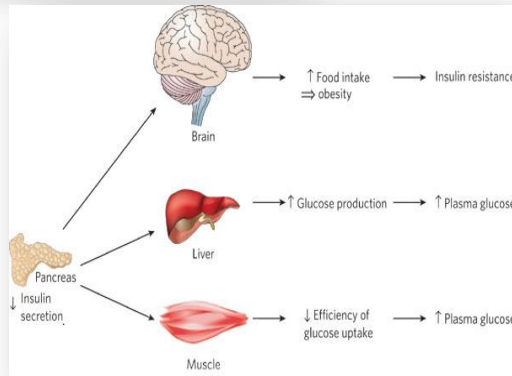
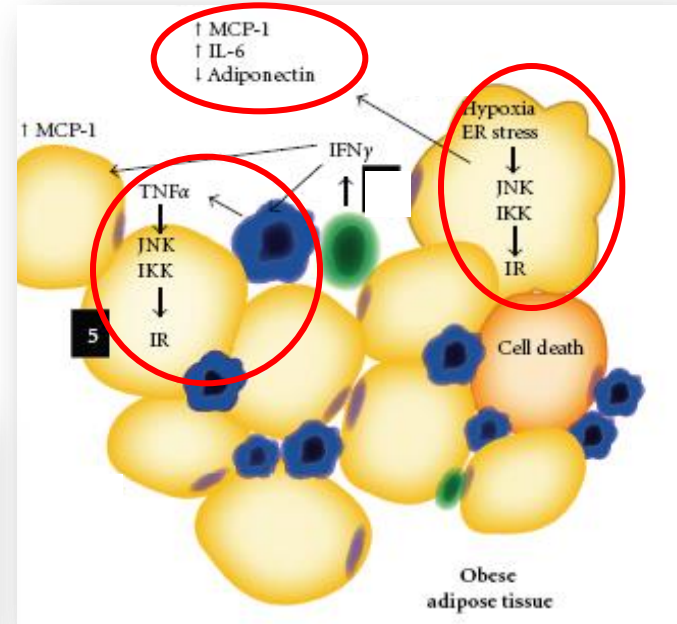
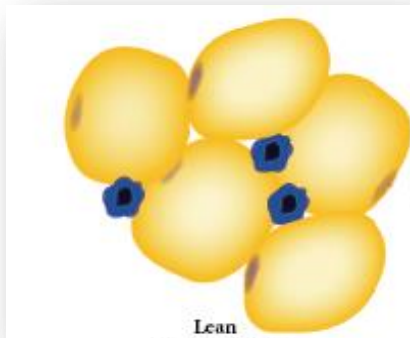
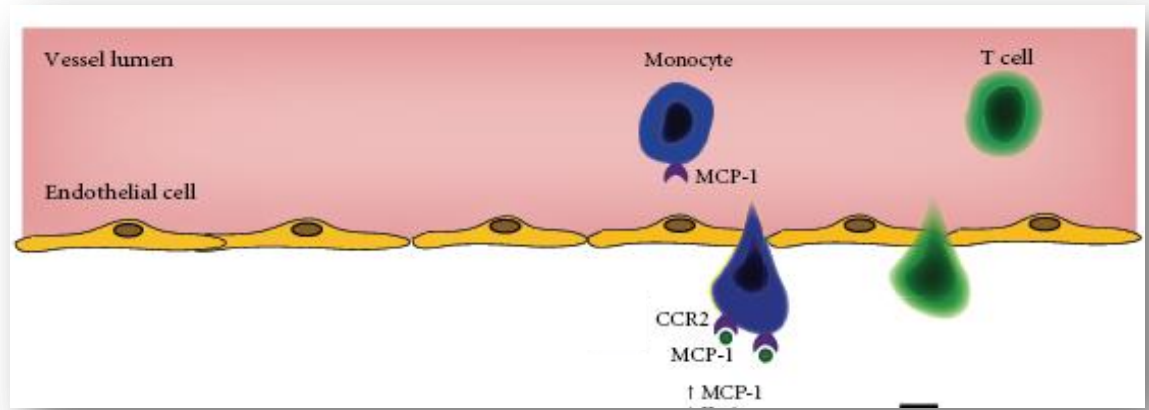


Tweak: a new cytokine within the context of obesity

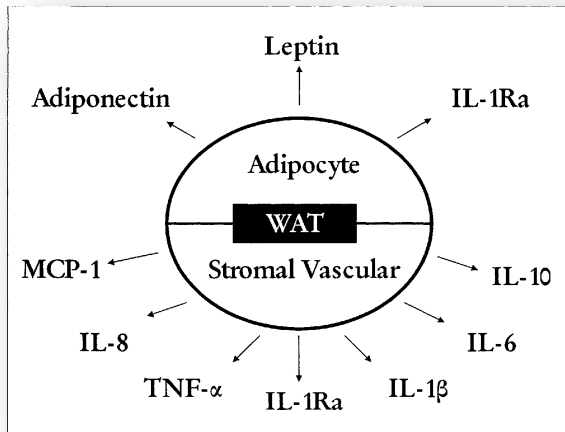
Matilde Rodríguez Chacón Ph.D
“Miguel Servet” Investigator
Institut d’Investigació Sanitària Pere Virgili
Tarragona

inflammation in obesity



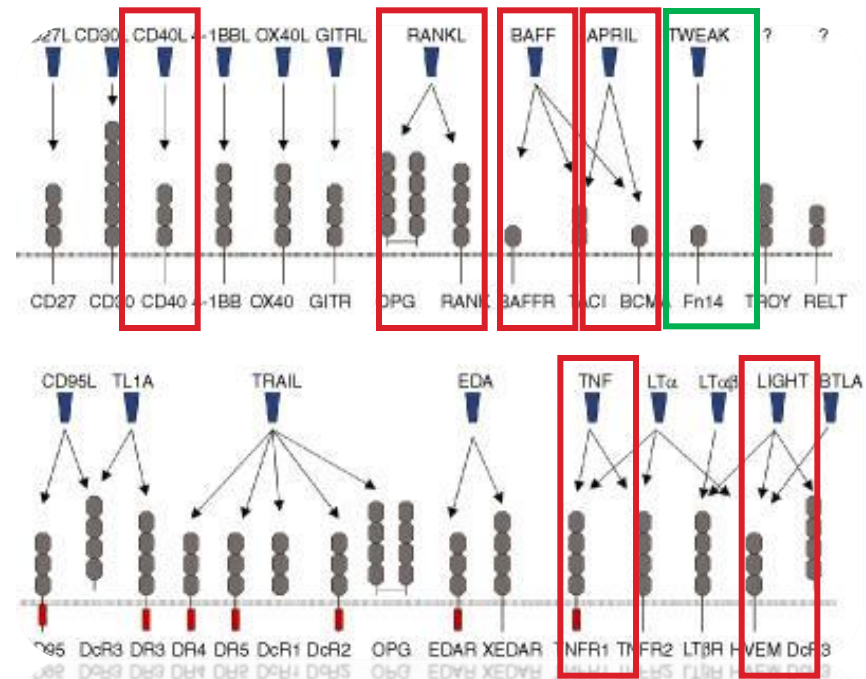
Inflammatory cytokines

Altered cytokines /adipokines/ chemokines in obesity



TNF-superfamily

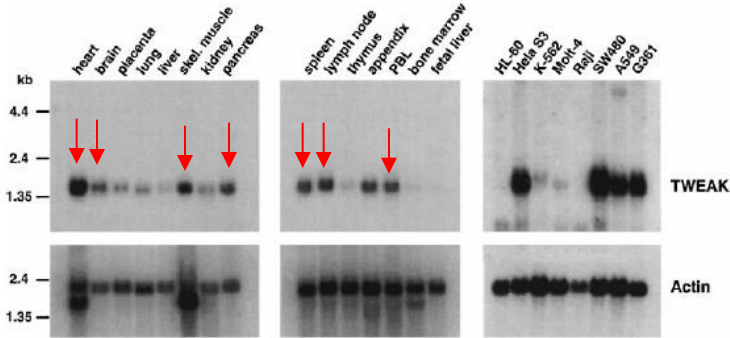
Members of the tumor necrosis factor (TNF) superfamily are potent regulators of inflammation and cell survival and consist of 20 ligands that signal through 29 different receptors.



Tweak (Tumor necrosis factor like weak inducer of apoptosis)

Background

➤ TWEAK is a widely expressed cytokine

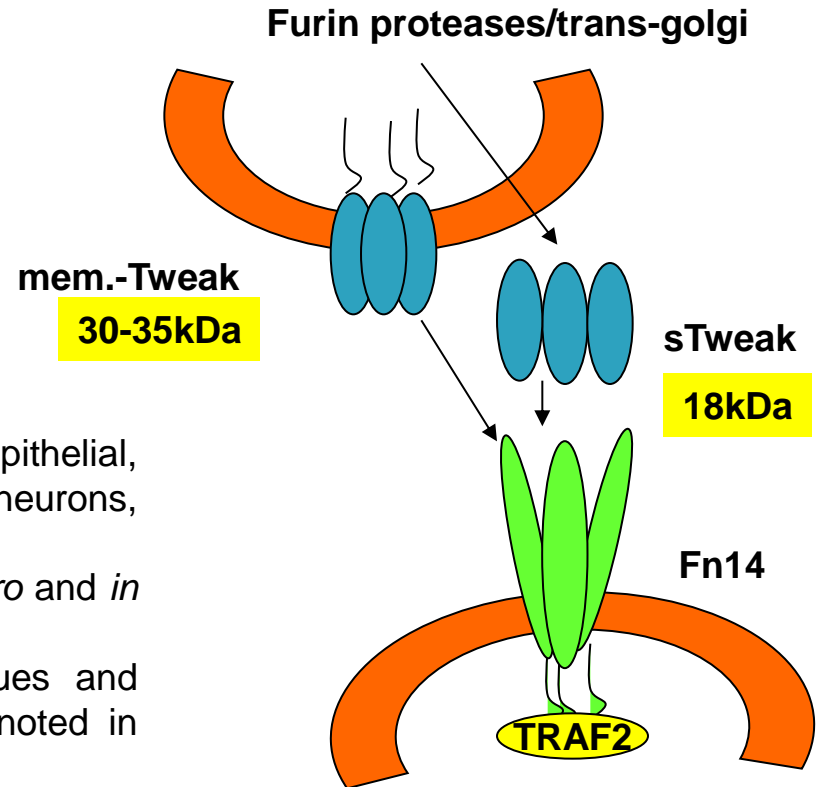
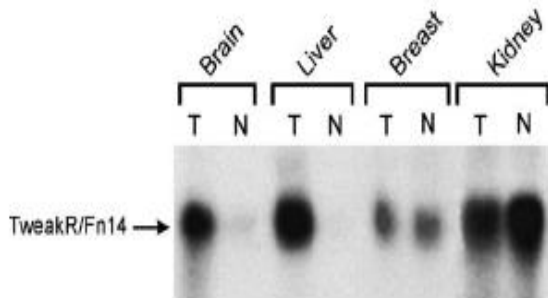


