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Down-regulation of miR-205 promotes stemness of hepatocellular carcinoma cells by targeting PLCβ1 and increasing CD24 expression

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Hepatocellular carcinoma (HCC) is a particularly lethal form of cancer. Overall survival eve after liver surgery is unsatisfactory due to high metastatic capacity and recurrence rates. Cancer stem cells (CSCs) were recently proposed to elucidate the molecular mechanism of HCC metastasis and recurrence. In our study, we found that down-regulation of miR-205 promoted stem cell inhibition of HCC.

Expression of miR-205 and PLCβ1 was investigated by qRT-PCR. MiR-205 and PLCB1 expression were associated with disease free survival(DFS) by log-rank test. Computational predicting software was used to predict potential targets of miR-205. MiR-205 and PLCβ1 were transfected into cells to analyze the stem cell inhibition.

MiR-205 was significantly down-regulated and PLCβ1 dramatically up-regulated in tumors compared with matched tissues ($P<0.0001$). High miR-205 and low PLCβ1 expression was found to be associated with better DFS. PLCβ1 was one of the potential targets of miR-205 and the dual luciferase report system demonstrated that PLCβ1 was a direct target of miR-205 in cells. When miR-205 and PLCβ1 were transfected into cells, we found that the number of spheres increased and the CD24+ subpopulation of HCC cells dramatically increased.

Down-regulation of miR-205 promotes stem cell inhibition of HCC by targeting PLCβ1 and increasing CD24 expression.

Key words: miR-205, HCC, PLCB1, stem cell inhibition

Hepatocellular carcinoma (HCC) is the sixth most common malignancy and globally the third-leading cause of cancer-related death [1]. The incidence of HCC is dramatically increasing in developing countries such as China, in which hepatitis B virus (HBV) infection is prevalent, and HBV has been shown to be closely associated with hepatocarcinogenesis [2,3]. Due to the often late diagnosis and lack of effective treatment, most HCC develops to the advanced stages, where surgery is not an option, which generally results in poor prognosis [4]. Thus, more effective treatments are urgently needed for HCC. Cancer stem cells (CSCs), also known as tumor-initiating cells, have been demonstrated in HCC cells and are considered the master regulators of HCC initiation, metastasis and chemotherapeutic drug resistance [5-7]. Hence, hepatic CSCs may serve as better therapeutic targets for treating HCC patients. Despite the clinical importance, the regulation of hepatic CSCs remains elusive.

MicroRNAs (miRNAs), the small endogenous non-coding RNA, play an important role in modulating diverse cellular processes including growth, differentiation and apoptosis, by targeting the protein coding genes or even long noncoding RNAs [8]. Thus, the discovery of miRNAs extends our knowledge about gene expression and regulation. It is estimated that approximately one third of all human genes are regulated by miRNAs [9]. Recent evidence has highlighted the function of miRNAs in modulating and controlling the self-renewal and pluripotency of stem cells [10]. Currently, some miRNA clusters, which are highly expressed in embryonic stem cells, have been shown to promote induced pluripotent stem cells (iPS cells) reprogramming [11]. For instance, miR-134, miR-296,

and miR-470 significantly increased during the differentiation of mouse embryonic stem cells [12]. In HCC, the modulation of hepatic CSCs is largely unknown. Some evidence has shown that miRNAs and other noncoding RNAs play important roles in the regulation of hepatic CSCs.

In order to elucidate the role of miR-205 in the regulation of hepatic CSCs in HCC cells, we first analyzed the expression of miR-205 in HCC tumors and matched normal tissues and found that miR-205 was significantly down-regulated in HCC tumors. Moreover, when these patients were followed-up after surgery, we found that the down-regulation of miR-205 was closely associated with longer disease free survival (DFS), indicating that it could be a prognostic biomarker in HCC. We further demonstrated that phospholipase C β1 (PLCβ-1) was one of the potential targets of miR-205 using online predicting software and remained the downstream target in cells. PLCβ-1 was also closely related to the DFS when patients underwent surgery. When PLCβ-1 and miR-205 were transfected into HCC cells, we found that they could regulate the stem cell inhibition of HCC by increasing the CD24+ cell population. Taken together, miR-205 can regulate the stem cell inhibition of HCC by targeting PLCβ-1 and can also be a prognostic biomarker of HCC in clinical settings.

Materials and methods

Reagents and cell culture. The human HCC cell lines were cultured in modified RPMI-1640 or DMEM (Invitrogen, Carlsbad, CA, USA) with 10% fetal bovine serum (FBS) and 100 units/mL of penicillin and 100 μg/mL of streptomycin (GIBCO, Grand Island, NY, USA). The SuperScript III First-Strand Synthesis System kit for RT-PCR was purchased from Life Technologies (Carlsbad, CA, USA). The SsoFast™ EvaGreen® Supermix for qPCR was from Bio-Rad (Hercules, CA, USA). The HCC tumors and matched normal tissues were obtained from and the Department of General Surgery, the First Affiliated Hospital of Anhui Medical University. The informed consents were obtained from patients and this study was approved by the ethics committee of Anhui Medical University.

RNA extraction and Real-Time Quantitative Reverse-Transcription PCR (qRT-PCR). Total RNA from HCC tumors or matched normal tissue samples or cell lines was extracted using TRIzol reagent (Life Technologies, USA). The quality and quantity of isolated total RNA was assessed using the NanoDrop ND-1000 Spectrophotometer. For mRNA detection, the total RNA was reverse-transcribed using the SuperScript III First-Strand Synthesis System kit and then amplification was performed using the SsoFast™ EvaGreen® Supermix. The primers for PLCβ1 were 5'-GGGGTACCCCAAATGCTTGTCTGGCCTCC-3'(F), and 5'-GCTCTAGAGCCTGGTGAACTATATTCAGCC-3'(R)[13]; The primers for HPRT1 were TGACACTGGCAAAACAATGCA (F) and GGTCCTTTTCACCAGCAAGCT (R). For miRNA detection, the total RNA was polyadenylated and reverse-transcribed for quantitative RT-PCR using the NCode™ VILO™ miRNA cDNA Synthesis and EXPRESS SYBR® GreenER™ miRNA qRT-PCR kits (Life Technologies, USA), according to the manufacturer's instructions. HPRT1 and U6 internal control were used as endogenous controls, and fold changes were calculated via relative quantification ($2^{-\Delta Ct}$).

Western blotting. The transfected cells were washed twice with cold PBS and solubilized in radioimmunoprecipitation assay (RIPA) lysis buffer with the halt protease inhibitor cocktail (Pierce, Rockford, IL, USA). The protein concentrations were determined using the Bradford protein assay (Bio-Rad, Hercules, CA, USA). Heat-denatured protein samples (20 μg per lane) were resolved by SDS-polyacrylamide gel electrophoresis (PAGE) and transferred to the nitrocellulose membrane using the iBlot® Dry blotting transfer system (Life Technologies, USA). The membrane was incubated for 2 h in PBS containing 0.1% Tween 20 and 5% skimmed milk to block non-specific binding, followed by incubation overnight at 4°C with a primary rabbit polyclonal antibody against PLCβ1 (1:500 dilution) (Abcam, UK) or goat anti-GAPDH polyclonal antibody (1:1000) (GenScript, NJ). The membrane was washed three times for 10 min each in PBS with 0.1% Tween 20 and then incubated for 1-2 h with the secondary antibody. The membrane was washed thoroughly in PBS containing 0.1% Tween 20 and subjected to Pierce ECL Western blotting (Pierce, Rockford, IL), according to the manufacturer's instructions.

Sphere formation assay. Single-cells (1×10^3) were plated onto a 24-well ultralow-attachment plate (Corning, Corning, NY) in serum-free DMEM-F12, supplemented with 10 ng/mL basic fibroblast growth factor, 20 ng/mL epidermal growth factor, 0.4% bovine serum albumin and B-27 supplement (1:50 dilution; Invitrogen). After 14 days of culture, the number of formed tumor spheres (diameter > 40 μm) were counted under an inverted microscope.

Flow cytometry. Stably transfected cells (1×10^6) were resuspended in 100 μl of staining buffer (eBioscience, San Diego, CA) containing 1% FBS and placed on ice for 20 min to block Fc receptors. After incubation with primary phycoerythrin-conjugated anti-human CD24 antibodies (BD Biosciences, USA) for another 45 min on ice in the dark, cells were washed twice with 1 ml ice-cold staining buffer and centrifuged at 400 × g for 5 min at 4°C. Cells resuspended in 0.5 ml of 2% formaldehyde fixation buffer were analyzed using theBD FACSCanto II flow cytometer (BD Biosciences, USA) and FlowJo software. All flow cytometry results were obtained from two independent experiments performed in triplicate.

Luciferase reporter assay. The potential microRNAs targeting PLCβ1 were selected by bioinformatic analysis. The 3'-UTR sequence of PLCβ1, which is predicted to interact with the microRNAs, was synthesized and inserted into the *Xba*I and *Fse*I sites of the pGL3 control vector (Promega, Madison, WI). For the reporter assay, HEK293 cells were plated onto 24-well plates and transfected with the above constructs and

miR-205 mimics or mimic-controls using the Lipofectamine 3000 transfection reagent (Life Technologies, USA). A Renilla luciferase vector pRL-SV50 (Promega, Madison, WI) was also co-transfected to normalize the differences in transfection efficiency. After transfection for 48 h, cells were harvested and assayed with the Dual-Luciferase Reporter Assay System (Promega, Madison, WI) according to the manufacturer's instructions. This experiment was performed in duplicate in three independent experiments.

Survival and statistical analysis. The experimental data are presented as the mean ± standard deviation (SD). All statistical analyses were performed using ANOVA or a two-tailed Student's *t* test (GraphPad Prism 5). Disease free survival (DFS) was measured from the date of hepatic resection to the date of death or the last follow-up. The survival curves were calculated using the Kaplan-Meier method and statistically compared using a log-rank test. Differences were considered statistically significant when the P-values were less than 0.05.

