	application	NGS-CN recommendations
short reads, Illumina	**RNAseq and miRNAseq**	0,5µg total RNA, concentration range >10ng/µl, at least 10µl volume. DNA free, no degradation (RIN > 7, delta RIN < =1 RIN Stufe), OD260/280 = 1,8-2,1. Low input RNA Seq experiments on request.
	Genome Sequencing, PCR-free	2µg high molecular DNA, concentration >50ng/µl (at least 15µl volume), no degradation
	Amplicon sequencing	50 ng purified PCR-Product (at least 10µl volume, minimum concentration 5 ng/µl). Make sure that the read length chosen fits to the size of your amplicons.
	ChIPseq	>10 ng ds ChIP DNA bead cleaned, >1ng/µl, >15µl. dsDNA fragments should be in a range of 200-600bp.
	WES, gene panel	> 500ng genomic DNA, > 25ng/ul, at least 20µl volume. No degradation.
	User-supplied libraries	Concentration: 10-20 nM, Volume: At least 20µL in Tris-Cl 10mM Buffer, pH 8,5 (Qiagen EB or Illumina RSB) and addition of Tween-20 to the sample to a final concentration of 0,1% Tween. Always use DNA low bind tubes. Please provide us with TapeStation or Bioanyzer traces of your samples.
	Single Cell RNA seq:	700-2000 cells/µL concentration Viability (> 80 %; >90 % desired), Medium: supported by 10x (normally PBS+ 0,04% BSA; but also DMEM, FBS, HBBS), Diameter <40µm (<70 µm on own risk for clogging) , single cell suspension, free of debris and cell aggregates.
long reads, ONT	**ONT -Direct cDNA Sequencing**	> 100 ng PolyA RNA of good quality or > 200 ng already prepped cDNA
	ONT - long-range PCR	> 200 ng purified DNA of good quality (quantified by Qubit, absorbance ratios A260/280 >1,9, A260/230 >1,9).
	ONT – Genome	> bacteria: 3 µg purified DNA of good quality (quantified by Qubit, absorbance ratios A260/280 >1,9, A260/230 >1,9). Fragment length determines output fragment length. Human: > 6 µg of purified DNA with absorbance ratios of 260/280 1.8-2.0; 230/260: > 2.0. Depending on fragment length distribution of the DNA sample (i.e. shearing and size selection needed), then > 10 µg would be requested.
	ONT – Genome rapid	>500 ng purified DNA of good quality (quantified by Qubit, absorbance ratios A260/280 >1,9, A260/230 >1,9). Fragment length determines output fragment length.
	ONT – 16S	>100 ng DNA (quantified by Qubit, absorbance ratios A260/280 >1,9, A260/230 >1,9). Fragment length determines output fragment length.
	ONT – direct mRNA Seq	Direct RNA Seq: 1 µg PolyA-RNA in at least 20 µL water
	ONT – Ultra Long reads	> 15 µg purified HMW DNA of good quality (quantified by Qubit, absorbance ratios A260/280 >1,9, A260/230 >1,9). Fragment length determines output fragment length. *Output (GB) is low.*
	ONT – Amplicons	> 1 nmol amplicon DNA
	ONT - Native Barcoding	> 1 µg purified DNA of good quality (quantified by Qubit, absorbance ratios A260/280 >1,9, A260/230 >1,9). Fragment length determines output fragment length.
long reads, Pac Bio	**PacBio - Amplicons/16S**	Sample requirements for PacBio amplicon sequencing: 50 ng purified PCR-Product (at least 10µl volume, minimum concentration 5 ng/µl). Pooled amplicons should be of same size.
	PacBio - large insert WGS/microbial WGS	Sample requirements for PacBio WGS; HiFi: 10-15ug high molecular weight DNA (HMW DNA), 10kb Insert: >1ug HMW DNA, >15kb insert: >3 ug HMW DNA, >30kb insert: >5ug HMW DNA; 50-250ng/ul; low input (genome size up to 1Gb): >500ng; Nanodrop: 260/280 1.7-2.0; 230/260: 1.9-2.3; Difference between Nanodrop and Qubit <25%, fragment size > 50kb
	PacBio - RNA	Sample requirements for IsoSeq: 1µg, ≥50ng/ul, RIN > 8, DNAse digested, Nanodrop: 260/280:~2.0; 230/260: >2.0