

# NGS library prep service *from RNA*

Processed

Send request to: Functional Genomics Laboratory, 255 Life Sciences Addition, Berkeley, CA 94720-3200

Please contact Justin (jygchoi@berkeley.edu) Tel: (510) 642-1165

Date \_\_\_/\_\_\_/\_\_\_

User Information		*UC Funding Code/PO#:		
Name			Fund Manager Information	
Email				
Dept./Inst.		Name		
P.I.		Email		
TEL		TEL		

<b>Info about your samples</b>	Possible Biohazard	Yes**/ No	Requesting for rRNA depletion	Yes/No	<input type="checkbox"/> PolyA selection		
	<b>Type of your RNA</b>	<input type="checkbox"/> total RNA			<i>Info about Library</i>	<input type="checkbox"/> RiboZero	
		<input type="checkbox"/> rRNA depleted RNA				<input type="checkbox"/> _____	
		<input type="checkbox"/> PolyA selected RNA	Multiplexing	Yes / No			
		<input type="checkbox"/> small or miRNA	Desired insert size	Range ____~____			
	<input type="checkbox"/> _____						
<b>Purity</b>	A <sub>260/280</sub> _____	<i>Info about Sequencing</i>	Length (cycle)	SR/PE & 50/100/150/_____	Please sign & submit the sequencing form when you receive a bioanalyzer trace for your samples from the FGL.  <i>Without a signed form, the samples cannot be submitted for sequencing</i>		
	A <sub>260/230</sub> _____						
Integrity* on a Fragment analyzer	RIN _____ ~ _____						
Model Organism							

	User sample I.D. <i>(Your samples name)</i>	FGL I.D. <i>(We may assign a different name)</i>	* Grouping	Type of RNA	Used Sol.	Ratio		Conc. (ng or µg /µl)	Total vol. (~50µ L)	Total amount (0.2~5µg)
						A260 /280	A260 /230			
ex			A	Total RNA	Water	1.9	1.8	20.5ng/ul	12	1.0 µg
1										
2										
3										
4										
5										
6										

\*Please note that we will **not process** without QC of purified samples on Bioanalyzer. \*\* Please contact FGL before submitting your samples if your samples are possibly infectious

<b>For Office Use Only</b>		Recharge account:	<b>APOLLO</b>
<b>User Affiliation</b>	<i>Other used chemicals-</i>	Used other chemicals:	= _____
<b>UC / Affiliated / Outside</b>		Lib_ prep :	_____ X \$ = _____
		<b>Order Total:</b>	

User sample I.D.	FGL I.D.	*Grouping	Type of RNA	Used Sol.	Ratio		Conc. (ng or $\mu\text{g}$ / $\mu\text{l}$ )	Total vol. ( $\mu\text{L}$ )	Total amount ( $\mu\text{g}$ )
					A260 /280	A260 /230			

\*Grouping-To minimize processing effects (a same treatment or experiment) since we can process only 8 samples on the robot at a time. Please use a letter, number or symbol for a same experiment.