

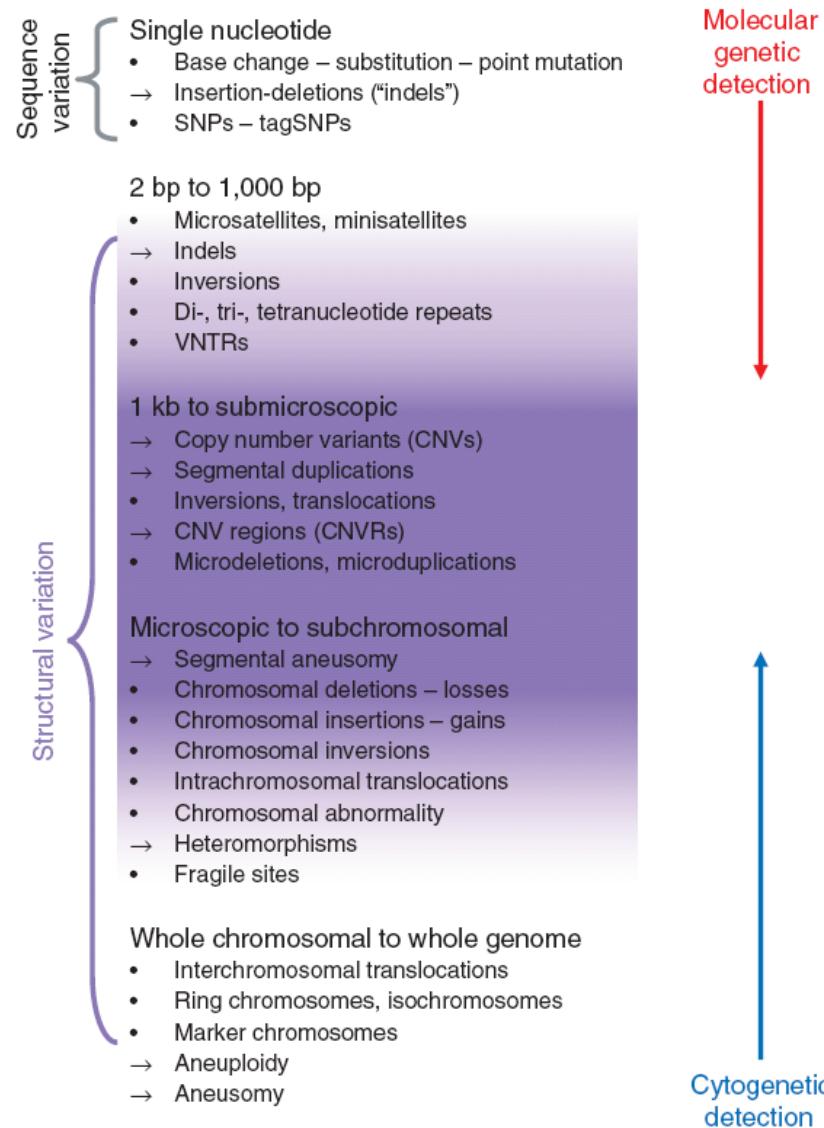
The Human Genome and its Dynamics

Matthias Platzer

Genome Analysis
Leibniz Institute for Age Research
- Fritz-Lipmann Institute (FLI)

Genetic variation

Lexicon



Scherer et al., *Nat Genet Suppl* 39:s7 2007

Genetic variation

Terminology

Mutation

= **event** causing genetic **variation**
substitution, insertion, deletion, inversion

Polymorphism

= **condition** of a **variation**, when it is established
with frequency **$\geq 1\%$** in a **population**

Mutation in medical genetics

= rare variation with a population frequency **<1%**

Genetic variation

Single Nucleotide Polymorphism (SNP)

ATTCGAC**G**TATTG

ATTCG**A**TGTATTG

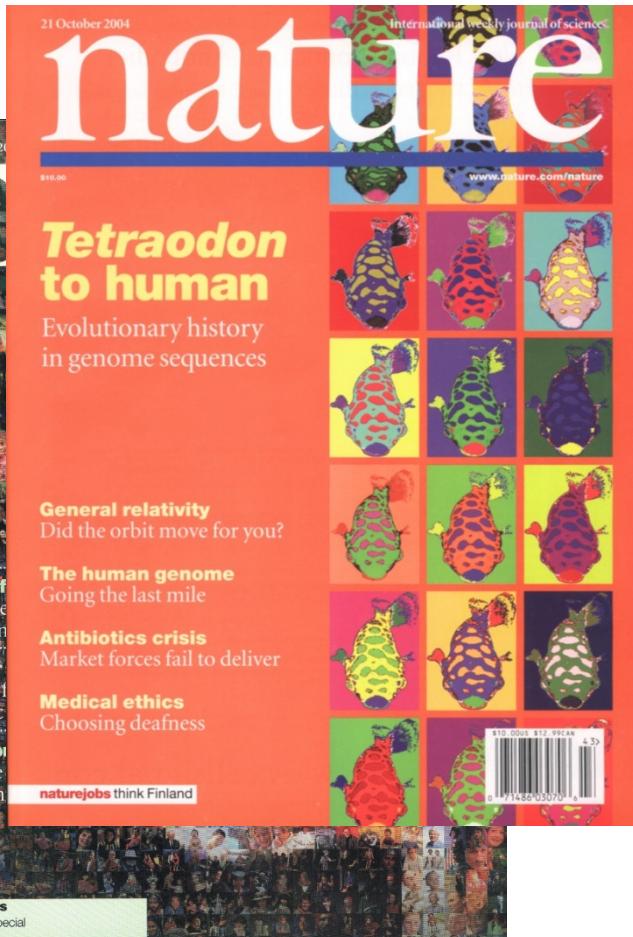
↑
SNP

- as a rule bi-allelic
- 12 Mio SNPs genom-wide 1/250 bp
- 2 individuals differ in ~300.000 SNPs 1/10.000 bp
- ~5% of SNPs, e.g. 600.000 SNPs with phenotyp (?)
50-100.000 SNPs with clinical relevance (?)

Sequencing of the Human Genome

Publications

2004



2001

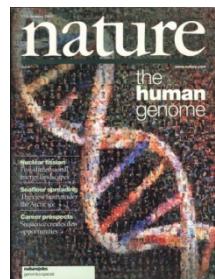


2001

International academic
consortium

Human Genome

Working Draft versions February 2001



Academic



Private

Initial Sequencing & Analysis...

The Sequence of ...

2.72 Gb	Sequenced Bases	2.65 Gb
1,000	Clone gaps	54,000
146,000	Sequence gaps	116,000
147,000	Gaps	170,000

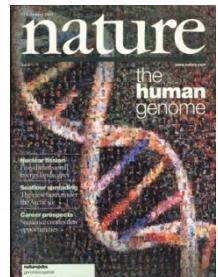
overall coverage:

94%

quality of unfinished data : **< 1 error/10kb in 91%**

Human Genome

Final version October 2004



Initial Seq...



Finishing the euchromatic sequence...

Academic

Private



The Sequence of ...

2.72 Gb	2.85 Gb	Sequenced Bases	2.65 Gb
1,000	283	Clone gaps	54,000
146,000	58	Sequence gaps	116,000
147,000	341	Gaps	170,000

near-complete sequence:
extremely high quality:

