Resource Summary Report

Generated by <u>dkNET</u> on Apr 30, 2025

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

Funding:

Resource Name: HapCUT

Resource ID: SCR_010791

Alternate IDs: OMICS_00198

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250420T014509+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 <u>dkNET</u>.

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.

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.

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.

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.

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.

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.

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

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

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.

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.

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

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