Additional file 5: Figure S4. Correlation of normalized read counts (RPKM) for unigenes in orthogroups shared between the interface transcriptomes and reference assembly TrVeBC1 (ppgp.huck.psu.edu). Reads from each interface transcriptome were mapped to a reference assembly (TrVeBC2, ppgp.huck.psu.edu) that included whole haustorium data from *T. versicolor* grown on *M. truncatula*. A subset of unigenes is more highly expressed in the interface transcriptome of *T. versicolor* grown on *M. truncatula*; a similar pattern is not observed for *T. versicolor* grown on *Z. mays*. This is due to a bias for *Medicago* grown *Triphysaria* unigenes in the reference dataset TrVeBC2, which was constructed with reads from *Medicago* grown *Triphysaria*. For unigenes in shared orthogroups, the RPKM values are highly correlated (Pearson’s R = 0.81) between interface transcriptomes indicating that technical and biological variation is low.