NGS sample specifications - WGS

	Library Type	Sample Type	Input	Volume	Amount
WGS	TruSeq DNA Nano	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 20 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 50 µl)	at least 300 ng in 15 µl
	Illumina DNA prep	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 1 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 10µl TE-Buffer (max. 55µl)	at least 5 ng in 10µl
	Illumina DNA PCR-Free	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 5 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 10µl TE-Buffer (max. 55µl)	At least 50 ng in 10 µl
	Sequel II SMRTBell HIFI	gDNA (double-stranded – *high molecular weigth*)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 100 ng/µl ≤ 500 ng/µl (based on Qubit)	in ≥ 20 µl TE-Buffer (max. 40 µl)	at least 1.5 µg/Gb haploid genome in 20 µl
	Sequel SMRTBell microbial multiplexed genomes	gDNA (double-stranded – *high molecular weigth*)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 100 ng/µl ≤ 500 ng/µl (based on Qubit)	in ≥ 20 µl TE-Buffer (max. 40 µl)	at least 1 µg in 20 µl

NGS sample specifications – targeted sequencing

	Library Type	Sample Type	Input	Volume	Amount
Targeted Sequencing	Illumina DNA Prep with Enrichment IDT xGen Exome	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 10 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 50 µl)	at least 150 ng in 15 µl
	Custom panels (contact first)	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 10 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 50 µl)	at least 150 ng in 15 µl
	HLA typing	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 30 ng/µl ≤ 500 ng/µl (based on Qubit)	in ≥ 40 µl TE-Buffer (max. 100 µl)	at least 1 200 ng in 40 µl

NGS sample specifications – methylome sequencing

	Library Type	Sample Type	Input	Volume	Amount
Methylome sequencing	RRBS	gDNA (double-stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 20 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 10µl TE-Buffer (max. 25µl)	at least 200 ng in 10 µl
	NEB Em-Seq	gDNA (double stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 1 ng/µl ≤ 200ng/µl (based on Qubit)	in ≥ 15µl TE-Buffer (max. 55µl)	at least 15 ng in 15 µl
	Sequel SMRTBell	gDNA (double-stranded – *high molecular weigth*)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 150 ng/µl ≤ 500 ng/µl (based on Qubit)	in ≥ 20 µl TE-Buffer (max. 40 µl)	at least 1.5 µg/Gb haploid genome in 20 µl

NGS sample specifications – self made libraries and microbiome sequening

	Library Type	Sample Type	Input	Volume	Amount
selfmade libraries	Ready to sequence libryries (P5/P7 adapter ligated	any	**concentration ≥ 10ng/µl ≤ 200ng/µl or > 2 nM** (based on Qubit)	in ≥ 15 µl TE-Buffer	-
Microbiome/Amplicon	Amplicon PacBio SMRTBell (up to 8 kb)	Amplicon with universal overhang	PCR product of first round of amplification described in this pdf **concentration ≥ 1 ng/µl ≤ 10ng/µl (based on Qubit AFTER clean up)**	in ≥ 15 µl Tris-Buffer	-
	Shotgun Metagenome Sequencing	gDNA (double stranded)	$OD_{260/280}$ ≥ 1,8 concentration ≥ 1 ng/µl ≤ 200 ng/µl (based on Qubit)	in ≥ 10 µl TE-Buffer (max. 55µl)	at least 5 ng in 10 µl
	Bacterial 16S Amplicon V1/V2 Bacterial 16S Amplicon V3/V4 Archaeal 16S Amplicon Fungal ITS		Please contact Corinna Bang (C.bang@ikmb.uni-kiel.de)		

NGS sample specifications – transcriptome sequencing

	Library Type	Sample Type	Input	Volume	Amount
RNA libraries	TruSeq stranded RNA	total RNA	DNA free pure ($OD_{260/280}$ ≥ 1,8) RIN (Agilent Bioanalyzer 2100) ≥ 8 **concentration ≥ 40 ng/µl ≤ 200ng/µl** (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 30 µl)	at least 600 ng in 15µl
		mRNA	DNA free pure ($OD_{260/280}$ ≥ 1,8) RIN (Agilent Bioanalyzer 2100) ≥ 8 **concentration ≥ 40 ng/µl ≤ 200ng/µl** (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 50 µl)	at least 600 ng in 15µl
	Illumina stranded RNA	Total RNA with RiboZero plus (H/M/R + bacteria)	DNA free pure ($OD_{260/280}$ ≥ 1,8) RIN (Agilent Bioanalyzer 2100) ≥ 8 **concentration ≥ 10 ng/µl ≤ 200ng/µl** (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 30 µl)	at least 150 ng in 15µl
		mRNA	DNA free pure ($OD_{260/280}$ ≥ 1,8) RIN (Agilent Bioanalyzer 2100) ≥ 8 **concentration ≥ 2 ng/µl ≤ 200ng/µl** (based on Qubit)	in ≥ 15 µl TE-Buffer (max. 30 µl)	at least 30 ng in 15µl
	NextFlex smallRNA	total RNA	DNA free pure ($OD_{260/280}$ ≥ 1,8) RIN (Agilent Bioanalyzer 2100) ≥ 8 **concentration ≥ 0.5 ng/µl** (based on Qubit)	in 15 µl TE-Buffer	at least 7.5 ng in 15 µl
		micro RNA	DNA free pure ($OD_{260/280}$ ≥ 1,8) **Amount ≥ micro RNA fraction of ≥ 1,2 µg total RNA** (based on Qubit)	in 15 µl TE-Buffer	-
	PacBio IsoSeq	total RNA	DNA free pure ($OD_{260/280}$ ≥ 1,8) RIN (Agilent Bioanalyzer 2100) ≥ 8 **concentration ≥ 150 ng/µl ≤ 400ng/µl** (based on Qubit)	in ≥ 10 µl Tris Buffer or nuclease free water	at least 800 ng in 10 µl

NGS sample specifications – single cell sequencing

	Library Type	Sample Type	Input	Volume	Amount
	Chromium single-cell RNAseq (contact us before)	Cell suspension	**> 500 Cells/sample** Viability at least 95 %	in ≥ 10 µl buffer (max. 40 µl)	-