Supplementary Table S1. Neural Stem Cell Genes Upregulated with Coculture

Gene	Official symbol	Gene ID	Mean SI		Fold change
			CC	Neural stem cell	
Prostate transmembrane protein, androgen induced 1	*Pmepa1*	311676	5149.44	248.37	20.73
Putative ISG12(b) protein	*Isg12(b)*	299269	986.1	97.5	10.11
Adrenomedullin	*Adm*	25026	76.38	10.08	7.57
Reelin	*Reln*	24718	1532.76	251.19	6.1
S100 calcium binding protein A10 (calpactin)	*S100a10*	81778	6310.98	1201.41	5.25
Neuronal pentraxin receptor	*Nptxr*	81005	1731.65	366.06	4.73
Lymphoid enhancer binding factor 1	*Lef1*	161452	980.99	238.54	4.11
Procollagen, type IV, alpha 2 (predicted)	*Col4a2*	306628	695.04	178.45	3.89
Carbonhydrate sulfotransferase 2 (predicted)	*Chst2*	367145	2177.71	589.44	3.69
Tenascin R	*Tnr*	25567	736.91	199.83	3.69[a]
Procollagen, type IV, alpha 1	*Col4a1*	290905	3986.83	1128.57	3.53
Retinol binding protein 1, cellular	*Rbp1*	25056	719.51	211.61	3.4
Cyclin-dependent kinase inhibitor 1C (P57)	*Cdkn1c*	246060	2029.79	614.93	3.3
ATPase, Na+/K+transporting, beta 2 polypeptide	*Atp1b2*	24214	796.92	254.67	3.13
Early growth response 2	*Egr2*	114090	284.26	91.27	3.11
Cyclin D2	*Ccnd2*	64033	3779.89	1238.54	3.05
Procollagen, type XI, alpha 1	*Col11a1*	25654	450.83	150.55	2.99
Protein S (alpha)	*Pros1*	81750	541.73	183.93	2.95
Activating transcription factor 3	*Atf3*	25389	259.16	94.13	2.75
Septin 4	*Sept4*	287606	537.43	195.96	2.74
Bone morphogenetic protein 4	*Bmp4*	25296	841.93	307.96	2.73
Complement component 1, q subcomponent-like 1 (predicted)	*C1ql1*	363686	2889.56	1138.25	2.54
Protein kinase C, eta	*Prkch*	81749	117.86	47.76	2.47
Tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	*Tnfrsf11b*	25341	776.83	314.04	247[a]
Matrix metallopeptidase 11	*Mmp11*	25481	215.18	89.25	2.41
Early growth response 1	*Egr1*	24330	6612.23	2821.33	2.34
Coagulation factor III	*F3*	25584	1306.03	557.82	2.34
Calcitonin receptor-like	*Calcrl*	25029	735.92	317.79	2.32
Dipeptidylpeptidase 6	*Dpp6*	29272	161.37	71.33	2.26
Glutamate receptor, ionotropic, AMPA3 (alpha 3)	*Gria3*	29628	287.22	128.93	2.23
Plasma membrane proteolipid	*Pllp*	64364	3038.5	1366.5	2.22
Fas apoptotic inhibitory molecule	*Faim*	140930	2661.26	1209.6	2.2
Ribose 5-phosphate isomerase A (predicted)	*Rpia*	362383	598.48	271.61	2.2
Meteorin, glial cell differentiation regulator	*Metrn*	287151	4441.11	2042.79	2.17
Immediate early response 2	*Ier2*	494344	1979.92	923.6	2.14
Signal transducer and activator of transcription 3	*Stat3*	25125	1707.16	803.09	2.13
G0/G1 switch gene 2	*G0s2*	289388	1231.9	580.46	2.12
Sulfatase 2	*Sulf2*	311642	5972.93	2822.77	2.12
Fibroblast growth factor receptor-like 1	*Fgfrl1*	360903	1788.7	849.07	2.11
Chondroitin sulfate proteoglycan 2	*Cspg2*	114122	2106.94	1018.83	2.07

[a] Multiple probes met the filtering criteria. Representative signal intensities and fold change are given for a single probe.

