Supplemental Table 1. Fold changes and significance of microRNA target gene sets in CCA vs FPA comparison. Only the highly abundant microRNAs (qPCR Ct value < 30) are included.

Total CCA vs FPA

microRNA	Fold Change	p-value	Significant target genes	Fold change	p-value
miR-98	0.77	0.043	SLC35D2	1.37	0.015
miR-98	0.77	0.043	IGF1R	1.67	0.009
miR-107	0.69	0.016	GALNT7	1.35	0.014
miR-107	0.69	0.016	ANKFY1	1.19	0.035
miR-107	0.69	0.016	ACVR2B	1.26	0.047
miR-107	0.69	0.016	RASSF5	1.45	0.041
miR-107	0.69	0.016	NEDD9	1.47	0.043
miR-107	0.69	0.016	YWHAH	1.14	0.049
miR-107	0.69	0.016	HTR4	1.46	0.048
miR-130b	0.72	0.014	EPS15	1.25	<0.001
miR-130b	0.72	0.014	SMAD5	1.57	0.022
miR-130b	0.72	0.014	SNX5	1.13	0.024
miR-130b	0.72	0.014	AKAP11	1.25	0.022
miR-130b	0.72	0.014	PTPRM	1.39	0.046
miR-130b	0.72	0.014	USP33	1.28	0.047
miR-130b	0.72	0.014	UBL3	1.24	0.055
miR-15b	0.72	0.027	IGF1R	1.67	0.009
miR-15b	0.72	0.027	ZADH2	1.37	0.016
miR-15b	0.72	0.027	SMAD5	1.57	0.022
miR-15b	0.72	0.027	AP1GBP1	1.29	0.031
miR-15b	0.72	0.027	GRIN1	1.56	0.043
miR-15b	0.72	0.027	GNA12	1.33	0.048
miR-15b	0.72	0.027	DNAJA2	1.33	0.056
miR-195	0.57	0.006	BTG2	1.45	0.049
miR-497	0.62	0.001	OSBPL7	1.35	0.034
miR-16	0.74	0.008	GORASP2	1.3	0.049
miR-20a	0.66	0.002	EZH1	1.42	0.023
miR-20a	0.66	0.002	RIPK5	1.51	0.031
miR-20a	0.66	0.002	BNIP2	1.49	0.038
miR-20a	0.66	0.002	NAGK	1.23	0.042
miR-20a	0.66	0.002	CXADR	1.21	0.051
miR-93	0.65	<0.001	PTGFRN	1.23	0.012
miR-93	0.65	<0.001	NPAS2	1.47	0.014

miR-93	0.65	<0.001	HDAC4	1.51	0.022
miR-93	0.65	<0.001	NEDD4L	1.16	0.057
miR-18a	0.65	0.015	PTGFRN	1.23	0.012
miR-18a	0.65	0.015	NOTCH2	1.45	0.013
miR-18a	0.65	0.015	NCOA1	1.32	0.011
miR-18a	0.65	0.015	LAT	1.55	0.018
miR-18a	0.65	0.015	WBP2	1.33	0.019
miR-18a	0.65	0.015	TMEM1	1.20	0.017
miR-18a	0.65	0.015	AEBP2	1.19	0.024
miR-18a	0.65	0.015	FNBP1	1.23	0.033
miR-18a	0.65	0.015	NEDD9	1.47	0.043
miR-19b	0.63	<0.001	GDA	1.26	0.011
miR-19b	0.63	<0.001	WBP2	1.33	0.022

Polysomal CCA vs FPA

microRNA	Fold Change	p-value	Significant target genes	Fold change	p-value
miR-130b	0.72	0.014	AKAP1	4.04	0.012
miR-130b	0.72	0.014	MTF1	1.52	0.013
miR-15b	0.72	0.027	GRID1	1.18	0.057
miR-15b	0.72	0.027	SYNJ1	1.49	0.048
miR-15b	0.72	0.027	SMAD5	1.25	0.046
miR-15b	0.72	0.027	GGA3	1.40	0.044
miR-15b	0.72	0.027	CYP26B1	1.52	0.042
miR-15b	0.72	0.027	CDS2	3.55	0.038
miR-15b	0.72	0.027	LYPLA2	1.58	0.031
miR-15b	0.72	0.027	CASR	1.71	0.022
miR-15b	0.72	0.027	DLGAP2	1.23	0.011
miR-15b	0.72	0.027	EIF4E	1.97	0.012
miR-15b	0.72	0.027	ABCG4	1.95	0.008
miR-15b	0.72	0.027	BCL9L	1.67	<0.001
miR-15b	0.72	0.027	IHPK1	1.56	<0.001
miR-16	0.74	0.008	ADRB2	1.37	0.043
miR-16	0.74	0.008	CDC42EP2	1.21	0.012
miR-16	0.74	0.008	RET	1.82	0.006
miR-497	0.62	0.001	LPHN1	2.04	0.034
miR-93	0.65	<0.001	PPP2R2A	1.41	0.046
miR-93	0.65	<0.001	EGR2	1.45	0.041
miR-93	0.65	<0.001	SLC9A2	1.4	0.022

