

.LIB Library Fragments

The format of LIB (Simulated Library) files is simple and condenses the information needed to describe a fragment (RNA or cDNA) of an original transcripts. Each line corresponds to one such fragments and in 3 tab-delimited fields the *estart*, *eend* in the spliced sequence (exonic) of the transcript with transcript_id of the original annotation.

Nr	Name	Type	Description
1	estart	Integer	exonic start and end position, 0-based. Values larger than the transcript length indicate positions in the poly-A tail, negative values are caused by variations of the transcription start site to upstream positions.
2	eend	Integer	
3	transcript identifier	String	an string uniquely identifying the transcript. As by UCSC, the prefix of the reference sequence name is joined by an '@' symbol
4	number of copies	Integer	the number of identical copies of this fragment

Example

1456	1686	chr1:4847775-4887990W@NM_011541	0
2238	2441	chr1:4847775-4887990W@NM_011541	0
116	290	chr1:4847775-4887990W@NM_011541	0
199	423	chr1:4847775-4887990W@NM_011541	0
1510	1711	chr1:4847775-4887990W@NM_011541	0
1196	1361	chr1:4847775-4887990W@NM_011541	0
1669	1875	chr1:4847775-4887990W@NM_011541	0
270	480	chr1:4847775-4887990W@NM_011541	0

Note: because the simulated transcription start and length of the poly-A tail may vary from the annotation in the reference, values for *estart* can drop below , and values for *eend* can take values higher than the transcript length.

Example