University of Pennsylvania

**Penn Genomic Analysis Core - DNA Sequencing Laboratory**

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**Request for Ion Torrent S5 Sequencing Service**

### PI \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Fund/PO No \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

## Tel\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Date\_\_\_\_\_\_\_\_\_\_

**Contact person (full name) \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Tel \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**\*E-mail (Required) \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_**

**Ion Torrent S5 is an upgrade of Proton with various throughput capabilities.**

 **Applications:** Targeted Sequencing of custom and ready-to-use gene panels e.g.

Comprehensive Cancer Panel & Inherited Disease Panel; RNA-Seq and AmpliSeq Transcriptome;

Exome & AmpliSeq Exome; Bacterial Genome

**Only 1 sample is run on a chip. No waiting is necessary to fill up a plate/flow cell/slide.**

|  |
| --- |
| ***ExpEExpected Run Results (200 and 400b sequencing) and Cost (effective Jan 1, 2018)*** |
|  | **520 chip** | **530 chip** | **540 chip** |
| **Read Length** | **200b & 400b** | **200b & 400b** | **200b only** |
|  **No of Reads** | **5 - 7M** | **16 - 22M** | **70 - 90M** |
|  **Throughput** | **1Gb - 2Gb**  | **3.5Gb - 7GB**  | **~12Gb** |
| **§ Sequencing****(pooled libraries submitted)** | **$1,090** | **$1,230** | **$1,400** |
| **Barcoded library, gDNA or long amplicons, with Pippin Prep size selection,****1 – 3 libraries - $100 each; 4 or more libraries - $75 each**  |
|  **Barcoded Cancer Hotspot Panel v2 library,** **8 minimum - $130 each, more for fewer samples** |
| **Comprehensive Cancer Panel or Custom Panel Library - Contact us** |
| **RNA-Seq & AmpliSeq Transcriptome Library - Contact us** |
| **Exome & AmpliSeq Exome Library - Contact us** |
| **Volume discount - Contact us** |

**§The sequencing price includes emPCR, sequencing, and preliminary data analysis to provide FASTQ, BAM and BAI files, as well as sequence alignment and variant calls.**

**Library prep & QC not included.**

**Note – Downstream data analysis (provided after consultation with the user): $100/hr**

Ion Torrent S5 Service

**Please Fill Out-**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **No** | **Sample Name** | **Barcode** | **Fragment size** | **Concentration (ng/µl)** | **Total amount (ng)** |
| **1** |  |  |  |  |  |
| **2** |  |  |  |  |  |
| **3** |  |  |  |  |  |
| **4** |  |  |  |  |  |
| **5** |  |  |  |  |  |
| **6** |  |  |  |  |  |
| **7** |  |  |  |  |  |

***\*\* gDNA or pooled amplicons***

***Required 300 - 400 ng by fluorometry or 1 – 1.5 µg by Nanodrop, Volume 30 – 50 µl***

***\*\* Amplicon library with Ion adaptors attached***

***Required 100 – 200 ng by fluorometry or 300 - 600 ng by Nanodrop, Volume 30 –50 µl***

***Please Check the Following-***

***Gel Picture Submitted ( ) Quantitation Method: Nanodrop ( ) or Fluorometry ( )***

**Samples Pooled: ( ) Barcoded: ( )**

***Throughput Desired for Each Sample No of reads \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_, No of bases \_\_\_\_\_\_\_\_\_\_\_\_\_***

***Use chip ( ) Use 200 b ( ) or 400b ( ) sequencing***

Note: Please mention barcode sequences in the project description if different from Ion Torrent’s.

**Project description with a title (required)** *Use separate page if necessary*

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