



taxon		
<u>taxon_id</u>	int	<pk>
genus	text	
species	text	
sub_species	text	
common_name	text	
classification	text	

chromosome		
<u>chr_id</u>	int	<pk>
taxon_id	int	<fk>
chr_name	text	
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	longtext	
left_extand	int	
right_extand	int	
indel_gc	double	
indel_freq	int	
indel_occured	char(128)	
indel_type	char(8)	
indel_slippage	double	
indel_coding	double	
indel_repeats	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_te	double	
align_paralog	double	
align_coding_runlist	text	
align_repeats_runlist	text	
align_te_runlist	text	
align_paralog_runlist	text	

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_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	char(128)	
ref_base	char(1)	
mutant_to	char(128)	
snp_freq	int	
snp_occured	char(128)	
snp_coding	double	
snp_repeats	double	
snp_cpg	double	

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	

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_multiexons	int	
gene_tc_runlist	text	
gene_tl_runlist	text	
gene_description	text	
gene_go	char(64)	
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	

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

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	

window		
<u>window_id</u>	int	<pk>
<u>align_id</u>	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	

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_wave_length	int	
gsw_amplitude	double	
gsw_trough_gc	double	
gsw_gradient	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	