

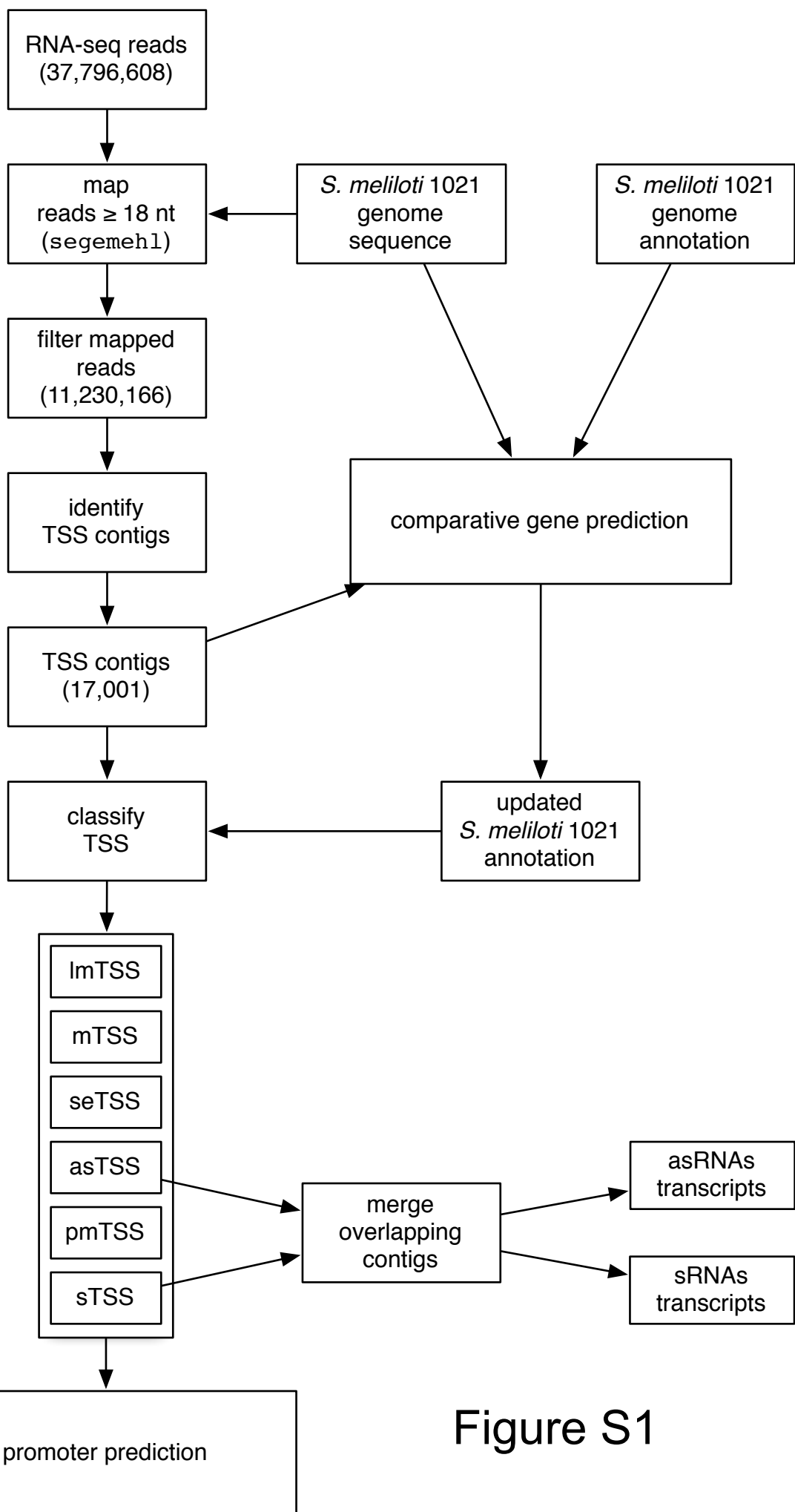


