</i>	0.03	0.04	0.03	2.56	1.27	2.41
<i>hebp2</i>	0.39	0.54	0.34	1.11	1.22	0.72
<i>slc24a3</i>	0.02	0.04	0.04	2.47	2.90	1.77
<i>rin2</i>	0.40	0.18	0.28	9.18	6.68	7.57
<i>loc104933667</i>	7.81	5.78	5.76	5.17	5.10	5.92
<i>ncapd3</i>	12.61	12.12	21.80	21.08	16.63	18.48
<i>calhm2</i>	0.00	0.00	0.00	0.26	0.21	0.05
<i>tubb4b</i>	0.77	0.32	1.46	69.89	81.61	46.89
<i>vps8</i>	8.79	8.69	12.54	12.00	12.94	13.33
<i>zic3</i>	1.36	0.98	1.03	11.33	7.34	10.97
<i>pcca</i>	38.74	35.64	45.08	24.82	21.15	23.04
<i>tm9sf2</i>	2.91	3.48	3.91	13.34	13.28	9.69
<i>piezo1</i>	0.34	0.25	0.40	2.51	2.40	2.24
<i>cdt1</i>	120.65	114.69	117.53	16.34	13.05	15.83
<i>aprt</i>	7.07	8.04	8.44	6.92	10.33	4.94
<i>tk2</i>	4.28	4.28	2.68	23.83	22.26	26.57
<i>tubb6</i>	41.48	39.91	45.56	751.79	525.84	887.52
<i>nvl</i>	23.74	22.54	29.57	9.25	8.27	8.49
<i>degs1</i>	7.78	8.44	6.17	16.54	19.00	14.90
<i>fbxo28</i>	5.62	6.00	7.86	8.46	10.11	7.44
<i>polr1c</i>	88.55	87.51	56.92	16.75	20.10	14.66
<i>gprin2</i>	0.00	0.00	0.07	0.25	0.12	0.24
<i>ndst2</i>	2.77	2.10	3.52	14.66	10.20	13.97

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>zswim8</i>	8.87	5.66	12.04	51.89	33.17	64.03
<i>prss12</i>	0.42	0.30	0.55	1.60	1.04	0.92
<i>chchd1</i>	55.36	68.49	42.76	7.94	13.93	5.53
<i>rap1gds1</i>	0.11	0.08	0.12	0.36	0.40	0.22
<i>galm</i>	16.90	18.42	14.78	10.07	7.26	8.75
<i>hnrnp1l</i>	0.06	0.11	0.16	9.95	5.09	9.24
<i>ctu2</i>	13.70	8.08	10.85	5.17	4.60	4.45
<i>rnfl66</i>	0.65	0.70	0.61	3.64	3.71	5.20
<i>snai2</i>	0.00	0.00	0.00	1.70	1.95	0.83
<i>cyp17a1</i>	0.48	0.22	0.08	71.98	48.40	59.51
<i>borcs7</i>	1.81	1.81	1.33	5.71	4.42	4.52
<i>nt5c2</i>	0.17	0.23	0.17	10.13	8.50	8.09
<i>loc124063885</i>	0.86	0.79	2.82	130.09	103.38	90.35
<i>wbp1l</i>	3.49	2.66	2.94	27.37	33.16	29.30
<i>fbxw4</i>	17.39	16.71	14.53	15.45	18.72	12.31
<i>fgf8</i>	0.00	0.07	0.00	1.59	1.89	2.58
<i>slc2a9</i>	0.04	0.00	0.00	0.20	0.13	0.17
<i>lbx1</i>	0.07	0.08	0.07	0.72	0.48	0.67
<i>tlx1</i>	0.00	0.08	0.00	0.72	0.44	0.58
<i>hells</i>	12.61	11.20	16.45	36.57	38.32	27.07
<i>rab1a</i>	8.89	11.64	6.93	57.96	87.76	54.09
<i>cep68</i>	6.36	4.34	6.64	8.23	8.40	9.50
<i>sdhaf4</i>	40.09	48.22	37.40	31.02	48.81	19.16
<i>calhm3</i>	0.45	0.22	0.13	0.57	0.28	0.11
<i>loc109629162</i>	0.05	0.04	0.03	0.56	0.47	0.29
<i>prkg2a</i>	0.00	0.00	0.00	0.26	0.38	0.26
<i>col13a1</i>	0.00	0.00	0.03	0.76	0.68	0.39
<i>h2afy2</i>	10.34	13.09	13.38	99.06	88.63	81.84
<i>gbf1</i>	1.59	1.28	2.29	7.30	5.52	7.59
<i>pitx3</i>	0.00	0.16	0.07	1.76	1.48	1.84
<i>pnliprp1</i>	7.03	15.71	2.33	0.24	0.09	0.34
<i>hspa12a</i>	0.40	0.56	0.53	5.45	4.17	3.09
<i>loc124053561</i>	0.33	0.30	0.06	5.37	3.57	5.24
<i>eno4</i>	0.23	0.26	0.42	50.03	89.79	56.18
<i>shn1</i>	1.33	0.72	0.71	3.11	3.52	2.16
<i>atp6v1b2</i>	22.69	20.53	26.21	23.53	17.64	19.57
<i>vax1</i>	0.00	0.00	0.00	0.33	0.00	0.00
<i>pla2g4f</i>	0.00	0.03	0.03	0.06	0.03	0.00
<i>kcnk18</i>	0.00	0.06	0.16	1.40	0.80	1.36
<i>slc18a2</i>	0.00	0.00	0.00	0.71	1.54	0.89
<i>pdzd8</i>	0.96	0.56	1.11	8.30	4.67	6.05

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>edaradd</i>	0.27	0.66	0.40	2.47	3.75	1.90
<i>loc104929388</i>	0.00	0.00	0.00	0.11	0.02	0.03
<i>exo1</i>	21.51	20.12	15.02	9.42	12.17	11.84
<i>yipf4</i>	16.30	21.47	17.99	10.00	22.50	9.24
<i>birc6</i>	2.69	1.94	3.06	17.35	13.25	19.12
<i>ltbp1</i>	0.06	0.17	0.04	2.54	1.67	2.17
<i>ttc27</i>	14.78	12.62	24.81	6.90	6.59	5.20
<i>fam98a</i>	13.06	14.47	16.91	13.63	12.42	10.83
<i>loc115596078</i>	5.92	7.05	6.29	4.16	4.74	3.14
<i>cdh1</i>	10.60	8.24	9.56	7.17	4.74	4.80
<i>cd53</i>	0.00	0.08	0.00	0.00	0.08	0.00
<i>sub1</i>	42.46	50.32	25.64	28.99	40.81	23.61
<i>loc112139785</i>	0.23	0.13	0.11	0.45	2.10	0.47
<i>npr3</i>	0.53	0.60	0.52	3.99	4.28	3.08
<i>pdzd2</i>	0.19	0.11	0.09	2.32	1.51	0.95
<i>golp3</i>	8.98	7.63	6.36	9.10	10.17	8.02
<i>dtx3</i>	0.05	0.00	0.00	1.32	1.40	0.91
<i>isl1</i>	0.06	0.07	0.12	5.71	3.87	7.97
<i>pgbd2</i>	0.00	0.00	0.00	0.05	0.05	0.04
<i>ccdc125</i>	0.14	0.26	0.31	1.83	2.52	1.77
<i>rad17</i>	14.71	14.25	18.35	22.01	26.60	17.77
<i>ak6</i>	8.42	9.01	7.99	4.88	4.66	3.65
<i>ydjc</i>	0.72	0.59	0.26	4.15	4.29	3.90
<i>ube2l3</i>	52.43	79.91	61.38	37.72	47.75	29.99
<i>pias2</i>	5.33	5.93	4.80	8.66	6.54	7.74
<i>arid3a</i>	0.04	0.00	0.00	1.46	0.94	0.98
<i>tesk1</i>	0.06	0.19	0.00	3.92	5.67	3.17
<i>b3galt2</i>	0.42	0.41	0.47	1.71	2.15	1.49
<i>tnc</i>	0.06	0.05	0.04	0.78	0.64	0.61
<i>traf2</i>	7.66	4.65	4.65	7.16	7.34	5.58
<i>rabl6</i>	0.78	1.00	0.86	15.16	17.23	11.71
<i>imp4</i>	92.41	96.52	75.93	21.12	23.54	17.68
<i>araf</i>	2.72	2.30	2.67	7.73	9.34	8.18
<i>orf2</i>	0.00	0.00	0.07	2.89	1.97	0.88
<i>pnpla7</i>	1.40	0.92	0.93	9.11	6.96	9.78
<i>mrpl4l</i>	18.76	14.02	15.49	13.92	13.51	12.39
<i>dph7</i>	82.49	65.14	33.28	29.09	22.76	27.20
<i>sh3glb2</i>	2.81	3.32	3.53	4.66	5.67	3.78
<i>lta</i>	0.05	0.13	0.05	1.86	3.27	2.44
<i>megf9</i>	0.47	0.47	0.43	4.42	4.74	3.92
<i>ppp6c</i>	0.78	0.69	0.77	56.31	70.98	51.02

