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Supplementary Materials

Computational Analysis of Epstein-Barr Virus *Bam*HI A Rightward Transcript (BART) MicroRNAs (miRNAs) Regulation on Messenger RNAs and Long Non-Coding RNAs in Nasopharyngeal Cancer

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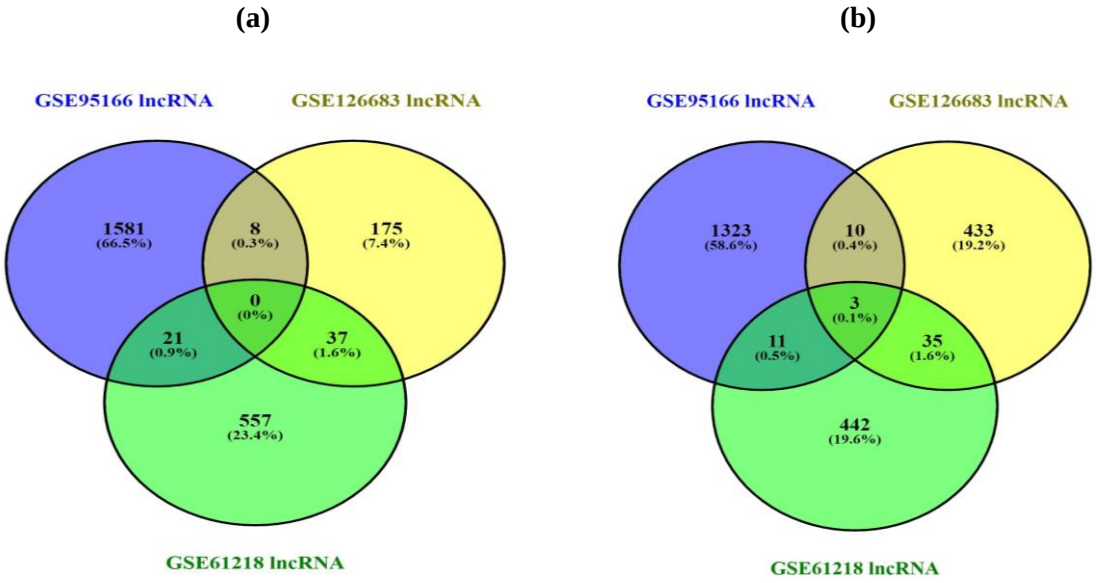
Supplementary Table 1. The information on miRNA, lncRNA and mRNA datasets retrieved from the NCBI between the year 2020 and 2023

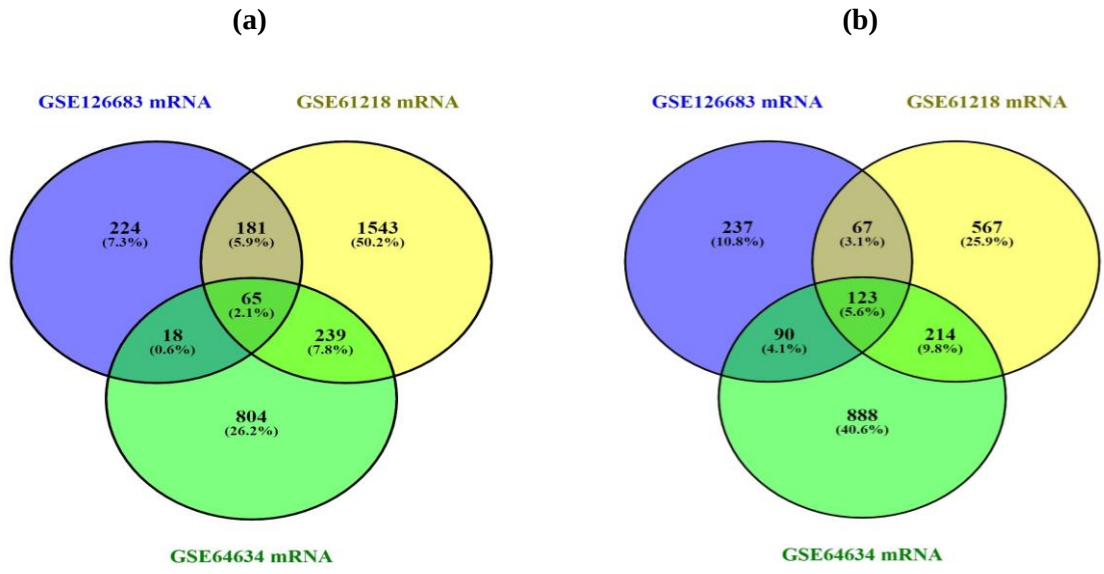
Accession Number	**Platform**	**Sample Number**		**Reference**	**PMID**	**Year**
		Normal	NPC			
GSE70970	GPL20699 nCounter® Human miRNA Assay (v1.0, Nanostring)	17	198	Bruce et al.	25738365	2015
GSE95166	GPL15314 Arraystar Human LncRNA microarray V2.0 (Agilent-033010 Probe Name version)	4	4	Zhang et al.	Unknown	2019
GSE126683	GPL16956 Agilent-045997 Arraystar human lncRNA microarray V3 (Probe Name Version)	3	3	Zheng et al.	31331909	2019
GSE61218	GPL19061 Agilent-043965 custom human array oelinc_xw	6	10	Fan et al.	32972383	2020
GSE64634	GPL570 [HG-U133_Plus_2] Affymetrix Human Genome U133 Plus 2.0 Array	4	12	Bo et al.	26246469	2017

Supplementary Table 2. The number of miRNAs, lncRNAs and mRNAs which are differentially expressed, assayed via GEO2R

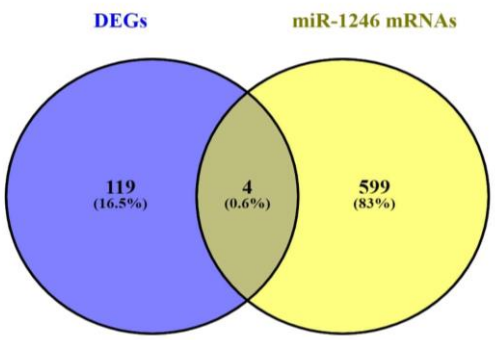
Accession Number	**Differentially expressed RNAs**			
	RNAs	**Up-regulated**	**Down-regulated**	**Total**
GSE70970	miRNAs	38	33	71
GSE95166	lncRNAs	1,861	1,775	3,636
GSE126683	mRNA	579	599	1,178
	lncRNA	264	539	803
GSE61218	lncRNA	789	567	1,356
	mRNA	2,752	4,876	7,628
GSE64634	mRNA	1,424	1,605	3,029

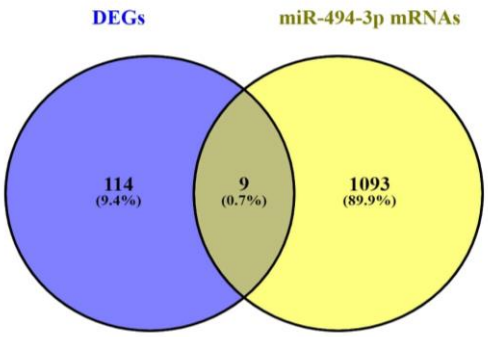


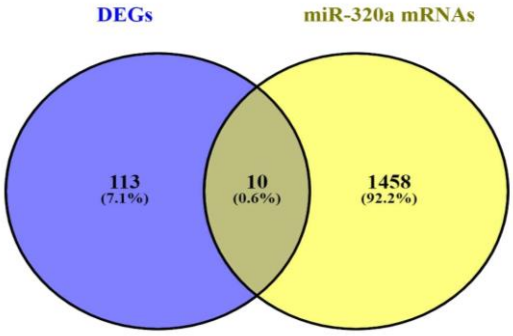
Supplementary Figure 1. Venn chart of comparison among differentially expressed lncRNA datasets of GSE95166, GSE126683 and GSE61218: (a) no common up-regulated lncRNAs between the three datasets, and (b) three common lncRNAs down-regulated shared between the three datasets, namely CASC2, TPTE2P1and ARHGEF26-AS1

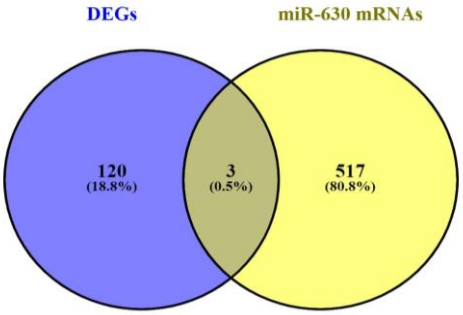


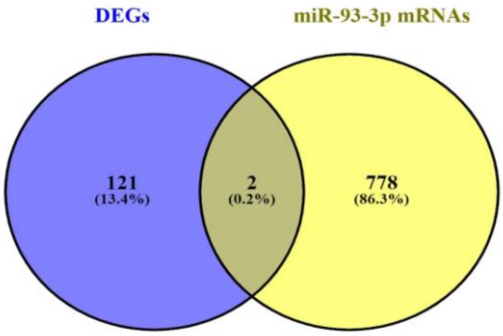
Supplementary Figure 2. Venn chart of comparison among differentially expressed mRNAs datasets of GSE64634, GSE126683 and GSE61218: (a) 65 up-regulated mRNAs are shared between the three datasets, and (b) 123 down-regulated mRNAs are shared between the three datasets

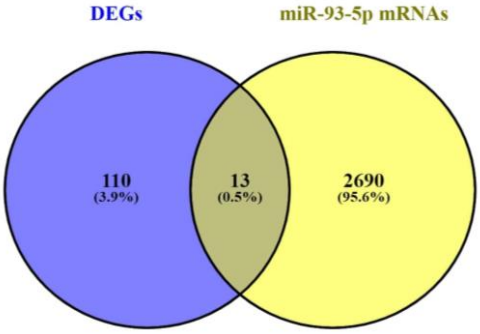

DEGs
miR-1246 mRNAs
119
(16.5%)
4
(0.6%)
599
(83%)

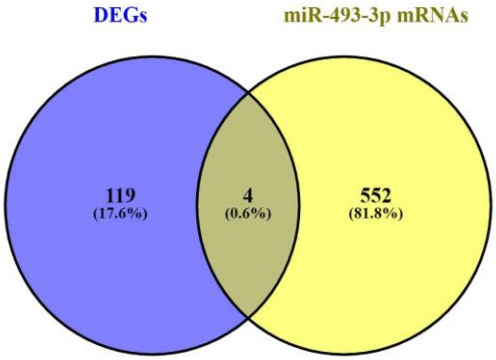

DEGs
miR-494-3p mRNAs
114
(9.4%)
9
(0.7%)
1093
(89.9%)

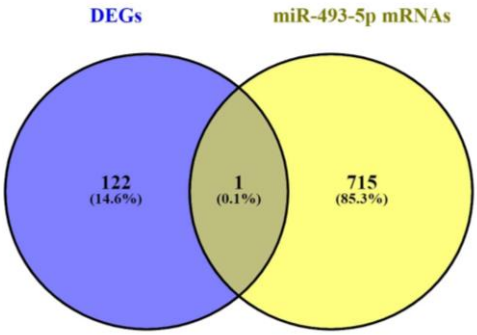

DEGs
miR-320a mRNAs
113
(7.1%)
10
(0.6%)
1458
(92.2%)

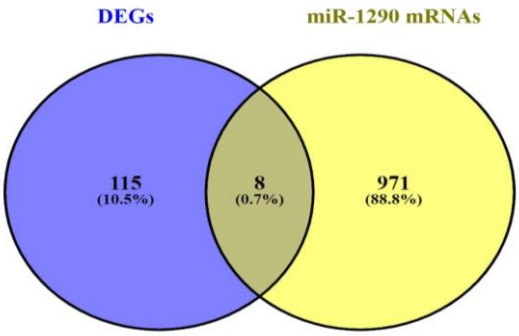

DEGs
miR-630 mRNAs
120
(18.8%)
3
(0.5%)
517
(80.8%)

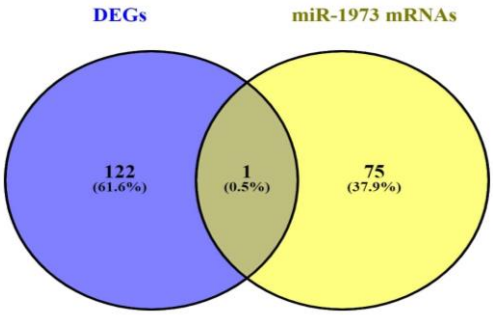

DEGs
miR-93-3p mRNAs
121
(13.4%)
2
(0.2%)
778
(86.3%)

