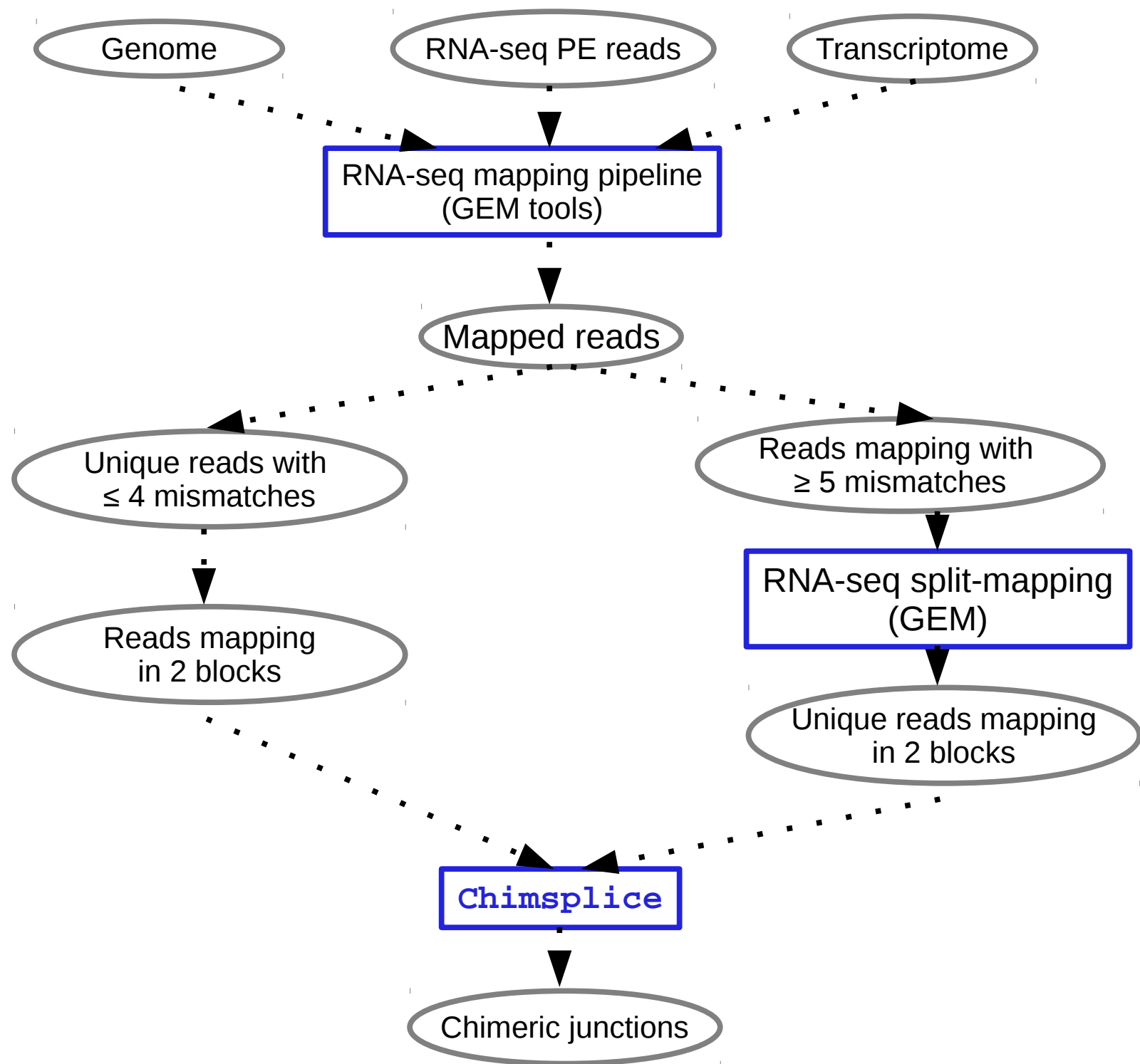
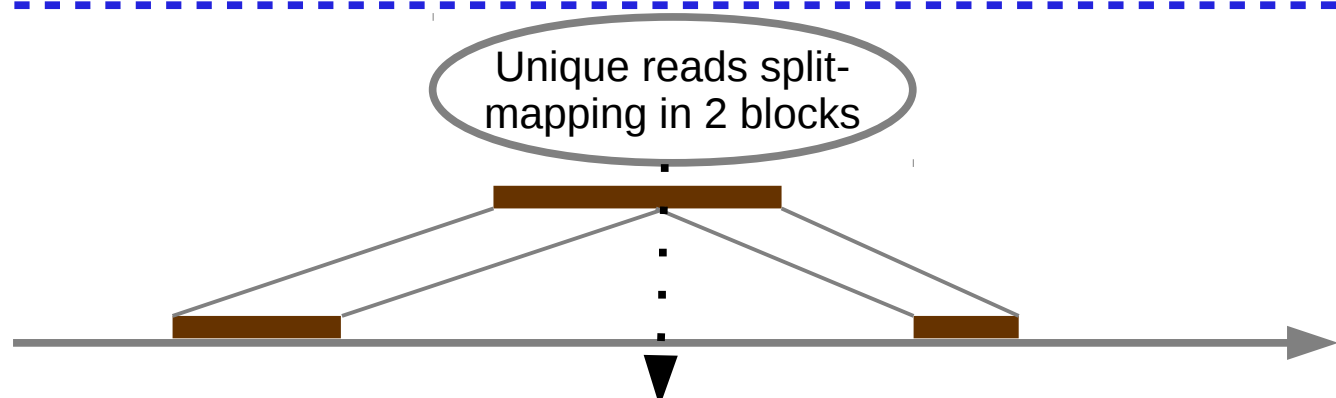


Method: ChimPipe





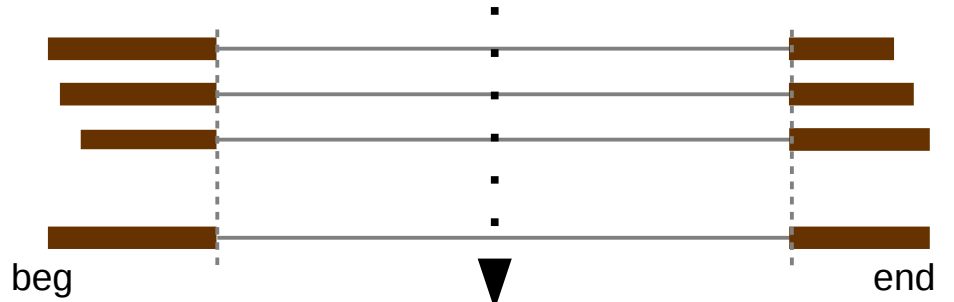
Keep reads where the two blocks overlap exons\* from different genes

\* Here only exons belonging to one gene are considered.

Chimeric reads connecting two different genes

Collapse reads into chimeric junctions associated to number of staggered and total supporting reads

Chimsplice —



3 staggered split-mappings

junction with beginning and end

Keep junctions with  $\geq x$  staggered reads  
( $x$  is chosen depending on sequencing depth)

Reliable chimeric junctions