SUPPLEMENTARY DATA

Microarray Studies and Data Analysis:

Labeled cRNA was prepared by linear amplification of the Poly(A)+ RNA population within the total RNA sample. Total RNA (1 μg) was reverse transcribed after priming with a DNA oligonucleotide containing the T7 RNA polymerase promoter 5' to a d(T)24 sequence. After second-strand cDNA synthesis and purification of double-stranded cDNA, *in vitro* transcription was performed using T7 RNA polymerase. The quantity and quality of the cRNA was assayed by spectrophotometry and on the Agilent Bioanalyzer. We fragmented 1 μg of purified cRNA to uniform size and hybridized to Human Whole Genome 4x44k arrays (Agilent Technologies) at 37° C for 18 hrs in a rotating incubator. Arrays were washed and scanned with a G2565 Microarray Scanner (Agilent Technologies).

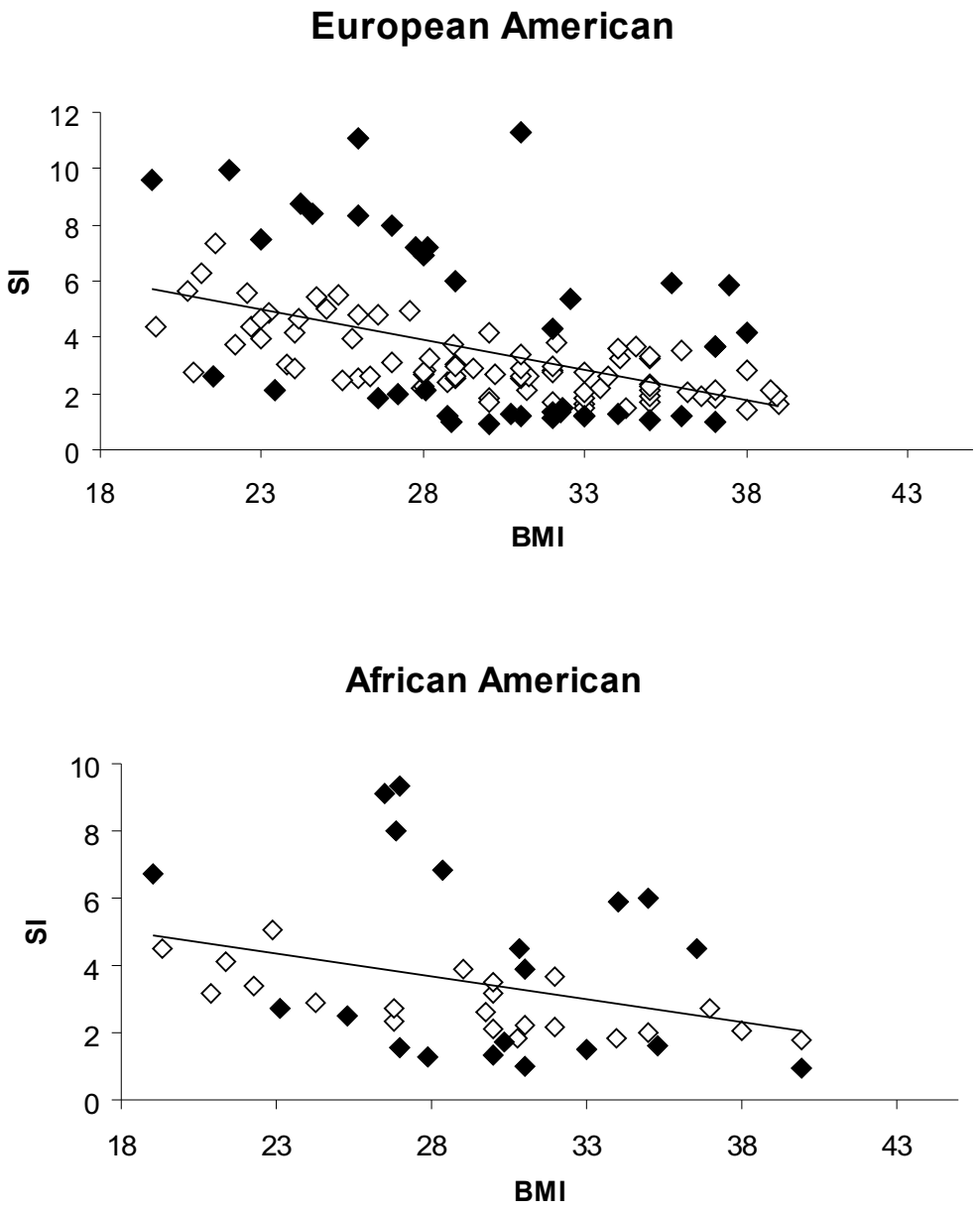
Arrays were processed and background corrected with default settings of the Agilent Feature Extraction software v.9.5.3.1 (Agilent Technologies). Agilent FE plug- in converts the complex set of 16 binary flag columns into three- levels of GeneSpring flags: Absent (A), Marginal (M). or Present (P). Raw data were analyzed with GeneSpring GX v7.3 software (Agilent Technologies). To compare individual expression values across arrays, raw intensity data from each gene were quantile normalized to the 75th percentile intensity of each array. Only genes with GeneSpring feature extraction flag P (present) in at least n-3 samples in one of the two comparison groups were included in further analyses.

