

Table S1. Prediction of potential candidate target genes of miR-3662 using TargetScan analysis

Target gene	Representative transcript	Gene name	3P-seq tags + 5	Total sites	8mer sites	7mer-m8 sites	7mer-A1 sites	6mer sites	Representative miRNA	Cumulative weighted context ++ score	Total context ++ score	Aggregate PCT
GUCY1A2	ENST00000526355.2	guanylate cyclase 1, soluble, alpha 2	24	11	0	6	5	5	hsa-miR-3662	-0.19	-1.14	N/A
KCNJ6	ENST00000609713.1	potassium inwardly-rectifying channel, subfamily J, member 6	5	5	0	3	2	10	hsa-miR-3662	-1.07	-1.07	N/A
STX7	ENST00000367941.2	syntaxin 7	1395	10	3	5	2	15	hsa-miR-3662	-0.03	-0.95	N/A
NCKAP1	ENST00000361354.4	NCK-associated protein 1	700	14*	3	7	3	5	hsa-miR-3662	-0.06	-0.94	N/A
UBE2D3	ENST00000453744.2	ubiquitin-conjugating enzyme E2D 3	2312	9	0	2	7	8	hsa-miR-3662	-0.01	-0.87	N/A
PTPN4	ENST00000263708.2	protein tyrosine phosphatase, non-receptor type 4 (megakaryocyte)	215	12	1	3	8	9	hsa-miR-3662	-0.36	-0.81	N/A
VWC2	ENST00000340652.4	von Willebrand factor C domain containing 2	5	7	3	1	3	7	hsa-miR-3662	-0.79	-0.79	N/A
PGAP1	ENST00000354764.4	post-GPI attachment to proteins 1	106	11	2	4	5	7	hsa-miR-3662	-0.51	-0.79	N/A
HSD17B12	ENST00000278353.4	hydroxysteroid (17-beta) dehydrogenase 12	1422	6	1	2	3	8	hsa-miR-3662	-0.06	-0.67	N/A
CSRNP3	ENST00000314499.7	cysteine-serine-rich nuclear protein 3	24	6	1	2	3	8	hsa-miR-3662	-0.6	-0.6	N/A
XKR4	ENST00000327381.6	XK, Kell blood group complex subunit-related family, member 4	5	12	2	9	1	12	hsa-miR-3662	-0.57	-0.57	N/A
LY75-CD302	ENST00000504764.1	LY75-CD302 readthrough	855	4	0	1	3	5	hsa-miR-3662	-0.34	-0.56	N/A
LY75	ENST00000554112.1	lymphocyte antigen 75	855	4	0	1	3	5	hsa-miR-3662	-0.34	-0.56	N/A
CAMTA1	ENST00000473578.1	calmodulin binding transcription activator 1	1674	3	0	3	0	0	hsa-miR-3662	-0.54	-0.55	N/A
GJE1	ENST00000450456.2	gap junction protein, epsilon 1, 23kDa	5	2	1	1	0	0	hsa-miR-3662	-0.51	-0.51	N/A
QKI	ENST00000392127.2	QKI, KH domain containing, RNA binding	323	9	0	3	6	9	hsa-miR-3662	-0.1	-0.48	N/A
MGST3	ENST00000367889.3	microsomal glutathione S-transferase 3	938	1	1	0	0	3	hsa-miR-3662	-0.38	-0.46	N/A
ZBTB20	ENST00000462705.1	zinc finger and BTB domain containing 20	5	17	5	6	6	11	hsa-miR-3662	-0.04	-0.45	N/A
GPR18	ENST00000397473.2	G protein-coupled receptor 18	5	1	1	0	0	1	hsa-miR-3662	-0.45	-0.45	N/A
CCDC50	ENST00000392455.3	coiled-coil domain containing 50	961	5	0	2	3	6	hsa-miR-3662	-0.25	-0.45	N/A
TMEM106B	ENST00000396667.3	transmembrane protein 106B	615	9	0	5	4	7	hsa-miR-3662	-0.01	-0.44	N/A
SUPT4H1	ENST00000225504.3	suppressor of Ty 4 homolog 1 (S. cerevisiae)	6325	2	2	0	0	3	hsa-miR-3662	-0.42	-0.42	N/A
AP5M1	ENST00000261558.3	adaptor-related protein complex 5, mu 1 subunit	198	10	1	6	3	5	hsa-miR-3662	-0.14	-0.41	N/A
UNC5C	ENST00000453304.1	unc-5 homolog C (C. elegans)	60	3	0	3	0	7	hsa-miR-3662	-0.29	-0.4	N/A
SMIM15	ENST00000339020.3	small integral membrane protein 15	1037	5	0	1	4	4	hsa-miR-3662	-0.09	-0.4	N/A
PTS	ENST00000525803.1	6-pyruvoyltetrahydropterin synthase	1526	2	1	1	0	1	hsa-miR-3662	-0.13	-0.4	N/A
C12orf76	ENST00000546651.2	chromosome 12 open reading frame 76	62	2	1	1	0	1	hsa-miR-3662	-0.36	-0.4	N/A
AIMP2	ENST00000223029.3	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	2844	1	1	0	0	0	hsa-miR-3662	0	-0.4	N/A
AGO2	ENST00000220592.5	argonaute RISC catalytic component 2	350	1	0	0	1	1	hsa-miR-3662	-0.02	-0.4	N/A
PKIA	ENST00000396418.2	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	542	10	4	5	1	7	hsa-miR-3662	-0.1	-0.39	N/A
ISCA2	ENST00000554924.1	iron-sulfur cluster assembly 2	135	5	2	0	3	0	hsa-miR-3662	-0.22	-0.39	N/A
ZNF66	ENST00000594534.1	zinc finger protein 66	2	3	1	1	1	0	hsa-miR-3662	-0.38	-0.38	N/A

PPM1L	ENST00000498165.1	protein phosphatase, Mg2+/Mn2+ dependent, 1L	59	8	1	3	4	6	hsa-miR-3662	-0.16	-0.38	N/A
LRP12	ENST00000424843.2	low density lipoprotein receptor-related protein 12	378	4	1	1	2	4	hsa-miR-3662	-0.1	-0.38	N/A
MND1	ENST00000240488.3	meiotic nuclear divisions 1 homolog (S. cerevisiae)	1780	1	1	0	0	0	hsa-miR-3662	-0.36	-0.37	N/A
CFHR2	ENST00000367421.3	complement factor H-related 2	5	3	0	3	0	3	hsa-miR-3662	-0.32	-0.36	N/A
PPBP	ENST00000296028.3	pro-platelet basic protein (chemokine (C-X-C motif) ligand 7)	5	3	1	1	1	2	hsa-miR-3662	-0.12	-0.36	N/A
FZD3	ENST00000240093.3	frizzled family receptor 3	192	12	4	4	4	7	hsa-miR-3662	-0.31	-0.36	N/A
CMC1	ENST00000466830.1	COX assembly mitochondrial protein 1 homolog (S. cerevisiae)	1203	3	1	2	0	6	hsa-miR-3662	-0.3	-0.36	N/A
RP11-9B6.1	ENST00000504213.1	HCG2045747; Uncharacterized protein	5	1	0	1	0	2	hsa-miR-3662	-0.35	-0.35	N/A
NUDCD2	ENST00000302764.4	NudC domain containing 2	308	12	1	6	5	7	hsa-miR-3662	-0.09	-0.35	N/A
FCN3	ENST00000270879.4	ficolin (collagen/fibrinogen domain containing) 3	5	1	1	0	0	0	hsa-miR-3662	-0.35	-0.35	N/A
ABI2	ENST00000295851.5	abl-interactor 2	877	6	0	1	5	13	hsa-miR-3662	-0.01	-0.35	N/A
C8orf22	ENST00000303202.8	chromosome 8 open reading frame 22	5	2	0	2	0	2	hsa-miR-3662	-0.34	-0.34	N/A
DNAJC10	ENST00000264065.7	DnaJ (Hsp40) homolog, subfamily C, member 10	709	15	1	7	7	8	hsa-miR-3662	-0.01	-0.34	N/A
CREB1	ENST00000432329.2	cAMP responsive element binding protein 1	295	9	2	3	4	9	hsa-miR-3662	-0.14	-0.34	N/A
BCL2L15	ENST00000393316.3	BCL2-like 15	5	6	1	4	1	4	hsa-miR-3662	-0.25	-0.34	N/A
ADAT2	ENST00000606514.1	adenosine deaminase, tRNA-specific 2	303	9	1	4	4	3	hsa-miR-3662	-0.05	-0.34	N/A
TMEM182	ENST00000412401.2	transmembrane protein 182	69	3	1	2	0	3	hsa-miR-3662	-0.27	-0.33	N/A
