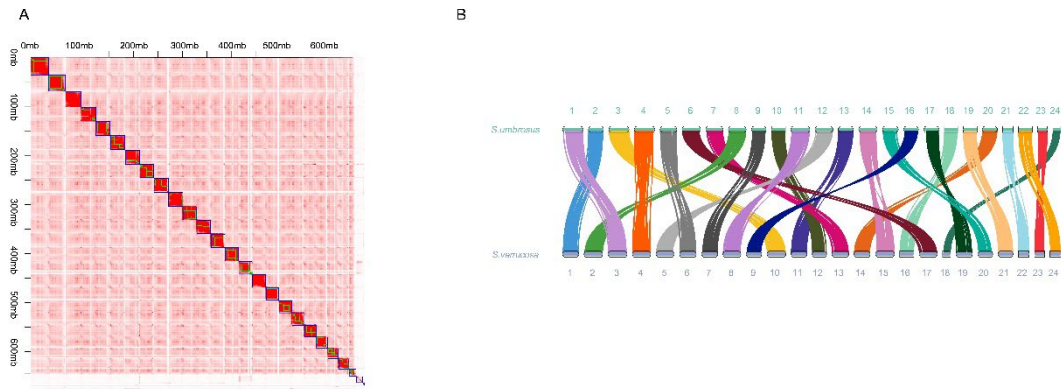
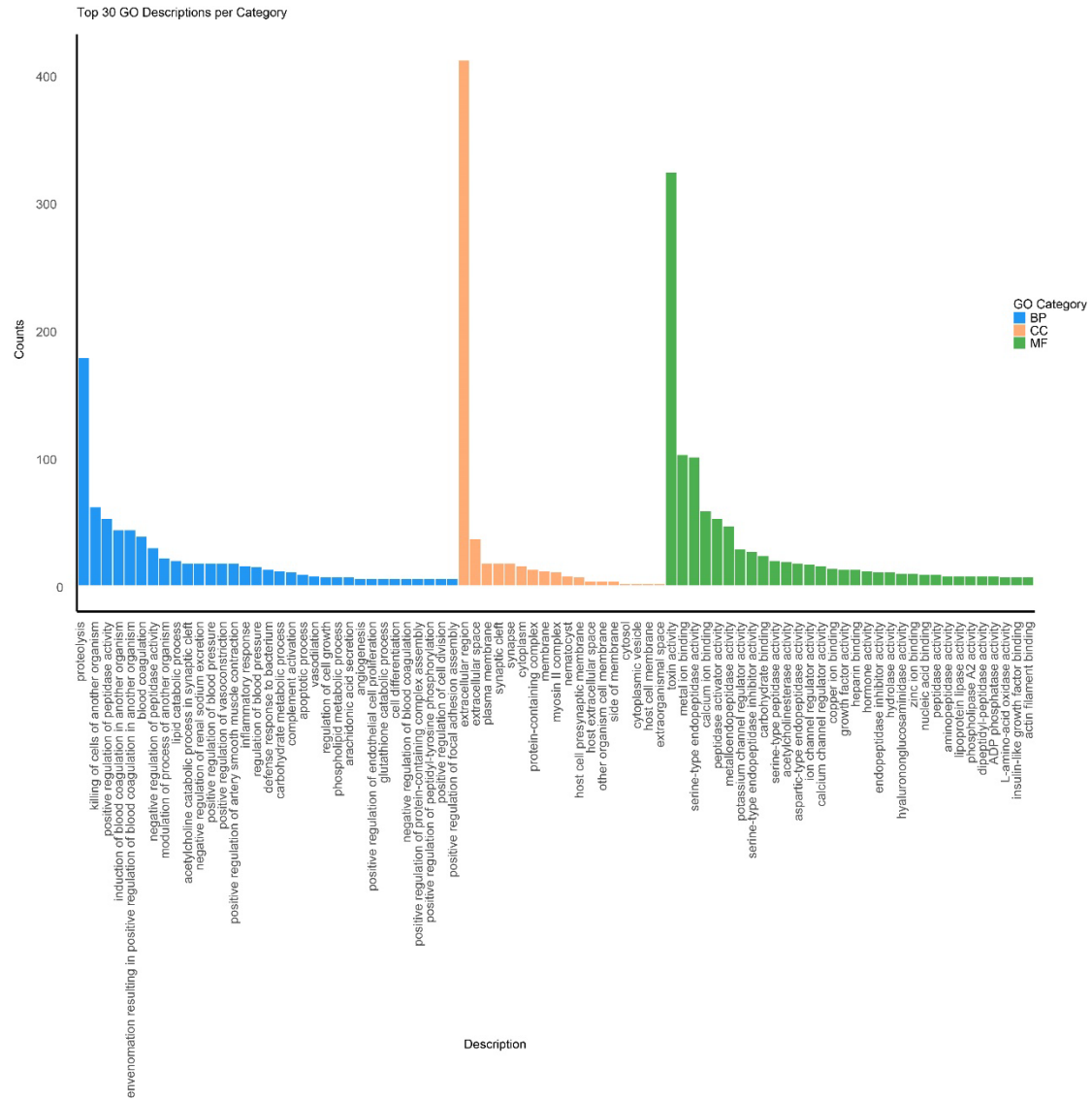




