Index supplemental tables:

Based on our functional data we aimed to identify three types of gene regulation that mirror a) cell type independent regulation after MPA in both sensitive cell types HDMVEC and Fibroblasts b) endothelial cell specific response to MPA c) fibroblast specific MPA response.

a) The co-regulated genes in MPA sensitive cell types were selected by two sided t-test, HDMVEC and Fibroblats vs. U87 $p<0.01$ after 1000 permutations and standard Bonferroni correction, combined with correlation analysis using Pavlidis template matching (PTM, correlation coefficient >0.74) (supplemental table a).

b) The predominant expression pattern found was a gradient of gene regulation from the most MPA sensitive endothelial cells (up- or down-regulation) to fibroblasts (intermediate regulation) to the resistant U87 glioblastoma (no- or inverse regulation compared to HDMVEC over time, at 6 and 12 h post treatment). Therefore, we performed significance analysis of microarray (SAM) using the gradient of gene regulation from endothelial cell over fibroblasts to U87 as the template. Genes were selected based on 1000 permutations and a false discovery rate (FDR) $\leq 5\%$ (supplemental table b).

c) Fibroblast specific genes were selected based on their differential regulation after MPA treatment in fibroblasts vs. other cell types. T-test with 1000 permutations were performed ($p<0.01$, supplemental table c).

For all tables: ratios = $\lg_2$, MPA treatment/control.