

# Genome Variant Format

## Genome Variant Format (GVF)

We are also able to process data provided in GVF version 1.05 or 1.06.

chr1	VCF	SNV	3537996	3537996	.
	+	.			
	ID=6;Reference_seq=T;Variant_seq=C;Variant_feature=exonic;Gene=WRAP73;Genotype=heterozygous				

The first eight columns are as per the GVF standard and represent:

Chromosome

Source (unused)

\*Sequence Ontology type

\*The following Sequence Ontology types are recognized by this tool:

SNV, MNP, complex\_substitution, insertion, inversion, deletion, indel, copy\_number\_variation, gap

Start location

End location

Score (unused)

Strand

Phase (unused)

The last column is a series of value/type pairs.

The following are currently recognized by the tool and itemized for i2b2: Variant\_feature, Gene and Genotype.