LCGC Sequencing Price List@2021				
Service Type	**Unit**	**Deliverables**		**LCGC List Price**
Purified Plasmid/PCR Product Sequencing Service	Reaction	High quality ~800 bases per reaction with chromatogram and fasta file.		522.38
Unpurified Plasmid/PCR Product Sequencing Service	Reaction	Purification of PCR product and High quality ~800 bases per reaction with chromatogram and fasta file.		835.80
Primer Walk Sequencing Service	Nucleotide (Base)	Report containing consensus sequence of entire product, with chromatograms and fasta files.	upto 1.5kb	3,134.25
Microbial Identification service (MID)				-
MID-S:- Microbial Identification of Bacteria /Yeast/ Fungus	Sample	Sequencing data of ribosomal genes or other regions of <1500 bp with chromatogram and fasta file.	DNA extraction - INR 500+	6,268.50
MID-C:- Microbial Identification of Bacteria/Yeast/ Fungus	Sample	Sequencing data of ribosomal genes or other regions of <1500 bp and Contig Report with chromatogram and fasta file.	DNA extraction - INR 500+	6,268.50
MID-R:- Microbial Identification of Bacteria/Yeast/ Fungus	Sample	Sequencing data of ribosomal genes or other regions of <1500 bp. comprehensive report includes genus and species level identification with top10 matches, electrophoretogram, phylogenetic tree and distance matrix for representation of the relationships, to obtain organism lineage and taxonomy	DNA extraction - INR 500+	6,268.50
Instrument Run on MiSeq				
Service Type	Unit	Chemistry	Data output	
MiSeq-Lane-PE300	Lane	2X300	~15 Gb/ 25M PE Reads	4,26,258.00
Instrument Run on HiSeq				
HiSeq-Lane-PE150	Lane	2x150	~110 Gb	2,29,845.00
HiSeq-Lane-PE250	Lane	2x250	~75 Gb	9,27,738.00
HiSeq-Lane- SE50	Lane	1x50	~12 Gb	1,48,354.50
Whole Genome Sequencing on Illumina MiSeq				
MiSeq-WGS-10Gb-PE	Sample	2X300/2x250	~10 Gb/13-15 Million PE Reads	5,55,221.94
MiSeq-WGS-6Gb-PE	Sample	2X300/2x250	~6 Gb/11-12 Million PE Reads	2,92,530.00
MiSeq-WGS-4Gb-PE	Sample	2X300/2x250	~4 Gb/7-8 Million PE Reads	1,85,073.28
MiSeq-WGS-3Gb-PE	Sample	2X300/2x250	~3 Gb/5-6 Million PE Reads	1,38,805.49
MiSeq-WGS-2Gb-PE	Sample	2X300/2x250	~2 Gb/3-4 Million PE Reads	1,11,044.39
Whole Genome Sequencing on Illumina HiSeq				
HiSeq-WGS-30Gb-PE	Sample	2X150	~30 Gb/90-100 Million PE Reads	1,62,981.00
HiSeq-WGS-20Gb-PE	Sample	2X150	~20 Gb/60-70 Million PE Reads	64,774.50
HiSeq-WGS-15Gb-PE	Sample	2X150	~15 Gb/45-50 Million PE Reads	55,371.75
HiSeq-WGS-10Gb-PE	Sample	2X150	~10 Gb/32-36 Million PE Reads	43,879.50
HiSeq-WGS-7.5Gb-PE	Sample	2X150	~7.5 Gb/22-25 Million PE Reads	37,611.00

HiSeq-WGS-5Gb-PE	Sample	2X150	~5 Gb/11-16 Million PE Reads	32,387.25
HiSeq-WGS-2.5Gb-PE	Sample	2X150	~2.5 Gb/5-8 Million PE Reads	27,163.50
Whole Transcriptome Sequencing on Illumina MiSeq				
MiSeq-RNASeq-5Gb	Sample	2X150	~6 Gb/13-15 Million PE Reads	2,86,783.88
MiSeq-RNASeq-2.5Gb	Sample	2X150	~6 Gb/7-8 Million PE Reads	1,43,391.94
MiSeq-RNASeq-2Gb	Sample	2X150	~6 Gb/5-6 Million PE Reads	95,594.63
MiSeq-RNASeq-1Gb	Sample	2X150	~6 Gb/2.5-3 Million PE Reads	1,14,922.50
Whole Transcriptome Sequencing on Illumina HiSeq				
HiSeq-RNASeq-10Gb	Sample	2X150	~10 Gb/45-50 Million PE Reads	43,879.50
HiSeq-RNASeq-8Gb	Sample	2X150	~8 Gb/36-40 Million PE Reads	39,282.60
HiSeq-RNASeq-6Gb	Sample	2X150	~6 Gb/28-30 Million PE Reads	33,432.00
HiSeq-RNASeq-4Gb	Sample	2X150	~4 Gb/18-20 Million PE Reads	31,342.50
HiSeq-RNASeq-2Gb	Sample	2X150	~2 Gb/9-10 Million PE Reads	25,074.00
16S/ITS/18S Amplicon Sequencing				
MiSeq-16SMetaG-150Mb	Sample	2X300/2x250	~100-150 Mb/0.15-0.25 Million PE Reads	18,805.50
MiSeq-16SMetaG-150Mb	Sample	2X300/2x250	~200-300 Mb/0.3-0.5 Million PE Reads	37,611.00
XGC-HiSeq-16SMetaG-150Mb	Sample	2X250	~100-150 Mb/0.3 Million PE Reads	16,298.10
XGC-HiSeq-16SMetaG-150Mb	Sample	2X250	~200-300 Mb/0.6 Million PE Reads	29,253.00
