Supplemental Material

Treatment protocols

Patients were treated on one of the following intensive cytarabine/daunorubicin-based Cancer and Leukemia Group B (CALGB) frontline treatment protocols: 8525 (n=18),[1] 8923 (n=10),[2] 9420 (n=5),[3] 9720 (n=89),[4,5] or 10201 (n=57).[6] The analyzed patient subset (n=179) performed similarly to comparable *de novo* CN-AML patients which have not been included in our dataset [n=151; complete remission (CR): *P*=.31, disease-free survival (DFS): *P*=.40, overall survival (OS): *P*=.99].

Among these protocols, CALGB 9420, 9720, and 10201 included investigational agents other than chemotherapy. CALGB 9720[4,5] was initiated as a phase III trial in untreated acute myeloid leukemia (AML) patients 60 years and older evaluating multidrug resistance (MDR) modulation by valspodar (PSC-833) during induction and consolidation therapy with cytarabine, daunorubicin, and etoposide. The valspodar (PSC-833) arm was closed after randomized assignment of 120 patients because of excessive early deaths. Enrollment on this protocol continued on the chemotherapy-only control arm. CALGB 10201[6] evaluated the *BCL2* antisense, oblimersen sodium (Genasense; G3139) administered with induction and consolidation chemotherapy; preliminary results showed no impact of the antisense on outcome. CALGB 9420[3] and CALGB 9720[4,5] evaluated a subcutaneous IL-2 regimen in older AML patients as maintenance therapy, which was demonstrated to induce no clear benefit. Per the protocols, patients enrolled on these studies did not receive stem cell transplantation in first CR.

Sample preparation and *miR-3151* and *BAALC* expression analyses

Patients enrolled on the aforementioned treatment protocols were also enrolled on the companion protocols CALGB 9665 (Leukemia Tissue Bank) and CALGB 20202 (molecular studies in AML), and gave informed consent for pretreatment marrow and blood collection and their research use in accordance with the Declaration of Helsinki. Mononuclear cells from pretreatment blood were enriched by Ficoll-Hypaque gradient and cryopreserved in liquid nitrogen until they were thawed at 37°C for analysis. DNA and total RNA sample extraction and quality control were performed as reported previously.[7-10] Briefly, total RNA was extracted using the Trizol method and complementary DNA was synthesized from total RNA using the MicroRNA Reverse Transcription Kit (Invitrogen, Carlsbad, CA) and SuperScript®III (Invitrogen, Carlsbad, CA) respectively according to protocol instructions. Custom made RT-PCR primers for *miR-3151* were obtained from ABI (Life Technologies Corporation/Applied Biosystems, Carlsbad, CA). The TaqMan assays were carried out for each sample in triplicate using Taqman Primer-Probe sets for *BAALC* and *miR-3151* and the respective house-keeping genes *18S* and *RNU44 (*Life Technologies Corporation/Applied Biosystems, Carlsbad, CA) according to protocol instructions. To determine the relative levels of expression of *miR-3151* and *BAALC*, the comparative C_T method was used *(*Life Technologies Corporation/Applied Biosystems, Carlsbad, CA *)*. First, the parameter threshold cycle (C_T) was determined for *miR-3151* and *RNU44* as well as for *BAALC* and *18S,* and the cycle number difference (*RNU44* − *miR-3151* and *18S* − *BAALC* = ΔC_T) was calculated for each replicate. If *miR-3151* or *BAALC* failed to reach the threshold, the sample was considered below the detection limit. If *RNU44* or *18S* amplification failed, the sample was omitted from the analysis. Finally, the mean ΔC_T from the three replicates was generated [$(\Sigma\Delta C_T)/3 = MC_T$], normalizing *miR-3151* expression to *RNU44* expression and *BAALC* expression to *18S* expression. Negative controls were included in each assay.

Gene- expression profiling (GEP)

For GEP, total RNA was extracted from pretreatment bone marrow (BM) or blood mononuclear cells of 156 patients with material available. Gene-expression of samples from patients enrolled on CALGB 9720 and 10201 was profiled using the Affymetrix U133 plus 2.0 array (Affymetrix, Santa Clara, CA) as previously reported.[11] For expression profiling, summary measures of gene-expression were computed simultaneously for all samples using the robust multichip average (RMA) method, which incorporates quantile normalization of arrays.[12] Expression values were logged (base 2) before analysis. A filtering step was performed to remove probe-sets that did not display significant variation in expression across arrays. In this procedure, a chi-square test was used to test whether the observed variance in expression of a probe set was significantly larger than the median observed variance in expression for all probe-sets using α=.01 as the significance level; 24,649 probe-sets passed the filtering criterion and were included in subsequent analyses. An expression signature was derived by comparing gene expression between low and high *miR-3151* expressers. A univariable significance level of .001 was used to determine the probe-sets that comprised the signature. A global test of significance based on a permutation procedure was performed to determine whether or not the number of differentially expressed probe sets was more than expected by chance; if not, no signature is reported for the comparison.

MicroRNA expression profiling (MEP)

For MEP total RNA was extracted from pretreatment BM or blood mononuclear cells of 135 patients with material available. MicroRNA expression was profiled using The Ohio State University custom microRNA array (OSU_CCC version 4.0) as previously reported.[11] For expression profiling, signal intensities were calculated for each spot, with an adjustment made for local background. Spots that were flagged due to low signal-to-noise ratio on more than 75% of arrays were excluded from analysis. Signal intensities were log-transformed and quantile normalization was performed on arrays using spots for all human and mouse microRNA probes represented on the array. Log-signal intensities from replicate spots (ie, spots representing the same probe) were averaged. For each microRNA probe, an adjustment was made for batch effects (ie, differences in expression related to the batch in which arrays were hybridized). Further analysis was limited to 460 unique human probes that passed the filtering criterion. An expression signature was derived by comparing microRNA expression between low and high *miR-3151* expressers. A univariable significance level of <.005 was used to determine the probes that comprised the signature. A global test of significance based on a permutation procedure was performed to determine whether or not the number of differentially expressed probes was more than expected by chance; if not, no signature is reported for the comparison.

