

Supplementary Figure Legends:

Figure S1. The complexity of the *de novo* transcriptome assembly of *T. amboinensis*. (A) Distribution of the number of transcripts (isoforms) in each sub-component of the *de novo* transcriptome assembly. (B) Distribution of the number of protein-coding genes annotated on each transcript.

Figure S2. Expression levels of “conserved”, “orphan” and transposon-coding genes *T. amboinensis* chemosensory appendages and whole body samples. In the box-plot, red, green, and blue colors indicate “conserved” genes (i.e. genes with homolog in the NR database), “orphan” genes (i.e. genes without homolog in the NR database), and transposon-coding genes, respectively. The RPKM value was used as the measurement of gene expression level.

Figure S3. Distribution of single-gene trees supporting alternative placements of *T. amboinensis* in the mosquito phylogeny. Blue: gene trees supporting a sister relationship between *T. amboinensis* and *Ae. aegypti*; orange: gene trees supporting a sister relationship between *T. amboinensis* and *C. quinquefasciatus*; grey: gene trees supporting a basal position of *T. amboinensis* to the grouping of *Ae. aegypti* and *C. quinquefasciatus*.

Figure S4. Gene tree for the GRs of four mosquito species. Phylogeny of the GR-family of chemoreceptors with branches color coded by the respective species. The heat maps at the branch tips represent the RPKM-percent composition of each GR family member within the maxillary palp of the three species whose expression was profiled in this study. The gene family members from *C. quinquefasciatus* are included here for phylogenetic reference, but no transcriptome profile for this species was available.

Figure S5. Maximum likelihood tree with length of the ORs of four mosquito species. Phylogeny of the OR-family of chemoreceptors with branches color coded by the respective species. ML tree is based upon amino acid sequence.

Figure S6 Maximum likelihood tree with length of the GRs of four mosquito species. Phylogeny of the GR-family of chemoreceptors with branches color coded by the respective species. ML tree is based upon amino acid sequence

Figure S7. Maximum likelihood tree with length of the IRs of four mosquito species. Phylogeny of the IR-family of chemoreceptors with branches color coded by the respective species. ML tree is based upon amino acid sequence

Figure S1

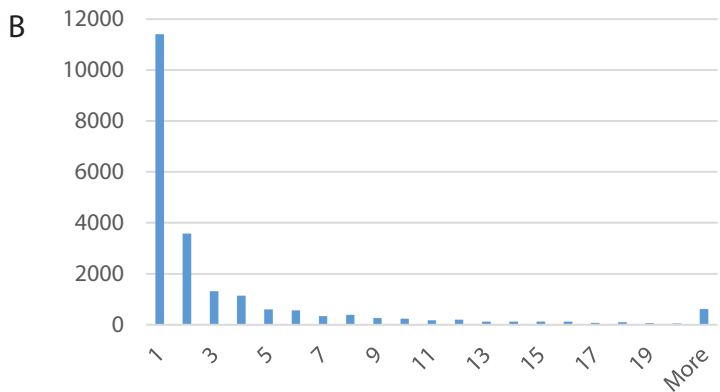
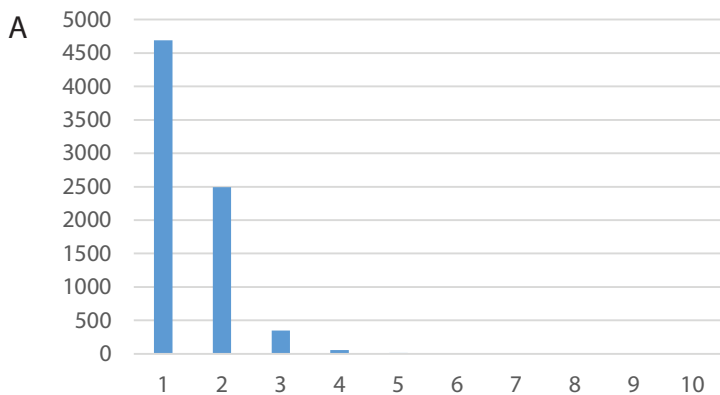


