Supplementary Figures

Comparative venomics of *C. flavidus* and *C. frigidus* and closely related vermivorous cone snails.

Himaya S.W.A.[1,*], Alexander Arkhipov[1,2], Wai Ying Yum [1] and Richard J. Lewis[1,*]

[1] Institute for Molecular Bioscience, The University of Queensland, St Lucia, QLD 4072, Brisbane, Australia
[2] Current address - School of Agriculture and Food Science, The University of Queensland, St Lucia, QLD 4072, Brisbane, Australia
* Correspondence to: R.J.L. r.lewis@uq.edu.au; Tel.: +61 7 334 62984; H.S.W.A. h.sddhihalu@imb.uq.edu.au; Tel.: +61 7 334 62722

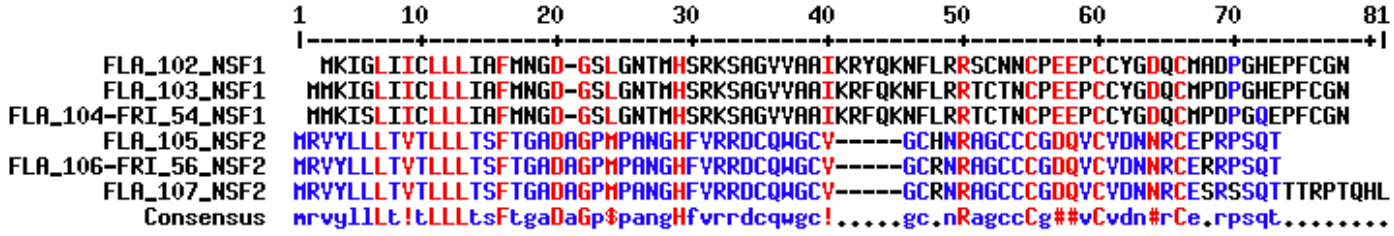

Figure S1: Sequence alignment of the New Superfamily 1 (NSF1) and 2 (NSF2) precursors

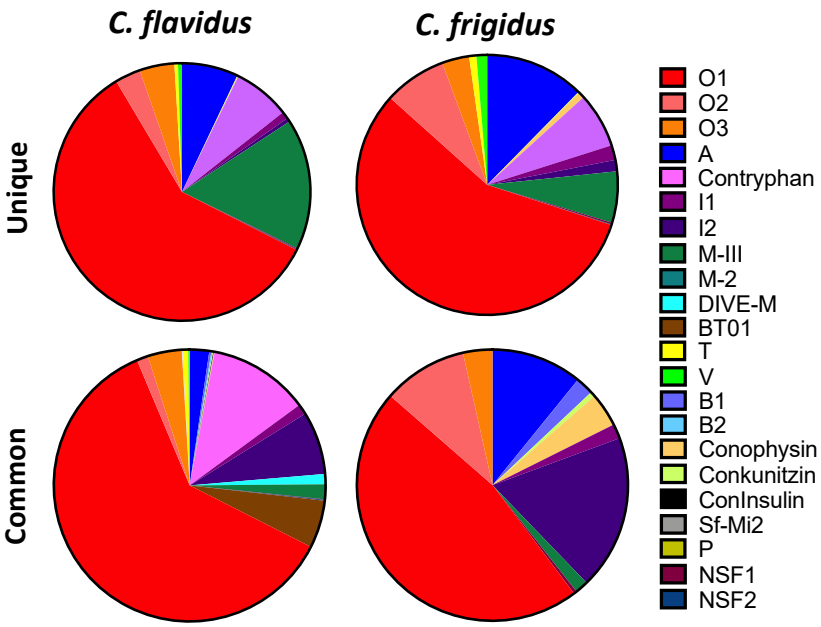

Figure S2: The superfamily expression profile of the unique (only found in one species) and common (found in both species) sequences in *C. flavidus* and *C. frigidus* transcriptomes.

