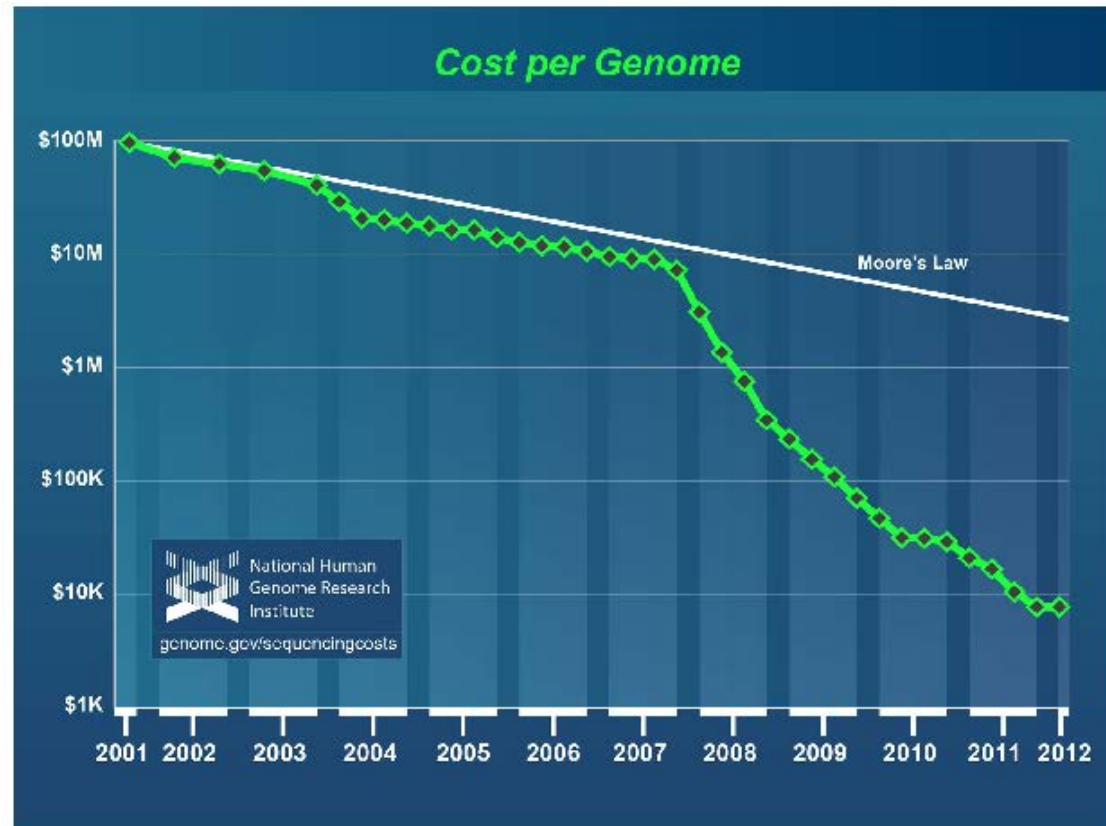
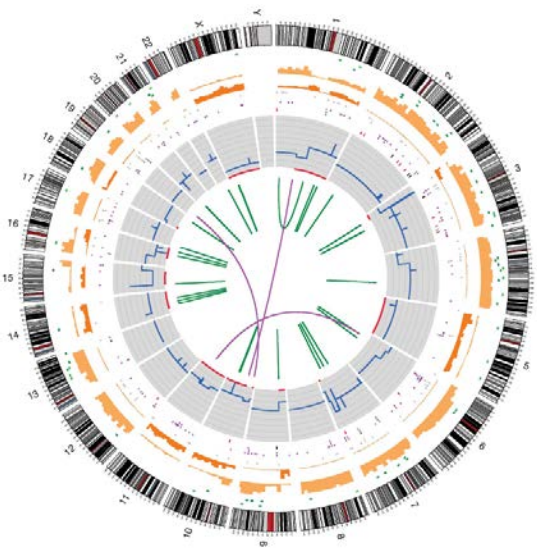




