PHASE GENOMICS

Proximo™ Genome Scaffolding Platform

Convert Contigs to Chromosomes

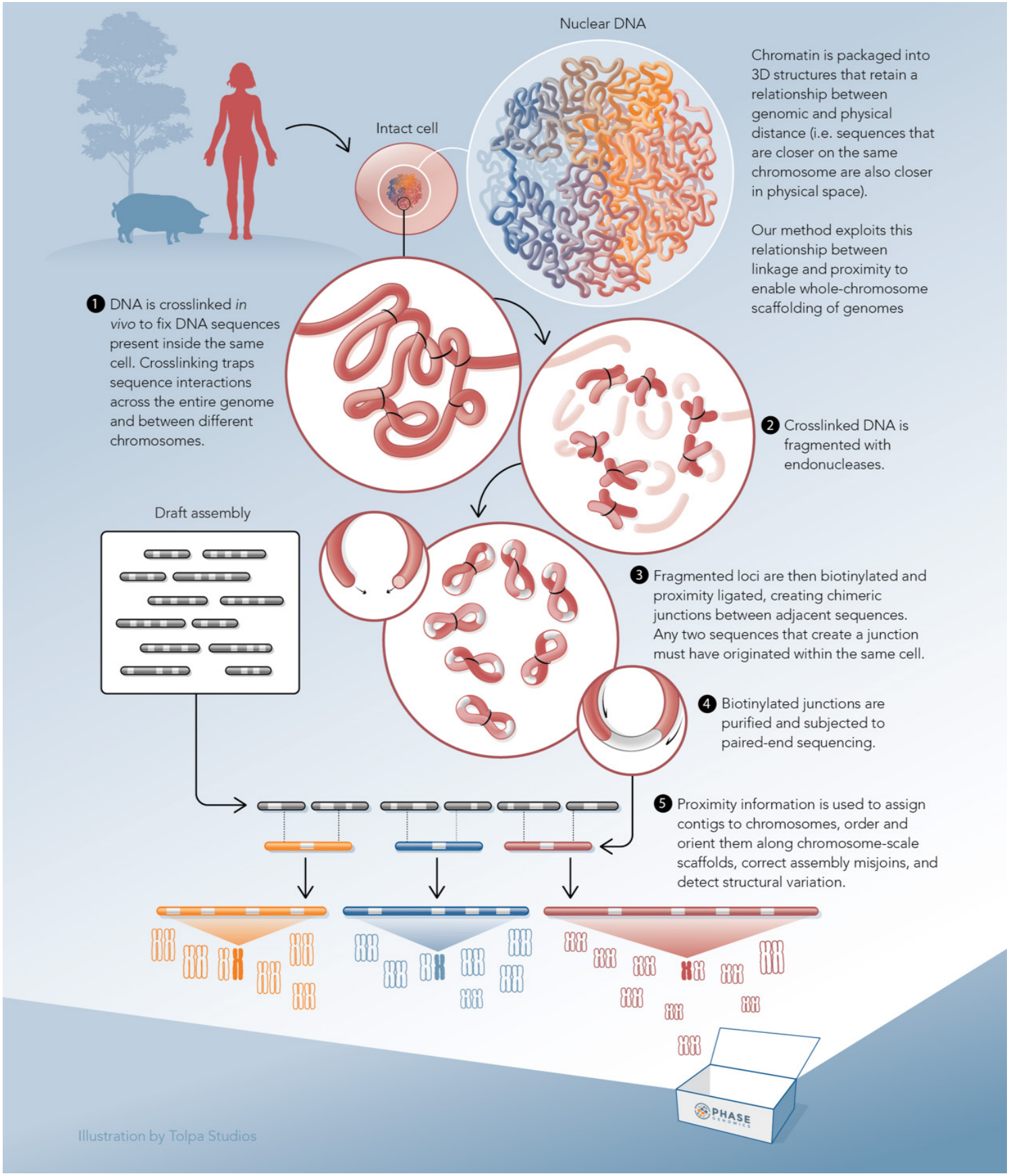
Haplotype-resolved, chromosome-scale platinum genomes

The Proximo Hi-C method employs cost-effective proximity ligation data generated using **in vivo** Hi-C to orient and order contigs into chromosome-scale scaffolds, and generate reference-quality genome assemblies for virtually any organism. Go beyond the sequence to phase haplotypes and detect structural variation; and help deliver on the promise of genomics across a wide range of many applications in agriculture and medicine.

