

Figure S1. “Molecular Function” GO enrichment of the 147 miRNA-targeted genes identified through miRCancerdb.

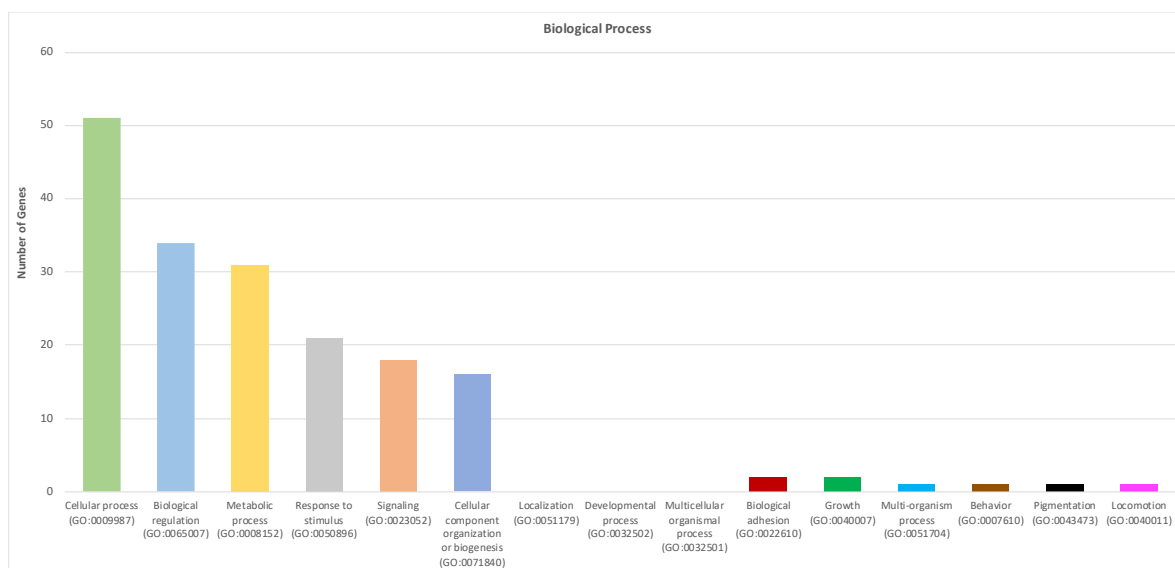


Figure S2. “Biological Process” GO enrichment of the 147 miRNA-targeted genes identified through miRCancerdb.

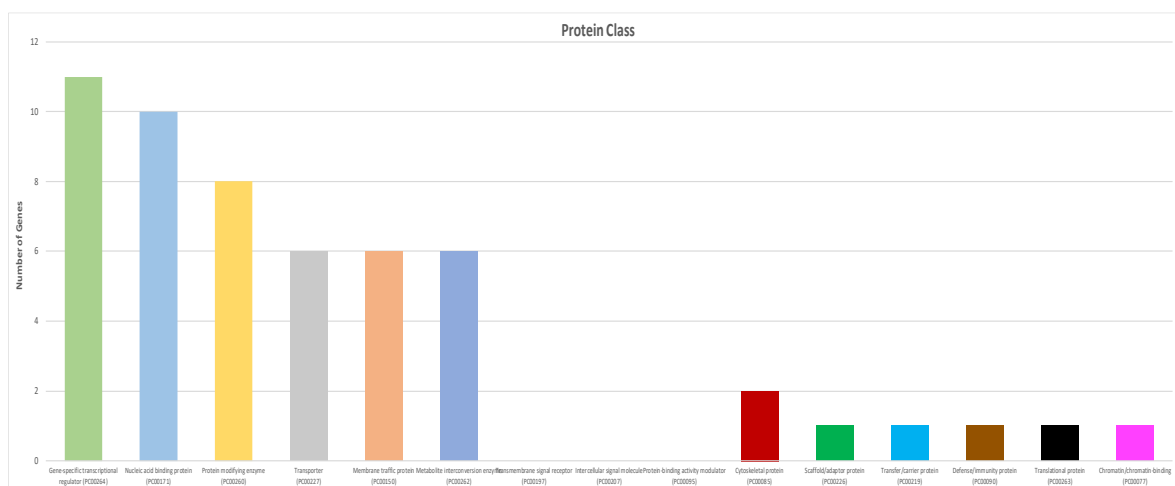


Figure S3. “Protein Class” GO enrichment of the 147 miRNA-targeted genes identified through miRCancerdb.

