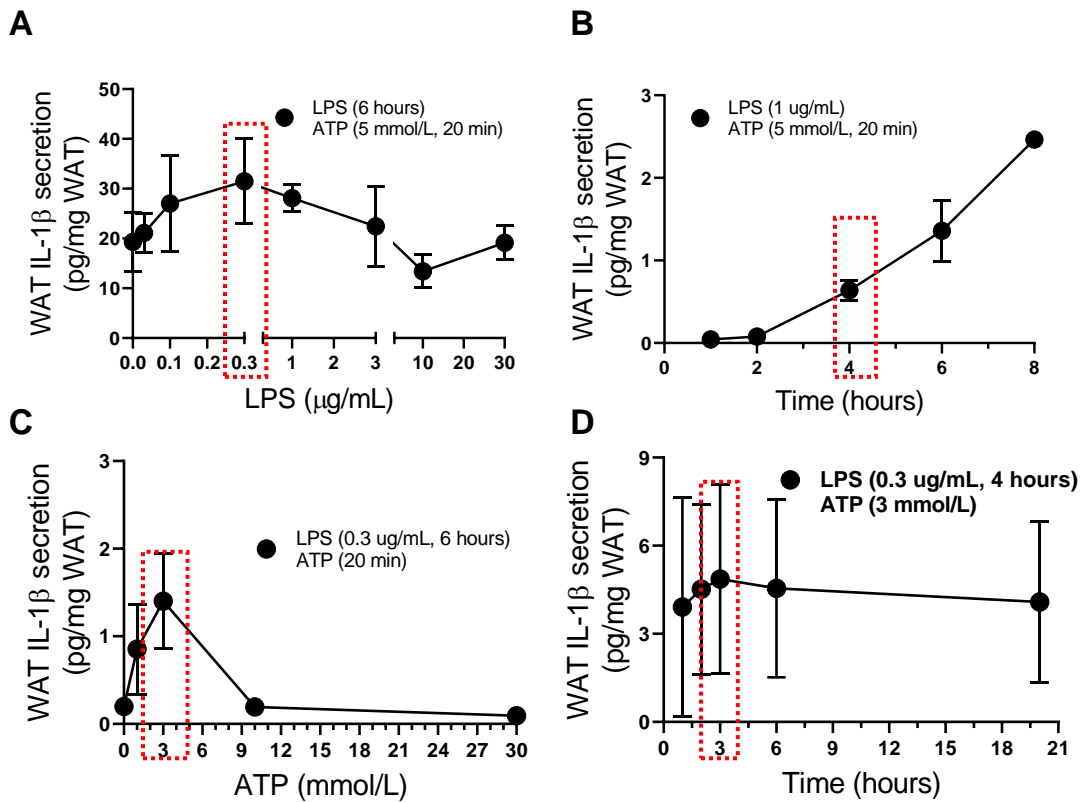


**Native low-density lipoproteins are priming signals of the NLRP3 inflammasome/
interleukin-1 β pathway in human adipose tissue and macrophages**

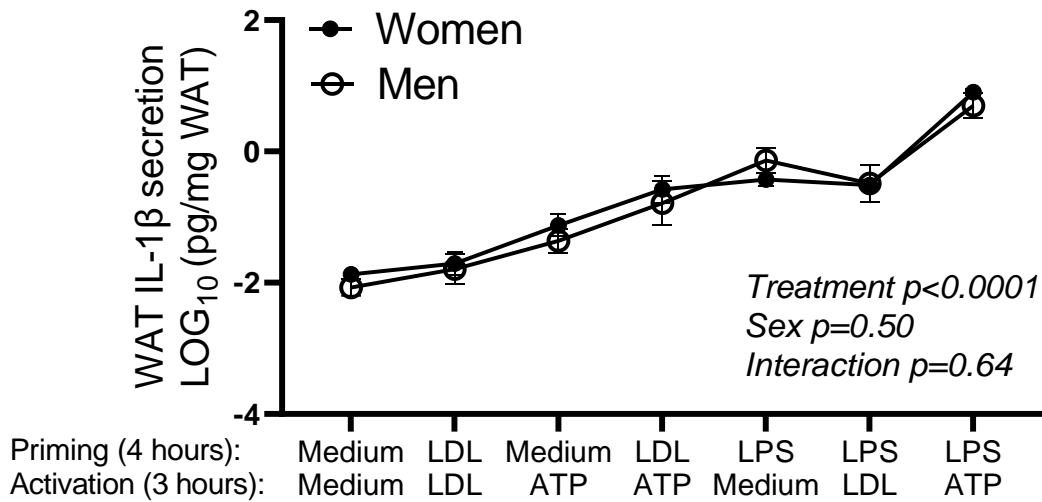
Simon Bissonnette^{1,2,3}, Valérie Lamantia^{1,2,3}, Benjamin Ouimet^{1,2}, Yannick Cyr^{1,2,3}, Marie Devaux^{1,2}, Remi Rabasa-Lhoret^{1,2,3}, Michel Chrétien^{1,2}, Maya Saleh^{4,5}, May Faraj^{1,2,3,4}

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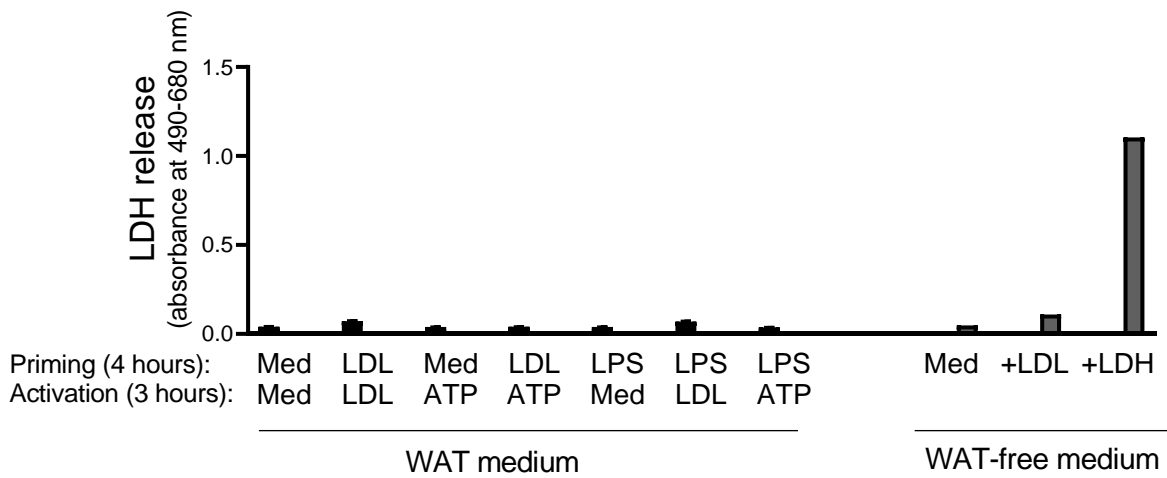
Supplemental Figure 1: Pilot kinetic studies conducted in fasting white adipose tissue (WAT) of 4 subjects to optimize experimental conditions to be used for LPS and ATP as *priming* and *activation* positive controls of WAT NLRP3 inflammasome, respectively. Shown here is WAT IL-1 β -secretion following incubation with (A) LPS concentration-curve for 6 hours followed by 5 mmol/L ATP for 20 min, N=1; (B) 1 μ g/mL LPS time-curve followed by 5 mmol/L ATP for 20 min, N=1; (C) 0.3 μ g/ml LPS for 6 hours followed by ATP concentration-curve for 20 minutes, N=3; and (D) 0.3 μ g/ml LPS for 4 hours followed by 3 mmol/L ATP time-curve, N=2. Minimal LPS and ATP concentrations and incubation period that induced maximal WAT IL-1 β -secretion were then used as positive controls for all experiments described in manuscript and were: **0.3 μ g/ml LPS for 4 hours followed by 3 mmol/L ATP for 3 hours** (highlighted in red rectangular below). N.B. LPS was used for 4 hours for practical reasons to account for the 8 hours needed to complete experiments in postprandial WAT (not included in this manuscript).