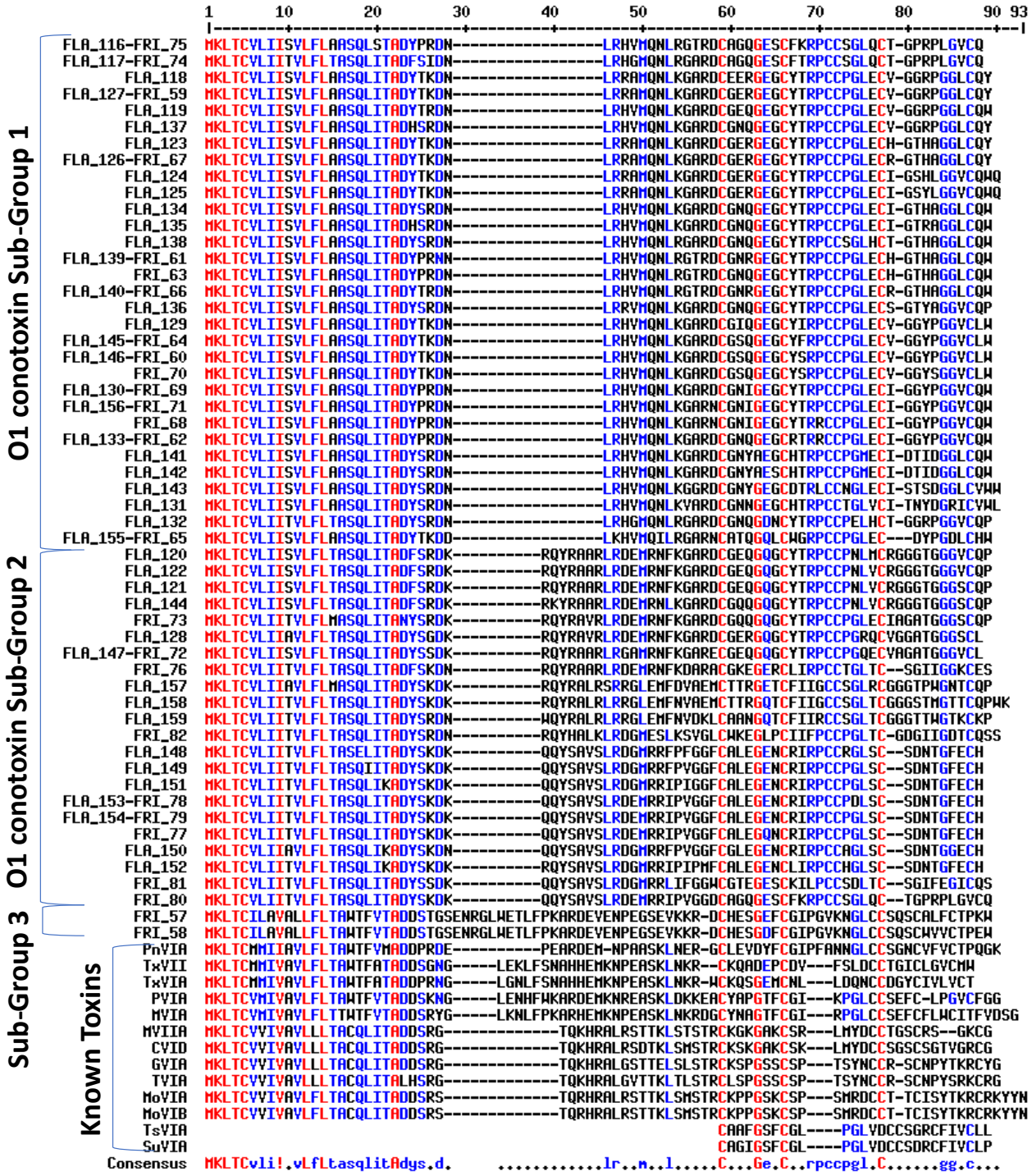

Figure S3 : Alignment of O1 conotoxin precursors found in *C. flavidus* and *C. frigidus* transcriptomes. The precursor sequences were classified into three subgroups based on the sequence similarity. Known O1 superfamily ω- and δ-conotoxins from fish, mollusk and worm hunting cone snails were aligned with the *C. flavidus* and *C. frigidus* O1 precursors using Clustal Omega. Conserved amino acids are highlighted and the consensus sequence shown at the bottom.

