

SUPPLEMENTARY TABLE S1. mRNA MICROARRAY RESULTS

<i>Symbol</i>	<i>Entrez gene name</i>	<i>Log ratio</i>	<i>P-value</i>
<i>CHI3L1</i>	Chitinase 3-like 1 (cartilage glycoprotein-39)	1.654	4.81E-02
<i>RPS4Y1</i>	Ribosomal protein S4, Y-linked 1	1.390	2.16E-01
<i>TRIB1</i>	Tribbles homolog 1 (<i>Drosophila</i>)	1.024	4.31E-02
<i>GAS1</i>	Growth arrest-specific1	0.941	2.21E-02
<i>SRSF6</i>	Serine/arginine-rich splicing factor 6	0.935	3.54E-03
<i>COLEC12</i>	Collectin subfamily member 12	0.925	1.35E-01
<i>HES1</i>	Hairy and enhancer of split 1 (<i>Drosophila</i>)	0.915	3.55E-02
<i>PTGS2</i>	Prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase)	0.879	7.52E-02
<i>LRRC15</i>	Leucine-rich repeat containing 15	0.850	1.58E-01
<i>CTSK</i>	Cathepsin K	0.835	5.46E-02
<i>NR4A2</i>	Nuclear receptor subfamily 4, group A, member 2	0.834	1.16E-01
<i>ENPP1</i>	Ectonucleotide pyrophosphatase/phosphodiesterase 1	0.793	4.88E-02
<i>CH25H</i>	Cholesterol 25-hydroxylase	0.785	8.53E-02
<i>BAALC</i>	Brain and acute leukemia, cytoplasmic	0.782	3.07E-02
<i>FOS</i>	FBJ murine osteosarcoma viral oncogene homolog	0.763	2.17E-01
<i>IGFBP5</i>	Insulin-like growth factor binding protein 5	0.705	3.56E-03
<i>HAS1</i>	Hyaluronan synthase 1	0.703	1.01E-01
<i>TNC</i>	Tenascin C	0.696	3.37E-02
<i>SRPX</i>	Sushi-repeat containing protein, X-linked	0.660	8.02E-03
<i>CTBP1</i>	C-terminal binding protein 1	0.649	1.07E-01
<i>EIF1AY</i>	Eukaryotic translation initiation factor 1A, Y-linked	0.647	2.06E-01
<i>BHLHE40</i>	Basic helix-loop-helix family, member e40	0.637	8.87E-02
<i>RAB3B</i>	RAB3B, member RAS oncogene family	0.612	2.46E-02
<i>GSTT2/GSTT2B</i>	Glutathione S-transferase theta-2	0.607	1.52E-03
<i>ETV1</i>	Ets variant 1	0.584	2.30E-02
<i>FBN2</i>	Fibrillin-2	0.583	2.25E-01
<i>MATN2</i>	Matrilin-2	0.580	7.64E-03
<i>MAFB</i>	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian)	0.566	5.12E-02
<i>DDX3Y</i>	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	0.558	2.96E-01
<i>FOSB</i>	FBJ murine osteosarcoma viral oncogene homolog B	0.550	2.10E-01
<i>OLFML3</i>	Olfactomedin-like 3	0.548	9.79E-02
<i>ATF3</i>	Activating transcription factor 3	0.544	1.43E-01
<i>INSIG1</i>	Insulin-induced gene 1	0.536	1.82E-01
<i>PTN</i>	Pleiotrophin	0.532	5.33E-03
<i>NUCKS1</i>	Nuclear casein kinase and cyclin-dependent kinase substrate 1	0.527	2.96E-02
<i>APOBEC3B</i>	Apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3B	0.524	3.67E-03
<i>ACAT2</i>	Acetyl-CoA acetyltransferase 2	0.524	3.96E-02
<i>EIF2S3</i>	Eukaryotic translation initiation factor 2, subunit 3 gamma, 52 kDa	0.513	8.23E-02
<i>PTX3</i>	Pentraxin 3, long	-0.500	4.03E-01
<i>CNN1</i>	Calponin 1, basic, smooth muscle	-0.504	1.78E-02
<i>ITGBL1</i>	Integrin, beta-like 1 (with EGF-like repeat domains)	-0.516	7.01E-02
<i>TXNIP</i>	Thioredoxin-interacting protein	-0.517	8.55E-02
<i>CYTL1</i>	Cytokine-like 1	-0.517	4.11E-01
<i>MCAM</i>	Melanoma cell adhesion molecule	-0.519	9.54E-02
<i>TIMP3</i>	TIMP metalloproteinase inhibitor 3	-0.520	4.11E-02
<i>IFI27</i>	Interferon, alpha-inducible protein 27	-0.521	1.71E-01
<i>FST</i>	Follistatin	-0.530	2.23E-01
<i>MFAP5</i>	Microfibrillar-associated protein 5	-0.532	1.21E-01
<i>FHL1</i>	Four and a half LIM domains 1	-0.535	6.07E-02
<i>JAG1</i>	Jagged 1	-0.549	2.32E-01
<i>ACAN</i>	Aggrecan	-0.565	8.00E-02
<i>KRT18</i>	Keratin 18	-0.565	4.25E-01
<i>LTBP1</i>	Latent transforming growth factor beta-binding protein 1	-0.567	1.19E-02
<i>EPAS1</i>	Endothelial PAS domain protein 1	-0.571	4.00E-02
<i>SLC7A11</i>	Solute carrier family 7 (anionic amino acid transporter light chain, xc- system), member 11	-0.573	6.99E-02
<i>DDIT4</i>	DNA-damage-inducible transcript 4	-0.592	1.80E-01
<i>ASNS</i>	Asparagine synthetase (glutamine-hydrolyzing)	-0.600	1.83E-01
<i>LIMCH1</i>	LIM and calponin homology domains 1	-0.600	1.12E-01
<i>EFEMP1</i>	EGF containing fibulin-like extracellular matrix protein 1	-0.602	3.69E-02
<i>MTHFD2</i>	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	-0.607	4.80E-02

