Table S8. Identification of putative miR-663 target sites predicted by TargetScan

Target gene	Representative transcript	Gene name	Conserved	sites			Poorly con	served sites	3		Representative miRNA	Total context+ score	Aggregate PCT	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A				
АВО	NM_020469	ABO blood group (transferase A, alpha 1-3-N- acetylgalactosaminyltransferase; transferase B, alpha 1-3- galactosyltransferase)	O	0	0	0	3	3	0	0	hsa-miR-663	-1.61	N/A	Sites in UTR
MDGA1	NM_153487	MAM domain containing glycosylphosphatidylinositol anchor 1	1	1	0	0	4	2	0	2	hsa-miR-1908	-1.49	N/A	Sites in UTR
C1orf86	NM_182533	chromosome 1 open reading frame 86	O	0	0	0	4	2	2	. 0	hsa-miR-663	-1.48	N/A	Sites in UTR
NFIX	NM_002501	nuclear factor I/X (CCAAT-binding transcription factor)	0	0	0	0	9	0	9	0	hsa-miR-663	-1.32	N/A	Sites in UTR
STK11	NM_000455	serine/threonine kinase 11	0	0	0	0	4	2	2	2 0	hsa-miR-663	-1.27	N/A	Sites in UTR
ZFR2	NM_001145640	zinc finger RNA binding protein 2	O	0	0	0	5	0	5	0	hsa-miR-663	-1.25	N/A	Sites in UTR
KIAA0415	NM_014855	KIAA0415	O	0	0	0	8	2	4	2	hsa-miR-663	-1.24	N/A	Sites in UTR
PCSK1N	NM_013271	proprotein convertase subtilisin/kexin type 1 inhibitor	0	0	0	0	3	2	0	1	hsa-miR-663	-1.23	N/A	Sites in UTR
GJD3	NM_152219	gap junction protein, delta 3, 31.9kDa	0	0	0	0	4	2	2	2 0	hsa-miR-663	-1.2	N/A	Sites in UTR
ABCD1	NM_000033	ATP-binding cassette, sub-family D (ALD), member 1	0	0	0	0	4	1	3	0	hsa-miR-663	-1.17	N/A	Sites in UTR
PRSS22	NM_022119	protease, serine, 22	0	0	0	0	5	0	5	0	hsa-miR-1908	-1.16	N/A	Sites in UTR
DPF1	NM_001135155	D4, zinc and double PHD fingers family 1	1	0	1	0	4	1	3	0	hsa-miR-663	-1.15	N/A	Sites in UTR
FKBP8	NM_012181	FK506 binding protein 8, 38kDa	0	0	0	0	3	1	2	2 0	hsa-miR-663	-1.11	N/A	Sites in UTR
CLSTN1	NM_001009566	calsyntenin 1	0	0	0	0	4	1	3	0	hsa-miR-663	-1.1	N/A	Sites in UTR
ARAF	NM_001654	v-raf murine sarcoma 3611 viral oncogene homolog	O	0	0	0	3	2	1	. 0	hsa-miR-1908	-1.1	N/A	Sites in UTR
PABPC1L2A	NM_001012977	poly(A) binding protein, cytoplasmic 1-like 2A	O	0	0	0	3	1	2	0	hsa-miR-663	-1.04	N/A	Sites in UTR
PABPC1L2B	NM_001042506	poly(A) binding protein, cytoplasmic 1-like 2B	0	0	0	0	3	1	2	0	hsa-miR-663	-1.04	N/A	Sites in UTR

HSPG2	NM_005529	heparan sulfate proteoglycan 2	1	1	0	0	2	0 2	2 0	hsa-miR-663	-1.03	N/A	Sites in UTR
HDAC10	NM_001159286	histone deacetylase 10	0	0	0	0	4	0 4	1 0	hsa-miR-1908	-1.02	N/A	Sites in UTR
NRARP	NM_001004354	NOTCH-regulated ankyrin repeat protein	0	0	0	0	4	1 2	2 1	hsa-miR-663	-1	N/A	Sites in UTR
TNFRSF4	NM_003327	tumor necrosis factor receptor superfamily, member 4	0	0	0	0	2	2 0	0	hsa-miR-663	-0.97	N/A	Sites in UTR
MMP25	NM_022468	matrix metallopeptidase 25	0	0	0	0	4	1 3	3 0	hsa-miR-663	-0.96	N/A	Sites in UTR
ST3GAL2	NM_006927	ST3 beta-galactoside alpha-2,3-sialyltransferase 2	1	1	0	0	2	0 1	1	hsa-miR-663	-0.96	N/A	Sites in UTR
GRIN2D	NM_000836	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	2	1	1	0	1	0 1	L C	hsa-miR-663	-0.96	N/A	Sites in UTR
SCRT1	NM_031309	scratch homolog 1, zinc finger protein (Drosophila)	0	0	0	0	7	0 6	5 1	hsa-miR-663	-0.95	N/A	Sites in UTR
CMIP	NM_030629	c-Maf-inducing protein	0	0	0	0	4	1 3	3 0	hsa-miR-663	-0.95	N/A	Sites in UTR
PRRT1	NM_030651	proline-rich transmembrane protein 1	1	0	1	0	2	0 2	2 0	hsa-miR-663	-0.9	N/A	Sites in UTR
SLC22A13	NM_004256	solute carrier family 22 (organic anion transporter), member 13	0	0	0	0	3	0 3	3 0	hsa-miR-663	-0.89	N/A	Sites in UTR
DLGAP4	NM_001042486	discs, large (Drosophila) homolog-associated protein 4	0	0	0	0	3	2 1	L C	hsa-miR-663	-0.88	N/A	Sites in UTR
CYTH1	NM_004762	cytohesin 1	0	0	0	0	3	1 2	2 0	hsa-miR-663	-0.87	N/A	Sites in UTR
PPP5C	NM_001204284	protein phosphatase 5, catalytic subunit	0	0	0	0	3	1 2	2 0	hsa-miR-1908	-0.87	N/A	Sites in UTR
ЕРНА2	NM_004431	EPH receptor A2	0	0	0	0	2	2 0	) (	hsa-miR-663	-0.86	N/A	Sites in UTR
EEF1A2	NM_001958	eukaryotic translation elongation factor 1 alpha 2	1	1	0	0	2	0 2	2 0	hsa-miR-663	-0.86	N/A	Sites in UTR
LSP1	NM_001013253	lymphocyte-specific protein 1	0	0	0	0	2	1 1		hsa-miR-663	-0.85	N/A	Sites in UTR
DPP9	NM_139159	dipeptidyl-peptidase 9	0	0	0	0	2	1 1		hsa-miR-663	-0.85	N/A	Sites in UTR
SEC14L2	NM_001204204	SEC14-like 2 (S. cerevisiae)	0	0	0	0	4	2 0	) 2	hsa-miR-663	-0.85	N/A	Sites in UTR
FGFRL1	NM_001004356	fibroblast growth factor receptor-like 1	0	0	0	0	3	0 3	3	hsa-miR-663	-0.84	N/A	Sites in UTR

CCDC144A	NM_014695	coiled-coil domain containing 144A	0	0	0	0	2	1 0	1 hsa-miR-663	-0.82	N/A	Sites in UTR
VWA1	NM_022834	von Willebrand factor A domain containing 1	0	0	0	0	5	0 4	1 hsa-miR-663	-0.82	N/A	Sites in UTR
RAB11B	NM_004218	RAB11B, member RAS oncogene family	0	0	0	0	2	1 1	. 0 hsa-miR-663	-0.82	N/A	Sites in UTR
GGA3	NM_001172703	golgi-associated, gamma adaptin ear containing, ARF binding protein 3	0	0	0	0	2	2 0	0 hsa-miR-663	-0.82	N/A	Sites in UTR
SHOX	NM_000451	short stature homeobox	0	0	0	0	3	0 3	0 hsa-miR-663	-0.82	N/A	Sites in UTR
COL8A2	NM_005202	collagen, type VIII, alpha 2	0	0	0	0	2	2 0	0 hsa-miR-663	-0.81	N/A	Sites in UTR
KIAA0284	NM_001112726	KIAA0284	0	0	0	0	3	0 3	0 hsa-miR-663	-0.81	N/A	Sites in UTR
PITPNM2	NM_020845	phosphatidylinositol transfer protein, membrane- associated 2	0	0	0	0	3	1 2	0 hsa-miR-1908	-0.81	N/A	Sites in UTR
BBS5	NM_152384	Bardet-Biedl syndrome 5	0	0	0	0	6	1 4	1 hsa-miR-1908	-0.81	N/A	Sites in UTR
C3orf70	NM_001025266	chromosome 3 open reading frame 70	0	0	0	0	3	0 2	1 hsa-miR-1908	-0.8	N/A	Sites in UTR
C7orf26	NM_024067	chromosome 7 open reading frame 26	0	0	0	0	2	1 1	0 hsa-miR-1908	-0.8	N/A	Sites in UTR
всам	NM_005581	basal cell adhesion molecule (Lutheran blood group)	0	0	0	0	3	0 3	0 hsa-miR-663	-0.8	N/A	Sites in UTR
FAM73B	NM_032809	family with sequence similarity 73, member B	0	0	0	0	4	0 4	0 hsa-miR-663	-0.8	N/A	Sites in UTR
MFI2	NM_005929	antigen p97 (melanoma associated) identified by monoclonal antibodies 133.2 and 96.5	0	0	0	0	6	0 3	3 hsa-miR-663	-0.79	N/A	Sites in UTR
CNN2	NM_004368	calponin 2	0	0	0	0	2	1 1	. 0 hsa-miR-663	-0.78	N/A	Sites in UTR
C9orf167	NM_017723	chromosome 9 open reading frame 167	0	0	0	0	5	0 3	2 hsa-miR-663	-0.78	N/A	Sites in UTR
PIP5K1C	NM_001195733	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	0	0	0	0	3	1 2	0 hsa-miR-1908	-0.76	N/A	Sites in UTR
ISLR2	NM_001130136	immunoglobulin superfamily containing leucine-rich repeat 2	0	0	0	0	2	1 1	. 0 hsa-miR-1908	-0.76	N/A	Sites in UTR
GRASP	NM_181711	GRP1 (general receptor for phosphoinositides 1)- associated scaffold protein	0	0	0	0	2	1 1	0 hsa-miR-1908	-0.75	N/A	Sites in UTR
MKNK2	NM_199054	MAP kinase interacting serine/threonine kinase 2	0	0	0	0	4	0 3	1 hsa-miR-663	-0.75	N/A	Sites in UTR

ARHGAP6	NM_013423	Rho GTPase activating protein 6	0	0	0	0	2	1 1	L (	hsa-miR-663	-0.75	N/A	Sites in UTR
RER1	NM_007033	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	0	0	0	0	3	1 2	L 1	hsa-miR-663	-0.75	N/A	Sites in UTR
TBL1X	NM_001139466	transducin (beta)-like 1X-linked	0	0	0	0	2	2 (	) (	hsa-miR-1908	-0.74	N/A	Sites in UTR
TMEM120B	NM_001080825	transmembrane protein 120B	0	0	0	0	2	1	1 (	hsa-miR-1908	-0.74	N/A	Sites in UTR
ZNF512B	NM_020713	zinc finger protein 512B	0	0	0	0	3	0 8	3 (	hsa-miR-1908	-0.74	N/A	Sites in UTR
DDA1	NM_024050	DET1 and DDB1 associated 1	0	0	0	0	3	0 2	2 1	. hsa-miR-663	-0.74	N/A	Sites in UTR
DIS3L2	NM_152383	DIS3 mitotic control homolog (S. cerevisiae)-like 2	0	0	0	0	3	0 2	2 1	. hsa-miR-663	-0.73	N/A	Sites in UTR
ZNF385A	NM_001130967	zinc finger protein 385A	3	0	3	0	0	0 0		hsa-miR-1908	-0.73	N/A	Sites in UTR
USP11	NM_004651	ubiquitin specific peptidase 11	0	0	0	0	2	1	. (	hsa-miR-663	-0.73	N/A	Sites in UTR
SNCB	NM_001001502	synuclein, beta	0	0	0	0	3	0 3	3 (	hsa-miR-663	-0.72	N/A	Sites in UTR
KIFC2	NM_145754	kinesin family member C2	0	0	0	0	2	1	L C	hsa-miR-1908	-0.72	N/A	Sites in UTR
AP2A2	NM_001242837	adaptor-related protein complex 2, alpha 2 subunit	0	0	0	0	3	0 2	2 1	. hsa-miR-663	-0.7	N/A	Sites in UTR
DUSP8	NM_004420	dual specificity phosphatase 8	0	0	0	0	4	0 3	3	. hsa-miR-663	-0.7	N/A	Sites in UTR
STX1A	NM_001165903	syntaxin 1A (brain)	0	0	0	0	3	0 3	3	hsa-miR-1908	-0.7	N/A	Sites in UTR
C6orf223	NM_001171992	chromosome 6 open reading frame 223	0	0	0	0	3	1 2	2	hsa-miR-1908	-0.7	N/A	Sites in UTR
MYL9	NM_006097	myosin, light chain 9, regulatory	1	1	0	0	1	0	) 1	. hsa-miR-663	-0.68	N/A	Sites in UTR
G6PD	NM_000402	glucose-6-phosphate dehydrogenase	0	0	0	0	2	1 (	) 1	. hsa-miR-663	-0.68	N/A	Sites in UTR
YIF1B	NM_001039671	Yip1 interacting factor homolog B (S. cerevisiae)	0	0	0	0	2	1	1 (	hsa-miR-663	-0.68	N/A	Sites in UTR
SCAMP4	NM_079834	secretory carrier membrane protein 4	0	0	0	0	2	1 :	1 (	hsa-miR-663	-0.68	N/A	Sites in UTR
FBXL16	NM_153350	F-box and leucine-rich repeat protein 16	0	0	0	0	3	1 2	2	hsa-miR-663	-0.68	N/A	Sites in UTR

PAX2	NM_000278	paired box 2	1	0	1	0	3	0	2	hsa-miR-663	-0.67	N/A	Sites in UTR
ARHGEF18	NM_001130955	Rho/Rac guanine nucleotide exchange factor (GEF) 18	0	0	0	0	2	1	0 :	. hsa-miR-663	-0.67	N/A	Sites in UTR
wwox	NM_130844	WW domain containing oxidoreductase	0	0	0	0	1	1	0 0	hsa-miR-663	-0.67	N/A	Sites in UTR
SOLH	NM_005632	small optic lobes homolog (Drosophila)	0	0	0	0	3	0	2 1	hsa-miR-1908	-0.66	N/A	Sites in UTR
GNG7	NM_052847	guanine nucleotide binding protein (G protein), gamma 7	0	0	0	0	2	1	0 1	. hsa-miR-1908	-0.66	N/A	Sites in UTR
RFX1	NM_002918	regulatory factor X, 1 (influences HLA class II expression)	0	0	0	0	3	1	2 (	hsa-miR-663	-0.66	N/A	Sites in UTR
SLC25A35	NM_201520	solute carrier family 25, member 35	1	0	1	0	3	0	1 2	! hsa-miR-663	-0.66	N/A	Sites in UTR
NKIRAS2	NM_001001349	NFKB inhibitor interacting Ras-like 2	0	0	0	0	2	1	0 2	hsa-miR-663	-0.66	N/A	Sites in UTR
FAM43B	NM_207334	family with sequence similarity 43, member B	0	0	0	0	3	O	2 1	. hsa-miR-663	-0.66	N/A	Sites in UTR
LINGO1	NM_032808	leucine rich repeat and Ig domain containing 1	0	0	0	0	2	1	1 (	hsa-miR-663	-0.65	N/A	Sites in UTR
SIX2	NM_016932	SIX homeobox 2	0	0	0	0	2	1	1 (	hsa-miR-663	-0.65	N/A	Sites in UTR
5-Sep	NM_001009939	septin 5	0	0	0	0	3	O	2 1	. hsa-miR-663	-0.65	N/A	Sites in UTR
ATAT1	NM_001190724	alpha tubulin acetyltransferase 1	0	0	0	0	2	1	1 (	hsa-miR-663	-0.64	N/A	Sites in UTR
MYO1D	NM_015194	myosin ID	0	0	0	0	3	0	3 (	hsa-miR-663	-0.64	N/A	Sites in UTR
KIAA0930	NM_001009880	кіАА0930	0	0	0	0	3	0	2 1	. hsa-miR-663	-0.64	N/A	Sites in UTR
NTN5	NM_145807	netrin 5	0	0	0	0	1	1	0 (	hsa-miR-663	-0.64	N/A	Sites in UTR
GNAI2	INIVI UUTTAAA25	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	0	0	0	0	2	0	2 (	hsa-miR-663	-0.63	N/A	Sites in UTR
MXD4	NM_006454	MAX dimerization protein 4	0	0	0	0	2	1	0 1	. hsa-miR-1908	-0.63	N/A	Sites in UTR
SHC3	NM_016848	SHC (Src homology 2 domain containing) transforming protein 3	0	0	0	0	3	2	1 (	hsa-miR-663	-0.63	N/A	Sites in UTR
NF2	NM_000268	neurofibromin 2 (merlin)	0	0	0	0	2	1	1 (	hsa-miR-1908	-0.63	N/A	Sites in UTR

ZNF710	NM_198526	zinc finger protein 710	0	0	0	0	3	0	2 1	L hsa-miR-663	-0.63	N/A	Sites in UTR
FLCN	NM_144997	folliculin	0	0	0	0	2	1	0 1	l hsa-miR-1908	-0.63	N/A	Sites in UTR
EXTL1	NM_004455	exostoses (multiple)-like 1	0	0	0	0	2	1	1 0	hsa-miR-663	-0.62	N/A	Sites in UTR
EFNA2	NM_001405	ephrin-A2	0	0	0	0	3	0	3 (	hsa-miR-663	-0.62	N/A	Sites in UTR
TMEM143	NM_018273	transmembrane protein 143	0	0	0	0	2	0	2 0	) hsa-miR-1908	-0.62	N/A	Sites in UTR
ACSL3	NM_004457	acyl-CoA synthetase long-chain family member 3	0	0	0	0	1	1	0 0	) hsa-miR-1908	-0.62	N/A	Sites in UTR
RGS6	NM_001204416	regulator of G-protein signaling 6	0	0	0	0	2	1	1 0	) hsa-miR-1908	-0.61	N/A	Sites in UTR
PROP1	NM_006261	PROP paired-like homeobox 1	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.61	N/A	Sites in UTR
NR5A1	NM_004959	nuclear receptor subfamily 5, group A, member 1	0	0	0	0	3	0	2 1	L hsa-miR-663	-0.61	N/A	Sites in UTR
WIPF3	NM_001080529	WAS/WASL interacting protein family, member 3	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.61	N/A	Sites in UTR
TFAP2B		transcription factor AP-2 beta (activating enhancer binding protein 2 beta)	0	0	0	0	3	0	3 (	) hsa-miR-1908	-0.61	N/A	Sites in UTR
SYT7	NM_004200	synaptotagmin VII	0	0	0	0	3	1	1 1	l hsa-miR-1908	-0.61	N/A	Sites in UTR
CCDC67	NM_181645	coiled-coil domain containing 67	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.6	N/A	Sites in UTR
SRCIN1	NM_025248	SRC kinase signaling inhibitor 1	0	0	0	0	3	0	3 (	) hsa-miR-663	-0.6	N/A	Sites in UTR
IL17REL	NM_001001694	interleukin 17 receptor E-like	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.6	N/A	Sites in UTR
SLC24A6	NM_024959	solute carrier family 24 (sodium/potassium/calcium exchanger), member 6	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.6	N/A	Sites in UTR
C10orf90	NM_001004298	chromosome 10 open reading frame 90	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.59	N/A	Sites in UTR
C8orf82	NM_001001795	chromosome 8 open reading frame 82	0	0	0	0	3	0	3 (	) hsa-miR-663	-0.59	N/A	Sites in UTR
GLO1	NM_006708	glyoxalase I	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.59	N/A	Sites in UTR
ILK	NM_001014794	integrin-linked kinase	0	0	0	0	2	0	2 (	) hsa-miR-1908	-0.59	N/A	Sites in UTR

OSBPL7	NM_145798	oxysterol binding protein-like 7	0	0	0	0	2	0	2 0 hsa	a-miR-663	-0.59	N/A	Sites in UTR
RMND5A	NM_022780	required for meiotic nuclear division 5 homolog A (S. cerevisiae)	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.58	N/A	Sites in UTR
ТТҮН3	NM_025250	tweety homolog 3 (Drosophila)	0	0	0	0	5	1	1 3 hsa	a-miR-663	-0.58	N/A	Sites in UTR
GBP5	NM_001134486	guanylate binding protein 5	0	0	0	0	2	1	1 0 hsa	a-miR-663	-0.58	N/A	Sites in UTR
WDR5	NM_017588	WD repeat domain 5	0	0	0	0	2	1	0 1 hsa	a-miR-663	-0.58	N/A	Sites in UTR
CELSR1	NM_014246	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	0	0	0	0	3	0	0 hsa	a-miR-663	-0.58	N/A	Sites in UTR
TSPAN33	NM_178562	tetraspanin 33	0	0	0	0	3	0	2 1 hsa	a-miR-1908	-0.58	N/A	Sites in UTR
IGHMBP2	NM_002180	immunoglobulin mu binding protein 2	0	0	0	0	1	1	0 hsa	a-miR-663	-0.58	N/A	Sites in UTR
GIGYF1	NM_022574	GRB10 interacting GYF protein 1	0	0	0	0	3	0	2 1 hsa	a-miR-663	-0.57	N/A	Sites in UTR
CYP3A43	NM_022820	cytochrome P450, family 3, subfamily A, polypeptide 43	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.57	N/A	Sites in UTR
PTGDS	NM_000954	prostaglandin D2 synthase 21kDa (brain)	0	0	0	0	1	1	0 hsa	a-miR-663	-0.57	N/A	Sites in UTR
URB1	NM_014825	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.57	N/A	Sites in UTR
ESPN	NM_031475	espin	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.57	N/A	Sites in UTR
MAFB	NM_005461	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	0	0	0	0	2	1	1 0 hsa	a-miR-663	-0.57	N/A	Sites in UTR
NXPH4	NM_007224	neurexophilin 4	0	0	0	0	2	0	1 1 hsa	a-miR-1908	-0.57	N/A	Sites in UTR
ZNF784	NM_203374	zinc finger protein 784	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.57	N/A	Sites in UTR
REG4	NM_001159352	regenerating islet-derived family, member 4	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.56	N/A	Sites in UTR
FHL3	NM_004468	four and a half LIM domains 3	0	0	0	0	1	1	0 0 hsa	a-miR-1908	-0.56	N/A	Sites in UTR
GMIP	NM_016573	GEM interacting protein	0	0	0	0	1	1	0 0 hsa	a-miR-663	-0.56	N/A	Sites in UTR
PDIA2	NM_006849	protein disulfide isomerase family A, member 2	0	0	0	0	1	1	0 hsa	a-miR-663	-0.56	N/A	Sites in UTR

CCL22	NM_002990	chemokine (C-C motif) ligand 22	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.56	5 N/A	Sites in UTR
ZNF787	NM_001002836	zinc finger protein 787	0	0	0	0	2	0	2 0 hsa	a-miR-663	-0.56	5 N/A	Sites in UTR
STK33	NM_030906	serine/threonine kinase 33	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.56	5 N/A	Sites in UTR
КСР	NM_001135914	kielin/chordin-like protein	0	0	0	0	1	1	0 hsa	a-miR-663	-0.56	5 N/A	Sites in UTR
SIGLEC8	NM_014442	sialic acid binding Ig-like lectin 8	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.56	5 N/A	Sites in UTR
OPA3	NM_001017989	optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia)	0	0	0	0	2	0	2 0 hsa	a-miR-1908	-0.56	5 N/A	Sites in UTR
отоѕ	NM_148961	otospiralin	0	0	0	0	1	1	0 hsa	a-miR-663	-0.5!	N/A	Sites in UTR
DISC1	NM_001012957	disrupted in schizophrenia 1	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.5!	N/A	Sites in UTR
C2orf65	NM_138804	chromosome 2 open reading frame 65	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.5!	N/A	Sites in UTR
IL11	NM_000641	interleukin 11	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.5!	N/A	Sites in UTR
SLC17A7	NM_020309	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	1	1	0	0	0	0	0 hsa	a-miR-1908	-0.5!	N/A	Sites in UTR
LPIN2	NM_014646	lipin 2	0	0	0	0	3	0	2 1 hsa	a-miR-663	-0.5!	N/A	Sites in UTR
CARM1	NM_199141	coactivator-associated arginine methyltransferase 1	0	0	0	0	3	0	3 0 hsa	a-miR-663	-0.5!	N/A	Sites in UTR
APC2	NM_005883	adenomatosis polyposis coli 2	0	0	0	0	3	0	3 0 hsa	a-miR-663	-0.5!	N/A	Sites in UTR
CCR7	NM_001838	chemokine (C-C motif) receptor 7	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.5!	5 N/A	Sites in UTR
CRTC1	NM_001098482	CREB regulated transcription coactivator 1	0	0	0	0	2	1	1 hsa	a-miR-663	-0.5!	N/A	Sites in UTR
PRDM15	NM_001040424	PR domain containing 15	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.5!	5 N/A	Sites in UTR
ТМВІМ1	NM_022152	transmembrane BAX inhibitor motif containing 1	0	0	0	0	1	1	0 hsa	a-miR-1908	-0.5!	5 N/A	Sites in UTR
DCTN5	NM_001199743	dynactin 5 (p25)	0	0	0	0	1	1	0 hsa	a-miR-663	-0.5!	5 N/A	Sites in UTR
UNC13D	NM_199242	unc-13 homolog D (C. elegans)	0	0	0	0	1	1	0 hsa	a-miR-663	-0.55	5 N/A	Sites in UTR

NLE1	NM_001014445	notchless homolog 1 (Drosophila)	0	0	0	0	2	O	2 (	) hsa-miR-663	-0.55	N/A	Sites in UTR
EPB41L1	NM_012156	erythrocyte membrane protein band 4.1-like 1	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.55	N/A	Sites in UTR
ROD1	NM_001163788	ROD1 regulator of differentiation 1 (S. pombe)	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.55	N/A	Sites in UTR
UBXN6	NM_001171091	UBX domain protein 6	0	0	0	0	1	1	0 0	hsa-miR-663	-0.55	N/A	Sites in UTR
NT5C3L	NM_052935	5'-nucleotidase, cytosolic III-like	0	0	0	0	1	1	0 0	) hsa-miR-1908	-0.54	N/A	Sites in UTR
ZBTB22	NM_001145338	zinc finger and BTB domain containing 22	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.54	N/A	Sites in UTR
PI4K2A	NM_018425	phosphatidylinositol 4-kinase type 2 alpha	0	0	0	0	2	1	1 0	) hsa-miR-663	-0.54	N/A	Sites in UTR
ADRBK1	NM_001619	adrenergic, beta, receptor kinase 1	0	0	0	0	2	O	1 1	l hsa-miR-1908	-0.54	N/A	Sites in UTR
LDOC1	NM_012317	leucine zipper, down-regulated in cancer 1	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.54	N/A	Sites in UTR
BEGAIN	NM_001159531	brain-enriched guanylate kinase-associated homolog (rat)	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.54	N/A	Sites in UTR
SLX4	NM_032444	SLX4 structure-specific endonuclease subunit homolog (S. cerevisiae)	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.54	N/A	Sites in UTR
C1QTNF6	NM_031910	C1q and tumor necrosis factor related protein 6	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.54	N/A	Sites in UTR
SBF1	NM_002972	SET binding factor 1	2	0	2	0	1	0	0 1	L hsa-miR-663	-0.53	N/A	Sites in UTR
MX2	NM_002463	myxovirus (influenza virus) resistance 2 (mouse)	0	0	0	0	1	1	0 0	) hsa-miR-1908	-0.53	N/A	Sites in UTR
RASD2	NM_014310	RASD family, member 2	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.53	N/A	Sites in UTR
PDXP	NM_020315	pyridoxal (pyridoxine, vitamin B6) phosphatase	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.53	N/A	Sites in UTR
CSNK2A1	NM_001895	casein kinase 2, alpha 1 polypeptide	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.53	N/A	Sites in UTR
SOHLH2	NM_017826	spermatogenesis and oogenesis specific basic helix-loop- helix 2	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.53	N/A	Sites in UTR
C13orf38-SOHLH2	NM_001198910	C13orf38-SOHLH2 readthrough	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.53	N/A	Sites in UTR
AK1	NM_000476	adenylate kinase 1	0	0	0	0	2	O	2 (	) hsa-miR-1908	-0.53	N/A	Sites in UTR

CBX2	NM_032647	chromobox homolog 2	0	0	0	0	1	1 0	0	hsa-miR-1908	-0.53	N/A	Sites in UTR
ASB13	NM_024701	ankyrin repeat and SOCS box containing 13	0	0	0	0	2	0 1	1 1	hsa-miR-1908	-0.53	N/A	Sites in UTR
APLNR	NM_005161	apelin receptor	0	0	0	0	2	0 2	0	hsa-miR-663	-0.53	N/A	Sites in UTR
TNKS1BP1	NM_033396	tankyrase 1 binding protein 1, 182kDa	0	0	0	0	1	1 0	0	hsa-miR-663	-0.53	N/A	Sites in UTR
BLK	NM_001715	B lymphoid tyrosine kinase	0	0	0	0	2	0 2	0	hsa-miR-663	-0.53	N/A	Sites in UTR
AKT1S1	NM_001098632	AKT1 substrate 1 (proline-rich)	1	0	1	0	1	0 1	0	hsa-miR-663	-0.53	N/A	Sites in UTR
TMEM132A	NM_017870	transmembrane protein 132A	0	0	0	0	1	1 0	0	hsa-miR-1908	-0.53	N/A	Sites in UTR
ALPPL2	NM_031313	alkaline phosphatase, placental-like 2	0	0	0	0	2	0 2	0	hsa-miR-1908	-0.53	N/A	Sites in UTR
ZBTB7B	NM_015872	zinc finger and BTB domain containing 7B	1	0	1	0	2	0 2	0	hsa-miR-1908	-0.53	N/A	Sites in UTR
IFI35	NM_005533	interferon-induced protein 35	0	0	0	0	1	1 0	0	hsa-miR-663	-0.53	N/A	Sites in UTR
HRAS	NM_001130442	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	0	0	0	0	2	0 2	0	hsa-miR-663	-0.52	N/A	Sites in UTR
C6orf221	NM_001017361	chromosome 6 open reading frame 221	0	0	0	0	2	0 2	0	hsa-miR-663	-0.52	N/A	Sites in UTR
POLM	NM_013284	polymerase (DNA directed), mu	0	0	0	0	1	1 0	0	hsa-miR-1908	-0.52	N/A	Sites in UTR
SLC25A40	NM_018843	solute carrier family 25, member 40	0	0	0	0	1	1 0	0	hsa-miR-663	-0.52	N/A	Sites in UTR
SPRY4	NM_001127496	sprouty homolog 4 (Drosophila)	0	0	0	0	1	1 0	0	hsa-miR-1908	-0.52	N/A	Sites in UTR
CTIF	NM_001142397	CBP80/20-dependent translation initiation factor	0	0	0	0	2	1 0	1	hsa-miR-663	-0.52	N/A	Sites in UTR
DYSFIP1	NM_001007533	dysferlin interacting protein 1	0	0	0	0	1	1 0	0	hsa-miR-663	-0.52	N/A	Sites in UTR
PRKCG	NM_002739	protein kinase C, gamma	0	0	0	0	2	0 2	0	hsa-miR-663	-0.52	N/A	Sites in UTR
TTC22	NM_001114108	tetratricopeptide repeat domain 22	0	0	0	0	2	0 2	0	hsa-miR-663	-0.52	N/A	Sites in UTR
HSPB1	NM_001540	heat shock 27kDa protein 1	0	0	0	0	1	1 0	0	hsa-miR-1908	-0.52	N/A	Sites in UTR

EZR	NM_001111077	ezrin	0	0	0	0	1	1 (	0 hsa-miR-663	-0.52	N/A	Sites in UTR
DENND1A	NM_020946	DENN/MADD domain containing 1A	0	0	0	0	1	1 (	0 hsa-miR-663	-0.52	N/A	Sites in UTR
MYO1G	NM_033054	myosin IG	0	0	0	0	1	1 (	0 hsa-miR-1908	-0.52	N/A	Sites in UTR
ZC3H18	NM_144604	zinc finger CCCH-type containing 18	0	0	0	0	2	0 2	2 0 hsa-miR-663	-0.52	N/A	Sites in UTR
тмсо6	NM_018502	transmembrane and coiled-coil domains 6	0	0	0	0	1	1	0 hsa-miR-1908	-0.52	N/A	Sites in UTR
FAM125A	NM_138401	family with sequence similarity 125, member A	0	0	0	0	1	1	0 hsa-miR-1908	-0.52	N/A	Sites in UTR
ZFPM1	NM_153813	zinc finger protein, multitype 1	0	0	0	0	1	1 (	0 hsa-miR-663	-0.52	N/A	Sites in UTR
SLC12A5	NM_001134771	solute carrier family 12 (potassium/chloride transporter), member 5	1	0	1	0	2	0 2	0 hsa-miR-663	-0.52	N/A	Sites in UTR
GTPBP5	NM_015666	GTP binding protein 5 (putative)	0	0	0	0	2	0 2	2 0 hsa-miR-663	-0.52	N/A	Sites in UTR
ACAP1	NM_014716	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	0	0	0	0	1	1	0 hsa-miR-1908	-0.52	N/A	Sites in UTR
LCN15	NM_203347	lipocalin 15	0	0	0	0	2	0 2	0 hsa-miR-1908	-0.52	N/A	Sites in UTR
FASN	NM_004104	fatty acid synthase	0	0	0	0	2	1	0 hsa-miR-663	-0.52	N/A	Sites in UTR
CHRNA4	NM_000744	cholinergic receptor, nicotinic, alpha 4	0	0	0	0	2	0 2	0 hsa-miR-1908	-0.52	N/A	Sites in UTR
LRRC4B	NM_001080457	leucine rich repeat containing 4B	0	0	0	0	1	1	0 hsa-miR-1908	-0.51	N/A	Sites in UTR
CORO6	NM_032854	coronin 6	0	0	0	0	2	0 2	2 0 hsa-miR-663	-0.51	N/A	Sites in UTR
PLXNA4	NM_020911	plexin A4	0	0	0	0	2	2	0 hsa-miR-1908	-0.51	N/A	Sites in UTR
P4HTM	NM_177938	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	0	0	0	0	1	1	0 hsa-miR-1908	-0.51	N/A	Sites in UTR
LOC100507050	NM_001195528	hypothetical LOC100507050	0	0	0	0	2	0 2	0 hsa-miR-1908	-0.51	N/A	Sites in UTR
TNIP2	NM_001161527	TNFAIP3 interacting protein 2	0	0	0	0	1	1 (	0 hsa-miR-1908	-0.51	N/A	Sites in UTR
FAM84A	NM_145175	family with sequence similarity 84, member A	0	0	0	0	2	1	0 hsa-miR-1908	-0.51	N/A	Sites in UTR

CDKN2A	NM_000077	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)	0	0	0	0	1	1	0	) hsa-miR-663	-0.51	N/A	Sites in UTR
IQCE	NM_001100390	IQ motif containing E	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.51	N/A	Sites in UTR
HAPLN3	NM_178232	hyaluronan and proteoglycan link protein 3	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.51	N/A	Sites in UTR
FAM43A	NM_153690	family with sequence similarity 43, member A	0	0	0	0	1	1	0 0	) hsa-miR-1908	-0.51	N/A	Sites in UTR
SMCR8	NM_144775	Smith-Magenis syndrome chromosome region, candidate 8	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.51	N/A	Sites in UTR
GRM4	NM_000841	glutamate receptor, metabotropic 4	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.51	N/A	Sites in UTR
ZBTB45	NM_032792	zinc finger and BTB domain containing 45	0	0	0	0	2	0	1	L hsa-miR-663	-0.51	N/A	Sites in UTR
IPO9	NM_018085	importin 9	0	0	0	0	2	0	2 (	) hsa-miR-1908	-0.51	N/A	Sites in UTR
MAD1L1	NM_001013836	MAD1 mitotic arrest deficient-like 1 (yeast)	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.51	N/A	Sites in UTR
EPO	NM_000799	erythropoietin	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.5	N/A	Sites in UTR
C9orf142	NM_183241	chromosome 9 open reading frame 142	0	0	0	0	1	1	0 0	) hsa-miR-1908	-0.5	N/A	Sites in UTR
FNBP1	NM_015033	formin binding protein 1	0	0	0	0	3	2	1 (	) hsa-miR-663	-0.5	N/A	Sites in UTR
PRKDC	NM_001081640	protein kinase, DNA-activated, catalytic polypeptide	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.5	N/A	Sites in UTR
TSPAN9	NM_001168320	tetraspanin 9	0	0	0	0	2	1	1 (	) hsa-miR-663	-0.5	N/A	Sites in UTR
C1orf201	NM_001199012	chromosome 1 open reading frame 201	0	0	0	0	1	1	0 0	) hsa-miR-1908	-0.49	N/A	Sites in UTR
RAB3A	NM_002866	RAB3A, member RAS oncogene family	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.49	N/A	Sites in UTR
UBE2M	NM_003969	ubiquitin-conjugating enzyme E2M	1	1	0	0	0	0	0 0	) hsa-miR-1908	-0.49	N/A	Sites in UTR
NCDN	NM_001014839	neurochondrin	1	1	0	0	0	0	0 (	) hsa-miR-1908	-0.49	N/A	Sites in UTR
CERS4	NM_024552	ceramide synthase 4	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.49	N/A	Sites in UTR
TBX1	NM_080647	T-box 1	0	0	0	0	2	0	2	) hsa-miR-663	-0.49	N/A	Sites in UTR

TOMM40	NM_001128916	translocase of outer mitochondrial membrane 40 homolog (yeast)	0	0	0	0	2	1	1	0	hsa-miR-1908	-0.49	N/A	Sites in UTR
SLC26A1	NM_022042	solute carrier family 26 (sulfate transporter), member 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.49	N/A	Sites in UTR
SNX8	NM_013321	sorting nexin 8	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.49	N/A	Sites in UTR
HRH3	NM_007232	histamine receptor H3	0	0	0	0	2	0	2	0	hsa-miR-663	-0.49	N/A	Sites in UTR
ITGB4	NM_000213	integrin, beta 4	0	0	0	0	1	1	0	0	hsa-miR-663	-0.49	N/A	Sites in UTR
PNMAL2	NM_020709	PNMA-like 2	0	0	0	0	2	0	2	0	hsa-miR-663	-0.49	N/A	Sites in UTR
IQSEC3	NM_001170738	IQ motif and Sec7 domain 3	0	0	0	0	4	0	2	2	hsa-miR-1908	-0.49	N/A	Sites in UTR
SLC25A44	NM_014655	solute carrier family 25, member 44	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.49	N/A	Sites in UTR
HNRNPUL1	NM_007040	heterogeneous nuclear ribonucleoprotein U-like 1	0	0	0	0	1	1	0	0	hsa-miR-663	-0.49	N/A	Sites in UTR
FBXW5	NM_018998	F-box and WD repeat domain containing 5	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.49	N/A	Sites in UTR
PPP1R12C	NM_017607	protein phosphatase 1, regulatory (inhibitor) subunit 12C	0	0	0	0	2	0	1	1	hsa-miR-663	-0.49	N/A	Sites in UTR
MNT	NM_020310	MAX binding protein	0	0	0	0	2	0	2	0	hsa-miR-663	-0.49	N/A	Sites in UTR
SPTBN4	NM_020971	spectrin, beta, non-erythrocytic 4	0	0	0	0	2	0	2	0	hsa-miR-663	-0.49	N/A	Sites in UTR
GPER	NM_001039966	G protein-coupled estrogen receptor 1	0	0	0	0	1	1	0	0	hsa-miR-663	-0.48	N/A	Sites in UTR
CDHR1	NM_033100	cadherin-related family member 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
SOX1	NM_005986	SRY (sex determining region Y)-box 1	0	0	0	0	2	0	2	0	hsa-miR-663	-0.48	N/A	Sites in UTR
H6PD	NM_004285	hexose-6-phosphate dehydrogenase (glucose 1- dehydrogenase)	0	0	0	0	1	1	0	0	hsa-miR-663	-0.48	N/A	Sites in UTR
CYS1	NM_001037160	cystin 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
RIN3	NM_024832	Ras and Rab interactor 3	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
ANKRD13B	NM_152345	ankyrin repeat domain 13B	0	0	0	0	1	1	0	0	hsa-miR-663	-0.48	N/A	Sites in UTR