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>golgal</i>	1.60	1.60	2.30	7.56	8.08	7.54
<i>rpl35</i>	1222.24	1078.16	488.00	714.68	533.20	698.03
<i>loc119891964</i>	0.00	0.00	0.00	0.18	0.10	0.15
<i>olfml2a</i>	0.06	0.08	0.07	3.52	4.10	3.12
<i>nr6a1</i>	0.07	0.29	0.07	1.57	0.35	1.23
<i>nr5a1</i>	11.53	10.60	9.83	16.07	11.40	12.20
<i>adgrd2</i>	0.00	0.00	0.00	0.45	0.58	0.51
<i>lhx2</i>	0.76	0.17	1.35	7.52	3.02	5.29
<i>crb2</i>	0.03	0.01	0.01	0.54	0.37	0.38
<i>fpgs</i>	0.00	0.00	0.00	0.38	0.42	0.24
<i>bcl2l16</i>	0.00	0.00	0.00	0.13	0.17	0.15
<i>loc101061694</i>	5016.14	4165.59	3820.73	1421.72	995.97	1278.52
<i>glipr2</i>	0.00	0.00	0.10	1.37	1.84	0.99
<i>nrde2</i>	6.79	6.19	9.40	12.19	10.87	11.95
<i>trim35</i>	0.00	0.00	0.00	0.13	0.15	0.08
<i>hs3st1b</i>	0.43	0.55	0.24	9.36	9.80	8.51
<i>h2afv</i>	26.36	29.64	32.77	67.47	72.42	44.15
<i>purb</i>	2.69	3.78	3.82	19.85	17.39	18.20
<i>loc104923460</i>	1.84	2.91	1.99	13.01	13.68	7.53
<i>ckap2l</i>	13.46	30.55	39.25	17.89	22.34	17.21
<i>il1b</i>	0.00	0.10	0.41	0.32	0.35	0.23
<i>cnnm4</i>	0.62	0.59	0.85	2.64	2.03	2.48
<i>atp8b2</i>	0.10	0.10	0.19	2.29	1.71	1.82
<i>dapk1</i>	1.21	1.00	1.42	17.99	16.80	23.30
<i>ctsl</i>	59.18	66.83	109.37	47.89	34.16	35.37
<i>fbp2</i>	0.00	0.00	0.00	0.10	0.06	0.04
<i>fbp1</i>	161.02	138.05	146.96	19.58	14.09	17.24
<i>kank1</i>	2.77	3.31	4.61	4.94	3.54	4.48
<i>cfap157</i>	0.69	2.08	0.61	28.29	38.43	33.64
<i>dmrt1Y</i>	0.16	0.09	0.00	32.98	47.61	32.52
<i>dmrt3</i>	0.24	0.05	0.05	3.83	2.71	3.79
<i>dmrt2</i>	0.11	0.04	0.11	3.73	4.57	3.77
<i>snf2l2</i>	1.52	1.66	2.55	32.58	31.81	37.21
<i>pol</i>	0.00	0.00	0.00	0.15	0.05	0.08
<i>adamts3</i>	0.03	0.02	0.02	1.05	1.16	0.91
<i>npffr2</i>	0.00	0.00	0.00	0.05	0.16	0.08
<i>slc4a4</i>	0.12	0.20	0.15	1.35	1.47	1.19
<i>rufy3</i>	3.81	4.54	4.09	11.29	11.73	8.10
<i>grsf1</i>	111.55	123.58	57.22	14.05	15.50	11.88
<i>trim16</i>	0.04	0.04	0.00	1.45	1.19	0.72
<i>mapk1</i>	0.93	1.12	1.39	11.25	9.62	13.03

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>ypel1</i>	0.63	0.78	0.68	9.28	11.99	10.12
<i>ppil2</i>	71.72	87.02	103.91	24.32	27.44	20.09
<i>slc39a14</i>	2.74	2.61	3.34	10.36	7.09	10.15
<i>ascc2</i>	4.52	4.69	3.51	21.77	17.07	20.32
<i>mf215</i>	1.50	0.78	0.79	6.66	5.67	7.48
<i>sec14l2</i>	0.04	0.00	0.02	1.04	1.65	1.34
<i>unc13b</i>	0.13	0.13	0.12	0.33	0.31	0.25
<i>loc124057552</i>	2408.34	2054.10	2890.14	24.83	11.66	36.02
<i>rusc2</i>	0.77	0.57	0.85	10.37	7.12	9.86
<i>sh3bgrl</i>	0.00	0.07	0.47	4.44	5.94	3.04
<i>ccl19</i>	0.00	0.25	0.00	0.44	0.00	0.00
<i>wdfy3</i>	0.45	0.35	0.54	6.54	3.49	6.53
<i>cds1</i>	0.12	0.13	0.12	6.06	6.13	5.95
<i>tmem175</i>	0.73	1.18	0.64	14.16	11.33	16.28
<i>zscan20</i>	17.95	20.47	17.01	7.28	7.16	5.67
<i>rasgef1b</i>	2.32	1.96	1.09	8.30	9.06	5.77
<i>prkg2b</i>	0.03	0.03	0.03	1.54	1.14	1.43
<i>bmp3</i>	0.09	0.00	0.04	0.89	0.84	0.72
<i>cunh4orf22</i>	13.89	12.46	8.25	171.82	220.86	199.14
<i>fgf5</i>	0.00	0.00	0.00	1.00	1.00	1.23
<i>prdm8</i>	0.00	0.00	0.00	1.67	1.31	1.07
<i>antxr2</i>	1.88	1.80	2.06	6.85	6.24	6.21
<i>paqr3</i>	0.55	0.89	1.02	16.92	13.72	12.36
<i>bmp2k</i>	0.89	0.87	0.93	5.58	4.08	5.46
<i>fras1</i>	0.11	0.14	0.16	4.40	2.40	3.49
<i>mrpl1</i>	115.01	121.30	84.11	25.64	22.51	20.17
<i>cnot6l</i>	0.57	0.51	0.69	3.10	3.33	2.64
<i>fam102a</i>	0.17	0.29	0.18	6.06	6.66	4.88
<i>slc25a25a</i>	87.36	133.68	128.58	5.84	6.58	5.83
<i>zdhhc12</i>	0.48	0.09	0.08	1.47	0.86	1.38
<i>pkn2</i>	0.15	0.06	0.10	7.88	6.21	5.89
<i>odf2</i>	1.88	2.48	3.55	41.24	53.55	51.84
<i>gle1</i>	19.64	19.85	27.90	38.66	48.32	48.05
<i>ptges2</i>	33.64	33.74	26.22	10.33	11.09	8.03
<i>ralgds</i>	0.18	0.08	0.15	8.99	4.19	9.05
<i>smarcb1</i>	51.04	43.70	72.40	40.17	31.87	32.68
<i>sh2d3c</i>	0.03	0.00	0.05	3.95	2.94	3.27
<i>strbp</i>	1.79	1.66	1.74	15.80	12.49	13.79
<i>gpr21</i>	0.00	0.00	0.00	0.17	0.13	0.10
<i>p2rx7</i>	18.50	12.97	15.03	5.54	6.68	4.78
<i>gstt3</i>	0.72	0.91	0.47	3.56	7.14	4.15

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>loc100708255</i>	3.59	0.58	1.79	19.68	31.71	23.25
<i>mmp11</i>	0.00	0.00	0.00	0.61	0.29	0.62
<i>loc100692885</i>	0.00	0.10	0.09	0.27	1.08	0.30
<i>loc102079727</i>	0.00	0.00	0.00	2.55	2.11	1.78
<i>tor2a</i>	4.00	4.39	3.05	8.70	12.42	9.42
<i>ptrh1</i>	17.71	14.94	11.84	6.56	6.52	5.34
<i>loc124057810</i>	0.00	0.00	0.00	0.81	1.00	1.10
<i>loc124057819</i>	0.05	0.06	0.16	0.05	0.06	0.09
<i>fam163b</i>	0.00	0.13	0.12	2.21	1.54	2.06
<i>adamtsl2</i>	0.02	0.07	0.00	0.35	0.20	0.35
<i>ttc16</i>	0.38	0.23	0.44	29.42	43.01	37.98
<i>slc2a8</i>	0.39	0.38	0.46	4.67	4.20	4.48
<i>hira</i>	1.82	1.84	2.43	45.27	61.99	59.86
<i>il6st</i>	0.00	0.06	0.03	0.50	0.78	0.60
<i>nudt12</i>	2.34	2.49	1.87	6.85	6.87	6.25
<i>slc12a2l</i>	0.10	0.08	0.13	0.99	0.66	0.71
<i>gramd2b</i>	0.00	0.00	0.00	0.12	0.10	0.13
<i>znf608</i>	0.00	0.03	0.02	0.44	0.46	0.54
<i>cepl20</i>	2.46	2.58	3.73	11.76	12.05	14.60
<i>ppic</i>	0.00	0.00	0.00	0.39	0.60	0.26
<i>snx2</i>	1.40	1.39	1.44	4.81	6.43	3.97
<i>rnf214</i>	76.05	68.18	67.37	13.59	8.80	12.99
<i>sncaip</i>	0.49	0.43	0.42	5.15	5.39	3.82
<i>lox</i>	0.06	0.06	0.11	18.54	23.44	23.51
<i>ddr2</i>	0.44	0.60	0.62	12.98	6.67	14.61
<i>ier3</i>	1.26	1.41	2.25	2.40	1.24	1.62
<i>loc124057473</i>	0.34	0.05	0.19	27.04	49.21	40.49
<i>rnf223</i>	18.77	21.26	20.85	0.45	0.43	0.72
<i>piwil2</i>	35.54	31.54	42.33	91.38	86.00	103.18
<i>htr7</i>	0.00	0.06	0.10	2.13	0.86	2.17
<i>atad1a</i>	1.33	0.96	1.19	7.08	9.48	5.77
<i>galnt9</i>	0.00	0.06	0.02	0.72	0.55	0.59
<i>fbrsl1</i>	0.17	0.08	0.20	6.12	3.66	4.68
<i>chfr</i>	31.10	24.63	22.95	16.01	13.78	17.84
<i>loc104921085</i>	6.18	6.70	6.67	4.26	4.18	4.07
<i>golga3</i>	1.79	1.50	1.90	37.25	48.42	51.19
<i>ankle2</i>	11.42	11.41	12.84	69.92	86.06	82.36
<i>pgam5</i>	99.64	90.07	85.95	16.94	13.39	14.26
<i>zdhhc8</i>	9.01	7.93	10.45	3.70	2.84	3.64
<i>ranbp1</i>	131.08	163.80	198.97	98.70	89.63	71.50
<i>trmt2a</i>	96.76	92.34	72.51	34.85	28.66	35.04

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>dgcr8</i>	26.76	23.93	22.17	24.31	17.71	19.57
<i>tango2</i>	4.80	4.48	2.57	15.88	17.21	14.69
<i>arvcf</i>	0.12	0.06	0.11	13.17	14.76	10.81
<i>txnrd2</i>	1.17	1.33	1.15	9.25	7.41	5.75
<i>gnb1l</i>	44.37	31.69	38.52	10.48	8.53	7.35
<i>tbx1</i>	0.04	0.05	0.08	4.89	3.32	4.29

