scaling factor. The scaling factor was derived by dividing 5000 (arbitrarily selected) by the 75 percentile value of the non-control features for each chip (obtained from the Agilent signal extraction software), so that each chip had a 75 percentile signal of 5000. Features that failed in any of the following 4 criteria in either the obese or lean groups were excluded – (i) non-uniform outlier in >25% samples in either group, (ii) population outlier in >25% samples in either group, (iii) positively and significantly different from background in <50% samples in both groups, (iv) >50% saturated pixels in either group. Additionally, features with unknown gene annotation were removed. A total of 35543 features were retained for further analysis post-filtering. Unless otherwise specified, gene expression signals were log transformed (base 2) for downstream analysis. Sample outliers were evaluated by principal components analysis of logged gene expression data using the Simca P+ 12.0 software (Umetrics, Uppsala, Sweden).

METHOD 2: Quantitative PCR analysis: For RT-PCR validation, 500ng of total RNA was used for cDNA synthesis using the RT-First Strand kit (Qiagen, CA) according to the manufacturers' protocol. Quantitative SybrGreen PCR was performed in multi-well plates using the RT-PCR master mix (Qiagen) according to protocol. Amplification was performed using the Roche LC480 instrument (Roche Applied Biosystems, CA). Triplicate aliquots of each RNA sample were used in the same reactions. For quality control, all multi-well PCR reactions were analyzed for reverse transcription controls and genomic DNA contamination using the provided control wells. For all experimental samples, the relative fold difference of each gene between the obese subjects and lean controls was determined by means of the $\Delta\Delta$Ct (threshold cycle) method (Roche Applied Biosystems, CA).