



Protocol abstract

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Chromatin immunoprecipitation (ChIP) of plant transcription factors followed by sequencing (ChIP-SEQ) or hybridization to whole genome arrays (ChIP-CHIP)

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Abstract

Chromatin immunoprecipitation (ChIP) is a powerful technique to study interactions between transcription factors (TFs) and DNA *in vivo*. For genome-wide *de novo* discovery of TF-binding sites, the DNA that is obtained in ChIP experiments needs to be processed for sequence identification. The sequences can be identified by direct sequencing (ChIP-SEQ) or hybridization to microarrays (ChIP-CHIP). Given the small amounts of DNA that are usually obtained in ChIP experiments, successful and reproducible sample processing is challenging. Here we provide a detailed procedure for ChIP of plant TFs, as well as protocols for sample preparation for ChIP-SEQ and for ChIP-CHIP. Our ChIP procedure is optimized for high signal-to-noise ratio starting with tissue fixation, followed by nuclei isolation, immunoprecipitation, DNA amplification and purification. We also provide a guide for primary data analysis of ChIP-SEQ data. The complete protocol for ChIP-SEQ/ChIP-CHIP sample preparation starting from plant harvest takes ~7 d.

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