Supplemental Material to:

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Mesenchymal stem cells in mammary adipose tissue stimulate progression of breast cancer resembling the basal-type

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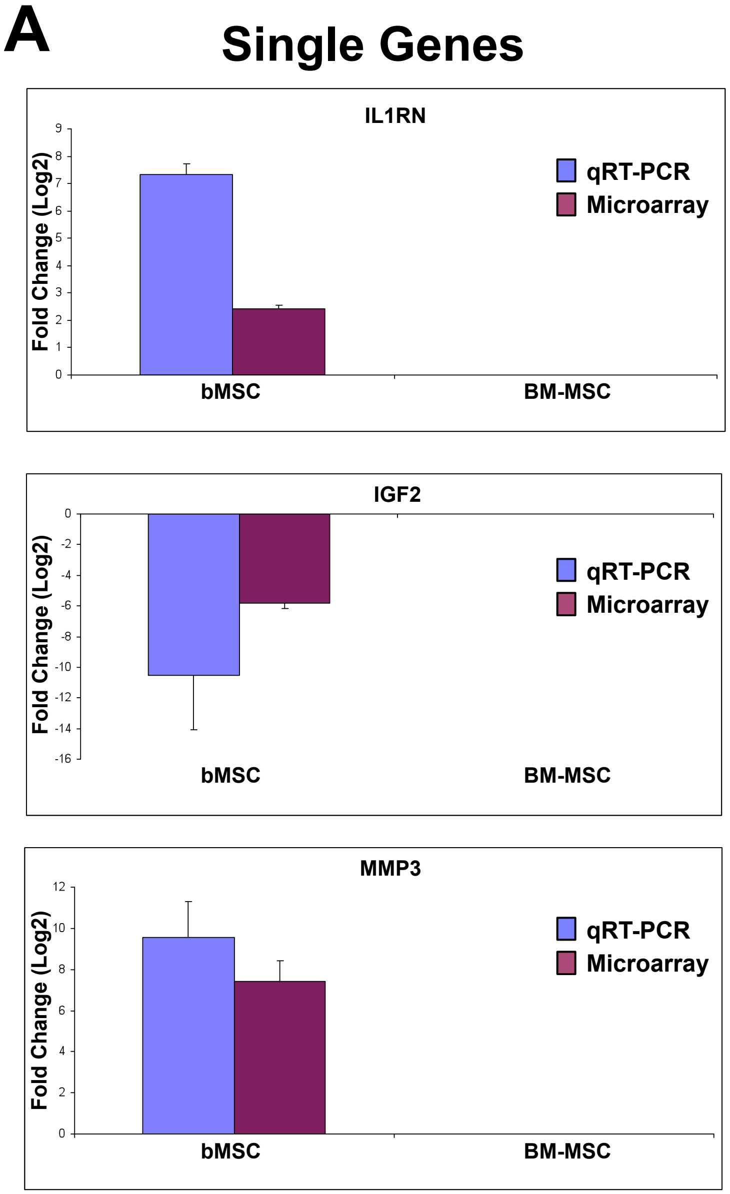
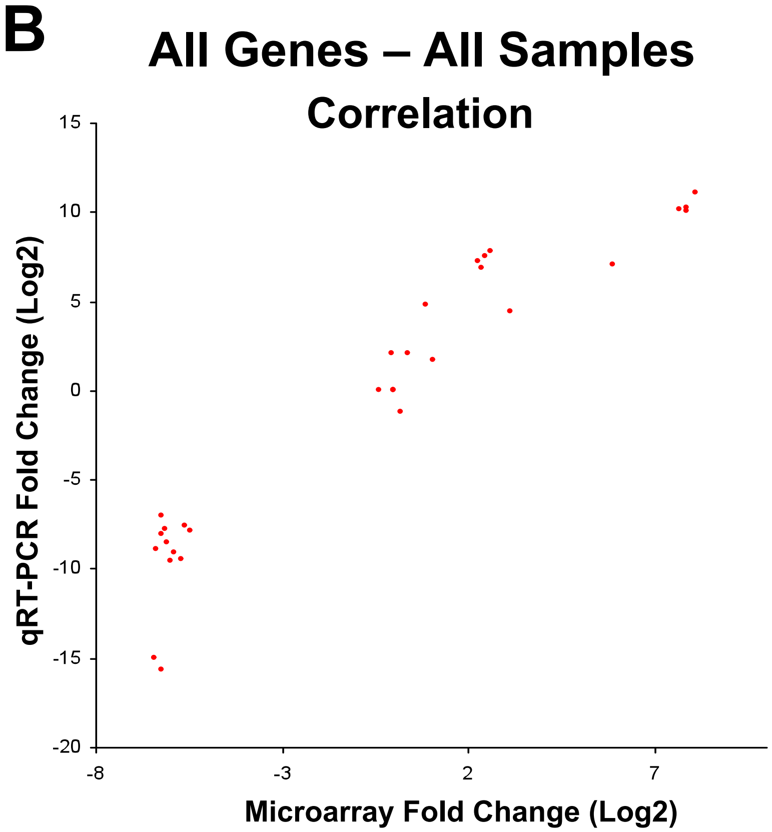
Supplemental Figure 1. qRT-PCR confirms the differential expression of 3 genes. Probes and primer sets for detection of MMP3, IGF2 and IL1RA transcripts were obtained from inventoried assays (Applied Biosystems, Foster City, CA). For all of the samples, cyclophilin A (PPIA) from the Predeveloped TaqMan® Assay reagents was used as an endogenous control. (A) single genes; (B) all genes-all sample.

