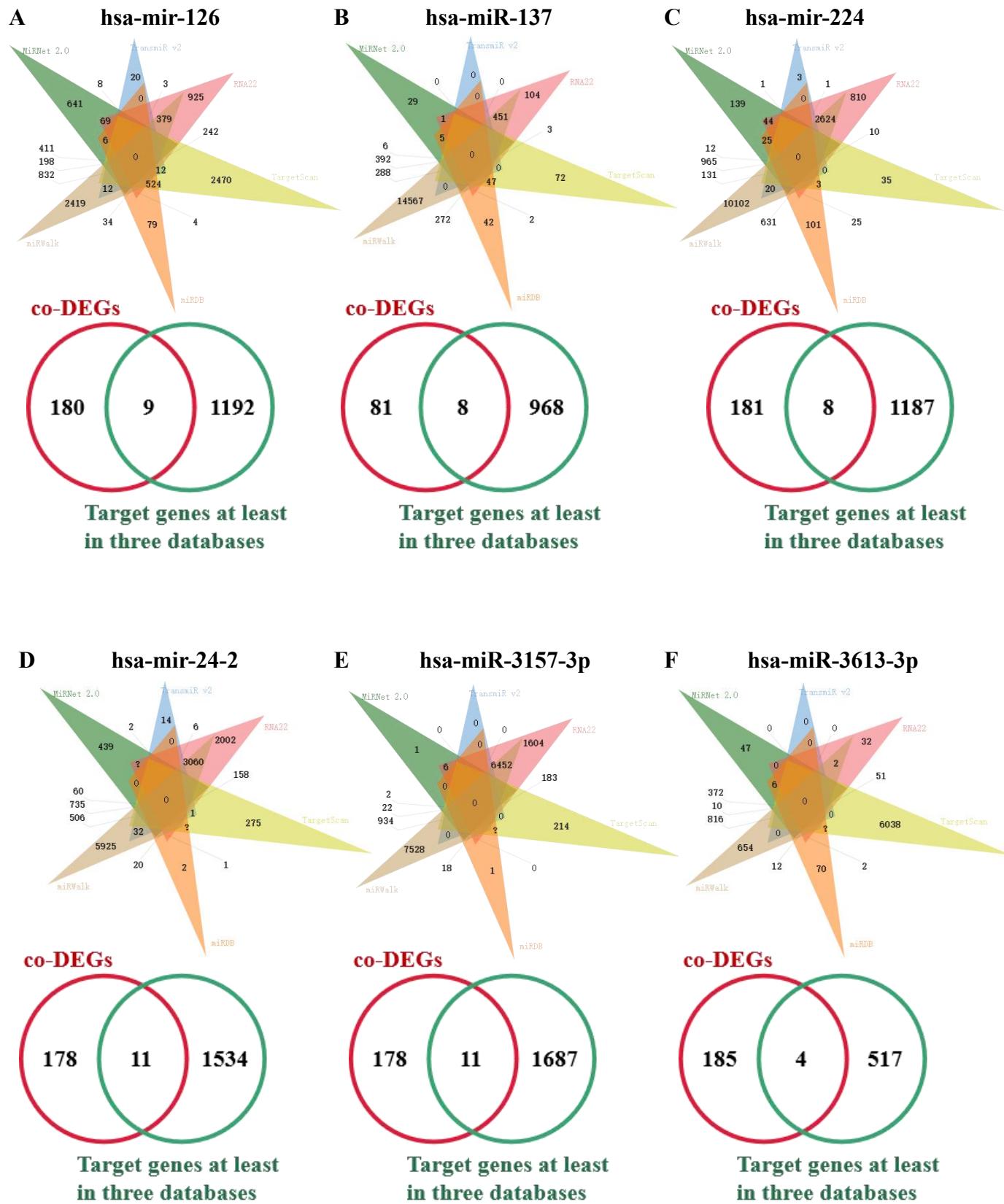
