Email the completed form and Bioanalyzer traces (if available) to DNATECH@UCDAVIS.EDU **and** submit a printed copy of these together with your samples.

Sequencing Submission Form - Customer Prepared Library

Indicate the Illumina sequencing platform:

___MiSeq | X_NextSeq | __HiSeq2500 __ | HiSeq4000

PI on Genome Center Account:	craig.nelson	Date:	7/8/16
PI email:	craig.nelson@hawaii.edu	Your Name:	Craig Nelson
Institute:	University of Hawai'i	Email:	craig.nelson@hawaii.edu (UC address if applicable)
Account to be billed (required):	credit card	Phone No.	805-705-3497 (cell) or 808-956-0566 (office)
(enter DaFIS account, Chart String for inter-campus payments, PO number, or "credit card")			

	Example	Library #1	Library #2	Library #3	Library #4	Library #5	Library #6	Library #7
Library Name	*XYZ012*	G021	G048	G068	G088 #2	R020 re-amp	R023 re-amp	R060 re-amp
Organism (Scientific and Common Name)	*mouse, Mus Musculus*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*
Bioanalyzer traces are required. Do you need us to run the Bioanalyzer library QC (at extra cost)?	*yes*	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted
What **library type** (genome shotgun, RNA-seq, RAD/GBS, Amplicon, 16S Amplicon, **PCR-free**) & which kit (TruSeq, Kapa, custom)?	*RNA-Seq, TruSeq kit*	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded
Sample concentration (ng/ul and nM) 5 nM minimum From:__ **Nanodrop** | __ **Qubit** | _x_ **BioAnalyzer**	*2 ng/ul (7 nM)*	138 nM	53.2 nM	4.1 nM	3.97 nM	2.19 nM	30.18 nM	10.35 nM
Sample **volume** (ul) 15 ul minimum	*20 ul*	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul
Library size with adapters (e.g. 250 bp, 450 bp)	*450*	352	309	254	308	229	296	281
Specify **indices** and **length** (none, single, dual, **in-line?**, 6bp, 8bp)	*single, 8 bp*	TruSeq dual, 8bp D704, D505	TruSeq dual, 8bp D704, D506	TruSeq dual, 8bp D704, D507	TruSeq dual, 8bp D704, D508	TruSeq dual, 8bp D705, D505	TruSeq dual, 8bp D705, D506	TruSeq dual, 8bp D705, D507
Do we need to **demultiplex**? (included)	*Yes*	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Pooling requested (at extra cost), **if YES**: (i.e. "all into 1 pool", or the **Pool Name** [**A, B, C, ...**]) Libraries need to have similar insert sizes.	*Pool **A***	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool
No. of seq. **lanes** requested (for pool if applicable)	*1 lane Pool A*	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output
Type of sequencing run (SR50, SR90Si, PE100, PE150, PE300, Rapid PE250)	*PE100*	SR80	SR80	SR80	SR80	SR80	SR80	SR80
Is the library enriched for **low complexity** regions? (i.e. enzyme recognition sites, GC or AT rich areas, in-line barcodes, amplicons)	*no*	no	no	no	no	no	no	no
Special Instructions (i.e. custom seq. primers; % of high complexity control spike-in , e.g. PhiX)	*N/A*	none	none	none	none	none	none	none

	Library #8	Library #9	Library #10	Library #11	Library #12	Library #13	Library #14	Library #15
Library Name	G023	G041	G066	G091	R004	R025	R049	G029
Organism (Scientific and Common Name)	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*
Bioanalyzer traces are required. Do you need us to run the Bioanalyzer library QC (at extra cost)?	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted
What **library type** (genome shotgun, RNA-seq, RAD/GBS, Amplicon, 16S Amplicon, **PCR-free**) & which kit (TruSeq, Kapa, custom)?	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded
Sample concentration (ng/ul and nM) 5 nM minimum From:__ **Nanodrop** | __ **Qubit** | _x_ **BioAnalyzer**	5.9 nM	43.65 nM	36 nM	61.5 nM	90 nM	70 nM	95 nM	63.5 nM
Sample **volume** (ul) 15 ul minimum	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul
Library size with adapters (e.g. 250 bp, 450 bp)	270	336	379	347	341	339	349	352
Specify **indices** and **length** (none, single, dual, **in-line?**, 6bp, 8bp)	TruSeq dual, 8bp D705, D508	TruSeq dual, 8bp D706, D505	TruSeq dual, 8bp D706, D506	TruSeq dual, 8bp D706, D507	TruSeq dual, 8bp D706, D508	TruSeq dual, 8bp D707, D505	TruSeq dual, 8bp D707, D506	TruSeq dual, 8bp D707, D507
Do we need to **demultiplex**? (included)	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Pooling requested (at extra cost), **if YES**: (i.e. "all into 1 pool", or the **Pool Name** [**A, B, C, ...**]) Libraries need to have similar insert sizes.	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool
No. of seq. **lanes** requested (for pool if applicable)	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output
Type of sequencing run (SR50, SR90Si, PE100, PE150, PE300, Rapid PE250)	SR80	SR80	SR80	SR80	SR80	SR80	SR80	SR80
Is the library enriched for **low complexity** regions? (i.e. enzyme recognition sites, GC or AT rich areas, in-line barcodes, amplicons)	no	no	no	no	no	no	no	no
Special Instructions (i.e. custom seq. primers; % of high complexity control spike-in , e.g. PhiX)	none	none	none	none	none	none	none	none

