UNIVERSITÄTSMEDIZIN GÖTTINGEN UMG
NGS Integrative Genomics
Core Unit Göttingen
Institute Human Genetics
NIG

DNA / RNA SEQUENCING CONTACT (NIG)

Date:

Project number (filled by NIG) :

Project title (with one sentence) :

Project Description :

CONTACT INFORMATION

Contact person	Group leader/Principal investigator
Name :	Name :
Email :	Email :
Address :	Address :
Phone :	Phone :

PROJECT INFORMATION HiSeq PROTOCOL INFORMATION

Library type

single-end library　paired-end library

Read length

☐ Hiseq2500　☐ Hiseq4000　☐ Miseq　☐ Minion

☐ 50 bp　☐ 100 bp　☐ 150bp　☐ 250bp

Analysis application type

total RNA-seq	mRNA-seq	ATAC-Seq
miRNA-seq	smallRNA-seq	Amplicon-Seq
ChIP-seq	RRBS	
Bisulfite sequencing	Targeted DNA-seq	
de novo genome sequencing	genome resequencing	% PhiX

Sample pooling　Yes　No

if yes, how many samples will be pooled together? ___________________________

Total number of samples (including biological replicates) :

Organism:

Sample type :

DNA / RNA extraction method :

Other possible pre-processing done to the samples (please specify all applied protocols)

Dnase treatment:

Sample Name	conc.	µl	Sample Name	conc.	µl	Sample Name	conc.	µl
1.			10.			19.		
2.			11.			20.		
3.			12.			21.		
4.			13.			22.		
5.			14.			23.		
6.			15.			24.		
7.			16.			25.		
8.			17.			26.		
9.			18.			27.		

Data Analysis

☐ Basic (sequencing quality control, data conversion, FASTQ only)
☐ Advanced (mapping, statistics, visualisation)
☐ Individual ____

Group descriptions

Please give a short description of each sample group (add rows if needed)

Sample group	Num. of biological replicates	Description

Changing your sample setup:

Please note that if you have changed your original sample setup from the one discussed with our bioinformaticians, you should contact them (tal@gwdg.de) to discuss the changes before continuing further. This concerns especially those projects where the data analysis service is used.

COMPARISON TO A SET OF PREVIOUS RESULTS If you are planning to compare these results with a previous set of results produced using our service, please indicate here the time when the previous samples were processed	
COMPARISON TO A SET OF FUTURE RESULTS If you are planning to compare these results directly with a possible future set of samples that will be processed using our service, please indicate this here and also give us some estimate when these samples will be processed. (It should be noted that after longer time the same equipment and protocols may not be available anymore, complicating the integration between earlier and later data set)	
LEFT OVER MATERIAL DISPOSAL The TAL will discard the left over sample material after 1 year. P**lease indicate** if you wish to have it returned. In such case please note that the user has to cover the possible costs related to the returning of the sample material	
NOTE: ABOUT STORING THE RESULT DATA The TAL will store data only for a short time and the **customer is responsible for storing the raw data** after the project is finished and the data has been delivered to the user.	

☐ I have read the "Nutzerordnung" / policy and accept it.
http://www.med.uni-goettingen.de/de/media/G1-1_forschung_einrichtungen/TAL_Nutzerordnung_AM_I_Nr_50_2013_10_23.pdf

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signature