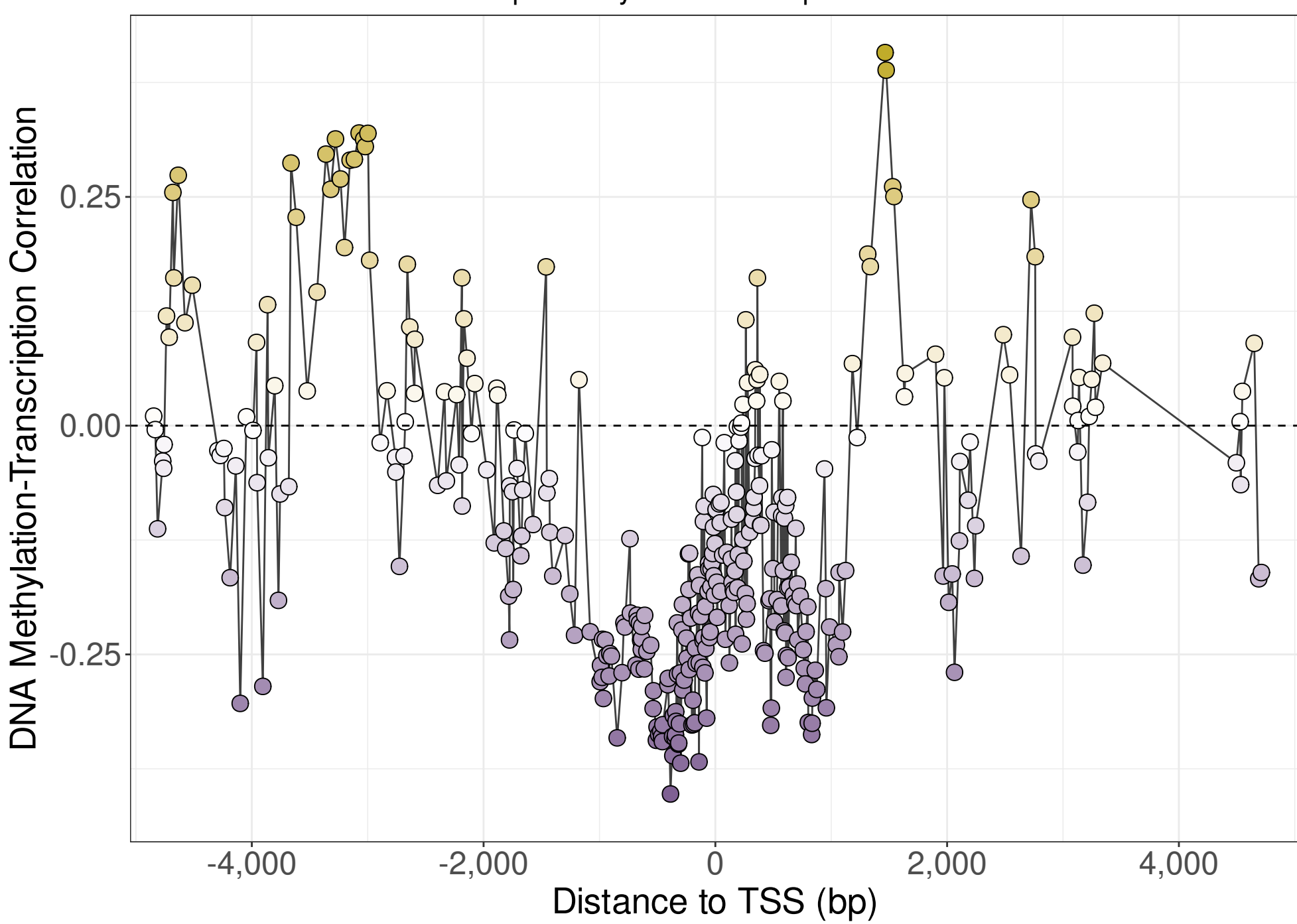
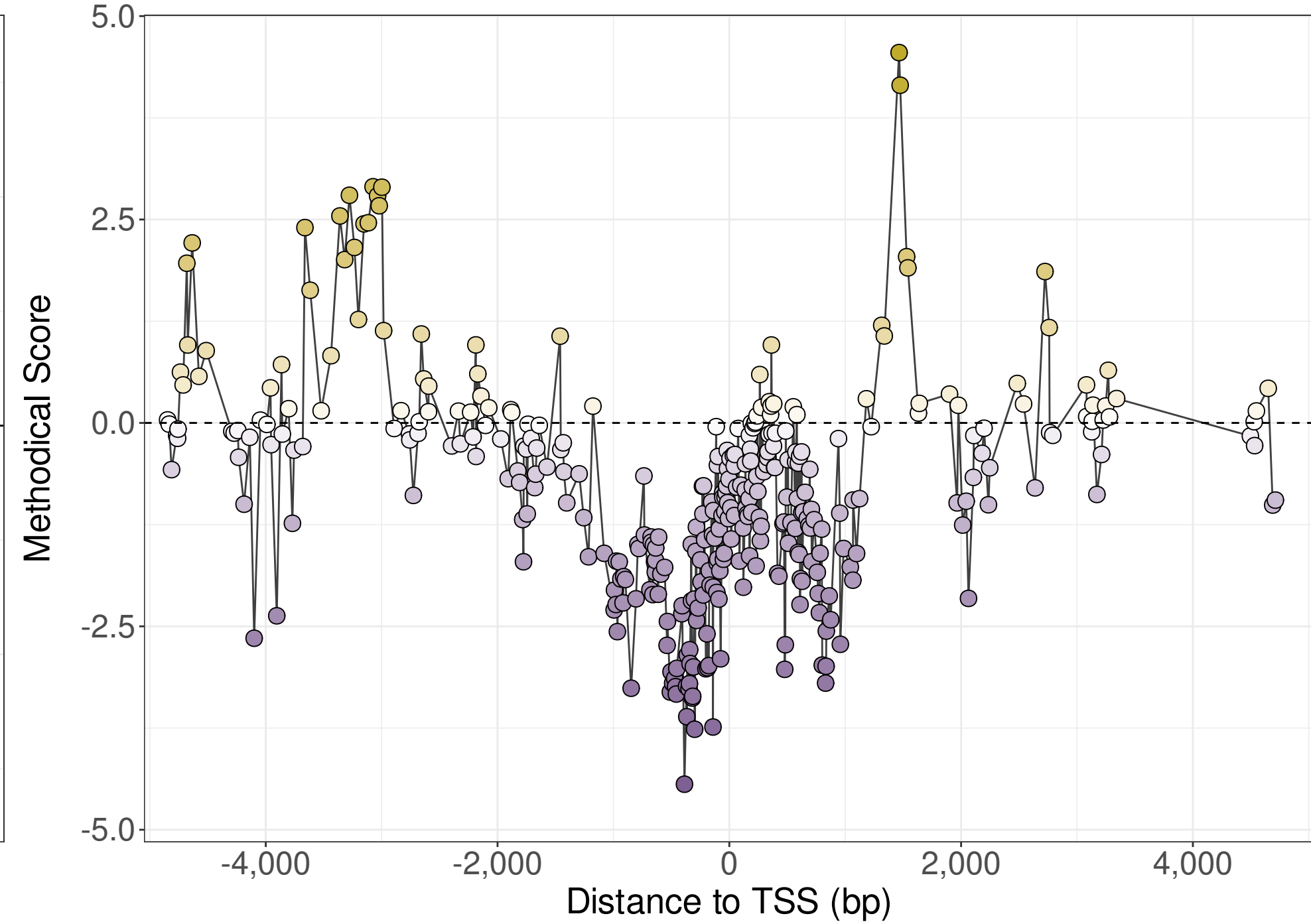