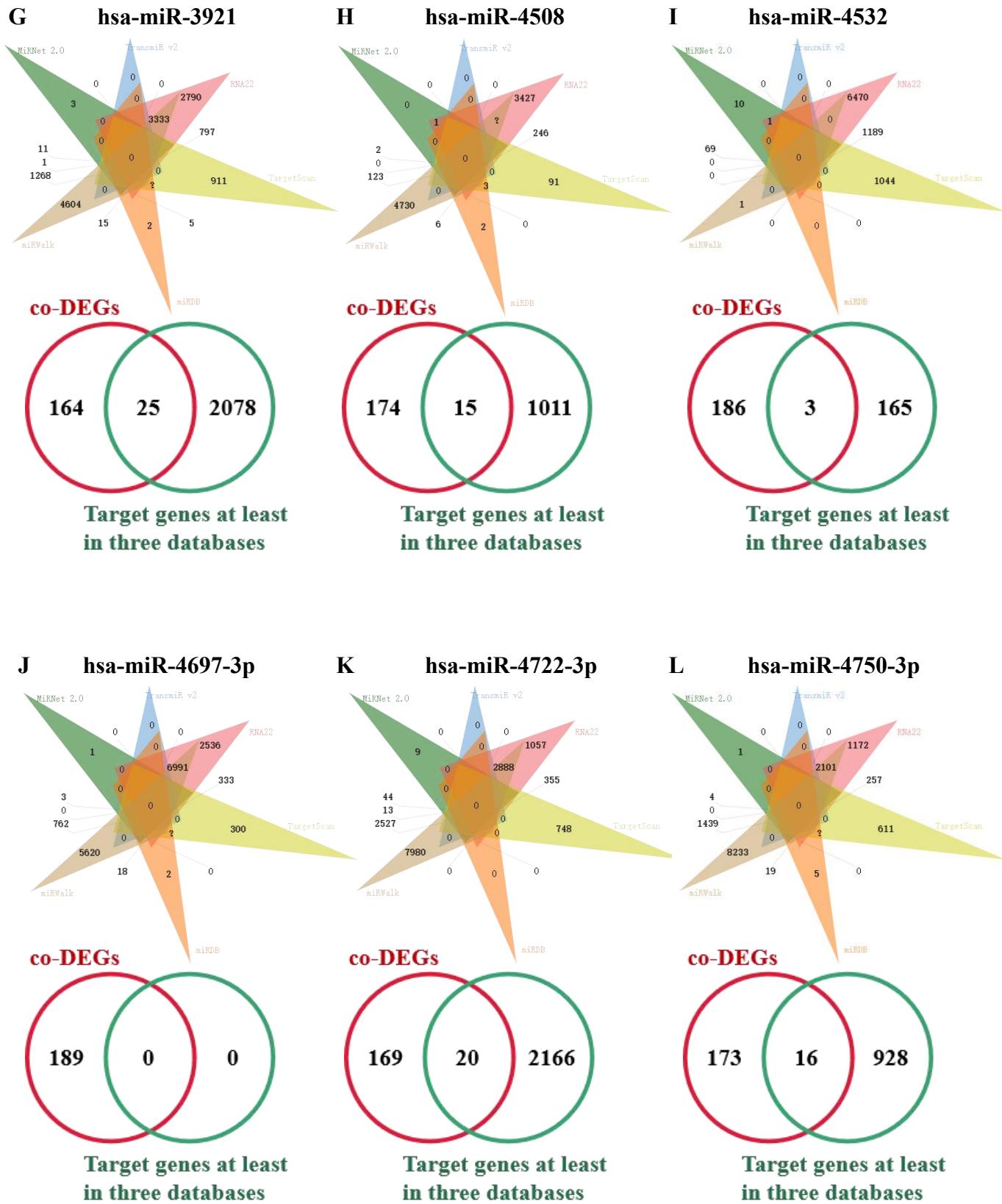


