| Abbreviation | Detailed explanations |
|---|---|
| CHROM | Chromosome. |
| POS | The reference position, with the 1st base having position 1. |
| REF | Reference base(s). |
| ALT | Alternate base(s). |
| DP | Total read depth at the locus. |
| RO | Reference allele observation count, with partial observations recorded fractionally. |
| AO | Alternate allele observations, with partial observations recorded fractionally. |
| ALLELE | Allele (or ALT): In case of multiple ALT fields, this helps to identify which ALT we are referring to. |
| EFFECT | Annotation (a.k.a. effect): Annotated using Sequence Ontology terms. Multiple effects can be concatenated using '&'. |
| IMPACT | Putative_impact: A simple estimation of putative impact / deleteriousness : {HIGH, MODERATE, LOW, MODIFIER}. |
| FEATURE | Which type of feature is in the next field (e.g. transcript, motif, miRNA, etc.). |
| FEATUREID | Depending on the annotation, this may be: Transcript ID (preferably using version number), Motif ID, miRNA, ChipSeq peak, Histone mark, etc. |
| GENE | Common gene name (HGNC). Optional: use closest gene when the variant is "intergenic". |
| GENEID | Gene ID. |
| BIOTYPE | Transcript biotype:The bare minimum is at least a description on whether the transcript is {Coding, Noncoding}. Whenever possible, use ENSEMBL biotypes. |
| HGVS_C | Variant using HGVS notation (DNA level). |
| HGVS_P | If variant is coding, this field describes the variant using HGVS notation (Protein level). Since transcript ID is already mentioned in feature ID, it may be omitted here. |

*Refer to these weblinks:*
*http://snpeff.sourceforge.net/SnpEff_manual.html#input*
*https://samtools.github.io/hts-specs/VCFv4.2.pdf*