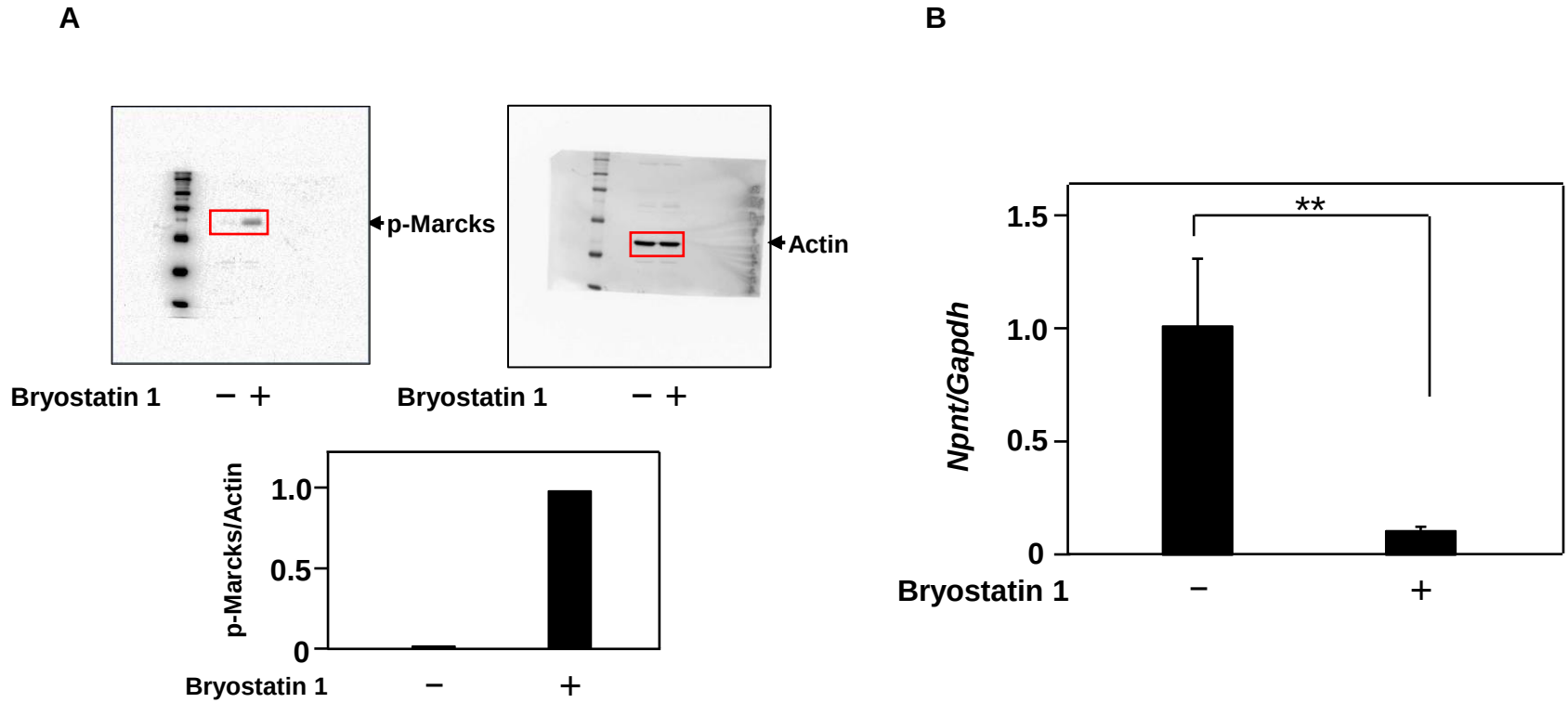
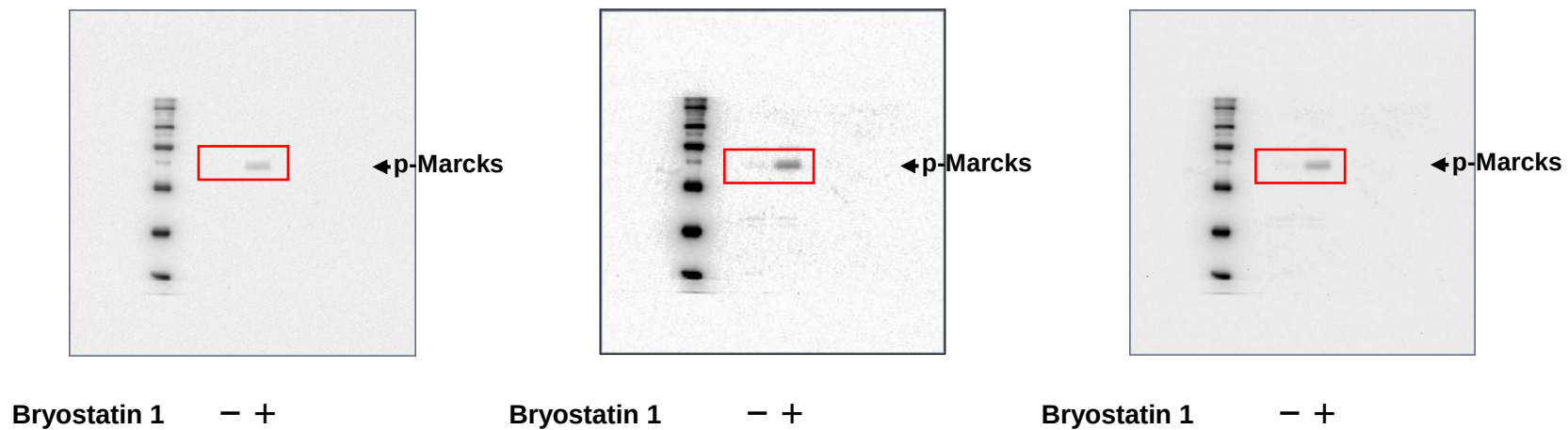




