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Maternal and paternal gene copies are not always expressed in a 50:50 ratio. Transcriptional imbalance, called allele-specific expression (ASE), has been demonstrated in model organisms and may have evolutionary importance. We are developing a bioinformatics pipeline to detect ASE in RNAseq reads from model plants. The pipeline requires RNAseq reads from homozygous parents, plus RNAseq reads from heterozygous offspring. The pipeline uses software for reference-based assembly, transcript alignment, and differential expression analysis. The pipeline outputs lists of genes whose expression ratios differ significantly from the 50:50 null model prediction. We tested the pipeline on genes commonly expressed in seed endosperm tissue using three strains of *Arabidopsis thaliana*. Previous studies of this system had relied on counting RNAseq reads that contain known, isolated SNPs. On our data, the two methods had correlations between 0.84 and 0.98 across four experiments. In ongoing work, while developing a version in Python, we aim to demonstrate that the new pipeline is actually more accurate than the isolated SNPs method.