Quantification of tube formation (F) and chemotaxis assay using Boyden chambers (G) of HUVECs incubated with microparticles isolated from MCS-fed mice (control diet) and MCD-fed mice treated with VNN1 siRNA, control siRNA, or PBS (mock) (n = 5 mice per group). VEGF was used as a positive control, and serum-free medium as a negative control. Values in (C), (E), (F), and (G) represent means ± SD from three independent experiments. *P < 0.05; **P < 0.01; ***P < 0.001, Kruskal-Wallis with Bonferroni correction.

Supplemental Figure 1. HepG2 exposed to different saturated and unsaturated free fatty acids. Representative micrographs of Oil red-O staining for lipid droplets in HepG2 exposed to 1% BSA (control) or 0.25 mM of oleic, palmitic and stearic acid for 24 h. 20X magnification was used for acquisition of the pictures.

Supplemental Figure 2. Effect of lipotoxic FFAs is counteracted by non-lipotoxic FFAs. HepG2 were exposed to 0.25 mM of palmitic acid, oleic acid and a mixture of both up to 24 hrs. MPs were isolated from the supernatant and Annexin V+ positive MPs were detected by flow cytometry and quantity is reported in the graph. Values represent mean ± S.D. * P < 0.05; ** P < 0.01; ***P < 0.001 compared to controls.

Supplemental Figure 3. Cellular localization and molecular function of proteins from hepatocyte-derived MPs. All the proteins obtained by three different proteomics analysis of MPs from HepG2 cells exposed to palmitic acid were organized based on cellular localization (top pie chart) and molecular function (bottom pie chart). Percentages over the total number of proteins were reported in the pie charts.

Supplemental Figure 4. MPs released by fat-laden rat primary hepatocytes are potent inducers of angiogenesis. (A) Representative micrographs of tube formation of HUVECs after exposure up to 6 h to rat primary hepatocytes-derived MPs, MP-free supernatant or controls. (B) HUVECs total tube length has been measured and reported in the histogram. (C) Representative micrographs of chemotaxis assay (Boyden's chamber assay) of HUVECs were tested with primary hepatocytes-derived MPs, MP-free supernatant or controls, as described in Methods. A 10X magnification was used for microscopic pictures. (D) An average of HUVECs migrated into the filter was measured and reported in the graph. VEGF (100 ng/ml) was used as a positive control. Values represent mean ± S.D. from three independent experiments. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

Supplemental Figure 5. Pro-angiogenic effect of hepatocytes-derived MPs is dose-dependent. HepG2 were treated with 0.25 mM of palmitic acid up to 24 h and MPs were isolated from the supernatant by ultracentrifugation. MPs samples were quantified by BCA protein assay and the concentration has been determined. Different doses (50, 125, 250 and 500 µg/mL) have been used for assessing (**A**) HUVECs tube formation and (**B**) chemotaxis assay (Boyden's chamber assay). Quantification graphs are reported in the figure. A dose of 100 ng/mL of VEGF has been used as positive control. Values represent mean ± S.D. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

Supplemental Figure 6. Endothelial cells angiogenesis in vitro depends on internalization of MPs into HUVECs. Representative micrographs of tube formation of HUVECs after exposure to HepG2-derived $MPs^{Calcein}$ up to 6 hours. HUVECs tubes were detected by an Olympus FV1000 Spectral Confocal with 20X lens.

Supplemental Figure 7. Genetic suppression of VNN1 expression on MPs significantly reduced the pro-angiogenic effects of MPs on endothelial cell migration and tube formation. HepG2 were exposed to palmitic acid (PA) for 24 h and then treated with VNN1 siRNA or control RNA (Ctrl RNA). Representative micrographs of (**A**) tube formation and (**B**) chemotaxis (Boyden's chamber assay) of HUVECs treated with hepatocyte-derived MPs, MP-free supernatant (MP-free sup.) or controls for 6 h and 16 h, respectively. A dose of 100 ng/mL of VEGF was used as positive control. A 4X magnification was used for acquisition of pictures.

Supplemental Figure 8. Pro-angiogenic effect of hepatocytes-derived microparticles acts through VNN1-dependent internalization. (A) Fat-laden HepG2-derived MPs were stained with 1 μM of Calcein AM-FITC ($MPs^{Calcein}$), washed to removed unspecific bound and incubated with or without a neutralizing antibody anti-VNN1 (4 μg/mL) (VNN1 nAb) and anti-GAPDH for 30 minutes. MPs were then incubated with HUVECs for 6 hours and FITC-positive events were detected by FACS. (B) Number of FITC-positive HUVECs exposed to $MP^{Calcein}$ with or without VNN1 were reported in graph; (C) tube formation of HUVECs after exposure for 6 hours to HepG2-derived MPs with or without VNN1 or controls; (D) chemotaxis assay of HUVECs was performed with HepG2-derived MPs with or without VNN1 or controls as described in Methods. (E) Protein expression of endothelial cells markers activation, ICAM-1 and VCAM-1, after exposure up to 6 hours with hepatocytes-derived MPs or MPs pre-incubated with a VNN1 neutralizing antibody. GAPDH was used as loading control. (**F**) Glutathione activity assay analysis in HUVECs treated with HepG2-derived MPs with or without VNN1 or controls. Glutathione activity is reported in RFU. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$, compared to controls.

Supplemental Figure 9. Proangiogenic effects of VNN1 positive MPs are not mediated by induction of endothelial cell proliferation or modulation of PPAR-γ expression. Fat-laden HepG2-derived MPs were incubated with or without a rabbit polyclonal antibody anti-VNN1 (4 μg/mL) for 30 minutes. A BrdU proliferation assay has been performed with HUVECs incubated for 16 h with MPs, MPs and VNN1 neutralizing Ab or controls. (**A**) Flow cytometry analysis gating (P3) proliferating-FITC-positive HUVECs. A BrdU negative staining has been included as negative control. (**B**) RNA was isolated from HUVECs that were incubated for 16 h with MPs, MPs and VNN1 nAb or controls in order to determine the expression of PPAR-γ by quantitative PCR. The housekeeping gene 18S was used as an internal control. Values represent mean ± S.D. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

Supplemental Figure 10. Increase of VNN1 in hepatocytes during lipotoxicity is independent of PPARα and γ. (**A**) Quantitative PCR of PPARγ expression in HepG2 treated with 0.25 mM of palmitic acid (PA) or 1% BSA (vehicle) for 24 h. (**B**) Quantitative PCR for PPARα and (**C**) VNN1 in HepG2 treated with 1% BSA, 0.25 mM of palmitic acid (PA), oleic acid (OA) or palmitic acid/oleic acid mix for 24 h. (**D**) Quantitative PCR for PPARα and (**E**) VNN1 in HepG2 exposed to 1% BSA, 0.25 mM of palmitic acid (PA), oleic acid (OA) or palmitic acid/oleic acid mix for 24 h and treated with PPARα siRNA or control RNA (Ctrl RNA).

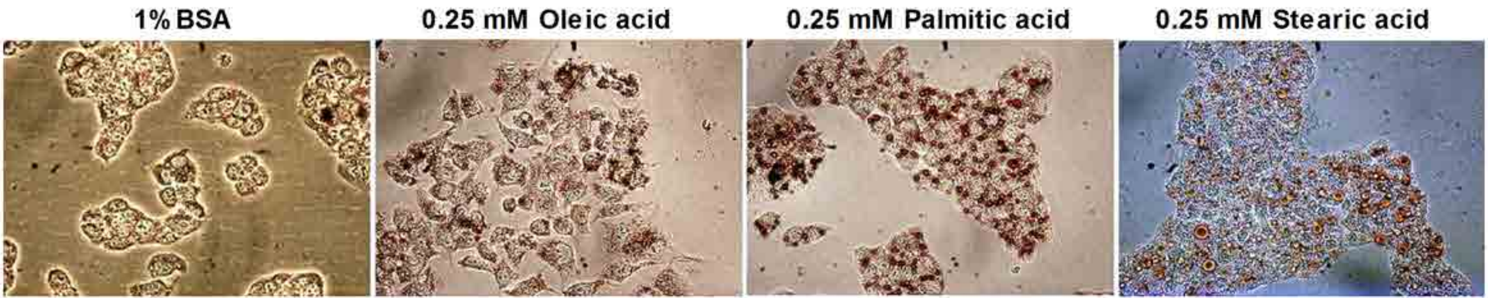
Supplementary Figure 11. Release of circulating microparticles depends on the stage of NASH. C57/B6 mice (n=5) were put on a MCD, high fat/high carbohydrates (HF/HCarb) or chow diet for 6 weeks. (**A**) Circulating MPs were isolated as described in Methods and Annexin V+ MPs were detected by flow cytometry. (**B**) H-E staining. (**C**) NAFLD activity score. Values represent mean ± S.D. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

