Service Code	Description	Public Institutions	Private companies
Microarrays	**Prices based on projects consisting of 50 samples maximum**		
MA1	Quality control	300	360
MA2	Differential expression	420	504
MA3	GSEA GO and KEGG	360	432
MA4	Pattern analysis (gaga)	540	648
MA5	Signature discovery	600	720
RNAseq	**Prices based on projects consisting of 50 samples maximum**		
RNAS1	Quality control + alignment*	60	72
RNAS2	Differential expression gene level	420	504
RNAS3	Differential expression isoform level	420	504
RNAS4	GSEA analysis GO and KEGG	420	504
RNAS5	Pattern analysis (gaga)	540	648
RNAS6	Isoform switching	660	792
RNAS7	SNP calling*	120	144
RIPSeq	**Prices based on projects consisting of 50 samples maximum**		
RIPS1	Quality control + alignment + rRNA cleaning	120	144
RIPS2	RBP site definition + annotation + visualization	600	720
RIPS3	Gene-level / UTR-level binding assessment	600	720
RIPS4	GSEA analysis GO and KEGG	480	576
RIPS5	Regulatory motif search & assessment	600	720
ChipSeq	**Prices based on projects consisting of 50 samples maximum**		
CHS1	Quality control + alignment*	60	72
CHS2	Peak definition + annotation + visualization	600	720
CHS3	Differential Binding + Integrative analysis	720	864
Whole Genome Sequencing	**Prices based on projects consisting of 25 samples maximum**		
WGS1	Quality control + alignment*	180	216
WGS2	SNP calling*	300	360
WGS3	Copy number alteration calling*	300	360
Whole Exome Sequencing	**Prices based on projects consisting of 25 samples maximum**		
WES1	Quality control + alignment*	180	216
WES2	SNP calling*	240	288
WES3	Copy number alteration calling*	240	288
Proteomics			
PR1	Quality control	300	360
PR2	Differential expression	420	504
PR3	GSEA GO and KEGG	360	432
Public databases mining/analysis			
PD1	Selection	600	720
PD2	Curation of clinical data	720	864
PD3	Processing of expression data	660	792
PD4	Analysis: association of expression and clinical data/ copy number/ mutations	720	864
TCGA analysis			
TCGA1	Exploratory analysis in all cancer types: association between expression and clinical variables	900	1080
TCGA2	Detailed analysis with curated clinical and technical variables: association with expression	780	936
TCGA3	Data integration: copy number, expression, mutations, etc	780	936
Microbiome			
MB1	Quality control + OTU estimation + differential abundance	240	288
MB2	Differential analysis	420	504
MB3	Phylogenetic analysis	600	720
Binding site prediction			
BS1	Prediction of binding sites for a given gene in a set of regions or genome wide	420	504
Single Cell Sequencing			
SCS1	Quality control + alignment*	60	72
SCS2	Differential expression	600	720
SCS3	Clustering + DE expression of clusters	480	576
SCS4	GSEA GO and KEGG	420	504
Consulting			
CONS1	Consulting / data analysis / custom service	60	72
STATREV	Statistical revision of publication (per test)	60	72
Mandatory items for all services	**Prices based on projects consisting of 50 samples maximum**		
SETUP	Initial meeting + experimental design + results delivery	600	720

* Items will be charged per sample