

Table S1. Characteristics of all the studies included in this systematic review.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post-RYGB vs obese)		Reference
	Patients data/ Recruitment country			Reported gene expression values (Obese; 8±5 months post-RYGB)	Calculated fold change [(Post-RYGB/Obese)-1]	
qPCR	Obese: 19 obese of ≥ 18 years	RYGB	Obese: 42± 5	Upregulated expression post-RYGB(+)		
Candidate genes involved in:		8±5 months	Post-RYGB: ~32 ± 6	<i>PLIN1 (1.00; 4.01)</i> <i>HSL (1.00; 2.19)</i> <i>CG158 (1.00; 2.19)</i> <i>ATGL (1.00; 1.72)</i>	Upregulated expression post-RYGB(+)	(Karki et al., 2015)
(a) Lipolysis (b) Triglyceride metabolism	Post-RYGB: 19 patients post-RYGB of ≥ 18 years	(3 a 15 months)	ΔBMI: ~10 kg/m ²		<i>PLIN1 (3.01)</i> <i>HSL (1.19)</i> <i>CG158 (1.19)</i> <i>ATGL (0.72)</i>	
	Boston, United States of America			Note: Approximate data of expression of the article		

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	Patients data/ Recruitment country			Calculated fold change [(Post-RYGB/Obese)-1]		
				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	
qPCR	Obese: 17 Obese of 46 ± 10 years		Obese: ~45 ± 3	<i>IL-6 (38.37)</i> <i>IL-8 (19.75)</i> <i>FASN (1.69)</i> <i>AQP9 (1.45)</i> <i>TNFα (0.86)</i> <i>LBP (0.72)</i> <i>SREBF1 (0.27)</i> <i>PPARG (0.20)</i> <i>SLC27A2 (0.07)</i> <i>ACLY (0.06)</i> <i>ELOVL6 (0.05)</i> <i>LEP (0.02)</i>	<i>ADIPOQ (-0.38)</i> <i>CEBPa (-0.28)</i> <i>IRS-1 (-0.23)</i> <i>GLUT4 (-0.23)</i> <i>ACACA (-0.09)</i>	
Genes involved in:	Post-RYGB: 17 patients post-RYGB of 46 ± 10 years	RYGB	Post-RYGB: Not changes			(Ortega et al., 2016)
(a) Inflammation (b) Lipid metabolism (c) Glucose metabolism	Barcelona, Spain	90-120 min	ΔBMI: Not changes			

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post-RYGB vs obese)				Reference
	Patients data/ Recruitment country			Reported gene expression values (Obese; 6 months post-RYGB)		Calculated fold change [(Post-RYGB/Obese)-1]		
qPCR				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB (-)			
Validation by qPCR of genes involved in:	Obese: 13 Obese of ~33±9 years		Obese: ~45± 6					
(a) Energy metabolism	Post-RYGB: 13 patients post-RYGB ~33±9 years Sao Paulo, Brazil	RYGB 6 months	Post-RYGB: ~35 ± 6 ΔBMI: ~10 kg/m ²	UCP2 (0.75; 1.27) Note: Approximate values from the graphs in the article	PLIN1 (1.16; 0.89) Note: Approximate values from the graphs in the article	Upregulated expression post-RYGB(+) UCP2 (0.69)	Downregulated expression post-RYGB (-) PLIN1 (-0.23) Note: Approximate values from the graphs in the article	(de Oliveira et al., 2017)

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	Patients data/ Recruitment country			Calculated fold change [(Post-RYGB/Obese)-1]				
				Upregulated expression post-RYGB (+)		Downregulated expression post-RYGB(-)		
qPCR								
Validation by qPCR of genes involved in:	Obese: 11 Obese of ~55±9 years		Obese: ~37± 4	ADIPOQ (3.81)	ACACA (0.22)			
(a) Adipogenesis	Post-RYGB: 11 patients post-RYGB ~55±9 years	RYGB 1 month	Post-RYGB: ~33 ± 3	PLIN1 (2.84)	ACLY (0.22)			
(b) Oxidation of fatty acids				FABP4 (1.7)	AKT1 (0.21)		IL-18 (-0.34)	
(c) Glucose metabolism	Uppsala, Sweden		ΔBMI: ~4 kg/m ²	LIPE (1.12)	IRS-1 (0.2)		MKI67 (-0.30)	(Katsogiannos et al., 2019)
				FAS (0.76)	CPT1A (0.16)		E2F1 (-0.29)	
				CD36 (0.68)	SLC2A1 (0.15)		LEP (-0.25)	
				CPT1B (0.53)	CASP3 (0.15)		ELOVL6 (-0.19)	
				SLC2A4 (0.32)	LPL (0.09)		SREBF1 (-0.19)	
				CEBPB (0.24)	PNPLA2 (0.07)		TNFA (-0.15)	
				IL-6 (0.23)				
				PPARG (0.22)				
				CEBPA (0.06)				

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post-RYGB vs obese)		Reference
	Patients data/ Recruitment country			Calculated fold change [(Post-RYGB/Obese)-1]		
				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	
qPCR	Obese: 12 obese of 55 ± 9 years	RyGB	Obese: 37 ± 4	ADIPOQ (11.15) FAS (4.67) SLC2A4 (2.57) FABP4 (1.91) PPARG (1.14) CPT1B (1.13) CEBPA (0.88) LIPE (0.86) ELOVL6 (0.68) IRS-1 (0.66) CEBPB (0.64) AKT1 (0.37) SLC2A1 (0.28) LEP (0.19)	E2F1 (-0.33)	(Katsogiannos et al., 2019)
Candidate genes involved in: a) Adipogenesis b) Oxidation of fatty acids c) Glucose metabolism	Post-RYGB: 12 patients post-RYGB of 55 ± 9 years Uppsala, Sweden	6 months	Post-RYGB: ~29 ± 3 ΔBMI: ~8 kg/m ² ;	Note: Upregulated expression involved in adipogenesis		Note: Downregulated genes involved in cell proliferation

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	Patients data	Gene expression fold change (Post-RYGB vs obese)		Reference		
	Patients data/ Recruitment country			Reported gene expression values (Obese; 3 months post-RYGB)				
				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB (-)	Calculated fold change [(Post-RYGB/Obese)-1]		
				Logarithmic conversion	Logarithmic conversion			
qPCR	Obese: 13 Obese of ~38±8 years	RyGB	Obese: ~42± 4	NRF2 (0.84; 4.50) AMPK (0.92; 4.14) ADIPOQ (0.80; 3.29) SIRT1 (0.84; 3.29) GNC2 (0.97; 3.07) ATF4 (0.82; 2.55) PGC1α (0.86; 2.28) SIRT3 (0.81; 1.88) SOD2 (0.93; 1.53) ATF6 (0.6; 0.96) CANX (0.59; 0.75) SOD3 (0.78; 0.91) CHOP (0.61; 0.71) XBP1 (0.91; 0.97) SOD1 (0.91; 0.95)	CALR (0.82; 0.05) EIF2AK3 (0.85; 0.15) MCP-1 (0.89; 0.25) TNFA (0.79; 0.28) IL-6 (0.86; 0.37) PPARG (0.97; 0.45) GRP78 (0.45; 0.25) CCT4 (0.91; 0.8) GADD34 (0.88; 0.84)	NRF2 (4.35) AMPK (3.5) ADIPOQ (3.11) SIRT1 (2.94) GNC2 (2.16) ATF4 (2.12) PGC1α (1.64) SIRT3 (1.33) SOD2 (0.65) ATF6 (0.59) CANX (0.27) SOD3 (0.16) CHOP (0.16) XBP1 (0.06) SOD1 (0.04)	CALR (-0.94) EIF2AK3 (-0.83) MCP-1 (-0.72) TNFA (-0.64) IL-6 (-0.57) PPARG (-0.53) GRP78 (-0.45) CCT4 (-0.13) GADD34 (-0.04)	(Ferraz-Bannitz et al., 2021)
Validation by qPCR of genes involved in (a) Inflammatory and anti-inflammatory cytokines (b) Lipid transport (c) Metabolic regulation (d) In caloric restriction (e)Glucose homeostasis (f) Oxidative stress	Post-RYGB: 13 patients of ~38±8 years Sao Paulo, Brazil	3 months	Post-RYGB: ~36 ± 5 ΔBMI: ~6 kg/m²	Note: Approximate values from the graphs in the article		Note: Approximate values from the graphs in the article		