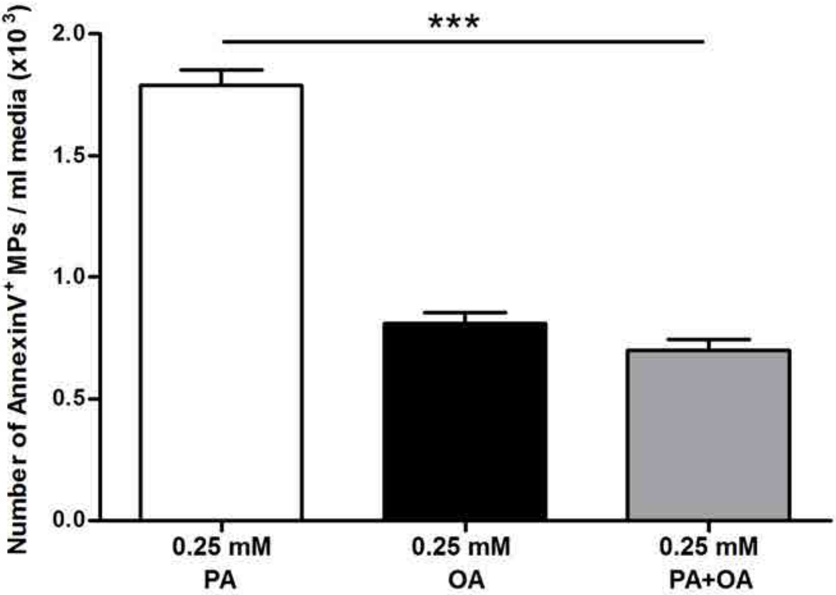
Supplementary Figure 12. Circulating MPs from mice with NASH stimulate angiogenesis ex vivo. C57/B6 mice were put on a MCD, high fat/high carbohydrates (HF/HCarb) and chow diet for 6 weeks, platelet-free plasma was harvested and MPs were isolated as described in Methods. MPs and MPs-free supernatant were used to induce HUVECs tube formation and oriented migration (Boyden's chamber assay) ex vivo. Quantification of (**A**) HUVECs tube formation (total tube length) and (**B**) chemotaxis assay (Boyden's chamber assay) is reported in the graph. A dose of 100 ng/mL of VEGF has been used as positive control. Values represent mean ± S.D. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

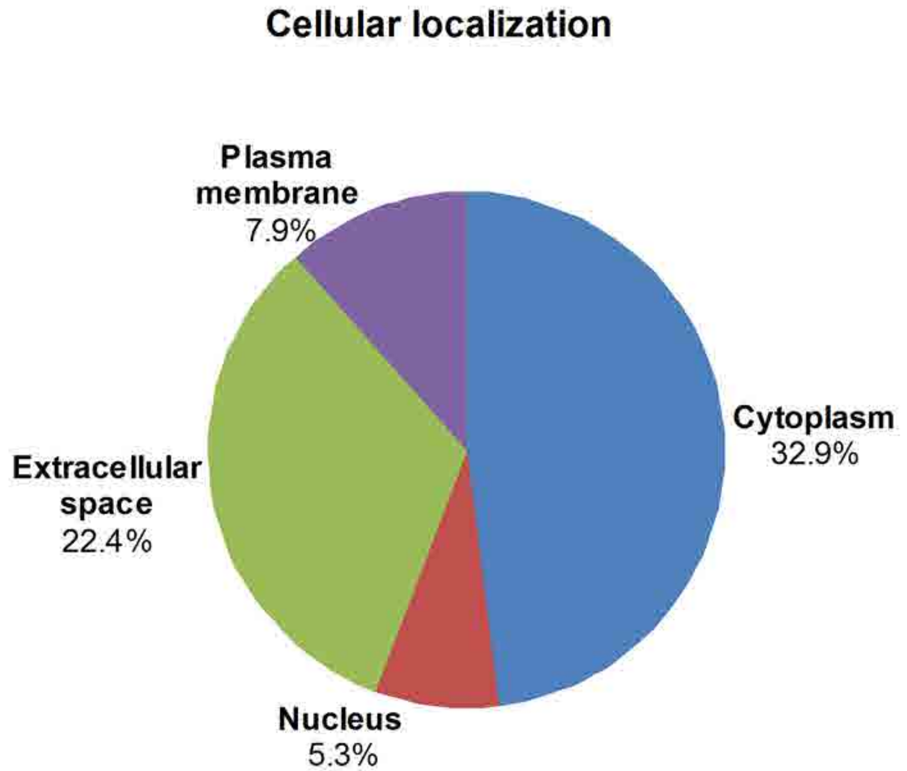
Supplemental Figure 13. Liver specific in vivo silencing of VNN1 does not affect VNN1 expression in other tissues. Expression of VNN1 was assessed in (**A**) kidney, (**B**) intestine and (**C**) spleen harvested from MCD-fed mice treated with VNN1 siRNA, control RNA (CTRL RNA) or PBS (Mock) to confirm the liver-specific knockdown of VNN1. The housekeeping gene 18S was used as an internal control. Values represent mean ± S.D. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

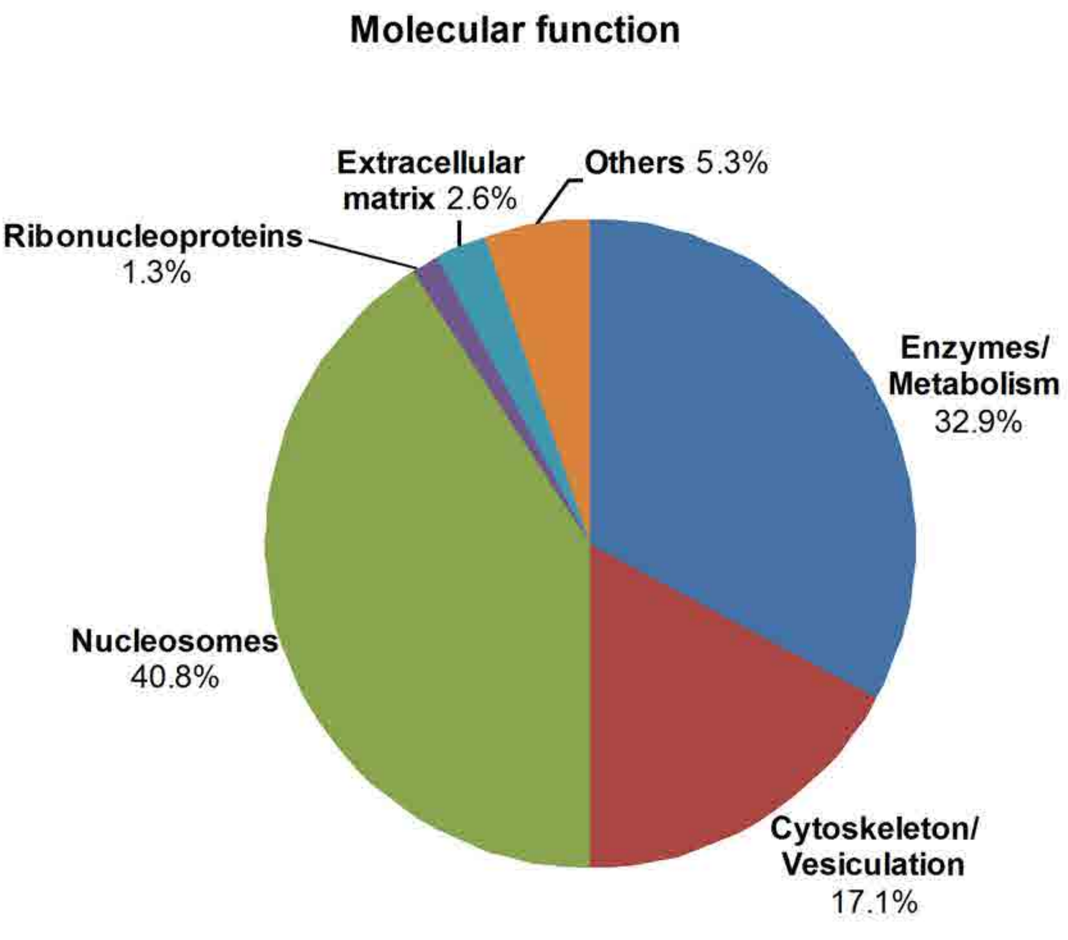
Supplemental Figure 14. Casp3-/- mice are protected from MCD-induced pathological angiogenesis and liver fibrosis. (A) Representative micrographs for H-E staining, immunostaining for CD-31, vonWillebrand factor (vWF) and Sirius red staining of liver specimens harvested from WT and Caspase-3 KO mice fed the MCD or control diet (MCS) diet for 6 weeks. A 10X magnification was used for micrographs. (**B**) Total area in pixel (px) is reported in the graph to show the quantification of CD31 immunostaining. (C) Percentage of fibrosis was measured by using Image J. (C) RNA was isolated from liver samples of C57BL/6 $Casp3^{-/-}$ and WT mice, fed a MCD or MCS diet. Analysis of the transcripts for the pro-angiogenic genes (VEGF-B and FGF-ß) and pro-fibrogenic genes (Collagen type I and α-SMA) was assessed by quantitative PCR. The housekeeping gene 18S was used as an internal control. Values represent mean ± S.D. * $P < 0.05$; ** $P < 0.01$; ***$P < 0.001$ compared to controls.

