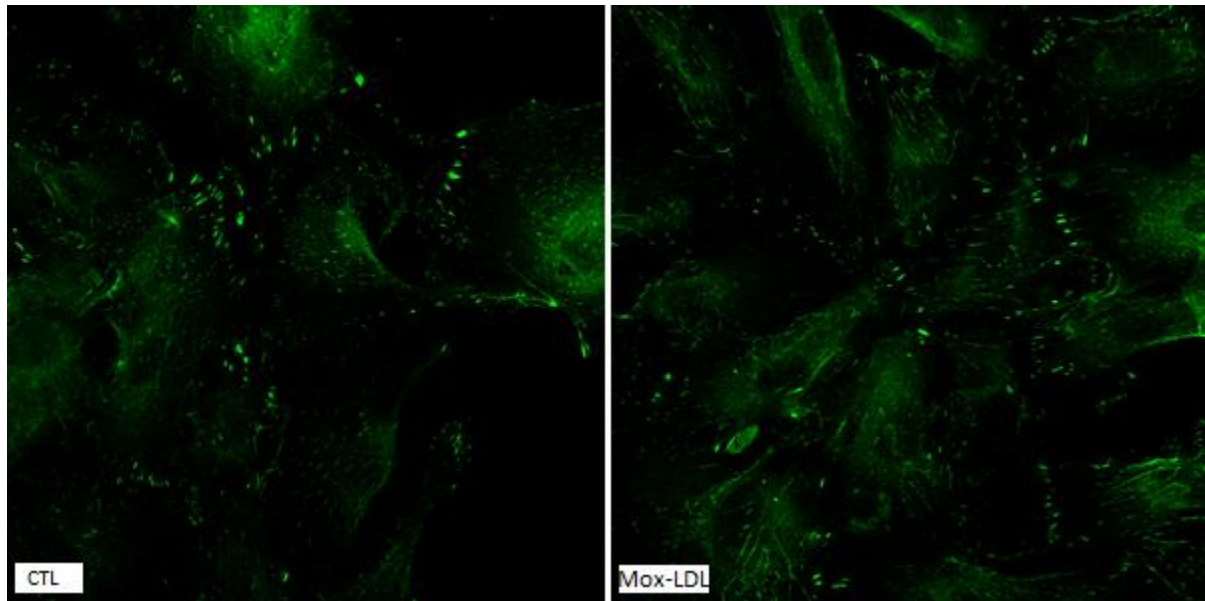
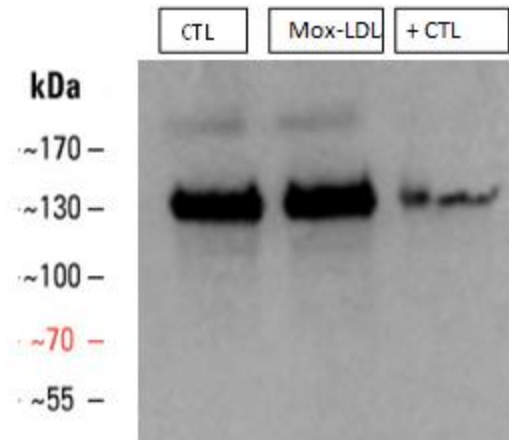


