Resource Summary Report

Generated by dkNET on Apr 17, 2025

SSAHASNP

RRID:SCR_009415
Type: Tool

Proper Citation

SSAHASNP (RRID:SCR_009415)

Resource Information

URL: http://www.sanger.ac.uk/science/tools/ssahasnp-0

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Description: A polymorphism detection tool that detects homozygous SNPs and indels by aligning shotgun reads to the finished genome sequence. Highly repetitive elements are filtered out by ignoring those kmer words with high occurrence numbers. For those less repetitive or non-repetitive reads, we place them uniquely on the reference genome sequence and find the best alignment according to the pair-wise alignment score if there are multiple seeded regions. From the best alignment, SNP candidates are screened, taking into account the quality value of the bases with variation as well as the quality values in the neighbouring bases, using neighbourhood quality standard (NQS). For insertions/deletions, we check if the same indel is mapped by more than one read, ensuring the detected indel with high confidence. (entry from Genetic Analysis Software)

Abbreviations: SSAHASNP

Synonyms: Sequence Search and Alignment by Hashing Algorithm for SNP detection

Resource Type: software resource, software application

Keywords: gene, genetic, genomic

Funding:

Resource Name: SSAHASNP

Resource ID: SCR_009415

Alternate IDs: nlx_154661

Record Creation Time: 20220129T080252+0000

Record Last Update: 20250416T063547+0000

Ratings and Alerts

No rating or validation information has been found for SSAHASNP.

No alerts have been found for SSAHASNP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Zhang N, et al. (2016) Transcriptome analysis of the Chinese bread wheat cultivar Yunong 201 and its ethyl methanesulfonate mutant line. Gene, 575(2 Pt 1), 285.

Liu ZK, et al. (2016) Transcriptomic Analysis of Eucryptorrhynchus chinensis (Coleoptera: Curculionidae) Using 454 Pyrosequencing Technology. Journal of insect science (Online), 16(1).

Harris RA, et al. (2016) Genomic Variants Associated with Resistance to High Fat Diet Induced Obesity in a Primate Model. Scientific reports, 6, 36123.

Gao J, et al. (2014) Transcriptome analysis of the differences in gene expression between testis and ovary in green mud crab (Scylla paramamosain). BMC genomics, 15(1), 585.