NUSeq Next-Gen Sequencing Option Selection – Quick Guide

Which NGS Application?

	10x Single Cell RNA-seq	Bulk RNA-seq	Whole Genome Seq (Mammalian)	Whole Exome Seq (Mammalian)	ChIP-seq	ATAC-seq
Sequencing Option (Regular)	10K-20K cells total: HiSeq flow cell, 1 lane, $1600 30K-40K cells total: NovaSeq S1 flow cell, 1 lane, $3400 60K cells total: NovaSeq S2 flow cell, 1 lane, $4800	1-12 samples: HiSeq flow cell, 1x50 bp reads, 1 lane, $800 12-72 samples: HiSeq flow cell, 1x50 bp length, multiple lanes, $800 for every 12 samples >72 samples: NovaSeq S4 flow cell, 150x150 bp, each lane accommodates up to 96 samples at $5400	1-7 samples: NovaSeq S4 flow cell, 150x150 bp reads, 1 lane, $5400 >7 samples: Novaseq S4 flow cell, 150x150 bp reads, multiple lanes, $5400 for every 7 samples	1-8 samples: NovaSeq SP flow cell, 150x150 bp reads, 1 lane, $2400 8-17 samples: NovaSeq S1 flow cell, 150x150 bp reads, 2 lane, $4200 18-54 samples: NovaSeq S4 flow cell, 150x150 bp reads, 1 lane, $5400 >54 samples: NovaSeq S4 flow cell, 150x150 bp reads, multiple lanes, $5400 for every 54 samples	1-12 samples: HiSeq flow cell, 1x50 bp reads, 1 lane, $800 >12 samples: HiSeq flow cell, 1x50 bp, multiple lanes, $800 for every 12 samples	1-8 samples: NextSeq high-output flow cell, 37x37 bp reads, $1960 >8 samples: NextSeq high-output flow cells, 37x37 bp reads, multiple flow cells, $1960 for every 8 samples
Sequencing Option (Urgent)	NovaSeq SP flow cell, 2 lanes, $4000 for up to 30K cells	NextSeq high-output flow cell, 1x75 bp reads, $1960 for up to 16 samples	NovaSeq 150x150 bp, SP flow cell ($2400, 1-2 samples), S1 ($4200, 3-4 samples), S2 ($13400, 5-12 samples), S4 ($21600, 13-29 samples)	NextSeq high-output flow cell, 75x75 bp reads, $3400 for up to 8 samples	NextSeq high-output flow cell, 1x75 bp reads, $1960 for up to 16 samples	NextSeq high-output flow cell, 37x37 bp reads, $1960 for up to 8 samples
Recommended Depth	*20-30K reads per cell*	*20-25 million reads per sample*	*30x per genome*	*100x per exome*	*20-25 million reads per sample*	*40-50 million read pairs per sample*