

| Application | Amount | Volume (μL) | Conc. (ng/ μL) | Quality | Size (bp) | Comment |
|---|-------------|-----------------------------|-------------------------------|--|--------------|---|
| Illumina Short-Read Sequencing | | | | | | |
| <i>Genome Sequencing</i> | | | | | | |
| <i>Whole Genome - Low input (incl. PCR)</i> | 100 – 300ng | 10 – 50 | >2 | high molecular for best results 260/280 ratio 1.8-2.0 | - | FFPE possible with constraints in output quality |
| <i>Whole Genome - PCR Free</i> | >300 ng | 10 – 50 | >25 | high molecular for best results 260/280 ratio 1.8-2.0 | - | |
| <i>Bacterial genome sequencing</i> | 10 ng | 10 | 1 | high molecular for best results 260/280 ratio 1.8-2.0 | | |
| <i>Whole Exome Sequencing</i> | >50 ng | 10 | 5 | 260/280 ratio 1.8-2.0 | - | FFPE possible if amount based on qPCR measurement is sufficient |
| <i>Gene Panel</i> | 600 ng | 10 | 20 | 260/280 ratio 1.7-2.2 260/230 ratio 1.2 | - | - |
| <i>Amplicons</i> | >50 ng | 10 | 5 | 260/280 ratio >1.5 | - | less material possible on request |
| <i>Microbiome</i> | | | | | | |
| <i>Microbiome 16S</i> | 100 ng | 10 | 10 | 260/280 ratio >1.5 | - | less material possible on request |
| <i>Microbiome Shotgun Metagenomics</i> | 50 ng | 10 | 5 | 260/280 ratio >1.5 | - | less material possible on request |

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|---|--------|----------------------|------------------------|--|--------------|--|
| Illumina Short-Read Sequencing | | | | | | |
| <i>Transcriptome</i> | | | | | | |
| <i>Whole Transcriptome – standard input</i> | 500 ng | 10 | 50 | 260/280 ratio >2.0 RQN \geq 8; Δ <1 DNase treated | - | - |
| <i>Whole Transcriptome - low input</i> | 1 ng | 10 | <1 | 260/280 ratio >2.0 RQN \geq 8; Δ <1 DNase treated | - | constraints in output quality possible if input amount is very low |
| <i>Expression Profiling (mRNA) – standard input</i> | 500 ng | 10 | 50 | 260/280 ratio >2.0 RQN \geq 8; Δ <1 DNase treated | - | - |
| <i>Expression Profiling (mRNA) – low input</i> | 1 ng | 10 | <1 | 260/280 ratio >2.0 RQN \geq 8; Δ <1 DNase treated | - | constraints in output quality possible if input amount is very low |
| <i>Small RNA Profiling (miRNA, lnc-RNA etc.)</i> | 50 ng | 10 | 50 | 260/280 ratio >2.0 RQN \geq 8; Δ <1 DNase treated | - | Low input possible on request |
| <i>Sequencing of prepared NGS libraries</i> | 50 ng | 10 | 5 | No primer dimer residuals | - | Buffer: TRIS-HCL 10 mM |

| Application | Amount | Volume (μL) | Conc. ($\text{ng}/\mu\text{L}$) | Quality | Size (bp) | Comment |
|---------------------------------------|---|-----------------------------|--------------------------------------|------------------------------------|----------------|---------|
| 10X Single-Cell RNA-Sequencing | | | | | | |
| <i>Single-Cell Transcriptomics</i> | 1.000 – 30.000 cells /sample | 50 μl | 500-1.000 cells/ μl | Vitality >70 % | - | - |
| <i>Spatial Transcriptomics</i> | Tissue sections placed on Visium slides, RNA extracted from tissue section RIN >7 | | | | | |
| Bionano Optical Mapping | | | | | | |
| <i>Bionano Saphyr Chip</i> | 1 μg | - | >36 | 260/280 = 1.8 260/230 = 2.0-2.2 | Megabase range | - |

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| Pacific Biosciences Long-Read Sequencing | | | | | | |
| <i>Transcriptome (Iso-Seq)</i> | >2 μg | >15 | >130 | RIN 8-10 260/280 = 2.0 260/230 = 2.2 | - | DNase digested, buffer: RNase free water |
| <i>Whole Genome Sequencing</i> | | | | | | |
| <i>HiFi Reads – Standard Protocol</i> | >6 μg | >120 | 50 | 260/280 = 1.8 260/230 = 2.0-2.2 | >50kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>HiFi Reads – Low Input</i> | >1 μg | >50 | 20 | 260/280 = 1.8 260/230 = 2.0-2.2 | >50kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>HiFi Reads – Ultra-Low Input</i> | >30 ng | >15 | 2 | - | >50kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>Continous Long Reads</i> | >6 μg | >120 | 50 | 260/280 = 1.8 260/230 = 2.0-2.2 | >50kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>Amplicon Sequencing</i> | 500 ng – 3 μg (depends on size) | 50 | - | - | - | clean, target-specific, buffer: EB |
| <i>Multiplexed Microbial</i> | >1 μg per sample | 20-100 | - | 260/280 = 1.8 260/230 = 2.0-2.2 | >20kb | - |

