Resource Summary Report

Generated by Kravitz on Sep 10, 2026

High Quality SNP Database

RRID:SCR_007230
Type: Tool

Proper Citation

High Quality SNP Database (RRID:SCR_007230)

Resource Information

URL: http://snpselector.duhs.duke.edu/hqsnp36.html

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Description: This is the HQSNP DB (high-quality SNP database) developed by CHG bioinformatics group. The high-quality SNP is defined as a SNP having allele frequency or genotyping data. The majority of the HQSNPs come from HapMap, others come from JSNP (Japanese SNP database), TSC (The SNP Consortium), Affymetrix 120K SNP, and Perlegen SNP. There are four kinds of SNP search you can do: * Get SNPs by dbSNP rs#: Choose this search if you have already selected a list of SNPs and you just want to get the SNP information. The program will generate a Excel file containing the SNP flanking sequence, variation, quality, function, etc. In the Excel file, there are 10 highlighted fields. You can send only those highlighted information to Illumina to get SNP pre-score. (The same fields are presented in other types of searches as well.) * Get gene SNPs by gene names: Choose this search if you have a list of gene names and you want to get the SNP information in these genes. The gene name can be official gene symbol, Ensembl gene ID, RefSeq accession ID, LocusLink number, etc. * Get gene SNPs by genome regions: Choose this search if you have a list of genome regions and you want to get all gene SNP information in these regions. The software will find all the Ensembl genes in the regions and find SNPs associated to each Ensembl gene. * Get genome scan SNPs by genome regions: Choose this search if you have a list of genome regions and you want to get evenly spaced SNPs in these regions. A SNP selection tool (SNPselector) was built upon HQSNP. It took snp ID list, gene name list, or genome region list as input and searched SNPs for genome scan or gene assoctiation study. It could take an optional ABI SNP file (exported from ABI SNP search web page) as input for checking whether the candidate SNP is available from ABI. It could also take an optional Illumina SNP pre-score file as input to select SNP for Illumina SNP assay. It generated results sorted by tag SNP in LD block, SNP quality, SNP function, SNP regulatory potential, and SNP mutation risk. SNPselector is now retired from public use (as of September 30, 2010).

Abbreviations: HQSNP DB

Synonyms: SNPselector and High Quality SNP Database, CHG DAS Data

Resource Type: data or information resource, database

Keywords: snp, genotyping, data, allele, bioinformatics, genome, study, gene

Resource Name: High Quality SNP Database

Resource ID: SCR_007230

Alternate IDs: nif-0000-30254

Record Creation Time: 20220129T080240+0000

Record Last Update: 20260905T133139+0000

Ratings and Alerts

No rating or validation information has been found for High Quality SNP Database.

No alerts have been found for High Quality SNP Database.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Walker CG, et al. (2011) Variation in the FFAR1 gene modifies BMI, body composition and beta-cell function in overweight subjects: an exploratory analysis. PloS one, 6(4), e19146.

Chien YL, et al. (2011) Association study of the CNS patterning genes and autism in Han Chinese in Taiwan. Progress in neuro-psychopharmacology & biological psychiatry, 35(6), 1512.

Edwards M, et al. (2010) Association of the OCA2 polymorphism His615Arg with melanin content in east Asian populations: further evidence of convergent evolution of skin pigmentation. PLoS genetics, 6(3), e1000867.