# Single Cell Services at IRB Barcelona: From Groundwork to Partnership

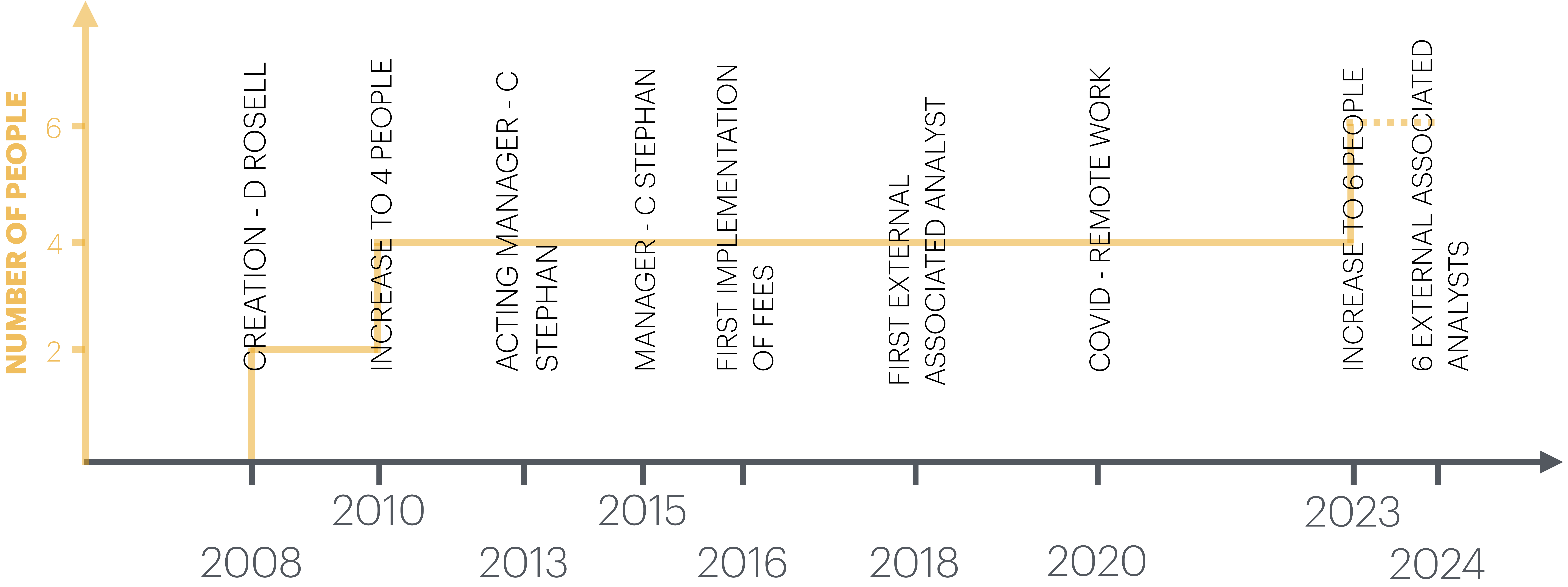
Kick-Off meeting - SCENTINEL PROJECT

