Supplemental figures:

Figures S1: Immunofluorescent analysis of WT and *Gli1*$^{-/-}$ for SPEM. Representative images of immunofluorescent staining for mucous neck cells with GSII lectin (green), GIF (red) and H^+,K^+-ATPase (white) antibodies in each group as indicated: WT uninfected mice (UI); WT plus *H. felis* (*Hf*) infection for 6 months (WT+*Hf*); Gli1$^{-/-}$ plus *H. felis* infection for 6 months (Gli1$^{-/-}$ +*Hf*). Mice receiving the BMT received cells from SLFN4-tdT$^+$ donor mice prior to infecting with *H. felis* (w/BMT). N=5 mice analyzed per group. Scale bar=50μm.

Figure S2: Analysis of major immune cell types in WT versus *pCMV-Shh* mice. Corpus cells from WT versus *pCMV-Shh* mice were analyzed for immune cell markers in uninfected mice: F4/80 (macrophages); CD11b (myeloid cell lineage); CD11c (dendritic cells); Ly6B.2 (neutrophils); CD3 (T cells). The percentage of labeled cells enumerated is shown in the representative dot plot graphs. The scatter graph shows the median and interquartile range for N=3 separate mice per group. Multiple T tests were performed to compare the differences between WT vs *pCMV-Shh* genotypes for each immune marker. *P<0.05.

Figure S3: Q-PCR analysis of SPEM markers. *Atp4α*, *Gif*, *Tff2* and clusterin (*Clu*) mRNA from WT and *pCMV-Shh* mouse corpi with and without 4 months of infection with *H. felis*. Shown is the median fold change relative to WT values and interquartile range for N=8-10 mice for 3 separate expts. One-way ANOVA followed by Tukey's multiple comparisons test on-log transformed values was performed. *P<0.05; ***P<0.001; ****P<0.0001; NS, not significant.

Figure S4: *H. felis*-infected *pCMV-Shh* corpus versus antrum. Representative images of 4-month infected **A**) Corpus; **B**) Antrum. N>10 mice analyzed. Scale bar =50μm.

Figure S5: Flow cytometric analysis of SLFN4-tdTomato$^+$ cells. A) The percentage of SLFN4$^+$ cells in BM, spleen and corpus over time from uninfected mice. N=3 separate mice per group. *P<0.05. SLFN4-tdT$^+$ cells vs SSC flow cytometry dot plot graphs for infected WT versus *pCMV-Shh* at indicated time points from **B**) BM, spleen and corpus (Summary graphs for these 3 tissues shown in Fig. **3**) and **C**) liver and small intestine. The percentage of SLFN4$^+$ cells is shown in the representative dot plot graphs. N=8-10 mice per group over 3 expts; **D**) Summary of **C**) as percent of SLFN4-tdT$^+$ cells. Shown is the median and interquartile range. Kruskal-Wallis ANOVA with Dunn's test of multiple comparisons was performed for **A** and **D**.

Figure S6: SHH responsive CD11b$^+$ cells at 4 and 6 months after *H. felis* infection. Corpus cells were isolated from WT and *pCMV-Shh* mice 4- and 6-month after *H. felis* infection. Gated CD11b$^+$ cells were analyzed for SLFN4-tdT fluorescence and the GR-1$^+$ surface marker. The percentage of gated cells is shown as median (interquartile range), N=5 mice per group over 2 independent experiments.

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Figure S8. IFNα induces *Slfn4* gene expression in primary myeloid cells. A) WT or *Gli1*$^{+/-}$ peritoneal myeloid cells analyzed by flow cytometry for CD11b (versus forward scatter, FSC). Gated CD11b$^+$ cells were treated with rIFNα and then analyzed for GR-1 and SLFN4 expression by flow cytometry. The percentage of gated cells is shown in the graph. **B**) Schematic experimental protocol. **C**) *Slfn4* mRNA analysis of CD11b$^+$/GR-1$^+$ versus CD11b$^+$/GR-1$^-$ cells. Shown for **A**) and **C**) are the median (interquartile range) for N= 3 experiments performed in triplicate. One-way ANOVA followed by Tukey's multiple comparisons test on log-transformed values was performed. * P<0.05.