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post-RYGB vs obese)			Reference
	Patients data/ Recruitment country			Reported gene expression values (Obese; 6 months post-RYGB)			
				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB (-)	Calculated fold change [(Post-RYGB/Obese)-1]	
				Logarithmic conversion	Logarithmic conversion	Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB (-)
qPCR	Obese: 13 Obese of ~38±8 years		Obese: ~42± 4	ADIPOQ (0.80; 4.89)		ADIPOQ (5.11)	
(a) Validation by qPCR of genes involved in:				SIRT1 (0.84; 2.85)	CALR (0.82; 0.14)	SIRT1 (2.41)	
(b) Inflammatory and anti-inflammatory cytokines				NRF2 (0.84; 2.75)	EIF2AK3 (0.85; 0.15)	NRF2 (2.27)	
(c) Lipid transport				AMPK (0.92; 2.68)	TNFα (0.79; 0.17)	AMPK (1.91)	CALR (-0.83)
(d) Adipogenesis				GNC2 (0.97; 2.5)	PPARG (0.97; 0.61)	GNC2 (1.57)	EIF2AK3 (-0.83)
(e) Metabolic regulation				ATF4 (0.82; 2.08)	GADD34 (0.88; 0.59)	ATF4 (1.55)	TNFα (-0.79)
(f) Amino acid metabolism				PGC1α (0.86; 1.77)	IL-6 (0.86; 0.66)	PGC1α (1.04)	PPARG (-0.37)
(g) In caloric restriction				SIRT3 (0.81; 1.59)	SOD1 (0.91; 0.8)	SIRT3 (0.97)	GADD34 (-0.33)
(h) Glucose homeostasis				ATF6 (0.60; 1.19)	CCT4 (0.91; 0.82)	ATF6 (0.97)	IL-6 (-0.23)
(i) Oxidative stress				GRP78 (0.45; 0.89)	MCP-1 (0.89; 0.86)	GRP78 (0.97)	SOD1 (-0.12)
				CHOP (0.61; 1.14)		CHOP (0.87)	CCT4 (-0.1)
				CANX (0.59; 0.82)		CANX (0.39)	MCP-1 (-0.03)
				SOD2 (0.93; 1.15)		SOD2 (0.24)	
				XBP1 (0.91; 1.05)		XBP1 (0.15)	
				SOD3 (0.78; 0.81)		SOD3 (0.04)	
				Note: Approximate values from article graphics	Note: Approximate values from article graphics		

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)				Reference
	Patients data/ Recruitment country			Microarrays		qPCR		
				Calculated fold change [(Post-RYGB/Obese)-1]				
				Downregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	Downregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	
	Microarrays		Microarrays					
. Microarrays								
SurePrint-G3 Human GE 8 x60 K microarray kit 62,000 transcripts	Obese: 8 Obese of ~41±11 years Post-RYGB: 8 patients		Obese: ~52± 7 Post-RYGB: ~34 ± 9	172 upregulated genes post-RYGB	731 downregulated genes post-RYGB			
qPCR			ΔBMI: ~18 kg/m ² ;	Validation genes: FASN (4.94) ACACA (2.13) SCD1 (2.13) IRS-1 (1.19)	Validation genes: IL-6 (-57.67) MSR1 (-10.69) TNFα (-4.75) FBP1 (-5.06)	FASN (5.88) ACACA (2.13) SCD1 (2.13) IRS-1 (1.5)	IL-6 (-7.56) MSR1 (-7.56) TNFα (-2.88) FBP1 (-3.50)	(González-Plaza et al., 2016)
Validation by qPCR of genes selected for antecedents of improving lipid metabolism and post-RYGB inflammation	qPCR	RYGB	qPCR					
	Obese: 20 obese of ~46 ± 10 years Post-RYGB: 20 patients	~2 years	Obese: ~56 ± 7 Post-RYGB: ~39 ± 10		Note: Downregulated genes involved in: (a) Immune system (b) Inflammatory processes (immune response, stress response, cell death, response to endogenous stimulus)			
	Malaga, Spain		ΔBMI: ~17 kg/m ² ;	Note: Upregulated expression implied in: (a) Biosynthetic processes				
In addition, those that were differentially expressed in Microarrays were selected.				Note: Approximate values from the graphs in the article	Note: Approximate values from the graphs in the article	Note: Approximate values from the graphs in the article	Note: Approximate values from the graphs in the article	

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

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Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)				Reference
	Patients data/ Recruitment country			Microarrays		qPCR		
				Calculated fold change [(Post-RYGB/Obese)-1]				
				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	
	Microarrays		Microarrays	<i>Logarithmic conversion</i>	<i>Logarithmic conversion</i>			
	OBESE: 8 Obese [4 down-insulin resistance (low-IR); 4 high-insulin resistance (high-IR)]		OBESE Low-IR: ~49±5 High-IR: ~52±7	153 upregulated genes post-RYGB: High-IR: <i>GLYCTK (2.18)</i> <i>IRS-1 (1.27)</i> <i>FADS1 (0.55)</i>	865 downregulated genes post-RYGB: High-IR: <i>ITPKC(-7.18)</i> <i>TNFα (-5.82)</i> <i>LIF (-4.73)</i> <i>UCHL1 (-4.36)</i> <i>CCND1 (-2.36)</i>	High-IR: <i>IRS-1 (2.73)</i> <i>FADS1 (1.64)</i> <i>GLYCTK (3.09)</i>	High-IR: <i>ITPKC (-5.27)</i> <i>LIF (-4.73)</i> <i>TNFα(-3.27)</i> <i>UCHL1 (-4.10)</i> <i>CCND1 (-2.55)</i>	
Microarrays SurePrint-G3 Human GE 8 x60 K microarray kit >55,077 transcripts Focus on genes involved in a state of low and high insulin resistance (IR), for a possible relationship with comorbidities.	Low-IR: ~39±13 years High-IR: ~43±11 years		POST-RYGB: Low-IR: ~32±6 High-IR: ~37±3	227 upregulated genes post-RYGB: Low-IR: <i>GLYCTK (4.73)</i> <i>FADS1 (2.55)</i> <i>IRS-1 (1.27)</i>	619 downregulated genes post-RYGB: Low-IR: <i>UCHL1 (-8.55)</i> <i>CCND1 (-5.09)</i> <i>TNFα (-4.64)</i> <i>ITPKC (-2.91)</i> <i>LIF (-2.91)</i>	Low-IR: <i>GLYCTK (4.55)</i> <i>FADS1 (3.45)</i> <i>IRS-1 (2.36)</i>	Low-IR: <i>UCHL1(-6.00)</i> <i>CCND1(-4.10)</i> <i>TNFα(-2.91)</i> <i>ITPKC (-5.27)</i> <i>LIF (-2.91)</i>	(González-Plaza et al., 2018)
qPCR Subsequent validation of genes identified.	qPCR OBESE: 9 obese (9 low-IR; 11 high-IR:) Low-IR: ~45±13 years High-IR: ~47±9 years Malaga, Spain	RYGB ~2 years	ΔBMI: Low-IR: ~17 kg/m ² High-IR: ~16 kg/m ² qPCR OBESE Low-IR: ~57±9 High-IR: ~55±6 POST-RYGB: Low-IR: ~39±9 High-IR: ~38±6 ΔBMI: Low-IR: ~18 kg/m ² High-IR: ~17 kg/m ²	Note: In low-IR, genes involved in carbohydrate metabolic processes Note: Approximate values from the graphs in the article	Note: In high-IR genes involved in cytokine-cytokine receptor, cancer chemokine signaling, and activation of transcription factors In low-IR, genes involved in glycosaminoglycan metabolism and translation regulation	Note: Approximate values from the graphs in the article	Note: Approximate values from the graphs in the article	