Results

miR-205 is down-regulated in HCC tumors and inversely associated with the expression of PLCβ1. Since miR-205 plays an important role in HCC carcinogenesis, it is interesting to investigate the expression of miR-205 in HCC patients. The expression of miR-205 and its potential target PLCβ1 in 30 samples of HCC tumors and matched normal tissues were compared by qRT-PCR. Interestingly, miR-205 was down-regulated in HCC tumors, while it was up-regulated in matched normal tissues (Fig. 1B). Computational software was used to predict the downstream target of miR-205, and PLCβ1 was of specific interest because it was involved in signal transduction cascades that influence many cellular events, including cell cycle, tumor progression and differentiation [14]. We performed qRT-PCR to analyze the expression of PLCβ1 in tumors and matched normal tissues. Conversely, it showed down-regulation of PLCβ1 in tumors when compared to matched normal tissues (Fig. 1A). Thus, the expression of miR-205 and PLCβ1 were inversely expressed in tumors and matched normal tissues (Fig.1 A&B). This indicates that PLCβ1 may be one of the direct targets of miR-205 in HCC tumors.

Clinical significance of miR-205 and PLCβ1 in HCC patients. To investigate the clinical significance of miR-205 and PLCβ1 in HCC patients, the expression of miR-205 in 30 examples of HCC patients was compared by qRT-PCR. Interestingly, we found that HCC patients with high miR-205 had longer DFS compared with patients with low miR-205 (P=0.034, Student's t-test, Fig. 2B). Next, we detected PLCβ1 in these 30 tumor samples. Consistently, low expression of PLCβ1 was significantly correlated with longer DFS of patients (P=0.044; Fig. 2A). In HCC, shorter DFS generally indicated that patients very often develop recurrence or metastasis and as well as resistance to chemotherapeutic therapies. Taking these results into account, miR-205, along with its downstream target- PLCβ1, may play a critical role in the development of therapeutic resistance and metastasis seen in HCC. Thus, they may serve as prognostic biomarkers or therapeutic targets for treating HCC patients.

Over-expression of PLCβ1 is associated with the loss of miR-205 in HCC. We have demonstrated the clinical significance of PLCβ1 and miR-205 in HCC; therefore, it is interesting to investigate the regulation of PLCβ1. Previous studies have suggested that at least one-third of human genes are estimated to be miRNA targets, so we used TargetScan/TargetScanS to predict whether there is interaction between PLCβ1 and miR-205. The 3'-UTR of PLCβ1 can be perfectly matched with miR-205 (Fig.3A&B), suggesting that PLCβ1

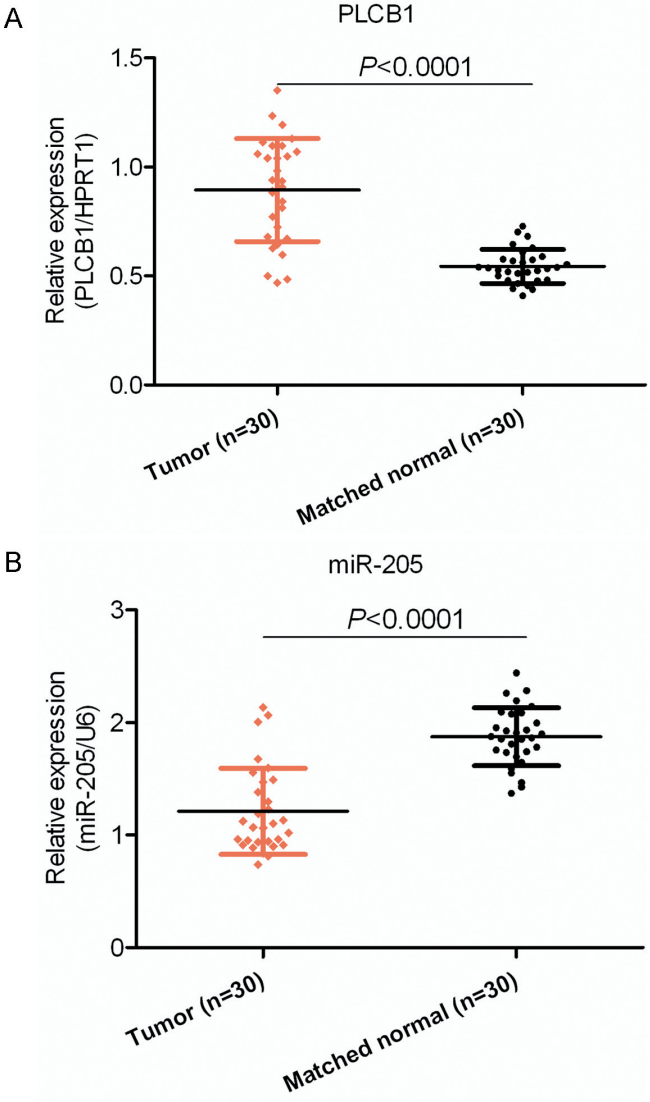

Figure 1. Overexpression of PLCβ1 was inversely associated with down-regulation of miR-205 in HCC samples. (A and B) The expression of PLCβ1 (A) and miR-205 (B) in 30 pairs of HCC tissue samples was examined by real time qRT-PCR analysis.

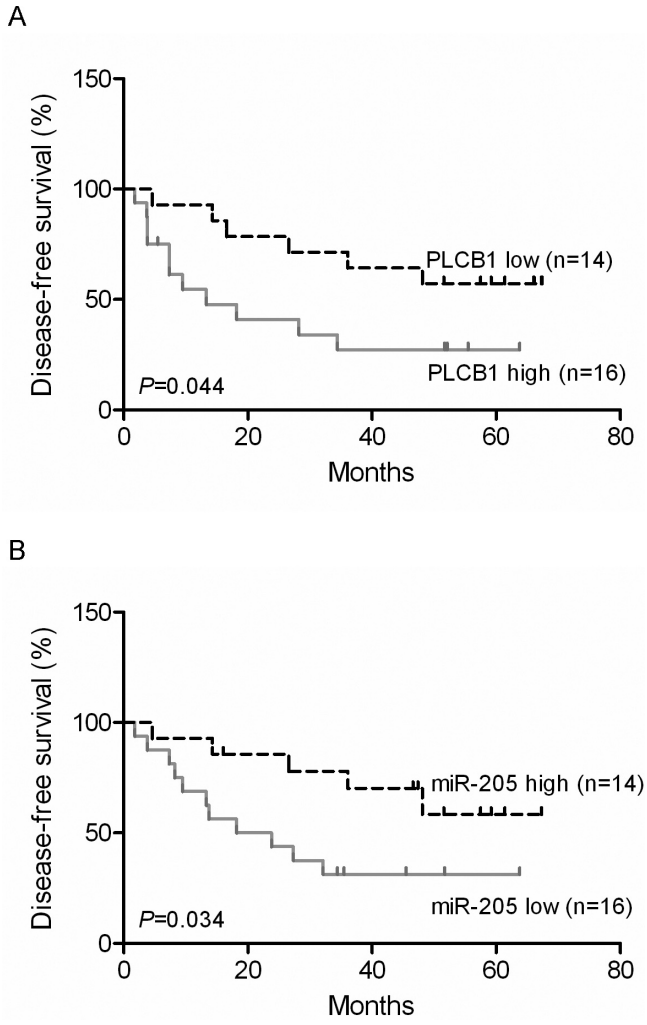

Figure 2. Overexpression of PLCB1 and down-regulation of miR-205 are associated with poor survival. (A and B) The median expression level of PLCβ1 (A) and miR-205 (B) in all 30 samples was chosen as the cut-off point. The Kaplan-Meier method was used to analyze survival in patients with HCC.

may be regulated by miR-205. To validate whether miR-205 directly recognizes the 3'-UTRs of PLCβ1 mRNA, we cloned the 3'UTR of PLCβ1 to the pGL3 luciferase reporter gene to generate pGL3- PLCβ1-3'UTR-wt or pGL3- PLCβ1-3'UTR-mut as a control vector. The vectors were then co-transfected with miR-205 plasmid or miR-205 controls into HEK293 cells. A renilla luciferase vector (pRL-TK) was used to normalize differences in transfection efficiency. Luciferase activity in cells co-transfected with miR-205 and pGL3- PLCβ1-3'UTR-wt vectors was decreased when compared with the control (Fig.3D). Next, we further detected the protein expression of PLCβ1 in cells after transfection with miR-205 or the control. The results showed that the over-expression of miR-205 decreased the expression of PLCβ1 (Fig. 3C). These data suggest that the over-expression of PLCβ1 is associated with a loss of miR-205 in HCC.

Overexpression of miR-205 promote stem cell inhibition of HCC cells. Recent studies have indicated that the emergence of cancer stem cells (CSCs) contributes to HCC chemoresistance, metastasis, recurrence and poor survival. Several biomarkers of HCC hepatic CSCs have been identified and CD24 is one of them. We assessed the self-renewal ability of HCC cancer cells by means of sphere formation, which is considered a hallmark of cancer stem-like cells. Interestingly, we also found that sphere formation ability was approximately 7- to 8-fold decreased when miR-205 was stably over-expressed in HCC cancer cells (Fig.4A and 4B). Next, we also analyzed the population of CD24+ cells, which are considered to be hepatic CSCs. Consistently, we found that when miR-205 was transfected into HCC cells, CD24+ cell number dramatically decreased compared with that when miR-205 control or both miR-205 and PLCβ1 were transfected into HCC cells. These results indicate that miR-205 promotes stemness of HCC by targeting PLCβ1 and increasing CD24 expression.

Discussion

Cancer stem cells (CSCs) compose a small fraction of tumor bulk, which show a high capacity of sphere forming, self-renewing and high resistance to chemoradiotherapy [15]. This bulk of CSCs may result in the initiation and propagation of cancer cell growth, metastasis, recurrence and chemoresistance. Targeting CSCs may represent a novel therapy for treating malignancies. Hepatic CSCs were first reported by Haraguchi and colleagues [6]. In recent studies, several biomarkers of hepatic CSCs have been identified, including CD90 [16], CD133 [17] and CD13 [18]. Another important biomarker is CD24 and CD24 positive HCC cells have been shown to be important for the maintenance, self-renewal and metastasis of HCC[19]. In our study, we found that the CD24+ cell population was increased while sphere formation capacity was also improved in stably transfected HCC cells, partly demonstrating that CD24 is an important biomarker for hepatic CSCs.

