Step 1: Identify SNPs between two groups of clinical isolates in the dataset titled "Aligned genome sequence reads - *C. auris* clinical isolates".

Step 2: Find genes that overlap with SNPs detected in Step 1.

Step 3: Search for genes that are predicted to encode a secretory signal peptide.

Step 4: Look for genes up-regulated in biofilm (4, 12, 24hr).

Step 5: Convert to orthologs in *Candida albicans*.

Step 6: Find genes up-regulated in *Candida albicans* during infection of murine macrophages. Macrophage data is in HostDB.

Step 7: Cross-reference with disease phenotype annotations from PHI-Base.