

Supplemental Table 6. miR-155 associated gene expression signature for positively correlated genes
Correlation of miR-155 expression in combined older and younger CN-AML patients.
154 positively correlated (FDR<.001) genes, ordered by decreasing correlation coefficient.

ProbeSet	Symbol	Name	Correlation coefficient	Parametric p-value
229437_at	MIR155HG	MIR155 host gene (non-protein coding)	0.819	< 1e-07
228372_at	C10orf128	chromosome 10 open reading frame 128	0.513	< 1e-07
211269_s_at	IL2RA	interleukin 2 receptor, alpha	0.49	< 1e-07
206341_at	IL2RA	interleukin 2 receptor, alpha	0.489	< 1e-07
209457_at	DUSP5	dual specificity phosphatase 5	0.482	< 1e-07
209695_at	PTP4A3	protein tyrosine phosphatase type IVA, member 3	0.457	< 1e-07
1554999_at	RASGEF1B	RasGEF domain family, member 1B	0.441	< 1e-07
204224_s_at	GCH1	GTP cyclohydrolase 1	0.41	< 1e-07
1554997_a_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.4	< 1e-07
241709_s_at	DOCK1	dedicator of cytokinesis 1	0.398	< 1e-07
212646_at	RFTN1	raftlin, lipid raft linker 1	0.396	< 1e-07
215078_at	SOD2	superoxide dismutase 2, mitochondrial	0.395	< 1e-07
206574_s_at	PTP4A3	protein tyrosine phosphatase type IVA, member 3	0.39	< 1e-07
212385_at	TCF4	transcription factor 4	0.39	< 1e-07
204103_at	CCL4	chemokine (C-C motif) ligand 4	0.387	< 1e-07
215034_s_at	TM4SF1	transmembrane 4 L six family member 1	0.386	< 1e-07
239835_at	KBTBD8	kelch repeat and BTB (POZ) domain containing 8	0.382	< 1e-07
204748_at	PTGS2	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.381	< 1e-07
226530_at	BMF	Bcl2 modifying factor	0.377	< 1e-07
203753_at	TCF4	transcription factor 4	0.376	< 1e-07
1563229_at	DLEU2	deleted in lymphocytic leukemia 2 (non-protein coding)	0.371	< 1e-07
202820_at	AHR	aryl hydrocarbon receptor	0.368	< 1e-07
228011_at	FAM92A1	family with sequence similarity 92, member A1	0.367	< 1e-07
207655_s_at	BLNK	B-cell linker	0.365	< 1e-07
228702_at	FLJ43663	hypothetical LOC378805	0.364	< 1e-07
230380_at	THAP2	THAP domain containing, apoptosis associated protein 2	0.364	< 1e-07
209386_at	TM4SF1	transmembrane 4 L six family member 1	0.364	< 1e-07
222146_s_at	TCF4	transcription factor 4	0.362	< 1e-07
202644_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	0.36	< 1e-07
201502_s_at	NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha	0.357	< 1e-07

