

Figure S1. Venom gland transcriptome of two individuals of *Bothrops cotiara*.

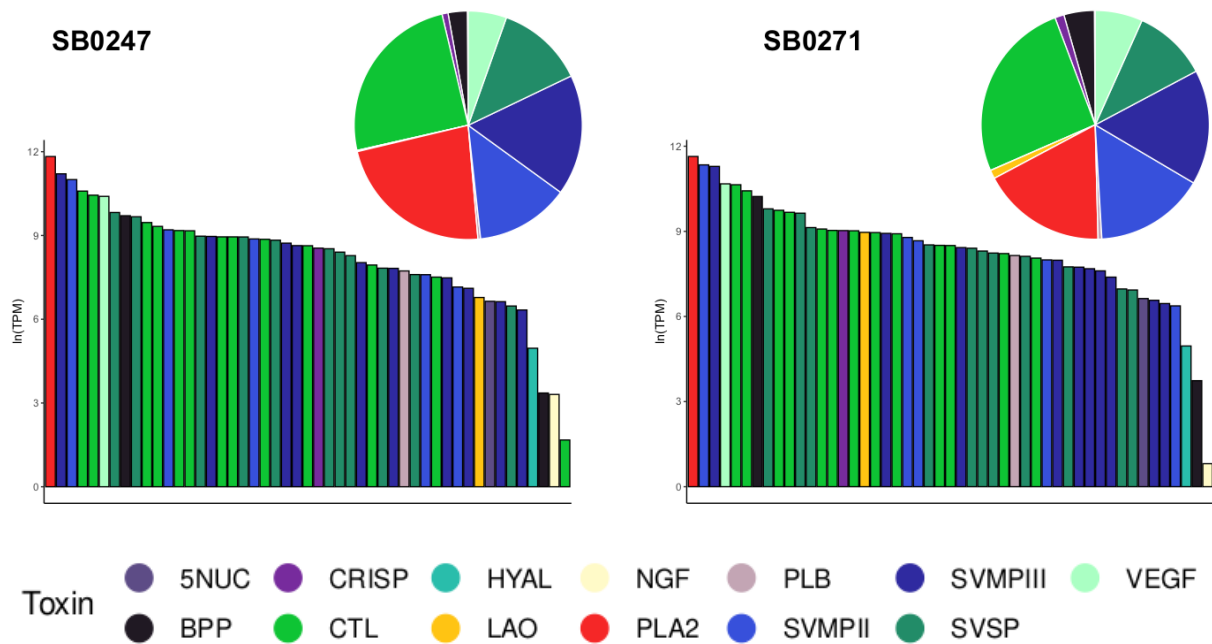


Figure S2. Venom gland transcriptome of two individuals of *Bothrops fonsecai*.

