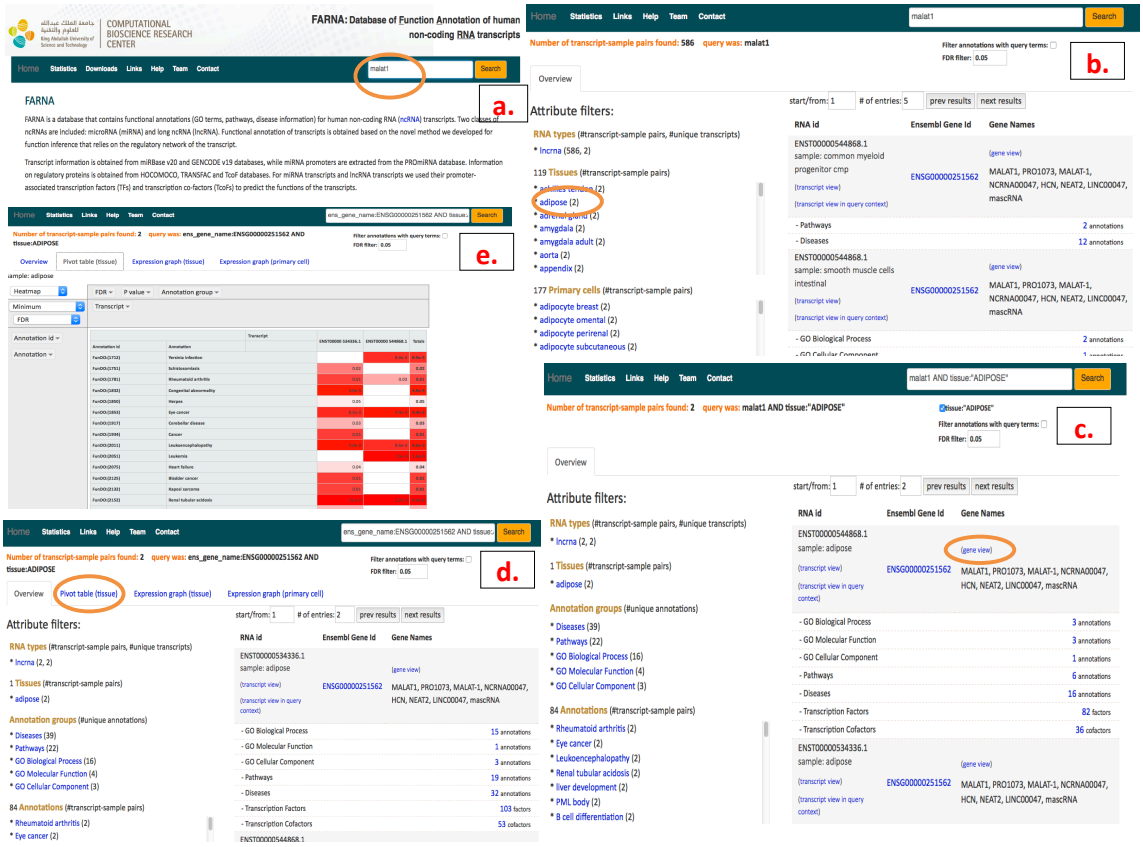
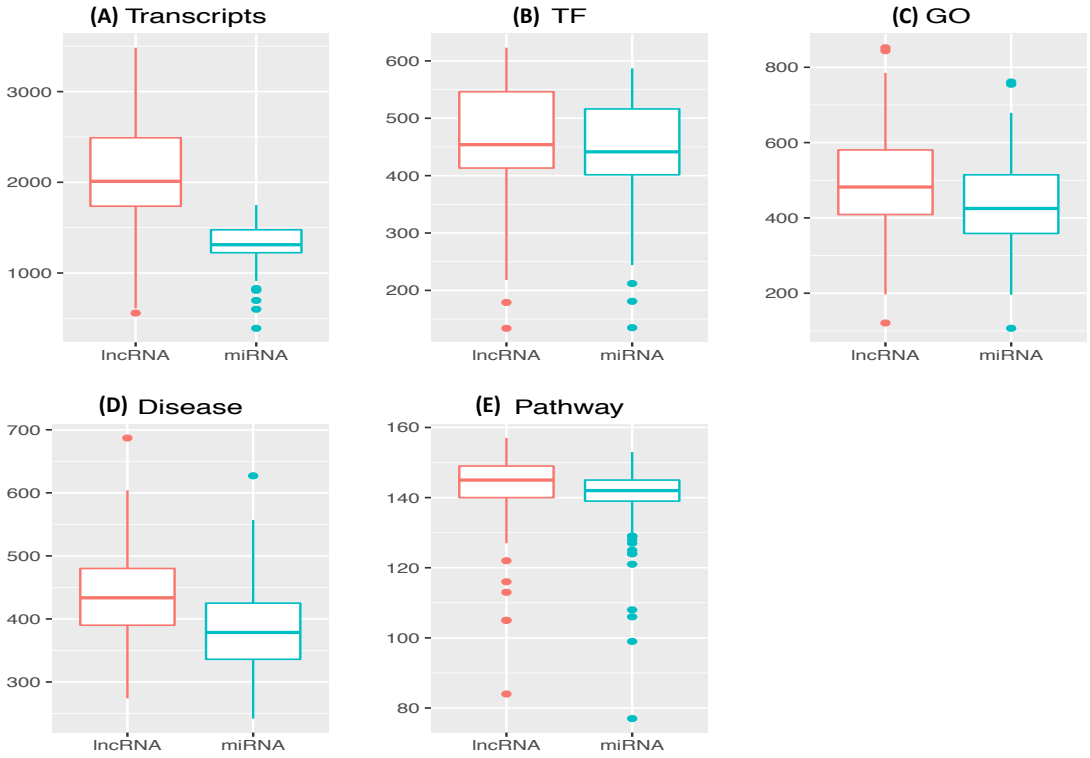