226545_at	CD109	CD109 molecule	0.356	< 1e-07
202643_s_at	TNFAIP3	tumor necrosis factor, alpha-induced protein 3	0.356	< 1e-07
209392_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.354	< 1e-07
235391_at	FAM92A1	family with sequence similarity 92, member A1	0.353	< 1e-07
212386_at	TCF4	transcription factor 4	0.352	< 1e-07
204440_at	CD83	CD83 molecule	0.35	< 1e-07
210839_s_at	ENPP2	ectonucleotide pyrophosphatase/phosphodiesterase 2	0.35	< 1e-07
229900_at	CD109	CD109 molecule	0.349	< 1e-07
202859_x_at	IL8	interleukin 8	0.349	< 1e-07
212387_at	TCF4	transcription factor 4	0.347	< 1e-07
39402_at	IL1B	interleukin 1, beta	0.346	< 1e-07
212382_at	TCF4	transcription factor 4	0.346	< 1e-07
209365_s_at	ECM1	extracellular matrix protein 1	0.345	< 1e-07
236898_at	LOC100288781	similar to hCG1994130	0.345	< 1e-07
203897_at	LYRM1	LYR motif containing 1	0.345	< 1e-07
1568695_s_at	INTS6	integrator complex subunit 6	0.344	< 1e-07
232504_at	LOC285628	hypothetical protein LOC285628	0.344	< 1e-07
200880_at	DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1	0.342	< 1e-07
225615_at	IFFO2	intermediate filament family orphan 2	0.342	< 1e-07
230123_at	NECAP2	NECAP endocytosis associated 2	0.342	< 1e-07
205067_at	IL1B	interleukin 1, beta	0.339	< 1e-07
236213_at	LOC100286920	hypothetical protein LOC100286920	0.338	< 1e-07
212365_at	MYO1B	myosin IB	0.338	< 1e-07
220669_at	OTUD4	OTU domain containing 4	0.337	1.00E-07
229054_at	C14orf181	chromosome 14 open reading frame 181	0.336	1.00E-07
201631_s_at	IER3	immediate early response 3	0.336	1.00E-07
203373_at	SOCS2	suppressor of cytokine signaling 2	0.336	1.00E-07
216016_at	NLRP3	NLR family, pyrin domain containing 3	0.335	1.00E-07
229744_at	SSFA2	sperm specific antigen 2	0.335	1.00E-07
201719_s_at	EPB41L2	erythrocyte membrane protein band 4.1 like 2	0.334	1.00E-07
225979_at	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	0.334	1.00E-07
232188_at	AKAP13	A kinase (PRKA) anchor protein 13	0.333	1.00E-07
209218_at	SQLE	squalene epoxidase	0.332	1.00E-07
213891_s_at	TCF4	transcription factor 4	0.331	1.00E-07
211506_s_at	IL8	interleukin 8	0.33	1.00E-07
203372_s_at	SOCS2	suppressor of cytokine signaling 2	0.33	1.00E-07
210656_at	EED	embryonic ectoderm development	0.328	1.00E-07
207075_at	NLRP3	NLR family, pyrin domain containing 3	0.326	2.00E-07
1559315_s_at	LOC144481	hypothetical protein LOC144481	0.325	2.00E-07
207426_s_at	TNFSF4	tumor necrosis factor (ligand) superfamily, member 4	0.325	2.00E-07
218810_at	ZC3H12A	zinc finger CCCH-type containing 12A	0.324	2.00E-07

226071_at	ADAMTSL4	ADAMTS-like 4	0.322	2.00E-07
214390_s_at	BCAT1	branched chain amino-acid transaminase 1, cytosolic	0.322	2.00E-07
216015_s_at	NLRP3	NLR family, pyrin domain containing 3	0.322	2.00E-07
213324_at	SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	0.322	2.00E-07
209326_at	SLC35A2	solute carrier family 35 (UDP-galactose transporter), member A2	0.321	3.00E-07
213562_s_at	SQLE	squalene epoxidase	0.321	3.00E-07
201718_s_at	EPB41L2	erythrocyte membrane protein band 4.1-like 2	0.32	3.00E-07
210299_s_at	FHL1	four and a half LIM domains 1	0.318	3.00E-07
219480_at	SNAI1	snail homolog 1 (Drosophila)	0.318	3.00E-07
201540_at	FHL1	four and a half LIM domains 1	0.317	4.00E-07
1554486_a_at	C6orf114	chromosome 6 open reading frame 114	0.316	4.00E-07
209530_at	CACNB3	calcium channel, voltage-dependent, beta 3 subunit	0.314	5.00E-07
239719_at	CD109	CD109 molecule	0.314	5.00E-07
235252_at	KSR1	kinase suppressor of ras 1	0.313	5.00E-07
225699_at	C7orf40	chromosome 7 open reading frame 40	0.309	7.00E-07
204363_at	F3	coagulation factor III (thromboplastin, tissue factor)	0.309	7.00E-07
203187_at	DOCK1	dedicator of cytokinesis 1	0.308	8.00E-07
207375_s_at	IL15RA	interleukin 15 receptor, alpha	0.308	8.00E-07
226390_at	STARD4	StAR-related lipid transfer (START) domain containing 4	0.308	8.00E-07
224496_s_at	TMEM107	transmembrane protein 107	0.308	8.00E-07
204794_at	DUSP2	dual specificity phosphatase 2	0.307	9.00E-07
201329_s_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.307	8.00E-07
202638_s_at	ICAM1	intercellular adhesion molecule 1	0.307	9.00E-07
226459_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	0.307	8.00E-07
206148_at	IL3RA	interleukin 3 receptor, alpha (low affinity)	0.306	1.00E-06
225344_at	NCOA7	nuclear receptor coactivator 7	0.306	1.00E-06
214581_x_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0.306	9.00E-07
204073_s_at	C11orf9	chromosome 11 open reading frame 9	0.305	1.00E-06
224606_at	KLF6	Kruppel-like factor 6	0.304	1.10E-06
205193_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0.303	1.20E-06
200787_s_at	PEA15	phosphoprotein enriched in astrocytes 15	0.303	1.20E-06
205298_s_at	BTN2A2	butyrophilin, subfamily 2, member A2	0.302	1.30E-06
218898_at	FAM57A	family with sequence similarity 57, member A	0.302	1.30E-06
214505_s_at	FHL1	four and a half LIM domains 1	0.302	1.30E-06
223159_s_at	NEK6	NIMA (never in mitosis gene a)-related kinase 6	0.302	1.30E-06

