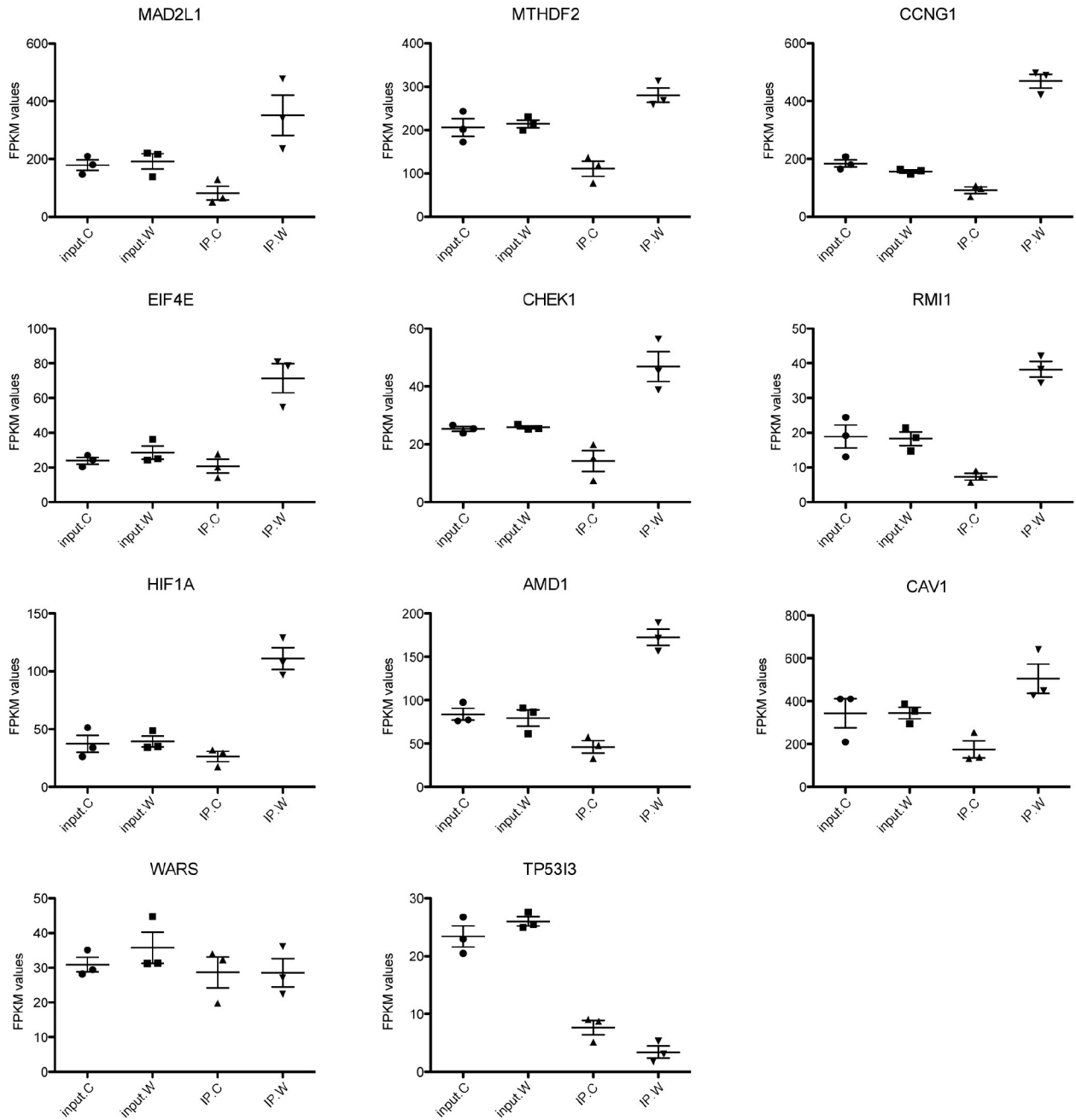
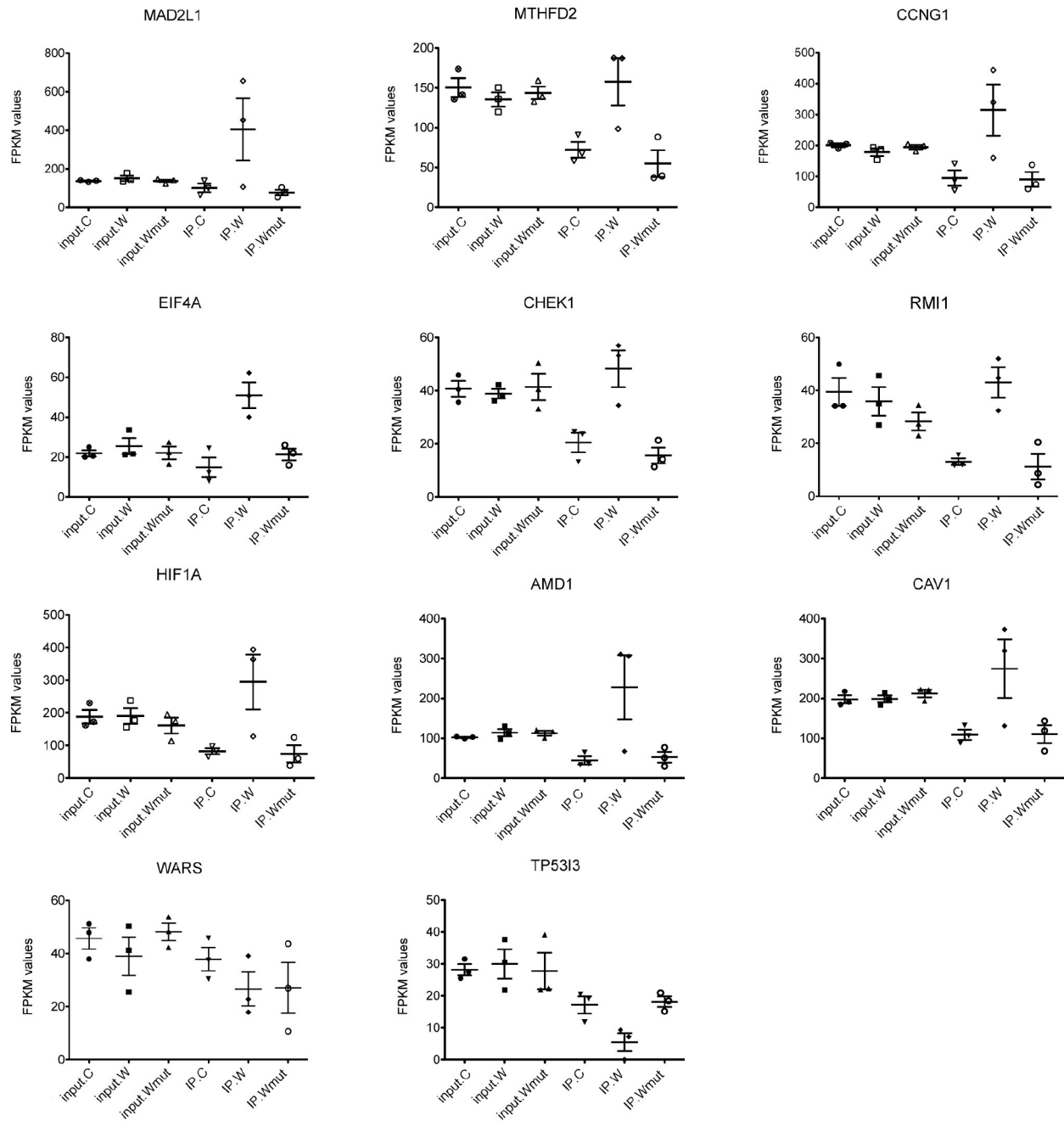


