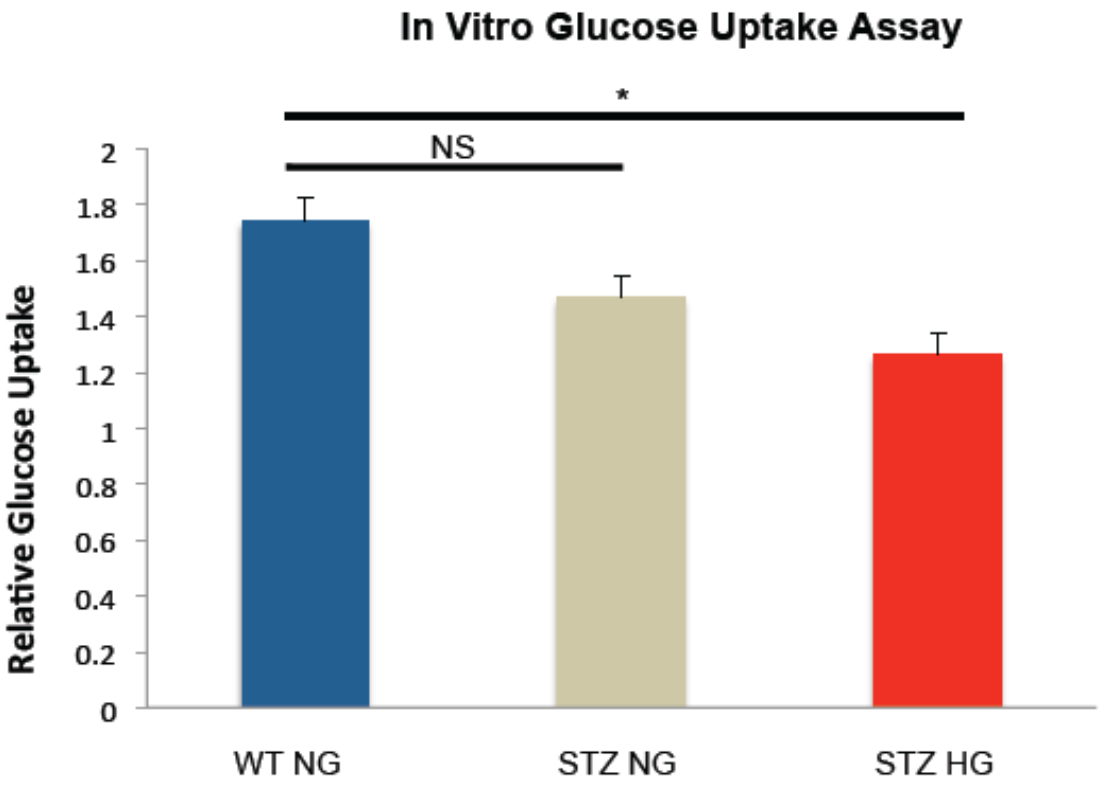
SUPPLEMENTARY DATA

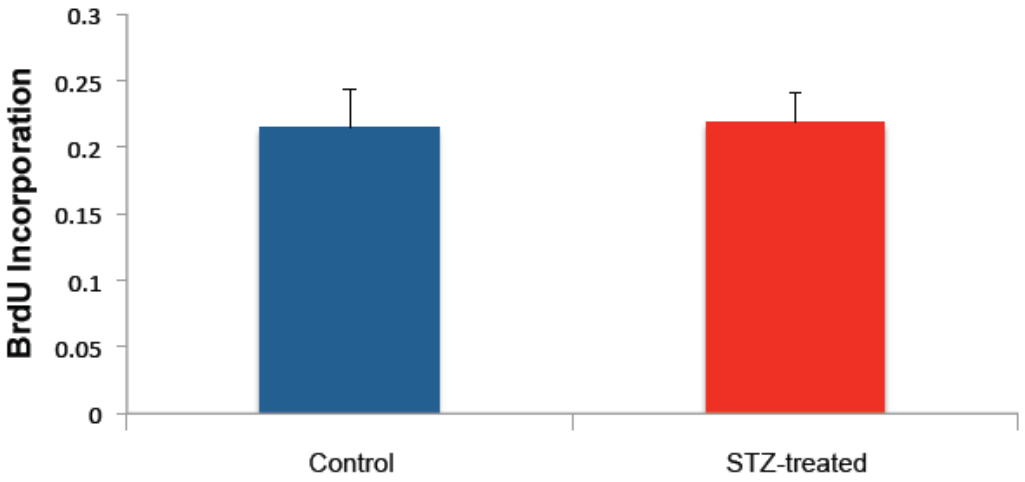
Supplementary Figure 1. Normoglycemic culture largely restores deficits in glucose uptake in diabetic BM-MPCs. MPCs isolated from the bone marrow of type 1 diabetic (modeled by STZ) and wildtype (WT) mice were cultured under either normoglycemic (NG; 1 g/L) or hyperglycaemic (HG; 4.5 g/L) glucose conditions. Diabetic BM-MPCs exhibited significantly impaired glucose uptake in hyperglycemic culture ($p = 0.01$) that was largely restored to WT levels by normoglycemic culture ($p = 0.07$). This suggests phenomenon other than direct glucose uptake are responsible for the persistent functional deficits of diabetic cells seen in **Figure 1** despite normalization of glycemic conditions. *, $p < 0.05$; NS, not significant.



