

Interspecies identification of *Brassica* chromosome segments: work in progress

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Diverse genome organization following 13 independent mesopolyploid events in Brassicaceae contrasts with convergent patterns of gene retention

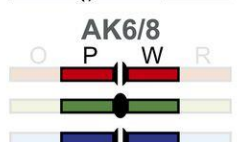
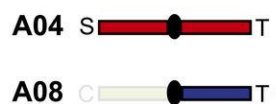
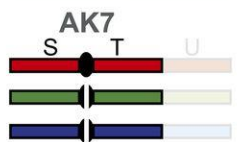
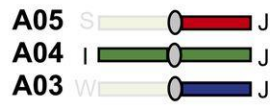
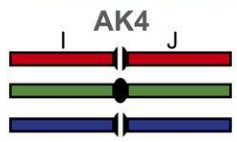
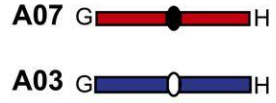
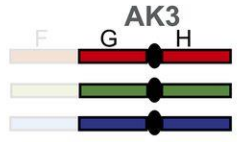
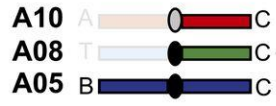
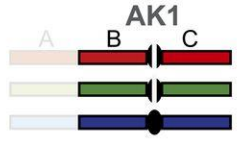
Terezie Mandáková¹, Zheng Li², Michael S. Barker² and Martin A. Lysak^{1,*}
¹Plant Cytogenomics Research Group, CEITEC-Central European Institute of Technology, Masaryk University, Brno 625 00, Czech Republic, and

ancestral and extant centromeres (upstream)

21 ancestral centromeres in the tPCK-like hexaploid

ancestral and extant centromeres (downstream)

A09 B



A05 S
A08 S

A02 P

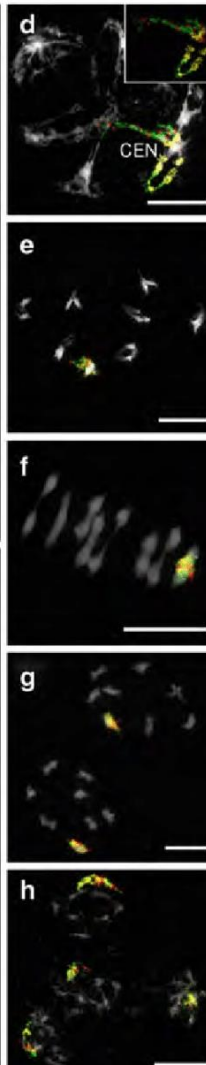
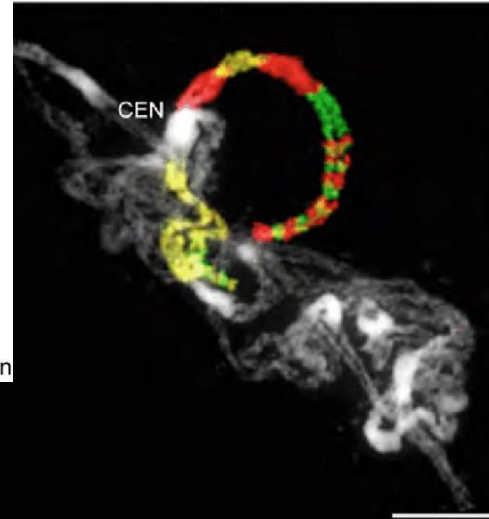
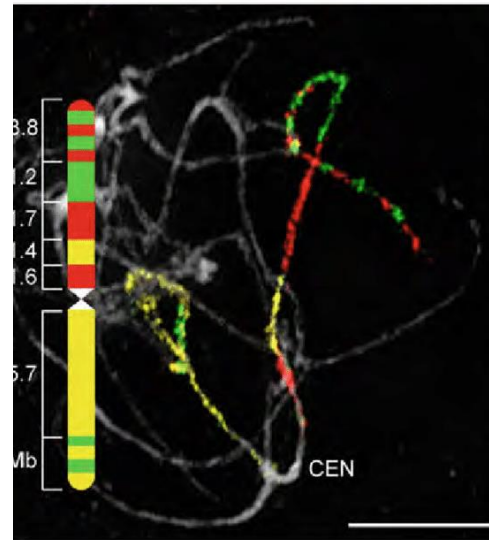
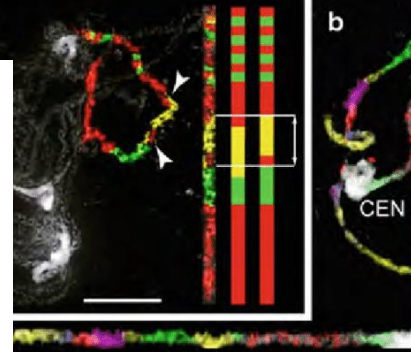
A06 M

A06 M

A03 D

A01 D

LF MF2 ● extant centromere ○ no centromere traces detected
MF1 ○ centromere traces detected (|) rearrangement in centromere region