SH3TC2	ENST00000502274.1	SH3 domain and tetratricopeptide repeats 2	31	18	2	10	6	8	hsa-miR-3662	0	-0.33	N/A
AC090186.1	ENST00000415643.1	Uncharacterized protein	5	2	0	2	0	0	hsa-miR-3662	-0.32	-0.32	N/A
RP11-3B7.1	ENST00000440528.3	Uncharacterized protein	8	2	1	1	0	0	hsa-miR-3662	-0.32	-0.32	N/A
REEP5	ENST00000545426.1	receptor accessory protein 5	4440	2	1	0	1	3	hsa-miR-3662	0	-0.32	N/A
MYCBP2	ENST00000544440.2	MYC binding protein 2, E3 ubiquitin protein ligase	343	1	0	1	0	4	hsa-miR-3662	-0.17	-0.32	N/A
IFIT1	ENST00000371804.3	interferon-induced protein with tetratricopeptide repeats 1	72	3	2	0	1	2	hsa-miR-3662	-0.28	-0.32	N/A
DOCK7	ENST00000251157.5	dedicator of cytokinesis 7	66	5	0	2	3	2	hsa-miR-3662	-0.19	-0.32	N/A
RGS17	ENST00000367225.2	regulator of G-protein signaling 17	11	6	2	3	1	8	hsa-miR-3662	-0.18	-0.31	N/A
RAB3B	ENST00000371655.3	RAB3B, member RAS oncogene family	611	4	0	2	2	3	hsa-miR-3662	-0.04	-0.31	N/A
PIK3C2G	ENST00000433979.1	phosphatidylinositol-4-phosphate 3-kinase, catalytic subunit type 2 gamma	5	1	1	0	0	0	hsa-miR-3662	-0.31	-0.31	N/A
ATP5S	ENST00000245448.6	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (fa	310	7	3	2	2	2	hsa-miR-3662	-0.06	-0.31	N/A
CCR8	ENST00000414803.1	chemokine (C-C motif) receptor 8	5	2	1	0	1	2	hsa-miR-3662	-0.3	-0.3	N/A
C21orf37	ENST00000440664.1	chromosome 21 open reading frame 37	5	1	1	0	0	0	hsa-miR-3662	-0.3	-0.3	N/A
IL22	ENST00000538666.1	interleukin 22	5	2	1	0	1	0	hsa-miR-3662	-0.3	-0.3	N/A
EBNA1BP2	ENST00000431635.2	EBNA1 binding protein 2	930	5	4	1	0	2	hsa-miR-3662	-0.17	-0.3	N/A
CCDC38	ENST00000546386.1	coiled-coil domain containing 38	10	2	1	1	0	1	hsa-miR-3662	-0.22	-0.3	N/A
CAMK4	ENST00000282356.4	calcium/calmodulin-dependent protein kinase IV	73	17	3	5	9	10	hsa-miR-3662	-0.21	-0.3	N/A
AGL	ENST00000370161.2	amylo-alpha-1, 6-glucosidase, 4-alpha-glucanotransferase	48	1	0	1	0	3	hsa-miR-3662	-0.3	-0.3	N/A
RP6-24A23.6	ENST00000563887.1	Uncharacterized protein	937	4	0	1	3	1	hsa-miR-3662	-0.14	-0.29	N/A
ZNF280C	ENST00000370978.4	zinc finger protein 280C	138	4	0	2	2	8	hsa-miR-3662	-0.19	-0.29	N/A
TBCB	ENST00000586868.1	tubulin folding cofactor B	1224	2	0	1	1	0	hsa-miR-3662	-0.29	-0.29	N/A
RAB30	ENST00000533486.1	RAB30, member RAS oncogene family	274	3	1	0	2	3	hsa-miR-3662	-0.18	-0.29	N/A

PPIL4	ENST00000340881.2	peptidylprolyl isomerase (cyclophilin)-like 4	1565	8	1	5	2	12	hsa-miR-3662	-0.05	-0.29	N/A
ITGA1	ENST00000282588.6	integrin, alpha 1	400	7	1	5	1	6	hsa-miR-3662	-0.09	-0.29	N/A
HOOK3	ENST00000307602.4	hook microtubule-tethering protein 3	403	15	3	8	4	7	hsa-miR-3662	-0.2	-0.29	N/A
GTF2A2	ENST00000396060.2	general transcription factor IIA, 2, 12kDa	1068	2	1	0	1	1	hsa-miR-3662	-0.24	-0.29	N/A
GLIPR1L1	ENST00000312442.2	GLI pathogenesis-related 1 like 1	5	1	1	0	0	0	hsa-miR-3662	-0.29	-0.29	N/A
ARL15	ENST00000502271.1	ADP-ribosylation factor-like 15	119	2	1	1	0	0	hsa-miR-3662	-0.29	-0.29	N/A
ZNF460	ENST00000360338.3	zinc finger protein 460	164	13	4	7	2	18	hsa-miR-3662	-0.25	-0.28	N/A
SSH2	ENST00000582084.1	slingshot protein phosphatase 2	190	6	0	4	2	0	hsa-miR-3662	-0.03	-0.28	N/A
PSMA8	ENST00000343848.6	proteasome (prosome, macropain) subunit, alpha type, 8	5	3	3	0	0	0	hsa-miR-3662	-0.28	-0.28	N/A
PPP2CB	ENST00000221138.4	protein phosphatase 2, catalytic subunit, beta isozyme	11	1	1	0	0	1	hsa-miR-3662	-0.24	-0.28	N/A
MKLN1	ENST00000352689.6	muskelin 1, intracellular mediator containing kelch motifs	477	4	0	3	1	4	hsa-miR-3662	-0.18	-0.28	N/A
KLRC2	ENST00000381902.2	killer cell lectin-like receptor subfamily C, member 2	5	3	1	1	1	0	hsa-miR-3662	-0.28	-0.28	N/A
EIF3E	ENST00000220849.5	eukaryotic translation initiation factor 3, subunit E	906	1	1	0	0	1	hsa-miR-3662	-0.28	-0.28	N/A
AC012360.2	ENST00000595531.1	LOC644617 protein; Uncharacterized protein	430	2	1	1	0	1	hsa-miR-3662	-0.22	-0.27	N/A
USP14	ENST00000261601.7	ubiquitin specific peptidase 14 (tRNA-guanine transglycosylase)	561	3	0	1	2	3	hsa-miR-3662	-0.17	-0.27	N/A
STRN	ENST00000263918.4	striatin, calmodulin binding protein	476	10	5	2	3	7	hsa-miR-3662	-0.17	-0.27	N/A
SSB	ENST00000260956.4	Sjogren syndrome antigen B (autoantigen La)	373	1	1	0	0	0	hsa-miR-3662	-0.27	-0.27	N/A
RNF217	ENST00000521654.2	ring finger protein 217	92	12	5	5	2	7	hsa-miR-3662	-0.07	-0.27	N/A
RFESD	ENST00000513950.2	Rieske (Fe-S) domain containing	15	3	1	0	2	2	hsa-miR-3662	-0.05	-0.27	N/A
PHYHIP1L	ENST00000373880.4	phytanoyl-CoA 2-hydroxylase interacting protein-like	26	4	1	1	2	3	hsa-miR-3662	-0.22	-0.27	N/A
GNG4	ENST00000450593.1	guanine nucleotide binding protein (G protein), gamma 4	1171	4	0	4	0	1	hsa-miR-3662	-0.23	-0.27	N/A
CPXCR1	ENST00000276127.4	CPX chromosome region, candidate 1	5	1	1	0	0	0	hsa-miR-3662	-0.27	-0.27	N/A
CLP1	ENST00000533682.1	cleavage and polyadenylation factor I subunit 1	208	1	1	0	0	0	hsa-miR-3662	-0.27	-0.27	N/A
GRXCR1	ENST00000399770.2	glutaredoxin, cysteine rich 1	5	1	1	0	0	0	hsa-miR-3662	-0.26	-0.26	N/A
C9orf53	ENST00000441769.2	chromosome 9 open reading frame 53	5	1	1	0	0	0	hsa-miR-3662	-0.26	-0.26	N/A
AMER2	ENST00000357816.2	APC membrane recruitment protein 2	7	4	0	0	4	7	hsa-miR-3662	-0.2	-0.26	N/A
SRSF1	ENST00000258962.4	serine/arginine-rich splicing factor 1	1430	11	1	6	4	9	hsa-miR-3662	-0.14	-0.26	N/A
NOL7	ENST00000451315.2	nucleolar protein 7, 27kDa	1168	2	1	0	1	0	hsa-miR-3662	-0.03	-0.26	N/A
MAP2K6	ENST00000590474.1	mitogen-activated protein kinase kinase 6	235	11	2	4	5	10	hsa-miR-3662	-0.03	-0.26	N/A
GPR34	ENST00000378142.4	G protein-coupled receptor 34	5	1	1	0	0	1	hsa-miR-3662	-0.26	-0.26	N/A
