

WashU Epigenome Browser - Bug # 188

Status:	Closed	Priority:	Normal
Author:	Xin Zhou	Category:	
Created:	04/20/2014	Assignee:	
Updated:	05/25/2014	Due date:	
Subject:	showing wrong reference sequence for a split read		
Description	<p>This bam file was from RNA-seq experiment (75bp, single end) and lots of reads are split over exon boundaries.</p> <p>http://epigenomegateway.wustl.edu/browser/?genome=hg19&#38;gftk=refGene,full&#38;coordinate=chr7:26708766-26710476&#38;bam=xx,http://vizhub.wustl.edu/hubSample/hg19/wgEncodeCaltechRnaSeqGm12878R1x75dAlignsRep1V2.bam,full</p> <p>Clicking on one such read and show the sequence alignment in tooltip, it showed lots of mismatches but in fact there's no mismatched. Wrong sequence is retrieved from the reference genome.</p>		

History

#1 - 05/02/2014 11:39 am - Xin Zhou

- Status changed from *New* to *Resolved*

fixed in 37.0.3 on test

click a split read here:

<http://epgg-test.wustl.edu/browser/?genome=hg19&gftk=refGene,full&coordinate=chr7:26708766-26710476&bam=xx,http://vizhub.wustl.edu/hubSample/hg19/wgEncodeCaltechRnaSeqGm12878R1x75dAlignsRep1V2.bam,full>

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

- Status changed from *Resolved* to *Closed*

Files

1.png	29.4 kB	04/20/2014	Xin Zhou
-------	---------	------------	----------