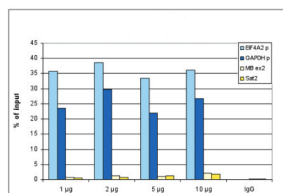
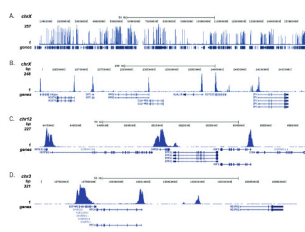


Product no **AS16 3190-10****H3K4me3 | Histone H3, trimethylated lysine 4 (H3K4me3) (10 µg)****Product information****Immunogen** | KLH-conjugated synthetic peptide**Host** | Rabbit**Clonality** | Polyclonal**Purity** | Immunogen affinity purified serum.**Format** | Liquid**Quantity** | 10 µg**Storage** | Store lyophilized/reconstituted at -20°C; once reconstituted make aliquots to avoid repeated freeze-thaw cycles. Please remember to spin the tubes briefly prior to opening them to avoid any losses that might occur from material adhering to the cap or sides of the tube.**Application information****Recommended dilution** | 1-5 µg/IP (ChIP-seq), 1 : 10 000 (Dot), 1 : 100 (ELISA), 1 : 200 (IF), 1 : 2000 (PA), 1 : 1000 (WB)**Confirmed reactivity** | Human**Predicted reactivity** | *Arabidopsis thaliana*, *Solanum lycopersicum*, *Oryza sativa*, *Populus sp.*, *Zea mays***Not reactive in** | No confirmed exceptions from predicted reactivity are currently known**application example**

ChIP assays were performed using human HeLa cells, the antibody against H3K4me3 and optimized PCR primer pairs for qPCR. ChIP was performed with the “Auto Histone ChIP-seq” kit, using sheared chromatin from 1 million cells. A titration consisting of 1, 2, 5 and 10 µg of antibody per ChIP experiment was analyzed. IgG (2 µg/IP) was used as a negative IP control. Quantitative PCR was performed with primers specific for the promoter of the active genes GAPDH and EIF4A2, used as positive controls, and for exon 2 of the inactive myoglobin (MB) gene and the Sat2 satellite repeat, used as negative controls. Figure 1 shows the recovery, expressed as a % of input (the relative amount of immunoprecipitated DNA compared to input DNA after qPCR analysis). These results are in accordance with the observation that trimethylation of K4 at histone H3 is associated with the promoters of active genes.



ChIP-seq was performed on sheared chromatin from 1 million HeLaS3 cells using 1 µg of the anti-H3K4me3 antibodies as described above. The IP'd DNA was subsequently analysed on an Illumina Genome Analyzer. Library preparation, cluster generation and sequencing were performed according to the manufacturer's instructions. The 36 bp tags were aligned to the human genome using the ELAND algorithm. Image shows the peak distribution along the complete sequence and a 600 kb region of the X-chromosome (A and B) and in two regions surrounding the GAPDH and EIF4A2 positive control genes, respectively (C and D). These results clearly show an enrichment of the H3K4 trimethylation at the promoters of active genes.

