

KaryoSolver

The Next Generation of Karyogenomics via Low-Pass Whole Genome Sequencing

Turnaround < 24h
Rapid same-day reporting

~50 kb Resolution
High-precision CNV & ROH calls

Data Privacy
BAM file local preprocessing

KaryoSolver represents a paradigm shift in molecular cytogenomics, replacing conventional karyotyping technologies with uniform low-pass whole genome sequencing.

KEY DIAGNOSTIC DETECTION CAPABILITIES:

Aneuploidies

Detects genome-wide numerical abnormalities and whole-chromosome gains/losses.

Segmental CNVs

Detects deletions and duplications down to ~50 kb across all autosomes & sex chromosomes.

Balanced Translocations

Detects chromosomal rearrangements that do not result in a net gain or loss of genetic material.

Mosaicism

Identifies mosaic CNVs and low-level numerical alterations at moderate fractions (> 10%).

ROH

Detects Loss of Heterozygosity (LOH) and Regions of Homozygosity for UPD & consanguinity.

ALL-IN-ONE SOLUTION

aCGH, SNP ARRAYS & OGM » **LOW-PASS WGS** + **KaryoSolver**

	Array CGH	SNP Array	OGM	KaryoSolver
Core Mechanism	Dual-color hybridization	Allele-specific hybridization	Direct imaging of UHMW	**Low-Pass WGS**
DNA Input Required	High (>500 ng)	Medium (>100 ng)	High (~750 ng)	**Ultra-low (≥ 50 ng)**
Sample Flexibility	Blood, Amniotic Fluid, CVS	High-quality DNA	UHMW DNA	**Blood, Amniotic fluid, CVS, WGA**
CNV Resolution	~100 - 200 kb	~50 - 100 kb	~100 - 200 kb	**~50 kb**
LOH / UPD Detection	No	Yes	Limited	**Yes**
Structural Variant Detection	No balanced SVs	No balanced SVs	Yes	**Yes**

CLINICAL APPLICATIONS

PRENATAL DIAGNOSTICS

- Chromosomal microarray analysis (CMA)
- Regions of Homozygosity (ROH) and Uniparental Disomy (UPD) investigation
- Product of Conception (POC) analysis, i.e. PGT

VALIDATED FOR:

- Chorionic villi
- Body fluids (amniotic fluid),
- tissues (foetal abortion tissue)
- Whole Genome Amplification (WGA)

POSTNATAL / CONSTITUTIONAL

- Developmental Delay (DD)
- Intellectual Disability (ID)
- Autism Spectrum Disorder (ASD)
- Multiple congenital anomalies

VALIDATED FOR:

- Peripheral Blood

CANCER GENOMICS

- Chromosomal copy-number alteration
- Loss of Heterozygosity (LOH) investigation
- Mosaicism and clonal architecture assessment

VALIDATED FOR:

- Peripheral Blood
- Bone Marrow

Clinical Application	Typical Indication	CNV Scale
PGT (A/SR)	Embryo screening	Whole-chr & large segmental
Prenatal (Large)	Abnormal ultrasound, positive NIPT	Whole-chr & large CNVs
Prenatal (Recurrent)	Syndromic fetal anomalies	Recurrent CNVs
Postnatal (Standard)	DD, ID, ASD, ADHD, Epilepsy	Pathogenic CNVs
Postnatal (Congenital)	CHD, syndromic phenotype	Large syndromic CNVs
Cancer (Large)	MDS, AML, MPN	CNVs and aneuploidies
Cancer (Recurrent)	Known risk regions	Recurrent deletions

Integrated 4bases Workflow

KaryoSolver is a NGS-based solution that redefines molecular karyotyping.
By combining the **lyophilized KaryoPrep library preparation**
with a dedicated, purpose-built data analysis pipeline.

PHASE 1 • WET LAB

KaryoPrep

NGS library preparation in less than 2 hours of hands-on time.

Features 100% **lyophilized reagents** for maximum stability without cold-chain constraints.