Stable expression of *miR-3151*

The stemloop of *miR-3151* with 200bp flanking sequence was cloned into the HIV based lentiviral dual promoter vector (pCDH-CMV-MCS-EF1-copGFP+Puro cDNA; System Biosciences, Mountain View, CA). As a control, lentiviral scramble control miR was used according to the manufacturer's instructions (miRZiP000, System Biosciences). 4500µg lentiviral construct was transfected into 293TN cells using 45µg pPACKH1 and 55µl PureFection (System Biosciences). After 48h and 72h, the supernatant containing the pseudoviral particles was collected and the virus was precipitated overnight at 4°C using 7.5ml PEG-IT virus precipitation solution (System Biosciences). 200µl Phosphate Buffered Saline and 25µM Hepes Buffer were used for resuspension of the pelleted virus. 200,000 KG1 cells/ml were infected in triplicate with 20 IU virus, using 5µl Transdux Infection Reagent (System Biosciences). Ten days later successfully infected cells were selected using Puromycin. To check for successful overexpression of *miR-3151,* RNA (1 million cells) was harvested on day 14 and reverse transcribed to cDNA using the TaqMan MicroRNA Reverse Transcription Kit (Life Technologies Corporation/Applied Biosystems, Carlsbad, CA). To analyze the effect of forced *miR-3151* expression on the predicted target genes, we used the Superscript III First-Strand cDNA Synthesis Kit (Life Technologies Corporation/Invitrogen). Both kits were used according to the manufacturer's instructions. Simultaneously, protein (from 4 million cells) was harvested and used for Western Blotting.

Western blot analysis

Western blotting was performed using the protein lysates, mixed with (6X) sodium dodecyl sulfate (SDS) loading buffer (125mM Tris pH 6.8, 4% SDS, 20% glycerol, 200 mM beta-mercaptoethanol, 0.2% [w/v] bromophenol blue) and boiled for 10 minutes. Protein samples were loaded onto a 4-20% Criterion Tris-HCl precast gel (Bio-Rad, Herkules, CA) and transferred to 0.45μm polyvinylidene fluoride (PVDF) membrane. Membranes were blocked using 5% milk and incubated in primary antibody overnight at 4º C on a rocking platform. Membranes were washed in Tris-Buffered Saline (TBS) buffer containing 0.1% Tween-20 and probed with secondary antibody for 2h. Following a final wash in TBS buffer containing Tween-20, membranes were incubated in ECL Western blotting detection reagents (GE Healthcare, Piscataway, NJ) and exposed to film (Denville Scientific, Metuchen, NJ). Antibodies used were: Actin (sc-1616, 1:1000), FBL20 (sc-242799, 1:200; Santa Cruz Biotechnologies, Santa Cruz, CA) and anti-goat HRP-linked.

Luciferase reporter assays

To assess the inhibiting potential of *miR-3151* on *FBXL20* and *USP40* gene expression, 500bp of the respective 3′-untranslated regions (UTR) containing the predicted *miR-3151* binding sites were cloned into a luciferase reporter vector (pGL4.24; Promega Corporation, Madison, WI). Mutation of the predicted binding sites was accomplished using bi-directional mutation primers, exchanging 3 nucleotides of the respective predicted binding sequences. Primer sequences and the corresponding annealing temperatures are listed in Supplemental Table 3. HEK 293T cells (American Type Culture Collection ATCC, Manassas, VA) were cultured in DMEM culture medium supplemented with 10% Fetal Bovine Serum, L-glutamine (200mM), and antibiotic/antimycotic agent (all Life Technologies Corporation/Gibco, Carlsbad, CA) and grown at 37ºC with 5% CO_2. When the culture reached 80% confluency, the cells were transfected in triplicate with reporter and control constructs (Renilla, pGL4.74; Promega Corporation,) using Lipofectamin 2000 transfection reagent (Life Technologies Corporation/Invitrogen). Cells were co-transfected with 10pmol of either MIR-3151 (Pre-miR miRNA Precursor, Life Technologies Corporation/Ambion) or scramble control-miR (negative Control Pre-miR #1, Ambion). Transfected cells were incubated for 24h at 37ºC with 5% CO_2 in Opti-MEM II medium containing the Lipofectamine/plasmid combination. Protein lysates were assessed for firefly luciferase and *Renilla* luciferase activities according to the recommendations detailed in the Dual-Luciferase Reporter Assay System (Promega Corporation). For further analysis, relative expression was normalized using co-transfected *Renilla* luciferase.

Statistical analyses

Patients were divided into quartile groups – based on expression levels of *miR-3151* and assessed for outcome associations by the trend test for DFS (*P*=.03) and OS (*P*=.001); based on these results a median cut was used in all statistical analyses.[13] A median cut for *BAALC* was used in all statistical analyses, as previously published.[14]

For analysis of the *ERG* expression data, complete case analysis was used to handle missing expression data of the patients.

Definition of clinical endpoints

CR was defined as recovery of morphologically normal BM and blood counts (ie, neutrophils ≥1,500/µl and platelets >100,000/µl), and no circulating leukemic blasts or evidence of extramedullary leukemia. DFS was measured from the date of CR until date of relapse or death, regardless of cause. OS was measured from the date on study until date of death. Patients alive at last follow-up were censored for both DFS and OS.

Multivariable models

Variables in addition to *miR-3151* and *BAALC* expression that were considered for univariable analyses for CR were age, sex, race, hemoglobin, platelet count, white blood count (WBC), *NPM1* (mutated vs wild-type), *FLT3*-ITD (present vs absent), *FLT3*-TKD (present vs absent), *CEBPA* (mutated vs wild-type), ELN Genetic Group (Favorable vs Intermediate-I), *TET2* (mutated vs wild-type), *ASXL1* (mutated vs wild-type), *DNMT3A* (mutated vs wild-type), *RUNX1* (mutated vs wild-type), *MLL*-PTD (present vs absent), *IDH1* (mutated vs wild-type), *IDH2* (mutated vs wild-type), *WT1* (mutated vs wild-type) and *ERG* expression (high vs low). Variables considered for inclusion in the logistic models were those significant at α=.20 from the univariable models. Variables remaining in the final models were significant at α=.05.

Variables in addition to *miR-3151* expression that were considered for univariable analyses for DFS and OS were age, sex, race, hemoglobin, platelet count, WBC, *NPM1* (mutated vs wild-type), *FLT3*-ITD (present vs absent), *FLT3*-TKD (present vs absent), *CEBPA* (mutated vs wild-type), ELN Genetic Group (Favorable vs Intermediate-I), *TET2* (mutated vs wild-type), *ASXL1* (mutated vs wild-type), *DNMT3A* (mutated vs wild-type), *RUNX1* (mutated vs wild-type), *MLL*-PTD (present vs absent), *IDH1* (mutated vs wild-type), *IDH2* (mutated vs wild-type), *WT1* (mutated vs wild-type) and *BAALC* and *ERG* expression (high vs low). Variables significant at α=.20 from the univariable analyses were considered for multivariable analyses. The proportional hazards assumption was checked for each variable individually. If the proportional hazards assumption was not met for a particular variable, then an artificial time dependent covariate was included in all models that contained that variable.[14]

Supplemental Tables

Supplemental Table 1. Bivariable models for outcome according to the expression status of *miR-3151* and *BAALC* in older patients with cytogenetically normal acute myeloid leukemia

A Complete Remission

Variable	Categories	*P*-value	Odds Ratio* (95% CI)
miR-3151 expression	High vs Low (median cut)	<.001	0.47 (0.23, 0.96)
BAALC expression	High vs Low (median cut)	<.001	0.30 (0.14, 0.64)

B Disease-Free Survival

Variable	Categories	*P*-value	Hazard Ratio† (95% CI)
miR-3151 expression	High vs Low (median cut)	.01	1.68 (1.13, 2.48)
BAALC expression	High vs Low (median cut)	.003	1.82 (1.24, 2.69)

C Overall Survival

Variable	Categories	*P*-value	Hazard Ratio† (95% CI)
miR-3151 expression	High vs Low (median cut)	.002	1.68 (1.20, 2.36)
BAALC expression	High vs Low (median cut)	<.001	2.01 (1.45, 2.81)

*An odds ratio>1 (<1) corresponds to a higher (lower) odds of achieving a CR for the first level listed of a dichotomous variable.

