

**The interplay between dose and immune system activation determines fungal infection
outcome in the African malaria mosquito, *Anopheles gambiae***

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Supplementary Materials:

Supplementary Figure Legends

Figures S1-6

Supplementary Figure Legends

Fig. S1. Primer efficiencies for RT-qPCR analysis. Primer efficiencies were measured using dilutions of the cDNA of untreated 2-3 day-old female *An. gambiae* for RT-qPCR analysis. Graphs show Ct values plotted against log values of the dilutions for ribosomal protein S7 (*rpS7*) (a), and genes of interest, *RELI* (b) and *Cactus* (c). r^2 = goodness of fit.

Fig. S2. Individual biological replicates of survival analyses of *An. gambiae* after exposure to *B. bassiana*. (a-f) Individual biological replicates of survival curves after exposure to 0, low, medium, and high *B. bassiana* conidial doses corresponding to data shown in Figure 1 of the main manuscript. Survival curves are presented as percent survival and each biological replicate utilized 35 adult, female mosquitoes per treatment. Statistical significant differences between survival curves were assessed by Log Rank Test, with resulting *P* values shown in the figure.

Fig. S3. Individual biological replicates of the *RELI* and *Cactus* relative expression time course following exposure to *B. bassiana*. Individual biological replicates of the relative expression of *An. gambiae* (a) *RELI* and (b) *Cactus* transcripts after exposure to the high dose of *B. bassiana* conidia in adult, female mosquitoes. Graphs depict transcript levels at 1, 2, 4, and 6 days post exposure for oil-only and *B. bassiana*-exposed mosquitoes relative to untreated, day 0 controls. Quantitative RT-qPCR results were analyzed using *rpS7* as the reference gene and untreated mosquitoes as calibrator condition.

Fig. S4. Percent knockdown of *RELI* and *Cactus* transcripts by RNAi. Mosquitoes were analyzed for knockdown efficiency by quantitative RT-qPCR. Relative expression of *An.*

gambiae (a) *RELI* and (b) *Cactus* transcripts three days after injection of dsRNA [3.0 µg/µL] specific to each transcript in adult, female mosquitoes. Graphs depict mean transcript levels relative to ds*GFP*-injected controls. Quantitative RT-qPCR results were analyzed using *rpS7* as the reference gene and untreated mosquitoes as calibrator condition. Data are presented as mean ± 1 SEM from three biological replicates.

Fig. S5. Individual biological replicates of survival analyses of *An. gambiae* following exposure to *B. bassiana*. (a-c) Figure shows the individual biological replicates of survival curves after RNAi treatments (uninjected, ds*GFP*, ds*RELI*, ds*Cactus*) and exposure to oil-only, low, medium, and high *B. bassiana* conidial doses, corresponding to data shown in Figure 3 of the main manuscript. Survival curves are presented as percent survival and each biological replicate utilizing 35 female mosquitoes per treatment. Statistically significant differences between survival curves were assessed by Log Rank Test, with resulting *P* values shown in the figure.

Fig. S6. Smoothed percent daily mortality curves of *An. gambiae* following exposure to *B. bassiana*. (a-d) Combined percent daily mortality rate from proportional survivals shown in Figure 3 of the main manuscript. Curves represent the average of three biological replicates. Peaks within ds*RELI*- and ds*Cactus*-injected treatments indicated with an asterisk (first peak) or a square (second peak).