Supplementary Table S2. Neural Stem Cell Genes Downregulated with Coculture

			Mean SI		
Gene	*Official symbol*	*Gene ID*	*Neural stem cell*	*CC*	*Fold change*
Matrix metallopeptidase 13	*Mmp13*	171052	22.44	1[a]	−22.44
ATPase, H+transporting, Iysosmoal V0 subunit a isoform 2	*Atp6v0a2*	116455	18.06	1[a]	−18.06
Taste receptor, type 2, member 105	*Tas2r105*	78985	17.7	1[a]	−17.7
Vav 1 oncogene	*Vav1*	25156	38.46	2.91[a]	−13.24
Minichromosome maintenance deficient 3 (S. cerevisiae) associated protein	*Mcm3ap*	294339	40.47	30.6[a]	−13.21
Sialic acid binding Ig-like lectin 10 (predicted)	*Siglec10*	292844	26.9	3.02[a]	−8.91
RT1 class lb, locus M3	*RT1-M3*	24747	29.05	5.04[a]	−5.76
TBK1 binding protein 1	*Tbkbp1*	266764	21.3	4.21[a]	−5.06
Carboxypeptidase×2 (M14 family) (predicted)	*Cpxm2*	293566	32.74	6.57[a]	−4.98
FCH and double SH3 domains 2 (predicted)	*Fchsd2*	308864	58.6	12.75	−4.6
FERM and PDZ domain containing 1 (predicted)	*Frmpd1*	313244	52.36	11.78[a]	−4.44
Carbonic anhydrase 3	*Ca3*	54232	15.96	3.69[a]	−4.33
Caspase 12	*Casp12*	156117	48.63	11.42[a]	−4.26[b]
Urinary protein 2	*Rup2*	619560	35.82	9.05[a]	−3.96
MAM domain containing 4	*Mamdc4*	252882	58.3	15.18[a]	−3.84
Otoferlin	*Otof*	84573	23.91	6.52[a]	−3.67
Cadherin 11	*Cdh11*	84407	54.49	15.09[a]	−3.61
Ubiquitin specific protease 42 (predicted)	*Usp42*	288482	57.88	16.58[a]	−3.49
DnaJ (Hsp40) homolog, subfamily C, member 2	*Dnajc2*	116456	37.48	11.25	−3.33
Lipoprotein lipase	*Lpl*	24539	277.89	83.45[a]	−3.33
Plexin C1 (predicted)	*Plxnc1*	362873	135.4	40.68	−3.33
Insulin-like growth factor 1	*lgf1*	24482	30.3	9.56[a]	−3.17
Gamma-aminobutyric acid (GABA) A receptor, subunit gamma 3	*Gabrg3*	79211	178.41	59.56[a]	−3
Apelin, AGTRL1 ligand	*Apln*	58812	76.34	25.81[a]	−2.96
Chemokine orphan receptor 1	*Cmkor1*	84348	219.09	75.63	−2.9
Solute carrier family 33 (acetyl-CoA transporter), member 1	*Slc33a1*	64018	26.28	9.44[a]	−2.78
Retinal G protein coupled receptor (predicted)	*Rgr*	306307	356.73	145.6	−2.45
Dihydropyrimidinase-like 5	*Dpysl5*	65208	153.41	63.52[a]	−2.41
ATPase, Na+/K+transporting, beta 3 polypeptide	*Apt1b3*	25390	32.29	14.03[a]	−2.3

[a] Signal absent in coculture.

[b] Multiple probes met the filtering criteria. Representative signal intensities and fold change are given for a single probe.