Fig. S1



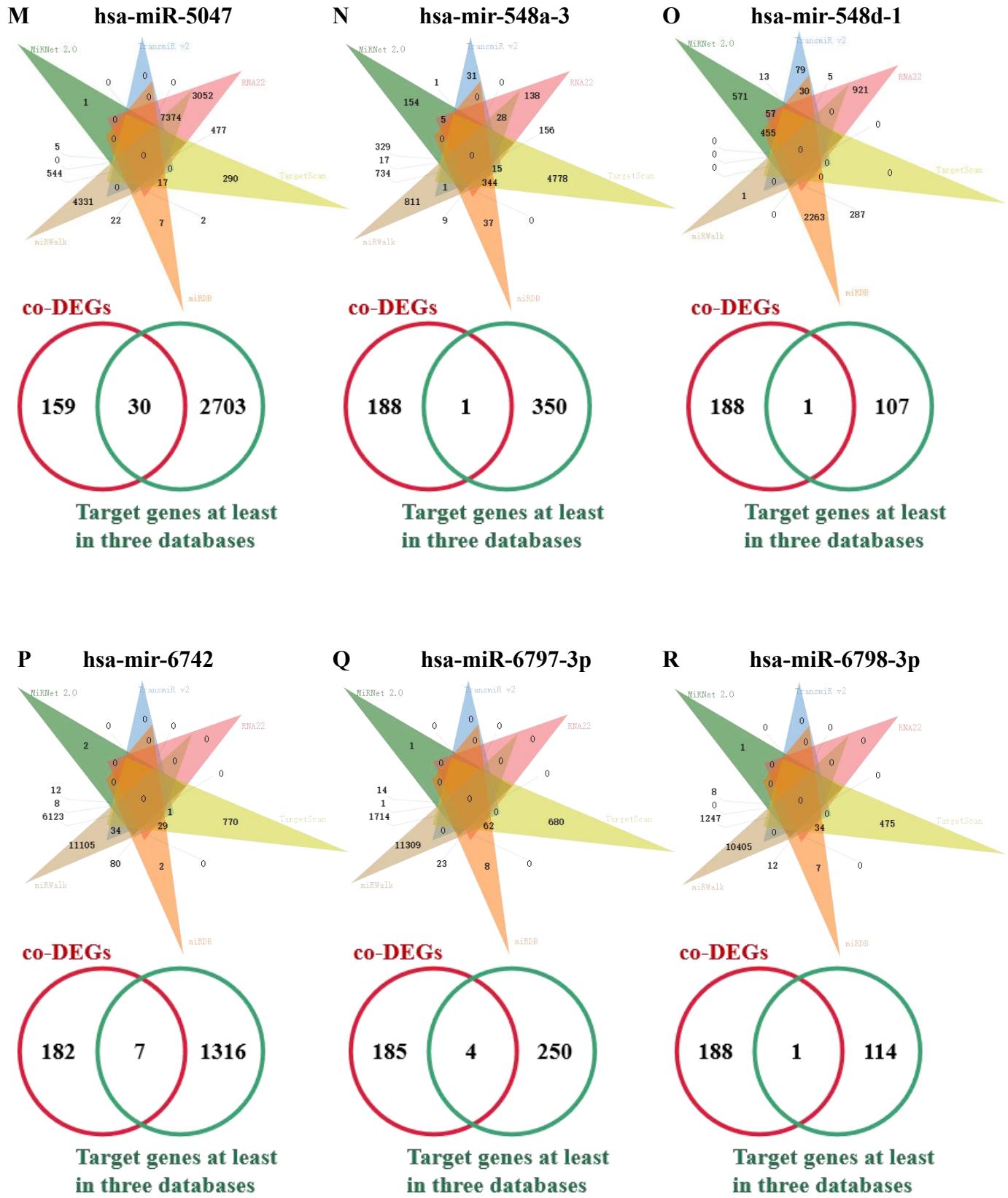
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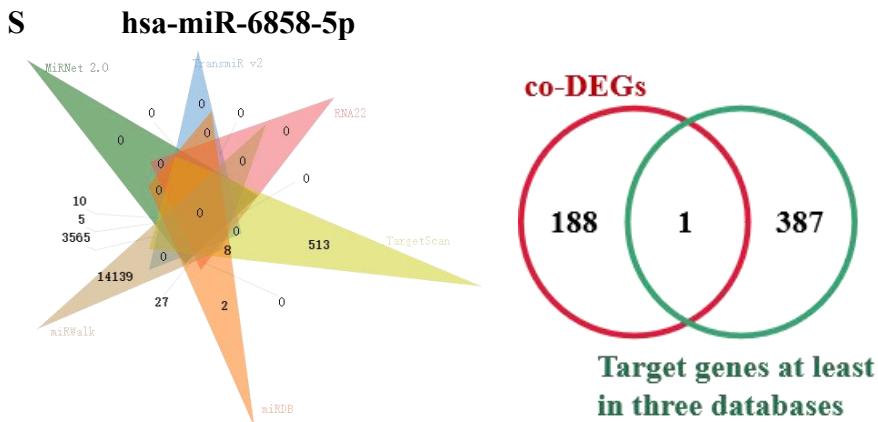


