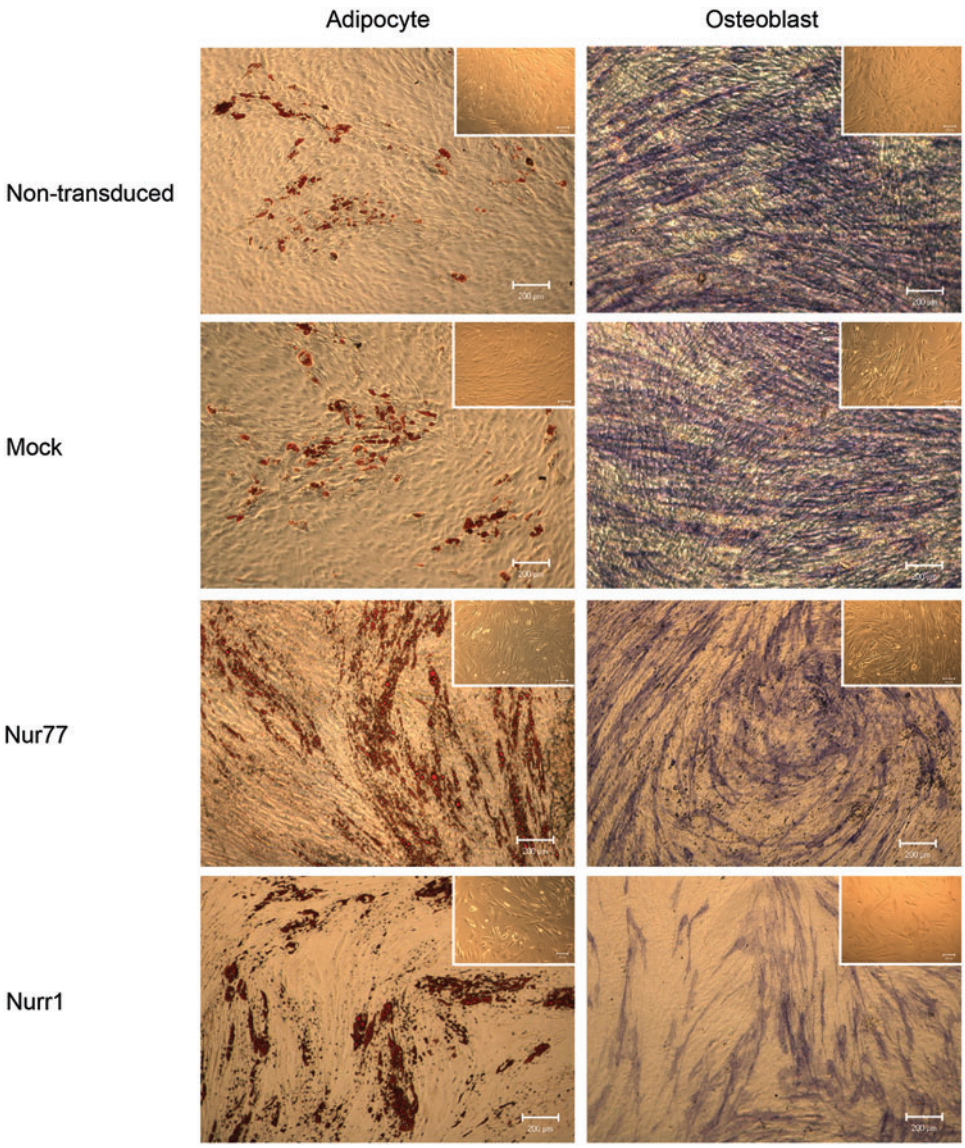
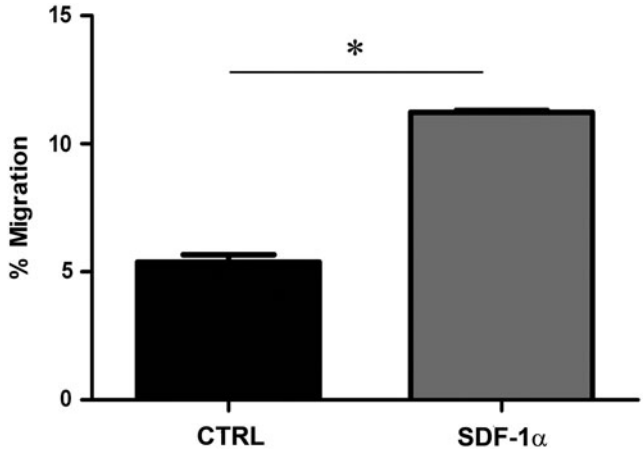