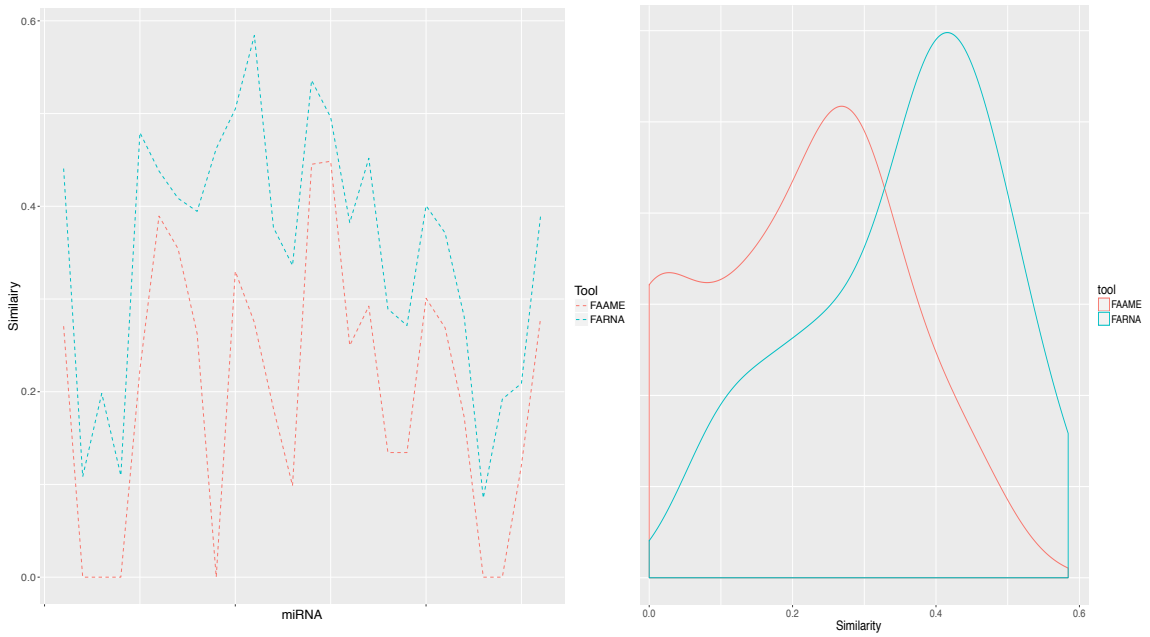


