METHOD 3: Differential gene expression analysis: For differential gene expression analysis, redundant features and features with an intra-group coefficient of variation >25% or absolute fold-change of less than 1.5-fold between obese and lean groups were excluded, resulting in 3006 features. Differentially expressed genes were identified via the Comparative Marker Selection algorithm in GenePattern software (http://www.broadinstitute.org/cancer/software/genepattern/) using standard t-tests and asymptotic p-values for ascertainment of statistical significance. A false-discovery rate (FDR) was calculated to control for multiple testing