**For accounting questions, contact the recharge finance analyst, Christine Owen, cjowen@berkeley.edu, (510) 642-3506**

### Illumina MiSeq Sequencing Request Form

http://qb3.berkeley.edu/gsl

Library Drop-off Locations:
- B206 Stanley Hall  M-F 10am-5pm (510) 666-3372
- 255 LSA (Life Science Add.)  M-F 10am-5pm (510) 642-1165

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<table>
<thead>
<tr>
<th>Library Name* (per lane basis)</th>
<th>Sample Type (gDNA, ChIP, RNA, RADtag etc.)</th>
<th>Organism</th>
<th>Nano (~1M Reads) (Circle)</th>
<th>V3 Chemistry (~20-25M Reads) (Circle)</th>
<th># of Tubes Submitted</th>
<th>Bioanalyzer</th>
<th>qPCR</th>
<th>Bead Clean</th>
<th>Pippin Prep</th>
<th>Additional QC Required for all Tubes Submitted**</th>
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</table>

*Standard Naming convention is PI initials, Your initials, Number, ex: DRMC001. Please do not submit samples with the same names you have used in the past.

*For multiplexed samples submitted individually, label tubes with the same library name, as explained above, followed by a letter (A-Z), ex: DRMC001A, DRMC001B = 2 samples/1 lane

**Additional QC is required for multiplexing samples submitted as separate tubes. ex: If you are submitting 8 tubes for 1 lane, you will need 7 additional qPCR preps

**Bioanalyzer traces are not included in the base sequencing price but must be provided or performed by the sequencing facility. Please write down the number of samples requiring a trace.

Please provide us with additional details regarding your sample: (Truseq/Nextera/Custom Barcodes at R1/Custom Sequencing Primer/Low Diversity/Amplicon...) Please print here or provide us with an Excel Sheet with Sample names and corresponding index sequences listed (required for multiplexed samples):

Please email a spreadsheet formatted list of sample names and actual index sequences (Truseq/Nextera names ok) to vecgsl.qb3@gmail.com, with any Bioanalyzer traces that need to be provided at the time of sample submission.

**PLEASE BE ADVISED THAT LIBRARIES AND FINAL DATA WILL NOT BE STORED INDEFINITELY!!!! PLEASE DO NOT SEND ALL LIBRARY AND/OR ARRANGE TO PICKUP YOUR SAMPLES. DOWNLOAD DATA DROM THE FTP SERVER WITHIN 1 MONTH OF ITS POST. A $100 REPROCESSING FEE WILL BE CHARGED FOR ANY REPOSTS DUE TO USER DELIQUENCY. ORGINAL LIBRARIES WILL BE STORED FOR UP TO A YEAR. RUN DATA WILL BE STORED AS LONG AS SPACE ALLOWS.

SIGNATURE:

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Please provide the following information:

- **Library Name**
- **Sample Type**
- **Organism**
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- **V3 Chemistry (~20-25M Reads) (Circle)**
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- **qPCR**
- **Bead Clean**
- **Pippin Prep**
- **Additional QC Required for all Tubes Submitted**

**INDEX INFORMATION (circle)**

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<tr>
<th>Length (bases)</th>
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<th>TruSeq</th>
<th>Nextera</th>
<th>Other</th>
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</tbody>
</table>

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**User Affiliation**

- **UC / Affiliate / Academic / Outside**
- **Cycle Number**
- **Chemistry version**
- **Sequencing Total**
- **Bioanalyzer**
- **qPCR**
- **Bead Clean / Pippin Prep**
- **Order Total**
- **Date Completed**

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- **Name:**
- **Date:**
- **Lab:**
- **Dept./Inst.:**
- **Phone:**
- **Email:**
- **Fund Admin Name:**
- **Phone:**
- **Email address:**

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