U.S. National Library of Medicine
National Center for Biotechnology Information

SNP FAQ Archive
NCBI Help Manual

National Center for Biotechnology Information
U.S. National Library of Medicine

Finding Specific Data in dbSNP's FTP Files

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Finding Functional Class Data

I noticed that the coding non-synonymous function code has been subdivided. Can you list and define the subdivisions?

Function Code 41: "Nonsense" (coding nonsynonymous)

changes to the Stop codon

Function Code 42: "Missense" (coding nonsynonymous)

alters codon to make an altered amino acid in protein product

Function Code 44: "Frameshift" (coding nonsynonymous)

indel SNP causing frameshift

You can find up-to-date function codes and their definitions in the SnpFunctionCode.bcp.gz table located in the /shared_data directory of the dbSNP FTP site. (**10/27/08**)

Where can I find a flat file where the non-synonymous SNPs are mapped to their respective positions in the corresponding proteins along with the SNP and protein IDs?

Please see the Functional (synonymous, non-synonymous, etc.)Data Table section of this archive, and the SNPContigLocusId Table section of this archive to get information about retrieving non-synonymous SNPs. You can download the SNPContigLocusId table from dbSNP's FTP site in the organism_data directory(this link takes you to the directory for human) for your organism of interest. (**07/25/08**)

I noticed that b127 SNPs are no longer associated with function class codes 1,2,5, and 7. Does dbSNP no longer use these function class codes?

As of build 127, function codes 1, 5 and 7 have been modified into two digit codes that will more precisely indicate the location of a SNP. The two digit codes have function codes 1, 5 or 7 as the first digit, each of these numbers keeping its original meaning, and 3 or 5 as the second digit, indicating whether the SNP is 3' or 5' to the region of interest. So the new function codes are as follows:

Function code13: "nearGene-3"

Where:
1=locus region
3= SNP is 3' to and 0.5kb away from gene

Function code 15: "nearGene-5"

Where:
1=locus region
5= SNP is 5' to and 2kb away from gene

Function code 53: "UTR-3"

Where:
5= UTR (untranslated region)
3= SNP located in the 3' untranslated region

Function code 55: "UTR-5"

Where:
5= UTR (untranslated region)
5(as the second digit)= SNP located in the 5' untranslated region

Function code 73: "splice-3"

Where:
7=splice site
3=3' acceptor dinucleotide

Function code 75: "splice-5"

Where:
7=splice site
5=5' donor dinucleotide

Function code 2, however, was retired permanently as of b127, as it identified a SNP as being in the coding region of a gene, but that other details about its location were unknown. Since mapping and annotation have improved dramatically since function code 2 was defined, it is no longer used. (**4/30/07**)

Where do I find information on SNP functional classes?

Information on SNP functional classes is located in the SNPFunctionCode table. You can find a description of this table by doing the following:

1. Click on Database dictionary in the documentation section of the left blue sidebar on the dbSNP home page.
2. Type SNPFunctionCode in the text box located in the light blue "Search by" box located at the top of the page, and then click on the "Search" button located below the text box.
3. Click on the SNPFunctionCode link on the response page to get a full description of the SNPFunctionCode table. (**1/18/06**)

Does dbSNP have ftp tables that contains splice site SNP location data?

Look in the shared_data directory for your organism on the dbSNP ftp site and download SnpFunctionCode.bcp.gz, which defines the codes used for function class. It indicates that a splice-site associated with the SNP is either code 73 (splice-3: 3 prime acceptor dinucleotide) or code 75 (splice-5:5 prime donor dinucleotide)

Then go to the organism_data directory(this link takes you to the directory for human) for your organism of interest, and download SNPContigLocusId.bcp.gz, which contains the snp_id and the functional class code for eachSNP. You can find a description of the columns in the SNPContigLocusId table online. Please note that the "locus_id" column of this table stores the NCBI gene ID. (**11/15/07**)

How do I search for information regarding the number of SNPs found in coding regions within a gene using the gi, NM, or XM ID numbers?

Go to the organism_data directory located in your organism's database and click on SNPContigLocusId.bcp.gz. This is an ASCII image of the database table containing all of our snp-to-gene information as gathered from the NCBI assembly processing. See below for column headings.

You probably only want to keep rows where fxn_class is 3, 4, or 8.