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>tomm20</i>	48.35	15.56	20.61	41.94
<i>arid4b</i>	2.83	3.82	20.56	23.22
<i>ggpps</i>	0.00	0.00	0.00	0.00
<i>b3galnt2</i>	1.24	0.57	9.18	13.25
<i>gng4</i>	0.00	0.00	24.94	29.70
<i>lyst</i>	0.68	0.30	3.59	5.52
<i>nid1</i>	0.03	0.12	1.34	0.47
<i>gpr137b</i>	0.00	0.00	0.00	0.00
<i>egln1</i>	11.00	18.20	16.99	10.15
<i>tsnax</i>	10.31	11.32	32.03	24.12
<i>disc1</i>	2.21	1.77	2.99	4.77
<i>sipal12</i>	2.83	3.17	12.77	7.23
<i>map10</i>	0.06	0.08	1.03	0.95
<i>ntpcr</i>	5.47	2.51	6.60	7.25
<i>sptbn5</i>	0.23	1.08	0.04	0.03
<i>npas4</i>	0.00	0.00	0.00	0.00
<i>tmem121</i>	0.00	0.00	0.69	6.29
<i>pacs1</i>	0.00	0.00	1.63	3.31
<i>mrpl2</i>	27.86	12.06	28.50	19.60
<i>klc1</i>	6.20	5.61	68.58	33.80
<i>ptk7</i>	1.17	0.63	3.87	4.53
<i>srf</i>	4.59	2.36	14.04	11.21
<i>fam160b1</i>	0.00	0.00	0.00	0.00
<i>ablim1</i>	0.04	0.10	9.79	7.26
<i>trim11</i>	0.00	0.00	0.00	0.00
<i>habp2</i>	50.89	538.07	0.19	0.26
<i>trim25</i>	3.69	1.67	15.97	2.08
<i>aldh18a1</i>	4.63	8.38	8.11	0.40
<i>ate1</i>	18.47	2.35	8.27	9.55
<i>fgfr2</i>	14.58	18.72	54.28	41.62
<i>wdr11</i>	4.75	6.02	17.17	23.96
<i>plpp4</i>	0.27	0.20	2.96	21.69
<i>cdh23</i>	0.00	0.05	0.51	0.01
<i>EIF3L</i>	42.03	75.68	70.67	19.76
<i>smoc2</i>	0.07	0.33	36.59	10.48
<i>dact2</i>	2.25	6.20	2.27	5.25
<i>lrrfip2</i>	18.55	18.08	11.62	9.70
<i>mlh1</i>	1.43	1.45	6.41	4.98
<i>fam83ha</i>	0.00	0.00	0.00	0.00

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>adtrp</i>	0.00	0.00	0.03	0.00
<i>herc4</i>	5.89	8.82	36.31	24.35
<i>cox5b</i>	334.41	180.48	251.38	279.98
<i>dnajc12</i>	6.18	0.00	0.00	18.75
<i>sirt1</i>	1.61	1.17	8.80	5.60
<i>cacul1</i>	2.70	1.15	4.69	4.72
<i>mypn</i>	0.00	0.01	0.00	0.01
<i>pkd2l1</i>	0.01	0.00	0.72	0.01
<i>tial1</i>	11.93	3.93	8.57	12.78
<i>bag3</i>	3.28	4.05	6.99	10.70
<i>inpp5f</i>	0.66	0.56	9.42	10.15
<i>mcmbp</i>	8.62	7.01	8.78	4.37
<i>sec23ip</i>	16.77	6.81	14.56	11.45
<i>csgalnact2</i>	1.66	3.12	10.85	5.18
<i>ret</i>	0.00	0.01	5.34	1.47
<i>hgsnat</i>	2.43	0.00	0.06	6.91
<i>pcdb1</i>	0.00	0.00	0.00	0.00
<i>sgpl1</i>	5.43	4.90	12.33	9.53
<i>neurog3</i>	0.00	0.00	0.08	0.00
<i>pdlim1</i>	16.49	6.04	27.00	15.36
<i>sh3d5</i>	0.00	0.00	0.00	0.00
<i>pik3ap1</i>	1.87	1.44	8.24	3.73
<i>fam204a</i>	2.40	2.79	7.42	6.15
<i>rab11fip2</i>	1.69	1.21	5.47	4.48
<i>emx2</i>	0.00	0.00	0.03	14.54
<i>elf3a</i>	60.12	94.26	64.28	48.20
<i>fam45a</i>	0.00	0.00	0.00	0.00
<i>sfxn4</i>	5.26	3.70	18.85	16.53
<i>prdx3</i>	61.41	106.09	90.51	56.09
<i>tm9sf3</i>	20.84	9.06	21.85	17.96
<i>abhd12</i>	0.00	70.42	3.60	7.42
<i>mocos</i>	6.83	9.48	1.98	0.97
<i>pcbp3</i>	0.01	0.05	191.16	7.70
<i>vwc2</i>	0.00	0.00	2.04	7.73
<i>ikzf1</i>	0.55	0.60	3.48	1.61
<i>fign1</i>	0.25	0.07	0.46	0.38
<i>tll</i>	1.51	0.96	6.44	7.60
<i>polr1b</i>	8.24	3.36	4.06	2.75
<i>nanp</i>	3.24	0.18	2.88	2.62
<i>cyp1b1</i>	1.46	0.41	7.94	0.88
<i>rmdn2</i>	3.95	19.17	3.36	2.69

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>cdc42ep3</i>	0.34	0.21	3.04	8.72
<i>opn3</i>	0.61	0.00	0.06	4.42
<i>kmo</i>	102.42	61.65	28.61	15.16
<i>ide</i>	6.94	3.67	6.04	6.35
<i>march5</i>	0.00	0.00	0.00	0.00
<i>cpeb3</i>	1.17	1.97	4.33	6.52
<i>btaf1</i>	4.44	2.69	10.95	14.94
<i>ccnj</i>	0.55	0.44	0.83	1.19
<i>znf518a</i>	0.24	2.34	1.94	0.55
<i>blnk</i>	1.98	1.42	15.45	5.77
<i>hs3st1a</i>	0.00	0.00	0.00	0.00
<i>vent1</i>	0.00	0.00	0.08	0.04
<i>pv.1</i>	0.00	0.00	0.00	0.10
<i>kndc1</i>	0.00	0.03	11.79	11.24
<i>adgral</i>	0.03	0.00	3.64	3.86
<i>gabrp</i>	0.00	0.00	2.02	5.28
<i>cfap46</i>	0.00	0.00	4.37	2.81
<i>valopa</i>	0.00	0.00	0.00	0.00
<i>nkx6-2</i>	0.05	0.00	19.58	25.58
<i>inpp5a</i>	3.11	1.71	27.39	22.25
<i>pwwp2b</i>	2.47	1.54	6.31	6.51
<i>lrrc27</i>	0.01	0.01	2.32	4.55
<i>stk32c</i>	0.10	0.32	13.45	7.43
<i>plac9</i>	0.00	43.37	19.31	0.00
<i>srr</i>	0.00	0.00	0.00	0.00
<i>tnfrsf25</i>	233.03	133.31	19.38	13.47
<i>otx5</i>	0.00	0.00	0.00	0.00
<i>rhoq</i>	1.90	1.51	7.72	16.48
<i>socs5</i>	3.33	0.94	5.45	4.72
<i>prop1</i>	0.00	0.00	0.00	0.00
<i>mef2d</i>	230.93	167.32	15.26	13.15
<i>ttc7a</i>	1.42	8.83	0.12	0.11
<i>muc4</i>	0.00	0.00	0.02	0.01
<i>epcam</i>	28.24	0.00	0.00	1.43
<i>plekhh2</i>	0.08	0.00	0.81	0.40
<i>thada</i>	2.15	1.00	2.99	1.14
<i>zfp36l2</i>	0.03	0.00	0.14	0.23
<i>hcar2</i>	1.66	7.27	0.00	0.00
<i>haao</i>	125.19	42.95	0.10	0.02
<i>papolg</i>	7.98	3.13	9.86	15.84
<i>rel</i>	33.70	16.38	5.14	3.92

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>pex13</i>	9.44	13.25	23.07	12.96
<i>sanbr</i>	0.00	0.00	0.00	0.00
<i>xpo1</i>	7.65	4.33	24.85	16.65
<i>loc102297702</i>	0.00	0.00	0.00	0.00
<i>mf122</i>	0.12	0.95	9.33	15.00
<i>pcgf6</i>	4.03	0.83	0.48	0.84
<i>ina</i>	0.06	0.15	0.54	0.89
<i>srtad2</i>	1.76	0.94	6.31	2.67
<i>slc1a4</i>	2.06	0.19	5.02	8.63
<i>smap1</i>	20.12	0.35	14.29	32.81
<i>b3gat2</i>	1.06	1.04	54.28	37.49
<i>ogfrl1</i>	0.15	0.06	26.78	18.65
<i>asrgl1</i>	4.81	0.09	27.69	3.40
<i>rims1</i>	0.01	0.02	94.73	56.78
<i>bcl11a</i>	0.00	0.01	6.38	0.84
<i>fanc1</i>	0.41	0.35	1.16	0.41
<i>vrk2</i>	1.08	1.69	5.19	3.11
<i>loc108881720</i>	0.00	0.00	0.00	0.00
<i>ccdc85a</i>	0.00	0.00	10.53	2.56
<i>hebp2</i>	0.07	0.00	2.70	404.01
<i>slc24a3</i>	0.01	0.00	2.37	12.68
<i>rin2</i>	0.81	2.21	3.32	2.08
<i>loc104933667</i>	0.00	0.00	0.00	0.00
<i>ncapd3</i>	0.61	0.29	0.65	0.47
<i>calhm2</i>	0.01	0.01	0.04	0.14
<i>tubb4b</i>	7.40	0.53	1.27	465.80
<i>vps8</i>	3.60	4.15	19.21	16.61
<i>zic3</i>	0.01	0.01	73.55	43.99
<i>pcca</i>	12.00	9.54	17.97	9.54
<i>tm9sf2</i>	40.07	15.24	33.56	29.31
<i>piezol</i>	0.12	0.61	1.05	1.00
<i>cdt1</i>	0.57	0.32	1.46	2.36
<i>aprt</i>	6.88	16.59	17.08	3.92
<i>tk2</i>	6.74	2.97	13.57	22.78
<i>tubb6</i>	0.00	0.00	0.00	0.00
<i>nvl</i>	4.42	3.90	5.57	2.64
<i>degs1</i>	29.04	24.48	24.13	26.60
<i>fbxo28</i>	2.55	1.80	6.93	12.96
<i>polr1c</i>	9.99	7.13	10.30	7.01
<i>gprin2</i>	0.00	0.00	0.00	0.00
<i>ndst2</i>	13.72	9.79	4.56	5.73

