

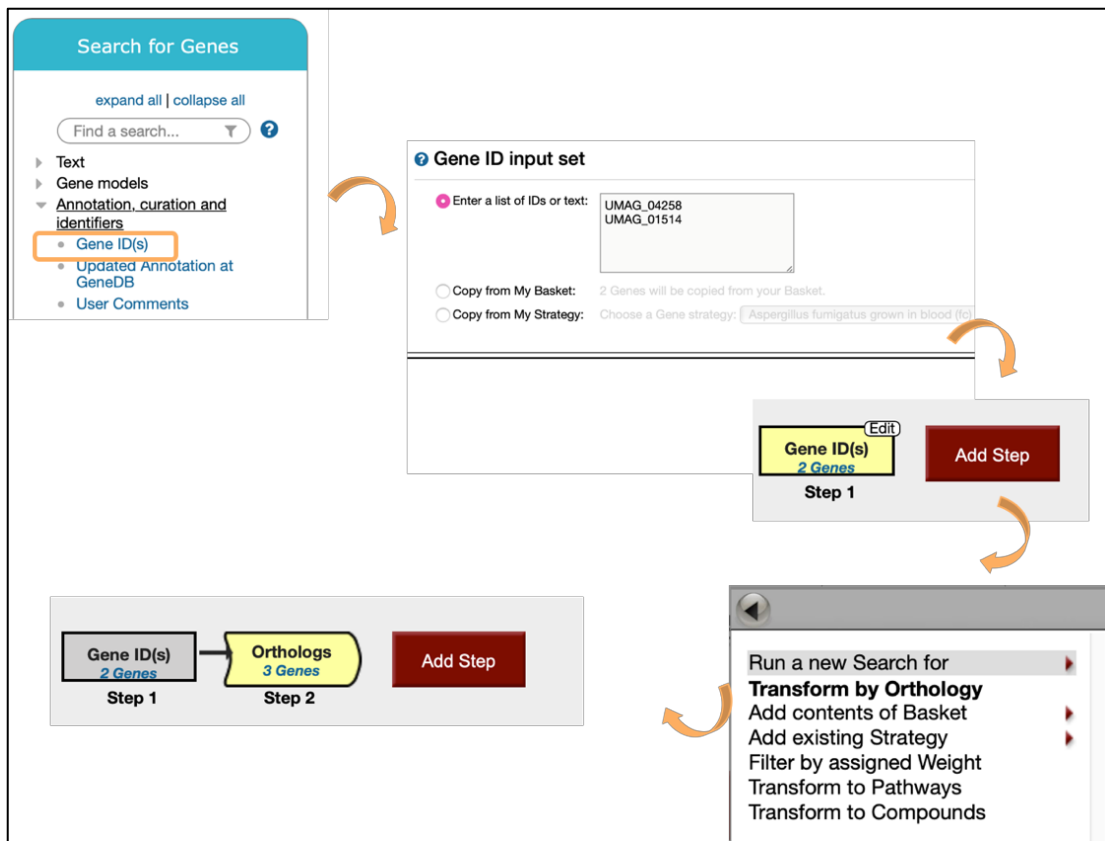
Enriching your analysis with data from EnsemblFungi BioMart and FungiDB

- Navigate to BioMart and identify genes that have PHI-Base annotation.

- Determine which genes are annotated in PHI-Base with loss of pathogenicity due to a mutation in *Zea mays*:

- Copy a list of genes and create a GeneID search in FungiDB and then identify orthologs of these genes in *F. graminearum* PH-1

Gene stable ID	Transcript stable ID
UMAG_04258	KIS67763
UMAG_01514	KIS70344



- Why do you think you identified more genes in *F. graminearum* than in *U. maydis*?

Note: This approach can be used with any organisms for which the data is loaded in FungiDB and EnsemblFungi BioMart.