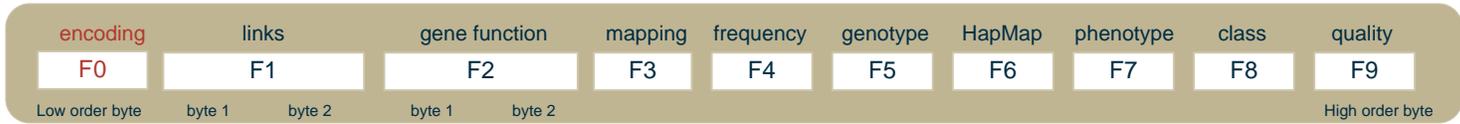




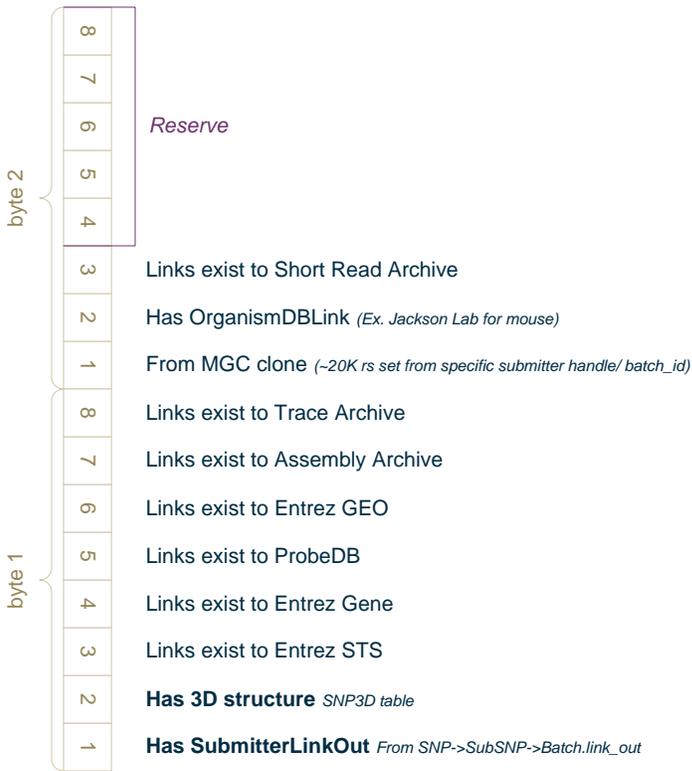
12 byte structure



The dbSNP bitfield structure is a 12-byte object that defines variation properties in 9 areas.

- F1 and F2 are 2-byte structures
- F0 (lowest order byte) is the version of the encoding schema used for the data, see page 2 for definition.
- Bits labeled in **bold** are currently populated by dbSNP

### F1 – resource link properties



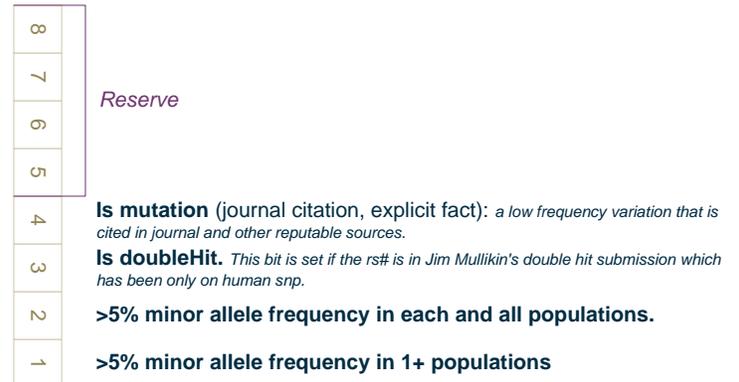
### F2 – gene function properties



### F3 – mapping properties



### F4 – allele frequency properties





### F5 – genotype properties

8	Reserve
7	
6	
5	
4	
3	<b>Marker is on high density genotyping kit</b> (50K density or greater). <i>The snp may have phenotype associations present in dbGaP.</i>
2	In Haplotype tagging set
1	<b>Genotypes available.</b> <i>The snp has individual genotype (in SubInd table).</i>

### F6 – HapMap properties

8	Reserve
7	
6	
5	
4	
3	Phase 3 genotyped: filtered, non-redundant.
2	<b>Phase 2 genotyped:</b> filtered, non-redundant.
1	Phase 1 genotyped: filtered, non-redundant.

### F7 – phenotype properties

8	Has MeSH is linked to a disease.
7	<b>Variation is interrogated in a clinical diagnostic assay</b>
6	Has transcription factor
5	<b>Submitted from a locus-specific database.</b>
4	Has significant association in dbGaP study
3	Has LOD score
2	Has SnpRIF
1	<b>Has OMIM/OMIA</b>

### F8 – variation class

8	Reserve
7	
6	
5	
4	0001 = single base polymorphism SNP 0010 = dips (deletion/insertion) 0011 = HETEROZYGOUS 0100 = Microsatellite 0101 = Named variation, e.g. (Alu) 0110 = NOVARIATION 0111 = mixed class 1000 = multi-base polymorphism
3	
2	
1	

### F9 – quality check

8	Reserve
7	
6	
5	<b>Contig allele not present in SNP allele list.</b> <i>The reference sequence allele at the mapped position is not present in the SNP allele list, adjusted for orientation.</i>
4	<b>Is Withdrawn by submitter</b> <i>If one member ss is withdrawn by submitter, then this bit is set. If all member ss' are withdrawn, then the rs is deleted to SNPHistory.</i>
3	<b>Rs cluster has non-overlapping allele sets.</b> <i>True when rs set has more than 2 alleles from different submissions and these sets share no alleles in common.</i>
2	Is a strain-specific fixed difference
1	<b>Has Genotype Conflict</b> <i>Same (rs, ind), different genotype. N/N is not included.</i>

### F0 – Version encoding

8	Reserve
7	
6	
5	
4	
3	<b>Bitmap schema version.</b> <i>Versions increment as integer value (current is version 2, version 1.2 is encoded as version 1)</i>
2	
1	