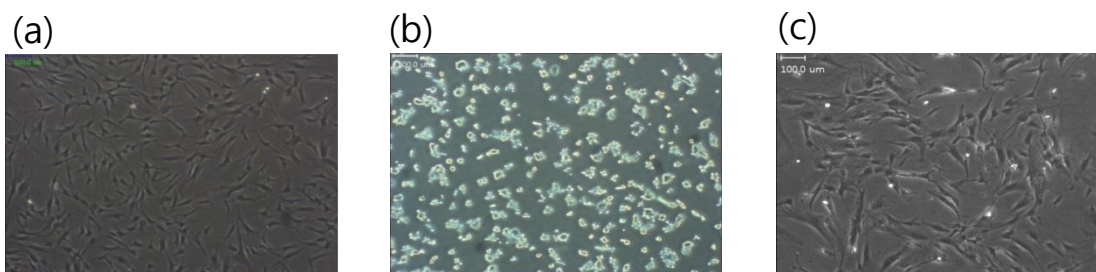
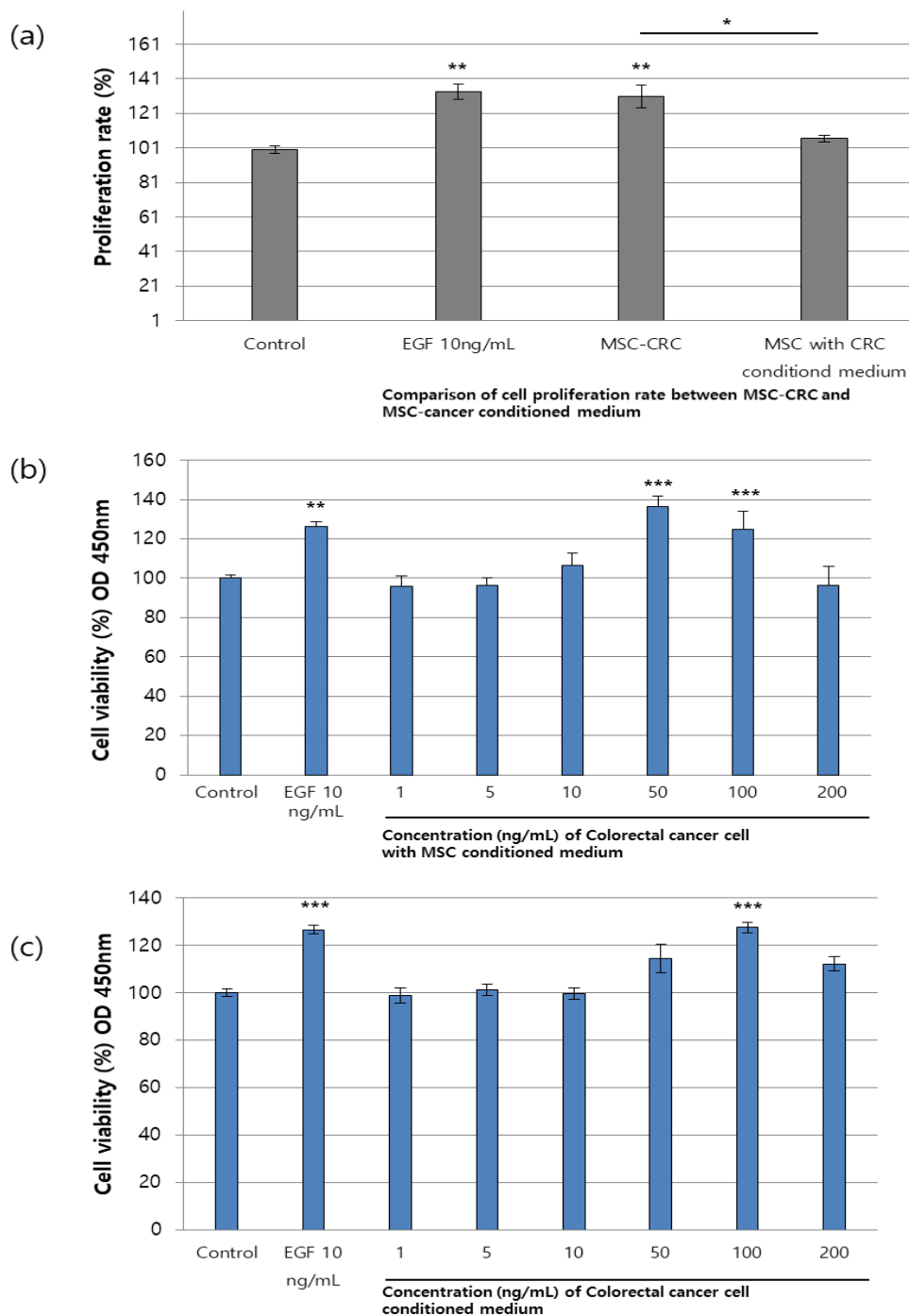