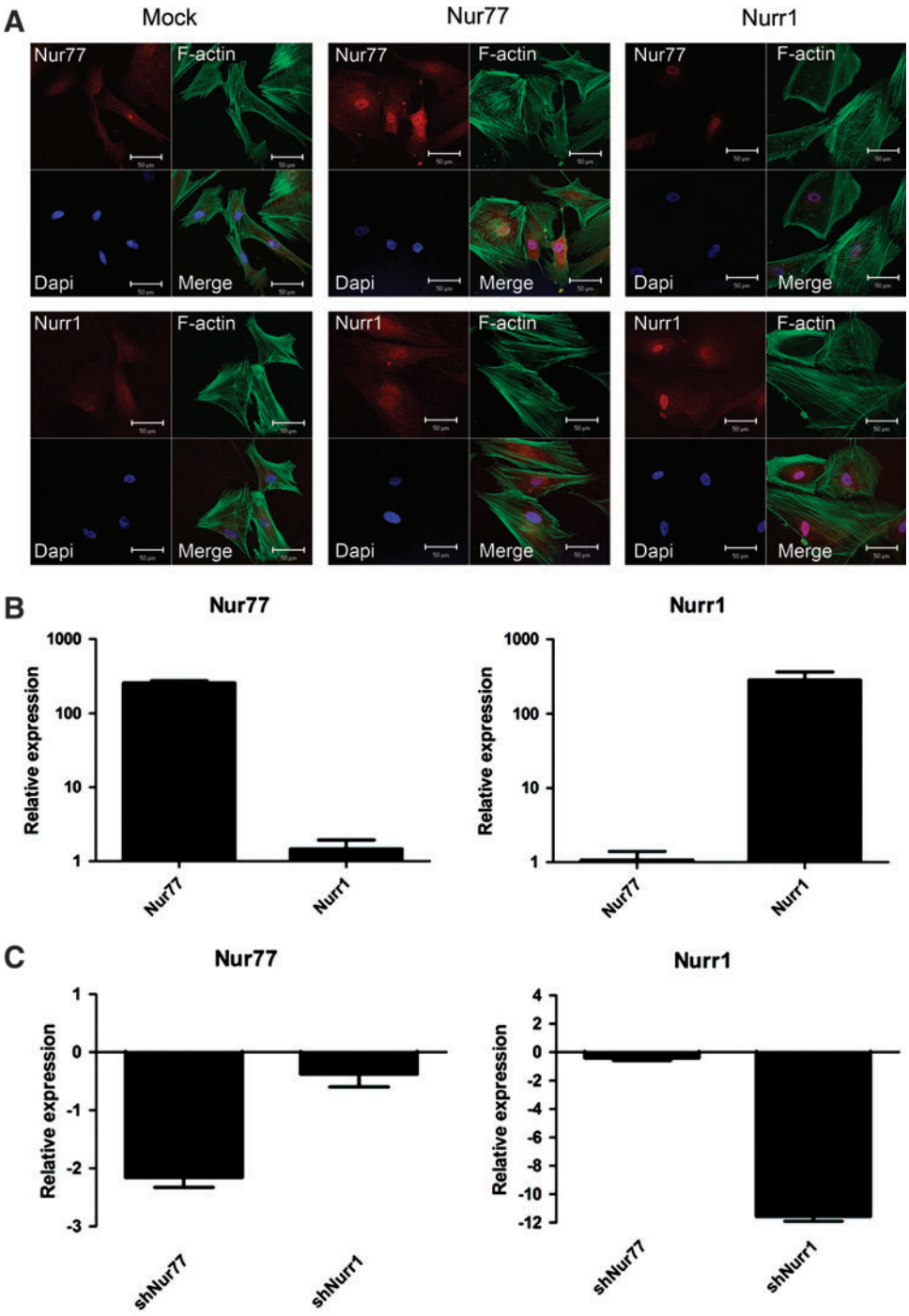
Supplementary Data



