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A Draft Human Pangenome Reference

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35	GBZ File Format for Pangenome Graphs.		
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31	Recombination between heterologous human acrocentric chromosomes.		0
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20	Ensembl 2023.	1
19	From the reference human genome to human pangenome: Premise, promise and challenge. 13,	0
18	GENCODE: reference annotation for the human and mouse genomes in 2023.	0
17	Assembly of 43 diverse human Y chromosomes reveals extensive complexity and variation.	0
16	The complete sequence of a human Y chromosome.	0
15	NPGREAT: assembly of human subtelomere regions with the use of ultralong nanopore reads and linked-reads. 2022, 23,	0
14	Method of the year: long-read sequencing. 2023, 20, 6-11	2
13	Haplotype-aware pantranscriptome analyses using spliced pangenome graphs.	0
12	Scalable Nanopore sequencing of human genomes provides a comprehensive view of haplotype-resolved variation and methylation.	0
11	Comprehensive variant discovery in the era of complete human reference genomes. 2023, 20, 17-19	0
10	The Dynamic Structure and Rapid Evolution of Human Centromeric Satellite DNA. 2023, 14, 92	0
9	StratoMod: Predicting sequencing and variant calling errors with interpretable machine learning.	0
8	A sheep pangenome reveals the spectrum of structural variations and their effects on tail phenotypes. 2023, 33, 463-477	0
7	Genomic structural variation: A complex but important driver of human evolution.	0
6	A deep population reference panel of tandem repeat variation.	0
5	Benchmarking datasets for assembly-based variant calling using high-fidelity long reads. 2023, 24,	0
4	Sequence toGraph Alignment Using Gap-Sensitive Co-linear Chaining. 2023, 58-73	0
3	Building pangenome graphs.	0

- 2 Variant calling and benchmarking in an era of complete human genome sequences. ☐
- 1 Every base everywhere all at once: pangenomics comes of age. **2023**, 616, 618-620 ☐