Modeling ChIP sequencing *in silico* with applications

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Supplementary table 1. The goodness of fit between the simulated and the actual curves. [1]

Among sites		Background			
		Uniform		Varying	
Uniform	**A**	Enrichment coef. t	Mean squared error	**B** Enrichment coef. t	Mean squared error
		5	1.586998897	5	0.990667305
		10	0.863164925	10	0.889633664
		12	0.725042018	12	0.771627405
		15	0.754559600	15	0.679462299
		20	0.629474980	20	0.484540718
		Average	0.911848	Average	0.7631863
Varying	**C**	Enrichment coef. t	Mean squared error	**D** Enrichment coef. t	Mean squared error
		5	0.353800760	5	0.239834829
		10	0.092974392	10	0.004265812
		12	0.090004782	12	0.007199094
		15	0.103924481	15	0.021765468
		20	0.131689485	20	0.042511183
		Average	0.1544788	Average	0.06311528

1. See Figure 4 for the corresponding curves in each panel.