**Methods**

**Annotation**

**BLASTp + phylomeDB:**

In order to annotate the amino acid sensing mechanism of the mTOR pathway, component genes were identified using the Kyoto Encyclopedia of Genes and Genomes (KEGG (Kanehisa and Goto 2000)). Amino acid sequences of previously annotated mTOR genes within *Drosophila melanogaster* were gathered using FlyBase (Gramates et al. 2017). These were used to BLASTp the 2.0 *A. pisum* genome (NBCI taxon ID 7029). BLASTp for *A. pisum* were carried out using NCBI Blast tools.

After BLASTS identified likely orthologs within *A. pisum,* phylomeDB (Huerta-Cepas et al. 2014) was used to confirm the identity of orthologs and check any suggested duplicates within the Aphid genome. To confirm the identity of a potential ortholog it had to occur in the same phylogeny as its *D. melanogaster* ortholog, as did any duplications. The genomic locations of duplicated genes were also checked on aphidbase (bipaa.genouest.org/is/aphidbase) to ensure that suspected duplications were separate genes, along with adjacent predicted genes.

When *A. pisum* orthologs of mTOR pathway genes were confirmed, their amino acid sequences were used to BLASTp against the genome of the G006 clone of *M. persicae* on Aphidbase. Again orthologs within *M. persicae* were confirmed by checking their positions on phylogenies in phylomeDB (Huerta-Cepas et al. 2014).

**HMMer search:**

Hidden Markov Models (HMMs) were used to search both aphid genomes. HMMs were taken from PantherDB (Mi et al. 2017) were they had already been constructed based on previous gene annotations. HMMs were then used to search the aphid genomes using the ‘hmmsearch’ command from HMMer3. HMM searches supported earlier orthologs and duplications identified from BLASTp and phylogeny searches. Where HMM searches of the genome did not support the same peptides as BLASTps from *D. melanogaster* genes (SKP2, Sec13, Wdr24, LAMTOR4 and LAMTOR5), annotated *Drosophila* genes were used in PantherDB to verify the HMM’s accuracy. Where they were not included in the HMMs presented by PantherDB, EggNog sequence search (Huerta-Cepas et al. 2016) was used instead to confirm annotation and find HMMs. These HMMs were then used to search the genome and identified the same sequences as BLASTp searches. EggNog was also used where where PantherDB did not agree with phylomeDB. FlyBase IDs and HMM IDs can be found in table S2.

**Identifying cross species orthologs using synteny:**

In cases where there was more than one copy of a gene in either aphid species, orthologs could not be ascertained by multiple sequence alignments. Instead surrounding genes were entered into PantherDB (Doerks et al. 2002) to find their PTHR families and subfamilies. Orthologs between the two species were then identified by looking for synteny in the adjacent gene’s identity and position in the genome (fig. S3).

**Transcriptomes**

**Sample material**

RNAseq data were generated in a previous study by Duncan *et al.,* 2016 for the *M. persicae* lines USDA, G002, and G006. *A. pisum* RNAseq data were generated in previous studies by Feng et al., 2018 and Jaquiery et al, 2018, and were only used to interrogate the expression of genes at a binary level.

**Transcriptome assembly**

Transcriptomes were constructed using Hisat2 v2.0.0 (Kim et al. 2015), SeqMonk (Andrews 2007), and DESeq2 (Love et al. 2014). Transcriptomes were constructed using the *M. persicae* G006 OGS v1.0 and the *A. pisum* LRS1 2.1b OGS as a reference due to the previously constructed *de novo* transcriptomes being unable to differentiate between highly similar duplicated genes.

**Quality control and Data preparation**

Paired reads were first examined in FastQC (Andrews 2010) to test for presence of adaptor sequences, and to test the quality of the RNAseq data. The Illumina universal adaptor sequence was present in all reads. The adaptor sequence was trimmed using Trim galore v0.4.3 (Kruger 2012). RNAseq data were mapped against reference genomes available on aphidbase (bipaa.genouest.org/is/aphidbase) using Hisat2 (Kim et al. 2015) allowing no mismatches in the seed region (‘-K 0').The most recent available genomeswere used as references (version 2.1b for *A. pisum* and version 1 of the G006 clone line for *M. persicae*).

**SeqMonk**

A genome was constructed in SeqMonk (Andrews 2007) using the same reference genomes as were used in Hisat2, and with the most recent official gene sets (2.1b for *A. pisum* and 1.0 for *M. persicae*). The reference genome was constructed in 25 pseudo-chromosomes. The outputs from Hisat2 were loaded into SeqMonk with a minimum mapping quality of 255, the value Hisat2 give unique alignments in order to stop transcripts from paralog genes counting towards multiple genes in the final transcriptome. Probes and raw counts were then generated in the RNA-seq quantitation pipeline. Differential expression analysis was carried out using DESeq2 in SeqMonk.

**Statistical Analysis**

A principle component analysis was carried out on the *M. persicae* transcriptome data to see if any batch effect was present in the data. This analysis demonstrated that the transcriptomes grouped clearly by tissue type rather than by genetic line or by time the transcriptomes were made, so batch effect removal was deemed unnecessary (fig. S1).