NGS sample specifications – methylome sequencing

	Library Type	Sample Type	Input	Volume	Amount
Methylome sequencing	RRBS	gDNA (double-stranded)	$OD_{260/280} \geq 1,8$ 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)	$OD_{260/280} \geq 1,8$ 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*)	$OD_{260/280} \geq 1,8$ 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