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>zswim8</i>	1.18	1.02	6.39	5.88
<i>prss12</i>	0.01	0.00	3.34	2.15
<i>chchd1</i>	24.58	1.80	6.73	21.66
<i>rap1gds1</i>	0.00	0.04	0.00	0.00
<i>galn</i>	43.87	50.99	15.77	9.40
<i>hnrnp11</i>	0.61	0.36	27.74	28.37
<i>ctu2</i>	3.95	1.88	5.44	6.29
<i>rnf166</i>	1.04	0.66	2.37	8.81
<i>snai2</i>	2.78	0.87	0.67	0.39
<i>cyp17a1</i>	0.00	0.06	0.73	0.28
<i>borcs7</i>	1.20	1.16	5.62	9.42
<i>nt5c2</i>	2.13	0.79	3.67	1.92
<i>loc124063885</i>	0.00	0.00	0.00	0.00
<i>wbp11</i>	2.02	2.11	1.41	1.65
<i>fbxw4</i>	2.39	3.74	29.64	4.38
<i>fgf8</i>	0.00	0.00	0.00	0.00
<i>slc2a9</i>	0.00	0.05	0.13	0.01
<i>lbx1</i>	0.00	0.00	1.55	0.60
<i>tlx1</i>	0.01	0.00	0.02	0.00
<i>hells</i>	0.60	0.44	0.73	0.28
<i>rab1a</i>	64.34	29.92	83.08	55.96
<i>cep68</i>	0.43	0.58	6.14	6.03
<i>sdhaf4</i>	6.96	12.25	45.89	17.86
<i>calhm3</i>	0.09	0.03	0.46	0.12
<i>loc109629162</i>	0.00	0.00	0.00	0.00
<i>prkg2a</i>	0.00	0.00	0.00	0.00
<i>coll3a1</i>	11.67	7.52	0.46	2.43
<i>h2afy2</i>	0.00	0.00	0.00	0.00
<i>gbf1</i>	10.44	1.24	4.04	10.47
<i>pitx3</i>	0.01	0.00	0.00	0.49
<i>pnliprpl</i>	0.02	0.00	0.00	0.00
<i>hspa12a</i>	0.48	0.21	3.14	12.67
<i>loc124053561</i>	0.00	0.00	0.00	0.00
<i>eno4</i>	0.00	0.00	0.87	1.51
<i>shtn1</i>	6.13	0.91	12.79	0.06
<i>atp6v1b2</i>	25.53	12.57	203.14	210.92
<i>vax1</i>	0.00	0.00	0.00	0.00
<i>pla2g4f</i>	0.00	0.00	0.00	0.00
<i>kcnk18</i>	0.01	0.00	0.31	0.07
<i>slc18a2</i>	0.01	0.01	1.38	1.85
<i>pdzd8</i>	0.89	0.95	4.35	4.74

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>edaradd</i>	0.12	0.05	0.80	0.39
<i>loc104929388</i>	0.00	0.00	0.00	0.00
<i>exo1</i>	0.40	0.06	0.23	0.05
<i>yipf4</i>	25.88	13.06	28.96	28.47
<i>birc6</i>	4.06	3.06	7.69	9.08
<i>ltbp1</i>	5.93	6.74	2.66	4.34
<i>ttc27</i>	14.50	7.07	8.86	6.33
<i>fam98a</i>	8.95	6.59	16.12	12.93
<i>loc115596078</i>	0.00	0.00	0.00	0.00
<i>cdh1</i>	11.46	24.81	8.24	5.66
<i>cd53</i>	2.54	1.13	17.42	6.09
<i>sub1</i>	40.25	36.17	77.86	66.90
<i>loc112139785</i>	0.00	0.00	0.00	0.00
<i>npr3</i>	0.13	0.00	0.79	2.29
<i>pdzd2</i>	0.00	0.00	0.20	0.25
<i>golph3</i>	19.08	6.48	17.10	21.32
<i>dtx3</i>	1.09	1.67	0.73	11.70
<i>isl1</i>	0.00	0.01	0.28	0.23
<i>pcbd2</i>	0.15	0.00	0.00	2.26
<i>ccdc125</i>	1.25	1.82	2.68	1.15
<i>rad17</i>	3.83	2.39	8.16	6.98
<i>ak6</i>	11.17	1.51	4.52	15.13
<i>ydjc</i>	3.54	1.34	5.03	6.50
<i>ube2l3</i>	72.65	16.67	95.80	97.22
<i>pias2</i>	5.09	1.11	3.02	9.58
<i>arid3a</i>	0.00	0.00	0.17	0.66
<i>tesk1</i>	1.09	0.38	7.24	5.67
<i>b3galt2</i>	0.21	0.01	0.05	0.44
<i>tnc</i>	0.01	0.05	2.15	23.39
<i>traf2</i>	9.00	0.03	6.64	3.91
<i>rabl6</i>	4.04	2.40	7.19	8.37
<i>imp4</i>	30.28	11.37	27.74	18.46
<i>araf</i>	1.72	1.26	3.75	0.40
<i>orf2</i>	0.00	0.00	0.00	0.00
<i>pnpla7</i>	2.90	2.59	7.23	8.30
<i>mrpl41</i>	56.21	14.75	22.41	22.37
<i>dph7</i>	7.29	6.04	7.36	4.69
<i>sh3glb2</i>	1.91	0.28	8.51	7.97
<i>lta</i>	0.13	0.45	0.57	0.44
<i>megf9</i>	1.18	0.79	16.36	16.16
<i>ppp6c</i>	19.58	6.81	29.09	31.37

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>golgal</i>	2.51	1.14	6.04	5.97
<i>rpl35</i>	2878.14	979.35	710.29	1426.46
<i>loc119891964</i>	0.00	0.00	0.00	0.00
<i>olfml2a</i>	0.05	0.56	2.97	2.24
<i>nr6a1</i>	0.00	0.00	0.00	0.00
<i>nr5a1</i>	0.00	0.00	0.00	0.00
<i>adgrd2</i>	0.00	0.00	8.16	0.02
<i>lhx2</i>	0.01	0.00	0.46	7.85
<i>crb2</i>	0.00	0.00	0.00	0.00
<i>fpgs</i>	0.00	12.58	3.13	0.00
<i>bcl2l16</i>	0.00	0.00	0.00	0.00
<i>loc101061694</i>	0.00	0.00	0.00	0.00
<i>glipr2</i>	0.00	0.00	13.59	14.52
<i>nrde2</i>	0.35	1.38	5.79	0.94
<i>trim35</i>	1.03	0.01	0.05	0.40
<i>hs3st1b</i>	0.00	0.00	0.00	0.00
<i>h2afv</i>	0.00	0.00	0.00	0.00
<i>purb</i>	5.83	18.27	133.78	25.26
<i>loc104923460</i>	0.00	0.00	0.00	0.00
<i>ckap2l</i>	1.11	0.09	0.52	0.72
<i>il1b</i>	0.40	0.38	4.71	5.49
<i>cnnm4</i>	1.05	0.02	1.02	5.82
<i>atp8b2</i>	0.91	7.08	0.12	0.89
<i>dapk1</i>	2.15	1.57	6.72	16.93
<i>ctsl</i>	141.76	0.27	0.08	82.04
<i>fbp2</i>	0.10	0.14	7.93	3.94
<i>fbp1</i>	2.92	516.38	0.34	6.10
<i>kank1</i>	5.92	5.03	0.58	3.63
<i>cfap157</i>	0.00	0.00	0.53	0.54
<i>dmrt1</i>	0.16	0.00	0.00	0.00
<i>dmrt3</i>	0.00	0.00	0.15	0.00
<i>dmrt2</i>	0.00	0.00	0.00	0.00
<i>snf2l2</i>	0.00	0.00	0.00	0.00
<i>pol</i>	0.01	0.00	0.62	0.06
<i>adamts3</i>	0.23	0.72	1.96	0.67
<i>npffr2</i>	0.00	0.00	0.25	0.20
<i>slc4a4</i>	2.93	0.29	0.03	0.06
<i>rufy3</i>	2.24	2.36	166.90	88.92
<i>grsf1</i>	28.95	5.76	14.20	19.84
<i>trim16</i>	0.30	0.89	1.30	0.48
<i>mapk1</i>	0.18	2.44	7.88	1.59

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>ypel1</i>	0.23	0.72	3.38	8.62
<i>ppil2</i>	4.23	5.05	15.42	7.78
<i>slc39a14</i>	3.08	0.26	3.20	5.36
<i>ascc2</i>	10.94	7.45	14.35	11.87
<i>mf215</i>	0.32	0.75	5.72	5.79
<i>sec14l2</i>	0.33	198.15	1.11	5.57
<i>unc13b</i>	0.11	0.97	0.27	0.02
<i>loc124057552</i>	0.00	0.00	0.00	0.00
<i>rusc2</i>	1.09	0.01	4.00	28.86
<i>sh3bgrl</i>	5.70	3.36	38.71	33.52
<i>ccl19</i>	38.19	0.00	0.00	4.07
<i>wdfy3</i>	1.18	0.45	7.90	16.93
<i>cds1</i>	0.82	0.65	8.20	16.88
<i>tmem175</i>	1.45	1.04	8.02	14.96
<i>zscan20</i>	1.69	2.04	4.73	3.29
<i>rasgef1b</i>	0.00	0.00	0.00	0.00
<i>prkg2b</i>	0.00	0.00	0.00	0.00
<i>bmp3</i>	0.00	0.00	0.48	0.24
<i>cunh4orf22</i>	0.00	0.00	0.00	0.00
<i>fgf5</i>	0.00	0.00	0.00	0.13
<i>prdm8</i>	0.00	0.00	3.62	2.71
<i>antxr2</i>	41.23	54.05	8.18	5.64
<i>paqr3</i>	4.43	2.03	8.41	10.99
<i>bmp2k</i>	0.01	1.40	4.43	0.04
<i>fras1</i>	0.00	0.00	0.05	0.00
<i>mrpl1</i>	16.53	9.30	18.73	12.80
<i>cnot6l</i>	5.94	10.95	3.34	3.17
<i>fam102a</i>	0.07	0.03	1.41	2.45
<i>slc25a25a</i>	50.23	9.85	1.55	1.16
<i>zdhhc12</i>	0.00	0.00	0.00	0.00
<i>pkn2</i>	1.90	2.43	1.69	0.91
<i>odf2</i>	1.05	0.15	1.76	8.46
<i>gle1</i>	1.38	0.54	2.43	2.70
<i>ptges2</i>	11.36	4.16	15.36	15.10
<i>ralgds</i>	1.25	9.15	6.49	2.69
<i>smarcb1</i>	14.62	0.79	5.89	20.22
<i>sh2d3c</i>	3.05	0.11	8.49	22.71
<i>strbp</i>	0.18	0.17	11.65	11.68
<i>gpr21</i>	0.01	0.00	0.00	0.10
<i>p2rx7</i>	0.52	0.33	7.86	17.33
<i>gstt3</i>	168.17	242.54	1.62	30.29