KRTAP9-3	ENST00000411528.2	keratin associated protein 9-3	5	1	1	0	0	0	hsa-miR-3662	-0.25	-0.25	N/A
ZBTB37	ENST00000367701.5	zinc finger and BTB domain containing 37	213	7	2	4	1	8	hsa-miR-3662	-0.23	-0.25	N/A
TIMM21	ENST00000169551.6	translocase of inner mitochondrial membrane 21 homolog (yeast)	306	1	1	0	0	1	hsa-miR-3662	-0.08	-0.25	N/A
SOD2	ENST00000538183.2	superoxide dismutase 2, mitochondrial	993	5	0	4	1	9	hsa-miR-3662	-0.02	-0.25	N/A
SNAPIN	ENST00000368685.5	SNAP-associated protein	1843	2	1	1	0	0	hsa-miR-3662	-0.23	-0.25	N/A
SLC41A2	ENST00000258538.3	solute carrier family 41 (magnesium transporter), member 2	224	3	0	2	1	4	hsa-miR-3662	-0.1	-0.25	N/A
MCTS1	ENST00000371317.5	malignant T cell amplified sequence 1	6611	8	1	2	5	5	hsa-miR-3662	0	-0.25	N/A
LRRC40	ENST00000370952.3	leucine rich repeat containing 40	88	11	4	3	4	7	hsa-miR-3662	-0.04	-0.25	N/A
KLF12	ENST00000377669.2	Kruppel-like factor 12	251	12	2	7	3	6	hsa-miR-3662	-0.23	-0.25	N/A

FBXO43	ENST00000428847.2	F-box protein 43	133	4	1	1	2	0	hsa-miR-3662	-0.16	-0.25	N/A
EXOC5	ENST00000413566.2	exocyst complex component 5	242	8	2	3	3	7	hsa-miR-3662	-0.2	-0.25	N/A
ENSA	ENST00000369014.5	endosulfine alpha	167	3	2	0	1	0	hsa-miR-3662	-0.21	-0.25	N/A
C17orf67	ENST00000397861.2	chromosome 17 open reading frame 67	5	2	1	0	1	0	hsa-miR-3662	-0.25	-0.25	N/A
ARMC1	ENST00000276569.3	armadillo repeat containing 1	93	3	0	1	2	2	hsa-miR-3662	-0.2	-0.25	N/A
CLEC6A	ENST00000382073.3	C-type lectin domain family 6, member A	5	3	1	1	1	0	hsa-miR-3662	-0.24	-0.24	N/A
GPHA2	ENST00000279168.2	glycoprotein hormone alpha 2	8	1	1	0	0	0	hsa-miR-3662	-0.24	-0.24	N/A
RIF1	ENST00000243326.5	RAP1 interacting factor homolog (yeast)	213	6	0	3	3	6	hsa-miR-3662	-0.1	-0.24	N/A
NUP62CL	ENST00000372461.3	nucleoporin 62kDa C-terminal like	73	2	1	0	1	4	hsa-miR-3662	-0.06	-0.24	N/A
MMGT1	ENST00000305963.2	membrane magnesium transporter 1	113	4	0	1	3	1	hsa-miR-3662	-0.07	-0.24	N/A
LIN7C	ENST00000278193.2	lin-7 homolog C (C. elegans)	1701	4	1	3	0	4	hsa-miR-3662	-0.21	-0.24	N/A
EIF4E	ENST00000450253.2	eukaryotic translation initiation factor 4E	876	9	2	3	4	3	hsa-miR-3662	-0.07	-0.24	N/A
DPYS	ENST00000351513.2	dihydropyrimidinase	7	2	1	1	0	0	hsa-miR-3662	-0.24	-0.24	N/A
DGKH	ENST00000261491.5	diacylglycerol kinase, eta	46	11	4	5	2	10	hsa-miR-3662	-0.15	-0.24	N/A
TMEM9B	ENST00000309134.5	TMEM9 domain family, member B	195	1	1	0	0	2	hsa-miR-3662	-0.19	-0.23	N/A
PTAR1	ENST00000377200.5	protein prenyltransferase alpha subunit repeat containing 1	161	10	5	3	2	6	hsa-miR-3662	-0.15	-0.23	N/A
MELK	ENST00000536987.1	maternal embryonic leucine zipper kinase	5978	5	1	1	3	6	hsa-miR-3662	0	-0.23	N/A
LOX	ENST00000231004.4	lysyl oxidase	3441	8	3	3	2	0	hsa-miR-3662	-0.07	-0.23	N/A
IMPG1	ENST00000369963.3	interphotoreceptor matrix proteoglycan 1	5	6	2	3	1	4	hsa-miR-3662	-0.23	-0.23	N/A
FAM208B	ENST00000328090.5	family with sequence similarity 208, member B	42	5	2	3	0	1	hsa-miR-3662	-0.18	-0.23	N/A
FAM104B	ENST00000472571.2	family with sequence similarity 104, member B	599	2	0	1	1	0	hsa-miR-3662	-0.11	-0.23	N/A
CTHRC1	ENST00000330295.5	collagen triple helix repeat containing 1	1504	2	0	1	1	1	hsa-miR-3662	-0.22	-0.23	N/A
CGGBP1	ENST00000309534.6	CGG triplet repeat binding protein 1	990	5	1	2	2	2	hsa-miR-3662	-0.11	-0.23	N/A
C17orf80	ENST00000359042.2	chromosome 17 open reading frame 80	740	2	1	0	1	1	hsa-miR-3662	-0.22	-0.23	N/A
BRWD1	ENST00000342449.3	bromodomain and WD repeat domain containing 1	96	10	1	6	3	7	hsa-miR-3662	-0.05	-0.23	N/A
ARHGEF6	ENST00000370620.1	Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6	15	2	1	1	0	2	hsa-miR-3662	-0.17	-0.23	N/A
ALG11	ENST00000523764.1	ALG11, alpha-1,2-mannosyltransferase	121	1	1	0	0	0	hsa-miR-3662	-0.01	-0.23	N/A
PRAMEF2	ENST00000240189.2	PRAME family member 2	5	1	0	1	0	0	hsa-miR-3662	-0.22	-0.22	N/A
TMPRSS11B	ENST00000332644.5	transmembrane protease, serine 11B	5	3	3	0	0	1	hsa-miR-3662	-0.22	-0.22	N/A
JHDM1D	ENST00000397560.2	jumonji C domain containing histone demethylase 1 homolog D (S. cere	470	10	3	6	1	4	hsa-miR-3662	-0.19	-0.22	N/A
FMO3	ENST00000367755.4	flavin containing monooxygenase 3	5	1	0	0	1	2	hsa-miR-3662	-0.08	-0.22	N/A
ZNF736	ENST00000423484.2	zinc finger protein 736	36	4	1	1	2	3	hsa-miR-3662	-0.12	-0.22	N/A
TP53INP1	ENST00000448464.2	tumor protein p53 inducible nuclear protein 1	39	8	1	4	3	4	hsa-miR-3662	-0.14	-0.22	N/A
TAF7L	ENST00000372907.3	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associat	51	1	1	0	0	0	hsa-miR-3662	-0.22	-0.22	N/A
SGCE	ENST00000265735.7	sarcoglycan, epsilon	57	1	1	0	0	1	hsa-miR-3662	-0.22	-0.22	N/A
PERP	ENST00000421351.3	PERP, TP53 apoptosis effector	437	4	3	0	1	3	hsa-miR-3662	-0.14	-0.22	N/A
MLLT11	ENST00000368921.3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosopl	308	2	1	0	1	0	hsa-miR-3662	-0.16	-0.22	N/A
METRNL	ENST00000320095.7	meteorin, glial cell differentiation regulator-like	353	1	1	0	0	0	hsa-miR-3662	-0.1	-0.22	N/A
HRH4	ENST00000256906.4	histamine receptor H4	5	2	0	1	1	2	hsa-miR-3662	-0.22	-0.22	N/A

FGF5	ENST00000456523.3	fibroblast growth factor 5	1478	6	2	1	3	6	hsa-miR-3662	-0.1	-0.22	N/A
CDK13	ENST00000181839.4	cyclin-dependent kinase 13	32	5	1	2	2	3	hsa-miR-3662	-0.11	-0.22	N/A
CADM2	ENST00000383699.3	cell adhesion molecule 2	5	7	0	3	4	12	hsa-miR-3662	-0.22	-0.22	N/A
C21orf91	ENST00000400558.3	chromosome 21 open reading frame 91	998	7	3	1	3	4	hsa-miR-3662	-0.19	-0.22	N/A
BMPR2	ENST00000374574.2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	287	10	0	3	7	6	hsa-miR-3662	-0.06	-0.22	N/A
