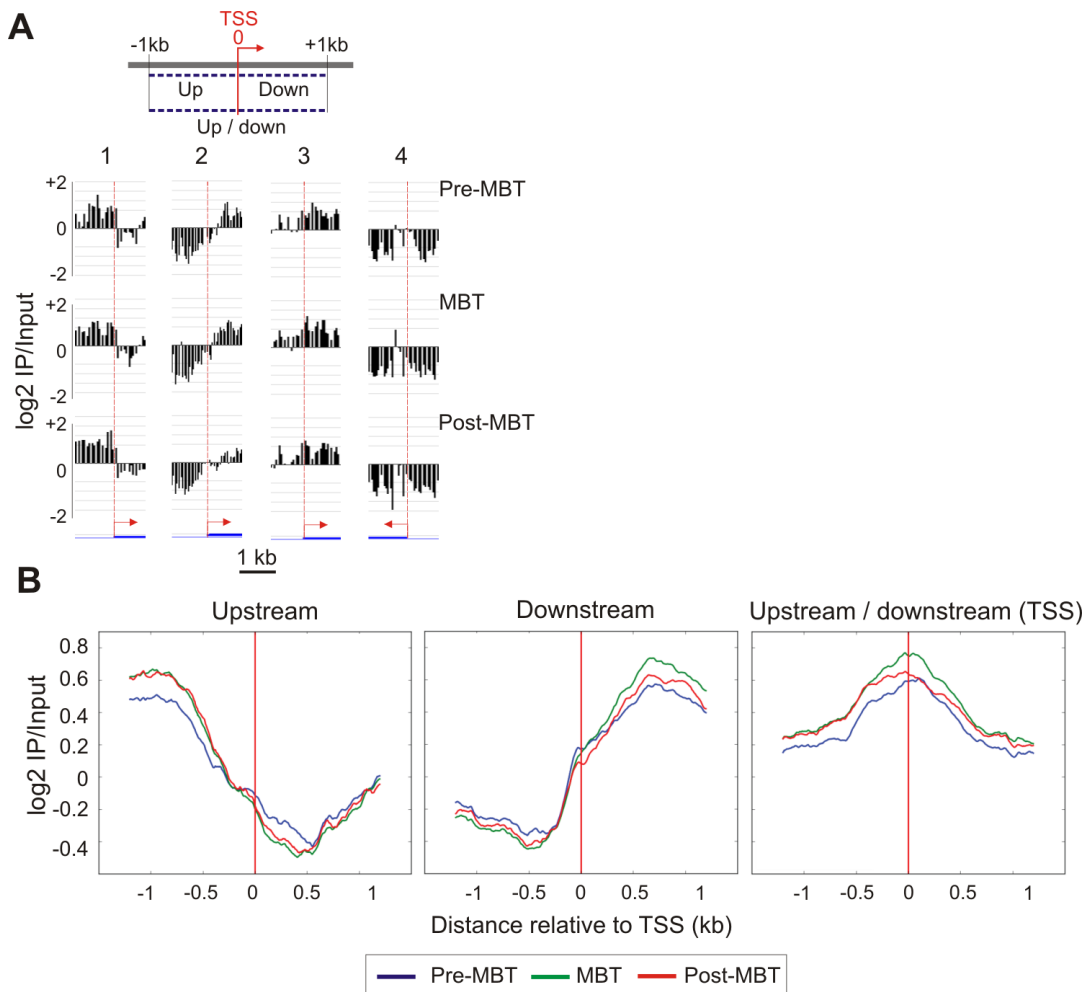




Additional file 4. Partitioning of tiled regions reveals developmentally-linked dynamic methylation upstream of TSS. **(A)** Partitioning of the -1 to +1 kb region relative to the TSS, and browser representation of (1) upstream methylation (ENSDART00000037383), (2) downstream methylation (*zgc:56306*), (3) up/downstream methylation (*atf7ip*) and (4) no methylation (*lef1*). Blue marls (bottom track) indicates genes; red arrows indicate TSSs. **(B)** Metagene profiles of average DNA methylation in upstream, downstream and upstream/downstream partitions at the pre-MBT, MBT and MBT stages.