	Description	Public Institutions F	rivate companies
Microarrays	Prices based on projects consisting of 50 samples maximum		
MA1	Quality control	300	360
MA2	Differential expression	420	50-
MA3	GSEA GO and KEGG	360	433
MA4	Pattern analysis (gaga)	540	64
MA5	Signature discovery	600	72
DNIA	Di 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
RNAseq	Prices based on projects consisting of 50 samples maximum	40	7
RNAS1	Quality control + alignment*	60 420	7.
RNAS2 RNAS3	Differential expression gene level Differential expression isoform level	420	50
RNAS4	GSEA analysis GO and KEGG	420	50 50
RNAS5	Pattern analysis (gaga)	540	64
RNAS6	Isoform switching	660	79
RNAS7	SNP calling*	120	14
RIPSeq	Prices based on projects consisting of 50 samples maximum		
RIPS1	Quality control + alignment + rRNA cleaning	120	14
RIPS2	RBP site definition + annotation + visualization	600	72
RIPS3	Gene-level / UTR-level binding assessment	600	72
RIPS4	GSEA analysis GO and KEGG	480	57
RIPS5	Regulatory motif search & assessment	600	72
Cl · C			
ChipSeq	Prices based on projects consisting of 50 samples maximum	40	
CHS1	Quality control + alignment*	60	7.
CHS2 CHS3	Peak definition + annotation + visualization Differential Binding + Integrative analysis	600 720	72 86
CH53	Differential binding + integrative analysis	720	86
Whole Genome Sequencing	Prices based on projects consisting of 25 samples maximum		
WGS1	Quality control + alignment*	180	21
WGS2	SNP calling*	300	36
WGS3	Copy number alteration calling*	300	360
Whole Exome Sequencing	Prices based on projects consisting of 25 samples maximum		
WES1	Quality control + alignment*	180	21
WES2	SNP calling*	240	28
WES3	Copy number alteration calling*	240	28
Proteomics			
PR1	Quality control	300	360
PR2	Differential expression	420	50
PR3	GSEA GO and KEGG	360	433
Public databases mining/analysis			
PD1	Selection	600	72
PD2	Curation of clinical data	720	86
PD3	Processing of expression data	660	79
PD4	Analysis: association of expression and clinical data/		
	copy number/ mutations	720	86-
TCGA analysis			
TCGA1	Exploratory analysis in all cancer types: association		
	Exploratory driatysis in all cancer types, association		
	between expression and clinical variables	900	108
TCGA2	between expression and clinical variables	900	108
TCGA2	between expression and clinical variables Detailed analysis with curated clinical and technical	900	108
TCGA2	·	900 780	
TCGA2	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression,	780	93
	Detailed analysis with curated clinical and technical variables: association with expression		93
TCGA3	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression,	780	93
TCGA3 Microbiome	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc	780	93
TCGA3	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential	780	93
TCGA3 Microbiome	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc	780 780	93 93 28
TCGA3 Microbiome MB1	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance	780 780	93 93 28 50
TCGA3 Microbiome MB1 MB2	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis	780 780 240 420	93i 93i 28i 50
Microbiome MB1 MB2 MB3 Binding site prediction	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis	780 780 240 420	93i 93i 28i 50
Microbiome MB1 MB2 MB3	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set	780 780 240 420 600	93 93 28 50 72
Microbiome MB1 MB2 MB3 Binding site prediction	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis	780 780 240 420	93 93 28 50 72
Microbiome MB1 MB2 MB3 Binding site prediction BS1	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set	780 780 240 420 600	93 93 28 50 72
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide	780 780 240 420 600	93 93 28 50 72
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment*	780 780 240 420 600	93i 93i 28i 50i 72i
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression	780 780 240 420 600 420	93 93 28 50 72 50
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS3	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters	780 780 240 420 600 420 600 600 480	93 93 28 50 72 50
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression	780 780 240 420 600 420	93 93 28 50 72 50
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS2 SCS3 SCS4	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters	780 780 240 420 600 420 600 600 480	93 93 28 50 72 50
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS3 SCS4 Consulting	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters GSEA GO and KEGG	780 780 240 420 600 420 600 480 420	93 93 28 50 72 50 7 7 72 57 50
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS2 SCS3 SCS4	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters GSEA GO and KEGG	780 780 240 420 600 420 600 600 480	93i 93i 28i 50i 72i 50i 77: 72i 57i 50i
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS3 SCS4 Consulting CONS1	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters GSEA GO and KEGG	780 780 240 420 600 420 600 480 420	93i 93i 28i 50i 72i 50i 77: 72i 57i 50i
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS3 SCS4 Consulting CONS1	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters GSEA GO and KEGG Consulting / data analysis / custom service Statistical revision of publication (per test)	780 780 240 420 600 420 600 480 420	93i 93i 28i 50i 72i 50i 77: 72i 57i 50i
Microbiome MB1 MB2 MB3 Binding site prediction BS1 Single Cell Sequencing SCS1 SCS2 SCS3 SCS4 Consulting CONS1 STATREV	Detailed analysis with curated clinical and technical variables: association with expression Data integration: copy number, expression, mutations, etc Quality control + OTU estimation + differential abundance Differential analysis Phylogenetic analysis Prediction of binding sites for a given gene in a set of regions or genome wide Quality control + alignment* Differential expression Clustering + DE expression of clusters GSEA GO and KEGG	780 780 240 420 600 420 600 480 420	108i 93i 93i 28i 50- 72i 57: 72i 57: 77:

^{*} Items will be charged per sample