

Introduction to high-throughput deep-sequencing platforms: 454 (Roche), SOLiD (ABI) en Solexa (Illumina)

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Researcher: which mutations in a genomic region "REG" cause disease "DIS" ?

Experiment: ?? how do we collect data about the DNA sequence?

Inspiration from cell biology: <http://www.youtube.com/watch?v=983lhh20rGY>



Sequencing-by-synthesis:

Can we also read the genome base-by-base and output not mRNA but a text-file?



1. Speaking the Language

2. Mastering the Lab

3. Understanding Data Files

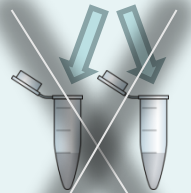
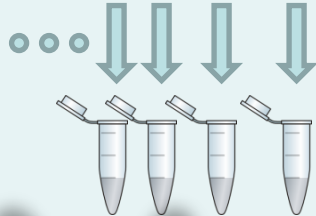


4. Playing the Game!

Sample preparation

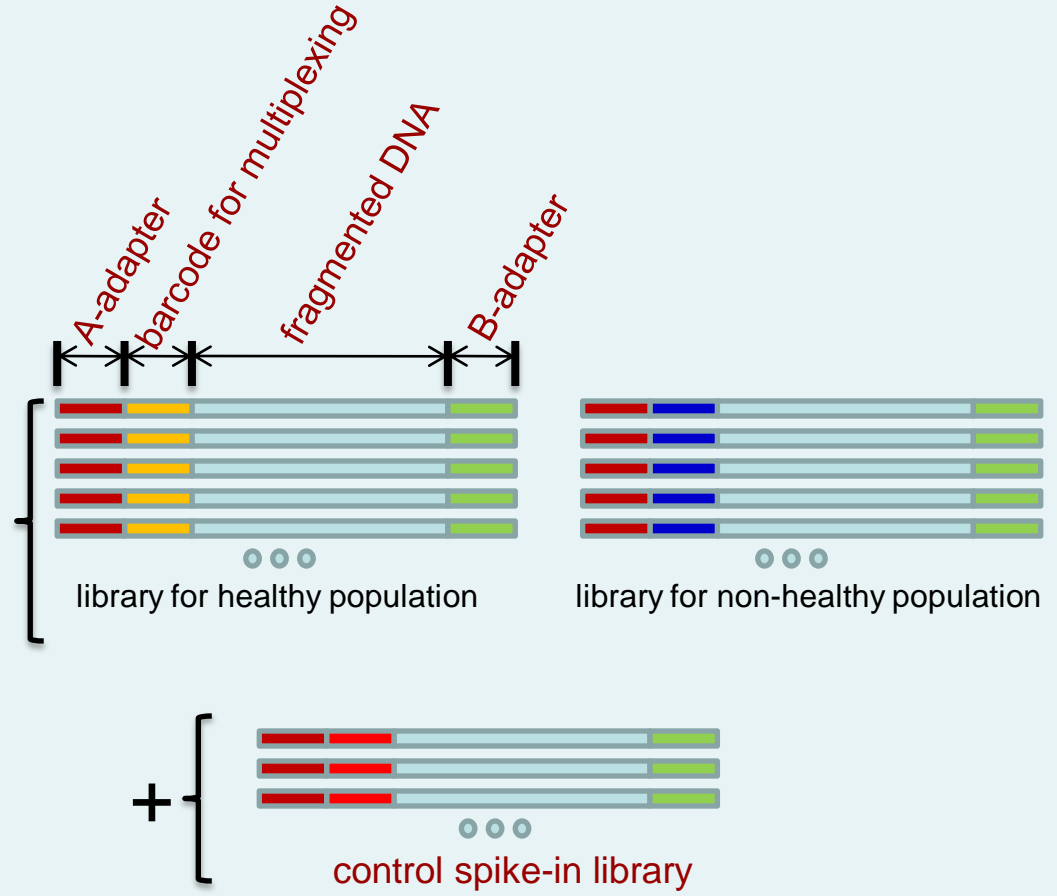


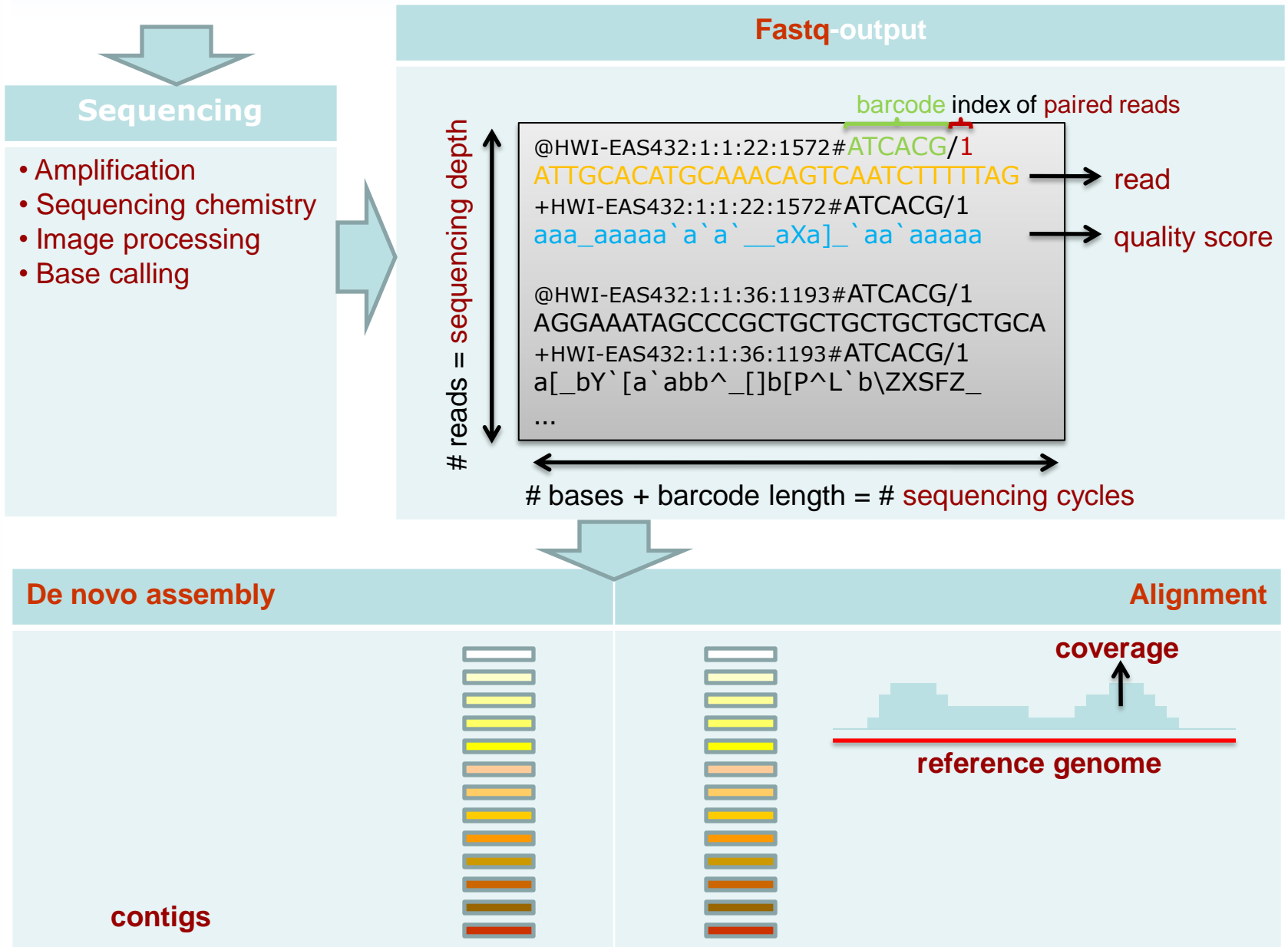
biological replicates



~~technical replicates~~

Library preparation





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	GS FLX Titanium	GA IIx Solexa	SOLiD 3 Plus