Figure S2

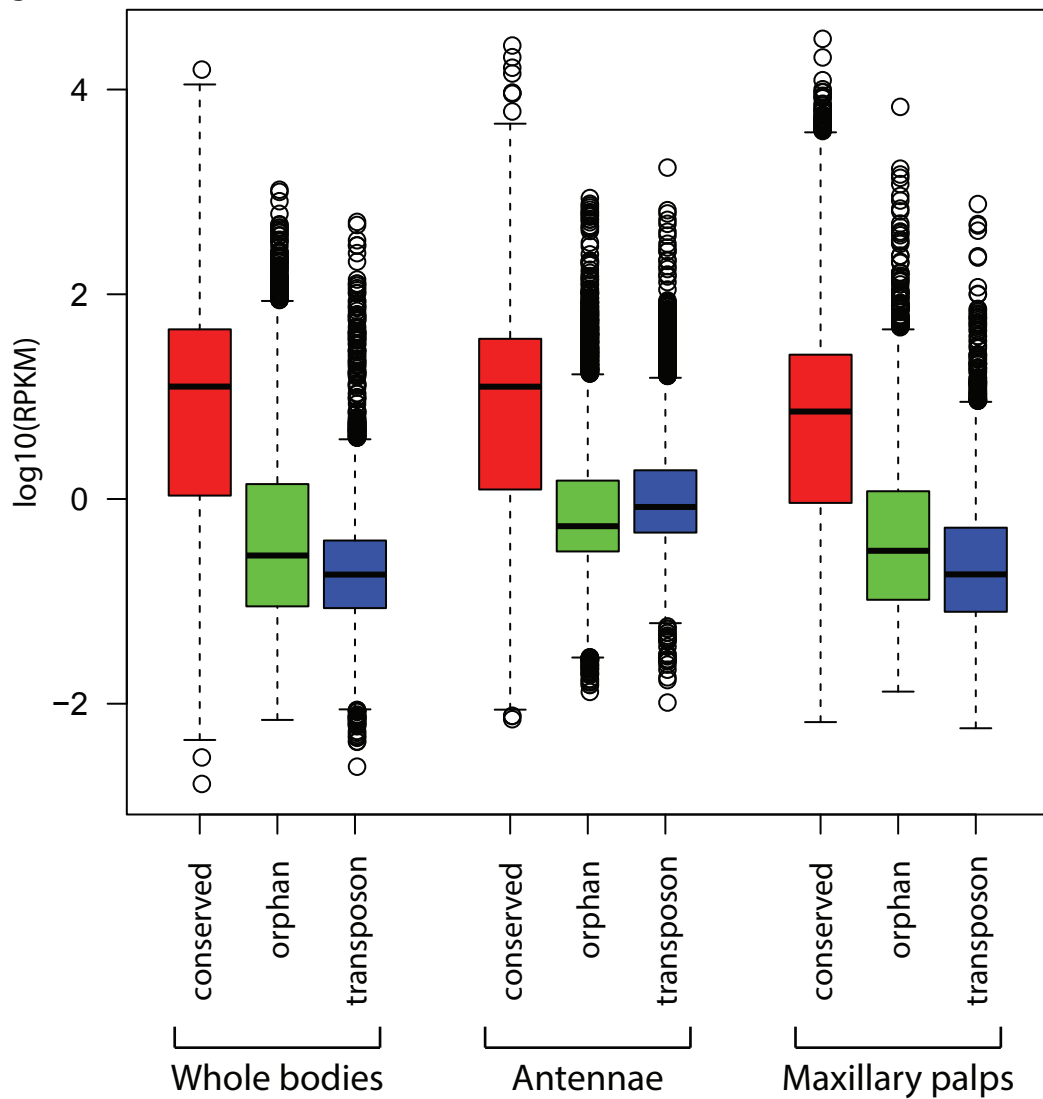
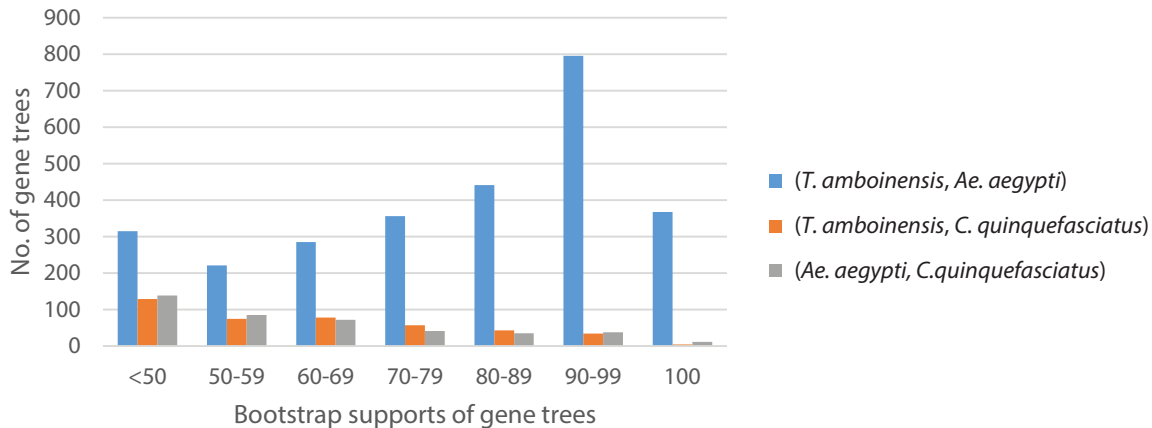