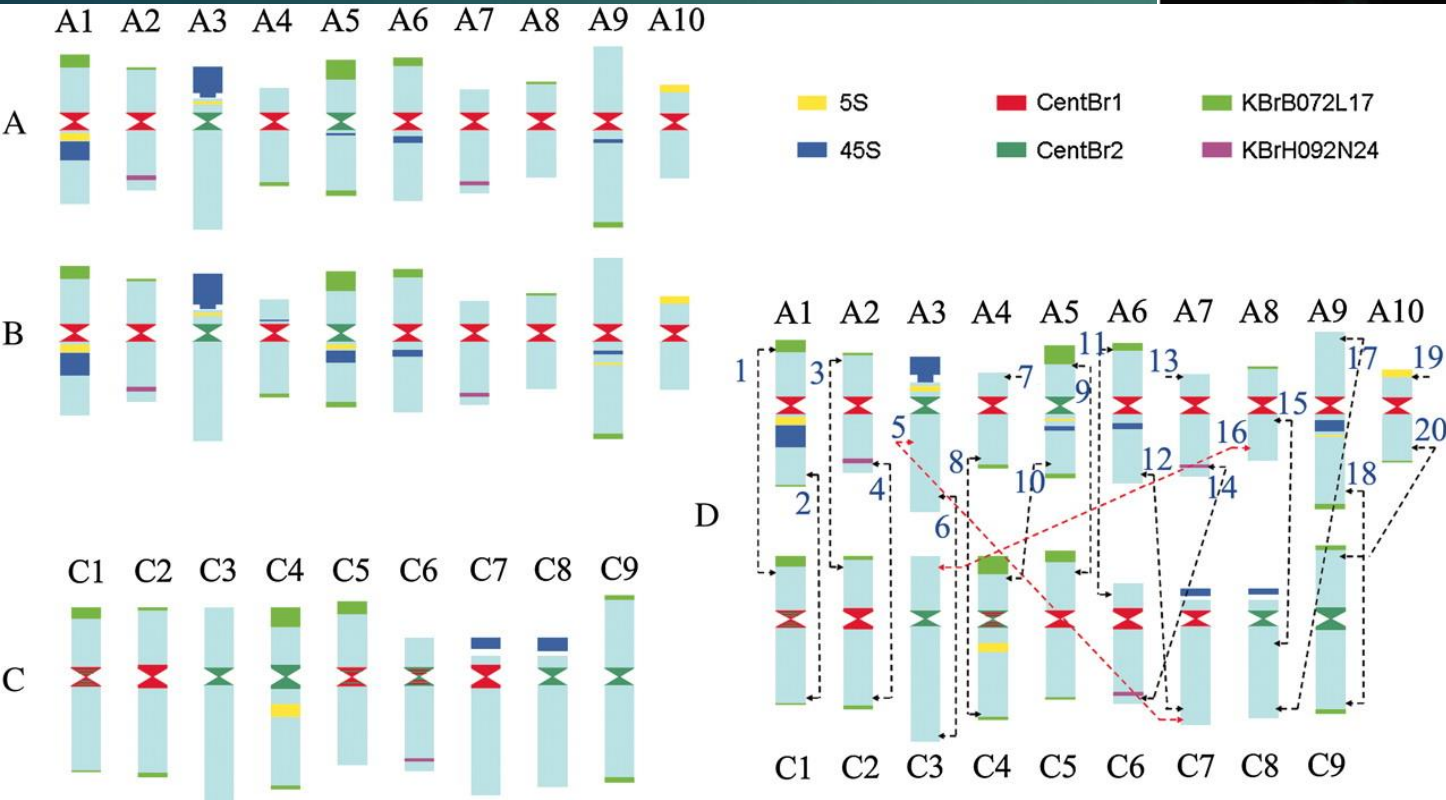
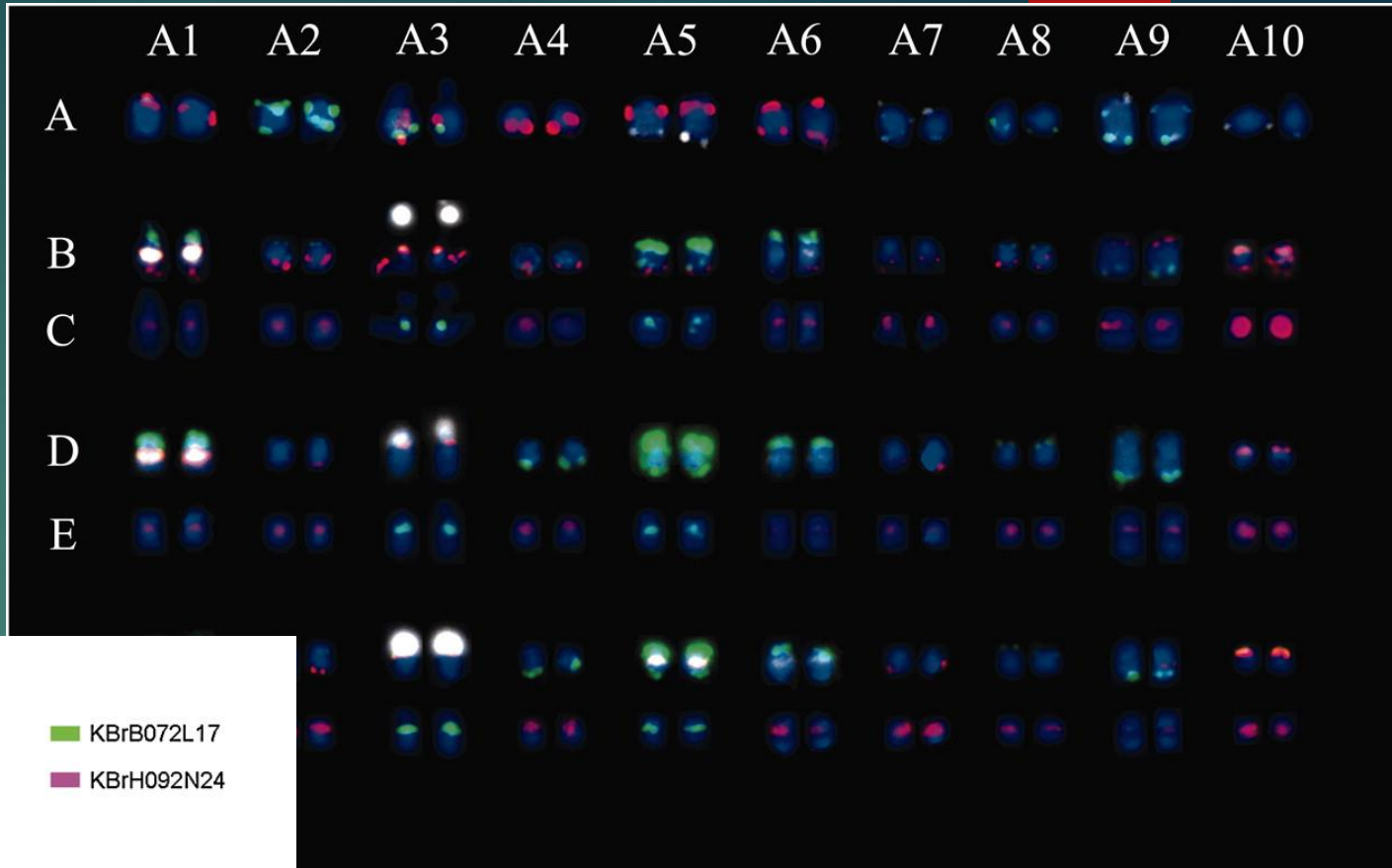
Deciphering the Diploid Ancestral Genome of the Meso-hexaploid Brassica rapa
Feng Cheng, Terezie Mandáková, Jian Wu, Qi Xie, Martin A. Lysak, Xiaowu Wang

Plant Cell 2013 25: 1541-1554
DOI: 10.1105/tpc.113.110486

Analysis of Plant Meiotic Chromosomes by Chromosome Painting

2013 Methods in molecular biology 990(2):13-24

DOI: 10.1007/978-1-62703-333-6_2
Martin Lysak Terezie Mandáková



▶ Zhiyong Xiong and J Chris Pires
 ▶ Karyotype and Identification of All Homoeologous Chromosomes of Allopolyploid *Brassica napus* and Its Diploid Progenitors
 ▶ Genetics (2011) 187: 37-49 DOI 10.1534/genetics.110.122473