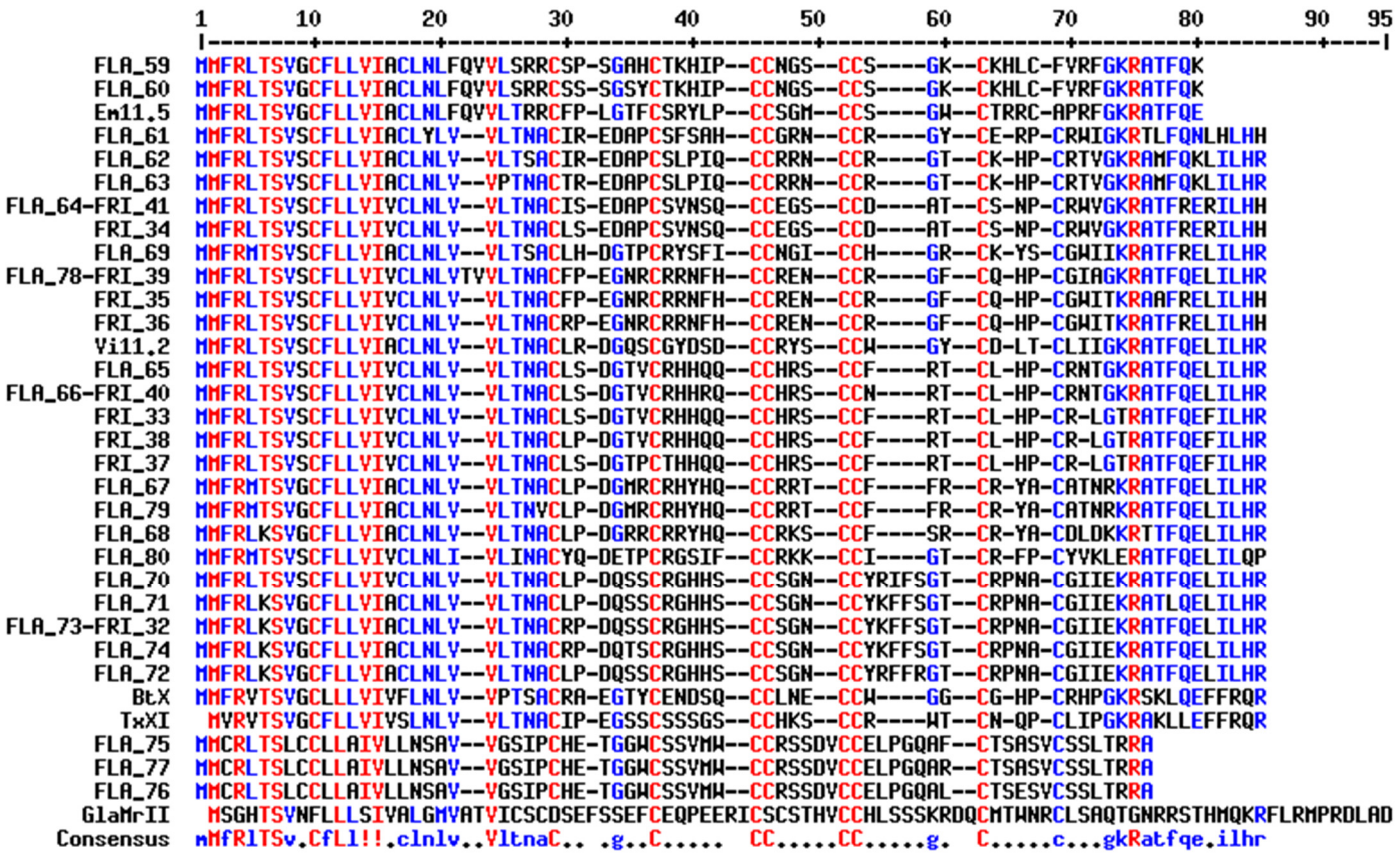

Figure S4 : I2 conotoxin precursors aligned with known I2 conotoxin precursors from other Cone snails (Vi11.2, Btx, TxXI and GlaMrII).

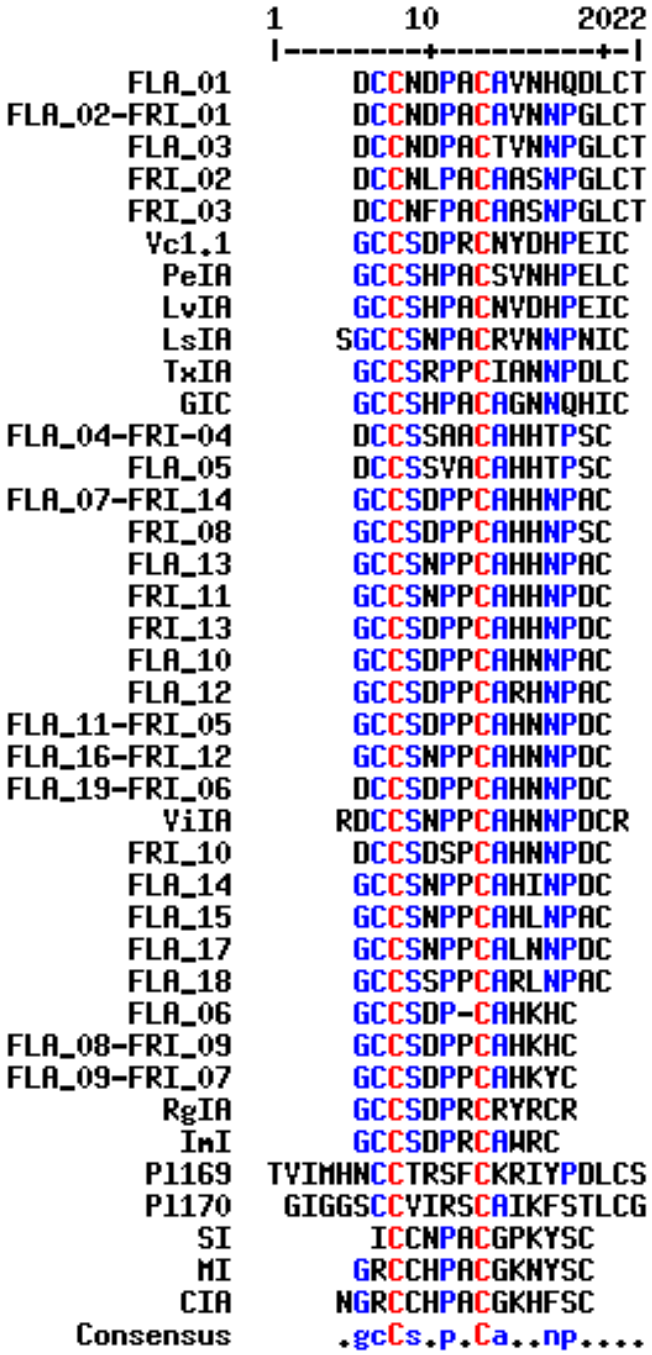

Figure S5: A conotoxins aligned with known A conotoxins from other fish (SI, MI, CIA, GIC), mollusk (TxIA) and worm hunters (PeIA, LvIA, LsIA, ViIA, RgIA, ImI, Pl169, Pl170).

