**Table S10. Identification of putative miR-647 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 | | | | |
| ARHGEF15 | NM_025014 | Rho guanine nucleotide exchange factor (GEF) 15 | 1 | 1 | 0 | 0 | 3 | 2 | 0 | 1 | hsa-miR-647 | -1.25 | N/A | Sites in UTR |
| FAM109B | NM_001002034 | family with sequence similarity 109, member B | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.76 | N/A | Sites in UTR |
| MUDENG | NM_018229 | MU-2/AP1M2 domain containing, death-inducing | 0 | 0 | 0 | 0 | 3 | 1 | 1 | 1 | hsa-miR-647 | -0.76 | N/A | Sites in UTR |
| ICOS | NM_012092 | inducible T-cell co-stimulator | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.76 | N/A | Sites in UTR |
| WWTR1 | NM_001168278 | WW domain containing transcription regulator 1 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | hsa-miR-647 | -0.76 | N/A | Sites in UTR |
| PFKM | NM_000289 | phosphofructokinase, muscle | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.75 | N/A | Sites in UTR |
| THOC5 | NM_001002877 | THO complex 5 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.69 | N/A | Sites in UTR |
| STRA6 | NM_001142617 | stimulated by retinoic acid gene 6 homolog (mouse) | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.69 | N/A | Sites in UTR |
| ATG7 | NM_001136031 | ATG7 autophagy related 7 homolog (S. cerevisiae) | 2 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.69 | N/A | Sites in UTR |
| RUNX2 | NM_001015051 | runt-related transcription factor 2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.68 | N/A | Sites in UTR |
| SLC7A1 | NM_003045 | solute carrier family 7 (cationic amino acid transporter, y+ system), member 1 | 0 | 0 | 0 | 0 | 4 | 2 | 2 | 0 | hsa-miR-647 | -0.68 | N/A | Sites in UTR |
| ATP8A2 | NM_016529 | ATPase, aminophospholipid transporter, class I, type 8A, member 2 | 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.66 | N/A | Sites in UTR |
| ZBTB37 | NM_001122770 | zinc finger and BTB domain containing 37 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.65 | N/A | Sites in UTR |
| S1PR5 | NM_001166215 | sphingosine-1-phosphate receptor 5 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.65 | N/A | Sites in UTR |
| TMEM143 | NM_018273 | transmembrane protein 143 | 1 | 0 | 0 | 1 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.65 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LMO4 | NM_006769 | LIM domain only 4 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.65 | N/A | Sites in UTR |
| CUEDC1 | NM_017949 | CUE domain containing 1 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.64 | N/A | Sites in UTR |
| CPEB2 | NM_001177381 | cytoplasmic polyadenylation element binding protein 2 | 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.64 | N/A | Sites in UTR |
| LOC284385 | NM_001242812 | hypothetical LOC284385 | 0 | 0 | 0 | 0 | 4 | 0 | 1 | 3 | hsa-miR-647 | -0.64 | N/A | Sites in UTR |
| COMMD9 | NM_001101653 | COMM domain containing 9 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.64 | N/A | Sites in UTR |
| C11orf21 | NM_001142946 | chromosome 11 open reading frame 21 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.64 | N/A | Sites in UTR |
| HADHA | NM_000182 | hydroxyacyl-CoA dehydrogenase/3-ketoacyl-CoA thiolase/enoyl-CoA hydratase (trifunctional protein), alpha subunit | 0 | 0 | 0 | 0 | 3 | 1 | 0 | 2 | hsa-miR-647 | -0.63 | N/A | Sites in UTR |
| UBE2Q2 | NM_001145335 | ubiquitin-conjugating enzyme E2Q family member 2 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.63 | N/A | Sites in UTR |
| PTTG1IP | NM_004339 | pituitary tumor-transforming 1 interacting protein | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.62 | N/A | Sites in UTR |
| BMP1 | NM_006129 | bone morphogenetic protein 1 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.61 | N/A | Sites in UTR |
| IL1RAP | NM_001167930 | interleukin 1 receptor accessory protein | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.6 | N/A | Sites in UTR |
| NETO1 | NM_138966 | neuropilin (NRP) and tolloid (TLL)-like 1 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.6 | N/A | Sites in UTR |
| VSTM4 | NM_001031746 | V-set and transmembrane domain containing 4 | 0 | 0 | 0 | 0 | 4 | 1 | 1 | 2 | hsa-miR-647 | -0.6 | N/A | Sites in UTR |
| CAMK2G | NM_001204492 | calcium/calmodulin-dependent protein kinase II gamma | 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.59 | N/A | Sites in UTR |
| DNAH5 | NM_001369 | dynein, axonemal, heavy chain 5 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.58 | N/A | Sites in UTR |
| KIRREL2 | NM_032123 | kin of IRRE like 2 (Drosophila) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.58 | N/A | Sites in UTR |
| ZFAND3 | NM_021943 | zinc finger, AN1-type domain 3 | 0 | 0 | 0 | 0 | 4 | 0 | 4 | 0 | hsa-miR-647 | -0.58 | N/A | Sites in UTR |
| PSMF1 | NM_006814 | proteasome (prosome, macropain) inhibitor subunit 1 (PI31) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.58 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RHOJ | NM_020663 | ras homolog gene family, member J | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.58 | N/A | Sites in UTR |
| ABCC1 | NM_004996 | ATP-binding cassette, sub-family C (CFTR/MRP), member 1 | 2 | 0 | 2 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.57 | N/A | Sites in UTR |
| C1orf183 | NM_019099 | chromosome 1 open reading frame 183 | 0 | 0 | 0 | 0 | 5 | 0 | 4 | 1 | hsa-miR-647 | -0.57 | N/A | Sites in UTR |
| PRRX1 | NM_006902 | paired related homeobox 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.57 | N/A | Sites in UTR |
| ENDOD1 | NM_015036 | endonuclease domain containing 1 | 1 | 0 | 1 | 0 | 3 | 1 | 0 | 2 | hsa-miR-647 | -0.57 | N/A | Sites in UTR |
| ZBTB44 | NM_014155 | zinc finger and BTB domain containing 44 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.57 | N/A | Sites in UTR |
| C6orf89 | NM_152734 | chromosome 6 open reading frame 89 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.57 | N/A | Sites in UTR |
| ST3GAL3 | NM_006279 | ST3 beta-galactoside alpha-2,3-sialyltransferase 3 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.56 | N/A | Sites in UTR |
| ENDOU | NM_001172439 | endonuclease, polyU-specific | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.56 | N/A | Sites in UTR |
| DENND5B | NM_144973 | DENN/MADD domain containing 5B | 0 | 0 | 0 | 0 | 3 | 2 | 0 | 1 | hsa-miR-647 | -0.56 | N/A | Sites in UTR |
| RAPGEF5 | NM_012294 | Rap guanine nucleotide exchange factor (GEF) 5 | 0 | 0 | 0 | 0 | 4 | 1 | 1 | 2 | hsa-miR-647 | -0.55 | N/A | Sites in UTR |
| ERCC2 | NM_001130867 | excision repair cross-complementing rodent repair deficiency, complementation group 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.55 | N/A | Sites in UTR |
| NFIX | NM_002501 | nuclear factor I/X (CCAAT-binding transcription factor) | 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.55 | N/A | Sites in UTR |
| TP73 | NM_001126240 | tumor protein p73 | 0 | 0 | 0 | 0 | 4 | 1 | 3 | 0 | hsa-miR-647 | -0.55 | N/A | Sites in UTR |
| NR6A1 | NM_001489 | nuclear receptor subfamily 6, group A, member 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.55 | N/A | Sites in UTR |
| ALCAM | NM_001627 | activated leukocyte cell adhesion molecule | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.55 | N/A | Sites in UTR |
| GK | NM_000167 | glycerol kinase | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.54 | N/A | Sites in UTR |
| F13A1 | NM_000129 | coagulation factor XIII, A1 polypeptide | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.54 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAGEB1 | NM_002363 | melanoma antigen family B, 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| MAP3K3 | NM_002401 | mitogen-activated protein kinase kinase kinase 3 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| C9orf66 | NM_152569 | chromosome 9 open reading frame 66 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| FAM75D3 | NM_207416 | family with sequence similarity 75, member D3 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| IL5 | NM_000879 | interleukin 5 (colony-stimulating factor, eosinophil) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| KAZN | NM_201628 | kazrin, periplakin interacting protein | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| PLCL2 | NM_001144382 | phospholipase C-like 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| CA10 | NM_001082533 | carbonic anhydrase X | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.53 | N/A | Sites in UTR |
| C11orf34 | NM_001145024 | chromosome 11 open reading frame 34 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| GRIPAP1 | NM_020137 | GRIP1 associated protein 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| ULBP1 | NM_025218 | UL16 binding protein 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| PNPO | NM_018129 | pyridoxamine 5'-phosphate oxidase | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| ZNF629 | NM_001080417 | zinc finger protein 629 | 0 | 0 | 0 | 0 | 3 | 1 | 0 | 2 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| RND3 | NM_005168 | Rho family GTPase 3 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| AFF3 | NM_001025108 | AF4/FMR2 family, member 3 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| CREG2 | NM_153836 | cellular repressor of E1A-stimulated genes 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| SYVN1 | NM_032431 | synovial apoptosis inhibitor 1, synoviolin | 2 | 0 | 2 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.52 | N/A | Sites in UTR |
| C16orf82 | NM_001145545 | chromosome 16 open reading frame 82 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.51 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| IGDCC3 | NM_004884 | immunoglobulin superfamily, DCC subclass, member 3 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.51 | N/A | Sites in UTR |
| SCRN3 | NM_001193528 | secernin 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.51 | N/A | Sites in UTR |
| FAM149B1 | NM_173348 | family with sequence similarity 149, member B1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| ARNT | NM_001197325 | aryl hydrocarbon receptor nuclear translocator | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| DCX | NM_000555 | doublecortin | 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| UBE2L6 | NM_004223 | ubiquitin-conjugating enzyme E2L 6 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| CDHR1 | NM_033100 | cadherin-related family member 1 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| SETBP1 | NM_015559 | SET binding protein 1 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| C2orf61 | NM_173649 | chromosome 2 open reading frame 61 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| MLEC | NM_014730 | malectin | 0 | 0 | 0 | 0 | 4 | 1 | 2 | 1 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| DDHD1 | NM_001160147 | DDHD domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| SESN2 | NM_031459 | sestrin 2 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| TPPP2 | NM_173846 | tubulin polymerization-promoting protein family member 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| MRGPRF | NM_001098515 | MAS-related GPR, member F | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| DNAJC27 | NM_001198559 | DnaJ (Hsp40) homolog, subfamily C, member 27 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.5 | N/A | Sites in UTR |
| EGF | NM_001178130 | epidermal growth factor | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| EXOC5 | NM_006544 | exocyst complex component 5 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| ZNF202 | NM_003455 | zinc finger protein 202 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PKDCC | NM_138370 | protein kinase domain containing, cytoplasmic homolog (mouse) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| DCUN1D3 | NM_173475 | DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| SLC24A4 | NM_153646 | solute carrier family 24 (sodium/potassium/calcium exchanger), member 4 | 1 | 0 | 1 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| PCGF6 | NM_001011663 | polycomb group ring finger 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| RHPN1 | NM_052924 | rhophilin, Rho GTPase binding protein 1 | 0 | 0 | 0 | 0 | 4 | 0 | 2 | 2 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| DCK | NM_000788 | deoxycytidine kinase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| TECRL | NM_001010874 | trans-2,3-enoyl-CoA reductase-like | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.49 | N/A | Sites in UTR |
| TMEM91 | NM_001042595 | transmembrane protein 91 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| HCFC1 | NM_005334 | host cell factor C1 (VP16-accessory protein) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| C1orf122 | NM_001142726 | chromosome 1 open reading frame 122 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| KIAA1143 | NM_020696 | KIAA1143 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| PPM1F | NM_014634 | protein phosphatase, Mg2+/Mn2+ dependent, 1F | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| SYT6 | NM_205848 | synaptotagmin VI | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| C19orf24 | NM_017914 | chromosome 19 open reading frame 24 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| MYCT1 | NM_025107 | myc target 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| MLIP | NM_138569 | muscular LMNA-interacting protein | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| FOXJ2 | NM_018416 | forkhead box J2 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| GSDMB | NM_001042471 | gasdermin B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RAB1A | NM_004161 | RAB1A, member RAS oncogene family | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.48 | N/A | Sites in UTR |
| FN1 | NM_002026 | fibronectin 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| L2HGDH | NM_024884 | L-2-hydroxyglutarate dehydrogenase | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| EPB41L4A | NM_022140 | erythrocyte membrane protein band 4.1 like 4A | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| C5orf46 | NM_206966 | chromosome 5 open reading frame 46 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| HSF5 | NM_001080439 | heat shock transcription factor family member 5 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| LCP1 | NM_002298 | lymphocyte cytosolic protein 1 (L-plastin) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| TRAF2 | NM_021138 | TNF receptor-associated factor 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| C1orf127 | NM_001170754 | chromosome 1 open reading frame 127 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| MOSPD2 | NM_001177475 | motile sperm domain containing 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| GTDC1 | NM_001006636 | glycosyltransferase-like domain containing 1 | 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| DNALI1 | NM_003462 | dynein, axonemal, light intermediate chain 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| CD3D | NM_000732 | CD3d molecule, delta (CD3-TCR complex) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| SRF | NM_003131 | serum response factor (c-fos serum response element-binding transcription factor) | 2 | 0 | 1 | 1 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| HELZ | NM_014877 | helicase with zinc finger | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| IFIT2 | NM_001547 | interferon-induced protein with tetratricopeptide repeats 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| PSMD13 | NM_002817 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |
| SAE1 | NM_001145713 | SUMO1 activating enzyme subunit 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.47 | N/A | Sites in UTR |

| | | | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC100130357 | NM_001242698 | hypothetical LOC100130357 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| STIL | NM_001048166 | SCL/TAL1 interrupting locus | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| ZNF19 | NM_006961 | zinc finger protein 19 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| ZNF521 | NM_015461 | zinc finger protein 521 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| ALOXE3 | NM_001165960 | arachidonate lipoxygenase 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| TCEB1 | NM_001204857 | transcription elongation factor B (SIII), polypeptide 1 (15kDa, elongin C) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| DKK2 | NM_014421 | dickkopf homolog 2 (Xenopus laevis) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| TMEM159 | NM_020422 | transmembrane protein 159 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| C17orf65 | NM_178542 | chromosome 17 open reading frame 65 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| MLL2 | NM_003482 | myeloid/lymphoid or mixed-lineage leukemia 2 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| GABRB2 | NM_000813 | gamma-aminobutyric acid (GABA) A receptor, beta 2 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.46 | N/A | Sites in UTR |
| GJB7 | NM_198568 | gap junction protein, beta 7, 25kDa | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| TUBB6 | NM_032525 | tubulin, beta 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| YIPF5 | NM_001024947 | Yip1 domain family, member 5 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| TNFAIP2 | NM_006291 | tumor necrosis factor, alpha-induced protein 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| PTPRB | NM_001109754 | protein tyrosine phosphatase, receptor type, B | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| RNF165 | NM_152470 | ring finger protein 165 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| THAP6 | NM_144721 | THAP domain containing 6 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CYTH4 | NM_013385 | cytohesin 4 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| PITPNM3 | NM_001165966 | PITPNM family member 3 | 2 | 0 | 1 | 1 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| PAK6 | NM_001128628 | p21 protein (Cdc42/Rac)-activated kinase 6 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| 3-Sep | NM_019106 | septin 3 | 0 | 0 | 0 | 0 | 3 | 1 | 1 | 1 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| ABHD6 | NM_020676 | abhydrolase domain containing 6 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| FGFBP3 | NM_152429 | fibroblast growth factor binding protein 3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| HPCA | NM_002143 | hippocalcin | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| YIPF3 | NM_015388 | Yip1 domain family, member 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.45 | N/A | Sites in UTR |
| C19orf63 | NM_175063 | chromosome 19 open reading frame 63 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| APLF | NM_173545 | aprataxin and PNKP like factor | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| TRPS1 | NM_014112 | trichorhinophalangeal syndrome I | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| PTAFR | NM_000952 | platelet-activating factor receptor | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| ODF2L | NM_001007022 | outer dense fiber of sperm tails 2-like | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| FBXO17 | NM_024907 | F-box protein 17 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| ORMDL3 | NM_139280 | ORM1-like 3 (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| ARID1A | NM_006015 | AT rich interactive domain 1A (SWI-like) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| TRAK2 | NM_015049 | trafficking protein, kinesin binding 2 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| SCN2B | NM_004588 | sodium channel, voltage-gated, type II, beta | 0 | 0 | 0 | 0 | 4 | 1 | 3 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RNF208 | NM_031297 | ring finger protein 208 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| ZNF652 | NM_001145365 | zinc finger protein 652 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| HNRNPF | NM_001098204 | heterogeneous nuclear ribonucleoprotein F | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| LOC388630 | NM_001194986 | UPF0632 protein A | 2 | 2 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| SCN8A | NM_001177984 | sodium channel, voltage gated, type VIII, alpha subunit | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| C19orf59 | NM_174918 | chromosome 19 open reading frame 59 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.44 | N/A | Sites in UTR |
| DAPK3 | NM_001348 | death-associated protein kinase 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| CLVS1 | NM_173519 | clavesin 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| ZNF195 | NM_001130519 | zinc finger protein 195 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| ZNF480 | NM_144684 | zinc finger protein 480 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| FOXP3 | NM_001114377 | forkhead box P3 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| GINS2 | NM_016095 | GINS complex subunit 2 (Psf2 homolog) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| CHRAC1 | NM_017444 | chromatin accessibility complex 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| CRHR2 | NM_001202475 | corticotropin releasing hormone receptor 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| C1orf159 | NM_017891 | chromosome 1 open reading frame 159 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| NEBL | NM_001173484 | nebulette | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| XAF1 | NM_017523 | XIAP associated factor 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| ZFHX4 | NM_024721 | zinc finger homeobox 4 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| BEND6 | NM_152731 | BEN domain containing 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| TXNL4B | NM_001142317 | thioredoxin-like 4B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| UPF3B | NM_023010 | UPF3 regulator of nonsense transcripts homolog B (yeast) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| GDNF | NM_000514 | glial cell derived neurotrophic factor | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.43 | N/A | Sites in UTR |
| SORL1 | NM_003105 | sortilin-related receptor, L(DLR class) A repeats containing | 1 | 0 | 1 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| PLAG1 | NM_001114634 | pleiomorphic adenoma gene 1 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| NETO2 | NM_001201477 | neuropilin (NRP) and tolloid (TLL)-like 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| ORAI3 | NM_152288 | ORAI calcium release-activated calcium modulator 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| CNOT2 | NM_001199302 | CCR4-NOT transcription complex, subunit 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| ISM1 | NM_080826 | isthmin 1 homolog (zebrafish) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| SCNN1B | NM_000336 | sodium channel, nonvoltage-gated 1, beta | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| ZFP41 | NM_173832 | zinc finger protein 41 homolog (mouse) | 0 | 0 | 0 | 0 | 4 | 0 | 1 | 3 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| PHYH | NM_001037537 | phytanoyl-CoA 2-hydroxylase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| FAM75D4 | NM_001145197 | family with sequence similarity 75, member D4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| PRRC2C | NM_015172 | proline-rich coiled-coil 2C | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| C6orf136 | NM_001109938 | chromosome 6 open reading frame 136 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| LAIR1 | NM_002287 | leukocyte-associated immunoglobulin-like receptor 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| MOCS1 | NM_001075098 | molybdenum cofactor synthesis 1 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DAB2 | NM_001343 | disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| SLC25A4 | NM_001151 | solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| MKRN2 | NM_014160 | makorin ring finger protein 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| GRIA2 | NM_000826 | glutamate receptor, ionotropic, AMPA 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| PTPN18 | NM_001142370 | protein tyrosine phosphatase, non-receptor type 18 (brain-derived) | 0 | 0 | 0 | 0 | 4 | 0 | 1 | 3 | hsa-miR-647 | -0.42 | N/A | Sites in UTR |
| ADAT1 | NM_012091 | adenosine deaminase, tRNA-specific 1 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| GGCX | NM_000821 | gamma-glutamyl carboxylase | 2 | 0 | 1 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| GPN1 | NM_001145047 | GPN-loop GTPase 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| EFEMP1 | NM_001039348 | EGF containing fibulin-like extracellular matrix protein 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| PDE8A | NM_002605 | phosphodiesterase 8A | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| SLC23A2 | NM_005116 | solute carrier family 23 (nucleobase transporters), member 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| HNF1A | NM_000545 | HNF1 homeobox A | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| CCDC80 | NM_199511 | coiled-coil domain containing 80 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| PLD1 | NM_001130081 | phospholipase D1, phosphatidylcholine-specific | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| CDH20 | NM_031891 | cadherin 20, type 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| SYNJ2 | NM_001178088 | synaptojanin 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| CHST3 | NM_004273 | carbohydrate (chondroitin 6) sulfotransferase 3 | 0 | 0 | 0 | 0 | 4 | 1 | 2 | 1 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| SSC5D | NM_001195267 | scavenger receptor cysteine rich domain containing (5 domains) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SURF4 | NM_033161 | surfeit 4 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| CHST6 | NM_021615 | carbohydrate (N-acetylglucosamine 6-O) sulfotransferase 6 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| RNFT2 | NM_001109903 | ring finger protein, transmembrane 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| AP3M1 | NM_012095 | adaptor-related protein complex 3, mu 1 subunit | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| ABCC9 | NM_020297 | ATP-binding cassette, sub-family C (CFTR/MRP), member 9 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.41 | N/A | Sites in UTR |
| TTN | NM_003319 | titin | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| CLEC7A | NM_022570 | C-type lectin domain family 7, member A | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| CXorf1 | NM_004709 | chromosome X open reading frame 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| CRIPT | NM_014171 | cysteine-rich PDZ-binding protein | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| SNX15 | NM_013306 | sorting nexin 15 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| PLA2G4E | NM_001206670 | phospholipase A2, group IVE | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| EFNA5 | NM_001962 | ephrin-A5 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| CRTC1 | NM_001098482 | CREB regulated transcription coactivator 1 | 0 | 0 | 0 | 0 | 3 | 2 | 1 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| TRIM52 | NM_032765 | tripartite motif containing 52 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| LOC253044 | NM_001242772 | hypothetical protein LOC253044 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| CERS6 | NM_203463 | ceramide synthase 6 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| EAF1 | NM_033083 | ELL associated factor 1 | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| PPP1R14D | NM_001130143 | protein phosphatase 1, regulatory (inhibitor) subunit 14D | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| BARHL2 | NM_020063 | BarH-like homeobox 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| MC2R | NM_000529 | melanocortin 2 receptor (adrenocorticotropic hormone) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| PXDN | NM_012293 | peroxidasin homolog (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| BMP8B | NM_001720 | bone morphogenetic protein 8b | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| PTPRT | NM_007050 | protein tyrosine phosphatase, receptor type, T | 0 | 0 | 0 | 0 | 5 | 0 | 3 | 2 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| CERS5 | NM_147190 | ceramide synthase 5 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| ZBTB41 | NM_194314 | zinc finger and BTB domain containing 41 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| C6orf106 | NM_022758 | chromosome 6 open reading frame 106 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| PTPN14 | NM_005401 | protein tyrosine phosphatase, non-receptor type 14 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| C9orf139 | NM_207511 | chromosome 9 open reading frame 139 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| ZRANB2 | NM_005455 | zinc finger, RAN-binding domain containing 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| LPPR1 | NM_017753 | lipid phosphate phosphatase-related protein type 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| TMEM115 | NM_007024 | transmembrane protein 115 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| PTGER3 | NM_198715 | prostaglandin E receptor 3 (subtype EP3) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.4 | N/A | Sites in UTR |
| LDOC1 | NM_012317 | leucine zipper, down-regulated in cancer 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| ANK2 | NM_001127493 | ankyrin 2, neuronal | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| EXOC3L4 | NM_001077594 | exocyst complex component 3-like 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| TMEM174 | NM_153217 | transmembrane protein 174 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FBN2 | NM_001999 | fibrillin 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| FAM107A | NM_001076778 | family with sequence similarity 107, member A | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| DNAJB12 | NM_001002762 | DnaJ (Hsp40) homolog, subfamily B, member 12 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| FAM123B | NM_152424 | family with sequence similarity 123B | 0 | 0 | 0 | 0 | 3 | 1 | 1 | 1 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| TRMT2A | NM_022727 | TRM2 tRNA methyltransferase 2 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| RASGRF1 | NM_001145648 | Ras protein-specific guanine nucleotide-releasing factor 1 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| C17orf51 | NM_001113434 | chromosome 17 open reading frame 51 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| KRT31 | NM_002277 | keratin 31 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| HEPHL1 | NM_001098672 | hephaestin-like 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| CISD3 | NM_001136498 | CDGSH iron sulfur domain 3 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.39 | N/A | Sites in UTR |
| FAM127A | NM_001078171 | family with sequence similarity 127, member A | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| MYLK2 | NM_033118 | myosin light chain kinase 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| ARL8A | NM_138795 | ADP-ribosylation factor-like 8A | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| XYLT1 | NM_022166 | xylosyltransferase I | 1 | 0 | 1 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| CDADC1 | NM_001193478 | cytidine and dCMP deaminase domain containing 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| EIF2C1 | NM_012199 | eukaryotic translation initiation factor 2C, 1 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| SIRT5 | NM_001193267 | sirtuin 5 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| C12orf53 | NM_153685 | chromosome 12 open reading frame 53 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PRODH | NM_001195226 | proline dehydrogenase (oxidase) 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| PPPDE2 | NM_015704 | PPPDE peptidase domain containing 2 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| PLCB3 | NM_000932 | phospholipase C, beta 3 (phosphatidylinositol-specific) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| MOBKL2C | NM_145279 | MOB1, Mps One Binder kinase activator-like 2C (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| FKBP4 | NM_002014 | FK506 binding protein 4, 59kDa | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| PRKG1 | NM_001098512 | protein kinase, cGMP-dependent, type I | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| GALNTL1 | NM_001168368 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 1 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.38 | N/A | Sites in UTR |
| MYCBP | NM_012333 | c-myc binding protein | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| WDR31 | NM_001012361 | WD repeat domain 31 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| SIN3B | NM_015260 | SIN3 homolog B, transcription regulator (yeast) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| CXCR5 | NM_001716 | chemokine (C-X-C motif) receptor 5 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| INMT | NM_001199219 | indolethylamine N-methyltransferase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| SMPD4 | NM_001171083 | sphingomyelin phosphodiesterase 4, neutral membrane (neutral sphingomyelinase-3) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| TSSK6 | NM_032037 | testis-specific serine kinase 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| ALKBH5 | NM_017758 | alkB, alkylation repair homolog 5 (E. coli) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| STX16 | NM_001001433 | syntaxin 16 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| SLC25A25 | NM_001006641 | solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 25 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| DAK | NM_015533 | dihydroxyacetone kinase 2 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CACNG8 | NM_031895 | calcium channel, voltage-dependent, gamma subunit 8 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| SMURF1 | NM_001199847 | SMAD specific E3 ubiquitin protein ligase 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| ZNF497 | NM_001207009 | zinc finger protein 497 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| TOR3A | NM_022371 | torsin family 3, member A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| SNX22 | NM_024798 | sorting nexin 22 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| SHPK | NM_013276 | sedoheptulokinase | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| CXorf49 | NM_001145140 | chromosome X open reading frame 49 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| CXorf49B | NM_001145139 | chromosome X open reading frame 49B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| TOM1L2 | NM_001033551 | target of myb1-like 2 (chicken) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| MUS81 | NM_025128 | MUS81 endonuclease homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.37 | N/A | Sites in UTR |
| HMGXB3 | NM_014983 | HMG box domain containing 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| TMEM110 | NM_198563 | transmembrane protein 110 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| TJP2 | NM_001170630 | tight junction protein 2 (zona occludens 2) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| FCHO2 | NM_001146032 | FCH domain only 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| ZC3H18 | NM_144604 | zinc finger CCCH-type containing 18 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| HIP1R | NM_003959 | huntingtin interacting protein 1 related | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| PLA2G2D | NM_012400 | phospholipase A2, group IID | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| HSPC159 | NM_014181 | galectin-related protein | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LGI4 | NM_139284 | leucine-rich repeat LGI family, member 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| CLEC5A | NM_013252 | C-type lectin domain family 5, member A | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| CDK1 | NM_001786 | cyclin-dependent kinase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| NSUN4 | NM_199044 | NOP2/Sun domain family, member 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| SYT2 | NM_001136504 | synaptotagmin II | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| GIGYF1 | NM_022574 | GRB10 interacting GYF protein 1 | 1 | 1 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| IFNG | NM_000619 | interferon, gamma | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| FBXL19 | NM_001099784 | F-box and leucine-rich repeat protein 19 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| FCRL4 | NM_031282 | Fc receptor-like 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| STX1B | NM_052874 | syntaxin 1B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| C13orf31 | NM_001128303 | chromosome 13 open reading frame 31 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.36 | N/A | Sites in UTR |
| HEATR6 | NM_022070 | HEAT repeat containing 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| ABCC6 | NM_001171 | ATP-binding cassette, sub-family C (CFTR/MRP), member 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| NEK9 | NM_033116 | NIMA (never in mitosis gene a)- related kinase 9 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| PHKB | NM_000293 | phosphorylase kinase, beta | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| PAX3 | NM_000438 | paired box 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| WIPI2 | NM_001033518 | WD repeat domain, phosphoinositide interacting 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| AMOTL1 | NM_130847 | angiomotin like 1 | 1 | 0 | 0 | 1 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PAFAH1B2 | NM_001184748 | platelet-activating factor acetylhydrolase 1b, catalytic subunit 2 (30kDa) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| CRTC3 | NM_001042574 | CREB regulated transcription coactivator 3 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| ALDH4A1 | NM_001161504 | aldehyde dehydrogenase 4 family, member A1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| MFSD4 | NM_181644 | major facilitator superfamily domain containing 4 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| HECTD2 | NM_173497 | HECT domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| NAGPA | NM_016256 | N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| ETNK2 | NM_018208 | ethanolamine kinase 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| RASSF2 | NM_014737 | Ras association (RalGDS/AF-6) domain family member 2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| TTR | NM_000371 | transthyretin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| CDH1 | NM_004360 | cadherin 1, type 1, E-cadherin (epithelial) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| CACNA1B | NM_000718 | calcium channel, voltage-dependent, N type, alpha 1B subunit | 1 | 0 | 0 | 1 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| SHB | NM_003028 | Src homology 2 domain containing adaptor protein B | 0 | 0 | 0 | 0 | 3 | 1 | 1 | 1 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| HEMK1 | NM_016173 | HemK methyltransferase family member 1 | 0 | 0 | 0 | 0 | 4 | 0 | 4 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| PLEKHA4 | NM_001161354 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 4 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| MTF1 | NM_005955 | metal-regulatory transcription factor 1 | 0 | 0 | 0 | 0 | 4 | 1 | 1 | 2 | hsa-miR-647 | -0.35 | N/A | Sites in UTR |
| CCDC141 | NM_173648 | coiled-coil domain containing 141 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| KIF26A | NM_015656 | kinesin family member 26A | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| ZNF319 | NM_020807 | zinc finger protein 319 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TBC1D30 | NM_015279 | TBC1 domain family, member 30 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| GADD45A | NM_001199741 | growth arrest and DNA-damage-inducible, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| NR1D2 | NM_001145425 | nuclear receptor subfamily 1, group D, member 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| HUNK | NM_014586 | hormonally up-regulated Neu-associated kinase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| SERINC3 | NM_006811 | serine incorporator 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| FBXW8 | NM_012174 | F-box and WD repeat domain containing 8 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| OXCT1 | NM_000436 | 3-oxoacid CoA transferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| ZMYM6 | NM_007167 | zinc finger, MYM-type 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| ROR2 | NM_004560 | receptor tyrosine kinase-like orphan receptor 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| NIPBL | NM_015384 | Nipped-B homolog (Drosophila) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| C10orf81 | NM_001193434 | chromosome 10 open reading frame 81 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| FSCB | NM_032135 | fibrous sheath CABYR binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| PPP1R3F | NM_001184745 | protein phosphatase 1, regulatory (inhibitor) subunit 3F | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| AQPEP | NM_173800 | laeverin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| MMP8 | NM_002424 | matrix metallopeptidase 8 (neutrophil collagenase) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| ITPRIP | NM_033397 | inositol 1,4,5-trisphosphate receptor interacting protein | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| CHIT1 | NM_003465 | chitinase 1 (chitotriosidase) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| BAIAP2L1 | NM_018842 | BAI1-associated protein 2-like 1 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TMEM132D | NM_133448 | transmembrane protein 132D | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| ARHGAP22 | NM_021226 | Rho GTPase activating protein 22 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| VSIG10L | NM_001163922 | V-set and immunoglobulin domain containing 10 like | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| PLCE1 | NM_001165979 | phospholipase C, epsilon 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| SLC6A20 | NM_020208 | solute carrier family 6 (proline IMINO transporter), member 20 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| EIF4EBP1 | NM_004095 | eukaryotic translation initiation factor 4E binding protein 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| TPRG1L | NM_182752 | tumor protein p63 regulated 1-like | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.34 | N/A | Sites in UTR |
