Figure S1. STR analysis of HepG2 cells. Genomic DNA was extracted and PCR was performed to amplify the STR locus. STR analysis was performed using Genemapper 5 by Bionics Co., Ltd. HepG2 was matched to HB-8065, CRL-11997, MRA-975 and CRL-10741.

HepG2

STR analysis result

Marker	Allele 1	Allele 2	Peak 1	Allele 1-ht	Peak 2	Allele 2-ht
AMEL	X	Y	107.67	1564	113.11	1623
CSF1PO	10	11	320.31	1026	324.33	878
D13S317	9	13	222.04	2742	237.88	2931
D16S539	12	13	280.77	5074	284.7	2441
D18S51	13	14	288.9	2223	293.01	1843
D19S433	15.2		127.53	3435		
D21S11	29	31	205.03	604	212.97	724
D2S1338	19	20	323.8	1884	327.99	4144
D3S1358	15	16	125.26	2338	129.33	2439
D5S818	11	12	152.37	1207	156.46	1367
D7S820	10		272.27	1231		
D8S1179	15	16	154.98	1014	159.01	1262
FGA	22	25	237.26	1382	249.56	1232
TH01	9		184.02	6880		
TPOX	8	9	230.93	2271	234.89	5435
vWA	17		179.41	4684		

CLA analysis result

% Match	100.0	100.0	100.0	93.0
Atcc Number	HB-8065	CRL-11997	MRA-975	CRL-10741
Designation	Hep G2 Hepatocellular Carcinoma Human	HEP G2/2.2.1 CELL LINE	HC-04	C3A (HepG2/C3A) Hepatocellular CarcinomaHuman
D5S818	11,12	11,12	11,12	11,13
D13S317	9,13	9,13	9,13	9,13
D7S820	10	10	10	10
D16S539	12,13	12,13	12	12,13
vWA	17	17	17	17
TH01	9	9	9	9
AMEL	X,Y	X,Y	X,Y	X,Y
TPOX	8,9	8,9	8,9	8,9
CSF1PO	10,11	10,11	10,11	10,11

Figure S2. Exosomes from T-MSCs were detected by Nanosight particle tracking analysis. Left, T-MSCs of different origins; right, overall size of the exosomes isolated from T-MSCs of different origins. T-MSC, tonsil-derived mesenchymal stem cell.

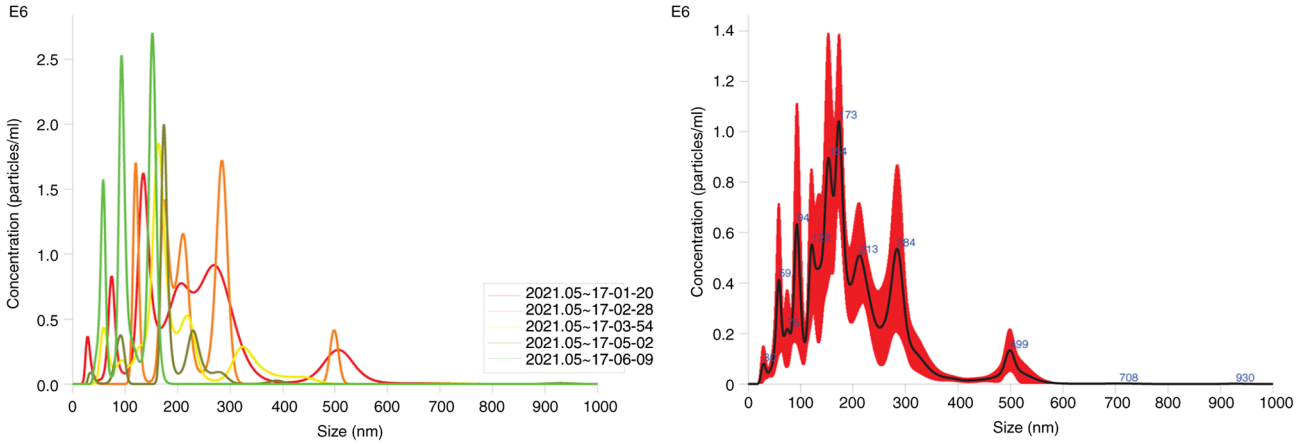
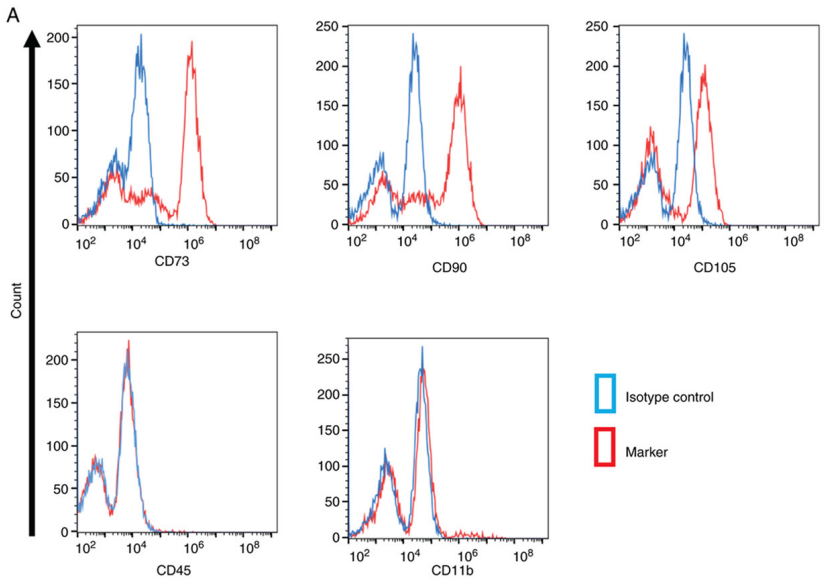


