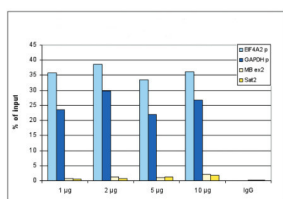
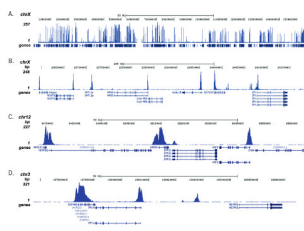


Product no **AS16 3190****H3K4me3 | Histone H3, trimethylated lysine 4 (H3K4me3)****Product information****Immunogen** | KLH-conjugated synthetic peptide**Host** | Rabbit**Clonality** | Polyclonal**Purity** | Antigen affinity purified**Format** | Liquid**Quantity** | 50 µg**Storage** | Store lyophilized/reconstituted 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.**Additional information** | Antibody is provided in PBS containing 0,05% azide and 0,05% ProClin 300 at concentration of 1.3 µg/µl.**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, *Solanum lycopersicum***Predicted reactivity** | *Arabidopsis thaliana*, Mouse, *Oryza sativa*, *Populus sp.*, *Zea mays*  
Species of your interest not listed? [Contact us](#)**Not reactive in** | No confirmed exceptions from predicted reactivity are currently known**Selected references** | [Mursalimov et al. \(2019\)](#). Cytological Techniques to Study Cytomixis in Plant Male Meiosis. *Methods Mol Biol.* 2020;2061:117-129. doi: 10.1007/978-1-4939-9818-0\_9.  
[Liu et al. \(2018\)](#). Transcriptomics analyses reveal the molecular roadmap and long noncoding RNA landscape of sperm cell lineage development. *Plant J.* 2018 Jul 26. doi: 10.1111/tbj.14041.**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