Key features:

- Scaffold chromosome-scale genomes
- Generate high-quality, long-range sequencing data
- No high-molecular-weight DNA or culturing required
- Short-read compatible; yields libraries for Illumina® sequencing
- User-friendly, 2-pack Proximo Hi-C Kits with Proximo Genome Scaffolding Analysis service

Technology



Applications

Assemble high-quality reference genomes

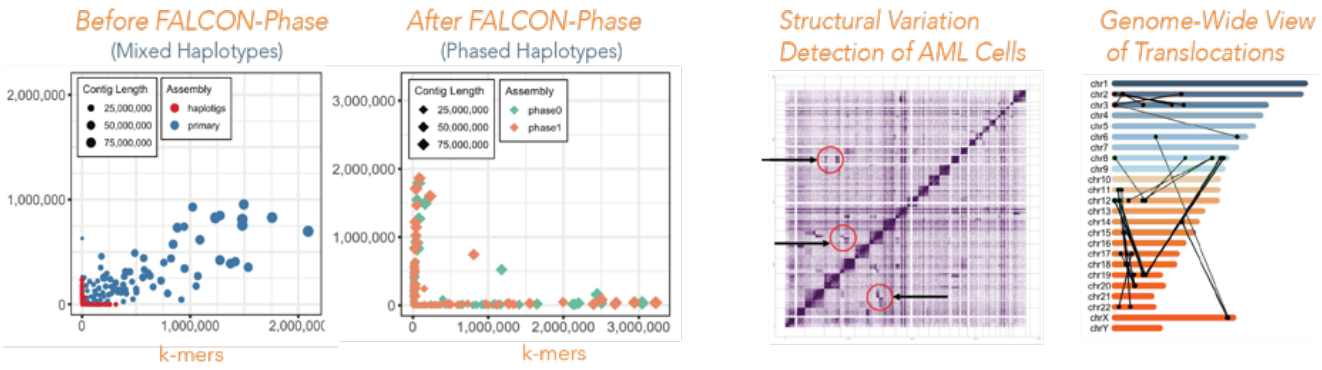
Transform your draft assemblies into high-quality genomes. Proximo™, the most published Hi-C scaffolding method, dependably yields high-quality, end-to-end chromosome scaffolds for diverse species, from diverse sample types. Hi-C data and Proximo may also be integrated with other computational approaches (e.g. FALCON-Phase™), to enable the production of "gold" and "platinum" eukaryotic genomes.

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]	1.41 Gb	37	99.51	5.4 Mb	38.0 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
Honey Bee[6]	223 Mb	7	98.40	1.21 Mb	31.86 Mb
Clownfish[7]	904 Mb	24	97.97	1.86 Mb	38.1 Mb
Black Raspberry[8]	291 Mb	7	100.0	5.19 Mb	41.1 Mb
Firefly[9]	473 Mb	10	94.64	175 kb	49.2 Mb

1: Bickhart et al. Nat. Genet. 2017; 49: 643. 2: Pennisi, Science 2017; 357: 10. 3: Peichel et al. J. Hered. 2017; 108: 693. 4: Lightfoot et al. BMC Biol. 2017; 15: 74. 5: Burton et al. Nat. Biotechnol. 2013; 31: 1119. 6: Wallberg et al. BMC Genomics 2019; 20: 275. 7:Lehmann et al. BioRxiv March 2018. 8: VanBuren et al. GigaScience 2018; 7: giy094. 9: Fallon et al. BioRxiv December 2017. For a complete list of eukaryotes for which reference genomes have been generated or improved with the Proximo Platform, visit http://phasegenomics.com/publications/#papers.

Phase haplotypes and detect structural variants

Hi-C captures both short-range and long-range genomic contiguity. The Hi-C signal increases as the genomic distance between any two loci across the genome decreases. FALCON-Phase uses this information to phase genomes. Proximo SV detects complex rearrangements, including balanced translocations, chromothripsis, and copy number changes across the entire genome. Collect SNV, CNV, SV, and phase data from a single library prep.



Proximo captures the complexities of the genome and structural aberrations in cancer by generating phased, end-to-end chromosome scaffolds.

Kits & Services

Complete Sample-to-Analysis Solution

Accelerate your genomics research with our user-friendly sample prep kits, customized for different sample types, and the Proximo Genome Scaffolding software. Hi-C kits yield a dual-indexed proximity ligation library, to be sequenced on an Illumina® sequencer.

Hi-C kits are available for plant, fungal, animal, microbial and human samples.

Proximo Hi-C Kits

- Everything needed for two sample preps, starting from intact cells
- Only 3 hours hands-on time
- Unique dual-indexed Illumina adapters included

Take advantage of our expertise

Interested in additional computational analyses? Contact us to learn more about the services listed below:

Proximo SV

- Identify large-scale structural variation and determine epigenetic changes using Hi-C data.

FALCON-Phase™

- Integrate PacBio long-read assemblies with Hi-C data to generate phased, diploid genome assemblies.

Not doing genomics research? **Contact us to find out about our metagenomics platform and services.**

ProxiMeta™ Metagenome Deconvolution Platform

- Go beyond 16S and binning techniques to obtain complete genomes directly from a mixed samples.

PHASE GENOMICS

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