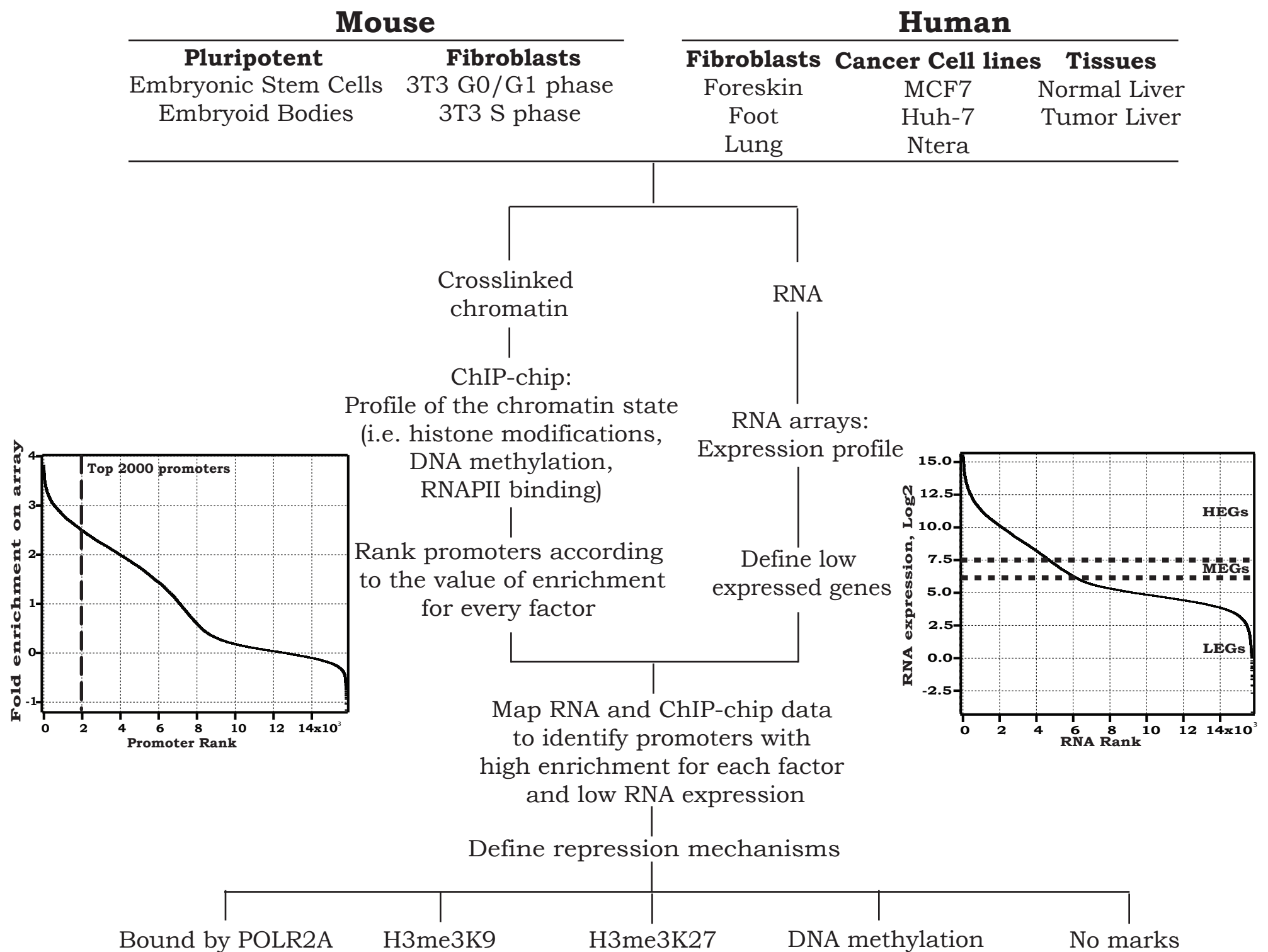


Figure S1. Experimental Flow Chart



The different mouse and human cell lines and the types of analyses performed in this study are shown. Regions on the promoter arrays bound by the individual factors were determined using the Maxfour peak calling method (see Methods). These regions were ranked according to the fold enrichment value and the top 2000 promoters were considered. RNA expression data was ranked according to the p-value (see Methods) and three different expression categories were obtained: low expressed genes (LEGs; $0.05 \leq p\text{-value} \leq 1$), middle expressed genes (MEGs; $0 < p\text{-value} < 0.05$) and highly expressed genes (HEGs; $p\text{-value} = 0$). RNA expression values on a Log2 scale approximately equal to the defined p-value ranges are shown on the figure.