Figure S3

Number of single-gene trees supporting alternative phylogenetic positions of *T. amboinensis*



- *An. gambiae*
- *C. quinquefasciatus*
- *Ae. aegypti*
- *T. amboinensis*

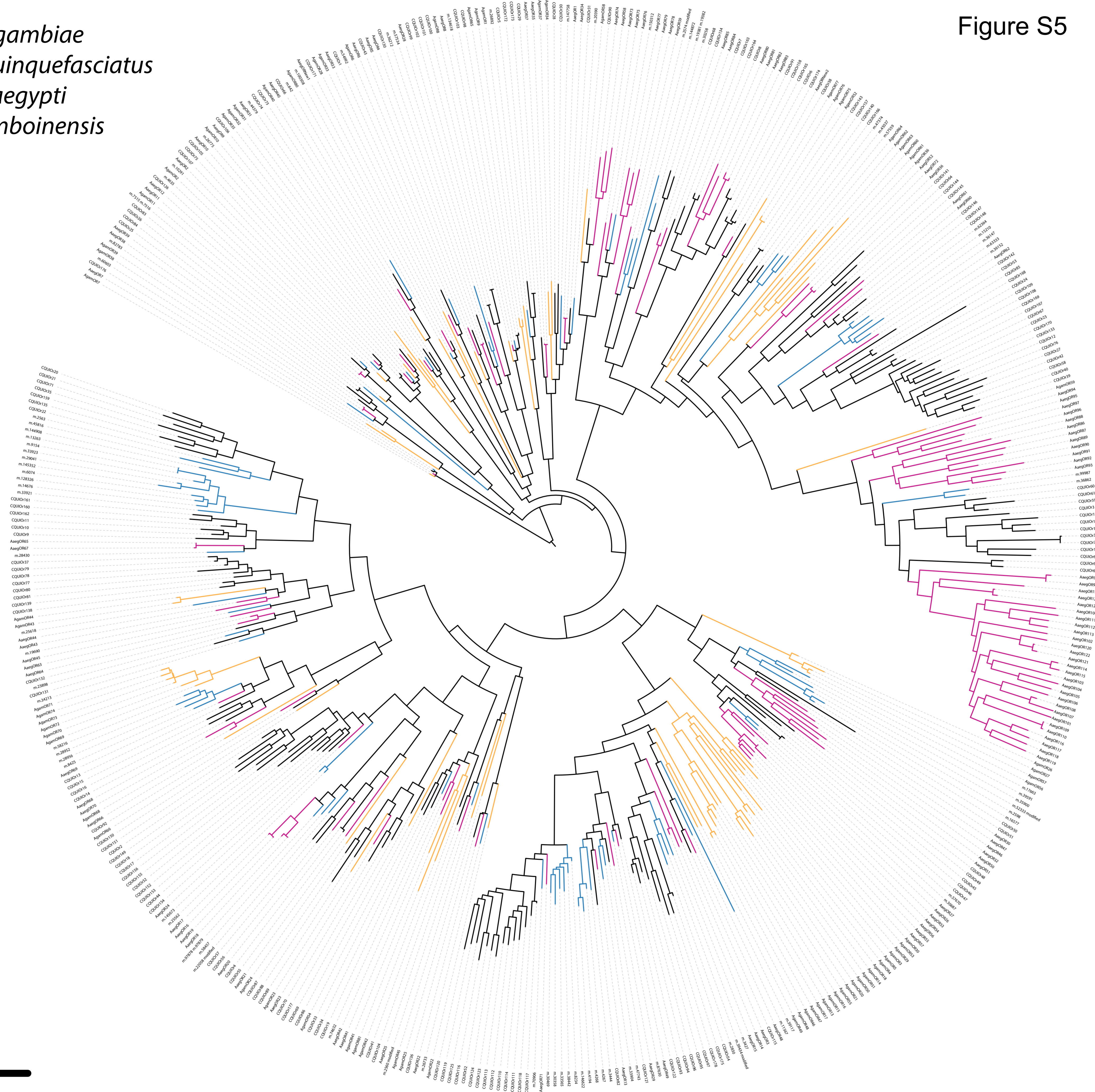




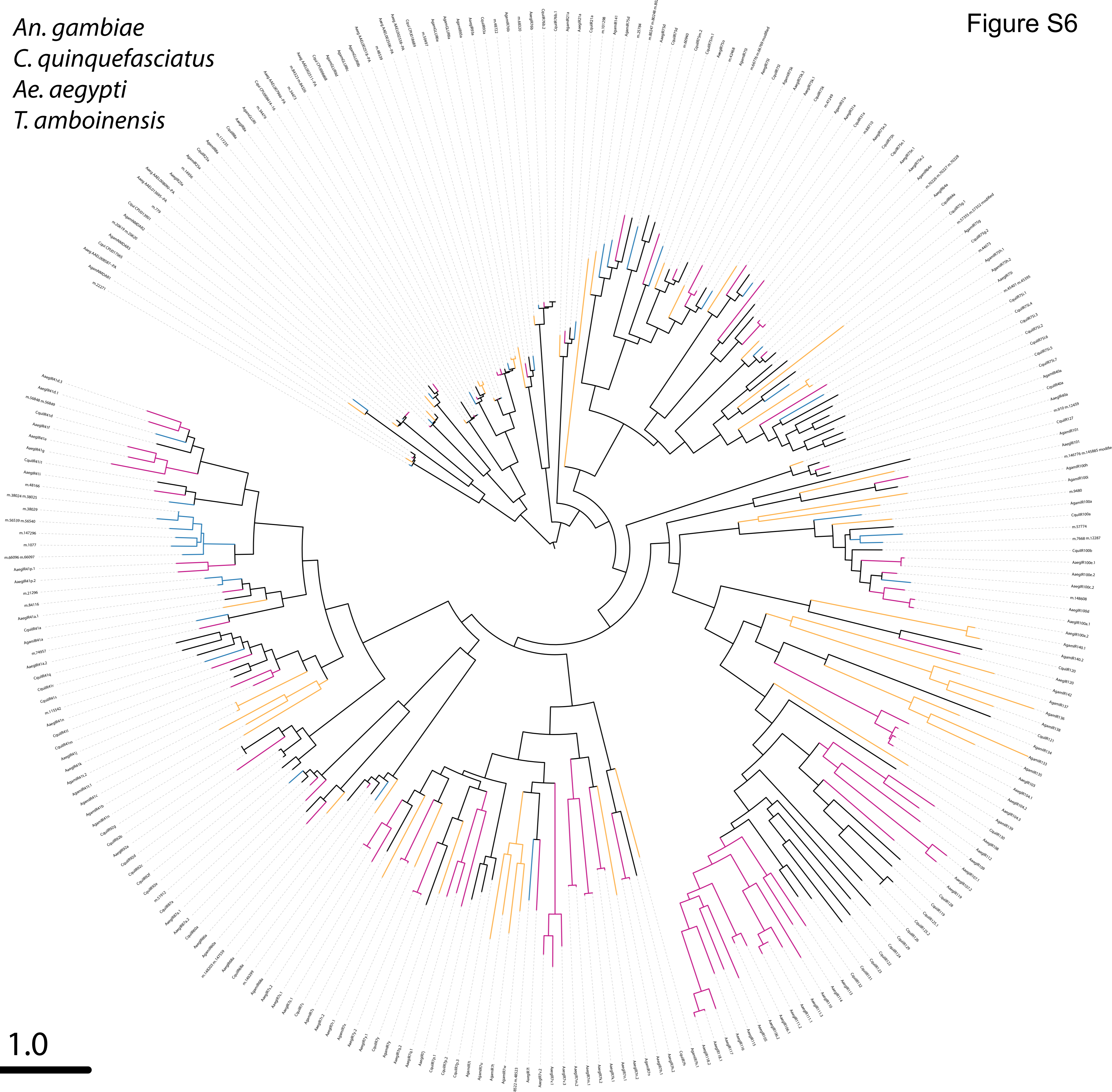


Figure S6

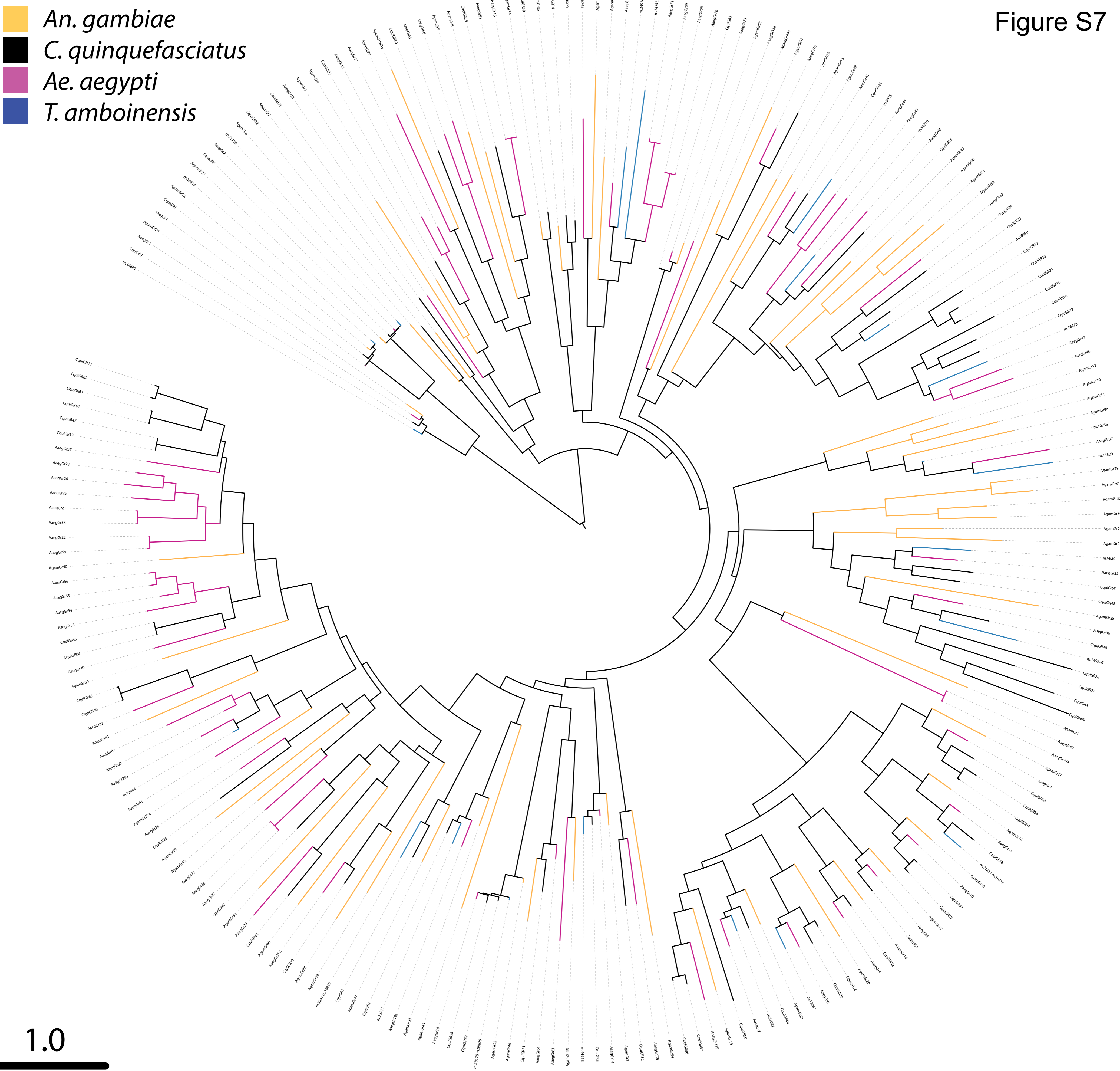
 *An. gambiae*
 *C. quinquefasciatus*
 *Ae. aegypti*
 *T. amboinensis*



1.0

Figure S7

- *An. gambiae*
- *C. quinquefasciatus*
- *Ae. aegypti*
- *T. amboinensis*



1.0