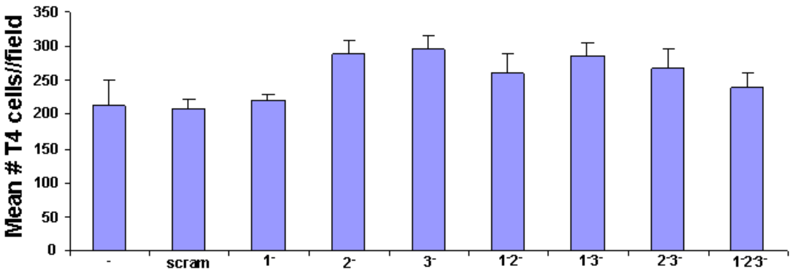




n	32	
r statistic	0.96	
95% CI	0.91 to 0.98	**(normal approximation)**
t statistic	17.79	
DF	30	
2-tailed p	<0.0001	**(t approximation)**

Zhao et al Supp. Figure 1

Supplemental Figure 2. **Potentiation of T4 invasion by bMSCs is not dependent on MMP 1, MMP2 and/or MMP3 expression**. Si-RNA technology was used to transiently knockdown expression of MMP1, MMP2 and/or MMP3. Forty-eight hours post transfection, cell were seeded onto Matrigel®-coated transwell inserts and subjected to our standard *in vitro* invasion assay and pelleted for total RNA isolation followed by qRT-PCR to assess relative levels of the respective MMPs. Below the graph, relative quantitation (as described in Materials and Methods) is shown with underlined values representing significant knockdown from the uninfected control. Shown graphically are the mean numbers of T4 breast epithelial cells migrating to the under side of the transwell inserts. Values represent the mean number of cells per microscopic field based on 3 fields/insert and 3 inserts per condition. A 2 tailed student t-test was conducted and none of the knockdown conditions resulted in a significant difference in the potentiation of T4 cancer cells by bMSCs.



