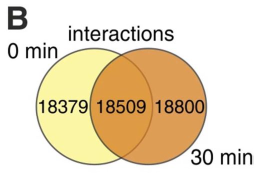
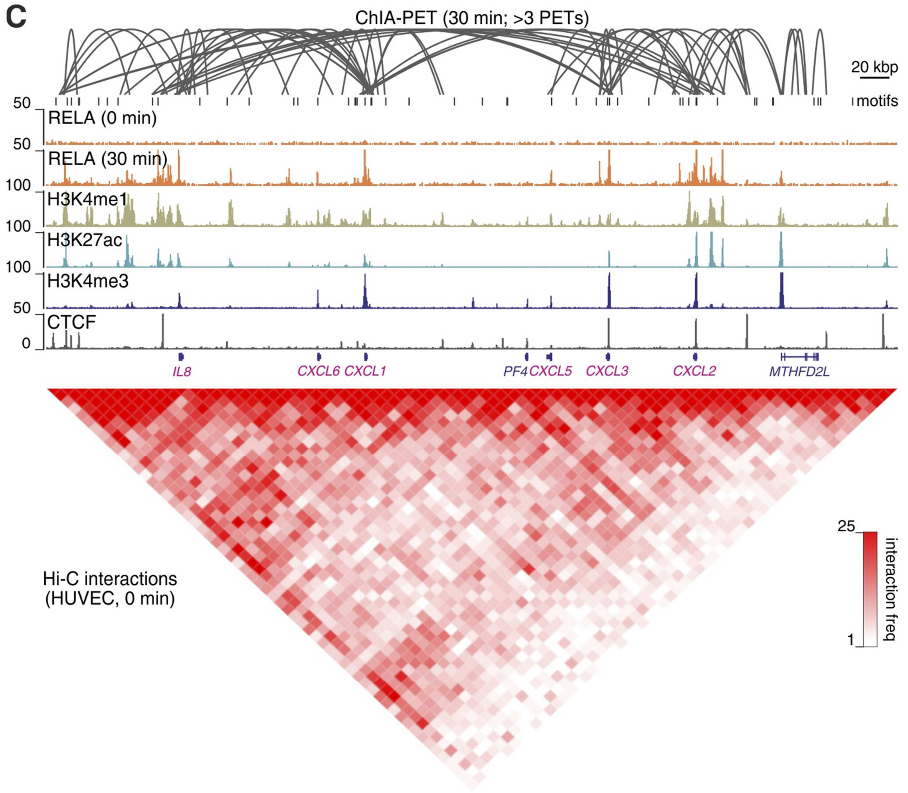
A

ChIA-PET datasets

library ID	total reads	mapped reads	total interactions	>3 PETs
0 min	35,9 million	10,8 million	1,529,513	36,888
30 min	36,4 million	8,8 million	1,547,177	37,309





Supplemental Fig. S3. Features of the RNAPII–ChIA-PET data from HUVECs stimulated with TNF for 0 or 30 min. ChIA-PET was performed using antisera against active RNA polymerase II isoforms for pulling-down chromatin complexes. (***A***) Details on the total numbers of generated and successfully mapped reads after sequencing the 0- and 30-min ChIA-PET libraries (Papantonis et al. 2012). The total number of interactions detected, and those used in the analysis here (supported by ≥3 PETs) are also shown. (***B***) The Venn diagram depicts the number of unique and shared interactions between the 0- and 30-min ChIA-PET filtered datasets. (***C***) A typical view of ChIA-PET interaction maps showing the 30-min contacts that develop in a 0.5-Mbp locus carrying TNF-responsive genes. The Hi-C contact map shown below (25-kbp resolution; Rao et al. 2014) is in agreement with the ChIA-PET data.