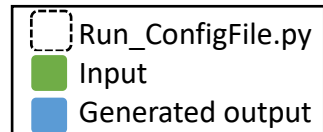


VCF (phased haplotype)  
RNAseq fastq



### Process RNAseq and VCF

./Process\_RNAseq/Process\_RNAseq\_pipeline\_I\_trim.sh

./Process\_RNAseq/Process\_RNAseq\_pipeline\_II\_align.sh

./Process\_VCF/Process\_VCF\_pipeline\_I.extractVCF.sh

./Process\_VCF/Process\_VCF\_pipeline\_II\_hetsMeta.sh

./Process\_RNAseq/Process\_RNAseq\_pipeline\_III\_mpileup.sh

### Phasing

./Phasing/step1\_prepareVCF.sh

./Phasing/step2\_phasing.sh

### BEASTIE

./BEASTIE/stan\_wrapper.py

./BEASTIE/output\_analysis.py

To be uploaded

ASE prob  
( $\theta > \lambda/\theta \leq \lambda$ )

ASE point  
estimate

Gene list with  
extreme ASE