# 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 |
| 15 | Removed header and associated data from CSQ field | Pass | Code executed and generated required output | 1 |
| 16 | Added additional header and empty data field to CSQ field | Fail | See CommentsOnCode.docx issue 24 | 1 |
| 17 | Removed command line argument -V | Pass | Incorrect arguments exception correctly raised including execution of catch() block | 1 |
| 18 | Set -V flag active with no associated path to a file | Pass | Missing argument exception correctly raised | 1 |
| 19 | Added option -K (only report known RefSeq transcripts) | Fail | See CommentsOnCode.docx issue 29 | 1 |
| 20 | Set -T flag active with no associated path to a file | Pass | Missing argument exception correctly raised | 1 |
| 21 | Set -T flag active with incorrect path to a file | Pass | IOException correctly raised including execution of catch() block | 1 |
| 22 | Set -C flag active with no associated path to a file | Pass | Missing argument exception correctly raised | 1 |
| 23 | Set -C flag active with incorrect path to a file | Fail | See CommentsOnCode.docx issue 30 | 1 |
| 24 | Removed write permissions from folder where code executes | Pass | Access is denied message correctly raised with wrapping text specified in catch() block | 1 |
| 25 | Left intended output file open in another program (Excel) |  | File being used by another process message correctly raised with wrapping text specified in catch() block |  |
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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.

Auto-generated @Override code has not been tested.

To do (06/02/2017):

* Note: Not tested operation of variant classification nor preferred transcript list (06/02/2017)- files in correct format required.
  + Test correct operation of code and output is as specified
  + Attempt test to see result of passing in malformed file
* Note: Not explored deserialize classes as unsure how they work- reading required

## 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