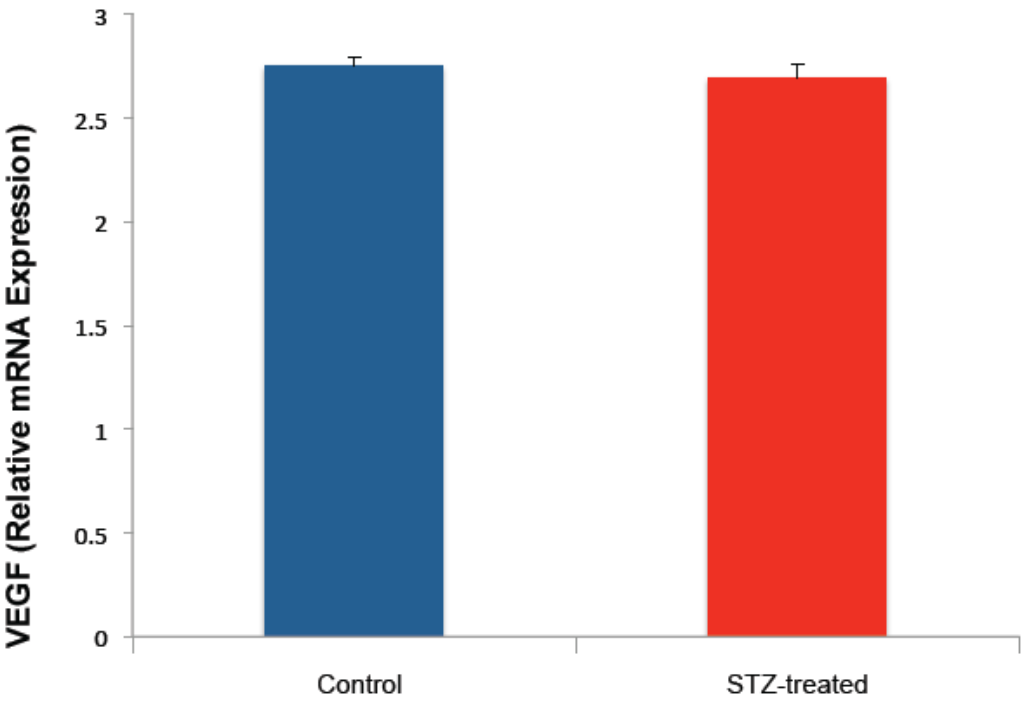
SUPPLEMENTARY DATA

Supplementary Figure 2. Streptozotocin does not directly impair BM-MPCs function *in vitro.* MPCs isolated from the bone marrow of wildtype mice were cultured in medium with or without streptozotocin (STZ). No differences in **(a)** proliferation or **(b)** VEGF expression in STZ-treated cells was observed, suggesting that the functional impairments in cells harvested from STZ-induced diabetic mice are not due to direct cellular effects of STZ.

