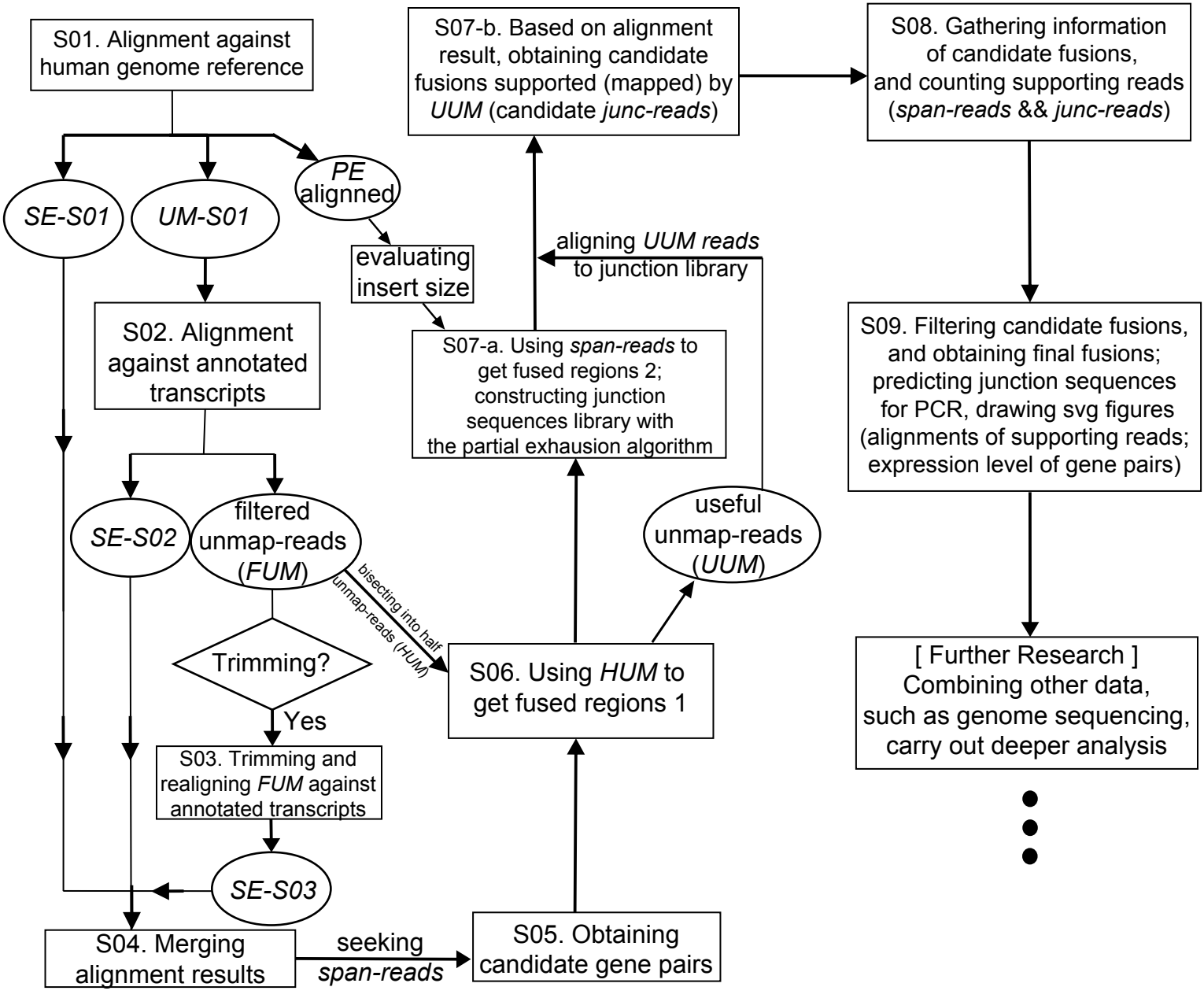
Figure S2


S01. Alignment against human genome reference
SE-S01
UM-S01
PE alignned
evaluating insert size
S02. Alignment against annotated transcripts
SE-S02
filtered unmap-reads (FUM)
Trimming?
Yes
S03. Trimming and realigning FUM against annotated transcripts
SE-S03
S04. Merging alignment results
seeking span-reads
S05. Obtaining candidate gene pairs
bisecting into half unmap-reads (HUM)
S06. Using HUM to get fused regions 1
S07-a. Using span-reads to get fused regions 2; constructing junction sequences library with the partial exhausion algorithm
aligning UUM reads to junction library
useful unmap-reads (UUM)
S07-b. Based on alignment result, obtaining candidate fusions supported (mapped) by UUM (candidate junc-reads)
S08. Gathering information of candidate fusions, and counting supporting reads (span-reads && junc-reads)
S09. Filtering candidate fusions, and obtaining final fusions; predicting junction sequences for PCR, drawing svg figures (alignments of supporting reads; expression level of gene pairs)
[Further Research] Combining other data, such as genome sequencing, carry out deeper analysis