



University of North Carolina at Chapel Hill

High Throughput Sequencing Facility - 1

Form associated with:

Service Project HTSF--JL-147 at High Throughput Sequencing Facility - 1

Owner: Joshua Leon (Mitchell, Charles (UNC-CH) Lab)

HTSF Nanopore Submission Form DNA

*** I will be submitting DNA for:**

- ☐ Ligation Sequencing (SQK-LSK114)
- ☐ Ligation Sequencing with Barcoding (SQK-NBD114.96)
- ☐ Rapid Sequencing (SQK-RAD114)
- ☒ Rapid Sequencing with Barcoding (SQK-RBK114.24)

*** Type of Sample**

- ☐ High Molecular Weight DNA / gDNA
- ☐ Fragmented DNA
- ☒ PCR Amplicons
- ☐ cDNA

*** Do these samples contain human DNA? (required)**

- ☐ Yes
- ☒ No

Source Organism:

Fungi from plant leave tissue

Sample Buffer:

- ☒ EB
- ☐ Nuclease-Free Water

*** Sample Information:**

	Sample Name	Volume (μL)	Qubit Conc. (ng/μL)	Nanodrop Conc. (ng/μL)	A ₂₆₀ /A ₂₈₀ ratio	A ₂₆₀ /A ₂₃₀ ratio
1	1	2		298.9	1.84	
2	3	2		314.05	1.84	
3	5	2		348.2	1.84	
4	6	2		346.75	1.84	
5	10	2		294.1	1.84	
6	13	2		225.9	1.84	

	Sample Name	Volume (μL)	Qubit Conc. (ng/μL)	Nanodrop Conc. (ng/μL)	A ₂₆₀ /A ₂₈₀ ratio	A ₂₆₀ /A ₂₃₀ ratio
7	14	2		367.85	1.84	
8	17	2		274.85	1.84	
9	19	2		189.1	1.84	
10	24	2		160.8	1.84	
11	25	2		265.75	1.84	
12	26	2		277.15	1.83	
13	27	2		210.2	1.84	
14	30	2		260.25	1.83	
15	32	2		281.85	1.85	
16	33	2		293.75	1.83	
17	37	2		340.9	1.83	
18	38	2		340.6	1.84	
19	39	2		238	1.83	
20	42	2		358.6	1.84	
21	46	2		223	1.84	
22	47	2		409.2	1.84	
23	48	2		307.55	1.83	
24	49	2		202.8	1.84	
25	52	2		254.45	1.84	
26	53	2		468.75	1.84	
27	54	2		234.2	1.84	
28	55	2		330.1	1.84	
29	56	2		286.6	1.84	
30	57	2		302.85	1.84	
31	58	2		390.55	1.83	
32	61	2		246.55	1.84	
33	64	2		234.55	1.84	
34	66	2		318.7	1.84	
35	72	2		282.2	1.84	
36	75	2		182.15	1.83	
37	77	2		263.45	1.84	
38	82	2		229.5	1.83	
39	85	2		289.25	1.83	
40	86	2		235	1.83	
41	87	2		286.6	1.84	
42	90	2		215.65	1.84	
43	91	2		347.4	1.84	
44	92	2		316.3	1.83	
45	93	2		267.5	1.86	
46	95	2		333.25	1.87	
47	96	2		270.45	1.85	
48	97	2		325.15	1.83	
49	101	2		302.8	1.84	
50	102	2		248.15	1.82	
51	105	2		284.05	1.84	
52	106	2		249.1	1.84	
53	110	2		215.55	1.84	
54	112	2		321.95	1.84	
55	113	2		254.45	1.84	
56	115	2		238.1	1.84	

	Sample Name	Volume (μL)	Qubit Conc. (ng/μL)	Nanodrop Conc. (ng/μL)	A ₂₆₀ /A ₂₈₀ ratio	A ₂₆₀ /A ₂₃₀ ratio
57	117	2		351.45	1.84	
58	118	2		306.45	1.84	
59	123	2		162.2	1.83	
60	125	2		270.95	1.84	
61	127	2		245.9	1.83	
62	129	2		305.65	1.84	
63	131	2		170.4	1.85	
64	133	2		259.7	1.82	
65	134	2		236.85	1.83	
66	138	2		162.15	1.84	
67	140	2		187.35	1.84	
68	143	2		255.9	1.84	
69	148	2		343.8	1.84	
70	149	2		255.75	1.84	
71	153	2		429.9	1.84	
72	154	2		290.7	1.84	
73	157	2		322.7	1.84	
74	158	2		344.1	1.84	
75	159	2		279.5	1.84	
76	160	2		308.3	1.84	
77	161	2		325.55	1.84	
78	162	2		288.25	1.85	
79	165	2		245.2	1.83	
80	166	2		350.8	1.84	
81	169	2		151.95	1.83	
82	170	2		361.65	1.85	
83	171	2		265.05	1.84	
84	173	2		420.8	1.84	
85	174	2		229.65	1.84	
86	176	2		236.2	1.84	
87	179	2		194.25	1.84	
88	180	2		186.7	1.84	
89	183	2		374.55	1.84	
90	186	2		166.3	1.84	
91	187	2		332.55	1.84	
92	190	2		112.7	1.84	
93	191	2		160.85	1.83	
94	195	2		239.4	1.84	
95	Positive control					
96	BLANK					
97						
98						
99						

*** Flow Cell Selection:**

- ☒ MinION Flow Cell
☐ PromethION Flow Cell

Approx. Genome Size 600

Approx. Coverage Needed 50x-100x

Estimated number of Flow Cells 1

Additional Comments / Special Needs

Amplicon length is 600 bp. Genome size is difficult to approximate as these are microbiome samples. For coverage, I am hoping to get anywhere between 30,000 - 100,000 reads per sample.

Bioinformatics and Data Delivery

I would like my data to be basecalled using:

- ☐ HAC (High Accuracy - Usually sufficient for most applications)
- ☒ SUP (Super-High Accuracy - Computing intensive and may add 1-2 weeks to data delivery)
- ☐ Methylation

File Format:

- ☒ FASTQ / BAM
- ☐ POD5 (only necessary if you wish to do basecalling on your own)

Data Delivery Notification email addresses:

joshleon@unc.edu

How would you like to retrieve your data from HTSF?

- ☒ Deliver my data to ITS Research Computing storage (/proj)
- ☒ Provide me with a URL to download my data via the web
- ☐ Pre-arranged data delivery method for this project
- ☐ Other

Note: For Bioinformatics Analysis and Consulting (Assembly, Custom Solutions, etc.) – Please contact the Bioinformatics and Analytics Research Collaborative (BARC) – may be subject to extra costs.