EPA and DHA inhibit LDL-induced upregulation of human adipose tissue NLRP3 inflammasome/IL-1β pathway and its association with diabetes risk factors

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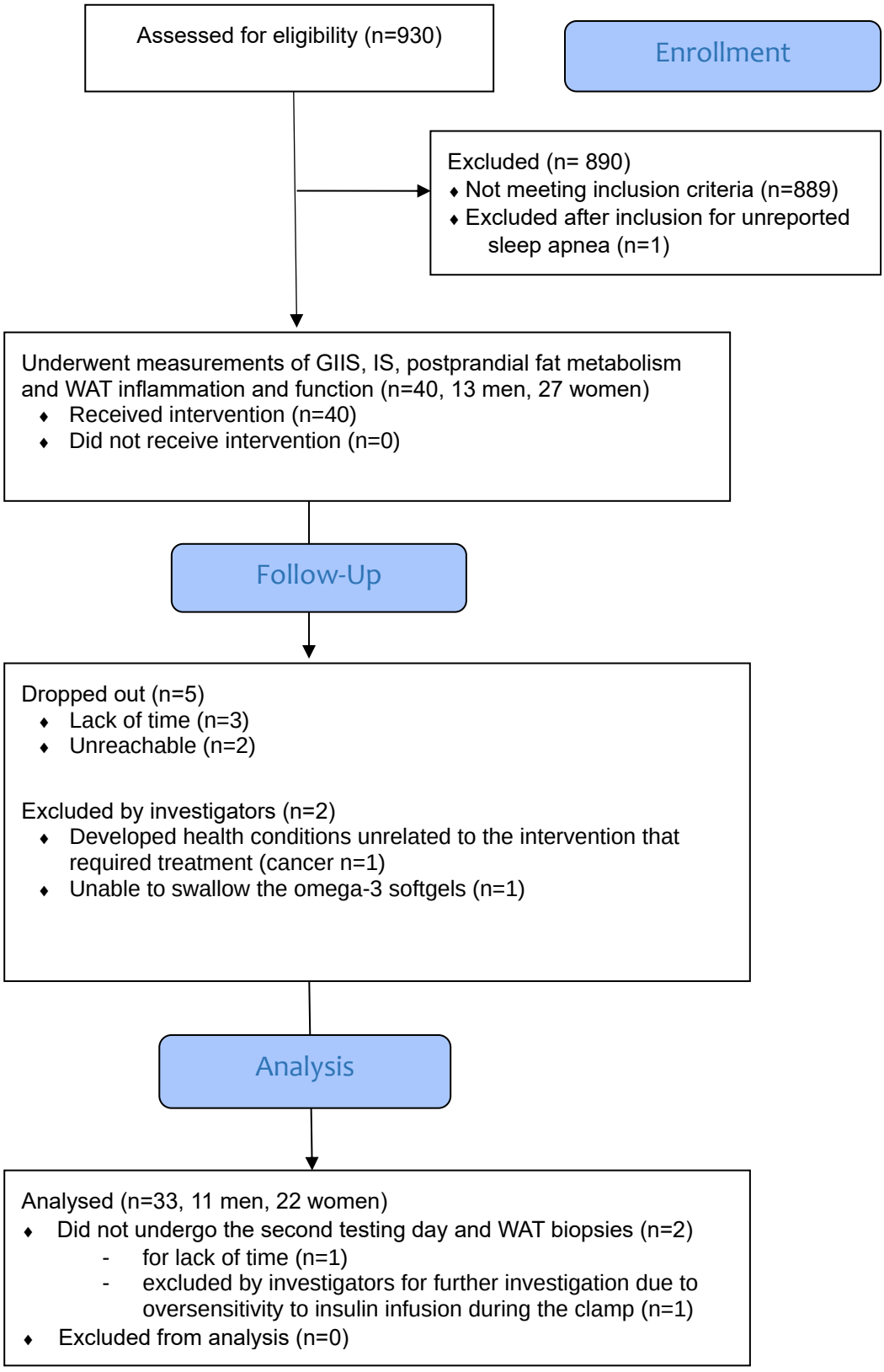