PHASE 2 • PRIVACY & DATA

KaryoCompanion

Secure on-premise software for BAM file preprocessing.

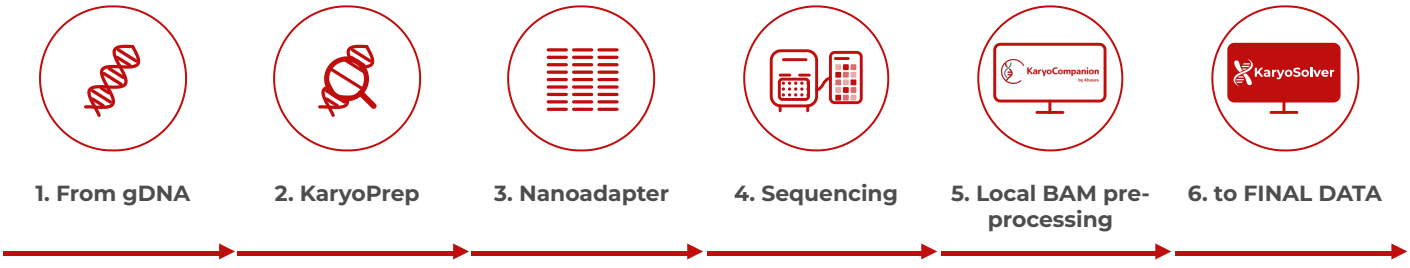
Guarantees complete clinical sample anonymization and strict compliance with global data privacy standards.

PHASE 3 • BIOINFORMATIC ANALYSES

KaryoSolver

Automated CNV/ROH segmentation.

Integrated with ClinGen/ACMG databases to generate standardized, ISCN-compliant diagnostic reports.

