



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	

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	

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

tvsql		
<u>tvsql_id</u>	int	<pk>
target_taxon_id	int	
target_name	text	
query_taxon_id	int	
query_name	text	
ref_taxon_id	int	
ref_name	text	

align		
<u>align_id</u>	int	<pk>
tvsql_id	int	<fk>
align_length	int	
comparable_bases	int	
identities	int	
differences	int	
gaps	int	
ns	int	
align_error	int	
pi	double	
align_target_gc	double	
align_average_gc	double	
comparable_runlist	text	
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	

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	
indel_insert	char(1)	
left_extand	int	
right_extand	int	
indel_gc	double	
indel_dG	double	
indel_occured	char(1)	
indel_type	char(1)	

snp_extra		
<u>snp_extra_id</u>	int	<pk>
snp_id	int	<fk>
snp_feature1	double	
snp_feature2	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)	
ref_base	char(1)	
snp_occured	char(1)	
snp_coding	double	
snp_repeats	double	
snp_cpg	double	

indel_extra		
<u>indel_extra_id</u>	int	<pk>
indel_id	int	<fk>
prev_indel_id	int	<fk>
indel_feature1	double	
indel_feature2	double	
indel_feature3	double	

isw		
<u>isw_id</u>	int	<pk>
indel_id	int	<fk>
prev_indel_id	int	<fk>
isw_start	int	
isw_end	int	
isw_length	int	
isw_type	char(1)	
isw_distance	int	
isw_density	int	
isw_pi	double	
isw_target_gc	double	
isw_average_gc	double	
isw_target_dG	double	
isw_query_dG	double	
isw_d_indel	double	
isw_d_noindel	double	
isw_d_complex	double	
isw_cpg_pi	double	

ssw		
<u>ssw_id</u>	int	<pk>
snp_id	int	<fk2>
window_id	int	<fk1>
ssw_type	char(1)	
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		

genesw			
<u>genesw_id</u>	int	<pk>	
window_id	int	<fk2>	
gene_id	int	<fk1>	
genesw_type	char(1)		
genesw_distance	int		

exonsw			
<u>exonsw_id</u>	int	<pk>	
window_id	int	<fk2>	
exon_id	int	<fk1>	
prev_exon_id	int	<fk1>	
exonsw_type	char(1)		
exonsw_distance	int		
exonsw_density	int		

codingsw			
<u>codingsw_id</u>	int	<pk>	
exon_id	int	<fk1>	
prev_exon_id	int	<fk1>	
window_id	int	<fk2>	
codingsw_type	char(1)		
codingsw_distance	int		

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		

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		

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_target_dG	double		
window_query_dG	double		
window_coding	double		
window_repeats	double		
window_ns_indel	double		

segment			
<u>segment_id</u>	int	<pk>	
window_id	int	<fk>	
segment_type	char(1)		
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(1)		
extreme_left_amplitude	double		
extreme_right_amplitude	double		
extreme_left_wave_length	double		
extreme_right_wave_length	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(1)		
ofgsw_distance	int		

gsw			
<u>gsw_id</u>	int	<pk>	
extreme_id	int	<fk2>	
prev_extreme_id	int	<fk2>	
window_id	int	<fk1>	
gsw_type	char(1)		
gsw_distance	int		
gsw_density	int		
gsw_amplitude	int		

