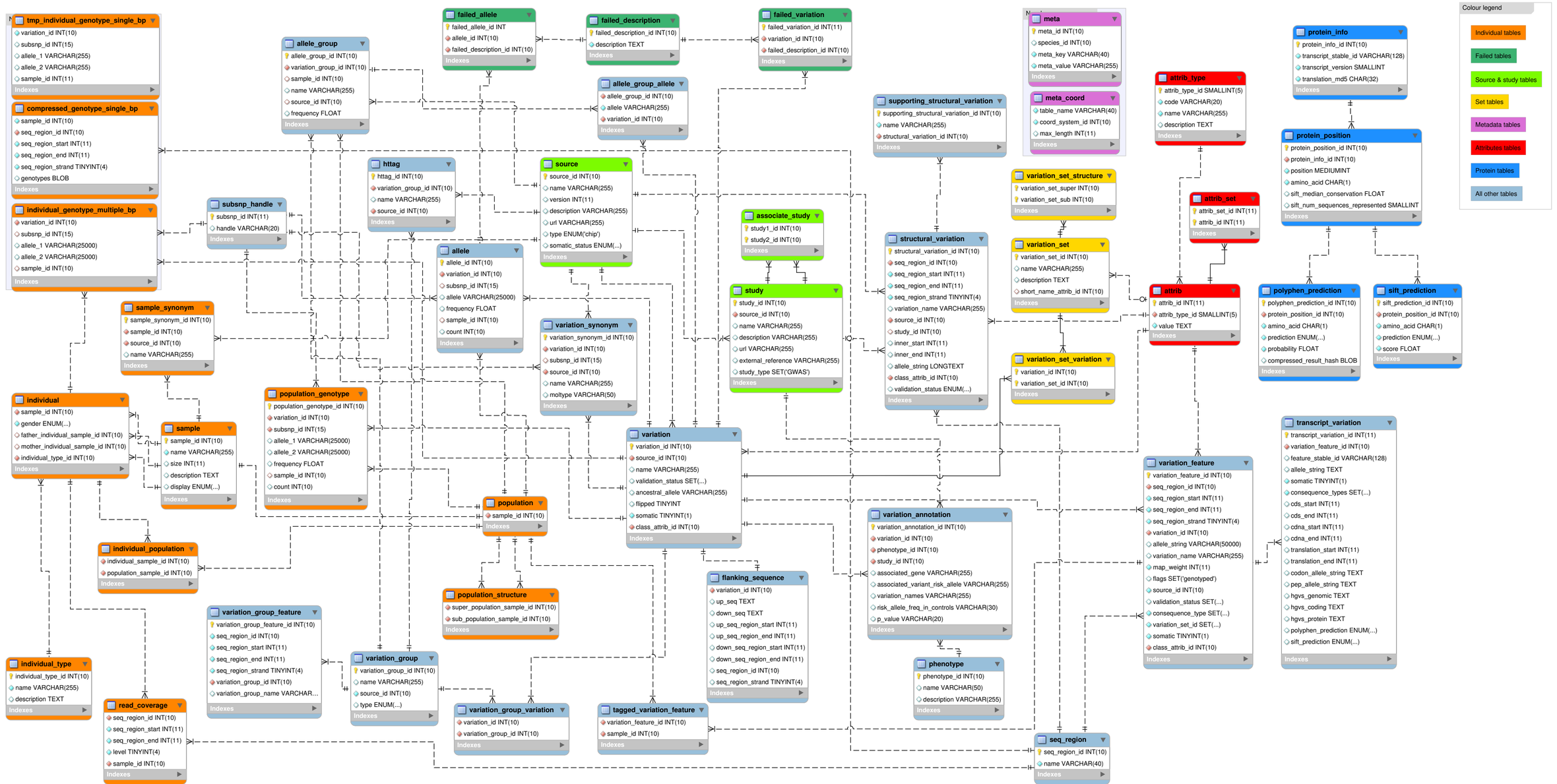
Colour legend
Individual tables
Failed tables
Source & study tables
Set tables
Metadata tables
Attributes tables
Protein tables
All other tables
tmp_individual_genotype_single_bp
variation_id INT(10)
subsnp_id INT(15)
allele_1 VARCHAR(255)
allele_2 VARCHAR(255)
sample_id INT(11)
Indexes
compressed_genotype_single_bp
sample_id INT(10)
seq_region_id INT(10)
seq_region_start INT(11)
seq_region_end INT(11)
seq_region_strand TINYINT(4)
genotypes BLOB
Indexes
individual_genotype_multiple_bp
variation_id INT(10)
subsnp_id INT(15)
allele_1 VARCHAR(25000)
allele_2 VARCHAR(25000)
sample_id INT(10)
Indexes
allele_group
allele_group_id INT(10)
variation_group_id INT(10)
sample_id INT(10)
name VARCHAR(255)
source_id INT(10)
frequency FLOAT
Indexes
failed_allele
failed_allele_id INT
allele_id INT(10)
failed_description_id INT(10)
Indexes
failed_description
failed_description_id INT(10)
description TEXT
Indexes
failed_variation
failed_variation_id INT(11)
variation_id INT(10)
failed_description_id INT(10)
Indexes
allele_group_allele
allele_group_id INT(10)
allele VARCHAR(255)
variation_id INT(10)
Indexes
meta
meta_id INT(10)
species_id INT(10)
meta_key VARCHAR(40)
meta_value VARCHAR(255)
Indexes
meta_coord
table_name VARCHAR(40)
coord_system_id INT(10)
max_length INT(11)
Indexes
supporting_structural_variation
supporting_structural_variation_id INT(10)
name VARCHAR(255)
structural_variation_id INT(10)
Indexes
attrib_type
attrib_type_id SMALLINT(5)
code VARCHAR(20)
