

Service Code	Description	per sample	Public Institutions	Private companies
Microarrays				
Prices based on projects consisting of 50 samples maximum				
MA1	Quality control	1	90	108
MA2	Differential expression	1	240	288
MA3	GSEA GO and KEGG	1	255	306
MA4	Pattern analysis (gaga)	1	360	432
MA5	Signature discovery	1	330	396
RNAseq				
Prices based on projects consisting of 50 samples maximum				
RNAS1	Quality control + alignment	0.1	27	32.4
RNAS2	Differential expression gene level	1	240	288
RNAS3	Differential expression isoform level	1	240	288
RNAS4	GSEA analysis GO and KEGG	1	255	306
RNAS5	Pattern analysis (gaga)	1	380	456
RNAS6	Isoform switching	1	240	288
RNAS7	SNP calling	0.1	31.5	37.8
ChipSeq				
Prices based on projects consisting of 50 samples maximum				
CHS1	Quality control + alignment	0.1	18	21.6
CHS2	Peak definition + annotation + visualization	1	315	378
CHS3	Differential Binding + Integrative analysis	1	360	432
Whole Genome Sequencing				
Prices based on projects consisting of 25 samples maximum				
WGS1	Quality control + alignment	0.1	72	86.4
WGS2	SNP calling	0.1	72	86.4
WGS3	Copy number alteration calling	0.05	42	50.4
Whole Exome Sequencing				
Prices based on projects consisting of 25 samples maximum				
WES1	Quality control + alignment	0.1	60	72
WES2	SNP calling	0.1	60	72
WES3	Copy number alteration calling	0.05	36	43.2
Proteomics				
PR1	Quality control	1	90	108
PR2	Differential expression	1	240	288
PR3	GSEA GO and KEGG	1	255	306
Public databases mining/analysis				
PD1	Selection	1	320	384
PD2	Curation of clinical data	1	520	624
PD3	Processing of expression data	1	360	432
PD4	Analysis: association of expression and clinical data/ copy number/ mutations	1	450	540
TCGA analysis				
TCGA1	Exploratory analysis in all cancer types: association between expression and clinical variables	1	660	792
TCGA2	Detailed analysis with curated clinical and technical variables: association with expression	1	720	864
TCGA3	Data integration: copy number, expression, mutations, etc	1	780	936
Microbiome				
MB1	Quality control + OTU estimation + differential abundance	1	750	900
MB2	Phylogenetic analysis	1	270	324
Binding site prediction				
BS1	Prediction of binding sites for a given gene in a set of regions or genome wide	1	360	432
Single Cell Sequencing				
SCS1	Quality control + alignment	0.1	24	28.8
SCS2	Differential expression	1	240	288
SCS3	Clustering + DE expression of clusters	1	600	720
SCS4	GSEA GO and KEGG	1	255	306
Consulting				
CONS1	Consulting / data analysis / custom service	1	102	122.4
Mandatory items for all services				
SETUP	Initial meeting + experimental design + results delivery	1	180	216