| C3orf43 | NM_001077657 | chromosome 3 open reading frame 43 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| TNIP1 | NM_006058 | TNFAIP3 interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| NLRP1 | NM_014922 | NLR family, pyrin domain containing 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| QTRTD1 | NM_024638 | queuine tRNA-ribosyltransferase domain containing 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| SECISBP2L | NM_001193489 | SECIS binding protein 2-like | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| PPL | NM_002705 | periplakin | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| SRRM4 | NM_194286 | serine/arginine repetitive matrix 4 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| HTRA4 | NM_153692 | HtrA serine peptidase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| IQCJ | NM_001042706 | IQ motif containing J | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| CXCL9 | NM_002416 | chemokine (C-X-C motif) ligand 9 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| LCLAT1 | NM_001002257 | lysocardiolipin acyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CENPB | NM_001810 | centromere protein B, 80kDa | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| TRAF1 | NM_001190945 | TNF receptor-associated factor 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| ZNF609 | NM_015042 | zinc finger protein 609 | 1 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| PDE8B | NM_001029851 | phosphodiesterase 8B | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| KIF3C | NM_002254 | kinesin family member 3C | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| RPRD1B | NM_021215 | regulation of nuclear pre-mRNA domain containing 1B | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| SS18 | NM_001007559 | synovial sarcoma translocation, chromosome 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| PIP4K2A | NM_005028 | phosphatidylinositol-5-phosphate 4-kinase, type II, alpha | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| SPRED2 | NM_001128210 | sprouty-related, EVH1 domain containing 2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| BTBD1 | NM_001011885 | BTB (POZ) domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| POU6F1 | NM_002702 | POU class 6 homeobox 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| SLC36A2 | NM_181776 | solute carrier family 36 (proton/amino acid symporter), member 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| PTMS | NM_002824 | parathymosin | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| SSR3 | NM_007107 | signal sequence receptor, gamma (translocon-associated protein gamma) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| KIAA1147 | NM_001080392 | KIAA1147 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| ZNF705D | NM_001039615 | zinc finger protein 705D | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| TSTD2 | NM_139246 | thiosulfate sulfurtransferase (rhodanese)-like domain containing 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| FMOD | NM_002023 | fibromodulin | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PLXNA4 | NM_001105543 | plexin A4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| C16orf5 | NM_001199054 | chromosome 16 open reading frame 5 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.33 | N/A | Sites in UTR |
| GPD1L | NM_015141 | glycerol-3-phosphate dehydrogenase 1-like | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| IL18R1 | NM_003855 | interleukin 18 receptor 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| RIN3 | NM_024832 | Ras and Rab interactor 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| KIAA0930 | NM_001009880 | KIAA0930 | 1 | 0 | 0 | 1 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| KDM5C | NM_001146702 | lysine (K)-specific demethylase 5C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| TSPAN33 | NM_178562 | tetraspanin 33 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| PADI2 | NM_007365 | peptidyl arginine deiminase, type II | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| COG5 | NM_001161520 | component of oligomeric golgi complex 5 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| PLA2G15 | NM_012320 | phospholipase A2, group XV | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| SH3PXD2B | NM_001017995 | SH3 and PX domains 2B | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| ZNF318 | NM_014345 | zinc finger protein 318 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| ZNF644 | NM_016620 | zinc finger protein 644 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| ITGA6 | NM_000210 | integrin, alpha 6 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| HNRNPUL2 | NM_001079559 | heterogeneous nuclear ribonucleoprotein U-like 2 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| KATNAL2 | NM_031303 | katanin p60 subunit A-like 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| ZDHHC22 | NM_174976 | zinc finger, DHHC-type containing 22 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZNF705A | NM_001004328 | zinc finger protein 705A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| MAVS | NM_001206491 | mitochondrial antiviral signaling protein | 0 | 0 | 0 | 0 | 5 | 0 | 3 | 2 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| PHF13 | NM_153812 | PHD finger protein 13 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| SMAD2 | NM_001003652 | SMAD family member 2 | 1 | 1 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| PRAME | NM_006115 | preferentially expressed antigen in melanoma | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| IVD | NM_001159508 | isovaleryl-CoA dehydrogenase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| TRABD | NM_025204 | TraB domain containing | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| CRY2 | NM_001127457 | cryptochrome 2 (photolyase-like) | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| HSD17B14 | NM_016246 | hydroxysteroid (17-beta) dehydrogenase 14 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| LSM14B | NM_144703 | LSM14B, SCD6 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| LHFPL2 | NM_005779 | lipoma HMGIC fusion partner-like 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.32 | N/A | Sites in UTR |
| SP100 | NM_001080391 | SP100 nuclear antigen | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| GGPS1 | NM_001037277 | geranylgeranyl diphosphate synthase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| MCTP2 | NM_001159643 | multiple C2 domains, transmembrane 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| GSG1 | NM_001080554 | germ cell associated 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| FUS | NM_001170634 | fused in sarcoma | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| USP46 | NM_001134223 | ubiquitin specific peptidase 46 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| KBTBD12 | NM_207335 | kelch repeat and BTB (POZ) domain containing 12 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZNF70 | NM_021916 | zinc finger protein 70 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| G3BP1 | NM_005754 | GTPase activating protein (SH3 domain) binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| PAPOLG | NM_022894 | poly(A) polymerase gamma | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| BTN2A1 | NM_001197233 | butyrophilin, subfamily 2, member A1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| CRTAP | NM_006371 | cartilage associated protein | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| C8orf83 | NM_001171795 | chromosome 8 open reading frame 83 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| GPR180 | NM_180989 | G protein-coupled receptor 180 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| ZIC4 | NM_001168378 | Zic family member 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| SMARCA5 | NM_003601 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| CSNK1G1 | NM_022048 | casein kinase 1, gamma 1 | 1 | 0 | 1 | 0 | 3 | 1 | 1 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| C7orf64 | NM_032120 | chromosome 7 open reading frame 64 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| GPR107 | NM_001136557 | G protein-coupled receptor 107 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| MAZ | NM_001042539 | MYC-associated zinc finger protein (purine-binding transcription factor) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| FAM3C | NM_001040020 | family with sequence similarity 3, member C | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| LRPAP1 | NM_002337 | low density lipoprotein receptor-related protein associated protein 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| PLXND1 | NM_015103 | plexin D1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| DTX1 | NM_004416 | deltex homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| MATN1 | NM_002379 | matrilin 1, cartilage matrix protein | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KPNA5 | NM_002269 | karyopherin alpha 5 (importin alpha 6) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| WLS | NM_001193334 | wntless homolog (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| CACNG4 | NM_014405 | calcium channel, voltage-dependent, gamma subunit 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| DPH3 | NM_001047434 | DPH3, KTI11 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| HLA-DOA | NM_002119 | major histocompatibility complex, class II, DO alpha | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.31 | N/A | Sites in UTR |
| C8orf22 | NM_001007176 | chromosome 8 open reading frame 22 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| IL13 | NM_002188 | interleukin 13 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| CHD1 | NM_001270 | chromodomain helicase DNA binding protein 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| ICA1 | NM_004968 | islet cell autoantigen 1, 69kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| KCNK1 | NM_002245 | potassium channel, subfamily K, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| SOX21 | NM_007084 | SRY (sex determining region Y)-box 21 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| CNNM3 | NM_017623 | cyclin M3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| RALGAPA2 | NM_020343 | Ral GTPase activating protein, alpha subunit 2 (catalytic) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| RASGEF1A | NM_145313 | RasGEF domain family, member 1A | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| PPP1R12B | NM_001197131 | protein phosphatase 1, regulatory (inhibitor) subunit 12B | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| SLC44A1 | NM_080546 | solute carrier family 44, member 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| SLC2A6 | NM_001145099 | solute carrier family 2 (facilitated glucose transporter), member 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| POLR1D | NM_001206559 | polymerase (RNA) I polypeptide D, 16kDa | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TXNDC6 | NM_178130 | thioredoxin domain containing 6 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| CHMP6 | NM_024591 | chromatin modifying protein 6 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| AAK1 | NM_014911 | AP2 associated kinase 1 | 1 | 1 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | 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-647 | -0.3 | N/A | Sites in UTR |
| COL18A1 | NM_030582 | collagen, type XVIII, alpha 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| DEFB132 | NM_207469 | defensin, beta 132 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| MCM6 | NM_005915 | minichromosome maintenance complex component 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| FAM91A1 | NM_144963 | family with sequence similarity 91, member A1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| IGSF10 | NM_001178145 | immunoglobulin superfamily, member 10 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| CHGB | NM_001819 | chromogranin B (secretogranin 1) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| ATP8B1 | NM_005603 | ATPase, aminophospholipid transporter, class I, type 8B, member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| MYBL1 | NM_001080416 | v-myb myeloblastosis viral oncogene homolog (avian)-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| CARD17 | NM_001007232 | caspase recruitment domain family, member 17 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| ZNF275 | NM_001080485 | zinc finger protein 275 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| FURIN | NM_002569 | furin (paired basic amino acid cleaving enzyme) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| PDE3B | NM_000922 | phosphodiesterase 3B, cGMP-inhibited | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| FAM192A | NM_024946 | family with sequence similarity 192, member A | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| SPOCK2 | NM_001134434 | sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DNAJB1 | NM_006145 | DnaJ (Hsp40) homolog, subfamily B, member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| GNAO1 | NM_138736 | guanine nucleotide binding protein (G protein), alpha activating activity polypeptide O | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.3 | N/A | Sites in UTR |
| SPRR2G | NM_001014291 | small proline-rich protein 2G | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| OGDHL | NM_001143996 | oxoglutarate dehydrogenase-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ADAMTSL2 | NM_001145320 | ADAMTS-like 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| CCBP2 | NM_001296 | chemokine binding protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| NCOA1 | NM_003743 | nuclear receptor coactivator 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| CBLL1 | NM_024814 | Cas-Br-M (murine) ecotropic retroviral transforming sequence-like 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| OPTN | NM_001008211 | optineurin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ZWILCH | NM_017975 | Zwilch, kinetochore associated, homolog (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ANKRD23 | NM_144994 | ankyrin repeat domain 23 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| STARD9 | NM_020759 | StAR-related lipid transfer (START) domain containing 9 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| GAL3ST4 | NM_024637 | galactose-3-O-sulfotransferase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| POLE3 | NM_017443 | polymerase (DNA directed), epsilon 3 (p17 subunit) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| C12orf68 | NM_001013635 | chromosome 12 open reading frame 68 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| SLC11A1 | NM_000578 | solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| UBE2L3 | NM_003347 | ubiquitin-conjugating enzyme E2L 3 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ELOVL7 | NM_001104558 | ELOVL fatty acid elongase 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NAB1 | NM_005966 | NGFI-A binding protein 1 (EGR1 binding protein 1) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| FAM105A | NM_019018 | family with sequence similarity 105, member A | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| 4-Mar | NM_020814 | membrane-associated ring finger (C3HC4) 4 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| FAM167A | NM_053279 | family with sequence similarity 167, member A | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| PDE6B | NM_000283 | phosphodiesterase 6B, cGMP-specific, rod, beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| FCGR2A | NM_001136219 | Fc fragment of IgG, low affinity IIa, receptor (CD32) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ZDHHC14 | NM_024630 | zinc finger, DHHC-type containing 14 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| NR2F2 | NM_001145155 | nuclear receptor subfamily 2, group F, member 2 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| LPPR5 | NM_001010861 | lipid phosphate phosphatase-related protein type 5 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| SLA | NM_001045556 | Src-like-adaptor | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| C22orf13 | NM_031444 | chromosome 22 open reading frame 13 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 3 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| SMCR8 | NM_144775 | Smith-Magenis syndrome chromosome region, candidate 8 | 1 | 0 | 1 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| MASP1 | NM_001879 | mannan-binding lectin serine peptidase 1 (C4/C2 activating component of Ra-reactive factor) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| C16orf46 | NM_152337 | chromosome 16 open reading frame 46 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| IDE | NM_001165946 | insulin-degrading enzyme | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| CAMKK1 | NM_032294 | calcium/calmodulin-dependent protein kinase kinase 1, alpha | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ANO9 | NM_001012302 | anoctamin 9 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| WIZ | NM_021241 | widely interspaced zinc finger motifs | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| STAG1 | NM_005862 | stromal antigen 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| UBL4B | NM_203412 | ubiquitin-like 4B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| C1orf229 | NM_207401 | chromosome 1 open reading frame 229 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| ODC1 | NM_002539 | ornithine decarboxylase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| SUDS3 | NM_022491 | suppressor of defective silencing 3 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| TRIM40 | NM_138700 | tripartite motif containing 40 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| EP400 | NM_015409 | E1A binding protein p400 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| MFNG | NM_001166343 | MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| LIPG | NM_006033 | lipase, endothelial | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| SLFN13 | NM_144682 | schlafen family member 13 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| RAPGEF3 | NM_001098531 | Rap guanine nucleotide exchange factor (GEF) 3 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.29 | N/A | Sites in UTR |
| HPGDS | NM_014485 | hematopoietic prostaglandin D synthase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| CPT1A | NM_001876 | carnitine palmitoyltransferase 1A (liver) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ANK1 | NM_000037 | ankyrin 1, erythrocytic | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| DUSP8 | NM_004420 | dual specificity phosphatase 8 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| KIN | NM_012311 | KIN, antigenic determinant of recA protein homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SLC39A1 | NM_014437 | solute carrier family 39 (zinc transporter), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| TRIM4 | NM_033017 | tripartite motif containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| C11orf85 | NM_001037225 | chromosome 11 open reading frame 85 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ARHGEF37 | NM_001001669 | Rho guanine nucleotide exchange factor (GEF) 37 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SAMD4B | NM_018028 | sterile alpha motif domain containing 4B | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| CAMKK2 | NM_172214 | calcium/calmodulin-dependent protein kinase kinase 2, beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| LY6K | NM_001160354 | lymphocyte antigen 6 complex, locus K | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| C1orf27 | NM_001164245 | chromosome 1 open reading frame 27 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SLC9A9 | NM_173653 | solute carrier family 9 (sodium/hydrogen exchanger), member 9 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ZNF660 | NM_173658 | zinc finger protein 660 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| LDOC1L | NM_032287 | leucine zipper, down-regulated in cancer 1-like | 1 | 0 | 1 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| KIAA1826 | NM_032424 | KIAA1826 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | 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-647 | -0.28 | N/A | Sites in UTR |
| C17orf100 | NM_001105520 | chromosome 17 open reading frame 100 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| VWA5B1 | NM_001039500 | von Willebrand factor A domain containing 5B1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SRSF2 | NM_001195427 | serine/arginine-rich splicing factor 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| CUL1 | NM_003592 | cullin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| KIF4B | NM_001099293 | kinesin family member 4B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| CHL1 | NM_006614 | cell adhesion molecule with homology to L1CAM (close homolog of L1) | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 3 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SH3TC2 | NM_024577 | SH3 domain and tetratricopeptide repeats 2 | 0 | 0 | 0 | 0 | 6 | 1 | 3 | 2 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DDTL | NM_001084393 | D-dopachrome tautomerase-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| PDCD1 | NM_005018 | programmed cell death 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SMG5 | NM_015327 | smg-5 homolog, nonsense mediated mRNA decay factor (C. elegans) | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SEC13 | NM_001136232 | SEC13 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SLC14A1 | NM_001128588 | solute carrier family 14 (urea transporter), member 1 (Kidd blood group) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ZSCAN23 | NM_001012455 | zinc finger and SCAN domain containing 23 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| PARK2 | NM_004562 | parkinson protein 2, E3 ubiquitin protein ligase (parkin) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| TMEM35 | NM_021637 | transmembrane protein 35 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| USP20 | NM_001008563 | ubiquitin specific peptidase 20 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| CCDC6 | NM_005436 | coiled-coil domain containing 6 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| RGS5 | NM_001195303 | regulator of G-protein signaling 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| RGS20 | NM_003702 | regulator of G-protein signaling 20 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ABCA9 | NM_080283 | ATP-binding cassette, sub-family A (ABC1), member 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SOX12 | NM_006943 | SRY (sex determining region Y)-box 12 | 1 | 0 | 1 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| PBLD | NM_022129 | phenazine biosynthesis-like protein domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| B4GALT6 | NM_004775 | UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 6 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ST6GALNAC6 | NM_013443 | ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| FAM196A | NM_001039762 | family with sequence similarity 196, member A | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| WDR64 | NM_144625 | WD repeat domain 64 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| MS4A2 | NM_000139 | membrane-spanning 4-domains, subfamily A, member 2 (Fc fragment of IgE, high affinity I, receptor for; beta polypeptide) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| RNF24 | NM_001134337 | ring finger protein 24 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| POMT2 | NM_013382 | protein-O-mannosyltransferase 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| ARFGAP1 | NM_018209 | ADP-ribosylation factor GTPase activating protein 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.28 | N/A | Sites in UTR |
| SRSF8 | NM_032102 | serine/arginine-rich splicing factor 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| HECW2 | NM_020760 | HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| FAM127C | NM_001078173 | family with sequence similarity 127, member C | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| FXC1 | NM_012192 | fracture callus 1 homolog (rat) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| FBXO44 | NM_001014765 | F-box protein 44 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| PRKD3 | NM_005813 | protein kinase D3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| CCND2 | NM_001759 | cyclin D2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| C6orf162 | NM_001042493 | chromosome 6 open reading frame 162 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| F2RL3 | NM_003950 | coagulation factor II (thrombin) receptor-like 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| GDAP2 | NM_017686 | ganglioside induced differentiation associated protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| TRIM7 | NM_203293 | tripartite motif containing 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| KLHDC7A | NM_152375 | kelch domain containing 7A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| DIDO1 | NM_001193370 | death inducer-obliterator 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PLIN4 | NM_001080400 | perilipin 4 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| SDHC | NM_001035511 | succinate dehydrogenase complex, subunit C, integral membrane protein, 15kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| ZNF507 | NM_001136156 | zinc finger protein 507 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| UHMK1 | NM_001184763 | U2AF homology motif (UHM) kinase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| ZNF488 | NM_153034 | zinc finger protein 488 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| RUNX3 | NM_001031680 | runt-related transcription factor 3 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| HTATIP2 | NM_001098520 | HIV-1 Tat interactive protein 2, 30kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| ICA1L | NM_138468 | islet cell autoantigen 1,69kDa-like | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| AIM1 | NM_001624 | absent in melanoma 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| GRIN3A | NM_133445 | glutamate receptor, ionotropic, N-methyl-D-aspartate 3A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | 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-647 | -0.27 | N/A | Sites in UTR |
| KIAA0564 | NM_015058 | KIAA0564 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| EIF2A | NM_032025 | eukaryotic translation initiation factor 2A, 65kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| ELOF1 | NM_032377 | elongation factor 1 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| ATP2A3 | NM_005173 | ATPase, Ca++ transporting, ubiquitous | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| SLC9A6 | NM_001042537 | solute carrier family 9 (sodium/hydrogen exchanger), member 6 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| FAM84B | NM_174911 | family with sequence similarity 84, member B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| C15orf2 | NM_018958 | chromosome 15 open reading frame 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CCDC78 | NM_001031737 | coiled-coil domain containing 78 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| BTN3A3 | NM_001242803 | butyrophilin, subfamily 3, member A3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| KCTD4 | NM_198404 | potassium channel tetramerisation domain containing 4 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| INPP5K | NM_001135642 | inositol polyphosphate-5-phosphatase K | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| LRRC46 | NM_033413 | leucine rich repeat containing 46 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| DZIP1 | NM_014934 | DAZ interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| KIF4A | NM_012310 | kinesin family member 4A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| SOSTDC1 | NM_015464 | sclerostin domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| UNC80 | NM_032504 | unc-80 homolog (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| TMEM212 | NM_001164436 | transmembrane protein 212 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| HIF3A | NM_022462 | hypoxia inducible factor 3, alpha subunit | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| TMEM201 | NM_001130924 | transmembrane protein 201 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| SPRN | NM_001012508 | shadow of prion protein homolog (zebrafish) | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| CHRND | NM_000751 | cholinergic receptor, nicotinic, delta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| VPS4A | NM_013245 | vacuolar protein sorting 4 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| NR2E3 | NM_016346 | nuclear receptor subfamily 2, group E, member 3 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.27 | N/A | Sites in UTR |
| RCC1 | NM_001048194 | regulator of chromosome condensation 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.27 | 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-647 | -0.27 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CALN1 | NM_001017440 | calneuron 1 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| UBE4A | NM_001204077 | ubiquitination factor E4A | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.26 | 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-647 | -0.26 | N/A | Sites in UTR |
| SOX9 | NM_000346 | SRY (sex determining region Y)-box 9 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| ASCL1 | NM_004316 | achaete-scute complex homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| ORC4 | NM_001190879 | origin recognition complex, subunit 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| SLC19A2 | NM_006996 | solute carrier family 19 (thiamine transporter), member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| FHDC1 | NM_033393 | FH2 domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| TSPAN11 | NM_001080509 | tetraspanin 11 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| ENOSF1 | NM_001126123 | enolase superfamily member 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| STMN3 | NM_015894 | stathmin-like 3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| MYOZ3 | NM_001122853 | myozenin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| KNDC1 | NM_152643 | kinase non-catalytic C-lobe domain (KIND) containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| LMLN | NM_001136049 | leishmanolysin-like (metallopeptidase M8 family) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| APBA1 | NM_001163 | amyloid beta (A4) precursor protein-binding, family A, member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| LRRC59 | NM_018509 | leucine rich repeat containing 59 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| ZZEF1 | NM_015113 | zinc finger, ZZ-type with EF-hand domain 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| MBNL3 | NM_001170701 | muscleblind-like 3 (Drosophila) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RLF | NM_012421 | rearranged L-myc fusion | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| SPOP | NM_001007226 | speckle-type POZ protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| SNAP29 | NM_004782 | synaptosomal-associated protein, 29kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| ART5 | NM_001079536 | ADP-ribosyltransferase 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| FBLN7 | NM_001128165 | fibulin 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| BBS12 | NM_001178007 | Bardet-Biedl syndrome 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| KRTCAP3 | NM_001168364 | keratinocyte associated protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| JAM3 | NM_001205329 | junctional adhesion molecule 3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| EGR4 | NM_001965 | early growth response 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| GRK5 | NM_005308 | G protein-coupled receptor kinase 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| TLK2 | NM_001112707 | tousled-like kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| TMCO1 | NM_019026 | transmembrane and coiled-coil domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| PPDPF | NM_024299 | pancreatic progenitor cell differentiation and proliferation factor homolog (zebrafish) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| MAP3K9 | NM_033141 | mitogen-activated protein kinase kinase kinase 9 | 2 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| RGS19 | NM_001039467 | regulator of G-protein signaling 19 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| NPY | NM_000905 | neuropeptide Y | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| UNG | NM_003362 | uracil-DNA glycosylase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| AWAT2 | NM_001002254 | acyl-CoA wax alcohol acyltransferase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PPIL1 | NM_016059 | peptidylprolyl isomerase (cyclophilin)-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| RBM4 | NM_001198844 | RNA binding motif protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| LHX9 | NM_001014434 | LIM homeobox 9 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| FUNDC2 | NM_023934 | FUN14 domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| SEC14L1 | NM_001039573 | SEC14-like 1 (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| MTHFD2 | NM_006636 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| TCTN3 | NM_001143973 | tectonic family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| SLC39A8 | NM_001135147 | solute carrier family 39 (zinc transporter), member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| ENO4 | NM_001242699 | enolase family member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| CBX5 | NM_001127321 | chromobox homolog 5 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| CLEC2D | NM_001004419 | C-type lectin domain family 2, member D | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.26 | N/A | Sites in UTR |
| TIGD3 | NM_145719 | tigger transposable element derived 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| CORO1C | NM_014325 | coronin, actin binding protein, 1C | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| LSM12 | NM_152344 | LSM12 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ITPRIPL2 | NM_001034841 | inositol 1,4,5-trisphosphate receptor interacting protein-like 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ENG | NM_000118 | endoglin | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ATF7IP2 | NM_024997 | activating transcription factor 7 interacting protein 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SLC35A4 | NM_080670 | solute carrier family 35, member A4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SLC22A23 | NM_015482 | solute carrier family 22, member 23 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ADORA3 | NM_001081976 | adenosine A3 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SLC35A5 | NM_017945 | solute carrier family 35, member A5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| POLR2J3 | NM_001097615 | polymerase (RNA) II (DNA directed) polypeptide J3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| CYR61 | NM_001554 | cysteine-rich, angiogenic inducer, 61 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SLCO2B1 | NM_001145211 | solute carrier organic anion transporter family, member 2B1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| JUB | NM_032876 | jub, ajuba homolog (Xenopus laevis) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| STK24 | NM_001032296 | serine/threonine kinase 24 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.25 | 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-647 | -0.25 | N/A | Sites in UTR |
| GDPD1 | NM_001165993 | glycerophosphodiester phosphodiesterase domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| FOXJ1 | NM_001454 | forkhead box J1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| GLT25D1 | NM_024656 | glycosyltransferase 25 domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| MAGT1 | NM_032121 | magnesium transporter 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SH3KBP1 | NM_001024666 | SH3-domain kinase binding protein 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| DUSP16 | NM_030640 | dual specificity phosphatase 16 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| KCNT1 | NM_020822 | potassium channel, subfamily T, member 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| LMF1 | NM_022773 | lipase maturation factor 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| CD84 | NM_001184879 | CD84 molecule | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RAB3B | NM_002867 | RAB3B, member RAS oncogene family | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| C17orf72 | NM_001164257 | chromosome 17 open reading frame 72 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SLC35E2B | NM_001110781 | solute carrier family 35, member E2B | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| CRCP | NM_001040647 | CGRP receptor component | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SVEP1 | NM_153366 | sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ANKS6 | NM_173551 | ankyrin repeat and sterile alpha motif domain containing 6 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| RAB15 | NM_198686 | RAB15, member RAS onocogene family | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| SOST | NM_025237 | sclerostin | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| APBA2 | NM_001130414 | amyloid beta (A4) precursor protein-binding, family A, member 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ZNF75A | NM_153028 | zinc finger protein 75a | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| C3orf23 | NM_173826 | chromosome 3 open reading frame 23 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| FADS2 | NM_004265 | fatty acid desaturase 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| BICD2 | NM_001003800 | bicaudal D homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ASB13 | NM_024701 | ankyrin repeat and SOCS box containing 13 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ARNT2 | NM_014862 | aryl-hydrocarbon receptor nuclear translocator 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| BTN3A2 | NM_001197246 | butyrophilin, subfamily 3, member A2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| MPND | NM_001159846 | MPN domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| LIX1 | NM_153234 | Lix1 homolog (chicken) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZC3H7B | NM_017590 | zinc finger CCCH-type containing 7B | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| ZCCHC2 | NM_017742 | zinc finger, CCHC domain containing 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.25 | N/A | Sites in UTR |
| GALC | NM_000153 | galactosylceramidase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| PTPN12 | NM_001131008 | protein tyrosine phosphatase, non-receptor type 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| INF2 | NM_032714 | inverted formin, FH2 and WH2 domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| FAM124A | NM_001242312 | family with sequence similarity 124A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| P2RY8 | NM_178129 | purinergic receptor P2Y, G-protein coupled, 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| TGFA | NM_001099691 | transforming growth factor, alpha | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ARHGDIA | NM_001185077 | Rho GDP dissociation inhibitor (GDI) alpha | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| FBXO32 | NM_001242463 | F-box protein 32 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| FOXF1 | NM_001451 | forkhead box F1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| HLA-DQB2 | NM_001198858 | major histocompatibility complex, class II, DQ beta 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CUL4B | NM_001079872 | cullin 4B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ABI3 | NM_001135186 | ABI family, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ZCCHC10 | NM_017665 | zinc finger, CCHC domain containing 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ERGIC1 | NM_001031711 | endoplasmic reticulum-golgi intermediate compartment (ERGIC) 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CDC42BPB | NM_006035 | CDC42 binding protein kinase beta (DMPK-like) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CDC42 | NM_001039802 | cell division cycle 42 (GTP binding protein, 25kDa) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KHSRP | NM_003685 | KH-type splicing regulatory protein | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| SEMA6C | NM_001178061 | sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| OAS3 | NM_006187 | 2'-5'-oligoadenylate synthetase 3, 100kDa | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| PPIF | NM_005729 | peptidylprolyl isomerase F | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CIT | NM_001206999 | citron (rho-interacting, serine/threonine kinase 21) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| TRIM50 | NM_178125 | tripartite motif containing 50 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| TGM4 | NM_003241 | transglutaminase 4 (prostate) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| MAGED2 | NM_014599 | melanoma antigen family D, 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ATP6V1D | NM_015994 | ATPase, H+ transporting, lysosomal 34kDa, V1 subunit D | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ZNF746 | NM_001163474 | zinc finger protein 746 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| SPTBN1 | NM_003128 | spectrin, beta, non-erythrocytic 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ATOH8 | NM_032827 | atonal homolog 8 (Drosophila) | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| RALGPS2 | NM_152663 | Ral GEF with PH domain and SH3 binding motif 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.24 | 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-647 | -0.24 | N/A | Sites in UTR |
| IKBKG | NM_001099856 | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| TNFSF10 | NM_001190942 | tumor necrosis factor (ligand) superfamily, member 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| IFIT5 | NM_012420 | interferon-induced protein with tetratricopeptide repeats 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| RNASEH2C | NM_032193 | ribonuclease H2, subunit C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CDRT4 | NM_001204477 | CMT1A duplicated region transcript 4 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| GRIK3 | NM_000831 | glutamate receptor, ionotropic, kainate 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| IL2RA | NM_000417 | interleukin 2 receptor, alpha | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| TANC1 | NM_001145909 | tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| LTBP2 | NM_000428 | latent transforming growth factor beta binding protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| GLYCTK | NM_145262 | glycerate kinase | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| TBX15 | NM_152380 | T-box 15 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ADAP2 | NM_018404 | ArfGAP with dual PH domains 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CHKA | NM_001277 | choline kinase alpha | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| PLXNA2 | NM_025179 | plexin A2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CTSS | NM_001199739 | cathepsin S | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | 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-647 | -0.24 | N/A | Sites in UTR |
| PBX1 | NM_001204961 | pre-B-cell leukemia homeobox 1 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| RNF144B | NM_182757 | ring finger protein 144B | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CPLX2 | NM_001008220 | complexin 2 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| CD177 | NM_020406 | CD177 molecule | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| KIAA0240 | NM_015349 | KIAA0240 | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ARHGEF40 | NM_018071 | Rho guanine nucleotide exchange factor (GEF) 40 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GDAP1L1 | NM_024034 | ganglioside-induced differentiation-associated protein 1-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| C1orf212 | NM_001164824 | chromosome 1 open reading frame 212 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| SLAMF8 | NM_020125 | SLAM family member 8 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.24 | N/A | Sites in UTR |