**99% of euchromatin
< 1 error/100kb**

Segmental Duplications

Problems of the human reference sequence

~50%

of the

273 interior euchromatic gaps

located in

segmentally duplicated regions

Segmental Duplication

Definition

genomic regions >1kb
with nt identity >90%

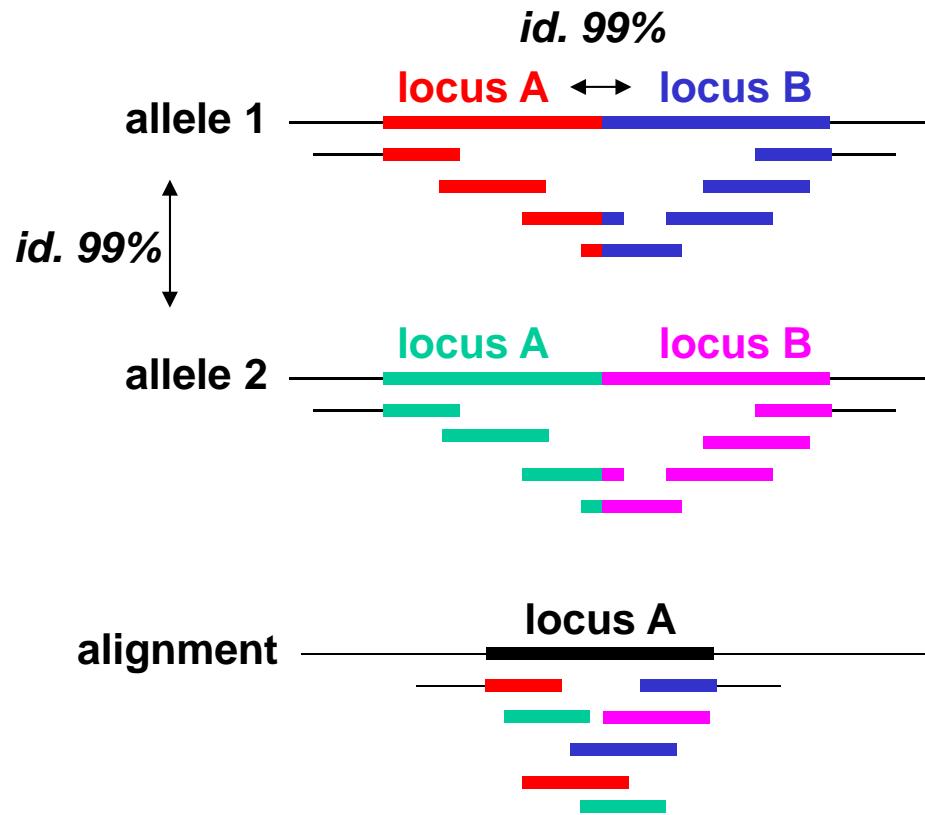
Human genome

5.3% segmentally duplicated

87% of all segmental duplications >50 kb

