



Supplemental Figure 2. Differential Remodeling of the Enhancer Landscape is Associated with the Transcriptional Response to Trametinib. (A) Quantification of cell cycle analysis following 24 hr treatment with DMSO or 30 nM trametinib. POS cells in G1 indicated by light blue, S in blue, G2 in dark blue. NEG cells in G1 indicated in pink, S in red, G2 in dark red. (B) Comparison of gene expression following trametinib treatment in POS subpopulation FACS-sorted from SUM-229PE with POS cells cultured in isolation for 6 weeks (left). Pearson correlation coefficient = 0.90. Comparison of gene expression following trametinib treatment in NEG subpopulation FACS-sorted from SUM-229PE with NEG cells cultured in isolation for 6 weeks (right). Pearson correlation coefficient = 0.92. (C) Unique differential gene expression in POS cells in response to acute trametinib treatment. Significant genes with a minimum mean expression of 25 reads and greater than two-fold difference in expression with a p-value < 0.05 are highlighted (UP indicated in blue, DOWN in light blue). (D) GO analysis of the molecular function of genes identified in Fig. S2C. Log2 fold change in expression of genes in the most enriched GO terms identified in upregulated genes (blue), and downregulated genes (light blue). (E) Unique differential gene expression in NEG cells in response to acute trametinib treatment. Significant genes with a minimum mean expression of 25 reads and greater than two-fold difference in expression with a p-value < 0.05 are highlighted (UP indicated in red, DOWN in pink). (F) GO analysis of the molecular function of genes identified in Fig. S2E. Log2 fold change in expression of genes in the most enriched GO terms identified in upregulated genes (red), and downregulated genes (pink).