

Table S1 Comparative characteristics of programs that can be used to search for miRNA BSs in mRNA target genes

Programs	Schemes of interactions of miRNA with mRNA
MirTarget	<pre> 5' -CUUCACCACCACCACCACCAC-3' 3' -AAAGUAGUAGUAGUAGUAGUA-5' </pre>
TAPIR	No BSs found
psRNATarget	<p>No BSs found</p> <pre> 21 AAAGUAGUAGUAGUAGUA 1 ::: ::: ::::: ::::: 886 UUUGAUCCUCAUCCAUCCAG 906 </pre>
RNA 22	<p>No BSs found</p> <pre> TTTGATCCTCATCACCATCAG AAAGTAGTAGTAGTAGTAGTA886 </pre>

miRNA: ath-miR5658-5p; Gene: GSB RNA2T00009950001; Start of BSs: 610 nt., mRNA region: CDS, ΔG : -87 kJ/mol, $\Delta G/\Delta G_m$: 85%, miRNA length: 21 nt. The predictions were compared with the results of psRNATarget, Tapir, RNA22, with their default parameters. The default criteria (the score cutoff value =4 and the free energy ratio cutoff value =0.7) for target prediction in Tapir website were used. The standard parameter set for target prediction in psRNATarget was as follows: penalty for (extending gap =0.5, opening gap =2, G.U pair =0.5, other mismatches =1), HSP size =19, seed region =2-13 nucleotides. The minimum expectation score =5.0. The RNA22 algorithm was run after defining standard settings. These include: Sensitivity and specificity values =63% and 61%, respectively, Seed size =7, with one unpaired base allowed in the seed region, Minimum number of paired-up bases in heteroduplex =12, Maximum folding energy for heteroduplex =-12 kcal/mol, Maximum number of G:U wobbles allowed in seed region = no limit. TAPIR, psRNATarget and RNA 22 analysis web servers did not find ath-miR5658-5p binding sites at positions 610 nt in the mRNA of the GSB RNA2T00009950001 gene, since the programs do not take into account hydrogen bonds between C and A. mRNA, messenger RNA; ath, *Arabidopsis thaliana*; miRNA, mRNA-inhibitory RNA; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BSs, binding sites; nt, nucleotide; CDS, coding domain sequence.

Table S2 Characteristics of zma-miR529-3p interaction with human mRNA genes

Gene	Start of BS, nt	Region of mRNA	ΔG , kJ/mol	$\Delta G/\Delta G_m$, %
ATP6V0A4	241	5'UTR	-106	94
CHD2	6,684	3'UTR	-106	94
MLL	11,418	CDS	-106	94
PDE4B	2,270	CDS	-106	94
LMO7	4,210	CDS	-102	91
LRTOMT	1,111	CDS	-102	91
LTB4R	3,117	3'UTR	-102	91
NUDC	455	CDS	-102	91
POMC	1,055	CDS	-102	91
SOX9	92	5'UTR	-102	91

mRNA, messenger RNA; zma, *Zea mays*; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BS, binding sites; nt, nucleotide; CDS, coding domain sequence; 3'UTR, 3'-untranslated region; 5'UTR, 5'-untranslated region.

Table S3 Nucleotide sequences of regions of human gene mRNA containing zma-miR529-3p BSs

Gene	Nucleotide sequences of mRNA regions
<i>ATP6V0A4</i>	UCUCUGAAGAGGAAGAAGAGAGAGAGACACAGCCAAGACCGA
<i>CHD2</i>	UUGGGGUGGAGAAGUAGAGAGAGGGCAACAGCUUCCACAAC
<i>MLL</i>	CCCCAUGAUGAAGAAGAGGAGGAGGUACAGCUGAAGUCAG
<i>PDE4B</i>	AAGGACCUGAGAAGGAGGGAGAGGGACACAGCUAUUUCAGC
<i>LMO7</i>	AACCCGAGCAGGAGAAGAGGAGAGGAGACAGCCACAAGAGG
<i>LRTOMT</i>	GGAACCCCAUUGGAGGAAGAGAAAGGGUUAUAGCAGGCCUUG
<i>LTB4R</i>	GAGUGGAGUGGAAGAAGAGGGAGAGGUGGAGCAAAGUGAGG
<i>NUDC</i>	GCUAACUGAUGAAGAGGCAGAGAGGCUGCAGCUAGAGAUUG
<i>POMC</i>	ACGCCUACAAAGAGGGCGAGUGAGGGCACAGCGGGGCCCCA
<i>SOX9</i>	CUUUGCAGGAGGAGAAGAGAAGGGGUGCAAGCGCCCCACU

The red type indicates nucleotide sequences of miRNA BSs. mRNA, messenger RNA; zma, *Zea mays*; miRNA, mRNA-inhibitory RNA; BSs, binding sites.

