Illumina Short-Read Sequencing

Application	Amount	Volume (µL)	Conc. (ng/µL)	Quality	Size (bp)	Comment
Genome Sequencing						
Whole Genome - Low input (incl. PCR)	50 – 1000 ng	10 – 50	>2	high molecular for best results 260/280 ratio 1.8-2.0	-	FFPE possible with constraints in output quality
Whole Genome - PCR Free	1.25 – 2.5 µg	10 – 50	>25	high molecular for best results 260/280 ratio 1.8-2.0	-	standard is 350 bp insert size, for 550 bp insert size >2000 ng
Whole Exome Sequencing	>50 ng	10	5	260/280 ratio 1.8-2.0	-	FFPE possible if amount based on qPCR measurement is sufficient
Gene Panel	600 ng	10	20	260/280 ratio 1.7-2.2 260/230 ratio 1.2	-	-
Amplicons	>50 ng	10	5	260/280 ratio >1.5	-	less material possible on request
Microbiome						
Microbiome 16S	100 ng	10	10	260/280 ratio >1.5	-	less material possible on request
Microbiome Shotgun Metagenomics	50 ng	10	5	260/280 ratio >1.5	-	less material possible on request

Illumina Short-Read Sequencing

Application	Amount	Volume (µL)	Conc. (ng/µL)	Quality	Size (bp)	Comment
Transcriptome						
Whole Transcriptome – standard input	500 ng	10	50	260/280 ratio >2.0 RQN>=8; Δ<1 DNAse treated	-	-
Whole Transcriptome - low input	1 ng	10	<1	260/280 ratio >2.0 RQN>=8; Δ<1 DNAse treated	-	constraints in output quality possible if input amount is very low
Expression Profiling (mRNA) – standard input	500 ng	10	50	260/280 ratio >2.0 RQN>=8; Δ<1 DNAse treated	-	-
Expression Profiling (mRNA) – low input	1 ng	10	<1	260/280 ratio >2.0 RQN>=8; Δ<1 DNAse treated	-	constraints in output quality possible if input amount is very low
Small RNA Profiling (miRNA, lnc-RNA etc.)	50 ng	10	50	260/280 ratio >2.0 RQN>=8; Δ<1 DNAse treated	-	-
Sequencing of prepared NGS libraries	50 ng	10	5	No primer dimer residuals	-	Buffer: TRIS-HCL 10 mM

Gene Expression Microarray

Application	Amount	Volume (µL)	Conc. (ng/µL)	Quality	Size (bp)	Comment
Transcriptome Profiling – standard input	500 ng	10	50	260/280 ratio 1.8 – 2.0 260/230 ratio >2.0 DNAse treated RQN>=8; Δ<1	-	-
Transcriptome Profiling – low input	>0.5 ng	10	>0.05	260/280 ratio 1.8 – 2.0 260/230 ratio >2.0 DNAse treated RQN>=8; Δ<1	-	constraints in output quality possible if input amount is very low

10X Single-Cell RNA-Sequencing

Single-Cell Transcriptomics	1.000 – 30.000 cells /sample	50 µl	500-1.000 cells/µl	Vitality >70 %	-	-
Spatial Transcriptomics	Tissue sections placed on Visium slides, RNA extracted from tissue section RIN >7					

Bionano Optical Mapping

Bionano Saphyr Chip	1 µg	-	>36	260/280 = 1.8 260/230 = 2.0-2.2	Megabase range	-

Pacific Biosciences Long-Read Sequencing

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

Oxford Nanopore Long-Read Sequencing

Application	Amount	Volume (µL)	Conc. (ng/µL)	Quality	Size (bp)	Comment
Transcriptome						
Direct mRNA Sequencing	>600 ng polyA+	>10	>60	260/280 = 2.0 260/230 = 2.0-2.2	-	DNase digested, buffer: RNase free water
cDNA Sequencing	>150 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
cDNA PCR Sequencing	>10 ng polyA+ or >75 ng Total-RNA	>10	>1	260/280 = 2.0 260/230 = 2.0-2.2	-	DNase digested, buffer: RNase free water
Whole Genome Sequencing						
Ligation Sequencing	>2 µg	10-50	>40	260/280 = 1.8 260/230 = 2.0-2.2	>30 kb	homogenous HMW DNA, RNase digested, buffer: EB
Native Barcoding	>1 µg per sample	10-50	>40	260/280 = 1.8 260/230 = 2.0-2.2	>30 kb	homogenous HMW DNA, RNase digested, buffer: EB
Ultra Long Reads	40 µg	750	>55	260/280 = 1.8 260/230 = 2.0-2.2	>100 kb	homogenous UHMW DNA, RNase digested, buffer: EEB (please inquire about EEB buffer)
Genome Rapid	>400 ng	10	>55	260/280 = 1.8 260/230 = 2.0-2.2	>30 kb	homogenous HMW DNA, RNase digested, buffer: EB
PCR Sequencing	>100 ng	>10 - 50	>2	260/280 = 1.8 260/230 = 2.0-2.2	-	clean, target-specific, buffer: EB

Application	Amount	Volume (µL)	Conc. (ng/µL)	Quality	Size (bp)	Comment
Oxford Nanopore Long-Read Sequencing						
Amplicon Sequencing						
Amplicons by Ligation	>1 µg per sample	10-50	>40	260/280 = 1.8 260/230 = 2.0-2.2	-	clean, target-specific, buffer: EB
16S	>10 ng	>10	>1	260/280 = 1.8 260/230 = 2.0-2.2	-	clean, target-specific, buffer: EB
Sanger Sequencing						
Full Service						
Plasmid	>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 10µM
	>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 10µM
	>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 10µM
Full Service / Xpress Service						
PCR-product	max. 10 ng	-	<2,5	260/280 = 1.8 260/230 = 2.0-2.2	<100 bp	purified PCR products Primer concentration 10µM
	50 ng	-	< 5ng	260/280 = 1.8 260/230 = 2.0-2.2	100 bp – 1 kb	purified PCR products Primer concentration 10µM
	400 ng	-	20 - 50	260/280 = 1.8 260/230 = 2.0-2.2	>1 kb	purified PCR products Primer concentration 10µM

Sanger Sequencing

Application	Amount	Volume (µL)	Conc. (ng/µL)	Quality	Size (bp)	Comment
Xpert Service	-	-	-	-	-	Sample requirements as for Full Service
Pre-mixed Service						
Plasmid	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
PCR-products	<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
Ready-to-load Service						
Plasmid, PCR-products	-	20	-	-	-	Purified sequencing reaction

Fragment Analysis

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