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>loc100708255</i>	0.00	0.00	0.00	0.00
<i>mmp11</i>	0.17	0.48	0.12	0.09
<i>loc100692885</i>	0.00	0.00	0.00	0.00
<i>loc102079727</i>	0.00	0.00	0.00	0.00
<i>tor2a</i>	3.30	4.45	12.52	5.64
<i>ptrh1</i>	18.11	1.57	3.31	7.04
<i>loc124057810</i>	0.00	0.00	0.00	0.00
<i>loc124057819</i>	0.00	0.00	0.00	0.00
<i>fam163b</i>	0.05	0.00	56.75	0.10
<i>adamtsl2</i>	0.00	0.00	0.15	0.48
<i>ttc16</i>	0.21	0.04	0.52	1.79
<i>slc2a8</i>	2.90	1.77	12.66	7.77
<i>hira</i>	2.43	1.30	4.82	4.26
<i>il6st</i>	15.07	0.06	2.20	16.13
<i>nudt12</i>	2.80	3.67	2.57	0.00
<i>slc12a2l</i>	0.00	0.00	0.00	0.00
<i>gramd2b</i>	7.29	0.38	3.03	13.65
<i>znf608</i>	0.00	0.01	3.48	8.33
<i>cep120</i>	0.71	0.68	2.31	1.91
<i>ppic</i>	0.00	0.00	0.96	0.89
<i>snx2</i>	1.56	1.16	6.47	7.78
<i>rmf214</i>	2.63	2.32	8.99	5.60
<i>sncalp</i>	1.20	0.35	1.66	3.16
<i>lox</i>	0.20	0.00	0.41	1.89
<i>ddr2</i>	4.16	0.03	0.83	4.09
<i>ier3</i>	0.00	0.00	0.00	0.00
<i>loc124057473</i>	0.00	0.00	0.00	0.00
<i>rmf223</i>	0.02	0.00	0.93	0.56
<i>piwil2</i>	0.00	0.00	0.07	0.16
<i>htr7</i>	0.00	0.02	5.24	0.87
<i>atad1a</i>	3.73	1.30	11.47	12.57
<i>galnt9</i>	0.00	0.00	23.72	13.57
<i>fbrsl1</i>	0.00	1.13	1.12	0.00
<i>chfr</i>	2.29	0.78	3.66	4.85
<i>loc104921085</i>	0.00	0.00	0.00	0.00
<i>golga3</i>	5.80	2.25	6.48	6.80
<i>ankle2</i>	6.42	10.54	10.13	12.66
<i>pgam5</i>	6.85	6.89	13.41	7.98
<i>zdhhc8</i>	0.00	0.00	0.00	0.00
<i>ranbp1</i>	51.65	17.67	45.87	27.36
<i>trmt2a</i>	16.23	4.53	13.31	18.79

Table S13. The expression of sex determining region genes in different tissues of *Sc. tetracanthus*

Gene	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>dgcr8</i>	8.36	6.35	22.81	19.78
<i>tango2</i>	7.44	7.27	8.28	12.12
<i>arvcf</i>	0.31	0.00	6.88	23.13
<i>txnrd2</i>	3.88	2.55	5.79	9.42
<i>gnb1l</i>	7.01	6.33	9.19	5.71
<i>tbx1</i>	0.27	0.14	0.50	0.00

Table S14. The expression of sex determining region genes in different tissues of *Se. multifasciata*

Gene name	Ovary- 1_fpk	Ovary- 2_fpk	Ovary- 3_fpk	Testis- 1_fpk	Testis- 2_fpk	Testis- 3_fpk
<i>syt14</i>	0.08	0.04	0.03	3.37	4.26	1.83
<i>nt5c1a</i>	18.64	19.94	27.68	9.36	7.14	5.96
<i>rdh14</i>	97.79	96.26	94.56	6.22	8.73	10.20
<i>il6st</i>	0.42	0.67	0.64	0.88	0.60	0.43
<i>rngtt</i>	22.07	19.06	21.02	9.95	11.33	6.85
<i>cnr1</i>	0.04	0.10	0.03	2.05	1.27	1.01
<i>akirin2</i>	70.24	68.26	77.22	16.61	22.91	18.05
<i>rars2</i>	9.05	6.34	5.80	11.75	11.29	8.86
<i>ypel5</i>	4.96	3.75	5.10	9.95	23.39	44.32
<i>sipall1</i>	1.13	1.49	1.11	19.81	15.83	13.47
<i>rgs6</i>	10.05	6.10	6.37	0.68	0.75	0.31
<i>lama2</i>	0.74	0.50	0.46	5.99	8.47	10.60
<i>slc32a1</i>	0.38	0.74	0.19	0.24	0.73	0.15
<i>ptprk</i>	1.11	2.00	1.40	20.94	11.45	8.41
<i>dlgap2</i>	0.13	0.25	0.16	1.33	1.53	0.85
<i>specc1</i>	9.55	9.15	7.46	3.27	4.75	6.15
<i>grcc10</i>	2.61	2.12	3.51	2.56	3.47	3.94
<i>saysd1</i>	10.28	10.77	6.90	3.02	4.80	2.32
<i>bpnt1</i>	4.11	4.38	3.14	7.86	29.82	88.18
<i>ppplc</i>	0.61	0.61	0.59	0.24	0.21	0.35
<i>plb1</i>	0.07	0.33	0.12	5.07	5.15	2.29
<i>rab15</i>	2.47	3.45	2.26	4.96	6.72	6.15
<i>fntb</i>	11.63	12.24	12.27	8.75	8.23	8.07
<i>max</i>	8.01	5.56	6.27	23.41	32.48	39.51
<i>srsf5</i>	7.90	5.63	5.86	26.08	20.17	15.92
<i>susd6</i>	1.26	1.79	1.28	25.53	28.97	45.93
<i>dmrt1Y</i>	0.08	0.21	0.07	125.29	103.77	49.48
<i>tcla</i>	0.11	0.10	0.05	0.57	0.71	12.40
<i>nrde2</i>	1.96	1.73	1.95	4.36	6.86	5.79
<i>acot22</i>	15.71	15.66	14.78	18.25	18.65	13.53
<i>gpr176</i>	0.00	0.00	0.00	1.24	1.19	0.31
<i>thbs1</i>	0.10	0.03	0.04	3.06	1.96	0.96
<i>katnbl</i>	20.73	21.92	25.06	8.96	15.14	26.10
<i>emc7</i>	107.36	90.05	91.07	26.51	21.80	19.89
<i>chrn5b</i>	3.17	2.22	1.89	10.38	11.45	10.47
<i>ld</i>	0.43	0.32	0.00	0.18	0.29	0.00
<i>grem1</i>	0.12	0.00	0.22	0.93	0.78	0.35
<i>scg5</i>	9.46	12.99	6.78	3.95	4.15	2.33
<i>arhgap11a</i>	187.76	279.37	237.88	0.75	0.55	1.74

Table S14. The expression of sex determining region genes in different tissues of *Se. multifasciata*

Gene name	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>acta2</i>	7.76	9.04	8.46	9.94	12.98	12.74
<i>ak7</i>	0.15	0.26	0.16	13.92	63.08	231.36
<i>scara3</i>	0.21	0.14	0.39	0.24	0.20	0.00
<i>clu</i>	2.48	3.30	1.25	407.43	213.60	126.42
<i>reps1</i>	4.00	3.37	4.38	8.85	8.67	9.46
<i>abracl</i>	35.59	35.63	34.57	26.22	19.15	12.64
<i>heca</i>	3.06	5.82	3.46	8.77	9.51	4.67
<i>mtif3</i>	26.22	26.64	29.63	13.54	11.60	7.26
<i>spag5</i>	13.35	10.42	11.54	5.54	12.66	14.23
<i>nudt14</i>	1.41	1.76	1.42	5.02	5.79	6.16
<i>jag2</i>	9.71	9.21	10.80	27.28	16.12	8.81
<i>esr2</i>	1.51	1.92	1.57	10.72	5.34	5.75
<i>syne2</i>	0.15	0.14	0.13	2.37	2.35	2.86
<i>hadha</i>	0.15	0.24	0.15	6.97	8.10	6.79
<i>hadhb</i>	39.37	32.88	38.24	60.69	41.36	27.01
<i>loc119264033</i>	0.01	0.09	0.05	1.28	1.75	0.45
<i>tfap2d</i>	0.13	0.25	0.14	2.51	1.83	0.70
<i>tfap2b</i>	0.08	0.17	0.16	0.87	0.88	0.59
<i>lrp11</i>	1.07	1.11	1.12	21.42	39.28	84.97
<i>pcmt</i>	28.73	30.21	31.74	17.71	18.21	16.34
<i>lats1</i>	1.26	1.29	1.32	7.26	8.87	7.79
<i>rab10</i>	51.94	54.41	63.45	81.55	88.62	75.59
<i>kif3c</i>	0.06	0.08	0.04	5.17	1.79	1.51
<i>tlr5</i>	0.90	1.85	2.10	3.83	6.88	4.94
<i>dtmb</i>	1.38	2.06	1.52	18.73	21.53	27.99
<i>dnmt3a</i>	0.04	0.30	0.14	2.70	1.31	3.03
<i>sun1</i>	0.24	0.14	0.28	6.30	2.40	13.93
<i>dpysl5</i>	0.36	0.95	0.45	7.43	7.65	7.13
<i>mapre3</i>	0.70	0.91	0.71	14.77	31.33	67.49
<i>tmem214</i>	84.68	62.51	71.91	33.14	39.37	43.55
<i>gtf2h5</i>	3.39	2.63	2.87	4.69	4.24	1.68
<i>serac1</i>	4.99	3.45	3.82	7.91	9.08	8.08
<i>myct1</i>	0.37	0.60	0.54	11.32	8.74	6.99
<i>esr1</i>	0.70	0.68	0.43	5.99	3.65	4.36
<i>arnt1</i>	13.54	11.78	10.60	10.58	13.44	8.15
<i>zbtb2</i>	2.61	3.16	3.64	7.85	9.57	11.09
<i>akap12</i>	2.88	3.39	3.61	24.32	19.07	12.94
<i>methfd11</i>	1.42	1.43	1.64	10.24	16.91	18.72
<i>stx11</i>	17.75	16.01	21.05	1.03	0.55	0.52
<i>utrn</i>	1.07	1.45	1.40	25.13	14.89	11.55
<i>epm2a</i>	1.20	1.22	1.04	2.10	2.57	1.80

