



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		

