Table S9. Identification of putative miR-622 target sites predicted by TargetScan

Target gene	Representative transcript	Gene name	Conserved sites				Poorly conserved sites				Representative miRNA	Total context+ score	Aggregate PCT	Links to sites in UTRs
			total	8mer	7mer-m8	7mer-1A	total	8mer	7mer-m8	7mer-1A				
INSIG2	NM_016133	insulin induced gene 2	1	1	0	0	1	0	1	0	hsa-miR-622	-0.68	N/A	Sites in UTR
SMARCAD1	NM_001128429	SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin, subfamily a, containing DEAD/H box 1	0	0	0	0	3	2	0	1	hsa-miR-622	-0.62	N/A	Sites in UTR
ANKS1A	NM_015245	ankyrin repeat and sterile alpha motif domain containing 1A	2	1	0	1	0	0	0	0	hsa-miR-622	-0.6	N/A	Sites in UTR
CASR	NM_000388	calcium-sensing receptor	0	0	0	0	2	2	0	0	hsa-miR-622	-0.59	N/A	Sites in UTR
USP44	NM_001042403	ubiquitin specific peptidase 44	0	0	0	0	2	1	0	1	hsa-miR-622	-0.56	N/A	Sites in UTR
TMEM14C	NM_001165258	transmembrane protein 14C	0	0	0	0	2	1	0	1	hsa-miR-622	-0.55	N/A	Sites in UTR
CCNJ	NM_001134375	cyclin J	0	0	0	0	3	0	2	1	hsa-miR-622	-0.54	N/A	Sites in UTR
LRRC27	NM_001143757	leucine rich repeat containing 27	0	0	0	0	2	2	0	0	hsa-miR-622	-0.54	N/A	Sites in UTR
ATF2	NM_001880	activating transcription factor 2	0	0	0	0	2	1	0	1	hsa-miR-622	-0.53	N/A	Sites in UTR
FAM104A	NM_001098832	family with sequence similarity 104, member A	0	0	0	0	2	1	1	0	hsa-miR-622	-0.53	N/A	Sites in UTR
DCUN1D1	NM_020640	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.52	N/A	Sites in UTR
C3orf23	NM_001029839	chromosome 3 open reading frame 23	0	0	0	0	2	1	0	1	hsa-miR-622	-0.52	N/A	Sites in UTR
DSEL	NM_032160	dermatan sulfate epimerase-like	1	0	1	0	2	1	0	1	hsa-miR-622	-0.52	N/A	Sites in UTR
ROCK2	NM_004850	Rho-associated, coiled-coil containing protein kinase 2	1	0	0	1	2	0	1	1	hsa-miR-622	-0.51	N/A	Sites in UTR
ELOVL2	NM_017770	ELOVL fatty acid elongase 2	1	0	0	1	2	1	1	0	hsa-miR-622	-0.51	N/A	Sites in UTR

CSRNP3	NM_001172173	cysteine-serine-rich nuclear protein 3	1	0	1	0	1	0	1	0	hsa-miR-622	-0.51	N/A	Sites in UTR
AGPAT4	NM_020133	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	0	0	0	0	3	1	2	0	hsa-miR-622	-0.5	N/A	Sites in UTR
CD247	NM_000734	CD247 molecule	0	0	0	0	2	1	1	0	hsa-miR-622	-0.5	N/A	Sites in UTR
SYNM	NM_015286	synemin, intermediate filament protein	0	0	0	0	5	0	5	0	hsa-miR-622	-0.5	N/A	Sites in UTR
JRKL	NM_003772	jerky homolog-like (mouse)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.49	N/A	Sites in UTR
ZDHHC3	NM_001135179	zinc finger, DHHC-type containing 3	0	0	0	0	5	3	1	1	hsa-miR-622	-0.48	N/A	Sites in UTR
FDX1	NM_004109	ferredoxin 1	0	0	0	0	2	1	1	0	hsa-miR-622	-0.48	N/A	Sites in UTR
CLPB	NM_030813	ClpB caseinolytic peptidase B homolog (E. coli)	0	0	0	0	2	2	0	0	hsa-miR-622	-0.48	N/A	Sites in UTR
LONRF2	NM_198461	LON peptidase N-terminal domain and ring finger 2	0	0	0	0	3	1	0	2	hsa-miR-622	-0.48	N/A	Sites in UTR
CYBASC3	NM_001161452	cytochrome b, ascorbate dependent 3	0	0	0	0	2	1	1	0	hsa-miR-622	-0.47	N/A	Sites in UTR
EYA1	NM_000503	eyes absent homolog 1 (Drosophila)	1	1	0	0	1	0	0	1	hsa-miR-622	-0.47	N/A	Sites in UTR
VIPAR	NM_001193314	VPS33B interacting protein, apical-basolateral polarity regulator	1	1	0	0	1	0	1	0	hsa-miR-622	-0.47	N/A	Sites in UTR
SLC5A3	NM_006933	solute carrier family 5 (sodium/myo-inositol cotransporter), member 3	1	1	0	0	1	0	1	0	hsa-miR-622	-0.46	N/A	Sites in UTR
TTC30A	NM_152275	tetratricopeptide repeat domain 30A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.46	N/A	Sites in UTR
LMO2	NM_001142315	LIM domain only 2 (rhombotin-like 1)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.46	N/A	Sites in UTR
RILPL1	NM_178314	Rab interacting lysosomal protein-like 1	0	0	0	0	2	1	1	0	hsa-miR-622	-0.46	N/A	Sites in UTR
BCL10	NM_003921	B-cell CLL/lymphoma 10	0	0	0	0	2	0	1	1	hsa-miR-622	-0.45	N/A	Sites in UTR
PPP1R2	NM_006241	protein phosphatase 1, regulatory (inhibitor) subunit 2	0	0	0	0	3	0	0	3	hsa-miR-622	-0.45	N/A	Sites in UTR

PGD	NM_002631	phosphogluconate dehydrogenase	0	0	0	0	1	1	0	0	hsa-miR-622	-0.45	N/A	Sites in UTR
USP9X	NM_001039590	ubiquitin specific peptidase 9, X-linked	1	1	0	0	1	0	0	1	hsa-miR-622	-0.45	N/A	Sites in UTR
ISY1	NM_001199469	ISY1 splicing factor homolog (S. cerevisiae)	0	0	0	0	3	2	1	0	hsa-miR-622	-0.45	N/A	Sites in UTR
CDK9	NM_001261	cyclin-dependent kinase 9	0	0	0	0	2	1	1	0	hsa-miR-622	-0.44	N/A	Sites in UTR
DDX51	NM_175066	DEAD (Asp-Glu-Ala-Asp) box polypeptide 51	0	0	0	0	3	2	1	0	hsa-miR-622	-0.44	N/A	Sites in UTR
STX18	NM_016930	syntaxin 18	0	0	0	0	2	1	1	0	hsa-miR-622	-0.44	N/A	Sites in UTR
DOT1L	NM_032482	DOT1-like, histone H3 methyltransferase (S. cerevisiae)	0	0	0	0	3	1	2	0	hsa-miR-622	-0.44	N/A	Sites in UTR
PDE11A	NM_001077196	phosphodiesterase 11A	0	0	0	0	4	1	2	1	hsa-miR-622	-0.44	N/A	Sites in UTR
TP53INP1	NM_001135733	tumor protein p53 inducible nuclear protein 1	1	1	0	0	1	0	0	1	hsa-miR-622	-0.43	N/A	Sites in UTR
CACNG2	NM_006078	calcium channel, voltage-dependent, gamma subunit 2	1	0	1	0	1	1	0	0	hsa-miR-622	-0.43	N/A	Sites in UTR
SUSD4	NM_017982	sushi domain containing 4	1	1	0	0	0	0	0	0	hsa-miR-622	-0.43	N/A	Sites in UTR
KHDRBS2	NM_152688	KH domain containing, RNA binding, signal transduction associated 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.43	N/A	Sites in UTR
PKHD1	NM_138694	polycystic kidney and hepatic disease 1 (autosomal recessive)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.43	N/A	Sites in UTR
RPS29	NM_001030001	ribosomal protein S29	0	0	0	0	1	1	0	0	hsa-miR-622	-0.42	N/A	Sites in UTR
DUS4L	NM_181581	dihydrouridine synthase 4-like (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.42	N/A	Sites in UTR
E2F8	NM_024680	E2F transcription factor 8	0	0	0	0	1	1	0	0	hsa-miR-622	-0.42	N/A	Sites in UTR
ERP29	NM_001034025	endoplasmic reticulum protein 29	0	0	0	0	1	1	0	0	hsa-miR-622	-0.42	N/A	Sites in UTR
HIST2H2BE	NM_003528	histone cluster 2, H2be	0	0	0	0	1	1	0	0	hsa-miR-622	-0.41	N/A	Sites in UTR

IL22RA2	NM_052962	interleukin 22 receptor, alpha 2	0	0	0	0	2	1	0	1	hsa-miR-622	-0.41	N/A	Sites in UTR
BOD1	NM_001159651	biorientation of chromosomes in cell division 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.41	N/A	Sites in UTR
RPP14	NM_001098783	ribonuclease P/MRP 14kDa subunit	1	0	0	1	1	1	0	0	hsa-miR-622	-0.41	N/A	Sites in UTR
GALNT10	NM_198321	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 10 (GalNAc-T10)	0	0	0	0	4	1	1	2	hsa-miR-622	-0.41	N/A	Sites in UTR
SAA2	NM_001127380	serum amyloid A2	0	0	0	0	2	1	0	1	hsa-miR-622	-0.41	N/A	Sites in UTR
TMEM14B	NM_001127711	transmembrane protein 14B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.41	N/A	Sites in UTR
AMPH	NM_001635	amphiphysin	0	0	0	0	1	1	0	0	hsa-miR-622	-0.41	N/A	Sites in UTR
WBP2NL	NM_152613	WBP2 N-terminal like	1	1	0	0	0	0	0	0	hsa-miR-622	-0.41	N/A	Sites in UTR
MORC3	NM_015358	MORC family CW-type zinc finger 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
KCNB1	NM_004975	potassium voltage-gated channel, Shab-related subfamily, member 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
ZBTB5	NM_014872	zinc finger and BTB domain containing 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
ELF1	NM_001145353	E74-like factor 1 (ets domain transcription factor)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
PPARD	NM_001171818	peroxisome proliferator-activated receptor delta	1	1	0	0	0	0	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
GPATCH1	NM_018025	G patch domain containing 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
MIER1	NM_001077700	mesoderm induction early response 1 homolog (Xenopus laevis)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
APOBEC3A	NM_145699	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
LRRC61	NM_001142928	leucine rich repeat containing 61	0	0	0	0	2	1	1	0	hsa-miR-622	-0.4	N/A	Sites in UTR
TTC22	NM_017904	tetratricopeptide repeat domain 22	0	0	0	0	2	1	0	1	hsa-miR-622	-0.4	N/A	Sites in UTR

LMAN1	NM_005570	lectin, mannose-binding, 1	0	0	0	0	2	1	1	0	hsa-miR-622	-0.4	N/A	Sites in UTR
FRAS1	NM_025074	Fraser syndrome 1	1	1	0	0	2	0	0	2	hsa-miR-622	-0.4	N/A	Sites in UTR
APPL1	NM_012096	adaptor protein, phosphotyrosine interaction, PH domain and leucine zipper containing 1	1	1	0	0	1	0	1	0	hsa-miR-622	-0.4	N/A	Sites in UTR
NPM1	NM_001037738	nucleophosmin (nucleolar phosphoprotein B23, numatrin)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
PRKAR2B	NM_002736	protein kinase, cAMP-dependent, regulatory, type II, beta	0	0	0	0	1	1	0	0	hsa-miR-622	-0.4	N/A	Sites in UTR
EIF1AX	NM_001412	eukaryotic translation initiation factor 1A, X-linked	1	1	0	0	0	0	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
MBD1	NM_001204137	methyl-CpG binding domain protein 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.39	N/A	Sites in UTR
HOXA9	NM_152739	homeobox A9	0	0	0	0	1	1	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
YTHDF1	NM_017798	YTH domain family, member 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
SFXN1	NM_022754	sideroflexin 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
KCNN3	NM_001204087	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3	0	0	0	0	3	2	1	0	hsa-miR-622	-0.39	N/A	Sites in UTR
1-Mar	NM_001166373	membrane-associated ring finger (C3HC4) 1	0	0	0	0	3	1	0	2	hsa-miR-622	-0.39	N/A	Sites in UTR
CNIH3	NM_152495	cornichon homolog 3 (Drosophila)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.39	N/A	Sites in UTR
NDST1	NM_001543	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1	1	1	0	0	2	0	1	1	hsa-miR-622	-0.39	N/A	Sites in UTR
SLFN5	NM_144975	schlafen family member 5	0	0	0	0	2	0	2	0	hsa-miR-622	-0.39	N/A	Sites in UTR
F2RL2	NM_004101	coagulation factor II (thrombin) receptor-like 2	0	0	0	0	3	1	1	1	hsa-miR-622	-0.39	N/A	Sites in UTR
MBTPS1	NM_003791	membrane-bound transcription factor peptidase, site 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
FAM72A	NM_001123168	family with sequence similarity 72, member A	1	1	0	0	0	0	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR

TBC1D5	NM_001134380	TBC1 domain family, member 5	0	0	0	0	3	1	2	0	hsa-miR-622	-0.39	N/A	Sites in UTR
BNIP3	NM_004052	BCL2/adenovirus E1B 19kDa interacting protein 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
TRAPPC8	NM_014939	trafficking protein particle complex 8	0	0	0	0	2	1	1	0	hsa-miR-622	-0.39	N/A	Sites in UTR
BTK	NM_000061	Bruton agammaglobulinemia tyrosine kinase	1	1	0	0	0	0	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
LAMA2	NM_000426	laminin, alpha 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.39	N/A	Sites in UTR
RILPL2	NM_145058	Rab interacting lysosomal protein-like 2	0	0	0	0	2	1	0	1	hsa-miR-622	-0.38	N/A	Sites in UTR
TRUB2	NM_015679	TruB pseudouridine (psi) synthase homolog 2 (E. coli)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.38	N/A	Sites in UTR
N6AMT1	NM_013240	N-6 adenine-specific DNA methyltransferase 1 (putative)	0	0	0	0	3	1	1	1	hsa-miR-622	-0.38	N/A	Sites in UTR
USP48	NM_032236	ubiquitin specific peptidase 48	0	0	0	0	1	1	0	0	hsa-miR-622	-0.38	N/A	Sites in UTR
NUAK1	NM_014840	NUAK family, SNF1-like kinase, 1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.38	N/A	Sites in UTR
G3BP1	NM_005754	GTPase activating protein (SH3 domain) binding protein 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.38	N/A	Sites in UTR
RBP7	NM_052960	retinol binding protein 7, cellular	0	0	0	0	1	1	0	0	hsa-miR-622	-0.38	N/A	Sites in UTR
SPTY2D1	NM_194285	SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.38	N/A	Sites in UTR
PIWIL3	NM_001008496	piwi-like 3 (Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.38	N/A	Sites in UTR
ZFYVE19	NM_001077268	zinc finger, FYVE domain containing 19	1	1	0	0	1	0	1	0	hsa-miR-622	-0.38	N/A	Sites in UTR
TXLNG	NM_001168683	taxilin gamma	1	0	1	0	1	1	0	0	hsa-miR-622	-0.38	N/A	Sites in UTR
UBE2K	NM_001111112	ubiquitin-conjugating enzyme E2K	1	0	0	1	2	1	1	0	hsa-miR-622	-0.38	N/A	Sites in UTR
CDK8	NM_001260	cyclin-dependent kinase 8	1	1	0	0	0	0	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR

SP4	NM_003112	Sp4 transcription factor	0	0	0	0	1	1	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
TTC17	NM_018259	tetratricopeptide repeat domain 17	1	1	0	0	0	0	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
MAPKAPK3	NM_004635	mitogen-activated protein kinase-activated protein kinase 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
ST8SIA3	NM_015879	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3	0	0	0	0	2	1	0	1	hsa-miR-622	-0.37	N/A	Sites in UTR
ADCYAP1R1	NM_001118	adenylate cyclase activating polypeptide 1 (pituitary) receptor type I	0	0	0	0	3	0	3	0	hsa-miR-622	-0.37	N/A	Sites in UTR
PRLR	NM_000949	prolactin receptor	0	0	0	0	2	1	0	1	hsa-miR-622	-0.37	N/A	Sites in UTR
LRRC10	NM_201550	leucine rich repeat containing 10	0	0	0	0	2	0	1	1	hsa-miR-622	-0.37	N/A	Sites in UTR
FAM72B	NM_001100910	family with sequence similarity 72, member B	1	1	0	0	0	0	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
FAM72D	NM_207418	family with sequence similarity 72, member D	1	1	0	0	0	0	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
NAA25	NM_024953	N(alpha)-acetyltransferase 25, NatB auxiliary subunit	1	1	0	0	0	0	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
AQP8	NM_001169	aquaporin 8	0	0	0	0	2	1	0	1	hsa-miR-622	-0.37	N/A	Sites in UTR
SKP1	NM_006930	S-phase kinase-associated protein 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.37	N/A	Sites in UTR
BMX	NM_001721	BMX non-receptor tyrosine kinase	0	0	0	0	2	0	1	1	hsa-miR-622	-0.36	N/A	Sites in UTR
ZNF518B	NM_053042	zinc finger protein 518B	0	0	0	0	2	0	1	1	hsa-miR-622	-0.36	N/A	Sites in UTR
C1orf150	NM_145278	chromosome 1 open reading frame 150	0	0	0	0	4	0	1	3	hsa-miR-622	-0.36	N/A	Sites in UTR
RRN3	NM_018427	RRN3 RNA polymerase I transcription factor homolog (S. cerevisiae)	0	0	0	0	2	1	1	0	hsa-miR-622	-0.36	N/A	Sites in UTR
SLC25A4	NM_001151	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	1	1	0	0	1	0	0	1	hsa-miR-622	-0.36	N/A	Sites in UTR
ANKRD13B	NM_152345	ankyrin repeat domain 13B	1	1	0	0	1	0	0	1	hsa-miR-622	-0.36	N/A	Sites in UTR

TRAF6	NM_004620	TNF receptor-associated factor 6	1	1	0	0	1	0	1	0	hsa-miR-622	-0.36	N/A	Sites in UTR
SRSF1	NM_001078166	serine/arginine-rich splicing factor 1	1	0	1	0	2	0	1	1	hsa-miR-622	-0.36	N/A	Sites in UTR
FLOT1	NM_005803	flotillin 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.36	N/A	Sites in UTR
SLAMF1	NM_003037	signaling lymphocytic activation molecule family member 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.36	N/A	Sites in UTR
FAM113B	NM_138371	family with sequence similarity 113, member B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.36	N/A	Sites in UTR
PLEKHG7	NM_001004330	pleckstrin homology domain containing, family G (with RhoGef domain) member 7	0	0	0	0	1	1	0	0	hsa-miR-622	-0.36	N/A	Sites in UTR
LRCH2	NM_020871	leucine-rich repeats and calponin homology (CH) domain containing 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.36	N/A	Sites in UTR
PTEN	NM_000314	phosphatase and tensin homolog	0	0	0	0	2	1	1	0	hsa-miR-622	-0.36	N/A	Sites in UTR
DIO3	NM_001362	deiodinase, iodothyronine, type III	0	0	0	0	1	1	0	0	hsa-miR-622	-0.35	N/A	Sites in UTR
WHSC1	NM_133334	Wolf-Hirschhorn syndrome candidate 1	1	0	0	1	2	1	0	1	hsa-miR-622	-0.35	N/A	Sites in UTR
SS18	NM_001007559	synovial sarcoma translocation, chromosome 18	1	1	0	0	0	0	0	0	hsa-miR-622	-0.35	N/A	Sites in UTR
MTRF1	NM_004294	mitochondrial translational release factor 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.35	N/A	Sites in UTR
PAN2	NM_001127460	PAN2 poly(A) specific ribonuclease subunit homolog (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.35	N/A	Sites in UTR
DYRK2	NM_003583	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 2	1	1	0	0	1	0	1	0	hsa-miR-622	-0.35	N/A	Sites in UTR
PHF17	NM_024900	PHD finger protein 17	0	0	0	0	1	1	0	0	hsa-miR-622	-0.35	N/A	Sites in UTR
PPP3R1	NM_000945	protein phosphatase 3, regulatory subunit B, alpha	0	0	0	0	1	1	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
NFAT5	NM_001113178	nuclear factor of activated T-cells 5, tonicity-responsive	1	1	0	0	1	1	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
ING1	NM_005537	inhibitor of growth family, member 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR

ITGB5	NM_002213	integrin, beta 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
TM4SF1	NM_014220	transmembrane 4 L six family member 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
SPIRE1	NM_001128626	spire homolog 1 (Drosophila)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
ADNP2	NM_014913	ADNP homeobox 2	0	0	0	0	2	1	0	1	hsa-miR-622	-0.34	N/A	Sites in UTR
TRPM6	NM_001177310	transient receptor potential cation channel, subfamily M, member 6	0	0	0	0	2	1	1	0	hsa-miR-622	-0.34	N/A	Sites in UTR
EFHC1	NM_001172420	EF-hand domain (C-terminal) containing 1	0	0	0	0	4	0	4	0	hsa-miR-622	-0.34	N/A	Sites in UTR
SRSF3	NM_003017	serine/arginine-rich splicing factor 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
CMTM3	NM_144601	CKLF-like MARVEL transmembrane domain containing 3	1	1	0	0	1	0	0	1	hsa-miR-622	-0.34	N/A	Sites in UTR
CSF2RB	NM_000395	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.34	N/A	Sites in UTR
GPC6	NM_005708	glypican 6	1	1	0	0	1	1	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
MBD2	NM_003927	methyl-CpG binding domain protein 2	1	1	0	0	1	0	1	0	hsa-miR-622	-0.34	N/A	Sites in UTR
ALS2CL	NM_001190707	ALS2 C-terminal like	0	0	0	1	1	0	0	0	hsa-miR-622	-0.34	N/A	Sites in UTR
SCN2B	NM_004588	sodium channel, voltage-gated, type II, beta	1	1	0	0	1	0	1	0	hsa-miR-622	-0.33	N/A	Sites in UTR
NR1H3	NM_001130101	nuclear receptor subfamily 1, group H, member 3	1	1	0	0	0	0	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
RTN4	NM_007008	reticulon 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
FLJ25363	NM_001145553	hypothetical LOC401082	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
CHTF18	NM_022092	CTF18, chromosome transmission fidelity factor 18 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.33	N/A	Sites in UTR
ZFP161	NM_001143823	zinc finger protein 161 homolog (mouse)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.33	N/A	Sites in UTR

ATP8B4	NM_024837	ATPase, class I, type 8B, member 4	0	0	0	0	2	1	0	1	hsa-miR-622	-0.33	N/A	Sites in UTR
LRIT3	NM_198506	leucine-rich repeat, immunoglobulin-like and transmembrane domains 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
GPR137B	NM_003272	G protein-coupled receptor 137B	0	0	0	0	2	0	1	1	hsa-miR-622	-0.33	N/A	Sites in UTR
KIAA0240	NM_015349	KIAA0240	1	1	0	0	0	0	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
ARID4B	NM_001206794	AT rich interactive domain 4B (RBP1-like)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.33	N/A	Sites in UTR
CUBN	NM_001081	cubilin (intrinsic factor-cobalamin receptor)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
FHOD3	NM_025135	formin homology 2 domain containing 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
S1PR3	NM_005226	sphingosine-1-phosphate receptor 3	0	0	0	0	2	1	0	1	hsa-miR-622	-0.33	N/A	Sites in UTR
SMCHD1	NM_015295	structural maintenance of chromosomes flexible hinge domain containing 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
DYRK4	NM_003845	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.33	N/A	Sites in UTR
CCL3L1	NM_021006	chemokine (C-C motif) ligand 3-like 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
CCL3L3	NM_001001437	chemokine (C-C motif) ligand 3-like 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
FAM53C	NM_001135647	family with sequence similarity 53, member C	1	1	0	0	0	0	0	0	hsa-miR-622	-0.33	N/A	Sites in UTR
PHACTR2	NM_001100164	phosphatase and actin regulator 2	1	1	0	0	1	0	0	1	hsa-miR-622	-0.32	N/A	Sites in UTR
CCL3	NM_002983	chemokine (C-C motif) ligand 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
TRIT1	NM_017646	tRNA isopentenyltransferase 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
ZEB2	NM_001171653	zinc finger E-box binding homeobox 2	1	1	0	0	0	0	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
ATG12	NM_004707	ATG12 autophagy related 12 homolog (S. cerevisiae)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.32	N/A	Sites in UTR

SLC35B4	NM_032826	solute carrier family 35, member B4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
UBE2Q2	NM_001145335	ubiquitin-conjugating enzyme E2Q family member 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
GLTP	NM_016433	glycolipid transfer protein	1	1	0	0	0	0	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
DBNDD2	NM_001048221	dysbindin (dystrobrevin binding protein 1) domain containing 2	1	1	0	0	0	0	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
ARID4A	NM_002892	AT rich interactive domain 4A (RBP1-like)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
KLHL4	NM_019117	kelch-like 4 (Drosophila)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.32	N/A	Sites in UTR
KRAS	NM_004985	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog	0	0	0	0	2	0	2	0	hsa-miR-622	-0.32	N/A	Sites in UTR
FPGS	NM_001018078	folylpolyglutamate synthase	0	0	0	0	1	1	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
CD276	NM_001024736	CD276 molecule	0	0	0	0	1	1	0	0	hsa-miR-622	-0.32	N/A	Sites in UTR
KIAA1598	NM_001127211	KIAA1598	0	0	0	0	2	0	1	1	hsa-miR-622	-0.31	N/A	Sites in UTR
HDX	NM_001177478	highly divergent homeobox	1	0	1	0	0	0	0	0	hsa-miR-622	-0.31	N/A	Sites in UTR
FKBP15	NM_015258	FK506 binding protein 15, 133kDa	1	1	0	0	0	0	0	0	hsa-miR-622	-0.31	N/A	Sites in UTR
GSTM5	NM_000851	glutathione S-transferase mu 5	0	0	0	0	2	1	1	0	hsa-miR-622	-0.31	N/A	Sites in UTR
EPT1	NM_033505	ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific)	0	0	0	0	3	0	2	1	hsa-miR-622	-0.31	N/A	Sites in UTR
MTR	NM_000254	5-methyltetrahydrofolate-homocysteine methyltransferase	0	0	0	0	4	1	1	2	hsa-miR-622	-0.31	N/A	Sites in UTR
EML4	NM_001145076	echinoderm microtubule associated protein like 4	0	0	0	0	2	0	1	1	hsa-miR-622	-0.31	N/A	Sites in UTR
ADAMTSL4	NM_019032	ADAMTS-like 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.31	N/A	Sites in UTR
PPM1E	NM_014906	protein phosphatase, Mg2+/Mn2+ dependent, 1E	0	0	0	0	2	1	1	0	hsa-miR-622	-0.31	N/A	Sites in UTR

IFI44L	NM_006820	interferon-induced protein 44-like	0	0	0	0	4	1	1	2	hsa-miR-622	-0.31	N/A	Sites in UTR
FOLR2	NM_000803	folate receptor 2 (fetal)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.3	N/A	Sites in UTR
THBD	NM_000361	thrombomodulin	0	0	0	0	2	0	2	0	hsa-miR-622	-0.3	N/A	Sites in UTR
SNED1	NM_001080437	sushi, nidogen and EGF-like domains 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
TMEM176A	NM_018487	transmembrane protein 176A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
TBC1D14	NM_001113361	TBC1 domain family, member 14	1	1	0	0	0	0	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
GLIS3	NM_001042413	GLIS family zinc finger 3	0	0	0	0	2	1	1	0	hsa-miR-622	-0.3	N/A	Sites in UTR
CERS3	NM_178842	ceramide synthase 3	0	0	0	0	2	0	2	0	hsa-miR-622	-0.3	N/A	Sites in UTR
AIMP1	NM_001142415	aminoacyl tRNA synthetase complex-interacting multifunctional protein 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
FOXJ3	NM_001198850	forkhead box J3	1	1	0	0	0	0	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
SPRY3	NM_005840	sprouty homolog 3 (Drosophila)	0	0	0	0	2	1	1	0	hsa-miR-622	-0.3	N/A	Sites in UTR
NFYA	NM_002505	nuclear transcription factor Y, alpha	1	0	1	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
GDPD5	NM_030792	glycerophosphodiester phosphodiesterase domain containing 5	1	1	0	0	0	0	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
OSBPL1A	NM_001242508	oxysterol binding protein-like 1A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
CD84	NM_001184879	CD84 molecule	0	0	0	0	2	1	0	1	hsa-miR-622	-0.3	N/A	Sites in UTR
GTF3C1	NM_001520	general transcription factor IIIC, polypeptide 1, alpha 220kDa	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
PEAR1	NM_001080471	platelet endothelial aggregation receptor 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
SLC35D1	NM_015139	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	1	0	1	0	2	0	1	1	hsa-miR-622	-0.3	N/A	Sites in UTR

GALNTL2	NM_054110	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 2	0	0	0	0	2	0	0	2	hsa-miR-622	-0.3	N/A	Sites in UTR
FAM63A	NM_001040217	family with sequence similarity 63, member A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
SCN1A	NM_001165963	sodium channel, voltage-gated, type I, alpha subunit	1	0	1	0	2	0	1	1	hsa-miR-622	-0.3	N/A	Sites in UTR
LRFN5	NM_152447	leucine rich repeat and fibronectin type III domain containing 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.3	N/A	Sites in UTR
PEX19	NM_001193644	peroxisomal biogenesis factor 19	0	0	0	0	2	0	2	0	hsa-miR-622	-0.3	N/A	Sites in UTR
RAB10	NM_016131	RAB10, member RAS oncogene family	1	1	0	0	0	0	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
ZCCHC11	NM_001009881	zinc finger, CCHC domain containing 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.3	N/A	Sites in UTR
PWWP2A	NM_001130864	PWWP domain containing 2A	0	0	0	0	2	0	1	1	hsa-miR-622	-0.3	N/A	Sites in UTR
ATF6	NM_007348	activating transcription factor 6	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
APOC2	NM_000483	apolipoprotein C-II	0	0	0	0	1	1	0	0	hsa-miR-622	-0.3	N/A	Sites in UTR
JMJD6	NM_001081461	jumonji domain containing 6	0	0	0	0	4	0	1	3	hsa-miR-622	-0.3	N/A	Sites in UTR
ANGPT2	NM_001118887	angiopoietin 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
BCAS4	NM_001010974	breast carcinoma amplified sequence 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
OSBPL11	NM_022776	oxysterol binding protein-like 11	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
MALL	NM_005434	mal, T-cell differentiation protein-like	1	1	0	0	0	0	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
ZNF706	NM_001042510	zinc finger protein 706	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
PPARA	NM_001001928	peroxisome proliferator-activated receptor alpha	1	0	0	1	3	1	0	2	hsa-miR-622	-0.29	N/A	Sites in UTR
AACS	NM_023928	acetoacetyl-CoA synthetase	0	0	0	0	2	1	1	0	hsa-miR-622	-0.29	N/A	Sites in UTR

PVRL2	NM_001042724	poliovirus receptor-related 2 (herpesvirus entry mediator B)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.29	N/A	Sites in UTR
C9orf66	NM_152569	chromosome 9 open reading frame 66	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
FAM154B	NM_001008226	family with sequence similarity 154, member B	0	0	0	0	3	0	2	1	hsa-miR-622	-0.29	N/A	Sites in UTR
SALL1	NM_001127892	sal-like 1 (Drosophila)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
CAMTA1	NM_015215	calmodulin binding transcription activator 1	1	0	1	0	1	0	1	0	hsa-miR-622	-0.29	N/A	Sites in UTR
MTHFS	NM_001199758	5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.29	N/A	Sites in UTR
ST20-MTHFS	NM_001199760	ST20-MTHFS readthrough	0	0	0	0	1	0	1	0	hsa-miR-622	-0.29	N/A	Sites in UTR
SLAIN2	NM_020846	SLAIN motif family, member 2	1	0	1	0	1	0	1	0	hsa-miR-622	-0.29	N/A	Sites in UTR
ANKRD20A3	NM_001012419	ankyrin repeat domain 20 family, member A3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
SLC24A1	NM_004727	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	0	0	0	0	3	0	1	2	hsa-miR-622	-0.29	N/A	Sites in UTR
LEF1	NM_001130713	lymphoid enhancer-binding factor 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.29	N/A	Sites in UTR
ARL4D	NM_001661	ADP-ribosylation factor-like 4D	1	0	0	1	1	0	1	0	hsa-miR-622	-0.29	N/A	Sites in UTR
TRDN	NM_006073	triadin	0	0	0	0	2	0	2	0	hsa-miR-622	-0.29	N/A	Sites in UTR
KCNJ8	NM_004982	potassium inwardly-rectifying channel, subfamily J, member 8	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
NUP50	NM_007172	nucleoporin 50kDa	0	0	0	0	1	1	0	0	hsa-miR-622	-0.29	N/A	Sites in UTR
PNN	NM_002687	pinin, desmosome associated protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.28	N/A	Sites in UTR
TBL1XR1	NM_024665	transducin (beta)-like 1 X-linked receptor 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.28	N/A	Sites in UTR
CCDC14	NM_022757	coiled-coil domain containing 14	1	1	0	0	0	0	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR

DNAH5	NM_001369	dynein, axonemal, heavy chain 5	0	0	0	0	3	0	1	2	hsa-miR-622	-0.28	N/A	Sites in UTR
PATZ1	NM_014323	POZ (BTB) and AT hook containing zinc finger 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.28	N/A	Sites in UTR
MAP6	NM_207577	microtubule-associated protein 6	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
MRPS27	NM_015084	mitochondrial ribosomal protein S27	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
MECOM	NM_001105077	MDS1 and EVI1 complex locus	0	0	0	0	1	0	1	0	hsa-miR-622	-0.28	N/A	Sites in UTR
METTL20	NM_001135863	methyltransferase like 20	0	0	0	0	1	0	1	0	hsa-miR-622	-0.28	N/A	Sites in UTR
OR13A1	NM_001004297	olfactory receptor, family 13, subfamily A, member 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
SORT1	NM_001205228	sortilin 1	1	0	1	0	1	0	0	1	hsa-miR-622	-0.28	N/A	Sites in UTR
UQCRFS1	NM_006003	ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.28	N/A	Sites in UTR
MCMBP	NM_024834	minichromosome maintenance complex binding protein	0	0	0	0	2	0	2	0	hsa-miR-622	-0.28	N/A	Sites in UTR
PAPLN	NM_173462	papilin, proteoglycan-like sulfated glycoprotein	0	0	0	0	2	0	2	0	hsa-miR-622	-0.28	N/A	Sites in UTR
TRIM25	NM_005082	tripartite motif containing 25	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
CNNM2	NM_199077	cyclin M2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
RNF215	NM_001017981	ring finger protein 215	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
RXRB	NM_021976	retinoid X receptor, beta	1	1	0	0	0	0	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
PKIG	NM_007066	protein kinase (cAMP-dependent, catalytic) inhibitor gamma	1	1	0	0	0	0	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
DTX4	NM_015177	deltex homolog 4 (Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
GAB4	NM_001037814	GRB2-associated binding protein family, member 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR

LARGE	NM_004737	like-glycosyltransferase	1	0	1	0	0	0	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
TNFRSF1B	NM_001066	tumor necrosis factor receptor superfamily, member 1B	0	0	0	0	2	0	2	0	hsa-miR-622	-0.28	N/A	Sites in UTR
STX6	NM_005819	syntaxin 6	1	1	0	0	0	0	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
FGD2	NM_173558	FYVE, RhoGEF and PH domain containing 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
KCNJ14	NM_013348	potassium inwardly-rectifying channel, subfamily J, member 14	0	0	0	0	3	0	0	3	hsa-miR-622	-0.28	N/A	Sites in UTR
CTNNA1	NM_001903	catenin (cadherin-associated protein), alpha 1, 102kDa	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
ITGA4	NM_000885	integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
MYH9	NM_002473	myosin, heavy chain 9, non-muscle	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
TIAL1	NM_001033925	TIA1 cytotoxic granule-associated RNA binding protein-like 1	1	1	0	0	1	0	0	1	hsa-miR-622	-0.28	N/A	Sites in UTR
TNFRSF19	NM_001204458	tumor necrosis factor receptor superfamily, member 19	1	0	0	1	2	1	0	1	hsa-miR-622	-0.28	N/A	Sites in UTR
KIF1B	NM_015074	kinesin family member 1B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.28	N/A	Sites in UTR
NFS1	NM_001198989	NFS1 nitrogen fixation 1 homolog (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
KIAA0748	NM_001098815	KIAA0748	0	0	0	0	1	1	0	0	hsa-miR-622	-0.28	N/A	Sites in UTR
RNF213	NM_020914	ring finger protein 213	0	0	0	0	3	0	3	0	hsa-miR-622	-0.27	N/A	Sites in UTR
DGKB	NM_145695	diacylglycerol kinase, beta 90kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
SLC25A26	NM_001164796	solute carrier family 25, member 26	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
TDRD9	NM_153046	tudor domain containing 9	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
XRCC2	NM_005431	X-ray repair complementing defective repair in Chinese hamster cells 2	0	0	0	0	3	0	1	2	hsa-miR-622	-0.27	N/A	Sites in UTR

RFWD3	NM_018124	ring finger and WD repeat domain 3	0	0	0	0	2	1	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
KIAA0586	NM_014749	KIAA0586	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
NRSN1	NM_080723	neurensin 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.27	N/A	Sites in UTR
CD200	NM_001004196	CD200 molecule	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
GUF1	NM_021927	GUF1 GTPase homolog (S. cerevisiae)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.27	N/A	Sites in UTR
ZNF12	NM_006956	zinc finger protein 12	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
RNF220	NM_018150	ring finger protein 220	1	1	0	0	0	0	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
SLC17A7	NM_020309	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
NCS1	NM_001128826	neuronal calcium sensor 1	1	1	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
CLK1	NM_001162407	CDC-like kinase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
SMOC2	NM_001166412	SPARC related modular calcium binding 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
CBLN2	NM_182511	cerebellin 2 precursor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
ANKRD29	NM_173505	ankyrin repeat domain 29	0	0	0	0	2	0	1	1	hsa-miR-622	-0.27	N/A	Sites in UTR
TPRG1	NM_198485	tumor protein p63 regulated 1	1	0	1	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
ATP2A3	NM_005173	ATPase, Ca++ transporting, ubiquitous	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
ZNF248	NM_021045	zinc finger protein 248	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
ESRRG	NM_001134285	estrogen-related receptor gamma	0	0	0	0	2	0	2	0	hsa-miR-622	-0.27	N/A	Sites in UTR
C12orf69	NM_001013698	chromosome 12 open reading frame 69	0	0	0	0	2	0	1	1	hsa-miR-622	-0.27	N/A	Sites in UTR

PDF	NM_022341	peptide deformylase (mitochondrial)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
SLC25A38	NM_017875	solute carrier family 25, member 38	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
UBL4B	NM_203412	ubiquitin-like 4B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
LOC100287036	NM_001242885	hypothetical LOC100287036	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
CDC42EP3	NM_006449	CDC42 effector protein (Rho GTPase binding) 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
PABPC1L2A	NM_001012977	poly(A) binding protein, cytoplasmic 1-like 2A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
PDE4DIP	NM_001198832	phosphodiesterase 4D interacting protein	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
TRDMT1	NM_004412	tRNA aspartic acid methyltransferase 1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.27	N/A	Sites in UTR
C9orf72	NM_145005	chromosome 9 open reading frame 72	0	0	0	0	1	0	1	0	hsa-miR-622	-0.27	N/A	Sites in UTR
ARIH1	NM_005744	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
FCGR2B	NM_001002273	Fc fragment of IgG, low affinity IIb, receptor (CD32)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.27	N/A	Sites in UTR
LOC388564	NM_001190764	hypothetical protein LOC388564	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
RBM3	NM_006743	RNA binding motif (RNP1, RRM) protein 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
PTGES	NM_004878	prostaglandin E synthase	0	0	0	0	1	1	0	0	hsa-miR-622	-0.27	N/A	Sites in UTR
RHBDL3	NM_138328	rhomboid, veinlet-like 3 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
SLC39A12	NM_001145195	solute carrier family 39 (zinc transporter), member 12	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
ST6GALNAC3	NM_152996	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
PAPOLA	NM_032632	poly(A) polymerase alpha	1	0	1	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR

MMP16	NM_005941	matrix metallopeptidase 16 (membrane-inserted)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
KDM6A	NM_021140	lysine (K)-specific demethylase 6A	1	0	1	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
GPR89B	NM_016334	G protein-coupled receptor 89B	1	0	1	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
GPR89A	NM_001097612	G protein-coupled receptor 89A	1	0	1	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
GPR89C	NM_001097616	G protein-coupled receptor 89C	1	0	1	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
CLEC4F	NM_173535	C-type lectin domain family 4, member F	0	0	0	0	1	1	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
IRX1	NM_024337	iroquois homeobox 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
TLE4	NM_007005	transducin-like enhancer of split 4 (E(sp1) homolog, Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.26	N/A	Sites in UTR
PAX3	NM_001127366	paired box 3	0	0	0	0	2	0	2	0	hsa-miR-622	-0.26	N/A	Sites in UTR
GRIN2D	NM_000836	glutamate receptor, ionotropic, N-methyl D-aspartate 2D	3	0	3	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
DLX6	NM_005222	distal-less homeobox 6	1	1	0	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
STX7	NM_003569	syntaxin 7	0	0	0	0	3	1	2	0	hsa-miR-622	-0.26	N/A	Sites in UTR
ATE1	NM_001001976	arginyltransferase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
TTC19	NM_017775	tetratricopeptide repeat domain 19	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
PI4KB	NM_001198773	phosphatidylinositol 4-kinase, catalytic, beta	0	0	0	0	1	1	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
C14orf43	NM_001043318	chromosome 14 open reading frame 43	2	0	1	1	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
SLC35E1	NM_024881	solute carrier family 35, member E1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.26	N/A	Sites in UTR
TMOD1	NM_001166116	tropomodulin 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR

PRR5L	NM_001160167	proline rich 5 like	0	0	0	0	1	1	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
WWC3	NM_015691	WWC family member 3	1	0	0	1	2	0	1	1	hsa-miR-622	-0.26	N/A	Sites in UTR
PCTP	NM_001102402	phosphatidylcholine transfer protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
TMEM47	NM_031442	transmembrane protein 47	1	0	1	0	0	0	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
PGRMC2	NM_006320	progesterone receptor membrane component 2	1	0	0	1	1	0	1	0	hsa-miR-622	-0.26	N/A	Sites in UTR
C15orf29	NM_024713	chromosome 15 open reading frame 29	0	0	0	0	2	0	1	1	hsa-miR-622	-0.26	N/A	Sites in UTR
11-Sep	NM_018243	septin 11	0	0	0	0	2	0	2	0	hsa-miR-622	-0.26	N/A	Sites in UTR
PDCD1LG2	NM_025239	programmed cell death 1 ligand 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
WDR65	NM_001167965	WD repeat domain 65	0	0	0	0	1	1	0	0	hsa-miR-622	-0.26	N/A	Sites in UTR
PRKAR2A	NM_004157	protein kinase, cAMP-dependent, regulatory, type II, alpha	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
RAB31	NM_006868	RAB31, member RAS oncogene family	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
PCGF5	NM_032373	polycomb group ring finger 5	0	0	0	0	2	1	0	1	hsa-miR-622	-0.25	N/A	Sites in UTR
EBF3	NM_001005463	early B-cell factor 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.25	N/A	Sites in UTR
MAP3K2	NM_006609	mitogen-activated protein kinase kinase kinase 2	1	0	1	0	2	1	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
GNL3	NM_014366	guanine nucleotide binding protein-like 3 (nucleolar)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
SMC2	NM_001042550	structural maintenance of chromosomes 2	0	0	0	0	2	0	1	1	hsa-miR-622	-0.25	N/A	Sites in UTR
FRS2	NM_001042555	fibroblast growth factor receptor substrate 2	1	0	0	1	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
MAPK1	NM_002745	mitogen-activated protein kinase 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.25	N/A	Sites in UTR

RTF1	NM_015138	Rtf1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	1	0	1	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
EIF4E1B	NM_001099408	eukaryotic translation initiation factor 4E family member 1B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
ADIPOQ	NM_001177800	adiponectin, C1Q and collagen domain containing	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
WIPF1	NM_001077269	WAS/WASL interacting protein family, member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
DLG5	NM_004747	discs, large homolog 5 (Drosophila)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.25	N/A	Sites in UTR
CNP	NM_033133	2',3'-cyclic nucleotide 3' phosphodiesterase	0	0	0	0	3	0	2	1	hsa-miR-622	-0.25	N/A	Sites in UTR
RGS20	NM_003702	regulator of G-protein signaling 20	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
MAFB	NM_005461	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
BTG1	NM_001731	B-cell translocation gene 1, anti-proliferative	1	0	0	1	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
PURB	NM_033224	purine-rich element binding protein B	0	0	0	0	2	0	2	0	hsa-miR-622	-0.25	N/A	Sites in UTR
TMF1	NM_007114	TATA element modulatory factor 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.25	N/A	Sites in UTR
SATB1	NM_001131010	SATB homeobox 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
MAP7	NM_001198608	microtubule-associated protein 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
FAM70A	NM_001104544	family with sequence similarity 70, member A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
SLC28A3	NM_001199633	solute carrier family 28 (sodium-coupled nucleoside transporter), member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
TSEN15	NM_001127394	tRNA splicing endonuclease 15 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.25	N/A	Sites in UTR
ERO1LB	NM_019891	ERO1-like beta (S. cerevisiae)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.25	N/A	Sites in UTR
HIRA	NM_003325	HIR histone cell cycle regulation defective homolog A (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR

ABCC9	NM_020297	ATP-binding cassette, sub-family C (CFTR/MRP), member 9	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
SH2D4B	NM_001145719	SH2 domain containing 4B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
MYLIP	NM_013262	myosin regulatory light chain interacting protein	0	0	0	0	1	1	0	0	hsa-miR-622	-0.25	N/A	Sites in UTR
SLC11A2	NM_000617	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 2	0	0	0	0	2	0	2	0	hsa-miR-622	-0.24	N/A	Sites in UTR
SIM2	NM_009586	single-minded homolog 2 (Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
CHSY1	NM_014918	chondroitin sulfate synthase 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
CCR5	NM_000579	chemokine (C-C motif) receptor 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
VTA1	NM_016485	Vps20-associated 1 homolog (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
FAM129A	NM_052966	family with sequence similarity 129, member A	0	0	0	0	3	0	1	2	hsa-miR-622	-0.24	N/A	Sites in UTR
ABHD5	NM_016006	abhydrolase domain containing 5	0	0	0	0	3	1	1	1	hsa-miR-622	-0.24	N/A	Sites in UTR
ZNF48	NM_001214906	zinc finger protein 48	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
GAPVD1	NM_015635	GTPase activating protein and VPS9 domains 1	1	0	1	0	1	0	0	1	hsa-miR-622	-0.24	N/A	Sites in UTR
SHISA2	NM_001007538	shisa homolog 2 (Xenopus laevis)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.24	N/A	Sites in UTR
ZDHHC2	NM_016353	zinc finger, DHHC-type containing 2	1	1	0	0	0	0	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
FPR3	NM_002030	formyl peptide receptor 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
GHR	NM_000163	growth hormone receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
NR3C1	NM_000176	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
ATP5L	NM_006476	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G	1	0	1	0	0	0	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR

SLC39A14	NM_001128431	solute carrier family 39 (zinc transporter), member 14	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
PCDH15	NM_001142763	protocadherin-related 15	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
SUV39H1	NM_003173	suppressor of variegation 3-9 homolog 1 (Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
DENND1A	NM_020946	DENN/MADD domain containing 1A	0	0	0	0	2	1	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
ZBTB7B	NM_015872	zinc finger and BTB domain containing 7B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
C5orf47	NM_001144954	chromosome 5 open reading frame 47	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
EZH1	NM_001991	enhancer of zeste homolog 1 (Drosophila)	1	1	0	0	1	0	0	1	hsa-miR-622	-0.24	N/A	Sites in UTR
PAFAH1B1	NM_000430	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
RRAGD	NM_021244	Ras-related GTP binding D	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
CDS2	NM_003818	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2	1	1	0	0	0	0	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
NUDT16	NM_001171905	nudix (nucleoside diphosphate linked moiety X)-type motif 16	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
CRK	NM_005206	v-crk sarcoma virus CT10 oncogene homolog (avian)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.24	N/A	Sites in UTR
TSKU	NM_015516	tsukushi small leucine rich proteoglycan homolog (Xenopus laevis)	1	0	1	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
ANO5	NM_001142649	anoctamin 5	0	0	0	0	3	0	0	3	hsa-miR-622	-0.24	N/A	Sites in UTR
SLC38A2	NM_018976	solute carrier family 38, member 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
SLAMF6	NM_001184714	SLAM family member 6	0	0	0	0	2	1	0	1	hsa-miR-622	-0.24	N/A	Sites in UTR
RIMBP2	NM_015347	RIMS binding protein 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
MAP1A	NM_002373	microtubule-associated protein 1A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR

XRCC3	NM_001100118	X-ray repair complementing defective repair in Chinese hamster cells 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
COG8	NM_032382	component of oligomeric golgi complex 8	0	0	0	0	1	1	0	0	hsa-miR-622	-0.24	N/A	Sites in UTR
KRTAP13-2	NM_181621	keratin associated protein 13-2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.24	N/A	Sites in UTR
PSEN1	NM_000021	presenilin 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
RGS1	NM_002922	regulator of G-protein signaling 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SDC2	NM_002998	syndecan 2	0	0	0	0	2	0	1	1	hsa-miR-622	-0.23	N/A	Sites in UTR
PAFAH2	NM_000437	platelet-activating factor acetylhydrolase 2, 40kDa	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
RARG	NM_000966	retinoic acid receptor, gamma	1	1	0	0	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SFRP2	NM_003013	secreted frizzled-related protein 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
ATP5L2	NM_001165877	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit G2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
CD300E	NM_181449	CD300e molecule	1	0	1	0	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
ARSI	NM_001012301	arylsulfatase family, member I	0	0	0	0	2	0	2	0	hsa-miR-622	-0.23	N/A	Sites in UTR
C3orf43	NM_001077657	chromosome 3 open reading frame 43	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
C1orf131	NM_152379	chromosome 1 open reading frame 131	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
DSC3	NM_001941	desmocollin 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.23	N/A	Sites in UTR
POU4F1	NM_006237	POU class 4 homeobox 1	1	0	0	1	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
COTL1	NM_021149	coactosin-like 1 (Dictyostelium)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
PRRC2B	NM_013318	proline-rich coiled-coil 2B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR

PRDM4	NM_012406	PR domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
ZNF260	NM_001012756	zinc finger protein 260	0	0	0	0	2	0	0	2	hsa-miR-622	-0.23	N/A	Sites in UTR
TPD52	NM_001025252	tumor protein D52	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
MEX3A	NM_001093725	mex-3 homolog A (C. elegans)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
ZNF865	NM_001195605	zinc finger protein 865	0	0	0	0	2	1	0	1	hsa-miR-622	-0.23	N/A	Sites in UTR
TAF7	NM_005642	TAF7 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 55kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
TECPR2	NM_001172631	tectonin beta-propeller repeat containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
MYL12A	NM_006471	myosin, light chain 12A, regulatory, non-sarcomeric	1	0	1	0	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
WFDC8	NM_181510	WAP four-disulfide core domain 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
EN1	NM_001426	engrailed homeobox 1	2	0	1	1	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SIAH3	NM_198849	seven in absentia homolog 3 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.23	N/A	Sites in UTR
NEDD4L	NM_001144964	neural precursor cell expressed, developmentally down-regulated 4-like	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
TRIB2	NM_021643	tribbles homolog 2 (Drosophila)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
RHD	NM_001127691	Rh blood group, D antigen	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
UBE2J1	NM_016021	ubiquitin-conjugating enzyme E2, J1, U	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SEH1L	NM_001013437	SEH1-like (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SEC16A	NM_014866	SEC16 homolog A (S. cerevisiae)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.23	N/A	Sites in UTR
CTDSPL	NM_001008392	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR

PARP6	NM_020214	poly (ADP-ribose) polymerase family, member 6	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SLCO2A1	NM_005630	solute carrier organic anion transporter family, member 2A1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.23	N/A	Sites in UTR
KLF3	NM_016531	Kruppel-like factor 3 (basic)	1	0	0	1	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
WSB1	NM_015626	WD repeat and SOCS box containing 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
SLC14A1	NM_001128588	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.23	N/A	Sites in UTR
PHTF2	NM_001127357	putative homeodomain transcription factor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
KLHL14	NM_020805	kelch-like 14 (Drosophila)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
FAM110C	NM_001077710	family with sequence similarity 110, member C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
CCDC86	NM_024098	coiled-coil domain containing 86	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
CCNG1	NM_004060	cyclin G1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
EPHA7	NM_004440	EPH receptor A7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
IRF2	NM_002199	interferon regulatory factor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
NPY1R	NM_000909	neuropeptide Y receptor Y1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
PKD1L1	NM_138295	polycystic kidney disease 1 like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
BCAT1	NM_001178091	branched chain amino-acid transaminase 1, cytosolic	0	0	0	0	2	0	1	1	hsa-miR-622	-0.23	N/A	Sites in UTR
TMEM100	NM_001099640	transmembrane protein 100	0	0	0	0	2	0	1	1	hsa-miR-622	-0.23	N/A	Sites in UTR
RNF125	NM_017831	ring finger protein 125	1	1	0	0	1	0	0	1	hsa-miR-622	-0.23	N/A	Sites in UTR
OSMR	NM_001168355	oncostatin M receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR

C9orf80	NM_021218	chromosome 9 open reading frame 80	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
CFHR5	NM_030787	complement factor H-related 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
ACBD5	NM_001042473	acyl-CoA binding domain containing 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
ACAT1	NM_000019	acetyl-CoA acetyltransferase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
FABP2	NM_000134	fatty acid binding protein 2, intestinal	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
POLR2H	NM_006232	polymerase (RNA) II (DNA directed) polypeptide H	0	0	0	0	1	0	1	0	hsa-miR-622	-0.23	N/A	Sites in UTR
EGFR	NM_005228	epidermal growth factor receptor	0	0	0	0	2	0	1	1	hsa-miR-622	-0.23	N/A	Sites in UTR
CLDN5	NM_001130861	claudin 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.23	N/A	Sites in UTR
DCUN1D5	NM_032299	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	1	0	0	1	2	0	1	1	hsa-miR-622	-0.22	N/A	Sites in UTR
LSM1	NM_014462	LSM1 homolog, U6 small nuclear RNA associated (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
ZNF436	NM_001077195	zinc finger protein 436	0	0	0	0	2	0	1	1	hsa-miR-622	-0.22	N/A	Sites in UTR
CLEC12B	NM_205852	C-type lectin domain family 12, member B	0	0	0	0	3	0	0	3	hsa-miR-622	-0.22	N/A	Sites in UTR
DPP10	NM_001004360	dipeptidyl-peptidase 10 (non-functional)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
TMCO1	NM_019026	transmembrane and coiled-coil domains 1	1	0	1	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
DDHD1	NM_001160147	DDHD domain containing 1	0	0	0	0	3	0	3	0	hsa-miR-622	-0.22	N/A	Sites in UTR
DYNC1LI2	NM_006141	dynein, cytoplasmic 1, light intermediate chain 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
RAB28	NM_001017979	RAB28, member RAS oncogene family	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
NT5DC3	NM_001031701	5'-nucleotidase domain containing 3	0	0	0	0	2	1	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR

HES2	NM_019089	hairy and enhancer of split 2 (Drosophila)	1	1	0	0	1	0	0	1	hsa-miR-622	-0.22	N/A	Sites in UTR
USP10	NM_005153	ubiquitin specific peptidase 10	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
RAB25	NM_020387	RAB25, member RAS oncogene family	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
CDH5	NM_001795	cadherin 5, type 2 (vascular endothelium)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.22	N/A	Sites in UTR
LYRM7	NM_181705	Lyrm7 homolog (mouse)	0	0	0	0	2	1	0	1	hsa-miR-622	-0.22	N/A	Sites in UTR
RALGPS1	NM_014636	Ral GEF with PH domain and SH3 binding motif 1	1	1	0	0	2	1	0	1	hsa-miR-622	-0.22	N/A	Sites in UTR
API5	NM_001142930	apoptosis inhibitor 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
LPAR2	NM_004720	lysophosphatidic acid receptor 2	0	0	0	0	2	0	1	1	hsa-miR-622	-0.22	N/A	Sites in UTR
LRAT	NM_004744	lecithin retinol acyltransferase (phosphatidylcholine--retinol O-acyltransferase)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
BST1	NM_004334	bone marrow stromal cell antigen 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
EIF2B1	NM_001414	eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa	1	1	0	0	0	0	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
PRRX1	NM_006902	paired related homeobox 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
ZC3H10	NM_032786	zinc finger CCCH-type containing 10	1	1	0	0	0	0	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
ATXN7L1	NM_020725	ataxin 7-like 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
HYAL1	NM_007312	hyaluronoglucosaminidase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
LYZ	NM_000239	lysozyme	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
SLC37A1	NM_018964	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
ZFYVE20	NM_022340	zinc finger, FYVE domain containing 20	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR

ALCAM	NM_001627	activated leukocyte cell adhesion molecule	0	0	0	0	1	1	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
SH2D7	NM_001101404	SH2 domain containing 7	0	0	0	0	1	1	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
DGKG	NM_001080744	diacylglycerol kinase, gamma 90kDa	0	0	0	0	2	1	0	1	hsa-miR-622	-0.22	N/A	Sites in UTR
VPS24	NM_001005753	vacuolar protein sorting 24 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
RNF103-VPS24	NM_001198954	RNF103-VPS24 readthrough	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
PDE7A	NM_002604	phosphodiesterase 7A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.22	N/A	Sites in UTR
ISM1	NM_080826	isthmin 1 homolog (zebrafish)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.22	N/A	Sites in UTR
NDRG3	NM_022477	NDRG family member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
HTRA4	NM_153692	HtrA serine peptidase 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.22	N/A	Sites in UTR
C9orf3	NM_001193331	chromosome 9 open reading frame 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.22	N/A	Sites in UTR
THUMPD3	NM_001114092	THUMP domain containing 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.22	N/A	Sites in UTR
HBEGF	NM_001945	heparin-binding EGF-like growth factor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
DKK2	NM_014421	dickkopf homolog 2 (Xenopus laevis)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
FGF3	NM_005247	fibroblast growth factor 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
COL4A3BP	NM_001130105	collagen, type IV, alpha 3 (Goodpasture antigen) binding protein	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
GFAP	NM_002055	glial fibrillary acidic protein	0	0	0	0	4	0	3	1	hsa-miR-622	-0.21	N/A	Sites in UTR
GP5	NM_004488	glycoprotein V (platelet)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
PRSS8	NM_002773	protease, serine, 8	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR

ALDH4A1	NM_001161504	aldehyde dehydrogenase 4 family, member A1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
ZNF234	NM_001144824	zinc finger protein 234	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
ATXN1	NM_000332	ataxin 1	0	0	0	0	2	1	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
PRR11	NM_018304	proline rich 11	0	0	0	0	5	0	0	5	hsa-miR-622	-0.21	N/A	Sites in UTR
SNRNP40	NM_004814	small nuclear ribonucleoprotein 40kDa (U5)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
MFSD4	NM_181644	major facilitator superfamily domain containing 4	0	0	0	0	2	0	1	1	hsa-miR-622	-0.21	N/A	Sites in UTR
TNFRSF9	NM_001561	tumor necrosis factor receptor superfamily, member 9	0	0	0	0	2	0	2	0	hsa-miR-622	-0.21	N/A	Sites in UTR
CYFIP2	NM_001037332	cytoplasmic FMR1 interacting protein 2	0	0	0	0	4	0	1	3	hsa-miR-622	-0.21	N/A	Sites in UTR
U2SURP	NM_001080415	U2 snRNP-associated SURP domain containing	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
TGIF1	NM_003244	TGFB-induced factor homeobox 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
TMEM233	NM_001136534	transmembrane protein 233	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
HTR2C	NM_000868	5-hydroxytryptamine (serotonin) receptor 2C	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
MRPL9	NM_031420	mitochondrial ribosomal protein L9	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
MYL12B	NM_001144944	myosin, light chain 12B, regulatory	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
SAMD4B	NM_018028	sterile alpha motif domain containing 4B	0	0	0	0	3	0	3	0	hsa-miR-622	-0.21	N/A	Sites in UTR
ERCC6	NM_000124	excision repair cross-complementing rodent repair deficiency, complementation group 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
AXIN2	NM_004655	axin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
RNF24	NM_001134337	ring finger protein 24	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR

SDCBP2	NM_001199784	syndecan binding protein (syntenin) 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
HEATR1	NM_018072	HEAT repeat containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
MYO5C	NM_018728	myosin VC	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
PMPCB	NM_004279	peptidase (mitochondrial processing) beta	0	0	0	0	2	0	2	0	hsa-miR-622	-0.21	N/A	Sites in UTR
RPUSD4	NM_001144827	RNA pseudouridylate synthase domain containing 4	0	0	0	0	2	0	2	0	hsa-miR-622	-0.21	N/A	Sites in UTR
HAPLN4	NM_023002	hyaluronan and proteoglycan link protein 4	0	0	0	0	2	1	0	1	hsa-miR-622	-0.21	N/A	Sites in UTR
RB1	NM_000321	retinoblastoma 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
USP25	NM_013396	ubiquitin specific peptidase 25	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
CHRFAM7A	NM_139320	CHRNA7 (cholinergic receptor, nicotinic, alpha 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) fusion	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
C9orf91	NM_153045	chromosome 9 open reading frame 91	1	0	0	1	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
HOXB9	NM_024017	homeobox B9	0	0	0	0	2	0	2	0	hsa-miR-622	-0.21	N/A	Sites in UTR
SIRPB1	NM_001135844	signal-regulatory protein beta 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
PSMD13	NM_002817	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
UQCR11	NM_006830	ubiquinol-cytochrome c reductase, complex III subunit XI	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
SLC16A10	NM_018593	solute carrier family 16, member 10 (aromatic amino acid transporter)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
PRR23C	NM_001134657	proline rich 23C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
MTRNR2L7	NM_001190489	MT-RNR2-like 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
DCDC5	NM_020869	doublecortin domain containing 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR

YWHAG	NM_012479	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide	0	0	0	0	1	1	0	0	hsa-miR-622	-0.21	N/A	Sites in UTR
FRMD4A	NM_018027	FERM domain containing 4A	0	0	0	0	2	1	0	1	hsa-miR-622	-0.21	N/A	Sites in UTR
ATP1B3	NM_001679	ATPase, Na+/K+ transporting, beta 3 polypeptide	0	0	0	0	1	0	1	0	hsa-miR-622	-0.21	N/A	Sites in UTR
LAMC2	NM_005562	laminin, gamma 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
PAX1	NM_006192	paired box 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
APOBEC3F	NM_145298	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3F	0	0	0	0	2	0	2	0	hsa-miR-622	-0.2	N/A	Sites in UTR
CYTH3	NM_004227	cytohesin 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
TOMM34	NM_006809	translocase of outer mitochondrial membrane 34	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
WSCD1	NM_015253	WSC domain containing 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
DPCR1	NM_080870	diffuse panbronchiolitis critical region 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
PEA15	NM_003768	phosphoprotein enriched in astrocytes 15	1	0	1	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
PIK3R5	NM_001142633	phosphoinositide-3-kinase, regulatory subunit 5	0	0	0	0	2	1	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
LCT	NM_002299	lactase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
FAM36A	NM_198076	family with sequence similarity 36, member A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
ONECUT2	NM_004852	one cut homeobox 2	0	0	0	0	3	0	2	1	hsa-miR-622	-0.2	N/A	Sites in UTR
TNPO3	NM_001191028	transportin 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
SRFBP1	NM_152546	serum response factor binding protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
GPHN	NM_001024218	gephyrin	1	0	0	1	1	0	0	1	hsa-miR-622	-0.2	N/A	Sites in UTR

ADM2	NM_024866	adrenomedullin 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
EPHA5	NM_004439	EPH receptor A5	0	0	0	0	2	1	0	1	hsa-miR-622	-0.2	N/A	Sites in UTR
E2F6	NM_198256	E2F transcription factor 6	0	0	0	0	2	0	2	0	hsa-miR-622	-0.2	N/A	Sites in UTR
PRF1	NM_001083116	perforin 1 (pore forming protein)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
SPTBN1	NM_003128	spectrin, beta, non-erythrocytic 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
AKAP7	NM_004842	A kinase (PRKA) anchor protein 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
CWC27	NM_005869	CWC27 spliceosome-associated protein homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
KCNC1	NM_004976	potassium voltage-gated channel, Shaw-related subfamily, member 1	1	0	1	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
MYH11	NM_001040113	myosin, heavy chain 11, smooth muscle	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
KSR1	NM_014238	kinase suppressor of ras 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
FAM13B	NM_001101800	family with sequence similarity 13, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
CYSLTR2	NM_020377	cysteinyl leukotriene receptor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
CEP19	NM_032898	centrosomal protein 19kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
SLC22A8	NM_001184732	solute carrier family 22 (organic anion transporter), member 8	0	0	0	0	2	0	0	2	hsa-miR-622	-0.2	N/A	Sites in UTR
ERP44	NM_015051	endoplasmic reticulum protein 44	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
KIAA0317	NM_001039479	KIAA0317	0	0	0	0	3	0	1	2	hsa-miR-622	-0.2	N/A	Sites in UTR
FAM105A	NM_019018	family with sequence similarity 105, member A	0	0	0	0	3	1	1	1	hsa-miR-622	-0.2	N/A	Sites in UTR
HLA-DQB1	NM_002123	major histocompatibility complex, class II, DQ beta 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR

CHDH	NM_018397	choline dehydrogenase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
LSM11	NM_173491	LSM11, U7 small nuclear RNA associated	1	0	1	0	0	0	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
SLC15A5	NM_001170798	solute carrier family 15, member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
LPGAT1	NM_014873	lysophosphatidylglycerol acyltransferase 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.2	N/A	Sites in UTR
AQP5	NM_001651	aquaporin 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
BMP4	NM_001202	bone morphogenetic protein 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
NIT1	NM_001185093	nitrilase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
SLC7A6OS	NM_032178	solute carrier family 7, member 6 opposite strand	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
KIAA0182	NM_001134473	KIAA0182	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
GLTPD1	NM_001029885	glycolipid transfer protein domain containing 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.2	N/A	Sites in UTR
VMA21	NM_001017980	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
LY75	NM_002349	lymphocyte antigen 75	0	0	0	0	2	0	0	2	hsa-miR-622	-0.2	N/A	Sites in UTR
WASL	NM_003941	Wiskott-Aldrich syndrome-like	0	0	0	0	2	0	1	1	hsa-miR-622	-0.2	N/A	Sites in UTR
B3GALNT2	NM_152490	beta-1,3-N-acetylgalactosaminyltransferase 2	0	0	0	0	2	0	1	1	hsa-miR-622	-0.2	N/A	Sites in UTR
DDX23	NM_004818	DEAD (Asp-Glu-Ala-Asp) box polypeptide 23	1	1	0	0	0	0	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
C15orf62	NM_001130448	chromosome 15 open reading frame 62	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
IL16	NM_001172128	interleukin 16	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
TAGAP	NM_054114	T-cell activation RhoGTPase activating protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR

RAD21	NM_006265	RAD21 homolog (S. pombe)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
RBMS1	NM_002897	RNA binding motif, single stranded interacting protein 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
KLF9	NM_001206	Kruppel-like factor 9	0	0	0	0	1	0	0	1	hsa-miR-622	-0.2	N/A	Sites in UTR
LSS	NM_001145436	lanosterol synthase (2,3-oxidosqualene-lanosterol cyclase)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
METTL13	NM_001007239	methyltransferase like 13	1	0	0	1	1	0	1	0	hsa-miR-622	-0.2	N/A	Sites in UTR
FAM22G	NM_001045477	family with sequence similarity 22, member G	0	0	0	0	1	1	0	0	hsa-miR-622	-0.2	N/A	Sites in UTR
EXOC7	NM_001013839	exocyst complex component 7	0	0	0	0	4	0	3	1	hsa-miR-622	-0.19	N/A	Sites in UTR
LAIR1	NM_002287	leukocyte-associated immunoglobulin-like receptor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
GALNT14	NM_024572	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 14 (GalNAc-T14)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
LOC284385	NM_001242812	hypothetical LOC284385	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
CCDC165	NM_015210	coiled-coil domain containing 165	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
FBXO22	NM_012170	F-box protein 22	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
C8orf4	NM_020130	chromosome 8 open reading frame 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
METTL15	NM_001113528	methyltransferase like 15	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
ETNK1	NM_018638	ethanolamine kinase 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.19	N/A	Sites in UTR
SLC25A30	NM_001010875	solute carrier family 25, member 30	0	0	0	0	2	0	1	1	hsa-miR-622	-0.19	N/A	Sites in UTR
RGS4	NM_001102445	regulator of G-protein signaling 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
EP400	NM_015409	E1A binding protein p400	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR

RBM12B	NM_203390	RNA binding motif protein 12B	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
CNTNAP2	NM_014141	contactin associated protein-like 2	1	0	0	1	1	0	0	1	hsa-miR-622	-0.19	N/A	Sites in UTR
SFRP1	NM_003012	secreted frizzled-related protein 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
MBNL1	NM_021038	muscleblind-like (Drosophila)	1	1	0	0	1	0	0	1	hsa-miR-622	-0.19	N/A	Sites in UTR
GABPB1	NM_005254	GA binding protein transcription factor, beta subunit 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
UBE2L6	NM_004223	ubiquitin-conjugating enzyme E2L 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
C1orf9	NM_014283	chromosome 1 open reading frame 9	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
ZNF713	NM_182633	zinc finger protein 713	0	0	0	0	2	0	0	2	hsa-miR-622	-0.19	N/A	Sites in UTR
RALGPS2	NM_152663	Ral GEF with PH domain and SH3 binding motif 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
EPB41L5	NM_001184937	erythrocyte membrane protein band 4.1 like 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
OTUD4	NM_001102653	OTU domain containing 4	0	0	0	0	2	1	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
YPEL2	NM_001005404	yippee-like 2 (Drosophila)	0	0	0	0	3	0	1	2	hsa-miR-622	-0.19	N/A	Sites in UTR
ALDH1B1	NM_000692	aldehyde dehydrogenase 1 family, member B1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
DFFA	NM_213566	DNA fragmentation factor, 45kDa, alpha polypeptide	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
USP24	NM_015306	ubiquitin specific peptidase 24	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
DLL4	NM_019074	delta-like 4 (Drosophila)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
IQCH	NM_001031715	IQ motif containing H	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
TMEM86A	NM_153347	transmembrane protein 86A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR

KIAA0174	NM_014761	KIAA0174	0	0	0	0	2	0	0	2	hsa-miR-622	-0.19	N/A	Sites in UTR
ZKSCAN1	NM_003439	zinc finger with KRAB and SCAN domains 1	0	0	0	0	3	1	0	2	hsa-miR-622	-0.19	N/A	Sites in UTR
HIF1A	NM_001530	hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
SIN3A	NM_001145357	SIN3 homolog A, transcription regulator (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
FAM32A	NM_014077	family with sequence similarity 32, member A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
PCNP	NM_020357	PEST proteolytic signal containing nuclear protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
ZNF329	NM_024620	zinc finger protein 329	0	0	0	0	2	0	0	2	hsa-miR-622	-0.19	N/A	Sites in UTR
SNX10	NM_001199835	sorting nexin 10	0	0	0	0	2	0	1	1	hsa-miR-622	-0.19	N/A	Sites in UTR
C20orf203	NM_182584	chromosome 20 open reading frame 203	0	0	0	0	2	1	0	1	hsa-miR-622	-0.19	N/A	Sites in UTR
C20orf112	NM_080616	chromosome 20 open reading frame 112	1	0	0	1	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
APC	NM_000038	adenomatous polyposis coli	0	0	0	0	1	0	0	1	hsa-miR-622	-0.19	N/A	Sites in UTR
CHRNA7	NM_000746	cholinergic receptor, nicotinic, alpha 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
EYA4	NM_004100	eyes absent homolog 4 (Drosophila)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
RLF	NM_012421	rearranged L-myc fusion	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
TIGD3	NM_145719	tigger transposable element derived 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
C12orf74	NM_001037671	chromosome 12 open reading frame 74	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
SMAD2	NM_001003652	SMAD family member 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
SMAD5	NM_001001419	SMAD family member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR

CLDN11	NM_001185056	claudin 11	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
FRY	NM_023037	furry homolog (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
TMEM43	NM_024334	transmembrane protein 43	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
AGAP3	NM_031946	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
ARHGDIA	NM_001185077	Rho GDP dissociation inhibitor (GDI) alpha	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	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	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
USP20	NM_001008563	ubiquitin specific peptidase 20	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
ROBO2	NM_001128929	roundabout, axon guidance receptor, homolog 2 (Drosophila)	1	0	0	1	2	0	0	2	hsa-miR-622	-0.19	N/A	Sites in UTR
CX3CR1	NM_001171171	chemokine (C-X3-C motif) receptor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.19	N/A	Sites in UTR
FLT4	NM_182925	fms-related tyrosine kinase 4	0	0	0	0	2	0	1	1	hsa-miR-622	-0.19	N/A	Sites in UTR
MASP1	NM_001031849	mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.19	N/A	Sites in UTR
E2F1	NM_005225	E2F transcription factor 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
RBM8A	NM_005105	RNA binding motif protein 8A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.19	N/A	Sites in UTR
SLC25A34	NM_207348	solute carrier family 25, member 34	0	0	0	0	3	0	2	1	hsa-miR-622	-0.19	N/A	Sites in UTR
RASA1	NM_002890	RAS p21 protein activator (GTPase activating protein) 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
ZNF282	NM_003575	zinc finger protein 282	1	0	1	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
C1orf212	NM_001164824	chromosome 1 open reading frame 212	0	0	0	0	2	0	2	0	hsa-miR-622	-0.18	N/A	Sites in UTR
PRKACA	NM_002730	protein kinase, cAMP-dependent, catalytic, alpha	1	1	0	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR

NMUR1	NM_006056	neuromedin U receptor 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
LY6K	NM_001160354	lymphocyte antigen 6 complex, locus K	0	0	0	0	1	1	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
NEK2	NM_002497	NIMA (never in mitosis gene a)-related kinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
MX1	NM_001144925	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
GGT6	NM_001122890	gamma-glutamyltransferase 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
AGR3	NM_176813	anterior gradient homolog 3 (Xenopus laevis)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
AFF3	NM_001025108	AF4/FMR2 family, member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
XPNPEP2	NM_003399	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
TBC1D8	NM_001102426	TBC1 domain family, member 8 (with GRAM domain)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
DTX3	NM_178502	deltex homolog 3 (Drosophila)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
ZNF627	NM_145295	zinc finger protein 627	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
SPRYD4	NM_207344	SPRY domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
OR2H1	NM_030883	olfactory receptor, family 2, subfamily H, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
PLCH1	NM_001130960	phospholipase C, eta 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
ACPL2	NM_001037172	acid phosphatase-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
TNRC6B	NM_001024843	trinucleotide repeat containing 6B	1	0	1	0	1	0	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
GLO1	NM_006708	glyoxalase I	0	0	0	0	1	0	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
GJB2	NM_004004	gap junction protein, beta 2, 26kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR

ZNF143	NM_003442	zinc finger protein 143	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
PPM1D	NM_003620	protein phosphatase, Mg2+/Mn2+ dependent, 1D	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
PAXIP1	NM_007349	PAX interacting (with transcription-activation domain) protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
SERAC1	NM_032861	serine active site containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
FKTN	NM_001079802	fukutin	0	0	0	0	1	1	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
FHL3	NM_004468	four and a half LIM domains 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
C1orf201	NM_001199012	chromosome 1 open reading frame 201	0	0	0	0	1	1	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
YTHDF2	NM_001172828	YTH domain family, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
MEGF11	NM_032445	multiple EGF-like-domains 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
KIAA1644	NM_001099294	KIAA1644	1	1	0	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
EIF2AK1	NM_001134335	eukaryotic translation initiation factor 2-alpha kinase 1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
MGST2	NM_001204366	microsomal glutathione S-transferase 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
PTK2	NM_001199649	PTK2 protein tyrosine kinase 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
TSPAN2	NM_005725	tetraspanin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
MAB21L2	NM_006439	mab-21-like 2 (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
TAF7L	NM_001168474	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
FGFRL1	NM_001004356	fibroblast growth factor receptor-like 1	0	0	0	0	2	1	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
SPATA2	NM_001135773	spermatogenesis associated 2	0	0	0	0	2	0	2	0	hsa-miR-622	-0.18	N/A	Sites in UTR

ABL1	NM_005157	c-abl oncogene 1, non-receptor tyrosine kinase	0	0	0	0	2	1	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
CEACAM7	NM_006890	carcinoembryonic antigen-related cell adhesion molecule 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
SETX	NM_015046	senataxin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
GOLGA4	NM_001172713	golgin A4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
KIF5C	NM_004522	kinesin family member 5C	1	0	1	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
RCN1	NM_002901	reticulocalbin 1, EF-hand calcium binding domain	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
HAO2	NM_001005783	hydroxyacid oxidase 2 (long chain)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
CXorf36	NM_024689	chromosome X open reading frame 36	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
C15orf44	NM_001136043	chromosome 15 open reading frame 44	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
KCNA6	NM_002235	potassium voltage-gated channel, shaker-related subfamily, member 6	1	0	1	0	1	0	0	1	hsa-miR-622	-0.18	N/A	Sites in UTR
ATP2B1	NM_001001323	ATPase, Ca++ transporting, plasma membrane 1	1	1	0	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
TIMP2	NM_003255	TIMP metallopeptidase inhibitor 2	1	0	1	0	2	0	1	1	hsa-miR-622	-0.18	N/A	Sites in UTR
POP1	NM_001145860	processing of precursor 1, ribonuclease P/MRP subunit (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.18	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-622	-0.18	N/A	Sites in UTR
EXO1	NM_003686	exonuclease 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
PDSS1	NM_014317	prenyl (decaprenyl) diphosphate synthase, subunit 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
C20orf177	NM_001190826	chromosome 20 open reading frame 177	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR
VMP1	NM_030938	vacuole membrane protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.18	N/A	Sites in UTR

UBR7	NM_175748	ubiquitin protein ligase E3 component n-recognin 7 (putative)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.18	N/A	Sites in UTR
FCHSD2	NM_014824	FCH and double SH3 domains 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.18	N/A	Sites in UTR
ARPM1	NM_032487	actin related protein M1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
RAB1A	NM_004161	RAB1A, member RAS oncogene family	1	0	1	0	0	0	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PLCB1	NM_015192	phospholipase C, beta 1 (phosphoinositide-specific)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PTCHD2	NM_020780	patched domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PRKCQ	NM_001242413	protein kinase C, theta	0	0	0	0	2	0	0	2	hsa-miR-622	-0.17	N/A	Sites in UTR
MPPED2	NM_001145399	metallophosphoesterase domain containing 2	0	0	0	0	2	0	1	1	hsa-miR-622	-0.17	N/A	Sites in UTR
LOC100507203	NM_001195597	hypothetical LOC100507203	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
ZNF648	NM_001009992	zinc finger protein 648	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
GYPA	NM_002099	glycophorin A (MNS blood group)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SLC22A18	NM_002555	solute carrier family 22, member 18	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
GPR68	NM_001177676	G protein-coupled receptor 68	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
RASAL1	NM_001193520	RAS protein activator like 1 (GAP1 like)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
IGF2BP2	NM_001007225	insulin-like growth factor 2 mRNA binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
ANKFY1	NM_016376	ankyrin repeat and FYVE domain containing 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
CSGALNACT1	NM_001130518	chondroitin sulfate N-acetylgalactosaminyltransferase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
NCAM2	NM_004540	neural cell adhesion molecule 2	0	0	0	0	2	0	0	2	hsa-miR-622	-0.17	N/A	Sites in UTR

GPSM3	NM_022107	G-protein signaling modulator 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.17	N/A	Sites in UTR
FGF9	NM_002010	fibroblast growth factor 9 (glia-activating factor)	1	0	1	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
RAB15	NM_198686	RAB15, member RAS onocogene family	0	0	0	0	2	0	1	1	hsa-miR-622	-0.17	N/A	Sites in UTR
GPR64	NM_001079858	G protein-coupled receptor 64	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TRAF1	NM_001190945	TNF receptor-associated factor 1	0	0	0	0	4	1	1	2	hsa-miR-622	-0.17	N/A	Sites in UTR
IL1B	NM_000576	interleukin 1, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
STARD8	NM_001142503	StAR-related lipid transfer (START) domain containing 8	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SYT11	NM_152280	synaptotagmin XI	1	0	0	1	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
ACOX1	NM_001185039	acyl-CoA oxidase 1, palmitoyl	0	0	0	0	2	0	2	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PLEKHG4	NM_001129727	pleckstrin homology domain containing, family G (with RhoGef domain) member 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
HPS3	NM_032383	Hermansky-Pudlak syndrome 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
EPB41L4A	NM_022140	erythrocyte membrane protein band 4.1 like 4A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PNPLA3	NM_025225	patatin-like phospholipase domain containing 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TM4SF18	NM_001184723	transmembrane 4 L six family member 18	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
C2orf72	NM_001144994	chromosome 2 open reading frame 72	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
ABI2	NM_005759	abl-interactor 2	0	0	0	0	2	0	0	2	hsa-miR-622	-0.17	N/A	Sites in UTR
TOR1AIP2	NM_001199260	torsin A interacting protein 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
C9orf47	NM_001001938	chromosome 9 open reading frame 47	0	0	0	0	3	0	1	2	hsa-miR-622	-0.17	N/A	Sites in UTR

IGSF3	NM_001007237	immunoglobulin superfamily, member 3	0	0	0	0	3	0	3	0	hsa-miR-622	-0.17	N/A	Sites in UTR
GGT7	NM_178026	gamma-glutamyltransferase 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TLK2	NM_001112707	tousled-like kinase 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
HABP2	NM_001177660	hyaluronan binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
BUB3	NM_004725	budding uninhibited by benzimidazoles 3 homolog (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
FAIM3	NM_001142473	Fas apoptotic inhibitory molecule 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SLC23A2	NM_005116	solute carrier family 23 (nucleobase transporters), member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PSIP1	NM_001128217	PC4 and SFRS1 interacting protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TRAPPC3	NM_014408	trafficking protein particle complex 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
LGR4	NM_018490	leucine-rich repeat containing G protein-coupled receptor 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
RAB20	NM_017817	RAB20, member RAS oncogene family	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SPSB2	NM_001146316	splA/ryanodine receptor domain and SOCS box containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
C9orf100	NM_032818	chromosome 9 open reading frame 100	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
KLF14	NM_138693	Kruppel-like factor 14	1	0	1	0	0	0	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SH3PXD2B	NM_001017995	SH3 and PX domains 2B	0	0	0	0	2	0	2	0	hsa-miR-622	-0.17	N/A	Sites in UTR
FAM164A	NM_016010	family with sequence similarity 164, member A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TM6SF1	NM_001144903	transmembrane 6 superfamily member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SEPN1	NM_020451	selenoprotein N, 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR

PLEKHA3	NM_019091	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
SLFN11	NM_001104587	schlafen family member 11	0	0	0	0	2	0	2	0	hsa-miR-622	-0.17	N/A	Sites in UTR
C6	NM_000065	complement component 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
COL2A1	NM_001844	collagen, type II, alpha 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TRIM31	NM_007028	tripartite motif containing 31	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
ESRRB	NM_004452	estrogen-related receptor beta	0	0	0	0	2	0	1	1	hsa-miR-622	-0.17	N/A	Sites in UTR
SAMD8	NM_001174156	sterile alpha motif domain containing 8	0	0	0	0	4	1	1	2	hsa-miR-622	-0.17	N/A	Sites in UTR
HORMAD1	NM_001199829	HORMA domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
FKBP2	NM_001135208	FK506 binding protein 2, 13kDa	1	0	1	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
ICOS	NM_012092	inducible T-cell co-stimulator	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
MPEG1	NM_001039396	macrophage expressed 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
C12orf61	NM_175895	chromosome 12 open reading frame 61	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
ROD1	NM_001163788	ROD1 regulator of differentiation 1 (S. pombe)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.17	N/A	Sites in UTR
TMEM120B	NM_001080825	transmembrane protein 120B	0	0	0	0	2	0	2	0	hsa-miR-622	-0.17	N/A	Sites in UTR
GADD45B	NM_015675	growth arrest and DNA-damage-inducible, beta	0	0	0	0	3	0	1	2	hsa-miR-622	-0.17	N/A	Sites in UTR
VWDE	NM_001135924	von Willebrand factor D and EGF domains	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
ERBB3	NM_001982	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
PHF20L1	NM_016018	PHD finger protein 20-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR

HAUS3	NM_024511	HAUS augmin-like complex, subunit 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
CNOT7	NM_054026	CCR4-NOT transcription complex, subunit 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
TAF9B	NM_015975	TAF9B RNA polymerase II, TATA box binding protein (TBP)-associated factor, 31kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.17	N/A	Sites in UTR
MAPK9	NM_001135044	mitogen-activated protein kinase 9	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
INADL	NM_176877	InaD-like (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
TMCC3	NM_020698	transmembrane and coiled-coil domain family 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.17	N/A	Sites in UTR
FAM60A	NM_001135811	family with sequence similarity 60, member A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
HHIPL1	NM_001127258	HHIP-like 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.17	N/A	Sites in UTR
INO80D	NM_017759	INO80 complex subunit D	0	0	0	0	3	0	2	1	hsa-miR-622	-0.16	N/A	Sites in UTR
TMEM180	NM_024789	transmembrane protein 180	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
ALPL	NM_000478	alkaline phosphatase, liver/bone/kidney	1	0	1	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
PAX4	NM_006193	paired box 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
TBX19	NM_005149	T-box 19	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
MORC4	NM_001085354	MORC family CW-type zinc finger 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
GRASP	NM_181711	GRP1 (general receptor for phosphoinositides 1)-associated scaffold protein	1	0	1	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
ANKRD11	NM_013275	ankyrin repeat domain 11	0	0	0	0	2	0	2	0	hsa-miR-622	-0.16	N/A	Sites in UTR
TOR1B	NM_014506	torsin family 1, member B (torsin B)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
UBQLN1	NM_013438	ubiquilin 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR

RNF2	NM_007212	ring finger protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
SNRPB2	NM_003092	small nuclear ribonucleoprotein polypeptide B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
TEX10	NM_001161584	testis expressed 10	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
B3GALNT1	NM_001038628	beta-1,3-N-acetylgalactosaminyltransferase 1 (globoside blood group)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
FTSJ2	NM_013393	FtsJ homolog 2 (E. coli)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
CEACAM21	NM_001098506	carcinoembryonic antigen-related cell adhesion molecule 21	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
CRTC3	NM_001042574	CREB regulated transcription coactivator 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
TARBP2	NM_004178	TAR (HIV-1) RNA binding protein 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
KCTD3	NM_016121	potassium channel tetramerisation domain containing 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
MRPS14	NM_022100	mitochondrial ribosomal protein S14	0	0	0	0	2	0	0	2	hsa-miR-622	-0.16	N/A	Sites in UTR
GPR4	NM_005282	G protein-coupled receptor 4	0	0	0	0	2	0	1	1	hsa-miR-622	-0.16	N/A	Sites in UTR
FHDC1	NM_033393	FH2 domain containing 1	0	0	0	0	3	0	2	1	hsa-miR-622	-0.16	N/A	Sites in UTR
DAZL	NM_001190811	deleted in azoospermia-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
C11orf73	NM_016401	chromosome 11 open reading frame 73	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
CYB5RL	NM_001031672	cytochrome b5 reductase-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
EYA3	NM_001990	eyes absent homolog 3 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.16	N/A	Sites in UTR
FAM19A5	NM_001082967	family with sequence similarity 19 (chemokine (C-C motif)-like), member A5	1	0	1	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
PODXL	NM_001018111	podocalyxin-like	0	0	0	0	3	0	3	0	hsa-miR-622	-0.16	N/A	Sites in UTR

NF2	NM_000268	neurofibromin 2 (merlin)	0	0	0	0	4	0	3	1	hsa-miR-622	-0.16	N/A	Sites in UTR
SERBP1	NM_001018067	SERPINE1 mRNA binding protein 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
OR12D3	NM_030959	olfactory receptor, family 12, subfamily D, member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
PAGE5	NM_001013435	P antigen family, member 5 (prostate associated)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
BICD1	NM_001003398	bicaudal D homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
USP4	NM_003363	ubiquitin specific peptidase 4 (proto-oncogene)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
SHANK2	NM_012309	SH3 and multiple ankyrin repeat domains 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
PKN3	NM_013355	protein kinase N3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
IPO11	NM_001134779	importin 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
PLXDC1	NM_020405	plexin domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
HOXA1	NM_005522	homeobox A1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
CMAS	NM_018686	cytidine monophosphate N-acetylneuraminic acid synthetase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
MCEE	NM_032601	methylmalonyl CoA epimerase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
RASGRF2	NM_006909	Ras protein-specific guanine nucleotide-releasing factor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
CHST4	NM_001166395	carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
ODZ2	NM_001122679	odz, odd Oz/ten-m homolog 2 (Drosophila)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
KCTD2	NM_015353	potassium channel tetramerisation domain containing 2	0	0	0	0	2	1	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
ZIC1	NM_003412	Zic family member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR

C2orf43	NM_021925	chromosome 2 open reading frame 43	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
LRRC34	NM_001172780	leucine rich repeat containing 34	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
KIF24	NM_194313	kinesin family member 24	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
CTSC	NM_001114173	cathepsin C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
RGS7	NM_002924	regulator of G-protein signaling 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
NAT9	NM_015654	N-acetyltransferase 9 (GCN5-related, putative)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
ISOC2	NM_001136201	isochorismatase domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
PARD6G	NM_032510	par-6 partitioning defective 6 homolog gamma (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
RNGTT	NM_003800	RNA guanylyltransferase and 5'-phosphatase	0	0	0	0	2	0	0	2	hsa-miR-622	-0.16	N/A	Sites in UTR
SNRNP25	NM_024571	small nuclear ribonucleoprotein 25kDa (U11/U12)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.16	N/A	Sites in UTR
PAK6	NM_001128628	p21 protein (Cdc42/Rac)-activated kinase 6	0	0	0	0	2	0	2	0	hsa-miR-622	-0.16	N/A	Sites in UTR
SPOPL	NM_001001664	speckle-type POZ protein-like	1	0	0	1	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
SELP	NM_003005	selectin P (granule membrane protein 140kDa, antigen CD62)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
SPDYE3	NM_001004351	speedy homolog E3 (Xenopus laevis)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
RAB21	NM_014999	RAB21, member RAS oncogene family	0	0	0	0	1	0	0	1	hsa-miR-622	-0.16	N/A	Sites in UTR
AIM1	NM_001624	absent in melanoma 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
KITLG	NM_000899	KIT ligand	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
MNT	NM_020310	MAX binding protein	1	0	1	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR

BTBD7	NM_001002860	BTB (POZ) domain containing 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
KIAA1211	NM_020722	KIAA1211	1	0	1	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
GIGYF1	NM_022574	GRB10 interacting GYF protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
RBM17	NM_001145547	RNA binding motif protein 17	0	0	0	0	1	0	1	0	hsa-miR-622	-0.16	N/A	Sites in UTR
RASSF8	NM_001164746	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	0	0	0	0	2	0	1	1	hsa-miR-622	-0.16	N/A	Sites in UTR
FAM127A	NM_001078171	family with sequence similarity 127, member A	0	0	0	0	2	0	2	0	hsa-miR-622	-0.16	N/A	Sites in UTR
FBXW7	NM_001013415	F-box and WD repeat domain containing 7	1	1	0	0	0	0	0	0	hsa-miR-622	-0.16	N/A	Sites in UTR
MDM4	NM_001204171	Mdm4 p53 binding protein homolog (mouse)	0	0	0	0	3	0	0	3	hsa-miR-622	-0.15	N/A	Sites in UTR
ACOT8	NM_005469	acyl-CoA thioesterase 8	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ELAVL1	NM_001419	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 1 (Hu antigen R)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
PLXND1	NM_015103	plexin D1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
EMCN	NM_001159694	endomucin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
SCN9A	NM_002977	sodium channel, voltage-gated, type IX, alpha subunit	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
PRPF4B	NM_003913	PRP4 pre-mRNA processing factor 4 homolog B (yeast)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FLRT3	NM_013281	fibronectin leucine rich transmembrane protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
SNX14	NM_020468	sorting nexin 14	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
KIAA1524	NM_020890	KIAA1524	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
POTEC	NM_001137671	POTE ankyrin domain family, member C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR

FAM155A	NM_001080396	family with sequence similarity 155, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ME1	NM_002395	malic enzyme 1, NADP(+)-dependent, cytosolic	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
RBM7	NM_016090	RNA binding motif protein 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
ARL15	NM_019087	ADP-ribosylation factor-like 15	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
LRP2BP	NM_018409	LRP2 binding protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
SHANK3	NM_001080420	SH3 and multiple ankyrin repeat domains 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
RMI2	NM_152308	RMI2, RecQ mediated genome instability 2, homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
MAP3K12	NM_001193511	mitogen-activated protein kinase kinase kinase 12	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
DEFB132	NM_207469	defensin, beta 132	0	0	0	0	2	0	1	1	hsa-miR-622	-0.15	N/A	Sites in UTR
MOBKL3	NM_001100819	MOB1, Mps One Binder kinase activator-like 3 (yeast)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
HSPE1-MOBKL3	NM_001202485	HSPE1-MOBKL3 readthrough	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
GSTM3	NM_000849	glutathione S-transferase mu 3 (brain)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.15	N/A	Sites in UTR
SMARCA5	NM_003601	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	0	0	0	0	3	0	0	3	hsa-miR-622	-0.15	N/A	Sites in UTR
CALB1	NM_004929	calbindin 1, 28kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
NDUFB6	NM_001199987	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 6, 17kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
PF4V1	NM_002620	platelet factor 4 variant 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
TFPI2	NM_006528	tissue factor pathway inhibitor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
C17orf78	NM_173625	chromosome 17 open reading frame 78	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR

PTPRCAP	NM_005608	protein tyrosine phosphatase, receptor type, C-associated protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
MAP4K4	NM_001242559	mitogen-activated protein kinase kinase kinase kinase 4	1	0	1	0	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FXR2	NM_004860	fragile X mental retardation, autosomal homolog 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
SCAMP1	NM_004866	secretory carrier membrane protein 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
DZIP1	NM_014934	DAZ interacting protein 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.15	N/A	Sites in UTR
SETD7	NM_030648	SET domain containing (lysine methyltransferase) 7	1	0	0	1	3	0	0	3	hsa-miR-622	-0.15	N/A	Sites in UTR
PPP2CB	NM_001009552	protein phosphatase 2, catalytic subunit, beta isozyme	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
LRRC2	NM_024512	leucine rich repeat containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
TRIM45	NM_001145635	tripartite motif containing 45	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
KRT31	NM_002277	keratin 31	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
UNG	NM_003362	uracil-DNA glycosylase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CLDN6	NM_021195	claudin 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
METTL21B	NM_015433	methyltransferase like 21B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
VARS2	NM_001167733	valyl-tRNA synthetase 2, mitochondrial (putative)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
HDHD2	NM_032124	haloacid dehalogenase-like hydrolase domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CNDP2	NM_001168499	CNDP dipeptidase 2 (metallopeptidase M20 family)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.15	N/A	Sites in UTR
B4GALT5	NM_004776	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FAM22D	NM_001009610	family with sequence similarity 22, member D	0	0	0	0	3	0	2	1	hsa-miR-622	-0.15	N/A	Sites in UTR

CMKLR1	NM_001142343	chemokine-like receptor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
SCP2	NM_001007099	sterol carrier protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ZNF69	NM_021915	zinc finger protein 69	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
CSAD	NM_015989	cysteine sulfinic acid decarboxylase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ARHGAP20	NM_020809	Rho GTPase activating protein 20	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ACTR6	NM_022496	ARP6 actin-related protein 6 homolog (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
PAGE2	NM_207339	P antigen family, member 2 (prostate associated)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
PAGE2B	NM_001015038	P antigen family, member 2B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
MAOA	NM_000240	monoamine oxidase A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CMTM6	NM_017801	CKLF-like MARVEL transmembrane domain containing 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
SHC4	NM_203349	SHC (Src homology 2 domain containing) family, member 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
PLDN	NM_012388	pallidin homolog (mouse)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
PDGFB	NM_002608	platelet-derived growth factor beta polypeptide	1	0	1	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
PFKFB4	NM_004567	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	0	0	0	0	2	0	2	0	hsa-miR-622	-0.15	N/A	Sites in UTR
MLL	NM_001197104	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
PHOX2B	NM_003924	paired-like homeobox 2b	0	0	0	0	2	0	2	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FYCO1	NM_024513	FYVE and coiled-coil domain containing 1	0	0	0	0	3	0	0	3	hsa-miR-622	-0.15	N/A	Sites in UTR
TCF7L2	NM_001146274	transcription factor 7-like 2 (T-cell specific, HMG-box)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR

PCLO	NM_014510	piccolo (presynaptic cytomatrix protein)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
SH3GLB1	NM_001206651	SH3-domain GRB2-like endophilin B1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
IP6K1	NM_001006115	inositol hexakisphosphate kinase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
PCDH17	NM_001040429	protocadherin 17	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FAM164C	NM_001042430	family with sequence similarity 164, member C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
C8orf45	NM_173518	chromosome 8 open reading frame 45	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
NRIP3	NM_020645	nuclear receptor interacting protein 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
DLK2	NM_023932	delta-like 2 homolog (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
VSTM4	NM_001031746	V-set and transmembrane domain containing 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
MAPK14	NM_001315	mitogen-activated protein kinase 14	0	0	0	0	2	1	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CXCR4	NM_001008540	chemokine (C-X-C motif) receptor 4	1	0	0	1	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
DYNLL1	NM_001037494	dynein, light chain, LC8-type 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ZNF460	NM_006635	zinc finger protein 460	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
SLC25A33	NM_032315	solute carrier family 25, member 33	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
HDDC2	NM_016063	HD domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
NRN1	NM_016588	neuritin 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
TMEM132E	NM_207313	transmembrane protein 132E	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
ASB15	NM_080928	ankyrin repeat and SOCS box containing 15	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR

MALT1	NM_006785	mucosa associated lymphoid tissue lymphoma translocation gene 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
NTRK2	NM_001007097	neurotrophic tyrosine kinase, receptor, type 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
ZFAND5	NM_001102420	zinc finger, AN1-type domain 5	1	0	0	1	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CLDN14	NM_001146077	claudin 14	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
KIAA1324	NM_020775	KIAA1324	1	0	0	1	0	0	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
KLK7	NM_001207053	kallikrein-related peptidase 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
PTPN3	NM_001145368	protein tyrosine phosphatase, non-receptor type 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CCDC76	NM_019083	coiled-coil domain containing 76	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
LARP1B	NM_032239	La ribonucleoprotein domain family, member 1B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
MCOLN3	NM_018298	mucolipin 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
PDGFC	NM_016205	platelet derived growth factor C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
CAMKK1	NM_032294	calcium/calmodulin-dependent protein kinase kinase 1, alpha	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FAM75D4	NM_001145197	family with sequence similarity 75, member D4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
FAM75D3	NM_207416	family with sequence similarity 75, member D3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
RAP2B	NM_002886	RAP2B, member of RAS oncogene family	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
TGFB3	NM_003239	transforming growth factor, beta 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.15	N/A	Sites in UTR
FAM105B	NM_138348	family with sequence similarity 105, member B	1	0	1	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
GREB1	NM_014668	growth regulation by estrogen in breast cancer 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR

PTPMT1	NM_001143984	protein tyrosine phosphatase, mitochondrial 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.15	N/A	Sites in UTR
C11orf41	NM_012194	chromosome 11 open reading frame 41	1	0	1	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
ATP1A1	NM_000701	ATPase, Na+/K+ transporting, alpha 1 polypeptide	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
PSG7	NM_001206650	pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
DDX47	NM_016355	DEAD (Asp-Glu-Ala-Asp) box polypeptide 47	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
C11orf30	NM_020193	chromosome 11 open reading frame 30	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
KIAA1407	NM_020817	KIAA1407	0	0	0	0	1	0	0	1	hsa-miR-622	-0.15	N/A	Sites in UTR
HRAS	NM_001130442	v-Ha-ras Harvey rat sarcoma viral oncogene homolog	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
SNAP47	NM_053052	synaptosomal-associated protein, 47kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.15	N/A	Sites in UTR
BRP44	NM_001143674	brain protein 44	0	0	0	0	2	0	0	2	hsa-miR-622	-0.15	N/A	Sites in UTR
NUDCD3	NM_015332	NudC domain containing 3	0	0	0	0	2	0	2	0	hsa-miR-622	-0.15	N/A	Sites in UTR
OGN	NM_014057	osteoglycin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
THBS1	NM_003246	thrombospondin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF235	NM_004234	zinc finger protein 235	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
TNFSF15	NM_001204344	tumor necrosis factor (ligand) superfamily, member 15	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
IMPG2	NM_016247	interphotoreceptor matrix proteoglycan 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
METTL4	NM_022840	methyltransferase like 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
VPS37A	NM_001145152	vacuolar protein sorting 37 homolog A (S. cerevisiae)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR

TWF1	NM_001242397	twinfilin, actin-binding protein, homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
GLCE	NM_015554	glucuronic acid epimerase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
C1orf106	NM_001142569	chromosome 1 open reading frame 106	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
PRKG1	NM_001098512	protein kinase, cGMP-dependent, type I	0	0	0	0	2	0	0	2	hsa-miR-622	-0.14	N/A	Sites in UTR
C22orf43	NM_016449	chromosome 22 open reading frame 43	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
WDR11	NM_018117	WD repeat domain 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
C20orf72	NM_052865	chromosome 20 open reading frame 72	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF285	NM_152354	zinc finger protein 285	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
CBLL1	NM_024814	Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
FAM92B	NM_198491	family with sequence similarity 92, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
KCNE1	NM_000219	potassium voltage-gated channel, Isk-related family, member 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
DENND4A	NM_001144823	DENN/MADD domain containing 4A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF783	NM_001195220	zinc finger family member 783	0	0	0	0	3	0	3	0	hsa-miR-622	-0.14	N/A	Sites in UTR
PDE8B	NM_001029851	phosphodiesterase 8B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ENOPH1	NM_021204	enolase-phosphatase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
CAB39L	NM_001079670	calcium binding protein 39-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
MYOCD	NM_001146313	myocardin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
NPPA	NM_006172	natriuretic peptide A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR

NSUN2	NM_001193455	NOP2/Sun domain family, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
PGAP3	NM_033419	post-GPI attachment to proteins 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
GSK3B	NM_001146156	glycogen synthase kinase 3 beta	0	0	0	0	1	1	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ABCD2	NM_005164	ATP-binding cassette, sub-family D (ALD), member 2	0	0	0	0	2	0	0	2	hsa-miR-622	-0.14	N/A	Sites in UTR
SAMD12	NM_001101676	sterile alpha motif domain containing 12	1	0	1	0	2	1	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ALDH6A1	NM_005589	aldehyde dehydrogenase 6 family, member A1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
RELL1	NM_001085400	RELT-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
SLC29A3	NM_001174098	solute carrier family 29 (nucleoside transporters), member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
BCORL1	NM_021946	BCL6 corepressor-like 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
C5orf20	NM_130848	chromosome 5 open reading frame 20	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
SPPL3	NM_139015	signal peptide peptidase-like 3	1	0	1	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
MEGF8	NM_001410	multiple EGF-like-domains 8	0	0	0	0	2	1	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF445	NM_181489	zinc finger protein 445	0	0	0	0	2	0	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
PTGFRN	NM_020440	prostaglandin F2 receptor negative regulator	1	0	0	1	2	0	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
RNF8	NM_003958	ring finger protein 8	0	0	0	0	3	1	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
UBE3C	NM_014671	ubiquitin protein ligase E3C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
EID2	NM_153232	EP300 interacting inhibitor of differentiation 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
LCORL	NM_001166139	ligand dependent nuclear receptor corepressor-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR

HAS3	NM_001199280	hyaluronan synthase 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
PRKCA	NM_002737	protein kinase C, alpha	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
C16orf70	NM_025187	chromosome 16 open reading frame 70	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
RCOR1	NM_015156	REST corepressor 1	0	0	0	0	3	0	2	1	hsa-miR-622	-0.14	N/A	Sites in UTR
PAK3	NM_001128166	p21 protein (Cdc42/Rac)-activated kinase 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
SATB2	NM_001172509	SATB homeobox 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
NCKIPSD	NM_016453	NCK interacting protein with SH3 domain	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
KCTD4	NM_198404	potassium channel tetramerisation domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
CIITA	NM_000246	class II, major histocompatibility complex, transactivator	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
USP2	NM_004205	ubiquitin specific peptidase 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
GFOD1	NM_001242628	glucose-fructose oxidoreductase domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
KIF12	NM_138424	kinesin family member 12	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
FN1	NM_054034	fibronectin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
HELLS	NM_018063	helicase, lymphoid-specific	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
RPS26	NM_001029	ribosomal protein S26	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
PHLPP1	NM_194449	PH domain and leucine rich repeat protein phosphatase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF451	NM_001031623	zinc finger protein 451	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
TAB3	NM_152787	TGF-beta activated kinase 1/MAP3K7 binding protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR

ZNF568	NM_001204835	zinc finger protein 568	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ARTN	NM_001136215	artemin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ZMYND19	NM_138462	zinc finger, MYND-type containing 19	1	0	1	0	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
CNTD1	NM_173478	cyclin N-terminal domain containing 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ZFP42	NM_174900	zinc finger protein 42 homolog (mouse)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
YPEL1	NM_013313	yippee-like 1 (Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
MUC20	NM_001098516	mucin 20, cell surface associated	0	0	0	0	2	0	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ITGA2	NM_002203	integrin, alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor)	0	0	0	0	3	0	0	3	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF555	NM_001172775	zinc finger protein 555	0	0	0	0	3	0	2	1	hsa-miR-622	-0.14	N/A	Sites in UTR
DNA2	NM_001080449	DNA replication helicase 2 homolog (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
STMN1	NM_001145454	stathmin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
HCFC2	NM_013320	host cell factor C2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF454	NM_001178089	zinc finger protein 454	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
OAS2	NM_001032731	2'-5'-oligoadenylate synthetase 2, 69/71kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
TFAP2C	NM_003222	transcription factor AP-2 gamma (activating enhancer binding protein 2 gamma)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
LUZP1	NM_001142546	leucine zipper protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
SLC39A6	NM_012319	solute carrier family 39 (zinc transporter), member 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
NCCRP1	NM_001001414	non-specific cytotoxic cell receptor protein 1 homolog (zebrafish)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR

ELMO1	NM_001039459	engulfment and cell motility 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
DDX5	NM_004396	DEAD (Asp-Glu-Ala-Asp) box polypeptide 5	1	0	0	1	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
GTF2H3	NM_001516	general transcription factor IIH, polypeptide 3, 34kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
DNAJB1	NM_006145	DnaJ (Hsp40) homolog, subfamily B, member 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
GPR180	NM_180989	G protein-coupled receptor 180	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ABHD3	NM_138340	abhydrolase domain containing 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
PDXDC1	NM_015027	pyridoxal-dependent decarboxylase domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ANKRD12	NM_001083625	ankyrin repeat domain 12	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
REV1	NM_001037872	REV1 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
SAV1	NM_021818	salvador homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
FBRS	NM_001105079	fibrosin	1	0	1	0	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
KLHDC7B	NM_138433	kelch domain containing 7B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
BMP8A	NM_181809	bone morphogenetic protein 8a	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
TFEC	NM_001018058	transcription factor EC	0	0	0	0	2	0	0	2	hsa-miR-622	-0.14	N/A	Sites in UTR
AGFG1	NM_001135187	ArfGAP with FG repeats 1	1	0	1	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
KCTD5	NM_018992	potassium channel tetramerisation domain containing 5	0	0	0	0	2	1	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
SH3TC2	NM_024577	SH3 domain and tetratricopeptide repeats 2	0	0	0	0	4	0	2	2	hsa-miR-622	-0.14	N/A	Sites in UTR
RYR2	NM_001035	ryanodine receptor 2 (cardiac)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR

KALRN	NM_001024660	kalirin, RhoGEF kinase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
EAF2	NM_018456	ELL associated factor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ZNF574	NM_022752	zinc finger protein 574	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
TRMT2B	NM_001167970	TRM2 tRNA methyltransferase 2 homolog B (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
TSHZ2	NM_001193421	teashirt zinc finger homeobox 2	1	0	0	1	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
EML5	NM_183387	echinoderm microtubule associated protein like 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
MEFV	NM_000243	Mediterranean fever	1	0	1	0	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ATP8A2	NM_016529	ATPase, aminophospholipid transporter, class I, type 8A, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
SRGAP1	NM_020762	SLIT-ROBO Rho GTPase activating protein 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
LRRC8C	NM_032270	leucine rich repeat containing 8 family, member C	0	0	0	0	2	0	1	1	hsa-miR-622	-0.14	N/A	Sites in UTR
PLCXD3	NM_001005473	phosphatidylinositol-specific phospholipase C, X domain containing 3	0	0	0	0	3	0	1	2	hsa-miR-622	-0.14	N/A	Sites in UTR
CHIT1	NM_003465	chitinase 1 (chitotriosidase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
DAZ1	NM_004081	deleted in azoospermia 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
LMX1A	NM_001174069	LIM homeobox transcription factor 1, alpha	1	0	0	1	0	0	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
MSRB2	NM_012228	methionine sulfoxide reductase B2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
C10orf118	NM_018017	chromosome 10 open reading frame 118	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
DAZ3	NM_020364	deleted in azoospermia 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
DAZ2	NM_001005785	deleted in azoospermia 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR

DAZ4	NM_001005375	deleted in azoospermia 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
WWC2	NM_024949	WW and C2 domain containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
AMAC1L2	NM_054028	acyl-malonyl condensing enzyme 1-like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
ADAT2	NM_182503	adenosine deaminase, tRNA-specific 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
C8orf84	NM_153225	chromosome 8 open reading frame 84	0	0	0	0	1	0	0	1	hsa-miR-622	-0.14	N/A	Sites in UTR
SRP19	NM_001204199	signal recognition particle 19kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
TRIB1	NM_025195	tribbles homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
ARIH2	NM_006321	ariadne homolog 2 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
RPH3A	NM_001143854	rabphilin 3A homolog (mouse)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
SPIRE2	NM_032451	spire homolog 2 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
AADACL3	NM_001103169	arylacetamide deacetylase-like 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.14	N/A	Sites in UTR
LRP11	NM_032832	low density lipoprotein receptor-related protein 11	0	0	0	0	2	0	0	2	hsa-miR-622	-0.14	N/A	Sites in UTR
MMAB	NM_052845	methylmalonic aciduria (cobalamin deficiency) cblB type	0	0	0	0	1	1	0	0	hsa-miR-622	-0.14	N/A	Sites in UTR
TBX15	NM_152380	T-box 15	0	0	0	0	2	0	0	2	hsa-miR-622	-0.13	N/A	Sites in UTR
BNIP2	NM_004330	BCL2/adenovirus E1B 19kDa interacting protein 2	1	0	0	1	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
NR2F6	NM_005234	nuclear receptor subfamily 2, group F, member 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
RARRES1	NM_002888	retinoic acid receptor responder (tazarotene induced) 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF165	NM_003447	zinc finger protein 165	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR

ZNF766	NM_001010851	zinc finger protein 766	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
IDH3B	NM_006899	isocitrate dehydrogenase 3 (NAD+) beta	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
MET	NM_000245	met proto-oncogene (hepatocyte growth factor receptor)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
NUPL1	NM_001008564	nucleoporin like 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.13	N/A	Sites in UTR
FAM108B1	NM_001025780	family with sequence similarity 108, member B1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
C6orf225	NM_001033564	chromosome 6 open reading frame 225	0	0	0	0	2	0	0	2	hsa-miR-622	-0.13	N/A	Sites in UTR
SPARC	NM_003118	secreted protein, acidic, cysteine-rich (osteonectin)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF714	NM_182515	zinc finger protein 714	0	0	0	0	2	0	1	1	hsa-miR-622	-0.13	N/A	Sites in UTR
C6orf168	NM_032511	chromosome 6 open reading frame 168	0	0	0	0	3	0	2	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ADORA3	NM_001081976	adenosine A3 receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
EED	NM_152991	embryonic ectoderm development	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
POT1	NM_001042594	protection of telomeres 1 homolog (S. pombe)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
CLDN22	NM_001111319	claudin 22	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
PRTFDC1	NM_020200	phosphoribosyl transferase domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
METTL14	NM_020961	methyltransferase like 14	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
FAM58A	NM_001130997	family with sequence similarity 58, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
MAP3K14	NM_003954	mitogen-activated protein kinase kinase kinase 14	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
CECR1	NM_017424	cat eye syndrome chromosome region, candidate 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR

SLITRK1	NM_052910	SLIT and NTRK-like family, member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
FAM174B	NM_207446	family with sequence similarity 174, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
VOPP1	NM_030796	vesicular, overexpressed in cancer, prosurvival protein 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.13	N/A	Sites in UTR
PRRC1	NM_130809	proline-rich coiled-coil 1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
PPM1H	NM_020700	protein phosphatase, Mg2+/Mn2+ dependent, 1H	0	0	0	0	1	1	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
CELF2	NM_001025076	CUGBP, Elav-like family member 2	1	0	0	1	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ZFYVE26	NM_015346	zinc finger, FYVE domain containing 26	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ZCCHC4	NM_024936	zinc finger, CCHC domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF581	NM_016535	zinc finger protein 581	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
FAM171B	NM_177454	family with sequence similarity 171, member B	1	0	0	1	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
CD68	NM_001040059	CD68 molecule	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
SOX11	NM_003108	SRY (sex determining region Y)-box 11	1	0	1	0	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
IQSEC1	NM_001134382	IQ motif and Sec7 domain 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
MYC	NM_002467	v-myc myelocytomatosis viral oncogene homolog (avian)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
SLC25A27	NM_004277	solute carrier family 25, member 27	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
TMEM87B	NM_032824	transmembrane protein 87B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
GDNF	NM_000514	glial cell derived neurotrophic factor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
GTF2E1	NM_005513	general transcription factor IIE, polypeptide 1, alpha 56kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR

RAB23	NM_016277	RAB23, member RAS oncogene family	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF548	NM_001172773	zinc finger protein 548	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
STIM1	NM_003156	stromal interaction molecule 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.13	N/A	Sites in UTR
PBX1	NM_001204961	pre-B-cell leukemia homeobox 1	1	0	1	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ENAH	NM_001008493	enabled homolog (Drosophila)	0	0	0	0	3	0	1	2	hsa-miR-622	-0.13	N/A	Sites in UTR
AQP4	NM_001650	aquaporin 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
PTPRG	NM_002841	protein tyrosine phosphatase, receptor type, G	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
RARRES3	NM_004585	retinoic acid receptor responder (tazarotene induced) 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
GJA5	NM_005266	gap junction protein, alpha 5, 40kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ISL2	NM_145805	ISL LIM homeobox 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
MICALCL	NM_032867	MICAL C-terminal like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ORMDL3	NM_139280	ORM1-like 3 (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF280B	NM_080764	zinc finger protein 280B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
NPLOC4	NM_017921	nuclear protein localization 4 homolog (S. cerevisiae)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.13	N/A	Sites in UTR
GRIA1	NM_000827	glutamate receptor, ionotropic, AMPA 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ELOVL4	NM_022726	ELOVL fatty acid elongase 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF238	NM_006352	zinc finger protein 238	1	0	0	1	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ZNF750	NM_024702	zinc finger protein 750	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR

RWDD4	NM_152682	RWD domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
KRT85	NM_002283	keratin 85	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
SIT1	NM_014450	signaling threshold regulating transmembrane adaptor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ECHDC2	NM_001198961	enoyl CoA hydratase domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
CHD7	NM_017780	chromodomain helicase DNA binding protein 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
CCDC130	NM_030818	coiled-coil domain containing 130	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
TMEM64	NM_001008495	transmembrane protein 64	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
PTPRD	NM_001040712	protein tyrosine phosphatase, receptor type, D	1	0	0	1	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
KMO	NM_003679	kynurenine 3-monooxygenase (kynurenine 3-hydroxylase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
PIWIL2	NM_001135721	piwi-like 2 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
SLAMF8	NM_020125	SLAM family member 8	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
C9orf128	NM_001012446	chromosome 9 open reading frame 128	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
KIAA0754	NM_015038	KIAA0754	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
6-Sep	NM_015129	septin 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
IFRD1	NM_001007245	interferon-related developmental regulator 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
ABHD12	NM_001042472	abhydrolase domain containing 12	1	0	0	1	0	0	0	0	hsa-miR-622	-0.13	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-622	-0.13	N/A	Sites in UTR
RASGEF1B	NM_152545	RasGEF domain family, member 1B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR

RNF145	NM_001199380	ring finger protein 145	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
LUZP2	NM_001009909	leucine zipper protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
C2orf74	NM_001143959	chromosome 2 open reading frame 74	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
BET1	NM_005868	blocked early in transport 1 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
PNPO	NM_018129	pyridoxamine 5'-phosphate oxidase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
SLC26A11	NM_001166347	solute carrier family 26, member 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
PTK6	NM_005975	PTK6 protein tyrosine kinase 6	0	0	0	0	2	0	1	1	hsa-miR-622	-0.13	N/A	Sites in UTR
COL4A4	NM_000092	collagen, type IV, alpha 4	0	0	0	0	2	0	2	0	hsa-miR-622	-0.13	N/A	Sites in UTR
YEATS2	NM_018023	YEATS domain containing 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
TRAF3	NM_001199427	TNF receptor-associated factor 3	2	0	1	1	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ALDH1L2	NM_001034173	aldehyde dehydrogenase 1 family, member L2	0	0	0	0	2	0	0	2	hsa-miR-622	-0.13	N/A	Sites in UTR
PHF15	NM_015288	PHD finger protein 15	0	0	0	0	2	0	1	1	hsa-miR-622	-0.13	N/A	Sites in UTR
GEMIN8	NM_001042479	gem (nuclear organelle) associated protein 8	0	0	0	0	2	0	1	1	hsa-miR-622	-0.13	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	0	hsa-miR-622	-0.13	N/A	Sites in UTR
CEBPD	NM_005195	CCAAT/enhancer binding protein (C/EBP), delta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
FZD3	NM_017412	frizzled family receptor 3	1	0	0	1	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
NNT	NM_012343	nicotinamide nucleotide transhydrogenase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
C17orf80	NM_001100621	chromosome 17 open reading frame 80	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR

ARRDC4	NM_183376	arrestin domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.13	N/A	Sites in UTR
LRRC32	NM_001128922	leucine rich repeat containing 32	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
PCSK6	NM_002570	proprotein convertase subtilisin/kexin type 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
PCM1	NM_006197	pericentriolar material 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.13	N/A	Sites in UTR
MDC1	NM_014641	mediator of DNA-damage checkpoint 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
INMT	NM_001199219	indolethylamine N-methyltransferase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
NCEH1	NM_001146276	neutral cholesterol ester hydrolase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
SEC16B	NM_033127	SEC16 homolog B (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.13	N/A	Sites in UTR
ADAMTS5	NM_007038	ADAM metallopeptidase with thrombospondin type 1 motif, 5	0	0	0	0	2	0	0	2	hsa-miR-622	-0.13	N/A	Sites in UTR
ADM	NM_001124	adrenomedullin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC6A2	NM_001172504	solute carrier family 6 (neurotransmitter transporter, noradrenalin), member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
FCF1	NM_015962	FCF1 small subunit (SSU) processome component homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ADPGK	NM_031284	ADP-dependent glucokinase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
GYPE	NM_198682	glycophorin E (MNS blood group)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
DNALI1	NM_003462	dynein, axonemal, light intermediate chain 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
SP140	NM_001005176	SP140 nuclear body protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C11orf49	NM_001003676	chromosome 11 open reading frame 49	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
FOXK2	NM_004514	forkhead box K2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR

GIMAP6	NM_024711	GTPase, IMAP family member 6	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
BMP3	NM_001201	bone morphogenetic protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CYR61	NM_001554	cysteine-rich, angiogenic inducer, 61	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
NTNG1	NM_001113226	netrin G1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ZC3HAV1	NM_020119	zinc finger CCCH-type, antiviral 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CNGA2	NM_005140	cyclic nucleotide gated channel alpha 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PPIP5K1	NM_001130858	diphosphoinositol pentakisphosphate kinase 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
GLIPR1	NM_006851	GLI pathogenesis-related 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PELI3	NM_001098510	pellino homolog 3 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
CCPG1	NM_004748	cell cycle progression 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
RCAN2	NM_005822	regulator of calcineurin 2	0	0	0	0	2	0	0	2	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC35F1	NM_001029858	solute carrier family 35, member F1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
KPNA1	NM_002264	karyopherin alpha 1 (importin alpha 5)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SIM1	NM_005068	single-minded homolog 1 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ZNF638	NM_001014972	zinc finger protein 638	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
C3orf38	NM_173824	chromosome 3 open reading frame 38	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ATP9B	NM_198531	ATPase, class II, type 9B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
KRTAP5-5	NM_001001480	keratin associated protein 5-5	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR

CDK14	NM_012395	cyclin-dependent kinase 14	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
TK2	NM_001172643	thymidine kinase 2, mitochondrial	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
VCL	NM_003373	vinculin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
TNFRSF10B	NM_003842	tumor necrosis factor receptor superfamily, member 10b	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
SUPT7L	NM_014860	suppressor of Ty 7 (S. cerevisiae)-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PITPNM2	NM_020845	phosphatidylinositol transfer protein, membrane-associated 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
GRID2IP	NM_001145118	glutamate receptor, ionotropic, delta 2 (Grid2) interacting protein	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C5orf63	NM_001164479	chromosome 5 open reading frame 63	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
EIF2S3	NM_001415	eukaryotic translation initiation factor 2, subunit 3 gamma, 52kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
GNS	NM_002076	glucosamine (N-acetyl)-6-sulfatase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
NCK1	NM_001190796	NCK adaptor protein 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
ZNF37A	NM_001007094	zinc finger protein 37A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CILP	NM_003613	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
MAP7D1	NM_018067	MAP7 domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
HACE1	NM_020771	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC15A4	NM_145648	solute carrier family 15, member 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
KCNK2	NM_001017424	potassium channel, subfamily K, member 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
ANGPTL2	NM_012098	angiopoietin-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR

SMUG1	NM_014311	single-strand-selective monofunctional uracil-DNA glycosylase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PARS2	NM_152268	prolyl-tRNA synthetase 2, mitochondrial (putative)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
ZFAND3	NM_021943	zinc finger, AN1-type domain 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
FAM160B2	NM_022749	family with sequence similarity 160, member B2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
DOK3	NM_001144875	docking protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PDIA3	NM_005313	protein disulfide isomerase family A, member 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.12	N/A	Sites in UTR
SSH1	NM_018984	slingshot homolog 1 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CEACAM5	NM_004363	carcinoembryonic antigen-related cell adhesion molecule 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CHRNA5	NM_000745	cholinergic receptor, nicotinic, alpha 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
RTN1	NM_021136	reticulon 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SDHD	NM_003002	succinate dehydrogenase complex, subunit D, integral membrane protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
UBP1	NM_001128160	upstream binding protein 1 (LBP-1a)	1	0	0	1	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
MAPRE1	NM_012325	microtubule-associated protein, RP/EB family, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
MUC13	NM_033049	mucin 13, cell surface associated	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
IL31RA	NM_001242637	interleukin 31 receptor A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CRKL	NM_005207	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
GPR17	NM_001161415	G protein-coupled receptor 17	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
WNT9B	NM_003396	wingless-type MMTV integration site family, member 9B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR

OBSL1	NM_001173408	obscurin-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
UBAP2	NM_018449	ubiquitin associated protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PDZD4	NM_032512	PDZ domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
LINGO1	NM_032808	leucine rich repeat and Ig domain containing 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C15orf55	NM_175741	chromosome 15 open reading frame 55	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
AGMO	NM_001004320	alkylglycerol monooxygenase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC7A11	NM_014331	solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	0	0	0	0	2	0	0	2	hsa-miR-622	-0.12	N/A	Sites in UTR
GPR85	NM_001146265	G protein-coupled receptor 85	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ST14	NM_021978	suppression of tumorigenicity 14 (colon carcinoma)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
TNFSF9	NM_003811	tumor necrosis factor (ligand) superfamily, member 9	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
CDKL2	NM_003948	cyclin-dependent kinase-like 2 (CDC2-related kinase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
NUDT3	NM_006703	nudix (nucleoside diphosphate linked moiety X)-type motif 3	1	0	0	1	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
HSD17B12	NM_016142	hydroxysteroid (17-beta) dehydrogenase 12	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
C4orf41	NM_021942	chromosome 4 open reading frame 41	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
GRIP2	NM_001080423	glutamate receptor interacting protein 2	1	0	0	1	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
RPS10-NUDT3	NM_001202470	RPS10-NUDT3 readthrough	1	0	0	1	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
BCR	NM_004327	breakpoint cluster region	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
AUTS2	NM_001127231	autism susceptibility candidate 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR

KRT76	NM_015848	keratin 76	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
SYK	NM_001135052	spleen tyrosine kinase	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
S100PBP	NM_022753	S100P binding protein	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ZNF696	NM_030895	zinc finger protein 696	0	0	0	0	2	0	1	1	hsa-miR-622	-0.12	N/A	Sites in UTR
C1orf88	NM_181643	chromosome 1 open reading frame 88	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PLA2G5	NM_000929	phospholipase A2, group V	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC25A16	NM_152707	solute carrier family 25 (mitochondrial carrier; Graves disease autoantigen), member 16	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
FOSL1	NM_005438	FOS-like antigen 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ARPP19	NM_006628	cAMP-regulated phosphoprotein, 19kDa	1	0	0	1	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
MEAF6	NM_022756	MYST/Esa1-associated factor 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
AHSA2	NM_152392	AHA1, activator of heat shock 90kDa protein ATPase homolog 2 (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
C10orf71	NM_001135196	chromosome 10 open reading frame 71	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
KRT74	NM_175053	keratin 74	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
TMEM215	NM_212558	transmembrane protein 215	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
USH1G	NM_173477	Usher syndrome 1G (autosomal recessive)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C18orf1	NM_001003674	chromosome 18 open reading frame 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
NRP2	NM_201264	neuropilin 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ILVBL	NM_006844	ilvB (bacterial acetolactate synthase)-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR

LTN1	NM_015565	listerin E3 ubiquitin protein ligase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
KIAA1797	NM_017794	KIAA1797	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
HEMGN	NM_018437	hemogen	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
AMAC1	NM_152462	acyl-malonyl condensing enzyme 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
COMT	NM_000754	catechol-O-methyltransferase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
CYP4A11	NM_000778	cytochrome P450, family 4, subfamily A, polypeptide 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C9orf7	NM_001135775	chromosome 9 open reading frame 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
BVES	NM_001199563	blood vessel epicardial substance	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
KLHL3	NM_017415	kelch-like 3 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C16orf5	NM_001199054	chromosome 16 open reading frame 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C10orf67	NM_153714	chromosome 10 open reading frame 67	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
CISD3	NM_001136498	CDGSH iron sulfur domain 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
FNBP1	NM_015033	formin binding protein 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.12	N/A	Sites in UTR
FNDC3A	NM_001079673	fibronectin type III domain containing 3A	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PRKD3	NM_005813	protein kinase D3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
TSSK1B	NM_032028	testis-specific serine kinase 1B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
MEIS1	NM_002398	Meis homeobox 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
TAF4	NM_003185	TAF4 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 135kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR

CEP68	NM_015147	centrosomal protein 68kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
MTHFD1L	NM_001242767	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SUV39H2	NM_001193424	suppressor of variegation 3-9 homolog 2 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
FAM198A	NM_001129908	family with sequence similarity 198, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
HLA-DPB1	NM_002121	major histocompatibility complex, class II, DP beta 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
XK	NM_021083	X-linked Kx blood group (McLeod syndrome)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
NRXN2	NM_015080	neurexin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
ATP6V0A2	NM_012463	ATPase, H+ transporting, lysosomal V0 subunit a2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
MPHOSPH8	NM_017520	M-phase phosphoprotein 8	1	0	1	0	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
SPINLW1	NM_020398	serine peptidase inhibitor-like, with Kunitz and WAP domains 1 (eppin)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
BRIP1	NM_032043	BRCA1 interacting protein C-terminal helicase 1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
DDO	NM_003649	D-aspartate oxidase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
KIAA1147	NM_001080392	KIAA1147	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
C10orf58	NM_032333	chromosome 10 open reading frame 58	1	0	0	1	0	0	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
DPY19L4	NM_181787	dpy-19-like 4 (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
PTTG1IP	NM_004339	pituitary tumor-transforming 1 interacting protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
PRIM2	NM_000947	primase, DNA, polypeptide 2 (58kDa)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
AKAP8	NM_005858	A kinase (PRKA) anchor protein 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR

GCN1L1	NM_006836	GCN1 general control of amino-acid synthesis 1-like 1 (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
ZMYND8	NM_012408	zinc finger, MYND-type containing 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
RHCG	NM_016321	Rh family, C glycoprotein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
KTI12	NM_138417	KTI12 homolog, chromatin associated (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
LHFPL2	NM_005779	lipoma HMGIC fusion partner-like 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
SESN2	NM_031459	sestrin 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.12	N/A	Sites in UTR
MACC1	NM_182762	metastasis associated in colon cancer 1	0	0	0	0	4	0	3	1	hsa-miR-622	-0.12	N/A	Sites in UTR
MAP3K4	NM_005922	mitogen-activated protein kinase kinase kinase 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC20A1	NM_005415	solute carrier family 20 (phosphate transporter), member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
AKAP12	NM_005100	A kinase (PRKA) anchor protein 12	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
YAF2	NM_001190977	YY1 associated factor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ARL2BP	NM_012106	ADP-ribosylation factor-like 2 binding protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
DAK	NM_015533	dihydroxyacetone kinase 2 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
SLC2A8	NM_014580	solute carrier family 2 (facilitated glucose transporter), member 8	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
ENOSF1	NM_001126123	enolase superfamily member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
RFTN2	NM_144629	raftlin family member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
AMAC1L3	NM_001102614	acyl-malonyl condensing enzyme 1-like 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.12	N/A	Sites in UTR
POP4	NM_006627	processing of precursor 4, ribonuclease P/MRP subunit (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR

CDR2L	NM_014603	cerebellar degeneration-related protein 2-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
CHST15	NM_015892	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
RUFY2	NM_001042417	RUN and FYVE domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
NCKAP5L	NM_001037806	NCK-associated protein 5-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
C9orf116	NM_001048265	chromosome 9 open reading frame 116	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
FAM127C	NM_001078173	family with sequence similarity 127, member C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.12	N/A	Sites in UTR
ERBB4	NM_001042599	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
FLNB	NM_001164317	filamin B, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
PPM1G	NM_177983	protein phosphatase, Mg2+/Mn2+ dependent, 1G	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
UCP3	NM_022803	uncoupling protein 3 (mitochondrial, proton carrier)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
VLDLR	NM_001018056	very low density lipoprotein receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
GEMIN5	NM_015465	gem (nuclear organelle) associated protein 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
DHRS7B	NM_015510	dehydrogenase/reductase (SDR family) member 7B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
DISC1	NM_001012957	disrupted in schizophrenia 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
LGSN	NM_001143940	lengsin, lens protein with glutamine synthetase domain	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
VPS33A	NM_022916	vacuolar protein sorting 33 homolog A (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
TXNRD3	NM_001173513	thioredoxin reductase 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
VGLL2	NM_153453	vestigial like 2 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR

SLCO4C1	NM_180991	solute carrier organic anion transporter family, member 4C1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SLC29A1	NM_001078174	solute carrier family 29 (nucleoside transporters), member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
MLF2	NM_005439	myeloid leukemia factor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
IL20RA	NM_014432	interleukin 20 receptor, alpha	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
TULP4	NM_001007466	tubby like protein 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
RPRD1B	NM_021215	regulation of nuclear pre-mRNA domain containing 1B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ERC1	NM_178039	ELKS/RAB6-interacting/CAST family member 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.11	N/A	Sites in UTR
PNMAL2	NM_020709	PNMA-like 2	0	0	0	0	2	0	2	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CHRM5	NM_012125	cholinergic receptor, muscarinic 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
PTPRO	NM_002848	protein tyrosine phosphatase, receptor type, O	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
BEST1	NM_004183	bestrophin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
GDA	NM_001242505	guanine deaminase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SPCS2	NM_014752	signal peptidase complex subunit 2 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
DSE	NM_001080976	dermatan sulfate epimerase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ZCCHC8	NM_017612	zinc finger, CCHC domain containing 8	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
B3GALTL	NM_194318	beta 1,3-galactosyltransferase-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
WDR16	NM_001080556	WD repeat domain 16	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SPTBN2	NM_006946	spectrin, beta, non-erythrocytic 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR

TRAF7	NM_032271	TNF receptor-associated factor 7	1	0	1	0	0	0	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
MORN4	NM_001098831	MORN repeat containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CHMP4B	NM_176812	chromatin modifying protein 4B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
C17orf102	NM_207454	chromosome 17 open reading frame 102	0	0	0	0	2	0	1	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SIDT2	NM_001040455	SID1 transmembrane family, member 2	1	1	0	0	0	0	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
PPP1R3A	NM_002711	protein phosphatase 1, regulatory (inhibitor) subunit 3A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ABCA8	NM_007168	ATP-binding cassette, sub-family A (ABC1), member 8	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
YAP1	NM_001130145	Yes-associated protein 1	0	0	0	0	2	1	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
MLLT11	NM_006818	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ABI3BP	NM_015429	ABI family, member 3 (NESH) binding protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
TMEM203	NM_053045	transmembrane protein 203	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ARL6IP6	NM_152522	ADP-ribosylation-like factor 6 interacting protein 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
TMEM192	NM_001100389	transmembrane protein 192	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ALDH1A3	NM_000693	aldehyde dehydrogenase 1 family, member A3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
PDGFA	NM_002607	platelet-derived growth factor alpha polypeptide	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
KLF7	NM_003709	Kruppel-like factor 7 (ubiquitous)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
NR2E3	NM_016346	nuclear receptor subfamily 2, group E, member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ZNF507	NM_001136156	zinc finger protein 507	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR

C1orf43	NM_001098616	chromosome 1 open reading frame 43	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
LRRC1	NM_018214	leucine rich repeat containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CWF19L2	NM_152434	CWF19-like 2, cell cycle control (S. pombe)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
FAM190A	NM_207491	family with sequence similarity 190, member A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
DUXA	NM_001012729	double homeobox A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
SEMA6A	NM_020796	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A	0	0	0	0	2	0	1	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ZBTB44	NM_014155	zinc finger and BTB domain containing 44	0	0	0	0	2	1	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
B7H6	NM_001202439	B7 homolog 6	0	0	0	0	4	0	4	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ISLR	NM_005545	immunoglobulin superfamily containing leucine-rich repeat	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SNX24	NM_014035	sorting nexin 24	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
PILRA	NM_013439	paired immunoglobin-like type 2 receptor alpha	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
NKRF	NM_001173487	NFKB repressing factor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
DACH2	NM_001139514	dachshund homolog 2 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
TMEM41B	NM_015012	transmembrane protein 41B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
EIF5A	NM_001143760	eukaryotic translation initiation factor 5A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
GJC2	NM_020435	gap junction protein, gamma 2, 47kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
FAM19A3	NM_001004440	family with sequence similarity 19 (chemokine (C-C motif)-like), member A3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
TIMP3	NM_000362	TIMP metallopeptidase inhibitor 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.11	N/A	Sites in UTR

ZNF19	NM_006961	zinc finger protein 19	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
TSC22D1	NM_006022	TSC22 domain family, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
GDF11	NM_005811	growth differentiation factor 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
C1orf109	NM_017850	chromosome 1 open reading frame 109	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
RNF150	NM_020724	ring finger protein 150	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
CXCL16	NM_001100812	chemokine (C-X-C motif) ligand 16	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ACTR5	NM_024855	ARP5 actin-related protein 5 homolog (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
C9orf123	NM_033428	chromosome 9 open reading frame 123	1	0	0	1	0	0	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
GORAB	NM_152281	golgin, RAB6-interacting	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
LRRC42	NM_052940	leucine rich repeat containing 42	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
BCL2L15	NM_001010922	BCL2-like 15	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
RIOK3	NM_003831	RIO kinase 3 (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ABCF2	NM_007189	ATP-binding cassette, sub-family F (GCN20), member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
MPZL2	NM_005797	myelin protein zero-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
LARS2	NM_015340	leucyl-tRNA synthetase 2, mitochondrial	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ZDHHC8	NM_001185024	zinc finger, DHHC-type containing 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CCDC88A	NM_001135597	coiled-coil domain containing 88A	1	0	1	0	0	0	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
TIFA	NM_052864	TRAF-interacting protein with forkhead-associated domain	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR

SLC36A2	NM_181776	solute carrier family 36 (proton/amino acid symporter), member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
RGSL1	NM_001137669	regulator of G-protein signaling like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CASP10	NM_001206524	caspase 10, apoptosis-related cysteine peptidase	0	0	0	0	2	0	2	0	hsa-miR-622	-0.11	N/A	Sites in UTR
SLC7A14	NM_020949	solute carrier family 7 (orphan transporter), member 14	0	0	0	0	2	0	1	1	hsa-miR-622	-0.11	N/A	Sites in UTR
GTF2H1	NM_001142307	general transcription factor IIH, polypeptide 1, 62kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
RGS2	NM_002923	regulator of G-protein signaling 2, 24kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
STAG1	NM_005862	stromal antigen 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
DOCK11	NM_144658	dedicator of cytokinesis 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
CHUK	NM_001278	conserved helix-loop-helix ubiquitous kinase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
EFNB1	NM_004429	ephrin-B1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
MAT1A	NM_000429	methionine adenosyltransferase I, alpha	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ZDHHC22	NM_174976	zinc finger, DHHC-type containing 22	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ALG1L2	NM_001136152	asparagine-linked glycosylation 1-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
C22orf46	NM_001142964	chromosome 22 open reading frame 46	0	0	0	0	2	0	2	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ATP6V0A1	NM_001130020	ATPase, H+ transporting, lysosomal V0 subunit a1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
PDK4	NM_002612	pyruvate dehydrogenase kinase, isozyme 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
CEP170	NM_001042404	centrosomal protein 170kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
UBA6	NM_018227	ubiquitin-like modifier activating enzyme 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR

SPAG17	NM_206996	sperm associated antigen 17	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
FAM26E	NM_153711	family with sequence similarity 26, member E	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ZNF491	NM_152356	zinc finger protein 491	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ZNF827	NM_178835	zinc finger protein 827	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CCDC85C	NM_001144995	coiled-coil domain containing 85C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
VAMP4	NM_001185127	vesicle-associated membrane protein 4	0	0	0	0	2	2	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
CHD1	NM_001270	chromodomain helicase DNA binding protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
MSTN	NM_005259	myostatin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ZNF195	NM_001130519	zinc finger protein 195	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
LDB1	NM_001113407	LIM domain binding 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
TMED10	NM_006827	transmembrane emp24-like trafficking protein 10 (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ERRFI1	NM_018948	ERBB receptor feedback inhibitor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
KIF26B	NM_018012	kinesin family member 26B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ODF2L	NM_001007022	outer dense fiber of sperm tails 2-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
DUSP21	NM_022076	dual specificity phosphatase 21	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ZNF397	NM_032347	zinc finger protein 397	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
KIAA1267	NM_001193465	KIAA1267	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
EDNRA	NM_001166055	endothelin receptor type A	1	0	1	0	0	0	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR

SYNPO	NM_007286	synaptopodin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
SLC44A2	NM_001145056	solute carrier family 44, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
EDA2R	NM_001199687	ectodysplasin A2 receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
SORBS1	NM_001034954	sorbin and SH3 domain containing 1	1	0	0	1	2	1	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SLC2A2	NM_000340	solute carrier family 2 (facilitated glucose transporter), member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
PITPNB	NM_012399	phosphatidylinositol transfer protein, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
C1orf56	NM_017860	chromosome 1 open reading frame 56	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
C6orf25	NM_025260	chromosome 6 open reading frame 25	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
AFAP1L2	NM_001001936	actin filament associated protein 1-like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
ABCC12	NM_033226	ATP-binding cassette, sub-family C (CFTR/MRP), member 12	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
CD300LG	NM_001168324	CD300 molecule-like family member g	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
SLC35F3	NM_173508	solute carrier family 35, member F3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
EDNRB	NM_000115	endothelin receptor type B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
PLEKHA5	NM_001190860	pleckstrin homology domain containing, family A member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
MESP1	NM_018670	mesoderm posterior 1 homolog (mouse)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
HPS4	NM_022081	Hermansky-Pudlak syndrome 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ARHGAP40	NM_001164431	Rho GTPase activating protein 40	0	0	0	0	1	0	1	0	hsa-miR-622	-0.11	N/A	Sites in UTR
ZBTB46	NM_025224	zinc finger and BTB domain containing 46	0	0	0	0	1	1	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR

MCOLN2	NM_153259	mucolipin 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.11	N/A	Sites in UTR
RNF170	NM_001160223	ring finger protein 170	0	0	0	0	2	0	2	0	hsa-miR-622	-0.11	N/A	Sites in UTR
RPS6KL1	NM_031464	ribosomal protein S6 kinase-like 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.11	N/A	Sites in UTR
FAM135B	NM_015912	family with sequence similarity 135, member B	0	0	0	0	2	1	0	1	hsa-miR-622	-0.11	N/A	Sites in UTR
COL19A1	NM_001858	collagen, type XIX, alpha 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZNF510	NM_014930	zinc finger protein 510	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
WDR52	NM_001164496	WD repeat domain 52	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
FAM111A	NM_001142519	family with sequence similarity 111, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
PLD5	NM_001195811	phospholipase D family, member 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
C4orf3	NM_001001701	chromosome 4 open reading frame 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MTA2	NM_004739	metastasis associated 1 family, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CDCP1	NM_022842	CUB domain containing protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
C12orf43	NM_022895	chromosome 12 open reading frame 43	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MEGF10	NM_032446	multiple EGF-like-domains 10	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GUCY1A3	NM_001130683	guanylate cyclase 1, soluble, alpha 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.1	N/A	Sites in UTR
DIS3	NM_001128226	DIS3 mitotic control homolog (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GMFB	NM_004124	glia maturation factor, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
PSMD7	NM_002811	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR

COBL	NM_015198	cordon-bleu homolog (mouse)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MTRF1L	NM_001114184	mitochondrial translational release factor 1-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TMUB2	NM_001076674	transmembrane and ubiquitin-like domain containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZNF547	NM_173631	zinc finger protein 547	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
GRSF1	NM_001098477	G-rich RNA sequence binding factor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
NFIB	NM_001190737	nuclear factor I/B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
HMGXB3	NM_014983	HMG box domain containing 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CIDEC	NM_001199551	cell death-inducing DFFA-like effector c	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
HIF3A	NM_022462	hypoxia inducible factor 3, alpha subunit	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CCDC3	NM_031455	coiled-coil domain containing 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
JDP2	NM_001135047	Jun dimerization protein 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TCEB3	NM_003198	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
ZNF84	NM_001127372	zinc finger protein 84	0	0	0	0	1	1	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
LRTOMT	NM_001145308	leucine rich transmembrane and 0-methyltransferase domain containing	1	1	0	0	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
IL11RA	NM_147162	interleukin 11 receptor, alpha	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZC3H11A	NM_014827	zinc finger CCCH-type containing 11A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
HAVCR1	NM_001099414	hepatitis A virus cellular receptor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
C20orf111	NM_016470	chromosome 20 open reading frame 111	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR

MRPS10	NM_018141	mitochondrial ribosomal protein S10	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZBTB26	NM_020924	zinc finger and BTB domain containing 26	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
PAPD5	NM_001040284	PAP associated domain containing 5	1	0	0	1	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
C15orf41	NM_032499	chromosome 15 open reading frame 41	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
NFXL1	NM_152995	nuclear transcription factor, X-box binding-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MMP15	NM_002428	matrix metallopeptidase 15 (membrane-inserted)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MYBPC3	NM_000256	myosin binding protein C, cardiac	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
FRAT1	NM_005479	frequently rearranged in advanced T-cell lymphomas	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
VAMP5	NM_006634	vesicle-associated membrane protein 5 (myobrevin)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
KIAA0368	NM_001080398	KIAA0368	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GTPBP2	NM_019096	GTP binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
ACSS2	NM_001076552	acyl-CoA synthetase short-chain family member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TJAP1	NM_001146016	tight junction associated protein 1 (peripheral)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
HENMT1	NM_001102592	HEN1 methyltransferase homolog 1 (Arabidopsis)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SLC16A14	NM_152527	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
STEAP2	NM_001040665	six transmembrane epithelial antigen of the prostate 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
KRT73	NM_175068	keratin 73	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
PCSK5	NM_001190482	proprotein convertase subtilisin/kexin type 5	0	0	0	0	2	0	0	2	hsa-miR-622	-0.1	N/A	Sites in UTR

C17orf51	NM_001113434	chromosome 17 open reading frame 51	0	0	0	0	2	0	2	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MPZL1	NM_001146191	myelin protein zero-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
RABGAP1L	NM_001035230	RAB GTPase activating protein 1-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ENAM	NM_031889	enamelin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MAEA	NM_001017405	macrophage erythroblast attacher	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
KDM1A	NM_001009999	lysine (K)-specific demethylase 1A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TBC1D12	NM_015188	TBC1 domain family, member 12	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
RPP25	NM_017793	ribonuclease P/MRP 25kDa subunit	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SLC25A23	NM_024103	solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TMC5	NM_001105248	transmembrane channel-like 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZNF396	NM_145756	zinc finger protein 396	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TAL1	NM_003189	T-cell acute lymphocytic leukemia 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SLC22A13	NM_004256	solute carrier family 22 (organic anion transporter), member 13	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
RUNDC3A	NM_001144826	RUN domain containing 3A	1	0	1	0	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CCDC134	NM_024821	coiled-coil domain containing 134	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
PIK3C2B	NM_002646	phosphoinositide-3-kinase, class 2, beta polypeptide	0	0	0	0	2	0	0	2	hsa-miR-622	-0.1	N/A	Sites in UTR
ERLIN2	NM_007175	ER lipid raft associated 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CACYBP	NM_001007214	calcyclin binding protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR

DROSHA	NM_001100412	drosha, ribonuclease type III	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CLEC2D	NM_001004419	C-type lectin domain family 2, member D	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
C7orf42	NM_017994	chromosome 7 open reading frame 42	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
VCPIP1	NM_025054	valosin containing protein (p97)/p47 complex interacting protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SIGLEC12	NM_033329	sialic acid binding Ig-like lectin 12 (gene/pseudogene)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
C9orf43	NM_152786	chromosome 9 open reading frame 43	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
GRK6	NM_001004106	G protein-coupled receptor kinase 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
NR3C2	NM_000901	nuclear receptor subfamily 3, group C, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TEAD3	NM_003214	TEA domain family member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TSPAN3	NM_001168412	tetraspanin 3	1	0	0	1	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
DPPA4	NM_018189	developmental pluripotency associated 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
WDR33	NM_001006623	WD repeat domain 33	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
USP47	NM_017944	ubiquitin specific peptidase 47	0	0	0	0	1	1	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
ITGB8	NM_002214	integrin, beta 8	0	0	0	0	2	0	0	2	hsa-miR-622	-0.1	N/A	Sites in UTR
MOBKL2B	NM_024761	MOB1, Mps One Binder kinase activator-like 2B (yeast)	1	0	0	1	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MEF2D	NM_005920	myocyte enhancer factor 2D	0	0	0	0	3	0	1	2	hsa-miR-622	-0.1	N/A	Sites in UTR
ITGA2B	NM_000419	integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
JARID2	NM_004973	jumonji, AT rich interactive domain 2	1	0	0	1	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR

VRTN	NM_018228	vertebrae development homolog (pig)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
KCTD14	NM_023930	potassium channel tetramerisation domain containing 14	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
EIF2A	NM_032025	eukaryotic translation initiation factor 2A, 65kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TAPT1	NM_153365	transmembrane anterior posterior transformation 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
DHRSX	NM_145177	dehydrogenase/reductase (SDR family) X-linked	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
NDUFC2-KCTD14	NM_001203260	NDUFC2-KCTD14 readthrough	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
EXT1	NM_000127	exostosin 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MMP11	NM_005940	matrix metallopeptidase 11 (stromelysin 3)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SLC25A36	NM_001104647	solute carrier family 25, member 36	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
WDR76	NM_001167941	WD repeat domain 76	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
NIPAL4	NM_001099287	NIPA-like domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TRPS1	NM_014112	trichorhinophalangeal syndrome I	1	1	0	0	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SARM1	NM_015077	sterile alpha and TIR motif containing 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SOX1	NM_005986	SRY (sex determining region Y)-box 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
LAPTM4A	NM_014713	lysosomal protein transmembrane 4 alpha	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
WDR6	NM_018031	WD repeat domain 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CCDC47	NM_020198	coiled-coil domain containing 47	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SSX2IP	NM_001166293	synovial sarcoma, X breakpoint 2 interacting protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR

UBLCP1	NM_145049	ubiquitin-like domain containing CTD phosphatase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
YTHDF3	NM_152758	YTH domain family, member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
RIMKLA	NM_173642	ribosomal modification protein rimK-like family member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
AQP6	NM_001652	aquaporin 6, kidney specific	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
FGFR1	NM_001174063	fibroblast growth factor receptor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
IL3RA	NM_002183	interleukin 3 receptor, alpha (low affinity)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MGLL	NM_001003794	monoglyceride lipase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TBC1D9B	NM_015043	TBC1 domain family, member 9B (with GRAM domain)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
PSME4	NM_014614	proteasome (prosome, macropain) activator subunit 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CNO	NM_018366	cappuccino homolog (mouse)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
DERL1	NM_001134671	Der1-like domain family, member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
STK40	NM_032017	serine/threonine kinase 40	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
UHMK1	NM_001184763	U2AF homology motif (UHM) kinase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CLDN4	NM_001305	claudin 4	0	0	0	0	2	0	0	2	hsa-miR-622	-0.1	N/A	Sites in UTR
SNCA	NM_000345	synuclein, alpha (non A4 component of amyloid precursor)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.1	N/A	Sites in UTR
KCNE3	NM_005472	potassium voltage-gated channel, Isk-related family, member 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.1	N/A	Sites in UTR
MR1	NM_001194999	major histocompatibility complex, class I-related	0	0	0	0	3	0	2	1	hsa-miR-622	-0.1	N/A	Sites in UTR
GTF3C2	NM_001035521	general transcription factor IIIC, polypeptide 2, beta 110kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR

HOXB4	NM_024015	homeobox B4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
IL9R	NM_002186	interleukin 9 receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MYOM2	NM_003970	myomesin (M-protein) 2, 165kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TRAF4	NM_004295	TNF receptor-associated factor 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
LYPLA1	NM_006330	lysophospholipase I	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SMG5	NM_015327	smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TBC1D22A	NM_014346	TBC1 domain family, member 22A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SYTL2	NM_001162951	synaptotagmin-like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TMLHE	NM_018196	trimethyllysine hydroxylase, epsilon	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
UBE2Q1	NM_017582	ubiquitin-conjugating enzyme E2Q family member 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
RCN3	NM_020650	reticulocalbin 3, EF-hand calcium binding domain	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CNTNAP5	NM_130773	contactin associated protein-like 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
LELP1	NM_001010857	late cornified envelope-like proline-rich 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CHRND	NM_000751	cholinergic receptor, nicotinic, delta	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TRPM5	NM_014555	transient receptor potential cation channel, subfamily M, member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
HDAC8	NM_001166418	histone deacetylase 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CTTNBP2NL	NM_018704	CTTNBP2 N-terminal like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GPAM	NM_020918	glycerol-3-phosphate acyltransferase, mitochondrial	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR

ZNF526	NM_133444	zinc finger protein 526	0	0	0	0	2	0	1	1	hsa-miR-622	-0.1	N/A	Sites in UTR
RD3	NM_001164688	retinal degeneration 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.1	N/A	Sites in UTR
STXBP4	NM_178509	syntaxin binding protein 4	1	1	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
EHD1	NM_006795	EH-domain containing 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CUX2	NM_015267	cut-like homeobox 2	1	0	0	1	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
DNAJC19	NM_001190233	DnaJ (Hsp40) homolog, subfamily C, member 19	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CC2D1B	NM_032449	coiled-coil and C2 domain containing 1B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
VSTM2B	NM_001146339	V-set and transmembrane domain containing 2B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
PKIA	NM_006823	protein kinase (cAMP-dependent, catalytic) inhibitor alpha	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SYNJ2	NM_001178088	synaptojanin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MAP3K13	NM_001242314	mitogen-activated protein kinase kinase kinase 13	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
URGCP	NM_001077663	upregulator of cell proliferation	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SHF	NM_138356	Src homology 2 domain containing F	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
UBN2	NM_173569	ubinuclein 2	0	0	0	0	2	1	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
IRF4	NM_001195286	interferon regulatory factor 4	0	0	0	0	2	0	1	1	hsa-miR-622	-0.1	N/A	Sites in UTR
FAM126B	NM_173822	family with sequence similarity 126, member B	1	0	0	1	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TBCC	NM_003192	tubulin folding cofactor C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ENDOU	NM_001172439	endonuclease, polyU-specific	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR

RPS6KA6	NM_014496	ribosomal protein S6 kinase, 90kDa, polypeptide 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
NXPH1	NM_152745	neurexophilin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SCYL2	NM_017988	SCY1-like 2 (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZNF395	NM_018660	zinc finger protein 395	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CHCHD7	NM_001011667	coiled-coil-helix-coiled-coil-helix domain containing 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
KIRREL3	NM_001161707	kin of IRRE like 3 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
PTGR2	NM_001146154	prostaglandin reductase 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
FAM116A	NM_152678	family with sequence similarity 116, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ZCCHC5	NM_152694	zinc finger, CCHC domain containing 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
CSF1R	NM_005211	colony stimulating factor 1 receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GNG4	NM_001098721	guanine nucleotide binding protein (G protein), gamma 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
MCL1	NM_001197320	myeloid cell leukemia sequence 1 (BCL2-related)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
RGS16	NM_002928	regulator of G-protein signaling 16	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GPR161	NM_153832	G protein-coupled receptor 161	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
GGA1	NM_001001561	golgi-associated, gamma adaptin ear containing, ARF binding protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
STIM2	NM_001169117	stromal interaction molecule 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR
RNF26	NM_032015	ring finger protein 26	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
NSUN7	NM_024677	NOP2/Sun domain family, member 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR

TMEM41A	NM_080652	transmembrane protein 41A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
WDR88	NM_173479	WD repeat domain 88	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TMEM150C	NM_001080506	transmembrane protein 150C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
PAIP2B	NM_020459	poly(A) binding protein interacting protein 2B	0	0	0	0	2	0	2	0	hsa-miR-622	-0.1	N/A	Sites in UTR
PPP1R16B	NM_001172735	protein phosphatase 1, regulatory (inhibitor) subunit 16B	0	0	0	0	4	1	2	1	hsa-miR-622	-0.1	N/A	Sites in UTR
LAD1	NM_005558	ladinin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
NFKBIE	NM_004556	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
SRP72	NM_006947	signal recognition particle 72kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TMEM216	NM_001173990	transmembrane protein 216	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
ARV1	NM_022786	ARV1 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
TTC39B	NM_001168339	tetratricopeptide repeat domain 39B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.1	N/A	Sites in UTR
MC1R	NM_002386	melanocortin 1 receptor (alpha melanocyte stimulating hormone receptor)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
SUMO3	NM_006936	SMT3 suppressor of mif two 3 homolog 3 (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
HCAR3	NM_006018	hydroxycarboxylic acid receptor 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
BATF	NM_006399	basic leucine zipper transcription factor, ATF-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
TNRC6C	NM_001142640	trinucleotide repeat containing 6C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
CDCA5	NM_080668	cell division cycle associated 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.1	N/A	Sites in UTR
FAM155B	NM_015686	family with sequence similarity 155, member B	0	0	0	0	1	1	0	0	hsa-miR-622	-0.1	N/A	Sites in UTR

GTF2H5	NM_207118	general transcription factor IIH, polypeptide 5	0	0	0	0	2	0	0	2	hsa-miR-622	-0.09	N/A	Sites in UTR
RDX	NM_002906	radixin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
EIF2B5	NM_003907	eukaryotic translation initiation factor 2B, subunit 5 epsilon, 82kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
SPG20	NM_001142294	spastic paraplegia 20 (Troyer syndrome)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
RBM22	NM_018047	RNA binding motif protein 22	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
SCYL3	NM_020423	SCY1-like 3 (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CDK16	NM_001170460	cyclin-dependent kinase 16	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
MAPK3	NM_001040056	mitogen-activated protein kinase 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TFF3	NM_003226	trefoil factor 3 (intestinal)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
MTMR3	NM_021090	myotubularin related protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
FAM82B	NM_016033	family with sequence similarity 82, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
KANK4	NM_181712	KN motif and ankyrin repeat domains 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
FKRP	NM_001039885	fukutin related protein	0	0	0	0	2	0	1	1	hsa-miR-622	-0.09	N/A	Sites in UTR
IRS1	NM_005544	insulin receptor substrate 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.09	N/A	Sites in UTR
GJC1	NM_001080383	gap junction protein, gamma 1, 45kDa	0	0	0	0	3	0	1	2	hsa-miR-622	-0.09	N/A	Sites in UTR
POLR3F	NM_006466	polymerase (RNA) III (DNA directed) polypeptide F, 39 kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
INTS7	NM_001199809	integrator complex subunit 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PIP4K2C	NM_001146258	phosphatidylinositol-5-phosphate 4-kinase, type II, gamma	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR

LEPR	NM_001003679	leptin receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
WFS1	NM_001145853	Wolfram syndrome 1 (wolframin)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
SERF1A	NM_021967	small EDRK-rich factor 1A (telomeric)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
KIAA1024	NM_015206	KIAA1024	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
CTDNEP1	NM_001143775	CTD nuclear envelope phosphatase 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR
SYT9	NM_175733	synaptotagmin IX	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ZNF773	NM_198542	zinc finger protein 773	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
SERF1B	NM_022978	small EDRK-rich factor 1B (centromeric)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
CYP11B1	NM_000497	cytochrome P450, family 11, subfamily B, polypeptide 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.09	N/A	Sites in UTR
IRF6	NM_001206696	interferon regulatory factor 6	0	0	0	0	2	0	0	2	hsa-miR-622	-0.09	N/A	Sites in UTR
KSR2	NM_173598	kinase suppressor of ras 2	0	0	0	0	2	0	2	0	hsa-miR-622	-0.09	N/A	Sites in UTR
KIF2A	NM_001098511	kinesin heavy chain member 2A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
POU2AF1	NM_006235	POU class 2 associating factor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ARHGEF10	NM_014629	Rho guanine nucleotide exchange factor (GEF) 10	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
NDUFAF4	NM_014165	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, assembly factor 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
TTC26	NM_001144920	tetratricopeptide repeat domain 26	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
IRX2	NM_033267	iroquois homeobox 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
VWA3B	NM_144992	von Willebrand factor A domain containing 3B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR

NHLRC2	NM_198514	NHL repeat containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
FAM49A	NM_030797	family with sequence similarity 49, member A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
CYP4F11	NM_001128932	cytochrome P450, family 4, subfamily F, polypeptide 11	0	0	0	0	2	0	1	1	hsa-miR-622	-0.09	N/A	Sites in UTR
GOSR1	NM_001007024	golgi SNAP receptor complex member 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.09	N/A	Sites in UTR
CGNL1	NM_032866	cingulin-like 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.09	N/A	Sites in UTR
C8orf33	NM_023080	chromosome 8 open reading frame 33	0	0	0	0	2	0	1	1	hsa-miR-622	-0.09	N/A	Sites in UTR
EIF5AL1	NM_001099692	eukaryotic translation initiation factor 5A-like 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.09	N/A	Sites in UTR
FOSB	NM_001114171	FBJ murine osteosarcoma viral oncogene homolog B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ZNF41	NM_007130	zinc finger protein 41	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
DNPEP	NM_012100	aspartyl aminopeptidase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PLA2G3	NM_015715	phospholipase A2, group III	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ZNF770	NM_014106	zinc finger protein 770	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
SELRC1	NM_023077	Sel1 repeat containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ALPK1	NM_001102406	alpha-kinase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
RNASEH2C	NM_032193	ribonuclease H2, subunit C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CXCR5	NM_001716	chemokine (C-X-C motif) receptor 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
GRAP	NM_006613	GRB2-related adaptor protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
KIAA1715	NM_030650	KIAA1715	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR

TDRD10	NM_001098475	tudor domain containing 10	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
IGLON5	NM_001101372	IgLON family member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ZFP3	NM_153018	zinc finger protein 3 homolog (mouse)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR
MTX3	NM_001010891	metaxin 3	0	0	0	0	2	1	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
CSTB	NM_000100	cystatin B (stefin B)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
HPS1	NM_000195	Hermansky-Pudlak syndrome 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
MYL1	NM_079420	myosin, light chain 1, alkali; skeletal, fast	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
FILIP1L	NM_001042459	filamin A interacting protein 1-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
KLHDC5	NM_020782	kelch domain containing 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
C13orf18	NM_025113	chromosome 13 open reading frame 18	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
L3MBTL2	NM_031488	l(3)mbt-like 2 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
RCSD1	NM_052862	RCSD domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PRR20A	NM_198441	proline rich 20A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
KIF19	NM_153209	kinesin family member 19	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
EME1	NM_001166131	essential meiotic endonuclease 1 homolog 1 (S. pombe)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CA13	NM_198584	carbonic anhydrase XIII	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PRR20B	NM_001130404	proline rich 20B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PRR20C	NM_001130405	proline rich 20C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR

PRR20D	NM_001130406	proline rich 20D	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PRR20E	NM_001130407	proline rich 20E	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CHRNA2	NM_000742	cholinergic receptor, nicotinic, alpha 2 (neuronal)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
E2F4	NM_001950	E2F transcription factor 4, p107/p130-binding	1	0	1	0	0	0	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR
H2AFX	NM_002105	H2A histone family, member X	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
IL12RB1	NM_153701	interleukin 12 receptor, beta 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
AMOTL1	NM_130847	angiomotin like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TREML4	NM_198153	triggering receptor expressed on myeloid cells-like 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
SNX27	NM_030918	sorting nexin family member 27	0	0	0	0	4	0	1	3	hsa-miR-622	-0.09	N/A	Sites in UTR
NQO1	NM_000903	NAD(P)H dehydrogenase, quinone 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
RRP1	NM_003683	ribosomal RNA processing 1 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CLDN2	NM_001171092	claudin 2	0	0	0	1	0	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
SART3	NM_014706	squamous cell carcinoma antigen recognized by T cells 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PHB2	NM_001144831	prohibitin 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
LIMCH1	NM_001112717	LIM and calponin homology domains 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
FBXL3	NM_012158	F-box and leucine-rich repeat protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CMPK1	NM_001136140	cytidine monophosphate (UMP-CMP) kinase 1, cytosolic	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
APOBR	NM_018690	apolipoprotein B receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR

SIPA1L2	NM_020808	signal-induced proliferation-associated 1 like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
LOC253044	NM_001242772	hypothetical protein LOC253044	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
DRD2	NM_000795	dopamine receptor D2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
GABRE	NM_004961	gamma-aminobutyric acid (GABA) A receptor, epsilon	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
GRIA3	NM_000828	glutamate receptor, ionotrophic, AMPA 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ZNF142	NM_001105537	zinc finger protein 142	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
DAP3	NM_001199849	death associated protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
YKT6	NM_006555	YKT6 v-SNARE homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
POGZ	NM_001194937	pogo transposable element with ZNF domain	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
PPPDE1	NM_016076	PPPDE peptidase domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TBC1D22B	NM_017772	TBC1 domain family, member 22B	1	0	1	0	0	0	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR
RNF126	NM_194460	ring finger protein 126	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
AEN	NM_022767	apoptosis enhancing nuclease	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
SLC2A11	NM_001024938	solute carrier family 2 (facilitated glucose transporter), member 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
MRPS25	NM_022497	mitochondrial ribosomal protein S25	1	0	0	1	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
PFKFB2	NM_006212	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	0	0	0	0	2	0	1	1	hsa-miR-622	-0.09	N/A	Sites in UTR
SSR1	NM_003144	signal sequence receptor, alpha	1	0	1	0	1	1	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR
CDH8	NM_001796	cadherin 8, type 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR

HERC3	NM_014606	hect domain and RLD 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
VAX1	NM_199131	ventral anterior homeobox 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
FETUB	NM_014375	fetuin B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
MLH3	NM_001040108	mutL homolog 3 (E. coli)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
STARD3NL	NM_032016	STARD3 N-terminal like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
IGFL2	NM_001002915	IGF-like family member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
RIBC1	NM_144968	RIB43A domain with coiled-coils 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
NANOS1	NM_199461	nanos homolog 1 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
FBLN1	NM_006485	fibulin 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ODZ1	NM_001163278	odz, odd Oz/ten-m homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TAB1	NM_006116	TGF-beta activated kinase 1/MAP3K7 binding protein 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR
EHD4	NM_139265	EH-domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
REEP2	NM_016606	receptor accessory protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
CELF5	NM_001172673	CUGBP, Elav-like family member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ZBTB3	NM_024784	zinc finger and BTB domain containing 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ZNF709	NM_152601	zinc finger protein 709	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
C8orf46	NM_152765	chromosome 8 open reading frame 46	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ASB4	NM_016116	ankyrin repeat and SOCS box containing 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.09	N/A	Sites in UTR

SHE	NM_001010846	Src homology 2 domain containing E	0	0	0	0	2	0	2	0	hsa-miR-622	-0.09	N/A	Sites in UTR
LOC100507462	NM_001242740	hypothetical LOC100507462	0	0	0	0	2	1	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
LIPA	NM_000235	lipase A, lysosomal acid, cholesterol esterase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CNTN3	NM_020872	contactin 3 (plasmacytoma associated)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ATP2C1	NM_001199179	ATPase, Ca++ transporting, type 2C, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
KCNK4	NM_033310	potassium channel, subfamily K, member 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
CCDC60	NM_178499	coiled-coil domain containing 60	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
SKA3	NM_001166017	spindle and kinetochore associated complex subunit 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
DLX3	NM_005220	distal-less homeobox 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ATF7	NM_001130059	activating transcription factor 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
PISD	NM_014338	phosphatidylserine decarboxylase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
BCAP29	NM_001008405	B-cell receptor-associated protein 29	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
C13orf30	NM_182508	chromosome 13 open reading frame 30	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
AMZ1	NM_133463	archaelysin family metallopeptidase 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TMEM217	NM_145316	transmembrane protein 217	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TBC1D28	NM_001039397	TBC1 domain family, member 28	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
PEG10	NM_001040152	paternally expressed 10	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ABHD14B	NM_001146314	abhydrolase domain containing 14B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR

FBXO48	NM_001024680	F-box protein 48	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
ZFP36L2	NM_006887	zinc finger protein 36, C3H type-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
B3GALT5	NM_006057	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
WDR5	NM_017588	WD repeat domain 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
UNC93A	NM_001143947	unc-93 homolog A (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
TMEM209	NM_032842	transmembrane protein 209	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
HINT3	NM_138571	histidine triad nucleotide binding protein 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.09	N/A	Sites in UTR
DLX2	NM_004405	distal-less homeobox 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
GDF2	NM_016204	growth differentiation factor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
RALBP1	NM_006788	ralA binding protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
NHLRC3	NM_001012754	NHL repeat containing 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
P2RY6	NM_004154	pyrimidinergic receptor P2Y, G-protein coupled, 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
GPR55	NM_005683	G protein-coupled receptor 55	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
MTHFSD	NM_001159377	methenyltetrahydrofolate synthetase domain containing	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
ADAMTS14	NM_080722	ADAM metallopeptidase with thrombospondin type 1 motif, 14	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
SYNPO2	NM_133477	synaptopodin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.09	N/A	Sites in UTR
MDGA1	NM_153487	MAM domain containing glycosylphosphatidylinositol anchor 1	1	0	0	1	1	0	0	1	hsa-miR-622	-0.09	N/A	Sites in UTR
GPX5	NM_001509	glutathione peroxidase 5 (epididymal androgen-related protein)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR

LAMP2	NM_002294	lysosomal-associated membrane protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SRA1	NM_001035235	steroid receptor RNA activator 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ST7L	NM_017744	suppression of tumorigenicity 7 like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
KLHL15	NM_030624	kelch-like 15 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
EAF1	NM_033083	ELL associated factor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
RASSF3	NM_001242691	Ras association (RalGDS/AF-6) domain family member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	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	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
OSBPL2	NM_014835	oxysterol binding protein-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
C1orf198	NM_001136494	chromosome 1 open reading frame 198	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
HCAR2	NM_177551	hydroxycarboxylic acid receptor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
C2orf68	NM_001013649	chromosome 2 open reading frame 68	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
PTPN21	NM_007039	protein tyrosine phosphatase, non-receptor type 21	0	0	0	0	1	1	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
CDHR3	NM_152750	cadherin-related family member 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.08	N/A	Sites in UTR
QKI	NM_006775	quaking homolog, KH domain RNA binding (mouse)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.08	N/A	Sites in UTR
CBX5	NM_001127321	chromobox homolog 5	1	0	1	0	2	0	2	0	hsa-miR-622	-0.08	N/A	Sites in UTR
CD55	NM_000574	CD55 molecule, decay accelerating factor for complement (Cromer blood group)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
EEF1D	NM_001130053	eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SIRT5	NM_001193267	sirtuin 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR

SHISA5	NM_016479	shisa homolog 5 (Xenopus laevis)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SUSD3	NM_145006	sushi domain containing 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
PIRT	NM_001101387	phosphoinositide-interacting regulator of transient receptor potential channels	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
POU6F1	NM_002702	POU class 6 homeobox 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
DBF4	NM_006716	DBF4 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
SIK3	NM_025164	SIK family kinase 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
HUNK	NM_014586	hormonally up-regulated Neu-associated kinase	0	0	0	0	2	0	1	1	hsa-miR-622	-0.08	N/A	Sites in UTR
CTGF	NM_001901	connective tissue growth factor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
GAB1	NM_002039	GRB2-associated binding protein 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
TRIM37	NM_015294	tripartite motif containing 37	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
TCEA1	NM_006756	transcription elongation factor A (SII), 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SIRPG	NM_001039508	signal-regulatory protein gamma	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
LRRC4	NM_022143	leucine rich repeat containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ZNF576	NM_001145347	zinc finger protein 576	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
RUNDC3B	NM_001134405	RUN domain containing 3B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
GLOD5	NM_001080489	glyoxalase domain containing 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ERVFRD-1	NM_207582	endogenous retrovirus group FRD, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
HMX1	NM_018942	H6 family homeobox 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR

KCNK3	NM_002246	potassium channel, subfamily K, member 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
ZDHHC14	NM_024630	zinc finger, DHHC-type containing 14	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
STRN	NM_003162	striatin, calmodulin binding protein	0	0	0	0	1	1	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
BNC1	NM_001717	basonuclin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
TAF1	NM_004606	TAF1 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 250kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
GPR88	NM_022049	G protein-coupled receptor 88	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
FAM134B	NM_001034850	family with sequence similarity 134, member B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SCUBE2	NM_001170690	signal peptide, CUB domain, EGF-like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ZNF431	NM_133473	zinc finger protein 431	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
DHFRL1	NM_001195643	dihydrofolate reductase-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
KLK2	NM_001002231	kallikrein-related peptidase 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
PPL	NM_002705	periplakin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
RAD50	NM_005732	RAD50 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
RASD2	NM_014310	RASD family, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
GOLGA6L1	NM_001001413	golgin A6 family-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
HECA	NM_016217	headcase homolog (Drosophila)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.08	N/A	Sites in UTR
HMBS	NM_000190	hydroxymethylbilane synthase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SNRPE	NM_003094	small nuclear ribonucleoprotein polypeptide E	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR

KLHL28	NM_017658	kelch-like 28 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
TXNDC16	NM_001160047	thioredoxin domain containing 16	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
HSH2D	NM_032855	hematopoietic SH2 domain containing	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
MMS22L	NM_198468	MMS22-like, DNA repair protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
FAM111B	NM_001142703	family with sequence similarity 111, member B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
GTF3C5	NM_001122823	general transcription factor IIIC, polypeptide 5, 63kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
RAB14	NM_016322	RAB14, member RAS oncogene family	1	0	1	0	0	0	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
RGMA	NM_001166283	RGM domain family, member A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
NDRG4	NM_001130487	NDRG family member 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
TYSND1	NM_001040273	trypsin domain containing 1	0	0	0	0	2	0	2	0	hsa-miR-622	-0.08	N/A	Sites in UTR
DMD	NM_000109	dystrophin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
FABP3	NM_004102	fatty acid binding protein 3, muscle and heart (mammary-derived growth inhibitor)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
PHF1	NM_002636	PHD finger protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SERPINB5	NM_002639	serpin peptidase inhibitor, clade B (ovalbumin), member 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SLC5A1	NM_000343	solute carrier family 5 (sodium/glucose cotransporter), member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
KCNH8	NM_144633	potassium voltage-gated channel, subfamily H (eag-related), member 8	0	0	0	1	0	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SPRED1	NM_152594	sprouty-related, EVH1 domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ADAMTS18	NM_199355	ADAM metallopeptidase with thrombospondin type 1 motif, 18	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR

DZIP1L	NM_173543	DAZ interacting protein 1-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ANKRD13D	NM_207354	ankyrin repeat domain 13 family, member D	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
EPHA2	NM_004431	EPH receptor A2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
F2RL1	NM_005242	coagulation factor II (thrombin) receptor-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
ATG4B	NM_013325	ATG4 autophagy related 4 homolog B (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
DBNDD1	NM_001042610	dysbindin (dystrobrevin binding protein 1) domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
BPIL1	NM_025227	bactericidal/permeability-increasing protein-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
APH1B	NM_001145646	anterior pharynx defective 1 homolog B (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
MYADML2	NM_001145113	myeloid-associated differentiation marker-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
GOLGA6L6	NM_001145004	golgin A6 family-like 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
PANK1	NM_138316	pantothenate kinase 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.08	N/A	Sites in UTR
LAMP3	NM_014398	lysosomal-associated membrane protein 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.08	N/A	Sites in UTR
RASGRP1	NM_001128602	RAS guanyl releasing protein 1 (calcium and DAG-regulated)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
OPHN1	NM_002547	oligophrenin 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.08	N/A	Sites in UTR
KHNYN	NM_015299	KH and NYN domain containing	1	1	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SCAI	NM_001144877	suppressor of cancer cell invasion	1	0	0	1	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
ZNF621	NM_001098414	zinc finger protein 621	0	0	0	0	3	0	2	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ANK3	NM_001149	ankyrin 3, node of Ranvier (ankyrin G)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR

PRDM1	NM_001198	PR domain containing 1, with ZNF domain	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
F7	NM_000131	coagulation factor VII (serum prothrombin conversion accelerator)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
GRIA4	NM_000829	glutamate receptor, ionotrophic, AMPA 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
PA2G4	NM_006191	proliferation-associated 2G4, 38kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SLC35D2	NM_007001	solute carrier family 35, member D2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
FGFR1OP2	NM_001171887	FGFR1 oncogene partner 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
RRP15	NM_016052	ribosomal RNA processing 15 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
HERC6	NM_001165136	hect domain and RLD 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
EFHA2	NM_181723	EF-hand domain family, member A2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
LHFP	NM_005780	lipoma HMGIC fusion partner	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
LATS2	NM_014572	LATS, large tumor suppressor, homolog 2 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
A2LD1	NM_001195087	AIG2-like domain 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
HEPHL1	NM_001098672	hephaestin-like 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.08	N/A	Sites in UTR
TCF3	NM_001136139	transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ATCAY	NM_033064	ataxia, cerebellar, Cayman type	0	0	0	0	2	0	1	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SV2B	NM_001167580	synaptic vesicle glycoprotein 2B	0	0	0	0	2	1	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
CD97	NM_001025160	CD97 molecule	1	0	0	1	0	0	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
PTGS2	NM_000963	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR

STAU1	NM_001037328	staufen, RNA binding protein, homolog 1 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
SIX2	NM_016932	SIX homeobox 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
WWTR1	NM_001168278	WW domain containing transcription regulator 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
KIAA1274	NM_014431	KIAA1274	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
ELTD1	NM_022159	EGF, latrophilin and seven transmembrane domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
PTPRB	NM_001109754	protein tyrosine phosphatase, receptor type, B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
MAN1A2	NM_006699	mannosidase, alpha, class 1A, member 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
GNL3L	NM_001184819	guanine nucleotide binding protein-like 3 (nucleolar)-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
C18orf25	NM_001008239	chromosome 18 open reading frame 25	0	0	0	0	1	1	0	0	hsa-miR-622	-0.08	N/A	Sites in UTR
DHFR	NM_000791	dihydrofolate reductase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
NDUFS1	NM_001199981	NADH dehydrogenase (ubiquinone) Fe-S protein 1, 75kDa (NADH-coenzyme Q reductase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
WDR48	NM_020839	WD repeat domain 48	0	0	0	1	0	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
BAALC	NM_001024372	brain and acute leukemia, cytoplasmic	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
LRRTM4	NM_024993	leucine rich repeat transmembrane neuronal 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
TSGA13	NM_052933	testis specific, 13	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
AEBP2	NM_153207	AE binding protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.08	N/A	Sites in UTR
PCGF3	NM_006315	polycomb group ring finger 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
MLC1	NM_015166	megalencephalic leukoencephalopathy with subcortical cysts 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR

TMEM104	NM_017728	transmembrane protein 104	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
XPNPEP3	NM_022098	X-prolyl aminopeptidase (aminopeptidase P) 3, putative	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
KRI1	NM_023008	KRI1 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
FOPNL	NM_144600	FGFR1OP N-terminal like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.08	N/A	Sites in UTR
JMY	NM_152405	junction mediating and regulatory protein, p53 cofactor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ITGAL	NM_001114380	integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
WNT11	NM_004626	wingless-type MMTV integration site family, member 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TBK1	NM_013254	TANK-binding kinase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
PRICKLE4	NM_013397	prickle homolog 4 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ZFYVE21	NM_001198953	zinc finger, FYVE domain containing 21	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RNASEK	NM_001004333	ribonuclease, RNase K	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ROR2	NM_004560	receptor tyrosine kinase-like orphan receptor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
PHLDA3	NM_012396	pleckstrin homology-like domain, family A, member 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
DCDC2	NM_001195610	doublecortin domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
PARP8	NM_001178055	poly (ADP-ribose) polymerase family, member 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
PRR3	NM_001077497	proline rich 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
FAM83C	NM_178468	family with sequence similarity 83, member C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ZNF506	NM_001099269	zinc finger protein 506	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR

ATXN7L3B	NM_001136262	ataxin 7-like 3B	0	0	0	0	2	0	1	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SGCG	NM_000231	sarcoglycan, gamma (35kDa dystrophin-associated glycoprotein)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SPRR2E	NM_001024209	small proline-rich protein 2E	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
MFAP3L	NM_001009554	microfibrillar-associated protein 3-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RPL13A	NM_012423	ribosomal protein L13a	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
BCL2L13	NM_015367	BCL2-like 13 (apoptosis facilitator)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
UBR5	NM_015902	ubiquitin protein ligase E3 component n-recognin 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ORAI3	NM_152288	ORAI calcium release-activated calcium modulator 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
FBXO45	NM_001105573	F-box protein 45	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TLX1	NM_001195517	T-cell leukemia homeobox 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
IL4R	NM_000418	interleukin 4 receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
BRE	NM_004899	brain and reproductive organ-expressed (TNFRSF1A modulator)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ICOSLG	NM_015259	inducible T-cell co-stimulator ligand	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
DNAJC11	NM_018198	DnaJ (Hsp40) homolog, subfamily C, member 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
CYP4V2	NM_207352	cytochrome P450, family 4, subfamily V, polypeptide 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ARL10	NM_173664	ADP-ribosylation factor-like 10	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
LOC100293516	NM_001204818	zinc finger protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
TLE3	NM_001105192	transducin-like enhancer of split 3 (E(sp1) homolog, Drosophila)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR

EIF5	NM_001969	eukaryotic translation initiation factor 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
FGFR3	NM_000142	fibroblast growth factor receptor 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ITGA6	NM_000210	integrin, alpha 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
PDK2	NM_001199898	pyruvate dehydrogenase kinase, isozyme 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RAD52	NM_134424	RAD52 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SKAP2	NM_003930	src kinase associated phosphoprotein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
BZW1	NM_001207067	basic leucine zipper and W2 domains 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
MGA	NM_001080541	MAX gene associated	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
PEX5L	NM_016559	peroxisomal biogenesis factor 5-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
PDP1	NM_001161778	pyruvate dehyrogenase phosphatase catalytic subunit 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
BSDC1	NM_001143888	BSD domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
MLL3	NM_170606	myeloid/lymphoid or mixed-lineage leukemia 3	1	0	0	1	0	0	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ERI1	NM_153332	exoribonuclease 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RC3H1	NM_172071	ring finger and CCCH-type domains 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
MOCS1	NM_001075098	molybdenum cofactor synthesis 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
BATF3	NM_018664	basic leucine zipper transcription factor, ATF-like 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
MID1IP1	NM_001098790	MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish))	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
SLC25A43	NM_145305	solute carrier family 25, member 43	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR

KCNIP3	NM_001034914	Kv channel interacting protein 3, calsenilin	0	0	0	0	2	0	2	0	hsa-miR-622	-0.07	N/A	Sites in UTR
WIPF3	NM_001080529	WAS/WASL interacting protein family, member 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
PAPD7	NM_001171805	PAP associated domain containing 7	0	0	0	0	2	0	2	0	hsa-miR-622	-0.07	N/A	Sites in UTR
GNAO1	NM_138736	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SLC47A1	NM_018242	solute carrier family 47, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
STEAP4	NM_001205315	STEAP family member 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TMEM132D	NM_133448	transmembrane protein 132D	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
METAP1D	NM_199227	methionyl aminopeptidase type 1D (mitochondrial)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
NEO1	NM_001172623	neogenin 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
NEURL1B	NM_001142651	neuralized homolog 1B (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ASB13	NM_024701	ankyrin repeat and SOCS box containing 13	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
UNC119B	NM_001080533	unc-119 homolog B (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	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	1	1	hsa-miR-622	-0.07	N/A	Sites in UTR
PIP5K1C	NM_001195733	phosphatidylinositol-4-phosphate 5-kinase, type I, gamma	0	0	0	0	2	0	1	1	hsa-miR-622	-0.07	N/A	Sites in UTR
EXD2	NM_001193360	exonuclease 3'-5' domain containing 2	0	0	0	0	3	0	1	2	hsa-miR-622	-0.07	N/A	Sites in UTR
ATP5G3	NM_001002258	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3 (subunit 9)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	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	hsa-miR-622	-0.07	N/A	Sites in UTR
IL17A	NM_002190	interleukin 17A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR

RFXAP	NM_000538	regulatory factor X-associated protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TCF4	NM_001083962	transcription factor 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RECQL5	NM_001003715	RecQ protein-like 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RNF139	NM_007218	ring finger protein 139	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ZFP30	NM_014898	zinc finger protein 30 homolog (mouse)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
C12orf4	NM_020374	chromosome 12 open reading frame 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ZFP90	NM_133458	zinc finger protein 90 homolog (mouse)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
GPS1	NM_004127	G protein pathway suppressor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
IPO5	NM_002271	importin 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
MAP4	NM_030885	microtubule-associated protein 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
POLR2L	NM_021128	polymerase (RNA) II (DNA directed) polypeptide L, 7.6kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
RRP1B	NM_015056	ribosomal RNA processing 1 homolog B (S. cerevisiae)	0	0	0	0	1	1	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
DRG2	NM_001388	developmentally regulated GTP binding protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
MSR1	NM_002445	macrophage scavenger receptor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SAP18	NM_005870	Sin3A-associated protein, 18kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RGL1	NM_015149	ral guanine nucleotide dissociation stimulator-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TPK1	NM_001042482	thiamin pyrophosphokinase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SLC22A17	NM_016609	solute carrier family 22, member 17	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR

MTFP1	NM_001003704	mitochondrial fission process 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
FAM204A	NM_001134672	family with sequence similarity 204, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
GPBP1	NM_001127235	GC-rich promoter binding protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SLCO5A1	NM_001146008	solute carrier organic anion transporter family, member 5A1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
C6orf89	NM_152734	chromosome 6 open reading frame 89	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
COL1A1	NM_000088	collagen, type I, alpha 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
FLI1	NM_001167681	Friend leukemia virus integration 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
NINJ1	NM_004148	ninjurin 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
FAM65B	NM_014722	family with sequence similarity 65, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
TNK2	NM_001010938	tyrosine kinase, non-receptor, 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
STX3	NM_001178040	syntaxin 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
NAA50	NM_025146	N(alpha)-acetyltransferase 50, NatE catalytic subunit	0	0	0	0	3	1	0	2	hsa-miR-622	-0.07	N/A	Sites in UTR
LIMK2	NM_005569	LIM domain kinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
MTRR	NM_002454	5-methyltetrahydrofolate-homocysteine methyltransferase reductase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SPRR2B	NM_001017418	small proline-rich protein 2B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TRAM1	NM_014294	translocation associated membrane protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TINF2	NM_012461	TERF1 (TRF1)-interacting nuclear factor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
BCL11B	NM_022898	B-cell CLL/lymphoma 11B (zinc finger protein)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR

SFXN5	NM_144579	sideroflexin 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TMEM188	NM_153261	transmembrane protein 188	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SSTR3	NM_001051	somatostatin receptor 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
TRIOBP	NM_001039141	TRIO and F-actin binding protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
PHLPP2	NM_015020	PH domain and leucine rich repeat protein phosphatase 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
GLYCTK	NM_145262	glycerate kinase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
SHISA4	NM_198149	shisa homolog 4 (Xenopus laevis)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
NXPH3	NM_007225	neurexophilin 3	0	0	0	0	2	1	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
H2AFV	NM_138635	H2A histone family, member V	0	0	0	0	2	0	2	0	hsa-miR-622	-0.07	N/A	Sites in UTR
IRAK2	NM_001570	interleukin-1 receptor-associated kinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ACCS	NM_001127219	1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
EDARADD	NM_080738	EDAR-associated death domain	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RPS6KB1	NM_003161	ribosomal protein S6 kinase, 70kDa, polypeptide 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
FAM127B	NM_001078172	family with sequence similarity 127, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
CCDC149	NM_001130726	coiled-coil domain containing 149	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ERLIN1	NM_001100626	ER lipid raft associated 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
CPPED1	NM_001099455	calcineurin-like phosphoesterase domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
UBFD1	NM_019116	ubiquitin family domain containing 1	1	0	0	1	0	0	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR

KCMF1	NM_020122	potassium channel modulatory factor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ABLIM2	NM_001130088	actin binding LIM protein family, member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
LGALS12	NM_001142535	lectin, galactoside-binding, soluble, 12	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
UBXN10	NM_152376	UBX domain protein 10	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SMAD4	NM_005359	SMAD family member 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
BZRAP1	NM_004758	benzodiazapine receptor (peripheral) associated protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
C5orf4	NM_032385	chromosome 5 open reading frame 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
GADD45G	NM_006705	growth arrest and DNA-damage-inducible, gamma	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
SND1	NM_014390	staphylococcal nuclease and tudor domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
SCML4	NM_198081	sex comb on midleg-like 4 (Drosophila)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
FIGNL2	NM_001013690	fidgetin-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
TIMM8A	NM_001145951	translocase of inner mitochondrial membrane 8 homolog A (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ITPRIP	NM_033397	inositol 1,4,5-trisphosphate receptor interacting protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
FAM59B	NM_001168241	family with sequence similarity 59, member B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
C9orf163	NM_152571	chromosome 9 open reading frame 163	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
FLJ44635	NM_207422	TPT1-like protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
DPAGT1	NM_001382	dolichyl-phosphate (UDP-N-acetylglucosamine) N-acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
CPSF2	NM_017437	cleavage and polyadenylation specific factor 2, 100kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR

ASPHD2	NM_020437	aspartate beta-hydroxylase domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
ZSWIM4	NM_023072	zinc finger, SWIM-type containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
SPTB	NM_001024858	spectrin, beta, erythrocytic	0	0	0	0	2	0	1	1	hsa-miR-622	-0.07	N/A	Sites in UTR
CREBZF	NM_001039618	CREB/ATF bZIP transcription factor	0	0	0	0	2	0	1	1	hsa-miR-622	-0.07	N/A	Sites in UTR
BMP6	NM_001718	bone morphogenetic protein 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
IL1RAP	NM_001167928	interleukin 1 receptor accessory protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
RPA1	NM_002945	replication protein A1, 70kDa	1	0	0	1	0	0	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR
LEFTY2	NM_001172425	left-right determination factor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
NTN1	NM_004822	netrin 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ASCC3	NM_022091	activating signal cointegrator 1 complex subunit 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
C2orf18	NM_017877	chromosome 2 open reading frame 18	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
TMEM108	NM_001136469	transmembrane protein 108	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
LIN28A	NM_024674	lin-28 homolog A (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
SPRED2	NM_001128210	sprouty-related, EVH1 domain containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
ARGFX	NM_001012659	arginine-fifty homeobox	0	0	0	0	1	0	0	1	hsa-miR-622	-0.07	N/A	Sites in UTR
NAP1L1	NM_004537	nucleosome assembly protein 1-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
TBC1D24	NM_001199107	TBC1 domain family, member 24	0	0	0	0	1	0	1	0	hsa-miR-622	-0.07	N/A	Sites in UTR
CPEB2	NM_001177381	cytoplasmic polyadenylation element binding protein 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.07	N/A	Sites in UTR

SLC25A15	NM_014252	solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	0	0	0	0	2	0	2	0	hsa-miR-622	-0.06	N/A	Sites in UTR
SOBP	NM_018013	sine oculis binding protein homolog (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
CDH23	NM_052836	cadherin-related 23	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
TMEM182	NM_144632	transmembrane protein 182	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
FAM19A2	NM_178539	family with sequence similarity 19 (chemokine (C-C motif)-like), member A2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
ACVR1B	NM_004302	activin A receptor, type IB	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
ST3GAL1	NM_003033	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.06	N/A	Sites in UTR
SLC6A1	NM_003042	solute carrier family 6 (neurotransmitter transporter, GABA), member 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
CECR2	NM_031413	cat eye syndrome chromosome region, candidate 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
SYS1	NM_001099791	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
SNX19	NM_014758	sorting nexin 19	0	0	0	0	2	0	1	1	hsa-miR-622	-0.06	N/A	Sites in UTR
ZMYM2	NM_001190964	zinc finger, MYM-type 2	1	1	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
EPHB3	NM_004443	EPH receptor B3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
VAPB	NM_001195677	VAMP (vesicle-associated membrane protein)-associated protein B and C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
NCOR1	NM_001190440	nuclear receptor corepressor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
JOSD1	NM_014876	Josephin domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
GALNTL1	NM_001168368	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
MOSC1	NM_022746	MOCO sulphurase C-terminal domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR

MMP28	NM_024302	matrix metallopeptidase 28	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
TMX1	NM_030755	thioredoxin-related transmembrane protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
LRIT2	NM_001017924	leucine-rich repeat, immunoglobulin-like and transmembrane domains 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
POLR2D	NM_004805	polymerase (RNA) II (DNA directed) polypeptide D	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
RGS11	NM_003834	regulator of G-protein signaling 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
ZSCAN22	NM_181846	zinc finger and SCAN domain containing 22	0	0	0	0	2	0	0	2	hsa-miR-622	-0.06	N/A	Sites in UTR
GFI1	NM_001127215	growth factor independent 1 transcription repressor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SPRR2F	NM_001014450	small proline-rich protein 2F	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
EML2	NM_001193268	echinoderm microtubule associated protein like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
HCAR1	NM_032554	hydroxycarboxylic acid receptor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
CPNE8	NM_153634	copine VIII	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
C8orf74	NM_001040032	chromosome 8 open reading frame 74	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
MAPK11	NM_002751	mitogen-activated protein kinase 11	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
UBE3B	NM_130466	ubiquitin protein ligase E3B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
C3orf62	NM_198562	chromosome 3 open reading frame 62	0	0	0	0	2	0	1	1	hsa-miR-622	-0.06	N/A	Sites in UTR
CLASP1	NM_001142273	cytoplasmic linker associated protein 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SRD5A2	NM_000348	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
WARS2	NM_015836	tryptophanyl tRNA synthetase 2, mitochondrial	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR

ZDHHC23	NM_173570	zinc finger, DHHC-type containing 23	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
C1orf229	NM_207401	chromosome 1 open reading frame 229	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
ADAM8	NM_001109	ADAM metallopeptidase domain 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
IGF2	NM_000612	insulin-like growth factor 2 (somatomedin A)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
CLIC5	NM_001114086	chloride intracellular channel 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
ZNF845	NM_138374	zinc finger protein 845	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
ATG9B	NM_173681	ATG9 autophagy related 9 homolog B (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
MTHFR	NM_005957	methylenetetrahydrofolate reductase (NAD(P)H)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.06	N/A	Sites in UTR
FAM190B	NM_018999	family with sequence similarity 190, member B	0	0	0	0	2	1	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
NPTX2	NM_002523	neuronal pentraxin II	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
USP13	NM_003940	ubiquitin specific peptidase 13 (isopeptidase T-3)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
RUSC2	NM_001135999	RUN and SH3 domain containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
FAM83A	NM_032899	family with sequence similarity 83, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
MTRNR2L4	NM_001190476	MT-RNR2-like 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
GCNT1	NM_001097633	glucosaminyl (N-acetyl) transferase 1, core 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
PLP1	NM_000533	proteolipid protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
SDC3	NM_014654	syndecan 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.06	N/A	Sites in UTR
FLJ45513	NM_001242791	hypothetical LOC729220	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR

SCN4B	NM_001142348	sodium channel, voltage-gated, type IV, beta	0	0	0	0	2	0	0	2	hsa-miR-622	-0.06	N/A	Sites in UTR
SPRR2A	NM_005988	small proline-rich protein 2A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SUSD5	NM_015551	sushi domain containing 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
MYOZ2	NM_016599	myozenin 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
ANKRD40	NM_052855	ankyrin repeat domain 40	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
PLEKHA7	NM_175058	pleckstrin homology domain containing, family A member 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
ZYG11B	NM_024646	zyg-11 homolog B (C. elegans)	1	0	1	0	0	0	0	0	hsa-miR-622	-0.06	N/A	Sites in UTR
PMAIP1	NM_021127	phorbol-12-myristate-13-acetate-induced protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
PTPRF	NM_002840	protein tyrosine phosphatase, receptor type, F	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SORL1	NM_003105	sortilin-related receptor, L(DLR class) A repeats containing	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SNAP29	NM_004782	synaptosomal-associated protein, 29kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
PLA2G2D	NM_012400	phospholipase A2, group IID	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
EXOC2	NM_018303	exocyst complex component 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
KLHL12	NM_021633	kelch-like 12 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
TYW5	NM_001039693	tRNA-yW synthesizing protein 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
KIAA0226	NM_001145642	KIAA0226	1	0	1	0	0	0	0	0	hsa-miR-622	-0.06	N/A	Sites in UTR
KLHL24	NM_017644	kelch-like 24 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
ZNF276	NM_001113525	zinc finger protein 276	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR

SNX20	NM_001144972	sorting nexin 20	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
TRA2B	NM_004593	transformer 2 beta homolog (Drosophila)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.06	N/A	Sites in UTR
PLEKHM3	NM_001080475	pleckstrin homology domain containing, family M, member 3	0	0	0	0	2	1	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
VCAN	NM_001126336	versican	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SHC1	NM_001130040	SHC (Src homology 2 domain containing) transforming protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
HERC2	NM_004667	hect domain and RLD 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
DTL	NM_016448	denticleless homolog (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
TBC1D8B	NM_017752	TBC1 domain family, member 8B (with GRAM domain)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
HMBOX1	NM_001135726	homeobox containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
TRIM52	NM_032765	tripartite motif containing 52	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
TWISTNB	NM_001002926	TWIST neighbor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
ZNF740	NM_001004304	zinc finger protein 740	1	0	0	1	0	0	0	0	hsa-miR-622	-0.06	N/A	Sites in UTR
CD274	NM_014143	CD274 molecule	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
IER5	NM_016545	immediate early response 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
APLNR	NM_005161	apelin receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
BAK1	NM_001188	BCL2-antagonist/killer 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
HLF	NM_002126	hepatic leukemia factor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
RPS23	NM_001025	ribosomal protein S23	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR

SENP1	NM_014554	SUMO1/sentrin specific peptidase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
C1orf95	NM_001003665	chromosome 1 open reading frame 95	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SHROOM2	NM_001649	shroom family member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
DIAPH1	NM_001079812	diaphanous homolog 1 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
GSPT1	NM_001130006	G1 to S phase transition 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
MTMR6	NM_004685	myotubularin related protein 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
KDM2A	NM_012308	lysine (K)-specific demethylase 2A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
COASY	NM_001042529	CoA synthase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
CABLES2	NM_031215	Cdk5 and Abl enzyme substrate 2	0	0	0	0	2	0	2	0	hsa-miR-622	-0.06	N/A	Sites in UTR
SIGLEC1	NM_023068	sialic acid binding Ig-like lectin 1, sialoadhesin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
PSME3	NM_005789	proteasome (prosome, macropain) activator subunit 3 (PA28 gamma; Ki)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SIK2	NM_015191	salt-inducible kinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
CPSF7	NM_001136040	cleavage and polyadenylation specific factor 7, 59kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
FAM192A	NM_024946	family with sequence similarity 192, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
C9orf170	NM_001001709	chromosome 9 open reading frame 170	0	0	0	0	1	0	0	1	hsa-miR-622	-0.06	N/A	Sites in UTR
SLC12A4	NM_001145961	solute carrier family 12 (potassium/chloride transporters), member 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
KRT75	NM_004693	keratin 75	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR
TNPO2	NM_001136195	transportin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.06	N/A	Sites in UTR

NID1	NM_002508	nidogen 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
NR2F2	NM_001145155	nuclear receptor subfamily 2, group F, member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
WNT6	NM_006522	wingless-type MMTV integration site family, member 6	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ATP13A1	NM_020410	ATPase type 13A1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
CASP2	NM_001224	caspase 2, apoptosis-related cysteine peptidase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
DPP4	NM_001935	dipeptidyl-peptidase 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
MYCL1	NM_005376	v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
SP2	NM_003110	Sp2 transcription factor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
C17orf75	NM_022344	chromosome 17 open reading frame 75	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
IFITM10	NM_001170820	interferon induced transmembrane protein 10	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
KIF5B	NM_004521	kinesin family member 5B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
OXTR	NM_000916	oxytocin receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SULT2A1	NM_003167	sulfotransferase family, cytosolic, 2A, dehydroepiandrosterone (DHEA)-preferring, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
C9orf5	NM_032012	chromosome 9 open reading frame 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ZNF606	NM_025027	zinc finger protein 606	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
GLYATL3	NM_001010904	glycine-N-acyltransferase-like 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
COQ7	NM_001190983	coenzyme Q7 homolog, ubiquinone (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
BAZ2A	NM_013449	bromodomain adjacent to zinc finger domain, 2A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR

ARHGEF18	NM_001130955	Rho/Rac guanine nucleotide exchange factor (GEF) 18	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CENPH	NM_022909	centromere protein H	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
UNC5D	NM_080872	unc-5 homolog D (C. elegans)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
DCLK3	NM_033403	doublecortin-like kinase 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.05	N/A	Sites in UTR
GUCA1B	NM_002098	guanylate cyclase activator 1B (retina)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
RBBP4	NM_001135255	retinoblastoma binding protein 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SNTB1	NM_021021	syntrophin, beta 1 (dystrophin-associated protein A1, 59kDa, basic component 1)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
TNFAIP3	NM_006290	tumor necrosis factor, alpha-induced protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SLC27A4	NM_005094	solute carrier family 27 (fatty acid transporter), member 4	1	0	0	1	0	0	0	0	hsa-miR-622	-0.05	N/A	Sites in UTR
RABGAP1	NM_012197	RAB GTPase activating protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
PIGR	NM_002644	polymeric immunoglobulin receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
PKP2	NM_001005242	plakophilin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CTSA	NM_000308	cathepsin A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CORO2A	NM_003389	coronin, actin binding protein, 2A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
C14orf126	NM_080664	chromosome 14 open reading frame 126	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
FGD4	NM_139241	FYVE, RhoGEF and PH domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
SLC9A9	NM_173653	solute carrier family 9 (sodium/hydrogen exchanger), member 9	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
GAS8	NM_001481	growth arrest-specific 8	0	0	0	0	1	1	0	0	hsa-miR-622	-0.05	N/A	Sites in UTR

CDHR1	NM_033100	cadherin-related family member 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.05	N/A	Sites in UTR
KIAA0895	NM_001100425	KIAA0895	0	0	0	0	2	0	1	1	hsa-miR-622	-0.05	N/A	Sites in UTR
FSTL4	NM_015082	follistatin-like 4	0	0	0	0	2	0	2	0	hsa-miR-622	-0.05	N/A	Sites in UTR
RBFOX2	NM_001031695	RNA binding protein, fox-1 homolog (C. elegans) 2	0	0	0	0	2	0	2	0	hsa-miR-622	-0.05	N/A	Sites in UTR
RASL10B	NM_033315	RAS-like, family 10, member B	0	0	0	0	2	0	2	0	hsa-miR-622	-0.05	N/A	Sites in UTR
TJP1	NM_003257	tight junction protein 1 (zona occludens 1)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ENC1	NM_003633	ectodermal-neural cortex 1 (with BTB-like domain)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ANGPTL7	NM_021146	angiopoietin-like 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ZHX1	NM_001017926	zinc fingers and homeoboxes 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SMOC1	NM_001034852	SPARC related modular calcium binding 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
NKAIN2	NM_001040214	Na+/K+ transporting ATPase interacting 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
MSL1	NM_001012241	male-specific lethal 1 homolog (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
C5orf56	NM_001207003	chromosome 5 open reading frame 56	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
HSPG2	NM_005529	heparan sulfate proteoglycan 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
JRK	NM_001077527	jerky homolog (mouse)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
NCAPH2	NM_001185011	non-SMC condensin II complex, subunit H2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
C5orf51	NM_175921	chromosome 5 open reading frame 51	0	0	0	0	1	1	0	0	hsa-miR-622	-0.05	N/A	Sites in UTR
GPR56	NM_001145770	G protein-coupled receptor 56	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR

ZMYND11	NM_001202464	zinc finger, MYND-type containing 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
RIOK2	NM_001159749	RIO kinase 2 (yeast)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.05	N/A	Sites in UTR
ZNF304	NM_020657	zinc finger protein 304	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SHROOM3	NM_020859	shroom family member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
RHOU	NM_021205	ras homolog gene family, member U	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
C19orf18	NM_152474	chromosome 19 open reading frame 18	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ADAR	NM_001025107	adenosine deaminase, RNA-specific	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CSNK1G2	NM_001319	casein kinase 1, gamma 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
FNTB	NM_002028	farnesyltransferase, CAAX box, beta	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
ZNF208	NM_007153	zinc finger protein 208	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CHMP4C	NM_152284	chromatin modifying protein 4C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
PACRGL	NM_001130727	PARK2 co-regulated-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CHURC1-FNTB	NM_001202558	CHURC1-FNTB readthrough	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
ATOH8	NM_032827	atonal homolog 8 (Drosophila)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CDKN2B	NM_004936	cyclin-dependent kinase inhibitor 2B (p15, inhibits CDK4)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
CDK17	NM_001170464	cyclin-dependent kinase 17	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
TMEM63C	NM_020431	transmembrane protein 63C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
IGSF11	NM_001015887	immunoglobulin superfamily, member 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR

RTKN2	NM_145307	rhotekin 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
RIN1	NM_004292	Ras and Rab interactor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
ANGPTL4	NM_001039667	angiopoietin-like 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
BRWD1	NM_001007246	bromodomain and WD repeat domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
COL6A6	NM_001102608	collagen, type VI, alpha 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
FBXL16	NM_153350	F-box and leucine-rich repeat protein 16	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
CES4A	NM_001190201	carboxylesterase 4A	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
RER1	NM_007033	RER1 retention in endoplasmic reticulum 1 homolog (S. cerevisiae)	0	0	0	0	2	0	2	0	hsa-miR-622	-0.05	N/A	Sites in UTR
SLC31A2	NM_001860	solute carrier family 31 (copper transporters), member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
IFIT2	NM_001547	interferon-induced protein with tetratricopeptide repeats 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
KCNJ13	NM_001172416	potassium inwardly-rectifying channel, subfamily J, member 13	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
PIPOX	NM_016518	pipecolic acid oxidase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SYVN1	NM_032431	synovial apoptosis inhibitor 1, synoviolin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
TCEANC2	NM_153035	transcription elongation factor A (SII) N-terminal and central domain containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
CBLN3	NM_001039771	cerebellin 3 precursor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
UHRF1	NM_001048201	ubiquitin-like with PHD and ring finger domains 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
AJAP1	NM_001042478	adherens junctions associated protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
PIK3CD	NM_005026	phosphoinositide-3-kinase, catalytic, delta polypeptide	0	0	0	0	2	0	1	1	hsa-miR-622	-0.05	N/A	Sites in UTR

ARAF	NM_001654	v-raf murine sarcoma 3611 viral oncogene homolog	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
DLST	NM_001933	dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
FCGR1A	NM_000566	Fc fragment of IgG, high affinity Ia, receptor (CD64)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
PTPN2	NM_002828	protein tyrosine phosphatase, non-receptor type 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SFTPB	NM_000542	surfactant protein B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
F2RL3	NM_003950	coagulation factor II (thrombin) receptor-like 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
CPEB4	NM_030627	cytoplasmic polyadenylation element binding protein 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
KNCN	NM_001097611	kinocilin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
KCTD7	NM_001167961	potassium channel tetramerisation domain containing 7	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
C16orf52	NM_001164579	chromosome 16 open reading frame 52	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
SYNGR1	NM_004711	synaptogyrin 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
FBXW8	NM_012174	F-box and WD repeat domain containing 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
SNX15	NM_013306	sorting nexin 15	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
IL34	NM_001172771	interleukin 34	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
C17orf28	NM_030630	chromosome 17 open reading frame 28	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
IRF2BP2	NM_001077397	interferon regulatory factor 2 binding protein 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.05	N/A	Sites in UTR
DMPK	NM_001081560	dystrophia myotonica-protein kinase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
STAC	NM_003149	SH3 and cysteine rich domain	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR

WWOX	NM_016373	WW domain containing oxidoreductase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ESRP1	NM_001034915	epithelial splicing regulatory protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
ZNF528	NM_032423	zinc finger protein 528	0	0	0	0	1	0	0	1	hsa-miR-622	-0.05	N/A	Sites in UTR
DCAF10	NM_024345	DDB1 and CUL4 associated factor 10	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
HSD3B7	NM_001142777	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
GAL3ST3	NM_033036	galactose-3-O-sulfotransferase 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
MYOZ3	NM_001122853	myozenin 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
C8orf73	NM_001100878	chromosome 8 open reading frame 73	0	0	0	0	1	0	1	0	hsa-miR-622	-0.05	N/A	Sites in UTR
DNAJC30	NM_032317	DnaJ (Hsp40) homolog, subfamily C, member 30	0	0	0	0	1	1	0	0	hsa-miR-622	-0.05	N/A	Sites in UTR
TP53RK	NM_033550	TP53 regulating kinase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
ARNT	NM_001197325	aryl hydrocarbon receptor nuclear translocator	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CAMKK2	NM_006549	calcium/calmodulin-dependent protein kinase kinase 2, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
RBBP9	NM_006606	retinoblastoma binding protein 9	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
DTWD1	NM_001144955	DTW domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
JHDM1D	NM_030647	jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
EDN2	NM_001956	endothelin 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
FAM115A	NM_001206938	family with sequence similarity 115, member A	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SEMA3G	NM_020163	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3G	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR

ZNF776	NM_173632	zinc finger protein 776	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
ATXN1L	NM_001137675	ataxin 1-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
USP31	NM_020718	ubiquitin specific peptidase 31	0	0	0	0	1	1	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
HNRNPA2B1	NM_002137	heterogeneous nuclear ribonucleoprotein A2/B1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
KIF3B	NM_004798	kinesin family member 3B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
YLPM1	NM_019589	YLP motif containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
BLK	NM_001715	B lymphoid tyrosine kinase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
LRP3	NM_002333	low density lipoprotein receptor-related protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
PPP2R1B	NM_001177562	protein phosphatase 2, regulatory subunit A, beta	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
SLC6A8	NM_001142805	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
EEF2K	NM_013302	eukaryotic elongation factor-2 kinase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
FKBP10	NM_021939	FK506 binding protein 10, 65 kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
ZNF483	NM_133464	zinc finger protein 483	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
GSG1L	NM_001109763	GSG1-like	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
RBM14	NM_001198836	RNA binding motif protein 14	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SF3A3	NM_006802	splicing factor 3a, subunit 3, 60kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SF3B3	NM_012426	splicing factor 3b, subunit 3, 130kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SEZ6L	NM_001184773	seizure related 6 homolog (mouse)-like	1	0	0	1	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR

ZBTB4	NM_001128833	zinc finger and BTB domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
THSD4	NM_024817	thrombospondin, type I, domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CACNA2D4	NM_172364	calcium channel, voltage-dependent, alpha 2/delta subunit 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
ORC4	NM_001190879	origin recognition complex, subunit 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
RAB5B	NM_002868	RAB5B, member RAS oncogene family	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
SH3BP5L	NM_030645	SH3-binding domain protein 5-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
SLC38A5	NM_033518	solute carrier family 38, member 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
CYP4F22	NM_173483	cytochrome P450, family 4, subfamily F, polypeptide 22	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
DCBLD2	NM_080927	discoidin, CUB and LCCL domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
FAM116B	NM_001001794	family with sequence similarity 116, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
MAPT	NM_001123066	microtubule-associated protein tau	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
TNFSF14	NM_003807	tumor necrosis factor (ligand) superfamily, member 14	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CDC42BPB	NM_006035	CDC42 binding protein kinase beta (DMPK-like)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
PALLD	NM_001166108	palladin, cytoskeletal associated protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
KIAA1467	NM_020853	KIAA1467	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
MTPN	NM_145808	myotrophin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
ETF1	NM_004730	eukaryotic translation termination factor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
MYO1E	NM_004998	myosin IE	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR

TOB2	NM_016272	transducer of ERBB2, 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
MIER2	NM_017550	mesoderm induction early response 1, family member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
UBAC2	NM_001144072	UBA domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
RBM41	NM_001171080	RNA binding motif protein 41	0	0	0	0	2	0	0	2	hsa-miR-622	-0.04	N/A	Sites in UTR
DCP2	NM_001242377	DCP2 decapping enzyme homolog (S. cerevisiae)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CACNB2	NM_000724	calcium channel, voltage-dependent, beta 2 subunit	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
MDFIC	NM_001166345	MyoD family inhibitor domain containing	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
NAV2	NM_001111018	neuron navigator 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
MOBKL1A	NM_173468	MOB1, Mps One Binder kinase activator-like 1A (yeast)	1	1	0	0	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
GPI	NM_000175	glucose-6-phosphate isomerase	0	0	0	0	2	0	2	0	hsa-miR-622	-0.04	N/A	Sites in UTR
ITGB1BP1	NM_004763	integrin beta 1 binding protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
TBC1D30	NM_015279	TBC1 domain family, member 30	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SFRP5	NM_003015	secreted frizzled-related protein 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
DSTYK	NM_015375	dual serine/threonine and tyrosine protein kinase	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
BBC3	NM_001127240	BCL2 binding component 3	1	0	1	0	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
NSFL1C	NM_001206736	NSFL1 (p97) cofactor (p47)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
PTBP2	NM_021190	polypyrimidine tract binding protein 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
MAPK1IP1L	NM_144578	mitogen-activated protein kinase 1 interacting protein 1-like	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR

FGFBP3	NM_152429	fibroblast growth factor binding protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
SLC7A2	NM_001008539	solute carrier family 7 (cationic amino acid transporter, y+ system), member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
C3orf19	NM_016474	chromosome 3 open reading frame 19	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
PHIP	NM_017934	pleckstrin homology domain interacting protein	1	0	0	1	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
STAMBP	NM_006463	STAM binding protein	0	0	0	0	1	1	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
RHOBTB3	NM_014899	Rho-related BTB domain containing 3	0	0	0	0	1	1	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
CNN1	NM_001299	calponin 1, basic, smooth muscle	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
NFE2L1	NM_003204	nuclear factor (erythroid-derived 2)-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
CD164	NM_001142401	CD164 molecule, sialomucin	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
SCD5	NM_001037582	stearoyl-CoA desaturase 5	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
IFNAR1	NM_000629	interferon (alpha, beta and omega) receptor 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
INPP5B	NM_005540	inositol polyphosphate-5-phosphatase, 75kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SLC17A4	NM_005495	solute carrier family 17 (sodium phosphate), member 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
DUSP16	NM_030640	dual specificity phosphatase 16	1	0	0	1	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
PLA2G4E	NM_001206670	phospholipase A2, group IVE	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
SRRM3	NM_001110199	serine/arginine repetitive matrix 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
FBXW2	NM_012164	F-box and WD repeat domain containing 2	0	0	0	0	1	1	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
TSPYL5	NM_033512	TSPY-like 5	0	0	0	0	1	1	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR

CNGB1	NM_001297	cyclic nucleotide gated channel beta 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
PRKAA2	NM_006252	protein kinase, AMP-activated, alpha 2 catalytic subunit	1	0	1	0	0	0	0	0	hsa-miR-622	-0.04	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-622	-0.04	N/A	Sites in UTR
NLN	NM_020726	neurolysin (metallopeptidase M3 family)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
PRRG4	NM_024081	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
FAM102A	NM_001035254	family with sequence similarity 102, member A	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
RIC3	NM_001135109	resistance to inhibitors of cholinesterase 3 homolog (C. elegans)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
MYCBP	NM_012333	c-myc binding protein	1	0	0	1	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
ZNF701	NM_001172655	zinc finger protein 701	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
PAPD4	NM_001114393	PAP associated domain containing 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
C14orf182	NM_001012706	chromosome 14 open reading frame 182	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CTDSPL2	NM_016396	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase like 2	1	0	1	0	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
SYAP1	NM_032796	synapse associated protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
GNL1	NM_005275	guanine nucleotide binding protein-like 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
ATXN3	NM_001127696	ataxin 3	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CALN1	NM_001017440	calneuron 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
FZD1	NM_003505	frizzled family receptor 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
MPDU1	NM_004870	mannose-P-dolichol utilization defect 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR

TRIM62	NM_018207	tripartite motif containing 62	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
ZKSCAN2	NM_001012981	zinc finger with KRAB and SCAN domains 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CACNA1D	NM_000720	calcium channel, voltage-dependent, L type, alpha 1D subunit	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
ZNF747	NM_023931	zinc finger protein 747	1	0	1	0	0	0	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
TIGD6	NM_030953	tigger transposable element derived 6	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
C16orf54	NM_175900	chromosome 16 open reading frame 54	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
DLG2	NM_001142699	discs, large homolog 2 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-622	-0.04	N/A	Sites in UTR
UBIAD1	NM_013319	UbiA prenyltransferase domain containing 1	0	0	0	0	1	1	0	0	hsa-miR-622	-0.04	N/A	Sites in UTR
DACH1	NM_004392	dachshund homolog 1 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
PRKACB	NM_001242857	protein kinase, cAMP-dependent, catalytic, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
RP2	NM_006915	retinitis pigmentosa 2 (X-linked recessive)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
UBE2R2	NM_017811	ubiquitin-conjugating enzyme E2R 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
PSAPL1	NM_001085382	prosaposin-like 1 (gene/pseudogene)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.04	N/A	Sites in UTR
CTSH	NM_004390	cathepsin H	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
DGCR14	NM_022719	DiGeorge syndrome critical region gene 14	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
GAB2	NM_012296	GRB2-associated binding protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
UBN1	NM_001079514	ubinuclein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
ZC3H12C	NM_033390	zinc finger CCCH-type containing 12C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR

C19orf25	NM_152482	chromosome 19 open reading frame 25	0	0	0	0	1	0	1	0	hsa-miR-622	-0.04	N/A	Sites in UTR
TP73	NM_001126240	tumor protein p73	0	0	0	0	1	1	0	0	hsa-miR-622	-0.03	N/A	Sites in UTR
CD36	NM_001001548	CD36 molecule (thrombospondin receptor)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
KDR	NM_002253	kinase insert domain receptor (a type III receptor tyrosine kinase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
MAP3K9	NM_033141	mitogen-activated protein kinase kinase kinase 9	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ZFYVE16	NM_001105251	zinc finger, FYVE domain containing 16	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
SLC39A9	NM_018375	solute carrier family 39 (zinc transporter), member 9	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ATG9A	NM_001077198	ATG9 autophagy related 9 homolog A (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
SGIP1	NM_032291	SH3-domain GRB2-like (endophilin) interacting protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
GLP1R	NM_002062	glucagon-like peptide 1 receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
MRAS	NM_001085049	muscle RAS oncogene homolog	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
ACTR8	NM_022899	ARP8 actin-related protein 8 homolog (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
DUSP18	NM_152511	dual specificity phosphatase 18	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
DAB2IP	NM_032552	DAB2 interacting protein	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
LARP4	NM_001170803	La ribonucleoprotein domain family, member 4	0	0	0	0	1	1	0	0	hsa-miR-622	-0.03	N/A	Sites in UTR
ABCC1	NM_004996	ATP-binding cassette, sub-family C (CFTR/MRP), member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
SYP	NM_003179	synaptophysin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
MOSPD1	NM_019556	motile sperm domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR

TNRC18	NM_001080495	trinucleotide repeat containing 18	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
CDK2	NM_001798	cyclin-dependent kinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
WNT7B	NM_058238	wingless-type MMTV integration site family, member 7B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ProSAPiP1	NM_014731	ProSAPiP1 protein	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
POLD3	NM_006591	polymerase (DNA-directed), delta 3, accessory subunit	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
C2orf88	NM_001042519	chromosome 2 open reading frame 88	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
FXR1	NM_001013438	fragile X mental retardation, autosomal homolog 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
CA5B	NM_007220	carbonic anhydrase VB, mitochondrial	1	0	1	0	0	0	0	0	hsa-miR-622	-0.03	N/A	Sites in UTR
REXO1L1	NM_172239	REX1, RNA exonuclease 1 homolog (S. cerevisiae)-like 1	0	0	0	0	2	0	1	1	hsa-miR-622	-0.03	N/A	Sites in UTR
C11orf58	NM_014267	chromosome 11 open reading frame 58	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
KIAA1755	NM_001029864	KIAA1755	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
METTL2A	NM_181725	methyltransferase like 2A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
SH2B3	NM_005475	SH2B adaptor protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
IKZF1	NM_001220765	IKAROS family zinc finger 1 (Ikaros)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
SLC24A2	NM_001193288	solute carrier family 24 (sodium/potassium/calcium exchanger), member 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
TMEM135	NM_001168724	transmembrane protein 135	0	0	0	0	2	0	1	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ADRA2B	NM_000682	adrenergic, alpha-2B-, receptor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
RIPK1	NM_003804	receptor (TNFRSF)-interacting serine-threonine kinase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR

HOXB13	NM_006361	homeobox B13	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	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-622	-0.03	N/A	Sites in UTR
NCOR2	NM_001077261	nuclear receptor corepressor 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
GPRC5B	NM_016235	G protein-coupled receptor, family C, group 5, member B	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
APOLD1	NM_001130415	apolipoprotein L domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
NUDT4	NM_019094	nudix (nucleoside diphosphate linked moiety X)-type motif 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ZNF654	NM_018293	zinc finger protein 654	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
SLC35E3	NM_018656	solute carrier family 35, member E3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
EIF5A2	NM_020390	eukaryotic translation initiation factor 5A2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ARF1	NM_001024226	ADP-ribosylation factor 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
TPCN1	NM_001143819	two pore segment channel 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
CYP26B1	NM_019885	cytochrome P450, family 26, subfamily B, polypeptide 1	1	0	1	0	0	0	0	0	hsa-miR-622	-0.03	N/A	Sites in UTR
NPAS4	NM_178864	neuronal PAS domain protein 4	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
ENG	NM_000118	endoglin	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
FOXP1	NM_032682	forkhead box P1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
TATDN2	NM_014760	TatD DNase domain containing 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
DRAM1	NM_018370	DNA-damage regulated autophagy modulator 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
INTS2	NM_020748	integrator complex subunit 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR

SEC62	NM_003262	SEC62 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
AMMECR1	NM_001025580	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region gene 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
CCDC88C	NM_001080414	coiled-coil domain containing 88C	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
CORO1C	NM_014325	coronin, actin binding protein, 1C	0	0	0	0	2	0	0	2	hsa-miR-622	-0.03	N/A	Sites in UTR
OCRL	NM_000276	oculocerebrorenal syndrome of Lowe	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
PTGIS	NM_000961	prostaglandin I2 (prostacyclin) synthase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
UNC5B	NM_170744	unc-5 homolog B (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
SMG1	NM_015092	smg-1 homolog, phosphatidylinositol 3-kinase-related kinase (C. elegans)	0	0	0	0	2	0	0	2	hsa-miR-622	-0.03	N/A	Sites in UTR
CYP27C1	NM_001001665	cytochrome P450, family 27, subfamily C, polypeptide 1	0	0	0	0	2	0	0	2	hsa-miR-622	-0.03	N/A	Sites in UTR
BMS1	NM_014753	BMS1 homolog, ribosome assembly protein (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
SF3A1	NM_001005409	splicing factor 3a, subunit 1, 120kDa	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
SIRPB2	NM_001122962	signal-regulatory protein beta 2	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
EYS	NM_001142801	eyes shut homolog (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.03	N/A	Sites in UTR
ITGA11	NM_001004439	integrin, alpha 11	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
TMEM213	NM_001085429	transmembrane protein 213	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
NWD1	NM_001007525	NACHT and WD repeat domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
ZCCHC16	NM_001004308	zinc finger, CCHC domain containing 16	0	0	0	0	1	0	0	1	hsa-miR-622	-0.03	N/A	Sites in UTR
RRM2B	NM_001172477	ribonucleotide reductase M2 B (TP53 inducible)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR

GABRB3	NM_000814	gamma-aminobutyric acid (GABA) A receptor, beta 3	0	0	0	0	2	0	0	2	hsa-miR-622	-0.02	N/A	Sites in UTR
SYNPO2L	NM_001114133	synaptopodin 2-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
SPIN3	NM_001010862	spindlin family, member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
ADORA2A	NM_000675	adenosine A2a receptor	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR
TLX3	NM_021025	T-cell leukemia homeobox 3	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR
TTC23	NM_001040655	tetratricopeptide repeat domain 23	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR
SCARB2	NM_001204255	scavenger receptor class B, member 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
IL1R1	NM_000877	interleukin 1 receptor, type I	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
LTBP3	NM_001130144	latent transforming growth factor beta binding protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
VHL	NM_000551	von Hippel-Lindau tumor suppressor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
ATP8A1	NM_001105529	ATPase, aminophospholipid transporter (APLT), class I, type 8A, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
TGIF2	NM_001199513	TGFB-induced factor homeobox 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
OTX1	NM_001199770	orthodenticle homeobox 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR
PML	NM_033238	promyelocytic leukemia	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR
ZIC3	NM_003413	Zic family member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
ANKRD22	NM_144590	ankyrin repeat domain 22	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
CELSR1	NM_014246	cadherin, EGF LAG seven-pass G-type receptor 1 (flamingo homolog, Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR
CTNNBIP1	NM_001012329	catenin, beta interacting protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	-0.02	N/A	Sites in UTR

CA7	NM_001014435	carbonic anhydrase VII	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
MAP3K3	NM_002401	mitogen-activated protein kinase kinase kinase 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
RABEP1	NM_001083585	rabaptin, RAB GTPase binding effector protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
PCYOX1	NM_016297	prenylcysteine oxidase 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
FAM46C	NM_017709	family with sequence similarity 46, member C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
SLITRK4	NM_001184749	SLIT and NTRK-like family, member 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
BRWD3	NM_153252	bromodomain and WD repeat domain containing 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
PKNOX1	NM_004571	PBX/knotted 1 homeobox 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
RNF185	NM_001135825	ring finger protein 185	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
FRYL	NM_015030	FRY-like	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
ARRB1	NM_004041	arrestin, beta 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
NAMPT	NM_005746	nicotinamide phosphoribosyltransferase	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
RAB4B	NM_016154	RAB4B, member RAS oncogene family	1	0	0	1	0	0	0	0	hsa-miR-622	-0.02	N/A	Sites in UTR
ARHGAP31	NM_020754	Rho GTPase activating protein 31	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
ADIPOR2	NM_024551	adiponectin receptor 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
VAV3	NM_001079874	vav 3 guanine nucleotide exchange factor	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
TGM2	NM_004613	transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
CUL3	NM_003590	cullin 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR

SCAMP5	NM_001178111	secretory carrier membrane protein 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
ANKRD23	NM_144994	ankyrin repeat domain 23	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
PDE3B	NM_000922	phosphodiesterase 3B, cGMP-inhibited	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
PI15	NM_015886	peptidase inhibitor 15	0	0	0	0	1	0	0	1	hsa-miR-622	-0.02	N/A	Sites in UTR
OPA1	NM_015560	optic atrophy 1 (autosomal dominant)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
CNTN2	NM_005076	contactin 2 (axonal)	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
AMOTL2	NM_016201	angiomotin like 2	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
ARID2	NM_152641	AT rich interactive domain 2 (ARID, RFX-like)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.01	N/A	Sites in UTR
PLIN4	NM_001080400	perilipin 4	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
TRAK1	NM_014965	trafficking protein, kinesin binding 1	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
KIAA1456	NM_001099677	KIAA1456	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
KIF3C	NM_002254	kinesin family member 3C	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
ANKH	NM_054027	ankylosis, progressive homolog (mouse)	1	0	0	1	0	0	0	0	hsa-miR-622	-0.01	N/A	Sites in UTR
FAM73A	NM_198549	family with sequence similarity 73, member A	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
PPP3R2	NM_147180	protein phosphatase 3, regulatory subunit B, beta	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
CPSF6	NM_007007	cleavage and polyadenylation specific factor 6, 68kDa	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
RBM15B	NM_013286	RNA binding motif protein 15B	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
TM7SF3	NM_016551	transmembrane 7 superfamily member 3	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR

FNDC5	NM_001171940	fibronectin type III domain containing 5	0	0	0	0	1	0	0	1	hsa-miR-622	-0.01	N/A	Sites in UTR
TP53INP2	NM_021202	tumor protein p53 inducible nuclear protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
VPS13C	NM_001018088	vacuolar protein sorting 13 homolog C (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FAM199X	NM_207318	family with sequence similarity 199, X-linked	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ADCY1	NM_021116	adenylate cyclase 1 (brain)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AK2	NM_001199199	adenylate kinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AK4	NM_001005353	adenylate kinase 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
BDNF	NM_001143805	brain-derived neurotrophic factor	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RUNX1T1	NM_001198625	runt-related transcription factor 1; translocated to, 1 (cyclin D-related)	1	0	0	1	0	0	0	0	hsa-miR-622	> -0.01	N/A	Sites in UTR
CEBPG	NM_001806	CCAAT/enhancer binding protein (C/EBP), gamma	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
COX15	NM_004376	COX15 homolog, cytochrome c oxidase assembly protein (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CREBBP	NM_001079846	CREB binding protein	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DBT	NM_001918	dihydrolipoamide branched chain transacylase E2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.01	N/A	Sites in UTR
DUSP3	NM_004090	dual specificity phosphatase 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
E2F3	NM_001949	E2F transcription factor 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
EMP2	NM_001424	epithelial membrane protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ENSA	NM_207043	endosulfine alpha	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
EPB41L1	NM_012156	erythrocyte membrane protein band 4.1-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

ETV1	NM_001163147	ets variant 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NR5A2	NM_003822	nuclear receptor subfamily 5, group A, member 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GABRA4	NM_000809	gamma-aminobutyric acid (GABA) A receptor, alpha 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
B4GALT1	NM_001497	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ARHGAP35	NM_004491	Rho GTPase activating protein 35	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
HK2	NM_000189	hexokinase 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
HNF4G	NM_004133	hepatocyte nuclear factor 4, gamma	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
HNRNPU	NM_004501	heterogeneous nuclear ribonucleoprotein U (scaffold attachment factor A)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
IGF1R	NM_000875	insulin-like growth factor 1 receptor	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
IVD	NM_001159508	isovaleryl-CoA dehydrogenase	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KCNA1	NM_000217	potassium voltage-gated channel, shaker-related subfamily, member 1 (episodic ataxia with myokymia)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KCNQ3	NM_001204824	potassium voltage-gated channel, KQT-like subfamily, member 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KCNS1	NM_002251	potassium voltage-gated channel, delayed-rectifier, subfamily S, member 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
LEP	NM_000230	leptin	1	0	0	1	0	0	0	0	hsa-miR-622	> -0.01	N/A	Sites in UTR
LPP	NM_001167671	LIM domain containing preferred translocation partner in lipoma	1	0	0	1	0	0	0	0	hsa-miR-622	> -0.01	N/A	Sites in UTR
LRP6	NM_002336	low density lipoprotein receptor-related protein 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SMAD3	NM_001145102	SMAD family member 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MAP1B	NM_005909	microtubule-associated protein 1B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

MGAT3	NM_001098270	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MKI67	NM_001145966	antigen identified by monoclonal antibody Ki-67	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MYO6	NM_004999	myosin VI	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NFATC4	NM_001136022	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NPR3	NM_000908	natriuretic peptide receptor C/guanylate cyclase C (atrionatriuretic peptide receptor C)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PCDH7	NM_001173523	protocadherin 7	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PDE4C	NM_000923	phosphodiesterase 4C, cAMP-specific	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PDGFRA	NM_006206	platelet-derived growth factor receptor, alpha polypeptide	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PGR	NM_000926	progesterone receptor	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PLCB3	NM_000932	phospholipase C, beta 3 (phosphatidylinositol-specific)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
POLH	NM_006502	polymerase (DNA directed), eta	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MAPK10	NM_002753	mitogen-activated protein kinase 10	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PTGER3	NM_198715	prostaglandin E receptor 3 (subtype EP3)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PTGS1	NM_000962	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RORA	NM_002943	RAR-related orphan receptor A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RPL27A	NM_000990	ribosomal protein L27a	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	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	hsa-miR-622	> -0.01	N/A	Sites in UTR
ATXN7	NM_000333	ataxin 7	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

SOX12	NM_006943	SRY (sex determining region Y)-box 12	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SP1	NM_003109	Sp1 transcription factor	1	0	0	1	0	0	0	0	hsa-miR-622	> -0.01	N/A	Sites in UTR
SPN	NM_001030288	sialophorin	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MED22	NM_181491	mediator complex subunit 22	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	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-622	> -0.01	N/A	Sites in UTR
NR2C2	NM_003298	nuclear receptor subfamily 2, group C, member 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
UMPS	NM_000373	uridine monophosphate synthetase	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
UQCRB	NM_001199975	ubiquinol-cytochrome c reductase binding protein	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZFX	NM_001178084	zinc finger protein, X-linked	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
EVI5	NM_005665	ecotropic viral integration site 5	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ST8SIA4	NM_005668	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
BRAP	NM_006768	BRCA1 associated protein	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FZD4	NM_012193	frizzled family receptor 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PPFIA4	NM_015053	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GAS7	NM_001130831	growth arrest-specific 7	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TNKS	NM_003747	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CACNA1I	NM_001003406	calcium channel, voltage-dependent, T type, alpha 1I subunit	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SEC22C	NM_032970	SEC22 vesicle trafficking protein homolog C (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

XPR1	NM_001135669	xenotropic and polytropic retrovirus receptor 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
STK17B	NM_004226	serine/threonine kinase 17b	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
H6PD	NM_004285	hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
HS2ST1	NM_012262	heparan sulfate 2-O-sulfotransferase 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FAM53B	NM_014661	family with sequence similarity 53, member B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
EDEM1	NM_014674	ER degradation enhancer, mannosidase alpha-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ULK2	NM_014683	unc-51-like kinase 2 (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FAM131B	NM_001031690	family with sequence similarity 131, member B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
UTP14C	NM_021645	UTP14, U3 small nucleolar ribonucleoprotein, homolog C (yeast)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MLEC	NM_014730	malectin	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ATG13	NM_001142673	ATG13 autophagy related 13 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RNF144A	NM_014746	ring finger protein 144A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PLEKHM1	NM_014798	pleckstrin homology domain containing, family M (with RUN domain) member 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
EPM2AIP1	NM_014805	EPM2A (laforin) interacting protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PIGK	NM_005482	phosphatidylinositol glycan anchor biosynthesis, class K	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
APC2	NM_005883	adenomatosis polyposis coli 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TLR6	NM_006068	toll-like receptor 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SPON1	NM_006108	spondin 1, extracellular matrix protein	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

CRTAP	NM_006371	cartilage associated protein	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TGOLN2	NM_001206840	trans-golgi network protein 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
EXOC5	NM_006544	exocyst complex component 5	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PNMA2	NM_007257	paraneoplastic antigen MA2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZBTB6	NM_006626	zinc finger and BTB domain containing 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PDE10A	NM_001130690	phosphodiesterase 10A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FGL2	NM_006682	fibrinogen-like 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PTPRT	NM_007050	protein tyrosine phosphatase, receptor type, T	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GALNT6	NM_007210	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AAK1	NM_014911	AP2 associated kinase 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ATG14	NM_014924	ATG14 autophagy related 14 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ELL2	NM_012081	elongation factor, RNA polymerase II, 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NT5C2	NM_001134373	5'-nucleotidase, cytosolic II	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KLHDC10	NM_014997	kelch domain containing 10	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZNF609	NM_015042	zinc finger protein 609	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CDK19	NM_015076	cyclin-dependent kinase 19	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NFASC	NM_001005388	neurofascin	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
HIC2	NM_015094	hypermethylated in cancer 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

LPIN1	NM_145693	lipin 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
LARP4B	NM_015155	La ribonucleoprotein domain family, member 4B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TRIM2	NM_001130067	tripartite motif containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TTC28	NM_001145418	tetratricopeptide repeat domain 28	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KIAA1045	NM_015297	KIAA1045	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AHCYL2	NM_001130720	adenosylhomocysteinase-like 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	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	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CARHSP1	NM_001042476	calcium regulated heat stable protein 1, 24kDa	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KPNA6	NM_012316	karyopherin alpha 6 (importin alpha 7)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C3orf17	NM_015412	chromosome 3 open reading frame 17	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NSL1	NM_001042549	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CNNM1	NM_020348	cyclin M1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AP3M1	NM_012095	adaptor-related protein complex 3, mu 1 subunit	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PDE7B	NM_018945	phosphodiesterase 7B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SLCO3A1	NM_013272	solute carrier organic anion transporter family, member 3A1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMOD3	NM_014547	tropomodulin 3 (ubiquitous)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SLC39A3	NM_213568	solute carrier family 39 (zinc transporter), member 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NOX4	NM_001143836	NADPH oxidase 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

MYEF2	NM_016132	myelin expression factor 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZDHHC9	NM_001008222	zinc finger, DHHC-type containing 9	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PHF21A	NM_001101802	PHD finger protein 21A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CHIC1	NM_001039840	cysteine-rich hydrophobic domain 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SHC3	NM_016848	SHC (Src homology 2 domain containing) transforming protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KCNK10	NM_021161	potassium channel, subfamily K, member 10	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMEM106B	NM_001134232	transmembrane protein 106B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RSBN1	NM_018364	round spermatid basic protein 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SMU1	NM_018225	smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
VPS53	NM_001128159	vacuolar protein sorting 53 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AGPAT5	NM_018361	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
LIN7C	NM_018362	lin-7 homolog C (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SYNJ2BP	NM_018373	synaptojanin 2 binding protein	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MED29	NM_017592	mediator complex subunit 29	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMEM127	NM_001193304	transmembrane protein 127	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PARVA	NM_018222	parvin, alpha	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PAG1	NM_018440	phosphoprotein associated with glycosphingolipid microdomains 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C1orf183	NM_019099	chromosome 1 open reading frame 183	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

