a
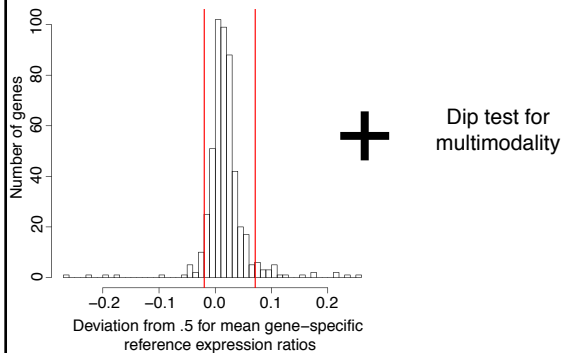
SNP filtering criteria

- Exclude PAR regions of the X-chromosome
- Require a minimum of 10 reads per allele
- Filter known escape genes
- SNPs must be included in dbSNP
- Exclude SNPs with total expression greater than 3000 reads
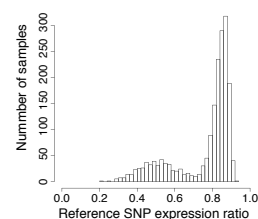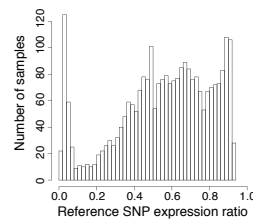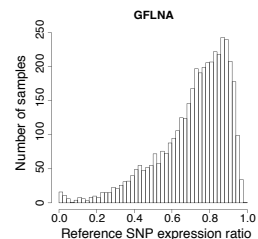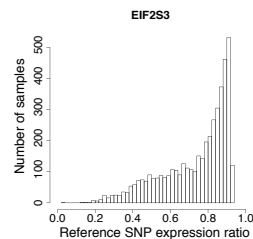- Filter genes exhibiting reference bias and bimodal reference SNP distributions

+ Dip test for multimodality

b

Non-biased examples: ACOT9, PIGA
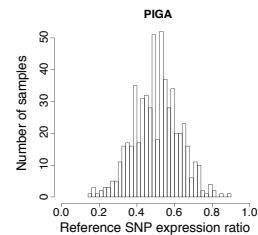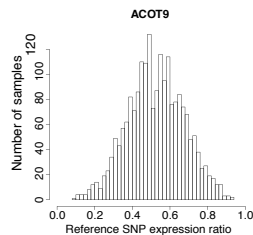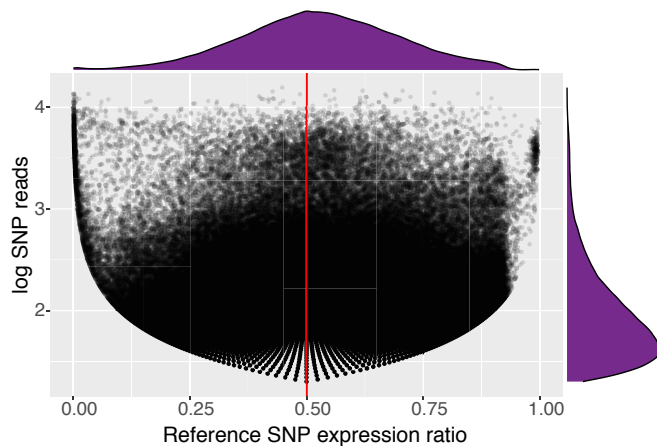
Bimodal examples: RPL10, KDM5C

Reference biased examples: EIF2S3, GFLNA

c All heterozygous SNPs before gene filtering

d All heterozygous SNPs after gene filtering. Representing 542 genes