

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

HapCUT

RRID:SCR_010791

Type: Tool

Proper Citation

HapCUT (RRID:SCR_010791)

Resource Information

URL: <https://sites.google.com/site/vibansal/software/hapcut>

Proper Citation: HapCUT (RRID:SCR_010791)

Description: A max-cut based algorithm for haplotype assembly using sequence reads from the two chromosomes of an individual.

Abbreviations: HapCUT

Resource Type: software resource

Resource Name: HapCUT

Resource ID: SCR_010791

Alternate IDs: OMICS_00198

Record Creation Time: 20220129T080300+0000

Record Last Update: 20260912T195723+0000

Ratings and Alerts

No rating or validation information has been found for HapCUT.

No alerts have been found for HapCUT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 17 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Yang C, et al. (2024) LRTK: a platform agnostic toolkit for linked-read analysis of both human genome and metagenome. *GigaScience*, 13.

Lu X, et al. (2022) A high-quality assembled genome and its comparative analysis decode the adaptive molecular mechanism of the number one Chinese cotton variety CRI-12. *GigaScience*, 11.

Bell AD, et al. (2020) Insights into variation in meiosis from 31,228 human sperm genomes. *Nature*, 583(7815), 259.

Kryvokhyzha D, et al. (2019) Parental legacy, demography, and admixture influenced the evolution of the two subgenomes of the tetraploid *Capsella bursa-pastoris* (Brassicaceae). *PLoS genetics*, 15(2), e1007949.

Kryvokhyzha D, et al. (2019) Towards the new normal: Transcriptomic convergence and genomic legacy of the two subgenomes of an allopolyploid weed (*Capsella bursa-pastoris*). *PLoS genetics*, 15(5), e1008131.

Vendramin V, et al. (2019) Genomic tools for durum wheat breeding: de novo assembly of Svevo transcriptome and SNP discovery in elite germplasm. *BMC genomics*, 20(1), 278.

Kamal N, et al. (2019) Characterization of genes and alleles involved in the control of flowering time in grapevine. *PloS one*, 14(7), e0214703.

Song M, et al. (2019) Mapping cis-regulatory chromatin contacts in neural cells links neuropsychiatric disorder risk variants to target genes. *Nature genetics*, 51(8), 1252.

Wolfe MD, et al. (2019) Historical Introgressions from a Wild Relative of Modern Cassava Improved Important Traits and May Be Under Balancing Selection. *Genetics*, 213(4), 1237.

Choi Y, et al. (2018) Comparison of phasing strategies for whole human genomes. *PLoS genetics*, 14(4), e1007308.

Challa GS, et al. (2018) De novo assembly of wheat root transcriptomes and transcriptional signature of longitudinal differentiation. *PloS one*, 13(11), e0205582.

Edge P, et al. (2017) HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. *Genome research*, 27(5), 801.

Lovell JT, et al. (2017) Mutation Accumulation in an Asexual Relative of *Arabidopsis*. *PLoS genetics*, 13(1), e1006550.

Huang J, et al. (2016) The Jujube Genome Provides Insights into Genome Evolution and the Domestication of Sweetness/Acidity Taste in Fruit Trees. *PLoS genetics*, 12(12), e1006433.

Castel SE, et al. (2016) Rare variant phasing and haplotypic expression from RNA sequencing with phASER. *Nature communications*, 7, 12817.

Chopra R, et al. (2016) Transcriptome Sequencing of Diverse Peanut (*Arachis*) Wild Species and the Cultivated Species Reveals a Wealth of Untapped Genetic Variability. *G3* (Bethesda, Md.), 6(12), 3825.

Li C, et al. (2016) An accurate clone-based haplotyping method by overlapping pool sequencing. *Nucleic acids research*, 44(12), e112.