Figure S3. Characterization of T-MSCs. (A) Surface markers of T-MSCs of different origins were analyzed by flow cytometry. (B) Adipogenic differentiation of T-MSCs of different origins. The lipid droplets were visualized red under phase contrast microscope. T-MSC, tonsil-derived mesenchymal stem cell.



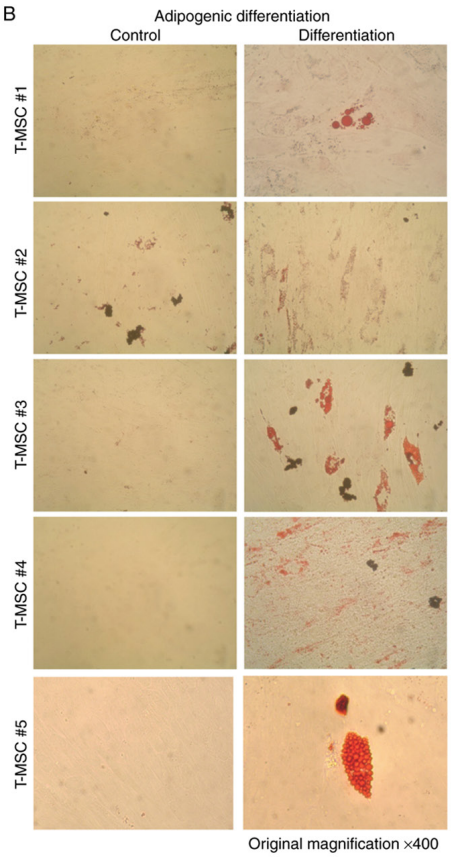


Figure S4. miRNA sequencing comparison of T-CM and DMEM. (A) Heat map of one-way hierarchical clustering. (B) Significant mature miRNA count by fold change. n=5 in CM group; n=1 in DMEM group. miRNAs exhibiting $log_2FC>2$ were considered to be differentially expressed. (C) Hierarchical clustering analysis. Using each sample's normalized value, the high expression similarities were grouped together. Distance metric=Euclidean distance; linkage method=complete linkage. T-CM, tonsil-derived mesenchymal stem cell conditioned medium; miRNA, microRNA; DMEM-C, DMEM-only negative control.

