Genome Structural Variation

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Who am I?

- Canadian and American
- 1991-1995--Ph.D. Baylor College of Medicine with David Nelson : triplet repeat instability and Fragile X
- 1995-1997- Postdoc –LLNL Human Genome Project
- 1997-2004 Assistant & Associate Professor Case Western Reserve Univ
- 2004-present Professor and HHMI investigator at University of Washington, Seattle
- Recently duplicated genes and dynamic regions of structural variation their role in human disease and evolution
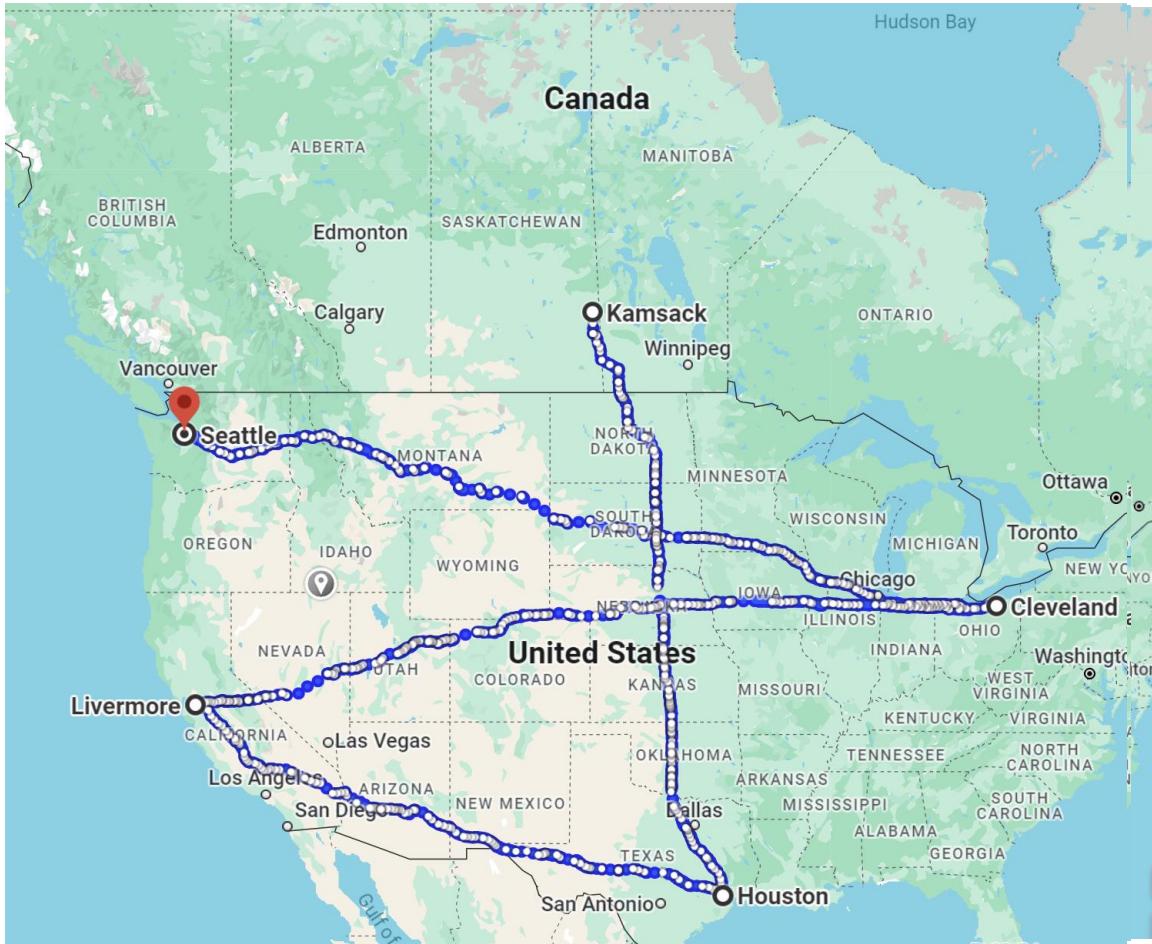
Genetic Variation

Types

Sequence

- Single base-pair changes – point mutations

- Small insertions/deletions– frameshift, microsatellite, minisatellite

- Mobile elements—retroelement insertions (300bp -10 kb in size)

- Large-scale genomic variation (>1 kb)

  – Large-scale Deletions, Inversion, translocations

  – Segmental Duplications

- Chromosomal variation—translocations, inversions, fusions.

*Cytogenetics*

Genome Structural Variation
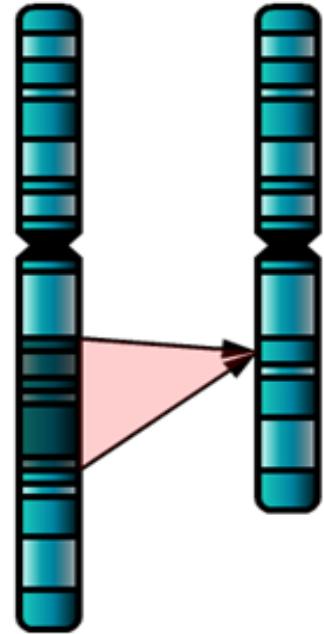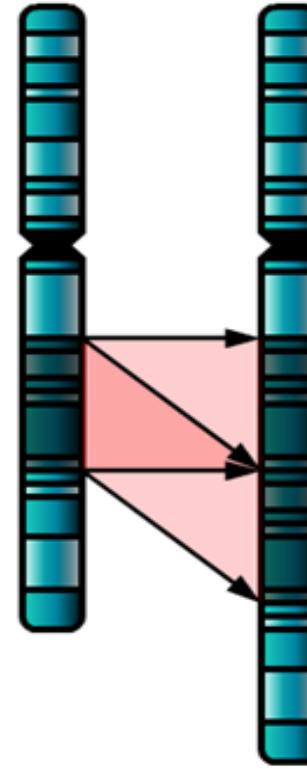
Deletion   Duplication   Inversion
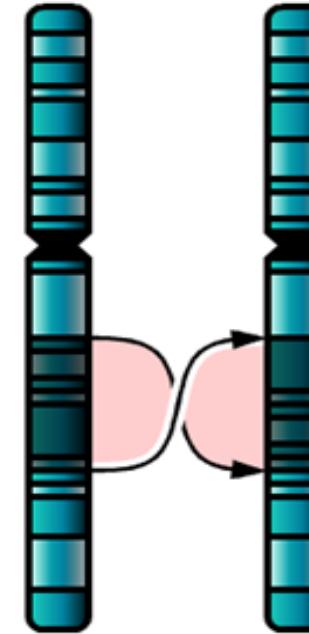
Introduction

- **Genome structural variation :** gains and losses of DNA (copy-number variation (CNV)) as well as balanced events such as inversions and translocations—operationally defined $>=50$ bp

- **Objectives**
  1. Genomic architecture and disease impact.
  2. Detection and characterization methods
  3. Primate genome evolution

Copy number polymorphism in *Fcgr3* predisposes to glomerulonephritis in rats and humans

Timothy J. Aitman[1], Rong Dong[1]*, Timothy J. Vyse[2]*, Penny J. Norsworthy[1]*, Michelle D. Johnson[1], Jennifer Smith[3], Jonathan Mangion[1], Cheri Roberton-Lowe[1,2], Amy J. Marshall[1], Enrico Petretto[1], Matthew D. Hodges[1], Gurjeet Bhangal[3], Sheetal G. Patel[1], Kelly Sheehan-Rooney[1], Mark Duda[1,3], Paul R. Cook[1,3], David J. Evans[3], Jan Domin[3], Jonathan Flint[4], Joseph J. Boyle[5], Charles D. Pusey[3] & H. Terence Cook[5]

The Influence of *CCL3L1* Gene–Containing Segmental Duplications on HIV-1/AIDS Susceptibility

Enrique Gonzalez,[1]* Hemant Kulkarni,[1]* Hector Bolivar,[1]*† Andrea Mangano,[2]* Racquel Sanchez,[1]‡ Gabriel Catano,[1]‡ Robert J. Nibbs,[3]‡ Barry I. Freedman,[4]‡ Marlon P. Quinones,[1]‡ Michael J. Bamshad,[5] Krishna K. Murthy,[6] Brad H. Rovin,[7] William Bradley,[8,9] Robert A. Clark,[1] Stephanie A. Anderson,[8,9] Robert J. O'Connell,[9,10] Brian K. Agan,[9,10] Seema S. Ahuja,[1] Rosa Bologna,[11] Luisa Sen,[2] Matthew J. Dolan,[9,10,12]§ Sunil K. Ahuja[1]§

Discovery of previously unidentified genomic disorders from the duplication architecture of the human genome

Andrew J Sharp[1], Sierra Hansen[1], Rebecca R Selzer[2], Ze Cheng[1], Regina Regan[3], Jane A Hurst[4], Helen Stewart[4], Sue M Price[4], Edward Blair[4], Raoul C Hennekam[5,6], Carrie A Fitzpatrick[7], Rick Segraves[8], Todd A Richmond[2], Cheryl Guiver[3], Donna G Albertson[8,9], Daniel Pinkel[8], Peggy S Eis[2], Stuart Schwartz[7], Samantha J L Knight[3] & Evan E Eichler[1]

## Association between Microdeletion and Microduplication at 16p11.2 and Autism

Lauren A. Weiss, Ph.D., Yiping Shen, Ph.D., Joshua M. Korn, B.S., Dan E. Arking, Ph.D., David T. Miller, M.D., Ph.D., Ragnheidur Fossdal, B.Sc., Evald Saemundsen, B.A., Hreinn Stefansson, Ph.D., Manuel A.R. Ferreira, Ph.D., Todd Green, B.S., Orah S. Platt, M.D., Douglas M. Ruderfer, M.S., Christopher A. Walsh, M.D., Ph.D., David Altshuler, M.D., Ph.D., Aravinda Chakravarti, Ph.D., Rudolph E. Tanzi, Ph.D., Kari Stefansson, M.D., Ph.D., Susan L. Santangelo, Sc.D., James F. Gusella, Ph.D., Pamela Sklar, M.D., Ph.D., Bai-Lin Wu, M.Med., Ph.D., and Mark J. Daly, Ph.D., for the Autism Consortium

Schizophrenia risk from complex variation of complement component 4

Aswin Sekar, Allison R. Bialas, Heather de Rivera, Avery Davis, Timothy R. Hammond, Nolan Kamitaki, Katherine Tooley, Jessy Presumey, Matthew Baum, Vanessa Van Doren, Giulio Genovese, Samuel A. Rose, Robert E. Handsaker, Schizophrenia Working Group of the Psychiatric Genomics Consortium, Mark J. Daly, Michael C. Carroll, Beth Stevens & Steven A. McCarroll ✉

Strong Association of De Novo Copy Number Mutations with Autism

Jonathan Sebat,[1]* B. Lakshmi,[1] Dheeraj Malhotra,[1]* Jennifer Troge,[1]* Christa Lese-Martin,[2] Tom Walsh,[3] Boris Yamrom,[1] Seungtai Yoon,[1] Alex Krasnitz,[1] Jude Kendall,[1] Anthony Leotta,[1] Deepa Pai,[1] Ray Zhang,[1] Yoon-Ha Lee,[1] James Hicks,[1] Sarah J. Spence,[4] Annette T. Lee,[5] Kaija Puura,[6] Terho Lehtimäki,[7] David Ledbetter,[2] Peter K. Gregersen,[5] Joel Bregman,[8] James S. Sutcliffe,[9] Vaidehi Jobanputra,[10] Wendy Chung,[10] Dorothy Warburton,[10] Mary-Claire King,[3] David Skuse,[11] Daniel H. Geschwind,[12] T. Conrad Gilliam,[13] Kenny Ye,[14] Michael Wigler[1]†

Perspective: Segmental Duplications (SD)

Definition: Continuous portion of genomic sequence represented more than once in the genome (>90% and > 1kb in length)=historical copy number variation


Intrachromosomal

Interchromosomal

Distribution

Interspersed

Tandem

Configuration
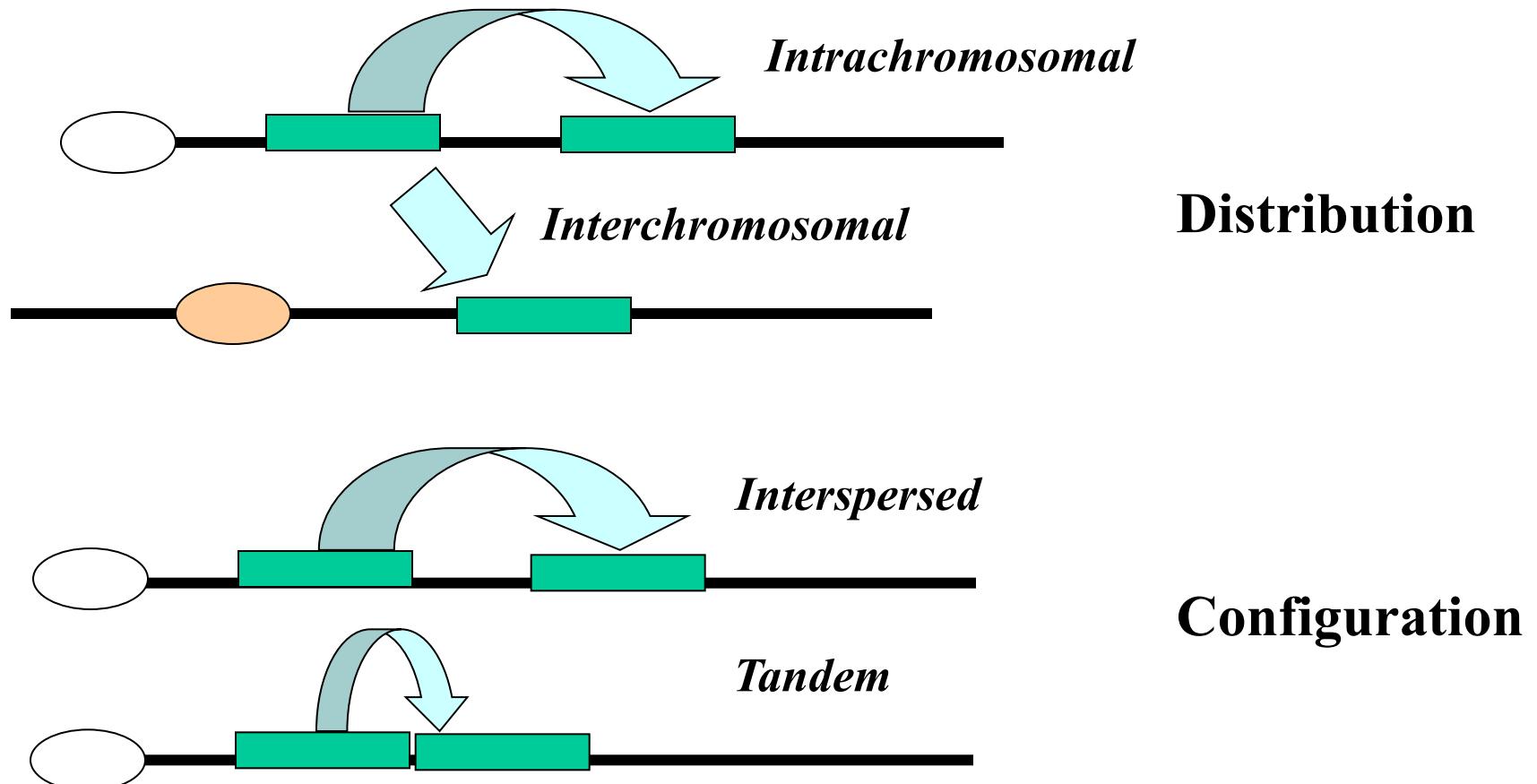
Importance:
SDs promote genome structural variation

GAMETES

Non Allelic Homologous Recombination
NAHR

Human Disease
Triplosensitive, Haploinsufficient and Imprinted Genes
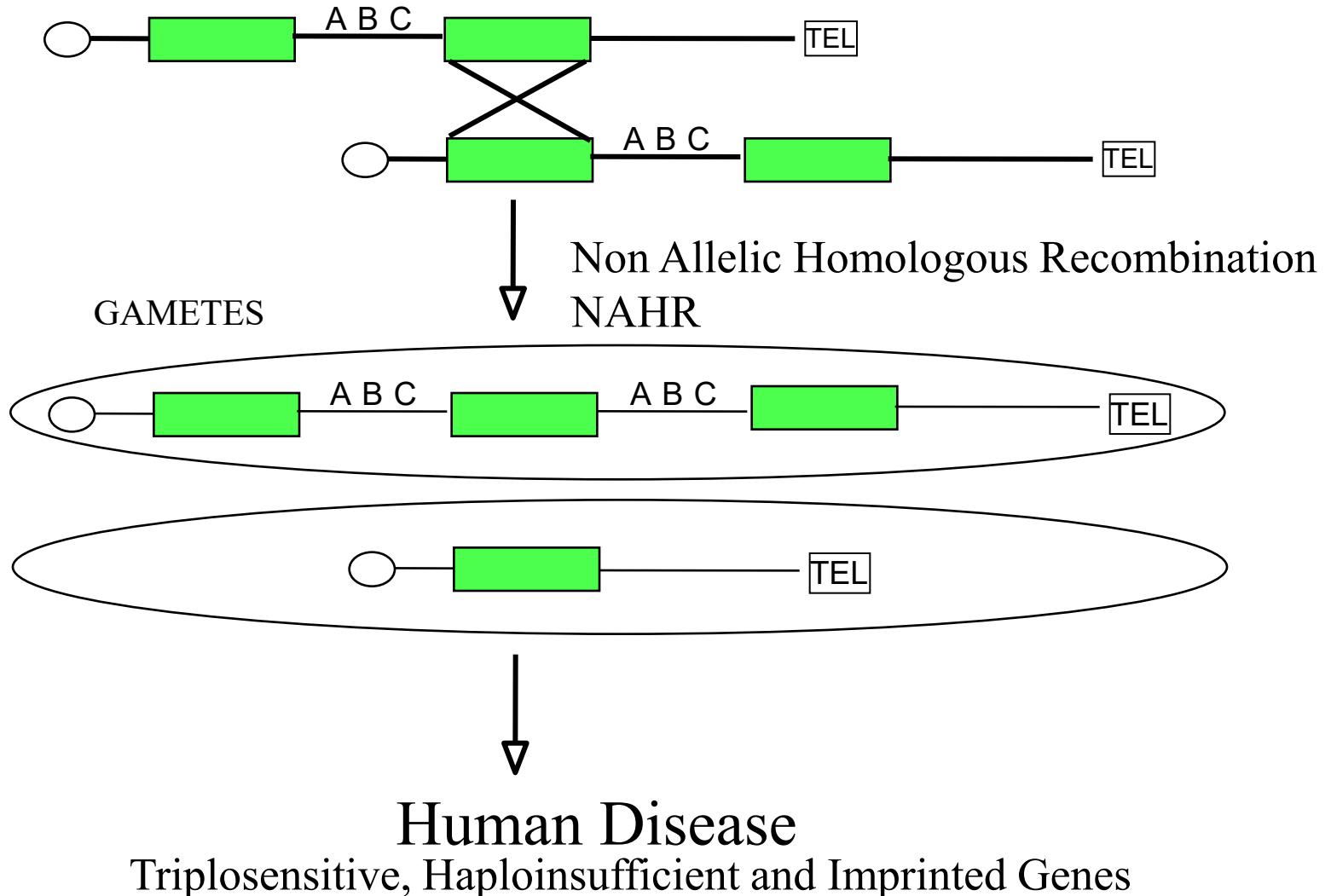
Importance: Evolution of New Gene Function

GeneA → Duplication → **GeneA'**

GeneA → Mutation → Maintain old Function

GeneA' → Mutation → Acquire New/ Modified Function

GeneA' → Mutation → Loss of Function

Human Genome Segmental Duplication Pattern

- ~4% duplication (125 Mb)
- \>20 kb, >95%
- **59.5% interspersed**
  - Gene/transcript rich
  - Associated with Alu repeat
  - 50% of all CNV > 1 kbp
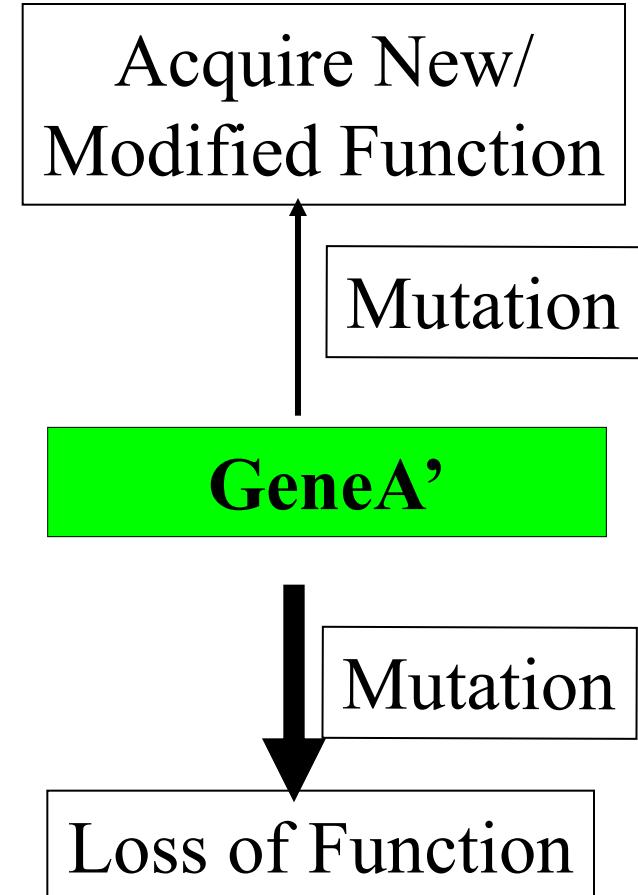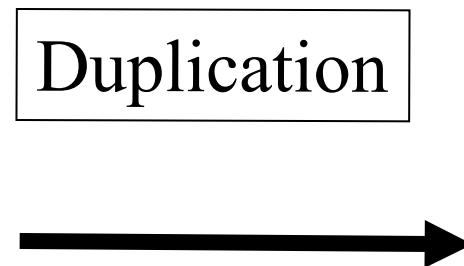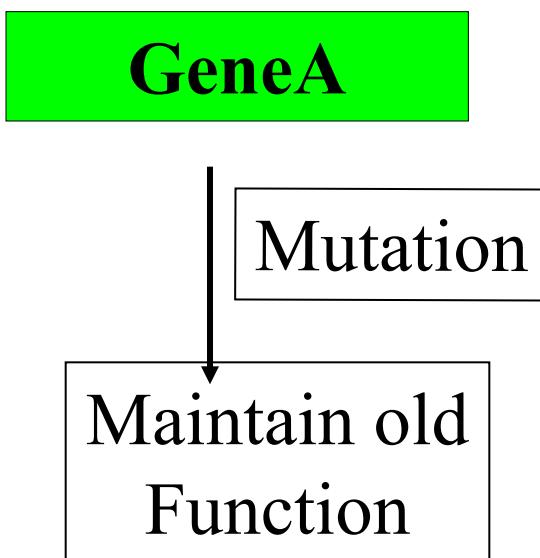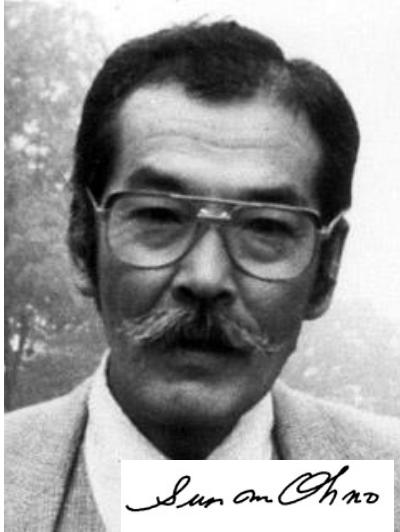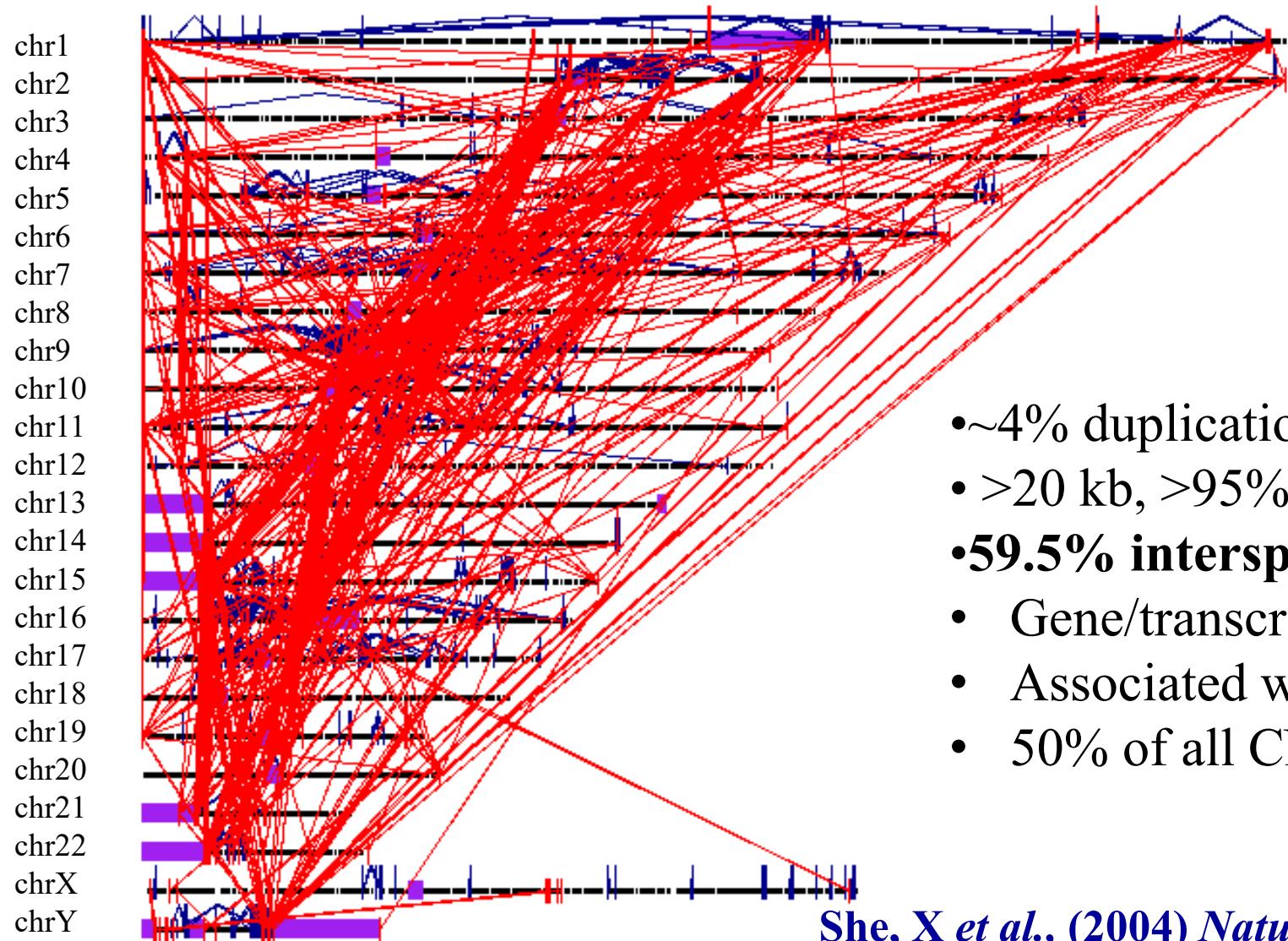
She, X *et al.,* (2004) *Nature* 431:927-30

Mouse Segmental Duplication Pattern
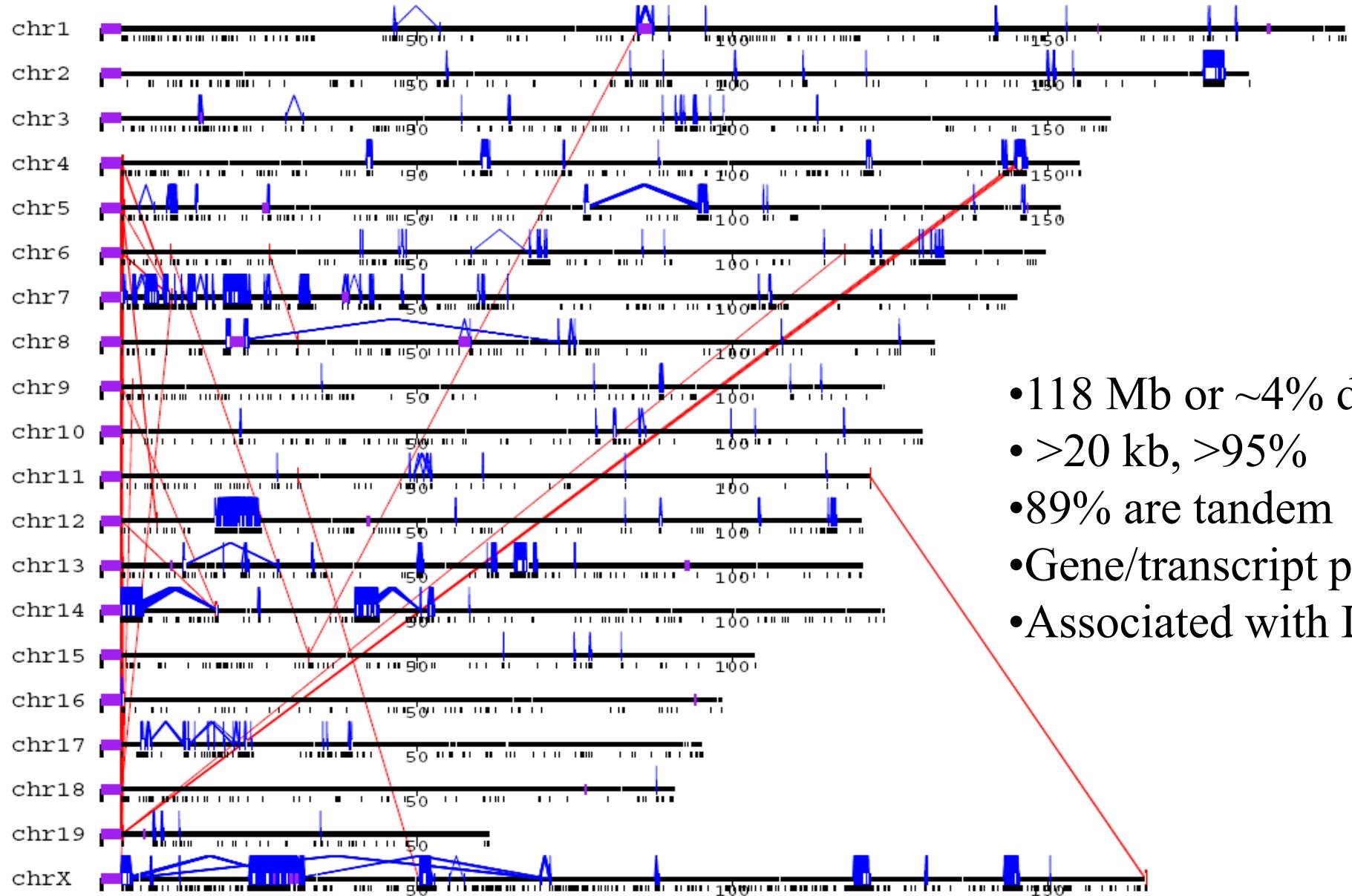
- 118 Mb or ~4% dup
- >20 kb, >95%
- 89% are tandem
- Gene/transcript poor
- Associated with LINEs