Heraklion - 21st June 2024

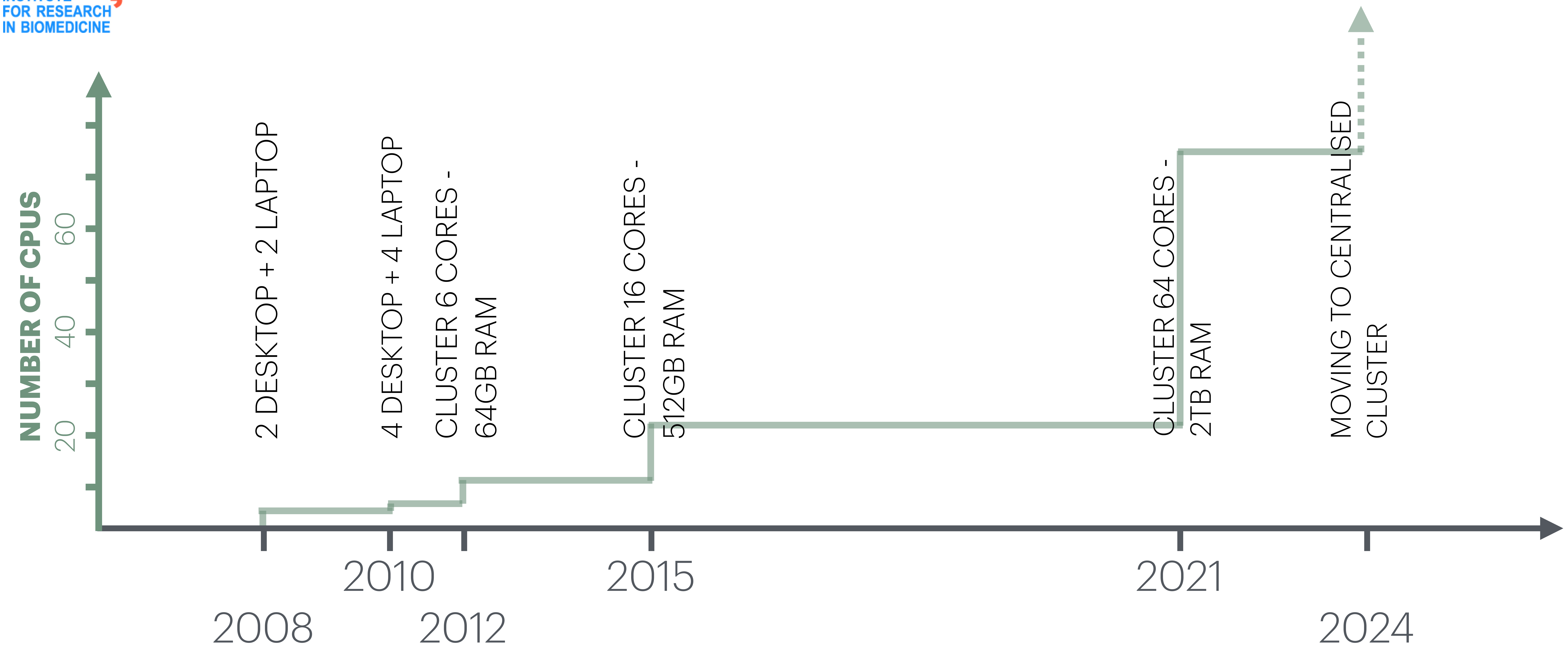
Camille Stephan-Otto Attolini. Biostatistics and Bioinformatics Unit, IRB Barcelona