Figure S1

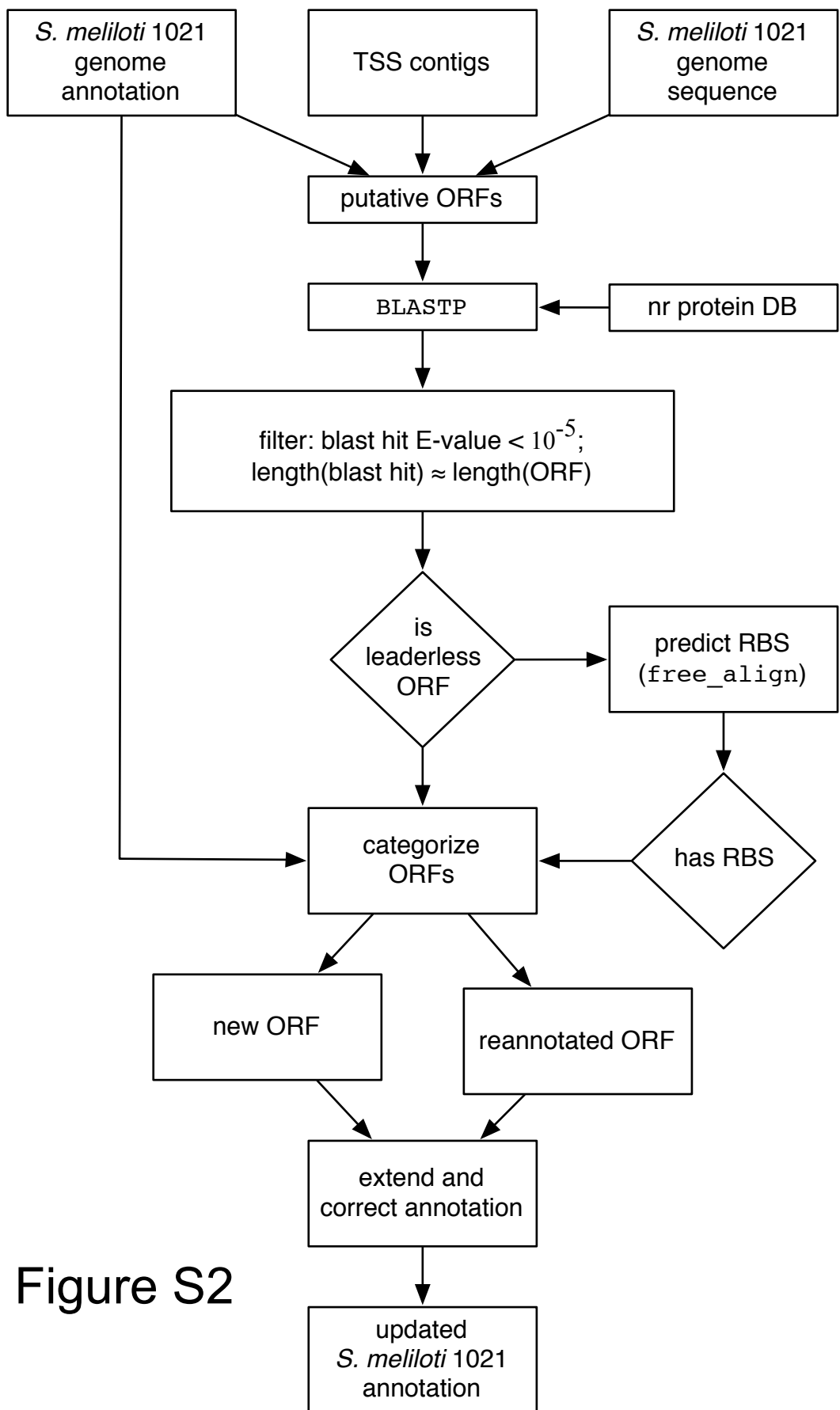