AC144568.2	ENST00000522481.3	Uncharacterized protein	5	1	1	0	0	0	hsa-miR-3662	-0.21	-0.21	N/A
AF165138.7	ENST00000400562.1	Protein LOC388813	5	1	1	0	0	0	hsa-miR-3662	-0.21	-0.21	N/A
SLC9C2	ENST00000367714.3	solute carrier family 9, member C2 (putative)	5	1	1	0	0	0	hsa-miR-3662	-0.21	-0.21	N/A
TRIM43	ENST00000272395.2	tripartite motif containing 43	5	1	1	0	0	1	hsa-miR-3662	-0.21	-0.21	N/A
RP11-664D7	ENST00000512294.3	HCG1787533; Uncharacterized protein	14	6	0	2	4	1	hsa-miR-3662	-0.15	-0.21	N/A
AC117395.1	ENST00000593416.1	LOC646903 protein; Uncharacterized protein	22	3	2	1	0	0	hsa-miR-3662	-0.14	-0.21	N/A
RASSF9	ENST00000361228.3	Ras association (RalGDS/AF-6) domain family (N-terminal) member 9	9	6	2	2	2	6	hsa-miR-3662	-0.12	-0.21	N/A
TRAT1	ENST00000295756.6	T cell receptor associated transmembrane adaptor 1	5	5	0	4	1	4	hsa-miR-3662	0	-0.21	N/A
ZRANB2	ENST00000254821.6	zinc finger, RAN-binding domain containing 2	4196	3	0	1	2	1	hsa-miR-3662	-0.11	-0.21	N/A
ZNF626	ENST00000291750.6	zinc finger protein 626	24	6	0	4	2	4	hsa-miR-3662	-0.1	-0.21	N/A
ZNF45	ENST00000269973.5	zinc finger protein 45	359	6	0	4	2	4	hsa-miR-3662	-0.09	-0.21	N/A
UBE2E2	ENST00000396703.1	ubiquitin-conjugating enzyme E2E 2	794	4	3	1	0	1	hsa-miR-3662	-0.07	-0.21	N/A
SLC8A1	ENST00000406785.2	solute carrier family 8 (sodium/calcium exchanger), member 1	61	11	3	4	4	17	hsa-miR-3662	-0.08	-0.21	N/A
SHFM1	ENST00000248566.2	split hand/foot malformation (ectrodactyly) type 1	96	1	1	0	0	0	hsa-miR-3662	-0.01	-0.21	N/A
RPS6KA6	ENST00000262752.2	ribosomal protein S6 kinase, 90kDa, polypeptide 6	156	7	2	2	3	10	hsa-miR-3662	-0.1	-0.21	N/A
RNF152	ENST00000312828.3	ring finger protein 152	57	9	3	3	3	7	hsa-miR-3662	-0.13	-0.21	N/A
NAA38	ENST00000249299.2	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	458	6	1	0	5	8	hsa-miR-3662	-0.08	-0.21	N/A
ILF2	ENST00000361891.4	interleukin enhancer binding factor 2	5746	1	1	0	0	0	hsa-miR-3662	-0.01	-0.21	N/A
FAM227B	ENST00000558594.1	family with sequence similarity 227, member B	44	3	1	2	0	3	hsa-miR-3662	-0.21	-0.21	N/A
ERBB4	ENST00000342788.4	v-erb-b2 avian erythroblastic leukemia viral oncogene homolog 4	27	6	0	5	1	7	hsa-miR-3662	-0.2	-0.21	N/A
ARL5A	ENST00000295087.8	ADP-ribosylation factor-like 5A	112	6	2	2	2	9	hsa-miR-3662	-0.05	-0.21	N/A
ALG10B	ENST00000308742.4	ALG10B, alpha-1,2-glucosyltransferase	471	9	0	5	4	6	hsa-miR-3662	-0.2	-0.21	N/A
POU1F1	ENST00000350375.2	POU class 1 homeobox 1	5	1	1	0	0	0	hsa-miR-3662	-0.2	-0.2	N/A
TSHB	ENST00000256592.1	thyroid stimulating hormone, beta	5	1	0	1	0	0	hsa-miR-3662	-0.2	-0.2	N/A
C6orf211	ENST00000367294.3	chromosome 6 open reading frame 211	65	1	0	0	1	3	hsa-miR-3662	-0.15	-0.2	N/A
PGR	ENST00000325455.5	progesterone receptor	8	8	5	1	2	10	hsa-miR-3662	-0.14	-0.2	N/A
EFHC2	ENST00000420999.1	EF-hand domain (C-terminal) containing 2	5	1	0	1	0	3	hsa-miR-3662	-0.09	-0.2	N/A
WASF1	ENST00000392587.2	WAS protein family, member 1	55	1	1	0	0	0	hsa-miR-3662	-0.2	-0.2	N/A
TMPPE	ENST00000416695.2	transmembrane protein with metallophosphoesterase domain	22	9	2	5	2	6	hsa-miR-3662	-0.07	-0.2	N/A
SLC5A3	ENST00000608209.1	sodium/myo-inositol cotransporter	24	9	3	5	1	3	hsa-miR-3662	-0.12	-0.2	N/A
SLC16A7	ENST00000261187.4	solute carrier family 16 (monocarboxylate transporter), member 7	73	9	2	5	2	11	hsa-miR-3662	-0.06	-0.2	N/A
PRRG1	ENST00000378628.4	proline rich Gla (G-carboxyglutamic acid) 1	1122	6	1	4	1	2	hsa-miR-3662	-0.2	-0.2	N/A
PDSS1	ENST00000376203.5	prenyl (decaprenyl) diphosphate synthase, subunit 1	41	1	1	0	0	0	hsa-miR-3662	-0.2	-0.2	N/A
PAQR3	ENST00000512733.1	progesterin and adipoQ receptor family member III	217	10	1	4	5	6	hsa-miR-3662	-0.12	-0.2	N/A

LEPROT	ENST00000371065.4	leptin receptor overlapping transcript	397	4	0	1	3	7	hsa-miR-3662	-0.06	-0.2	N/A
KLRC1	ENST00000359151.3	killer cell lectin-like receptor subfamily C, member 1	5	2	1	1	0	0	hsa-miR-3662	-0.2	-0.2	N/A
INO80D	ENST00000403263.1	INO80 complex subunit D	5	13	1	4	8	6	hsa-miR-3662	-0.2	-0.2	N/A
IL6	ENST00000404625.1	interleukin 6 (interferon, beta 2)	472	2	0	0	2	0	hsa-miR-3662	-0.11	-0.2	N/A
IKZF5	ENST00000368886.5	IKAROS family zinc finger 5 (Pegasus)	83	5	2	1	2	3	hsa-miR-3662	-0.09	-0.2	N/A
HIST1H3B	ENST00000244661.2	histone cluster 1, H3b	7	3	1	0	2	2	hsa-miR-3662	-0.04	-0.2	N/A
GUCY1A3	ENST00000296518.7	guanylate cyclase 1, soluble, alpha 3	42	9	3	5	1	7	hsa-miR-3662	-0.05	-0.2	N/A
GIF	ENST00000257248.2	gastric intrinsic factor (vitamin B synthesis)	5	1	1	0	0	0	hsa-miR-3662	-0.2	-0.2	N/A
FGG	ENST00000404648.3	fibrinogen gamma chain	488	3	2	1	0	0	hsa-miR-3662	-0.15	-0.2	N/A
CSTF2	ENST00000415585.2	cleavage stimulation factor, 3' pre-RNA, subunit 2, 64kDa	385	2	2	0	0	1	hsa-miR-3662	-0.17	-0.2	N/A
CENPK	ENST00000514814.1	centromere protein K	212	2	0	1	1	1	hsa-miR-3662	-0.19	-0.2	N/A
CCL16	ENST00000293275.3	chemokine (C-C motif) ligand 16	5	2	1	1	0	0	hsa-miR-3662	-0.2	-0.2	N/A
C6orf62	ENST00000378119.4	chromosome 6 open reading frame 62	300	6	0	6	0	6	hsa-miR-3662	-0.12	-0.2	N/A
BAALC	ENST00000438105.2	brain and acute leukemia, cytoplasmic	137	4	1	3	0	1	hsa-miR-3662	-0.14	-0.2	N/A
ATP6V1D	ENST00000554236.1	ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D	1271	1	1	0	0	2	hsa-miR-3662	-0.2	-0.2	N/A
ANXA1	ENST00000257497.6	annexin A1	365	2	0	1	1	1	hsa-miR-3662	-0.16	-0.2	N/A
AL441883.1	ENST00000600057.1	Uncharacterized protein	5	1	0	1	0	0	hsa-miR-3662	-0.19	-0.19	N/A
C10orf40	ENST00000521074.1	chromosome 10 open reading frame 40	5	4	0	0	4	1	hsa-miR-3662	-0.19	-0.19	N/A