Figure S1

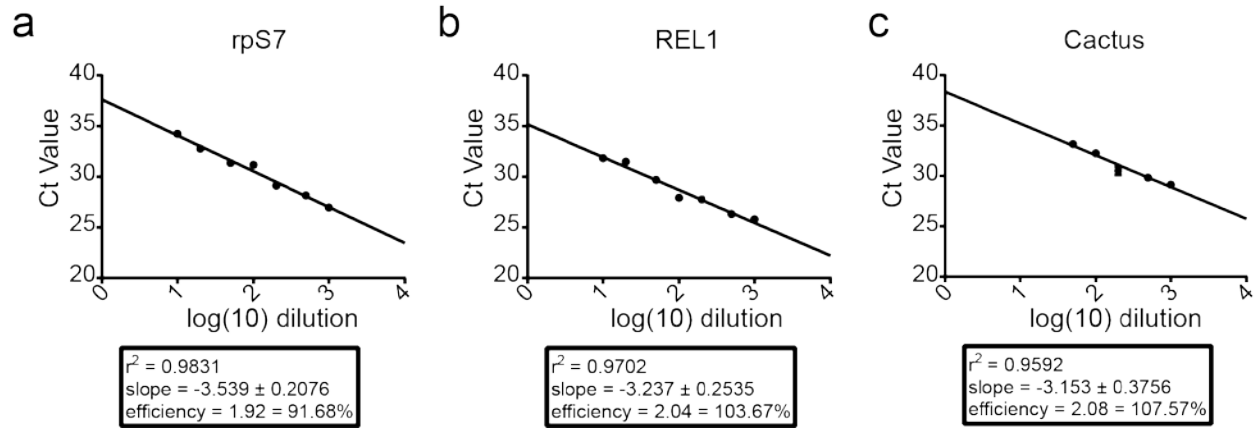


Figure S2

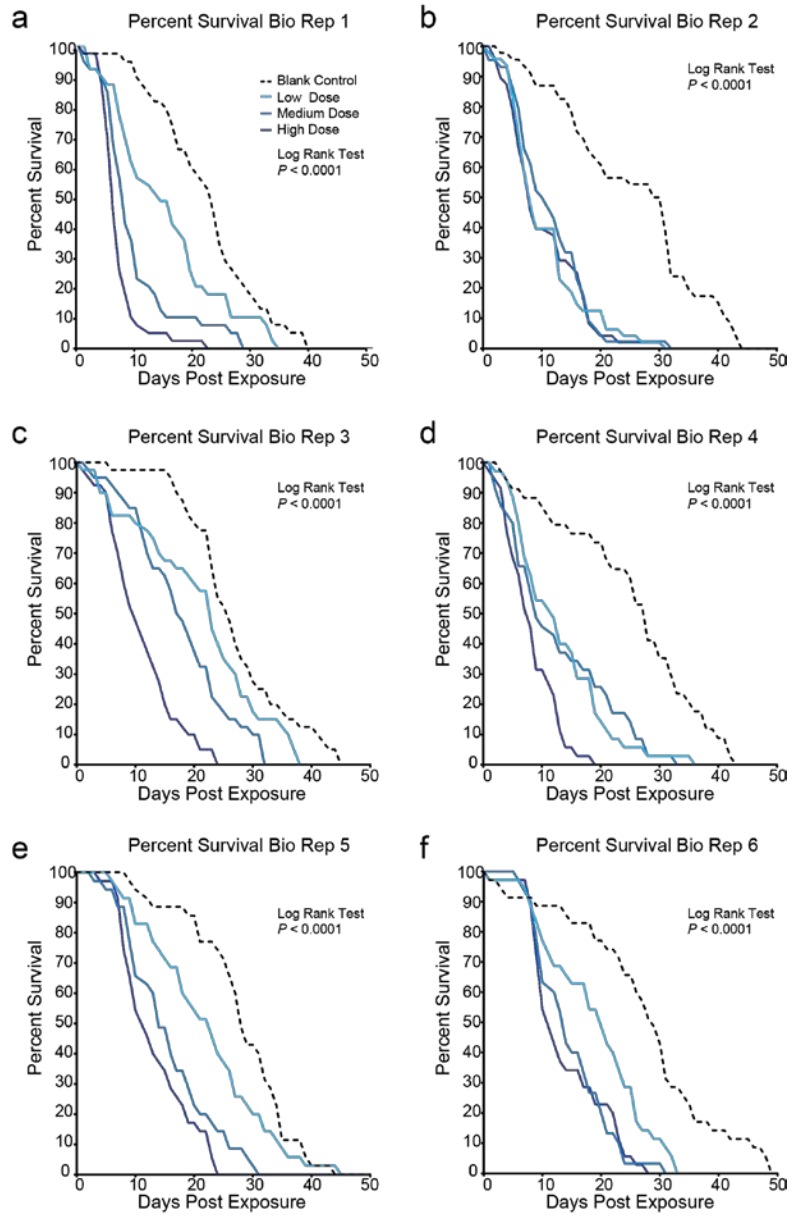
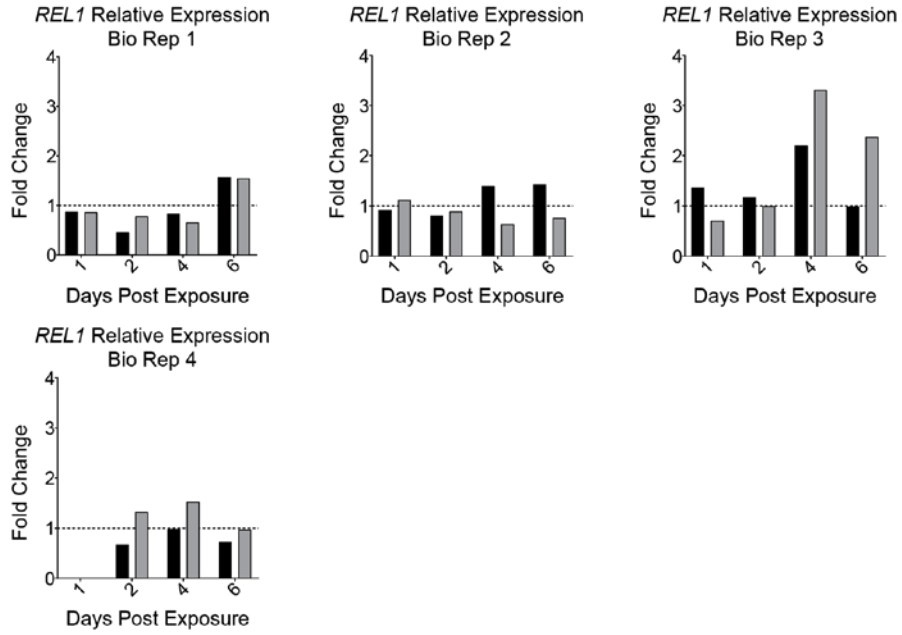