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Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)						Reference
	Patients data/ Recruitment country			Microarrays	qPCR					
				Calculated fold change [(PostRYGB/Obese)-1]	Reported fold change values (Obese; 2 years post-RYGB)		Calculated fold change [(Post-RYGB/Obese)-1]			
					Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)				
				Logarithmic conversion			Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)		
<u>Microarrays</u>	<u>Microarrays</u>		<u>Microarrays</u>	Downregulated expression post-RYGB(+)		<i>IL-6</i> <i>(0.01695; 0.0006)</i>				
Affymetrix GeneChip Human Gene 2.0 ST Array	Obese: 16 obese of 48 ± 10 years		Obese: ~46 ± 6			<i>TNFA</i> <i>(0.00302; 0.00074)</i>				
13,885 transcripts post-RYGB VS obese (Ortega et al., 2015)	Post-RYGB: 16 patients		Post-RYGB: Not mentioned	<i>TLR8 (-0.53)</i> <i>TLR7 (-0.48)</i> <i>TLR1 (-0.44)</i> <i>TLR2 (-0.36)</i> <i>TLR5 (-0.35)</i> <i>TLR6 (-0.34)</i> <i>TLR4 (-0.13)</i> <i>TLR3 (-0.12)</i> <i>TLR10 (-0.05)</i> <i>TLR9 (-0.05)</i>		<i>TLR8</i> <i>(0.00032; 0.00011)</i>			<i>IL-6</i> <i>(-0.96)</i> <i>TNFA</i> <i>(-0.75)</i> <i>TLR8</i> <i>(-0.66)</i> <i>LEP</i> <i>(-0.66)</i> <i>TLR1</i> <i>(-0.51)</i> <i>TLR7</i> <i>(-0.37)</i> <i>TLR4</i> <i>(-0.33)</i> <i>TLR5</i> <i>(-0.32)</i> <i>TLR2</i> <i>(-0.3)</i> <i>TLR6</i> <i>(-0.28)</i> <i>TLR3</i> <i>(-0.18)</i>	
	<u>qPCR</u>	RYGB ~2 years	<u>qPCR</u>			<i>LEP</i> <i>(0.9706; 0.3327)</i>				
	Obese: 22 obese of 49 ± 8 years		Obese: ~43 ± 5		<i>GLUT4</i> <i>(0.04472; 0.08758)</i>	<i>TLR1</i> <i>(0.01177; 0.00582)</i>	<i>GLUT4 (0.96)</i> <i>ADIPOQ (0.41)</i> <i>IRS-1 (0.35)</i>			
Candidate genes involved in: (a) Inflammatory (b) Toll-like receptors (TLRs)	Post-RYGB: 22 patients of 53 ± 8 years		Post-RYGB: ~30 ± 5		<i>ADIPOQ</i> <i>(3.24; 4.57)</i>	<i>TLR7</i> <i>(0.00737; 0.00466)</i>				
			ΔBMI: ~13 kg/m ²		<i>IRS-1</i> <i>(0.0107; 0.01438)</i>	<i>TLR4</i> <i>(0.02932; 0.0196)</i>				
	Barcelona, Spain					<i>TLR5</i> (0.00398; 0.00269) <i>TLR2</i> (0.00821; 0.00575) <i>TLR6</i> (0.00666; 0.00482) <i>TLR3</i> <i>(0.01014; 0.00828)</i>				
				Note: Microarray results from Ortega et al., 2015						(Latorre et al., 2018)

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post-RYGB vs obese)			Reference
	Patients data/ Recruitment country			Calculated fold change [(Post-RYGB/Obese)-1]			
				Upregulated expression post-RYGB (+)	Downregulated expression post-RYGB (-)		
<p>. Microarrays</p> <p>Human HT12 v4.0 BeadChip 47,231 transcripts</p> <p>Selection of genes involved in:</p> <ul style="list-style-type: none"> • Matrix fibers • Cross-linking enzymes • Profibrotic proteins • Glycosaminoglycan proteins • Multitensive glycoproteins • MMPs/TIMPs <p>Post-transcriptional modification of collagen</p>	<p>Microarrays</p> <p>Obese: 42 obese of ~43±11 years</p> <p>Post-RYGB: 42 patients</p> <p>Paris, France</p>	RYGB	<p>Microarrays</p> <p>Obese: ~47± 6</p> <p>Post-RYGB: ~33 ± 5</p> <p>ΔBMI: ~15 kg/m²;</p>	<p>4, 236 upregulated genes post-RYGB</p> <p>TIMP4 (0.52)</p> <p>LAMB1 (0.43)</p> <p>COL1A1 (0.36)</p> <p>COL6A3 (0.26)</p> <p>THBS2 (0.24)</p> <p>LAMA2 (0.17)</p> <p>P3H2 (0.16)</p> <p>ADAMTS9 (0.16)</p> <p>TGM2 (0.14)</p> <p>FBLN1 (0.14)</p> <p>TBHS4 (0.14)</p> <p>HSPG2 (0.1)</p> <p>LAMA3 (0.1)</p> <p>LAMA4 (0.1)</p> <p>P3H3 (0.09)</p> <p>COL4A2 (0.05)</p> <p>VIT (0.05)</p> <p>TGM3 (0.03)</p> <p>PLOD1 (0.03)</p> <p>MMP2 (0.03)</p> <p>LAMA5 (0)</p>	<p>2,989 downregulated genes post-RYGB</p> <p>MMP9 (-0.62)</p> <p>SPP1 (-0.59)</p> <p>LOX (-0.41)</p> <p>SPARC (-0.36)</p> <p>COL6A2 (-0.31)</p> <p>CTGF (-0.28)</p> <p>TIMP1 (-0.28)</p> <p>COL6A1 (-0.240)</p> <p>LOXL4 (-0.240)</p> <p>HSPA5 (-0.23)</p> <p>COL3A1 (-0.2)</p> <p>TGM1 (-0.17)</p> <p>TNC (-0.17)</p> <p>GLT25D1 (-0.16)</p> <p>HSP47 (-0.16)</p> <p>PLOD2 (-0.14)</p> <p>CANX (-0.14)</p> <p>ADAMTSL4 (-0.14)</p> <p>PDIA6 (-0.13)</p> <p>P4HA2 (-0.11)</p> <p>P4HB (-0.11)</p> <p>BMP1 (-0.11)</p>	<p>PLOD3 (-0.1)</p> <p>TIMP2 (-0.09)</p> <p>ADAMTS1 (-0.09)</p> <p>ADAMTS5 (-0.09)</p> <p>P4HA2 (-0.09)</p> <p>PDIA4 (-0.08)</p> <p>ELN (-0.07)</p> <p>THBS1 (-0.07)</p> <p>DNAJC10 (-0.07)</p> <p>P4HA1 (-0.05)</p> <p>P3H1 (-0.05)</p> <p>HSP90AA1 (-0.05)</p> <p>HSP90B1 (-0.05)</p> <p>ERP29 (-0.05)</p> <p>ADAMTS2 (-0.05)</p> <p>COL4A1 (-0.04)</p> <p>COL4A5 (-0.04)</p> <p>MMP11 (-0.02)</p> <p>LOXL1 (-0.02)</p>	(Liu et al., 2016)
				Note: Approximate values from graphics in the article		Note: Downregulated genes encoding cross-linking enzymes	
						Note: Approximate values from graphics in the article	