Figure S9. Primary myeloid cells exhibit T cell suppressor function after IFNα treatment. Primary myeloid cells from the WT and *Gli1*$^{+/-}$ mice were treated with rIFNα and then flow sorted for SLFN4-tdT$^+$ and SLFN4-tdT$^-$ cells. These two subpopulations were analyzed for **A**) *iNos* mRNA or **B**) *Arg1* mRNA. One-way ANOVA followed by Tukey's multiple comparisons test on log-transformed values was performed. *P<0.05. NS, not significant. **C**) The CFSE T suppression assay was performed using sorted cells by co-culturing with activated splenic T cells in a ratio of 1:10. The percentage of proliferating T cells is shown. For **A**-**C**), shown are the median and interquartile range for N= 3 experiments performed in triplicate. *P<0.05. NS, not significant.

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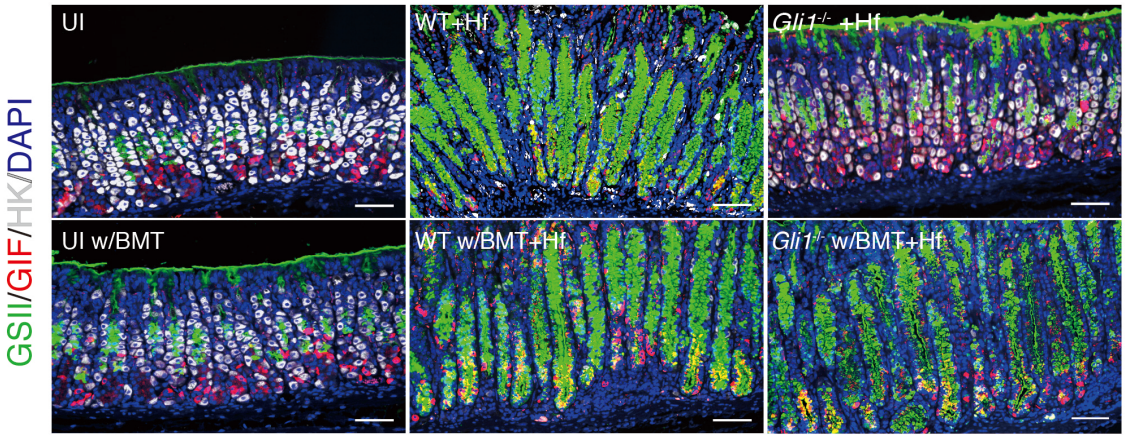

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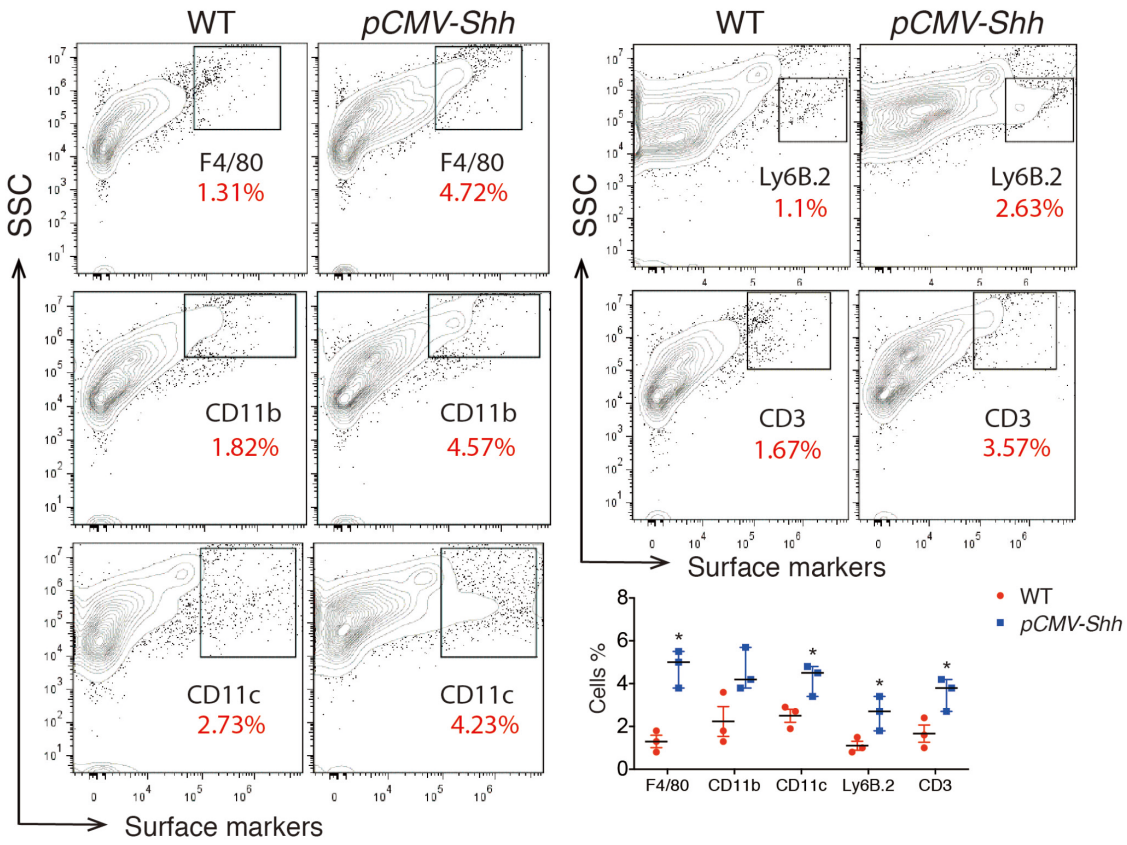