†A hazard ratio>1 (<1) corresponds to a higher (lower) risk for the first level listed of a dichotomous variable.

Supplemental Table 2. Outcome analysis according to *miR-3151* expression status and ELN genetic group in older patients with cytogenetically normal acute myeloid leukemia

Outcome	**Favorable**			**Intermediate-I**		
	Low *miR-3151* n=50	**High *miR-3151* n=35**	***P***	**Low *miR-3151* n=40**	**High *miR-3151* n=52**	***P***
Complete remission rate, no. (%)	42 (84)	26 (74)	.29	31 (78)	27 (52)	.02
Disease-free Survival			.55			<.001
Median, y	1.1	1.0		1.1	0.6	
Disease-free at 3 y, % (95% CI)	29 (16-43)	15 (5-31)		23 (10-38)	0	
Overall Survival			.18			<.001
Median, y	1.5	1.4		1.0	0.7	
Alive at 3 y, % (95% CI)	36 (23-49)	20 (9-34)		28 (15-42)	4 (1-12)	

Abbreviations: y, years; CI, confidence interval.

* The ELN Favorable Genetic Group comprises patients with mutated *CEBPA* and those with mutated *NPM1* without *FLT3*-ITD; the ELN Intermediate-I Genetic Group includes patients with *CEBPA* wild-type who are either *FLT3*-ITD-positive and *NPM1*-mutated, *FLT3*-ITD-negative and *NPM1* wild-type or *FLT3*-ITD-positive and *NPM1* wild-type.

Supplemental Table 3. Primer sequences and corresponding annealing temperatures for cloning and mutational sequence changes of the *FBXL20* and *USP40* 3′-UTRs.

Amplicon	**Primer Sequence (5´-3´)**	**Annealing Temperature**
FBXL20 cloning F	cgtcgaattcGTTGCCTTGAAATCACTGTG	58 °C
FBXL20 cloning R	cgtcgaattcATGCAAACTGTAAACACGAC	
FBXL20 mutation F	CTGTTGCTCCCCTTTACACTCTTG	52 °C
FBXL20 mutation R	CAAGAGTGTAAAGGGGAGCAACAG	52 °C
USP40 cloning F	cgtcgaattcGGCTTCTCACAGTGTCTCAG	58 °C
USP40 cloning R	cgtcgaattcCTCGTGGAAAGAGCTCGCAC	
USP40 mutation F	GACTTCATGGCCTTTACTCGTTC	52 °C
USP40 mutation R	GAACGAGTAAAGGCCATGAAGTC	52 °C

Supplemental Table 4. *miR-3151*-associated gene expression signature in CN-AML patients: Upregulated genes. High *miR-3151* expresser status was associated with the upregulation of 192 probe sets (116 annotated genes) out of 24,649 investigated (Global test *P*-value = .001).

Probe set	**Gene Symbol**	**Fold-change: *miR-3151* High/Low**	***P*-value**
202912_at	*ADM*	2.91	1.00E-07
1566363_at	*DNTT*	2.60	0.000311
218899_s_at	*BAALC*	2.55	1.20E-06
210487_at	*DNTT*	2.49	0.0003485
222780_s_at	*BAALC*	2.44	1.00E-06
1562433_at	*FLJ10489*	2.08	4.10E-06
201540_at	*FHL1*	2.02	3.70E-06
205330_at	*MN1*	2.00	0.0001118
229390_at	*FAM26F*	1.99	3.66E-05
230896_at	*BEND4*	1.91	0.0002137
204057_at	*IRF8*	1.91	0.0003184
243819_at		1.88	7.27E-05
215078_at	*SOD2*	1.88	0.0001314
205984_at	*CRHBP*	1.87	4.71E-05
209823_x_at	*HLA-DQB1*	1.87	0.000231
202283_at	*SERPINF1*	1.84	9.10E-05
210299_s_at	*FHL1*	1.81	1.23E-05
228376_at	*GGTA1*	1.80	9.50E-06
219648_at	*MREG*	1.80	9.13E-05
229391_s_at	*FAM26F*	1.77	2.80E-05
223467_at	*RASD1*	1.77	2.42E-05
213931_at		1.76	4.39E-05
242814_at	*SERPINB9*	1.76	1.12E-05
224435_at	*C10orf58*	1.74	0.0001958
214505_s_at	*FHL1*	1.74	1.42E-05
209723_at	*SERPINB9*	1.74	0.0006185
1559425_at		1.73	9.90E-06
233223_at		1.73	1.01E-05
211656_x_at		1.72	0.0005121
215990_s_at	*BCL6*	1.70	0.0006403
1564796_at	*EMP1*	1.70	0.0002895
242064_at	*SDK2*	1.70	1.21E-05
202388_at	*RGS2*	1.68	0.0001906