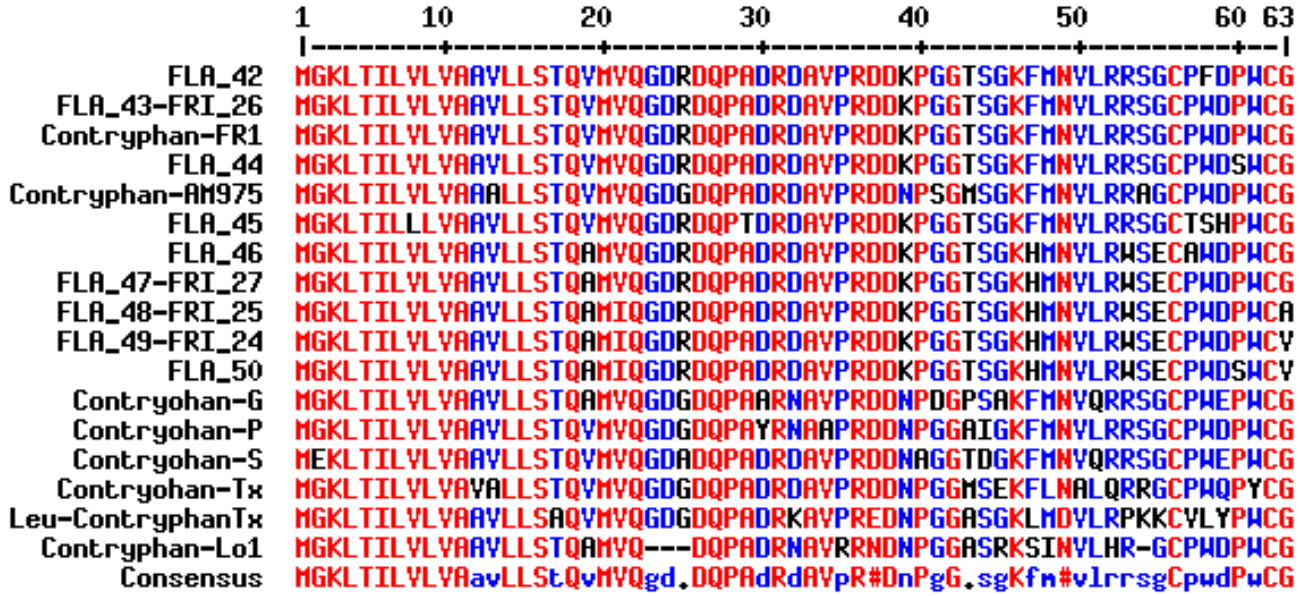

Figure S6: Contryphan precursors aligned with known Contryphan precursors from other fish (Contryphan-G, Contryphan-S Contryphan-P), mollusk (Contryphan-Tx, Leu-Contryphan-Tx) and worm (Contryphan-Lo1) hunters.