SUPPLEMENTARY FIGURES AND TABLES

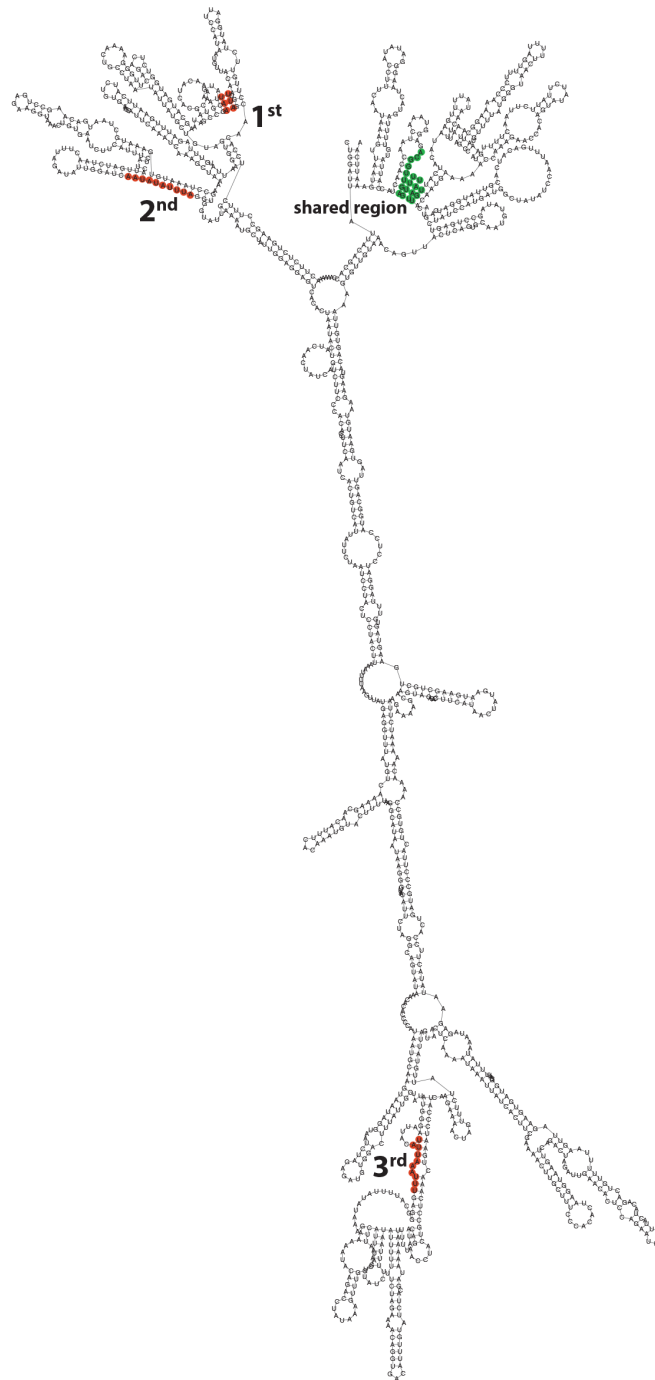


Supplementary Figure S1: FPKM values calculated in the triplicates RIP-Seq experiments per sample for the selected targets in HCT116 cells.



