

## **Rokatoarivelo et al., Supplementary data**

### **Supplementary Figure 1. Expression of housekeeping genes in the analyzed samples**

Gene expression of *GADPH* and *LRP10* in the adipose tissues of all the samples.

### **Supplementary Figure 2. Expression of cytokines in the sera of patients**

Indicated cytokines were measured in the sera of patients and controls. N= 5 BMI<30 (kg/m<sup>2</sup>); n=5 no diabetes BMI ≥30 (kg/m<sup>2</sup>); n=7 diabetes BMI ≥30 (kg/m<sup>2</sup>).

### **Supplementary Figure 3. Expression of CRP in the sera of patients**

CRP levels were measured in the sera of patients and controls using hsCRP kit. N= 5 BMI<30 (kg/m<sup>2</sup>); n=25 no diabetes BMI ≥30 (kg/m<sup>2</sup>); n=9 pre-diabetes BMI ≥30 (kg/m<sup>2</sup>); n=25 diabetes BMI ≥30 (kg/m<sup>2</sup>).

### **Supplementary Figure 4. Expression of other cytokines in visceral and subcutaneous adipose tissues of patients**

Indicated cytokines were measured in 41 visceral and 42 subcutaneous adipose tissues of patients and controls. N= 9 and 8 BMI<30 (kg/m<sup>2</sup>); n=12 no diabetes BMI ≥30 (kg/m<sup>2</sup>); n=11 and 9 pre-diabetes BMI ≥30 (kg/m<sup>2</sup>); n=10 and 12 diabetes BMI ≥30 (kg/m<sup>2</sup>). (VAT and SAT).

### **Supplementary Figure 5. Expression of *IFNG*, *IL18*, *IL15* and *IL15RA* cytokines in visceral and subcutaneous adipose tissues of patients**

Gene expression of *IFNG*, *IL18*, *IL15* and *IL15RA* in the visceral and subcutaneous adipose tissues. n= 4-11 BMI<30 (kg/m<sup>2</sup>); n=34 - 40 no diabetes BMI ≥30 (kg/m<sup>2</sup>); n=12-17 pre-diabetes BMI ≥30 (kg/m<sup>2</sup>); n=38 diabetes BMI ≥30 (kg/m<sup>2</sup>). None of the data was statistically significant.

### **Supplementary Figure 6. Correlation between protein and gene expression in adipose tissues**

Correlation between protein and gene transcripts for TNF $\alpha$ , IL6, IL-1 $\beta$  and IL15 in visceral and subcutaneous adipose tissues is shown in the figure. n= 24 - 30.

**Supplementary Figure 7. Expression patterns of select cytokines in the visceral and subcutaneous adipose tissues**

Expression pattern of the indicated cytokines in the visceral and subcutaneous adipose tissues from a given patient. A line of a particular color in both the depots indicates data from each patient. The points have been joined for easy visualization. Dotted lines do not have the corresponding data in the other adipose tissue depot. The straight lines represent the data presented in Fig. 4.

**Supplementary Figure 8. Expression patterns of select cytokine genes in the visceral and subcutaneous adipose tissues**

Expression pattern of the indicated cytokines in the visceral and subcutaneous adipose tissues from a given patient. Each line indicates data from each patient. The points have been joined for easy visualization.

**Supplementary Figure 9. Chemokine levels in adipose tissues**

Expression of select chemokines in the visceral and subcutaneous adipose tissues. n= 9 and 8 BMI<30 (kg/m<sup>2</sup>); n=12 no diabetes BMI  $\geq$ 30 (kg/m<sup>2</sup>); n=11 and 9 pre-diabetes BMI  $\geq$ 30 (kg/m<sup>2</sup>); n=10 and 12 diabetes BMI  $\geq$ 30 (kg/m<sup>2</sup>). None of the data was statistically significant.

**Supplementary Figure 10. Expression of chemokines in adipose tissues**

**A)** Gene expression of *CCL2*, *CCL5* and *CXCL10* in the visceral and subcutaneous adipose tissues. n= 8-11 BMI<30 (kg/m<sup>2</sup>); n=34 - 40 no diabetes BMI  $\geq$ 30 (kg/m<sup>2</sup>); n=12 - 17 pre-diabetes BMI  $\geq$ 30 (kg/m<sup>2</sup>); n=38 diabetes BMI  $\geq$ 30 (kg/m<sup>2</sup>). None of the data was statistically significant. **B)** Correlation between chemokines (*CCL2*, *CCL5*) and cytokines (*TNFA*, *IL6*) at the level of gene expression. Pooled data (BMI<30 (kg/m<sup>2</sup>) and BMI  $\geq$ 30 (kg/m<sup>2</sup>)) was used for the analysis. n= 29. **C)** Correlation between

chemokines (CCL2, CCL5 and CXCL10) and cytokines (TNF $\alpha$ , IL6 and IFN $\gamma$ ). Pooled data (BMI<30 (kg/m<sup>2</sup>) and BMI  $\geq$ 30 (kg/m<sup>2</sup>)) was used for the analysis. n= 42.

**Supplementary Figure 11. Correlation between *CD68*, *TNFA* and *IL6* gene expression in adipose tissues**

Correlation between gene transcripts for *CD68*, *TNFA* and *IL6* in visceral and subcutaneous adipose tissues is shown in the figure. n= 30 - 61.

**Supplementary Figure 12. VEGF and PDGF in adipose tissues**

Expression of VEGF-A, PDGF-BB and PDGF-AA in the visceral and subcutaneous adipose tissues and sera. None of the data was statistically significant.

**Supplementary Figure 13. Correlation between VEGF and select cytokines in adipose tissues**

Correlation between the growth factors (VEGF-A, PDGF-BB and PDGF-AA) and inflammatory cytokines (IL-6, TNF $\alpha$ , IL-1 $\beta$  and IL-15) in visceral and subcutaneous adipose tissues is shown in the figure. n= 42.

