motility	
id INT	P
sub_id CHAR	F
cl_id CHAR	F
avg_end_to_end_dist FLOAT	
avg_total_dist FLOAT	
avg_speed FLOAT	
end_to_end_dist_st_dev FLOAT	
total_dist_st_dev FLOAT	
speed_st_dev FLOAT	
end_to_end_dist_st_err FLOAT	
total_dist_st_err FLOAT	
speed_st_err FLOAT	

motility_measurements	
id INT	Q P
sub_id CHAR	
cl_id CHAR	
distance FLOAT	
pixel_value FLOAT	
slice INT	
track INT	
velocity FLOAT	
x FLOAT	
y FLOAT	

stiffness		
id INT	P	
atomic_force_measurement_id CHAR		+
calc_ramp_ex_nm FLOAT		'
calc_ramp_rt_nm FLOAT		
defl_nm_ex FLOAT		
defl_nm_rt FLOAT		
time s ex FLOAT		

time_s_rt FLOAT

stiffness_measurements	
id INT	₽
sub_id CHAR	
cl_id CHAR	
atomic_force_measurement_id CHAR	
date DATE	
young_modulus FLOAT	
spring_constant FLOAT	

contractility	
id INT	P
sub_id CHAR	G
cl_id CHAR	G
traction_force FLOAT	
nuclear_volume FLOAT	
cell_volume FLOAT	
cell_area FLOAT	

id INT	Q P
sub_id CHAR	
cl_id CHAR	
aspect_ratio FLOAT	
circularity FLOAT	
area FLOAT	

proliferation_measurement_timing		
id INT	P	
cl_id CHAR		
p1t1 FLOAT		
p1t2 FLOAT		
p1t3 FLOAT		
p2t1 FLOAT		
p2t2 FLOAT		
p2t3 FLOAT		

proteomics_iBAQ		
id INT		P
sub_id CHAR		G
cl_id CHAR		G
UPS2 BOOLEAN		
replicate INT		
prob FLOAT		
protein CHAR		
total_filtered_peptides INT		
unique_filtered_peptides IN7	Γ	
pep_prophet FLOAT		
peptide CHAR		
description TEXT		

proteomics_phospho	
id INT	Q P
sub_id CHAR	
cl_id CHAR	
accession CHAR	
score FLOAT	
coverage FLOAT	
sequence CHAR	
num_peptides INT	
unique_peptides INT	
modifications CHAR	
x_corr FLOAT	
description TEXT	
replicate INT	

proteomics_tmt	
id INT	
cl_id CHAR	
accessions CHAR	
score FLOAT	
sequence CHAR	
modifications CHAR	
x_corr FLOAT	
description TEXT	
modifications_all_sites CHAR	
sample INT	
abundance_ratio_F1_127N_F1_126 FLOAT	
abundance_ratio_F1_127C_F1_126 FLOAT	
abundance_ratio_F1_128N_F1_126 FLOAT	
abundance_ratio_F1_128C_F1_126 FLOAT	
abundance_ratio_F1_129N_F1_126 FLOAT	
abundance_ratio_F1_129C_F1_126 FLOAT	
abundance_ratio_F1_130N_F1_126 FLOAT	
abundance_ratio_F1_130C_F1_126 FLOAT	
abundance_ratio_F1_131_F1_126 FLOAT	
abundance_ratio_log2_F1_127N_F1_126 FL	OAT
abundance_ratio_log2_F1_127C_F1_126 FL	OAT
abundance_ratio_log2_F1_128N_F1_126 FL	OAT
abundance_ratio_log2_F1_128C_F1_126 FL	OAT
abundance_ratio_log2_F1_129N_F1_126 FL	OAT
abundance_ratio_log2_F1_129C_F1_126 FL	OAT
abundance_ratio_log2_F1_130N_F1_126 FL	OAT
abundance_ratio_log2_F1_130C_F1_126 FL	OAT
abundance_ratio_log2_F1_131_F1_126 FLO	AT

		mRNA_sequencing_files
		id INT
		sub_id CHAR
		cl_id CHAR
		raw_fastqc_files CHAR
		trim_reads_fq_files CHAR
		accepted_hits_bam_file CHAR
		accepted_hits_bai_file CHAR
		unmapped_bam_file CHAR
		deletions_bed_file CHAR
		junctions_bed_file CHAR
		insertions_bed_file CHAR
		transcripts_transdecoder_files CHAR
		cufflinks_files CHAR
		NCBI_genome_build CHAR
		variant_analysis_calls_vcf_file CHAR
AR • G		transcript_sequences_file CHAR
o_end_dist FLOAT		miRNA_differential_expression_files
dist FLOAT \\		id INT
FLOAT		sub_id CHAR
d_dist_st_dev FLOAT 📵		cl_id CHAR
st_dev FLOAT 📄 \ \	/ /	

substrate

sub_id CHAR

matrix CHAR

cell_line

id INT

substrate CHAR
stiffness CHAR

integrin_ligand CHAR

cl_id CHAR

cell_line CHAR

disease CHAR

tissue CHAR

P

exome_sequencing_files

raw_fastqc_files CHAR

trim_fastqc_files CHAR

nt_sequences_fa_file CHAR

coding_sequences_fa_file CHAR

peptide_translation_aa_file CHAR

variant_analysis_calls_vcf CHAR copy_number_variation_vcf CHAR

exome_variant_analysis_annotation

gene_accession_coordinates_bed_file CHAR

id INT

exome_id INT bam_file CHAR

bai_file CHAR

exome_id INT

position INT

accession INT

rs_ID INT

function_GVS INT

function_dbSNP INT

protein_position INT

cDNA_position CHAR

grantham_score CHAR

score_phast_cons CHAR
cons_score_GERP CHAR

dbSNP_validation CHAR

repeat_masker CHAR

tandem_repeat CHAR

kegg_pathway CHAR

cpg_islands CHAR

amino_acids CHAR
poly_phen FLOAT

african_hap_map_freq CHAR

asian_hap_map_freq CHAR

distance_to_splice CHAR

has_genotype CHAR

micro_RNAs CHAR

genome_esp CHAR

protein_sequence CHAR

tfbs CHAR

ppi CHAR

european_hap_map_freq CHAR

dbSNP VARCHAR(255)