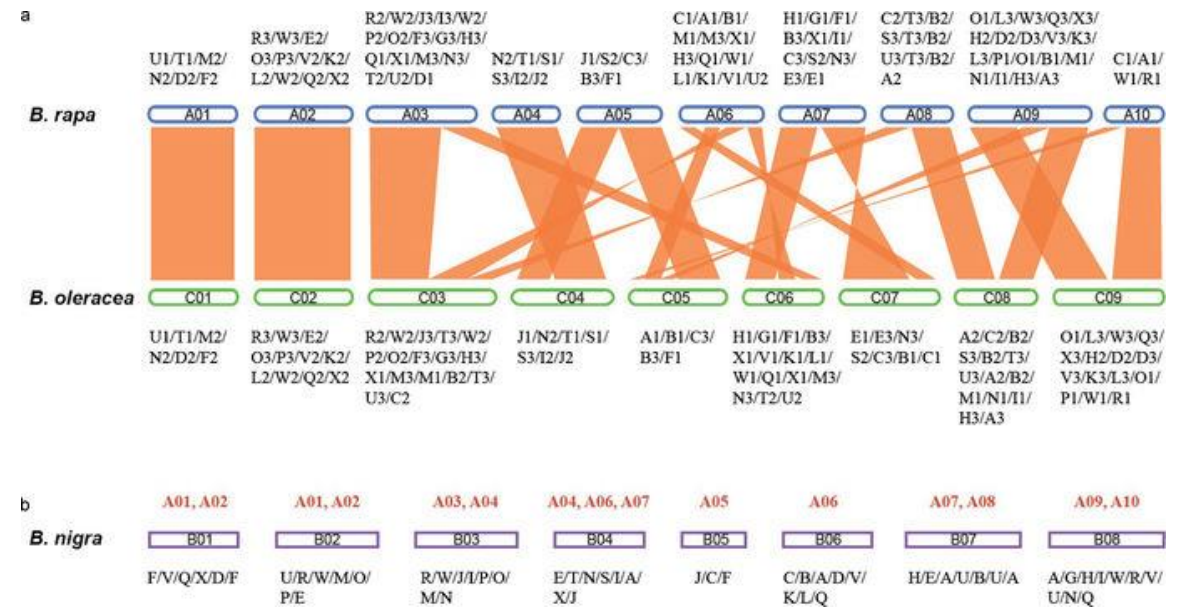
▶ FROM

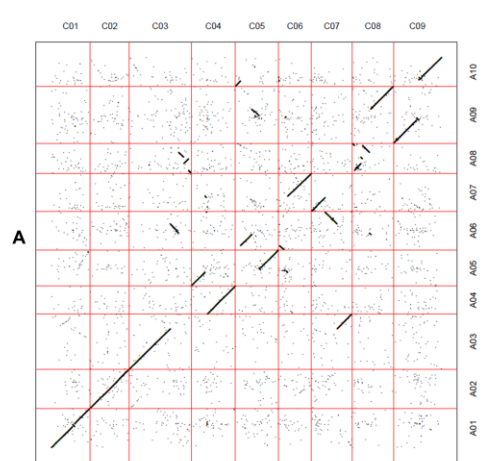
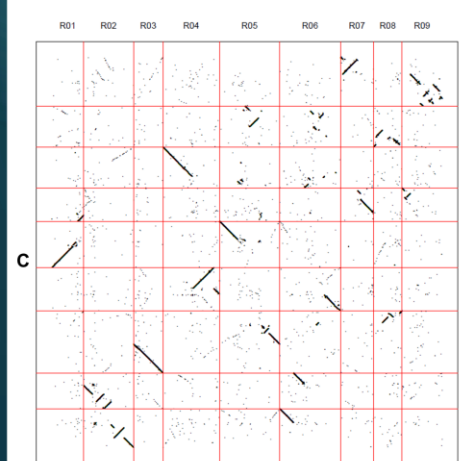
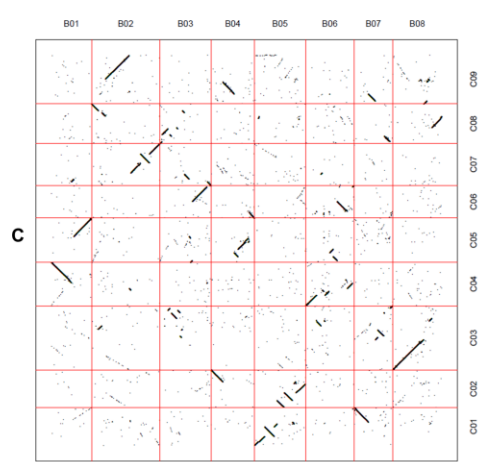
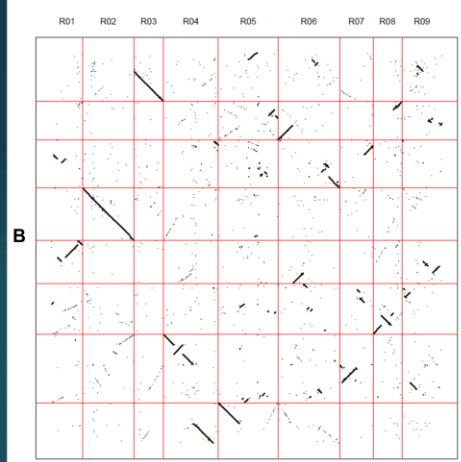
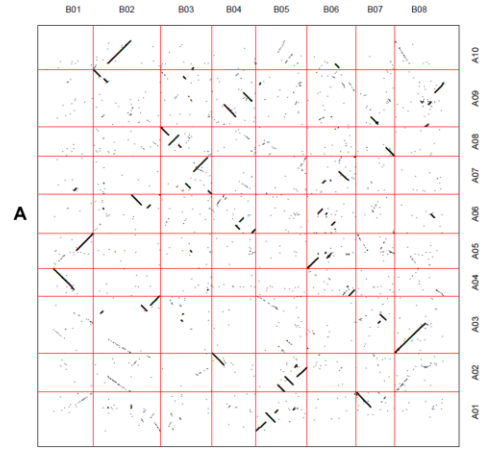
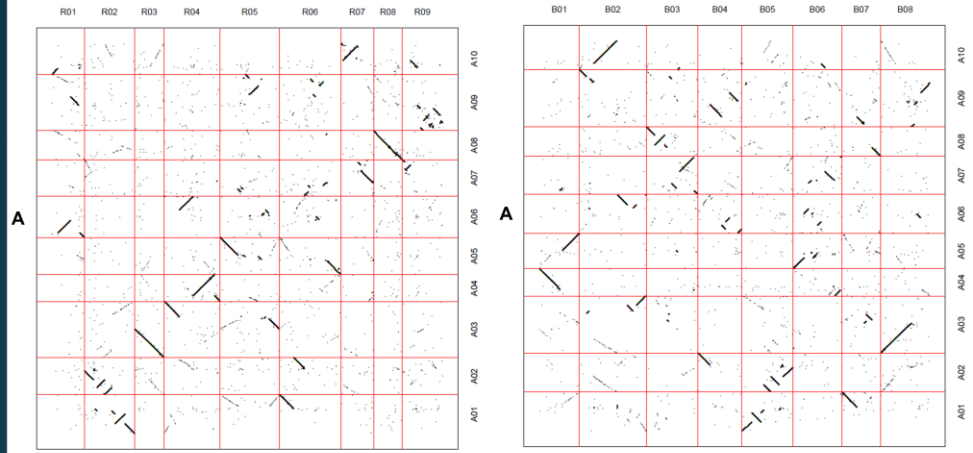
▶ Genome triplication drove the diversification of Brassica plants

