# *VALET* pipeline

INPUT:
assembly.fasta
lib_1.fastq
lib_2.fastq

Filter assembly based on **coverage** and **length**.

Depth of coverage

Breakpoint detection

Bin contigs by coverage

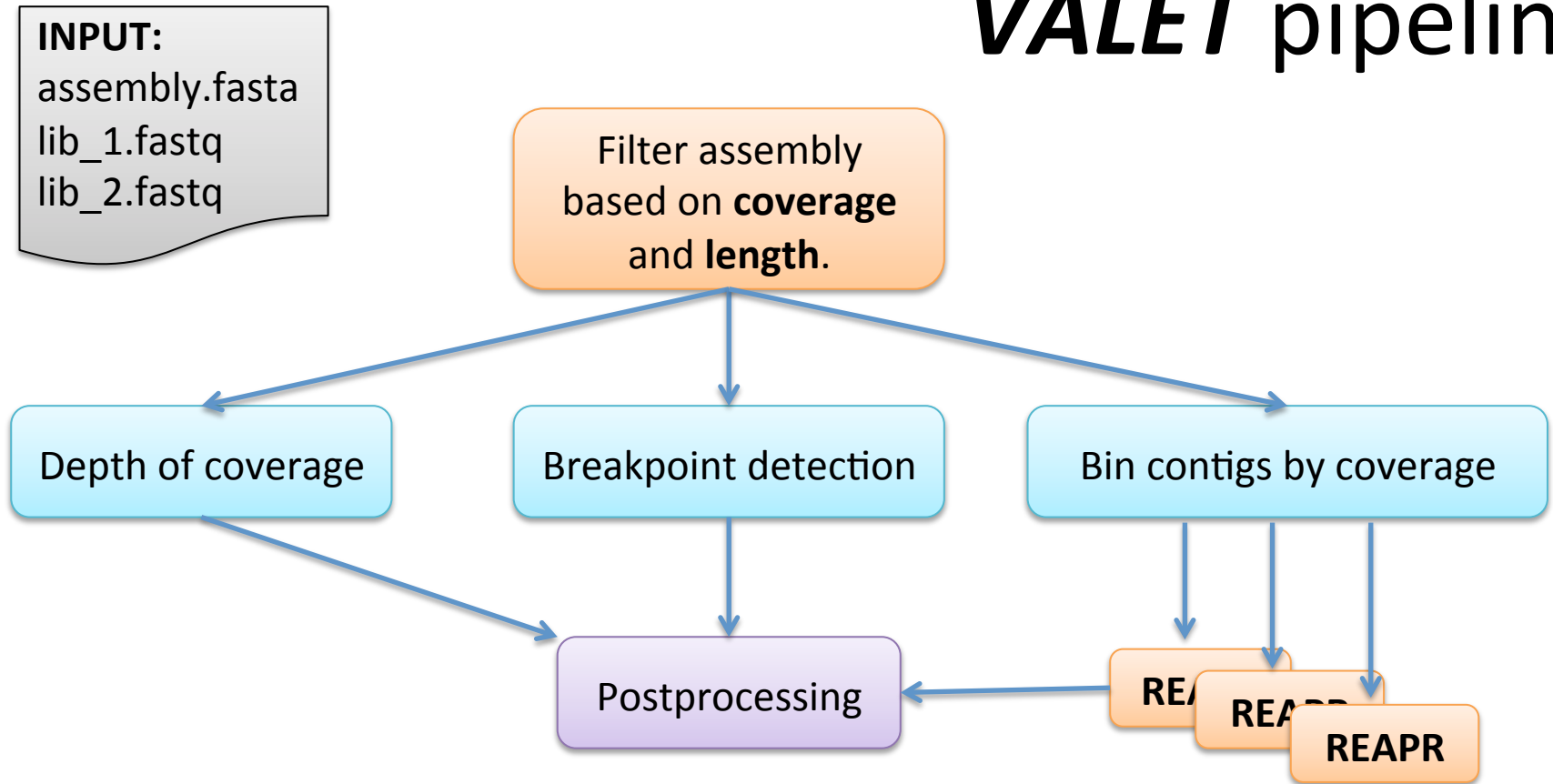Postprocessing

REAPR

REAPR

REAPR

**OUTPUT:**

**summary.gff & suspicious.gff**

```
scaffold_0_0    DEPTH_COV        Low_coverage    101    503…
scaffold_0_0    DEPTH_COV        Low_coverage    101    503…
scaffold_0_0    REAPR   Read_cov         101    103…
```

**summary.tsv**

```
#contig_name       length      abun   low_cov low_cov_bps…
scaffold_0        502453      54     4       1630…
scaffold_100      28452       108    4       1458…
scaffold_101      26395       105    4       1744…
…
```

igv Integrative Genomics Viewer