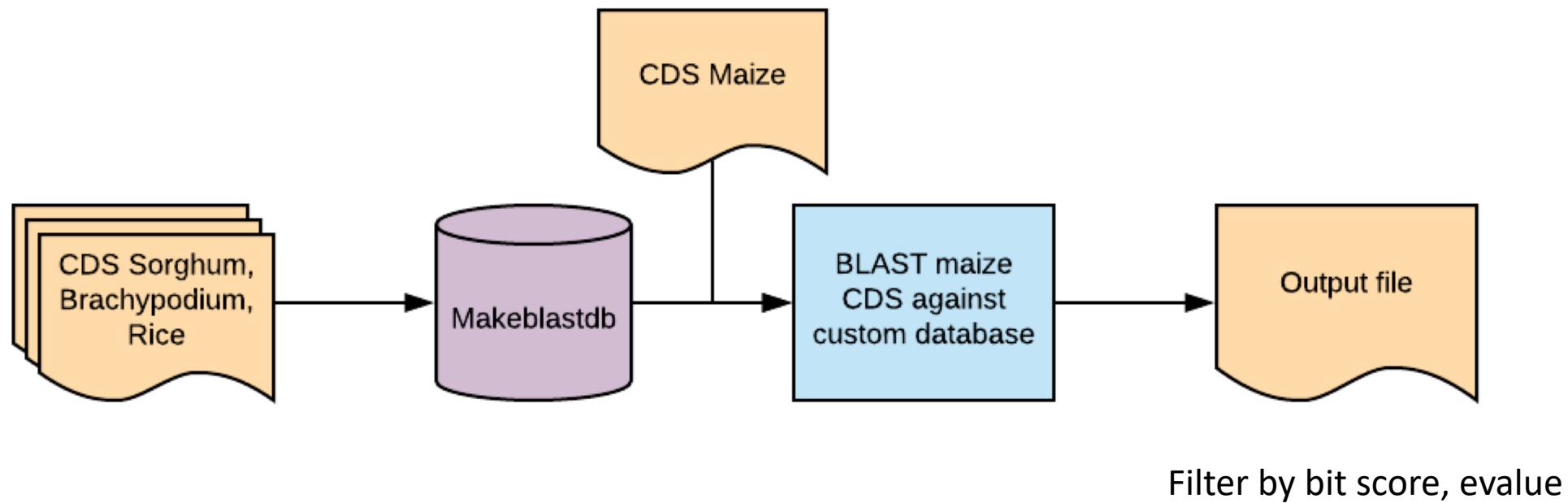


BLAST searches on maize coding DNA sequences for PHG reference ranges

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Buckler Lab Presentation
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Methods



Results

- For some genes:
 - BLAST search was able to reduce #of possible transcripts to 1
 - Others had duplicates, different transcripts had same bit scores & e-values
- First CDS not always most conserved
 - Often transcripts 2-86 had highest conservation
- Some IDs in CDS file → “ZeamMpxxx”, “ZeamaCpxxx”
- Extract new coordinates

Item	Count
# CDS maize IDs	131,585
Total # matches across 3 genomes	848,886
Final # of transcripts for PHG ref-ranges	34,547