▶ Feng Cheng, Jian Wu & Xiaowu Wang

▶ Horticulture Research volume 1, Article number: 14024 (2014)

▶ doi:10.1038/hortres.2014.24



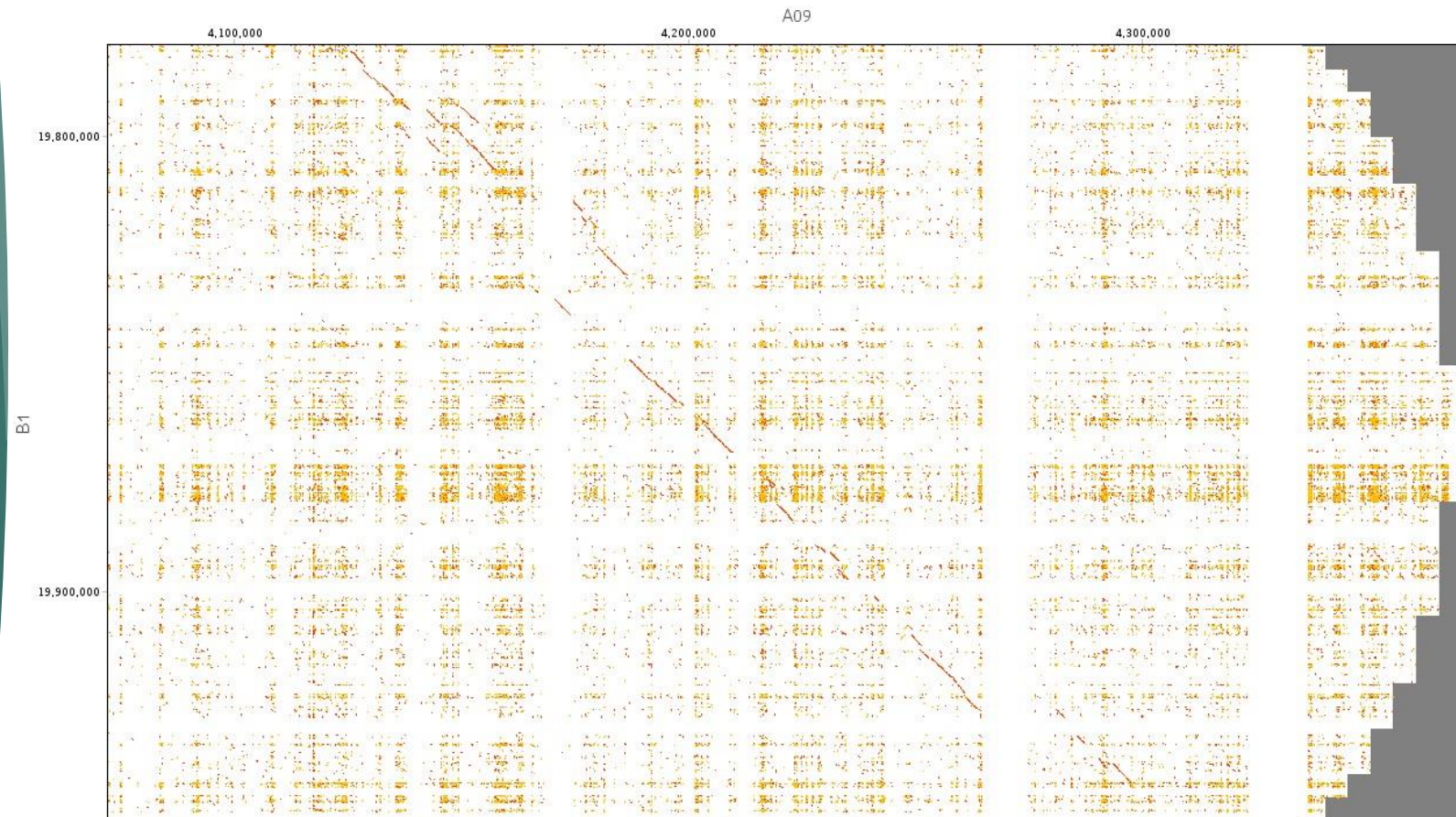


Interspecies dotplots

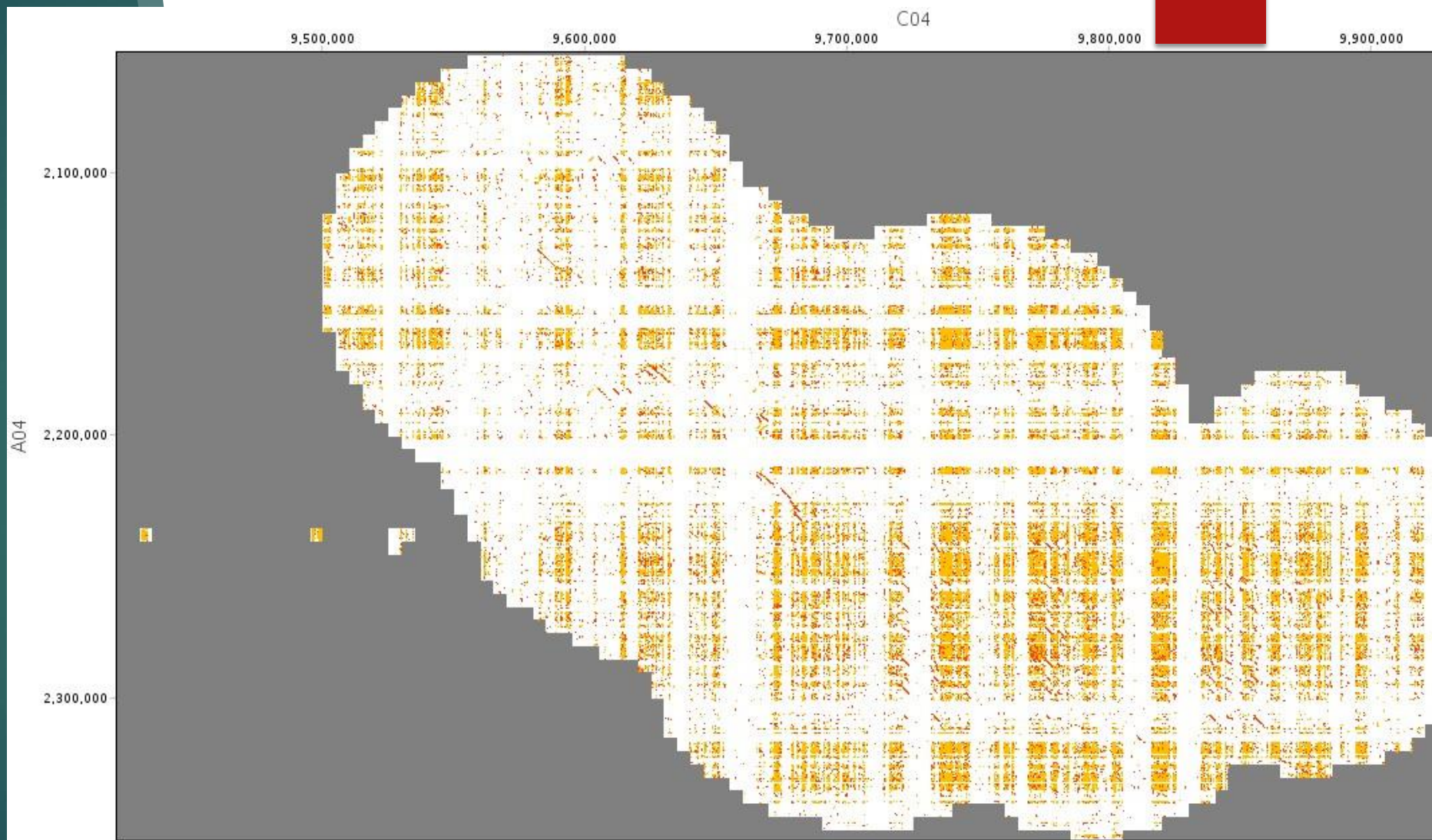
FROM IAN BANCROFT & YORK COLLEAGUES




A09 4.2M to B01 19.9M



A04 vs C04





Interspecies identification of *Brassica* chromosome segments: work in progress

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Massive oligonucleotide pools –
>20,000 c. 50-mers = >1,000,000 bp

- ▶ Designed along chromosome, then screened to remove sequences that have homology to other sites or repetitive DNA

Genetics, Vol. 208, 513–523 February 2018

HIGHLIGHTED ARTICLE
GENETICS | INVESTIGATION

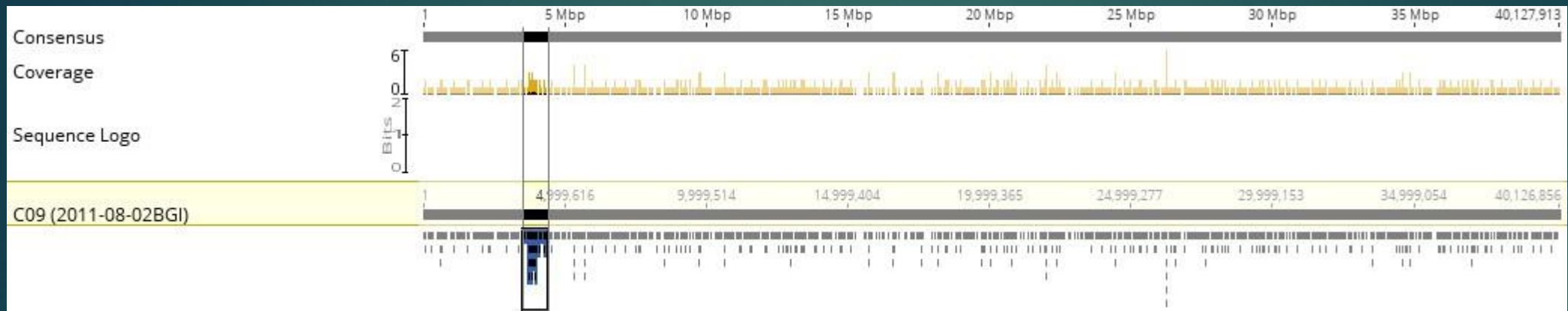