242814_at	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0.302	1.30E-06
221881_s_at	CLIC4	chloride intracellular channel 4	0.301	1.40E-06
213038_at	RNF19B	ring finger protein 19B	0.3	1.60E-06
218856_at	TNFRSF21	tumor necrosis factor receptor superfamily, member 21	0.3	1.60E-06
213075_at	OLFML2A	olfactomedin-like 2A	0.298	1.90E-06
36564_at	RNF19B	ring finger protein 19B	0.298	1.80E-06
218429_s_at	C19orf66	chromosome 19 open reading frame 66	0.297	2.00E-06
215925_s_at	CD72	CD72 molecule	0.297	2.00E-06
232052_at	LOC440944	hypothetical LOC440944	0.297	2.00E-06
36711_at	MAFF	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0.296	2.10E-06
209544_at	RIPK2	receptor-interacting serine-threonine kinase 2	0.296	2.10E-06
216841_s_at	SOD2	superoxide dismutase 2, mitochondrial	0.296	2.10E-06
1554508_at	PIK3AP1	phosphoinositide-3-kinase adaptor protein 1	0.295	2.40E-06
201939_at	PLK2	polo-like kinase 2	0.295	2.30E-06
1569203_at	CXCL2	chemokine (C-X-C motif) ligand 2	0.294	2.40E-06
210117_at	SPAG1	sperm associated antigen 1	0.294	2.50E-06
207113_s_at	TNF	tumor necrosis factor	0.294	2.50E-06
204057_at	IRF8	interferon regulatory factor 8	0.293	2.70E-06
1569020_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	0.293	2.80E-06
202637_s_at	ICAM1	intercellular adhesion molecule 1	0.292	2.90E-06
223158_s_at	NEK6	NIMA (never in mitosis gene a)-related kinase 6	0.292	2.90E-06
219499_at	SEC61A2	Sec61 alpha 2 subunit (<i>S. cerevisiae</i>)	0.291	3.10E-06
1566363_at	DNMT	deoxynucleotidyltransferase, terminal	0.29	3.30E-06
231887_s_at	KIAA1274	KIAA1274	0.29	3.50E-06
228607_at	OAS2	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0.29	3.40E-06
204430_s_at	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5	0.29	3.50E-06
218789_s_at	C11orf71	chromosome 11 open reading frame 71	0.289	3.80E-06
203716_s_at	DPP4	dipeptidyl-peptidase 4	0.289	3.80E-06
230363_s_at	INPP5F	inositol polyphosphate-5-phosphatase F	0.289	3.70E-06
205599_at	TRAF1	TNF receptor-associated factor 1	0.289	3.60E-06
220507_s_at	UPB1	ureidopropionase, beta	0.289	3.80E-06
213895_at	EMP1	epithelial membrane protein 1	0.288	4.10E-06
205582_s_at	GGT5	gamma-glutamyltransferase 5	0.288	4.00E-06
221477_s_at	SOD2	superoxide dismutase 2, mitochondrial	0.288	3.90E-06
210815_s_at	CALCRL	calcitonin receptor-like	0.287	4.50E-06
201328_at	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	0.287	4.30E-06