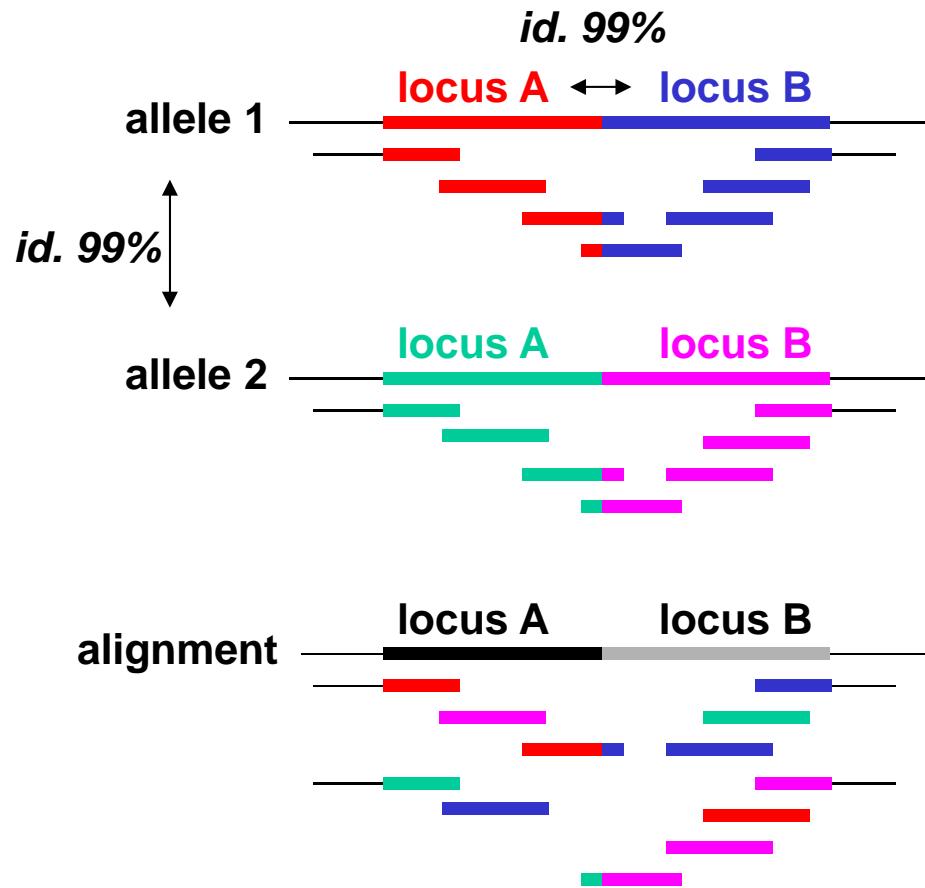
Segmental Tandem Duplications

Assembly problems



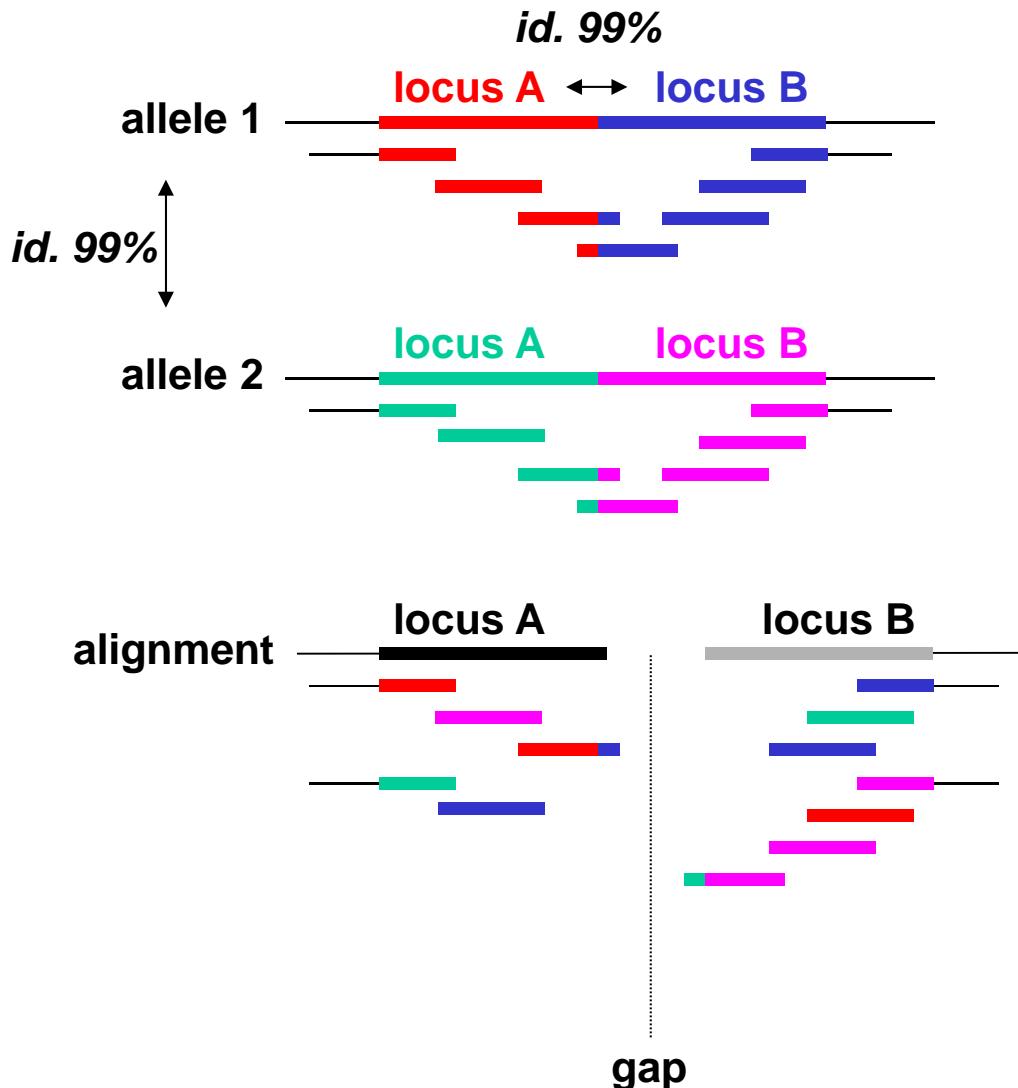
Segmental Tandem Duplications

Assembly problems



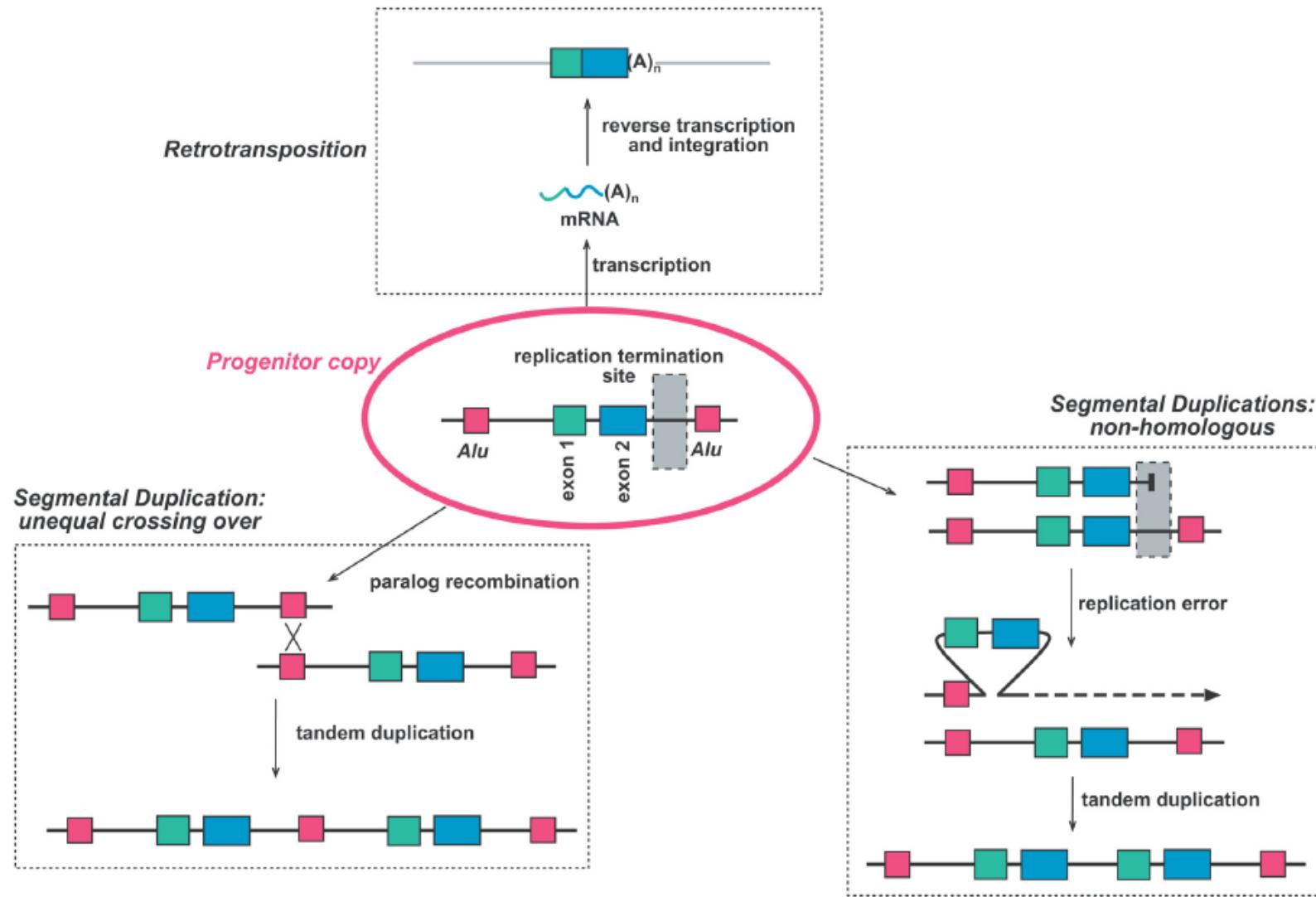
Segmental Tandem Duplications

Assembly problems



Segmental duplications

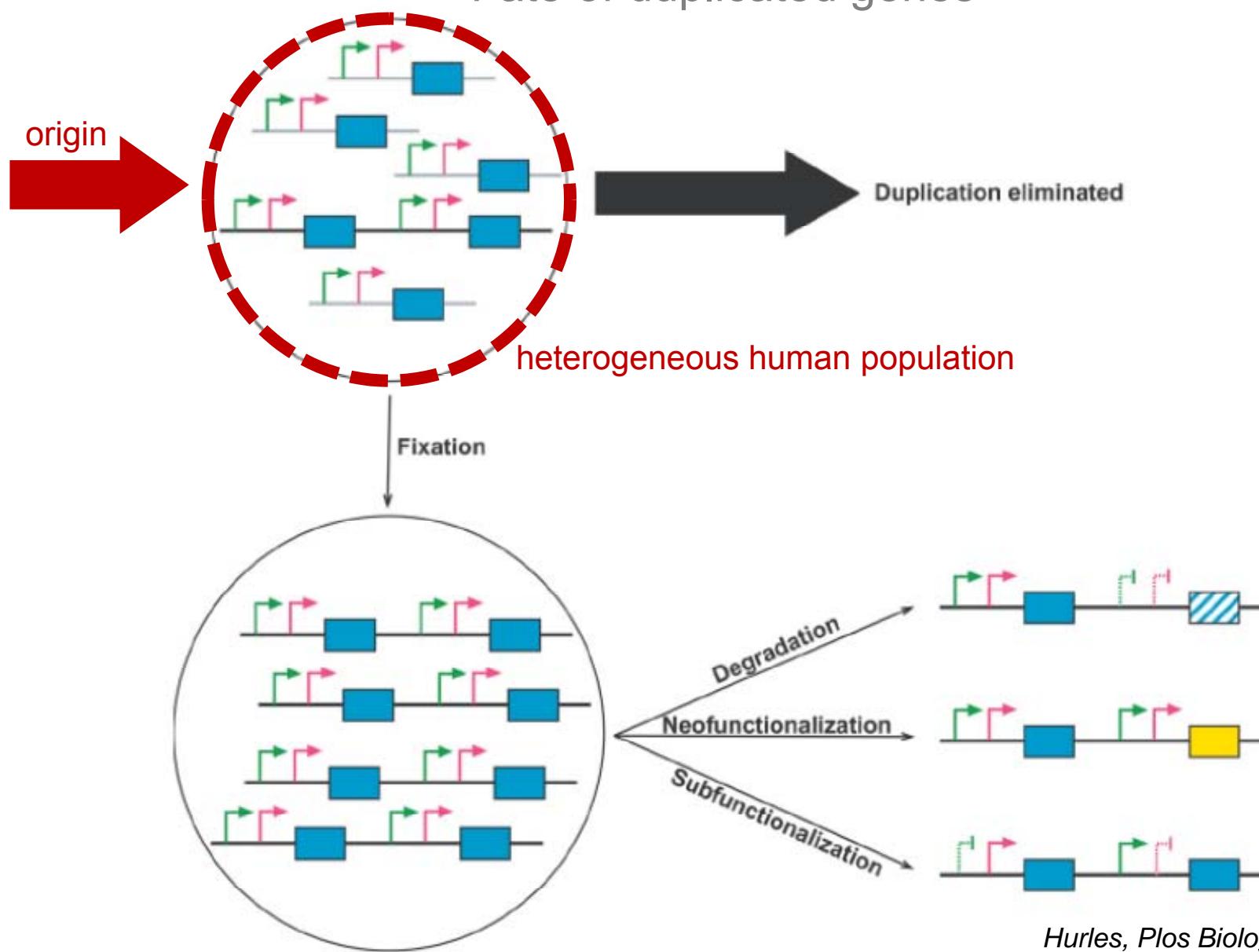
Mechanisms



Hurles, Plos Biology 2:900 (2004)