Supplementary Figure 1 Genome assembly of *S. verrucosa*

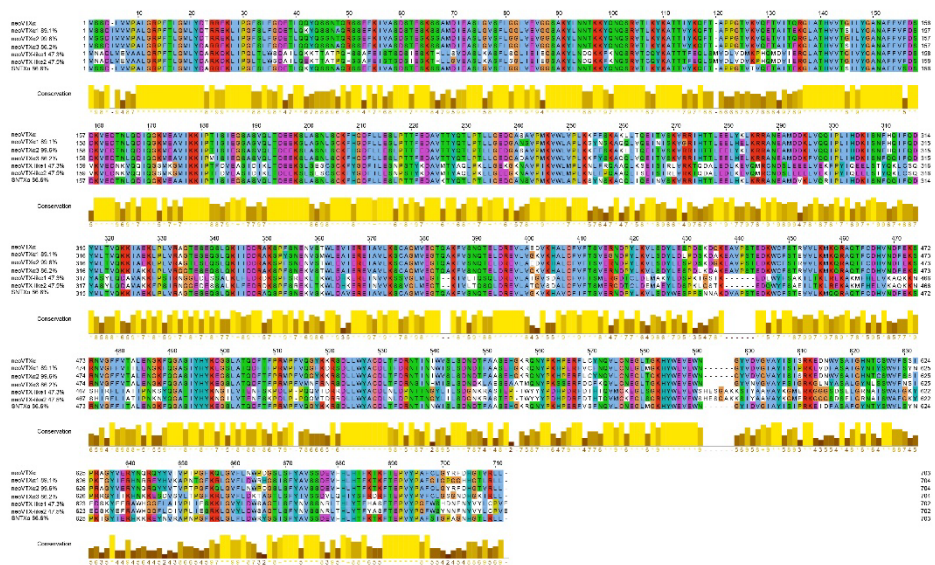
A) Hi-C contact map showing genome-wide pairwise chromatin interactions of 24 chromosomes. B) Synteny between the chromosomes of *S. verrucosa* and *S. umbrosus*. The links inside referred to internal syntenic blocks within the genomes.