		Library #16	Library #17	Library #18	Library #19	Library #20	Library #21	Library #22	Library #23
Library Name		G053	G079	R059	R009	R038	G096 #2	G024	G056
Organism (Scientific and Common Name)		Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*
Bioanalyzer traces are required. Do you need us to run the Bioanalyzer library QC (at extra cost)?		no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted
What **library type** (genome shotgun, RNA-seq, RAD/GBS, Amplicon, 16S Amplicon, **PCR-free**) & which kit (TruSeq, Kapa, custom)?		RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded
Sample concentration (ng/ul and nM) 5 nM minimum From:__ **Nanodrop** | __ **Qubit** | _x_ **BioAnalyzer**		256.4 nM	65.9 nM	109 nM	118.5 nM	180.3 nM	47.1 nM	150 nM	190.1 nM
Sample **volume** (ul) 15 ul minimum		15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul
Library size with adapters (e.g. 250 bp, 450 bp)		351	349	348	345	335	355	341	335
Specify **indices** and **length** (none, single, dual, **in-line?**, 6bp, 8bp)		TruSeq dual, 8bp D707, D508	TruSeq dual, 8bp D708, D505	TruSeq dual, 8bp D708, D506	TruSeq dual, 8bp D708, D507	TruSeq dual, 8bp D708, D508	TruSeq dual, 8bp D709, D505	TruSeq dual, 8bp D709, D506	TruSeq dual, 8bp D709, D507
Do we need to **demultiplex**? (included)		Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Pooling requested (at extra cost), **if YES**: (i.e. "all into 1 pool", or the **Pool Name** [**A, B, C, ...**])		all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool
No. of seq. **lanes** requested (for pool if applicable)		NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output
Type of sequencing run (SR50, SR90Si, PE100, PE150, PE300, Rapid PE250)		SR80	SR80	SR80	SR80	SR80	SR80	SR80	SR80
Is the library enriched for **low complexity** regions? (i.e. enzyme recognition sites, GC or AT rich areas, in-line barcodes, amplicons)		no	no	no	no	no	no	no	no
Special Instructions (i.e. custom seq. primers; % of high complexity control spike-in , e.g. PhiX)		none	none	none	none	none	none	none	none

	Library #24	Library #25	Library #26	Library #27	Library #28	Library #29	Library #30	Library #31
Library Name	G077	G094	R003	R021	R048	G028	G060	R046
Organism (Scientific and Common Name)	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*
Bioanalyzer traces are required. Do you need us to run the Bioanalyzer library QC (at extra cost)?	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted
What **library type** (genome shotgun, RNA-seq, RAD/GBS, Amplicon, 16S Amplicon, **PCR-free**) & which kit (TruSeq, Kapa, custom)?	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded
Sample concentration (ng/ul and nM) 5 nM minimum From:__ **Nanodrop** | __ **Qubit** | _x_ **BioAnalyzer**	205.2 nM	80.1 nM	74.3 nM	96 nM	62.7	55.7 nM	101.2 nM	85.5 nM
Sample **volume** (ul) 15 ul minimum	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul	15 ul
Library size with adapters (e.g. 250 bp, 450 bp)	348	343	343	350	346	354	345	353
Specify **indices** and **length** (none, single, dual, **in-line?**, 6bp, 8bp)	TruSeq dual, 8bp D709, D508	TruSeq dual, 8bp D710, D505	TruSeq dual, 8bp D710, D506	TruSeq dual, 8bp D710, D507	TruSeq dual, 8bp D710, D508	TruSeq dual, 8bp D711, D505	TruSeq dual, 8bp D711, D506	TruSeq dual, 8bp D711, D507
Do we need to **demultiplex**? (included)	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Pooling requested (at extra cost), **if YES**: (i.e. "all into 1 pool", or the **Pool Name** [**A, B, C, ...**])	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool
No. of seq. **lanes** requested (for pool if applicable)	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output
Type of sequencing run (SR50, SR90Si, PE100, PE150, PE300, Rapid PE250)	SR80	SR80	SR80	SR80	SR80	SR80	SR80	SR80
Is the library enriched for **low complexity** regions? (i.e. enzyme recognition sites, GC or AT rich areas, in-line barcodes, amplicons)	no	no	no	no	no	no	no	no
Special Instructions (i.e. custom seq. primers; % of high complexity control spike-in , e.g. PhiX)	none	none	none	none	none	none	none	none