Here are the columns. The example is the first NON_SYNON encountered from the top:

```
Columns          Example              COMMENT

snp_id                47            snp_id
contig_acc      NT_007819           contig accession
contig_ver            14            contig version
asn_from         10876794           contig position
asn_to           10876794           contig position
locus_id            23249           locus link identifier
locus_symbol      KIAA0960          gene name
mrna_acc         XM_371877          mrna accession
mrna_ver              2             mrna version
protein_acc      XP_371877          protein accession
protein_ver           2             protein version
fxn_class             4             2,3,4,8 are coding, 6=intron, 5=utr
reading_frame         1
allele                G             allele as found on mrna_acc
residue               D             residue as found on protein_acc
aa_position          514            position of residue I protein_acc
build_id            34_3            Genome build; assembly context
                                    is a property of contig
```

Is it possible to download a report that includes SNP function x gene model relationships?

The dbSNP XML format provides extensive information on SNP function x gene model relationships as a potential sub-property of each contig location defined for the variation. Protein structure data is provided in the complex element NSE-rs_structure-data when available.

If you are interested in a specific set of SNPs or genes (i.e. a small set of data), you can get the data via dbSNP's batch query service by selecting one of the XML reports in the "submission format" toggle menu at the bottom of the Batch query page.

If you are interested in the complete set of SNP functional data, it is available on the dbSNP FTP site. The data are dumped by organism & chromosome when a reference genome is available to organize the data.

OMIM functional mapping for human variations are currently not part of the XML file, but you can download the entire table of SNPxOMIM data from the ftp site as a relational table. The relational table has the following structure:

```
CREATE TABLE [SNP2Omim]
([omim_id] [int] NOT NULL ,
[var_id] [char] (4) COLLATE Latin1_General_BIN NOT NULL ,
[locus_id] [int] NOT NULL ,
[snp_id] [int] NOT NULL ,
[aa1] [char] (1) COLLATE Latin1_General_BIN NOT NULL ,
[aa_pos] [int] NOT NULL ,
[aa2] [char] (1) COLLATE Latin1_General_BIN NOT NULL) ON [PRIMARY]
GO
```

(7/22/05)

Finding Population Diversity Data

Which FTP file contains the population diversity data tables?

The ftp file that contains the genotype and allele frequency data for Human is:

ftp://ftp.ncbi.nih.gov/snp/organisms/human_9606/genotype/ (**4/21/06**)

Finding Hardy Weinburg Probabilities

Where can I download population diversity data such as Hardy Weinburg Probabilities via FTP for all of the SNPs described in dbSNP?

The information you are looking for is located in the "genotype" file for the particular organism you are interested in. For example, if you are interested in population diversity data for human, go to the dbSNP FTP site, select the organisms directory, then select the human directory, and then select the genotype file. The format of these files is described online. (**10/5/06**)

Finding Average Heterozygosity, Allele Frequency and Genotype Frequency

Is there a table that shows that most common CYP2C9 alleles in Caucasians?

dbSNP doesn't have data for common alleles sorted by race. We only provide the allele frequency of populations defined by the submitter, some of which may be Caucasians. The dbSNP Genotype and Allele Frequency Report for CYP2C9 may help you find the common alleles you are looking for. (**09/07/07**)

How do I download the data located in the variation summary section of the refSNP report for all human SNPs? Would I get it on your ftp site?

You can get the data from the following three database table dump files located in the dbSNP ftp site:

SNP.bcp.gz (the relevant fields are: snp_id is the rs#, avg_heterozygosity)

SNPAlleleFreq.bcp.gz

SNPGtyFreq.bcp.gz

Also located in the ftp directory are the Allele.bcp.gz and the UniGty.bcp.gz tables, where you can find the meaning of each allele_id and/or unigty_id. The column descriptions for all the tables can be found in the dbSNP Data Dictionary. (**4/1/05**)

Finding All Alleles for a Given SNP

Where is the .bcp file that contains the alleles for any given SNP?

We don't have a table that keeps all alleles for a given refSNP. That's why you can't find a single .bcp file that has this information. You can get all the alleles for a given refSNP through the relationship between the following tables. Please see the ER diagram for table relationships:

SNPSubSNPLink, SubSNP, ObsVariation, VariAllele

When the submitted SNP is on a reverse strand with the refSNP (SNPSubSNPLink.substrand_reversed_flag=1), you need to also reverse the alleles of the submitted SNP. Another complication is that our current data model also allows submitters to submit new alleles (not reported in assay reports) with frequency or genotype on an existing SNP.