Chicheportiche et al.. *JBC* 19 (1997), 32401–32410,

➤ Fn14 is expressed by many cell types including epithelial, mesenchymal and endothelial cells, as well as neurons, astrocytes etc..

➤ *Fn14* gene expression is highly regulated both *in vitro* and *in vivo*.

➤ Fn14 is expressed at low levels in normal tissues and significantly higher levels of expression have been noted in multiple tumor specimens.



Signal transduction/pathway activation
NF-κB can, non-can, MAPK

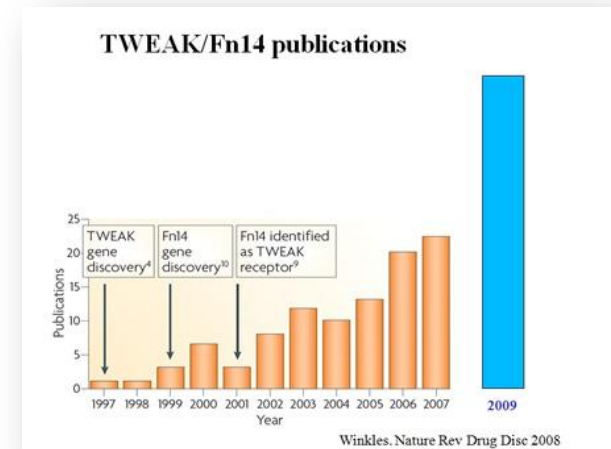
Inflammation, Cell growth, angiogenesis
Cell death, Cell survival etc..

Pathogenic role of TWEAK in human diseases


- TWEAK-dependent Fn14 signaling can contribute to the clinical severity of autoimmune inflammatory diseases: rheumatoid arthritis, SLE (lupus nephritis), multiple sclerosis, atopic dermatitis, autoimmune encephalomyelitis.


Others:

- chronic renal failure: Kidney injury
- Cancer: prostate cancer, renal carcinomas, breast tumors, esophageal adenocarcinoma, endometrial cancer, Glial tumors
- Ulcerative colitis
- Periodontitis
- Cardiovascular component (Heart failure, cardiomyopathy, atherosclerosis, abdominal aortic aneurysm, non-dialysis Chronic Kidney Disease, pulmonary artery hypertension and acute myocardial infarction.
- ischemic stroke (cerebral ischemia)



Tweak circulating levels as potential biomarker

❖ Autoimmune disease 
rheumatoid arthritis
SLE
multiple sclerosis

❖ Cardiovascular component 
Heart failure
Cardiomyopathy
Atherosclerosis
Abdominal aortic aneurysm
Non-dialysis chronic kidney disease
Pulmonary artery hypertension
Acute myocardial infarction

TWEAK/Fn14 IN OBESITY

1. Selected Cohorts

Clinical and anthropometrical characteristics of the studied cohorts

	Obesity study				Type 2 diabetes study			Severe obesity study		
	Lean BMI<25 n=19	Overweight 25=<BMI<30 n=28	Obese 30=<BMI<40 n=15	<i>p</i>	Control n=36	Type 2 diabetic n=11	<i>p</i>	Control n=35	Severe obesity n=23	<i>p</i>
Age (years)	51.7 ± 16.0	57.1 ± 15.0	57.4 ± 12.8	ns	61.6 ± 10.6	66.1 ± 8.6	ns	44.5±8.3	40±0.4	ns
Gender (n, male/female)	13/6	16/12	9/6	ns	21/15	5/6	ns	23/12	9/14	ns
BMI (kg/m ²)	23.6 (24.2)	27.2 (27.9)	32.1 (33.6)	<0.001	28.6 (31.5)	28.7 (30.4)	ns	26.2±3.6	57.4±7.3	<0.001
Waist circumference (cm)	83.0 (90.0)	97.0 (100.0)	107.0 (117.2)	<0.001	100.0 (107.0)	97.0 (102.0)	ns	90.8±13	146.2±23.5	<0.001
FFA (mM)	0.8 (1.2)	0.7 (0.9)	0.8 (1.0)	ns	0.8 ± 0.3	0.9 ± 0.4	ns	0.9±0.5	0.6±0.4	ns
Cholesterol (mM)	5.2 ± 1.2	4.9 ± 1.0	5.2 ± 0.8	ns	5.1 ± 0.9	4.7 ± 1.2	ns	4.8 (5.6)	5.2 (5.5)	ns
HDL-cholesterol (mM)	1.5 ± 0.5	1.3 ± 0.3	1.4 ± 0.3	ns	1.4 (1.6)	1.2 (1.9)	ns	1.3 (1.5)	1 (1.5)	ns
Triglycerides (mM)	1.0 (1.6)	1.1 (1.5)	1.0 (1.3)	ns	1.0 (1.5)	1.7 (2.3)	<0.001	0.9 (1.5)	1.2 (1.6)	ns
Glucose (mM)	4.8 ± 0.7	5.5 ± 0.5 ^a	5.6 ± 0.5 ^b	<0.001	5.6 (5.8)	8.3 (10.1)	<0.001	5 (5.7)	5.4 (6.1)	ns
Insulin (μIU/ml)	3.4 (6.7)	4.0 (7.2)	6.6 (16.5)	ns	4.5 (7.7)	10.2 (21.4)	ns	4 (7.6)	23 (51)	<0.001
HOMA-IR	0.75 (1.83)	1.01 (2.09)	1.60 (4.79)	0.028	1.22 (2.10)	3.66 (23.66)	<0.001	1 (2)	5.4 (13)	<0.001
sIL-6 (pg/ml)	1.4 (2.5)	1.0 (2.2)	2.5 (5.2)	0.022	1.4 (2.6)	1.5 (2.4)	ns	1.3 (2.6)	5.5 (8.9)	<0.001

^a Differences vs lean

^b Differences vs overweight

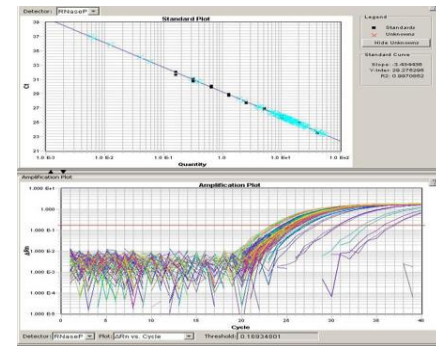
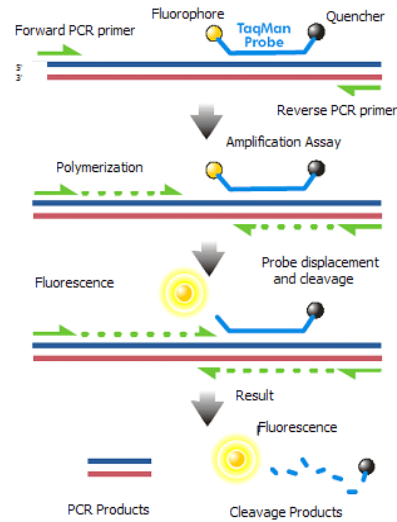
ns: not significant

ND: not determined

Applied Biosystems Fast Real Time

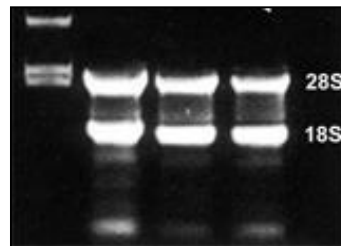


SAT and VAT
500mg



Measured gene expression
TWEAK and Fn14

RNA isolation by RNAsy[®]
Mini Kit (Qiagen)



2. TWEAK/Fn14 expression study in SAT-VAT paired samples

Differential expression levels of TWEAK and Fn14 in the studied cohorts (A). Depot specific analysis (B)

A.