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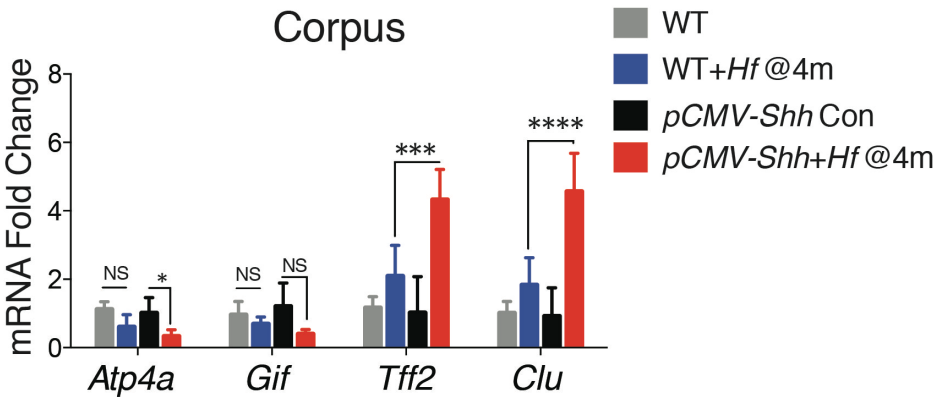

