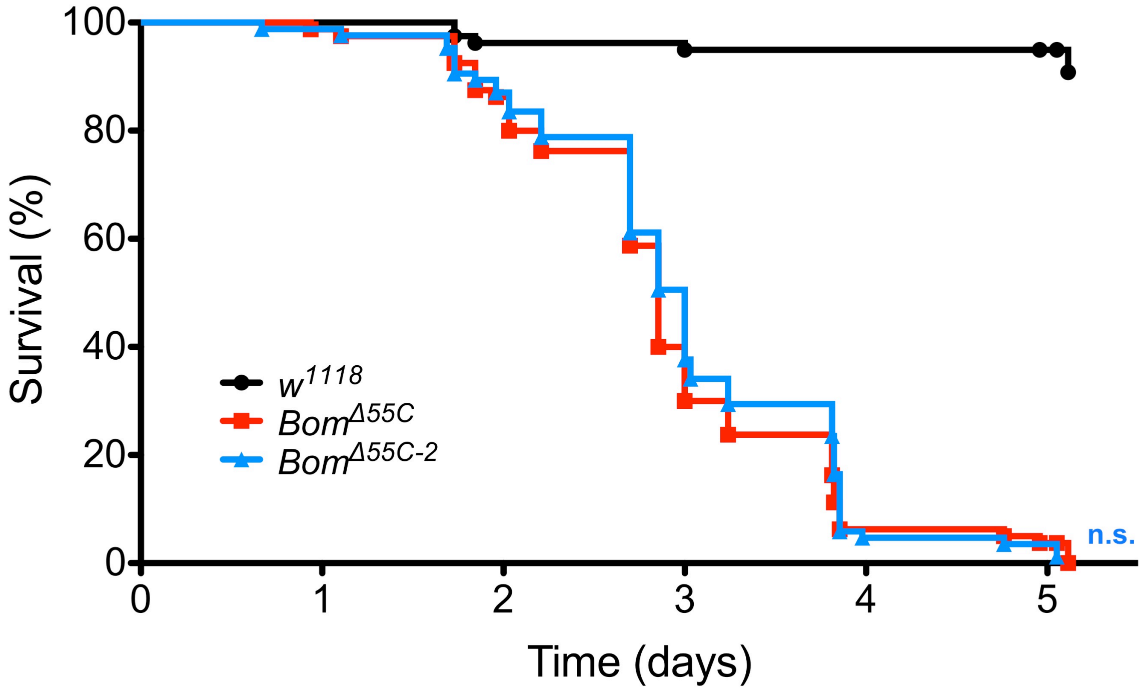
Supplementary Table 1. Induced *Bom* transcript levels measured in wild-type and transgenic flies.

Genotype	**Induced *Bom* transcript level**[†]			
	Bom3	*Bom836*	*Bom065*	*Bom068*
w^{1118}	18 ± 1.1	2.8 ± .26	25 ± 4.0	3.2 ± .04
$Bom^{\Delta 55C}$; {55C-Right}	19 ± .78	3.5 ± .36	30 ± .80	6.5 ± .07
$Bom^{\Delta 55C}$; {Bom3}	18 ± .84	na	na	na
$Bom^{\Delta 55C}$; {Bom836}	na	3.0 ± .34	na	na
$Bom^{\Delta 55C}$; {Bom065}	na	na	24 ± 1.2	na
$Bom^{\Delta 55C}$; {Bom068}	na	na	na	8.9 ± .48

[†] Total RNA was extracted, using Trizol, from three separate groups of flies (2-7 day old adult males, n =6) for each genotype 24 hours after Toll induction with heat-killed *M. luteus*. RNA was reverse-transcribed (SuperScript II, Invitrogen) and real-time PCR was carried out using iQ SYBR Green Supermix (Bio-Rad) with an iCycler iQ instrument. Transcript levels are shown relative to *rp49*, quantified using the $2^{-\Delta\Delta Ct}$ method, and corrected for primer amplification efficiencies. Standard error of the mean is indicated. "na" = not applicable.



Supplementary Figure 1. *Bom*$^{\Delta 55C\text{-}2}$ phenocopies *Bom*$^{\Delta 55C}$. Survival of flies after *C. glabrata* infection was monitored for wild type (*w*^{1118}), TALEN-generated Δ*Bom*55C (*Bom*$^{\Delta 55C}$), and CRISPR-generated Δ*Bom*55C (*Bom*$^{\Delta 55C\text{-}2}$). Data were captured and analyzed as in Fig. 2. Significance is shown relative to *Bom*$^{\Delta 55C}$ (n.s. = not significant, $p>0.05$).