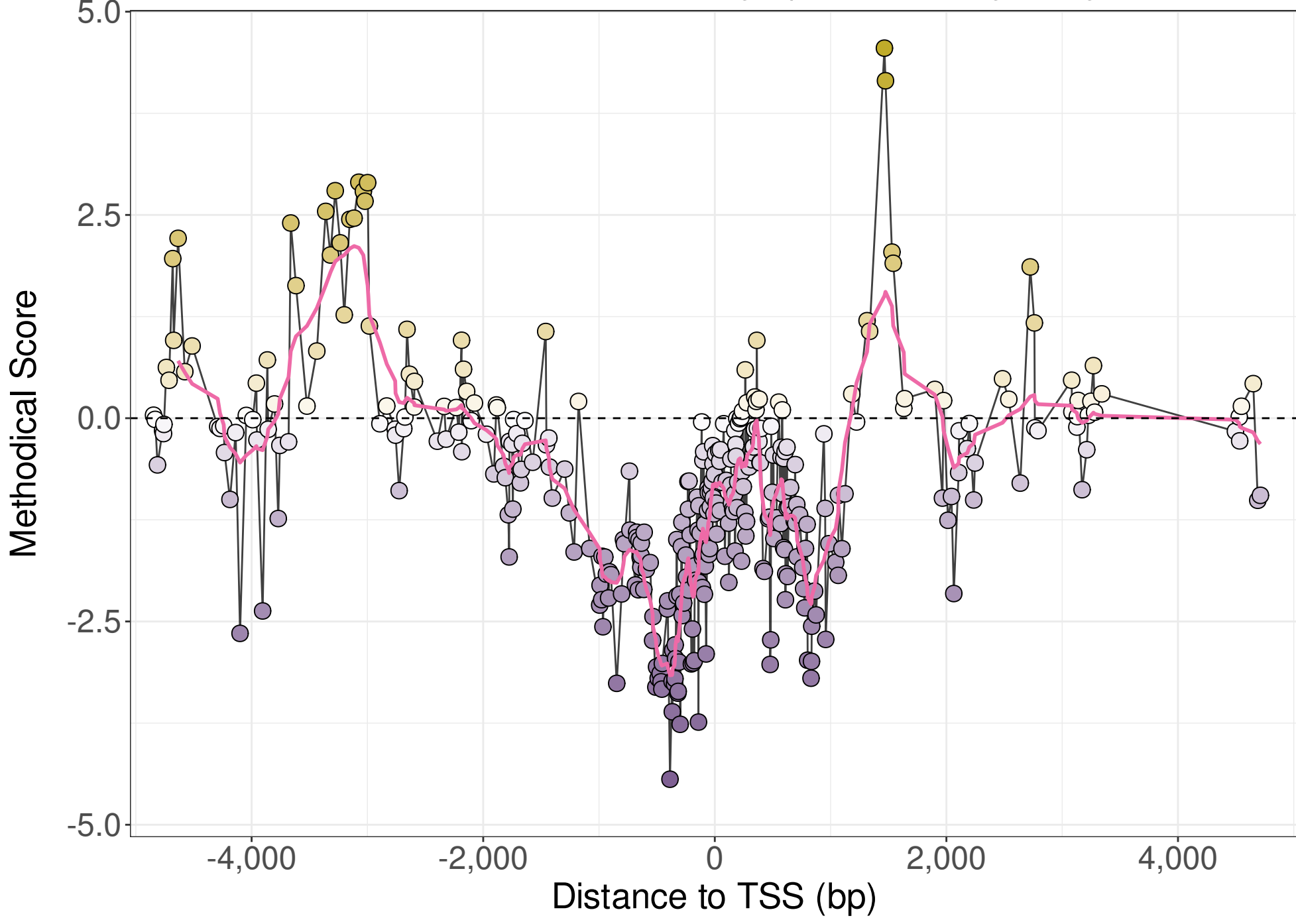
1: Calculate CpG methylation-transcription correlation