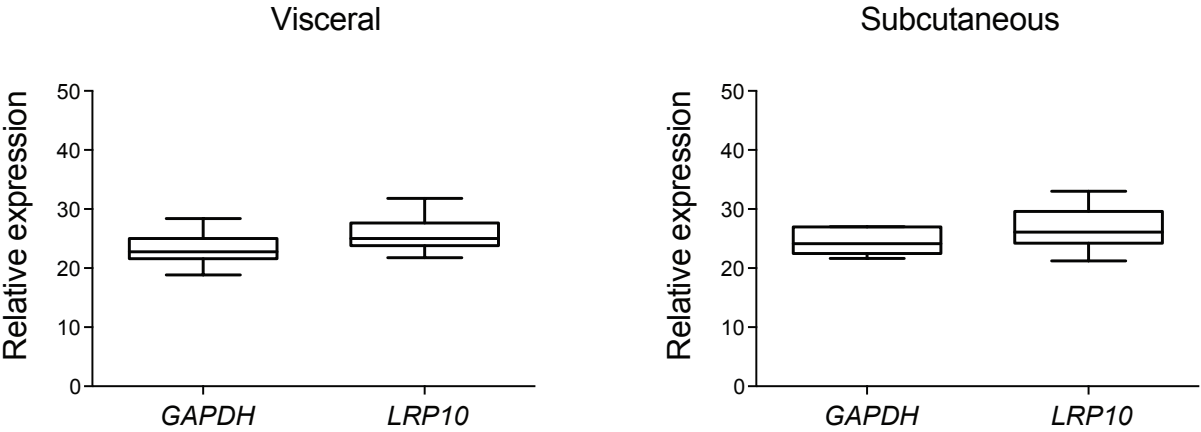
## Supplementary Table 1: List of primers used in this study

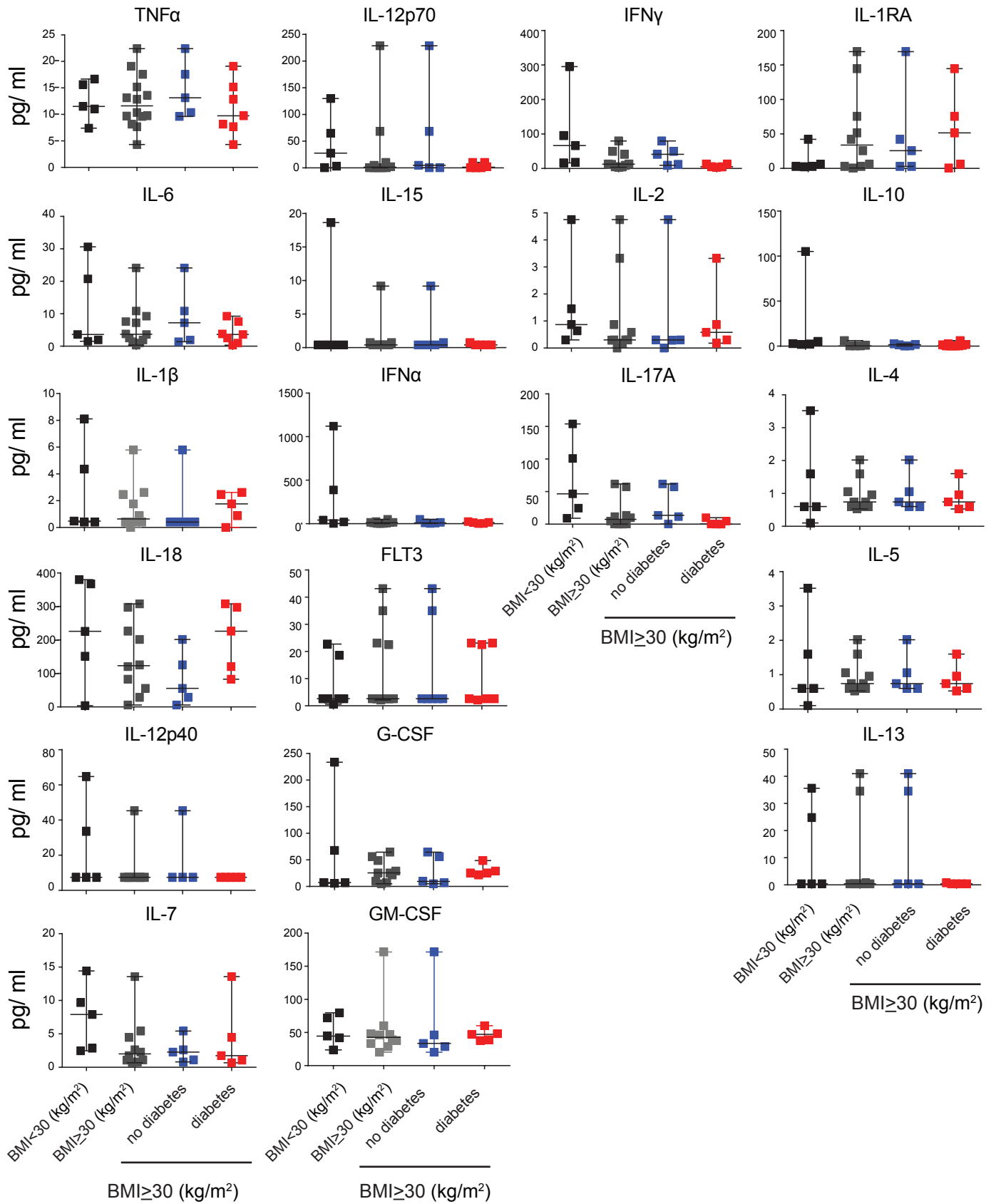
Gene name	Gene ID	Sense primer	Anti-sense primer	Amplicon size	Primer efficiency
<i>IL1B</i>	NM_000576.2	TGACCTGAGCACCTTCTTTC	CCACTTGTGCTCCATATCC	205bp	1.92
<i>IL6</i>	NM_000600	CCACTCACCTCTTCAGAACG	CATCTTTGGAAGGTTCAGGTTG	150bp	2.1
<i>TNFA</i>	NM_0005943	CAGCCTCTTCTCCTTCTGAT	GCCAGAGGGCTGATTAGAGA	122bp	2.03
<i>IL15</i>	NM_172175.2	CAAACAACAGTTTGTCTTCTAAT GG	GACAATATGTACAAAACCTGCAAAA A	112pb	2.2
<i>IL15RA</i>	NM_001351097.1	AGACAACAGCCAAGAACTGG	TTGCCTTGACTTGAGGTAGC	166bp	2.1
<i>IL18</i>	NM_001562	CATTGACCAAGGAAATCGGC	CACAGAGATAGTTACAGCCATACC	136bp	2.1
<i>IL10</i>	NM_000572	CGCATGTGAACTCCCTGG	TAGATGCCTTTCTCTTGAGC	145bp	ND
<i>LRP10</i>	NM_014045	GGATGGAGGCTGAGATTGTG	CTGTAGCAGAGAACGCAGG	146bp	1.9
<i>GAPDH</i>	NM_002046.5	GATGACATCAAGAAGGTGGTG AA	GTCTTACTCCTTGGAGGCCATGT	245bp	2.02
<i>IFNG</i>	NM_000619	GCATCGTTTTGGGTTCTCTTG	AGTTCCATTATCCGCTACATCTG	113bp	ND
<i>IL4</i>	NM_000589	AGCTGATCCGATTCTGAAAC	AACGTACTCTGGTTGGCTTC	94pb	ND
<i>CD4</i>	NM_000616.4	TCAAATAGACATCGTGGTGCT	ACCTGTTCCCCCTTTTCTTA	72bp	2.08
<i>CD8</i>	NM_001768.6	TCATGGCCTTACCAGTGACC	AGGTTCCAGGTCCGATCC	105bp	2.0
<i>CD68</i>	NM_001251	CATCTCTGACTGAACCCCAAC	CCATGTAGCTCAGGTAGACAAC	149bp	1.98
<i>PPARG</i>	NM_138711.3	AGTCCTCACAGCTGTTTGCCAA GC	GAGCGGGTGAAGACTCATGTCTGT	124bp	2.06
<i>IL1RN</i>	NM_173843	CCTCATGCTCTGTTCTTGGG	TGTCCTGCTTTCTGTTCTCG	130pb	1.87