Human Segmental Duplications Properties

- Large (>10 kb)
- Recent (>95% identity)
- **Interspersed (60% are separated by more than 1 Mb)**
- Modular in organization
- Difficult to resolve

Rare Structural Variation & Disease

Human Disease
Triplosensitive, Haploinsufficient and Imprinted Genes
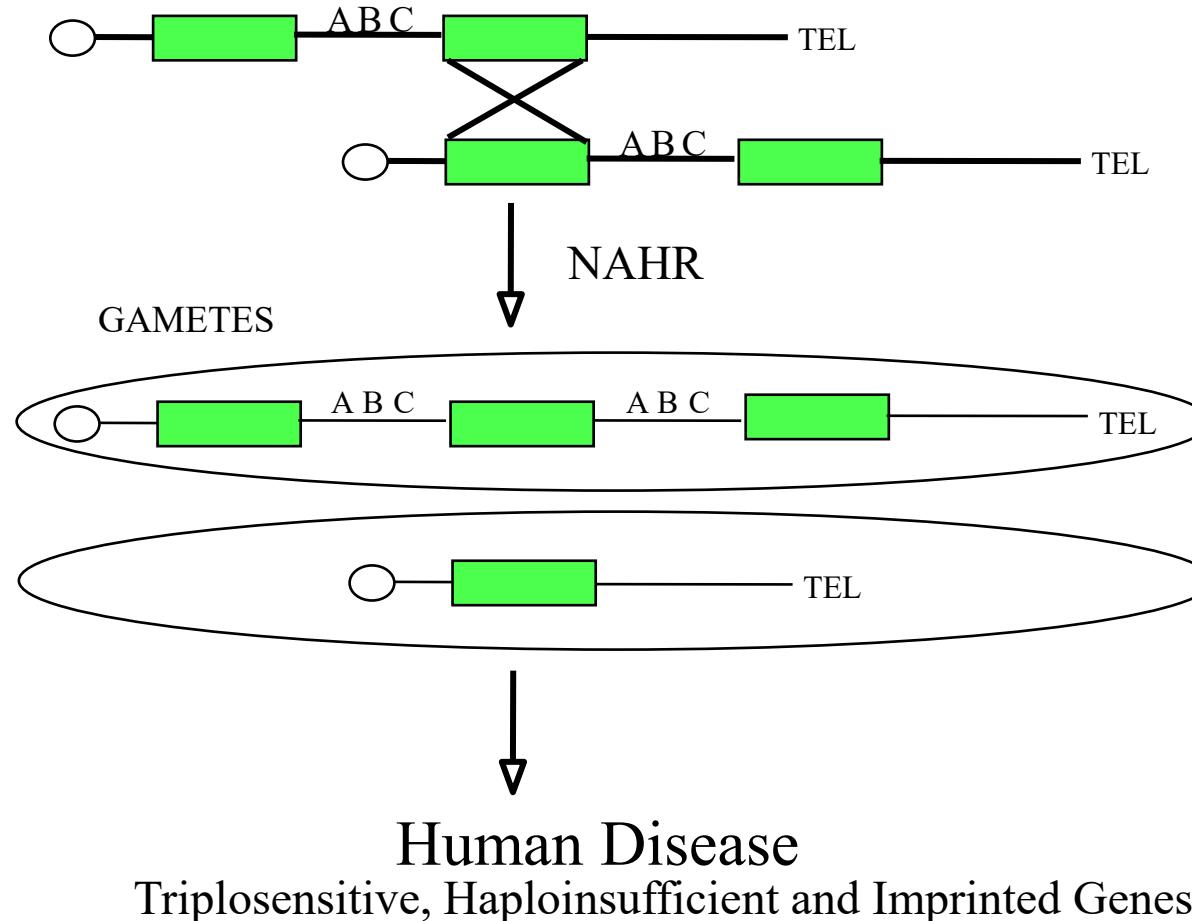
•**Genomic Disorders:** A group of diseases that results from genome rearrangement mediated mostly by non-allelic homologous recombination. (*Inoue & Lupski , 2002*).

DiGeorge/VCFS/22q11 Syndrome

Chromosome 22 diagram with DGCR markers: D22S427, D22S75, D22S941, D22S944, TBX1, D22S264, cos 82 pH17

A Normal heart

Pulmonary artery (to lungs)

Oxygenated blood flow in left heart

Aorta (to body)

Right atrium

Deoxygenated blood flow in right heart

Right and left ventricles

B Heart with tetrology of Fallot

Increased outflow in aorta

Partial obstruction (stenosis) of right ventricular outflow (to lungs) and pulmonary valve

Ventricular septal defect

Thickened right ventricle (hypertrophy)

1/3000 live births
180 phenotypes
75-80% are sporadic (not inherited)
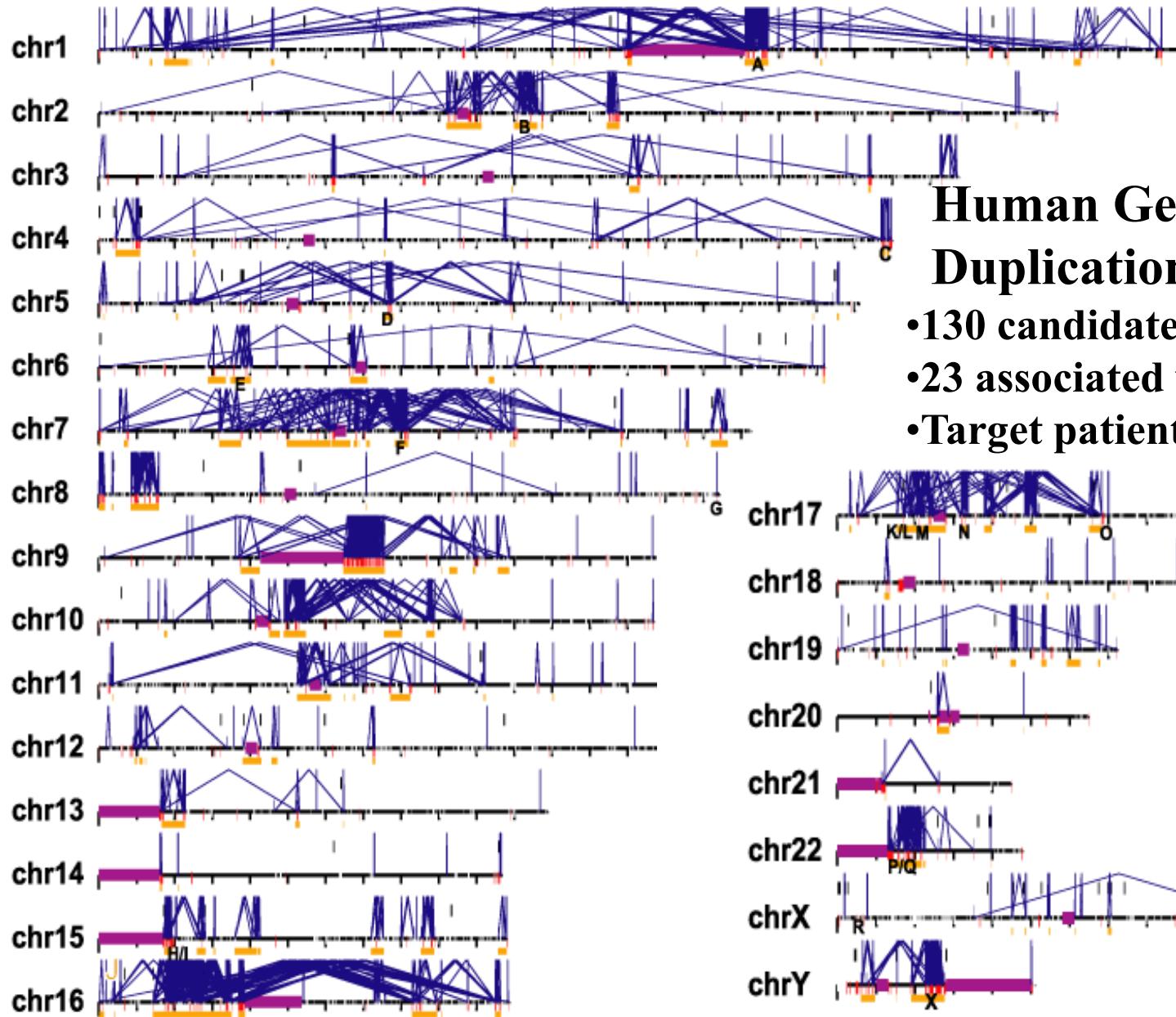
Human Genome Segmental Duplication Map
- 130 candidate regions (298 Mb)
- 23 associated with genetic disease
- Target patients array CGH

Bailey *et al.* (2002), *Science*
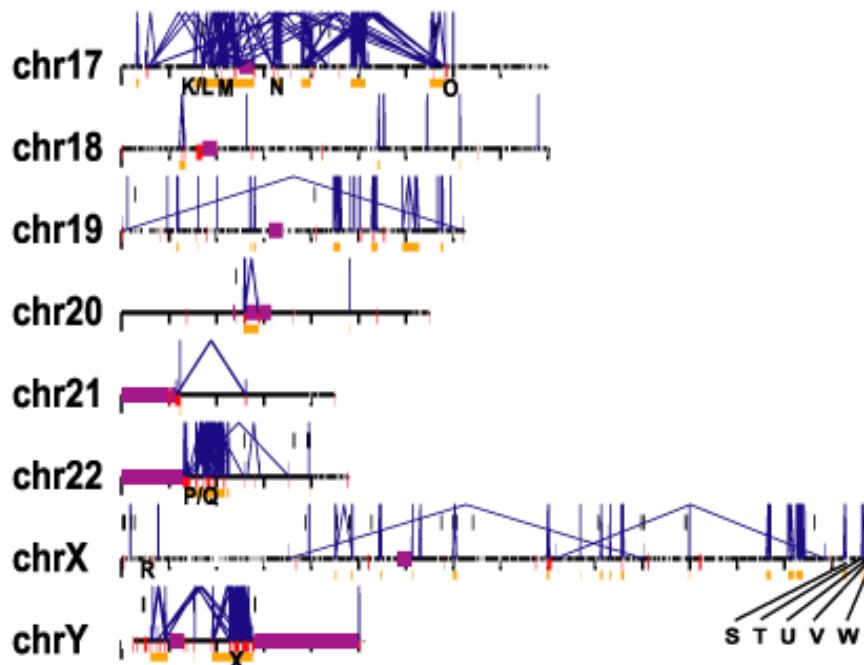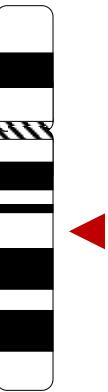
Chromosome 17

Chromosome 15
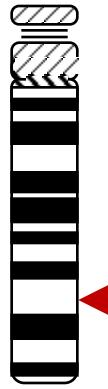
Chromosome 15
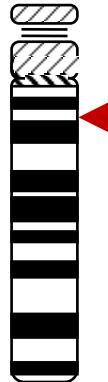
Genome Wide CNV Burden
(15,767 cases of ID,DD,MCA vs. 8,328 controls)

**Developmental Delay Cases**

Controls

~14.2% of genetic cause of developmental delay explained by large CNVs (>500 kbp)

Percentage of Population

Minimum Size of CNV (kbp)

Cooper et al., *Nat. Genet*, 2011
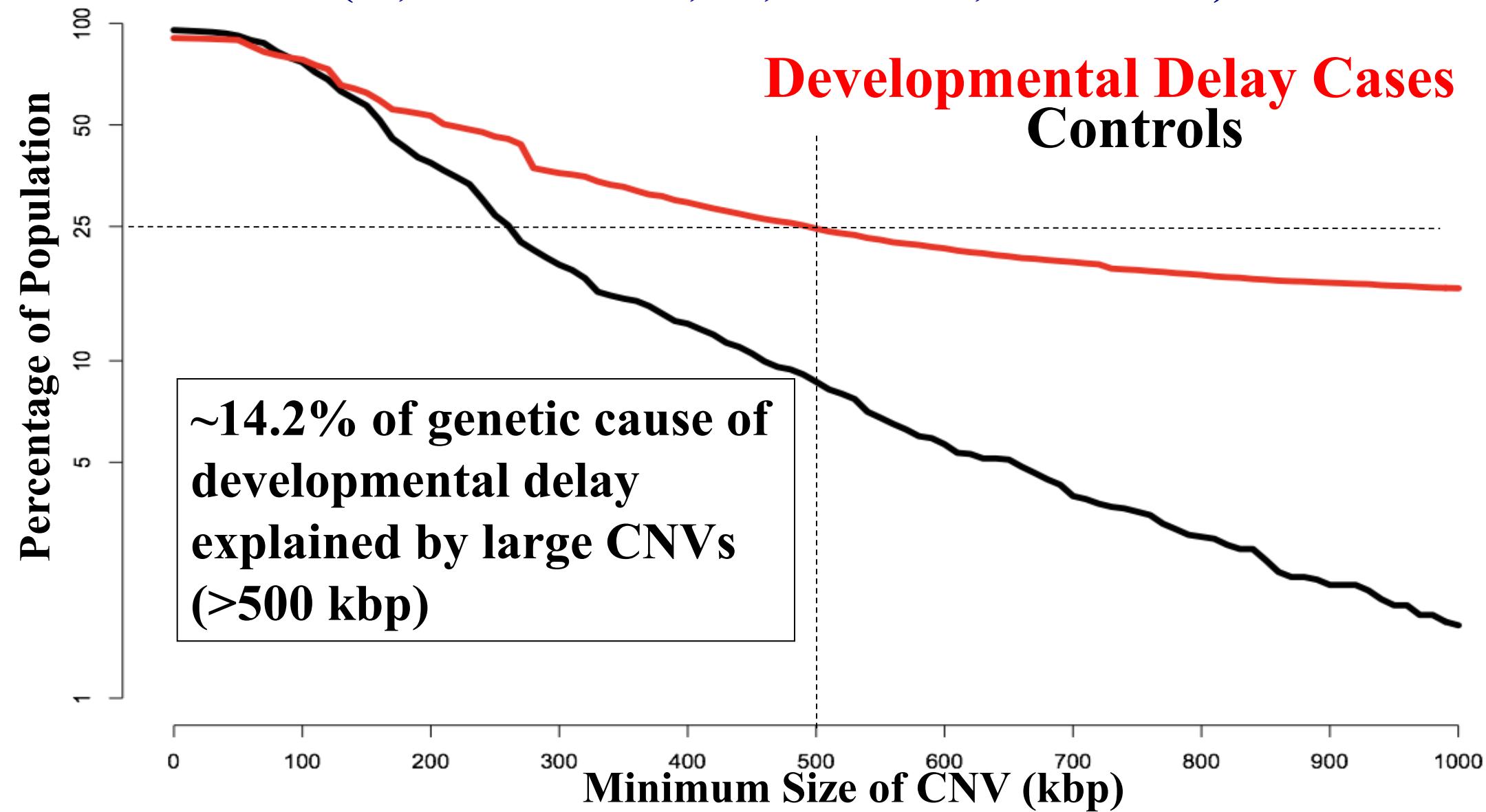
# Common and rare structural variation are linked 17q21.31 deletion syndrome
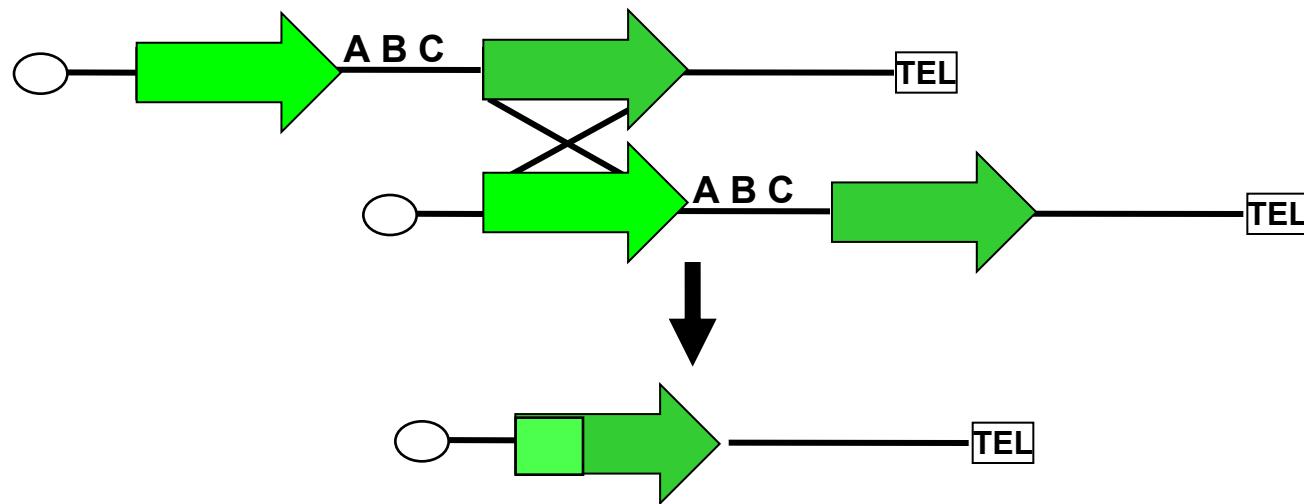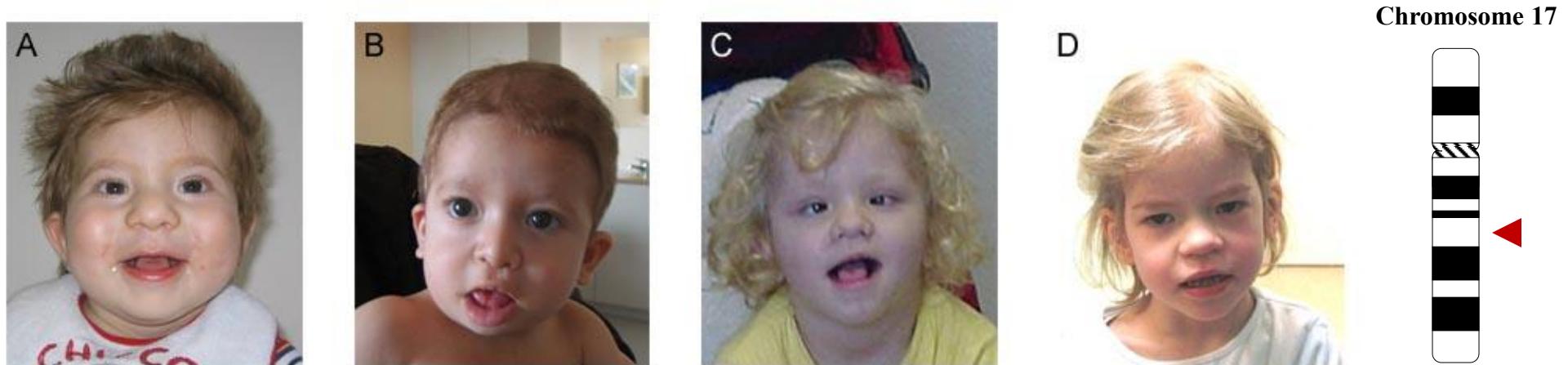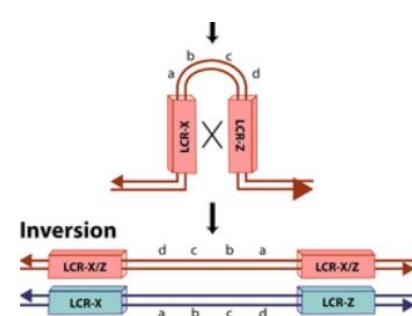
17q21.31 inversion
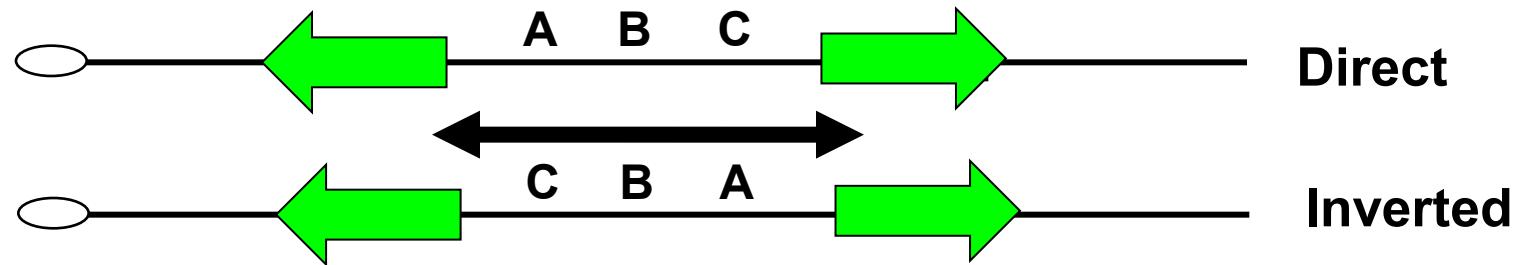
- Region of recurrent deletion is a site of common inversion polymorphism in the human population

- Inversion is largely restricted to European populations

  - >20% frequency in Northern European populations

- **Inversion is associated with increase in global recombination and increased fecundity**

Stefansson, K *et al., (2005) Nature Genetics*

A common inversion polymorphism
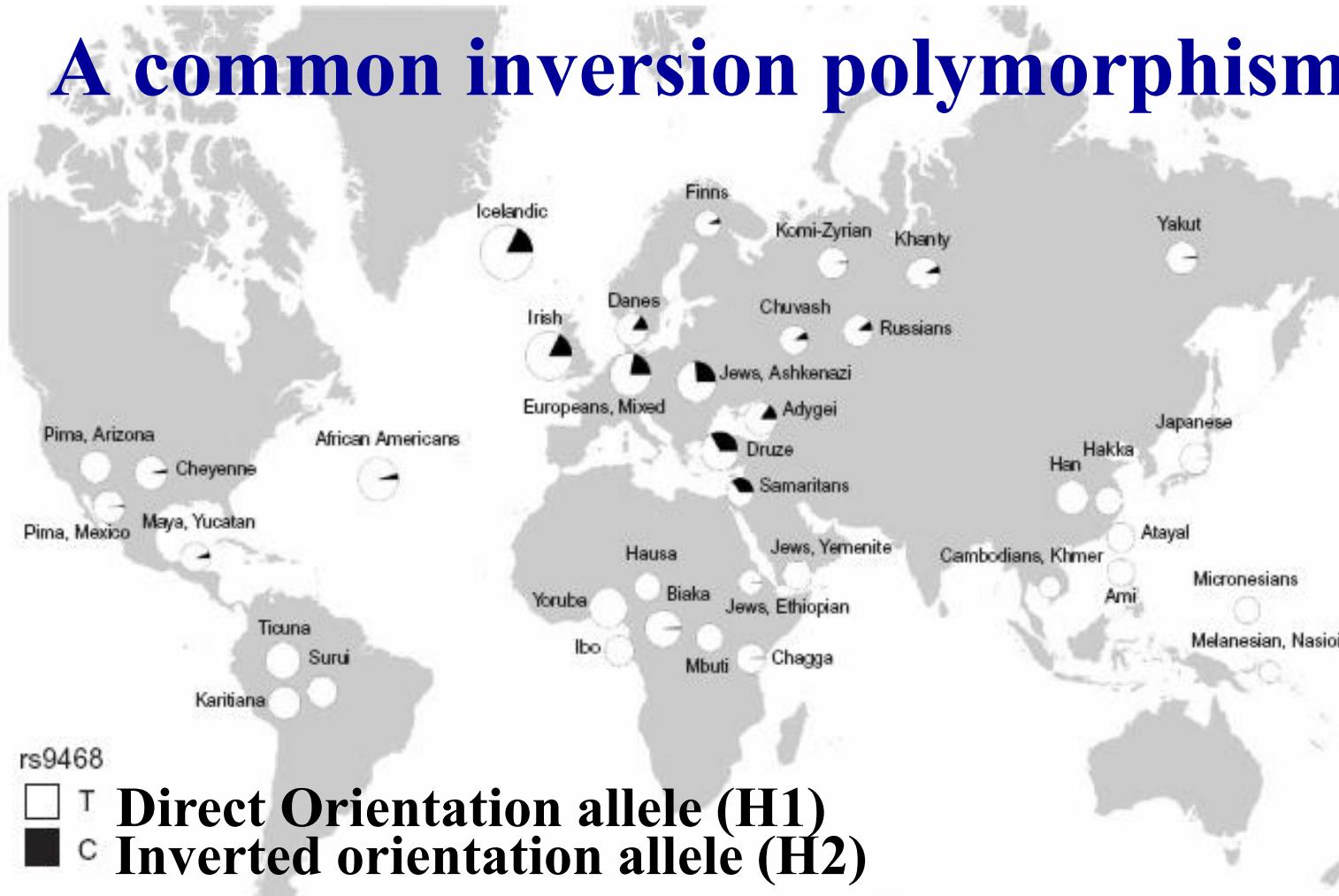
•Tested 17 parents of children with microdeletion and found that every parent within whose germline the deletion occurred carried an inversion
•Inversion polymorphism is a risk factor for the microdeletion event

Duplication Architecture of 17q21.31 Inversion (H2) vs. Direct (H1) Haplotype

- Inversion occurred 2.3 million years ago and was mediated by the LRRC37A core duplicon
- H2 haplotype acquired human-specific duplications in direct orientation that mediate rearrangement and disrupts *KANSL1* gene

Zody *et al.*, *Nat. Genet*. 2008, Itsara et al., Am J. Human Genet 2012

Summary

- Human genome is enriched for segmental duplications which predisposes to recurrent large CNVs during germ-cell production

- 14-15% of neurodevelopmental disease in intellectual disabled children is "caused" by large CNVs—8% of normal individuals carry large events

- Segmental duplications enriched >10 fold for structural variation because of increased probability of non-allelic homologous recombination

- Increased complexity is beneficial and deleterious: Ancestral duplication predisposes to inversion polymorphism, inversion polymorphisms acquires duplication, haplotype becomes positively selected and now predispose to microdeletion

II. Genome-wide SV Discovery Approaches

Hybridization-based

- Iafrate et al., 2004, Sebat et al., 2004

- SNP microarrays: McCarroll *et al.*, 2008, Cooper *et al.*, 2008, Itsara *et al.*, 2009

- Array CGH: Redon *et al.* 2006, Conrad *et al.,* 2010, Park *et al.,* 2010, WTCCC, 2010

Single molecule mapping

- Optical mapping**:** Teague et al., 2010 e.g. Bionano Genomics: Levy-Sakin et al, 2019

Sequencing-based

- Read-depth: Bailey et al, 2002

- Fosmid ESP: Tuzun *et al.* 2005, Kidd *et al.* 2008

- Next-gen sequencing: Korbel *et al.* 2007*,* Yoon *et al.*, 2009, Alkan et al., 2009, Chen *et al.* 2009; Mills 1000 Genomes Project, 2011, Sudmant *et al.* 2015a,

- Long-read sequencing and assembly: Chaisson *et al.,* 2015, 2019, Pendleton *et al.,* 2015, Sedlazeck et al., 2018 Audano *et al*, 2019, Ebert et al,, 2021

Array Comparative Genomic Hybridization

Array of DNA Molecules

Test individual DNA Sample

Normal reference DNA Sample

**Hybridization**

Cy5 Channel

Cy3 Channel

Merge

12 mm

One copy gain = $\log_2(3/2) = 0.57$ (3 copies vs. 2 copies in reference)

