Figure S2 (Wontakal et. al.)

A. 

![Graph showing percentage of peaks vs. distance from TSS (bp). The x-axis represents distance from TSS in base pairs, and the y-axis represents the percentage of peaks. The graph includes three lines: black for overlap, blue for MEL enriched, and red for ES-EP enriched. Each line is marked at different distance intervals: <50, <200, <800, <3200, <12800, and <51200 base pairs.]

B. 

![Sequence alignment showing nucleotide positions and their corresponding coding regions. The alignment highlights specific sequences marked with green bars.]

[Figure S2 details the distribution of peaks in relation to the transcription start site (TSS) for different enrichment categories, illustrating the overlap and enrichment patterns across various distance intervals. The sequence alignment further elucidates the specific nucleotide sequences and their coding potential, marked by green bars for ease of identification.]