How many files do I need to run the Flux Simulator?

Dear Micha:

I got a quick question while using Flux Simulator: in the .PAR file, I need to provide several files, but I am not quite sure how to get them. Currently I assume:

REF_FILE_NAME: GTF annotation file directly downloaded from Ensembl?

PRO_FILE_NAME: results from Flux Capacitor?

LIB_FILE_NAME: not sure how to get this file…

SEQ_FILE_NAME: junctions.bed file from TopHat? How about insertions.bed and deletions.bed?

GEN_DIR: a directory containing .fa files of chromosome considered (say, Chr1 and Chr2)?

Thank you again for your kind help!