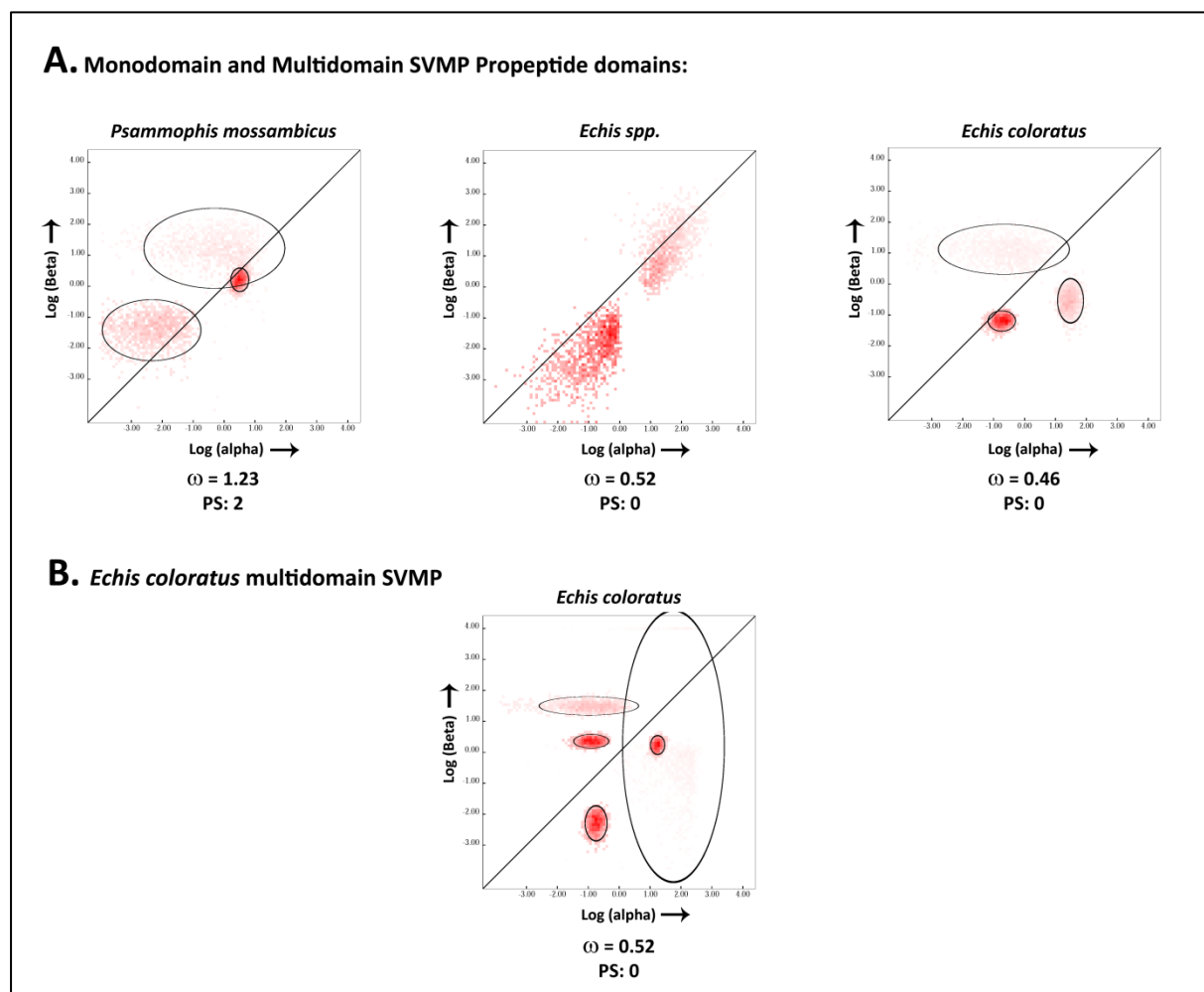## Supplementary Figure 1: Evolutionary Fingerprint of SVMPs

Estimates of the distribution of synonymous (alpha) and non-synonymous (beta) substitution rates inferred for the propeptide domain from *Psammophis mossambicus, Echis spp* and *Echis coloratus* (Panel A) and the entire *E coloratus* multidomain SVMP (Panel B), are shown here. The ellipses reflect a Gaussian-approximated variance in each individual rate estimate, and coloured pixels show the density of the posterior sample of the distribution for a given rate. The diagonal line represents the idealized neutral evolution regime (ω = 1), points above and below the line correspond to positive selection (ω>1) and negative selection (ω<1), respectively. The evolutionary fingerprinting of these genes reveals a good proportion of positively-selected sites in *P mossambicus* propeptide monodomain and the entire multidomain of *E coloratus* propeptide SVMP. On the contrary, almost all the sites in *E spp* and *E coloratus* monodomain SVMPs seem to be evolving under the regime of negative-selection; a small proportion of sites in these that fall above the line of neutrality, do not have any statistical support.