



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

sequence			
<u>seq_id</u>	int	<pk>	
align_id	int	<fk2>	
chr_id	int	<fk1>	
seq_role	char(8)		
seq_position	int		
common_name	char(64)		
chr_name	char(64)		
chr_start	int		
chr_end	int		
chr_strand	char(1)		
seq_length	int		
seq_gc	double		
seq_runlist	text		
seq_seq	longtext		

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_outgroup_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		

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_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		

isw			
<u>isw_id</u>	int	<pk>	
indel_id	int	<fk1>	
prev_indel_id	int	<fk1>	
align_id	int	<fk2>	
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_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		

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

snp			
<u>snp_id</u>	int	<pk>	
isw_id	int	<fk2>	
align_id	int	<fk1>	
snp_pos	int		
snp_target_base	char(1)		
snp_query_base	char(1)		
snp_all_bases	text		
snp_outgroup_base	char(1)		
snp_mutant_to	char(64)		
snp_freq	int		
snp_occured	text		
snp_coding	double		
snp_repeats	double		
snp_cpg	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		

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	text		
exon_peptide	text		

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_gc	double		
window_coding	double		
window_repeats	double		

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		

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		

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		