

ReporterExpression		
P	* reporter_expression_id	Integer
F	protocol_app_node_id	Integer
F	reporter_id	Integer
	value	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 ReporterExpression_PK (reporter_expression_id)		

NaFeatureExpression		
P	* na_feat_expression_id	Integer
F	* protocol_app_node_id	Integer
	* na_feature_id	Integer
	value	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 NaFeatureExpression_PK (na_feat_expression_id)		

RnaExpression		
P	* rna_expression_id	Integer
F	protocol_app_node_id	Integer
	* rna_id	Integer
	value	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 RnaExpression_PK (rna_expression_id)		

GeneExpression		
P	* gene_expression_id	Integer
F	protocol_app_node_id	Integer
F	gene_id	Integer
	value	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 GeneExpression_PK (gene_expression_id)		

ProteinExpression		
P	* protein_expression_id	Integer
F	protocol_app_node_id	Integer
	* protein_id	Integer
	value	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 ProteinExpression_PK (protein_expression_id)		

FamilyExpression		
P	* family_expression_id	Integer
F	protocol_app_node_id	Integer
	* family_id	Integer
	value	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 FamilyExpression_PK (family_expression_id)		

SegmentResult		
P	* segment_result_id	Integer
F	protocol_app_node_id	Integer
	na_sequence_id	Integer
	start	Integer
	end	Integer
	on_reverse_strand	Boolean (1)
	na_feature_id	Integer
	genetic_location	VARCHAR (30)
	score1	FLOAT
	score2	FLOAT
	p_value	FLOAT
	fdr	FLOAT
	confidence	FLOAT
	standard_error	FLOAT
	categorical_value	VARCHAR (100)
🔗 SegmentResult_PK (segment_result_id)		

SegmentDiffResult		
P	* segment_diff_res_id	Integer
F	protocol_app_node_id	Integer
	na_sequence_id	Integer
	start	Integer
	end	Integer
	on_reverse_strand	Boolean (1)
	na_feature_id	Integer
	mean1	FLOAT
	sd1	FLOAT
	mean2	FLOAT
	sd2	FLOAT
	fold_change	FLOAT
	test_statistic	FLOAT
	p_value	FLOAT
	adj_p_value	FLOAT
	q_value	FLOAT
	fdr	FLOAT
	confidence_up	FLOAT
	confidence_down	FLOAT
🔗 SegmentDiffResult_PK (segment_diff_res_id)		

EditingEvent		
P	* editing_event_id	Integer
F	protocol_app_node_id	Integer
	na_sequence_id	Integer
	start	Integer
	end	Integer
	na_feature_id	Integer
F	editing_type_id	Integer
	alternate_sequence	VARCHAR (200)
	frequency	FLOAT
	p_value	FLOAT
🔗 EditingEvent_PK (editing_event_id)		

ReporterDiffExpr

RnaDiffExpr

NaFeatureDiffExpr

GeneDiffExpr		
P	* gene_diff_expr_id	Integer
F	protocol_app_node_id	Integer
F	gene_id	Integer
	mean1	FLOAT
	sd1	FLOAT
	mean2	FLOAT
	sd2	FLOAT
	fold_change	FLOAT
	test_statistic	FLOAT
	p_value	FLOAT
	adj_p_value	FLOAT
	q_value	FLOAT
	fdr	FLOAT
	confidence_up	FLOAT
	confidence_down	FLOAT
	time_max	VARCHAR (100)
	time_min	VARCHAR (100)
🔗 GeneDiffExpr_PK (gene_diff_expr_id)		

ProteinDiffExpr

FamilyDiffExpr

SnpResult		
P	* snp_result_id	Integer
F	protocol_app_node_id	Integer
	name	VARCHAR (30)
	na_sequence_id	Integer
	location	Integer
	na_feature_id	Integer
F	external_database_release_id	Integer
	source_id	VARCHAR (50)
	description	VARCHAR (4000)
F	taxon_id	Integer
	reference_na	VARCHAR (4000)
	reference_strain	VARCHAR (4000)
	reference_aa	VARCHAR (4000)
	major_allele	VARCHAR (4000)
	major_product	VARCHAR (4000)
	minor_allele	VARCHAR (4000)
	minor_product	VARCHAR (4000)
	strains	VARCHAR (4000)
	strains_revcomp	VARCHAR (4000)
	major_allele_count	Integer
	minor_allele_count	Integer
	is_coding	Boolean (1)
	position_in_cds	Integer
	position_in_protein	Integer
	has_nonsynonymous_allele	Boolean (1)
🔗 SnpResult_PK (snp_result_id)		

GeneSimilarity		
P	* gene_similarity_id	Integer
F	protocol_app_node_id	Integer
F	gene1_id	Integer
F	gene2_id	Integer
	* similarity	FLOAT
🔗 GeneSimilarity_PK (gene_similarity_id)		

SegmentProximity		
P	* segment_proximity_id	Integer
F	protocol_app_node_id	Integer
	na_sequence_id1	Integer
	start1	Integer
	end1	Integer
	on_reverse_strand1	BLOB
	na_feature_id1	Integer
	na_sequence_id2	Integer
	start2	Integer
	end2	Integer
	on_reverse_strand2	Boolean (1)
	ns_feature_id2	Integer
	* score	FLOAT
🔗 SegmentProximity_PK (segment_proximity_id)		