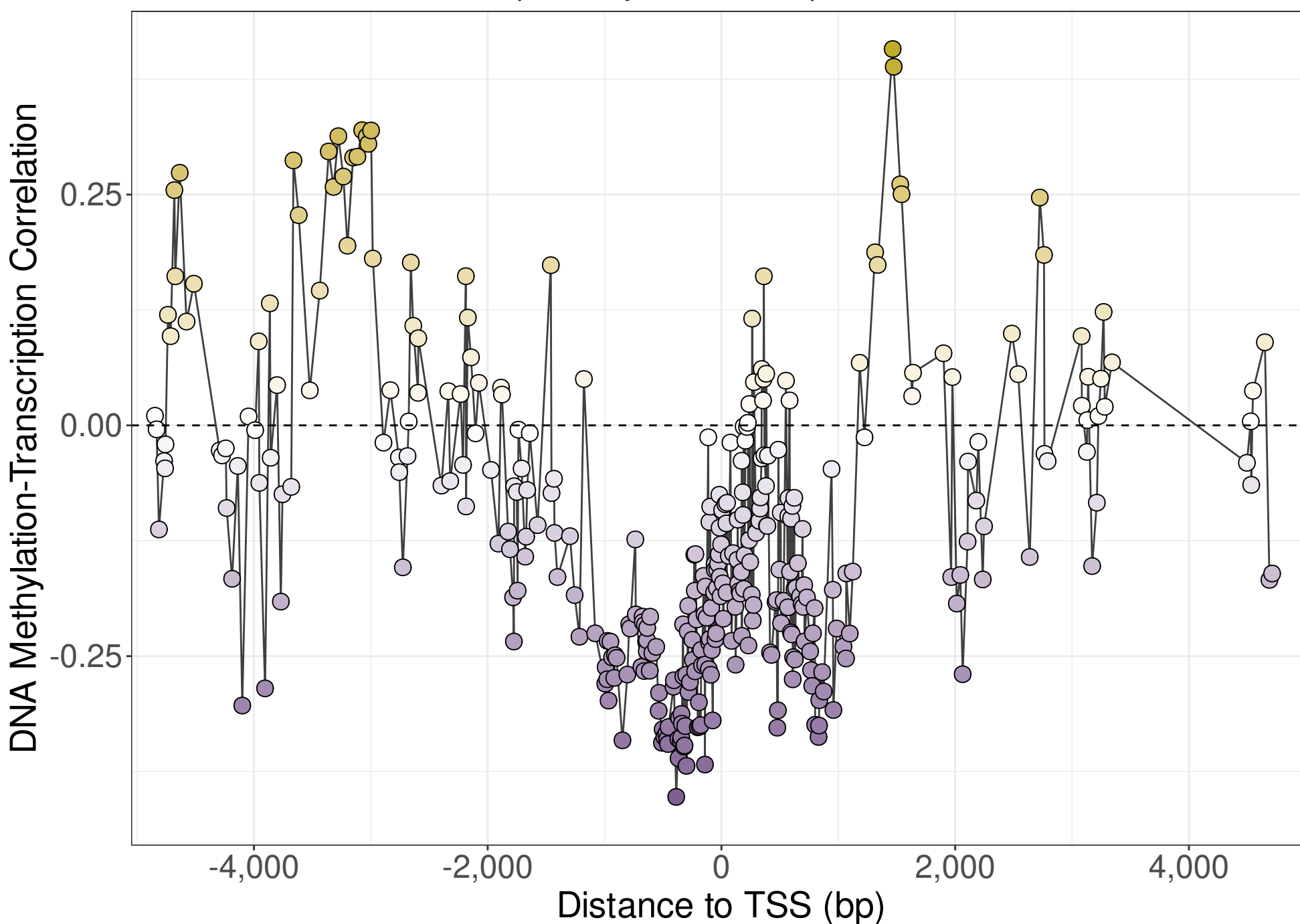
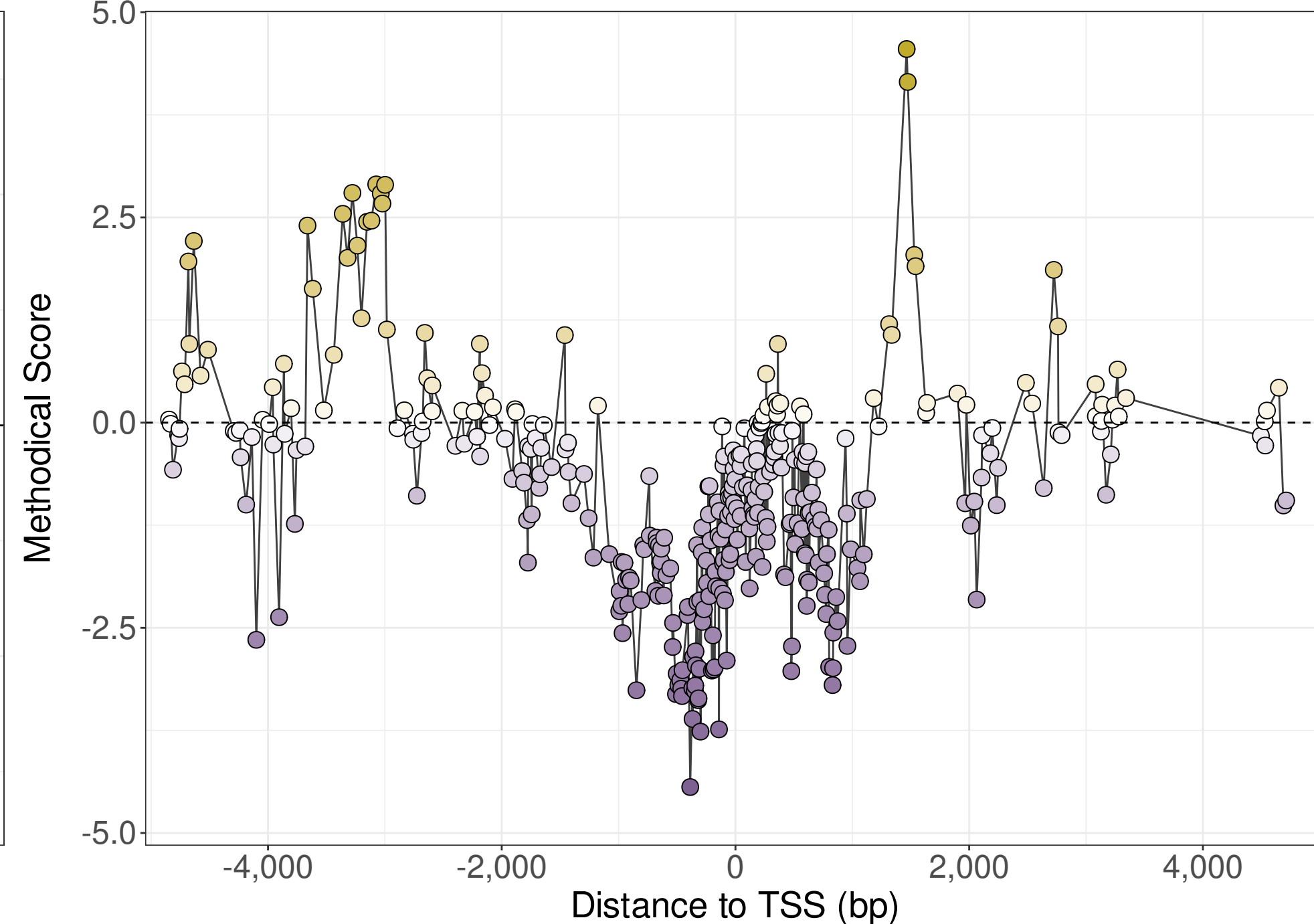