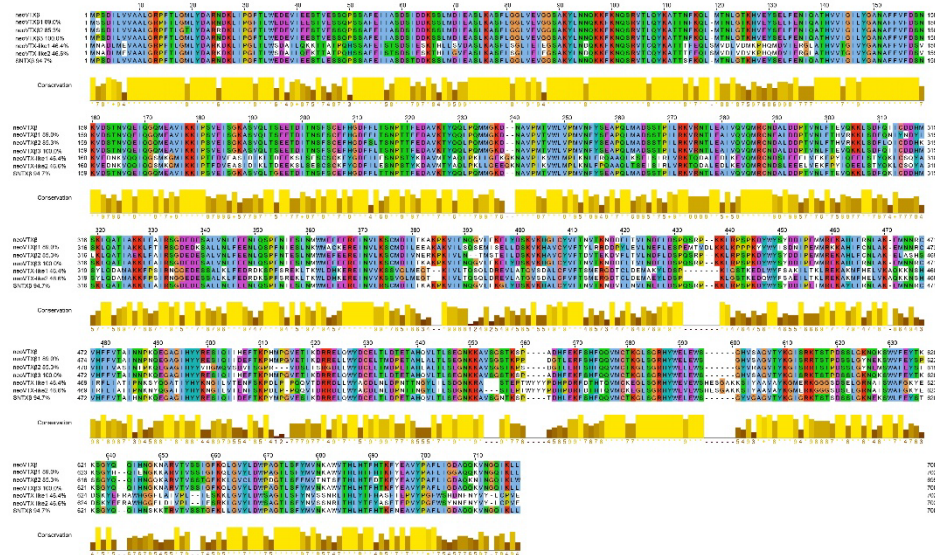
Supplementary Figure 2 Gene ontology enrichment analysis of putative toxin genes

Enriched GO terms of all the annotated 478 toxin genes in biological process (BP), cellular components (CC); and molecular function (MF).

