How to quantify the expression value of transcript in RPKM

Dear All,

I am trying to measure the expression values (in RPKM) for gencode IncRNA uploaded in your site, using flux capacitor. But it shows RPKM 0.000 for all transcript. Can you please suggest a sample command in details?

I am using following command with no luck, all output RPKM is 0.000

sh flux-capacitor -i myinput.bam -a gencode.v12.annotation.patched_contigs.gtf -o myoutput.txt --threads 2

Here is a sample output:

1 HAVANA transcript 12010 13670 . + . transcript_id "ENST00000450305.2"; locus_id "1:11869-14412W"; gene_id "ENSG00000223972.4"; reads 0.000000; length 632; RPKM 0.000000