

A

Read Pre-processing	Debarcode (Custom Perl Script) Combine paired-end reads into single sequence (e.g. <code>`pear -f FOR_READS -r REV_READS -o LIBRARY_NAME`</code>)
Dscam1 Isoform Index	Create all 4,6,&9 ligamer combinations Assign unique name to each combination (e.g. <code>`>9v9:6v30:4v2`</code>) Create bowtie2 index of combinations (<code>`bowtie2-build dscam.ligamer.combinations.fa dscam1`</code>)
Read Alignment	Align reads to all possible Dscam1 ligamer combinations (e.g. <code>`bowtie2 --local --very-sensitive-local -no-discordant`</code>)
Data Analysis	Filter for high-confidence alignments (e.g. <code>`samtools view -q 31 -b5`</code>) Analyze using R and R packages (e.g. <code>dplyr()</code> , <code>ggplot()</code> , <code>DESeq()</code>)

B

In Vitro Isoform Template-Switched isoform Source-unknown isoform Near-cognate ligation In vivo isoform