Comparative Oligo-FISH Mapping: An Efficient and Powerful Methodology To Reveal Karyotypic and Chromosomal Evolution

Guilherme T. Braz,^{*,†,1} Li He,^{*,†,1} Hainan Zhao,^{*,1} Tao Zhang,^{*,§,1} Cassandra Semrau,^{**}
Jean-Marie Rouillard,^{**,††} Giovana A. Torres,[†] and Jiming Jiang^{*,**,§§,2}

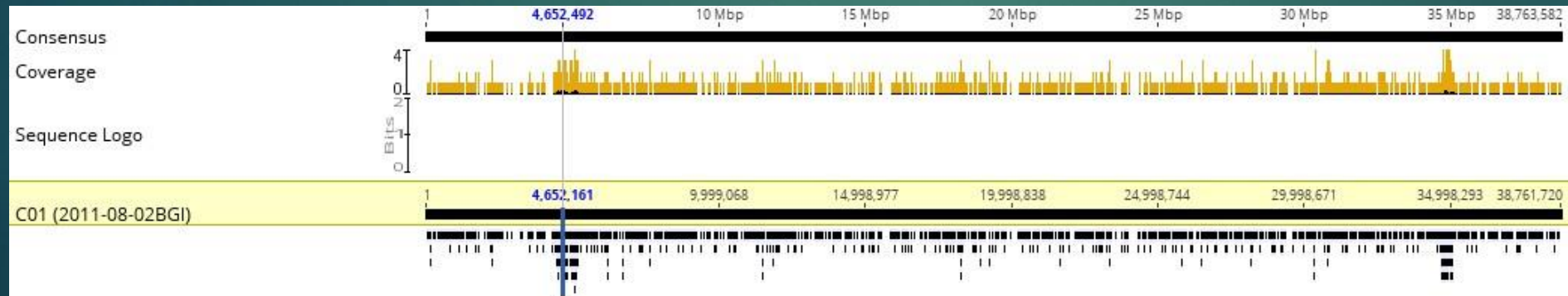
ABSTRACT Developing the karyotype of a eukaryotic species relies on identification of individual chromosomes, which has been a major challenge for most nonmodel plant and animal species. We developed a novel chromosome identification system by selecting and labeling oligonucleotides (oligos) located in specific regions on every chromosome. We selected a set of 54,672 oligos (45 nt)



