ScreenSeq Pipeline

Version:

- feature/simpleScripts (2020-12-23)

Description of results:

Counts and QC-Stats

- `<ProjectNo>____STATS.xlsx` — Overall QC stats for run; table columns are:

Column	Description
Sample	SampleId
Total	Total number of reads
Num.Processed	Number of reads that had a valid sgRNA sequence
Num.Library	Number of reads found in sgRNA library
PCT.Useable	Num.Library / Total

`PCT.Useable` gives a measure of the quality of the library. If it is low or if there is one or more samples whose values are much lower than the others this may indicate some QC issues.

- `<ProjectNo>____COUNTS.xlsx` — Raw count file.

Raw (unnormalized) counts for each sample

Column	Description
sgRNA	Sequence of sgRNA
Gene	Gene targeted
ProbeID	Unique Probe Id
LibName	Library Name
Samp1	Sample 1 counts
…	…
SampN	Sample N counts