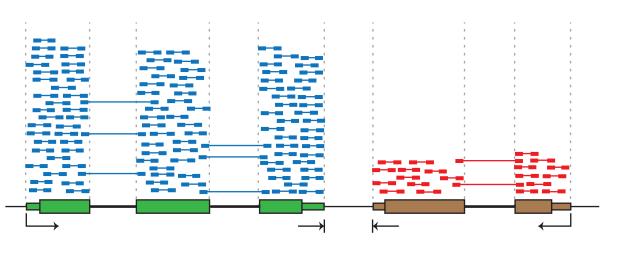
A. Depiction of cDNA fragments from an unstranded library

Legend Transcription start site and direction PolyA site (transcription end) Read sequenced from positive strand (forward) Read sequenced from negative strand (reverse)

B. Depiction of cDNA fragments from an stranded library



C. Analysis software settings by strandedness

Library Kit	5' to 3' IGV	TopHat	HTSeq	Picard	Stranded
TruSeq Strand Specific Total RNA	F2R1	fr-firststrand	reverse	SECOND_READ_TR ANSCRIPTION_STR AND	Yes
NuGEN Encore	F1R2	fr-secondstrand	yes	FIRST_READ_TRAN SCRIPTION_STRAN D	Yes
NuGEN OvationV2	F2R1 or F1R2	fr-unstranded	no	NONE	No

D. Viewing strand of aligned reads in IGV