TMEM14E	ENST00000408960.3	transmembrane protein 14E	5	2	0	2	0	2	hsa-miR-3662	-0.19	-0.19	N/A
SLC6A5	ENST00000525748.1	solute carrier family 6 (neurotransmitter transporter), member 5	5	5	2	2	1	4	hsa-miR-3662	-0.19	-0.19	N/A
ZNF431	ENST00000311048.7	zinc finger protein 431	93	10	2	5	3	10	hsa-miR-3662	-0.11	-0.19	N/A
ZMAT3	ENST00000311417.2	zinc finger, matrin-type 3	459	10	1	7	2	9	hsa-miR-3662	-0.15	-0.19	N/A
TGFBR2	ENST00000359013.4	transforming growth factor, beta receptor II (70/80kDa)	2168	8	1	5	2	3	hsa-miR-3662	-0.03	-0.19	N/A
STPG2	ENST00000295268.3	sperm-tail PG-rich repeat containing 2	5	1	1	0	0	0	hsa-miR-3662	-0.19	-0.19	N/A
SSR1	ENST00000244763.4	signal sequence receptor, alpha	12917	6	1	4	1	8	hsa-miR-3662	-0.04	-0.19	N/A
SIKE1	ENST00000369528.5	suppressor of IKBKE 1	281	7	1	3	3	5	hsa-miR-3662	-0.01	-0.19	N/A
RAP2B	ENST00000323534.2	RAP2B, member of RAS oncogene family	594	8	3	5	0	7	hsa-miR-3662	-0.07	-0.19	N/A
PEX13	ENST00000295030.5	peroxisomal biogenesis factor 13	484	3	0	1	2	2	hsa-miR-3662	-0.06	-0.19	N/A
ONECUT2	ENST00000491143.2	one cut homeobox 2	847	5	0	2	3	11	hsa-miR-3662	-0.15	-0.19	N/A
NCOA7	ENST00000392477.2	nuclear receptor coactivator 7	2967	1	0	1	0	4	hsa-miR-3662	-0.19	-0.19	N/A
MED28	ENST00000237380.7	mediator complex subunit 28	1483	5	2	3	0	9	hsa-miR-3662	-0.11	-0.19	N/A
LNPEP	ENST00000231368.5	leucyl/cystinyl aminopeptidase	28	10	2	5	3	7	hsa-miR-3662	-0.05	-0.19	N/A
KRTAP4-8	ENST00000333822.4	keratin associated protein 4-8	5	3	1	2	0	0	hsa-miR-3662	-0.19	-0.19	N/A
IMPACT	ENST00000284202.4	impact RWD domain protein	250	1	1	0	0	2	hsa-miR-3662	-0.15	-0.19	N/A
GPR63	ENST00000229955.3	G protein-coupled receptor 63	5	6	1	2	3	6	hsa-miR-3662	-0.19	-0.19	N/A
FRG2B	ENST00000443774.1	FSHD region gene 2 family, member B	5	2	2	0	0	0	hsa-miR-3662	-0.19	-0.19	N/A
FRG2	ENST00000504750.1	FSHD region gene 2	5	2	2	0	0	0	hsa-miR-3662	-0.19	-0.19	N/A
FKBP1A	ENST00000400137.4	FK506 binding protein 1A, 12kDa	72	2	1	1	0	0	hsa-miR-3662	-0.19	-0.19	N/A
EFCAB7	ENST00000371088.4	EF-hand calcium binding domain 7	113	1	1	0	0	1	hsa-miR-3662	-0.19	-0.19	N/A

DPP4	ENST00000360534.3	dipeptidyl-peptidase 4	49	3	1	2	0	0	hsa-miR-3662	-0.19	-0.19	N/A
DNAJC2	ENST00000249270.7	DnaJ (Hsp40) homolog, subfamily C, member 2	221	1	0	1	0	2	hsa-miR-3662	-0.06	-0.19	N/A
CREBZF	ENST00000398294.2	CREB/ATF bZIP transcription factor	1115	10	2	5	3	4	hsa-miR-3662	-0.12	-0.19	N/A
CHMP1B	ENST00000526991.2	charged multivesicular body protein 1B	3248	1	1	0	0	1	hsa-miR-3662	-0.05	-0.19	N/A
C2ORF15	ENST00000302513.2	Uncharacterized protein C2orf15	166	5	2	0	3	7	hsa-miR-3662	-0.15	-0.19	N/A
BMP3	ENST00000282701.2	bone morphogenetic protein 3	36	5	2	2	1	6	hsa-miR-3662	-0.09	-0.19	N/A
ABCD2	ENST00000308666.3	ATP-binding cassette, sub-family D (ALD), member 2	5	3	1	1	1	5	hsa-miR-3662	-0.1	-0.19	N/A
AAED1	ENST00000375234.3	AhpC/TSA antioxidant enzyme domain containing 1	5	3	0	1	2	1	hsa-miR-3662	-0.19	-0.19	N/A
KRBOX1	ENST00000426937.1	KRAB box domain containing 1	28	1	0	1	0	1	hsa-miR-3662	-0.18	-0.18	N/A
GABRA4	ENST00000264318.3	gamma-aminobutyric acid (GABA) A receptor, alpha 4	5	10	1	6	3	2	hsa-miR-3662	-0.18	-0.18	N/A
FRG2C	ENST00000308062.3	FSHD region gene 2 family, member C	7	2	2	0	0	1	hsa-miR-3662	-0.18	-0.18	N/A
GPR174	ENST00000276077.1	G protein-coupled receptor 174	5	5	1	3	1	1	hsa-miR-3662	0	-0.18	N/A
ZNF148	ENST00000360647.4	zinc finger protein 148	230	11	1	4	6	2	hsa-miR-3662	-0.12	-0.18	N/A
ZNF117	ENST00000282869.6	zinc finger protein 117	21	9	2	5	2	7	hsa-miR-3662	-0.11	-0.18	N/A
UBA3	ENST00000415609.2	ubiquitin-like modifier activating enzyme 3	96	2	0	1	1	1	hsa-miR-3662	-0.12	-0.18	N/A
TMOD3	ENST00000308580.7	tropomodulin 3 (ubiquitous)	1533	3	1	0	2	3	hsa-miR-3662	-0.13	-0.18	N/A
SYNCRIP	ENST00000355238.6	synaptotagmin binding, cytoplasmic RNA interacting protein	4864	3	1	2	0	3	hsa-miR-3662	-0.06	-0.18	N/A
SPHAR	ENST00000366688.3	S-phase response (cyclin related)	202	2	1	1	0	2	hsa-miR-3662	0	-0.18	N/A
SLC30A7	ENST00000370112.4	solute carrier family 30 (zinc transporter), member 7	204	11	3	1	7	7	hsa-miR-3662	-0.07	-0.18	N/A
SDHC	ENST00000367975.2	succinate dehydrogenase complex, subunit C, integral membrane protei	172	2	1	0	1	0	hsa-miR-3662	-0.17	-0.18	N/A
RNF170	ENST00000534961.1	ring finger protein 170	203	5	1	1	3	0	hsa-miR-3662	-0.01	-0.18	N/A
RCHY1	ENST00000451788.1	ring finger and CHY zinc finger domain containing 1, E3 ubiquitin protei	821	3	0	2	1	2	hsa-miR-3662	-0.05	-0.18	N/A
PRKACB	ENST00000370689.2	protein kinase, cAMP-dependent, catalytic, beta	344	6	3	0	3	1	hsa-miR-3662	-0.05	-0.18	N/A
PLCL1	ENST00000428675.1	phospholipase C-like 1	31	6	0	4	2	7	hsa-miR-3662	-0.09	-0.18	N/A
OGFRL1	ENST00000370435.4	opioid growth factor receptor-like 1	607	8	3	4	1	7	hsa-miR-3662	-0.02	-0.18	N/A
NSL1	ENST00000422588.2	NSL1, MIS12 kinetochore complex component	180	4	0	3	1	8	hsa-miR-3662	-0.05	-0.18	N/A
NFIL3	ENST00000297689.3	nuclear factor, interleukin 3 regulated	7439	2	0	0	2	1	hsa-miR-3662	0	-0.18	N/A
NFAT5	ENST00000354436.2	nuclear factor of activated T-cells 5, tonicity-responsive	128	8	2	5	1	8	hsa-miR-3662	-0.08	-0.18	N/A
NDUFAF4	ENST00000316149.7	NADH dehydrogenase (ubiquinone) complex I, assembly factor 4	2444	3	0	1	2	1	hsa-miR-3662	-0.16	-0.18	N/A
LCOR	ENST00000371103.3	ligand dependent nuclear receptor corepressor	94	7	2	2	3	6	hsa-miR-3662	-0.18	-0.18	N/A
HLA-DRA	ENST00000395388.2	major histocompatibility complex, class II, DR alpha	58	1	1	0	0	1	hsa-miR-3662	-0.18	-0.18	N/A
HIF1A	ENST00000323441.6	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcript	1955	8	1	3	4	0	hsa-miR-3662	-0.06	-0.18	N/A