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)		Reference				
qPCR	Patients data/Recruitment country			Reported gene expression values (Obese; 1 week post-RYGB)		Calculated fold change [(Post-RYGB/Obese)-1]				
				Upregulated expression post-RYGB (+)						
				Validation by qPCR of genes involved in: (a) Mitochondrial biogenesis (b) Oxidative stress	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Upregulated expression post-RYGB (+)	(Jahansouz et al., 2015)	
										Post-RYGB: ~39 ± 2
Post-RYGB: ~39 ± 2										
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2		
	Obese: 8 obese of ~50 ± 3 years	RYGB	Obese: ~40 ± 2	Obese: ~40 ± 2	Obese: ~40 ± 2					
Post-RYGB: ~39 ± 2						RYGB				

Lean vs obese

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)		Reference	
	Patients data/ Recruitment country	BMI (kg/m ²)	Reported gene expression values (Obese; Lean)		Calculated fold change [(Lean/Obese)-1]	
			Upregulated expression in lean	Downregulated genes in lean (-)		
qPCR	Lean: 8 lean of 45 ± 6 years				Downregulated genes in lean (-)	
Candidate genes involved in:						
(a) Mitochondrial biogenesis	Obese: 16 obese of 46 ± 3 years	Lean: 24±0.9 kg/m ²	<i>CytC</i> (0.040; 1.00) <i>eNOS</i> (0.20; 1.00) <i>NRF1</i> (0.260; 1.00)	Not reported	<i>CytC</i> (24.00) <i>eNOS</i> (4.00) <i>NRF1</i> (2.85)	(Jahansouz et al., 2015)
(b) Oxidative stress		Obese: 41± 1 kg/m ²	<i>TFAM</i> (0.48; 1.00) <i>PGC1α</i> (0.60; 1.00)		<i>TFAM</i> (1.08) <i>PGC1α</i> (0.67)	
	Minnesota, United States of America					
			Note: Approximate values from article graphics			

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post-RYGB vs Obese)		Reference
	Patients data/ Recruitment country			Reported gene expression values (Obese; 1 year post-RYGB)		
				Upregulated expression post-RYGB (+)	Downregulated expression post-RYGB (-)	Calculated fold change [(Post-RYGB/Obese)-1]
qPCR						
Candidate genes involved in:	Obese: 26 obese of ~42±12 years		Obese: ~46± 6		IL-6 (1.00; 0) <i>FGF1 (1.00; 0.01)</i> <i>IRS-2 (1.00; 0.07)</i> <i>CCL3 (1.00; 0.09)</i> <i>IL-10 (1.02; 0.10)</i> PPARG (1.01; 0.11) ADIPOQ (1.00; 0.12)	Upregulated expression post-RYGB(+) Downregulated expression post-RYGB(-) IL-6 (-1.00) <i>FGF1 (-0.99)</i> <i>IRS-2 (-0.93)</i> <i>CCL3 (-0.91)</i> <i>IL-10 (-0.9)</i> PPARG (-0.89) ADIPOQ (-0.88) <i>IL1B (-0.88)</i> <i>CD68 (-0.87)</i> <i>CIDEA (-0.87)</i> <i>PLIN1 (-0.87)</i> <i>IGF1 (-0.81)</i> <i>CD144 (-0.73)</i> SLC2A4 (-0.69) <i>HLA-DR (-0.57)</i> <i>CD3E (-0.55)</i> VEGFC (-0.04)
(a) Inflammatory cytokines	Post-RYGB: 26 patients	RYGB	Post-RYGB: ~31 ± 6			
(b) Growth factors	of ~43±12 years	~1 year	ΔBMI: ~15 kg/m ² ;	TNFα (1.00; 2.72)	<i>CD144 (0.92; 0.25)</i>	
(c) Metabolic markers (lipolysis)				CASP3 (1.00; 1.64)	SLC2A4 (1.01; 0.31)	
(d) Cell surface markers (apoptosis)	Vienna, Austria			<i>CD40 (0.97; 1.02)</i>	<i>HLA-DR (0.92; 0.40)</i> <i>CD3E (0.94; 0.42)</i> VEGFC (1.00; 0.96)	
					Note: Of the genes downregulated post-RYGB, 4 are metabolic markers.	
				Note: Values calculated from the graphs of the article (without %)	Note: Values calculated from the graphs of the article (without %)	(Jürets et al., 2017)

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Lean vs obese

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)		Reference
	Patients data/ Recruitment country	BMI (kg/m ²)	Reported gene expression values (Obese; Lean)		Calculated fold change [(Lean/Obese)-1]
			Upregulated expression in lean (+)	Downregulated expression in lean (-)	
					Upregulated expression in lean(+) Downregulated expression in lean (-)
qPCR	qPCR	qPCR			
Candidate genes involved in:	Lean: 20 lean of 43 ± 9 years	Lean: ~25 ± 3	<i>CIDEA</i> (1.00; 1.52) <i>CD40</i> (1.00; 1.17) <i>ADIPOQ</i> (1.00; 1.13) <i>SLC2A4</i> (1.00; 1.10) <i>IGF1</i> (1.00; 1.08) <i>IRS-2</i> (1.00; 1.08) <i>PLIN1</i> (1.00; 1.04) <i>CD3E</i> (1.00; 1.03)	<i>IL-6</i> (1.00; 0.17) <i>IL-10</i> (1.00; 0.37) <i>FGF1</i> (1.00; 0.42) <i>CCL3</i> (1.00; 0.5) <i>IL1B</i> (1.00; 0.50) <i>CASP3</i> (1.00; 0.66) <i>CD68</i> (1.00; 0.70) <i>HLA-DR</i> (1.00; 0.75) <i>CD144</i> (1.00; 0.75) <i>VEGFC</i> (1.00; 0.75) <i>PPARG</i> (1.00; 0.88) <i>TNFα</i> (1.00; 0.92)	<i>CIDEA</i> (0.52) <i>CD40</i> (0.17) <i>ADIPOQ</i> (0.13) <i>SLC2A4</i> (0.10) <i>IGF1</i> (0.08) <i>IRS-2</i> (0.08) <i>PLIN1</i> (0.04) <i>CD3E</i> (0.03)
(a) Inflammatory cytokines (b) Growth factors (c) Metabolic markers (lipids and glucose) (d) Cell surface markers (apoptosis)	Obese: 26 obese of 42 ± 12 years Vienna, Austria	Obese: ~46 ± 6			<i>IL-6</i> (-0.83) <i>IL-10</i> (-0.63) <i>FGF1</i> (-0.58) <i>CCL3</i> (-0.50) <i>IL1B</i> (-0.50) <i>CASP3</i> (-0.34) <i>CD68</i> (-0.30) <i>HLA-DR</i> (-0.25) <i>CD144</i> (-0.25) <i>VEGFC</i> (-0.25) <i>PPARG</i> (-0.12) <i>TNFα</i> (-0.08)
			Note: Approximate values from graphics in the article	Note: Approximate values from graphics in the article	(Jürets et al., 2017)