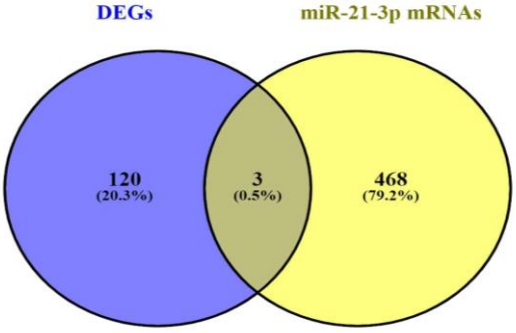

DEGs
miR-93-5p mRNAs
110
(3.9%)
13
(0.5%)
2690
(95.6%)

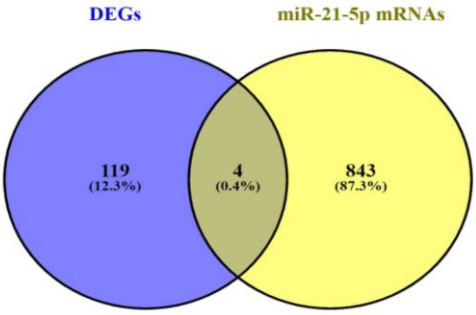

DEGs
miR-493-3p mRNAs
119
(17.6%)
4
(0.6%)
552
(81.8%)

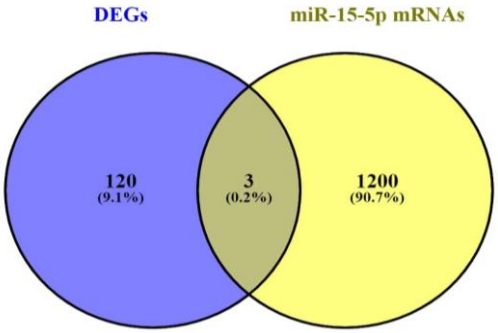

DEGs
miR-493-5p mRNAs
122
(14.6%)
1
(0.1%)
715
(85.3%)

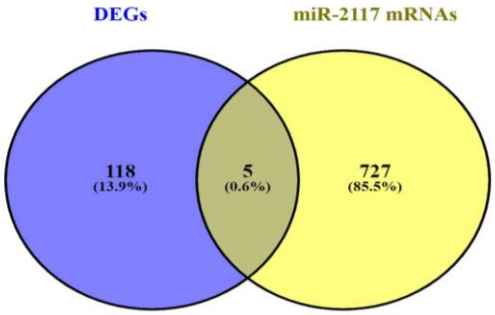

DEGs
miR-1290 mRNAs
115
(10.5%)
8
(0.7%)
971
(88.8%)

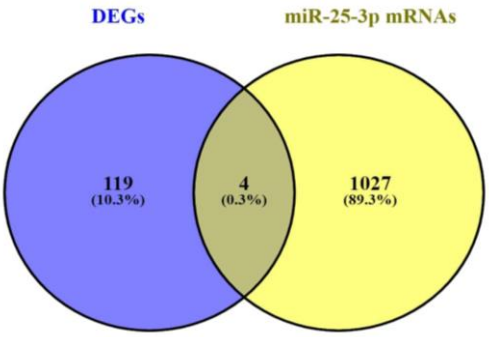

DEGs
miR-1973 mRNAs
122
(61.6%)
1
(0.5%)
75
(37.9%)

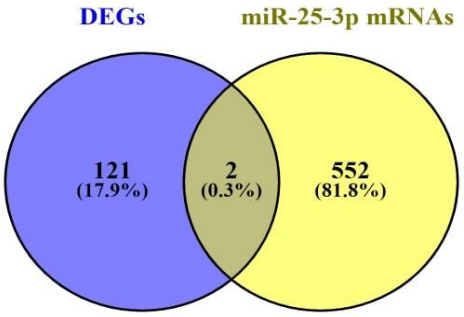

DEGs
miR-21-3p mRNAs
120
(20.3%)
3
(0.5%)
468
(79.2%)

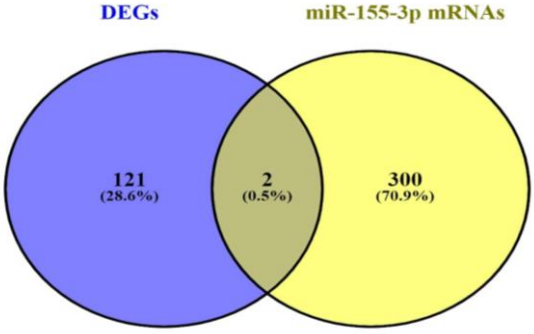

DEGs
miR-21-5p mRNAs
119
(12.3%)
4
(0.4%)
843
(87.3%)

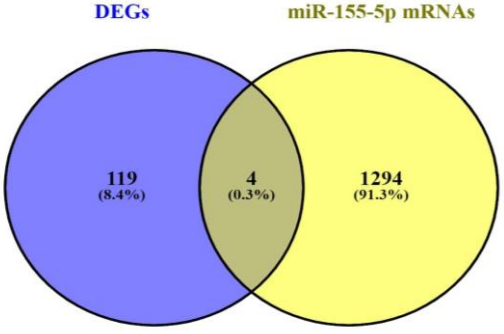

DEGs
miR-15-5p mRNAs
120
(9.1%)
3
(0.2%)
1200
(90.7%)

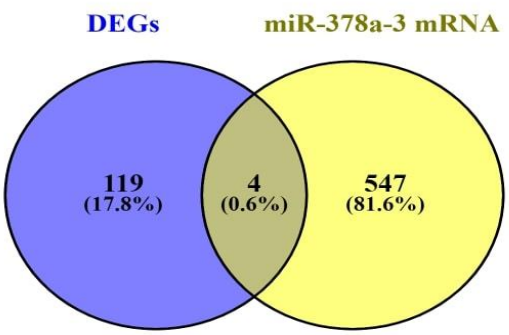

DEGs
miR-2117 mRNAs
118
(13.9%)
5
(0.6%)
727
(85.5%)

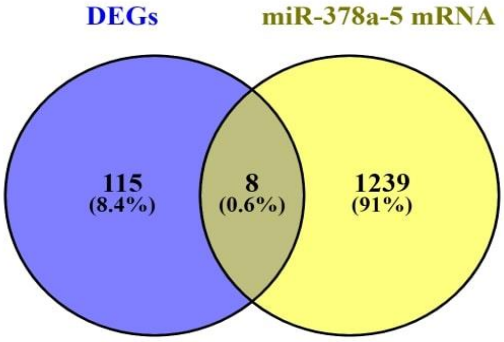

DEGs
miR-25-3p mRNAs
119
(10.3%)
4
(0.3%)
1027
(89.3%)

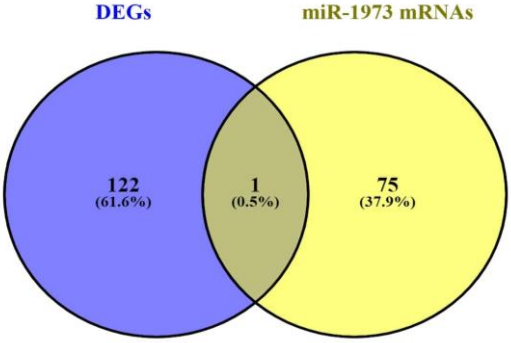

DEGs
miR-25-3p mRNAs
121
(17.9%)
2
(0.3%)
552
(81.8%)

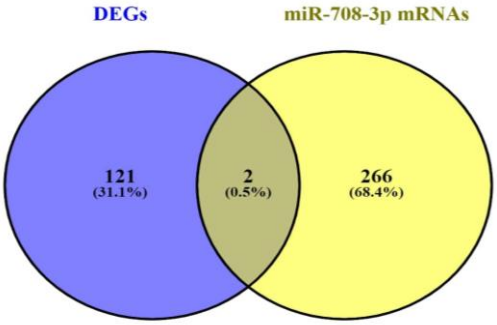

DEGs
miR-155-3p mRNAs
121
(28.6%)
2
(0.5%)
300
(70.9%)

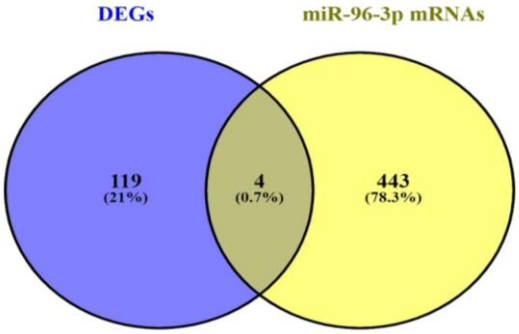

DEGs
miR-155-5p mRNAs
119
(8.4%)
4
(0.3%)
1294
(91.3%)

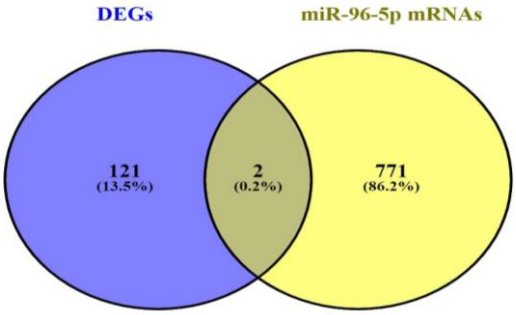

DEGs
miR-378a-3 mRNA
119
(17.8%)
4
(0.6%)
547
(81.6%)

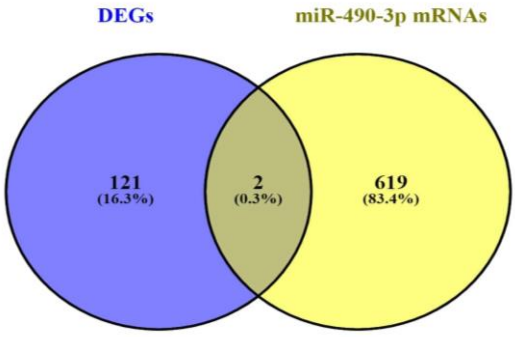

DEGs
miR-378a-5 mRNA
115
(8.4%)
8
(0.6%)
1239
(91%)

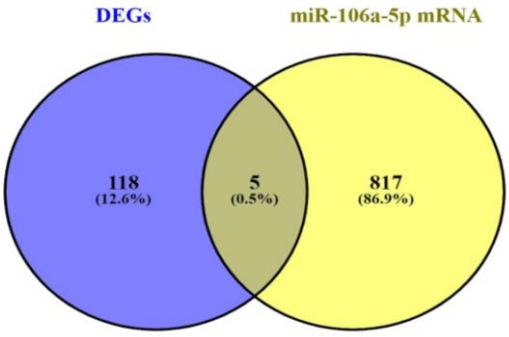

DEGs
miR-1973 mRNAs
122
(61.6%)
1
(0.5%)
75
(37.9%)

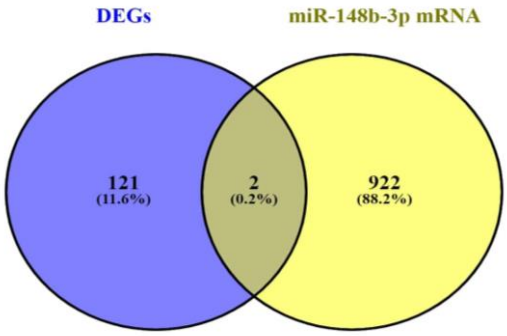

DEGs
miR-708-3p mRNAs
121
(31.1%)
2
(0.5%)
266
(68.4%)

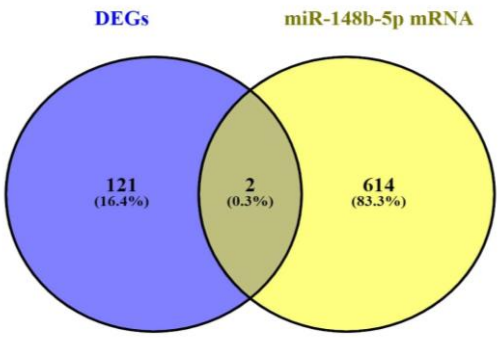

DEGs
miR-96-3p mRNAs
119
(21%)
4
(0.7%)
443
(78.3%)

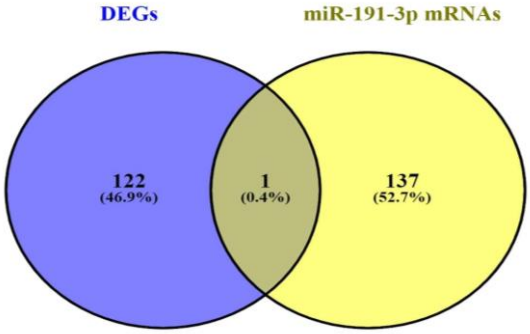

DEGs
miR-96-5p mRNAs
121
(13.5%)
2
(0.2%)
771
(86.2%)