# The Biostatistics and bioinformatics Unit

## History

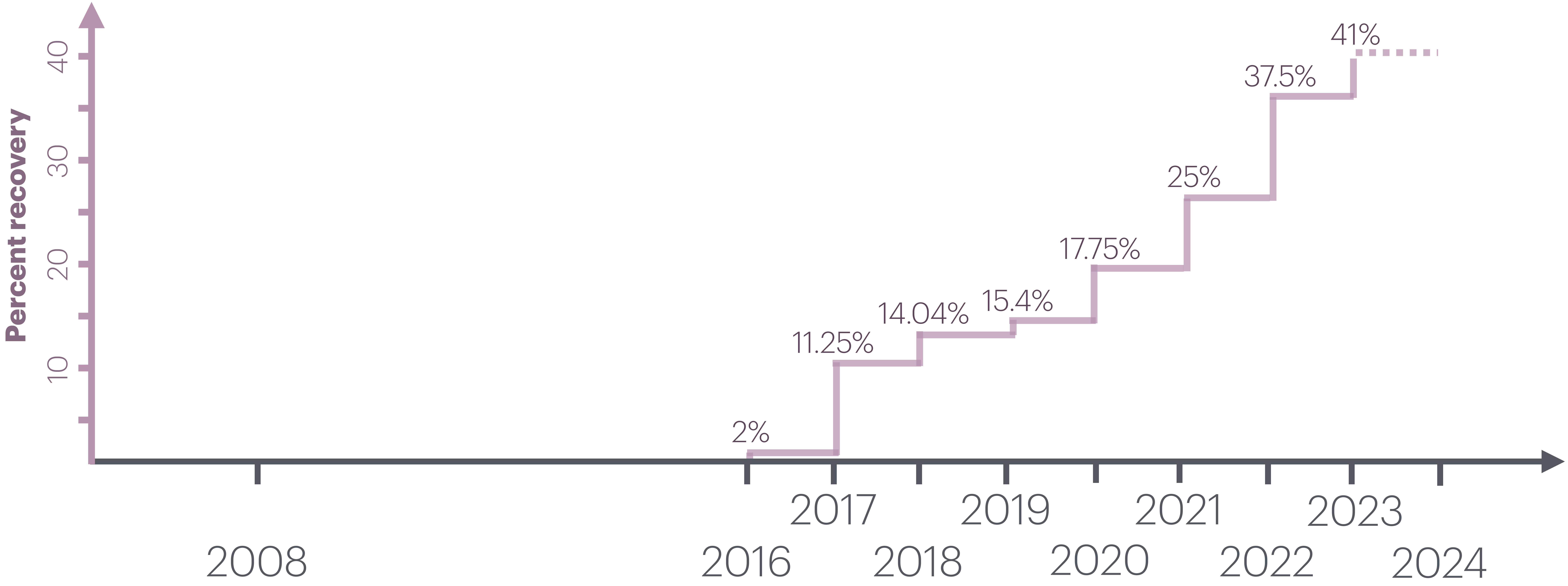


# Computational resources



IRB BARCELONA
INSTITUTE FOR RESEARCH IN BIOMEDICINE

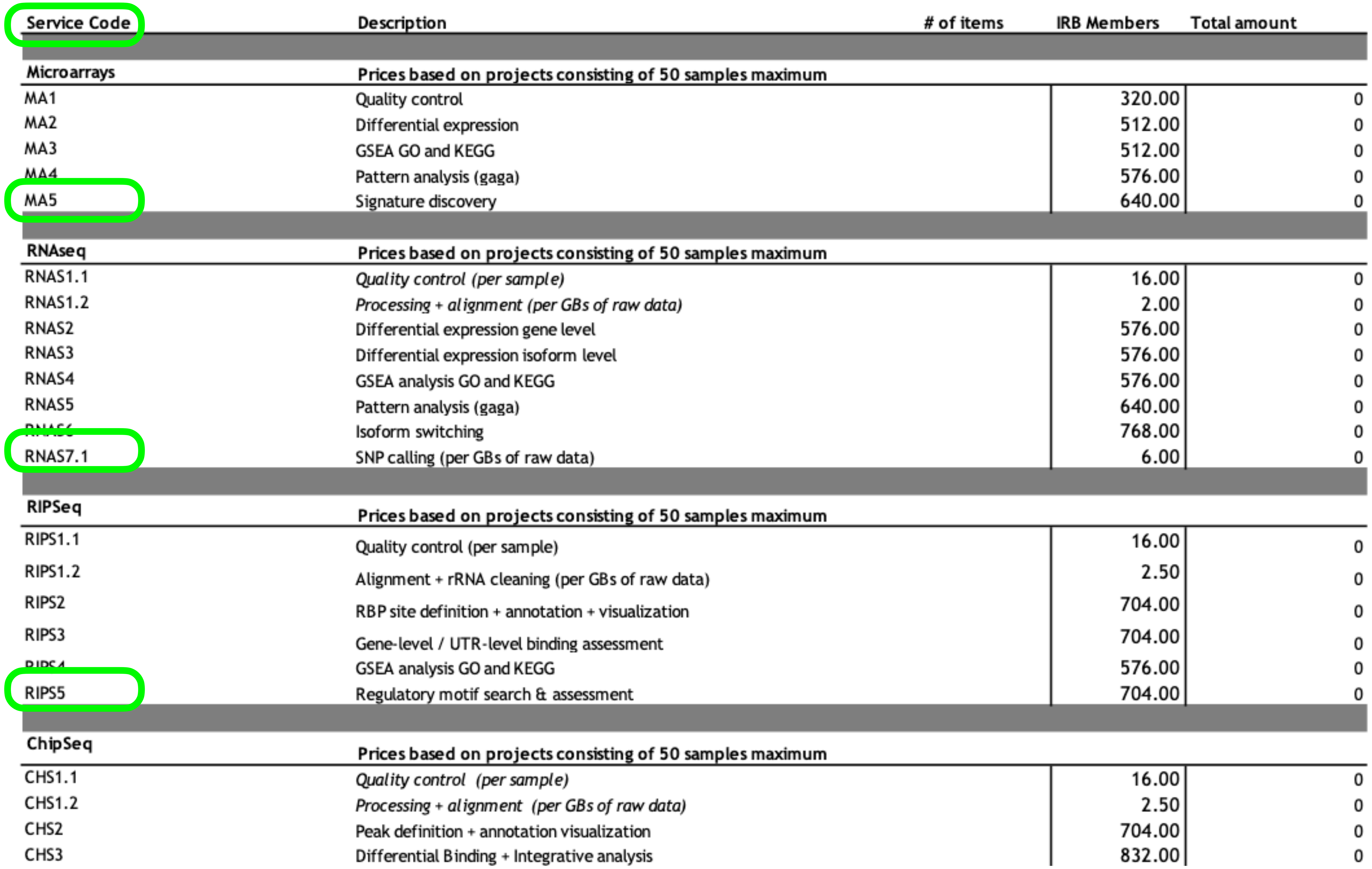