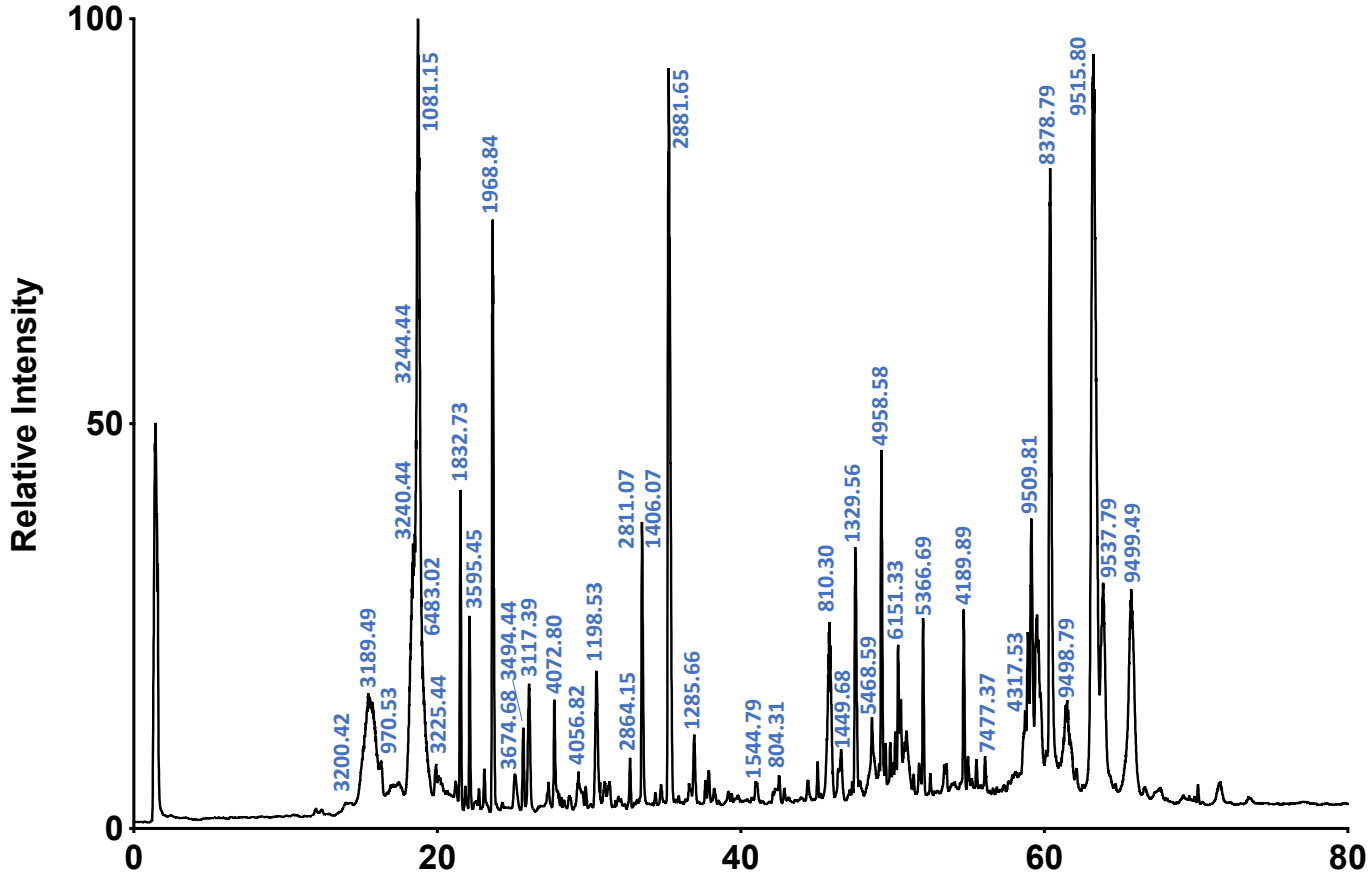

Figure S7: TIC of the *C. flavidus* Proximal venom duct showing dominant masses eluting under major peaks.

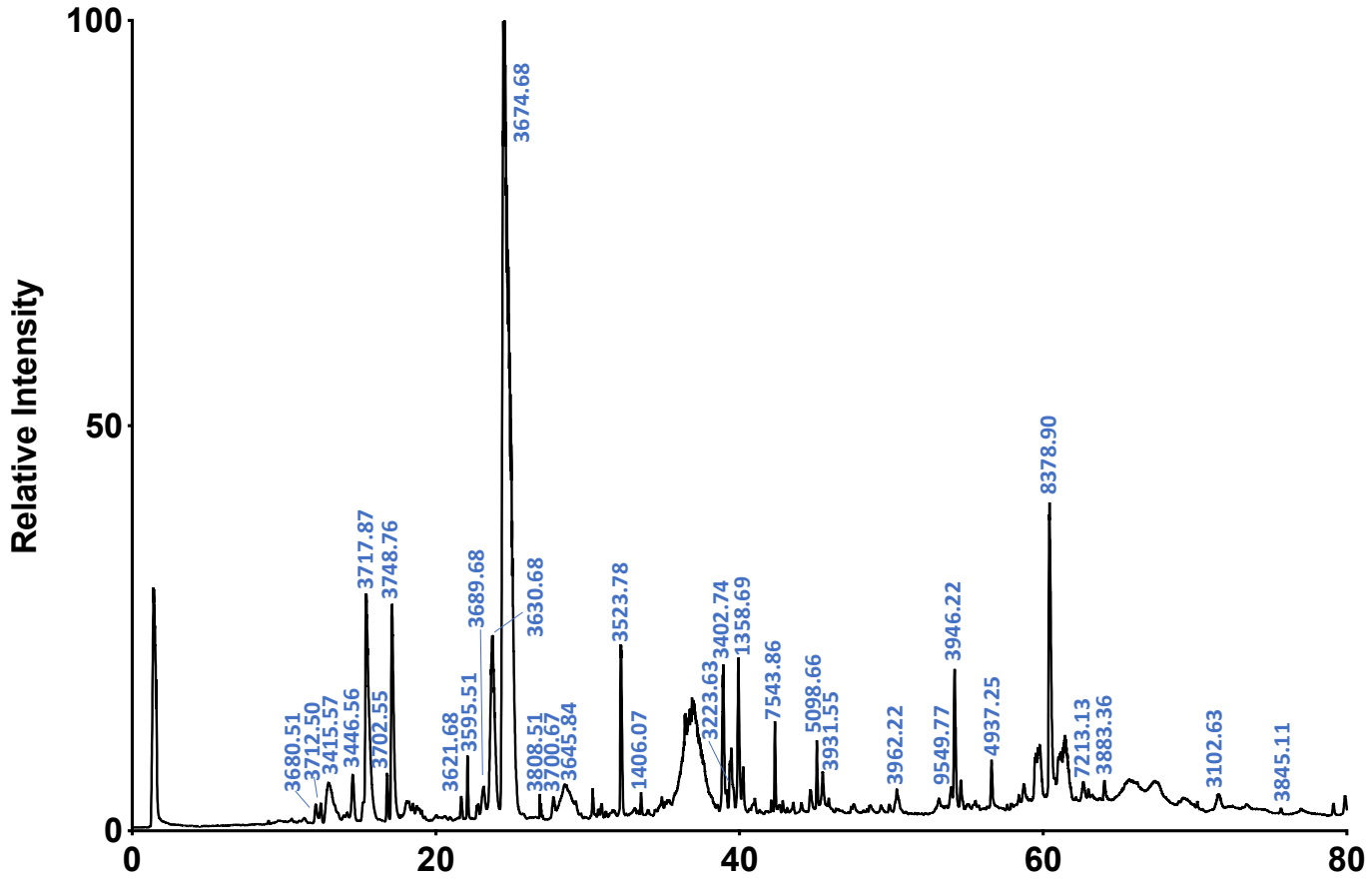

Figure S8: TIC of the *C. flavidus* Distal venom duct showing dominant masses eluting under major peaks.

