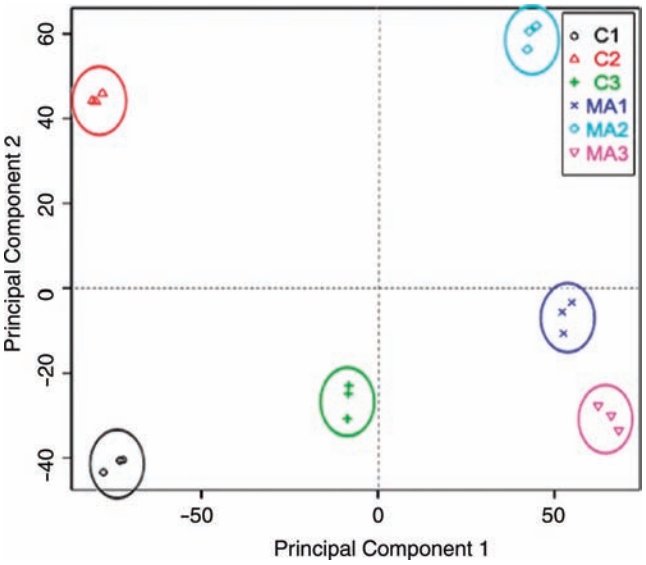
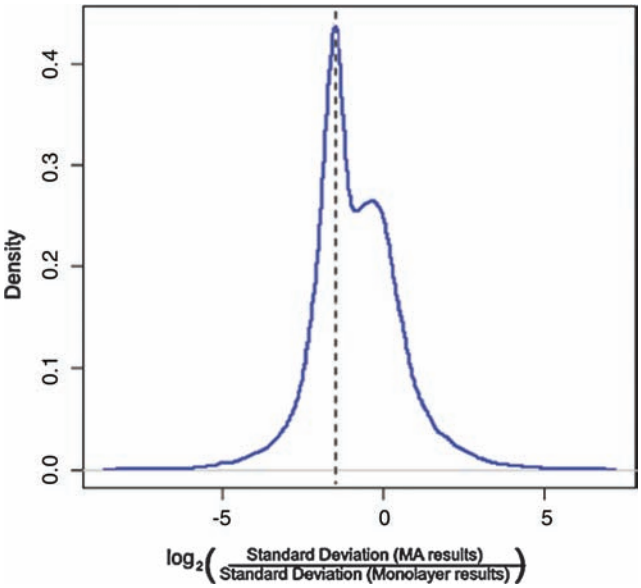
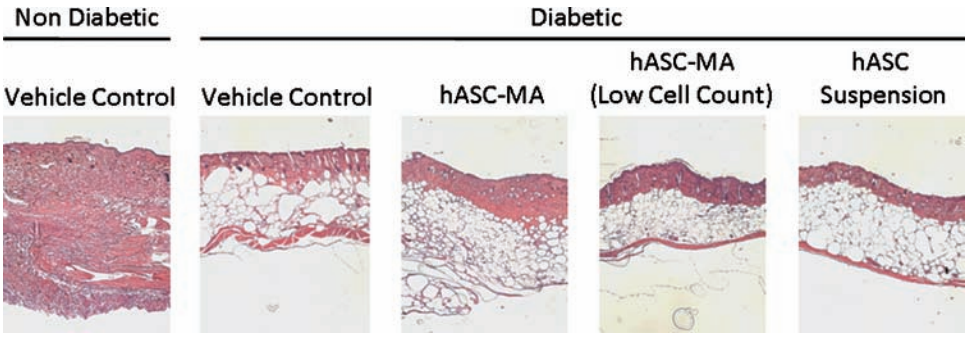


SUPPLEMENTAL FIG. S1. Principal component analysis plot of three replicate arrays for each of three patients whose cells were grown as multicellular aggregates (MAs) or in monolayers. As highlighted by ovals, the replicated arrays were tightly clustered together, demonstrating that the variation due to method of culture (MA vs. monolayer [C1, C2, C3]) and distinct patient expression profiles was much greater than the variation among replicates. The dominant axis of variation is the first principal component (PC1 along the x-axis) and the secondary axis of variation is the second principal component (PC2 along the y-axis). Samples grown as MAs were significantly shifted from those grown in monolayer along PC1, indicating that culture method was the dominant source of variation in expression profiles. Patient profiles were separated along PC2, indicating that variation in individual expression profiles was a secondary source of gene expression change/variability compared to culture method.



SUPPLEMENTAL FIG. S2. Distribution plot of the $\log_2$ ratio of the standard deviation in gene expression among patients whose cells were grown in MA over those whose cells were grown in monolayer for each gene. The dotted line indicates the mode of the distribution, which is near negative one, indicating that a large population of genes exhibit a twofold smaller standard deviation in gene expression from cells grown as MAs compared to those grown as monolayers.



SUPPLEMENTAL FIG. S3. Hematoxylin and eosin–stained cross sections of healed wounds (day 21). As expected, the composition of the dermis in the diabetic animals has a higher content of endogenous adipose tissue relative to the nondiabetic control mouse. Treatment with vehicle control, human adipose-derived stromal cell (hASC) MAs, or hASC single-cell suspensions creates no observable differences in the thickness of the epidermis or dermis or gross morphological differences in healing outcomes.