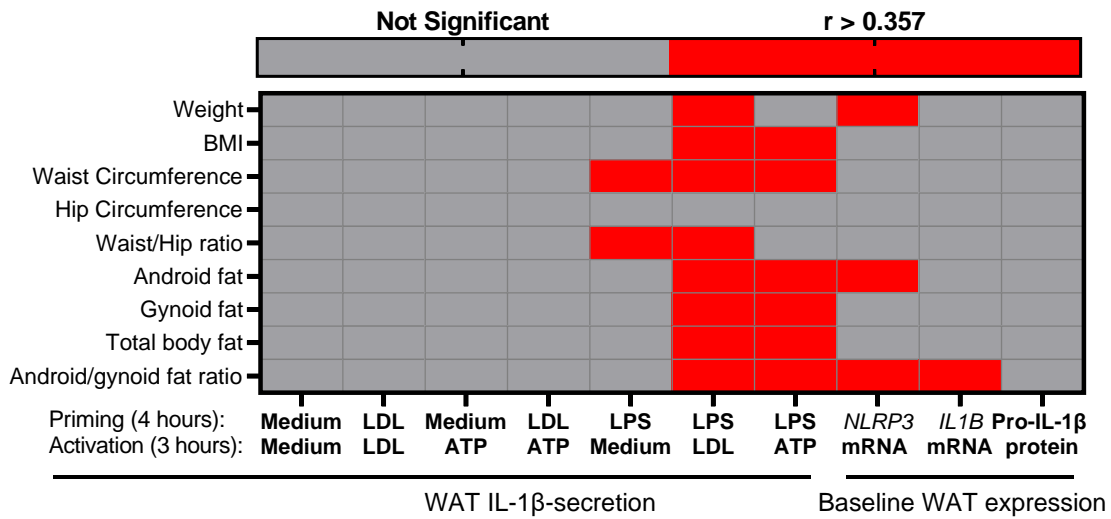
Supplemental Figure 2: Sex differences in fasting WAT IL-1 β -secretion induced by 5% FBS medium/medium (baseline or negative control), LDL/LDL, medium/ATP, LDL/ATP, LPS/medium, LPS/LDL, or LPS/ATP (positive control) for the priming/activation periods of the NLRP3 inflammasome. Data was analyzed by mixed-model analysis with treatment and sex interaction as in methods and presented as average \pm SEM. N=23 women and N=11 men except with LDL/LDL, where N=21 women and N=11 men for missing data.



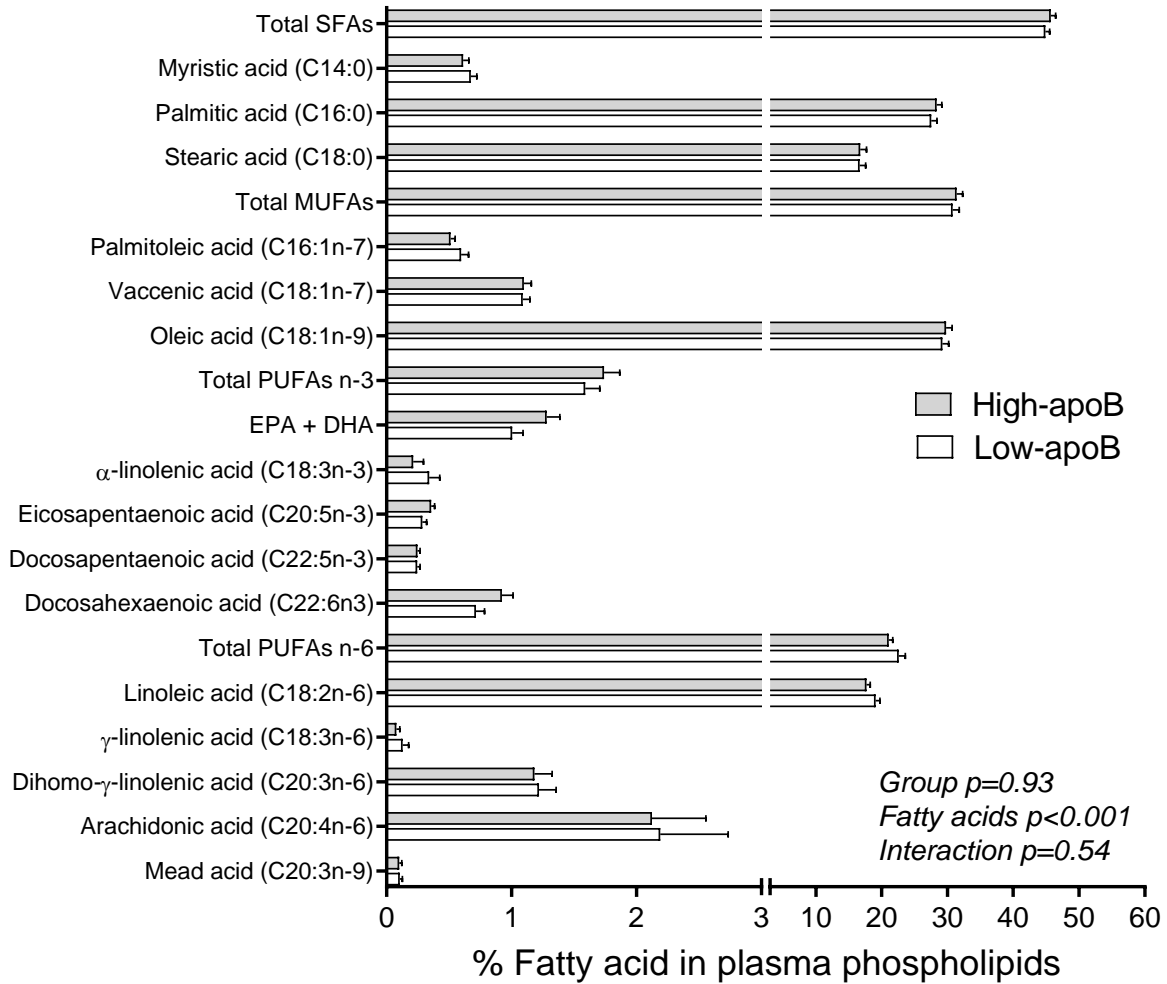
Supplemental Figure 3: Cytotoxic assay measuring LDH release into WAT medium induced by 5% FBS medium/medium (baseline or negative control), LDL/LDL, medium/ATP, LDL/ATP, LPS/medium, LPS/LDL, or LPS/ATP (positive control) for the priming/activation periods of the NLRP3 inflammasome. Also shown are LDH concentrations measured in WAT-free medium alone or supplemented with 1.2 g/L apoB incubated for 3 hours compared to the LDH positive control provided by