

1 **FIG. S1. Placement of the *E. anopheles* MSU001 16S rRNA sequence into a phylogenetic**
2 **tree, revealing affinity with *E. anophelis*.** An approximately 1.3-kb region of the 16S rRNA
3 gene was amplified using forward primer 63f and reverse primer 1387r and sequenced
4 (Materials and Methods). The phylogenetic tree was constructed by neighbor-joining analysis
5 of partial 16S rRNA sequences according to MEGA version 5.2 (54). The bar represents 2%
6 sequence divergence. The GenBank accession numbers for 16s rRNA sequences for selected
7 strains are listed in parenthesis.

8 **FIG. S2.** Time course of growth in WT, SCH814 and SCH837. The cells were grown in LB,
9 sampled at the specific time point and determined the OD_{600nm}.

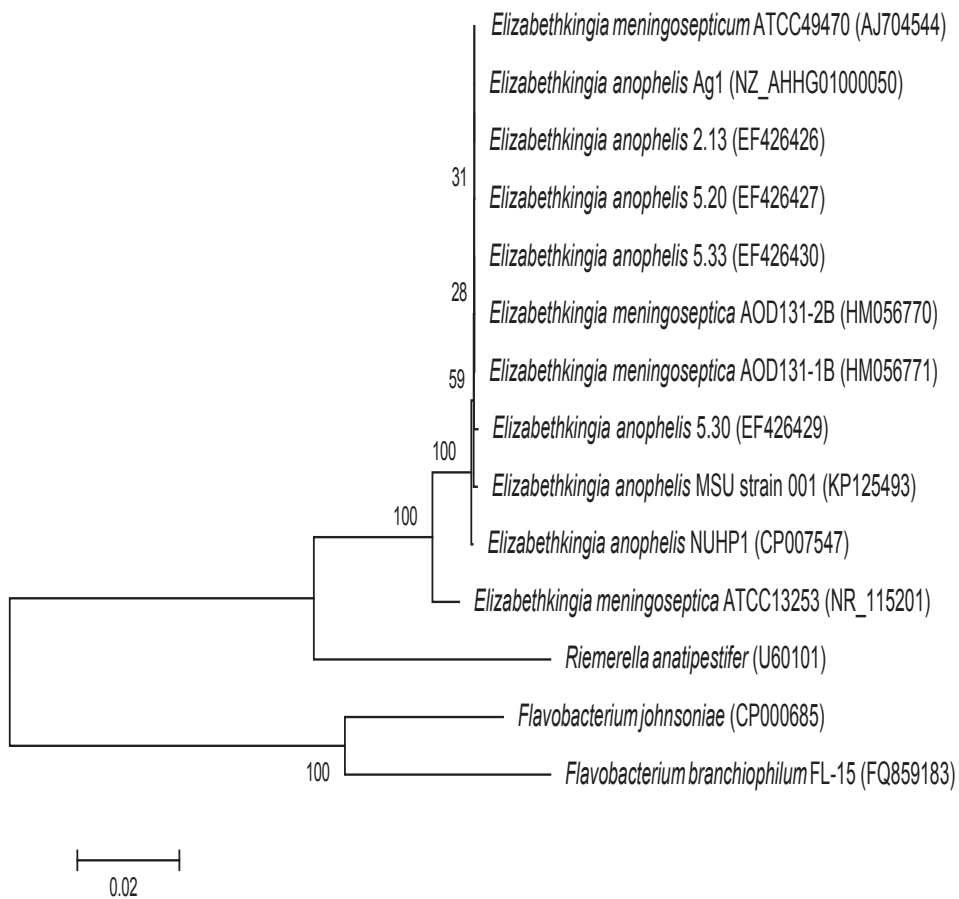
10 **FIG. S3. Properties of NanoLuc reporter in *E. anophelis* and its application.** (A)
11 NanoLuc-tagged *E. anophelis* was grown in LB. Growth was determined by measuring
12 OD_{600nm}. (B) Expression of *nluc* under promoter *PompA*. NanoLuc luciferase was determined
13 in *E. anophelis* sampled at the specific time points according to the procedures described in
14 Methods and Materials. (C) Effects of the growth phase on relative luciferase activity. The
15 relative activity was expressed as normalization of the total luciferase activity with OD_{600nm}.
16 (D) Relationship between the CFUs and NanoLuc activity.