ND- the data set did not permit the determination of primer efficiency

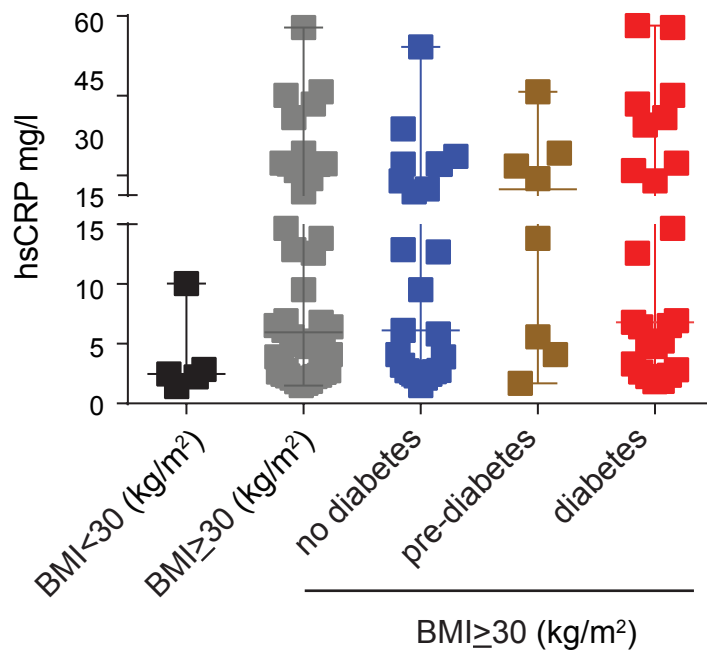
### **Gene names**

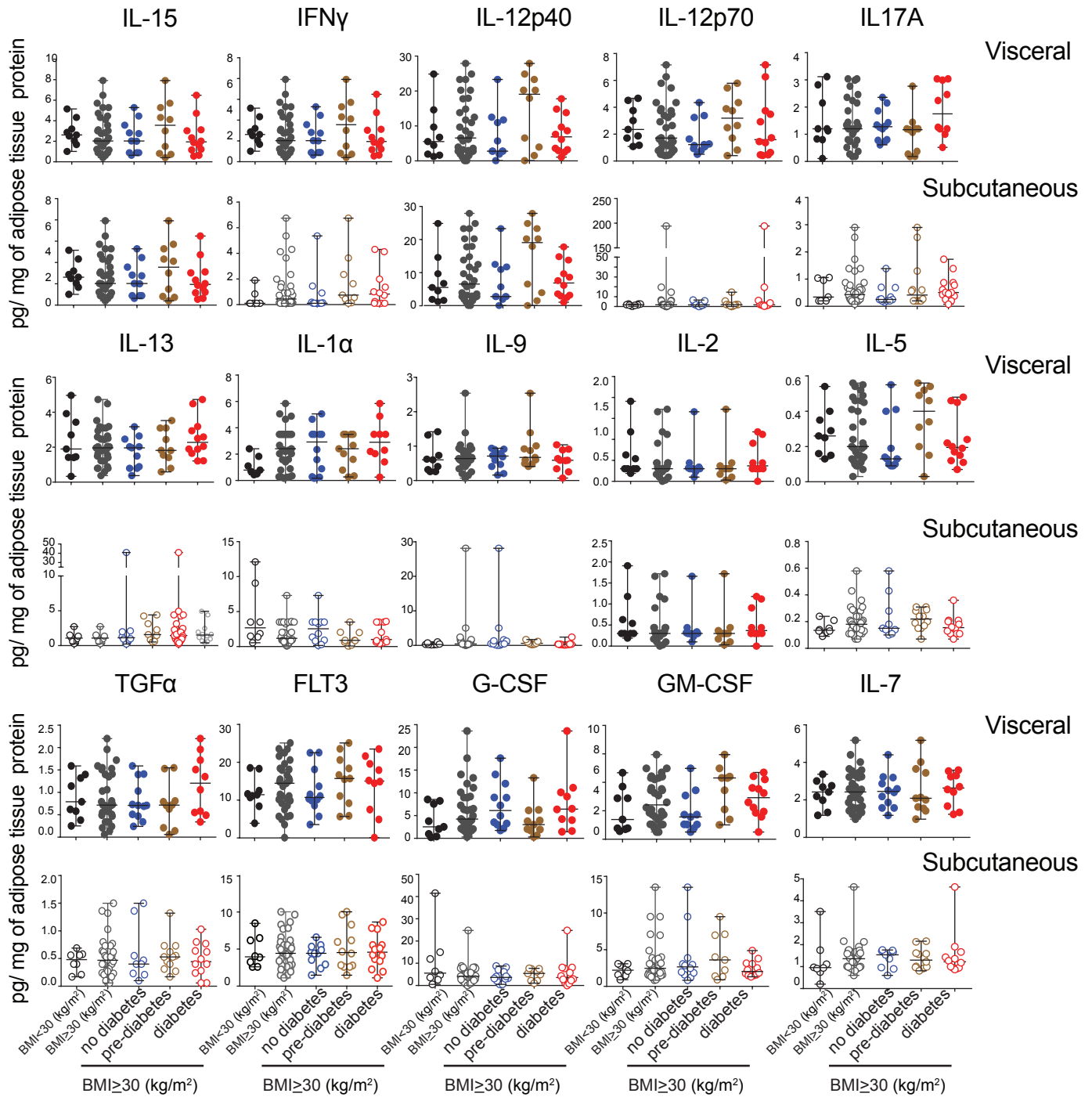
*IL1B*, Interleukin-1 beta  
*IL6*, Interleukin-6 beta  
*TNFA*, Tumor necrosis factor, alpha  
*IL15*, Interleukin-15  
*IL15RA*, Interleukin-15, receptor subunit alpha  
*IL18*, Interleukin-18  
*IL10*, Interleukin-10  
*LRP10*, LDL receptor related protein 10  
*GAPDH*, Glyceraldehyde-3-phosphate dehydrogenase  
*IFNG*, Interferon gamma  
*IL4*, Interleukin-4  
*CD4*, CD4 molecule  
*CD8*, CD8a molecule  
*CD68*, CD68a molecule  
*PPARG*, Peroxisome proliferator activated receptor gamma  
*IL1RN*, Interleukin-1 receptor antagonist



