Supporting information

Lipid Surface Modifications Increases Mesoporous Silica Nanoparticles Labeling Properties in Mesenchymal Stem Cells

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Table S1. Significantly up and down-regulated proteins found in MSN labelled hMSCs compared to control cells (protein discoverer, cut-off is >1,5 fold and < 0,5).

Accession number	Protein name	fold-change	p-value
Q9Y618-1	Nuclear receptor corepressor 2	3,437	5,1E-07
Q14192-2	Isoform 2 of Four and a half LIM domains protein 2	2,644	2,3E-08
P02656	Apolipoprotein C-III	2,17	8,8E-07
P51397	Death-associated protein 1	2,119	5,1E-07
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	2,037	6,6E-03
P01344	Insulin-like growth factor II	2,016	5,7E-06
Q96Q89-1	Kinesin-like protein KIF20B	1,822	8,0E-07
O14983	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	1,793	7,4E-05
Q5BKZ1	DBIRD complex subunit ZNF326	1,741	1,1E-01
O75531	Barrier-to-autointegration factor	1,732	7,0E-04
P02458-2	Collagen alpha-1(II) chain	1,707	8,9E-02
Q76M96-2	Isoform 2 of Coiled-coil domain-containing protein 80	1,686	9,1E-02
Q76M96-1	Coiled-coil domain-containing protein 80	1,686	9,1E-02
Q7RTV0	PHD finger-like domain-containing protein 5A	1,669	5,4E-02
Q6P1N9-1	Putative deoxyribonuclease TATDN1	1,609	1,8E-01
Q96N16-5	Isoform 5 of Janus kinase and microtubule-interacting protein 1	1,584	1,3E-01
Q96N16-2	Isoform 2 of Janus kinase and microtubule-interacting protein 1	1,584	1,3E-01
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	1,508	1,8E-03
Q13564-1	NEDD8-activating enzyme E1 regulatory subunit	0,499	7,2E-03
P42677	40S ribosomal protein S27	0,495	7,8E-13
P29558-1	RNA-binding motif, single-stranded-interacting protein 1	0,494	4,1E-07
O60256-1	Phosphoribosyl pyrophosphate synthase-associated protein 2	0,493	7,1E-03
Q14558	Phosphoribosyl pyrophosphate synthase-associated protein 1	0,493	7,1E-03
P62244	40S ribosomal protein S15a	0,49	3,5E-09
Q9NRY4	Rho GTPase-activating protein 35	0,489	1,8E-02
P63173	60s ribosomal protein l38	0,477	2,7E-14
P30405-2	Isoform 2 of Peptidyl-prolyl cis-trans isomerase F, mitochondrial	0,473	5,9E-04
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	0,473	5,9E-04
Q6BAA4	Fc receptor-like B	0,473	5,9E-04
Q6NVY1	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	0,464	8,1E-03
Q58FG1	Putative heat shock protein HSP 90-alpha A4	0,453	7,5E-03
P07996	thrombospondin-1	0,451	4,1E-16
P61011-1	signal recognition particle 54 kDa protein	0,427	3,4E-04
Q9NP77	RNA polymerase II subunit A C-terminal domain phosphatase SSU72	0,418	1,4E-03
P62701	40S ribosomal protein S4, X isoform	0,418	4,1E-16
Q8TD47	40S ribosomal protein S4, Y isoform 2	0,411	4,1E-16
P17096-2	Isoform HMG-Y of High mobility group protein HMG-I/HMG-Y	0,41	1,3E-05
P22090	40S ribosomal protein S4, Y isoform 1	0,386	4,1E-16
P62269	40S ribosomal protein S18	0,358	4,1E-16
P62280	40S ribosomal protein S11	0,337	4,1E-16
P62277	40S ribosomal protein S13	0,322	4,1E-16
P39019	40S ribosomal protein S19	0,312	4,1E-16
P62249	40S ribosomal protein S16	0,258	4,1E-16

Q99962	Endophilin-A1	0,25	5,3E-11

Table S2. Significantly up and down-regulated proteins found in MSN-LIP labelled hMSCs compared to control cells (protein discoverer, cut-off is >1,5 fold and < 0,5).