Supplementary Table S3. Mesenchymal Stromal Cell Genes Upregulated with Coculture

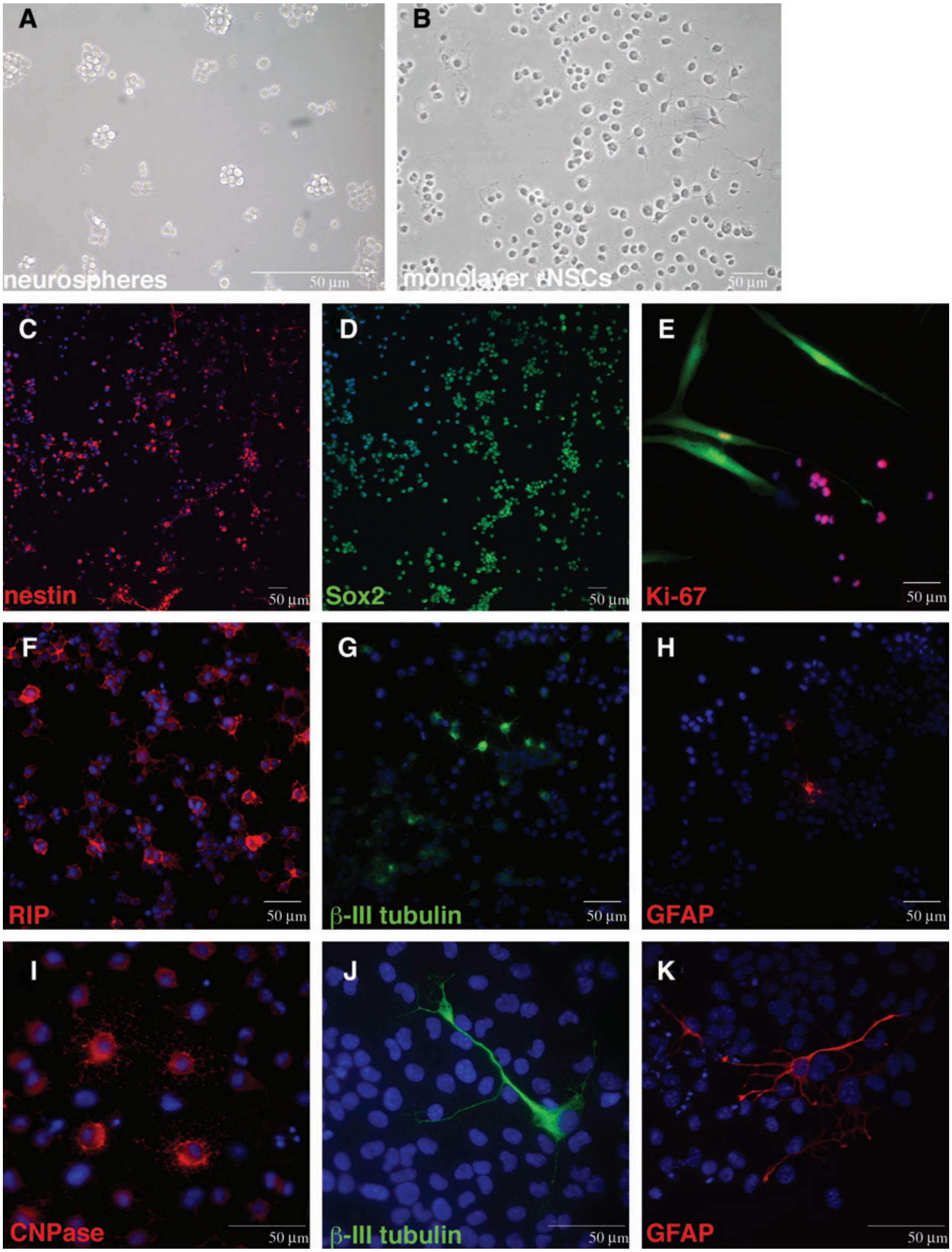
Gene	Official symbol	Gene ID	Mean SI		Fold change
			CC	Mesenchymal stromal cell	
ATP-binding cassette, sub-family A (ABC1), member 1	*ABCA1*	19	4140.54	92.66	44.68
Collagen, type IV, alpha 1	*COL4A1*	1282	6827.88	783.75	8.71
Inhibitor of DNA binding 3, dominant negative helix-loop-helix protein	*ID3*	3399	1999.21	237.79	8.41
Endothelin receptor type A	*EDNRA*	1909	2929.32	463.59	6.32^{a}
Hairy and enhancer of split 1 (Drosophila)	*HES1*	3280	2912.21	540.21	5.39^{a}
Notch homolog 3 (Drosophila)	*NOTCH3*	4854	3441.03	684.13	5.03
Solute carrier family 7 (cationic amino acid transporter, y+system) member 11	*SLC7A11*	23657	2587.2	568.35	4.55^{a}
Immediate early response 5-like	*IER5L*	389792	508.25	112.55	4.52
Unc-5 homolog B (C. elegans)	*UNC5B*	219699	2290.89	544.09	4.21
Biglycan	*BGN*	633	5785.87	1380.49	4.19^{a}
Jagged 1 (Alagille syndrome)	*JAG1*	182	2368.63	567.35	4.17^{a}
Collagen, type IV, alpha 2	*COL4A2*	1284	8265.82	2075.16	3.98^{a}
Endothelial differentiation, sphingolipid G-protein-coupled receptor, 3	*EDG3*	1903	1858.04	481.63	3.86
Collagen, type 1, alpha 1	*COL1A1*	1277	9801.77	2548.83	3.85^{a}
SRY (sex determining region Y)-box 4	*SOX4*	6659	1375.41	363.36	3.79
Tumor necrosis factor, alpha-induced protein 6	*TNFAIP6*	7130	1891.21	503.71	3.75^{a}
Syndecan 2	*SDC2*	6383	4269.44	1164.59	3.67^{a}
Sphingosine kinase 1	*SPHK1*	8877	2190.19	597.8	3.66
G0/G1switch 2	*GOS2*	50486	2765.57	791.02	3.5
Collagen, type V, alpha 1	*COL5A1*	1289	2178.9	630.53	3.46^{a}