Segmental duplications

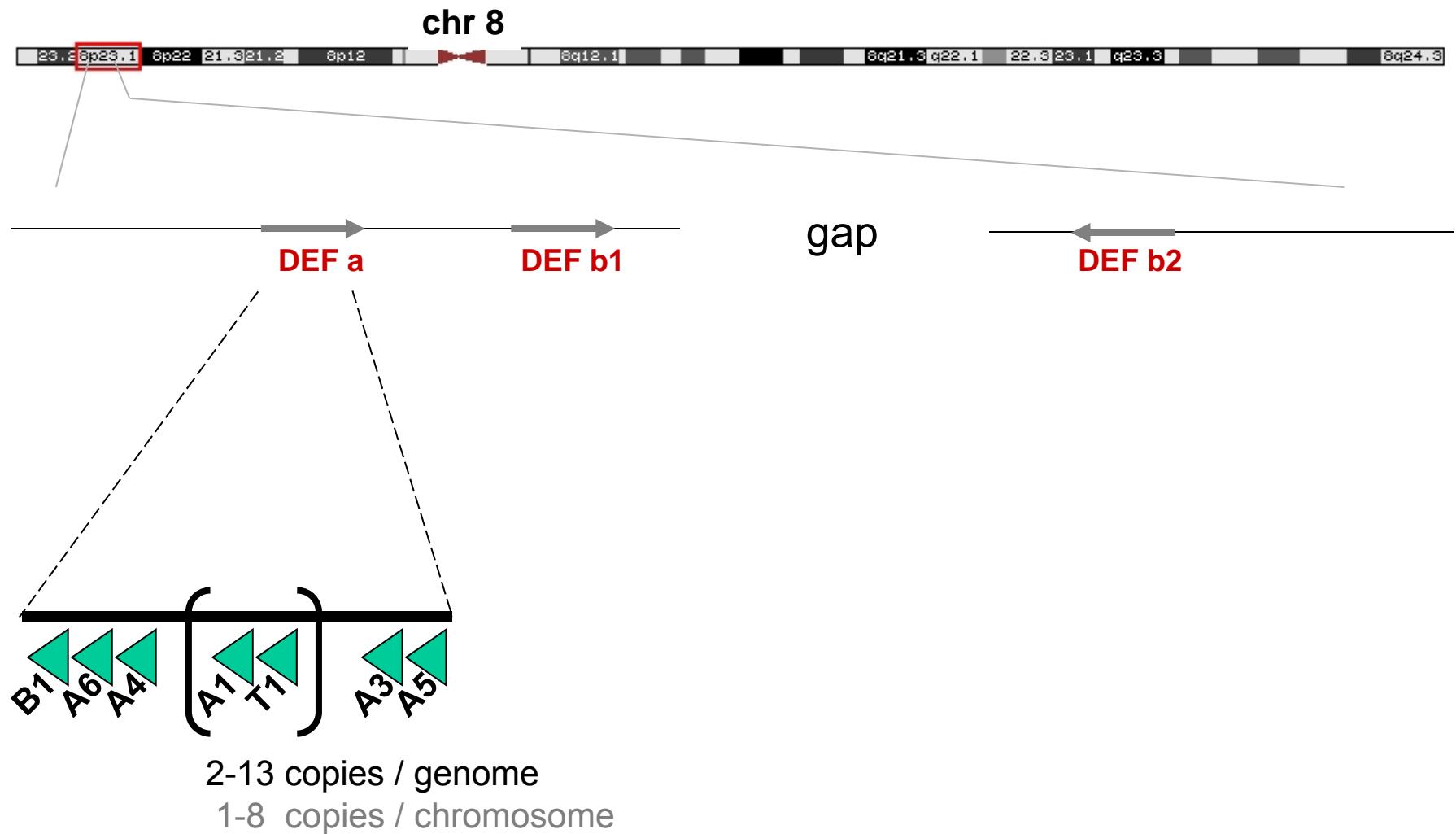
Fate of duplicated genes



Hurles, Plos Biology 2:900 (2004)

DEF cluster at 8p23.1

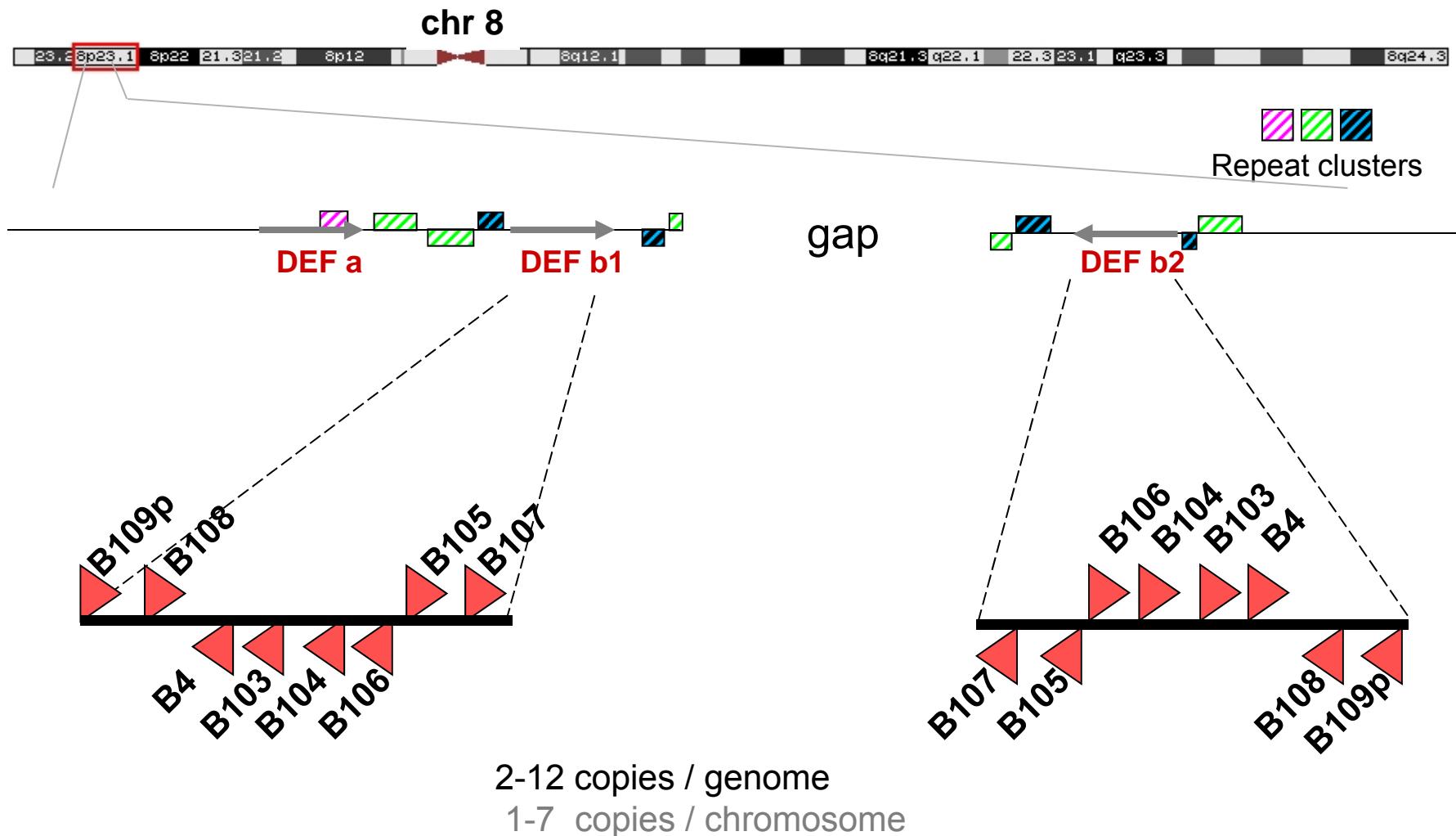
hg16: 6.3-8.3 Mb



Taudien et al., BMC Genomics 5:92 (2004)

DEF cluster at 8p23.1

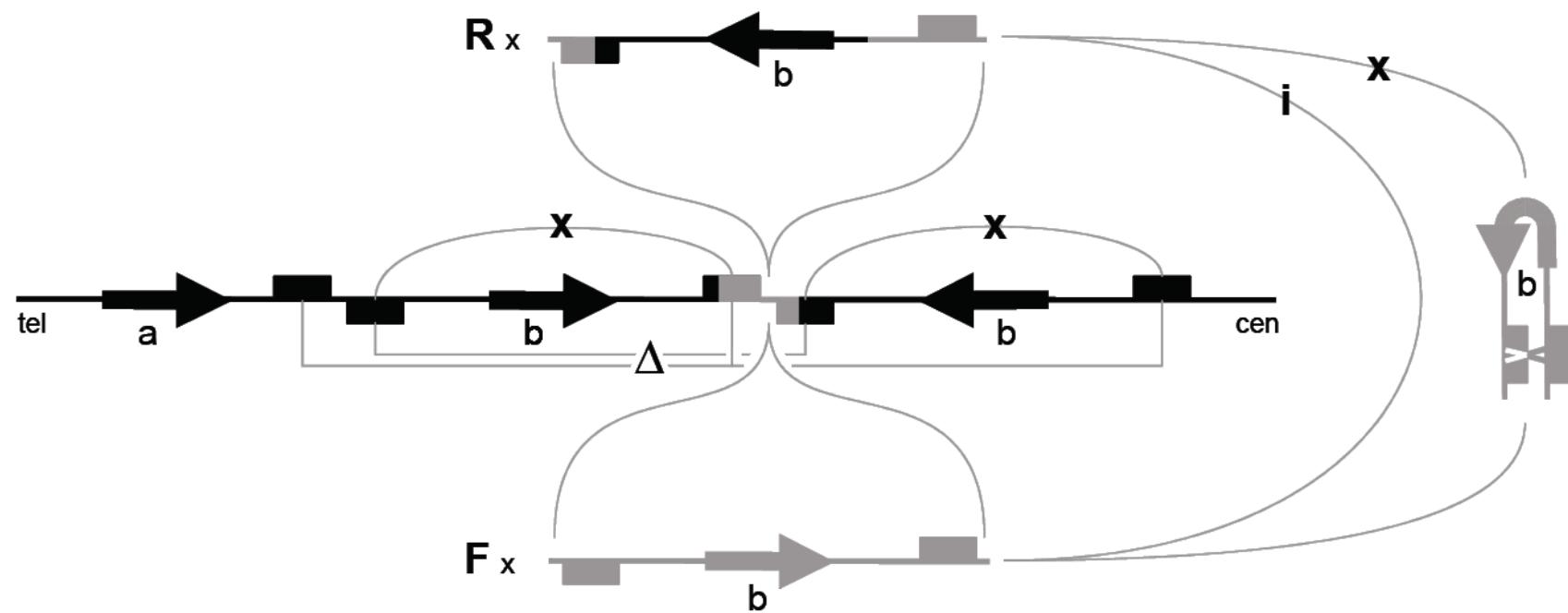
hg16: 6.3-8.3 Mb



Taudien et al., BMC Genomics 5:92 (2004)