Accession number	**protein name**	**fold change**	**p-value**
Q9Y618-1	Nuclear receptor corepressor 2	5,114	3,5E-16
Q14192-2	Isoform 2 of Four and a half LIM domains protein 2	3,678	2,01E-11
Q06828	Fibromodulin	2,586	3,76E-06
Q13308-5	Isoform 5 of Inactive tyrosine-protein kinase 7	2,383	3,87E-05
Q15369-2	Isoform 2 of Transcription elongation factor B polypeptide 1	2,197	0,000297
P22626-2	Isoform A2 of Heterogeneous nuclear ribonucleoproteins A2/B1	2,132	0,000605
Q16629	serine/arginine-rich splicing factor 7	2,11	0,00074
Q99962	Endophilin-A1	2,047	0,001452
Q13595-1	Transformer-2 protein homolog alpha	2,038	0,001581
Q96Q89-1	Kinesin-like protein KIF20B	2,017	0,00195
P51397	Death-associated protein 1	1,991	0,00256
Q9NPQ8-3	Isoform 3 of Synembryn-A	1,921	0,004918
O14983	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	1,907	0,005548
P09012	U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A	1,9	0,005804
Q9UNH7-2	Isoform 2 of Sorting nexin-6	1,84	0,010167
Q96N16-5	Isoform 5 of Janus kinase and microtubule-interacting protein 1	1,825	0,011733
Q96N16-2	Isoform 2 of Janus kinase and microtubule-interacting protein 1	1,825	0,011733
P29354-1	Growth factor receptor-bound protein 2	1,781	0,017536
P62993-2	Isoform 2 of Growth factor receptor-bound protein 2	1,781	0,017536
Q8WUD1	Ras-related protein Rab-2B	1,738	0,026806
Q9HAU6	Putative translationally-controlled tumor protein-like protein TPT1P8	1,678	0,046673
P14735	insulin-degrading enzyme	0,499	0,001034
Q14651	Plastin-1	0,494	0,000817
P25445-1	Tumor necrosis factor receptor superfamily member 6	0,492	0,000741
Q9H694-1	Protein bicaudal C homolog 1	0,492	0,000747
Q13564-1	NEDD8-activating enzyme E1 regulatory subunit	0,491	0,000737
P53611	Geranylgeranyl transferase type-2 subunit beta	0,491	0,00074
Q8WXF1	Paraspeckle component 1	0,489	0,000678
Q14568	Heat shock protein HSP 90-alpha A2	0,489	0,00067
Q9UMX5	Neudesin	0,488	0,000649
P04181-2	Isoform 2 of Ornithine aminotransferase, mitochondrial	0,487	0,000628
Q9H254	Spectrin beta chain, non-erythrocytic 4	0,482	0,000495
P18085	ADP-ribosylation factor 4	0,473	0,000302
Q15287-1	RNA-binding protein with serine-rich domain 1	0,472	0,000297
Q96IU4-2	Isoform 2 of Protein ABHD14B	0,467	0,000229
P09960-2	Isoform 2 of Leukotriene A-4 hydrolase	0,467	0,000229
P09960-3	Isoform 3 of Leukotriene A-4 hydrolase	0,467	0,000229
P07951-1	Tropomyosin beta chain	0,455	0,000115

P06703	protein S100-A6	0,453	0,000105
P80723-2	Isoform 2 of Brain acid soluble protein 1	0,453	0,000105
Q5JTH9-1	RRP12-like protein	0,452	0,000104
P63167	Dynein light chain 1, cytoplasmic	0,451	9,52E-05
P62328	Thymosin beta-4	0,45	9,25E-05
Q8N556-2	Isoform 2 of Actin filament-associated protein 1	0,449	8,77E-05
Q8N556-1	actin filament-associated protein 1	0,449	8,77E-05
P54132	Bloom syndrome protein	0,448	8,2E-05
O94919	endonuclease domain-containing 1 protein	0,447	7,89E-05
P67809	Nuclease-sensitive element-binding protein 1	0,438	4,47E-05
Q9Y224	UPF0568 protein C14orf166	0,432	3,14E-05
Q5JXB2	Putative ubiquitin-conjugating enzyme E2 N-like	0,429	2,57E-05
O43852-9	Isoform 9 of Calumenin	0,423	1,76E-05
Q5T1M5	FK506-binding protein 15	0,403	4,3E-06
Q9P299	coatomer subunit zeta-2	0,399	3,14E-06
O95399	Urotensin-2	0,397	2,9E-06
P06454-1	Prothymosin alpha	0,391	1,7E-06
P06454-2	Isoform 2 of Prothymosin alpha	0,391	1,7E-06
P16989-3	Isoform 3 of Y-box-binding protein 3	0,388	1,45E-06
P63172	Dynein light chain Tctex-type 1	0,378	6,41E-07
Q9NS69	Mitochondrial import receptor subunit TOM22 homolog	0,377	5,59E-07
O43237	Cytoplasmic dynein 1 light intermediate chain 2	0,376	5,12E-07
P29536-1	Leiomodin-1	0,374	4,47E-07
O60762	Dolichol-phosphate mannosyltransferase subunit 1	0,373	3,97E-07
P51858-3	Isoform 3 of Hepatoma-derived growth factor	0,369	2,94E-07
Q5JSH3	WD repeat-containing protein 44	0,369	2,9E-07
Q58FF8	Putative heat shock protein HSP 90-beta 2	0,357	9,81E-08
Q969X5	Endoplasmic reticulum-Golgi intermediate compartment protein 1	0,355	8,54E-08
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	0,333	9,48E-09
O00193	Small acidic protein	0,331	8,44E-09
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	0,329	6,69E-09
Q13217	DnaJ homolog subfamily C member 3	0,322	3,07E-09
P29966	Myristoylated alanine-rich C-kinase substrate	0,312	9,5E-10
Q32MZ4-4	Isoform 4 of Leucine-rich repeat flightless-interacting protein 1	0,311	8,5E-10
O00232-1	26s proteasome non-atpase regulatory subunit 12	0,299	1,97E-10
P30405-2	Isoform 2 of Peptidyl-prolyl cis-trans isomerase F, mitochondrial	0,296	1,39E-10
P30405	Peptidyl-prolyl cis-trans isomerase F, mitochondrial	0,296	1,39E-10
Q6BAA4	Fc receptor-like B	0,296	1,39E-10
O75410-8	Isoform 8 of Transforming acidic coiled-coil-containing protein 1	0,292	7,39E-11
O75607	Nucleoplasmin-3	0,286	3,63E-11
O95319-1	CUGBP Elav-like family member 2	0,269	2,99E-12
O95319-5	Isoform 5 of CUGBP Elav-like family member 2	0,269	2,99E-12
O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal	0,264	1,43E-12
Q58FG0	Putative heat shock protein HSP 90-alpha A5	0,253	2,05E-13
P60903	Protein S100-A10	0,23	3,5E-16