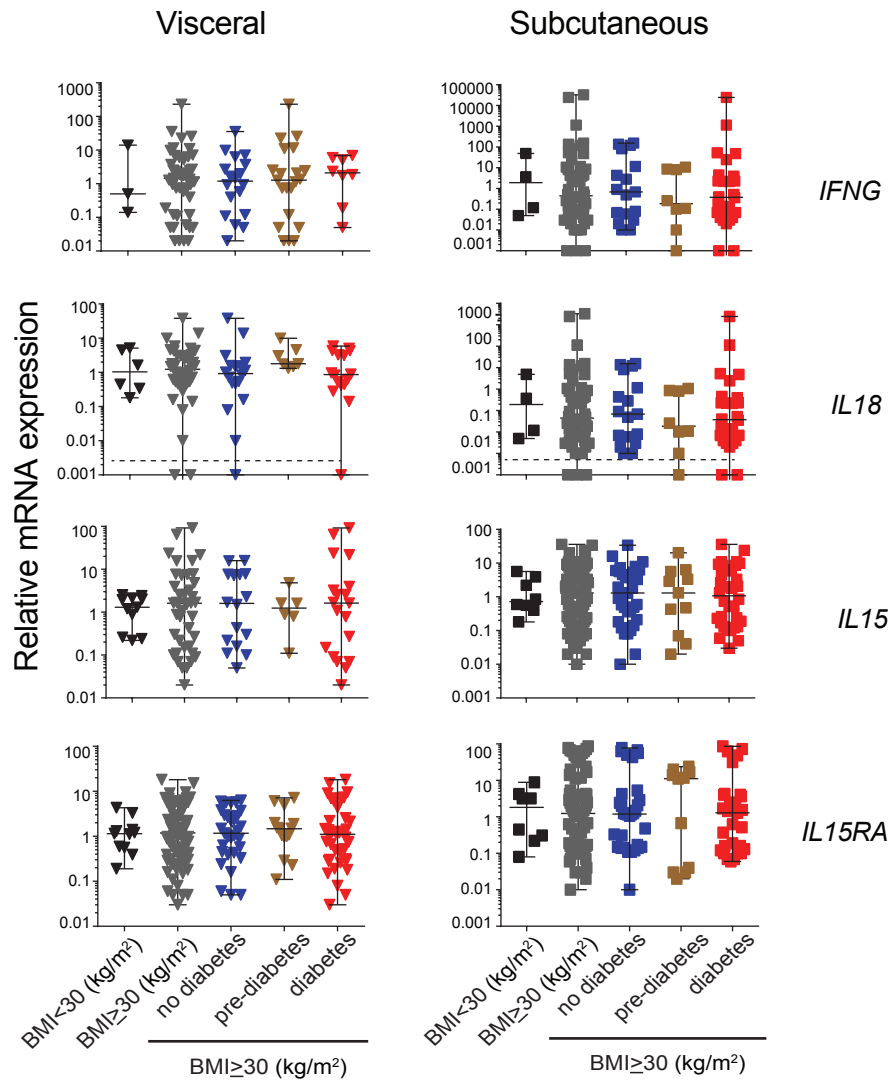


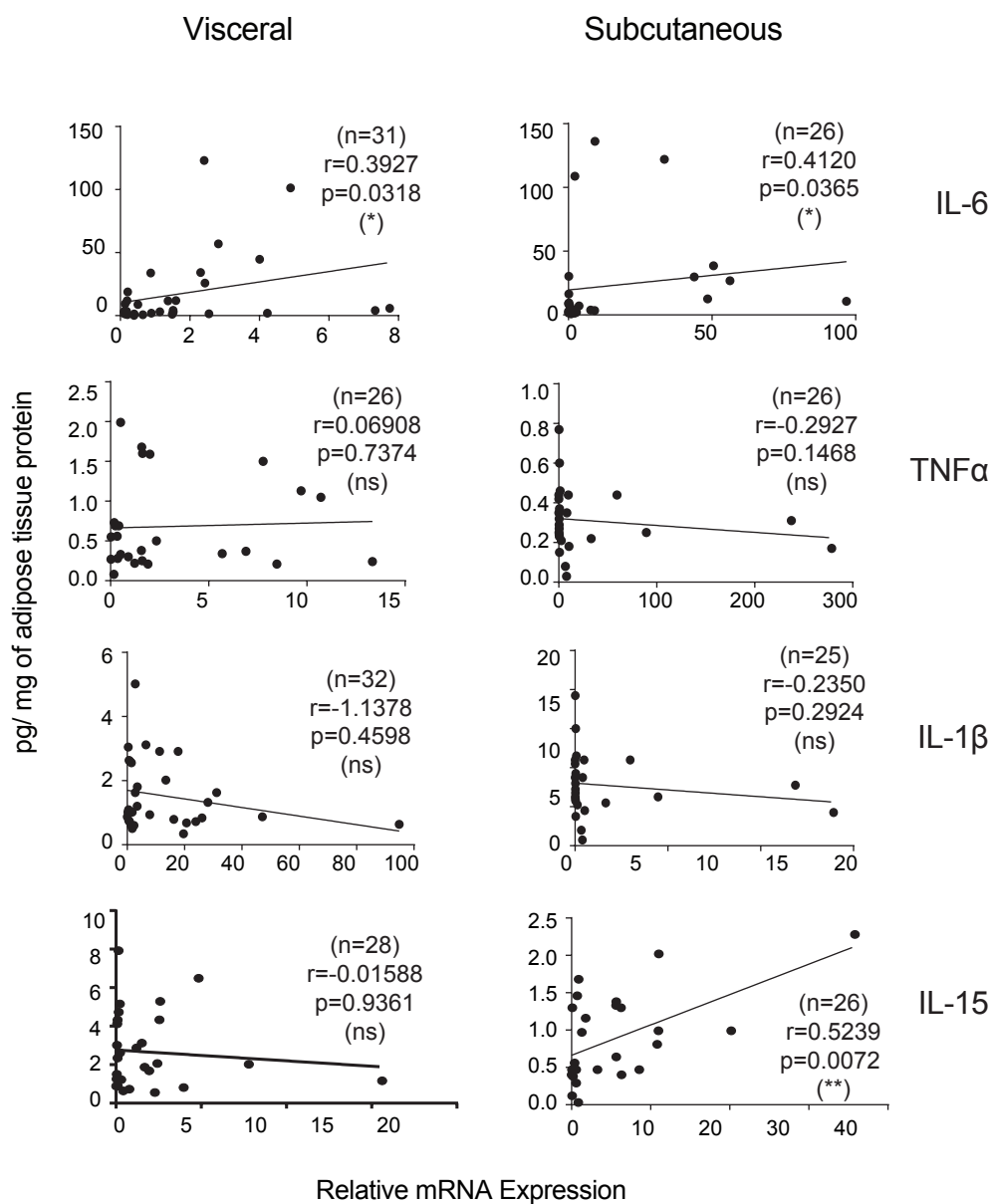
Rakotoarivelo et al., Supplementary Figure 3