GRIN2B	ENST00000609686.1	glutamate receptor, ionotropic, N-methyl D-aspartate 2B	5	12	1	4	7	7	hsa-miR-3662	-0.18	-0.18	N/A
GNG10	ENST00000374293.4	guanine nucleotide binding protein (G protein), gamma 10	407	2	0	1	1	0	hsa-miR-3662	-0.18	-0.18	N/A
GLIPR2	ENST00000396613.3	GLI pathogenesis-related 2	218	2	1	0	1	0	hsa-miR-3662	-0.09	-0.18	N/A
EXOC8	ENST00000360394.2	exocyst complex component 8	129	9	2	5	2	5	hsa-miR-3662	-0.05	-0.18	N/A
ERICH2	ENST00000409885.1	glutamate-rich 2	13	1	0	0	1	0	hsa-miR-3662	-0.11	-0.18	N/A
C4orf36	ENST00000473559.1	chromosome 4 open reading frame 36	5	3	1	2	0	2	hsa-miR-3662	-0.18	-0.18	N/A
C12orf50	ENST00000298699.2	chromosome 12 open reading frame 50	5	1	0	0	1	0	hsa-miR-3662	-0.18	-0.18	N/A

BRWD3	ENST00000373275.4	bromodomain and WD repeat domain containing 3	506	9	3	1	5	10	hsa-miR-3662	-0.12	-0.18	N/A
RP11-1102P1	ENST00000523987.1	Uncharacterized protein	5	2	0	1	1	3	hsa-miR-3662	-0.17	-0.17	N/A
PRAMEF14	ENST00000344998.3	PRAME family member 14	5	2	0	2	0	0	hsa-miR-3662	-0.17	-0.17	N/A
AC107021.1	ENST00000422482.1	HCG1786590; PRO2533; Uncharacterized protein	5	1	1	0	0	0	hsa-miR-3662	-0.17	-0.17	N/A
MANSC4	ENST00000381273.3	MANSC domain containing 4	0	1	0	1	0	0	hsa-miR-3662	-0.17	-0.17	N/A
ZKSCAN8	ENST00000330236.6	zinc finger with KRAB and SCAN domains 8	281	8	2	5	1	7	hsa-miR-3662	-0.17	-0.17	N/A
XRCC5	ENST00000392133.3	X-ray repair complementing defective repair in Chinese hamster cells 5	14802	11	2	2	7	4	hsa-miR-3662	0	-0.17	N/A
TOMM6	ENST00000398884.3	translocase of outer mitochondrial membrane 6 homolog (yeast)	2735	3	2	0	1	1	hsa-miR-3662	0	-0.17	N/A
TNRC6B	ENST00000335727.9	trinucleotide repeat containing 6B	69	10	1	5	4	9	hsa-miR-3662	-0.13	-0.17	N/A
TMEM100	ENST00000424486.2	transmembrane protein 100	86	1	1	0	0	1	hsa-miR-3662	-0.17	-0.17	N/A
TMC1	ENST00000297784.5	transmembrane channel-like 1	5	1	1	0	0	0	hsa-miR-3662	-0.17	-0.17	N/A
THEMIS2	ENST00000373925.1	thymocyte selection associated family member 2	41	2	1	0	1	0	hsa-miR-3662	-0.17	-0.17	N/A
TFEC	ENST00000265440.7	transcription factor EC	5	5	2	3	0	2	hsa-miR-3662	-0.17	-0.17	N/A
SRSF10	ENST00000343255.5	serine/arginine-rich splicing factor 10	1920	9	2	4	3	3	hsa-miR-3662	-0.13	-0.17	N/A
SPCS3	ENST00000503362.1	signal peptidase complex subunit 3 homolog (S. cerevisiae)	1645	4	1	1	2	2	hsa-miR-3662	-0.08	-0.17	N/A
SOX30	ENST00000265007.6	SRY (sex determining region Y)-box 30	5	3	1	1	1	3	hsa-miR-3662	-0.14	-0.17	N/A
SOGA3	ENST00000556132.1	SOGA family member 3	95	7	2	4	1	4	hsa-miR-3662	-0.03	-0.17	N/A
PUS10	ENST00000398658.2	pseudouridylate synthase 10	72	1	1	0	0	1	hsa-miR-3662	-0.17	-0.17	N/A
PCDH17	ENST00000377918.3	protocadherin 17	477	9	2	2	5	7	hsa-miR-3662	-0.03	-0.17	N/A
MBNL3	ENST00000370839.3	muscleblind-like splicing regulator 3	593	11	2	2	7	4	hsa-miR-3662	-0.12	-0.17	N/A
LRIG2	ENST00000361127.5	leucine-rich repeats and immunoglobulin-like domains 2	348	7	3	4	0	2	hsa-miR-3662	-0.16	-0.17	N/A
LPP	ENST00000312675.4	LIM domain containing preferred translocation partner in lipoma	1894	5	0	2	3	12	hsa-miR-3662	-0.17	-0.17	N/A
LIN7A	ENST00000552864.1	lin-7 homolog A (C. elegans)	86	6	0	4	2	4	hsa-miR-3662	-0.07	-0.17	N/A
INTS6	ENST00000311234.4	integrator complex subunit 6	433	6	1	5	0	6	hsa-miR-3662	-0.11	-0.17	N/A
IMPAD1	ENST00000262644.4	inositol monophosphatase domain containing 1	1488	8	1	7	0	3	hsa-miR-3662	-0.07	-0.17	N/A
IL36G	ENST00000259205.4	interleukin 36, gamma	5	3	1	2	0	1	hsa-miR-3662	-0.17	-0.17	N/A
IL1A	ENST00000263339.3	interleukin 1, alpha	5	3	1	2	0	1	hsa-miR-3662	-0.17	-0.17	N/A
HSPH1	ENST00000320027.5	heat shock 105kDa/110kDa protein 1	4109	4	1	2	1	2	hsa-miR-3662	0	-0.17	N/A
HEXIM1	ENST00000332499.2	hexamethylene bis-acetamide inducible 1	179	2	1	1	0	3	hsa-miR-3662	-0.13	-0.17	N/A
HBP1	ENST00000222574.4	HMG-box transcription factor 1	167	1	0	0	1	0	hsa-miR-3662	-0.17	-0.17	N/A
GUCY1B3	ENST00000264424.8	guanylate cyclase 1, soluble, beta 3	729	2	0	2	0	0	hsa-miR-3662	-0.02	-0.17	N/A
GTPBP10	ENST00000222511.6	GTP-binding protein 10 (putative)	489	10	0	7	3	2	hsa-miR-3662	-0.01	-0.17	N/A
GPR180	ENST00000376958.4	G protein-coupled receptor 180	161	5	0	3	2	5	hsa-miR-3662	-0.07	-0.17	N/A
FGFR1OP	ENST00000366847.4	FGFR1 oncogene partner	552	9	2	3	4	3	hsa-miR-3662	-0.06	-0.17	N/A
FAM229A	ENST00000432622.1	family with sequence similarity 229, member A	59	2	0	0	2	0	hsa-miR-3662	-0.17	-0.17	N/A
DNAJB4	ENST00000370763.5	DnaJ (Hsp40) homolog, subfamily B, member 4	633	7	1	1	5	6	hsa-miR-3662	-0.02	-0.17	N/A
DGKI	ENST00000453654.2	diacylglycerol kinase, iota	16	10	1	5	4	7	hsa-miR-3662	-0.05	-0.17	N/A
COL4A4	ENST00000396625.3	collagen, type IV, alpha 4	133	7	1	4	2	4	hsa-miR-3662	-0.15	-0.17	N/A
COL19A1	ENST00000322773.4	collagen, type XIX, alpha 1	5	9	2	4	3	6	hsa-miR-3662	-0.13	-0.17	N/A

CELF2	ENST00000379261.4	CUGBP, Elav-like family member 2	45	8	2	5	1	4	hsa-miR-3662	-0.17	-0.17	N/A
CCT7	ENST00000540468.1	chaperonin containing TCP1, subunit 7 (eta)	13211	1	1	0	0	0	hsa-miR-3662	-0.17	-0.17	N/A
CALCRL	ENST00000392370.3	calcitonin receptor-like	18	8	3	3	2	1	hsa-miR-3662	-0.07	-0.17	N/A
C1QBP	ENST00000225698.4	complement component 1, q subcomponent binding protein	2957	1	0	1	0	0	hsa-miR-3662	-0.16	-0.17	N/A
C18orf32	ENST00000579820.1	chromosome 18 open reading frame 32	733	5	0	3	2	0	hsa-miR-3662	0	-0.17	N/A
AQR	ENST00000156471.5	aquarius intron-binding spliceosomal factor	314	4	1	1	2	6	hsa-miR-3662	-0.04	-0.17	N/A