P84101-3	Isoform 3 of Small EDRK-rich factor 2	0,226	3,5E-16

Table S3. Significantly up and down-regulated proteins found in MSN-PEG2000 labelled hMSCs compared to control cells (protein discoverer, cut-off is >1,5 fold and < 0,5).

Accession number	protein name	fold change	p-value
Q13308-5	Isoform 5 of Inactive tyrosine-protein kinase 7	2,467	7,51E-08
Q96Q89-1	Kinesin-like protein KIF20B	1,904	2,63E-09
Q9Y618-1	Nuclear receptor corepressor 2	1,888	0,014032
Q16629	serine/arginine-rich splicing factor 7	1,865	6E-06
Q15369-2	Isoform 2 of Transcription elongation factor B polypeptide 1	1,819	2,08E-09
Q96N16-5	Isoform 5 of Janus kinase and microtubule-interacting protein 1	1,728	0,004393
Q96N16-2	Isoform 2 of Janus kinase and microtubule-interacting protein 1	1,728	0,004393
P51397	Death-associated protein 1	1,696	0,000561
Q9HAU6	Putative translationally-controlled tumor protein-like protein TPT1P8	1,69	3,03E-05
P61077-1	Ubiquitin-conjugating enzyme E2 D3	1,673	3,11E-05
Q86UE4	protein LYRIC	1,579	0,040764
P28065	Proteasome subunit beta type-9	1,554	0,010654
P54727-2	Isoform 2 of UV excision repair protein RAD23 homolog B	1,532	0,000985
P29354-1	Growth factor receptor-bound protein 2	1,513	0,008493
P62993-2	Isoform 2 of Growth factor receptor-bound protein 2	1,513	0,008493
Q58FF6	Putative heat shock protein HSP 90-beta 4	1,511	0,000188
Q969E4	transcription elongation factor A protein-like 3	0,464	2,5E-10
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	0,463	3,5E-05
Q9H254	Spectrin beta chain, non-erythrocytic 4	0,46	3,22E-16
O75607	Nucleoplasmin-3	0,447	2,11E-05
P06454-1	Prothymosin alpha	0,444	3,22E-16
P06454-2	Isoform 2 of Prothymosin alpha	0,444	3,22E-16
P60903	Protein S100-A10	0,438	3,22E-16
P10915	Hyaluronan and proteoglycan link protein 1	0,414	3,22E-16
Q13242	serine/arginine-rich splicing factor 9	0,393	5,13E-12
Q32MZ4-4	Isoform 4 of Leucine-rich repeat flightless-interacting protein 1	0,369	1,06E-09
Q96G03	Phosphoglucomutase-2	0,287	3,22E-16

Table S4. Significantly up and down-regulated proteins found in MSN-PEG750 labelled hMSCs compared to control cells (protein discoverer, cut-off is >1,5 fold and < 0,5).

Accession number	protein name	fold change	p-value
Q5JSH3	WD repeat-containing protein 44	3,205	2,7E-07
Q9Y618-1	Nuclear receptor corepressor 2	2,455	3,0E-04
O75489	NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial	2,317	3,4E-04
O14602	Eukaryotic translation initiation factor 1A, Y-chromosomal	2,228	4,5E-05
Q96Q89-1	Kinesin-like protein KIF20B	1,99	8,0E-09
O95319-1	CUGBP Elav-like family member 2	1,916	1,1E-03
O95319-5	Isoform 5 of CUGBP Elav-like family member 2	1,916	1,1E-03