1552542_s_at	*TAGAP*	1.67	4.16E-05
213506_at	*F2RL1*	1.66	0.0009492
210298_x_at	*FHL1*	1.65	0.0001137
211302_s_at	*PDE4B*	1.65	0.0007491
239979_at		1.63	0.0001418
204794_at	*DUSP2*	1.62	9.77E-05
201539_s_at	*FHL1*	1.62	5.28E-05
209305_s_at	*GADD45B*	1.62	0.0002034
200832_s_at	*SCD*	1.61	7.70E-06
224823_at	*MYLK*	1.60	0.0007962
215223_s_at	*SOD2*	1.60	0.0005505
228758_at	*BCL6*	1.59	0.0006702
207574_s_at	*GADD45B*	1.59	0.000571
209304_x_at	*GADD45B*	1.58	0.0003232
208937_s_at	*ID1*	1.58	0.0004095
222315_at		1.58	0.0001866
226878_at	*HLA-DOA*	1.57	0.0006173
216016_at	*NLRP3*	1.57	0.0004723
1556209_at	*CLEC2B*	1.54	0.0008631
202481_at	*DHRS3*	1.54	0.0005449
209457_at	*DUSP5*	1.54	0.0002859
209582_s_at	*CD200*	1.53	0.000115
229543_at	*FAM26F*	1.53	0.0004945
202177_at	*GAS6*	1.53	3.95E-05
201566_x_at	*ID2*	1.53	0.000287
206682_at	*CLEC10A*	1.52	0.0006437
203523_at	*LSP1*	1.52	0.0005851
227108_at	*STARD9*	1.52	0.000233
201565_s_at	*ID2*	1.51	0.0007525
236898_at		1.51	0.0008993
230212_at	*SPRY1*	1.51	0.0002686
201531_at	*ZFP36*	1.51	0.0009634
243465_at		1.50	0.0002234
202340_x_at	*NR4A1*	1.50	2.76E-05
219480_at	*SNAI1*	1.49	1.00E-07
204918_s_at	*MLLT3*	1.48	0.0003138
234050_at	*TAGAP*	1.48	0.000557
235574_at	*GBP4*	1.47	0.0001027
208436_s_at	*IRF7*	1.46	0.0002375
209615_s_at	*PAK1*	1.46	0.000625
229054_at	*C14orf181*	1.45	4.38E-05

214537_at	*HIST1H1D*	1.45	0.0004494
223217_s_at	*NFKBIZ*	1.44	0.0009275
227478_at	*SETBP1*	1.43	0.0008673
214390_s_at	*BCAT1*	1.42	0.0004886
228618_at	*PEAR1*	1.42	0.0003346
235175_at	*GBP4*	1.41	5.53E-05
1566232_at		1.41	0.0001209
201841_s_at	*HSPB1*	1.40	0.0004139
202555_s_at	*MYLK*	1.40	0.0007748
241387_at		1.40	0.0001764
215671_at	*PDE4B*	1.40	0.0001311
212667_at	*SPARC*	1.40	0.0003604
222773_s_at	*GALNT12*	1.39	0.0006944
233867_at		1.39	0.0001436
239901_at		1.39	0.0004709
1558411_at	*C3orf50*	1.38	0.0002312
221900_at	*COL8A2*	1.38	0.0006902
209722_s_at	*SERPINB9*	1.38	0.000104
225762_x_at	*LOC284801*	1.37	0.000939
223129_x_at	*MYLIP*	1.37	9.50E-06
225775_at	*TSPAN33*	1.37	0.0007704
232239_at	*hCG_2024094*	1.36	0.0003539
220319_s_at	*MYLIP*	1.36	4.56E-05
240671_at		1.36	0.0006524
202014_at	*PPP1R15A*	1.36	0.0003242
233138_at	*C18orf1*	1.35	7.46E-05
235205_at	*LOC346887*	1.35	0.0007481
244087_at		1.35	0.0001114
221261_x_at		1.35	0.0001938
244876_at		1.35	0.0003286
223218_s_at	*NFKBIZ*	1.35	0.0008108
227053_at	*PACSIN1*	1.35	3.24E-05
227006_at	*PPP1R14A*	1.35	1.07E-05
207821_s_at	*PTK2*	1.35	0.0002505
238949_at	*RNF145*	1.35	0.0001135
1552541_at	*TAGAP*	1.35	3.61E-05
1598_g_at	*GAS6*	1.34	7.70E-06
237571_at		1.34	0.0009857
37028_at	*PPP1R15A*	1.34	0.0003758
1555579_s_at	*PTPRM*	1.34	0.000501
242738_s_at	*ZFHX3*	1.34	0.0003126

223130_s_at	*MYLIP*	1.33	9.40E-05
1565034_s_at		1.33	0.0001131
241577_at		1.33	0.0002603
204121_at	*GADD45G*	1.32	0.000359
206313_at	*HLA-DOA*	1.31	0.0004997
231887_s_at	*KIAA1274*	1.31	0.0007634
210313_at	*LILRA4*	1.31	1.42E-05
242868_at		1.31	0.000714
218611_at	*IER5*	1.30	0.0008784
206429_at	*F2RL1*	1.29	0.0003835
1567224_at	*HMGA2*	1.29	0.0003882
232682_at	*MREG*	1.29	0.0003514
229484_at	*PPM1J*	1.29	1.18E-05
233379_at	*PRR5L*	1.29	0.0006499
204713_s_at	*F5*	1.28	0.0006393
204454_at	*LDOC1*	1.28	0.0007596
228098_s_at	*MYLIP*	1.28	0.0002199
1563357_at		1.28	0.0002197
242551_at		1.28	0.0007152
223839_s_at	*SCD*	1.28	0.000563
202308_at	*SREBF1*	1.28	0.00045
212654_at	*TPM2*	1.28	1.80E-06
239272_at	*MMP28*	1.27	0.0006608
223313_s_at		1.27	0.0001821
223304_at	*SLC37A3*	1.27	0.0001288
237315_at		1.26	7.76E-05
236322_at		1.26	0.000648
229062_at	*ARL9*	1.25	0.0003144
223385_at	*CYP2S1*	1.25	4.60E-06
228263_at	*GRASP*	1.25	0.0004894
1570362_at	*LOC100288009*	1.25	4.73E-05
223932_at		1.25	0.0002419
1557223_at		1.25	0.0005938
211143_x_at	*NR4A1*	1.25	9.70E-06
208779_x_at	*DDR1*	1.24	2.70E-06
210749_x_at	*DDR1*	1.24	3.88E-05
206896_s_at	*GNG7*	1.24	0.0008744
241877_at		1.24	1.67E-05
212528_at		1.24	5.65E-05
203329_at	*PTPRM*	1.24	0.0001066
211708_s_at	*SCD*	1.24	4.76E-05

1552301_a_at	*CORO6*	1.23	0.0005449
1559529_at	*PTK2*	1.23	0.000399
204811_s_at	*CACNA2D2*	1.22	0.0005027
239317_at	*CEACAM21*	1.22	0.0003081
239273_s_at	*MMP28*	1.22	0.0001238
224771_at	*NAV1*	1.22	0.0003001
224773_at	*NAV1*	1.22	0.000377
227486_at	*NT5E*	1.22	0.0003515
40148_at	*APBB2*	1.21	0.0005349
214781_at		1.21	0.0002272
216470_x_at		1.21	0.0006018
236459_at	*PRKCE*	1.21	0.0002985
1553493_a_at	*TDH*	1.21	0.0004184
205494_at	*ZNF821*	1.21	0.0003261
212817_at	*DNAJB5*	1.20	0.0001555
228403_at	*ENHO*	1.20	0.0003024
244429_at		1.20	0.0009389
227584_at	*NAV1*	1.20	0.0009954
208711_s_at	*CCND1*	1.19	0.0005108
207205_at	*CEACAM4*	1.19	0.0003577
52651_at	*COL8A2*	1.19	7.57E-05
205225_at	*ESR1*	1.19	0.0007502
212707_s_at		1.19	0.0002102
232290_at		1.19	0.0004165
209325_s_at	*RGS16*	1.19	0.0008462
209320_at	*ADCY3*	1.18	0.00046
202986_at	*ARNT2*	1.18	0.0004949
226985_at	*FGD5*	1.18	0.0007412
203726_s_at	*LAMA3*	1.18	5.14E-05
220006_at	*CCDC48*	1.17	0.0006156
238986_at	*FLJ43663*	1.17	0.0001125
226499_at	*NRARP*	1.17	0.000448
203756_at	*ARHGEF17*	1.16	0.000761
220448_at	*KCNK12*	1.16	0.000976
1568795_at		1.16	0.0008143
225909_at	*tcag7.1196*	1.16	0.0006626

