

Supplementary Table 1 summarises the main content (RQ1) of each article according to the PICO principle, which includes Population, Indicator, Comparison and Outcome measures. The earliest reported study meeting the eligibility criteria was Højlund et al. published in 2003 (Hojlund et al. 2003), therefore the current review considers literature over a 12 year study period from 2003 to 2016.

Note-OB is obesity, MOB is Morbidly obese, T2DM is type 2 diabetes mellitus, HT is hypertension, OWHLT is overweight with healthy, LEHLT is lean with healthy, LEOW is lean with slightly overweight, NGT is non-glucose tolerance, OCs is Obese-control

*presented significant difference at p-value <0.05 or under

Reference	Participants (M/F)	Study groups		Method in proteomics	Outcome measures		
		Case	Control		Uniprot accession number	Protein name (gene name)*	
Højlund et al. 2003	N=15 (8/7) Vastus lateralis (biopsy & cell)	T2DM	OWHLT	2D-DIGE	Up-regulation (6)		
		n = 9 (5/4)	n = 6 (3/3)	pH 4-7	P08238	Heat shock protein HSP 90-beta	HSP90AB1 (HSP90AB1 HSP90B, HSPC2, HSPCB)
		age 45 ± 2 y	age 46 ± 2 y		P11021	78 kDa glucose-regulated protein	GRP78 (HSPA5 GRP78)
		BMI 33.3± 1.9 kg.m ⁻²	BMI 25.7 ± 1.2 kg.m ⁻²	MALDI-TOF (P-32)	P12109	Collagen alpha-1(VI) chain	COL6A1 (COL6A1)
					P12277	Creatine kinase B-type	KCRB (CKB CKBB)
					P36871	Phosphoglucomutase-1	PGM1 (PGM1)
					Q96A32	Myosin regulatory light chain 2, skeletal muscle isoform	MLRS (MYLPF)
					Down-regulation (2)		
					P06576	ATP synthase subunit beta, mitochondrial	ATPB (ATP5B)
					P10916	Myosin regulatory light chain 2, ventricular/cardiac muscle isoform	MLRV
Hittel et al. 2005	N=18 (0/18) Rectus abdominus	OW/OB	LEHLT	2D-DIGE	Up-regulation (3)		
		n = 6 (0/6)	n = 6	pH 3-10 11 cm			
		age 44 ± 3 y	age 45 ± 3 y				
		BMI 30.2 ± 0.81 kg.m ⁻²	BMI 23.8 ± 0.58 kg.m ⁻²	MALDI-TOF	P00568	Adenylate kinase isoenzyme 1	KAD1 (AK1)
					P04075	Fructose-bisphosphate aldolase A	ALDOA (ALDOA ALDA)
		MOB			P04406	Glyceraldehyde-3-phosphate dehydrogenase	G3P (GAPDH GAPD, CDABP0047, OK/SW-cl.12)
		n = 6 (0/6)			Down-regulation (0)		
		age 38 ± 3 y					
		BMI 53.8 ± 3.5 kg.m ⁻²					
		Lefort et al. 2010	N = 34 (18/16) Vastus lateralis	OB (with pre-HT/pre-DM)	LEOW (with pre-HT)	1D-SDS-PAGE (12%)	Up-regulation (10)
n = 14 (7/7)	n = 20 (11/9)			HPLC-MS/MS	A6NNS2	Dehydrogenase/reductase SDR family member 7C	DRS7C (DHRS7C SDR32C2)
age 38 ± 4 y	age 38 ± 3 y				O14983	Sarcoplasmic/endoplasmic reticulum calcium ATPase 1	AT2A1 (SERCA1)
BMI 36 ± 1 kg.m ⁻²	BMI 25 ± 1 kg.m ⁻²				P02647	Apolipoprotein A-I	APOA1 (APOA1)
					P11217	Glycogen phosphorylase, muscle form	PYGM (PYGM)
					P12882	Myosin-1	MYH1 (MYH1)
					P27105	Erythrocyte band 7 integral membrane protein	STOM (STOM)
					P32119	Peroxisedoxin-2	PRDX2 (Prdx2 Tdpx1, Tpx)