Sample requirements	>5 µg of dsDNA in a 10 µL volume	0.1-1µg of dsDNA ; 10µg for mate pairs	10ng-5µg of dsDNA ; 5µg-20µg for mate pairs
Multiplexing	16 regions x 12 barcodes	8 lanes x 12 barcodes	2 cells x 8 samples/cell x 16 barcodes
Paired ends separation	3kb-20kb (half of the read length for each end)	200bp-10kb	600bp-10kb
Amplification	Emulsion PCR	Bridge amplification	Emulsion PCR
Sequencing chemistry	Pyrosequencing	Polymerase based sequencing-by-synthesis	Sequencing by ligation
Read length	400 bp average - 500 bp modal (variable)	2 x 35, 50, 75 and 100bp (fixed)	35 and 50 (fixed)
Reads per run	> 1 M	225-250M	>1000M
Mbp per run	400 Mbp – 600 Mbp	25 Gbp	60Gbp
Accuracy	99% accuracy at the 400th base and higher for preceding bases	99,9% accuracy and higher for more than 70% of the bases;	99,9% accuracy and higher for more than 80% of the bases
Specifics	no complex optics or lasers		data is recorded in ABI color space

Introduction video

<http://www.appliedbiosystems.com/solid4>

	SOLiD 3 Plus
Sample requirements	10ng-5µg of dsDNA ; 5µg-20µg for mate pairs
