Sample Submission Guidelines

Thank you for choosing CD Genomics for your project. Our portfolio of services covers genomics, transcriptomics, metagenomics, epigenomics, single cell sequencing, genotyping, microarray, and more. When considering any of our NGS services, please take note of the sample requirements and instructions for packaging, labeling, and shipping your samples. This will help to guarantee the success and quality of your project. You will need to provide the completed ***Sample Submission Form***, clearly listing all the samples you are providing for sequencing. Make sure the sample names on the form match the labels on the sample tubes. We also ask that you submit an electronic copy of the form and any required QC data via email. Please label the top of the lid of each tube - with a maximum of 4 alpha-numeric characters (for example: 4B01).

Shipping Guidelines

1. When sending samples, the standard sample submission form provided by our company should be included (electronic version sent by email, or paper version sent with the sample). Please carefully check and ensure that the sample name and quantity filled in the information sheet are completely consistent with the sample name identification and sample quantity actually sent.

2. We suggest loading samples in 1.5 mL centrifuge tubes when possible. Please seal the tube with parafilm for transportation. In order to prevent the centrifuge tubes from being crushed and broken during transportation (leading to sample loss) it is better to insert sample tubes into 50 mL centrifuge tubes (or other rigid supports), which can also be packed with cotton, foam, etc.

3. Samples for large scale projects can be submitted in well-sealed 96-well semi- or fully-skirted PCR plates, or in strip-tubes with individually attached caps. To prevent sample loss and/or cross contamination, we recommend tightly sealing all wells of the plate with an adhesive sheet/foil. You can protect the plates or strip tubes in a sturdy box with plenty of cushioning. Sample shipments of plates should be carried out on frozen blue ice or on dry ice, to ensure that the samples remain frozen through the shipment.

5. Do not write the sample name and other information directly on the tube wall or tube cover with an oil pen. It is better to write sample names at the top and the side of each tube with black permanent marker.

6. If a DNA sample is stored in 70% ethanol, it can be transported at room temperature. If a DNA sample is dissolved in H_2O or TE buffer, it needs to be transported with ice packs.

7. RNA, cells, bacteria and frozen tissue samples should be stored in liquid nitrogen for quick freezing and then transported with dry ice.

Note: The amount of dry ice and ice bags to be added during transportation depends on the season, the length of transportation, and the thickness of the foam box.

8. For blood samples, we recommend 5-10 mL plastic anticoagulant blood collection vessels for loading. In order to prevent the blood collection vessels from being damaged due to extrusion during transportation, it is necessary to wrap the body of each blood collection vessel with bubble wrap and then place it in a rigid box.

9. Before sending the samples, the sample sender shall send a timely notice by mail, which should include the Sample Submission Form and the tracking number (for timely registration and processing after the arrival of the samples). Since we are not available to receive packages on weekends, please make sure your samples arrive on weekdays.

10. CD Genomics recommends that you use FedEx, DHL or UPS for the shipment.

DNA Sequencing Service Sample Requirements

DNA can be submitted in DNase-free Water, Elution Buffer, or 10mM Tris pH 8.0. DNA samples require an OD260/280 as close to 1.8~2.0 as possible. All DNA should be RNase-treated and should show no degradation or contamination. Ship with ice packs. The total amount of DNA required depends on the specific application. Please refer to the Sample Requirements table for general guidance.
NOTE: The concentrations listed below should be determined by fluorometry (e.g. Picogreen/Qubit/RiboGreen). If you do not have access to a fluorometry-based assay and are relying on spectrophotometry (e.g. Nanodrop), increase concentrations by ~2 fold.