P06454-1	Prothymosin alpha	1,889	1,2E-09
P06454-2	Isoform 2 of Prothymosin alpha	1,889	1,2E-09
P62328	Thymosin beta-4	1,844	5,8E-09
P63172	Dynein light chain Tctex-type 1	1,769	6,5E-03
Q9Y608	Leucine-rich repeat flightless-interacting protein 2	1,717	1,4E-02
P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	1,701	1,1E-02
Q15287-1	RNA-binding protein with serine-rich domain 1	1,698	9,4E-03
P16989-3	Isoform 3 of Y-box-binding protein 3	1,673	1,3E-02
P60903	Protein S100-A10	1,633	6,6E-06
O75531	Barrier-to-autointegration factor	1,631	7,5E-03
P25445-1	Tumor necrosis factor receptor superfamily member 6	1,628	1,1E-01
Q9H254	Spectrin beta chain, non-erythrocytic 4	1,61	1,9E-05
P80723-2	Isoform 2 of Brain acid soluble protein 1	1,56	6,4E-05
P05114	Non-histone chromosomal protein HMG-14	1,56	4,4E-03
Q9UMX5	Neudesin	1,541	6,1E-03
O43852-9	Isoform 9 of Calumenin	1,507	3,0E-04
P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A	0,476	7,0E-09
P02656	Apolipoprotein C-III	0,476	4,8E-04
Q5VT25-1	Serine/threonine-protein kinase MRCK alpha	0,452	2,6E-03
Q09666-2	Isoform 2 of Neuroblast differentiation-associated protein AHNAK	0,444	1,7E-05
Q58FG1	Putative heat shock protein HSP 90-alpha A4	0,443	4,4E-03
P22692-2	Isoform 2 of Insulin-like growth factor-binding protein 4	0,439	2,9E-04
P22692	insulin-like growth factor-binding protein 4	0,439	2,9E-04
Q7L2H7	Eukaryotic translation initiation factor 3 subunit M	0,436	8,4E-05
Q7L2H7-2	Isoform 2 of Eukaryotic translation initiation factor 3 subunit M	0,425	1,5E-04
P07996	thrombospondin-1	0,416	3,3E-16
P68402-1	platelet-activating factor acetylhydrolase IB subunit beta	0,413	1,9E-07
Q9NRY4	Rho GTPase-activating protein 35	0,402	8,1E-04
Q9BRK5-2	Isoform 2 of 45 kDa calcium-binding protein	0,367	7,8E-05
P84101-3	Isoform 3 of Small EDRK-rich factor 2	0,302	5,2E-12
Q9Y6K9	NF-kappa-B essential modulator	0,254	4,7E-09

Table S5.Identified enriched molecular functions in MSN exposed hMSCs (STRING).

	#pathway ID	**pathway description**	**observed gene count**	**false discovery rate**
MSN	GO.0003735	structural constituent of ribosome	8	4.32e-09
	GO.0019843	rRNA binding	5	1.25e-06
	GO.0003723	RNA binding	10	0.00282
	GO.0004749	ribose phosphate diphosphokinase activity	2	0.0108
MSN-LIP	GO.0005198	structural molecule activity	11	0.00337
	GO.0005200	structural constituent of cytoskeleton	5	0.0251
MSN-PEG750	GO.0005198	structural molecule activity	7	0.000977

Table S6.Identified enriched cellular component in MSN exposed hMSCs (STRING).

	pathway ID	**pathway description**	**observed gene count**	**false discovery rate**
MSN	GO.0022627	cytosolic small ribosomal subunit	8	2.82e-14
	GO.0022626	cytosolic ribosome	9	3.36e-13
	GO.0015935	small ribosomal subunit	7	1.38e-10
	GO.0005840	ribosome	9	2.34e-10
	GO.0044391	ribosomal subunit	8	3.47e-10
	GO.0030529	ribonucleoprotein complex	9	3.7e-06
	GO.0005829	cytosol	14	0.000191
	GO.0002189	ribose phosphate diphosphokinase complex	2	0.00024
	GO.0005925	focal adhesion	5	0.00751
	GO.0032991	macromolecular complex	13	0.0297
MSN-LIP	GO.0005856	cytoskeleton	20	8.41e-05
	GO.0031988	membrane-bounded vesicle	27	8.41e-05
	GO.0044421	extracellular region part	28	8.41e-05
	GO.0044430	cytoskeletal part	17	8.41e-05
	GO.0070062	extracellular exosome	24	8.41e-05
	GO.0045111	intermediate filament cytoskeleton	8	9.9e-05
	GO.0005576	extracellular region	30	0.000123
	GO.0005737	cytoplasm	46	0.000596
	GO.0043232	intracellular non-membrane-bounded organelle	25	0.000663
	GO.0044446	intracellular organelle part	38	0.00183
	GO.0005882	intermediate filament	6	0.00222
	GO.0005868	cytoplasmic dynein complex	3	0.00873
	GO.0015629	actin cytoskeleton	7	0.015
	GO.0043234	protein complex	23	0.0224
	GO.0043229	intracellular organelle	45	0.0256
	GO.0044444	cytoplasmic part	34	0.0275
	GO.0005829	cytosol	20	0.0299
MSN-PEG750	GO.0070062	extracellular exosome	13	5.08e-06
	GO.0044421	extracellular region part	14	7.87e-06
	GO.0005576	extracellular region	14	4.67e-05
	GO.0045111	intermediate filament cytoskeleton	5	0.000264
	GO.0005856	cytoskeleton	9	0.00101
	GO.0005882	intermediate filament	4	0.00236
	GO.0043232	intracellular non-membrane-bounded organelle	11	0.00236

