

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: IDs and links to Hi-C, ChIP-seq, and RNA-seq datasets used in this study

File Name: Supplementary Data 2

Description: Complete domain hierarchies inferred by CALDER from 127 Hi-C contact maps

File Name: Supplementary Data 3

Description: Percentage of the genome assigned to each sub-compartment by Calder and SNIPER for 38 Hi-C datasets.

File Name: Supplementary Data 4

Description: Correlation between sub-compartment calls and gene expression for SNIPER and CALDER

File Name: Supplementary Data 5

Description: Matrix of sub-compartment domain assignments for 127 Hi-C contact maps used for the clustering analysis in Figure 3

File Name: Supplementary Data 6

Description: Gene set enrichment analysis (mSigDB) results for high entropy ($S > 0.95$) and low entropy ($S < 0.15$) genes

File Name: Supplementary Data 7

Description: Repositioned compartment domains between normal and cancer cell lines derived from breast, prostate, and pancreatic tissue samples