



C

	Symbol	Entrez Gene Name	Fold Change	Location	Type(s)
Network1	<i>cnr1</i>	cannabinoid receptor 1 (brain)	-31,627	Plasma Membrane	G-protein coupled receptor
	<i>areg/aregb</i>	amphiregulin	-31,481	Extracellular Space	growth factor
	<i>efnb2</i>	ephrin-B2	-26,049	Plasma Membrane	other
	<i>fkbp5</i>	FK506 binding protein 5	-19,747	Nucleus	enzyme
	<i>hsd11b1</i>	hydroxysteroid (11-beta) dehydrogenase 1	-19,149	Cytoplasm	enzyme
	<i>ptger2</i>	prostaglandin E receptor 2 (subtype EP2), 53kDa	-15,357	Plasma Membrane	G-protein coupled receptor
	<i>hgf</i>	hepatocyte growth factor (hepapoietin A; scatter factor)	-5,638	Extracellular Space	growth factor
Network2	<i>cpm</i>	carboxypeptidase M	-21,249	Plasma Membrane	peptidase
	<i>maoa</i>	monoamine oxidase A	-16,804	Cytoplasm	enzyme
	<i>zbtb16</i>	zinc finger and BTB domain containing 16	-6,652	Nucleus	transcription regulator
	<i>alox15b</i>	arachidonate 15-lipoxygenase, type B	-4,850	Cytoplasm	enzyme
	<i>cc120</i>	chemokine (C-C motif) ligand 20	-3,985	Extracellular Space	cytokine

SUPPLEMENTARY FIG. S1. Possible biological processes involving the differentially expressed genes. Gene expression in FP-ASCs and hASCs was analyzed using the Human Gene 1.0 ST array (Affymetrix) and subjected to an Ingenuity Knowledge Base search using the IPA application. Molecular interaction networks detected were (A) “Cell Growth and Proliferation, Cell Morphology and Cell Death” Network 1, score = 82. (B) “Cell Movement, Cell Signaling and Cell–Cell Interaction, and Cell Development” Network 2, score = 34. Indicative graphs showing genes differentially expressed in FP-ASCs and hASCs, shown in *green* (FP-ASCs > MSCs) or *red* (FP-ASCs < MSCs). Color intensity reflects the fold change (FC) in expression. *Uncolored symbols* connect genes excluded from the list of selected genes. (C) Table of array results showing expression levels for genes selected for validation by real-time polymerase chain reaction (RT-PCR) in the different networks. hASCs, human adipose-tissue-derived MSCs; FP-ASCs, fast-proliferating phenotype; MSCs, mesenchymal stromal cells; IPA, Ingenuity Pathway Analysis.