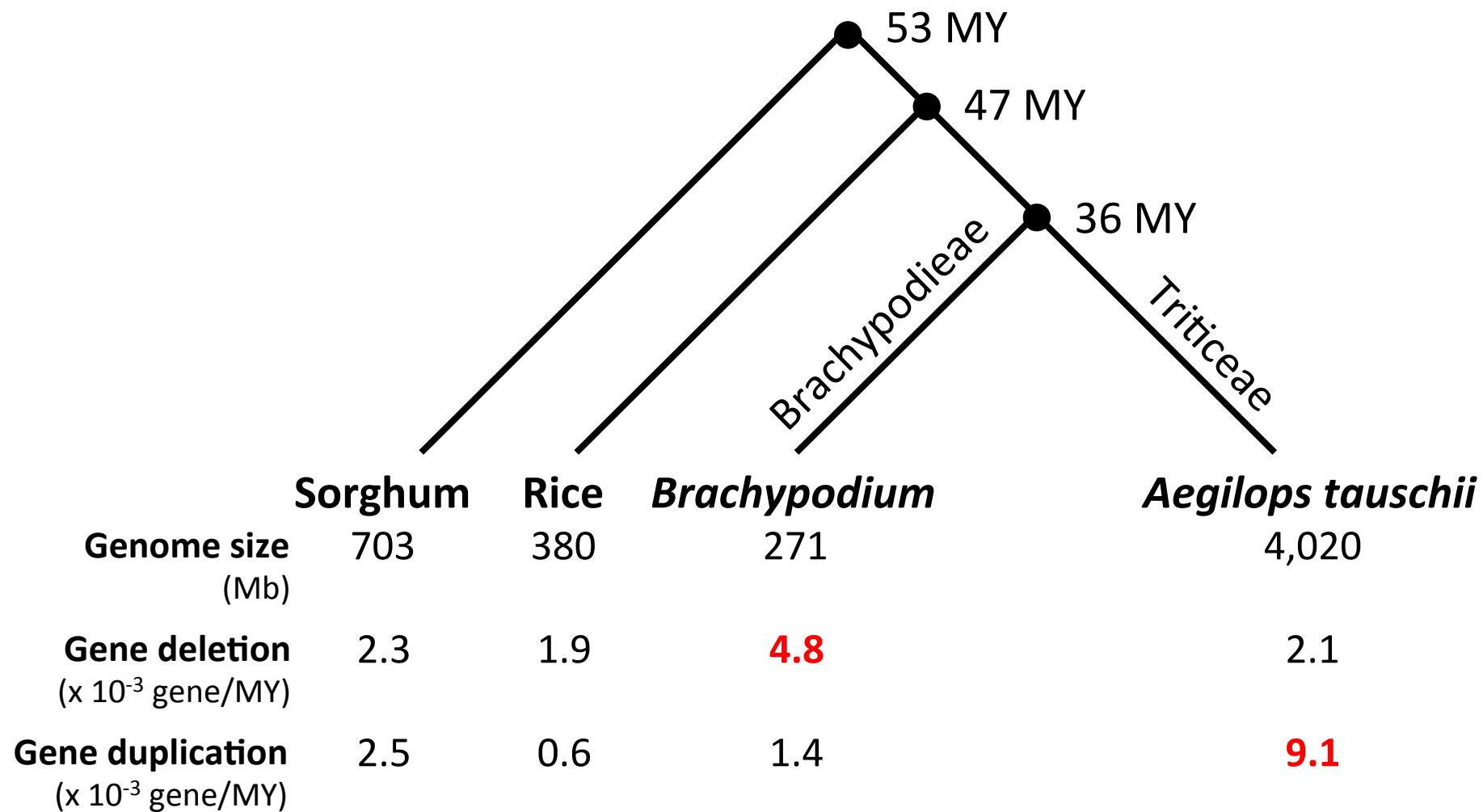


Whole-genome Nanomap comparison reveals dynamics of genome structural evolution

Tingting Zhu

Department of Plant Sciences, University of California, Davis

Genome dynamics in grasses



Driving force of gene deletion/duplication

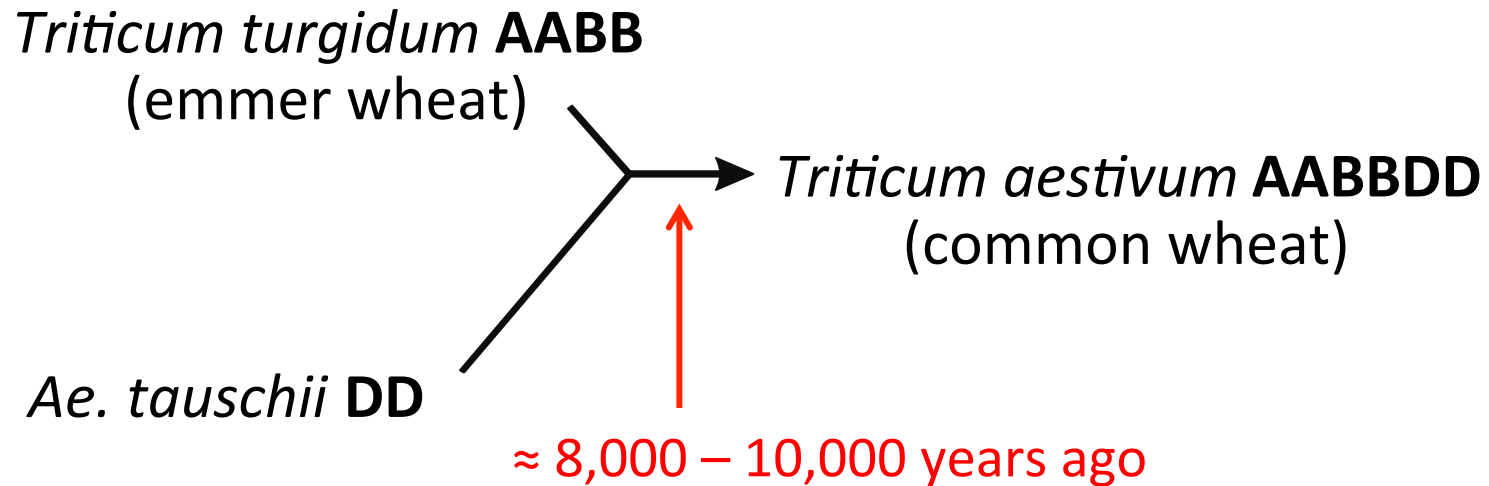
- The gene deletion/duplication rates are correlated with recombination rates along chromosome arms.
- The gene deletion/duplication rates decrease from distal region to proximal region along the chromosomal axis.

NSF funded project

Sequencing the *Aegilops tauschii* genome

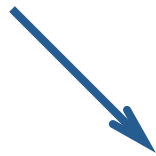
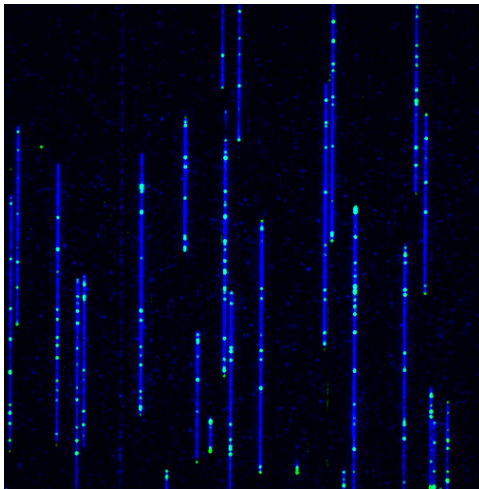
NSF-IOS-1238231

