Supplementary Figure S6



Supplementary Figure S6

A., B. and C. Heatmaps representing dCas9-KRAB signal intensity over all Tigger3a elements present in the human genome in clone 1 (A), clone2 (B) and clone 3 (C) dCas9-KRAB 22Rv1 cells (each obtained from two independent nucleofections with Tigger3a gRNAs combination). D. and E. Violin plots showcasing the dCas9-KRAB signal intensity over top 25% Tigger3a elements compared to matched flanking 1.5kb regions in clone 1 (D) and clone 3 (E) dCas9-KRAB dCas9-KRAB cells (upstream = -1.5kb, downstream = +1.5kb - right panel). p-value results of wilcoxon test are showcased on the violin plot.

F., G. and H. Heatmaps representing dCas9-KRAB signal intensity over all Tigger3b or Charlie7 elements present in the human genome in dCas9-KRAB 22Rv1 clone 1 (F), clone 2 (G) and clone 3 (H) (each obtained from two independent nucleofections with Tigger3a gRNAs combination).

I., J. and K. dCas9-KRAB signal difference among transposable element families. Violin plots showcasing the level of dCas9-KRAB signal over the top 25% elements for Tigger3a, Tigger3b and Charlie7 transposable element families. p-value results of wilcoxon test are showcased on the violin plot.

L., M. and N. Distribution of dCas9-KRAB signal over the entire set of Tigger3a elements. Every dot corresponds to one Tigger3a element. Red and and dotted vertical lines identify the quartile of Tigger3a elements with high dCas9-KRAB signal (top 25%) and the quartile with low dCas9-KRAB signal (bottom 25%) in dCas9-KRAB 22Rv1 clone 1 (L), clone 2 (M) and clone 3 (N).

O., P. and Q. Violin plots showcasing the dCas9-KRAB signal intensity over bottom 25% Tigger3a elements compared to matched flanking 1.5kb regions (upstream = -1.5kb, downstream = +1.5kb) in dCas9-KRAB 22Rv1 clone 1 (O), clone 2 (P) and clone 3 (Q). p-value results of wilcoxon test are showcased on the violin plots.

R. and S. Violin plots showcasing the H3K27ac signal distribution in clone 1 (R) and clone 3 (S) dCas9-KRAB 22Rv1 cells nucleofected with Control (gray) or Tigger3a (purple) gRNAs combinations over Tigger3a elements with high dCas9-KRAB signal (top 25%) or low dCas9-KRAB signal (bottom 25%). p-value results of wilcoxon test are showcased on the violin plot.

T. and U. H3K27ac signal over top 25% dCas9-KRAB bound Tigger3a elements in clone 1 (T) and clone 3 (U) dCas9-KRAB 22Rv1 cells nucleofected with Control or Tigger3a gRNA combinations. Every dot corresponds to one Tigger3a element, x-axis represents the log2 of the normalized H3K27ac signal intensity in two independent nucleofection with Control gRNAs combination, while the y-axis represents the log2 normalized H3K27ac signal intensity in two independent nucleofection with Control gRNAs combination, while the y-axis represents the log2 normalized H3K27ac signal intensity in two independent nucleofection with Tigger3a gRNAs combination.

V., W. and X. Violin plot showcasing the H3K27ac signal distribution in clone 1 (V), clone 2 (W) and clone 3 (X) dCas9-KRAB 22Rv1 cells nucleofected with Control (gray) or Tigger3a (purple) gRNAs combinations over Tigger3b or Charlie7 elements with high dCas9-KRAB signal (top 25%). p-value results of wilcoxon test are showcased on the violin plot.