Instructions for sample preparation, QC, storage & shipment

Application	Library	Sample preparation	Minimal amount , concentration & method of quantification	QC	Comment
DNA sequencing (Illumina)	Sonication & PCR amplification	***Method 1*** Proteinase K, ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation ***Method 2*** PureLink Genomic DNA kit (Thermo Fisher Sci.) or similar	400 ng 20 ng/µL $T_{10}E_1$ or H_2O microfluorimetry (*e.g.* Qubit).	260/230 ≥ 2 ; 260/280 ≥ 1.8 Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.
DNA sequencing (Illumina)	Tagmentation & PCR amplification	***Method 1*** Proteinase K, ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation ***Method 2*** PureLink Genomic DNA kit (Thermo Fisher Sci.) or similar	2 ng 0.1 ng/µL H_2O microfluorimetry (*e.g.* Qubit).	Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.
DNA sequencing (Illumina)	Sonication, PCR-free	***Method 1*** Proteinase K, ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation ***Method 2*** PureLink Genomic DNA kit (Thermo Fisher Sci.) or similar	2 µg 40 ng/µL $T_{10}E_1$ or H_2O microfluorimetry (*e.g.* Qubit).	260/230 ≥ 2 ; 260/280 ≥ 1.8 Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.

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DNA sequencing (Illumina)	Tagmentation, PCR-free	***Method 1*** Proteinase K, ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation. ***Method 2*** PureLink Genomic DNA kit (Thermo Fisher Sci.) or similar.	50 ng 1 ng/µL H_2O microfluorimetry (*e.g.* Qubit).	Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.
DNA sequencing (MinION)	Long reads	Use a method that is appropriate to prepare (very) long DNA fragments. Might be species specific.	5 µg 100 ng/µL H_2O microfluorimetry (*e.g.* Qubit).	260/230 ≥ 2 ; 260/280 ≥ 1.8 Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation Store @ 4°C. Ship @ 4°C.
TF binding sites, histones modif.	ChIP-seq	Immunoprecipitated chromatin is heated to reverse the DNA-protein crosslinks, incubated with RNase, then proteinase K. Glycogen may be added, if necessary. ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation.	20 ng 0.66 ng/µL $T_{10}E_1$ or H_2O microfluorimetry (*e.g.* Qubit).	Using purified chromatin input, check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	Store @ -20°C. Ship @ 4°C.

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Genotyping	RAD-seq	PureLink Genomic DNA kit (Thermo Fisher Sci.), DNeasy Blood & Tissue Kit (Qiagen) or similar product.	2µg 25ng/µL H_2O microfluorimetry (*e.g.* Qubit).	260/230 ≥ 2 ; 260/280 ≥ 1.8 Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Mandatory** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.
DNA methylation	WGBS	***Method 1*** Proteinase K, ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation. Do NOT use Trizol ! ***Method 2*** PureLink Genomic DNA kit (Thermo Fisher Sci.) or similar.	200 ng 5 ng/µL H_2O microfluorimetry (*e.g.* Qubit).	260/230 ≥ 2 ; 260/280 ≥ 1.8 Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.
DNA methylation	RRBS	***Method 1*** Proteinase K, ϕol/$CHCl_3$ extraction, EtOH/NaOAc precipitation. Do NOT use Trizol ! ***Method 2*** PureLink Genomic DNA kit (Thermo Fisher Sci.) or similar. Do NOT vortex samples !!	200 ng 5 ng/µL H_2O microfluorimetry (*e.g.* Qubit).	260/230 ≥ 2 ; 260/280 ≥ 1.8 Check DNA integrity, *i.e.* agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** RNase treatment, then inactivation. Store @ -20°C. Ship @ 4°C.

Application	Library	Sample preparation	Minimal amount , concentration & method of quantification	QC	Comment
RNA sequencing (Illumina)	RNAseq, polyA+	***Method 1*** Trizol-like. After addition of $CHCl_3$ to the Trizol lysate and centrifugation, extract the aqueous upper phase with $CHCl_3$ again. After EtOH/NaOAc precipitation, wash the pellet TWICE with 70 % EtOH. ***Method 2*** Quick RNA (Zymo) or similar.	2 µg 200 ng/µL H_2O spectrophotometry	260/230 ≥ 2 ; 260/280 ≥ 2. Check RNA integrity, *i.e.* denaturing agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** DNase treatment, then inactivation. Store @ -80°C. Ship on dry ice.
RNA sequencing (Illumina)	RNAseq, polyA+, small amounts	***Method 1*** Trizol-like. After addition of $CHCl_3$ to the Trizol lysate and centrifugation, extract the aqueous upper phase with $CHCl_3$ again. After EtOH/NaOAc precipitation, wash the pellet TWICE with 70 % EtOH. ***Method 2*** Quick RNA (Zymo) or similar.	20 ng 0.15 ng/µL H_2O capillary electrophoresis	Check RNA integrity, *i.e.* capillary electrophoresis (*e.g.* BioAnalyzer).	**Mandatory** DNase treatment, then inactivation. Store @ -80°C. Ship on dry ice.

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RNA sequencing (Illumina)	RNAseq, rRNA-depleted	***Method 1*** Trizol-like. After addition of $CHCl_3$ to the Trizol lysate and centrifugation, extract the aqueous upper phase with $CHCl_3$ again. After EtOH/NaOAc precipitation, wash the pellet TWICE with 70 % EtOH. ***Method 2*** Quick RNA (Zymo) or similar.	*Bacteria, NEBNext® rRNA Depletion Kit* → 2 µg *Mammals, Illumina Ribo-Zero Plus rRNA Depletion Kit* → 200 ng *For both kits*, 200 ng/µL H_2O spectrophotometry	260/230 ≥ 2 ; 260/280 ≥ 2. Check RNA integrity, *i.e.* denaturing agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Mandatory** DNase treatment, then inactivation. Store @ -80°C. Ship on dry ice.
RNA sequencing (MinION)	Direct RNAseq	***Method 1*** Trizol-like. After addition of $CHCl_3$ to the Trizol lysate and centrifugation, extract the aqueous upper phase with $CHCl_3$ again. After EtOH/NaOAc precipitation, wash the pellet TWICE with 70 % EtOH. ***Method 2*** Quick RNA (Zymo) or similar.	80 µg 100 ng/µL H_2O spectrophotometry	260/230 ≥ 2 ; 260/280 ≥ 2. Check RNA integrity, *i.e.* denaturing agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** DNase treatment, then inactivation. Store @ -80°C. Ship on dry ice.

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Small RNA sequencing (Illumina)	small RNAseq	***Method 1*** Trizol-like. After addition of $CHCl_3$ to the Trizol lysate and centrifugation, extract the aqueous upper phase with $CHCl_3$ again. After EtOH/NaOAc precipitation, wash the pellet TWICE with 70 % EtOH. ***Method 2*** Quick RNA (Zymo) or similar.	2 ng 0.1 ng/µL H_2O capillary electrophoresis	260/230 ≥ 2 ; 260/280 ≥ 2. Check RNA integrity, *i.e.* denaturing agarose gel or capillary electrophoresis (*e.g.* BioAnalyzer).	**Highly recommended** DNase treatment, then inactivation. Store @ -80°C . Ship on dry ice.
Ready-to-load library	Illumina compatible library	Any methods that produces Illumina compatible library.	10 nM in 20µl H_2O/EB capillary electrophoresis qPCR	Less than 1 % adapter doublets and PCR primer Homogenous insert sizes for libraries to be mutliplexed in the same lane/flow cell	**Highly recommended** Construction method that includes Unique Dual Adapters (UDI)