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_138383 r	metastasis suppressor 1-like	0	0	0	0	2	0	2	0	hsa-miR-663	-0.48	N/A	Sites in UTR
_003824 F	Fas (TNFRSF6)-associated via death domain	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
_015258 F	FK506 binding protein 15, 133kDa	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
_052896	CUB and Sushi multiple domains 2	1	0	1	0	1	0	1	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
000837		0	0	0	0	1	1	0	0	hsa-miR-663	-0.48	N/A	Sites in UTR
_024652	leucine-rich repeat kinase 1	0	0	0	0	1	1	0	0	hsa-miR-663	-0.48	N/A	Sites in UTR
_022773 li	lipase maturation factor 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
_022480 k	kelch-like 25 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-663	-0.48	N/A	Sites in UTR
_001029885 g	glycolipid transfer protein domain containing 1	0	0	0	0	2	0	2	0	hsa-miR-663	-0.48	N/A	Sites in UTR
_001570 i	interleukin-1 receptor-associated kinase 2	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
_001024937 r	misshapen-like kinase 1	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.48	N/A	Sites in UTR
_001102371 F	FAD-dependent oxidoreductase domain containing 2	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.48	N/A	Sites in UTR
_002725 p	proline/arginine-rich end leucine-rich repeat protein	0	0	0	0	2	1	0	1	hsa-miR-663	-0.48	N/A	Sites in UTR
002019		0	0	0	0	1	1	0	0	hsa-miR-663	-0.48	N/A	Sites in UTR
_000091	collagen, type IV, alpha 3 (Goodpasture antigen)	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
_018207 t	tripartite motif containing 62	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
_001080524	chromosome 16 open reading frame 90	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
_001084393	D-dopachrome tautomerase-like	0	0	0	0	1	1	0	0	hsa-miR-663	-0.47	N/A	Sites in UTR
UXU55/		0	0	0	0	2	0	2	0	hsa-miR-663	-0.47	N/A	Sites in UTR
_031866 f	frizzled family receptor 8	0	0	0	0	2	0	1	1	hsa-miR-663	-0.47	N/A	Sites in UTR
	03824  15258  52896  00837  24652  22773  22480  01029885  01570  01024937  01102371  02725  02019  00091  18207  01080524  01084393  80552	Fas (TNFRSF6)-associated via death domain  FK506 binding protein 15, 133kDa  CUB and Sushi multiple domains 2  glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)  Leucine-rich repeat kinase 1  lipase maturation factor 1  kelch-like 25 (Drosophila)  glycolipid transfer protein domain containing 1  linterleukin-1 receptor-associated kinase 2  linterleukin-1 receptor-associated kinase 2  misshapen-like kinase 1  PAD-dependent oxidoreductase domain containing 2  proline/arginine-rich end leucine-rich repeat protein  fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)  collagen, type IV, alpha 3 (Goodpasture antigen)  tripartite motif containing 62  chromosome 16 open reading frame 90  D-dopachrome tautomerase-like  solute carrier family 32 (GABA vesicular transporter), member 1	Fas (TNFRSF6)-associated via death domain 0 15258 FK506 binding protein 15, 133kDa 0 152896 CUB and Sushi multiple domains 2 1 100837 glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding) 0 14652 leucine-rich repeat kinase 1 0 122773 lipase maturation factor 1 0 122480 kelch-like 25 (Drosophila) 0 101029885 glycolipid transfer protein domain containing 1 0 101570 interleukin-1 receptor-associated kinase 2 0 101024937 misshapen-like kinase 1 1 101102371 FAD-dependent oxidoreductase domain containing 2 0 102725 proline/arginine-rich end leucine-rich repeat protein 0 102019 fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) 0 18207 tripartite motif containing 62 0 18207 tripartite motif containing 62 0 101080524 chromosome 16 open reading frame 90 0 101084393 D-dopachrome tautomerase-like 0 10080552 solute carrier family 32 (GABA vesicular transporter), member 1	D3824 Fas (TNFRSF6)-associated via death domain 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		13824   Fas (TNFRSF6)-associated via death domain   0   0   0   0   0   0   0   0   0	15258	1   1   1   1   1   1   1   1   1   1		Page   Page		23824 Fest (TNRFSSF) associated via death domain	203224 Fas (NAFSSSS) associated via death domain

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NCS1	NM_001128826	neuronal calcium sensor 1	0	0	0	0	3	0	2	1	hsa-miR-1908	-0.47	N/A	Sites in UTR
SPI1	INIVI UUTUSUS47	spleen focus forming virus (SFFV) proviral integration oncogene spi1	0	0	0	0	2	1	1	. 0	hsa-miR-663	-0.47	N/A	Sites in UTR
ARL8A	NM_138795	ADP-ribosylation factor-like 8A	0	0	0	0	2	0	2	0	hsa-miR-663	-0.47	N/A	Sites in UTR
C16orf5	NM_001199054	chromosome 16 open reading frame 5	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
IGF2	NM_000612	insulin-like growth factor 2 (somatomedin A)	0	0	0	0	2	1	1	. 0	hsa-miR-663	-0.47	N/A	Sites in UTR
CDX1	NM_001804	caudal type homeobox 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
VAT1	NM_006373	vesicle amine transport protein 1 homolog (T. californica)	0	0	0	0	1	1	0	0	hsa-miR-663	-0.47	N/A	Sites in UTR
OTOF	NM_004802	otoferlin	0	0	0	0	2	0	1	. 1	hsa-miR-1908	-0.47	N/A	Sites in UTR
DNM1	NM_001005336	dynamin 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
FAM18A	NM_001079512	family with sequence similarity 18, member A	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
HOXC11	NM_014212	homeobox C11	0	0	0	0	2	0	2	0	hsa-miR-663	-0.47	N/A	Sites in UTR
LIME1	NM_017806	Lck interacting transmembrane adaptor 1	0	0	0	0	2	0	2	0	hsa-miR-663	-0.47	N/A	Sites in UTR
CDC42EP4	NM_012121	CDC42 effector protein (Rho GTPase binding) 4	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
NKX3-2	NM_001189	NK3 homeobox 2	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
RAD51B	NM_133509	RAD51 homolog B (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR
DEF8	NM_001242816	differentially expressed in FDCP 8 homolog (mouse)	0	0	0	0	2	0	1	. 1	hsa-miR-663	-0.47	N/A	Sites in UTR
SUFU	NM_016169	suppressor of fused homolog (Drosophila)	0	0	0	0	2	1	1	. 0	hsa-miR-663	-0.47	N/A	Sites in UTR
CSF1	NM_172212	colony stimulating factor 1 (macrophage)	0	0	0	0	1	1	0	0	hsa-miR-663	-0.47	N/A	Sites in UTR
MFSD10	NM_001120	major facilitator superfamily domain containing 10	0	0	0	0	1	1	0	0	hsa-miR-663	-0.47	N/A	Sites in UTR
ZDHHC7	NM_001145548	zinc finger, DHHC-type containing 7	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.47	N/A	Sites in UTR

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C14orf180	NM_001008404	chromosome 14 open reading frame 180	0	0	0	0	1	1	0	0	hsa-miR-663	-0.47	N/A	Sites in UTR
HAND2	NM_021973	heart and neural crest derivatives expressed 2	0	0	0	0	1	1	0	0	hsa-miR-663	-0.47	N/A	Sites in UTR
SETD4	NM_017438	SET domain containing 4	0	0	0	0	1	1	0	0	hsa-miR-663	-0.46	N/A	Sites in UTR
C2orf72	NM_001144994	chromosome 2 open reading frame 72	0	0	0	0	2	0	2	0	hsa-miR-663	-0.46	N/A	Sites in UTR
CC2D1A	NM_017721	coiled-coil and C2 domain containing 1A	0	0	0	0	1	1	0	0	hsa-miR-663	-0.46	N/A	Sites in UTR
ACAP3	NM_030649	ArfGAP with coiled-coil, ankyrin repeat and PH domains 3	0	0	0	0	2	0	2	. 0	hsa-miR-663	-0.46	N/A	Sites in UTR
SERINC2	NM_001199037	serine incorporator 2	0	0	0	0	1	1	0	0	hsa-miR-663	-0.46	N/A	Sites in UTR
ARHGDIA	NM_001185077	Rho GDP dissociation inhibitor (GDI) alpha	0	0	0	0	2	0	2	0	hsa-miR-663	-0.46	N/A	Sites in UTR
CD79A	NM_001783	CD79a molecule, immunoglobulin-associated alpha	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.46	N/A	Sites in UTR
TTBK1	NM_032538	tau tubulin kinase 1	0	0	0	0	1	1	0	0	hsa-miR-663	-0.46	N/A	Sites in UTR
LMX1B	NM_001174146	LIM homeobox transcription factor 1, beta	1	0	0	1	1	0	1	. 0	hsa-miR-1908	-0.46	N/A	Sites in UTR
AGRN	NM_198576	agrin	0	0	0	0	2	0	2	0	hsa-miR-663	-0.46	N/A	Sites in UTR
RAX2	NM_032753	retina and anterior neural fold homeobox 2	0	0	0	0	1	1	0	0	hsa-miR-663	-0.46	N/A	Sites in UTR
TMEM110	NM_198563	transmembrane protein 110	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.46	N/A	Sites in UTR
ADAR	NM_001025107	adenosine deaminase, RNA-specific	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.46	N/A	Sites in UTR
ZCCHC24	NM_153367	zinc finger, CCHC domain containing 24	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.46	N/A	Sites in UTR
SPEF1	NM_015417	sperm flagellar 1	0	0	0	0	2	0	1	. 1	hsa-miR-1908	-0.46	N/A	Sites in UTR
PCDHA9	NM_031857	protocadherin alpha 9	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHAC2	NM_018899	protocadherin alpha subfamily C, 2	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHAC1	NM_018898	protocadherin alpha subfamily C, 1	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR

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PCDHA13	NM_018904	protocadherin alpha 13	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA12	NM_018903	protocadherin alpha 12	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA11	NM_018902	protocadherin alpha 11	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA10	NM_018901	protocadherin alpha 10	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA8	NM_018911	protocadherin alpha 8	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA7	NM_018910	protocadherin alpha 7	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA6	NM_018909	protocadherin alpha 6	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA5	NM_018908	protocadherin alpha 5	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA4	NM_018907	protocadherin alpha 4	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA3	NM_018906	protocadherin alpha 3	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA2	NM_018905	protocadherin alpha 2	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PCDHA1	NM_018900	protocadherin alpha 1	1	1	0	0	0	0	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
PNCK		pregnancy up-regulated non-ubiquitously expressed CaM kinase	0	0	0	0	1	1	0	0	hsa-miR-663	-0.45	N/A	Sites in UTR
ZC3H12D	NM_207360	zinc finger CCCH-type containing 12D	0	0	0	0	2	0	1	1	hsa-miR-663	-0.45	N/A	Sites in UTR
CBFA2T3		core-binding factor, runt domain, alpha subunit 2; translocated to, 3	0	0	0	0	2	0	1	1	hsa-miR-663	-0.45	N/A	Sites in UTR
LLGL1	NM_004140	lethal giant larvae homolog 1 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-663	-0.45	N/A	Sites in UTR
STX16	NM_001001433	syntaxin 16	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.45	N/A	Sites in UTR
KIAA0889	NM_080627	KIAA0889	0	0	0	0	2	0	1	1	hsa-miR-663	-0.45	N/A	Sites in UTR
PLIN4	NM_001080400	perilipin 4	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.45	N/A	Sites in UTR
C1QL1	NM_006688	complement component 1, q subcomponent-like 1	0	0	0	0	2	0	2	0	hsa-miR-663	-0.45	N/A	Sites in UTR

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CDK5R1	NM_003885	cyclin-dependent kinase 5, regulatory subunit 1 (p35)	0	0	0	0	1	1	0	0 hsa-miR-663	-0.45	N/A	Sites in UTR
TIMM13	NM_012458	translocase of inner mitochondrial membrane 13 homolog (yeast)	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.45	N/A	Sites in UTR
SH3GL1	NM_001199943	SH3-domain GRB2-like 1	0	0	0	0	3	0	3	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
SORBS3	NM_001018003	sorbin and SH3 domain containing 3	0	0	0	0	2	0	2	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
P2RY11	NM_002566	purinergic receptor P2Y, G-protein coupled, 11	0	0	0	0	1	1	0	0 hsa-miR-663	-0.44	N/A	Sites in UTR
PPAN-P2RY11	NM_001040664	PPAN-P2RY11 readthrough	0	0	0	0	1	1	0	0 hsa-miR-663	-0.44	N/A	Sites in UTR
BARHL1	NM_020064	BarH-like homeobox 1	0	0	0	0	1	1	0	0 hsa-miR-663	-0.44	N/A	Sites in UTR
RIMS3	NM_014747	regulating synaptic membrane exocytosis 3	0	0	0	0	2	1	1	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
SLC25A1	NM_005984	solute carrier family 25 (mitochondrial carrier; citrate transporter), member 1	0	0	0	0	2	0	1	1 hsa-miR-663	-0.44	N/A	Sites in UTR
AK3	NM_001199852	adenylate kinase 3	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
C15orf41	NM_001130010	chromosome 15 open reading frame 41	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
SNAI3	NM_178310	snail homolog 3 (Drosophila)	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
LRCH4	NM_002319	leucine-rich repeats and calponin homology (CH) domain containing 4	0	0	0	0	2	0	2	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
AATF	NM_012138	apoptosis antagonizing transcription factor	0	0	0	0	1	0	1	0 hsa-miR-663	-0.44	N/A	Sites in UTR
MCF2L2	NM_015078	MCF.2 cell line derived transforming sequence-like 2	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.44	N/A	Sites in UTR
PLEKHG4B	NM_052909	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	0	0	0	0	3	1	2	0 hsa-miR-1908	-0.44	N/A	Sites in UTR
LLGL2	NM_001031803	lethal giant larvae homolog 2 (Drosophila)	0	0	0	0	1	1	0	0 hsa-miR-663	-0.43	N/A	Sites in UTR
SLC2A4RG	NM_020062	SLC2A4 regulator	0	0	0	0	1	1	0	0 hsa-miR-663	-0.43	N/A	Sites in UTR
SKI	NM_003036	v-ski sarcoma viral oncogene homolog (avian)	0	0	0	0	2	0	2	0 hsa-miR-663	-0.43	N/A	Sites in UTR
NCAM1	NM_001076682	neural cell adhesion molecule 1	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.43	N/A	Sites in UTR

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MED15	NM_001003891	mediator complex subunit 15	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
SLC6A1		solute carrier family 6 (neurotransmitter transporter, GABA), member 1	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.43	N/A	Sites in UTR
GREM2	NM_022469	gremlin 2	0	0	0	0	2	0	2	0	hsa-miR-663	-0.43	N/A	Sites in UTR
ZNF275	NM_001080485	zinc finger protein 275	0	0	0	0	2	1	1	0	hsa-miR-1908	-0.43	N/A	Sites in UTR
ATP1B2	NM_001678	ATPase, Na+/K+ transporting, beta 2 polypeptide	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
TNFRSF8	NM_001243	tumor necrosis factor receptor superfamily, member 8	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
ST14	NM_021978	suppression of tumorigenicity 14 (colon carcinoma)	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.43	N/A	Sites in UTR
EXOC4	NM_021807	exocyst complex component 4	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
RILPL1	NM_178314	Rab interacting lysosomal protein-like 1	0	0	0	0	2	0	0	2	hsa-miR-1908	-0.43	N/A	Sites in UTR
ІТРКВ	NM_002221	inositol-trisphosphate 3-kinase B	0	0	0	0	2	0	2	0	hsa-miR-663	-0.43	N/A	Sites in UTR
C17orf39	NM_024052	chromosome 17 open reading frame 39	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
KIFC3	NM_001130099	kinesin family member C3	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.43	N/A	Sites in UTR
KCNQ4	NM_004700	potassium voltage-gated channel, KQT-like subfamily, member 4	0	0	0	0	2	0	1	1	hsa-miR-663	-0.43	N/A	Sites in UTR
SLC11A1	NM_000578	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	0	0	0	0	2	1	0	1	hsa-miR-663	-0.43	N/A	Sites in UTR
EVC	NM_153717	Ellis van Creveld syndrome	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
ZDHHC8	NM_013373	zinc finger, DHHC-type containing 8	0	0	0	0	1	1	0	0	hsa-miR-663	-0.43	N/A	Sites in UTR
LIMS2	NM_001136037	LIM and senescent cell antigen-like domains 2	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.43	N/A	Sites in UTR
CERS1	NM_021267	ceramide synthase 1	0	0	0	0	3	0	3	0	hsa-miR-663	-0.43	N/A	Sites in UTR
TMEM184B	NM_001195071	transmembrane protein 184B	0	0	0	0	1	1	0	0	hsa-miR-663	-0.42	N/A	Sites in UTR
SOST	NM_025237	sclerostin	0	0	0	0	2	0	1	1	hsa-miR-663	-0.42	N/A	Sites in UTR

TNRC18	NM_001080495	trinucleotide repeat containing 18	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.42	N/A	Sites in UTR
PALM	NM_001040134	paralemmin	0	0	0	0	1	1	0	0	hsa-miR-663	-0.42	N/A	Sites in UTR
ZNF653	NM_138783	zinc finger protein 653	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.42	N/A	Sites in UTR
CALML3	NM_005185	calmodulin-like 3	0	0	0	0	1	1	0	0	hsa-miR-663	-0.42	N/A	Sites in UTR
AZU1	NM_001700	azurocidin 1	0	0	0	0	2	0	2	0	hsa-miR-663	-0.42	N/A	Sites in UTR
FAM22G	NM_001045477	family with sequence similarity 22, member G	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.42	N/A	Sites in UTR
HSPA12B	NM_001197327	heat shock 70kD protein 12B	0	0	0	0	2	0	1	1	hsa-miR-663	-0.42	N/A	Sites in UTR
PRR12	NM_020719	proline rich 12	0	0	0	0	3	0	3	0	hsa-miR-663	-0.42	N/A	Sites in UTR
DGKQ	NM_001347	diacylglycerol kinase, theta 110kDa	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.42	N/A	Sites in UTR
EFNA5	NM_001962	ephrin-A5	0	0	0	0	2	0	2	0	hsa-miR-663	-0.42	N/A	Sites in UTR
NXPH3	NM_007225	neurexophilin 3	0	0	0	0	1	1	0	0	hsa-miR-663	-0.42	N/A	Sites in UTR
NRGN	NM_001126181	neurogranin (protein kinase C substrate, RC3)	1	0	1	0	1	0	1	0	hsa-miR-663	-0.42	N/A	Sites in UTR
MYLK2	NM_033118	myosin light chain kinase 2	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.42	N/A	Sites in UTR
PPFIA3	NM_003660	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	1	0	1	0	1	0	1	0	hsa-miR-1908	-0.42	N/A	Sites in UTR
MDM4	NM_001204171	Mdm4 p53 binding protein homolog (mouse)	0	0	0	0	3	0	2	1	hsa-miR-663	-0.41	N/A	Sites in UTR
FLRT1	NM_013280	fibronectin leucine rich transmembrane protein 1	0	0	0	0	2	0	1	1	hsa-miR-663	-0.41	N/A	Sites in UTR
VASH1	NM_014909	vasohibin 1	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.41	N/A	Sites in UTR
CLEC2L	NM_001080511	C-type lectin domain family 2, member L	0	0	0	0	2	0	2	0	hsa-miR-663	-0.41	N/A	Sites in UTR
CYBASC3	NM_001161452	cytochrome b, ascorbate dependent 3	0	0	0	0	1	1	0	0	hsa-miR-663	-0.41	N/A	Sites in UTR
FOXK2	NM_004514	forkhead box K2	0	0	0	0	2	0	1	1	hsa-miR-663	-0.41	N/A	Sites in UTR

IQSEC2	NM_001111125	IQ motif and Sec7 domain 2	0	0	0	0	1	1	0	) hsa-miR-1908	-0.41	N/A	Sites in UTR
C12orf61	NM_175895	chromosome 12 open reading frame 61	0	0	0	0	1	1	0	hsa-miR-1908	-0.41	N/A	Sites in UTR
GALNT2	NM_004481	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N- acetylgalactosaminyltransferase 2 (GalNAc-T2)	0	0	0	0	3	0	3	) hsa-miR-663	-0.41	N/A	Sites in UTR
SCN1B	NM_001037	sodium channel, voltage-gated, type I, beta	0	0	0	0	3	0	3	) hsa-miR-1908	-0.41	N/A	Sites in UTR
HOMER2	NM_004839	homer homolog 2 (Drosophila)	0	0	0	0	2	0	2	) hsa-miR-663	-0.41	N/A	Sites in UTR
LRRC27	NM_001143757	leucine rich repeat containing 27	0	0	0	0	2	0	0 2	hsa-miR-663	-0.41	N/A	Sites in UTR
C1QTNF8	NM_207419	C1q and tumor necrosis factor related protein 8	0	0	0	0	2	0	0 2	hsa-miR-663	-0.41	N/A	Sites in UTR
ANAPC2	NM_013366	anaphase promoting complex subunit 2	0	0	0	0	2	0	1 :	L hsa-miR-663	-0.41	N/A	Sites in UTR
CLCN7	NM_001114331	chloride channel 7	0	0	0	0	2	0	2	) hsa-miR-1908	-0.41	N/A	Sites in UTR
SLC34A2	NM_001177998	solute carrier family 34 (sodium phosphate), member 2	0	0	0	0	2	0	2	) hsa-miR-663	-0.41	N/A	Sites in UTR
CALCOCO2	NM_005831	calcium binding and coiled-coil domain 2	0	0	0	0	1	1	0	) hsa-miR-663	-0.41	N/A	Sites in UTR
NCLN	NM_020170	nicalin	0	0	0	0	2	0	2	) hsa-miR-663	-0.4	N/A	Sites in UTR
SP2	NM_003110	Sp2 transcription factor	0	0	0	0	1	1	0	) hsa-miR-1908	-0.4	N/A	Sites in UTR
TNRC6C	NM_001142640	trinucleotide repeat containing 6C	0	0	0	0	1	1	0	) hsa-miR-663	-0.4	N/A	Sites in UTR
FKBP7	NM_001135212	FK506 binding protein 7	0	0	0	0	2	0	1 :	L hsa-miR-663	-0.4	N/A	Sites in UTR
CYP4F22	NM_173483	cytochrome P450, family 4, subfamily F, polypeptide 22	1	0	1	0	1	0	1 (	) hsa-miR-663	-0.4	N/A	Sites in UTR
ELAVL3	NM_001420	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 3 (Hu antigen C)	0	0	0	0	3	1	2 (	) hsa-miR-663	-0.4	N/A	Sites in UTR
ASB6	NM_001202403	ankyrin repeat and SOCS box containing 6	0	0	0	0	3	0	2	L hsa-miR-1908	-0.4	N/A	Sites in UTR
PHF21B	NM_001135862	PHD finger protein 21B	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.4	N/A	Sites in UTR
PDDC1	NM_182612	Parkinson disease 7 domain containing 1	0	0	0	0	2	0	2 (	) hsa-miR-1908	-0.4	N/A	Sites in UTR

	1			1					1	1		ı	ı	1
тмем63С	NM_020431	transmembrane protein 63C	0	0	0	0	1	1	0	O	hsa-miR-1908	-0.4	N/A	Sites in UTR
HCN2	NM_001194	hyperpolarization activated cyclic nucleotide-gated potassium channel 2	0	0	0	0	2	0	2	0	hsa-miR-663	-0.4	N/A	Sites in UTR
MYADM	NM_001020818	myeloid-associated differentiation marker	0	0	0	0	2	0	2	O	hsa-miR-663	-0.4	N/A	Sites in UTR
CSDC2	NM_014460	cold shock domain containing C2, RNA binding	0	0	0	0	1	1	0	0	hsa-miR-663	-0.4	N/A	Sites in UTR
RGMA	NM_001166283	RGM domain family, member A	0	0	0	0	2	0	1	1	hsa-miR-663	-0.4	N/A	Sites in UTR
MGAT4B	NM_014275	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N- acetylglucosaminyltransferase, isozyme B	0	0	0	0	2	0	2	C	hsa-miR-663	-0.4	N/A	Sites in UTR
СМТМЗ	NM_144601	CKLF-like MARVEL transmembrane domain containing 3	0	0	0	0	1	1	0	O	hsa-miR-663	-0.39	N/A	Sites in UTR
TGFB1	NM_000660	transforming growth factor, beta 1	3	0	3	0	0	0	0	O	hsa-miR-663	-0.39	N/A	Sites in UTR
C16orf55	NM_153025	chromosome 16 open reading frame 55	0	0	0	0	2	0	2	О	hsa-miR-1908	-0.39	N/A	Sites in UTR
UBE2NL	NM_001012989	ubiquitin-conjugating enzyme E2N-like	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.39	N/A	Sites in UTR
NBEAL2	NM_015175	neurobeachin-like 2	0	0	0	0	2	0	2	O	hsa-miR-663	-0.39	N/A	Sites in UTR
CTAGE5	NM_005930	CTAGE family, member 5	0	0	0	0	1	0	1	0	hsa-miR-663	-0.39	N/A	Sites in UTR
KIAA0247	NM_014734	KIAA0247	0	0	0	0	2	0	1	1	hsa-miR-663	-0.39	N/A	Sites in UTR
WBP2	NM_012478	WW domain binding protein 2	0	0	0	0	1	1	0	O	hsa-miR-663	-0.39	N/A	Sites in UTR
DLX2	NM_004405	distal-less homeobox 2	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.39	N/A	Sites in UTR
CABLES1	NM_001100619	Cdk5 and Abl enzyme substrate 1	0	0	0	0	1	1	0	O	hsa-miR-663	-0.39	N/A	Sites in UTR
ARFGAP1	NM_018209	ADP-ribosylation factor GTPase activating protein 1	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.39	N/A	Sites in UTR
GRIN1	NM_000832	glutamate receptor, ionotropic, N-methyl D-aspartate 1	0	0	0	0	2	0	1	1	hsa-miR-663	-0.39	N/A	Sites in UTR
CCR1	NM_001295	chemokine (C-C motif) receptor 1	0	0	0	0	1	1	0	C	hsa-miR-663	-0.39	N/A	Sites in UTR
PAFAH1B2		platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa)	0	0	0	0	1	1	0	C	hsa-miR-663	-0.39	N/A	Sites in UTR

									1			
NM_182894	visual system homeobox 2	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.38	N/A	Sites in UTR
NM_012393	phosphoribosylformylglycinamidine synthase	0	0	0	0	1	0	1 0	hsa-miR-1908	-0.38	N/A	Sites in UTR
NM_001128210	sprouty-related, EVH1 domain containing 2	0	0	0	0	2	0	1 1	. hsa-miR-663	-0.38	N/A	Sites in UTR
NM_015254	kinesin family member 13B	0	0	0	0	1	1	0 0	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_005597	nuclear factor I/C (CCAAT-binding transcription factor)	0	0	0	0	1	1	0 0	hsa-miR-1908	-0.38	N/A	Sites in UTR
NM_001145536	chromosome 17 open reading frame 107	0	0	0	0	3	0	3 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_001080434	lemur tyrosine kinase 3	0	0	0	0	2	0	2 (	hsa-miR-1908	-0.38	N/A	Sites in UTR
NM_005650	transcription factor 20 (AR1)	0	0	0	0	2	0	2 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_152769	chromosome 19 open reading frame 26	0	0	0	0	2	0	2 (	hsa-miR-1908	-0.38	N/A	Sites in UTR
NM_001145102	SMAD family member 3	0	0	0	0	2	1	1 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_001134774	kinesin light chain 2	1	0	1	0	1	0	1 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_058164	olfactomedin 2	0	0	0	0	1	0	1 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_001242659	hypothetical LOC643988	0	0	0	0	2	0	1 1	. hsa-miR-1908	-0.38	N/A	Sites in UTR
NIVI UUTT91060	solute carrier family 25 (mitochondrial carrier: glutamate), member 22	0	0	0	0	2	0	1 1	. hsa-miR-663	-0.38	N/A	Sites in UTR
	pleckstrin homology domain containing, family G (with RhoGef domain) member 5	1	0	1	0	1	0	1 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_005276	glycerol-3-phosphate dehydrogenase 1 (soluble)	0	0	0	0	1	1	0 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_006465	AT rich interactive domain 3B (BRIGHT-like)	0	0	0	0	1	1	0 (	hsa-miR-663	-0.38	N/A	Sites in UTR
NM_032109	orthopedia homeobox	0	0	0	0	2	0	0 2	! hsa-miR-1908	-0.38	N/A	Sites in UTR
NM_002086	growth factor receptor-bound protein 2	0	0	0	0	2	0	2 (	hsa-miR-663	-0.37	N/A	Sites in UTR
NM_033113	zinc finger protein 628	0	0	0	0	1	0	1 (	hsa-miR-663	-0.37	N/A	Sites in UTR
	NM_012393  NM_001128210  NM_001128210  NM_0015254  NM_005597  NM_001145536  NM_001080434  NM_005650  NM_152769  NM_001134774  NM_058164  NM_001242659  NM_001191060  NM_001042663  NM_005276  NM_006465  NM_006465  NM_032109  NM_002086	phosphoribosylformylglycinamidine synthase  NM_001128210 sprouty-related, EVH1 domain containing 2  NM_015254 kinesin family member 13B  NM_005597 nuclear factor I/C (CCAAT-binding transcription factor)  NM_001145536 chromosome 17 open reading frame 107  NM_001080434 lemur tyrosine kinase 3  NM_005650 transcription factor 20 (AR1)  NM_152769 chromosome 19 open reading frame 26  NM_001145102 SMAD family member 3  NM_001134774 kinesin light chain 2  NM_058164 olfactomedin 2  NM_001242659 hypothetical LOC643988  NM_001191060 solute carrier family 25 (mitochondrial carrier: glutamate), member 22  pleckstrin homology domain containing, family G (with RhoGef domain) member 5  NM_005276 glycerol-3-phosphate dehydrogenase 1 (soluble)  NM_006465 AT rich interactive domain 3B (BRIGHT-like)  NM_002086 growth factor receptor-bound protein 2	NM_012393         phosphoribosylformylglycinamidine synthase         0           NM_001128210         sprouty-related, EVH1 domain containing 2         0           NM_015254         kinesin family member 13B         0           NM_005597         nuclear factor I/C (CCAAT-binding transcription factor)         0           NM_001145536         chromosome 17 open reading frame 107         0           NM_001080434         lemur tyrosine kinase 3         0           NM_005650         transcription factor 20 (AR1)         0           NM_152769         chromosome 19 open reading frame 26         0           NM_001145102         SMAD family member 3         0           NM_00114774         kinesin light chain 2         1           NM_0134774         kinesin light chain 2         1           NM_0190142659         hypothetical LOC643988         0           NM_001191060         solute carrier family 25 (mitochondrial carrier: glutamate), member 2         0           NM_001042663         pleckstrin homology domain containing, family G (with RhoGef domain) member 5         1           NM_005276         glycerol-3-phosphate dehydrogenase 1 (soluble)         0           NM_006465         AT rich interactive domain 3B (BRIGHT-like)         0           NM_002086         growth factor receptor-bound protein 2	NM_012393         phosphoribosylformylglycinamidine synthase         0         0           NM_001128210         sprouty-related, EVH1 domain containing 2         0         0           NM_015254         kinesin family member 13B         0         0           NM_005597         nuclear factor I/C (CCAAT-binding transcription factor)         0         0           NM_001145536         chromosome 17 open reading frame 107         0         0           NM_00180434         lemur tyrosine kinase 3         0         0           NM_005650         transcription factor 20 (AR1)         0         0           NM_152769         chromosome 19 open reading frame 26         0         0           NM_001145102         SMAD family member 3         0         0           NM_001134774         kinesin light chain 2         1         0           NM_058164         olfactomedin 2         0         0           NM_01191060         solute carrier family 25 (mitochondrial carrier: glutamate), member 22         0         0           NM_001191060         pleckstrin homology domain containing, family G (with RhoGef domain) member 5         1         0           NM_005276         glycerol-3-phosphate dehydrogenase 1 (soluble)         0         0           NM_005465         AT rich interac	NM_012393         phosphoribosylformylglycinamidine synthase         0         0         0           NM_0123210         sprouty-related, EVH1 domain containing 2         0         0         0           NM_015254         kinesin family member 13B         0         0         0           NM_005597         nuclear factor I/C (CCAAT-binding transcription factor)         0         0         0           NM_001145536         chromosome 17 open reading frame 107         0         0         0           NM_001080434         lemur tyrosine kinase 3         0         0         0           NM_005650         transcription factor 20 (AR1)         0         0         0           NM_058164         chromosome 19 open reading frame 26         0         0         0           NM_001145102         SMAD family member 3         0         0         0           NM_001134774         kinesin light chain 2         1         0         1           NM_058164         olfactomedin 2         0         0         0           NM_001191060         solute carrier family 25 (mitochondrial carrier: glutamate), member 22         0         0         0           NM_001042663         pleckstrin homology domain containing, family G (with shoged domain) member 5         1	NM_012393   phosphoribosylformylglycinamidine synthase	NM_012393         phosphoribosylformylglycinamidine synthase         0         0         0         0         1           NM_0128210         sprouty-related, EVH1 domain containing 2         0         0         0         0         2           NM_015254         kinesin family member 138         0         0         0         0         1           NM_005597         nuclear factor I/C (CCAAT-binding transcription factor)         0         0         0         0         1           NM_001145336         chromosome 17 open reading frame 107         0         0         0         0         3           NM_001080434         lemur tyrosine kinase 3         0         0         0         0         2           NM_005650         transcription factor 20 (AR1)         0         0         0         0         2           NM_152769         chromosome 19 open reading frame 26         0         0         0         0         2           NM_001145102         SMAD family member 3         0         0         0         0         2           NM_01134774         kinesin light chain 2         1         0         1         0         1           NM_058164         olfactomedin 2         0         0         <	NM_012393         phosphoribosylformylglycinamidine synthase         0         0         0         0         1         0           NM_001128210         sprouty-related, EVH1 domain containing 2         0         0         0         0         2         0           NM_015254         kinesin family member 138         0         0         0         0         1         1           NM_005597         nuclear factor I/C (CCAAT-binding transcription factor)         0         0         0         0         1         1           NM_001145536         chromosome 17 open reading frame 107         0         0         0         0         0         0         0         2         0           NM_001080434         lemur tyrosine kinase 3         0         0         0         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         0         0         2         1         1         0         1<	NM_012393         phosphoribosylformylglycinamidine synthase         0         0         0         1         0         1         0         1         0         1         0         1         0         1         0         1         0         1         0         1         0         0         1         0         0         1         1         0         0         1         1         0         0         0         1         1         0         0         0         1         1         0         0         0         1         1         0         0         0         1         1         0         0         0         0         1         1         0         0         0         0         1         1         0         0         0         0         1         1         0         0         0         0         0         1         1         0         0         0         0         0         0         0         0         0         0         2         0         2         0         2         0         0         0         0         0         0         0         0         0         0         0 <t< td=""><td>NM_012833 phosphor/bosylformylglycinamidine synthase 0 0 0 0 0 1 1 0 1 0 has miR-1908 NM_001128210 sprouty-related, EVH1 domain containing 2 0 0 0 0 0 2 0 1 1 has-miR-1908 NM_0015254 kinesin family member 13B 0 0 0 0 1 1 1 0 0 has-miR-663 NM_005397 nuclear factor I/C (CCAAT-binding transcription factor) 0 0 0 0 1 1 1 0 0 has-miR-1908 NM_001185316 chromosome 17 open reading frame 107 0 0 0 0 1 1 1 0 0 has-miR-1908 NM_001185316 chromosome 17 open reading frame 107 0 0 0 0 0 2 0 2 0 has-miR-1908 NM_001080434 temur tyrosine kinase 3 0 0 0 0 0 2 0 2 0 has-miR-1908 NM_00160500 transcription factor 20 (AR1) 0 0 0 0 2 0 2 0 has-miR-1908 NM_005600 transcription factor 20 (AR1) 0 0 0 0 2 0 2 0 has-miR-1908 NM_00134769 chromosome 19 open reading frame 26 0 0 0 0 2 2 0 2 0 has-miR-1908 NM_00134774 kinesin light chain 2 1 0 1 0 1 0 has-miR-663 NM_00134774 kinesin light chain 2 1 0 1 0 1 0 has-miR-663 NM_00134774 kinesin light chain 2 1 0 0 0 0 0 2 0 1 1 has-miR-663 NM_00134769 hypothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_00134669 hypothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_00134669 hypothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 0 2 0 0 1 1 1 0 0 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0</td><td>NM_012393</td><td>NM_012833   phosphorbopy/formylglycinamidin synthase   0   0   0   1   0   1   1   Na-miR-1508   -0.38   NA   NM_0128210   sprouty-related, EVH1 domain containing 2   0   0   0   0   1   1   Na-miR-663   -0.38   NA   NM_0128210   sprouty-related, EVH1 domain containing 2   0   0   0   0   1   1   0   0   Na-miR-663   -0.38   NA   NM_0128210   suncinc factor (VC (CCAAT binding transcription factor)   0   0   0   1   1   0   0   Na-miR-1008   -0.38   NA   NM_012836   chromosome 17 open reading frame 107   0   0   0   0   1   1   0   0   Na-miR-1008   -0.38   NA   NM_01010844   emur tyrosine listuse 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_01010844   emur tyrosine listuse 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_010560   transcription factor 20 (AH1)   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_0101145102   MAP family member 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_01011461102   MAP family member 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_01011461102   MAP family member 3   0   0   0   0   0   2   0   1   0   Na-miR-663   -0.38   NA   NM_01011461102   MAP family member 3   0   0   0   0   0   0   0   0   0  </td></t<>	NM_012833 phosphor/bosylformylglycinamidine synthase 0 0 0 0 0 1 1 0 1 0 has miR-1908 NM_001128210 sprouty-related, EVH1 domain containing 2 0 0 0 0 0 2 0 1 1 has-miR-1908 NM_0015254 kinesin family member 13B 0 0 0 0 1 1 1 0 0 has-miR-663 NM_005397 nuclear factor I/C (CCAAT-binding transcription factor) 0 0 0 0 1 1 1 0 0 has-miR-1908 NM_001185316 chromosome 17 open reading frame 107 0 0 0 0 1 1 1 0 0 has-miR-1908 NM_001185316 chromosome 17 open reading frame 107 0 0 0 0 0 2 0 2 0 has-miR-1908 NM_001080434 temur tyrosine kinase 3 0 0 0 0 0 2 0 2 0 has-miR-1908 NM_00160500 transcription factor 20 (AR1) 0 0 0 0 2 0 2 0 has-miR-1908 NM_005600 transcription factor 20 (AR1) 0 0 0 0 2 0 2 0 has-miR-1908 NM_00134769 chromosome 19 open reading frame 26 0 0 0 0 2 2 0 2 0 has-miR-1908 NM_00134774 kinesin light chain 2 1 0 1 0 1 0 has-miR-663 NM_00134774 kinesin light chain 2 1 0 1 0 1 0 has-miR-663 NM_00134774 kinesin light chain 2 1 0 0 0 0 0 2 0 1 1 has-miR-663 NM_00134769 hypothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_00134669 hypothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_00134669 hypothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 2 0 0 1 1 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 0 2 0 0 1 1 1 0 0 has-miR-663 NM_0013666 phosphothetical ICDG83988 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	NM_012393	NM_012833   phosphorbopy/formylglycinamidin synthase   0   0   0   1   0   1   1   Na-miR-1508   -0.38   NA   NM_0128210   sprouty-related, EVH1 domain containing 2   0   0   0   0   1   1   Na-miR-663   -0.38   NA   NM_0128210   sprouty-related, EVH1 domain containing 2   0   0   0   0   1   1   0   0   Na-miR-663   -0.38   NA   NM_0128210   suncinc factor (VC (CCAAT binding transcription factor)   0   0   0   1   1   0   0   Na-miR-1008   -0.38   NA   NM_012836   chromosome 17 open reading frame 107   0   0   0   0   1   1   0   0   Na-miR-1008   -0.38   NA   NM_01010844   emur tyrosine listuse 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_01010844   emur tyrosine listuse 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_010560   transcription factor 20 (AH1)   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_0101145102   MAP family member 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_01011461102   MAP family member 3   0   0   0   0   2   0   2   0   Na-miR-1008   -0.38   NA   NM_01011461102   MAP family member 3   0   0   0   0   0   2   0   1   0   Na-miR-663   -0.38   NA   NM_01011461102   MAP family member 3   0   0   0   0   0   0   0   0   0

CD40LG	NM_000074	CD40 ligand	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.37	N/A	Sites in UTR
JUNB	NM_002229	jun B proto-oncogene	1	0	1	0	1	0	1	) hsa-miR-663	-0.37	N/A	Sites in UTR
MAPK8IP3	NM_001040439	mitogen-activated protein kinase 8 interacting protein 3	0	0	0	0	2	0	2	) hsa-miR-1908	-0.37	N/A	Sites in UTR
MMP24	NM_006690	matrix metallopeptidase 24 (membrane-inserted)	0	0	0	0	2	0	1	L hsa-miR-663	-0.37	N/A	Sites in UTR
CIAO1	NM_004804	cytosolic iron-sulfur protein assembly 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.37	N/A	Sites in UTR
FAM83H	NM_198488	family with sequence similarity 83, member H	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.37	N/A	Sites in UTR
STARD3	NM_001165937	StAR-related lipid transfer (START) domain containing 3	0	0	0	0	2	0	2	) hsa-miR-663	-0.37	N/A	Sites in UTR
DHTKD1	NM_018706	dehydrogenase E1 and transketolase domain containing 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.37	N/A	Sites in UTR
MAP2K7	NM_145185	mitogen-activated protein kinase kinase 7	0	0	0	0	2	0	2	) hsa-miR-663	-0.37	N/A	Sites in UTR
TBR1	NM_006593	T-box, brain, 1	0	0	0	0	2	0	1 :	L hsa-miR-663	-0.37	N/A	Sites in UTR
NLRP8	NM_176811	NLR family, pyrin domain containing 8	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.37	N/A	Sites in UTR
RAX	NM_013435	retina and anterior neural fold homeobox	0	0	0	0	2	0	0 :	hsa-miR-1908	-0.37	N/A	Sites in UTR
CASZ1	NM_001079843	castor zinc finger 1	1	0	1	0	1	0	0 :	L hsa-miR-663	-0.37	N/A	Sites in UTR
СЕВРА	NM_004364	CCAAT/enhancer binding protein (C/EBP), alpha	0	0	0	0	2	0	0 2	hsa-miR-663	-0.37	N/A	Sites in UTR
DOT1L	NM_032482	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	0	0	0	0	2	0	1 :	L hsa-miR-663	-0.37	N/A	Sites in UTR
CYP8B1	NM_004391	cytochrome P450, family 8, subfamily B, polypeptide 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.36	N/A	Sites in UTR
SARS	NM_006513	seryl-tRNA synthetase	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.36	N/A	Sites in UTR
ANKRD23	NM_144994	ankyrin repeat domain 23	0	0	0	0	3	0	3 (	) hsa-miR-1908	-0.36	N/A	Sites in UTR
WDR7	NM_015285	WD repeat domain 7	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.36	N/A	Sites in UTR
TLX3	NM_021025	T-cell leukemia homeobox 3	0	0	0	0	2	0	2	) hsa-miR-1908	-0.36	N/A	Sites in UTR

