Column Heading	Description
Slide name	Slide name
Scan name	Scan name
ROI name	ROI name (application generated)
Segment name	Name given to segment at time of generation
Tags	Unique descriptor of a variable group (ie. MAPK+)
X	X location within the image
Y	Y location within the image
Factors	a descriptor group that encompasses the entire data set (ie. Gender)
Surface area	surface area of the ROI in square microns (μm^2)
Nuclei count	number of nuclei detected in the segment
Sequencing set	is derived from the sequencing run, more like another run identifier. Depending on SW version of the GeoMx NGS Pipeline, this may be absent/present and if SeqSetId is missing, there are no downstream effects when creating a study in DSPDA.
Sequencing saturation	is a measure of the fraction of library complexity that was sequenced in a given experiment. The inverse of the sequencing saturation can be interpreted as the number of additional reads it would take to detect a new transcript. GeoMx default = 50% cutoff
Raw reads	reads not yet analyzed in any way to be used for data analysis. The number of reads that pass filter from the flow cell represented in the FASTQ file. GeoMx NGS Pipeline starts with FASTQ files.
readout tag sequence identifier (RTS ID)	indentifies a specific target
Stitched reads	represents consensus from the overlapping sequence of read 1 and 2. This is a % of the aligned reads that were overlapped and consensus confirmed, usually upward of 80% but less in terms of number of reads than aligned reads.

Aligned reads	is a sequence that has been aligned to a gene/probe. Typically these reads can number from the hundreds of thousands to tens of millions. In GeoMx alignment is via mapping the **RTS ID** to a white list of sequences that represent targets.
Deduplicated reads	is the replacement of blocks of duplicate data with a Virtual Index Pointer linking the new sub-block to the existing block of data in a duplicate repository. This is used to reduce the amount of space need to store the data.
In Situ Negative median	is the median of all negative control probes for a given segment. A measure of signal to background for each segment
Biological probe median	is the median count from all probes except the negative control probes. A measure of signal to background for each segment
Unique molecular identifiers (UMIs)	The molecular barcode that uniquely identifies each DNA molecule. During PCR amplification all duplicate molecules contain that barcode.
UMI Q30	**UMIs** are a type of molecular barcoding that provides error correction and increased accuracy during sequencing. A Q30 score has 1:1000 probability of an incorrect base call.
Tag sequence Q30	refer to base calling accuracy of the tag sequence. A Q30 score has 1:1000 probability of an incorrect base call.
GeoMx NGS Pipeline version	Current version of Pipeline software