Illumina Service	Sample Type	Recommended Quantity	Minimum Quantity	Minimum Concentration
Whole Genome Sequencing	Genomic DNA	⩾ 500 ng	200 ng	10 ng/μL
Whole Genome Sequencing (PCR-free)	Genomic DNA	⩾ 1 μg	500 ng	20 ng/μL
Whole Exome Sequencing	Genomic DNA	⩾ 500 ng	100 ng	10 ng/μL
Complete Plasmid DNA Sequencing	Plasmid DNA	⩾ 1 μg	500 ng	20 ng/μL
Human/Mouse Mitochondrial DNA (mtDNA) Sequencing-multiplex PCR	Genomic DNA	⩾ 200 ng	50 ng	5 ng/μL
Human/Mouse Mitochondrial DNA (mtDNA) Sequencing-probes	Genomic DNA	⩾ 500 ng	200 ng	10 ng/μL
Chloroplast DNA (cpDNA) Sequencing	Plants tissue (Green tissue)	⩾ 5 g		
Viral Genome Sequencing	Genomic DNA	⩾ 1 μg	500 ng	20 ng/μL
Amplicon Sequencing	Purified Amplicon	⩾ 1 μg	500 ng	20 ng/μL
GBS/ddRAD	Genomic DNA	⩾ 300 ng	100 ng	10 ng/μL
BSA (Bulk Segregant Analysis)	Genomic DNA	⩾ 2 μg	500 ng	20 ng/μL
2b-RAD	Genomic DNA	⩾ 200 ng	50 ng	5 ng/μL
Metagenome Sequencing	Metagenome DNA	⩾ 500 ng	20 ng	5 ng/μL
16S/18S/ITS Sequencing	Genomic DNA	⩾ 100 ng	10 ng	1 ng/μL
SNP Microarray	Genomic DNA	⩾ 300 ng	100 ng	8 ng/μL
DNA Methylation Microarray	Genomic DNA	⩾ 1 μg	500 ng	8 ng/μL
SSR Genotyping	Genomic DNA	⩾ 500 ng	200 ng	10 ng/μL

HLA Typing	Genomic DNA	⩾ 200 ng	
	Cell, PMBC	⩾ 1×10^6	
	Blood	⩾ 1 mL	
	Buccal Swab	2	
	Dried blood spot (DBS)	2 completely filled spots, each 10 mm in diameter	
TCR-Seq	Genomic DNA	⩾ 2 μg	20 ng/μL
	PMBC	⩾ 2×10^5	
	Animal tissue	⩾ 500 mg	
	Blood	⩾ 0.5 mL	

Long Read Sequencing

Service	Sample Type	Recommended Quantity	Minimum Quantity	Minimum Concentration
Whole Genome Sequencing (PacBio)	Genomic DNA	⩾ 3 μg		80 ng/μL
Whole Genome Sequencing (Nanopore)	Genomic DNA	⩾ 5 μg		20 ng/μL
Plasmid Sequencing (Nanopore)	Genomic DNA	⩾ 1 μg	500 ng	10 ng/μL
Full-Length 16S/18S/ITS Amplicon Sequencing	Genomic DNA	⩾ 500ng		10 ng/μL
	Tissue	1-3g	1 g	
	Thallus	5 g	3 g	
	Interstitial Fluid	3-5 mL	1 mL	
	Environmental Samples	3-5g	1 g	
	Water filter membrane	3	1	
Long-Read Metagenomic Sequencing	Genomic DNA	⩾ 2 ug		30ng/μL
	Tissue	2 g	1 g	
	Interstitial Fluid	6-10 mL, sediment 2g	2 mL, sediment	
	Environmental Samples	6g	2 g	
	Water filter membrane	6	2	