Multiplexing	2 cells x 8 samples/cell x 16 barcodes
Paired ends separation	600bp-10kb
Amplification	Emulsion PCR
Sequencing chemistry	Sequencing by ligation
Read length	35 and 50 (fixed)
Reads per run	>1000M
Mbp per run	60Gbp
Accuracy	99,9% accuracy and higher for more than 80% of the bases
Specifics	data is recorded in ABI color space

Introduction video http://www.illumina.com/technology/sequencing_technology.ilmn

	GA IIx Solexa
Sample requirements	0.1-1µg of dsDNA ; 10µg for mate pairs
Multiplexing	8 lanes x 12 barcodes
Paired ends separation	200bp-10kb
Amplification	Bridge amplification
Sequencing chemistry	Polymerase based sequencing-by-synthesis
Read length	2 x 35, 50, 75 and 100bp (fixed)
Reads per run	225-250M
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Introduction video

<http://www.youtube.com/watch?v=bFNjxKHP8Jc>

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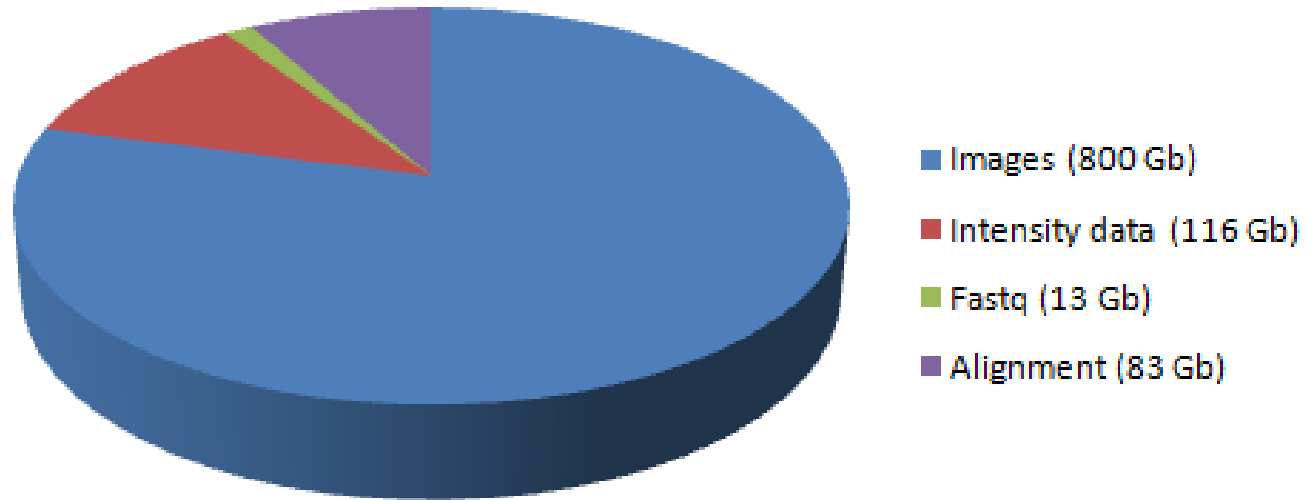
3. Understanding Data Files