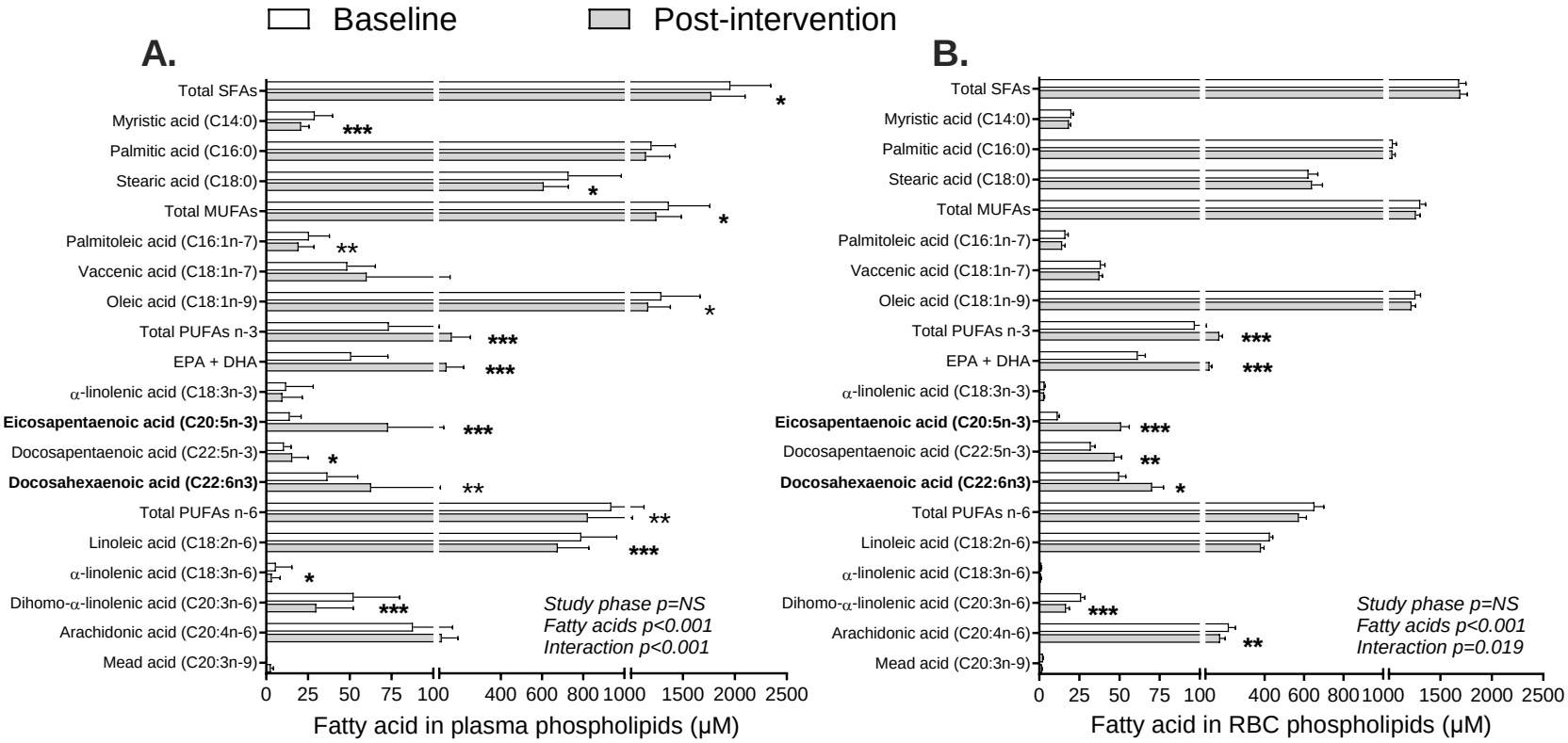
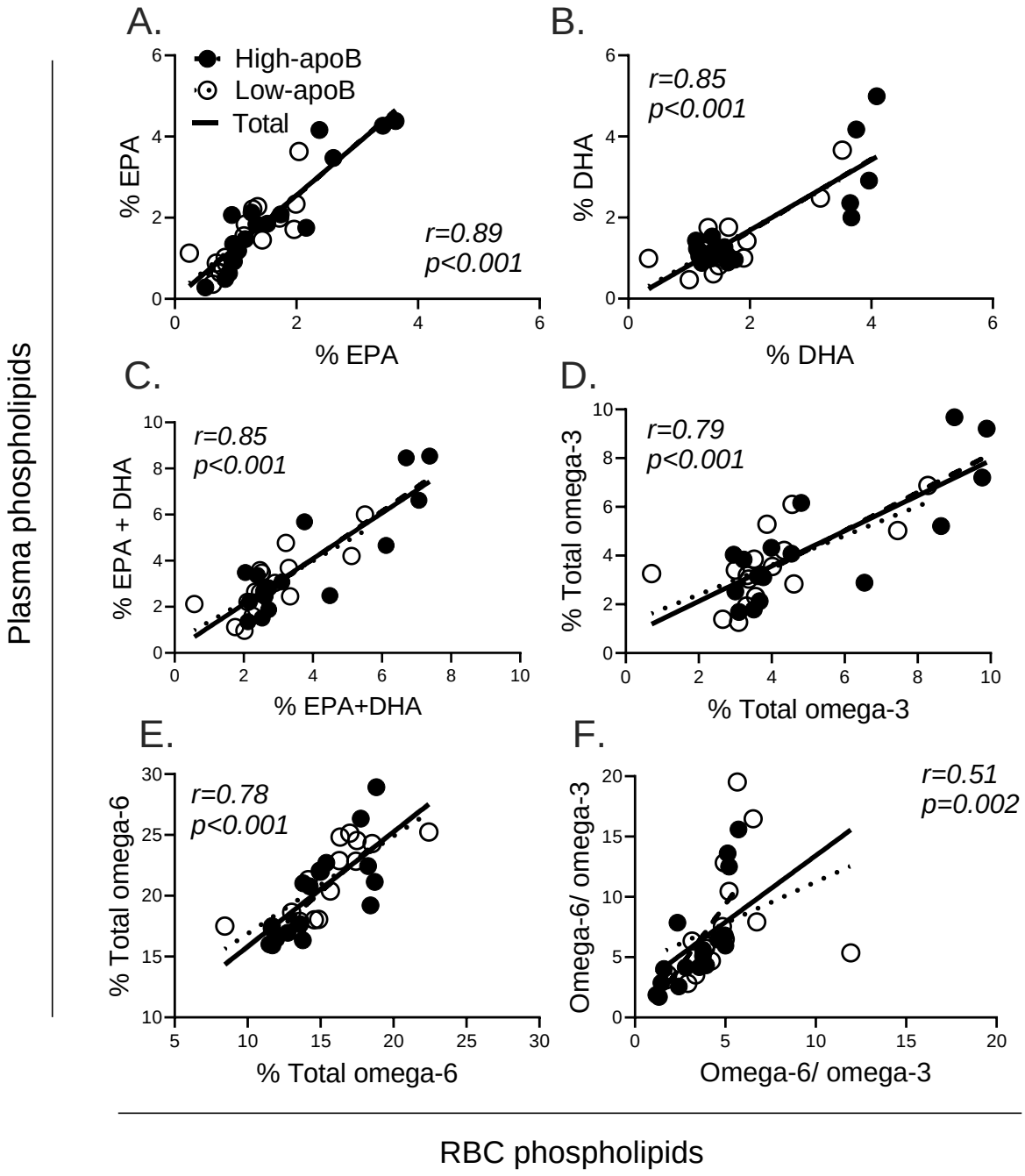
Supplemental Figure 1: Subject flow chart



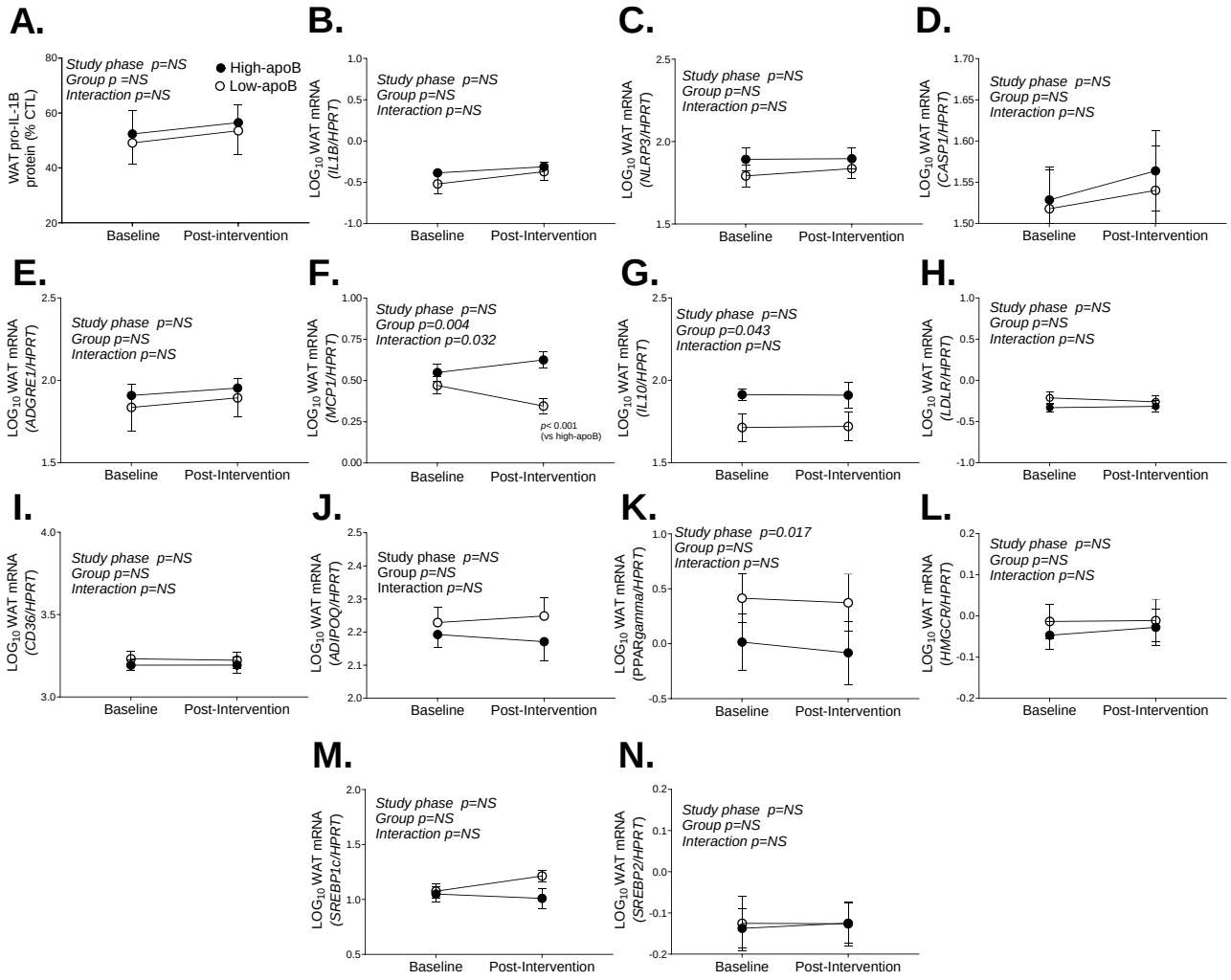
Supplemental Figure 2: Fatty acid concentrations in the phospholipid layer of A) plasma (i.e. lipoproteins) and B) red blood cells (RBC) at baseline and following the 12-week supplementation with EPA and DHA (2.7 g/d) in the 33 subjects who completed the trial. Data was analyzed by mixed-model analysis with interaction. * for $p<0.05$, ** for $p<0.01$ and *** for $p<0.001$ versus baseline. N.B. Mead acid was excluded from analysis as only N=2 subjects had measurable post-intervention concentration in RBC-PL.



