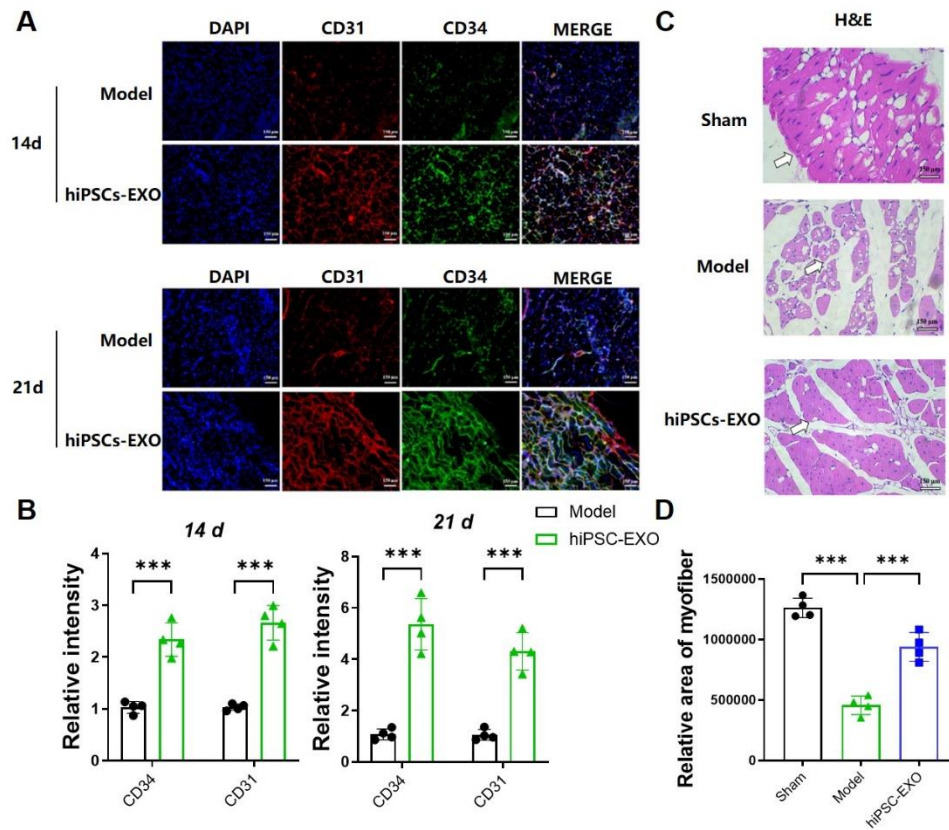
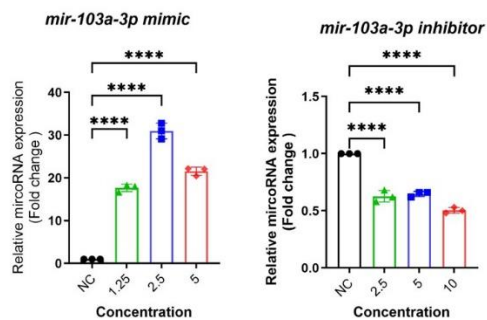


Supplementary information

Human-Induced Pluripotent Stem Cell Derived Exosomal miR-103a-3p Accelerate Urethral Injury Recovery by Promoting Angiogenesis Via TGFBR3/VEGF/FAK Axis

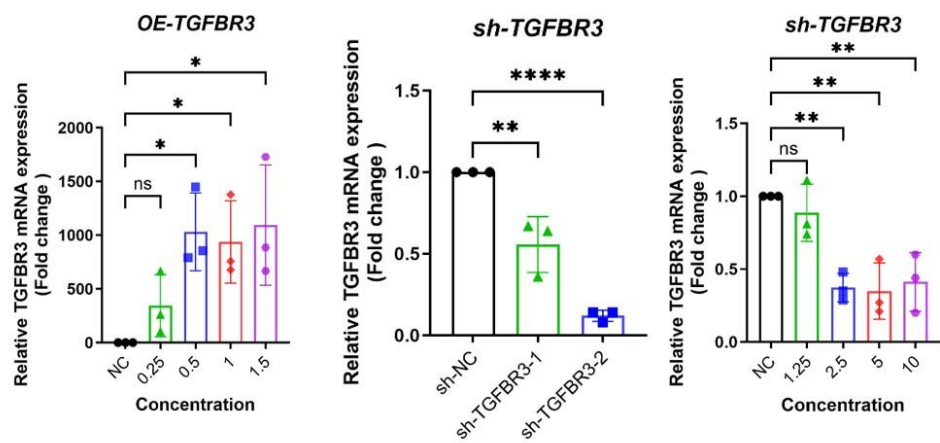


Supplementary Figure 1 A, B: Microscopic images stained with CD31, and CD34 after 14, and 21 days between model group and hiPSC-Exo group. C, D: HE staining of the quadriceps muscle on postoperative days 21.

