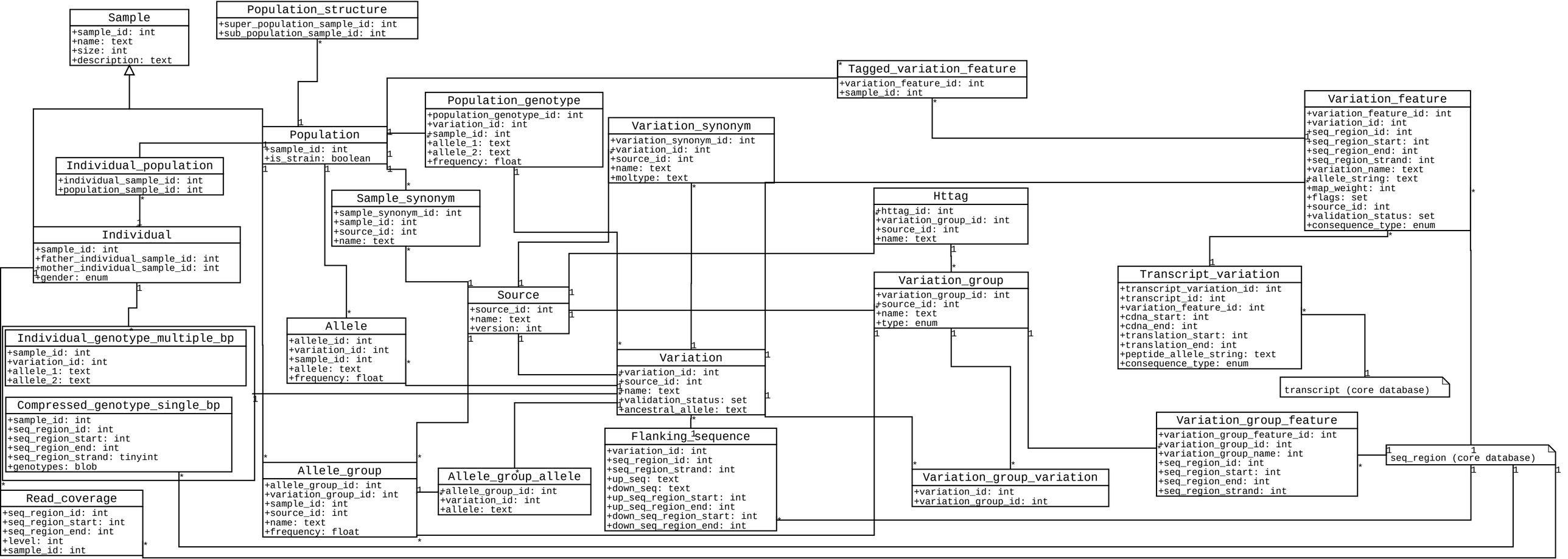
Sample
+sample_id: int
+name: text
+size: int
+description: text
Population_structure
+super_population_sample_id: int
+sub_population_sample_id: int
Tagged_variation_feature
+variation_feature_id: int
+sample_id: int
Population_genotype
+population_genotype_id: int
+variation_id: int
+sample_id: int
+allele_1: text
+allele_2: text
+frequency: float
Variation_synonym
+variation_synonym_id: int
+variation_id: int
+source_id: int
+name: text
+moltype: text
Variation_feature
+variation_feature_id: int
+variation_id: int
+seq_region_id: int
+seq_region_start: int
+seq_region_end: int
+seq_region_strand: int
+variation_name: text
+allele_string: text
+map_weight: int
+flags: set
+source_id: int
+validation_status: set
+consequence_type: enum
Population
+sample_id: int
+is_strain: boolean
Individual_population
+individual_sample_id: int
+population_sample_id: int
Sample_synonym
+sample_synonym_id: int
+sample_id: int
+source_id: int
+name: text
Individual
+sample_id: int
+father_individual_sample_id: int
+mother_individual_sample_id: int
+gender: enum
Httag
+httag_id: int
+variation_group_id: int
+source_id: int
+name: text
Variation_group
+variation_group_id: int
+source_id: int
+name: text
+type: enum
Transcript_variation
+transcript_variation_id: int
+transcript_id: int
+variation_feature_id: int
+cdna_start: int
+cdna_end: int
+translation_start: int
+translation_end: int
+peptide_allele_string: text
+consequence_type: enum
Source
+source_id: int
+name: text
+version: int
Allele
+allele_id: int
+variation_id: int
+sample_id: int
+allele: text
+frequency: float
Individual_genotype_multiple_bp
+sample_id: int
+variation_id: int
+allele_1: text
+allele_2: text
Variation
+variation_id: int
+source_id: int
+name: text
+validation_status: set
+ancestral_allele: text
transcript (core database)
Compressed_genotype_single_bp
+sample_id: int
+seq_region_id: int
+seq_region_start: int
+seq_region_end: int
+seq_region_strand: tinyint
+genotypes: blob
Variation_group_feature
+variation_group_feature_id: int
+variation_group_id: int
+variation_group_name: int
+seq_region_id: int
+seq_region_start: int
+seq_region_end: int
+seq_region_strand: int
Flanking_sequence
+variation_id: int
+seq_region_id: int
+seq_region_strand: int
+up_seq: text
+down_seq: text
+up_seq_region_start: int
+up_seq_region_end: int
+down_seq_region_start: int
+down_seq_region_end: int
seq_region (core database)
Allele_group
+allele_group_id: int
+variation_group_id: int
+sample_id: int
+source_id: int
+name: text
+frequency: float
Allele_group_allele
+allele_group_id: int
+variation_id: int
+allele: text
Variation_group_variation
+variation_id: int
+variation_group_id: int
Read_coverage
+seq_region_id: int
+seq_region_start: int
+seq_region_end: int
+level: int
+sample_id: int