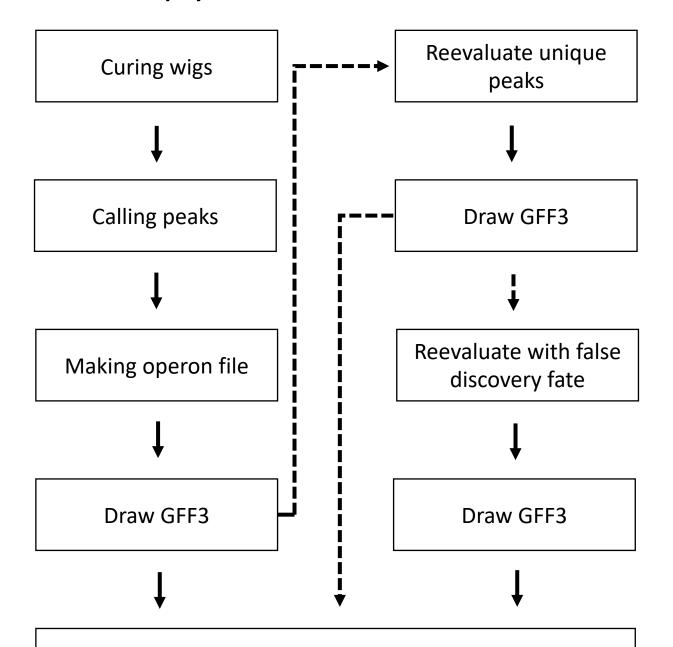
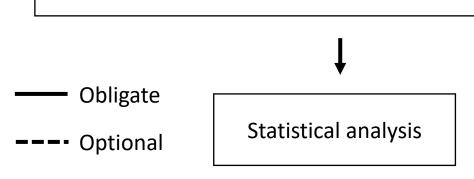
pyRAP flowchart



Post-processing:

- Transfer features and names from old annotation file
 - Categorize sRNAs
 - Categorize operons
 - Supply genes with no coverage



pyRAP flowchart

