Center for Health Genomics and Informatics

Illumina Experiment Manager

Cheat Sheet for Sample Sheets only (not sample plates)

For official Illumina IEM support, visit:
https://support.illumina.com/sequencing/sequencing_software/experiment_manager/documentation.html

For MiSeq runs:

1) Open IEM
2) Select “Create Sample Sheet”
3) In Instrument Selection window - select “MiSeq” and Next
4) MiSeq Application Selection window:
   a) Select Category and Application and Next
      i) Examples:
         (1) 16S libraries: category “Targeted Resequencing”, application “Metagenomics 16S rRNA”
         (2) Standard fragment libraries (e.g. Nextera XT, NEB Ultra, etc.): category “Small Genomic Sequencing”, application “Resequencing”
         (3) Amplicon libraries: category “Other”, application “FASTQ only”
   b) Note that many applications require a Manifest to be uploaded to the sequencing instrument prior to run set up. If you do not have this, select category “other” and “FASTQ only” as application.
5) Workflow Parameters window:
   a) Reagent Cartridge Barcode: enter “SampleSheet” or a Project Name. This is the name under which the generated .csv file will be saved as.
   b) Library Prep Workflow: select your library prep kit. If you do not see your kit or are using a custom library prep kit, select the kit that the indexes you used to make your libraries are compatible with. See document: https://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/experiment-design/illumina-adapter-sequences-1000000002694-09.pdf
   c) Index Adapters: select the kit that your indexes are from (this will then provide the indexes for ONLY that kit in the next window)
   d) Index Reads:
      i) 0 (None) - library is not indexed
      ii) 1 (Single) - libraries have only one 6-bp index attached
      iii) 2 (Dual) - libraries each have two 8-bp indexes attached
   e) Enter an experiment name. Enter the investigator name and project description. These should be the same as entered on the CHGI Sample Submission excel worksheet.
   f) Select Read Type
      i) Paired End – run includes Read 1 and Read 2 (2 x bp read, e.g. 2x150bp)
      ii) Single Read – run includes only Read 1 (a single direction sequencing run, e.g. 75bp in one direction only)

g) Cycles per Read: enter one more than the number of cycles for each read. E.g. for a 300 cycle cartridge with paired end reads of 2 x 150bp, enter 151 for both reads.
h) Leave Workflow-Specific Settings in the right hand table as default.

6) Sample Selection window:
   a) If a previous sample plate has not been created, add a blank row for each of your libraries.
   b) For each library enter information in the table (only Sample ID and index information are required), selecting the correct index for each sample, the index sequence will auto-populate and you can cross check with your kit.

<u>For NextSeq runs:</u>

1) Open IEM
2) Select “Create Sample Sheet”
3) In Instrument Selection window - select “NextSeq/MiniSeq” and Next
4) NextSeq Application Selection window:
   a) “NextSeq FASTQ only” is the only option, select Next.
5) Workflow Parameters window:
   a) Reagent Cartridge Barcode: enter “SampleSheet” or a Project Name.
   b) Library Prep Workflow: select your library prep kit. If you do not see your kit or are using a custom library prep kit then select the kit that the indexes you used to make your libraries are compatible with. See document https://support.illumina.com/content/dam/illumina-support/documents/documentation/chemistry_documentation/experiment-design/illumina-adapter-sequences-1000000002694-09.pdf
   c) Index Adapters: select the kit that your indexes are from (this will then provide the indexes for ONLY that kit in the next window)
   d) Index Reads:
      i) 0 (None) - library is not indexed
      ii) 1 (Single) - libraries have only one 6bp index attached
      iii) 2 (Dual) - libraries each have two 8bp indexes attached
   e) Enter Experiment name, investigator name, and project description
   f) Select Read Type
      i) Paired End reads – run will include Read 1 and Read 2 (2 x bp read)
      ii) Single Read – run will include only Read 1 (a single direction sequencing run, e.g. 75bp in one direction only)
   g) Cycles per Read: enter one more than the number of cycles for each read. E.g. for a 300 cycle cartridge with paired end reads of 2 x 150bp, enter 151 for both reads.
   h) Leave Workflow-Specific Settings in the right hand table as default.
6) Sample Selection window:
   a) If a previous sample plate has not been created, add a blank row for each of your libraries.
   b) For each library enter information in the table (only Sample ID and index information are required), selecting the correct index for each sample, the index sequence will auto-populate and you can cross check with your kit.