**Diagram, schematic

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**Supplementary Figure 4: Weak correlation of TE expression induction with DNA methylation change and viral mimicry activation.** **A.** Boxplot illustrating the average TE expression (counts per million) in tumor samples. Dotted lines connect tumor pairs from same patient. **B.** Heatmaps representing the average DNA methylation change, intergenic LTR/LINE expression fold-change and viral mimicry gene expression fold-change comparing pre-treatment and post-treatment UC tumors from this study. **C.** Correlation between TE expression fold-change and DNA methylation change induced by combination therapy.