Supplementary Figure S1: This figure demonstrates how a user can find predicted function of MALAT1 in a tissue. Figures are ordered in clock-wise manner.

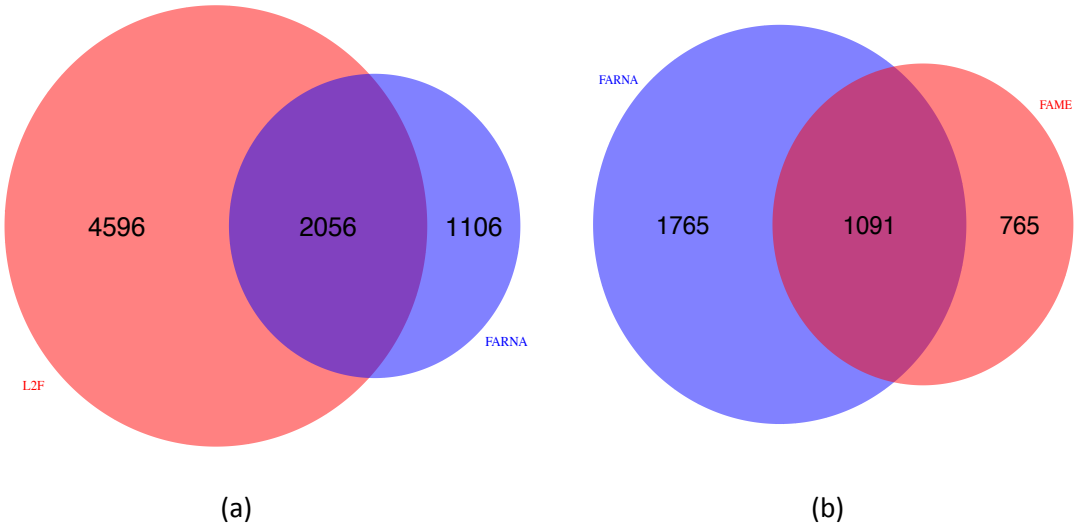
- **a. Type "malat1" in search box**
- **b. Select a tissue of interest. We select "adipose".**
- **c. Click "gene view"**
- **d. Click "Pivot Table" to view result**
- **e. Final result of pivot table**



Supplementary Figure S2: This figures summarizes the statistics of FARNA from different perspective.
(A) This figure shows the number of RNA transcripts expressed in different cells/tissues.
(B) This figure shows the number of unique TFs involved in different cells/tissues regulating the RNA transcripts.
(C) This figure shows the number of statistically significant unique GO terms in different cells/tissues.
(D) This figure shows the number of statistically significant unique disease terms in different cells/tissues.
(E) This figure shows the number of statistically significant unique pathways in different cells/tissues.



Supplementary Figure S3: Comparison of predictions from FARNA and FAME against known miRNA annotations from AMIGO based on semantic similarity. We used Lin's similarity measure with Resnik information content with best matching average (bma) option from "The semantic measures library and toolkit".



Supplementary Figure S4: Overlap of GO terms annotations for FARNA, FAME and LncRNA2Function (L2F). (a) This figure shows the overlap of GO term annotations provided by FARNA and LncRNA2Function (L2F). It shows that LncRNA2Function covers 65.02% of annotations provided by FARNA, and 30.90% annotations of LncRNA2Function are covered by FARNA. (b) This figure shows the overlap of GO term annotations provided by FARNA and FAME. It shows that 38.20% of annotations provided by FARNA are covered by FAME, and 58.78% annotations of FAME are covered by FARNA

Supplementary Table S1. Evidence form miRNAs and lncRNAs to validate the predictions from FARNA

Gene/Transcript	Comparison between known evidences and FARNA demonstrations
miR-122	It is also shown that miR-122 may be involved in liver damage (113). And miR-122 is involved in liver disease via IFN-alpha/beta pathways (114) and Nuclear factor-κB (NF-κB) system is activated in response to several stresses and may cause liver damage (113). FARNA suggest "GO:0001889 liver development", "GO:0044255 cellular lipid metabolic process", "GO:0038061 NIK/NF-kappaB signaling", "GO:0033256 I-kappaB/NF-kappaB complex", "REACT_25024 TRAF6 mediated induction of NFkB and MAP kinases upon TLR7/8 or 9 activation", "REACT_13537 p75NTR signals via NF-kB", REACT_22258 Metabolism of lipids and lipoproteins", "REACT_19241 Regulation of lipid metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)" and "REACT_25359: RIG-I/MDA5 mediated induction of IFN-alpha/beta pathways" in "liver" tissue. miR-122 has also been linked to skin-related diseases (115). FARNA further suggest "GAD:(KOBAS:40244) Lupus vulgaris" and "NHGRI GWAS Catalog:(KOBAS:8815) Psoriasis". miR-122 has also been shown to be significantly upregulated in the serum of patients with osteoporosis [PMID: 24431276] and has been identified as a biomarker for bone diseases [PMID: 26525415]. FARNA retrieved associated annotations such as KEGG DISEASE:(KOBAS:372) Cancers of soft tissues and bone, GAD:(KOBAS:14214) Osteosarcoma and FunDO:(2188) Bone marrow disease.
miR-200	miR-200 family that has been identified as biomarkers for epithelial-to-mesenchymal transition (EMT). In EMT epithelial cells morphologically and phenotypically transdifferentiate into mesenchymal cells and the major pathological process implicated in proliferative vitreoretinopathy (PVR) (116), renal fibrosis (117), cancer (118) and development (119). This miR-200 family have been demonstrated to target the E-cadherin transcriptional repressors zinc finger E-box binding homeobox 1(ZEB1) and ZEB2 for EMT (120-122). Some TFs such as SNAI1 and SNAI2 play a crucial role in EMT (123,124). SNAI2 indirectly regulates ZEB1 and ZEB2 by regulating the miR-200 family transcript, and in turn the miR-200 family regulates ZEB1 and ZEB2. ETS1, another TF, is a suggested upstream regulator of ZEB1 and ZEB2 (125) and has also been identified as a biomarker of EMT. FARNA predicts that TFs SNAI1, SNAI2, ZEB1 and ETS1 binds the miR-200a promoter region and that miR-200a is expressed in "eye vitreous humor" tissue and in "monocyte and renal epithelial cells". FARNA also returns several related annotations such as GO:0048048 Embryonic eye morphogenesis; GO:0031076 embryonic camera-type eye development; REACT_11061 Signalling by NGF (126); REACT_13776 p75 NTR receptor-mediated signaling (126); FunDO:(2152) Renal tubular acidosis; GO:0072160 nephron tubule epithelial cell differentiation; REACT_6966 Toll-Like Receptors Cascades (127). miR-200 is shown to be involved in renal cells for EMT transition (128). FARNA annotates miR-200 in "renal epithelial cells" primary cell with "GO:0010631 epithelial cell migration".
miR-146a	This miRNA is found in lung and monocytic cell line (129) and known to be involved in innate immune sensing (130). FARNA suggest "REACT_6802 Innate Immune System" in

