**Supplemental data**

**Figure S1. HSC derived adipocytes in multiple sites *in vivo*.** Peritoneal (A-D and M-P), omental (E-H) and peri-nephric (I-L) fat pads from mice transplanted with a clonal population of cells derived from a single $EGFP^+$ HSC were sectioned (5 μm) and examined using high magnification epi-fluorescent and DIC microscopy. Shown are representative sections from each. Numerous $EGFP^+$ cells (A, E, I, M, arrows) with characteristic morphology of adipocytes (B, F, J, N, arrows), were observed. Sections were stained using antibodies to leptin (C, G, K, O). Superimposition of the green EGFP images and red images of leptin demonstrate co-expression of EGFP and leptin (D, H, L, P, arrows). Panels M-P show EGFP expression, DIC and negative control for leptin staining, respectively. Scale bar in A-P equals 25 μm.

**Figure S2. Analysis of nuclear DNA content of cultured adipocytes.** The adipocytes were fixed in 70% ethanol and stained with propidium iodide in the presence of RNase. Controls are B16 melanoma cells and peripheral blood (PB) MNCs. The left peaks indicate cells in $G_0/G_1$ and the right peaks $G_2$/M states in adipocytes and PB MNCs.

**Table S1. PCR primer sequences and GeneBank Accession Numbers**

| Primer Name | Sequence 5`-3` | | GeneBank Accession # | Amplicon Size | Ta °C |
|---|---|---|---|---|---|
| *Resistin* | TTGGCAGGACTGAGGTTCCAT | CCACTGAATCATCTCACCAGCC | NM_022984 | 211 | 58 |
| *PPAR-γ* | GTGCCAGTTTCGATCCGTAGAA | TCCCTGGTCATGAATCCTTGG | NM_011146 | 201 | 58 |
| *PAI1* | ACATGTTTAGTGCAACCCTGGC | GCCGAACCACAAAGAGAAAGG | NM_008871 | 201 | 60 |
| *Leptin* | CATGTCCCTGTGGTTAGACCCT | ATCCCGTGTCAACAGTGTGCT | NM_008493 | 217 | 60 |
| *C/EBP-α* | GCCCCTCAGTCCCTGTCTTTAG | ATGGTCCCCGTGTCCTCCTA | NM_007678 | 302 | 60 |
| *FABP4* | TGAAATCACCGCAGACGACA | AGGCCTCTTCCTTTGGCTCAT | NM_024406 | 201 | 59 |
| *Sox9* | TCCCAAAACCGACGTGCAA | TGCCGTAACTGCCAGTGTAGGT | NM_011448 | 242 | 62 |
| *HPRT* | GCTGGTGAAAAGGACCTCTC | ATGGCCACAGGACTAGAACAC | J00423 | 254 | 62 |

TnQTable2Ta, annealing temperature; PPAR-γ, peroxisome proliferator-activated receptor-γ; PAI1, plasminogen activator inhibitor type 1; C/EBP-α, CCAAT/enhancer binding protein-α; FABP4, fatty acid binding protein 4; Sox9, SRY-box containing gene 9; HPRT, hypoxanthine phosphoribosyl transferase.