					P54289	Voltage-dependent calcium channel subunit alpha-2/delta-1	CA2D1 (CACNA2D1 CACNL2A, CCHL2A, MHS3)
					Q9UHG3	Prenylcysteine oxidase 1	PCYOX (PCYOX1 KIAA0908, PCL1, UNQ597/PRO1183)
					Q9UKX2	Myosin-2	MYH2 (MYH2 MYHSA2)
					Down-regulation (11)		
					E9PQ53	NADH dehydrogenase [ubiquinone] 1 subunit C2, isoform 2	NDUCR (NDUFC2-KCTD14)
					O14958	Calsequestrin-2	CASQ2 (CASQ2)
					O75306	NADH dehydrogenase [ubiquinone] iron-sulfur protein 2, mitochondrial	NDUS2 (NDUFS2)
					O95169	NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 8, mitochondrial	NDUB8 (NDUFB8)
					P05166	Propionyl-CoA carboxylase beta chain, mitochondrial	PCCB (PCCB)
					P10606	Cytochrome c oxidase subunit 5B, mitochondrial	COX5B (COX5B)
					P51970	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 8	NDUA8 (NDUFA8)
					Q02252	Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	MMSA (ALDH6A1 MMSDH)
					Q6ZMU5	Tripartite motif-containing protein 72	TRI72 (TRIM72 MG53)
					Q86Y39	NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 11	NDUAB (NDUFA11)
					Q92523	Carnitine O-palmitoyltransferase 1, muscle isoform	CPT1B
Hwang et al. 2010	N = 24 (12/12) Vastus lateralis	OB (with pre-DM)	LEHLT	1D-SDS-PAGE	Up-regulation (9)		
		n = 8 (4/4)	n= 8 (4/4)	(4-20%)	O94760	N(G),N(G)-dimethylarginine dimethylaminohydrolase 1	DDAH1 (DDAH1 DDAH)
		age 44 ± 3 y	age 37 ± 4 y	HPLC-MS/MS	P30101	Protein disulfide-isomerase A3	PDIA3 (PDIA3 ERP57, ERP60, GRP58)
		BMI 31.6 ± 0.8 kg.m ⁻²	BMI 24.3 ± 0.8 kg.m ⁻²		P47897	Glutamine--tRNA ligase	SYQ (QARS)
					P49720	Proteasome subunit beta type-3	PSB3 (PSMB3)

				T2DM n= 8 (4/4) age 48 ± 3 y BMI 29.0 ± 1.1 kg.m ⁻²		P50990 T-complex protein 1 subunit theta P50991 T-complex protein 1 subunit delta Q16543 Hsp90 co-chaperone Cdc37 Q93034 Cullin-5 Q9Y2K3 Myosin-15 Down-regulation (5) Cytochrome c oxidase subunit 6C (Cytochrome c oxidase polypeptide VIc) P14927 Cytochrome b-c1 complex subunit 7 P35609 Alpha-actinin-2 Q9NP98 Myozenin-1 Q9NX63 MICOS complex subunit MIC19	TCPQ (CCT8 C21orf112, CCTQ, KIAA0002) TCPD (CCT4 CCTD, SRB) CDC37 (CDC37 CDC37A) CUL5 (CUL5 VACM1) MYH15 (MYH15 KIAA1000) COX6C (COX6C) QCR7 (UQCRB UQBP) ACTN2 (ACTN2) MYOZ1 MIC19 (CHCHD3 MIC19, MINOS3)
Thingholm et al	N=30	OB	LEHLT			Up-regulation (6) P05413 Fatty acid-binding protein, heart P11055 Myosin-3 P13535 Myosin-8 P24821 Tenascin P60842 Eukaryotic initiation factor 4A-I Q9UKX2 Myosin-2 Down-regulation (6) O14558 Heat shock protein beta-6 P00325 Alcohol dehydrogenase 1B P00813 Adenosine deaminase P02647 Apolipoprotein A-I P40121 Macrophage-capping protein P69905 Hemoglobin subunit alpha	FABPH (FABP3 FABP11, MDGI) MYH3 (MYH3) MYH8 (MYH8) TENA (TNC) IF4A1 (EIF4A1) MYH2 (MYH2 MYHSA2) HSPB6 (HSPB6) ADHB1 (ADH1B ADH2) ADA (ADA ADA1) APOA1 (APOA1) CAPG (CAPG AFCP, MCP) HBA (HBA1 HBA2)
