WashU Epigenome Browser - Bug # 205

Status:	Rejected	**Priority:**	Normal
Author:	Daofeng Li	**Category:**	
Created:	07/18/2014	**Assignee:**	
Updated:	07/18/2014	**Due date:**	
Subject:	custom BAM track could not be used for Genome Snapshot?		
Description			

- not sure it's a bug or design
- submit a custom BAM track, like https://cgs.wustl.edu/~dli/CAGE/PE/DACSB_Aligned.out_unique.bam
- trying to do genome snapshot of this track, could not find it from the track list

History

#1 - 07/18/2014 11:27 am - Xin Zhou

- Status changed from New to Rejected

Design not bug. Bam files are usually too big to generate whole genome read count.

#2 - 07/18/2014 12:31 pm - Daofeng Li

- I supposed to mean in density mode.