values



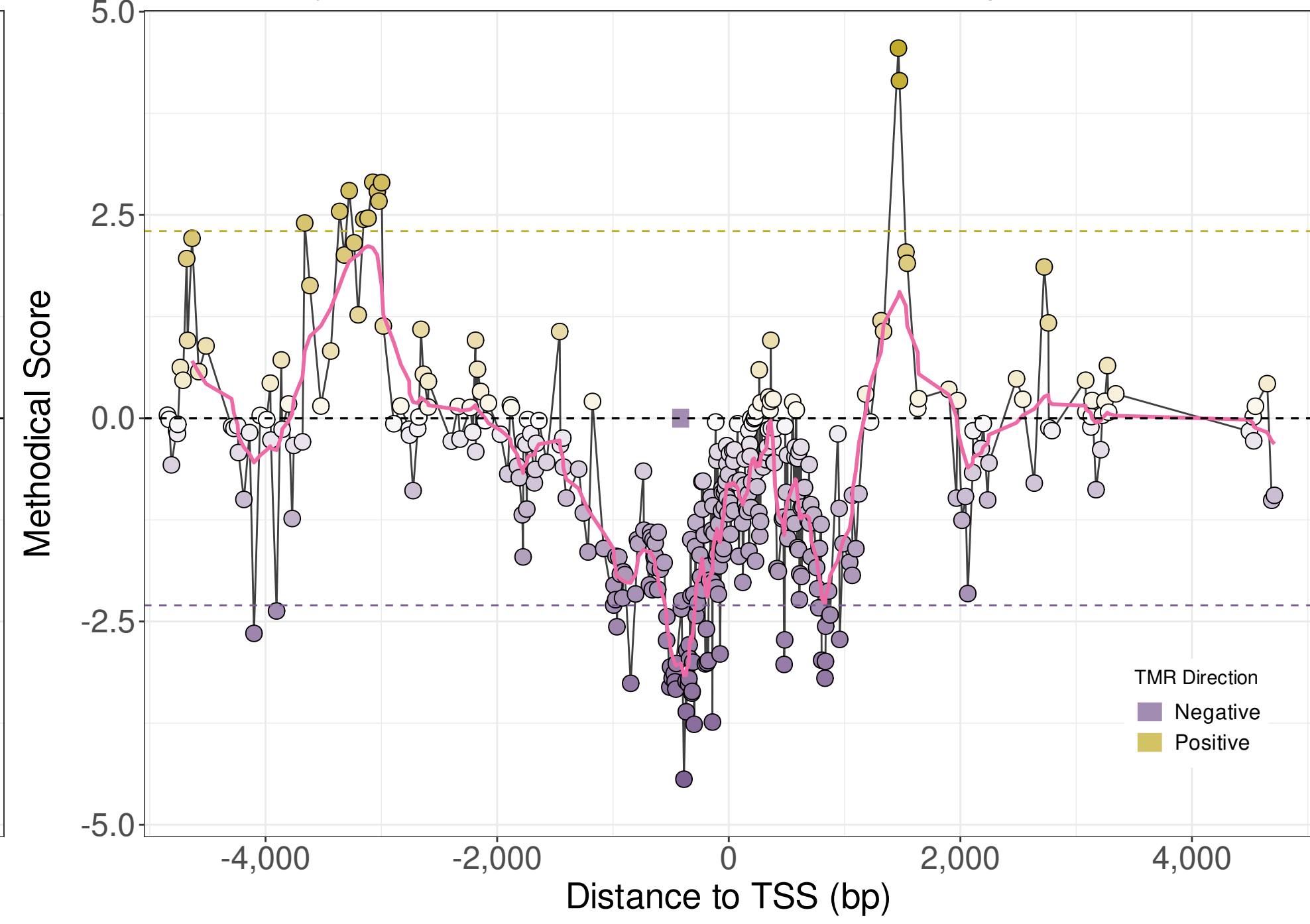
2: Convert correlation values to