Supplementary Table S1. Types of visualization in OMView

Types of visualization	**Functions**
Regional view	Display alignments as an overview at a selected region
Anchor view	Display alignments that match selected signals to validate structural variations
Alignment view	Display alignment detail of a single molecule
Multiple alignment view	Display the multiple alignment of all queries for genome comparison
Molecule view	Display molecules for data inspection

Supplementary Table S2. Features in OMView

	Details
Visualization types	Supported multiple visualization types for different objectives, including overview of alignment at a region, structural variations validations, detailed view of an alignment, multiple alignment and inspection of data quality
Visualization Interface	Color representation on segment stretching in molecules
	Tabbed browsing
	Multiple panels for direct comparison across different samples
	Command-line arguments input for easy graphics generation
Performance	High loading speed, especially on visualizing large data set
Supported data formats	Supported a wide range of data, alignment and annotation formats in optical mapping
	Supported vector graphics export

Supplementary Table S3. Types of supported data formats in OMTools.

OMTools supports data formats used by OpGen Inc. and BioNano Genomics Inc., alignment results by different alignment methods and various common annotation formats. OMView also supports image export in different formats.

	Formats
Optical mapping molecules	REF, FA01, SPOTS, DATA, SDATA, BNX, CMAP, OPT, SILICO, and OpGen XML formats
Alignment results	OMA, OMD, XMAP, Valouev *et al.*, SOMA v2 Unique Match, and Twin PSL formats
Annotation	BED, GFF/GTF/GVF, and OSV
Image	SVG, PNG and JPEG/JPG

Supplementary Table S4. List of modules in OMTools

Modules	**Description**
Mapper	
OMBlastMapper	Aligns query optical maps to reference optical maps using the OMBlast algorithm
OMHAMapper	Aligns query optical maps to reference optical maps using the OMHA algorithm
OMFMMapper	Aligns query optical maps to reference optical maps using the OMFM algorithm
PairwiseAlignment	Performs pairwise alignment between each pair of optical map data sets from multiple optical map files.
FastaTools	
FastaToOM	Performs an *in silico* digestion on DNA sequence and provides statistics for nicking site breaks
Data Tools	
DataTools	Provides basic functions for manipulation of optical mapping data
DataStatistics	Generates basic statistics for optical mapping data
DuplicatedMoleculesDetection	Detects duplicated entries in an optical map data set
DuplicatedMoleculesRemover	Removes duplicated entries in an optical map data set
Simulation	
OptMapDataGenerator	Generates simulated optical mapping data from a reference according to specified error model
RandomReferenceGenerator	Generates random reference according to the given signal density
Alignment Tools	
ResultTools	Provides basic functions for manipulation of alignment results
ResultMerger	Merges alignment results from different alignment methods
ResultStatistics	Generates basic statistics for alignment results
PrecisiongRecallGraphDataGenerator	Generates precision-recall graph data for alignment performance analysis
Visualization	
OMView	Provides visualization of optical maps