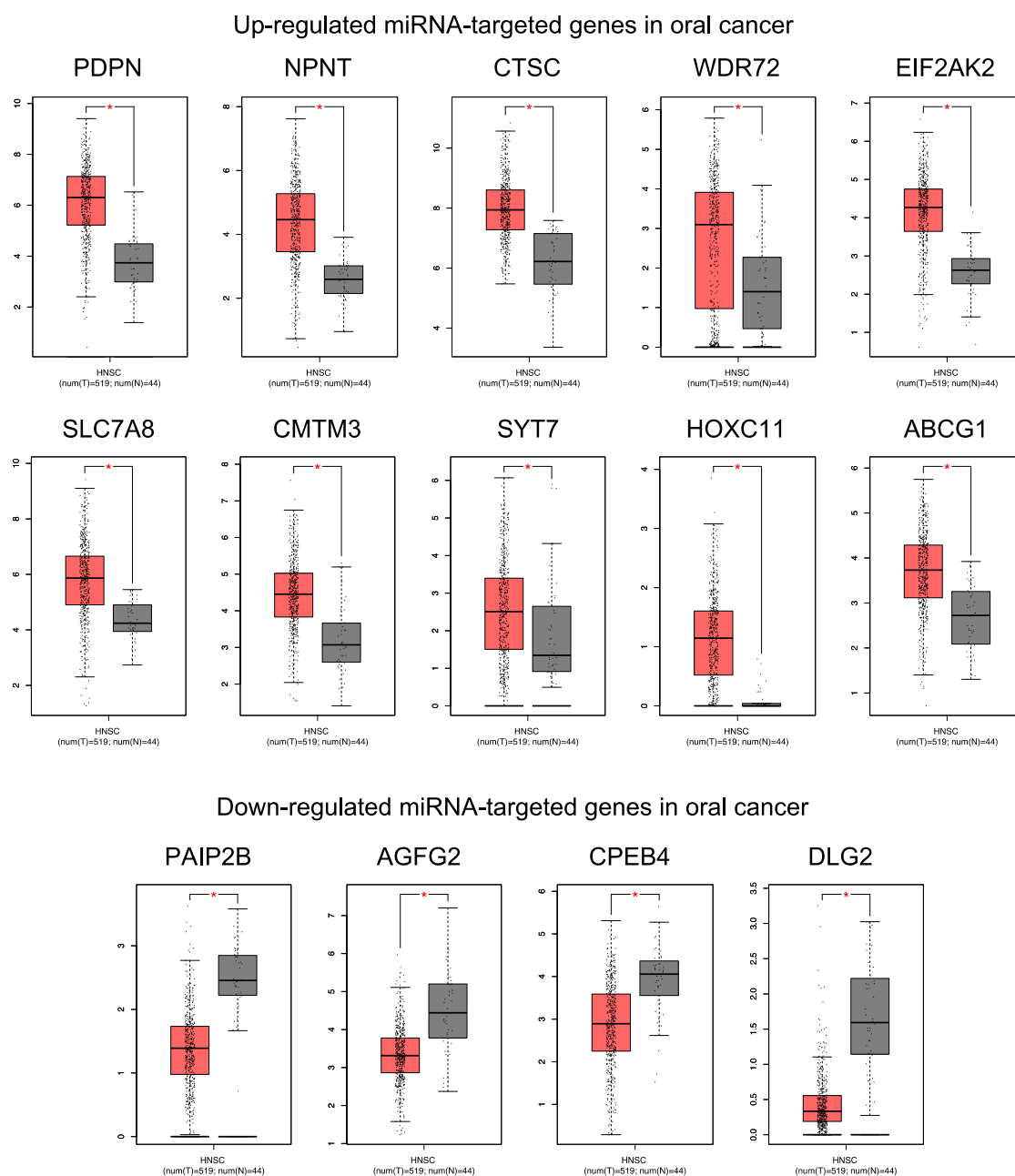


Figure S4. GEPIA analysis of the miRNA-targeted genes differentially expressed between oral cancer and healthy donors.

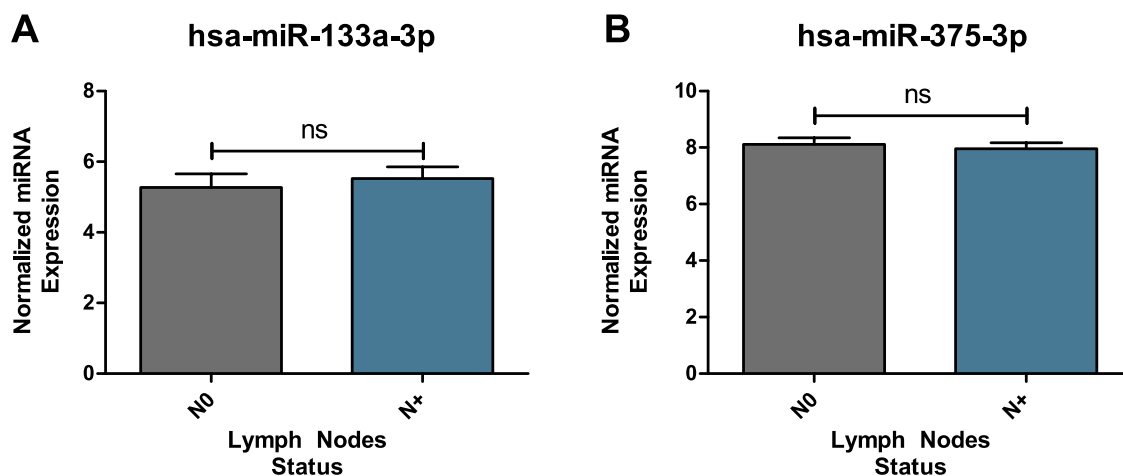


Figure S5. Panel A) No statistical difference observed for hsa-miR-133a-3p expression between oral cancer patients with positive lymph nodes and oral cancer patients without lymph nodes involvement according to the TCGA HNSC data; Panel B) No statistical difference observed for hsa-miR-375-3p expression between oral cancer patients with positive lymph nodes and oral cancer patients without lymph nodes involvement according to the TCGA HNSC data.

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