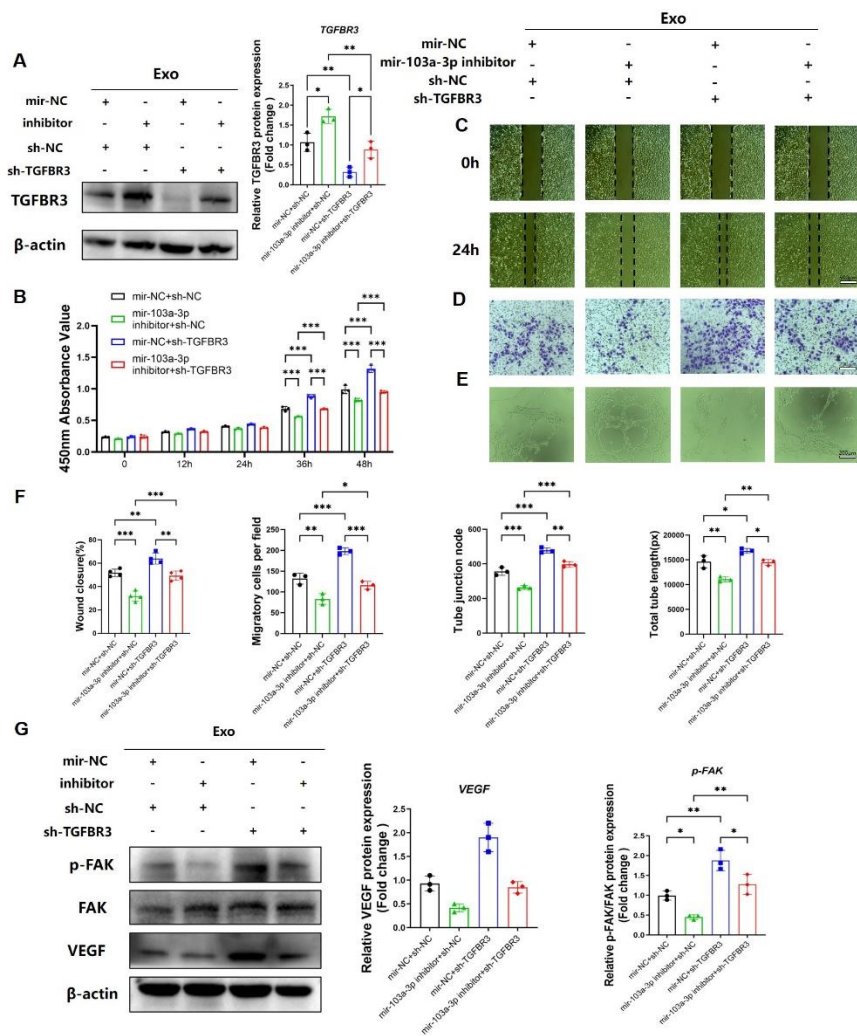


Supplementary Figure 2 The qPCR results of relative miR-103a-3p expression after

transfection.

