For processing the amplicons through the tiler program, we will want to generate BED files. This will just allow us to pass everything by reference.

Let’s just biomart on the list of genes to get an annotated database for export to bed file format:

Use the R script - make\_BED\_file\_from\_ENSEMBL\_IDs.R

It generates a bed file that we can use.

We use the Bed to soft-mask the exons, then swap case for all items (including tags within):

sed -i 'y/acgntACGNT/ACGNTacgnt/' someFileNameHere