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		Please contact Corinna Bang (C.bang@ikmb.uni-kiel.de)		
	Bacterial 16S Amplicon V3/V4				
	Archaeal 16S Amplicon				
	Fungal ITS				