

## Supplementary Figures

### **Transcriptome assembly and differential gene expression of the invasive avian malaria parasite *Plasmodium relictum* in Hawai‘i**

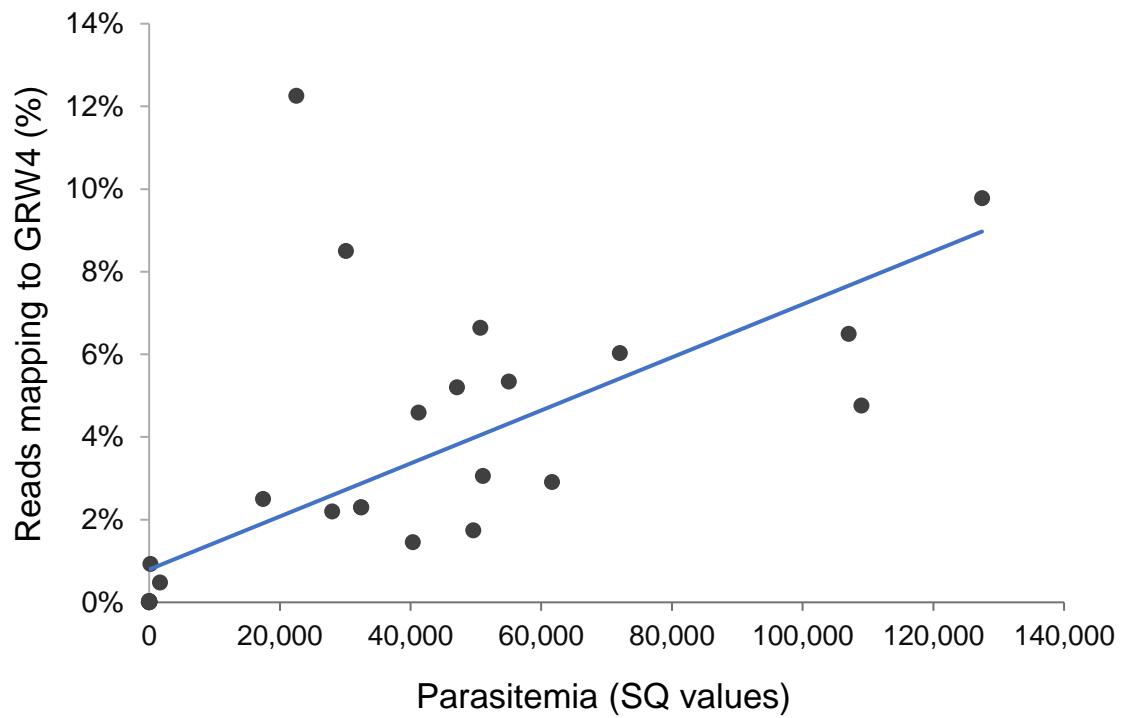
Elin Videvall<sup>1</sup>, Kristina L. Paxton<sup>1,2</sup>, Michael G. Campana<sup>1</sup>, Loren Cassin-Sackett<sup>1,3</sup>,  
Carter T. Atkinson<sup>4</sup>, Robert C. Fleischer<sup>1</sup>

<sup>1</sup> Center for Conservation Genomics, Smithsonian Conservation Biology Institute, National Zoological Park, Washington, DC 20008, USA

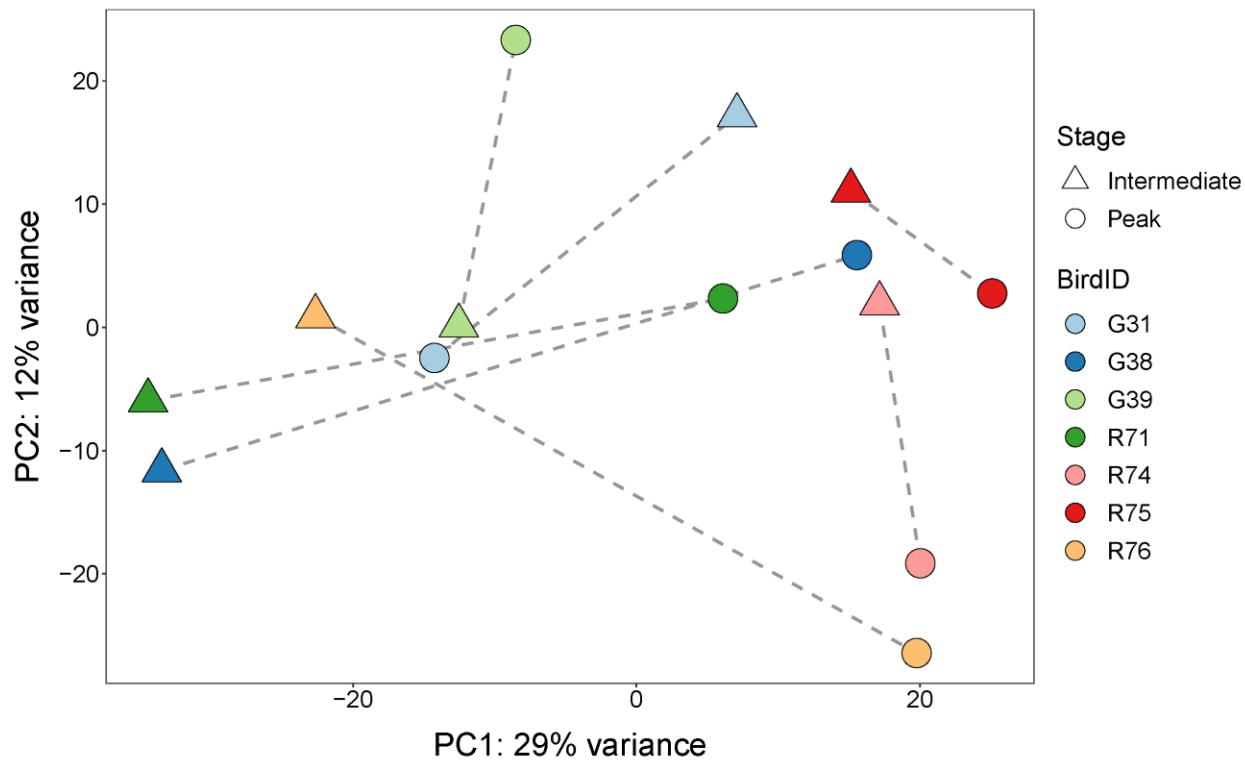
<sup>2</sup> Current address: Hawai‘i Cooperative Studies Unit, University of Hawai‘i at Hilo, PO Box 44, Hawai‘i National Park, HI 96718, USA

<sup>3</sup> Department of Biology, University of Louisiana, Lafayette, LA 70503, USA

<sup>4</sup> U.S. Geological Survey Pacific Island Ecosystems Research Center, Kilauea Field Station, PO Box 44, Hawai‘i National Park, HI 96718, USA



**Figure S1.** Parasitemia intensity (SQ values obtained from qPCR) and percent of total reads mapping to the assembled *Plasmodium relictum* GRW4 transcriptome. The blue line indicates the linear relationship (Pearson's correlation test:  $t = 5.51$ ,  $df = 32$ ,  $p = 4.52\text{e-}06$ ,  $r = 0.70$ ).



**Figure S2.** PCA of *Plasmodium relictum* GRW4 transcriptomes in all paired samples (host individuals with parasite transcriptional data at both intermediate and peak infection stages). Dashed lines connect parasite transcriptomes from the same host individual.