CSCs appear to arise by epigenetic mechanisms. MicroRNAs (miRs), 18-24nt long RNAs, have emerged as one of the most important epigenetic modulators, playing an important role in multiple biological processes such as cell growth, differentiation, apoptosis and survival[20]. The interaction between miRNAs and CSCs has been implicated in many studies. CSCs, compared with tumors or matched normal tissues, showed dramatic differently expressed miRNA patterns[21]. Furthermore, MiRNAs were proven to regulate CSCs and be crucial in maintaining CSC self-renewal and differentiation by effecting implicated signaling pathways and protein-coding genes. However, the role of a specific miRNA in CSCs maintenance or regulation is not clear. In our study, we investigated the role of miR-205 to uncover the mecha-

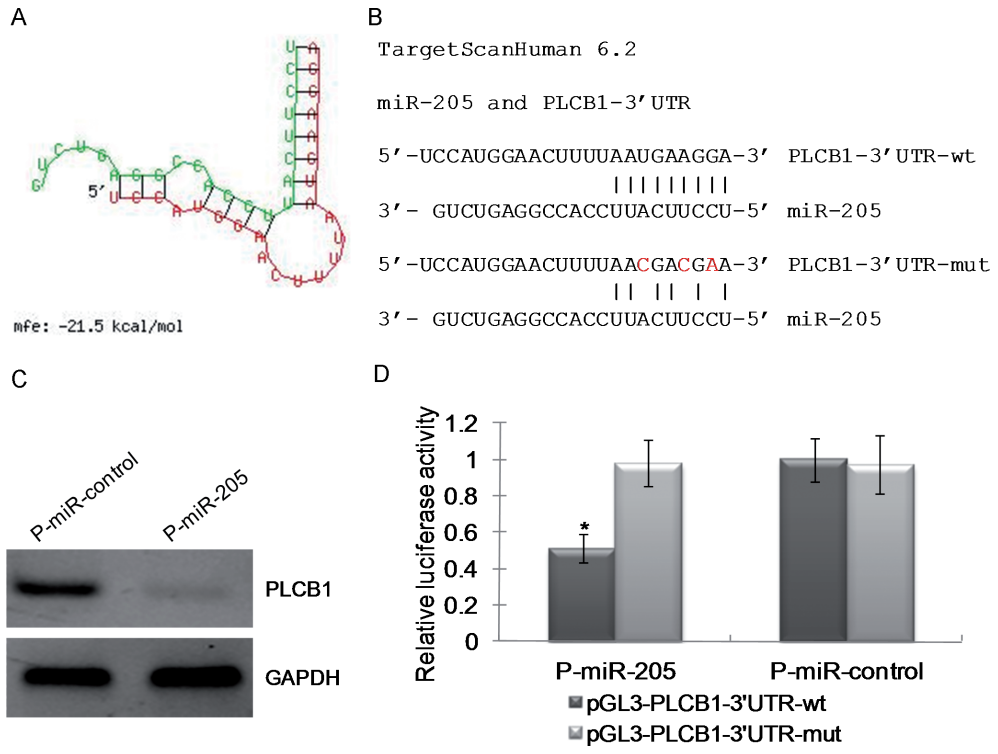

Figure 3. PLCB1 is a direct downstream target of miR-205. (A and B) The bioinformatic prediction of the binding sequence or mutation of the 3'-UTRs of PLCβ1 mRNA. (C) Western blot analysis of PLCβ1 in the cell lysates extracted from p-miR-205 or p-miR-control transfected cells. (D) Luciferase activity in cells co-transfected with p-miR-205 or p-miR-control and pGL3-PLCβ1-3'UTR-wt or pGL3-PLCβ1-3'UTR-mut vector.

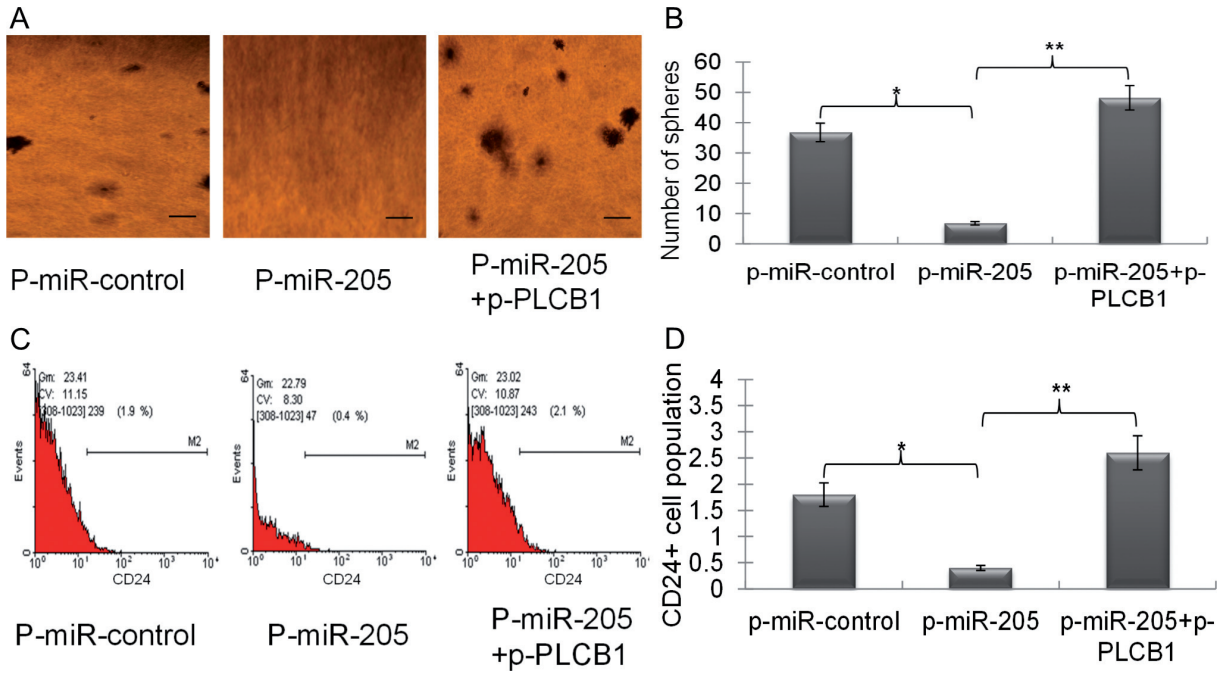

Figure 4. Down-regulation of miR-205 promotes stemness of hepatocellular carcinoma cells by targeting PLCB1 and increasing CD24 expression. (A) The representative images of tumor spheres from the sphere formation assay. (B) The bar graph indicates the number of tumor spheres (mean ± S.D.) generated after 2–3 weeks of single-cell culture in each group. (C) Flow cytometry analysis of CD24+ cell distribution in established stable cells. (D) The bar graph indicates the quantification of CD24+ cell distribution in two independent experiments performed in triplicate.* $P<0.05$, ** $P<0.01$

nism of miR-205 in the regulation or maintenance stem cell inhibition of HCC CSCs.

As many characteristics of miR-205 have been revealed, it appears to exert an effect as either an oncogenes or tumor suppressor gene, determined by the specific cancer context or its target genes [22,23]. The expression level of miR-205 is controversial as it can be down-regulated or up-regulated depending on the cell type. In our study, we found that it was down-regulated in HCC tumor tissues, indicating its role as a tumor suppressor in HCC. Previous studies have shown that it can be associated with stem cell properties in lung cancer. Consistently, we also found that miR-205 can promote stemness in HCC by targeting PLCβ1.

PLCβ1 is an important enzyme in nuclear lipid signal transduction that plays a critical role in cell cycle progression[24]. PLCβ1 presents in two forms, 150-kDa PLCβ1a and 140-kDa PLCβ1b, both of which mostly exist in the nucleus of cells. Previous studies have shown that the over-expression of PLCβ1 induces cell cycle progression by targeting cyclin D3, along with its specific kinase[25]. It was also demonstrated to regulate the expression of CD24 in mouse models[14]. In our study, comparing HCC tumor tissues and matched normal tissues, we found that PLCβ1 was significantly expressed in tumors, indicating its important role in tumorigenesis. Moreover, the computational software shows that PLCβ1 is a potential downstream target of miR-205, and the luciferase reporting system demonstrates that it is an authentic target of miR-205 in cells. Importantly, we also found that miR-205 was inversely expressed with PLCβ1 in tumor tissues. All of these results demonstrate that the miR-205/PLCβ1 axis may play an important role in HCC tumorigenesis and stemness maintenance.

We also investigated the clinical significance of miR-205 and PLCβ1 in HCC tumors. The expression of miR-205 and PLCβ1 in 30 samples of HCC was compared by qRT-PCR. Interestingly, we found that HCC patients with low miR-205 or high PLCβ1 had longer disease free survival (DFS) compared with patients with high miR-205 or low PLCβ1. In HCC, shorter DFS means that patients easily developed recurrence or metastasis. From these results, it can be seen that miR-205, along with the significantly modulated PLCβ1, may play a critical role in the recurrence or metastasis of HCC. Thus, they may serve as prognostic biomarkers for HCC.

In conclusion, we found that the miR-205/PLCβ1 axis may play an important role in HCC stemness maintenance and the increased CD24 subpopulation, thus it may be a therapeutic target for the treatment of HCC in the future.

Supplementary information is available in the online version of the paper.