Table S14. The expression of sex determining region genes in different tissues of *Se. multifasciata*

Gene name	Ovary- 1 fpkm	Ovary- 2 fpkm	Ovary- 3 fpkm	Testis- 1 fpkm	Testis- 2 fpkm	Testis- 3 fpkm
<i>aloxe3</i>	105.70	146.98	154.89	0.30	0.49	1.09
<i>fbxo30</i>	6.98	6.46	7.01	8.80	11.15	12.40
<i>grm1</i>	0.05	0.00	0.01	1.93	2.42	1.74
<i>rab32</i>	10.01	10.72	8.12	11.61	8.50	5.11
<i>adgb</i>	2.18	3.60	4.71	13.29	34.91	75.12
<i>stxbp5</i>	0.15	0.18	0.16	2.01	1.25	2.01
<i>sash1</i>	4.96	3.18	4.76	9.93	5.70	5.97

Table S14. The expression of sex determining region genes in different tissues of *Se. multifasciata*

Gene name	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>syt14</i>	0.02	0.03	4.22	4.80
<i>nt5c1a</i>	0.58	0.57	1.73	1.56
<i>rdh14</i>	8.35	7.61	14.73	13.80
<i>il6st</i>	0.61	0.27	0.93	0.75
<i>mgtt</i>	3.20	3.86	7.16	7.29
<i>cnr1</i>	0.05	0.07	68.74	71.72
<i>akirin2</i>	9.96	8.49	11.12	11.03
<i>rars2</i>	3.98	5.36	11.20	11.72
<i>ypel5</i>	0.33	0.14	18.56	17.65
<i>sipa111</i>	0.34	0.53	16.89	17.68
<i>rgs6</i>	0.01	0.00	5.45	4.00
<i>lama2</i>	0.00	0.00	1.04	0.75
<i>slc32a1</i>	0.00	0.00	0.14	0.13
<i>ptprk</i>	2.25	2.86	19.43	21.63
<i>dlgap2</i>	0.53	0.58	0.69	0.75
<i>specc1</i>	0.00	0.01	11.53	10.67
<i>grcc10</i>	0.65	0.61	0.81	0.76
<i>saysd1</i>	2.51	3.73	3.67	3.81
<i>bpnt1</i>	0.79	1.12	14.58	15.53
<i>ppp1c</i>	0.89	0.76	0.91	0.86
<i>plb1</i>	0.06	0.03	0.30	0.25
<i>rab15</i>	0.01	0.03	23.96	23.43
<i>fntb</i>	23.11	25.21	27.02	25.66
<i>max</i>	33.18	61.80	121.00	126.11
<i>srsf5</i>	29.12	31.96	140.38	143.54
<i>susd6</i>	0.00	0.00	0.00	0.00
<i>dmrt1</i>	0.00	0.01	0.00	0.03
<i>tcla</i>	0.00	0.00	0.00	0.00
<i>nrde2</i>	0.72	0.91	5.57	6.08
<i>acot22</i>	25.10	30.71	26.00	29.86
<i>gpr176</i>	0.00	0.01	6.22	6.32
<i>thbs1</i>	0.94	0.71	3.85	5.06
<i>katnbl</i>	0.00	0.00	0.00	0.00
<i>emc7</i>	39.27	42.68	111.46	111.19
<i>chrm5b</i>	0.04	0.03	13.00	13.58
<i>ld</i>	0.00	0.00	0.16	0.21
<i>grem1</i>	0.06	0.03	6.23	5.16
<i>scg5</i>	4.85	4.26	298.35	298.11
<i>arhgap11a</i>	0.00	0.00	0.08	0.04

Table S14. The expression of sex determining region genes in different tissues of *Se. multifasciata*

Gene name	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>acta2</i>	0.00	0.00	0.00	0.02
<i>ak7</i>	0.00	0.01	1.04	0.60
<i>scara3</i>	0.06	0.02	1.63	1.29
<i>clu</i>	39.52	31.09	622.14	536.44
<i>reps1</i>	1.94	2.32	6.55	6.58
<i>abracl</i>	0.00	0.00	0.00	0.00
<i>heca</i>	0.23	0.24	3.80	3.99
<i>mtif3</i>	3.67	2.52	1.99	2.11
<i>spag5</i>	0.00	0.16	0.57	0.38
<i>nudt14</i>	0.47	0.54	13.96	13.70
<i>jag2</i>	1.49	1.40	11.16	11.10
<i>esr2</i>	4.72	5.94	22.16	18.90
<i>syne2</i>	0.21	0.25	1.00	1.05
<i>hadha</i>	0.04	0.02	0.21	0.36
<i>hadhb</i>	46.00	65.09	23.63	23.17
<i>loc119264033</i>	0.00	0.00	0.11	0.03
<i>tfap2d</i>	0.00	0.00	0.46	0.22
<i>tfap2b</i>	0.00	0.00	2.68	1.77
<i>lrp11</i>	9.00	16.40	39.07	39.16
<i>pcmt</i>	4.09	4.42	38.02	40.09
<i>lats1</i>	1.30	1.74	2.90	3.15
<i>rab10</i>	28.40	32.53	98.52	92.56
<i>kif3c</i>	0.04	0.10	25.66	26.76
<i>tlr5</i>	7.52	3.15	0.16	0.17
<i>dtmb</i>	4.25	3.03	2.12	1.58
<i>dnmt3a</i>	0.36	0.53	1.70	1.49
<i>sun1</i>	1.77	1.46	15.62	14.59
<i>dpysl5</i>	0.02	0.05	78.91	70.88
<i>mapre3</i>	46.98	49.57	18.36	18.01
<i>tmem214</i>	81.73	81.58	15.20	14.13
<i>gtf2h5</i>	3.54	5.01	11.08	11.04
<i>serac1</i>	11.63	13.72	8.62	8.85
<i>myct1</i>	2.26	2.03	1.23	1.48
<i>esr1</i>	1.35	0.77	1.48	2.00
<i>arnt1</i>	2.06	2.27	11.78	12.09
<i>zbtb2</i>	3.60	2.25	3.49	3.34
<i>akap12</i>	3.02	3.12	12.62	14.10
<i>methfd1l</i>	0.11	0.23	0.94	0.63
<i>stx11</i>	0.01	0.01	0.10	0.01
<i>utrn</i>	2.60	2.54	9.19	9.22
<i>epm2a</i>	3.39	3.28	3.48	3.38

Table S14. The expression of sex determining region genes in different tissues of *Se. multifasciata*

Gene name	Female-Liver_fpk	Male-Liver_fpk	Female-Brain_fpk	Male-Brain_fpk
<i>aloxe3</i>	0.02	0.03	0.04	0.02
<i>fbxo30</i>	0.00	0.00	0.00	0.00
<i>grm1</i>	0.01	0.01	23.74	22.72
<i>rab32</i>	1.06	1.60	3.62	3.37
<i>adgb</i>	0.13	0.24	2.68	1.78
<i>stxbp5</i>	0.02	0.02	33.73	35.26
<i>sash1</i>	0.54	0.54	15.09	17.07

Table S15. Distribution of transposable elements in *dmrt1s* of three Scatophagidae species

<i>Sc. argus</i> (Class I)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	3944	3989	LINE
<i>dmrt1Y</i>	11397	13007	LINE
<i>dmrt1Y</i>	14583	14714	LINE
<i>dmrt1Y</i>	20853	20890	LINE
<i>dmrt1Y</i>	20987	21042	LINE
<i>dmrt1Y</i>	21005	21058	LINE
<i>dmrt1Y</i>	31865	32016	LINE
<i>dmrt1Y</i>	33691	33800	LINE
<i>dmrt1Y</i>	34100	34166	LINE
<i>dmrt1Y</i>	36060	36219	LINE
<i>dmrt1Y</i>	38226	38238	LINE
<i>dmrt1Y</i>	38239	38260	LINE
<i>dmrt1Y</i>	4364	4441	LTR
<i>dmrt1Y</i>	10347	10399	LTR
<i>dmrt1Y</i>	20354	20430	LTR
<i>dmrt1Y</i>	20968	21025	LTR
<i>dmrt1Y</i>	32473	32525	LTR
<i>dmrt1ΔX</i>	4210	4251	LINE
<i>dmrt1ΔX</i>	4252	4595	LINE
<i>dmrt1ΔX</i>	8176	8257	LINE
<i>dmrt1ΔX</i>	10628	10720	LINE
<i>dmrt1ΔX</i>	12029	12156	LINE
<i>dmrt1ΔX</i>	12664	12797	LINE
<i>dmrt1ΔX</i>	14560	14626	LINE
<i>dmrt1ΔX</i>	16957	16970	LINE
<i>dmrt1ΔX</i>	20585	20762	LINE
<i>dmrt1ΔX</i>	20807	21796	LINE
<i>dmrt1ΔX</i>	25140	25360	LINE
<i>dmrt1ΔX</i>	26847	27060	LINE
<i>dmrt1ΔX</i>	30337	30491	LINE
<i>dmrt1ΔX</i>	31014	31239	LINE
<i>dmrt1ΔX</i>	31687	31786	LINE
<i>dmrt1ΔX</i>	21250	21795	LTR
<i>dmrt1ΔX</i>	24056	24114	LTR
<i>dmrt1ΔX</i>	24625	24890	LTR