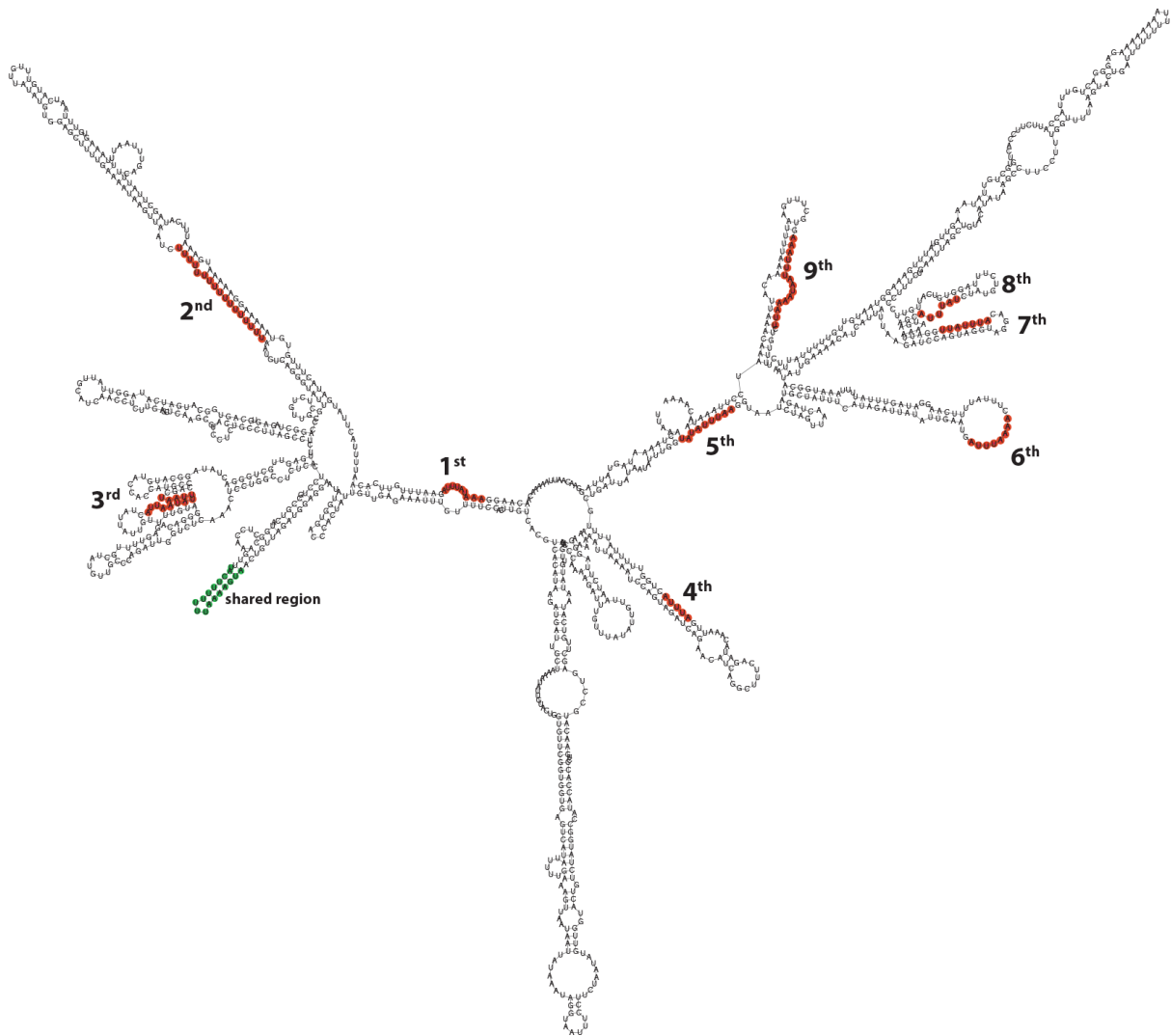
Supplementary Figure S2: FPKM values calculated in the triplicates RIP-Seq experiments per sample for the selected targets in Saos-2 cells.

a. CCNG1



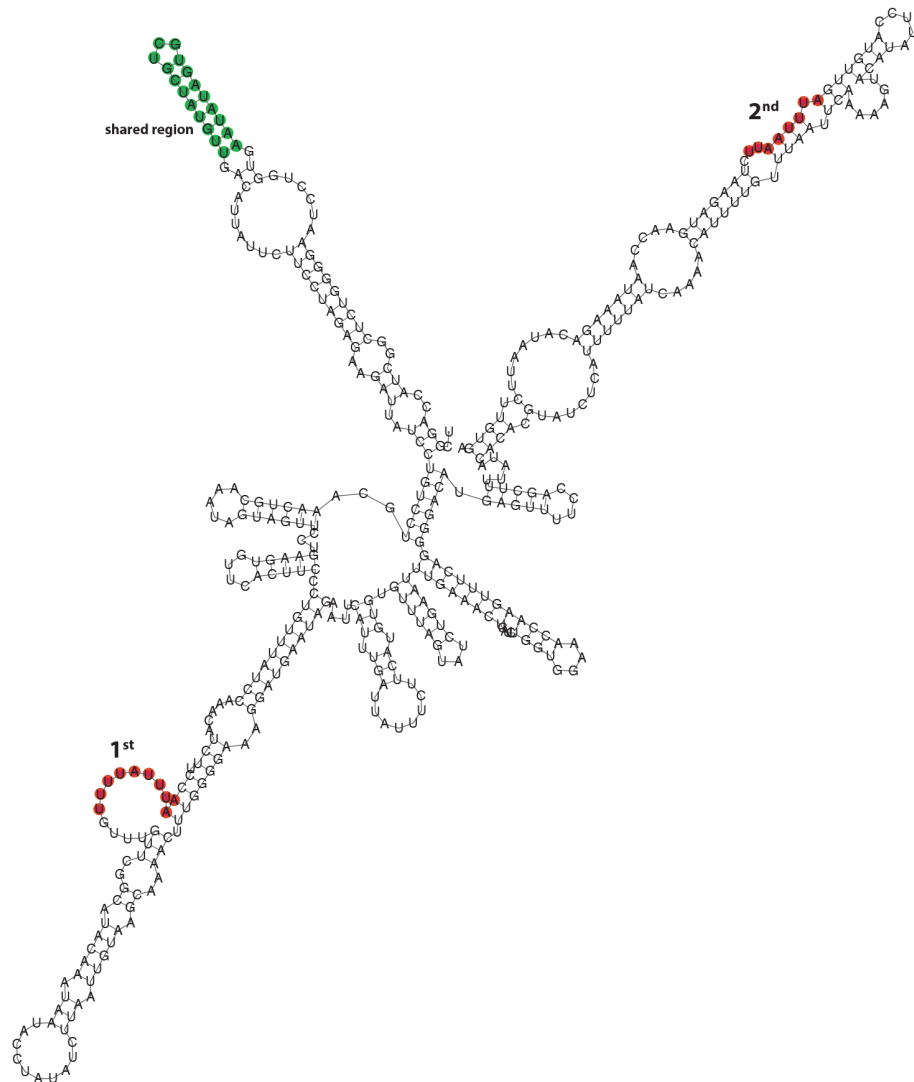
Supplementary Figure S3: 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as “shared motif”). A. CCNG1. (Continued).

