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miRNA Target Gene Identification: Sourcing miRNA Target Gene Relationships for the Analyses of TCGA Illumina MiSeq and RNA-Seq Hiseq Platform Data

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ABSTRACT Disruption in homeostatic levels of gene expression can lead directly to disease phenotype. miRNAs have key regulatory roles in modulating gene expression and have been shown to act as oncogenes, with their altered expression disrupting homeostatic biological mechanisms and adding to a disease phenotype. Using the Illumina MiSeq and HiSeq RNA sequencing platform data from the TCGA online resource, the objectives of the current research were to 1 Assess and quantify the existing online resource for miRNA target gene (TG) association, and 2 Define TG lists that can be used for genome-wide miRNA-mRNA-disease association analyses. Using the integration of miRNA lists from the Illumina platform and validated TG online databases, the researchers identified 307 miRNAs mapping to 3,358 validated TG's, with 9,858 miRNA-TG connections. From eight online predicted TG databases, they find 547 miRNAs that map to 18,271 unique TG's, with nearly three and a half million connections. Using the genomic location of miRNA and mRNAs assessed on the Illumina platforms, they identified 434 genes where miRNAs are co-located, and suggest that hypo/hyper methylation of these sites may play a key role in aberrant miRNA expression. In conclusion, using the Illumina miRNA and mRNA sequencing platforms, the researchers have created informative databases for the analyses of the complex interactions between miRNA and their target genes. The researchers' approaches can be applied to similar data sets for any other disease.