Mitochondrial DNA Sequencing on Illumina HiSeq				
HiSeq-Mito3G	Sample	2X150	~ 3 Gb/8-10 Million PE Reads	11,701.20
HiSeq-Mito2G	Sample	2X150	~ 2 Gb/5-6 Million PE Reads	11,701.20
HiSeq-Mito1G	Sample	2X150	~1 Gb/3-3.2 Million PE Reads	11,701.20
ChIP Sequencing				
NextSeq-ChIPSeq-20-1	Sample	2X150	~6 Gb/20 Million PE Reads	62,685.00
NextSeq-ChIPSeq-10-1	Sample	2X150	~3 Gb/10 Million PE Reads	54,849.38
HiSeq-ChIPSeq-20-1	Sample	2X150	~6 Gb/20 Million PE Reads	62,685.00
HiSeq-ChIPSeq-10-1	Sample	2X150	~3 Gb/10 Million PE Reads	52,237.50
Whole exome Sequencing				
NextSeq-ExomeSeq	Sample	2X150	~4Gb/20 Million PE Reads	73,132.50
NextSeq-Clinical ExomeSeq	Sample	2X150	~5Gb/20 Million PE Reads	94,027.50
Microarray services				
One-color gene expression profiling	Array	Sample labeling, Hybridization, Run QC	8x60K	3,980.00
Two-color gene expression profiling	Array	Sample labeling, Hybridization, Run QC	8x60K	4,975.00
Custom designed gene expression profiling	Array	Sample labeling, Hybridization, Run QC	8x60K	4,975.00

CGH & CNV arrays (1M)	Array	Sample labeling, Hybridization, Run QC	1x1M	9,950.00
CGH & CNV arrays (180K)	Array	Sample labeling, Hybridization, Run QC	4x180K	4,378.00
CGH & CNV arrays (15K)	Array	Sample labeling, Hybridization, Run QC	8x15K	2,985.00
miRNA profiling	Array	Sample labeling, Hybridization, Run QC	8x15K	3,582.00
Splice variant analysis	Array	Sample labeling, Hybridization, Run QC	8x15K	3,980.00
Chip-on-chip 1M	Array	Sample labeling, Hybridization, Run QC	1x1M	9,552.00
Chip-on-chip 400K	Array	Sample labeling, Hybridization, Run QC	2x400K	6,965.00
Methylation profiling 244K	Array	Sample labeling, Hybridization, Run QC	2x244K	8,955.00
Methylation profiling 105K	Array	Sample labeling, Hybridization, Run QC	2x105K	6,368.00
Nucleic Acid Extraction Services				
DNA extraction for Genotyoing	Sample	DNA extraction, Nanodrop QC	Extraction Report	2,089.50
DNA extraction for NGS library prep	Sample	DNA extraction, Nanodrop/ Qubit, Tapestation QC	Extraction Report	4,179.00
RNA extraction for Microarray	Sample	RNA extraction, Nanodrop/ Qubit, Tapestation QC	Extraction Report	7,313.25
RNA extraction for NGS library prep	Sample	RNA extraction, Nanodrop/ Qubit, Tapestation QC	Extraction Report	10,447.50
small RNA extraction for NGS library prep	Sample	RNA extraction, Nanodrop/ Qubit, Tapestation QC	Extraction Report	16,716.00
Bioinformatics Analysis				
Prokaryotes: WGS-Denovo	Sample	1Gb data	Raw data ----> Report	16,716.00
Prokaryotes: WGS-Resequencing	Sample	1Gb data	Raw data ----> Report	14,626.50
Eukaryotes: WGS-Denovo	Sample	1Gb data	Raw data ----> Report	20,895.00
Eukaryotes: WGS-Resequencing	Sample	1Gb data	Raw data ----> Report	18,805.50
Eukaryotes: WGS-Targeted/Exome	Sample	1Gb data	Raw data ----> Report	16,716.00
Prokaryotes: Transcriptome-Resequencing	Sample	1Gb data	Raw data ----> Report	14,626.50
Eukaryotes: Transcriptome-Resequencing	Sample	1Gb data	Raw data ----> Report	16,716.00
Eukaryotes: Transcriptome-Denovo	Sample	1Gb data	Raw data ----> Report	20,895.00
ChIP Sequencing	Sample	1Gb data	Raw data ----> Report	20,895.00
Metagenome Sequencing	Sample	1Gb data	Raw data ----> Report	12,537.00
SmallRNA/miRNA Sequencing	Sample	1Gb data	Raw data ----> Report	14,626.50
Microbiome Sequencing	Sample	10Gb data	Raw data ----> Report	31,342.50
Bisulphite Sequencing	Sample	10Gb data	Raw data ----> Report	25,074.00
Microarray - Gene expression	Sample	60k, 15k, 1M data	Raw data ----> Report	10,447.50
Microarray - ChIP-Chip analysis	Sample	60k, 15k, 1M data	Raw data ----> Report	10,447.50
Microarray - Methylation analysis	Sample	60k, 15k, 1M data	Raw data ----> Report	10,447.50
Microarray - CGH analysis	Sample	60k, 15k, 1M data	Raw data ----> Report	10,447.50
Microarray - custom data analysis	Sample	60k, 15k, 1M data	Raw data ----> Report	10,447.50