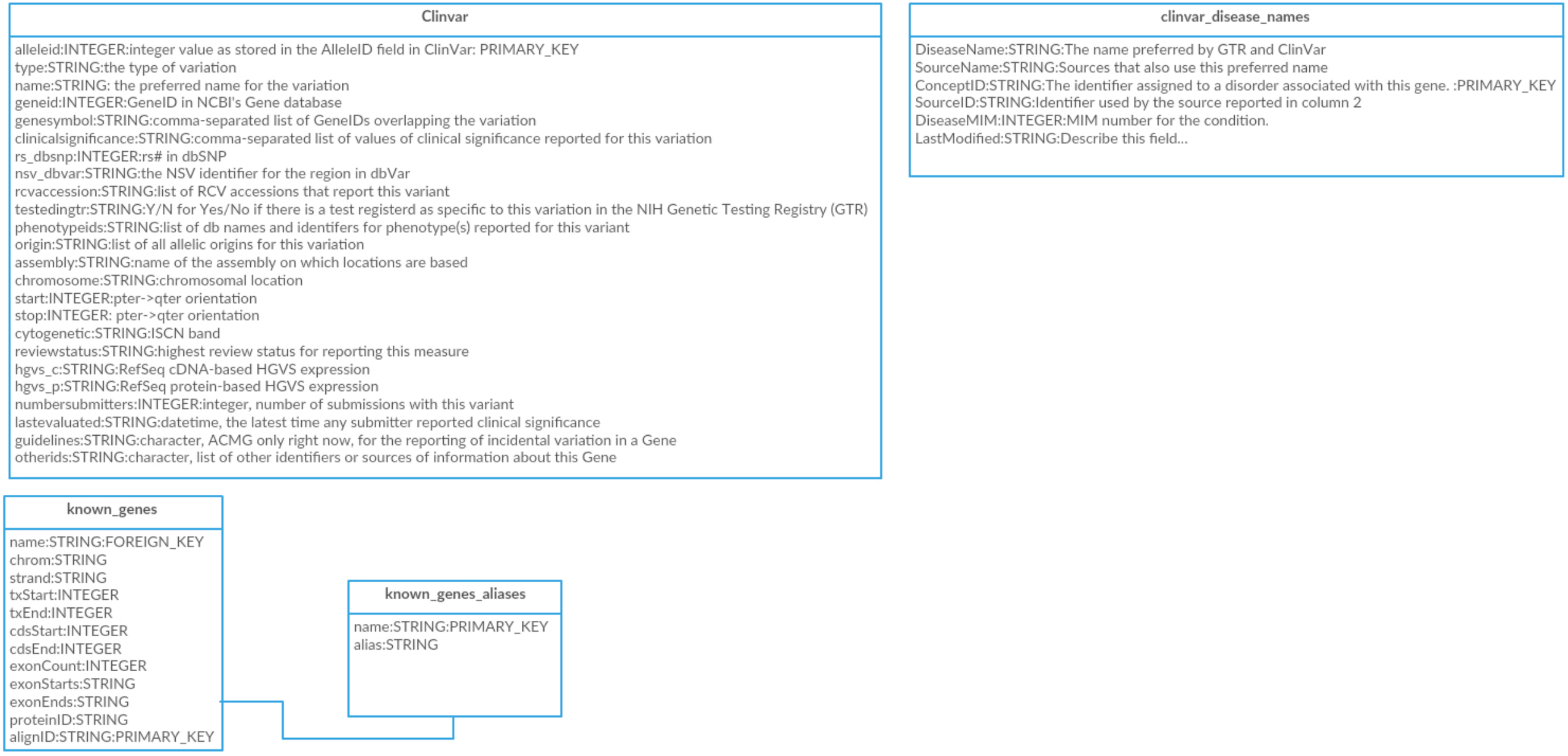
Clinvar
alleleid:INTEGER:integer value as stored in the AlleleID field in ClinVar: PRIMARY_KEY
type:STRING:the type of variation
name:STRING: the preferred name for the variation
geneid:INTEGER:GeneID in NCBI's Gene database
genesymbol:STRING:comma-separated list of GeneIDs overlapping the variation
clinicalsignificance:STRING:comma-separated list of values of clinical significance reported for this variation
rs_dbsnp:INTEGER:rs# in dbSNP
nsv_dbvar:STRING:the NSV identifier for the region in dbVar
rcvaccession:STRING:list of RCV accessions that report this variant
testedingtr:STRING:Y/N for Yes/No if there is a test registerd as specific to this variation in the NIH Genetic Testing Registry (GTR)
phenotypeids:STRING:list of db names and identifers for phenotype(s) reported for this variant
origin:STRING:list of all allelic origins for this variation
assembly:STRING:name of the assembly on which locations are based
chromosome:STRING:chromosomal location
start:INTEGER:pter->qter orientation
stop:INTEGER: pter->qter orientation
cytogenetic:STRING:ISCN band
reviewstatus:STRING:highest review status for reporting this measure
hgvs_c:STRING:RefSeq cDNA-based HGVS expression
hgvs_p:STRING:RefSeq protein-based HGVS expression
numbersubmitters:INTEGER:integer, number of submissions with this variant
lastevaluated:STRING:datetime, the latest time any submitter reported clinical significance
guidelines:STRING:character, ACMG only right now, for the reporting of incidental variation in a Gene
otherids:STRING:character, list of other identifiers or sources of information about this Gene
clinvar_disease_names
DiseaseName:STRING:The name preferred by GTR and ClinVar
SourceName:STRING:Sources that also use this preferred name
ConceptID:STRING:The identifier assigned to a disorder associated with this gene. :PRIMARY_KEY
SourceID:STRING:Identifier used by the source reported in column 2
DiseaseMIM:INTEGER:MIM number for the condition.
LastModified:STRING:Describe this field...
known_genes
name:STRING:FOREIGN_KEY
chrom:STRING
strand:STRING
txStart:INTEGER
txEnd:INTEGER
cdsStart:INTEGER
cdsEnd:INTEGER
exonCount:INTEGER
exonStarts:STRING
exonEnds:STRING
proteinID:STRING
alignID:STRING:PRIMARY_KEY
known_genes_aliases
name:STRING:PRIMARY_KEY
alias:STRING