Table S7. Identical upregulated proteins identified in MSN labeled hMSCs

sample	**total**	**swissprot ID number and protein name**
MSN, MSN-LIP, MSN-LIPPEG2000, MSN-PEG2000, MSN-PEG750	1	Q9Y618-1Nuclear receptor corepressor 2
MSN, MSN-LIP, MSN-LIPPEG2000, MSN-PEG2000	2	Q96N16-2Isoform 2 of Janus kinase and microtubule-interacting protein 1
		Q96N16-5Isoform 5 of Janus kinase and microtubule-interacting protein 1
MSN, MSN-LIP, MSN-PEG2000, MSN-PEG750	1	Q96Q89-1Kinesin-like protein KIF20B
MSN, MSN-LIP, MSN-LIPPEG2000	2	Q14192-2Isoform 2 of Four and a half LIM domains protein 2
		O14983Sarcoplasmic/endoplasmic reticulum calcium ATPase 1
MSN, MSN-LIP, MSN-PEG2000	1	P51397Death-associated protein 1
MSN, MSN-LIPPEG2000, MSN-PEG750	2	O75489NADH dehydrogenase [ubiquinone] iron-sulfur protein 3
		O75531Barrier-to-autointegration factor
MSN-LIP, MSN-LIPPEG2000, MSN-PEG2000	1	Q13308-5Isoform 5 of Inactive tyrosine-protein kinase 7
MSN, MSN-LIPPEG2000	2	P02656Apolipoprotein C-III
		Q6P1N9-1Putative deoxyribonuclease TATDN1
MSN-LIP, MSN-LIPPEG2000	1	Q99962Endophilin-A1
MSN-LIP, MSN-PEG2000	7	P62993-2Isoform 2 of Growth factor receptor-bound protein 2
		Q9HAU6Putative translationally-controlled tumor protein-like protein TPT1P8
		Q15369-2Isoform 2 of Transcription elongation factor B polypeptide 1
		Q86UE4protein LYRIC
		Q16629serine/arginine-rich splicing factor 7
		P29354-1Growth factor receptor-bound protein 2
		P61077-1Ubiquitin-conjugating enzyme E2 D3
MSN-LIPPEG2000, MSN-PEG750	1	Q5JSH3WD repeat-containing protein 44

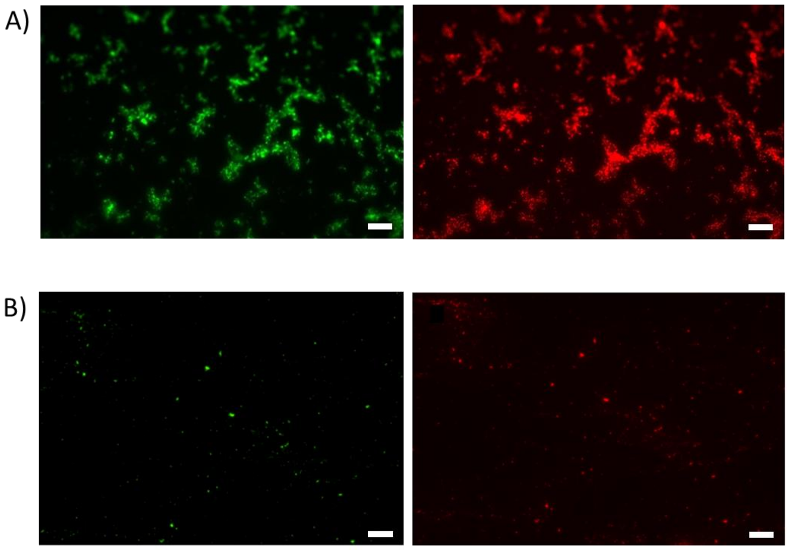

Figure S1. A) MSNs are functionalized on their surface with amine groups (labelled with FITC-NHS,green), and in their core with thiol groups (labeled with ATTO633 maleimide, red). B) Lipid bilayers are covering MSNs as shown by co-labeling; MSN labeled with ATTO633 maleimide (red) to the core thiol groups and lipid bilayer labeling by incorporating fluorescently tagged phospholipid in the lipid bilayer (green). Scale bar is 50 µm.

