# Tests on the VEP VCF parser

## Snapshot of the code from 5pm 02/02/2016, commit hash 7601efd

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| **Test number** | **Test** | **Pass/Fail** | **Additional Comments** | **Test file** |
| 1 | Successful code execution and write-out of tab-delimited file | Pass | Writes out file to directory containing code | 1 |
| 2 | Absent or incorrectly named input file | Fail | See CommentsOnCode.docx issue 1 | 1 |
| 3 | VCF file generated using different (older) version of Germline Enrichment pipeline (version 1.1.0) | Fail | See CommentsOnCode.docx issue 2 | 1 |
| 4 | Removed ##VEP header line from VCF | Pass | Code continues to execute to completion throwing a warning | 1 |
| 5 | Removed ##SAMPLE header line from VCF | Pass | Code execution stops, exception correctly thrown | 1 |
| 6 | Removed ##INFO header line from VCF | Fail | See CommentsOnCode.docx issue 3.1 | 1 |
| 7 | Removed ##CSQ from within ##INFO VCF header line | Fail | See CommentsOnCode.docx issue 3.2 | 1 |
| 8 | Removed sample name from the ##SAMPLE header line of the VCF | Fail | See CommentsOnCode.docx issue 4 | 1 |
| 9 | Checked sample name was correct to original VCF using a print statement on the variable and comparing to original VCF | Pass | N/A | 1 |
| 10 | Removed CSQ attribute tag in body of VCF | Pass | Code executes and generates output missing the annotations from the CSQ field | 1 |
| 11 | Created mixed genotype 0/. | Pass | Exception correctly thrown | 1 |
| 12 | Created mixed genotype 1/. | Pass | Exception correctly thrown | 1 |
| 13 | Created polyploid genotype 0/1/1 | Pass | Exception correctly thrown | 1 |
| 14 | Created simulated genotype with overlapping indel G > T,\* with genotype 0/2 | Pass | Code correctly continues to execute and does not write out this \* as an allele | 1 |
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Allele num association and handling of multisample vcfs unable to be tested without VCF generated by Germline Enrichment latest version (1.1.5) of the pipeline.

## Test Files

1. 160127\_M00766\_0001\_000000000-ALR2L\_16M00174\_filtered\_meta\_annotated.vcf
   * Generated using newest version of the Somatic Amplicon pipeline (1.3.6)
2. d