A

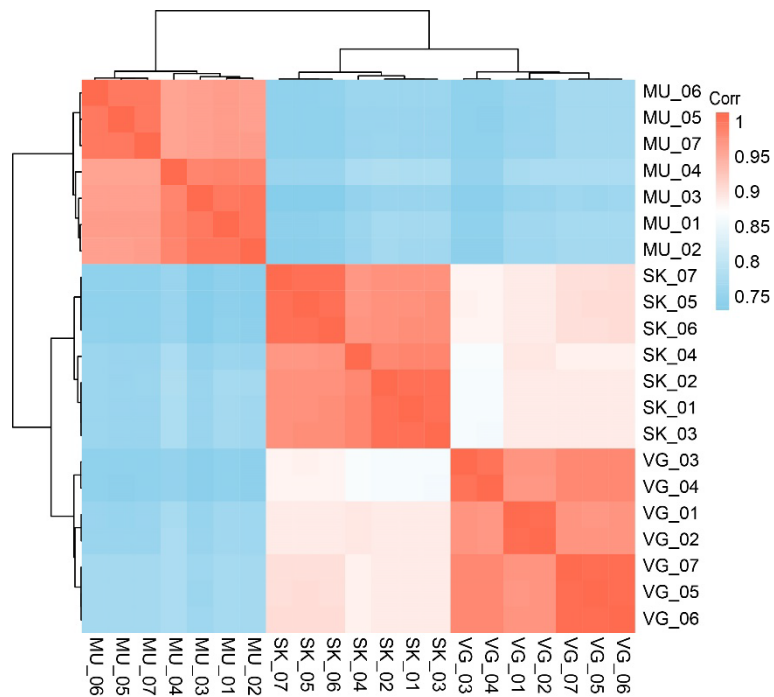


B



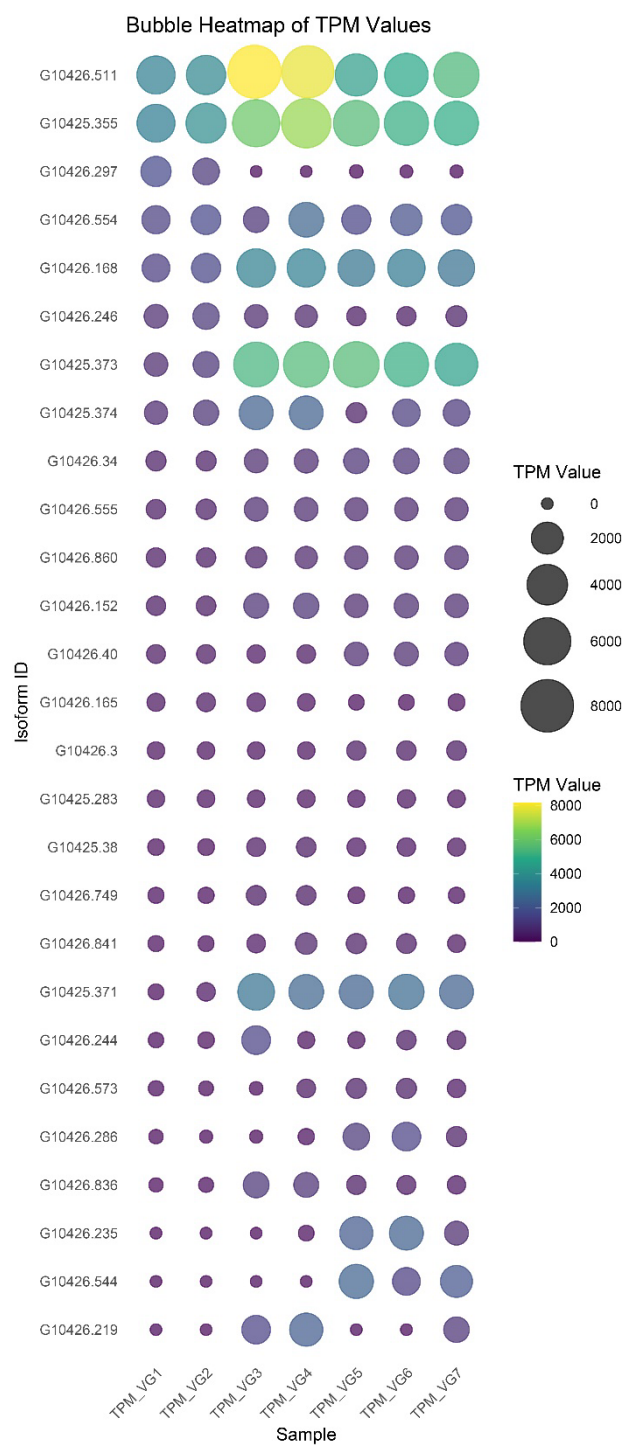
Supplementary Figure 3 Amino sequence alignment of the tandem-duplicated neoVTX genes

A) Pairwise alignment of neoVTX-α1, neoVTX-α2, neoVTX-α3, neoVTX-like1, neoVTX-like 2 and SNTXα (AAC60022) against with neoVTXα (BAF41221). B) Pairwise alignment of neoVTX-β1, neoVTX-β2, neoVTX-β3, neoVTX-like1, neoVTX-like2 and SNTXβ (AAC60021) against with neoVTXβ (BAF41222). Histogram at the top represented the conservation level (0 to 10) of each site.



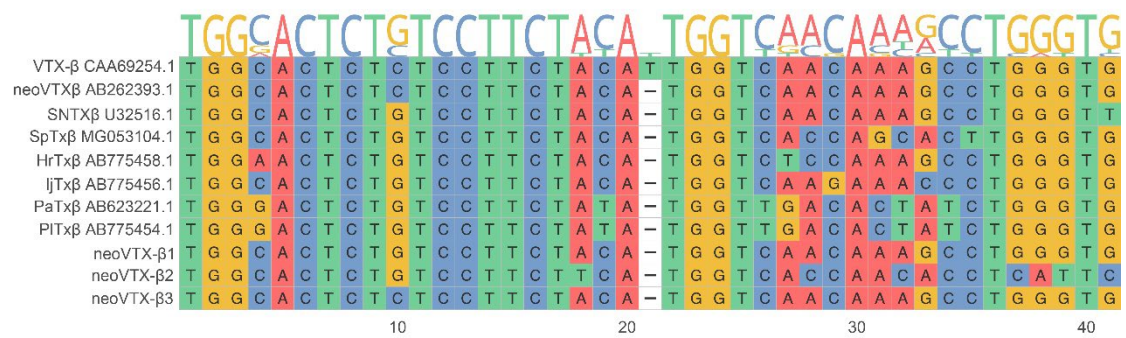
Supplementary Figure 4 Sample correlation analysis among venom gland, skin and muscle

Dendrograms displayed hierarchical clustering of rows and columns, representing the relationships among samples. Each cell represents the correlation coefficient between samples, with deeper colors indicating stronger correlations. Color from blue to red indicated the correlation level.