Epigenomics sequencing

Service	Sample Type	Recommended Quantity	Minimum Quantity	Minimum Concentration
MeDIP-Seq/hMeDIP-seq	Genomic DNA	⩾ 2 μg	1 μg	20 ng/μL
WGBS (Whole Genome Bisulfite Sequencing)	Genomic DNA	⩾ 1 μg	200 ng	10 ng/μL
	Cell	⩾ 1 x10^6		
	Tissue	⩾ 50 mg		
RRBS (Reduced representation bisulfite sequencing)	Genomic DNA	⩾ 1 μg	20 ng	20 ng/μL
	Cell	⩾ 5 x10^6	3×10^3	
	Tissue	⩾ 30 mg		
Targeted Bisulfite Sequencing	Genomic DNA	⩾ 500 ng	50 ng	10 ng/μL
	Cell	⩾ 1×10^6		
	Tissue	⩾ 20 mg		
oxWGBS-Seq	Genomic DNA	⩾ 3 μg	1 μg	30 ng/μL
oxRRBS-Seq	Genomic DNA	⩾ 2 μg		50 ng/μL
oxTBS-Seq	Genomic DNA	⩾ 1 μg		20 ng/μL
DNA 6mA-IP-Seq	Genomic DNA	⩾ 5 μg		20 ng/μL
Epityper	Genomic DNA	⩾ 1 μg		
ChIP-seq	ChIPed DNA	⩾ 10 ng	5 ng	1 ng/μL
	Cell	⩾ 2 x10^7	1 x10^5	
	Tissue	⩾ 500 mg		
DAP-seq	TF	⩾ 5 μg	1 μg	20 ng/μL
	Cell	⩾ 5 x10^6		
	Tissue	⩾ 500 mg	200 mg	
ATAC-seq	Cell	⩾ 1×10^6	5×10^4	
	Tissue	⩾ 500 mg	200mg	
CUT&Tag	Cell	⩾ 1×10^5	5×10^4	
	Tissue	⩾ 500 mg	200mg	

RNA Sequencing Service Sample Requirements

RNA can be submitted in RNase-free water, RNA Stabilization Reagent, or 10mM Tris pH 8.0. All total RNA samples should be DNA-free. RNA samples require an OD A260/A280 ratio ≥ 1.8, A260/230 ratio≥ 1.8 and a RIN ≥ 6. Ship with dry ice.

The total amount of RNA required depends on the specific application, please refer to the Sample Requirements table for general guidance.

NOTE: The concentrations listed below should be determined by fluorometry (e.g. Picogreen/Qubit/RiboGreen). If you do not have access to a fluorometry-based assay and are relying on spectrophotometry (e.g. Nanodrop), increase concentrations by ~2 fold.

Service	Sample Type	Recommended Quantity	Minimum Quantity	Minimum Concentration
Whole Transcriptome Sequencing	Total RNA	⩾ 3 μg	1 μg	20 ng/μL
Low input RNA Sequencing	Total RNA	⩾ 20 ng	20 pg	1 pg/μL
mRNA Sequencing	Total RNA	⩾ 500 ng	200 ng	20 ng/μL
	Cells	⩾ 1×10^6		
	Tissue	⩾ 50 mg	10 mg	
Total RNA/LncRNA Sequencing	Total RNA	⩾ 2 μg	500 ng	50 ng/μL
	Cells	⩾ 2×10^6		
	Tissue	⩾ 500 mg	100 mg	
Small Sequencing	Total RNA	⩾ 1 μg	200 ng	20 ng/μL
	Cells	⩾ 2×10^6		
	Tissue	⩾ 500 mg	100 mg	
CircRNA Sequencing (linear RNA digestion)	Total RNA	⩾ 5 μg	2 μg	50 ng/μL
	Cells	⩾ 2×10^6		
	Tissue	⩾ 500 mg	100 mg	
Metatranscriptome	Total RNA	⩾ 4 μg	3 μg	50 ng/μL
	Cells	⩾ 5×10^6		
	Environmental Samples	⩾ 1.5g		

Bacterial RNA Sequencing	Total RNA Cells	⩾ 1 μg ⩾ $1x10^7$		
Degradome sequencing	Total RNA	⩾ 20 μg	15 μg	100 ng/μL
TCR-seq	Total RNA	⩾ 100 ng		10 ng/μL
CAGE-seq	Total RNA Cells Tissue	⩾ 5 μg ⩾ $2×10^7$ ⩾ 500 mg	3 μg 200 mg	
Ribo-seq	Cells Tissue	⩾ $5×10^6$-10^7 ⩾ 400 mg	 200 mg	
Dual RNA-seq	Total RNA Cells Tissue	⩾ 1 μg ⩾ $5×10^6$ ⩾ 500 mg	200 ng 100 mg	10 ng/μL
Exosomal RNA Sequencing	Total RNA Cell supernatants Serum, plasma	⩾ 100 ng ⩾ 15 mL ⩾ 1 mL		20 ng/μL