	"lung" tissue, as well as KEGG DISEASE:(H00013) Small cell lung cancer and KEGG DISEASE:(KOBAS:762) Cancers of the lung and pleura It has additionally been demonstrated that a G > C polymorphism (rs2910164) is located in the stem region opposite to the mature miR-146a sequence, which results in a change from G:U pair to C:U mismatch in the stem structure of miR-146a precursor (131). FARNA predicts GO:0001889 liver development, GO:0071339 MLL1 complex, GAD:(KOBAS:34494) LIVER CIRRHOSIS, BILIARY and FunDO:(2022) Liver cancer hsa-mir-146a is also shown to be involved in the progression of Alzheimer's disease (132,133) . FARNA predicts "GO:0048708 astrocyte differentiation, REACT_268456 Programmed Cell Death, REACT_578 Apoptosis, REACT_6890 Activated TLR4 signalling, REACT_6894 Toll Like Receptor 4 (TLR4) Cascade, REACT_995 Apoptotic execution phase, REACT_1213 Apoptosis induced DNA fragmentation, GAD:(KOBAS:124) NEUROLOGICAL and FunDO:(1740) Alzheimer's disease" and show hsa-mir-146a to be highly expressed in "cd4+cd25 cd45ra memory regulatory t cells". hsa-mir-146a is also shown to be involved in Rheumatoid arthritis (134). FARNA predicts "NHGRI GWAS Catalog:(KOBAS:645) Rheumatoid arthritis and GAD:(KOBAS:15804) Arthritis, psoriatic".
miR-155	ELK3 was demonstrated to binds the miR-155 promoter via ChIP and quantitative polymerase chain reaction (QPCR) (135). Additionally, both hsa-miR-155 and ELK3 have been linked to the hypoxia response pathway (135). FARNA predicts that TF ELK3 binds the hsa-miR-155 promoter region and GO:0001666 response to hypoxia miR-155 is demonstrated to be involved in Rheumatoid arthritis (136,137). FARNA predicts "FunDO:(1781) Rheumatoid arthritis". This miRNA are mainly involved in monocytic and immune system cell line (138,139). FARNA suggest it is also expressed in "cd14+ monocyte derived endothelial": miR-155 is also shown to be involved in cystic fibrosis (140,141). FARNA show hsa-miR-155 to be expressed in "fibroblast lung" cell, as well as KEGG DISEASE:(KOBAS:762) Cancers of the lung and pleura and GAD:(KOBAS:644) Lung cancer hsa-mir-155 is shown to be involved in lymphoma (139) and FARNA predicts "FunDO:(2239) Lymphoma" in "cd19+ b cells", as well as GAD:(KOBAS:33584) Precursor cell lymphoblastic leukemia-lymphoma and GAD:(KOBAS:8444) Follicular lymphoma
miR-21	miR-21 was shown to be highly expressed in several cancer types such as colorectal cancer (142), breast cancer (143) and liver cancer (144). FARNA returns related GO, disease and pathway annotation such as GO:0008285 negative regulation of cell proliferation; GO:0006921 cellular component disassembly involved in execution phase of apoptosis; GO:0016605 PML body and REACT_995 Apoptotic execution phase. FARNA further returns 24 different types of cancer for miR-21 in different cells/tissues that include Adenoid cystic cancer, Bladder cancer, Breast cancer, Colon cancer, Colorectal cancer, Endometrial cancer, Esophageal cancer, Esophagus cancer, Eye cancer,

