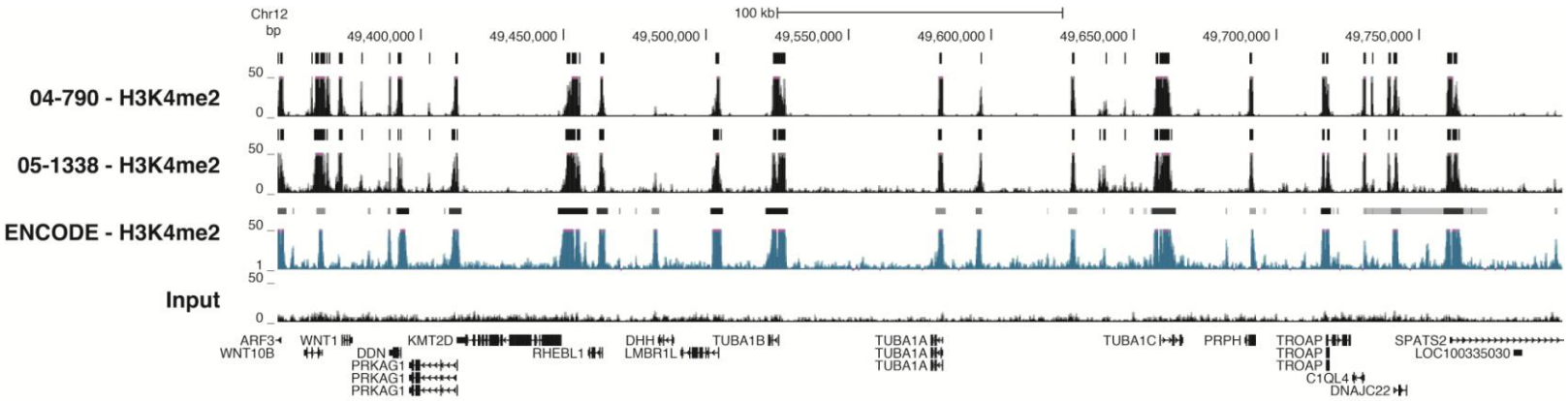

ChIP-seq Analysis

Chromatin immunoprecipitation was performed using the Magna ChIP™ HiSens kit (17-10460), anti-dimethyl-Histone H3 (Lys4) antibody (2 µL of cat# 04-790; 2 µg of cat# 05-1338), 20 µL Protein A/G beads, and 1e6 crosslinked HeLa cell chromatin followed by DNA purification using magnetic beads. Libraries were prepared from Input and ChIP DNA samples using standard protocols with Illumina barcoded adapters, and analyzed on an Illumina HiSeq™ instrument. An excess of sixteen million reads from FastQ files were mapped using Bowtie (http://bowtie-bio.sourceforge.net/manual.shtml) following TagDust (http://genome.gsc.riken.jp/osc/english/dataresource/) tag removal. Peaks were identified using MACS (http://luelab.dfci.harvard.edu/MACS/), with peaks and reads visualized as a custom track in UCSC Genome Browser (http://genome.ucsc.edu) from BigWig and BED files. The highest 25% of peaks identified in the 04-790 and 05-1338 datasets showed 92 and 90% overlap with peaks identified in the ENCODE H3K4me2 BROAD Histone track for HeLa S3. Data in the region of the transcriptionally active housekeeping gene *TUBA1A* (Tubulin, alpha 1A) is shown.