	Library #32	Library #33	Library #34	Library #35				
Library Name	R015	G085 #2	R026	G075				
Organism (Scientific and Common Name)	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*	Lace Coral, *Pocillopora damicornis*				
Bioanalyzer traces are required. Do you need us to run the Bioanalyzer library QC (at extra cost)?	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted	no, BA traces submitted				
What **library type** (genome shotgun, RNA-seq, RAD/GBS, Amplicon, 16S Amplicon, **PCR-free**) & which kit (TruSeq, Kapa, custom)?	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded	RNA-Seq, Kapa mRNA Stranded				
Sample concentration (ng/ul and nM) 5 nM minimum	89.6	33.6 nM	480 nM	50 nM				
Sample **volume** (ul) 15 ul minimum	15 ul	15 ul	15 ul	15 ul				
Library size with adapters (e.g. 250 bp, 450 bp)	356	334	343	351				
Specify **indices** and **length** (none, single, dual, **in-line?**, 6bp, 8bp)	TruSeq dual, 8bp D711, D508	TruSeq dual, 8bp D712, D505	TruSeq dual, 8bp D712, D506	TruSeq dual, 8bp D712, D507				
Do we need to **demultiplex**? (included)	Yes	Yes	Yes	Yes				
Pooling requested (at extra cost), **if YES**: (i.e. "all into 1 pool", or the **Pool Name** [**A, B, C, ...**])	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool	all (35) into 1 pool				
No. of seq. **lanes** requested (for pool if applicable)	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output	NextSeq 75cyc High-Output				
Type of sequencing run (SR50, SR90Si, PE100, PE150, PE300, Rapid PE250)	SR80	SR80	SR80	SR80				
Is the library enriched for **low complexity** regions? (i.e. enzyme recognition sites, GC or AT rich areas, in-line barcodes, amplicons)	no	no	no	no				
Special Instructions (i.e. custom seq. primers; % of high complexity control spike-in , e.g. PhiX)	none	none	none	none				

If you have made multiplex libraries which you need us to demultiplex, provide the barcode information below; if you used dual indexing also fill out Columns E and F.
Please ensure your sample IDs and barcodes are unique; additional labor charges are applied for re-demultiplexing because of incorrect submission info.

SampleName	**Barcodesequence**	**Index 1 (i7) Description**	**only for dual indexing**	**2nd index (i5) Description**
e.g. ABX1	**e.g.ATGCCA**	**e.g. N701, TruSeq99**	**2nd Barcode sequence**	**e.g. S503**
G021	GAGATTCC	D704	CTTCGCCT	D505
G048	GAGATTCC	D704	TAAGATTA	D506
G068	GAGATTCC	D704	ACGTCCTG	D507
G088	GAGATTCC	D704	GTCAGTAC	D508
R020	ATTCAGAA	D705	CTTCGCCT	D505
R023	ATTCAGAA	D705	TAAGATTA	D506
R060	ATTCAGAA	D705	ACGTCCTG	D507
G023	ATTCAGAA	D705	GTCAGTAC	D508
G041	GAATTCGT	D706	CTTCGCCT	D505
G066	GAATTCGT	D706	TAAGATTA	D506
G091	GAATTCGT	D706	ACGTCCTG	D507
R004	GAATTCGT	D706	GTCAGTAC	D508
R025	CTGAAGCT	D707	CTTCGCCT	D505
R049	CTGAAGCT	D707	TAAGATTA	D506
G029	CTGAAGCT	D707	ACGTCCTG	D507
G053	CTGAAGCT	D707	GTCAGTAC	D508
G079	TAATGCGC	D708	CTTCGCCT	D505
R059	TAATGCGC	D708	TAAGATTA	D506
R009	TAATGCGC	D708	ACGTCCTG	D507
R038	TAATGCGC	D708	GTCAGTAC	D508
G096	CGGCTATG	D709	CTTCGCCT	D505
G024	CGGCTATG	D709	TAAGATTA	D506
G056	CGGCTATG	D709	ACGTCCTG	D507
G077	CGGCTATG	D709	GTCAGTAC	D508
G094	TCCGCGAA	D710	CTTCGCCT	D505
R003	TCCGCGAA	D710	TAAGATTA	D506
R021	TCCGCGAA	D710	ACGTCCTG	D507
R048	TCCGCGAA	D710	GTCAGTAC	D508
G028	TCTCGCGC	D711	CTTCGCCT	D505
G060	TCTCGCGC	D711	TAAGATTA	D506
R046	TCTCGCGC	D711	ACGTCCTG	D507
R015	TCTCGCGC	D711	GTCAGTAC	D508
G085	AGCGATAG	D712	CTTCGCCT	D505
R026	AGCGATAG	D712	TAAGATTA	D506
G075	AGCGATAG	D712	ACGTCCTG	D507