

Supplementary Materials:

Figure S1. Flow chart of the overall phases of the *in silico* analyses of both let-7a and miR-34a including the used programs in each phase.

Figure S2. Network of the overlapping target genes of let-7a and miR-34a supporting their coordinated regulation. The 63 highly significant shared targets represent the intersection between the two miRs and they include: FNDC3B, IGF2, SOX4, POLL, HMGA, CSF1R, MAGEA1, WNT, CTNNB1, MAP4K3, MAP3K1, IFNLR1, UHRF2, SAR1A, QDPP, SPTBN1, ZNF644, LIN28B, CDC34, IGF1R, CSF1R, ONECUT2, COL1A1, TGFBR1, ACSL4, PLAG1, PPP2R3A, LEF1, UBE2H, PD-1, CTLA4, TERT, HGF, VCL, GORASP2, MFSD8, FKBP8, GTF3C1, HUWE1, UBAP2, ITGB3, BCL2L11, CDK6, FAM104A, HIST1H1D, EFHD2, FUT8, FUT10, BCL2, SURF4, ATG4C, HIST1H4D, BAZ2A, MAGEA6, SYT1, YAP1, ATXN2L, IGF2BP1, IGF2BP2, IGF2BP3, AGO1, MYC, LARP1. Notably, each miR has specific panel of its predicted targets which are shadowed as orange circles and represented far away from the network.

Table S1. Designed and used stem loop primers of miRs and RT qPCR primers of miRs and mRNA of targets.

Table S2. The common hepatocarcinogenic targets of both let-7a and mir-34a based on miRWalk target prediction. These targets were arranged in descending order according to sum of programs which predict its co-regulation by both miRs. Notably, the sum of programs of target prediction is 12.

Table S3. Results of the sanger sequencing of the ligation products of let-7a and miR-34a.