Figure S7

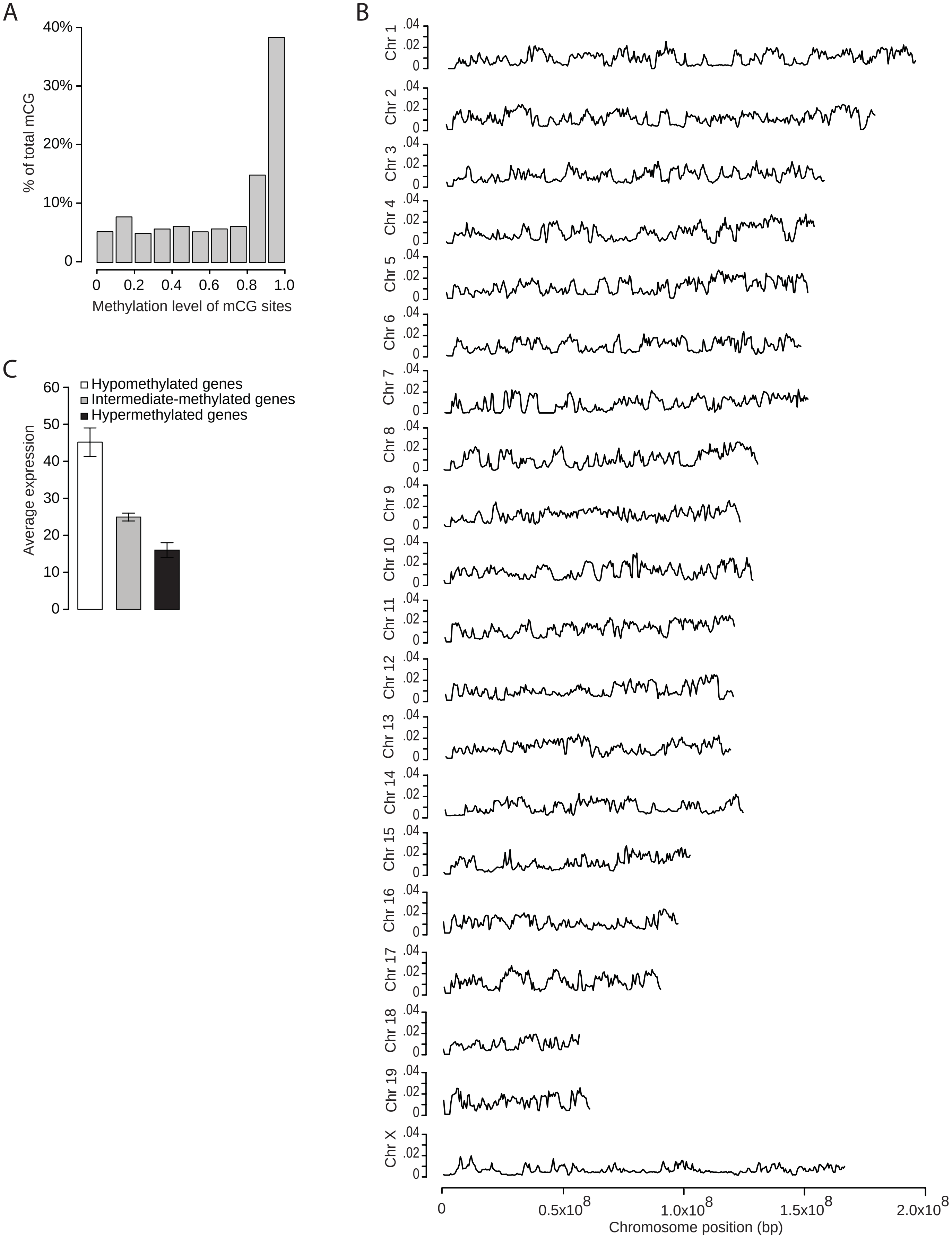

Figure S7. Global DNA methylation patterns in 129TF. **A.** Histogram of methylation level of mCG sites. Methylation level is measured by the number of methylcytosine reads divided by the number of total reads at a cytosine site in a CG context (only sites with at least one methylcytosine read and at least 5 total reads are included). **B.** Methylation profile across all chromosomes. Y-axis is mCG density per base pair; X-axis is chromosome positions in base pairs. **C.** Promoter methylation is anti-correlated with expression. Genes are classified based on promoter methylation levels as described in the main text. Expression level is measured in TPG.