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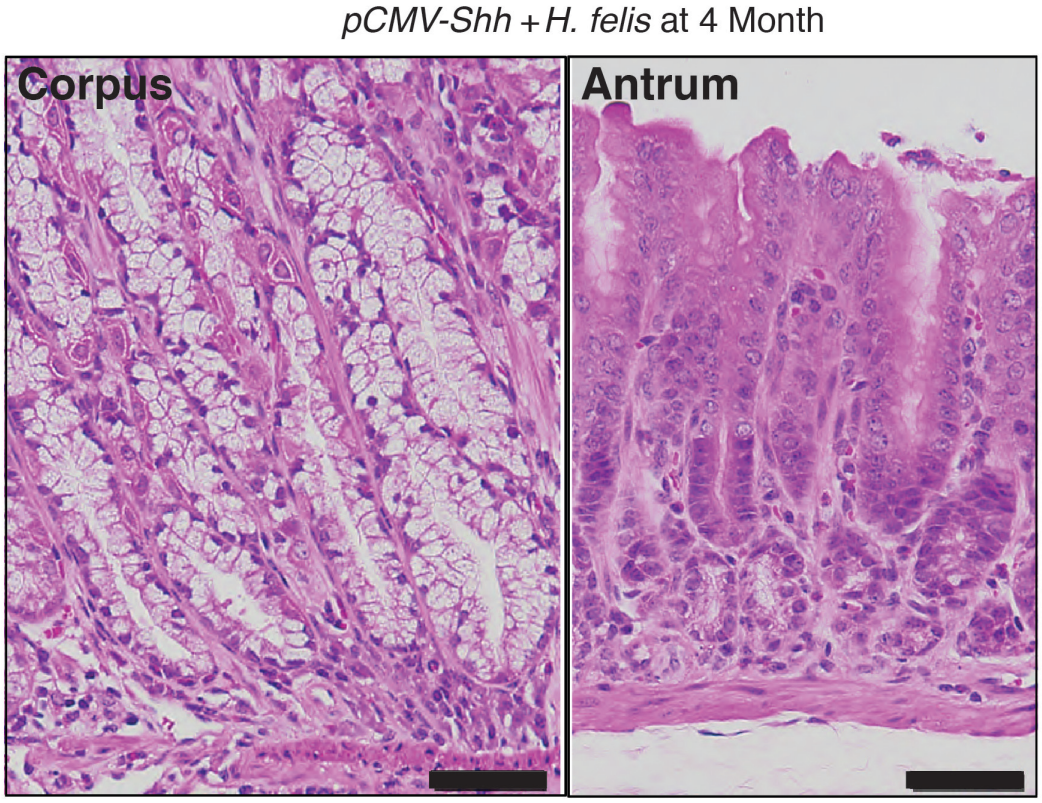

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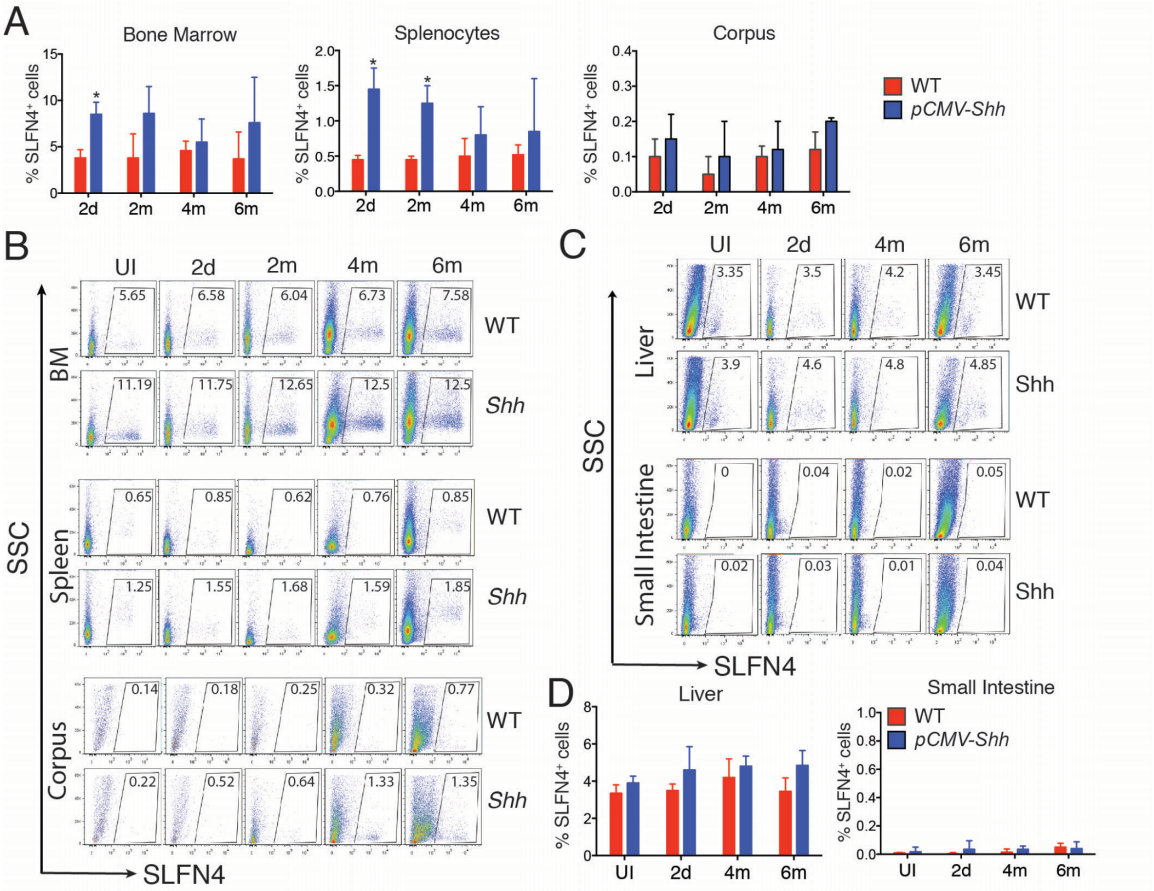

