

Selective Toxicity of the Anthelmintic Emodepside Revealed by Heterologous Expression of Human KCNMA1 in *Caenorhabditis elegans*

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Molecular Pharmacology

Supplementary Information S2.

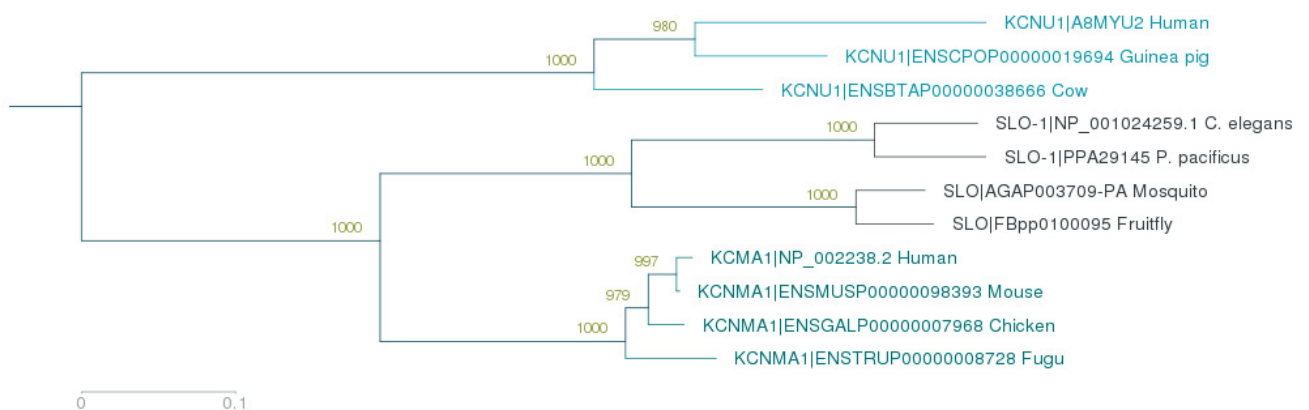


Figure S2. Minimum evolution molecular phylogeny (1000 bootstraps) of invertebrate SLO-1 with vertebrate homologues KCNMA1 and KCNU1. Mid-point rooting identifies KCNU1 as the outgroup, supporting the orthologous relationship of SLO-1 and KCNMA1. Sequences were aligned with MAFFT (Kato et al., 2005) and the phylogeny constructed with FastTree (Price et al., 2009).

Kato, K., Kuma, K., Toh, H. and Miyata, T. (2005) MAFFT version 5: improvement in accuracy of multiple sequence alignment. *Nucleic Acids Res*, **33**, 511-518.

Price, M.N., Dehal, P.S. and Arkin, A.P. (2009) FastTree: computing large minimum evolution trees with profiles instead of a distance matrix. *Mol Biol Evol*, **26**, 1641-1650.