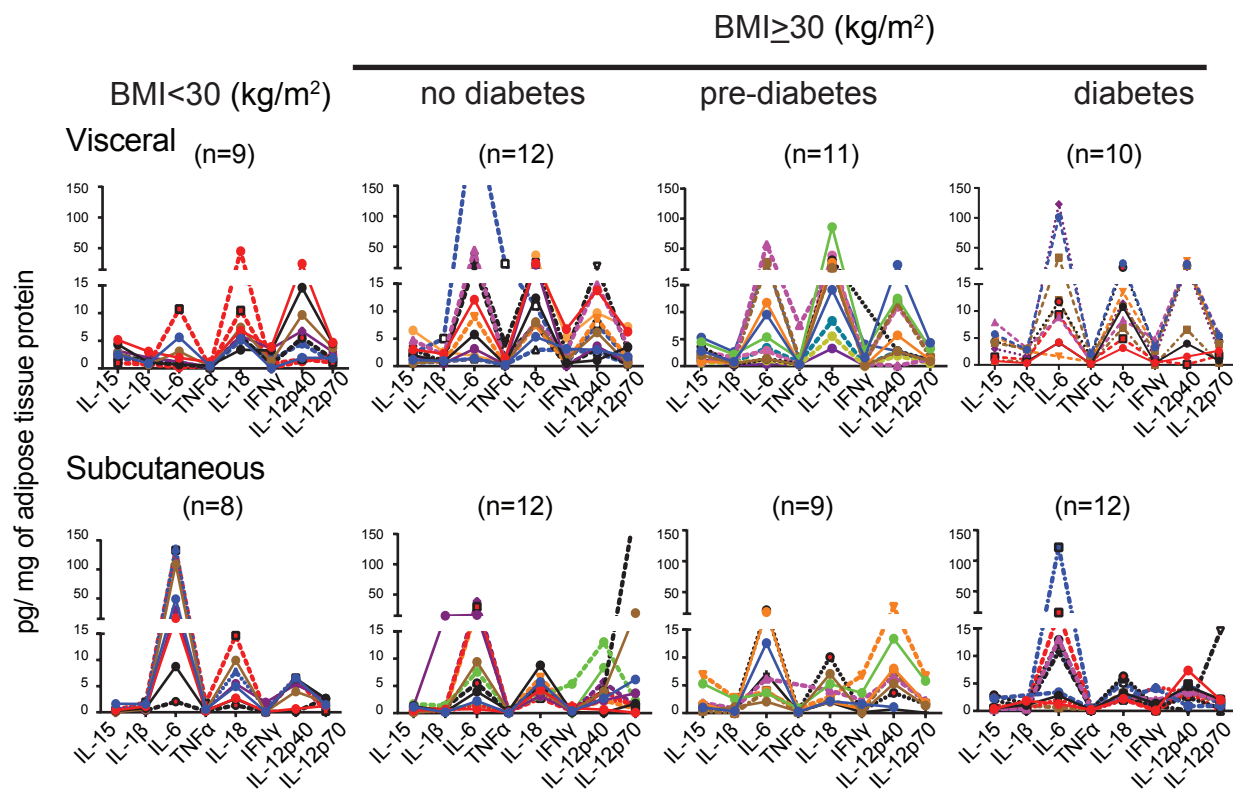


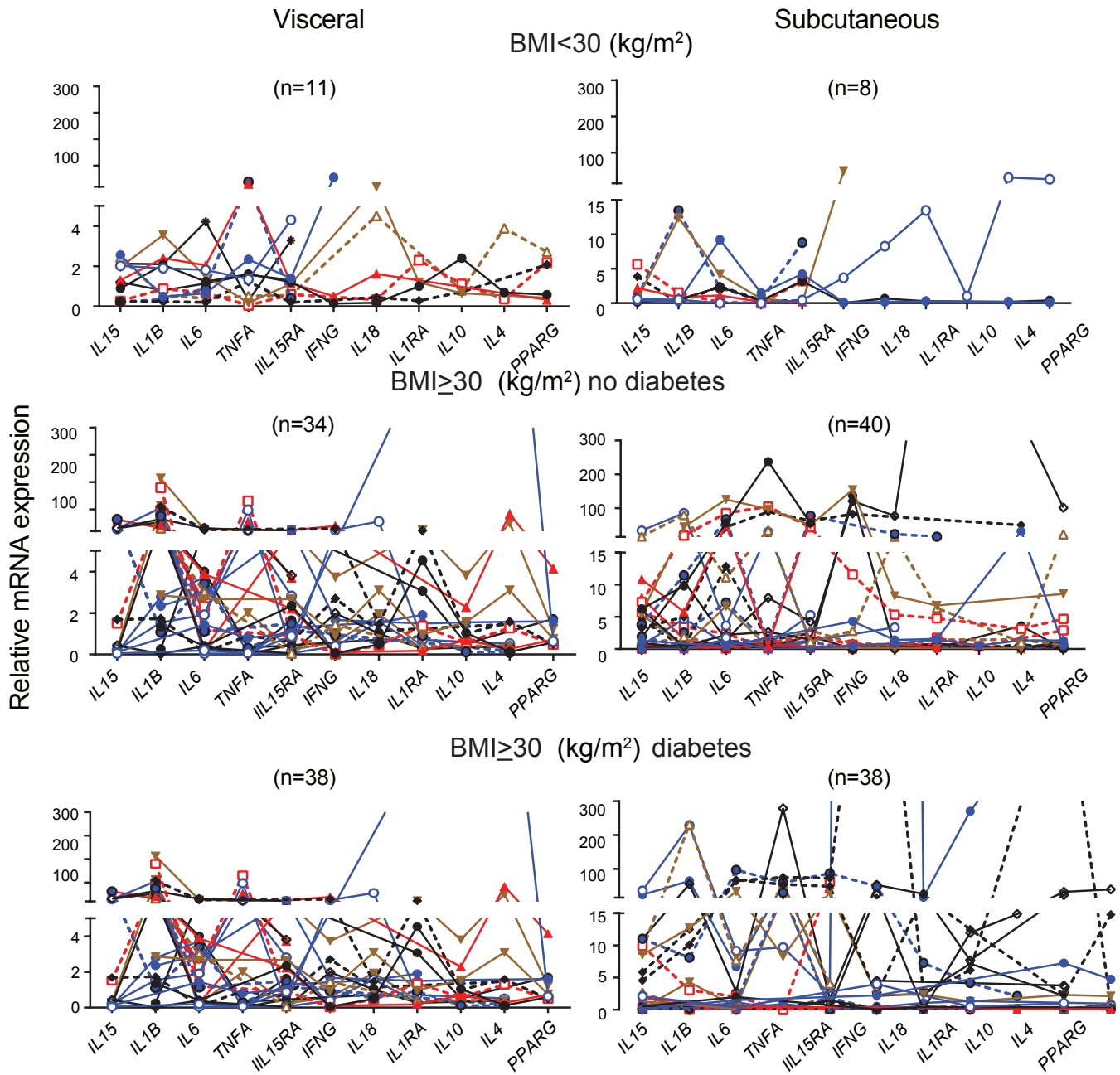




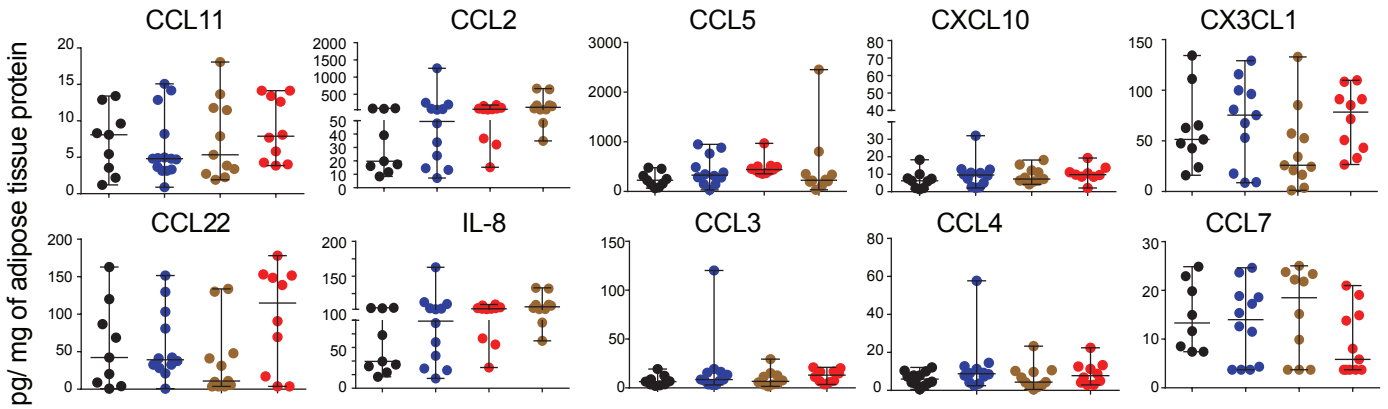


