



dbSNP Data Quality Control

Created: July 23, 2005; Updated: February 18, 2014.

Does dbSNP require any quality control from its submitters or does dbSNP perform quality control itself prior to the release of a SNP record?

Submitters are entirely responsible for the quality of the data they provide in submitted assay reports and abstracted SNP objects. dbSNP does, however, provide submitters with [Locus Validation Fields](#) they can complete during their submission which allows them to provide an assessment of their data quality for the dbSNP user. When a submission is mapped, from time to time sequence errors are detected when the SNP fails to map to a known genome location. In such a case, dbSNP notifies the submitter, who will then submit an update to the original submission correcting the sequence.

If you have questions regarding the quality of a submitted SNP that are not answered by the data provided in the SNP reports, contact the submitter directly. (2/21/07)

I'm concerned that submitted SNPs based on cDNA sequence could be artifacts of RNA editing. Does dbSNP track potential RNA-edited artifacts?

We do not directly track SNPs that could be potential RNA-edited artifacts. However, we do flag SNPs derived from cDNA that DO NOT map to the genome contigs but DO map to RefSeq transcripts.

How do I verify dbSNP's genotype data sources?

Population descriptions are provided to dbSNP by the submitter, and as such, the submitter is entirely responsible for any quality control of the submitted population description. You will therefore have to ask the submitter about the source of the genotype data. Please contact snp-admin@ncbi.nlm.nih.gov if you need help contacting the submitter.