NM_001142633	phosphoinositide-3-kinase, regulatory subunit 5	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.36	N/A	Sites in UTR
NM_001083909	G protein-coupled receptor 123	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.36	N/A	Sites in UTR
NM_194272	RNA binding protein with multiple splicing 2	0	0	0	0	2	0	2	) hsa-miR-1908	-0.36	N/A	Sites in UTR
NM_001002838	WNK lysine deficient protein kinase 3	0	0	0	0	1	0	1	) hsa-miR-663	-0.36	N/A	Sites in UTR
NM_001199989	RAS, dexamethasone-induced 1	0	0	0	0	2	0	1	hsa-miR-663	-0.36	N/A	Sites in UTR
NM_001004426	phospholipase A2, group VI (cytosolic, calcium- independent)	0	0	0	0	1	0	1	) hsa-miR-663	-0.36	N/A	Sites in UTR
NM_006422	A kinase (PRKA) anchor protein 3	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.36	N/A	Sites in UTR
NM_018489	ash1 (absent, small, or homeotic)-like (Drosophila)	1	1	0	0	0	0	0 (	) hsa-miR-1908	-0.36	N/A	Sites in UTR
NM_020134	dihydropyrimidinase-like 5	0	0	0	0	2	0	2 (	) hsa-miR-1908	-0.35	N/A	Sites in UTR
NM_080836	serine/threonine kinase 35	0	0	0	0	3	1	1 :	l hsa-miR-1908	-0.35	N/A	Sites in UTR
NM_152654	DAN domain family, member 5	0	0	0	0	2	0	0 2	hsa-miR-663	-0.35	N/A	Sites in UTR
NM_006651	complexin 1	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.35	N/A	Sites in UTR
NM_006206	platelet-derived growth factor receptor, alpha polypeptide	0	0	0	0	1	1	0 (	) hsa-miR-663	-0.35	N/A	Sites in UTR
NM_033036	galactose-3-O-sulfotransferase 3	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.35	N/A	Sites in UTR
NM_001012508	shadow of prion protein homolog (zebrafish)	0	0	0	0	3	0	1 7	hsa-miR-663	-0.35	N/A	Sites in UTR
NM_213568	solute carrier family 39 (zinc transporter), member 3	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.35	N/A	Sites in UTR
NM_024086	methyltransferase like 16	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.35	N/A	Sites in UTR
NM_022825	porcupine homolog (Drosophila)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.35	N/A	Sites in UTR
NM_002699	POU class 3 homeobox 1	1	0	1	0	1	0	1 (	) hsa-miR-663	-0.35	N/A	Sites in UTR
NM_001145204	shisa homolog 9 (Xenopus laevis)	0	0	0	0	1	O	1 (	) hsa-miR-1908	-0.34	N/A	Sites in UTR
	NM_001083909  NM_194272  NM_001002838  NM_001199989  NM_001004426  NM_018489  NM_020134  NM_080836  NM_152654  NM_006651  NM_006651  NM_006206  NM_033036  NM_0131568  NM_011012508  NM_213568  NM_024086  NM_022825  NM_002699	NM_001083909	NM_001083909         G protein-coupled receptor 123         0           NM_194272         RNA binding protein with multiple splicing 2         0           NM_001002838         WNK lysine deficient protein kinase 3         0           NM_001199989         RAS, dexamethasone-induced 1         0           NM_001004426         phospholipase A2, group VI (cytosolic, calcium-independent)         0           NM_006422         A kinase (PRKA) anchor protein 3         0           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1           NM_080836         serine/threonine kinase 35         0           NM_080836         serine/threonine kinase 35         0           NM_05651         complexin 1         0           NM_06651         complexin 1         0           NM_06206         platelet-derived growth factor receptor, alpha polypeptide         0           NM_033036         galactose-3-O-sulfotransferase 3         0           NM_0112508         shadow of prion protein homolog (zebrafish)         0           NM_213568         solute carrier family 39 (zinc transporter), member 3         0           NM_024086         methyltransferase like 16         0           NM_02699         POU class 3 homeobox 1         1	NM_001083909         G protein-coupled receptor 123         0         0           NM_194272         RNA binding protein with multiple splicing 2         0         0           NM_001002838         WNK lysine deficient protein kinase 3         0         0           NM_00119989         RAS, dexamethasone-induced 1         0         0           NM_00104426         phospholipase A2, group VI (cytosolic, calcium-independent)         0         0           NM_006422         A kinase (PRKA) anchor protein 3         0         0           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1           NM_020134         dihydropyrimidinase-like 5         0         0           NM_080836         serine/threonine kinase 35         0         0           NM_152654         DAN domain family, member 5         0         0           NM_006051         complexin 1         0         0           NM_006206         platelet-derived growth factor receptor, alpha polypeptide         0         0           NM_033036         galactose-3-0-sulfotransferase 3         0         0           NM_012508         shadow of prion protein homolog (zebrafish)         0         0           NM_213568         solute carrier family 39 (zinc transporter), member 3<	NM_001083909         G protein-coupled receptor 123         0         0         0           NM_194272         RNA binding protein with multiple splicing 2         0         0         0           NM_001002838         WNK lysine deficient protein kinase 3         0         0         0           NM_001199989         RAS, dexamethasone-induced 1         0         0         0           NM_00104426         phospholipase A2, group VI (cytosolic, calciumindependent)         0         0         0           NM_006422         A kinase (PRKA) anchor protein 3         0         0         0           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1         0           NM_020134         dihydropyrimidinase-like 5         0         0         0           NM_080836         serine/threonine kinase 35         0         0         0           NM_152654         DAN domain family, member 5         0         0         0           NM_006651         complexin 1         0         0         0           NM_006206         platelet-derived growth factor receptor, alpha polypeptide         0         0           NM_033036         galactose-3-O-sulfotransferase 3         0         0         0 <t< td=""><td>NM_001083909         G protein-coupled receptor 123         0         0         0         0           NM_194272         RNA binding protein with multiple splicing 2         0         0         0         0           NM_001002838         WNK lysine deficient protein kinase 3         0         0         0         0           NM_00119989         RAS, dexamethasone-induced 1         0         0         0         0           NM_001004426         phospholipase A2, group VI (cytosolic, calciumindependent)         0         0         0         0           NM_006422         A kinase (PRKA) anchor protein 3         0         0         0         0           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1         0         0           NM_020134         diltydropyrimidinase-like 5         0         0         0         0           NM_080836         serine/threonine kinase 35         0         0         0         0           NM_152654         DAN domain family, member 5         0         0         0         0           NM_006651         complexin 1         0         0         0         0         0           NM_033036         galactose-3-0-sulfotransferase 3         0<td>NM_001083909         G protein-coupled receptor 123         0         0         0         0         1           NM_194272         RNA binding protein with multiple splicing 2         0         0         0         0         2           NM_001002838         WNK lysine deficient protein kinase 3         0         0         0         0         0         1           NM_001109989         RAS, dexamethasone-induced 1         0         0         0         0         0         2           NM_0010004426         phospholipase A2, group VI (rytosolic, calciumingendent)         0         0         0         0         0         1           NM_006422         A kinase (PRKA) anchor protein 3         0         0         0         0         0         1           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1         0         0         0         0         0         1         1           NM_020134         dihydropyrimidinase-like 5         0         0         0         0         2         2           NM_080836         serine/threonine kinase 35         0         0         0         0         2           NM_080836         serine/threonine kinase 35         0</td><td>NM_001083309</td><td>NM_001083909</td><td>NM_001083909</td><td>Not_001002436</td><td>Mal_001038899</td></td></t<>	NM_001083909         G protein-coupled receptor 123         0         0         0         0           NM_194272         RNA binding protein with multiple splicing 2         0         0         0         0           NM_001002838         WNK lysine deficient protein kinase 3         0         0         0         0           NM_00119989         RAS, dexamethasone-induced 1         0         0         0         0           NM_001004426         phospholipase A2, group VI (cytosolic, calciumindependent)         0         0         0         0           NM_006422         A kinase (PRKA) anchor protein 3         0         0         0         0           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1         0         0           NM_020134         diltydropyrimidinase-like 5         0         0         0         0           NM_080836         serine/threonine kinase 35         0         0         0         0           NM_152654         DAN domain family, member 5         0         0         0         0           NM_006651         complexin 1         0         0         0         0         0           NM_033036         galactose-3-0-sulfotransferase 3         0 <td>NM_001083909         G protein-coupled receptor 123         0         0         0         0         1           NM_194272         RNA binding protein with multiple splicing 2         0         0         0         0         2           NM_001002838         WNK lysine deficient protein kinase 3         0         0         0         0         0         1           NM_001109989         RAS, dexamethasone-induced 1         0         0         0         0         0         2           NM_0010004426         phospholipase A2, group VI (rytosolic, calciumingendent)         0         0         0         0         0         1           NM_006422         A kinase (PRKA) anchor protein 3         0         0         0         0         0         1           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1         0         0         0         0         0         1         1           NM_020134         dihydropyrimidinase-like 5         0         0         0         0         2         2           NM_080836         serine/threonine kinase 35         0         0         0         0         2           NM_080836         serine/threonine kinase 35         0</td> <td>NM_001083309</td> <td>NM_001083909</td> <td>NM_001083909</td> <td>Not_001002436</td> <td>Mal_001038899</td>	NM_001083909         G protein-coupled receptor 123         0         0         0         0         1           NM_194272         RNA binding protein with multiple splicing 2         0         0         0         0         2           NM_001002838         WNK lysine deficient protein kinase 3         0         0         0         0         0         1           NM_001109989         RAS, dexamethasone-induced 1         0         0         0         0         0         2           NM_0010004426         phospholipase A2, group VI (rytosolic, calciumingendent)         0         0         0         0         0         1           NM_006422         A kinase (PRKA) anchor protein 3         0         0         0         0         0         1           NM_018489         ash1 (absent, small, or homeotic)-like (Drosophila)         1         1         0         0         0         0         0         1         1           NM_020134         dihydropyrimidinase-like 5         0         0         0         0         2         2           NM_080836         serine/threonine kinase 35         0         0         0         0         2           NM_080836         serine/threonine kinase 35         0	NM_001083309	NM_001083909	NM_001083909	Not_001002436	Mal_001038899

CSNK1G2	NM_001319	casein kinase 1, gamma 2	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
АТР9А	NM_006045	ATPase, class II, type 9A	0	0	0	0	1	1	0	0 hsa-miR-663	-0.34	N/A	Sites in UTR
POFUT2	NM_015227	protein O-fucosyltransferase 2	0	0	0	0	3	0	2	1 hsa-miR-663	-0.34	N/A	Sites in UTR
CYP2B6	NM_000767	cytochrome P450, family 2, subfamily B, polypeptide 6	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
C20orf27	NM_001039140	chromosome 20 open reading frame 27	0	0	0	0	2	0	2	0 hsa-miR-663	-0.34	N/A	Sites in UTR
RAB36	NM_004914	RAB36, member RAS oncogene family	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
NXF1	NM_001081491	nuclear RNA export factor 1	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
AMPD2	NM_004037	adenosine monophosphate deaminase 2	0	0	0	0	1	0	1	0 hsa-miR-663	-0.34	N/A	Sites in UTR
CALR	NM_004343	calreticulin	0	0	0	0	1	0	1	0 hsa-miR-663	-0.34	N/A	Sites in UTR
ETV6	NM_001987	ets variant 6	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
FAM81A	NM_152450	family with sequence similarity 81, member A	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
MLLT6	NM_005937	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6	0	0	0	0	2	0	2	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
LIN28A	NM_024674	lin-28 homolog A (C. elegans)	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.34	N/A	Sites in UTR
TNN	NM_022093	tenascin N	0	0	0	0	1	0	1	0 hsa-miR-663	-0.34	N/A	Sites in UTR
ELF4	NM_001127197	E74-like factor 4 (ets domain transcription factor)	0	0	0	0	1	1	0	0 hsa-miR-663	-0.34	N/A	Sites in UTR
C19orf29	NM_001080543	chromosome 19 open reading frame 29	0	0	0	0	1	0	1	0 hsa-miR-663	-0.34	N/A	Sites in UTR
MYH14	NM_001077186	myosin, heavy chain 14, non-muscle	0	0	0	0	1	0	1	0 hsa-miR-663	-0.34	N/A	Sites in UTR
C20orf144	NM_080825	chromosome 20 open reading frame 144	0	0	0	0	1	0	1	0 hsa-miR-663	-0.34	N/A	Sites in UTR
PHF15	NM_015288	PHD finger protein 15	0	0	0	0	2	0	2	0 hsa-miR-1908	-0.34	N/A	Sites in UTR
ЕРНВ2	NM_004442	EPH receptor B2	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.34	N/A	Sites in UTR

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NM_001109	ADAM metallopeptidase domain 8	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_004745	discs, large (Drosophila) homolog-associated protein 2	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_001005505	calcium channel, voltage-dependent, alpha 2/delta subunit 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_001008563	ubiquitin specific peptidase 20	0	0	0	0	1	0	1	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_001220765	IKAROS family zinc finger 1 (Ikaros)	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_020765	ubiquitin protein ligase E3 component n-recognin 4	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_001049	somatostatin receptor 1	0	0	0	0	2	0	0	2	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_146388	mitochondrial ribosomal protein L4	0	0	0	0	2	0	2	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_001099456	neuropeptide W	0	0	0	0	2	0	2	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_001127649	peroxisomal biogenesis factor 26	0	0	0	0	1	1	0	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_006772	synaptic Ras GTPase activating protein 1	0	0	0	0	2	0	1	1	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_007014	WW domain containing E3 ubiquitin protein ligase 2	0	0	0	0	2	0	0	2	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_001039517	RUSC1 antisense RNA 1 (non-protein coding)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_016069	presequence translocase-associated motor 16 homolog (S. cerevisiae)	0	0	0	0	2	0	2	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_001201479	CORO7-PAM16 readthrough	0	0	0	0	2	0	2	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_178557	N-acetyltransferase 8-like (GCN5-related, putative)	0	0	0	0	3	0	3	0	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_003032	ST6 beta-galactosamide alpha-2,6-sialyltranferase 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_001042402	N-acylethanolamine acid amidase	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.33	N/A	Sites in UTR
NM_032779	coiled-coil domain containing 142	0	0	0	0	1	0	1	0	hsa-miR-663	-0.33	N/A	Sites in UTR
NM_001008693	cystatin 9 (testatin)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.33	N/A	Sites in UTR
	NM_004745  NM_001005505  NM_001008563  NM_001220765  NM_020765  NM_001049  NM_146388  NM_001099456  NM_001127649  NM_006772  NM_007014  NM_007014  NM_016069  NM_01201479  NM_178557  NM_003032  NM_001042402  NM_001042402  NM_032779	NM_00103505 discs, large (Drosophila) homolog-associated protein 2  NM_001005505 calcium channel, voltage-dependent, alpha 2/delta subunit 2  NM_001008563 ubiquitin specific peptidase 20  NM_001220765 IKAROS family zinc finger 1 (Ikaros)  NM_020765 ubiquitin protein ligase E3 component n-recognin 4  NM_001049 somatostatin receptor 1  NM_146388 mitochondrial ribosomal protein L4  NM_001099456 neuropeptide W  NM_001127649 peroxisomal biogenesis factor 26  NM_006772 synaptic Ras GTPase activating protein 1  NM_007014 WW domain containing E3 ubiquitin protein ligase 2  NM_001039517 RUSC1 antisense RNA 1 (non-protein coding)  NM_016069 presequence translocase-associated motor 16 homolog (S. cerevisiae)  NM_001201479 CORO7-PAM16 readthrough  NM_178557 N-acetyltransferase 8-like (GCN5-related, putative)  NM_003032 ST6 beta-galactosamide alpha-2,6-sialyltranferase 1  NM_001042402 N-acylethanolamine acid amidase  NM_032779 coiled-coil domain containing 142	NM_001005505 calcium channel, voltage-dependent, alpha 2/delta subunit 2 0  NM_001005505 ubiquitin specific peptidase 20 0  NM_001008563 ubiquitin specific peptidase 20 0  NM_001220765 IKAROS family zinc finger 1 (Ikaros) 0  NM_001049 somatostatin receptor 1 0  NM_001049 somatostatin receptor 1 0  NM_001099456 neuropeptide W 0  NM_001099456 peroxisomal biogenesis factor 26 0  NM_001722 synaptic Ras GTPase activating protein 1 0  NM_007014 WW domain containing E3 ubiquitin protein ligase 2 0  NM_001039517 RUSC1 antisense RNA 1 (non-protein coding) 0  NM_016069 presequence translocase-associated motor 16 homolog (S. cerevisiae) 0  NM_0178557 N-acetyltransferase 8-like (GCN5-related, putative) 0  NM_003032 ST6 beta-galactosamide alpha-2,6-sialyltranferase 1 0  NM_001042402 N-acylethanolamine acid amidase 0  NM_032779 coiled-coil domain containing 142 0	NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0           NM_001008563         ubiquitin specific peptidase 20         0         0           NM_0010220765         IKAROS family zinc finger 1 (likaros)         0         0           NM_020765         ubiquitin protein ligase E3 component n-recognin 4         0         0           NM_020765         ubiquitin protein ligase E3 component n-recognin 4         0         0           NM_01049         somatostatin receptor 1         0         0           NM_146388         mitochondrial ribosomal protein L4         0         0           NM_01099456         neuropeptide W         0         0           NM_001127649         peroxisomal biogenesis factor 26         0         0           NM_006772         synaptic Ras GTPase activating protein 1         0         0           NM_007014         WW domain containing E3 ubiquitin protein ligase 2         0         0           NM_001039517         RUSC1 antisense RNA 1 (non-protein coding)         0         0           NM_016069         presequence translocase-associated motor 16 homolog (S. cerevisiae)         0         0	NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0         0           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0           NM_001220765         IKAROS family zinc finger 1 (Ikaros)         0         0         0         0           NM_020765         ubiquitin protein ligase E3 component n-recognin 4         0         0         0         0           NM_021049         somatostatin receptor 1         0         0         0         0           NM_146388         mitochondrial ribosomal protein L4         0         0         0         0           NM_020199456         neuropeptide W         0         0         0         0         0           NM_00172649         peroxisomal biogenesis factor 26         0         0         0         0           NM_006772         synaptic Ras GTPase activating protein 1         0         0         0           NM_007014         WW domain containing E3 ubiquitin protein ligase 2         0         0         0           NM_010669         gresquence translocase-associated motor 16 homolog (s. cerevisiae)	NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         0           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0         0         0           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0           NM_001220765         IKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0           NM_020765         ubiquitin protein ligase E3 component n-recognin 4         0         0         0         0           NM_021049         somatostatin receptor 1         0         0         0         0         0           NM_01049         somatostatin receptor 1         0         0         0         0         0         0           NM_01499         somatostatin receptor 1         0         0         0         0         0         0         0           NM_01569         neuropeptide W         0         0         0         0         0         0         0         0         0           NM_00127649         peroxisomal biogenesis factor 26         0         0         0         0         0         0         0 <td>NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         0         2           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0         0         0         0         1           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0         0         1           NM_001220765         IKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0         0         0         1           NM_001049         somatostatin receptor 1         0         0         0         0         0         2           NM_146388         mitochondrial ribosomal protein L4         0         0         0         0         2           NM_001099456         neuropeptide W         0         0         0         0         2           NM_001127649         peroxisomal biogenesis factor 26         0         0         0         0         1           NM_007772         synaptic Ras GTPase activating protein I         0         0         0         0         2           NM_007014         WW domain containing E3 ubiquitin protein ligase 2         0         0</td> <td>NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         0         2         0           NM_001008505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0         0         0         1         0           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0         1         0           NM_00120765         MKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0         2         0           NM_020765         ubiquitin protein ligase E3 component n-recognin 4         0         0         0         0         1         0           NM_0201099         somatostatin receptor 1         0         0         0         0         2         0           NM_146388         mitochondrial ribosomal protein L4         0         0         0         0         2         0           NM_001099456         neuropeptide W         0         0         0         0         2         0           NM_001027649         peroxisomal biogenesis factor 26         0         0         0         0         1         1           NM_006772         synaptic</td> <td>NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         2         0         1           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta         0         0         0         0         1         0         1           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0         0         1         0         1           NM_001220765         IKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0         1         0         1         1           NM_0010965         ubiquitin protein ligase E3 component n-recognin 4         0         0         0         0         1         0         1         1         1           NM_001099         somatostatin receptor 1         0         0         0         0         2         0         0         0         2         0         0         0         2         0         0         0         2         0         2         0         0         2         0         0         2         0         0         2         0         2         0         2         0         2         <td< td=""><td>NM_00108505</td><td>NM_004745 discs, large (Drosophila) homolog-associated protein 2 0 0 0 0 0 1 1 1 has miR-1908  NM_001005505 calcium channel, voltage-dependent, alpha 2/delta obubula?  NM_001008563 ubiquith spacific peptidase 20 0 0 0 0 1 1 0 1 0 has miR-1908  NM_00120765 RAROS family zinc finger 1 (Raros) 0 0 0 0 0 1 1 0 1 1 has miR-1908  NM_00120765 ubiquith protein ligase E3 component n-recognin 4 0 0 0 0 1 1 0 1 0 has miR-1908  NM_001049 somatostatin receptor 1 0 0 0 0 0 2 0 0 1 has miR-1908  NM_001049 somatostatin receptor 1 0 0 0 0 0 2 0 0 2 has miR-663  NM_001049 neuropeptide W 0 0 0 0 2 0 0 2 0 has miR-663  NM_001079456 neuropeptide W 0 0 0 0 2 0 0 2 0 has miR-663  NM_001127849 prososomal biogenesis factor 26 0 0 0 0 1 1 0 0 has miR-663  NM_006772 synaptic Ras GTPase activating protein 1 0 0 0 0 2 0 1 1 has miR-1908  NM_007014 WW domain containing E3 ubiquitin protein ligase 2 0 0 0 0 2 1 0 has miR-663  NM_010109517 RUSC1 antisense RNA 1 (non protein coding) 0 0 0 0 2 0 2 0 2 0 has miR-663  NM_015666 presequence translocase-associated motor 16 homolog 6 C cerevisiae)  NM_015677 Nacepharase 8 like (GCNS related, putative) 0 0 0 0 1 1 0 1 0 has miR-663  NM_00101201479 CORO7-PAMAIS readthrough 0 0 0 0 1 1 0 1 0 has miR-663  NM_00103012 ST6 bets galactosamide alpha 2.6 slalytranferase 1 0 0 0 0 1 1 0 1 0 has miR-1908  NM_001042402 N-acylethanolamine acid amidase 0 0 0 0 1 1 0 1 0 has miR-1908</td><td>MM_004715 discs, large (1/thooganila) homolog associated protein 2</td><td>MM_00108565 should be calculated and a control of the control of t</td></td<></td>	NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         0         2           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0         0         0         0         1           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0         0         1           NM_001220765         IKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0         0         0         1           NM_001049         somatostatin receptor 1         0         0         0         0         0         2           NM_146388         mitochondrial ribosomal protein L4         0         0         0         0         2           NM_001099456         neuropeptide W         0         0         0         0         2           NM_001127649         peroxisomal biogenesis factor 26         0         0         0         0         1           NM_007772         synaptic Ras GTPase activating protein I         0         0         0         0         2           NM_007014         WW domain containing E3 ubiquitin protein ligase 2         0         0	NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         0         2         0           NM_001008505         calcium channel, voltage-dependent, alpha 2/delta subunit 2         0         0         0         0         1         0           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0         1         0           NM_00120765         MKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0         2         0           NM_020765         ubiquitin protein ligase E3 component n-recognin 4         0         0         0         0         1         0           NM_0201099         somatostatin receptor 1         0         0         0         0         2         0           NM_146388         mitochondrial ribosomal protein L4         0         0         0         0         2         0           NM_001099456         neuropeptide W         0         0         0         0         2         0           NM_001027649         peroxisomal biogenesis factor 26         0         0         0         0         1         1           NM_006772         synaptic	NM_004745         discs, large (Drosophila) homolog-associated protein 2         0         0         0         2         0         1           NM_001005505         calcium channel, voltage-dependent, alpha 2/delta         0         0         0         0         1         0         1           NM_001008563         ubiquitin specific peptidase 20         0         0         0         0         0         0         1         0         1           NM_001220765         IKAROS family zinc finger 1 (Ikaros)         0         0         0         0         0         1         0         1         1           NM_0010965         ubiquitin protein ligase E3 component n-recognin 4         0         0         0         0         1         0         1         1         1           NM_001099         somatostatin receptor 1         0         0         0         0         2         0         0         0         2         0         0         0         2         0         0         0         2         0         2         0         0         2         0         0         2         0         0         2         0         2         0         2         0         2 <td< td=""><td>NM_00108505</td><td>NM_004745 discs, large (Drosophila) homolog-associated protein 2 0 0 0 0 0 1 1 1 has miR-1908  NM_001005505 calcium channel, voltage-dependent, alpha 2/delta obubula?  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LAMB3	NM_000228	laminin, beta 3	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
PPID	NM_005038	peptidylprolyl isomerase D	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
NEUROD2	NM_006160	neurogenic differentiation 2	1	0	1	0	2	0	2	0	hsa-miR-663	-0.32	N/A	Sites in UTR
PITPNB	NM_012399	phosphatidylinositol transfer protein, beta	0	0	0	0	1	1	0	0	hsa-miR-663	-0.32	N/A	Sites in UTR
HEYL	NM_014571	hairy/enhancer-of-split related with YRPW motif-like	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
ADAMTS15		ADAM metallopeptidase with thrombospondin type 1 motif, 15	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
MAD2L2	NM_001127325	MAD2 mitotic arrest deficient-like 2 (yeast)	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
LRRC8A	NM_001127244	leucine rich repeat containing 8 family, member A	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
C7orf29	NM_138434	chromosome 7 open reading frame 29	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
PPIL2	NM_014337	peptidylprolyl isomerase (cyclophilin)-like 2	0	0	0	0	2	0	1	. 1	hsa-miR-663	-0.32	N/A	Sites in UTR
FOXI2	NM_207426	forkhead box I2	0	0	0	0	1	1	0	0	hsa-miR-663	-0.32	N/A	Sites in UTR
SIGLEC7	NM_014385	sialic acid binding Ig-like lectin 7	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
SPSB3	NM_080861	spIA/ryanodine receptor domain and SOCS box containing 3	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
SH2D1B	NM_053282	SH2 domain containing 1B	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
C6orf141	NM_001145652	chromosome 6 open reading frame 141	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
GYS1	NM_001161587	glycogen synthase 1 (muscle)	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
GDAP1L1	INIVI UZ4U34	ganglioside-induced differentiation-associated protein 1- like 1	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
SRRM4	NM_194286	serine/arginine repetitive matrix 4	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.32	N/A	Sites in UTR
AQP10	NM_080429	aquaporin 10	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.32	N/A	Sites in UTR
RHBDD1	NM_001167608	rhomboid domain containing 1	0	0	0	0	1	1	0	0	hsa-miR-663	-0.32	N/A	Sites in UTR

KIF21B	NM_017596	kinesin family member 21B	0	0	0	0	3	1	2	) hsa-miR-663	-0.32	N/A	Sites in UTR
SOBP	NM_018013	sine oculis binding protein homolog (Drosophila)	0	0	0	0	2	0	2	) hsa-miR-663	-0.32	N/A	Sites in UTR
SEC22C	NM_032970	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	0	0	0	0	1	1	0	) hsa-miR-1908	-0.32	N/A	Sites in UTR
PLOD3	NM_001084	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 3	0	0	0	0	1	0	1	) hsa-miR-663	-0.32	N/A	Sites in UTR
ADCYAP1R1	NM_001118	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.32	N/A	Sites in UTR
EEPD1	NM_030636	endonuclease/exonuclease/phosphatase family domain containing 1	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.32	N/A	Sites in UTR
DENND5A	NM_015213	DENN/MADD domain containing 5A	0	0	0	0	1	0	0 :	1 hsa-miR-1908	-0.31	N/A	Sites in UTR
ASB16	NM_080863	ankyrin repeat and SOCS box containing 16	0	0	0	0	1	0	1	) hsa-miR-663	-0.31	N/A	Sites in UTR
CYTH2	NM_004228	cytohesin 2	1	0	1	0	1	0	0 :	1 hsa-miR-663	-0.31	N/A	Sites in UTR
CNBP	NM_001127192	CCHC-type zinc finger, nucleic acid binding protein	0	0	0	0	3	0	1	2 hsa-miR-1908	-0.31	N/A	Sites in UTR
GPSM3	NM_022107	G-protein signaling modulator 3	0	0	0	0	1	0	1	) hsa-miR-1908	-0.31	N/A	Sites in UTR
САМКМТ	NM_024766	calmodulin-lysine N-methyltransferase	0	0	0	0	1	0	1	) hsa-miR-1908	-0.31	N/A	Sites in UTR
ZNF490	NM_020714	zinc finger protein 490	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.31	N/A	Sites in UTR
ABLIM3	NM_014945	actin binding LIM protein family, member 3	0	0	0	0	1	1	0	) hsa-miR-1908	-0.31	N/A	Sites in UTR
NACC2	NM_144653	NACC family member 2, BEN and BTB (POZ) domain containing	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.31	N/A	Sites in UTR
RBCK1	NM_006462	RanBP-type and C3HC4-type zinc finger containing 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.31	N/A	Sites in UTR
MAPKBP1	NM_001128608	mitogen-activated protein kinase binding protein 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.31	N/A	Sites in UTR
FOXN4	NM_213596	forkhead box N4	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.31	N/A	Sites in UTR
VPS37D	NM_001077621	vacuolar protein sorting 37 homolog D (S. cerevisiae)	1	0	1	0	0	0	0 (	) hsa-miR-663	-0.31	N/A	Sites in UTR
RS1	NM_000330	retinoschisin 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.31	N/A	Sites in UTR

PCIF1	NM_022104	PDX1 C-terminal inhibiting factor 1	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.31	N/A	Sites in UTR
KCTD2	NM_015353	potassium channel tetramerisation domain containing 2	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.31	N/A	Sites in UTR
KALRN	NM_003947	kalirin, RhoGEF kinase	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.31	N/A	Sites in UTR
SNRNP200	NM_014014	small nuclear ribonucleoprotein 200kDa (U5)	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.31	N/A	Sites in UTR
OTUB1	NM_017670	OTU domain, ubiquitin aldehyde binding 1	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.31	N/A	Sites in UTR
FIZ1	NM_032836	FLT3-interacting zinc finger 1	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.31	N/A	Sites in UTR
GLI3	NM_000168	GLI family zinc finger 3	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.31	N/A	Sites in UTR
KIAA0556	NM_015202	KIAA0556	0	0	0	0	2	0	0	2	hsa-miR-1908	-0.31	N/A	Sites in UTR
MMP15	NM_002428	matrix metallopeptidase 15 (membrane-inserted)	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.31	N/A	Sites in UTR
TSPAN31	NM_005981	tetraspanin 31	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.31	N/A	Sites in UTR
CELF5	NM_001172673	CUGBP, Elav-like family member 5	0	0	0	0	2	0	1	. 1	hsa-miR-663	-0.31	N/A	Sites in UTR
TBC1D30	NM_015279	TBC1 domain family, member 30	0	0	0	0	1	0	1		hsa-miR-663	-0.3	N/A	Sites in UTR
DUSP14	NM_007026	dual specificity phosphatase 14	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.3	N/A	Sites in UTR
PACSIN2	NM_001184970	protein kinase C and casein kinase substrate in neurons 2	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.3	N/A	Sites in UTR
ZNF219	NM_001101672	zinc finger protein 219	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.3	N/A	Sites in UTR
GAS7	NM_001130831	growth arrest-specific 7	0	0	0	0	2	0	0	2	hsa-miR-663	-0.3	N/A	Sites in UTR
ZBTB7A	NM_015898	zinc finger and BTB domain containing 7A	0	0	0	0	2	0	2	. 0	hsa-miR-663	-0.3	N/A	Sites in UTR
CDC42EP1	NM_152243	CDC42 effector protein (Rho GTPase binding) 1	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.3	N/A	Sites in UTR
SEZ6	NM_001098635	seizure related 6 homolog (mouse)	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.3	N/A	Sites in UTR
RASL12	NM_016563	RAS-like, family 12	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.3	N/A	Sites in UTR

NM_017712	pyroglutamyl-peptidase I	0	0	0	0	1	0	1	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_001170686	mindbomb homolog 2 (Drosophila)	0	0	0	0	1	0	1	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_020382	SET domain containing (lysine methyltransferase) 8	0	0	0	0	1	0	1	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_001440	exostoses (multiple)-like 3	0	0	0	0	2	0	2	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_000501	elastin	0	0	0	0	1	0	1	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_152569	chromosome 9 open reading frame 66	0	0	0	0	1	0	1	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_032329	inhibitor of growth family, member 5	0	0	0	0	3	0	2	L hsa-miR-663	-0.3	N/A	Sites in UTR
NM_001077238	signal peptide peptidase-like 2B	0	0	0	0	2	0	0 :	2 hsa-miR-663	-0.3	N/A	Sites in UTR
NM_017409	homeobox C10	1	0	1	0	0	0	0 (	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_015431	tripartite motif containing 58	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_153018	zinc finger protein 3 homolog (mouse)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_183373	chromosome 6 open reading frame 145	0	0	0	0	1	0	1	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_021943	zinc finger, AN1-type domain 3	0	0	0	0	2	0	2 (	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_033259	calcium/calmodulin-dependent protein kinase II inhibitor 2	0	0	0	0	2	O	2 (	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_001142622	GH3 domain containing	0	0	0	0	1	O	1 (	) hsa-miR-663	-0.3	N/A	Sites in UTR
NM_001145873	CD8a molecule	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_001135147	solute carrier family 39 (zinc transporter), member 8	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_001163323	coiled-coil domain containing 120	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_002360	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	0	0	0	0	2	0	0 :	hsa-miR-1908	-0.3	N/A	Sites in UTR
NM_001199723	cellular retinoic acid binding protein 2	0	0	0	0	1	O	1 (	) hsa-miR-663	-0.3	N/A	Sites in UTR
	NM_001170686  NM_001440  NM_000501  NM_152569  NM_032329  NM_001077238  NM_017409  NM_015431  NM_153018  NM_153018  NM_183373  NM_021943  NM_033259  NM_001142622  NM_001145873  NM_001135147  NM_001163323  NM_002360	NM_001170686 mindbomb homolog 2 (Drosophila)  NM_020382 SET domain containing (lysine methyltransferase) 8  NM_001440 exostoses (multiple)-like 3  NM_000501 elastin  NM_152569 chromosome 9 open reading frame 66  NM_032329 inhibitor of growth family, member 5  NM_001077238 signal peptide peptidase-like 2B  NM_017409 homeobox C10  NM_015431 tripartite motif containing 58  NM_153018 zinc finger protein 3 homolog (mouse)  NM_183373 chromosome 6 open reading frame 145  NM_021943 zinc finger, AN1-type domain 3  NM_033259 calcium/calmodulin-dependent protein kinase II inhibitor 2  NM_001142622 GH3 domain containing  NM_001145873 CD8a molecule  NM_001135147 solute carrier family 39 (zinc transporter), member 8  NM_001163323 coiled-coil domain containing 120  V-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	NM_001170686         mindbomb homolog 2 (Drosophila)         0           NM_020382         SET domain containing (lysine methyltransferase) 8         0           NM_001440         exostoses (multiple)-like 3         0           NM_000501         elastin         0           NM_152569         chromosome 9 open reading frame 66         0           NM_032329         inhibitor of growth family, member 5         0           NM_017409         homeobox C10         1           NM_017409         homeobox C10         1           NM_153018         zinc finger protein 3 homolog (mouse)         0           NM_153018         zinc finger protein 3 homolog (mouse)         0           NM_021943         zinc finger, AN1-type domain 3         0           NM_033259         calcium/calmodulin-dependent protein kinase II inhibitor 2         0           NM_033259         Calcium/calmodulin-dependent protein kinase II inhibitor 2         0           NM_01142622         GH3 domain containing         0           NM_01145873         CD8a molecule         0           NM_01163323         coiled-coil domain containing 120         0           NM_002360         v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)         0	NM_001170686         mindbomb homolog 2 (Drosophila)         0         0           NM_020382         SET domain containing (lysine methyltransferase) 8         0         0           NM_001440         exostoses (multiple)-like 3         0         0           NM_000501         elastin         0         0           NM_000501         elastin         0         0           NM_152569         chromosome 9 open reading frame 66         0         0           NM_032329         inhibitor of growth family, member 5         0         0           NM_017409         signal peptide peptidase-like 2B         0         0           NM_017409         homeobox C10         1         0           NM_015431         tripartite motif containing 58         0         0           NM_153018         zinc finger protein 3 homolog (mouse)         0         0           NM_183373         chromosome 6 open reading frame 145         0         0           NM_021943         zinc finger, AN1-type domain 3         0         0           NM_033259         calcium/calmodulin-dependent protein kinase II inhibitor 2         0         0           NM_001145873         CD8a molecule         0         0           NM_001163323         colled-coil domain	NM_001170686         mindbomb homolog 2 (Drosophila)         0         0         0           NM_020382         SET domain containing (lysine methyltransferase) 8         0         0         0           NM_0201440         exostoses (multiple)-like 3         0         0         0           NM_000501         elastin         0         0         0           NM_152569         chromosome 9 open reading frame 66         0         0         0           NM_032329         inhibitor of growth family, member 5         0         0         0           NM_017409         homeobox C10         1         0         1           NM_015431         tripartite motif containing 58         0         0         0           NM_153018         zinc finger protein 3 homolog (mouse)         0         0         0           NM_183373         chromosome 6 open reading frame 145         0         0         0           NM_03259         calcium/calmodulin-dependent protein kinase II inhibitor         0         0         0           NM_03145873         CD8a molecule         0         0         0           NM_001145873         CD8a molecule         0         0         0           NM_00163323         colled-coil domain containing 12	NM_001170686         mindbomb homolog 2 (Drosophila)         0         0         0         0           NM_020382         SET domain containing (lysine methyltransferase) 8         0         0         0         0           NM_001440         exostoses (multiple)-like 3         0         0         0         0           NM_000501         elastin         0         0         0         0           NM_152569         chromosome 9 open reading frame 66         0         0         0         0           NM_032329         inhibitor of growth family, member 5         0         0         0         0           NM_017409         homeobox C10         1         0         1         0         0           NM_015431         tripartite motif containing 58         0         0         0         0           NM_153018         zinc finger protein 3 homolog (mouse)         0         0         0         0           NM_183373         chromosome 6 open reading frame 145         0         0         0         0           NM_021943         zinc finger, AN1-type domain 3         0         0         0         0           NM_033259         calclum/calmodulin-dependent protein kinase II inhibitor         0         0	NM_001170686         mindbomb homolog 2 (Drosophila)         0         0         0         0         0         1           NM_020382         SET domain containing (lysine methyltransferase) 8         0         0         0         0         0         1           NM_001440         exostoses (multiple)-like 3         0         0         0         0         0         0         2           NM_000501         elastin         0         0         0         0         0         0         1           NM_152569         chromosome 9 open reading frame 66         0         0         0         0         0         1           NM_032329         inhibitor of growth family, member 5         0         0         0         0         0         3           NM_017409         homeobox C10         1         0         1         0         0         0         2           NM_015431         tripartite motif containing 58         0         0         0         0         1           NM_153018         zinc finger protein 3 homolog (mouse)         0         0         0         0         1           NM_153318         zinc finger, AN1-type domain 3         0         0         0         0 </td <td>NM_001170686         mindbomb homolog 2 (Drosophila)         0         0         0         0         1         0           NM_020382         SET domain containing (lysine methyltransferase) 8         0         0         0         0         1         0           NM_001440         exostoses (multiple)-like 3         0         0         0         0         0         2         0           NM_000501         elastin         0         0         0         0         0         1         0           NM_152569         chromosome 9 open reading frame 66         0         0         0         0         0         1         0           NM_032329         inhibitor of growth family, member 5         0         0         0         0         0         3         0           NM_017409         homeobox C10         1         0         1         0         1         0         0</td> <td>NM_001170686 mindbomb homolog 2 (torosophila) 0 0 0 0 0 1 0 0 1 0 1 0 1 0 0 1 1 0 0 0 1 1 0</td> <td>NM_00170868   mindbomb homolog 2 (Drosophila)   0   0   0   0   0   1   0   1   0   Na-miR-1908   NM_001868   mindbomb homolog 2 (Drosophila)   0   0   0   0   0   0   1   0   1   0   Na-miR-1908   NM_001400   exostoses (multiple) like 3   0   0   0   0   0   0   0   2   0   0</td> <td>MM_001170666 mendebamb benoteg 2 (Drosophila)</td> <td>Md_C011706666 mindbomb homolog 2 (Drosophila)</td>	NM_001170686         mindbomb homolog 2 (Drosophila)         0         0         0         0         1         0           NM_020382         SET domain containing (lysine methyltransferase) 8         0         0         0         0         1         0           NM_001440         exostoses (multiple)-like 3         0         0         0         0         0         2         0           NM_000501         elastin         0         0         0         0         0         1         0           NM_152569         chromosome 9 open reading frame 66         0         0         0         0         0         1         0           NM_032329         inhibitor of growth family, member 5         0         0         0         0         0         3         0           NM_017409         homeobox C10         1         0         1         0         1         0         0	NM_001170686 mindbomb homolog 2 (torosophila) 0 0 0 0 0 1 0 0 1 0 1 0 1 0 0 1 1 0 0 0 1 1 0	NM_00170868   mindbomb homolog 2 (Drosophila)   0   0   0   0   0   1   0   1   0   Na-miR-1908   NM_001868   mindbomb homolog 2 (Drosophila)   0   0   0   0   0   0   1   0   1   0   Na-miR-1908   NM_001400   exostoses (multiple) like 3   0   0   0   0   0   0   0   2   0   0	MM_001170666 mendebamb benoteg 2 (Drosophila)	Md_C011706666 mindbomb homolog 2 (Drosophila)

