Chromatin immunoprecipitation (ChIP)-sequencing

ChIP assays were done as previously described[10]. Briefly, **2X107** cells were prepared, crosslinked with 1% formaldehyde, unreacted formaldehyde was quenched with 1 ml of 10× glycine, and then lysed with lysate buffer. Sonication was used to break genomic DNA into small DNA fragments. **Anti-FLAG antibody** was added and used to immunoprecipitate DNA fragments corresponding to the promoter regions. Input was used as a control. The DNA fragments bound by proteins were then isolated and sequenced using the Illumina HiSeq X-ten platform (Shanghai Biotechnology Co., China). Sequencing raw reads were preprocessed by filtering out sequencing adapters, short-fragment reads and other low-quality reads. Bowtie (version 0.12.8) was then used to map the clean reads to the human hg19 reference genome. Peak detection was performed by MACS (version 1.4.2; https://pypi.python.org/pypi/MACS/1.4.2). The protein-binding motifs were identified using HOMER software (http://homer.ucsd.edu/homer/).