

Supplementary Table 2

Species	# of sequences	total # of bases	average sequence length	average sequence quality	% GC
<i>Acanthophis wellsi</i>	55,372	15,197,836	274	30.71	50.34
<i>Brachyuropis roperi</i>	55,694	15,892,775	285	30.42	45.89
<i>Cacophis squamulosus</i>	38,985	14,068,260	360	32.21	48.73
<i>Denisonia devisii</i>	28,275	8,059,988	285	30.52	49.75
<i>Echiopsis curta</i>	59,740	17,191,872	287	30.40	49.76
<i>Furina ornate</i>	46,190	13,117,708	283	30.39	49.19
<i>Hemiaspis signata</i>	48,904	18,095,514	370	32.13	57.09
<i>Hoplocephalus bungaroides</i>	47,675	13,050,675	273	32.37	56.52
<i>Pseudonaja modesta</i>	51,984	14,959,557	287	30.51	48.99
<i>Suta fasciata</i>	90,963	26,698,687	293	30.35	47.26
<i>Vermicella annulata</i>	49,960	14,653,238	293	32.71	55.39

Supplementary Table 3

Species	# of contigs	Assembled bases	Average bases per contig
<i>Acanthophis wellsi</i>	2,657	1,284,940	484
<i>Brachyuropis semifasciata</i>	5,493	2,794,630	509
<i>Denisonia devisi</i>	1,572	774,029	492
<i>Echiopsis curta</i>	2,998	1,534,906	512
<i>Furina ornata</i>	3,137	1,555,634	496
<i>Cacophis squamulosus</i>	3,015	1,638,379	543
<i>Hemiaspis signata</i>	1,431	728,481	509
<i>Hoplocephalus bungaroides</i>	3,939	2,150,604	546
<i>Pseudonaja modesta</i>	3,335	1,708,478	512
<i>Suta fasciata</i>	6,180	3,391,483	549
<i>Vermicella annulata</i>	3,711	1,842,636	497