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SLC1A7	NM_006671	solute carrier family 1 (glutamate transporter), member 7	0	0	0	0	1	0 1	0 hsa-miR-1908	-0.3	N/A	Sites in UTR
FSCN1	NM_003088	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus)	0	0	0	0	1	0	L 0 hsa-miR-663	-0.3	B N/A	Sites in UTR
STAM2	NM_005843	signal transducing adaptor molecule (SH3 domain and ITAM motif) 2	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.3	N/A	Sites in UTR
HCST	NM_001007469	hematopoietic cell signal transducer	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.3	N/A	Sites in UTR
ZCCHC3	NM_033089	zinc finger, CCHC domain containing 3	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.3	B N/A	Sites in UTR
SIM2	NM_005069	single-minded homolog 2 (Drosophila)	0	0	0	0	1	0 2	l 0 hsa-miR-1908	-0.29	N/A	Sites in UTR
PGS1	NM_024419	phosphatidylglycerophosphate synthase 1	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.29	N/A	Sites in UTR
OLFM1	NM_014279	olfactomedin 1	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.29	N/A	Sites in UTR
TUBA8	NM_001193414	tubulin, alpha 8	0	0	0	0	1	0 2	0 hsa-miR-1908	-0.29	N/A	Sites in UTR
GPR173	NM_018969	G protein-coupled receptor 173	0	0	0	0	1	0 2	0 hsa-miR-1908	-0.29	N/A	Sites in UTR
C2CD4C	NM_001136263	C2 calcium-dependent domain containing 4C	0	0	0	0	1	0 3	0 hsa-miR-663	-0.29	N/A	Sites in UTR
DACT2	NM_214462	dapper, antagonist of beta-catenin, homolog 2 (Xenopus laevis)	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.29	N/A	Sites in UTR
MAP2K2	NM_030662	mitogen-activated protein kinase kinase 2	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.29	N/A	Sites in UTR
MIS18A	NM_018944	MIS18 kinetochore protein homolog A (S. pombe)	0	0	0	0	1	0 3	l 0 hsa-miR-1908	-0.29	N/A	Sites in UTR
FLJ22184	NM_001190467	hypothetical protein FLJ22184	0	0	0	0	2	0 2	2 0 hsa-miR-663	-0.29	N/A	Sites in UTR
NPHP4	NM_015102	nephronophthisis 4	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.29	N/A	Sites in UTR
9-Sep	NM_001113491	septin 9	0	0	0	0	2	0 3	l hsa-miR-663	-0.29	N/A	Sites in UTR
HUWE1	NM_031407	HECT, UBA and WWE domain containing 1	0	0	0	0	1	0 2	l 0 hsa-miR-1908	-0.29	N/A	Sites in UTR
ENTPD2	NM_001246	ectonucleoside triphosphate diphosphohydrolase 2	0	0	0	0	1	0 3	L 0 hsa-miR-1908	-0.29	N/A	Sites in UTR
NAV1	NM_001167738	neuron navigator 1	0	0	0	0	1	0 2	l 0 hsa-miR-1908	-0.29	N/A	Sites in UTR

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NM_033329	sialic acid binding Ig-like lectin 12 (gene/pseudogene)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_173821	chromosome 2 open reading frame 85	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_001296	chemokine binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_020982	claudin 9	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_006342	transforming, acidic coiled-coil containing protein 3	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_012296	GRB2-associated binding protein 2	0	0	0	0	1	1	0	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_014346	TBC1 domain family, member 22A	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
		0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_014232	vesicle-associated membrane protein 2 (synaptobrevin 2)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_014704	centrosomal protein 104kDa	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_001144888	BAI1-associated protein 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_015362	chromosome 17 open reading frame 81	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_001199803	centromere protein O	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_001029998	solute carrier family 10 (sodium/bile acid cotransporter family), member 7	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_001242481	eukaryotic translation initiation factor 1A domain containing	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
NM_001024226	ADP-ribosylation factor 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_000748	cholinergic receptor, nicotinic, beta 2 (neuronal)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_001195303	regulator of G-protein signaling 5	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_001130020	ATPase, H+ transporting, lysosomal V0 subunit a1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.29	N/A	Sites in UTR
NM_001204961	pre-B-cell leukemia homeobox 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
	NM_173821  NM_001296  NM_001296  NM_006342  NM_012296  NM_014346  NM_014346  NM_014232  NM_014704  NM_01144888  NM_0115362  NM_001199803  NM_001029998  NM_001024226  NM_001024226  NM_000748  NM_001195303  NM_001130020	NM_01296 chemokine binding protein 2  NM_020982 claudin 9  NM_020982 transforming, acidic coiled-coil containing protein 3  NM_012296 GRB2-associated binding protein 2  NM_012296 GRB2-associated binding protein 2  NM_014346 TBC1 domain family, member 22A  NM_02917 RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase  NM_014232 vesicle-associated membrane protein 2 (synaptobrevin 2)  NM_014704 centrosomal protein 104kDa  NM_0114488 BAI1-associated protein 2  NM_015362 chromosome 17 open reading frame 81  NM_01199803 centromere protein 0  NM_010199803 solute carrier family 10 (sodium/bile acid cotransporter family), member 7  NM_001029998 eukaryotic translation initiation factor 1A domain containing  NM_001024226 ADP-ribosylation factor 1  NM_000748 cholinergic receptor, nicotinic, beta 2 (neuronal)  NM_001130020 ATPase, H+ transporting, lysosomal V0 subunit a1	NM_173821         chromosome 2 open reading frame 85         0           NM_001296         chemokine binding protein 2         0           NM_020982         claudin 9         0           NM_06342         transforming, acidic coiled-coil containing protein 3         0           NM_012296         GRB2-associated binding protein 2         0           NM_014346         TBC1 domain family, member 22A         0           NM_014346         TBC1 domain family, member 22A         0           NM_02917         RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase         0           NM_014232         vesicle-associated membrane protein 2 (synaptobrevin 2)         0           NM_014704         centrosomal protein 104kDa         0           NM_01144888         BAl1-associated protein 2         0           NM_015362         chromosome 17 open reading frame 81         0           NM_01199803         centromere protein O         0           NM_001199803         centromere protein O         0           NM_001242481         eukaryotic translation initiation factor 1A domain containing         0           NM_001242481         eukaryotic translation initiation factor 1A domain containing         0           NM_000748         cholinergic receptor, nicotinic, beta 2 (neuronal)         0	NM_173821         chromosome 2 open reading frame 85         0         0           NM_001296         chemokine binding protein 2         0         0           NM_020982         claudin 9         0         0           NM_006342         transforming, acidic coiled-coil containing protein 3         0         0           NM_012296         GRB2-associated binding protein 2         0         0           NM_014346         TBC1 domain family, member 22A         0         0           NM_02917         RFNG O-fucosylpeptide 3-beta-Nacetylglucosaminyltransferase         0         0           NM_014232         vesicle-associated membrane protein 2 (synaptobrevin 2)         0         0           NM_014704         centrosomal protein 104kDa         0         0           NM_014704         centrosomal protein 2         0         0           NM_01144888         BAI1-associated protein 2         0         0           NM_015362         chromosome 17 open reading frame 81         0         0           NM_00199803         centromere protein O         0         0           NM_00129998         solute carrier family 10 (sodium/bile acid cotransporter family), member 7         0         0           NM_001242481         eukaryotic translation initiation factor 1A domain containi	NM_173821         chromosome 2 open reading frame 85         0         0         0           NM_001296         chemokine binding protein 2         0         0         0           NM_020982         claudin 9         0         0         0           NM_006342         transforming, acidic coiled-coil containing protein 3         0         0         0           NM_012296         GRB2-associated binding protein 2         0         0         0           NM_014346         TBC1 domain family, member 22A         0         0         0           NM_014346         TBC1 domain family, member 22A         0         0         0           NM_014704         RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase         0         0         0           NM_014704         centrosomal protein 104kDa         0         0         0           NM_014704         centrosomal protein 104kDa         0         0         0           NM_01144888         BAI1-associated protein 2         0         0         0           NM_015362         chromosome 17 open reading frame 81         0         0         0           NM_019803         centromere protein 0         0         0         0           NM_00129998         solute carr	NM_173821         chromosome 2 open reading frame 85         0         0         0         0           NM_001296         chemokine binding protein 2         0         0         0         0           NM_020982         claudin 9         0         0         0         0           NM_006342         transforming, acidic coiled-coil containing protein 3         0         0         0         0           NM_012296         GR82-associated binding protein 2         0         0         0         0         0           NM_014346         TBC1 domain family, member 22A         0         0         0         0         0           NM_02917         RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase         0         0         0         0           NM_014232         vesicle-associated membrane protein 2 (synaptobrevin 2)         0         0         0         0           NM_014704         centrosomal protein 104kDa         0         0         0         0         0           NM_01144888         BAl1-associated protein 2         0         0         0         0         0           NM_015362         chromosome 17 open reading frame 81         0         0         0         0         0	NM_173821         chromosome 2 open reading frame 85         0         0         0         0         1           NM_001296         chemokine binding protein 2         0         0         0         0         0         1           NM_020982         claudin 9         0         0         0         0         0         1           NM_006342         transforming, acidic coiled-coil containing protein 3         0         0         0         0         1           NM_012296         GR82-associated binding protein 2         0         0         0         0         0         1           NM_014346         TBC1 domain family, member 22A         0         0         0         0         0         1           NM_002917         RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminytransferase         0         0         0         0         0         1           NM_014732         vesicle-associated membrane protein 2 (synaptobrevin 2)         0         0         0         0         1           NM_014704         centrosomal protein 104kDa         0         0         0         0         1           NM_015362         chromosome 17 open reading frame 81         0         0         0         0         1 <td>NM_173821 chromosome 2 open reading frame 85</td> <td>NM_133821 chromosome 2 open reading frame 85</td> <td>NM_173821 chromosome 2 open reading frame 85</td> <td>NM_173821</td> <td>MA_173821</td> <td>M. 173821 chromosome 2 open reading frame 85</td>	NM_173821 chromosome 2 open reading frame 85	NM_133821 chromosome 2 open reading frame 85	NM_173821 chromosome 2 open reading frame 85	NM_173821	MA_173821	M. 173821 chromosome 2 open reading frame 85

TFE3	NM 006521	transcription factor binding to IGHM enhancer 3	0	0	0	0	1	0	1		hsa-miR-1908	-0.29	N/A	Sites in UTR
11123		transcription factor binding to formive emianter 3	0	· ·	-	0	1		1		134-1111/ 1300	0.23	IV/A	Sites in OTK
PHB2	NM_001144831	prohibitin 2	0	0	0	0	1	0	1	O	hsa-miR-1908	-0.29	N/A	Sites in UTR
ARHGAP31	NM_020754	Rho GTPase activating protein 31	0	0	0	0	1	1	0	C	hsa-miR-663	-0.29	N/A	Sites in UTR
PDE4C	NM_000923	phosphodiesterase 4C, cAMP-specific	0	0	0	0	1	0	1	O	hsa-miR-1908	-0.29	N/A	Sites in UTR
FAM90A1	NM_018088	family with sequence similarity 90, member A1	0	0	0	0	1	0	1	O	hsa-miR-663	-0.29	N/A	Sites in UTR
TRIM65	NM_173547	tripartite motif containing 65	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
FAM90A7	NM_001136572	family with sequence similarity 90, member A7	0	0	0	0	1	0	1	0	hsa-miR-663	-0.29	N/A	Sites in UTR
SCML4	NM_198081	sex comb on midleg-like 4 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.28	N/A	Sites in UTR
FHIT	NM_001166243	fragile histidine triad gene	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
GPR124	NM_032777	G protein-coupled receptor 124	0	0	0	0	1	0	1	O	hsa-miR-1908	-0.28	N/A	Sites in UTR
SRGAP1	NM_020762	SLIT-ROBO Rho GTPase activating protein 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
FAM167B	NM_032648	family with sequence similarity 167, member B	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
LATS1	NM_004690	LATS, large tumor suppressor, homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
BET1L	NM_001098787	blocked early in transport 1 homolog (S. cerevisiae)-like	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
PYDC1	NM_152901	PYD (pyrin domain) containing 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
KIAA0240	NM_015349	KIAA0240	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
KRT6C	NM_173086	keratin 6C	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
RGAG4	NM_001024455	retrotransposon gag domain containing 4	0	0	0	0	1	0	1	a	hsa-miR-663	-0.28	N/A	Sites in UTR
SYNGR1	NM_004711	synaptogyrin 1	0	0	0	0	2	0	2	a	hsa-miR-663	-0.28	N/A	Sites in UTR
PTPN18	NM_001142370	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	0	0	0	0	1	1	0	0	hsa-miR-663	-0.28	N/A	Sites in UTR

ALAD	NM 000031	aminolevulinate dehydratase	0	0		0	1	0	1 0 hsa-miR-663	-0.28	N/A	Sites in UTR
712712		animolevalinate delivaratase	Ů						o lisa liilik oos	0.20	14//	Sites III O III
RFX2	NM_000635	regulatory factor X, 2 (influences HLA class II expression)	0	0	0	0	1	0	0 hsa-miR-663	-0.28	N/A	Sites in UTR
DENND4B	NM_014856	DENN/MADD domain containing 4B	0	0	0	0	1	0	0 hsa-miR-1908	-0.28	N/A	Sites in UTR
CDH23	NM_001171931	cadherin-related 23	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
ZYX	NM_001010972	zyxin	0	0	0	0	1	0	0 hsa-miR-1908	-0.28	N/A	Sites in UTR
SLC7A8	NM_012244	solute carrier family 7 (amino acid transporter light chain, L system), member 8	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
RPP25	NM_017793	ribonuclease P/MRP 25kDa subunit	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
PLEKHA2	NM_021623	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.28	N/A	Sites in UTR
CD180	NM_005582	CD180 molecule	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
PET112	NM_004564	PET112 homolog (yeast)	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.28	N/A	Sites in UTR
CNIH2	NM_182553	cornichon homolog 2 (Drosophila)	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
THSD4	NM_024817	thrombospondin, type I, domain containing 4	0	0	0	0	2	0	0 hsa-miR-663	-0.28	N/A	Sites in UTR
AKAP13	NM_006738	A kinase (PRKA) anchor protein 13	0	0	0	0	2	0	2 0 hsa-miR-663	-0.28	N/A	Sites in UTR
GPX4	NM_001039847	glutathione peroxidase 4 (phospholipid hydroperoxidase)	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.28	N/A	Sites in UTR
SAP18	NM_005870	Sin3A-associated protein, 18kDa	0	0	0	0	1	0	0 hsa-miR-1908	-0.28	N/A	Sites in UTR
SHPK	NM_013276	sedoheptulokinase	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
HES2	NM_019089	hairy and enhancer of split 2 (Drosophila)	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.28	N/A	Sites in UTR
WBSCR17	NM_022479	Williams-Beuren syndrome chromosome region 17	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR
STEAP3	NM_001008410	STEAP family member 3	0	0	0	0	1	1	0 hsa-miR-663	-0.28	N/A	Sites in UTR
SLC7A4	NM_004173	solute carrier family 7 (orphan transporter), member 4	0	0	0	0	1	0	L 0 hsa-miR-663	-0.28	N/A	Sites in UTR

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SETD3	NM_199123	SET domain containing 3	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
LOC100130705	NM_001195150	hypothetical protein LOC100130705	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
GPR83	NM_016540	G protein-coupled receptor 83	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.28	N/A	Sites in UTR
CRISP1	NM_001131	cysteine-rich secretory protein 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
CYB561	NM_001017916	cytochrome b-561	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
FPGS	NM_001018078	folylpolyglutamate synthase	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
TGM3	NM_003245	transglutaminase 3 (E polypeptide, protein-glutamine- gamma-glutamyltransferase)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
ADAMTSL4	NM_019032	ADAMTS-like 4	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
ACTR10	NM_018477	actin-related protein 10 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
CREB3L3	NM_032607	cAMP responsive element binding protein 3-like 3	0	0	0	0	2	1	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
LRTM2	NM_001039029	leucine-rich repeats and transmembrane domains 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
ATF7	NM_001130059	activating transcription factor 7	0	0	0	0	1	1	0	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
CRAT	NM_000755	carnitine O-acetyltransferase	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
SUSD4	NM_017982	sushi domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.28	N/A	Sites in UTR
ANKRD52	NM_173595	ankyrin repeat domain 52	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
PTGER3	NM_198714	prostaglandin E receptor 3 (subtype EP3)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.28	N/A	Sites in UTR
ZIC2	NM_007129	Zic family member 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
DLC1	NM_001164271	deleted in liver cancer 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
LPIN1	NM_145693	lipin 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR
AGAP2	NM_001122772	ArfGAP with GTPase domain, ankyrin repeat and PH domain 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.28	N/A	Sites in UTR

ANPEP	NM_001150	alanyl (membrane) aminopeptidase	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
LRP1	NM_002332	low density lipoprotein receptor-related protein 1	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
SCGB3A1	NM_052863	secretoglobin, family 3A, member 1	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
CDAN1	NM_138477	congenital dyserythropoietic anemia, type I	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
MUM1	NM_032853	melanoma associated antigen (mutated) 1	0	0	0	0	2	0	1	1	. hsa-miR-663	-0.27	N/A	Sites in UTR
ЕРНВ4	NM_004444	EPH receptor B4	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
ZNF19	NM_006961	zinc finger protein 19	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
TENC1	NM_015319	tensin like C1 domain containing phosphatase (tensin 2)	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
FAM63A	NM_001040217	family with sequence similarity 63, member A	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
CCDC64B	NM_001103175	coiled-coil domain containing 64B	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
RAP1GAP2	NM_001100398	RAP1 GTPase activating protein 2	0	0	0	0	1	1	0	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
CTBP1	NM_001012614	C-terminal binding protein 1	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
POU2F2	NM_001207025	POU class 2 homeobox 2	1	0	1	0	0	0	0	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
PACSIN1	NM_001199583	protein kinase C and casein kinase substrate in neurons 1	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
NCKAP5L	NM_001037806	NCK-associated protein 5-like	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
CD27	NM_001242	CD27 molecule	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
GTF3C1	NIVI UUTSZU	general transcription factor IIIC, polypeptide 1, alpha 220kDa	0	0	0	0	1	0	1	C	hsa-miR-663	-0.27	N/A	Sites in UTR
DGKD	NM_003648	diacylglycerol kinase, delta 130kDa	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
HIF1AN	NM_017902	hypoxia inducible factor 1, alpha subunit inhibitor	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR
C8orf73	NM_001100878	chromosome 8 open reading frame 73	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.27	N/A	Sites in UTR

MTRF1L	NM_001114184	mitochondrial translational release factor 1-like	0	0	0	0	1	1	0 0	) hsa-miR-663	-0.27	N/A	Sites in UTR
MPST	NM_001013436	mercaptopyruvate sulfurtransferase	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
RAB5C	NM_004583	RAB5C, member RAS oncogene family	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
GPR37L1	NM_004767	G protein-coupled receptor 37 like 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
PHPT1	NM_001135861	phosphohistidine phosphatase 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.27	N/A	Sites in UTR
NUB1	NM_016118	negative regulator of ubiquitin-like proteins 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
CTDSP1	NM_001206878	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
RCOR2	NM_173587	REST corepressor 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
MUC21	NM_001010909	mucin 21, cell surface associated	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
FOXL2	NM_023067	forkhead box L2	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
MEN1	NM_000244	multiple endocrine neoplasia I	0	0	0	0	1	0	1	) hsa-miR-1908	-0.27	N/A	Sites in UTR
ROR2	NM_004560	receptor tyrosine kinase-like orphan receptor 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
PRSS33	NM_152891	protease, serine, 33	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
SH2D5	NM_001103160	SH2 domain containing 5	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
RPS6KA2	NM_001006932	ribosomal protein S6 kinase, 90kDa, polypeptide 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
<b>ГКВР</b> 9	NM_007270	FK506 binding protein 9, 63 kDa	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
SDHAF2	NM_017841	succinate dehydrogenase complex assembly factor 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
KLK15	NM_017509	kallikrein-related peptidase 15	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
KRT71	NM_033448	keratin 71	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
SYNGR2	NM_004710	synaptogyrin 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
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ARFRP1	NM_001134758	ADP-ribosylation factor related protein 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
ATL2	NM_001135673	atlastin GTPase 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.27	N/A	Sites in UTR
PASD1	NM_173493	PAS domain containing 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.27	N/A	Sites in UTR
MSLN	NM_001177355	mesothelin	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
XPO6	NM_015171	exportin 6	0	0	0	0	1	0	1	) hsa-miR-1908	-0.27	N/A	Sites in UTR
SUN2	NM_001199579	Sad1 and UNC84 domain containing 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.27	N/A	Sites in UTR
BEND3	NM_001080450	BEN domain containing 3	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
C10orf95	NM_024886	chromosome 10 open reading frame 95	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
FAM123A	NM_152704	family with sequence similarity 123A	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
GP1BB	NM_000407	glycoprotein Ib (platelet), beta polypeptide	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
CORO2B	NM_001190456	coronin, actin binding protein, 2B	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.27	N/A	Sites in UTR
MAP1LC3A	NM_032514	microtubule-associated protein 1 light chain 3 alpha	0	0	0	0	1	0	1	) hsa-miR-663	-0.27	N/A	Sites in UTR
HS3ST5	NM_153612	heparan sulfate (glucosamine) 3-O-sulfotransferase 5	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.26	N/A	Sites in UTR
RGS19	NM_001039467	regulator of G-protein signaling 19	0	0	0	0	1	0	1	) hsa-miR-663	-0.26	N/A	Sites in UTR
FBXW8	NM_012174	F-box and WD repeat domain containing 8	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
ASCL4	NM_203436	achaete-scute complex homolog 4 (Drosophila)	0	0	0	0	1	0	1	) hsa-miR-663	-0.26	N/A	Sites in UTR
NPAS4	NM_178864	neuronal PAS domain protein 4	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
MUC13	NM_033049	mucin 13, cell surface associated	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.26	N/A	Sites in UTR
TIAM1	NM_003253	T-cell lymphoma invasion and metastasis 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.26	N/A	Sites in UTR
H2AFY2	NM_018649	H2A histone family, member Y2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR

TRIM36	NM_001017398	tripartite motif containing 36	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
LRRC3	NM_030891	leucine rich repeat containing 3	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
FIGNL2	NM_001013690	fidgetin-like 2	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
SBK1	NM_001024401	SH3-binding domain kinase 1	0	0	0	0	2	0	2	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
LGI2	NM_018176	leucine-rich repeat LGI family, member 2	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
FOXK1	NM_001037165	forkhead box K1	0	0	0	0	2	1	1	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
PRICKLE3	NM_006150	prickle homolog 3 (Drosophila)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
MVD	NM_002461	mevalonate (diphospho) decarboxylase	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
CIB2	NM_006383	calcium and integrin binding family member 2	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
KAT5	NM_001206833	K(lysine) acetyltransferase 5	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
ATP5D	NM_001001975	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
DLG4	NM_001128827	discs, large homolog 4 (Drosophila)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
SIN3B	NM_015260	SIN3 homolog B, transcription regulator (yeast)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
SS18L1	NM_198935	synovial sarcoma translocation gene on chromosome 18- like 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
ARHGAP39	NM_025251	Rho GTPase activating protein 39	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
OLIG1	NM_138983	oligodendrocyte transcription factor 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
IL34	NM_001172771	interleukin 34	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
SNRNP48	NM_152551	small nuclear ribonucleoprotein 48kDa (U11/U12)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR
PLAGL2	NM_002657	pleiomorphic adenoma gene-like 2	0	0	0	0	2	0	2	0 hsa-miR-663	-0.26	N/A	Sites in UTR
SPTB	NM_000347	spectrin, beta, erythrocytic	0	0	0	0	1	0	1	0 hsa-miR-663	-0.26	N/A	Sites in UTR

DPPA4	NM_018189	developmental pluripotency associated 4	0	0	0	0	1	O	1	) hsa-miR-663	-0.26	N/A	Sites in UTR
MAVS	NM_001206491	mitochondrial antiviral signaling protein	0	0	0	0	3	0	1 2	2 hsa-miR-663	-0.26	N/A	Sites in UTR
DBN1	NM_004395	drebrin 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.26	N/A	Sites in UTR
PRRG2	NM_000951	proline rich Gla (G-carboxyglutamic acid) 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.26	N/A	Sites in UTR
PRAP1	NM_001145201	proline-rich acidic protein 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.26	N/A	Sites in UTR
XRRA1	NM_182969	X-ray radiation resistance associated 1	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
IL4R	NM_000418	interleukin 4 receptor	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
UNC13A	NM_001080421	unc-13 homolog A (C. elegans)	1	0	1	0	0	0	0 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
CNTF	NM_000614	ciliary neurotrophic factor	0	0	0	0	1	O	0 :	l hsa-miR-1908	-0.26	N/A	Sites in UTR
EN1	NM_001426	engrailed homeobox 1	0	0	0	0	1	O	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
CDK5R2	NM_003936	cyclin-dependent kinase 5, regulatory subunit 2 (p39)	0	0	0	0	1	O	1 (	) hsa-miR-663	-0.26	N/A	Sites in UTR
SOCS6	NM_004232	suppressor of cytokine signaling 6	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
PITPNM3	NM_001165966	PITPNM family member 3	1	0	1	0	0	0	0 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
KLF16	NM_031918	Kruppel-like factor 16	0	0	0	0	1	O	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
FGD3	NM_001083536	FYVE, RhoGEF and PH domain containing 3	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.26	N/A	Sites in UTR
S100A16	NM_080388	S100 calcium binding protein A16	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.26	N/A	Sites in UTR
PIM3	NM_001001852	pim-3 oncogene	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.26	N/A	Sites in UTR
TGFB1I1	NM_001042454	transforming growth factor beta 1 induced transcript 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.26	N/A	Sites in UTR
CGGBP1	NM_001008390	CGG triplet repeat binding protein 1	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR
ARTN	NM_001136215	artemin	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.26	N/A	Sites in UTR

PGBD5	NM_024554	piggyBac transposable element derived 5	0	0	0	0	1	0	0 hsa-miR-1908	-0.26	N/A	Sites in UTR
C1orf95	NM_001003665	chromosome 1 open reading frame 95	0	0	0	0	2	0 2	2 0 hsa-miR-663	-0.26	N/A	Sites in UTR
PTPRF	NM_002840	protein tyrosine phosphatase, receptor type, F	0	0	0	0	1	0 1	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
MAP4K2	NM_004579	mitogen-activated protein kinase kinase kinase kinase 2	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
DGKZ	NM_001105540	diacylglycerol kinase, zeta	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PAK4	NM_001014831	p21 protein (Cdc42/Rac)-activated kinase 4	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PCSK4	NM_017573	proprotein convertase subtilisin/kexin type 4	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
ТНТРА	NM_001126339	thiamine triphosphatase	0	0	0	0	1	0 3	0 hsa-miR-1908	-0.25	N/A	Sites in UTR
RELL2	NM_001130029	RELT-like 2	0	0	0	0	1	0 2	l 0 hsa-miR-1908	-0.25	N/A	Sites in UTR
APOE	NM_000041	apolipoprotein E	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
KCNAB3	NM_004732	potassium voltage-gated channel, shaker-related subfamily, beta member 3	1	0	1	0	0	0 0	0 hsa-miR-663	-0.25	N/A	Sites in UTR
STMN3	NM_015894	stathmin-like 3	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PARP10	NM_032789	poly (ADP-ribose) polymerase family, member 10	0	0	0	0	1	0 2	0 hsa-miR-1908	-0.25	N/A	Sites in UTR
ADAMTS14	NM_080722	ADAM metallopeptidase with thrombospondin type 1 motif, 14	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
ZNF865	NM_001195605	zinc finger protein 865	0	0	0	0	1	0 3	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
FLNA	NM_001110556	filamin A, alpha	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
МАРТ	NM_001123066	microtubule-associated protein tau	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PNPLA2	NM_020376	patatin-like phospholipase domain containing 2	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PDZD4	NM_032512	PDZ domain containing 4	0	0	0	0	1	0 2	L 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PRDM12	NM_021619	PR domain containing 12	0	0	0	0	2	0 2	0 hsa-miR-1908	-0.25	N/A	Sites in UTR

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SH2D4A	NM_001174159	SH2 domain containing 4A	0	0	0	0	1	O	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
TNS4	NM_032865	tensin 4	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
DOK7	NM_001164673	docking protein 7	0	0	0	0	1	0	1	) hsa-miR-663	-0.25	N/A	Sites in UTR
TBX10	NM_005995	T-box 10	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
SAMD4A	NM_001161576	sterile alpha motif domain containing 4A	0	0	0	0	1	1	0	) hsa-miR-663	-0.25	N/A	Sites in UTR
BRF1	NM_001242786	BRF1 homolog, subunit of RNA polymerase III transcription initiation factor IIIB (S. cerevisiae)	0	0	0	0	1	0	1	) hsa-miR-663	-0.25	N/A	Sites in UTR
S1PR2	NM_004230	sphingosine-1-phosphate receptor 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.25	N/A	Sites in UTR
STARD8	NM_001142503	StAR-related lipid transfer (START) domain containing 8	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
EFR3B	NM_014971	EFR3 homolog B (S. cerevisiae)	0	0	0	0	1	0	1	) hsa-miR-663	-0.25	N/A	Sites in UTR
DDN	NM_015086	dendrin	0	0	0	0	1	0	1	) hsa-miR-663	-0.25	N/A	Sites in UTR
C4orf3	NM_001001701	chromosome 4 open reading frame 3	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
GAS1	NM_002048	growth arrest-specific 1	0	0	0	0	2	0	2	) hsa-miR-1908	-0.25	N/A	Sites in UTR
KCNG1	NM_002237	potassium voltage-gated channel, subfamily G, member 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
MIER2	NM_017550	mesoderm induction early response 1, family member 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
SLITRK1	NM_052910	SLIT and NTRK-like family, member 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.25	N/A	Sites in UTR
PLD4	NM_138790	phospholipase D family, member 4	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
TLX2	NM_016170	T-cell leukemia homeobox 2	1	0	0	1	0	0	0	) hsa-miR-663	-0.25	N/A	Sites in UTR
FAM157A	NM_001145248	family with sequence similarity 157, member A	0	0	0	0	1	0	0 :	1 hsa-miR-663	-0.25	N/A	Sites in UTR
ARRB2	NM_004313	arrestin, beta 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR
HNF4A	NM_000457	hepatocyte nuclear factor 4, alpha	0	0	0	0	1	0	1	) hsa-miR-1908	-0.25	N/A	Sites in UTR

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KLHL6	NM_130446	kelch-like 6 (Drosophila)	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	N/A	Sites in UTR
KCNC1	NM_004976	potassium voltage-gated channel, Shaw-related subfamily, member 1	0	0	0	0	2	0	1 1 hsa-miR-663	-0.25	N/A	Sites in UTR
SYCE1L	NM_001129979	synaptonemal complex central element protein 1-like	0	0	0	0	1	0	0 1 hsa-miR-1908	-0.25	N/A	Sites in UTR
PBMUCL1	NM_001198815	panbronchiolitis related mucin-like 1	0	0	0	0	1	0	0 1 hsa-miR-663	-0.25	N/A	Sites in UTR
ADAM11	NM_002390	ADAM metallopeptidase domain 11	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.25	N/A	Sites in UTR
PITX1	NM_002653	paired-like homeodomain 1	0	0	0	0	2	0	2 0 hsa-miR-663	-0.25	N/A	Sites in UTR
SALL1	NM_001127892	sal-like 1 (Drosophila)	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	N/A	Sites in UTR
KLF10	NM_001032282	Kruppel-like factor 10	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.25	5 N/A	Sites in UTR
GIPC1	NM_005716	GIPC PDZ domain containing family, member 1	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	5 N/A	Sites in UTR
GUF1	NM_021927	GUF1 GTPase homolog (S. cerevisiae)	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.25	N/A	Sites in UTR
PGAP3	NM_033419	post-GPI attachment to proteins 3	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.25	N/A	Sites in UTR
FAM78A	NM_033387	family with sequence similarity 78, member A	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	5 N/A	Sites in UTR
ZNF324B	NM_207395	zinc finger protein 324B	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.25	5 N/A	Sites in UTR
C14orf119	NM_017924	chromosome 14 open reading frame 119	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.25	5 N/A	Sites in UTR
CPNE5	NM_020939	copine V	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	N/A	Sites in UTR
OTUD6A	NM_207320	OTU domain containing 6A	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	N/A	Sites in UTR
MTR	NM_000254	5-methyltetrahydrofolate-homocysteine methyltransferase	0	0	0	0	2	0	1 1 hsa-miR-1908	-0.25	N/A	Sites in UTR
ЕРНВЗ	NM_004443	EPH receptor B3	1	0	1	0	0	0	0 hsa-miR-663	-0.25	N/A	Sites in UTR
MN1	NM_002430	meningioma (disrupted in balanced translocation) 1	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	N/A	Sites in UTR
PDCD1	NM_005018	programmed cell death 1	0	0	0	0	1	0	1 0 hsa-miR-663	-0.25	N/A	Sites in UTR

NPLOC4	NM_017921	nuclear protein localization 4 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.25	N/A	Sites in UTR
HR	NM_005144	hairless homolog (mouse)	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.25	N/A	Sites in UTR
LPCAT1	NM_024830	lysophosphatidylcholine acyltransferase 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.25	N/A	Sites in UTR
ZNF696	NM_030895	zinc finger protein 696	0	0	0	0	1	0	1	0 hsa-miR-663	-0.25	N/A	Sites in UTR
SH3TC2	NM_024577	SH3 domain and tetratricopeptide repeats 2	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.24	N/A	Sites in UTR
FAM89A	NM_198552	family with sequence similarity 89, member A	0	0	0	0	1	0	0	1 hsa-miR-663	-0.24	N/A	Sites in UTR
KCNJ11	NM_000525	potassium inwardly-rectifying channel, subfamily J, member 11	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
IL32	NM_001012631	interleukin 32	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
HHLA3	NM_001031693	HERV-H LTR-associating 3	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
ZBTB4	NM_001128833	zinc finger and BTB domain containing 4	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
VSTM2L	NM_080607	V-set and transmembrane domain containing 2 like	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
IGFBP6	NM_002178	insulin-like growth factor binding protein 6	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
SFRP5	NM_003015	secreted frizzled-related protein 5	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
MACROD1	NM_014067	MACRO domain containing 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
RTBDN	NM_001080997	retbindin	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
MAMDC4	NM_206920	MAM domain containing 4	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
GP5	NM_004488	glycoprotein V (platelet)	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
PVRL2	NM_002856	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
RAB35	NM_001167606	RAB35, member RAS oncogene family	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
CALY	NM_015722	calcyon neuron-specific vesicular protein	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR

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MKL1	NM_020831	megakaryoblastic leukemia (translocation) 1	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
UNKL	NM_001193388	unkempt homolog (Drosophila)-like	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
PPDPF	NM_024299	pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish)	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
KLK9	NM_012315	kallikrein-related peptidase 9	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
TNRC6B	NM_001024843	trinucleotide repeat containing 6B	0	0	0	0	1	1	0	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
CDH8	NM_001796	cadherin 8, type 2	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.24	N/A	Sites in UTR
SFN	NM_006142	stratifin	0	0	0	0	2	0	1	1 hsa-miR-663	-0.24	N/A	Sites in UTR
SYN2	NM_133625	synapsin II	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
HSPB7	NM_014424	heat shock 27kDa protein family, member 7 (cardiovascular)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
ZNF671	NM_024833	zinc finger protein 671	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.24	N/A	Sites in UTR
KCNC3		potassium voltage-gated channel, Shaw-related subfamily, member 3	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
STAM	NM_003473	signal transducing adaptor molecule (SH3 domain and ITAM motif) 1	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
MCOLN1	NM_020533	mucolipin 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
NDOR1	NM_001144026	NADPH dependent diflavin oxidoreductase 1	0	0	0	0	2	0	2	0 hsa-miR-663	-0.24	N/A	Sites in UTR
PXMP4	NM_007238	peroxisomal membrane protein 4, 24kDa	0	0	0	0	2	0	0	2 hsa-miR-663	-0.24	N/A	Sites in UTR
CD5L	NM_005894	CD5 molecule-like	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
INPPL1	NM_001567	inositol polyphosphate phosphatase-like 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.24	N/A	Sites in UTR
C1orf93	NM_001195736	chromosome 1 open reading frame 93	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
C7orf51	NM_173564	chromosome 7 open reading frame 51	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
KIAA0040	NM_001162893	KIAA0040	0	0	0	0	1	1	0	0 hsa-miR-663	-0.24	N/A	Sites in UTR

ACCN1	NM_001094	amiloride-sensitive cation channel 1, neuronal	0	0	0	0	1	0	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
LCN1	NM_002297	lipocalin 1 (tear prealbumin)	0	0	0	0	1	0	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
MYOD1	NM_002478	myogenic differentiation 1	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
SLC6A8	NM_001142805	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
CLDN6	NM_021195	claudin 6	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
LHPP	NM_001167880	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
ZFHX2	NM_033400	zinc finger homeobox 2	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
DCAF15	NM_138353	DDB1 and CUL4 associated factor 15	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
SPTBN2	NM_006946	spectrin, beta, non-erythrocytic 2	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
TATDN2	NM_014760	TatD DNase domain containing 2	0	0	0	0	1	0 :	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
PRX	NM_020956	periaxin	0	0	0	0	2	1	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR
KREMEN1	NM_001039570	kringle containing transmembrane protein 1	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
LRRC33	NM_198565	leucine rich repeat containing 33	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
C9orf171	NM_207417	chromosome 9 open reading frame 171	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
MPRIP	NM_015134	myosin phosphatase Rho interacting protein	0	0	0	0	2	0 :	l hsa-miR-663	-0.24	N/A	Sites in UTR
PCGF3	NM_006315	polycomb group ring finger 3	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
TNFAIP8L1	NM_001167942	tumor necrosis factor, alpha-induced protein 8-like 1	0	0	0	0	1	0 :	0 hsa-miR-1908	-0.24	N/A	Sites in UTR
DPY19L3	NM_001172774	dpy-19-like 3 (C. elegans)	0	0	0	0	1	1 (	0 hsa-miR-663	-0.24	N/A	Sites in UTR
RAPGEFL1	NM_016339	Rap guanine nucleotide exchange factor (GEF)-like 1	0	0	0	0	1	0 (	) 1 hsa-miR-1908	-0.24	N/A	Sites in UTR
RPL28	NM_000991	ribosomal protein L28	0	0	0	0	1	0	L 0 hsa-miR-663	-0.24	N/A	Sites in UTR

STXBP1	NM_001032221	syntaxin binding protein 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.24	N/A	Sites in UTR
PDCD11	NM_014976	programmed cell death 11	0	0	0	0	1	0	1	) hsa-miR-663	-0.24	N/A	Sites in UTR
DHX37	NM_032656	DEAH (Asp-Glu-Ala-His) box polypeptide 37	0	0	0	0	1	0	1	) hsa-miR-663	-0.24	N/A	Sites in UTR
MAPK15	NM_139021	mitogen-activated protein kinase 15	0	0	0	0	1	0	1	) hsa-miR-1908	-0.24	N/A	Sites in UTR
DIS3	NM_001128226	DIS3 mitotic control homolog (S. cerevisiae)	0	0	0	0	1	1	0	) hsa-miR-663	-0.24	N/A	Sites in UTR
GBP4	NM_052941	guanylate binding protein 4	0	0	0	0	1	0	0	1 hsa-miR-663	-0.23	N/A	Sites in UTR
GPC1	NM_002081	glypican 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NPTX2	NM_002523	neuronal pentraxin II	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
TCEB3	NM_003198	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
TNRC6A	NM_014494	trinucleotide repeat containing 6A	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
CCDC106	NM_013301	coiled-coil domain containing 106	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
CD1A	NM_001763	CD1a molecule	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
CHST15	NM_015892	carbohydrate (N-acetylgalactosamine 4-sulfate 6-0) sulfotransferase 15	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
SFTPB	NM_000542	surfactant protein B	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
ULK1	NM_003565	unc-51-like kinase 1 (C. elegans)	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
DGKE	NM_003647	diacylglycerol kinase, epsilon 64kDa	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
TLR6	NM_006068	toll-like receptor 6	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NGB	NM_021257	neuroglobin	0	0	0	0	2	0	2	) hsa-miR-663	-0.23	N/A	Sites in UTR
CACNG7	NM_031896	calcium channel, voltage-dependent, gamma subunit 7	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
FAM55C	NM_001134456	family with sequence similarity 55, member C	1	0	1	0	0	0	0	) hsa-miR-663	-0.23	N/A	Sites in UTR