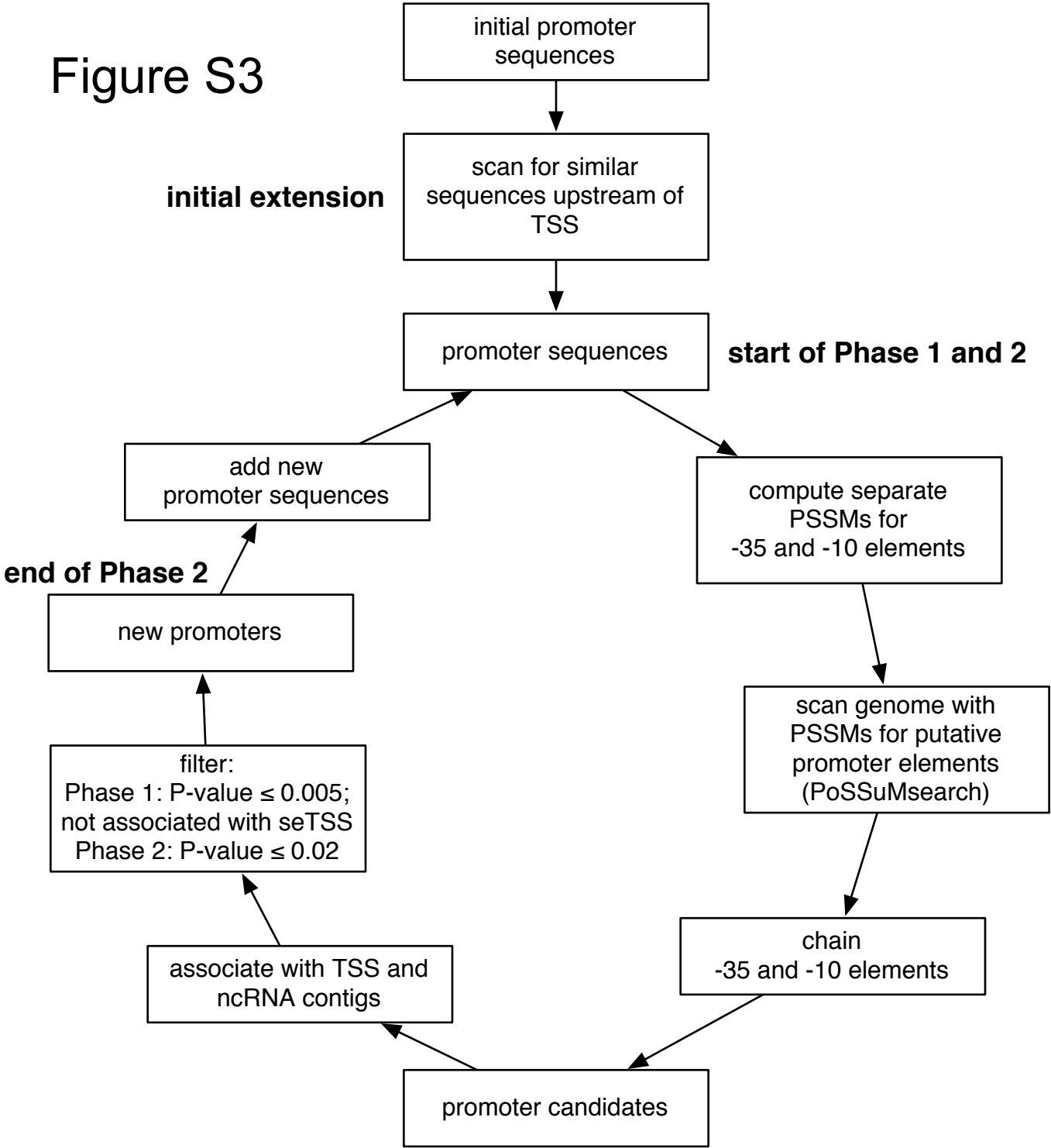