Table S15. Distribution of transposable elements in *dmrt1s* of three Scatophagidae species

<i>Sc. argus</i> (Class II)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	3953	4005	CMC-EnSpm
<i>dmrt1Y</i>	20446	20467	CMC-EnSpm
<i>dmrt1Y</i>	23844	24095	CMC-EnSpm
<i>dmrt1Y</i>	24639	25333	CMC-EnSpm
<i>dmrt1Y</i>	25418	25752	CMC-EnSpm
<i>dmrt1Y</i>	25923	26061	CMC-EnSpm
<i>dmrt1Y</i>	26655	26742	CMC-EnSpm
<i>dmrt1Y</i>	27382	27492	CMC-EnSpm
<i>dmrt1Y</i>	2235	2370	hAT-Ac
<i>dmrt1Y</i>	4386	4570	hAT-Ac
<i>dmrt1Y</i>	6716	7084	hAT-Ac
<i>dmrt1Y</i>	7106	7439	hAT-Ac
<i>dmrt1Y</i>	9586	9667	hAT-Ac
<i>dmrt1Y</i>	10913	11058	hAT-Ac
<i>dmrt1Y</i>	32354	32478	hAT-Ac
<i>dmrt1Y</i>	38142	38317	hAT-Ac
<i>dmrt1Y</i>	29510	29612	hAT-Charlie
<i>dmrt1Y</i>	29692	30076	hAT-Charlie
<i>dmrt1Y</i>	30116	30209	hAT-Charlie
<i>dmrt1Y</i>	33114	33166	MULE-MuDR
<i>dmrt1Y</i>	36935	37170	P
<i>dmrt1Y</i>	37001	37063	P
<i>dmrt1Y</i>	37216	37267	P
<i>dmrt1Y</i>	20380	20445	Sola-3
<i>dmrt1Y</i>	20387	20454	TcMar-m44
<i>dmrt1Y</i>	4442	4503	TcMar-Tc1
<i>dmrt1Y</i>	10319	10381	TcMar-Tc1
<i>dmrt1Y</i>	20462	20485	TcMar-Tc1
<i>dmrt1Y</i>	30850	30930	TcMar-Tc1
<i>dmrt1Y</i>	30947	31142	TcMar-Tc1
<i>dmrt1Y</i>	31907	31934	TcMar-Tc1
<i>dmrt1ΔX</i>	31014	31828	CMC-EnSpm
<i>dmrt1ΔX</i>	31869	31928	CMC-EnSpm
<i>dmrt1ΔX</i>	30980	31067	Crypton-V
<i>dmrt1ΔX</i>	27822	27891	hAT-Ac
<i>dmrt1ΔX</i>	28459	28622	hAT-Ac
<i>dmrt1ΔX</i>	30322	30491	hAT-Ac
<i>dmrt1ΔX</i>	26661	27060	hAT-Charlie
<i>dmrt1ΔX</i>	27090	27509	hAT-Charlie
<i>dmrt1ΔX</i>	25401	25448	hAT-hAT5
<i>dmrt1ΔX</i>	25082	25394	hAT-hobo

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Sc. argus</i> (Class II)			
Gene	Start	End	TE type
<i>dmrt1ΔX</i>	24554	24578	P
<i>dmrt1ΔX</i>	24579	24630	P
<i>dmrt1ΔX</i>	23413	23464	PIF-Harbinger
<i>dmrt1ΔX</i>	22694	22857	TcMar-Tc1
<i>dmrt1ΔX</i>	23349	23457	TcMar-Tc1

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Sc. tetracanthus</i> (Class I)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	33843	33898	LTR
<i>dmrt1Y</i>	11934	12050	LTR
<i>dmrt1Y</i>	22796	22879	LTR
<i>dmrt1Y</i>	30467	30701	LINE
<i>dmrt1Y</i>	30359	30595	LINE
<i>dmrt1Y</i>	30458	30580	LINE
<i>dmrt1Y</i>	30839	30904	LINE
<i>dmrt1Y</i>	12403	12543	LINE
<i>dmrt1Y</i>	12538	13796	LINE
<i>dmrt1Y</i>	13800	13864	LINE
<i>dmrt1Y</i>	33904	34308	LINE
<i>dmrt1Y</i>	12413	12536	LINE
<i>dmrt1Y</i>	12571	13805	LINE
<i>dmrt1Y</i>	34249	34310	LINE
<i>dmrt1Y</i>	12366	12575	LINE
<i>dmrt1Y</i>	12390	12542	LINE
<i>dmrt1Y</i>	12402	12572	LINE
<i>dmrt1Y</i>	12538	13716	LINE
<i>dmrt1Y</i>	13709	13795	LINE
<i>dmrt1Y</i>	34260	34358	LINE
<i>dmrt1Y</i>	15856	16036	LINE
<i>dmrt1Y</i>	15946	16036	LINE
<i>dmrt1Y</i>	23245	23306	LINE
<i>dmrt1ΔX</i>	22509	22602	LTR
<i>dmrt1ΔX</i>	12766	12871	LTR
<i>dmrt1ΔX</i>	12477	12524	LTR
<i>dmrt1ΔX</i>	24080	24136	LTR
<i>dmrt1ΔX</i>	16728	16818	LTR
<i>dmrt1ΔX</i>	16760	16836	LTR
<i>dmrt1ΔX</i>	29738	30221	LTR
<i>dmrt1ΔX</i>	27723	29739	LTR
<i>dmrt1ΔX</i>	29733	29804	LTR
<i>dmrt1ΔX</i>	27711	29677	LTR
<i>dmrt1ΔX</i>	17704	17721	LTR
<i>dmrt1ΔX</i>	17464	17526	LTR
<i>dmrt1ΔX</i>	28128	29657	LTR
<i>dmrt1ΔX</i>	27724	28170	LTR
<i>dmrt1ΔX</i>	6913	7058	LTR
<i>dmrt1ΔX</i>	9640	9674	LINE
<i>dmrt1ΔX</i>	12340	12400	LINE
<i>dmrt1ΔX</i>	4569	4649	LINE

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Sc. tetracanthus</i> (Class I)			
Gene	Start	End	TE type
<i>dmrt1ΔX</i>	24668	24749	LINE
<i>dmrt1ΔX</i>	24650	24790	LINE
<i>dmrt1ΔX</i>	24605	24790	LINE
<i>dmrt1ΔX</i>	1320	1511	LINE
<i>dmrt1ΔX</i>	23433	23444	LINE
<i>dmrt1ΔX</i>	22595	22814	LINE
<i>dmrt1ΔX</i>	1051	1296	LINE
<i>dmrt1ΔX</i>	22600	22654	LINE
<i>dmrt1ΔX</i>	1292	1525	LINE
<i>dmrt1ΔX</i>	22507	22584	LINE
<i>dmrt1ΔX</i>	11131	11309	LINE
<i>dmrt1ΔX</i>	11329	11372	LINE
<i>dmrt1ΔX</i>	11219	11309	LINE
<i>dmrt1ΔX</i>	11131	11228	LINE
<i>dmrt1ΔX</i>	11195	11362	LINE
<i>dmrt1ΔX</i>	11195	11305	LINE
<i>dmrt1ΔX</i>	17671	17732	LINE

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Sc. tetracanthus</i> (Class II)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	25757	25791	DNA
<i>dmrt1Y</i>	17392	17523	DNA/CMC-EnSpm
<i>dmrt1Y</i>	14605	14707	DNA/CMC-EnSpm
<i>dmrt1Y</i>	22740	22872	DNA/CMC-EnSpm
<i>dmrt1Y</i>	22815	22900	DNA/CMC-EnSpm
<i>dmrt1Y</i>	23269	23332	DNA/CMC-EnSpm
<i>dmrt1Y</i>	748	1123	DNA/hAT-Ac
<i>dmrt1Y</i>	4499	4583	DNA/hAT-Ac
<i>dmrt1Y</i>	6720	7057	DNA/hAT-Ac
<i>dmrt1Y</i>	7093	7378	DNA/hAT-Ac
<i>dmrt1Y</i>	9696	10221	DNA/hAT-Ac
<i>dmrt1Y</i>	10242	10364	DNA/hAT-Ac
<i>dmrt1Y</i>	10397	10455	DNA/hAT-Ac
<i>dmrt1Y</i>	11150	11868	DNA/hAT-Ac
<i>dmrt1Y</i>	20604	20678	DNA/hAT-Ac
<i>dmrt1Y</i>	971	1124	DNA/hAT-Ac
<i>dmrt1Y</i>	11150	11220	DNA/hAT-Ac
<i>dmrt1Y</i>	11174	11231	DNA/hAT-Ac
<i>dmrt1Y</i>	11787	11868	DNA/hAT-Ac
<i>dmrt1Y</i>	6028	6095	DNA/hAT-Tip100
<i>dmrt1Y</i>	23275	23340	DNA/Maverick
<i>dmrt1Y</i>	14643	14720	DNA/Merlin
<i>dmrt1Y</i>	22880	22894	DNA/Merlin
<i>dmrt1Y</i>	32395	32763	DNA/P
<i>dmrt1Y</i>	14633	14709	DNA/P
<i>dmrt1Y</i>	32592	32806	DNA/P
<i>dmrt1Y</i>	14721	14737	DNA/TcMar
<i>dmrt1Y</i>	18245	18290	DNA/TcMar-Stowaway
<i>dmrt1Y</i>	1831	2517	DNA/TcMar-Tc1
<i>dmrt1Y</i>	2510	3348	DNA/TcMar-Tc1
<i>dmrt1Y</i>	3306	3355	DNA/TcMar-Tc1
<i>dmrt1Y</i>	4165	4206	DNA/TcMar-Tc1
<i>dmrt1Y</i>	26718	27010	DNA/TcMar-Tc1
<i>dmrt1Y</i>	1832	2517	DNA/TcMar-Tc1
<i>dmrt1Y</i>	2512	3344	DNA/TcMar-Tc1
<i>dmrt1Y</i>	26723	26816	DNA/TcMar-Tc1
<i>dmrt1Y</i>	2514	3083	DNA/TcMar-Tc1
<i>dmrt1Y</i>	29654	29689	DNA/TcMar-Tc2
<i>dmrt1Y</i>	30285	30319	DNA/TcMar-Tc2

