motility	
id INT	P
sub_id CHAR	G
cl_id CHAR	
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	
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	

substrate

sub_id CHAR

substrate CHAR

stiffness CHAR

matrix CHAR

cell_line

integrin_ligand CHAR

cl_id CHAR

cell_line CHAR

disease CHAR

tissue CHAR

Q D

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

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

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

cpg_islands CHAR
amino_acids CHAR
poly_phen FLOAT

dbSNP VARCHAR(255)

ref_base VARCHAR(255)

sample_alleles CHAR

alleles_dbSNP CHAR

chromosome VARCHAR(255)

sample_genotype VARCHAR(255)

Q D

morphology	
id INT	₽
sub_id CHAR	
cl_id CHAR	
aspect_ratio FLOAT	
circularity FLOAT	
area FLOAT	

proliferation	
id INT	₽
sub_id CHAR	
cl_id CHAR	
plate INT	
trial INT	
single INT	
touching INT	
frame_num INT	

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

proteomics_iBAQ		
id INT		G
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	

replicate IN I	
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 FLOAT

	mRNA_sequencing_files
	id INT
\mathcal{H}	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
	transcript_sequences_file CHAR
	miRNA_differential_expression_files

	miRNA_differential_expression_files	
	id INT	
\forall	sub_id CHAR	
	cl_id CHAR	
	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
\dashv	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	

mRNA_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 FLOA	Г

NCBI_genome_build 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

miRNA_mapping_id INT
miRDeep2_score FLOAT

transcript_ids CHAR

expected_count INT

effective_length FLOAT

length FLOAT

TPM FLOAT

FPKM 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	
mRNA_gene_transcript_map_id INT	
gene id VARCHAR(255)	

	exome_structural_variants
	id INT
\in	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)