Giebelstein et al	N=31 (17/14)	OB (pre-DM)	LEHLT	2D-DIGE		Up-regulation (20) O75323 Protein NipSnap homolog 2 P02679 Fibrinogen gamma chain P04406 Glyceraldehyde-3-phosphate dehydrogenase P05976 Myosin light chain 1/3, skeletal muscle isoform P06732 Creatine kinase M-type P11217 Glycogen phosphorylase, muscle form P13929 Beta-enolase P14618 Pyruvate kinase PKM P15259 Phosphoglycerate mutase 2 P40925 Malate dehydrogenase, cytoplasmic P45378 Troponin T, fast skeletal muscle P54652 Heat shock-related 70 kDa protein 2 P55084 Trifunctional enzyme subunit beta, mitochondrial P63267 Actin, gamma-enteric smooth muscle P69905 Hemoglobin subunit alpha Q13011 Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial Q14469 Transcription factor HES-1 Q96A32 Myosin regulatory light chain 2, skeletal muscle isoform Q9H7C9 Mth938 domain-containing protein Q9Y281 Cofilin-2 Down-regulation (6) P08590 Myosin light chain 3 P10916 Myosin regulatory light chain 2, ventricular/cardiac muscle isoform P13805 Troponin T, slow skeletal muscle P17661 Desmin P40123 Adenylyl cyclase-associated protein 2 P62736 Actin, aortic smooth muscle	NIPS2 (GBAS NIPSNAP2) FIBG (FGG PRO2061) G3P (GAPDH GAPD, CDABP0047, OK/SW-cl.12) MYL1 KCRM (KCRM) PYGM (PYGM) ENOB (ENO3) KYPM (PKM OIP3, PK2, PK3, PKM2) PGAM2 (PGAM2 PGAMM) MDHC (MDH1, MDHA) TNNT3 (TNNT3) HSP72 (HSPA2) ECHB (HADHB MSTP029) ACTH (ACTG2 ACTA3, ACTL3, ACTSG) HBA (HBA1 HBA2) ECH1 HES1 (HES1 BHLHB39, HL, HRY) MLRS (MYLPF) AAMDC (AAMDC C11orf67, PTD015) COF2 (CFL2) MYL3 (MYL3) MLRV TNNT1 (TNNT1 TNT) DESM (DES) CAP2 (CAP2) ACTA (ACTA2 ACTSA, ACTVS, GIG46)

Al-Khalili et al 2014a	N=20 (na/na)	T2DM n=10	NGT n=10	2D-DIGE pH 3-11 24cm LC-MS/MS (CyDye)	Up-regulation (8)	
	Vastus lateralis (cell line)				P04792 Heat shock protein beta-1	HSPB1 (HSPB1 HSP27, HSP28)
					P25786 Proteasome subunit alpha type-1	PSA1 (PSMA1 HC2, NU, PROS30, PSC2)
					P25789 Proteasome subunit alpha type-4	PSA4 (PSMA4 HC9, PSC9)
					P49721 Proteasome subunit beta type-2	PSB2 (PSMB2)
					P60900 Proteasome subunit alpha type-6	PSA6 (PSMA6)
					P62195 26S protease regulatory subunit 8	PRS8 (PSMC5 SUG1)
					Q9BT22 Dehydrogenase/reductase SDR family member 4	DHRS4 (DHRS4 SDR25C2, UNQ851/PRO1800)
					Q9UBQ0 Vacuolar protein sorting-associated protein 29	VPS29 (VPS29 DC15, DC7, MDS007)
					Down-regulation (3)	
					O75083 WD repeat-containing protein 1	WDR1 (WDR1)
					P14866 Heterogeneous nuclear ribonucleoprotein L	HNRPL (HNRNPL HNRPL, P/OKcl.14)
					Q13838 Spliceosome RNA helicase DDX39B	DX39B (DDX39B BAT1, UAP56)
Al-Khalili et al 2014b	N=20 (20/0)	T2DM (10/0)	NGT (10/0)	2D-DIGE pH 3-11 24cm LC-MS/MS (CyDye)	Up-regulation (29)	
	Vastus lateralis (cell line)				O75390 Citrate synthase, mitochondrial	CISY (CS)