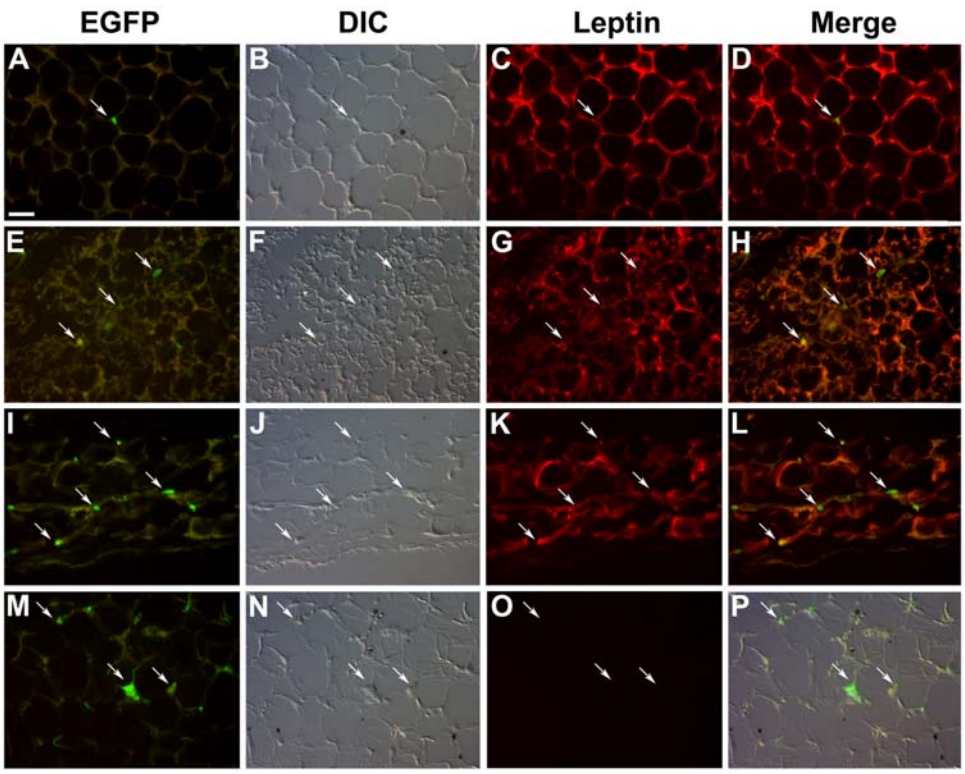
**Table S2. Relationship between hematopoietic lineage expression and adipogenesis observed from single hematopoietic progenitors**