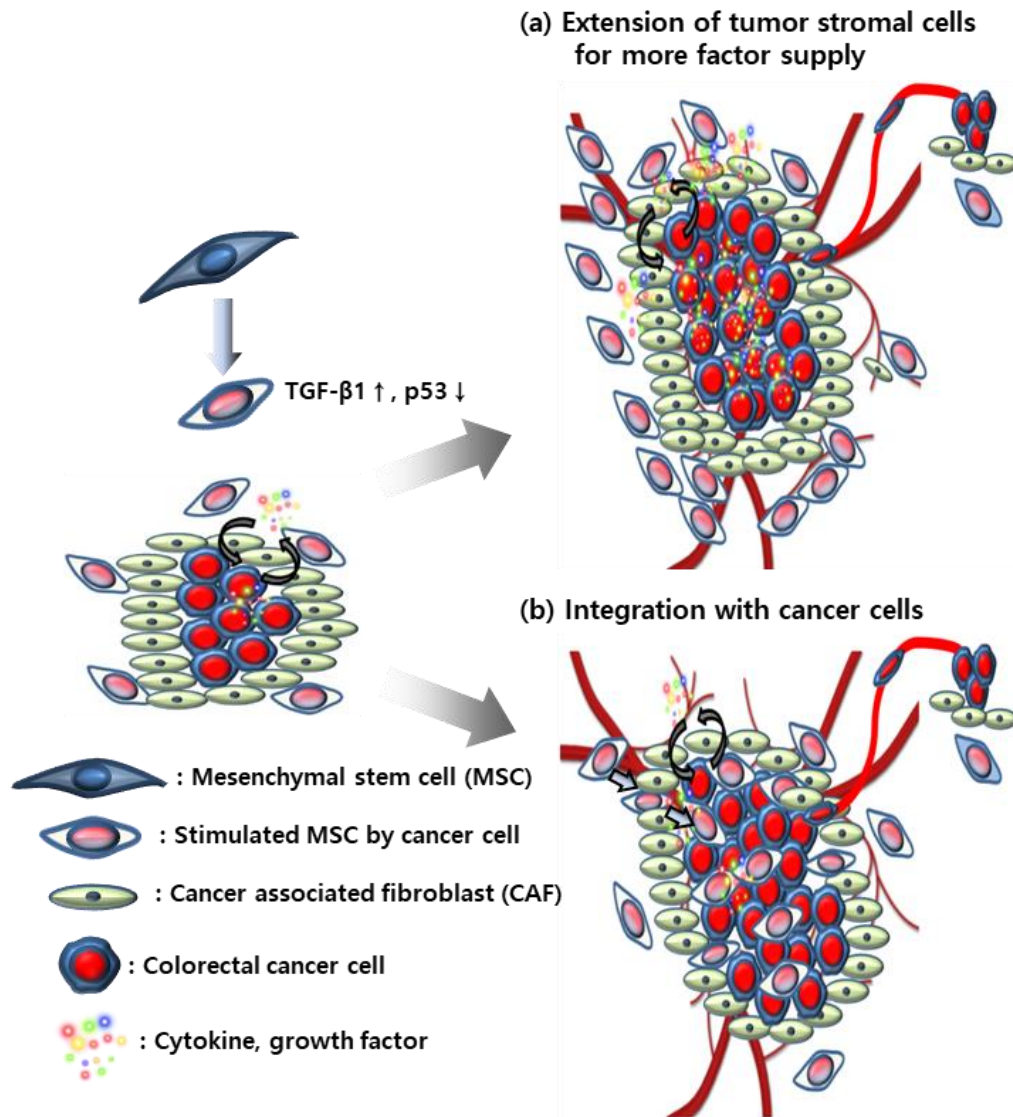
Supplementary Figure 1. Micrograph showing representative cell morphology of the used cell line. (a) Micrograph showing representative morphology of the used human amniotic membrane-derived stem cells (bcellbio-hAM-00) cultured for 3 days. (b) Representative morphology of human colorectal adenocarcinoma cells (ATCC® CCL-227™). (c) Representative morphology of CCD-18 Co normal colon fibroblasts (ATCC® CRL-1459™).