Supporting information

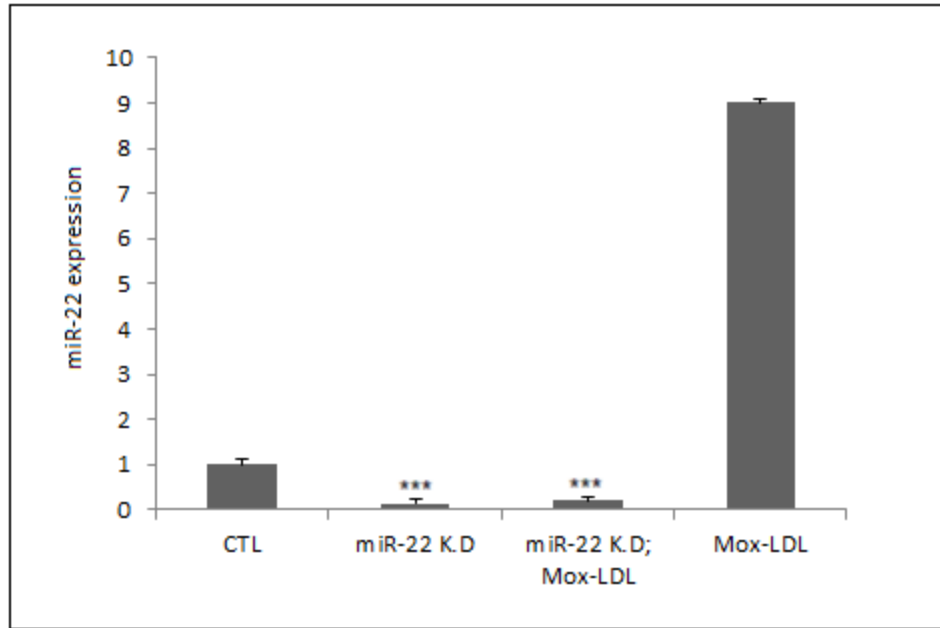
Supplementary figures



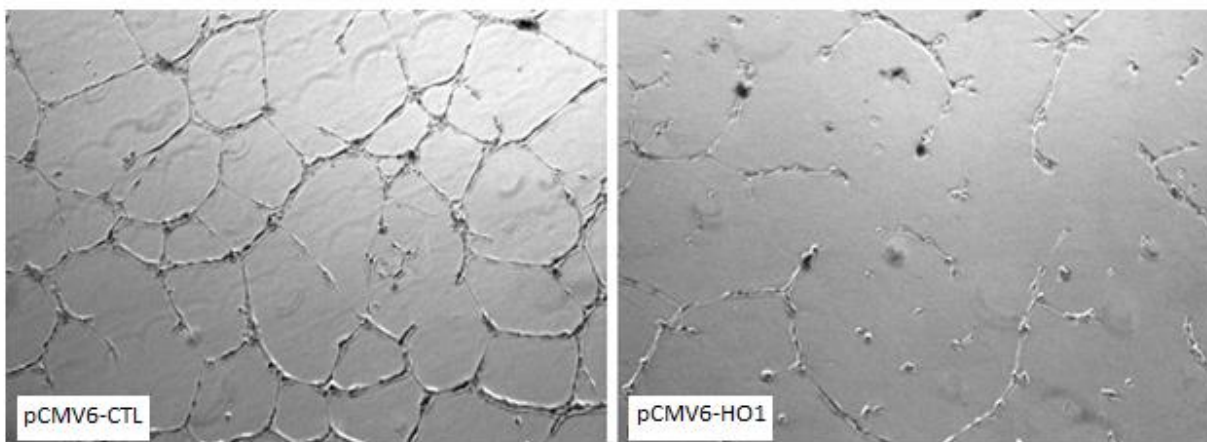
Supplementary Figure I. Control (CTL) mock-treated and Mox-LDL (Mox-LDL) treated HUVECs were subjected to confocal microscopy analysis to detect the patterning of focal adhesions using paxillin IF staining. Cells were cultured in the presence or absence of Mox-LDL for 24 hours, fixed and processed for immunofluorescence.



Supplementary Figure II. Western blot analysis of control (CTL) mock-treated and Mox-LDL (Mox-LDL) treated HUVECs using an anti phospho-FAK antibody. Cells were cultured in the presence or absence of Mox-LDL for 24 hours. HepG2 protein extract was used as a positive control (+ CTL).



Supplementary Figure III. Differential miR-22 expression between HUVECs submitted to different treatments: CTL (control mock-treated cells), miR-22 K.D (cells treated with miR-22 inhibitor), miR-22 K.D ; Mox-LDL (cells treated with miR-22 inhibitor and Mox-LDL) and Mox-LDL (cells treated with Mox-LDL). Total RNA was extracted and analyzed by qRT-PCR using miR-22-specific primers. Pooled data from 3 independent experiments are shown. ***, $p < 0.001$ (Student's t test).



Supplementary Figure VI. The effect of HO-1 overexpression on HUVEC tubulogenesis . A) Representative fields of HUVEC cultures in tubulogenic conditions. HUVECs were transfected with either a control empty pCMV6 vector or the same vector containing HO-1 ORF for overexpression. Afterwards, cells were cultured for 24 hours. HUVECs were then seeded on MATRIGEL™ and incubated overnight.

Supplementary tables

Rank	Gene Name	Fold Change
1	HMOX1 (HO-1)	11.098827
2	ANGPTL4	3.54599
3	FLT1	-2.048766
4	TNF	49.373841
5	ANG	1.862989
6	ERBB2	2.042583
7	GDF5	-2.042658
8	ITGB3	-2.446958
9	F3	2.259589
10	MMP14	1.94062
11	STC1	-4.21923
12	VEGFC	-1.617768
13	MET	-1.926857
14	PTEN	-1.994231
15	CXCR4	1.463703
16	BIRC5	-1.896081
17	IL18	1.734897
18	PTN	7.617571
19	ENG	2.058152
20	AKT1	1.793787
21	CTGF	-1.834454
22	FGF2	-1.461817
23	ITGB1	-1.794913
24	IL6	-1.533378
25	ITGAV	-1.44376
26	HIF1A	-1.273682
27	MYC	-2.207365
28	TNFSF15	1.521195
29	HOXD3	1.334072
30	CSF1	1.704672
31	KDR	-1.601133
32	EPHB4	1.568042
33	CAV1	-1.571543
34	Hs18s	1.338716

