Cross-talk of epigenetic and transcriptional programs in liver regeneration

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The capacity of the liver to regenerate is likely to be encoded as a plasticity of molecular networks within the liver. We found that histone H3K4 was tri-methylated at the promoter regions of many loci during liver regeneration, among which only a fraction including cell-cycle-related genes were transcriptionally up-regulated. A cistrome analysis guided by the histone methylation patterns and the transcriptome identified FOXM1 as a key transcription factor promoting liver regeneration. The promoter regions of cell-cycle-related genes and Foxm1 acquired higher levels of H3K4me3, suggesting that epigenetic regulations of these key regulatory genes define quiescence and regeneration of the liver cells.