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| Oxford Nanopore Long-Read Sequencing | | | | | | |
| <i>Transcriptome</i> | | | | | | |
| <i>Direct mRNA Sequencing</i> | >100 ng polyA+ or 1 μg Total-RNA | >10 | >10 | 260/280 = 2.0 260/230 = 2.0-2.2 | - | DNase digested, buffer: RNase free water |
| <i>cDNA Sequencing</i> | >200 ng polyA+ | >10 | >15 | 260/280 = 2.0 260/230 = 2.0-2.2 | - | 200 ng cDNA can be used as input DNase digested, buffer: RNase free water |
| <i>cDNA PCR Sequencing</i> | >10 ng polyA+ or >400 ng Total-RNA | >10 | >1 | 260/280 = 2.0 260/230 = 2.0-2.2 | - | DNase digested, buffer: RNase free water |
| <i>Whole Genome Sequencing</i> | | | | | | |
| <i>Ligation Sequencing</i> | >2 μg | >50 | >40 | 260/280 = 1.8 260/230 = 2.0-2.2 | >30 kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>Native Barcoding</i> | >1 μg per sample | >50 | >20 | 260/280 = 1.8 260/230 = 2.0-2.2 | >30 kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>Ultra Long Reads</i> | >50 μg | >750 | >70 | 260/280 = 1.8 260/230 = 2.0-2.2 | >100 kb | homogenous UHMW DNA, RNase digested, buffer: EEB (please inquire about EEB buffer) |
| <i>Genome Rapid</i> | >400 ng | >10 | >40 | 260/280 = 1.8 260/230 = 2.0-2.2 | >30 kb | homogenous HMW DNA, RNase digested, buffer: EB |
| <i>PCR Sequencing</i> | >200 ng | >50 | >4 | 260/280 = 1.8 260/230 = 2.0-2.2 | - | clean, target-specific, buffer: EB |

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|---|--------------------|-----------------------------|--------------------------------------|------------------------------------|--------------|---------------------------------------|
| Oxford Nanopore Long-Read Sequencing | | | | | | |
| <i>Amplicon Sequencing</i> | | | | | | |
| <i>Amplicons by Ligation</i> | >500 ng per sample | >10 | >50 | 260/280 = 1.8 260/230 = 2.0-2.2 | - | clean, target-specific, buffer: EB |
| 16S | >20 ng | >10 | >2 | 260/280 = 1.8 260/230 = 2.0-2.2 | - | clean, target-specific, buffer: EB |

Sanger Sequencing

| | | | | | | |
|--------------------------------------|--------------------|---|--------------|------------------------------------|---------------|--|
| <i>Full Service</i> | | | | | | |
| <i>Plasmid</i> | >500 ng | - | 100 – 250 | 260/280 = 1.8 260/230 = 2.0-2.2 | <5 kb | Buffer: 10 mM Tris/HCl or water Primer concentration 10 μM |
| | >800 ng | - | 150 – 600 | 260/280 = 1.8 260/230 = 2.0-2.2 | 5 kb – 15 kb | Buffer: 10 mM Tris/HCl or water Primer concentration 10 μM |
| | >1,5 μg | - | >600 | 260/280 = 1.8 260/230 = 2.0-2.2 | >15 kb | Buffer: 10 mM Tris/HCl or water Primer concentration 10 μM |
| <i>Full Service / Xpress Service</i> | | | | | | |
| <i>PCR-product</i> | max. 10 ng | - | <2,5 | 260/280 = 1.8 260/230 = 2.0-2.2 | <100 bp | purified PCR products Primer concentration 10 μM |
| | 50 ng | - | < 5ng | 260/280 = 1.8 260/230 = 2.0-2.2 | 100 bp – 1 kb | purified PCR products Primer concentration 10 μM |
| | 400 ng | - | 20 - 50 | 260/280 = 1.8 260/230 = 2.0-2.2 | >1 kb | purified PCR products Primer concentration 10 μM |

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|------------------------------|------------------------------|-----------------------------|--------------------------------------|---------|--------------|---|
| Sanger Sequencing | | | | | | |
| <i>Xpert Service</i> | - | - | - | - | - | Sample requirements as for Full Service |
| <i>Pre-mixed Service</i> | | | | | | |
| | <i>Plasmid</i> | 300 – 600 ng | - | - | - | <10 kb 5 pmol Primer/reaction 7,5 μL total volume |
| | | >700 ng | - | - | - | >10 kb 5 pmol Primer/reaction 7,5 μL total volume |
| | <i>PCR-products</i> | <100 ng | - | - | - | 100 bp – 1 kb 5 pmol Primer/reaction 7,5 μL total volume |
| | | >100 ng | - | - | - | >1 kb 5 pmol Primer/reaction 7,5 μL total volume |
| <i>Ready-to-load Service</i> | | | | | | |
| | <i>Plasmid, PCR-products</i> | - | 20 | - | - | Purified sequencing reaction |

Fragment Analysis

| | | | | | | |
|---------------------|---------------------|-------|----|---|------------------------------------|---|
| | <i>Ready-to-run</i> | - | 20 | - | - | <600 bp Fully prepared samples dissolved in formamide |
| | <i>Pre-pared</i> | - | 10 | - | - | <600 bp samples dissolved in formamide without length standard |
| <i>STR analysis</i> | | 50 ng | - | 5 | 260/280 = 1.8 260/230 = 2.0-2.2 | - Buffer: 10 mM Tris/HCl, low TE or water |