TruPath™ Genome

Confident variant calling in difficult-to-map genomic regions

TruPath Genome delivers haplotype-resolved calls, gene/pseudogene disambiguation, and copy-number–aware insights, providing the clarity needed to accurately interpret clinically relevant and paralogous genes.

Multi-region joint detection (MRJD)

Making the most challenging regions of the genome readable

MRJD is a specialized variant-calling method within TruPath Genome that jointly analyzes paralogous regions to build phased haplotypes and resolve copy number—delivering long-read-level clarity from standard WGS data.

Key capabilities

- Joint analysis across duplicated regions
- De novo, phased, copy-number–aware small variant calls
- No reliance on population haplotypes
- TruPath Genome's MRJD supports 15 medically relevant paralogous genes at launch (Table 1).

Table 1:

Gene / Locus	Associated Condition / Research Area
PMS2	Lynch Syndrome
SMN1-SMN2	Spinal Muscular Atrophy
NCF1	Chronic Granulomatous Disease
RCCX (CYP21A2, TNXB)	Congenital Adrenal Hyperplasia, Ehlers-Danlos syndrome
STRC	Recessive Nonsyndromic Hearing Loss
CYP2D6	Pharmacogenetics
CYP11B1-CYP11B2	Glucocorticoid-remediable Aldosteronism
CFHR1-CFHR2-CFHR3-CFHR4	Atypical Hemolytic Uremic Syndrome
USP18	Type I Interferonopathy

Haplotype-resolved variant calling in complex, medically relevant paralogous genes

Confidently differentiates functional genes from pseudogenes (e.g., *PMS2* vs. *PMS2CL*)

Detection of whole-gene copy number gain or loss in segmental duplications

Haplotype-resolved variant calling in complex paralogous regions

Short-read data often makes it difficult to determine which copy a variant belongs to, whether it's the functional gene versus pseudogene. MRJD resolves this ambiguity using haplotype information, enabling more confident interpretation in complex paralogous regions (see Figure 1).

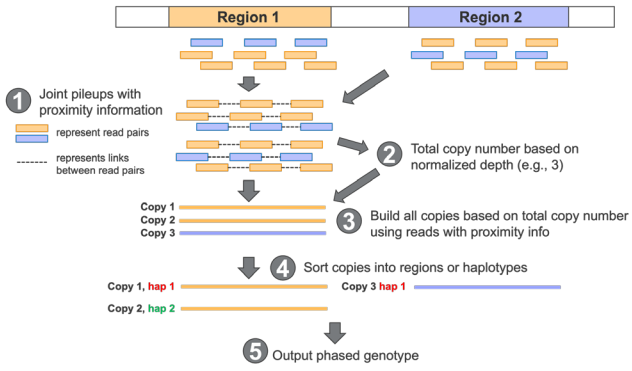

Figure 1: Proximity-based haplotype reconstruction with MRJD

Identify disease-driving genes in highly homologous regions

MRJD addresses persistent challenges in short-read analysis by resolving gene-level ambiguity across a wide range of highly homologous regions.

- Differentiates functional genes from pseudogenes, such as *PMS2* vs. *PMS2CL* (see Figure 2)
- Delivers long-read-level clarity for key clinical research applications, including hereditary cancer, carrier screening, newborn screening, and rare disease genomics