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)				Reference																						
<p>Microarrays</p> <p>Affymetrix GeneChip Human Gene 2.0 ST Array</p> <p>13,885 transcripts post-RYGB vs obese</p> <p>qPCR</p> <p>Candidate genes involved in:</p> <p>(a) Cell cycle</p> <p>(b) Development</p> <p>(c) Lipid metabolism</p> <p>(d) Inflammatory response</p> <p>In addition, the genes that were most regulated post-RYGB were selected.</p>	Patients data/ Recruitment country	RYGB	~2 years	~43 ± 5	~29 ± 6	~14 kg/m ² ;	Microarrays and qPCR	Obese: ~43 ± 5	Post-RYGB: ~29 ± 6	ΔBMI ~14 kg/m ² ;	Calculated fold change [(Post-RYGB/Obese)-1]																			
	Microarrays												Obese: 16 obese of 48±10 years	Post-RYGB: 16 patients of 51 ± 9 years	qPCR	Obese: 25 obese of 48±10 years	Post-RYGB: 25 patients of 51 ± 9 years	Girona, Spain	Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)	Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(-)								
																							Logarithmic conversion	Logarithmic conversion						
																											2,432 upregulated genes	2,586 downregulated genes		
SLC27A2 (3.79)	FOS (-0.86)	ELOVL6 (12.54)	IL-6 (-0.96)																											
ELOVL6 (1.91)	EGFL6 (-0.79)	FOS (-0.96)	FOS (-0.96)																											
FASN (1.87)	AQP9 (-0.78)	RGS1 (-0.94)	RGS1 (-0.94)																											
STOX1 (1.77)	PRG4 (-0.78)	AQP9 (-0.90)	AQP9 (-0.90)																											
GYS2 (1.71)	FOSB (-0.73)	SPP1 (-0.87)	SPP1 (-0.87)																											
MOGAT1 (1.58)	MT1A (-0.71)	EGR1 (-0.84)	EGR1 (-0.84)																											
SNORA71B (1.58)	DUSP1 (-0.7)	DUSP1 (-0.83)	DUSP1 (-0.83)																											
LGALS12 (1.46)	RGS1 (-0.69)	PRG4 (-0.81)	PRG4 (-0.81)																											
C6 (1.45)	EGR1 (-0.68)	EGFL6 (-0.8)	EGFL6 (-0.8)																											
TF (1.45)	SPP1 (-0.67)	TNFα (-0.75)	TNFα (-0.75)																											
PKP2 (1.43)	LYZ (-0.67)	LYZ (-0.68)	LYZ (-0.68)																											
OLFM2 (1.35)	C5AR1 (-0.66)	IQ6GAP2 (-0.51)	IQ6GAP2 (-0.51)																											
ACLY (1.35)	IFI30 (-0.66)	KPNA2 (-0.48)	KPNA2 (-0.48)																											
	HSD11B1 (-0.65)																													
	CD69 (-0.63)																													
	IL8 (-0.63)																													
	CLEC7A (-0.63)																													
	JUNB (-0.62)																													
	RANBP3L (-0.62)																													
	ZFP36 (-0.62)																													
	THBS1 (-0.62)																													
	PLA2G7 (-0.62)																													
	IGSF6 (-0.61)																													
	C3AR1 (-0.59)																													
	CHI3L1 (-0.59)																													
	MMP9 (-0.59)																													
	NQO1 (-0.59)																													
	MS4A6E (-0.59)																													
	CXorf21 (-0.59)																													
	MS4A7 (-0.58)																													
	NPR3 (-0.58)																													
	MS4A14 (-0.58)																													
	CCL8 (-0.58)																													
	P2RY13 (-0.58)																													
	ITGAX (-0.58)																													
	JUN (-0.58)																													
	MS4A4E (-0.57)																													
	ADAM12 (-0.57)																													
	MNDA (-0.57)																													
	CES1 (-0.56)																													

				<p>Upregulated genes involved in:</p> <p>(a) Cancer pathways (b) Hematologic disease (c) Post-transcriptional modification of RNA (d) Development of connective tissue (e) Metabolic disease</p>	<p>Note: Downregulated genes involved in:</p> <p>(a) Lipid metabolism (b) Transportation (c) Cell-cell interaction signaling (d) Carbohydrate metabolism (e) Development and function of connective tissue</p>			
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Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Lean vs obese

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)		Reference
	Patients data/ Recruitment country	BMI (kg/m ²)	Reported fold change [(Lean/Obese)-1]		
			Upregulated expression in lean (+)	Downregulated expression in lean (-)	
			3,576 upregulated genes in lean	2,420 downregulated genes in lean	
gPCR Candidate genes from microarray data Affymetrix GeneChip Human Gene 2.0 ST array >24,838 transcripts between post-surgery vs Obese	Lean: 26 lean of 45±5 years	Lean: ~24±2	EGR1 (5.34) FOS (2.97) PKP2 (2.20) ELOVL6 (2.00) DUSP1 (1.85) GYS2 (1.76) SLC27A2 (1.14) IL-6 (0.66) GLUT4 (0.63) <i>RGS1 (0.52)</i> DECRI (0.51) OLFM2 (0.51) ACSL1 (0.47) LGALS12 (0.44) FASN (0.43) ACLY (0.43) THRSP14 (0.43) IRS-1 (0.42) ECI1 (0.29) <i>TNFα (0.18)</i> <i>SCD1 (0.12)</i> <i>ACACA (0.03)</i>	LYZ (-0.70) SPP1 (-0.70) PRG4 (-0.69) EGFL6 (-0.64) AQP9 (-0.56) IQ6GAP2 (-0.52) KPNA2 (-0.29)	(Ortega et al., 2015)
Candidate genes involved in: (a) Cell cycle (b) Development (c) Lipid metabolism (d) Inflammatory response	Obese: 25 obese of 48±10 years Girona, Spain	Obese: ~43±5			
			Note: Fold change reported without percentage	Note: Fold change reported without percentage	

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs Obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)		Reference
	Patients data/ Recruitment country			Reported gene expression	Calculated fold change [(Post-RYGB/Obese)-1]	
Microarrays				Upregulated expression post-RYGB (+)		
Affymetrix Human Gene 1.1 (Affymetrix , Inc., Santa Clara, CA) >28,000 transcripts	Obese: 16 obese of ~46 ± 2 years	RYGB	Obese: ~41 ± 1	<i>TGFB1</i> <i>CXCL2</i> <i>FGF2</i> <i>OGN</i> <i>PDGFD</i>	Not calculated	(Petrus et al., 2018)
They focused on associated genes with adipocyte number change in obesity and post-RYGB.	Post-RYGB: 16 patients of ~48 ± 2 years Stockholm, Sweden	2 years	Post-RYGB: ~25 ± 1 ΔBMI: ~16 kg/m ²	Upregulated genes involved in growth factors and extracellular matrix organization		

Lean vs Obese

Method	Characteristics of the groups	BMI (kg/m ²)	Gene expression fold change (Lean vs Obese)		Reference
	Patients data/ Recruitment country		Reported gene expression	Calculated fold change [(Lean/Obese)-1]	
Microarrays			Upregulated genes in lean (+)	Downregulated genes in lean (-)	
Affymetrix Human Gene 1.1 (Affymetrix , Inc., Santa Clara, CA) >28,000 transcripts	Lean: 16 lean of ~48 ± 2 years	Lean: ~25 kg/m ²			(Petrus et al., 2018)
	Obese: 16 obese of ~46 ± 2 years Stockholm, Sweden	Obese: ~41 ± 1 kg/m ²	Not reported	<i>TGFB1</i> <i>TGFB3</i>	Not calculated

