**Master Regulator Analysis**

Gene-regulatory network inference from expression data has become a valuable method to describe transcriptional relationships characterizing a well-defined phenotypic state (1). It has been shown that transcriptional events behind complex cellular processes can be explained by the action of relatively few transcription factors, termed as Master Regulators (2). The identification of most influencing factors driving a determined phenotypic state by inferring them from a gene-regulatory network is known as Master Regulator Analysis (MRA) (3-4). In this study, MRA was performed by comparing interferon treated samples, in the presence of TEPA and interferon only treated cells with the mra algorithm included in the corto R package (5), using default parameters and a neuroblastoma co-expression network. Before MRA, VST-normalized genes whose expression showed a variance less than 0.01 throughout the dataset were filtered out from the analysis (6). The neuroblastoma network was generated by applying the corto algorithm to the high-risk neuroblastoma RNA-seq dataset from the TARGET Project (7) using a list of 1191 unique transcriptional regulators.

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