# Billing



# Current status

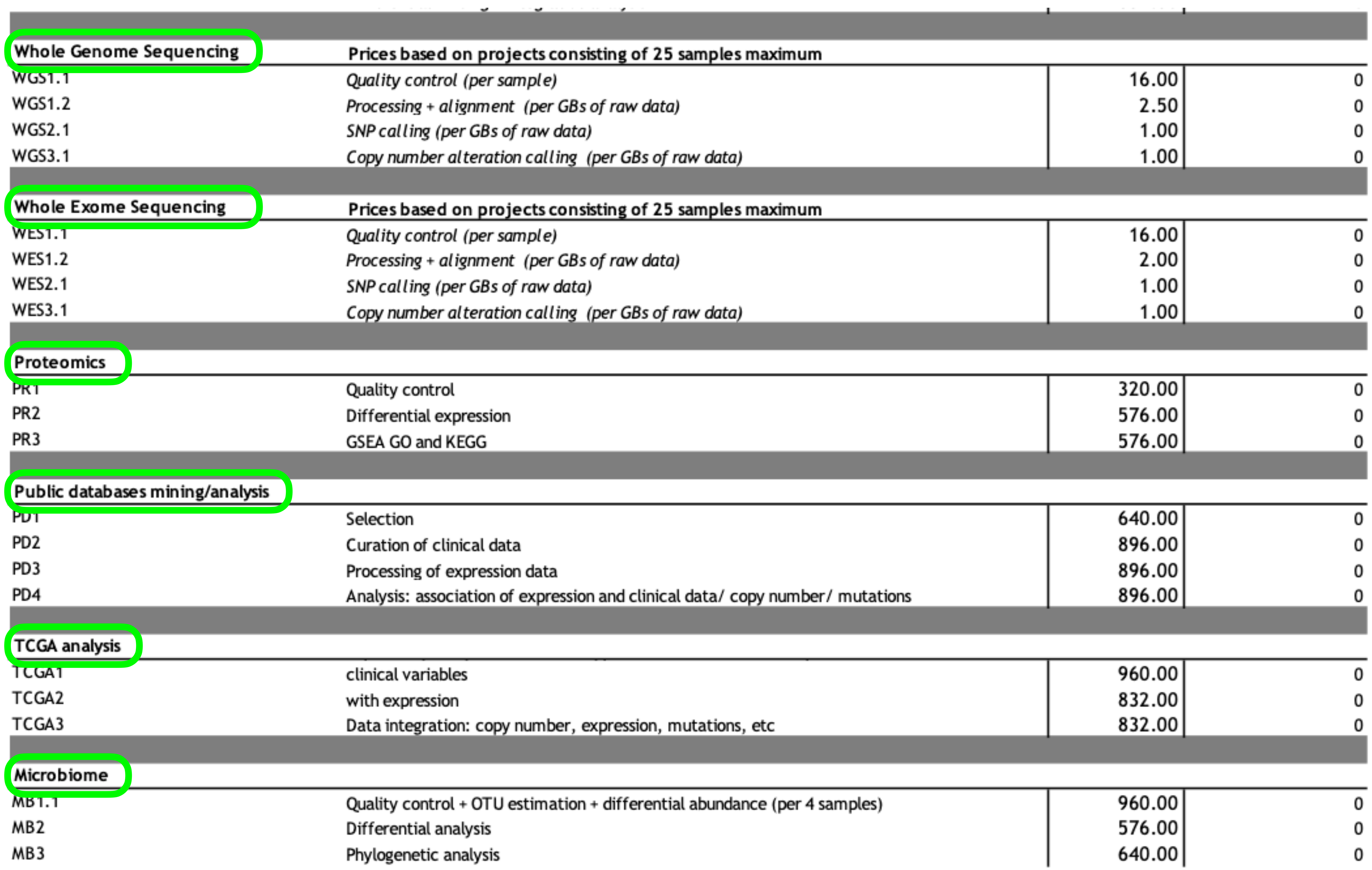
- Number of standard analyses offered: 64
- Number of projects (to date): 66
- Number of projects in 2023: 117
- Services to internal, public and private institutions
- Course on basic statistical concepts
- Co-authorship of (countless) papers
- Authors of 5 methodological papers
- Some PhD students and summer students