	Gastric cancer, Kidney cancer, Liver cancer, Lung cancer, Non-small cell lung cancer, Oral cancer, Ovarian cancer, Pancreatic cancer, Penile cancer, Pituitary cancer, Prostate cancer, Small cell lung cancer, Squamous cell cancer, Stomach cancer, Thyroid cancer. It has additionally been shown that miR-21 contributes to myocardial disease by stimulating MAP kinase signalling through SPRY1 in fibroblasts (145). Generally, patients with rheumatoid arthritis (RA) have higher levels of inflammation in their bodies, which may affect other organs and tissues besides the joints. People with RA have up to twice the risk of heart disease and development of heart failure (146). FARNA suggest "FunDO:(1781) Rheumatoid arthritis", "GAD:(KOBAS:1134) Atherosclerosis, coronary" and "GAD:(KOBAS:33284) Coronary disease". miR-21 is shown to be involved in cardiac hypertrophy(147) and FARNA predicts "GAD:(KOBAS:33194) Hypertrophy, left ventricular" in "heart tricuspid valve".
miR-375	miR-375 was shown to be is down-regulated in pancreatic cancer (148,149) and it has been shown that specific cofactors of SWI/SNF chromatin remodeling complex have roles in pancreatic cancer. FARNA suggest "GO:0070603 SWI/SNF superfamily-type complex" and NHGRI GWAS Catalog:(KOBAS:5145) Pancreatic cancer and also shows miR-375 (trx 2) to be highly expressed in "pancreatic" tissue. It has also been demonstrated that miR-375 overexpression in mouse hippocampus potently reduced dendrite density. FARNA suggest miR-375 to be highly expressed in "hippocampus" tissue and predicts GO:0030425 dendrite miR-375 is also shown to be involved in head and neck squamous cell carcinoma (HNSCC)(150) and has been identified as a microRNA that is differentially expressed between lung squamous cell carcinoma and lung adenocarcinoma. FARNA suggest miR-375 to be highly expressed in "lung" tissue and predicts KEGG DISEASE:(KOBAS:702) Head and neck cancers.
miR-16	miR-15 and miR-16 families have been demonstrated as transcriptional targets of E2F, which, in turn, modulates E2F activity [PMID: 21454377]. FARNA predicts that TF E2F4 binds the miR-16 promoter region. miR-16 is being considered as a potential biomarker for predicting melanoma prognosis (150). FARNA suggest "GAD:(KOBAS:8644) Melanoma", "KEGG DISEASE:(KOBAS:7442) Skin and soft tissue diseases" and "KEGG DISEASE:(KOBAS:7432) Skin diseases". miR-16 is also down-regulated during insulin resistance and controls skeletal muscle protein accretion (151). FARNA suggest "GAD:(KOBAS:34) Diabetes, type 1" and KEGG DISEASE:(H00409) Type II diabetes mellitus. Inhibitors of the WNT pathway are being explored as a novel therapeutic target in the reversal of the age-related thymic involution (152). miR-16 exhibited differential expression in the senescent thymus (152) , and have previously been implicated in thymus involution caused by aging (153). FARNA suggest "GO:0007420 brain development" and show miR-16 to be highly expressed in "thymus" and "pituitary gland" tissue
XIST	XIST (http://www.lncrnadb.org/xist/) is known to acts as a major effector of the X