One-copy loss = $\log_2(1/2) = -1$
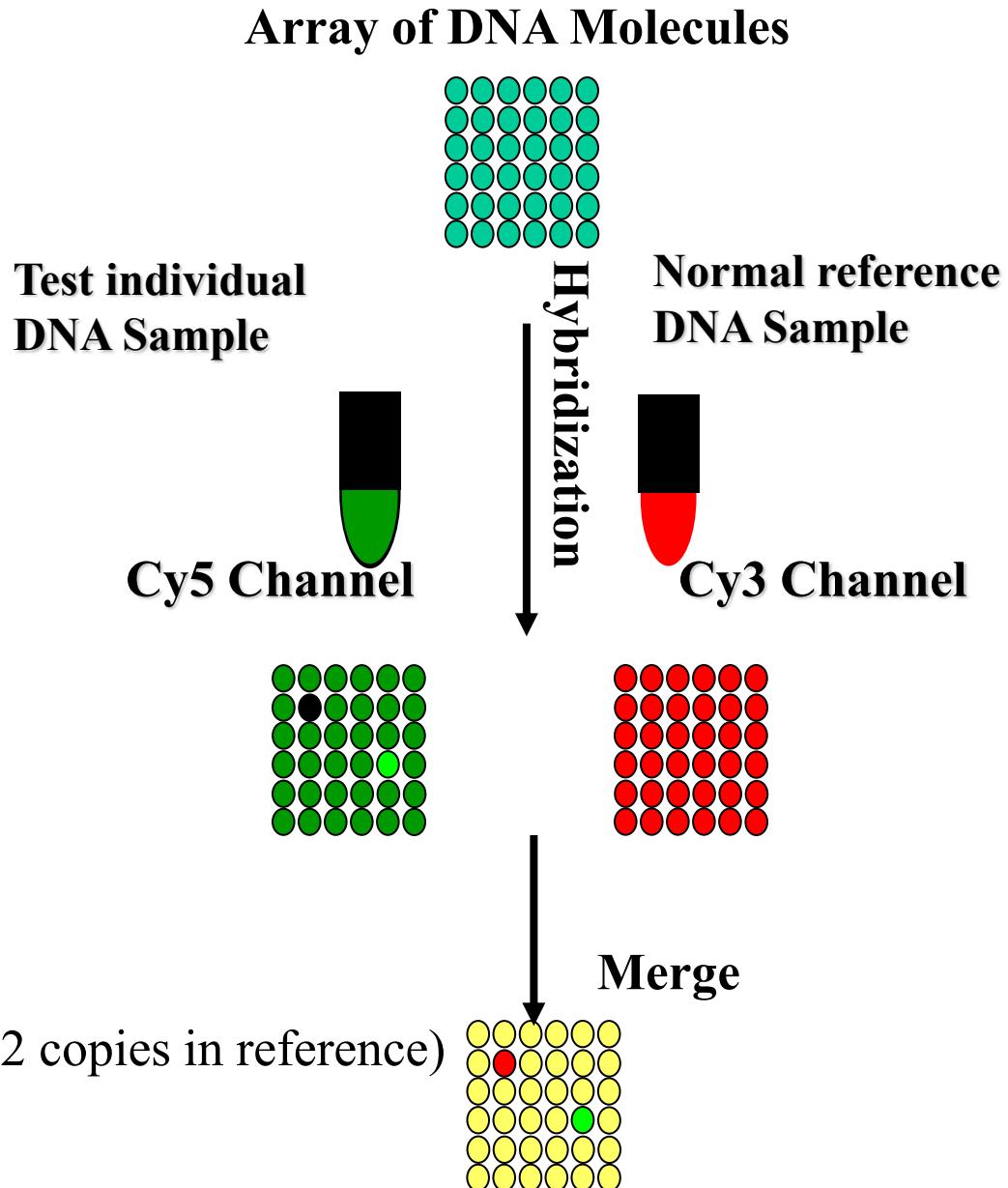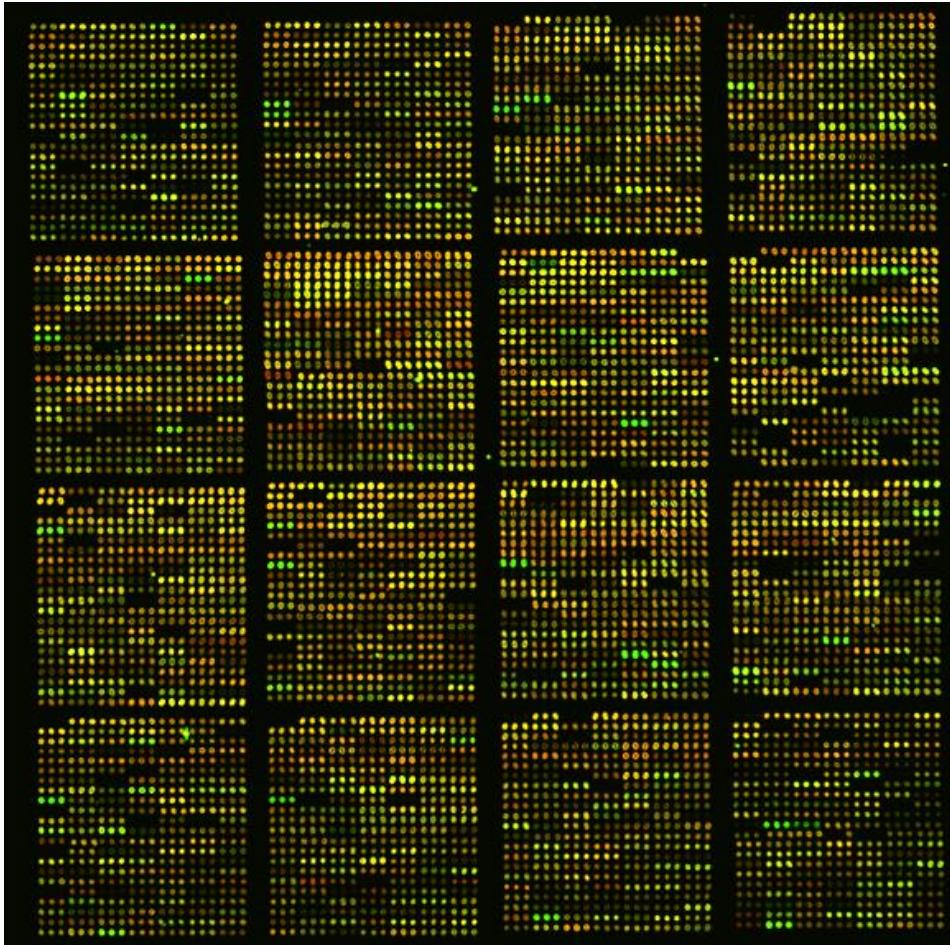
# SNP Microarray detection of Deletion (Illumina)

LogR and B-Allele Frequency

Human chromosome 3 position

A- or B-

AB

AB

~55 kbp
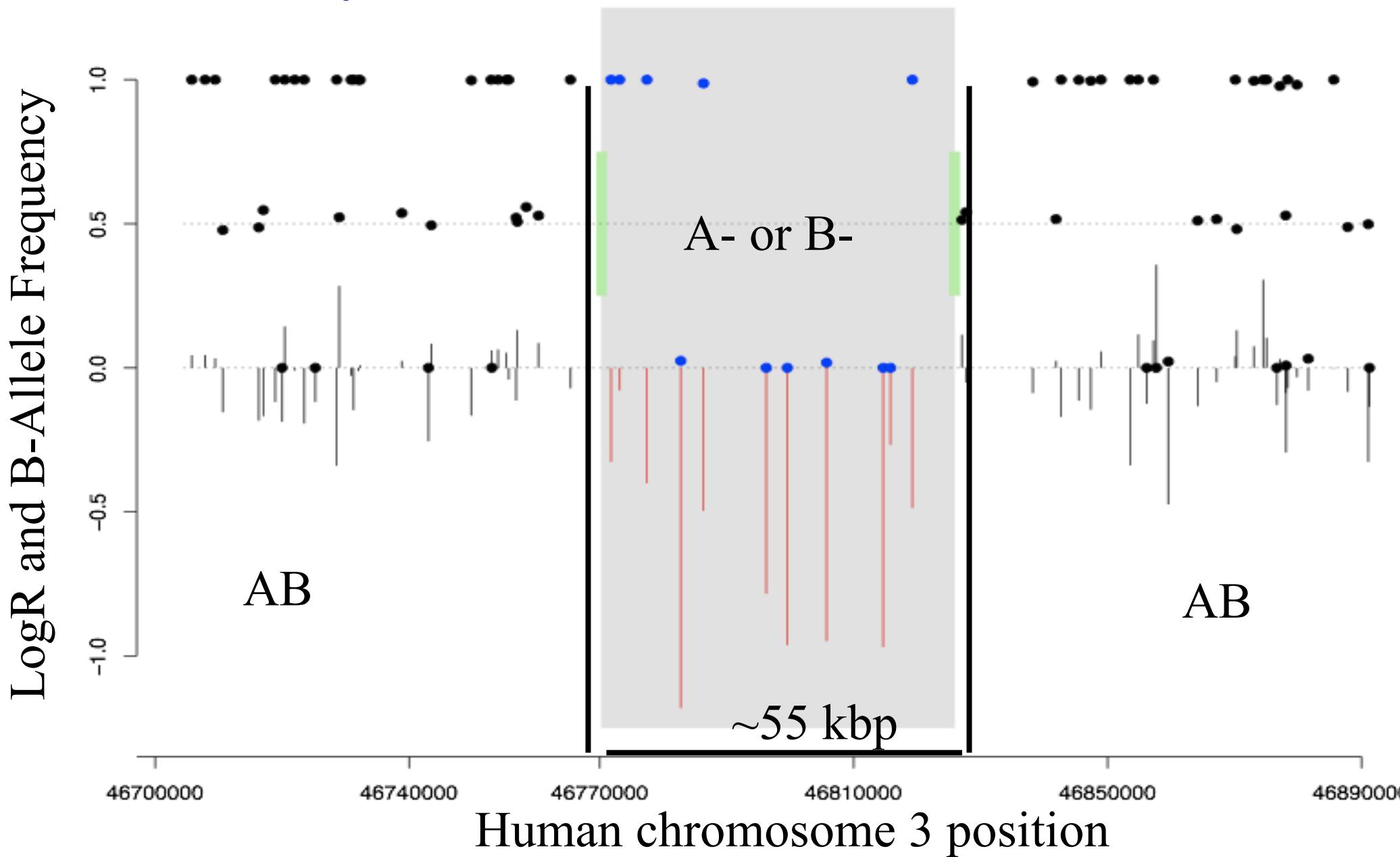
SNP Microarray detection of duplication

LogR and B-Allele Intensity

Human chromosome 2 position

AB

ABB
or AAB

AB
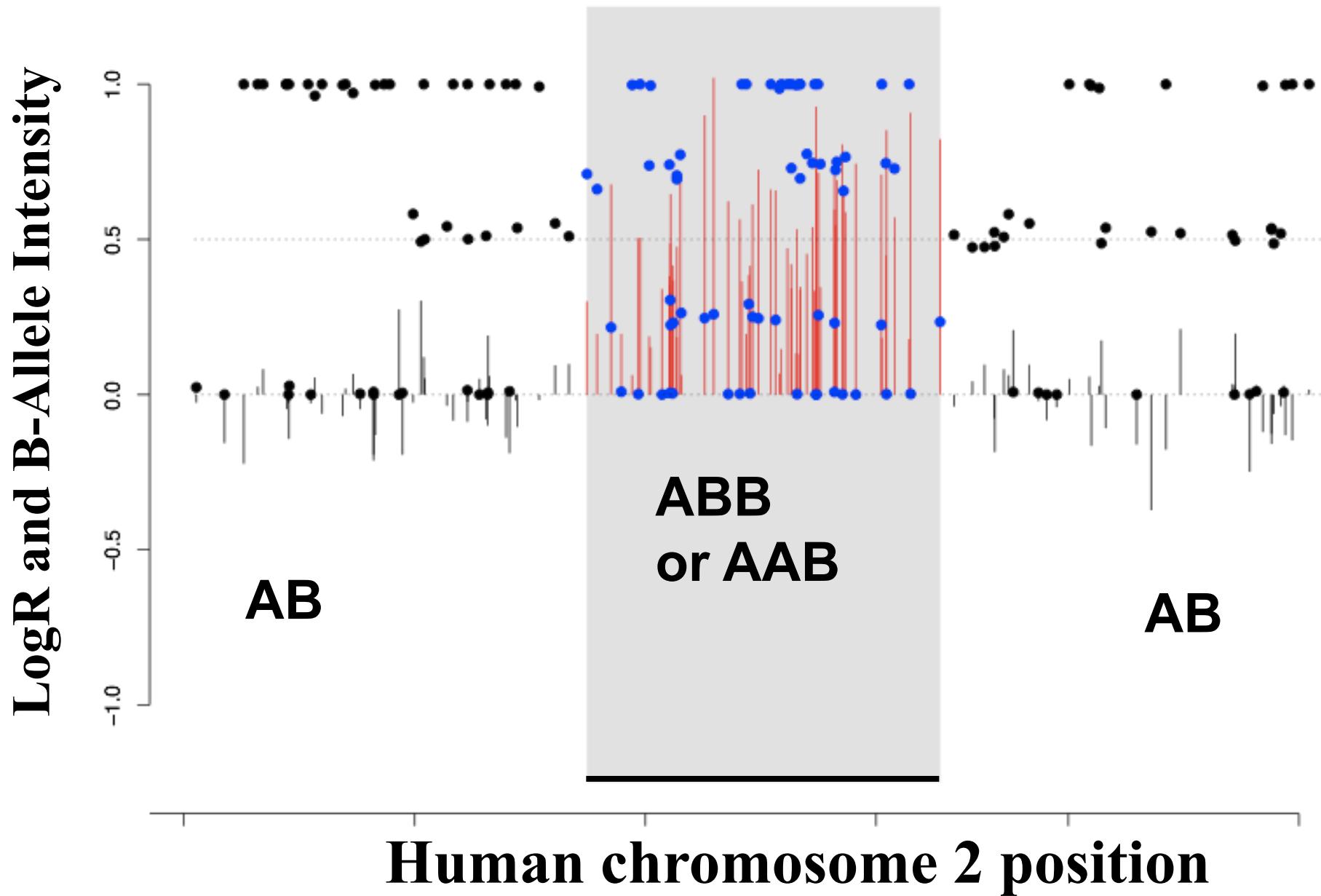
Using sequence read pairs to detect structural variation

Human Genomic DNA

Human DNA

Genomic Library (1 million clones)

Sequence ends of genomic inserts & map paired-ends to human genome

Concordant **Insertion** **Deletion** **Inversions**

Fosmid

> < > < > < < <

Build35
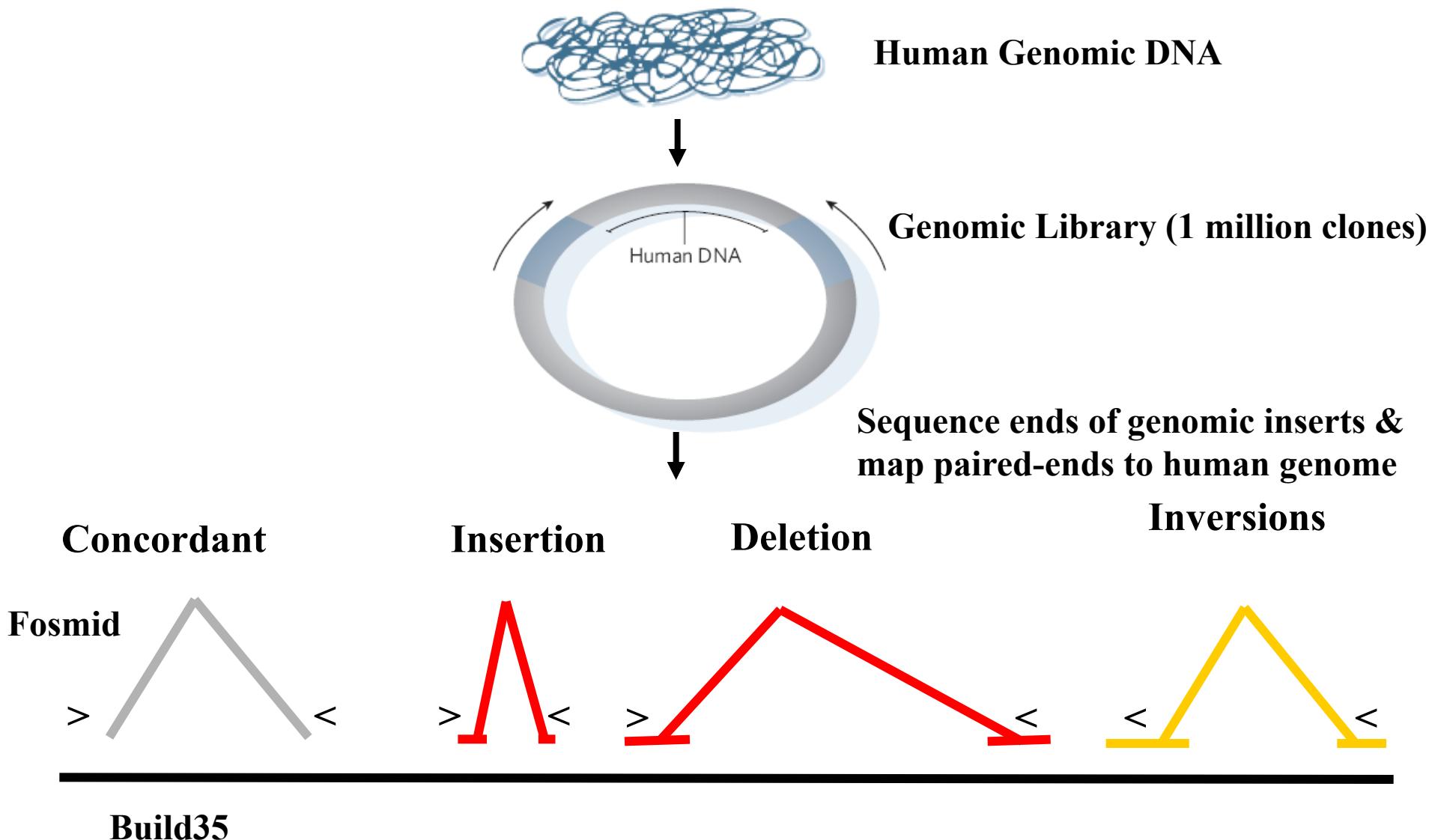
Dataset: 1,122,408 fosmid pairs preprocessed (15.5X genome coverage)
639,204 fosmid pairs BEST pairs (8.8 X genome coverage)

Genome-wide detection of structural variation (>8kb) by end-sequence pairs or "mate pairs"


a) Insertion, Deletion, Inversion

Span <32 kb

Span >48 kb

Inconsistent orientation

b) Fosmid Size Distribution(G248)

Number of Fosmids

< 32 kb Putative Insertion

>48 kb Putative Deletion

Fosmid_Insert_Size

c)

discordant by orientation (yellow/gold)

discordant size (red)

duplication track

Tuzun et al, *Nat. Genetics*, 2005; Kidd et al., *Nature*, 2008
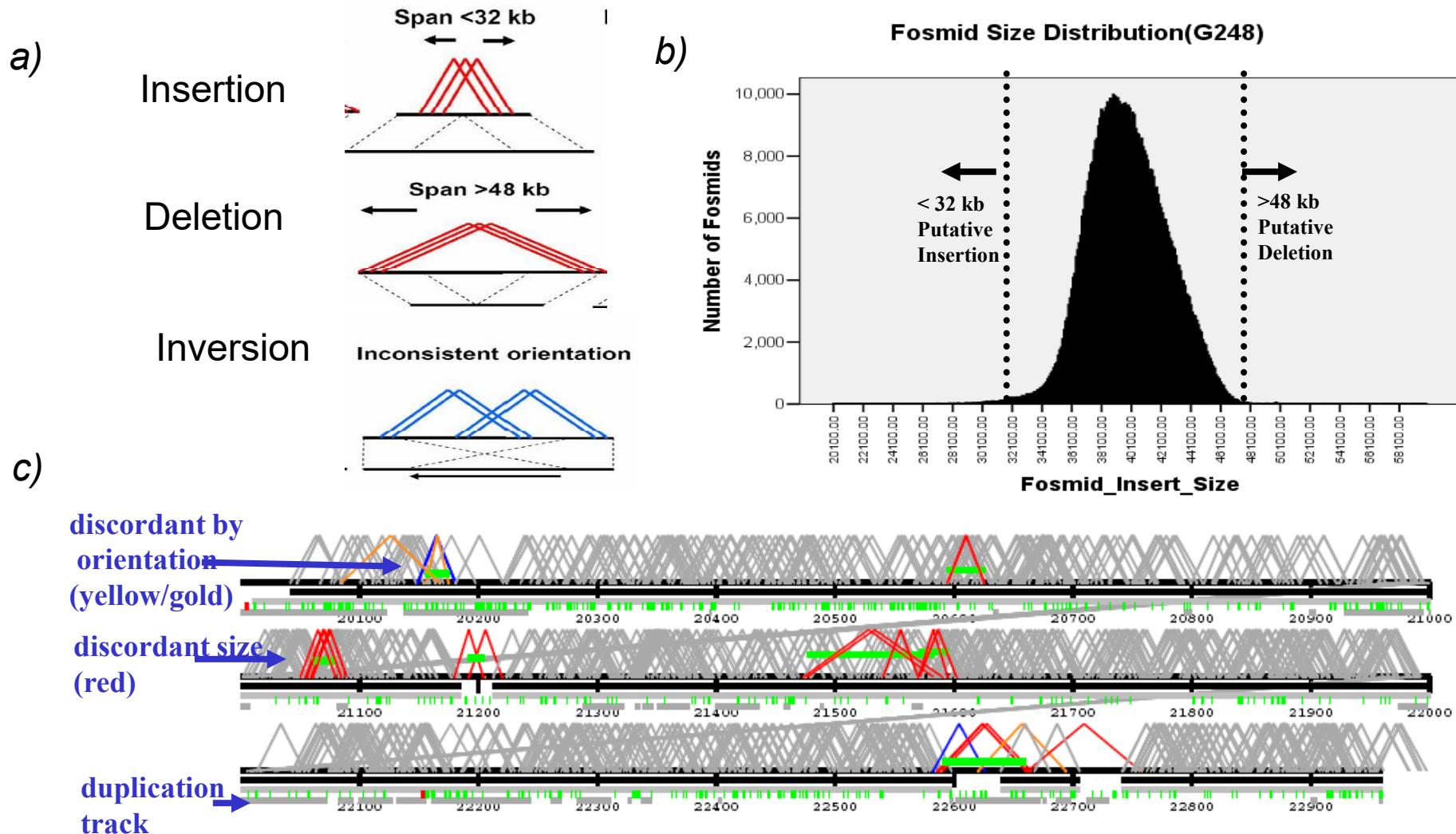
Next-Generation Sequencing Methods

- **Read pair analysis**
  - Deletions, small novel insertions, inversions, transposons
  - Size and breakpoint resolution dependent to insert size
- **Read depth analysis**
  - Deletions and duplications (CNV) only
  - Relatively poor breakpoint resolution
- **Split read analysis**
  - Small novel insertions/deletions, and mobile element insertions
  - 1bp breakpoint resolution
- **Local and *de novo* assembly**
  - SV in unique segments
 - 1bp breakpoint resolution

Alkan et al., *Nat Rev Genet, 2011*
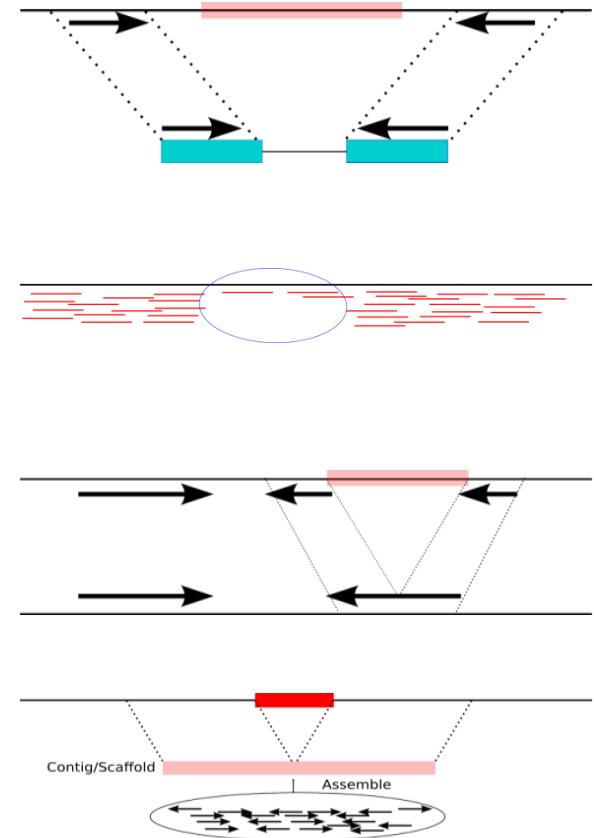
Using Sequence Read Depth

- **Map whole genome sequence to reference genome**
  - Variation in copy number correlates linearly with read-depth

**Illumina Sequence**

Reference Sequence

Sequence to Test
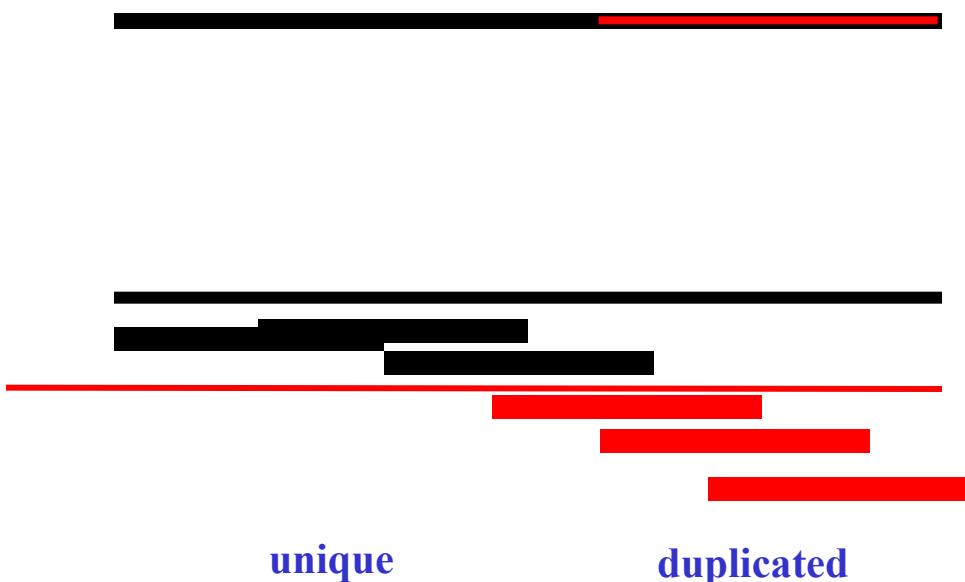
~~Celera's 27.3 million reads~~

Random Genome Sample

unique   duplicated

Bailey et al., Science, 2002

Personalized Duplication or Copy-Number Variation Maps
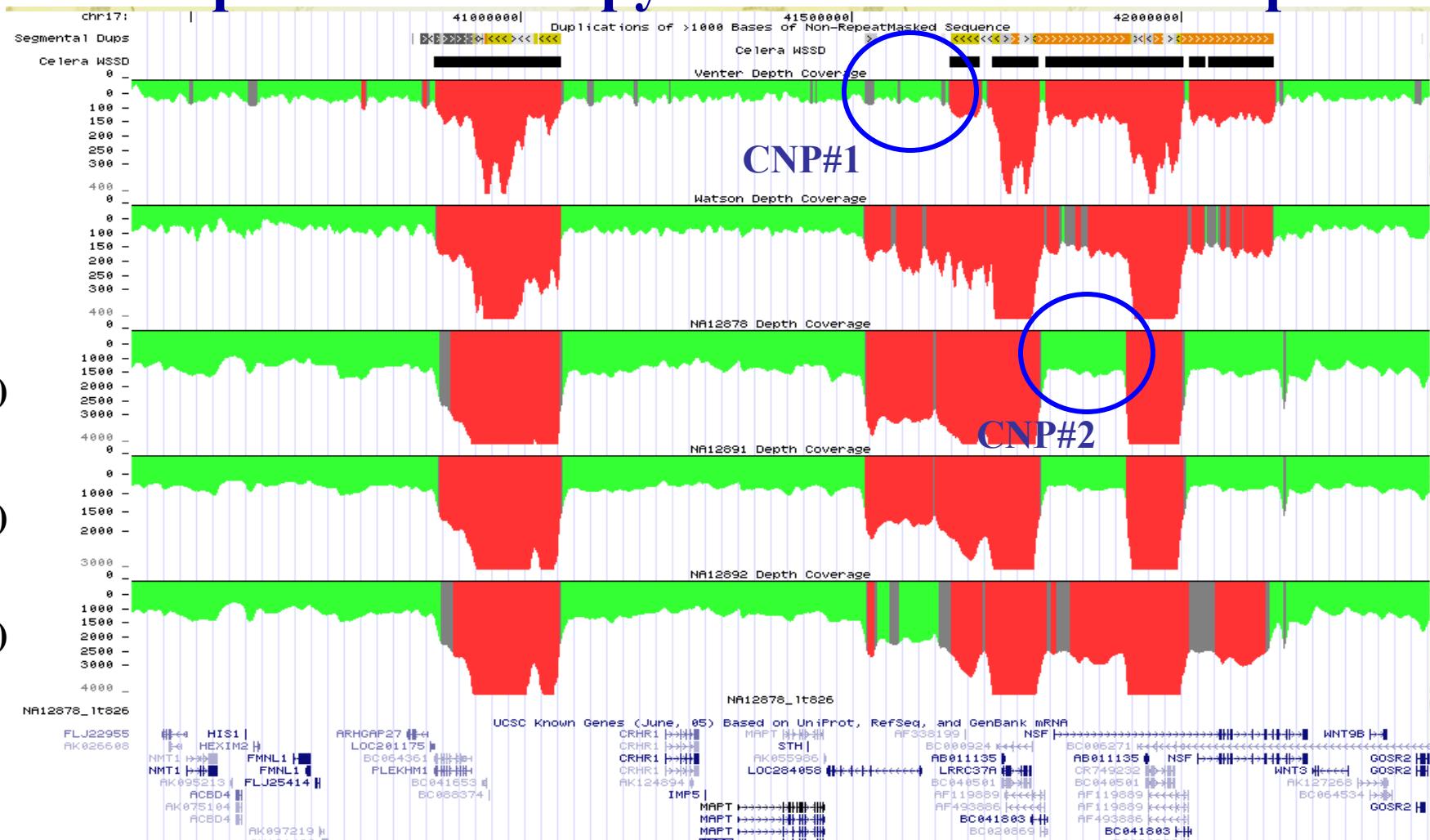
- Two known ~70 kbp CNPs, CNP#1 duplication absent in Venter but predicted in Watson and NA12878, CNP#2 present mother but neither father or child

