



**Supplementary Figure 1:** Gene expression profiles of the 22 genes (significantly discriminating MMECs vs. MGECs) in the 15 samples (5 HUVECs, 5 MGECs, 5 MMECs) dataset by means of SAM multiclass supervised analysis. The matrix has been generated by means of dChip software (13). The color scale bar represents the relative gene-expression changes normalized by the standard deviation, and the color changes in each row represent gene expression relative to the mean across the samples. Gene symbols are indicated.

Annotation cluster n°	Enrichment score	Representative annotation terms	Gene count
1	9.37	Cell motility	39
2	8.33	Hemostasis	18
3	8.19	Glycosaminoglycan binding	18
4	7.77	Blood vessel development	24
5	7.26	Anion transport	21
6	5.25	Blood vessel morphogenesis	20
7	4.98	Regulation of cell migration	11
8	3.61	Skeletal muscle development	11
9	2.98	Cell death	40
10	2.52	Cell projection morphogenesis	16
11	2.50	Embryonic limb morphogenesis	7
12	2.41	Tissue remodeling	12
13	2.38	Neurogenesis	19
14	2.33	Signal transducer activity	96
15	2.29	Cell growth	14
16	2.25	Regulation of kinase activity	16
17	2.21	Muscle cell proliferation	5
18	2.05	Cellular calcium ion homeostasis	11
19	1.98	Chemotaxis	11
20	1.85	Hemopoiesis	13
21	1.82	Myoblast development	4
22	1.82	Adaptive immune response	8
23	1.81	Amine metabolic process	24
24	1.80	Lipid homeostasis	4
25	1.76	Negative regulation of apoptosis	14
26	1.62	Neuron development	12
27	1.58	Cell cycle process	32
28	1.52	Positive regulation of kinase activity	10
29	1.46	Positive regulation of chemotaxis	3
30	1.33	Activation of immune response	6
31	1.32	L-serine biosynthetic process	3
32	1.30	Regulation of heart contraction	5
33	1.30	Positive regulation of immune response	7

**Supplementary Table 1:** The 663 probesets resulting as the highly variable ones (2AVEFC) in the 15 samples (5 HUVECs, 5 MGECs, 5 MMECs) dataset by unsupervised analysis were analyzed by means of the Database for Annotation, Visualization and Integrated Discovery (DAVID) Tool 2008, using the Functional Annotation Clustering Tool (Huang et al.: Systematic and integrative analysis of large gene lists using DAVID Bioinformatics Resources. Nature Protoc 2009;4:44-57). Specifically, Gene Ontology (GO) Biological Process (BP) and Molecular Function (MF) terms were selected as annotation categories and high classification stringency was set for the analysis. Only the 33 annotation clusters (out of the 83 clusters globally identified) with an Enrichment score superior than 1.3 value are represented. The reported annotation terms were manually selected and the corresponding gene counts were referred to the recognized 528 DAVID IDs.

<b>Probe Set ID</b>	<b>Gene Symbol</b>	<b>Score(d)</b>	<b>contrast-HUVECs</b>	<b>contrast-MGECs</b>	<b>contrast-MMECs</b>	<b>q-value (%)</b>
201438_at	<b>COL6A3</b>	8.8181	-8.4716	7.5555	0.9162	0
201645_at	<b>TNC</b>	6.3761	-4.2176	6.6452	-2.4276	0
202465_at	<b>PCOLCE</b>	5.8817	-4.4325	5.9748	-1.5423	0
211981_at	<b>COL4A1</b>	5.3555	-4.6854	-0.3868	5.0722	0
212940_at	<b>COL6A1</b>	4.4675	-3.7602	4.3404	-0.5803	0
202283_at	<b>SERPINF1</b>	3.9504	-2.8381	4.0608	-1.2226	0
202450_s_at	<b>CTSK</b>	3.8119	-2.8219	3.8904	-1.0686	0
206481_s_at	<b>LDB2</b>	3.6556	-2.1070	3.8535	-1.7464	0
209283_at	<b>CRYAB</b>	3.4938	-2.9635	-0.4135	3.3769	0
204955_at	<b>SRPX</b>	3.1723	2.8800	0.0342	-2.9142	0
210809_s_at	<b>POSTN</b>	3.0492	-2.8298	2.7358	0.0940	0
209687_at	<b>CXCL12</b>	2.9551	-2.5189	2.8475	-0.3286	0
218934_s_at	<b>HSPB7</b>	2.6951	-1.9148	-0.8615	2.7763	0.06
219087_at	<b>ASPN</b>	2.3892	-1.3848	2.5209	-1.1361	0.14
201858_s_at	<b>SRGN</b>	2.3023	1.9379	-2.2347	0.2968	0.16
201849_at	<b>BNIP3</b>	2.2948	-1.8779	-0.3832	2.2611	0.16
204472_at	<b>GEM</b>	2.2635	-1.3776	2.3784	-1.0008	0.16
201983_s_at	<b>EGFR</b>	2.1466	-1.2541	2.2603	-1.0062	0.27
201194_at	<b>SEPW1</b>	1.8334	0.5880	-1.8893	1.3012	0.83
215506_s_at	<b>DIRAS3</b>	1.4824	-0.8212	1.5636	-0.7423	2.58
209016_s_at	<b>KRT7</b>	1.1885	-0.8353	-0.3916	1.2269	7.28
201631_s_at	<b>IER3</b>	1.0796	-0.5794	1.1382	-0.5588	9.82

**Supplementary Table 2:** The 22 genes discriminating MMECs from MGECs were also identified among the significantly differentially expressed probe sets in HUVECs, MGECs and MMECs by means of supervised multiclass analysis (SAM, FDR  $\leq 10\%$ ). Genes are ordered according to their SAM *score(d)*. The *contrast* value for each gene in each class is also shown (positive score means positive correlation) and the *q*-value for each gene is reported.