a

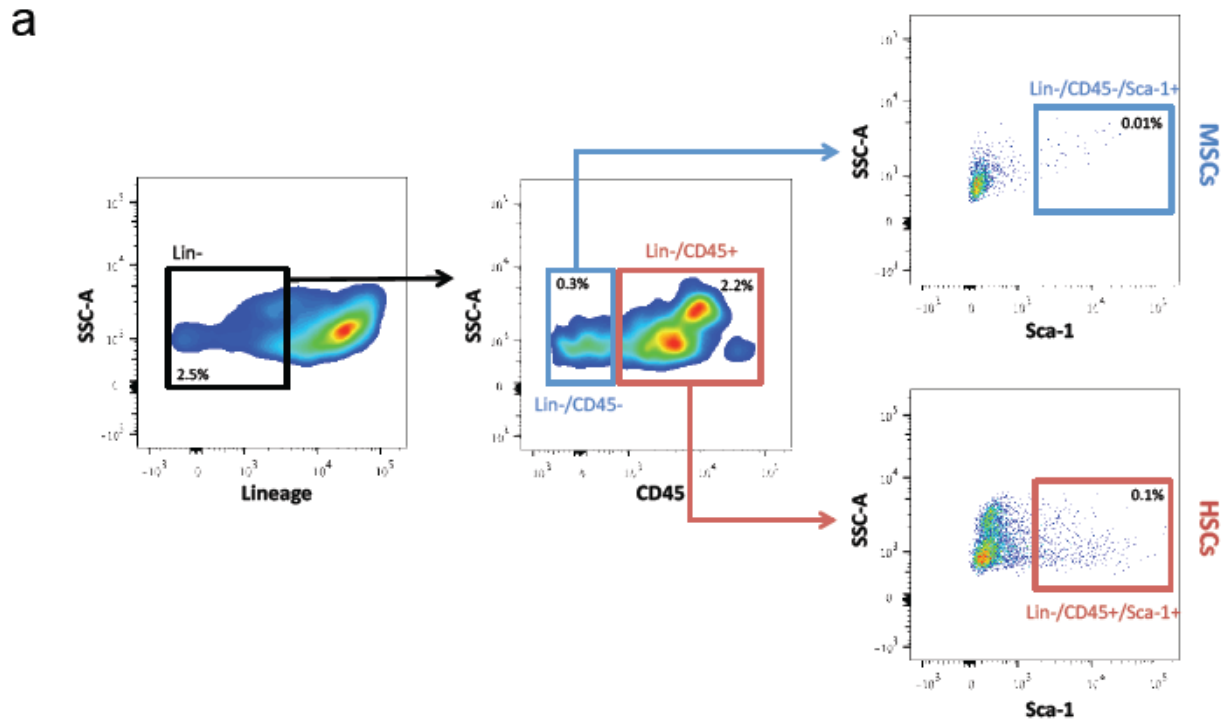


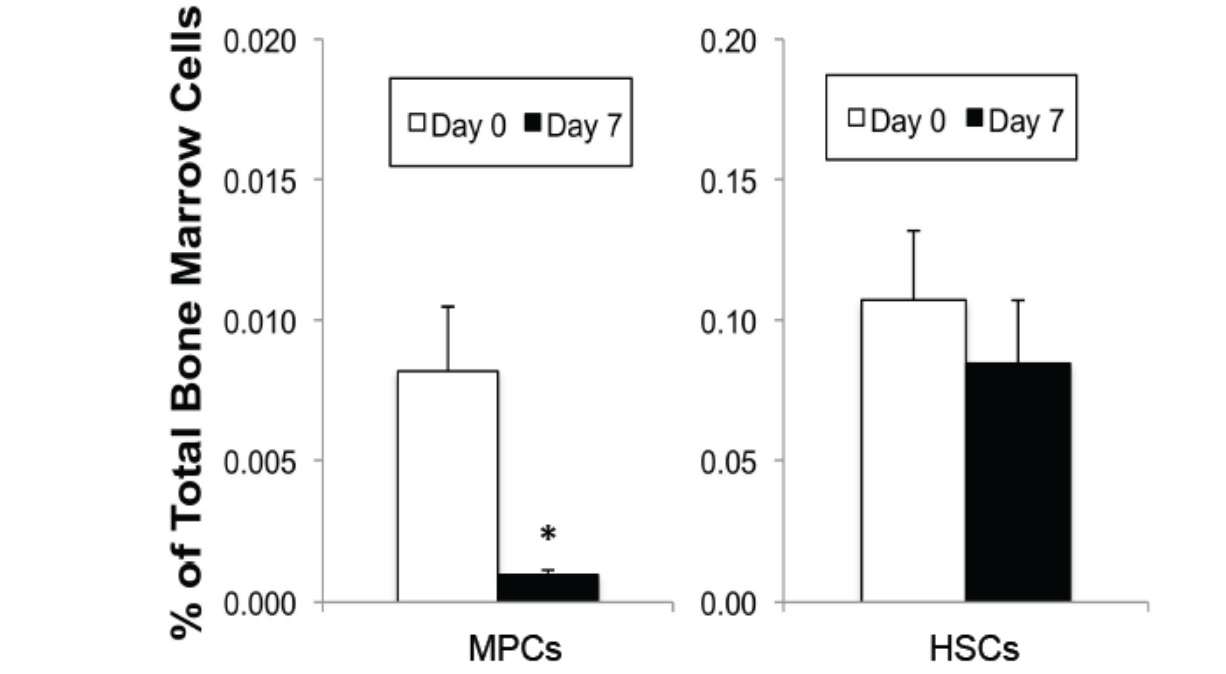
b



SUPPLEMENTARY DATA

Supplementary Figure 3. Only non-hematopoietic cells are mobilized from the bone marrow in response to peripheral ischemia. (a) Flow cytometic gating of Lin-/CD45-/Sca-1+ bone marrow mesenchymal progenitor cells (BM-MPCs) and Lin-/CD45+/Sca-1+ hematopoietic stem cells (HSCs). (b) Bone marrow isolated from wildtype mice was significantly depleted of BMMPCs at day 7 following ischemic insult (left), whereas levels of HSCs remained unchanged(right).