Table S4 Characteristics of zma-miR159e-5p interaction with human mRNA genes

Gene	Start of BS, nt	Region of mRNA	ΔG , kJ/mol	$\Delta G/\Delta G_m$, %
<i>BZRAP1</i>	72	5'UTR	-104	91
<i>FEN1</i>	1,040	CDS	-104	91
<i>LZTS1</i>	1,524	CDS	-106	93
<i>PDE6B</i>	218	CDS	-104	91
<i>PRCD</i>	755	3'UTR	-104	91

mRNA, messenger RNA; zma, *Zea mays*; miRNA, mRNA-inhibitory RNA; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BS, binding sites; nt, nucleotide; CDS, coding domain sequence; 3'UTR, 3'-untranslated region; 5'UTR, 5'-untranslated region.

Table S5 Nucleotide sequences of regions of human gene mRNA containing zma-miR159e-5p BSs

Gene	Nucleotide sequences of mRNA regions
<i>BZRAP1</i>	GCAGUCCCCAGAGCAGAGGCCAGCAGGGGCUGAGACUAUGA
<i>FEN1</i>	AAUUCACCUGAGCCGGAUUCUGCAGGAGCUGGGCCUGAAC
<i>LZTS1</i>	UCCUCGACGAGAGCAGAUGGCUGCAGCAGCUGCCAGACCUA
<i>PDE6B</i>	AGGUGGAGGAGAGCACGGCGCUGCUGGAGCUGGUGCAGGAU
<i>PRCD</i>	CCAGAUCAGGAGCAGACCCUGCAGGCAGCUGCUCCUGAUG

The red type indicates nucleotide sequences of miRNA BSs. mRNA, messenger RNA; zma, *Zea mays*; miRNA, mRNA-inhibitory RNA; BSs, binding sites.

Table S6 Characteristics of zma-miR164b-3p interaction with human mRNA genes

Gene	Start of BS, nt	Region of mRNA	ΔG , kJ/mol	$\Delta G/\Delta G_m$, %
<i>DYSF</i>	5,983	CDS	-100	92
<i>EXOC7</i>	2,252	CDS	-102	94
<i>HPD</i>	954	CDS	-100	92
<i>ITGA7</i>	3,496	CDS	-102	94
<i>PTPRF</i>	3,163	CDS	-100	92
<i>ZNF37A</i>	5,222	3'UTR	-102	94

mRNA, messenger RNA; zma, *Zea mays*; miRNA, mRNA-inhibitory RNA; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BS, binding sites; nt, nucleotide; CDS, coding domain sequence; 3'UTR, 3'-untranslated region.

Table S7 Nucleotide sequences of regions of human gene mRNA containing zma-miR164b-3p BSs

Gene	Nucleotide sequences of mRNA regions
<i>DYSF</i>	UGAGCCUCACGGGGGAGAAGAUGAGCGACAUUUUAUGUGAA
<i>EXOC7</i>	UCAAGUACGGGGUGGAGCAGGUGGGCGACAU GAUCGAUCG
<i>HPD</i>	CACACACCCUGGUGGAGAAGAUGAACUACAU CGGCCAAUU
<i>ITGA7</i>	AGCAGUUCAAGGAGGAGAAGACGGGCACCAUCCUGAGGAA
<i>PTPRF</i>	CGCCAGUGCUGGCGGAGAGGAACGGGCGCAUCAUCAGCUA
<i>ZNF37A</i>	GGAAGGGACA GGGGGAGGAGAUGGGCAGCAUUGUUGAGAG

The red type indicates nucleotide sequences of miRNA binding sites. mRNA, messenger RNA; zma, *Zea mays*; miRNA, mRNA-inhibitory RNA; BSs, binding sites.

Table S8 Characteristics of tae-miR408-3p interaction with human mRNA genes

Gene	Start of BS, nt	Region of mRNA	ΔG , kJ/mol	$\Delta G/\Delta G_m$, %
<i>RBMS2</i>	7,343	3'UTR	-113	95
<i>NGB</i>	218	5'UTR	-108	91
<i>ALPK3</i>	602	CDS	-108	91
<i>EDEM1</i>	354	CDS	-108	91
<i>PAQR6</i>	1,079	CDS	-110	93
<i>UNG</i>	260	CDS	-108	91

mRNA, messenger RNA; tae, *Triticum aestivum*; miRNA, mRNA-inhibitory RNA; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BS, binding sites; nt, nucleotide; CDS, coding domain sequence; 3'UTR, 3'-untranslated region; 5'UTR, 5'-untranslated region.

Table S9 Nucleotide sequences of regions of human gene mRNA containing tae-miR408-3p BSs

Gene	Nucleotide sequences of mRNA regions
<i>RBMS2</i>	GCUGUGAUAGGCCAGGGGAGUAGGCUGUGCAGUGACGGCUU
<i>NGB</i>	UCUCUCCCGCGCCAGGGAAGGAGCGGCUGCGGCCCCCGCCG
<i>ALPK3</i>	GUCGGGCCAGGCCAGGGGAGGGACAGCAGCAGGUGACGACG
<i>EDEM1</i>	GGCUGCAGCCGCCGGGGACCGGGGCAGCGCAGAGCCCGCGC
<i>PAQR6</i>	GCCUGGCCCGGCCCGGAAGAGGCAGGGGCAGAUGCCUUC
<i>UNG</i>	AGCUGCGGACGCCUGGGAAGGGGCCGUCGAGCUCUUGAGC

The red type indicates nucleotide sequences of miRNA BSs. mRNA, messenger RNA; tae, *Triticum aestivum*; miRNA, mRNA-inhibitory RNA; BSs, binding sites.