Supplementary Figure 2. Effect of MSC-CRC and conditioned medium (CM) on the proliferation of MSCs. (a) Cell proliferation between MSC-CRC group and CRC-CM group were compared after 48 hours. Cell proliferation rate was counted using a microscope and compared with the control group. Proliferation rate was increased in the MSC-CRC group and this not observed in the MSC-CM group. (b) Cell proliferation rate was measured 48 h after treatment with concentrated MSC-CRC CM (1–200 $\mu\text{g/mL}$). MSC groups treated with cancer-CM of 50 and 100 $\mu\text{g/mL}$ concentrations were the only ones that showed significantly enhanced proliferation. (c) The cell proliferation rate was measured 48 h after concentrated MSC-CM (1–200 $\mu\text{g/mL}$) treatment. 100 $\mu\text{g/mL}$ concentration of CM was observed to be the most effective. Serum-free culture medium was used as a negative control and EGF was used as a positive control. Error bars represent three independent experiments carried out in triplicate (Statistical analysis was performed by ANOVA with Tukey's multiple comparison test. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$).



Supplementary Figure 3. Schematic diagram. The schematic diagram shows the tumor development with the following two roles of the MSC changed by the colorectal cancer cells. (a) Extension of tumor stromal cells for more factor supply. (b) Integration with cancer cells.



Supplementary Table 1. List of genes present in the microarray gene datasets and reported in literature to be involved in cancer association. Fold change (FC) represents increasing events in the MSC-CRC sample when compared to the MSC-A sample.

p53

Gene Accession	Gene Symbol	Gene Description	FC (fold change)	P Value
NM_001031685	TP53BP2	tumor protein p53 binding protein, 2	1.695588	0.004342
NM_001251964	TP53AIP1	tumor protein p53 regulated apoptosis inducing protein 1	1.378506	0.874367
NM_016058	TPRKB	TP53RK binding protein	-1.2528	0.932319
NM_000546	TP53	tumor protein p53	-1.26064	0.394961
ENST00000316024	WRAP53	WD repeat containing, antisense to TP53	-1.29272	0.696636
NM_002393	MDM4	Mdm4 p53 binding protein homolog (mouse)	-1.30188	0.239469
NM_001172477	RRM2B	ribonucleotide reductase M2 B (TP53 inducible)	-1.30568	0.387107
NM_001258320	TP53I11	tumor protein p53 inducible protein 11	-1.31302	0.598831
NM_022045	MTBP	Mdm2, transformed 3T3 cell double minute 2, p53 binding protein (mouse) binding protein, 104 kDa	-1.62813	0.011169
ENST00000372114	TP53RK	TP53 regulating kinase	-1.71391	0.021333
ENST00000342697	TP53INP1	tumor protein p53 inducible nuclear protein 1	-1.7527	0.002458

Tumor suppressor genes

Gene Accession	Gene Symbol	Gene Description	FC	P Value
ENST00000371953	PTEN	phosphatase and tensin homolog	-1.41238	0.028239
NM_005418	ST5	suppression of tumorigenicity 5	-1.8249	0.003851
NM_017744	ST7L	suppression of tumorigenicity 7 like	-1.43845	0.176188
NM_007275	TUSC2	tumor suppressor candidate 2	-1.34661	0.300948
NM_145341	PDCD4	programmed cell death 4 (neoplastic transformation inhibitor)	-1.44278	0.001038