Figure S3

a



b

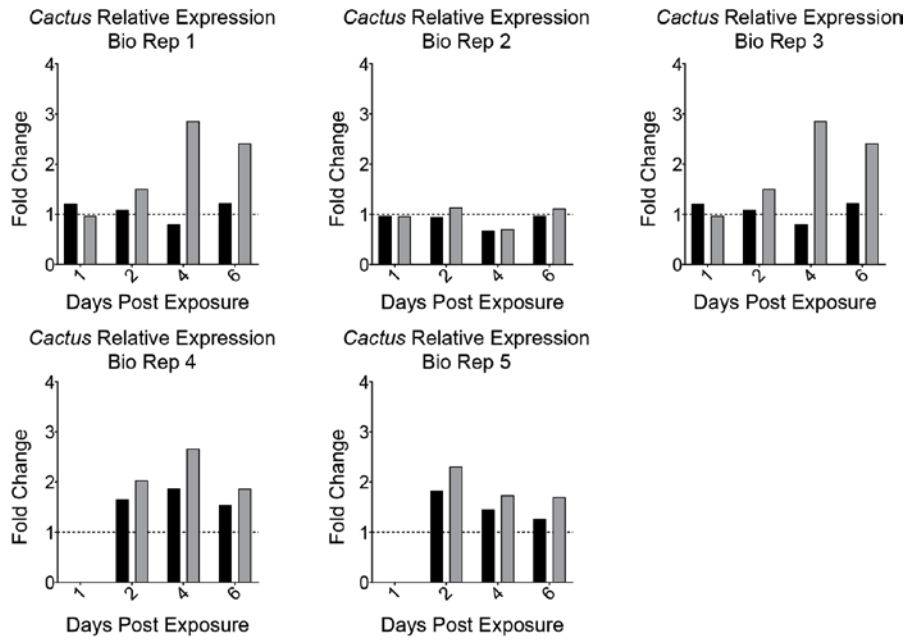


Figure S4