					O75534 Cold shock domain-containing protein E1	CSDE1 (CSDE1 D1S155E, KIAA0885, NRU, UNR)
					O96008 Mitochondrial import receptor subunit TOM40 homolog	TOM40 (TOMM40 C19orf1, PEREC1, TOM40)
					P13010 X-ray repair cross-complementing protein 5	XRCC5 (XRCC5 G22P2)
					P14061 Estradiol 17-beta-dehydrogenase 1	DHB1 (HSD17B1 E17KSR, EDH17B1, EDH17B2, EDHB17, SDR28C1)
					P14866 Heterogeneous nuclear ribonucleoprotein L	HNRPL (HNRNPL HNRPL, P/OKcl.14)
					P23786 Carnitine O-palmitoyltransferase 2, mitochondrial	CPT2 (CPT2 CPT1)
					P25705 ATP synthase subunit alpha, mitochondrial	ATPA (ATP5A1 ATP5A, ATP5AL2, ATPM)
					P30044 Peroxiredoxin-5, mitochondrial	PRDX5 (PRDX5 ACR1, SBBI10)
					P31040 Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	SDHA
					P34897 Serine hydroxymethyltransferase, mitochondrial	GLYM (SHMT2)
					P38117 Electron transfer flavoprotein subunit beta	ETFB (ETFB FP585)
					P40926 Malate dehydrogenase, mitochondrial	MDHM (MDH2)
					P42765 3-ketoacyl-CoA thiolase, mitochondrial	THIM (ACAA2)
					P47897 Glutamine--tRNA ligase	SYQ (QARS)
					P49411 Elongation factor Tu, mitochondria	EFTU (TUFM)
					P49748 Very long-chain specific acyl-CoA dehydrogenase, mitochondrial	ACADV (ACADVL)
					P50213 Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial	IDH3A (IDH3A)
					P83111 Serine beta-lactamase-like protein LACTB, mitochondrial	LACTB (LACTB MRPL56, UNQ843/PRO1781)
					Q02809 Procollagen-lysine,2-oxoglutarate 5-dioxygenase 1	PLOD1 (PLOD1 LLH, PLOD)
					Q12906 Interleukin enhancer-binding factor 3	ILF3 (ILF3 DRBF, MPHOSPH4, NF90)
					Q12931 Heat shock protein 75 kDa, mitochondrial	TRAP1 (TRAP1 HSP75)
					Q13263 Transcription intermediary factor 1-beta	TIF1B (TRIM28 KAP1, RNF96, TIF1B)
					Q14191 Werner syndrome ATP-dependent helicase	WRN (WRN RECO3, RECQL2)
					Q92499 ATP-dependent RNA helicase DDX1	DDX1 (DDX1)
					Q92945 Far upstream element-binding protein 2	FUBP2 (KHSPRP FUBP2)
					Q99798 Aconitate hydratase, mitochondrial	ACON (ACO2)
					Q9HCC0 Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial	MCCB (MCCC2)
					Q9NSD9 Phenylalanine--tRNA ligase beta subunit	SYFB (FARSB FARSLB, FRSB, HSPC173)
					Down-regulation (18)	
					P04792 Heat shock protein beta-1	HSPB1 (HSPB1 HSP27, HSP28)
					P06733 Alpha-enolase	ENOA (ENO1 ENO1L1, MBPB1, MPB1)
					P07900 Heat shock protein HSP 90-alpha	HSP90A (HSP90AA1 HSP90A, HSPC1, HSPCA)
					P09211 Glutathione S-transferase P	GSTP1 (GSTP1 FAEES3, GST3)
					P13797 Plastin-3	PLST (PLS3)
					P16152 Carbonyl reductase [NADPH] 1	CBR1 (CBR1)
					P28161 Glutathione S-transferase Mu 2	GSTM2 (GSTM2 GST4)
					P30084 Enoyl-CoA hydratase, mitochondrial	ECHM (ECHS1)
					P30711 Glutathione S-transferase theta-1	GSTT1 (GSTT1)

					P35080	Profilin-2	PROF2 (PFN2)