Supplemental Table 5. *miR-3151*-associated gene expression signature in CN-AML patients: Downregulated genes. High *miR-3151* expresser status was associated with the downregulation of 405 probe sets (258 annotated genes) out of 24,649 investigated (Global test *P*-value = .001). Seventy-three of the downregulated genes are *in-silico* predicted targets of *miR-3151* (microrna.org). Highlighted in grey are the six probe-sets corresponding to annotated genes of the *in-silico* targets which showed ≥25% downregulation with a *P*-value <.0001.

Probe set	**Gene Symbol**	**Fold-change: *miR-3151* High/Low**	***P*-value**	***miR-3151 in-silico* predicted Target**
236892_s_at	*hCG_2042068*	0.44	0.0006833	n.a.[#]
1558871_at		0.46	4.18E-05	
219737_s_at	*PCDH9*	0.48	0.0002818	no
238784_at	*DPY19L2*	0.49	0.0003588	yes
204082_at	*PBX3*	0.53	5.20E-06	no
239791_at	*hCG_2042068*	0.54	0.0003422	n.a.
242172_at	*MEIS1*	0.55	0.000455	yes
215767_at	*ZNF804A*	0.55	1.70E-05	no
242321_at		0.55	0.0006427	
205801_s_at	*RASGRP3*	0.56	0.0007374	no
240747_at		0.57	5.46E-05	
236193_at	*HIST1H2BC*	0.58	0.00091	no
230743_at	*hCG_2042068*	0.59	0.0001059	n.a.
220416_at	*ATP8B4*	0.60	0.0002586	no
1559266_s_at	*C10orf140*	0.60	0.0004956	no
240772_at		0.60	5.11E-05	
205942_s_at	*ACSM3*	0.61	0.0007281	no
210377_at	*ACSM3*	0.63	0.0005425	no
234145_at	*PBX3*	0.64	2.22E-05	no
212606_at	*WDFY3*	0.64	0.0003402	yes
241497_at		0.66	0.0002142	
238919_at		0.66	0.0008977	
226736_at	*CHURC1*	0.67	0.0002505	yes
227367_at	*SLCO3A1*	0.67	3.70E-06	yes
227031_at	*SNX13*	0.67	3.64E-05	no
243082_at		0.67	0.0005293	

212651_at	*RHOBTB1*	0.68	0.0003549	no
239033_at		0.68	0.0001358	
1556818_at		0.68	0.0009934	
232412_at	*FBXL20*	0.69	6.32E-05	yes
227224_at	*RALGPS2*	0.69	2.38E-05	no
1568964_x_at	*SPN*	0.69	0.0007393	yes
227533_at		0.69	4.39E-05	
1562280_at		0.69	0.0004659	
228108_at		0.69	0.0007252	
223513_at	*CENPJ*	0.70	0.0008215	no
230166_at	*KIAA1958*	0.70	4.90E-06	yes
227036_at	*RASAL2*	0.70	0.0001915	yes
228696_at	*SLC45A3*	0.70	0.000363	yes
203869_at	*USP46*	0.70	0.0002599	yes
239482_x_at	*ZNF708*	0.70	6.72E-05	no
236002_at		0.70	5.46E-05	
233239_at		0.70	0.0001189	
1558605_at		0.70	0.0002599	
238043_at		0.70	0.0007307	
1563453_at		0.70	0.000981	
221522_at	*ANKRD27*	0.71	7.84E-05	no
225731_at	*ANKRD50*	0.71	0.0004392	yes
224943_at	*BTBD7*	0.71	7.40E-06	no
203763_at	*DYNC2LI1*	0.71	0.0001115	no
218618_s_at	*FNDC3B*	0.71	0.0003876	no
202660_at	*ITPR2*	0.71	0.0004874	yes
235970_at	*LCORL*	0.71	1.75E-05	no
240592_at	*LCORL*	0.71	7.61E-05	no
239392_s_at	*POGK*	0.71	9.44E-05	yes
232500_at	*RALGAPA2*	0.71	0.000644	no
1553148_a_at	*SNX13*	0.71	6.23E-05	no
243469_at		0.71	0.0005396	
232599_at	*EXOC6*	0.72	0.0005936	no
225032_at	*FNDC3B*	0.72	2.90E-05	no
213392_at	*IQCK*	0.72	0.0005533	yes
224726_at	*MIB1*	0.72	0.0004097	no
239406_at	*ZNF193*	0.72	0.0002445	no
225176_at		0.72	5.01E-05	
63825_at	*ABHD2*	0.73	0.0005065	yes
222266_at	*C19orf2*	0.73	0.0004023	no
1570571_at	*CCDC91*	0.73	0.0005321	no

222587_s_at	*GALNT7*	0.73	0.00075	no
203955_at	*KIAA0649*	0.73	3.31E-05	yes
209925_at	*OCLN*	0.73	0.0004003	no
222630_at	*RFX7*	0.73	0.0001535	yes
204633_s_at	*RPS6KA5*	0.73	0.0001815	no
226366_at	*SHPRH*	0.73	0.0006594	no
225085_at	*USP40*	0.73	5.02E-05	yes
205928_at	*ZNF443*	0.73	0.0002221	no
204291_at	*ZNF518A*	0.73	0.0006949	no
243003_at		0.73	0.0001094	
233713_at		0.73	0.000377	
242343_x_at		0.73	0.0006754	
241906_at		0.73	0.0008831	
244022_at		0.73	0.0009613	
213304_at	*FAM179B*	0.74	0.0002543	no
218313_s_at	*GALNT7*	0.74	0.0009507	no
227931_at	*INO80D*	0.74	0.0005216	yes
242458_at	*RALGPS2*	0.74	6.30E-06	no
217707_x_at	*SMARCA2*	0.74	0.0004349	no
230759_at	*SNX14*	0.74	3.23E-05	no
223282_at	*TSHZ1*	0.74	0.0006712	yes
205739_x_at	*ZNF107*	0.74	0.0008872	no
215307_at	*ZNF529*	0.74	0.0008217	yes
239731_at		0.74	0.0001179	
233228_at		0.74	0.0004784	
214820_at	*BRWD1*	0.75	0.0003919	no
225633_at	*DPY19L3*	0.75	0.0006495	no
235030_at	*FAM55C*	0.75	0.0009935	no
224016_at	*HIPK2*	0.75	0.0009617	yes
214457_at	*HOXA2*	0.75	0.0002601	no
224725_at	*MIB1*	0.75	0.0002309	no
223464_at	*OSBPL5*	0.75	7.85E-05	yes
238890_at	*PSMG1*	0.75	0.0006195	no
203883_s_at	*RAB11FIP2*	0.75	4.17E-05	no
202088_at	*SLC39A6*	0.75	9.53E-05	no
235890_at	*TBL1XR1*	0.75	0.0004402	no
1553118_at	*THEM4*	0.75	0.0008293	no
230029_x_at	*UBR3*	0.75	0.0001777	no
226562_at	*ZSCAN29*	0.75	6.40E-06	no
237096_at		0.75	0.0002812	
240478_at		0.75	0.0002859	

