Supporting Information

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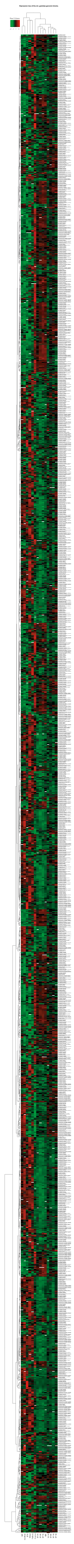

Fig. S1. Expression tree of the *Anopheles gambiae* genomic blocks. This figure shows the genomic expression tree of Fig. 2*A* in detail; readers may use it to analyze other traits with other sets of training genes or to analyze other loci.

Three expression-tree branches enriched with immune genomic blocks.

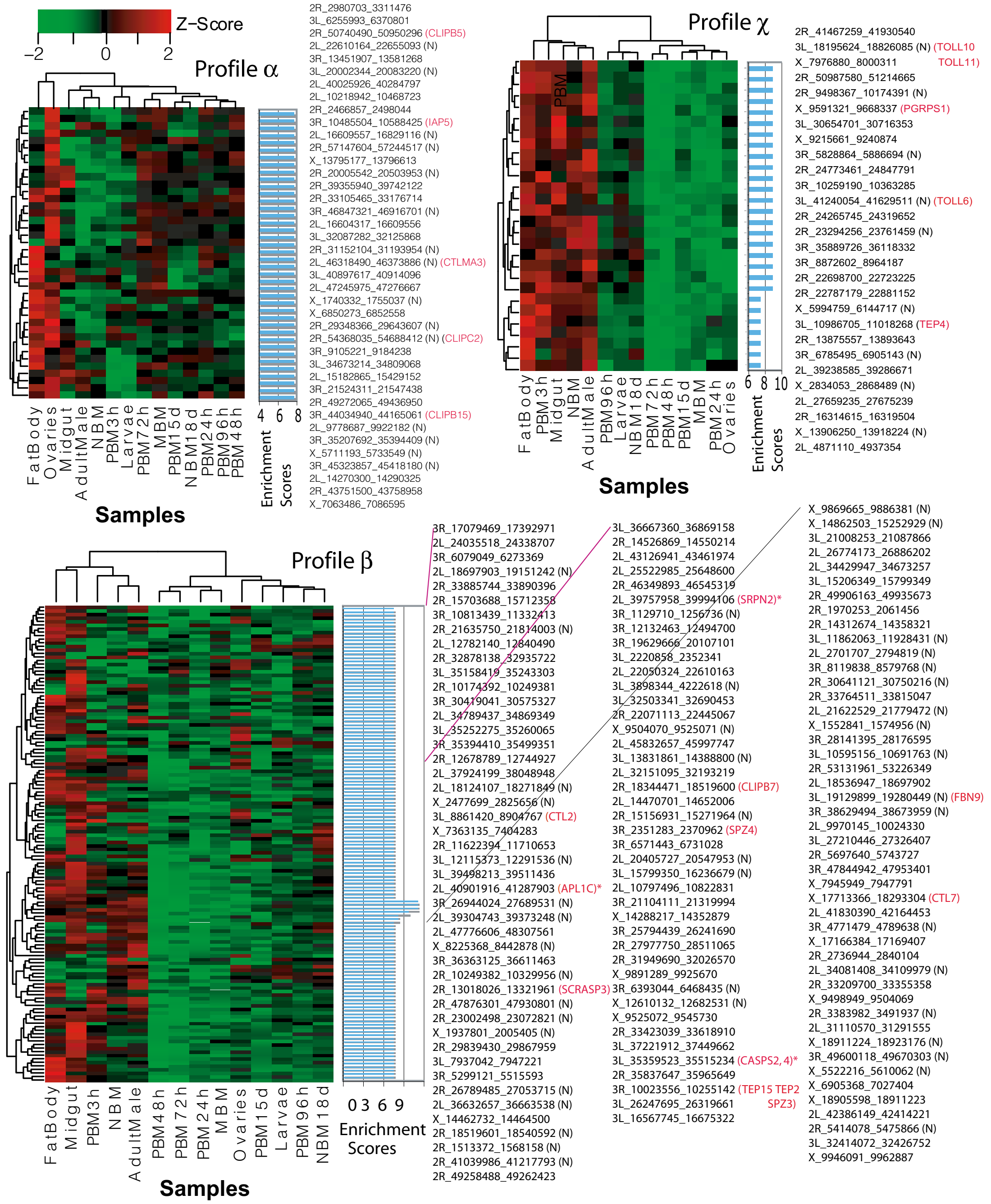

Fig. S2. Three expression-tree branches enriched with immune genomic blocks. Block name convention: chromosome_start_end. The nonconserved blocks are labeled "N" at the end. Immune genes from the known immune gene sets are labeled in red within blocks. The enrichment score profiles show the corresponding leaf scores. The immune gene enrichment scores were not smoothed in this figure because fewer points were used in the profile. Genes in profile α have products that may function as immune modulators. Profile β genes include a signature expression pattern for the defense against malaria parasites. Profile χ genes may be related to the defense against Gram-positive bacteria and fungi.

Table S1. Syntenic blocks between *An. gambiae* and *Culex quinquefasciatus*

Table S1

Table S2. List of known immune genes for characteristic chromosomal block expression pattern detection

Table S2

Table S3. The immune gene enrichment scores for the leaves in the *An. gambiae* genomic block expression tree

Table S3

Table S4. Nonsynonymous single-nucleotide polymorphisms (SNPs) in the five candidate genomic regions and their associated *P* values with *P. falciparum* infection from nine wild-derived *An. gambiae* from Kenya

Table S4

Table S5. Phenotypes (number of *P. falciparum* oocysts in midguts) and genotypes of the five candidate SNPs in the five genes from the 22 wild-derived *An. gambiae* from Kenya

Table S5

Table S6. Primers for cloning the candidate genomic DNA fragments, RT-PCR and nested PCR

Table S6