Variant Ionotropic Receptors in the Malaria Vector Mosquito *Anopheles gambiae*Tuned to Amines and Carboxylic Acids.

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Supplemental Figure S1. *In situ* and immunohistochemistry localization controls.

(A-D) Double *in situ* hybridization using sense RNA probes *AgIr76b* (green) and *AgOrco* (red). (E-H) *In situ* hybridization control using an *AgIr76b* sense RNA probe (green) plus immunohistochemical localization of *AgOr*co using an anti-Orco antibody (red). Scale bars ~50 μm.

Supplemental Figure S2. Control responses of *Xenopus laevis* oocytes to amine/imines.

Responses to unitary compounds [10^{-4} M] from oocytes that were co-injected with cRNAs encoding the subunits indicated in the color keys. Mean responses (+/-SEM) were normalized against the maximum responses to pyrrolidine of *AgIr41a* + *AgIr25a/76b* (A), or *AgIr41c* + *AgIr25a/76b* (B). n = 4 oocytes each.

Supplemental Figure S3. Control responses of *Xenopus laevis* oocytes to carboxylic acids.

Mean responses (+/-SEM) to blends of compounds (each at $[10^{-4} \text{ M}]$) from oocytes that were coinjected with cRNAs encoding the subunits indicated in the color keys. Responses were normalized against the maximum responses to carboxylic acid blend #15 (see Table S1) of AgIr75k + AgIr8a. AgIr75l + AgIr8a responded with very low amplitude (~50 nA) to blend #15 in a single trial, while no other AgIr combinations responded to either blend. n = 3-5 oocytes each.

Supplemental Table S1. *AgIr* transcript abundances in *An. gambiae* chemosensory tissues. Units are given in Reads per Kilobase per Million Reads (RPKM).

Supplemental Table S2. Compounds used for screening *AgIr* responses in *Xenopus laevis* oocytes and arranged by chemical class (column A), compound name (column B) and blend groupings used in the initial screens (column C).

Supplemental Table S3. Effective concentrations at half maximal compound responses (EC_{50}) for listed *AgIr* complexes expressed in *Xenopus laevis* oocytes.

Supplemental Table S4. Cloning primers and peptide translations for full-length *AgIr* transcripts functionally characterized in this study.

Fig. S1

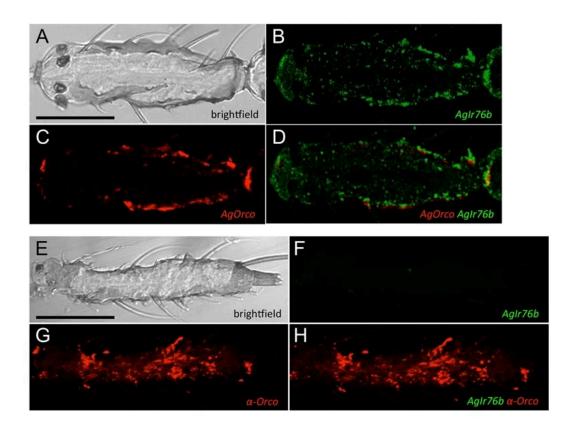


Fig. S2

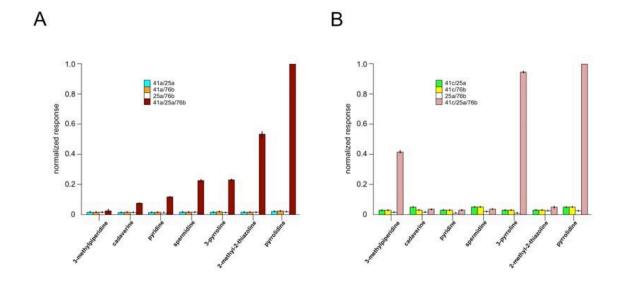


Fig. S3