Figure S2

Figure S3



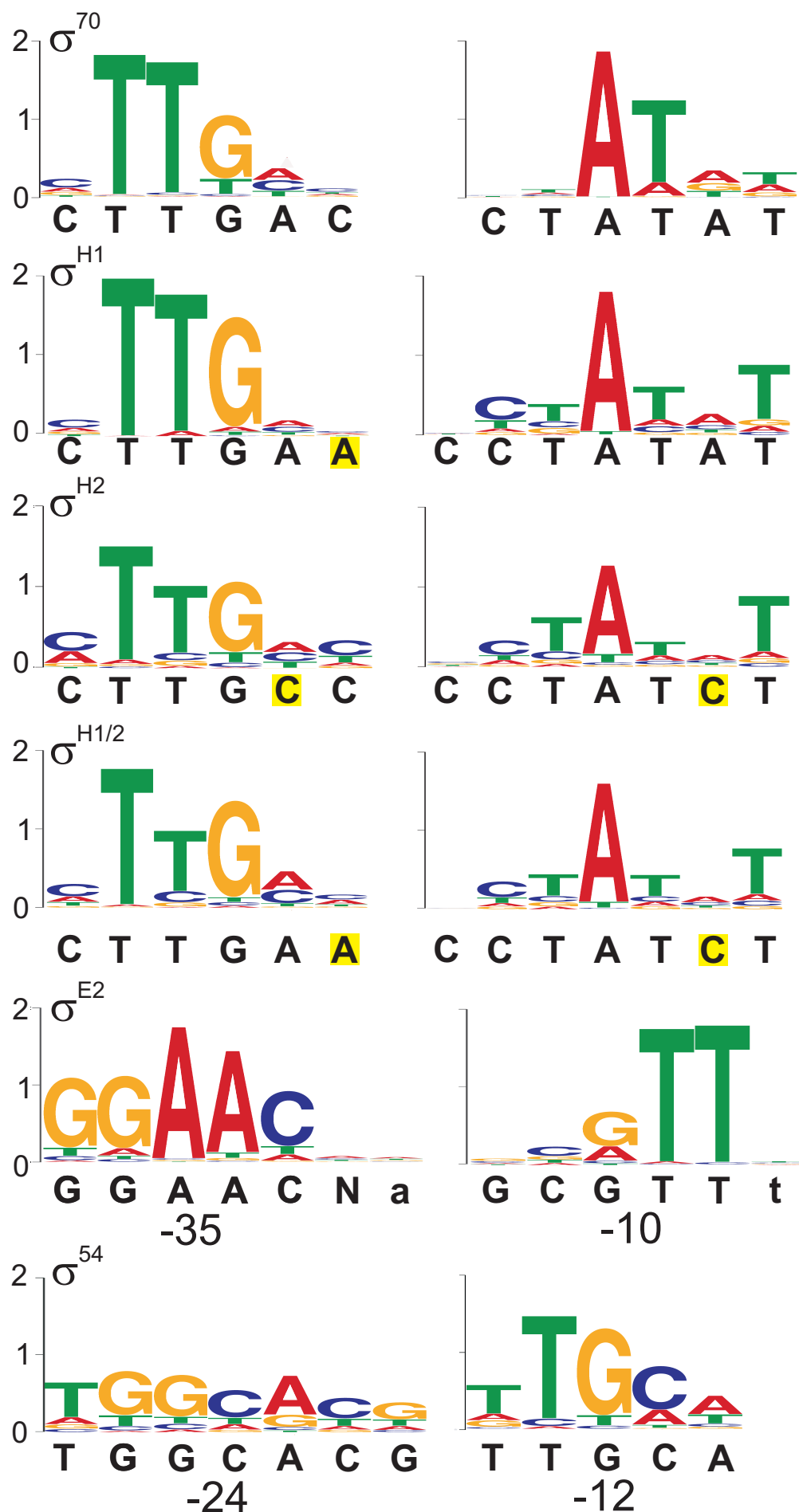
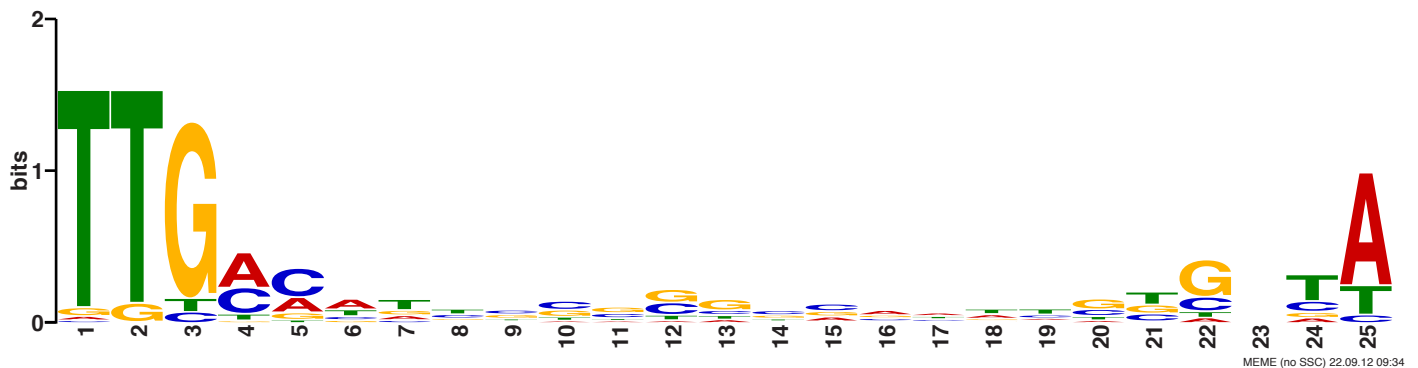
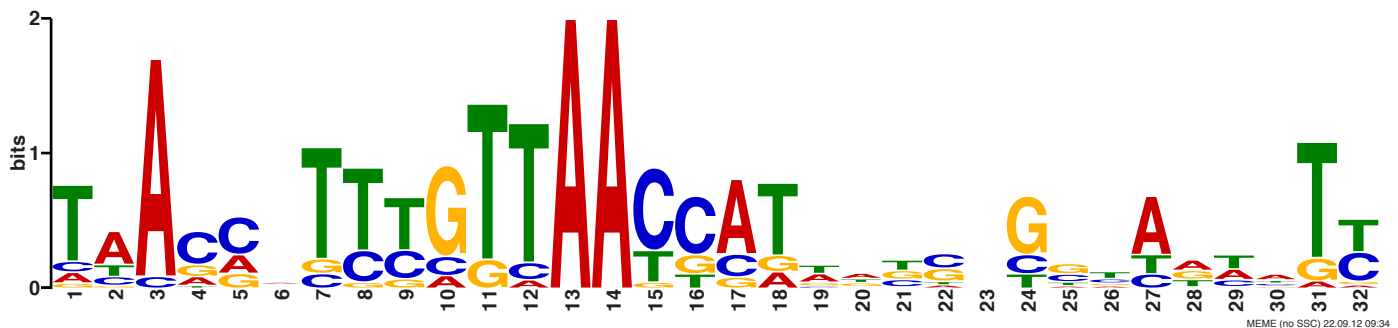