Uveal autoantigen with coiled-coil domains and ankyrin repeats	*UACA*	55075	3474.18	1048.37	3.31
Bone morphogenetic protein 1	*BMP1*	649	905.83	276.86	3.27^{a}
Collagen, type III, alpha 1	*COL3A1*	1281	12297	3763.29	3.27
Phosphoglycerate dehydrogenase	*PHGDH*	26227	2425.24	785.16	3.09
Hydroxyacylglutathione hydrolase	*HAGH*	3029	820	271.7	3.02
Kruppel-like factor 9	*KLF9*	687	566.4	190.59	2.97
Growth differentiation factor 15	*GDF15*	9518	916.03	317.01	2.89
Pleckstrin homology, Sec7 and coiled-coil domains 3	*PSCD3*	9265	1195.05	418.69	2.85
Olfactomedin-like 2B	*OLFML2B*	25903	1033.2	364.24	2.84
Snail homolog 2 (Drosophila)	*SNAI2*	6591	6154.47	2178.95	2.82
Matrix metallopeptidase 14 (membrane-inserted)	*MMP14*	4323	3488.5	1239.89	2.81^{a}
SMAD family member 3	*SMAD3*	4088	1092.02	405.37	2.69^{a}
Versican	*VCAN*	1462	3976.6	1480.22	2.69
Sine oculis homeobox homolog 2	*SIX2*	10736	1674.3	628.2	2.67
Phosphoserine aminotransferase 1	*PSAT1*	29968	1049.7	404.93	2.59
Platelet-derived growth factor receptor, beta polypeptide	*PDGFRB*	5159	8776.75	3419.68	2.57
Transmembrane protein with epidermal growth factor-like and 2 follistatin-like domains 2	*TMEFF2*	23671	516.4	206.26	2.5
Sulfatase 1	*SULF1*	23213	2079.53	839.63	2.48^{a}
Collagen, type V, alpha 2	*COL5A2*	1290	8902.25	3613.43	2.46
Periostin, osteoblast specific factor	*POSTN*	10631	5311.35	2162.62	2.46
Protein kinase C substrate 80K-H	*PRKCSH*	5589	6619.26	2692.38	2.46
Collagen, type VI, alpha 1	*COL6A1*	1291	6216.84	2537.67	2.45^{a}
Non-POU domain contaiing, octamer-binding	*NONO*	4841	4272.48	1774	2.41

