

Physical Data Model	
Model:	alignDB
Package:	
Diagram:	alignDB
Author:	vagrant
Date:	1/19/2016
Version:	

chromosome			
<u>chr_id</u>	int	<pk>	
common_name	char(64)		
taxon_id	int		
chr_name	char(64)		
chr_length	int		

target			
<u>target_id</u>	int	<pk>	
seq_id	int	<fk>	

query			
<u>query_id</u>	int	<pk>	
seq_id	int	<fk>	
query_strand	char(1)		
query_position	int		

reference			
<u>ref_id</u>	int	<pk>	
seq_id	int	<fk>	
ref_raw_seq	longtext		
ref_complex_indel	text		

sequence			
<u>seq_id</u>	int	<pk>	
align_id	int	<fk2>	
chr_id	int	<fk1>	
chr_start	int		
chr_end	int		
chr_strand	char(1)		
seq_length	int		
seq_seq	longtext		
seq_gc	double		
seq_runlist	text		

indel			
<u>indel_id</u>	int	<pk>	
<u>prev_indel_id</u>	int	<pk>	
align_id	int	<fk>	
indel_start	int		
indel_end	int		
indel_length	int		
indel_seq	text		
indel_all_seqs	text		
indel_ref_seq	text		
left_extand	int		
right_extand	int		
indel_gc	double		
indel_freq	int		
indel_occured	text		
indel_type	char(8)		
indel_slippage	double		
indel_coding	double		
indel_repeats	double		

isw			
<u>isw_id</u>	int	<pk>	
indel_id	int	<fk>	
prev_indel_id	int	<fk>	
isw_indel_id	int		
isw_start	int		
isw_end	int		
isw_length	int		
isw_type	char(8)		
isw_distance	int		
isw_density	int		
isw_differences	int		
isw_pi	double		
isw_target_gc	double		
isw_average_gc	double		
isw_cv	double		
isw_d_indel	double		
isw_d_noindel	double		
isw_d_complex	double		
isw_d_bii	double		
isw_d_bnn	double		
isw_d_indel2	double		
isw_d_noindel2	double		
isw_d_complex2	double		
isw_d_bii2	double		
isw_d_bnn2	double		
isw_d_indel3	double		
isw_d_noindel3	double		
isw_d_complex3	double		
isw_d_bii3	double		
isw_d_bnn3	double		
isw_coding	double		
isw_repeats	double		
isw_cpg_pi	double		

snp			
<u>snp_id</u>	int	<pk>	
isw_id	int	<fk2>	
align_id	int	<fk1>	
snp_pos	int		
target_base	char(1)		
query_base	char(1)		
all_bases	text		
ref_base	char(1)		
mutant_to	char(64)		
snp_freq	int		
snp_occured	text		
snp_coding	double		
snp_repeats	double		
snp_cpg	double		

align			
<u>align_id</u>	int	<pk>	
align_length	int		
align_comparables	int		
align_identities	int		
align_differences	int		
align_gaps	int		
align_ns	int		
align_error	int		
align_pi	double		
align_indels	int		
align_target_gc	double		
align_average_gc	double		
align_comparable_runlist	text		
align_indel_runlist	text		
align_coding	double		
align_repeats	double		
align_coding_runlist	text		
align_repeats_runlist	text		

ssw			
<u>ssw_id</u>	int	<pk>	
snp_id	int	<fk2>	
window_id	int	<fk1>	
ssw_type	char(8)		
ssw_distance	int		
ssw_d_snp	double		
ssw_d_nosnp	double		
ssw_d_complex	double		

meta			
<u>meta_id</u>	int	<pk>	
meta_key	text		
meta_value	text		

gene		
<u>gene_id</u>	int	<pk>
window_id	int	<fk>
gene_stable_id	char(64)	<ak>
gene_external_name	char(64)	
gene_biotype	char(64)	
gene_strand	char(1)	
gene_is_full	int	
gene_is_known	int	
gene_multitrans	int	
gene_multitexons	int	
gene_tc_runlist	text	
gene_tl_runlist	text	
gene_description	text	
gene_feature4	double	
gene_feature5	double	

codingsw		
<u>codingsw_id</u>	int	<pk>
exon_id	int	<fk1>
prev_exon_id	int	<fk1>
window_id	int	<fk2>
codingsw_type	char(8)	
codingsw_distance	int	
codingsw_cv	double	

exon		
<u>exon_id</u>	int	<pk>
<u>prev_exon_id</u>	int	<pk>
window_id	int	<fk1>
gene_id	int	<fk2>
exon_stable_id	char(64)	<ak>
exon_strand	char(1)	
exon_phase	int	
exon_end_phase	int	
exon_frame	int	
exon_rank	int	
exon_is_full	int	
exon_tl_runlist	text	
exon_seq	longtext	
exon_peptide	longtext	

segment		
<u>segment_id</u>	int	<pk>
window_id	int	<fk>
segment_type	char(8)	
segment_gc_mean	double	
segment_gc_std	double	
segment_gc_cv	double	
segment_gc_mdcw	double	

extreme		
<u>extreme_id</u>	int	<pk>
<u>prev_extreme_id</u>	int	<pk>
window_id	int	<fk>
extreme_type	char(8)	
extreme_left_amplitude	double	
extreme_right_amplitude	double	
extreme_left_wave_length	int	
extreme_right_wave_length	int	

gsw		
<u>gsw_id</u>	int	<pk>
extreme_id	int	<fk2>
prev_extreme_id	int	<fk2>
window_id	int	<fk1>
gsw_type	char(8)	
gsw_distance	int	
gsw_distance_crest	int	
gsw_wave_length	int	
gsw_amplitude	double	
gsw_trough_gc	double	
gsw_crest_gc	double	
gsw_gradient	double	
gsw_cv	double	

window		
<u>window_id</u>	int	<pk>
align_id	int	<fk>
window_start	int	
window_end	int	
window_length	int	
window_runlist	text	
window_comparables	int	
window_identities	int	
window_differences	int	
window_indel	int	
window_pi	double	
window_target_gc	double	
window_average_gc	double	
window_coding	double	
window_repeats	double	
window_ns_indel	double	

ofg		
<u>ofg_id</u>	int	<pk>
window_id	int	<fk>
ofg_tag	char(64)	
ofg_type	char(64)	

ofgsw		
<u>ofgsw_id</u>	int	<pk>
ofg_id	int	<fk1>
window_id	int	<fk2>
ofgsw_type	char(8)	
ofgsw_distance	int	
ofgsw_cv	double	