Phylogeny of wheat

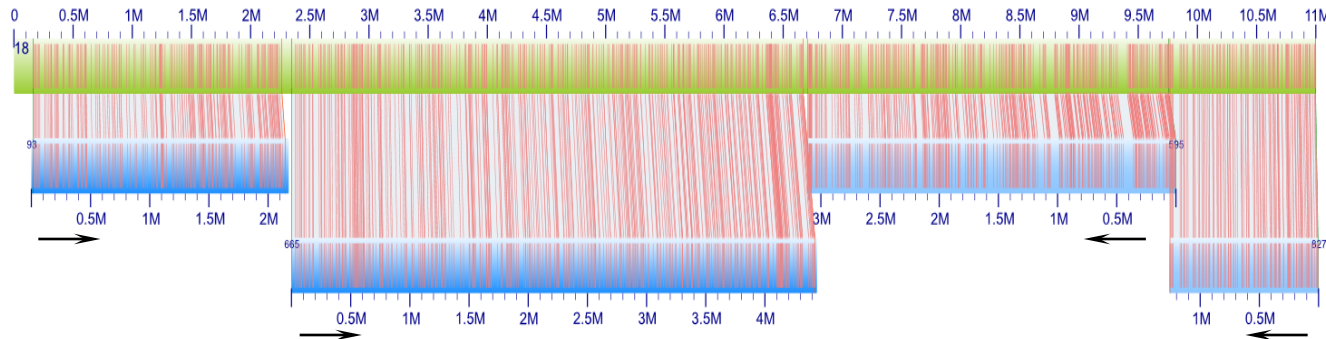


Ae. tauschii ssp. *strangulata* acc. **AL8/78**.
(Dvorak *et al.*, 1998)

BNG map assisted genome assembly



BioNano genome (BNG) map assembly



in silico digestion of NGS assembly

```
>2027.1 218487 HD470E21.RP HI306D22.RP
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GCTTGCATTGCTTCTACTTTGTGAACGCAATAGCTTAGTTTACACATCGTG
```

Reference sequence of *Ae. tauschii* genome

- **7** pseudomolecules: total **4,025 Mb**.

Birth place of the hexaploid wheat

Ae. tauschii AL8/78
(Dvorak *et al.*, 1998)



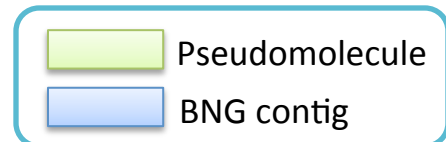
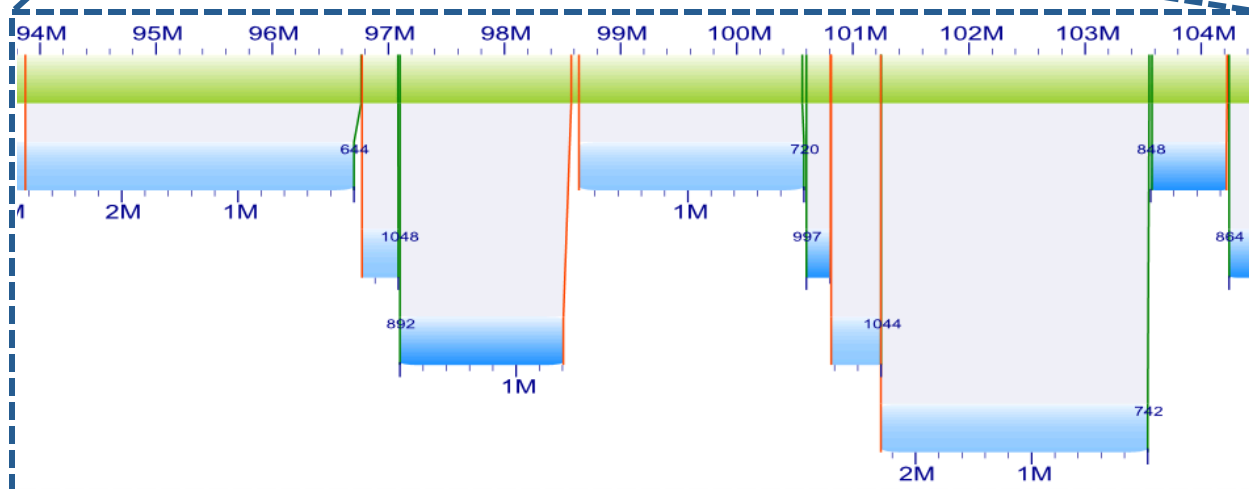
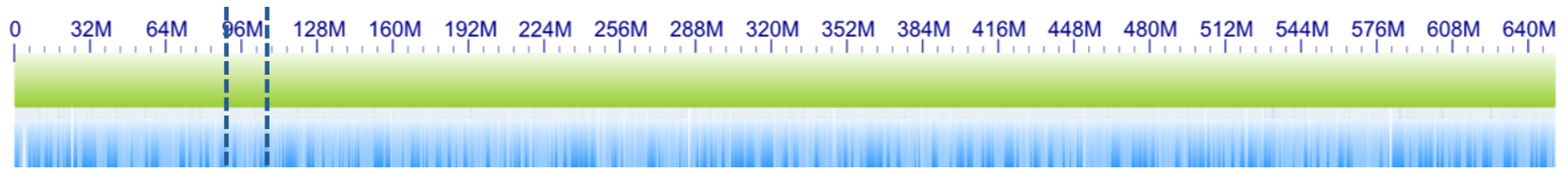
Ae. tauschii Clae23
(Wang *et al.*, 2013)