Long Read Sequencing

Service	Sample Type	Recommended Quantity	Minimum Quantity	Minimum Concentration
Iso-Seq	Total RNA	⩾ 2 μg	600 ng	30 ng/μL
Nanopore Full-Length Transcripts Sequencing	Total RNA	⩾ 2 μg		
Nanopore Direct RNA Sequencing	Total RNA	⩾ 15 μg		

* **The Long Read Sequencing has high requirements for RNA quality, RNA samples are required to RIN ≥ 8.**

RNA Epigenomics Sequencing

Service	Sample Type	Recommended Quantity	Minimum Quantity	Minimum Concentration
RIP-seq	IPed RNA	≥ 100 ng	40 ng	5 ng/μL
	Cell	≥ 5×10^7		
	Tissue	≥ 500 mg	200 mg	
eCLIP-Seq	IPed RNA	≥ 100 ng	40 ng	5 ng/μL
	Cell	≥ 3×10^7		
	Tissue	≥ 500 mg	200 mg	
MeRIP (Methylated RNA Immunoprecipitation)	Total RNA	≥ 10 μg	2 μg	1 ng/μL
	Cell	≥ 1×10^7		
	Tissue	≥ 500 mg	200 mg	
RNA BS-seq (RNA Bisulfite Sequencing)	Total RNA	≥ 10 μg		
	Cell	≥ 1×10^7		
	Tissue	≥ 500 mg	100 mg	

Single Cell Sequencing/Spatiotemporal Genomics

Service	Sample Type	Recommended Quantity & Quality	Minimum Quantity & Quality
ScRNA-seq	Single cell suspension, Fresh tissue	2×10^6 cells	1×10^6 cells
SnRNA-seq	Snap frozen tissue	⩾ 100mg(Please contact us for details)	
10X Visium Spatial Transcriptome	OCT embedded tissue, FFPE	6.5mm×6.5mm	
Smart-Seq2	Fresh living intact cells, not suitable for samples that have been fixed, stained, etc.; mammalian cells or other eukaryotic cells without cell wall structures	Cell suspension volume ⩽1 μL, 1~500 single cells/sample, ⩾3 biological replicates	
scATAC-seq	Single cell nuclei suspension	1×10^6, Nuclei < 40 μm, complete nuclear membrane, and the proportion of nuclei > 95%	5×10^5
	Single cell suspension	⩾1×10^6Cell Viability>80%, Cell concentration 700~1200 cells/μL,	5×10^5
	Fresh tissue	200 mg	
	Whole blood anticoagulated with EDTA	⩾ 5mL	
Single Cell Genome Sequencing	Cells	1-10^3, Single cells are stored in 1xPBS buffer (without Ca^{2+}, Mg^{2+}), the volume is within 2 μL	
	DNA	⩾ 0.5pg	
ScWGBS	Cell lines, primary cells, fresh tissue, frozen cells	Use 200μl PCR tubes to store cells (single or multiple cells), 5μl of lysate per tube, and no more than 1μl of buffer when collecting cells. ⩾3 biological replicates	

ScRRBS	Cell lines, primary cells, fresh tissue, frozen cells	Use 200μl PCR tubes to store cells (single or multiple cells), 5μl of lysate per tube, and no more than 1μl of buffer when collecting cells. ⩾3 biological replicates

Pre-made Library Sequencing

The quality inspection method of the sizes and concentrations of the library is Qubit, Agilent bioanalyzer.