ALDH3A2	ENST00000339618.4	aldehyde dehydrogenase 3 family, member A2	940	2	2	0	0	0	hsa-miR-3662	-0.02	-0.17	N/A
ADHFE1	ENST00000396623.3	alcohol dehydrogenase, iron containing, 1	33	4	1	2	1	0	hsa-miR-3662	-0.01	-0.17	N/A
AC006455.1	ENST00000456890.1		5	1	1	0	0	1	hsa-miR-3662	-0.16	-0.16	N/A
PRAMEF13	ENST00000376132.3	PRAME family member 13	5	2	0	2	0	0	hsa-miR-3662	-0.16	-0.16	N/A
KRTAP20-2	ENST00000330798.2	keratin associated protein 20-2	45	1	0	1	0	0	hsa-miR-3662	-0.16	-0.16	N/A
GAGE1	ENST00000381700.6	G antigen 1	5	3	0	2	1	1	hsa-miR-3662	-0.13	-0.16	N/A
C4orf40	ENST00000344526.5	chromosome 4 open reading frame 40	5	3	0	1	2	3	hsa-miR-3662	0	-0.16	N/A
ZADH2	ENST00000322342.3	zinc binding alcohol dehydrogenase domain containing 2	207	8	3	2	3	1	hsa-miR-3662	-0.05	-0.16	N/A
XRCC4	ENST00000511817.1	X-ray repair complementing defective repair in Chinese hamster cells 4	573	2	1	0	1	0	hsa-miR-3662	-0.16	-0.16	N/A
WDFY2	ENST00000298125.5	WD repeat and FYVE domain containing 2	85	9	2	3	4	3	hsa-miR-3662	-0.03	-0.16	N/A
TTLL7	ENST00000260505.8	tubulin tyrosine ligase-like family, member 7	93	8	2	4	2	3	hsa-miR-3662	-0.14	-0.16	N/A
TMEM69	ENST00000372025.4	transmembrane protein 69	20	1	1	0	0	1	hsa-miR-3662	-0.16	-0.16	N/A
TMEM241	ENST00000383233.3	transmembrane protein 241	115	8	1	6	1	0	hsa-miR-3662	-0.11	-0.16	N/A
TMEM135	ENST00000340353.7	transmembrane protein 135	963	7	0	5	2	6	hsa-miR-3662	-0.03	-0.16	N/A
TLR4	ENST00000355622.6	toll-like receptor 4	47	8	2	4	2	7	hsa-miR-3662	-0.03	-0.16	N/A
TAOK1	ENST00000261716.3	TAO kinase 1	164	10	2	2	6	8	hsa-miR-3662	-0.14	-0.16	N/A
SLC30A4	ENST00000261867.4	solute carrier family 30 (zinc transporter), member 4	19	8	2	4	2	1	hsa-miR-3662	-0.11	-0.16	N/A
SLC1A2	ENST00000278379.3	solute carrier family 1 (glial high affinity glutamate transporter), member	5	8	1	6	1	7	hsa-miR-3662	-0.16	-0.16	N/A
SH2D1B	ENST00000367929.2	SH2 domain containing 1B	5	2	0	0	2	1	hsa-miR-3662	-0.16	-0.16	N/A
SGIP1	ENST00000371036.3	SH3-domain GRB2-like (endophilin) interacting protein 1	180	7	3	3	1	6	hsa-miR-3662	-0.03	-0.16	N/A
SERINC1	ENST00000339697.4	serine incorporator 1	2408	8	1	6	1	4	hsa-miR-3662	-0.02	-0.16	N/A
RLIM	ENST00000332687.6	ring finger protein, LIM domain interacting	662	8	3	2	3	1	hsa-miR-3662	-0.08	-0.16	N/A
RFT1	ENST00000296292.3	RFT1 homolog (S. cerevisiae)	392	2	1	1	0	2	hsa-miR-3662	-0.13	-0.16	N/A
RDX	ENST00000343115.4	radixin	44	9	2	3	4	9	hsa-miR-3662	-0.09	-0.16	N/A
RBM7	ENST00000541475.1	RNA binding motif protein 7	46	7	3	3	1	4	hsa-miR-3662	-0.14	-0.16	N/A
PRAMEF1	ENST00000332296.7	PRAME family member 1	5	2	0	2	0	0	hsa-miR-3662	-0.16	-0.16	N/A
PPIP5K2	ENST00000321521.9	diphosphoinositol pentakisphosphate kinase 2	203	8	2	4	2	10	hsa-miR-3662	-0.01	-0.16	N/A
PDK3	ENST00000441463.2	pyruvate dehydrogenase kinase, isozyme 3	659	8	2	4	2	5	hsa-miR-3662	-0.09	-0.16	N/A
NFYC	ENST00000447388.3	nuclear transcription factor Y, gamma	777	1	1	0	0	2	hsa-miR-3662	-0.11	-0.16	N/A
NDUFB1	ENST00000553514.1	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 1, 7kDa	534	1	0	0	1	0	hsa-miR-3662	-0.16	-0.16	N/A
NAA30	ENST00000556492.1	N(alpha)-acetyltransferase 30, NatC catalytic subunit	418	8	1	3	4	6	hsa-miR-3662	-0.06	-0.16	N/A
MTAP	ENST00000380172.4	methylthioadenosine phosphorylase	1575	8	0	5	3	5	hsa-miR-3662	-0.06	-0.16	N/A
MPHOSPH6	ENST00000258169.4	M-phase phosphoprotein 6	139	1	1	0	0	0	hsa-miR-3662	-0.16	-0.16	N/A

LSM3	ENST00000306024.3	LSM3 homolog, U6 small nuclear RNA associated (<i>S. cerevisiae</i>)	304	2	0	2	0	3	hsa-miR-3662	-0.13	-0.16	N/A
KCTD16	ENST00000507359.3	potassium channel tetramerization domain containing 16	36	9	1	5	3	5	hsa-miR-3662	-0.07	-0.16	N/A
GRSF1	ENST00000254799.6	G-rich RNA sequence binding factor 1	4414	5	2	1	2	2	hsa-miR-3662	0	-0.16	N/A
GABPA	ENST00000354828.3	GA binding protein transcription factor, alpha subunit 60kDa	8	6	4	2	0	2	hsa-miR-3662	-0.14	-0.16	N/A
FER	ENST00000281092.4	fer (<i>fps/fes</i> related) tyrosine kinase	665	8	1	6	1	3	hsa-miR-3662	-0.16	-0.16	N/A
EIF4E3	ENST00000425534.3	eukaryotic translation initiation factor 4E family member 3	475	8	2	2	4	7	hsa-miR-3662	-0.01	-0.16	N/A
EFCAB2	ENST00000366523.1	EF-hand calcium binding domain 2	204	5	1	2	2	1	hsa-miR-3662	-0.09	-0.16	N/A
CPEB4	ENST00000265085.5	cytoplasmic polyadenylation element binding protein 4	472	10	0	6	4	5	hsa-miR-3662	-0.15	-0.16	N/A
CFHR1	ENST00000320493.5	complement factor H-related 1	5	1	0	1	0	0	hsa-miR-3662	-0.16	-0.16	N/A
C6orf48	ENST00000375633.1	chromosome 6 open reading frame 48	5498	1	0	0	1	0	hsa-miR-3662	-0.16	-0.16	N/A
APOLD1	ENST00000356591.4	apolipoprotein L domain containing 1	27	7	3	3	1	4	hsa-miR-3662	-0.12	-0.16	N/A
ANKRD49	ENST00000544253.1	ankyrin repeat domain 49	32	7	3	2	2	1	hsa-miR-3662	-0.14	-0.16	N/A
TMSB15A	ENST00000289373.4	thymosin beta 15a	14	1	0	1	0	0	hsa-miR-3662	-0.15	-0.15	N/A
FUT9	ENST00000302103.5	fucosyltransferase 9 (alpha (1,3) fucosyltransferase)	5	5	0	3	2	6	hsa-miR-3662	-0.15	-0.15	N/A
C1orf141	ENST00000371007.2	chromosome 1 open reading frame 141	5	1	0	0	1	2	hsa-miR-3662	-0.15	-0.15	N/A
AFF2	ENST00000370460.2	AF4/FMR2 family, member 2	8	8	1	5	2	3	hsa-miR-3662	-0.1	-0.15	N/A
KIAA0408	ENST00000483725.3	KIAA0408	95	7	2	4	1	4	hsa-miR-3662	-0.02	-0.15	N/A
ZNF708	ENST00000356929.3	zinc finger protein 708	16	10	0	5	5	7	hsa-miR-3662	-0.03	-0.15	N/A
ZNF704	ENST00000327835.3	zinc finger protein 704	124	5	1	3	1	8	hsa-miR-3662	-0.08	-0.15	N/A
ZMYM1	ENST00000373330.1	zinc finger, MYM-type 1	215	7	1	6	0	2	hsa-miR-3662	-0.12	-0.15	N/A
ZDHHC3	ENST00000296127.3	zinc finger, DHHC-type containing 3	426	10	1	3	6	6	hsa-miR-3662	-0.07	-0.15	N/A