EVI5L	NM_001159944	ecotropic viral integration site 5-like	0	0	0	0	1	0	0	1 hsa-miR-663	-0.23	N/A	Sites in UTR
NONO	NM_001145408	non-POU domain containing, octamer-binding	0	0	0	0	1	0	1	hsa-miR-1908	-0.23	N/A	Sites in UTR
ZNF70	NM_021916	zinc finger protein 70	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
TSPYL4	NM_021648	TSPY-like 4	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
PTCHD2	NM_020780	patched domain containing 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
C11orf95	NM_001144936	chromosome 11 open reading frame 95	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
MARVELD1	NM_031484	MARVEL domain containing 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
RLIM	NM_016120	ring finger protein, LIM domain interacting	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
ZNF585B	NM_152279	zinc finger protein 585B	0	0	0	0	1	1	0	) hsa-miR-1908	-0.23	N/A	Sites in UTR
SLC24A4	NM_153646	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	0	0	0	0	1	1	0	) hsa-miR-663	-0.23	N/A	Sites in UTR
TRIM9	NM_052978	tripartite motif containing 9	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
KCTD19	NM_001100915	potassium channel tetramerisation domain containing 19	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
MYBPHL	NM_001010985	myosin binding protein H-like	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
GSK3A	NM_019884	glycogen synthase kinase 3 alpha	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
MPZ	NM_000530	myelin protein zero	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
PRODH	NM_001195226	proline dehydrogenase (oxidase) 1	0	0	0	0	2	0	1	1 hsa-miR-663	-0.23	N/A	Sites in UTR
REEP2	NM_016606	receptor accessory protein 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
RAPGEF5	NM_012294	Rap guanine nucleotide exchange factor (GEF) 5	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
HMGA1	NM_002131	high mobility group AT-hook 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
KCNN1	NM_002248	potassium intermediate/small conductance calcium- activated channel, subfamily N, member 1	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.23	N/A	Sites in UTR

NFIA	NM 001134673	augles feeter I/A	0	0	0	0	1	0	1		hsa-miR-1908	-0.23	NI/A	Sites in UTR
INFIA	NINI_001134073	nuclear factor I/A	0		0	0	1	0	1		1124-11114-1300	-0.23	N/A	Sites III OTK
ENPP1	NM_006208	ectonucleotide pyrophosphatase/phosphodiesterase 1	0	0	0	0	1	0	1		hsa-miR-1908	-0.23	N/A	Sites in UTR
SPOCK2		sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2	0	0	0	0	1	0	1	. (	hsa-miR-663	-0.23	N/A	Sites in UTR
MMRN1	NM_007351	multimerin 1	0	0	0	0	1	0	1		hsa-miR-663	-0.23	N/A	Sites in UTR
PHLDB3	NM_198850	pleckstrin homology-like domain, family B, member 3	1	0	1	0	1	0	1		hsa-miR-1908	-0.23	N/A	Sites in UTR
CERS2	NM_022075	ceramide synthase 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.23	N/A	Sites in UTR
HUS1	NM_004507	HUS1 checkpoint homolog (S. pombe)	0	0	0	0	1	0	1	. (	hsa-miR-1908	-0.23	N/A	Sites in UTR
PTBP1	NM_002819	polypyrimidine tract binding protein 1	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.23	N/A	Sites in UTR
ADAMTSL2	NM_001145320	ADAMTS-like 2	0	0	0	0	1	0	1	. (	hsa-miR-1908	-0.23	N/A	Sites in UTR
ZDHHC12	NM_032799	zinc finger, DHHC-type containing 12	0	0	0	0	1	0	1	. (	hsa-miR-663	-0.23	N/A	Sites in UTR
FAM199X	NM_207318	family with sequence similarity 199, X-linked	0	0	0	0	1	0	1	. (	hsa-miR-1908	-0.23	N/A	Sites in UTR
VSTM4	NM_144984	V-set and transmembrane domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.23	N/A	Sites in UTR
BBC3	NM_001127240	BCL2 binding component 3	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.23	N/A	Sites in UTR
PAK6	NM_001128628	p21 protein (Cdc42/Rac)-activated kinase 6	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.23	N/A	Sites in UTR
PRDM8	NM_001099403	PR domain containing 8	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.23	N/A	Sites in UTR
PLSCR3	NM_001201576	phospholipid scramblase 3	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.23	N/A	Sites in UTR
TRMT2B	NM_001167970	TRM2 tRNA methyltransferase 2 homolog B (S. cerevisiae)	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.23	N/A	Sites in UTR
MSRA	NM_001135670	methionine sulfoxide reductase A	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.23	N/A	Sites in UTR
PTPN9	NM_002833	protein tyrosine phosphatase, non-receptor type 9	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.23	N/A	Sites in UTR
ТВХЗ	NM_005996	T-box 3	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.23	N/A	Sites in UTR

NM_001204077	ubiquitination factor E4A	0	0	0	0	1	0	0	l hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_001122841	FERM domain containing 1	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.23	N/A	Sites in UTR
NM_004943	dystrophia myotonica, WD repeat containing	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_000992	ribosomal protein L29	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_015103	plexin D1	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_001104554	progestin and adipoQ receptor family member V	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_024954	ubiquitin domain containing 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_145865	ankyrin repeat and sterile alpha motif domain containing 4B	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_052858	MARVEL domain containing 3	0	0	0	0	1	O	0 :	L hsa-miR-663	-0.23	N/A	Sites in UTR
NM_004174	solute carrier family 9 (sodium/hydrogen exchanger), member 3	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_003370	vasodilator-stimulated phosphoprotein	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_145270	chromosome 16 open reading frame 11	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_145272	chromosome 17 open reading frame 50	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_199461	nanos homolog 1 (Drosophila)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_198285	WD repeat domain 86	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_014753	BMS1 homolog, ribosome assembly protein (yeast)	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_024306	fatty acid 2-hydroxylase	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.23	N/A	Sites in UTR
NM_000144	frataxin	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_000431	mevalonate kinase	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_004561	ovo-like 1(Drosophila)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.23	N/A	Sites in UTR
	NM_001122841  NM_004943  NM_000992  NM_015103  NM_001104554  NM_024954  NM_145865  NM_052858  NM_004174  NM_003370  NM_145270  NM_145272  NM_199461  NM_198285  NM_014753  NM_024306  NM_000144  NM_000431	NM_001122841 FERM domain containing 1  NM_004943 dystrophia myotonica, WD repeat containing  NM_000992 ribosomal protein L29  NM_015103 plexin D1  NM_001104554 progestin and adipoQ receptor family member V  NM_024954 ubiquitin domain containing 1  NM_145865 ankyrin repeat and sterile alpha motif domain containing 4B  NM_052858 MARVEL domain containing 3  NM_004174 solute carrier family 9 (sodium/hydrogen exchanger), member 3  NM_003370 vasodilator-stimulated phosphoprotein  NM_145270 chromosome 16 open reading frame 11  NM_145272 chromosome 17 open reading frame 50  NM_199461 nanos homolog 1 (Drosophila)  NM_198285 WD repeat domain 86  NM_014753 BMS1 homolog, ribosome assembly protein (yeast)  NM_024306 fatty acid 2-hydroxylase  NM_000144 frataxin  NM_000431 mevalonate kinase	NM_001122841         FERM domain containing 1         0           NM_004943         dystrophia myotonica, WD repeat containing         0           NM_000992         ribosomal protein L29         0           NM_015103         plexin D1         0           NM_01104554         progestin and adipoQ receptor family member V         0           NM_024954         ubiquitin domain containing 1         0           NM_145865         ankyrin repeat and sterile alpha motif domain containing 48         0           NM_052858         MARVEL domain containing 3         0           NM_04174         solute carrier family 9 (sodium/hydrogen exchanger), member 3         0           NM_03370         vasodilator-stimulated phosphoprotein         0           NM_145270         chromosome 16 open reading frame 11         0           NM_145272         chromosome 17 open reading frame 50         0           NM_199461         nanos homolog 1 (Drosophila)         0           NM_198285         WD repeat domain 86         0           NM_014753         BMS1 homolog, ribosome assembly protein (yeast)         0           NM_024306         fatty acid 2-hydroxylase         0           NM_000144         frataxin         0           NM_000431         mevalonate kinase <t< td=""><td>NM_001122841         FERM domain containing 1         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0           NM_000992         ribosomal protein L29         0         0           NM_015103         plexin D1         0         0           NM_001104554         progestin and adipoQ receptor family member V         0         0           NM_024954         ubiquitin domain containing 1         0         0           NM_145865         ankyrin repeat and sterile alpha motif domain containing 4B         0         0           NM_052858         MARVEL domain containing 3         0         0           NM_004174         solute carrier family 9 (sodium/hydrogen exchanger), member 3         0         0           NM_003370         vasodilator-stimulated phosphoprotein         0         0           NM_145270         chromosome 16 open reading frame 11         0         0           NM_145272         chromosome 17 open reading frame 50         0         0           NM_198285         WD repeat domain 86         0         0           NM_014753         BMS1 homolog, ribosome assembly protein (yeast)         0         0           NM_024306         fatty acid 2-hydroxylase         0         0     &lt;</td><td>NM_001122841         FERM domain containing 1         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0           NM_000992         ribosomal protein L29         0         0         0           NM_015103         plexin D1         0         0         0           NM_01104554         progestin and adipoQ receptor family member V         0         0         0           NM_024954         ubiquitin domain containing 1         0         0         0           NM_145865         ankyrin repeat and sterile alpha motif domain containing 48         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0<!--</td--><td>NM_001122841         FERM domain containing 1         0         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0           NM_004943         ribosomal protein L29         0         0         0         0         0           NM_015103         plexin D1         0         0         0         0         0         0         0           NM_024954         ubiquitin domain containing 1         0</td><td>NM_001122841         FERM domain containing 1         0         0         0         0         0         1           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0         0         1           NM_000992         ribosomal protein L29         0         0         0         0         0         1           NM_015103         plexin D1         0         0         0         0         0         1           NM_01104554         progestin and adipoQ receptor family member V         0         0         0         0         0         1           NM_024954         ubiquitin domain containing 1         0         0         0         0         0         1           NM_145865         alk givrin repeat and sterile alpha motif domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_00</td><td>NM_001122841 FERM domain containing 1</td><td>NM_001122841 FERM domain containing 1 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0</td><td>NM_001122811</td><td>MA_001126911 FERM domain containing 1</td><td>NA_001124581 FERM domain containing 1</td></td></t<>	NM_001122841         FERM domain containing 1         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0           NM_000992         ribosomal protein L29         0         0           NM_015103         plexin D1         0         0           NM_001104554         progestin and adipoQ receptor family member V         0         0           NM_024954         ubiquitin domain containing 1         0         0           NM_145865         ankyrin repeat and sterile alpha motif domain containing 4B         0         0           NM_052858         MARVEL domain containing 3         0         0           NM_004174         solute carrier family 9 (sodium/hydrogen exchanger), member 3         0         0           NM_003370         vasodilator-stimulated phosphoprotein         0         0           NM_145270         chromosome 16 open reading frame 11         0         0           NM_145272         chromosome 17 open reading frame 50         0         0           NM_198285         WD repeat domain 86         0         0           NM_014753         BMS1 homolog, ribosome assembly protein (yeast)         0         0           NM_024306         fatty acid 2-hydroxylase         0         0     <	NM_001122841         FERM domain containing 1         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0           NM_000992         ribosomal protein L29         0         0         0           NM_015103         plexin D1         0         0         0           NM_01104554         progestin and adipoQ receptor family member V         0         0         0           NM_024954         ubiquitin domain containing 1         0         0         0           NM_145865         ankyrin repeat and sterile alpha motif domain containing 48         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0         0           NM_052858         MARVEL domain containing 3         0         0         0 </td <td>NM_001122841         FERM domain containing 1         0         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0           NM_004943         ribosomal protein L29         0         0         0         0         0           NM_015103         plexin D1         0         0         0         0         0         0         0           NM_024954         ubiquitin domain containing 1         0</td> <td>NM_001122841         FERM domain containing 1         0         0         0         0         0         1           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0         0         1           NM_000992         ribosomal protein L29         0         0         0         0         0         1           NM_015103         plexin D1         0         0         0         0         0         1           NM_01104554         progestin and adipoQ receptor family member V         0         0         0         0         0         1           NM_024954         ubiquitin domain containing 1         0         0         0         0         0         1           NM_145865         alk givrin repeat and sterile alpha motif domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_00</td> <td>NM_001122841 FERM domain containing 1</td> <td>NM_001122841 FERM domain containing 1 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0</td> <td>NM_001122811</td> <td>MA_001126911 FERM domain containing 1</td> <td>NA_001124581 FERM domain containing 1</td>	NM_001122841         FERM domain containing 1         0         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0           NM_004943         ribosomal protein L29         0         0         0         0         0           NM_015103         plexin D1         0         0         0         0         0         0         0           NM_024954         ubiquitin domain containing 1         0	NM_001122841         FERM domain containing 1         0         0         0         0         0         1           NM_004943         dystrophia myotonica, WD repeat containing         0         0         0         0         0         1           NM_000992         ribosomal protein L29         0         0         0         0         0         1           NM_015103         plexin D1         0         0         0         0         0         1           NM_01104554         progestin and adipoQ receptor family member V         0         0         0         0         0         1           NM_024954         ubiquitin domain containing 1         0         0         0         0         0         1           NM_145865         alk givrin repeat and sterile alpha motif domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_052858         MARVEL domain containing 3         0         0         0         0         1           NM_00	NM_001122841 FERM domain containing 1	NM_001122841 FERM domain containing 1 0 0 0 0 0 0 1 0 0 0 0 0 1 0 0 0 0 0	NM_001122811	MA_001126911 FERM domain containing 1	NA_001124581 FERM domain containing 1

	<u> </u>											
NM_001185080	claudin 15	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_052859	RFT1 homolog (S. cerevisiae)	0	0	0	0	1	0	1 (	hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_181843	nudix (nucleoside diphosphate linked moiety X)-type motif 8	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_017565	family with sequence similarity 20, member A	0	0	0	0	1	0	0 2	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_020901	PHD and ring finger domains 1	0	0	0	0	1	0	0 2	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_001033560	dyslexia susceptibility 1 candidate 1	0	0	0	0	1	0	0 3	1 hsa-miR-663	-0.23	N/A	Sites in UTR
NM_001114617	mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N- acetylglucosaminyltransferase	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_006941	SRY (sex determining region Y)-box 10	0	0	0	0	1	0	1	) hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_152380	T-box 15	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_015995	Kruppel-like factor 13	0	0	0	0	2	0	1	1 hsa-miR-1908	-0.23	N/A	Sites in UTR
NM_017957	epsin 3	0	0	0	0	2	0	2	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_001130111	family with sequence similarity 108, member A1	0	0	0	0	1	0	1	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_001111307	phosphodiesterase 4A, cAMP-specific	0	0	0	0	2	0	2	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_015049	trafficking protein, kinesin binding 2	0	0	0	0	1	1	0	) hsa-miR-663	-0.23	N/A	Sites in UTR
NM_001083314	chromatin modifying protein 1A	0	0	0	0	1	0	1	) hsa-miR-663	-0.22	N/A	Sites in UTR
NM_020832	zinc finger protein 687	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
NM_001001794	family with sequence similarity 116, member B	0	0	0	0	1	0	1 (	hsa-miR-1908	-0.22	N/A	Sites in UTR
NM_001080531	chromosome 4 open reading frame 51	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
NM_000151	glucose-6-phosphatase, catalytic subunit	0	0	0	0	1	0	0 1	1 hsa-miR-1908	-0.22	N/A	Sites in UTR
NM_014817	TLR4 interactor with leucine-rich repeats	0	0	0	0	1	0	0 :	1 hsa-miR-1908	-0.22	N/A	Sites in UTR
	NM_052859  NM_181843  NM_017565  NM_020901  NM_001033560  NM_001114617  NM_006941  NM_152380  NM_015995  NM_017957  NM_01130111  NM_001130111  NM_001111307  NM_0010805314  NM_001080531  NM_0000151	NM_052859 RFT1 homolog (S. cerevisiae)  NM_181843 nudix (nucleoside diphosphate linked moiety X)-type motif 8  NM_017565 family with sequence similarity 20, member A  NM_020901 PHD and ring finger domains 1  NM_001033560 dyslexia susceptibility 1 candidate 1  NM_001114617 mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase  NM_006941 SRY (sex determining region Y)-box 10  NM_152380 T-box 15  NM_015995 Kruppel-like factor 13  NM_017957 epsin 3  NM_01130111 family with sequence similarity 108, member A1  NM_001111307 phosphodiesterase 4A, cAMP-specific  NM_015049 trafficking protein, kinesin binding 2  NM_0100103314 chromatin modifying protein 1A  NM_020832 zinc finger protein 687  NM_001001794 family with sequence similarity 116, member B  NM_0101080531 chromosome 4 open reading frame 51  NM_000151 glucose-6-phosphatase, catalytic subunit	NM_052859         RFT1 homolog (S. cerevisiae)         0           NM_181843         nudix (nucleoside diphosphate linked moiety X)-type motif 8         0           NM_017565         family with sequence similarity 20, member A         0           NM_020901         PHD and ring finger domains 1         0           NM_01033560         dyslexia susceptibility 1 candidate 1         0           NM_001114617         mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase         0           NM_006941         SRY (sex determining region Y)-box 10         0           NM_152380         T-box 15         0           NM_015995         Kruppel-like factor 13         0           NM_017957         epsin 3         0           NM_01130111         family with sequence similarity 108, member A1         0           NM_00113071         phosphodiesterase 4A, cAMP-specific         0           NM_015049         trafficking protein, kinesin binding 2         0           NM_010083314         chromatin modifying protein 1A         0           NM_001001794         family with sequence similarity 116, member B         0           NM_001001794         family with sequence similarity 116, member B         0           NM_001080531         chromosome 4 open reading frame 51         0	NM_052859         RFT1 homolog (5. cerevisiae)         0         0           NM_181843         nudix (nucleoside diphosphate linked moiety X)-type moitf 8         0         0           NM_017565         family with sequence similarity 20, member A         0         0           NM_020901         PHD and ring finger domains 1         0         0           NM_001033560         dyslexia susceptibility 1 candidate 1         0         0           NM_00114617         mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase         0         0           NM_006941         SRY (sex determining region Y)-box 10         0         0           NM_0152380         T-box 15         0         0           NM_015995         Kruppel-like factor 13         0         0           NM_017957         epsin 3         0         0           NM_0113011         family with sequence similarity 108, member A1         0         0           NM_00113011         family with sequence similarity 108, member A1         0         0           NM_011307         phosphodiesterase 4A, cAMP-specific         0         0           NM_011307         trafficking protein, kinesin binding 2         0         0           NM_020332         zinc finger protein 687         0	NM_052859         RFT1 homolog (S. cerevisiae)         0         0         0           NM_181843         nudix (nucleoside diphosphate linked moiety X)-type motif 8         0         0         0           NM_017565         family with sequence similarity 20, member A         0         0         0           NM_020901         PHD and ring finger domains 1         0         0         0           NM_001033560         dyslexia susceptibility 1 candidate 1         0         0         0           NM_001114617         mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase         0         0         0           NM_006941         SRY (sex determining region Y)-box 10         0         0         0           NM_152380         T-box 15         0         0         0           NM_015995         Kruppel-like factor 13         0         0         0           NM_017957         epsin 3         0         0         0           NM_0113011         family with sequence similarity 108, member A1         0         0           NM_0113049         trafficking protein, kinesin binding 2         0         0           NM_01083314         chromatin modifying protein 1A         0         0           NM_020832         zinc finge	NM_052859         RFT1 homolog (S. cerevisiae)         0         0         0         0         0           NM_181843         nudix (nucleoside diphosphate linked molety X)-type motif 8         0         0         0         0         0           NM_017565         family with sequence similarity 20, member A         0         0         0         0           NM_020901         PHD and ring finger domains 1         0         0         0         0           NM_001033560         dyslexia susceptibility 1 candidate 1         0         0         0         0           NM_001114617         mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase         0         0         0         0           NM_006941         SRY (sex determining region Y)-box 10         0         0         0         0           NM_152380         T-box 15         0         0         0         0         0           NM_015995         Kruppel-like factor 13         0         0         0         0           NM_01130111         family with sequence similarity 108, member A1         0         0         0           NM_001130111         family with sequence similarity 108, member A1         0         0         0           NM_015049	NM_052859         RFT1 homolog (s. cerevisiae)         0         0         0         0         0         1           NM_181843         nudix (nucleoside diphosphate linked moiety XI-type motif 8         0         0         0         0         1           NM_017565         family with sequence similarity 20, member A         0         0         0         0         1           NM_020901         PHD and ring finger domains 1         0         0         0         0         1           NM_001033560         dyslexia susceptibility 1 candidate 1         0         0         0         0         1           NM_00114617         mannosyl (alpha-1,3-)-glycoprotein beta-1,2-N-acetylglucosaminyttransferase         0         0         0         0         1           NM_006941         SRY (sex determining region Y)-box 10         0         0         0         0         1           NM_015995         Kruppel-like factor 13         0         0         0         0         1           NM_017957         epsin 3         0         0         0         0         2           NM_001130111         family with sequence similarity 108, member A1         0         0         0         1           NM_015049         trafficking pr	NM_052859 RFT1 homolog (S. cerevisiae)	NM_052859 RFT1 homolog (s. cerevisiae) 0 0 0 0 1 0 1 0 1 0 1 0 1 0 1 0 1 1 1 0 1 1 1 0 1 1 1 1 0 1 1 1 1 0 1	NM_052859	ML_052899	M_C02899

FAM60A	NM_001135811	family with sequence similarity 60, member A	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.22	N/A	Sites in UTR
CACNA1D	NM_000720	calcium channel, voltage-dependent, L type, alpha 1D subunit	0	0	0	0	1	0	1	) hsa-miR-663	-0.22	N/A	Sites in UTR
CTF1	NM_001142544	cardiotrophin 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.22	N/A	Sites in UTR
нохв8	NM_024016	homeobox B8	1	0	1	0	0	0	0	) hsa-miR-663	-0.22	N/A	Sites in UTR
UCK2	NM_012474	uridine-cytidine kinase 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.22	N/A	Sites in UTR
RIPK1	NM_003804	receptor (TNFRSF)-interacting serine-threonine kinase 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
ERC1	NM_178039	ELKS/RAB6-interacting/CAST family member 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
SYNDIG1L	NM_001105579	synapse differentiation inducing 1-like	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
NKX2-1	NM_001079668	NK2 homeobox 1	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.22	N/A	Sites in UTR
C9orf89	NM_032310	chromosome 9 open reading frame 89	0	0	0	0	1	0	0 :	L hsa-miR-1908	-0.22	N/A	Sites in UTR
СМТМ5	NM_001037288	CKLF-like MARVEL transmembrane domain containing 5	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.22	N/A	Sites in UTR
C19orf51	NM_178837	chromosome 19 open reading frame 51	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.22	N/A	Sites in UTR
SLC6A18	NM_182632	solute carrier family 6, member 18	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
RNF165	NM_152470	ring finger protein 165	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
ZDHHC3	NM_001135179	zinc finger, DHHC-type containing 3	0	0	0	0	2	1	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
HN1L	NM_144570	hematological and neurological expressed 1-like	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.22	N/A	Sites in UTR
C17orf109	NM_001162995	chromosome 17 open reading frame 109	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.22	N/A	Sites in UTR
TAOK2	NM_004783	TAO kinase 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
VPS8	NM_001009921	vacuolar protein sorting 8 homolog (S. cerevisiae)	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.22	N/A	Sites in UTR
FBXL18	NM_024963	F-box and leucine-rich repeat protein 18	0	0	0	0	2	0	1 :	L hsa-miR-663	-0.22	N/A	Sites in UTR

TMEM184A	NM_001097620	transmembrane protein 184A	0	0	0	0	2	0	0	2	hsa-miR-663	-0.22	N/A	Sites in UTR
IL17RD	NM_017563	interleukin 17 receptor D	0	0	0	0	1	1	0	(	hsa-miR-1908	-0.22	N/A	Sites in UTR
BAD	NM_004322	BCL2-associated agonist of cell death	0	0	0	0	1	0	1	(	) hsa-miR-663	-0.22	N/A	Sites in UTR
CALB2	NM_001740	calbindin 2	0	0	0	0	1	0	1	(	) hsa-miR-663	-0.22	N/A	Sites in UTR
SEMA3F	NM_004186	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3F	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
SLC9A3R2	NM_001130012	solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 2	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
C10orf116	NM_006829	chromosome 10 open reading frame 116	0	0	0	0	1	0	0	1	l hsa-miR-1908	-0.22	N/A	Sites in UTR
TBX21	NM_013351	T-box 21	0	0	0	0	1	0	0	1	l hsa-miR-1908	-0.22	N/A	Sites in UTR
ABLIM1	NM_001003407	actin binding LIM protein 1	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
BRD3	NM_007371	bromodomain containing 3	0	0	0	0	1	0	1	(	) hsa-miR-663	-0.22	N/A	Sites in UTR
SASH3	NM_018990	SAM and SH3 domain containing 3	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
MRM1	NM_024864	mitochondrial rRNA methyltransferase 1 homolog (S. cerevisiae)	0	0	0	0	1	0	1	(	) hsa-miR-663	-0.22	N/A	Sites in UTR
CRB2	NM_173689	crumbs homolog 2 (Drosophila)	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
CDC14B	NM_001077181	CDC14 cell division cycle 14 homolog B (S. cerevisiae)	0	0	0	0	1	1	0	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
SLC17A9	NM_022082	solute carrier family 17, member 9	0	0	0	0	1	0	0	1	L hsa-miR-663	-0.22	N/A	Sites in UTR
MRPS26	NM_030811	mitochondrial ribosomal protein S26	0	0	0	0	1	0	0	1	l hsa-miR-1908	-0.22	N/A	Sites in UTR
NR4A1	NM_001202233	nuclear receptor subfamily 4, group A, member 1	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
GLTSCR1	NM_015711	glioma tumor suppressor candidate region gene 1	0	0	0	0	1	0	1	(	) hsa-miR-1908	-0.22	N/A	Sites in UTR
NSD1	NM_022455	nuclear receptor binding SET domain protein 1	0	0	0	0	1	0	1	(	) hsa-miR-663	-0.22	N/A	Sites in UTR
ССТ6А	NM_001009186	chaperonin containing TCP1, subunit 6A (zeta 1)	0	0	0	0	1	0	0	1	l hsa-miR-1908	-0.22	N/A	Sites in UTR

NM_006078	calcium channel, voltage-dependent, gamma subunit 2	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.22	N/A	Sites in UTR
NM_000597	insulin-like growth factor binding protein 2, 36kDa	0	0	0	0	1	0	1	) hsa-miR-663	-0.22	N/A	Sites in UTR
NM_002646	phosphoinositide-3-kinase, class 2, beta polypeptide	0	0	0	0	1	0	1	) hsa-miR-663	-0.22	N/A	Sites in UTR
NM_001195059	pleckstrin homology domain containing, family O member 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.22	N/A	Sites in UTR
NM_001014447	carboxypeptidase Z	0	0	0	0	1	0	0 :	1 hsa-miR-663	-0.21	N/A	Sites in UTR
NM_003704	family with sequence similarity 193, member A	0	0	0	0	1	0	0 :	1 hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_001190943	tumor necrosis factor (ligand) superfamily, member 10	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_000265	neutrophil cytosolic factor 1	0	0	0	0	1	0	0 :	1 hsa-miR-663	-0.21	N/A	Sites in UTR
NM_004040	ras homolog gene family, member B	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_052838	septin 1	0	0	0	0	2	0	2	) hsa-miR-663	-0.21	N/A	Sites in UTR
NM_012218	interleukin enhancer binding factor 3, 90kDa	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
NM_001113182	bromodomain containing 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_006426	dihydropyrimidinase-like 4	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
NM_001007225	insulin-like growth factor 2 mRNA binding protein 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
NM_001114099	seizure related 6 homolog (mouse)-like 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_001024216	filamin binding LIM protein 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_001142643	CASK interacting protein 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.21	N/A	Sites in UTR
NM_031895	calcium channel, voltage-dependent, gamma subunit 8	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
NM_145232	cytosolic thiouridylase subunit 1 homolog (S. pombe)	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
NM_020120	UDP-glucose glycoprotein glucosyltransferase 1	0	0	0	0	2	0	2	) hsa-miR-663	-0.21	N/A	Sites in UTR
	NM_000597  NM_000597  NM_0001195059  NM_001014447  NM_003704  NM_001190943  NM_000265  NM_004040  NM_052838  NM_012218  NM_01113182  NM_001113182  NM_001007225  NM_0010114099  NM_001114099  NM_001142643  NM_031895  NM_145232	insulin-like growth factor binding protein 2, 36kDa  phosphoinositide-3-kinase, class 2, beta polypeptide  pleckstrin homology domain containing, family O member 2  carboxypeptidase Z  NM_001014447  carboxypeptidase Z  NM_001190943  tumor necrosis factor (ligand) superfamily, member 10  NM_000265  neutrophil cytosolic factor 1  NM_004040  ras homolog gene family, member B  NM_052838  septin 1  NM_012218  interleukin enhancer binding factor 3, 90kDa  NM_001113182  bromodomain containing 2  dihydropyrimidinase-like 4  NM_001007225  insulin-like growth factor 2 mRNA binding protein 2  seizure related 6 homolog (mouse)-like 2  NM_001142643  CASK interacting protein 2  NM_031895  calcium channel, voltage-dependent, gamma subunit 8  NM_145232  cytosolic thiouridylase subunit 1 homolog (5. pombe)	NM_000597 insulin-like growth factor binding protein 2, 36kDa 0  NM_002646 phosphoinositide-3-kinase, class 2, beta polypeptide 0  NM_001195059 pleckstrin homology domain containing, family 0 member 2  NM_001014447 carboxypeptidase Z 0  NM_003704 family with sequence similarity 193, member A 0  NM_001190943 tumor necrosis factor (ligand) superfamily, member 10 0  NM_000265 neutrophil cytosolic factor 1 0  NM_004040 ras homolog gene family, member B 0  NM_052838 septin 1 0  NM_012218 interleukin enhancer binding factor 3, 90kDa 0  NM_001113182 bromodomain containing 2 0  NM_001007225 insulin-like growth factor 2 mRNA binding protein 2 0  NM_001114099 seizure related 6 homolog (mouse)-like 2 0  NM_001142643 CASK interacting protein 2 0  NM_001142643 calcium channel, voltage-dependent, gamma subunit 8 0  NM_031895 calcium channel, voltage-dependent, gamma subunit 8	NM_000597         insulin-like growth factor binding protein 2, 36kDa         0         0           NM_002646         phosphoinositide-3-kinase, class 2, beta polypeptide         0         0           NM_001195059         pleckstrin homology domain containing, family 0 member 2         0         0           NM_001195059         pleckstrin homology domain containing, family 0 member 2         0         0           NM_001194447         carboxypeptidase Z         0         0           NM_003704         family with sequence similarity 193, member A         0         0           NM_001190943         tumor necrosis factor (ligand) superfamily, member 10         0         0           NM_000265         neutrophil cytosolic factor 1         0         0           NM_0004040         ras homolog gene family, member B         0         0           NM_052838         septin 1         0         0           NM_012218         interleukin enhancer binding factor 3, 90kDa         0         0           NM_0113182         bromodomain containing 2         0         0           NM_006426         dihydropyrimidinase-like 4         0         0           NM_00107225         insulin-like growth factor 2 mRNA binding protein 2         0         0           NM_001142643         CAS	NM_000597         insulin-like growth factor binding protein 2, 36kDa         0         0         0           NM_002646         phosphoinositide-3-kinase, class 2, beta polypeptide         0         0         0           NM_001195059         pleckstrin homology domain containing, family O member 2         0         0         0           NM_001195059         pleckstrin homology domain containing, family O member 0         0         0         0           NM_001194447         carboxypeptidase Z         0         0         0         0           NM_003704         family with sequence similarity 193, member A         0         0         0           NM_001190943         tumor necrosis factor (ligand) superfamily, member 10         0         0         0           NM_000265         neutrophil cytosolic factor 1         0         0         0         0           NM_004040         ras homolog gene family, member B         0         0         0         0           NM_012218         interleukin enhancer binding factor 3, 90kDa         0         0         0           NM_012113182         bromodomain containing 2         0         0         0           NM_006426         dihydropyrimidinase-like 4         0         0         0           NM_00114099<	Insulin-like growth factor binding protein 2, 36kDa	NM_000597         insulin-like growth factor binding protein 2, 36kDa         0         0         0         0         1           NM_002646         phosphoinositide-3-kinase, class 2, beta polypeptide         0         0         0         0         1           NM_001195059         pleckstrin homology domain containing, family O member         0         0         0         0         1           NM_001194447         carboxypeptidase Z         0         0         0         0         0         1           NM_003704         family with sequence similarity 193, member A         0         0         0         0         1           NM_003704         family with sequence similarity 193, member A         0         0         0         0         1           NM_003704         family with sequence similarity 193, member A         0         0         0         0         1           NM_001190943         tumor necrosis factor (ligand) superfamily, member 10         0         0         0         1           NM_0002655         neutrophil cytosolic factor 1         0         0         0         0         1           NM_052838         septin 1         0         0         0         0         1           NM_0113182	NM_000597         Insulin-like growth factor binding protein 2, 36kDa         0         0         0         1         0           NM_000597         Insulin-like growth factor binding protein 2, 36kDa         0         0         0         1         0           NM_001966         phosphoinositide-3-kinase, class 2, beta polypeptide         0         0         0         0         1         0           NM_001195059         2         pleckstrin homology domain containing, family O member         0         0         0         1         0           NM_001104447         carboxypeptidase Z         0         0         0         0         1         0           NM_003704         family with sequence similarity 193, member A         0         0         0         1         0           NM_0019943         tumor necrosis factor (ligand) superfamily, member 10         0         0         0         1         0           NM_000265         neutrophil cytosolic factor 1         0         0         0         0         1         0           NM_004040         ras homolog gene family, member B         0         0         0         0         1         0           NM_052838         septin 1         0         0         0	NM_000597         insulin-like growth factor binding protein 2, 36kDa         0         0         0         1         0         0         1         0         0         1         0         0         1         0         0         1         0         0         0         1         0         0         0         1         0         0         0         0         0         1         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0         0	NM_000597	MM_000597 Insulin-tike growth factor binding protein 2, 260a 0 0 0 0 1 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 1 0 0 0 0 0 0 0 1 0 0 1 0	MM_000697

		<u> </u>												
DUSP7	NM_001947	dual specificity phosphatase 7	0	0	0	0	1	0	0	1 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
SEMA6A	NM_020796	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	0	0	0	0	1	0	0	) 1 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
H2AFX	NM_002105	H2A histone family, member X	0	0	0	0	1	0	1	0 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
TM2D2	NM_001024380	TM2 domain containing 2	0	0	0	0	1	0	1	0 h	nsa-miR-663	-0.21	N/A	Sites in UTR
FAM125B	NM_033446	family with sequence similarity 125, member B	0	0	0	0	1	0	1	0 h	nsa-miR-663	-0.21	N/A	Sites in UTR
IER5L	NM_203434	immediate early response 5-like	0	0	0	0	1	0	1	0 h	nsa-miR-663	-0.21	N/A	Sites in UTR
RASGEF1C	NM_175062	RasGEF domain family, member 1C	0	0	0	0	1	0	0	1 h	nsa-miR-663	-0.21	N/A	Sites in UTR
TLN1	NM_006289	talin 1	0	0	0	0	1	0	1	0 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
CDC123	NM_006023	cell division cycle 123 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
NOL10	NM_024894	nucleolar protein 10	0	0	0	0	1	0	1	0 h	nsa-miR-663	-0.21	N/A	Sites in UTR
GLT1D1	NM_144669	glycosyltransferase 1 domain containing 1	0	0	0	0	2	0	2	0 h	nsa-miR-663	-0.21	N/A	Sites in UTR
C20orf151	NM_080833	chromosome 20 open reading frame 151	0	0	0	0	1	0	0	1 h	nsa-miR-663	-0.21	N/A	Sites in UTR
C1orf144	NM_001114600	chromosome 1 open reading frame 144	0	0	0	0	1	0	1	0 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
ANKRD40	NM_052855	ankyrin repeat domain 40	0	0	0	0	1	0	1	0 h	nsa-miR-663	-0.21	N/A	Sites in UTR
МАРЗК10	NM_002446	mitogen-activated protein kinase kinase kinase 10	0	0	0	0	1	0	0	) 1 h	nsa-miR-663	-0.21	N/A	Sites in UTR
МҮОЗА	NM_017433	myosin IIIA	0	0	0	0	1	0	0	1 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
SLC12A7	NM_006598	solute carrier family 12 (potassium/chloride transporters), member 7	0	0	0	0	1	0	1	0 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
CNTNAP2	NM_014141	contactin associated protein-like 2	0	0	0	0	2	0	1	1 h	nsa-miR-1908	-0.21	N/A	Sites in UTR
СҮВА	NM_000101	cytochrome b-245, alpha polypeptide	0	0	0	0	1	0	0	1 h	nsa-miR-663	-0.21	N/A	Sites in UTR
SH3BP4	NM_014521	SH3-domain binding protein 4	0	0	0	0	1	0	0	1 h	nsa-miR-1908	-0.21	N/A	Sites in UTR

POLN	NM_181808	polymerase (DNA directed) nu	0	0	0	0	1	0	0	1	hsa-miR-663	-0.21	N/A	Sites in UTR
NRTN	NM_004558	neurturin	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
TBX2	NM_005994	T-box 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.21	N/A	Sites in UTR
CTDP1	NM_001202504	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
MCAT	NM_014507	malonyl CoA:ACP acyltransferase (mitochondrial)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.21	N/A	Sites in UTR
CD209	NM_001144893	CD209 molecule	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
RNPEPL1	NM_018226	arginyl aminopeptidase (aminopeptidase B)-like 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
ISL2	NM_145805	ISL LIM homeobox 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
ZNF579	NM_152600	zinc finger protein 579	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.21	N/A	Sites in UTR
PPP2R5C	NM_001161725	protein phosphatase 2, regulatory subunit B', gamma	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.21	N/A	Sites in UTR
CBX4	NM_003655	chromobox homolog 4	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.21	N/A	Sites in UTR
RBM5	NM_005778	RNA binding motif protein 5	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.21	N/A	Sites in UTR
DAPK2	NM_014326	death-associated protein kinase 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.21	N/A	Sites in UTR
DBR1	NM_016216	debranching enzyme homolog 1 (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.21	N/A	Sites in UTR
PLAC8	NM_001130716	placenta-specific 8	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.21	N/A	Sites in UTR
CD37	NM_001040031	CD37 molecule	0	0	0	0	2	0	2	0	hsa-miR-663	-0.21	N/A	Sites in UTR
UBE2K	NM_001111112	ubiquitin-conjugating enzyme E2K	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
DCUN1D2	NM_001014283	DCN1, defective in cullin neddylation 1, domain containing 2 (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
BCORL1	NM_021946	BCL6 corepressor-like 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR
MGAT5B	NM_001199172	mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl- glucosaminyltransferase, isozyme B	0	0	0	0	1	0	1	0	hsa-miR-663	-0.21	N/A	Sites in UTR

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НРСА	NM_002143	hippocalcin	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.21	N/A	Sites in UTR
KIAA1210	NM_020721	KIAA1210	0	0	0	0	1	0	0 2	l hsa-miR-663	-0.21	N/A	Sites in UTR
GLIS1	NM_147193	GLIS family zinc finger 1	0	0	0	0	1	0	0 2	l hsa-miR-663	-0.21	N/A	Sites in UTR
DTX3	NM_178502	deltex homolog 3 (Drosophila)	0	0	0	0	1	0	0 2	l hsa-miR-663	-0.21	N/A	Sites in UTR
GFRAL	NM_207410	GDNF family receptor alpha like	0	0	0	0	1	0	0 2	l hsa-miR-1908	-0.21	N/A	Sites in UTR
GMDS	NM_001500	GDP-mannose 4,6-dehydratase	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
NGFR	NM_002507	nerve growth factor receptor	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
SLITRK5	NM_015567	SLIT and NTRK-like family, member 5	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
GIGYF2	NM_001103146	GRB10 interacting GYF protein 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
BLOC1S3	NM_212550	biogenesis of lysosomal organelles complex-1, subunit 3	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
ITGA11	NM_001004439	integrin, alpha 11	0	0	0	0	1	0	0 3	l hsa-miR-663	-0.21	N/A	Sites in UTR
ATP6V0C	NM_001198569	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
СКМ	NM_001824	creatine kinase, muscle	1	0	1	0	0	0	0 (	) hsa-miR-1908	-0.21	N/A	Sites in UTR
ARL4C	NM_005737	ADP-ribosylation factor-like 4C	1	0	1	0	0	0	0 (	) hsa-miR-1908	-0.21	N/A	Sites in UTR
ARC	NM_015193	activity-regulated cytoskeleton-associated protein	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
PWWP2A	NM_052927	PWWP domain containing 2A	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
PIGA	NM_002641	phosphatidylinositol glycan anchor biosynthesis, class A	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.21	N/A	Sites in UTR
S100B	NM_006272	S100 calcium binding protein B	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.21	N/A	Sites in UTR
SLC39A13	NM_001128225	solute carrier family 39 (zinc transporter), member 13	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.21	N/A	Sites in UTR
LRRC25	NM_145256	leucine rich repeat containing 25	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.21	N/A	Sites in UTR

