Table S2: The function of piR-1245 targets and their expression in CRC

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| --- | --- | --- | --- | --- |
| Gene | Expression\* | Function\*\* | Process\*\* | Component\*\* |
| MXD1 | down | RNA polymerase II core promoter proximal region sequence-specific DNA binding protein binding protein dimerization activity transcription cofactor activity transcription corepressor activitytranscription factor activity, sequence-specific DNA bindingtranscriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding | cell proliferationmulticellular organism developmentnegative regulation of transcription from RNA polymerase II promoter transcription, DNA-templated | nuclear chromatinnucleus |
| DUSP5 | down | MAP kie tyrosine/serine/threonine phosphae activityphosphae activityprotein bindingprotein tyrosine phosphae activity protein tyrosine/serine/threonine phosphae activityprotein tyrosine/serine/threonine phosphae activity | MAPK cascade activation of MAPK activitydephosphorylationendoderm formationinactivation of MAPK activity peptidyl-threonine dephosphorylationpeptidyl-tyrosine dephosphorylationprotein dephosphorylation | nucleoplasm |
| BTG1 | down | enzyme binding kie bindingprotein binding transcription cofactor activity | cell migration negative regulation of cell growth negative regulation of cell proliferation positive regulation of angiogenesis positive regulation of endothelial cell differentiationpositive regulation of fibroblast apoptotic process positive regulation of myoblast differentiationpositive regulation of myoblast differentiation regulation of transcription, DNA-templated | cytoplasm cytoplasmnucleus nucleus |
| TP53INP1 | down | antioxnt activity protein binding | apoptotic process autophagic cell death autophagosome assembly cell cycle arrest cellular oxnt detoxification cellular response to cellular response to ethanol cellular response to hydroperoxide cellular response to methyl methanesulfonatenegative regulation of cell migration negative regulation of cell proliferation positive regulation of apoptotic signaling pathway positive regulation of autophagypositive regulation of transcription, DNA-templated regulation of apoptotic process regulation of signal transduction by p53 class mediator response to heat response to stress transcription, DNA-templated | PML body autophagosomecytoplasm cytoplasmic vesicle cytosol nucleoplasm nucleus |
| FAS | down | identical protein binding kie binding protease binding protein binding protein complex binding receptor activity signal transducer activity tumor necrosis factor-activated receptor activity | B cell mediated immunity activation of cysteine-type endopeptse activity involved in apoptotic process activation of cysteine-type endopeptse activity involved in apoptotic signaling pathway activation-induced cell death of T cells aging apoptotic process apoptotic signaling pathway brain development cellular response to cobalt ion cellular response to estrogen stimulus cellular response to glucose stimulus cellular response to hydrogen peroxide cellular response to hydrostatic pressure cellular response to hyperoxiacellular response to hypoxia cellular response to interleukin-1 cellular response to lithium ion cellular response to mechanical stimulus cellular response to phenylalanine chordate embryonic development circadian rhythm dendrite regeneration extrinsic apoptotic signaling pathway extrinsic apoptotic signaling pathway in absence of ligand extrinsic apoptotic signaling pathway via death domain receptors | CD95 death-inducing signaling complex apical dendrite apical plasma membrane cell surface cytoplasm cytosol death-inducing signaling complex external side of plasma membrane extracellular exosome extracellular space integral component of plasma membrane membrane raft neuron projectionneuronal cell body nucleus nucleus perinuclear region of cytoplasm plasma membrane plasma membrane plasma membrane |