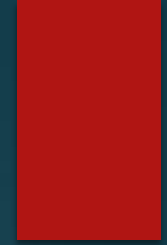
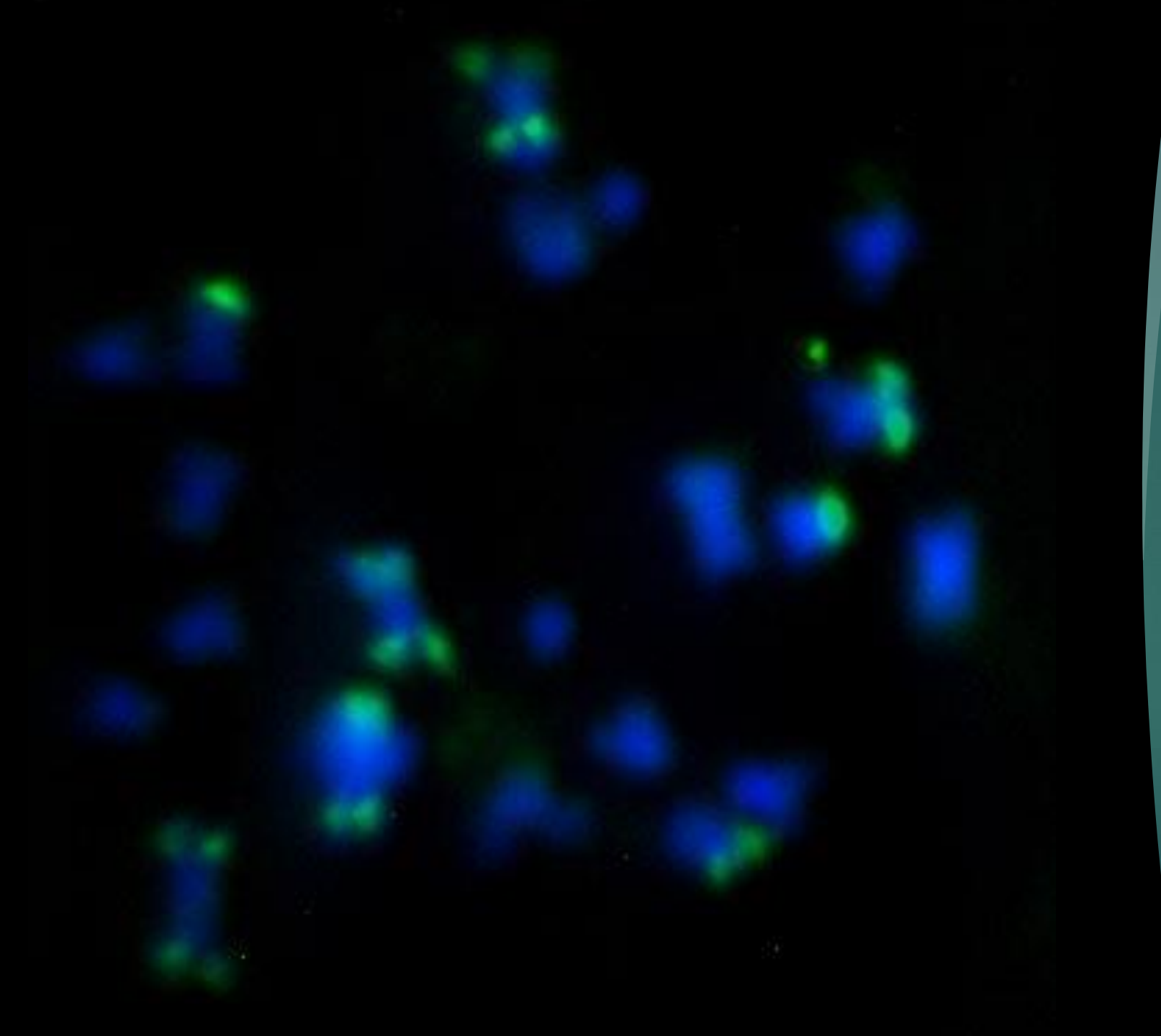
▶ A05:12000000-12500000:492740-492787 ATATAAAATTGAGAAAAATGGCAAAAAAGATTATGATCAACTAGAAG
▶ A05:12000000-12500000:493030-493077 CAGAGACAGACTTTACCAAAAAGCAATAAAAATTAATAAATATCAAT
▶ A05:12000000-12500000:493220-493267 ATTAAGAAAAAAGGTTAACCTAAATTGGTGGTACAAAATATAATGAA
▶ A05:12000000-12500000:497420-497467 AACAAATTGGAGAAAAATTTAACTTATTTTGAGGGAAAATATGAAG
▶ A01:4000000-4500000:990-1037 ATATGTTGCAGCATTTAATGTTGTCAAATTATATAGCAGAAATATAA
▶ A01:4000000-4500000:1040-1087 AAAAAACTAGTTGGCAGTACAAATAATGTAACCATAAAAAAAATCTA
▶ A01:4000000-4500000:1830-1877 ATTTTGTAAGATGTTGAAGTATGGAATAAACATAAATTCTTTGTTC
▶ A01:4000000-4500000:2190-2237 TCCAAATGCAGAAAATAAAATATTAATAATGAAACATCCAAATAGCT
▶ A01:4000000-4500000:3310-3357 CGGACACTATATAATATTGAAAGCAATAAAAAGATATGAATAAATGA
▶ A01:4000000-4500000:3670-3717 TCCTATAAAAATGAATTATTTGTAAGAAATATGATCACTCTCATACA
▶ A01:4000000-4500000:4270-4317 AGGTTCAAGTTATTATTTAATCTTTCTTTCTACGTTTGTGTTAAT
▶ A01:4000000-4500000:4540-4587 ATATATATGTATACAATGCGATATTAATTGTCTATTCCATGTATGT