Figure S1. The target genes of differentially expressed microRNAs, and Veen diagram of target genes and co-DEGs in metabolically unhealthy obesity. (A) The target genes of hsa-mir-126 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-mir-126 (down). (B) The target genes of hsa-miR-137 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-137 (down). (C) The target genes of hsa-mir-224 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-mir-224 (down). (D) The target genes of hsa-mir-24-2 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-mir-24-2 (down). (E) The target genes of hsa-miR-3157-3p predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-3157-3p (down). (F) The target genes of hsa-miR-3613-3p predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-3613-3p (down). (G) The target genes of hsa-miR-3921 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-3921 (down). (H) The target genes of hsa-miR-4508 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-4508 (down). (I) The target genes of hsa-miR-4532 predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-4532 (down). (J) The target genes of hsa-miR-4697-3p predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-4697-3p (down). (K) The target genes of hsa-miR-4722-3p predicted by MiRNet 2.0, TransmiR v2.0, RNA22, TargetScan 7.2, miRDB and miRWalk (up). The Veen diagram of co-DEGs and target genes of hsa-miR-4722-3p (down). (L) The target genes of hsa-miR-4750-3p (up). The Veen diagram of co-DEGs and target genes of hsa-miR-4750-3p (down). (M) The target genes of hsa-miR-5047 (up). The Veen diagram of co-DEGs and target genes of hsa-miR-5047 (down). (N) The target genes of hsa-miR-548a-3 (up). The Veen diagram of co-DEGs and target genes of hsa-miR-548a-3 (down). (O) The target genes of hsa-miR-548d-1 (up). The Veen diagram of co-DEGs and target genes of hsa-miR-548d-1 (down). (P) The target genes of hsa-miR-6742 (up). The Veen diagram of co-DEGs and target genes of hsa-miR-6742 (down). (Q) The target genes of hsa-miR-6797-3p (up). The Veen diagram of co-DEGs and target genes of hsa-miR-6797-3p (down). (R) The target genes of hsa-miR-6798-3p (up). The Veen diagram of co-DEGs and target genes of hsa-miR-6798-3p (down). (S) The target genes of hsa-miR-6858-5p (left). The Veen diagram of co-DEGs and target genes of hsa-miR-6858-5p (right). DEGs: differentially expressed genes.

Supplementary Table 1. Details of differentially expressed microRNAs in blood of the MUO group

miRNAs	MUO vs MHO	Sequence Type	Sequence	Potential functions
hsa-mir-126	Down	stem-loop	CGCUGGCGACGGGA CAUUAUUACUUUUG GUACGCGCUGUGAC ACUUCAAACUCGUA CCGUGAGUAUAAU GCGCCGUCCACGGC A	<ul style="list-style-type: none"> 1. Increased in bromocriptine-resistant prolactinomas [1], in blood of patients with diabetic kidney disease [2] and in exosomal of colorectal cancer [3]. 2. Decreased in human obesity [4], in blood of metabolically unhealthy obese [5], in plasma of type 2 diabetes [6], in urinary of patients with diabetic kidney disease [7], in non-small cell lung cancer [8-11], pancreatic adenocarcinoma [12, 13], in glioblastoma[14, 15] and in the serum of COVID-19 patients [16]. 3. Potential biomarkers in Natural Killer Cells of Patients with Chronic Fatigue Syndrome / Myalgic Encephalomyelitis [7, 17] and in peripheral blood mononuclear cell of gestational diabetes mellitus patients [18] 4. Suppressed PAK4 expression in ovarian cancer SKOV3 cells [19]. 5. Down-regulates dengue virus replication in Huh-7 cells [20].

miRNAs	MUO vs MHO	Sequence Type	Sequence	Potential functions
hsa-miR-137	Up	miRNA	UUAUUGCUUAAGAA UACGCGUAG	<ol style="list-style-type: none"> Increased in blood of metabolically unhealthy obese [5], in gestational diabetes mellitus [21], hepatocellular carcinoma [22], in ovarian cancer [23, 24], in Parkinson's disease [25] and in colonic tissue of Lynch syndrome [26]. Decreased in astrocytoma [27], in glioblastoma [28], in oligodendroglial tumors [29], in non-small cell lung cancer [30], in gastrointestinal stromal tumor [31], in colorectal carcinoma [32], in papillary thyroid carcinoma [33], in prolactinomas [34], in pancreatic cancer [35, 36], in acute lymphoblastic leukemia [37], renal cell carcinoma [38, 39], in multiple myeloma [40], in cartilage tissue of osteoarthritis [41], in pediatric high-grade gliomas [42], in schizophrenia [43-45], in multiple sclerosis [46], knee osteoarthritis [47] and during the osteogenic differentiation of human adipose-derived stem cells [48]. Potential therapeutic target for melanoma [49-51], pituitary adenomas [52], acute myeloid leukemia [53], breast cancer [54-56], endometrial cancer [57], Alzheimer's Disease [58] and hypertrophic scars [59].