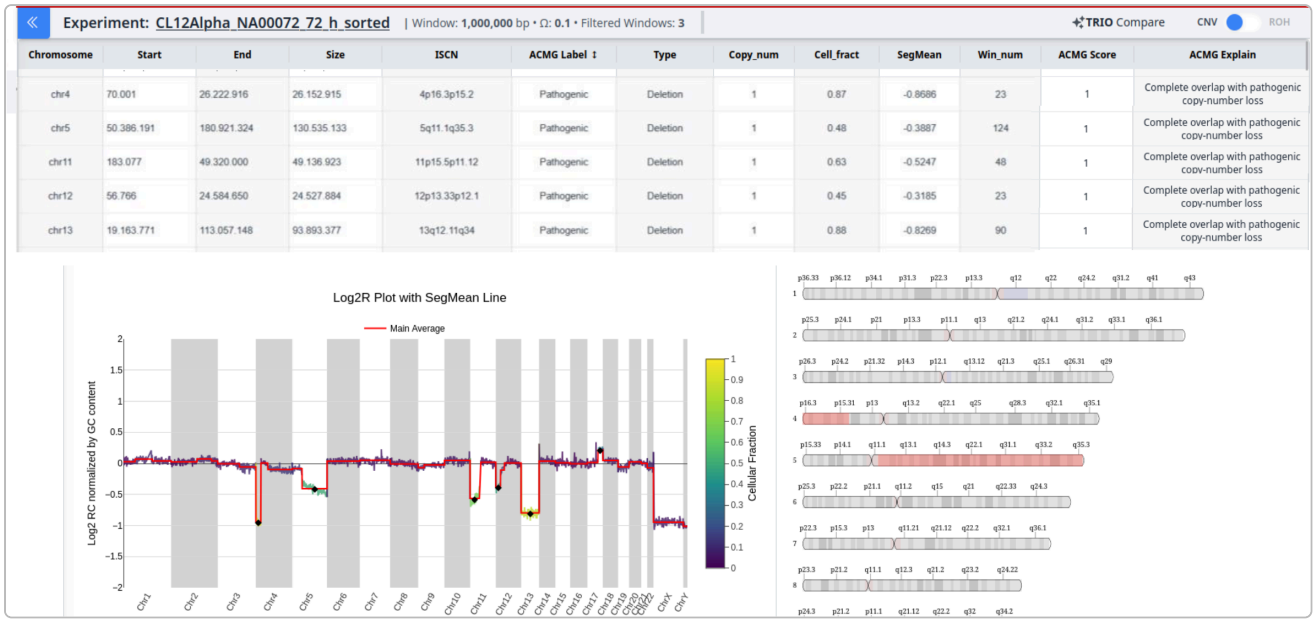


lpWGS Performance & Throughput

Resolution	Detection capability	Samples/ Promethion	Samples/ MiniON
~ 5Mb	Large CNVs	> 96 samples	72 samples
~ 1Mb	CNVs	96 samples	16 samples
~ 500kb	CNVs	72 samples	12 samples
~ 200kb	High-resolution CNVs	48 samples	8 samples
~ 100kb	High-resolution CNVs	24 samples	4 samples
~ 50kb	Ultra-high-resolution CNVs	16 samples	2 samples
ROH	LOH, UPD	16 samples	2 samples
Balanced SVs	Balanced structural variants	4 samples	-

Constitutional CNVs: from genomic imbalance to clinical interpretation

CASE 1 | Wolf-Hirschhorn syndrome with chromosomes deletions and duplications

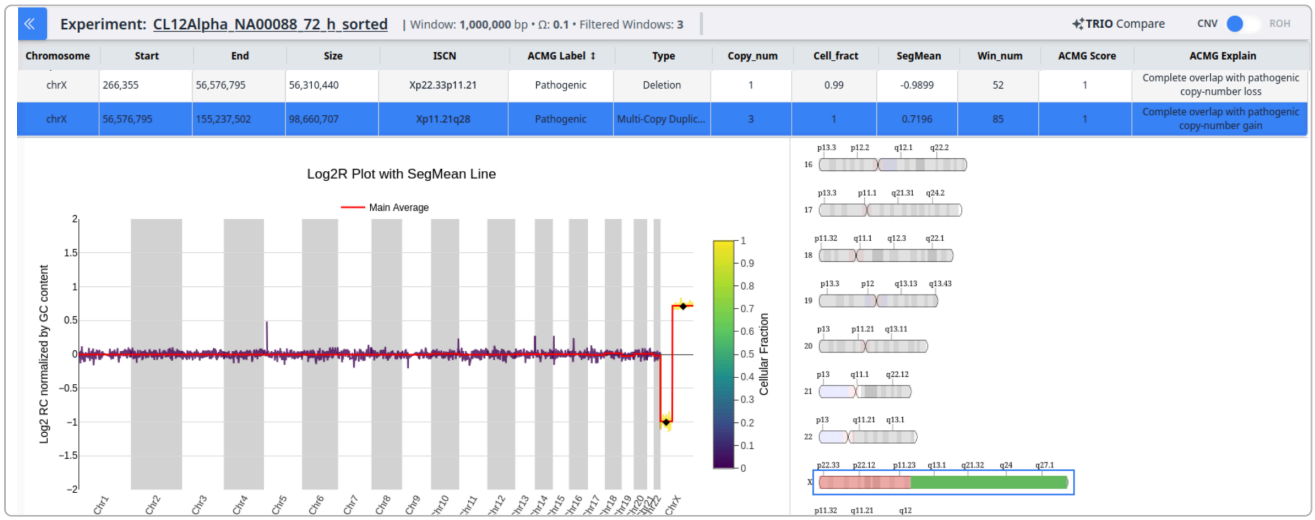


Experiment: CL12Alpha_NA00072_72_h_sorted | Window: 1,000,000 bp • Ω: 0.1 • Filtered Windows: 3

