



Supplemental Fig. S5. Validation of TF ChIP-seq. (A). Western Blot of 8 chromatin factors that were profiled by ChIP-seq (Fig. 6a) at indicated times after VEGFA stimulation. Phosphorylation of ERK indicated activation by VEGFA. Appearance of N1CD, the intracellular domain of NOTCH1, illustrated the activation of NOTCH signaling. (B). Summary of the number of regions occupied by the indicated transcriptional regulator at H0, H1, H4, and H12. (C) Motifs enriched among regions bound by the indicated factor at the indicated time point following VEGFA treatment. (D). ChIP-qPCR validating the static and ynamic sites of ETS1 and FLI1. (E). Correlation test of static and dynamic peaks of 8 examined TFs across time. H0 peaks have stronger correlation with peaks from other three time points in static clusters than in unique clusters, indicating more dramatic changes at dynamic peaks.