Methodical scores



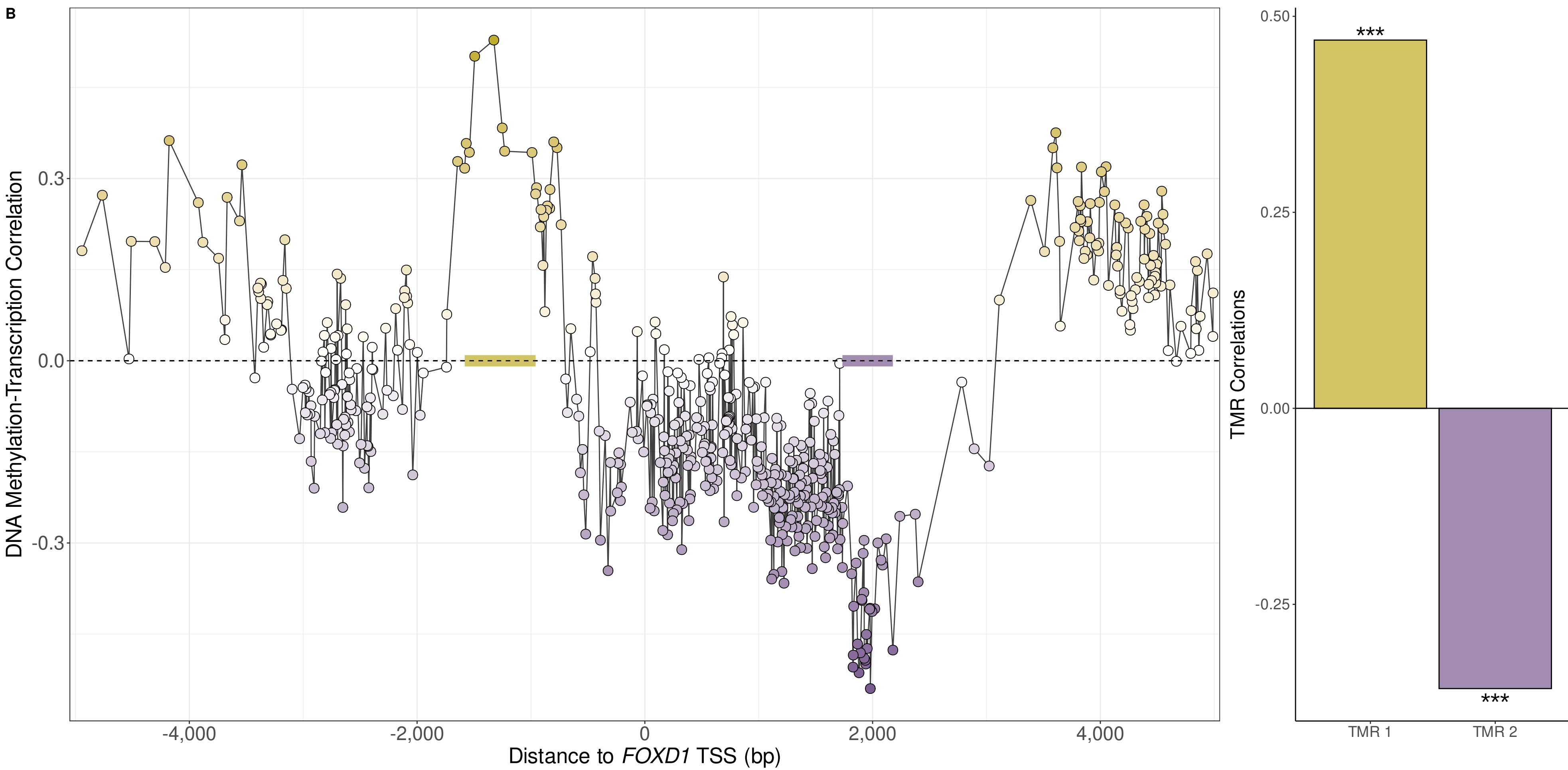
3: Smooth Methodical scores