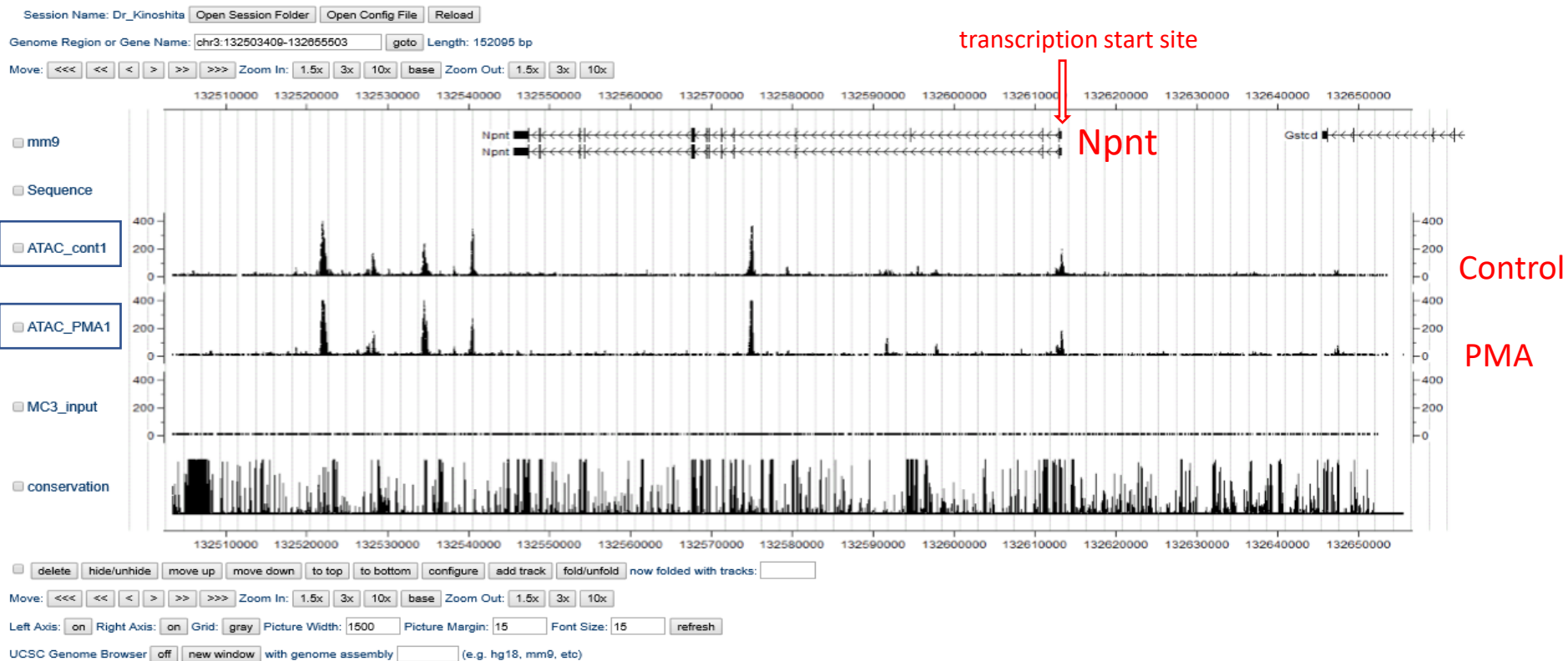
(A) Activation of PKC by Bryostatin 1. MC3T3-E1 cells were starved for 16 hours in serum-free medium. Cells were treated with or without Bryostatin (10 nM) for five minutes, then proteins were extracted and subjected to Western blotting to detect phosphorylation of Marcks (p-Marcks) and Actin.

(B) Effects of Bryostatin 1 on *Npnt* gene expression.

MC3T3-E1 cells were treated with Bryostatin (10 nM) for 24 hours. Total cellular RNA was extracted, and mRNA levels of *Npnt* and *Gapdh* were examined using quantitative real-time PCR analysis. Results are shown as the mean  $\pm$  SD of 3 samples. \*\* $P < 0.01$ , Student's t-test, as compared to presence or absence of Bryostatin 1.



**Appendix Figure 1-1. Multiple exposure images of Appendix Figure 1.**



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The ATAC-seq was performed as described previously [Buenrostro JD et al., *Nat Methods*. 2013 Dec; 10(12):1213-8.]. Briefly, MC3T3-E1 cells were treated in the absence or presence of PMA (100nM) for 24 hours, and then 50,000 cells were collected and lysed with lysis buffer containing 10 mM Tris-HCl, 10 mM NaCl, 3 mM MgCl<sub>2</sub>, and 0.1% IGEPAL CA-630. Tn5 transposase reaction using the Tagment DNA Enzyme 1 (TDE1) (Illumina) was carried out at 37 ° C for 30 min. The reacted DNA was purified using QIAGEN MinElute PCR purification kit and amplified for 8–15 cycles to produce libraries for sequencing. The ATAC-seq libraries were sequenced on Illumina HiSeq X sequencer. The sequence reads were aligned to the mouse genome reference sequence mm9 by bowtie aligner [Langmead B et al., *Genome Biol*. 2009; 10(3):R25.]. Peak calling was performed by two-sample analysis on CisGenome software [Ji H et al., *Nat Biotechnol*. 2008 Nov; 26(11):1293-300.].