Platform	Minimum Concentration	Data Amount	Volume Requirement
Novaseq-PE150	2 ng/μL	X<30G	⩾15 μL
		30G⩽X < 100G	⩾25 μL
		100G⩽X⩽400G	⩾50 μL
		400G < X < 800G	⩾70 μL
		800G	⩾100 μL (additional 70μL for one more lane)
Nova- PE250	2 ng/μL	X<30GM	⩾15 μL
		30M⩽X < 100M	⩾25 μL
		100M⩽X<400M	⩾50 μL
		400M	⩾100 μL (additional 70μL for one more lane)
HiSeq-PE150	1 ng/μL	1 Lane	⩾10 μL
MiSeq-PE300	1 ng/μL	1 Flowcell	⩾10 μL

Suggestions of sampling

We all know that quality nucleic acid input equals quality sequencing data output , and so CD Genomics offers a complete line of sample extraction services for any sample type. We can consult to provide effective solutions for any sample type.

Sample Type	Quantity Recommended	Shipping Method
Cell	1×10^6 cells	Dry ice
Fresh Frozen Tissue	10 mg	Dry ice
FFPE	⩾ 4 FFPE slides, thickness 5~20 μm, area >150 mm^2	Room temperature/Blue Ice
Viral Particles	$5x10^9$	Dry ice
Stool	100 mg	Dry ice
Swabs	2 tubes/sample, 1 swap/tube	Room temperature
Saliva	1 mL	Dry ice/blue ice
Soil	100 mg	Room temperature/Blue Ice
Water	50 mL	Room temperature/Blue Ice
Plasma/Serum	10 mL	Dry ice
Whole Blood	2 mL Fresh blood in EDTA tube	Blue Ice
	4 mL Frozen blood in EDTA tube	Dry ice
	2.5 mL Frozen blood in PAXgene tube	Dry ice
	3 mL Frozen blood in Tempus Blood RNA Tube	Dry ice
Bodily Fluids	500 μL (gDNA)	Blue Ice
	500-10,000 μL (cell free DNA)	Dry ice

Adherent cells
1) Observe the cells under the microscope and confirm that they are in good growth condition (the polymerization degree of normal cells is about 80%).
2) Remove the culture medium, and quickly wash it twice with precooled PBS buffer solution.
3) Place the culture dish on ice, add an appropriate amount of pre cooled PBS into the culture dish. Scrape the cells on one side of the culture dish with a clean cell scraper, and place the culture dish on the ice at an angle to make the buffer flow to one side. Pipette the dissolved products into the precooled centrifuge tube, and after 500-600 g centrifugation, discard the supernatant.
4) Store at - 80 °C after liquid nitrogen quick freezing.

Cell Suspension
1) The cells in the culture bottle/dish were gently blown and mixed with a pipette gun, and transferred to a 15 mL centrifuge tube.
2) Horizontal centrifuge, centrifuge 400g~1000g at 4 °C for 5-10 minutes to collect cells and discard the supernatant.
3) Carefully wash the flake sediment twice with precooled PBS, place it on ice, and discard the supernatant.
4) Quickly freeze with liquid nitrogen, and storage at - 80 °C.

Animal tissue samples
Quick-freezing fresh tissue in liquid nitrogen
1) After fresh tissue is isolated, connective tissue, adipose tissue and other tissue types that are not required for the study shall be removed immediately. If the tissue volume is large, try to cut small pieces (length, width and height ≤ 0.5 cm).
2) Quickly wash the tissue with precooled normal saline or PBS, and dry it with dust-free paper. Place it in a 1.5 mL or 2 mL centrifuge tube for quick freezing and then store it at - 80 °C; If the sample size is large, please divide into aliquots.

Plant tissue samples
Quick-freezing fresh tissue in liquid nitrogen
1) After taking fresh plant samples, wash them with DEPC water immediately and dry them with dust-free paper.
2) Divide the plant tissue sample into 1-2 cm or 50-100 mg small pieces with scissors and place them in 2 mL, 15 mL or 50 mL EP tubes.
3) Quickly freeze with liquid nitrogen, and storage at - 80 °C.

Bacterial sample
Quick-freezing bacteria liquid nitrogen
1) Collect an appropriate amount of bacterial liquid into a 50 mL centrifuge tube, centrifugate at a low speed (3000-5000g/10min) with a 4 °C horizontal centrifuge to collect bacteria, and remove the culture medium as clean as possible;
2) Add 5-10 mL sterile water or PBS solution to wash twice, then transfer it to a 1.5 mL or 2.0 mL centrifuge tube, centrifuge at 1500 rpm at 4 °C for 10min, remove the supernatant, and retain the precipitated bacteria.
3) Quickly freeze with liquid nitrogen, and storage at - 80 °C.

