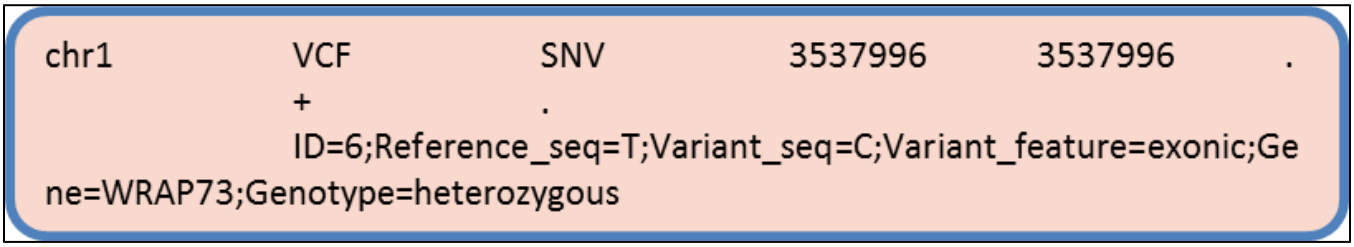
Genome Variant Format

Genome Variant Format (GVF)

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



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.