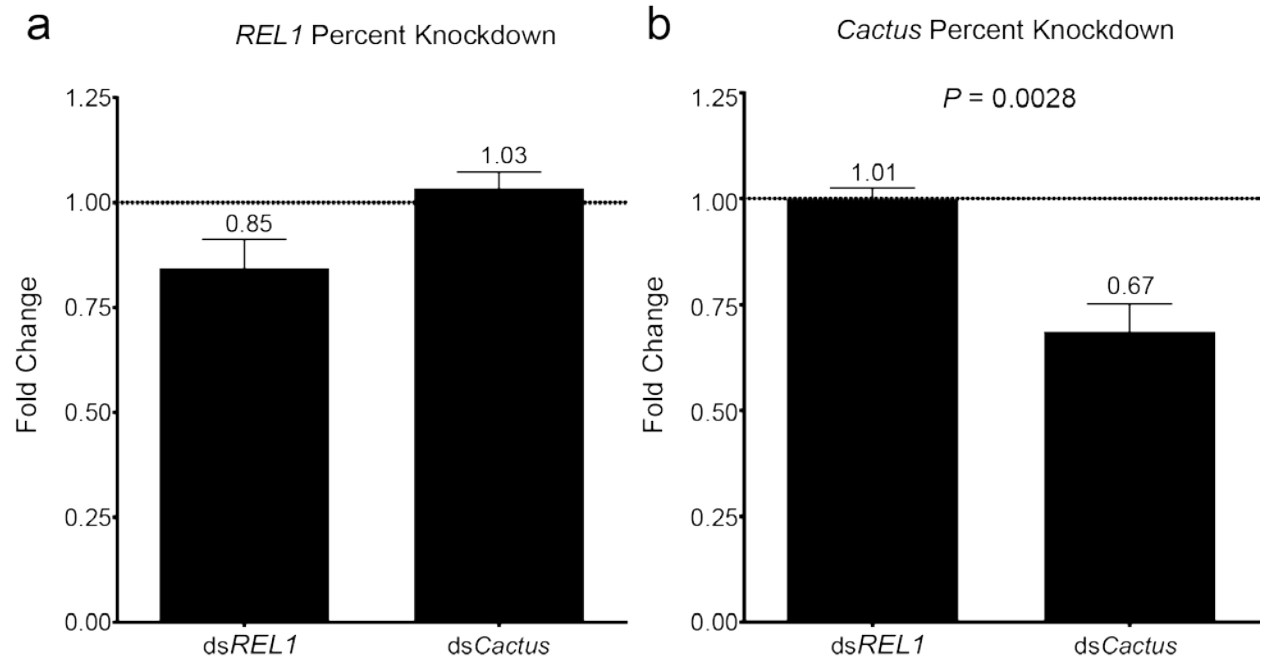


Figure S5

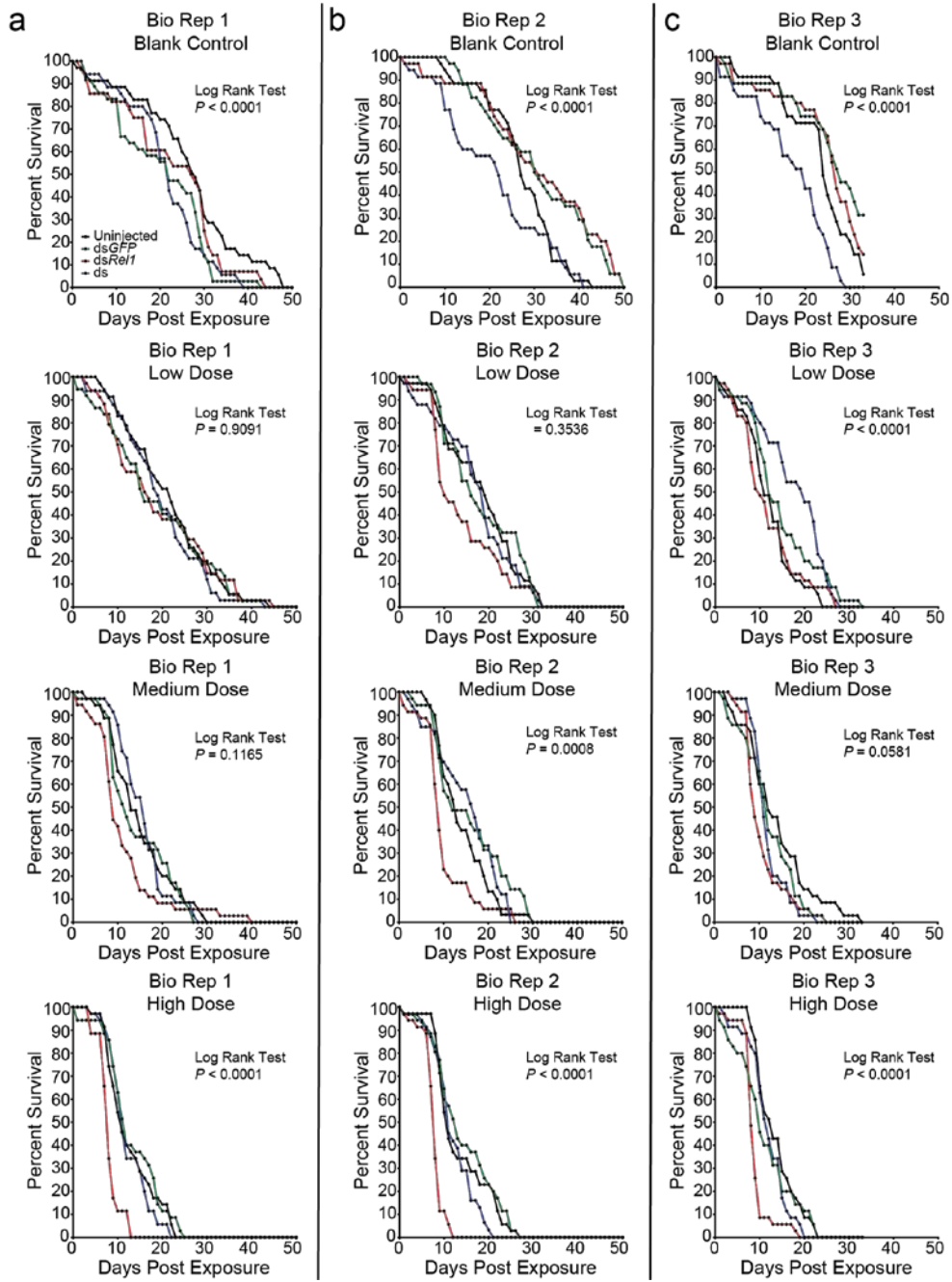


Figure S6

