

NGS sample specifications - WGS

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