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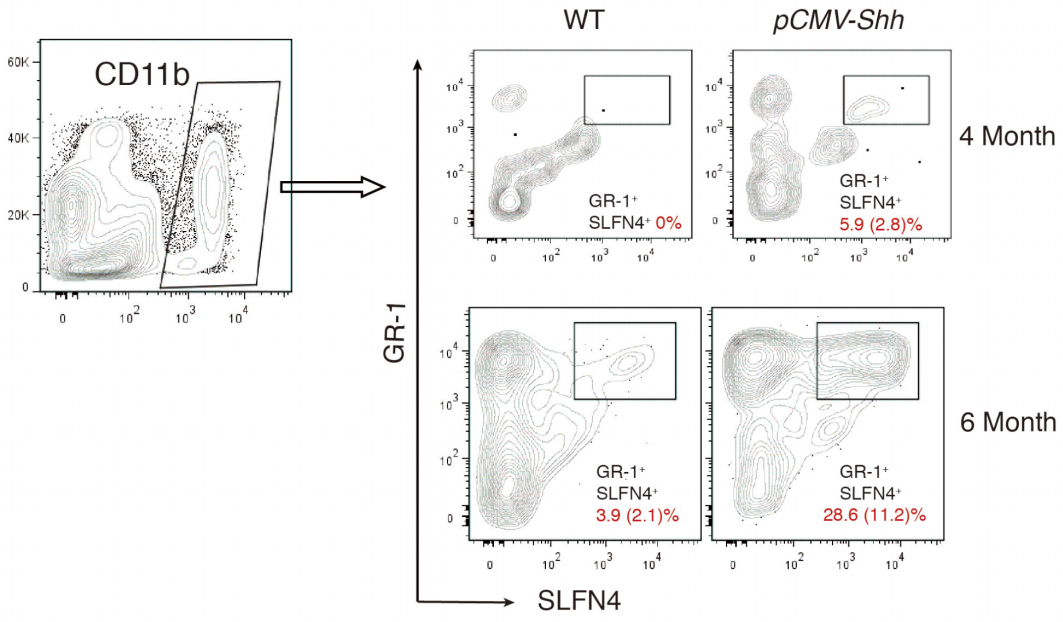

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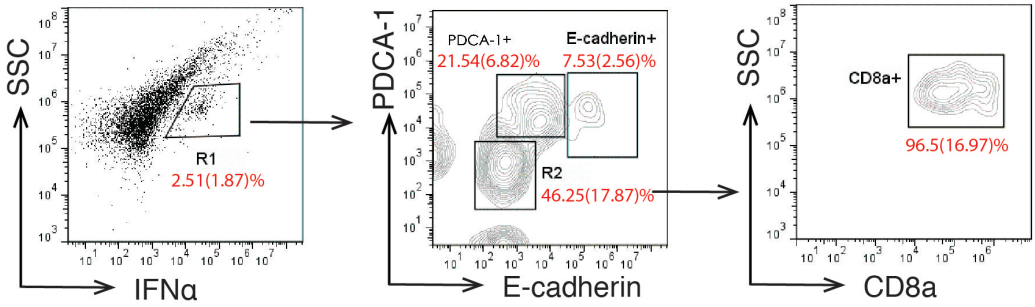