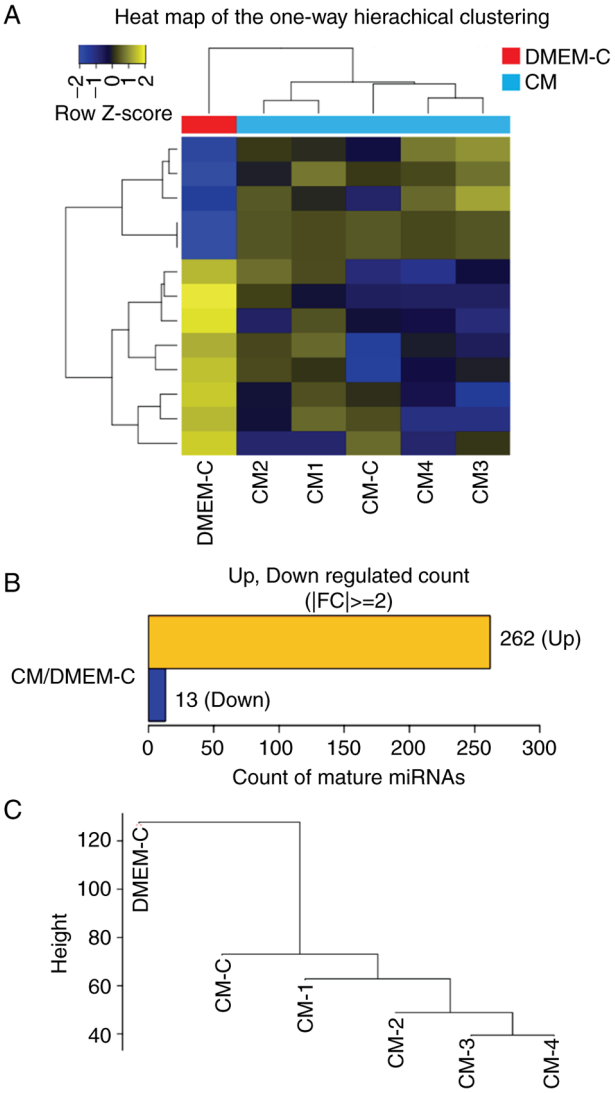


Figure S5. miRNA pathway analysis. The top 20 miRNAs identified in tonsil-derived mesenchymal stem cell exosomes were subjected to analysis using mirDIP, an integrative database of human miRNA target predictions, to determine whole miRNA target genes with high confidence. A total of 3,393 genes derived from mirDIP were further analyzed by Database for Annotation, Visualization and Integrated Discovery v6.8 to identify enriched biological pathways. miRNA, microRNA.

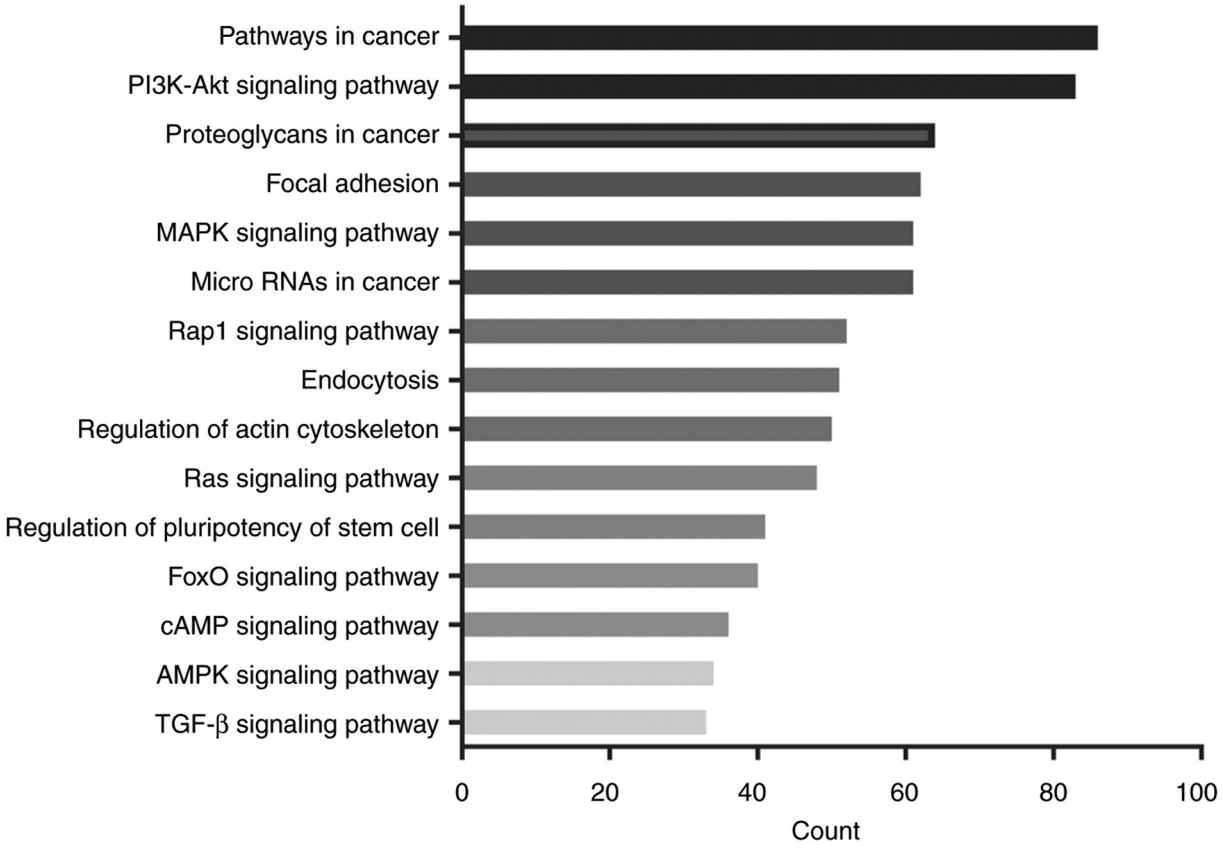


Figure S6. Transfection efficiency of miR-199a-3p inhibitor. The expression of hsa-miR-199a-3p and RNU6-1 in HepG2 cells transfected with negative control of miRNA inhibitor or has-miR-199a-3p inhibitor was compared by reverse transcription-quantitative PCR in normal (purple) and HepG2 cells transfected with control inhibitor (black) or miR199a-3p inhibitor (green). Relative expression was compared by one-way ANOVA with multiple comparison by Sidak test. Data are presented as the mean ± standard error of the mean. ****P<0.0001 vs. miR-199a-3p inhibitor). miR, microRNA; NL, normal HepG2 cells; CONT inhibitor, negative control of miRNA inhibitor; TF, transfectant.