de novo assembly of BNG map

Assembly	# Contigs	Contig N50 (Mb)	Total length (Gb)
AL8/78_1	4,072	1.56	4.07
AL8/78_2	2,563	2.17	3.88
Clae23	2,494	2.42	4.12
Chinese Spring	12,808	1.40	14.24

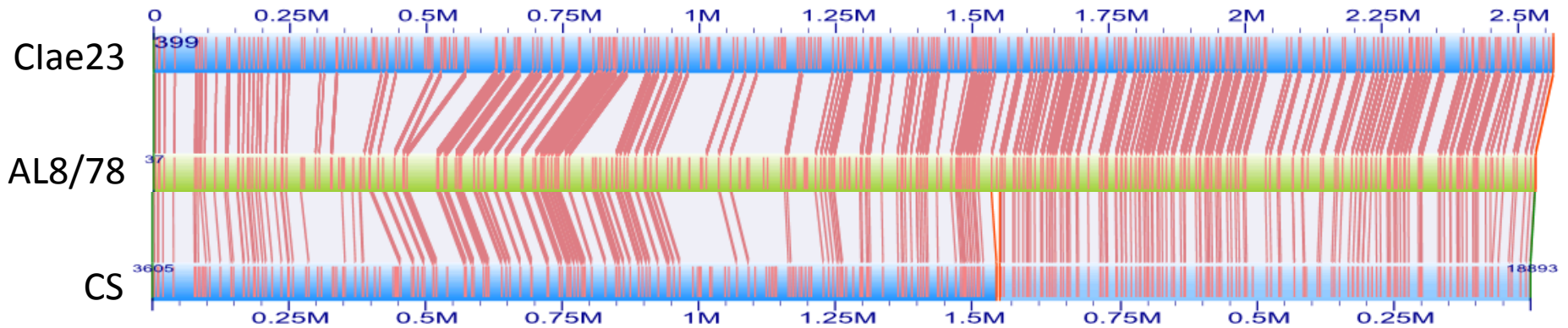
Pseudomolecule of AL8/78

Chr2D

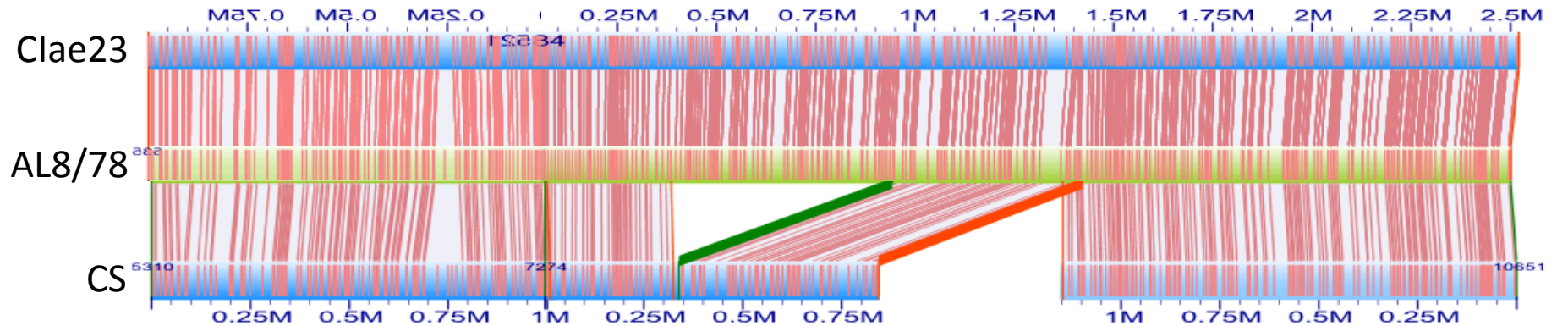


Structural variations (SVs)