228468_at	MASTL	microtubule associated serine/threonine kinase-like	0.287	4.40E-06
204269_at	PIM2	pim-2 oncogene	0.287	4.50E-06
1557352_at	SQLE	squalene epoxidase	0.287	4.40E-06
208296_x_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	0.287	4.40E-06
221718_s_at	AKAP13	A kinase (PRKA) anchor protein 13	0.286	4.60E-06
224884_at	AKAP13	A kinase (PRKA) anchor protein 13	0.286	4.90E-06
220658_s_at	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.285	5.10E-06
209732_at	CLEC2B	C-type lectin domain family 2, member B	0.285	5.10E-06
204533_at	CXCL10	chemokine (C-X-C motif) ligand 10	0.285	5.10E-06
218823_s_at	KCTD9	potassium channel tetramerisation domain containing 9	0.285	5.00E-06
201647_s_at	SCARB2	scavenger receptor class B, member 2	0.285	5.20E-06
226517_at	BCAT1	branched chain amino-acid transaminase 1, cytosolic	0.284	5.60E-06
210233_at	IL1RAP	interleukin 1 receptor accessory protein	0.284	5.80E-06
204059_s_at	ME1	malic enzyme 1, NADP(+)-dependent, cytosolic	0.284	5.70E-06
1552301_a_at	CORO6	coronin 6	0.283	6.20E-06
224983_at	SCARB2	scavenger receptor class B, member 2	0.283	6.20E-06
210260_s_at	TNFAIP8	tumor necrosis factor, alpha-induced protein 8	0.283	5.90E-06
217826_s_at	UBE2J1	ubiquitin-conjugating enzyme E2, J1 (UBC6 homolog, yeast)	0.283	6.10E-06
200788_s_at	PEA15	phosphoprotein enriched in astrocytes 15	0.282	6.70E-06
1555486_a_at	PRR5L	proline rich 5 like	0.282	6.30E-06
207076_s_at	ASS1	argininosuccinate synthase 1	0.281	7.30E-06
206082_at	HCP5	HLA complex P5	0.281	7.10E-06
53720_at	C19orf66	chromosome 19 open reading frame 66	0.279	8.20E-06
202910_s_at	CD97	CD97 molecule	0.279	7.90E-06
209774_x_at	CXCL2	chemokine (C-X-C motif) ligand 2	0.279	8.20E-06
201325_s_at	EMP1	epithelial membrane protein 1	0.279	8.40E-06
230067_at	FAM124A	family with sequence similarity 124A	0.279	8.10E-06
210298_x_at	FHL1	four and a half LIM domains 1	0.279	8.40E-06
244080_at	LOC100287039	hypothetical protein LOC100287039	0.279	8.10E-06
218086_at	NPDC1	neural proliferation, differentiation and control, 1	0.279	8.00E-06
210519_s_at	NQO1	NAD(P)H dehydrogenase, quinone 1	0.279	8.00E-06
224204_x_at	ARNTL2	aryl hydrocarbon receptor nuclear translocator-like 2	0.278	9.20E-06
227808_at	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15	0.278	9.10E-06
201539_s_at	FHL1	four and a half LIM domains 1	0.278	8.70E-06
1552329_at	RBBP6	retinoblastoma binding protein 6	0.278	8.60E-06
237016_at	TMEM217	transmembrane protein 217	0.278	8.50E-06
48531_at	TNIP2	TNFAIP3 interacting protein 2	0.278	9.20E-06

1553736_at	ZFC3H1	zinc finger, C3H1-type containing	0.278	8.70E-06
224739_at	PIM3	pim-3 oncogene	0.277	9.80E-06
213134_x_at	BTG3	BTG family, member 3	0.276	1.03E-05
233986_s_at	PLEKHG2	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	0.276	9.90E-06
210365_at	RUNX1	runt-related transcription factor 1	0.276	1.02E-05
228747_at	SEC61A2	Sec61 alpha 2 subunit (<i>S. cerevisiae</i>)	0.276	9.90E-06
1555832_s_at	KLF6	Kruppel-like factor 6	0.275	1.13E-05
1559777_at	LOC731424	hypothetical LOC731424	0.275	1.14E-05
200797_s_at	MCL1	myeloid cell leukemia sequence 1 (BCL2-related)	0.275	1.09E-05
213577_at	SQLE	squalene epoxidase	0.275	1.14E-05
1552755_at	C9orf66	chromosome 9 open reading frame 66	0.274	1.17E-05
206429_at	F2RL1	coagulation factor II (thrombin) receptor like 1	0.274	1.15E-05
211139_s_at	NAB1	NGFI-A binding protein 1 (EGR1 binding protein 1)	0.274	1.23E-05
224579_at	SLC38A1	solute carrier family 38, member 1	0.274	1.20E-05
222243_s_at	TOB2	transducer of ERBB2, 2	0.274	1.21E-05
206331_at	CALCRL	calcitonin receptor-like	0.273	1.26E-05
235688_s_at	TRAF4	TNF receptor-associated factor 4	0.273	1.25E-05
220246_at	CAMK1D	calcium/calmodulin-dependent protein kinase ID	0.272	1.39E-05
244074_at	LOC100129104	hypothetical LOC100129104	0.272	1.38E-05
225949_at	NRBP2	nuclear receptor binding protein 2	0.272	1.43E-05
227420_at	TNFAIP8L1	tumor necrosis factor, alpha-induced protein 8-like 1	0.272	1.35E-05
217853_at	TNS3	tensin 3	0.272	1.35E-05
206756_at	CHST7	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 7	0.271	1.47E-05
225970_at	DDHD1	DDHD domain containing 1	0.271	1.55E-05
212070_at	GPR56	G protein-coupled receptor 56	0.27	1.56E-05
202150_s_at	NEDD9	neural precursor cell expressed, developmentally down-regulated 9	0.27	1.57E-05
223218_s_at	NFKBIZ	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	0.27	1.58E-05
204484_at	PIK3C2B	phosphoinositide-3-kinase, class 2, beta polypeptide	0.27	1.61E-05

