1. Build a custom bed file with all the regions we care about (really just a list of genes).
   1. make\_BED\_file\_from\_ENSEMBL\_IDs.R
2. Create a custom bed file of canonical transcripts describing exonic regions.
   1. create\_Ensemble\_Exon\_bedFile\_reference.R
3. Create a custom-masked reference fasta so we can pull exons introns.
   1. bedtools
4. Pull all the bases from the custom-masked reference fasta using the custom bed file with regions we care about
   1. Samtools
5. Pull in the sequence and the tile information from the custom bed file with regions we care about to generate a tile objects
   1. tileBuilder.class