WashU Epigenome Browser - Bug # 160

Status:	Closed	**Priority:**	Normal
Author:	Rebecca Lowdon	**Category:**	
Created:	02/13/2014	**Assignee:**	Xin Zhou
Updated:	05/25/2014	**Due date:**	
Subject:	Custom PE BAM files unstable		

Description

BAM tracks of paired-end alignments appear unstable on the browser. Relocating or zooming in/out causes reads to "move" and change position.

Browser session app isn't working.... Load these 2 tracks:

1 PE: http://cgs.wustl.edu/~rlowdon/iPCR_Jan2013/sample1.sorted.mapped_only.bam
1 softclipped SE: http://cgs.wustl.edu/~rlowdon/iPCR_Jan2013/softclipped/sample1_bt2.mapped.bam

And jump to: chr4:32115941-32116000

Scroll left/right. Even just with scrolling, you can see that the PE BAM alignments appear to "move", it is unclear where exactly the read is aligned to.
In contrast, the single-end alignments don't change position along the chromosome (but they do appear to rearrange their order **vertically** along the y-axis of the track -- probably fine).

History

#1 - 02/15/2014 01:09 pm - Xin Zhou

- Status changed from New to Resolved

Fixed in v32.1.4

http://epigenomegateway.wustl.edu/browser/?genome=danRer7&custombam=xx,http://cgs.wustl.edu/~rlowdon/iPCR_Jan2013/sample1.sorted.
apped_only.bam,full&coordinate=chr19:19053110-19055265

#2 - 05/25/2014 12:12 am - Daofeng Li

- Status changed from Resolved to Closed