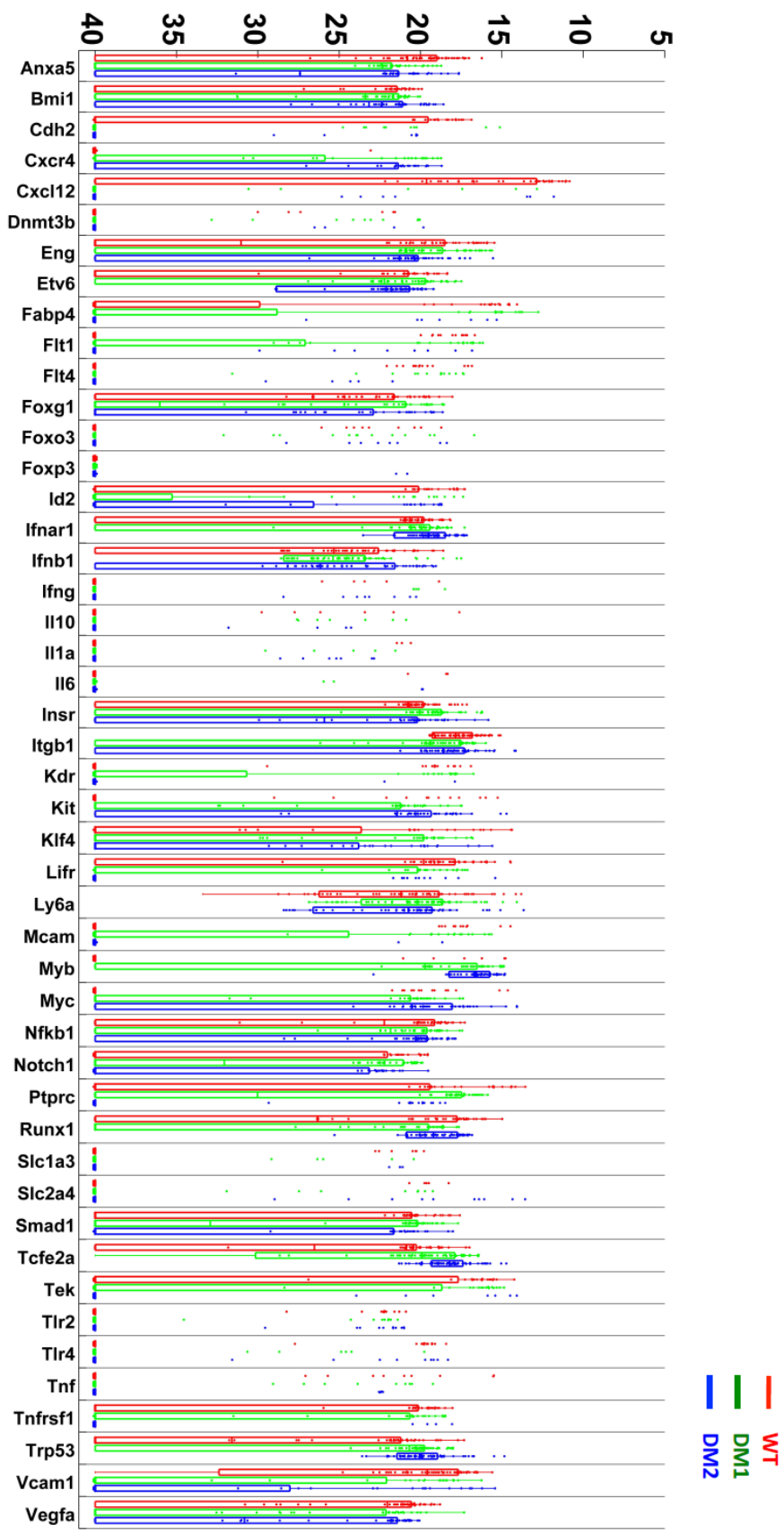




SUPPLEMENTARY DATA

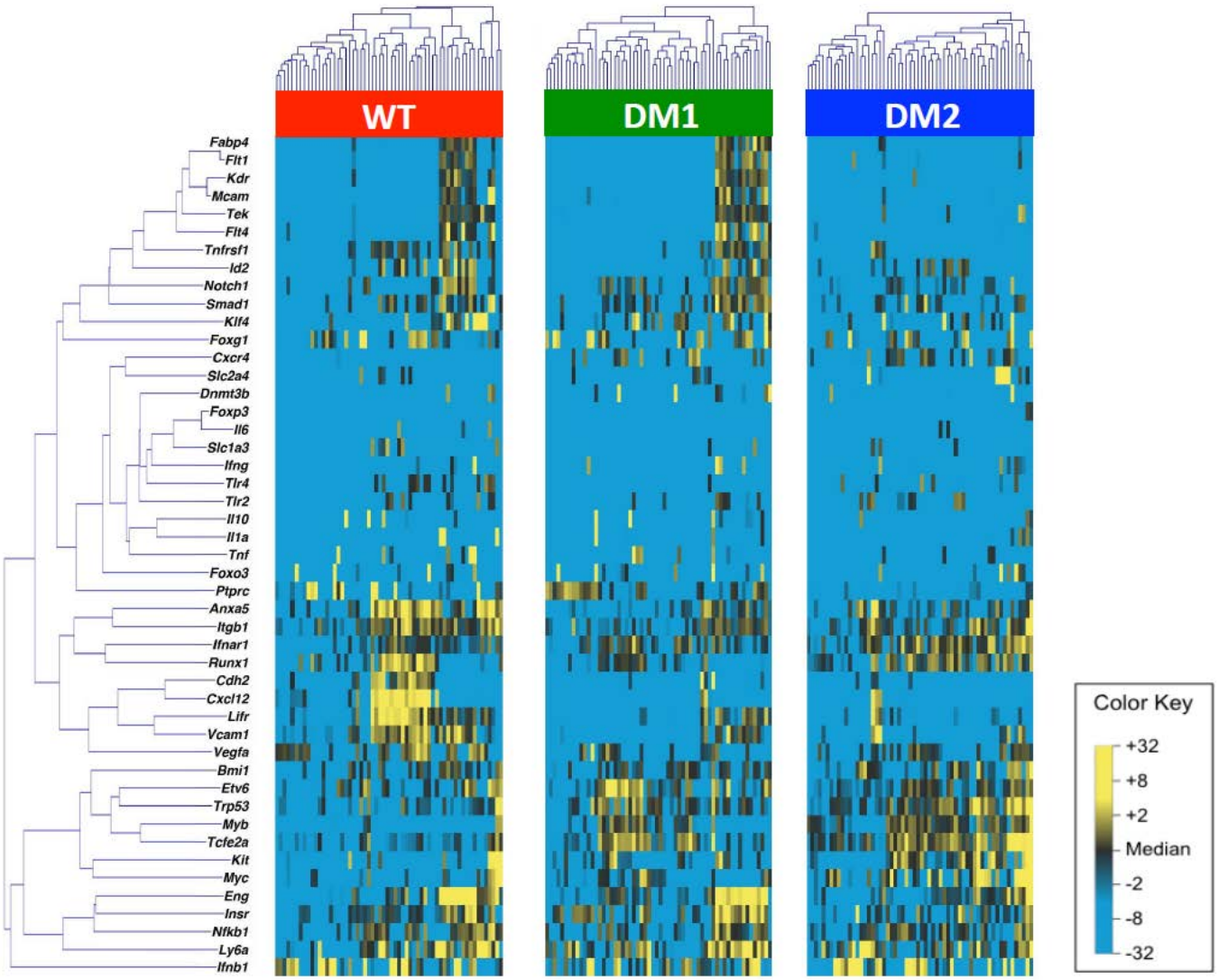
Supplementary Figure 4. Whisker plots presenting raw qPCR cycle threshold values for each gene across all wildtype and diabetic MPCs. Individual dots represent single gene/cell qPCR reactions, with increased cycle threshold values corresponding to decreased mRNA content. Cycle threshold values of 40 were assigned to all reactions that failed to achieve detectable levels of amplification within 40 qPCR cycles. Cells isolated from wildtype, STZ (type 1) diabetic, and db/db (type 2) diabetic mice are colored in red, green, and blue, respectively. Boxes enclose lower and upper quartiles, and whiskers delimit lowest/highest data points within 1.5 inter-quartile ranges (IQR) or lower/upper quartiles.