| ABCA4 | NM_000350 | ATP-binding cassette, sub-family A (ABC1), member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ZNF473 | NM_001006656 | zinc finger protein 473 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ATP5S | NM_001003803 | ATP synthase, H+ transporting, mitochondrial Fo complex, subunit s (factor B) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| C17orf87 | NM_207103 | chromosome 17 open reading frame 87 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| TTF2 | NM_003594 | transcription termination factor, RNA polymerase II | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LANCL2 | NM_018697 | LanC lantibiotic synthetase component C-like 2 (bacterial) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| PHC2 | NM_004427 | polyhomeotic homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| DPYSL2 | NM_001197293 | dihydropyrimidinase-like 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| BTN3A1 | NM_001145008 | butyrophilin, subfamily 3, member A1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ZNF621 | NM_001098414 | zinc finger protein 621 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| EFS | NM_005864 | embryonal Fyn-associated substrate | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| GPR161 | NM_153832 | G protein-coupled receptor 161 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LINGO2 | NM_152570 | leucine rich repeat and Ig domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ZNF662 | NM_001134656 | zinc finger protein 662 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ADPRH | NM_001125 | ADP-ribosylarginine hydrolase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PKHD1 | NM_170724 | polycystic kidney and hepatic disease 1 (autosomal recessive) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| SLC5A6 | NM_021095 | solute carrier family 5 (sodium-dependent vitamin transporter), member 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| DVL3 | NM_004423 | dishevelled, dsh homolog 3 (Drosophila) | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| MINK1 | NM_001024937 | misshapen-like kinase 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| CD101 | NM_004258 | CD101 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ARMC8 | NM_015396 | armadillo repeat containing 8 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ZNF671 | NM_024833 | zinc finger protein 671 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| KIAA1267 | NM_001193465 | KIAA1267 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| CDV3 | NM_001134422 | CDV3 homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| UBXN2B | NM_001077619 | UBX domain protein 2B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LAMP2 | NM_013995 | lysosomal-associated membrane protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| PMM2 | NM_000303 | phosphomannomutase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| SETD1A | NM_014712 | SET domain containing 1A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| TELO2 | NM_016111 | TEL2, telomere maintenance 2, homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| COBRA1 | NM_015456 | cofactor of BRCA1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| IL36RN | NM_012275 | interleukin 36 receptor antagonist | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| AGGF1 | NM_018046 | angiogenic factor with G patch and FHA domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| RBM41 | NM_001171080 | RNA binding motif protein 41 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ELMO2 | NM_133171 | engulfment and cell motility 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| FLOT2 | NM_004475 | flotillin 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LRRC20 | NM_018205 | leucine rich repeat containing 20 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| BEST3 | NM_032735 | bestrophin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ZNF827 | NM_178835 | zinc finger protein 827 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ACER3 | NM_018367 | alkaline ceramidase 3 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| PRR14L | NM_173566 | proline rich 14-like | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| CATSPERB | NM_024764 | cation channel, sperm-associated, beta | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| SAR1B | NM_001033503 | SAR1 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| PLEKHF2 | NM_024613 | pleckstrin homology domain containing, family F (with FYVE domain) member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| PPAPDC2 | NM_203453 | phosphatidic acid phosphatase type 2 domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| RFX2 | NM_000635 | regulatory factor X, 2 (influences HLA class II expression) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| PVR | NM_001135768 | poliovirus receptor | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| MR1 | NM_001194999 | major histocompatibility complex, class I-related | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| DIP2C | NM_014974 | DIP2 disco-interacting protein 2 homolog C (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| UMODL1 | NM_001004416 | uromodulin-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| MPP7 | NM_173496 | membrane protein, palmitoylated 7 (MAGUK p55 subfamily member 7) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| TMEM154 | NM_152680 | transmembrane protein 154 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PRELP | NM_002725 | proline/arginine-rich end leucine-rich repeat protein | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| CD4 | NM_000616 | CD4 molecule | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| DNASE1L1 | NM_001009932 | deoxyribonuclease I-like 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| SUCLA2 | NM_003850 | succinate-CoA ligase, ADP-forming, beta subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LSM14A | NM_001114093 | LSM14A, SCD6 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LDLRAP1 | NM_015627 | low density lipoprotein receptor adaptor protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| CLSPN | NM_001190481 | claspin | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| LBH | NM_030915 | limb bud and heart development homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| ADAMTS17 | NM_139057 | ADAM metallopeptidase with thrombospondin type 1 motif, 17 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.23 | N/A | Sites in UTR |
| HAAO | NM_012205 | 3-hydroxyanthranilate 3,4-dioxygenase | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| RIBC1 | NM_144968 | RIB43A domain with coiled-coils 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| TTC24 | NM_001105669 | tetratricopeptide repeat domain 24 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| LRCH1 | NM_001164213 | leucine-rich repeats and calponin homology (CH) domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| RNF121 | NM_018320 | ring finger protein 121 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| KCNN3 | NM_001204087 | potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ARF6 | NM_001663 | ADP-ribosylation factor 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| TOMM22 | NM_020243 | translocase of outer mitochondrial membrane 22 homolog (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| SETX | NM_015046 | senataxin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PITPNB | NM_012399 | phosphatidylinositol transfer protein, beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| MYL10 | NM_138403 | myosin, light chain 10, regulatory | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| C1orf65 | NM_152610 | chromosome 1 open reading frame 65 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| RHBDL3 | NM_138328 | rhomboid, veinlet-like 3 (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| RPS10 | NM_001014 | ribosomal protein S10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ARSD | NM_001669 | arylsulfatase D | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ACSL3 | NM_004457 | acyl-CoA synthetase long-chain family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| THRSP | NM_003251 | thyroid hormone responsive | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| MRPS5 | NM_031902 | mitochondrial ribosomal protein S5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| C5orf44 | NM_001093755 | chromosome 5 open reading frame 44 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| FAM185A | NM_001145268 | family with sequence similarity 185, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ABCE1 | NM_001040876 | ATP-binding cassette, sub-family E (OABP), member 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| RANBP10 | NM_020850 | RAN binding protein 10 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| SNRNP48 | NM_152551 | small nuclear ribonucleoprotein 48kDa (U11/U12) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ADCYAP1R1 | NM_001118 | adenylate cyclase activating polypeptide 1 (pituitary) receptor type I | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| JMJD6 | NM_001081461 | jumonji domain containing 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| FAM20A | NM_017565 | family with sequence similarity 20, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| EMILIN3 | NM_052846 | elastin microfibril interfacer 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZAK | NM_133646 | sterile alpha motif and leucine zipper containing kinase AZK | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| MRPL30 | NM_145212 | mitochondrial ribosomal protein L30 | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 3 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ALOX12 | NM_000697 | arachidonate 12-lipoxygenase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| SSH1 | NM_001161330 | slingshot homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| CRYAA | NM_000394 | crystallin, alpha A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| EVPL | NM_001988 | envoplakin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| GBGT1 | NM_021996 | globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| TRIM11 | NM_145214 | tripartite motif containing 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| PCSK9 | NM_174936 | proprotein convertase subtilisin/kexin type 9 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| BEAN1 | NM_001136106 | brain expressed, associated with NEDD4, 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| PLCZ1 | NM_033123 | phospholipase C, zeta 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| C8orf34 | NM_001195639 | chromosome 8 open reading frame 34 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| MPZ | NM_000530 | myelin protein zero | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| MAPK7 | NM_002749 | mitogen-activated protein kinase 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| AHNAK2 | NM_138420 | AHNAK nucleoprotein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| GFER | NM_005262 | growth factor, augmenter of liver regeneration | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| FUT10 | NM_032664 | fucosyltransferase 10 (alpha (1,3) fucosyltransferase) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| ALX3 | NM_006492 | ALX homeobox 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TRANK1 | NM_014831 | tetratricopeptide repeat and ankyrin repeat containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| TNS3 | NM_022748 | tensin 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| PFKFB4 | NM_004567 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.22 | N/A | Sites in UTR |
| BNC2 | NM_017637 | basonuclin 2 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.22 | 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-647 | -0.21 | N/A | Sites in UTR |
| MLH3 | NM_001040108 | mutL homolog 3 (E. coli) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PKN3 | NM_013355 | protein kinase N3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| RTN4R | NM_023004 | reticulon 4 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| GGA2 | NM_015044 | golgi-associated, gamma adaptin ear containing, ARF binding protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| C1orf226 | NM_001085375 | chromosome 1 open reading frame 226 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| SLC9A8 | NM_015266 | solute carrier family 9 (sodium/hydrogen exchanger), member 8 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| C5orf64 | NM_173667 | chromosome 5 open reading frame 64 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| MKS1 | NM_001165927 | Meckel syndrome, type 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ZSCAN18 | NM_001145542 | zinc finger and SCAN domain containing 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ODZ4 | NM_001098816 | odz, odd Oz/ten-m homolog 4 (Drosophila) | 2 | 0 | 1 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| HJURP | NM_018410 | Holliday junction recognition protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PUS1 | NM_001002019 | pseudouridylate synthase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| KPNA1 | NM_002264 | karyopherin alpha 1 (importin alpha 5) | 3 | 1 | 1 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| C1orf21 | NM_030806 | chromosome 1 open reading frame 21 | 1 | 1 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CD53 | NM_000560 | CD53 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| LMX1A | NM_001174069 | LIM homeobox transcription factor 1, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PDLIM5 | NM_001011515 | PDZ and LIM domain 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| MFAP3L | NM_001009554 | microfibrillar-associated protein 3-like | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| UBE2H | NM_001202498 | ubiquitin-conjugating enzyme E2H | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| TBC1D16 | NM_019020 | TBC1 domain family, member 16 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| KIF5B | NM_004521 | kinesin family member 5B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ROR1 | NM_001083592 | receptor tyrosine kinase-like orphan receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| C21orf33 | NM_004649 | chromosome 21 open reading frame 33 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| EHD3 | NM_014600 | EH-domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| GLT25D2 | NM_015101 | glycosyltransferase 25 domain containing 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ZBTB7C | NM_001039360 | zinc finger and BTB domain containing 7C | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| BACE1 | NM_001207048 | beta-site APP-cleaving enzyme 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| COPB1 | NM_001144061 | coatomer protein complex, subunit beta 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| FAT3 | NM_001008781 | FAT tumor suppressor homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CYP11A1 | NM_000781 | cytochrome P450, family 11, subfamily A, polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| SLC1A7 | NM_006671 | solute carrier family 1 (glutamate transporter), member 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TCP11 | NM_001093728 | t-complex 11 homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| USH1C | NM_005709 | Usher syndrome 1C (autosomal recessive, severe) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| POLQ | NM_199420 | polymerase (DNA directed), theta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| MAP2K4 | NM_003010 | mitogen-activated protein kinase kinase 4 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| AP2A2 | NM_001242837 | adaptor-related protein complex 2, alpha 2 subunit | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| MAP2K7 | NM_145185 | mitogen-activated protein kinase kinase 7 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| IL28RA | NM_170743 | interleukin 28 receptor, alpha (interferon, lambda receptor) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| TMEM183A | NM_138391 | transmembrane protein 183A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CD27 | NM_001242 | CD27 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PECAM1 | NM_000442 | platelet/endothelial cell adhesion molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| AKAP17A | NM_005088 | A kinase (PRKA) anchor protein 17A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| SYNPO | NM_007286 | synaptopodin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ELMOD3 | NM_001135021 | ELMO/CED-12 domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| TYW1B | NM_001145440 | tRNA-yW synthesizing protein 1 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA9 | NM_031857 | protocadherin alpha 9 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHAC2 | NM_018899 | protocadherin alpha subfamily C, 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHAC1 | NM_018898 | protocadherin alpha subfamily C, 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA13 | NM_018904 | protocadherin alpha 13 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PCDHA12 | NM_018903 | protocadherin alpha 12 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA11 | NM_018902 | protocadherin alpha 11 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA10 | NM_018901 | protocadherin alpha 10 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA8 | NM_018911 | protocadherin alpha 8 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA7 | NM_018910 | protocadherin alpha 7 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA6 | NM_018909 | protocadherin alpha 6 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA5 | NM_018908 | protocadherin alpha 5 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA4 | NM_018907 | protocadherin alpha 4 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA3 | NM_018906 | protocadherin alpha 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA2 | NM_018905 | protocadherin alpha 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PCDHA1 | NM_018900 | protocadherin alpha 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| LRRTM2 | NM_015564 | leucine rich repeat transmembrane neuronal 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CCDC90A | NM_001031713 | coiled-coil domain containing 90A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CYP11B2 | NM_000498 | cytochrome P450, family 11, subfamily B, polypeptide 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PRDX1 | NM_001202431 | peroxiredoxin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ITSN1 | NM_003024 | intersectin 1 (SH3 domain protein) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| TLE2 | NM_001144761 | transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| DDX3Y | NM_001122665 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AKAP2 | NM_001004065 | A kinase (PRKA) anchor protein 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| STK38 | NM_007271 | serine/threonine kinase 38 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| POGZ | NM_001194937 | pogo transposable element with ZNF domain | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| C10orf12 | NM_015652 | chromosome 10 open reading frame 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PPM1H | NM_020700 | protein phosphatase, Mg2+/Mn2+ dependent, 1H | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| C16orf92 | NM_001109659 | chromosome 16 open reading frame 92 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PALM2-AKAP2 | NM_007203 | PALM2-AKAP2 readthrough | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| SLC25A27 | NM_001204051 | solute carrier family 25, member 27 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| DRAM1 | NM_018370 | DNA-damage regulated autophagy modulator 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| AGPAT6 | NM_178819 | 1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.21 | 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 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| KCMF1 | NM_020122 | potassium channel modulatory factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| SH3RF3 | NM_001099289 | SH3 domain containing ring finger 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| RCOR3 | NM_001136223 | REST corepressor 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| PPP1R9A | NM_001166160 | protein phosphatase 1, regulatory (inhibitor) subunit 9A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| THAP5 | NM_001130475 | THAP domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ITGB3 | NM_000212 | integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ATP6V1G1 | NM_004888 | ATPase, H+ transporting, lysosomal 13kDa, V1 subunit G1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| R3HDM1 | NM_015361 | R3H domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| DDIT4 | NM_019058 | DNA-damage-inducible transcript 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CHRNA10 | NM_020402 | cholinergic receptor, nicotinic, alpha 10 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| KLHL25 | NM_022480 | kelch-like 25 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| WSCD1 | NM_015253 | WSC domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| CASP14 | NM_012114 | caspase 14, apoptosis-related cysteine peptidase | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| ATF7 | NM_001130059 | activating transcription factor 7 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| SPTY2D1 | NM_194285 | SPT2, Suppressor of Ty, domain containing 1 (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| C9orf167 | NM_017723 | chromosome 9 open reading frame 167 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| RABL3 | NM_173825 | RAB, member of RAS oncogene family-like 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| AKT3 | NM_005465 | v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| RGAG4 | NM_001024455 | retrotransposon gag domain containing 4 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.21 | N/A | Sites in UTR |
| USP53 | NM_019050 | ubiquitin specific peptidase 53 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| NAMPT | NM_005746 | nicotinamide phosphoribosyltransferase | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| EXOC2 | NM_018303 | exocyst complex component 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| FREM3 | NM_001168235 | FRAS1 related extracellular matrix 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| FXYD3 | NM_001136008 | FXYD domain containing ion transport regulator 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KDM4C | NM_001146695 | lysine (K)-specific demethylase 4C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| WWC3 | NM_015691 | WWC family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| NARFL | NM_022493 | nuclear prelamin A recognition factor-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ADRA2C | NM_000683 | adrenergic, alpha-2C-, receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| P2RY11 | NM_002566 | purinergic receptor P2Y, G-protein coupled, 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PTGFRN | NM_020440 | prostaglandin F2 receptor negative regulator | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| TUFT1 | NM_001126337 | tuftelin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| NFE2L3 | NM_004289 | nuclear factor (erythroid-derived 2)-like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| RBM19 | NM_016196 | RNA binding motif protein 19 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | 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-647 | -0.2 | N/A | Sites in UTR |
| TYW1 | NM_018264 | tRNA-yW synthesizing protein 1 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PPAN-P2RY11 | NM_001040664 | PPAN-P2RY11 readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| RNF103-VPS24 | NM_001198954 | RNF103-VPS24 readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| EEPD1 | NM_030636 | endonuclease/exonuclease/phosphatase family domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| POFUT1 | NM_015352 | protein O-fucosyltransferase 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PNMA3 | NM_013364 | paraneoplastic antigen MA3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| NOVA1 | NM_002515 | neuro-oncological ventral antigen 1 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KCNH1 | NM_002238 | potassium voltage-gated channel, subfamily H (eag-related), member 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| STAT5A | NM_003152 | signal transducer and activator of transcription 5A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TMEM70 | NM_001040613 | transmembrane protein 70 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| URM1 | NM_001135947 | ubiquitin related modifier 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CCDC126 | NM_138771 | coiled-coil domain containing 126 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | 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-647 | -0.2 | N/A | Sites in UTR |
| MAT1A | NM_000429 | methionine adenosyltransferase I, alpha | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| IQUB | NM_178827 | IQ motif and ubiquitin domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| MAGEA6 | NM_005363 | melanoma antigen family A, 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KRT38 | NM_006771 | keratin 38 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CYP2S1 | NM_030622 | cytochrome P450, family 2, subfamily S, polypeptide 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| NT5M | NM_020201 | 5',3'-nucleotidase, mitochondrial | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SYTL4 | NM_001129896 | synaptotagmin-like 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| STX1A | NM_001165903 | syntaxin 1A (brain) | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CLMN | NM_024734 | calmin (calponin-like, transmembrane) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CPT2 | NM_000098 | carnitine palmitoyltransferase 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PEG3 | NM_001146184 | paternally expressed 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PFKP | NM_001242339 | phosphofructokinase, platelet | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SFRP1 | NM_003012 | secreted frizzled-related protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| POFUT2 | NM_015227 | protein O-fucosyltransferase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SYPL2 | NM_001040709 | synaptophysin-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ANGPTL1 | NM_004673 | angiopoietin-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | 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-647 | -0.2 | N/A | Sites in UTR |
| AP3B2 | NM_004644 | adaptor-related protein complex 3, beta 2 subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SEC61A2 | NM_001142628 | Sec61 alpha 2 subunit (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| FAHD1 | NM_001018104 | fumarylacetoacetate hydrolase domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| FADS6 | NM_178128 | fatty acid desaturase domain family, member 6 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ESPNL | NM_194312 | espin-like | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| STARD3NL | NM_032016 | STARD3 N-terminal like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| MAGEA3 | NM_005362 | melanoma antigen family A, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| MAGEA12 | NM_001166386 | melanoma antigen family A, 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| RPL28 | NM_000991 | ribosomal protein L28 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KCNK7 | NM_005714 | potassium channel, subfamily K, member 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| MOSPD3 | NM_001040097 | motile sperm domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| C1orf35 | NM_024319 | chromosome 1 open reading frame 35 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| MFSD9 | NM_032718 | major facilitator superfamily domain containing 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| C15orf42 | NM_152259 | chromosome 15 open reading frame 42 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| RIPPLY1 | NM_001171706 | ripply1 homolog (zebrafish) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PASD1 | NM_173493 | PAS domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CGNL1 | NM_032866 | cingulin-like 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| TRMT61A | NM_152307 | tRNA methyltransferase 61 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PIGY | NM_032906 | phosphatidylinositol glycan anchor biosynthesis, class Y | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| RSPRY1 | NM_133368 | ring finger and SPRY domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CXorf59 | NM_173695 | chromosome X open reading frame 59 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ADCY7 | NM_001114 | adenylate cyclase 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| T | NM_003181 | T, brachyury homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KIAA0040 | NM_001162893 | KIAA0040 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| HGS | NM_004712 | hepatocyte growth factor-regulated tyrosine kinase substrate | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| HAPLN1 | NM_001884 | hyaluronan and proteoglycan link protein 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| TEK | NM_000459 | TEK tyrosine kinase, endothelial | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| TTC4 | NM_004623 | tetratricopeptide repeat domain 4 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | 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-647 | -0.2 | N/A | Sites in UTR |
| ELMO3 | NM_024712 | engulfment and cell motility 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SPATA13 | NM_001166271 | spermatogenesis associated 13 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KIAA1462 | NM_020848 | KIAA1462 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| EIF4A2 | NM_001967 | eukaryotic translation initiation factor 4A2 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TEX15 | NM_031271 | testis expressed 15 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ZNF765 | NM_001040185 | zinc finger protein 765 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| MAP4 | NM_030885 | microtubule-associated protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| BCL2L11 | NM_001204106 | BCL2-like 11 (apoptosis facilitator) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| RBPJL | NM_014276 | recombination signal binding protein for immunoglobulin kappa J region-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| NTSR2 | NM_012344 | neurotensin receptor 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SOCS4 | NM_080867 | suppressor of cytokine signaling 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ARFIP2 | NM_001242854 | ADP-ribosylation factor interacting protein 2 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SLC26A1 | NM_022042 | solute carrier family 26 (sulfate transporter), member 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| FAM125B | NM_001011703 | family with sequence similarity 125, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PIK3AP1 | NM_152309 | phosphoinositide-3-kinase adaptor protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| HSD11B1 | NM_001206741 | hydroxysteroid (11-beta) dehydrogenase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| CEACAM6 | NM_002483 | carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| OPHN1 | NM_002547 | oligophrenin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PDE6D | NM_002601 | phosphodiesterase 6D, cGMP-specific, rod, delta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| PDE7A | NM_001242318 | phosphodiesterase 7A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SPG7 | NM_199367 | spastic paraplegia 7 (pure and complicated autosomal recessive) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KAT6B | NM_012330 | K(lysine) acetyltransferase 6B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NKIRAS2 | NM_001001349 | NFKB inhibitor interacting Ras-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ALG12 | NM_024105 | asparagine-linked glycosylation 12, alpha-1,6-mannosyltransferase homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| KCNJ14 | NM_013348 | potassium inwardly-rectifying channel, subfamily J, member 14 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| ZNF512B | NM_020713 | zinc finger protein 512B | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| SMU1 | NM_018225 | smu-1 suppressor of mec-8 and unc-52 homolog (C. elegans) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.2 | N/A | Sites in UTR |
| JMY | NM_152405 | junction mediating and regulatory protein, p53 cofactor | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| GOSR1 | NM_001007024 | golgi SNAP receptor complex member 1 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| BSN | NM_003458 | bassoon (presynaptic cytomatrix protein) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| MGLL | NM_001003794 | monoglyceride lipase | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| FBN1 | NM_000138 | fibrillin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SUCLG1 | NM_003849 | succinate-CoA ligase, alpha subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CHST9 | NM_031422 | carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PNP | NM_000270 | purine nucleoside phosphorylase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| HS3ST4 | NM_006040 | heparan sulfate (glucosamine) 3-O-sulfotransferase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| STON1 | NM_001198595 | stonin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SH3BP4 | NM_014521 | SH3-domain binding protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ZNF607 | NM_001172677 | zinc finger protein 607 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ZNF48 | NM_001214906 | zinc finger protein 48 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S100A7A | NM_176823 | S100 calcium binding protein A7A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| RPP14 | NM_001098783 | ribonuclease P/MRP 14kDa subunit | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ARHGEF9 | NM_001173479 | Cdc42 guanine nucleotide exchange factor (GEF) 9 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CACNA1I | NM_001003406 | calcium channel, voltage-dependent, T type, alpha 1I subunit | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| MYOT | NM_001135940 | myotilin | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CYTIP | NM_004288 | cytohesin 1 interacting protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| EIF2B1 | NM_001414 | eukaryotic translation initiation factor 2B, subunit 1 alpha, 26kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| USP35 | NM_020798 | ubiquitin specific peptidase 35 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PGAP1 | NM_024989 | post-GPI attachment to proteins 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| BMP8A | NM_181809 | bone morphogenetic protein 8a | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ATG13 | NM_001142673 | ATG13 autophagy related 13 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| GPT2 | NM_001142466 | glutamic pyruvate transaminase (alanine aminotransferase) 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PRKAA1 | NM_006251 | protein kinase, AMP-activated, alpha 1 catalytic subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| AP4S1 | NM_001128126 | adaptor-related protein complex 4, sigma 1 subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| KDM5A | NM_001042603 | lysine (K)-specific demethylase 5A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| COL16A1 | NM_001856 | collagen, type XVI, alpha 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| L1CAM | NM_000425 | L1 cell adhesion molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| MAGEA2 | NM_005361 | melanoma antigen family A, 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZNF24 | NM_006965 | zinc finger protein 24 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| FGF19 | NM_005117 | fibroblast growth factor 19 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| TRIM17 | NM_001024940 | tripartite motif containing 17 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| MAGEA2B | NM_153488 | melanoma antigen family A, 2B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| C22orf29 | NM_024627 | chromosome 22 open reading frame 29 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| IL8 | NM_000584 | interleukin 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | 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 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| AP1B1 | NM_001127 | adaptor-related protein complex 1, beta 1 subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ANXA13 | NM_001003954 | annexin A13 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CLTC | NM_004859 | clathrin, heavy chain (Hc) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| KALRN | NM_001024660 | kalirin, RhoGEF kinase | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| RPP30 | NM_001104546 | ribonuclease P/MRP 30kDa subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| MYO15A | NM_016239 | myosin XVA | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| C19orf10 | NM_019107 | chromosome 19 open reading frame 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | 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-647 | -0.19 | N/A | Sites in UTR |
| ATPAF2 | NM_145691 | ATP synthase mitochondrial F1 complex assembly factor 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ANKRD22 | NM_144590 | ankyrin repeat domain 22 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| MTMR6 | NM_004685 | myotubularin related protein 6 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MGEA5 | NM_001142434 | meningioma expressed antigen 5 (hyaluronidase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PPCDC | NM_021823 | phosphopantothenoylcysteine decarboxylase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| TANC2 | NM_025185 | tetratricopeptide repeat, ankyrin repeat and coiled-coil containing 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PAFAH2 | NM_000437 | platelet-activating factor acetylhydrolase 2, 40kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ZNF770 | NM_014106 | zinc finger protein 770 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ENSA | NM_004436 | endosulfine alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| IKBKE | NM_001193321 | inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| NCOA5 | NM_020967 | nuclear receptor coactivator 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PVRL4 | NM_030916 | poliovirus receptor-related 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| FAM59B | NM_001168241 | family with sequence similarity 59, member B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PPIL6 | NM_001111298 | peptidylprolyl isomerase (cyclophilin)-like 6 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| KLF12 | NM_007249 | Kruppel-like factor 12 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SLC35E2 | NM_182838 | solute carrier family 35, member E2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SUMO2 | NM_001005849 | SMT3 suppressor of mif two 3 homolog 2 (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| HTR3D | NM_001145143 | 5-hydroxytryptamine (serotonin) receptor 3 family member D | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SKA2 | NM_001100595 | spindle and kinetochore associated complex subunit 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| N4BP1 | NM_153029 | NEDD4 binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SGK2 | NM_001199264 | serum/glucocorticoid regulated kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RASGRP3 | NM_001139488 | RAS guanyl releasing protein 3 (calcium and DAG-regulated) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| C12orf23 | NM_152261 | chromosome 12 open reading frame 23 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SPSB4 | NM_080862 | splA/ryanodine receptor domain and SOCS box containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CRAT | NM_000755 | carnitine O-acetyltransferase | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SESTD1 | NM_178123 | SEC14 and spectrin domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| OR52I2 | NM_001005170 | olfactory receptor, family 52, subfamily I, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| SERPINB8 | NM_002640 | serpin peptidase inhibitor, clade B (ovalbumin), member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ZNF646 | NM_014699 | zinc finger protein 646 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | 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-647 | -0.19 | N/A | Sites in UTR |
| RIPK4 | NM_020639 | receptor-interacting serine-threonine kinase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| POLDIP3 | NM_032311 | polymerase (DNA-directed), delta interacting protein 3 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CADM3 | NM_001127173 | cell adhesion molecule 3 | 2 | 0 | 2 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| GLTPD1 | NM_001029885 | glycolipid transfer protein domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| IDS | NM_000202 | iduronate 2-sulfatase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| GLS2 | NM_013267 | glutaminase 2 (liver, mitochondrial) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| EML4 | NM_001145076 | echinoderm microtubule associated protein like 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| ZNF280C | NM_017666 | zinc finger protein 280C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| TMEM181 | NM_020823 | transmembrane protein 181 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| HCP5 | NM_006674 | HLA complex P5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| P2RY13 | NM_176894 | purinergic receptor P2Y, G-protein coupled, 13 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| CCDC85C | NM_001144995 | coiled-coil domain containing 85C | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| PER2 | NM_022817 | period homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| VAPB | NM_001195677 | VAMP (vesicle-associated membrane protein)-associated protein B and C | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.19 | N/A | Sites in UTR |
| TP53 | NM_000546 | tumor protein p53 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| MYO19 | NM_001163735 | myosin XIX | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| BTF3L4 | NM_001136497 | basic transcription factor 3-like 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| TCEAL6 | NM_001006938 | transcription elongation factor A (SII)-like 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SLC15A1 | NM_005073 | solute carrier family 15 (oligopeptide transporter), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| TPR | NM_003292 | translocated promoter region (to activated MET oncogene) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ATRN | NM_139321 | attractin | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| RNPS1 | NM_006711 | RNA binding protein S1, serine-rich domain | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| C3orf27 | NM_007354 | chromosome 3 open reading frame 27 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZNF500 | NM_021646 | zinc finger protein 500 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZDHHC11 | NM_024786 | zinc finger, DHHC-type containing 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| H1F0 | NM_005318 | H1 histone family, member 0 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SUFU | NM_016169 | suppressor of fused homolog (Drosophila) | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KCNJ16 | NM_018658 | potassium inwardly-rectifying channel, subfamily J, member 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CCDC28A | NM_015439 | coiled-coil domain containing 28A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| C7orf42 | NM_017994 | chromosome 7 open reading frame 42 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CELF4 | NM_001025087 | CUGBP, Elav-like family member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| TBL1XR1 | NM_024665 | transducin (beta)-like 1 X-linked receptor 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| FCRL3 | NM_052939 | Fc receptor-like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| IDAS | NM_001190787 | Idas protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| WNT8B | NM_003393 | wingless-type MMTV integration site family, member 8B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| EIF2S2 | NM_003908 | eukaryotic translation initiation factor 2, subunit 2 beta, 38kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SGSM2 | NM_001098509 | small G protein signaling modulator 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| OGFR | NM_007346 | opioid growth factor receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| DSCAML1 | NM_020693 | Down syndrome cell adhesion molecule like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| C5orf62 | NM_032947 | chromosome 5 open reading frame 62 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| GRAMD2 | NM_001012642 | GRAM domain containing 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.18 | 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-647 | -0.18 | N/A | Sites in UTR |