					P60981	Destrin	DEST (DSTN ACTDP, DSN)
					P61086	Ubiquitin-conjugating enzyme E2 K	UBE2K (UBE2K HIP2, LIG)
					P62937	Peptidyl-prolyl cis-trans isomerase A	PPIA (PPIA CYPA)
					P82279	Protein crumbs homolog 1	CRUM1 (CRB1)
					Q16555	Dihydropyrimidinase-related protein 2	DPYL2 (DPYSL2 CRMP2, ULIP2)
					Q99497	Protein deglycase DJ-1	PARK7
					Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3	SH3L3 (SH3BGR13 P1725)
					Q9Y617	Phosphoserine aminotransferase	SERC (PSAT1 PSA)
Caruso et al	N=22 (14/8)	OCs (pre-DM)	LCs	1D-SDS-PAGE	Up-regulation (9)		
2014		n=7 (5/2)	n=8 (5/3)	HPLC-MS/MS	O14732	Inositol monophosphatase 2	IMPA2 (IMPA2 IMP.18P)
	Vastus lateralis biopsy	age 44 ± 4 y	age 46 ± 4 y		P19474	E3 ubiquitin-protein ligase TRIM21	RO52 (TRIM21 RNF81, RO52, SSA1)
		BMI 32.5 ± 1.4 kg.m ⁻²	BMI 23.2 ± 0.5 kg.m ⁻²		P21980	Protein-glutamine gamma-glutamyltransferase 2	TGM2 (TGM2)
					P27986	Phosphatidylinositol 3-kinase regulatory subunit alpha	P85A (PIK3R1 GRB1)
		T2DM			P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform	2AAA (PPP2R1A)
		n=7 (4/3)			P62753	40S ribosomal protein S6	RS6 (RPS6 OK/SW-cl.2)
		age 53 ± 4 y			P62993	Growth factor receptor-bound protein 2	GRB2 (GRB2 ASH)
		BMI 32.8 ± 1.5 kg.m ⁻²			P67775	Serine/threonine-protein phosphatase 2A catalytic subunit alpha isoform	PP2AA (PPP2CA/B)
					Q13061	Triadin	TRDN (TRDN)
					Down-regulation (4)		
					O75083	WD repeat-containing protein 1	WDR1 (WDR1)
					P05091	Aldehyde dehydrogenase, mitochondrial	ALDH2 (ALDH2 ALDM)
					P33176	Kinesin-1 heavy chain	KINH (KIF5B KNS, KNS1)
					Q92901	60S ribosomal protein L3-like	RL3L (RPL3L)
Hussey	N = 12 (8/4) at rest	T2DM	Control	1D-SDS-PAGE (4-20%)	Up-regulation (2)		
2013		n = 6 (4/2)	n = 6 (4/2)		P02765	Alpha-2-HS-glycoprotein	FETUA (AHSG FETUA, PRO2743)
	Vastus lateralis	age 54 ± 4 y	age 48 ± 2 y	HPLC-MS/MS	P02787	Serotransferrin	TF (TRFE)
		BMI 29 ± 2 kg.m ⁻²	BMI 28 ± 3 kg.m ⁻²		Down-regulation (13)		
					P00403	Cytochrome c oxidase subunit 2	COX2 (MT-CO2 COII, COXII, MTCO2)
					P00505	Aspartate aminotransferase, mitochondrial	AATM (GOT2)
					P12882	Myosin-1	MYH1 (MYH1)
					P15121	Aldose reductase	ALDR (AKR1B1 ALDR1)
					P17174	Aspartate aminotransferase, cytoplasmic	AATC (GOT1)
					P24539	ATP synthase F(0) complex subunit B1, mitochondrial	ATP5F1 (ATP5F1)
					P25705	ATP synthase subunit alpha, mitochondrial	ATPA (ATP5A1 ATP5A, ATP5AL2, ATPM)
					P40926	Malate dehydrogenase, mitochondrial	MDHM (MDH2)
					Q13011	Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	ECH1
					Q7Z4W1	L-xylulose reductase	DCXR (DCXR SDR20C1)
					Q8N335	Glycerol-3-phosphate dehydrogenase 1-like protein	GPD1L (GPD1L KIAA0089)
					Q99623	Prohibitin-2	PHB2 (PHB2 BAP, REA)
					Q9UDW1	Cytochrome b-c1 complex subunit 9	UCR9 (UQCR10 UCR1, HSPC119)