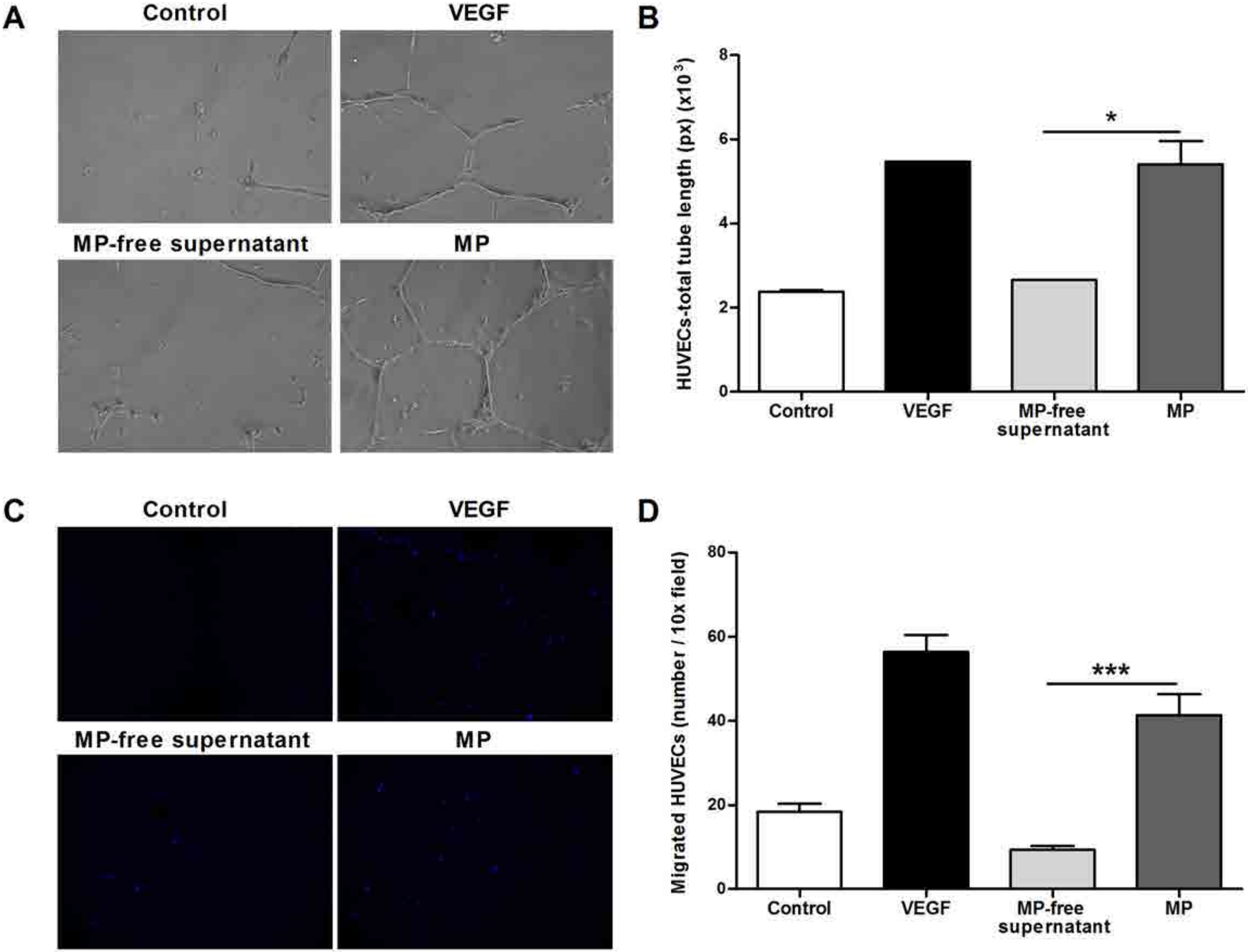
Supplemental Table 1. Identification of the whole hepatocytes-derived microparticles proteins based on the LC-MS/MS-derived sequences. Pure hepatocytes-derived microparticles were isolated and processed for a complete proteomics analysis as described in the 'Methods' paragraph. The proteins detected are listed in the table with the corresponding uniprot accession code, number of peptides, biological function and cellular localization.


1% BSA
0.25 mM Oleic acid
0.25 mM Palmitic acid
0.25 mM Stearic acid

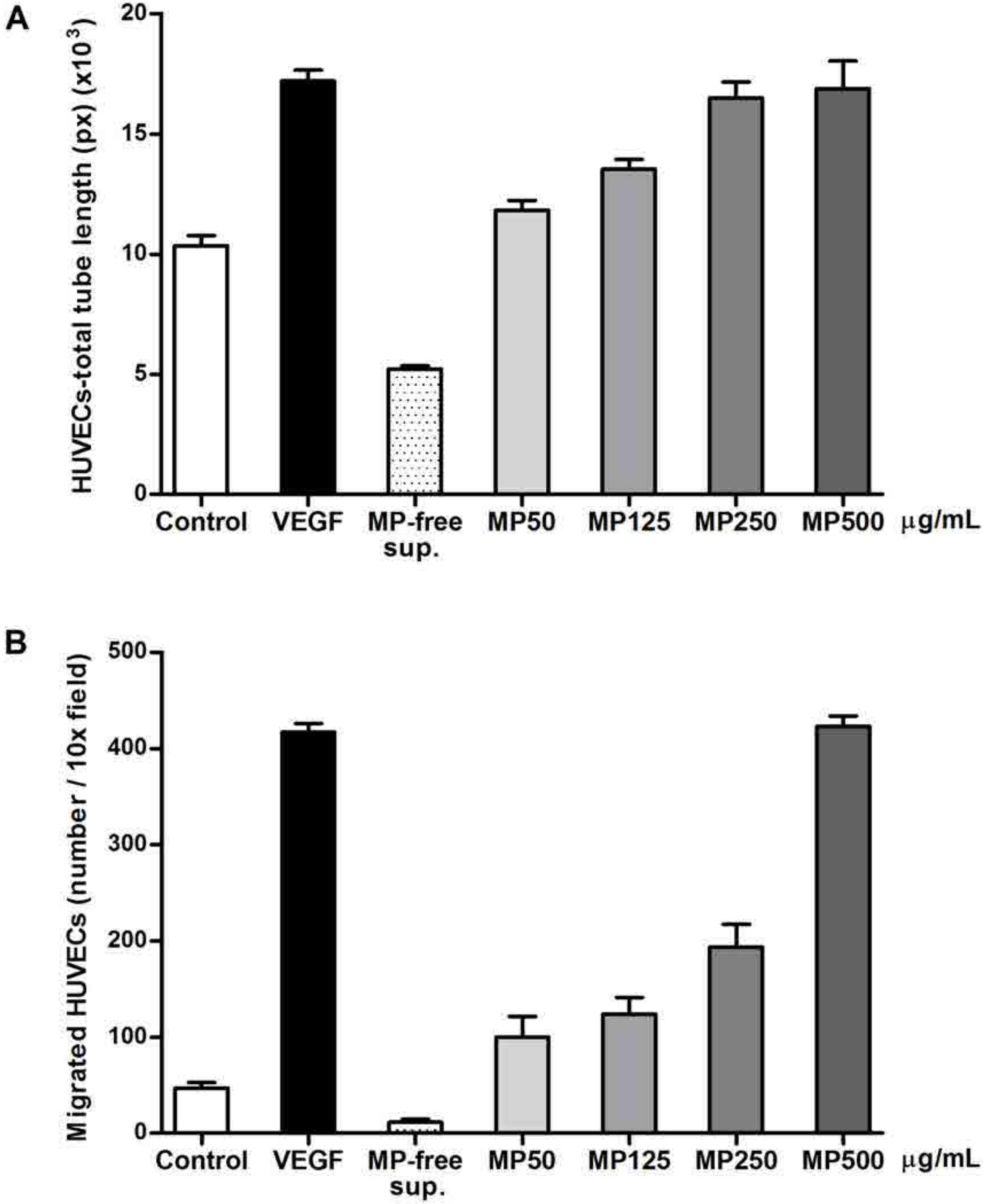

***
Number of AnnexinV$^+$ MPs / ml media (x10^3)
2.0
1.5
1.0
0.5
0.0
0.25 mM PA
0.25 mM OA
0.25 mM PA+OA


Cellular localization
Plasma membrane 7.9%
Cytoplasm 32.9%
Extracellular space 22.4%
Nucleus 5.3%

