S3 _ File

Filtering criteria used in XomAnnotate to detect variations of high impact lying within the exonic boundaries.

```
# Objective: This is the configuration file for xominer software.
# The xominer software is to mine variations from exome genomic data.
# The xominer program reads the configuration parameters from this file
# to tune its behavior. The name of this file is always <toolname>.cfg.
#
# NOTICE:
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# otherwise, arising from, out of or in connection with the software
# or the use or other dealings in the software.
#
concordanceCutoff = 8              # The minimum vote to select a locus for SV
qualityThreshold = 20              # Minimum MAPQ threshold for SAM file
EvidenceScore = 0.0005             # Exclude Lumpy record if it is greater
BasesInDelete = 500                # Number of minimum Bases in Lumpy Delete

Effect_Skip = SYNONYMOUS_CODING # Skip all SNP with this Effect
Effect_Impact = MODERATE           # MODERATE & HIGH
UnifiedGenotyper_Quality = 50      # 50 is PASS for GATK UnifiedGenotyper
FreeBayes_Quality = 50             # Only High quality mutations for Freebayes
AlleleFrequency = 0.05             # Only High quality MAF to be included
```