b. RMI1



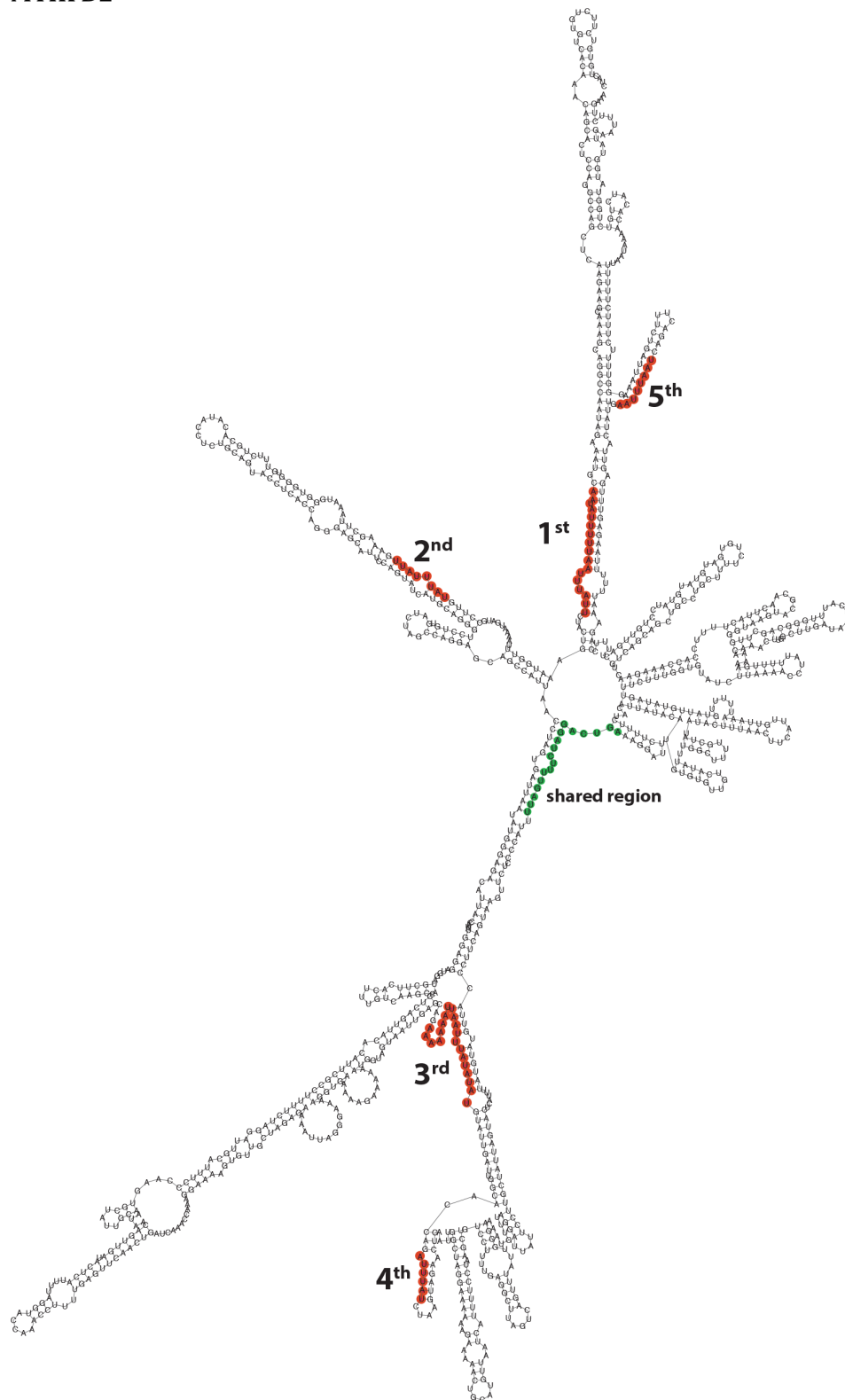
Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif"). B.RMI1. (Continued)

c. CHEK1



Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif"). C. CHEK1. (Continued)