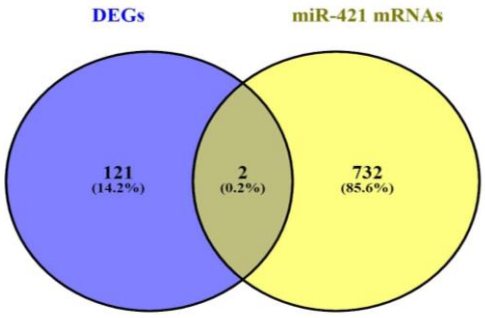

DEGs
miR-490-3p mRNAs
121
(16.3%)
2
(0.3%)
619
(83.4%)

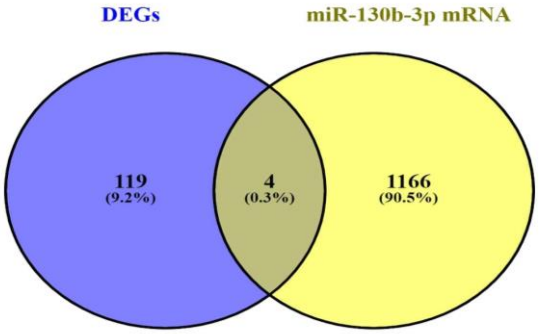

DEGs
miR-106a-5p mRNA
118
(12.6%)
5
(0.5%)
817
(86.9%)

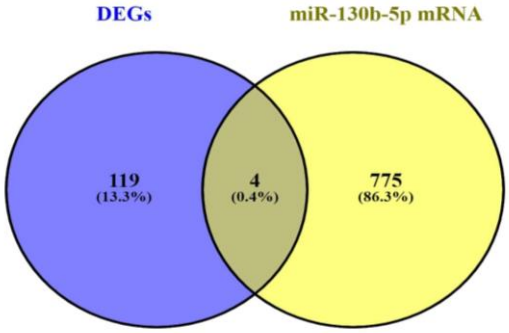

DEGs
miR-148b-3p mRNA
121
(11.6%)
2
(0.2%)
922
(88.2%)

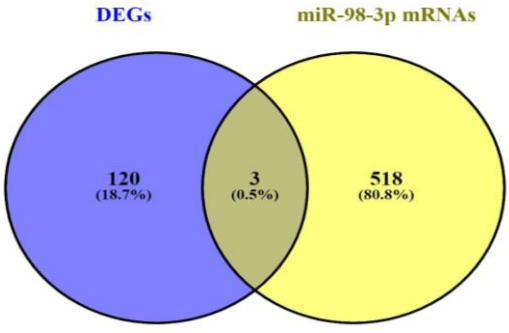

DEGs
miR-148b-5p mRNA
121
(16.4%)
2
(0.3%)
614
(83.3%)

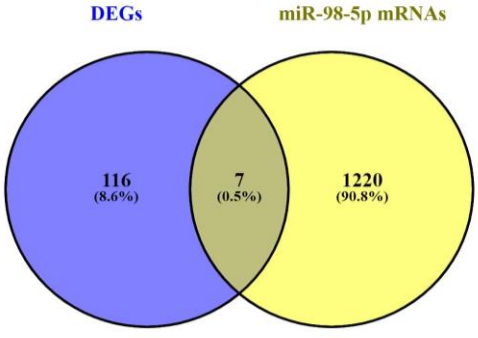

DEGs
miR-191-3p mRNAs
122
(46.9%)
1
(0.4%)
137
(52.7%)

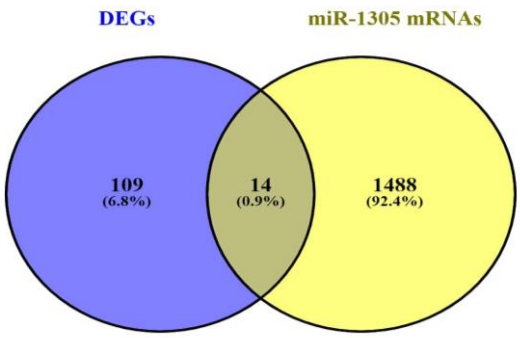

DEGs
miR-421 mRNAs
121
(14.2%)
2
(0.2%)
732
(85.6%)

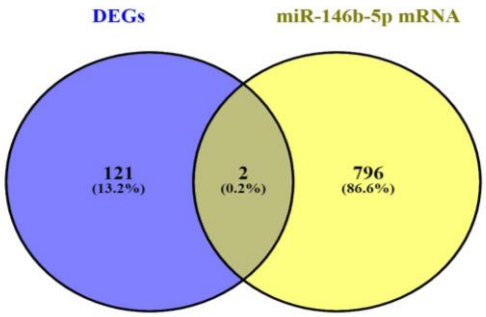

DEGs
miR-130b-3p mRNA
119
(9.2%)
4
(0.3%)
1166
(90.5%)

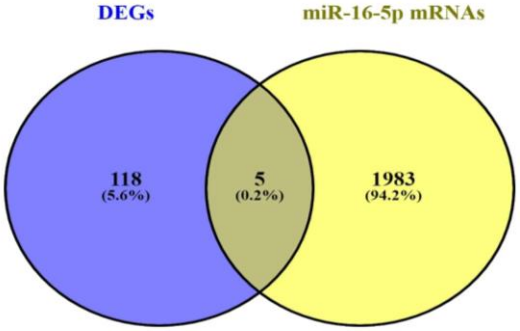

DEGs
miR-130b-5p mRNA
119
(13.3%)
4
(0.4%)
775
(86.3%)

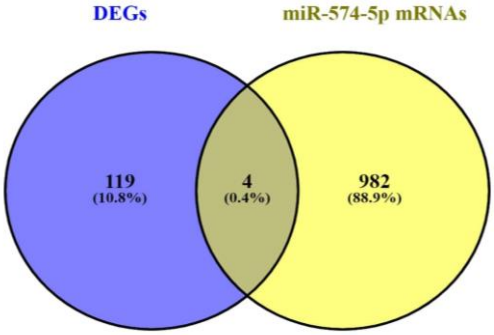

DEGs
miR-98-3p mRNAs
120
(18.7%)
3
(0.5%)
518
(80.8%)

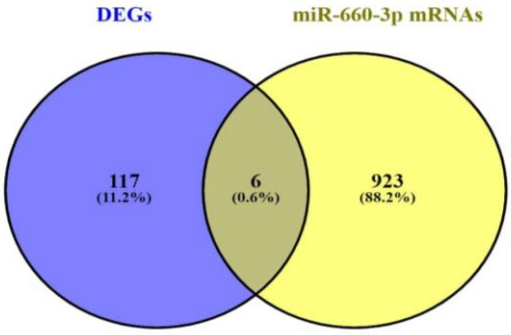

DEGs
miR-98-5p mRNAs
116
(8.6%)
7
(0.5%)
1220
(90.8%)

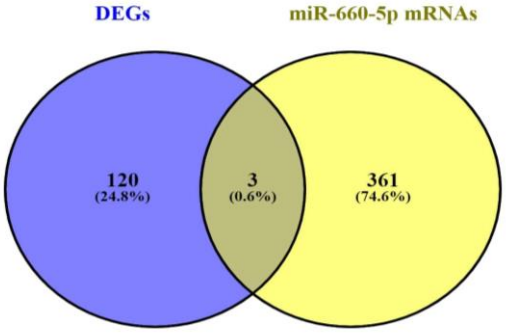

DEGs
miR-1305 mRNAs
109
(6.8%)
14
(0.9%)
1488
(92.4%)

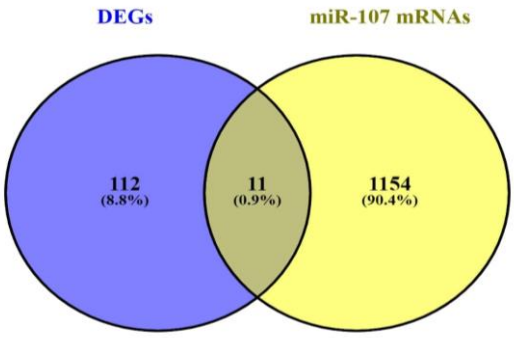

DEGs
miR-146b-5p mRNA
121
(13.2%)
2
(0.2%)
796
(86.6%)

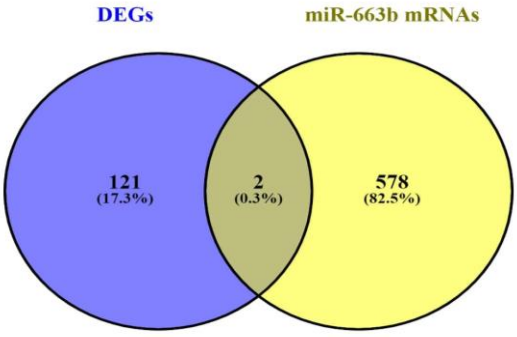

DEGs
miR-16-5p mRNAs
118
(5.6%)
5
(0.2%)
1983
(94.2%)

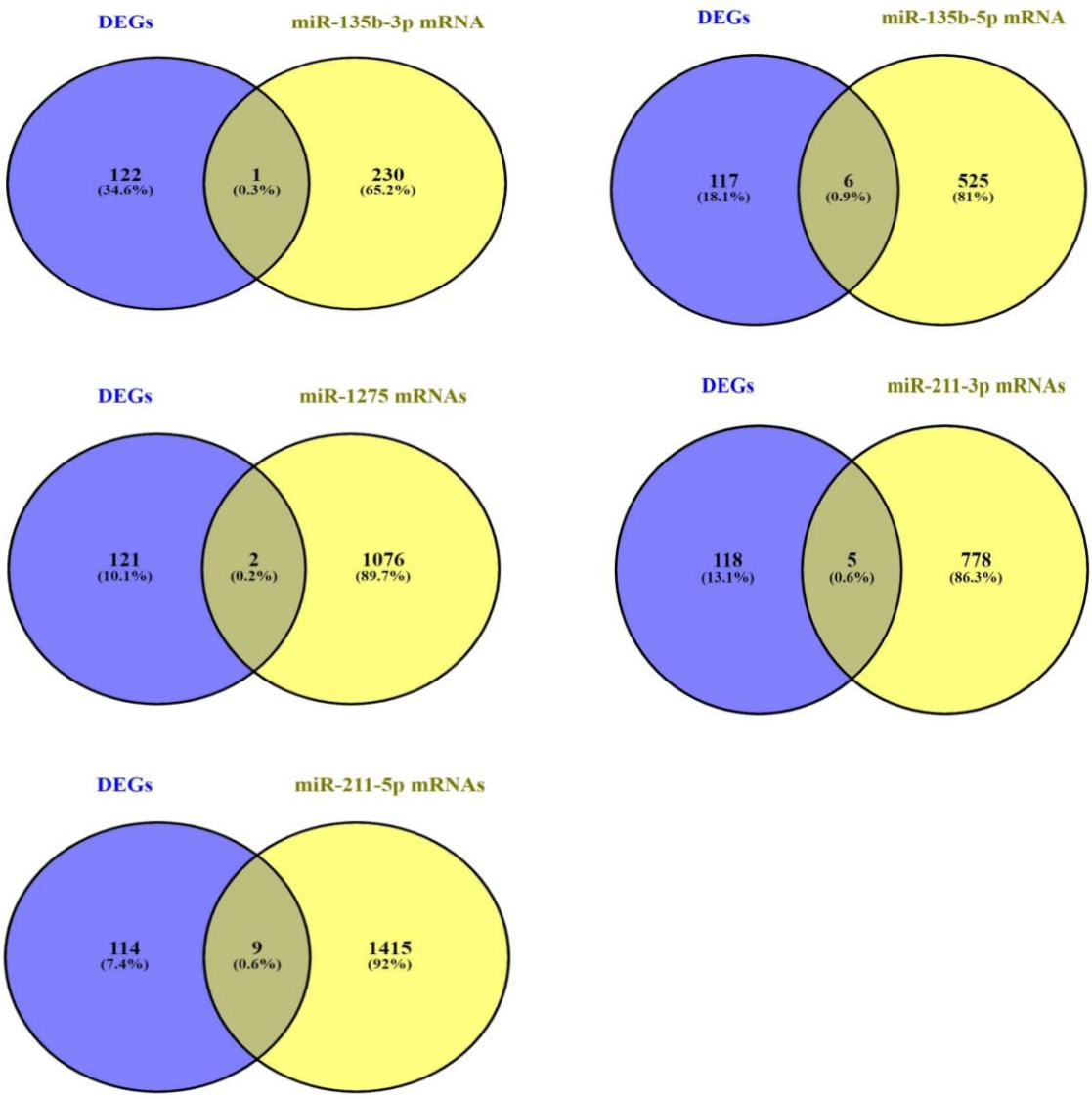

DEGs
miR-574-5p mRNAs
119
(10.8%)
4
(0.4%)
982
(88.9%)