Chromosome	Start	End	Size	ISCN	ACMG Label	Type	Copy_num	Cell_fract	SegMean	Win_num	ACMG Score	ACMG Explain
chr4	70.001	26.222.916	26.152.915	4p16.3p15.2	Pathogenic	Deletion	1	0.87	-0.8686	23	1	Complete overlap with pathogenic copy-number loss
chr5	50.386.191	180.921.324	130.535.133	5q11.1q35.3	Pathogenic	Deletion	1	0.48	-0.3887	124	1	Complete overlap with pathogenic copy-number loss
chr11	183.077	49.320.000	49.136.923	11p15.5p11.12	Pathogenic	Deletion	1	0.63	-0.5247	48	1	Complete overlap with pathogenic copy-number loss
chr12	56.766	24.584.650	24.527.884	12p13.33p12.1	Pathogenic	Deletion	1	0.45	-0.3185	23	1	Complete overlap with pathogenic copy-number loss
chr13	19.163.771	113.057.148	93.893.377	13q12.11q34	Pathogenic	Deletion	1	0.88	-0.8269	90	1	Complete overlap with pathogenic copy-number loss

KaryoSolver highlights the pathogenic **4p deletion** directly in the CNV profile and links the finding to genomic coordinates and annotation. The visual pattern makes the clinically relevant imbalance easy to recognize and supports a rapid interpretation consistent with Wolf–Hirschhorn syndrome.

CASE 2 | Turner syndrome — pattern consistent with isochromosome Xq



Experiment: CL12Alpha_NA00088_72_h_sorted | Window: 1,000,000 bp • Ω: 0.1 • Filtered Windows: 3

Chromosome	Start	End	Size	ISCN	ACMG Label	Type	Copy_num	Cell_fract	SegMean	Win_num	ACMG Score	ACMG Explain
chrX	266,355	56,576,795	56,310,440	Xp22.33p11.21	Pathogenic	Deletion	1	0.99	-0.9899	52	1	Complete overlap with pathogenic copy-number loss
chrX	56,576,795	155,237,502	98,660,707	Xp11.21q28	Pathogenic	Multi-Copy Duplic...	3	1	0.7196	85	1	Complete overlap with pathogenic copy-number gain

How to read the pattern

Xp22.33–p11.21: CN = 1
loss of the short arm (Xp)

