DCLS SARS-CoV-2 Sequencing, Helpful Hints:

* Samples with low cT values (~15) should be diluted 1:10
* Samples with High cT values (seems to be ~30+) should be run for 30-35 cycles for PCR
* Due to the high variation in concentration for cDNA, I've been manually adjusting sample input volumes for flex tagmentation to achieve 100-500ng total DNA (I try to get them as consistent as possible across all samples)
* DO NOT use the pulsenet bead clean-up during flex library prep, there is an adjustment in the illumina product insert for short amplicon (Single bead wash with 81ul SPB). The Pulsenet clean-up is designed for longer amplicon and you will lose most of your library.
* If there are any samples that did not reach ~100ng total DNA input for tagmentation, manual normalization post library is required. I would not recommend quantifying the pool as auto-normalization only occurs when you reach that DNA input.
* I am loading the run at 8pM- due to shorter library fragments 8pM is giving ~1000 cluster density
* 5% phiX spike in, since this is amplicon sequencing my assumption is that higher PhiX% will preserve fluorescence diversity
* If doing mixed organism runs, I would recommend bioanalzying and adjusting the pool concentrations to account for the significantly shorter library fragments for SC2
* Expected values:
  + cDNA amplicon should be roughly 400bp with a sharp peak
  + Library fragments are 250-300bp
  + cDNA yields vary wildly (4-120ng/ul - based on original cT value)