

# Resource Summary Report

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## HapMap 3 and ENCODE 3

RRID:SCR\_004563

Type: Tool

### Proper Citation

HapMap 3 and ENCODE 3 (RRID:SCR\_004563)

### Resource Information

**URL:** <http://www.hgsc.bcm.tmc.edu/content/hapmap-3-and-encode-3>

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**Description:** Draft release 3 for genome-wide SNP genotyping and targeted sequencing in DNA samples from a variety of human populations (sometimes referred to as the HapMap 3 samples). This release contains the following data: \* SNP genotype data generated from 1184 samples, collected using two platforms: the Illumina Human1M (by the Wellcome Trust Sanger Institute) and the Affymetrix SNP 6.0 (by the Broad Institute). Data from the two platforms have been merged for this release. \* PCR-based resequencing data (by Baylor College of Medicine Human Genome Sequencing Center) across ten 100-kb regions (collectively referred to as ENCODE 3) in 712 samples. Since this is a draft release, please check this site regularly for updates and new releases. The HapMap 3 sample collection comprises 1,301 samples (including the original 270 samples used in Phase I and II of the International HapMap Project) from 11 populations, listed below alphabetically by their 3-letter labels. Five of the ten ENCODE 3 regions overlap with the HapMap-ENCODE regions; the other five are regions selected at random from the ENCODE target regions (excluding the 10 HapMap-ENCODE regions). All ENCODE 3 regions are 100-kb in size, and are centered within each respective ENCODE region. The HapMap 3 and ENCODE 3 data are downloadable from the ftp site.

**Abbreviations:** HapMap 3 and ENCODE 3

**Resource Type:** data or information resource, database

**Keywords:** human, gene, genotype, sequence, single nucleotide polymorphism, dna, software

**Funding:** Wellcome Trust ;  
NHGRI ;  
NIDCD

**Resource Name:** HapMap 3 and ENCODE 3

**Resource ID:** SCR\_004563

**Alternate IDs:** nlx\_143820

**Old URLs:** <http://www.hgsc.bcm.tmc.edu/project-medseq-hm-hapmap3encode3.hgsc?pageLocation=hapmap3encode3>

**Record Creation Time:** 20220129T080225+0000

**Record Last Update:** 20260905T133124+0000

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## Ratings and Alerts

No rating or validation information has been found for HapMap 3 and ENCODE 3.

No alerts have been found for HapMap 3 and ENCODE 3.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 3 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Tjader NP, et al. (2024) Association of ESR1 Germline Variants with TP53 Somatic Variants in Breast Tumors in a Genome-wide Study. Cancer research communications, 4(6), 1597.

Gupta R, et al. (2021) Human genetic analyses of organelles highlight the nucleus in age-related trait heritability. eLife, 10.

Factor DC, et al. (2020) Cell Type-Specific Intralocus Interactions Reveal Oligodendrocyte Mechanisms in MS. Cell, 181(2), 382.