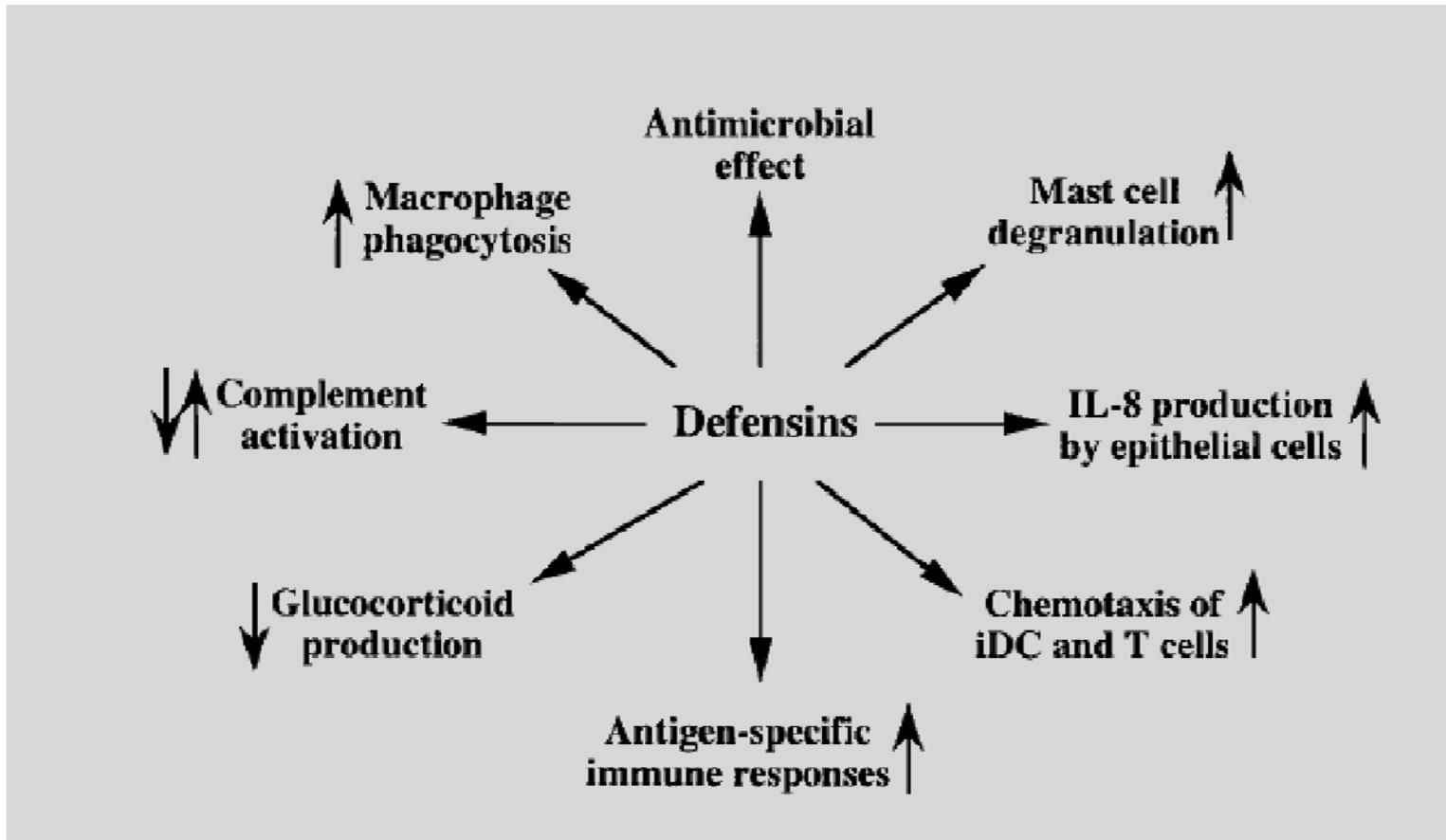
Genomic variability of 8p23.1 DEF locus

Hypothetical organisation



Defensins (DEF)

Multiple roles



Immunity & Cancer

Complex phenotypes / diseases

Structural variations

Gene	Type	Locus	Size (kb)	Phenotype	Copy number
<i>UGT2B17</i>	Deletion	4q13	150	Variable testosterone levels, risk of prostate cancer	0-2
<i>DEFB4</i>	VNTR	8p23.1	20	Colonic Crohn's disease	2-10
<i>FCGR3</i>	Deletion	1q23.3	>5	Glomerulonephritis, systemic lupus erythematosus	0-14
<i>OPN1LW/OPN1MW</i>	VNTR	Xq28	13-15	Red/green colour blindness	0-4/0-7
<i>LPA</i>	VNTR	6q25.3	5.5	Altered coronary heart disease risk	2-38
<i>CCL3L1/CCL4L1</i>	VNTR	17q12	Not known*	Reduced HIV infection; reduced AIDS susceptibility	0-14
<i>RHD</i>	Deletion	1p36.11	60	Rhesus blood group sensitivity	0-2
<i>CYP2A6</i>	Deletion	19q13.2	7	Altered nicotine metabolism	2-3

*Precise boundaries of the copy-number variant are not known.

VNTR, variable number tandem repeats.

Complex phenotypes / diseases

Structural variations

FCGR3 copy number & **glomerulonephritis** in humans
and rats

Nature 439:851 (2006)

Strong association of *de novo* copy number mutations
with **autism**

Science 316: 445 (2007)

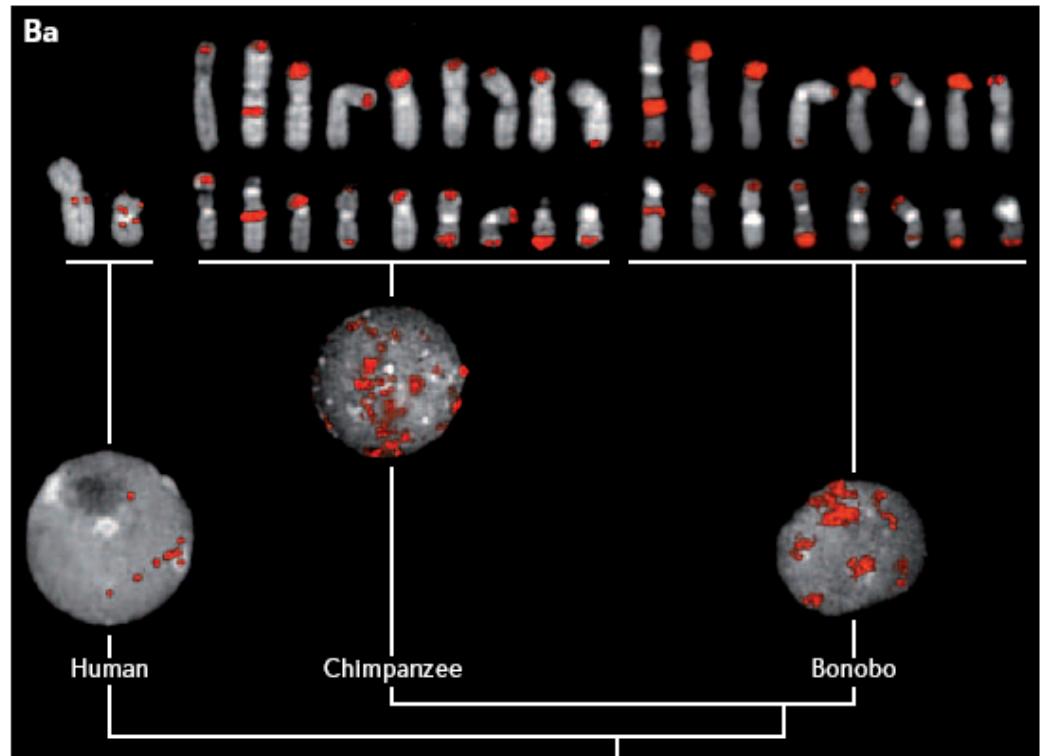
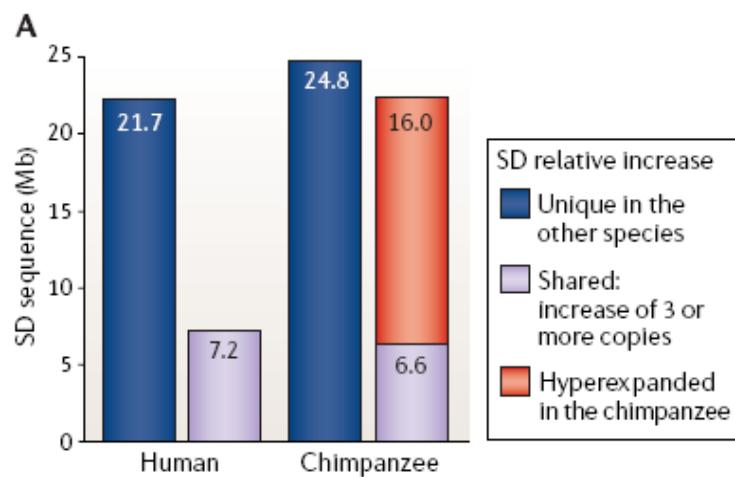
Segmental duplications