Alkan, Nat. Genet, 2009

Read-Depth CNV Heat Maps vs. FISH
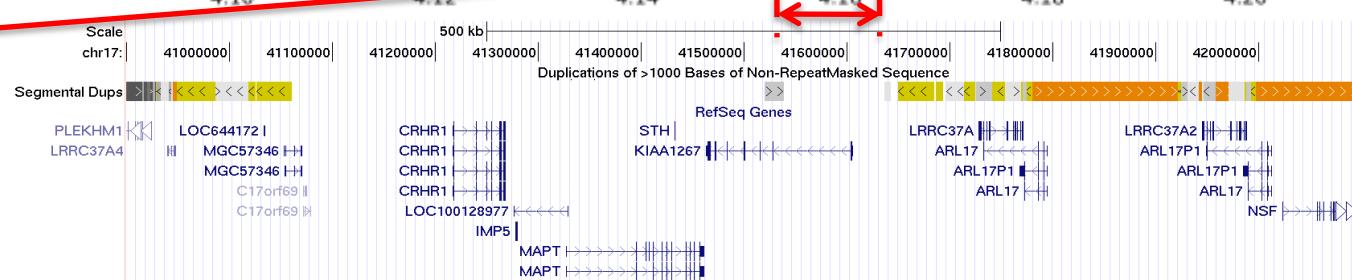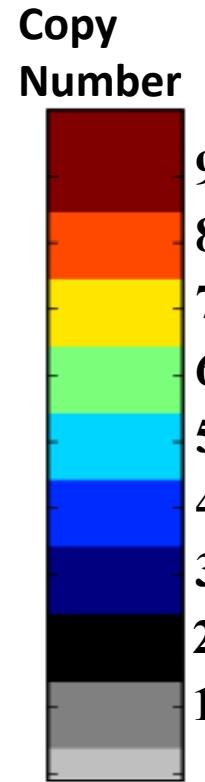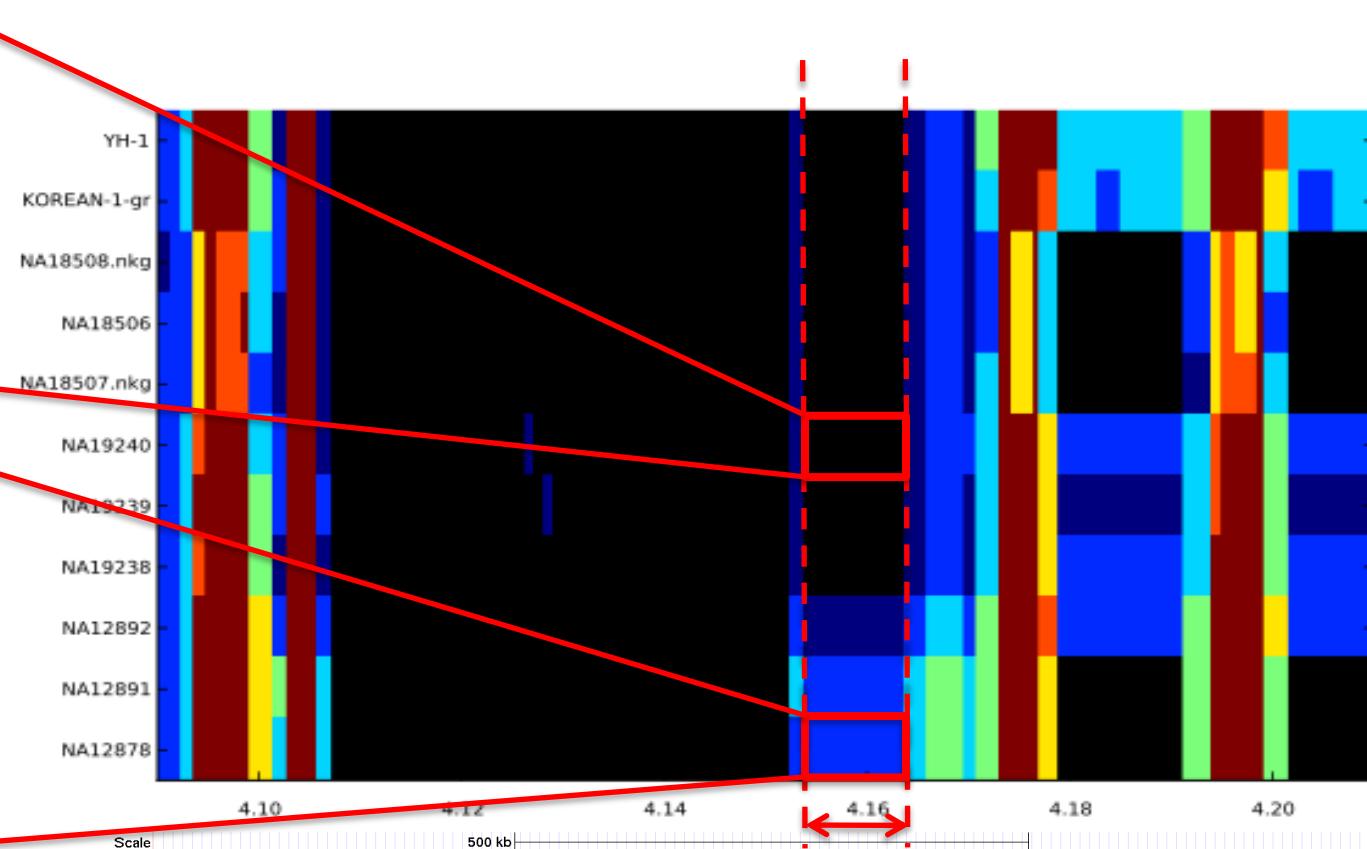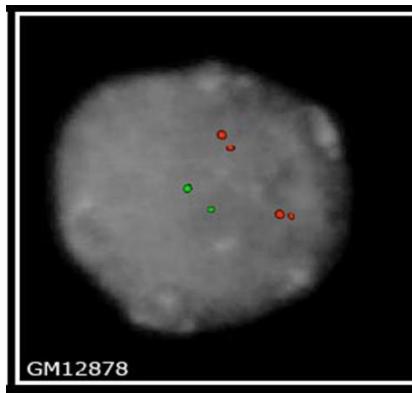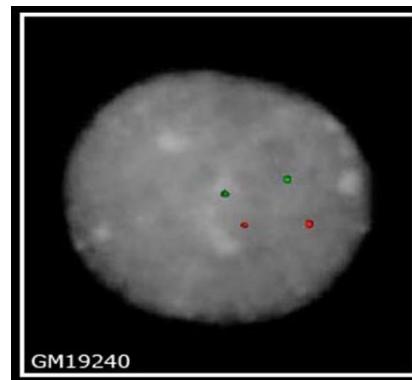
Challenges with indirect short-read approaches

- Repeat biases—a large fraction of events mediated by repeats are missed
- Size biases—read-pair methods limited by insert size while read-depth typically requires > 5kbp
- Class bias: deletions>>>duplications>>>>balanced events (inversions)
- Multiallelic copy number states—incomplete references and the complexity of repetitive DNA
- False negatives.

Long read Genome Sequencing Revolution
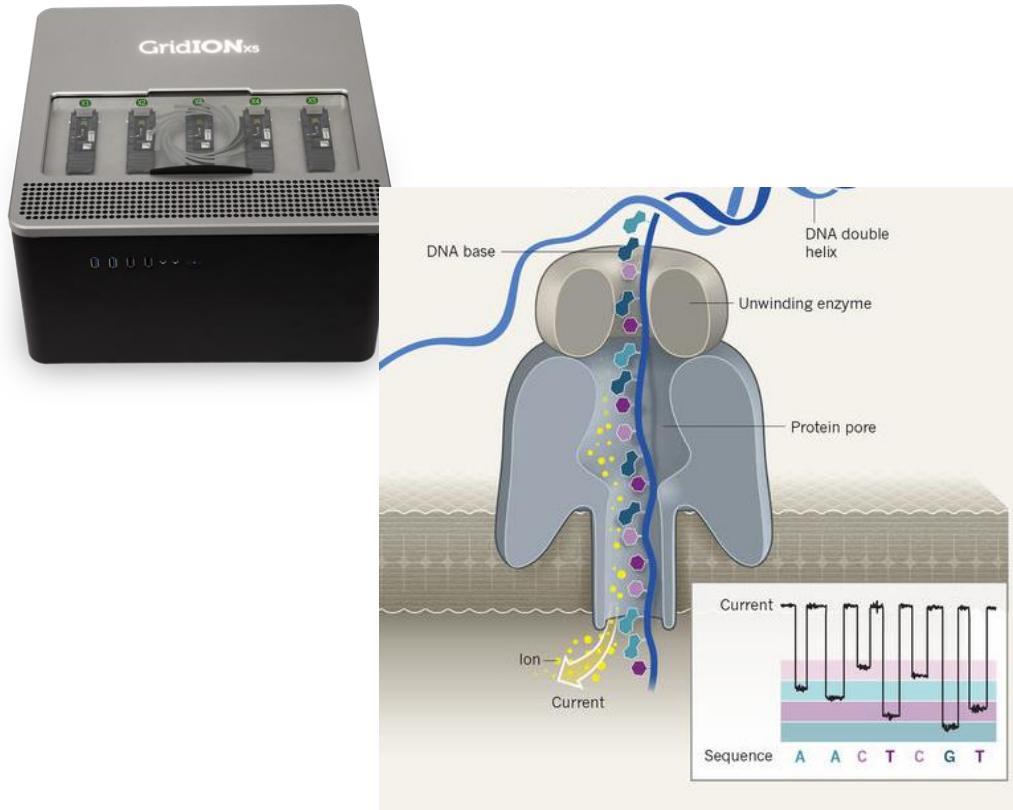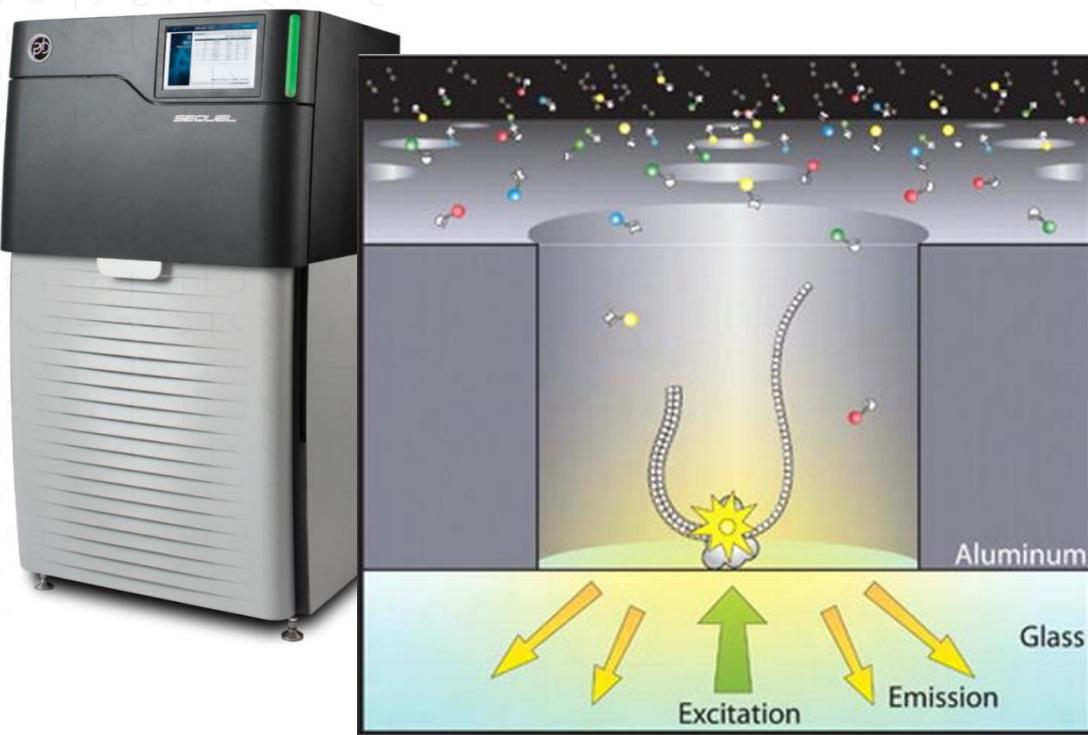
Pacific Biosciences (PacBio)—single-molecule real-time sequence (SMRT) data (15-50) kbp sequence reads
ONT (Oxford Nanopore Technology)—higher error rate but, portable, scalable native DNA sequencing of long-reads

Advances in long-read sequencing

HiFi Pac Bio Sequencing
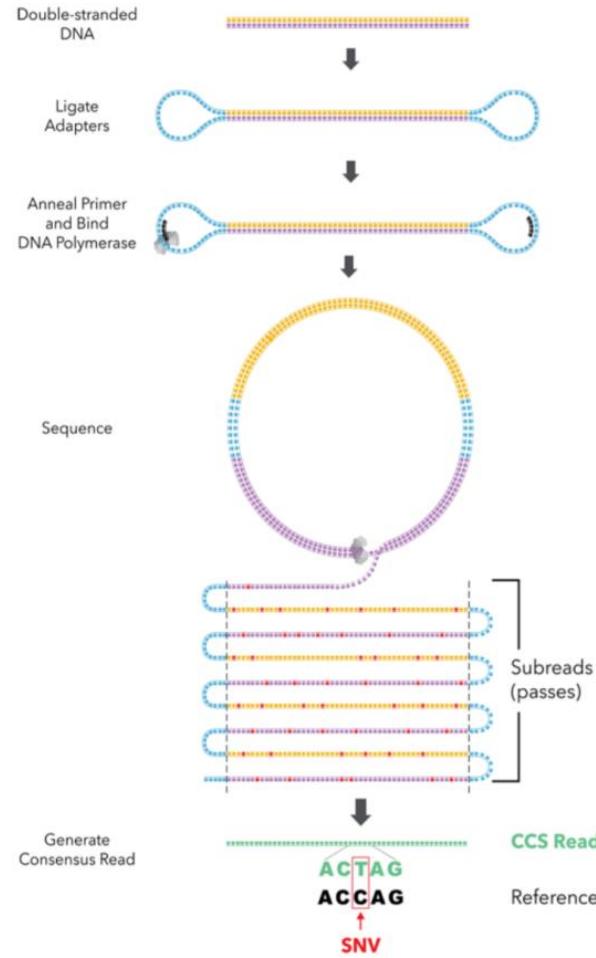
99.9% accurate 18-23 kbp reads

Ultra-long reads ONT

19.5X coverage

Median=36.7
Mean=67.3
N50=139.9
N1=631.9
Max=1538.3

Number of reads

Length (kbp), Total Gb = 62.56
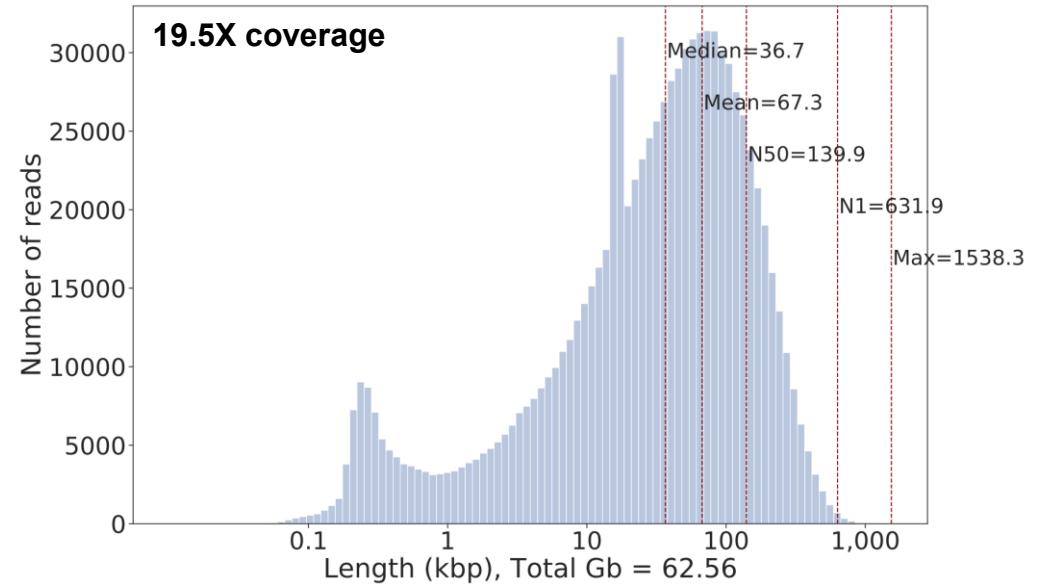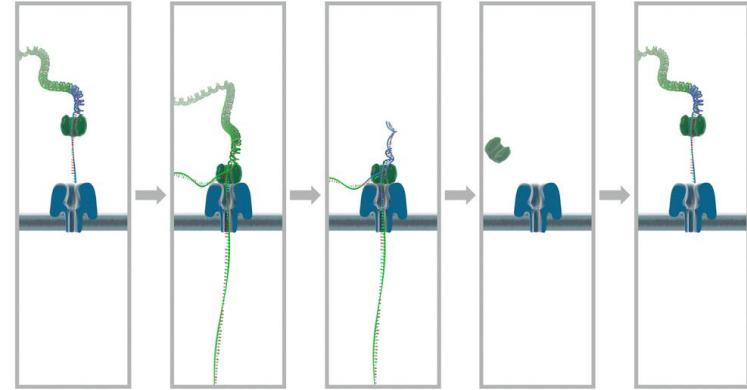
>100 kbp in length

Advantages of long read sequencing

Ultra-long Oxford Nanopore Technology (ONT)
~139 kbp

HiFi PacBio

~18-20 kbp

Illumina
150-300 bp

More uniform coverage and sequencing of native DNA

SHANK3

PacBio Sequence Coverage

Illumina Sequence Coverage
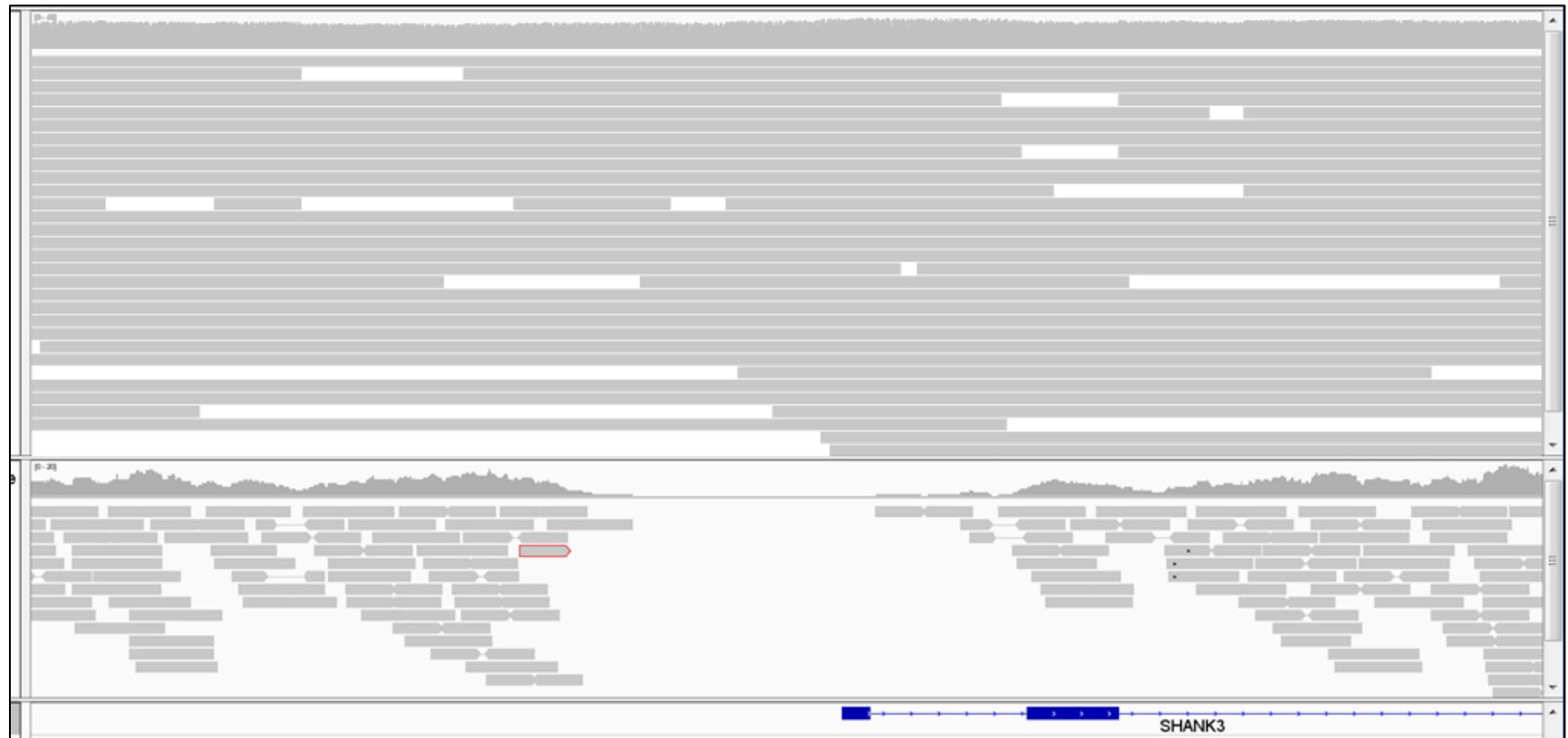
Increased sensitivity for structural variation (SV)
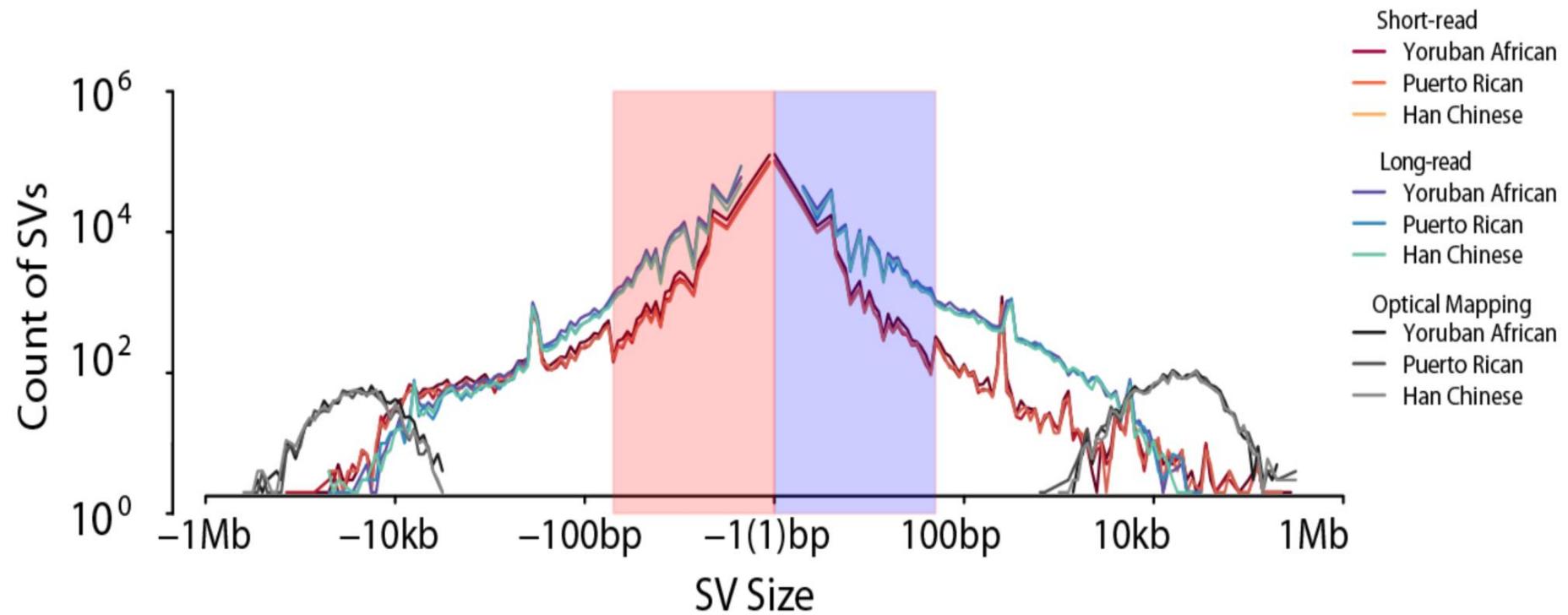
- ~25,000 PacBio SVs vs. 11,000 Illumina SVs >50 bp
- Eleven Illumina callers combined detect 49% of deletions and 11% of insertions in a human genome--**NGS misses 75% of SVs**

Chaisson et al, Nature, 2015; Chaisson et al., Nat Comm, 2019

Complete sequence of a human genome
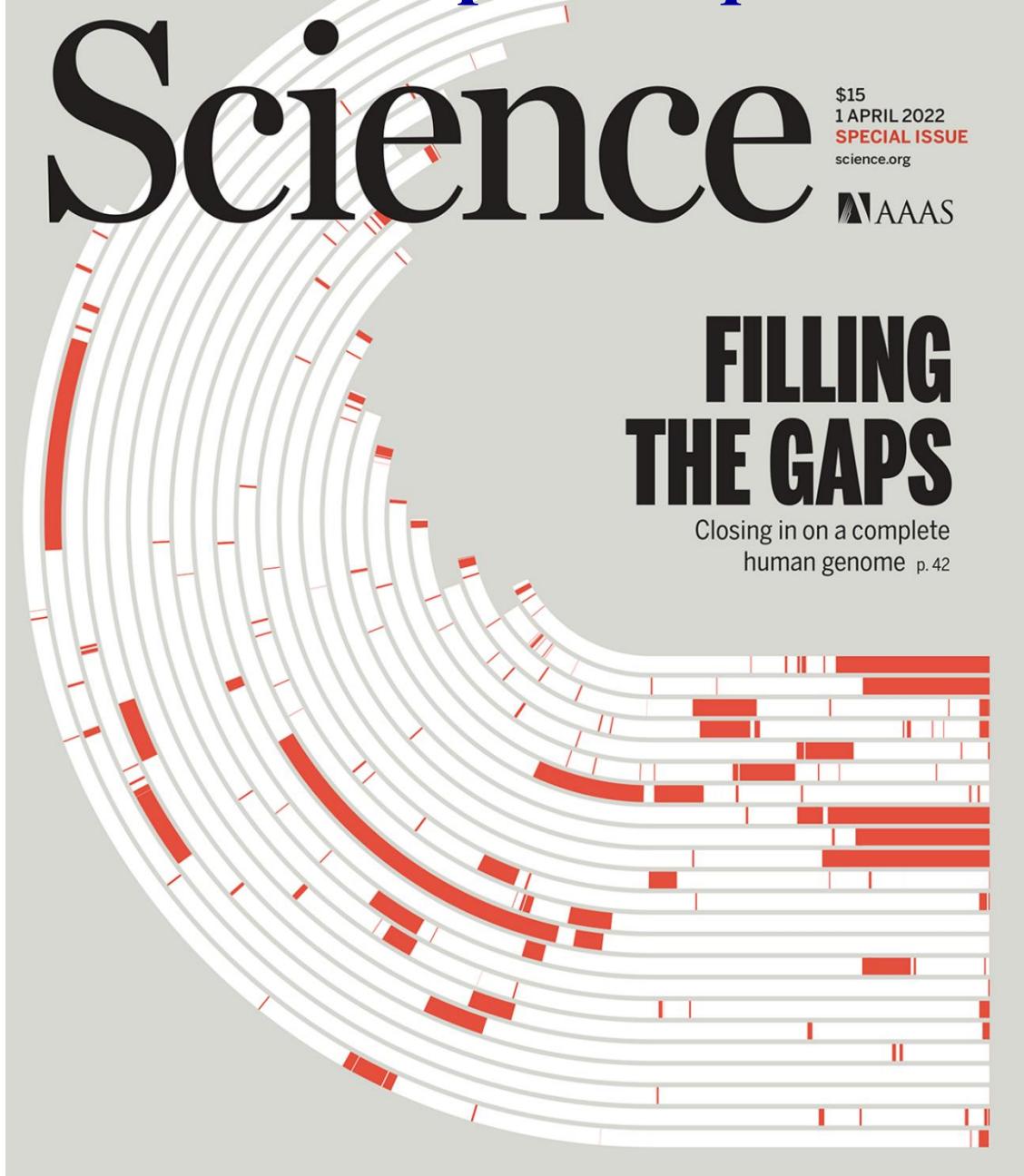
- 8% of missing genome sequence added (>200 Mbp)
- Complete sequence of centromeres, acrocentric and segmental duplications
- Adds 1956 gene predictions of which 130-190 are protein coding
- Framework for understanding the genetically most complex regions of our genome.

So how did we do it?