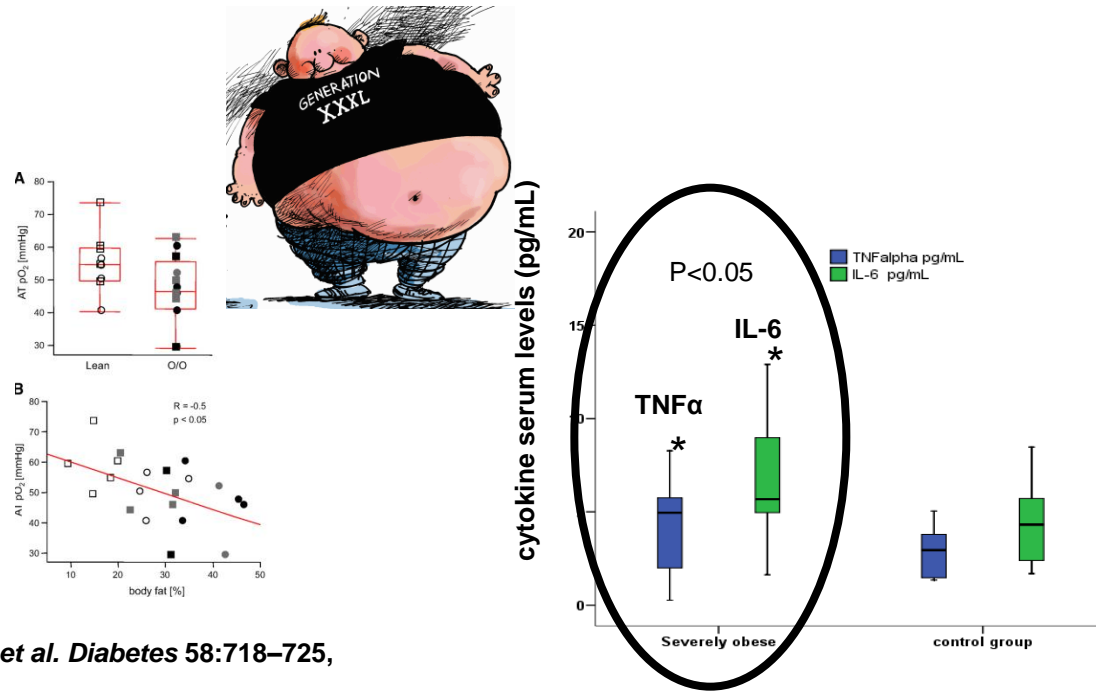
	Obesity study				Type 2 diabetes study			Severe obesity study		
	Lean BMI<25 n=19	Overweight 25=<BMI<30 n=28	Obese 30=<BMI<40 n=15	<i>p</i>	Control n=36	Type 2 diabetes n=11	<i>p</i>	Control n=35	Severe obesity n=23	<i>p</i>
Gene expression levels (arbitrary units)										
SAT TWEAK	0.94±0.21	1.06±0.22	0.92±0.33	ns	1.01 ±0.3	1.16±0.3	ns	0.98±0.3	1.35±0.43	0.001
VAT TWEAK	0.80±0.18	0.90±0.18	0.89±0.38	ns	0.89±0.25	0.89±1.16	ns	0.87±0.2	1.34±0.7	0.004
SAT Fn14	0.78±0.46	0.67±0.30	0.93±0.53	ns	0.8±0.4	1.6±1.3	ns	0.64 (1.03)	2.6 (13.3)	<0.001
VAT Fn14	1.4 (3.9)	0.8 (1.7)	0.8 (1.4)	ns	0.9 (1.6)	1.4 (1.7)	ns	0.84 (1.7)	5.7 (35.1)	<0.001

B.

	Lean	Overweight	Obese	Severely obese	Type 2 Diabetes
TWEAK	SAT>VAT p=0.015	SAT>VAT p=0.02	SAT=VAT p=0.578	SAT=VAT p=0.848	SAT>VAT p=0.06
Fn14	SAT<VAT p=0.002	SAT<VAT p=0.024	SAT=VAT p=0.609	SAT<VAT p=0.033	SAT=VAT p=0.477

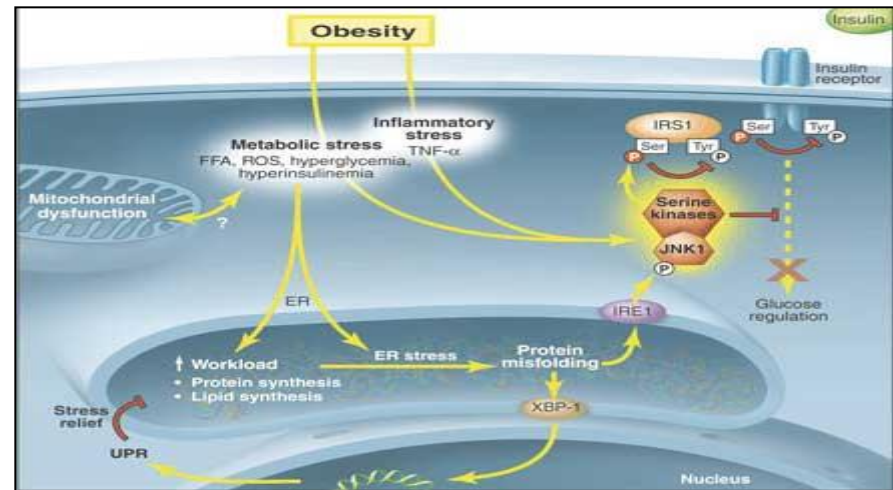
What is inducing the over-expression of Tweak/Fn14 in severely obese subjects?

'hypoxia hypothesis' suggested that the dysregulation of the production of inflammation-related adipokines in obesity, linked to the development of the metabolic syndrome and other obesity-associated disorders, is a specific response to relative hypoxia in clusters of adipocytes that become distant from the vasculature as adipose tissue mass expands (Trayhurn P & Wood IS Br J Nutr (2008) 92, 347–355)



Pasarica et al. *Diabetes* 58:718–725, 2009

endoplasmic reticulum (ER) stress In the transformation of a healthy functional adipocyte to a hypertrophic, dysfunctional adipocyte, mitochondrial function is lost, and multiple stress-signaling cascades are initiated from the ER (Hotamisligil GS. *Cell*. (2010) 140,900-17).



Selected candidate genes

	Gene	Function
Hypoxia regulated	<i>VISFATIN</i>	Pro-inflammatory and potentially insulin-mimetic adipokine. HIF-1 hypoxia regulated gene.
	<i>FIAF</i>	Lipid metabolism. Highly up-regulated during hypoxia
	<i>HIF-1α</i>	Key transcription factor in hypoxia
	<i>HYOU1</i>	Oxygen-regulated protein (150 kDa) has been reported to be linked to type 2 diabetes and obesity.
	<i>GLUT1</i>	Glucose transporter 1 gene in human adipocytes. It has been found to be increased under hypoxia.
	<i>VEGF</i>	Mediator of inflammation and an angiogenic factor and it is hypoxia regulated.
ER stress	<i>GRP78</i>	Protein strongly related with glucose metabolism and ER stress.
	<i>XBP-1</i>	Transcription factor that modulates the ER stress response.

Have our studied subjects altered the expression of hypoxia and ER regulated genes?

Gene expression analysis of hypoxia and ER genes in SAT and VAT samples in obesity (arbitrary units)

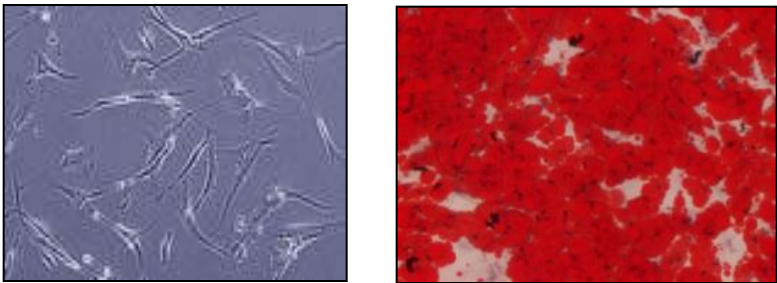
Depot	Obesity study						Severe obesity study			
	Lean n=19		Overweight n=28		Obese n=15		Overweight control group n=35		Severe Obese n=23	
	SAT	VAT	SAT	VAT	SAT	VAT	SAT	VAT	SAT	VAT
Adipokynes										
<i>VISFATIN</i>	1.2 (2.7)	0.8 (1.3)	0.9 (1.4)	0.8 (1.1)	1 (1.9)	0.8 (1.1)	1.2 (2.5)	0.9 (1.3)	1.6 (7.2)*	6.6 (27.8)*#
Hypoxia										
<i>FIAF</i>	2±0.9#	1.1±0.6	1.8±0.6#	0.9±0.6	1.5±0.5	1.3±0.9	1.7±0.72#	1.14±0.7	2.8±1.54*	1.8±1.34*#
<i>HIF-1α</i>	0.9 (1.9)	1 (1.2)	0.9 (1)	0.9 (1)	1 (1.3)	1 (1.3)	0.9 (1.1)	1 (1.3)#	1.8 (4.5)*	3.2 (5.3)*#
<i>HYOU1</i>	0.8±0.2	1±0.2#	0.9±0.1	0.9±0.2	0.9±0.2	0.9±0.1	0.8 (1)	0.9 (1)	1.4 (1.6)*	1.4 (1.7)*
<i>GLUT1</i>	1 (1.8)	1.6 (2.3)#	0.9 (1.2)	1.1 (1.6)#	0.9 (1.2)	1.3 (1.7)	1 (1.1)	1.1 (1.7)#	2.8 (4.8)	5.1 (9.4)*#
<i>VEGF</i>	1.4 (2)*	1.5 (1.7)*	1 (1.3)	1 (1.5)	1 (1.5)	1 (1.2)	1.3 (1.8)	1.2 (1.5)	2.5 (4.3)*	6.5 (9)*#
ER stress										
<i>GRP78</i>	0.9±0.2	1.1±0.2#	0.8±0.1	1±0.3#	0.9±0.3	1±0.2	0.9±0.2	1±0.2#	1.4±0.6*	1.8±1*
<i>XBP-1</i>	0.8±0.2	1±0.3#	0.8±0.1	1±0.2#	0.8±0.2	0.8±0.1	0.8±0.2	1±0.3#	0.9±0.5*	1.6±0.9*#

