



Fig. S2. ESRR A inhibition induces antitumor immunity *in vivo*.

(A, B) Validation of BipotentR-identified targets. (A) Effect of knockout/knockdown of target identified by BipotentR on expression of genes in energy metabolism pathways. (B) Gene expression changes in energy metabolism pathways by knockout of bipotent (immune-metabolic) TFCRs vs. other TFCRs. (C, D) Benchmarking BipotentR against other TFCR identification approaches: Effect of knockout/knockdown of target identified by BipotentR on the expression of genes in energy metabolism pathways benchmarked with (C) LISA-identified and (D) BARTWeb-identified targets. (E) Effect of knockout of target identified by BipotentR on T-cell mediated killing of cancer cells. (F, G) Effect of concentration on proximity (alphascreen signal) between compounds (39 and 29) and ligand-binding domain of WT or mutated ESRR A. (H) The distribution of ESRR A regulatory potentials (sum of ChIP-seq signal weighted by distance from target transcription start sites) for background genes and genes inhibited by siRNA knockdown or drug inhibition of ESRR A. (I, J) LISA analysis of up- and down-regulated gene sets by ESRR A inhibition through drug (I) or siRNA (J). (K) ESRR A expression in tumor infiltrating immune cells in 4T1 mouse model.

(L) The relative proportion of CD8⁺ T cells and Tregs in the T-cell populations between ESRRAi and control groups in scRNA-seq data. (M) The change in tumor volume over time in ESRRAi and control B16F10 mice (n =10 per group). (N) The correlation between tumor volume and fraction of active CD8⁺ T cells for the ESRRAi treated mice. (O, P) Macrophage polarity shifted by ESRRAi shown by M1 (O) and M2 (P) marker expression density. (Q) Differentially expressed genes of macrophages between ESRRAi and control mice. Labeled genes are M1 and M2 markers. P-value estimated by permutation test (Methods). (R) The change of tumor volumes over time (days) in mice after removing tumors by surgery.