Arima CiFi^{TM} Kit

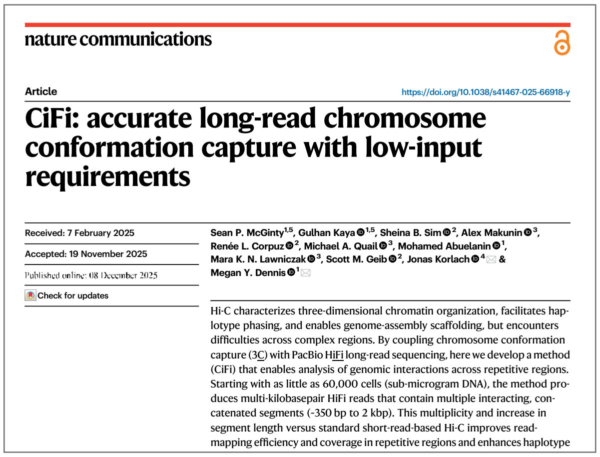
Enables chromatin capture that integrates with downstream PacBio long read sequencing for greater resolution in repetitive and complex genomic regions

Combine Hi-C and Long-Read Sequencing for Complete Genome Insights

Short-read sequencing, while well established, leaves critical gaps in repetitive and complex regions – limiting the depth and completeness of your research. By integrating Hi-C chromatin capture with PacBio HiFi sequencing, CiFi generates multi-contact reads that deliver significantly improved performance – enabling chromosome-scale scaffolding, resolution of complex 3D genome structure, and comprehensive analysis from low input samples.

Benefits of the Arima CiFi Kit

- **One platform, complete data:** integrate scaffolding, phasing, and sequencing without separate Hi-C and HiFi runs
- **Flexible sample compatibility:** work with plants, animals, invertebrates, or low input down to single organisms
- **Built-in quality assurance:** designed to support reliable, reproducible results suitable for publication
- **Ready-to-use convenience:** 8-reaction kit with optimized protocol for fast, efficient setup



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CiFi: accurate long-read chromosome conformation capture with low-input requirements

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Hi-C characterizes three-dimensional chromatin organization, facilitates haplotype phasing, and enables genome-assembly scaffolding, but encounters difficulties across complex regions. By coupling chromosome conformation capture (3C) with PacBio HiFi long-read sequencing, here we develop a method (CiFi) that enables analysis of genomic interactions across repetitive regions. Starting with as little as 60,000 cells (sub-microgram DNA), the method produces multi-kilobasepair HiFi reads that contain multiple interacting, concatenated segments (~350 bp to 2 kbp). This multiplicity and increase in segment length versus standard short-read-based Hi-C improves read-mapping efficiency and coverage in repetitive regions and enhances haplotype

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From Contigs to Phased Chromosomes in One Platform

The authors developed CiFi , and applied it to generate chromosome-scale assemblies and chromatin interaction maps from human cell lines, single mosquitos, and single fruit flies. Key findings include superior mapping in repetitive regions (83-89% vs. 33-37% for short-read Hi-C), improved haplotype phasing (80.3% vs. 10.9%), and successful assembly from as few as 62,000 cells.

McGinty, S.P., Kaya, G., Sim, S.B. et al. CiFi: accurate long-read chromosome conformation capture with low-input requirements. Nat Commun 17, 215 (2026).

CiFi Workflow

CiFi Prep

Easy to follow protocol

Library Prep

Generate high-quality PacBio libraries

Sequencing

Process on recommended PacBio platform

Analysis

Analyze data with suggested pipeline

Product List

Product	Description	Size	SKU
Arima CiFi Kit	Includes chromatin capture reagents	8 reaction kit	A101050
Arima CiFi Library Prep Service	Service performed at Arima Genomics (PacBio sequencing can be added for an additional fee)	Custom project	A201040

Specifications

Category	Specification (minimum)
Sample Input	Fresh frozen tissue: 50mg Whole blood: 1mL Plant tissue: 2.5g Cells: >1 million cells
Sequencing Requirements	PacBio long read sequencing (coverage varies based on # of samples pooled, genome size and application)
Analysis Pipeline	Primary data: BAM file Downstream analysis: Follow McGinty paper protocol

Contact Arima Genomics for a quote or project consultation.

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