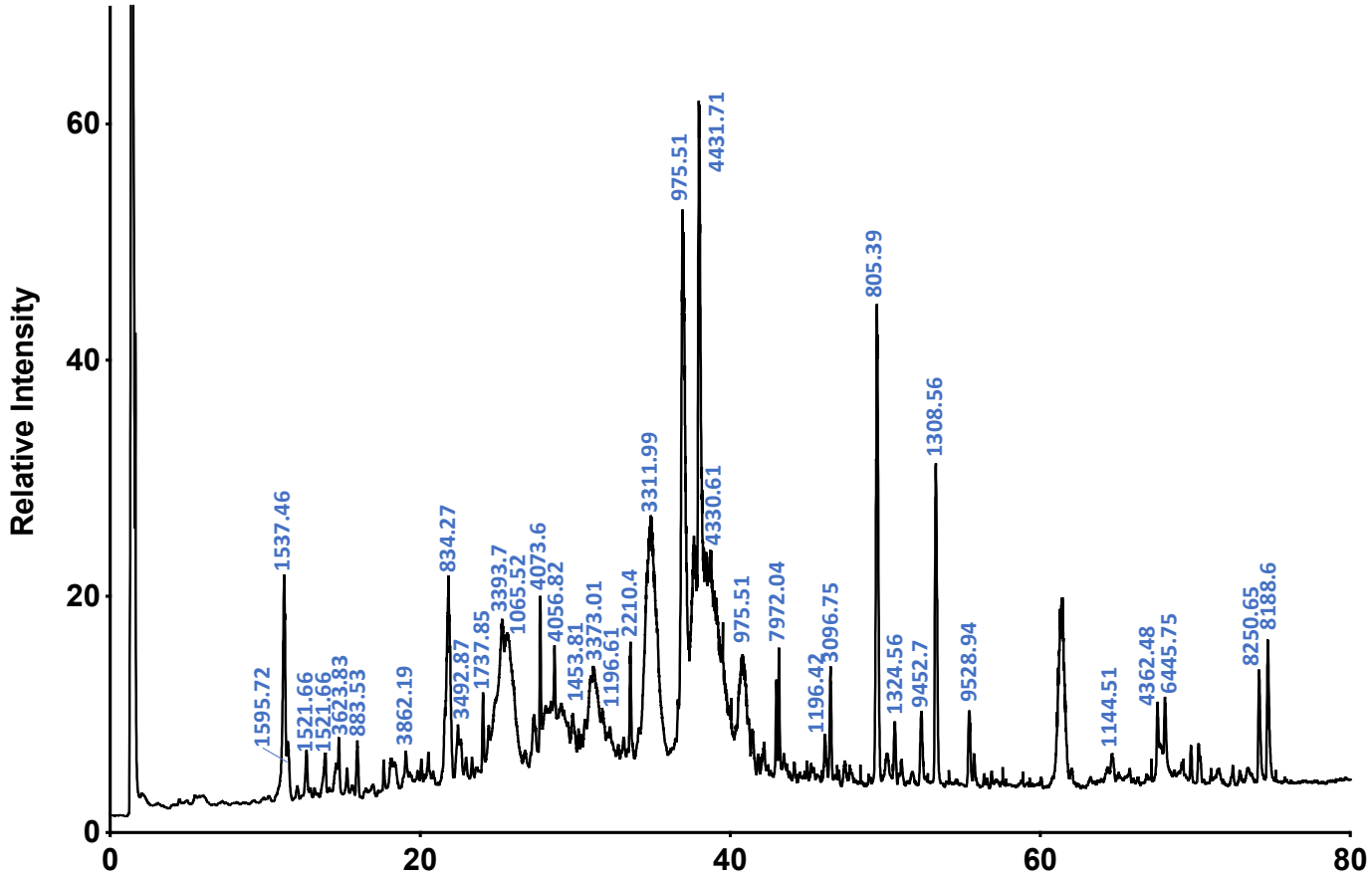

Figure S9: TIC of the *C. frigidus* Proximal venom duct showing dominant masses eluting under major peaks.