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Understanding Data Files

Platform	Solexa – GA II / GAP v1.3
Single reads	1000 Gb for 8 lanes
Paired reads & 76 cycles	4000 Gb for 8 lanes



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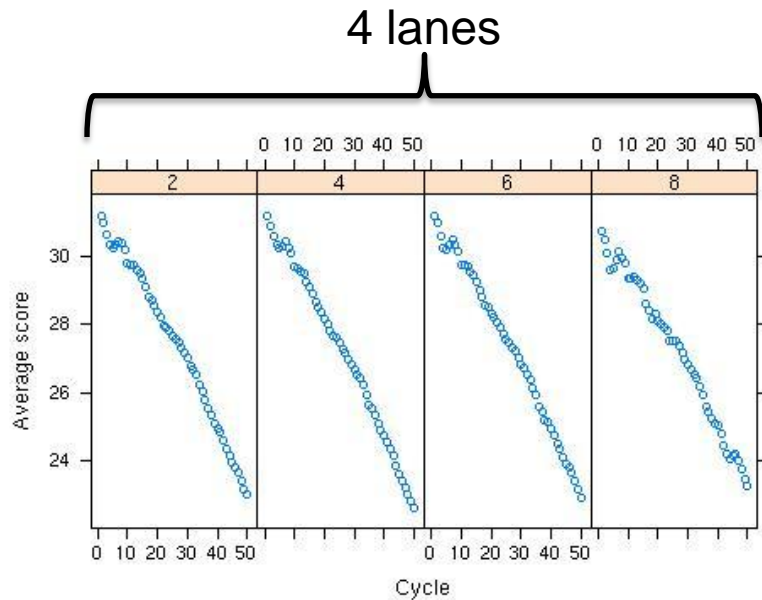
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Playing the Game

Introduction video http://www.illumina.com/technology/sequencing_technology.ilmn

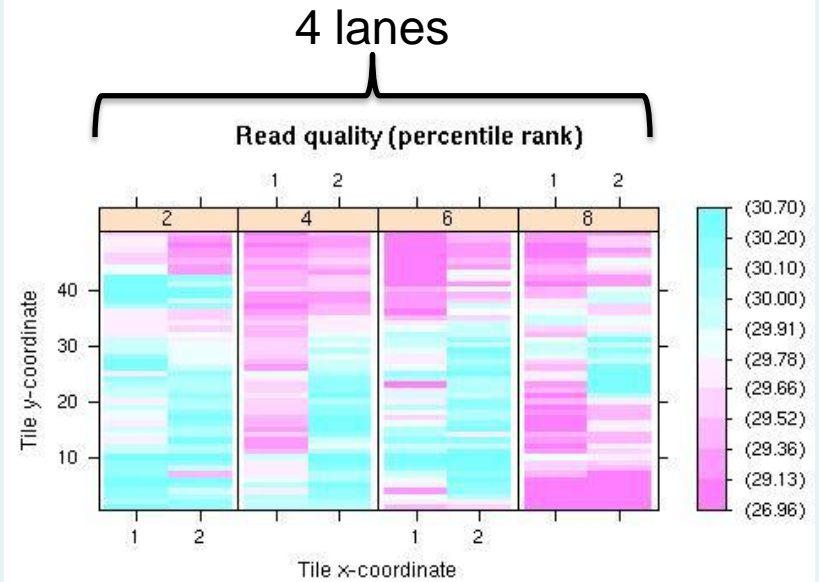
Quality Control Report

Base quality per cycle



50 cycles

Base quality per tile



CCD camera takes pictures of 1 tile at a time

	GS FLX Titanium	GA Iix Solexa	SOLiD 3 Plus
Time per run	10 hours	2 days (2x35) - 9.5 days (2x100)	8.5 days (2x35) - 13 days (2x50)
Cost per run	9,000 EURO	10,000 EURO (1x35) - 35,000 EURO (2x75)	45,000 EURO (1x50)
Cost per Mbp	< 18 EURO	< 1.8 EURO	< 1.8 EURO

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