35	FLT4	1.591639
36	VEGFA	-1.219629
37	BMX	-1.529389
38	IGFBP3	-1.44343
39	ANGPT1	-2.116423
40	ANPEP	1.195922
41	TEK	-1.472871
42	EFNB2	-1.356693
43	FIGF	1.223317
44	PECAM1	-1.329769
45	PGF	1.71445
46	AGTR1	1.815252
47	RAC1	-1.151049
48	HSGenomic	1.767624
49	SPP1	2.69479
50	DLL4	-1.151107
51	ANGPT4	-2.084858
52	ACVRL1	1.620393
53	NOS3	-1.208613
54	VEGFB	1.116112
55	ANGPT2	-1.166612
56	EPHA2	1.337519
57	EDN1	-1.148181
58	ETS1	-1.376352
59	COL18A1	1.180191
60	ANGPTL6	1.120029
61	SSTR2	-273.450392
62	HPSE	-1.070885
63	PDGFB	1.621356
64	TGFB1	-2.243904
65	TIMP1	-1.176056
66	CEACAM1	-1.058709
67	HGF	1.853062
68	MIF	1.281158
69	SPARC	1.040428
70	SERPINE1	1.250923
71	NOS2	-215.498894

72	PTGS2	1.064404
73	NRP1	1.018726
74	ITGA5	1.141821
75	THBS1	1.067319
76	CYR61	-1.12108
77	MAPK7	1.153725
78	EPOR	1.097062
79	TYMP	1.156345
80	STAT3	1.097638
81	VASH1	1.088242
82	TP53	-1.02341
83	ID1	1.030433
84	BSG	1.117271
85	MMP2	1.046882
86	CXCL12	1.366611
87	SERPINF1	-1.06559
88	ANGPTL3	-1.403216
89	CCL2	1.01938
90	MMP9	-1.0471
91	IL1B	2.809877
92	ANGPTL1	1.954176
93	FGF1	1.520392
94	SERPINB5	15.988917
95	CXCR2	8.999235
96	LEP	-261.630054

Supplementary Table I. Shows the results of the human Angiogenesis StellarArray™ technique which was used to study the expression of 94 pre-selected genes involved in angiogenesis pathways. The table shows the complete list of genes with their fold change in expression levels in Mox-LDL treated condition as compared to the control condition (control mock-treated). Treatment of HUVECs with Mox-LDL significantly altered the expression of only one gene, the Heme Oxygenase 1 (HO-1) gene, which saw an 11-fold increase in its expression level.

microRNA	Fold Change
hsa-miR-107	2.4313
hsa- miR-133a	6.935
hsa- miR-134	0.3036
hsa- miR-188-3p	3.3762
hsa- miR-200b	3.9903
hsa- miR-203	16.5497
hsa- miR-22	550.8621
hsa- miR-29c	2.124
hsa- miR-449a	0.5709
hsa- miR-449b	0.5709
hsa- miR-502-3p	11.3658
hsa- miR-505	0.0081
hsa- miR-518b	0.0947
hsa- miR-629	8.2102
hsa- miR-636	0.1267
hsa- miR-652	0.2063
hsa- miR-672	0.19
hsa- miR-708	3.7797

Supplementary Table II. TLDA results showing the list of miRs that were identified to be differentially expressed exclusively in Mox-LDL treated HUVECs with their fold change in expression levels as compared to the control condition (control mock-treated). HUVEC were incubated for 24 hours in culture medium supplemented with mock medium, native LDL or Mox-LDL. Total RNA was extracted and analyzed by making use of the Taqman Low Density Array (TLDA) method.

microRNA	Fold Change
hsa- miR-133a	4.021
hsa- miR-203	2.480
hsa- miR-22	8.503
hsa- miR-672	0.331

Supplementary Table III. Shows the validated list of miRs that were confirmed to be differentially expressed exclusively in Mox-LDL treated HUVECs with their fold change in expression levels as compared to the control condition (Control mock-treated). HUVEC were incubated for 24 hours in culture medium supplemented with mock medium, native LDL or Mox-LDL. Individual qRT-PCR was used to validate the results of the TLDA high-throughput experiments. Total RNA was extracted and analyzed by qRT-PCR conducted on each of the differentially expressed miRs using specific primers.