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SALP, a new single-stranded DNA library preparation method especially useful for the high-throughput characterization of chromatin openness states

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Based on a novel kind of single strand adaptor (SSA), this study developed a new method to construct next-generation sequencing (NGS) library, named as SALP, representing single strand adaptor library preparation. The key creativity of the method lies in the design and verification of a special adaptor that can be efficiently linked to the 3' end of single-stranded DNA, which is a double-stranded oligonucleotide with a 3' overhang of 3 random nucleotides. This method can start with the denatured DNAs or chromatins fragmented by different methods such as Tn5 tagmentation, enzyme digestion and sonication. When applied to Tn5-tagmented chromatin, SALP overcomes the key limitation of the current ATAC-seq method and develops a high-throughput NGS library construction and sequencing approach, SALP-seq, which can be used to comparatively characterize the chromatin openness state of multiple cells simply and unbiasedly. In this way, the comparative chromatin openness states of four different cell lines, including GM12878, HepG2, HeLa and 293T, were successfully characterized. This study also demonstrated that SALP-seq could characterize the chromatin openness states with 105 to 500 cells, indicating the high sensitivity of SALP-seq in characterizing chromatin state of cells. SALP could have wide applications in the future biological sciences and biomedicine.

Biography

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