# Standard pipelines I



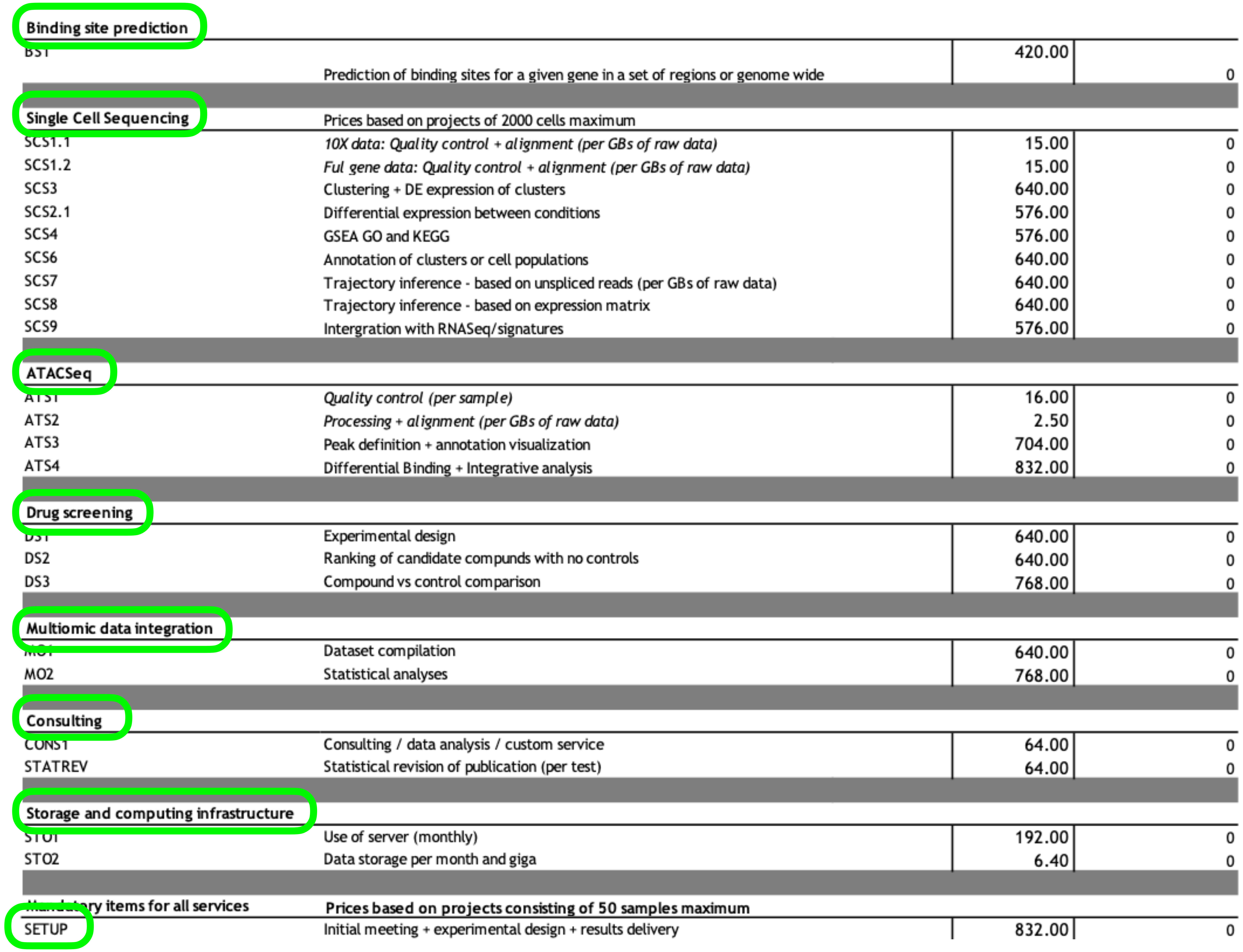
| Service Code | Description | # of items | IRB Members | Total amount |
|---|---|---|---|---|
| **Microarrays** | **Prices based on projects consisting of 50 samples maximum** | | | |
| MA1 | Quality control | | 320.00 | 0 |
| MA2 | Differential expression | | 512.00 | 0 |
| MA3 | GSEA GO and KEGG | | 512.00 | 0 |
| MA4 | Pattern analysis (gaga) | | 576.00 | 0 |
| MA5 | Signature discovery | | 640.00 | 0 |
| **RNAseq** | **Prices based on projects consisting of 50 samples maximum** | | | |
| RNAS1.1 | *Quality control (per sample)* | | 16.00 | 0 |
| RNAS1.2 | *Processing + alignment (per GBs of raw data)* | | 2.00 | 0 |
| RNAS2 | Differential expression gene level | | 576.00 | 0 |
| RNAS3 | Differential expression isoform level | | 576.00 | 0 |
| RNAS4 | GSEA analysis GO and KEGG | | 576.00 | 0 |
| RNAS5 | Pattern analysis (gaga) | | 640.00 | 0 |
| RNAS6 | Isoform switching | | 768.00 | 0 |
| RNAS7.1 | SNP calling (per GBs of raw data) | | 6.00 | 0 |
| **RIPSeq** | **Prices based on projects consisting of 50 samples maximum** | | | |
| RIPS1.1 | Quality control (per sample) | | 16.00 | 0 |
| RIPS1.2 | Alignment + rRNA cleaning (per GBs of raw data) | | 2.50 | 0 |
| RIPS2 | RBP site definition + annotation + visualization | | 704.00 | 0 |
| RIPS3 | Gene-level / UTR-level binding assessment | | 704.00 | 0 |
| RIPS4 | GSEA analysis GO and KEGG | | 576.00 | 0 |
| RIPS5 | Regulatory motif search & assessment | | 704.00 | 0 |
| **ChipSeq** | **Prices based on projects consisting of 50 samples maximum** | | | |
| CHS1.1 | *Quality control (per sample)* | | 16.00 | 0 |
| CHS1.2 | *Processing + alignment (per GBs of raw data)* | | 2.50 | 0 |
| CHS2 | Peak definition + annotation visualization | | 704.00 | 0 |
| CHS3 | Differential Binding + Integrative analysis | | 832.00 | 0 |