	inactivation process. X inactivation is an early developmental process in mammalian females that transcriptionally silences one of the pair of X chromosomes, thus providing dosage equivalence between males and females, that is, dosage compensation (154,155). XIST RNA is expressed from inactive X-chromosome and recruit different chromatin modifier in X-chromosome. Sample collected from hippocampus shows that majority of female mouse have random X-chromosome inactivation (XCI) (156). For XIST, in "globus pallidus" brain tissue FARNA returned the following GO terms: from Cellular Compartment: GO:0016514 SWI/SNF complex; GO:0071565 nBAF complex; GO:0071564 npBAF complex; from Biological Process: GO:0006337 nucleosome disassembly, as well KEGG DISEASE:(H00773) Non-syndromic autosomal dominant mental retardation and KEGG DISEASE:(KOBAS:302) Cancers of the breast and female genital organs. FARNA retrieving these GO terms are reasonable as the study of dosage compensation revealed the existence of an amazing number of interacting chromatin remodeling mechanisms that affect the function of entire chromosomes. The SWI/SNF subunits were shown to play a key role in chromatin remodeling (157). Additionally, mammalian BAF complexes include SWI/SNF subunits that are altered in response to the changes in epigenetic regulation that accompany the evolution of multicellularity. Moreover, the X-chromosome has been a target in many studies looking for causes of Non-syndromic autosomal dominant mental retardation because of the high male to female ratio in the Non-syndromic autosomal dominant mental retardation population. The result is that most of the known Non-syndromic autosomal dominant mental retardation genes are X-linked (158,159). Dosage compensation is the term used to describe equalization of the expression of genes between members of different biological sexes. In humans, females (XX) silence the transcription of one X chromosome, thus having the same number of expressed X-linked genes as do males (XY) (both genders having essentially one X chromosome per cell from which to transcribe and express genes) (160,161). Dosage compensation has been shown to be involved in global rebalancing of aneuploidy genomes and aneuploidies have been associated with a variety of developmental defects and malignant aberrations such as certain breast cancers (162). Thus, it is reasonable for FARNA to retrieve sex organ-specific cancers such as "Cancers of the breast and female genital organs". In summary, we find that the GO terms we highlighted and KEGG Diseases actually fit quite well to the "essential role in X chromosome dosage compensation" and that the relevance of brain tissue is warranted.
GAS5	Down-regulation of GAS5 has been demonstrated to increase pancreatic cancer cell proliferation by regulating CDK6 (163). FARNA predict "GAD:(KOBAS:32574) Pancreatic neoplasms" and show GAS5 to be highly expressed in normal "pancreas" tissue. GAS5 has also been implicated in autoimmune disease (164). FARNA predicts "REACT_6802 Innate Immune System", "KEGG DISEASE:(KOBAS:992) Primary immunodeficiency", "KEGG DISEASE:(KOBAS:802) Immune system diseases" and "REACT_75913 Nucleotide-binding domain, leucine rich repeat containing receptor (NLR) signaling pathways".

	GAS5 is also down-regulated in breast cancer and its expression induces growth arrest and apoptosis (165). FARNA shows that GAS5 is highly expressed in “breast” tissue and it is annotated with “KEGG DISEASE:(KOBAS:302) Cancers of the breast and female genital organs”, “FunDO:(1944) Breast cancer”
PCA3	PCA3 is known to be involved in prostate cancer (166). FARNA predicts “OMIM:(176807) Prostate cancer”, “GO:2000134 negative regulation of G1/S transition of mitotic cell cycle”, “GO:0043518 negative regulation of DNA damage response, signal transduction by p53 class mediator”, GO:0016605 PML body”, “GO:0051403 stress-activated MAPK cascade” and suggest PCA3 to be highly expressed in normal “prostate” and “penis” tissue.
PVT1	PVT1 is shown to be involved in apoptosis inhibition in colorectal cancers (167). FARNA annotate PVT1 function in terms of "GO:0016605 PML body”, “KEGG DISEASE:(H00020) Colorectal cancer”, “GO:0043066 negative regulation of apoptotic process” and “GO:0008285 negative regulation of cell proliferation”. PVT1 is known to be involved in type 1 diabetes (168). FARNA also predicts “KEGG DISEASE:(KOBAS:4532) Diabetes” and “FunDO:(1904) Diabetes mellitus”. PVT1 has also been implicated in the pathogenesis of ovarian and breast cancers (169). FARNA suggest “KEGG DISEASE:(H00027) Ovarian cancer”, “KEGG DISEASE:(KOBAS:302) Cancers of the breast and female genital organs” and show PVT1 to be expressed in breast tissue.
RMST	This brain specific lncRNA interact with SOX2 and play key role in neurogenesis (170). FARNA predicted SOX2 in the TF list of RMST and predict “REACT_264135 Organelle biogenesis and maintenance”. Additionally FARNA suggest its expression in “cerebellum adult” tissue. RMST is known to be necessary for neuronal differentiation (170). FARNA annotated RMST in “medulla oblongata” tissue with "GO:0045595 Regulation of cell differentiation" ," GO:0030099 myeloid cell differentiation ".
H19	H19 is shown to be involved in bladder cancer (171,172) and FARNA suggest “KEGG DISEASE:(KOBAS:602) Cancers of the urinary system and male genital organs” and “FunDO:(2125) Bladder cancer” disease in “bladder” tissue. This lncRNA is an oncogene and tumor suppressor (173). It is shown to be involved in embryonic growth and development(174). FARNA suggest “REACT_111045 Developmental Biology”, “GO:0043588 skin development”, “GO:0000578 embryonic axis specification”, “GO:0048596 embryonic camera-type eye morphogenesis” and FunDO:(1853) Eye cancer, including more than twenty other cancer types.
ANRIL	lncRNA ENSG00000240498 commonly known as ANRIL has been implicated in the progression of several cancer types such as prostate cancer (175), esophageal squamous cell carcinoma (176), Malignant glioma (177), bladder cancer (178) and breast cancer (179) . ANRIL inhibits p15 (INK4b) through the TGFβ1 signaling pathway in human ANRIL interaction with TGF-β pathway and increased expression of TGF-β and p-Smad2/3 (180). FARNA suggest “GO:0030219 megakaryocyte differentiation”, “FunDO:(1944) Breast