name VARCHAR(255)
description TEXT
Indexes
protein_info
protein_info_id INT(10)
transcript_stable_id VARCHAR(128)
transcript_version SMALLINT
translation_md5 CHAR(32)
Indexes
protein_position
protein_position_id INT(10)
protein_info_id INT(10)
position MEDIUMINT
amino_acid CHAR(1)
sift_median_conservation FLOAT
sift_num_sequences_represented SMALLINT
Indexes
subsnp_handle
subsnp_id INT(11)
handle VARCHAR(20)
Indexes
httag
httag_id INT(10)
variation_group_id INT(10)
name VARCHAR(255)
source_id INT(10)
Indexes
source
source_id INT(10)
name VARCHAR(255)
version INT(11)
description VARCHAR(255)
url VARCHAR(255)
type ENUM('chip')
somatic_status ENUM(...)
Indexes
associate_study
study1_id INT(10)
study2_id INT(10)
Indexes
variation_set_structure
variation_set_super INT(10)
variation_set_sub INT(10)
Indexes
attrib_set
attrib_set_id INT(11)
attrib_id INT(11)
Indexes
allele
allele_id INT(10)
variation_id INT(10)
subsnp_id INT(15)
allele VARCHAR(25000)
frequency FLOAT
sample_id INT(10)
count INT(10)
Indexes
study
study_id INT(10)
source_id INT(10)
name VARCHAR(255)
description VARCHAR(255)
url VARCHAR(255)
external_reference VARCHAR(255)
study_type SET('GWAS')
Indexes
structural_variation
structural_variation_id INT(10)
seq_region_id INT(10)
seq_region_start INT(11)
seq_region_end INT(11)
seq_region_strand TINYINT(4)
variation_name VARCHAR(255)
source_id INT(10)
study_id INT(10)
inner_start INT(11)
inner_end INT(11)
allele_string LONGTEXT
class_attrib_id INT(10)
validation_status ENUM(...)
