Calculating the sequencing time and output

* Flowcell (R10.4.1)-FLO-MIN-114 flowcells sequence at a rate of ~400-450 bases/second and perform high accuracy base-calling at 400 bases/second (bps).
* For a flow cell with 800 available pores; assuming ~500 pores are actively sequencing. Then theoretically in 60 minutes of sequencing, you would obtain the following:
  + 400 bps X 3600 seconds (60 minutes) = 1440000 bases
  + 1440000 bases X 500 pores = 720000000 bases
  + 720000000 bases = 360000000 basepairs = 0.36 GB
* So, if you run the sequencing for 3 hours in total, you will have 1.08 GB data at the end. Accounting for some failure during base-calling, let’s suppose you get 1GB base-called data for analysis.
* If you have sequenced 24 samples in the run, then you will have ~41MB data/sample for analysis.
* Similarly for 1 GB basecalled data, if you have sequenced 96 samples then you will have ~10MB data/sample for analysis.
* Based on current data, an output of 40-60 MB/sample should be sufficient for analysis, although this may be subject to change as the protocol is tested on more samples and will be updated here.