Chromatin immunoprecipitation (ChIP) followed by next-generation sequencing (ChIP-Seq) has been widely used to identify genomic loci of transcription factor (TF) binding and histone modifications. ChIP-Seq data analysis involves multiple steps from read mapping and peak calling to data integration and interpretation. It remains challenging and time-consuming to process large amounts of ChIP-Seq data derived from different antibodies or experimental designs using the same approach. To address this challenge, there is a need for a comprehensive analysis pipeline with flexible settings to accelerate the utilization of this powerful technology in epigenetics research.