Indexes
variation_set
variation_set_id INT(10)
name VARCHAR(255)
description TEXT
short_name_attrib_id INT(10)
Indexes
attrib
attrib_id INT(11)
attrib_type_id SMALLINT(5)
value TEXT
Indexes
polyphen_prediction
polyphen_prediction_id INT(10)
protein_position_id INT(10)
amino_acid CHAR(1)
prediction ENUM(...)
probability FLOAT
compressed_result_hash BLOB
Indexes
sift_prediction
sift_prediction_id INT(10)
protein_position_id INT(10)
amino_acid CHAR(1)
prediction ENUM(...)
score FLOAT
Indexes
sample_synonym
sample_synonym_id INT(10)
sample_id INT(10)
source_id INT(10)
name VARCHAR(255)
Indexes
variation_synonym
variation_synonym_id INT(10)
variation_id INT(10)
subsnp_id INT(15)
source_id INT(10)
name VARCHAR(255)
moltype VARCHAR(50)
Indexes
variation_set_variation
variation_id INT(10)
variation_set_id INT(10)
Indexes
individual
sample_id INT(10)
gender ENUM(...)
father_individual_sample_id INT(10)
mother_individual_sample_id INT(10)
individual_type_id INT(10)
Indexes
population_genotype
population_genotype_id INT(10)
variation_id INT(10)
subsnp_id INT(15)
allele_1 VARCHAR(25000)
allele_2 VARCHAR(25000)
frequency FLOAT
sample_id INT(10)
count INT(10)
Indexes
sample
sample_id INT(10)
name VARCHAR(255)
size INT(11)
description TEXT
display ENUM(...)
Indexes
variation
variation_id INT(10)
source_id INT(10)
name VARCHAR(255)
validation_status SET(...)
ancestral_allele VARCHAR(255)
flipped TINYINT
somatic TINYINT(1)
class_attrib_id INT(10)
Indexes
variation_feature
variation_feature_id INT(10)
seq_region_id INT(10)
seq_region_start INT(11)
seq_region_end INT(11)
seq_region_strand TINYINT(4)
variation_id INT(10)
allele_string VARCHAR(50000)
variation_name VARCHAR(255)
map_weight INT(11)
flags SET('genotyped')
source_id INT(10)
validation_status SET(...)
consequence_type SET(...)
variation_set_id SET(...)
somatic TINYINT(1)
class_attrib_id INT(10)
Indexes
transcript_variation
transcript_variation_id INT(11)
variation_feature_id INT(10)
feature_stable_id VARCHAR(128)
allele_string TEXT
somatic TINYINT(1)
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)
codon_allele_string TEXT
pep_allele_string TEXT
hgvs_genomic TEXT
hgvs_coding TEXT
hgvs_protein TEXT
polyphen_prediction ENUM(...)
sift_prediction ENUM(...)
Indexes
population
sample_id INT(10)
Indexes
variation_annotation
variation_annotation_id INT(10)
variation_id INT(10)
phenotype_id INT(10)
study_id INT(10)
associated_gene VARCHAR(255)
associated_variant_risk_allele VARCHAR(255)
variation_names VARCHAR(255)
risk_allele_freq_in_controls VARCHAR(30)
p_value VARCHAR(20)
Indexes
individual_population
individual_sample_id INT(10)
population_sample_id INT(10)
Indexes
population_structure
super_population_sample_id INT(10)
sub_population_sample_id INT(10)
Indexes
flanking_sequence
variation_id INT(10)
up_seq TEXT
down_seq TEXT
up_seq_region_start INT(11)
up_seq_region_end INT(11)
down_seq_region_start INT(11)
down_seq_region_end INT(11)
seq_region_id INT(10)
seq_region_strand TINYINT(4)
Indexes
variation_group_feature
variation_group_feature_id INT(10)
seq_region_id INT(10)
seq_region_start INT(11)
seq_region_end INT(11)
seq_region_strand TINYINT(4)
variation_group_id INT(10)
variation_group_name VARCHAR...
Indexes
variation_group
variation_group_id INT(10)
name VARCHAR(255)
source_id INT(10)
type ENUM(...)
Indexes
phenotype
phenotype_id INT(10)
name VARCHAR(50)
description VARCHAR(255)
Indexes
individual_type
individual_type_id INT(10)
name VARCHAR(255)
description TEXT
Indexes
read_coverage
seq_region_id INT(10)
seq_region_start INT(11)
seq_region_end INT(11)
level TINYINT(4)
sample_id INT(10)
Indexes
variation_group_variation
variation_id INT(10)
variation_group_id INT(10)
Indexes
tagged_variation_feature
variation_feature_id INT(10)
sample_id INT(10)
Indexes
seq_region
seq_region_id INT(10)
name VARCHAR(40)
Indexes