Gene Regulation in
Complex Human Disease



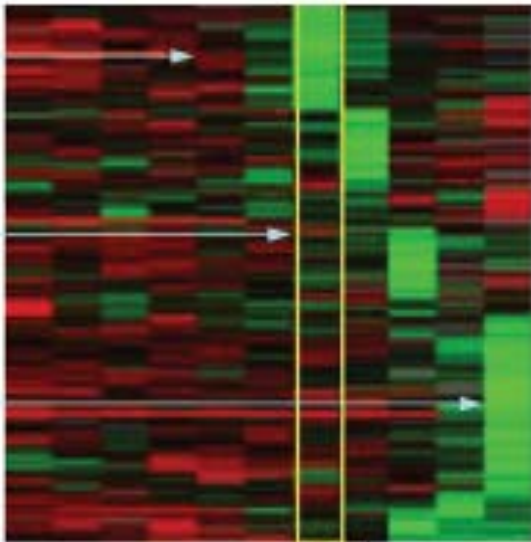
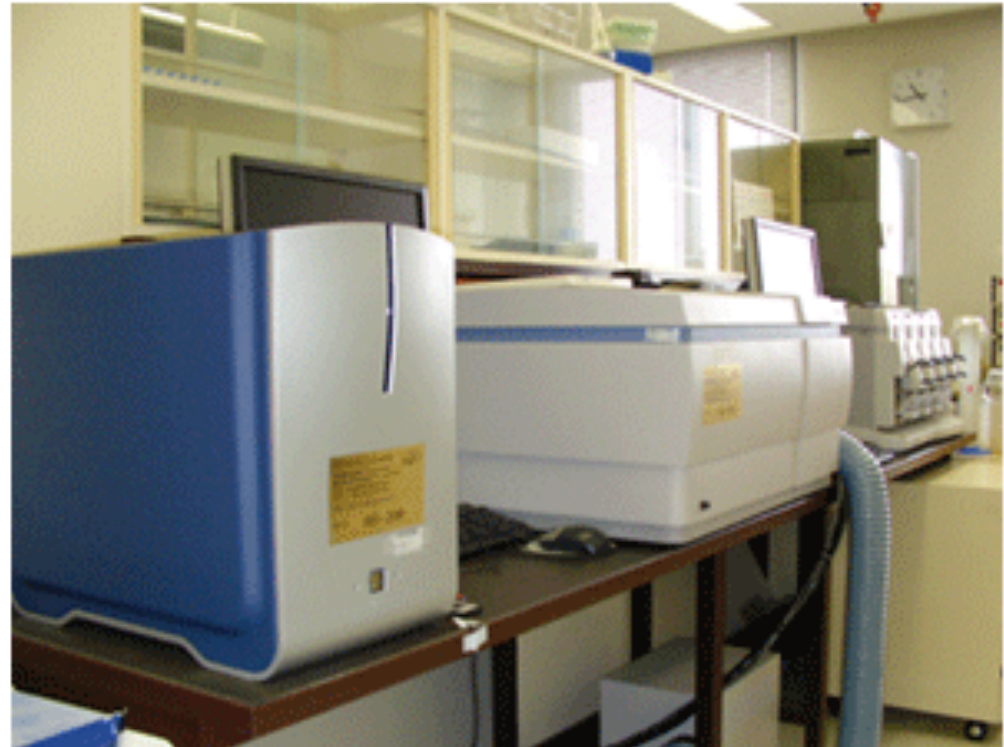
I-CORE Gene Regulation in Complex Human Disease