Content of sequenced animal genomes

	<i>Caenorhabditis elegans</i>	<i>Drosophila melanogaster</i>	Human	Mouse	Rat	Chicken	Chimpanzee*
SDs of >1 kb	4.3%	1.2%	5.2%	2.7%	1.6%	2.7%	N.D.
SDs of >10 kb	0.7%	0.1%	4.5%	2.2%	1.5%	0.3%	N.D.
SDs of >20 kb	N.D.	N.D.	4.0%	1.7%	0.9%	0.0%	~4.8%
Genome size	97	123	2,866	2,506	2,566	1,040	2,866

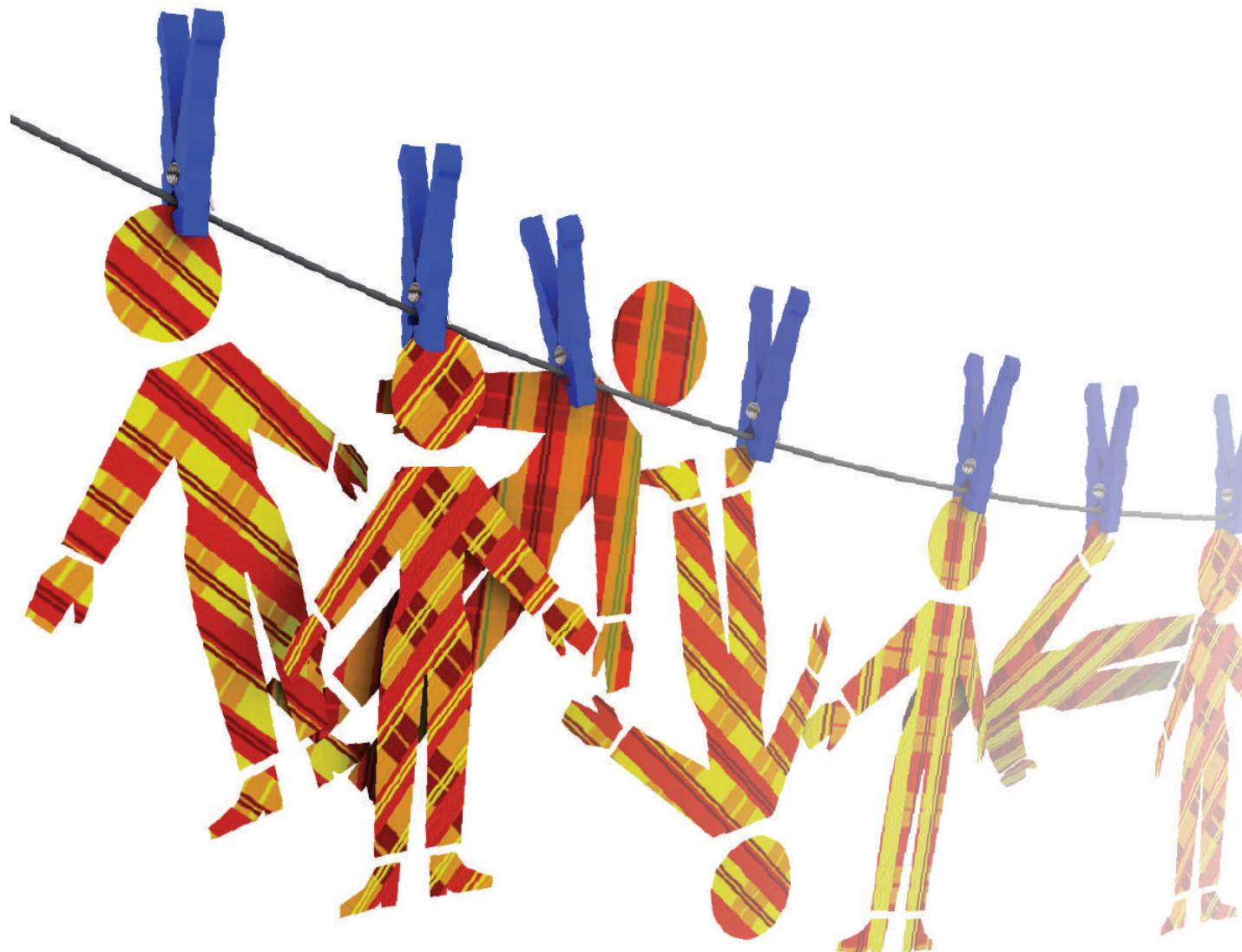
Segmental duplication content of hominoids

Hyperexpansions in chimpanzee



Genome Dynamics

Patchwork people ?



News Feature, Nature 437:1084 (2005)

Conclusions

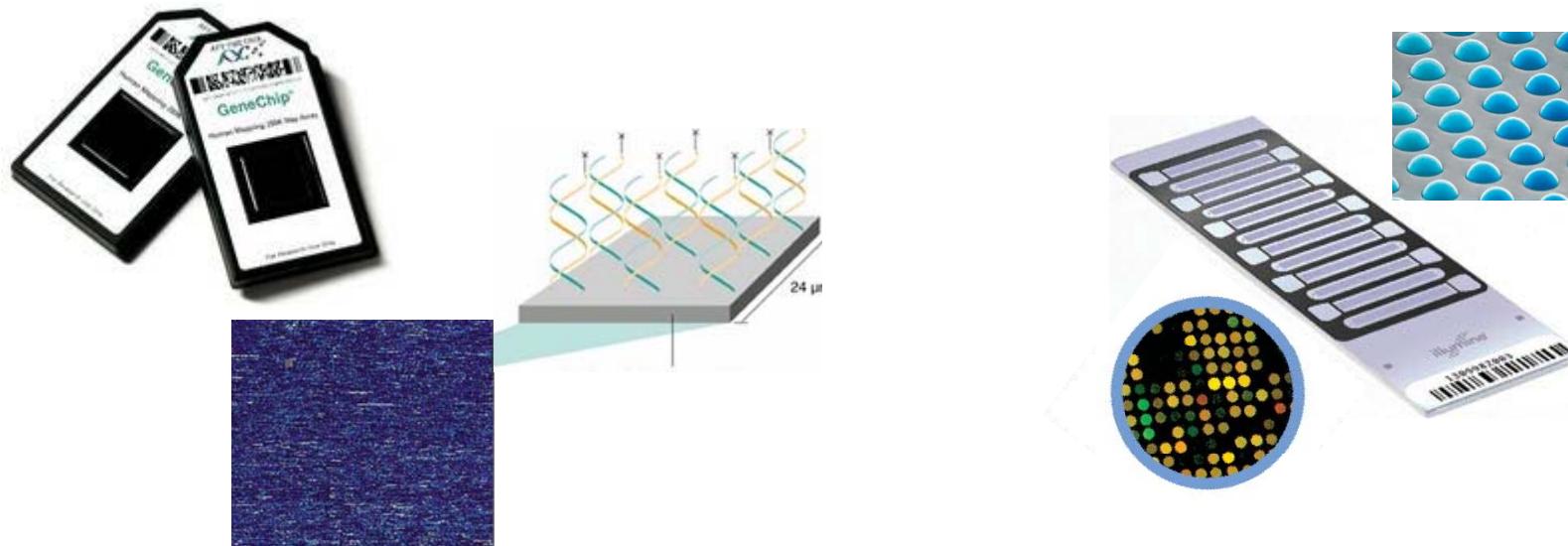
Genomes of any two individuals in the human population **differ more at the structural level than at the nucleotide sequence level.**