| SESN2 | down | leucine binding oxidoreduce activity, acting on peroxide as acceptor protein binding sulfiredoxin activity NOT sulfiredoxin activity | DNA damage response, signal transduction by p53 class mediator autophagy cellular oxnt detoxification NOT cellular oxnt detoxification cellular oxnt detoxification cellular response to amino acid stimulus cellular response to leucine cellular response to oxtive stress fatty acid beta-oxtion glucose ort mitochondrial DNA metabolic process negative regulation of TORC1 signaling negative regulation of cell growth negative regulation of translation in response to endoplasmic reticulum stress positive regulation of macroautophagypositive regulation of protein localization to nucleuspositive regulation of transcription from RNA polymerase II promoter in response to oxtive stressprotein kie B signaling reactive oxygen species metabolic processregulation of cAMP-dependent protein kie activityregulation of gluconeogenesis involved in cellular glucose homeosisregulation of protein phosphorylation regulation of response to reactive oxygen speciesresponse to glucose response to insulin | colocalizes\_with ATG1/ULK1 kie complex colocalizes\_with GATOR2 complex colocalizes\_with TORC2 complex cytoplasm cytosol mitochondrion colocalizes\_with nucleotide-activated protein kie complex nucleus |
| NFKBIA | down | NF-kappaB binding NF-kappaB binding enzyme binding heat shock protein binding identical protein binding nuclear localization sequence binding protein bindingprotein complex binding transcription factor binding ubiquitin protein ligase binding | Fc-epsilon receptor signaling pathway T cell receptor signaling pathway apoptotic process cellular response to cold cellular response to cytokine stimulus cellular response to organic cyclic compound cytoplasmic sequestering of NF-kappaB cytoplasmic sequestering of transcription factor lipopolysaccharide-mediated signaling pathway negative regulation of DNA binding negative regulation of NF-kappaB transcription factor activity negative regulation of Notch signaling pathway negative regulation of apoptotic process negative regulation of ld storage negative regulation of macrophage derived foam cell differentiation negative regulation of myeloid cell differentiation nucleotide-binding oligomerization domain containing 1 signaling pathway nucleotide-binding oligomerization domain containing 2 signaling pathway positive regulation of NF-kappaB transcription factor activity positive regulation of cellular protein metabolic process positive regulation of cholesterol efflux positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA polymerase II promoter protein ort into nucleus, translocation regulation of NF-kappaB ort into nucleus | I-kappaB/NF-kappaB complex cytoplasm cytosol nucleus plasma membrane |
| UPP1 | down | uridine phosphorylase activity | UMP salvage cellular response to glucose starvation nucleobase-containing compound metabolic process nucleotide catabolic process pyrimidine nucleoside catabolic process pyrimidine nucleoside salvage uridine catabolic process | cytosol |
| ATF3 | down | RNA polymerase II core promoter proximal region sequence-specific DNA binding RNA polymerase II regulatory region sequence-specific DNA binding identical protein binding protein binding protein heterodimerization activity protein homodimerization activity transcription corepressor activity transcription factor activity, RNA polymerase II core promoter proximal region sequence-specific binding transcription factor activity, sequence-specific DNA binding transcription regulatory region DNA binding transcription regulatory region sequence-specific DNA binding transcriptional activator activity, RNA polymerase II transcription regulatory region sequence-specific binding transcriptional repressor activity, RNA polymerase II core promoter proximal region sequence-specific binding | PERK-mediated unfolded protein response cellular response to amino acid starvation gluconeogenesis negative regulation of ERK1 and ERK2 cascade negative regulation of transcription from RNA polymerase II promoter positive regulation of TRAIL-activated apoptotic signaling pathway positive regulation of cell proliferation positive regulation of transcription from RNA polymerase II promoter positive regulation of transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress regulation of transcription from RNA polymerase II promoter in response to arsenic-containing substance skeletal muscle cell differentiation transcription from RNA polymerase II promoter | CHOP-ATF3 complex nucleolus nucleoplasm nucleus |

\*To compare the expression of target genes in cancer and normal tissues, Oncomine database was analyzed (Rhodes, D.R., et al. ONCOMINE: a cancer microarray database and integrated data-mining platform. Neoplasia,2004 6, 1-6).

\*\* The function of target gene was provided by Gene Ontology Annotation (UniProt-GOA) Database