## Methods

A homology model of the *A. gambiae* sodium channel (AGAP004707) was generated using the 3.8 Å resolution structure of the Periplaneta americana sodium channel NavPaS (PDB code 5X0M) (Shen et al., 2017)). Sequences were aligned using Clustal Omega (Sievers et al., 2011). 50 starting models were generated using MODELLER (Eswar et al., 2007). The internal scoring function of MODELLER was used to select 10 models, which were visually inspected and submitted to the VADAR webserver (Willard et al., 2003) to assess stereochemistry in order to select the best final model. Figures were produced using PyMOL (DeLano Scientific, San Carlos, CA, USA).

## References

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## Figure legend 1

Figure ? Location of allele variants. The variant positions are shown as red circles in a transmembrane topology map of the *A. gambiae* sodium channel (AGAP004707) and as red space-fill in a homology model of the channel.

## Figure legend 2

Figure ? Location of allele variants. Variant positions are shown as red circles in a transmembrane topology map of the *A. gambiae* sodium channel (AGAP004707) and as red space-fill in a homology model of the channel. Purple circles in the topology map are amino acids absent from the model due to the lack of modelled structure in these regions.