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Supplementary Information

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Supplementary table

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
ZNF606	NM_025027	zinc finger protein 606	**1**	1	0	0	**3**	2	0	1	hsa-miR-205	-0,89	< 0.1		Sites in UTR
CMTM4	NM_181521	CKLF-like MARVEL transmembrane domain containing 4	**2**	1	0	1	**4**	1	2	1	hsa-miR-205	-0,89	0,43		Sites in UTR
DMXL2	NM_001174116	Dmx-like 2	**1**	1	0	0	**1**	1	0	0	hsa-miR-205	-0,58	0,16	2005, 2007	Sites in UTR
BTBD3	NM_014962	BTB (POZ) domain containing 3	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,52	0,68	2005, 2007, 2009	Sites in UTR
LPCAT1	NM_024830	lysophosphatidylcholine acyltransferase 1	**1**	1	0	0	**2**	1	1	0	hsa-miR-205	-0,51	0,64	2007, 2009	Sites in UTR
SECISBP2L	NM_001193489	SECIS binding protein 2-like	**2**	1	1	0	**0**	0	0	0	hsa-miR-205	-0,5	0,23		Sites in UTR
YES1	NM_005433	v-yes-1 Yamaguchi sarcoma viral oncogene homolog 1	**1**	0	1	0	**2**	1	1	0	hsa-miR-205	-0,49	0,27	2005, 2007, 2009	Sites in UTR
C16orf52	NM_001164579	chromosome 16 open reading frame 52	**1**	1	0	0	**3**	0	0	3	hsa-miR-205	-0,48	0,44		Sites in UTR
CHN1	NM_001025201	chimerin (chimaerin) 1	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,47	0,27	2005, 2007, 2009	Sites in UTR
DLG2	NM_001142699	discs, large homolog 2 (Drosophila)	**1**	1	0	0	**1**	1	0	0	hsa-miR-205	-0,47	0,67	2005, 2007, 2009	Sites in UTR
ZFYVE16	NM_001105251	zinc finger, FYVE domain containing 16	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,46	< 0.1		Sites in UTR
CCNJ	NM_001134375	cyclin J	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,45	0,7	2005, 2007, 2009	Sites in UTR
PTCHD1	NM_173495	patched domain containing 1	**1**	0	1	0	**2**	0	1	1	hsa-miR-205	-0,44	0,26	2009	Sites in UTR
TBX18	NM_001080508	T-box 18	**2**	1	1	0	**1**	0	1	0	hsa-miR-205	-0,43	0,18	2009	Sites in UTR
MED1	NM_004774	mediator complex subunit 1	**3**	2	1	0	**1**	0	1	0	hsa-miR-205	-0,43	0,7	2005, 2007, 2009	Sites in UTR
LRRK2	NM_198578	leucine-rich repeat kinase 2	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,42	0,66	2007, 2009	Sites in UTR
MGRN1	NM_001142289	mahogunin, ring finger 1	**2**	2	0	0	**0**	0	0	0	hsa-miR-205	-0,42	0,27	2005, 2007, 2009	Sites in UTR
KPNA1	NM_002264	karyopherin alpha 1 (importin alpha 5)	**1**	0	0	1	**2**	1	1	0	hsa-miR-205	-0,4	0,3	2009	Sites in UTR
ACSL1	NM_001995	acyl-CoA synthetase long-chain family member 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,4	0,14	2005, 2007, 2009	Sites in UTR
PPP1R15B	NM_032833	protein phosphatase 1, regulatory (inhibitor) subunit 15B	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,4	0,14	2005, 2007, 2009	Sites in UTR
RAB11FIP1	NM_001002814	RAB11 family interacting protein 1 (class I)	**3**	1	0	2	**2**	2	0	0	hsa-miR-205	-0,4	0,37	2005, 2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
TAPT1	NM_153365	transmembrane anterior posterior transformation 1	**1**	0	1	0	**2**	0	2	0	hsa-miR-205	-0,4	0,27	2009	Sites in UTR
C11orf86	NM_001136485	chromosome 11 open reading frame 86	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,39	0,23		Sites in UTR
CDK19	NM_015076	cyclin-dependent kinase 19	**1**	1	0	0	**4**	0	1	3	hsa-miR-205	-0,39	0,52	2003, 2005, 2007, 2009	Sites in UTR
COX11	NM_004375	COX11 cytochrome c oxidase assembly homolog (yeast)	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,39	0,2	2009	Sites in UTR
KLF12	NM_007249	Kruppel-like factor 12	**2**	0	2	0	**2**	1	0	1	hsa-miR-205	-0,39	0,58	2005, 2007, 2009	Sites in UTR
ETNK1	NM_018638	ethanolamine kinase 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,39	0,14	2007, 2009	Sites in UTR
CDK14	NM_012395	cyclin-dependent kinase 14	**1**	1	0	0	**2**	0	2	0	hsa-miR-205	-0,38	0,18	2009	Sites in UTR
TNFAIP8	NM_001077654	tumor necrosis factor, alpha-induced protein 8	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,38	0,14	2009	Sites in UTR
RBM47	NM_001098634	RNA binding motif protein 47	**2**	0	1	1	**1**	0	0	1	hsa-miR-205	-0,38	0,58	2005, 2007, 2009	Sites in UTR
NEU1	NM_000434	sialidase 1 (lysosomal sialidase)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,38	0,45	2009	Sites in UTR
CHIC1	NM_001039840	cysteine-rich hydrophobic domain 1	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,38	< 0.1		Sites in UTR
TGFA	NM_001099691	transforming growth factor, alpha	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,38	0,27	2009	Sites in UTR
NSF	NM_006178	N-ethylmaleimide-sensitive factor	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,37	0,14	2009	Sites in UTR
ADAMTS9	NM_182920	ADAM metallopeptidase with thrombospondin type 1 motif, 9	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,37	0,58	2005, 2007, 2009	Sites in UTR
LRP1	NM_002332	low density lipoprotein receptor-related protein 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,36	0,67	2005, 2007, 2009	Sites in UTR
PHF16	NM_001077445	PHD finger protein 16	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,36	0,48	2009	Sites in UTR
CADM1	NM_001098517	cell adhesion molecule 1	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,35	0,41	2009	Sites in UTR
SLC30A8	NM_001172811	solute carrier family 30 (zinc transporter), member 8	**1**	0	0	1	**3**	1	1	1	hsa-miR-205	-0,35	0,27		Sites in UTR
SYT13	NM_020826	synaptotagmin XIII	**1**	1	0	0	**2**	0	0	2	hsa-miR-205	-0,35	0,1		Sites in UTR
ENC1	NM_003633	ectodermal-neural cortex 1 (with BTB-like domain)	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,34	0,19	2009	Sites in UTR
PJA2	NM_014819	praja ring finger 2	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,34	0,18	2005, 2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
CASC4	NM_138423	cancer susceptibility candidate 4	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,34	< 0.1	2009	Sites in UTR
LYSMD3	NM_198273	LysM, putative peptidoglycan-binding, domain containing 3	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,34	0,14	2007, 2009	Sites in UTR
ABI2	NM_005759	abl-interactor 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,34	0,14	2009	Sites in UTR
PHC2	NM_004427	polyhomeotic homolog 2 (Drosophila)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,33	0,67	2005, 2007, 2009	Sites in UTR
GRAMD1C	NM_001172105	GRAM domain containing 1C	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,33	< 0.1	2009	Sites in UTR
HS3ST1	NM_005114	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,33	0,1	2005, 2007, 2009	Sites in UTR
IMPG2	NM_016247	interphotoreceptor matrix proteoglycan 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,33	< 0.1		Sites in UTR
EFHA2	NM_181723	EF-hand domain family, member A2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,33	0,61	2009	Sites in UTR
EPB41	NM_001166005	erythrocyte membrane protein band 4.1 (elliptocytosis 1, RH-linked)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,33	0,45	2005, 2007, 2009	Sites in UTR
RBPMS2	NM_194272	RNA binding protein with multiple splicing 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	0,14	2007, 2009	Sites in UTR
DUSP7	NM_001947	dual specificity phosphatase 7	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	0,51		Sites in UTR
TP53BP2	NM_001031685	tumor protein p53 binding protein, 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	0,68	2005, 2007, 2009	Sites in UTR
SLC35A1	NM_001168398	solute carrier family 35 (CMP-sialic acid transporter), member A1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	< 0.1	2009	Sites in UTR
MAGI2	NM_012301	membrane associated guanylate kinase, WW and PDZ domain containing 2	**1**	1	0	0	**2**	0	0	2	hsa-miR-205	-0,32	0,19	2007, 2009	Sites in UTR
HSD17B11	NM_016245	hydroxysteroid (17-beta) dehydrogenase 11	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	0,15	2007, 2009	Sites in UTR
ZDHHC9	NM_001008222	zinc finger, DHHC-type containing 9	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	0,14		Sites in UTR
C10orf131	NM_001130446	chromosome 10 open reading frame 131	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,32	0,53		Sites in UTR
NACC2	NM_144653	NACC family member 2, BEN and BTB (POZ) domain containing	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,31	0,68	2007	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
ENPP4	NM_014936	ectonucleotide pyrophosphatase/ phosphodiesterase 4 (putative)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,31	< 0.1	2009	Sites in UTR
IL1R1	NM_000877	interleukin 1 receptor, type I	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,31	0,16	2009	Sites in UTR
CENPF	NM_016343	centromere protein F, 350/400kDa (mitosin)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,31	< 0.1	2009	Sites in UTR
PTPRM	NM_001105244	protein tyrosine phosphatase, receptor type, M	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,31	0,14	2005, 2007, 2009	Sites in UTR
PCDH20	NM_022843	protocadherin 20	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	0,14	2009	Sites in UTR
CLTC	NM_004859	clathrin, heavy chain (Hc)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	0,68	2005, 2007, 2009	Sites in UTR
FOXF1	NM_001451	forkhead box F1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	0,68	2009	Sites in UTR
SLC35B3	NM_001142540	solute carrier family 35, member B3	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	0,14	2005, 2007, 2009	Sites in UTR
SMAD4	NM_005359	SMAD family member 4	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	0,14	2009	Sites in UTR
PLCB1	NM_015192	phospholipase C, beta 1 (phosphoinositide-specific)	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,3	< 0.1	2005, 2007	Sites in UTR
TIMM17A	NM_006335	translocase of inner mitochondrial membrane 17 homolog A (yeast)	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,3	0,19	2009	Sites in UTR
ZCCHC14	NM_015144	zinc finger, CCHC domain containing 14	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	0,68	2005, 2007, 2009	Sites in UTR
PHC3	NM_024947	polyhomeotic homolog 3 (Drosophila)	**1**	0	0	1	**2**	0	2	0	hsa-miR-205	-0,3	0,3	2009	Sites in UTR
UNC5C	NM_003728	unc-5 homolog C (C. elegans)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	< 0.1		Sites in UTR
TC2N	NM_001128595	tandem C2 domains, nuclear	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	< 0.1	2009	Sites in UTR
HERC3	NM_014606	hect domain and RLD 3	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	< 0.1	2005, 2007, 2009	Sites in UTR
USP13	NM_003940	ubiquitin specific peptidase 13 (isopeptidase T-3)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,3	< 0.1		Sites in UTR
LHFPL2	NM_005779	lipoma HMGIC fusion partner-like 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,29	< 0.1	2005, 2007, 2009	Sites in UTR
C21orf63	NM_058187	chromosome 21 open reading frame 63	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,29	0,14	2005, 2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
ERBB3	NM_001982	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,29	0,67	2005, 2007, 2009	Sites in UTR
CTPS2	NM_001144002	CTP synthase II	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,29	0,44	2009	Sites in UTR
SORBS1	NM_001034954	sorbin and SH3 domain containing 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,29	0,14	2005, 2007, 2009	Sites in UTR
ERBB4	NM_001042599	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	**1**	1	0	0	**3**	1	0	2	hsa-miR-205	-0,29	0,76	2007, 2009	Sites in UTR
PRKCE	NM_005400	protein kinase C, epsilon	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,29	< 0.1	2005, 2007, 2009	Sites in UTR
CALCRL	NM_005795	calcitonin receptor-like	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,29	0,71	2005, 2007, 2009	Sites in UTR
ZBTB38	NM_001080412	zinc finger and BTB domain containing 38	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,29	0,15	2009	Sites in UTR
VEGFA	NM_001025366	vascular endothelial growth factor A	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	0,2	2007, 2009	Sites in UTR
SPATA13	NM_001166271	spermatogenesis associated 13	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	< 0.1		Sites in UTR
GRAMD2	NM_001012642	GRAM domain containing 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	< 0.1	2009	Sites in UTR
OCIAD1	NM_001079839	OCIA domain containing 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	0,14	2009	Sites in UTR
NFAT5	NM_001113178	nuclear factor of activated T-cells 5, tonicity-responsive	**3**	0	2	1	**1**	1	0	0	hsa-miR-205	-0,28	0,69	2005, 2007, 2009	Sites in UTR
TRAK2	NM_015049	trafficking protein, kinesin binding 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	0,62	2007, 2009	Sites in UTR
SATB2	NM_001172509	SATB homeobox 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	< 0.1	2005, 2007, 2009	Sites in UTR
LCA5	NM_001122769	Leber congenital amaurosis 5	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	< 0.1	2009	Sites in UTR
NAA25	NM_024953	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	0,68	2007, 2009	Sites in UTR
CALU	NM_001130674	calumenin	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,28	0,67	2005, 2007, 2009	Sites in UTR
CXorf21	NM_025159	chromosome X open reading frame 21	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,27	< 0.1	2009	Sites in UTR
TLK1	NM_001136554	tousled-like kinase 1	**2**	0	1	1	**0**	0	0	0	hsa-miR-205	-0,27	0,25	2009	Sites in UTR
LAMC1	NM_002293	laminin, gamma 1 (formerly LAMB2)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,27	0,16	2005, 2007, 2009	Sites in UTR
SUSD1	NM_022486	sushi domain containing 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,27	< 0.1	2009	Sites in UTR
SBF2	NM_030962	SET binding factor 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,27	0,14	2005, 2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
PCNX	NM_014982	pecanex homolog (Drosophila)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,26	0,12	2009	Sites in UTR
TFDP2	NM_001178138	transcription factor Dp-2 (E2F dimerization partner 2)	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,26	0,18		Sites in UTR
FRK	NM_002031	fyn-related kinase	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,26	< 0.1	2005, 2007, 2009	Sites in UTR
BMPER	NM_133468	BMP binding endothelial regulator	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,26	0,14	2005, 2007, 2009	Sites in UTR
HHLA1	NM_001145095	HERV-H LTR-associating 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,26	< 0.1		Sites in UTR
SEMA7A	NM_001146029	semaphorin 7A, GPI membrane anchor (John Milton Hagen blood group)	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,26	0,27		Sites in UTR
PDE3B	NM_000922	phosphodiesterase 3B, cGMP-inhibited	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,26	< 0.1	2005, 2007	Sites in UTR
MMD	NM_012329	monocyte to macrophage differentiation-associated	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,26	< 0.1	2005, 2007, 2009	Sites in UTR
ACACB	NM_001093	acetyl-CoA carboxylase beta	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,26	0,23		Sites in UTR
WHSC1	NM_007331	Wolf-Hirschhorn syndrome candidate 1	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,25	0,23		Sites in UTR
MAGI1	NM_001033057	membrane associated guanylate kinase, WW and PDZ domain containing 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,25	0,56	2007, 2009	Sites in UTR
MLL	NM_001197104	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,25	< 0.1		Sites in UTR
B4GALT5	NM_004776	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 5	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,25	0,14	2009	Sites in UTR
FBXO22	NM_147188	F-box protein 22	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,25	0,14	2005, 2007, 2009	Sites in UTR
SRSF10	NM_001191005	serine/arginine-rich splicing factor 10	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,25	< 0.1	2007, 2009	Sites in UTR
INHBA	NM_002192	inhibin, beta A	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,25	< 0.1	2005, 2007, 2009	Sites in UTR
KY	NM_178554	kyphoscoliosis peptidase	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,24	0,23	2009	Sites in UTR
EZR	NM_001111077	ezrin	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	< 0.1	2009	Sites in UTR
INPPL1	NM_001567	inositol polyphosphate phosphatase-like 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	0,63	2005, 2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
CBX1	NM_001127228	chromobox homolog 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	0,14	2009	Sites in UTR
VASN	NM_138440	vasorin	**2**	0	1	1	**0**	0	0	0	hsa-miR-205	-0,24	0,26	2007, 2009	Sites in UTR
NR3C2	NM_000901	nuclear receptor subfamily 3, group C, member 2	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,24	0,19	2005, 2007, 2009	Sites in UTR
TSHZ3	NM_020856	teashirt zinc finger homeobox 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,24	< 0.1	2009	Sites in UTR
HSF5	NM_001080439	heat shock transcription factor family member 5	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	< 0.1		Sites in UTR
