Source of strong bias towards 5' ends

Hello,

I was wondering of why there is such a strong and pronounced bias towards the 3' end of the genes as show below (lots of reads map at the 5' end, no reads are present at the 3' end). This image is obtained from the example.fastq file distributed from the site using a very simple parameter file

http://i.imgur.com/pWoUb.png

---- parameter file ----

```
REF_FILE_NAME chrI.gtf
GEN_DIR genome

NB_MOLECULES 100000
READ_NUMBER 1000000
EXPRESSION_K 0

# use default 76-bp error model
ERR_FILE 76

# create a fastq file
FASTA YES
```