



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(8)	
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(8)	
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(8)	
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	

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	double	
extreme_right_wave_length	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_density	int	
gsw_amplitude	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	