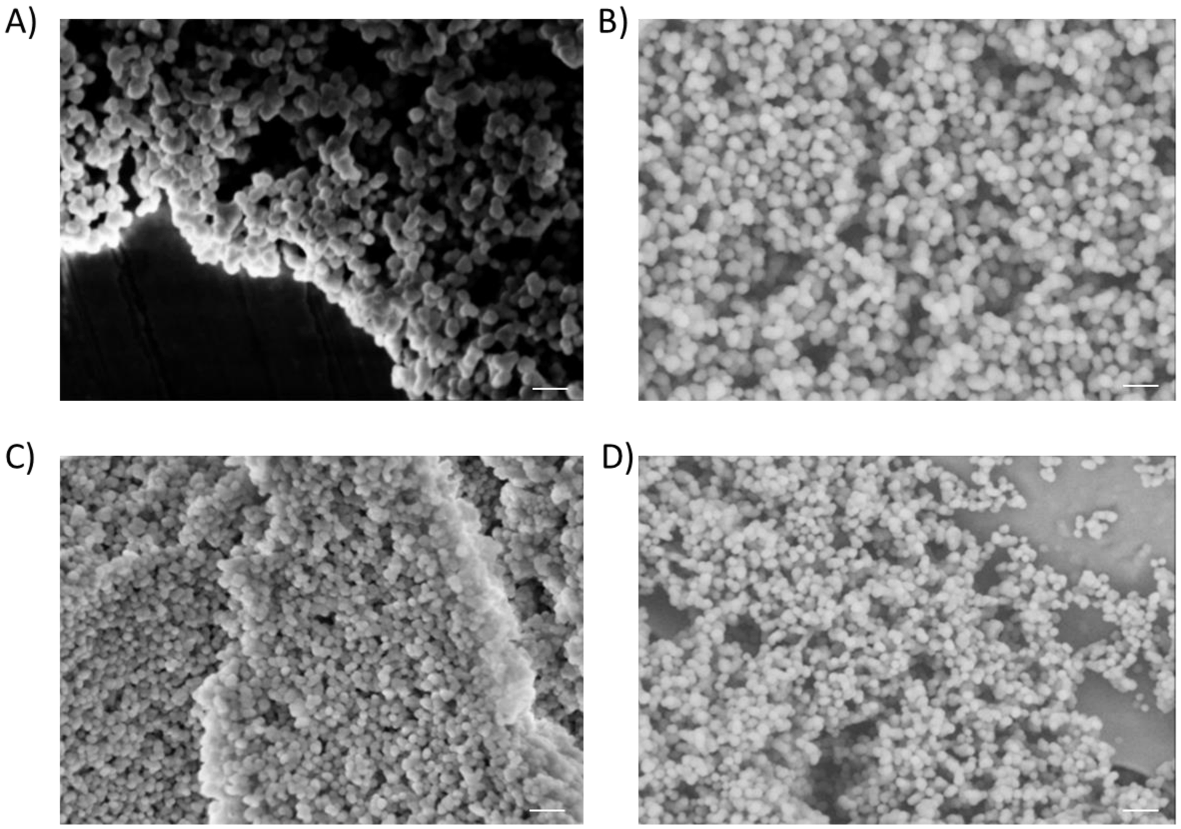

Figure S2. SEM images of A) MSN-LIP, B) MSN-LIP-PEG2000, C) MSN-PEG750 and D) MSN-PEG2000. Scale bar is 200 nm.

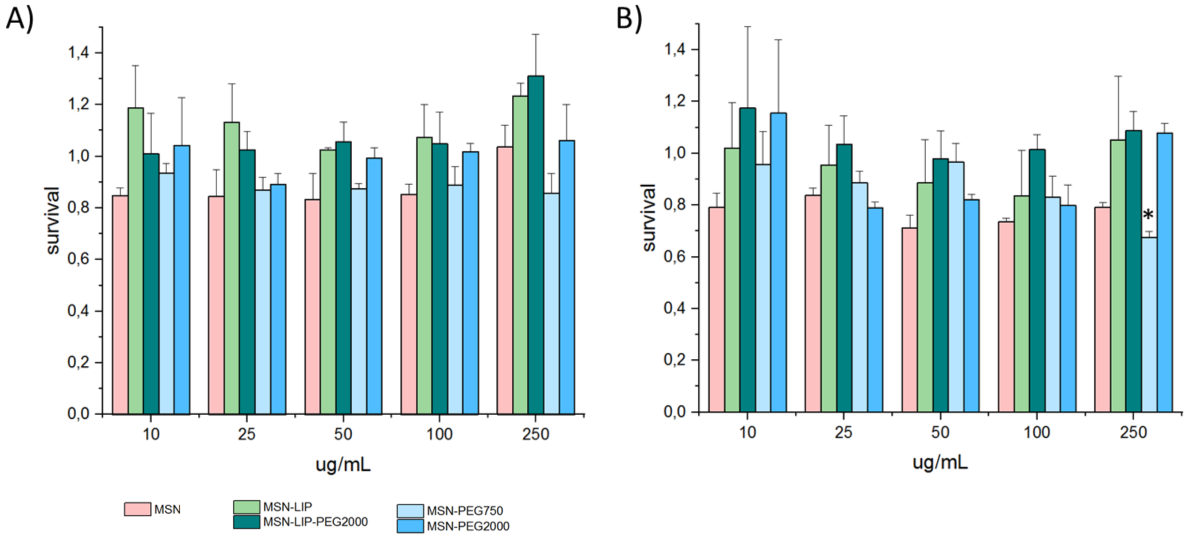

Figure S3. Effect of MSN labeling on hMSC cell metabolism (D313) using the MTT assay showing no dose-responsive effects on metabolic activity after; A) after 24 h of exposure and B) after 72 h of exposure. A small but significant decrease of cell survival was observed for hMSCs exposed to 250 µg/mL MSN-PEG750 (* $p<0.05$).