Finding Reference Alleles

How do I get the reference allele (ie the allele on the reference contig) for each refSNP in human build 128?

The alleles at the SNP contig position are in table SNPContigLoc.

Specifically for b128, it is in file b128_SNPContigLoc_36_2 which is located in the organism_data subdirectory for human. The column descriptions for SNPContigLoc are located in dbSNP's data dictionary. (**02/26/08**)

Finding a Report of Allele Frequencies across Major Populations

I want to download flat files that list all SNPs for which allele frequencies exist across the major human populations (European, East Asian, and African). Where can I find such data?

We currently do not have a flat file report of allele frequencies across major populations for all human SNPs. If you can work with XML files, you can find FTP files of genotype data (including genotype and allele frequency data) in the dbSNP FTP site. They are organized by chromosomes:

ftp://ftp.ncbi.nlm.nih.gov/snp/organisms/human_9606/genotype/

ftp://ftp.ncbi.nlm.nih.gov/snp/organisms/human_9606/genotype_by_gene/

If you are working with a set of SNPs, you could use eutils to fetch the allele frequency information.

In the meantime, we will look at making a new FTP file format for reporting SNP frequencies. (**7/24/07**)

Finding Genotypes

I need to identify SNPs that are different between C57BL/J and A/J mice from a list of 50,000 SNPs. Downloading the data by chromosome is very time consuming. Is there a better was to do this?

All the mouse genotype data submitted to dbSNP are available on the FTP site. Go to the mouse organism database, and select "genotype" from the list of available files. You can then download all of the data and do your own analysis.(**6/19/06**)

Finding IDs

Which SNP tables/columns do I have to parse to find the local_snp_ids for all SNPs I submitted?

To find the local IDs for specific submitted SNP (ss) numbers, all you need are the SubSNP.subsnp_id, SubSNP.loc_snp_id columns from SubSNP.bcp.gz located in the organism_data subdirectory for the organism of choice (the links above go to human). The SubSNP table column definitions are in dbSNP_sup_table.sql.gz, which is located in the organism_schema subdirectory of a particular organism (again, the links go to human). (**05/28/08**)

How do I download a complete list of refSNP (rs) IDs for the most recent SNP release?

You can get a list of valid rs for each organism for which dbSNP has data from the organism directory of the dbSNP FTP site.

All report types in the dbSNP FTP site include the rs ID numbers. The most compact report you can download is "Chromosome Reports" (chr_rpts).(**11/23/07**)

Where can I find a file that contains the relationship between Ensembl IDs and RefSNP IDs?

We don't have a file that shows the relationship between Ensembl IDs and RefSNP IDs. On our refSNP page, however, we do have a link to Ensembl that you can use to examine the Ensembl entry for a particular SNP. Go to the refSNP page for a particular refSNP, say rs3180392. Look at the top of the page to the right of the "Allele" section. Here you will find some small, blue text: "Links". Click on "links" to release a drop-down menu. Click on "Ensembl" to go the Ensembl page for this SNP. (ud:**03/19/08**).

How do I fetch data for a given refSNP ID (rsID) in XML format using a simple URL-request?

Please see the online short course for using eutils (**9/15/06**)

Finding Mapping Data

Where can I find a flat file where the non-synonymous SNPs are mapped to their respective positions in the corresponding proteins along with the SNP and protein IDs?

Please see the Functional (synonymous, non-synonymous, etc.)Data Table section of this archive, and the SNPContigLocusId Table section of this archive to get information about retrieving non-synonymous SNPs. You can download the SNPContigLocusId table from dbSNP's FTP site in the organism_data directory(this link takes you to the directory for human) for your organism of interest. (**07/25/08**)

Where in the FTP site do I find a table with coordinates of refSNPs (or subSNPs) in the genome (build 36)?

You can find the latest chromosome position of a refSNP in the phys_pos_from column of the b129_SNPContigLoc_36_3 table. (**07/10/08**)

I'm working with a local copy of dbSNP and need to know where I can find information that relates the orientation of a gene with the orientation of a SNP on that gene.

SNPContigLoc stores rs to Contig orientation and ContigExon stores mRNA to contig orientation.

Please see the "Forward vs. Reverse strand Orientation" section in the Mapping Process section of this archive. (**05/08/08**)

Is there an easy way to get SNP/human assembly mapping information from dbSNP, or do getting these require the downloading of the entire sql database?

