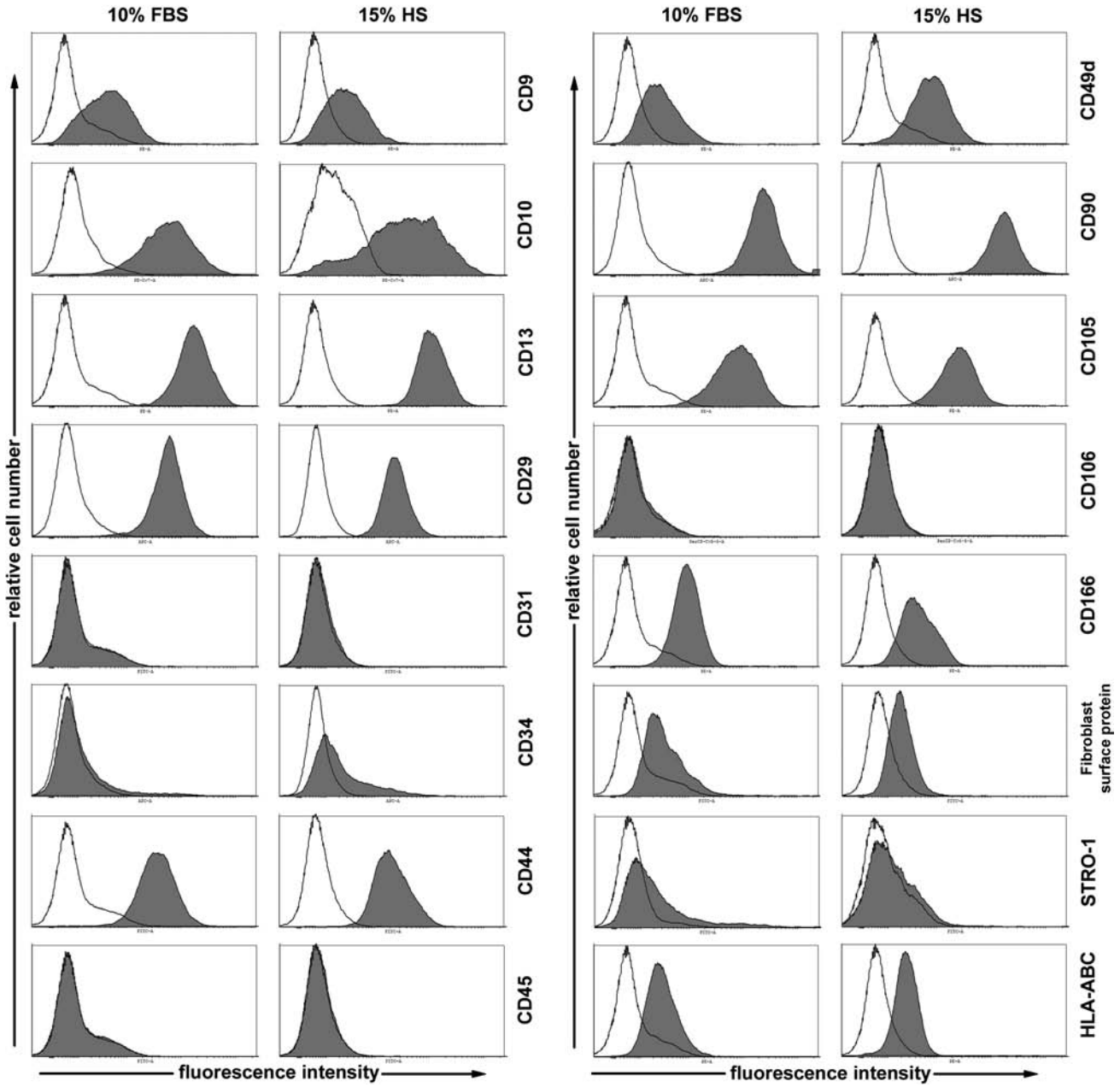
SUPPLEMENTAL ONLINE DATA S1. Characterization of adipose stem cells (ASCs). Surface marker expression of undifferentiated ASCs analyzed by flow cytometric analysis of 10,000 cells. Data are presented as mean ± standard deviation obtained from the number of donors indicated in parentheses.