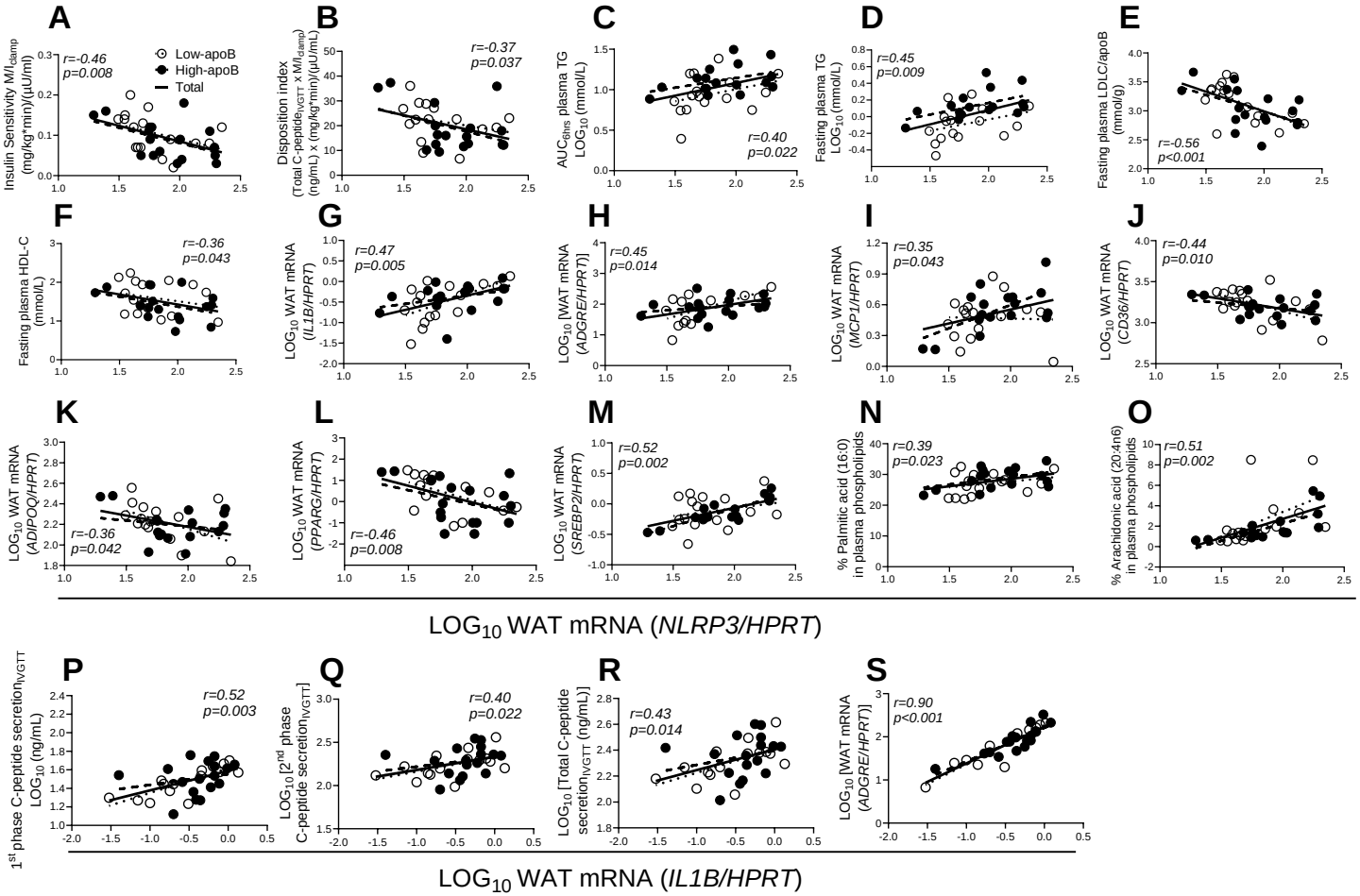
Supplemental Figure 3: Correlation between RBC and plasma phospholipids content of % EPA (**A**), % DHA (**B**), % EPA and DHA (**C**), % total omega-3 (**D**), % total omega-6 (**E**), and omega-6/omega-3 ratio (**F**) in subjects with low-apoB (N=16, open circle) and high-apoB (N=17, closed circle) who completed 12-week supplementation with EPA and DHA (2.7 g/d). Solid regression line represents correlation in all subjects. Data was analyzed by Pearson correlation as in methods.