Chr2D



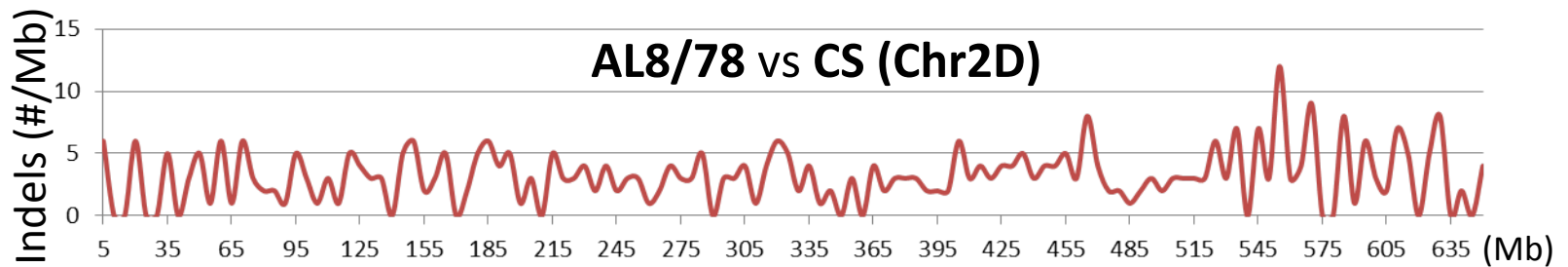
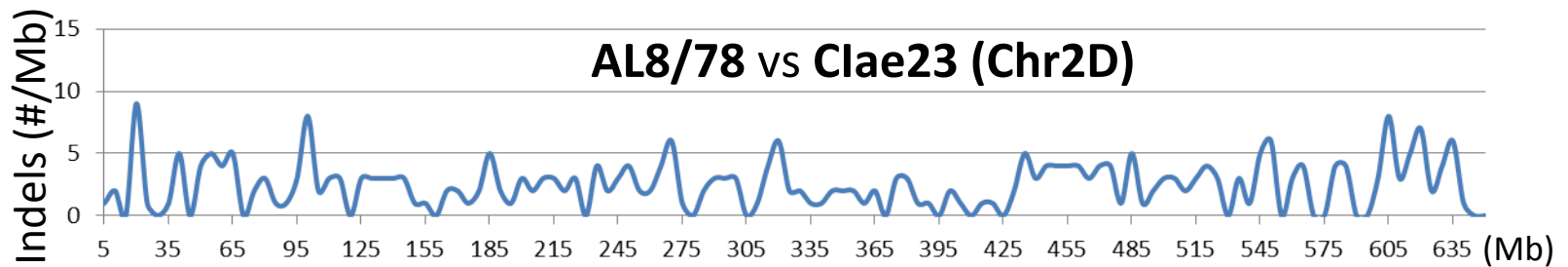
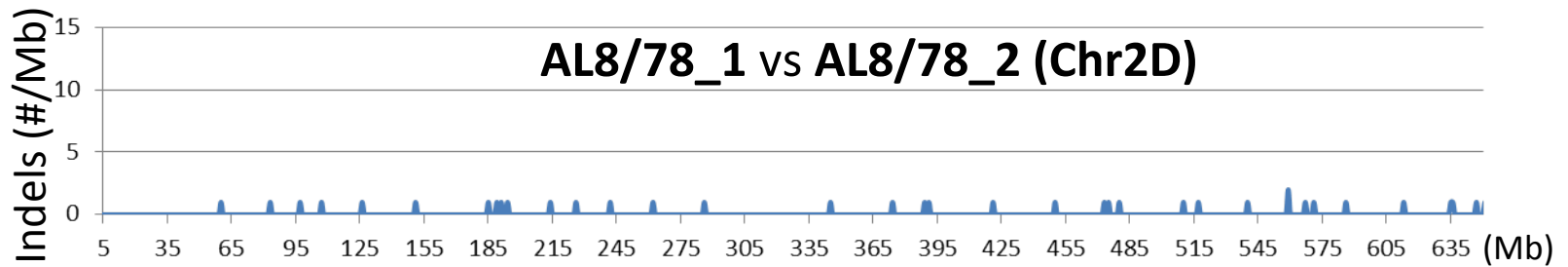
Chr4D



