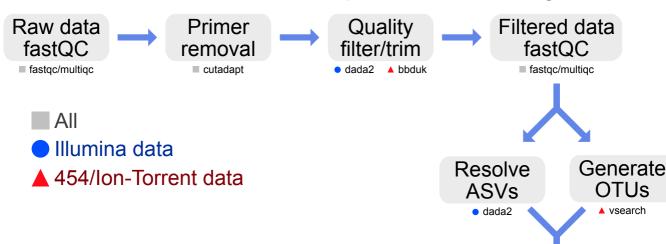
## **Amplicon Processing Overview**



## **Primary outputs:**

- Recovered ASV/OTU sequences (fasta)
- Counts of sequences per sample
- Taxonomic classifications of sequences

## Assign taxonomy

- DECIPHER
- SILVA DB for 16S
- UNITE DB for ITS