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CCDC140	NM_153038	coiled-coil domain containing 140	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.21	N/A	Sites in UTR
ATP2B3	NM_001001344	ATPase, Ca++ transporting, plasma membrane 3	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
DAGLA	NM_006133	diacylglycerol lipase, alpha	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
DDR1	NM_001202521	discoidin domain receptor tyrosine kinase 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
MAF	NM_001031804	v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.21	N/A	Sites in UTR
PRKCD	NM_006254	protein kinase C, delta	0	0	0	0	1	0	1	) hsa-miR-663	-0.21	N/A	Sites in UTR
TLK2	NM_001112707	tousled-like kinase 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.21	N/A	Sites in UTR
FAM19A5	NM_001082967	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.21	N/A	Sites in UTR
ADCY5	NM_001199642	adenylate cyclase 5	0	0	0	0	1	0	0 :	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
BCAN	NM_021948	brevican	0	0	0	0	1	0	0 :	1 hsa-miR-663	-0.2	N/A	Sites in UTR
ACAN	NM_001135	aggrecan	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
GPR44	NM_004778	G protein-coupled receptor 44	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
RELT	NM_032871	RELT tumor necrosis factor receptor	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
PIN1	NM_006221	peptidylprolyl cis/trans isomerase, NIMA-interacting 1	0	0	0	0	1	0	0 :	1 hsa-miR-663	-0.2	N/A	Sites in UTR
CCND1	NM_053056	cyclin D1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
ЕМР3	NM_001425	epithelial membrane protein 3	0	0	0	0	2	0	2	) hsa-miR-1908	-0.2	N/A	Sites in UTR
PYY	NM_004160	peptide YY	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.2	N/A	Sites in UTR
USP5	NM_001098536	ubiquitin specific peptidase 5 (isopeptidase T)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.2	N/A	Sites in UTR
NRXN3	NM_001105250	neurexin 3	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.2	N/A	Sites in UTR
TBC1D22B	NM_017772	TBC1 domain family, member 22B	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.2	N/A	Sites in UTR

PPM1H	NM_020700	protein phosphatase, Mg2+/Mn2+ dependent, 1H	0	0	0 (	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
BAHCC1	NM_001080519	BAH domain and coiled-coil containing 1	0	0	0 (	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
TINAGL1	NM_001204414	tubulointerstitial nephritis antigen-like 1	0	0	0 0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
HTRA3	NM_053044	HtrA serine peptidase 3	0	0	0 0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
JOSD2	NM_138334	Josephin domain containing 2	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
AMOTL1	NM_130847	angiomotin like 1	0	0	0	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
MS4A15	NM_001098835	membrane-spanning 4-domains, subfamily A, member 15	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
KLF15	NM_014079	Kruppel-like factor 15	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
MPHOSPH8	NM_017520	M-phase phosphoprotein 8	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
uqcc	NM_001184977	ubiquinol-cytochrome c reductase complex chaperone	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
TMPRSS3	NM_024022	transmembrane protease, serine 3	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
DNAJB13	NM_153614	DnaJ (Hsp40) homolog, subfamily B, member 13	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
GRK6	NM_001004106	G protein-coupled receptor kinase 6	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
TRAF1	NM_001190945	TNF receptor-associated factor 1	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
KHSRP	NM_003685	KH-type splicing regulatory protein	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
GRAP	NM_006613	GRB2-related adaptor protein	0	0	0	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
WSCD1	NM_015253	WSC domain containing 1	0	0	0 (	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
MIER1	NM_001077700	mesoderm induction early response 1 homolog (Xenopus laevis)	0	0	0 (	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
NANOS2	NM_001029861	nanos homolog 2 (Drosophila)	0	0	0 0	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
SEC13	NM_001136232	SEC13 homolog (S. cerevisiae)	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR

TERF2	NM_005652	telomeric repeat binding factor 2	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
ULK3	NM 001099436	unc-51-like kinase 3 (C. elegans)	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
02113	001033 130	une 31 like killade 3 (e. elegand)					_			1 1100 11111 1300	0.2		Jones III O III
C19orf28	NM_174983	chromosome 19 open reading frame 28	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
B3GNT6	NM_138706	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase)	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
ACSF3	NM_174917	acyl-CoA synthetase family member 3	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
CCPG1	NM_004748	cell cycle progression 1	0	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
PACS2	NM_001100913	phosphofurin acidic cluster sorting protein 2	0	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
DAGLB	NM_001142936	diacylglycerol lipase, beta	0	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
ARID3A	NM_005224	AT rich interactive domain 3A (BRIGHT-like)	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
MEFV	NM_000243	Mediterranean fever	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
XPNPEP2	NM_003399	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
DBNDD1	NM_001042610	dysbindin (dystrobrevin binding protein 1) domain containing 1	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
MEIR5	NM_001002759	MEI5 meiotic recombination protein homolog (S. cerevisiae)	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
ATP2A2	NM_170665	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	0	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
INSM1	NM_002196	insulinoma-associated 1	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
MLL2	NM_003482	myeloid/lymphoid or mixed-lineage leukemia 2	0	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR
LPIN3	NM_022896	lipin 3	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.2	N/A	Sites in UTR
B3GALT4	NM_003782	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
NUDCD3	NM_015332	NudC domain containing 3	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
ACHE	NM_015831	acetylcholinesterase	0	0	0	0	1	0	1	0 hsa-miR-663	-0.2	N/A	Sites in UTR

ST3GAL1	NM_003033	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
RNMT	NM_003799	RNA (guanine-7-) methyltransferase	0	0	0	0	1	0	1	hsa-miR-1908	-0.2	N/A	Sites in UTR
FXYD6	NM_001164831	FXYD domain containing ion transport regulator 6	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
CADM3	NM_001127173	cell adhesion molecule 3	0	0	0	0	1	0	1	D hsa-miR-663	-0.2	N/A	Sites in UTR
LHX5	NM_022363	LIM homeobox 5	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
СРМ	NM_001005502	carboxypeptidase M	0	0	0	0	1	1	0	) hsa-miR-1908	-0.2	N/A	Sites in UTR
ASCL2	NM_005170	achaete-scute complex homolog 2 (Drosophila)	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
CASP8	NM_001080124	caspase 8, apoptosis-related cysteine peptidase	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
CHRNA7	NM_000746	cholinergic receptor, nicotinic, alpha 7	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
NEK2	NM_001204183	NIMA (never in mitosis gene a)-related kinase 2	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
PRR5	NM_001017528	proline rich 5 (renal)	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
PVRL1	NM_002855	poliovirus receptor-related 1 (herpesvirus entry mediator C)	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
SNAPC2	NM_003083	small nuclear RNA activating complex, polypeptide 2, 45kDa	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
TNFRSF1B	NM_001066	tumor necrosis factor receptor superfamily, member 1B	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
TMEM179	NM_207379	transmembrane protein 179	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
UGDH	NM_001184700	UDP-glucose 6-dehydrogenase	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
C6orf89	NM_152734	chromosome 6 open reading frame 89	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
TSKU	NM_015516	tsukushi small leucine rich proteoglycan homolog (Xenopus laevis)	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
TOLLIP	NM_019009	toll interacting protein	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
PRIC285	NM_001037335	peroxisomal proliferator-activated receptor A interacting complex 285	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR

DRG2	NM_001388	developmentally regulated GTP binding protein 2	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
STX18	NM_016930	syntaxin 18	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR
CCDC124	NM_001136203	coiled-coil domain containing 124	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
FGD5	NM_152536	FYVE, RhoGEF and PH domain containing 5	0	0	0	0	1	0	0	1 hsa-miR-663	-0.2	N/A	Sites in UTR
CAPS	NM_004058	calcyphosine	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
MSX2	NM_002449	msh homeobox 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
PRKAR1B	NM_001164758	protein kinase, cAMP-dependent, regulatory, type I, beta	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
CDCA4	NM_017955	cell division cycle associated 4	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
TET3	NM_144993	tet oncogene family member 3	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
LOC728392	NM_001162371	hypothetical protein LOC728392	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
NACC1	NM_052876	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	0	0	0	0	2	0	2	) hsa-miR-663	-0.2	N/A	Sites in UTR
FOSB	NM_001114171	FBJ murine osteosarcoma viral oncogene homolog B	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
MYO1F	NM_012335	myosin IF	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
SLC16A3	NM_001042422	solute carrier family 16, member 3 (monocarboxylic acid transporter 4)	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
MGRN1	NM_001142289	mahogunin, ring finger 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
AGPAT3	NM_001037553	1-acylglycerol-3-phosphate O-acyltransferase 3	0	0	0	0	1	0	1	) hsa-miR-1908	-0.2	N/A	Sites in UTR
TMUB1	NM_001136044	transmembrane and ubiquitin-like domain containing 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
JDP2	NM_001135047	Jun dimerization protein 2	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
MAFA	NM_201589	v-maf musculoaponeurotic fibrosarcoma oncogene homolog A (avian)	0	0	0	0	1	0	1	) hsa-miR-663	-0.2	N/A	Sites in UTR
МАРК3	NM_001040056	mitogen-activated protein kinase 3	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.2	N/A	Sites in UTR

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MAPK13	NM_002754	mitogen-activated protein kinase 13	0	0	0	0	1	0	0 1 hsa-miR-663	-0.2	N/A	Sites in UTR
NUDT19	NM_001105570	nudix (nucleoside diphosphate linked moiety X)-type motif 19	0	0	0	0	1	0	0 1 hsa-miR-663	-0.2	? N/A	Sites in UTR
ACTC1	NM_005159	actin, alpha, cardiac muscle 1	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.2	? N/A	Sites in UTR
RAC3	NM_005052	ras-related C3 botulinum toxin substrate 3 (rho family, small GTP binding protein Rac3)	0	0	0	0	1	0	1 0 hsa-miR-663	-0.2	? N/A	Sites in UTR
HDGFRP2	NM_001001520	hepatoma-derived growth factor-related protein 2	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.2	? N/A	Sites in UTR
C19orf6	NM_001033026	chromosome 19 open reading frame 6	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.2	? N/A	Sites in UTR
FOXD2	NM_004474	forkhead box D2	0	0	0	0	1	0	0 1 hsa-miR-1908	-0.19	N/A	Sites in UTR
HCFC1	NM_005334	host cell factor C1 (VP16-accessory protein)	0	0	0	0	1	0	0 1 hsa-miR-1908	-0.19	N/A	Sites in UTR
TNPO3	NM_001191028	transportin 3	0	0	0	0	1	0	0 1 hsa-miR-663	-0.19	N/A	Sites in UTR
PLEKHN1	NM_001160184	pleckstrin homology domain containing, family N member 1	0	0	0	0	1	0	0 1 hsa-miR-663	-0.19	N/A	Sites in UTR
CCDC127	NM_145265	coiled-coil domain containing 127	0	0	0	0	1	0	0 1 hsa-miR-1908	-0.19	N/A	Sites in UTR
IRF4	NM_001195286	interferon regulatory factor 4	0	0	0	0	1	0	1 0 hsa-miR-663	-0.19	N/A	Sites in UTR
RAB8A	NM_005370	RAB8A, member RAS oncogene family	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.19	N/A	Sites in UTR
BRSK2	NM_003957	BR serine/threonine kinase 2	0	0	0	0	1	0	1 0 hsa-miR-663	-0.19	N/A	Sites in UTR
NRG2	NM_001184935	neuregulin 2	0	0	0	0	2	0	2 0 hsa-miR-663	-0.19	N/A	Sites in UTR
EML3	NM_153265	echinoderm microtubule associated protein like 3	0	0	0	0	1	0	1 0 hsa-miR-663	-0.19	N/A	Sites in UTR
KLHL29	NM_052920	kelch-like 29 (Drosophila)	0	0	0	0	1	0	0 1 hsa-miR-663	-0.19	N/A	Sites in UTR
SLC22A12	NM_144585	solute carrier family 22 (organic anion/urate transporter), member 12	0	0	0	0	1	0	0 1 hsa-miR-1908	-0.19	N/A	Sites in UTR
BCL9L	NM_182557	B-cell CLL/lymphoma 9-like	0	0	0	0	1	0	0 1 hsa-miR-1908	-0.19	N/A	Sites in UTR
GGA1	NM_001001560	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	0	0	0	0	1	0	1 0 hsa-miR-1908	-0.19	N/A	Sites in UTR

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REM2	NM_173527	RAS (RAD and GEM)-like GTP binding 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
CBS	NM_000071	cystathionine-beta-synthase	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
GJA3	NM_021954	gap junction protein, alpha 3, 46kDa	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
CABP1	NM_001033677	calcium binding protein 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
TBC1D14	NM_001113361	TBC1 domain family, member 14	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
C17orf62	NM_001033046	chromosome 17 open reading frame 62	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
YPEL3	NM_001145524	yippee-like 3 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
C3orf21	NM_152531	chromosome 3 open reading frame 21	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
MBOAT1	NM_001080480	membrane bound O-acyltransferase domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
BCL2L13	NM_015367	BCL2-like 13 (apoptosis facilitator)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
KIAA1522	NM_001198972	KIAA1522	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
TOM1L2	NM_001033551	target of myb1-like 2 (chicken)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
CDK6	NM_001145306	cyclin-dependent kinase 6	0	0	0	0	3	0	3	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
SCNM1	NM_001204856	sodium channel modifier 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
TNFAIP8L2-SCNM1	NM_001204848	TNFAIP8L2-SCNM1 readthrough	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
OSBP2	NM_030758	oxysterol binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
PANX2	NM_001160300	pannexin 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.19	N/A	Sites in UTR
VIPR2	NM_003382	vasoactive intestinal peptide receptor 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
COTL1	NM_021149	coactosin-like 1 (Dictyostelium)	0	0	0	0	2	1	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
ACOXL	NM_001142807	acyl-CoA oxidase-like	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR

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NM_020422	transmembrane protein 159	0	0	0	0	1	0	0 1	hsa-miR-1908	-0.19	N/A	Sites in UTR
NM_198532	chromosome 19 open reading frame 35	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.19	N/A	Sites in UTR
NM_017857	slingshot homolog 3 (Drosophila)	0	0	0	0	1	0	1 0	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_002756	mitogen-activated protein kinase kinase 3	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.19	N/A	Sites in UTR
NM_012455	pleckstrin and Sec7 domain containing 4	0	0	0	0	1	0	0 1	. hsa-miR-1908	-0.19	N/A	Sites in UTR
NM_001002840	stromal antigen 3-like 1	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.19	N/A	Sites in UTR
NM_001849	collagen, type VI, alpha 2	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_148896	neuropeptide B	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_001167820	bladder cancer associated protein	0	0	0	0	1	0	0 1	. hsa-miR-1908	-0.19	N/A	Sites in UTR
NM_017560	zinc finger protein 853	0	0	0	0	1	0	0 1	. hsa-miR-1908	-0.19	N/A	Sites in UTR
	core 1 synthase, glycoprotein-N-acetylgalactosamine 3- beta-galactosyltransferase, 1	0	0	0	0	1	1	0 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_000389	cyclin-dependent kinase inhibitor 1A (p21, Cip1)	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_000093	collagen, type V, alpha 1	0	0	0	0	1	0	1 0	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_001099335	phytanoyl-CoA 2-hydroxylase interacting protein	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_024816	rabaptin, RAB GTPase binding effector protein 2	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_013318	proline-rich coiled-coil 2B	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_173618	INO80 complex subunit E	0	0	0	0	1	0	1 (	hsa-miR-663	-0.19	N/A	Sites in UTR
NM_001127190	c-src tyrosine kinase	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.19	N/A	Sites in UTR
NM_001098576	transmembrane BAX inhibitor motif containing 6	0	0	0	0	1	0	0 1	. hsa-miR-1908	-0.19	N/A	Sites in UTR
NM_001136264	DAZ associated protein 2	0	0	0	0	1	0	0 1	hsa-miR-1908	-0.19	N/A	Sites in UTR
	IM_198532 IM_017857 IM_0017857 IM_0017857 IM_0012455 IM_001002840 IM_001849 IM_148896 IM_001167820 IM_017560 IM_020156 IM_000093 IM_000093 IM_001099335 IM_024816 IM_013318 IM_173618 IM_173618 IM_001127190 IM_001098576	IM_198532 chromosome 19 open reading frame 35  IM_017857 slingshot homolog 3 (Drosophila)  IM_002756 mitogen-activated protein kinase kinase 3  IM_012455 pleckstrin and Sec7 domain containing 4  IM_01002840 stromal antigen 3-like 1  IM_001849 collagen, type VI, alpha 2  IM_143896 neuropeptide B  IM_001167820 bladder cancer associated protein  IM_017560 zinc finger protein 853  IM_020156 core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1  IM_000389 cyclin-dependent kinase inhibitor 1A (p21, Cip1)  IM_000093 collagen, type V, alpha 1  IM_001099335 phytanoyl-CoA 2-hydroxylase interacting protein  IM_024816 rabaptin, RAB GTPase binding effector protein 2  IM_013318 proline-rich coiled-coil 2B  IM_013318 INO80 complex subunit E  IM_001127190 c-src tyrosine kinase  IM_001098576 transmembrane BAX inhibitor motif containing 6	IM_198532         chromosome 19 open reading frame 35         0           IM_017857         slingshot homolog 3 (Drosophila)         0           IM_002756         mitogen-activated protein kinase kinase 3         0           IM_012455         pleckstrin and Sec7 domain containing 4         0           IM_001002840         stromal antigen 3-like 1         0           IM_001849         collagen, type VI, alpha 2         0           IM_0148896         neuropeptide B         0           IM_017560         zinc finger protein 853         0           IM_020156         core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1         0           IM_000389         cyclin-dependent kinase inhibitor 1A (p21, Cip1)         0           IM_000093         collagen, type V, alpha 1         0           IM_001099335         phytanoyl-CoA 2-hydroxylase interacting protein         0           IM_013318         proline-rich coiled-coil 2B         0           IM_013318         INO80 complex subunit E         0           IM_001127190         c-src tyrosine kinase         0           IM_001098576         transmembrane BAX inhibitor motif containing 6         0	IM_198532         chromosome 19 open reading frame 35         0         0           IM_017857         slingshot homolog 3 (Drosophila)         0         0           IM_002756         mitogen-activated protein kinase kinase 3         0         0           IM_012455         pleckstrin and Sec7 domain containing 4         0         0           IM_010002840         stromal antigen 3-like 1         0         0           IM_01849         collagen, type VI, alpha 2         0         0           IM_018896         neuropeptide B         0         0           IM_0167820         bladder cancer associated protein         0         0           IM_017560         zinc finger protein 853         0         0           IM_020156         core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1         0         0           IM_000389         cyclin-dependent kinase inhibitor 1A (p21, Cip1)         0         0           IM_00093         collagen, type V, alpha 1         0         0           IM_001099335         phytanoyl-CoA 2-hydroxylase interacting protein         0         0           IM_013318         proline-rich coiled-coil 2B         0         0           IM_013318         INO80 complex subunit E         0         0	IM_198532         chromosome 19 open reading frame 35         0         0         0           IM_017857         slingshot homolog 3 (Drosophila)         0         0         0           IM_002756         mitogen-activated protein kinase kinase 3         0         0         0           IM_012455         pleckstrin and Sec7 domain containing 4         0         0         0           IM_001002840         stromal antigen 3-like 1         0         0         0           IM_001849         collagen, type VI, alpha 2         0         0         0           IM_0148896         neuropeptide B         0         0         0           IM_017560         zinc finger protein 853         0         0         0           IM_017560         zinc finger protein 853         0         0         0           IM_020156         core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1         0         0           IM_000389         cyclin-dependent kinase inhibitor 1A (p21, Cip1)         0         0           IM_000933         collagen, type V, alpha 1         0         0           IM_00199335         phytanoyl-CoA 2-hydroxylase interacting protein         0         0           IM_013318         proline-rich coiled-coil 2B	M_198532         chromosome 19 open reading frame 35         0         0         0         0           M_017857         slingshot homolog 3 (Drosophila)         0         0         0         0           M_002756         mitogen-activated protein kinase kinase 3         0         0         0         0           M_012455         pleckstrin and Sec7 domain containing 4         0         0         0         0           M_001002840         stromal antigen 3-like 1         0         0         0         0           M_01849         collagen, type VI, alpha 2         0         0         0         0           M_01167820         bladder cancer associated protein         0         0         0         0           M_017560         zinc finger protein 853         0         0         0         0           M_020156         core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1         0         0         0           M_000389         cyclin-dependent kinase inhibitor 1A (p21, Cip1)         0         0         0           M_000093         collagen, type V, alpha 1         0         0         0           M_000199335         phytanoyi-CoA 2-hydroxylase interacting protein         0         0         0	M_198532         chromosome 19 open reading frame 35         0         0         0         0         1           M_017857         slingshot homolog 3 (Drosophila)         0         0         0         0         1           M_002756         mitogen-activated protein kinase kinase 3         0         0         0         0         1           M_012455         pleckstrin and Sec7 domain containing 4         0         0         0         0         1           M_001002840         stromal antigen 3-like 1         0         0         0         0         1           M_001849         collagen, type VI, alpha 2         0         0         0         0         1           M_148896         neuropeptide 8         0         0         0         0         1           M_001167820         bladder cancer associated protein         0         0         0         1           M_017560         zinc finger protein 853         0         0         0         0         1           M_00389         cyclin-dependent kinase inhibitor 1A (p21, Cip1)         0         0         0         1           M_00389         cyclin-dependent kinase inhibitor protein         0         0         0         1	M_198532 chromosome 19 open reading frame 35	M_198532 chromosome 19 open reading frame 35	M_017857 directions and service services are serviced by the services and services are serviced by the services and services are serviced by the s	M_108532 chromosome 19 open reading frame 3S	M_ 198532

SLU7	NM_006425	SLU7 splicing factor homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
ZC3H3	NM_015117	zinc finger CCCH-type containing 3	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
C7orf50	NM_001134395	chromosome 7 open reading frame 50	0	0	0	0	1	0	0	1	hsa-miR-663	-0.19	N/A	Sites in UTR
VPS53	NM_001128159	vacuolar protein sorting 53 homolog (S. cerevisiae)	0	0	0	0	2	0	1	1	hsa-miR-663	-0.19	N/A	Sites in UTR
JUP	NM_002230	junction plakoglobin	0	0	0	0	1	0	1	0	hsa-miR-663	-0.19	N/A	Sites in UTR
CDK16	NM_001170460	cyclin-dependent kinase 16	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
SGPL1	NM_003901	sphingosine-1-phosphate lyase 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.19	N/A	Sites in UTR
CYP2W1	NM_017781	cytochrome P450, family 2, subfamily W, polypeptide 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
PLCXD1	NM_018390	phosphatidylinositol-specific phospholipase C, X domain containing 1	0	0	0	0	2	0	0	2	hsa-miR-1908	-0.19	N/A	Sites in UTR
VENTX	NM_014468	VENT homeobox	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
RTN4R	NM_023004	reticulon 4 receptor	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.19	N/A	Sites in UTR
ITPK1	NM_001142594	inositol-tetrakisphosphate 1-kinase	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.19	N/A	Sites in UTR
PDRG1	NM_030815	p53 and DNA-damage regulated 1	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
TP53l11	NM_001076787	tumor protein p53 inducible protein 11	0	0	0	0	1	0	1	0	hsa-miR-663	-0.18	N/A	Sites in UTR
ANK1	NM_000037	ankyrin 1, erythrocytic	0	0	0	0	2	0	2	0	hsa-miR-663	-0.18	N/A	Sites in UTR
RORC	NM_001001523	RAR-related orphan receptor C	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
ARHGAP11A	NM_014783	Rho GTPase activating protein 11A	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
FBXO21	NM_015002	F-box protein 21	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
TSPEAR	NM_144991	thrombospondin-type laminin G domain and EAR repeats	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
QPCTL	NM_001163377	glutaminyl-peptide cyclotransferase-like	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR

NM_001206645	A kinase (PRKA) interacting protein 1	0	0	0	0	1	0	0 2	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001199847	SMAD specific E3 ubiquitin protein ligase 1	0	0	0	0	1	0	0 2	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_024915	grainyhead-like 2 (Drosophila)	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001031726	chromosome 19 open reading frame 12	0	0	0	0	1	0	0 2	hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_153334	scavenger receptor class F, member 2	0	0	0	0	1	0	0 2	hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_152346	solute carrier family 43, member 2	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_207117	solute carrier family 25, member 47	0	0	0	0	1	0	0 3	. hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_005194	CCAAT/enhancer binding protein (C/EBP), beta	0	0	0	0	1	0	1 (	hsa-miR-663	-0.18	N/A	Sites in UTR
NM_003378	VGF nerve growth factor inducible	0	0	0	0	1	0	1 (	hsa-miR-663	-0.18	N/A	Sites in UTR
NM_015111	NEDD4 binding protein 3	0	0	0	0	1	0	1 (	hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_000875	insulin-like growth factor 1 receptor	0	0	0	0	2	1	1 (	hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001007559	synovial sarcoma translocation, chromosome 18	0	0	0	0	1	0	0 1	. hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_005434	mal, T-cell differentiation protein-like	0	0	0	0	1	0	0 :	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001242832	ADP-ribosylation factor GTPase activating protein 2	0	0	0	0	1	O	0 1	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001286	chloride channel 6	0	0	0	0	1	O	1 (	hsa-miR-663	-0.18	N/A	Sites in UTR
NM_003021	small glutamine-rich tetratricopeptide repeat (TPR)- containing, alpha	0	0	0	0	1	0	1 (	hsa-miR-663	-0.18	N/A	Sites in UTR
NM_005112	WD repeat domain 1	0	0	0	0	2	0	2 (	hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001130417	solute carrier family 8 (sodium/calcium exchanger), member 3	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_007107	signal sequence receptor, gamma (translocon-associated protein gamma)	0	0	0	0	1	0	0 1	. hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001017396	zinc finger protein 2	0	0	0	0	1	O	0 :	. hsa-miR-1908	-0.18	N/A	Sites in UTR
	NM_001199847  NM_001199847  NM_024915  NM_001031726  NM_153334  NM_152346  NM_207117  NM_005194  NM_003378  NM_015111  NM_000875  NM_001007559  NM_001007559  NM_005434  NM_001242832  NM_001286  NM_003021  NM_005112  NM_005112  NM_007107	NM_001199847 SMAD specific E3 ubiquitin protein ligase 1  NM_024915 grainyhead-like 2 (Drosophila)  NM_01031726 chromosome 19 open reading frame 12  NM_153334 scavenger receptor class F, member 2  NM_152346 solute carrier family 43, member 2  NM_207117 solute carrier family 25, member 47  NM_005194 CCAAT/enhancer binding protein (C/EBP), beta  NM_003378 VGF nerve growth factor inducible  NM_015111 NEDD4 binding protein 3  NM_000875 insulin-like growth factor 1 receptor  NM_001007559 synovial sarcoma translocation, chromosome 18  NM_001434 mal, T-cell differentiation protein-like  NM_001242832 ADP-ribosylation factor GTPase activating protein 2  NM_001286 chloride channel 6  NM_003021 small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha  NM_005112 WD repeat domain 1  NM_001130417 solute carrier family 8 (sodium/calcium exchanger), member 3  NM_007107 signal sequence receptor, gamma (translocon-associated protein gamma)	NM_001199847 SMAD specific E3 ubiquitin protein ligase 1 0  NM_024915 grainyhead-like 2 (Drosophila) 0  NM_01031726 chromosome 19 open reading frame 12 0  NM_153334 scavenger receptor class F, member 2 0  NM_153334 solute carrier family 43, member 2 0  NM_207117 solute carrier family 25, member 47 0  NM_005194 CCAAT/enhancer binding protein (C/EBP), beta 0  NM_003378 VGF nerve growth factor inducible 0  NM_015111 NEDD4 binding protein 3 0  NM_000875 insulin-like growth factor 1 receptor 0  NM_001007559 synovial sarcoma translocation, chromosome 18 0  NM_005434 mal, T-cell differentiation protein-like 0  NM_001242832 ADP-ribosylation factor GTPase activating protein 2 0  NM_001286 chloride channel 6 0  NM_003021 small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha 0  NM_005112 WD repeat domain 1 0  NM_00130417 solute carrier family 8 (sodium/calcium exchanger), member 3  NM_007107 signal sequence receptor, gamma (translocon-associated protein gamma)	NM_001199847         SMAD specific E3 ubiquitin protein ligase 1         0         0           NM_024915         grainyhead-like 2 (Drosophila)         0         0           NM_01031726         chromosome 19 open reading frame 12         0         0           NM_153334         scavenger receptor class F, member 2         0         0           NM_152346         solute carrier family 43, member 2         0         0           NM_207117         solute carrier family 25, member 47         0         0           NM_005194         CCAAT/enhancer binding protein (C/EBP), beta         0         0           NM_03378         VGF nerve growth factor inducible         0         0           NM_015111         NEDD4 binding protein 3         0         0           NM_000875         insulin-like growth factor 1 receptor         0         0           NM_001007559         synovial sarcoma translocation, chromosome 18         0         0           NM_005434         mal, T-cell differentiation protein-like         0         0           NM_0012286         chloride channel 6         0         0           NM_003021         small glutamine-rich tetratricopeptide repeat (TPR)-containing, alpha         0           NM_005112         WD repeat domain 1         0         0<	NM_001199847         SMAD specific E3 ubiquitin protein ligase 1         0         0         0           NM_024915         grainyhead-like 2 (Drosophila)         0         0         0           NM_001031726         chromosome 19 open reading frame 12         0         0         0           NM_153334         scavenger receptor class F, member 2         0         0         0           NM_152346         solute carrier family 43, member 2         0         0         0           NM_207117         solute carrier family 25, member 47         0         0         0           NM_005194         CCAAT/enhancer binding protein (C/EBP), beta         0         0         0           NM_03378         VGF nerve growth factor inducible         0         0         0           NM_015111         NEDD4 binding protein 3         0         0         0           NM_000875         insulin-like growth factor 1 receptor         0         0         0           NM_00107559         synovial sarcoma translocation, chromosome 18         0         0         0           NM_001242832         ADP-ribosylation factor GTPase activating protein 2         0         0         0           NM_001286         chioride channel 6         0         0         0	NM_001199847         SMAD specific E3 ubiquitin protein ligase 1         0         0         0         0           NM_024915         grainyhead-like 2 (Drosophila)         0         0         0         0           NM_001031726         chromosome 19 open reading frame 12         0         0         0         0           NM_153334         scavenger receptor class F, member 2         0         0         0         0           NM_152346         solute carrier family 43, member 2         0         0         0         0           NM_207117         solute carrier family 25, member 47         0         0         0         0           NM_005194         CCAAT/enhancer binding protein (C/EBP), beta         0         0         0         0           NM_003378         VGF nerve growth factor inducible         0         0         0         0           NM_015111         NEDD4 binding protein 3         0         0         0         0           NM_000875         insulin-like growth factor 1 receptor         0         0         0           NM_001344         mal, T-cell differentiation protein-like         0         0         0           NM_005434         mal, T-cell differentiation protein-like         0         0         0<	NM_00119847         SMAD specific E3 ubiquitin protein ligase 1         0         0         0         0         0         1           NM_024915         grainyhead-like 2 (Drosophila)         0         0         0         0         0         1           NM_021031726         chromosome 19 open reading frame 12         0         0         0         0         1           NM_153334         scavenger receptor class F, member 2         0         0         0         0         1           NM_152346         solute carrier family 43, member 2         0         0         0         0         1           NM_207117         solute carrier family 25, member 47         0         0         0         0         1           NM_005194         CCAAT/enhancer binding protein (C/EBP), beta         0         0         0         0         1           NM_003378         VGF nerve growth factor inducible         0         0         0         0         1           NM_015111         NEDD4 binding protein 3         0         0         0         0         1           NM_001007559         synovial sarcoma translocation, chromosome 18         0         0         0         0         1           NM_005434         ma	NM_001199847         SMAD specific E3 ubiquitin protein ligase 1         0         0         0         0         1         0           NM_024915         grainyhead-like 2 (Drosophila)         0         0         0         0         0         1         0           NM_001031726         chromosome 19 open reading frame 12         0         0         0         0         1         0           NM_153334         scavenger receptor class F, member 2         0         0         0         0         1         0           NM_152346         solute carrier family 43, member 2         0         0         0         0         1         0           NM_207117         solute carrier family 25, member 47         0         0         0         0         1         0           NM_005194         CCAAT/enhancer binding protein (C/EBP), beta         0         0         0         0         1         0           NM_003378         VGF nerve growth factor inducible         0         0         0         0         1         0           NM_0051511         NEDD4 binding protein 3         0         0         0         0         0         1         0           NM_000875         insulin-like growth factor 1 recepto	NM_001199847 SMAD specific E3 ubiquitin protein ligase 1 0 0 0 0 0 1 0 0 1 0 0 0 0 0 0 0 0 0	NM_001199847 SMAD specific E3 ubiquitifi protein ligase 1 0 0 0 0 0 0 1 0 0 0 1 1 0 0 0 1 1 has-miR-653  NM_00129126 grainyhead-like 2 (Drosophila) 0 0 0 0 0 0 0 0 1 0 0 0 1 1 has-miR-653  NM_001031726 chromosome 19 open reading frame 12 0 0 0 0 0 0 0 1 0 0 0 1 1 0 0 0 1 has-miR-653  NM_001031726 solute carrier family 43, member 2 0 0 0 0 0 0 0 1 0 0 0 1 1 0 0 0 1 has-miR-653  NM_153334 solute carrier family 25, member 2 0 0 0 0 0 0 0 1 0 0 0 1 1 0 0 0 1 has-miR-653  NM_005194 CCAAT/enhancer binding protein (C/F8P), beta 0 0 0 0 0 0 1 0 0 1 0 0 1 1 0 0 1 1 has-miR-663  NM_003378 VGF nerve growth factor inducible 0 0 0 0 0 0 0 1 0 0 1 0 0 1 0 has-miR-663  NM_003378 VGF nerve growth factor 1 receptor 0 0 0 0 0 0 0 0 1 0 0 1 0 0 1 1 0 0 has-miR-663  NM_003578 should be growth factor 1 receptor 0 0 0 0 0 0 0 0 1 0 0 1 1 0 0 has-miR-663  NM_003578 should be growth factor 1 receptor 0 0 0 0 0 0 0 0 1 0 0 0 1 1 0 0 has-miR-663  NM_005194 should be growth factor 1 receptor 0 0 0 0 0 0 0 0 1 1 0 0 0 1 has-miR-663  NM_003578 should be growth factor 1 receptor 0 0 0 0 0 0 0 0 0 1 1 0 0 0 1 has-miR-663  NM_0013614 mal, T cell differentiation protein like 0 0 0 0 0 0 0 0 1 0 0 0 1 has-miR-663  NM_005434 mal, T cell differentiation protein like 0 0 0 0 0 0 0 0 1 0 0 0 1 has-miR-663  NM_001242832 APP ribosylation factor GFPsis activating protein 2 0 0 0 0 0 0 0 0 1 0 0 0 1 has-miR-663  NM_001266 chloride channel crick tetratricopaptide repeat (TPR) 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	MA_001198477 SMAD specific E3 whisquishin protein lignor 1	MA_00199847

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ZSWIM1	NM_080603	zinc finger, SWIM-type containing 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
ZNF543	NM_213598	zinc finger protein 543	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
IGLON5	NM_001101372	IgLON family member 5	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
ARHGAP1	NM_004308	Rho GTPase activating protein 1	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.18	N/A	Sites in UTR
JUND	NM_005354	jun D proto-oncogene	1	0	1	0	0	0	0	0	hsa-miR-663	-0.18	N/A	Sites in UTR
RANBP3	NM_003624	RAN binding protein 3	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.18	N/A	Sites in UTR
PODNL1	NM_001146254	podocan-like 1	1	0	1	0	0	0	0	0	hsa-miR-1908	-0.18	N/A	Sites in UTR
RASL10B	NM_033315	RAS-like, family 10, member B	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR
PSPH	NM_004577	phosphoserine phosphatase	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
TBCCD1	NM_001134415	TBCC domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
ADCY1	NM_021116	adenylate cyclase 1 (brain)	0	0	0	0	1	0	1	. 0	hsa-miR-663	-0.18	N/A	Sites in UTR
ATP2B2	NM_001001331	ATPase, Ca++ transporting, plasma membrane 2	0	0	0	0	2	0	0	2	hsa-miR-1908	-0.18	N/A	Sites in UTR
TAB1	NM_153497	TGF-beta activated kinase 1/MAP3K7 binding protein 1	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR
KIAA0664	NM_015229	KIAA0664	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR
SH3BP5L	NM_030645	SH3-binding domain protein 5-like	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR
OSR1	NM_145260	odd-skipped related 1 (Drosophila)	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR
LTBP4	NM_001042544	latent transforming growth factor beta binding protein 4	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
SLC27A1	NM_198580	solute carrier family 27 (fatty acid transporter), member 1	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
TK2	NM_001172643	thymidine kinase 2, mitochondrial	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR
C19orf63	NM_175063	chromosome 19 open reading frame 63	0	0	0	0	1	0	1	. 0	hsa-miR-1908	-0.18	N/A	Sites in UTR