236385_at		0.75	0.0004943	
240625_at		0.75	0.0008147	
228694_at		0.75	0.0009289	
212289_at	*ANKRD12*	0.76	0.0002169	no
226901_at	*C17orf58*	0.76	0.0006642	no
223210_at	*CHURC1*	0.76	8.47E-05	yes
1554154_at	*GDAP2*	0.76	5.02E-05	yes
226191_at	*GSK3B*	0.76	0.0001726	yes
212057_at	*KIAA0182*	0.76	0.0003039	yes
227569_at	*LNX2*	0.76	3.93E-05	no
229664_at	*MAPK8*	0.76	0.0003438	no
232613_at	*PBRM1*	0.76	1.57E-05	no
212688_at	*PIK3CB*	0.76	0.0004898	no
219802_at	*PYROXD1*	0.76	0.0006364	no
220338_at	*RALGPS2*	0.76	0.0001018	no
227268_at	*RNFT1*	0.76	0.0002366	no
204635_at	*RPS6KA5*	0.76	5.62E-05	no
213694_at	*RSBN1*	0.76	0.0009087	yes
212921_at	*SMYD2*	0.76	0.0001919	no
241731_x_at	*ZNF440*	0.76	1.51E-05	no
222028_at	*ZNF45*	0.76	0.0001961	no
1556432_at		0.76	8.57E-05	
233393_at		0.76	0.0001948	
225318_at		0.76	0.0006019	
242920_at		0.76	0.0006517	
226030_at	*ACADSB*	0.77	0.0001613	yes
212500_at	*ADO*	0.77	6.58E-05	yes
221825_at	*ANGEL2*	0.77	0.0008929	no
212798_s_at	*ANKMY2*	0.77	0.0001912	no
203525_s_at	*APC*	0.77	0.0003005	no
224945_at	*BTBD7*	0.77	0.0003606	no
219972_s_at	*C14orf135*	0.77	0.0009821	no
223983_s_at	*C19orf12*	0.77	4.56E-05	yes
228149_at	*C7orf60*	0.77	0.0001894	no
212981_s_at	*FAM115A*	0.77	0.000427	no
202915_s_at	*FAM20B*	0.77	1.01E-05	no
202271_at	*FBXO28*	0.77	0.0002156	yes
223215_s_at	*JKAMP*	0.77	6.59E-05	no
215698_at	*KDM5A*	0.77	0.0001753	yes
232112_at	*RALGPS2*	0.77	9.73E-05	no
218499_at	*RP6-213H19.1*	0.77	0.0005841	no

222790_s_at	*RSBN1*	0.77	0.0002179	yes
204156_at	*SIK3*	0.77	5.02E-05	yes
236600_at	*SPG20*	0.77	0.0005169	no
218521_s_at	*UBE2W*	0.77	0.0007051	no
234982_at	*UBR3*	0.77	6.58E-05	no
220243_at	*ZBTB44*	0.77	0.0005526	yes
229022_at	*ZFX*	0.77	0.0003904	no
204523_at	*ZNF140*	0.77	0.0009089	no
209989_at	*ZNF268*	0.77	0.000987	no
60794_f_at	*ZNF814*	0.77	0.0007416	no
218639_s_at	*ZXDC*	0.77	4.19E-05	yes
239830_at		0.77	5.16E-05	
244456_at		0.77	8.90E-05	
1555325_s_at		0.77	0.0001902	
237341_at		0.77	0.0002003	
1559723_s_at		0.77	0.0003648	
1556306_at		0.77	0.0008414	
229692_at		0.77	0.0008903	
223297_at	*AMMECR1L*	0.78	0.0009393	yes
228594_at	*C5orf33*	0.78	0.0001565	yes
204373_s_at	*CEP350*	0.78	0.0005026	no
203078_at	*CUL2*	0.78	0.0001172	no
228032_s_at	*DENND1B*	0.78	0.0008005	no
201025_at	*EIF5B*	0.78	5.36E-05	yes
1563483_at	*FAM91A2*	0.78	4.79E-05	no
201724_s_at	*GALNT1*	0.78	0.0002851	no
201722_s_at	*GALNT1*	0.78	0.0008337	no
240602_at	*HBS1L*	0.78	0.0009194	no
203011_at	*IMPA1*	0.78	0.0005389	no
212056_at	*KIAA0182*	0.78	7.78E-05	yes
209255_at	*KLHDC10*	0.78	0.000236	no
227601_at	*METTL14*	0.78	3.83E-05	no
205408_at	*MLLT10*	0.78	0.0001901	yes
212483_at	*NIPBL*	0.78	0.0001484	no
223238_s_at	*PBRM1*	0.78	0.0002493	no
219459_at	*POLR3B*	0.78	0.0009418	no
213049_at	*RALGAPA1*	0.78	0.0003032	no
203775_at	*SLC25A13*	0.78	0.0002159	no
225881_at	*SLC35B4*	0.78	0.0007477	yes
202089_s_at	*SLC39A6*	0.78	0.0003745	no
204496_at	*STRN3*	0.78	0.0008479	no