Anti-oxidant genes

Gene Accession	Gene Symbol	Gene Description	FC	P Value
NM_002061	GCLM	glutamate-cysteine ligase, modifier subunit	-3.42147	8.66E-20
NM_201397	GPX1	glutathione peroxidase 1	-1.5374	0.116637
ENST00000320623	NQO1	NAD(P)H dehydrogenase, quinone 1	-1.50795	9.02E-05
NM_001752	CAT	catalase	-1.36128	0.076412
NM_001008397	GPX8	glutathione peroxidase 8 (putative)	-1.35885	0.03716
NM_001145412	NFE2L2	nuclear factor (erythroid-derived 2)-like 2	-1.29909	0.236304

Oncogenes

Gene Accession	Gene Symbol	Gene Description	FC	P Value
ENST00000371222	JUN	jun proto-oncogene	3.458496	0
NM_001143820	ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	3.097517	0
NM_001127500	MET	met proto-oncogene (hepatocyte growth factor receptor)	2.800247	0
NM_007314	ABL2	v-abl Abelson murine leukemia viral oncogene homolog 2	2.681566	1.11E-12
NM_000222	KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog	2.238577	0.000202
NM_004163	RAB27B	RAB27B, member RAS oncogene family	2.194765	0.012712
ENST00000257017	RAB33A	RAB33A, member RAS oncogene family	2.165543	1.89E-05
NM_170662	CBLB	Cbl proto-oncogene, E3 ubiquitin protein ligase B	2.121365	9.15E-12
NM_001256295	ETS2	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian)	1.990579	5.32E-08
NM_005402	RALA	v-ral simian leukemia viral oncogene homolog A (ras related)	1.962577	0.004787
ENST00000295025	REL	v-rel reticuloendotheliosis viral oncogene homolog (avian)	1.830371	4.72E-06
NM_001172663	RAB40C	RAB40C, member RAS oncogene family	1.666959	0.004254
NM_017817	RAB20	RAB20, member RAS oncogene family	1.66306	0.058073
NM_002866	RAB3A	RAB3A, member RAS oncogene family	1.470861	0.336716
NM_006834	RAB32	RAB32, member RAS oncogene family	1.433811	0.125178
NM_006270	RRAS	related RAS viral (r-ras) oncogene homolog	1.43294	0.001888

NM_005207	CRKL	v-crk sarcoma virus CT10 oncogene homolog (avian)-like	1.420233	0.017156
NM_006875	PIM2	pim-2 oncogene	1.414471	0.692839
NR_000039	RAB9BP1	RAB9B, member RAS oncogene family pseudogene 1	1.408603	0.501703
NM_016277	RAB23	RAB23, member RAS oncogene family	1.394545	0.011186
NM_002360	MAFK	v-maf musculoaponeurotic fibrosarcoma oncogene homolog K (avian)	1.378013	0.220002
NM_001031834	RAB40AL	RAB40A, member RAS oncogene family-like	1.369403	0.962948
NM_002867	RAB3B	RAB3B, member RAS oncogene family	1.366038	0.070021
NM_032846	RAB2B	RAB2B, member RAS oncogene family	1.345272	0.14785
NM_001001852	PIM3	pim-3 oncogene	1.336936	0.262947
NM_016322	RAB14	RAB14, member RAS oncogene family	1.321471	0.049022
NM_032711	MAFG	v-maf musculoaponeurotic fibrosarcoma oncogene homolog G (avian)	1.312744	0.680149
NM_005252	FOS	FBJ murine osteosarcoma viral oncogene homolog	1.307629	0.758151
NM_005354	JUND	jun D proto-oncogene	1.297015	0.261528

Growth factors/etc

Gene Accession	Gene Symbol	Gene Description	FC	P Value
NM_002506	NGF	nerve growth factor (beta polypeptide)	2.500558	8.78E-08
NM_000660	TGFB1	transforming growth factor, beta 1	1.97916	9.85E-09
NM_004750	CRLF1	cytokine receptor-like factor 1	1.721763	1.69E-06
ENST00000361188	PRC1	protein regulator of cytokinesis 1	1.689911	0.006902
NM_000601	HGF	hepatocyte growth factor (hepapoietin A; scatter factor)	1.65331	0.024311
NM_004112	FGF11	fibroblast growth factor 11	1.586894	0.170769
NM_002059	GH2	growth hormone 2	1.540906	0.07246
ENST00000275493	EGFR	epidermal growth factor receptor	1.53724	0.001064
NM_001025366	VEGFA	vascular endothelial growth factor A	2.718992	0
NM_001243733	VEGFB	vascular endothelial growth factor B	1.297331	0.421236
NM_000963	PTGS2	prostaglandin-endoperoxide synthase 2	2.174502	0
NM_006516	SLC2A1	solute carrier family 2 (facilitated glucose transporter), member 1	6.590226	0