ref_base VARCHAR(255)

sample_alleles CHAR
alleles_dbSNP CHAR

chromosome VARCHAR(255)

sample_genotype VARCHAR(255)

P

miRNA_differential_expression_files	
id INT	P
sub_id CHAR	
cl_id CHAR	G
miRNA_differential_expression_id INT	
raw_fastq_files CHAR	
trim_reads_fq_files CHAR	
sorted_25nt_bam_file CHAR	
sorted_25nt_bai_file CHAR	
unmapped_25nt_fq_file CHAR	
miRanalyzer_files CHAR	
NCBI_genome_build CHAR	

miRNA_differential_expression	
id INT	P
sub_id CHAR	F
tissue_1 CHAR	
tissue_2 CHAR	
miRNA_accession_id CHAR	
base_mean FLOAT	
log2_fold_change FLOAT	
IfcSE FLOAT	
stat FLOAT	
p_value FLOAT	
p_adj FLOAT	
NCBI_genome_build CHAR	

miRNA_mapping	
id INT	P
sub_id CHAR	
cl_id CHAR	
raw_fastq_file CHAR	
NCBI_genome_build CHAR	

nRNA_gene_transcript_map		
id INT	P	
sub_id CHAR		
cl_id CHAR		
raw_fastq_files CHAR		
NCBI_genome_build CHAR		
sorted_STAR_bam_file CHAR		
sorted_STAR_bai_file CHAR		

exome_sequencing_summary	
id INT	P
sub_id CHAR	
cl_id CHAR	
num_exons INT	
total_size_exons INT	
longest_exon INT	
shortest_exon INT	
mean_exon_size INT	
median_exon_size INT	
N50_exon_length INT	
L50_exon_count INT	
exon_percent_A FLOAT	
exon_percent_C FLOAT	
exon_percent_G FLOAT	
exon_percent_T FLOAT	
exon_percent_N FLOAT	
exon_percent_GC FLOAT	
exon_percent_other_nt FLOAT	
exon_num_other_nt FLOAT	
mean_exon_completeness FLOAT	
mean_exon_coverage_per_base FLOAT	

NCBI_genome_build CHAR

$mRNA seq_variant_call_annotation$
id INT
mRNAseq_id INT
HUGO_symbol VARCHAR(255)
Chromosome VARCHAR(255)
Start_position INT
End_position INT
Reference_Allele VARCHAR
Variant_Classification VARCHAR
Variant_Type CHAR
Mutation_Status CHAR
Exon_Number INT
Transcript_ID INT
Protein_Position CHAR
Codons CHAR
BIOTYPE CHAR

miRNA_mapping_annotation
id INT
miRNA_mapping_id INT
miRDeep2_score FLOAT
provisional_id CHAR
true_positive_prob CHAR
rfam_alert CHAR
total_read_count INT
mature_read_count INT
loop_read_count INT
star_read_count INT
significant_randfold_p_value FLOAT
miRBase_miRNA VARCHAR(255)
same_seed_example_miRBase_miRNA VARCHAR(255)
UCSC_browser VARCHAR(255)
NCBI_blastn VARCHAR(255)
consensus_mature_seq CHAR
consensus_star_seq CHAR
consensus_precursor_seq CHAR
precursor_coordinate CHAR
novel BOOLEAN
mature BOOLEAN

miRNA_mapping_summary	
id INT	(
miRNA_mapping_id INT	(
miRDeep2_score FLOAT	
novel_miRNAs_reported INT	
novel_miRNAs_false_positive_est CHAR	
novel_miRNAs_true_positive_est CHAR	
known_miRNAs_total INT	
known_miRNAs_data INT	
known_miRNA_detected INT	
SNR_est FLOAT	
excision_gearing INT	

mRNA_gene_transcript_annotation	
id INT	P
mRNA_gene_transcript_map_id INT	
gene_id VARCHAR(255)	
transcript_ids CHAR	
length FLOAT	
effective_length FLOAT	
expected_count INT	
TPM FLOAT	
FPKM FLOAT	
	id INT mRNA_gene_transcript_map_id INT gene_id VARCHAR(255) transcript_ids CHAR length FLOAT effective_length FLOAT expected_count INT TPM FLOAT

	exome_structural_variants
	id INT
\langle	exome_id INT
	cluster_id CHAR
	left_chromosome INT
	left_breakpoint CHAR
	right_chromosome INT
	right_breakpoint CHAR
	num_prs INT
	localization FLOAT
	type VARCHAR(255)

exome_mutation_annotation	
id INT	P
exome_id INT	
HUGO_symbol VARCHAR(255)	
Chromosome VARCHAR(255)	
Start_position INT	
End_position INT	
Reference_Allele VARCHAR	
Variant_Classification VARCHAR	
Variant_Type CHAR	
Mutation_Status CHAR	
Exon_Number INT	
Transcript_ID INT	
Protein_Position CHAR	
Codons CHAR	
BIOTYPE CHAR	