

VBCF NGS Project Agreement 7500

Created on February 22, 2019

Scientist	
Cost assignment	(none)
Submission	2019-02-22
Sequencing Type	Illumina HiSeqV4 SR100
Demultiplexing	Yes
Alignment	No
BioComp Support	No
Lanes	2 with many samples
Multiplexes	7746, 7745

Comments

Please sequence on two lanes, as indicated. The purchase order number to be neioned on the invoice is 139/sv/2019. Thank you

The *Cost Assignment* field should reflect the budget this request is billed to, e.g. "START project budget", invoices for a specific group will be split by this reference.

Lanes

Lane 1

Use **NEBNext Dual** adaptors with dual indexing.

6 Samples

ld		Тад	Exptype	Ratio	Prep	Multiplex
83686	710	TCCGCGAA	8M10	1	RNA, stranded	7746
	503	CCTATCCT				
83687	701	ATTACTCG	8M12	1	RNA, stranded	7746
	507	CAGGACGT				
83688	706	GAATTCGT	8N1	1	RNA, stranded	7746
	503	CCTATCCT				
83689	711	TCTCGCGC	8N3	1	RNA, stranded	7746
	505	AGGCGAAG				
83690	709	CGGCTATG	16M8	1	RNA, stranded	7746
	508	GTACTGAC				
83691	705	ATTCAGAA	16M13	1	RNA, stranded	7746
	501	TATAGCCT				

Lane 2

Use **NEBNext Dual** adaptors with dual indexing.

6 Samples

ld		Tag	Exptype	Ratio	Prep	Multiplex
83680	707	CTGAAGCT	16N1	1	RNA, stranded	7745
	505	AGGCGAAG				
83681	709	CGGCTATG	16N5	1	RNA, stranded	7745
	508	GTACTGAC				
83682	710	TCCGCGAA	24M1	1	RNA, stranded	7745
	508	GTACTGAC				
83683	711	TCTCGCGC	24M2	1	RNA, stranded	7745
	504	GGCTCTGA				
					Continued	

ld		Тад	Exptype	Ratio	Prep	Multiplex
83684	704	GAGATTCC	24N1	1	RNA, stranded	7745
	505	AGGCGAAG				
83685	706	GAATTCGT	24N5	1	RNA, stranded	7745
	507	CAGGACGT				

Estimated Costs

Description	Price	Count	Total
mRNA Library preparation (polyA enrichment, NEB)	150.00	12	1800.00
Library Quality Control	40.00	12	480.00
Sequencing 100bp single read HiSeq	1290.00	2	2580.00
Demultiplexing	20.00	2	40.00
Total			4900.00 E

VAT not included. This is a non-binding estimate based on the current request data. Final billing may differ if additional lab work, bioinformatics or sequencing runs are necessary.

Terms and Conditions

All requests submitted to the VBCF NGS are subject to the general cooperation conditions of the VBCF as well as VBCF NGS policy if no additional agreement exists.

General cooperation conditions, current price list and User guide (containing VBCF NGS policy) can be downloaded at: http://ngs.vbcf.ac.at/forskalle

The signature commits the PI to add the VBCF NGS facility into the acknowledgements of any publication containing data generated at the VBCF NGS facility.

Signatures

Scientist Date

Group leader Date

Submission guide

Samples submitted to the facility need to fullfill certain criteria, otherwise they cannot be accepted. Please go through the checklist before you deliver the samples:

General Criteria

- □ Samples are in **1.5 ml Eppendorf tubes**.
- □ Samples are labelled with the 5-digit **sample number** or the 4-digit **multiplex number** for pooled samples created by forskalle (Examples: M1234 or 54321)
- □ Labelling is done with a permanent marker, **NO stickers**.
- □ The delivery volume is at least 15 µl
- □ For user prepared libraries: concentration is at least 5 nmol
- □ The **cost assignment** is correct

Additional Criteria for Facility Prepared Samples

DNA Samples for delivery of genomic DNA or cDNA

- □ The amount of sheared DNA is at least 10 ng
- \Box The minimum concentration is 0.167 ng/µl
- □ The majority of DNA fragments is **between 100 bp and 900 bp**

RNA Samples We generally request **high quality total RNA** (RIN >7 and DV200 >70%, the higher the better results will be). Minimum amount and concentration depend on the preparation method:

	Min. amount	Min. conc.
NEB poly-A	200 ng	4 ng∕µl
NEB total RNA	100 ng	$20 \text{ ng}/\mu$ l
Epicenter Ribozero	500 ng	$17 \mathrm{ng}/\mathrm{\mu l}$
Lexogen Sense	200 ng	$20\mathrm{ng}/\mathrm{\mu}\mathrm{l}$
Lexogen Quant-Seq	50 ng	$10{ m ng}/{ m \mu l}$
NEB Small RNA	200 ng	$33\mathrm{ng}/\mathrm{\mu l}$

DNAse treatment by the user is mandatory for rRNA depletion protocols!

Maximum turnover times

- User prepared samples: 2 weeks lab turnover plus sequencing time (about 1 week)
- Facility prepared samples: 4 weeks lab plus sequencing time (about 1 week)