Differences between individuals

- CNV: >4 Mb >1/800 bp **> 0.12 %**
- SNP: 2.5 Mb 1/1,200 bp **0.08 %**

High-throughput SNP genotyping

High-throughput array-based genotyping



Affymetrix

Human SNP Array 6.0

>1.8 million markers

906,600 SNPs

946,000 for CNVs

Illumina

Human 660W-Quad BeadChip

2.6 million markers / four samples

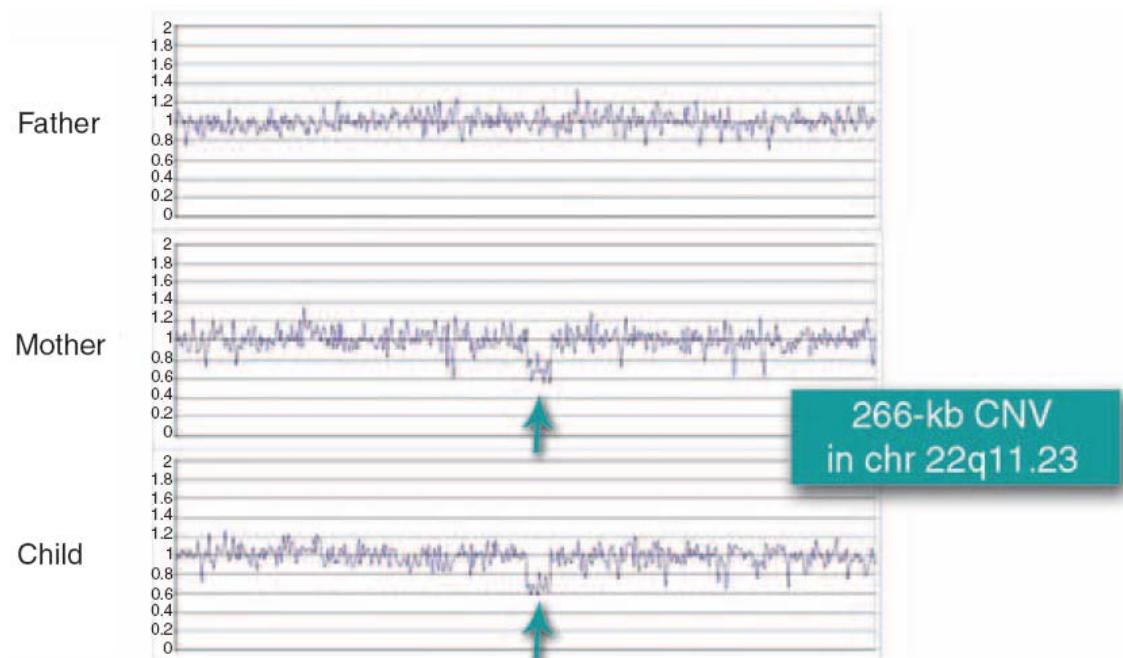
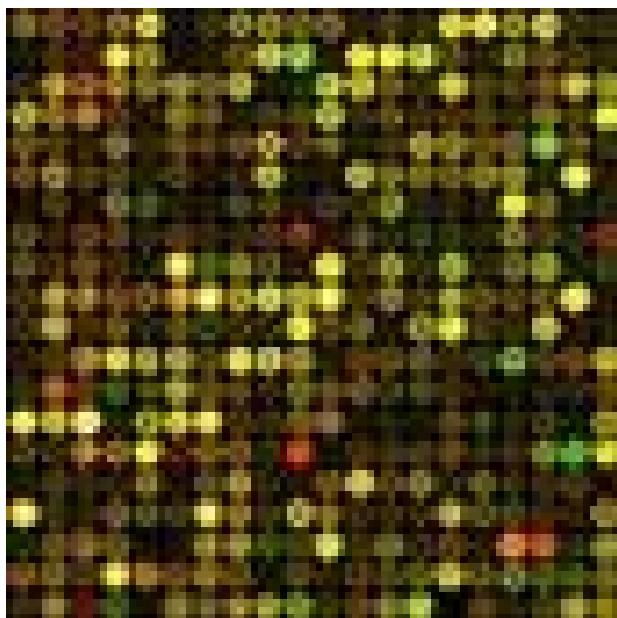
550,000 tag SNPs

100,000 for CNVs

5,000 common CNVs

Copy number variation (CNV)

Detection by DNA microarrays



- 0.5-2 Mio data points
- comparative hybridization vs. a reference

Lee et al., *Nat Genet Suppl* 39:s48 (2007)