NM_022114	PR domain containing 16	0	0	0	0	2	0	1 1	l hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_021907	dystrobrevin, beta	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_000175	glucose-6-phosphate isomerase	0	0	0	0	1	0	0 3	l hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_014564	LIM homeobox 3	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.18	N/A	Sites in UTR
NM_012101	tripartite motif containing 29	0	0	0	0	1	0	0 3	L hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_003714	stanniocalcin 2	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.18	N/A	Sites in UTR
MM 001047535	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_001013659	zinc finger protein 793	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.18	N/A	Sites in UTR
NM_006499	lectin, galactoside-binding, soluble, 8	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_004717	diacylglycerol kinase, iota	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001190411	rabphilin 3A-like (without C2 domains)	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_022493	nuclear prelamin A recognition factor-like	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_001042697	zinc finger, SWIM-type containing 7	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.18	N/A	Sites in UTR
VIVI 001168388	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.18	N/A	Sites in UTR
NM_138496	cysteine/histidine-rich 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.18	N/A	Sites in UTR
NM_052897	methyl-CpG binding domain protein 6	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.18	N/A	Sites in UTR
NM_001076680	chromosome 17 open reading frame 108	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.18	N/A	Sites in UTR
NM_016037	UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.18	N/A	Sites in UTR
NM_005231	cortactin	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.18	N/A	Sites in UTR
NM_002586	pre-B-cell leukemia homeobox 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.18	N/A	Sites in UTR
	M_021907  M_00175  M_014564  M_012101  M_003714  M_001042535  M_001013659  M_006499  M_004717  M_001190411  M_022493  M_001042697  M_01168388  M_138496  M_052897  M_001076680  M_016037  M_005231	M_001907 dystrobrevin, beta  M_00175 glucose-6-phosphate isomerase  M_014564 LIM homeobox 3  M_012101 tripartite motif containing 29  M_003714 stanniocalcin 2  M_001042535 ArfGAP with GTPase domain, ankyrin repeat and PH domain 3  M_001013659 zinc finger protein 793  M_006499 lectin, galactoside-binding, soluble, 8  M_004717 dlacylglycerol kinase, iota  M_001190411 rabphilin 3A-like (without C2 domains)  M_022493 nuclear prelamin A recognition factor-like  M_001042697 zinc finger, SWIM-type containing 7  Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2  Cysteine/histidine-rich 1  M_052897 methyl-CpG binding domain protein 6  Chromosome 17 open reading frame 108  M_016037 UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)  M_005231 cortactin	M_021907         dystrobrevin, beta         0           M_000175         glucose-6-phosphate isomerase         0           M_014564         LIM homeobox 3         0           M_012101         tripartite motif containing 29         0           M_003714         stanniocalcin 2         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0           M_00103659         zinc finger protein 793         0           M_006499         lectin, galactoside-binding, soluble, 8         0           M_004717         diacylglycerol kinase, iota         0           M_001190411         rabphilin 3A-like (without C2 domains)         0           M_022493         nuclear prelamin A recognition factor-like         0           M_00142697         zinc finger, SWIM-type containing 7         0           M_00168388         Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2         0           M_138496         cysteine/histidine-rich 1         0           M_052897         methyl-CpG binding domain protein 6         0           M_0010076680         chromosome 17 open reading frame 108         0           M_016037         UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast)         0           M_005231 <td>M_021907         dystrobrevin, beta         0         0           M_000175         glucose-6-phosphate isomerase         0         0           M_014564         LIM homeobox 3         0         0           M_012101         tripartite motif containing 29         0         0           M_003714         stanniocalcin 2         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0           M_001013659         zinc finger protein 793         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0           M_00190411         rabphilin 3A-like (without C2 domains)         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0           M_0012493         nuclear prelamin A recognition factor-like         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0           M_001168388         Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2         0         0           M_138496         cysteine/histidine-rich 1         0         0           M_052897         methyl-CpG binding domain protein 6         0         0</td> <td>M_021907         dystrobrevin, beta         0         0         0           M_000175         glucose-6-phosphate isomerase         0         0         0           M_014564         LIM homeobox 3         0         0         0           M_012101         tripartite motif containing 29         0         0         0           M_003714         stanniocalcin 2         0         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0         0           M_00113659         zinc finger protein 793         0         0         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0         0         0           M_004717         diacylglycerol kinase, iota         0         0         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0         0           M_022493         nuclear prelamin A recognition factor-like         0         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0         0           M_0168388         Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2         0         0<!--</td--><td>M_021907         dystrobrevin, beta         0         0         0         0           M_000175         glucose-6-phosphate isomerase         0         0         0         0           M_014564         LIM homeobox 3         0         0         0         0           M_012101         tripartite motif containing 29         0         0         0         0           M_003714         stanniocalcin 2         0         0         0         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0         0         0         0           M_001013659         zinc finger protein 793         0         0         0         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0         0         0           M_004717         diacylglycerol kinase, iota         0         0         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0         0           M_022493         nuclear prelamin A recognition factor-like         0         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0         0     <td>M_00175 dystrobrevin, beta 0 0 0 0 0 0 1  M_00175 glucose-6-phosphate isomerase 0 0 0 0 0 1  M_014564 LIM homeobox 3 0 0 0 0 0 1  M_012101 tripartite motif containing 29 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_001042535 ArfGAP with GTPase domain, ankyrin repeat and PH 0 0 0 0 0 1  M_001013659 zinc finger protein 793 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 1  M_001190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1  M_002493 nuclear prelamin A recognition factor-like 0 0 0 0 1  M_001042697 zinc finger, SWIM-type containing 7 0 0 0 0 1  M_001168388 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2  M_138496 cysteine/histidine-rich 1 0 0 0 0 1  M_052897 methyl-CpG binding domain protein 6 0 0 0 0 1  M_001076680 chromosome 17 open reading frame 108 0 0 0 0 1  M_0016037 UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) 0 0 0 0 1  M_005231 cortactin 0 0 0 0 0 1</td><td>M_021907</td><td>M_0021907</td><td>M_002197 dystrobrevin, beta 0 0 0 0 1 0 0 1 hss=miR-1908  M_002175 glucose-6-phosphate komerase 0 0 0 0 0 1 0 0 1 hss=miR-1908  M_014564 UM homeobox 3 0 0 0 0 1 0 0 1 hss=miR-1908  M_012101 tripartite motif containing 29 0 0 0 0 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 hss=miR-1908  M_001042535 ArfGAV with GTYpase domain, ankyrin repeat and PH 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 hss=miR-1908  M_00499 lectin, galactoside binding, soluble, 8 0 0 0 0 1 0 0 1 hss=miR-1908  M_004717 diacylglycerol kinase, lota 0 0 0 0 1 0 0 1 hss=miR-1908  M_00190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1 0 0 1 hss=miR-1908  M_001042697 ininc finger, SWIM type containing 7 0 0 0 1 0 0 1 hss=miR-1908  M_00168388 Caplya00-interacting transactivator, with Glu/Asp-rich or carboxy-terminal domains, 2 carboxy-term</td><td>M_00175</td><td>M_021867 obstrokrym, beta 0 0 0 0 0 1 1 0 0 1 1 hs-milk-1908 -0.18 N/A M_000775 glucoe 6 phosphate isomerase 0 0 0 0 0 1 0 0 1 hs-milk-1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000771 unit for milk 1908 -0.18 N/A M_0007774 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_000777 unit for milk 19</td></td></td>	M_021907         dystrobrevin, beta         0         0           M_000175         glucose-6-phosphate isomerase         0         0           M_014564         LIM homeobox 3         0         0           M_012101         tripartite motif containing 29         0         0           M_003714         stanniocalcin 2         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0           M_001013659         zinc finger protein 793         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0           M_00190411         rabphilin 3A-like (without C2 domains)         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0           M_0012493         nuclear prelamin A recognition factor-like         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0           M_001168388         Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2         0         0           M_138496         cysteine/histidine-rich 1         0         0           M_052897         methyl-CpG binding domain protein 6         0         0	M_021907         dystrobrevin, beta         0         0         0           M_000175         glucose-6-phosphate isomerase         0         0         0           M_014564         LIM homeobox 3         0         0         0           M_012101         tripartite motif containing 29         0         0         0           M_003714         stanniocalcin 2         0         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0         0           M_00113659         zinc finger protein 793         0         0         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0         0         0           M_004717         diacylglycerol kinase, iota         0         0         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0         0           M_022493         nuclear prelamin A recognition factor-like         0         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0         0           M_0168388         Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2         0         0 </td <td>M_021907         dystrobrevin, beta         0         0         0         0           M_000175         glucose-6-phosphate isomerase         0         0         0         0           M_014564         LIM homeobox 3         0         0         0         0           M_012101         tripartite motif containing 29         0         0         0         0           M_003714         stanniocalcin 2         0         0         0         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0         0         0         0           M_001013659         zinc finger protein 793         0         0         0         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0         0         0           M_004717         diacylglycerol kinase, iota         0         0         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0         0           M_022493         nuclear prelamin A recognition factor-like         0         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0         0     <td>M_00175 dystrobrevin, beta 0 0 0 0 0 0 1  M_00175 glucose-6-phosphate isomerase 0 0 0 0 0 1  M_014564 LIM homeobox 3 0 0 0 0 0 1  M_012101 tripartite motif containing 29 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_001042535 ArfGAP with GTPase domain, ankyrin repeat and PH 0 0 0 0 0 1  M_001013659 zinc finger protein 793 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 1  M_001190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1  M_002493 nuclear prelamin A recognition factor-like 0 0 0 0 1  M_001042697 zinc finger, SWIM-type containing 7 0 0 0 0 1  M_001168388 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2  M_138496 cysteine/histidine-rich 1 0 0 0 0 1  M_052897 methyl-CpG binding domain protein 6 0 0 0 0 1  M_001076680 chromosome 17 open reading frame 108 0 0 0 0 1  M_0016037 UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) 0 0 0 0 1  M_005231 cortactin 0 0 0 0 0 1</td><td>M_021907</td><td>M_0021907</td><td>M_002197 dystrobrevin, beta 0 0 0 0 1 0 0 1 hss=miR-1908  M_002175 glucose-6-phosphate komerase 0 0 0 0 0 1 0 0 1 hss=miR-1908  M_014564 UM homeobox 3 0 0 0 0 1 0 0 1 hss=miR-1908  M_012101 tripartite motif containing 29 0 0 0 0 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 hss=miR-1908  M_001042535 ArfGAV with GTYpase domain, ankyrin repeat and PH 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 hss=miR-1908  M_00499 lectin, galactoside binding, soluble, 8 0 0 0 0 1 0 0 1 hss=miR-1908  M_004717 diacylglycerol kinase, lota 0 0 0 0 1 0 0 1 hss=miR-1908  M_00190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1 0 0 1 hss=miR-1908  M_001042697 ininc finger, SWIM type containing 7 0 0 0 1 0 0 1 hss=miR-1908  M_00168388 Caplya00-interacting transactivator, with Glu/Asp-rich or carboxy-terminal domains, 2 carboxy-term</td><td>M_00175</td><td>M_021867 obstrokrym, beta 0 0 0 0 0 1 1 0 0 1 1 hs-milk-1908 -0.18 N/A M_000775 glucoe 6 phosphate isomerase 0 0 0 0 0 1 0 0 1 hs-milk-1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000771 unit for milk 1908 -0.18 N/A M_0007774 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_000777 unit for milk 19</td></td>	M_021907         dystrobrevin, beta         0         0         0         0           M_000175         glucose-6-phosphate isomerase         0         0         0         0           M_014564         LIM homeobox 3         0         0         0         0           M_012101         tripartite motif containing 29         0         0         0         0           M_003714         stanniocalcin 2         0         0         0         0         0           M_001042535         ArfGAP with GTPase domain, ankyrin repeat and PH domain 3         0         0         0         0         0           M_001013659         zinc finger protein 793         0         0         0         0         0           M_006499         lectin, galactoside-binding, soluble, 8         0         0         0         0           M_004717         diacylglycerol kinase, iota         0         0         0         0           M_001190411         rabphilin 3A-like (without C2 domains)         0         0         0           M_022493         nuclear prelamin A recognition factor-like         0         0         0           M_001042697         zinc finger, SWIM-type containing 7         0         0         0 <td>M_00175 dystrobrevin, beta 0 0 0 0 0 0 1  M_00175 glucose-6-phosphate isomerase 0 0 0 0 0 1  M_014564 LIM homeobox 3 0 0 0 0 0 1  M_012101 tripartite motif containing 29 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_001042535 ArfGAP with GTPase domain, ankyrin repeat and PH 0 0 0 0 0 1  M_001013659 zinc finger protein 793 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 1  M_001190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1  M_002493 nuclear prelamin A recognition factor-like 0 0 0 0 1  M_001042697 zinc finger, SWIM-type containing 7 0 0 0 0 1  M_001168388 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2  M_138496 cysteine/histidine-rich 1 0 0 0 0 1  M_052897 methyl-CpG binding domain protein 6 0 0 0 0 1  M_001076680 chromosome 17 open reading frame 108 0 0 0 0 1  M_0016037 UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) 0 0 0 0 1  M_005231 cortactin 0 0 0 0 0 1</td> <td>M_021907</td> <td>M_0021907</td> <td>M_002197 dystrobrevin, beta 0 0 0 0 1 0 0 1 hss=miR-1908  M_002175 glucose-6-phosphate komerase 0 0 0 0 0 1 0 0 1 hss=miR-1908  M_014564 UM homeobox 3 0 0 0 0 1 0 0 1 hss=miR-1908  M_012101 tripartite motif containing 29 0 0 0 0 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 hss=miR-1908  M_001042535 ArfGAV with GTYpase domain, ankyrin repeat and PH 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 hss=miR-1908  M_00499 lectin, galactoside binding, soluble, 8 0 0 0 0 1 0 0 1 hss=miR-1908  M_004717 diacylglycerol kinase, lota 0 0 0 0 1 0 0 1 hss=miR-1908  M_00190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1 0 0 1 hss=miR-1908  M_001042697 ininc finger, SWIM type containing 7 0 0 0 1 0 0 1 hss=miR-1908  M_00168388 Caplya00-interacting transactivator, with Glu/Asp-rich or carboxy-terminal domains, 2 carboxy-term</td> <td>M_00175</td> <td>M_021867 obstrokrym, beta 0 0 0 0 0 1 1 0 0 1 1 hs-milk-1908 -0.18 N/A M_000775 glucoe 6 phosphate isomerase 0 0 0 0 0 1 0 0 1 hs-milk-1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000771 unit for milk 1908 -0.18 N/A M_0007774 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_000777 unit for milk 19</td>	M_00175 dystrobrevin, beta 0 0 0 0 0 0 1  M_00175 glucose-6-phosphate isomerase 0 0 0 0 0 1  M_014564 LIM homeobox 3 0 0 0 0 0 1  M_012101 tripartite motif containing 29 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_003714 stanniocalcin 2 0 0 0 0 0 1  M_001042535 ArfGAP with GTPase domain, ankyrin repeat and PH 0 0 0 0 0 1  M_001013659 zinc finger protein 793 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 0 1  M_004717 dlacylglycerol kinase, iota 0 0 0 0 1  M_001190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1  M_002493 nuclear prelamin A recognition factor-like 0 0 0 0 1  M_001042697 zinc finger, SWIM-type containing 7 0 0 0 0 1  M_001168388 Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2  M_138496 cysteine/histidine-rich 1 0 0 0 0 1  M_052897 methyl-CpG binding domain protein 6 0 0 0 0 1  M_001076680 chromosome 17 open reading frame 108 0 0 0 0 1  M_0016037 UTP11-like, U3 small nucleolar ribonucleoprotein, (yeast) 0 0 0 0 1  M_005231 cortactin 0 0 0 0 0 1	M_021907	M_0021907	M_002197 dystrobrevin, beta 0 0 0 0 1 0 0 1 hss=miR-1908  M_002175 glucose-6-phosphate komerase 0 0 0 0 0 1 0 0 1 hss=miR-1908  M_014564 UM homeobox 3 0 0 0 0 1 0 0 1 hss=miR-1908  M_012101 tripartite motif containing 29 0 0 0 0 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 1 hss=miR-1908  M_003714 stanniocalcin 2 0 0 0 0 1 1 0 0 hss=miR-1908  M_001042535 ArfGAV with GTYpase domain, ankyrin repeat and PH 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 0 hss=miR-1908  M_001013659 ininc finger protein 793 0 0 0 0 1 0 1 0 1 hss=miR-1908  M_00499 lectin, galactoside binding, soluble, 8 0 0 0 0 1 0 0 1 hss=miR-1908  M_004717 diacylglycerol kinase, lota 0 0 0 0 1 0 0 1 hss=miR-1908  M_00190411 rabphilin 3A-like (without C2 domains) 0 0 0 0 1 0 0 1 hss=miR-1908  M_001042697 ininc finger, SWIM type containing 7 0 0 0 1 0 0 1 hss=miR-1908  M_00168388 Caplya00-interacting transactivator, with Glu/Asp-rich or carboxy-terminal domains, 2 carboxy-term	M_00175	M_021867 obstrokrym, beta 0 0 0 0 0 1 1 0 0 1 1 hs-milk-1908 -0.18 N/A M_000775 glucoe 6 phosphate isomerase 0 0 0 0 0 1 0 0 1 hs-milk-1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000776 unit for milk 1908 -0.18 N/A M_000771 unit for milk 1908 -0.18 N/A M_0007774 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_0007777 unit for milk 1908 -0.18 N/A M_000777 unit for milk 19

		protein prenyltransferase alpha subunit repeat containing												
PTAR1	NM_001099666	1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.18	N/A	Sites in UTR
CACNA1B	NM_000718	calcium channel, voltage-dependent, N type, alpha 1B subunit	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
CAMK2G	NM_001204492	calcium/calmodulin-dependent protein kinase II gamma	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
KCNJ15	NM_002243	potassium inwardly-rectifying channel, subfamily J, member 15	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
SEC14L1	NM_001143998	SEC14-like 1 (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
FLYWCH1	NM_032296	FLYWCH-type zinc finger 1	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
KCNG4	NM_172347	potassium voltage-gated channel, subfamily G, member 4	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
SLC25A45	NM_001077241	solute carrier family 25, member 45	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
HSD17B13	NM_001136230	hydroxysteroid (17-beta) dehydrogenase 13	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
ADAP1	NM_006869	ArfGAP with dual PH domains 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.18	N/A	Sites in UTR
NAT15	NM_001083600	N-acetyltransferase 15 (GCN5-related, putative)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.18	N/A	Sites in UTR
CNGB1	NM_001297	cyclic nucleotide gated channel beta 1	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
RPS6KB2	NM_003952	ribosomal protein S6 kinase, 70kDa, polypeptide 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
CACNA1H	NM_001005407	calcium channel, voltage-dependent, T type, alpha 1H subunit	0	0	0	0	1	0	0	1	hsa-miR-663	-0.18	N/A	Sites in UTR
BRD4	NM_058243	bromodomain containing 4	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
PCDHB11	NM_018931	protocadherin beta 11	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.18	N/A	Sites in UTR
MLLT1	NM_005934	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.18	N/A	Sites in UTR
PAFAH1B1	NM_000430	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.18	N/A	Sites in UTR
AKAP11	NM_016248	A kinase (PRKA) anchor protein 11	0	0	0	0	1	0	1	0	hsa-miR-663	-0.18	N/A	Sites in UTR
SLC9A8	NM_015266	solute carrier family 9 (sodium/hydrogen exchanger), member 8	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.18	N/A	Sites in UTR

TP53INP1	NM 001135733	tumor protein p53 inducible nuclear protein 1	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.17	N/A	Sites in UTR
		potent position position protein 2											
C9orf91	NM_153045	chromosome 9 open reading frame 91	0	0	0	0	1	1	0	D hsa-miR-663	-0.17	N/A	Sites in UTR
OBFC2A	NM_001031716	oligonucleotide/oligosaccharide-binding fold containing 2A	0	0	0	0	1	O	0	1 hsa-miR-1908	-0.17	N/A	Sites in UTR
GLG1	NM_001145666	golgi glycoprotein 1	0	0	0	0	2	0	0	2 hsa-miR-1908	-0.17	N/A	Sites in UTR
SRC	NM_005417	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.17	N/A	Sites in UTR
USP2	NM_004205	ubiquitin specific peptidase 2	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
RASA3	NM_007368	RAS p21 protein activator 3	0	0	0	0	1	0	1	0 hsa-miR-663	-0.17	N/A	Sites in UTR
WWC3	NM_015691	WWC family member 3	0	0	0	0	1	0	1	0 hsa-miR-663	-0.17	N/A	Sites in UTR
C15orf52	NM_207380	chromosome 15 open reading frame 52	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
RXRA	NM_002957	retinoid X receptor, alpha	0	0	0	0	2	0	2	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
NSUN7	NM_024677	NOP2/Sun domain family, member 7	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.17	N/A	Sites in UTR
BCL2L15	NM_001010922	BCL2-like 15	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.17	N/A	Sites in UTR
SOCS3	NM_003955	suppressor of cytokine signaling 3	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
ZNF618	NM_133374	zinc finger protein 618	0	0	0	0	2	1	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
VPS13C	NM_017684	vacuolar protein sorting 13 homolog C (S. cerevisiae)	0	0	0	0	1	0	0	1 hsa-miR-663	-0.17	N/A	Sites in UTR
MTMR10	NM_017762	myotubularin related protein 10	0	0	0	0	1	0	0	1 hsa-miR-663	-0.17	N/A	Sites in UTR
SLMO1	NM_001142405	slowmo homolog 1 (Drosophila)	0	0	0	0	1	0	1	0 hsa-miR-663	-0.17	N/A	Sites in UTR
CYP46A1	NM_006668	cytochrome P450, family 46, subfamily A, polypeptide 1	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
PTCD1	NM_015545	pentatricopeptide repeat domain 1	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR
ATP5J2-PTCD1	NM_001198879	ATP5J2-PTCD1 readthrough	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.17	N/A	Sites in UTR

		ı		1	1	1	1		1	1	T	ı		1
PIK3R2	NM_005027	phosphoinositide-3-kinase, regulatory subunit 2 (beta)	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
TECPR1	NM_015395	tectonin beta-propeller repeat containing 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
SPATS2L	NM_001100422	spermatogenesis associated, serine-rich 2-like	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
SDF4	NM_016176	stromal cell derived factor 4	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
TMEM222	NM_032125	transmembrane protein 222	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
SLC29A4	NM_001040661	solute carrier family 29 (nucleoside transporters), member 4	0	0	0	0	2	0	1	1	hsa-miR-663	-0.17	N/A	Sites in UTR
PURB	NM_033224	purine-rich element binding protein B	0	0	0	0	1	0	1	0	hsa-miR-663	-0.17	N/A	Sites in UTR
KIF3A	NM_007054	kinesin family member 3A	0	0	0	0	1	0	1	0	hsa-miR-663	-0.17	N/A	Sites in UTR
EHMT1	NM_024757	euchromatic histone-lysine N-methyltransferase 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.17	N/A	Sites in UTR
ATP6V0E2	NM_001100592	ATPase, H+ transporting V0 subunit e2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.17	N/A	Sites in UTR
TAF1C	NM_005679	TATA box binding protein (TBP)-associated factor, RNA polymerase I, C, 110kDa	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
нохв6	NM_018952	homeobox B6	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.17	N/A	Sites in UTR
SMG7	NM_001174061	smg-7 homolog, nonsense mediated mRNA decay factor (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.17	N/A	Sites in UTR
GLB1L2	NM_138342	galactosidase, beta 1-like 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.17	N/A	Sites in UTR
KIAA1143	NM_020696	KIAA1143	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.17	N/A	Sites in UTR
C6orf25	NM_025260	chromosome 6 open reading frame 25	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR
нохс6	NM_004503	homeobox C6	0	0	0	0	1	0	1	0	hsa-miR-663	-0.17	N/A	Sites in UTR
NFASC	NM_001005388	neurofascin	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.17	N/A	Sites in UTR
ZNF850	NM_001193552	zinc finger protein 850	0	0	0	0	2	0	1	1	hsa-miR-1908	-0.17	N/A	Sites in UTR
NANOG	NM_024865	Nanog homeobox	0	0	0	0	1	0	0	1	hsa-miR-663	-0.17	N/A	Sites in UTR

NM_015056	ribosomal RNA processing 1 homolog B (S. cerevisiae)	0	0	0	0	1	0	1	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_001008220	complexin 2	0	0	0	0	2	1	1	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_005026	phosphoinositide-3-kinase, catalytic, delta polypeptide	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.17	N/A	Sites in UTR
NM_003842	tumor necrosis factor receptor superfamily, member 10b	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_152458	zinc finger protein 785	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_207401	chromosome 1 open reading frame 229	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.17	N/A	Sites in UTR
NM_001035	ryanodine receptor 2 (cardiac)	0	0	0	0	1	0	1	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_016235	G protein-coupled receptor, family C, group 5, member B	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_001079906	zinc finger protein 331	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_000789	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.17	N/A	Sites in UTR
NM_014898	zinc finger protein 30 homolog (mouse)	0	0	0	0	1	0	0 :	L hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_014901	ring finger protein 44	0	0	0	0	1	0	0 :	L hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_015042	zinc finger protein 609	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_145262	glycerate kinase	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_002074	guanine nucleotide binding protein (G protein), beta polypeptide 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_001199770	orthodenticle homeobox 1	1	0	1	0	0	0	0 (	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_173354	salt-inducible kinase 1	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_153042	lysine (K)-specific demethylase 1B	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.17	N/A	Sites in UTR
NM_000587	complement component 7	0	0	0	0	1	0	0 :	L hsa-miR-1908	-0.17	N/A	Sites in UTR
NM_001142857	EF-hand calcium binding domain 1	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.17	N/A	Sites in UTR
	NM_001008220  NM_005026  NM_003842  NM_152458  NM_207401  NM_001035  NM_016235  NM_001079906  NM_000789  NM_014898  NM_014898  NM_014901  NM_015042  NM_145262  NM_002074  NM_001199770  NM_173354  NM_153042  NM_000587	NM_001008220 complexin 2  NM_005026 phosphoinositide-3-kinase, catalytic, delta polypeptide  NM_003842 tumor necrosis factor receptor superfamily, member 10b  NM_152458 zinc finger protein 785  NM_207401 chromosome 1 open reading frame 229  NM_001035 ryanodine receptor 2 (cardiac)  NM_016235 G protein-coupled receptor, family C, group 5, member B  NM_001079906 zinc finger protein 331  NM_0010789 angiotensin I converting enzyme (peptidyl-dipeptidase A)  1  NM_014898 zinc finger protein 30 homolog (mouse)  NM_014901 ring finger protein 44  NM_015042 zinc finger protein 609  NM_145262 glycerate kinase  NM_002074 guanine nucleotide binding protein (G protein), beta polypeptide 1  NM_001199770 orthodenticle homeobox 1  NM_173354 salt-inducible kinase 1  NM_153042 lysine (K)-specific demethylase 1B  NM_000587 complement component 7	NM_001008220         complexin 2         0           NM_005026         phosphoinositide-3-kinase, catalytic, delta polypeptide         0           NM_003842         tumor necrosis factor receptor superfamily, member 10b         0           NM_152458         zinc finger protein 785         0           NM_207401         chromosome 1 open reading frame 229         0           NM_001035         ryanodine receptor 2 (cardiac)         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0           NM_01079906         zinc finger protein 331         0           NM_000789         angiotensin I converting enzyme (peptidyl-dipeptidase A) 1         0           NM_014898         zinc finger protein 30 homolog (mouse)         0           NM_014901         ring finger protein 609         0           NM_015042         glycerate kinase         0           NM_145262         glycerate kinase         0           NM_002074         guanine nucleotide binding protein (G protein), beta polypeptide 1         0           NM_001199770         orthodenticle homeobox 1         1           NM_173354         salt-inducible kinase 1         0           NM_153042         lysine (K)-specific demethylase 1B         0           NM_000587	NM_001008220         complexin 2         0         0           NM_005026         phosphoinositide-3-kinase, catalytic, delta polypeptide         0         0           NM_003842         tumor necrosis factor receptor superfamily, member 10b         0         0           NM_152458         zinc finger protein 785         0         0           NM_207401         chromosome 1 open reading frame 229         0         0           NM_001035         ryanodine receptor 2 (cardiac)         0         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0         0           NM_00179906         zinc finger protein 331         0         0           NM_000789         angiotensin I converting enzyme (peptidyl-dipeptidase A)         0         0           NM_014898         zinc finger protein 30 homolog (mouse)         0         0           NM_014901         ring finger protein 609         0         0           NM_145262         glycerate kinase         0         0           NM_002074         guanine nucleotide binding protein	NM_001008220         complexin 2         0         0         0           NM_005026         phosphoinositide-3-kinase, catalytic, delta polypeptide         0         0         0           NM_003842         tumor necrosis factor receptor superfamily, member 10b         0         0         0           NM_152458         zinc finger protein 785         0         0         0         0           NM_207401         chromosome 1 open reading frame 229         0         0         0         0           NM_001035         ryanodine receptor 2 (cardiac)         0         0         0         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0         0         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0         0         0           NM_016235         G protein-coupled receptor, family C, group 5, member B         0         0         0           NM_00179906         zinc finger protein 331         0         0         0         0           NM_000789         angiotensin I converting enzyme (peptidyl-dipeptidase A)         0         0         0           NM_014898         zinc finger protein 30 homolog (mouse)         0         0         0	NM_001008220         complexin 2         0	NM_001008220         complexin 2         0         0         0         0         0         2           NM_005026         phosphoinositide-3-kinase, catalytic, delta polypeptide         0         0         0         0         1           NM_003842         tumor necrosis factor receptor superfamily, member 10b         0         0         0         0         0         1           NM_152458         zinc finger protein 785         0         0         0         0         0         0         1           NM_207401         chromosome 1 open reading frame 229         0         0         0         0         0         0         1           NM_001035         ryanodine receptor 2 (cardiac)         0         0         0         0         0         0         1           NM_016235         G protein-coupled receptor, family C, group S, member B         0         0         0         0         1         1           NM_016235         G protein-coupled receptor, family C, group S, member B         0         0         0         0         1         1           NM_0016296         zinc finger protein 331         0         0         0         0         0         1         1           NM_000789	NM_001008220 complexin 2 0 0 0 0 0 2 1 1  NM_005026 phosphoinostide-3-kinase, catalytic, delta polypeptide 0 0 0 0 0 0 1 0 1 0 0  NM_003842 tumor necrosis factor receptor superfamily, member 10b 0 0 0 0 0 1 1 0 0  NM_152458 zinc finger protein 785 0 0 0 0 0 0 1 1 0 0  NM_207401 chromosome 1 open reading frame 229 0 0 0 0 0 0 1 1 0 0  NM_001035 ryanodine receptor 2 (cardiac) 0 0 0 0 0 1 1 0 0  NM_016235 G protein-coupled receptor, family C, group 5, member B 0 0 0 0 0 1 1 0 0  NM_001079906 zinc finger protein 331 0 0 0 0 0 1 1 0 0  NM_001079906 zinc finger protein 331 0 0 0 0 0 1 1 0 0  NM_001089 angiotensin I converting enzyme (peptidyl-dipeptidase A) 0 0 0 0 1 1 0 0  NM_014901 ring finger protein 30 homolog (mouse) 0 0 0 0 0 1 1 0 0  NM_015042 zinc finger protein 609 0 0 0 0 0 1 0 0 1 0 0  NM_002074 guarine nucleotide binding protein (G protein), beta 0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0	NM_001008220 complexin 2	NM_001009220 complexin 2	No. 0,0008200 compressor 2 comp	Mc_001038220 comprisent 2

GJB4	NM_153212	gap junction protein, beta 4, 30.3kDa	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.17	N/A	Sites in UTR
VCL	NM_003373	vinculin	0			0	1	0	0	1	hsa-miR-1908	-0.17	N/A	Sites in UTR
VCL	WW_003373	Vincuini					1	-		1	1134-11111/ 1300	-0.17		Sites in OTK
KLLN	NM_001126049	killin, p53-regulated DNA replication inhibitor	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
IGDCC3	NM_004884	immunoglobulin superfamily, DCC subclass, member 3	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
SPECC1L	NM_001145468	sperm antigen with calponin homology and coiled-coil domains 1-like	0	0	0	0	1	0	1	0	hsa-miR-663	-0.16	N/A	Sites in UTR
LYZ	NM_000239	lysozyme	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
SPCS3	NM_021928	signal peptidase complex subunit 3 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
DNAJB2	NM_006736	DnaJ (Hsp40) homolog, subfamily B, member 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
LMNA	NM_170707	lamin A/C	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
CHST11	NM_001173982	carbohydrate (chondroitin 4) sulfotransferase 11	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
CD99L2	NM_001184808	CD99 molecule-like 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.16	N/A	Sites in UTR
CYB5R3	NM_000398	cytochrome b5 reductase 3	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR
UBA52	NM_001033930	ubiquitin A-52 residue ribosomal protein fusion product 1	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NSFL1C	NM_001206736	NSFL1 (p97) cofactor (p47)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
SPRYD7	NM_001127482	SPRY domain containing 7	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
PAPOLG	NM_022894	poly(A) polymerase gamma	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR
SPPL3	NM_139015	signal peptide peptidase-like 3	0	0	0	0	1	0	1	0	hsa-miR-663	-0.16	N/A	Sites in UTR
GNAO1	NM_020988	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR
AASS	NM_005763	aminoadipate-semialdehyde synthase	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR
HIF3A	NM_022462	hypoxia inducible factor 3, alpha subunit	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR

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NM_002596	cyclin-dependent kinase 18	0	0	0	0	1	0	1	O	hsa-miR-1908	-0.16	N/A	Sites in UTR
INIVI UTZSTA		0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_001198681	leptin receptor overlapping transcript	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR
NM_170743	interleukin 28 receptor, alpha (interferon, lambda receptor)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_001017369	sterol-C4-methyl oxidase-like	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_024654	nucleolar protein 9	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_001144989	zinc finger protein 814	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_003108	SRY (sex determining region Y)-box 11	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_182925	fms-related tyrosine kinase 4	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_001142651	neuralized homolog 1B (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.16	N/A	Sites in UTR
NM_024771	N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_014911	AP2 associated kinase 1	0	0	0	0	2	0	1	1	hsa-miR-663	-0.16	N/A	Sites in UTR
INIVI UUS ISU		0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_031444	chromosome 22 open reading frame 13	0	0	0	0	1	0	1	0	hsa-miR-663	-0.16	N/A	Sites in UTR
NM_025224	zinc finger and BTB domain containing 46	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_207645	chromosome 11 open reading frame 87	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_005157	c-abl oncogene 1, non-receptor tyrosine kinase	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_001039350	dipeptidyl-peptidase 6	0	0	0	0	1	0	0	1	hsa-miR-663	-0.16	N/A	Sites in UTR
NM_003677	density-regulated protein	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
NM_003924	paired-like homeobox 2b	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.16	N/A	Sites in UTR
	NM_012318  NM_001198681  NM_170743  NM_001017369  NM_024654  NM_001144989  NM_003108  NM_182925  NM_001142651  NM_024771  NM_014911  NM_003150  NM_031444  NM_025224  NM_005157  NM_001039350  NM_003677	Interleukin 28 receptor overlapping transmembrane protein 1  NM_001198681 leptin receptor overlapping transcript  interleukin 28 receptor, alpha (interferon, lambda receptor)  NM_001017369 sterol-C4-methyl oxidase-like  NM_0010144989 zinc finger protein 9  NM_003108 SRY (sex determining region Y)-box 11  NM_182925 fms-related tyrosine kinase 4  NM_001142651 neuralized homolog 1B (Drosophila)  NM_024771 N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae)  NM_014911 AP2 associated kinase 1  NM_003150 signal transducer and activator of transcription 3 (acute-phase response factor)  NM_031444 chromosome 22 open reading frame 13  NM_025224 zinc finger and BTB domain containing 46  NM_207645 chromosome 11 open reading frame 87  NM_001039350 dipeptidyl-peptidase 6  NM_001039350 density-regulated protein	NM_012318   leucine zipper-EF-hand containing transmembrane protein 1	NM_012318         leucine zipper-EF-hand containing transmembrane protein 1         0         0           NM_001198681         leptin receptor overlapping transcript         0         0           NM_170743         interleukin 28 receptor, alpha (interferon, lambda receptor)         0         0           NM_001017369         sterol-C4-methyl oxidase-like         0         0           NM_0014654         nucleolar protein 9         0         0           NM_001144989         zinc finger protein 814         0         0           NM_003108         SRY (sex determining region Y)-box 11         0         0           NM_182925         fms-related tyrosine kinase 4         0         0           NM_001142651         neuralized homolog 1B (Drosophila)         0         0           NM_024771         N(alpha)-acetyltransferase 40, NatD catalytic subunit, homolog (S. cerevisiae)         0         0           NM_014911         AP2 associated kinase 1         0         0           NM_014911         AP2 associated kinase 1         0         0           NM_03150         signal transducer and activator of transcription 3 (acute-phase response factor)         0         0           NM_031444         chromosome 22 open reading frame 13         0         0           NM_025224	NM_012318   leucine zipper-EF-hand containing transmembrane	NM_012318         leucine zipper-EF-hand containing transmembrane protein 1         0<	NM_012318   leucine zipper-EF-hand containing transmembrane   0   0   0   0   0   1	NM_012318   lequin etipper-EF-hand containing transmembrane protein 1   0   0   0   0   0   1   0   0   0	NM_012318   Public Pipper-EF-hand containing transmembrane protein 1   0   0   0   0   0   1   0   0   0	NM_012318   leucine pipper EF-hand containing transmembrane profein 1   0   0   0   0   0   1   0   0   0	NM_012318   Section 2 Secretary of the protein 1   Section 2 Section 2   Section 2   Section 2   Section 3   Secti	NA_02318   elusine ripper 5F hand containing transcener brane grades in 1   0   0   0   1   1   0   0   1   1	NA_0122181

	T		,	-	1	1	1	1			<u> </u>		
CCDC122	NM_144974	coiled-coil domain containing 122	0	0	0	0	1	0	0	) 1 hsa-miR-1	908 -0.16	N/A	Sites in UTR
RAPGEF3	NM_001098531	Rap guanine nucleotide exchange factor (GEF) 3	0	0	0	0	1	0	1	. 0 hsa-miR-6	-0.16	N/A	Sites in UTR
KIAA1161	NM_020702	KIAA1161	0	0	0	0	1	0	1	. 0 hsa-miR-1!	908 -0.16	N/A	Sites in UTR
SLC6A14	INIVI UU7731	solute carrier family 6 (amino acid transporter), member 14	0	0	0	0	1	0	0	1 hsa-miR-1	-0.16	N/A	Sites in UTR
TMEM41B	NM_015012	transmembrane protein 41B	0	0	0	0	1	0	0	1 hsa-miR-6	-0.16	N/A	Sites in UTR
CCNG2	NM_004354	cyclin G2	0	0	0	0	1	1	0	0 hsa-miR-19	908 -0.16	N/A	Sites in UTR
SOX13	NM_005686	SRY (sex determining region Y)-box 13	0	0	0	0	1	0	1	. 0 hsa-miR-6	-0.16	N/A	Sites in UTR
CEP63	NM_001042383	centrosomal protein 63kDa	0	0	0	0	1	0	1	. 0 hsa-miR-1	908 -0.16	N/A	Sites in UTR
POLR2E	NM_002695	polymerase (RNA) II (DNA directed) polypeptide E, 25kDa	0	0	0	0	1	0	1	. 0 hsa-miR-6	-0.15	N/A	Sites in UTR
C9orf7	NM_001135775	chromosome 9 open reading frame 7	0	0	0	0	1	0	1	. 0 hsa-miR-1	908 -0.15	N/A	Sites in UTR
ATP8B2	NM_020452	ATPase, class I, type 8B, member 2	0	0	0	0	1	0	1	. 0 hsa-miR-6	-0.15	N/A	Sites in UTR
L3MBTL2	NM_031488	I(3)mbt-like 2 (Drosophila)	0	0	0	0	1	0	0	1 hsa-miR-6	-0.15	N/A	Sites in UTR
SFXN1	NM_022754	sideroflexin 1	0	0	0	0	1	0	0	1 hsa-miR-6	-0.15	N/A	Sites in UTR
PLA2G4E	NM_001206670	phospholipase A2, group IVE	0	0	0	0	1	0	0	) 1 hsa-miR-1!	908 -0.15	N/A	Sites in UTR
CDC42BPB	NM_006035	CDC42 binding protein kinase beta (DMPK-like)	0	0	0	0	1	0	1	. 0 hsa-miR-1	908 -0.15	N/A	Sites in UTR
WTIP	NM_001080436	Wilms tumor 1 interacting protein	0	0	0	0	1	0	1	. 0 hsa-miR-1	908 -0.15	N/A	Sites in UTR
GOSR1	NM_001007024	golgi SNAP receptor complex member 1	0	0	0	0	3	0	3	0 hsa-miR-1	908 -0.15	N/A	Sites in UTR
ATG13	NM_001142673	ATG13 autophagy related 13 homolog (S. cerevisiae)	0	0	0	0	1	0	1	. 0 hsa-miR-1!	908 -0.15	N/A	Sites in UTR
EMX1	NM_004097	empty spiracles homeobox 1	0	0	0	0	1	0	0	1 hsa-miR-6	-0.15	N/A	Sites in UTR
KIAA0825	NM_001145678	KIAA0825	0	0	0	0	1	0	0	1 hsa-miR-6	-0.15	N/A	Sites in UTR

TBC1D24	NM_001199107	TBC1 domain family, member 24	0	0	0	0	2	0	2	) hsa-miR-663	-0.15	N/A	Sites in UTR
PFKFB3	NM_001145443	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	0	0	0	0	1	0	1	hsa-miR-1908	-0.15	N/A	Sites in UTR
MAPK1IP1L	NM_144578	mitogen-activated protein kinase 1 interacting protein 1-like	0	0	0	0	2	0	0	2 hsa-miR-1908	-0.15	N/A	Sites in UTR
MSI2	NM_170721	musashi homolog 2 (Drosophila)	0	0	0	0	1	0	1	) hsa-miR-1908	-0.15	N/A	Sites in UTR
FGF1	NM_000800	fibroblast growth factor 1 (acidic)	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.15	N/A	Sites in UTR
ESPNL	NM_194312	espin-like	0	0	0	0	1	0	0	1 hsa-miR-663	-0.15	N/A	Sites in UTR
RPTOR	NM_001163034	regulatory associated protein of MTOR, complex 1	0	0	0	0	1	0	1	) hsa-miR-1908	-0.15	N/A	Sites in UTR
ZNF345	NM_001242472	zinc finger protein 345	0	0	0	0	1	0	0	1 hsa-miR-663	-0.15	N/A	Sites in UTR
NXN	NM_001205319	nucleoredoxin	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.15	N/A	Sites in UTR
DGCR14	NM_022719	DiGeorge syndrome critical region gene 14	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR
TNKS	NM_003747	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR
SLC35E1	NM_024881	solute carrier family 35, member E1	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR
NTNG2	NM_032536	netrin G2	0	0	0	0	2	0	2	) hsa-miR-1908	-0.15	N/A	Sites in UTR
ADAMTS17	NM_139057	ADAM metallopeptidase with thrombospondin type 1 motif, 17	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR
EFHD2	NM_024329	EF-hand domain family, member D2	0	0	0	0	1	0	0	1 hsa-miR-663	-0.15	N/A	Sites in UTR
NUAK2	NM_030952	NUAK family, SNF1-like kinase, 2	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.15	N/A	Sites in UTR
USP6	NM_004505	ubiquitin specific peptidase 6 (Tre-2 oncogene)	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR
GATAD2A	NM_017660	GATA zinc finger domain containing 2A	0	0	0	0	1	0	1	) hsa-miR-1908	-0.15	N/A	Sites in UTR
TMEM8A	NM_021259	transmembrane protein 8A	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR
TSPAN14	NM_001128309	tetraspanin 14	0	0	0	0	1	0	1	) hsa-miR-663	-0.15	N/A	Sites in UTR

SORCS3	NM_014978	sortilin-related VPS10 domain containing receptor 3	0	0	0	0	1	0	0 1	l hsa-miR-663	-0.15	N/A	Sites in UTR
C14orf43	NM_001043318	chromosome 14 open reading frame 43	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.15	N/A	Sites in UTR
CX3CL1	NM_002996	chemokine (C-X3-C motif) ligand 1	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.15	N/A	Sites in UTR
SERPINB9	NM_004155	serpin peptidase inhibitor, clade B (ovalbumin), member 9	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.15	N/A	Sites in UTR
C17orf101	NM_024648	chromosome 17 open reading frame 101	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.15	N/A	Sites in UTR
PPM1E	NM_014906	protein phosphatase, Mg2+/Mn2+ dependent, 1E	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.15	N/A	Sites in UTR
INO80D	NM_017759	INO80 complex subunit D	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.15	N/A	Sites in UTR
OR2C3	NM_198074	olfactory receptor, family 2, subfamily C, member 3	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.15	N/A	Sites in UTR
TMEM154	NM_152680	transmembrane protein 154	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.15	N/A	Sites in UTR
DBH	NM_000787	dopamine beta-hydroxylase (dopamine beta- monooxygenase)	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.14	N/A	Sites in UTR
ZNF516	NM_014643	zinc finger protein 516	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.14	N/A	Sites in UTR
WASF2	NM_001201404	WAS protein family, member 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.14	N/A	Sites in UTR
SLC2A3	NM_006931	solute carrier family 2 (facilitated glucose transporter), member 3	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.14	N/A	Sites in UTR
WNT3A	NM_033131	wingless-type MMTV integration site family, member 3A	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.14	N/A	Sites in UTR
MKI67	NM_001145966	antigen identified by monoclonal antibody Ki-67	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.14	N/A	Sites in UTR
C1orf115	NM_024709	chromosome 1 open reading frame 115	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.14	N/A	Sites in UTR
CSNK1E	NM_001894	casein kinase 1, epsilon	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.14	N/A	Sites in UTR
ZNF697	NM_001080470	zinc finger protein 697	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.14	N/A	Sites in UTR
KIAA1549	NM_001164665	KIAA1549	0	0	0	0	1	1	0 (	) hsa-miR-1908	-0.14	N/A	Sites in UTR
KLHL30	NM_198582	kelch-like 30 (Drosophila)	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.14	N/A	Sites in UTR

