

DETECTION | 1



process contig-to-genome alignments

classify alignment topologies

identify gap and split candidates

add gene and repeat annotations

SUPPORT | 2



process read-to-contig alignments

differentiate strongly/weakly supporting reads

FILTERING | 3



apply confidence criteria

PREDICTION | 4



predict fusions

predict PTDs

predict ITDs

COVERAGE | 5

calculate relative coverage of chimeric transcripts