Chromosome Reports (This linked chr_rpts is for human) give the contig position and chromosome coordinates, plus the gene identifier if the SNP is in the locus of a gene. If you use chromosome reports, be aware that chromosome 7 has two complete assemblies, and the only way to differentiate them in the chromosome report is to look for "7" versus "7b" in the ctg ID field. For example, rs7 hits both the reference assembly on Hs7_8090_34 at chromosome position 91391586 and the alternate assembly Hs7b_79660_34 at chromosome position 90737098. The thing that will drive you nuts if you're not careful is that the chromosome coordinates in the two assemblies are fairly close but not identical.

Can I determine if a SNP is uniquely mapped if I find a map location for the SNP in b126_SNPContigLoc_36_1, and if the following two mapping conditions are met: rf_ngbr - lf_ngbr - 1 = 1 and rf_ngbr - lf_ngbr = rc_ngbr - lc_ngbr ?

What you are doing is generally correct, but SNPContigLoc has mapping data for all assemblies (e.g. the human data includes both the NCBI and Celera assemblies), so you'll need to determine which assembly you have by joining with the ContigInfo table. Also, rf_ngbr - lf_ngbr - 1 = 1 may also include other types of variations, as a result of the method we use to code the variation in rs FASTA: we always use "N" for any length of indel, mixed SNP, MNP, etc. Anything that not using the the IUPAC code letters, we make an "N". As a result, many variations may fit in the two conditions you listed.

There is an online description of the SNPContigLoc table that includes an example sql showing how to determine all trueSNPs that have unique mapping on one assembly. (**8/21/06**)

How do I determine all trueSNPs that have unique mapping on one assembly?

The online description of the SNPContigLoc table includes an example sql that shows how to determine all trueSNPs that have unique mapping on one assembly.(**8/21/06**)

I'm looking for a SNP that seems to have no genome mapping positions. I thought it would be in the 126 XML ds_chUn or ds_chNotOn files, but can't find it. Where is it?

The SNP you are looking for is in the ds_ch11.xml file of the human XML directory. This SNP maps to the Celera assembly only, so it will not appear in your Entrez search results since Entrez indexes only SNPs that map to the NCBI reference assembly.(**8/30/06**)

Finding Orientation Data

I have a huge list of human rs numbers, how do I get a list of their alleles in forward orientation?

This information is available in the SNPContigLoc and ContigInfo tables.

SNPContigLoc contains the rs allele on the contig, while ContigInfo contains information about the contig position and orientation on the genome(chromosome), so from these two tables you should be able to derive the genomic allele orientation.

You will find descriptions for the SNPContigLoc and ContigInfo tables using the dbSNP Database Dictionary.(**11/14/08**)

Finding Sequence Data in CSV Format

I am submitting sequence to Illumina for Golden Gate assay oligo design, which requires a Microsoft Excel file in csv format, where each FASTA sequence is in a single cell of the file. Can I retrieve data from dbSNP in this format?

Both flanks and the alleles need to be in the same cell of an excel file. An adjacent cell in the same row would have the rsID number.

The data you need can be obtained from dbSNP's current FTP reports.

For example, you can look at the FASTA report for dog

Please note that the sequences are directly from submissions. You may want to verify the sequences during your oligo design.(**06/02/08**)

Finding Microarray Data

Do you have any AFFY or ILLUMINA array data available?

What we have is located in the dbSNP FTP site in the human GWAS_arrays directory.(**10/08/08**)

Where can I download individual 1M Illumina SNP data from dbSNP?

The data is available in XML format in the "/organisms/human_9606/" directory of the dbSNP FTP site. Go to "GWAS arrays" and then select /ILLUMINA.ILLUMINA_Human_1M.xml.gz(**11/28/08**)

We are using Illumina HumanHap550 V1, but Illumina provides chromosome positions based on Build 35. Can you give me the chromosome positions based on Build 36?

Please check the Human GWAS array directory, located in the dbSNP FTP site dbSNP ftp site (**06/02/08**)

Finding Merged RefSNP (rs) Data

I want to find all the refSNPs that got merged in build 127, but when I downloaded RsMergeArch.bcp.gz, I couldn't find a single entry for Build 127.

You are right that the build_id in RsMergeArch should be set to 127. This will be fixed for the next build.

For now, please use the following rule to find all the merged refSNPs in build 127: Since build 126 was released on May 4, 2006, find all the rows in RsMergeArch that were created after May 4, 2006.