| CRB1 | NM_001193640 | crumbs homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| HEBP1 | NM_015987 | heme binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PADI6 | NM_207421 | peptidyl arginine deiminase, type VI | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ITGAV | NM_001144999 | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| MTR | NM_000254 | 5-methyltetrahydrofolate-homocysteine methyltransferase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PML | NM_002675 | promyelocytic leukemia | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| DISC1 | NM_001012958 | disrupted in schizophrenia 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZNF589 | NM_016089 | zinc finger protein 589 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CYP21A2 | NM_000500 | cytochrome P450, family 21, subfamily A, polypeptide 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PSMD11 | NM_002815 | proteasome (prosome, macropain) 26S subunit, non-ATPase, 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| KCNMB2 | NM_005832 | potassium large conductance calcium-activated channel, subfamily M, beta member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| IFNK | NM_020124 | interferon, kappa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZNF474 | NM_207317 | zinc finger protein 474 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| MCHR1 | NM_005297 | melanin-concentrating hormone receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PSMB8 | NM_004159 | proteasome (prosome, macropain) subunit, beta type, 8 (large multifunctional peptidase 7) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| VAX2 | NM_012476 | ventral anterior homeobox 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| KCNK17 | NM_001135111 | potassium channel, subfamily K, member 17 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| WDFY2 | NM_052950 | WD repeat and FYVE domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| C9orf100 | NM_032818 | chromosome 9 open reading frame 100 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.18 | 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-647 | -0.18 | N/A | Sites in UTR |
| TFCP2L1 | NM_014553 | transcription factor CP2-like 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CCDC50 | NM_174908 | coiled-coil domain containing 50 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CXorf36 | NM_176819 | chromosome X open reading frame 36 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| GPD2 | NM_000408 | glycerol-3-phosphate dehydrogenase 2 (mitochondrial) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ADPGK | NM_031284 | ADP-dependent glucokinase | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| DBT | NM_001918 | dihydrolipoamide branched chain transacylase E2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| WDFY3 | NM_014991 | WD repeat and FYVE domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| BTLA | NM_001085357 | B and T lymphocyte associated | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| DAGLA | NM_006133 | diacylglycerol lipase, alpha | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| APLN | NM_017413 | apelin | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| TRAM2 | NM_012288 | translocation associated membrane protein 2 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| FUT8 | NM_004480 | fucosyltransferase 8 (alpha (1,6) fucosyltransferase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| GLI2 | NM_005270 | GLI family zinc finger 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CLEC3A | NM_005752 | C-type lectin domain family 3, member A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PRKX | NM_005044 | protein kinase, X-linked | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| WDHD1 | NM_001008396 | WD repeat and HMG-box DNA binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| HBP1 | NM_012257 | HMG-box transcription factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CAMKV | NM_024046 | CaM kinase-like vesicle-associated | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PIGO | NM_001201484 | phosphatidylinositol glycan anchor biosynthesis, class O | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TMEM217 | NM_001162900 | transmembrane protein 217 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| KIAA1310 | NM_001115016 | KIAA1310 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| NEFH | NM_021076 | neurofilament, heavy polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PGRMC2 | NM_006320 | progesterone receptor membrane component 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| AMD1 | NM_001033059 | adenosylmethionine decarboxylase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| FGF11 | NM_004112 | fibroblast growth factor 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| IL4R | NM_000418 | interleukin 4 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| KIAA0415 | NM_014855 | KIAA0415 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| TRAK1 | NM_001042646 | trafficking protein, kinesin binding 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SH3BGRL2 | NM_031469 | SH3 domain binding glutamic acid-rich protein like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| KIRREL3 | NM_001161707 | kin of IRRE like 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PAPLN | NM_173462 | papilin, proteoglycan-like sulfated glycoprotein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| DSTYK | NM_015375 | dual serine/threonine and tyrosine protein kinase | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SIRPA | NM_001040022 | signal-regulatory protein alpha | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| LONRF2 | NM_198461 | LON peptidase N-terminal domain and ring finger 2 | 0 | 0 | 0 | 0 | 4 | 3 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| YRDC | NM_024640 | yrdC domain containing (E. coli) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CCDC82 | NM_024725 | coiled-coil domain containing 82 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| MEP1A | NM_005588 | meprin A, alpha (PABA peptide hydrolase) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MRPS12 | NM_021107 | mitochondrial ribosomal protein S12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SNAPC4 | NM_003086 | small nuclear RNA activating complex, polypeptide 4, 190kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CLDN22 | NM_001111319 | claudin 22 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| TMEM40 | NM_018306 | transmembrane protein 40 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PARP9 | NM_001146106 | poly (ADP-ribose) polymerase family, member 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ACCS | NM_001127219 | 1-aminocyclopropane-1-carboxylate synthase homolog (Arabidopsis)(non-functional) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PGAM5 | NM_138575 | phosphoglycerate mutase family member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| KIF1C | NM_006612 | kinesin family member 1C | 1 | 1 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| OBFC1 | NM_024928 | oligonucleotide/oligosaccharide-binding fold containing 1 | 0 | 0 | 0 | 0 | 4 | 1 | 1 | 2 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| RASSF8 | NM_007211 | Ras association (RalGDS/AF-6) domain family (N-terminal) member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SUMO4 | NM_001002255 | SMT3 suppressor of mif two 3 homolog 4 (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SLC4A8 | NM_001039960 | solute carrier family 4, sodium bicarbonate cotransporter, member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SIPA1L3 | NM_015073 | signal-induced proliferation-associated 1 like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SMPDL3B | NM_014474 | sphingomyelin phosphodiesterase, acid-like 3B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZRANB1 | NM_017580 | zinc finger, RAN-binding domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| RIC8B | NM_018157 | resistance to inhibitors of cholinesterase 8 homolog B (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| MCCC2 | NM_022132 | methylcrotonoyl-CoA carboxylase 2 (beta) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| LRFN4 | NM_024036 | leucine rich repeat and fibronectin type III domain containing 4 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FAM58A | NM_001130997 | family with sequence similarity 58, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CNTNAP5 | NM_130773 | contactin associated protein-like 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| CSAG1 | NM_001102576 | chondrosarcoma associated gene 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZADH2 | NM_175907 | zinc binding alcohol dehydrogenase domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| GOLGA1 | NM_002077 | golgin A1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| ZNF132 | NM_003433 | zinc finger protein 132 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| SIGLEC5 | NM_003830 | sialic acid binding Ig-like lectin 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PDLIM1 | NM_020992 | PDZ and LIM domain 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| AKAP10 | NM_007202 | A kinase (PRKA) anchor protein 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| RHOT1 | NM_001033566 | ras homolog gene family, member T1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| FAM81B | NM_152548 | family with sequence similarity 81, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| BAD | NM_004322 | BCL2-associated agonist of cell death | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| INHBB | NM_002193 | inhibin, beta B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| PPM1A | NM_021003 | protein phosphatase, Mg2+/Mn2+ dependent, 1A | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| MAPK11 | NM_002751 | mitogen-activated protein kinase 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| RGS11 | NM_003834 | regulator of G-protein signaling 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| BVES | NM_001199563 | blood vessel epicardial substance | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |
| NFAM1 | NM_145912 | NFAT activating protein with ITAM motif 1 | 0 | 0 | 0 | 0 | 4 | 0 | 2 | 2 | hsa-miR-647 | -0.18 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CCDC144A | NM_014695 | coiled-coil domain containing 144A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| WWP1 | NM_007013 | WW domain containing E3 ubiquitin protein ligase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| MOXD1 | NM_015529 | monooxygenase, DBH-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| UNC93A | NM_001143947 | unc-93 homolog A (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | 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-647 | -0.17 | N/A | Sites in UTR |
| P2RX4 | NM_002560 | purinergic receptor P2X, ligand-gated ion channel, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZNF397 | NM_001135178 | zinc finger protein 397 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| SCARF2 | NM_153334 | scavenger receptor class F, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| APPBP2 | NM_006380 | amyloid beta precursor protein (cytoplasmic tail) binding protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PLEKHG4B | NM_052909 | pleckstrin homology domain containing, family G (with RhoGef domain) member 4B | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| EGLN2 | NM_053046 | egl nine homolog 2 (C. elegans) | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TMPRSS11A | NM_001114387 | transmembrane protease, serine 11A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | 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-647 | -0.17 | N/A | Sites in UTR |
| EXOG | NM_001145464 | endo/exonuclease (5'-3'), endonuclease G-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ANKRD12 | NM_001083625 | ankyrin repeat domain 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| KCNH4 | NM_012285 | potassium voltage-gated channel, subfamily H (eag-related), member 4 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| SPDEF | NM_012391 | SAM pointed domain containing ets transcription factor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| NAT9 | NM_015654 | N-acetyltransferase 9 (GCN5-related, putative) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FNIP2 | NM_020840 | folliculin interacting protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| SAMD11 | NM_152486 | sterile alpha motif domain containing 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| KCTD20 | NM_173562 | potassium channel tetramerisation domain containing 20 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C11orf91 | NM_001166692 | chromosome 11 open reading frame 91 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| LCOR | NM_001170765 | ligand dependent nuclear receptor corepressor | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZBTB42 | NM_001137601 | zinc finger and BTB domain containing 42 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.17 | 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-647 | -0.17 | N/A | Sites in UTR |
| FOXJ3 | NM_001198850 | forkhead box J3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| 6-Mar | NM_005885 | membrane-associated ring finger (C3HC4) 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| MYL12A | NM_006471 | myosin, light chain 12A, regulatory, non-sarcomeric | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CPLX1 | NM_006651 | complexin 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| YTHDF2 | NM_001172828 | YTH domain family, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| IL17RB | NM_018725 | interleukin 17 receptor B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TMEM9B | NM_020644 | TMEM9 domain family, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| FAM160B1 | NM_001135051 | family with sequence similarity 160, member B1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| VSTM2L | NM_080607 | V-set and transmembrane domain containing 2 like | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| BTN2A2 | NM_001197237 | butyrophilin, subfamily 2, member A2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CRB3 | NM_139161 | crumbs homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NAIF1 | NM_197956 | nuclear apoptosis inducing factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| LCP2 | NM_005565 | lymphocyte cytosolic protein 2 (SH2 domain containing leukocyte protein of 76kDa) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C11orf61 | NM_024631 | chromosome 11 open reading frame 61 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PDGFRA | NM_006206 | platelet-derived growth factor receptor, alpha polypeptide | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CXCR1 | NM_000634 | chemokine (C-X-C motif) receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TSC1 | NM_000368 | tuberous sclerosis 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| B4GALT7 | NM_007255 | xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CLEC16A | NM_015226 | C-type lectin domain family 16, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| NUPR1 | NM_001042483 | nuclear protein, transcriptional regulator, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PLEKHH2 | NM_172069 | pleckstrin homology domain containing, family H (with MyTH4 domain) member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| LSM11 | NM_173491 | LSM11, U7 small nuclear RNA associated | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| MGAT5B | NM_001199172 | mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetyl-glucosaminyltransferase, isozyme B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| FAM18B2-CDRT4 | NM_001204478 | FAM18B2-CDRT4 readthrough | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| B3GAT1 | NM_018644 | beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| HDX | NM_001177478 | highly divergent homeobox | 1 | 0 | 0 | 1 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| SIKE1 | NM_001102396 | suppressor of IKBKE 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PVRL1 | NM_002855 | poliovirus receptor-related 1 (herpesvirus entry mediator C) | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CAPN2 | NM_001146068 | calpain 2, (m/II) large subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| VCAN | NM_001126336 | versican | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PRR12 | NM_020719 | proline rich 12 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CD151 | NM_001039490 | CD151 molecule (Raph blood group) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| EDN2 | NM_001956 | endothelin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| MARK3 | NM_001128918 | MAP/microtubule affinity-regulating kinase 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | 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-647 | -0.17 | N/A | Sites in UTR |
| ANKRD16 | NM_019046 | ankyrin repeat domain 16 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZNF461 | NM_153257 | zinc finger protein 461 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C22orf40 | NM_207327 | chromosome 22 open reading frame 40 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CAMSAP1 | NM_015447 | calmodulin regulated spectrin-associated protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| KITLG | NM_000899 | KIT ligand | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ASPH | NM_001164750 | aspartate beta-hydroxylase | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| UNC5C | NM_003728 | unc-5 homolog C (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ESM1 | NM_001135604 | endothelial cell-specific molecule 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PKD1L1 | NM_138295 | polycystic kidney disease 1 like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | 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-647 | -0.17 | N/A | Sites in UTR |
| RGS14 | NM_006480 | regulator of G-protein signaling 14 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| EXOC7 | NM_001013839 | exocyst complex component 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| C3orf52 | NM_001171747 | chromosome 3 open reading frame 52 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CCDC68 | NM_001143829 | coiled-coil domain containing 68 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| UCN2 | NM_033199 | urocortin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TRUB1 | NM_139169 | TruB pseudouridine (psi) synthase homolog 1 (E. coli) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| STX6 | NM_005819 | syntaxin 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CFLAR | NM_001127183 | CASP8 and FADD-like apoptosis regulator | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| F9 | NM_000133 | coagulation factor IX | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| FLNA | NM_001110556 | filamin A, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| UCHL5 | NM_001199261 | ubiquitin carboxyl-terminal hydrolase L5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ANKHD1 | NM_001197030 | ankyrin repeat and KH domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PTPRN | NM_001199763 | protein tyrosine phosphatase, receptor type, N | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TAGLN | NM_001001522 | transgelin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CREB5 | NM_001011666 | cAMP responsive element binding protein 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TSPAN15 | NM_012339 | tetraspanin 15 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| SDHAF2 | NM_017841 | succinate dehydrogenase complex assembly factor 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| FSD1L | NM_207647 | fibronectin type III and SPRY domain containing 1-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZDHHC18 | NM_032283 | zinc finger, DHHC-type containing 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CMTM4 | NM_181521 | CKLF-like MARVEL transmembrane domain containing 4 | 0 | 0 | 0 | 0 | 4 | 0 | 3 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KCNQ3 | NM_001204824 | potassium voltage-gated channel, KQT-like subfamily, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| HHAT | NM_001122834 | hedgehog acyltransferase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| FOXP2 | NM_001172766 | forkhead box P2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ALS2CL | NM_001190707 | ALS2 C-terminal like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TRDMT1 | NM_004412 | tRNA aspartic acid methyltransferase 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C8A | NM_000562 | complement component 8, alpha polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| UPK1B | NM_006952 | uroplakin 1B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| VEGFC | NM_005429 | vascular endothelial growth factor C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ANKRD26 | NM_014915 | ankyrin repeat domain 26 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| COBL | NM_015198 | cordon-bleu homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZNF419 | NM_001098491 | zinc finger protein 419 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| RSPH3 | NM_031924 | radial spoke 3 homolog (Chlamydomonas) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| LYSMD4 | NM_152449 | LysM, putative peptidoglycan-binding, domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PTPN9 | NM_002833 | protein tyrosine phosphatase, non-receptor type 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TPX2 | NM_012112 | TPX2, microtubule-associated, homolog (Xenopus laevis) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C10orf28 | NM_014472 | chromosome 10 open reading frame 28 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| NUB1 | NM_016118 | negative regulator of ubiquitin-like proteins 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| GAB1 | NM_002039 | GRB2-associated binding protein 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| BAK1 | NM_001188 | BCL2-antagonist/killer 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZNF45 | NM_003425 | zinc finger protein 45 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CEP350 | NM_014810 | centrosomal protein 350kDa | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZNF789 | NM_001013258 | zinc finger protein 789 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| AMIGO2 | NM_001143668 | adhesion molecule with Ig-like domain 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| EFNB1 | NM_004429 | ephrin-B1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| EPOR | NM_000121 | erythropoietin receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| RPS24 | NM_001142285 | ribosomal protein S24 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| S1PR4 | NM_003775 | sphingosine-1-phosphate receptor 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C2CD2 | NM_015500 | C2 calcium-dependent domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C19orf6 | NM_001033026 | chromosome 19 open reading frame 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| UROC1 | NM_001165974 | urocanase domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| PHF16 | NM_001077445 | PHD finger protein 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CASS4 | NM_001164114 | Cas scaffolding protein family member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C22orf39 | NM_001166242 | chromosome 22 open reading frame 39 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| CYBB | NM_000397 | cytochrome b-245, beta polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | 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-647 | -0.17 | N/A | Sites in UTR |
| RAD23A | NM_005053 | RAD23 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SGSH | NM_000199 | N-sulfoglucosamine sulfohydrolase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ZNF217 | NM_006526 | zinc finger protein 217 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TBC1D1 | NM_015173 | TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| TXN2 | NM_012473 | thioredoxin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| JOSD1 | NM_014876 | Josephin domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| C10orf26 | NM_001083913 | chromosome 10 open reading frame 26 | 1 | 0 | 1 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.17 | N/A | Sites in UTR |
| ARHGAP35 | NM_004491 | Rho GTPase activating protein 35 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| DDAH1 | NM_001134445 | dimethylarginine dimethylaminohydrolase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PIK3R4 | NM_014602 | phosphoinositide-3-kinase, regulatory subunit 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ADAMTS9 | NM_182920 | ADAM metallopeptidase with thrombospondin type 1 motif, 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| NKAIN2 | NM_001040214 | Na+/K+ transporting ATPase interacting 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| KRT3 | NM_057088 | keratin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| TEAD3 | NM_003214 | TEA domain family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ABHD12 | NM_001042472 | abhydrolase domain containing 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PHPT1 | NM_001135861 | phosphohistidine phosphatase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SEPX1 | NM_016332 | selenoprotein X, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| DHX35 | NM_001190809 | DEAH (Asp-Glu-Ala-His) box polypeptide 35 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ARMC6 | NM_001199196 | armadillo repeat containing 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FGD5 | NM_152536 | FYVE, RhoGEF and PH domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FZD2 | NM_001466 | frizzled family receptor 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ST8SIA1 | NM_003034 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| HDAC4 | NM_006037 | histone deacetylase 4 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ATP2B3 | NM_001001344 | ATPase, Ca++ transporting, plasma membrane 3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| LUM | NM_002345 | lumican | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| MEA1 | NM_014623 | male-enhanced antigen 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| C10orf46 | NM_153810 | chromosome 10 open reading frame 46 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CCDC39 | NM_181426 | coiled-coil domain containing 39 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ZNF470 | NM_001001668 | zinc finger protein 470 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| KLF5 | NM_001730 | Kruppel-like factor 5 (intestinal) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CYP1A1 | NM_000499 | cytochrome P450, family 1, subfamily A, polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| HLA-E | NM_005516 | major histocompatibility complex, class I, E | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SPARC | NM_003118 | secreted protein, acidic, cysteine-rich (osteonectin) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CREB3L3 | NM_032607 | cAMP responsive element binding protein 3-like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PABPN1L | NM_001080487 | poly(A) binding protein, nuclear 1-like (cytoplasmic) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| DSC2 | NM_004949 | desmocollin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SP140 | NM_007237 | SP140 nuclear body protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MOBKL1B | NM_018221 | MOB1, Mps One Binder kinase activator-like 1B (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | 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-647 | -0.16 | N/A | Sites in UTR |
| CD5 | NM_014207 | CD5 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FBLN1 | NM_006486 | fibulin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| GABRA3 | NM_000808 | gamma-aminobutyric acid (GABA) A receptor, alpha 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PTPRJ | NM_002843 | protein tyrosine phosphatase, receptor type, J | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| TP63 | NM_001114978 | tumor protein p63 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ARID2 | NM_152641 | AT rich interactive domain 2 (ARID, RFX-like) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| MAP3K5 | NM_005923 | mitogen-activated protein kinase kinase kinase 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SP140L | NM_138402 | SP140 nuclear body protein-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ZNF558 | NM_144693 | zinc finger protein 558 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ANKRD18A | NM_147195 | ankyrin repeat domain 18A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CSPG4 | NM_001897 | chondroitin sulfate proteoglycan 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| NFRKB | NM_001143835 | nuclear factor related to kappaB binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| LHX6 | NM_001242333 | LIM homeobox 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| HOOK1 | NM_015888 | hook homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FEZF2 | NM_018008 | FEZ family zinc finger 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| BCAN | NM_021948 | brevican | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| HPDL | NM_032756 | 4-hydroxyphenylpyruvate dioxygenase-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| NKD1 | NM_033119 | naked cuticle homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ZNF192 | NM_006298 | zinc finger protein 192 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| IRAK3 | NM_001142523 | interleukin-1 receptor-associated kinase 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| TRIM32 | NM_001099679 | tripartite motif containing 32 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| GLCE | NM_015554 | glucuronic acid epimerase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SULF2 | NM_001161841 | sulfatase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| EIF2C3 | NM_024852 | eukaryotic translation initiation factor 2C, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ZNF618 | NM_133374 | zinc finger protein 618 | 2 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ACTB | NM_001101 | actin, beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | 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-647 | -0.16 | N/A | Sites in UTR |
| MTL5 | NM_001039656 | metallothionein-like 5, testis-specific (tesmin) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PLCH2 | NM_014638 | phospholipase C, eta 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| RAB20 | NM_017817 | RAB20, member RAS oncogene family | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| LRRC3 | NM_030891 | leucine rich repeat containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| C5orf20 | NM_130848 | chromosome 5 open reading frame 20 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| KIF21B | NM_017596 | kinesin family member 21B | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| NCOR2 | NM_001077261 | nuclear receptor corepressor 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ACTN3 | NM_001104 | actinin, alpha 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| APOC2 | NM_000483 | apolipoprotein C-II | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FCGR2C | NM_201563 | Fc fragment of IgG, low affinity IIc, receptor for (CD32) (gene/pseudogene) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| KRTAP1-1 | NM_030967 | keratin associated protein 1-1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| DEFB125 | NM_153325 | defensin, beta 125 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| H2BFM | NM_001164416 | H2B histone family, member M | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| KLHL30 | NM_198582 | kelch-like 30 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| DUSP4 | NM_001394 | dual specificity phosphatase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| EMP1 | NM_001423 | epithelial membrane protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ITGA9 | NM_002207 | integrin, alpha 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ARHGEF2 | NM_001162383 | Rho/Rac guanine nucleotide exchange factor (GEF) 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CCDC165 | NM_015210 | coiled-coil domain containing 165 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| RGMA | NM_001166283 | RGM domain family, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PCBP4 | NM_001174100 | poly(rC) binding protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PLA2G2F | NM_022819 | phospholipase A2, group IIF | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| 3-Mar | NM_178450 | membrane-associated ring finger (C3HC4) 3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| TULP4 | NM_001007466 | tubby like protein 4 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ARL6IP5 | NM_006407 | ADP-ribosylation-like factor 6 interacting protein 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PBOV1 | NM_021635 | prostate and breast cancer overexpressed 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ASXL3 | NM_030632 | additional sex combs like 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| TADA2B | NM_152293 | transcriptional adaptor 2B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CXCL17 | NM_198477 | chemokine (C-X-C motif) ligand 17 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| MMP14 | NM_004995 | matrix metallopeptidase 14 (membrane-inserted) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SDPR | NM_004657 | serum deprivation response | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SDS | NM_006843 | serine dehydratase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SLC48A1 | NM_017842 | solute carrier family 48 (heme transporter), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| XPO5 | NM_020750 | exportin 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| CDCA5 | NM_080668 | cell division cycle associated 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SGK494 | NM_001174103 | uncharacterized serine/threonine-protein kinase SgK494 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| GPR111 | NM_153839 | G protein-coupled receptor 111 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| DDX51 | NM_175066 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 51 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ARHGAP26 | NM_001135608 | Rho GTPase activating protein 26 | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ACACB | NM_001093 | acetyl-CoA carboxylase beta | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| MLX | NM_170607 | MAX-like protein X | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| PNKD | NM_001077399 | paroxysmal nonkinesigenic dyskinesia | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| APOLD1 | NM_001130415 | apolipoprotein L domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MAP2 | NM_001039538 | microtubule-associated protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| RPL36A | NM_001199972 | ribosomal protein L36a | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ZNF460 | NM_006635 | zinc finger protein 460 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | 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 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| GPATCH8 | NM_001002909 | G patch domain containing 8 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| NECAP1 | NM_015509 | NECAP endocytosis associated 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| JMJD4 | NM_001161465 | jumonji domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ALPK2 | NM_052947 | alpha-kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FAM122C | NM_001170780 | family with sequence similarity 122C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FAM120C | NM_017848 | family with sequence similarity 120C | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FOXO4 | NM_001170931 | forkhead box O4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| ZNF135 | NM_001164529 | zinc finger protein 135 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| FAM118A | NM_001104595 | family with sequence similarity 118, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| OSR1 | NM_145260 | odd-skipped related 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| SRRM3 | NM_001110199 | serine/arginine repetitive matrix 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| IL6ST | NM_001190981 | interleukin 6 signal transducer (gp130, oncostatin M receptor) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.16 | N/A | Sites in UTR |
| TCF21 | NM_198392 | transcription factor 21 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.16 | 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-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SLC1A1 | NM_004170 | solute carrier family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ZBBX | NM_001199201 | zinc finger, B-box domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ELL3 | NM_025165 | elongation factor RNA polymerase II-like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| DAOA | NM_001161812 | D-amino acid oxidase activator | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TMEM194B | NM_001142645 | transmembrane protein 194B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RNF40 | NM_001207033 | ring finger protein 40 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| BAI1 | NM_001702 | brain-specific angiogenesis inhibitor 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| GNAT1 | NM_144499 | guanine nucleotide binding protein (G protein), alpha transducing activity polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RNF103 | NM_001198952 | ring finger protein 103 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | 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 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PLEKHB2 | NM_001100623 | pleckstrin homology domain containing, family B (evectins) member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| UBE2QL1 | NM_001145161 | ubiquitin-conjugating enzyme E2Q family-like 1 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SHC3 | NM_016848 | SHC (Src homology 2 domain containing) transforming protein 3 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RPS6KA3 | NM_004586 | ribosomal protein S6 kinase, 90kDa, polypeptide 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| NFYA | NM_002505 | nuclear transcription factor Y, alpha | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TTBK1 | NM_032538 | tau tubulin kinase 1 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FTL | NM_000146 | ferritin, light polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| 2-Sep | NM_001008491 | septin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KCNQ1 | NM_000218 | potassium voltage-gated channel, KQT-like subfamily, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MAX | NM_002382 | MYC associated factor X | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TPD52L2 | NM_003288 | tumor protein D52-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ZNF3 | NM_032924 | zinc finger protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RASSF7 | NM_001143993 | Ras association (RalGDS/AF-6) domain family (N-terminal) member 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CCR9 | NM_006641 | chemokine (C-C motif) receptor 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ING4 | NM_001127582 | inhibitor of growth family, member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SETD4 | NM_017438 | SET domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| NKAIN1 | NM_024522 | Na+/K+ transporting ATPase interacting 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| IL34 | NM_001172771 | interleukin 34 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MMD2 | NM_001100600 | monocyte to macrophage differentiation-associated 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FLNB | NM_001164317 | filamin B, beta | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SCNN1G | NM_001039 | sodium channel, nonvoltage-gated 1, gamma | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SIX3 | NM_005413 | SIX homeobox 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRDX6 | NM_004905 | peroxiredoxin 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ZCCHC11 | NM_001009881 | zinc finger, CCHC domain containing 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FIGNL1 | NM_001042762 | fidgetin-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| C15orf41 | NM_032499 | chromosome 15 open reading frame 41 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CCDC149 | NM_001130726 | coiled-coil domain containing 149 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ZDHHC20 | NM_153251 | zinc finger, DHHC-type containing 20 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| LPP | NM_001167671 | LIM domain containing preferred translocation partner in lipoma | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| AK3 | NM_001199852 | adenylate kinase 3 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| NHSL1 | NM_001144060 | NHS-like 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| G6PC3 | NM_138387 | glucose 6 phosphatase, catalytic, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ZNF25 | NM_145011 | zinc finger protein 25 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRRT4 | NM_001114726 | proline-rich transmembrane protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| GTF2H5 | NM_207118 | general transcription factor IIH, polypeptide 5 | 0 | 0 | 0 | 0 | 2 | 2 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| NAA50 | NM_025146 | N(alpha)-acetyltransferase 50, NatE catalytic subunit | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| C18orf1 | NM_001003674 | chromosome 18 open reading frame 1 | 1 | 1 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| DYNC1LI2 | NM_006141 | dynein, cytoplasmic 1, light intermediate chain 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CSF1 | NM_000757 | colony stimulating factor 1 (macrophage) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SERPINA1 | NM_000295 | serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PLEKHA2 | NM_021623 | pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MRPS26 | NM_030811 | mitochondrial ribosomal protein S26 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MMEL1 | NM_033467 | membrane metallo-endopeptidase-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SLC25A29 | NM_001039355 | solute carrier family 25, member 29 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ENPEP | NM_001977 | glutamyl aminopeptidase (aminopeptidase A) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | 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 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MMGT1 | NM_173470 | membrane magnesium transporter 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TCF20 | NM_005650 | transcription factor 20 (AR1) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| HAP1 | NM_001079870 | huntingtin-associated protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| 10-Mar | NM_001100875 | membrane-associated ring finger (C3HC4) 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SYNPO2 | NM_001128933 | synaptopodin 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SLC25A34 | NM_207348 | solute carrier family 25, member 34 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FAM160B2 | NM_022749 | family with sequence similarity 160, member B2 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SLC30A7 | NM_001144884 | solute carrier family 30 (zinc transporter), member 7 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SOX5 | NM_006940 | SRY (sex determining region Y)-box 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| WNT2 | NM_003391 | wingless-type MMTV integration site family member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MAGI1 | NM_001033057 | membrane associated guanylate kinase, WW and PDZ domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RASGRP1 | NM_001128602 | RAS guanyl releasing protein 1 (calcium and DAG-regulated) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| AIDA | NM_022831 | axin interactor, dorsalization associated | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FCHSD1 | NM_033449 | FCH and double SH3 domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRR20A | NM_198441 | proline rich 20A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| DGAT2L6 | NM_198512 | diacylglycerol O-acyltransferase 2-like 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PRR20B | NM_001130404 | proline rich 20B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRR20C | NM_001130405 | proline rich 20C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRR20D | NM_001130406 | proline rich 20D | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRR20E | NM_001130407 | proline rich 20E | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ACE | NM_000789 | angiotensin I converting enzyme (peptidyl-dipeptidase A) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| HIP1 | NM_005338 | huntingtin interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CCL21 | NM_002989 | chemokine (C-C motif) ligand 21 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| GOSR2 | NM_004287 | golgi SNAP receptor complex member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FBXO9 | NM_012347 | F-box protein 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MIER1 | NM_001077700 | mesoderm induction early response 1 homolog (Xenopus laevis) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SMTNL1 | NM_001105565 | smoothelin-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MKX | NM_001242702 | mohawk homeobox | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ARID5B | NM_032199 | AT rich interactive domain 5B (MRF1-like) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| GPX7 | NM_015696 | glutathione peroxidase 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| KIF2A | NM_001098511 | kinesin heavy chain member 2A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| NFATC1 | NM_172390 | nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| C1orf38 | NM_001039477 | chromosome 1 open reading frame 38 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| GOLIM4 | NM_014498 | golgi integral membrane protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PBRM1 | NM_018165 | polybromo 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CNKSR3 | NM_173515 | CNKSR family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TMEM233 | NM_001136534 | transmembrane protein 233 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CLLU1 | NM_001025233 | chronic lymphocytic leukemia up-regulated 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TEC | NM_003215 | tec protein tyrosine kinase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TMEM194A | NM_001130963 | transmembrane protein 194A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| HSD17B12 | NM_016142 | hydroxysteroid (17-beta) dehydrogenase 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SYT13 | NM_020826 | synaptotagmin XIII | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| FAM100B | NM_182565 | family with sequence similarity 100, member B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| HAS3 | NM_001199280 | hyaluronan synthase 3 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| BTBD9 | NM_001099272 | BTB (POZ) domain containing 9 | 0 | 0 | 0 | 0 | 4 | 0 | 4 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CREBL2 | NM_001310 | cAMP responsive element binding protein-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | 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-647 | -0.15 | N/A | Sites in UTR |