A oligos to C9

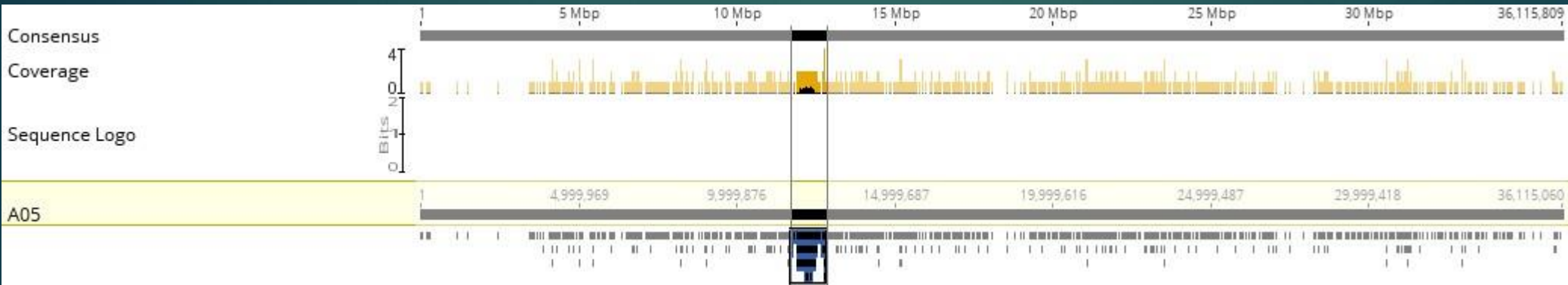


A oligos to C1

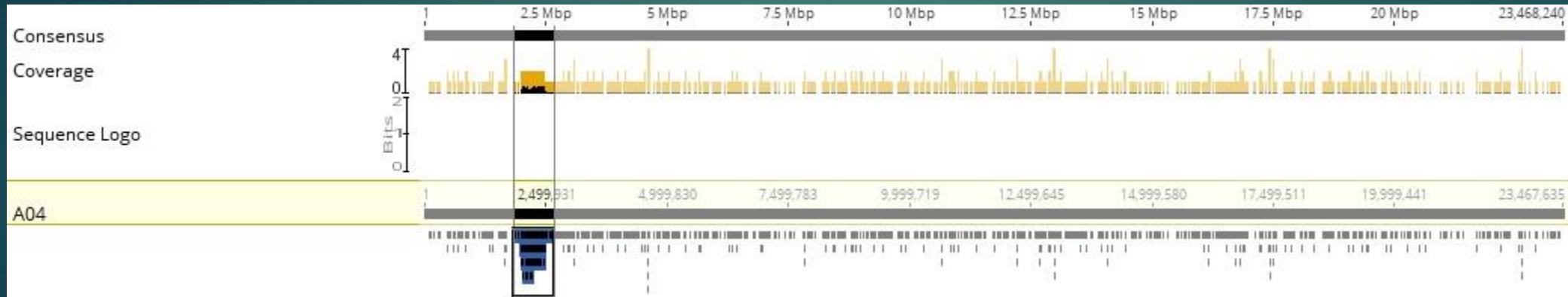


Oligo pool
Brassica rapa AA

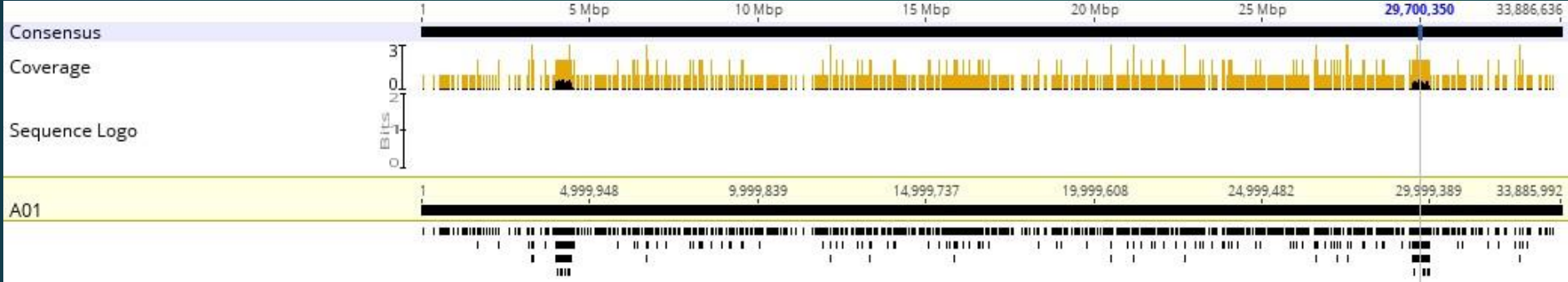
2 pairs both ends
2 pairs one end