DEGs
miR-660-3p mRNAs
117
(11.2%)
6
(0.6%)
923
(88.2%)


DEGs
miR-660-5p mRNAs
120
(24.8%)
3
(0.6%)
361
(74.6%)


DEGs
miR-107 mRNAs
112
(8.8%)
11
(0.9%)
1154
(90.4%)


DEGs
miR-663b mRNAs
121
(17.3%)
2
(0.3%)
578
(82.5%)



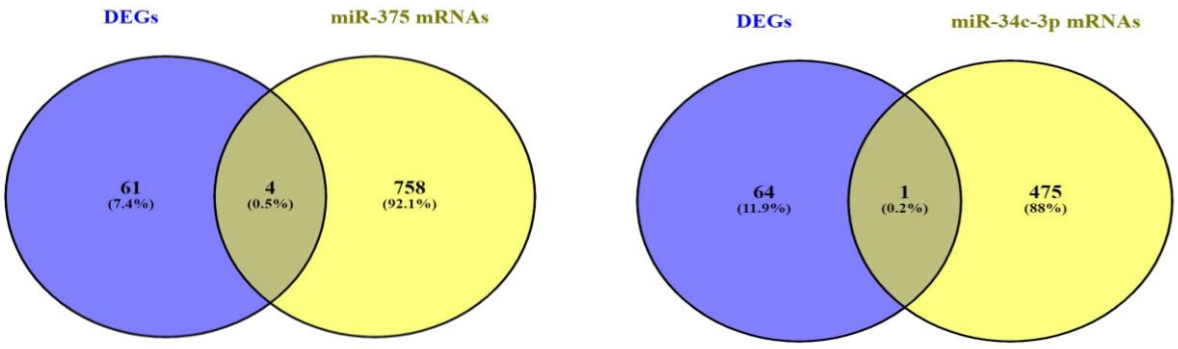
Supplementary Figure 3. Venn diagram of target mRNAs for up-regulated miRNAs from the combined databases of miRwalk 2.0 and miRTarBase databases compared with down-regulated DEmRNAs

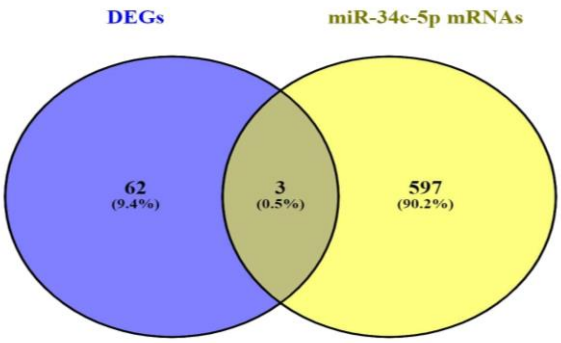
Supplementary Table 3. The overlapped target mRNAs of up-regulated DEmiRNAs from the combined databases of miRwalk 2.0 and miRTarBase databases with down-regulated DEmRNAs

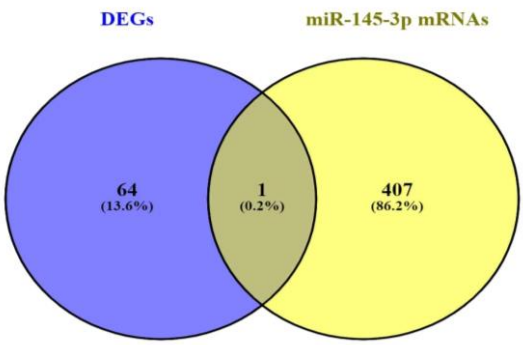
Up-regulated DEmiRNAs	**Overlapped target mRNAs with Down-regulated DEmRNAs**
hsa-miR-1246	EFHB, BCAS1,EYA1,NEK5
hsa-miR-494-3p	MAK, LRRC34, GULP1, ZBBX, EFCAB1, C11orf16, SRPX, NEK5, CH25H
hsa-miR-320a	IQCA1 KIF6, DNALI1, CHP2, MAK, TTC29, FBXL13, LEPR, NQO1, DYNC2H1
hsa-miR-630	CASC1, EFCAB1, C11orf70

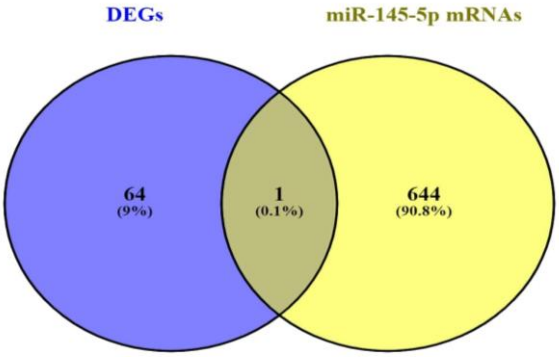
hsa-miR-93-3p	CHP2, LRRC34
hsa-miR-93-5p	C11orf63, TMEM45B, KIF6, MAK, FBXL13, EYA4, TMC5, EYA1, BCAS1, SORBS2, C11orf70, TTC9, SPEF2
hsa-miR-493-3p	KCNRG, MAK, EFCAB1, C11orf88
hsa-miR-493-5p	LEPR
hsa-miR-1290	BBS9, MAK, TTC29, TMC5, BCAS1, NEK11, ADH1C, NEK5
hsa-miR-1973	BCAS1
hsa-miR-21-3p	KIF6, MORN5, CH25H
hsa-miR-21-5p	FBXL13, SPEF2, C11orf70, ST6GALNAC1
hsa-miR-15b-5p	OSCP1, BCAS1, EYA1
hsa-miR-2117	KIF6, LRRC23, STEAP4, FAM153A, PRSS23
hsa-miR-25-3p	ENKUR, GULP1, CCDC113, SNTN
hsa-miR-25-5p	LRTOMT, PIGR
hsa-miR-155-3p	NEK11, CCDC65
hsa-miR-155-5p	SYTL2, SPEF2, AKR1C3, DYNC2H1
hsa-miR-378a-3p	SPA17, CRYM, LEPR, LRRC6
hsa-miR-378a-5p	SLC44A4, TMEM45B, RRAD, CASC1, FBXL13, TMC5, BCAS1, LRTOMT
hsa-miR-708-3p	IQCA1, SPAG16
hsa-miR-96-3p	MORN2, ZBBX, SORBS2, FAM153A
hsa-miR-96-5p	MAK, CCDC65
hsa-miR-490-3p	LRTOMT, PIGR
hsa-miR-106a-5p	C10orf107, EFCAB1, NEK11, SORBS2, DYNC2H1
hsa-miR-148b-3p	EYA4, STEAP4
hsa-miR-148b-5p	LEPR, EYA1
hsa-miR-191-3p	RRAD
hsa-miR-421	MAK, ENKUR
hsa-miR-130b-3p	RIBC1, STEAP4, NEK5, FAM153A

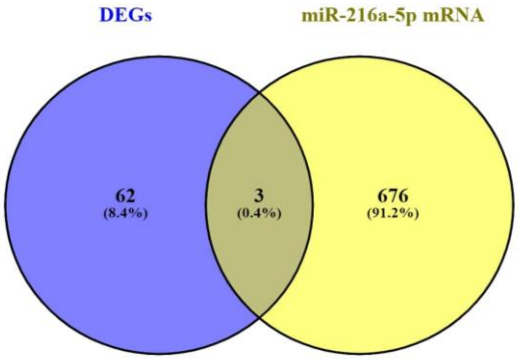
hsa-miR-130b-5p	SPATA6, DNAH2, C11orf70, SPEF2
hsa-miR-98-3p	IQCA1, SPATA18, MAK
hsa-miR-98-5p	SPATA18, RRAD, CCDC81, AKR1C3, LRTOMT, NQO1
hsa-miR-1305	SLC22A4, RSPH4A, MAK, C10orf107, GULP1, LEPR, C4orf47, NEK11, DNAH5, LRRC6, DHRS9, SPAG16, MACROD2, SPEF2
hsa-miR-146b-5p	CRYM, LRTOMT
hsa-miR-16-5p	OSCP1, TPPP3, EYA4, EYA1, BCAS1
hsa-miR-574-5p	SLC22A4, BCAS1, CCDC65, SPATA6
hsa-miR-660-3p	SPA17, VSIG2, BCAS1, TSPAN1, MACROD2, SORBS2
hsa-miR-660-5p	MAK, ENKUR, LEPR
hsa-miR-107	OSCP1, TPPP3, KCNRG, MAK, CASC1, ENKUR, CCDC81, BCAS1, CRYM
hsa-miR-663b	KIF6
hsa-miR-135b-5p	KIF6, DNALI1, KCNRG, GULP1, DNAH2, EBF1
hsa-miR-1275	LRTOMT
hsa-miR-211-3p	C1orf115, EFCAB1, CCDC113, CAPS, DHRS9
hsa-miR-211-5p	BBS9, DHRS9, SPAG16, SPEF2, EBF1

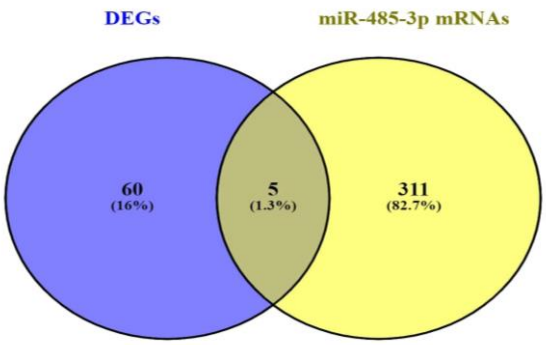


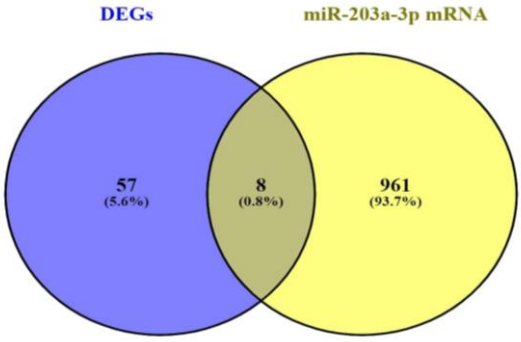

DEGs
miR-34c-5p mRNAs
62
(9.4%)
3
(0.5%)
597
(90.2%)

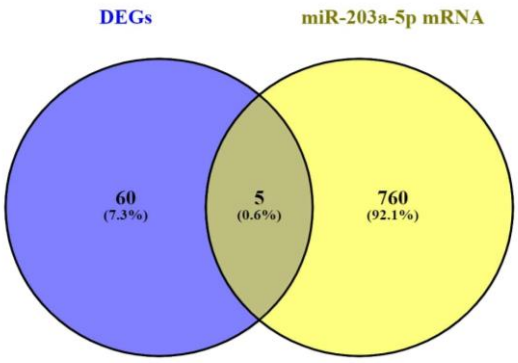

DEGs
miR-145-3p mRNAs
64
(13.6%)
1
(0.2%)
407
(86.2%)

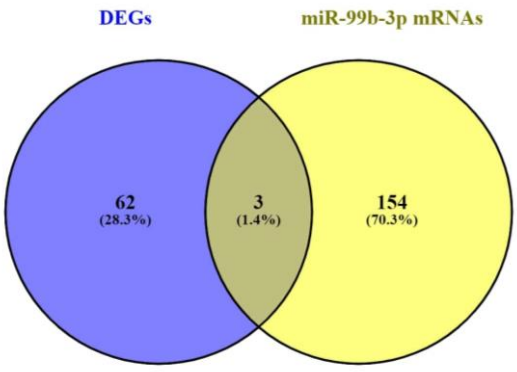

DEGs
miR-145-5p mRNAs
64
(9%)
1
(0.1%)
644
(90.8%)

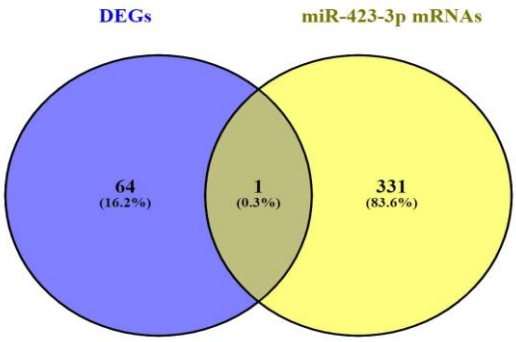

DEGs
miR-216a-5p mRNA
62
(8.4%)
3
(0.4%)
676
(91.2%)