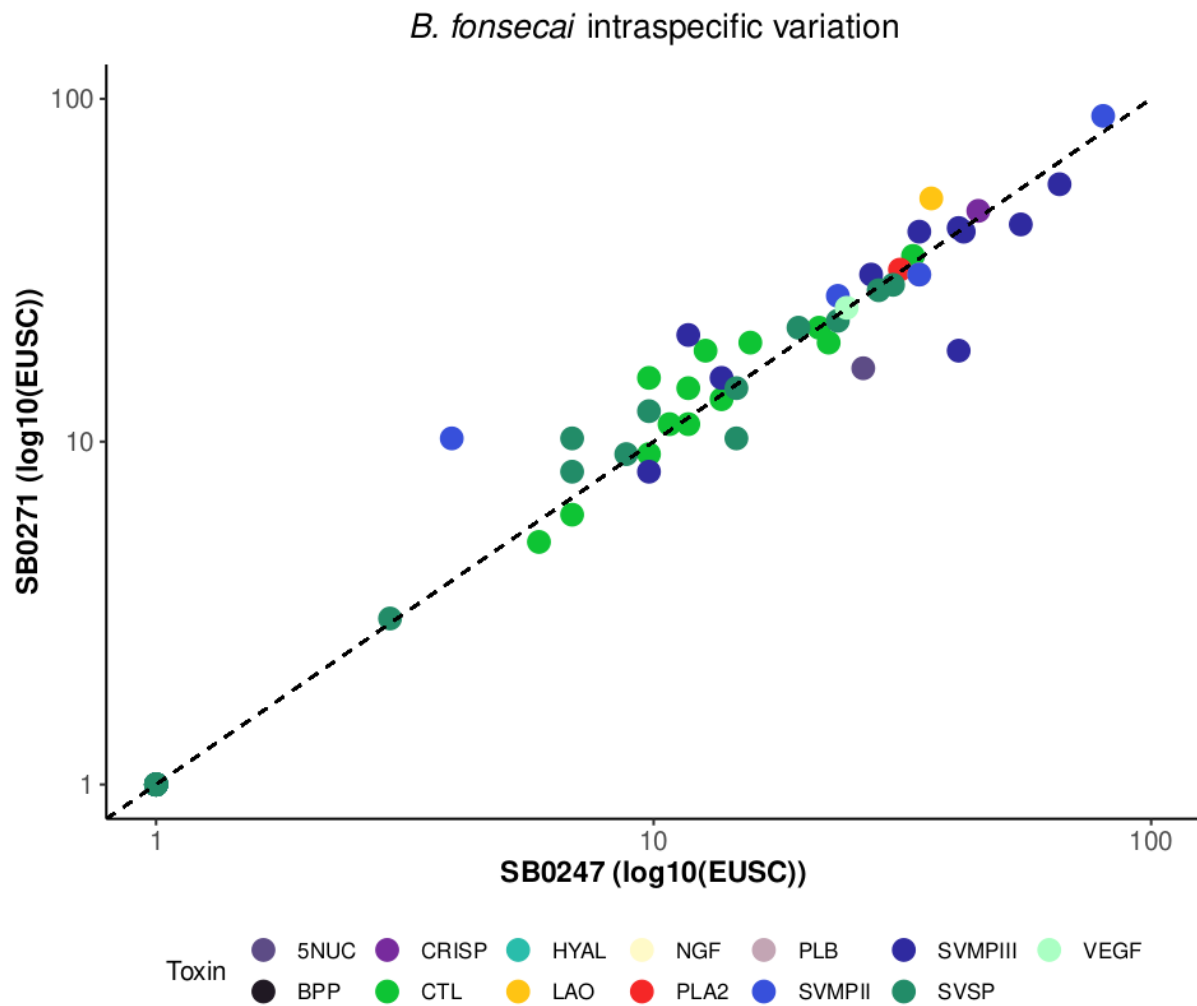


Figure S3. Intraspecific variation in the venom proteome of *Bothrops fonsecai*. The dashed line indicates a hypothetical correspondence of protein abundances between individuals.

