**UCSF Genomics CoLab Project Description Form**

[http://functionalgenomicscore.ucsf.edu](http://functionalgenomics.ucsf.edu)

|  |  |
| --- | --- |
| Principal Investigator: (last, first name) |  |
| Department/Institution: |  |
| PI e-mail: |  |
| Lead Scientist ( last, first name) |  |
| Lead Scientist e-mail |  |
| Lead Scientist phone # |  |
| Project Title ( required) |  |
| Genomics Technology (bulk RNA-seq, single cell RNA-seq, exome, etc) |  |

**Other Personnel Involved in Project (optional)**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Role in project | E-mail | Telephone |
|  |  |  |  |
|  |  |  |  |

|  |
| --- |
| Brief Description of Scientific Background and Goals/Questions/Hypothesis (one paragraph is sufficient): |
|  |

**List of Experimental Groups** *Group labels must be 1-8 characters and include only letters, numbers, and dashes (-)*

|  |  |  |
| --- | --- | --- |
| Group label | Description of the group | Number of samples |
|  |  |  |
|  |  |  |
|  |  |  |
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|  |  |  |
|  |  |  |

*Insert additional rows as needed*

|  |  |
| --- | --- |
| Total number of samples: |  |

**Data Analysis**

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| --- |
| *What are the group comparisons of interest? (List pairwise comparisons using group labels):* |
|  |
| *Please describe expected differences in specific genes between the groups, if known:* |
|  |

**Sample Information**

|  |  |  |  |
| --- | --- | --- | --- |
| Species: |  | Tissue/cell type: |  |
| Number of cells per sample if known: |  | Amount of nucleic acid per sample if known: |  |

**Comments**

|  |
| --- |
| Do you have any special requests? If you have preferences about which methods should be used for processing the samples, sequencing depth, or read length, please let us know. |
|  |

**After completing the above sections, please e-mail the completed form to** **GenomicsCoLab@ucsf.edu** **and we will contact you to schedule a project meeting.**

**FOR CORE USE ONLY**

|  |  |  |  |
| --- | --- | --- | --- |
| Project number: | XXXX | Project meeting date: |  |
| Analysis by core: |  | Fragment Analyzer QC: |  |
| Library prep: |  | NovaSeq/HiSeq: |  |
| Max. Lanes: | 1 | SE/PE: | PE | Read Depth: | 150 |

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| --- |
| Pricing |
|  |
| Timetable |
|  |
| Analysis notes |
|  |
| Other notes |
|  |

**Project log**

|  |  |  |
| --- | --- | --- |
| Date | Author | Note |
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