

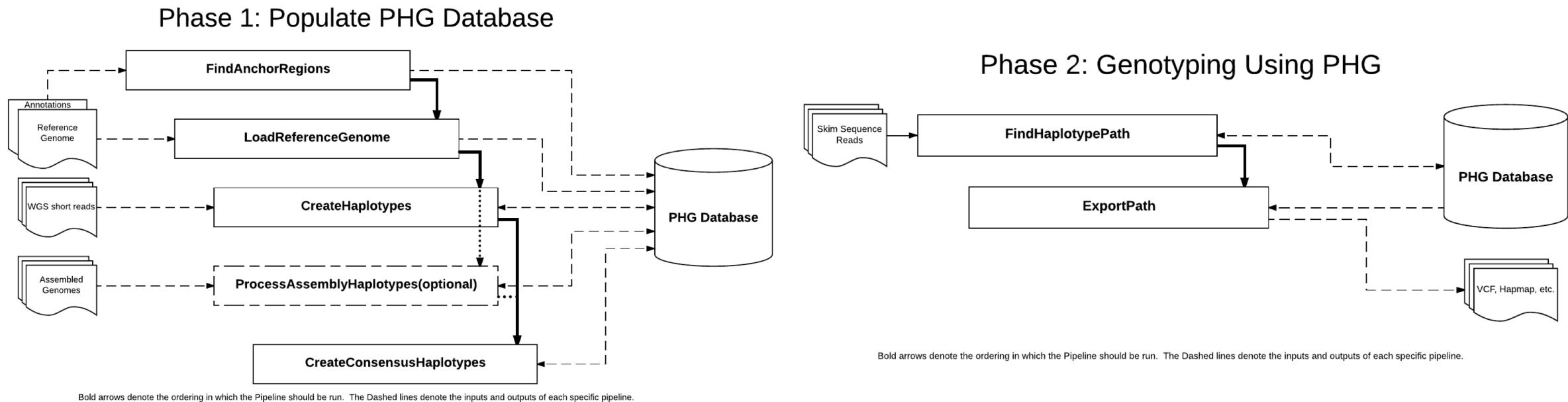
# Merritt Burch

Lab Meeting

2019-07-10

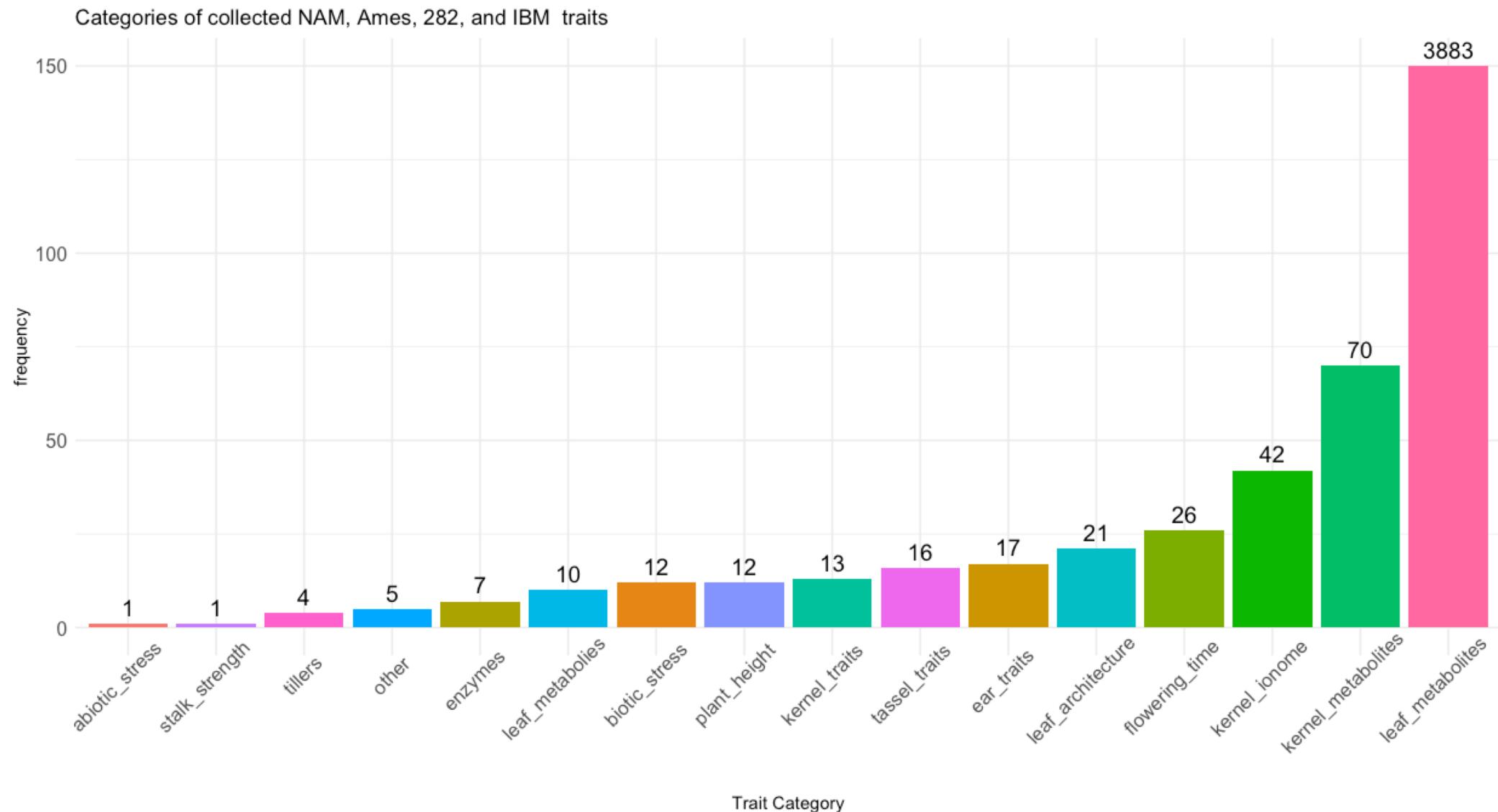
# Ran PHG Pipeline

- Populated database and genotyped test data



# Phenotype collection

- Not 10k metabolites, ~4k mass-features
- Typo in Zhou abstract and methods



## Next steps

- Combining phenotypes (it's messy)
  - 1 file per population + data type
- Running tests in TASSEL with NAM+flowering time
  - VNC to CBSU machines for TASSEL GUI
  - Filtering by table sites is *very important*

