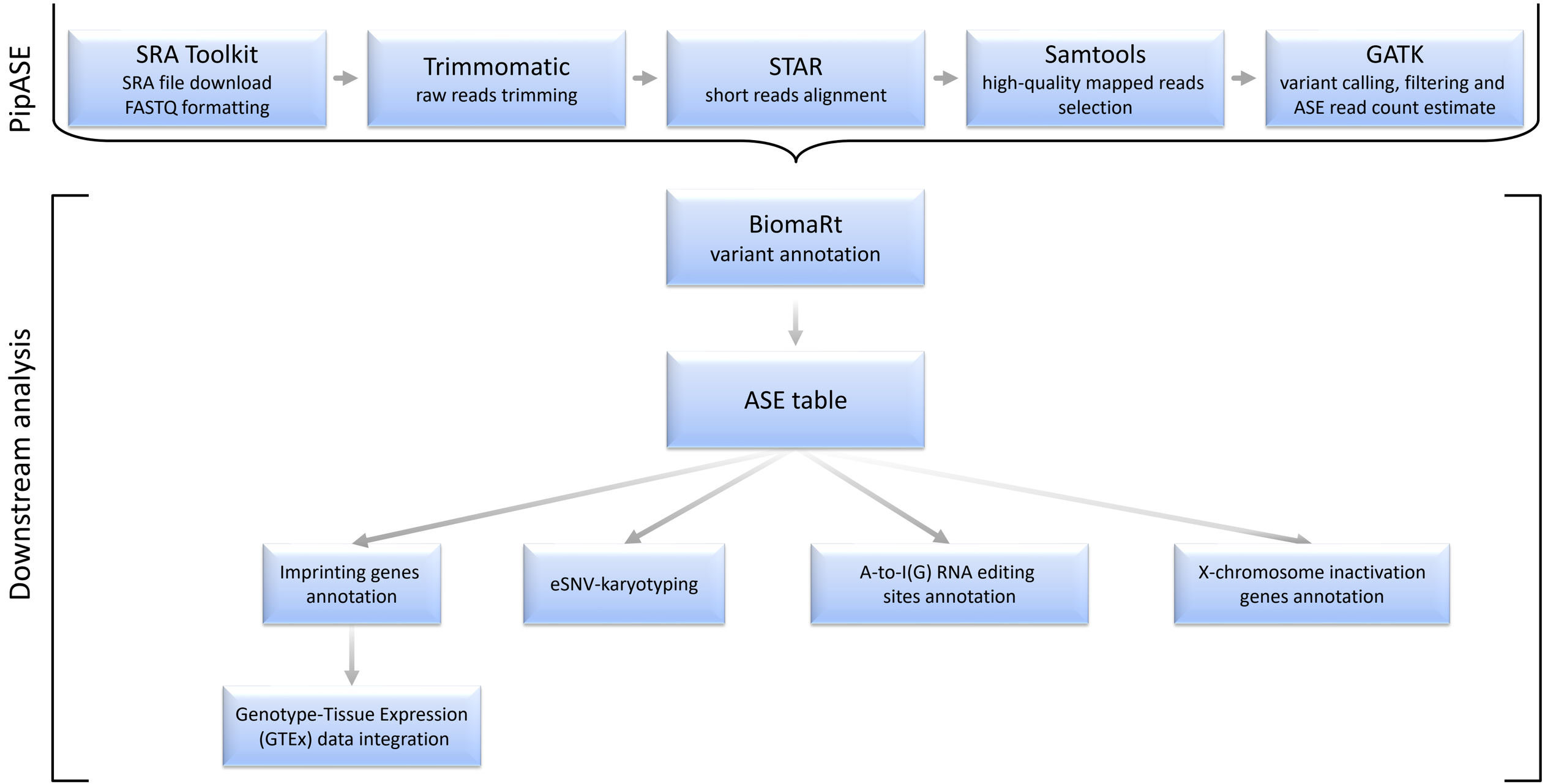
Figure S2


PipASE
SRA Toolkit
SRA file download
FASTQ formatting
Trimmomatic
raw reads trimming
STAR
short reads alignment
Samtools
high-quality mapped reads
selection
GATK
variant calling, filtering and
ASE read count estimate
Downstream analysis
BiomaRt
variant annotation
ASE table
Imprinting genes
annotation
eSNV-karyotyping
A-to-I(G) RNA editing
sites annotation
X-chromosome inactivation
genes annotation
Genotype-Tissue Expression
(GTEx) data integration