

Table S1. Number of reads obtained after sequencing by Illumina of the mRNA present in the Philodryadini venom glands and the number of contigs generated after *De novo* assembly.

Snake Code	Species	Merged reads	% of Merged*	Number of Contigs generated
SB0512	<i>Chlorosoma laticeps</i>	13.240.744	85.49%	204.864
SB0307	<i>Philodryas nattereri</i>	15.939.987	90.31%	263.673
SB0132	<i>Philodryas olfersii latirostris</i>	13.401.460	91.04%	162.859
SB0001	<i>Philodryas olfersii</i>	2.403.169	98.26%	57.270
SB0026	<i>Philodryas olfersii</i>	3.413.445	98.60%	82.665
SB0235	<i>Philodryas patagoniensis</i>	23.939.713	87.12%	183.351
SB0183	<i>Philodryas agassizii</i>	13.705.159	85.30%	213.881
SB0559	<i>Chlorosoma viridissimum</i>	16.716.391	84.49%	180.929
SB1590	<i>Xenoxybelis argenteus</i>	8.515.040	82.90%	171.648
SB1881	<i>Philodryas mattogrossensis</i>	7.508.732	82.41%	239.553

*The paired reads were merged based on their 3' overlaps using PEAR version 0.9.6 (Zhang et al. 2014).