Rakotoarivelo et al., Supplementary Figure 7

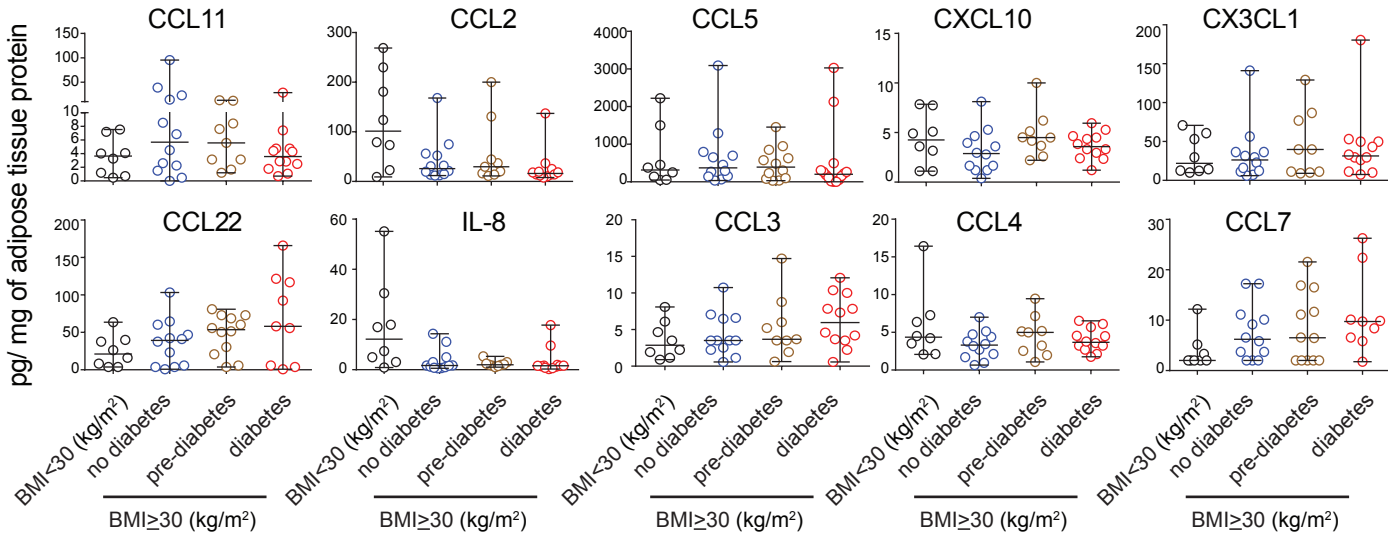




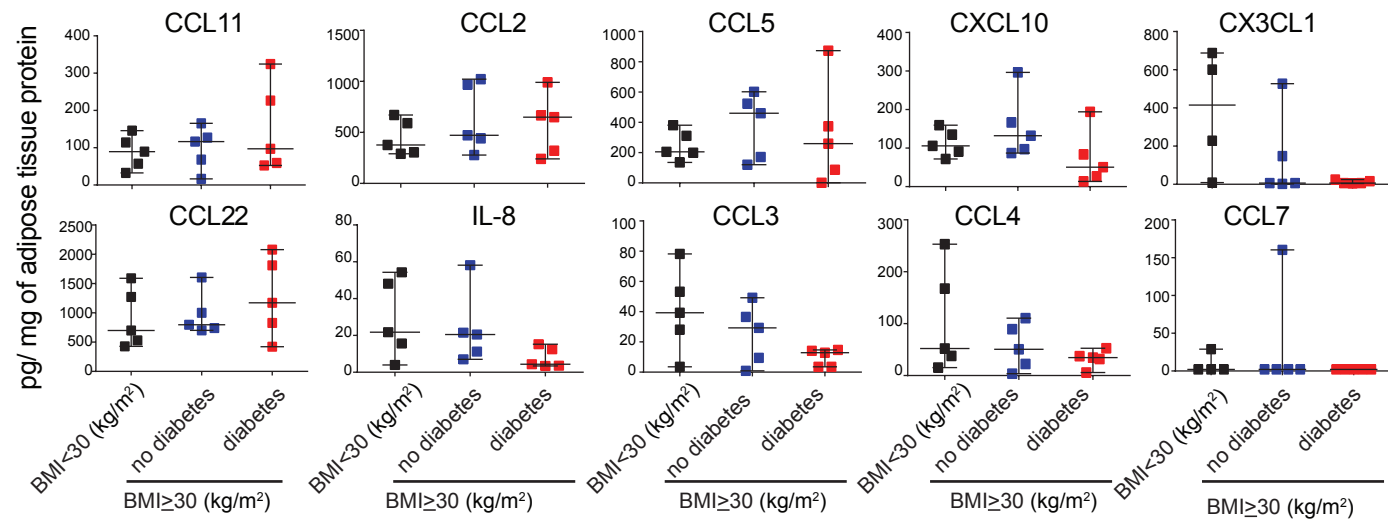