For example, the sql could be:

select * from RsMergeArch where create_time > '5/4/06'

There should be 324938 merged pairs of human SNPs for build 127. (**5/28/07**)

Do you have a table of merged SNPs somewhere within dbSNP?

The rs merge table (RsMergeArch) is on the dbSNP ftp site, and the column definitions for it are located in dbSNP_main_table.sql.gz, which can be found in the shared_schema directory of the dbSNP FTP site. The rsHigh column in the RsMergeArch table contains the rsID numbers that merged away (rsHigh is merged to rsLow). Due to multiple merge events, sometimes rsLow is merged even further. The "rsCurrent" column refers to the current refSNP. (**11/14/07**)

How do I query dbSNP so that it will return a flat or xml file containing the new RefSNP (rs) ID number into which a previously valid rs recently merged?

You can get the rs merge history of all rs numbers from your organism's (human in this case) RsMergeArch table located in on the dbSNP ftp site.

The following example shows that rs4344934 has been merged to rs1107123:

```
gzcat RsMergeArch.bcp.gz | grep 4344934
4344934 1107123 123      1      2004-09-24 18:49:00      2004-10-10
11:55:00      1107123 1
```

Also, you can now retrieve a list of merged rs numbers from Entrez SNP. Just type "mergedrs" (without the quotation marks) in the text box at the top of the page and click the "go" button. Each entry in the returned list will include the old rs numbers that has merged, and the new rs number it has merged into (with a link to the refSNPpage for the new rs number). You can limit the output to merged rs numbers within a certain species by clicking on the "Limits" tab and then selecting the organism you wish from the organism selection box. (**5/25/05:11/03/08**)

Finding Deleted (no longer used) refSNP Numbers

The "rsCurrent" field in RsMergeArch contains 129,000 rs numbers not in the ASN.1 flat files or in a dbSNP web search. Is there a list of expired rs numbers?

Let me explain how we track both merged and deleted (an entirely different process from merging) refSNP (rs) numbers, by using a hypothetical example where a "chain merge" (multiple rs numbers merge into each other) occurs:

For example, let us say rs "A" merged into rs "B", and later, rs "B" merged into rs "C". As a result of the first merge, the entry for rs "A" in rsCurrent is updated to rs "B"; after the second merge, rsCurrent is then updated to rs "C". Now, if rs "C"'s submitters withdraw all the member ss numbers within the refSNP cluster rs "C", then rs "C" will get an entry in the SNPHistory table (the SNPHistory table ONLY contains SNPs that have "become history" — that is, SNPs that have been completely deleted). Please see ftp file for SNPHistory.bcp (located in the snp/database/organism_data/species of interest directory). To find the column names for the SNPHistory table, download the human_9606_table.sql, which is located in the human organism_schema directory.

Getting back to RsMergeArch: since "withdrawing rs "C" is not a merge action, the table RsMergeArch is not updated. RsMergeArch is used to track "rs merge" actions only. I can see that this might be confusing, so when time allows, we will add the following explanation to the RsMergeAch table definition, to make the RsMergeArch.rsCurrent meaning clearer:

RsMergeArch is used to track each rs merge event.

If an rs number in RsMergeArch.rsCurrent is withdrawn from dbSNP by submitter request, then an the rs number of the same value as that in rsCurrent will be entered into the SNPHistory table (which contains deleted rs numbers only).

Please note: "rsCurrent" in RsMergeArch does not mean the "current rs number" in the current dbSNP build". (**08/12/08**)

Finding Method Data

Where can I find a SNP file that contains method information?

Go to the shared_data directory of the dbSNP FTP site, and look at the Method and MethodLine .bcp files for information on the methods used by submittors for their submissions. (**1/18/06**)

Finding SNP data for NCBI Genome Builds

How can I get the SNP data for NCBI's genome build 34?

To get the mapping coordinates for build 34.3, please see the SNPContigLoc_34_3.bcp.gz table for the species of interest on the dbSNP FTP site.

You might also wish to consult tables b125_SNPMapInfo_34_5 and b125_ContigInfo_34_5. in the same FTP directory. Please see the Data Dictonary for table descriptions of the above tables.

