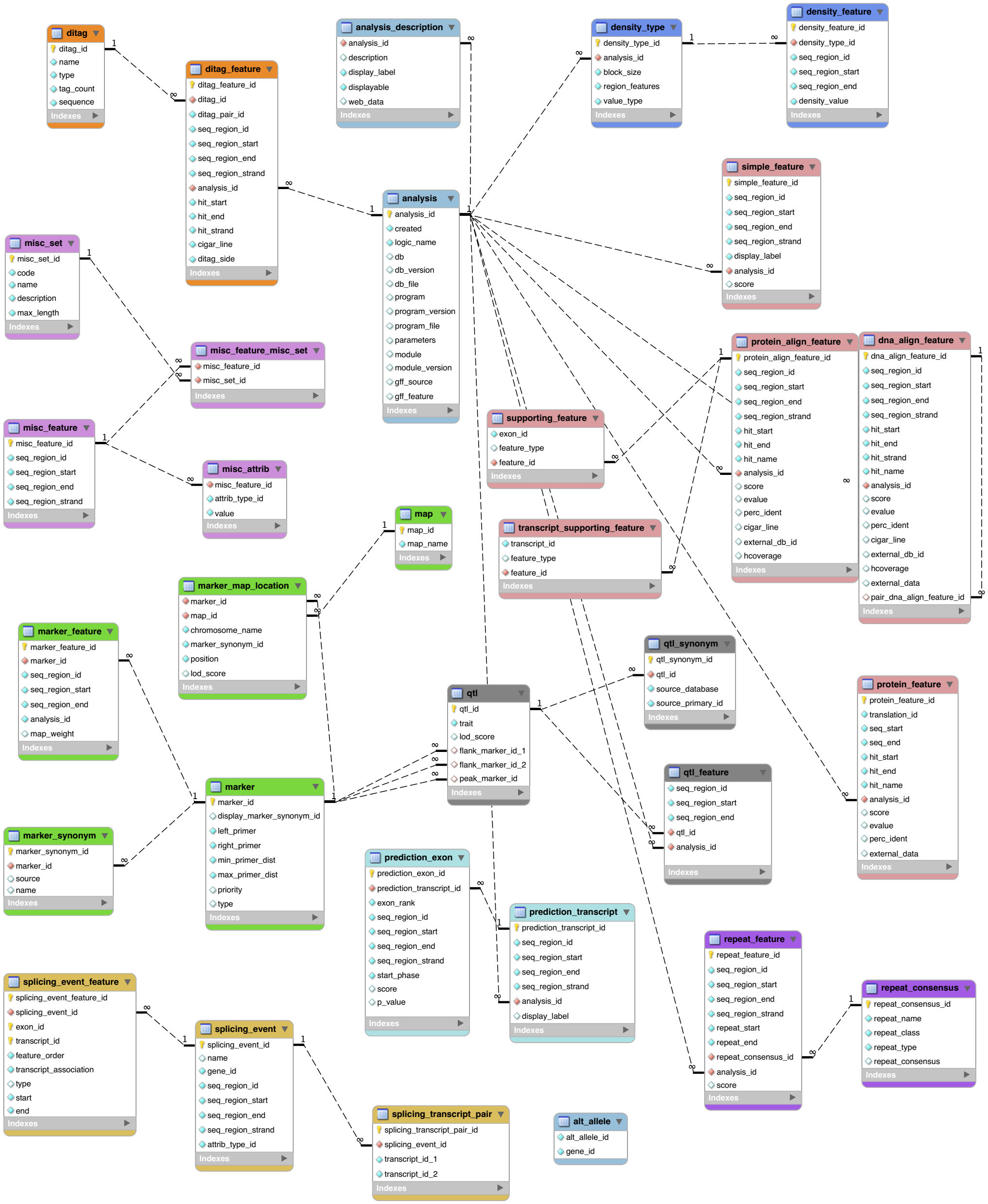
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name
type
tag_count
sequence
Indexes
ditag_feature
ditag_feature_id
ditag_id
ditag_pair_id
seq_region_id
seq_region_start
seq_region_end
seq_region_strand
analysis_id
hit_start
hit_end
hit_strand
cigar_line
ditag_side
Indexes
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analysis_id
description
display_label
displayable
web_data
Indexes
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density_type_id
analysis_id
block_size
region_features
value_type
Indexes
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density_type_id
seq_region_id
seq_region_start
seq_region_end
density_value
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seq_region_start
seq_region_end
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analysis_id
score
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db
db_version
db_file
program
program_version
program_file
parameters
module
module_version
gff_source
gff_feature
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misc_set_id
code
name
description
max_length
Indexes
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misc_feature_id
misc_set_id
Indexes
misc_feature
misc_feature_id
seq_region_id
seq_region_start
seq_region_end
seq_region_strand
Indexes
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misc_feature_id
attrib_type_id
value
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seq_region_end
seq_region_strand
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seq_region_strand
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hit_strand
hit_name
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perc_ident
cigar_line
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hcoverage
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transcript_id
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marker_id
map_id
chromosome_name
marker_synonym_id
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source_primary_id
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flank_marker_id_2
peak_marker_id
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hit_start
hit_end
hit_name
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seq_region_strand
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seq_region_end
seq_region_strand
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repeat_class
repeat_type
repeat_consensus
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splicing_event_id
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transcript_id
feature_order
transcript_association
type
start
end
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seq_region_end
seq_region_strand
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splicing_event_id
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transcript_id_2
Indexes
alt_allele
alt_allele_id
gene_id