UGGT1	NM_020120	UDP-glucose glycoprotein glucosyltransferase 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TWSG1	NM_020648	twisted gastrulation homolog 1 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C15orf17	NM_020447	chromosome 15 open reading frame 17	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NIPAL3	NM_020448	NIPA-like domain containing 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KIAA1143	NM_020696	KIAA1143	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SLC12A5	NM_001134771	solute carrier family 12 (potassium/chloride transporter), member 5	1	0	0	1	0	0	0	0	hsa-miR-622	> -0.01	N/A	Sites in UTR
CNOT6	NM_015455	CCR4-NOT transcription complex, subunit 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RPTOR	NM_001163034	regulatory associated protein of MTOR, complex 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TRMT5	NM_020810	TRM5 tRNA methyltransferase 5 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
WDFY1	NM_020830	WD repeat and FYVE domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DIP2B	NM_173602	DIP2 disco-interacting protein 2 homolog B (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RANBP10	NM_020850	RAN binding protein 10	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KIAA1609	NM_020947	KIAA1609	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GNB4	NM_021629	guanine nucleotide binding protein (G protein), beta polypeptide 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
LMBR1	NM_022458	limb region 1 homolog (mouse)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZFP106	NM_022473	zinc finger protein 106 homolog (mouse)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CSMD1	NM_033225	CUB and Sushi multiple domains 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NUCKS1	NM_022731	nuclear casein kinase and cyclin-dependent kinase substrate 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

UBE2Z	NM_023079	ubiquitin-conjugating enzyme E2Z	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KCTD15	NM_024076	potassium channel tetramerisation domain containing 15	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMEM185B	NM_024121	transmembrane protein 185B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CENPO	NM_001199803	centromere protein O	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ATP13A3	NM_024524	ATPase type 13A3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
METTL8	NM_024770	methyltransferase like 8	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CYBRD1	NM_001127383	cytochrome b reductase 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
WDR82	NM_025222	WD repeat domain 82	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AKNA	NM_030767	AT-hook transcription factor	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
APOL6	NM_030641	apolipoprotein L, 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AIF1L	NM_001185095	allograft inflammatory factor 1-like	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DNAL1	NM_001201366	dynein, axonemal, light chain 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MARVELD1	NM_031484	MARVEL domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMTC1	NM_001193451	transmembrane and tetratricopeptide repeat containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KATNAL1	NM_001014380	katanin p60 subunit A-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DCTN5	NM_001199743	dynactin 5 (p25)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DIXDC1	NM_001037954	DIX domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GTPBP10	NM_001042717	GTP-binding protein 10 (putative)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

FCHSD1	NM_033449	FCH and double SH3 domains 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FMNL3	NM_175736	formin-like 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SYT12	NM_001177880	synaptotagmin XII	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GALNT13	NM_052917	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 13 (GalNAc-T13)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
OSBPL6	NM_001201480	oxysterol binding protein-like 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C1QTNF3	NM_030945	C1q and tumor necrosis factor related protein 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NUS1	NM_138459	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S. cerevisiae)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GRIN3A	NM_133445	glutamate receptor, ionotropic, N-methyl-D-aspartate 3A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
THEM4	NM_053055	thioesterase superfamily member 4	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RAB3IP	NM_001024647	RAB3A interacting protein (rabin3)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GIPC3	NM_133261	GIPC PDZ domain containing family, member 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KLF17	NM_173484	Kruppel-like factor 17	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
UBE2QL1	NM_001145161	ubiquitin-conjugating enzyme E2Q family-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CD109	NM_001159587	CD109 molecule	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
AGPAT6	NM_178819	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ASB6	NM_001202403	ankyrin repeat and SOCS box containing 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DUSP19	NM_001142314	dual specificity phosphatase 19	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CCBE1	NM_133459	collagen and calcium binding EGF domains 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

ZNF578	NM_001099694	zinc finger protein 578	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DIRAS1	NM_145173	DIRAS family, GTP-binding RAS-like 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SYT6	NM_205848	synaptotagmin VI	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SMYD1	NM_198274	SET and MYND domain containing 1	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
FAM84A	NM_145175	family with sequence similarity 84, member A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
GPR155	NM_001033045	G protein-coupled receptor 155	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
CCDC50	NM_174908	coiled-coil domain containing 50	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
THAP6	NM_144721	THAP domain containing 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SLC2A12	NM_145176	solute carrier family 2 (facilitated glucose transporter), member 12	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMEM229B	NM_182526	transmembrane protein 229B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C18orf54	NM_173529	chromosome 18 open reading frame 54	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
DENND1B	NM_001195215	DENN/MADD domain containing 1B	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
PRICKLE2	NM_198859	prickle homolog 2 (Drosophila)	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RASSF6	NM_177532	Ras association (RalGDS/AF-6) domain family member 6	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TMEM184A	NM_001097620	transmembrane protein 184A	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C9orf25	NM_001184940	chromosome 9 open reading frame 25	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C3orf58	NM_001134470	chromosome 3 open reading frame 58	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SENP5	NM_152699	SUMO1/sentrin specific peptidase 5	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR

C11orf45	NM_145013	chromosome 11 open reading frame 45	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NAPEPLD	NM_001122838	N-acyl phosphatidylethanolamine phospholipase D	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
MSRB3	NM_001031679	methionine sulfoxide reductase B3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
NPNT	NM_001033047	nephronectin	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C19orf54	NM_198476	chromosome 19 open reading frame 54	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
RABL3	NM_173825	RAB, member of RAS oncogene family-like 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
SH3RF3	NM_001099289	SH3 domain containing ring finger 3	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZNF829	NM_001037232	zinc finger protein 829	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ILDR2	NM_199351	immunoglobulin-like domain containing receptor 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
TLCD2	NM_001164407	TLC domain containing 2	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
C6orf35	NM_018452	chromosome 6 open reading frame 35	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ISPD	NM_001101417	isoprenoid synthase domain containing	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
ZBTB42	NM_001137601	zinc finger and BTB domain containing 42	0	0	0	0	1	0	0	1	hsa-miR-622	> -0.01	N/A	Sites in UTR
KLHL21	NM_014851	kelch-like 21 (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ABR	NM_001092	active BCR-related gene	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ADCY5	NM_001199642	adenylate cyclase 5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
AHR	NM_001621	aryl hydrocarbon receptor	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ARCN1	NM_001142281	archain 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

ATP6V1C1	NM_001695	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CACNA1C	NM_000719	calcium channel, voltage-dependent, L type, alpha 1C subunit	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CAV3	NM_033337	caveolin 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CCND2	NM_001759	cyclin D2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CDK6	NM_001145306	cyclin-dependent kinase 6	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CFL2	NM_021914	cofilin 2 (muscle)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CRY2	NM_001127457	cryptochrome 2 (photolyase-like)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DMWD	NM_004943	dystrophia myotonica, WD repeat containing	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DUSP4	NM_001394	dual specificity phosphatase 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MEGF9	NM_001080497	multiple EGF-like-domains 9	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ELN	NM_000501	elastin	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MARK2	NM_001039469	MAP/microtubule affinity-regulating kinase 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FANCC	NM_000136	Fanconi anemia, complementation group C	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FANCF	NM_022725	Fanconi anemia, complementation group F	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FBN1	NM_000138	fibrillin 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FECH	NM_000140	ferrochelatase	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FGF2	NM_002006	fibroblast growth factor 2 (basic)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FLT1	NM_001159920	fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

GFRA1	NM_001145453	GDNF family receptor alpha 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GNRHR	NM_000406	gonadotropin-releasing hormone receptor	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GRIK3	NM_000831	glutamate receptor, ionotropic, kainate 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
AGFG2	NM_006076	ArfGAP with FG repeats 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
HUS1	NM_004507	HUS1 checkpoint homolog (S. pombe)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KCNC4	NM_001039574	potassium voltage-gated channel, Shaw-related subfamily, member 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KCNH1	NM_002238	potassium voltage-gated channel, subfamily H (eag-related), member 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KCNN1	NM_002248	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
LOX	NM_001178102	lysyl oxidase	1	0	1	0	0	0	0	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
LSAMP	NM_002338	limbic system-associated membrane protein	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
AFF1	NM_001166693	AF4/FMR2 family, member 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MPL	NM_005373	myeloproliferative leukemia virus oncogene	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NCAM1	NM_001076682	neural cell adhesion molecule 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NFIX	NM_002501	nuclear factor I/X (CCAAT-binding transcription factor)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NMT1	NM_021079	N-myristoyltransferase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PAX6	NM_000280	paired box 6	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PDE6A	NM_000440	phosphodiesterase 6A, cGMP-specific, rod, alpha	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PDK3	NM_001142386	pyruvate dehydrogenase kinase, isozyme 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

PLXNA2	NM_025179	plexin A2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PVRL1	NM_002855	poliovirus receptor-related 1 (herpesvirus entry mediator C)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
THRB	NM_000461	thyroid hormone receptor, beta (erythroblastic leukemia viral (v-erb-a) oncogene homolog 2, avian)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FZD5	NM_003468	frizzled family receptor 5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CCDC6	NM_005436	coiled-coil domain containing 6	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ST8SIA2	NM_006011	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SNN	NM_003498	stannin	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PDXK	NM_003681	pyridoxal (pyridoxine, vitamin B6) kinase	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
HS6ST1	NM_004807	heparan sulfate 6-O-sulfotransferase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
RAB36	NM_004914	RAB36, member RAS oncogene family	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZNF516	NM_014643	zinc finger protein 516	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
LPIN2	NM_014646	lipin 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
LRRC14	NM_014665	leucine rich repeat containing 14	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
TRAM2	NM_012288	translocation associated membrane protein 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SNPH	NM_014723	syntaphilin	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KIAA0513	NM_014732	KIAA0513	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MATR3	NM_001194954	matrin 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SCRN1	NM_001145513	secernin 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

DNAJC6	NM_014787	DnaJ (Hsp40) homolog, subfamily C, member 6	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
URB1	NM_014825	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZBTB39	NM_014830	zinc finger and BTB domain containing 39	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SRGAP3	NM_001033117	SLIT-ROBO Rho GTPase activating protein 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ATP9A	NM_006045	ATPase, class II, type 9A	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
RASA4	NM_001079877	RAS p21 protein activator 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
WASF2	NM_001201404	WAS protein family, member 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DCAF7	NM_005828	DDB1 and CUL4 associated factor 7	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
9-Sep	NM_001113491	septin 9	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
TSPAN9	NM_001168320	tetraspanin 9	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FAM107A	NM_001076778	family with sequence similarity 107, member A	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ATXN2L	NM_007245	ataxin 2-like	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ANKRD6	NM_001242809	ankyrin repeat domain 6	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
UBOX5	NM_014948	U-box domain containing 5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
EXPH5	NM_015065	exophilin 5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ARHGAP26	NM_001135608	Rho GTPase activating protein 26	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MCF2L2	NM_015078	MCF.2 cell line derived transforming sequence-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GRAMD4	NM_015124	GRAM domain containing 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

NCDN	NM_001014839	neurochondrin	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FBXO28	NM_001136115	F-box protein 28	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
IQCE	NM_001100390	IQ motif containing E	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DNAJC16	NM_015291	DnaJ (Hsp40) homolog, subfamily C, member 16	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
HAUS5	NM_015302	HAUS augmin-like complex, subunit 5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PSD3	NM_015310	pleckstrin and Sec7 domain containing 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	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-622	> -0.02	N/A	Sites in UTR
TTC9	NM_015351	tetratricopeptide repeat domain 9	1	0	1	0	0	0	0	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZNF346	NM_012279	zinc finger protein 346	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SPATS2L	NM_001100422	spermatogenesis associated, serine-rich 2-like	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C1orf144	NM_001114600	chromosome 1 open reading frame 144	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CCDC69	NM_015621	coiled-coil domain containing 69	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CNNM3	NM_017623	cyclin M3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
AFF4	NM_014423	AF4/FMR2 family, member 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NDOR1	NM_001144026	NADPH dependent diflavin oxidoreductase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GPKOW	NM_015698	G patch domain and KOW motifs	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
HIPK2	NM_001113239	homeodomain interacting protein kinase 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SOX8	NM_014587	SRY (sex determining region Y)-box 8	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

IL21R	NM_021798	interleukin 21 receptor	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SEPSECS	NM_016955	Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GDE1	NM_016641	glycerophosphodiester phosphodiesterase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KLF13	NM_015995	Kruppel-like factor 13	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C21orf91	NM_001100420	chromosome 21 open reading frame 91	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
WNT4	NM_030761	wingless-type MMTV integration site family, member 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
TBC1D13	NM_018201	TBC1 domain family, member 13	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CRLS1	NM_001127458	cardiolipin synthase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
BNC2	NM_017637	basonuclin 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ALKBH5	NM_017758	alkB, alkylation repair homolog 5 (E. coli)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PTCD3	NM_017952	Pentatricopeptide repeat domain 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PPP1R9A	NM_001166160	protein phosphatase 1, regulatory (inhibitor) subunit 9A	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MCTP2	NM_001159643	multiple C2 domains, transmembrane 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SPPL2B	NM_001077238	signal peptide peptidase-like 2B	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
RALGAPB	NM_020336	Ral GTPase activating protein, beta subunit (non-catalytic)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DOLPP1	NM_001135917	dolichyl pyrophosphate phosphatase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KIAA1244	NM_020340	KIAA1244	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KIAA1462	NM_020848	KIAA1462	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

GPR107	NM_001136557	G protein-coupled receptor 107	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
HRH4	NM_001143828	histamine receptor H4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NAPB	NM_022080	N-ethylmaleimide-sensitive factor attachment protein, beta	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CCDC90A	NM_001031713	coiled-coil domain containing 90A	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NSD1	NM_022455	nuclear receptor binding SET domain protein 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CREB3L2	NM_194071	cAMP responsive element binding protein 3-like 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C6orf106	NM_022758	chromosome 6 open reading frame 106	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CERK	NM_022766	ceramide kinase	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
WNK3	NM_001002838	WNK lysine deficient protein kinase 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
OTUB2	NM_023112	OTU domain, ubiquitin aldehyde binding 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NAA16	NM_024561	N(alpha)-acetyltransferase 16, NatA auxiliary subunit	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SRD5A3	NM_024592	steroid 5 alpha-reductase 3	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C16orf57	NM_001204911	chromosome 16 open reading frame 57	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NOL9	NM_024654	nucleolar protein 9	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CLMN	NM_024734	calmin (calponin-like, transmembrane)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
RBFA	NM_001171967	ribosome binding factor A (putative)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ERMP1	NM_024896	endoplasmic reticulum metallopeptidase 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PQLC1	NM_001146343	PQ loop repeat containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

CEP63	NM_001042383	centrosomal protein 63kDa	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DNAJC5	NM_025219	DnaJ (Hsp40) homolog, subfamily C, member 5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ITIH5	NM_030569	inter-alpha (globulin) inhibitor H5	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C22orf13	NM_031444	chromosome 22 open reading frame 13	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SETDB2	NM_001160308	SET domain, bifurcated 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NCALD	NM_001040624	neurocalcin delta	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZIC4	NM_001168378	Zic family member 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
LDOC1L	NM_032287	leucine zipper, down-regulated in cancer 1-like	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SRRM4	NM_194286	serine/arginine repetitive matrix 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PLEKHA8	NM_001197026	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
LMNB2	NM_032737	lamin B2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
PPP1R15B	NM_032833	protein phosphatase 1, regulatory (inhibitor) subunit 15B	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FBXL20	NM_001184906	F-box and leucine-rich repeat protein 20	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ARHGAP19	NM_001204300	Rho GTPase activating protein 19	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SNX29	NM_001080530	sorting nexin 29	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MTDH	NM_178812	metadherin	1	0	1	0	0	0	0	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NACC1	NM_052876	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MYSM1	NM_001085487	Myb-like, SWIRM and MPN domains 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

LRRC58	NM_001099678	leucine rich repeat containing 58	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FOXP4	NM_001012426	forkhead box P4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
RFFL	NM_001017368	ring finger and FYVE-like domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZNF488	NM_153034	zinc finger protein 488	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SFXN2	NM_178858	sideroflexin 2	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SLC24A4	NM_153646	solute carrier family 24 (sodium/potassium/calcium exchanger), member 4	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C18orf19	NM_001098801	chromosome 18 open reading frame 19	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
MOBKL2A	NM_130807	MOB1, Mps One Binder kinase activator-like 2A (yeast)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SYT2	NM_001136504	synaptotagmin II	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZNF362	NM_152493	zinc finger protein 362	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
METTL21A	NM_001127395	methyltransferase like 21A	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DTX3L	NM_138287	deltex 3-like (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GBP6	NM_198460	guanylate binding protein family, member 6	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ADAMTS17	NM_139057	ADAM metallopeptidase with thrombospondin type 1 motif, 17	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DNAJC18	NM_152686	DnaJ (Hsp40) homolog, subfamily C, member 18	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZCCHC24	NM_153367	zinc finger, CCHC domain containing 24	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
FOXK1	NM_001037165	forkhead box K1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C7orf41	NM_152793	chromosome 7 open reading frame 41	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR

PRR14L	NM_173566	proline rich 14-like	1	0	1	0	0	0	0	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C17orf103	NM_152914	chromosome 17 open reading frame 103	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
KIAA0284	NM_001112726	KIAA0284	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
GDPD1	NM_182569	glycerophosphodiester phosphodiesterase domain containing 1	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
DOK7	NM_001164673	docking protein 7	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
NAT8L	NM_178557	N-acetyltransferase 8-like (GCN5-related, putative)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C15orf52	NM_207380	chromosome 15 open reading frame 52	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
IYD	NM_001164694	iodotyrosine deiodinase	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
C3orf72	NM_001040061	chromosome 3 open reading frame 72	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZNF716	NM_001159279	zinc finger protein 716	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
RNF165	NM_152470	ring finger protein 165	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
POTEM	NM_001145442	POTE ankyrin domain family, member M	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
TMEM236	NM_001098844	transmembrane protein 236	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SLC35E2B	NM_001110781	solute carrier family 35, member E2B	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
SHISA9	NM_001145204	shisa homolog 9 (Xenopus laevis)	0	0	0	0	1	0	1	0	hsa-miR-622	> -0.02	N/A	Sites in UTR
CYLD	NM_001042355	cylindromatosis (turban tumor syndrome)	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
IGFBP5	NM_000599	insulin-like growth factor binding protein 5	1	0	0	1	1	0	0	1	hsa-miR-622	> -0.02	N/A	Sites in UTR
RAB3B	NM_002867	RAB3B, member RAS oncogene family	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR

SLC1A2	NM_001195728	solute carrier family 1 (glial high affinity glutamate transporter), member 2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
UBE2G2	NM_001202489	ubiquitin-conjugating enzyme E2G 2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
RAB7L1	NM_001135662	RAB7, member RAS oncogene family-like 1	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
KIF1C	NM_006612	kinesin family member 1C	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
MID2	NM_012216	midline 2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
TMOD2	NM_001142885	tropomodulin 2 (neuronal)	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
TRPM7	NM_017672	transient receptor potential cation channel, subfamily M, member 7	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
ACER3	NM_018367	alkaline ceramidase 3	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
SCN3B	NM_001040151	sodium channel, voltage-gated, type III, beta	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
RAD18	NM_020165	RAD18 homolog (S. cerevisiae)	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
CYP20A1	NM_177538	cytochrome P450, family 20, subfamily A, polypeptide 1	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
EPG5	NM_020964	ectopic P-granules autophagy protein 5 homolog (C. elegans)	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
PEAK1	NM_024776	NKF3 kinase family member	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
TREML2	NM_024807	triggering receptor expressed on myeloid cells-like 2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
ANKRD13C	NM_030816	ankyrin repeat domain 13C	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
RAB11FIP4	NM_032932	RAB11 family interacting protein 4 (class II)	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
ST6GAL2	NM_001142351	ST6 beta-galactosamide alpha-2,6-sialyltranferase 2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
SESTD1	NM_178123	SEC14 and spectrin domains 1	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR

PALM2	NM_001037293	paralemmin 2	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
SLC30A7	NM_001144884	solute carrier family 30 (zinc transporter), member 7	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
CLYBL	NM_206808	citrate lyase beta like	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
ANKRD52	NM_173595	ankyrin repeat domain 52	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
ZNF470	NM_001001668	zinc finger protein 470	0	0	0	0	2	0	0	2	hsa-miR-622	> -0.02	N/A	Sites in UTR
AP1G1	NM_001030007	adaptor-related protein complex 1, gamma 1 subunit	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
NOTCH2	NM_024408	notch 2	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
RPS6KA2	NM_001006932	ribosomal protein S6 kinase, 90kDa, polypeptide 2	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
SLC6A6	NM_001134367	solute carrier family 6 (neurotransmitter transporter, taurine), member 6	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
USH2A	NM_206933	Usher syndrome 2A (autosomal recessive, mild)	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
PIP4K2B	NM_003559	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
CREB5	NM_001011666	cAMP responsive element binding protein 5	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
SPIN1	NM_006717	spindlin 1	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
SZT2	NM_015284	seizure threshold 2 homolog (mouse)	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
ZNF629	NM_001080417	zinc finger protein 629	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
ZDHHC17	NM_015336	zinc finger, DHHC-type containing 17	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
CCDC113	NM_001142302	coiled-coil domain containing 113	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
TET2	NM_001127208	tet oncogene family member 2	1	1	0	0	0	0	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR

C20orf11	NM_017896	chromosome 20 open reading frame 11	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
TRERF1	NM_033502	transcriptional regulating factor 1	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
PDP2	NM_020786	pyruvate dehyrogenase phosphatase catalytic subunit 2	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
NECAB1	NM_022351	N-terminal EF-hand calcium binding protein 1	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
NFAM1	NM_145912	NFAT activating protein with ITAM motif 1	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
SLC36A1	NM_078483	solute carrier family 36 (proton/amino acid symporter), member 1	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
RBM20	NM_001134363	RNA binding motif protein 20	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
KY	NM_178554	kyphoscoliosis peptidase	0	0	0	0	1	1	0	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
ABLIM1	NM_001003407	actin binding LIM protein 1	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
LMX1B	NM_001174146	LIM homeobox transcription factor 1, beta	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
NOS1	NM_000620	nitric oxide synthase 1 (neuronal)	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
TMPO	NM_001032283	thymopoietin	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
RAPGEF3	NM_001098531	Rap guanine nucleotide exchange factor (GEF) 3	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
UNC13A	NM_001080421	unc-13 homolog A (C. elegans)	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
TANC2	NM_025185	tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2	1	0	1	0	1	0	0	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
TFCP2L1	NM_014553	transcription factor CP2-like 1	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
NAA38	NM_016200	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
CYCS	NM_018947	cytochrome c, somatic	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR

PLEKHB2	NM_001100623	pleckstrin homology domain containing, family B (evectins) member 2	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
PDPR	NM_017990	pyruvate dehydrogenase phosphatase regulatory subunit	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
ZNF490	NM_020714	zinc finger protein 490	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
NUFIP2	NM_020772	nuclear fragile X mental retardation protein interacting protein 2	2	0	1	1	1	0	1	0	hsa-miR-622	> -0.03	N/A	Sites in UTR
ZMAT3	NM_022470	zinc finger, matrin-type 3	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
ZXDC	NM_001040653	ZXD family zinc finger C	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
ORAI2	NM_001126340	ORAI calcium release-activated calcium modulator 2	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
SLC38A1	NM_001077484	solute carrier family 38, member 1	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
KLHL6	NM_130446	kelch-like 6 (Drosophila)	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
SLFN13	NM_144682	schlafen family member 13	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
DENND5B	NM_144973	DENN/MADD domain containing 5B	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
ZNF780B	NM_001005851	zinc finger protein 780B	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
P2RY8	NM_178129	purinergic receptor P2Y, G-protein coupled, 8	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
RAB43	NM_001204883	RAB43, member RAS oncogene family	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
PTAR1	NM_001099666	protein prenyltransferase alpha subunit repeat containing 1	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
ISY1-RAB43	NM_001204890	ISY1-RAB43 readthrough	0	0	0	0	2	0	1	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
TOMM70A	NM_014820	translocase of outer mitochondrial membrane 70 homolog A (S. cerevisiae)	0	0	0	0	2	1	0	1	hsa-miR-622	> -0.03	N/A	Sites in UTR
ARL3	NM_004311	ADP-ribosylation factor-like 3	0	0	0	0	2	1	0	1	hsa-miR-622	> -0.04	N/A	Sites in UTR

DCX	NM_000555	doublecortin	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
ELK4	NM_001973	ELK4, ETS-domain protein (SRF accessory protein 1)	0	0	0	0	2	1	0	1	hsa-miR-622	> -0.04	N/A	Sites in UTR
RBMS2	NM_002898	RNA binding motif, single stranded interacting protein 2	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
TNNI1	NM_003281	troponin I type 1 (skeletal, slow)	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
SH3PXD2A	NM_014631	SH3 and PX domains 2A	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
ZBTB40	NM_001083621	zinc finger and BTB domain containing 40	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
SEC23IP	NM_007190	SEC23 interacting protein	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
KLHL18	NM_025010	kelch-like 18 (Drosophila)	0	0	0	0	2	1	0	1	hsa-miR-622	> -0.04	N/A	Sites in UTR
ODZ4	NM_001098816	odz, odd Oz/ten-m homolog 4 (Drosophila)	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
MCTS1	NM_001137554	malignant T cell amplified sequence 1	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
CSNK1G1	NM_022048	casein kinase 1, gamma 1	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
ZNF471	NM_020813	zinc finger protein 471	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
CLSPN	NM_001190481	claspin	0	0	0	0	2	1	0	1	hsa-miR-622	> -0.04	N/A	Sites in UTR
C22orf29	NM_024627	chromosome 22 open reading frame 29	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
ING5	NM_032329	inhibitor of growth family, member 5	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
CBX2	NM_005189	chromobox homolog 2	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
OLFML2A	NM_182487	olfactomedin-like 2A	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
GK5	NM_001039547	glycerol kinase 5 (putative)	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR

TSPAN11	NM_001080509	tetraspanin 11	0	0	0	0	2	0	2	0	hsa-miR-622	> -0.04	N/A	Sites in UTR
PPM1A	NM_021003	protein phosphatase, Mg2+/Mn2+ dependent, 1A	0	0	0	0	3	0	1	2	hsa-miR-622	> -0.04	N/A	Sites in UTR
MAVS	NM_001206491	mitochondrial antiviral signaling protein	0	0	0	0	3	0	1	2	hsa-miR-622	> -0.04	N/A	Sites in UTR
STX11	NM_003764	syntaxin 11	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
ZNF264	NM_003417	zinc finger protein 264	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
PTPN18	NM_001142370	protein tyrosine phosphatase, non-receptor type 18 (brain-derived)	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
GDAP2	NM_017686	ganglioside induced differentiation associated protein 2	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
PAQR5	NM_001104554	progestin and adipoQ receptor family member V	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
PGPEP1	NM_017712	pyroglutamyl-peptidase I	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
PLXNA4	NM_020911	plexin A4	0	0	0	0	2	1	1	0	hsa-miR-622	> -0.05	N/A	Sites in UTR
ABHD2	NM_007011	abhydrolase domain containing 2	0	0	0	0	3	0	2	1	hsa-miR-622	> -0.05	N/A	Sites in UTR
IPO9	NM_018085	importin 9	0	0	0	0	3	1	0	2	hsa-miR-622	> -0.05	N/A	Sites in UTR
SSH2	NM_033389	slingshot homolog 2 (Drosophila)	0	0	0	0	3	0	2	1	hsa-miR-622	> -0.05	N/A	Sites in UTR
LOC646851	NM_001013647	hypothetical LOC646851	0	0	0	0	3	0	2	1	hsa-miR-622	> -0.05	N/A	Sites in UTR
ANTXR2	NM_058172	anthrax toxin receptor 2	0	0	0	0	4	0	1	3	hsa-miR-622	> -0.05	N/A	Sites in UTR
PLEKHG4B	NM_052909	pleckstrin homology domain containing, family G (with RhoGef domain) member 4B	0	0	0	0	4	0	1	3	hsa-miR-622	> -0.05	N/A	Sites in UTR
NFIA	NM_001134673	nuclear factor I/A	0	0	0	0	3	1	1	1	hsa-miR-622	> -0.06	N/A	Sites in UTR
WWC1	NM_001161661	WW and C2 domain containing 1	0	0	0	0	3	0	3	0	hsa-miR-622	> -0.06	N/A	Sites in UTR

ZNF704	NM_001033723	zinc finger protein 704	0	0	0	0	3	1	1	1	hsa-miR-622	> -0.06	N/A	Sites in UTR
LOC100507421	NM_001195278	transmembrane protein 178-like	0	0	0	0	4	0	2	2	hsa-miR-622	> -0.06	N/A	Sites in UTR
ACVR2B	NM_001106	activin A receptor, type IIB	0	0	0	0	3	1	2	0	hsa-miR-622	> -0.07	N/A	Sites in UTR
PTPN14	NM_005401	protein tyrosine phosphatase, non-receptor type 14	0	0	0	0	3	1	2	0	hsa-miR-622	> -0.07	N/A	Sites in UTR
HEYL	NM_014571	hairy/enhancer-of-split related with YRPW motif-like	1	0	1	0	2	1	1	0	hsa-miR-622	> -0.07	N/A	Sites in UTR
KLF12	NM_007249	Kruppel-like factor 12	1	1	0	0	3	0	1	2	hsa-miR-622	> -0.07	N/A	Sites in UTR
PLEKHA6	NM_014935	pleckstrin homology domain containing, family A member 6	0	0	0	0	4	0	3	1	hsa-miR-622	> -0.07	N/A	Sites in UTR
CACNG8	NM_031895	calcium channel, voltage-dependent, gamma subunit 8	0	0	0	0	5	1	0	4	hsa-miR-622	> -0.07	N/A	Sites in UTR
C6orf223	NM_001171992	chromosome 6 open reading frame 223	3	1	2	0	6	0	6	0	hsa-miR-622	> -0.19	N/A	Sites in UTR
CHD4	NM_001273	chromodomain helicase DNA binding protein 4	0	0	0	0	1	1	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
FOXG1	NM_005249	forkhead box G1	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
GUSB	NM_000181	glucuronidase, beta	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
SP110	NM_004509	SP110 nuclear body protein	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
IL7R	NM_002185	interleukin 7 receptor	0	0	0	0	1	1	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
ITK	NM_005546	IL2-inducible T-cell kinase	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
KCNA5	NM_002234	potassium voltage-gated channel, shaker-related subfamily, member 5	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
PFN2	NM_053024	profilin 2	1	0	1	0	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
PIN4	NM_006223	protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin)	1	0	0	1	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR

SEMA3B	NM_001005914	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
REEP5	NM_005669	receptor accessory protein 5	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
CREG1	NM_003851	cellular repressor of E1A-stimulated genes 1	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
HTR3B	NM_006028	5-hydroxytryptamine (serotonin) receptor 3B	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
MED23	NM_004830	mediator complex subunit 23	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
PPIH	NM_006347	peptidylprolyl isomerase H (cyclophilin H)	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
SYNCRIP	NM_001159673	synaptotagmin binding, cytoplasmic RNA interacting protein	1	0	0	1	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
SCGN	NM_006998	secretagogin, EF-hand calcium binding protein	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
EPB41L4B	NM_018424	erythrocyte membrane protein band 4.1 like 4B	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
ZDHHC7	NM_001145548	zinc finger, DHHC-type containing 7	0	0	0	0	1	1	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
SLC7A10	NM_019849	solute carrier family 7 (neutral amino acid transporter light chain, asc system), member 10	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
NAT14	NM_020378	N-acetyltransferase 14 (GCN5-related, putative)	0	0	0	0	1	1	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
SH3RF1	NM_020870	SH3 domain containing ring finger 1	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
FAM38B	NM_022068	family with sequence similarity 38, member B	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
TMC7	NM_001160364	transmembrane channel-like 7	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
ST6GALNAC5	NM_030965	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
FAM167A	NM_053279	family with sequence similarity 167, member A	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
RNASE7	NM_032572	ribonuclease, RNase A family, 7	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR

TMEM55B	NM_001100814	transmembrane protein 55B	1	0	1	0	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
UAP1L1	NM_207309	UDP-N-acteylglucosamine pyrophosphorylase 1-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
ADAMTSL1	NM_052866	ADAMTS-like 1	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
GCFC1	NM_016631	GC-rich sequence DNA-binding factor 1	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
ADSSL1	NM_152328	adenylosuccinate synthase like 1	0	0	0	0	1	1	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
KBTBD5	NM_152393	kelch repeat and BTB (POZ) domain containing 5	0	0	0	0	1	1	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
LIN54	NM_001115007	lin-54 homolog (C. elegans)	0	0	0	0	1	0	0	1	hsa-miR-622	N/A	N/A	Sites in UTR
NCOA7	NM_001122842	nuclear receptor coactivator 7	1	0	1	0	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
NOTUM	NM_178493	notum pectinacetylesterase homolog (Drosophila)	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
FAM78B	NM_001017961	family with sequence similarity 78, member B	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
C6orf94	NM_001013623	chromosome 6 open reading frame 94	1	0	1	0	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR
C8orf37	NM_177965	chromosome 8 open reading frame 37	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
ACSF3	NM_001127214	acyl-CoA synthetase family member 3	0	0	0	0	1	0	1	0	hsa-miR-622	N/A	N/A	Sites in UTR
TTLL6	NM_001130918	tubulin tyrosine ligase-like family, member 6	1	0	1	0	0	0	0	0	hsa-miR-622	N/A	N/A	Sites in UTR