

Table S1. RepeatMasker usage results and features of the sequence elements masked in the adult *C. s. simus* venom gland transcriptomes. Total contigs analyzed: 6484; Total length of sequences: 5043749 nucleotides; GC level: 41.81% number of bases masked: 97204 (1.93% of the total adult *C. s. simus* venom gland transcriptome).

	number of elements	nucleotides	% contig sequences
Retroelements	297	44474	0.88
<u>SINEs:</u>	62	7243	0.14
Penelope	24	2135	0.04
<u>LINEs:</u>	159	29857	0.59
CRE/SLACS	0	0	0.00
L2/CR1/Rex	95	15861	0.31
R1/LOA/Jockey	0	0	0.00
R2/R4/NeSL	6	1580	0.03
RTE/Bov-B	26	8435	0.17
L1/CIN4	8	1846	0.04
<u>LTR elements:</u>	76	7374	0.15
BEL/Pao	1	84	0.00
Ty1/Copia	0	0	0.00
Gypsy/DIRS1	17	1347	0.03
Retroviral	56	5859	0.12
DNA transposons	148	18708	0.37
hobo-Activator	94	11341	0.22
Tc1-IS630-Pogo	40	6558	0.13
En-Spm	0	0	0.00
MuDR-IS905	0	0	0.00
PiggyBac	2	103	0.00
Tourist/Harbinger	1	136	0.00
Other (Mirage, P-element, Transib)	0	0	0.00
Rolling-circles	0	0	0.00
Unclassified:	3	316	0.01
Total interspersed repeats:		63498	1.26
Small RNA:	18	5082	0.10
Satellites:	7	1177	0.02
Simple repeats:	275	11819	0.23
Low complexity:	432	15728	0.31

Table S2. RepeatMasker usage results and features of the sequence elements masked in the neonate *C. s. simus* venom gland transcriptomes. Total contigs analyzed: 6047; Total length of sequences: 3391553 nucleotides; GC level: 42.1%; number of bases masked: 65742 (1.94% of the total newborn *C. s. simus* venom gland transcriptome).

	number of elements	nucleotides	% contig sequences
Retroelements	189	28724	0.85
<u>SINEs:</u>	33	3873	0.11
Penelope	12	929	0.03
<u>LINEs:</u>	95	18524	0.55
CRE/SLACS	0	0	0.00
L2/CR1/Rex	59	9771	0.29
R1/LOA/Jockey	0	0	0.00
R2/R4/NeSL	3	834	0.02
RTE/Bov-B	16	6197	0.18
L1/CIN4	6	846	0.02
<u>LTR elements:</u>	61	6327	0.19
BEL/Pao	3	377	0.01
Ty1/Copia	0	0	0.00
Gypsy/DIRS1	17	2063	0.06
Retroviral	39	3803	0.11
DNA transposons	96	9494	0.28
hobo-Activator	63	5348	0.16
Tc1-IS630-Pogo	22	3686	0.11
En-Spm	0	0	0.00
MuDR-IS905	0	0	0.00
PiggyBac	1	55	0.00
Tourist/Harbinger	0	0	0.00
Other (Mirage, P-element, Transib)	0	0	0.00
Rolling-circles	0	0	0.00
Unclassified:	2	157	0.00
Total interspersed repeats:		38375	1.13
Small RNA:	50	11190	0.33
Satellites:	6	965	0.03
Simple repeats:	172	6799	0.20
Low complexity:	221	8557	0.25