# Standard pipelines II



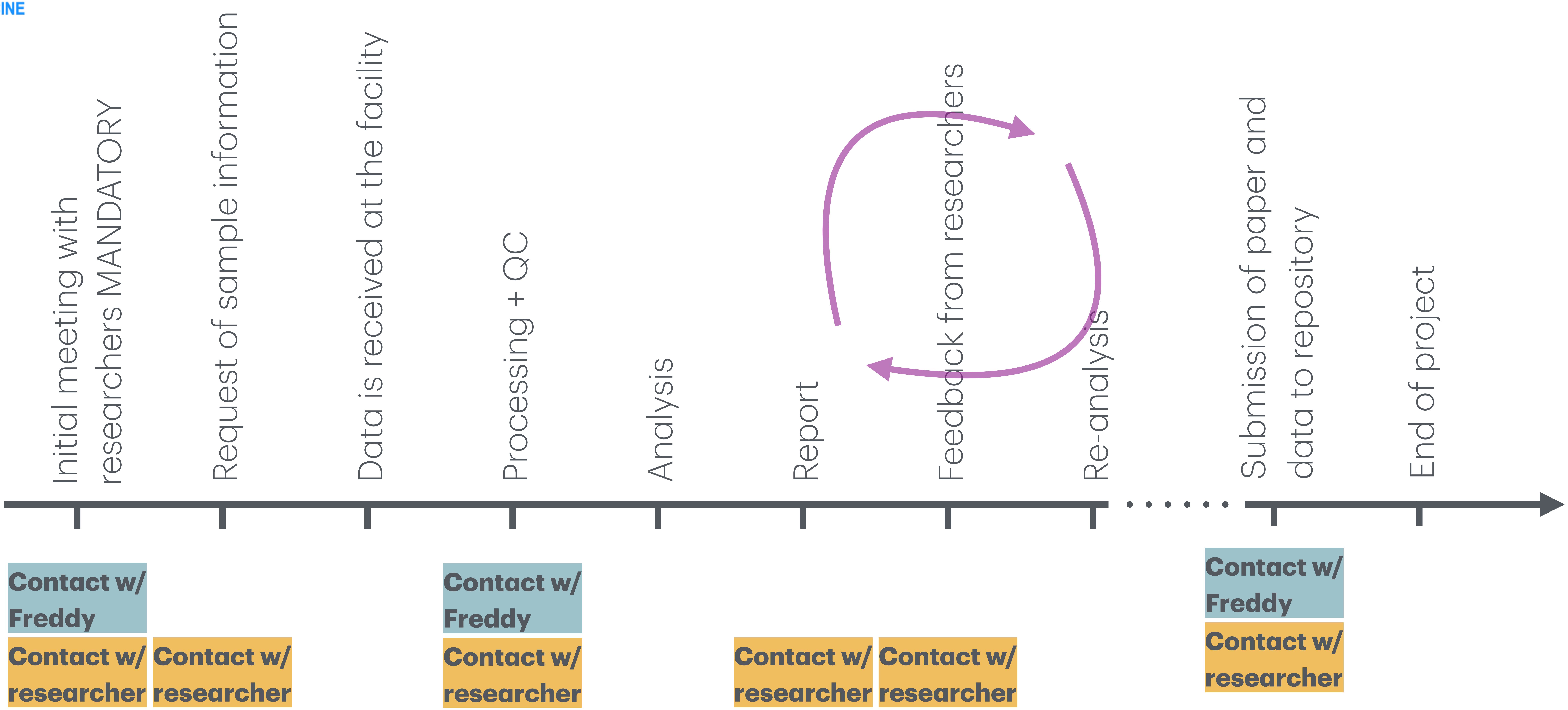
| | | | |
|---|---|---|---|
| **Whole Genome Sequencing** | **Prices based on projects consisting of 25 samples maximum** | | |
| WGS1.1 | *Quality control (per sample)* | 16.00 | 0 |
| WGS1.2 | *Processing + alignment (per GBs of raw data)* | 2.50 | 0 |
| WGS2.1 | *SNP calling (per GBs of raw data)* | 1.00 | 0 |
| WGS3.1 | *Copy number alteration calling (per GBs of raw data)* | 1.00 | 0 |
| **Whole Exome Sequencing** | **Prices based on projects consisting of 25 samples maximum** | | |
| WES1.1 | *Quality control (per sample)* | 16.00 | 0 |
| WES1.2 | *Processing + alignment (per GBs of raw data)* | 2.00 | 0 |
| WES2.1 | *SNP calling (per GBs of raw data)* | 1.00 | 0 |
| WES3.1 | *Copy number alteration calling (per GBs of raw data)* | 1.00 | 0 |
| **Proteomics** | | | |
| PR1 | Quality control | 320.00 | 0 |
| PR2 | Differential expression | 576.00 | 0 |
| PR3 | GSEA GO and KEGG | 576.00 | 0 |
| **Public databases mining/analysis** | | | |
| PD1 | Selection | 640.00 | 0 |
| PD2 | Curation of clinical data | 896.00 | 0 |
| PD3 | Processing of expression data | 896.00 | 0 |
| PD4 | Analysis: association of expression and clinical data/ copy number/ mutations | 896.00 | 0 |
| **TCGA analysis** | | | |
| TCGA1 | clinical variables | 960.00 | 0 |
| TCGA2 | with expression | 832.00 | 0 |
| TCGA3 | Data integration: copy number, expression, mutations, etc | 832.00 | 0 |
| **Microbiome** | | | |
| MB1.1 | Quality control + OTU estimation + differential abundance (per 4 samples) | 960.00 | 0 |
| MB2 | Differential analysis | 576.00 | 0 |
| MB3 | Phylogenetic analysis | 640.00 | 0 |