d. MTHFD2



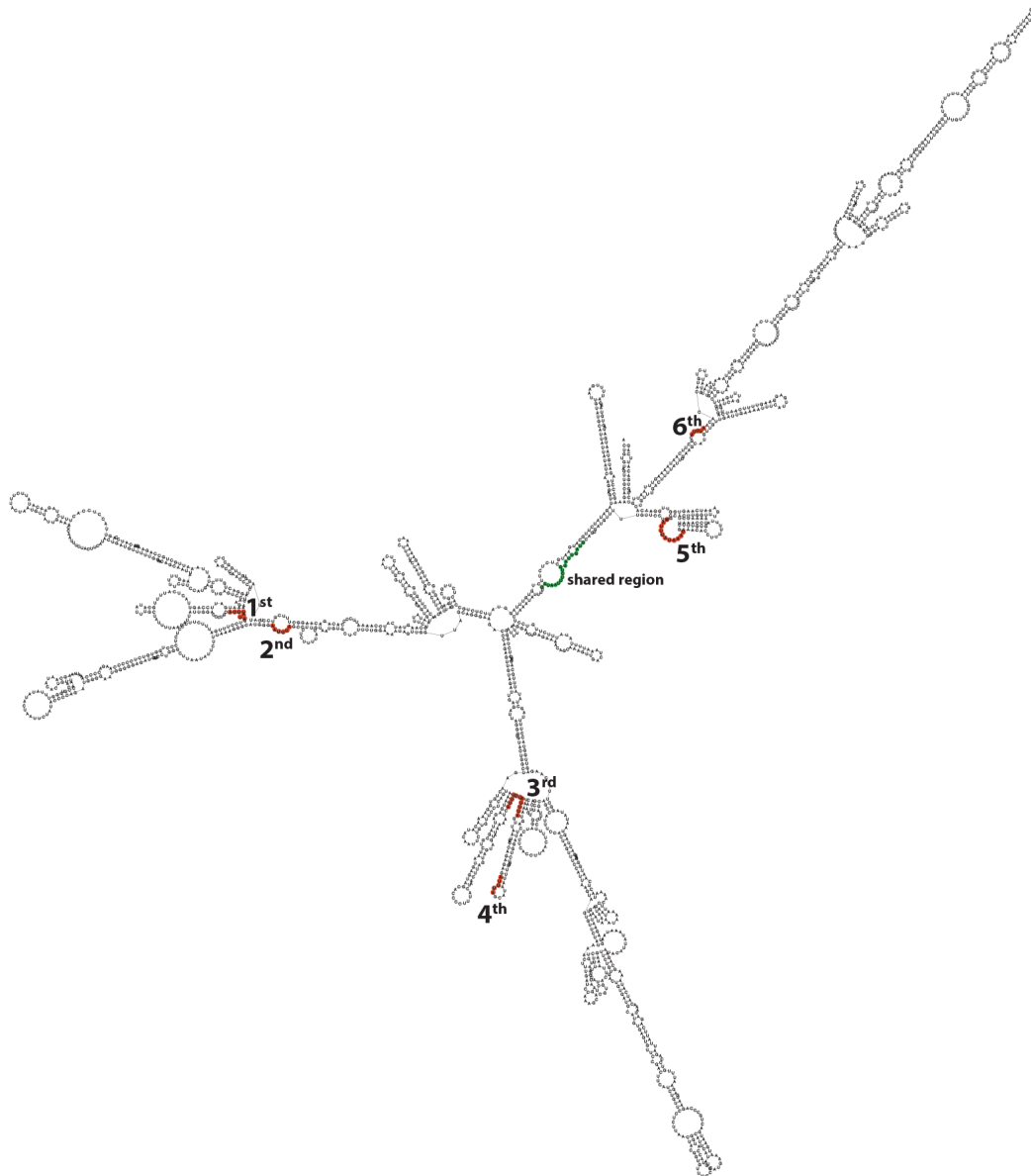
Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif").
D. MTHFD2 (Continued)

e. CAV1



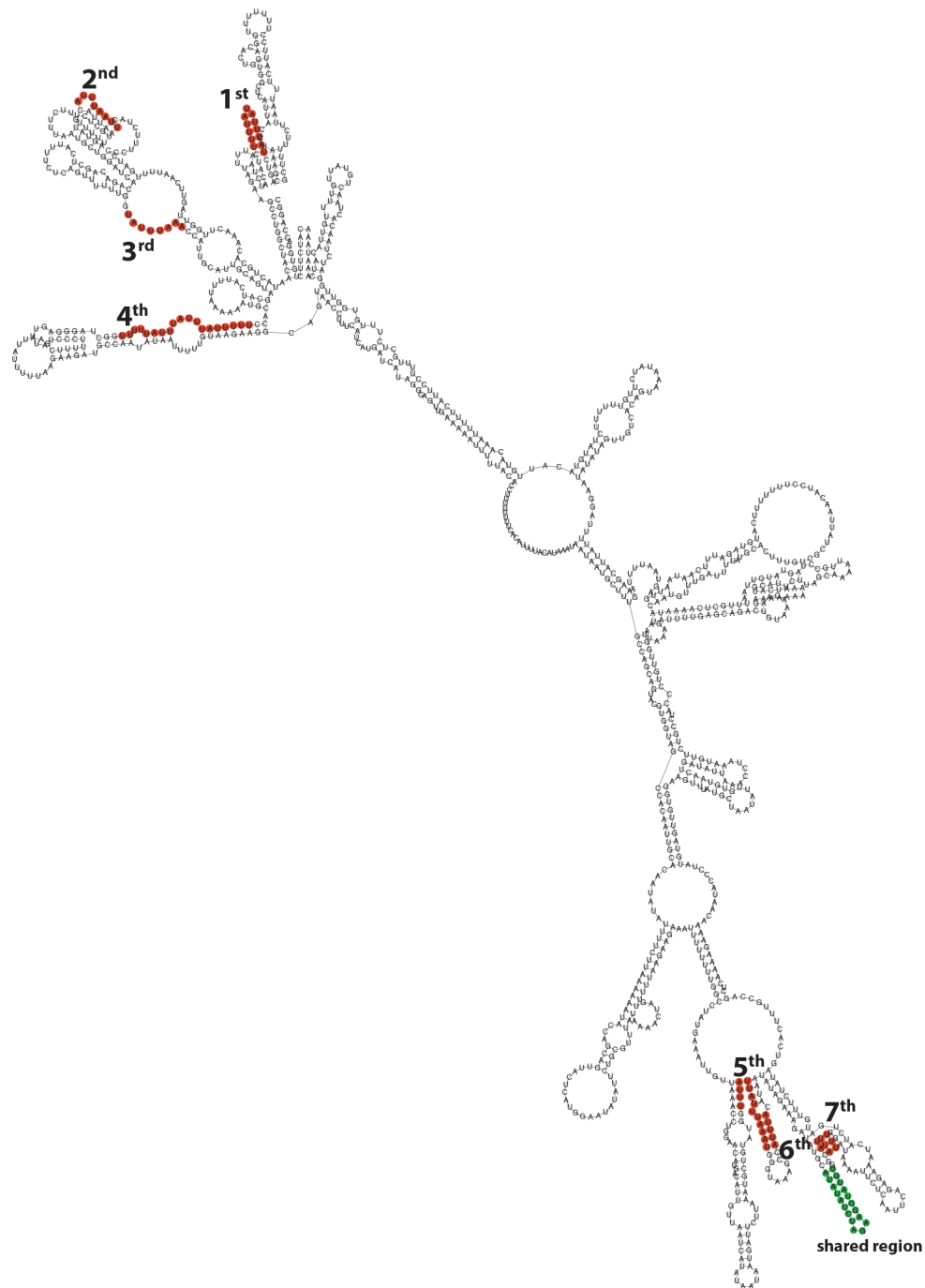
Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif"). E. CAV1. (Continued)

