



Fig. S1. Gene structures of Aerolysin homologues from *Nematostella vectensis* (sea anemone; GI 156403083), *Hydra magnipapillata* (hydra; GI 221104132), *Ixodes scapularis* (tick; GI 241568118) and *Coprinopsis cinerea* (basidiomycete fungus; GI 299746325). Boxes represent exons and lines represent introns. The red background corresponds to exon regions encoding amino acids with homology to a pore-forming toxin domain.