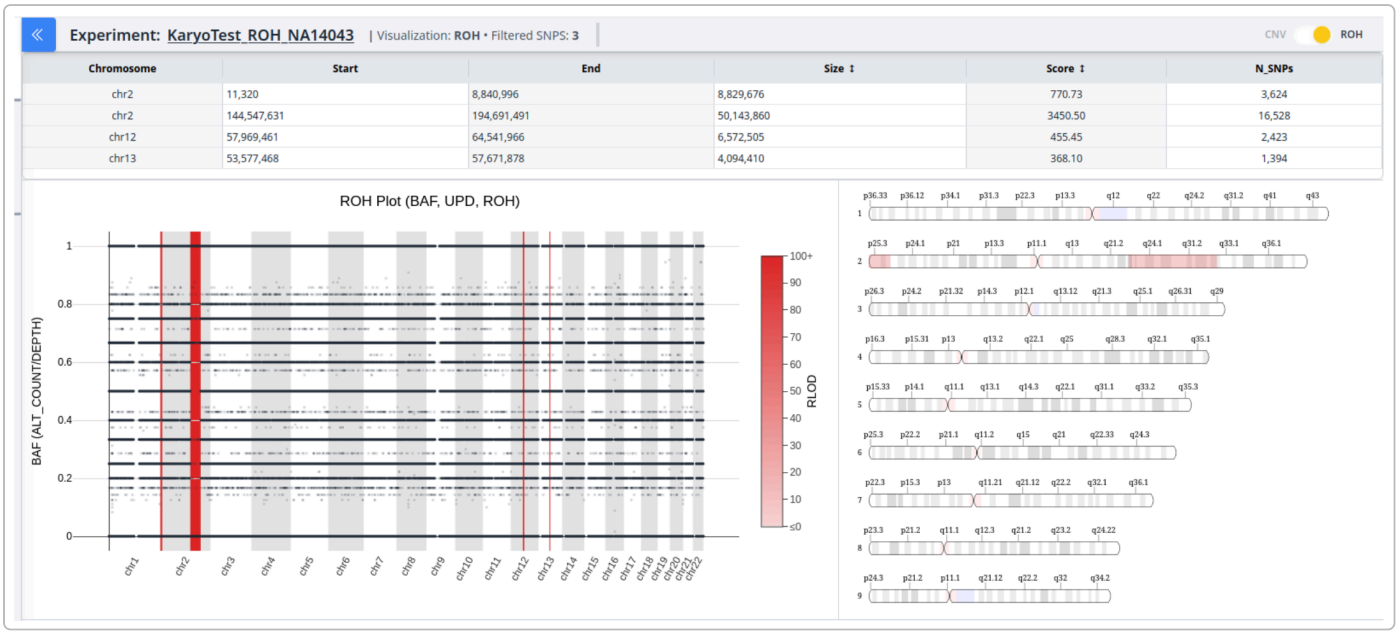
+

Xp11.21–q28: CN = 3
gain of most of the long arm (Xq)

→ The complementary loss + gain pattern is consistent with an i(Xq): one normal X plus an isochromosome composed of two Xq arms.

ROH, UPD and consanguinity: adding allelic information to CNV analysis

CASE 3 | Consanguinity



Chromosome	Start	End	Size	Score	N_SNPs
chr2	11,320	8,840,996	8,829,676	770.73	3,624
chr2	144,547,631	194,691,491	50,143,860	3450.50	16,528
chr12	57,969,461	64,541,966	6,572,505	455.45	2,423
chr13	53,577,468	57,671,878	4,094,410	368.10	1,394

Example shown: a large ROH on chromosome 2 can be immediately visualized, quantified and reviewed in the appropriate clinical context.

KaryoSolver detects extended regions of homozygosity (ROH) across the genome. Their size, distribution and chromosome specificity help the laboratory decide whether the pattern is more suggestive of parental relatedness or whether a chromosome-specific event should be evaluated for possible uniparental disomy.

Detect

Identify long homozygous segments from SNP information.

Put in context

Assess whether ROH are distributed across multiple chromosomes or concentrated on one chromosome.

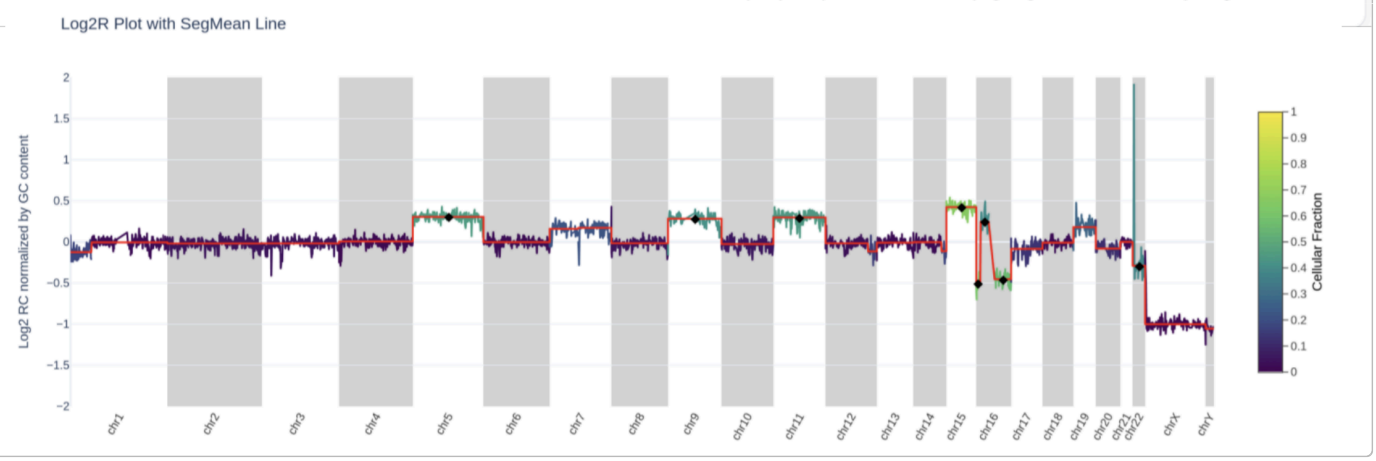
Support interpretation

Use the pattern to guide follow-up for consanguinity, UPD or recessive-disease investigation.