## We used an *effectively haploid* human cell line known as CHM13

CHM13 is a <u>c</u>omplete <u>h</u>ydatidiform <u>m</u>ole

23,X → 23,X 23,X → 46,XX

Fertilization

Loss of maternal pronucleus

Paternal chromosome endoreplication

A diploid genome with only one haplotype
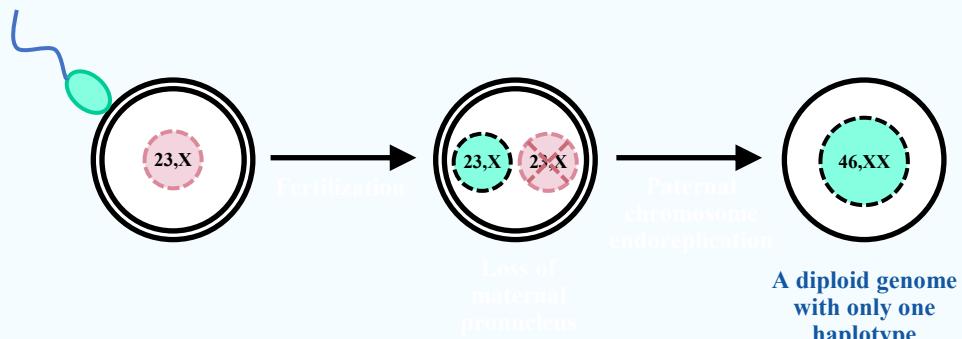
This greatly simplifies this problem because it allows us to assemble each chromosome without interference from a second set of chromosomes

We used two long-read sequencing technologies with complementary strengths

1. Pacific Biosciences (PacBio) high-fidelity (HiFi)
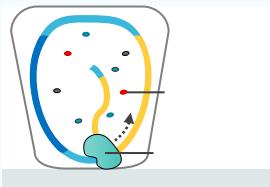
- **15-25 kbp long**
- **>99% accurate (similar to Illumina)**
- **Strength: Extremely accurate**

2. Oxford Nanopore Technologies (ONT)
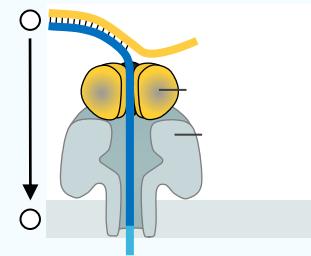
- **No limit in read length!**
- **93-99% accurate**
- **Strength: Extremely long**

Trio-based verkko assemblies of HG002

Total contigs: 81
Total contigs size: 3.03 Gbp
N50: 112.27 Mbp
AuN: 120.34 Mbp

Total contigs: 174
Total contigs size: 2.95 Gbp
N50: 133.99 Mbp
AuN: 139.56 Mbp

Plotted contigs: 45
Plotted contigs size: 3.02 Gbp

Plotted contigs: 51
Plotted contigs size: 2.93 Gbp

Haploype

Maternal

Paternal
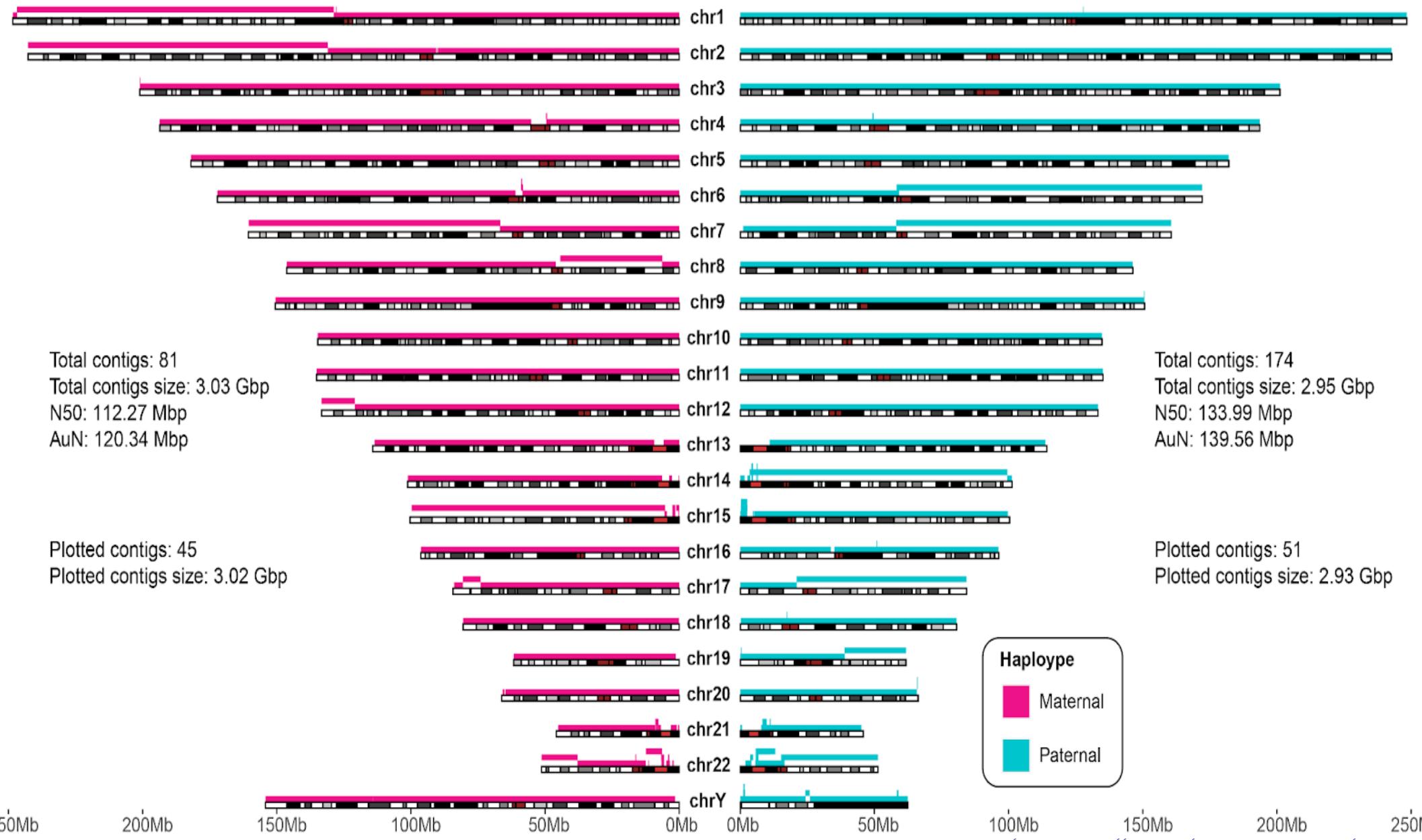
# LRS has transformed how we characterize copy number and structural variation

2015

Short-read copy number (CN) profile (reference-based)

2023

DupMasker profile of phased genome assemblies (reference-free)
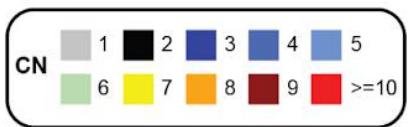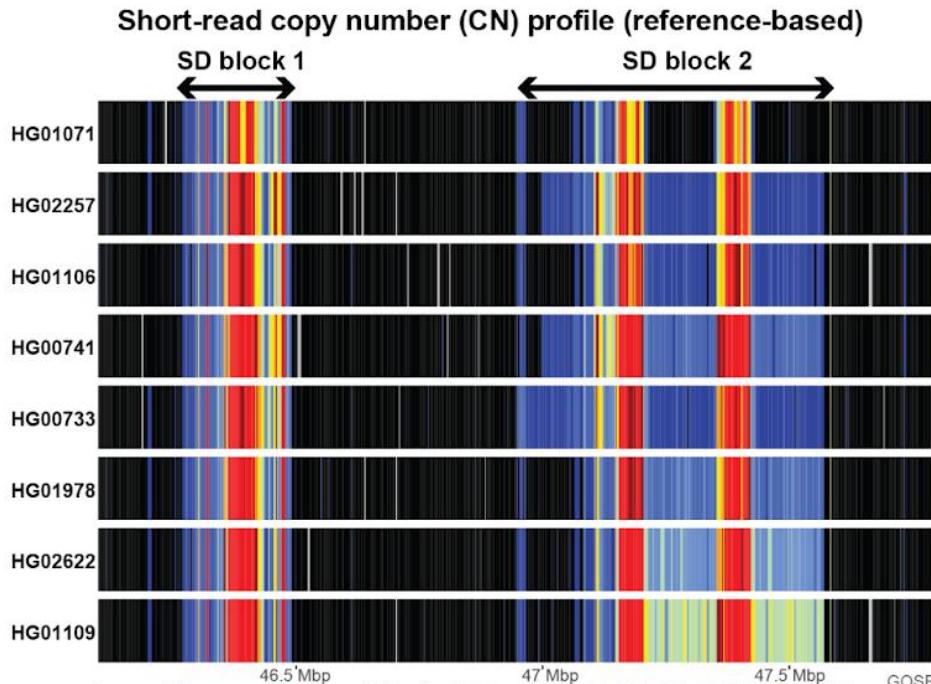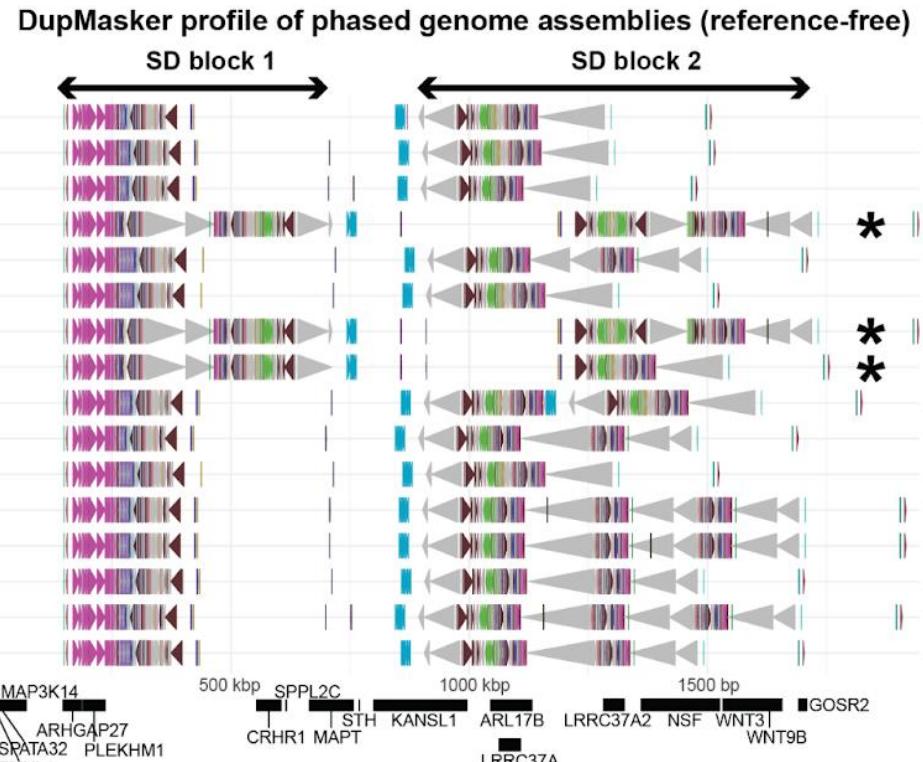
Primate phased genome assembly efforts

Human (~300 genomes)

4.5-6 mya

6-8 mya

Chimpanzee (2)

12-16 mya

Gorilla (2)

18-20 mya

Orangutan (2)

25-33 mya

Gibbon (1)

Macaque (1)

Kronenberg et al, *Science*, 2017; Ebert et al., Science, 2021; Liao/HPRC Nature, 2023; Yoo et al, bioRxiv, 2024
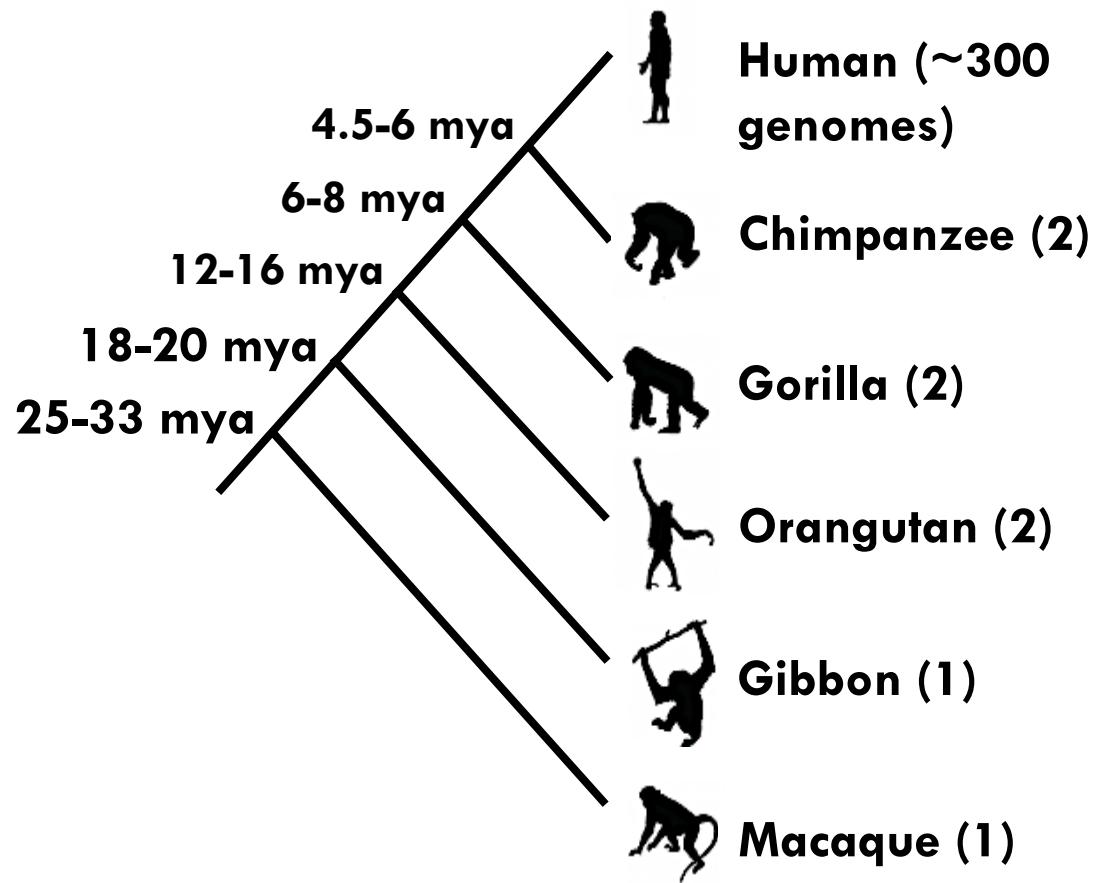
Ape telomere-to-telomere sequencing
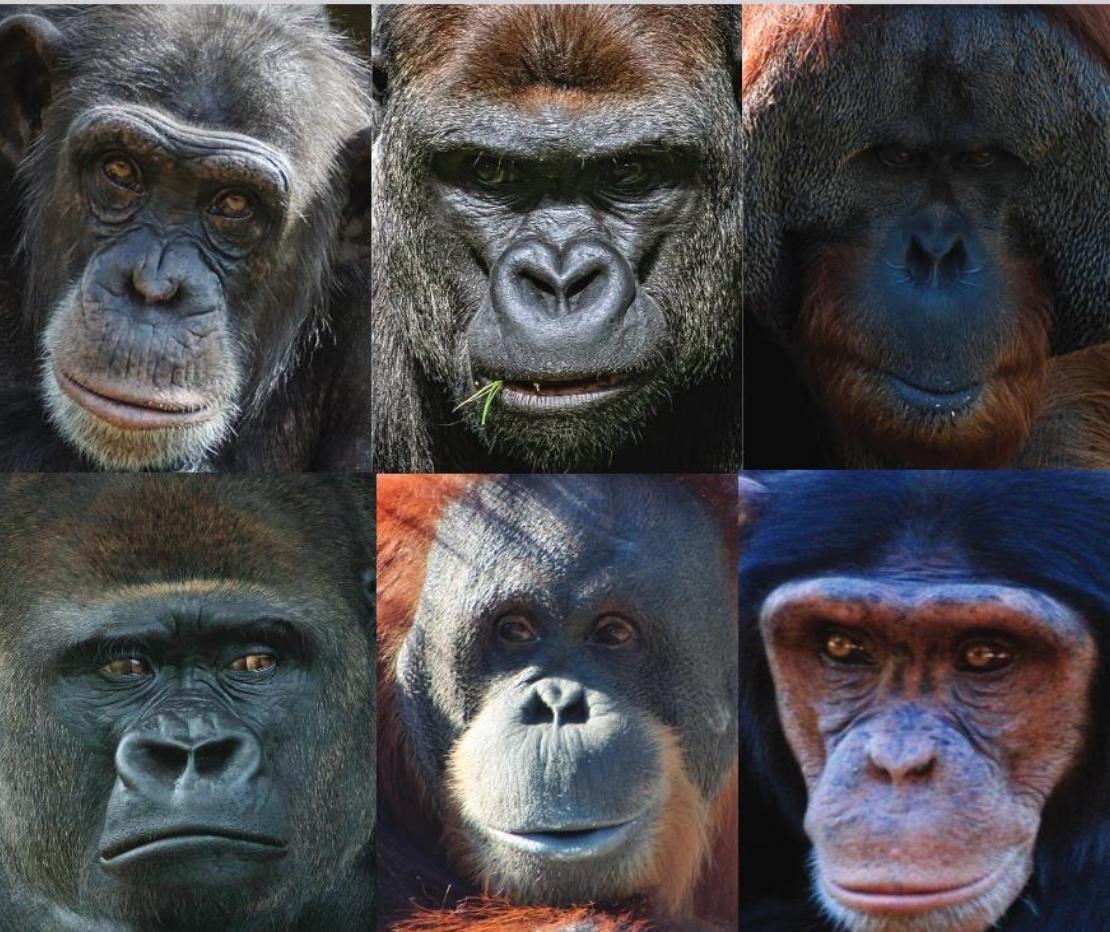
- Chimpanzee, bonobo, Western lowland gorilla, Bornean orangutan, Sumatran orangutan, Siamang
  - **led by UW, Penn State, NIH (60 labs)**
  - **Assembled** 12 genomes **(99.98-99.99% complete)**
- 94% non-rDNA chromosomes **T2T**
- **QV of 61.7-66.4 -- less than 1 error per 2.7 million base pairs**

Yoo et al, bioRxiv, 2024, Nature, 2025

Complete sequencing of ape chromosomes (SVbyEye "stacked" plot)

Chromosome 12
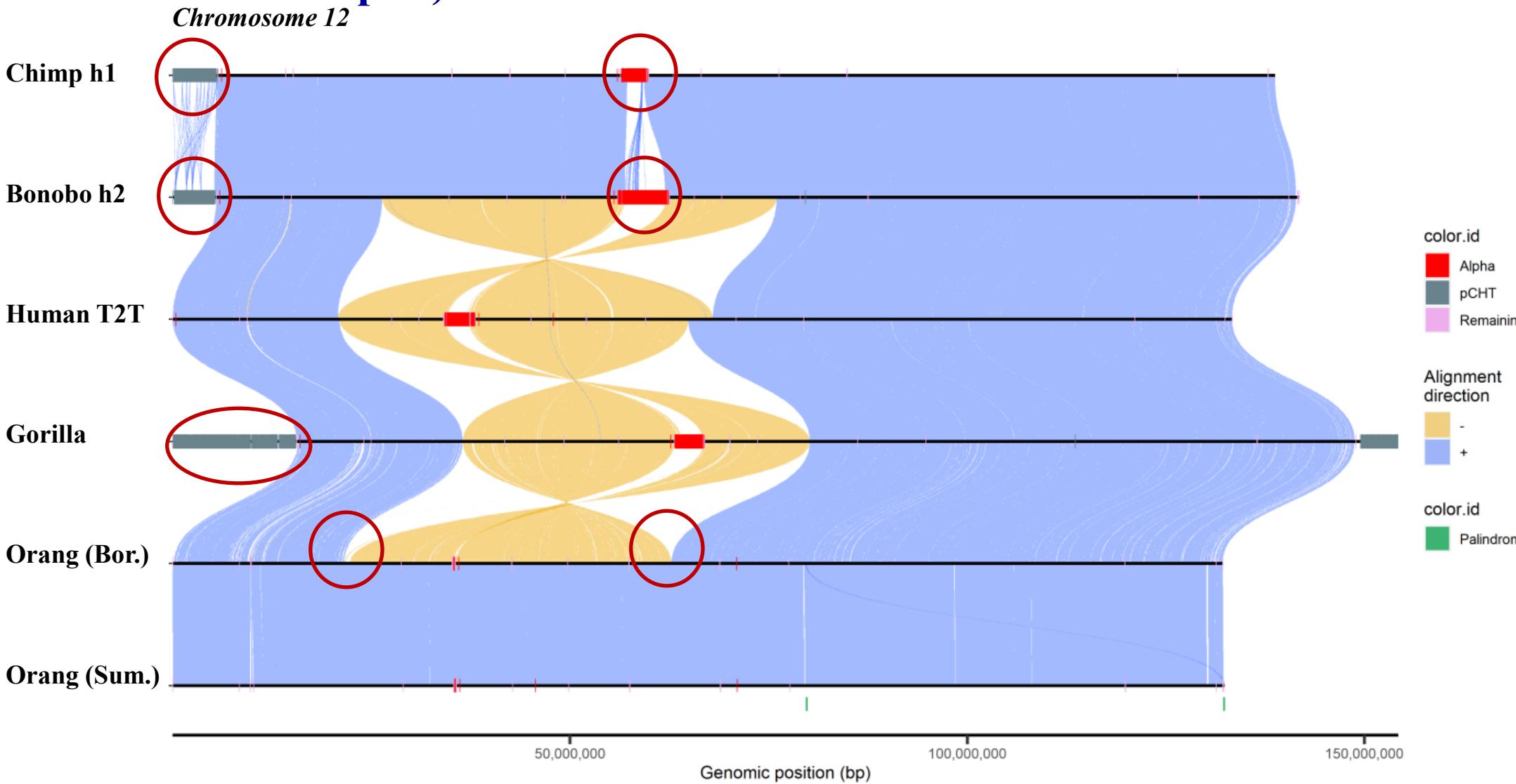
Complete sequencing of ape chromosomes


Chromosome 16
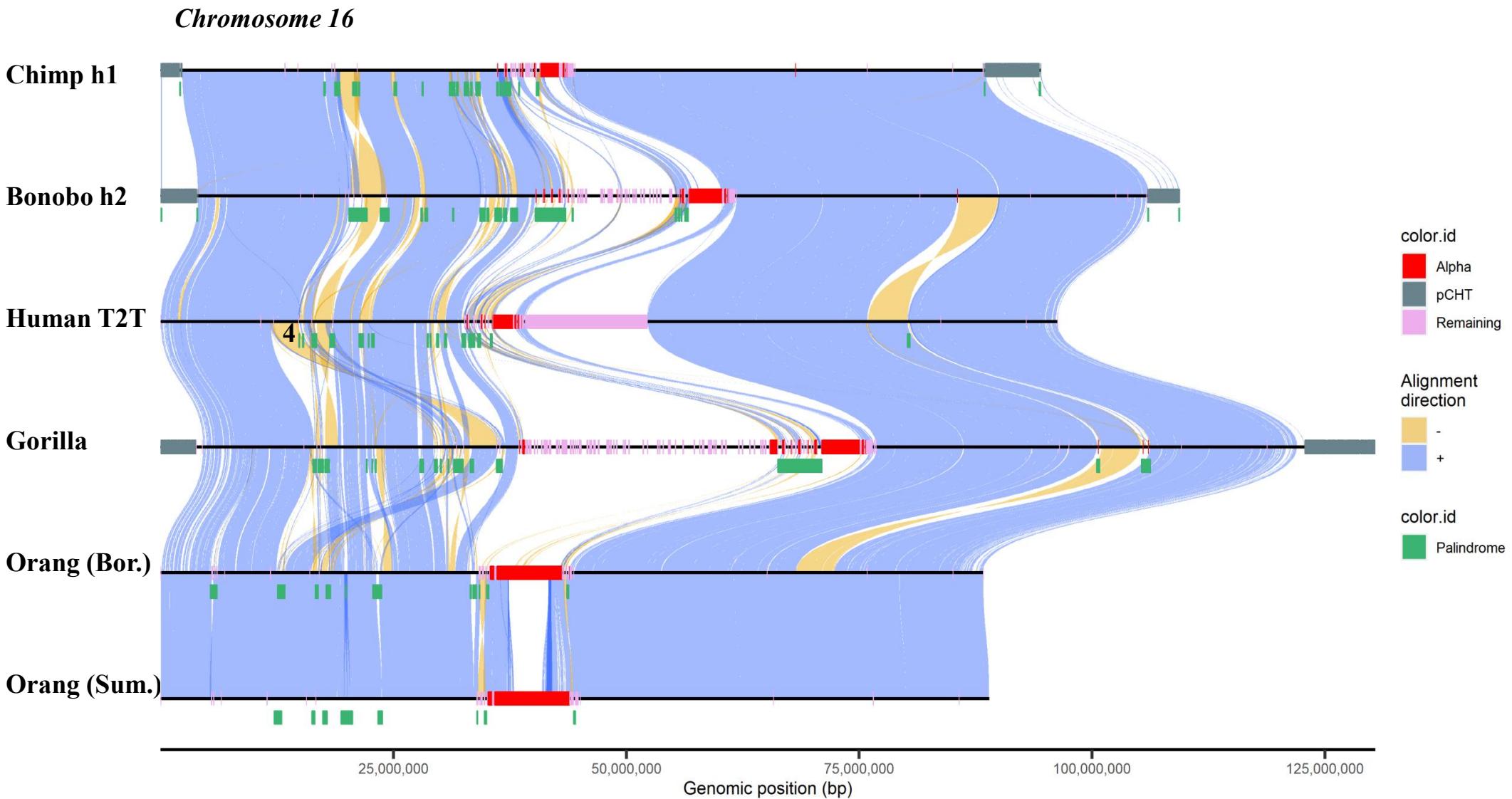
Inversions & SDs are the largest and most abundant form of structural variation affecting genes
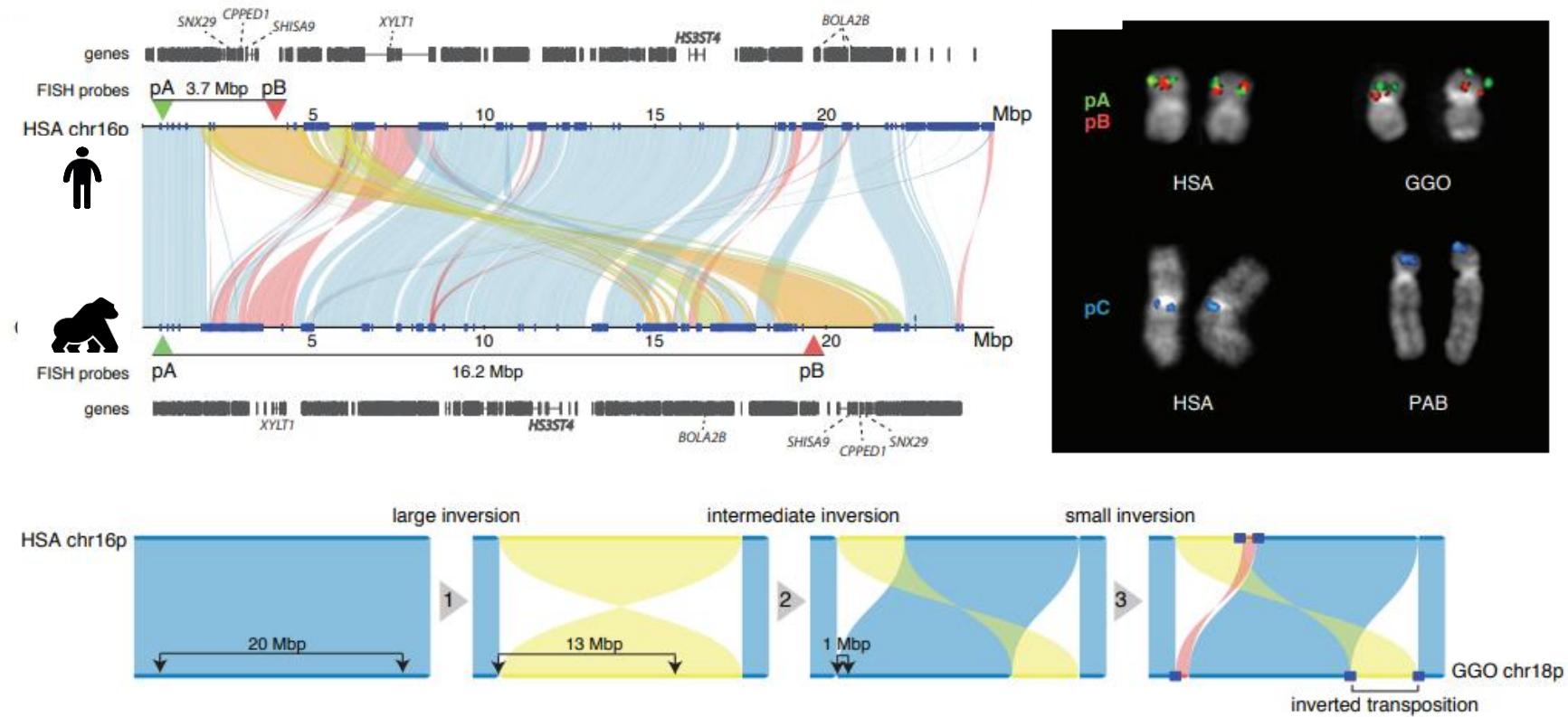

- Discovered a total of 1,140 inversions between ape species--522 are novel; 63.5% are flanked by large highly identical duplications

# Lineage-specific duplicate genes emerge at the edges of large-scale inversions
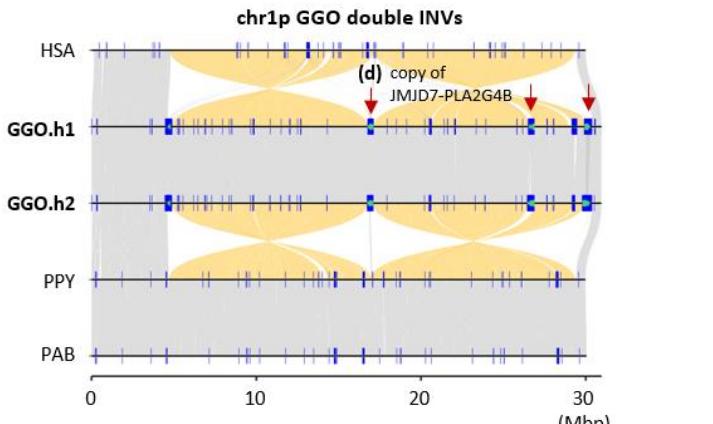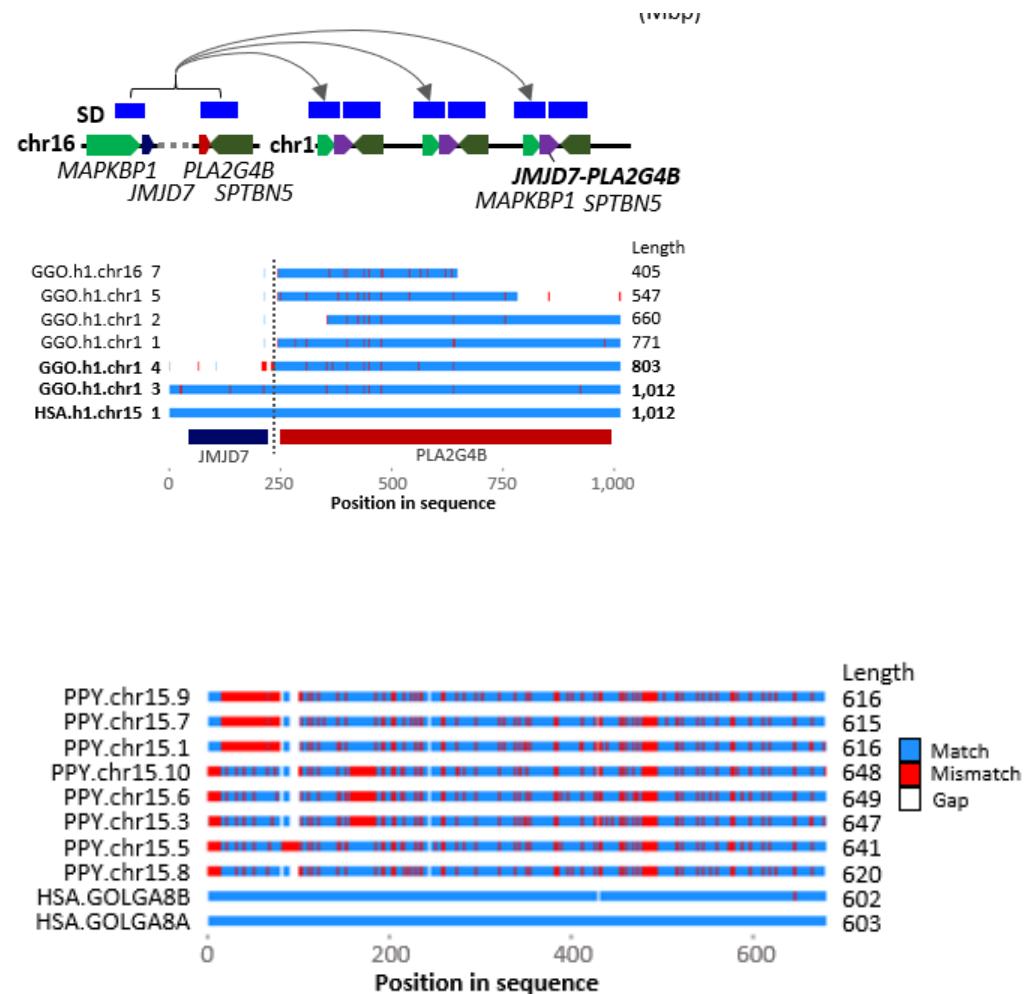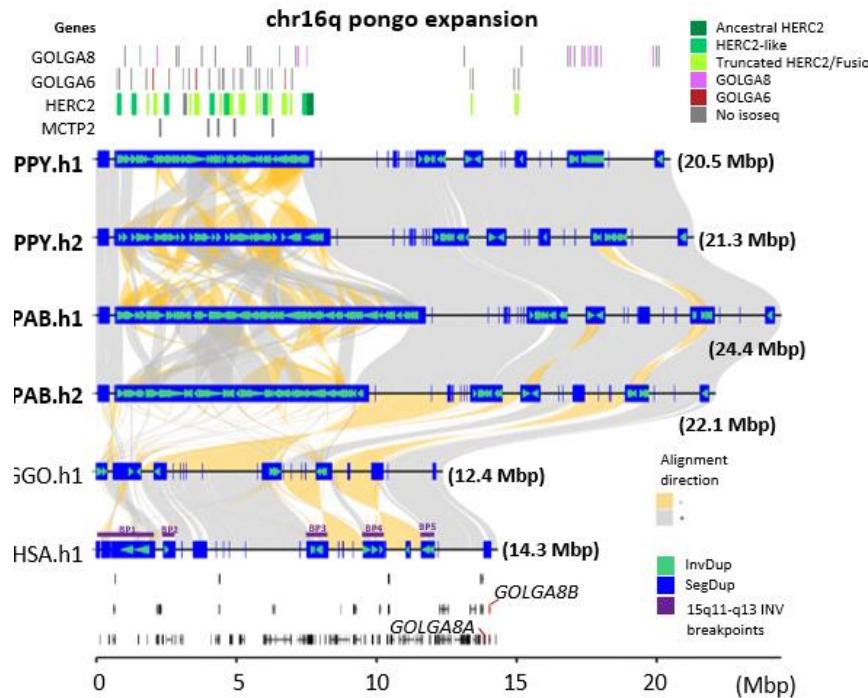
Lineage-specific ape protein-coding genes

