Bionano Data Services Intake Form

Document Number: 30378

Document Revision: 1

Customer Information:

Date of Request:

Service Requestors Information-

Customer Company/Institute Name:	
Primary Customer Contact Name:	
Customer Department:	
Customer Title:	
Customer Email:	
Customer Phone:	

Requestors Purchasing Contact Information-

Purchasing Contact Name:	
Purchasing Contact Title:	
Purchasing Contact Email:	
Purchasing Contact Phone:	

Requestors Bionano Business/Salesperson Contact Information-

Bionano Contact Name:	

Project Plans and Goals (provide a written description of the project):

References:

Sample Information:

Please indicate the number and type of samples in the table below. Two or more aliquots per sample are required to be submitted with one being used as a backup. Each aliquot should be prepared from a fresh sample, meaning no sample should have been previously subjected to any freeze/thaw cycles. All samples should be frozen as soon as possible, never thawed and shipped on dry ice.

Sample Type††	Minimum Quantity Per Aliquot	Number of Samples
Frozen blood (EDTA)	650 uL	
Frozen blood (Heparin)	† 650 uL (with Bionano DNA stabilizer added)	
Frozen cell line (cryopreservative)	1.5 million cells (in cryopreservative)	
Frozen cell line (dry pellet)	‡ 1.5 million cells (washed in Bionano DNA stabilizing buffer)	
Frozen bone marrow aspirate (EDTA)	1 mL	
Frozen bone marrow aspirate (Heparin)	† 1 mL (with Bionano DNA stabilizer added)	
Frozen tissue, standard yield	≥ 10 mg*	
Frozen tissue, low yield	≥ 60 mg**	
	Total:	

† heparin blood and heparin bone marrow aspirates require the addition of Bionano DNA Stabilizer prior to freezing (PN 20398).

‡ when preparing frozen dry cell pellets without cryopreservation medium, it is recommended to wash cells in DNA Stabilizing Buffer (PN 20394 and 20397) to remove residual growth medium before freezing.

†† see details in shipping guidelines documents

* Tissues with higher nuclei content relative to tissue mass: spleen, brain, liver, lung, kidney, thyroid, colon, bladder, ovary, testes, colon, prostate, and most breast tissue.

** Tissues with lower nuclei content relative to tissue mass: Some fatty tissues, including fatty breast tissue, and most muscle tissue.

Sample Storage Conditions-

What is your protocol for storing samples?	
What temperature were samples kept at before freezing?	
How long were they kept at the above temperature?	
At what temperature were the frozen samples stored?	
How long have the samples been kept frozen?	
Have the samples ever been thawed and refrozen?	
Did you count or weigh the samples before freezing?	
What system did you use for counting cells?	
Did you account for cell viability before freezing?	
What is the range of cell viability for all samples?	

Have any other assays or QCs been done on the sample (e.g. Bionanalyzer)?	

Sample Safety/Biohazard-

Is there a risk of danger to operators?	
If so, specify?	
What is the biosafety level of your samples?	

Note: Only biosafety levels 1 and 2 are accepted.

Privacy-

Have your samples been de-identified?	**Yes** ☐ **/ No** ☐

Note: No protected health information (PHI) should be included with your sample. If samples are received with PHI, they will be returned

Analysis Information:

Background-

Does the sample derive from an individual with a known cancer or genetic disease?	**Yes** ☐ **/ No** ☐
If yes, specify…	
What is the expected level of heterogeneity?	
What allele frequency sensitivity is expected/required for relevant variants?	
Are you expecting a specific Structural Variant (SV)?	**Yes** ☐ **/ No** ☐
If yes, what is the expected size?	
If yes, what are the expected coordinates?	

Study Design-

How many samples for the following applications:	
FSHD EnFocus analysis?	
Germ line variation detection (400 Gbp)?	
Somatic/mosaic variation detection (1.3 Tbp)?	
Are control samples provided?	
If yes, please describe the sample information below:	
What reference genome do you want used for SV calling and annotation?	GRCh37/hg19 ☐ or GRCh38/hg38 ☐
Do you have custom application needs (at an additional cost)? Please describe:	

Data Delivery-

Use https://bionanoaccess.com for visualization, filtering, report generation and download?	
If not, how do you want data transferred?	
Do you agree to allow Bionano to use the data for internal development?	

Note: All data will be removed after 6 and before 12 months of storage unless otherwise specified.

Important Notes:

Please note some important limitations to analysis with Saphyr:

- Heterochromatic regions of the genome are often not assembled in the human reference and Bionano may not have enough information to analyze these regions (this includes Robertsonian translocations and balanced translocations with centromeric breakpoints).
- In diploid samples, unbalanced SVs can be detected ≥ 500 bp and balanced SVs ≥ 30 – 50 kbp.
- With 1.3 Tbp and the rare variant pipeline, Bionano can detect variants as low as 5% allele fraction but is limited to SVs ≥ 5kbp (see SV Calling Theory of Operation document for more details).
- Loss of heterozygosity (LOH) is currently not supported with Bionano optical mapping.

Other Questions:

Publication Information-

Would you be interested in presenting this work at a conference?	
Do you have plans to publish this work?	

Sample Return-

Do you have any specific requests for the remnant sample and DNA?	

Note: Returning sample will incur a shipping cost. All samples and related material will be destroyed after 6 and before 12 months of storage unless otherwise specified.

Control Database Contribution-

Bionano is building a database of control data to help interpret variants by providing allele frequency in a population or information about a variant's previous detection in a clinical case. We are looking for customers willing to allow Bionano to use your data in this way. All data will be anonymized, no protected health information will be used or stored.

Please sign if you are willing to share your data for Bionano control structural variant database:

I, _____(type your name), ☐ **Consent** / ☐ **Do Not Consent** to share data with Bionano Genomics for use in an anonymized control database.

Technical Assistance

For technical assistance, contact Bionano Genomics Technical Support.

You can retrieve documentation on Bionano products, SDS's, certificates of analysis, frequently asked questions, and other related documents from the Support website or by request through e-mail and telephone.

Type	Contact
Email	support@bionanogenomics.com
Phone	Hours of Operation: Monday through Friday, 9:00 a.m. to 5:00 p.m., PST US: +1 (858) 888-7663
Website	www.bionanogenomics.com/support

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