GCB
Duke Center for Genomic
and Computational Biology

**Genome Sequencing
Shared Resource**

HISEQ SAMPLE SUBMISSION FORM

Order#:		Quote#:		**Shipping address:** Att: Illumina HiSeq Sequencing GCB Genome Sequencing Shared Resource Rm 119 Biology Bldg Duke University 130 Science Dr. Durham, NC, 27708 USA
Name:	Sergio Verjovski-Almeida	INTERNAL USE		
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

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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)*
TC15	Stranded mRNA-Seq	Total RNA	TC15	619	40	
TC16	Stranded mRNA-Seq	Total RNA	TC16	275	40	
TC19	Stranded mRNA-Seq	Total RNA	TC19	832	40	
TC20	Stranded mRNA-Seq	Total RNA	TC20	377	40	
TC21	Stranded mRNA-Seq	Total RNA	TC21	544	40	
TC22	Stranded mRNA-Seq	Total RNA	TC22	714	40	
TC25	Stranded mRNA-Seq	Total RNA	TC25	242	40	
TC26	Stranded mRNA-Seq	Total RNA	TC26	165	40	
TC27	Stranded mRNA-Seq	Total RNA	TC27	210	40	
TC28	Stranded mRNA-Seq	Total RNA	TC28	299	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

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