Please note that some refSNP (rs) numbers might have been merged (if they are found to map the same location at a later build). The rs merge history is located in the RsMergeArch table, located in the same FTP directory as the aforementioned tables, or you can retrieve a list of merged rs numbers from Entrez SNP. Just type "mergedrs" (without the quotation marks) in the text box at the top of the page and click the "go" button. Each entry in the returned list will include the old rs numbers that has merged, and the new rs number it has merged into (with a link to the refSNPpage for the new rs number). You can limit the output to merged rs numbers within a certain species by clicking on the "Limits" tab and then selecting the organism you wish from the organism selection box. (**4/28/06:11/03/08**)

Finding Submitter Data

Although I can search dbSNP for CSHL-HAPMAP, the output is too large and lists SNPs submitted by CSHL-HAPMAP and others, while I need just those submitted originally by HAPMAP.

CSHL-HAPMAP genotyped about 4 million of the 10 million refSNPs in dbSNP, so I'm assuming you'd like to find those SNPs that have genotype data from HapMap as opposed to novel SNP assays submitted by HapMap,

When you said the EntrezSNP gives you too much output, what display format did you choose? If you select the "brief" format, you will get a list of just the search's resulting refSNP numbers. Or, you can take a look at eUtils as a means of retrieving data in batches.

Another alternative would be to use the *.bcp file approach:

A *.bcp file is a text file of table column values separated by tabs. If you can work with *.bcp files either by using scripts or databases, then you can achieve what you want by using two tables: SNP_bitfield and SNPChrPosOnRef, both of which are located in the organism_data directory of the dbSNP FTP site. First, take a look at page 2 (F6-HapMpa properties) of the bitfield pdf. Here, you'll see that when the SNP_bitfield.hapmap_prop equals 2, it means that the SNP has had a HapMap geneotype (phase2) submitted. By using this information in conjunction with the data in SNPChrPosOnRef, which lists the chromosome and position for each SNP on reference assembly, you can get the list of refSNP numbers you wanted.

For future queries of this sort, you can use the *.bcp file approach or check back with us for a SNP Genome Workbench plug in which will allow flexible queries and reporting using the data in SNP_bitfield within Genome Workbench. This system is currently under development, and should be available soon.(**11/01/07**)

Where do I find a list of submitters and the number of submitted SNP (ss) and refSNP (rs) clusters that each has submitted?

You can get this information from the dn_handleCount.bcp table for your organism on the dbSNP ftp site. If you know the submitter handle for the lab you are interested in, try the following:

1. Find the "Submitter Information" section of the dbSNP home page, and click on the words"By Submitter".
2. You will get a page with a text box. Enter the handle of the lab of interest in the text box (e.g. SNP500CANCER) and click the "Search" button.

You will receive a report that includes the submitter's name, their institution, batch types as well as the ss counts and the rs counts for that submitter. **(1/4/05)**

Finding Submitter Referenced Genbank Accessions

Are SNP submitter referenced Genbank accessions available for down load?

You can find SNP submitter referenced accessions in the SubSNPAcc.bcp.gz and SubSNP.bcp.gz tables located in the organism_data sub-directory for your particular organism on the dbSNP the FTP site. You'll have to join these tables using subsnp_id to get the submitted accession for the refSNP (rs) numbers of interest. (**3/10/06**).

Finding Validation Data

Where can I find a variation status field as defined in HGVbase for the mouse genome in dbSNP?

The validation fields are in the XML dump. The complete dbSNP XML mouse data dump is on the FTP site. The validation fields are defined in the docsum_2005. (ud:**03/19/08**)

Finding Variation Class Data

If I want to download all the indels from dbSNP, do I download the SNP table? If so, where is it?

Before I give you the steps to download the SNP table, I would like to mention that you can also get all the indels housed in dbSNP using an Entrez Search:

1. Go to the Entrez SNP page, click on the grey "Limits" tab near the top of the page.
2. Once you are on the limits page, go to the "SNP Class" box, and click on "in del".

Here are the steps for downloading the SNP table:

1. Go to the left blue side bar on the dbSNP home page, and Click on "General".
2. From the released set of choices, click on "FTP Download".
3. For the purpose of this example, I will assume you need the SNP table for human. To find it, you would go to the human /database/organism_data/ directory.

(**10/08/08**)

Finding SNPs for a Specific Organism

How do I download all the SNPs for Bos taurus? I need the SNP positions on each chromosome and the bovine reference build (Btau3.1 or Btau4).

You can download all of the SNPs for an organism from the dbSNP FTP site in various formats. The XML, ASN.1, flat file, or chromosome report should have the SNP positions.(**05/22/08**)