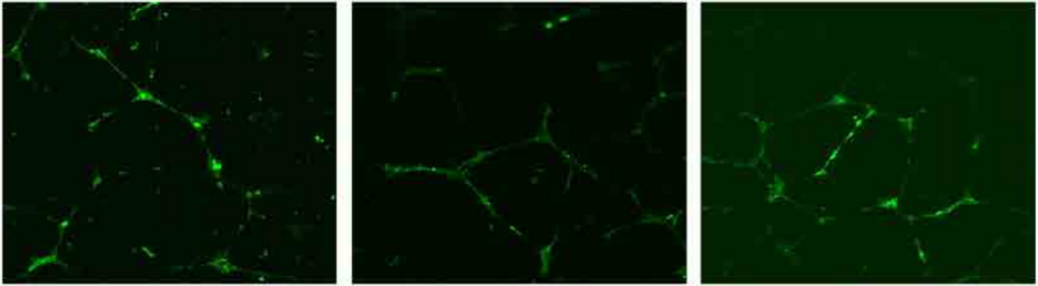

Molecular function
Extracellular matrix 2.6%
Others 5.3%
Ribonucleoproteins 1.3%
Enzymes/ Metabolism 32.9%
Nucleosomes 40.8%
Cytoskeleton/ Vesiculation 17.1%

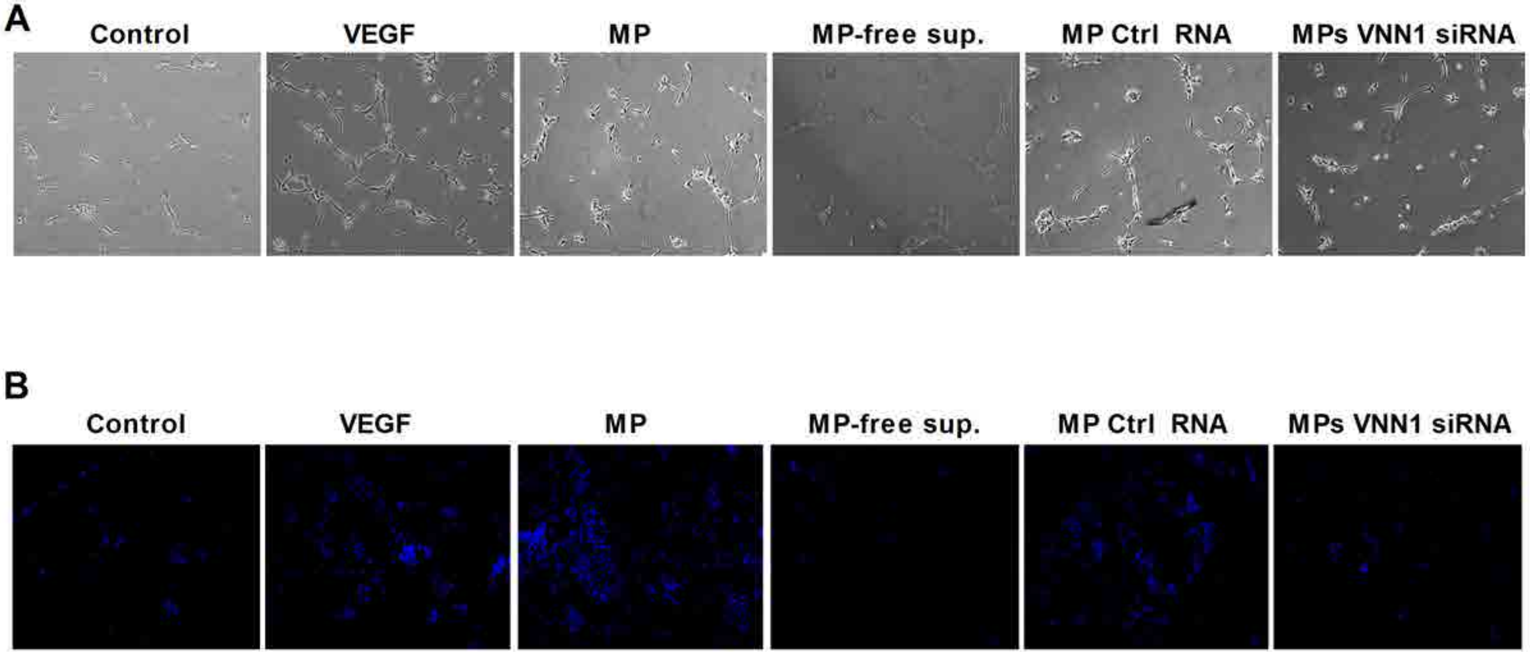


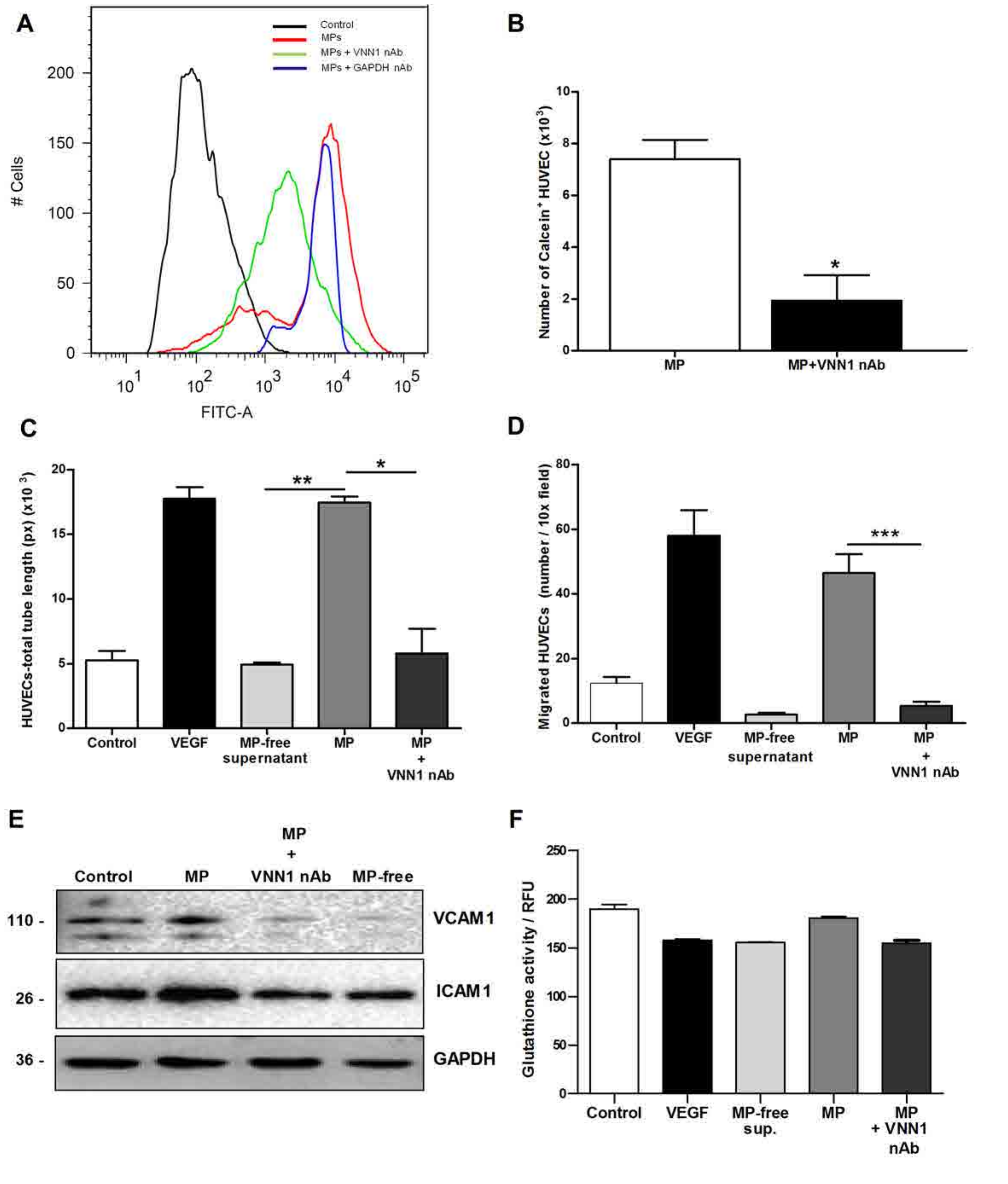
A
Control
VEGF
MP-free supernatant
MP
B
HUVECs-total tube length (px) (x10³)
8
6
4
2
0
*
Control
VEGF
MP-free supernatant
MP
C
Control
VEGF
MP-free supernatant
MP
D
Migrated HUVECs (number / 10x field)
80
60
40
20
0
***
Control
VEGF
MP-free supernatant
MP