USP44	ENST00000552440.1	ubiquitin specific peptidase 44	29	5	2	1	2	0	hsa-miR-3662	-0.12	-0.15	N/A
USP15	ENST00000353364.3	ubiquitin specific peptidase 15	286	6	3	3	0	8	hsa-miR-3662	-0.01	-0.15	N/A
UFL1	ENST00000369278.4	UFM1-specific ligase 1	298	5	0	1	4	3	hsa-miR-3662	-0.11	-0.15	N/A
TVP23B	ENST00000307767.8	trans-golgi network vesicle protein 23 homolog B (<i>S. cerevisiae</i>)	5	2	0	0	2	1	hsa-miR-3662	-0.06	-0.15	N/A
TOP3B	ENST00000357179.5	topoisomerase (DNA) III beta	5	1	0	0	1	0	hsa-miR-3662	-0.15	-0.15	N/A
SOX6	ENST00000316399.6	SRY (sex determining region Y)-box 6	22	7	2	4	1	3	hsa-miR-3662	-0.05	-0.15	N/A
SNX24	ENST00000513881.1	sorting nexin 24	352	3	1	0	2	2	hsa-miR-3662	-0.12	-0.15	N/A
SLC7A11	ENST00000280612.5	solute carrier family 7 (anionic amino acid transporter light chain, xc- sys	61	10	0	5	5	3	hsa-miR-3662	-0.05	-0.15	N/A
SH3D19	ENST00000409598.4	SH3 domain containing 19	245	8	1	5	2	2	hsa-miR-3662	-0.05	-0.15	N/A
RPAP2	ENST00000610020.1	RNA polymerase II associated protein 2	222	6	3	3	0	7	hsa-miR-3662	0	-0.15	N/A
RORA	ENST00000335670.6	RAR-related orphan receptor A	102	7	1	6	0	8	hsa-miR-3662	-0.13	-0.15	N/A
REEP3	ENST00000373758.4	receptor accessory protein 3	1095	6	2	1	3	3	hsa-miR-3662	-0.09	-0.15	N/A
RAB27B	ENST00000262094.5	RAB27B, member RAS oncogene family	5	7	1	5	1	1	hsa-miR-3662	-0.15	-0.15	N/A
PSMB1	ENST00000262193.6	proteasome (prosome, macropain) subunit, beta type, 1	25836	4	0	2	2	0	hsa-miR-3662	0	-0.15	N/A
PRPF18	ENST00000378572.3	pre-mRNA processing factor 18	551	1	1	0	0	0	hsa-miR-3662	-0.15	-0.15	N/A
PRIM2	ENST00000607273.1	primase, DNA, polypeptide 2 (58kDa)	32	1	0	1	0	1	hsa-miR-3662	-0.12	-0.15	N/A
PREPL	ENST00000541738.1	prolyl endopeptidase-like	612	7	2	3	2	3	hsa-miR-3662	-0.07	-0.15	N/A
PPP1R12A	ENST00000261207.5	protein phosphatase 1, regulatory subunit 12A	276	8	2	3	3	1	hsa-miR-3662	-0.11	-0.15	N/A

PLCH1	ENST00000494598.1	phospholipase C, eta 1	19	1	0	1	0	0	hsa-miR-3662	-0.15	-0.15	N/A
PEX7	ENST00000541292.1	peroxisomal biogenesis factor 7	661	3	1	2	0	1	hsa-miR-3662	-0.1	-0.15	N/A
NUSAP1	ENST00000260359.6	nucleolar and spindle associated protein 1	686	1	1	0	0	0	hsa-miR-3662	-0.13	-0.15	N/A
NPR3	ENST00000265074.8	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptic	517	9	1	4	4	2	hsa-miR-3662	-0.09	-0.15	N/A
NPL	ENST00000367553.1	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase)	19	1	1	0	0	1	hsa-miR-3662	-0.15	-0.15	N/A
NEGR1	ENST00000357731.5	neuronal growth regulator 1	28	7	1	1	5	13	hsa-miR-3662	-0.04	-0.15	N/A
NAA20	ENST00000310450.4	N(alpha)-acetyltransferase 20, NatB catalytic subunit	1586	1	1	0	0	0	hsa-miR-3662	-0.15	-0.15	N/A
MYL12A	ENST00000217652.3	myosin, light chain 12A, regulatory, non-sarcomeric	52535	1	0	1	0	2	hsa-miR-3662	-0.15	-0.15	N/A
MSANTD2	ENST00000239614.4	Myb/SANT-like DNA-binding domain containing 2	50	5	0	5	0	0	hsa-miR-3662	-0.08	-0.15	N/A
MRPL42	ENST00000549982.1	mitochondrial ribosomal protein L42	1172	3	0	0	3	2	hsa-miR-3662	-0.03	-0.15	N/A
MBLAC2	ENST00000316610.6	metallo-beta-lactamase domain containing 2	498	2	1	1	0	1	hsa-miR-3662	-0.11	-0.15	N/A
KRTAP4-11	ENST00000391413.2	keratin associated protein 4-11	5	2	1	1	0	0	hsa-miR-3662	-0.15	-0.15	N/A
KIAA1958	ENST00000337530.6	KIAA1958	117	8	1	5	2	6	hsa-miR-3662	-0.11	-0.15	N/A
IPMK	ENST00000373935.3	inositol polyphosphate multikinase	196	6	2	1	3	4	hsa-miR-3662	-0.04	-0.15	N/A
HIST1H4H	ENST00000289352.1	histone cluster 1, H4h	10	2	0	1	1	0	hsa-miR-3662	-0.15	-0.15	N/A
HILPDA	ENST00000257696.4	hypoxia inducible lipid droplet-associated	431	2	1	0	1	0	hsa-miR-3662	-0.15	-0.15	N/A
HECTD2	ENST00000371667.1	HECT domain containing E3 ubiquitin protein ligase 2	1514	3	0	1	2	1	hsa-miR-3662	-0.14	-0.15	N/A
HDAC2	ENST00000519065.1	histone deacetylase 2	1701	6	1	2	3	4	hsa-miR-3662	-0.08	-0.15	N/A
GPRC5A	ENST00000014914.5	G protein-coupled receptor, family C, group 5, member A	341	6	2	2	2	2	hsa-miR-3662	0	-0.15	N/A
FAM199X	ENST00000493442.1	family with sequence similarity 199, X-linked	856	7	2	4	1	2	hsa-miR-3662	-0.12	-0.15	N/A
EPB41L4B	ENST00000374557.4	erythrocyte membrane protein band 4.1 like 4B	135	5	1	3	1	3	hsa-miR-3662	-0.03	-0.15	N/A
EIF5A2	ENST00000474096.1	eukaryotic translation initiation factor 5A2	443	6	3	0	3	3	hsa-miR-3662	-0.03	-0.15	N/A
DYNLL2	ENST00000579991.2	dynein, light chain, LC8-type 2	1162	5	0	2	3	10	hsa-miR-3662	-0.02	-0.15	N/A
CPEB3	ENST00000412050.4	cytoplasmic polyadenylation element binding protein 3	48	7	2	4	1	2	hsa-miR-3662	-0.13	-0.15	N/A
CNOT2	ENST00000229195.3	CCR4-NOT transcription complex, subunit 2	1189	8	2	3	3	7	hsa-miR-3662	-0.02	-0.15	N/A
CERS6	ENST00000305747.6	ceramide synthase 6	1932	6	2	1	3	3	hsa-miR-3662	-0.13	-0.15	N/A
CD226	ENST00000581982.1	CD226 molecule	8	5	0	5	0	5	hsa-miR-3662	-0.06	-0.15	N/A
CCDC126	ENST00000307471.3	coiled-coil domain containing 126	846	1	1	0	0	2	hsa-miR-3662	-0.14	-0.15	N/A
C1orf210	ENST00000523677.1	chromosome 1 open reading frame 210	43	2	0	2	0	1	hsa-miR-3662	-0.01	-0.15	N/A
C16orf45	ENST00000300006.4	chromosome 16 open reading frame 45	60	2	1	0	1	2	hsa-miR-3662	-0.12	-0.15	N/A
BEND4	ENST00000504360.1	BEN domain containing 4	187	6	3	1	2	4	hsa-miR-3662	-0.14	-0.15	N/A
ATG12	ENST00000500945.2	autophagy related 12	1822	2	1	1	0	3	hsa-miR-3662	-0.11	-0.15	N/A
ATF7IP	ENST00000261168.4	activating transcription factor 7 interacting protein	667	8	2	3	3	3	hsa-miR-3662	-0.14	-0.15	N/A
ACADSB	ENST00000358776.4	acyl-CoA dehydrogenase, short/branched chain	239	7	3	2	2	2	hsa-miR-3662	-0.07	-0.15	N/A