SUPPLEMENTARY DATA



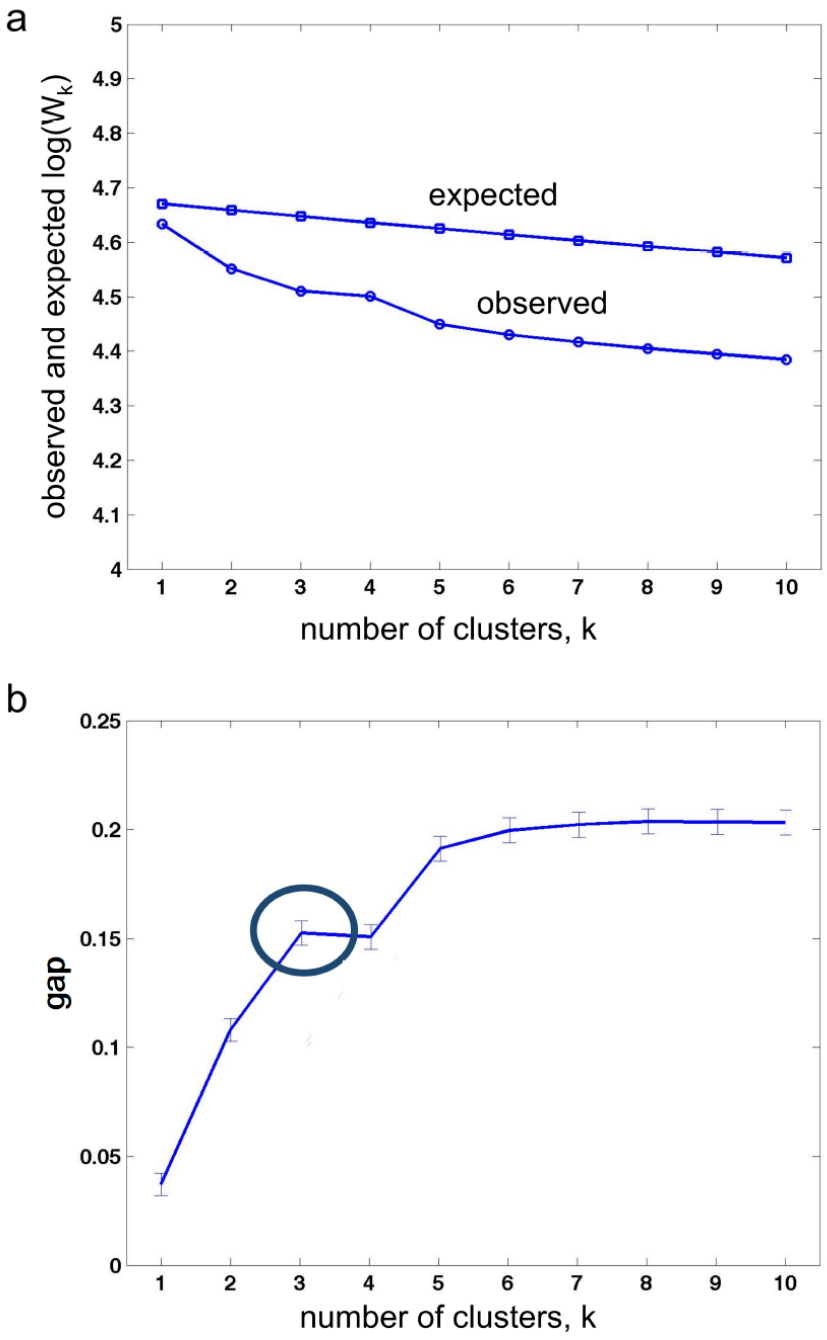
SUPPLEMENTARY DATA

Supplementary Figure 5. Unsupervised clustering of complete single cell gene expression data for bone marrow-derived MPCs. Hierarchical clustering of simultaneous gene expression for 60 individual cells from wildtype (WT; left), STZ-induced diabetic (DM1; middle), and db/db diabetic (DM2; right) mice across 47 gene targets. Gene expression is presented as fold change from median on a color scale from yellow (high expression, 32-fold above median) to blue (low expression, 32- fold below median).



SUPPLEMENTARY DATA

Supplementary Figure 6. Estimating the number of clusters in single cell gene expression data using the gap statistic. In order to estimate the appropriate number of subgroups present within our dataset, we employed the gap statistic as described by Tibshirani et al., which is a highly generalizable method for determining cluster number without the aide of a response variable.(56) Briefly, the within-cluster dispersion (W_k) is calculated as the sum of pairwise intra-cluster distances for each *k* number of clusters. **(a)** These W_k are compared with the expected values obtained through 100,000 Monte Carlo simulations over a reference distribution generated through the uniform distribution across the range of observed qPCR values. **(b)** The optimal number of clusters is designated as that which maximizes the gap between the log of W_k in our data and the expected value obtained from the reference distribution; this corresponded to four clusters in our dataset.