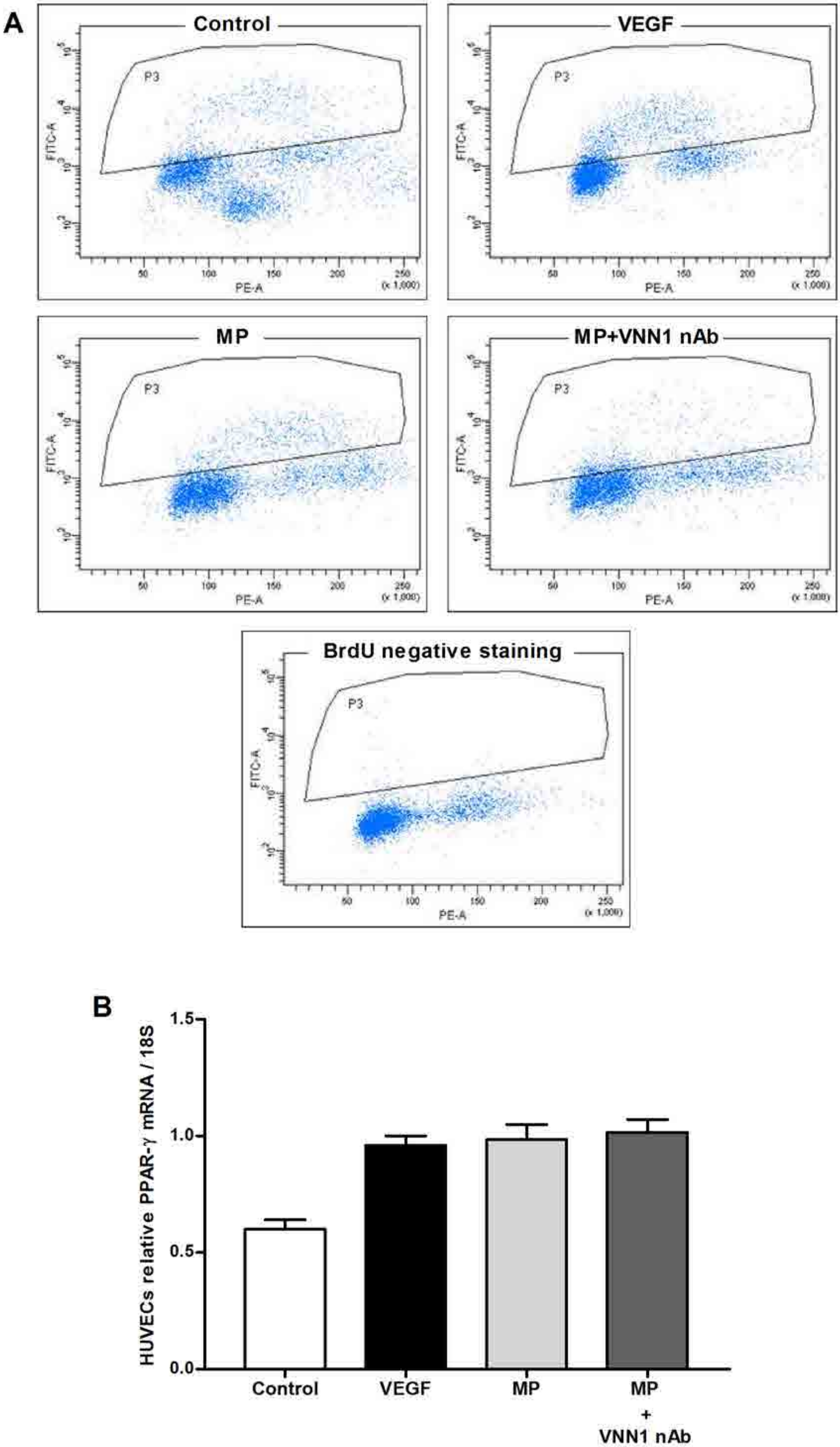

A
HUVECs-total tube length (px) (x10³)
20
15
10
5
0
Control
VEGF
MP-free sup.
MP50
MP125
MP250
MP500
μg/mL
B
Migrated HUVECs (number / 10x field)
500
400
300
200
100
0
Control
VEGF
MP-free sup.
MP50
MP125
MP250
MP500
μg/mL

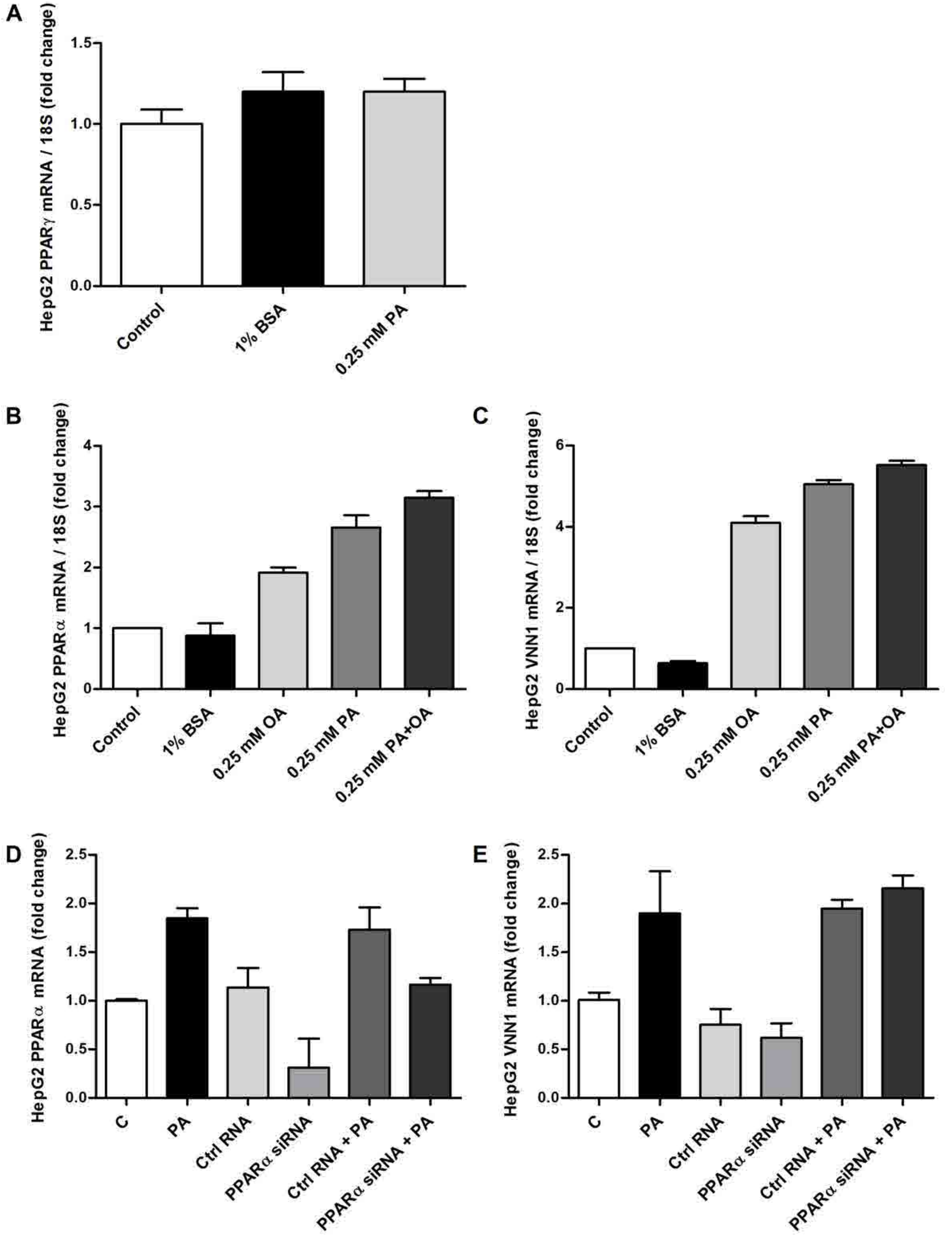
Calcein^{+} HUVECs tubes after treatment with MPs^{Calcein}

