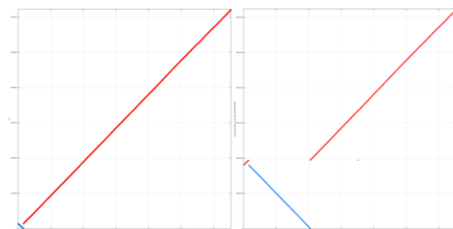


# Proximo™ Hi-C Chromosome-Scale Scaffolding

## SCAFFOLD LARGE GENOMES, NO HMW DNA REQUIRED

Proximo Hi-C organizes a *de novo* mammalian genome assembly into a reference-quality set of chromosome-scale scaffolds. Subsequent gap-filling closes 53.9% of gaps, leaving only 663 gaps in the entire assembly.



Goat	PacBio (PB)	+BioNano (BN)	+Proximo
Contigs/Scaffolds	3110	1575	31
Scaffold Length	2.6 Gb	2.7 Gb	2.7 Gb
Scaffold N50	4.7 Mb	22.3 Mb	91.7 Mb

(Bickhart et al. Nature Genetics, 2017)

## DECONTAMINATE ASSEMBLIES, START WITH RAW SAMPLES

Proximo Hi-C uses intact cells and tissues, eliminating the need for high-molecular-weight DNA extraction. This also allows it to remove contaminant DNA from an assembly. In the example below, 174 Mb of contaminant sequence was removed.

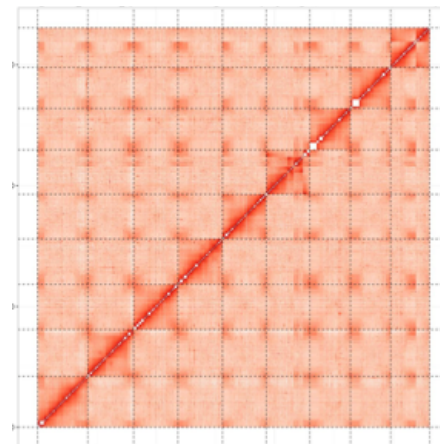


Contaminated Plant	Illumina	+Proximo
Contigs/Scaffolds	12,787	11
Scaffold Length	471 Mb	295 Mb
Scaffold N50	3.8 kb	26.3 Mb
Assembly % Expected Size	158.6%	99.3%
Fungal contigs in assembly	1471	4
Bacterial contigs in assembly	1582	0

# Proximo™ Hi-C Chromosome-Scale Scaffolding

## COMPATIBLE WITH OTHER ASSEMBLY METHODS

Proximo Hi-C works well with Illumina, PacBio, or any other core sequencing technology. It can also be used in combination with other scaffolding technologies to yield even better results, improving genomes already in relatively good states.



Sugar Beet	PB	PB+BN	PB +Proximo	PB+BN +Proximo
Contigs/ Scaffolds	938	86	10	10
Scaffold Length	563 Mb (contigs)	533 Mb	558 Mb	512 Mb
Scaffold N50	1.4 Mb (contig)	12.5 Mb	64.8 Mb	64.9 Mb

Sugar Beet	Illumina (IL)	IL+Dovetail (DT)	IL+DT +Proximo
Contigs/Scaffolds	1,935,503	10,485	10
Scaffold Length	640 Mb (contigs)	506 Mb	492 Mb
Scaffold N50	<10kb (contig)	4.0 Mb	57.1 Mb