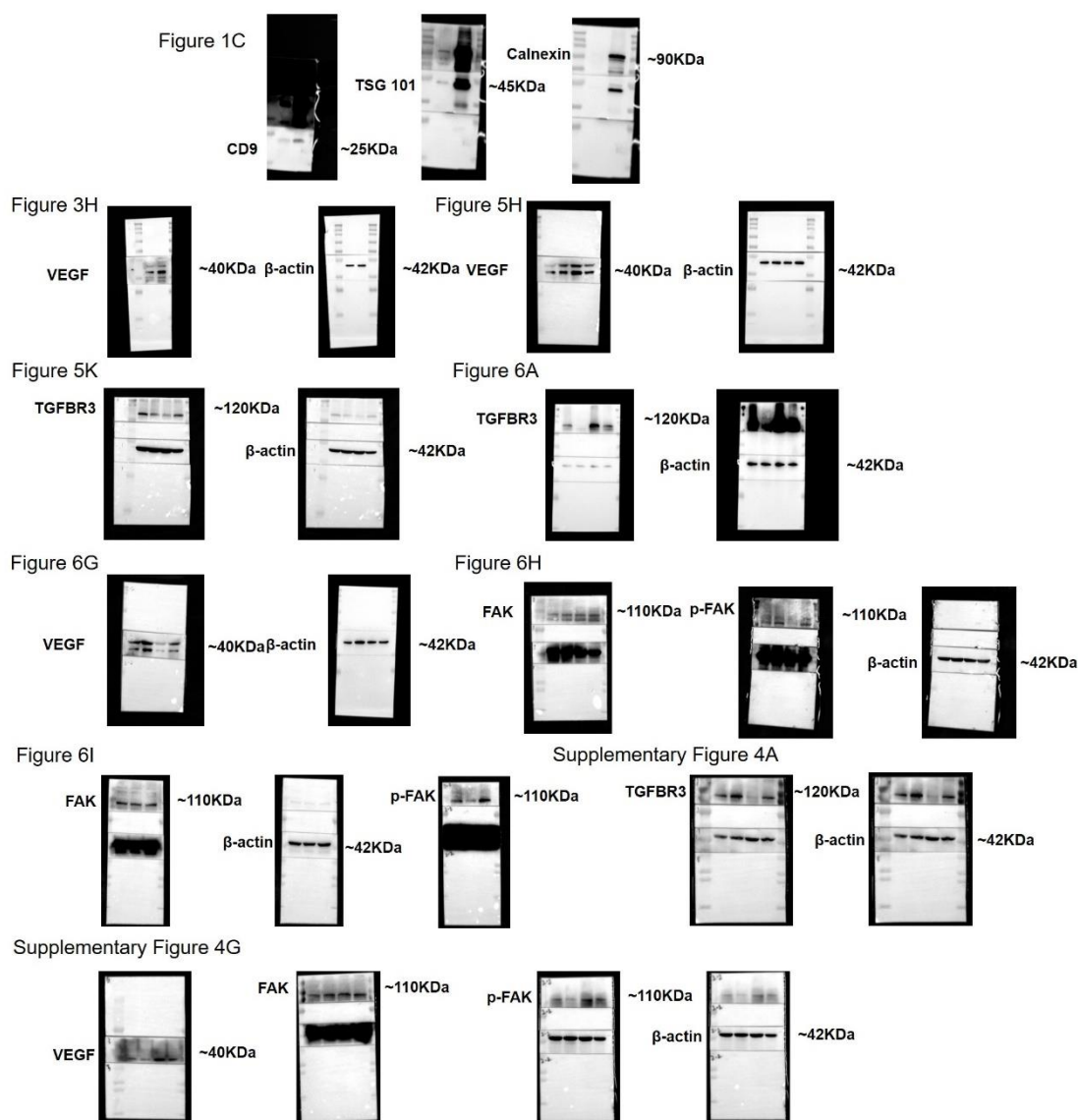


Supplementary Figure 3 The qPCR results of relative TGFBR3 expression after transfection.



Supplementary Figure 4 miR-103a-3p regulates HUVEC function via

TGFBR3/VEGF/FAK. (A) Western blot analysis to detect TGFBR3 expression after inhibitor virus transfection. (B) CCK-8 assay to assess the proliferative ability under different treatment conditions. (C) Representative images of wound healing of HUVEC under different treatment conditions after 24 h. (D) Representative images of migrative ability of HUVEC. (E) Representative images of tube formation of HUVEC under different treatment conditions after 6 h. (F) Statistical analysis of wound closure rate, migratory cells, total tubule length and junction node. (G) Western blot analysis of VEGF expression and phosphorylation activation of downstream FAK under different treatment conditions.



Supplementary Figure 5 Uncropped full length Western blots in Figure 1-6 and supplementary Figure 4.

Supplementary Table S1 Primers sequence used for qRT-PCR in this study.