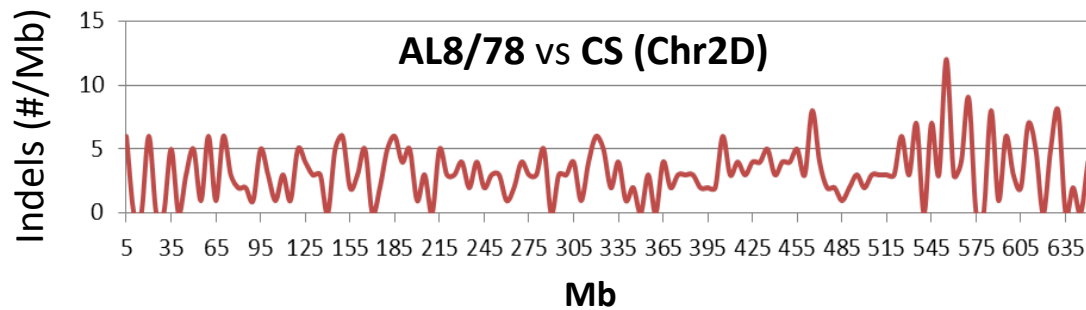
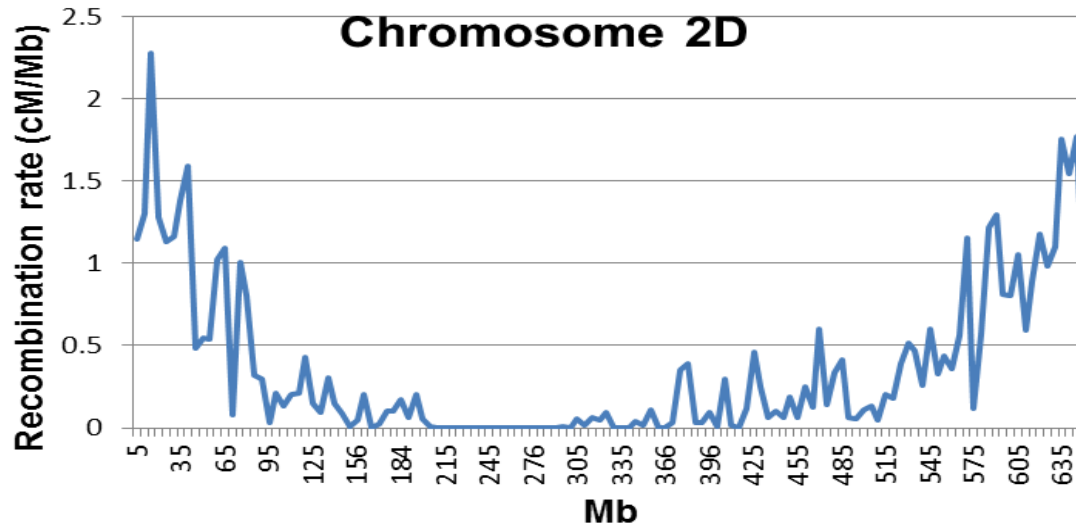
Indels among three genome comparisons

	# Indels/Mb	Length (Mb)	Max (Kb)	Min (Kb)	Mean (Kb)
AL8/78 vs Clae23	2.85	200	273	5	18.9
AL8/78 vs CS	2.69	147	145	5	16.3
Clae23 vs CS	1.82	109	198	5	18.0

SVs along chromosome



Recombination rate along chromosome



Summary

- BioNano genome map can facilitate analysis of whole-genome structural variation.
- Long stretch indels are abundant in large genomes.
- No obvious correlations observed between long stretch indels and recombination rates along chromosomal axis.

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