Comparative Assessment of Low Input ChIP-seq Library Kits

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Low input ChIP-seq libraries are often beset by low complexity, a high degree of PCR duplicates and unmappable reads. When preparing quality low input ChIP libraires, optimization of adapter ligation and avoidance of PCR amplification bias must be accounted for. This makes the choice of library preparation kit an important factor to consider. Given the varying underlying methodologies of different library prep kits, which kits will provide the highest quality sequencing data from low input ChIP samples in terms of complexity, duplication rate and mappable reads? To assess the results returned from low input ChIP libraries, we surveyed four different library preparation kits including KAPA's Hyper Prep, Epicypher's CUTANA, IDT's ssDNA and Low Input DNA, and Watchmaker's ER/AT kit and compared the quality of the sequencing data from each. Varying amounts of input DNA ranging from 10ng down to .01ng were utilized and three technical replicants were implemented for each sample of varying input to make statistical analysis possible. The criteria used to assess and compare these kits included duplication rate, alignment rate, map to read percentage, uniquely mapped read percentage, peak comparison and changes in library complexity given varying input amounts.