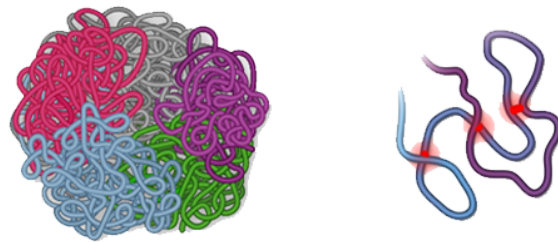
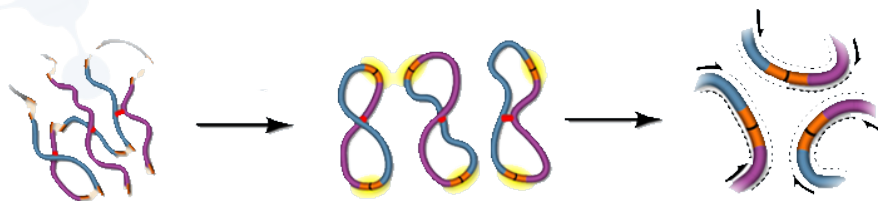


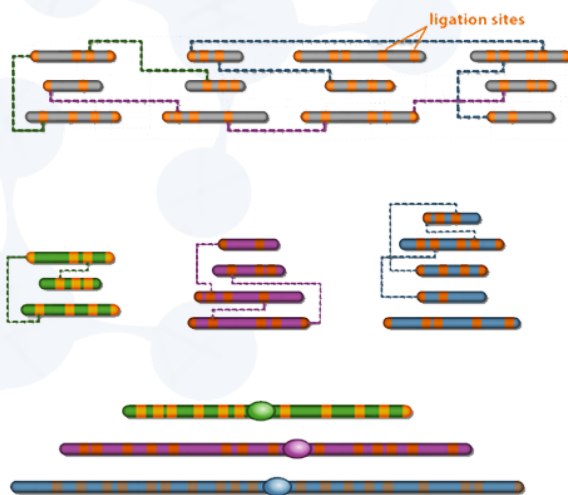
HOW IT WORKS



Physical proximity of nuclear DNA is inversely correlated with genomic distance. Chromatin proximity is captured through *in vivo* crosslinking, preserving contiguity information across entire chromosomes.



Crosslinked chromatin is fragmented and junctions are extracted. Fragmented junctions are proximity ligated and paired-end sequenced. Sequencing data encapsulates the chromatin proximity signal.

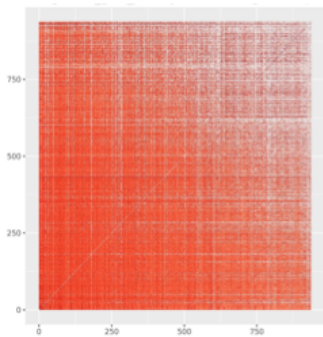


Proximity data establishes relationships among contigs at ligation sites.

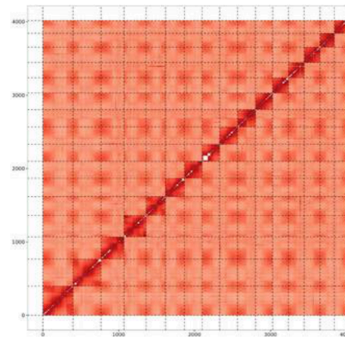
Contigs are placed into chromosome groups based on proximity signal...

... then ordered and oriented by proximity signal onto chromosome-scale scaffolds.

CHROMOSOME-LEVEL HI-C SCAFFOLDING OF PLANT AND ANIMAL GENOMES



Before Proximo Hi-C



After Proximo Hi-C

Lightfoot et al., *BMC Biol* 2017

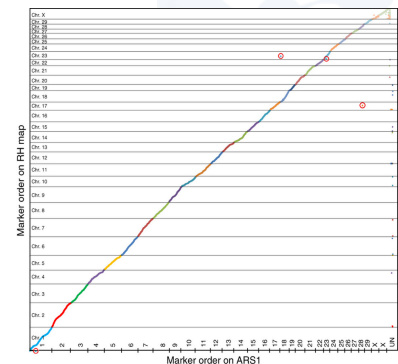
HIGH-ACCURACY
SCAFFOLDS

NO HMW-DNA REQUIRED

RAPID PROJECT
TURNAROUND

Proximo Hi-C-assembled
genomes are highly congruent
with genetic maps

Take any genome assembly to the chromosome level,
improve your contig N50, and resolve structural
variation with the newest Hi-C technology.



Bickhart et al., *Nature Genetics* 2017

PROVEN SCIENTIFIC TRACK RECORD

Proximo Hi-C has been used to scaffold hundreds of assemblies.
Recently published examples are listed below:

Organism	Genome Assembly Size	Final Scaffolds	Scaffolded Length (%)	Starting (N50)	Final (N50)
Goat ¹	2.62 Gb	31	98.74 %	13.9 Mb	91.7 Mb
Hummingbird ²	1.0 Gb	43	99.51 %	5.4 Mb	39.1 Mb
Stickleback ³	446 Mb	21	97.52 %	87.5 kb	20.6 Mb
Amaranth ⁴	400 Mb	16	98.09%	404 kb	24.1 Mb
Human ⁵	2.74 Gb	23	98.02 %	437 kb	125.7 Mb

1: Bickhart et al., *Nature Genetics*, 2017; 2: Pennisi., *Science*, Vol. 357, Issue 6346, pp. 10-11 3: Peichel et al., *Journal of Heredity*, 2017; 4: Maughan et al., *BMC Biology*, 2017; 5: Burton et al., *Nature Biotechnology*, 2013.