

Genomic/epigenomic services available at the CESCG and their costs

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The sequencing and informatics prices are listed as direct costs, to be used to calculate “CESCG Resources Direct Costs” in line “1) CESCO Resources Budget” of the Part D Budget Template. The informatics costs are to be applied only to the CESCO portion of Comprehensive budgets.

General notes:

- Prices are subject to change as vendor prices can change.
- b = bases read length
- We recommend that investigators plan for a whole sequencing lane (e.g. 6 samples where applicable) to avoid heterogeneity.

If libraries are provided by the research group the sequencing costs per lane are:

\$2,400 per lane, 100 b paired end

\$1,600 per lane, 100 b single end

Informatics costs per sample are provided in Table T1:

| Type | #Samples / Lane | Informatics cost per sample |
|---|-----------------|-----------------------------|
| ChIP-Seq | 6 | \$60 |
| RNA-Seq | 6 | \$100 |
| Exome-Seq | 6 | \$80 |
| Single cell analysis (RNA-Seq, genome-wide) | | \$120 |
| Whole genome sequencing | 1 | \$550 |
| Whole genome methylation | 1/7 | \$1,435 |

Table T1: Informatics costs per sample

If investigators supply cells or tissue, the sequencing and informatics costs per sample are provided in Table T2:

| Type | #Samples / Lane | Sequencing cost per sample including preparation of libraries | Informatics cost per sample |
|---|-----------------|---|-----------------------------|
| ChIP-Seq | 6 | \$950 (see note 1) | \$60 |
| RNA-Seq | 6 | \$1,000 (see note 2) | \$100 |
| Exome-Seq | 6 | \$1,000 (see note 3) | \$80 |
| Single cell analysis (RNA-Seq, genome-wide) | | Inquire | \$120 |
| Whole genome sequencing | 1 | \$1,550 (see note 4) | \$550 |
| Whole genome methylation | 1/7 | \$11,245 (see note 5) | \$1,435 |
| Hi-C Analysis | | \$5,418 (see note 6) | |

Table T2: Sequencing and Informatics cost per sample

Notes for Table T2:

1. **ChIP-Seq:** Cost provided for 100 b paired end. Validated antibody must be provided, except for well-characterized chromatin modifications H3K4me3, H3K4me1, H3K27ac, H3K27me3, H3K9me3, and H3K36me3. Should result in an estimated >25M reads per sample. Note Input or IgG controls need to be performed in parallel.
2. **RNA-Seq:** Cost provided for 100 b paired end, not strand specific. Inquire for strand specific. Should result in an estimated >25M reads per sample.
3. **Exome-Seq:** Cost provided for 100 b paired end.
4. **Whole Genome Sequencing:** Sequenced in batches of 10 or more. If less than 10 are submitted, samples will be combined with others until 10 or more are received. 3 micrograms of DNA required.
5. **Whole Genome Methylation:** Note that we need 7 lanes per sample. Cost provided for 100 b single end.
6. **Hi-C Analysis:** If library is provided cost is \$4,311.

Informatics consulting direct costs are provided in Table T3:

| Days/week | Cost/week | Cost/year |
|------------------|------------------|------------------|
| 1 | \$600 | \$31,200 |
| 2 | \$1,200 | \$62,400 |
| 3 | \$1,800 | \$93,600 |
| 4 | \$2,400 | \$124,800 |
| 5 | \$3,000 | \$156,000 |

Table T3: Informatics consulting direct costs

Notes for Table T3:

1. Informatics costs reported in Table T3 are for any additional analyses performed beyond standard informatics analyses and associated costs reported in Tables T1 and T2.