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ISBN	1-59693-095-0
Descrizione fisica	1 online resource (275 p.)
Altri autori (Persone)	KimSun <1962-> TangHaixu MardisElaine <1962->
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Soggetti	Genomes - Analysis Nucleotide sequence Electronic books.
Lingua di pubblicazione	Inglese
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Note generali	Description based upon print version of record.
Nota di bibliografia	Includes bibliographical references and index.
Nota di contenuto	An overview of new DNA sequencing technology -- Array-based pyrosequencing technology -- The role of resequencing arrays in revolutionizing DNA sequencing -- Polony sequencing -- Genome sequencing: a complex path to personalized medicine -- Overview of genome assembly techniques -- Fragment assembly algorithms -- Assembly for double-ended short read sequencing technologies -- Genome characterization in the post-human genome project era -- The haplotyping problem: an overview of computational models and solutions -- Analysis of genomic alterations in cancer -- High-throughput assessments of epigenomics in human disease -- Comparative sequencing, assembly, and anchoring.
Sommario/riassunto	"From a who's who of pioneers in the field comes a unique resource covering the latest advances in next generation genome sequencing and assembly. This groundbreaking book includes non-conventional techniques that are paving the way to potential new biomedical applications. Practitioners find unparalleled access to state-of-the-art DNA sequencing technologies, new algorithmic sequence assembly techniques, and emerging methods for both resequencing and de novo

genome analysis, which all together offer the most solid foundation possible for tackling the full range of experimental and computational challenges in the genome sciences today."--Jacket.