Species	Human transcripts mapped	Orthologous loci	Novel Loci with Isoseq support	Novel loci overlapping SDs	Novel isoforms Outside of novel loci
Bonobo (PPA)	99.82%	93.52%	1482 (6.48%)	1004	1708 (2.1%)
Chimp (PTR)	99.77%	94.82%	1167 (5.16%)	904	2560 (2.9%)
Gorilla (GGO)	99.80%	94.98%	1153 (5.12%)	812	2105 (2.6%)
S. Orang (PAB)	99.44%	94.01%	1328 (5.99%)	909	2363 (2.9%)
B. Orang (PPY)	99.40%	93.95%	1336 (6.05%)	906	2239 (2.8%)
Siamang (SSY)	99.27%	96.51%	770 (3.49%)	471	3638 (5.1%)

*Number of protein coding genes annotated: > 200 AA protein length filter, 50% protein homology percentage filter, IsoSeq filter applied

- **5-6% novel, multi-exonic protein coding per ape genes -70-80% driven by lineage-specific SDs** Yoo et al, bioRxiv, 2024, Nature, 2025

Human Segmental duplication polymorphism

Jeong et al, bioRxiv, 2024, *Nat Genet, 2025,* Yoo et al, unpublished
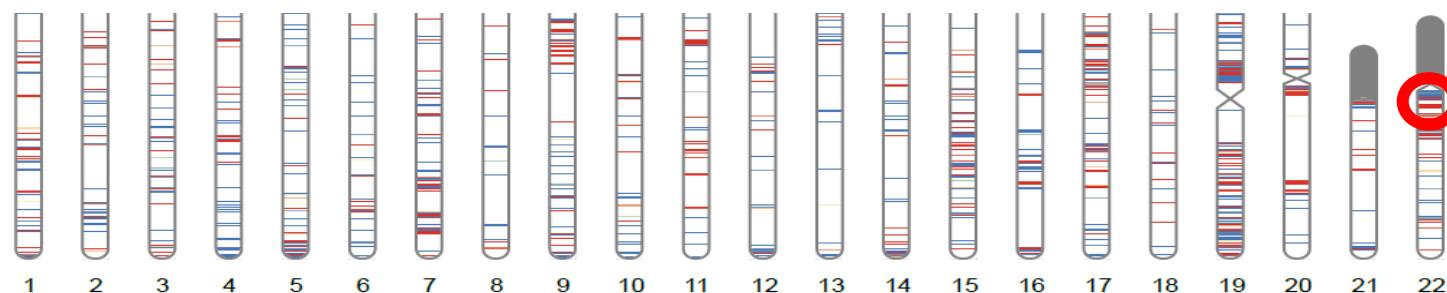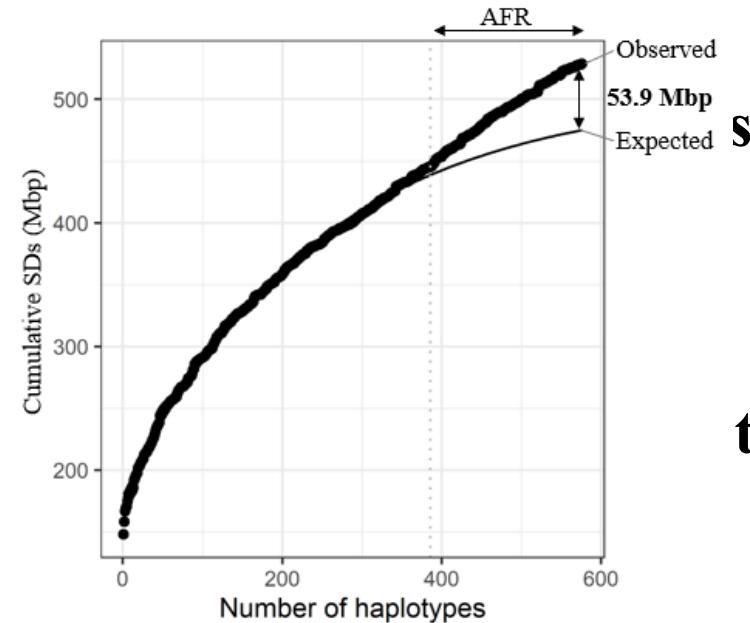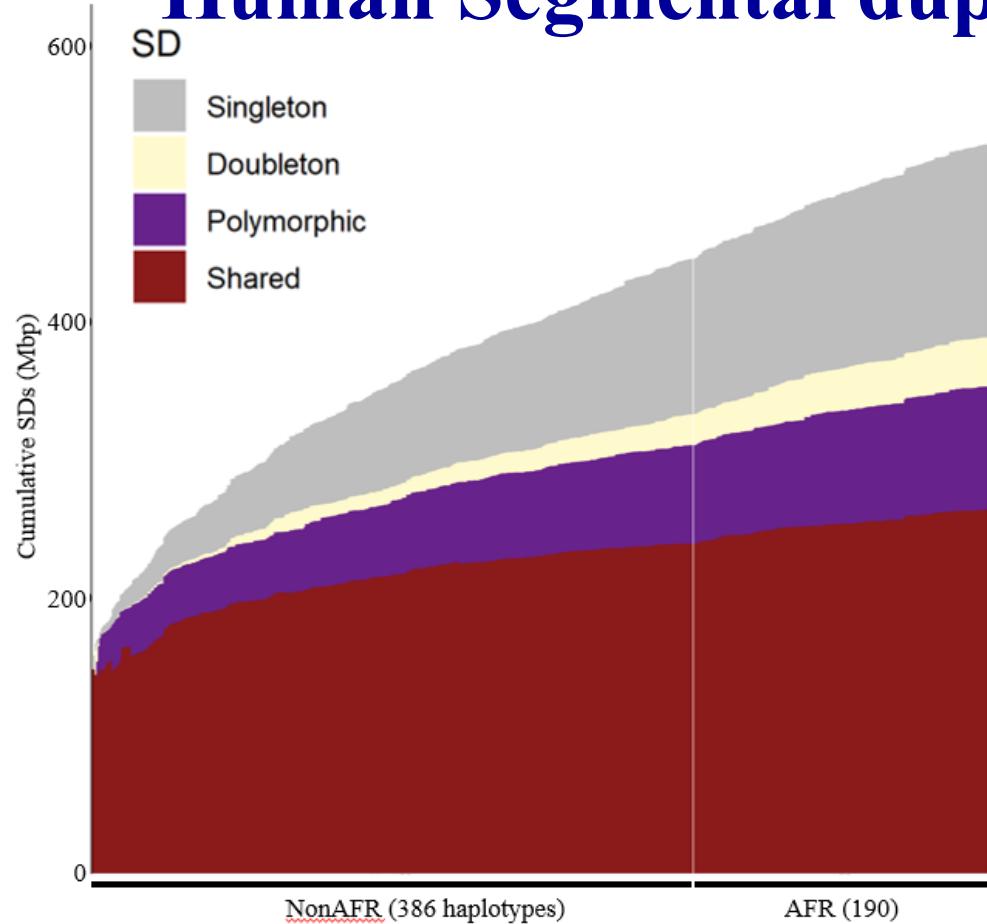
22q11 syndrome LCRA.
Complexity of normal human variation

Rearrangement-associate

Rearrangement-associated

50 diverse haplotypes of block A

superpop
- AFR
- AMR
- EAS
- EUR
- SAS

Haplotype count

Porubsky et al, bioRxiv, 2025
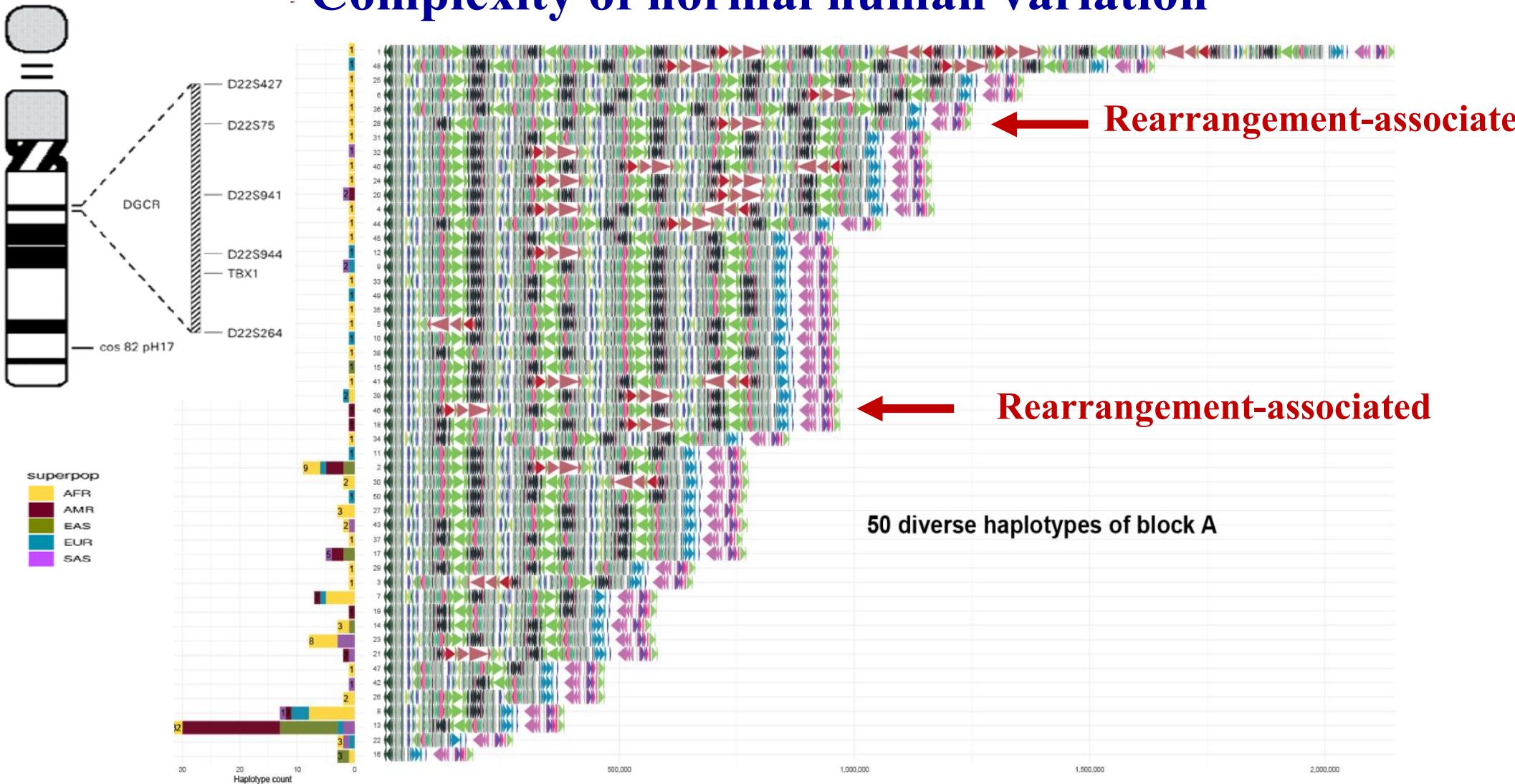
# Copy number and structural variation of *TBC1D3*
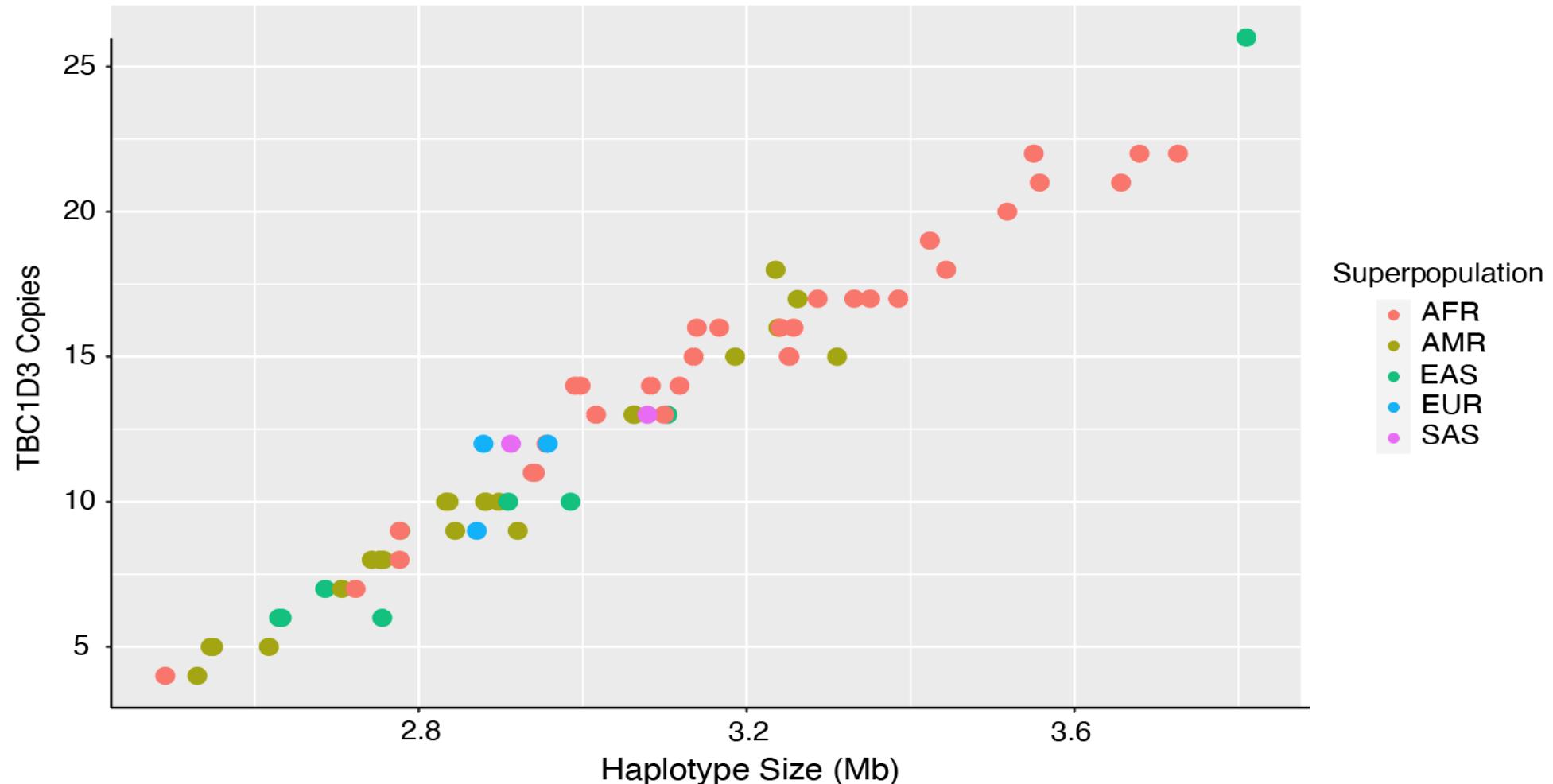
# A graph can capture such variation e.g. Minigraph

1. **Generate phase genome assemblies**
2. **Iteratively introduce assembly sequence to a graph.**
3. **Distinguish query sequence already present in graph from novel sequence**
4. **Include novel sequence as new segments or edges between segments in graph.**
5. **Repeat with next assembly**

Guitart, X
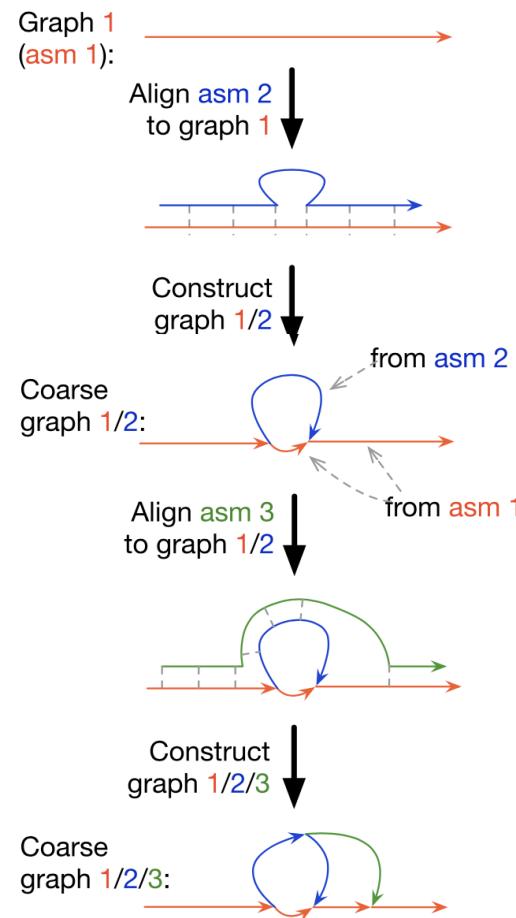
# A graph-based representation of structural variation
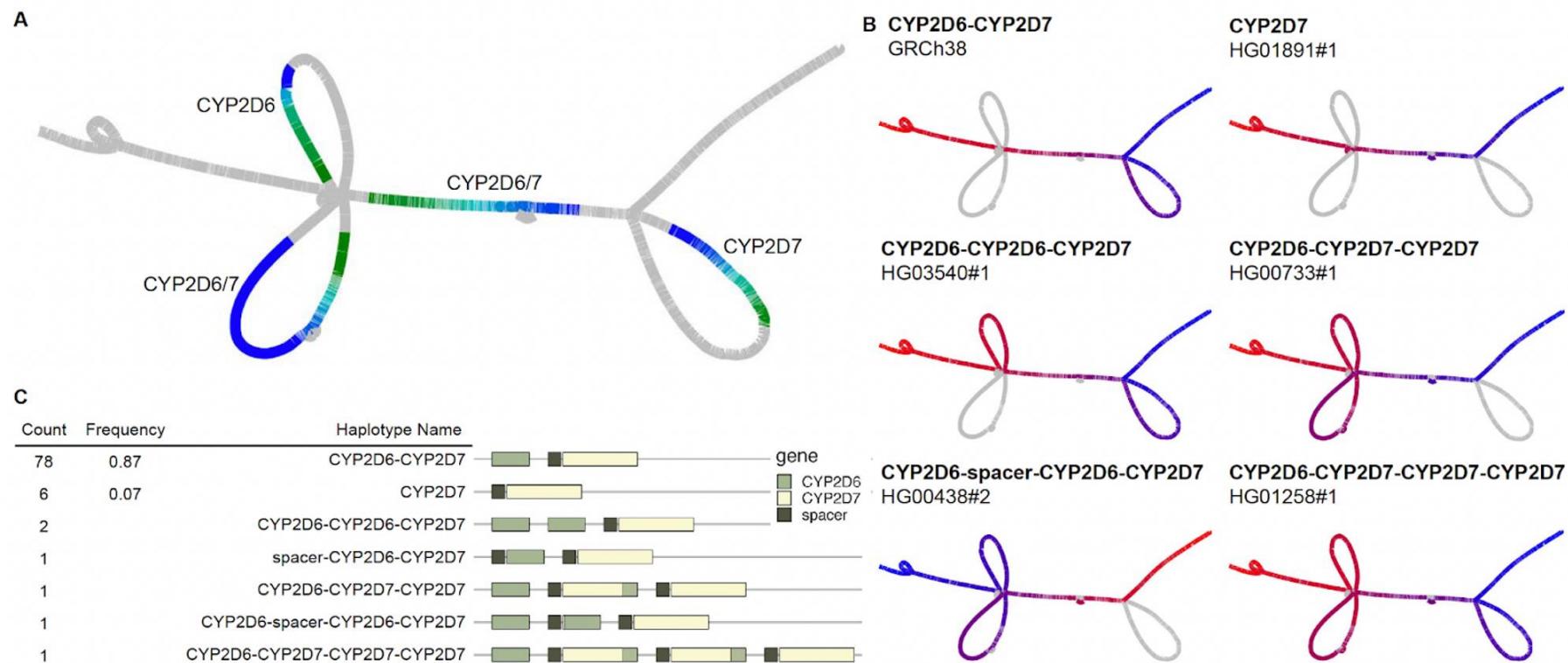
A graph-based representation of the entire human genome as a conceptual new reference.

Summary

- Short read NGS approaches
  - Multiple methods are needed—readpair+read-depth+splitread often with orthogonal validation such as SNP microarray
  - ~75% of SVs are missed because SVs are non-randomly distributed to repetitive regions where mapping quality is low
  - Read-depth approaches allow CNV prediction but not structure

- Long-read sequencing methods provide complete SV but currently limited throughput
  - Read-based versus assembly-based approaches
  - Telomere-to-telomere assemblies of human genomes now possible or nearly so for diploid—**complete genetic information where all variants are phased.**
  - First human pangenomes now available—a new concept to eventually replace a singular reference.

III. Why?
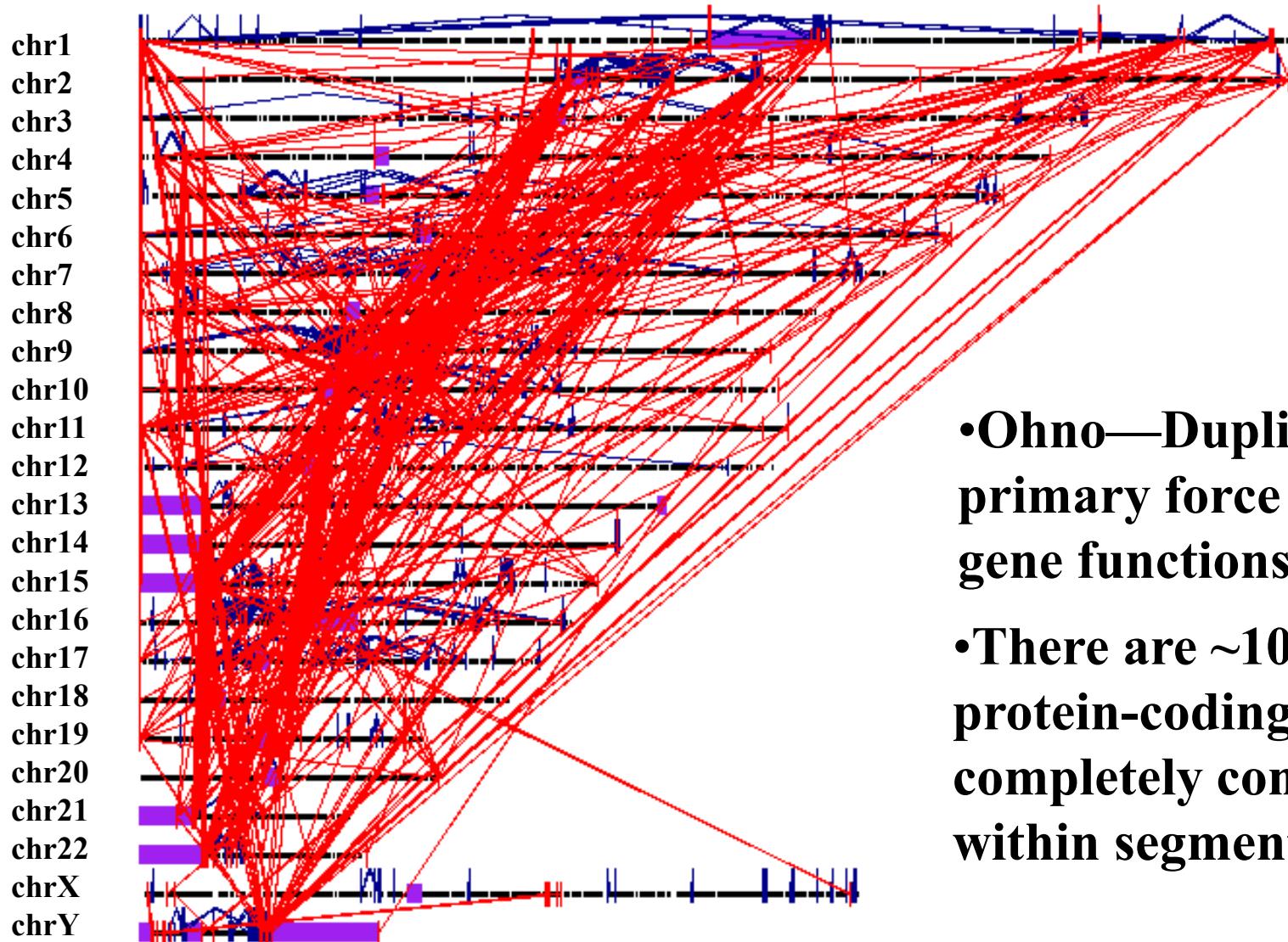
- **Ohno—Duplication is the primary force by which new gene functions are created**

- **There are ~1000 annotated protein-coding genes completely contained within segmental duplications**

Dynamic Genetic Variation
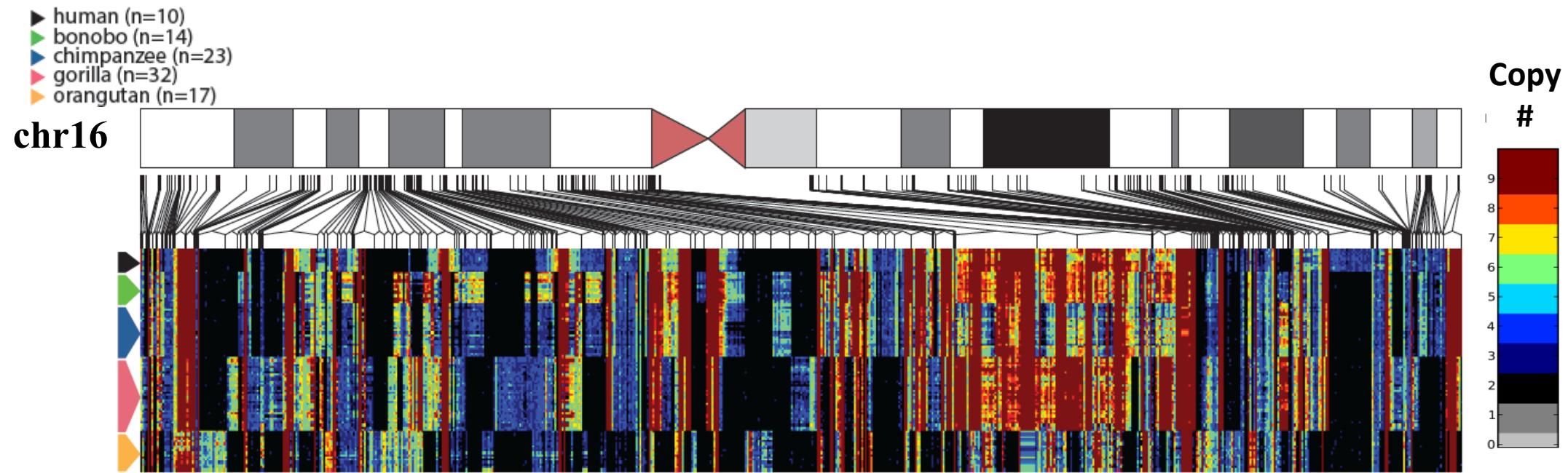
- Genomic copy number changes contributes more genetic difference between apes and humans than SNVs
- 468 Mbp CNV vs. 167 Mbp SNVs (ration: 2.8)