the commercial kit (Invitrogen). Notably, LDL presence alone (without WAT) represent a modest false positive signal for LDH measurement above baseline (medium).



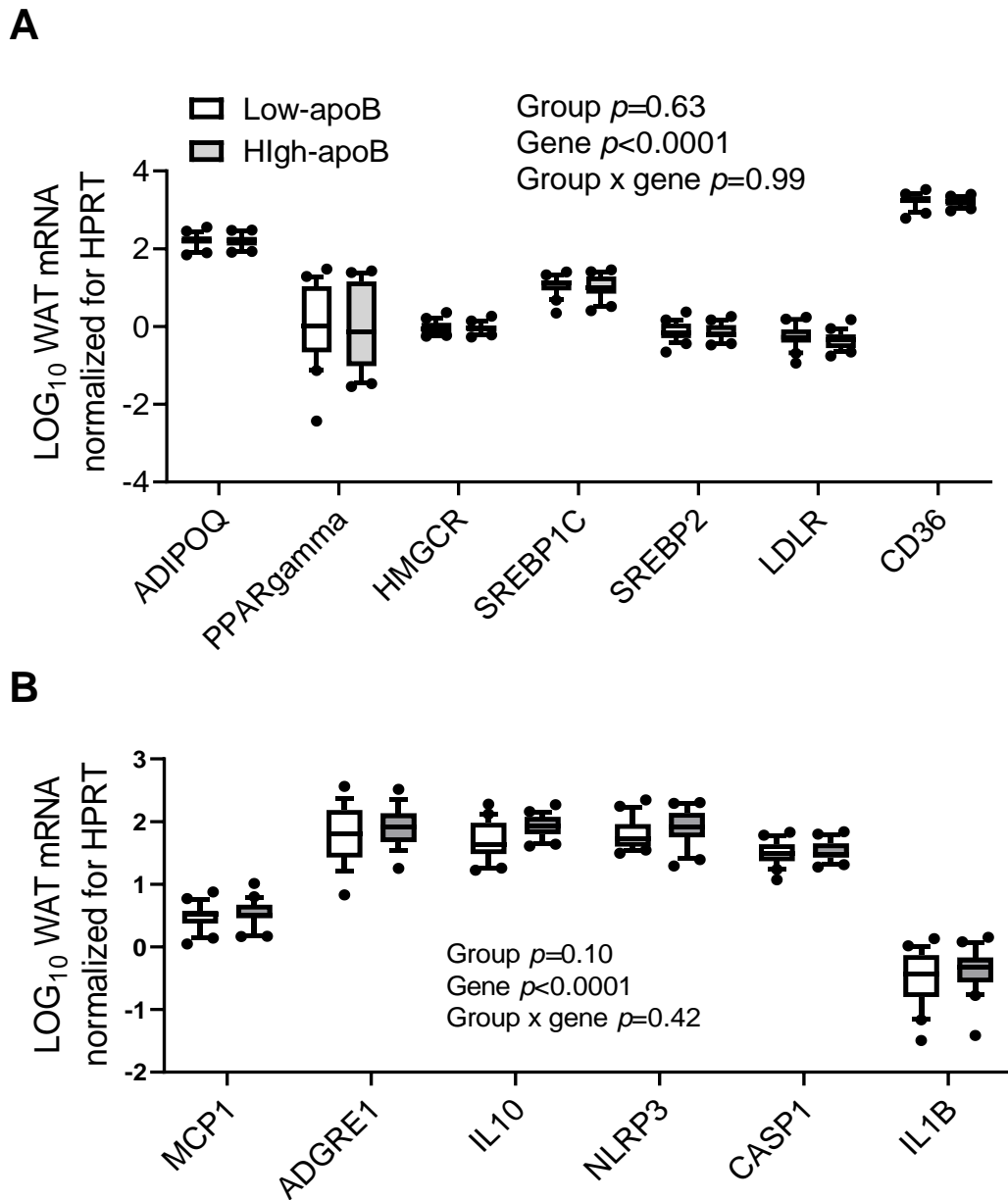
Supplemental Figure 4: Heat map representing Pearson correlation of subject weight, BMI, waist circumference, hip circumference, waist/hip ratio, android fat, gynoid fat, total body fat, android/gynoid fat ratio with fasting LOG₁₀ WAT IL-1 β -secretion at baseline (medium/medium) and following incubation with LDL/LDL, medium/ATP, LDL/ATP, LPS/medium, LPS/LDL, or LPS/ATP for the priming/activation periods, and with LOG₁₀WAT *NLRP3*, LOG₁₀WAT *IL1B* mRNA and WAT pro-IL-1 β protein in all subjects. N=40 for WAT mRNA and pro-IL-1 β data and N=34 for all WAT IL-1 β -secretion conditions except with LDL/LDL when N=31 for missing data. Grey cells represent insignificant and red cells represent significant positive correlations.



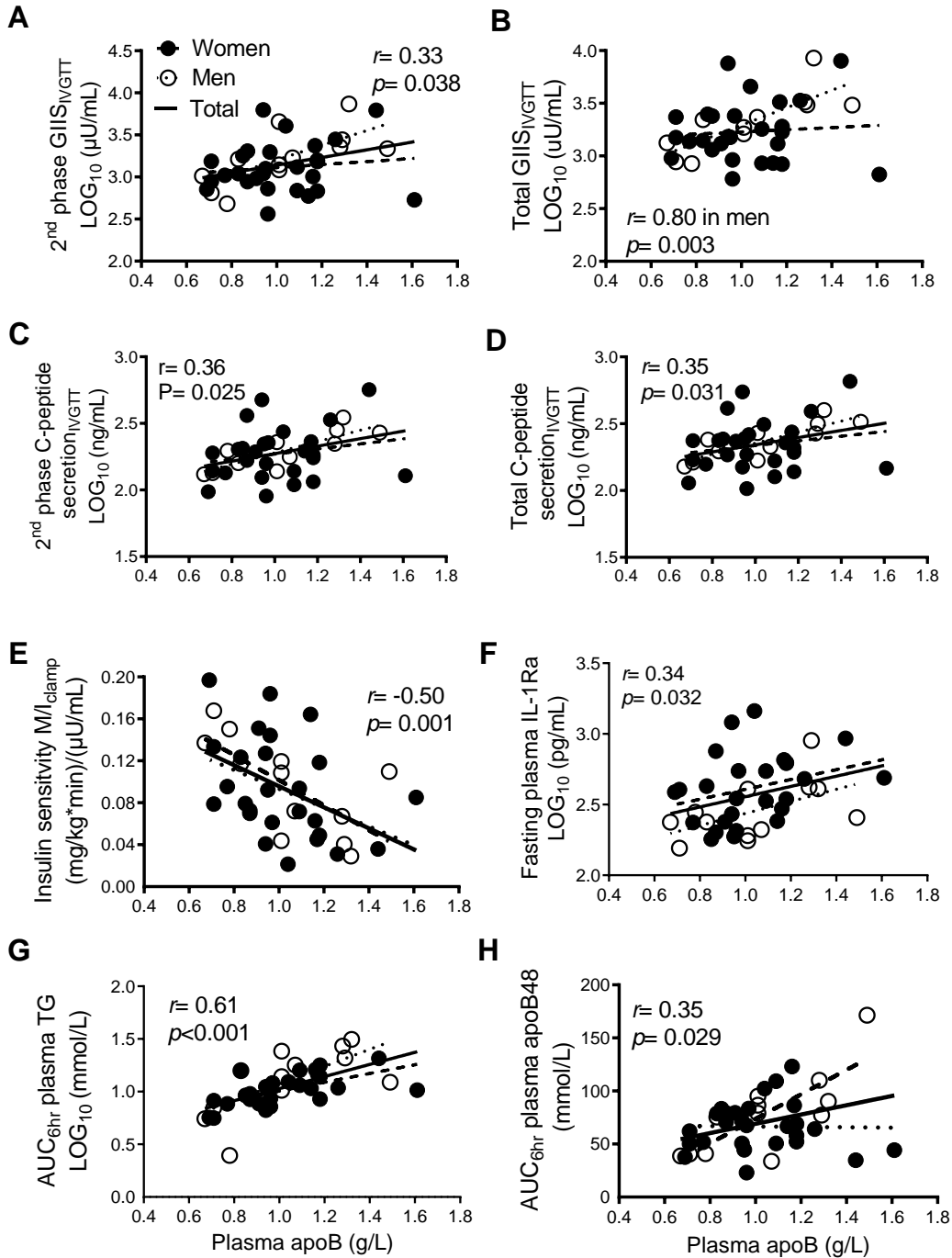
