fds 1/14/2010 version 3

Product Sheet (call or email Dr. Ryan Kim for pricing 505-995-4419 / rwk@ncgr.org) 10% off prepaid orders

Packages

Whole Genome Sequencing (WGS)	includes sample prep, ~30x's coverage (~90Gbp) , SNP report.
Exome sequencing	includes sample enrichment, ~100x's coverage (~4Gbp), SNP and target coverage reports.

Ala carte

PacBioRS

Library Prep	Long read or circular consensus

Sequencing	**~ read length (bp)**	**~ Mbp/SMRTCell**	**Automated preliminary draft assembly**
long read	1000	15	included
circ. consensus	150	2.25	N/A

ILLUMINA LIBRARY PREP

Low-throughput	RNA / smRNA / DNA / ChIP
Low-throughput	DSN RNA
Low-throughput	Long insert / mate-pair
High-throughput	48 samples well-plate format

ILLUMINA GAIIx

- o Flexible for low and high-throughput needs, single & multiple lane needs
- o Up to 12-plex per lane
- o Typically faster turnaround times then HiSeq

single / paired	by	cycles		Average passing reads per lane	~Gbp / lane
1	x	36		25,000,000	0.9
1	x	54		25,000,000	1.4
1	x	72		25,000,000	1.8
1	x	90		25,000,000	2.3
1	x	108		25,000,000	2.7
1	x	125		25,000,000	3.1
2	x	36		25,000,000	1.8
2	x	54		25,000,000	2.7
2	x	72		25,000,000	3.6
2	x	90		25,000,000	4.5
2	x	108		25,000,000	5.4
2	x	125		25,000,000	6.3
2	x	150		25,000,000	7.5

ILLUMINA HiSeq 2000

- o Good for high-throughput needs, multiple lane needs
- o Up to 12-plex per lane
- o Turnaround time dependent on projects ability to fill all lanes of flowcell (or wait for other projects to fill flowcell).

		cycles		Average passing reads per lane	~Gbp / lane
1	x	50		80,000,000	4
1	x	100		80,000,000	8
2	x	50		80,000,000	8
2	x	100		80,000,000	16
2	x	125		80,000,000	20
2	x	150		80,000,000	24

INFORMATICS

Award winning Alpheus variant, expression, and target detection

References	*Mouse, Human, Rat, Arabidopsis, Medicago, Soy, Maize*
	Reports only
	Website/DB version
	Custom analysis available

GENOTYPING

Choose chips to use below and call for pricing. Discount on large quantities.

Ag http://www.illumina.com/applications.ilmn#whole_genome_genotyping_and_copy_number_variation_analysis

Human http://www.illumina.com/applications.ilmn#whole_genome_genotyping_and_copy_number_variation_analysis

Other services, please inquire