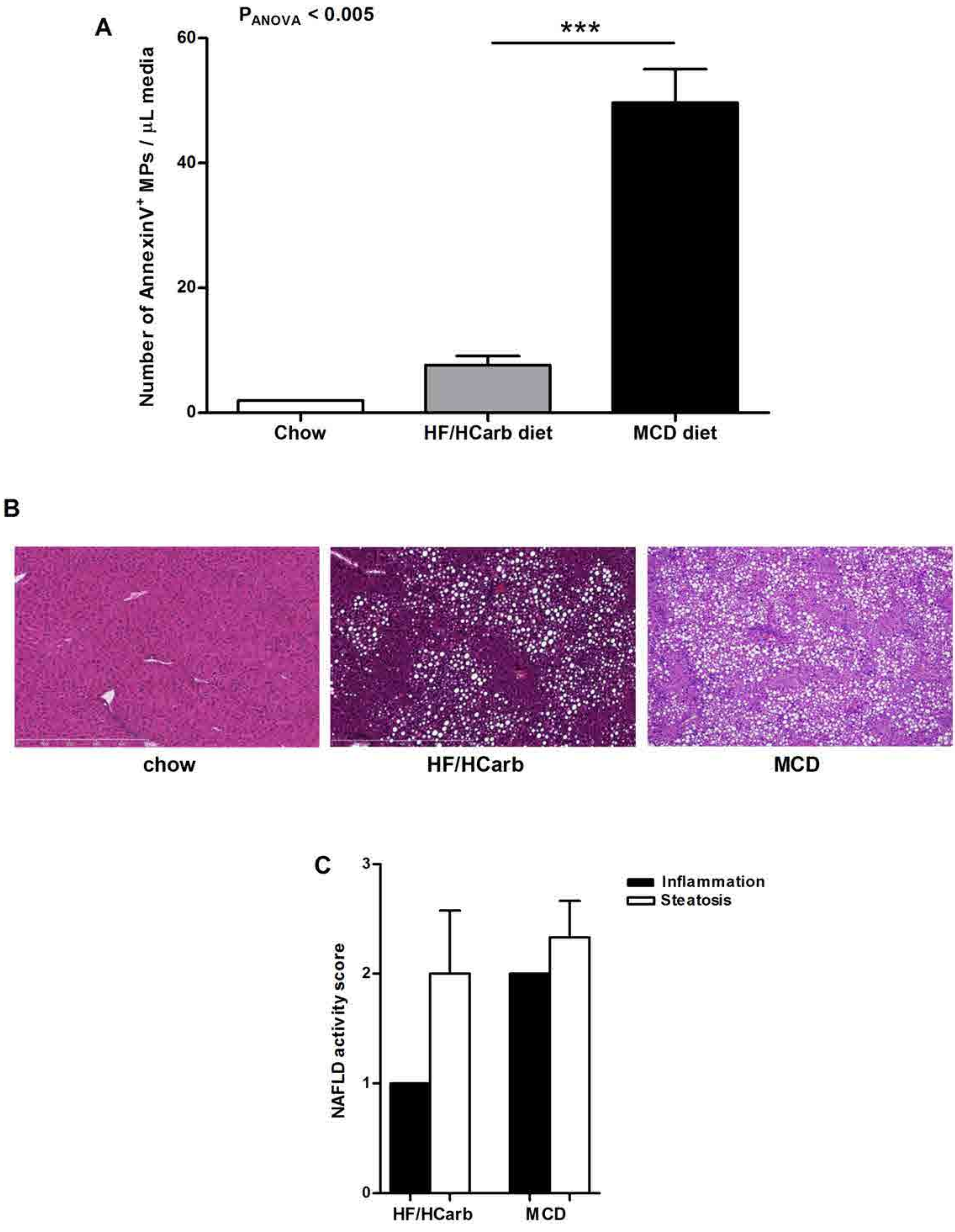


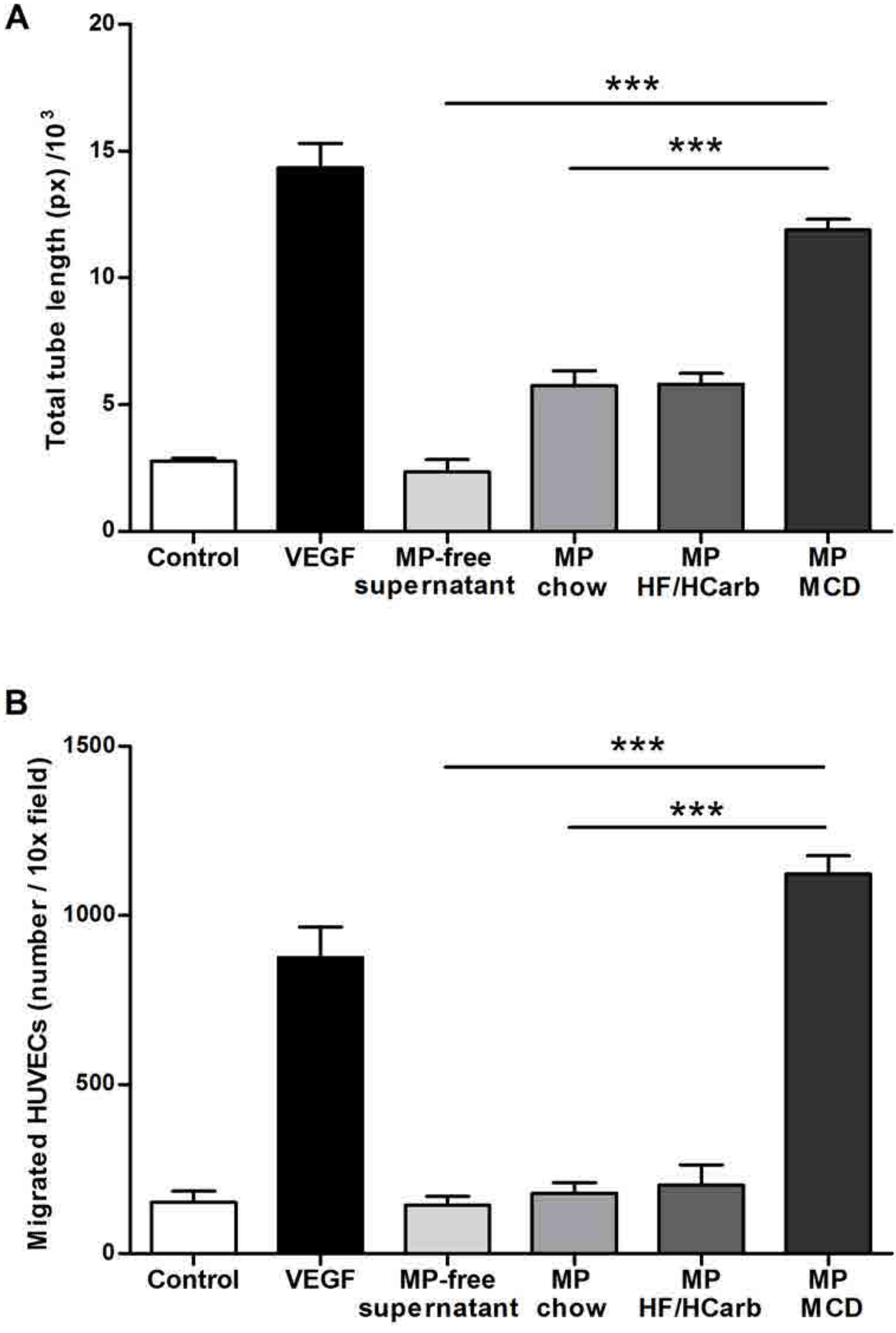

A
Control
VEGF
MP
MP-free sup.
MP Ctrl RNA
MPs VNN1 siRNA
B
Control
VEGF
MP
MP-free sup.
MP Ctrl RNA
MPs VNN1 siRNA