Supplemental Figure 5: Differences between subjects with low-apoB versus high-apoB in % fasting plasma phospholipid fatty acids. N=19 for low-apoB and N=20 for high-apoB for all fatty acids except for % C17:0 where N=5 for low and N=2 for high-apoB, % C16:1n-7 where N=16 for low-apoB, and % C18:3n-6 where N=18 for low and N=19 for high-apoB as the sample for one subject with low-apoB could not be measured and the named fatty acids were below detection limit of the GC-MS in some subjects.



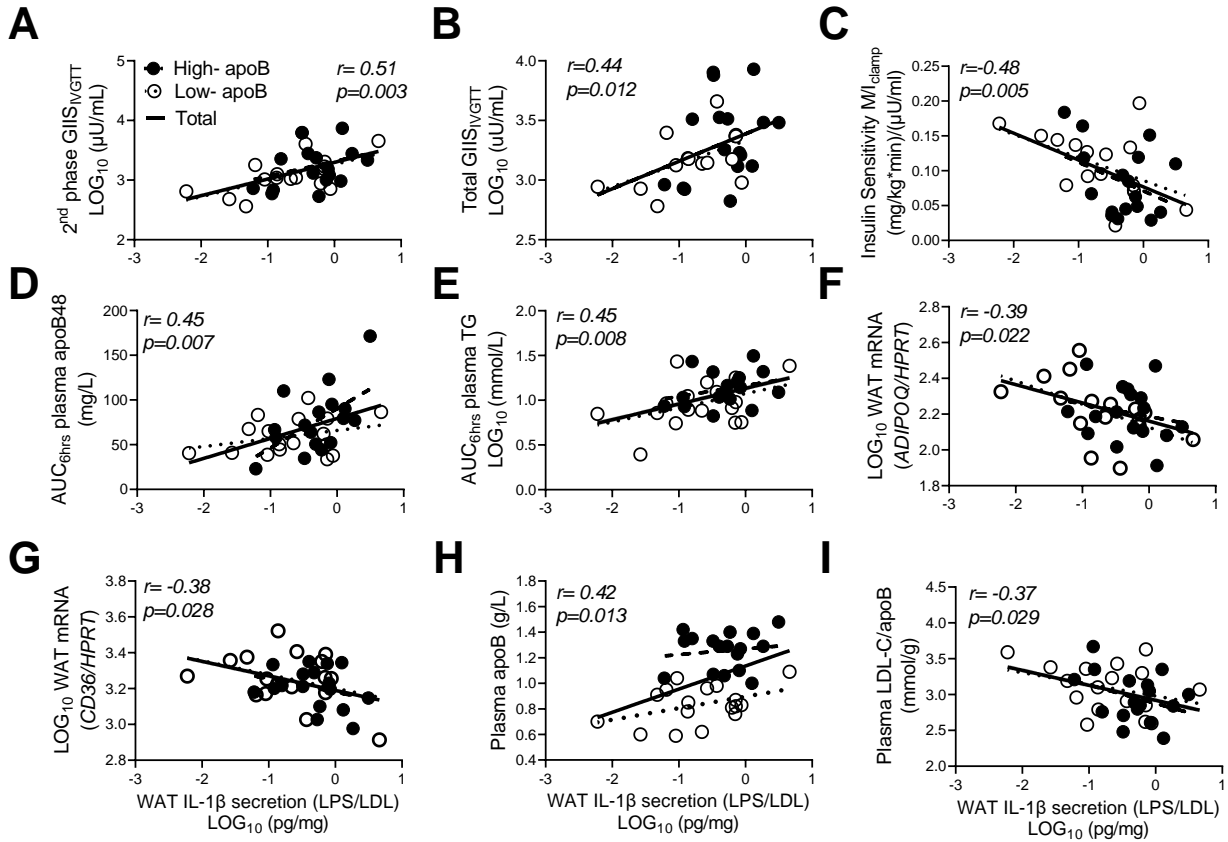
Supplemental Figure 6: Differences between subjects with low-apoB versus high-apoB in fasting baseline WAT mRNA expression of *ADIPOQ*, *PPARG*, *HMGCR*, *SREBP1C*, *SREBP2*, *LDLR*, and *CD36* normalized for *HPRT* (A), and of *MCP1*, *ADGRE1*, *IL10*, *NLRP3*, *CASP1*, and *IL1B* normalized for *HPRT* (B) analyzed by mixed-model analysis with group x gene interaction and presented as boxes with whiskers representing 10th – 90th percentile and line at the average. N=20 for low and N=20 for high plasma apoB.