Supplementary Table 2. DAVID functional annotation bioinformatics by microarray analysis of the top significantly increased genes. 594 upregulated genes identified in our microarray data set were entered and all annotation categories were used (Only terms with Fold change ≥ 1.5 , p-value ≤ 0.01). Pathway enrichment analysis of the upregulated DEGs.

Category	Term	Count	%	P Value	Genes	Benjamini	FDR
KEGG_PATHWAY	hsa05322:Systemic lupus erythematosus	18	0.02092	4.65E-06	HIST1H2AC, HIST2H2AA4, HIST1H2BC, HIST1H2BD, HIST1H2BG, HIST1H2AD, HIST1H2AE, HIST2H4B, HIST2H3D, HIST2H2AB, HIST1H2BM, HIST1H2BL, HIST2H2BE, HIST1H4B, HIST1H2AI, HIST1H3B, HIST1H4D, HIST1H3H	0.001013	0.005908
KEGG_PATHWAY	hsa04141:Protein processing in endoplasmic reticulum	20	0.02324	7.78E-06	HERPUD1, HSP90AA1, CRYAB, RNF185, HSPA1A, HSPA1B, PDIA4, EDEM1, DDIT3, NGLY1, HYOU1, HSP90B1, HSPA2, HSPA4L, HSPA6, YOD1, HSPA5, DNAJB1, PPP1R15A, SEC61G	8.48E-04	0.009893
KEGG_PATHWAY	hsa05034:Alcoholism	20	0.02324	1.52E-05	HIST1H2AC, HIST2H2AA4, HIST1H2BC, HIST1H2BD, HIST1H2BG, HIST1H2AD, HIST1H2AE, PPP1CB, HIST2H4B, HIST2H3D, HIST2H2AB, HIST1H2BM, HIST1H2BL, HIST2H2BE, HIST1H4B, HIST1H2AI, HIST1H3B, GNG2, HIST1H4D, HIST1H3H	0.001107	0.019378
KEGG_PATHWAY	hsa04710:Circadian rhythm	8	0.00929	8.43E-05	NR1D1, PRKAG2, PRKAB2, PER1, BHLHE40, RORA, PER3, BHLHE41	0.004584	0.107104
KEGG_PATHWAY	hsa04010:MAPK signaling pathway	21	0.02440	6.45E-04	EGFR, LAMTOR3, DUSP10, CACNB1, HSPA1A, HSPA1B, STK4, DDIT3, TGFB1, DUSP4, DUSP3, HSPA2, DUSP1, JUN, HSPA6, HSPB1, GADD45B, GADD45A, IL1A, RASA2, NGF	0.027754	0.817179
KEGG_PATHWAY	hsa04068:FoxO signaling pathway	14	0.01627	9.20E-04	EGFR, IRS2, PRKAB2, PRKAG2, SMAD4, BNIP3, CCNG2, STK4, TGFB1, S1PR1, PLK1, FBXO32, GADD45B, GADD45A	0.032899	1.163472
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	9	0.01046	0.00182	EGFR, PDK1, SLC2A1, MET, PGAM1, HK2, PFKP, KIT, SLC7A5	0.055138	2.288258
KEGG_PATHWAY	hsa04066:HIF-1 signaling pathway	11	0.01278	0.002088	EGFR, PDK1, PFKFB3, HMOX1, VEGFA, SLC2A1, SERPINE1, ENO2, HK2, IL6R, ENO1	0.055363	2.62164
KEGG_PATHWAY	hsa00010:Glycolysis / Gluconeogenesis	8	0.00929	0.009398	LDHA, ALDOC, ENO2, PGAM1, HK2, PFKP, PGK1, ENO1	0.204453	11.31011
