A Cross-Sectional Study for Variant Interpretation and Reporting of NGS Data Adopting Tertiary Analysis Software: Navify® Mutation Profiler

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Navify mutation Profiler successfully interpretes
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Allow correct RNA analysis.

In order to generate a report on NMP software by using "Oncomine_Fusions_only" assay, input VCF files was modified following listed workflow parameters:

1. IonReporterSoftwareVersion=5.14.0.0

2. IonReporterWorkflowVersion=ir514

3. OncomineVariantAnnotationToolVersion=3.0.8

Briefly, these modifications allow VCF files analysis of RNA-derived samples on NMP system. It has been suggested to assess these technical specifications opening the VCF file as "text editor". After technical modification, file can be saved and loaded on NMP.

Figure: Screenshots of RNA VCF files before (left) and after (right) required modifications by using Windows "text editor".