Table S1. Correlation coefficients among the studied variables: the level of neutral polymorphism (θ_{neu}), he level of normalized neutral polymorphism (P_{neu}=θ_{neu}/d_{neu}), recombination rate (RR), GC content (GC), the density of simple repeats (RD), the depth of sequencing coverage (SC), the divergence at coding sites (D_n), the divergence at conserved noncoding region (D_x), the number of codons (FD_n), the number of conserved noncoding sites (FD_x), and the level of neutral divergence (d_{neu}). Spearman's ρ and Kendall's τ are given at the upper and lower diagonal parts of the table, respectively. The values of θ_{neu} and P_{neu} are based on the Watson data.

	θ_{neu}	P_{neu}	RR	GC	RD	SC	D_n	D_x	FD_n	FD_x	d_{neu}
θ_{neu}	—	0.9007**	0.3155**	-0.0875**	-0.0775**	0.1183**	-0.1855**	-0.1143**	-0.2247**	-0.2403**	0.3663**
P_{neu}	0.7361**	—	0.2098**	-0.0514**	-0.1086**	0.1364**	-0.1363**	-0.1075**	-0.1290**	-0.1384**	-0.0122 (0.0631)
RR	0.2149**	0.1412**	—	0.3432**	-0.2738**	0.0819**	0.0373**	-0.0519**	0.0189*	-0.0315**	0.3024**
GC	-0.0586**	-0.0342**	0.2351**	—	-0.0554**	-0.4729**	0.5789**	0.1934**	0.6192**	0.5183**	-0.1069**
RD	-0.0520**	-0.0730**	-0.1856**	-0.0370**	—	-0.4839**	0.0300**	0.0622**	-0.0147 (0.0256)	-0.0265**	0.0415**
SC	0.0787**	0.0912**	0.0564**	-0.3175**	-0.3415**	—	-0.4579**	-0.2683**	-0.4321**	-0.3821**	-0.0159 (0.0155)
D_n	-0.1304**	-0.0950**	0.0263**	0.4218**	0.0217**	-0.3279**	—	0.3078**	0.8964**	0.6824**	-0.1550**
D_x	-0.0790**	-0.0742**	-0.0358**	0.1319**	0.0429**	-0.1867**	0.2239**	—	0.3028**	0.4962**	-0.0260**
FD_n	-0.1540**	-0.0872**	0.0136*	0.4479**	-0.0095 (0.0329)	-0.2968**	0.7411**	0.2131**	—	0.8283**	-0.2748**
FD_x	-0.1617**	-0.0921**	-0.0205**	0.3610**	-0.0179**	-0.2587**	0.5099**	0.3519**	0.6533**	—	-0.2926**
d_{neu}	0.2553**	-0.0087 (0.0478)	0.2075**	-0.0734**	0.0280**	-0.0099 (0.0242)	-0.1124**	-0.0188**	-0.1903**	-0.1990**	—

** Correlation is significant at the 0.001 level (2-tailed).

* Correlation is significant at the 0.01 level (2-tailed).