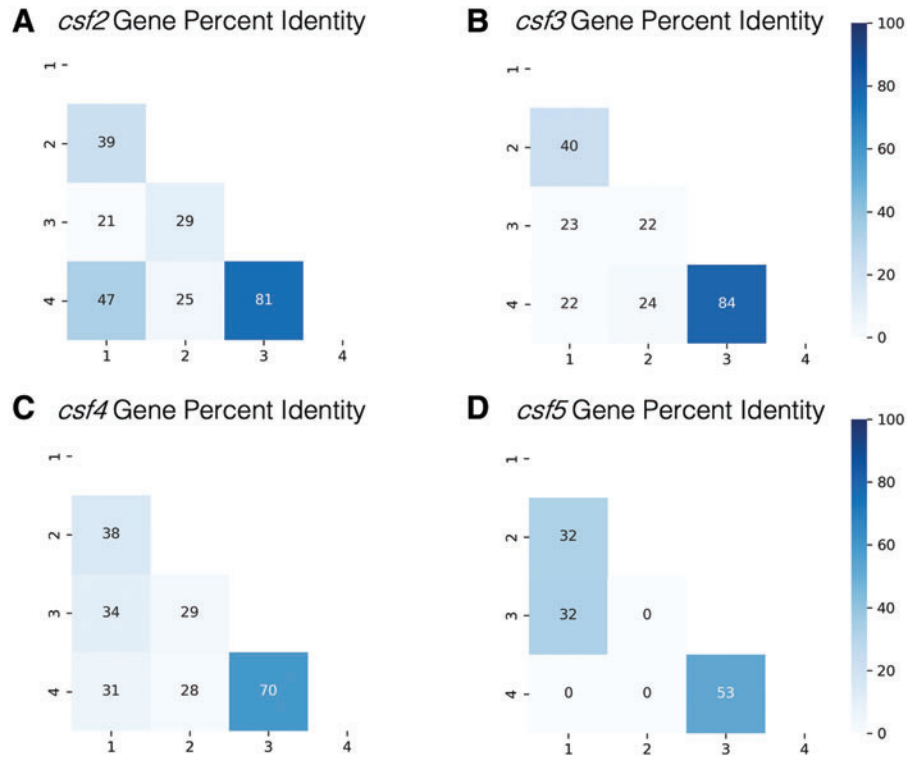# Supplementary Data

SUPPLEMENTARY FIG. S1. Representative amino acid sequences from each variant for each conserved gene were compared by identity. Each sequence was aligned using blastp using the BLOSUM62 scoring matrix. **(A)** Csf2 compared against Csf2. **(B)** Csf3 compared against Csf3. **(C)** Csf4/DinG compared against Csf4/DinG. **(D)** Csf5/Cas6 compared against Csf5/Cas6.