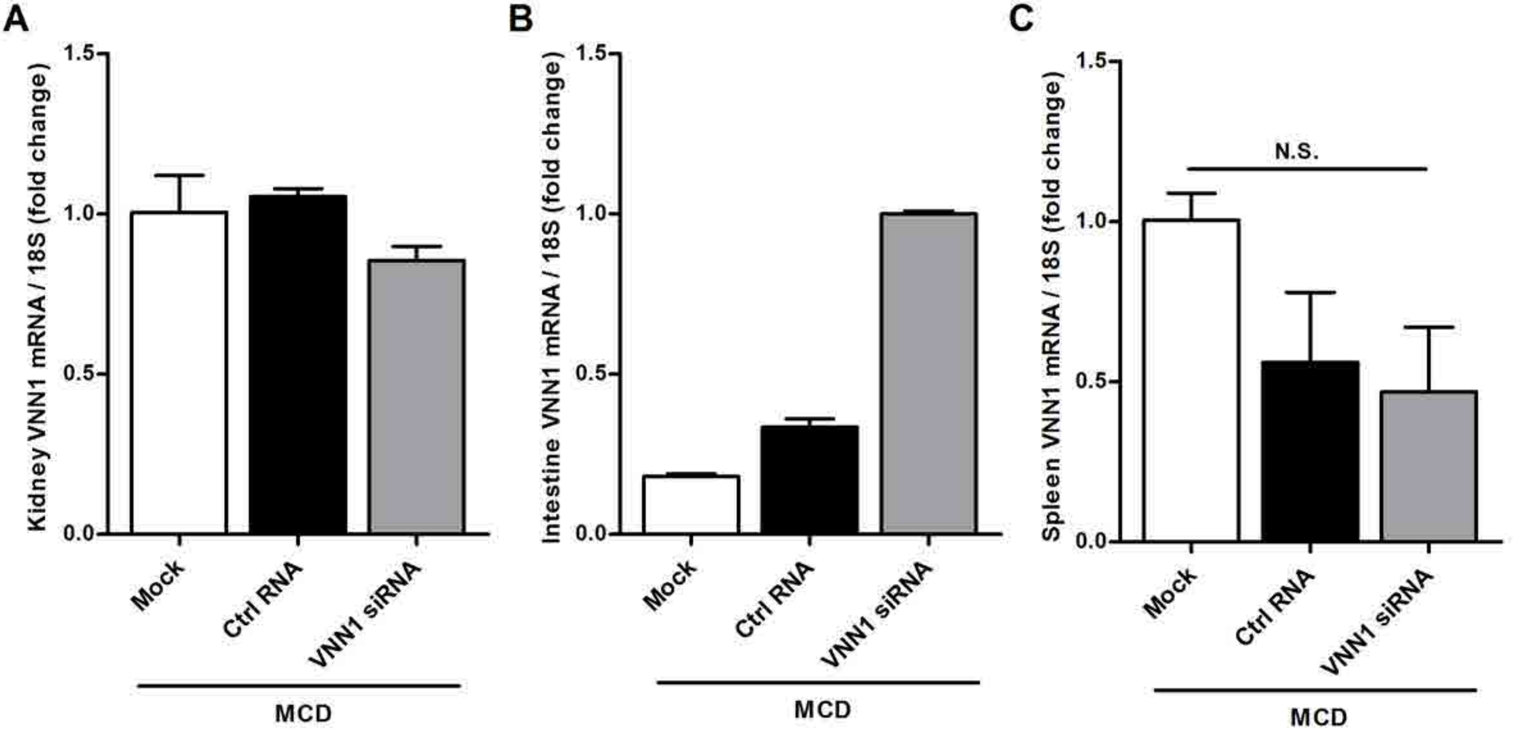

A
Control
MPs
MPs + VNN1 nAb
MPs + GAPDH nAb
Cells
FITC-A
B
Number of Calcein+ HUVEC (x10^3)
MP
MP+VNN1 nAb
C
HUVECs-total tube length (px) (x10^3)
Control
VEGF
MP-free supernatant
MP
MP + VNN1 nAb
D
Migrated HUVECs (number / 10x field)
Control
VEGF
MP-free supernatant
MP
MP + VNN1 nAb
E
Control
MP
MP + VNN1 nAb
MP-free
VCAM1
ICAM1
GAPDH
110 -
26 -
36 -
F
Glutathione activity / RFU
Control
VEGF
MP-free sup.
MP
MP + VNN1 nAb


A
Control
VEGF
MP
MP+VNN1 nAb
BrdU negative staining
P3
FITC-A
PE-A
(x 1,000)
B
HUVECs relative PPAR-γ mRNA / 18S
1.5
1.0
0.5
0.0
Control
VEGF
MP
MP
+
VNN1 nAb

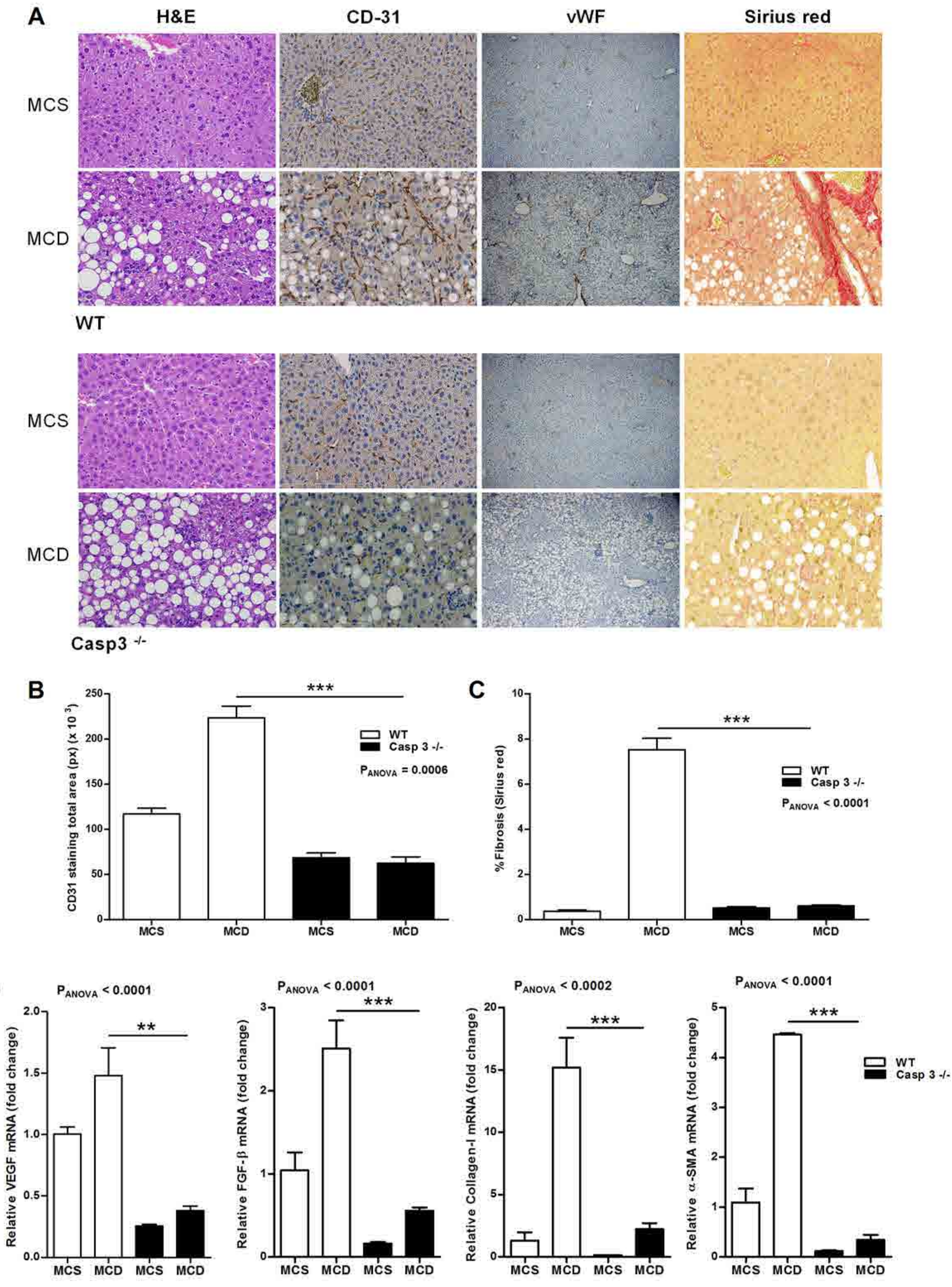

A
HepG2 PPARγ mRNA / 18S (fold change)
0.0
0.5
1.0
1.5
Control
1% BSA
0.25 mM PA
B
HepG2 PPARα mRNA / 18S (fold change)
0
1
2
3
4
Control
1% BSA
0.25 mM OA
0.25 mM PA
0.25 mM PA+OA
C
HepG2 VNN1 mRNA / 18S (fold change)
0
2
4
6
Control
1% BSA
0.25 mM OA
0.25 mM PA
0.25 mM PA+OA
D
HepG2 PPARα mRNA (fold change)
0.0
0.5
1.0
1.5
2.0
2.5
C
PA
Ctrl RNA
PPARα siRNA
Ctrl RNA + PA
PPARα siRNA + PA
E
HepG2 VNN1 mRNA (fold change)
0.0
0.5
1.0
1.5
2.0
2.5
C
PA
Ctrl RNA
PPARα siRNA
Ctrl RNA + PA
PPARα siRNA + PA


A
P ANOVA < 0.005
***
60
40
20
0
Number of AnnexinV+ MPs / μL media
Chow
HF/HCarb diet
MCD diet
B
chow
HF/HCarb
MCD
C
3
2
1
0
NAFLD activity score
Inflammation
Steatosis
HF/HCarb
MCD