Figure S4. Consensus motifs of σ^{70} , σ^H , σ^{E2} , and σ^{54} promoters after addition of promoters predicted in this study. Previously published promoter consensus motifs are printed in black below the consensus motifs, with those that differ in the new consensus sequences highlighted in yellow.

Motif 1



Motif 2



Motif 3

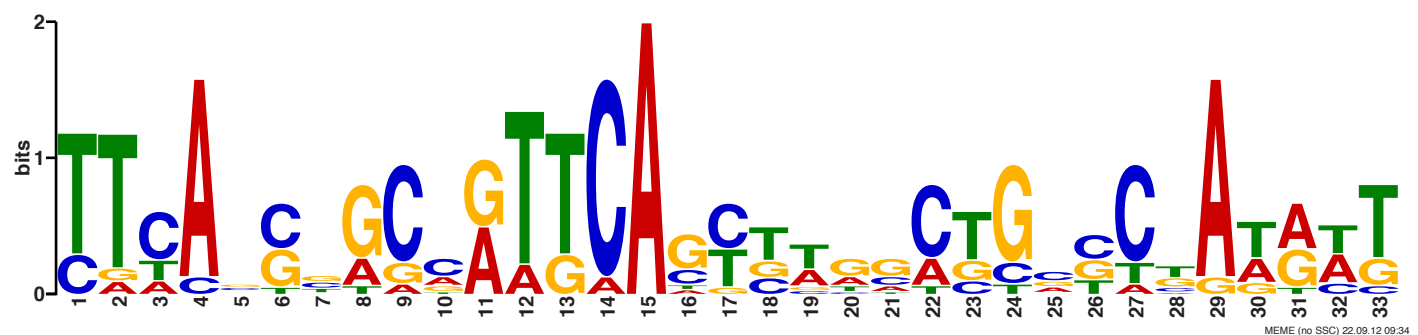


Figure S5. Motifs identified by *de novo* promoter prediction. Colored sequence logos were generated using MEME (Methods). The total information content of each logo is given in bits; the height of each nucleotide in the logo represents the positional probability of that nucleotide multiplied by the information content of the logo.