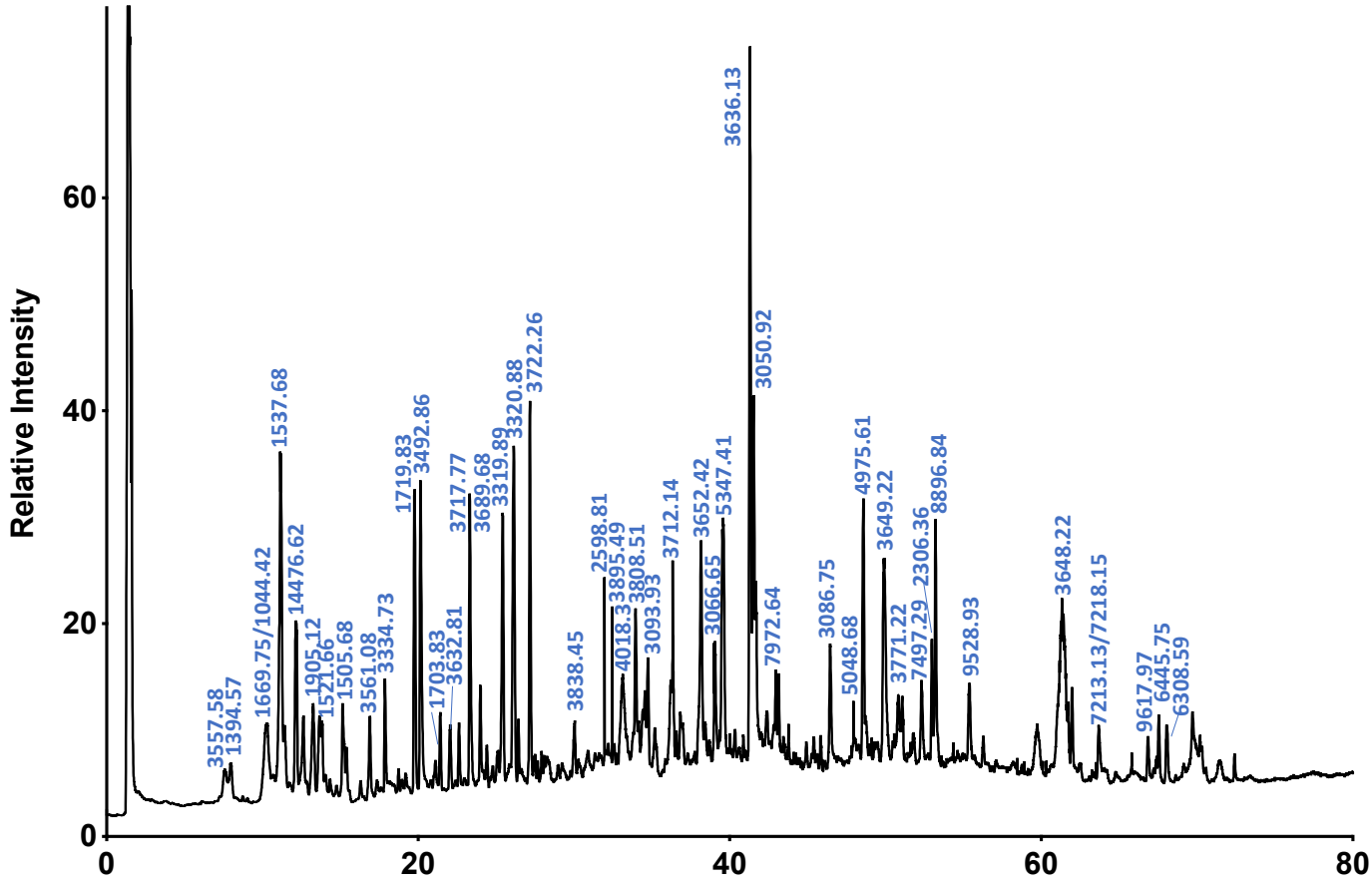

Figure S10: TIC of the *C. frigidus* Distal venom duct showing dominant masses eluting under major peaks.

