



Figure S10. Mean coverage (relative to the genome average) by DNase I hypersensitive zones, as a function of the distance to the closest U-domain border in H0287 (blue solid line : DNase GM06990, genome-wide mean value = 0.0107), in TL010 (blue dashed line : DNase GM06990, genome-wide mean value = 0.0107), in BJ R1 (light blue solid line : DNase BJtert, genome-wide mean value = 0.0164), in BJ R2 (light blue dashed line : DNase BJtert, genome-wide mean value = 0.0164), in HeLa R1 (magenta solid line : DNase HeLa S3, genome-wide mean value = 0.0136), in HeLa R2 (magenta dashed line : DNase HeLa S3, genome-wide mean value = 0.0136).