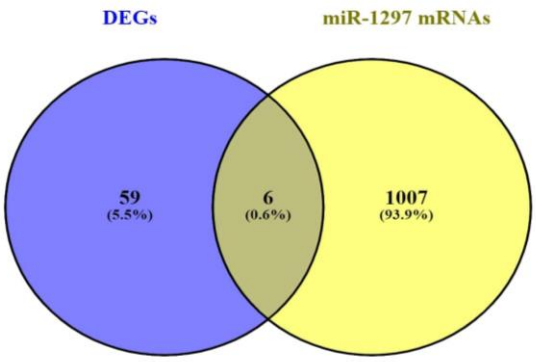

DEGs
miR-485-3p mRNAs
60
(16%)
5
(1.3%)
311
(82.7%)

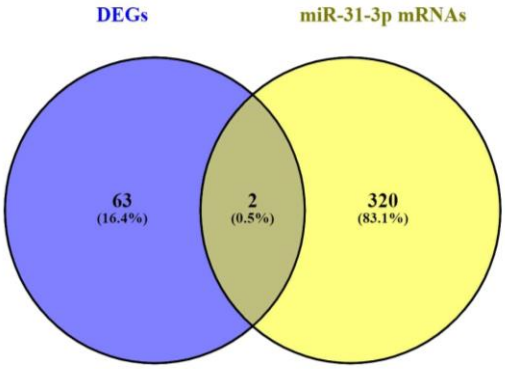

DEGs
miR-203a-3p mRNA
57
(5.6%)
8
(0.8%)
961
(93.7%)

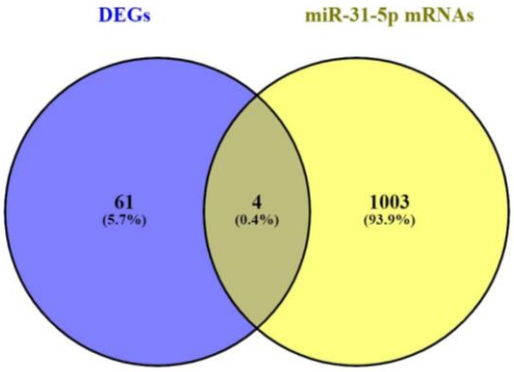

DEGs
miR-203a-5p mRNA
60
(7.3%)
5
(0.6%)
760
(92.1%)

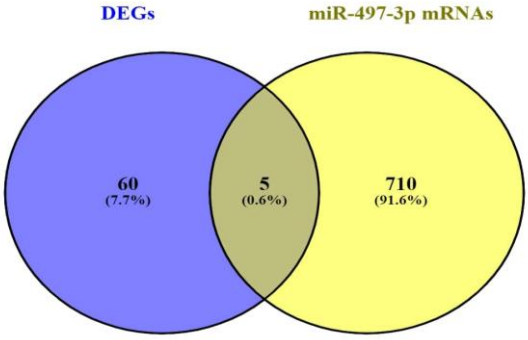

DEGs
miR-99b-3p mRNAs
62
(28.3%)
3
(1.4%)
154
(70.3%)

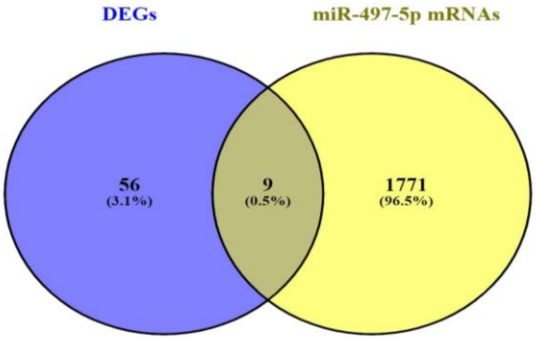

DEGs
miR-423-3p mRNAs
64
(16.2%)
1
(0.3%)
331
(83.6%)

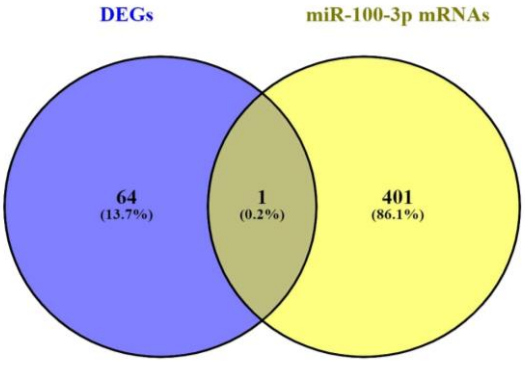

DEGs
miR-1297 mRNAs
59
(5.5%)
6
(0.6%)
1007
(93.9%)

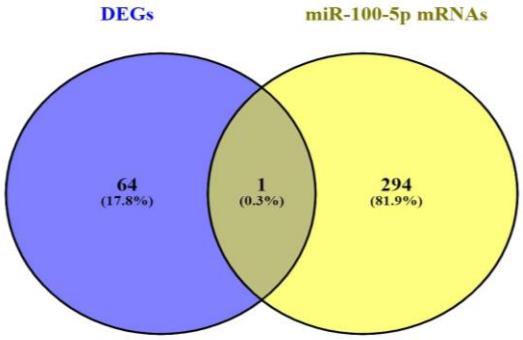

DEGs
miR-31-3p mRNAs
63
(16.4%)
2
(0.5%)
320
(83.1%)

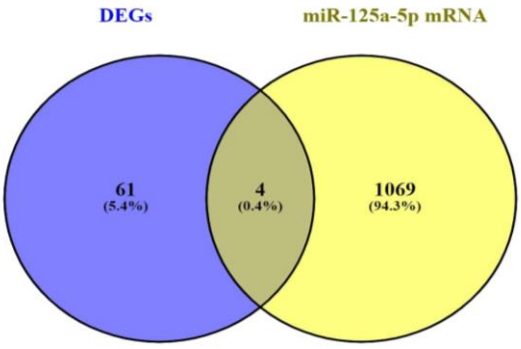

DEGs
miR-31-5p mRNAs
61
(5.7%)
4
(0.4%)
1003
(93.9%)

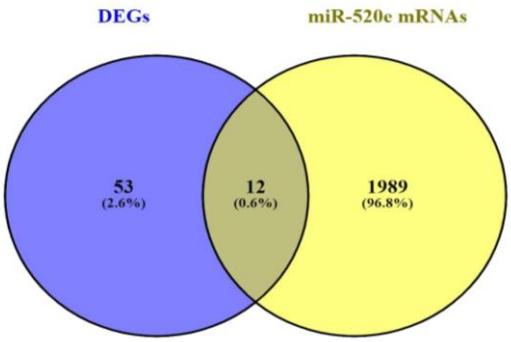

DEGs
miR-497-3p mRNAs
60
(7.7%)
5
(0.6%)
710
(91.6%)

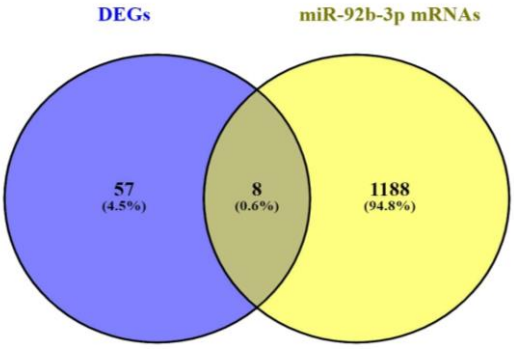

DEGs
miR-497-5p mRNAs
56
(3.1%)
9
(0.5%)
1771
(96.5%)

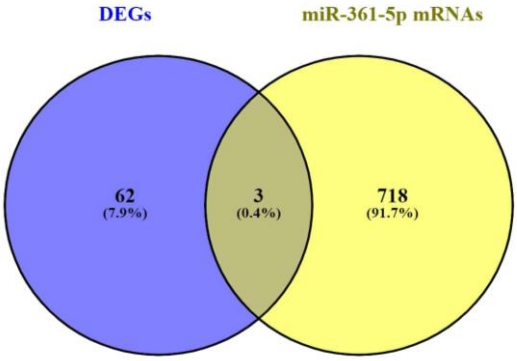

DEGs
miR-100-3p mRNAs
64
(13.7%)
1
(0.2%)
401
(86.1%)

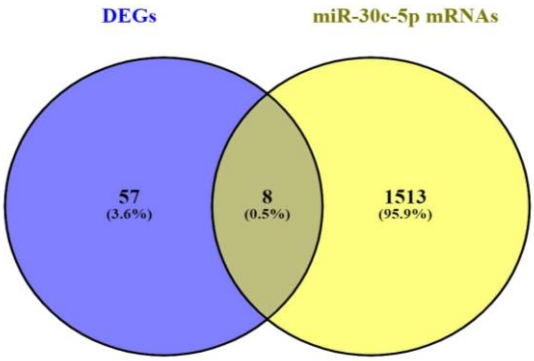

DEGs
miR-100-5p mRNAs
64
(17.8%)
1
(0.3%)
294
(81.9%)

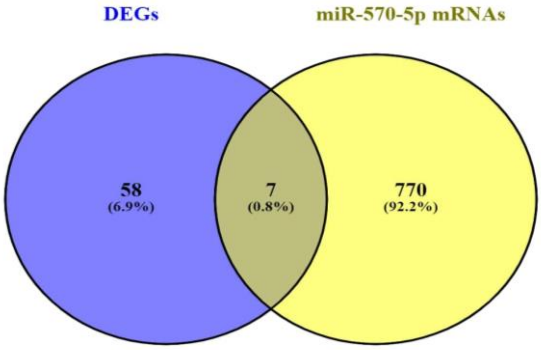

DEGs
miR-125a-5p mRNA
61
(5.4%)
4
(0.4%)
1069
(94.3%)

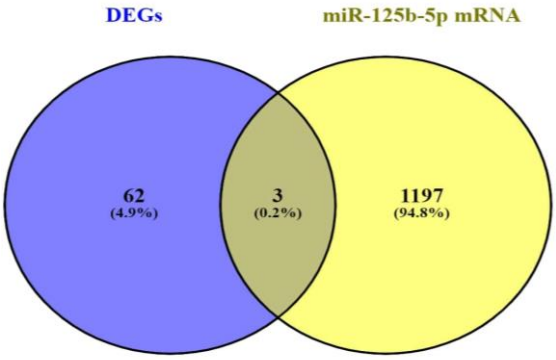

DEGs
miR-520e mRNAs
53
(2.6%)
12
(0.6%)
1989
(96.8%)

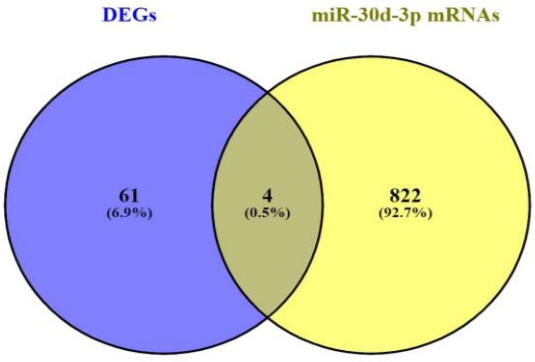

DEGs
miR-92b-3p mRNAs
57
(4.5%)
8
(0.6%)
1188
(94.8%)

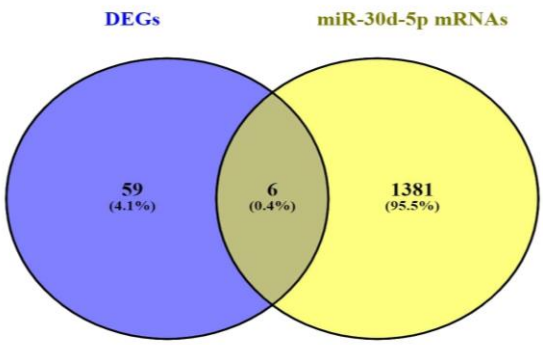

DEGs
miR-361-5p mRNAs
62
(7.9%)
3
(0.4%)
718
(91.7%)

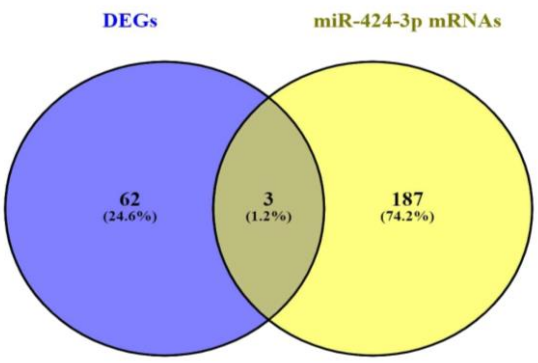

DEGs
miR-30c-5p mRNAs
57
(3.6%)
8
(0.5%)
1513
(95.9%)

