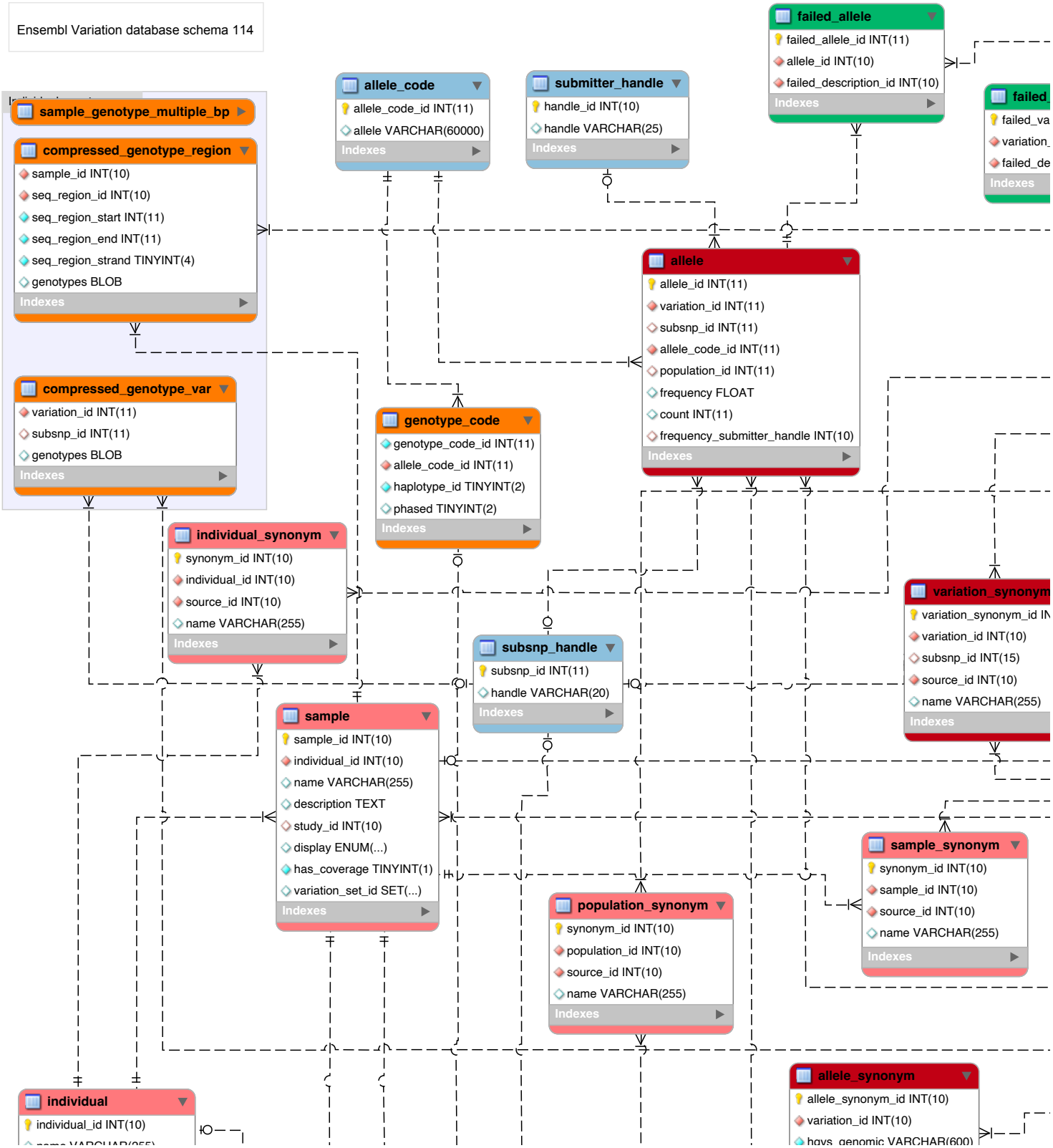
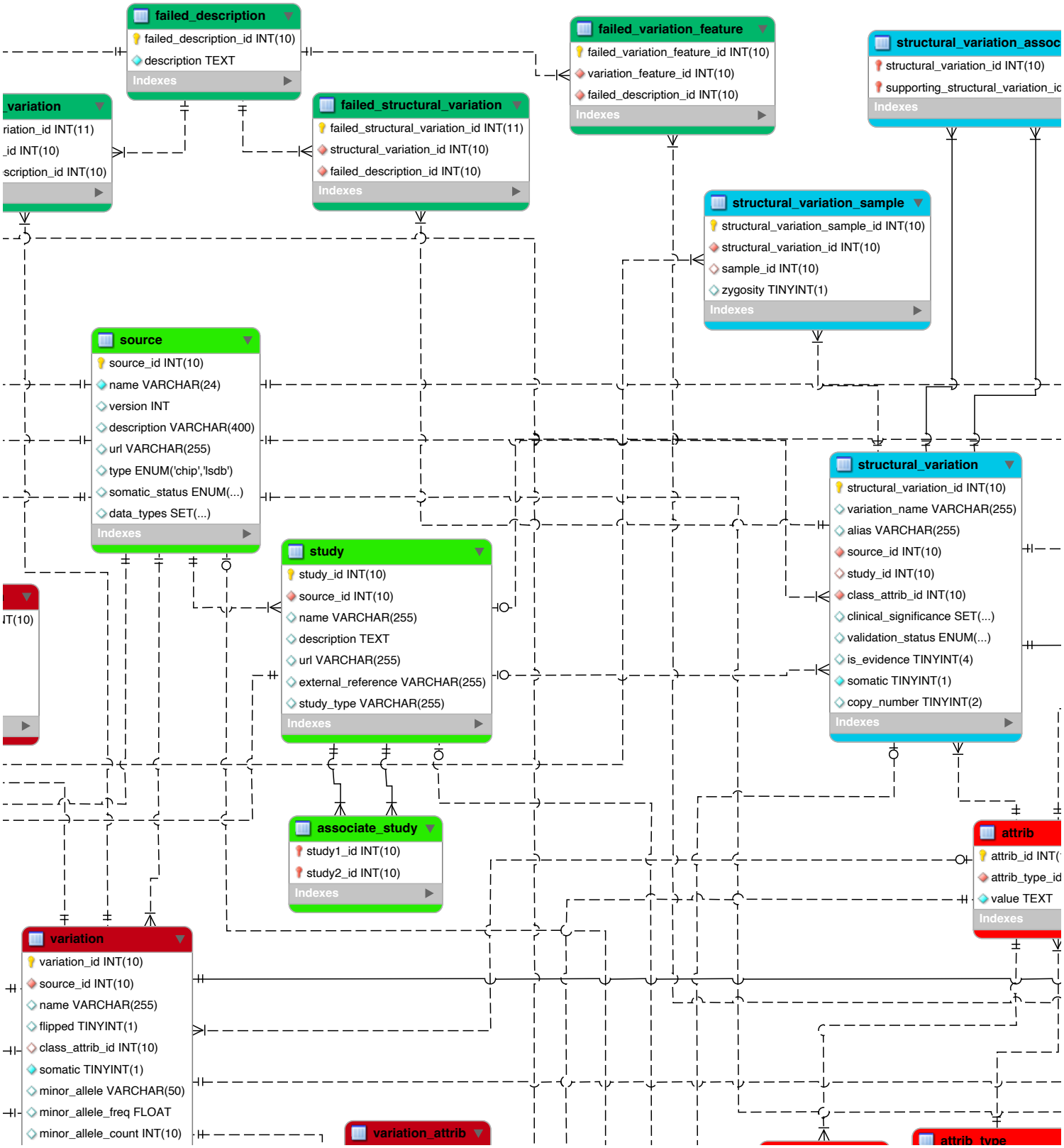
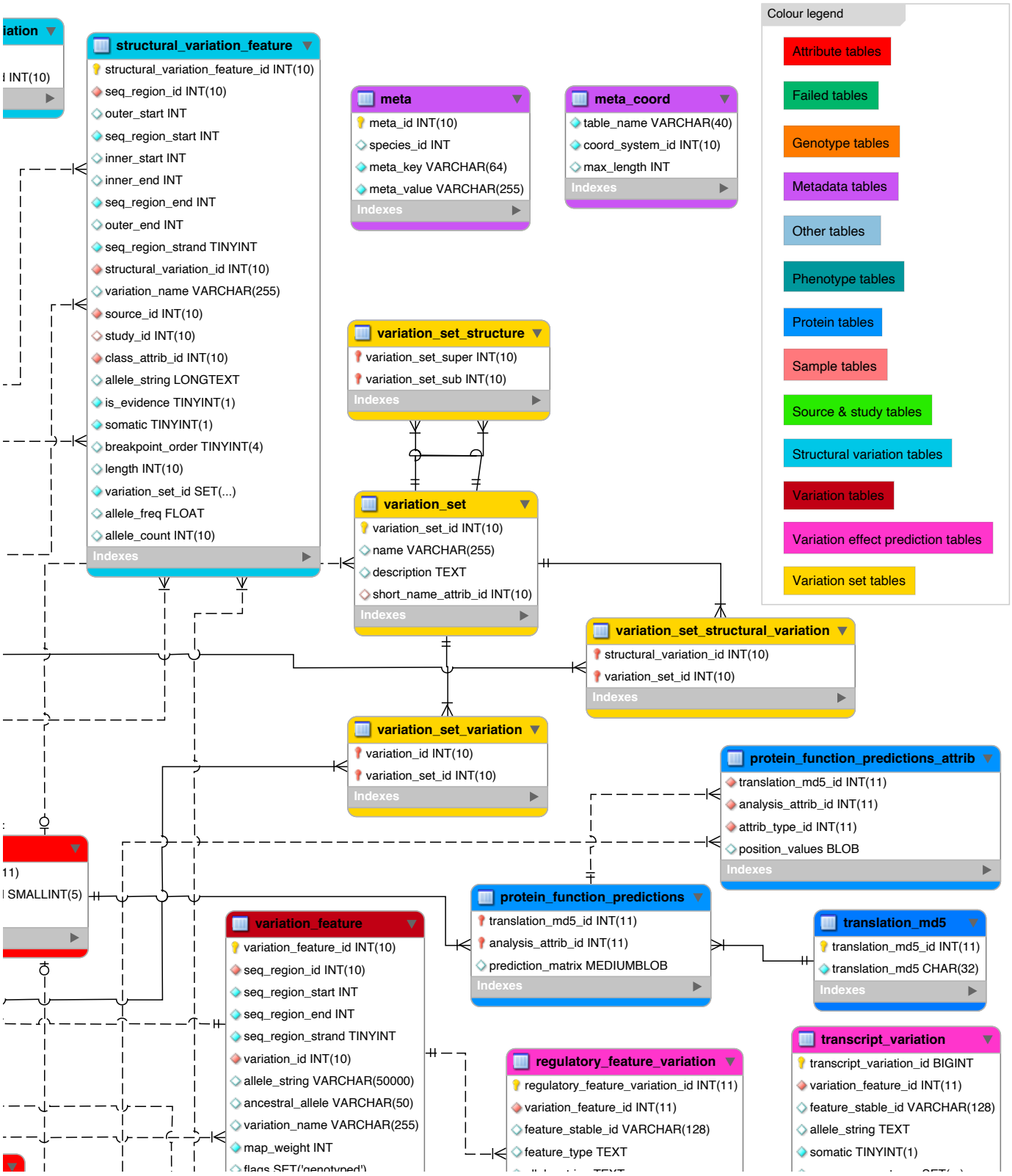
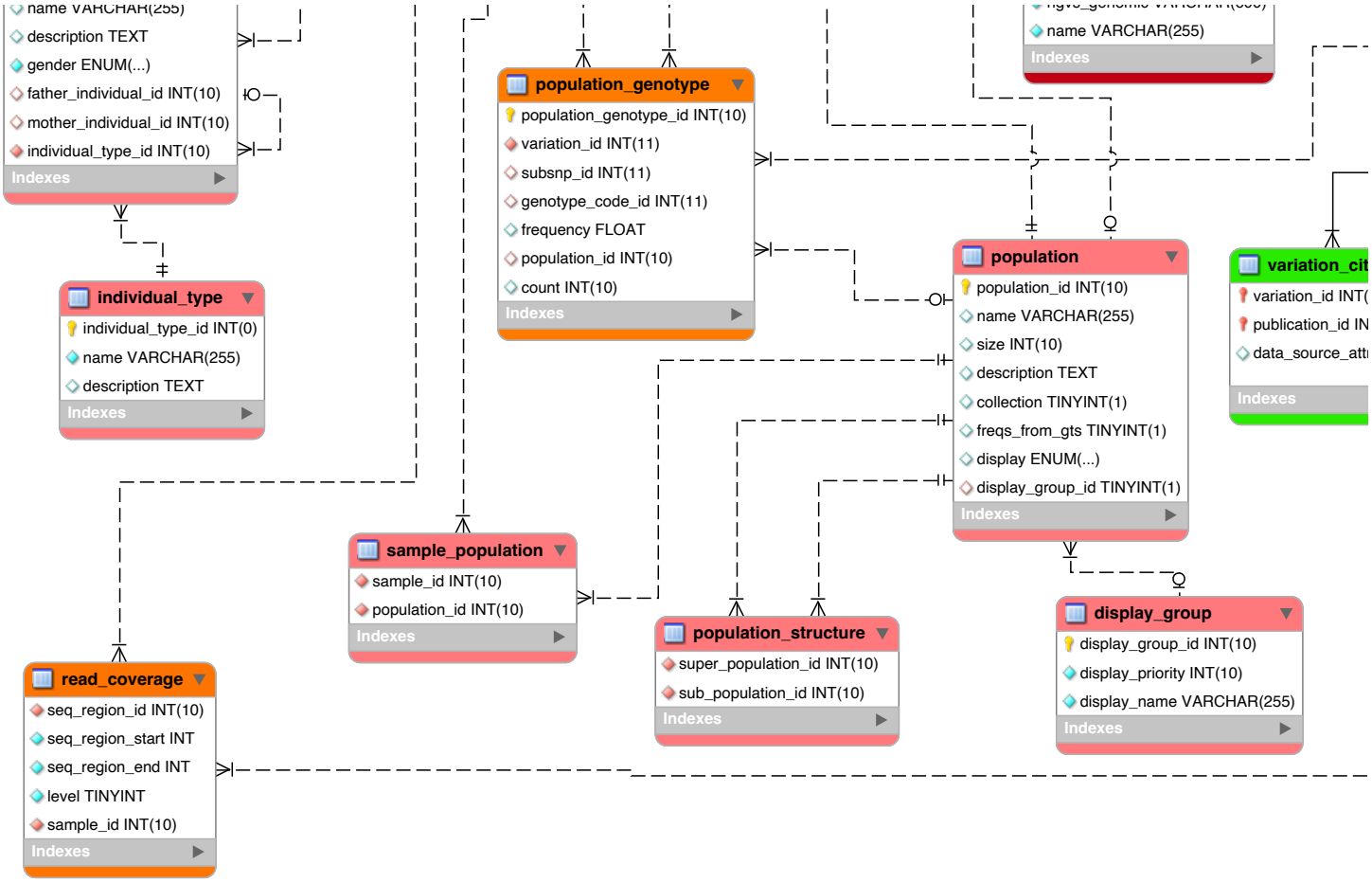
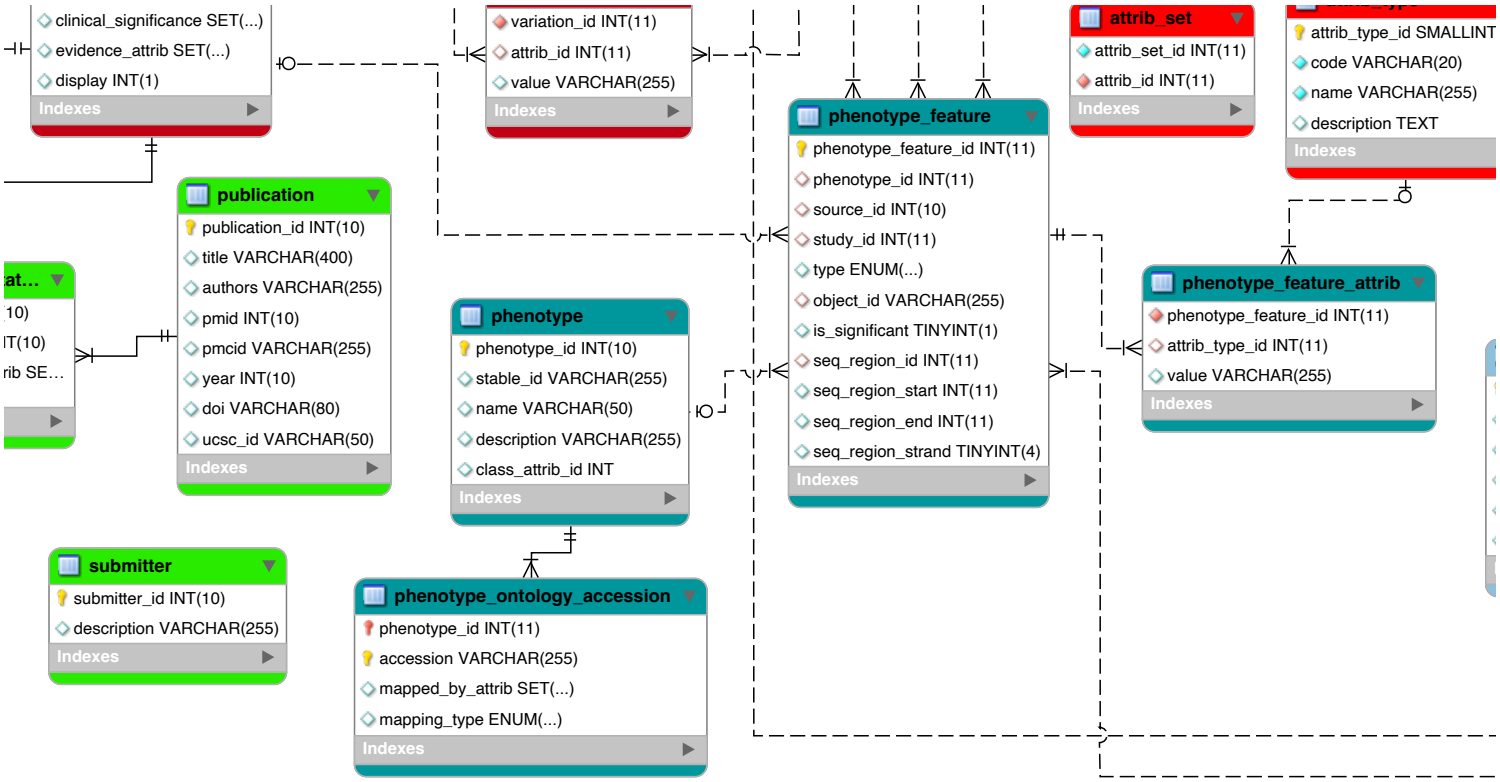
Ensembl Variation database schema 114




failed_description
failed_description_id INT(10)
description TEXT
Indexes
failed_variation_feature
failed_variation_feature_id INT(10)
variation_feature_id INT(10)
failed_description_id INT(10)
Indexes
structural_variation_assoc
structural_variation_id INT(10)
supporting_structural_variation_id
Indexes
_variation
riation_id INT(11)
_id INT(10)
scription_id INT(10)
failed_structural_variation
failed_structural_variation_id INT(11)
structural_variation_id INT(10)
failed_description_id INT(10)
Indexes
structural_variation_sample
structural_variation_sample_id INT(10)
structural_variation_id INT(10)
sample_id INT(10)
zygosity TINYINT(1)
Indexes
source
source_id INT(10)
name VARCHAR(24)
version INT
description VARCHAR(400)
url VARCHAR(255)
type ENUM('chip','lsdb')
somatic_status ENUM(...)
data_types SET(...)