17 **FIG. S4. Comparisons of SCH814 in the male and female mosquitoes.** Male or female
18 mosquitoes were fed with 10% of sucrose supplemented with SCH814. After 24 hours, the
19 sugar diet was replaced with fresh sterile sucrose without SCH814. The male (4 adults) and
20 female (4 adults) mosquitoes were randomly sampled on days 1, 3 and 14. Mosquito samples
21 were processed and NanoLuc reporter activity was determined as described in Materials and
22 Methods.

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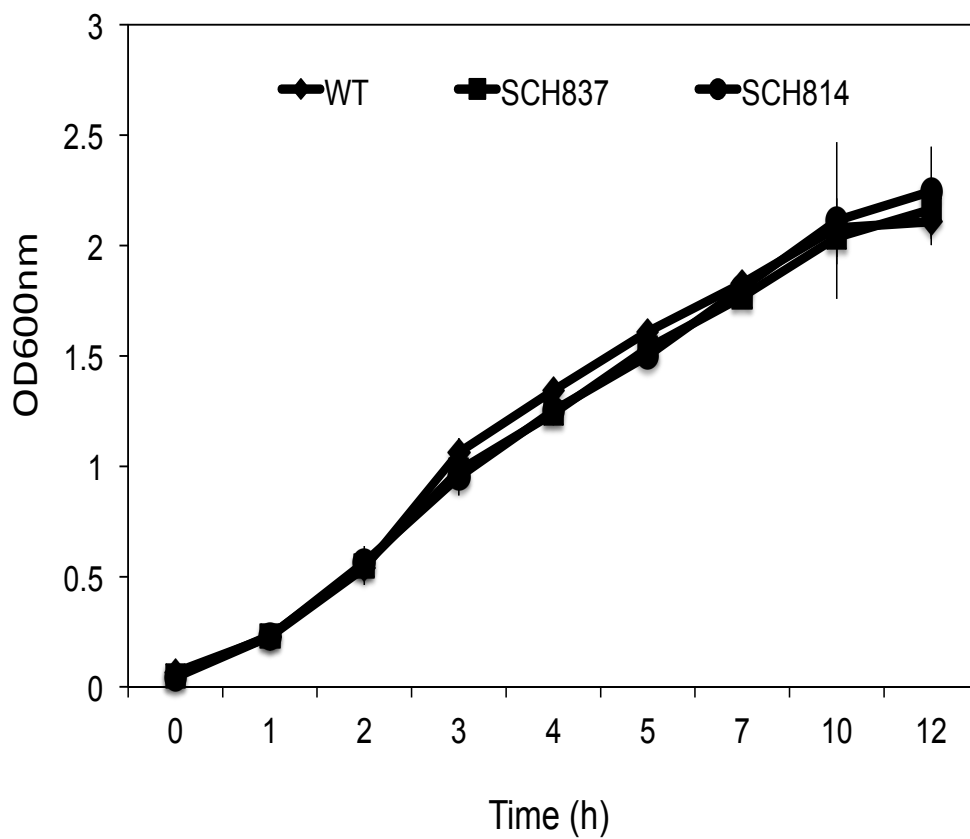


