Supplementary figures

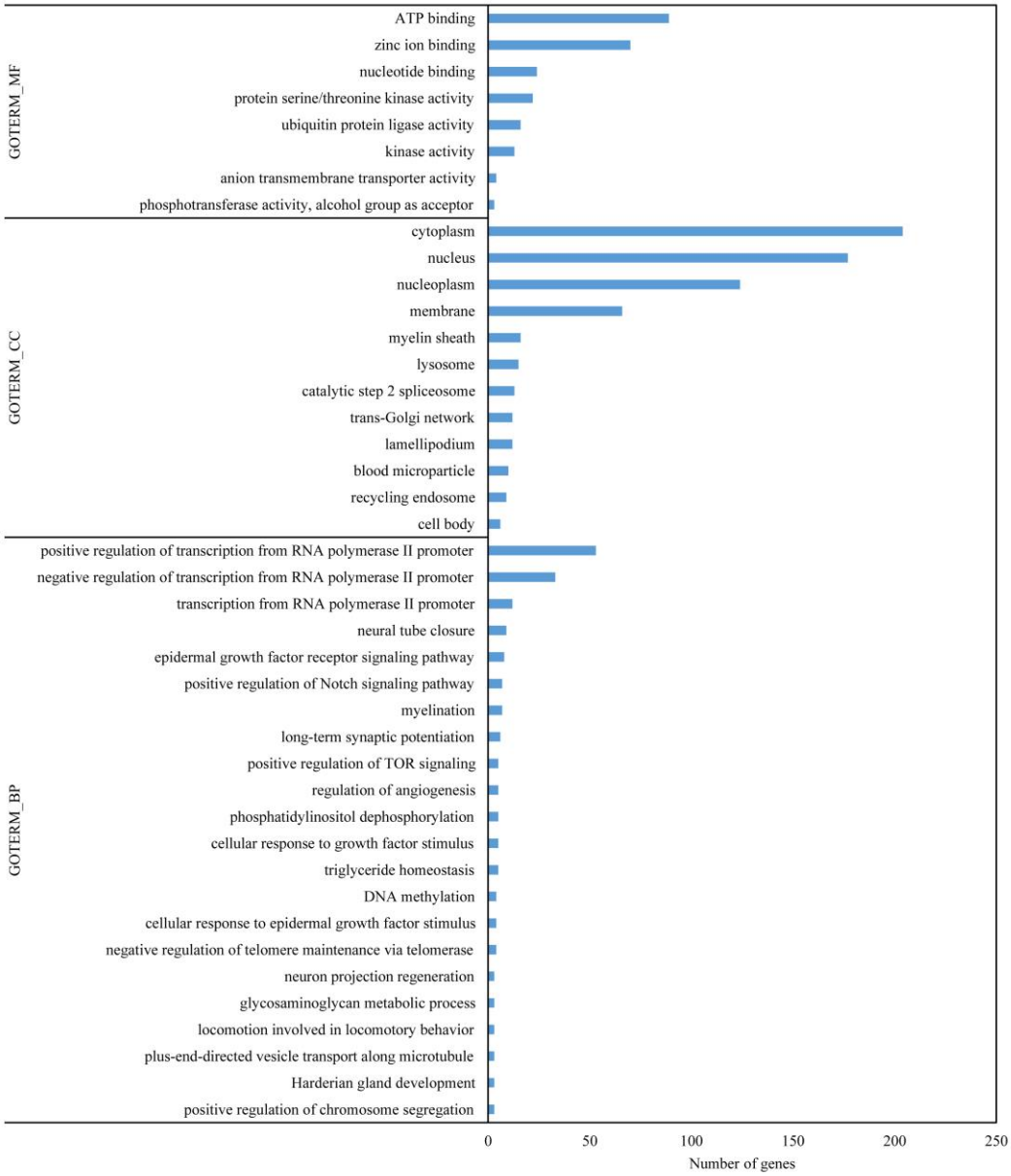

Figure S1. Gene ontology (GO) functional analysis of the potential targets of the top nine most abundant miRNAs (ssc-miR-148a-3p, ssc-let-7g, ssc-let-7f, ssc-miR-26a, ssc-miR-451, ssc-miR-21, ssc-miR-30d, ssc-miR-99a and ssc-miR-103). We displayed the enriched pathway terms with P value < 0.05 according to DAVID (6.8).

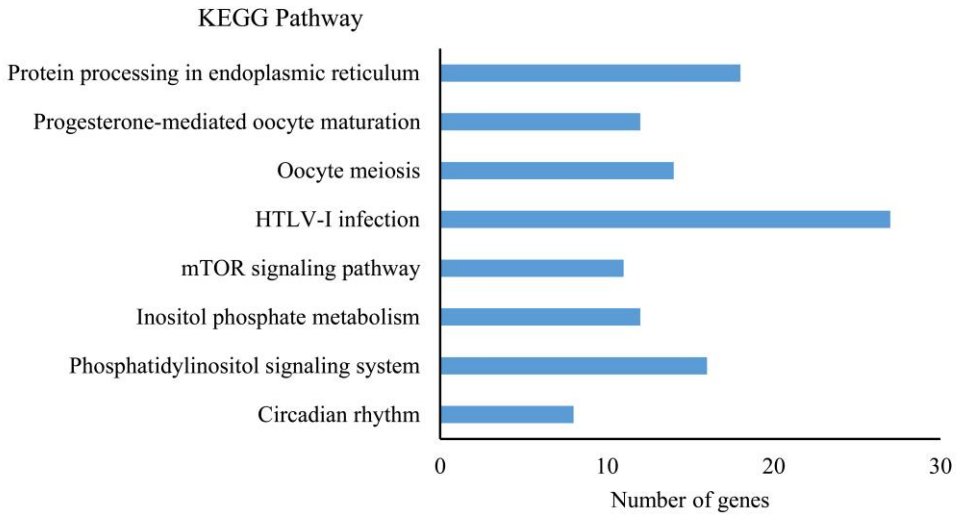

Figure S2. KEGG pathway analysis of the potential targets of the top nine most abundant miRNAs (ssc-miR-148a-3p, ssc-let-7g, ssc-let-7f, ssc-miR-26a, ssc-miR-451, ssc-miR-21, ssc-miR-30d, ssc-miR-99a and ssc-miR-103). We displayed the enriched pathway terms with P value < 0.05 according to DAVID (6.8).