**Stokes et al 2020 Data repository READme file.**

**Data used for Fig2 (B,C,E,F panels).** (B/C) Purified Ae. aegypti and H. sapiens SUMO, Ubc9, and SAE1/2 recombinant proteins (50 ng each per reaction, Figure S1) were incubated in the presence of 5 mM ATP for the indicated time points (minutes, min). Quantitation of the accumulation of HMW SUMO conjugates at 28 or 37˚C (B and C, respectively). N≥3 independent reactions per condition; values normalized to T=0 min (T0); mean and standard error of mean plotted. (E) Ae. aegypti SUMOylation pathway enzymes were incubated in the presence of WT or catalytically inactive (C371A) AaPIAS (10 ng) for the indicated time points at 28˚C. Quantitation of the accumulation of HMW SUMO conjugates (as described in B). (F) Ae. aegypti SUMOylation pathway enzymes (SAE1/2 and Ubc9) were incubated in the presence of chimaeric SUMO (amino acids 1-14 of HsSUMO3 [including WT or mutant (K11R) SCM] in frame with the C-terminus of AaSUMO) for the indicate time points at 28˚C. Western blots were quantified for the accumulation of HMW SUMO conjugates (as described in B). Membranes were imaged and quantified using a LiCor Odyssey Imaging System.

**Data used for Fig4A and S4.** RT-qPCR sumo expression in tissues Ae. aegypti females. Data analysed according to Taylor method. Three independent replicates per pool of tissues. S7 was used to normalise sumo expression. Normalized expression values (yellow) were used for the graph and Log2 values (red) were used for the statistics (ANOVA). Multiple comparison to carcass sample (Dunnett s correction) shown in Fig4 and multiple comparison between all tissues (Tukey s correction) shown in FigS4.

**Data used for Fig5 (A,D,G panels) qPCR.** RT-qPCR analysis of mRNA levels of ago2, SUMO, Ubc9, or PIAS within depleted (ago2, SUMO, Ubc9, or PIAS respectively) and infected AF5 cells. N=5 independent biological replicates; values normalized to ribosomal S7 and expressed relative to dsLacZ-treated control samples set to 1 for each replicate and each target gene; RQ mean and SD plotted. Data analysed according to the the 2−ΔΔCt (cycle threshold) method using the qPCR software. Statistical analysis, one sample (two-tailed) t test to a hypothetical mean of 1 (dsLacZ control).

**Data used for Fig5 (B, E, H panels) Luciferase assays.** Luciferase readings from BUNV, SFV, or ZIKV infected samples. N=15 independent biological replicates per condition; values expressed relative to dsLacZ-treated control samples (set to 1); mean and SD plotted. Statistical analysis, one sample (two-tailed) t test to a hypothetical mean of 1 (dsLacZ control).

**Data used for Fig5 (C, F, I panels) qPCR.** Viral RNA (vRNA) levels from BUNV, SFV, or ZIKV infected samples. N=5 independent biological replicates; Data analysed according to the the 2−ΔΔCt (cycle threshold) method with qPCR software: values normalized to ribosomal S7 and expressed relative to dsLacZ-treated control samples set to 1 for each replicate, RQ mean and SD plotted. Statistical analysis, one sample (two-tailed) t test to a hypothetical mean of 1 (dsLacZ control).

All other data are available in the manuscript or in supplementary files.