miRNAs	MUO vs MHO	Sequence Type	Sequence	Potential functions
hsa-mir-224	Up	stem-loop	GGGCUUCAAGUCA CUAGUGGUUCCGUU UAGUAGAUGAUUGU GCAUUGUUUCAAAA UGGUGCCCAGUGA CUACAAAGCCC	<ol style="list-style-type: none"> Increased in lung adenocarcinoma tissues from patients with lymph node metastasis [60], in plasma of patients with hepatocellular carcinoma [61] and CD4+ cells from asymptomatic patients with systemic lupus erythematosus [62]. Decreased in medullary thyroid carcinoma [63], during osteogenesis of unrestricted somatic stem cells (USSC) line 1 [64], during lobular neoplasia progression [65], in neuroblastoma [66] and in nasal mucosa of allergic rhinitis [67]. Potential biomarkers of breast cancer [68] and colon cancer [69]. Moderate expression in the inner tumor and tumor front of squamous cell lung carcinoma [70].
hsa-mir-24-2	Up	stem-loop	CUCUGCCUCCCGUG CCUACUGAGCUGAA ACACAGUUGGUUUG UGUACACUGGCUCA GUUCAGCAGGAACA GGG	Potential biomarkers of breast cancer [71] and metastasis of cervical squamous cell carcinoma [72].
hsa-miR-3157-3p	Up	miRNA	CUGCCCUAGUCUAG CUGAACGU	<ol style="list-style-type: none"> Increased in blood of metabolically unhealthy obese [5]. Potential biomarkers of schizophrenia [73].
hsa-miR-3613-3p	Down	miRNA	ACAAAAAAAGC CCAACCCUUC	<ol style="list-style-type: none"> Increased in HEK293 cells expressing H5N1 avian influenza virus non-structural protein 1 [74]. Decreased in colon carcinoma [75]. Affects cell proliferation and cell cycle in hepatocellular carcinoma [76].
hsa-miR-3921	Up	miRNA	UCUCUGAGUACCAU AUGCCUUGU	Decreased in urine of current smokers [77].

miRNAs	MUO vs MHO	Sequence Type	Sequence	Potential functions
hsa-miR-4508	Down	miRNA	GCGGGGCUGGGCGC GCG	<ul style="list-style-type: none"> 1. Increased after administration of dexmedetomidine [78]. 2. Decreased in blood of metabolically unhealthy obese [5] and in pediatric patients with β-thalassemia [79].
hsa-miR-4532	Up	miRNA	CCCCGGGGAGCCCC GCG	<ul style="list-style-type: none"> 1. Increased in blood of metabolically unhealthy obese [5] and in urine of diabetic nephropathy [80, 81]. 2. Potential biomarkers of schizophrenia [82]. 3. Carried by acute myeloid leukemia cells -derived exosomes [83]. 4. Inhibition of miR-4532 protects HLECs from UVR-induced oxidative injury [84].
hsa-miR-4697-3p	Up	miRNA	UGUCAGUGACUCCU GCCCUUGGU	Increased in blood of metabolically unhealthy obese [5].
hsa-miR-4722-3p	Down	miRNA	ACCUGCCAGCACCU CCCUGCAG	Unknown
hsa-miR-4750-3p	Down	miRNA	CCUGACCCACCCCCU CCCGCAG	Unknown
hsa-miR-5047	Down	miRNA	UUGCAGCUGCGGUU GUAAGGU	Decreased in blood of metabolically unhealthy obese [5].
hsa-mir-548a-3	Down	stem-loop	UACCAUUACUUCA AUGGCAAAACUGGC AAUUACUUUUGCAC CAACGUAAUACUU	Unknown

miRNAs	MUO vs MHO	Sequence Type	Sequence	Potential functions
hsa-mir-548d-1	Up	stem-loop	AAACAAGUUUAUU AGGUUGGUGCAAAA GUAAUUGUGGUUUU UGCCUGUAAAAGUA AUGGCAAAACCAC AGUUUCUUUUGCAC CAGACUAAUAAAG GAGGGAGUGGGGUG GGACCCAGCUGUUG	Increased in blood of metabolically unhealthy obese [5].
hsa-mir-6742	Down	stem-loop	GCCAUGGCGACAAC ACCUGGGUUGUCCC CUCUAG UGCAUGACCCUUCC CUCCCCAC	Increased in CVID patients by Ig infusion [85].
hsa-miR-6797-3p	Up	miRNA	CUACCCCCCAUCCCC	Unknown
hsa-miR-6798-3p	Up	miRNA	CUGUAG GUGAGGAGGGCUG	Increased in blood of metabolically unhealthy obese [5] and in plasma of patients with venous thrombosis [86].
hsa-miR-6858-5p	Up	miRNA	GCAGGGAC	Unknown

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