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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#  
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# 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 = 0.00005  # 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