using exponential moving average



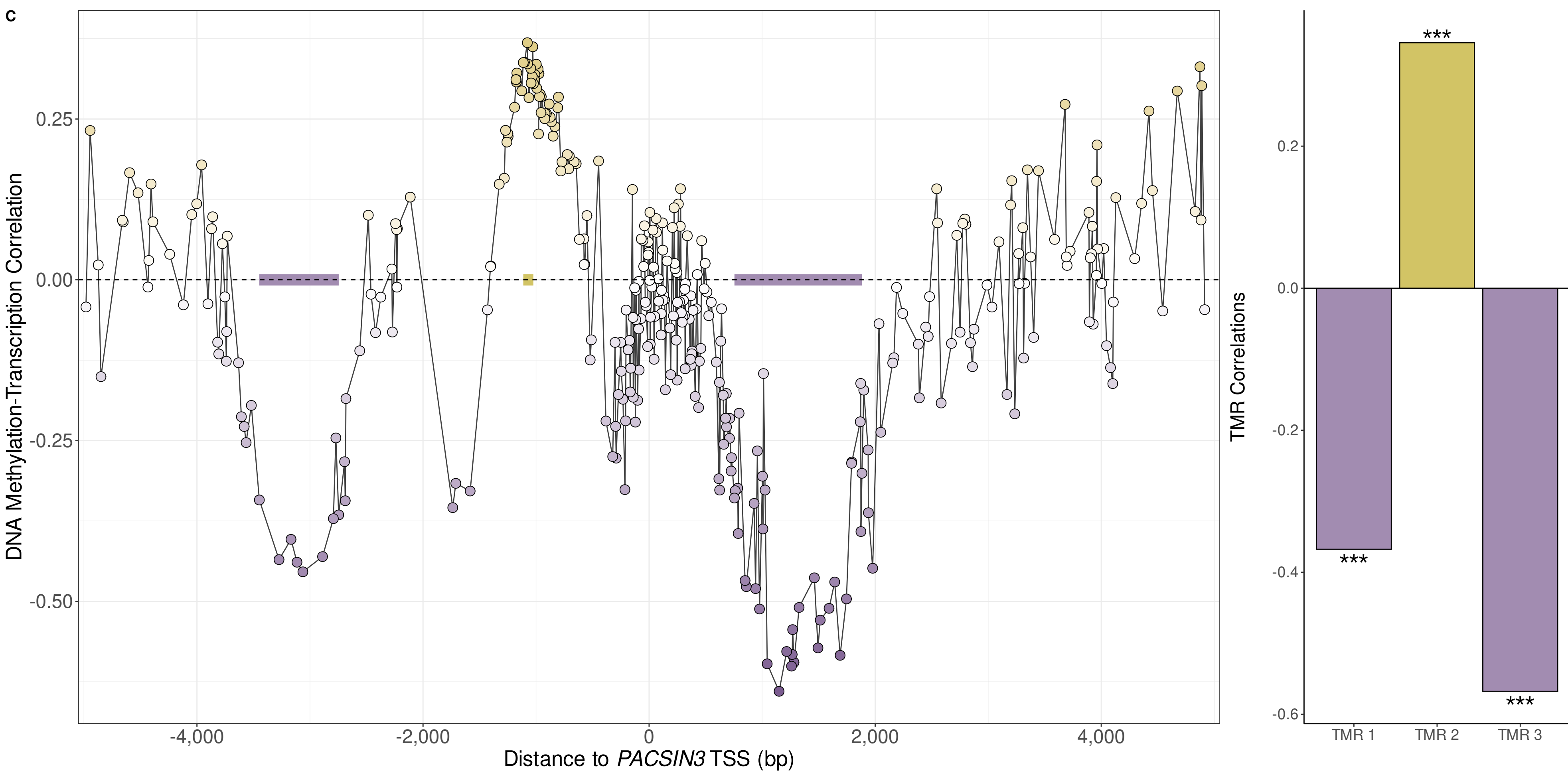
4: Identify TMRs where smoothed Methodical curve crosses significance thresholds



B



C



D