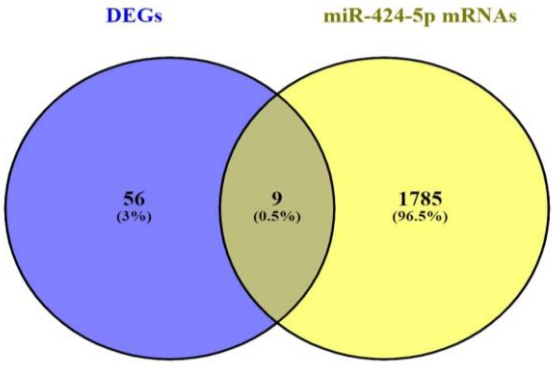

DEGs
miR-570-5p mRNAs
58
(6.9%)
7
(0.8%)
770
(92.2%)

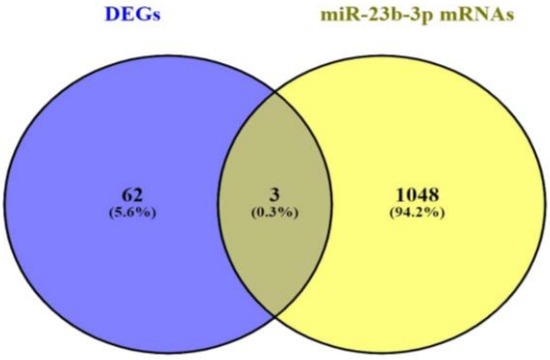

DEGs
miR-125b-5p mRNA
62
(4.9%)
3
(0.2%)
1197
(94.8%)

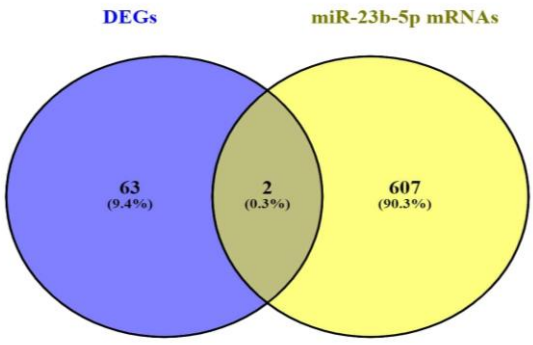

DEGs
miR-30d-3p mRNAs
61
(6.9%)
4
(0.5%)
822
(92.7%)

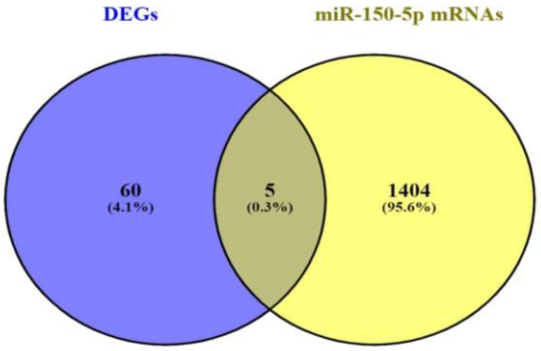

DEGs
miR-30d-5p mRNAs
59
(4.1%)
6
(0.4%)
1381
(95.5%)

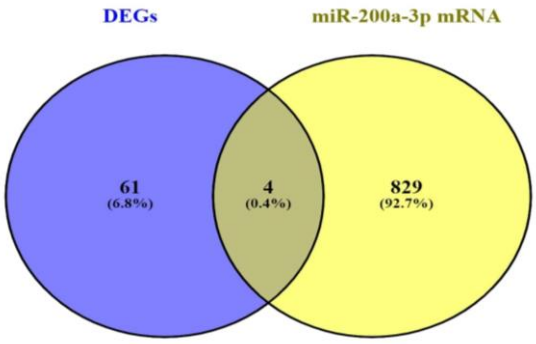

DEGs
miR-424-3p mRNAs
62
(24.6%)
3
(1.2%)
187
(74.2%)

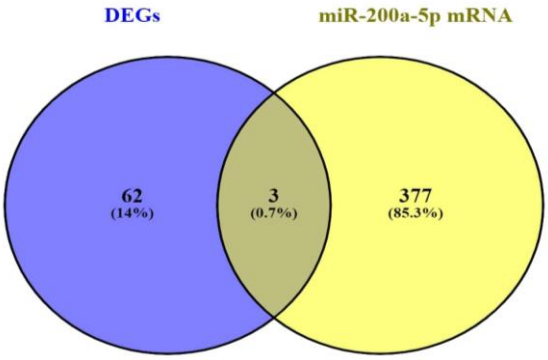

DEGs
miR-424-5p mRNAs
56
(3%)
9
(0.5%)
1785
(96.5%)

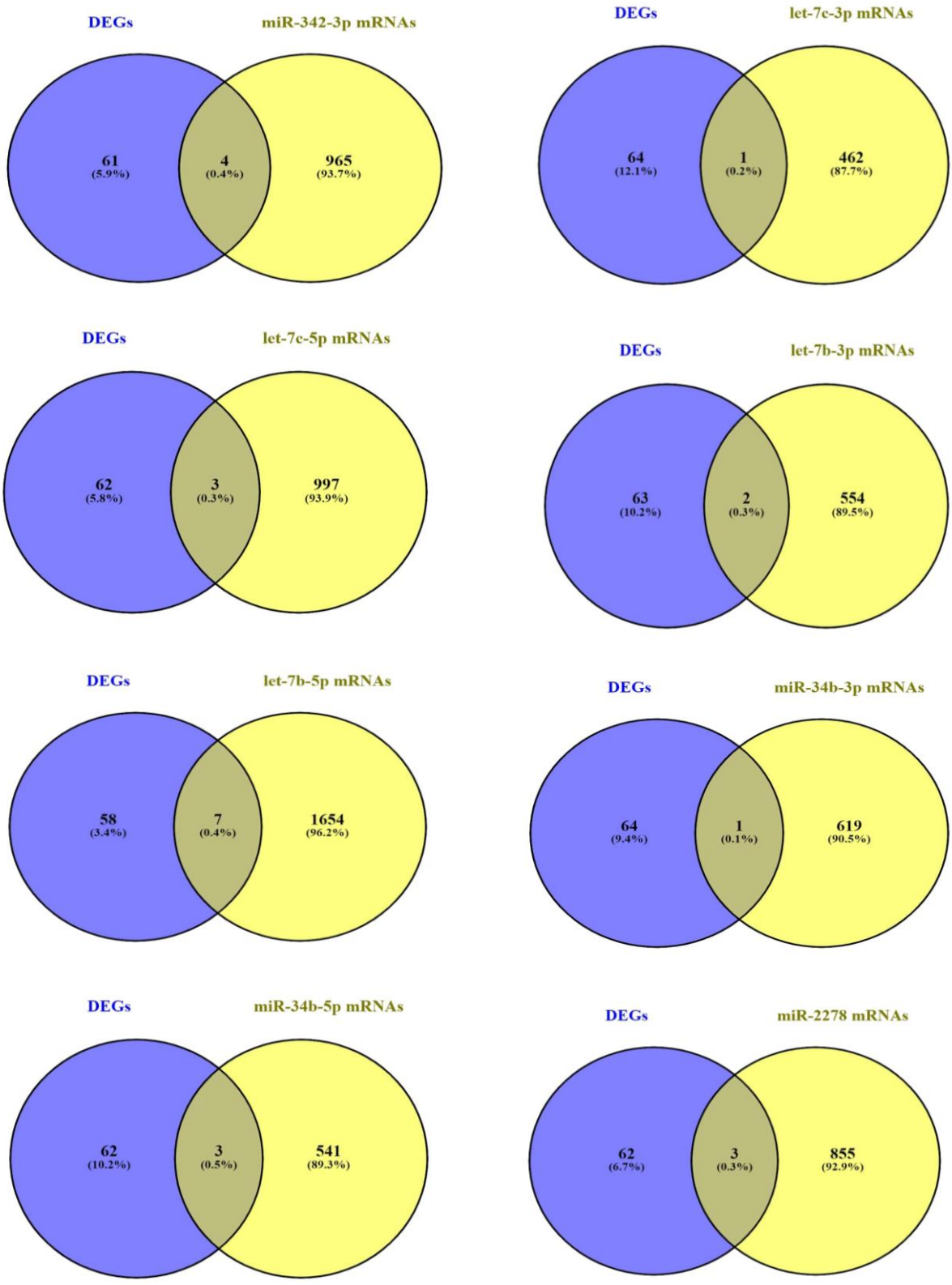

DEGs
miR-23b-3p mRNAs
62
(5.6%)
3
(0.3%)
1048
(94.2%)


DEGs
miR-23b-5p mRNAs
63
(9.4%)
2
(0.3%)
607
(90.3%)


DEGs
miR-150-5p mRNAs
60
(4.1%)
5
(0.3%)
1404
(95.6%)


DEGs
miR-200a-3p mRNA
61
(6.8%)
4
(0.4%)
829
(92.7%)


DEGs
miR-200a-5p mRNA
62
(14%)
3
(0.7%)
377
(85.3%)

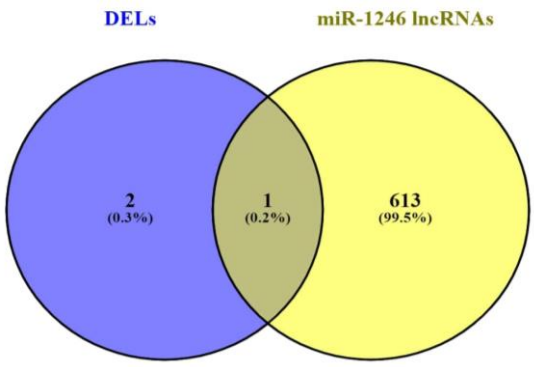


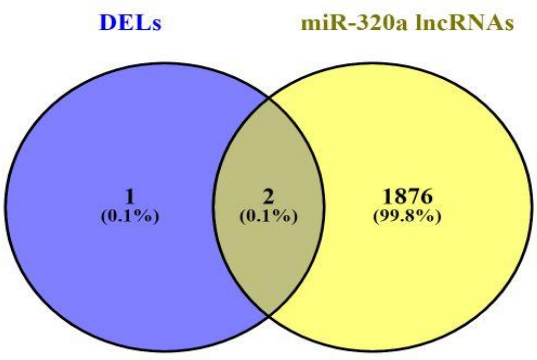
Supplementary Figure 4. Venn diagram of target mRNAs for down-regulated miRNAs from the combined databases of miRwalk 2.0 and miRTarBase databases compared with DEmRNAs

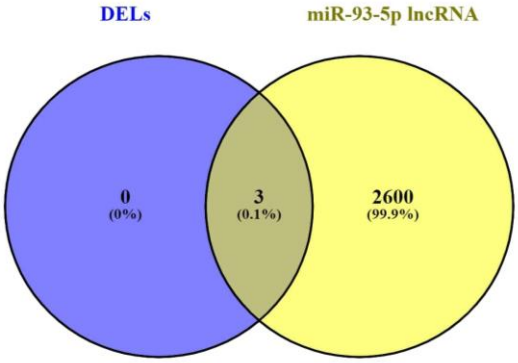
Supplementary Table 4. The overlapped target mRNAs of down-regulated DEmiRNAs from the combined databases of miRwalk 2.0 and miRTarBase databases with the up-regulated DEmRNAs

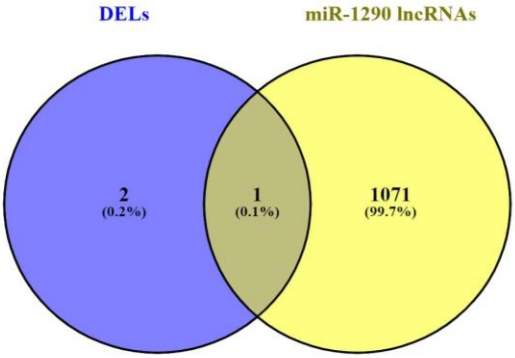
Down-regulated DEmiRNAs	**Overlapped target mRNAs with Up-regulated DEmRNAs**
hsa-miR-375	PLK4, TYMS, EXO1, CENPF
hsa-miR-34c-3p	PLK4
hsa-miR-34c-5p	PLK4, CCNE2, ULBP2
hsa-miR-145-3p	BUB1
hsa-miR-145-5p	PSAT1
hsa-miR-216a-5p	TPX2, KIF14, DEPDC1
hsa-miR-485-3p	WHSC1, KPNA2, PSAT1, CENPI, OLA1
hsa-miR-203a-3p	CHCHD3, GINS4, BIRC5, TYMS, PSAT1, CENPI, RAN, ICAM1
hsa-miR-203a-5p	CHCHD3, GINS4, TYMS, CENPI, ICAM1
hsa-miR-99b-3p	MSR1, CENPN, BRCA1
hsa-miR-423-3p	CHCHD3
hsa-miR-1297	BRCA1, KPNA2, PSAT1, DEPDC1, CDKN3, MAD2L1
hsa-miR-31-3p	AURKA, RAN
hsa-miR-31-5p	DMD, MKI67, DEPDC1, ICAM1
hsa-miR-497-3p	MSR1, KPNA2, DMD, RAN, BUB1
hsa-miR-497-5p	AHCY, KIF23, GINS4, BIRC5, CCNE2, WHSC1, PSAT1, CENPW, C1QB
hsa-miR-100-3p	CLEC7A
hsa-miR-100-5p	KPNA2
hsa-miR-125a-5p	ENO1, CHCHD3, MAGOHB, PRC1
hsa-miR-520e	GINS4, ATAD2, CENPN, PBK, BRCA1, WHSC1, KPNA2, KIF14, RAD51, CEP152, SSTR2, MCM7
hsa-miR-92b-3p	MSR1, NEIL3, AURKA, RFC3, RAD51, RAN, CEP152, ICAM1
hsa-miR-361-5p	CHCHD3, CENPN, TPX2
hsa-miR-30c-5p	AHCY, CHI3L1, BRIP1, BIRC5, CCNE2, DMD, CEP152, SSTR2