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)		Reference
	Patients data/ Recruitment country			Calculated fold change [(Post-RYGB/Obese)-1]		
				Upregulated expression post-RYGB (+)	Downregulated expression post-RYGB (-)	
				2,420 upregulated genes post-RYGB	3,576 downregulated genes post-RYGB	
					<p><i>GPR183</i> (-0.66)</p> <p><i>LYZ</i> (-0.65)</p> <p><i>CLEC7A</i> (-0.63)</p> <p><i>LCP1</i> (-0.63)</p> <p><i>NDUFS2</i> (-0.63)</p> <p><i>VSIG4</i> (-0.63)</p> <p><i>MS4A7</i> (-0.62)</p> <p><i>AQP9</i> (-0.61)</p> <p><i>NCKAP1L</i> (-0.6)</p> <p><i>CTSS</i> (-0.59)</p> <p><i>GLIPR1</i> (-0.59)</p> <p><i>CYBB</i> (-0.58)</p> <p><i>IGSF6</i> (-0.58)</p> <p><i>PLEK</i> (-0.58)</p> <p><i>CD163</i> (-0.57)</p> <p><i>MS4A6A</i> (-0.57)</p> <p><i>TLR8</i> (-0.57)</p> <p><i>BCAT1</i> (-0.56)</p> <p><i>TYROBP</i> (-0.56)</p> <p><i>AIF1</i> (-0.55)</p> <p><i>CD53</i> (-0.55)</p> <p><i>FCGR2A</i> (-0.55)</p> <p><i>CD68</i> (-0.54)</p> <p><i>FCGR3A</i> (-0.54)</p> <p><i>TBXAS1</i> (-0.54)</p> <p><i>CTD-2370N5.3</i> (-0.53)</p> <p><i>RNASE6</i> (-0.53)</p> <p><i>CPVL</i> (-0.52)</p> <p><i>F13A1</i> (-0.51)</p> <p><i>SAMSN1</i> (-0.51)</p> <p><i>CD4</i> (-0.5)</p> <p><i>FOLR2</i> (-0.49)</p> <p><i>IQGAP2</i> (-0.49)</p>	
					<p><i>PTPRC</i> (-0.49)</p> <p><i>KYNU</i> (-0.48)</p> <p><i>VAMP8</i> (-0.48)</p> <p><i>RGS10</i> (-0.47)</p> <p><i>CR1</i> (-0.46)</p> <p><i>ITGAM</i> (-0.46)</p> <p><i>LYVE1</i> (-0.45)</p> <p><i>SELPLG</i> (-0.45)</p> <p><i>ADAP2</i> (-0.44)</p> <p><i>ALOX5AP</i> (-0.44)</p> <p><i>AMICA1</i> (-0.44)</p> <p><i>ARRB2</i> (-0.44)</p> <p><i>CSF1R</i> (-0.44)</p> <p><i>ARHGAP30</i> (-0.43)</p> <p><i>BIN2</i> (-0.43)</p> <p><i>RPS6KA1</i> (-0.43)</p> <p><i>SLC7A7</i> (-0.42)</p> <p><i>GPR137B</i> (-0.4)</p> <p><i>RASSF2</i> (-0.4)</p> <p><i>CD300A</i> (-0.39)</p> <p><i>SYK</i> (-0.39)</p> <p><i>CD163L1</i> (-0.38)</p> <p><i>CHST11</i> (-0.37)</p> <p><i>DOCK10</i> (-0.37)</p> <p><i>PIK3R5</i> (-0.37)</p> <p><i>RNASET2</i> (-0.35)</p> <p><i>CATG0000007766.1</i> (-0.34)</p> <p><i>CHST15</i> (-0.33)</p> <p><i>CTSH</i> (-0.33)</p> <p><i>HCLS1</i> (-0.33)</p> <p><i>PPT1</i> (-0.33)</p> <p><i>SAMHD1</i> (-0.33)</p> <p><i>SMAP2</i> (-0.31)</p> <p><i>SRGN</i> (-0.31)</p> <p><i>PTPLAD2</i> (-0.3)</p>	
Microarrays	Obese:		Obese:			
ClariomTM D arrays	50 obese of 43±9 years		43±5			
19,418 transcripts excluding non-coding mRNAs		RYGB				
Focused on inflammatory genes with cutt-of of p-value 10 ⁻⁸	Post-RYGB:	2 years	Post-RYGB:			
	49 patients post-RYGB of 45±9 years		29±4			
	The surgery candidates		ΔBMI:			
			~14 kg/m ²			
	Stockholm, Sweden					
						Kerr et al., 2020

Note: Upregulated expression related to protein translation, cell differentiation, and metabolism.

Note: Some genes with p-value cut-off different than 10^{-8} but if $p < 0.05$, were (Calculated fold change at 2 years post-RYGB):

SLC2A4 (1.00)
IRS-1 (0.39)
ACSL1 (0.15)
PLIN1 (0.12)
ADIPOQ (0.09)

HGF (-0.29)
PYCARD (-0.29)
QPCT (-0.29)
FUCA1 (-0.27)
NAIP (-0.27)
PIK3AP1 (-0.26)
RNASE1 (-0.25)
SLC18B1 (-0.25)
EZR (-0.22)
CNPY3 (-0.19)

Note: downregulated and involved in immune and inflammatory responses.

Note: Some genes with p-value cut-off different than 10^{-8} but if $p < 0.05$, were (Calculated fold change at 2 years post-RYGB):

IL-6 (-0.42)

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Post-RYGB vs obese

Method	Characteristics of the groups	Bariatric surgery data	BMI data (kg/m ²)	Gene expression fold change (Post RYGB vs Obese)			Reference
				Calculated fold change [(Post-RYGB/Obese)-1]			
				Upregulated expression post-RYGB(+)	Downregulated expression post-RYGB(+)		
Microarrays ClariomTM D arrays 19,418 transcripts excluding non-coding mRNAs Focused on inflammatory genes with p-value cut-off 10 ⁻⁸	Obese: 50 Obese of 43±9 years Post-RYGB: 38 post-RYGB of 47±10 years Stockholm, Sweden	RYGB 5 years	Obese: 43±5 Post-RYGB: 32±6 ΔBMI: ~11 kg/m ²	1,653 upregulated genes post-RYGB	3,930 downregulated genes post-RYGB	<i>PTPRC</i> (-0.63) <i>BIN2</i> (-0.61) <i>ADAP2</i> (-0.61) <i>SELPLG</i> (-0.61) <i>LYVE1</i> (-0.6) <i>KYNU</i> (-0.6) <i>IQGAP2</i> (-0.6) <i>ALOX5AP</i> (-0.59) <i>CSF1R</i> (-0.59) <i>CR1</i> (-0.59) <i>VAMP8</i> (-0.59) <i>DOCK10</i> (-0.57) <i>RPS6KA1</i> (-0.57) <i>ITGAM</i> (-0.57) <i>ARRB2</i> (-0.56) <i>ARHGAP30</i> (-0.55) <i>SYK</i> (-0.54) <i>RASSF2</i> (-0.54) <i>SLC4A4</i> (-0.53) <i>PIK3R5</i> (-0.51) <i>CD300A</i> (-0.51) <i>CD163L1</i> (-0.5) <i>CHST11</i> (-0.49) <i>RNASET2</i> (-0.48) <i>SRGN</i> (-0.46) <i>CTSH</i> (-0.46) <i>CHST15</i> (-0.45) <i>SAMHD1</i> (-0.45) <i>SMAP2</i> (-0.44) <i>SLC7A7</i> (-0.44) <i>PTPLAD2</i> (-0.43) <i>PPT1</i> (-0.43) <i>QPCT</i> (-0.42) <i>CATG00000077766.1</i> (-0.42) <i>FUCA1</i> (-0.4) <i>EZR</i> (-0.39) <i>PIK3AP1</i> (-0.38) <i>PYCARD</i> (-0.38) <i>RNASE1</i> (-0.36) <i>NAIP</i> (-0.34) <i>SLC18B1</i> (-0.33) <i>CNPY3</i> (-0.28)	(Kerr et al., 2020)
				Reported fold change (Post-RYGB/Obese)	Reported fold change (Post-RYGB/Obese)	<i>AQP9</i> (-0.77) <i>LYZ</i> (-0.78) <i>CLEC7A</i> (-0.77) <i>LCP1</i> (-0.76) <i>MS4A7</i> (-0.75) <i>NDUFS2</i> (-0.75) <i>VSIG4</i> (-0.75) <i>FCGR3A</i> (-0.72) <i>TBXAS1</i> (-0.72) <i>CD53</i> (-0.72) <i>CYBB</i> (-0.72) <i>IGSF6</i> (-0.72) <i>CTSS</i> (-0.72) <i>TYROBP</i> (-0.71) <i>NCKAP1L</i> (-0.71) <i>HGF</i> (-0.7) <i>HCLS1</i> (-0.7) <i>GPR137B</i> (-0.7) <i>CD163</i> (-0.7) <i>GL IPR1</i> (-0.7) <i>GPR183</i> (-0.7) <i>MS4A6A</i> (-0.69) <i>TLR8</i> (-0.69) <i>CPVL</i> (-0.68) <i>FCGR2A</i> (-0.68) <i>SAMSN1</i> (-0.67) <i>CTD-2370N5.3</i> (-0.67) <i>AIF1</i> (-0.67) <i>BCAT1</i> (-0.66) <i>C1QB</i> (-0.65) <i>FOLR2</i> (-0.65) <i>F13A1</i> (-0.65) <i>RNASE6</i> (-0.65) <i>CD4</i> (-0.64) <i>CD68</i> (-0.63) <i>AMICA1</i> (-0.63) <i>RGS10</i> (-0.63)	
				<i>PKP2</i> (2.09) <i>FASN</i> (1.14) <i>COX14</i> (0.74) <i>NEDD4L</i> (0.56) <i>RNF157</i> (0.51) <i>PDE3B</i> (0.43) <i>PLEK</i> (0.43) <i>TENM3</i> (0.41) <i>PRKAR2B</i> (0.4) <i>AQP7</i> (0.4)			
				Note: Upregulated genes involved in lipid metabolism, adipocyte differentiation and function.			
				Note: Some genes with p-value cut-off different than 10 ⁻⁸ but if p<0.05, were (Calculated fold change at 2 years post-RYGB):			
				<i>SLC2A4</i> (1.13) <i>IRS-1</i> (0.39) <i>ACSL1</i> (0.20) <i>PLIN1</i> (0.15) <i>ADIPOQ</i> (0.09)			
						Note: Downregulated genes involved in immune response and cytokines production Note: Some genes with p-value cut-off different than 10 ⁻⁸ but if p<0.05, were (Calculated fold change at 2 years post-RYGB): <i>IL-6</i> (-0.48)	