(continued)

SUPPLEMENTARY TABLE S1. (CONTINUED)

<i>Symbol</i>	<i>Entrez gene name</i>	<i>Log ratio</i>	<i>P-value</i>
<i>C10orf116</i>	Chromosome 10 open reading frame 116	-0.617	3.85E-02
<i>CLIC3</i>	Chloride intracellular channel 3	-0.636	5.97E-03
<i>PSAT1</i>	Phosphoserine aminotransferase 1	-0.640	8.73E-02
<i>COL4A2</i>	Collagen, type IV, alpha 2	-0.655	2.86E-03
<i>DEPTOR</i>	DEP domain containing MTOR-interacting protein	-0.670	1.54E-01
<i>SLC7A5</i>	Solute carrier family 7 (amino acid transporter light chain, L system), member 5	-0.686	4.01E-02
<i>COL1A1</i>	Collagen type I, alpha 1	-0.700	9.37E-02
<i>ALDH1A3</i>	Aldehyde dehydrogenase 1 family, member A3	-0.748	9.99E-02
<i>COL4A1</i>	Collagen type IV, alpha 1	-0.749	2.43E-03
<i>KRT14</i>	Keratin 14	-0.776	6.33E-03
<i>PPP1R3C</i>	Protein phosphatase 1, regulatory subunit 3C	-0.783	7.34E-03
<i>DKK1</i>	Dickkopf 1 homolog (<i>Xenopus laevis</i>)	-0.790	1.10E-01
<i>TNFRSF11B</i>	Tumor necrosis factor receptor superfamily, member 11b	-0.817	2.11E-02
<i>XIST</i>	X (inactive)-specific transcript (nonprotein coding)	-0.892	2.03E-01
<i>PTGIS</i>	Prostaglandin I2 (prostacyclin) synthase	-0.900	2.41E-02
<i>ELN</i>	Elastin	-0.923	3.67E-02
<i>RGS4</i>	Regulator of G-protein signaling 4	-0.949	2.08E-01
<i>SULF1</i>	Sulfatase 1	-0.994	7.93E-03
<i>STC2</i>	Stanniocalcin-2	-0.999	2.03E-02

Regulated genes with log ratio of difference between good and low-performing donors of at least 0.5. According significance levels for each gene are displayed, but genes were not selected on significance.