Surface Protein	*Antigen*	*Manufacturer*	*Fetal bovine serum (n=15)*	*Human serum (n=15)*
CD9	Tetraspanin receptor	BD	16.8 ± 9.9	12.9 ± 11.3
CD10	CALLA	BD	75.8 ± 16.9	76.8 ± 19.6
CD13	Aminopeptidase N	BD	99.6 ± 0.7	99.5 ± 0.7
CD29	Integrin β1	BD	98.1 ± 3.2	97.4 ± 2.9
CD31	PECAM	IT	0.5 ± 0.5	0.5 ± 0.5
CD34	Sialomucin-like adhesion molecule	IT	20.4 ± 27.5	10.8 ± 20.2
CD44	Hyaluronate, HCAM	IT	81.7 ± 17.7	77.1 ± 24.7
CD45	Leukocyte common antigen	MB	0.6 ± 0.5	0.5 ± 0.3
CD49d	Integrin α2, VLA-4	BD	25.6 ± 13.6	32.0 ± 25.0
CD90	Thy-1	BD	99.0 ± 1.2	99.1 ± 1.1
CD105	SH-2, endoglin	RD	94.5 ± 5.9	87.9 ± 10.1
CD106	VCAM-1	BD	0.8 ± 1.0	0.8 ± 0.7
CD166	ALCAM	BD	29.7 ± 21.2	32.9 ± 29.8
HLA-ABC	Major histocompatibility class I antigen	IT	11.5 ± 9.0	18.0 ± 14.7
	Fibroblast surface protein	Sigma	8.6 ± 10.7	6.4 ± 10.4
	STRO-1	RD	3.2 ± 2.7	3.6 ± 5.9

CALLA, common leukocyte lymphocytic leukemia antigen; PECAM, platelet endothelial cell adhesion molecule; HCAM, lymphocyte homing-associated cell adhesion molecule; VCAM, vascular cell adhesion molecule; ALCAM, activated leukocyte cell adhesion molecule; Thy-1, T cell surface glycoprotein; STRO-1, putative mesenchymal stem cell marker

BD, BDBiosciences, Erembodegem, Belgium; IT, Immunotools GmbH Friesoythe, Germany; RD, R&D Systems Inc, MN, USA; MB, Miltenyi Biotech, Bergisch Gladbach, Germany; Sigma; Sigma, St. Louis, MO, USA

Characterization of ASCs. Relative cell number (y-axis) and fluorescence intensity (x-axis). Unstained control cells (empty histograms) and cells stained with antibodies against the surface proteins (filled histograms).



SUPPLEMENTAL ONLINE DATA S2. Microarray data quality control 1. To control data quality, RNA degradation plots were produced of the raw data and ensured to have resembling slopes and profiles (**A**). To verify adequate normalization, the comparability of the density histograms and box plots (**B, C**) of all samples and the linearity of the MA plot, a plot of log-intensity ratios (M) versus log-intensity averages (A), of each donor (human serum [HS] vs. fetal bovine serum [FBS]) were ensured. The average MA plot across all donors is presented (**D**). Microarray data quality control 2. To control data quality, a QC Report was produced. The QC Report assesses overall signal quality, 3′:5′ ratios of spiked-in and control genes, percentages of present calls, background levels, hybridization and gridding problems, background fluctuations, and outlier samples.[60] The approaches demonstrated good data quality across all samples.

SUPPLEMENTAL VIDEOS S3 A AND B. Automated monitoring of ASCs. The growth and morphologic characteristics of ASCs cultured in either 10% FBS (**A**) or 15% allogeneic human serum (alloHS) (**B**) were monitored using an online cell culture platform[104,105] (Cell-IQ®; Chip-man Technologies). This software allows time-lapse imaging of 500×670 μm areas in the culture wells. The video material was produced from the 2×2 time-lapse images (size, 1000×1340 μm) of a 3-day monitoring period, with time-lapse images captured approximately every 15 min.

SUPPLEMENTAL ONLINE DATA S4. Genes overexpressed and underexpressed in ASCs expanded in alloHS as compared to FBS.

SUPPLEMENTAL ONLINE DATA S5. Significantly enriched Gene Ontology (GO) Biological Processes and Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways.

SUPPLEMENTAL ONLINE DATA S6. Differentially expressed genes on the human KEGG Cell cycle and transforming growth factor beta (TGF-β) signaling pathways.