| WDR41 | NM_018268 | WD repeat domain 41 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CHD9 | NM_025134 | chromodomain helicase DNA binding protein 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| EXD1 | NM_152596 | exonuclease 3'-5' domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TMEM81 | NM_203376 | transmembrane protein 81 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| MTHFD2L | NM_001144978 | methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NKX2-5 | NM_001166175 | NK2 homeobox 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SYT4 | NM_020783 | synaptotagmin IV | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CHERP | NM_006387 | calcium homeostasis endoplasmic reticulum protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SPSB1 | NM_025106 | splA/ryanodine receptor domain and SOCS box containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ATAD1 | NM_032810 | ATPase family, AAA domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TMEM80 | NM_001042463 | transmembrane protein 80 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| POTEF | NM_001099771 | POTE ankyrin domain family, member F | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| KCTD15 | NM_001129994 | potassium channel tetramerisation domain containing 15 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ICK | NM_014920 | intestinal cell (MAK-like) kinase | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TTLL5 | NM_015072 | tubulin tyrosine ligase-like family, member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ERLEC1 | NM_001127397 | endoplasmic reticulum lectin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PAK7 | NM_020341 | p21 protein (Cdc42/Rac)-activated kinase 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SLC47A2 | NM_001099646 | solute carrier family 47, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| BTNL9 | NM_152547 | butyrophilin-like 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ITPR2 | NM_002223 | inositol 1,4,5-trisphosphate receptor, type 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TPMT | NM_000367 | thiopurine S-methyltransferase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PACSIN2 | NM_001184970 | protein kinase C and casein kinase substrate in neurons 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CCDC13 | NM_144719 | coiled-coil domain containing 13 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZC3H12D | NM_207360 | zinc finger CCCH-type containing 12D | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| CBLN3 | NM_001039771 | cerebellin 3 precursor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| D2HGDH | NM_152783 | D-2-hydroxyglutarate dehydrogenase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RGS6 | NM_001204416 | regulator of G-protein signaling 6 | 0 | 0 | 0 | 0 | 4 | 1 | 1 | 2 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| KIAA1045 | NM_015297 | KIAA1045 | 1 | 0 | 1 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SMPD3 | NM_018667 | sphingomyelin phosphodiesterase 3, neutral membrane (neutral sphingomyelinase II) | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| WASF2 | NM_001201404 | WAS protein family, member 2 | 1 | 1 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| SYN2 | NM_003178 | synapsin II | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PPIL2 | NM_014337 | peptidylprolyl isomerase (cyclophilin)-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| POLDIP2 | NM_015584 | polymerase (DNA-directed), delta interacting protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| ERI2 | NM_001142725 | ERI1 exoribonuclease family member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PTBP1 | NM_002819 | polypyrimidine tract binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| HHLA1 | NM_001145095 | HERV-H LTR-associating 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| KRI1 | NM_023008 | KRI1 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| C3orf25 | NM_207307 | chromosome 3 open reading frame 25 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| RNF180 | NM_001113561 | ring finger protein 180 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| PRKCA | NM_002737 | protein kinase C, alpha | 0 | 0 | 0 | 0 | 3 | 1 | 1 | 1 | hsa-miR-647 | -0.15 | N/A | Sites in UTR |
| TFAM | NM_003201 | transcription factor A, mitochondrial | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KDM6A | NM_021140 | lysine (K)-specific demethylase 6A | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RUFY3 | NM_014961 | RUN and FYVE domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ADCK3 | NM_020247 | aarF domain containing kinase 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RFWD2 | NM_001001740 | ring finger and WD repeat domain 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NSUN7 | NM_024677 | NOP2/Sun domain family, member 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ATP2B2 | NM_001001331 | ATPase, Ca++ transporting, plasma membrane 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BGN | NM_001711 | biglycan | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RYR2 | NM_001035 | ryanodine receptor 2 (cardiac) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CCL25 | NM_001201359 | chemokine (C-C motif) ligand 25 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PRPF4 | NM_004697 | PRP4 pre-mRNA processing factor 4 homolog (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NSUN5 | NM_001168347 | NOP2/Sun domain family, member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| LRRC8A | NM_001127244 | leucine rich repeat containing 8 family, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NAV1 | NM_001167738 | neuron navigator 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.14 | 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 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ATG2B | NM_018036 | ATG2 autophagy related 2 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RRP7A | NM_015703 | ribosomal RNA processing 7 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| KLF6 | NM_001160124 | Kruppel-like factor 6 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| E2F6 | NM_198256 | E2F transcription factor 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LRRC14 | NM_014665 | leucine rich repeat containing 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| KDM3B | NM_016604 | lysine (K)-specific demethylase 3B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RAPH1 | NM_203365 | Ras association (RalGDS/AF-6) and pleckstrin homology domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MAPKAP1 | NM_001006617 | mitogen-activated protein kinase associated protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FAM124B | NM_001122779 | family with sequence similarity 124B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| C1QL2 | NM_182528 | complement component 1, q subcomponent-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SLC26A5 | NM_206883 | solute carrier family 26, member 5 (prestin) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| OAS2 | NM_016817 | 2'-5'-oligoadenylate synthetase 2, 69/71kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RNF8 | NM_003958 | ring finger protein 8 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RAX | NM_013435 | retina and anterior neural fold homeobox | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ARHGAP39 | NM_025251 | Rho GTPase activating protein 39 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ABHD15 | NM_198147 | abhydrolase domain containing 15 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DUSP15 | NM_001012644 | dual specificity phosphatase 15 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TAF8 | NM_138572 | TAF8 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 43kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RD3 | NM_001164688 | retinal degeneration 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TMPPE | NM_001039770 | transmembrane protein with metallophosphoesterase domain | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SOLH | NM_005632 | small optic lobes homolog (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| IL16 | NM_001172128 | interleukin 16 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| AFF1 | NM_001166693 | AF4/FMR2 family, member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DNAJC5 | NM_025219 | DnaJ (Hsp40) homolog, subfamily C, member 5 | 0 | 0 | 0 | 0 | 5 | 0 | 5 | 0 | hsa-miR-647 | -0.14 | 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-647 | -0.14 | N/A | Sites in UTR |
| EDNRA | NM_001166055 | endothelin receptor type A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TGFBR2 | NM_001024847 | transforming growth factor, beta receptor II (70/80kDa) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ACOX3 | NM_001101667 | acyl-CoA oxidase 3, pristanoyl | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TBX18 | NM_001080508 | T-box 18 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PDCD6IP | NM_001162429 | programmed cell death 6 interacting protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SCLY | NM_016510 | selenocysteine lyase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SFXN3 | NM_030971 | sideroflexin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZNF491 | NM_152356 | zinc finger protein 491 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BOK | NM_032515 | BCL2-related ovarian killer | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SULT1C2 | NM_001056 | sulfotransferase family, cytosolic, 1C, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TNK1 | NM_003985 | tyrosine kinase, non-receptor, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| VWA1 | NM_022834 | von Willebrand factor A domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BAHCC1 | NM_001080519 | BAH domain and coiled-coil containing 1 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| AARS | NM_001605 | alanyl-tRNA synthetase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ABCF1 | NM_001025091 | ATP-binding cassette, sub-family F (GCN20), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| COL11A1 | NM_001190709 | collagen, type XI, alpha 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NRG1 | NM_001159995 | neuregulin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ELMO1 | NM_001039459 | engulfment and cell motility 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| KLF3 | NM_016531 | Kruppel-like factor 3 (basic) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NLGN3 | NM_001166660 | neuroligin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| GPRC5C | NM_018653 | G protein-coupled receptor, family C, group 5, member C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| METTL21D | NM_001040662 | methyltransferase like 21D | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NLRC5 | NM_032206 | NLR family, CARD domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CCDC135 | NM_032269 | coiled-coil domain containing 135 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MRFAP1 | NM_033296 | Morf4 family associated protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NXNL2 | NM_145283 | nucleoredoxin-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| EPS15 | NM_001159969 | epidermal growth factor receptor pathway substrate 15 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NR1I2 | NM_003889 | nuclear receptor subfamily 1, group I, member 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DDN | NM_015086 | dendrin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ARHGEF10L | NM_001011722 | Rho guanine nucleotide exchange factor (GEF) 10-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ANKS1B | NM_001204065 | ankyrin repeat and sterile alpha motif domain containing 1B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| VPS37B | NM_024667 | vacuolar protein sorting 37 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TMEM129 | NM_001127266 | transmembrane protein 129 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LPIN2 | NM_014646 | lipin 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ARHGEF38 | NM_001242729 | Rho guanine nucleotide exchange factor (GEF) 38 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ESR1 | NM_000125 | estrogen receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| GP1BA | NM_000173 | glycoprotein Ib (platelet), alpha polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| OPRM1 | NM_000914 | opioid receptor, mu 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CSRP3 | NM_001127656 | cysteine and glycine-rich protein 3 (cardiac LIM protein) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SPEN | NM_015001 | spen homolog, transcriptional regulator (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| HINFP | NM_015517 | histone H4 transcription factor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NRN1 | NM_016588 | neuritin 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FANCM | NM_020937 | Fanconi anemia, complementation group M | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NADK | NM_001198993 | NAD kinase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| EFHC1 | NM_001172420 | EF-hand domain (C-terminal) containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ASCL4 | NM_203436 | achaete-scute complex homolog 4 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TXLNB | NM_153235 | taxilin beta | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| LFNG | NM_001040167 | LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SLC38A3 | NM_006841 | solute carrier family 38, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FTO | NM_001080432 | fat mass and obesity associated | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| C19orf44 | NM_032207 | chromosome 19 open reading frame 44 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| BBS5 | NM_152384 | Bardet-Biedl syndrome 5 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| GJA5 | NM_005266 | gap junction protein, alpha 5, 40kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| GOLGB1 | NM_004487 | golgin B1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CD200 | NM_001004196 | CD200 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TNFSF13B | NM_001145645 | tumor necrosis factor (ligand) superfamily, member 13b | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MRPL42 | NM_014050 | mitochondrial ribosomal protein L42 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BRK1 | NM_018462 | BRICK1, SCAR/WAVE actin-nucleating complex subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| UNC45B | NM_001033576 | unc-45 homolog B (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SPRYD4 | NM_207344 | SPRY domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| C2orf71 | NM_001029883 | chromosome 2 open reading frame 71 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DNASE1L2 | NM_001374 | deoxyribonuclease I-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DPYSL3 | NM_001197294 | dihydropyrimidinase-like 3 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| 9-Sep | NM_001113491 | septin 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BET1L | NM_001098787 | blocked early in transport 1 homolog (S. cerevisiae)-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ENAH | NM_001008493 | enabled homolog (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -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-647 | -0.14 | N/A | Sites in UTR |
| UBTD1 | NM_024954 | ubiquitin domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ITFG3 | NM_032039 | integrin alpha FG-GAP repeat containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RBM8A | NM_005105 | RNA binding motif protein 8A | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TRIM67 | NM_001004342 | tripartite motif containing 67 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MLLT1 | NM_005934 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SNPH | NM_014723 | syntaphilin | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CD52 | NM_001803 | CD52 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| HNRNPA1 | NM_002136 | heterogeneous nuclear ribonucleoprotein A1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PDZK1IP1 | NM_005764 | PDZK1 interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SLC35D2 | NM_007001 | solute carrier family 35, member D2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| UBR5 | NM_015902 | ubiquitin protein ligase E3 component n-recognin 5 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FAM190B | NM_018999 | family with sequence similarity 190, member B | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| AGK | NM_018238 | acylglycerol kinase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| HNRNPA1L2 | NM_001011724 | heterogeneous nuclear ribonucleoprotein A1-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| AQP11 | NM_173039 | aquaporin 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MAP3K10 | NM_002446 | mitogen-activated protein kinase kinase kinase 10 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| HIVEP3 | NM_001127714 | human immunodeficiency virus type I enhancer binding protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TMEM198 | NM_001005209 | transmembrane protein 198 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CDC42BPA | NM_003607 | CDC42 binding protein kinase alpha (DMPK-like) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CDC25C | NM_001790 | cell division cycle 25 homolog C (S. pombe) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DPYS | NM_001385 | dihydropyrimidinase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MYO10 | NM_012334 | myosin X | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZNF193 | NM_001199479 | zinc finger protein 193 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MRPS2 | NM_016034 | mitochondrial ribosomal protein S2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BCL11A | NM_018014 | B-cell CLL/lymphoma 11A (zinc finger protein) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CT62 | NM_001102658 | cancer/testis antigen 62 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| LARS2 | NM_015340 | leucyl-tRNA synthetase 2, mitochondrial | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ABTB2 | NM_145804 | ankyrin repeat and BTB (POZ) domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MFSD6 | NM_017694 | major facilitator superfamily domain containing 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZNF395 | NM_018660 | zinc finger protein 395 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| HAUS3 | NM_024511 | HAUS augmin-like complex, subunit 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PPAPDC3 | NM_032728 | phosphatidic acid phosphatase type 2 domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FIBCD1 | NM_001145106 | fibrinogen C domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SCRT2 | NM_033129 | scratch homolog 2, zinc finger protein (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TBC1D20 | NM_144628 | TBC1 domain family, member 20 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| HOXB13 | NM_006361 | homeobox B13 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.14 | 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-647 | -0.14 | N/A | Sites in UTR |
| BMP6 | NM_001718 | bone morphogenetic protein 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PMP2 | NM_002677 | peripheral myelin protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RING1 | NM_002931 | ring finger protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| IDI2 | NM_033261 | isopentenyl-diphosphate delta isomerase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZNF773 | NM_198542 | zinc finger protein 773 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MIA3 | NM_198551 | melanoma inhibitory activity family, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZNF43 | NM_003423 | zinc finger protein 43 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| LRRFIP1 | NM_001137550 | leucine rich repeat (in FLII) interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| BMS1 | NM_014753 | BMS1 homolog, ribosome assembly protein (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MZB1 | NM_016459 | marginal zone B and B1 cell-specific protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| EPN3 | NM_017957 | epsin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PPP1R3B | NM_001201329 | protein phosphatase 1, regulatory (inhibitor) subunit 3B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| THAP9 | NM_024672 | THAP domain containing 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| CENPP | NM_001012267 | centromere protein P | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NUDCD3 | NM_015332 | NudC domain containing 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DMP1 | NM_001079911 | dentin matrix acidic phosphoprotein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| INSL3 | NM_005543 | insulin-like 3 (Leydig cell) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MPI | NM_002435 | mannose phosphate isomerase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MAPK9 | NM_002752 | mitogen-activated protein kinase 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TNFSF13 | NM_001198622 | tumor necrosis factor (ligand) superfamily, member 13 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RALBP1 | NM_006788 | ralA binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SPTBN5 | NM_016642 | spectrin, beta, non-erythrocytic 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| LYPD6 | NM_001195685 | LY6/PLAUR domain containing 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FAM170B | NM_001164484 | family with sequence similarity 170, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ACER2 | NM_001010887 | alkaline ceramidase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TNFSF12-TNFSF13 | NM_172089 | TNFSF12-TNFSF13 readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZDHHC7 | NM_001145548 | zinc finger, DHHC-type containing 7 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| H2AFX | NM_002105 | H2A histone family, member X | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PAPD5 | NM_001040284 | PAP associated domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZNF598 | NM_178167 | zinc finger protein 598 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SPECC1 | NM_001033553 | sperm antigen with calponin homology and coiled-coil domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ZFYVE27 | NM_001002261 | zinc finger, FYVE domain containing 27 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TMEM105 | NM_178520 | transmembrane protein 105 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FAIM2 | NM_012306 | Fas apoptotic inhibitory molecule 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NUDT2 | NM_001161 | nudix (nucleoside diphosphate linked moiety X)-type motif 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| F5 | NM_000130 | coagulation factor V (proaccelerin, labile factor) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MTAP | NM_002451 | methylthioadenosine phosphorylase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SUPT16H | NM_007192 | suppressor of Ty 16 homolog (S. cerevisiae) | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| PRMT6 | NM_018137 | protein arginine methyltransferase 6 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SRCRB4D | NM_080744 | scavenger receptor cysteine rich domain containing, group B (4 domains) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| NEURL2 | NM_080749 | neuralized homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| METRNL | NM_001004431 | meteorin, glial cell differentiation regulator-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| SHROOM2 | NM_001649 | shroom family member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| ENTPD3 | NM_001248 | ectonucleoside triphosphate diphosphohydrolase 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| EPHA8 | NM_020526 | EPH receptor A8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| MUC6 | NM_005961 | mucin 6, oligomeric mucus/gel-forming | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TBC1D25 | NM_002536 | TBC1 domain family, member 25 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TMOD1 | NM_001166116 | tropomodulin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| TSPAN5 | NM_005723 | tetraspanin 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DMRTB1 | NM_033067 | DMRT-like family B with proline-rich C-terminal, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -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-647 | -0.14 | N/A | Sites in UTR |
| APOL6 | NM_030641 | apolipoprotein L, 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| RASL10B | NM_033315 | RAS-like, family 10, member B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| DEGS2 | NM_206918 | degenerative spermatocyte homolog 2, lipid desaturase (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |
| FAM65C | NM_080829 | family with sequence similarity 65, member C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.14 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NFASC | NM_001005388 | neurofascin | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ST3GAL2 | NM_006927 | ST3 beta-galactoside alpha-2,3-sialyltransferase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MPDU1 | NM_004870 | mannose-P-dolichol utilization defect 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| BRP44 | NM_001143674 | brain protein 44 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ZNF285 | NM_152354 | zinc finger protein 285 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | 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-647 | -0.13 | N/A | Sites in UTR |
| C15orf54 | NM_207445 | chromosome 15 open reading frame 54 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| IL6R | NM_000565 | interleukin 6 receptor | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PDE2A | NM_001143839 | phosphodiesterase 2A, cGMP-stimulated | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PET112 | NM_004564 | PET112 homolog (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| FKBP6 | NM_001135211 | FK506 binding protein 6, 36kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| VMAC | NM_001017921 | vimentin-type intermediate filament associated coiled-coil protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SFTPA1 | NM_001093770 | surfactant protein A1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PHF2 | NM_005392 | PHD finger protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CDK2 | NM_001798 | cyclin-dependent kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MEIS1 | NM_002398 | Meis homeobox 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| BACE2 | NM_012105 | beta-site APP-cleaving enzyme 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ARRDC2 | NM_001025604 | arrestin domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CPPED1 | NM_001099455 | calcineurin-like phosphoesterase domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MEGF11 | NM_032445 | multiple EGF-like-domains 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PATE4 | NM_001144874 | prostate and testis expressed 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| FBXO47 | NM_001008777 | F-box protein 47 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PRR9 | NM_001195571 | proline rich 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RABIF | NM_002871 | RAB interacting factor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SPTB | NM_000347 | spectrin, beta, erythrocytic | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TAB1 | NM_006116 | TGF-beta activated kinase 1/MAP3K7 binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SUN2 | NM_001199579 | Sad1 and UNC84 domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | 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-647 | -0.13 | N/A | Sites in UTR |
| CACNG7 | NM_031896 | calcium channel, voltage-dependent, gamma subunit 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ATHL1 | NM_025092 | ATH1, acid trehalase-like 1 (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TRPM6 | NM_001177310 | transient receptor potential cation channel, subfamily M, member 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| NRBP2 | NM_178564 | nuclear receptor binding protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TRIM62 | NM_018207 | tripartite motif containing 62 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MED22 | NM_181491 | mediator complex subunit 22 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| DIEXF | NM_014388 | digestive organ expansion factor homolog (zebrafish) | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| HOXC9 | NM_006897 | homeobox C9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PKIA | NM_006823 | protein kinase (cAMP-dependent, catalytic) inhibitor alpha | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RAC2 | NM_002872 | ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TRIM26 | NM_001242783 | tripartite motif containing 26 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SOX13 | NM_005686 | SRY (sex determining region Y)-box 13 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CDK20 | NM_001039803 | cyclin-dependent kinase 20 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MTUS1 | NM_001001924 | microtubule associated tumor suppressor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| EPS8L2 | NM_022772 | EPS8-like 2 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CCNL2 | NM_001039577 | cyclin L2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CACNB3 | NM_000725 | calcium channel, voltage-dependent, beta 3 subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| VIPR1 | NM_004624 | vasoactive intestinal peptide receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | 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-647 | -0.13 | N/A | Sites in UTR |
| HEATR2 | NM_017802 | HEAT repeat containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| KPNA4 | NM_002268 | karyopherin alpha 4 (importin alpha 3) | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PARP14 | NM_017554 | poly (ADP-ribose) polymerase family, member 14 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| DERL3 | NM_001002862 | Der1-like domain family, member 3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| C11orf41 | NM_012194 | chromosome 11 open reading frame 41 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| IQSEC3 | NM_001170738 | IQ motif and Sec7 domain 3 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ARF4 | NM_001660 | ADP-ribosylation factor 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NCAM1 | NM_000615 | neural cell adhesion molecule 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PCDH7 | NM_002589 | protocadherin 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TATDN2 | NM_014760 | TatD DNase domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ZEB2 | NM_001171653 | zinc finger E-box binding homeobox 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PHIP | NM_017934 | pleckstrin homology domain interacting protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ATPAF1 | NM_001042546 | ATP synthase mitochondrial F1 complex assembly factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CCDC115 | NM_032357 | coiled-coil domain containing 115 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CAPN6 | NM_014289 | calpain 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PTK2B | NM_004103 | PTK2B protein tyrosine kinase 2 beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| C4orf36 | NM_144645 | chromosome 4 open reading frame 36 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| C15orf52 | NM_207380 | chromosome 15 open reading frame 52 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CX3CL1 | NM_002996 | chemokine (C-X3-C motif) ligand 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ACADSB | NM_001609 | acyl-CoA dehydrogenase, short/branched chain | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| COL17A1 | NM_000494 | collagen, type XVII, alpha 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| EFNB3 | NM_001406 | ephrin-B3 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| P2RX7 | NM_002562 | purinergic receptor P2X, ligand-gated ion channel, 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| VEGFB | NM_003377 | vascular endothelial growth factor B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| LAPTM5 | NM_006762 | lysosomal protein transmembrane 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| WTAP | NM_152857 | Wilms tumor 1 associated protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MRPL11 | NM_016050 | mitochondrial ribosomal protein L11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| GALNT12 | NM_024642 | UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 12 (GalNAc-T12) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| HPS3 | NM_032383 | Hermansky-Pudlak syndrome 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| EGR3 | NM_001199880 | early growth response 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PTP4A1 | NM_003463 | protein tyrosine phosphatase type IVA, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| UBL4A | NM_014235 | ubiquitin-like 4A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TMEM87A | NM_001110503 | transmembrane protein 87A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MOV10L1 | NM_001164104 | Mov10l1, Moloney leukemia virus 10-like 1, homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| 11-Sep | NM_018243 | septin 11 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PIRT | NM_001101387 | phosphoinositide-interacting regulator of transient receptor potential channels | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| WDR20 | NM_001242414 | WD repeat domain 20 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| S100Z | NM_130772 | S100 calcium binding protein Z | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| METTL15 | NM_001113528 | methyltransferase like 15 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PCGF3 | NM_006315 | polycomb group ring finger 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MLLT6 | NM_005937 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PIN4 | NM_001170747 | protein (peptidylprolyl cis/trans isomerase) NIMA-interacting, 4 (parvulin) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| GPANK1 | NM_001199237 | G patch domain and ankyrin repeats 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RNLS | NM_018363 | renalase, FAD-dependent amine oxidase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| KIAA1377 | NM_020802 | KIAA1377 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ERAP2 | NM_001130140 | endoplasmic reticulum aminopeptidase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CD300LB | NM_174892 | CD300 molecule-like family member b | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| FAM161B | NM_152445 | family with sequence similarity 161, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| COL6A1 | NM_001848 | collagen, type VI, alpha 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| OS9 | NM_001017956 | osteosarcoma amplified 9, endoplasmic reticulum lectin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TMEM104 | NM_017728 | transmembrane protein 104 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RGPD1 | NM_001024457 | RANBP2-like and GRIP domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SDC3 | NM_014654 | syndecan 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| DAO | NM_001917 | D-amino-acid oxidase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| NRP1 | NM_003873 | neuropilin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SYNJ1 | NM_001160302 | synaptojanin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CIAPIN1 | NM_020313 | cytokine induced apoptosis inhibitor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SLC38A10 | NM_001037984 | solute carrier family 38, member 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TIFAB | NM_001099221 | TRAF-interacting protein with forkhead-associated domain, family member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ZSCAN30 | NM_001112734 | zinc finger and SCAN domain containing 30 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MCF2L | NM_001112732 | MCF.2 cell line derived transforming sequence-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CHST15 | NM_014863 | carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RCC2 | NM_001136204 | regulator of chromosome condensation 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PAQR4 | NM_152341 | progestin and adipoQ receptor family member IV | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| TMEM132E | NM_207313 | transmembrane protein 132E | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ZNF280B | NM_080764 | zinc finger protein 280B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| DIRAS1 | NM_145173 | DIRAS family, GTP-binding RAS-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RASGEF1C | NM_175062 | RasGEF domain family, member 1C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ZFP106 | NM_022473 | zinc finger protein 106 homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ACVRL1 | NM_000020 | activin A receptor type II-like 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| INSR | NM_000208 | insulin receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RBBP9 | NM_006606 | retinoblastoma binding protein 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CLDN19 | NM_001123395 | claudin 19 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PPM1L | NM_139245 | protein phosphatase, Mg2+/Mn2+ dependent, 1L | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| ARF3 | NM_001659 | ADP-ribosylation factor 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| CISH | NM_013324 | cytokine inducible SH2-containing protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| COL6A2 | NM_001849 | collagen, type VI, alpha 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| MBP | NM_001025100 | myelin basic protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| SIK2 | NM_015191 | salt-inducible kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TMEM140 | NM_018295 | transmembrane protein 140 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| LYNX1 | NM_023946 | Ly6/neurotoxin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| QSER1 | NM_001076786 | glutamine and serine rich 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| KIFC2 | NM_145754 | kinesin family member C2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| WNT5A | NM_003392 | wingless-type MMTV integration site family, member 5A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| RLIM | NM_016120 | ring finger protein, LIM domain interacting | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| C20orf203 | NM_182584 | chromosome 20 open reading frame 203 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| FAM22G | NM_001045477 | family with sequence similarity 22, member G | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.13 | N/A | Sites in UTR |
| PKD2 | NM_000297 | polycystic kidney disease 2 (autosomal dominant) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PLA2G4C | NM_001159322 | phospholipase A2, group IVC (cytosolic, calcium-independent) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SEZ6L | NM_001184773 | seizure related 6 homolog (mouse)-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ABHD14B | NM_001146314 | abhydrolase domain containing 14B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| TARP | NM_001003799 | TCR gamma alternate reading frame protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LOC100130451 | NM_001242575 | hypothetical protein LOC100130451 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PCYT2 | NM_001184917 | phosphate cytidylyltransferase 2, ethanolamine | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| RET | NM_020630 | ret proto-oncogene | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| TFAP4 | NM_003223 | transcription factor AP-4 (activating enhancer binding protein 4) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NUP62 | NM_001193357 | nucleoporin 62kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PTCHD2 | NM_020780 | patched domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| C16orf53 | NM_024516 | chromosome 16 open reading frame 53 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NAGS | NM_153006 | N-acetylglutamate synthase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ACSF3 | NM_001127214 | acyl-CoA synthetase family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SLC1A2 | NM_001195728 | solute carrier family 1 (glial high affinity glutamate transporter), member 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NR4A3 | NM_006981 | nuclear receptor subfamily 4, group A, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| EIF1 | NM_005801 | eukaryotic translation initiation factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| RAMP1 | NM_005855 | receptor (G protein-coupled) activity modifying protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -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-647 | -0.12 | N/A | Sites in UTR |
