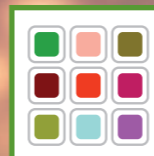


Standard Bioinformatics Analysis for Bacterial Whole Genome and Eukaryotic RNA Sequencing



Next-Generation Sequencing

Bacteria Whole Genome Sequencing (HiSeq 150 PE)

Standard Bioinformatics Analysis - Bacterial Whole Genome Sequencing
Reference Mapping / de novo Assembly
Gene Component Analysis: Gene Annotation/ Gene Structure Prediction Repeat Sequences Non-coding RNAs
Gene Function Annotation: NR GO COG KEGG

Eukaryotic RNA-seq (HiSeq 150 PE)

Standard Bioinformatics Analysis - Eukaryotic RNA Sequencing with Reference Genome
Reference Mapping
Gene Expression Quantification
Correlation Analysis (For biological replicates only)
Differential Expression Analysis (For two or more groups of samples)
GO Enrichment Analysis of Differentially Expressed Genes (DEGs) (For two or more groups of samples)
KEGG Pathway Enrichment Analysis of Differentially Expressed Genes (DEGs) (For two or more groups of samples)

Standard Bioinformatics Analysis - Eukaryotic RNA Sequencing without Reference Genome
de novo Assembly
Gene Functional Prediction using 7 Databases – NR, NT, KOG, KO, Swiss-Prot, GO and PFAM
GO, COG, KEGG Classification
CDS Prediction
Gene Expression Analysis
Correlation Analysis (For biological replicates only)
Differential Expression Analysis (For two or more groups of samples)
GO Enrichment Analysis of Differentially Expressed Genes (DEGs) (For two or more groups of samples)
KEGG Pathway Enrichment Analysis of Differentially Expressed Genes (DEGs) (For two or more groups of samples)

More NGS services are available, please contact our local distributor for your NGS enquiries.

Product Highlights: Next Generation Sequencing for Amplicon, Bacterial Whole Genome and Eukaryote transcriptome

Amplicon Sequencing

16S/ 18S/ ITS metagenomics amplicon sequencing with free standard bioinformatics analysis, which are OTU clustering & filtering, species annotation, Alpha & Beta Diversity at 3 choices:

- (i) 30,000 raw tags (~ 60,000 reads)
- (ii) 50,000 raw tags (~ 100,000 reads)
- (iii) 100,000 raw tags (~ 200,000 reads)

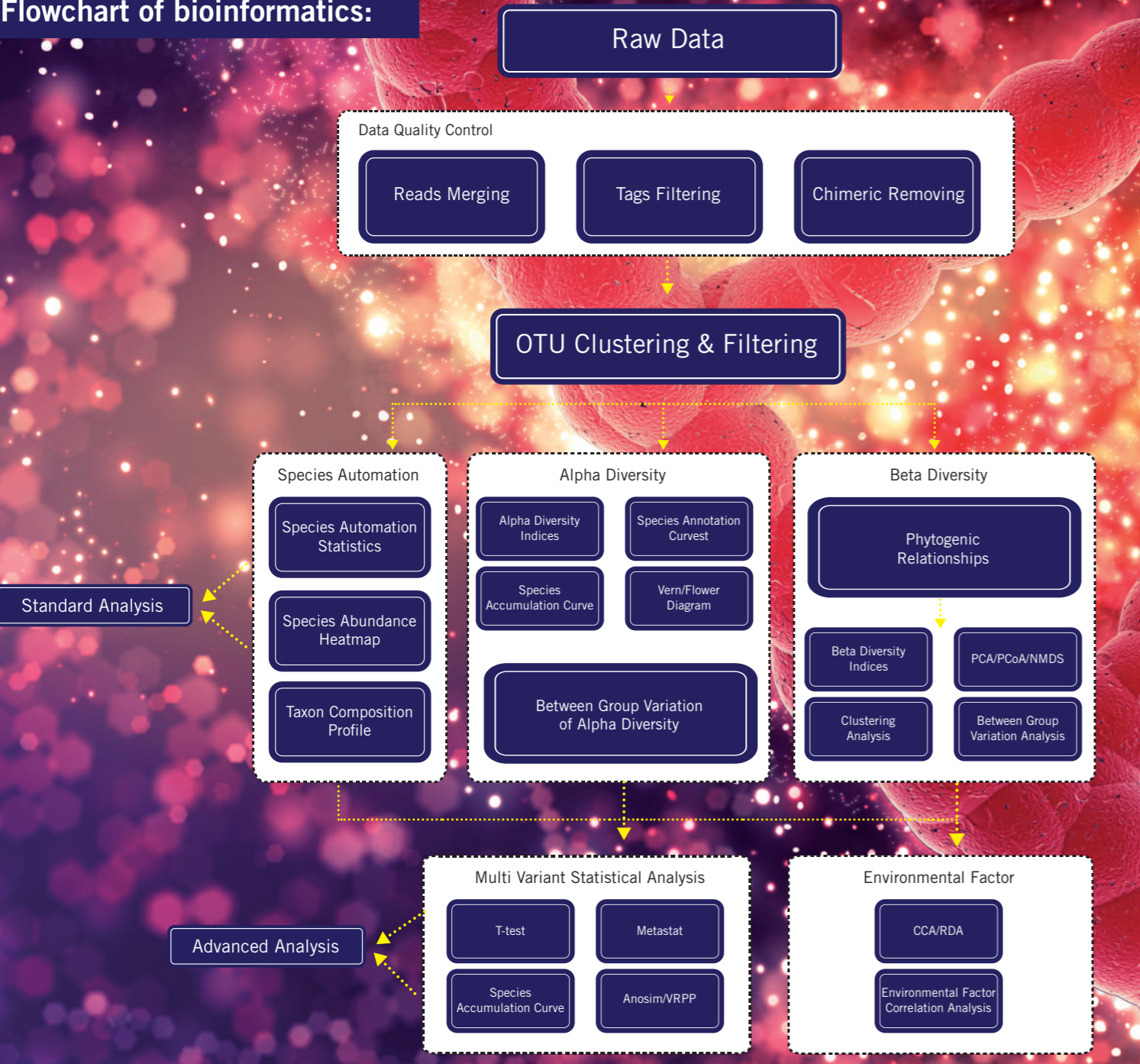
Various choice of Primers:

Types	Region	Fragment Length	Primer
Bacterial16S	V4	292 bp	515F
			806R
	*V3-V4	466 bp	341F
			806R
	V4-V5	393 bp	515F
			907R
Archaeal16S	*V4	288 bp	U519F
			806R
Fungal18S	V4	179 bp	528F
			706R
	V9	131 bp	1380F
			1510R
Fungal ITS	ITS1	307 bp	ITS5-1737F
			ITS5-1737F
	*ITS2	386 bp	ITS3
			ITS4

*Popular choices

For ordering and enquiries, please contact local distributor:





1) Higher quality of Q30 in HiSeq vs MiSeq

Actual sequencing quality by HiSeq 250 PE run:

Sample Name	Raw PE(#)	Combined(#)	Qualified(#)	Nochime(#)	Base(nt)	AvgLen(nt)	Q20	Q30	GC%	Effective%
Sample 1	128,890	123,477	113,269	99,409	42,595,983	428	98.75	97.41	52.54	77.13
Sample 2	122,870	117,054	107,045	88,166	37,670,275	427	98.74	97.43	53.23	71.76
Sample 3	125,694	118,185	106,892	72,944	31,134,638	427	98.64	97.24	53.31	58.03
Sample 4	122,638	117,109	106,980	98,734	42,109,339	426	98.65	97.21	53.35	80.51
Sample 5	122,202	116,784	106,616	92,986	39,725,135	427	98.63	97.16	53.4	76.09
Sample 6	127,001	120,838	109,699	92,529	39,627,392	428	98.64	97.14	54.09	72.86
Sample 7	120,609	115,370	107,529	98,473	40,584,142	412	98.74	97.4	54.4	81.65
Sample 8	125,129	118,791	108,041	96,099	41,188,943	429	98.75	97.41	52.71	76.8
Sample 9	126,076	119,714	108,762	95,033	40,720,930	428	98.77	97.43	53.16	75.38
Sample 10	130,996	124,552	113,130	101,222	43,351,395	428	98.76	97.41	52.51	77.27

Actual sequencing quality by MiSeq 300 PE run:

Table 1. Raw data Stats

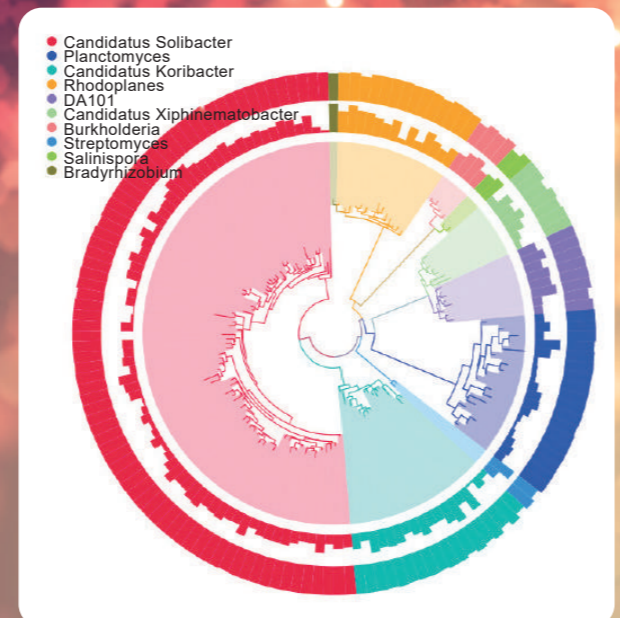
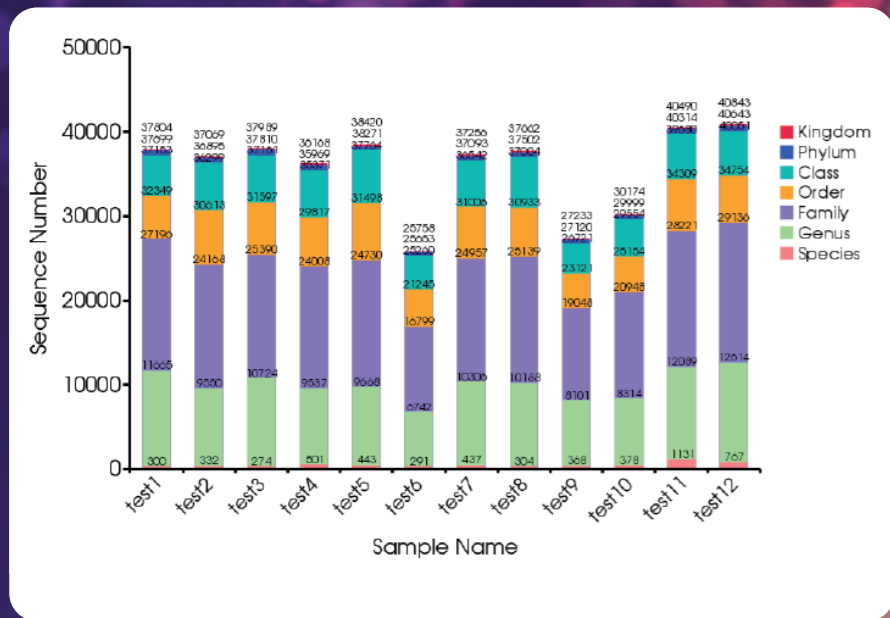
Sample ID	Total read bases (bp)	Total reads	CC(%)	AT(%)	Q20(%)	Q30(%)
1	256,529,762	858,212	58.233	41.77	75.286	60.508
2	236,175,031	786,836	58.398	41.6	75.259	60.508
3	231,879,252	772,820	58.410	41.59	75.262	60.546
4	263,438,836	879,626	58.954	41.05	75.406	60.611
5	250,572,014	837,304	59.149	40.85	75.891	61.186
6	278,201,129	929,298	59.450	40.55	75.110	60.201
7	321,024,326	1,074,090	57.810	42.19	75.249	60.536
8	272,400,636	910,644	58.150	41.85	74.950	60.049
9	260,691,692	869,800	58.619	41.38	74.840	59.910
10	289,893,547	967,216	57.476	42.52	75.123	60.295
11	265,199,289	883,502	57.196	42.8	75.552	60.874
12	241,720,364	805,268	57.339	42.66	75.345	60.633

2) Higher alignment efficiency from hypervariable regions

	RawR1 Q20%	RawR1 Q30%	RawR2 Q20%	RawR2 Q30%	Alignment Efficiency in %
HiSeq 250 PE	88.27	83.22	88.13	83.25	73.12
MiSeq 300 PE	88.48	78.96	89.42	80.37	49.39

3) Higher throughput and thus lower cost to run in HiSeq

Examples of charts in 16s metagenomics report



Note: The request of BI advanced analysis, which are multi-variant statistical and environmental factor is available at separate charges.