*differences when comparing same depot between obesity group study p<0.05

#differences when comparing depots within same obesity group p<0.05

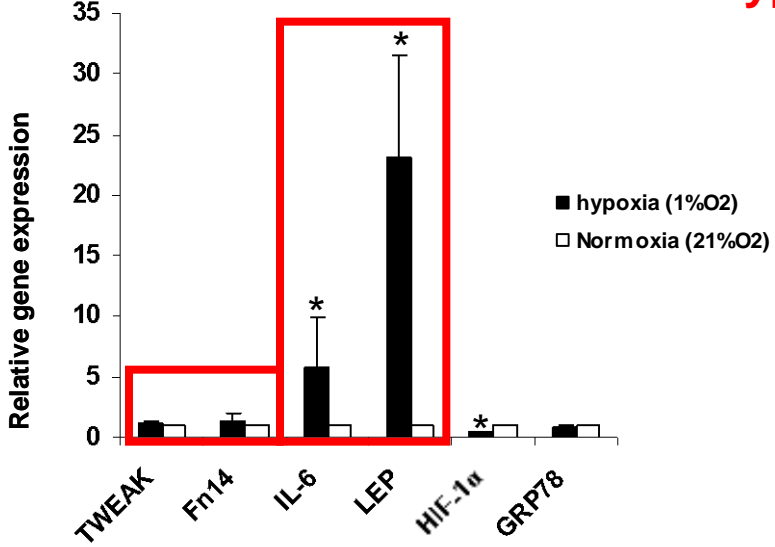
Study of effect of hypoxia, inflammation and ER stress on *TWEAK* and *Fn14* gene expression in human SGBS adipocytes

Simpson-Golabi-Behmel syndrome

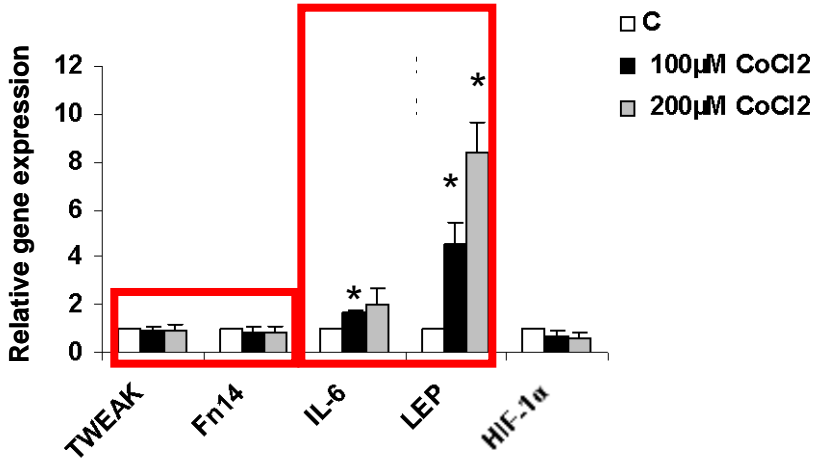


d0 d14

Hypoxia

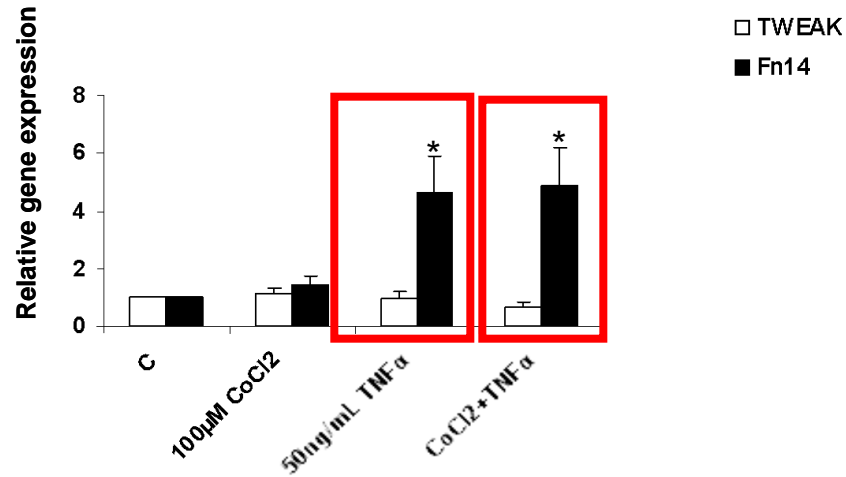


1% O₂

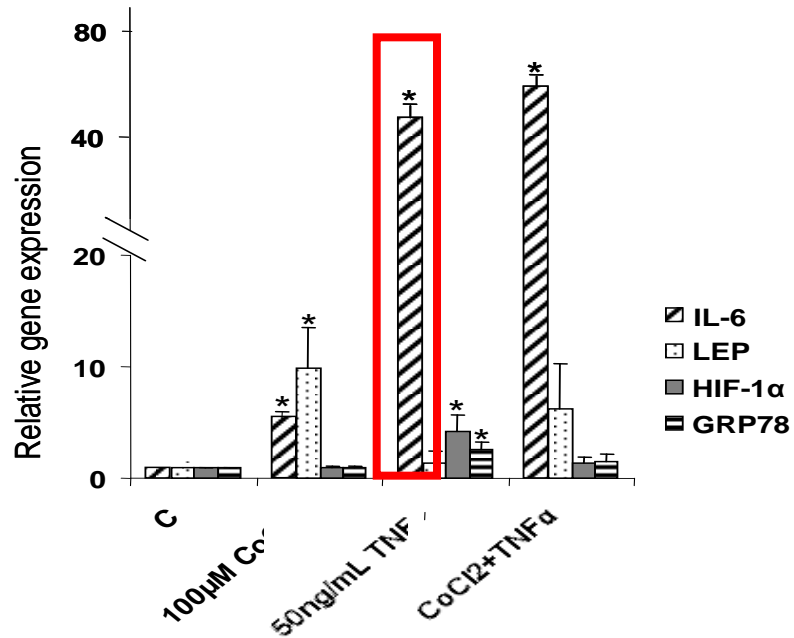


CoCl₂

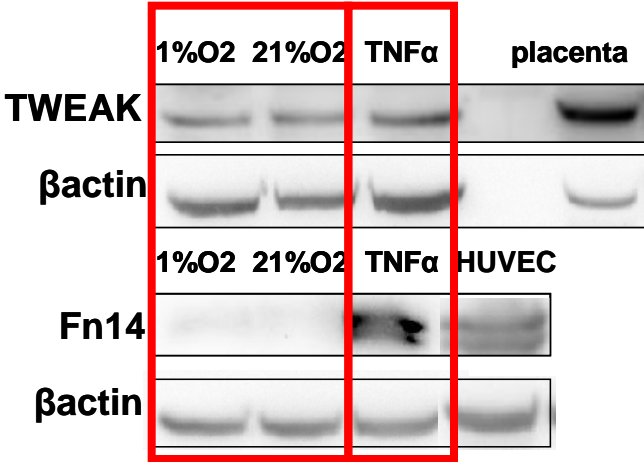
Infammatory stimulus (TNF α) Infammation + Hypoxia



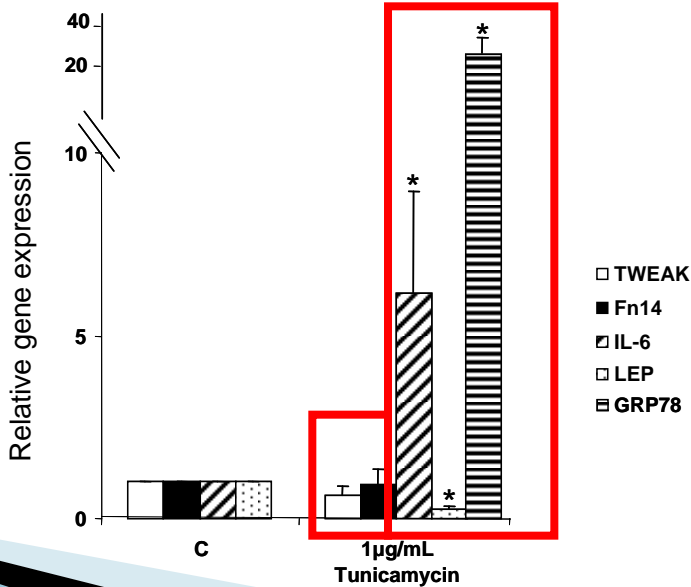
Infammatory stimulus



Hypoxia and inflammation on TWEAK and Fn14 protein expression in human SGBS adipocytes

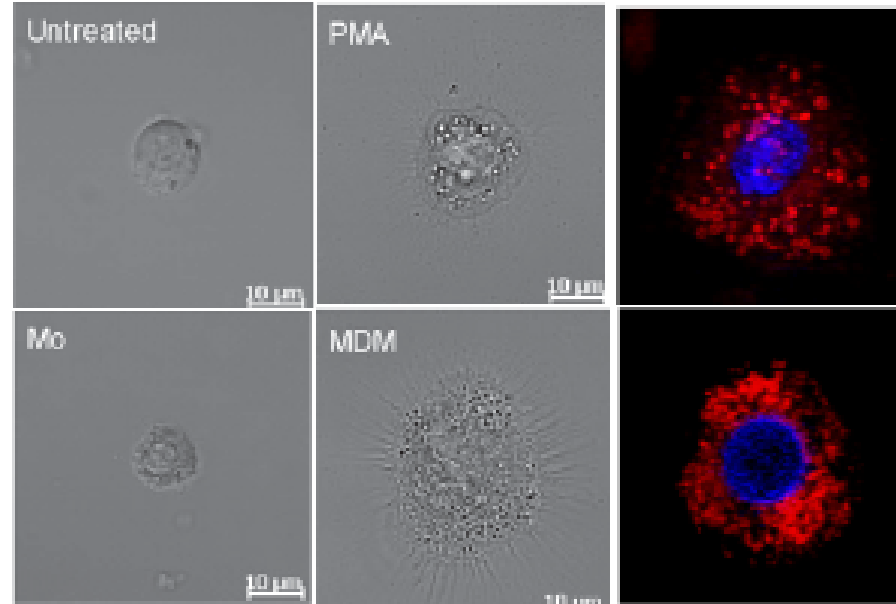


Effect of ER stress on TWEAK and Fn14 gene expression in human SGBS adipocytes



Study the effect of hypoxia, inflammation and ER stress on *TWEAK* and *Fn14* gene expression in THP-1 human macrophages