RQ:	**1.0**	**1.1**	**0.03**	**1.7**	**1.6**	**0.2**	**0.1**	**2.4**	**0.2**	**MMP1**
RQ:	**1.0**	**0.7**	**1.2**	**0.06**	**0.7**	**0.04**	**0.5**	**0.04**	**0.02**	**MMP2**
RQ:	**1.0**	**1.7**	**1.6**	**1.6**	**0.03**	**1.7**	**0.08**	**0.15**	**0.16**	**MMP3**

Zhao et al Supplemental Figure 2

Supplemental Table 1. Significant functional networks differentially expressed in breast MSCs vs. BM-MSCs

ID	Molecules in Network	Score	Focus Molecules	Top Functions
1	**ADCY7**, BAI2, C11ORF67, C22ORF28, C7ORF10, CD44, CLCN4, CTGF, CYP1B1*, CYP2J2, ENF1, EGR2, EIF4A1, **ELK3,** ERBB2, ETS1, FMO3, FMO4, GHR, GMDS, HNF4A, IL15, Integrin, IRF6, LPPR4, NDUFB3, NRG2 (includes EG:9542), ONECUT1, PALMD, SERPINE1, SIX2, **SLC1A6**, TAT (includes EG:6898), TEC, **TLN1**	33	16	Organismal Development, Cardiovascular System Development and Function, Lymphoid Tissue Structure and Development
2	Akt, Ap1, CD79, CLEC3B, Creb, ERK1/2, FOXC1, HGF*, HLA-DPA1*, HLA-DRA*, IFN Beta, IGF2, igfbp, IL1, IL2, IL12 (complex), **IL1RN**, Interferon alpha, Jnk, Laminin, LBP*, LDL, MHC Class II, Mhc2 Alpha, **MMP3**, NFkB (complex), P38 MAPK, p70 S6k, PI3K, RNASE2*, SAA@, TFPI, Tqf beta, Tlr, VCAM1	28	14	Organismal Injury and Abnormalities, Tissue Morphology, Cell-mediated Immune Response
3	ANXA1, beta-estradiol, CDO1, **CEP170**, CLTC, CYR61, DISC1, DNAJC6, FBXO2, FOXN3, FURIN, HBEGF, **HOXB2**, IGF2R, Igfbp, IGFBP6, KLF12, KYNU (includes eg:8942)*, Mmp, **MMS19**, MYC, MYOD1, PRPF8, RAP1GAP (includes eg:5909, retinoic acid, SMAD2, SOD2, ST8SIA1, STK11, **TCF4**, TGFB3, TNC, YWHAZ, ZNF423	28	14	Cell Morphology, Cancer, Cellular Movement
4	A2M, ALB, ANGPT1, ANXA1, **ARNTL2**, CADM1, CEBPA, CFD, CLN5, CYR61, ERK, FGF1, FURIN, geranylgeranyl pyrophosphate, HBEGF, Igf, IL17A (includes EG:3605), KRT8, MAOB, Mapk, NOV, NTRK, NTRK2*, OSR2, P2RY2, **PMCH**, PTGER4, Ras, RGS3, SEMA3F, SERPINI1, TGFB1, THBD, TNC	21	11	Cellular Movement, Cellular Growth and Proliferation, Cell-to-Cell Signaling and Interaction
5	DACH1, EYA1, SIX1	2	1	Developmental Disorder, Organ Morphology, Renal Hypoplasia
6	DVL1L1, Frizzled, FZD5, LRP6	2	1	Cardiovascular System Development and Function, Cell Death, Embryonic Development

Bold indicates that particular molecule is expressed at significantly higher levels in breast MSCs compared to BM-MSCs. Underlined indicates the converse. GEO Accession Number: GSE24433

