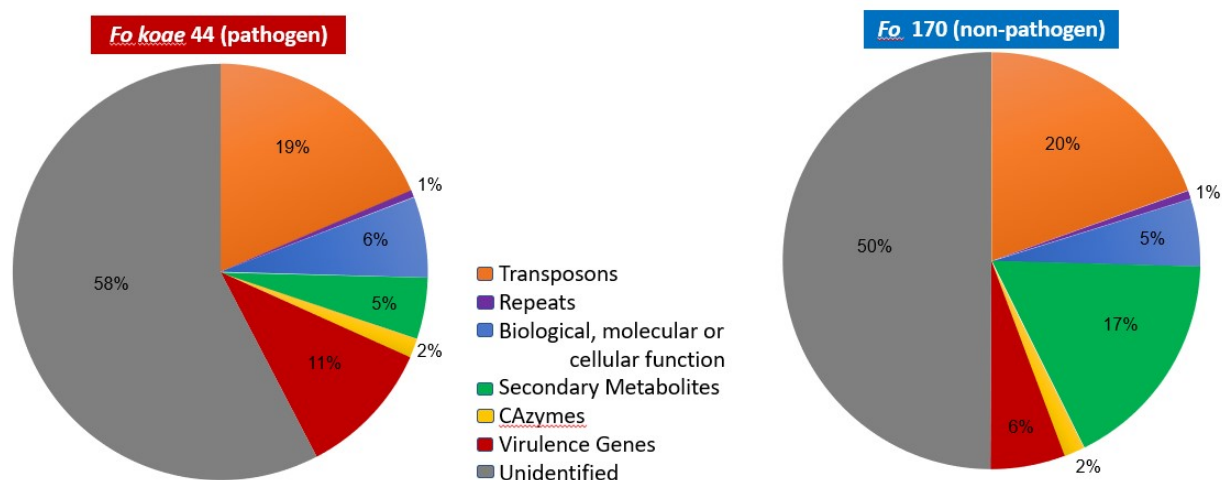




Additional File 8. Proportion of predicted genes with putative function of the lineage specific DNA (LSX) of the *Acacia koa* wilt pathogen *Fusarium oxysporum* f. sp. *koae* (*Fo koae* 44) and the *F. oxysporum* (*Fo* 170) isolate characterized as non-pathogenic to *A. koa*. Both isolates had similar proportions of transposons, repeats, carbohydrate active enzymes (CAZymes), and genes identified through gene ontology and protein families. *Fo koae* 44 had a higher proportion of virulence associated genes and *Fo* 170 had a higher proportion of secondary metabolite genes on the LSX.