miR20a	0.66	0.002	RIPK5	1.62	0.034
miR20a	0.66	0.002	MTF1	1.52	0.013
miR20a	0.66	0.002	SMOC2	1.66	0.007
miR-182	0.74	0.013	GRID1	1.18	0.057
miR-182	0.74	0.013	ACCN1	1.42	0.046
miR-182	0.74	0.013	NCAM1	1.37	0.036
miR-182	0.74	0.013	PLCG1	1.24	0.032
miR-182	0.74	0.013	LPHN1	2.04	0.034
miR-182	0.74	0.013	FOXO3	1.29	0.018
miR-182	0.74	0.013	SLC9A2	1.4	0.022
miR-182	0.74	0.013	PPP1R9B	1.39	0.013
miR-182	0.74	0.013	DLGAP2	1.23	0.011
miR-182	0.74	0.013	CDC42BPA	1.28	0.011
miR-182	0.74	0.013	TGFBI	1.34	0.008
miR-182	0.74	0.013	STK10	1.39	0.012
miR-183	0.74	0.009	SMPD3	2.1	0.037
miR-183	0.74	0.009	SLC6A6	1.64	0.012
miR-183	0.74	0.009	CX3CL1	1.49	0.008
miR-18a	0.65	0.015	MTF1	1.52	0.013
miR-18a	0.65	0.015	LAT	1.43	0.013
miR-18a	0.65	0.015	XYTLT2	1.46	0.002
miR-19b	0.63	<0.001	MAPK6	1.6	0.033
miR-196b	0.70	0.002	HABP4	1.34	0.042

Supplemental Table 2. Fold changes and significance of microRNA target gene sets in CCA vs FPA comparison. Only the low abundant microRNAs (qPCR Ct value > 30) are included.

Total CCA vs FPA

microRNA	Fold Change	p-value	Significant target genes	Fold change	p-value
miR-219	0.44	0.008	NCOA1	1.32	0.011
miR-219	0.44	0.008	DAZAP1	1.32	0.047
miR-9	1.68	<0.001	AAK1	0.60	<0.001
miR-9	1.68	<0.001	PAK6	0.59	0.042
miR-9	1.68	<0.001	NMT2	0.63	0.047
miR-9	1.68	<0.001	UHRF1	0.59	0.046
miR-9	1.68	<0.001	DIO2	0.39	0.058

Polysomal CCA vs FPA

microRNAs	Fold Change	p-value	Significant target genes	Fold change	p-value
miR-219	0.44	0.008	PIP5K1C	1.62	0.044
miR-219	0.44	0.008	GTPBP1	1.25	0.03
miR-9	1.68	<0.001	ARFGEF2	0.61	0.048
miR-9	1.68	<0.001	CPEB4	0.61	0.036
miR-9	1.68	<0.001	PGRMC2	0.69	0.028
miR-9	1.68	<0.001	CCNG1	0.77	0.019
miR-9	1.68	<0.001	STK3	0.69	0.018
miR-9	1.68	<0.001	CNOT6L	0.60	0.017
miR-9	1.68	<0.001	SHC1	0.69	0.015
miR-9	1.68	<0.001	TLK1	0.74	0.009
miR-9	1.68	<0.001	SYNJ2BP	0.61	0.007
miR-9	1.68	<0.001	EIF5	0.65	0.001
miR-9	1.68	<0.001	XPO4	0.74	<0.001

Supplemental Table 3. Association of direct microRNA targets with biological processes in the fat x fiber x carcinogen comparison. GO analysis was performed to identify the enrichment of biological processes associated with the putative targets**.**

microRNA	ID	Term	p-value
miR-101	GO:0006468	protein amino acid phosphorylation	0.011
	GO:0016310	phosphorylation	0.016
	GO:0045859	regulation of protein kinase activity	0.018
	GO:0051338	regulation of transferase activity	0.022
	GO:0006796	phosphate metabolic process	0.025
	GO:0006793	phosphorus metabolic process	0.025
	GO:0010033	response to organic substance	0.032
	GO:0044237	cellular metabolic process	0.034
	GO:0042325	regulation of phosphorylation	0.038
	GO:0043687	post-translational protein modification	0.042
miR-107	GO:0007165	signal transduction	0.008
	GO:0007242	intracellular signaling cascade	0.029
	GO:0010817	regulation of hormone levels	0.049
	GO:0019219	regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.099
miR-140	GO:0048468	cell development	0.004
	GO:0016043	cellular component organization	0.013
	GO:0044238	primary metabolic process	0.016
	GO:0043170	macromolecule metabolic process	0.030
	GO:0019538	protein metabolic process	0.030
	GO:0008152	metabolic process	0.035
	GO:0030154	cell differentiation	0.038
	GO:0048869	cellular developmental process	0.042
miR-15b	GO:0030154	cell differentiation	0.006
	GO:0048869	cellular developmental process	0.006
	GO:0045935	positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	0.013
	GO:0010557	positive regulation of macromolecule biosynthetic process	0.014
	GO:0031328	positive regulation of cellular biosynthetic process	0.015
	GO:0009891	positive regulation of biosynthetic process	0.016

	GO:0007166	cell surface receptor linked signal transduction	0.029
	GO:0022604	regulation of cell morphogenesis	0.040
	GO:0022414	reproductive process	0.016
miR-93	GO:0048519	negative regulation of biological process	0.044
miR-18a	GO:0010556	regulation of macromolecule biosynthetic process	0.023
	GO:0010468	regulation of gene expression	0.024
	GO:0031326	regulation of cellular biosynthetic process	0.027
	GO:0009889	regulation of biosynthetic process	0.028
	GO:0009605	response to external stimulus	0.036
	GO:0080090	regulation of primary metabolic process	0.042
	GO:0031323	regulation of cellular metabolic process	0.048
	GO:0019222	regulation of metabolic process	0.058
	GO:0050794	regulation of cellular process	0.067
	GO:0050789	regulation of biological process	0.085