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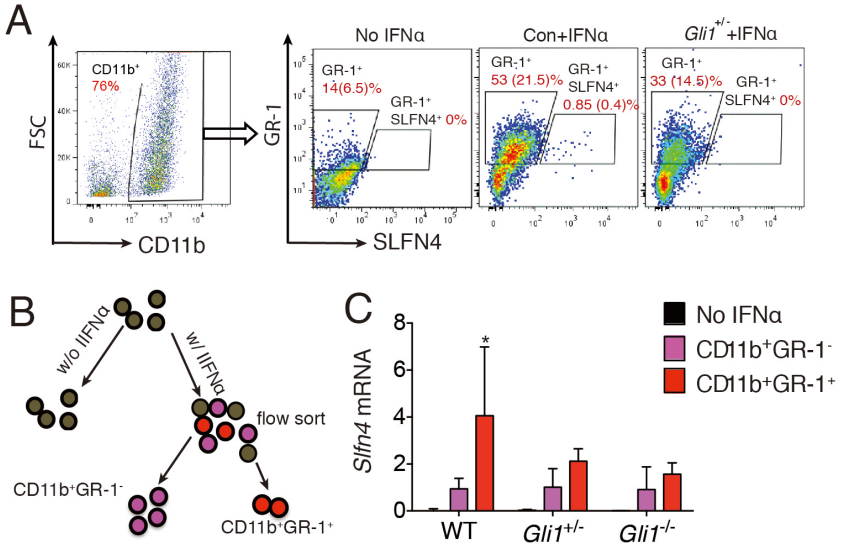

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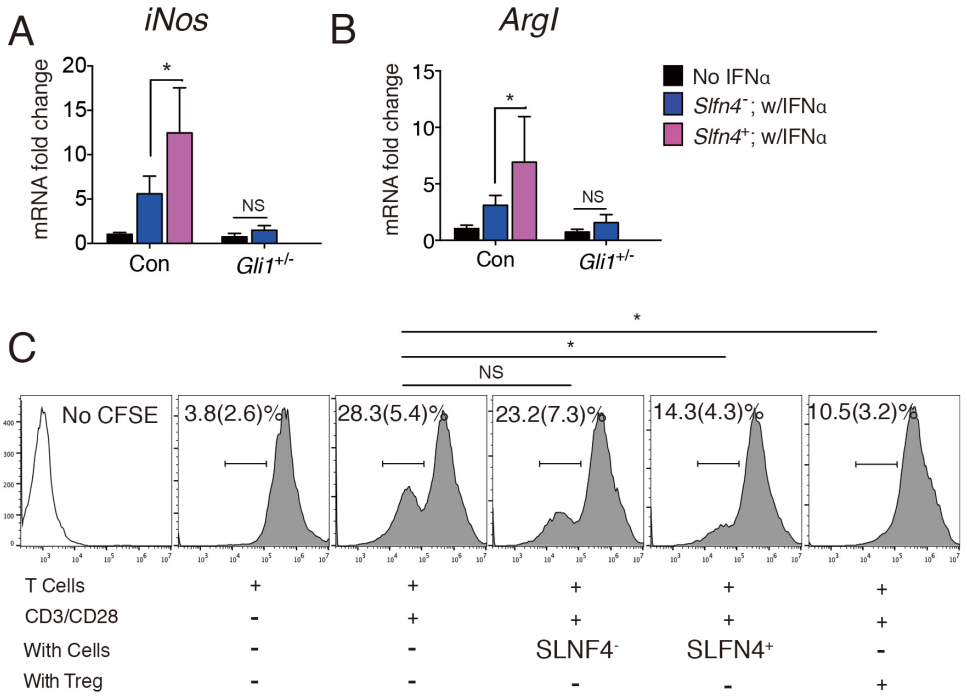

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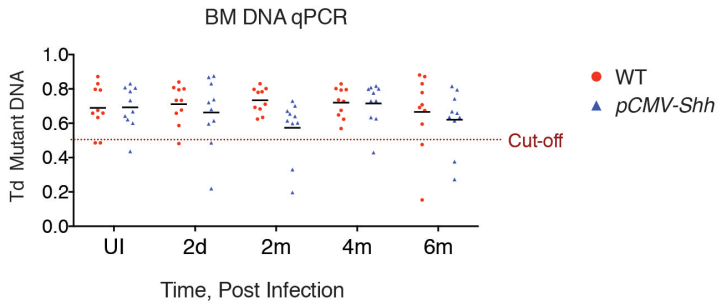

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