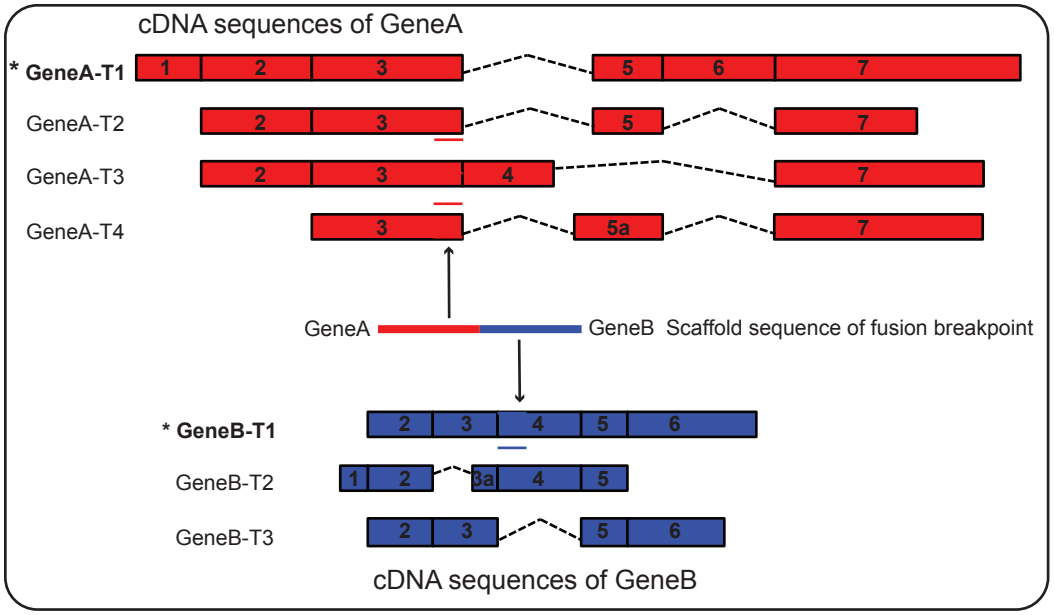
Make reference sequences
(GeneA, GeneB and scaffold)

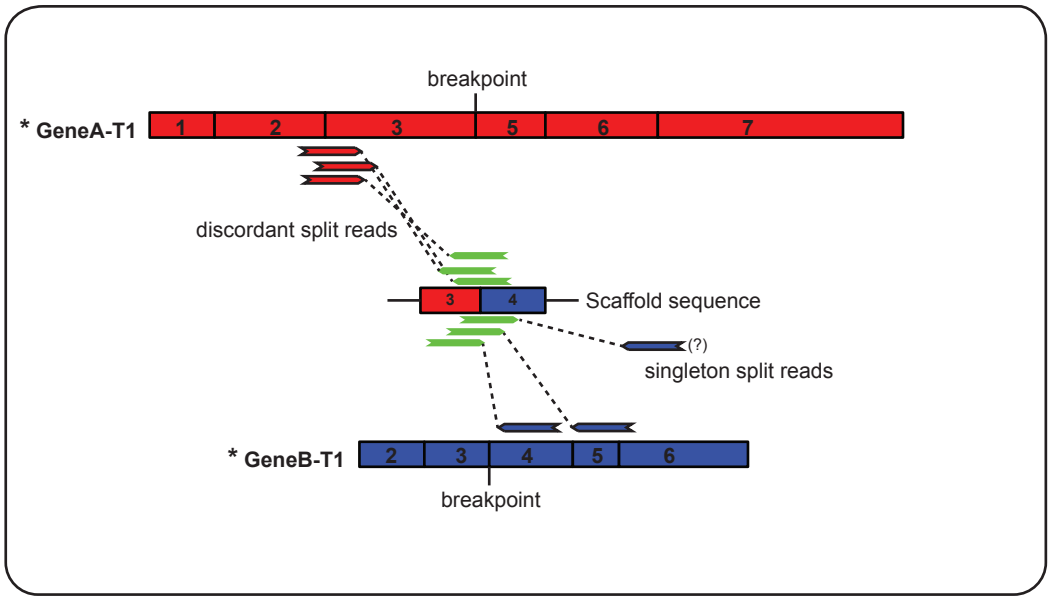
Align reads to reference sequences
(no splicing alignment model)

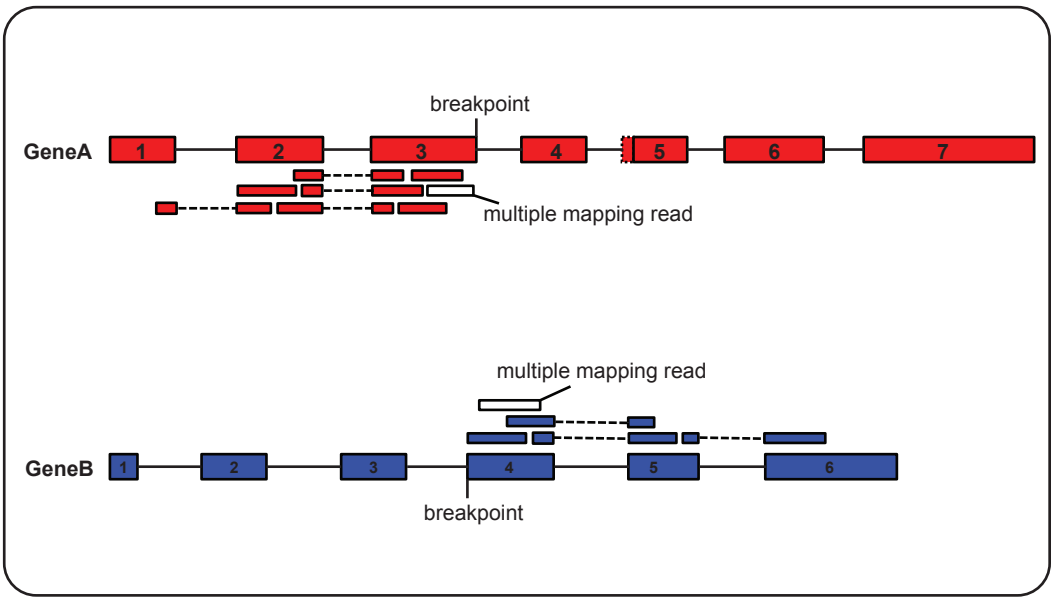
Extract spanning and
discordant/singleton split reads

Realign reads to genome seqeunces
(splicing alignment model)

Filtering spanning and
discordant/singleton split reads
(remove unspecific mapping reads)







Flow chart of scaffold alignment approach