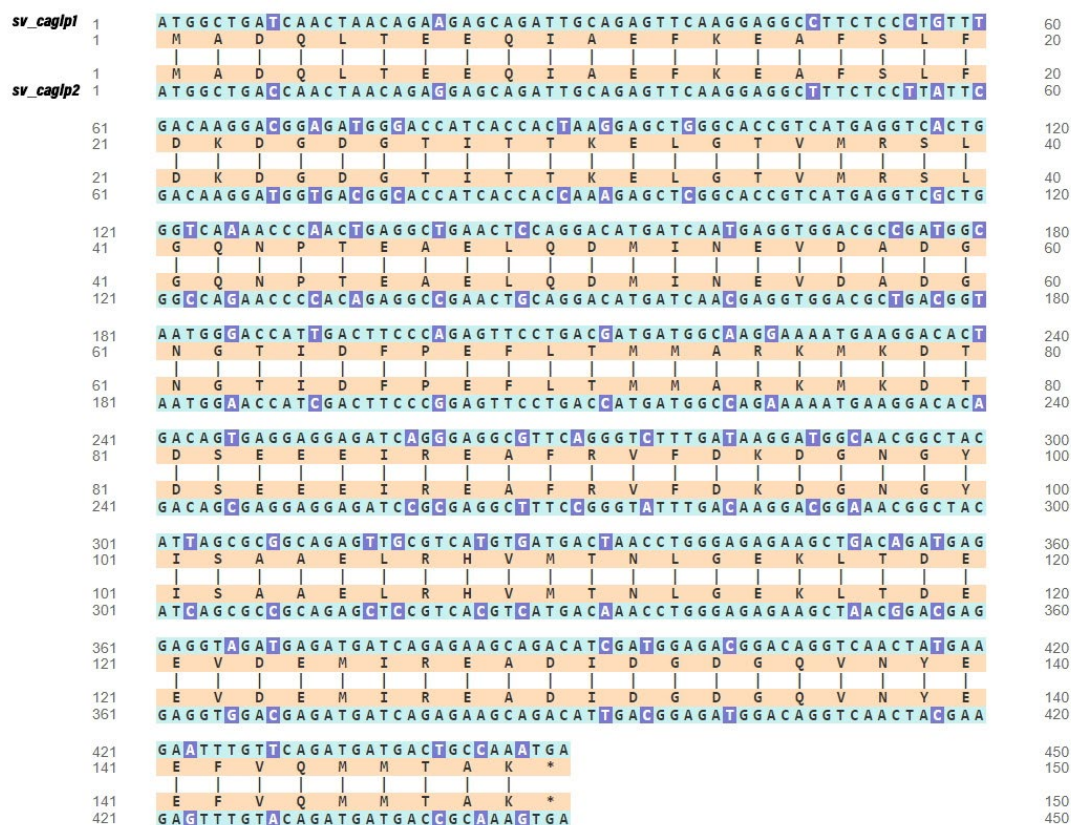
Supplementary Figure 5 Bubble plot analysis of heterogenous expression pattern of the AS isoforms

Expression pattern of the neoVTX major isoforms in all the 7 venom gland samples. Bubble size and color were both used to indicate the expression level.



Supplementary Figure 6 Alignment of a discriminative loci in the neoVTX β subunit genes

A discriminative among all the neoVTX β subunit homologue genes were shown. SpTxβ, *Scorpaena plumieri*; HrTxβ, *Hypodytes rubripinnis*; IjTxβ, *Inimicus japonicus*; PaTxβ, *Peterois antennata*; PlTxβ, *Pterois lunulate*.



Supplementary Figure 7 Sequence similarity between CAGLP1 with CAGLP2.

Alignment of CDS and amino acid sequences of *sv_caglp2* and *sv_caglp2*, with non-consensus sites highlighted