Supplemental Figure 4: Baseline and post-intervention of WAT protein expression of pro-IL-1β (**A**) and WAT mRNA expression of *IL1B* (**B**), *NLRP3* (**C**), *CASP1* (**D**). *ADGRE1* **(E)**, *MCP1* (**F**), *IL10* (**G**), *LDLR* (**H**), *CD36* (**I**), *ADIPOQ* (**J**), *PPARG* (**K**), *HMGCR* (**L**) *SREBP1c* (**M**) and *SREBP2* (**N**) normalized to *HPRT* in subjects with low-apoB (baseline N=16, post-intervention N=14) and high-apoB (baseline N=17, post-intervention N=16) for missing data. Data analyzed by mixed-model analysis with group x time interaction.



Supplemental Figure 5: Pearson correlation of fasting baseline WAT mRNA expression of *NLRP3* normalized for *HPRT* with insulin sensitivity as M/I_{clamp} (**A**), total disposition index (total C-peptide$_{IVGTT}$ x M/I_{clamp}) (**B**), AUC_{6hrs} plasma TG (**C**), fasting plasma TG (**D**), estimated fasting LDL size (**E**), fasting plasma HDL-C (**F**), and WAT mRNA expression of *IL1B* (**G**), *ADGRE1* (**H**), *MCP1* (**I**), *CD36* (**J**), *ADIPOQ* (**K**), *PPARG* (**L**), and *SREBP2* (**M**) normalized to *HPRT*, and % fasting plasma phospholipid palmitate (**N**), and arachidonate (**O**), and correlation of fasting baseline WAT mRNA expression of *IL1B* with 1st phase (**P**), 2nd phase (**Q**), total C-peptide secretion$_{IVGTT}$ (**R**), and WAT mRNA expression of *ADGRE1* normalized to *HPRT* (**S**) in subjects with low-apoB (N=16, open circles, dotted regression line) and high-apoB (N=17, closed circles, dashed regression line) who completed the trial. Solid regression line represents pooled data for all subjects.



Supplemental Figure 6: Pearson correlation of fasting post-intervention WAT mRNA expression of *NLRP3* normalized for *HPRT* with insulin sensitivity as M/I_{clamp} (**A**), total disposition index (total C-peptide$_{IVGTT}$ x M/I_{clamp}) (**B**), AUC_{6hrs} plasma TG (**C**), fasting plasma TG (**D**), estimated fasting LDL size (**E**), fasting plasma HDL-C (**F**), and WAT mRNA expression of *IL1B* (**G**), *ADGRE1* (**H**), *MCP1* (**I**), *CD36* (**J**), *ADIPOQ* (**K**), *PPARG* (**L**), and *SREBP2* (**M**) normalized to *HPRT*, and % fasting plasma phospholipid palmitate (**N**), and arachidonate (**O**), and correlation of fasting baseline WAT mRNA expression of *IL1B* with 1st phase (**P**), 2nd phase (**Q**), total C-peptide secretion$_{IVGTT}$ (**R**), and WAT mRNA expression of *ADGRE1* normalized to *HPRT* (**S**) in subjects with low-apoB (N=15, open circles, dotted regression line) and high-apoB (N=1, closed circles, dashed regression line) who completed the trial and have post-intervention WAT data. Solid regression line represents pooled data for all subjects.