S01. Alignment against human genome reference

S02. Alignment against annotated transcripts

SE-S01

UM-S01

Trimming?

Yes

S03. Trimming and realigning FUM against annotated transcripts

S04. Merging alignment results

S05. Obtaining candidate gene pairs

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 exhaustion algorithm

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