Genome analysis

DNA sequencing platforms

ABI 3730xl

4/2004 & 6/2006



1 Mb/day, 850 nt reads

Roche/454 GS FLX

12/2006



800 Gb/23h, 800 nt reads

Illumina/Solexa GAIIx

12/2008 & 11/2009



80 Gb/14d, 2x150 nt reads

HiSeq 2000

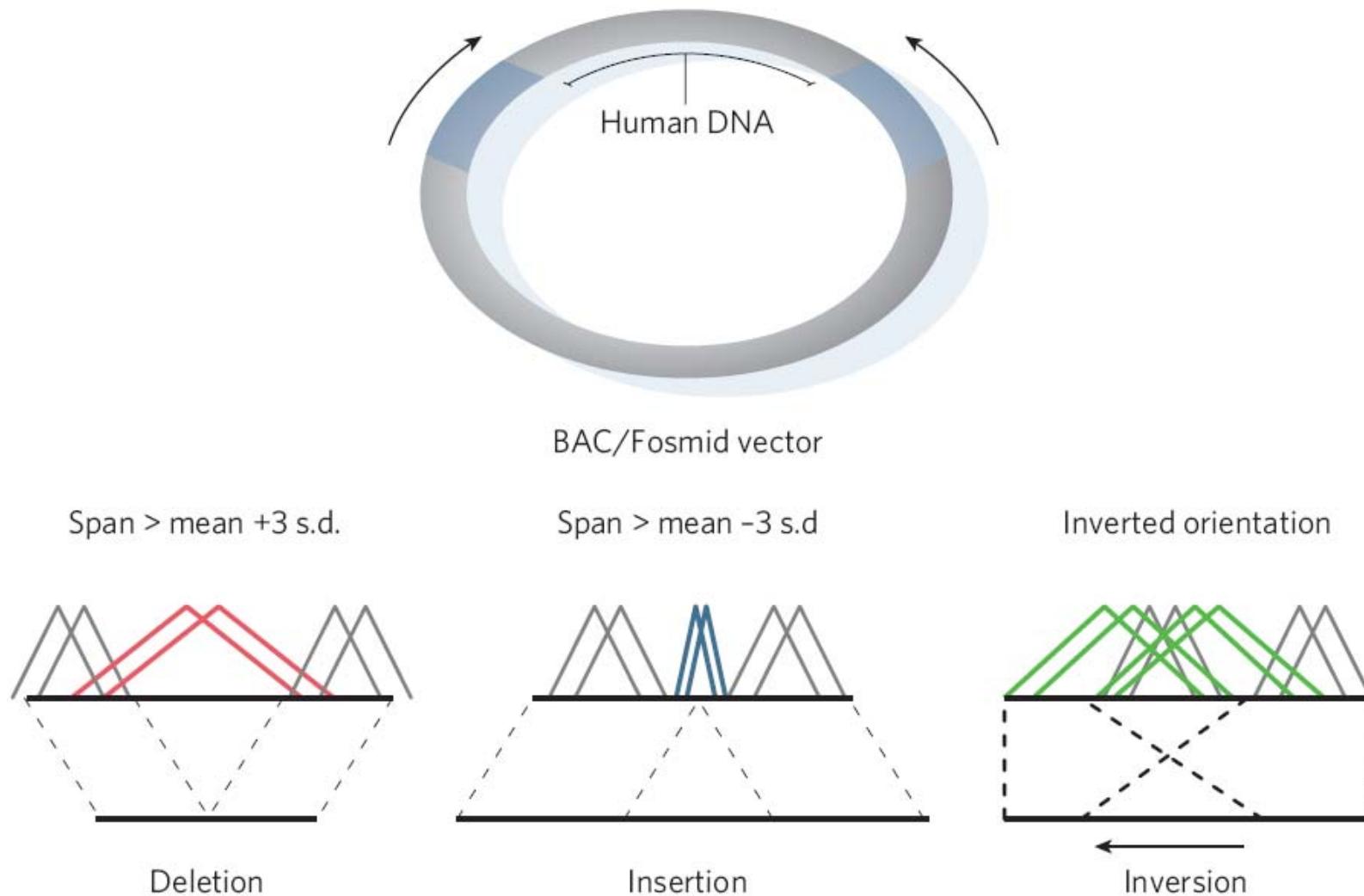
12/2010



600 Gb/10d, 2x100 nt reads

Completing the map of human genetic variation

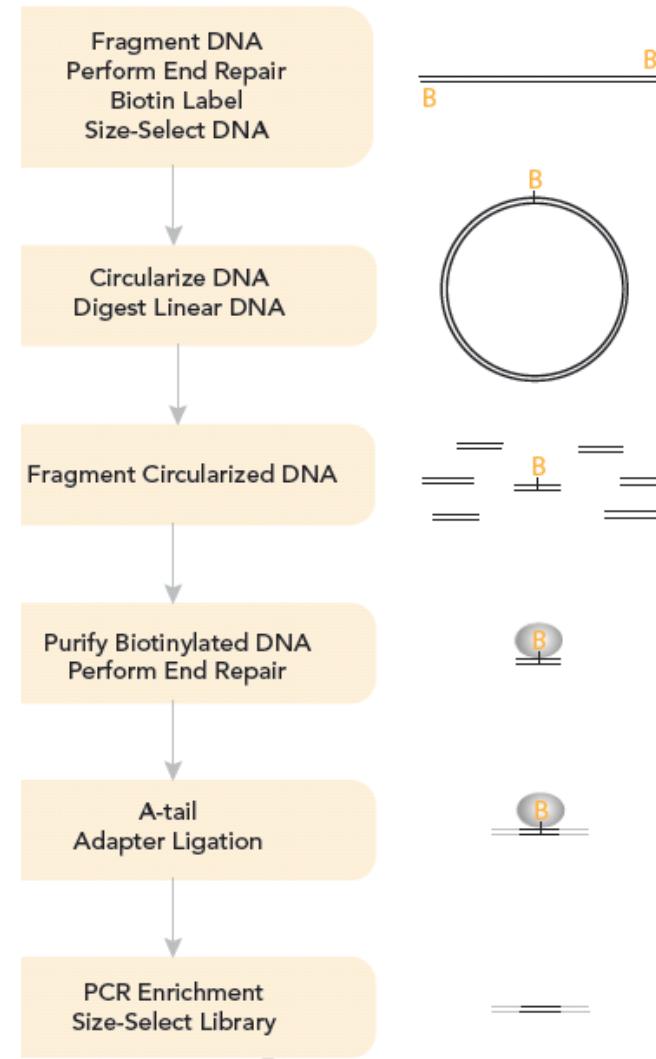
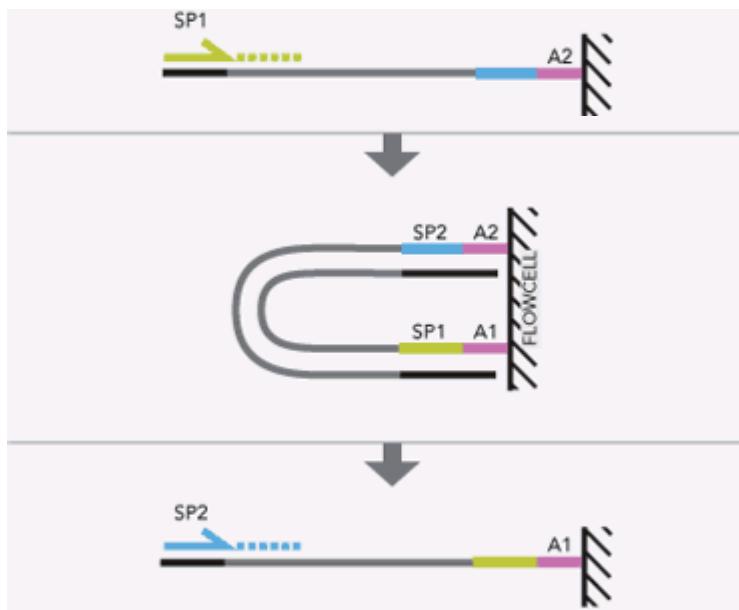
Mapping structural variations



Eichler et al., Nature 447:161 (2007)

Illumina/Solexa

Paired ends & Mate pairs



Human Genome Resequencing

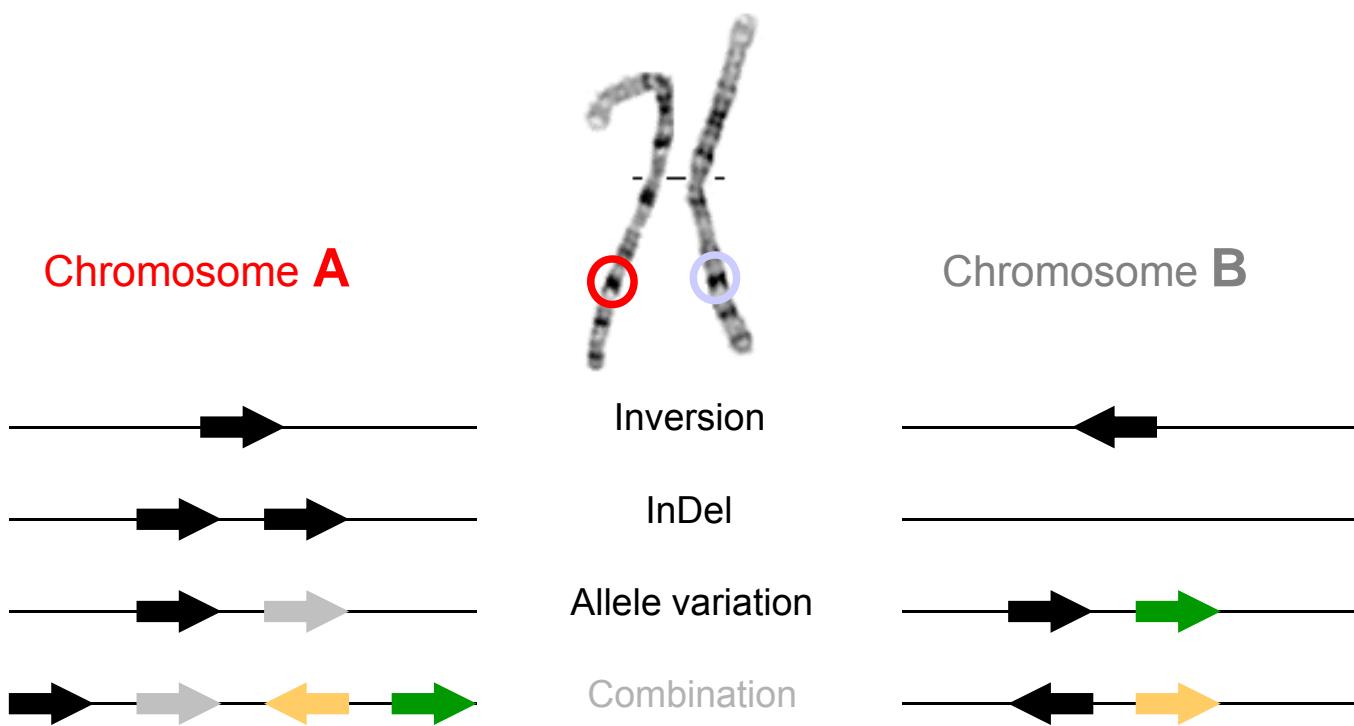
The screenshot shows the homepage of Complete Genomics. At the top, there's a navigation bar with links: Corporate, Technology, Services, Data Release, Future Applications, Resources, and Contact Us. Below the navigation is a banner for the '2009 Emerging Technology Award—Biotech' from the Silicon Valley/San Jose Business Journal. The main content area features a large blue banner with the text 'Accurate, Affordable, Complete Human Genome Studies Are Within Your Reach.' and a 'View Data' button. To the right, there's a photograph of two men in a laboratory setting, identified as the 'Commercial-scale Genome Center'.

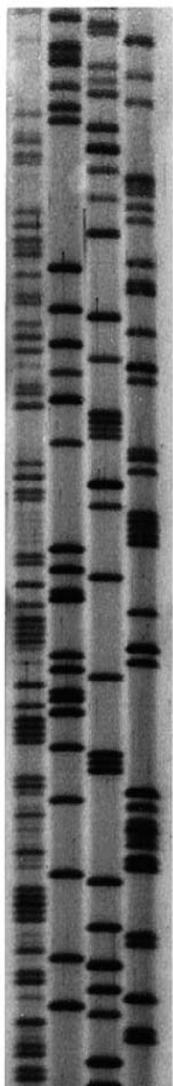
- launched by mid-2010
- 2010: ~600 human genomes
- 2011: ~4,000 genomes

- end 2011: 800-1200 genomes/month
- mid 2012: new machines with 6 genomes/day
- end 2012: <3,000 \$/genome

Genetic Variability

Structural variations





genome.fli-leibniz.de

Lectures