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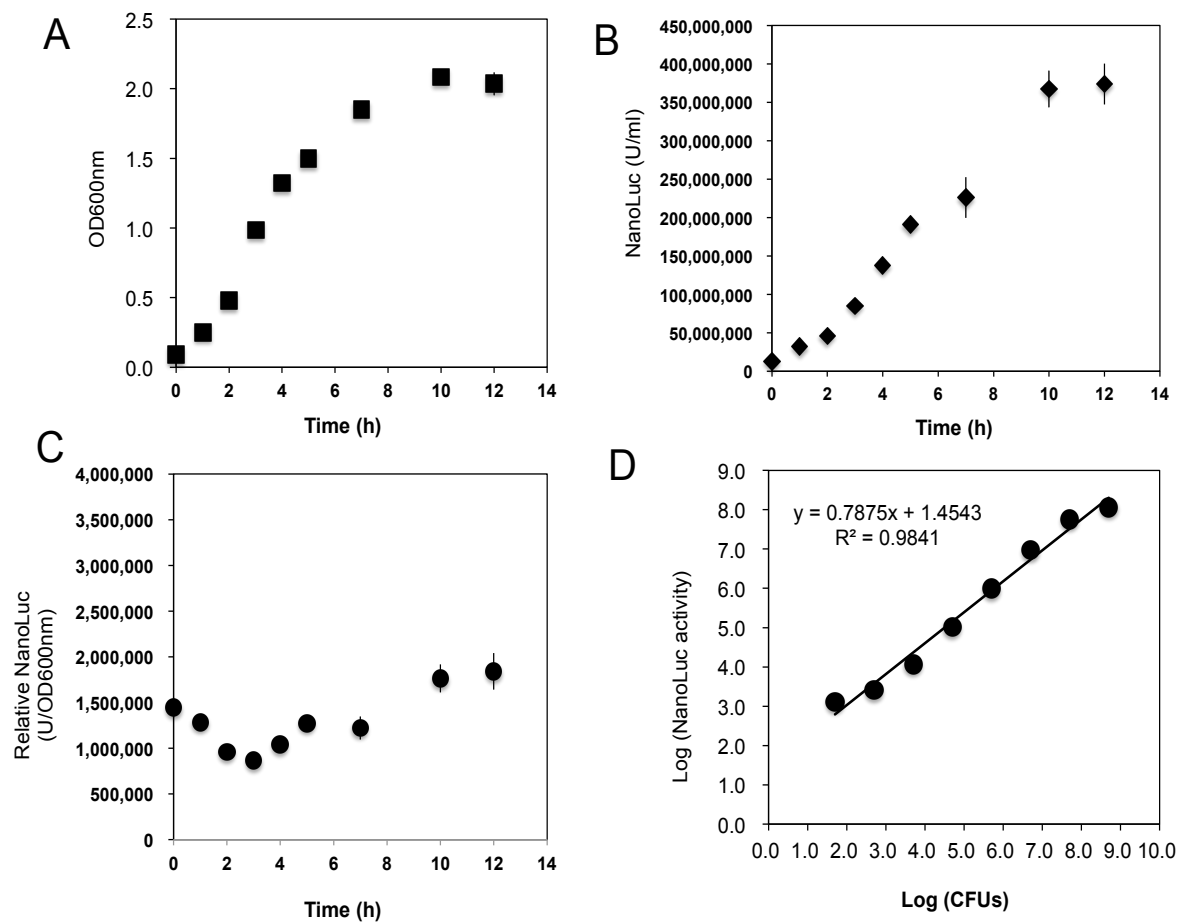
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31 Fig.S2

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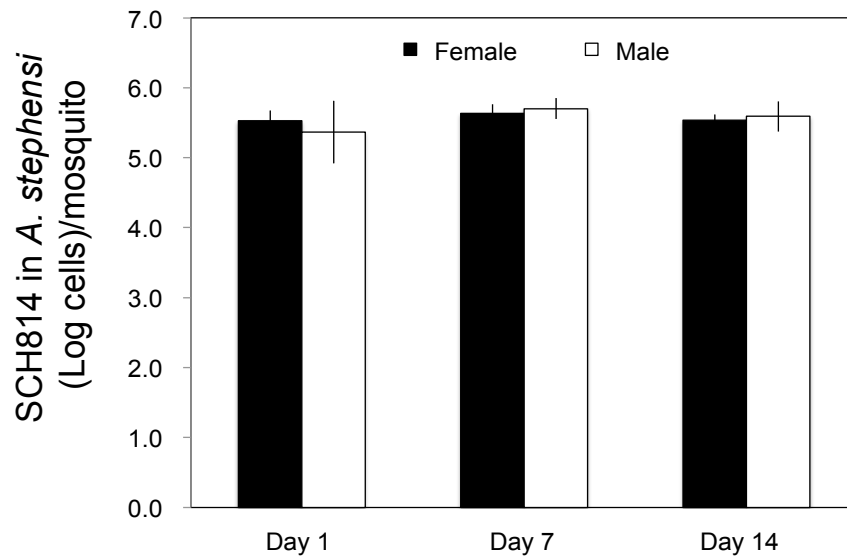
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