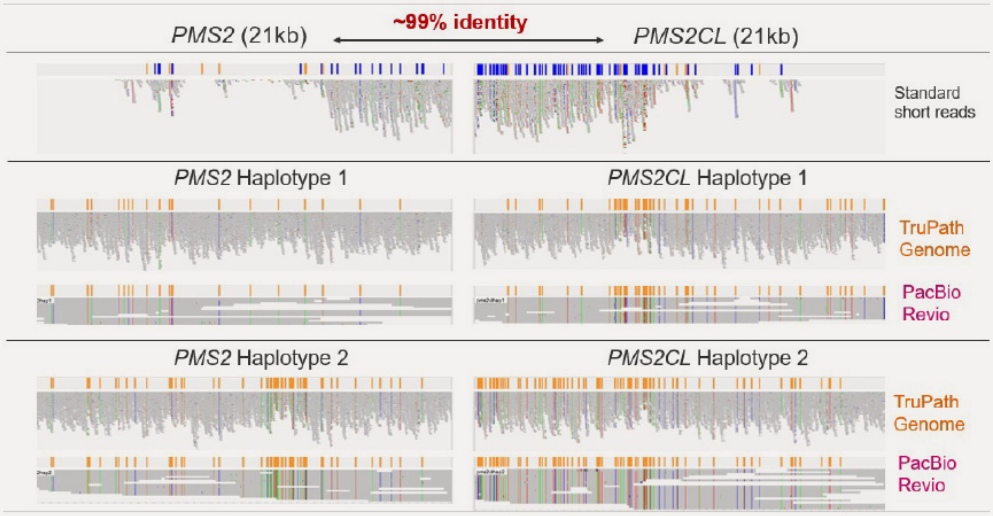

Figure 2: Resolving *PMS2* from *PMS2CL* in Lynch syndrome

Detect whole-gene gains and losses with confidence

- Accurate copy-number-variant (CNV) detection in segmental duplication with MRJD's evidence-based analysis
- Reliable support for genomic research, including carrier assessment, genetic counseling workflows, and confident interpretation of clinically important locii

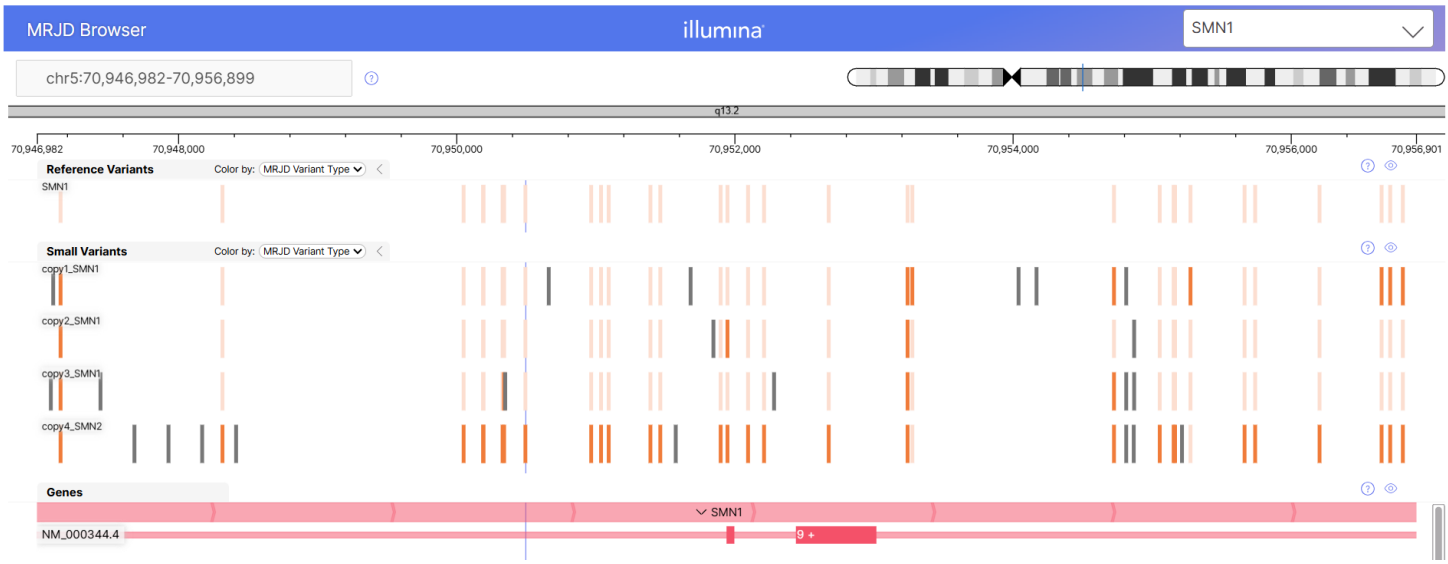

Figure 3: Example of visualizing MRJD results in DRAGEN reports

In DRAGEN™ Reports, the dark orange represents alternative allele for a reference difference site between the paralogous regions, the light orange represents reference allele for a reference difference site, while the grey represents non-reference difference site variant.

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