SUPPLEMENTARY DATA

Supplementary Table 1. TaqMan assays used to interrogate gene expression within murine MPCs. All assays were obtained from Applied Biosystems (Foster City, CA).

Gene ID	Assay ID	Gene ID	Assay ID
Alcam	Mm00711623 m1	*Lifr*	Mm00442942 m1
Alpl	Mm00475834 m1	*Lpl*	Mm00434764 m1
Anxa5	Mm01293059 m1	*Ly6a*	Mm00726565 s1
Bmi1	Mm00776122 gH	*Mcam*	Mm00522397 m1
Ccna2	Mm01292244 m1	*Myb*	Mm00501741 m1
Cdh2	Mm00483213 m1	*Myc*	Mm00487803 m1
Cdkn1a	Mm01303209 m1	*Nanog*	Mm02019550 s1
Cxcl12	Mm00445552 m1	*Nes*	Mm00450205 m1
Dnmt3b	Mm00599800 m1	*Nfkb1*	Mm00476361 m1
Eng	Mm00468256 m1	*Notch1*	Mm00435249 m1
Etv6	Mm00468390 m1	*Podxl*	Mm00449829 m1
Fgf2	Mm00433287 m1	*Ptk2*	Mm00433203 m1
Fgf9	Mm00442795 m1	*Ptprc*	Mm00448463 m1
Flt1	Mm00438980 m1	*Rb1*	Mm00485586 m1
Flt4	Mm01292611 m1	*Runx1*	Mm01213405 m1
Foxo3	Mm00490673 m1	*Smad1*	Mm00484721 m1
Gata2	Mm00492301 m1	*Sox2**	Mm00488369 s1
Id2	Mm00711781 m1	*Tal1*	Mm01187033 m1
Itga2	Mm00434371 m1	*Tcfe2a*	Mm01175585 m1
Itgb1	Mm01253227 m1	*Tek*	Mm01256898 m1
Jun	Mm00495062 s1	*Tert*	Mm00436933 m1
Kdr	Mm01222431 m1	*Trp53*	Mm01731287 m1
Kit	Mm00445212 m1	*Vcam1*	Mm01320970 m1
Klf4	Mm00516104 m1	*Vegfa*	Mm01281447 m1

* assay did not produce exponential amplification, excluded from analysis