Indexes
structural_variation
structural_variation_id INT(10)
variation_name VARCHAR(255)
alias VARCHAR(255)
source_id INT(10)
study_id INT(10)
class_attrib_id INT(10)
clinical_significance SET(...)
validation_status ENUM(...)
is_evidence TINYINT(4)
somatic TINYINT(1)
copy_number TINYINT(2)
Indexes
study
study_id INT(10)
source_id INT(10)
name VARCHAR(255)
description TEXT
url VARCHAR(255)
external_reference VARCHAR(255)
study_type VARCHAR(255)
Indexes
associate_study
study1_id INT(10)
study2_id INT(10)
Indexes
attrib
attrib_id INT(
attrib_type_id
value TEXT
Indexes
variation
variation_id INT(10)
source_id INT(10)
name VARCHAR(255)
flipped TINYINT(1)
class_attrib_id INT(10)
somatic TINYINT(1)
minor_allele VARCHAR(50)
minor_allele_freq FLOAT
minor_allele_count INT(10)
variation_attrib
attrib_type


structural_variation_feature
structural_variation_feature_id INT(10)
seq_region_id INT(10)
outer_start INT
seq_region_start INT
inner_start INT
inner_end INT
seq_region_end INT
outer_end INT
seq_region_strand TINYINT
structural_variation_id INT(10)
variation_name VARCHAR(255)
source_id INT(10)
study_id INT(10)
class_attrib_id INT(10)
allele_string LONGTEXT
is_evidence TINYINT(1)
somatic TINYINT(1)
breakpoint_order TINYINT(4)
length INT(10)
variation_set_id SET(...)
allele_freq FLOAT
allele_count INT(10)
Indexes
meta
meta_id INT(10)
species_id INT
meta_key VARCHAR(64)
meta_value VARCHAR(255)
Indexes
meta_coord
table_name VARCHAR(40)
coord_system_id INT(10)
max_length INT
Indexes
variation_set_structure
variation_set_super INT(10)
variation_set_sub INT(10)
Indexes
variation_set
variation_set_id INT(10)
name VARCHAR(255)
description TEXT
short_name_attrib_id INT(10)
Indexes
variation_set_structural_variation
structural_variation_id INT(10)
variation_set_id INT(10)
Indexes
variation_set_variation
variation_id INT(10)
variation_set_id INT(10)
Indexes
protein_function_predictions_attrib
translation_md5_id INT(11)
analysis_attrib_id INT(11)
attrib_type_id INT(11)
position_values BLOB
Indexes
protein_function_predictions
translation_md5_id INT(11)
analysis_attrib_id INT(11)
prediction_matrix MEDIUMBLOB
Indexes
translation_md5
translation_md5_id INT(11)
translation_md5 CHAR(32)
Indexes
variation_feature
variation_feature_id INT(10)
seq_region_id INT(10)
seq_region_start INT
seq_region_end INT
seq_region_strand TINYINT
variation_id INT(10)
allele_string VARCHAR(50000)
ancestral_allele VARCHAR(50)
variation_name VARCHAR(255)
map_weight INT
regulatory_feature_variation
regulatory_feature_variation_id INT(11)
variation_feature_id INT(11)
feature_stable_id VARCHAR(128)
feature_type TEXT
transcript_variation
transcript_variation_id BIGINT
variation_feature_id INT(11)
feature_stable_id VARCHAR(128)
allele_string TEXT
somatic TINYINT(1)
Colour legend
Attribute tables
Failed tables
Genotype tables
Metadata tables
Other tables
Phenotype tables
Protein tables
Sample tables
Source & study tables
Structural variation tables
Variation tables
Variation effect prediction tables
Variation set tables


name VARCHAR(255)
description TEXT
gender ENUM(...)
father_individual_id INT(10)
mother_individual_id INT(10)
individual_type_id INT(10)
Indexes
individual_type
individual_type_id INT(0)
name VARCHAR(255)
description TEXT
Indexes
population_genotype
population_genotype_id INT(10)
variation_id INT(11)
subsnp_id INT(11)
genotype_code_id INT(11)
frequency FLOAT
population_id INT(10)
count INT(10)
Indexes
name VARCHAR(255)
Indexes
population
population_id INT(10)
name VARCHAR(255)
size INT(10)
description TEXT
collection TINYINT(1)
freqs_from_gts TINYINT(1)
display ENUM(...)