204067_at	*SUOX*	0.78	0.0006076	yes
218882_s_at	*WDR3*	0.78	0.0004948	no
212402_at	*ZC3H13*	0.78	0.0001191	no
207304_at	*ZNF45*	0.78	0.0006085	no
222851_at	*ZNF654*	0.78	0.0005023	no
241348_at	*ZNF654*	0.78	0.0006106	no
229506_at		0.78	6.34E-05	
240351_at		0.78	0.000228	
242772_x_at		0.78	0.0005289	
233976_at		0.78	0.000621	
225935_at		0.78	0.0007008	
1570264_at		0.78	0.0007658	
203291_at	*CNOT4*	0.79	0.0003755	no
210320_s_at	*DDX52*	0.79	4.48E-05	no
212908_at	*DNAJC16*	0.79	0.0002277	yes
203693_s_at	*E2F3*	0.79	0.00058	no
226270_at	*EXOC2*	0.79	0.0001111	yes
226752_at	*FAM174A*	0.79	0.0008696	no
239223_s_at	*FBXL20*	0.79	0.0004156	yes
225022_at	*GOPC*	0.79	0.0005923	yes
204176_at	*KLHL20*	0.79	0.0003973	no
225452_at	*MED1*	0.79	0.0005078	yes
230528_s_at	*MGC2752*	0.79	5.27E-05	no
220925_at	*NAA35*	0.79	0.0002797	no
212629_s_at	*PKN2*	0.79	0.0004352	no
209296_at	*PPM1B*	0.79	0.0009847	no
231173_at	*PYROXD1*	0.79	0.0005597	no
226298_at	*RUNDC1*	0.79	0.0008398	yes
1554555_a_at	*SETD6*	0.79	0.0001971	no
213034_at	*SIK3*	0.79	9.10E-06	yes
229776_at	*SLCO3A1*	0.79	0.0001185	yes
228662_at	*SOCS7*	0.79	0.0006709	yes
201449_at	*TIA1*	0.79	0.0007791	no
203690_at	*TUBGCP3*	0.79	0.000182	no
218090_s_at	*WDR11*	0.79	2.52E-05	no
234991_at	*ZXDC*	0.79	0.0003971	yes
227547_at		0.79	2.70E-05	
232963_at		0.79	6.89E-05	
220900_at		0.79	0.0003081	
243997_x_at		0.79	0.0006967	
238431_at		0.79	0.0007433	

226542_at		0.79	0.0009825	
218434_s_at	*AACS*	0.80	0.0009915	no
203526_s_at	*APC*	0.80	9.69E-05	no
202631_s_at	*APPBP2*	0.80	0.0008188	yes
201879_at	*ARIH1*	0.80	0.0002033	no
201658_at	*ARL1*	0.80	1.98E-05	no
203486_s_at	*ARMC8*	0.80	0.000141	no
232515_at	*ASB3*	0.80	0.0006273	no
227777_at	*C10orf18*	0.80	0.0003238	no
217814_at	*CCDC47*	0.80	0.0001197	no
212911_at	*DNAJC16*	0.80	0.0008891	yes
243606_at	*FAM55C*	0.80	0.0008953	no
1555971_s_at	*FBXO28*	0.80	0.000216	yes
202272_s_at	*FBXO28*	0.80	0.0003735	yes
230454_at	*ICA1L*	0.80	0.0005581	yes
229429_x_at	*LOC728855*	0.80	0.0005025	no
225992_at	*MLLT10*	0.80	9.73E-05	yes
203207_s_at	*MTFR1*	0.80	0.0006053	no
218667_at	*PJA1*	0.80	0.0001621	no
212628_at	*PKN2*	0.80	0.0001619	no
227254_at	*POU2F1*	0.80	0.0003115	no
203253_s_at	*PPIP5K2*	0.80	0.0001916	yes
213878_at	*PYROXD1*	0.80	0.0002706	no
200928_s_at	*RAB14*	0.80	0.0004482	no
214855_s_at	*RALGAPA1*	0.80	0.0007877	no
224618_at	*ROD1*	0.80	0.0002432	yes
238005_s_at	*SIN3A*	0.80	0.0002709	yes
234268_at	*SLC2A13*	0.80	1.56E-05	no
210057_at	*SMG1*	0.80	0.000428	yes
203310_at	*STXBP3*	0.80	0.0005135	no
238045_at	*TMEM65*	0.80	0.0002501	no
225411_at	*TMEM87B*	0.80	0.0006145	no
208883_at	*UBR5*	0.80	0.0009669	no
235511_at		0.80	0.0001419	
1559347_at		0.80	0.0001514	
225543_at		0.80	0.0002055	
240016_at		0.80	0.000289	
1562957_at		0.80	0.0006838	
217259_at		0.80	0.0007146	
212502_at	*ADO*	0.81	0.0002688	yes
201880_at	*ARIH1*	0.81	0.0001679	no

225863_s_at	*C19orf12*	0.81	0.0001051	yes
217873_at	*CAB39*	0.81	7.94E-05	no
203533_s_at	*CUL5*	0.81	0.000121	no
203531_at	*CUL5*	0.81	0.0001771	no
226422_at	*ERGIC2*	0.81	0.0004973	no
218518_at	*FAM13B*	0.81	0.0007944	no
244396_at	*G3BP1*	0.81	0.000389	no
242361_at	*IMMT*	0.81	2.05E-05	no
212634_at	*KIAA0776*	0.81	0.000576	no
228446_at	*KIAA2026*	0.81	0.0006976	no
225268_at	*KPNA4*	0.81	0.0002119	yes
225267_at	*KPNA4*	0.81	0.0003695	yes
203208_s_at	*MTFR1*	0.81	5.72E-05	no
219362_at	*NAA35*	0.81	0.0001966	no
200813_s_at	*PAFAH1B1*	0.81	0.0006455	no
202239_at	*PARP4*	0.81	0.0001985	no
220355_s_at	*PBRM1*	0.81	0.0003826	no
209438_at	*PHKA2*	0.81	0.0003692	no
227176_at	*SLC2A13*	0.81	0.0008994	no
228254_at	*STAM2*	0.81	4.34E-05	no
1554287_at	*TRIM4*	0.81	0.000182	yes
225089_at	*USP40*	0.81	0.0002562	yes
227541_at	*WDR20*	0.81	0.000149	no
237208_at	*WDR61*	0.81	0.0005287	no
235819_at		0.81	6.33E-05	
1560048_at		0.81	0.000206	
243065_at		0.81	0.0004244	
240277_at		0.81	0.0004562	
226993_at		0.81	0.0006443	
1564690_at		0.81	0.0006942	
1556580_a_at		0.81	0.0008325	
1558624_at		0.81	0.0008887	
227815_at		0.81	0.0009967	
202629_at	*APPBP2*	0.82	0.0006803	yes
212819_at	*ASB1*	0.82	0.0007887	yes
211464_x_at	*CASP6*	0.82	0.0009132	no
223301_s_at	*CCDC82*	0.82	0.0006498	no
208896_at	*DDX18*	0.82	0.0005921	no
230974_at	*DDX19B*	0.82	0.0006995	no
220547_s_at	*FAM35A*	0.82	0.0001427	no
1557113_at	*LOC283588*	0.82	6.24E-05	n.a.