Supplemental Figure 7: Pearson correlation of fasting plasma apoB with 2nd phase GIIS_{IVGTT} (A), total GIIS_{IVGTT} (B), 2nd phase C-peptide secretion_{IVGTT} (C), total C-peptide secretion_{IVGTT} (D), insulin sensitivity as M/I_{clamp} (E), fasting plasma IL-1Ra (F), AUC_{6hr} plasma TG (G) and AUC_{6hr} plasma apoB48 (H) in women (N=27, closed circles, dotted regression line) and men (N=13, open circles, dashed regression line) except for panels A-D where N=11 men and panel E where N=12 men for missing data. Solid regression line represents pooled data for both sexes.



Supplemental Figure 8: Pearson correlation of fasting WAT IL-1 β -secretion induced by LPS/LDL with 2nd phase GIIS_{IVGTT} (A), total GIIS_{IVGTT} (B), insulin sensitivity as M/I_{clamp} (C), AUC_{6hrs} plasma apoB48 (D), AUC_{6hrs} plasma TG (E), fasting baseline WAT mRNA expression of *ADIPOQ* (F) and *CD36* (G) normalized for *HPRT* and fasting plasma apoB (H), and estimated LDL size as LDL-C/apoB ratio (I) in subjects with low-apoB (N=15, open circles) and high-apoB (N=19, closed circles). Solid regression line represents correlation in all subjects.



Supplemental Figure 9: Pearson correlation of fasting baseline WAT mRNA expression of *NLRP3* normalized for *HPRT* with 1st phase C-peptide secretion_{IVGTT} (**A**), 2nd phase C-peptide secretion_{IVGTT} (**B**), total C-peptide secretion_{IVGTT} (**C**), insulin sensitivity as M/I_{clamp} (**D**), total disposition index (total C-peptide_{IVGTT} x M/I_{clamp}) (**E**), AUC_{6hrs} plasma TG (**F**), fasting plasma IL-1Ra (**G**), TG (**H**), apoB/PCSK9 ratio (**I**), LDL-C/apoB ratio (**J**), and HDL-C (**K**), fasting baseline WAT mRNA expression of *PPARG* (**L**), *ADIPOQ* (**M**), *CD36* (**N**), *SREBP2* (**O**), *MCP1* (**P**), *ADGRE1* (**Q**), and *IL1B* (**R**) normalized to *HPRT*, and % fasting plasma phospholipid palmitate (**S**), arachidonate (**T**) and stearate (**U**) in subjects with low-apoB (N=20, open circles, dotted regression line) and high-apoB (N=20, closed circles, dashed regression line). Solid regression line represents pooled data for all subjects.

