

**Supplementary Table 1. Downregulation of 70 miR-200a targets as revealed by RNA-seq.**

Gene	miR-200a	aiR-200a-3	AKT1 siRNA-1	AKT1 siRNA-2
ACOT7	40%	34%	75%	77%
ACTA1	49%	48%	91%	86%
ARPC5	41%	37%	76%	80%
ATOH8	60%	127%	168%	136%
C22orf23	59%	110%	159%	130%
CBX1	49%	48%	92%	87%
CDK6	49%	49%	93%	88%
DCTN3	52%	55%	102%	92%
DKK1	50%	49%	95%	89%
DPY19L1	24%	19%	48%	24%
DR1	52%	61%	107%	94%
DTX3	55%	75%	125%	106%
EVI5L	58%	90%	136%	121%
FAM158A	54%	68%	116%	104%
FAM220A	59%	93%	140%	123%
FAM35B	48%	43%	87%	85%
FAM72B	55%	76%	126%	107%
FLJ32255	57%	89%	136%	116%
GEM	50%	53%	97%	90%
GNB1L	59%	95%	142%	124%
HINT3	57%	88%	135%	116%
HMOX1	52%	64%	108%	95%
HOXC13	53%	65%	110%	98%
HS6ST2	39%	34%	72%	75%
ITGB3	55%	72%	124%	106%
KCTD20	47%	42%	87%	84%
KIDINS220	43%	40%	79%	81%
LBR	34%	32%	71%	73%
LOC100130331	60%	158%	180%	146%
LOC100507032	58%	92%	138%	121%
LOC100653106	40%	35%	75%	79%
LOC100653136	59%	103%	155%	126%
LOC100653311	45%	41%	87%	84%
LOC729852	56%	78%	127%	110%
LOXL3	59%	106%	157%	127%
LRRC8B	51%	54%	100%	92%
MAP2K4	52%	55%	100%	92%
MAP3K3	53%	64%	110%	96%
NRP1	45%	41%	87%	84%
NUP43	55%	76%	125%	107%
PDGFA	56%	80%	132%	115%
PDHA1	55%	77%	127%	109%
PDXP	47%	43%	87%	85%
PEX12	59%	101%	150%	126%

PIF1	58%	89%	136%	119%
PORCN	56%	83%	134%	116%
PPP3CC	55%	72%	120%	106%
PPT2	28%	24%	65%	62%
PPT2-EGFL8	53%	66%	111%	99%
RNF5P1	59%	98%	149%	125%
SERPINE1	42%	38%	77%	81%
SLC16A3	52%	55%	106%	92%
SLC30A1	51%	54%	97%	91%
SLC35D1	50%	51%	95%	89%
SLC39A10	28%	23%	64%	61%
SMARCD3	59%	93%	141%	124%
SNRPB2	32%	31%	71%	68%
SRM	56%	78%	130%	111%
TMEM158	54%	70%	117%	106%
TRMT112	55%	77%	127%	108%
TSPAN12	53%	67%	112%	101%
TST	60%	145%	170%	144%
TUBB8	56%	80%	131%	114%
UBASH3B	52%	57%	106%	94%
UPRT	54%	67%	112%	102%
WHAMM	60%	198%	195%	160%
WIPI1	56%	83%	133%	115%
YWHAG	31%	30%	69%	63%
ZEB1	49%	47%	91%	85%
ZEB2	44%	40%	85%	82%

Gene downregulation was determined by referencing to the average readings of the negative control sample



es.