FDR	Permutation p-value
< 1e-07	< 1e-07
< 1e-07	< 1e-07
< 1e-07	< 1e-07
< 1e-07	< 1e-07
< 1e-07	< 1e-07
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< 1e-07	< 1e-07

3.97E-05	< 1e-07
3.97E-05	< 1e-07
3.97E-05	< 1e-07
3.97E-05	< 1e-07
5.62E-05	< 1e-07
5.62E-05	< 1e-07
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5.62E-05	< 1e-07
7.22E-05	< 1e-07
7.22E-05	< 1e-07
8.41E-05	< 1e-07
8.41E-05	< 1e-07
8.41E-05	< 1e-07
0.000113	< 1e-07
0.000113	< 1e-07
0.000123	< 1e-07
0.000123	< 1e-07
0.000123	1.00E-04
0.000123	< 1e-07
0.000135	< 1e-07
0.000123	< 1e-07
0.000135	1.00E-04
0.000123	< 1e-07
0.000147	< 1e-07
0.000147	< 1e-07
0.000135	< 1e-07
0.000147	< 1e-07
0.000155	< 1e-07
0.000164	< 1e-07
0.000164	< 1e-07
0.00017	< 1e-07
0.00017	< 1e-07
0.00017	< 1e-07
0.00017	< 1e-07

0.00017	< 1e-07
0.00018	< 1e-07
2.00E-04	< 1e-07
2.00E-04	< 1e-07
0.000229	< 1e-07
0.000223	< 1e-07
0.000236	< 1e-07
0.000236	< 1e-07
0.000236	< 1e-07
0.000242	< 1e-07
0.000242	< 1e-07
0.000242	< 1e-07
0.00027	< 1e-07
0.000262	< 1e-07
0.00027	< 1e-07
0.000278	< 1e-07
0.000278	< 1e-07
0.000297	< 1e-07
0.000303	< 1e-07
0.000308	1.00E-04
0.000308	< 1e-07
0.000326	< 1e-07
0.000345	< 1e-07
0.000353	< 1e-07
0.000352	< 1e-07
0.000353	< 1e-07
0.00037	< 1e-07
0.00037	< 1e-07
0.000366	< 1e-07
0.000359	< 1e-07
0.00037	< 1e-07
0.00039	< 1e-07
0.000382	< 1e-07
0.000378	< 1e-07
0.00041	< 1e-07
0.000405	< 1e-07

0.000406	< 1e-07
0.00041	< 1e-07
0.000406	< 1e-07
0.000406	< 1e-07
0.000415	< 1e-07
0.000438	< 1e-07
0.000448	< 1e-07
0.000448	< 1e-07
0.000448	< 1e-07
0.000445	< 1e-07
0.000455	< 1e-07
0.000485	< 1e-07
0.000496	< 1e-07
0.000492	< 1e-07
0.000515	< 1e-07
0.000515	< 1e-07
0.000498	< 1e-07
0.000511	< 1e-07
0.000549	< 1e-07
0.000521	< 1e-07
0.000589	< 1e-07
0.000575	< 1e-07
0.000625	< 1e-07
0.000617	< 1e-07
0.000625	< 1e-07
0.000631	< 1e-07
0.000622	< 1e-07
0.000631	< 1e-07
0.000622	2.00E-04
0.00062	< 1e-07
0.00062	< 1e-07
0.000673	< 1e-07
0.00067	< 1e-07
0.000643	< 1e-07
0.000641	< 1e-07
0.000636	< 1e-07
0.000673	< 1e-07

0.000643	< 1e-07
0.000706	< 1e-07
0.000731	< 1e-07
0.000708	< 1e-07
0.000727	< 1e-07
0.000708	< 1e-07
0.000785	< 1e-07
0.000787	1.00E-04
0.00076	< 1e-07
0.000787	< 1e-07
0.000802	< 1e-07
0.000791	< 1e-07
0.000829	1.00E-04
0.000817	< 1e-07
0.000818	< 1e-07
0.000843	< 1e-07
0.000839	< 1e-07
0.000902	< 1e-07
0.000899	1.00E-04
0.000919	< 1e-07
0.000888	< 1e-07
0.000888	< 1e-07
0.000939	< 1e-07
0.000984	< 1e-07
0.000984	< 1e-07
0.000984	< 1e-07
0.000987	< 1e-07
0.001	< 1e-07