# Standard pipelines III



| | | | |
|---|---|---|---|
| **Binding site prediction** | | | |
| BS1 | | 420.00 | |
| | Prediction of binding sites for a given gene in a set of regions or genome wide | | 0 |
| **Single Cell Sequencing** | Prices based on projects of 2000 cells maximum | | |
| SCS1.1 | *10X data: Quality control + alignment (per GBs of raw data)* | 15.00 | 0 |
| SCS1.2 | *Ful gene data: Quality control + alignment (per GBs of raw data)* | 15.00 | 0 |
| SCS3 | Clustering + DE expression of clusters | 640.00 | 0 |
| SCS2.1 | Differential expression between conditions | 576.00 | 0 |
| SCS4 | GSEA GO and KEGG | 576.00 | 0 |
| SCS6 | Annotation of clusters or cell populations | 640.00 | 0 |
| SCS7 | Trajectory inference - based on unspliced reads (per GBs of raw data) | 640.00 | 0 |
| SCS8 | Trajectory inference - based on expression matrix | 640.00 | 0 |
| SCS9 | Intergration with RNASeq/signatures | 576.00 | 0 |
| **ATACSeq** | | | |
| ATS1 | *Quality control (per sample)* | 16.00 | 0 |
| ATS2 | *Processing + alignment (per GBs of raw data)* | 2.50 | 0 |
| ATS3 | Peak definition + annotation visualization | 704.00 | 0 |
| ATS4 | Differential Binding + Integrative analysis | 832.00 | 0 |
| **Drug screening** | | | |
| DS1 | Experimental design | 640.00 | 0 |
| DS2 | Ranking of candidate compunds with no controls | 640.00 | 0 |
| DS3 | Compound vs control comparison | 768.00 | 0 |
| **Multiomic data integration** | | | |
| MO1 | Dataset compilation | 640.00 | 0 |
| MO2 | Statistical analyses | 768.00 | 0 |
| **Consulting** | | | |
| CONS1 | Consulting / data analysis / custom service | 64.00 | 0 |
| STATREV | Statistical revision of publication (per test) | 64.00 | 0 |
| **Storage and computing infrastructure** | | | |
| STO1 | Use of server (monthly) | 192.00 | 0 |
| STO2 | Data storage per month and giga | 6.40 | 0 |
| **Mandatory items for all services** | **Prices based on projects consisting of 50 samples maximum** | | |
| SETUP | Initial meeting + experimental design + results delivery | 832.00 | 0 |

# A happy project's life story



Initial meeting with researchers MANDATORY

Contact w/ Freddy

Contact w/ researcher

Request of sample information

Contact w/ researcher

Data is received at the facility

Processing + QC

Contact w/ Freddy

Contact w/ researcher

Analysis

Report

Contact w/ researcher

Feedback from researchers

Contact w/ researcher

Re-analysis

……

Submission of paper and data to repository

Contact w/ Freddy

Contact w/ researcher

End of project

# Challenges

- Many
- Project management and task follow up
- Tickets/queue system
- Percentage of hours billed to end user
- Methodology development
- Career progression

IRB BARCELONA

INSTITUTE FOR RESEARCH IN BIOMEDICINE

Thank you!