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Lean vs obese

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)		Reference
	Patients data/ Recruitment country	BMI (kg/m ²)	Reported gene expression values (Obese; Lean)	Calculated fold change [(Lean/Obese)-1]	
			Downregulated expression in lean (-)		
			Logarithmic conversion	Downregulated expression in lean (-)	
			<i>LCP1</i> (584.07;229.13)	<i>LCP1</i> (-0.61)	
			<i>GPR183</i> (265.03;108.38)	<i>GPR183</i> (-0.59)	
			<i>GLIPR1</i> (504.95;218.27)	<i>GLIPR1</i> (-0.57)	
			<i>VSIG4</i> (364.56;162.02)	<i>VSIG4</i> (-0.56)	
			<i>LYZ</i> (1710.26;765.36)	<i>LYZ</i> (-0.55)	
			<i>SAMSN1</i> (44.94;20.39)	<i>SAMSN1</i> (-0.55)	
			<i>CD53</i> (572.05;259.57)	<i>CD53</i> (-0.55)	
			<i>PLEK</i> (104.69;47.84)	<i>PLEK</i> (-0.54)	
			<i>NCKAP1L</i> (179.77;82.71)	<i>NCKAP1L</i> (-0.54)	
			<i>CTSS</i> (657.11;306.55)	<i>CTSS</i> (-0.53)	<i>SAMHD1</i> (-0.33)
			<i>CLEC7A</i> (113.77;53.08)	<i>CLEC7A</i> (-0.53)	<i>LGMN</i> (-0.32)
			<i>FCGR3A</i> (112.21;53.82)	<i>FCGR3A</i> (-0.52)	<i>HGF</i> (-0.31)
			<i>CYBB</i> (596.34;290.02)	<i>CYBB</i> (-0.51)	<i>CORO1A</i> (-0.31)
			<i>MNDA</i> (38.32;19.03)	<i>MNDA</i> (-0.5)	<i>S100A8</i> (-0.3)
			<i>TLR8</i> (34.54;17.39)	<i>TLR8</i> (-0.5)	<i>LY96</i> (-0.3)
			<i>CD68</i> (1089.92;556.41)	<i>CD68</i> (-0.49)	<i>CD48</i> (-0.29)
			<i>FCGR2A</i> (1009.9;519.15)	<i>FCGR2A</i> (-0.49)	<i>FCER1A</i> (-0.29)
			<i>TYROBP</i> (1686.71;879.17)	<i>TYROBP</i> (-0.48)	<i>FUCA1</i> (-0.27)
			<i>FCGR3B</i> (108.38;57.68)	<i>FCGR3B</i> (-0.47)	<i>QPCT</i> (-0.26)
			<i>AIF1</i> (1168.14;625.99)	<i>AIF1</i> (-0.46)	<i>NPC2</i> (-0.25)
			<i>IQGAP2</i> (126.24;67.65)	<i>IQGAP2</i> (-0.46)	<i>PIK3AP1</i> (-0.24)
			<i>BIN2</i> (89.88;49.52)	<i>BIN2</i> (-0.45)	<i>SELL</i> (-0.22)
			<i>VAMP8</i> (100.43;56.1)	<i>VAMP8</i> (-0.44)	<i>EZR</i> (-0.19)
			<i>CR1</i> (39.4;22.78)	<i>CR1</i> (-0.42)	<i>CTSC</i> (-0.19)
			<i>PTPRC</i> (439.59;254.23)	<i>PTPRC</i> (-0.42)	<i>CNPY3</i> (-0.17)
			<i>PRKCB</i> (61.82;36.5)	<i>PRKCB</i> (-0.41)	<i>GMFG</i> (-0.17)
			<i>RPS6KA1</i> (45.89;27.1)	<i>RPS6KA1</i> (-0.41)	<i>TNFRSF1B</i> (-0.14)
			<i>FOLR2</i> (265.03;157.59)	<i>FOLR2</i> (-0.41)	<i>ZC3HAV1</i> (-0.1)
			<i>SYK</i> (40.5;24.42)	<i>SYK</i> (-0.4)	<i>FGL2</i> (-0.07)
			<i>ITGAM</i> (121.1;73.01)	<i>ITGAM</i> (-0.4)	<i>CYLD</i> (-0.05)
			<i>FPR1</i> (63.56;38.59)	<i>ITGAM</i> (-0.4)	
			<i>CXCR4</i> (276.28;167.73)	<i>FPR1</i> (-0.39)	
			<i>LY86</i> (99.73;61.39)	<i>CXCR4</i> (-0.39)	
			<i>CD4</i> (148.06;91.14)	<i>LY86</i> (-0.38)	
			<i>C1QA</i> (430.54;265.03)	<i>CD4</i> (-0.38)	
			<i>ALOX5AP</i> (568.1;352.14)	<i>C1QA</i> (-0.38)	
			<i>ARRB2</i> (634.73;398.93)	<i>ALOX5AP</i> (-0.38)	
			<i>MYO1F</i> (245.57;158.68)	<i>ARRB2</i> (-0.37)	
			<i>RNASET2</i> (157.59;103.97)	<i>MYO1F</i> (-0.35)	
				<i>RNASET2</i> (-0.34)	
Microarrays	Lean: 28 lean of 44±9 years	Lean: 27±5			
ClariomTM D arrays >540,000 transcripts					
Focus on inflammatory genes	Obese: 50 obese of 43±9 years	Obese: 43±5			
	Stockholm, Sweden				
					(Kerr et al.,2020)