IRAK4	NM 001114182	interleukin-1 receptor-associated kinase 4	0	0	0	0	1	0	0	1 hsa-miR-1908	0.14	N/A	Sites in UTR
IIVAK4	NWI_001114182	interieukin-1 receptor-associateu kinase 4	0		0	0		-	0	1 1138-111111-1900	-0.14	N/A	Sites III OTK
TXNL4B	NM_001142317	thioredoxin-like 4B	0	0	0	0	1	0	0	1 hsa-miR-663	-0.14	N/A	Sites in UTR
NLRC3	NM_178844	NLR family, CARD domain containing 3	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.14	N/A	Sites in UTR
LRRC14	NM_014665	leucine rich repeat containing 14	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
TMEM132B	NM_052907	transmembrane protein 132B	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
PLEKHG1	NM_001029884	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.14	N/A	Sites in UTR
ERLIN2	NM_007175	ER lipid raft associated 2	0	0	0	0	1	1	0	0 hsa-miR-663	-0.14	N/A	Sites in UTR
RUNX3	NM_001031680	runt-related transcription factor 3	0	0	0	0	1	0	1	0 hsa-miR-663	-0.14	N/A	Sites in UTR
LDLRAP1	NM_015627	low density lipoprotein receptor adaptor protein 1	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
SYVN1	NM_032431	synovial apoptosis inhibitor 1, synoviolin	0	0	0	0	1	0	1	0 hsa-miR-663	-0.14	N/A	Sites in UTR
SHANK3	NM_001080420	SH3 and multiple ankyrin repeat domains 3	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
GPR107	NM_001136557	G protein-coupled receptor 107	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
SERTAD2	NM_014755	SERTA domain containing 2	0	0	0	0	1	0	0	1 hsa-miR-663	-0.14	N/A	Sites in UTR
LZTS1	NM_021020	leucine zipper, putative tumor suppressor 1	0	0	0	0	2	0	2	0 hsa-miR-663	-0.14	N/A	Sites in UTR
ZNF395	NM_018660	zinc finger protein 395	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
MTHFSD	NM_001159377	methenyltetrahydrofolate synthetase domain containing	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
ELOVL7	NM_001104558	ELOVL fatty acid elongase 7	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.14	N/A	Sites in UTR
MAP6	NM_207577	microtubule-associated protein 6	0	0	0	0	1	0	1	0 hsa-miR-663	-0.14	N/A	Sites in UTR
FSTL4	NM_015082	follistatin-like 4	0	0	0	0	1	0	1	0 hsa-miR-663	-0.14	N/A	Sites in UTR
CNNM4	NM_020184	cyclin M4	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.14	N/A	Sites in UTR

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LEMD2	NM_001143944	LEM domain containing 2	0	0	0	0	1	0	) 1 hsa-miR-663	-0.14	N/A	Sites in UTR
B4GALT5	NM_004776	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	0	0	0	0	1	0	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
KDELC2	NM_153705	KDEL (Lys-Asp-Glu-Leu) containing 2	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.14	N/A	Sites in UTR
TAF8	NM_138572	TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa	0	0	0	0	1	0	) 1 hsa-miR-1908	-0.14	N/A	Sites in UTR
CALHM1	NM_001001412	calcium homeostasis modulator 1	0	0	0	0	1	0	) 1 hsa-miR-663	-0.14	N/A	Sites in UTR
SKA2	NM_001100595	spindle and kinetochore associated complex subunit 2	0	0	0	0	1	0	) 1 hsa-miR-1908	-0.14	N/A	Sites in UTR
KCNMA1	NM_001014797	potassium large conductance calcium-activated channel, subfamily M, alpha member 1	0	0	0	0	1	0	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
PPP1R16B	NM_001172735	protein phosphatase 1, regulatory (inhibitor) subunit 16B	0	0	0	0	1	0	0 hsa-miR-1908	-0.14	N/A	Sites in UTR
GPSM1	NM_001145638	G-protein signaling modulator 1	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.14	N/A	Sites in UTR
WNT4	NM_030761	wingless-type MMTV integration site family, member 4	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.14	N/A	Sites in UTR
SETD1B	NM_015048	SET domain containing 1B	0	0	0	0	1	0	) 1 hsa-miR-663	-0.14	N/A	Sites in UTR
PDK3	NM_001142386	pyruvate dehydrogenase kinase, isozyme 3	0	0	0	0	1	0	0 hsa-miR-1908	-0.13	N/A	Sites in UTR
FXC1	NM_012192	fracture callus 1 homolog (rat)	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.13	B N/A	Sites in UTR
ММАВ	NM_052845	methylmalonic aciduria (cobalamin deficiency) cblB type	0	0	0	0	1	0	l 0 hsa-miR-1908	-0.13	B N/A	Sites in UTR
CRISPLD2	NM_031476	cysteine-rich secretory protein LCCL domain containing 2	0	0	0	0	1	0	) 1 hsa-miR-663	-0.13	B N/A	Sites in UTR
SLC25A42	NM_178526	solute carrier family 25, member 42	0	0	0	0	1	0	) 1 hsa-miR-663	-0.13	N/A	Sites in UTR
RASSF2	NM_014737	Ras association (RalGDS/AF-6) domain family member 2	0	0	0	0	1	0	) 1 hsa-miR-1908	-0.13	B N/A	Sites in UTR
HDAC4	NM_006037	histone deacetylase 4	0	0	0	0	1	0	L 0 hsa-miR-663	-0.13	N/A	Sites in UTR
RCC2	NM_001136204	regulator of chromosome condensation 2	0	0	0	0	1	0	0 hsa-miR-1908	-0.13	N/A	Sites in UTR
FOXP4	NM_001012426	forkhead box P4	0	0	0	0	1	0	L 0 hsa-miR-663	-0.13	N/A	Sites in UTR

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IL2RB	NM_000878	interleukin 2 receptor, beta	0	0	0	0	1	0	1	0	hsa-miR-663	-0.13	N/A	Sites in UTR
ТРРР	NM_007030	tubulin polymerization promoting protein	0	0	0	0	1	0	1	O	hsa-miR-1908	-0.13	N/A	Sites in UTR
STAC2	NM_198993	SH3 and cysteine rich domain 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.13	N/A	Sites in UTR
TNNI1	NM_003281	troponin I type 1 (skeletal, slow)	0	0	0	0	1	0	1	O	hsa-miR-663	-0.13	N/A	Sites in UTR
MGLL	NM_001003794	monoglyceride lipase	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.13	N/A	Sites in UTR
FAM168B	NM_001009993	family with sequence similarity 168, member B	0	0	0	0	1	0	1	0	hsa-miR-663	-0.13	N/A	Sites in UTR
QTRTD1	NM_024638	queuine tRNA-ribosyltransferase domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.13	N/A	Sites in UTR
ZNF737	NM_001159293	zinc finger protein 737	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.13	N/A	Sites in UTR
MTA1	NM_001203258	metastasis associated 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.13	N/A	Sites in UTR
UNK	NM_001080419	unkempt homolog (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.13	N/A	Sites in UTR
LBH	NM_030915	limb bud and heart development homolog (mouse)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.13	N/A	Sites in UTR
CACNA1E	NM_000721	calcium channel, voltage-dependent, R type, alpha 1E subunit	0	0	0	0	1	0	1	C	hsa-miR-1908	-0.12	N/A	Sites in UTR
CD93	NM_012072	CD93 molecule	0	0	0	0	1	0	1	0	hsa-miR-663	-0.12	N/A	Sites in UTR
UBE2G2	NM_001202489	ubiquitin-conjugating enzyme E2G 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.12	N/A	Sites in UTR
GMEB2	NM_012384	glucocorticoid modulatory element binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.12	N/A	Sites in UTR
NUFIP2	NM_020772	nuclear fragile X mental retardation protein interacting protein 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.12	N/A	Sites in UTR
AGFG1	NM_001135187	ArfGAP with FG repeats 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.12	N/A	Sites in UTR
SIK2	NM_015191	salt-inducible kinase 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.12	N/A	Sites in UTR
KIAA0754	NM_015038	KIAA0754	0	0	0	0	1	0	0	1	hsa-miR-663	-0.12	N/A	Sites in UTR
EIF2C1	NM_012199	eukaryotic translation initiation factor 2C, 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.12	N/A	Sites in UTR

CLMN	NM_024734	calmin (calponin-like, transmembrane)	0	0	0	0	1	0	1	) hsa-miR-663	-0.12	N/A	Sites in UTR
TGIF2	NM_001199513	TGFB-induced factor homeobox 2	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.12	N/A	Sites in UTR
EPB41L4A	NM_022140	erythrocyte membrane protein band 4.1 like 4A	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.12	N/A	Sites in UTR
HDLBP	NM_005336	high density lipoprotein binding protein	0	0	0	0	1	0	1	) hsa-miR-1908	-0.12	N/A	Sites in UTR
VANGL1	NM_001172411	vang-like 1 (van gogh, Drosophila)	0	0	0	0	1	0	1	) hsa-miR-663	-0.12	N/A	Sites in UTR
PPARA	NM_001001928	peroxisome proliferator-activated receptor alpha	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.12	N/A	Sites in UTR
MYO10	NM_012334	myosin X	0	0	0	0	1	1	0	) hsa-miR-663	-0.12	N/A	Sites in UTR
TIMP2	NM_003255	TIMP metallopeptidase inhibitor 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.12	N/A	Sites in UTR
SLC12A6	NM_001042494	solute carrier family 12 (potassium/chloride transporters), member 6	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.12	N/A	Sites in UTR
FAIM2	NM_012306	Fas apoptotic inhibitory molecule 2	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.12	N/A	Sites in UTR
PTPN1	NM_002827	protein tyrosine phosphatase, non-receptor type 1	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.12	N/A	Sites in UTR
CACNA1I	NM_001003406	calcium channel, voltage-dependent, T type, alpha 11 subunit	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.12	N/A	Sites in UTR
NAV2	NM_001111018	neuron navigator 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.12	N/A	Sites in UTR
TSTD2	NM_139246	thiosulfate sulfurtransferase (rhodanese)-like domain containing 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.12	N/A	Sites in UTR
GOLGA3	NM_005895	golgin A3	0	0	0	0	1	0	0 :	L hsa-miR-1908	-0.12	N/A	Sites in UTR
SGCD	NM_000337	sarcoglycan, delta (35kDa dystrophin-associated glycoprotein)	0	0	0	0	1	0	0 :	L hsa-miR-663	-0.12	N/A	Sites in UTR
ТОХ4	NM_014828	TOX high mobility group box family member 4	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.12	N/A	Sites in UTR
тох	NM_014729	thymocyte selection-associated high mobility group box	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.11	N/A	Sites in UTR
SZT2	NM_015284	seizure threshold 2 homolog (mouse)	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.11	N/A	Sites in UTR
TFCP2L1	NM_014553	transcription factor CP2-like 1	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.11	N/A	Sites in UTR

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CENPN	NM_001100624	centromere protein N	0	0	0	0	1	0	0	1	hsa-miR-663	-0.11	N/A	Sites in UTR
ANAPC16	NM_001242546	anaphase promoting complex subunit 16	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.11	N/A	Sites in UTR
BCDIN3D	NM_181708	BCDIN3 domain containing	0	0	0	0	1	0	0	1	hsa-miR-663	-0.11	N/A	Sites in UTR
KANK2	NM_001136191	KN motif and ankyrin repeat domains 2	0	0	0	0	1	0	1	0	hsa-miR-663	-0.11	N/A	Sites in UTR
C1orf183	NM_019099	chromosome 1 open reading frame 183	0	0	0	0	1	0	1	0	hsa-miR-663	-0.11	N/A	Sites in UTR
JAK3	NM_000215	Janus kinase 3	0	0	0	0	1	0	0	1	hsa-miR-663	-0.11	N/A	Sites in UTR
ARHGAP35	NM_004491	Rho GTPase activating protein 35	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.11	N/A	Sites in UTR
PDPK1	NM_002613	3-phosphoinositide dependent protein kinase-1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.11	N/A	Sites in UTR
LPHN1	NM_001008701	latrophilin 1	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.11	N/A	Sites in UTR
ТАРВР	NM_003190	TAP binding protein (tapasin)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.11	N/A	Sites in UTR
МТРАР	NM_018109	mitochondrial poly(A) polymerase	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.11	N/A	Sites in UTR
ZNF662	NM_001134656	zinc finger protein 662	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.11	N/A	Sites in UTR
C10orf54	NM_022153	chromosome 10 open reading frame 54	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.11	N/A	Sites in UTR
C6orf106	NM_022758	chromosome 6 open reading frame 106	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.11	N/A	Sites in UTR
MYT1L	NM_015025	myelin transcription factor 1-like	0	0	0	0	1	0	1	0	hsa-miR-663	-0.11	N/A	Sites in UTR
C6orf138	NM_207499	chromosome 6 open reading frame 138	0	0	0	0	1	0	0	1	hsa-miR-663	-0.11	N/A	Sites in UTR
KIAA1715	NM_030650	KIAA1715	0	0	0	0	1	0	0	1	hsa-miR-663	-0.11	N/A	Sites in UTR
CNP	NM_033133	2',3'-cyclic nucleotide 3' phosphodiesterase	1	0	1	0	0	0	0	0	hsa-miR-663	-0.1	N/A	Sites in UTR
TRIM59	NM_173084	tripartite motif containing 59	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.1	N/A	Sites in UTR
REXO1L1	NM_172239	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 1	0	0	0	0	1	0	1	0	hsa-miR-663	-0.1	N/A	Sites in UTR

FUT1	NM_000148	fucosyltransferase 1 (galactoside 2-alpha-L- fucosyltransferase, H blood group)	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.1	N/A	Sites in UTR
6-Mar	NM_005885	membrane-associated ring finger (C3HC4) 6	0	0	0	0	1	0	1	) hsa-miR-1908	-0.1	N/A	Sites in UTR
RRP7A	NM_015703	ribosomal RNA processing 7 homolog A (S. cerevisiae)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.1	N/A	Sites in UTR
SH3BP2	NM_001122681	SH3-domain binding protein 2	0	0	0	0	2	0	1	l hsa-miR-1908	-0.1	N/A	Sites in UTR
IRAK3	NM_001142523	interleukin-1 receptor-associated kinase 3	0	0	0	0	1	0	0 2	L hsa-miR-663	-0.1	N/A	Sites in UTR
DNAL1	NM_001201366	dynein, axonemal, light chain 1	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.1	N/A	Sites in UTR
SH3PXD2A	NM_014631	SH3 and PX domains 2A	0	0	0	0	1	0	1	) hsa-miR-1908	-0.1	N/A	Sites in UTR
N4BP1	NM_153029	NEDD4 binding protein 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.1	N/A	Sites in UTR
FAM131B	NM_001031690	family with sequence similarity 131, member B	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.1	N/A	Sites in UTR
SYT15	NM_031912	synaptotagmin XV	0	0	0	0	1	0	0 2	l hsa-miR-1908	-0.1	N/A	Sites in UTR
GSK3B	NM_001146156	glycogen synthase kinase 3 beta	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.1	N/A	Sites in UTR
ZNF562	NM_001130031	zinc finger protein 562	0	0	0	0	1	0	1	) hsa-miR-663	-0.1	N/A	Sites in UTR
KCNAB2	NM_001199860	potassium voltage-gated channel, shaker-related subfamily, beta member 2	0	0	0	0	2	0	1	l hsa-miR-1908	-0.1	N/A	Sites in UTR
SLC35E2	NM_182838	solute carrier family 35, member E2	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.1	N/A	Sites in UTR
ZNF701	NM_001172655	zinc finger protein 701	0	0	0	0	2	0	2 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
BTBD3	NM_014962	BTB (POZ) domain containing 3	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
FAM20B	NM_014864	family with sequence similarity 20, member B	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.09	N/A	Sites in UTR
HIC2	NM_015094	hypermethylated in cancer 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
MIDN	NM_177401	midnolin	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.09	N/A	Sites in UTR
SHISA6	NM_001173461	shisa homolog 6 (Xenopus laevis)	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR

мсс	NM_001085377	mutated in colorectal cancers	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.09	N/A	Sites in UTR
PTGIS	NM_000961	prostaglandin I2 (prostacyclin) synthase	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.09	N/A	Sites in UTR
WDR37	NM_014023	WD repeat domain 37	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.09	N/A	Sites in UTR
TEAD1	NM_021961	TEA domain family member 1 (SV40 transcriptional enhancer factor)	0	0	0	0	1	0	1 0	) hsa-miR-1908	-0.09	N/A	Sites in UTR
CECR6	NM_001163079	cat eye syndrome chromosome region, candidate 6	0	0	0	0	1	0	1 0	) hsa-miR-1908	-0.09	N/A	Sites in UTR
SHANK2	NM_012309	SH3 and multiple ankyrin repeat domains 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
TULP4	NM_001007466	tubby like protein 4	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.09	N/A	Sites in UTR
PLEKHG2	NM_022835	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	0	0	0	0	1	O	0 1	l hsa-miR-1908	-0.09	N/A	Sites in UTR
FAM53B	NM_014661	family with sequence similarity 53, member B	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
TECPR2	NM_014844	tectonin beta-propeller repeat containing 2	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
C17orf72	NM_001164257	chromosome 17 open reading frame 72	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.09	N/A	Sites in UTR
C1orf226	NM_001085375	chromosome 1 open reading frame 226	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.09	N/A	Sites in UTR
SCAI	NM_001144877	suppressor of cancer cell invasion	0	0	0	0	1	0	0 1	L hsa-miR-1908	-0.09	N/A	Sites in UTR
RNF169	NM_001098638	ring finger protein 169	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
RAB43	NM_001204883	RAB43, member RAS oncogene family	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
ISY1-RAB43	NM_001204890	ISY1-RAB43 readthrough	0	0	0	0	1	0	1 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
KIAA0513	NM_014732	KIAA0513	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.09	N/A	Sites in UTR
GDF11	NM_005811	growth differentiation factor 11	1	0	0	1	0	0	0 (	) hsa-miR-1908	-0.09	N/A	Sites in UTR
TOR1AIP2	NM_022347	torsin A interacting protein 2	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.09	N/A	Sites in UTR
CASP2	NM_001224	caspase 2, apoptosis-related cysteine peptidase	0	0	0	0	1	O	0 1	l hsa-miR-1908	-0.08	N/A	Sites in UTR

PHKG2	NM_000294	phosphorylase kinase, gamma 2 (testis)	O	0	0	0	1	0	0	1	hsa-miR-663	-0.08	N/A	Sites in UTR
DNAJC21	NM_001012339	DnaJ (Hsp40) homolog, subfamily C, member 21	0	0	0	0	1	0	0	1	hsa-miR-663	-0.08	N/A	Sites in UTR
PIP4K2B	NM_003559	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
TSPAN18	NM_130783	tetraspanin 18	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
AHRR	NM_001242412	aryl-hydrocarbon receptor repressor	0	0	0	0	1	0	1	0	hsa-miR-663	-0.08	N/A	Sites in UTR
MAU2	NM_015329	MAU2 chromatid cohesion factor homolog (C. elegans)	O	0	0	0	1	0	1	0	hsa-miR-1908	-0.08	N/A	Sites in UTR
нтт	NM_002111	huntingtin	O	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
IGFBP5	NM_000599	insulin-like growth factor binding protein 5	a	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
YAF2	NM_001190980	YY1 associated factor 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
SHISA7	NM_001145176	shisa homolog 7 (Xenopus laevis)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
SLC6A6	NM_001134367	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	O	0	0	0	1	0	1	0	hsa-miR-1908	-0.08	N/A	Sites in UTR
MUC20	NM_001098516	mucin 20, cell surface associated	O	0	0	0	1	0	0	1	hsa-miR-663	-0.08	N/A	Sites in UTR
KDM2A	NM_012308	lysine (K)-specific demethylase 2A	0	0	0	0	1	0	1	0	hsa-miR-663	-0.08	N/A	Sites in UTR
FAM22D	NM_001009610	family with sequence similarity 22, member D	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.08	N/A	Sites in UTR
INPP4A	NM_001134224	inositol polyphosphate-4-phosphatase, type I, 107kDa	0	0	0	0	1	0	0	1	hsa-miR-663	-0.08	N/A	Sites in UTR
SMAD4	NM_005359	SMAD family member 4	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.08	N/A	Sites in UTR
SNPH	NM_014723	syntaphilin	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.08	N/A	Sites in UTR
SH3PXD2B	NM_001017995	SH3 and PX domains 2B	0	0	0	0	2	0	2	0	hsa-miR-1908	-0.08	N/A	Sites in UTR
ADARB2	NM_018702	adenosine deaminase, RNA-specific, B2	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.08	N/A	Sites in UTR
FYTTD1	NM_001011537	forty-two-three domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-663	-0.08	N/A	Sites in UTR

RRP15	NM_016052	ribosomal RNA processing 15 homolog (S. cerevisiae)	0	0	0	0	1	0	1	O	hsa-miR-1908	-0.07	N/A	Sites in UTR
ТМСС3	NM_020698	transmembrane and coiled-coil domain family 3	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
ADCY9	NM_001116	adenylate cyclase 9	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR
ACSL6	NM_001009185	acyl-CoA synthetase long-chain family member 6	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
ACAP2	NM_012287	ArfGAP with coiled-coil, ankyrin repeat and PH domains 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
CBFA2T2	NM_001032999	core-binding factor, runt domain, alpha subunit 2; translocated to, 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR
RNF216	NM_207111	ring finger protein 216	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
TMEM33	NM_018126	transmembrane protein 33	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
APOOL	NM_198450	apolipoprotein O-like	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR
FZR1	NM_001136197	fizzy/cell division cycle 20 related 1 (Drosophila)	0	0	0	0	1	0	1	α	hsa-miR-663	-0.07	N/A	Sites in UTR
ZNF555	NM_001172775	zinc finger protein 555	0	0	0	0	1	0	1	C	hsa-miR-663	-0.07	N/A	Sites in UTR
MLL	NM_001197104	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
ST8SIA2	NM_006011	ST8 alpha-N-acetyl-neuraminide alpha-2,8- sialyltransferase 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
GATAD2B	NM_020699	GATA zinc finger domain containing 2B	0	0	0	0	1	0	1	O	hsa-miR-663	-0.07	N/A	Sites in UTR
ABR	NM_001092	active BCR-related gene	0	0	0	0	1	0	0	1	hsa-miR-663	-0.07	N/A	Sites in UTR
GNG4	NM_001098721	guanine nucleotide binding protein (G protein), gamma 4	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR
NFAM1	NM_145912	NFAT activating protein with ITAM motif 1	0	0	0	0	2	0	2	O	hsa-miR-1908	-0.07	N/A	Sites in UTR
ZNF805	NM_001023563	zinc finger protein 805	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR
SLC1A2	NM_001195728	solute carrier family 1 (glial high affinity glutamate transporter), member 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR
TFDP2	NM_001178138	transcription factor Dp-2 (E2F dimerization partner 2)	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.07	N/A	Sites in UTR

SCD	NM_005063	stearoyl-CoA desaturase (delta-9-desaturase)	0	0	0	0	1	0	1 (	hsa-miR-663	-0.06	N/A	Sites in UTR
MESDC2	NM_015154	mesoderm development candidate 2	0	0	0	0	1	0	1 (	hsa-miR-1908	-0.06	N/A	Sites in UTR
IRGQ	NM_001007561	immunity-related GTPase family, Q	0	0	0	0	1	0	0 2	l hsa-miR-1908	-0.06	N/A	Sites in UTR
MEF2D	NM_005920	myocyte enhancer factor 2D	0	0	0	0	1	0	1	) hsa-miR-1908	-0.06	N/A	Sites in UTR
FMNL3	NM_175736	formin-like 3	0	0	0	0	1	0	1	) hsa-miR-663	-0.06	N/A	Sites in UTR
CALML4	NM_001031733	calmodulin-like 4	0	0	0	0	1	0	1	) hsa-miR-1908	-0.06	N/A	Sites in UTR
ELFN2	NM_052906	extracellular leucine-rich repeat and fibronectin type III domain containing 2	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.06	N/A	Sites in UTR
ZNF264	NM_003417	zinc finger protein 264	0	0	0	0	1	0	0 :	L hsa-miR-1908	-0.06	N/A	Sites in UTR
ноокз	NM_032410	hook homolog 3 (Drosophila)	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.06	N/A	Sites in UTR
STEAP2	NM_001040665	six transmembrane epithelial antigen of the prostate 2	0	0	0	0	1	0	0 2	l hsa-miR-1908	-0.06	N/A	Sites in UTR
ORAI2	NM_001126340	ORAI calcium release-activated calcium modulator 2	0	0	0	0	1	0	1	) hsa-miR-1908	-0.06	N/A	Sites in UTR
TBC1D15	NM_001146213	TBC1 domain family, member 15	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.06	N/A	Sites in UTR
PGAP1	NM_024989	post-GPI attachment to proteins 1	0	0	0	0	1	0	0 2	l hsa-miR-1908	-0.06	N/A	Sites in UTR
MMS22L	NM_198468	MMS22-like, DNA repair protein	0	0	0	0	1	0	0 2	l hsa-miR-1908	-0.06	N/A	Sites in UTR
SC5DL	NM_001024956	sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.06	N/A	Sites in UTR
ESR1	NM_000125	estrogen receptor 1	0	0	0	0	1	0	1	) hsa-miR-663	-0.06	N/A	Sites in UTR
STK17B	NM_004226	serine/threonine kinase 17b	0	0	0	0	1	0	1 (	) hsa-miR-663	-0.06	N/A	Sites in UTR
PAK2	NM_002577	p21 protein (Cdc42/Rac)-activated kinase 2	0	0	0	0	1	0	0 :	l hsa-miR-1908	-0.06	N/A	Sites in UTR
CYCS	NM_018947	cytochrome c, somatic	0	0	0	0	1	0	0 1	l hsa-miR-1908	-0.06	N/A	Sites in UTR
ZNF780B	NM_001005851	zinc finger protein 780B	0	0	0	0	1	0	0 1	L hsa-miR-663	-0.06	N/A	Sites in UTR

TRAF6	NM_004620	TNF receptor-associated factor 6	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.06	N/A	Sites in UTR
CA5B	NM_007220	carbonic anhydrase VB, mitochondrial	0	0	0	0	1	0	0	1	hsa-miR-663	-0.06	N/A	Sites in UTR
C/102	WW_007220	carbonic anniqui asc vb, mitochonanai	9	Ŭ						_	I I I I I I I I I I I I I I I I I I I	0.00	1477	Sices in Oth
ICK	NM_014920	intestinal cell (MAK-like) kinase	0	0	0	0	1	0	0	1	hsa-miR-663	-0.06	N/A	Sites in UTR
GNL3L	NM_001184819	guanine nucleotide binding protein-like 3 (nucleolar)-like	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.05	N/A	Sites in UTR
CBL	NM_005188	Cas-Br-M (murine) ecotropic retroviral transforming sequence	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.05	N/A	Sites in UTR
SFMBT2	NM_001018039	Scm-like with four mbt domains 2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.05	N/A	Sites in UTR
FAM18B2	NM_001135036	family with sequence similarity 18, member B2	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.05	N/A	Sites in UTR
GRAMD4	NM_015124	GRAM domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-663	-0.05	N/A	Sites in UTR
RBFA	NM_001171967	ribosome binding factor A (putative)	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.05	N/A	Sites in UTR
KCTD12	NM_138444	potassium channel tetramerisation domain containing 12	0	0	0	0	1	0	1	0	hsa-miR-663	-0.05	N/A	Sites in UTR
LHFPL4	NM_198560	lipoma HMGIC fusion partner-like 4	0	0	0	0	1	0	1	0	hsa-miR-663	-0.05	N/A	Sites in UTR
RPL27A	NM_000990	ribosomal protein L27a	0	0	0	0	1	0	0	1	hsa-miR-663	-0.05	N/A	Sites in UTR
HIPK2	NM_001113239	homeodomain interacting protein kinase 2	0	0	0	0	2	0	2	0	hsa-miR-663	-0.05	N/A	Sites in UTR
ST6GAL2	NM_001142351	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	0	0	0	0	1	0	0	1	hsa-miR-663	-0.05	N/A	Sites in UTR
LPP	NM_001167671	LIM domain containing preferred translocation partner in lipoma	0	0	0	0	1	0	0	1	hsa-miR-1908	-0.05	N/A	Sites in UTR
FBXL20	NM_001184906	F-box and leucine-rich repeat protein 20	0	0	0	0	1	0	0	1	hsa-miR-663	-0.05	N/A	Sites in UTR
QKI	NM_006775	quaking homolog, KH domain RNA binding (mouse)	0	0	0	0	1	0	1	0	hsa-miR-663	-0.04	N/A	Sites in UTR
ZDHHC20	NM_153251	zinc finger, DHHC-type containing 20	0	0	0	0	1	0	1	0	hsa-miR-663	-0.04	N/A	Sites in UTR
MRAS	NM_001085049	muscle RAS oncogene homolog	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.04	N/A	Sites in UTR
ку	NM_178554	kyphoscoliosis peptidase	0	0	0	0	1	0	1	0	hsa-miR-1908	-0.04	N/A	Sites in UTR

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ZNF652	NM_001145365	zinc finger protein 652	0	0	0	0	1	0	1	0 hsa-miR-663	-0.04	N/A	Sites in UTR
ZNF250	NM_001109689	zinc finger protein 250	0	0	0	0	1	0	1	0 hsa-miR-663	-0.04	N/A	Sites in UTR
TUSC5	NM_172367	tumor suppressor candidate 5	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.04	N/A	Sites in UTR
PCDH19	NM_001105243	protocadherin 19	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.03	N/A	Sites in UTR
SOX12	NM_006943	SRY (sex determining region Y)-box 12	1	0	1	0	0	0	0	0 hsa-miR-1908	-0.03	N/A	Sites in UTR
BTBD9	NM_001099272	BTB (POZ) domain containing 9	0	0	0	0	1	0	1	0 hsa-miR-1908	-0.03	N/A	Sites in UTR
SLC7A5	NM_003486	solute carrier family 7 (amino acid transporter light chain, L system), member 5	0	0	0	0	1	0	1	0 hsa-miR-663	-0.03	N/A	Sites in UTR
NPTX1	NM_002522	neuronal pentraxin I	0	0	0	0	1	0	1	0 hsa-miR-663	-0.03	N/A	Sites in UTR
FAM101B	NM_182705	family with sequence similarity 101, member B	0	0	0	0	1	0	0	1 hsa-miR-1908	-0.03	N/A	Sites in UTR
CALN1	NM_001017440	calneuron 1	0	0	0	0	2	0	1	1 hsa-miR-1908	> -0.02	N/A	Sites in UTR
METTL21A	NM_001127395	methyltransferase like 21A	0	0	0	0	1	0	1	0 hsa-miR-1908	> -0.02	N/A	Sites in UTR
ACO2	NM_001098	aconitase 2, mitochondrial	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
ACTN1	NM_001102	actinin, alpha 1	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
ADORA1	NM_000674	adenosine A1 receptor	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
ALDOB	NM_000035	aldolase B, fructose-bisphosphate	0	0	0	0	1	0	0	1 hsa-miR-1908	N/A	N/A	Sites in UTR
АРР	NM_000484	amyloid beta (A4) precursor protein	0	0	0	0	1	1	0	0 hsa-miR-1908	N/A	N/A	Sites in UTR
EPHX1	NM_000120	epoxide hydrolase 1, microsomal (xenobiotic)	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
FECH	NM_000140	ferrochelatase	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
HMX1	NM_018942	H6 family homeobox 1	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
HPD	NM_001171993	4-hydroxyphenylpyruvate dioxygenase	1	0	1	0	0	0	0	0 hsa-miR-1908	N/A	N/A	Sites in UTR

ITGA3	NM_002204	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
LAD1	NM_005558	ladinin 1	0	0	0	0	1	1	0	0	hsa-miR-1908	N/A	N/A	Sites in UTR
PITX3	NM_005029	paired-like homeodomain 3	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
PPP4C	NM_002720	protein phosphatase 4, catalytic subunit	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
CLEC11A	NM_002975	C-type lectin domain family 11, member A	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
SLC7A1	NM_003045	solute carrier family 7 (cationic amino acid transporter, y+ system), member 1	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
STXBP2	NM_001127396	syntaxin binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
TEF	NM_001145398	thyrotrophic embryonic factor	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
TFAP2A	NM_001032280	transcription factor AP-2 alpha (activating enhancer binding protein 2 alpha)	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
USF2	NM_003367	upstream transcription factor 2, c-fos interacting	0	0	0	0	1	0	0	1	hsa-miR-1908	N/A	N/A	Sites in UTR
BTG2	NM_006763	BTG family, member 2	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
CST7	NM_003650	cystatin F (leukocystatin)	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
PDXK	NM_003681	pyridoxal (pyridoxine, vitamin B6) kinase	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
PPAP2C	NM_003712	phosphatidic acid phosphatase type 2C	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
FGF18	NM_003862	fibroblast growth factor 18	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
SLC5A6	NM_021095	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
MAPK8IP1	NM_005456	mitogen-activated protein kinase 8 interacting protein 1	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
SPAG7	NM_004890	sperm associated antigen 7	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
KLF2	NM_016270	Kruppel-like factor 2 (lung)	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
SLC2A6	NM_001145099	solute carrier family 2 (facilitated glucose transporter), member 6	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR

NM_007254	polynucleotide kinase 3'-phosphatase	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001080424	lysine (K)-specific demethylase 6B	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001161572	v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)	0	0	0	0	1	1	0	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_012466	tetraspanin 16	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_015694	zinc finger protein 777	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_014012	RAS (RAD and GEM)-like GTP-binding 1	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_013358	peptidyl arginine deiminase, type I	0	0	0	0	1	0	0	1 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_017422	calmodulin-like 5	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_017436	alpha 1,4-galactosyltransferase	0	0	0	0	1	0	0	1 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_018467	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_019612	immunity-related GTPase family, cinema	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001033561	PHD finger protein 12	0	0	0	0	1	1	0	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_021630	PDZ and LIM domain 2 (mystique)	0	0	0	0	1	0	0	1 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_006648	WNK lysine deficient protein kinase 2	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001168222	TBC1 domain family, member 17	0	0	0	0	1	1	0	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_025204	TraB domain containing	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001185095	allograft inflammatory factor 1-like	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_032569	glyoxylate reductase 1 homolog (Arabidopsis)	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001136493	major facilitator superfamily domain containing 2A	0	0	0	0	1	0	0	1 hsa-miR-1908	N/A	N/A	Sites in UTR
NM_001039374	KIAA1984	0	0	0	0	1	0	1	0 hsa-miR-1908	N/A	N/A	Sites in UTR
	NM_001080424  NM_001161572  NM_012466  NM_015694  NM_013358  NM_017422  NM_017436  NM_018467  NM_019612  NM_001033561  NM_021630  NM_021630  NM_006648  NM_001168222  NM_001185095  NM_032569  NM_001136493	NM_001080424   lysine (K)-specific demethylase 6B   NM_001161572   v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)   NM_012466   tetraspanin 16   NM_015694   zinc finger protein 777   NM_014012   RAS (RAD and GEM)-like GTP-binding 1   NM_013358   peptidyl arginine deiminase, type I   NM_017422   calmodulin-like 5   NM_017426   alpha 1,4-galactosyltransferase   NM_018467   unconventional SNARE in the ER 1 homolog (S. cerevisiae)   NM_019612   immunity-related GTPase family, cinema   NM_01033561   PHD finger protein 12   NM_021630   PDZ and LIM domain 2 (mystique)   NM_006648   WNK lysine deficient protein kinase 2   NM_001168222   TBC1 domain family, member 17   NM_025204   TraB domain containing   NM_001185095   allograft inflammatory factor 1-like   NM_032569   glyoxylate reductase 1 homolog (Arabidopsis)   NM_001136493   major facilitator superfamily domain containing 2A	NM_001080424         lysine (K)-specific demethylase 6B         0           NM_001161572         v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)         0           NM_012466         tetraspanin 16         0           NM_015694         zinc finger protein 777         0           NM_014012         RAS (RAD and GEM)-like GTP-binding 1         0           NM_013358         peptidyl arginine deiminase, type I         0           NM_017422         calmodulin-like 5         0           NM_017436         alpha 1,4-galactosyltransferase         0           NM_018467         unconventional SNARE in the ER 1 homolog (S. cerevisiae)         0           NM_019612         immunity-related GTPase family, cinema         0           NM_019612         immunity-related GTPase family, cinema         0           NM_01630         PDZ and LIM domain 2 (mystique)         0           NM_021630         PDZ and LIM domain 2 (mystique)         0           NM_0016822         TBC1 domain family, member 17         0           NM_001185095         allograft inflammatory factor 1-like         0           NM_001136493         major facilitator superfamily domain containing 2A         0	NM_001080424         lysine (K)-specific demethylase 6B         0         0           NM_001161572         v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)         0         0           NM_012466         tetraspanin 16         0         0           NM_015694         zinc finger protein 777         0         0           NM_014012         RAS (RAD and GEM)-like GTP-binding 1         0         0           NM_013358         peptidyl arginine deiminase, type I         0         0           NM_017422         calmodulin-like 5         0         0           NM_017436         alpha 1,4-galactosyltransferase         0         0           NM_018467         unconventional SNARE in the ER 1 homolog (S. cerevisiae)         0         0           NM_019612         immunity-related GTPase family, cinema         0         0           NM_019636         PHD finger protein 12         0         0           NM_021630         PDZ and LIM domain 2 (mystique)         0         0           NM_0016848         WNK lysine deficient protein kinase 2         0         0           NM_025204         TraB domain containing         0         0           NM_02185095         allograft inflammatory factor 1-like         0         0	NM_001080424         lysine (K)-specific demethylase 6B         0         0         0           NM_001161572         v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian)         0         0         0           NM_012466         tetraspanin 16         0         0         0           NM_015694         zinc finger protein 777         0         0         0           NM_014012         RAS (RAD and GEM)-like GTP-binding 1         0         0         0           NM_013358         peptidyl arginine deiminase, type I         0         0         0           NM_017422         calmodulin-like 5         0         0         0           NM_017436         alpha 1,4-galactosyltransferase         0         0         0           NM_018467         unconventional SNARE in the ER 1 homolog (S. cerevisiae)         0         0         0           NM_019612         immunity-related GTPase family, cinema         0         0         0           NM_019612         immunity-related GTPase family, cinema         0         0         0           NM_021630         PDZ and LIM domain 2 (mystique)         0         0         0           NM_026488         WNK lysine deficient protein kinase 2         0         0         0	NM_001080424         lysine (K)-specific demethylase 6B         0 </td <td>NM_001080424         lysine (K)-specific demethylase 6B         0         0         0         0         0         1           NM_001161572         v-maf musculoaponeurotic fibrosarcoma oncogene homolog E (avian)         0         0         0         0         0         0         1           NM_012466         tetraspanin 16         0         0         0         0         0         0         1           NM_015694         zinc finger protein 777         0         0         0         0         0         0         1           NM_014012         RAS (RAD and GEM)-like GTP-binding 1         0         0         0         0         0         1           NM_013358         peptidyl arginine deiminase, type I         0         0         0         0         0         1           NM_017422         calmodulin-like 5         0         0         0         0         1           NM_017436         alpha 1,4-galactosyltransferase         0         0         0         0         1           NM_018467         unconventional SNARE in the ER 1 homolog (S. cerevisiae)         0         0         0         0         1           NM_019612         inmunity-related GTPase family, cinema         0         0<!--</td--><td>NM_001080424</td><td>NM_001080424   Pysine (K)-specific demethylase 68   0   0   0   0   0   1   0   1   1   1</td><td>NA_0011661242</td><td>MA_001080424</td><td>NA_001601A24   Visine Of-secultic demethylase 86   0   0   0   0   0   0   0   0   0  </td></td>	NM_001080424         lysine (K)-specific demethylase 6B         0         0         0         0         0         1           NM_001161572         v-maf musculoaponeurotic fibrosarcoma oncogene homolog E (avian)         0         0         0         0         0         0         1           NM_012466         tetraspanin 16         0         0         0         0         0         0         1           NM_015694         zinc finger protein 777         0         0         0         0         0         0         1           NM_014012         RAS (RAD and GEM)-like GTP-binding 1         0         0         0         0         0         1           NM_013358         peptidyl arginine deiminase, type I         0         0         0         0         0         1           NM_017422         calmodulin-like 5         0         0         0         0         1           NM_017436         alpha 1,4-galactosyltransferase         0         0         0         0         1           NM_018467         unconventional SNARE in the ER 1 homolog (S. cerevisiae)         0         0         0         0         1           NM_019612         inmunity-related GTPase family, cinema         0         0 </td <td>NM_001080424</td> <td>NM_001080424   Pysine (K)-specific demethylase 68   0   0   0   0   0   1   0   1   1   1</td> <td>NA_0011661242</td> <td>MA_001080424</td> <td>NA_001601A24   Visine Of-secultic demethylase 86   0   0   0   0   0   0   0   0   0  </td>	NM_001080424	NM_001080424   Pysine (K)-specific demethylase 68   0   0   0   0   0   1   0   1   1   1	NA_0011661242	MA_001080424	NA_001601A24   Visine Of-secultic demethylase 86   0   0   0   0   0   0   0   0   0

ZNF598	NM_178167	zinc finger protein 598	0	0	0	0	1	0	0	1	hsa-miR-1908	N/A	N/A	Sites in UTR
C20orf54	NM_033409	chromosome 20 open reading frame 54	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
SLC25A29	NM_001039355	solute carrier family 25, member 29	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
CCDC105	NM_173482	coiled-coil domain containing 105	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
LYPD2	NM_205545	LY6/PLAUR domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
CNOT6L	NM_144571	CCR4-NOT transcription complex, subunit 6-like	0	0	0	0	1	1	0	0	hsa-miR-1908	N/A	N/A	Sites in UTR
BEST4	NM_153274	bestrophin 4	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
CCDC57	NM_198082	coiled-coil domain containing 57	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
C1QL4	NM_001008223	complement component 1, q subcomponent-like 4	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
CLEC4G	NM_198492	C-type lectin domain family 4, member G	0	0	0	0	1	0	1	0	hsa-miR-1908	N/A	N/A	Sites in UTR
IFITM10	NM_001170820	interferon induced transmembrane protein 10	0	0	0	0	1	0	0	1	hsa-miR-1908	N/A	N/A	Sites in UTR
ODF3B	NM_001014440	outer dense fiber of sperm tails 3B	0	0	0	0	1	0	0	1	hsa-miR-1908	N/A	N/A	Sites in UTR
RNF208	NM_031297	ring finger protein 208	0	0	0	0	1	0	0	1	hsa-miR-1908	N/A	N/A	Sites in UTR