display_group_id TINYINT(1)
Indexes
variation_cit
variation_id INT(
publication_id IN
data_source_att
Indexes
sample_population
sample_id INT(10)
population_id INT(10)
Indexes
population_structure
super_population_id INT(10)
sub_population_id INT(10)
Indexes
display_group
display_group_id INT(10)
display_priority INT(10)
display_name VARCHAR(255)
Indexes
read_coverage
seq_region_id INT(10)
seq_region_start INT
seq_region_end INT
level TINYINT
sample_id INT(10)
Indexes


clinical_significance SET(...)
evidence_attrib SET(...)
display INT(1)
Indexes
variation_id INT(11)
attrib_id INT(11)
value VARCHAR(255)
Indexes
attrib_set
attrib_set_id INT(11)
attrib_id INT(11)
Indexes
attrib_type_id SMALLINT
code VARCHAR(20)
name VARCHAR(255)
description TEXT
Indexes
phenotype_feature
phenotype_feature_id INT(11)
phenotype_id INT(11)
source_id INT(10)
study_id INT(11)
type ENUM(...)
object_id VARCHAR(255)
is_significant TINYINT(1)
seq_region_id INT(11)
seq_region_start INT(11)
seq_region_end INT(11)
seq_region_strand TINYINT(4)
Indexes
publication
publication_id INT(10)
title VARCHAR(400)
authors VARCHAR(255)
pmid INT(10)
pmcid VARCHAR(255)
year INT(10)
doi VARCHAR(80)
ucsc_id VARCHAR(50)
Indexes
phenotype_feature_attrib
phenotype_feature_id INT(11)
attrib_type_id INT(11)
value VARCHAR(255)
Indexes
phenotype
phenotype_id INT(10)
stable_id VARCHAR(255)
name VARCHAR(50)
description VARCHAR(255)
class_attrib_id INT
Indexes
submitter
submitter_id INT(10)
description VARCHAR(255)
Indexes
phenotype_ontology_accession
phenotype_id INT(11)
accession VARCHAR(255)
mapped_by_attrib SET(...)
mapping_type ENUM(...)
Indexes

(5)
source_id INT(10)
consequence_types SET(...)
variation_set_id SET(...)
class_attrib_id INT(10)
somatic TINYINT(1)
minor_allele VARCHAR(50)
minor_allele_freq FLOAT
minor_allele_count INT(10)
alignment_quality DOUBLE
evidence_attrib SET(...)
clinical_significance SET(...)
display INT(1)
Indexes
allele_string TEXT
somatic TINYINT(1)
consequence_types SET(...)
Indexes
consequence_types SET(...)
cds_start INT(11)
cds_end INT(11)
cdna_start INT(11)
cdna_end INT(11)
translation_start INT(11)
translation_end INT(11)
distance_to_transcript INT(11)
codon_allele_string TEXT
pep_allele_string TEXT
hgvs_genomic TEXT
hgvs_transcript TEXT
hgvs_protein TEXT
polyphen_prediction ENUM(...)
polyphen_score FLOAT
sift_prediction ENUM(...)
sift_score FLOAT
display INT(1)
Indexes
coord_system
coord_system_id INT(10)
species_id INT(10)
name VARCHAR(40)
version VARCHAR(255)
rank INT
attrib SET(...)
Indexes
motif_feature_variation
motif_feature_variation_id INT(11)
variation_feature_id INT(11)
feature_stable_id VARCHAR(128)
motif_feature_id INT(11)
allele_string TEXT
somatic TINYINT(1)
consequence_types SET(...)
binding_matrix_stable_id VARCHAR(60)
motif_start INT(11)
motif_end INT(11)
motif_score_delta FLOAT
in_informative_position TINYINT(1)
Indexes
seq_region
seq_region_id INT(10)
name VARCHAR(255)
coord_system_id INT(10)
Indexes