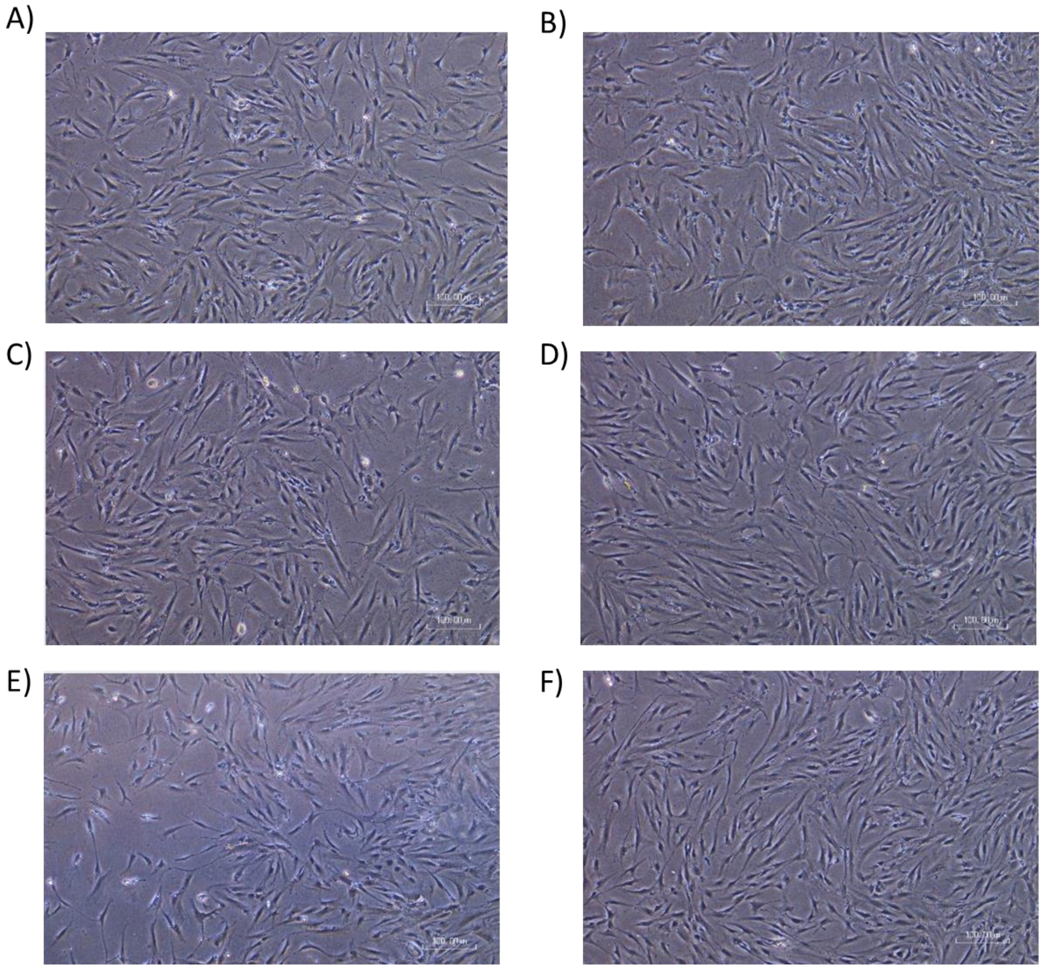

Figure S4. Light microscopy images taken from hMSCs exposed to MSNs (A), MSN-LIP (B), MSN-LIP-PEG2000 (C), MSN-PEG750 (D) and MSN-PEG2000 particles (E) at a concentration of 25 µg/mL for 24 hours. Control hMSCs are shown in F. Images were taken at a 4x magnification

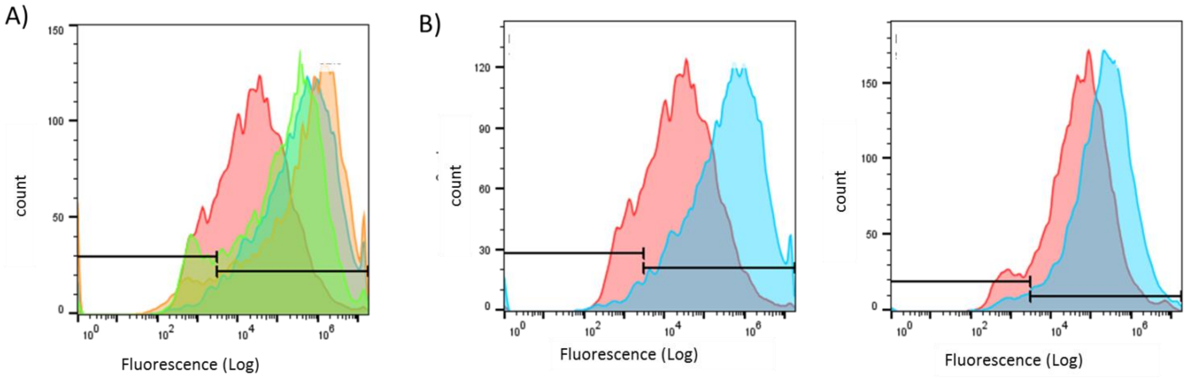

Figure S5. Flow cytometry histograms of A) hMSCs (D133A) exposed to MSN (red), MSN-PEG2000 (green), MSN-LIP-PEG2000 (orange) and MSN-LIP (blue) after 2h. B) hMSCs (D313) to MSN (red) and MSN-LIP (blue) after 2h (left) and 24h (right) .

