

WashU Epigenome Browser - Bug # 47

Status:	Closed	Priority:	Normal
Author:	Xin Zhou	Category:	
Created:	09/18/2013	Assignee:	Xin Zhou
Updated:	09/18/2013	Due date:	
Subject:	wrong Y axis range display		
Description			
showing hg18 mm1s default tracks			
- applying rpm/bp normalization method to the read density data			
- the five bam density tracks are in same group which means they should share same Y scale			

History

#1 - 09/18/2013 06:59 pm - Xin Zhou

- Status changed from New to Resolved

Fixed. Please test it thanks!

#2 - 09/18/2013 10:54 pm - Daofeng Li

- Status changed from Resolved to Closed

Solved and closed.

Files

28.png	113.4 kB	09/18/2013	Xin Zhou
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