THP-1

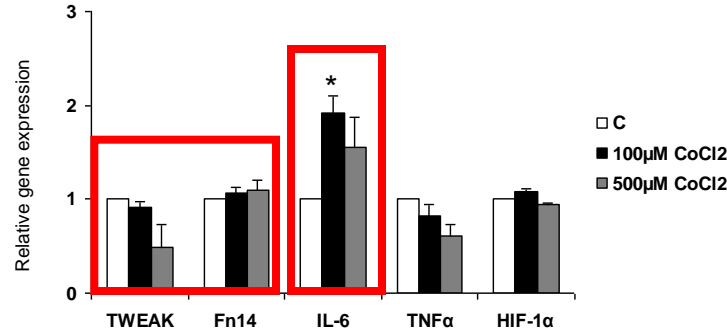


Human Monocytes

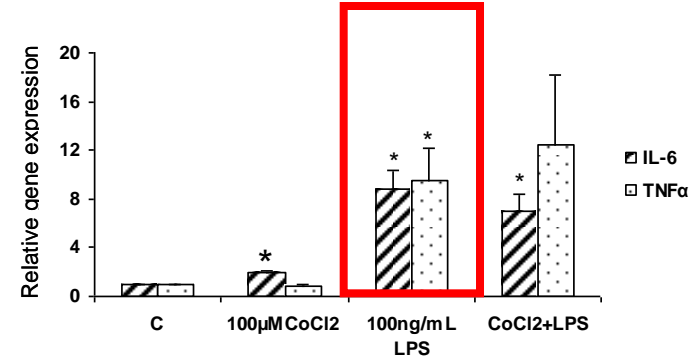
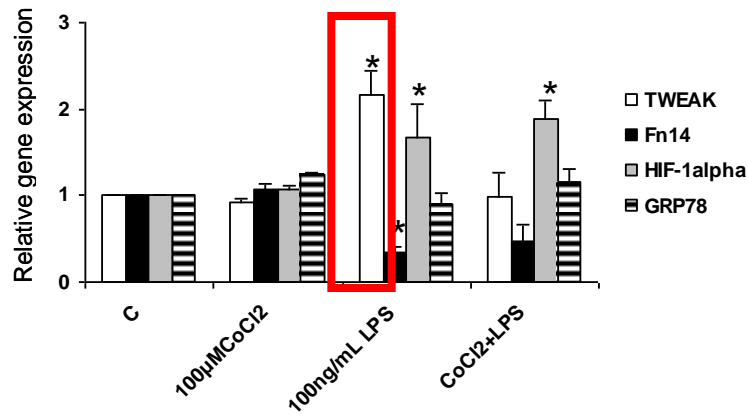
- Macrophage differentiation is associated with a reduction in the nucleocytoplasmic ratio due to an increase in cytoplasmic volume
- Increasing numbers of lysosomes and mitochondria with macrophage differentiation

Study the of hypoxia, inflammation and ER stress on *TWEAK* and *Fn14* gene expression in THP-1 human macrophages

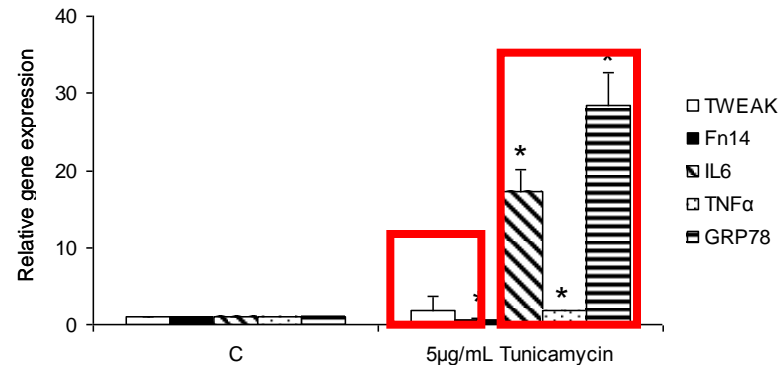
Hypoxia

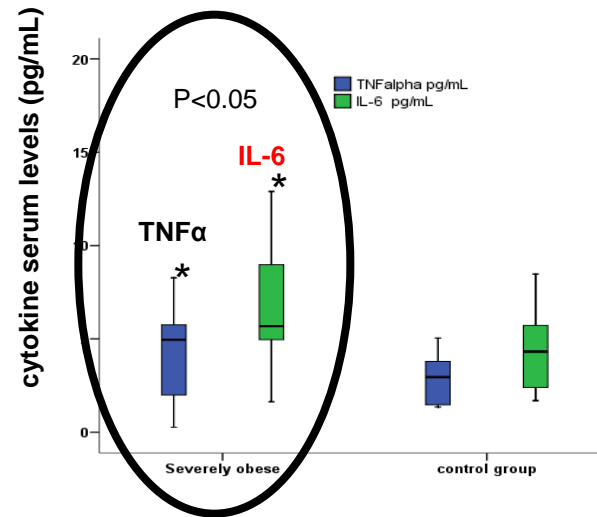


Inflammation



ER stress

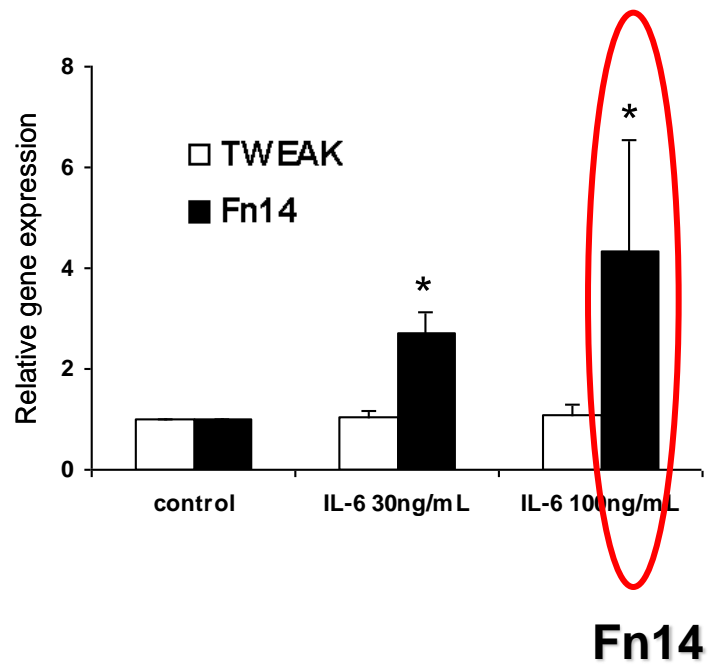




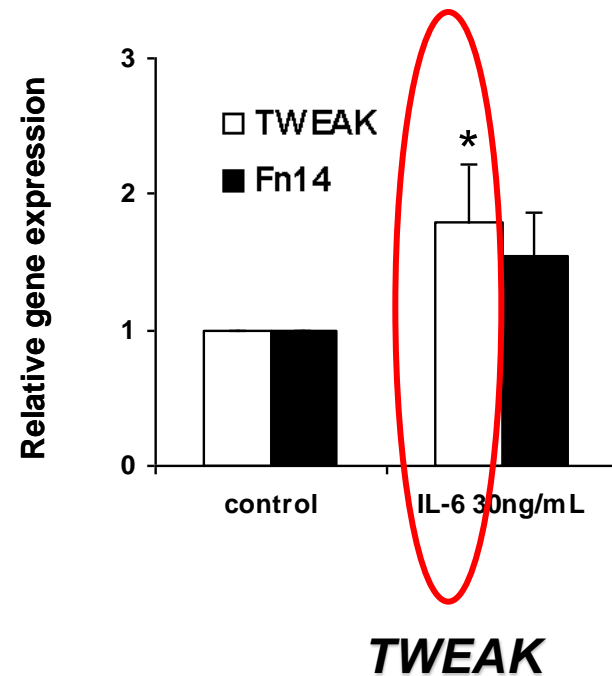
- Adipose Tissue of severely obese subjects have altered expression levels of Hypoxia and ER stress genes
- Hypoxia, ER and inflammatory stimuli strongly increases **IL-6** levels in adipocytes and macrophages
- **IL-6** is a potent inflammatory cytokine

Is IL-6 altering *TWEAK* and *Fn14* expression levels?