Visceral



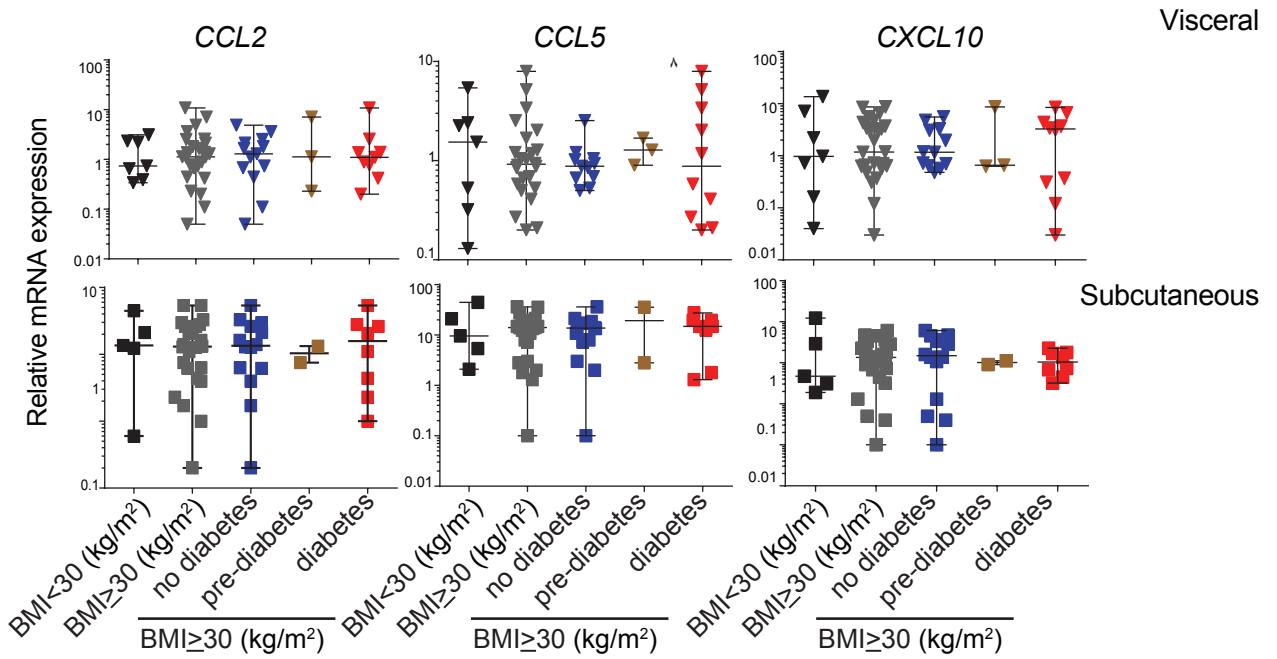
Subcutaneous



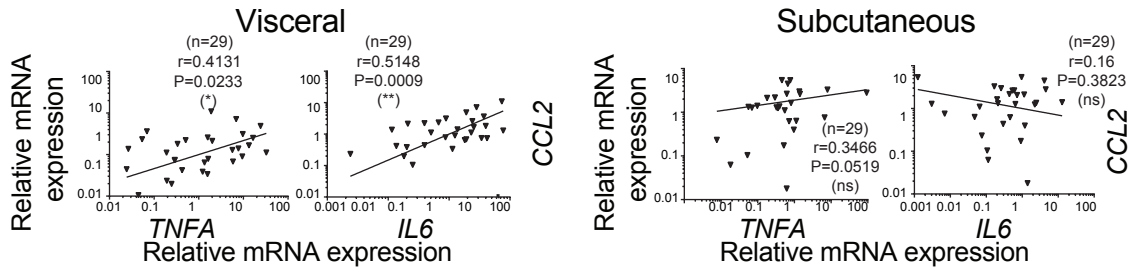
Serum