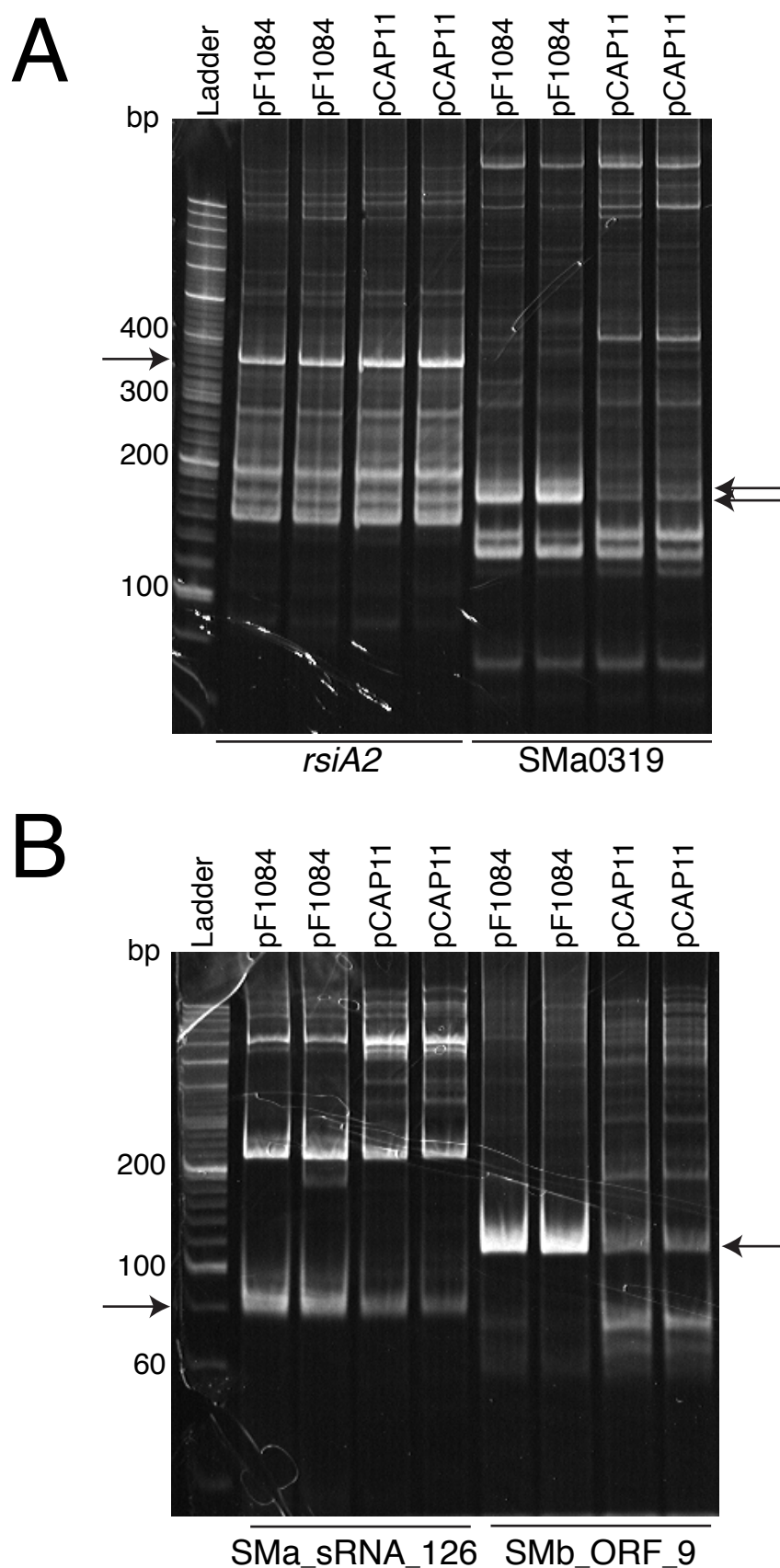


Figure S6. 5' RACE analysis of putative RpoE2 target genes. RNA from *S. meliloti* CL150 cells overexpressing *rpoE2* (pF1084) or carrying an empty vector (pCAP11) was ligated to an RNA primer and reverse transcribed to produce cDNA for 5' RACE. PCR products were resolved by polyacrylamide gel electrophoresis and visualized by SYBR Gold staining. Representative gels for two protein coding genes are shown in A). *rsiA2* (SMc04884) expression was not *rpoE2*-dependent in our Affymetrix experiments, whereas expression of SMa0319 was *rpoE2*-dependent. Gels for genes newly identified in this study are shown in B). Expression of a non-coding RNA (SMa_sRNA_126), and an ORF (SMb_ORF_9), is *rpoE2*-dependent. Bands that were excised and sequenced for transcription start site determination are indicated by an arrow.