	cancer", "FunDO:(2125) Bladder cancer", "NHGRI GWAS Catalog:(KOBAS:7855) Esophageal cancer" and "FunDO:(2214) Malignant glioma". ANRIL is also shown to be involved in atherosclerosis (181) and FARNA suggest "GAD:(KOBAS:1134) Atherosclerosis, coronary" disease in "fibroblast pulmonary artery".
PTCSC3	It has been demonstrated that PTCSC3 is a tumor suppressor and a target of miRNAs in thyroid cancer cells (182) . The expression of PTCSC3 is down-regulated in thyroid cancer (182), whereas in FARNA PTCSC3 is shown to be highly expressed in normal "thyroid" and "throat" tissue and very specific to these tissues, as well as return disease annotation "KEGG DISEASE:(H00032) Thyroid cancer"

Supplementary Table S2: List of miRNAs and their annotations downloaded from AMIGO site.

MIRNA	GO term	Reference
hsa-miR-133a-3p	GO:0010881	PMID:22378787
hsa-miR-19b-3p	GO:0008284	PMID:22378787
hsa-miR-19b-3p	GO:0010629	PMID:25765596
hsa-miR-19b-3p	GO:0035195	PMID:18728182
hsa-miR-19b-3p	GO:0035195	PMID:24998411
hsa-miR-19b-3p	GO:0035195	PMID:25084135
hsa-miR-19b-3p	GO:0035278	PMID:21796614
hsa-miR-19b-3p	GO:0042517	PMID:18728182
hsa-miR-19b-3p	GO:0048471	PMID:18728182
hsa-miR-19b-3p	GO:0050819	PMID:24998411
hsa-miR-19b-3p	GO:0060045	PMID:24998411
hsa-miR-19b-3p	GO:0072562	PMID:24998411
hsa-miR-19b-3p	GO:0090370	PMID:25084135
hsa-miR-19b-3p	GO:0090370	PMID:25765596
hsa-miR-19b-3p	GO:0097006	PMID:25765596
hsa-miR-19b-3p	GO:1901295	PMID:25765596
hsa-miR-19b-3p	GO:1903063	PMID:25765596
hsa-miR-19b-3p	GO:1903231	PMID:18728182
hsa-miR-19b-3p	GO:1903231	PMID:21796614
hsa-miR-19b-3p	GO:1903231	PMID:24998411
hsa-miR-19b-3p	GO:1903231	PMID:25084135
hsa-miR-19b-3p	GO:1904747	PMID:25084135
hsa-miR-19b-3p	GO:1905095	PMID:25084135
hsa-miR-19b-3p	GO:0038027|CL:0000517	PMID:25084135

hsa-miR-19b-3p	GO:2000188	PMID:25765596
hsa-miR-218-5p	GO:0032966	PMID:19913496
hsa-miR-218-5p	GO:0035278	PMID:19913496
hsa-miR-218-5p	GO:0035278	PMID:19913496
hsa-miR-218-5p	GO:1903231	PMID:19913496
hsa-miR-218-5p	GO:1903231	PMID:19913496
hsa-miR-378a-5p	GO:0000993	PMID:25336585
hsa-miR-19a-3p	GO:0010667	PMID:25336585
hsa-miR-19a-3p	GO:0035195	PMID:18728182
hsa-miR-19a-3p	GO:0035195	PMID:20940405
hsa-miR-19a-3p	GO:0035195	PMID:20940405
hsa-miR-19a-3p	GO:0035195	PMID:25785039
hsa-miR-19a-3p	GO:0042517	PMID:18728182
hsa-miR-19a-3p	GO:0070062	PMID:18728182
hsa-miR-19a-3p	GO:1903202	PMID:18728182
hsa-miR-19a-3p	GO:1903231	PMID:18728182
hsa-miR-19a-3p	GO:1903231	PMID:25785039
hsa-miR-19a-3p	GO:1903671	PMID:20299512
hsa-miR-31-5p	GO:0035195	PMID:19949084
hsa-miR-31-5p	GO:0035278	PMID:20826792
hsa-miR-31-5p	GO:1904995	PMID:19949084
hsa-miR-31-5p	GO:0071356	PMID:19949084
hsa-miR-31-5p	GO:1903231	PMID:19949084
hsa-miR-31-5p	GO:1903231	PMID:20826792
hsa-miR-31-5p	GO:0071356	PMID:19949084
hsa-miR-21-3p	GO:0008285	PMID:24098708
hsa-miR-21-3p	GO:0035195	PMID:24098708
hsa-miR-21-3p	GO:0043065	PMID:24098708
hsa-miR-21-3p	GO:1903231	PMID:24098708
hsa-miR-199b-5p	GO:0035195	PMID:15131085
hsa-miR-199b-5p	GO:1903231	PMID:15131085
hsa-miR-212-3p	GO:0035278	PMID:22880819
hsa-miR-212-3p	GO:1903231	PMID:22880819
hsa-miR-212-3p	GO:1903609	PMID:22880819
hsa-miR-208a-3p	GO:0002154	PMID:22880819
hsa-miR-208a-3p	GO:0035195	PMID:19726871
hsa-miR-208a-3p	GO:0042632	PMID:19726871
hsa-miR-208a-3p	GO:0045822	PMID:19726871
hsa-miR-208a-3p	GO:0061051	PMID:19726871
hsa-miR-208a-3p	GO:0070328	PMID:19726871