KEGG_PATHWAY	hsa04350:TGF-beta signaling pathway	9	0.01046	0.009753	INHBB, INHBA, NOG, SMAD9, ID2, ID1, SMAD4, ID3, TGFB1	0.19238	11.71309
KEGG_PATHWAY	hsa04152:AMPK signaling pathway	11	0.01278	0.012053	IRS2, CAB39L, TSC1, PFKFB4, PFKFB3, SCD, PRKAG2, PRKAB2, GYS1, PFKP, CCNA2	0.213627	14.2844
KEGG_PATHWAY	hsa01230:Biosynthesis of amino acids	8	0.00929	0.013712	ARG2, ALDOC, ENO2, PGAM1, PFKP, PGK1, PRPS1, ENO1	0.221839	16.09563
KEGG_PATHWAY	hsa05203:Viral carcinogenesis	15	0.01743	0.014441	HIST1H2BC, HIST1H2BD, VAC14, HIST1H2BG, HIST2H4B, HIST1H2BM, REL, HIST1H2BL, HIST1H4B, HIST2H2BE, JUN, HIST1H4D, RBPJ, CCNA2, RASA2	0.216453	16.8803
KEGG_PATHWAY	hsa04320:Dorso-ventral axis formation	5	0.00581	0.014455	EGFR, ETS1, ETS2, SPIRE1, CPEB1	0.202863	16.89576
KEGG_PATHWAY	hsa04931:Insulin resistance	10	0.01162	0.01451	IRS2, PPP1R3C, PPP1R3B, PRKAG2, PRKAB2, SLC2A1, MGEA5, GYS1, TRIB3, PPP1CB	0.191382	16.95503
KEGG_PATHWAY	hsa04915:Estrogen signaling pathway	9	0.01046	0.024364	EGFR, HSP90B1, HSP90AA1, PLCB4, HSPA2, JUN, HSPA6, HSPA1A, HSPA1B	0.285424	26.91254
KEGG_PATHWAY	hsa00051:Fructose and mannose metabolism	5	0.00581	0.025802	PFKFB4, PFKFB3, ALDOC, HK2, PFKP	0.284813	28.27001
KEGG_PATHWAY	hsa00500:Starch and sucrose metabolism	5	0.00581	0.028565	GBE1, ENPP1, GYS1, HK2, PGM2L1	0.296007	30.81336
KEGG_PATHWAY	hsa05211:Renal cell carcinoma	7	0.00813	0.029376	ETS1, JUN, VEGFA, SLC2A1, MET, FLCN, TGFB1	0.289727	31.54467
KEGG_PATHWAY	hsa04014:Ras signaling pathway	15	0.01743	0.030583	EGFR, MET, KIT, STK4, RASA4B, REL, ETS1, ETS2, VEGFA, RALA, GNG2, RASA4, ABL2, RASA2, NGF	0.287204	32.61858
KEGG_PATHWAY	hsa01200:Carbon metabolism	9	0.01046	0.047903	MUT, ALDOC, ENO2, PGAM1, HK2, PFKP, PGK1, PRPS1, ENO1	0.399255	46.41749
KEGG_PATHWAY	hsa04150:mTOR signaling pathway	6	0.00697	0.054624	CAB39L, TSC1, RICTOR, RRAAGD, DDIT4, RRAAGC	0.426858	51.03159
KEGG_PATHWAY	hsa04910:Insulin signaling pathway	10	0.01162	0.057334	IRS2, CBLB, PPP1R3C, PPP1R3B, TSC1, PRKAG2, PRKAB2, GYS1, HK2, PPP1CB	0.428578	52.786
KEGG_PATHWAY	hsa05410:Hypertrophic	7	0.00813	0.058687	ITGA5, PRKAG2, PRKAB2, CACNB1, ITGA1, ITGB3, TGFB1	0.422677	53.64003

