List of gene targets predicted for miR-320a, miR-361-5p, miR-21-5p and miR-103a-3p.

miRNA of Interest	Potential Gene Targets	Alternative Name of Gene	Relevant Literature (With Emphasis on Cancer)	P-values for miRNA-gene (<0.05 Threshold)
miR-361-5p	***ARCN1***	**Archain 1**	**In a screen to identify genes that control 2-deoxyglucose (2DG) sensitivity, *ARCN1* knockdown was found to sensitize cells to the glycolytic inhibitor. [1]**	**HiSeq_V1 P_1= 0.000544 HiSeq_V2 P_2= 7.72E-13**
	CREG1	Cellular Repressor of E1A stimulated Genes 1	There is conflicting literature for the role of *CREG1* in cancer. *CREG1* has been found to be overexpressed in non-small cell lung carcinoma cell lines with *KRAS* mutations and has also been found to be upregulated in gastric cancer tissues. [2,3] However, *CREG1* has also been found to be involved in cell senescence, to reduce cell proliferation, and to promote differentiation. [4-6]	P_1= 0.002726 P_2= 4.39E-07
	ELL3	Elongation Factor For RNA Polymerase II 3	In the breast cancer cell line MCF-7, *ELL3* expression has been found to promote cell proliferation and to increase cancer stem cell populations. [7] On the other hand, *ELL3* has been implicated in the stabilization process of p53, which ultimately results in increased cell apoptosis. [8]	P_1= 0.002395 P_2= 1.51E-07
	NCEH1	Arylacetamide Deacetylase-Like 1	*NCEH1* plays an important role in lipid metabolism and has been found to be overexpressed in numerous invasive cancer cell lines. [9-12] Knockdown of *NCEH1* in prostate cancer cells results in reduced cell migration, invasion, and survival. [13]	P_1= 0.002849782 P_2= 2.01E-08
miR-320a	*GSG2*	Germ Cell Associated 2 (Haspin)	*GSG2* plays a critical role in cell mitosis and has been found to be overexpressed in a number of neoplasms. *GSG2* has been suggested to be a potential therapeutic target for cancer. [14-16]	HiSeq_V1 P_1= 0.003303893 HiSeq_V2 P_2= 3.71E-06
	RAD51	**RAD51 Recombinase**	**In breast cancer, *RAD51* has been found to be overexpressed and to be associated with poor prognosis. [17] Another study has also shown that *RAD51* drives genomic instability in multiple breast cancer cell lines. [18] Additionally, downregulation of *RAD51* is associated with increased chemo-sensitivity. [19-20]**	**P_1= 0.000993014 P_2= 3.35E-07**
	RRP1B	**Ribosomal RNA Processing 1B**	**In one study, *RRP1B* was found to interact with metastasis modifier gene *SIPA1* to**	**P_1= 0.002623317 P_2= 6.55E-07**

			regulate tumor suppressor genes. [21] *RRP1B* has also been found to interact with splicing regulator *SRSF1* to repress metastasis. [22]	
	SYNGR2	Synaptogyrin 2	Expression of *SYNGR2* was included in a six-gene signature for thyroid tumors that could differentially diagnose malignant tumors and benign tumors. [23]	P_1= 0.000122781 P_2= 0.026343543
	TDG	**Thymine DNA Glycosylase**	**Deletion of *TDG* along with *PMS2* alterations contributes to a supermutator phenotype in both breast cancer and rectal cancer. [24-25]**	**P_1= 0.001831776** **P_2= 7.25E-08**
miR-21-5p	*ATXN10*	Ataxin 10	This gene has been found to be elevated in human cachectic cancer patients, and inducing *ATXN10* in cardiomyocytes proved to be sufficient in producing cachexia phenotypes. [26] On the other hand, it has also been found that *ATXN10* is associated with cell senescence in human fibroblasts, and that knockdown of *ATXN10* promoted cell senescence avoidance. [27]	HiSeq_V1 P_1= 0.002806202 HiSeq_V2 P_2= 7.05E-09
	GATAD2B	GATA Zinc Finger Domain Containing 2B	In human fibroblasts, combinatorial knockdown of *GATAD2B* along with *ELAVL2* and *TEAD1* produced CD105+ cell populations, demonstrating increased differentiation. [28] Another study found that the stabilization of *GATAD2B* from *LRRC42* induction helps to promote cell growth in lung cancer cells. [29]	P_1= 0.002524675 P_2= 2.19E-10
	MSH2	**MutS Homolog 2**	***MSH2* appears to play multiple roles in breast cancer, producing research suggesting that *MSH2* possesses a dual role as oncogene and tumor suppressor depending on the context. *MSH2* expression has been observed to have increased expression in breast cancer tissues compared to normal tissues, and has been observed to have a negative correlation with histological grade. [30, 31] In contrast, *MSH2* has also been reported to be a tumor suppressor for its role in the TGF- β pathway. [32, 33]**	**P_1= 0.000321851** **P_2= 1.88E-12**
	NKIRAS1	NFKB Inhibitor Interacting Ras-Like 1	In breast cancer and non-small cell lung cancer, *NKIRAS1* upregulation has been associated with the methylation of regulatory genes, potentially contributing to the	P_1= 0.004336416 P_2= 9.59E-10

			dysregulation of cell processes. [34, 35] However, *NKIRAS* has been found to be deleted or methylated in renal cancer. [36, 37]	
	PELI1	Pellino E3 Ubiquitin Protein Ligase 1	In leukemia, the constitutive expression of *PELI1* results in the development of lymphoid tumors. [38]	P_1= 0.001309759 P_2= 6.90E-06
	RMND5A	**Required For Meiotic Nuclear Division 5 Homolog A**	**In HeLa cells, the targeting of *RMND5A* through miR-138 dramatically reduces cell migration. [39] On the other hand, *RMND5A* expression has been found to increase after paclitaxel and carboplatin treatment for leukocyte gene expression. [40]**	**P_1= 0.001820747 P_2= 6.80E-14**
	STAG2	**Stromal Antigen 2**	***STAG2* is believed to play a tumor suppressing role for its function in the cohesion complex for both leukemia and pancreatic cancer. [41, 42] However, complete loss of *STAG2* in bladder cancer predicts good prognosis. [43]**	**P_1= 0.003000074 P_2= 1.93E-14**
	UBE2D3	**Ubiquitin Conjugating Enzyme E2 D3**	***UBE2D3* appears to act as a tumor suppressor in breast cancer because knockdown of *UBE2D3* in breast cancer cells augments cell proliferation and invasion. [44, 45] Additionally, inhibition of *UBE2D3* leads to radio-resistance. [44, 46]**	**P_1= 0.003901447 P_2= 2.03E-07**
	USP15	Ubiquitin Specific Peptidase 15	*USP15*'s role in enhancing TGF- β signaling has been found to be significant in glioblastomas, ovarian, and breast cancer. [47, 48] It has also been highlighted the *USP15* stabilizes MDM2, a negative regulator of p53, in cancer cells. [49]	P_1= 0.003470684 P_2= 3.27E-08
miR-103a-3p	*AMMECR1*	Alport Syndrome, Mental Retardation, Midface Hypoplasia And Elliptocytosis Chromosomal Region Gene 1	In ER+ breast cancer cells, miR-26 overexpression was found to inhibit estrogen-stimulated cell proliferation and tumor growth; *AMMECR1* was highlighted as a potential target of miR-26 as an estrogen responsive gene. [50]	HiSeq_V1 P_1= 0.004118655 HiSeq_V2 P_2= 2.55E-13

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