hsa-miR-208a-3p	GO:1903231	PMID:19726871
hsa-miR-208a-3p	GO:1903244	PMID:19726871
hsa-miR-208a-3p	GO:1903779	PMID:19726871
hsa-miR-208a-3p	GO:1905027	PMID:19726871
hsa-miR-141-3p	GO:0008284	PMID:16762633
hsa-miR-141-3p	GO:0035195	PMID:15131085
hsa-miR-141-3p	GO:0035195	PMID:16762633
hsa-miR-141-3p	GO:1903231	PMID:15131085
hsa-miR-181b-3p	GO:0035195	PMID:18728182
hsa-miR-181b-3p	GO:1903231	PMID:18728182
hsa-miR-93-5p	GO:0035195	PMID:18728182
hsa-miR-93-5p	GO:1903231	PMID:18728182
hsa-miR-30b-5p	GO:0035195	PMID:22387553
hsa-miR-30b-5p	GO:0042104	PMID:22387553
hsa-miR-30b-5p	GO:1903231	PMID:22387553
hsa-miR-30b-5p	GO:1903231	PMID:22387553
hsa-miR-107	GO:0035195	PMID:25033200
hsa-miR-107	GO:1903231	PMID:25033200
hsa-miR-15a-3p	GO:0006919	PMID:23353574
hsa-miR-15a-3p	GO:0035195	PMID:23353574
hsa-miR-15a-3p	GO:1903231	PMID:23353574
hsa-miR-29a-3p	GO:0010629	PMID:20570858
hsa-miR-29a-3p	GO:0035195	PMID:20570858
hsa-miR-29a-3p	GO:0035195	PMID:21761362
hsa-miR-29a-3p	GO:0061754	PMID:20570858
hsa-miR-29a-3p	GO:1903231	PMID:21761362
hsa-miR-451a	GO:0005615	PMID:20159880
hsa-miR-584-5p	GO:0000993	PMID:25336585
hsa-miR-21-5p	GO:0032869	PMID:25336585
hsa-miR-21-5p	GO:0001934	PMID:25336585
hsa-miR-21-5p	GO:0001934	PMID:16762633
hsa-miR-21-5p	GO:0001937	PMID:21347332
hsa-miR-21-5p	GO:0001937	PMID:23496142
hsa-miR-21-5p	GO:0003730	PMID:21376256
hsa-miR-21-5p	GO:0005737	PMID:23657402
hsa-miR-21-5p	GO:0007566	PMID:18556655
hsa-miR-21-5p	GO:0008284	PMID:16762633
hsa-miR-21-5p	GO:0008284	PMID:18384814
hsa-miR-21-5p	GO:0008284	PMID:21219636
hsa-miR-21-5p	GO:0008284	PMID:21376256

hsa-miR-21-5p	GO:0033554	PMID:19826040
hsa-miR-21-5p	GO:0008360	PMID:21817107
hsa-miR-21-5p	GO:0010596	PMID:21347332
hsa-miR-21-5p	GO:0010613	PMID:21347332
hsa-miR-21-5p	GO:0010614	PMID:21347332
hsa-miR-21-5p	GO:0010628	PMID:21376256
hsa-miR-21-5p	GO:0010629	PMID:17072344
hsa-miR-21-5p	GO:0010629	PMID:23684551
hsa-miR-21-5p	GO:0010667	PMID:23684551
hsa-miR-21-5p	GO:0071559	PMID:24887517
hsa-miR-21-5p	GO:0010838	PMID:21328460
hsa-miR-21-5p	GO:0001937|GO:0010596|GO:0061154	PMID:21347332
hsa-miR-21-5p	GO:0030334	PMID:20460403
hsa-miR-21-5p	GO:1904685	PMID:18591254
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