| Clone Number | Hematopoiesis | | | | | | Adipogenesis |
|---|---|---|---|---|---|---|---|
| | Type of clones | Differential counts, % | | | | | |
| | | n | m | E | M | Im | |
| 1 | nmEM | 84.0 | 6.5 | 7.5 | 2.0 | 0 | + |
| 2 | nmEM | 87.0 | 4.0 | 7.5 | 1.5 | 0 | + |
| 3 | nmEM | 62.5 | 12.0 | 20.5 | 2.0 | 3.0 | + |
| 4 | nm | 88.5 | 11.5 | 0 | 0 | 0 | + |
| 5 | nmEM | 57.5 | 12.5 | 29.5 | 0.5 | 0 | + |
| 6 | nm | 67.0 | 33.0 | 0 | 0 | 0 | + |
| 7 | nmEM | 56.5 | 33.0 | 10.0 | 0.5 | 0 | + |
| 8 | nmEM | 59.0 | 12.5 | 13.5 | 9.5 | 5.5 | + |
| 9 | nE | 92.0 | 0 | 8.0 | 0 | 0 | - |
| 10 | nmE | 79.0 | 6.0 | 15.0 | 0 | 0 | + |
| 11 | nmEM | 85.5 | 11.0 | 2.0 | 0.5 | 1.0 | + |
| 12 | nmE | 72.0 | 3.5 | 24.5 | 0 | 0 | + |
| 13 | nmE | 72.5 | 5.0 | 22.5 | 0 | 0 | + |
| 14 | nmE | 79.0 | 6.0 | 15.0 | 0 | 0 | + |
| 15 | nmE | 59.0 | 33.0 | 7.0 | 0 | 1.0 | + |
| 16 | nm | 67.5 | 30.5 | 0 | 0 | 2.0 | + |
| 17 | nmEM | 73.5 | 20.5 | 3.5 | 1.0 | 1.5 | + |
| 18 | nmE | 83.0 | 11.0 | 6.0 | 0 | 0 | + |
| 19 | nmEM | 43.5 | 22.5 | 28.5 | 1.0 | 4.5 | + |
| 20 | nmEM | 67.0 | 24.5 | 4.5 | 1.5 | 2.0 | + |
| 21 | nmM | 74.0 | 25.0 | 0 | 1.0 | 0 | - |
| 22 | nmE | 87.0 | 8.5 | 4.5 | 0 | 0 | + |
| 23 | nmE | 95.0 | 3.0 | 2.0 | 0 | 0 | + |
| 24 | nmEM | 40.0 | 8.5 | 49.5 | 2.0 | 0 | - |
| 25 | nmM | 76.0 | 23.0 | 0 | 1.0 | 0 | + |
| 26 | nmE | 91.5 | 4.5 | 4.0 | 0 | 0 | + |
| 27 | nm | 96.0 | 4.0 | 0 | 0 | 0 | + |
| 28 | nmEM | 69.0 | 5.5 | 19.0 | 1.5 | 5.0 | + |
| 29 | nmE | 81.0 | 9.0 | 8.0 | 0 | 2.0 | + |
| 30 | nmE | 68.5 | 10.5 | 20.5 | 0 | 0.5 | - |
| 31 | nE | 88.0 | 0 | 12.0 | 0 | 0 | - |
| 32 | nmE | 83.0 | 8.5 | 8.5 | 0 | 0 | + |
| 33 | nmEM | 60.0 | 10.0 | 27.5 | 2.5 | 0 | + |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 34 | n | 100 | 0 | 0 | 0 | 0 | - |
| 35 | nmE | 65.0 | 23.0 | 6.5 | 0 | 5.5 | + |
| 36 | nmE | 61.5 | 34.0 | 4.5 | 0 | 0 | + |
| 37 | nmEM | 77.5 | 11.5 | 7.5 | 1.0 | 2.5 | + |
| 38 | nmE | 88.5 | 8.0 | 2.5 | 0 | 1.0 | + |
| 39 | nm | 82.5 | 17.5 | 0 | 0 | 0 | + |
| 40 | nmE | 89.0 | 8.5 | 2.5 | 0 | 0 | - |
| 41 | nmEM | 72.0 | 3.0 | 24.0 | 1.0 | 0 | + |
| 42 | nmEM | 75.5 | 7.5 | 14.5 | 1.0 | 1.5 | + |
| 43 | nmEM | 84.0 | 12.5 | 3.0 | 0.5 | 0 | + |
| 44 | nmEM | 65.5 | 9.5 | 24.5 | 0.5 | 0 | + |
| 45 | nmEM | 89.0 | 6.5 | 3.0 | 1.5 | 0 | + |
| 46 | nmEM | 32.5 | 23.0 | 37.5 | 1.5 | 5.5 | + |
| 47 | nmEM | 33.0 | 36.5 | 20.0 | 1.0 | 9.5 | + |
| 48 | nmEM | 53.5 | 14.0 | 8.5 | 0.5 | 23.5 | + |
| 49 | nmE | 63.0 | 33.0 | 4.0 | 0 | 0 | + |
| 50 | nmE | 38.5 | 50.0 | 3.5 | 0 | 8.0 | + |
| 51 | nmEM | 55.5 | 20.5 | 14.0 | 5.5 | 4.5 | + |
| 52 | nmE | 63.5 | 23.5 | 13.0 | 0 | 0 | + |
| 53 | nE | 93.5 | 0 | 6.5 | 0 | 0 | - |
| 54 | nmEM | 18.0 | 53.5 | 25.0 | 0.5 | 3.0 | + |
| 55 | nmEM | 40.0 | 12.0 | 35.5 | 3.5 | 9.0 | + |
| 56 | nmEM | 19.5 | 8.5 | 46.0 | 2.0 | 24.0 | + |
| 57 | nmEM | 25.0 | 20.5 | 30.0 | 2.0 | 22.5 | + |
| 58 | nmE | 42.5 | 19.5 | 13.0 | 0 | 25.0 | + |
| 59 | nmEM | 66.5 | 7.0 | 12.5 | 2.0 | 12.0 | + |
| 60 | nmEM | 55.5 | 14.5 | 23.0 | 2.0 | 5.0 | + |
| 61 | nmE | 45.5 | 45.0 | 9.5 | 0 | 0 | + |
| 62 | nmE | 76.0 | 9.0 | 10.5 | 0 | 4.5 | + |
| 63 | nmEM | 70.0 | 18.5 | 3.5 | 0.5 | 7.5 | + |
| 64 | nmEM | 31.5 | 15.5 | 38.0 | 1.5 | 13.5 | + |
| 65 | nmE | 45.5 | 48.5 | 6.0 | 0 | 0 | + |
| 66 | nmE | 52.5 | 26.5 | 21.0 | 0 | 0 | + |
| 67 | nmEM | 70.0 | 12.0 | 10.5 | 1.0 | 6.5 | + |
| 68 | nmE | 54.0 | 28.5 | 7.5 | 0.5 | 9.5 | + |
| 69 | nmE | 74.0 | 15.0 | 11.0 | 0 | 0 | + |
| 70 | nmE | 81.5 | 7.0 | 11.5 | 0 | 0 | + |
| 71 | nmE | 43.5 | 40.0 | 11.0 | 0 | 5.5 | + |