Supplemental Table 2. Genes highly expressed in both breast MSCs and BM-MSCs

ID	Molecules in Network	Score	Focus Molecules	Top Functions
1	**ANXA2*, BTF3***, Ck2, **COL1A2, NEDD8**, NFkB (complex), **NPM1 (includes EG:4869), NUCKS1, POLR2E, POLR2J,** RNA polymerase II, **RPL7*, RPL8, RPL14, RPL15, RPL17, RPL18, RPL27, RPL29*, RPL21, RPL12 (includes EG:6136)*, RPL19 (includes EG:6143), RPL5 (includes EG:6125), RPL9 (includes EG:6133), RPS2*, RPS5, RPS7, RPS14, RPS18, RPS20*, RPS23, RPS26, RPS15A, UBA2**	65	32	Protein Synthesis, RNA Post-Transcriptional Modification, Cellular Assembly and Organization
2	Adaptor protein 2, **ADH5 (include EG:128)**, Akt, **AP2S1*, BGN, CALM3,** Calmodulin, **CLTC**, Collagen(s), **CYFIP1**, ERK, **FN1***, G protein beta gamma, **GNAS*, GNG5, GNG10, GTF3A, KTN1, NCKAP1**, P38 MAPK, Pdgf, **PDGFC** PI3K, PLC, **PPIA (includes EG:5748)*, RAC1*, RAP1A, RASA1, RHEB, RPS21, RPSA (includes EG:3921), SP3, SPARC,** Tgfbeta, VEGF	38	23	Cellular Assembly and Organization, Lymphoid Tissue Structure and Development, Skeletal and Muscular System Development and Function
3	**ANXA2***, CNBP, DDX56, **EEF1A1***, EEF1D, **EEF1G***, EIF4A1, EIF5A, GAS7, MAGEB2 (includes EG:4113), **MRCL3**, MYCN, **NEDD8**, NME2, **NPM1 (includes EG:4869)**, PA2G4, retinoic acid, **RPL6, RPL24, RPL30, RPL37, RPL13A*, RPL37A (includes EG:6168), RPL38 (includes EG:6169), RPLP0 (includes EG:6175)*, RPS15, RPS16*,** RPS19, **RPS12 (includes EG:6206), RPS24 (includes EG:6229), RPS3A*, SPARC,** STAU1, TGM2, **TMSB10**	35	21	Protein Synthesis, RNA Post-Transcriptional Modification, Cancer
4	APOA4, Coup-Tf, **CS, CXXC1, ERLIN1**, FAM46A, FH, FHIT, **HMGN4 (includes EG:10473)**, HNF4A, **LAPTM4A**, LIPC, malate dehydrogenase, **MDH2, MRPL33**, NAPA (includes EG:8775), **NR2F2, NSF, PCNP, PSMA1**, PSMD7, RABGEF1, RAD18, **RPL41**, RPLP1, SAP18, **SPCS2, SRPR**, SSR2, **TMEM30A**, TUBB4, **UBE2B, UBE2M**, WDR77	26	17	Gene Expression, Cellular Assembly and Organization, Cellular Function and Maintenance
5	APLP1, **ATG12**, BIRC6, C5ORF13, **CACYBP**, CBX1, **CBX3**, CDC34 (includes EG:997), CDKN2D, CHFR, **DAZAP2 (includes EG:9802), EEF1A1***, EEF1B2, HARS, Histone h3, MAGED2, Pkc(s), RAD23B, **RPS9, RPS29, SEPT2, SET, SF3B1*, SKP1***, STAB2, STAM, **SUMO3, TMSB4X**, TP53BP2, **TPT1 (includes EG:7178), UBC, UBE2D3**, Ubiquitin, UCHL1, USP8	24	16	Molecular Transport, Nucleic Acid Metabolism, Small Molecule Biochemistry
6	AGT, **AP3D1**, BRD8, CCL18, CCNF, CENPF, **COMT, GDI2, HUWE1**, hydrogen peroxide, IL15, ING3, MNAT1, **MORF4L1, MORF4L2**, MRFAP1, **MRLC2**, MYST1, **OAZ1**, PAFAH1B3, **PPIA (includes EG:5478)***, PTP4A1, **PTP4A2***, RB1, **RPL7A, RPS7, RPS17 (includes EG:6218)*, RPS3A*, SERBP1**, SERPINB5, TGFB2, TP53, UBA6, **UBA52, UQCRH**	24	17	Cellular Growth and Proliferation, Skeletal and Muscular System Development and Function, Cell Cycle
