



## dbSNP Haplotype Data

Created: July 7, 2005; Updated: February 18, 2014.

**The HapMap populations have the timestamp “2004-11-30”. Does this mean the population was defined in 2004?**

Yes. (07/08/08)

**What is the definition of “1 marker\_cnt = 31”?**

This refers to the number of markers used in the haplotype.

**What is the definition of “2 haplotype\_cnt =20”?**

This refers to the number of haplotypes estimated from the data.

**Is there somewhere within dbSNP that identifies htSNPs?**

dbSNP currently does not include the Haplotype tagging (ht) SNP property. We'll add this property when we get haplotype data and evidence substantiating the htSNPs. (2/28/05)

**Which program do people usually use to partition genotyped SNPs into different haplotype blocks?**

Such a user would look at [Haploview](#). (6/15/05)

**I want to design a SNP assay that will produce genotypes from which I can then infer SNP haplotype(s) (also known as "H2 allele(s)"). How do I create an alignment of the MHC gene(s) in rat?**

A site that might be of use to you is the [IPD-MHC RAT Sequence Database](#). Unfortunately, NCBI's [dbMHC website](#) is, at this time, devoted to human sequences.

**How do I tell if a SNP is uniquely mapped to the genome or if it appears in multiple places?**

The NCBI genome assembly now contains sequence from more than one haplotype. At the moment, we assemble one complete reference haplotype and two small alternative haplotypes that span the HLA region. SNPMapInfo.weight is a table that is designed to provide a measure of multiplicity in a single human haplotype, where a weight >1 implies that the SNP hits at more than one locus.