| CEACAM19 | NM_001127893 | carcinoembryonic antigen-related cell adhesion molecule 19 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ANKRD50 | NM_001167882 | ankyrin repeat domain 50 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ZSWIM5 | NM_020883 | zinc finger, SWIM-type containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | 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-647 | -0.12 | N/A | Sites in UTR |
| SLC13A5 | NM_001143838 | solute carrier family 13 (sodium-dependent citrate transporter), member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| INPP5D | NM_001017915 | inositol polyphosphate-5-phosphatase, 145kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| BARX2 | NM_003658 | BARX homeobox 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CAPN12 | NM_144691 | calpain 12 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PLCXD1 | NM_018390 | phosphatidylinositol-specific phospholipase C, X domain containing 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DTNA | NM_001198938 | dystrobrevin, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| FCGR2B | NM_001002273 | Fc fragment of IgG, low affinity IIb, receptor (CD32) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GNAZ | NM_002073 | guanine nucleotide binding protein (G protein), alpha z polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ABLIM1 | NM_001003407 | actin binding LIM protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NAA11 | NM_032693 | N(alpha)-acetyltransferase 11, NatA catalytic subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| FOXP4 | NM_001012426 | forkhead box P4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| B3GNTL1 | NM_001009905 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | 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-647 | -0.12 | N/A | Sites in UTR |
| FAM102B | NM_001010883 | family with sequence similarity 102, member B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LEP | NM_000230 | leptin | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| RIMKLA | NM_173642 | ribosomal modification protein rimK-like family member A | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PLEKHM1 | NM_014798 | pleckstrin homology domain containing, family M (with RUN domain) member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| AKR1D1 | NM_001190906 | aldo-keto reductase family 1, member D1 (delta 4-3-ketosteroid-5-beta-reductase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| IQSEC1 | NM_001134382 | IQ motif and Sec7 domain 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LPCAT3 | NM_005768 | lysophosphatidylcholine acyltransferase 3 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PAMR1 | NM_001001991 | peptidase domain containing associated with muscle regeneration 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GPKOW | NM_015698 | G patch domain and KOW motifs | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| AMOTL2 | NM_016201 | angiomotin like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NLGN4X | NM_020742 | neuroligin 4, X-linked | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CAPS | NM_004058 | calcyphosine | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ENTPD2 | NM_001246 | ectonucleoside triphosphate diphosphohydrolase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| C3orf70 | NM_001025266 | chromosome 3 open reading frame 70 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SP6 | NM_199262 | Sp6 transcription factor | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CD74 | NM_001025158 | CD74 molecule, major histocompatibility complex, class II invariant chain | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MAPK14 | NM_001315 | mitogen-activated protein kinase 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MCAM | NM_006500 | melanoma cell adhesion molecule | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MUT | NM_000255 | methylmalonyl CoA mutase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MPHOSPH8 | NM_017520 | M-phase phosphoprotein 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LEPROT | NM_001198681 | leptin receptor overlapping transcript | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CCNJL | NM_024565 | cyclin J-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PGLYRP3 | NM_052891 | peptidoglycan recognition protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| BDH1 | NM_004051 | 3-hydroxybutyrate dehydrogenase, type 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CLDN3 | NM_001306 | claudin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| DDX23 | NM_004818 | DEAD (Asp-Glu-Ala-Asp) box polypeptide 23 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ZNF335 | NM_022095 | zinc finger protein 335 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| OTUB2 | NM_023112 | OTU domain, ubiquitin aldehyde binding 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KIAA0319L | NM_024874 | KIAA0319-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| WDR82 | NM_025222 | WD repeat domain 82 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SFTPA2 | NM_001098668 | surfactant protein A2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| STK35 | NM_080836 | serine/threonine kinase 35 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SH3PXD2A | NM_014631 | SH3 and PX domains 2A | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| STC2 | NM_003714 | stanniocalcin 2 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MON2 | NM_015026 | MON2 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ALAD | NM_000031 | aminolevulinate dehydratase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GNGT2 | NM_001198754 | guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GREB1 | NM_014668 | growth regulation by estrogen in breast cancer 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| XPO6 | NM_015171 | exportin 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| TIPARP | NM_001184717 | TCDD-inducible poly(ADP-ribose) polymerase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CACNA1H | NM_001005407 | calcium channel, voltage-dependent, T type, alpha 1H subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| XPR1 | NM_001135669 | xenotropic and polytropic retrovirus receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SELENBP1 | NM_003944 | selenium binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LARGE | NM_004737 | like-glycosyltransferase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GPC6 | NM_005708 | glypican 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| FKBP15 | NM_015258 | FK506 binding protein 15, 133kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KCTD18 | NM_152387 | potassium channel tetramerisation domain containing 18 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| EVPLL | NM_001145127 | envoplakin-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| RRBP1 | NM_001042576 | ribosome binding protein 1 homolog 180kDa (dog) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SMG6 | NM_001170957 | smg-6 homolog, nonsense mediated mRNA decay factor (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CDC42EP4 | NM_012121 | CDC42 effector protein (Rho GTPase binding) 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SEC31B | NM_015490 | SEC31 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ONECUT2 | NM_004852 | one cut homeobox 2 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PLXDC1 | NM_020405 | plexin domain containing 1 | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| IGSF1 | NM_001170963 | immunoglobulin superfamily, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| DEK | NM_001134709 | DEK oncogene | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ARHGEF11 | NM_014784 | Rho guanine nucleotide exchange factor (GEF) 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SLC25A39 | NM_001143780 | solute carrier family 25, member 39 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NXN | NM_001205319 | nucleoredoxin | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| KCNIP4 | NM_001035003 | Kv channel interacting protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | 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-647 | -0.12 | N/A | Sites in UTR |
| THEMIS | NM_001010923 | thymocyte selection associated | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PRR23A | NM_001134659 | proline rich 23A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CYP11B1 | NM_000497 | cytochrome P450, family 11, subfamily B, polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| HRH3 | NM_007232 | histamine receptor H3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CENPO | NM_001199803 | centromere protein O | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CCDC48 | NM_024768 | coiled-coil domain containing 48 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SNX30 | NM_001012994 | sorting nexin family member 30 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GRM1 | NM_000838 | glutamate receptor, metabotropic 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NPAS2 | NM_002518 | neuronal PAS domain protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SCNN1A | NM_001038 | sodium channel, nonvoltage-gated 1 alpha | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| STAT3 | NM_003150 | signal transducer and activator of transcription 3 (acute-phase response factor) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PCSK7 | NM_004716 | proprotein convertase subtilisin/kexin type 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| UBE4B | NM_001105562 | ubiquitination factor E4B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LPPR2 | NM_001170635 | lipid phosphate phosphatase-related protein type 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| DIRC2 | NM_032839 | disrupted in renal carcinoma 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ULK2 | NM_014683 | unc-51-like kinase 2 (C. elegans) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CHM | NM_000390 | choroideremia (Rab escort protein 1) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| USP40 | NM_018218 | ubiquitin specific peptidase 40 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ANKRD40 | NM_052855 | ankyrin repeat domain 40 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| FAM109A | NM_001177996 | family with sequence similarity 109, member A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| C9orf96 | NM_153710 | chromosome 9 open reading frame 96 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ZNF605 | NM_001164715 | zinc finger protein 605 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| YPEL2 | NM_001005404 | yippee-like 2 (Drosophila) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CASP7 | NM_001227 | caspase 7, apoptosis-related cysteine peptidase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| IPO5 | NM_002271 | importin 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MC5R | NM_005913 | melanocortin 5 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SMARCC1 | NM_003074 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| STOML1 | NM_004809 | stomatin (EPB72)-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| RAI14 | NM_001145520 | retinoic acid induced 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GSTCD | NM_024751 | glutathione S-transferase, C-terminal domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| TMEM42 | NM_144638 | transmembrane protein 42 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ARL10 | NM_173664 | ADP-ribosylation factor-like 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| KAAG1 | NM_181337 | kidney associated antigen 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SLC8A2 | NM_015063 | solute carrier family 8 (sodium/calcium exchanger), member 2 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PODXL | NM_001018111 | podocalyxin-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PEX16 | NM_004813 | peroxisomal biogenesis factor 16 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| MED26 | NM_004831 | mediator complex subunit 26 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| TNRC6A | NM_014494 | trinucleotide repeat containing 6A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| NLE1 | NM_001014445 | notchless homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| C20orf29 | NM_001204446 | chromosome 20 open reading frame 29 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| THSD7A | NM_015204 | thrombospondin, type I, domain containing 7A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| FSTL1 | NM_007085 | follistatin-like 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ANO6 | NM_001025356 | anoctamin 6 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| LPHN1 | NM_001008701 | latrophilin 1 | 1 | 0 | 1 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | 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-647 | -0.12 | N/A | Sites in UTR |
| RALGPS1 | NM_001190730 | Ral GEF with PH domain and SH3 binding motif 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ABHD5 | NM_016006 | abhydrolase domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| GOLGA6C | NM_001164404 | golgin A6 family, member C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| CELSR2 | NM_001408 | cadherin, EGF LAG seven-pass G-type receptor 2 (flamingo homolog, Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| FOXE1 | NM_004473 | forkhead box E1 (thyroid transcription factor 2) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| PRKCE | NM_005400 | protein kinase C, epsilon | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| ST3GAL1 | NM_003033 | ST3 beta-galactoside alpha-2,3-sialyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| THRAP3 | NM_005119 | thyroid hormone receptor associated protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| KAT8 | NM_182958 | K(lysine) acetyltransferase 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| KNCN | NM_001097611 | kinocilin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| EIF2C4 | NM_017629 | eukaryotic translation initiation factor 2C, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |
| SPRY3 | NM_005840 | sprouty homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.12 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KLLN | NM_001126049 | killin, p53-regulated DNA replication inhibitor | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TP53I11 | NM_001076787 | tumor protein p53 inducible protein 11 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ATP2A2 | NM_001681 | ATPase, Ca++ transporting, cardiac muscle, slow twitch 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| CALM3 | NM_005184 | calmodulin 3 (phosphorylase kinase, delta) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| NCAM2 | NM_004540 | neural cell adhesion molecule 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| VEPH1 | NM_001167911 | ventricular zone expressed PH domain homolog 1 (zebrafish) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TRIM15 | NM_033229 | tripartite motif containing 15 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| CABLES1 | NM_001100619 | Cdk5 and Abl enzyme substrate 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| GATA4 | NM_002052 | GATA binding protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| FAM53B | NM_014661 | family with sequence similarity 53, member B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| POC1A | NM_001161580 | POC1 centriolar protein homolog A (Chlamydomonas) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DUSP13 | NM_001007271 | dual specificity phosphatase 13 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| FZR1 | NM_001136197 | fizzy/cell division cycle 20 related 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| RNF41 | NM_001242826 | ring finger protein 41 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| KIAA0889 | NM_080627 | KIAA0889 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| STOM | NM_004099 | stomatin | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| MUC7 | NM_001145006 | mucin 7, secreted | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PRKAB2 | NM_005399 | protein kinase, AMP-activated, beta 2 non-catalytic subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DYM | NM_017653 | dymeclin | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DHRSX | NM_145177 | dehydrogenase/reductase (SDR family) X-linked | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ZNF81 | NM_007137 | zinc finger protein 81 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| BTBD18 | NM_001145101 | BTB (POZ) domain containing 18 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| MED1 | NM_004774 | mediator complex subunit 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PEA15 | NM_003768 | phosphoprotein enriched in astrocytes 15 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | 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-647 | -0.11 | N/A | Sites in UTR |
| C17orf62 | NM_001033046 | chromosome 17 open reading frame 62 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ENPP7 | NM_178543 | ectonucleotide pyrophosphatase/phosphodiesterase 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| KAT2A | NM_021078 | K(lysine) acetyltransferase 2A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| IRF1 | NM_002198 | interferon regulatory factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TERT | NM_001193376 | telomerase reverse transcriptase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| NT5C2 | NM_001134373 | 5'-nucleotidase, cytosolic II | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| C17orf53 | NM_001171251 | chromosome 17 open reading frame 53 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| CLPTM1L | NM_030782 | CLPTM1-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DEF8 | NM_001242816 | differentially expressed in FDCP 8 homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ADAMTS5 | NM_007038 | ADAM metallopeptidase with thrombospondin type 1 motif, 5 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| KCNB1 | NM_004975 | potassium voltage-gated channel, Shab-related subfamily, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MOV10 | NM_001130079 | Mov10, Moloney leukemia virus 10, homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| GPR68 | NM_001177676 | G protein-coupled receptor 68 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| LEPROTL1 | NM_015344 | leptin receptor overlapping transcript-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| FAM54B | NM_001099625 | family with sequence similarity 54, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DNAJC30 | NM_032317 | DnaJ (Hsp40) homolog, subfamily C, member 30 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| NALCN | NM_052867 | sodium leak channel, non-selective | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| SMTNL2 | NM_001114974 | smoothelin-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ZNF805 | NM_001023563 | zinc finger protein 805 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PHYHIP | NM_001099335 | phytanoyl-CoA 2-hydroxylase interacting protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| C10orf116 | NM_006829 | chromosome 10 open reading frame 116 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| KIAA1467 | NM_020853 | KIAA1467 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| CSRNP3 | NM_001172173 | cysteine-serine-rich nuclear protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| OPCML | NM_001012393 | opioid binding protein/cell adhesion molecule-like | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| HIPK2 | NM_001113239 | homeodomain interacting protein kinase 2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| BDKRB2 | NM_000623 | bradykinin receptor B2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TLX1 | NM_001195517 | T-cell leukemia homeobox 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| NGFR | NM_002507 | nerve growth factor receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TIMM44 | NM_006351 | translocase of inner mitochondrial membrane 44 homolog (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TRIM38 | NM_006355 | tripartite motif containing 38 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| THAP10 | NM_020147 | THAP domain containing 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ZNF398 | NM_020781 | zinc finger protein 398 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TSLP | NM_033035 | thymic stromal lymphopoietin | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| SERINC2 | NM_001199037 | serine incorporator 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| C21orf2 | NM_004928 | chromosome 21 open reading frame 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| KIFC3 | NM_001130099 | kinesin family member C3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| OTUD5 | NM_001136157 | OTU domain containing 5 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.11 | 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-647 | -0.11 | N/A | Sites in UTR |
| FGF1 | NM_000800 | fibroblast growth factor 1 (acidic) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| WARS2 | NM_015836 | tryptophanyl tRNA synthetase 2, mitochondrial | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| RBPMS | NM_006867 | RNA binding protein with multiple splicing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| C9orf68 | NM_001039395 | chromosome 9 open reading frame 68 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TSGA14 | NM_018718 | testis specific, 14 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| COL8A2 | NM_005202 | collagen, type VIII, alpha 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| MAPT | NM_001123066 | microtubule-associated protein tau | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| RPS6KA2 | NM_001006932 | ribosomal protein S6 kinase, 90kDa, polypeptide 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| SLCO2A1 | NM_005630 | solute carrier organic anion transporter family, member 2A1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KCTD2 | NM_015353 | potassium channel tetramerisation domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DPYSL5 | NM_020134 | dihydropyrimidinase-like 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| FRMD1 | NM_001122841 | FERM domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| CNIH3 | NM_152495 | cornichon homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| GATAD2B | NM_020699 | GATA zinc finger domain containing 2B | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PPM1D | NM_003620 | protein phosphatase, Mg2+/Mn2+ dependent, 1D | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ENTPD1 | NM_001098175 | ectonucleoside triphosphate diphosphohydrolase 1 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DCC | NM_005215 | deleted in colorectal carcinoma | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| FGF9 | NM_002010 | fibroblast growth factor 9 (glia-activating factor) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| OSBP | NM_002556 | oxysterol binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| RAD9A | NM_004584 | RAD9 homolog A (S. pombe) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| SLC5A5 | NM_000453 | solute carrier family 5 (sodium iodide symporter), member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PCGF2 | NM_007144 | polycomb group ring finger 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ST8SIA5 | NM_013305 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| MED9 | NM_018019 | mediator complex subunit 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PDGFRB | NM_002609 | platelet-derived growth factor receptor, beta polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ZNF561 | NM_152289 | zinc finger protein 561 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| LEMD2 | NM_001143944 | LEM domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RRP15 | NM_016052 | ribosomal RNA processing 15 homolog (S. cerevisiae) | 1 | 0 | 1 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PITPNM2 | NM_020845 | phosphatidylinositol transfer protein, membrane-associated 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| MAN2A2 | NM_006122 | mannosidase, alpha, class 2A, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| UST | NM_005715 | uronyl-2-sulfotransferase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| GPR132 | NM_013345 | G protein-coupled receptor 132 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| RBFOX1 | NM_001142333 | RNA binding protein, fox-1 homolog (C. elegans) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| STK40 | NM_032017 | serine/threonine kinase 40 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| EDARADD | NM_080738 | EDAR-associated death domain | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ZNF783 | NM_001195220 | zinc finger family member 783 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| CD3EAP | NM_012099 | CD3e molecule, epsilon associated protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| RNF44 | NM_014901 | ring finger protein 44 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ASCC1 | NM_001198798 | activating signal cointegrator 1 complex subunit 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| DIRAS2 | NM_017594 | DIRAS family, GTP-binding RAS-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| PHC3 | NM_024947 | polyhomeotic homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| SCAMP4 | NM_079834 | secretory carrier membrane protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| GNG4 | NM_001098721 | guanine nucleotide binding protein (G protein), gamma 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| M6PR | NM_001207024 | mannose-6-phosphate receptor (cation dependent) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| LEMD3 | NM_001167614 | LEM domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RMND5B | NM_022762 | required for meiotic nuclear division 5 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| TEX19 | NM_207459 | testis expressed 19 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ELF4 | NM_001127197 | E74-like factor 4 (ets domain transcription factor) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| IHH | NM_002181 | Indian hedgehog | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ANKRD13B | NM_152345 | ankyrin repeat domain 13B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| ZNF655 | NM_001009960 | zinc finger protein 655 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.11 | N/A | Sites in UTR |
| IL1R1 | NM_000877 | interleukin 1 receptor, type I | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| P2RX1 | NM_002558 | purinergic receptor P2X, ligand-gated ion channel, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SDC1 | NM_001006946 | syndecan 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PTGES | NM_004878 | prostaglandin E synthase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| RPIA | NM_144563 | ribose 5-phosphate isomerase A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ATG2A | NM_015104 | ATG2 autophagy related 2 homolog A (S. cerevisiae) | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMEM39B | NM_018056 | transmembrane protein 39B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SLC10A7 | NM_001029998 | solute carrier family 10 (sodium/bile acid cotransporter family), member 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ZMYND17 | NM_001024593 | zinc finger, MYND-type containing 17 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MAGEA5 | NM_021049 | melanoma antigen family A, 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MKL1 | NM_020831 | megakaryoblastic leukemia (translocation) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CCDC120 | NM_001163321 | coiled-coil domain containing 120 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UBN2 | NM_173569 | ubinuclein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MAGEA10-MAGEA5 | NM_001204811 | MAGEA10-MAGEA5 readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CYP1B1 | NM_000104 | cytochrome P450, family 1, subfamily B, polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| HK2 | NM_000189 | hexokinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ST5 | NM_005418 | suppression of tumorigenicity 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| NAPA | NM_003827 | N-ethylmaleimide-sensitive factor attachment protein, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| NUMBL | NM_004756 | numb homolog (Drosophila)-like | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ADAMTS3 | NM_014243 | ADAM metallopeptidase with thrombospondin type 1 motif, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| BTNL3 | NM_197975 | butyrophilin-like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| WWP2 | NM_007014 | WW domain containing E3 ubiquitin protein ligase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SEMA4G | NM_017893 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4G | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PRR3 | NM_001077497 | proline rich 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMPRSS5 | NM_030770 | transmembrane protease, serine 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KCNJ10 | NM_002241 | potassium inwardly-rectifying channel, subfamily J, member 10 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| LIFR | NM_001127671 | leukemia inhibitory factor receptor alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| RANBP3 | NM_003624 | RAN binding protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| FAF2 | NM_014613 | Fas associated factor family member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SIDT1 | NM_017699 | SID1 transmembrane family, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NSFL1C | NM_001206736 | NSFL1 (p97) cofactor (p47) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ENGASE | NM_001042573 | endo-beta-N-acetylglucosaminidase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SIRPB2 | NM_001122962 | signal-regulatory protein beta 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CDH6 | NM_004932 | cadherin 6, type 2, K-cadherin (fetal kidney) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| DOCK1 | NM_001380 | dedicator of cytokinesis 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| EPHA3 | NM_005233 | EPH receptor A3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PSPH | NM_004577 | phosphoserine phosphatase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| THBS3 | NM_007112 | thrombospondin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ZNF155 | NM_003445 | zinc finger protein 155 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| NSD1 | NM_022455 | nuclear receptor binding SET domain protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMEM109 | NM_024092 | transmembrane protein 109 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ERLIN1 | NM_001100626 | ER lipid raft associated 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GJC2 | NM_020435 | gap junction protein, gamma 2, 47kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GLT1D1 | NM_144669 | glycosyltransferase 1 domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KCNQ5 | NM_001160130 | potassium voltage-gated channel, KQT-like subfamily, member 5 | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CASQ2 | NM_001232 | calsequestrin 2 (cardiac muscle) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SRL | NM_001098814 | sarcalumenin | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SYN3 | NM_001135774 | synapsin III | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GIPC1 | NM_005716 | GIPC PDZ domain containing family, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| COG4 | NM_001195139 | component of oligomeric golgi complex 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| FAM127B | NM_001078172 | family with sequence similarity 127, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CARKD | NM_001242881 | carbohydrate kinase domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| AARS2 | NM_020745 | alanyl-tRNA synthetase 2, mitochondrial (putative) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GPI | NM_000175 | glucose-6-phosphate isomerase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GIT1 | NM_001085454 | G protein-coupled receptor kinase interacting ArfGAP 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ZNF71 | NM_021216 | zinc finger protein 71 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SYT11 | NM_152280 | synaptotagmin XI | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ASAP3 | NM_001143778 | ArfGAP with SH3 domain, ankyrin repeat and PH domain 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GCOM1 | NM_001018100 | GRINL1A complex locus | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MUSTN1 | NM_205853 | musculoskeletal, embryonic nuclear protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMEM110-MUSTN1 | NM_001198974 | TMEM110-MUSTN1 readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| VAV2 | NM_001134398 | vav 2 guanine nucleotide exchange factor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| RECQL5 | NM_001003716 | RecQ protein-like 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TRIOBP | NM_001039141 | TRIO and F-actin binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| C12orf34 | NM_032829 | chromosome 12 open reading frame 34 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TNS4 | NM_032865 | tensin 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| GEN1 | NM_001130009 | Gen homolog 1, endonuclease (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SLC22A3 | NM_021977 | solute carrier family 22 (extraneuronal monoamine transporter), member 3 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | 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 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KLHDC10 | NM_014997 | kelch domain containing 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ZNF317 | NM_001190791 | zinc finger protein 317 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ZNF100 | NM_173531 | zinc finger protein 100 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CDHR3 | NM_152750 | cadherin-related family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| METTL10 | NM_212554 | methyltransferase like 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ACCN1 | NM_001094 | amiloride-sensitive cation channel 1, neuronal | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CRIP2 | NM_001312 | cysteine-rich protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| NFIC | NM_005597 | nuclear factor I/C (CCAAT-binding transcription factor) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SOX11 | NM_003108 | SRY (sex determining region Y)-box 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TSPAN9 | NM_001168320 | tetraspanin 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| BAHD1 | NM_014952 | bromo adjacent homology domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| BARHL1 | NM_020064 | BarH-like homeobox 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | 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-647 | -0.1 | N/A | Sites in UTR |
| PRR18 | NM_175922 | proline rich 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| FECH | NM_000140 | ferrochelatase | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NOS1 | NM_000620 | nitric oxide synthase 1 (neuronal) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PCSK1 | NM_000439 | proprotein convertase subtilisin/kexin type 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SEMA4D | NM_001142287 | sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| RPRD2 | NM_015203 | regulation of nuclear pre-mRNA domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMEM164 | NM_017698 | transmembrane protein 164 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TM4SF18 | NM_001184723 | transmembrane 4 L six family member 18 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| USH1G | NM_173477 | Usher syndrome 1G (autosomal recessive) | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PLAC4 | NM_182832 | placenta-specific 4 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| DLG3 | NM_001166278 | discs, large homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TUB | NM_003320 | tubby homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TRIM25 | NM_005082 | tripartite motif containing 25 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| THUMPD1 | NM_017736 | THUMP domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PLEKHO2 | NM_001195059 | pleckstrin homology domain containing, family O member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | 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-647 | -0.1 | N/A | Sites in UTR |
| IL17RA | NM_014339 | interleukin 17 receptor A | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TNFRSF10C | NM_003841 | tumor necrosis factor receptor superfamily, member 10c, decoy without an intracellular domain | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GUF1 | NM_021927 | GUF1 GTPase homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| C1QTNF7 | NM_001135170 | C1q and tumor necrosis factor related protein 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SGSM1 | NM_001039948 | small G protein signaling modulator 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KBTBD5 | NM_152393 | kelch repeat and BTB (POZ) domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMEM37 | NM_183240 | transmembrane protein 37 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MBD3 | NM_003926 | methyl-CpG binding domain protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MACROD2 | NM_001033087 | MACRO domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| DCLK2 | NM_001040260 | doublecortin-like kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CACNA1A | NM_000068 | calcium channel, voltage-dependent, P/Q type, alpha 1A subunit | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ADAM8 | NM_001109 | ADAM metallopeptidase domain 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ALDH3B1 | NM_000694 | aldehyde dehydrogenase 3 family, member B1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| IGF2R | NM_000876 | insulin-like growth factor 2 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MLL | NM_001197104 | myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SYNE1 | NM_033071 | spectrin repeat containing, nuclear envelope 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ZNF514 | NM_032788 | zinc finger protein 514 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ATP6V1C2 | NM_001039362 | ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| RAPGEF1 | NM_005312 | Rap guanine nucleotide exchange factor (GEF) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| FAM19A5 | NM_001082967 | family with sequence similarity 19 (chemokine (C-C motif)-like), member A5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CABLES2 | NM_031215 | Cdk5 and Abl enzyme substrate 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KCNAB2 | NM_001199860 | potassium voltage-gated channel, shaker-related subfamily, beta member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TBC1D10B | NM_015527 | TBC1 domain family, member 10B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| LTN1 | NM_015565 | listerin E3 ubiquitin protein ligase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| THAP3 | NM_138350 | THAP domain containing, apoptosis associated protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| BTBD11 | NM_001017523 | BTB (POZ) domain containing 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GOLGA6L9 | NM_198181 | golgin A6 family-like 9 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GJA3 | NM_021954 | gap junction protein, alpha 3, 46kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KCNJ12 | NM_021012 | potassium inwardly-rectifying channel, subfamily J, member 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| ACTR1B | NM_005735 | ARP1 actin-related protein 1 homolog B, centractin beta (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| PHF19 | NM_015651 | PHD finger protein 19 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| CCDC93 | NM_019044 | coiled-coil domain containing 93 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| C2orf18 | NM_017877 | chromosome 2 open reading frame 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| NDRG4 | NM_001130487 | NDRG family member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SAMD14 | NM_174920 | sterile alpha motif domain containing 14 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| KCNJ18 | NM_001194958 | potassium inwardly-rectifying channel, subfamily J, member 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GPC4 | NM_001448 | glypican 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| MTOR | NM_004958 | mechanistic target of rapamycin (serine/threonine kinase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| GABRP | NM_014211 | gamma-aminobutyric acid (GABA) A receptor, pi | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| TMEM64 | NM_001008495 | transmembrane protein 64 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| C2orf68 | NM_001013649 | chromosome 2 open reading frame 68 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| C20orf112 | NM_080616 | chromosome 20 open reading frame 112 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| SSX2IP | NM_001166293 | synovial sarcoma, X breakpoint 2 interacting protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| C5orf63 | NM_001164479 | chromosome 5 open reading frame 63 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.1 | N/A | Sites in UTR |
| LHFPL4 | NM_198560 | lipoma HMGIC fusion partner-like 4 | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ELF3 | NM_001114309 | E74-like factor 3 (ets domain transcription factor, epithelial-specific ) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| FZD4 | NM_012193 | frizzled family receptor 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| TNFRSF25 | NM_003790 | tumor necrosis factor receptor superfamily, member 25 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| UQCR11 | NM_006830 | ubiquinol-cytochrome c reductase, complex III subunit XI | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ACSL6 | NM_001009185 | acyl-CoA synthetase long-chain family member 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PSD4 | NM_012455 | pleckstrin and Sec7 domain containing 4 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SYNJ2BP | NM_018373 | synaptojanin 2 binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ZNF677 | NM_182609 | zinc finger protein 677 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| TRNP1 | NM_001013642 | TMF1-regulated nuclear protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| CALM1 | NM_006888 | calmodulin 1 (phosphorylase kinase, delta) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| AGPS | NM_003659 | alkylglycerone phosphate synthase | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| FGF23 | NM_020638 | fibroblast growth factor 23 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PIP5K1A | NM_001135636 | phosphatidylinositol-4-phosphate 5-kinase, type I, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SPTLC2 | NM_004863 | serine palmitoyltransferase, long chain base subunit 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MGRN1 | NM_001142289 | mahogunin, ring finger 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| LONP2 | NM_031490 | lon peptidase 2, peroxisomal | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ADCY1 | NM_021116 | adenylate cyclase 1 (brain) | 1 | 0 | 1 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SLC36A1 | NM_078483 | solute carrier family 36 (proton/amino acid symporter), member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| IREB2 | NM_004136 | iron-responsive element binding protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SLC13A1 | NM_022444 | solute carrier family 13 (sodium/sulfate symporters), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GAL3ST1 | NM_004861 | galactose-3-O-sulfotransferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| AADACL3 | NM_001103169 | arylacetamide deacetylase-like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| TMEM18 | NM_152834 | transmembrane protein 18 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| USP22 | NM_015276 | ubiquitin specific peptidase 22 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| STAT5B | NM_012448 | signal transducer and activator of transcription 5B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| CLIP2 | NM_003388 | CAP-GLY domain containing linker protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -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-647 | -0.09 | N/A | Sites in UTR |