7	ACAP1, Alpha catenin, **ANXA2*, AP2M1, AP2S1***, CDH5, CEACAM1, **CTNNA1**, CTNNB1, **CYB5R3**, DLGAP4, DOCK3, **FAT1**, GRB2, HTRA1, **LIMA1**, LMO7, LY9, **MATR3**, PDIA2, PKD1, PPP3CA, PSEN1, RPL10, **RPL13*, RPLP2, RPSA (includes EG:3921)**, RRAS, **SLC25A3**, SRC, SRP9, **SRP14, TGF, UGP2, YME1L1***	23	16	Cell-to-Cell Signaling and Interaction, Tissue Development, Renal and Urological System Development and Function
8	**C11ORF58, DYNC1I2, DYNLRB1**, EEF1B2, **EEF1G*, FKSG17**, HLA-B, **KARS**, LARS, NADH dehydrogenase, NADH2 dehydrogenase, NADH2 dehydrogenase (ubiquinone), ND3, **NDUFA4**, NDUFA5, NDUFA6, NDUFA9 (includes EG:4704), NDUFB3, **NDUFB4**, NDUFB10, **NDUFC1**, NDUFS1, NDUFS2, NDUFS4, NDUFS5, NDUFS6 (includes EG:4726), **NDUFV2**, PDCD5, **RARS, RPL4*, RPL32, PRS28, TOMM20***, TOMM22, TOMM40	22	15	Free Radical Scavenging, Genetic Disorder, Metabolic Disease
9	Ca2+, CALML5, CAMK2A, **CAPN2**, Caspase, **CHMP5**, COX1, COX2, COX17, **COX4I1, COX5A**, COX5B, **COX7A2**, COX7A2L, CXCL2, CXCL13, Cytochrome c oxidase, **EIF4G2**, GAS2, **GLO1, MCFD2**, MCL1, **NOTCH2***, PSME1, PTPN12, **RPL21 (includes EG:6144), RPS11**, SERPINB9, SPHK1, **STAG2**, TNF, USP6, **USP22, YWHAQ (includes EG:10971)***	20	14	Inflammatory Response, Cell-to-Cell Signaling and Interaction, Cell-mediated Immune Response
10	ACTA1, ATG5 (includes EG:9474), **CAPZA1, CAPZA2, CAPZB**, CCNA1, CD2, CD2AP, CDK4, **CMPK1, CSNK1A1, CUTA**, DAPK1, DFFA, EIF1B, FSH, GOLGA2, KRT18, M6PRBP1, magnesium, MAP2K1, MCC, **RAB1A**, RAB2A, **RPL39, SEC62**, SEC63, SGK1, STRN4, **TBCA**, TFRC, **TMED2, TMX1**, TWF2, **WIPI2**	18	13	Cell Morphology, Cellular Assembly and Organization, Cancer
11	aldosterone, **ANXA2*, C14ORF166, CALU**, CCAR1, CSE1L, EIF4A1, F2, FKBP4, GGCX, GTP, HNRNPC, **HSBP1**, Hsp70, **IPO5**, IQGAP2, **KLC1, NAGK**, NR3C1, NSFL1C, NUP50, PAK6, **PNRC1, PSMG2, RPL22*, RWDD1 (includes EG:51389)**, TERC (includes EG:7012), TERT, TNFRSF12A, **TNPO1**, TP53BP2, UCP2, **XBP1**, YBX1, YWHAZ	18	13	Endocrine System Development and Function, Lipid Metabolism, Small Molecule Biochemistry
12	ACTBM, Adensine-tetraphosphatase, ATP5A1, ATP5B, **ATP5C1***, ATP5D, ATP5E, **ATP5H (includes EG:10476), ATP5J2**, ATP5O, ATP6V1G2, **EIF1**, EIF1AX, EIF1B, EIF2S1, EIF3A, IEF3F, EIF3J, **EIF3K**, EIF3L, **EIF3M**, EIF4A2, EIF4G1, H+-transporting two-sector ATPase, L-methionyl-tRNA (Met), MME, NME2, PFN2, PNO1, **RPS10*, RTN4**, TRAF6	10	8	Energy Production, Nucleic Acid Metabolism, Small Molecule Biochemistry

Bolded molecules indicate those highly expressed; GEO Accession Number: GSE2443