(Continued)

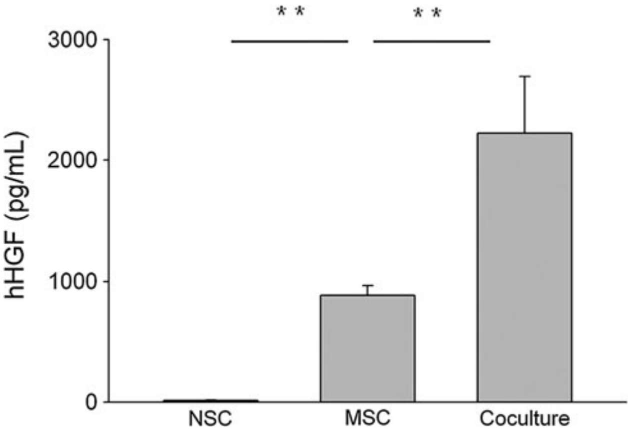
Supplementary Table S3. (Continued)

Gene	*Official symbol*	*Gene ID*	*Mean SI*		*Fold change*
			CC	*Mesenchymal stromal cell*	
Nidogen 2 (osteonidogen)	*NID2*	22795	3401.83	1418.5	2.4
ADP-ribosylation factor-like 4C	*ARL4C*	10123	3769.87	1579.94	2.39
Cystathionine-beta-synthase	*CBS*	875	1158.87	484.03	2.39
Transforming growth factor, beta 1	*TGFB1*	7040	3855.04	1630.09	2.36
Zinc finger protein 286A	*ZNF286A*	57335	78.77	33.48	2.35
Thy-1 cell surface antigen	*THY1*	7070	2911.47	1243.27	2.34
AE binding protein 1	*AEBP1*	165	2144.08	926	2.32
Cytochrome P450, family 1, subfamily B, polypeptide 1	*CYP1B1*	1545	1271.54	548.44	2.32[a]
KIT ligand	*KITLG*	4254	3485.92	1506.58	2.31
Glypican 1	*GPC1*	2817	4006.7	1738.92	2.3
Myristoylated alanine-rich protein kinase C substrate	*MARCKS*	4082	3402.36	1498.96	2.27
Nuclear protein 1	*NUPR1*	26471	1406.95	619.46	2.27
Endothelin converting enzyme 1	*ECE1*	1889	2132.1	944.14	2.26
Endothelial PAS domain protein 1	*EPAS1*	2034	4740.76	2110.07	2.25
Cysteine rich transmembrane BMP regulator 1 (chordin-like)	*CRIM1*	51232	3919.31	1782.58	2.2
GTP binding protein overexpressed in skeletal muscle	*GEM*	2669	2180.75	1009.98	2.16

[a] Multiple probes met the filtering criteria. Representative signal intensities and fold change are given for a single probe.



SUPPLEMENTARY FIG. S1. Characterization of rNSCs. (**A**) Before the start of experiments, rNSCs were propagated as nonadherent neurospheres in optimal rNSC growth medium. (**B**) For coculture experiments rNSCs were seeded on coated plates and grown as a monolayer (image was taken postfixation). Immunocytochemisty revealed that rNSCs grown in optimal growth medium expressed the characteristic NSC markers (**C**) nestin (red) and (**D**) Sox2 (green). (**E**) Both rNSCs and GFP+hMSCs in coculture expressed the cell proliferation marker Ki-67 (red). rNSCs cultured in differentiation medium expressed phenotypic markers of (**F**, **I**) oligodendrocytes (F-RIP and I-CNPase, red), (**G**, **J**) neurons (β-III tubulin, green), and (**H**, **K**) astrocytes (GFAP, red). (C–K) Nuclei were stained with DAPI (blue). All scale bars = 50 μm. rNSC, rat neural stem cell; hMSC, human mesenchymal stromal cell; GFAP, glial fibrillary acidic protein. GFP, green fluorescent protein; CNPase, 2′,3′-cyclic nucleotide 3′-phospho-diesterase; RIP, anti-oligodendrocytes antibody.



SUPPLEMENTARY FIG. S2. hMSCs increased secretion of HGF in cocultures. Human-specific ELISA of medium from cultures (*t*-test: $^{**}P < 0.01$ vs. coculture). HGF, hepatocyte growth factor.