

**Supplementary Table S3.** Diseases and functions predicted to be influenced in adipose-derived stem cells originating from three patients after RNA pooling and stimulation with PDGF2 (1 µg/mL) compared with parallel controls untreated with PDGF2

Diseases and Function Annotation	p	Predicted Activation State	z-Score	Number of Molecules Involved in the Process
Invasion of cells	7.01E-08	Increased	2.520	77
Cell cycle progression	1.55E-05	Increased	2.498	62
Proliferation of epithelial cell lines	1.84E-05	Increased	2.336	30
Binding of professional phagocytic cells	8.97E-07	Decreased	-2.001	22
Flux of cation	1.19E-06	Decreased	-2.037	26
Cell viability of lymphocytes	1.61E-04	Decreased	-2.051	10
Cell movement of lymphocytes	5.72E-07	Decreased	-2.103	30
Cell movement of phagocytes	1.51E-04	Decreased	-2.104	31
Binding of blood cells	2.60E-12	Decreased	-2.107	49
Migration of mononuclear leukocytes	7.85E-09	Decreased	-2.118	35
Cell death of cancer cells	1.13E-04	Decreased	-2.128	26
Lymphocyte migration	1.38E-07	Decreased	-2.141	29
Lymphopoiesis	1.08E-05	Decreased	-2.151	22
Flux of ion	2.17E-07	Decreased	-2.164	28
Cellular homeostasis	1.51E-05	Decreased	-2.214	82
Flux of Ca <sup>2+</sup>	1.25E-05	Decreased	-2.342	23
Lymphohematopoietic neoplasia	1.49E-14	Decreased	-2.345	319
Hematological neoplasia	3.76E-14	Decreased	-2.345	319
Cell movement of mononuclear leukocytes	7.26E-07	Decreased	-2.485	38
Cell movement of T lymphocytes	4.67E-05	Decreased	-2.486	18
T cell migration	6.95E-05	Decreased	-2.522	19
Binding of mononuclear leukocytes	1.08E-07	Decreased	-2.563	25
Mobilization of Ca <sup>2+</sup>	1.96E-06	Decreased	-2.944	30

The z-score is an algorithm in the IPA software designed to reduce the chance that random data will produce a significant prediction. It identifies functions with the strongest prediction for an increase (positive z-score) or a decrease (negative z-score). p-Score values <0.05 and z-score values ≤-2 or ≥2 were considered significant.

IPA, Ingenuity Pathway Analysis.

**Supplementary Table S4.** Diseases and functions predicted to be influenced in fibroblasts originating from three patients after RNA pooling and stimulation with PDGF2 (1 µg/mL) compared with parallel controls untreated with PDGF2

Diseases and Function Annotation	p	Predicted Activation State	z-Score	Number of Molecules Involved in the Process
Cell movements	2.83E-03	Increased	3.742	76
Cell migration	1.53E-03	Increased	3.445	70
L-Tyrosine phosphorylation	3.11E-02	Increased	2.449	8
Stem cell migration	4.20E-04	Increased	2.176	5
Invasion of cells	1.36E-02	Increased	2.073	40
Apoptosis	1.57E-03	Decreased	-2.016	88

The z-score is an algorithm in the IPA software designed to reduce the chance that random data will produce a significant prediction. It identifies functions with the strongest prediction for an increase (positive z-score) or a decrease (negative z-score). p-Score values <0.05 and z-score values ≤-2 or ≥2 were considered significant.