235884_at	*LOC644794*	0.82	9.42E-05	n.a.
225055_at	*LOC651250*	0.82	0.000945	n.a.
1557965_at	*MTERFD2*	0.82	0.0003913	no
212585_at	*OSBPL8*	0.82	0.0006901	no
215596_s_at	*RNF160*	0.82	0.0008331	no
222789_at	*RSBN1*	0.82	0.0002172	yes
224844_at	*SLAIN2*	0.82	9.05E-05	no
235241_at	*SLC38A9*	0.82	0.000563	no
202277_at	*SPTLC1*	0.82	1.73E-05	no
220486_x_at	*TMEM164*	0.82	0.0006555	yes
224704_at	*TNRC6A*	0.82	0.0009564	yes
238494_at	*TRAF3IP1*	0.82	0.0007156	no
225945_at	*ZNF655*	0.82	0.0007733	no
1556762_a_at		0.82	7.42E-05	
1561763_at		0.82	0.0002251	
241997_at		0.82	0.0003381	
243253_at		0.82	0.0008688	
240020_at		0.82	0.0009719	
202916_s_at	*FAM20B*	0.83	0.0002095	no
204703_at	*IFT88*	0.83	0.0002207	no
226367_at	*KDM5A*	0.83	0.0005376	yes
226919_at	*LYRM2*	0.83	0.0003668	no
242838_at	*MAP6D1*	0.83	0.0002232	no
203497_at	*MED1*	0.83	0.000444	yes
223115_at	*MED17*	0.83	0.0003178	no
235552_at	*METTL14*	0.83	0.0003597	no
212594_at	*PDCD4*	0.83	0.0002949	no
201603_at	*PPP1R12A*	0.83	0.0004046	no
224617_at	*ROD1*	0.83	0.0003319	yes
203704_s_at	*RREB1*	0.83	0.0003729	yes
226217_at	*SLC30A7*	0.83	0.0007446	no
214965_at	*SPATA2L*	0.83	0.0004362	yes
216941_s_at	*TAF1B*	0.83	0.0009691	yes
203732_at	*TRIP4*	0.83	0.0001709	no
233245_at	*UHRF1BP1*	0.83	0.0007008	yes
213120_at	*UHRF1BP1L*	0.83	0.0001656	no
224639_at	*UNQ1887*	0.83	0.0003873	no
202745_at	*USP8*	0.83	0.0006862	no
212267_at	*WAPAL*	0.83	0.0004935	no
212343_at	*YIPF6*	0.83	0.00023	no
202778_s_at	*ZMYM2*	0.83	0.0006963	no

228145_s_at	*ZNF398*	0.83	0.0006652	no
235448_at	*ZXDC*	0.83	8.30E-05	yes
1560171_at		0.83	0.0002508	
225137_at		0.83	0.0002751	
241184_x_at		0.83	0.0007175	
241152_at		0.83	0.0007638	
213282_at	*APOOL*	0.84	0.0002948	no
219116_s_at	*DCUN1D2*	0.84	0.0007572	no
201788_at	*DDX42*	0.84	0.0003808	yes
212375_at	*EP400*	0.84	0.0002203	yes
218297_at	*FAM188A*	0.84	0.0007626	no
224743_at	*IMPAD1*	0.84	0.0007519	yes
204177_s_at	*KLHL20*	0.84	8.15E-05	no
222506_at	*LMBR1*	0.84	0.0008285	no
223400_s_at	*PBRM1*	0.84	0.0007319	no
201493_s_at	*PUM2*	0.84	0.0003849	no
222445_at	*SLC39A9*	0.84	0.0002653	no
209523_at	*TAF2*	0.84	0.0005199	no
211987_at	*TOP2B*	0.84	0.0008433	no
213031_s_at	*WDR73*	0.84	0.0004511	yes
212637_s_at	*WWP1*	0.84	0.0005709	no
1552633_at	*ZNF101*	0.84	6.42E-05	no
226202_at	*ZNF398*	0.84	0.0009908	no
217922_at		0.84	0.0004547	
221079_s_at		0.84	0.0008952	
226893_at	*ABL2*	0.85	0.0007914	yes
212547_at	*BRD3*	0.85	0.0005158	no
219560_at	*C22orf29*	0.85	0.000416	yes
231995_at	*C9orf82*	0.85	0.0007887	no
225747_at	*COQ10A*	0.85	0.0006502	yes
223958_s_at	*DNAL1*	0.85	0.0004634	no
201056_at	*GOLGB1*	0.85	0.0004708	no
209254_at	*KLHDC10*	0.85	0.0005505	no
1557066_at	*LUC7L*	0.85	0.0003932	no
213224_s_at	*NCRNA00081*	0.85	0.0001204	n.a.
209221_s_at	*OSBPL2*	0.85	0.0008461	no
225073_at	*PPHLN1*	0.85	0.0001644	no
226527_at	*RPRD2*	0.85	0.0007514	yes
204587_at	*SLC25A14*	0.85	0.0009359	no
217758_s_at	*TM9SF3*	0.85	0.0001844	yes
234734_s_at	*TNRC6A*	0.85	0.0009006	yes

219163_at	*ZNF562*	0.85	0.0008627	yes
1563068_at		0.85	0.0004834	
241887_at		0.85	0.0005134	
237332_at		0.85	0.0005919	
212755_at	*MON2*	0.86	0.0008951	no
226626_at	*THOC2*	0.86	0.0009281	no
208773_s_at		0.86	0.000152	
236458_at		0.86	0.000897	
236204_at		0.86	0.0009051	
238552_at		0.87	0.0007762	

[#] The gene is not listed in the microrna.org database

Supplemental Table 6. Pathway analysis of the *miR-3151*-associated gene expression signature. Listed are the top ranking components of the categories biological functions and molecular/cellular functions.

Biological Functions	***P*-value**
Gene Expression (Transcriptional Regulation)	3.56E-07-1.95E-02
Cellular Development	8.86E-07-2.57E-02
Connective Tissue Development and Function	8.86E-07-1.95E-02
Cancer	1.16E-06-2.61E-02
Cell Cycle	2.16E-05-2.57E-02
Cellular Function and Maintenance	2.91E-05-2.41E-02
Skeletal and Muscular System Development and Function	2.91E-05-2.2E-02
Reproductive System Development and Function	7.17E-05-1.95E-02
Amino Acid Metabolism	1.06E-04-1.95E-02
Post-Translational Modification	1.06E-04-1.99E-02
Molecular and Cellular Functions	***P*-value**
Gene Expression (Transcriptional Regulation)	3.56E-07 - 1.95E-02
Cellular Development	8.86E-07 - 2.57E-02
Cell Cycle	2.16E-05 - 2.57E-02
Cellular Function and Maintenance	2.91E-05 - 2.41E-02
Amino Acid Metabolism	1.06E-04 - 1.95E-02

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