5'-peak in read coverage

Hello

I got a strong 5' bias. First positions in a transcript have a high(very high coverage) . The window that follows has almost no reads.

I believe the figure should speak for itself. I join also the parameters file used.

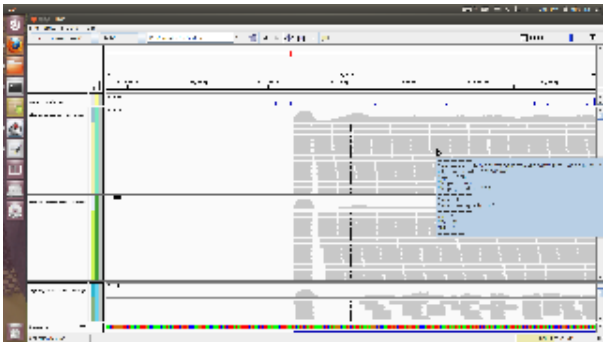
I noticed that accepting variability in TSS position reduces this bias but I want to simulate data with a fixed TSS.

Any suggestions on how to reduce this bias?

Thank you,

Bogdan

5bias.png



Parameters

```
NB_MOLECULES     50000
TSS_MEAN    NaN
POLYA_SCALE    50
POLYA_SHAPE     2


## Fragmentation
FRAG_SUBSTRATE  RNA
FRAG_METHOD     UR
FRAG_NB_LAMBDA 50


## RT parameters
RTRANSCRIPTION YES
RT_PRIMER      RH
RT_LOSSLESS    YES
RT_MIN        2000
RT_MAX        6000


## PCR / Filtering
## no [GC] bias to not observe sequence based biases


PCR_DISTRIBUTION  default
PCR_PROBABILITY 0.5
GC_MEAN NaN
FILTERING         YES
SIZE_SAMPLING     MH


# Sequencing
FASTA    true
READ_NUMBER     1000000
READ_LENGTH     50
PAIRED_END      NO
```