| FLJ45513 | NM_001242791 | hypothetical LOC729220 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SRGAP1 | NM_020762 | SLIT-ROBO Rho GTPase activating protein 1 | 0 | 0 | 0 | 0 | 3 | 1 | 0 | 2 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SH3BP5 | NM_001018009 | SH3-domain binding protein 5 (BTK-associated) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| OPN3 | NM_014322 | opsin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SLC30A8 | NM_001172811 | solute carrier family 30 (zinc transporter), member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ZNF850 | NM_001193552 | zinc finger protein 850 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| B3GALT6 | NM_080605 | UDP-Gal:betaGal beta 1,3-galactosyltransferase polypeptide 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GATA5 | NM_080473 | GATA binding protein 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PRND | NM_012409 | prion protein 2 (dublet) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| NAPB | NM_022080 | N-ethylmaleimide-sensitive factor attachment protein, beta | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| EARS2 | NM_001083614 | glutamyl-tRNA synthetase 2, mitochondrial (putative) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| C10orf10 | NM_007021 | chromosome 10 open reading frame 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MIS12 | NM_024039 | MIS12, MIND kinetochore complex component, homolog (S. pombe) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | 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-647 | -0.09 | N/A | Sites in UTR |
| CEP63 | NM_001042383 | centrosomal protein 63kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| LRRC27 | NM_001143757 | leucine rich repeat containing 27 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| NDUFA11 | NM_001193375 | NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11, 14.7kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| KRTAP5-10 | NM_001012710 | keratin associated protein 5-10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| VGLL3 | NM_016206 | vestigial like 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GCK | NM_000162 | glucokinase (hexokinase 4) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| HOXA11 | NM_005523 | homeobox A11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SLIT1 | NM_003061 | slit homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ATG5 | NM_004849 | ATG5 autophagy related 5 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| FRMPD4 | NM_014728 | FERM and PDZ domain containing 4 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SCARA3 | NM_016240 | scavenger receptor class A, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| C1QTNF6 | NM_031910 | C1q and tumor necrosis factor related protein 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ADM2 | NM_024866 | adrenomedullin 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ERCC1 | NM_001166049 | excision repair cross-complementing rodent repair deficiency, complementation group 1 (includes overlapping antisense sequence) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MVK | NM_000431 | mevalonate kinase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PLP1 | NM_000533 | proteolipid protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| RS1 | NM_000330 | retinoschisin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| C14orf129 | NM_016472 | chromosome 14 open reading frame 129 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| WNK3 | NM_001002838 | WNK lysine deficient protein kinase 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| KLC4 | NM_201521 | kinesin light chain 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| CXorf40A | NM_001171909 | chromosome X open reading frame 40A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GAS8 | NM_001481 | growth arrest-specific 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| HHIPL1 | NM_001127258 | HHIP-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GLP1R | NM_002062 | glucagon-like peptide 1 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MFAP4 | NM_001198695 | microfibrillar-associated protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PCSK6 | NM_002570 | proprotein convertase subtilisin/kexin type 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PLS1 | NM_001145319 | plastin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| RRAD | NM_001128850 | Ras-related associated with diabetes | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | 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-647 | -0.09 | N/A | Sites in UTR |
| ARHGEF6 | NM_004840 | Rac/Cdc42 guanine nucleotide exchange factor (GEF) 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PSD3 | NM_015310 | pleckstrin and Sec7 domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PRDM16 | NM_022114 | PR domain containing 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SH3BGRL3 | NM_031286 | SH3 domain binding glutamic acid-rich protein like 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ACACA | NM_198834 | acetyl-CoA carboxylase alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| COL4A2 | NM_001846 | collagen, type IV, alpha 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ADAM11 | NM_002390 | ADAM metallopeptidase domain 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GAS2L1 | NM_152237 | growth arrest-specific 2 like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| AP3M2 | NM_001134296 | adaptor-related protein complex 3, mu 2 subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| C19orf35 | NM_198532 | chromosome 19 open reading frame 35 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| TRIM66 | NM_014818 | tripartite motif containing 66 | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| CPNE3 | NM_003909 | copine III | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| UBTF | NM_001076683 | upstream binding transcription factor, RNA polymerase I | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| DDX19A | NM_018332 | DEAD (Asp-Glu-Ala-As) box polypeptide 19A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ALG9 | NM_001077690 | asparagine-linked glycosylation 9, alpha-1,2-mannosyltransferase homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ATXN7L1 | NM_020725 | ataxin 7-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ABCG2 | NM_004827 | ATP-binding cassette, sub-family G (WHITE), member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GNPDA1 | NM_005471 | glucosamine-6-phosphate deaminase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| NYNRIN | NM_025081 | NYN domain and retroviral integrase containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SV2B | NM_001167580 | synaptic vesicle glycoprotein 2B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| KIF1B | NM_183416 | kinesin family member 1B | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| FSHB | NM_000510 | follicle stimulating hormone, beta polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| RAB3IL1 | NM_013401 | RAB3A interacting protein (rabin3)-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| NRIP3 | NM_020645 | nuclear receptor interacting protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| CASKIN1 | NM_020764 | CASK interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| GJD3 | NM_152219 | gap junction protein, delta 3, 31.9kDa | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| FAM123C | NM_001105193 | family with sequence similarity 123C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| PTRF | NM_012232 | polymerase I and transcript release factor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| EFCAB1 | NM_001142857 | EF-hand calcium binding domain 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| ZNF594 | NM_032530 | zinc finger protein 594 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| FAM114A1 | NM_138389 | family with sequence similarity 114, member A1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| TPRG1 | NM_198485 | tumor protein p63 regulated 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MXRA7 | NM_001008529 | matrix-remodelling associated 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FSTL3 | NM_005860 | follistatin-like 3 (secreted glycoprotein) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| RAB35 | NM_001167606 | RAB35, member RAS oncogene family | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| REEP6 | NM_138393 | receptor accessory protein 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| AMZ1 | NM_133463 | archaelysin family metallopeptidase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| KIF6 | NM_145027 | kinesin family member 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SEPN1 | NM_020451 | selenoprotein N, 1 | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| AKAP13 | NM_006738 | A kinase (PRKA) anchor protein 13 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| HOXC5 | NM_018953 | homeobox C5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| SRGAP2 | NM_001170637 | SLIT-ROBO Rho GTPase activating protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| RNF185 | NM_001135825 | ring finger protein 185 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MIPOL1 | NM_001195296 | mirror-image polydactyly 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| CASP10 | NM_001206524 | caspase 10, apoptosis-related cysteine peptidase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| KIAA1609 | NM_020947 | KIAA1609 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| LMNB2 | NM_032737 | lamin B2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.09 | N/A | Sites in UTR |
| MDM2 | NM_002392 | Mdm2 p53 binding protein homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| EVC | NM_153717 | Ellis van Creveld syndrome | 0 | 0 | 0 | 0 | 3 | 0 | 0 | 3 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| CDC37 | NM_007065 | cell division cycle 37 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MGAT4A | NM_001160154 | mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SEPSECS | NM_016955 | Sep (O-phosphoserine) tRNA:Sec (selenocysteine) tRNA synthase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| KIAA1328 | NM_020776 | KIAA1328 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| C20orf118 | NM_080628 | chromosome 20 open reading frame 118 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| PSAPL1 | NM_001085382 | prosaposin-like 1 (gene/pseudogene) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ATP9A | NM_006045 | ATPase, class II, type 9A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| LRRC55 | NM_001005210 | leucine rich repeat containing 55 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MYH10 | NM_005964 | myosin, heavy chain 10, non-muscle | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ZDHHC3 | NM_001135179 | zinc finger, DHHC-type containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ELP3 | NM_018091 | elongation protein 3 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| TMC8 | NM_152468 | transmembrane channel-like 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MXD4 | NM_006454 | MAX dimerization protein 4 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| TNFRSF14 | NM_003820 | tumor necrosis factor receptor superfamily, member 14 (herpesvirus entry mediator) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| IQGAP1 | NM_003870 | IQ motif containing GTPase activating protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| DOK4 | NM_018110 | docking protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| RAVER1 | NM_133452 | ribonucleoprotein, PTB-binding 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SNX19 | NM_014758 | sorting nexin 19 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| USP6NL | NM_001080491 | USP6 N-terminal like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| C9orf5 | NM_032012 | chromosome 9 open reading frame 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CCDC113 | NM_001142302 | coiled-coil domain containing 113 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| C19orf12 | NM_001031726 | chromosome 19 open reading frame 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| DLGAP2 | NM_004745 | discs, large (Drosophila) homolog-associated protein 2 | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NPTXR | NM_014293 | neuronal pentraxin receptor | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| PEX19 | NM_001193644 | peroxisomal biogenesis factor 19 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SNTA1 | NM_003098 | syntrophin, alpha 1 (dystrophin-associated protein A1, 59kDa, acidic component) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| KDM4B | NM_015015 | lysine (K)-specific demethylase 4B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | 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-647 | -0.08 | N/A | Sites in UTR |
| MRTO4 | NM_016183 | mRNA turnover 4 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| RETSAT | NM_017750 | retinol saturase (all-trans-retinol 13,14-reductase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SAP30L | NM_001131062 | SAP30-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| LOC100132146 | NM_001195442 | hypothetical LOC100132146 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| TRH | NM_007117 | thyrotropin-releasing hormone | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| DGKE | NM_003647 | diacylglycerol kinase, epsilon 64kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| TCEANC2 | NM_153035 | transcription elongation factor A (SII) N-terminal and central domain containing 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ABCA1 | NM_005502 | ATP-binding cassette, sub-family A (ABC1), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ZBTB40 | NM_001083621 | zinc finger and BTB domain containing 40 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | 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-647 | -0.08 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FLG2 | NM_001014342 | filaggrin family member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| C8orf44 | NM_019607 | chromosome 8 open reading frame 44 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| DCTN5 | NM_001199743 | dynactin 5 (p25) | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| CEACAM1 | NM_001024912 | carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MAPKBP1 | NM_001128608 | mitogen-activated protein kinase binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| HCAR1 | NM_032554 | hydroxycarboxylic acid receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| POLK | NM_016218 | polymerase (DNA directed) kappa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| PGAP3 | NM_033419 | post-GPI attachment to proteins 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ASB14 | NM_001142733 | ankyrin repeat and SOCS box containing 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NEGR1 | NM_173808 | neuronal growth regulator 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ZNF678 | NM_178549 | zinc finger protein 678 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| GOLGA7B | NM_001010917 | golgin A7 family, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| AGPAT4 | NM_020133 | 1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| CEBPD | NM_005195 | CCAAT/enhancer binding protein (C/EBP), delta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| GSPT1 | NM_001130006 | G1 to S phase transition 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| GIT2 | NM_001135213 | G protein-coupled receptor kinase interacting ArfGAP 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SLFN11 | NM_001104587 | schlafen family member 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ZBTB46 | NM_025224 | zinc finger and BTB domain containing 46 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SPRED1 | NM_152594 | sprouty-related, EVH1 domain containing 1 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.08 | 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-647 | -0.08 | N/A | Sites in UTR |
| ADAP1 | NM_006869 | ArfGAP with dual PH domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MMACHC | NM_015506 | methylmalonic aciduria (cobalamin deficiency) cblC type, with homocystinuria | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| PYGO2 | NM_138300 | pygopus homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | 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-647 | -0.08 | N/A | Sites in UTR |
| IL17RD | NM_017563 | interleukin 17 receptor D | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SIK1 | NM_173354 | salt-inducible kinase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| KIF1A | NM_004321 | kinesin family member 1A | 1 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| DPP6 | NM_001039350 | dipeptidyl-peptidase 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| HNF4G | NM_004133 | hepatocyte nuclear factor 4, gamma | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| LAMC3 | NM_006059 | laminin, gamma 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | 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-647 | -0.08 | N/A | Sites in UTR |
| TMOD3 | NM_014547 | tropomodulin 3 (ubiquitous) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ZDHHC2 | NM_016353 | zinc finger, DHHC-type containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| C17orf63 | NM_001077498 | chromosome 17 open reading frame 63 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| REEP3 | NM_001001330 | receptor accessory protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | 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-647 | -0.08 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| TMED10 | NM_006827 | transmembrane emp24-like trafficking protein 10 (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| PCNX | NM_014982 | pecanex homolog (Drosophila) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| BMF | NM_001003940 | Bcl2 modifying factor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| HN1L | NM_144570 | hematological and neurological expressed 1-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| PPARGC1B | NM_001172698 | peroxisome proliferator-activated receptor gamma, coactivator 1 beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MEGF6 | NM_001409 | multiple EGF-like-domains 6 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| GRB2 | NM_002086 | growth factor receptor-bound protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| HMGA1 | NM_002131 | high mobility group AT-hook 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| CYTH2 | NM_004228 | cytohesin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SRSF12 | NM_080743 | serine/arginine-rich splicing factor 12 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| CYP4V2 | NM_207352 | cytochrome P450, family 4, subfamily V, polypeptide 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NEK6 | NM_001145001 | NIMA (never in mitosis gene a)-related kinase 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| APOL4 | NM_030643 | apolipoprotein L, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| MUC20 | NM_001098516 | mucin 20, cell surface associated | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| ZFP3 | NM_153018 | zinc finger protein 3 homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NRP2 | NM_003872 | neuropilin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NEURL | NM_004210 | neuralized homolog (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| RAB11FIP5 | NM_015470 | RAB11 family interacting protein 5 (class I) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CCM2 | NM_001029835 | cerebral cavernous malformation 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NR5A1 | NM_004959 | nuclear receptor subfamily 5, group A, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| RAI1 | NM_030665 | retinoic acid induced 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| GNPNAT1 | NM_198066 | glucosamine-phosphate N-acetyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| SPNS2 | NM_001124758 | spinster homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| DCAF7 | NM_005828 | DDB1 and CUL4 associated factor 7 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| NSL1 | NM_001042549 | NSL1, MIND kinetochore complex component, homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| COX19 | NM_001031617 | COX19 cytochrome c oxidase assembly homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.08 | N/A | Sites in UTR |
| FOXO1 | NM_002015 | forkhead box O1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| FLT4 | NM_182925 | fms-related tyrosine kinase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SMARCC2 | NM_001130420 | SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SULT4A1 | NM_014351 | sulfotransferase family 4A, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| RNF170 | NM_001160224 | ring finger protein 170 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TNFRSF8 | NM_001243 | tumor necrosis factor receptor superfamily, member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| MAP4K4 | NM_001242559 | mitogen-activated protein kinase kinase kinase kinase 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TMEM229B | NM_182526 | transmembrane protein 229B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| IBA57 | NM_001010867 | IBA57, iron-sulfur cluster assembly homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| IYD | NM_001164694 | iodotyrosine deiodinase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LOC100507421 | NM_001195278 | transmembrane protein 178-like | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TNFRSF9 | NM_001561 | tumor necrosis factor receptor superfamily, member 9 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SEC62 | NM_003262 | SEC62 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| CPLX4 | NM_181654 | complexin 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| C12orf76 | NM_207435 | chromosome 12 open reading frame 76 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TEAD1 | NM_021961 | TEA domain family member 1 (SV40 transcriptional enhancer factor) | 1 | 0 | 0 | 1 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TMEM132B | NM_052907 | transmembrane protein 132B | 0 | 0 | 0 | 0 | 2 | 1 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| DIO3 | NM_001362 | deiodinase, iodothyronine, type III | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SLC26A2 | NM_000112 | solute carrier family 26 (sulfate transporter), member 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| IGSF3 | NM_001007237 | immunoglobulin superfamily, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| NUAK1 | NM_014840 | NUAK family, SNF1-like kinase, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| MAPRE2 | NM_001143826 | microtubule-associated protein, RP/EB family, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| RASA3 | NM_007368 | RAS p21 protein activator 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ZNF250 | NM_001109689 | zinc finger protein 250 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| FBN3 | NM_032447 | fibrillin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PAQR8 | NM_133367 | progestin and adipoQ receptor family member VIII | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TTYH2 | NM_032646 | tweety homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TNFAIP8L1 | NM_001167942 | tumor necrosis factor, alpha-induced protein 8-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FAM110C | NM_001077710 | family with sequence similarity 110, member C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SMAD5 | NM_001001419 | SMAD family member 5 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| CELF2 | NM_001025076 | CUGBP, Elav-like family member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| GDF7 | NM_182828 | growth differentiation factor 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ADCYAP1 | NM_001099733 | adenylate cyclase activating polypeptide 1 (pituitary) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| S1PR3 | NM_005226 | sphingosine-1-phosphate receptor 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| MAOA | NM_000240 | monoamine oxidase A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| TRIM13 | NM_001007278 | tripartite motif containing 13 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| CECR6 | NM_001163079 | cat eye syndrome chromosome region, candidate 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| DEPDC1 | NM_001114120 | DEP domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| RNF213 | NM_020914 | ring finger protein 213 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| CDS2 | NM_003818 | CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ZNF510 | NM_014930 | zinc finger protein 510 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| AFF4 | NM_014423 | AF4/FMR2 family, member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SOCS7 | NM_014598 | suppressor of cytokine signaling 7 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| DCUN1D5 | NM_032299 | DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ARVCF | NM_001670 | armadillo repeat gene deleted in velocardiofacial syndrome | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| VAMP4 | NM_001185127 | vesicle-associated membrane protein 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NRXN3 | NM_001105250 | neurexin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| GPR64 | NM_001079858 | G protein-coupled receptor 64 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PNMAL2 | NM_020709 | PNMA-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ST8SIA2 | NM_006011 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.07 | 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-647 | -0.07 | N/A | Sites in UTR |
| BBC3 | NM_001127240 | BCL2 binding component 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| NPC1L1 | NM_001101648 | NPC1 (Niemann-Pick disease, type C1, gene)-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| DIP2B | NM_173602 | DIP2 disco-interacting protein 2 homolog B (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| MAP3K14 | NM_003954 | mitogen-activated protein kinase kinase kinase 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ZNF365 | NM_199451 | zinc finger protein 365 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| AHCYL2 | NM_001130720 | adenosylhomocysteinase-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| EIF2AK1 | NM_001134335 | eukaryotic translation initiation factor 2-alpha kinase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| MAP7D3 | NM_001173516 | MAP7 domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ANKRD13A | NM_033121 | ankyrin repeat domain 13A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| B3GNT6 | NM_138706 | UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6 (core 3 synthase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SYNGR1 | NM_004711 | synaptogyrin 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PATL1 | NM_152716 | protein associated with topoisomerase II homolog 1 (yeast) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| DGKQ | NM_001347 | diacylglycerol kinase, theta 110kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| ME2 | NM_001168335 | malic enzyme 2, NAD(+)-dependent, mitochondrial | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PCLO | NM_014510 | piccolo (presynaptic cytomatrix protein) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SOBP | NM_018013 | sine oculis binding protein homolog (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| MAK16 | NM_032509 | MAK16 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ALDH7A1 | NM_001182 | aldehyde dehydrogenase 7 family, member A1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| ProSAPiP1 | NM_014731 | ProSAPiP1 protein | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| THAP2 | NM_031435 | THAP domain containing, apoptosis associated protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PARD3B | NM_057177 | par-3 partitioning defective 3 homolog B (C. elegans) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| UBAC2 | NM_001144072 | UBA domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| CYP27C1 | NM_001001665 | cytochrome P450, family 27, subfamily C, polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PPP2R3A | NM_001190447 | protein phosphatase 2, regulatory subunit B', alpha | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| STXBP5L | NM_014980 | syntaxin binding protein 5-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| KIAA1755 | NM_001029864 | KIAA1755 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| AGAP2 | NM_001122772 | ArfGAP with GTPase domain, ankyrin repeat and PH domain 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| NIPAL4 | NM_001099287 | NIPA-like domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| FGFR1 | NM_001174063 | fibroblast growth factor receptor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| RPA1 | NM_002945 | replication protein A1, 70kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| FAM115A | NM_001206938 | family with sequence similarity 115, member A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| FAM105B | NM_138348 | family with sequence similarity 105, member B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| SDK1 | NM_152744 | sidekick homolog 1, cell adhesion molecule (chicken) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| THEM4 | NM_053055 | thioesterase superfamily member 4 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| GRB10 | NM_001001549 | growth factor receptor-bound protein 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PSKH1 | NM_006742 | protein serine kinase H1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| PNPLA4 | NM_001142389 | patatin-like phospholipase domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| RXFP3 | NM_016568 | relaxin/insulin-like family peptide receptor 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| DTL | NM_016448 | denticleless homolog (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| RAB23 | NM_016277 | RAB23, member RAS oncogene family | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| CPLX3 | NM_001030005 | complexin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.07 | N/A | Sites in UTR |
| C1orf95 | NM_001003665 | chromosome 1 open reading frame 95 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| DPM2 | NM_003863 | dolichyl-phosphate mannosyltransferase polypeptide 2, regulatory subunit | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CADM1 | NM_001098517 | cell adhesion molecule 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| RELT | NM_032871 | RELT tumor necrosis factor receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ZNF555 | NM_001172775 | zinc finger protein 555 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ZCCHC24 | NM_153367 | zinc finger, CCHC domain containing 24 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| DGCR14 | NM_022719 | DiGeorge syndrome critical region gene 14 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| FBXO41 | NM_001080410 | F-box protein 41 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RXRA | NM_002957 | retinoid X receptor, alpha | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| BCL2L1 | NM_001191 | BCL2-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PFKFB3 | NM_001145443 | 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CD2BP2 | NM_006110 | CD2 (cytoplasmic tail) binding protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ESYT2 | NM_020728 | extended synaptotagmin-like protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PDDC1 | NM_182612 | Parkinson disease 7 domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | 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-647 | -0.06 | N/A | Sites in UTR |
| TFRC | NM_001128148 | transferrin receptor (p90, CD71) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| JAKMIP3 | NM_001105521 | Janus kinase and microtubule interacting protein 3 | 0 | 0 | 0 | 0 | 3 | 0 | 3 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CAMK2A | NM_015981 | calcium/calmodulin-dependent protein kinase II alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SAP30BP | NM_013260 | SAP30 binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SLC2A4RG | NM_020062 | SLC2A4 regulator | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ALPPL2 | NM_031313 | alkaline phosphatase, placental-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PDK2 | NM_001199898 | pyruvate dehydrogenase kinase, isozyme 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SNX6 | NM_021249 | sorting nexin 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SHISA9 | NM_001145205 | shisa homolog 9 (Xenopus laevis) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| MYCL1 | NM_001033081 | v-myc myelocytomatosis viral oncogene homolog 1, lung carcinoma derived (avian) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CD209 | NM_001144893 | CD209 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PRPF40A | NM_017892 | PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| EFCAB2 | NM_001143943 | EF-hand calcium binding domain 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SNX1 | NM_003099 | sorting nexin 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ADARB2 | NM_018702 | adenosine deaminase, RNA-specific, B2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CCND1 | NM_053056 | cyclin D1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CCNT2 | NM_001241 | cyclin T2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| MDFI | NM_005586 | MyoD family inhibitor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| INTS6 | NM_001039937 | integrator complex subunit 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | 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-647 | -0.06 | N/A | Sites in UTR |
| CYB5RL | NM_001031672 | cytochrome b5 reductase-like | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ABCD1 | NM_000033 | ATP-binding cassette, sub-family D (ALD), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| POU2F1 | NM_001198783 | POU class 2 homeobox 1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SEC63 | NM_007214 | SEC63 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| TMEM79 | NM_032323 | transmembrane protein 79 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| RAB3IP | NM_001024647 | RAB3A interacting protein (rabin3) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CRAMP1L | NM_020825 | Crm, cramped-like (Drosophila) | 0 | 0 | 0 | 0 | 2 | 1 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| AK4 | NM_001005353 | adenylate kinase 4 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| MPPED2 | NM_001145399 | metallophosphoesterase domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| SNED1 | NM_001080437 | sushi, nidogen and EGF-like domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PAG1 | NM_018440 | phosphoprotein associated with glycosphingolipid microdomains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| FLYWCH1 | NM_032296 | FLYWCH-type zinc finger 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| TSPAN18 | NM_130783 | tetraspanin 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ADAMTSL1 | NM_001040272 | ADAMTS-like 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | 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-647 | -0.06 | N/A | Sites in UTR |
| PIK3R1 | NM_001242466 | phosphoinositide-3-kinase, regulatory subunit 1 (alpha) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | 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-647 | -0.06 | N/A | Sites in UTR |
| ZNF107 | NM_001013746 | zinc finger protein 107 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SCAI | NM_001144877 | suppressor of cancer cell invasion | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| GPC1 | NM_002081 | glypican 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGC3 | NM_002588 | protocadherin gamma subfamily C, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SEL1L | NM_005065 | sel-1 suppressor of lin-12-like (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGB4 | NM_003736 | protocadherin gamma subfamily B, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA8 | NM_032088 | protocadherin gamma subfamily A, 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA12 | NM_003735 | protocadherin gamma subfamily A, 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGC5 | NM_018929 | protocadherin gamma subfamily C, 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGC4 | NM_018928 | protocadherin gamma subfamily C, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PCDHGB7 | NM_018927 | protocadherin gamma subfamily B, 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGB6 | NM_018926 | protocadherin gamma subfamily B, 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGB5 | NM_018925 | protocadherin gamma subfamily B, 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGB3 | NM_018924 | protocadherin gamma subfamily B, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGB2 | NM_018923 | protocadherin gamma subfamily B, 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGB1 | NM_018922 | protocadherin gamma subfamily B, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA11 | NM_018914 | protocadherin gamma subfamily A, 11 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA10 | NM_018913 | protocadherin gamma subfamily A, 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA9 | NM_018921 | protocadherin gamma subfamily A, 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA7 | NM_018920 | protocadherin gamma subfamily A, 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA6 | NM_018919 | protocadherin gamma subfamily A, 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA5 | NM_018918 | protocadherin gamma subfamily A, 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA4 | NM_018917 | protocadherin gamma subfamily A, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA3 | NM_018916 | protocadherin gamma subfamily A, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA2 | NM_018915 | protocadherin gamma subfamily A, 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PCDHGA1 | NM_018912 | protocadherin gamma subfamily A, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CD44 | NM_000610 | CD44 molecule (Indian blood group) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| EPHA4 | NM_004438 | EPH receptor A4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| IGF1R | NM_000875 | insulin-like growth factor 1 receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| THSD4 | NM_024817 | thrombospondin, type I, domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SHE | NM_001010846 | Src homology 2 domain containing E | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| TRAF7 | NM_032271 | TNF receptor-associated factor 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ZBTB34 | NM_001099270 | zinc finger and BTB domain containing 34 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CBFA2T3 | NM_005187 | core-binding factor, runt domain, alpha subunit 2; translocated to, 3 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ERCC6 | NM_000124 | excision repair cross-complementing rodent repair deficiency, complementation group 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| FZD5 | NM_003468 | frizzled family receptor 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CNNM1 | NM_020348 | cyclin M1 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| WDR36 | NM_139281 | WD repeat domain 36 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SLC7A6 | NM_001076785 | solute carrier family 7 (amino acid transporter light chain, y+L system), member 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| MYO1D | NM_015194 | myosin ID | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| DLL4 | NM_019074 | delta-like 4 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ZNF557 | NM_001044387 | zinc finger protein 557 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| KIF24 | NM_194313 | kinesin family member 24 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| CUX1 | NM_001202543 | cut-like homeobox 1 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| ZNRF1 | NM_032268 | zinc and ring finger 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| HUS1 | NM_004507 | HUS1 checkpoint homolog (S. pombe) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PPP2R2C | NM_001206994 | protein phosphatase 2, regulatory subunit B, gamma | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| SLC33A1 | NM_004733 | solute carrier family 33 (acetyl-CoA transporter), member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| PLEKHF1 | NM_024310 | pleckstrin homology domain containing, family F (with FYVE domain) member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.06 | N/A | Sites in UTR |
| DGAT1 | NM_012079 | diacylglycerol O-acyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| VASH1 | NM_014909 | vasohibin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ZC3H4 | NM_015168 | zinc finger CCCH-type containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| GLIS2 | NM_032575 | GLIS family zinc finger 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| POU2AF1 | NM_006235 | POU class 2 associating factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| SCRN1 | NM_001145513 | secernin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| TMEM47 | NM_031442 | transmembrane protein 47 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ZNF862 | NM_001099220 | zinc finger protein 862 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ERC1 | NM_178039 | ELKS/RAB6-interacting/CAST family member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| IQCE | NM_001100390 | IQ motif containing E | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| DAB2IP | NM_032552 | DAB2 interacting protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ADD2 | NM_001185055 | adducin 2 (beta) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| PGR | NM_000926 | progesterone receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| FGD6 | NM_018351 | FYVE, RhoGEF and PH domain containing 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| MPP2 | NM_005374 | membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PRKCB | NM_002738 | protein kinase C, beta | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| GRIP2 | NM_001080423 | glutamate receptor interacting protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| SETD7 | NM_030648 | SET domain containing (lysine methyltransferase) 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| PDE4D | NM_001104631 | phosphodiesterase 4D, cAMP-specific | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| PPP6C | NM_001123355 | protein phosphatase 6, catalytic subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| CADM2 | NM_001167674 | cell adhesion molecule 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| GK5 | NM_001039547 | glycerol kinase 5 (putative) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| MAFF | NM_001161572 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog F (avian) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| PGPEP1 | NM_017712 | pyroglutamyl-peptidase I | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ZNF471 | NM_020813 | zinc finger protein 471 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| TOR1AIP2 | NM_022347 | torsin A interacting protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| MTX3 | NM_001010891 | metaxin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| MGA | NM_001080541 | MAX gene associated | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | 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-647 | -0.05 | N/A | Sites in UTR |