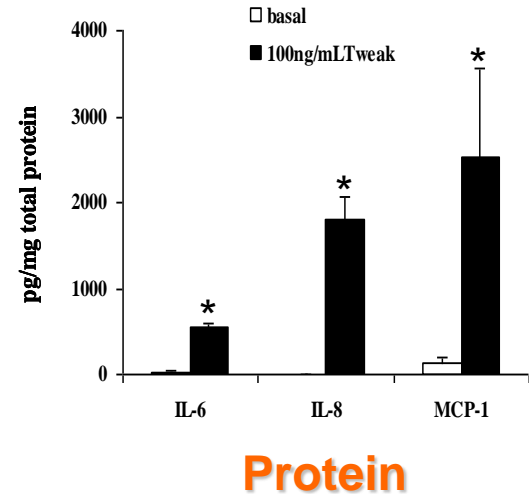
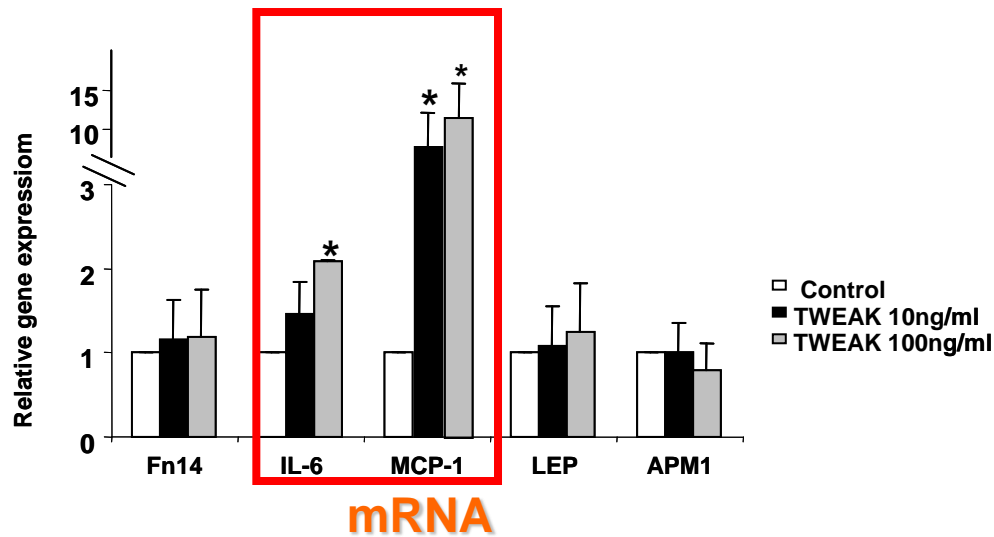
Human SGBS adipocytes



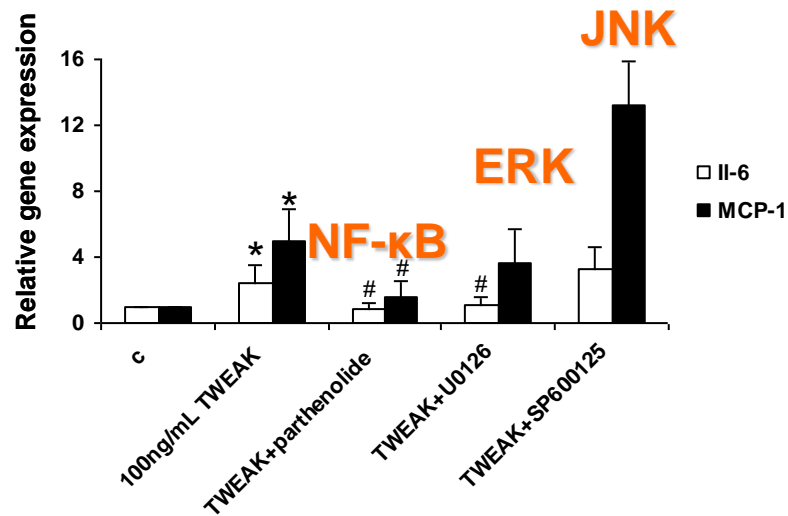
Human THP-1 macrophages



Is Tweak a Pro-inflammatory cytokine on human adipocytes



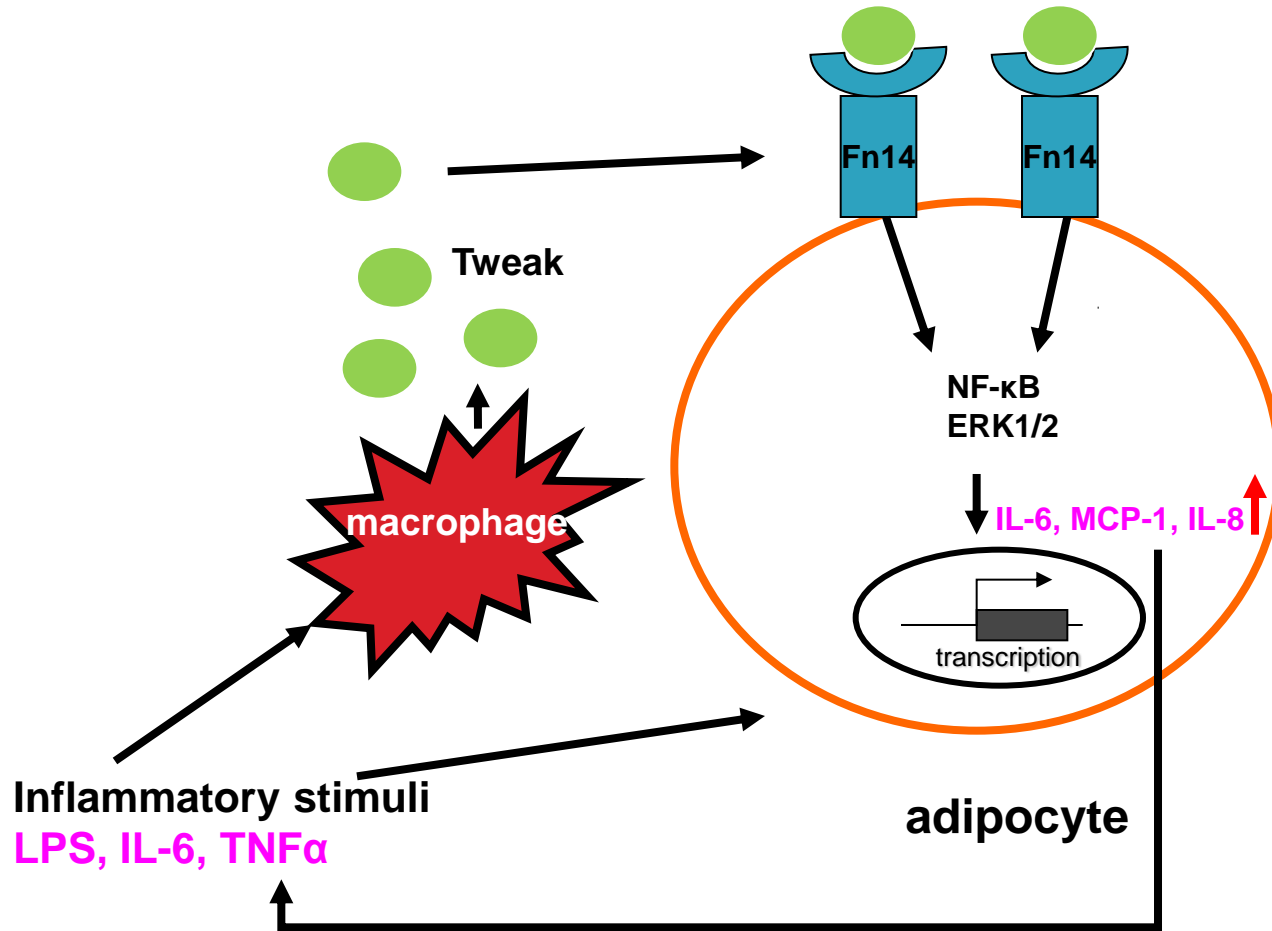
How is Tweak signaling in human adipocytes?



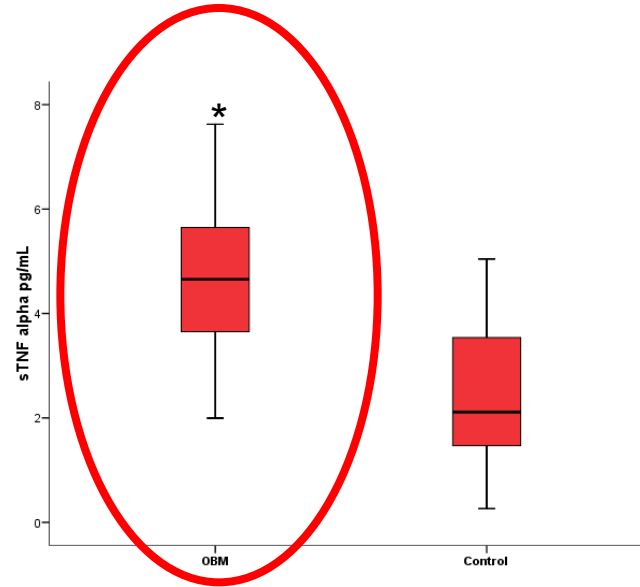
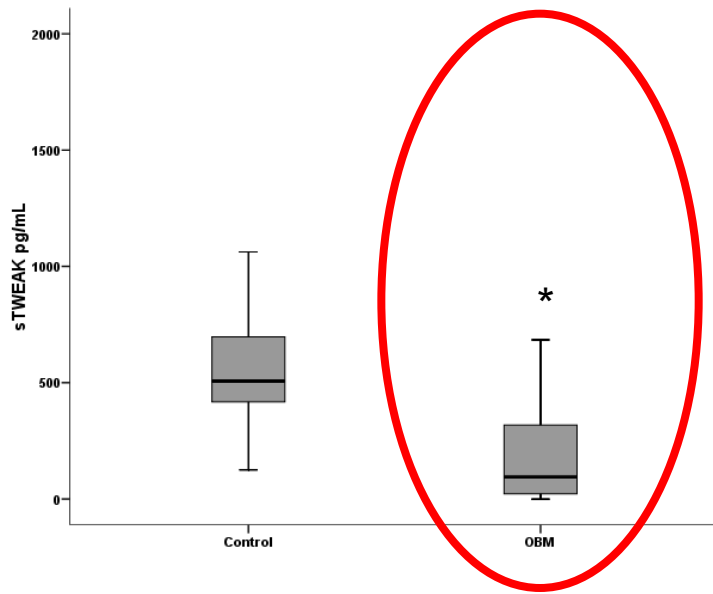
Summary

