

Supplementary Figure S1: *Bait RNA binding efficiency and AGO2 detection at the CDS and 3'-UTR of HLA-G*

(a) GTC gel electrophoresis after miTRAP procedure to estimate binding efficiency of HLA-G CDS+MS2 and MS2 control bait RNA to the MS2 loop binding protein. SN: supernatant, W: wash, E: eluate. (b) Western blot analysis of indicated proteins after miTRAP procedure using HLA-G 3'-UTR and CDS coupled to MS2 as bait RNA. AGO2 detection indicates the presence of co-purified miRNAs in the eluates. Actin is used as internal negative control. Probing for maltose binding protein (MBP) ensure equal loading of the resin.

Supplementary Figure S2: *Length distribution of sequenced reads after Illumina sequencing of miTRAP eluates*

Length distribution of sequenced co-purified small RNAs after miTRAP procedure using HLA-G CDS coupled to MS2 (a) or MS2 control (b) as bait RNA. Bars in red indicate typical length of miRNAs.

Supplementary Figure S3: *Analysis of JEG3 and HEK293T miRNA mimic transfection efficiency*

Flow cytometry-based analysis of miRNA mimic transfection efficiency in JEG3 and HEK293T cells using a FITC labelled miRNA mimic.

Supplementary Figure S4: *HLA-E protein detection after miRNA mimic transfection*

Western blot-based detection of HLA-E in JEG3 cells after transfection of miRNA mimic mock control, miR-16 and miR-744. GAPDH was used as housekeeper.

Supplementary Figure S5: *Effects of miR-16 on HLA-G mRNA stability and a luciferase reporter gene*

a) Transcriptional inhibition by Actinomycin D in JEG3 cells or JEG3 cells transfected with miRNA mimic control (mock) and miR-16, respectively. HLA-G mRNA levels were analyzed at the time points indicated. ALAS1 was used to normalize data. (b) Luciferase reporter assay using

wt HLA-G CDS. Relative luc activity was measured in the absence of miRNA mimics (plasmid only) and after transfection of a miRNA mimic control (mock) or miR-16, respectively.

Supplementary Table S1: Oligonucleotides used in this study

name	sequence	application
MF6_Fw_HLA-G CDS	GAATTCGTGGTCATGGCGCCC	amplification on HLA-G CDS
MF7_Rv_HLA-G CDS	CTCGAGTCAATCTGAGCTCTTCTTTCTCC	amplification on HLA-G CDS
MF8_Fw_GAPDH	AGGTCGGAGTCAACGGATTT	qRT-PCR
MF9_Rv_GAPDH	ATCTCGCTCCTGGAAGATGG	qRT-PCR
miRNA_rv	CCAGTGCAGGGTCCGAGGTA	qRT-PCR
MF139_miR 4749 3p ST	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC CTGTGG	qRT-PCR
MF140_miR 4749 3p_fw	CGCCCCCTCCTGCCCCC	qRT-PCR
MF141_miR 1915 5p ST	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC GGCCCCG	qRT-PCR
MF142_miR 1915 5p_fw	ACCTTGCCTTGCTGCCCCGG	qRT-PCR
MF143_miR 654 5p ST	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC GCACAT	qRT-PCR
MF144_miR 654 5p_fw	TGGTGGGCCCGCAGAACATGT	qRT-PCR
miR-0015a-5p qPCR FW	GCCCTAGCAGCACATAATGG	qRT-PCR
MiR-0015a-5p RT SL	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC CACAAA	qRT-PCR
MF502 miR-15b-	GTCGTATCCAGTGCAGGGTCCGAGGTATTCGCACTGGATACGAC	qRT-PCR

name	sequence	application
5p_STL	TGTAAA	
MF503 miR-15b-5p_qPCR	CACGCATAGCAGCACATCATG	qRT-PCR
MF374_miR-16-5p_STL	TCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACC GCCAA	qRT-PCR
MF375_miR-16-5p_Fw	CACGCATAGCAGCACGTAAAT	qRT-PCR
MF376_miR-424-5p_STL	TCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACT TCAA	qRT-PCR
MF377_miR-424-5p_Fw	CACGCACAGCAGCAATTCATG	qRT-PCR
MF382_miR-660-5p_STL	TCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACC AACTC	qRT-PCR
MF383_miR-660-5p_Fw	CGCATACCCATTGCATATCG	qRT-PCR
MF380_miR-744-5p_STL	TCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGACT GCTGT	qRT-PCR
MF381_miR-744-5p_Fw	GCATGCGGGGCTAGGGC	qRT-PCR
miR-0026a-5p qPCR FW	GCCCTTCAAGTAATCCAGGA	qRT-PCR
miR-0026a-5p RT SL	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGAC AGCCTA	qRT-PCR
miR-0030a-5p qPCR FW	GCCCTGTAAACATCCTCGAC	qRT-PCR
MiR-0030a-5p RT SL	GTCGTATCCAGTGCAGGGTCCGAGGTATTTCGCACTGGATACGAC CTTCCA	qRT-PCR
MF418_HLA-G_fw	GAGGAGACACGGAACACCAAG	qRT-PCR
MF419_HLA-G_rv	GTCGCAGCCAATCATCCACT	qRT-PCR
HLA-ABC RT FW	GCCTACGACGGCAAGGATTAC	qRT-PCR
HLA-ABC RT Rev	GGTGGCCTCATGGTCAGAGA	qRT-PCR
MF436_HLA G	GCTAGCGTGGTCATGGCGCCCCG	luciferase

