.BED Mapping Locations

The BED format is employed as default for describing reads produced in a Flux Simulator run by the genomic regions from which they are originating. Reads that fall partially in the poly-A tail are truncated to their respective content of genomic sequence.In contrast, reads that fall completely into the poly-A tail are described to be located on the special reference sequence 'poly-A'. The 12 tab-separated fields specified for the BED format are:

Nr	Name	Type	Description
1	chrom	String	The name of the chromosome (e.g. chr3, chrY, chr2_random) or scaffold (e.g. scaffold10671).
2	chromStart	Integer	The starting position of the feature in the chromosome or scaffold. The first base in a chromosome is numbered 0.
3	chromEnd	Integer	The ending position of the feature in the chromosome or scaffold. The *chromEnd* base is not included in the display of the feature. For example, the first 100 bases of a chromosome are defined as *chromStart=0, chromEnd=100*, and span the bases numbered 0-99.
4	name	String	Defines the name of the BED line. This label is displayed to the left of the BED line in the Genome Browser window when the track is open to full display mode or directly to the left of the item in pack mode.
5	score	Integer	Unused, set to '0'
6	strand	[+\-]	The absolute directionality of the read; '+' denotes the same directionality as the reference sequende, '-' denotes that the read sequence is a reverse-complement of the reference sequence.
7	thickStart	Integer	Unused, set to '.'
8	thickEnd	Integer	Unused, set to '.'
9	itemRgb	[0-9]+,[0-9]+,[0-9]+	Unused, set to '0,0,0'
10	blockCount	Integer	Number of alignment blocks for the read. Usually 1, but 2 or more in the case of reads that split-map.
11	blockSizes	comma-separated list	A comma-separated list of the block sizes. The number of items in this list should correspond to *blockCount*.
12	blockStarts	comma-separated list	A comma-separated list of block starts. All of the *blockStart* positions should be calculated relative to *chromStart*. The number of items in this list should correspond to *blockCount*.

Example

```
chr1 2082 2503 chr1:4847775-4887990W:NM_001159750:1:2668:917:1137:S/2 0 - 0 0 0,0,0 2 8,28 0,393
```

In this example, the complete region of the read spans from 2083 (note the 0-base in BED format) to position 2503 (which is the first excluded position in BED format and therefore directly translates to the last included position in a 1-based coordinate system) on the reference sequence chr1. The the read alignment is split in two parts, one from 2083 to 2083+8-1=2090, and the other one from 2083+393=2476 to 2476+28-1=2502. The 4th field encodes the read ID, more information about Flux Simulator read identifiers can be found in the Sequencing Section.