I-CORE
Israeli Centers of Research Excellence

I-CORE Genomics Center

DNA Microarray Technology



MiSeq Personal Sequencer

Illumina MiSeq



MiSeq System Performance Parameters

Read Length	Total Time*	Output
1 × 36 bp	~4 hours	540–610 Mb
2 × 25 bp	~5.5 hours	750–850 Mb
2 × 100 bp	~16.5 hours	3.0–3.4 Gb
2 × 150 bp	~24 hours	4.5–5.1 Gb
2 × 250 bp	~39 hours	7.5–8.5 Gb
2 × 300 bp**	> 48 hours	~15 Gb

Reads Passing Filter[†]

	Current	Future ^{**}
Single Reads	12–15 M	22–25 M
Paired-End Reads	24–30 M	44–50 M

Quality Scores^{††}

- > 90% bases higher than Q30 at 1 × 36 bp
- > 90% bases higher than Q30 at 2 × 25 bp
- > 85% bases higher than Q30 at 2 × 100 bp
- > 80% bases higher than Q30 at 2 × 150 bp
- > 75% bases higher than Q30 at 2 × 250 bp
- > 70% bases higher than Q30 at 2 × 300 bp**

Illumina HiSeq 2500



HiSeq 2500 Preliminary Performance Parameters*

Performance Parameter	High Output Mode	Rapid Run Mode	
Read length (bp)	2 × 100	2 × 100	2 × 150
Yield (Gb)	~600	~120	~180
Run time	~11 days	~27 hours	~39 hours
Bases > Q30	> 80%	> 80%	> 75%
Reads passing filter	> 90%	> 90%	> 90%
Number of flow cells	2	2	2
Lanes/flow cell	8	2	2
Cluster generation	cBot	onboard	onboard

*Anticipated performance specifications based on development instrument, subject to change.