Table S10 Characteristics of tae-miR444a,b-3p interaction in the CDS of human mRNA genes

Gene	Start of BS, nt	ΔG , kJ/mol	$\Delta G/\Delta G_m$, %
<i>AP1B1</i>	2,787	-104	91
<i>COL6A3</i>	9,106	-104	91
<i>DOCK1</i>	1,960	-104	91
<i>HIC1</i>	2,077	-104	91
<i>KRT6A</i>	460	-104	91
<i>KRT6B</i>	299	-104	91
<i>KRT6C</i>	299	-104	91
<i>RHBDF1</i>	1,071	-108	94
<i>RUNDC1</i>	1,191	-108	94

mRNA, messenger RNA; tae, *Triticum aestivum*; miRNA, mRNA-inhibitory RNA; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BS, binding sites; nt, nucleotide; CDS, coding domain sequence.

Table S11 Nucleotide sequences of regions of human gene mRNA containing tae-miR444a,b-3p BSs

Gene	Nucleotide sequences of mRNA regions
<i>AP1B1</i>	GAGGCUGCGAGCAGCAAGCUGCAGAGCAGCAACAUCUUCAC
<i>COL6A3</i>	GCCAGCAACGCGAGCGAAGCCUGUAGCAGCAAAGCCAGCAG
<i>DOCK1</i>	CCAGCCUGCUGCAGCAGAACUUGAGGCAGCUGAUGAAAGUC
<i>HIC1</i>	UCACGGCCGAGCAGCUGAGCCUGAAGCAGCAGGACAAGGCG
<i>KRT6A</i>	GGCGGCUAUGGCAGCAGAGCCGGAGGCAGCUAUGGCUUUGG
<i>KRT6B</i>	GGCGGCUAUGGCAGCAGAGCCGGAGGCAGCUAUGGCUUUGG
<i>KRT6C</i>	GGCGGCUAUGGCAGCAGAGCCGGAGGCAGCUAUGGCUUUGG
<i>RHBDF1</i>	GCCUGGACCGCAGCGAGCUUGAGCGCAGCACCCUGAUGCU
<i>RUNDC1</i>	ACAGAGUGAAGCAGCUAGCCUUGAGGCAGCAGCCACAUGAC

The red type indicates nucleotide sequences of miRNA BSs. mRNA, messenger RNA; tae, *Triticum aestivum*; miRNA, mRNA-inhibitory RNA; BSs, binding sites.

Table S12 Characteristics of tae-miR9653b-5p interaction in the CDS of human mRNA genes

Gene	Start of BS, nt	Region of mRNA	ΔG , kJ/mol	$\Delta G/\Delta G_m$, %
<i>ITIH4</i>	3,084	3'UTR	-106	93
<i>TMEM184A</i>	2,137	3'UTR	-104	91
<i>AOC3</i>	1,250	CDS	-113	98
<i>LOC101927064</i>	489	CDS	-104	91
<i>RBM19</i>	1,949	CDS	-104	91
<i>TEAD2</i>	245	CDS	-104	91
<i>TEAD3</i>	360	CDS	-104	91

mRNA, messenger RNA; tae, *Triticum aestivum*; miRNA, mRNA-inhibitory RNA; ΔG , free energy of miRNA binding; ΔG_m , free energy of miRNA binding to a fully complementary nucleotide sequence; BSs, binding sites; nt, nucleotide; CDS, coding domain sequence; 3'UTR, 3'-untranslated region.

Table S13 Nucleotide sequences of regions of human gene mRNA containing tae-miR9653b-5p BSs

Gene	Nucleotide sequences of mRNA regions
<i>ITIH4</i>	UUCCACUGUCAGCUCUCAAGAGCCCAUGGCCAGGAAGGCC
<i>TMEM184A</i>	UCCACACGCCAGCCACAGGGGAGCCUUGGCCAGGCGCCAG
<i>AOC3</i>	UUUUGAGAUUAGCCUCCAAGAGGCCUUGGCCAUUCUAUGGUG
<i>LOC101927064</i>	UCCACACGCCAGCCACAGGGGAGCCUUGGCCAGGCGCCAG
<i>RBM19</i>	CUGGCGGCCAGCUGCAGGAGACCUUCGGCCAUUUUGGCAG
<i>TEAD2</i>	CAUUGAGCAGAGCUUCCAGGAGGCCUUGGCCAUUCUAUCCAC
<i>TEAD3</i>	CAUCGAGCAGAGCUUCCAGGAGGCCUUGGCCAUUCUACCCGC

The red type indicates nucleotide sequences of miRNA BSs. mRNA, messenger RNA; tae, *Triticum aestivum*; miRNA, mRNA-inhibitory RNA; BSs, binding sites.

*Data in supplementary tables come in part from the PhD dissertation of AR: Characteristics of miRNAs binding with mRNAs of transcription factor genes of agricultural plants [dissertation]. Al-Farabi Kazakh National University; 2021