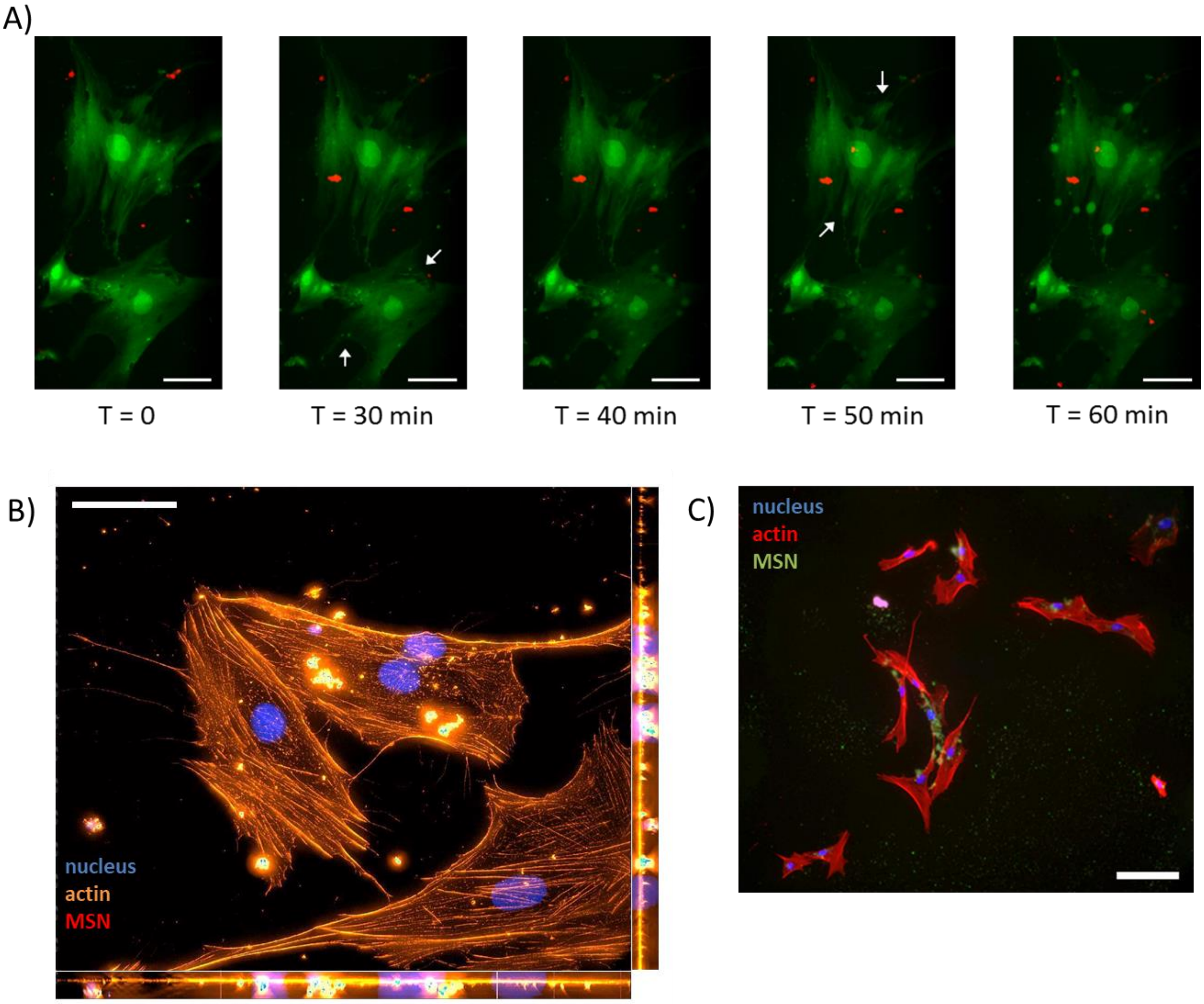

Figure S6. A) Live cell imaging of hMSCs stained with CellTracker (green). hMSCs were exposed to labelled MSNs (red) at a concentration of 25 µg/mL. T = 0 is directly after MSN exposure. Images were acquired at 30, 40, 50 and 60 minutes after MSN exposure using a 60x oil objective, scale bar is 50 µm. B) Maximum intensity projections of orthogonal views of hMSCs exposed to labeled MSNs (red), scale bar is 50 µm.C) hMSCs exposed to MSN-LIP (green), scale bar is 100 µm.

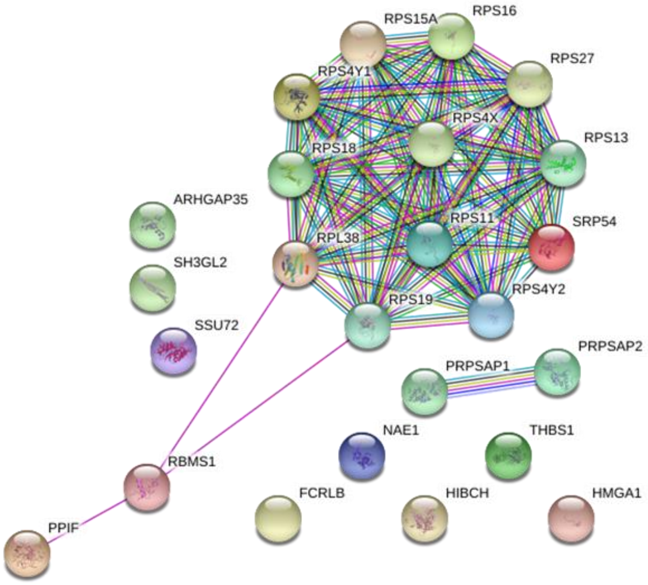

Figure S7. Network of proteins identified to be differentially regulated in hMSCs labeled with non-surface coated MSNs (STRING). (center proteins consist of RPS15A = Ribosomal protein S15a, RPS16 = Ribosomal protein S16, RPS4Y1 = Ribosomal protein S4, Y-linked 1, RPS4X = Ribosomal protein S4, X-linked, RPS27 = Ribosomal protein S27, RPS13 = Ribosomal protein S13, RPS11 = Ribosomal protein S11, RPS19 = Ribosomal protein S19, SRP54 = Signal recognition particle 54kDa, RPS4Y2 = Ribosomal protein S4, Y-linked 2, RPL38 = Ribosomal protein L38)