	cardiomyopathy (HCM)						
KEGG_PATHWAY	hsa04922:Glucagon signaling pathway	8	0.009298	0.062398	LDHA, PLCB4, PRKAG2, PRKAB2, SLC2A1, GYS1, PGAM1, SIK1	0.429834	55.91041
KEGG_PATHWAY	hsa05200:Pathways in cancer	21	0.024406	0.066801	GNA13, EGFR, HSP90AA1, PTGS2, MET, SMAD4, BDKRB1, KIT, STK4, TGFB1, LAMA1, HSP90B1, CBLB, PLCB4, ETS1, JUN, SLC2A1, VEGFA, CKS2, RALA, GNG2	0.439925	58.47083
KEGG_PATHWAY	hsa01130:Biosynthesis of antibiotics	13	0.015109	0.075308	LDHA, ALDOC, PFKP, HK2, PGAM1, UAP1L1, AK4, AMPD3, ARG2, ENO2, PGK1, ENO1, PRPS1	0.468557	63.03442
KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	7	0.008135	0.089152	CD55, ITGA5, ITGA1, IL6R, KIT, ITGB3, IL1A	0.516653	69.48367
KEGG_PATHWAY	hsa05120:Epithelial cell signaling in Helicobacter pylori infection	6	0.006973	0.0895	ATP6V1C1, EGFR, JUN, MET, ATP6V1H, ATP6V1B2	0.505804	69.63155
KEGG_PATHWAY	hsa05323:Rheumatoid arthritis	7	0.008135	0.092985	ATP6V1C1, JUN, VEGFA, ATP6V1H, ATP6V1B2, TGFB1, IL1A	0.507962	71.07647

Supplementary Table 3. List of heat shock proteins up-/downregulated in the microarray datasets. Fold change (FC) represents increasing or decreasing events in MSC-CRC sample when compared with the MSC-A sample.

Heat shock proteins

Gene Accession	Gene Symbol	Gene Description	FC	P Value
ENST00000430065	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	12.64146	0
ENST00000450744//ENST00000450744	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	12.60295	0
NM_005345	HSPA1A	heat shock 70 kDa protein 1A	12.142	0
ENST00000391555//ENST00000391555	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	11.96903	0
ENST00000542758//ENST00000542758	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	11.8167	0
ENST00000430065//ENST00000430065	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	11.56249	0
ENST00000430065//ENST00000430065	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	11.56249	0
ENST00000430065//ENST00000430065	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	11.56249	0
NM_005346	HSPA1B	heat shock 70 kDa protein 1B	10.85055	0
ENST00000450744//ENST00000450744	HSPA1B//HSPA1A	heat shock 70 kDa protein 1B//heat shock 70 kDa protein 1A	10.34194	0
AK023317	HSPA9	heat shock 70 kDa protein 9 (mortalin)	4.200864	0
NM_005347	HSPA5	heat shock 70 kDa protein 5 (glucose-regulated protein, 78 kDa)	3.312828	0
NM_002155	HSPA6	heat shock 70 kDa protein 6 (HSP70B')	2.317163	0.008745
NM_014424	HSPB7	heat shock 27 kDa protein family, member 7 (cardiovascular)	1.988287	0.000249
NR_024151	HSPA7	heat shock 70 kDa protein 7 (HSP70B)	1.798068	0.046102
NM_003299	HSP90B1	heat shock protein 90 kDa beta (Grp94), member 1	1.785849	1.01E-13
NM_001017963	HSP90AA1	heat shock protein 90 kDa alpha (cytosolic), class A member 1	1.739017	0.00059
NM_014278	HSPA4L	heat shock 70 kDa protein 4-like	1.716419	0.008524
NM_021979	HSPA2	heat shock 70 kDa protein 2	1.714436	9.12E-05
NM_001540	HSPB1	heat shock 27 kDa protein 1	1.613125	1.29E-05
NM_004134	HSPA9	heat shock 70 kDa protein 9 (mortalin)	1.451956	0.001334
NM_001136180	HSBP1L1	heat shock factor binding protein 1-like 1	1.418369	0.042399
NM_005527	HSPA1L	heat shock 70 kDa protein 1-like	1.400714	0.061484
NM_005527	HSPA1L	heat shock 70 kDa protein 1-like	1.387241	0.375167
NM_006308	HSPB3	heat shock 27 kDa protein 3	1.348573	0.560419
NM_014365	HSPB8	heat shock 22 kDa protein 8	1.285831	0.767025
NM_005526	HSF1	heat shock transcription factor 1	1.27882	0.493407
NM_006644	HSPH1	heat shock 105 kDa/110 kDa protein 1	1.25894	0.094029
NM_005527	HSPA1L	heat shock 70 kDa protein 1-like	1.252271	0.531485
NM_005527	HSPA1L	heat shock 70 kDa protein 1-like	1.252271	0.531485
NM_005527	HSPA1L	heat shock 70 kDa protein 1-like	1.252271	0.531485
NR_002927	HSP90AB4P	heat shock protein 90 kDa alpha (cytosolic), class B member 4, pseudogene	1.196783	0.980903
NM_001080439	HSF5	heat shock transcription factor family member 5	1.159665	0.991259
NM_001040667	HSF4	heat shock transcription factor 4	1.152137	0.997202
NM_006948	HSPA13	heat shock protein 70 kDa family, member 13	1.146232	0.214137
NM_012267	HSPBP1	HSPA (heat shock 70 kDa) binding protein, cytoplasmic cochaperone 1	1.139083	0.627941
NM_052970	HSPA12B	heat shock 70kDa protein 12B	1.13363	1
NM_004506	HSF2	heat shock transcription factor 2	1.105567	0.896224
NM_007355	HSP90AB1	heat shock protein 90 kDa alpha (cytosolic), class B member 1	1.092565	0.95244
NM_007031	HSF2BP	heat shock transcription factor 2 binding protein	1.087694	0.976131
NR_003130	HSP90B3P	heat shock protein 90 kDa beta (Grp94), member 3, pseudogene	1.072553	1
NM_002156	HSPD1	heat shock 60 kDa protein 1 (chaperonin)	-1.08591	1
NR_036694	HSP90AB3P	heat shock protein 90 kDa alpha (cytosolic), class B member 3, pseudogene	-1.10607	0.908047
NM_144617	HSPB6	heat shock protein, alpha-crystallin-related, B6	-1.10629	0.879613
NM_006597	HSPA8	heat shock 70 kDa protein 8	-1.12167	0.66895
NM_024610	HSPBAP1	HSPB (heat shock 27 kDa) associated protein 1	-1.16834	0.699368
NM_025015	HSPA12A	heat shock 70 kDa protein 12A	-1.17539	0.832846
ENST00000194214	HSPB11	heat shock protein family B (small), member 11	-1.19177	0.770917
BC041412	HSPA12A	heat shock 70 kDa protein 12A	-1.26006	0.686941
ENST00000378372	HSPA14	heat shock 70 kDa protein 14	-1.44767	0.297435
ENST00000304858	HSPA4	heat shock 70 kDa protein 4	-1.891	3.77E-06