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Sc. tetracanthus</i> (Class II)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	29663	29851	DNA/TcMar-Tc2
<i>dmrt1Y</i>	29853	30024	DNA/TcMar-Tc2
<i>dmrt1Y</i>	30020	30309	DNA/TcMar-Tc2
<i>dmrt1ΔX</i>	20288	20324	DNA
<i>dmrt1ΔX</i>	10383	10396	DNA/CMC-EnSpm
<i>dmrt1ΔX</i>	10267	10294	DNA/CMC-EnSpm
<i>dmrt1ΔX</i>	17690	17806	DNA/Ginger-1
<i>dmrt1ΔX</i>	30494	30589	DNA/hAT-Ac
<i>dmrt1ΔX</i>	8578	8761	DNA/hAT-Ac
<i>dmrt1ΔX</i>	6714	7030	DNA/hAT-Ac
<i>dmrt1ΔX</i>	4600	4668	DNA/hAT-Ac
<i>dmrt1ΔX</i>	50	275	DNA/hAT-Ac
<i>dmrt1ΔX</i>	17722	17847	DNA/hAT-Ac
<i>dmrt1ΔX</i>	114	267	DNA/hAT-Ac
<i>dmrt1ΔX</i>	10336	10444	DNA/hAT-Tip100
<i>dmrt1ΔX</i>	30242	30292	DNA/P
<i>dmrt1ΔX</i>	30242	30293	DNA/P
<i>dmrt1ΔX</i>	24067	24130	DNA/PIF-Harbinger
<i>dmrt1ΔX</i>	16772	16867	DNA/Sola-1
<i>dmrt1ΔX</i>	10307	10382	DNA/TcMar
<i>dmrt1ΔX</i>	23445	23490	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	21279	21569	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	1517	3008	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	960	1055	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	21379	21533	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	21284	21377	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	16715	16816	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	1517	3006	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	978	1055	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	1866	2747	DNA/TcMar-Tc1
<i>dmrt1ΔX</i>	10295	10306	DNA/Zisupton

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Se. multifasciata</i> (Class I)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	6592	6669	LINE
<i>dmrt1Y</i>	4126	4219	LINE
<i>dmrt1Y</i>	4030	4189	LINE
<i>dmrt1Y</i>	16256	16290	LINE
<i>dmrt1Y</i>	3997	4029	LINE
<i>dmrt1Y</i>	4190	4204	LINE
<i>dmrt1Y</i>	3752	4012	LINE
<i>dmrt1Y</i>	5504	6033	LINE
<i>dmrt1Y</i>	6664	7185	LINE
<i>dmrt1Y</i>	8341	9267	LINE
<i>dmrt1Y</i>	12882	12997	LINE
<i>dmrt1Y</i>	18641	19967	LINE
<i>dmrt1Y</i>	19161	19967	LINE
<i>dmrt1Y</i>	12782	12876	LINE
<i>dmrt1Y</i>	5315	5338	LTR
<i>dmrt1Y</i>	6563	6593	LTR
<i>dmrt1Y</i>	10510	10592	LTR
<i>dmrt1Y</i>	11868	11886	LTR
<i>dmrt1Y</i>	12020	12034	LTR
<i>dmrt1Y</i>	14065	14130	LTR
<i>dmrt1Y</i>	16188	16314	LTR
<i>dmrt1Y</i>	17631	17654	LTR
<i>dmrt1Y</i>	18487	18657	LTR
<i>dmrt1Y</i>	20722	20871	LTR
<i>dmrt1Y</i>	5334	5348	LTR
<i>dmrt1Y</i>	5452	5484	LTR
<i>dmrt1Y</i>	21135	22435	LTR
<i>dmrt1Y</i>	3410	3462	LTR
<i>dmrt1Y</i>	5452	5471	LTR
<i>dmrt1Y</i>	17481	17528	LTR
<i>dmrt1Y</i>	21196	21433	LTR
<i>dmrt1a</i>	25140	25304	LINE
<i>dmrt1a</i>	11204	11228	LINE
<i>dmrt1a</i>	16400	16453	LINE
<i>dmrt1a</i>	12532	12634	LINE
<i>dmrt1a</i>	9326	9472	LTR
<i>dmrt1a</i>	23223	23235	LTR
<i>dmrt1a</i>	23338	23377	LTR
<i>dmrt1a</i>	5838	5848	LTR
<i>dmrt1a</i>	5893	5905	LTR

Table S15. Distribution of transposable elements in *dmrt1* s of three Scatophagidae species

<i>Se. multifasciata</i> (Class II)			
Gene	Start	End	TE type
<i>dmrt1Y</i>	3420	3486	CMC-EnSpm
<i>dmrt1Y</i>	6018	6033	CMC-EnSpm
<i>dmrt1Y</i>	6201	6212	CMC-EnSpm
<i>dmrt1Y</i>	2667	2776	hAT-Ac
<i>dmrt1Y</i>	4395	4583	hAT-Ac
<i>dmrt1Y</i>	5365	5451	hAT-Ac
<i>dmrt1Y</i>	10160	10271	hAT-Ac
<i>dmrt1Y</i>	10285	10381	hAT-Ac
<i>dmrt1Y</i>	10404	10530	hAT-Ac
<i>dmrt1Y</i>	11903	11984	hAT-Ac
<i>dmrt1Y</i>	17529	17614	hAT-Ac
<i>dmrt1Y</i>	18430	18527	hAT-Ac
<i>dmrt1Y</i>	3380	3456	Maverick
<i>dmrt1Y</i>	6137	6210	Maverick
<i>dmrt1Y</i>	14871	14940	Maverick
<i>dmrt1Y</i>	17457	17595	Maverick
<i>dmrt1Y</i>	5472	5506	TcMar-Tc1
<i>dmrt1Y</i>	5622	5681	TcMar-Tc1
<i>dmrt1Y</i>	5702	5751	TcMar-Tc1
<i>dmrt1Y</i>	6034	6155	TcMar-Tc1
<i>dmrt1Y</i>	11885	11966	TcMar-Tc1
<i>dmrt1Y</i>	18314	18454	TcMar-Tc1
<i>dmrt1Y</i>	11064	11203	CMC-EnSpm
<i>dmrt1Y</i>	14127	14170	CMC-EnSpm
<i>dmrt1Y</i>	16414	16491	CMC-EnSpm
<i>dmrt1a</i>	18406	18445	CMC-EnSpm
<i>dmrt1a</i>	25467	25526	CMC-EnSpm
<i>dmrt1a</i>	4403	4607	hAT-Ac
<i>dmrt1a</i>	6607	6819	hAT-Ac
<i>dmrt1a</i>	9028	9267	hAT-Ac
<i>dmrt1a</i>	9296	9410	hAT-Ac
<i>dmrt1a</i>	23852	23964	hAT-Ac
<i>dmrt1a</i>	29240	29419	hAT-Ac
<i>dmrt1a</i>	2631	2683	TcMar-Tc1
<i>dmrt1a</i>	5849	5892	TcMar-Tc1
<i>dmrt1a</i>	11050	11114	TcMar-Tc1
<i>dmrt1a</i>	28560	28613	TcMar-Tc1
<i>dmrt1a</i>	31434	31766	TcMar-Tc1

Table S16. Primers used in this study

Species	Primer sequences (5' to 3')	Amplified fragments (bp)	Application	
<i>Sc. argus</i>	<i>Dmrt1</i> -Marker-4-F4 ^a : TCAGAGCACAATTGTTAGGCAAAGTGAAC	♀: 593 bp, ♂: 593 bp and 693 bp	Gender identification	
	<i>Dmrt1</i> -Marker-4-R4 ^a : TCGCTACTTTCACCAATACAGCATGA			
<i>Sc. tetracanthus</i>	Marker-1-F ^b : TGACCTAGTGGTGGGAATGAATAGAAGA	♀: 873 bp, ♂: 772 bp and 873 bp		
	Marker-1-R ^b : GAAGCAATATGAATGTGATGTG			
	Marker-3-F3 ^c : AGAGCTTGTTTCTCTGATAACTTAAG			♀: 373 bp, ♂: 373 bp and 294 bp
	Marker-3-R3 ^c : GTCACCATCGATGATGGAGCT			
<i>Se. multifasciata</i>	Fxy2: CATTTAGCCTACATTGCCTGTCTCAAG	♀: 436 bp, ♂: 436 bp and 519 bp		
	Rxy1: AAGACCTTTATTGTCATTGGACAGCG			
	Fx1: ACAGGTGTAGTAGATAATCCGACTGCT	♀: 256 bp, ♂: 256 bp	Validation of X chromosome specific fragment	
	Rx2: GGTTCTTGAACAGTCTGGTGAAGGC			
	Fxy1: GTGTGTTGTTCCATGATGTGGGACT	♀: 1443 bp, ♂: 1443 bp	Validation of inversion	
	Rx1: CACCAACAGCAGGACAGATGCTC			
	Fy1: AGTCTGTGAAGATCCACGACGTGT	♀: 0 bp, ♂: 1266 bp	Validation of Y chromosome specific insertion	
	Ry1: GGTTCAGCCTGCTGCAAGAGTTAA			
	Hsd3b-F: GGTAAGACAGTGCCTCAATGTTCTGAG	♀: 214 bp, ♂: 214 bp	RT-PCR internal reference	
	Hsd3b-R: GAAGTTGTAAACAGGAGTTGAAAGCAGC			
a,b,c: The primers were cited from our previous report (a: Huang, et al., 2021; b: Jiang et al., 2022; c: Peng et al., 2023). ♀: female, ♂: male.				

a,b,c: The primers were cited from our previous report (a: Huang, et al., 2021; b: Jiang et al., 2022; c: Peng et al., 2023). ♀: female, ♂: male.