| | | | | | | | |
|---|---|---|---|---|---|---|---|
| 72 | nmEM | 77.0 | 9.5 | 3.0 | 2.0 | 8.5 | + |
| 73 | nmE | 48.5 | 20.0 | 31.5 | 0 | 0 | + |
| 74 | nmEM | 69.5 | 16.0 | 9.0 | 2.0 | 3.5 | + |
| 75 | m | 0 | 100 | 0 | 0 | 0 | + |
| 76 | nmE | 72.0 | 11.0 | 14.5 | 0 | 2.5 | + |
| 77 | m | 0 | 100 | 0 | 0 | 0 | + |
| 78 | m | 0 | 100 | 0 | 0 | 0 | + |
| 79 | nmE | 53.5 | 29.0 | 17.5 | 0 | 0 | + |
| 80 | nmE | 39.0 | 18.0 | 18.0 | 0 | 25.0 | + |
| 81 | nmE | 56.5 | 37.5 | 6.0 | 0 | 0 | + |

TnQTable3Twelve days after single cell deposition and culture, smears were made from individual samples and stained with May-Grünwald Giemsa. Differential counting was carried out on 200 cells. n indicates neutrophil; m, macrophage/monocyte; E, erythrocyte; M, megakaryocyte and Im, immature cell.


EGFP
DIC
Leptin
Merge
A
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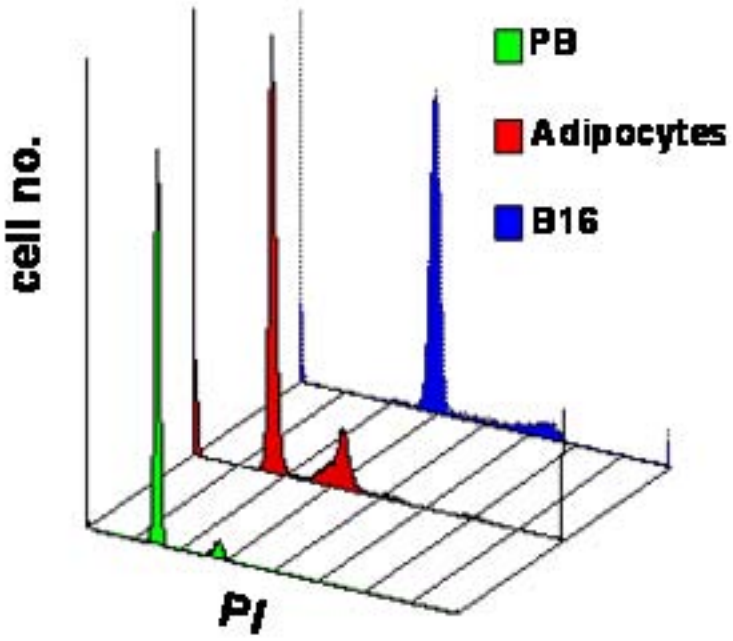
PB
Adipocytes
B16
cell no.
PI