f. AMD1



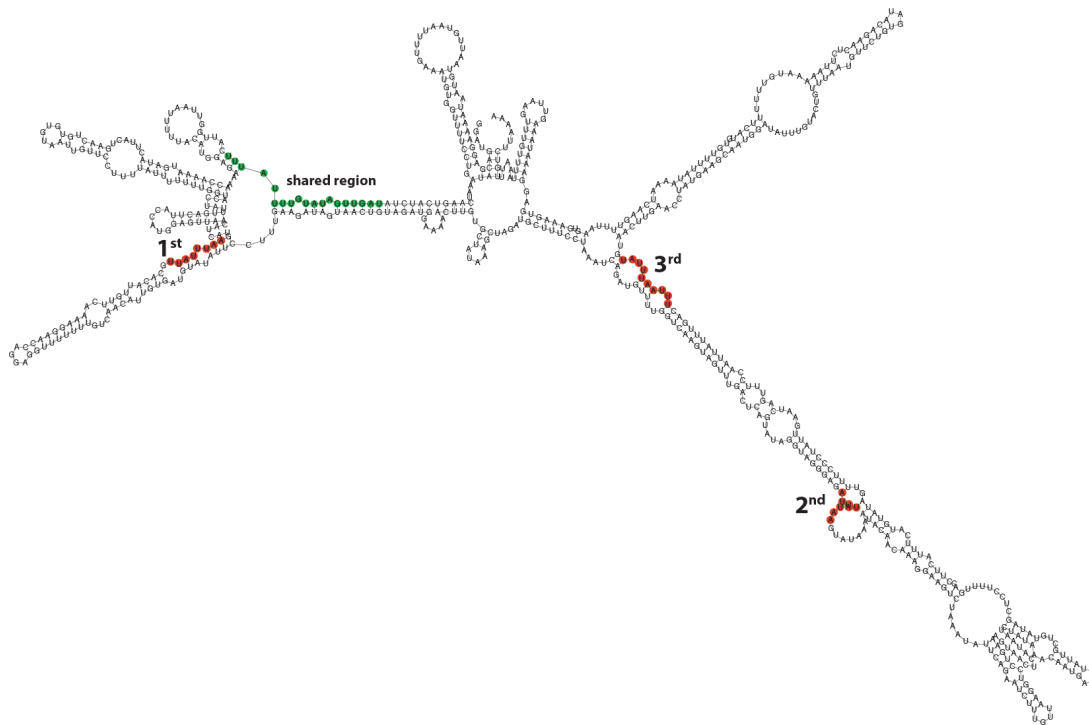
Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif"). F. AMD1. (Continued)