Whole Blood sample
1) Samples should be collected in suitable collection media such as QIAGEN PAXGene solution following the manufacturer's instructions.
2) Collect > 500 μL blood per tube and prepare 2 tubes per sample.
3) Fresh samples should be stored refrigerated and shipped refrigerated, with a wet/blue ice package.
4) Frozen samples should be shipped frozen by overnight delivery, packed with protective bubble pad. Make sure dry ice surrounds all sides of the specimens.
5) For whole blood sample volume in PAXgene blood RNA tubes, please ensure to collect > 2.5 mL blood, the yield should be approximately > 3 μg.

Plasma sample
1) Use a 5 mL blood collecting vessel containing EDTA (purple head tube) to extract the whole blood. A total of 10 mL is required. Gently mix up and down (the whole blood sample can be stored at 4°C when the centrifugation condition is limited, and the next processing can be carried out within 1h).
2) At 4°C, centrifuge 1900g with a bucket type rotating head for 10min. Carefully aspirate the supernatant for plasma, and finally discard 500 μL.
3) Centrifuge the obtained plasma again at 4 °C and 3000g for 15 min. Carefully aspirate, taking care not to disturb the sediment at the bottom and side.
4) Sub-pack the plasma into EP tubes and freeze at - 80 ° C before sample delivery to avoid repeated freezing and thawing.

Serum sample
1) Use a blood sampling needle and common serum tube (5 mL blood collecting vessel without anticoagulant) were used to collect 10 mL blood.
2) Let stand at room temperature for 30min, and at 4°C for 3-4h (blood clots can be seen at this time).
3) Use a pipette to aspirate the above pale yellow serum (about 4 mL) and transfer it into a 15 mL centrifuge tube. Centrifuge 3000g at 4 °C for 15min. Carefully transfer the supernatant into a new 15mL centrifuge tube to maximize the quality of serum.
4) After centrifugation, freeze the serum at - 80°C within 15 minutes to avoid repeated freezing and thawing.

PBMC samples
1) We recommend collecting at least 7.5 mL of blood for PBMC isolation.
2) Resuspend PBMC cells in RPMI 1640 containing 10% fetal bovine serum. Adjust the PBMC concentration to 1×10^6–1×10^7 cells/mL.
3) Centrifuge PBMC for a further 10–15 min at 350 x g. Remove and discard the supernatant.
4) Snap freeze the PBMC pellet in liquid nitrogen and store at - 80 °C for later DNA purification.
5) PBMC pellets must contain at least 10^6 cells in order to be processed. Pellets should be shipped on dry ice.

FFPE samples
1) We require approximately 80mg of tissue per sample.
2), After cleaning the tissue with PBS or physiological saline, completely immerse the tissue in formaldehyde fixing solution within half an hour of sampling. Seal the tube with sealing film.
3) The fresh tissue should be fixed with formaldehyde for no more than 24h. If a pretreatment kit is used, the fixing time shall be in accordance with the requirements of the kit. FFPE chips can be transported at room temperature.

Water body/membrane samples
1) Samples should be taken from at least 1-2 L of water or slightly turbid water.
2) Samples should be transported at low temperature.
3) Filter membranes with different pore size can be selected for filtration according to the research purpose.
4) After freezing with liquid nitrogen place sample in a sterile, RNAse-free centrifuge tube and ship on dry ice.

Urine
1) Use a 15 mL or 50 mL centrifuge tube to collect urine, 300g, centrifuged at 4 °C for 10min, and transfer the supernatant into a clean centrifuge tube to avoid touching the bottom sediment.
2) 3000g, centrifuged at 4 ° C for 15min, remove cells or cell fragments, retain the supernatant, and avoid touching the bottom sediment. Samples can be frozen at - 80 ° C prior to delivery to avoid repeated freezing and thawing.