name	sequence	application
CDS_pmiR		reporter
GLO_fw		assay
MF437_HLA G		luciferase
CDS_pmiR	GTCGACCTGAGCTCTTCTTTCTCCACAGC	reporter
GLO_rv		assay
MF492_HLA		luciferase
A_fw	CTCGAGGCCGTCATGGCGCCCCGAA	reporter
		assay
MF493_HLA		luciferase
A_rv	GTCGACTCACACTTTACAAGCTGTGAGGGACA	reporter
		assay
MF494_HLA		luciferase
B_fw	CTCGAGCTGGTCATGGCGCCCCGA	reporter
		assay
MF495_HLA		luciferase
B_rv	GTCGACGAGCCCTGGGCACTGTCG	reporter
		assay
MF496_HLA		luciferase
C_fw	CTCGAGGGGTCATGGCGCCCCGAG	reporter
		assay
MF497_HLA		luciferase
C_rv	GTCGACTCAGGCTTTACAAGTGATGAGAG	reporter
		assay
		luciferase
		reporter
		assay
MF514_mut.miR		(mutation
-744 BS_fw	GATCGGGGCGTGATCATACTGACCTGGCAGCG	of miR-744
		binding
		site)
		luciferase
		reporter
MF515_mut.miR		assay
-744 BS_rv	CCGATTGTCGTCACAGCACCTCAGGGTGGC	(mutation
		of miR-744
		binding

name	sequence	application
		site)
MF474_RNU47_ fw	GATGTAATGATTCTGCCAAATG	PCR (nuclei marker)
MF475_RNU47_ rv	CCTCAGAATCAAAATGGAACG	PCR (nuclei marker)
MF600_HPRT_f w	CATTATGCTGAGGATTTGGAAAGG	PCR (cytoplasm a marker)
MF601_HPRT_r v	CTTGAGCACACAGAGGGCTACA	PCR (cytoplasm a marker)
MF614_HLA G proximal Pro_ChIP_fw	CTTCCTGGATACTCACCGGG	ChIP Assay (prox. HLA-G Pro 1)
MF615_HLA G proximal Pro_ChIP_rv	TTGGCGTCTGGGGAGAATGA	ChIP Assay (prox. HLA-G Pro 1)
MF591_HLA G Pro2_fw	AGTGAGGGGCATTGTGACTG	ChIP Assay (distal HLA-G Pro 2)
MF592_HLA G Pro2_rv	TATGTTGCAACCAGGAGCCA	ChIP Assay (distal HLA-G Pro 2)
ALAS1_fw	TGAGACAGATGCTAATGGATGC	qRT-PCR
ALAS1_rv	CACCGTAGGGTAATTGATTGCT	qRT-PCR

Supplementary Table S2: Illumina small RNA-sequencing characteristics

sample	reads	low quality	total small RNAs	known miRNAs
HLA-G CDS + MS2	12.689.769	13.961 (0.11%)	7.034.456	1.466.584
MS2 control	12.832.780	30.990 (0.24%)	3.164.771	1.547.643

Supplementary Table S3: Indicated correlation data derived from cancerminer tool (35)

		miR-16			miR-744		
		REC score	p-value	FDR	REC score	p-value	FDR
pan-cancer	HLA-A	1.87	p < 0.05	0.25	-2.03	p < 0.01	0.21
	HLA-B	0.83	p > 0.05	0.68	-2.52	p < 0.01	0.11
	HLA-C	1.23	p = 0.05	0.48	-2.91	p < 0.01	0.07
	HLA-G	1.96	p < 0.05	0.22	-0.87	p > 0.05	0.66
breast carcinoma	HLA-A	5.88	p < 0.001	n.a.	-4.15	p < 0.001	n.a.
	HLA-B	2.42	p < 0.01	n.a.	-2.13	p < 0.01	n.a.
	HLA-C	3.47	p < 0.001	n.a.	-3.26	p < 0.001	n.a.
	HLA-G	4.66	p < 0.001	n.a.	-2.27	p < 0.01	n.a.
colon adenocarcinoma	HLA-A	2.48	p < 0.01	n.a.	-2.28	p < 0.01	n.a.
	HLA-B	2.32	p < 0.01	n.a.	-2.37	p < 0.01	n.a.
	HLA-C	2.19	p < 0.01	n.a.	-2.16	p < 0.01	n.a.
	HLA-G	2.33	p < 0.01	n.a.	-2.94	p < 0.01	n.a.

REC: association recurrence score; FDR: false discovery rate; n.a.: not analyzed

Supplementary Data 1: Summary of miRBase-mapped miRNA reads determined from indicated library using the HLA-G CDS coupled to MS2 and MS2 control as bait RNA