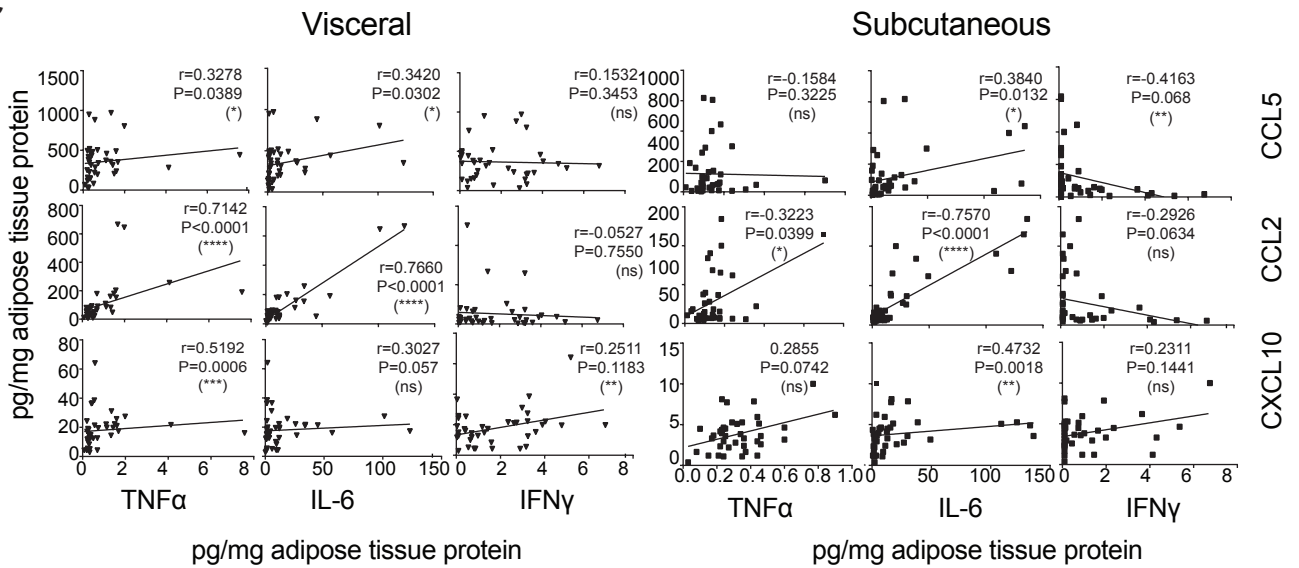
A

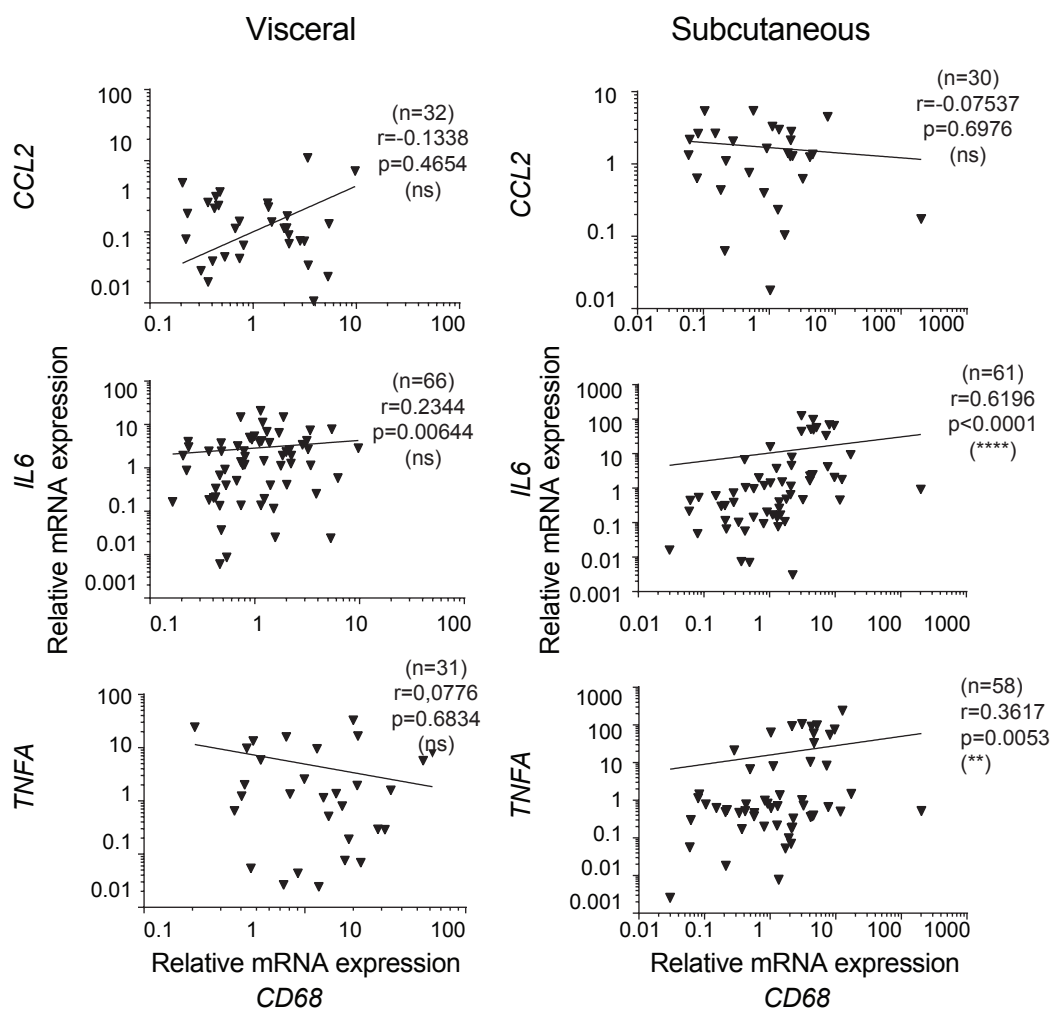


B



C





Rakotoarivelo et al., Supplementary Figure 12

