# Nothing clever here, just copying results to a single folder for gff conversion

mkdir Mackay\_MAGs\_diamond\_Greening\_metabolic\_marker\_genes\_pident\_cutoffs\_for\_gff\_conversion

for item in \*\_diamond\_Greening\_metabolic\_marker\_genes

do

sample\_name=${item/\_diamond\_Greening\_metabolic\_marker\_genes/}

cp ${item}/${sample\_name}\_diamond\_Greening\_metabolic\_marker\_genes\_combined\_pident\_cutoffs.tsv Mackay\_MAGs\_diamond\_Greening\_metabolic\_marker\_genes\_pident\_cutoffs\_for\_gff\_conversion

done