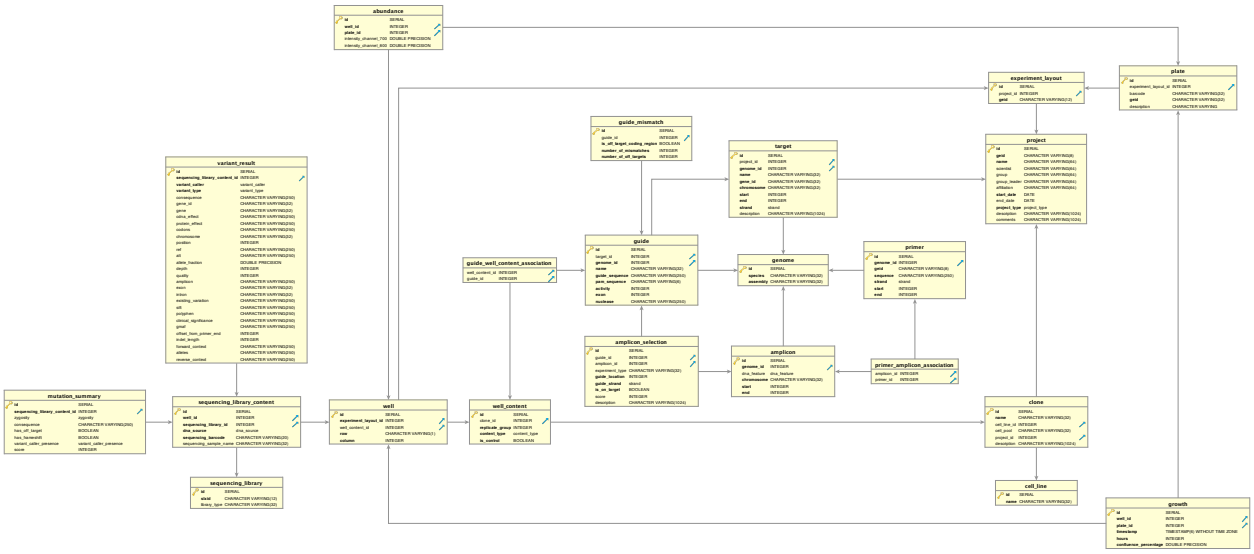
abundance
id SERIAL
well_id INTEGER
plate_id INTEGER
intensity_channel_700 DOUBLE PRECISION
intensity_channel_800 DOUBLE PRECISION
experiment_layout
id SERIAL
project_id INTEGER
grid CHARACTER VARYING(12)
plate
id SERIAL
experiment_layout_id INTEGER
barcode CHARACTER VARYING(32)
grid CHARACTER VARYING(32)
description CHARACTER VARYING
guide_mismatch
id SERIAL
guide_id INTEGER
is_off_target_coding_region BOOLEAN
number_of_mismatches INTEGER
number_of_off_targets INTEGER
target
id SERIAL
project_id INTEGER
genome_id INTEGER
name CHARACTER VARYING(32)
gene_id CHARACTER VARYING(32)
chromosome CHARACTER VARYING(32)
start INTEGER
end INTEGER
strand strand
description CHARACTER VARYING(1024)
project
id SERIAL
grid CHARACTER VARYING(8)
name CHARACTER VARYING(64)
scientist CHARACTER VARYING(64)
group CHARACTER VARYING(64)
group_leader CHARACTER VARYING(64)
affiliation CHARACTER VARYING(64)
start_date DATE
end_date DATE
project_type project_type
description CHARACTER VARYING(1024)
comments CHARACTER VARYING(1024)
variant_result
id SERIAL
sequencing_library_content_id INTEGER
variant_caller variant_caller
variant_type variant_type
consequence CHARACTER VARYING(250)
gene_id CHARACTER VARYING(32)
gene CHARACTER VARYING(32)
aa_effect CHARACTER VARYING(250)
protein_effect CHARACTER VARYING(250)
codons CHARACTER VARYING(250)
chromosome CHARACTER VARYING(32)
position INTEGER
id CHARACTER VARYING(250)
alt CHARACTER VARYING(250)
allele_fraction DOUBLE PRECISION
depth INTEGER
quality INTEGER
amplicon CHARACTER VARYING(250)
exon CHARACTER VARYING(32)
intron CHARACTER VARYING(32)
existing_variation CHARACTER VARYING(250)
ref CHARACTER VARYING(250)
polyphen CHARACTER VARYING(250)
polyphen_sig CHARACTER VARYING(250)
gnomad CHARACTER VARYING(250)
offset_from_primer_end INTEGER
scale_length INTEGER
forward_context CHARACTER VARYING(250)
allele CHARACTER VARYING(250)
reverse_context CHARACTER VARYING(250)
guide
id SERIAL
target_id INTEGER
genome_id INTEGER
name CHARACTER VARYING(64)
guide_sequence CHARACTER VARYING(250)
pam_sequence CHARACTER VARYING(50)
activity INTEGER
exon INTEGER
nuclease CHARACTER VARYING(250)
guide_well_content_association
well_content_id INTEGER
guide_id INTEGER
genome
id SERIAL
species CHARACTER VARYING(20)
assembly CHARACTER VARYING(20)
primer
id SERIAL
genome_id INTEGER
grid CHARACTER VARYING(8)
sequence CHARACTER VARYING(250)
strand strand
start INTEGER
end INTEGER
amplicon_selection
id SERIAL
guide_id INTEGER
amplicon_id INTEGER
experiment_type CHARACTER VARYING(32)
guide_location INTEGER
guide_strand strand
is_on_target BOOLEAN
rank INTEGER
description CHARACTER VARYING(1024)
amplicon
id SERIAL
genome_id INTEGER
dna_feature dna_feature
chromosome CHARACTER VARYING(32)
start INTEGER
end INTEGER
primer_amplicon_association
amplicon_id INTEGER
primer_id INTEGER
mutation_summary
id SERIAL
sequencing_library_content_id INTEGER
mutation_id BIGINT
consequence CHARACTER VARYING(250)
has_off_target BOOLEAN
has_farneseq BOOLEAN
variant_caller_presence variant_caller_presence
score INTEGER
sequencing_library_content
id SERIAL
well_id INTEGER
sequencing_library_id INTEGER
dna_source dna_source
sequencing_barcode CHARACTER VARYING(20)
sequencing_sample_name CHARACTER VARYING(32)
well
id SERIAL
experiment_layout_id INTEGER
well_content_id INTEGER
row CHARACTER VARYING(1)
column INTEGER
well_content
id SERIAL
clone_id INTEGER
replicate_group INTEGER
content_type content_type
is_control BOOLEAN
clone
id SERIAL
name CHARACTER VARYING(32)
cell_line_id INTEGER
cell_pool CHARACTER VARYING(32)
project_id INTEGER
description CHARACTER VARYING(1024)
sequencing_library
id SERIAL
shrid CHARACTER VARYING(10)
library_type CHARACTER VARYING(20)
cell_line
id SERIAL
name CHARACTER VARYING(32)
growth
id SERIAL
well_id INTEGER
plate_id INTEGER
timestamp TIMESTAMP(0) WITHOUT TIME ZONE
hours INTEGER
confluence_percentage DOUBLE PRECISION