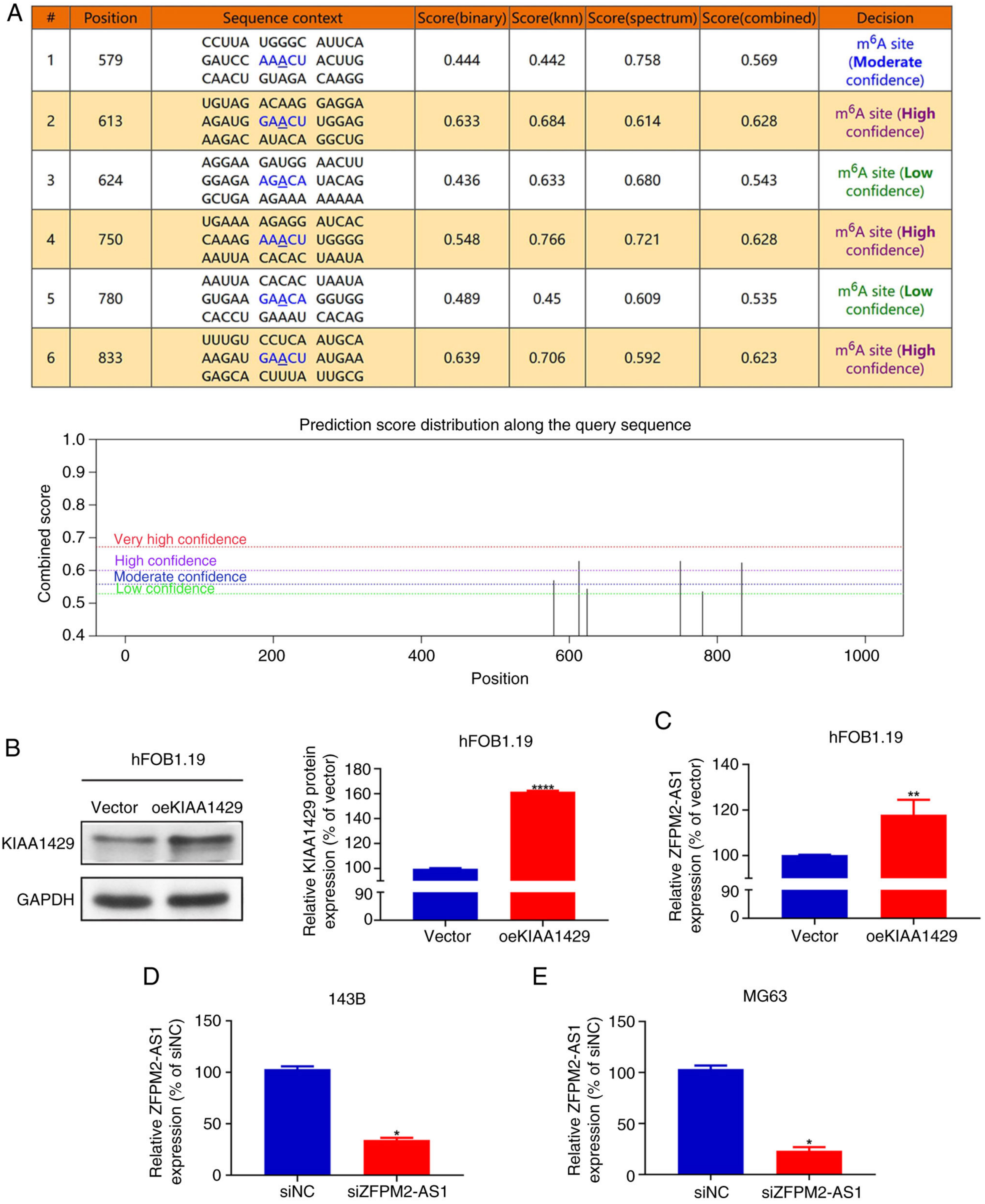
Figure S1. Prediction of m^{6}A modification sites in ZFPM2-AS1, and the effects of various transfections on KIAA1429 and ZFPM2-AS1 expression levels. (A) The m^{6}A modification sites in ZFPM2-AS1 were predicted using the SRAMP online tool. The table presents the positions of the predicted RRACH motifs in the query sequence, along with their flanking sequences and prediction scores. SRAMP predicted 3 high-confidence (95% specificity), 1 moderate-confidence (90% specificity), and 2 low-confidence (85% specificity) m^{6}A modification sites. The figure below the table shows the distribution of the predicted m^{6}A sites in the ZFPM2-AS1 sequence. (B) Western blotting and (C) RT-qPCR analysis of 143B and MG63 cells following transfection with oeKIAA1429 show that KIAA1429 protein and ZFPM2-AS1 expression levels were significantly increased. **P<0.01 and ****P<0.0001 vs. vector. RT-qPCR analysis of (D) 143B and (E) MG63 cells reveals that ZFPM2-AS1 was successfully knocked down following transfection with siZFPM2-AS1. *P<0.05 vs. shNC. All data are presented as the mean ± SD from three independent experiments. m^{6}A, N^6-methyladenosine; ZFPM2-AS1, friend of GATA family member 2-antisense 1; RT-qPCR, reverse transcription-quantitative PCR; oeKIAA1429, KIAA1429 overexpression; siZFPM2-AS1, siRNA targeting ZFPM2-AS1; siNC, negative control siRNA; siRNA, small interfering RNA.



#	Position	Sequence context	Score(binary)	Score(knn)	Score(spectrum)	Score(combined)	Decision
1	579	CCUUA UGGGC AUUCA GAUCC AAACU ACUUG CAACU GUAGA CAAGG	0.444	0.442	0.758	0.569	m^{6}A site (**Moderate** confidence)
2	613	UGUAG ACAAG GAGGA AGAUG GAACU UGGAG AAGAC AUACA GGCUG	0.633	0.684	0.614	0.628	m^{6}A site (**High** confidence)
3	624	AGGAA GAUGG AACUU GGAGA AGACA UACAG GCUGA AGAAA AAAAA	0.436	0.633	0.680	0.543	m^{6}A site (**Low** confidence)
4	750	UGAAA AGAGG AUCAC CAAAG AAACU UGGGG AAUUA CACAC UAAUA	0.548	0.766	0.721	0.628	m^{6}A site (**High** confidence)
5	780	AAUUA CACAC UAAUA GUGAA GAACA GGUGG CACCU GAAAU CACAG	0.489	0.45	0.609	0.535	m^{6}A site (**Low** confidence)
6	833	UUUGU CCUCA AUGCA AAGAU GAACU AUGAA GAGCA CUUUA UUGCG	0.639	0.706	0.592	0.623	m^{6}A site (**High** confidence)