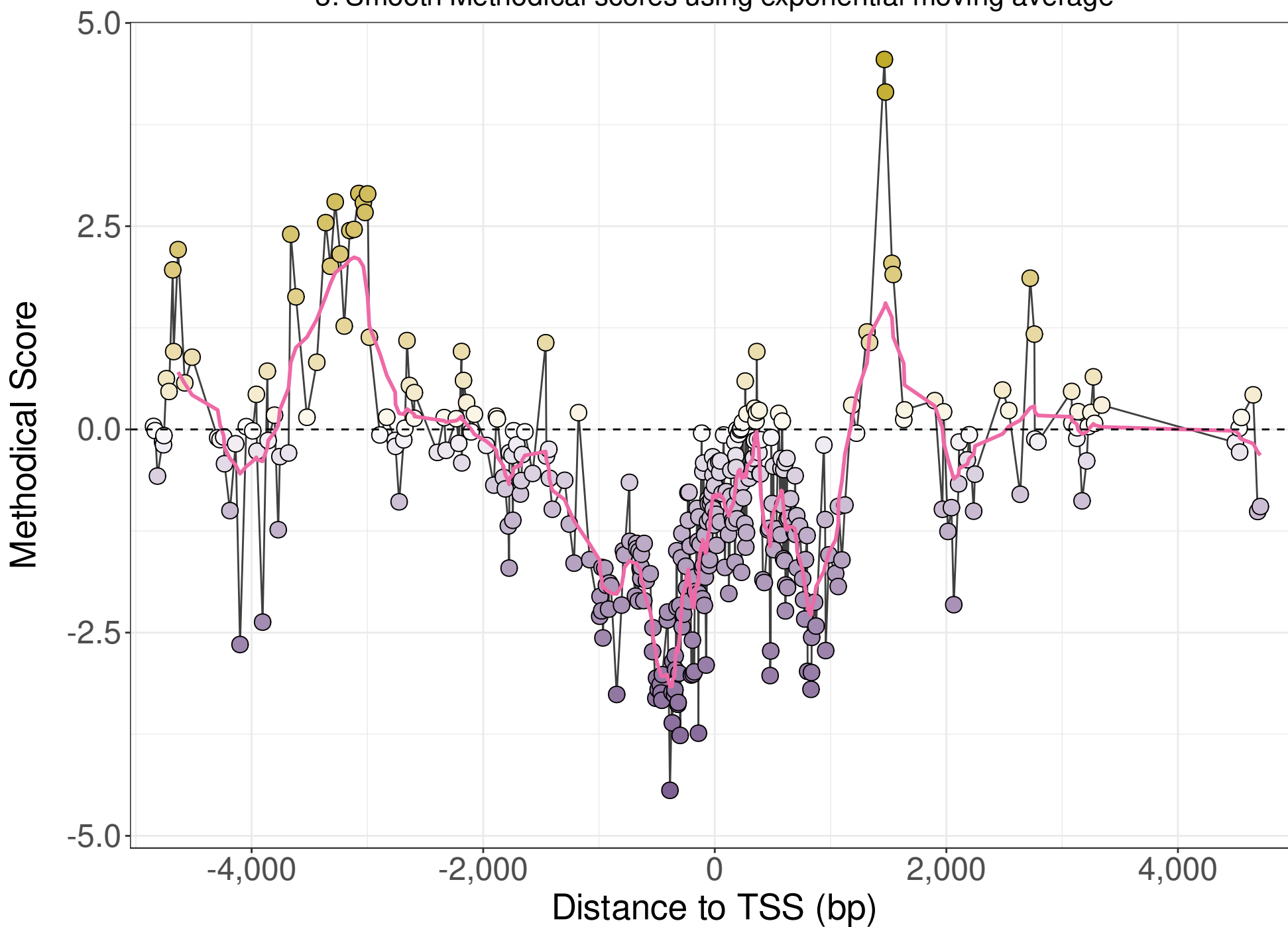
1: Calculate CpG methylation-transcription correlation values



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

