Supplementary

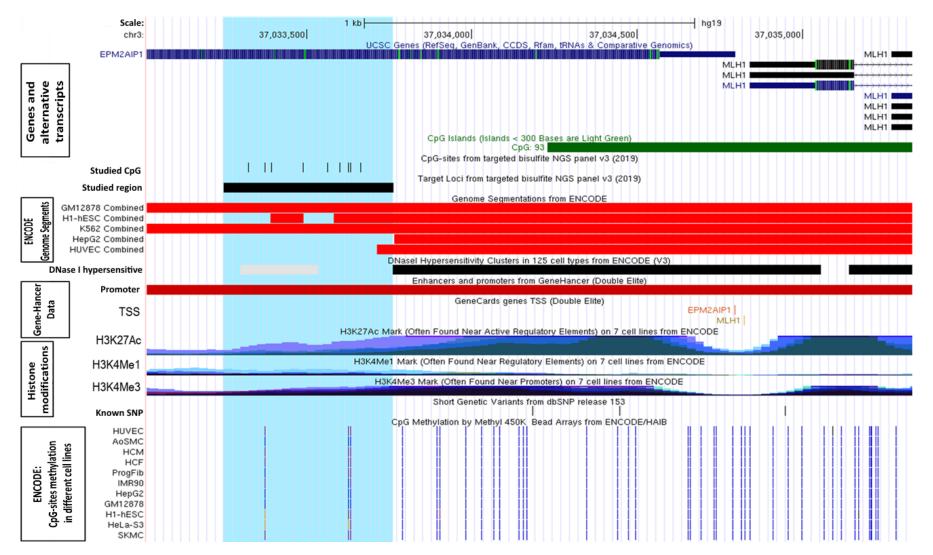


Figure 1 - Localization and epigenetic context of the studied MLH1 gene promoter region. The region studied is highlighted in blue. The designation of human cell lines studied in the ENCODE project: GM12878 - B cell derived cell line, H1-hESC - human embryonic stem cell line, K562 - cells derived from a patient with chronic myeloid leukemia in blast crisis, HepG2 - hepatoma cells, HUVEC - human umbilical vein endothelial cells, AoSMC - aortic smooth muscle cells, HCM - human cardiac myocytes, HCF - human cardiac fibroblasts, ProgFib - skin fibroblasts from a patient with Hutchinson-Gilford progeria syndrome, IMR90 - human fetal lung fibroblast cell line, HeLa-S3 - human cervical adenocarcinoma cells, SKMC - skeletal muscle cells (according to http://www.genome.ucsc.edu/)

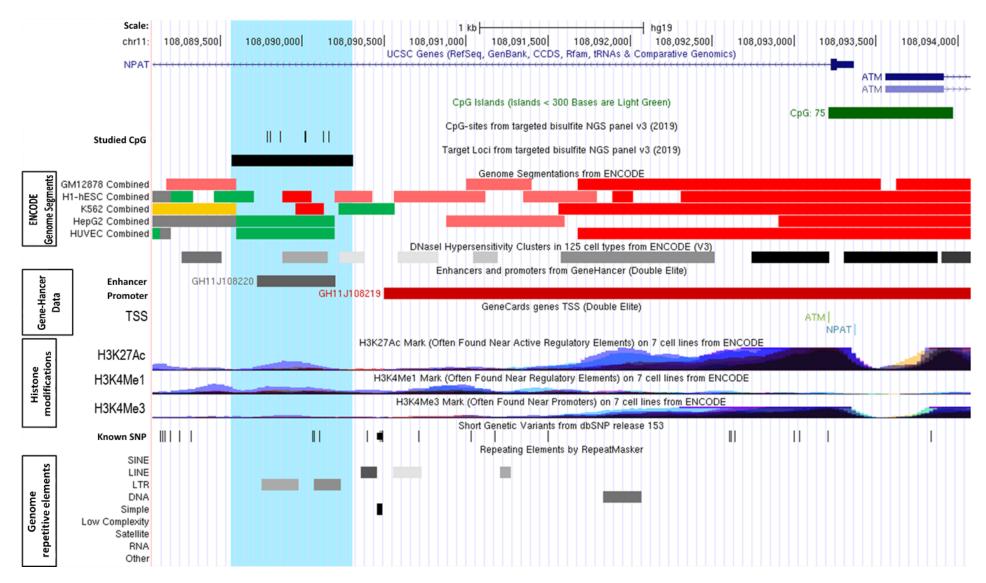


Figure 2 - Localization and epigenetic context of the putative ATM gene enhancer. The region studied is highlighted in blue, TSS means the transcription start site. The designation of human cell lines studied in the ENCODE project: GM12878 - B cell derived cell line, H1-hESC - human embryonic stem cell line, K562 - cells derived from a patient with chronic myeloid leukemia in blast crisis, HepG2 - hepatoma cells, HUVEC - human umbilical vein endothelial cells (according to http://www.genome.ucsc.edu/)