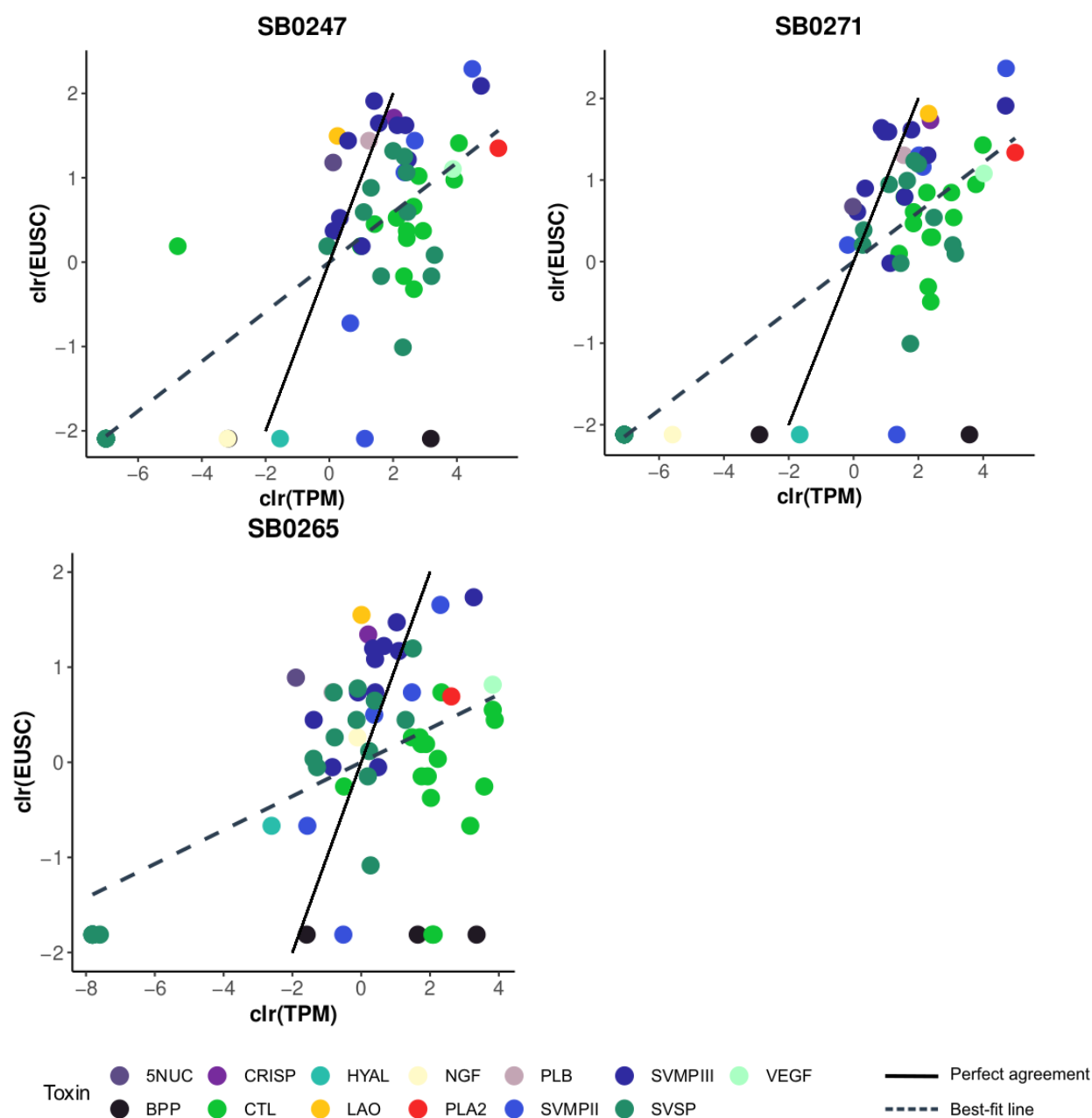


Figure S4. Comparison between levels of transcripts (TPM) and protein abundance (normalized EUSC - Exclusive Unique Spectrum Count) in the samples analyzed of *B. cotiara* (SB0265 [$p = 0.26$; $R = 0.49$]) and *B. fonsecai* (SB0247 [$p = 0.60$; $R = 0.78$] and SB0271 [$p = 0.61$; $R = 0.81$]). All data were centered log-ratio transformed (clr). Black lines indicate a perfect agreement between transcript and protein abundances. Dashed lines indicate the best-fit line between transcript and protein abundances.

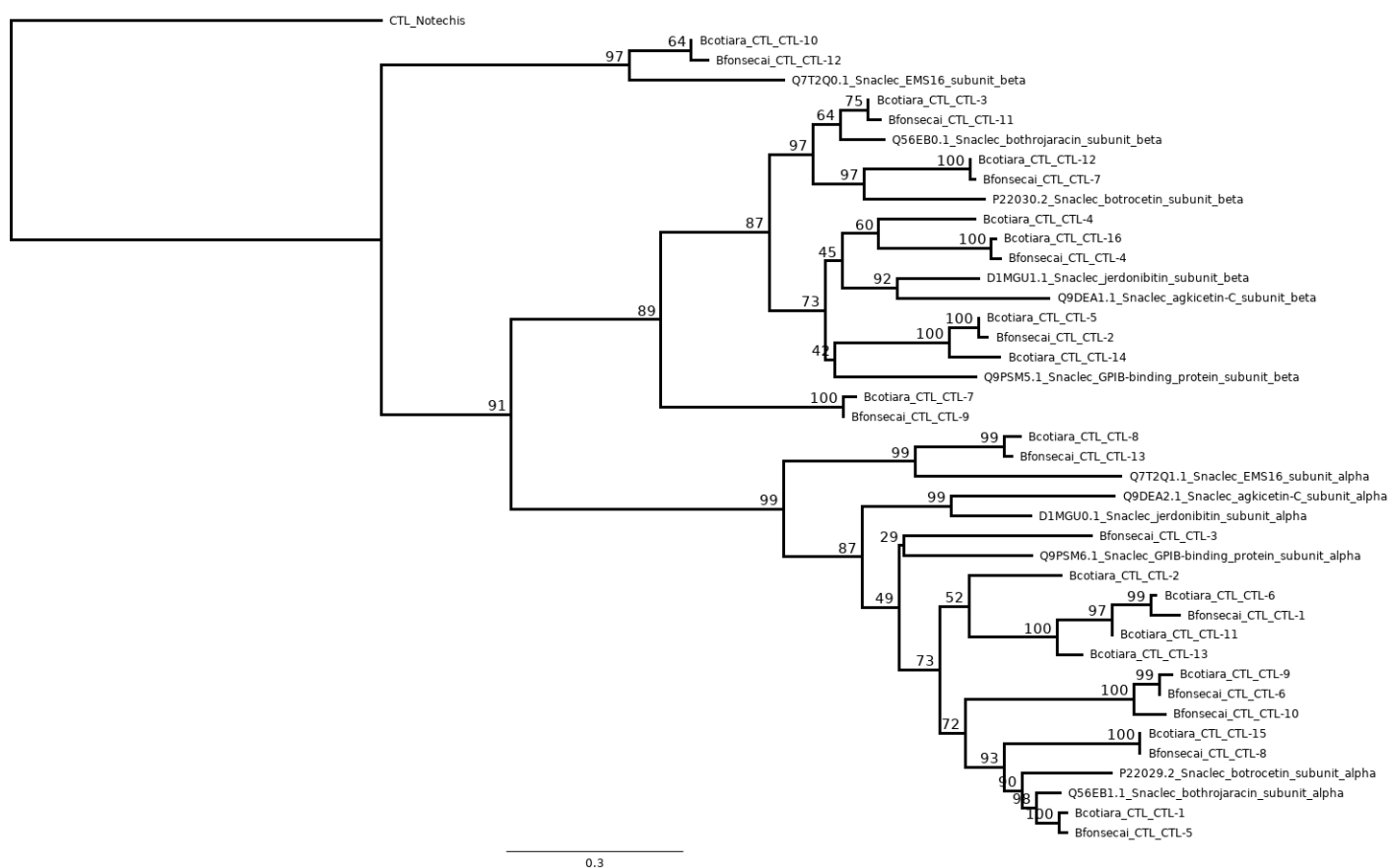


Figure S5. CTL phylogeny with known alpha and beta chain CTL homologs of several snake species. The support values of bootstrap are given in tree branches.

