



Supplemental Figure 1. Transcription elongation rates in K562 cells are not related to two- or three-dimensional localization. (A) Correlation between the elongation rate of a particular gene and the elongation rate of its nearest expressing neighbor. Data point frequency illustrated by a colored contour plot where solid line indicates a linear regression model. (B) Elongation rates of genes in relationship their two-dimensional chromosomal location. Genes were divided into four equal-sized groups according to ranked elongation rates (from slowest to fastest: black circles, blue squares, green diamonds, red triangles) and their chromosomal location are denoted for each chromosome. (C) Correlation between elongation rates and three-dimensional association using ChIA-PET data for K562 cells from ENCODE. Data point frequency illustrated by a colored contour plot where solid line indicates a linear regression model.