RORA	NM_002943	RAR-related orphan receptor A	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,24	0,69		Sites in UTR
HIATL1	NM_032558	hippocampus abundant transcript-like 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,24	< 0.1	2007, 2009	Sites in UTR
DOK4	NM_018110	docking protein 4	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	0,59	2005, 2007, 2009	Sites in UTR
CSPP1	NM_024790	centrosome and spindle pole associated protein 1	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,24	0,18	2009	Sites in UTR
DCHS1	NM_003737	dachsous 1 (Drosophila)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	< 0.1		Sites in UTR
ERRFI1	NM_018948	ERBB receptor feedback inhibitor 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,24	0,39	2007, 2009	Sites in UTR
TM9SF3	NM_020123	transmembrane 9 superfamily member 3	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,24	0,25	2007, 2009	Sites in UTR
NAA11	NM_032693	N(alpha)-acetyltransferase 11, NatA catalytic subunit	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	< 0.1		Sites in UTR
MARCKS	NM_002356	myristoylated alanine-rich protein kinase C substrate	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,24	0,63	2005, 2007, 2009	Sites in UTR
AGPAT6	NM_178819	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	**1**	0	0	1	**2**	1	1	0	hsa-miR-205	-0,24	0,23		Sites in UTR
AP1AR	NM_001128426	adaptor-related protein complex 1 associated regulatory protein	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,23	0,19	2005, 2007	Sites in UTR
MYO5B	NM_001080467	myosin VB	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,23	0,14		Sites in UTR
UBIAD1	NM_013319	UbiA prenyltransferase domain containing 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,23	< 0.1		Sites in UTR
SYPL2	NM_001040709	synaptophysin-like 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,23	0,51	2009	Sites in UTR
NKD1	NM_033119	naked cuticle homolog 1 (Drosophila)	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,23	0,72	2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												Links to sites in UTRs
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
B4GALT6	NM_004775	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 6	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,23	0,15	2005, 2007, 2009	Sites in UTR
FAM155A	NM_001080396	family with sequence similarity 155, member A	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,23	< 0.1	2007, 2009	Sites in UTR
PICALM	NM_001008660	phosphatidylinositol binding clathrin assembly protein	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,23	< 0.1		Sites in UTR
WWC1	NM_001161661	WW and C2 domain containing 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,23	0,56	2009	Sites in UTR
LPAR1	NM_001401	lysophosphatidic acid receptor 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,23	0,14	2009	Sites in UTR
FAM108B1	NM_001025780	family with sequence similarity 108, member B1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,23	< 0.1	2007, 2009	Sites in UTR
LSAMP	NM_002338	limbic system-associated membrane protein	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,23	0,23		Sites in UTR
MFNG	NM_001166343	MFNG O-fucosylpeptide 3-beta-N-acetylglu-cosaminyltransferase	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,23	0,13	2009	Sites in UTR
FAM84B	NM_174911	family with sequence similarity 84, member B	**2**	0	1	1	**0**	0	0	0	hsa-miR-205	-0,22	0,62	2007, 2009	Sites in UTR
CSF1	NM_000757	colony stimulating factor 1 (macrophage)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,22	0,14	2009	Sites in UTR
C14orf43	NM_001043318	chromosome 14 open reading frame 43	**1**	1	0	0	**2**	0	1	1	hsa-miR-205	-0,22	0,23	2009	Sites in UTR
ABCD1	NM_000033	ATP-binding cassette, sub-family D (ALD), member 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,22	0,14	2009	Sites in UTR
AFF1	NM_001166693	AF4/FMR2 family, member 1	**1**	1	0	0	**2**	0	1	1	hsa-miR-205	-0,22	0,27	2009	Sites in UTR
DNM1L	NM_005690	dynamin 1-like	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,21	< 0.1		Sites in UTR
PHYHIPL	NM_001143774	phytanoyl-CoA 2-hydroxylase interacting protein-like	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,21	< 0.1	2005, 2007, 2009	Sites in UTR
CUX2	NM_015267	cut-like homeobox 2	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,21	0,15	2009	Sites in UTR
PSD3	NM_015310	pleckstrin and Sec7 domain containing 3	**1**	0	0	1	**1**	1	0	0	hsa-miR-205	-0,21	0,14	2009	Sites in UTR
SRGAP1	NM_020762	SLIT-ROBO Rho GTPase activating protein 1	**1**	0	1	0	**3**	0	2	1	hsa-miR-205	-0,2	0,3		Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
DDHD1	NM_001160147	DDHD domain containing 1	**1**	0	0	1	**3**	0	2	1	hsa-miR-205	-0,2	0,34		Sites in UTR
AMOT	NM_001113490	angiomotin	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,2	0,15	2005, 2007, 2009	Sites in UTR
C12orf23	NM_152261	chromosome 12 open reading frame 23	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,2	< 0.1	2009	Sites in UTR
WDR35	NM_001006657	WD repeat domain 35	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,2	< 0.1		Sites in UTR
PTK7	NM_002821	PTK7 protein tyrosine kinase 7	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,2	0,17	2009	Sites in UTR
TBX3	NM_005996	T-box 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,2	< 0.1	2009	Sites in UTR
C11orf34	NM_001145024	chromosome 11 open reading frame 34	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,2	< 0.1		Sites in UTR
TTC19	NM_017775	tetratricopeptide repeat domain 19	**1**	0	0	1	**1**	1	0	0	hsa-miR-205	-0,2	0,27		Sites in UTR
ZNF536	NM_014717	zinc finger protein 536	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,2	< 0.1	2005, 2007, 2009	Sites in UTR
RAP2B	NM_002886	RAP2B, member of RAS oncogene family	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,19	0,27	2009	Sites in UTR
ACSL4	NM_004458	acyl-CoA synthetase long-chain family member 4	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,19	0,15	2009	Sites in UTR
CPSF6	NM_007007	cleavage and polyadenylation specific factor 6, 68kDa	**2**	0	0	2	**2**	0	0	2	hsa-miR-205	-0,19	0,34	2005, 2007, 2009	Sites in UTR
PI16	NM_001199159	peptidase inhibitor 16	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,19	0,26	2009	Sites in UTR
E2F1	NM_005225	E2F transcription factor 1	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,19	0,15	2005, 2007, 2009	Sites in UTR
SCMH1	NM_001031694	sex comb on midleg homolog 1 (Drosophila)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,19	0,56	2005, 2007, 2009	Sites in UTR
RAB9B	NM_016370	RAB9B, member RAS oncogene family	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,19	0,24		Sites in UTR
ZEB1	NM_001128128	zinc finger E-box binding homeobox 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,19	0,14		Sites in UTR
FAM126A	NM_032581	family with sequence similarity 126, member A	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1	2009	Sites in UTR
FAM196A	NM_001039762	family with sequence similarity 196, member A	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1	2009	Sites in UTR
TMEM136	NM_001198670	transmembrane protein 136	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,18	0,1		Sites in UTR
SH3BGRL3	NM_031286	SH3 domain binding glutamic acid-rich protein like 3	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1	2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
BMPR1B	NM_001203	bone morphogenetic protein receptor, type IB	**1**	0	1	0	**2**	1	0	1	hsa-miR-205	-0,18	0,14		Sites in UTR
DDX5	NM_004396	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,18	0,45	2005, 2007	Sites in UTR
SLC19A2	NM_006996	solute carrier family 19 (thiamine transporter), member 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1	2009	Sites in UTR
LRRC58	NM_001099678	leucine rich repeat containing 58	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1		Sites in UTR
LY75	NM_002349	lymphocyte antigen 75	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1		Sites in UTR
DUSP5	NM_004419	dual specificity phosphatase 5	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,18	0,19	2009	Sites in UTR
PHF17	NM_199320	PHD finger protein 17	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1	2007, 2009	Sites in UTR
ANGPT2	NM_001118887	angiopoietin 2	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1		Sites in UTR
PTPRJ	NM_002843	protein tyrosine phosphatase, receptor type, J	**1**	1	0	0	**1**	1	0	0	hsa-miR-205	-0,18	0,12	2009	Sites in UTR
AAK1	NM_014911	AP2 associated kinase 1	**3**	3	0	0	**4**	0	2	2	hsa-miR-205	-0,18	0,73	2007, 2009	Sites in UTR
LIN9	NM_173083	lin-9 homolog (C. elegans)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,18	< 0.1	2005, 2007, 2009	Sites in UTR
NOTCH2	NM_024408	notch 2	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,17	0,53	2009	Sites in UTR
ESRRG	NM_001134285	estrogen-related receptor gamma	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,17	0,16	2005, 2007, 2009	Sites in UTR
JPH4	NM_001146028	junctophilin 4	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,17	0,14	2005, 2007, 2009	Sites in UTR
RGS6	NM_001204416	regulator of G-protein signaling 6	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,17	0,23		Sites in UTR
C20orf111	NM_016470	chromosome 20 open reading frame 111	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,17	< 0.1		Sites in UTR
DGCR8	NM_001190326	DiGeorge syndrome critical region gene 8	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,17	< 0.1	2005, 2007	Sites in UTR
PDS5A	NM_001100399	PDS5, regulator of cohesion maintenance, homolog A (S. cerevisiae)	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,17	< 0.1		Sites in UTR
GXYLT1	NM_001099650	glucoside xylosyltransferase 1	**2**	1	0	1	**0**	0	0	0	hsa-miR-205	-0,17	0,14	2009	Sites in UTR
SS18	NM_001007559	synovial sarcoma translocation, chromosome 18	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,17	< 0.1	2009	Sites in UTR
RLIM	NM_016120	ring finger protein, LIM domain interacting	**1**	0	1	0	**2**	0	0	2	hsa-miR-205	-0,17	0,27		Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
GLIS3	NM_001042413	GLIS family zinc finger 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,17	0,56	2007, 2009	Sites in UTR
DNM3	NM_001136127	dynamin 3	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,16	0,14	2007	Sites in UTR
MGAT4A	NM_012214	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltrans-ferase, isozyme A	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,16	0,19	2009	Sites in UTR
GATA3	NM_001002295	GATA binding protein 3	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,16	0,35	2009	Sites in UTR
11.9	NM_018243	septin 11	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,16	0,25	2005, 2007, 2009	Sites in UTR
CLDN8	NM_199328	claudin 8	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1		Sites in UTR
NKX2-3	NM_145285	NK2 homeobox 3	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1	2007, 2009	Sites in UTR
NDUFA4	NM_002489	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4, 9kDa	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,16	0,49	2005, 2007, 2009	Sites in UTR
SIK2	NM_015191	salt-inducible kinase 2	**2**	0	0	2	**0**	0	0	0	hsa-miR-205	-0,16	0,27		Sites in UTR
CCDC93	NM_019044	coiled-coil domain containing 93	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1	2007, 2009	Sites in UTR
WWC3	NM_015691	WWC family member 3	**1**	0	0	1	**1**	1	0	0	hsa-miR-205	-0,16	0,14	2009	Sites in UTR
KIAA0182	NM_001134473	KIAA0182	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,16	0,14	2009	Sites in UTR
CDC42BPB	NM_006035	CDC42 binding protein kinase beta (DMPK-like)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1	2005, 2007, 2009	Sites in UTR
PAX9	NM_006194	paired box 9	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1	2009	Sites in UTR
WHSC1L1	NM_017778	Wolf-Hirschhorn syndrome candidate 1-like 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1	2009	Sites in UTR
SHROOM3	NM_020859	shroom family member 3	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,16	0,18	2009	Sites in UTR
PLEK	NM_002664	pleckstrin	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,16	< 0.1	2009	Sites in UTR
SYNJ2BP	NM_018373	synaptojanin 2 binding protein	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,16	0,23		Sites in UTR
HNRNPH3	NM_012207	heterogeneous nuclear ribonucleoprotein H3 (2H9)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,15	0,14	2005, 2007, 2009	Sites in UTR
PPP1R8	NM_002713	protein phosphatase 1, regulatory (inhibitor) subunit 8	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,15	< 0.1		Sites in UTR
SIAH1	NM_001006610	seven in absentia homolog 1 (Drosophila)	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,15	< 0.1	2007	Sites in UTR
STRBP	NM_001171137	spermatid perinuclear RNA binding protein	**1**	0	0	1	**1**	1	0	0	hsa-miR-205	-0,15	0,23	2005, 2007, 2009	Sites in UTR
LCOR	NM_001170765	ligand dependent nuclear receptor corepressor	**2**	2	0	0	**2**	1	0	1	hsa-miR-205	-0,15	0,19	2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
SELT	NM_016275	selenoprotein T	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,15	0,56	2005, 2007, 2009	Sites in UTR
STK3	NM_006281	serine/threonine kinase 3	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,15	0,14	2005, 2007, 2009	Sites in UTR
FAM176A	NM_001135032	family with sequence similarity 176, member A	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,15	< 0.1	2009	Sites in UTR
EREG	NM_001432	epiregulin	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,15	0,14	2005, 2007, 2009	Sites in UTR
AXIN2	NM_004655	axin 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,15	0,14	2005, 2007, 2009	Sites in UTR
CLDN11	NM_001185056	claudin 11	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,15	0,68	2005, 2007, 2009	Sites in UTR
CASD1	NM_022900	CAS1 domain containing 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,15	< 0.1		Sites in UTR
CDC27	NM_001114091	cell division cycle 27 homolog (S. cerevisiae)	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,14	0,14	2005, 2007	Sites in UTR
LOC401097	NM_001168214	hypothetical protein LOC401097	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,14	0,14		Sites in UTR
LIMS2	NM_001136037	LIM and senescent cell antigen-like domains 2	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,14	0,1	2007, 2009	Sites in UTR
LDLRAD3	NM_174902	low density lipoprotein receptor class A domain containing 3	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,14	0,19	2009	Sites in UTR
TPP2	NM_003291	tripeptidyl peptidase II	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,14	< 0.1		Sites in UTR
FAM174B	NM_207446	family with sequence similarity 174, member B	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,14	0,27		Sites in UTR
MGA	NM_001080541	MAX gene associated	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,14	0,23	2007, 2009	Sites in UTR
BAMBI	NM_012342	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,14	0,14	2005, 2007	Sites in UTR
COMMD10	NM_016144	COMM domain containing 10	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,14	0,14		Sites in UTR
TMEM87B	NM_032824	transmembrane protein 87B	**1**	0	0	1	**2**	0	1	1	hsa-miR-205	-0,14	0,27		Sites in UTR
UBE2N	NM_003348	ubiquitin-conjugating enzyme E2N	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,14	< 0.1	2005, 2007, 2009	Sites in UTR
RANBP2	NM_006267	RAN binding protein 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,14	0,14		Sites in UTR
VIP	NM_003381	vasoactive intestinal peptide	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,14	0,14	2009	Sites in UTR
ZNF148	NM_021964	zinc finger protein 148	**2**	0	0	2	**1**	0	0	1	hsa-miR-205	-0,14	0,3	2007, 2009	Sites in UTR
NSUN5	NM_001168347	NOP2/Sun domain family, member 5	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,14	0,14		Sites in UTR
ALX4	NM_021926	ALX homeobox 4	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,13	0,23		Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
DHCR24	NM_014762	24-dehydrocholesterol reductase	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,13	0,19	2009	Sites in UTR
C10orf53	NM_001042427	chromosome 10 open reading frame 53	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,13	0,14	2009	Sites in UTR
CREB1	NM_004379	cAMP responsive element binding protein 1	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,13	< 0.1		Sites in UTR
SLC4A4	NM_001098484	solute carrier family 4, sodium bicarbonate cotransporter, member 4	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,13	0,27	2009	Sites in UTR
MTF1	NM_005955	metal-regulatory transcription factor 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,13	0,14	2009	Sites in UTR
TMEM26	NM_178505	transmembrane protein 26	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,13	< 0.1	2009	Sites in UTR
PTEN	NM_000314	phosphatase and tensin homolog	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,13	< 0.1	2009	Sites in UTR
SULF1	NM_001128204	sulfatase 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,13	0,14	2009	Sites in UTR