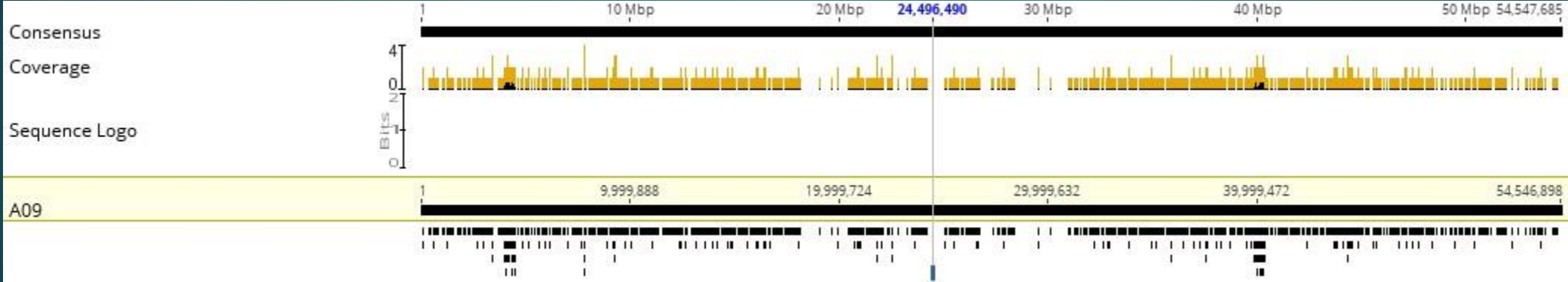
A oligos to A05



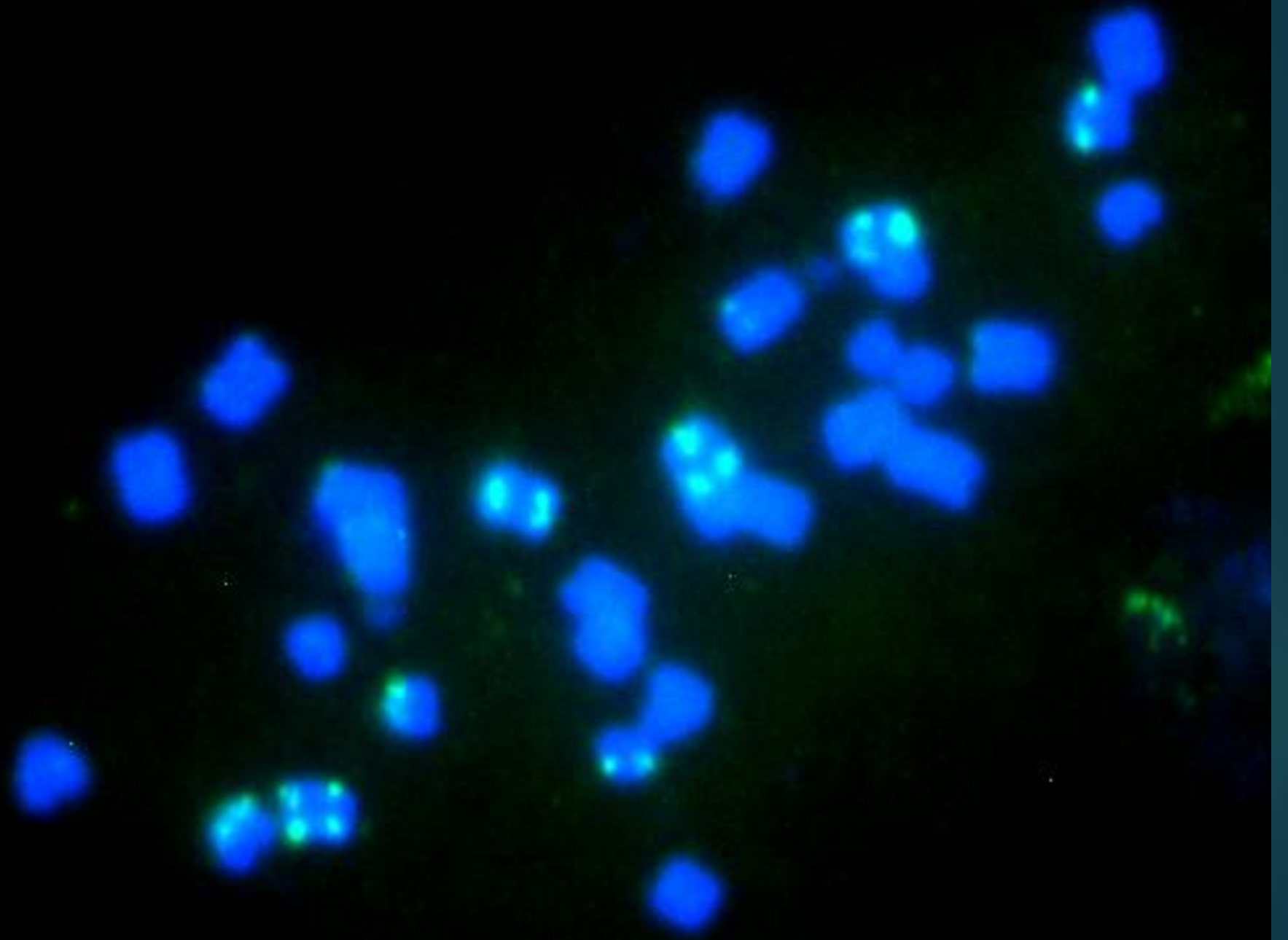
A oligos to A04

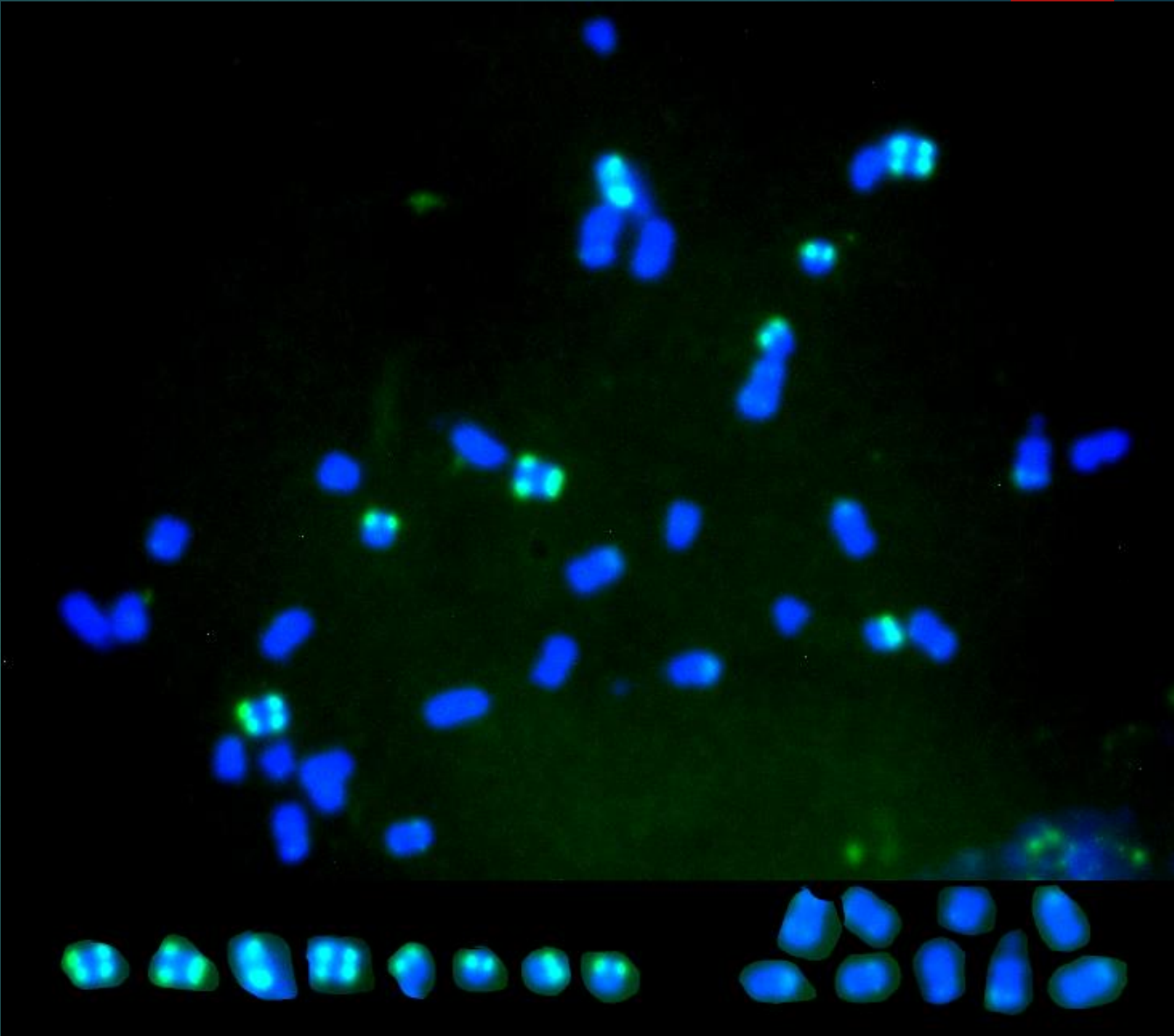



A oligos to A01



A oligos to A09







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