Onco-hematology: CNVs and balanced rearrangements in one view

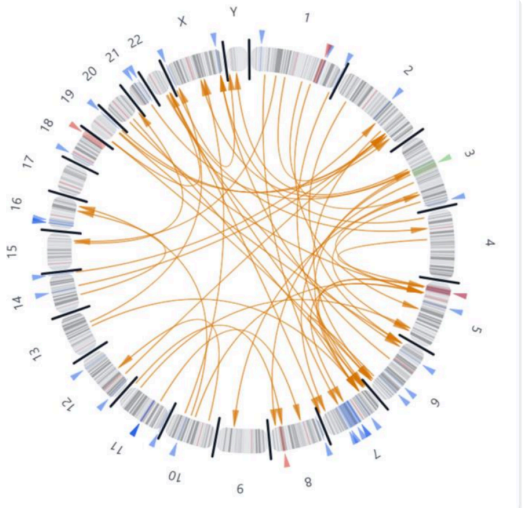
CASE 4A | Onco - hematological CNVs & Cellular fraction

Chr	Start	End	Size	CNV Type	Copy #	Cellular Fraction	ISCN Label	ACMG Score	ACMG Interpretation
chr5	82167	180921324	180839157	Duplication	3	0.45	5x3[0.45]	1	pathogenic
chr9	106230	137316454	137210224	Duplication	3	0.41	9x3[0.41]	1	pathogenic
chr11	183077	134010948	133827871	Duplication	3	0.44	11x3[0.44]	1	pathogenic
chr15	23314534	100591008	77276474	Duplication	3	0.66	15q11.2q26.3(23314534_100591008)x3[0.66]	1	pathogenic
chr16	36406	11036406	11000000	Deletion	1	0.61	16p13.3p13.13(36406_11036406)x1[0.61]	1	pathogenic
chr16	11036406	32526486	21490080	Duplication	3	0.39	16p13.13p11.2(11036406_32526486)x3[0.39]	1	pathogenic
chr16	46568590	89568590	43000000	Deletion	1	0.55	16q11.2q24.3(46568590_89568590)x1[0.55]	1	pathogenic
chr22	16580750	49389564	32808814	Deletion	1	0.38	22q11.1q13.33(16580750_49389564)x1[0.38]	1	pathogenic



Visualize multiple CNVs and their cellular fractions in a single genomic profile, providing an immediate view of the complex and heterogeneous copy-number landscape of multiple myeloma. Example: multiple mosaic gains and losses occurring at different cellular fractions, highlighting the presence of clonal and subclonal genomic alterations.

CASE 4B | Balanced translocations and complex rearrangements



Identify complex genomic rearrangements, including balanced translocations, and gain a comprehensive view of structural alterations in onco-hematological samples.

Example:
Circos plot revealing multiple chromosomal rearrangements and balanced translocations



4bases
Precision Matters

KaryoSolver

The Next Generation of Karyogenomics via Low-Pass Whole Genome Sequencing

One platform. A clearer view of the genome.

KaryoSolver transforms array and NGS data into clinically meaningful insights, supporting the detection and interpretation of CNVs, ROH and complex genomic rearrangements in **a single, intuitive workflow**.

Interested in learning more?
Contact our experts for further information or to request a personalized demo of KaryoSolver:
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Discover more at 4bases.ch

Precision Matters

4bases SA is a Swiss biotech company dedicated to developing certified companion diagnostics and NGS solutions for inherited gene mutations, clinical cytogenomics, and oncology.

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