RBFOX3	NM_001082575	RNA binding protein, fox-1 homolog (C. elegans) 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,13	0,15	2007, 2009	Sites in UTR
IVNS1ABP	NM_006469	influenza virus NS1A binding protein	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,13	0,15	2005, 2007, 2009	Sites in UTR
C17orf97	NM_001013672	chromosome 17 open reading frame 97	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,13	0,14		Sites in UTR
HNRNPK	NM_002140	heterogeneous nuclear ribonucleoprotein K	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2005, 2007, 2009	Sites in UTR
YAP1	NM_001130145	Yes-associated protein 1	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,12	0,19		Sites in UTR
TTI1	NM_014657	Tel2 interacting protein 1 homolog (S. pombe)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2005, 2007	Sites in UTR
LUC7L3	NM_016424	LUC7-like 3 (S. cerevisiae)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2007	Sites in UTR
DNAJA1	NM_001539	DnaJ (Hsp40) homolog, subfamily A, member 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14		Sites in UTR
NEK6	NM_001145001	NIMA (never in mitosis gene a)-related kinase 6	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2009	Sites in UTR
GALNT7	NM_017423	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
PTP4A1	NM_003463	protein tyrosine phosphatase type IVA, member 1	**1**	1	0	0	**2**	0	1	1	hsa-miR-205	-0,12	0,14		Sites in UTR
PTP4A2	NM_001195100	protein tyrosine phosphatase type IVA, member 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2009	Sites in UTR
TFE3	NM_006521	transcription factor binding to IGHM enhancer 3	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,12	< 0.1		Sites in UTR
LRP6	NM_002336	low density lipoprotein receptor-related protein 6	**1**	0	0	1	**1**	1	0	0	hsa-miR-205	-0,12	0,14	2009	Sites in UTR
BRCA1	NM_007294	breast cancer 1, early onset	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2009	Sites in UTR
KLHL15	NM_030624	kelch-like 15 (Drosophila)	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,12	0,14		Sites in UTR
RPS6KA3	NM_004586	ribosomal protein S6 kinase, 90kDa, polypeptide 3	**1**	1	0	0	**3**	0	2	1	hsa-miR-205	-0,12	0,34	2005, 2007, 2009	Sites in UTR
BEAN1	NM_001136106	brain expressed, associated with NEDD4, 1	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,12	0,19		Sites in UTR
KIAA1429	NM_015496	KIAA1429	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14		Sites in UTR
MID1IP1	NM_001098790	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,12	0,1	2005, 2007, 2009	Sites in UTR
LRP4	NM_002334	low density lipoprotein receptor-related protein 4	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,12	< 0.1	2009	Sites in UTR
MYLK4	NM_001012418	myosin light chain kinase family, member 4	**1**	0	1	0	**1**	1	0	0	hsa-miR-205	-0,12	< 0.1		Sites in UTR
NCOA1	NM_003743	nuclear receptor coactivator 1	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,12	0,23	2009	Sites in UTR
CBLL1	NM_024814	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,12	< 0.1		Sites in UTR
RAD17	NM_002873	RAD17 homolog (S. pombe)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2005, 2007	Sites in UTR
MORF4L2	NM_001142418	mortality factor 4 like 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2005, 2007, 2009	Sites in UTR
TOB2	NM_016272	transducer of ERBB2, 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
XPR1	NM_001135669	xenotropic and polytropic retrovirus receptor 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,12	0,1	2009	Sites in UTR
SH2D4A	NM_001174159	SH2 domain containing 4A	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,12	< 0.1		Sites in UTR
AP1G1	NM_001030007	adaptor-related protein complex 1, gamma 1 subunit	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,12	0,14	2005, 2007, 2009	Sites in UTR
INSR	NM_000208	insulin receptor	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,12	0,23	2009	Sites in UTR
ELF1	NM_001145353	E74-like factor 1 (ets domain transcription factor)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,12	0,14	2007, 2009	Sites in UTR
ZHX3	NM_015035	zinc fingers and homeoboxes 3	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,11	0,23	2007, 2009	Sites in UTR
MXD1	NM_001202513	MAX dimerization protein 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,11	0,14		Sites in UTR
TNR	NM_003285	tenascin R (restrictin, janusin)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,11	0,14	2009	Sites in UTR
RAB14	NM_016322	RAB14, member RAS oncogene family	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,11	0,19	2005, 2007	Sites in UTR
RBM12	NM_001198838	RNA binding motif protein 12	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,11	< 0.1		Sites in UTR
PAPD5	NM_001040284	PAP associated domain containing 5	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,11	0,69	2007, 2009	Sites in UTR
RUNX2	NM_001015051	runt-related transcription factor 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,11	0,31	2007, 2009	Sites in UTR
CENPO	NM_001199803	centromere protein O	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,11	< 0.1		Sites in UTR
NFIB	NM_001190737	nuclear factor I/B	**4**	0	2	2	**0**	0	0	0	hsa-miR-205	-0,1	0,41	2007, 2009	Sites in UTR
SMAD1	NM_001003688	SMAD family member 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2005, 2007, 2009	Sites in UTR
RBMS2	NM_002898	RNA binding motif, single stranded interacting protein 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,1	< 0.1		Sites in UTR
PPP3R1	NM_000945	protein phosphatase 3, regulatory subunit B, alpha	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2009	Sites in UTR
SCD5	NM_001037582	stearoyl-CoA desaturase 5	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,1	0,23	2009	Sites in UTR
CDC14B	NM_001077181	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2009	Sites in UTR
AEBP2	NM_001114176	AE binding protein 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2005, 2007, 2009	Sites in UTR
CCDC85C	NM_001144995	coiled-coil domain containing 85C	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14		Sites in UTR
GCOM1	NM_001018100	GRINL1A complex locus	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,1	< 0.1		Sites in UTR
9.9	NM_001113491	septin 9	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14		Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
FAM120A	NM_014612	family with sequence similarity 120A	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2007, 2009	Sites in UTR
TET1	NM_030625	tet oncogene 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,1	0,13	2009	Sites in UTR
LCORL	NM_001166139	ligand dependent nuclear receptor corepressor-like	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,1	< 0.1		Sites in UTR
AKAP11	NM_016248	A kinase (PRKA) anchor protein 11	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2005, 2007	Sites in UTR
UBFD1	NM_019116	ubiquitin family domain containing 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,1	0,14	2007, 2009	Sites in UTR
GAB2	NM_012296	GRB2-associated binding protein 2	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,1	< 0.1	2009	Sites in UTR
KIF26B	NM_018012	kinesin family member 26B	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,1	< 0.1	2007	Sites in UTR
FAM118B	NM_024556	family with sequence similarity 118, member B	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,09	0,41	2009	Sites in UTR
TIAL1	NM_001033925	TIA1 cytotoxic granule-associated RNA binding protein-like 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,09	0,14	2009	Sites in UTR
RARA	NM_000964	retinoic acid receptor, alpha	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,09	0,14	2005, 2007, 2009	Sites in UTR
IPO7	NM_006391	importin 7	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,09	0,25	2005, 2007, 2009	Sites in UTR
TRAM2	NM_012288	translocation associated membrane protein 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,09	0,14	2009	Sites in UTR
TXNRD1	NM_001093771	thioredoxin reductase 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,09	0,14	2009	Sites in UTR
EPS15	NM_001159969	epidermal growth factor receptor pathway substrate 15	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,09	0,1	2009	Sites in UTR
TNRC6C	NM_001142640	trinucleotide repeat containing 6C	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,09	0,36		Sites in UTR
IKZF4	NM_022465	IKAROS family zinc finger 4 (Eos)	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,09	< 0.1	2009	Sites in UTR
RNF213	NM_020914	ring finger protein 213	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	-0,09	0,18	2009	Sites in UTR
RNF157	NM_052916	ring finger protein 157	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	-0,09	0,1		Sites in UTR
AFF3	NM_001025108	AF4/FMR2 family, member 3	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,08	0,14	2009	Sites in UTR
MAP3K2	NM_006609	mitogen-activated protein kinase kinase kinase 2	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,08	< 0.1		Sites in UTR
CALM1	NM_006888	calmodulin 1 (phosphorylase kinase, delta)	**1**	0	0	1	**1**	0	1	0	hsa-miR-205	-0,08	0,23	2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
KAZN	NM_001017999	kazrin, periplakin interacting protein	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,08	0,14		Sites in UTR
ANK2	NM_001127493	ankyrin 2, neuronal	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2005, 2007, 2009	Sites in UTR
DOCK3	NM_004947	dedicator of cytokinesis 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,07	< 0.1		Sites in UTR
LRPPRC	NM_133259	leucine-rich PPR-motif containing	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,07	< 0.1		Sites in UTR
TNK2	NM_001010938	tyrosine kinase, non-receptor, 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14		Sites in UTR
CCDC43	NM_001099225	coiled-coil domain containing 43	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2007	Sites in UTR
HOOK3	NM_032410	hook homolog 3 (Drosophila)	**1**	1	0	0	**2**	0	2	0	hsa-miR-205	-0,07	0,18		Sites in UTR
DDX52	NM_007010	DEAD (Asp-Glu-Ala-Asp) box polypeptide 52	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2005, 2007, 2009	Sites in UTR
TMEM236	NM_001098844	transmembrane protein 236	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,07	0,1	2009	Sites in UTR
CHD2	NM_001271	chromodomain helicase DNA binding protein 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14		Sites in UTR
MAP3K13	NM_001242314	mitogen-activated protein kinase kinase kinase 13	**2**	2	0	0	**2**	0	0	2	hsa-miR-205	> -0.08	0,76		Sites in UTR
FZD3	NM_017412	frizzled family receptor 3	**1**	1	0	0	**2**	1	0	1	hsa-miR-205	> -0.07	0,31		Sites in UTR
ST8SIA3	NM_015879	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	**1**	1	0	0	**2**	1	0	1	hsa-miR-205	> -0.07	0,14		Sites in UTR
ZNF518B	NM_053042	zinc finger protein 518B	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2005, 2007, 2009	Sites in UTR
MIER3	NM_152622	mesoderm induction early response 1, family member 3	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2007, 2009	Sites in UTR
ITGA5	NM_002205	integrin, alpha 5 (fibronectin receptor, alpha polypeptide)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2009	Sites in UTR
IRF1	NM_002198	interferon regulatory factor 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,07	0,14	2009	Sites in UTR
DDX39B	NM_004640	DEAD (Asp-Glu-Ala-Asp) box polypeptide 39B	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,06	0,14	2009	Sites in UTR
SP6	NM_199262	Sp6 transcription factor	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	-0,06	< 0.1		Sites in UTR
SPRY1	NM_005841	sprouty homolog 1, antagonist of FGF signaling (Drosophila)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,06	0,14		Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
PPM1H	NM_020700	protein phosphatase, Mg2+/Mn2+ dependent, 1H	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,06	0,14	2009	Sites in UTR
MAGI3	NM_001142782	membrane associated guanylate kinase, WW and PDZ domain containing 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,06	< 0.1	2009	Sites in UTR
RNF4	NM_001185009	ring finger protein 4	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	-0,06	0,27	2005, 2007, 2009	Sites in UTR
HIF1AN	NM_017902	hypoxia inducible factor 1, alpha subunit inhibitor	**1**	1	0	0	**1**	1	0	0	hsa-miR-205	> -0.06	0,69	2009	Sites in UTR
EIF4E	NM_001130678	eukaryotic translation initiation factor 4E	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,06	0,14	2005, 2007	Sites in UTR
HMG20A	NM_018200	high mobility group 20A	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,06	0,14	2005, 2007	Sites in UTR
ZNF609	NM_015042	zinc finger protein 609	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,06	< 0.1	2007, 2009	Sites in UTR
TEAD1	NM_021961	TEA domain family member 1 (SV40 transcriptional enhancer factor)	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	-0,06	0,16	2005, 2007, 2009	Sites in UTR
BCL2	NM_000633	B-cell CLL/lymphoma 2	**1**	0	1	0	**1**	1	0	0	hsa-miR-205	-0,05	< 0.1	2005, 2007	Sites in UTR
ZNF652	NM_001145365	zinc finger protein 652	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	-0,05	0,23		Sites in UTR
EPB41L1	NM_012156	erythrocyte membrane protein band 4.1-like 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,05	< 0.1		Sites in UTR
SEMA4C	NM_017789	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,05	< 0.1	2007	Sites in UTR
XPO4	NM_022459	exportin 4	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,05	< 0.1	2009	Sites in UTR
TP53INP1	NM_001135733	tumor protein p53 inducible nuclear protein 1	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	> -0.05	0,53	2007, 2009	Sites in UTR
CPEB2	NM_001177381	cytoplasmic polyadenylation element binding protein 2	**1**	1	0	0	**1**	0	1	0	hsa-miR-205	> -0.05	0,52	2005, 2007, 2009	Sites in UTR
SLC30A7	NM_001144884	solute carrier family 30 (zinc transporter), member 7	**1**	0	1	0	**2**	0	1	1	hsa-miR-205	> -0.05	0,3		Sites in UTR
SLC5A3	NM_006933	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	**1**	1	0	0	**2**	0	0	2	hsa-miR-205	> -0.05	0,19	2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
ZNF436	NM_001077195	zinc finger protein 436	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,05	< 0.1		Sites in UTR
WDTC1	NM_015023	WD and tetratricopeptide repeats 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,05	0,14	2005, 2007, 2009	Sites in UTR
ZSWIM4	NM_023072	zinc finger, SWIM-type containing 4	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,05	0,14	2007	Sites in UTR
GTF3C2	NM_001035521	general transcription factor IIIC, polypeptide 2, beta 110kDa	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,05	< 0.1	2005, 2007, 2009	Sites in UTR
UBE2G1	NM_003342	ubiquitin-conjugating enzyme E2G 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,04	< 0.1	2005, 2007, 2009	Sites in UTR
PARD6B	NM_032521	par-6 partitioning defective 6 homolog beta (C. elegans)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,04	0,14	2007, 2009	Sites in UTR
PIP5K1A	NM_001135636	phosphatidylinositol-4-phosphate 5-kinase, type I, alpha	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,04	0,14		Sites in UTR
XRN1	NM_001042604	5'-3' exoribonuclease 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,04	0,14	2009	Sites in UTR
PEG3	NM_001146184	paternally expressed 3	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,04	< 0.1		Sites in UTR
FAM155B	NM_015686	family with sequence similarity 155, member B	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	> -0.04	0,66	2005, 2007, 2009	Sites in UTR
WWC2	NM_024949	WW and C2 domain containing 2	**1**	0	1	0	**1**	0	1	0	hsa-miR-205	> -0.04	0,26	2007, 2009	Sites in UTR
POU2F1	NM_001198783	POU class 2 homeobox 1	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	> -0.04	0,18		Sites in UTR
TNPO1	NM_002270	transportin 1	**2**	1	0	1	**0**	0	0	0	hsa-miR-205	> -0.04	0,14	2007, 2009	Sites in UTR
IFI44L	NM_006820	interferon-induced protein 44-like	**1**	1	0	0	**1**	0	0	1	hsa-miR-205	> -0.04	< 0.1	2009	Sites in UTR
SYT9	NM_175733	synaptotagmin IX	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,04	< 0.1	2009	Sites in UTR
HS3ST4	NM_006040	heparan sulfate (glucosamine) 3-O-sulfotransferase 4	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,04	< 0.1		Sites in UTR
RBMS1	NM_002897	RNA binding motif, single stranded interacting protein 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	0,59		Sites in UTR
SERTAD2	NM_014755	SERTA domain containing 2	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	0,22	2009	Sites in UTR
STS	NM_000351	steroid sulfatase (microsomal), isozyme S	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	0,2	2009	Sites in UTR
TAOK1	NM_020791	TAO kinase 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	0,14		Sites in UTR
SNX27	NM_030918	sorting nexin family member 27	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	0,14	2005, 2007, 2009	Sites in UTR