Supplementary Table 4. Primer sequences for RT-PCR.

Primer Sequence				
Name	Forward: 5' → 3'	Reverse: 5' → 3'	Expected	Annealing Temperature
β-actin	GGACTTCGAGCAAGAGATGG	AGCACTGTGTTGGCGTACAG	234 bp	57.5°C
VEGFa	CCTTGCTGCTCTACCAC	ATCTGCATGGTGATGTTGGA	280 bp	59.0°C
N-Ras	CTGTGGTCCTAAATCTGTCC	CAGTGCAGCTTGAAAGTG	682 bp	53°C
EGFR	CAGGGCATTTCACAGGTGCG	TCAGGTTACAGGGCACACAC	229 bp	58.5°C
p53	GCGTGTGGAGTATTTGGA	GAGAGGAGCTGGTGTTGT	344 bp	53°C
TGF-β1	TGRCACCGGAGTTGTGCG	GGCCGGTAGTGAACCCGT	131 bp	55°C

Supplementary Table 5. Comparison of colony formation by control and co-cultured MSCs.

Control MSC-A 8wk		MSC-NCF 8wk		MSC-CRC 8wk	
Number of cells	Colony formation/well	Number of cells	Colony formation/well	Number of cells	Colony formation/well
2×10^6	0/6	2×10^6	0/6	2×10^6	6/6
2×10^5	0/6	2×10^5	0/6	2×10^5	0/6
2×10^4	0/6	2×10^4	0/6	2×10^4	0/6

NOTE. Number of colony formations/number of well

Soft Agar Assays were performed in 6-well plates. After 21 days of growth, colonies > 100 μm in diameter were counted using a microscope.