Ion Proton

Human-scale genome sequencing

Whole transcriptome sequencing

Methylation analysis

Small genome sequencing

Small RNA sequencing

ChIP sequencing

Exome sequencing

Gene expression by sequencing

De novo sequencing

Gene sequencing



Ion Torrent

Barcoding solutions

384 barcodes supported by Torrent Suite Software

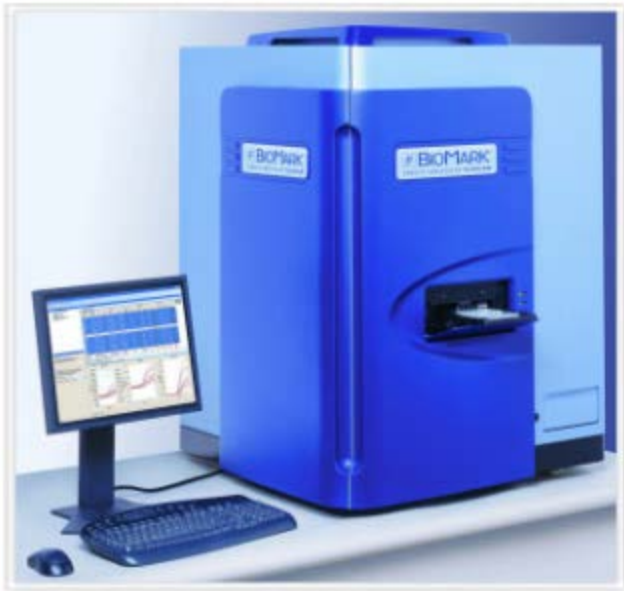
96 off-the-shelf barcodes for DNA

16 off-the-shelf barcodes for RNA

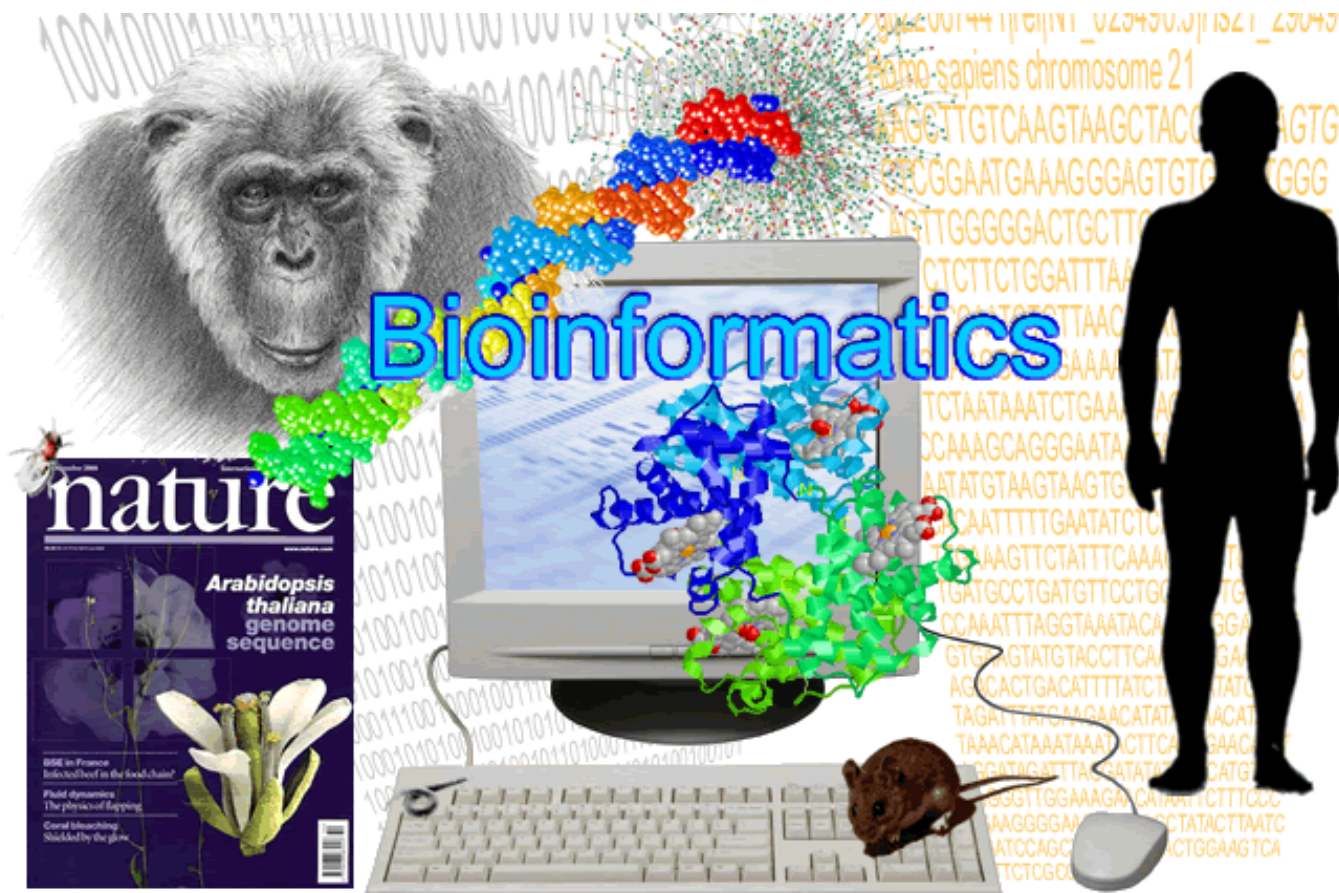


Ion Proton™ System performance specifications with Ion PI™ Chip	
Throughput	Up to 10 Gb (Note: The Ion PII™ Chip* will be available about six months after the Ion PI™ Chip. Ion PII™ Chip* will enable sample-to-variant analysis of a human genome in a single day, at up to 20x coverage.)
Read length	Up to 200-base fragment reads
Number of reads passing filter	60-80 million reads passing filter
Sequencing run time	2-4 hours

Fluidigm



I-CORE Genomics Center



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