- ✓ *TWEAK/Fn14* is expressed in SAT and VAT tissue
- ✓ TWEAK acts as a pro-inflammatory cytokine in human adipocyte cells
- ✓ We report an over expression of *TWEAK/Fn14*, hypoxia and ER characteristic genes in both SAT and VAT adipose tissue depots of severely obese patients
- ✓ However both *TWEAK* and *Fn14* genes were neither hypoxia nor ER stress sensitive but inflammation regulated
- ✓ The increment of *TWEAK* and *Fn14* expression in severe obesity may be due to the inflammatory environment, in particular that caused by the presence of IL-6, a cytokine that could be playing a key role in *TWEAK/Fn14* regulation

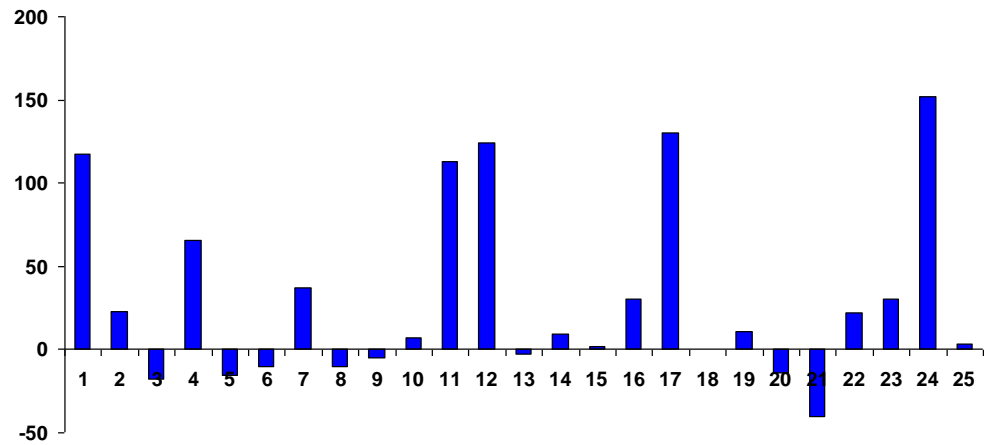
MODEL OF ACTION OF TWEAK-Fn14 IN ADIPOSE TISSUE



Circulating Tweak in severely obese subjects



%Δ sTweak

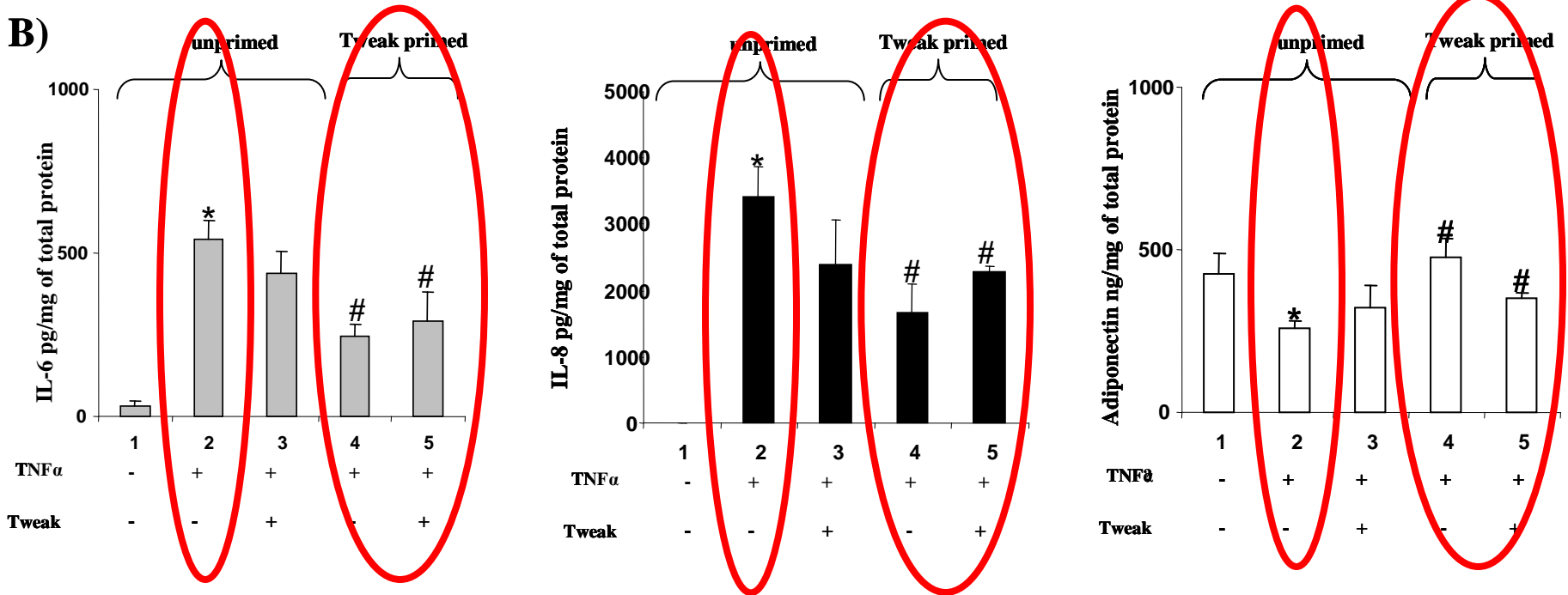


Could fluctuations in circulating Tweak have an impact on TNF α -induced inflammatory response?

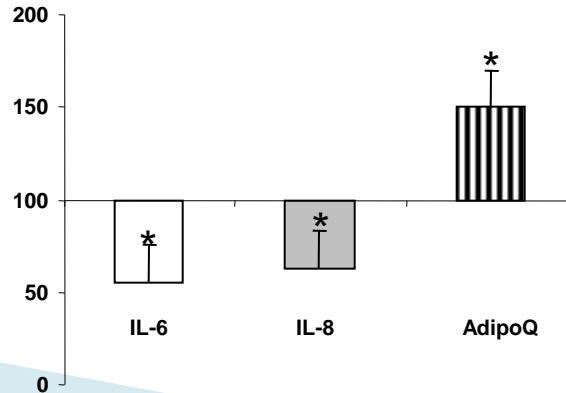
How the adipocyte responds in an environment where Tweak and TNF α are present?

Effect of Tweak in TNF α -induced cytokine secretion

B)

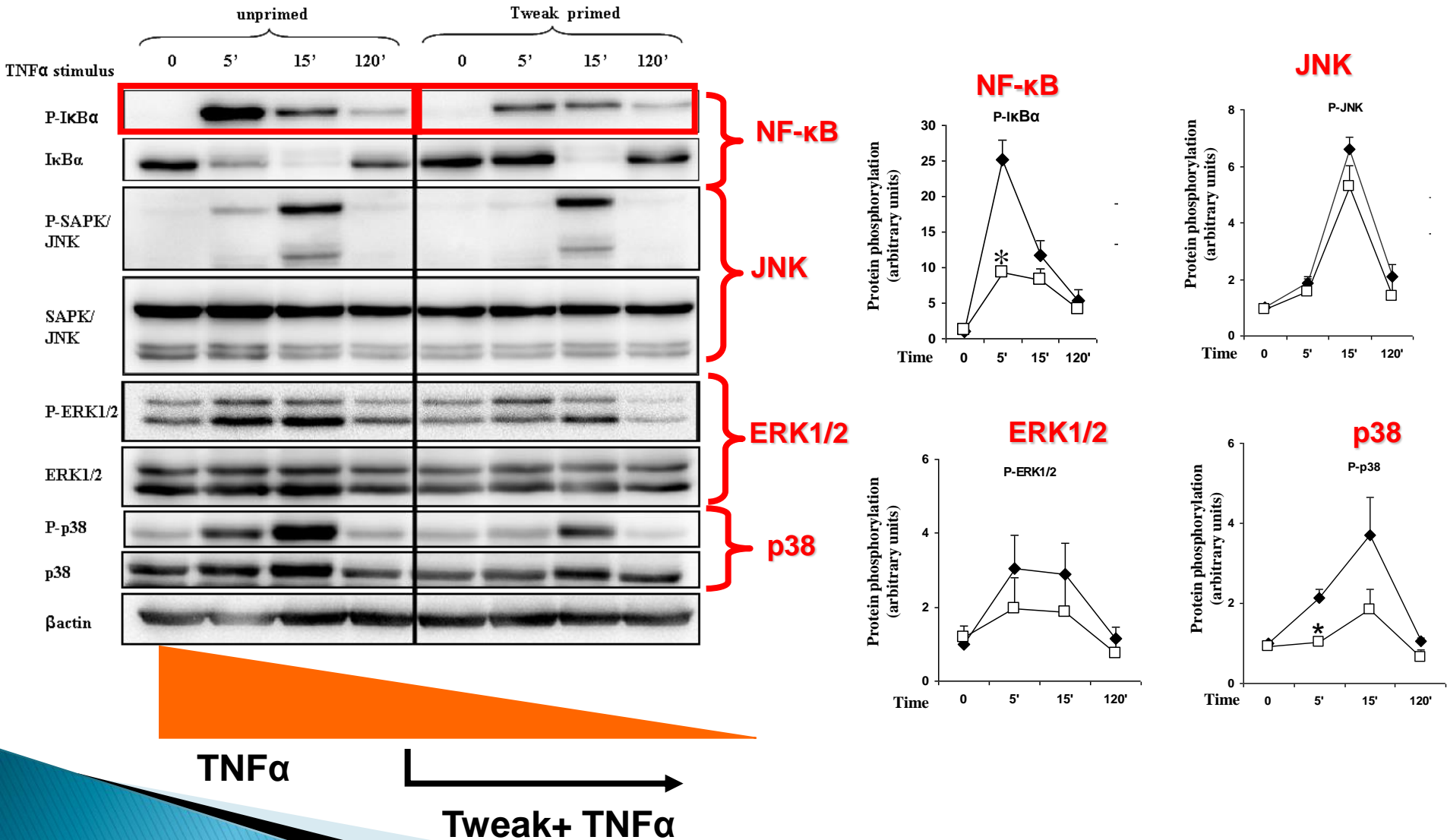


Cytokine production (%)