Processed arrays were analyzed using the nonparametric Wilcoxon statistic on normalized data in Statistical Analysis for Microarray (SAM) software (17). Comparison between AA and EA individuals were performed after considering IR and IS individuals as separate permutation group, while comparison between IR and IS individuals in all subjects were performed after assigning AA and EA individuals in separate permutation group. We considered results significant for a false discovery rate (q value) < 5%, and fold difference between IR and IS samples of >1.5, based on >400 permutations. Results driven by outliers were excluded by considering only results with single point t-test $p < 0.05$, and we report only on probes corresponding to transcripts with NCBI/Entrez identifiers and GeneCard (www.genecards.org) entries. Genes represented by multiple probes are considered significant only if at least one probe meet our stringent selection criteria and all probes are in same direction of differential expression.

Functional annotation of differentially expressed genes were performed by singular and modular enrichment analysis (SEA and MEA) using DAVID v6.7 functional annotation tool (18, 19) . Genes showing mean differential expression of 1.5 fold (q-value <5% and t-test $p<0.05$) for at least one probe were considered for SEA and MEA analysis to investigate the enrichment of these genes in known biological pathways or Gene ontology (GO) categories. Detailed analyses parameters for SEA and MEA using functional annotation chart and cluster analysis modules of DAVID respectively are described elsewhere (20). We also performed canonical pathway analysis and interaction network analysis for these differentially expressed genes using Ingenuity Pathway analysis (IPA ver8.7, https://analysis.ingenuity.com). A small number of genes showed mean 1.5 fold differential expression, thus we used all probes corresponding to transcripts with NCBI/Entrez identifiers irrespective of fold change for Gene Set Enrichment analysis (GSEA). The GSEA analysis was performed by GeneTrail (21) using a list of Entrez ids of genes ranked by mean fold change (IR/IS) for probes expressed over background and q-value <20%. GeneTrail was run with median occurrence for genes with multiple probes and considered only KEGG pathways and GO categories with 4 to 100 transcripts.