g. HIF1A



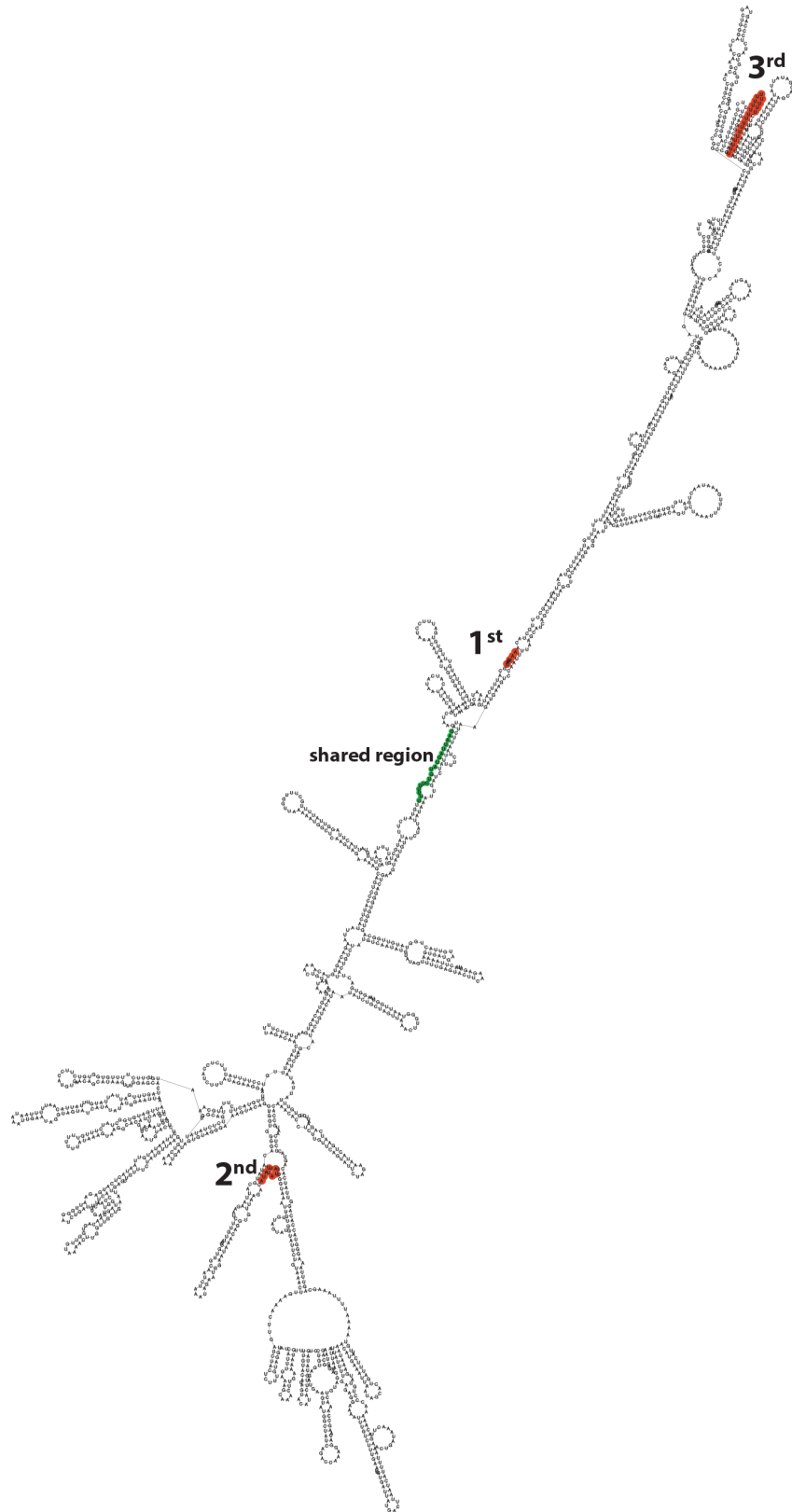
Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif"). G. HIF1A. (Continued)

h. MAD2L1



Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif"). H. MAD2L1. (Continued)

i. EIF4E



Supplementary Figure S3: (Continued) 2D sequence structures predicted by RNAfold for the 9 bound 3'UTR sequences. ARE elements are colored in red, consensus 2D motifs are colored in green (indicated as "shared motif").
I. EIF4E. (Continued)

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>RM11
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>CHEK1
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>CAV1
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 TCTCATCAACTGAATGAGGTCAGCATGTCTATTCAGTTCGTTTTATTTTCAAGAATAATCACGCTTTCTGAAATCCAACATAATCC

Supplementary Figure S4: (Continued) Sequences of the nine positively validated 3'UTRs bound by Wig-1. Putative ARE elements are highlighted in red, consensus 2D motifs are highlighted in green. (Continued)

ATCACCGGGTGGTTAGTGGCTCAACATTTGTGTTCCCATTTCCAGCTGATCAGTGGGCTCCAAGGAGGGGCTGTA AAAATGGAGGC
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>AMD1

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>HIF1A

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>MAD2L1

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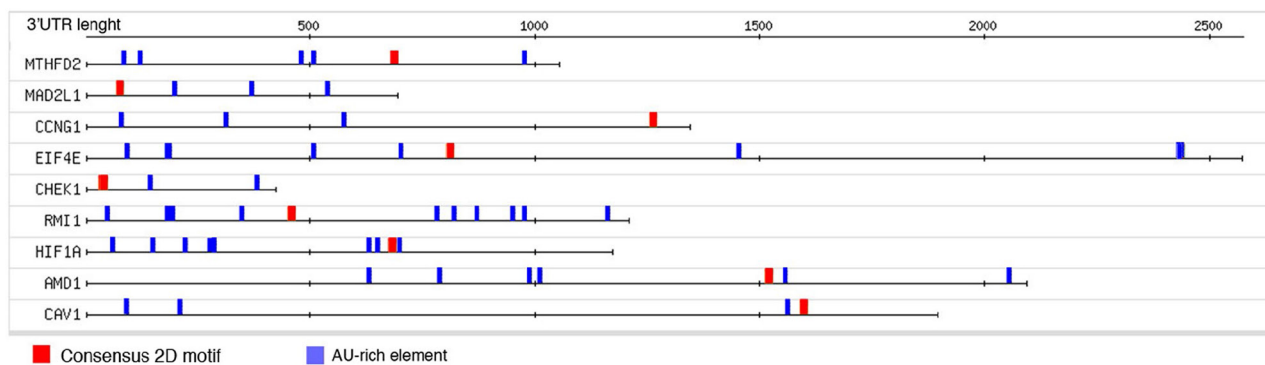
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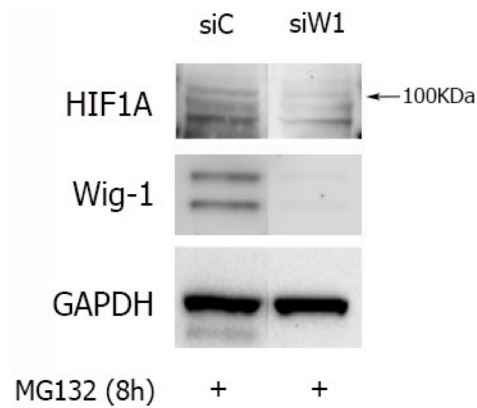
Supplementary Figure S4: (Continued) Sequences of the nine positively validated 3'UTRs bound by Wig-1. Putative ARE elements are highlighted in red, consensus 2D motifs are highlighted in green. (Continued)