RNA	Sequence
miR-302b-3p	TAAGTGCTTCCATGTTTTAGTAG
miR-302d-3p	TAAGTGCTTCCATGTTTGTGTGT
miR-302a-3p	TAAGTGCTTCCATGTTTTGGTGA
miR-302a-5p	ACTTAAACGTGGATGTACTTGCT
miR-1246	AATGGATTTTTGGAGCAGG
miR-302c-3p	TAAGTGCTTCCATGTTTCAGTGG
miR-148a-3p	TCAGTGCACTACAGAACTTTGT
miR-372-3p	AAAGTGCTGCGACATTTGAGCGT
miR-21-5p	CAGCTTATCAGACTGATGTTGA
miR-103a-3p	AGCAGCATTGTACAGGGCTATGA
T6	F: AACTTTGGCATTGTGGAAGG R: GGATGCAGGGATGATGTTCT
SNRK	F: CTCTCGGAAGAGGAGCACAACA R: TCAGCCAGCAGGAAGTATGTGG
ANO3	F: GTGGCTGTTTGATAGACCTCTGC R: ATGTCGTGACCACCAGTTCTGG
AGO4	F: ACAAGGTGCAGACAGTGTGGAG R: TCTCCAACACGTTTCACCTCCG
NF1	F: GCCTTGAGGAAAACCAGCGGAA R: TCCTACTGCACCGATGCTGTTC
NDEL1	F: GGCACAAAGTTCTCTCGATCAGG R: CTCACACACTGAGAGGCAGCAT
ZHX1	F: GAAACAGATGATAGTGACACTTGG R: TGATTCTCCTTCAACGTTTTAGGC
CAB39	F: GAGCATGGCTGTTCTGGAAAAGC R: GCTACTGCTTCTGTCTGAGGCT
ZCCHC2	F: AGACTCTCCACTCCTCAGCATG R: GGACTAGATGGAGAACTGTAATC
NEDD9	F: CCCATCCAGATACCAAAAGGACG R: CACTGGAAGTGAACACAGGGC
TGFBR3	F: TGGAGTCTCCTCTGAATGGCTG R: CCATTATCACCTGACTCCAGATC
GAPDH	F: GTCTCCTCTGACTTCAACAGCG R: ACCACCCTGTTGCTGTAGCCAA

Supplementary Table S2 The significant result of mircoRNA sequencing.

Gene	hips_exo1_ count	hips_exo1_ normalize	hips_exo2_ count	hips_exo2_ normalize
hsa-miR-302b-3p	74731	487809.8	168012	580342.3
hsa-miR-302d-3p	7233	47213.72	19747	68209.53
hsa-miR-302a-3p	4126	26932.64	17171	59311.58
hsa-miR-302a-5p	5961	38910.68	11597	40058.03

hsa-miR-1246	6326	41293.24	6386	22058.34
hsa-miR-302c-3p	1927	12578.58	5719	19754.41
hsa-miR-148a-3p	1621	10581.15	3960	13678.52
hsa-miR-372-3p	2018	13172.58	2620	9049.93
hsa-miR-21-5p	1184	7728.611	3030	10466.14
hsa-miR-103a-3p	1466	9569.378	1550	5353.966
hsa-miR-20a-5p	1124	7336.958	1346	4649.315
hsa-miR-1290	1163	7591.532	1271	4390.252
hsa-miR-92a-3p	1050	6853.92	1164	4020.656
hsa-miR-378a-3p	1083	7069.329	860	2970.588
hsa-miR-363-3p	676	4412.619	1258	4345.348
hsa-miR-512-3p	765	4993.57	616	2127.77
hsa-miR-7-5p	572	3733.755	801	2766.792
hsa-miR-17-5p	527	3440.015	781	2697.708
hsa-miR-4791	473	3087.528	694	2397.195
hsa-miR-151a-3p	487	3178.913	631	2179.582
hsa-miR-93-5p	475	3100.583	547	1889.432
hsa-miR-143-3p	13	84.85806	887	3063.85
hsa-miR-423-3p	439	2865.591	396	1367.852
hsa-miR-26a-5p	238	1553.555	564	1948.153
hsa-miR-20b-5p	305	1990.901	462	1595.827
hsa-miR-367-3p	257	1677.579	451	1557.831
hsa-miR-25-3p	305	1990.901	354	1222.777
hsa-miR-3182	433	2826.426	198	683.926
hsa-miR-221-3p	332	2167.144	273	942.9889
hsa-miR-106a-5p	307	2003.956	279	963.7139