A
Total tube length (px) /10^3
20
15
10
5
0
***
***
Control
VEGF
MP-free supernatant
MP chow
MP HF/HCarb
MP MCD
B
Migrated HUVECs (number / 10x field)
1500
1000
500
0
***
***
Control
VEGF
MP-free supernatant
MP chow
MP HF/HCarb
MP MCD



A
Kidney VNN1 mRNA / 18S (fold change)
1.5
1.0
0.5
0.0
Mock
Ctrl RNA
VNN1 siRNA
MCD
B
Intestine VNN1 mRNA / 18S (fold change)
1.5
1.0
0.5
0.0
Mock
Ctrl RNA
VNN1 siRNA
MCD
C
Spleen VNN1 mRNA / 18S (fold change)
1.5
1.0
0.5
0.0
N.S.
Mock
Ctrl RNA
VNN1 siRNA
MCD



A
H&E
CD-31
vWF
Sirius red
MCS
MCD
WT
MCS
MCD
Casp3 -/-
B
CD31 staining total area (px) (x 10 3)
250
200
150
100
50
0
MCS
MCD
MCS
MCD
***
WT
Casp 3 -/-
PANOVA = 0.0006
C
%Fibrosis (Sirius red)
10
8
6
4
2
0
MCS
MCD
MCS
MCD
***
WT
Casp 3 -/-
PANOVA < 0.0001
D
PANOVA < 0.0001
Relative VEGF mRNA (fold change)
2.0
1.5
1.0
0.5
0.0
**
MCS
MCD
MCS
MCD
PANOVA < 0.0001
Relative FGF-β mRNA (fold change)
3
2
1
0
***
MCS
MCD
MCS
MCD
PANOVA < 0.0002
Relative Collagen-I mRNA (fold change)
20
15
10
5
0
***
MCS
MCD
MCS
MCD
PANOVA < 0.0001
Relative α-SMA mRNA (fold change)
5
4
3
2
1
0
***
MCS
MCD
MCS
MCD
WT
Casp 3 -/-

Supplementary Table 1. IdentificationIdentification of the whole hepatocytes-derived microparticles proteins based on the LC-MS/MS-derived sequences

Protein name	Accession code	Number of peptides	Molecular function	Biological process	Cellular localization
CYTOSKELETON / VESICULATION / ENDOCYTOSIS					
Tubulin, alpha, ubiquitous	gi|57013276	2	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, alpha 1a	gi|17986283	2	Nucleotide binding	Mitosis / transport / protein folding / cytoskeleton organisation	Cytoplasm
Tubulin alpha 6	gi|14389309	2	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, alpha 3e	gi|46409270	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, alpha 3c	gi|17921993	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, alpha 3d	gi|156564363	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta, 2	gi|5174735	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta	gi|29788785	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta 8	gi|42558279	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta 2B	gi|29788768	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta 4	gi|21361322	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta polypeptide 4, member Q	gi|55770868	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
Tubulin, beta 6	gi|14210536	1	Nucleotide binding	Cytoskeleton organisation	Cytoplasm
ENZYMES / METABOLIC PROCESSES					
Albumin precursor	gi|4502027	42	Protein binding	Transport / response to stress / lipid metabolism	Extracellular space/ cytoplasm
Maltase-glucoamylase	gi|4758712	25	Glucosidase	Carbohydrate metabolism	Plasma membrane
Ceruloplasmin precursor	gi|4557485	55	Ferroxidase	Ion transport	Extracellular space

Apolipoprotein E precursor	gi|4557325	6	Lipid/protein binding	Lipid metabolism	Extracellular space / cytoplasm
Amine oxidase, copper containing 3 precursor	gi|4502119	12	Oxidase / binding	Catecholamine metabolism / adhesion / inflammation	Cytoplasm / plasma membrane
Vitamin D-binding protein precursor	gi|32483410	7	Protein binding	Vitamin D transport	Extracellular space
Isocitrate dehydrogenase 1 (NADP+), soluble	gi|28178825	4	Dehydrogenase	Isocitrate oxidative decarboxylation	Cytoplasm / mitochondrion / peroxisome
Fumarylacetoacetate hydrolase	gi|4557587	5	Hydrolase	Tyrosine catabolism	Cytoplasm
Apolipoprotein A-I preproprotein	gi|4557321	3	Lipid/protein binding	Lipid metabolism / platelet activation / endothelial cell proliferation	Extracellular space / cytoplasm / plasma membrane
Vanin-1 precursor	gi|4759312	3	Hydrolase / GPI anchor binding	Inflammatory response / anti-apoptosis / adhesion / cell migration	Plasma membrane
Eukaryotic translation elongation factor 1 alpha 1	gi|4503471	2	Nucleotide binding	Transcription / translation regulation	Cytoplasm / Nucleus
Clustein isoform 2	gi|42740907	2	ATPase / misfolded protein binding	Apoptosis regulation	Extracellular space / cytoplasm / mitochondrion
Clusterin isoform 1	gi|42716297	2	ATPase / misfolded protein binding	Apoptosis regulation	Extracellular space / cytoplasm / mitochondrion
Haptoglobin	gi|4826762	2	Catalytic activity	Hemoglobin binding / catabolic process	Extracellular space
Haptoglobin-related protein	gi|45580723	1	Catalytic activity	Hemoglobin binding	Extracellular space
Glyceraldehyde-3-phosphate dehydrogenase	gi|7669492	3	Dehydrogenase	Glycolisis	Cytoplasm
Dipeptidylpeptidase IV	gi|18765694	1	Aminopeptidase	Endothelial cell migration / adhesion / proteolysis	Plasma membrane / Golgi apparatus
Alpha 1 globin	gi|4504347	1	Transporter	Oxygen transport	Extracellular space
Alpha 2 globin	gi|4504345	1	Transporter	Oxygen transport	Extracellular space

Plasma glutamate carboxypeptidase	gi|7706387	3	Peptidase	Proteolysis	Cytoplasm / plasma membrane / nucleus
Eukaryotic translation elongation factor 1 alpha 2	gi|4503475	1	Nucleotide binding	Translation / anti-apoptosis	Cytoplasm / nucleus
Hornerin	gi|57864582	3	Isomerase	Tryptophan metabolic process	Extracellular space
Aspartate aminotransferase 1	gi|4504067	1	Transaminase	Amino acid degradation and biosynthesis	Cytoplasm
Lysozyme precursor	gi|4557894	1	Hydrolase / Lysozyme activity	Inflammatory response / cytolysis	Extracellular space
Serine (or cysteine) proteinase inhibitor, clade A, member 7	gi|4507377	1	Protein binding	Regulation of proteolysis	Extracellular space
RIBONUCLEOPROTEINS					
Ribosomal protein S10	gi|4506679	1	Protein binding	Translation	Nucleus
EXTRACELLULAR MATRIX					
Transforming growth factor, beta-induced, 68kDa	gi|4507467	3	Extracellular matrix binding	Angiogenesis / cell adhesion	Extracellular space
Vitronectin precursor	gi|88853069	2	Extracellular matrix binding	Cell-matrix adhesion / migration / integrin binding	Extracellular space
NUCLEOSOMES					
Histone cluster 2, H4b	gi|77539758	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 2, H4a	gi|4504323	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4i	gi|4504321	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4l	gi|4504317	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4e	gi|4504315	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4b	gi|4504313	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4h	gi|4504311	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4c	gi|4504309	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4k	gi|4504307	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4f	gi|4504305	2	DNA binding	Nucleosome assembly	Nucleus

Histone cluster 1, H4d	gi|4504303	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4a	gi|4504301	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 4, H4	gi|28173560	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H4j	gi|11415030	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 2, H2be	gi|4504277	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 3, H2bb	gi|28173554	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bj	gi|20336754	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bo	gi|16306566	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bb	gi|10800140	2	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 2, H2bf	gi|66912162	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bi	gi|4504271	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bh	gi|4504269	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bf	gi|4504265	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bm	gi|4504263	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bn	gi|4504261	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bl	gi|4504259	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bg	gi|4504257	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2be	gi|21396484	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bc	gi|21166389	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bd	gi|20336752	1	DNA binding	Nucleosome assembly	Nucleus
Histone cluster 1, H2bk	gi|18105048	1	DNA binding	Nucleosome assembly	Nucleus
OTHER PROTEINS					
Fibrinogen, alpha polypeptide isoform alpha-E preproprotein	gi|4503689	1	Protein binding	Coagulation	Extracellular space
Fibrinogen, alpha polypeptide isoform alpha preproprotein	gi|11761629	1	Protein binding	Coagulation	Extracellular space
Chemokine (C-C motif) ligand 20	gi|4759076	1	Chemokine	Chemotaxis / inflammation / signal transduction	Extracellular space
Growth differentiation factor 15	gi|153792495	1	Growth factor (TGF-β family)	Inflammation response / apoptosis	Cytoplasm