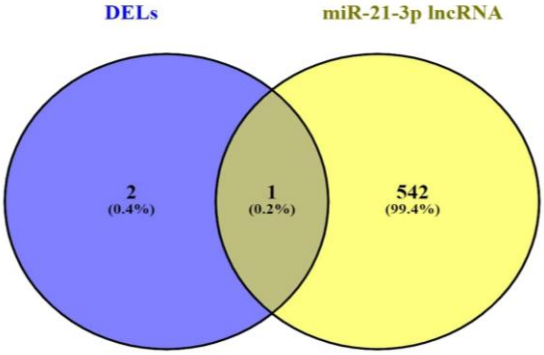
hsa-miR-570-5p	RFC5, BRIP1, MSR1, KIF14, NUF2, DEPDC1, OIP5
hsa-miR-125b-5p	CHCHD3, MAGOHB, PSAT1
hsa-miR-30d-3p	BRIP1, KIF23, FANCI, KPNA2
hsa-miR-30d-5p	AHCY, CHI3L1, BRIP1, CCNE2, DMD, SSTR2
hsa-miR-424-3p	CHCHD3, TPX2, BRCA1
hsa-miR-424-5p	KIF23, IFIH1, GINS4, BIRC5, CCNE2, WHSC1, PSAT1, CENPW, C1QB
hsa-miR-23b-3p	WHSC1, CDCA8, RAD51
hsa-miR-23b-5p	FANCI, TPX2
hsa-miR-150-5p	OASL, GINS1, BIRC5, CENPA, NLRP7
hsa-miR-200a-3p	CCNE2, PRC1, CEP152, CDKN3
hsa-miR-200a-5p	BIRC5, OLA1, OIP5
hsa-miR-342-3p	WHSC1, KPNA2, PSAT1, BUB1
hsa-let-7c-3p	GINS1
hsa-let-7c-5p	MSR1, FANCI, DMD
hsa-let-7b-3p	KIF23, DEPDC1
hsa-let-7b-5p	MSR1, BIRC5, TYMS, CDCA8, DMD, AURKA, MCM7
hsa-miR-34b-3p	BRIP1
hsa-miR-34b-5p	CCNE2, ICAM1, ULBP2
hsa-miR-2278	CLEC7A, CDCA8, KRT16






DELs
miR-93-5p lncRNA
0
(0%)
3
(0.1%)
2600
(99.9%)


DELs
miR-1290 lncRNAs
2
(0.2%)
1
(0.1%)
1071
(99.7%)


DELs
miR-21-3p lncRNA
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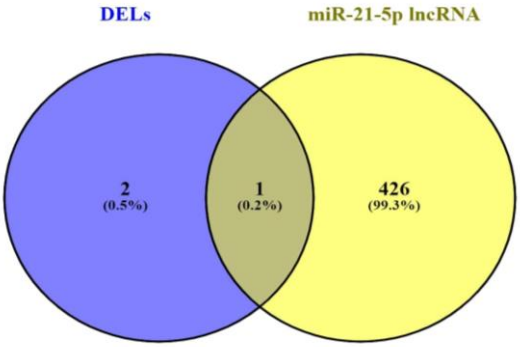
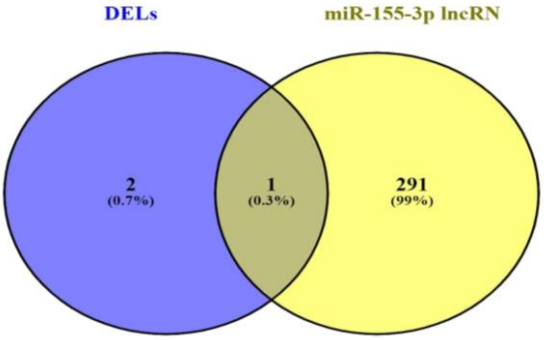
(0.4%)
1
(0.2%)
542
(99.4%)


DELs
miR-21-5p lncRNA
2
(0.5%)
1
(0.2%)
426
(99.3%)


DELs
miR-155-3p lncRN
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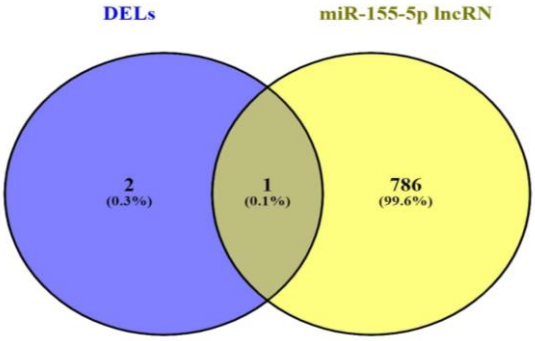
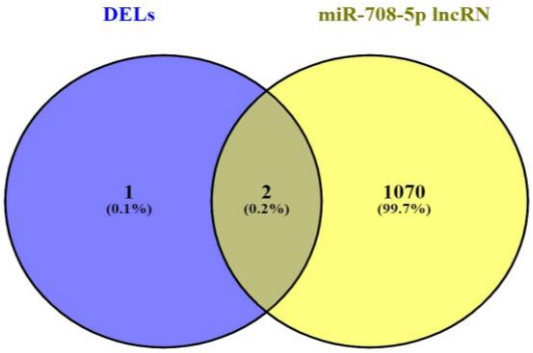
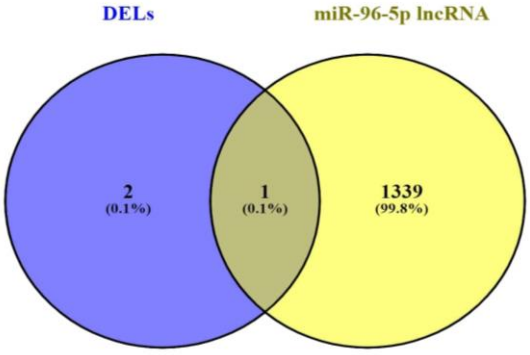
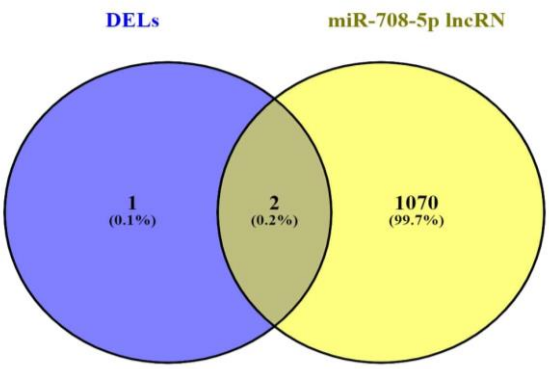
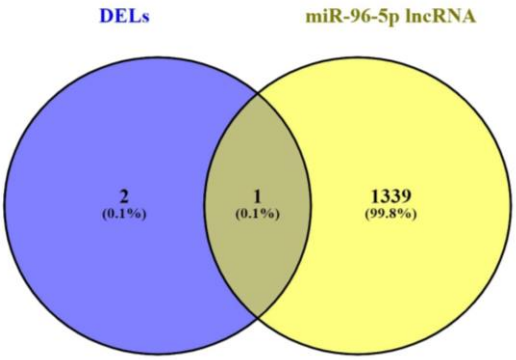
(0.7%)
1
(0.3%)
291
(99%)

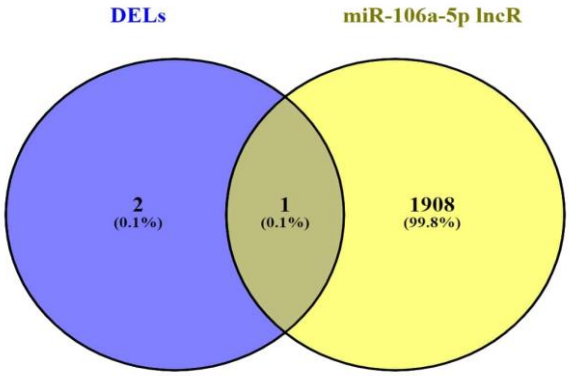

DELs
miR-155-5p lncRN
2
(0.3%)
1
(0.1%)
786
(99.6%)

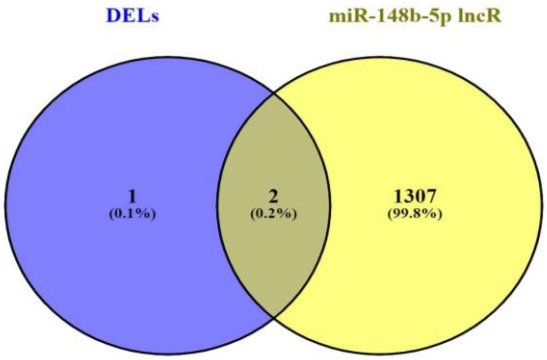

DELs
miR-708-5p lncRN
1
(0.1%)
2
(0.2%)
1070
(99.7%)

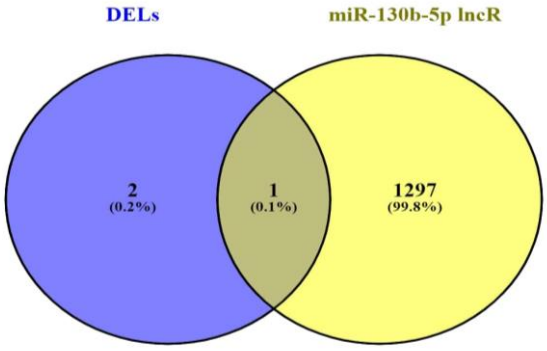

DELs
miR-96-5p lncRNA
2
(0.1%)
1
(0.1%)
1339
(99.8%)

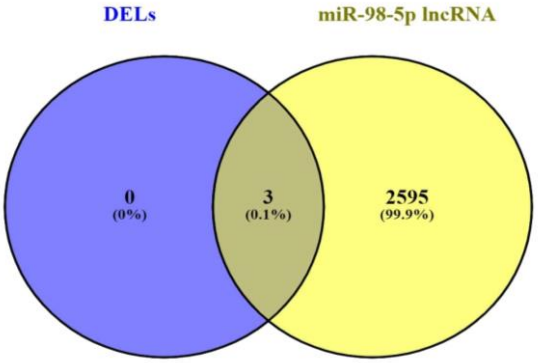

DELs
miR-708-5p lncRN
1
(0.1%)
2
(0.2%)
1070
(99.7%)

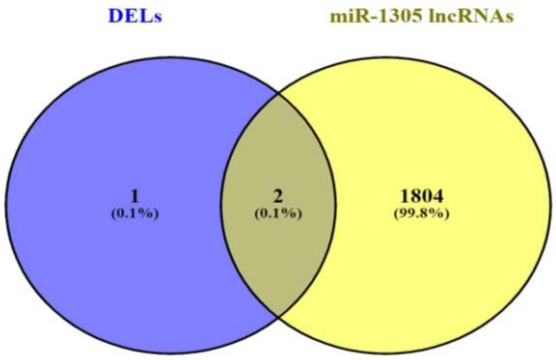

DELs
miR-96-5p lncRNA
2
(0.1%)
1
(0.1%)
1339
(99.8%)