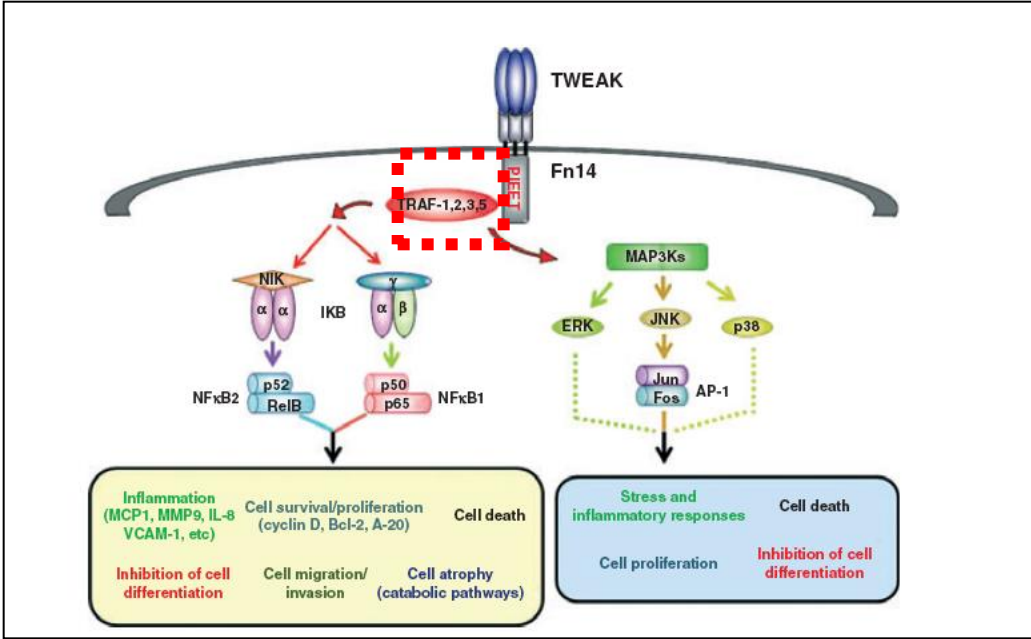


Regulation of TNF α signaling pathways after Tweak-priming

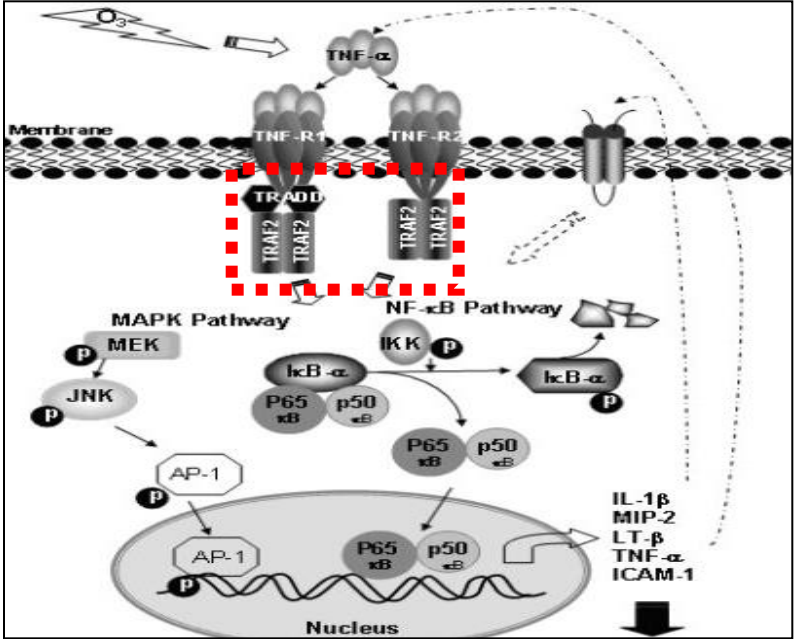
Mature human SGBS adipocytes



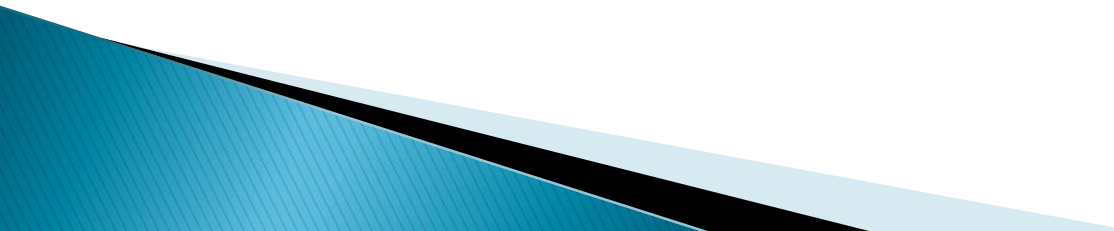
Tweak signaling



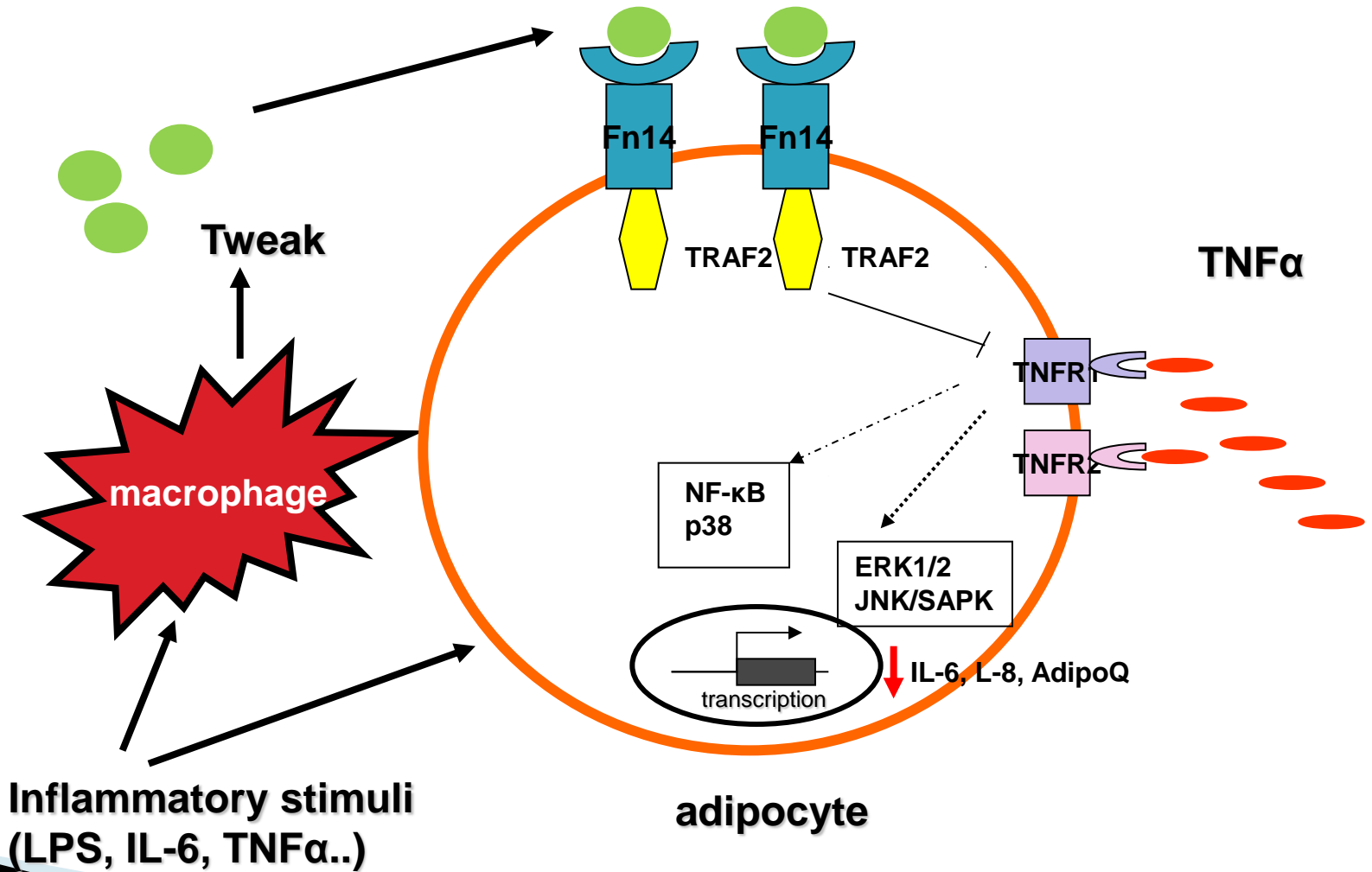
TNFα signaling



Conclusion

- ✓ Tweak modulates IL-6, IL-8 and Adiponectin production induced by TNF α in adipocytes
 - ✓ Tweak modulates TNF α signalling in part by TRAF2 cellular protein levels
 - ✓ Our observation of lower Tweak circulating levels in severely obese subjects could indicate that these subjects are prone to having a more potent inflammatory TNF α outcome
- 

Hypothesis for the mechanism of interaction between Tweak and TNF α





CIBERDEM

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Subdirección General de
Evaluación y Fomento de la
Investigación