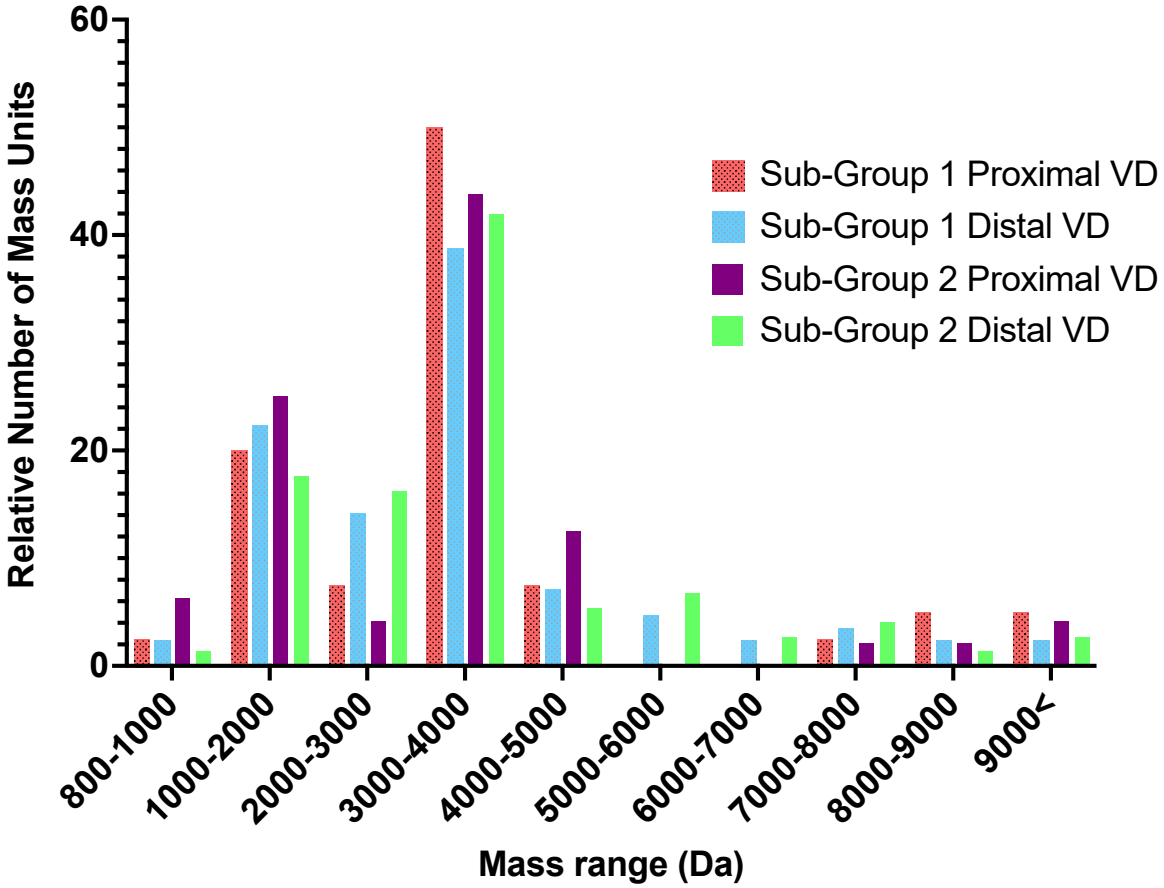

Figure S11: Mass distribution ranges in the reconstructed major masses of proximal and distal venom duct extracts of sub-groups 1 and 2.

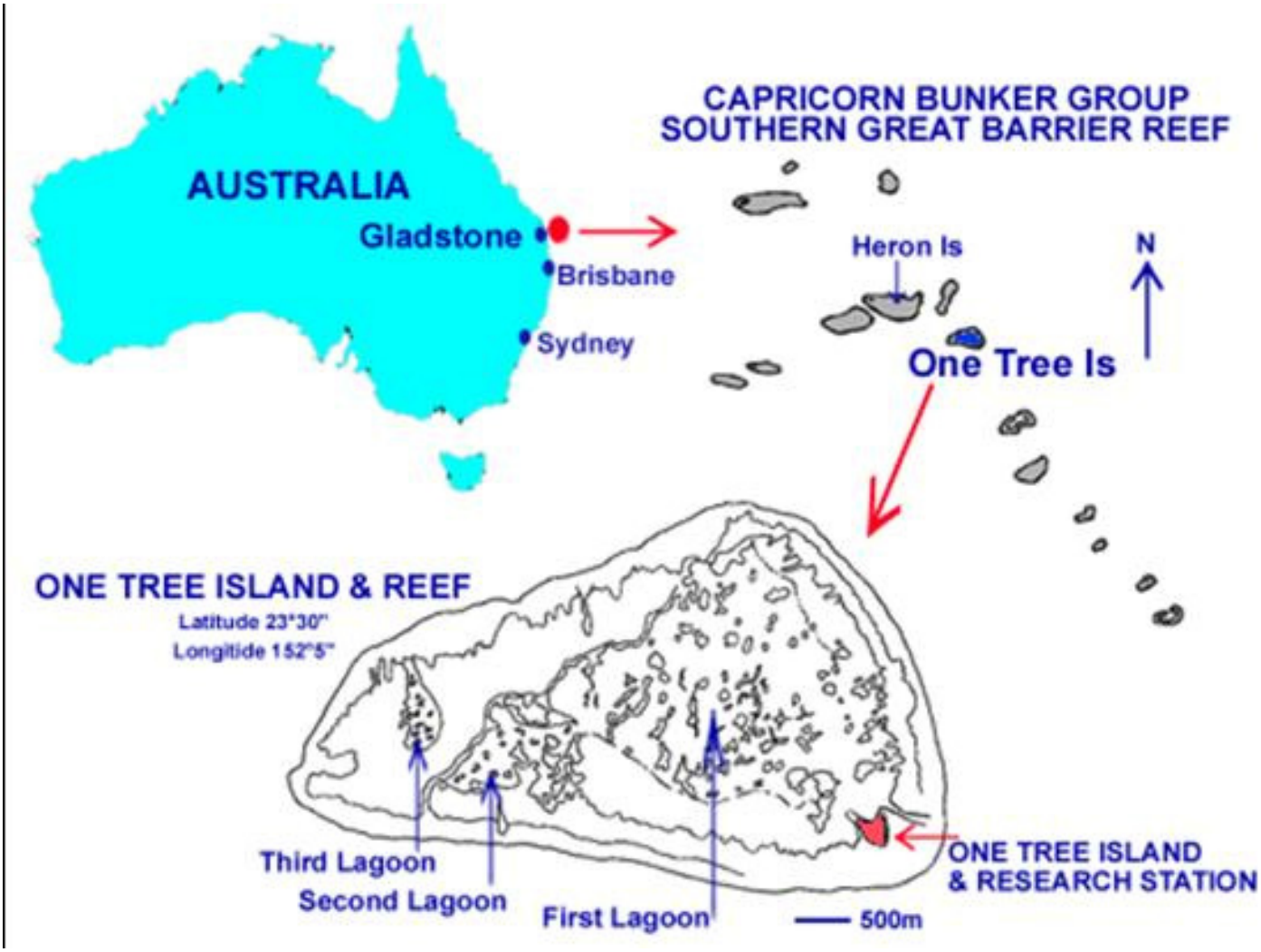

Figure S12. One Tree Island Map. The map is taken from the One Tree Island Research Station resources.