

Species	Clean reads	PCR duplicates	Assembled contigs	ORF			UTR		
				Gene recovered	Nucleotide recovered	On-target	Gene recovered	Nucleotide recovered	On-target
Ingroup									
<i>Plagiopholis styani</i>	60,795,890	20.36%	365,681	5,164	34.29%	16.44%	5,412	44.61%	25.85%
<i>Pseudoxenodon macrops</i>	78,044,194	24.34%	446,368	5,943	32.78%	8.50%	5,708	45.00%	21.27%
<i>Thermophis baileyi</i>	121,958,470	14.66%	758,196	7,380	44.11%	18.42%	6,999	52.85%	33.92%
<i>Heterodon platirhinos</i>	85,732,278	42.96%	548,110	5,509	27.26%	4.23%	5,072	40.59%	11.40%
<i>Amphiesma stolatum</i>	135,414,168	17.08%	782,280	7,768	50.71%	19.17%	7,143	54.23%	25.88%
<i>Sinonatrix annularis</i>	81,550,178	22.64%	596,605	6,824	38.30%	11.15%	6,523	48.97%	22.94%
<i>Rhabdophis tigrinus</i>	47,808,108	35.74%	372,907	4,603	25.27%	17.62%	4,317	41.82%	25.97%
<i>Xenochrophis flavipunctatus</i>	66,927,480	26.62%	417,738	5,783	34.74%	12.34%	5,715	44.46%	18.69%
<i>Opisthotropis maxwelli</i>	91,997,080	37.58%	616,961	5,972	31.12%	7.91%	5,482	44.47%	15.01%
<i>Hebius boulengeri</i>	115,780,018	43.83%	747,991	6,598	33.85%	10.54%	5,993	45.94%	13.99%
<i>Sibynophis chinensis</i>	67,980,026	27.18%	269,074	3,113	29.63%	11.71%	3,887	34.48%	27.72%
<i>Calamaria septentrionalis</i>	71,085,760	20.78%	475,129	5,687	32.37%	10.46%	5,401	44.10%	19.98%
<i>Dendrelaphis pictus</i>	82,339,908	16.23%	544,042	5,874	31.92%	12.56%	5,693	45.58%	29.65%
<i>Ahaetulla prasina</i>	81,929,996	19.86%	598,605	6,484	34.78%	11.96%	6,246	49.05%	24.15%
<i>Chrysopelea ornata</i>	87,456,898	14.21%	612,235	6,638	38.19%	14.18%	6,316	52.03%	30.75%
<i>Rhadinophis frenata</i>	96,678,378	22.00%	583,423	6,167	34.52%	11.91%	6,322	47.16%	29.88%
<i>Lycodon synaptor</i>	72,582,564	32.81%	603,426	5,957	27.72%	14.17%	5,613	45.05%	30.61%
<i>Oocatochus rufodorsatus</i>	62,153,044	19.04%	420,856	5,188	32.55%	12.02%	5,443	44.96%	33.31%
<i>Oreophis porphyraceus</i>	68,207,464	16.49%	655,878	6,555	33.80%	12.79%	6,101	46.57%	23.29%
<i>Cyclophiops major</i>	73,240,880	20.66%	524,248	6,128	35.06%	14.53%	6,170	47.18%	26.25%
<i>Boiga multomaculata</i>	85,813,374	19.60%	872,008	6,912	39.62%	10.90%	6,794	53.16%	24.57%
<i>Oligodon formosanus</i>	62,517,614	21.80%	449,851	5,995	35.69%	15.05%	6,156	47.88%	27.86%
<i>Elaphe carinata</i>	80,969,918	22.40%	492,163	5,742	32.80%	12.46%	6,055	48.23%	27.42%
<i>Euprepiophis perlacea</i>	87,007,252	21.04%	566,566	5,979	33.71%	16.55%	5,985	44.49%	32.79%
Outgroup									
<i>Achalinus spinalis</i>	36,768,628	25.49%	158,424	3,839	30.16%	9.98%	3,259	32.52%	11.65%
<i>Pareas margaritophorus</i>	52,202,066	41.27%	333,058	4,121	23.05%	5.17%	3,711	33.11%	18.23%
<i>Gloydius shedaoensis</i>	56,946,830	40.29%	514,229	5,958	27.46%	10.66%	5,288	38.94%	19.04%
<i>Daboia siamensis</i>	46,528,424	35.16%	397,272	4,925	25.79%	10.40%	4,326	37.60%	25.46%
<i>Azemiope feae</i>	60,036,632	39.61%	417,865	5,545	26.40%	8.66%	4,832	38.47%	15.00%
<i>Viridovipera stejnegeri</i>	72,691,804	40.07%	588,360	6,003	29.93%	7.66%	5,472	42.03%	16.46%
<i>Ovophis monticola</i>	40,247,260	36.22%	334,449	4,855	25.18%	12.01%	4,371	38.41%	20.04%
<i>Protobothrops jerdonii</i>	62,216,044	42.04%	568,009	6,297	30.54%	11.02%	5,543	41.62%	16.63%
<i>Sinomicrurus maclellandi</i>	40,974,674	14.08%	287,131	4,448	29.51%	11.67%	4,333	41.22%	25.90%
<i>Naja atra</i>	47,385,794	16.84%	319,872	4,897	30.14%	7.98%	4,700	41.30%	19.15%
<i>Bungarus multicinctus</i>	45,892,326	23.05%	292,234	4,577	29.73%	8.14%	4,408	39.74%	14.63%
<i>Myrrophis chinensis</i>	48,918,330	39.36%	462,418	5,266	26.54%	16.71%	4,850	40.15%	26.44%

Table 2. Capture and sequencing results and detailed information from the bioinformatic pipeline for each sample.