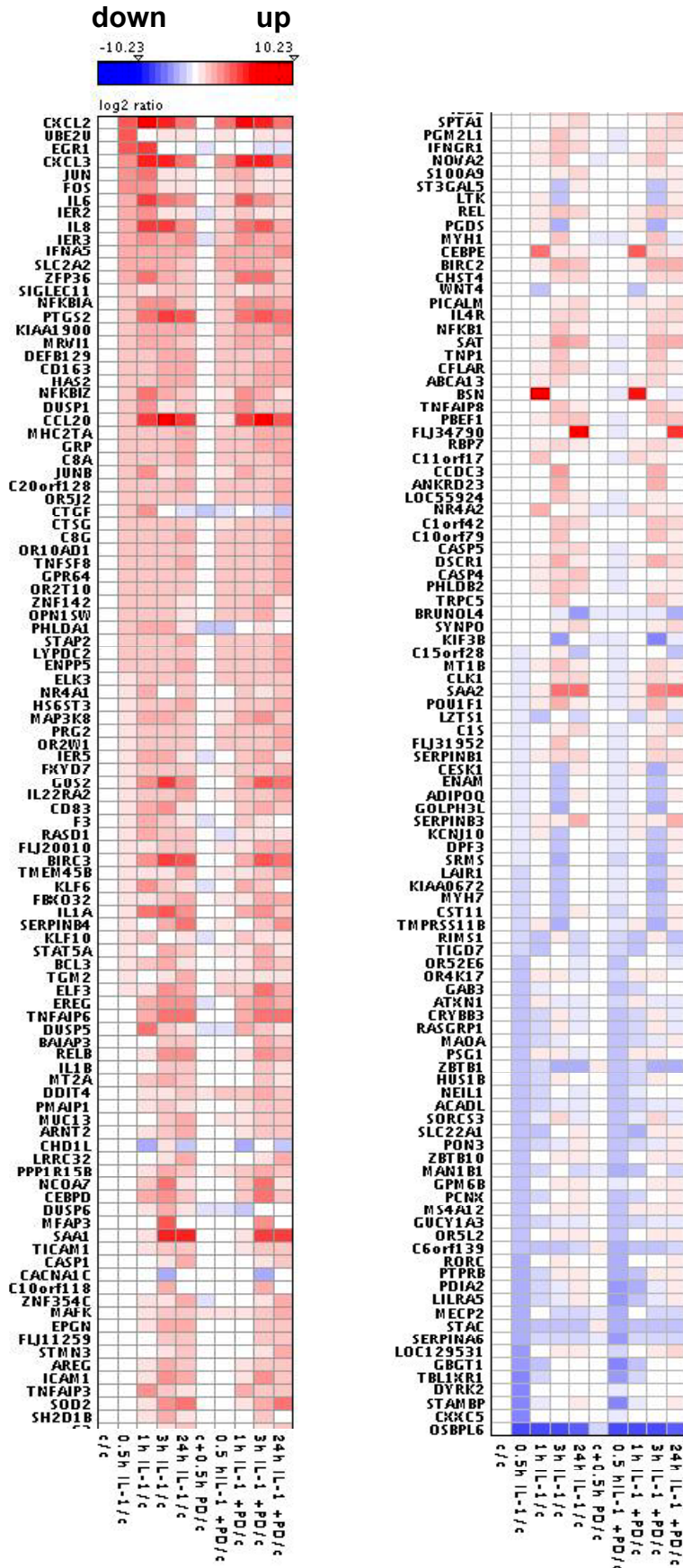




Example for genome wide analysis of IL-1-induced mRNA expression in human epidermal carcinoma KB cells.

Agilent 22k array experiments were performed using total RNA from experiments described in Fig.1 in Hoffmann et al., J.Biol.Chem., 2005). Arrays were filtered for genes that are repressed or induced by IL-1 at 0.5, 1, 3, and 24h of stimulation by at least 3-fold. 221 out of 295 genes had unique identifiers and were selected. Ratios of values from IL-1-treated samples against the unstimulated control (IL-1/c) were log2 transformed and sorted by regulation in response to IL-1 at 0.5, 1 and 3h of stimulation. Note the strong suppression of EGR1 and CTGF by the ERK inhibitor PD98059. Genes that are suppressed by at least 50% by PD are indicated. Ratio data are visualized as heat maps using mayday (<http://www.zbit.uni-tuebingen.de/pas/mayday/> Version 2.1). Mikroarray experiments were performed by Oliver Dittrich-Breiholz and Heike Schneider from the Cytokine Mikroarray Project, Medical School Hannover. Analysis and visualization was done by Axel Weber.