SUPPLEMENTARY FIG. S1. Adipocyte and osteoblast differentiation. Adipocyte or osteoblasts differentiation was induced in nontransduced FBMSC (*top panels*) and after transduction with mock-, Nur77-, or Nur77-containing lentivirus (representative donor shown; scale bar 200 μm). Overexpression of Nur77 or Nurr1 did not impair the differentiation potential of FBMSC. FBMSC, fetal bone marrow mesenchymal stromal cells. Insets depict undifferentiated FBMSC stained for adipocytes or osteoblasts.



SUPPLEMENTARY FIG. S2. SDF-1α-induced chemotaxis in FBMSC. To confirm SDF-1α-induced chemotaxis in the experiments from which cells were collected for gene expression profiling, 4 Transwell wells were evaluated to quantify the percentage of SDF-1α-induced migration. Wild-type FBMSC were allowed to migrate for 4 h toward SDF-1α (600 ng/mL). Medium alone served as a negative control. The number of migratory cells was counted by fluorescence microscopy. Bars represent the percentage (mean ± SD) of migrated MSC related to the cell number loaded in the upper compartment ($n = 4$). *$P \leq 0.05$. MSC, mesenchymal stromal cells; SDF-1α, stromal cell-derived factor 1α.



SUPPLEMENTARY FIG. S3. Validation of Nur77 and Nurr1 overexpression or knockdown. **(A)** Transduced MSC were seeded on fibronectin-coated glass slides, fixed, and stained for Nur77 or Nurr1 (red), F-actin by Phalloidin (green), and nuclei (blue). Clear nuclear localization of Nur77 or Nurr1 protein was observed in case of overexpression Nur77- (*middle*) or Nurr1-transduced FBMSC (*right*), respectively, whereas this was absent in mock-transduced FBMSC (*left*). Scale bar 50 μm. Please note that the anti-Nurr1 antibody gives more background than the anti-Nur77 antibody. **(B)** Quantification of *Nur77* or *Nurr1* overexpression by real-time quantitative (RQ)–polymerase chain reaction. Data (mean ± SD) were normalized to mock-transduced FBMSC. Overexpression of Nur77 (left) did not increase expression of *Nurr1* in the same cells and vice versa. **(C)** Quantification of Nur77 and Nurr1 knockdown by real-time quantitative–polymerase chain reaction. Data (mean ± SD) were normalized to short-hairpin control-transduced FBMSC. As basal expression of *Nur77* and *Nurr1* is low, the efficiency of lentiviral knockdown of Nur77 and Nurr1 is limited, whereas significant overexpression is easily achieved.

Supplementary Table S1. Primer Sequences

Gene name	*Sequence forward primer 5′–3′*	*Sequence reverse primer 5′–3′*
ABL	TGGAGATAACACTCTAAGCATAACTAAAGGT	TGGAGATAACACTCTAAGCATAACTAAAGGT
CYR61	CAGCTCCACCGCTCTGAAG	TTCCCCGTTTTGGTAGATTCTG
GFP	AGCAAAGACCCCAACGAGAA	GGCGGCGGTCACGAA
HGF	CCTCCTGCTCCCCATCG	TAGGGTAGTCTTTGCTGATTTTTTGA
HIST1H4B	GATAACATCCAAGGCATCACCA	ACCCCACCACGCCTAGC
IDO1	ACCATATTGATGAAGAAGTGGGC	TGAACATCCAGTCATTATAAAAATCAGG
NR4A1(NUR77)	AGGGCTGCAAGGGCTTCT	CCTTGTTAGCCAGGCAGATGTA
NR4A2(NURR1)	GCCCCCGGTGAGTCTGAT	GATAGTCAGGGTTCGCCTGG
NR4A3 (NOR1)	GTCAAGATTTCATCCCATACATGC	GAAGGGCTATATTGGGCTTGG
SMAD7	CCCGATGGATTTTCTCAAACC	CCCTGTTTCAGCGGAGGA
TGF-β1	AAGTGGACATCAACGGGTTC	CGTGGAGCTGAAGCAATAG

HGF, hepatocyte growth factor; IDO, indoleamine-2,3-dioxygenase; TGF-β1, transforming growth factor-β1.

Supplementary Table S2. Mesenchymal Stromal Cell Phenotype on Transduced Mesenchymal Stromal Cells

	NT	*Mock*	*Nur77*	*Nurr1*
CD73 (%)	98.4 ± 0.8	98.2 ± 2.5	97.0 ± 2.8	97.4 ± 2.0
CD90 (%)	97.4 ± 0.9	96.9 ± 2.3	97.5 ± 0.4	97.2 ± 0.4
CD105 (%)	94.7 ± 1.1	95.5 ± 0.7	95.6 ± 1.5	96.6 ± 0.9
CD45 (%)	3.1 ± 0.7	1.3 ± 1.4	2.2 ± 1.4	2.5 ± 0.8
CD34 (%)	2.0 ± 1.7	2.8 ± 0.3	2.1 ± 1.1	2.4 ± 1.2

Data expressed as percentage positive cells (mean ± SD, corrected for the isotype control from 3 individual donors) of the total population of MSC for the indicated group.

MSC, mesenchymal stromal cells; NT, nontransduced cells.