Sudmant *et al.*, Genome Res., 2013, Sudmant *et al*, Science, 2015

Rate of Duplication

Sudmant PH et al. , *Genome Res.* 2013
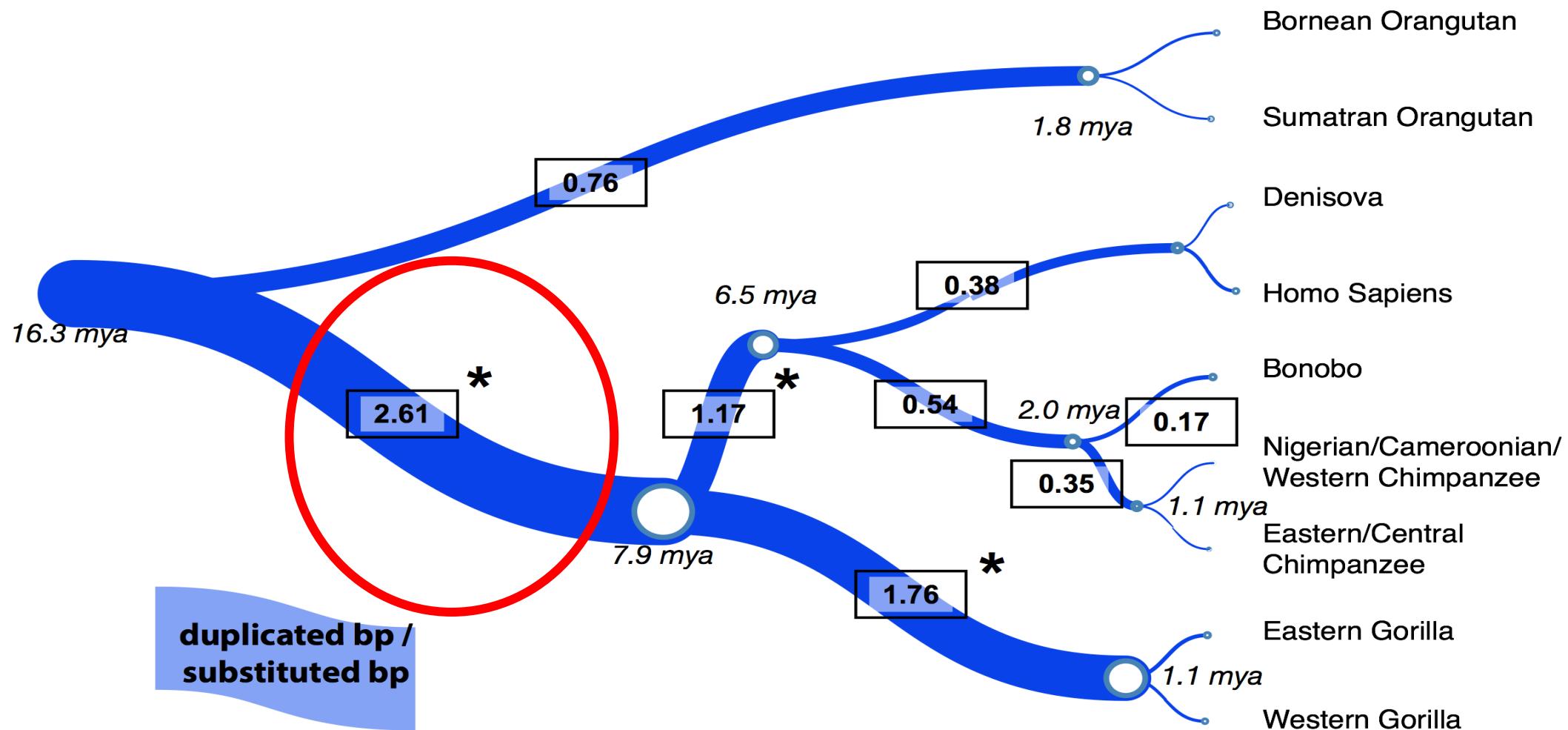
$p = 9.786 \times 10^{-12}$

Mosaic Architecture

Duplicons

Primary Duplicative Transpositions

Duplication Blocks

2p11

Secondary Block Duplications

16p   15q
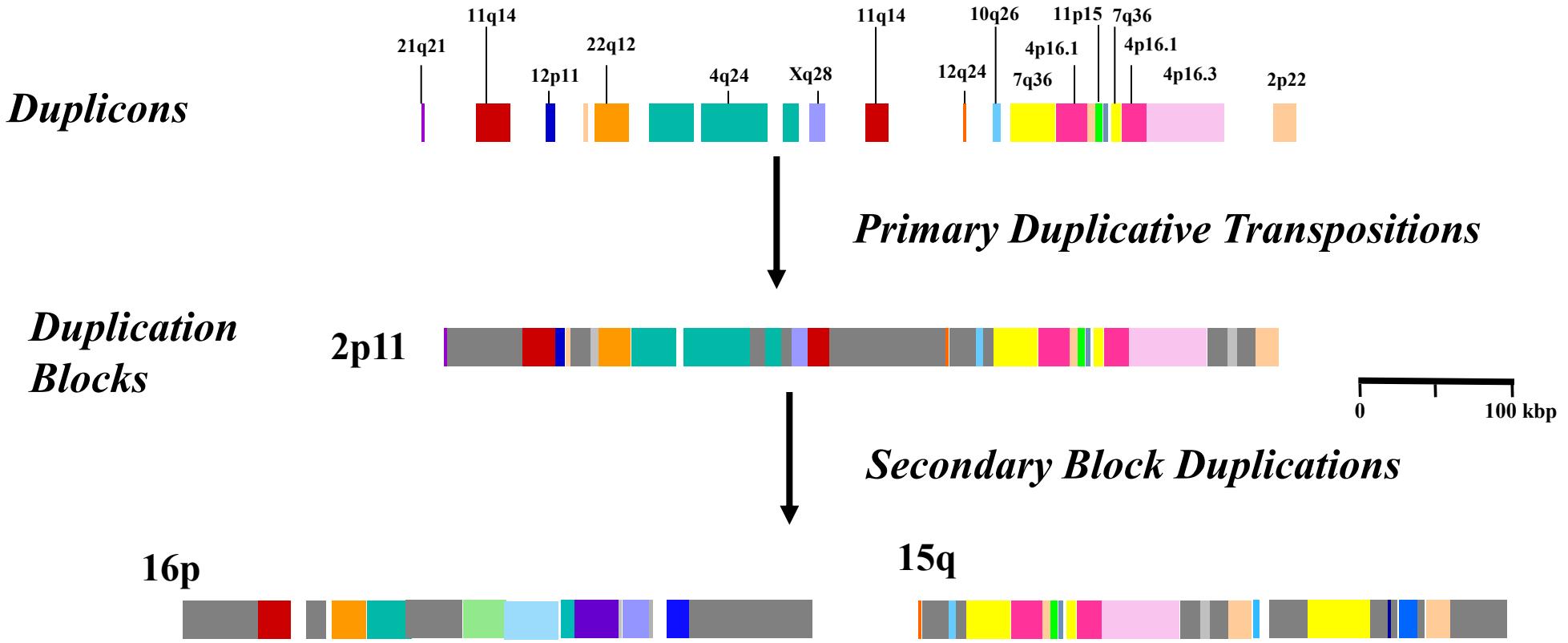
- A mosaic of recently transposed duplications
- Duplications within duplications.
- Potentiates "exon shuffling", regulatory innovation

Human Chromosome 16 Core Duplicon
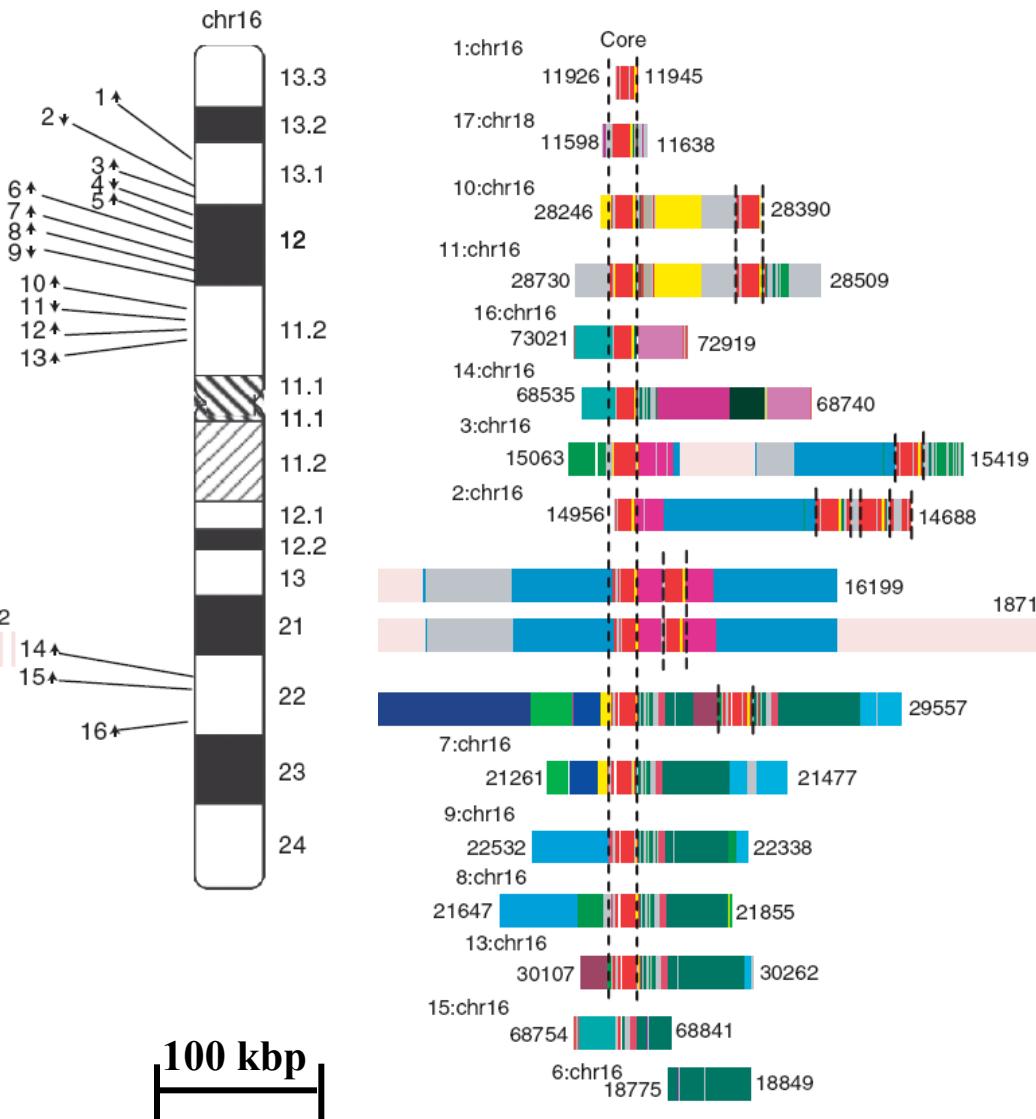
- The burst of segmental duplications 8-12 mya corresponds to core-associated duplications which have occurred on six human chromosomes (chromosomes 1,2, 7, 15, 16, 17)

- Most of the <u>recurrent</u> genomic disorders associated with developmental delay, epilepsy, intellectual disability, etc. are mediated by duplication blocks centered on a core.

Jiang et al, *Nat. Genet.*, 2007

Human/Great-ape "Core Duplicons" have led to the emergence of new genes
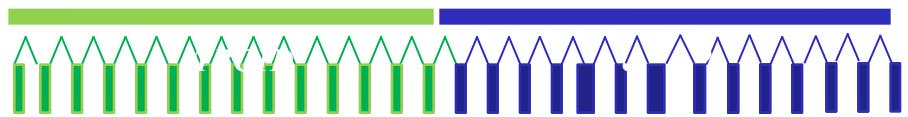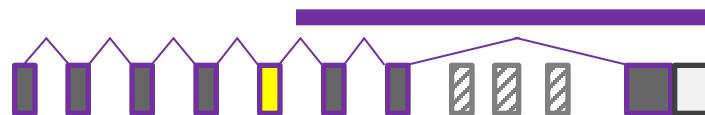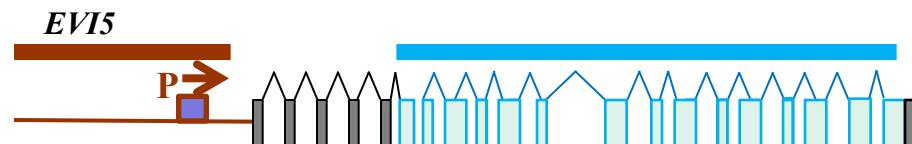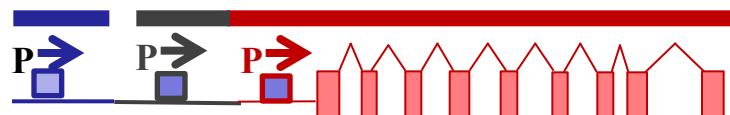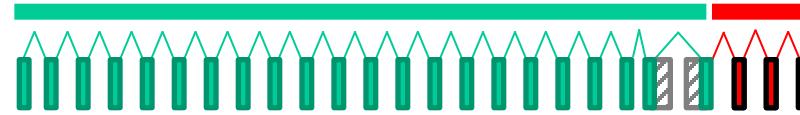

Features: No orthologs in mouse; multiple copies in chimp & human dramatic changes in expression profile; signatures of positive selection

Core Duplicon Hypothesis

The selective disadvantage of interspersed duplications is offset by the benefit of evolutionary plasticity and the emergence of new genes with new functions associated with core duplicons.

Marques-Bonet and Eichler, CSHL *Quant Biol,* 2008

Human-specific gene family expansions
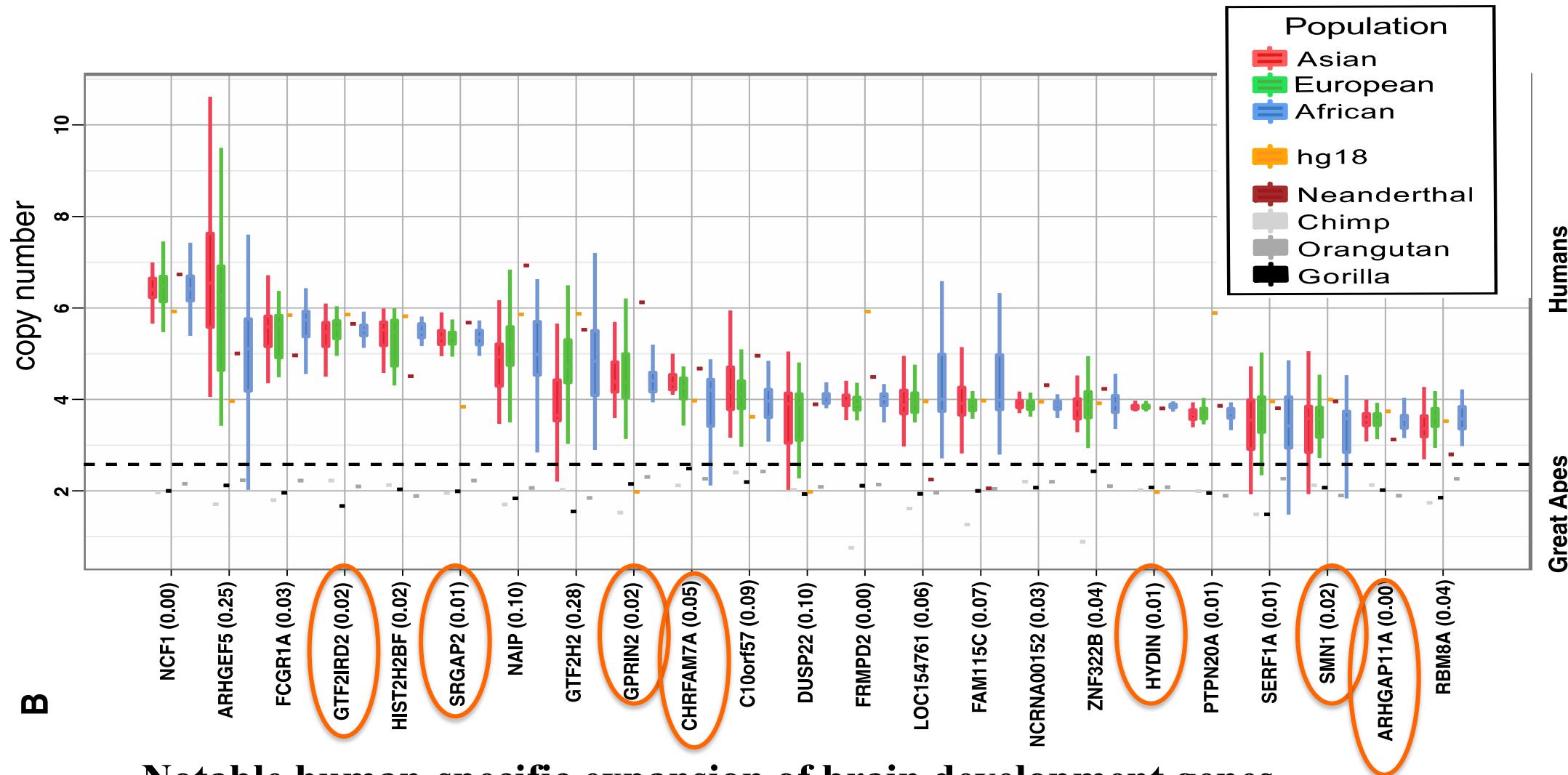
Notable human-specific expansion of brain development genes.
Neuronal cell death: p=5.7e-4; Neurological disease: p=4.6e-2

Sudmant et al., *Science*, 2010

SRGAP2 function

- *SRGAP2* (**SLIT**-ROBO Rho GTPase activating protein 2) functions to control migration of neurons and dendritic formation in the cortex

- Gene has been duplicated three times in human and no other mammalian lineage

- Duplicated loci not in human genome

Guerrier et al., *Cell*, 2009

SRGAP2 Human Specific Duplication

Dennis, Nuttle et al., *Cell,* 2012
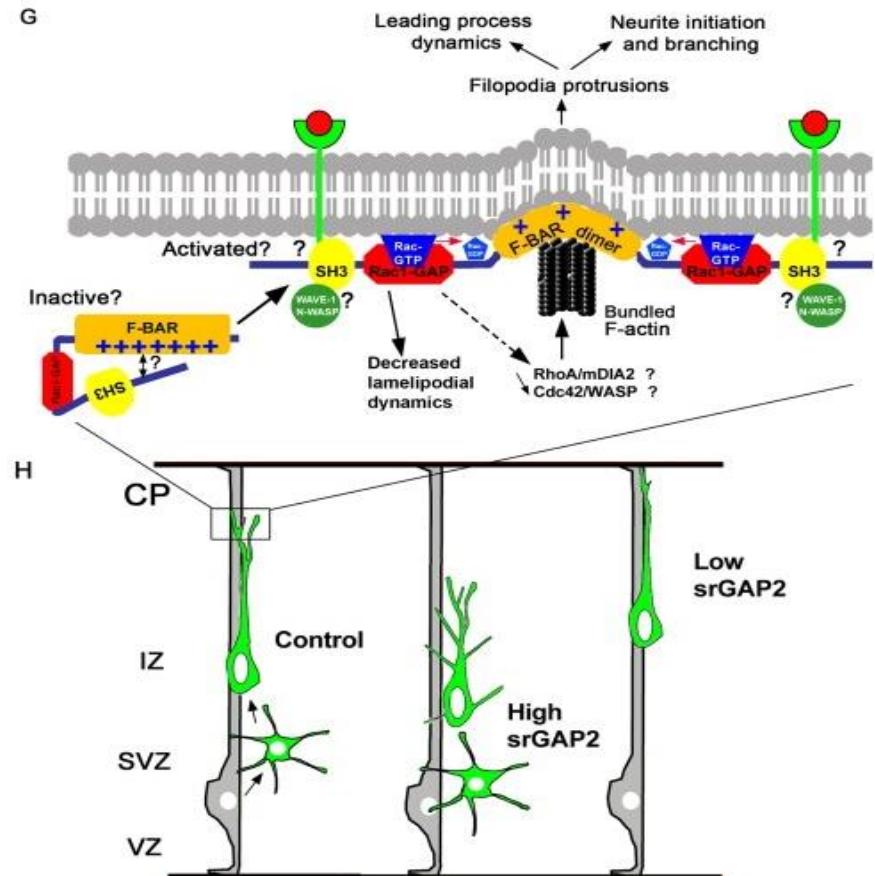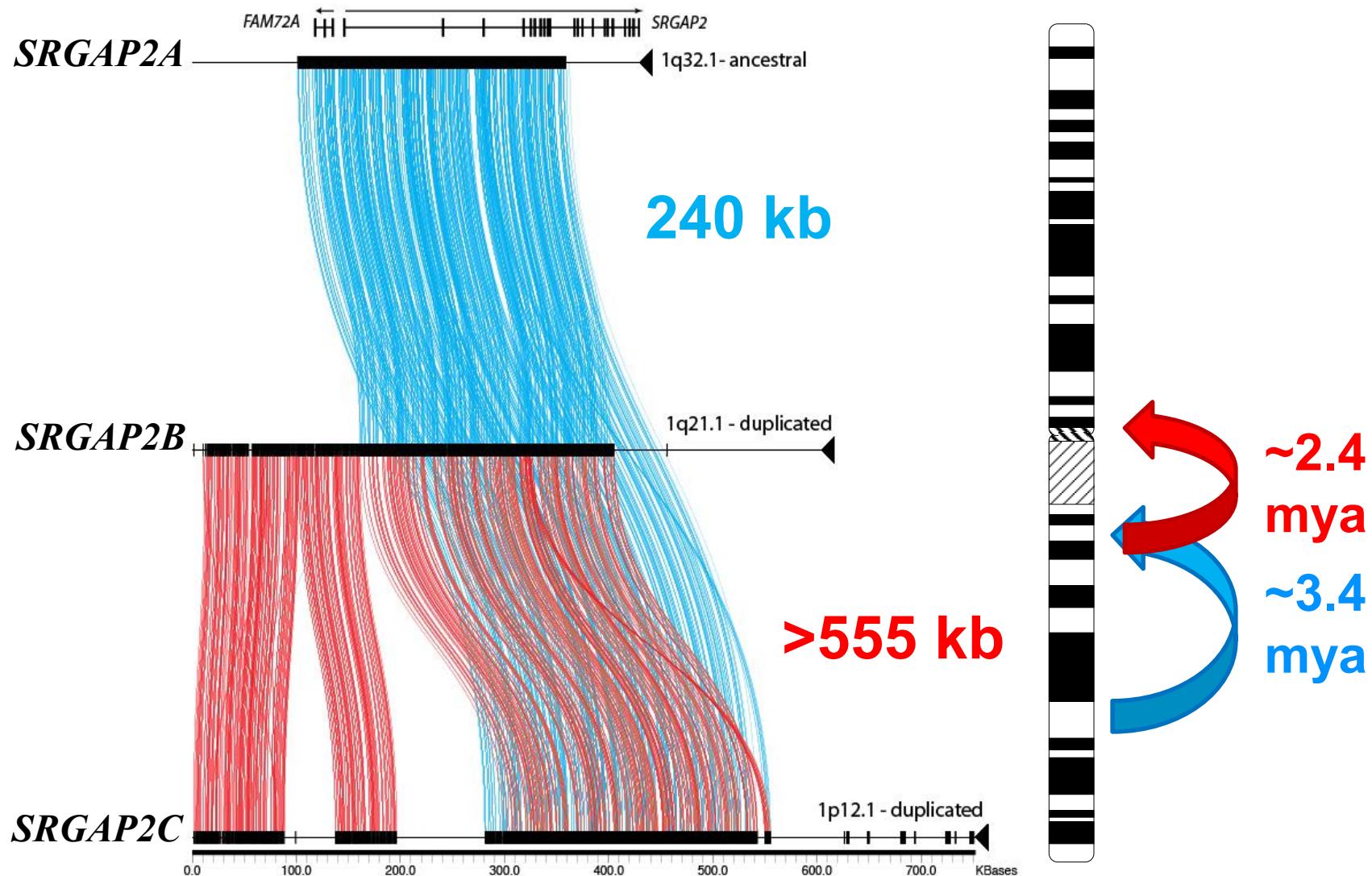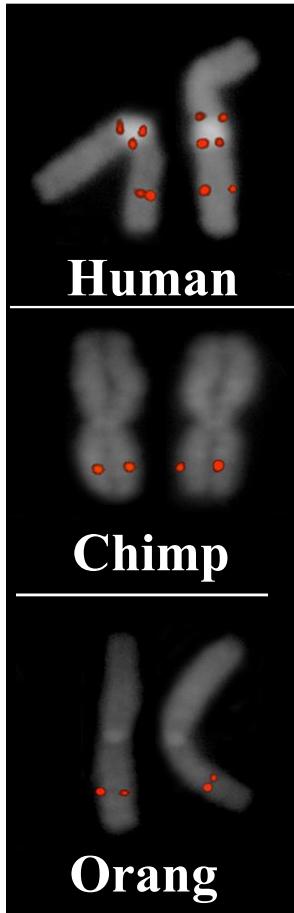
SRGAP2C is fixed in humans
(n=661 individual genomes)
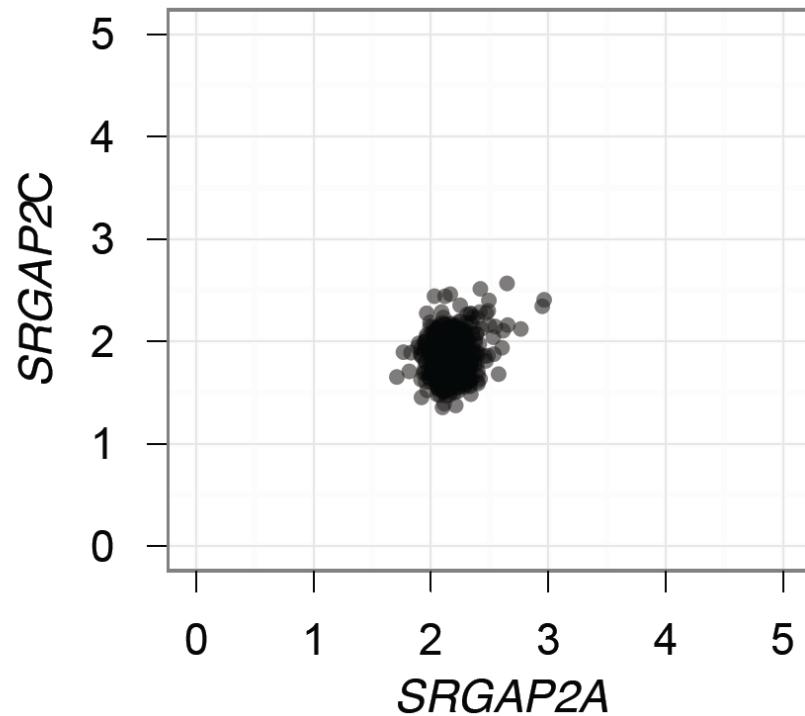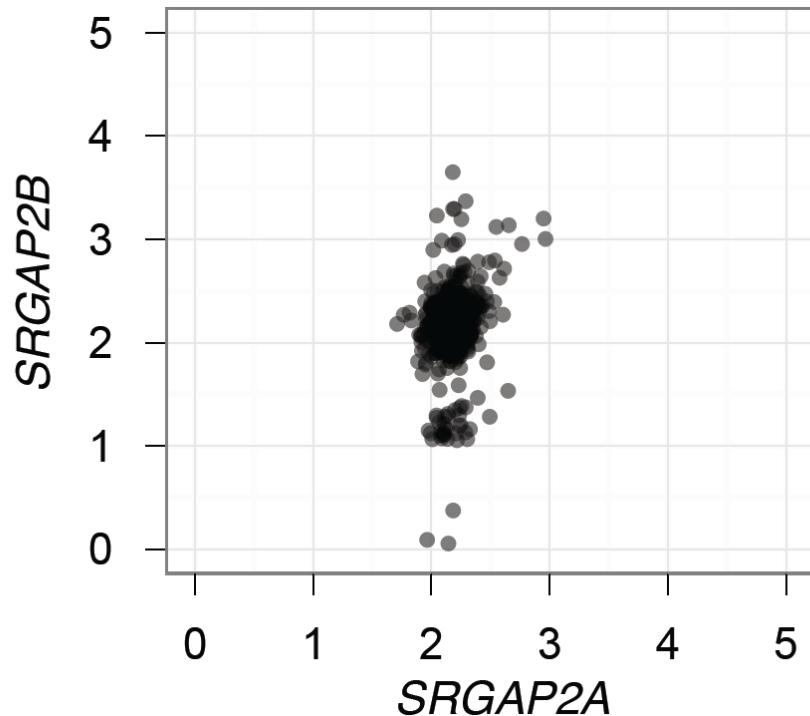
SRGAP2 duplicates are expressed

RNAseq

In situ

Cresyl violet   Duplicated srGAP2 (p12 or q21.1)   Human srGAP2 (q32.1)