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Lean vs obese

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)		Reference		
	Patients data/ Recruitment country	BMI (kg/m ²)	Reported gene expression values (Obese; Lean)		Calculated fold change [(Lean/Obese)-1]		
			Upregulated expression in lean (+)	Downregulated expression in lean (-)			
qPCR	Candidate genes involved in: (a) Adipogenic markers (b) Insulin signaling pathway (c) Remodeling of the extracellular matrix (ECM) (d) Inflammatory	Lean: 83 lean of ~23±2 years	Lean: ~22 ± 2				
		Obese: 19 obese of ~26±5 years	Obese: ~33 ± 3				
	Bialystok, Poland						
			SLC2A4 (0.20; 0.49) MAPK11 (0.04; 0.08) TLR2 (0.01; 0.02) CEBPB (0.10; 0.19) IRS-2 (0.58; 0.9) NFKBIA (0.17; 0.25) PIK3CA (0.13; 0.19) MAPK14 (0.56; 0.8) ADIPOQ (0.48; 0.68) PPARG (0.95; 1.34) VEGFA (0.29; 0.41) CEBPA (4.05; 5.69) TLR4 (0.14; 0.19) IRS-1 (0.59; 0.78) NFKBIL1 (0.18; 0.23) MMP2 (0.38; 0.48) AKT2 (2.32; 2.9) JUN (0.34; 0.42) COL1A1 (0.78; 0.95) MAPK8 (0.1; 0.12) RELA (0.45; 0.5) CCL3 (0.10; 0.11) RASA1 (0.34; 0.37) MAP3K1 (0.13; 0.14) GRB2 (0.57; 0.6) SREBF1 (0.28; 0.29) MAPK1 (0.31; 0.32) RAF1 (0.026; 0.028) CD8A (0.010; 0.013)	IL-18 (0.03; 0.01) MMP9 (0.26; 0.09) CCL2 (0.1; 0.05) CD14 (0.64; 0.35) ITGAM (0.07; 0.04) CD68 (0.31; 0.18) ITGAX (0.11; 0.07) CD19 (0.03; 0.02) CD86 (0.03; 0.02) NFKB2 (0.12; 0.09) IKBKB (0.04; 0.03) TIMP1 (0.34; 0.27) MIF (0.36; 0.31) CD40 (0.07; 0.06) NFKB1 (0.08; 0.07) CD4 (0.042; 0.040) CD3D (0.02; 0.01) FOXP3 (0.009; 0.007)	Upregulated expression in lean SLC2A4 (1.45) MAPK11 (1.00) TLR2 (1.00) CEBPB (0.90) IRS-2 (0.55) NFKBIA (0.47) PIK3CA (0.46) MAPK14 (0.43) ADIPOQ (0.42) PPARG (0.41) VEGFA (0.41) CEBPA (0.40) TLR4 (0.36) IRS-1 (0.32) NFKBIL1 (0.28) MMP2 (0.26) AKT2 (0.25) JUN (0.24) COL1A1 (0.22) MAPK8 (0.2) RELA (0.11) CCL3 (0.10) RASA1 (0.09) MAP3K1 (0.08) GRB2 (0.05) SREBF1 (0.04) MAPK1 (0.03) RAF1 (0.08) CD8A (0.30)	Downregulated expression in lean (-) IL-18 (-0.67) MMP9 (-0.65) CCL2 (-0.50) CD14 (-0.45) ITGAM (-0.43) CD68 (-0.42) ITGAX (-0.36) CD19 (-0.33) CD86 (-0.33) NFKB2 (-0.25) IKBKB (-0.25) TIMP1 (-0.21) MIF (-0.14) CD40 (-0.14) NFKB1 (-0.13) CD4 (-0.05) CD3D (-0.15) FOXP3 (-0.22)	(Matulewicz et al., 2017)
			Note: Approximate values from the graphs in the article	Note: Approximate values from the graphs in the article			

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)				Reference
	Patients data/ Recruitment country	BMI (kg/m ²)	Microarrays		qPCR		
			Upregulated expression in lean (+)	Downregulated expression in lean (-)	Reported gene expression values (Obese; Lean)	Calculated fold change [(Lean/Obese)-1]	
Microarrays							
Two-Color Microarray Based Gene Expression Analysis/Low Input Quick Amp Labeling >18,000 transcripts	Lean: 8 lean of ~36±9 years	Lean: ~24±1	ADPN, PPARG, IRS-2, CEBPB, MEF2A, MEF2D, MVD, ACSL1, ACSL3, GAPDHS, PGK1, LDHC, IRS, MAP3K2, MAP3K6, MAP3K9, MAP3K14, AKT1, ABCD1, CDKN2A, CASP4, CASP11, PNPLA3.	RETN, PPARA, SREBP2, HKI, CD40LG, VTN, ALOX5, RAPGEF1, BAX, BAX, CYP7A1, CYP19A1	Upregulated expression in lean (+)	Upregulated expression in lean (-)	
	Obese: 8 obese of ~41±9 years	Obese: ~33±3					
qPCR	qPCR						
qPCR validation of only 3 genes selected by the author	Lean: 35 patients						(Ronquillo et al., 2019)
	Obese: 37 obese						
	Mexico City, Mexico		Note: They do not present numeric expression values, only that they are upregulated.	Note: They do not present numeric expression values, only that they are overexpressed.			
			Genes involved in: (a) Endocrine function of the adipocyte (b) Cholesterol and triglyceride synthesis (c) Beta-oxidation of fatty acids (d) Insulin signaling (e) Leptin signaling (f) Cytochromes p450	Genes involved in: (a) Glycolysis and gluconeogenesis (b) Inflammation (c) Insulin signaling (d) Leptin signaling (e) TG synthesis (f) Carbohydrate metabolism (g) Oxidative stress (h) Cytochromes p450			
Note: In both cases, the selection criteria are not explained, only that they are involved in obesity.							
					Note: Approximate values from graphics in the article		

Lean vs obese

Method	Characteristics of the groups		Gene expression fold change (Lean vs Obese)		Reference
	Patients data/ Recruitment country	BMI (kg/m ²)	Reported gene expression		
			Upregulated genes in lean (+)	Downregulated genes in lean (-)	
Microarrays			91 upregulated genes in lean	130 downregulated genes in lean	
Affymetrix Human Gene 2.1ST array 10,000 transcripts	Lean: 9 lean of 50 ± 3 years	Lean: ~22 ± 2	<i>PPP1R1B</i> <i>NPR1</i> <i>HCAR3</i> <i>P1K3CA</i>	<i>CCL19</i> <i>CXCL10</i> <i>CXCL11</i> <i>TNFRSF11A</i> <i>TNFRSF25</i> <i>PDGFA</i> <i>GNB4</i> <i>ADCY1</i>	(Badoud et al., 2017)
Genes involved in: (a) Cytokine-cytokine receptor interaction (b) Chemokine signaling pathway	Obese: 11 Obese of 46 ± 1 years Ontario, Canada	Obese: ~35 ± 1	Note: Significantly upregulated genes involved in: (a) Lipolysis in adipocytes (b) cAMP signaling pathway	Note: Significantly downregulated genes involved in: (a) Cytokine-cytokine receptor interaction (b) Chemokine signaling pathway	

Genes, method, N, mean age, BMI (body mass index), reported or calculated fold change, upregulated or downregulated genes, reference. Highlighted genes are those found in the intersection of comparisons between post-RYGB vs obese and lean vs obese. Bold font appoints significance.