SUPPLEMENTARY DATA

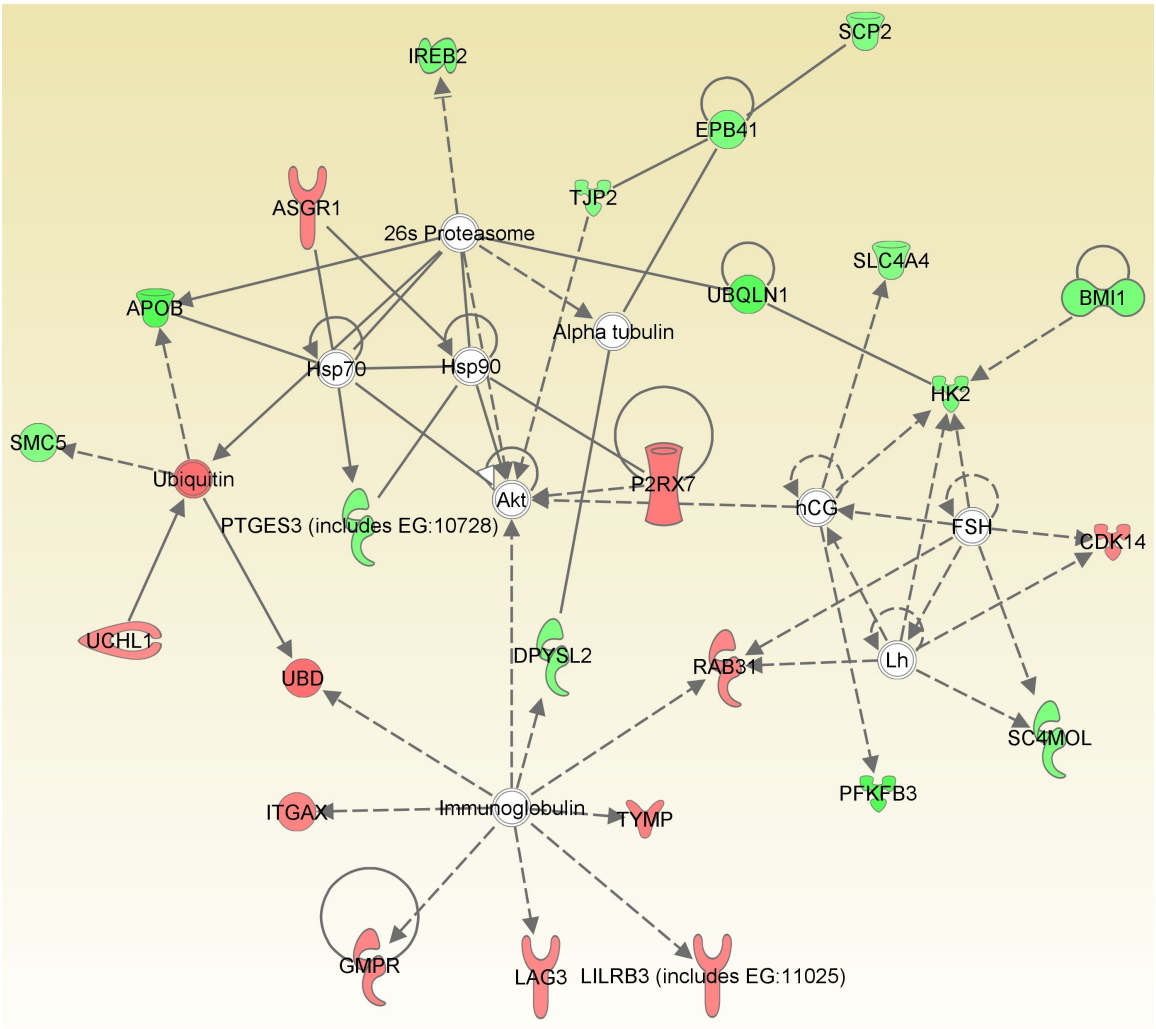
Supplementary Figure 1. Distribution of S_I and BMI in our study cohort. Subjects selected for microarray analysis based on standardized residual of S_I are shown as filled diamond (♦). S_I ($10^{?4}.min^{?1}$ $[?U/ml]^{?1}$) and BMI (kg/m^2) is shown as non log transformed values



SUPPLEMENTARY DATA

Supplementary Figure 2. Top interaction networks among genes differentially expressed (≥1.5 fold) in adipose tissue between European American IR and IS subjects. A) Network 1: cell mediated immune response (score= 42 with 25 differentially expressed genes) B) Network 2: Inflammatory response (score= 37 with 24 differentially expressed genes). Nodes of the interaction network containing up-regulated (IR/IS) genes are red and down regulated genes are green. Both direct and indirect interactions are included in the analysis.

A)



SUPPLEMENTARY DATA

B)