

Input:
Paired-End Sequence Data

Identify Index

Filter by Read Quality

Trim *Alu* (16 bp)
from junction read

Map Read Pairs
and Filter by
Mapping Quality

Map Read Pairs
and Filter by
Mapping Quality

Reference
Alu

Novel and
Reference *Alu*

Compute Junction Read end position

Group read pairs into *Alu* loci

Test for *Alu* sequence in junction read

Output:
Sample Genotypes
at *Alu* Loci

Reference *Alu*
Sensitivity:
Table 3

Comparison with
locus-by-locus
genotyping:
Table 6

Novel *Alu*
identification
and Specificity:
Table 4

Reproducibility:
Table 5