Target gene	Representative transcript	Gene name	Predicted potential of has-miR-205												
			Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
C5orf41	NM_153607	chromosome 5 open reading frame 41	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	0,11		Sites in UTR
GFRA1	NM_001145453	GDNF family receptor alpha 1	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	< 0.1		Sites in UTR
SP4	NM_003112	Sp4 transcription factor	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	< 0.1	2007	Sites in UTR
BCL9L	NM_182557	B-cell CLL/lymphoma 9-like	**1**	1	0	0	**0**	0	0	0	hsa-miR-205	> -0.03	< 0.1	2009	Sites in UTR
FAM120C	NM_017848	family with sequence similarity 120C	**1**	0	1	0	**1**	0	0	1	hsa-miR-205	> -0.03	0,23	2009	Sites in UTR
AFF4	NM_014423	AF4/FMR2 family, member 4	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,03	< 0.1	2009	Sites in UTR
EPG5	NM_020964	ectopic P-granules autophagy protein 5 homolog (C. elegans)	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,03	< 0.1		Sites in UTR
LPCAT2	NM_017839	lysophosphatidylcholine acyltransferase 2	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,02	0,14		Sites in UTR
C14orf101	NM_017799	chromosome 14 open reading frame 101	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	-0,02	< 0.1	2009	Sites in UTR
CNP	NM_033133	2‘,3‘-cyclic nucleotide 3‘ phosphodiesterase	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	0,41	2009	Sites in UTR
TRPS1	NM_014112	trichorhinophalangeal syndrome I	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	0,17	2005, 2007, 2009	Sites in UTR
ATP7A	NM_000052	ATPase, Cu++ transporting, alpha polypeptide	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	0,13	2005, 2007, 2009	Sites in UTR
SPOPL	NM_001001664	speckle-type POZ protein-like	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	0,11	2009	Sites in UTR
LYPD6	NM_001195685	LY6/PLAUR domain containing 6	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	0,1	2009	Sites in UTR
CANX	NM_001024649	calnexin	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	< 0.1	2005, 2007, 2009	Sites in UTR
GAB1	NM_002039	GRB2-associated binding protein 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	< 0.1		Sites in UTR
MMAB	NM_052845	methylmalonic aciduria (cobalamin deficiency) cblB type	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	< 0.1		Sites in UTR
DDX6	NM_004397	DEAD (Asp-Glu-Ala-Asp) box polypeptide 6	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	< 0.1	2005, 2007, 2009	Sites in UTR
WWP2	NM_199423	WW domain containing E3 ubiquitin protein ligase 2	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	< 0.1		Sites in UTR
CLASP1	NM_001142273	cytoplasmic linker associated protein 1	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	> -0.02	< 0.1	2009	Sites in UTR

