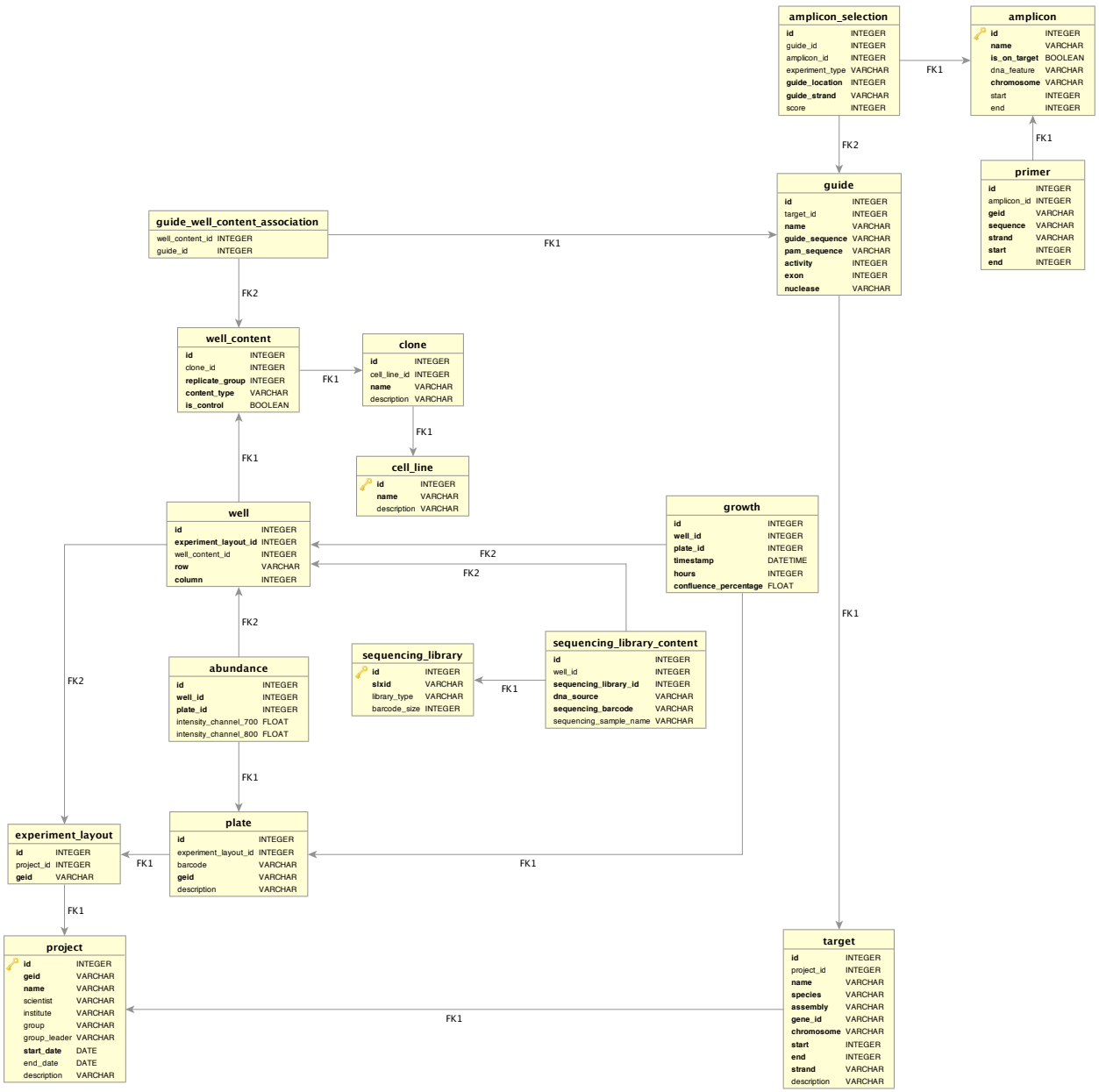
amplicon_selection
id INTEGER
guide_id INTEGER
amplicon_id INTEGER
experiment_type VARCHAR
guide_location INTEGER
guide_strand VARCHAR
score INTEGER
FK1
amplicon
id INTEGER
name VARCHAR
is_on_target BOOLEAN
dna_feature VARCHAR
chromosome VARCHAR
start INTEGER
end INTEGER
FK2
FK1
primer
id INTEGER
amplicon_id INTEGER
geid VARCHAR
sequence VARCHAR
strand VARCHAR
start INTEGER
end INTEGER
guide
id INTEGER
target_id INTEGER
name VARCHAR
guide_sequence VARCHAR
pam_sequence VARCHAR
activity INTEGER
exon INTEGER
nuclease VARCHAR
guide_well_content_association
well_content_id INTEGER
guide_id INTEGER
FK1
FK2
well_content
id INTEGER
clone_id INTEGER
replicate_group INTEGER
content_type VARCHAR
is_control BOOLEAN
FK1
clone
id INTEGER
cell_line_id INTEGER
name VARCHAR
description VARCHAR
FK1
cell_line
id INTEGER
name VARCHAR
description VARCHAR
FK1
well
id INTEGER
experiment_layout_id INTEGER
well_content_id INTEGER
row VARCHAR
column INTEGER
growth
id INTEGER
well_id INTEGER
plate_id INTEGER
timestamp DATETIME
hours INTEGER
confluence_percentage FLOAT
FK2
FK2
FK1
FK2
FK2
sequencing_library
id INTEGER
slxid VARCHAR
library_type VARCHAR
barcode_size INTEGER
FK1
sequencing_library_content
id INTEGER
well_id INTEGER
sequencing_library_id INTEGER
dna_source VARCHAR
sequencing_barcode VARCHAR
sequencing_sample_name VARCHAR
abundance
id INTEGER
well_id INTEGER
plate_id INTEGER
intensity_channel_700 FLOAT
intensity_channel_800 FLOAT
FK1
experiment_layout
id INTEGER
project_id INTEGER
geid VARCHAR
FK1
plate
id INTEGER
experiment_layout_id INTEGER
barcode VARCHAR
geid VARCHAR
description VARCHAR
FK1
FK1
project
id INTEGER
geid VARCHAR
name VARCHAR
scientist VARCHAR
institute VARCHAR
group VARCHAR
group_leader VARCHAR
start_date DATE
end_date DATE
description VARCHAR
target
id INTEGER
project_id INTEGER
name VARCHAR
species VARCHAR
assembly VARCHAR
gene_id VARCHAR
chromosome VARCHAR
start INTEGER
end INTEGER
strand VARCHAR
description VARCHAR
FK1