| CMTM3 | NM_144601 | CKLF-like MARVEL transmembrane domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| CABP7 | NM_182527 | calcium binding protein 7 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| CNTN2 | NM_005076 | contactin 2 (axonal) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| GPR26 | NM_153442 | G protein-coupled receptor 26 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MYO9B | NM_001130065 | myosin IXB | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| SLC25A44 | NM_014655 | solute carrier family 25, member 44 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| TPM4 | NM_001145160 | tropomyosin 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ZNF84 | NM_001127372 | zinc finger protein 84 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| C7orf51 | NM_173564 | chromosome 7 open reading frame 51 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| TBL1X | NM_001139466 | transducin (beta)-like 1X-linked | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| WNT4 | NM_030761 | wingless-type MMTV integration site family, member 4 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| FXN | NM_000144 | frataxin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | 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-647 | -0.05 | N/A | Sites in UTR |
| HEYL | NM_014571 | hairy/enhancer-of-split related with YRPW motif-like | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| GAB3 | NM_001081573 | GRB2-associated binding protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ZNF710 | NM_198526 | zinc finger protein 710 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| ZFP14 | NM_020917 | zinc finger protein 14 homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| DHCR24 | NM_014762 | 24-dehydrocholesterol reductase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| LIMS1 | NM_001193482 | LIM and senescent cell antigen-like domains 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| PARVA | NM_018222 | parvin, alpha | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| POM121C | NM_001099415 | POM121 membrane glycoprotein C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| STARD13 | NM_052851 | StAR-related lipid transfer (START) domain containing 13 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| DMWD | NM_004943 | dystrophia myotonica, WD repeat containing | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| PGP | NM_001042371 | phosphoglycolate phosphatase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| GNL3L | NM_001184819 | guanine nucleotide binding protein-like 3 (nucleolar)-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| SNX21 | NM_001042632 | sorting nexin family member 21 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| H2AFV | NM_138635 | H2A histone family, member V | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.05 | N/A | Sites in UTR |
| APAF1 | NM_001160 | apoptotic peptidase activating factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| RBFOX2 | NM_001031695 | RNA binding protein, fox-1 homolog (C. elegans) 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SHANK2 | NM_012309 | SH3 and multiple ankyrin repeat domains 2 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| AFF2 | NM_001169122 | AF4/FMR2 family, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| MYO6 | NM_004999 | myosin VI | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CD96 | NM_005816 | CD96 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| MCTS1 | NM_001137554 | malignant T cell amplified sequence 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ANAPC16 | NM_001242546 | anaphase promoting complex subunit 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ZNF704 | NM_001033723 | zinc finger protein 704 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SREK1IP1 | NM_173829 | SREK1-interacting protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ARPP19 | NM_006628 | cAMP-regulated phosphoprotein, 19kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| XKR5 | NM_207411 | XK, Kell blood group complex subunit-related family, member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| C7orf65 | NM_001123065 | chromosome 7 open reading frame 65 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RIMS3 | NM_014747 | regulating synaptic membrane exocytosis 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| NT5DC3 | NM_001031701 | 5'-nucleotidase domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| KLHL21 | NM_014851 | kelch-like 21 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ABCB8 | NM_007188 | ATP-binding cassette, sub-family B (MDR/TAP), member 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| RAB22A | NM_020673 | RAB22A, member RAS oncogene family | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| KCTD16 | NM_020768 | potassium channel tetramerisation domain containing 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| C1QTNF8 | NM_207419 | C1q and tumor necrosis factor related protein 8 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| EDA | NM_001005609 | ectodysplasin A | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CD93 | NM_012072 | CD93 molecule | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ST8SIA3 | NM_015879 | ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CELF5 | NM_001172673 | CUGBP, Elav-like family member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ZNF587 | NM_001204817 | zinc finger protein 587 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| MUM1 | NM_032853 | melanoma associated antigen (mutated) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| TSPYL5 | NM_033512 | TSPY-like 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ADCY2 | NM_020546 | adenylate cyclase 2 (brain) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| LAMTOR3 | NM_021970 | late endosomal/lysosomal adaptor, MAPK and MTOR activator 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ISLR2 | NM_001130136 | immunoglobulin superfamily containing leucine-rich repeat 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| COL5A1 | NM_000093 | collagen, type V, alpha 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| POM121 | NM_172020 | POM121 membrane glycoprotein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| KDM2A | NM_012308 | lysine (K)-specific demethylase 2A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| PRRC2B | NM_013318 | proline-rich coiled-coil 2B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| PDE10A | NM_001130690 | phosphodiesterase 10A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CCDC69 | NM_015621 | coiled-coil domain containing 69 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SPCS3 | NM_021928 | signal peptidase complex subunit 3 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| DCAF10 | NM_024345 | DDB1 and CUL4 associated factor 10 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| RUNX1 | NM_001001890 | runt-related transcription factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| MBD2 | NM_003927 | methyl-CpG binding domain protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| ZNF562 | NM_001130031 | zinc finger protein 562 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| GIPC3 | NM_133261 | GIPC PDZ domain containing family, member 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| KCNC1 | NM_004976 | potassium voltage-gated channel, Shaw-related subfamily, member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| RORA | NM_002943 | RAR-related orphan receptor A | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| NTN1 | NM_004822 | netrin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CLASP1 | NM_001142273 | cytoplasmic linker associated protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SYS1 | NM_001197129 | SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SPOCK1 | NM_004598 | sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| FBXL16 | NM_153350 | F-box and leucine-rich repeat protein 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| APBB2 | NM_001166050 | amyloid beta (A4) precursor protein-binding, family B, member 2 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| EPAS1 | NM_001430 | endothelial PAS domain protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SYT7 | NM_004200 | synaptotagmin VII | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CNTNAP2 | NM_014141 | contactin associated protein-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| COMMD2 | NM_016094 | COMM domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| CBX7 | NM_175709 | chromobox homolog 7 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| FLT1 | NM_002019 | fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| GRK6 | NM_001004106 | G protein-coupled receptor kinase 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SETD1B | NM_015048 | SET domain containing 1B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | 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 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| XRRA1 | NM_182969 | X-ray radiation resistance associated 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| BDNF | NM_001143805 | brain-derived neurotrophic factor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| RALGAPB | NM_020336 | Ral GTPase activating protein, beta subunit (non-catalytic) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| SPN | NM_001030288 | sialophorin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| PPIE | NM_006112 | peptidylprolyl isomerase E (cyclophilin E) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| FAM189A1 | NM_015307 | family with sequence similarity 189, member A1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| RPH3A | NM_001143854 | rabphilin 3A homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |
| EMR2 | NM_013447 | egf-like module containing, mucin-like, hormone receptor-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.04 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| YPEL1 | NM_013313 | yippee-like 1 (Drosophila) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| C9orf140 | NM_178448 | chromosome 9 open reading frame 140 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| PCGF5 | NM_032373 | polycomb group ring finger 5 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CD59 | NM_000611 | CD59 molecule, complement regulatory protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| FANCC | NM_000136 | Fanconi anemia, complementation group C | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| NEDD4L | NM_001144964 | neural precursor cell expressed, developmentally down-regulated 4-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CRLS1 | NM_001127458 | cardiolipin synthase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| PTGIS | NM_000961 | prostaglandin I2 (prostacyclin) synthase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| RND2 | NM_005440 | Rho family GTPase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CA5B | NM_007220 | carbonic anhydrase VB, mitochondrial | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| KLHDC5 | NM_020782 | kelch domain containing 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| BACH2 | NM_001170794 | BTB and CNC homology 1, basic leucine zipper transcription factor 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| MED29 | NM_017592 | mediator complex subunit 29 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| TAOK1 | NM_020791 | TAO kinase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CHURC1 | NM_001204063 | churchill domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| GDF11 | NM_005811 | growth differentiation factor 11 | 2 | 0 | 0 | 2 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| GABRG1 | NM_173536 | gamma-aminobutyric acid (GABA) A receptor, gamma 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| MAF | NM_001031804 | v-maf musculoaponeurotic fibrosarcoma oncogene homolog (avian) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MTUS2 | NM_001033602 | microtubule associated tumor suppressor candidate 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| RPRD1A | NM_018170 | regulation of nuclear pre-mRNA domain containing 1A | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| PPARA | NM_001001928 | peroxisome proliferator-activated receptor alpha | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| PACS2 | NM_001100913 | phosphofurin acidic cluster sorting protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| MKNK2 | NM_199054 | MAP kinase interacting serine/threonine kinase 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| LIN7C | NM_018362 | lin-7 homolog C (C. elegans) | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| C1GALT1 | NM_020156 | core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| KLHL6 | NM_130446 | kelch-like 6 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| SNX27 | NM_030918 | sorting nexin family member 27 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| SCRT1 | NM_031309 | scratch homolog 1, zinc finger protein (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| NANOS1 | NM_199461 | nanos homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| RSPO4 | NM_001029871 | R-spondin 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| ISPD | NM_001101417 | isoprenoid synthase domain containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| ARHGAP31 | NM_020754 | Rho GTPase activating protein 31 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| YWHAG | NM_012479 | tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, gamma polypeptide | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| HEG1 | NM_020733 | HEG homolog 1 (zebrafish) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CCDC117 | NM_173510 | coiled-coil domain containing 117 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| SLC6A17 | NM_001010898 | solute carrier family 6, member 17 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CXADR | NM_001207063 | coxsackie virus and adenovirus receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| NOL12 | NM_024313 | nucleolar protein 12 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CRX | NM_000554 | cone-rod homeobox | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| LGALS8 | NM_006499 | lectin, galactoside-binding, soluble, 8 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| C9orf69 | NM_152833 | chromosome 9 open reading frame 69 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| CASP2 | NM_001224 | caspase 2, apoptosis-related cysteine peptidase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| LYRM2 | NM_020466 | LYR motif containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| FASN | NM_004104 | fatty acid synthase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| PAX5 | NM_016734 | paired box 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| TMCC1 | NM_001017395 | transmembrane and coiled-coil domain family 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.03 | N/A | Sites in UTR |
| UBE2D4 | NM_015983 | ubiquitin-conjugating enzyme E2D 4 (putative) | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| SGCD | NM_000337 | sarcoglycan, delta (35kDa dystrophin-associated glycoprotein) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| SNX9 | NM_016224 | sorting nexin 9 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| DTX3L | NM_138287 | deltex 3-like (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| ARRB1 | NM_004041 | arrestin, beta 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| GFPT1 | NM_002056 | glutamine--fructose-6-phosphate transaminase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| STX11 | NM_003764 | syntaxin 11 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| ICMT | NM_012405 | isoprenylcysteine carboxyl methyltransferase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| UHRF1BP1 | NM_017754 | UHRF1 binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| IFFO2 | NM_001136265 | intermediate filament family orphan 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| VIPR2 | NM_003382 | vasoactive intestinal peptide receptor 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| PTAR1 | NM_001099666 | protein prenyltransferase alpha subunit repeat containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| NFIB | NM_001190737 | nuclear factor I/B | 1 | 0 | 0 | 1 | 1 | 0 | 0 | 1 | hsa-miR-647 | -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-647 | -0.02 | N/A | Sites in UTR |
| C6orf168 | NM_032511 | chromosome 6 open reading frame 168 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| IL13RA1 | NM_001560 | interleukin 13 receptor, alpha 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| C1orf52 | NM_198077 | chromosome 1 open reading frame 52 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | 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-647 | -0.02 | N/A | Sites in UTR |
| SLC15A2 | NM_001145998 | solute carrier family 15 (H+/peptide transporter), member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| VDR | NM_000376 | vitamin D (1,25- dihydroxyvitamin D3) receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| CEP104 | NM_014704 | centrosomal protein 104kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| DGCR2 | NM_001173533 | DiGeorge syndrome critical region gene 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| C10orf105 | NM_001164375 | chromosome 10 open reading frame 105 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| TTPAL | NM_001039199 | tocopherol (alpha) transfer protein-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | 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-647 | -0.02 | N/A | Sites in UTR |
| ERG | NM_001136154 | v-ets erythroblastosis virus E26 oncogene homolog (avian) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PAPPA | NM_002581 | pregnancy-associated plasma protein A, pappalysin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| SPRY4 | NM_001127496 | sprouty homolog 4 (Drosophila) | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| EHD1 | NM_006795 | EH-domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| MICAL3 | NM_001136004 | microtubule associated monoxygenase, calponin and LIM domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| CREBZF | NM_001039618 | CREB/ATF bZIP transcription factor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| EPT1 | NM_033505 | ethanolaminephosphotransferase 1 (CDP-ethanolamine-specific) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| CHML | NM_001821 | choroideremia-like (Rab escort protein 2) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| LOC100130705 | NM_001195150 | hypothetical protein LOC100130705 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| CENPN | NM_001100624 | centromere protein N | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.02 | N/A | Sites in UTR |
| AKNA | NM_030767 | AT-hook transcription factor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| BMPR2 | NM_001204 | bone morphogenetic protein receptor, type II (serine/threonine kinase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| PTPRD | NM_001040712 | protein tyrosine phosphatase, receptor type, D | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| NMT1 | NM_021079 | N-myristoyltransferase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| MAP3K13 | NM_001242314 | mitogen-activated protein kinase kinase kinase 13 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| C9orf91 | NM_153045 | chromosome 9 open reading frame 91 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| B7H6 | NM_001202439 | B7 homolog 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | -0.01 | N/A | Sites in UTR |
| MDM4 | NM_001204171 | Mdm4 p53 binding protein homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -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-647 | > -0.01 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| KCNMA1 | NM_001014797 | potassium large conductance calcium-activated channel, subfamily M, alpha member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ABAT | NM_000663 | 4-aminobutyrate aminotransferase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ACOX1 | NM_001185039 | acyl-CoA oxidase 1, palmitoyl | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ACVR2B | NM_001106 | activin A receptor, type IIB | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ASTN1 | NM_004319 | astrotactin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| CACNA1E | NM_000721 | calcium channel, voltage-dependent, R type, alpha 1E subunit | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| CLCN5 | NM_000084 | chloride channel 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| DSC3 | NM_001941 | desmocollin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| NDST1 | NM_001543 | N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| IRS1 | NM_005544 | insulin receptor substrate 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ITGB8 | NM_002214 | integrin, beta 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| MAPK1 | NM_002745 | mitogen-activated protein kinase 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| PSEN1 | NM_000021 | presenilin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| RREB1 | NM_001003698 | ras responsive element binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ATXN1 | NM_000332 | ataxin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| SCD | NM_005063 | stearoyl-CoA desaturase (delta-9-desaturase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| TPM3 | NM_152263 | tropomyosin 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| LRP8 | NM_001018054 | low density lipoprotein receptor-related protein 8, apolipoprotein e receptor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CDC14B | NM_001077181 | CDC14 cell division cycle 14 homolog B (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| BTRC | NM_003939 | beta-transducin repeat containing | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| LIMD1 | NM_014240 | LIM domains containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| VAPA | NM_003574 | VAMP (vesicle-associated membrane protein)-associated protein A, 33kDa | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| RASA4 | NM_001079877 | RAS p21 protein activator 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| TLR6 | NM_006068 | toll-like receptor 6 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| NFAT5 | NM_001113178 | nuclear factor of activated T-cells 5, tonicity-responsive | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | 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-647 | > -0.01 | N/A | Sites in UTR |
| FNBP1 | NM_015033 | formin binding protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| FBXO28 | NM_001136115 | F-box protein 28 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| TTC28 | NM_001145418 | tetratricopeptide repeat domain 28 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| NCS1 | NM_001128826 | neuronal calcium sensor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| PPP1R16B | NM_001172735 | protein phosphatase 1, regulatory (inhibitor) subunit 16B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| RSL1D1 | NM_015659 | ribosomal L1 domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| EEF2K | NM_013302 | eukaryotic elongation factor-2 kinase | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ANKFY1 | NM_016376 | ankyrin repeat and FYVE domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| TRIM33 | NM_015906 | tripartite motif containing 33 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| HES2 | NM_019089 | hairy and enhancer of split 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LGI2 | NM_018176 | leucine-rich repeat LGI family, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| CYP20A1 | NM_177538 | cytochrome P450, family 20, subfamily A, polypeptide 1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| TBC1D24 | NM_001199107 | TBC1 domain family, member 24 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| AHRR | NM_001242412 | aryl-hydrocarbon receptor repressor | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| PCDH19 | NM_001105243 | protocadherin 19 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| TNRC6C | NM_001142640 | trinucleotide repeat containing 6C | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ZMAT3 | NM_022470 | zinc finger, matrin-type 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| MRPS25 | NM_022497 | mitochondrial ribosomal protein S25 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| RMND5A | NM_022780 | required for meiotic nuclear division 5 homolog A (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| METTL8 | NM_024770 | methyltransferase like 8 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| FAM49A | NM_030797 | family with sequence similarity 49, member A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -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-647 | > -0.01 | N/A | Sites in UTR |
| CRISPLD2 | NM_031476 | cysteine-rich secretory protein LCCL domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| CBX2 | NM_005189 | chromobox homolog 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| CALML4 | NM_001031733 | calmodulin-like 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| MEX3A | NM_001093725 | mex-3 homolog A (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| LRRC58 | NM_001099678 | leucine rich repeat containing 58 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ZNF831 | NM_178457 | zinc finger protein 831 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NUDT16 | NM_001171905 | nudix (nucleoside diphosphate linked moiety X)-type motif 16 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| APOOL | NM_198450 | apolipoprotein O-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ZNF519 | NM_145287 | zinc finger protein 519 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -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-647 | > -0.01 | N/A | Sites in UTR |
| OLFML2A | NM_182487 | olfactomedin-like 2A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| SPIN3 | NM_001010862 | spindlin family, member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| FOXK1 | NM_001037165 | forkhead box K1 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| C7orf41 | NM_152793 | chromosome 7 open reading frame 41 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| SIAH3 | NM_198849 | seven in absentia homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| EIF4E3 | NM_001134649 | eukaryotic translation initiation factor 4E family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ATXN1L | NM_001137675 | ataxin 1-like | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| SAMD12 | NM_001101676 | sterile alpha motif domain containing 12 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| BCL2L15 | NM_001010922 | BCL2-like 15 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| LOC646851 | NM_001013647 | hypothetical LOC646851 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| ZBTB8A | NM_001040441 | zinc finger and BTB domain containing 8A | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| FAM22D | NM_001009610 | family with sequence similarity 22, member D | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| SHISA7 | NM_001145176 | shisa homolog 7 (Xenopus laevis) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | > -0.01 | N/A | Sites in UTR |
| BACH1 | NM_001186 | BTB and CNC homology 1, basic leucine zipper transcription factor 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CLN8 | NM_018941 | ceroid-lipofuscinosis, neuronal 8 (epilepsy, progressive with mental retardation) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -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-647 | > -0.02 | N/A | Sites in UTR |
| GNG7 | NM_052847 | guanine nucleotide binding protein (G protein), gamma 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| LMX1B | NM_001174146 | LIM homeobox transcription factor 1, beta | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| MXD1 | NM_001202513 | MAX dimerization protein 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| PAX6 | NM_000280 | paired box 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| PLAGL2 | NM_002657 | pleiomorphic adenoma gene-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SH3BP2 | NM_001122681 | SH3-domain binding protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SLC6A6 | NM_001134367 | solute carrier family 6 (neurotransmitter transporter, taurine), member 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| TNNI1 | NM_003281 | troponin I type 1 (skeletal, slow) | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| TNS1 | NM_022648 | tensin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| NR2C2 | NM_003298 | nuclear receptor subfamily 2, group C, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| UMPS | NM_000373 | uridine monophosphate synthetase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| WHSC1 | NM_133334 | Wolf-Hirschhorn syndrome candidate 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -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-647 | > -0.02 | N/A | Sites in UTR |
| ADAM19 | NM_033274 | ADAM metallopeptidase domain 19 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| MTMR3 | NM_021090 | myotubularin related protein 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| QKI | NM_006775 | quaking homolog, KH domain RNA binding (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| H6PD | NM_004285 | hexose-6-phosphate dehydrogenase (glucose 1-dehydrogenase) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SEC14L5 | NM_014692 | SEC14-like 5 (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| KIAA0513 | NM_014732 | KIAA0513 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| TBC1D5 | NM_001134380 | TBC1 domain family, member 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| GAB2 | NM_012296 | GRB2-associated binding protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| APC2 | NM_005883 | adenomatosis polyposis coli 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| CELF1 | NM_001025596 | CUGBP, Elav-like family member 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SPIN1 | NM_006717 | spindlin 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ABHD2 | NM_007011 | abhydrolase domain containing 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| WDR37 | NM_014023 | WD repeat domain 37 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| DTX4 | NM_015177 | deltex homolog 4 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| KIF13B | NM_015254 | kinesin family member 13B | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| USP24 | NM_015306 | ubiquitin specific peptidase 24 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| RYBP | NM_012234 | RING1 and YY1 binding protein | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| GIGYF2 | NM_001103146 | GRB10 interacting GYF protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| GMEB2 | NM_012384 | glucocorticoid modulatory element binding protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| PACSIN1 | NM_001199583 | protein kinase C and casein kinase substrate in neurons 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| KCNIP3 | NM_001034914 | Kv channel interacting protein 3, calsenilin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| CDON | NM_016952 | Cdon homolog (mouse) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| RAB6B | NM_016577 | RAB6B, member RAS oncogene family | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| NEURL1B | NM_001142651 | neuralized homolog 1B (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| C12orf5 | NM_020375 | chromosome 12 open reading frame 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SHROOM3 | NM_020859 | shroom family member 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| BEND3 | NM_001080450 | BEN domain containing 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ALX4 | NM_021926 | ALX homeobox 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| FYCO1 | NM_024513 | FYVE and coiled-coil domain containing 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| RIC3 | NM_001135109 | resistance to inhibitors of cholinesterase 3 homolog (C. elegans) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| FBXL18 | NM_024963 | F-box and leucine-rich repeat protein 18 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| OPA3 | NM_025136 | optic atrophy 3 (autosomal recessive, with chorea and spastic paraplegia) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ORAI2 | NM_001126340 | ORAI calcium release-activated calcium modulator 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| TLN2 | NM_015059 | talin 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ZNRF3 | NM_001206998 | zinc and ring finger 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| RAB11FIP4 | NM_032932 | RAB11 family interacting protein 4 (class II) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ATCAY | NM_033064 | ataxia, cerebellar, Cayman type | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| KIAA1644 | NM_001099294 | KIAA1644 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SHANK3 | NM_001080420 | SH3 and multiple ankyrin repeat domains 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| LRRC15 | NM_001135057 | leucine rich repeat containing 15 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ASB6 | NM_001202403 | ankyrin repeat and SOCS box containing 6 | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ASB7 | NM_198243 | ankyrin repeat and SOCS box containing 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| WIPF2 | NM_133264 | WAS/WASL interacting protein family, member 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| METTL21A | NM_001127395 | methyltransferase like 21A | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| PRICKLE2 | NM_198859 | prickle homolog 2 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SLC25A30 | NM_001010875 | solute carrier family 25, member 30 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -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-647 | > -0.02 | N/A | Sites in UTR |
| GLDN | NM_181789 | gliomedin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| BEND4 | NM_001159547 | BEN domain containing 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | > -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-647 | > -0.02 | N/A | Sites in UTR |
| RBMS2 | NM_002898 | RNA binding motif, single stranded interacting protein 2 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| KIAA1244 | NM_020340 | KIAA1244 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SHROOM4 | NM_020717 | shroom family member 4 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| SLC46A1 | NM_001242366 | solute carrier family 46 (folate transporter), member 1 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| RBM33 | NM_053043 | RNA binding motif protein 33 | 0 | 0 | 0 | 0 | 2 | 0 | 0 | 2 | hsa-miR-647 | > -0.02 | N/A | Sites in UTR |
| ADARB1 | NM_001112 | adenosine deaminase, RNA-specific, B1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| ZFHX3 | NM_001164766 | zinc finger homeobox 3 | 1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| NTRK2 | NM_001007097 | neurotrophic tyrosine kinase, receptor, type 2 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| SBNO1 | NM_001167856 | strawberry notch homolog 1 (Drosophila) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| SLC6A19 | NM_001003841 | solute carrier family 6 (neutral amino acid transporter), member 19 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| ABR | NM_001092 | active BCR-related gene | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| ZHX3 | NM_015035 | zinc fingers and homeoboxes 3 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| ZBTB43 | NM_001135776 | zinc finger and BTB domain containing 43 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| VPS53 | NM_001128159 | vacuolar protein sorting 53 homolog (S. cerevisiae) | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| TTYH3 | NM_025250 | tweety homolog 3 (Drosophila) | 0 | 0 | 0 | 0 | 3 | 0 | 2 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| ADAMTS15 | NM_139055 | ADAM metallopeptidase with thrombospondin type 1 motif, 15 | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| CLYBL | NM_206808 | citrate lyase beta like | 0 | 0 | 0 | 0 | 2 | 0 | 1 | 1 | hsa-miR-647 | > -0.03 | N/A | Sites in UTR |
| IGFBP5 | NM_000599 | insulin-like growth factor binding protein 5 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| MTHFR | NM_005957 | methylenetetrahydrofolate reductase (NAD(P)H) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| TK2 | NM_001172643 | thymidine kinase 2, mitochondrial | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| SLC7A5 | NM_003486 | solute carrier family 7 (amino acid transporter light chain, L system), member 5 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| JRK | NM_003724 | jerky homolog (mouse) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| WDR52 | NM_001164496 | WD repeat domain 52 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| PDLIM2 | NM_176871 | PDZ and LIM domain 2 (mystique) | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| KSR2 | NM_173598 | kinase suppressor of ras 2 | 0 | 0 | 0 | 0 | 2 | 0 | 2 | 0 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PDPK1 | NM_002613 | 3-phosphoinositide dependent protein kinase-1 | 0 | 0 | 0 | 0 | 3 | 0 | 1 | 2 | hsa-miR-647 | > -0.04 | N/A | Sites in UTR |
| MPRIP | NM_015134 | myosin phosphatase Rho interacting protein | 0 | 0 | 0 | 0 | 4 | 0 | 4 | 0 | hsa-miR-647 | > -0.08 | N/A | Sites in UTR |
| APOE | NM_000041 | apolipoprotein E | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| BRCA1 | NM_007294 | breast cancer 1, early onset | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| C3AR1 | NM_004054 | complement component 3a receptor 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| CTSK | NM_000396 | cathepsin K | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| EIF4G2 | NM_001042559 | eukaryotic translation initiation factor 4 gamma, 2 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| FABP6 | NM_001040442 | fatty acid binding protein 6, ileal | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| GSK3B | NM_001146156 | glycogen synthase kinase 3 beta | 1 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| GSTA3 | NM_000847 | glutathione S-transferase alpha 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| IGFBP2 | NM_000597 | insulin-like growth factor binding protein 2, 36kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| LAG3 | NM_002286 | lymphocyte-activation gene 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| LAMA5 | NM_005560 | laminin, alpha 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| MAGEA1 | NM_004988 | melanoma antigen family A, 1 (directs expression of antigen MZ2-E) | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| MAGEA4 | NM_001011548 | melanoma antigen family A, 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| PCSK5 | NM_006200 | proprotein convertase subtilisin/kexin type 5 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| PDGFA | NM_002607 | platelet-derived growth factor alpha polypeptide | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| RARRES3 | NM_004585 | retinoic acid receptor responder (tazarotene induced) 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| S100B | NM_006272 | S100 calcium binding protein B | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| CXCL12 | NM_199168 | chemokine (C-X-C motif) ligand 12 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| TSHR | NM_001018036 | thyroid stimulating hormone receptor | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| UBA7 | NM_003335 | ubiquitin-like modifier activating enzyme 7 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| APOL1 | NM_001136540 | apolipoprotein L, 1 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| FCN3 | NM_003665 | ficolin (collagen/fibrinogen domain containing) 3 (Hakata antigen) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| CHRD | NM_003741 | chordin | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| TRADD | NM_003789 | TNFRSF1A-associated via death domain | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| AP1M1 | NM_001130524 | adaptor-related protein complex 1, mu 1 subunit | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| CYTH1 | NM_004762 | cytohesin 1 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| ARPC3 | NM_005719 | actin related protein 2/3 complex, subunit 3, 21kDa | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| MTHFS | NM_001199758 | 5,10-methenyltetrahydrofolate synthetase (5-formyltetrahydrofolate cyclo-ligase) | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | 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-647 | N/A | N/A | Sites in UTR |
| APOL2 | NM_030882 | apolipoprotein L, 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| FBXL6 | NM_012162 | F-box and leucine-rich repeat protein 6 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| PKD2L2 | NM_014386 | polycystic kidney disease 2-like 2 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| ZNF446 | NM_017908 | zinc finger protein 446 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| CDK5RAP2 | NM_001011649 | CDK5 regulatory subunit associated protein 2 | 1 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| PDXP | NM_020315 | pyridoxal (pyridoxine, vitamin B6) phosphatase | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| ANKRD36B | NM_025190 | ankyrin repeat domain 36B | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| SPTBN4 | NM_025213 | spectrin, beta, non-erythrocytic 4 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| C14orf93 | NM_001130706 | chromosome 14 open reading frame 93 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| IRF2BPL | NM_024496 | interferon regulatory factor 2 binding protein-like | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| RAB17 | NM_022449 | RAB17, member RAS oncogene family | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| KLC2 | NM_001134774 | kinesin light chain 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| IPO4 | NM_024658 | importin 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| DHRS12 | NM_001031719 | dehydrogenase/reductase (SDR family) member 12 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| APOL3 | NM_145640 | apolipoprotein L, 3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| JHDM1D | NM_030647 | jumonji C domain containing histone demethylase 1 homolog D (S. cerevisiae) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| C3orf20 | NM_001184957 | chromosome 3 open reading frame 20 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| SGK196 | NM_032237 | protein kinase-like protein SgK196 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| HDGFRP2 | NM_001001520 | hepatoma-derived growth factor-related protein 2 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| CCNB3 | NM_033031 | cyclin B3 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| TGIF2LY | NM_139214 | TGFB-induced factor homeobox 2-like, Y-linked | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| SNX29 | NM_001080530 | sorting nexin 29 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| C20orf114 | NM_033197 | chromosome 20 open reading frame 114 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| RNF166 | NM_001171815 | ring finger protein 166 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| ARHGEF19 | NM_153213 | Rho guanine nucleotide exchange factor (GEF) 19 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| KRT78 | NM_173352 | keratin 78 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| TTLL10 | NM_001130045 | tubulin tyrosine ligase-like family, member 10 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| IGSF22 | NM_173588 | immunoglobulin superfamily, member 22 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| MYLK4 | NM_001012418 | myosin light chain kinase family, member 4 | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| DPPA5 | NM_001025290 | developmental pluripotency associated 5 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| IGF2 | NM_001042376 | insulin-like growth factor 2 (somatomedin A) | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| INS-IGF2 | NM_001042376 | INS-IGF2 readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 1 | 0 | hsa-miR-647 | N/A | N/A | Sites in UTR |
| ST20-MTHFS | NM_001199760 | ST20-MTHFS readthrough | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 1 | hsa-miR-647 | N/A | N/A | Sites in UTR |