

Table 1. Coefficients and Statistics of Poisson Regression Models Describing the Average Number of Breakpoints per Intergene as a Function of Intergene Length, %GC, and %CNE

	Coefficients					Goodness of Fit		
	Simple Regression	Stepwise Regression	P(> z)	Null Deviance (df)	Residual Deviance (df)	c ² p value	Stepwise c ² p value	Pseudo R ²
Model 1: length only								
Intergene length	0.28	—	< 2.10 ^{Å16a}	167.3 (10)	12.4 (9)	0.19 ^a	—	0.93 ^a
Model 2: length + %GC								
Intergene length	0.26	0.27	< 2.10 ^{Å16a}	137.8 (28)	25.7 (27)	0.53 ^a	—	0.81 ^a
%GC	—	0.003	0.44	137.8 (28)	25.1 (26)	0.52	0.42	0.82
Model 3: length + %CNE								
Intergene length	0.28	0.30	< 2.10 ^{Å16a}	179.2 (19)	26.3 (18)	0.09 ^a	—	0.85 ^a
%CNE	—	Å4.55	0.01 ^a	179.2 (19)	20.7 (17)	0.24 ^a	0.02 ^a	0.88 ^a
Simulation: 3D contacts in open chromatin								
Intergene length	0.28	—	< 2.10 ^{Å16}	253.8 (14)	29.6 (13)	0.005	—	0.88

A parameter significantly affecting the breakage rate has a regression coefficient statistically different from 0 (P(> jzj) < 0.05). The goodness of fit of each model is assessed by a c² test on the residual deviance and degrees of freedom (i.e., likelihood ratio test): a non-significant p value means that the residual deviance may be attributed to statistical noise. The effect of an additional parameter on the fit is assessed by a c² test on the difference in residual deviances and degrees of freedom with and without the parameter: a significant p value means that the fit is significantly better with the additional parameter. The pseudo R² corresponds to McFadden’s pseudo R² (proportion of null deviance explained by the model).

For methods, see the [Supplemental Information](#).

^aValues indicative of an improvement in the model.