

The table below shows the DNA input range for each platform. The higher the DNA input, the higher the library complexity will be, which translates into better sequencing data. Please add 25 ng to the quantities below for submission to complete QC, which is required for all samples.

Platforms	A1	A2	A3	Volume (µL)
	Optimal Quantity (ng)	Sub Optimal Quantity (ng)*	Not sufficient Quantity (ng)	
Illumina STP (formerly T200)	≥ 200	50-199	<50	55
Illumina L300	≥ 200	50-199	<50	55
Illumina WEX	≥ 200	50-199	<50	55
Illumina WGS	≥ 500	200 -499	< 200	55
RNAseq Capture	≥ 150	50 -149	< 50	55
RNAseq polyA Selection	≥ 300	50 -299	< 50	55
RNAseq-RiboZero	≥ 300	50 -299	< 50	55

* Any samples that qualify as: "acceptable, suboptimal" and "low input" and all FFPE might not reach the aimed coverage. Those samples can be repeated at the investigator's cost.

TABLE 4 – Nucleic acid amounts for NGS.