**Input**

- Read input data

**Pipeline internal**

- FAST genome alignment (Bowtie)
- Pairs of reads and large genomic bins
- Gapped genome alignment (BLAT)
- Gapped alignments
- Alignment processing
- Non-redundant gapped alignments
- Indel identification
- List of indel candidates (w/ \( \theta_u \) & \( \theta_{max} \))
- Thresholding, Homopolymer identification
- List of indels
- Calibrate
- Corrected indel number

**Output**

- Deletions + Insertions
- Rearrangement identification
- Novel deletions + Novel insertions + Duplication + Translocation

**Alignment processing**

**Gapped alignments**

**Non-redundant gapped alignments**

**Thresholding, Homopolymer identification**

**Calibrate**

**Corrected indel number**