Predicted potential of has-miR-205															
Target gene	Representative transcript	Gene name	Conserved sites				Poorly conserved sites				Repre-sentative miRNA	Total context+ score	Aggregate P_{CT}	Previous TargetScan publication(s)	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A					
TNRC6B	NM_001024843	trinucleotide repeat containing 6B	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	> -0.02	0,19	2007, 2009	Sites in UTR
SLC24A2	NM_001193288	solute carrier family 24 (sodium/potassium/ calcium exchanger), member 2	**1**	0	0	1	**1**	0	0	1	hsa-miR-205	> -0.02	0,19		Sites in UTR
KLF3	NM_016531	Kruppel-like factor 3 (basic)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,02	0,14	2009	Sites in UTR
ANKS1A	NM_015245	ankyrin repeat and sterile alpha motif domain containing 1A	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	-0,01	0,14	2009	Sites in UTR
NFIX	NM_002501	nuclear factor I/X (CCAAT-binding transcription factor)	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14		Sites in UTR
FXR1	NM_001013438	fragile X mental retardation, autosomal homolog 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14		Sites in UTR
SGPL1	NM_003901	sphingosine-1-phosphate lyase 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14	2009	Sites in UTR
PAQR5	NM_001104554	progestin and adipoQ receptor family member V	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14	2009	Sites in UTR
PRDM16	NM_022114	PR domain containing 16	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14	2009	Sites in UTR
DCAF10	NM_024345	DDB1 and CUL4 associated factor 10	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14		Sites in UTR
APOLD1	NM_001130415	apolipoprotein L domain containing 1	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14	2009	Sites in UTR
CA13	NM_198584	carbonic anhydrase XIII	**1**	0	0	1	**0**	0	0	0	hsa-miR-205	> -0.01	0,14		Sites in UTR
PAPLN	NM_173462	papilin, proteoglycan-like sulfated glycoprotein	**1**	0	1	0	**0**	0	0	0	hsa-miR-205	N/A	< 0.1	2005, 2007	Sites in UTR