Human embryos Gestational Week 12
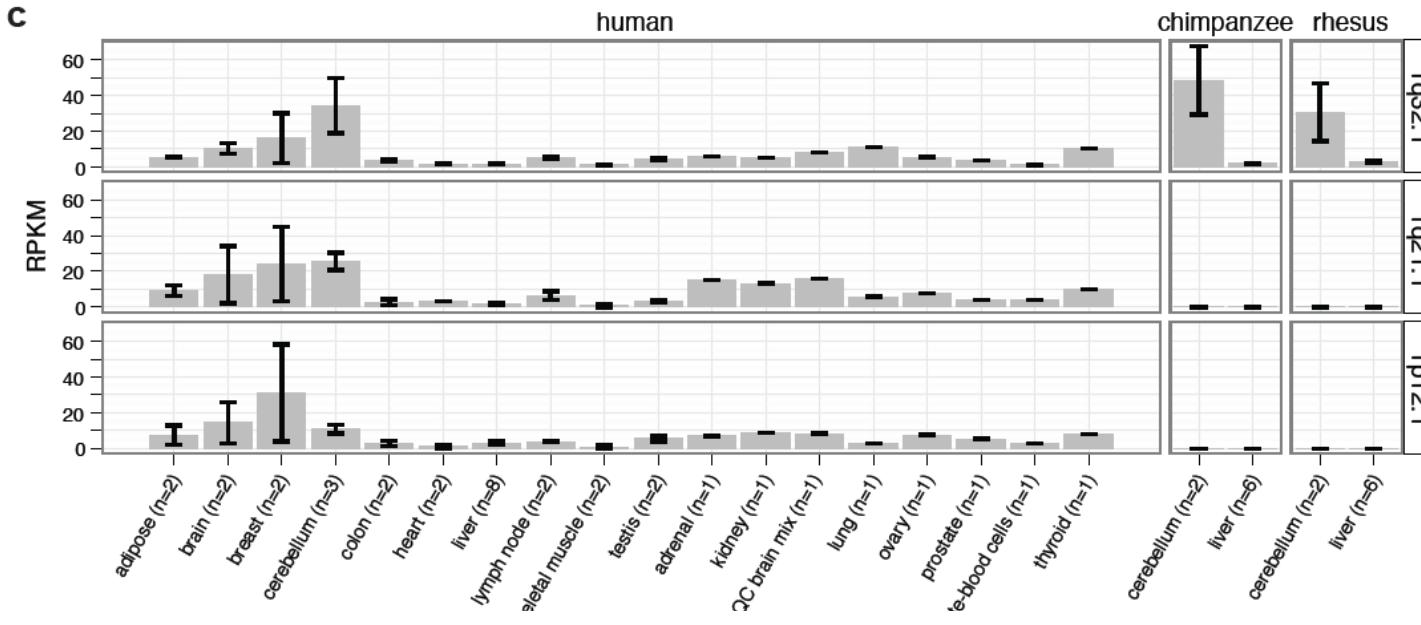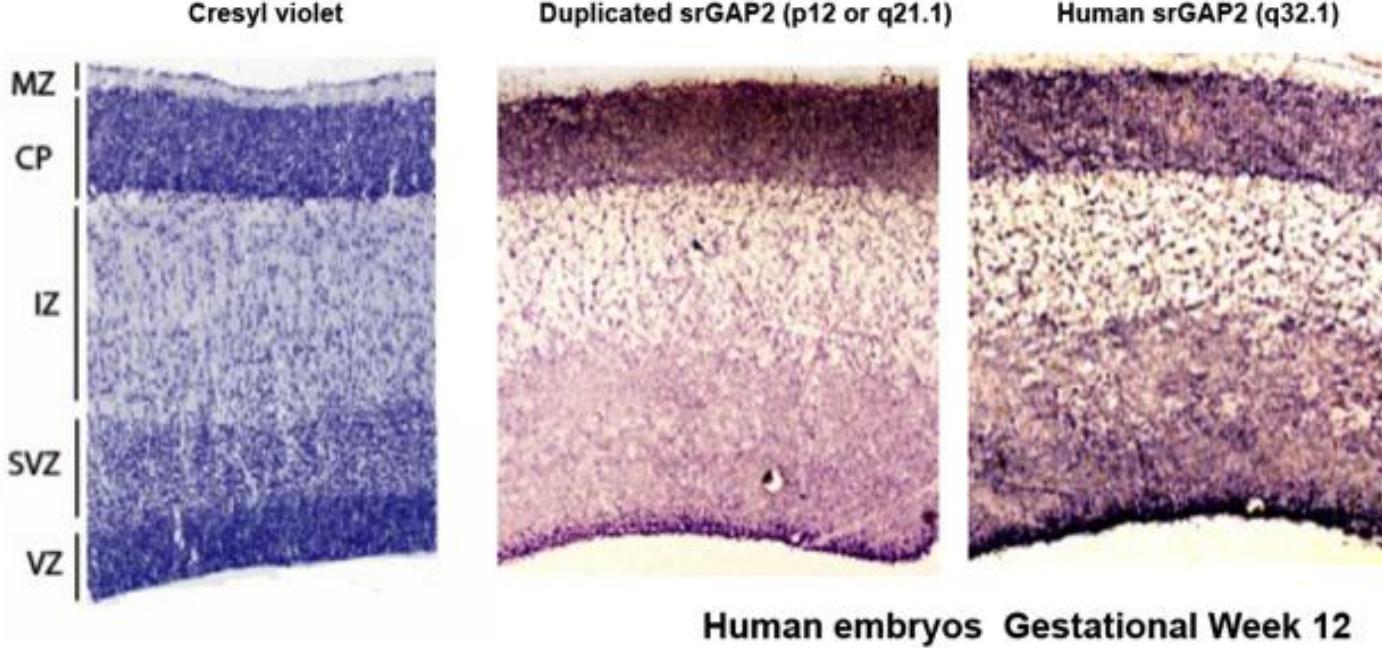
SRGAP2C duplicate antagonizes function
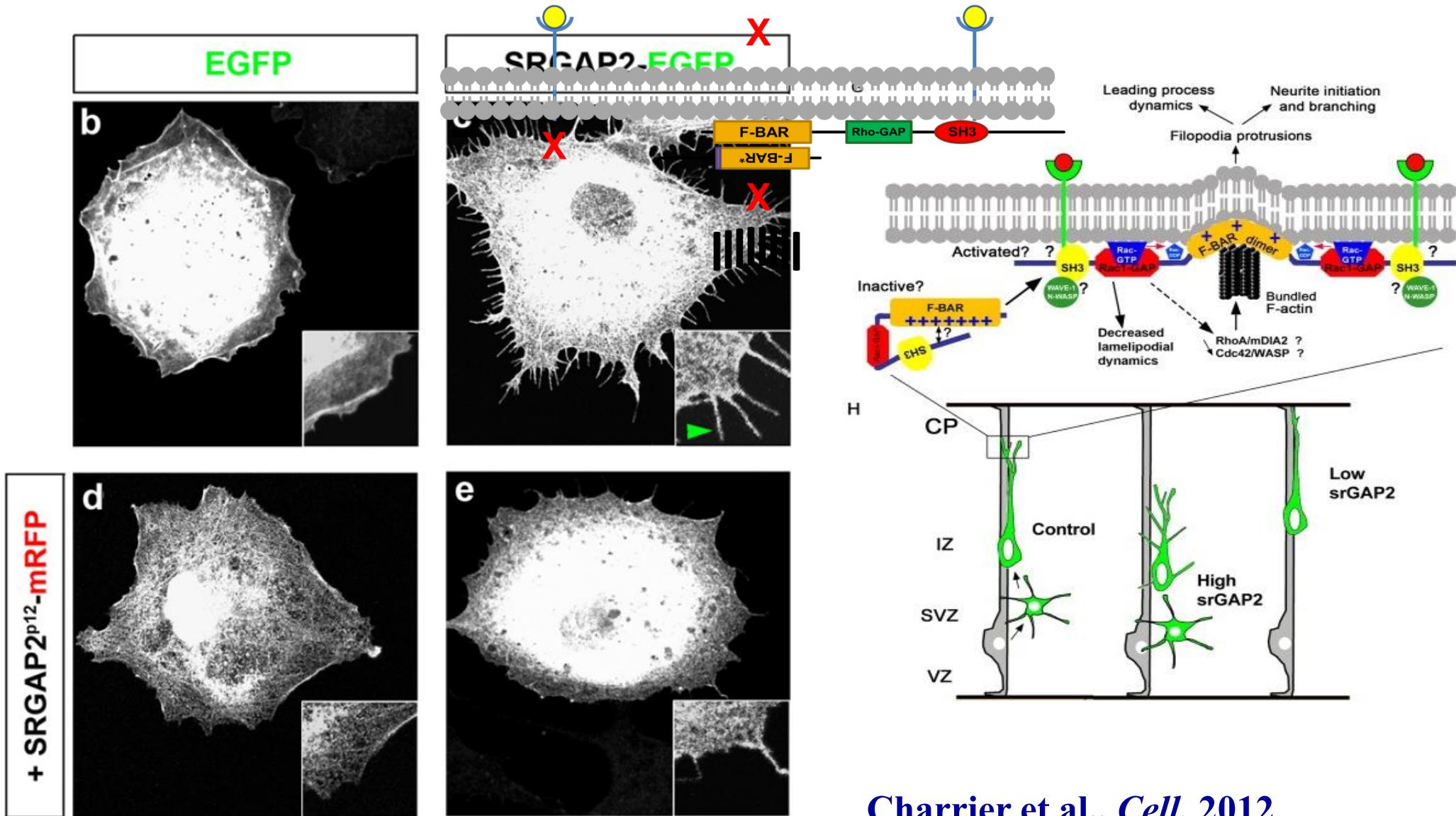
A

Fixed in human population and expressed in neurons

SRGAP2A   SRGAP2B,D$^{\psi}$ SRGAP2C

Dennis, Nuttle et al.
Cell (2012)

3.4 mya   2.4 mya

Sahelanthropus

Orrorin

K. platyops

Homo

A. anamensis

A. garhi

A. africanus

Ardipithecus

A. afarensis

A. aethiopicus

A. boisei

A. robustus

million   6 million   5 million   4 million   3 million   2 million   1 million
years ago

~350 cc   ~1000 cc
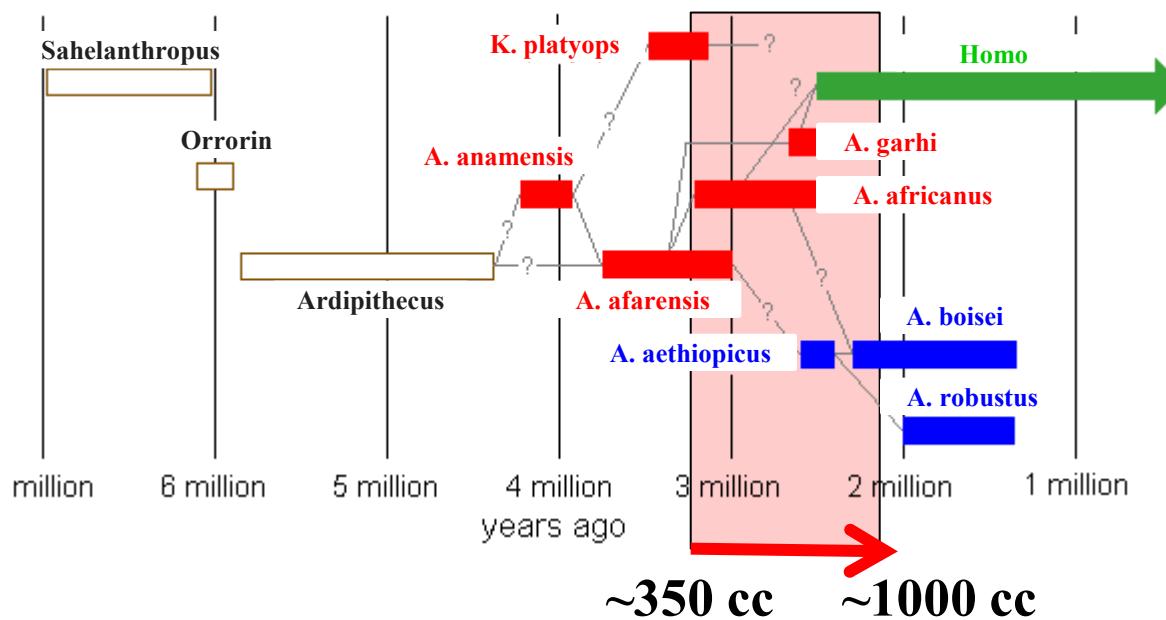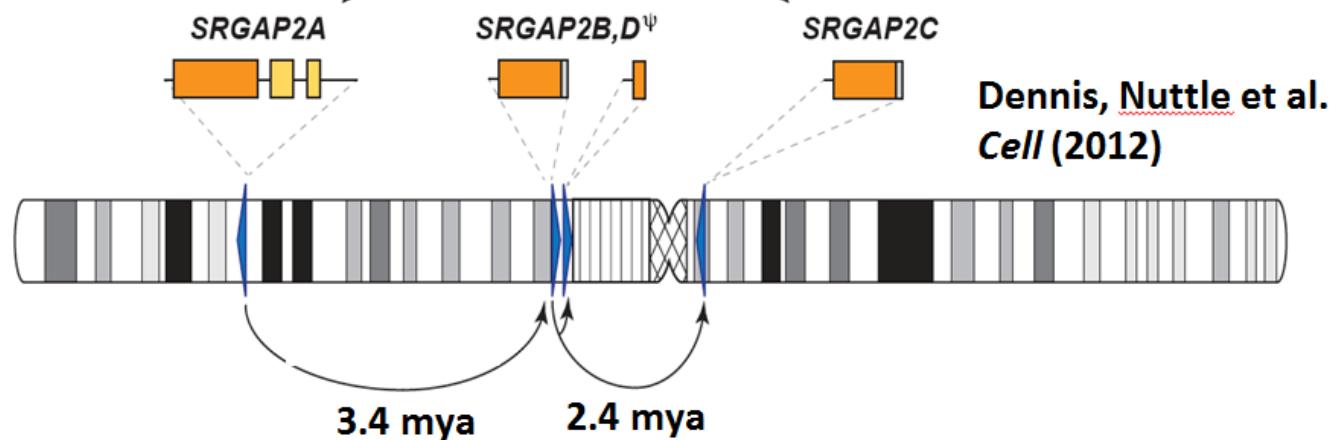
Australopithecus

Homo habilis

Example 2: Human-specific Duplication of *ARHGAP11B*

- Hypothesis: increase in number of basal radial glial cells or prolonged proliferation may lead to enlargement of the subventricular zone in humans

- Search for genes that are dramatically increased in concentration in basal radial glial cells as compared to neurons during development

- Only one gene of 56 not present in mouse *ARHGAP11B*
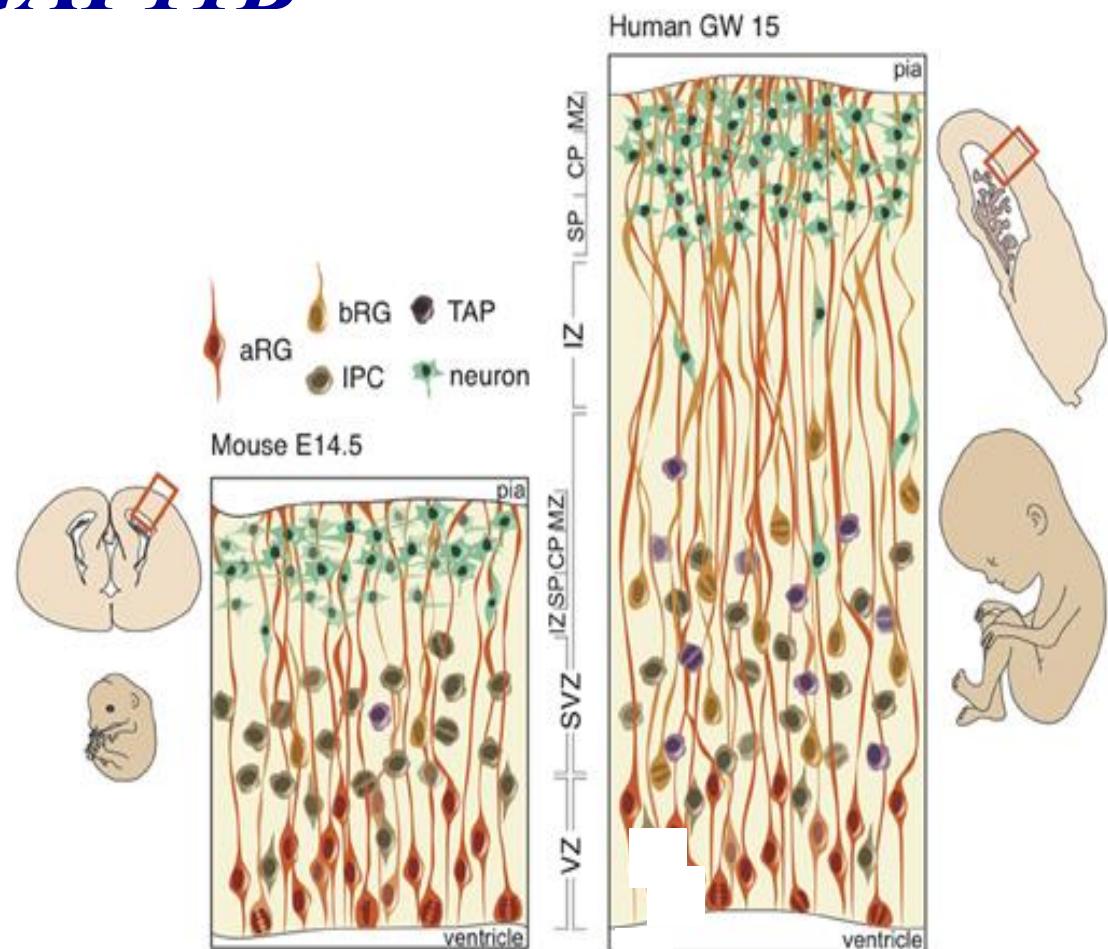
Florea *et al.*, *Science* 2015, Antonacci *et al.*, *Nat. Genet.*, 2014

ARHGAP11B induced gyrification of mouse brain

- E13.5 microinjection of *ARHGAP11B* induced folding in the neocortex by E18.5 in ½ of the cases– a significant increase in cortical area.
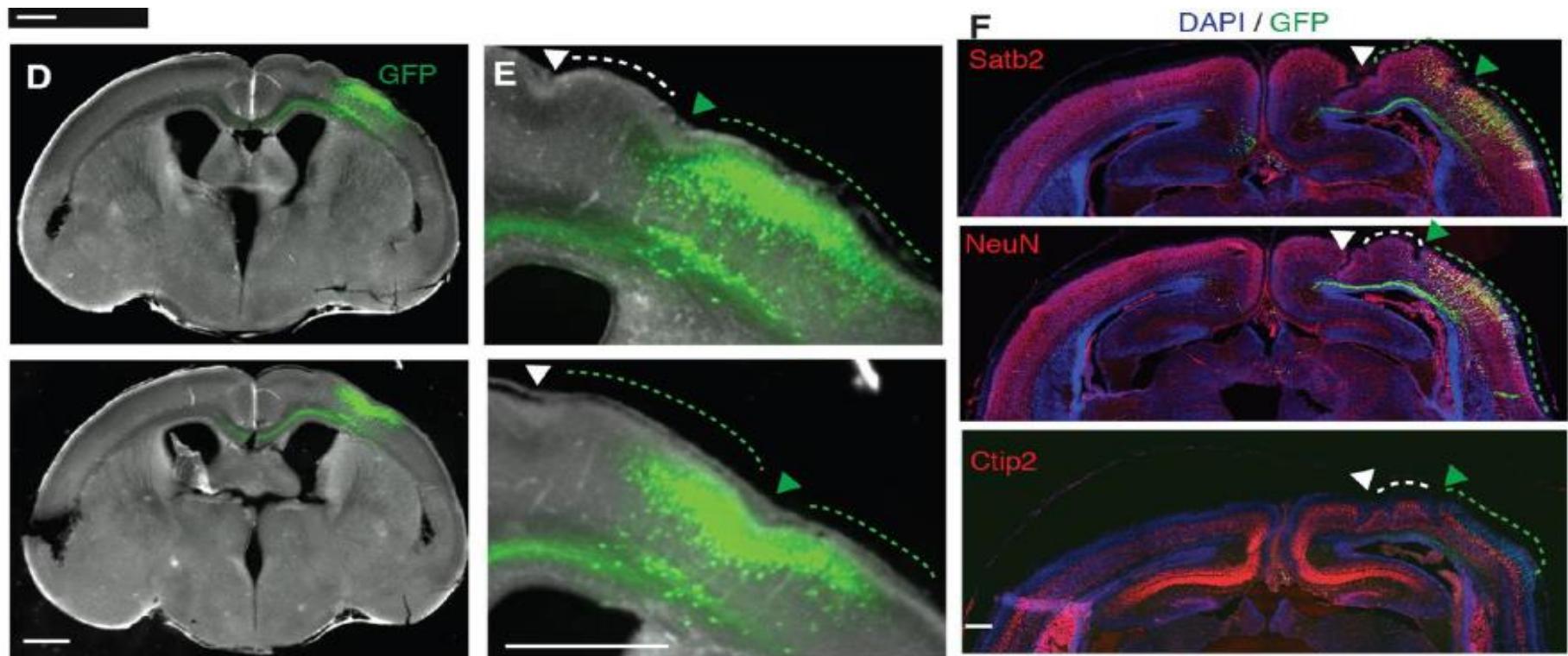
Transgenic human-specific duplicate *ARHGAP11B:* Marmoset fetal brain with human promoter
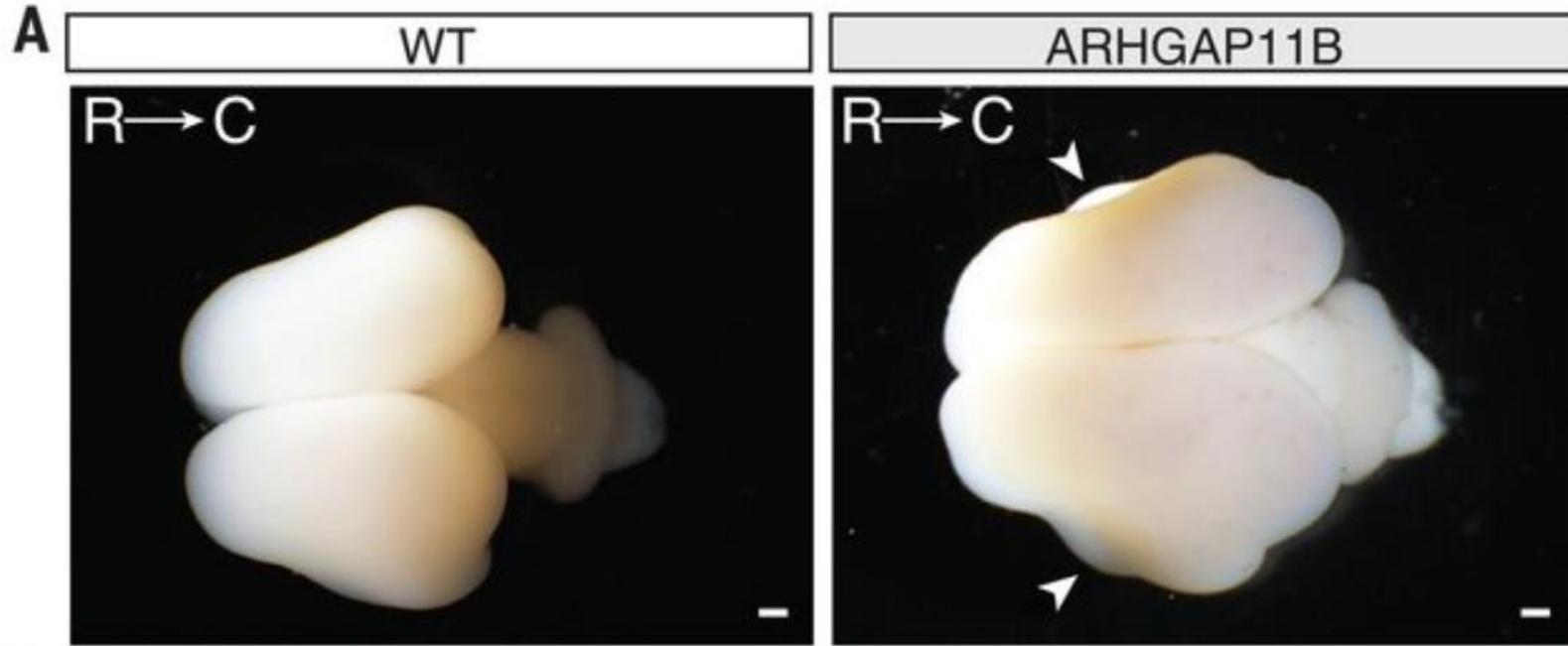
WT brain and brain expressing *ARHGAP11B* in neocortex (TG3). Arrowheads indicate cortical folds. R, rostral; C, caudal. Scale bars, 1 mm

- Increased the numbers of basal radial glia progenitors in the marmoset outer subventricular zone, increased the numbers of upper-layer neurons, enlarged the neocortex, and induced its folding.

Heide *et al., Science* 2020

Duplication of *ARHGAP11B* and 15q13.3 Syndrome
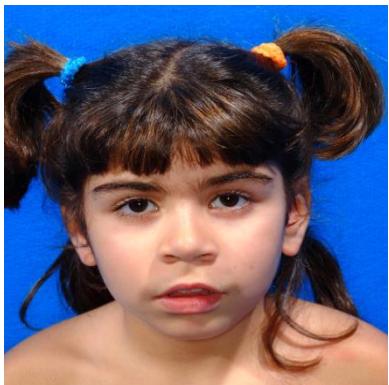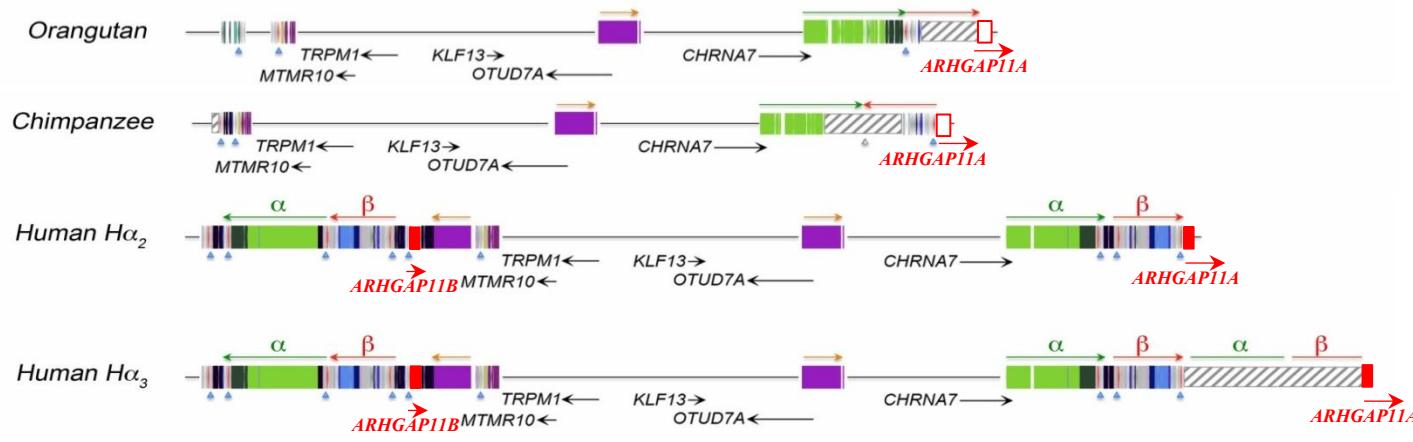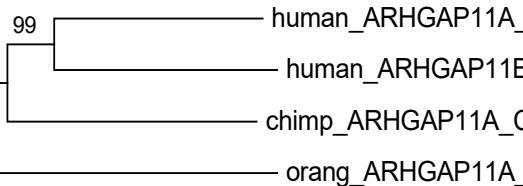
Duplication from *ARHGAP11A* to *ARHGAP11B* estimated to have occurred 5.3 +/- 0.5 million years ago.

Antonacci et al., *Nat Genet,* 2014,

Human-specific duplicated gene innovations and brain development

- *SRGAP2C*— 3.2 mya—produces a truncated protein that heterodimerizes with the parental product and alters neuronal migration, dendritic morphology and density of synapses (Dennis *et al.*, *Cell*, 2012; Charrier *et al*., *Cell*, 2012).

- *ARHGAP11B*— truncated duplicate is expressed in basal radial glial cells appears to expand neuronal count and expand subventricular zone (Antonacci *et al*., *Nat Genet*, 2014: Florio *et al*., *Science*, 2015,).

- *BOLA2B---* (256 kya) duplication of gene family specifically at root of Homo sapiens, rapid fixation and largest difference between Neandertals and human genomes and is important in iron homeostasis (Nuttle *et al*., *Nature,* 2016, Gianuzzi *et al*., *Am J Hum Genet* 2019).

- *NOTCH2NL--- (<3 mya)* partial duplication expressed in radial glial where interacts with NOTCH2 receptors and delays neuronal progenitor differentiation(Fiddes *et al*., *Cell,* 2018)

- Properties: Nearly fixed for copy number in the human population, predispose to disease instability and the duplications are incomplete with respect to gene structure. **NONE present in original human genome.**

1 cm
Human

Chimp
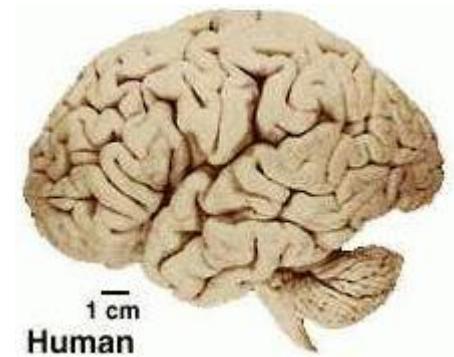
Genetic differences that make us uniquely human

Summary

- Interspersed duplication architecture sensitized our genome to copy-number variation increasing our species predisposition to disease—children with autism and intellectual disability

- Duplication architecture has evolved recently in a punctuated fashion around core duplicons which encode human great-ape specific gene innovations (eg. *NPIP, NBPF, LRRC37*, etc.).

- Cores have propagated in a stepwise fashion "transducing" flanking sequences---human-specific acquisitions flanks are associated with brain developmental genes.

- **Core Duplicon Hypothesis**: Selective disadvantage of these interspersed duplications offset by newly minted genes and new locations within our species. Eg. *SRGAP2C*

Overall Summary

- **I. Disease**: Role of CNVs in human disease—relationship of common and rare variants—biased toward interspersed SDs due to NAHR

- **II. Methods**: NGS Read-pair and read-depth methods to characterize SVs—long-read genomes can now be fully phased and assembled achieving complete telomere-to-telomere assembly & complete variation discovery.

- **III**: **Evolution**: Rapid evolution of complex human architecture that predisposes to disease also coupled to human-specific gene innovations that make us uniquely human

Disease

Evolution

Acknowledgements

Glossary

SV-structural variation

SD-segmental duplication

CNV- copy number variation

CNP—copy number polymorphism

NGS—next generation sequencing (eg. Illumina short read)

Indel-insertion/deletion event

SMRT-single-molecule real-time sequencing

CCS—circular consensus sequencing

HiFi-high fidelity long-read

CLR—continuous long-read sequencing

WGS—whole genome shotgun sequencing

ONT—Oxford Nanopore Technology

PacBio—Pacific Biosciences

ZMW-zero-mode wave guide

CDR—centromere dip region

NAHR—non-allelic homologous recombination

SV Software

- *PennCNV* (Kai Wang) and *CNVPartition*—calling CNVs from SNP microarray
- *Genomestrip*—Handsaker/McCarroll—combines read-depth and readpair data to identify potential sites of SV data from population genomic data; *Delly*—EMBL Rausch/Korbel—uses split-read and readpair signatures; *Lumpy* --Quinlan/Hall— uses probabilistic framework to integrate multiple SV such as discordant paired-end alignments and split-read alignments; *GATK-SV*—Talkowski—integrates multiple short reads signatures; *Manta*—Illumina split and paired-end reads followed by assembly
- *Conifer /XHMM*— Krumm/Eichler & Frommer/Purcell-exome CNV calling
- *PBSV*—Aaron Wenger (PacificBiosciences software) signatures from pbmm2 alignments; *SNIFFLES2*—Sedlaczeck/Schatz– NGLMR mapping of PacBio or ONT data using split-read alignments, high-mismatch regions, and coverage
- *PAV*—Audano/Eichler & *SVIM-asm*—Heller/Vingron--assembly-to-assembly based discovery of SVs using minimap and LRSassembled genomes
- *Verkko*—Koren/ Philippy & *HiFiasm*- Cheng/Li—graph based approaches to generate near T2T assemblies using UL-ONT and HiFi sequencing data
- *Saffire-SV*, *StainedGlass* & *SVbyEye*- (Vollger/ Porubsky/Eichler)—visualization tools to characterize chromosomal level SV and centromeric satellite DNA

SD-Mediated Rearrangements