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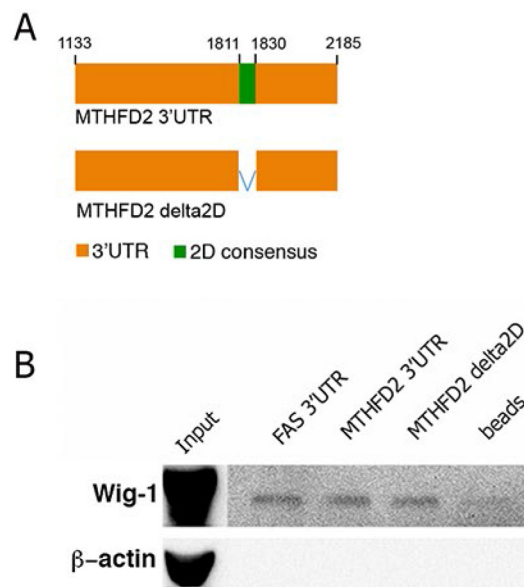
Supplementary Figure S4: (Continued) Sequences of the nine positively validated 3'UTRs bound by Wig- 1. Putative ARE elements are highlighted in red, consensus 2D motifs are highlighted in green.



Supplementary Figure S5: Visualization the position of the consensus 2D motifs and the ARE motifs in the 3'UTR sequences of the validated Wig-1 bound targets. Figure generated by RSAT.



Supplementary Figure S6: Wig-1 knockdown does not affect HIF1A protein levels. HCT116 cells were transfected with 10nM siRNA against Wig-1 (siW1) or control siRNA (siC). Forty-eight hours after transfections cells were treated with 20 μ M MG132 proteasome inhibitor for 8 h and the levels of nuclear HIF1A protein was measured by Western Blotting.



Supplementary Figure S7: A. Model of the MTHFD2 constructs used for biotin pulldown (see materials and methods for details). **B.** Biotin pull-down assay using the probes in (A.) or a FAS full-length 3'UTR probe as positive control followed by Western blotting for Wig-1 shows that Wig-1 binds to the full length FAS 3'UTR (positive control), the full length MTHFD2 3'UTR probe and the MTHFD2 3'UTR probe with consensus 2D motif deletion (MTHFD2 delta2D) with the same intensity.

Supplementary Table S1: Percentage of reads mapped to human genome

Samples (n=3)	Average number of paired reads sequenced (MEAN ± S.D.)	Percentage of reads mapped to human genome (MEAN % ± S.D.)	Percentage of reads after duplicate removal (MEAN % ± S.D.)
HCT116 input.C	15,446,432 ± 1,253,607	64 ± 2.55	41 ± 1.25
HCT116 input.W	15,403,089 ± 318,777	62 ± 0.95	38 ± 1.43
HCT116 IP.C	15,466,119 ± 1,577,956	58 ± 11.73	20 ± 7.79
HCT116 IP.W	15,870,292 ± 2,191,340	61 ± 3.39	34 ± 1.81
Saos2 input.C	16,683,516 ± 6,422,055	70 ± 4.56	52 ± 4.43
Saos2 input.W	17,592,957 ± 5,131,259	71 ± 5.57	51 ± 6.56
Saos2 input.Wmut	19,000,702 ± 3,109,401	71 ± 3.76	53 ± 3.53
Saos2 IP.C	20,610,044 ± 11,505,023	41 ± 3.36	12 ± 8.10
Saos2 IP.W	17,340,104 ± 3,692,727	46 ± 35.38	28 ± 27.12
Saos2 IP.Wmut	21,239,267 ± 7,806,368	42 ± 4.13	8 ± 1.67

Input.C: input control (empty vector); input.W: input Flag-Wig-1; input.Wmut: input Flag-Wig-1-point mutant; IP.C: IP control (empty vector); IP.W: IP Flag-Wig-1; IP.Wmut: IP Flag-Wig-1point mutant.

Supplementary Table S2: List of the 2335 Wig-1-bound RNAs in HCT116 cells.

Supplementary Table S3: List of the 354 Wig-1-bound RNAs in Saos-2 cells.

Supplementary Table S4: List of the 286 common Wig-1-bound RNAs in HCT116 and Saos2 cells.

Supplementary Table S5: List of transcripts that are bound by Wig-1 and whose gene expression levels are affected by Wig-1 silencing in HCT116 cells (GEO database GSE43046), at least 4-fold difference ($\log_2(\text{siRNA Wig-1}/\text{siRNA control})$) in at least two out of the three replicates.

Supplementary Table S6: Gene ontology Analysis of Wig-1-bound RNAs by DAVID.

Supplementary Table S7: List of the 300 pathways identified by network enrichment analysis as enriched at significance level $\text{FDR} < 0.01$.

Supplementary Table S8: List of the 133 Reactome pathways enriched at significant level of $\text{FDR} < 0.01$.

Supplementary Table S9: List of pathways identified by network enrichment analysis as enriched at significance level $\text{FDR} < 0.01$ for bound and regulated Wig-1 targets in HCT116 cell line.

Supplementary Table S10: List of the 286 RNAs included in the unbound group.

Supplementary Table S11: List of the TaqMan probes used for qRT-PCR.