**SUPPLEMENTAL MATERIAL**

**Figures:**

**Figure S1**. Principle Component Analysis of transcriptomes from bacteriome (Bc), gut (Gt), and whole insect (WI) tissue from three genotypes of *M. persicae*.



**Figure S2**. Log2 fold change in RPM between bacteriome and gut tissue of the mTOR pathway in three genotypes of *M. persicae*. Positive numbers indicate higher expression in bacteriome, negative numbers indicate higher expression in gut. Asterisks indicate FDR adjusted significant results. \* shows p < 0.05, \*\* shows p < 0.001, \*\*\* shows p < 0.00001





**Figure S3**. Identification of (A) RHEB, (B) Rag A/B, (C) Nup44A, and (D) Skp2 orthologs between *M. persicae* and *A. pisum* using the synteny of adjacent genes PTHR family.