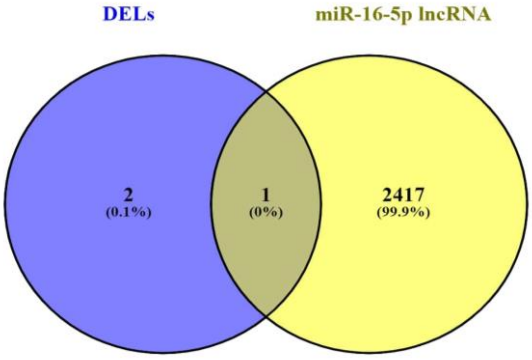

DELs
miR-106a-5p lncR
2
(0.1%)
1
(0.1%)
1908
(99.8%)

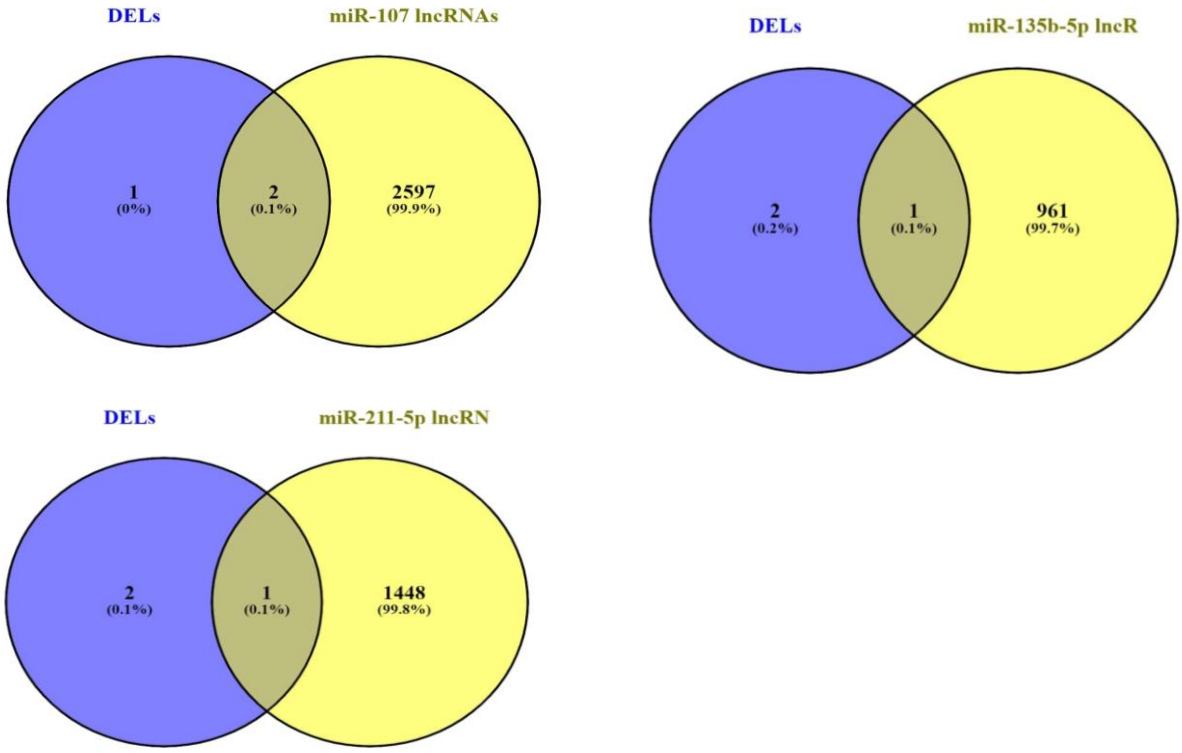

DELs
miR-148b-5p lncR
1
(0.1%)
2
(0.2%)
1307
(99.8%)


DELs
miR-130b-5p lncR
2
(0.2%)
1
(0.1%)
1297
(99.8%)


DELs
miR-98-5p lncRNA
0
(0%)
3
(0.1%)
2595
(99.9%)


DELs
miR-1305 lncRNAs
1
(0.1%)
2
(0.1%)
1804
(99.8%)


DELs
miR-16-5p lncRNA
2
(0.1%)
1
(0%)
2417
(99.9%)



Supplementary Figure 5. Venn diagram of target lncRNAs for the up-regulated miRNAs from the combined databases DIANA-lncBase V3, StarBase V2, miRcode and DIANA-LncBase V2 databases compared with the DElncRNAncRNAs

Supplementary Table 5. The overlapped target lncRNAs of down-regulated DEmiRNAs from the combined databases DIANA-LncBase V3, StarBase V2, miRcode and DIANA-LncBase V2 databases compared with up-regulated lncRNAs

Down-regulated DEmiRNAs	**Overlapped target lncRNAs with the GEO Up-regulated DElncRNAncRNAs**
hsa-miR-1246	ARHGEF26-AS1
hsa-miR-320a	CASC2, ARHGEF26-AS1
hsa-miR-93-5p	CASC2, TPTE2P1, ARHGEF26-AS1
hsa-miR-1290	ARHGEF26-AS1
hsa-miR-21-3p	CASC2
hsa-miR-21-5p	CASC2
hsa-miR-155-3p	CASC2
hsa-miR-155-5p	CASC2

hsa-miR-708-5p	CASC2, ARHGEF26-AS1
hsa-miR-96-5p	ARHGEF26-AS1
hsa-miR-106a-5p	CASC2
hsa-miR-148b-5p	CASC2, ARHGEF26-AS1
hsa-miR-130b-5p	CASC2
hsa-miR-98-5p	CASC2, TPTE2P1, ARHGEF26-AS1
hsa-miR-1305	CASC2, ARHGEF26-AS1
hsa-miR-16-5p	TPTE2P1
hsa-miR-107	CASC2, TPTE2P1
hsa-miR-135b-5p	CASC2
hsa-miR-211-5p	ARHGEF26-AS1

Supplementary Table 6. The interactions between DEmiRNAs, DEmRNAs and DElncRNAncRNAs within the competing endogenous RNA (ceRNA) network

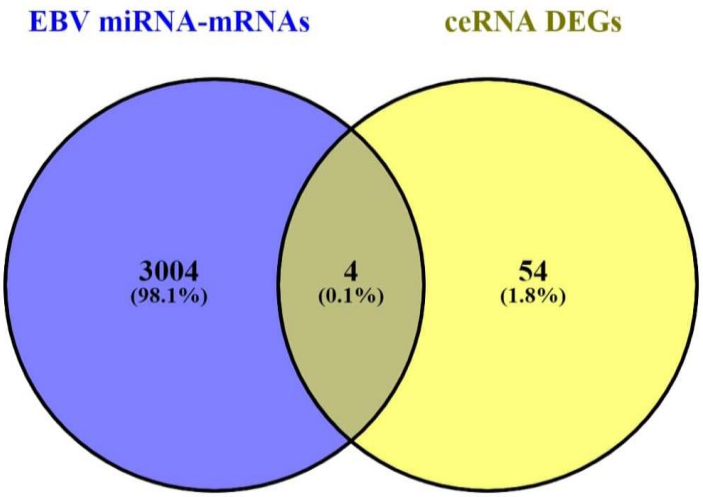
DEmiRNAs	**DEmRNAs**	**DElncRNAncRNAs**
hsa-miR-155-3p (interacts with)	CCDC65	CASC2
	NEK11	
hsa-miR-21-3p (interacts with)	CH25H	CASC2
	MORN5	
	KIF6	
hsa-miR-211-5p (interacts with)	DHRS9	ARHGEF26-AS1
	EBF1	
	SPAG16	
	SPEF2	
	SPATA6	

	STEAP4	
	DYNC2H1	
	ST6GALNAC1	
	BBS9	
hsa-miR-135b-5p (interacts with)	DNAH2	CASC2
	DNALI1	
	EBF1	
	GULP1	
	KCNRG	
	KIF6	
hsa-miR-135b-5p (interacts with)	DNAH2	CASC2
	DNALI1	
	EBF1	
	GULP1	
	KCNRG	
	KIF6	
hsa-miR-107 (interacts with)	BCAS1	CASC2
	CASC1	
	CCDC81	
	CRYM	
	ENKUR	TPTE2P1
	KCNRG	
	MAK	
	OSCP1	
	TPPP3	
	SELENBP1	
	SRPX	

hsa-miR-1305 (interacts with)	C10orf107	CASC2
	DHRS9	
	DNAH5	
	GULP1	
	MACROD2	ARHGEF26-AS1
	MAK	
	NEK11	
	RSPH4A	
	SLC22A4	
	SPAG16	
	SPEF2	
	LEPR	
	C4orf47	
	LRRC6	
hsa-miR-130b-5p (interacts with)	DNAH2	CASC2
	SPEF2	
	SPATA6	
	C11orf70	
hsa-miR-96-5p (interacts with)	CCDC65	ARHGEF26-AS1
	MAK	
hsa-miR-155-5p (interacts with)	SPEF2	CASC2
	SYTL2	
	AKR1C3	
	DYNC2H1	
hsa-miR-1290 (interacts with)	ADH1C	ARHGEF26-AS1
	BBS9	
	BCAS1	

	MAK	
	NEK11	
	TMC5	
	NEK5	
	TTC29	
hsa-miR-320a (interacts with)	CHP2	CASC2
	DNALI1	
	IQCA1	
	KIF6	
	MAK	
	TTC29	ARHGEF26-AS1
	LEPR	
	NQO1	
	DYNC2H1	
	FBXL13	
hsa-miR-1246 (interacts with)	BCAS1	ARHGEF26-AS1
	EFHB	
	EYA1	
	NEK5	
hsa-miR-16-5p (interacts with)	BCAS1	TPTE2P1
	EYA4	
	OSCP1	
	EYA1	
	TPPP3	
hsa-miR-98-5p (interacts with)	CCDC81	ARHGEF26-AS1
	LRTOMT	
	SPATA18	

	LEPR	TPTE2P1
	NQO1	
	AKR1C3	CASC2
	RRAD	
hsa-miR-106a-5p (interacts with)	C10orf107	CASC2
	EFCAB1	
	NEK11	
	SORBS2	
	DYNC2H1	
hsa-miR-21-5p (interacts with)	SPEF2	CASC2
	C11orf70	
	ST6GALNAC1	
	FBXL13	
hsa-miR-93-5p (interacts with)	BCAS1	ARHGEF26-AS1
	C11orf63	
	EYA4	
	FBXL13	
	MAK	TPTE2P1
	SORBS2	
	SPEF2	
	TMC5	
	TMEM45B	
	EYA1	CASC2
	C11orf70	
	KIF6	
	TTC9	

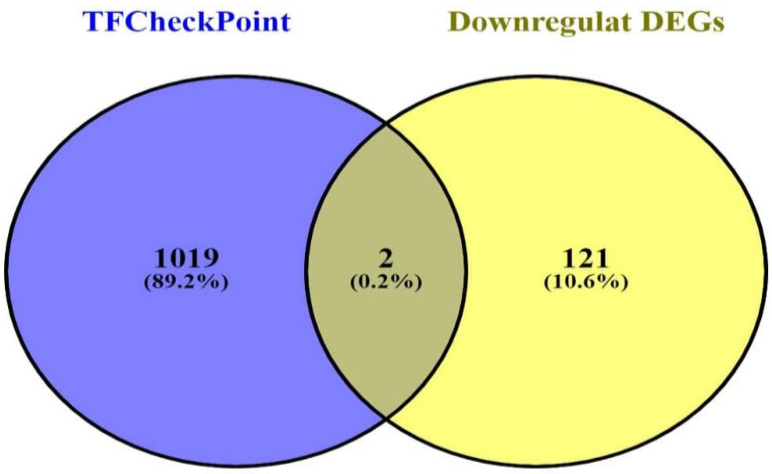


Supplementary Figure 6. Venn diagram of overlapping between the DEmRNAs targeted by Epstein-Barr Virus (EBV) *BamH1* A transcript (BART) miRNAs from ViRBase with the down-regulated DEmRNAs in the competing endogenous RNA (ceRNA) network revealed four common DEmRNAs which are EYA1, EYA4, EBF1 and MACROD2

Supplementary Table 7. Eighteen DEmRNAs with connectivity DEmRNAree greater than 5, according to Network Analyzer, showing DNAH5 has the highest connectivity DEmRNAree of 18, while both DNAAF1 and TEKT1 have the lowest connectivity DEmRNAree of 6

DEmRNAs	**Connectivity DEmRNAree**
TEKT1	6
DNAAF1	6
LRRC6	7
SPAG16	8
CCDC65	8
WDR78	8
SPEF2	8
DNAH2	9
SPAG6	9
DYNC2H1	10

DYNLRB2	10
DNAH12	10
RSPH4A	11
WDR63	11
RSPH1	13
DNAH6	14
DNALI1	17
DNAH5	18



Supplementary Figure 7. The Venn diagram of the overlapped two DEmRNAs common to all three GEO datasets (GSE64634, GSE126683 and GSE61218), as well as the transcription factors identified in the TFcheckpoint database, namely EBF1 and NR2F2