GCB
Duke Center for Genomic and Computational Biology

Genome Sequencing Shared Resource

HISEQ SAMPLE SUBMISSION FORM

Order#:		Quote#:		**Shipping address:**
Name:	Sergio Verjovski-Almeida	INTERNAL USE		Att: Illumina HiSeq Sequencing GCB Genome Sequencing Shared Resource Rm 119 Biology Bldg Duke University 130 Science Dr. Durham, NC, 27708 USA
Email:	verjo@iq.usp.br	Date:		
Department:	Department of Biochemistry Instituto de Química - USP	Receiver:		
Lab:	Laboratório de Expressão Gênica em Eucariotos	Location:		

IMPORTANT NOTES:

- Unless specified otherwise, leftover samples will be discarded two months after the sequencing is completed.
- Please attach your DUGSIM order form to this submission form when submitting your samples. If you are submitting more than 12 samples, please print a second page.
- An incomplete submission form will result in a delay with your order.
- If you are on campus please make arrangements ahead of time to drop off your sample(s) with Wendy Parris (wendy.parris@duke.edu).
- Data will distributed through our sftp server. Data will be available on our server for 30 days after it is has been delivered. Additional bioinformatics charges will be applied if alternative data distributions requested.

Here below are our default parameters. If you have any special conditions for your run and sample preparations, you must communicate them to us by email.

- Default loading concentration for all libraries is 6-10 pM depending on type and QC. Molarity will be estimated using a combination of Qubit and Bioanalyzer/Tapestation trace.
- Spike-in of 5 – 10% PhiX .
- Default insert size for DNA-Seq libraries is 200bp.

Sample requirements: Samples must be resuspended in nuclease free water. Note that the Nanodrop frequently over-estimates DNA concentration (~3x).

Library Type	Input	Concentration	Volume	Additional requirements
DNA-Seq	DNA	≥ 40 ng/µl	50 µl	
RNA-Seq	Total RNA	≥ 20 ng/µl	50 µl	RIN ≥ 7
ChIP-Seq	ChIP enriched DNA	≥ 1 ng/µl	30 µl	
smRNA-Seq	Total RNA	≥ 200 ng/µl	15 µl	RIN ≥ 7
Mate-Pair	DNA	≥ 200 ng/µl	50 µl	

I have read and understand the above information.

Signature: _____ Date: 23rd May 2016

Please check http://www.genome.duke.edu/cores/sequencing/Sequencing_Submission_Instructions.pdf

Samples

Code *(1)*	Library type	*Sample type (2)*	*Label (3)*	Conc. (ng/µl)	Vol. (µl)	*Frag. sz. (bp) (4)*
TC31	Stranded mRNA-Seq	Total RNA	TC31	485	40	
TC32	Stranded mRNA-Seq	Total RNA	TC32	219	40	
TC33	Stranded mRNA-Seq	Total RNA	TC33	291	40	
TC34	Stranded mRNA-Seq	Total RNA	TC34	213	40	
TC37	Stranded mRNA-Seq	Total RNA	TC37	542	40	
TC38	Stranded mRNA-Seq	Total RNA	TC38	566	40	
TC40	Stranded mRNA-Seq	Total RNA	TC40	504	40	
TC41	Stranded mRNA-Seq	Total RNA	TC41	397	40	
TC43	Stranded mRNA-Seq	Total RNA	TC43	437	40	
TC44	Stranded mRNA-Seq	Total RNA	TC44	510	40	

1 **Code:** Your initials-S-number (e.g. GC-S1, GC-S2, GC-S3); Mark each tube (cap and side) with its code when submitting your

2 **Sample type:** RNA, gDNA, plasmid, amplicon etc…

3 **Label:** This is to help you to keep track of your sample, so choose a label that's meaningful to you. This is optional.

4 **Frag. sz.:** Average Fragment Size (bp). (Amplicon, cDNA, ChIP) This is optional if over 50,000bp or RNA.

If you have any special instructions, please enter them on an attached sheet on the reverse side of this form.

1)
Please note that the rRNAs from this organism are composed of three more abundant species: alfa, beta and small (~1.7kb, ~2kb and ~2.5kb, respectively; according to Castro et al., 1980, doi:10.1016/0166-6851(81)90102-X) . So, take a look at the attachedBioanalyzer profile and see that these samples are not degraded.

2) As you can run up to 24 samples per lane, we ask you to combine the samples in order to run as follows:

Samples to be run on Lane 1:
TC1, TC2, TC7, TC8, TC13, TC14, TC19, TC20, TC25, TC26, TC31,TC32, TC37, TC38, TC43,TC44, TC49, TC52

Samples to be run on Lane 2:
TC3, TC4, TC9, TC10,TC15, TC16, TC21, TC22, TC27, TC28,TC33,TC34, TC40, TC41, TC46, TC47, TC50, TC51, TC53, TC55