Data-processing formula

Before performing the meta-analysis, the extracted data were converted to appropriate forms. For

the SELENOP concentration, data were expressed as the means and standard deviations (SDs). The

formula for the conversion of standard error (SE) to SD is

$$SD = SE \times \sqrt{n}, \tag{S1}$$

with n being the sample size [1]. For studies reporting the medians and interquartile range (IQR),

the medians were converted to means using

$$mean \approx \left(0.7 + \frac{0.39}{n}\right)\frac{q_1 + q_3}{2} + \left(0.3 - \frac{0.39}{n}\right)m, \tag{S2}$$

where q_1 is the first quartile, q_3 is the third quartile, and m is the median [2]. The IQR was

converted to SD using

$$SD \approx \frac{q_3 - q_1}{2\emptyset^{-1}(\frac{0.75n - 0.125}{n + 0.25})}, \tag{S3}$$

where Φ^{-1} is the inverse of the cumulative standard normal distribution [3,4]. For data expressed as

the geometric mean and SD, an online calculator

(https://www.rapidtables.com/calc/math/Log_Calculator.html) was used to find the antilog with

the base 10. The formula

$$r = 2\sin\left(r_s \times \frac{\pi}{6}\right), \tag{S4}$$

was used to convert the rho data reported as the Spearman correlation coefficient into the Pearson

correlation coefficient (PCC) (where r is the PCC and r_s is Spearman's rho) [5]. Finally, for the

original report and the converted correlation coefficient r values, the formula listed below

$$Fisher's\ Z = 0.5 \times ln\frac{1+r}{1-r}, \tag{S5}$$

was used to calculate the Fisher's Z value [6]. The summary Fisher's Z value (presented as the

effect size (ES) and 95% confidence interval in the forest plot) was obtained by the inverse

variance method [7]. Then, formula

$$summary\ r = \frac{e^{2Z} - 1}{e^{2Z} + 1}, (Z \text{ is summary Fisher's } Z \text{ value}) \tag{S6}$$

was used to convert the value of summary r [6], which was used to comprehensively evaluate the

correlation between SELENOP and glucose and lipid metabolism indicators. The degree of

correlation was judged by the range of absolute value: < 0.3 indicates poor correlation, 0.31–0.49 indicates moderate correlation, and ≥ 0.50 indicates strong correlation.
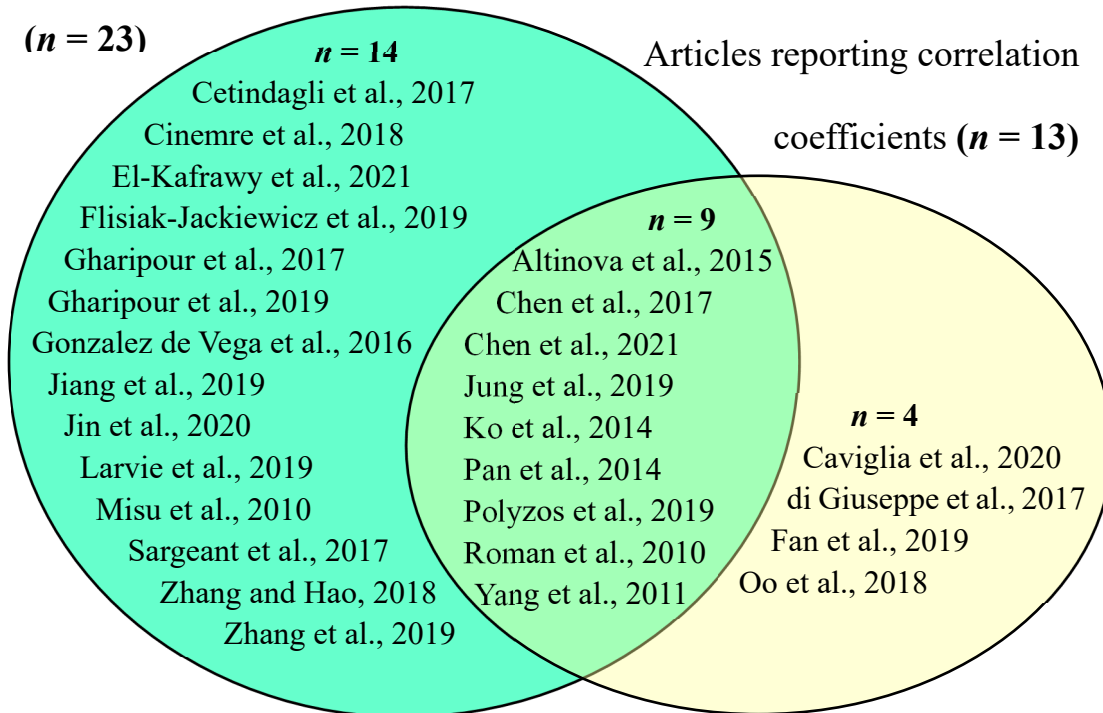
Articles reporting concentrations

(n = 23)

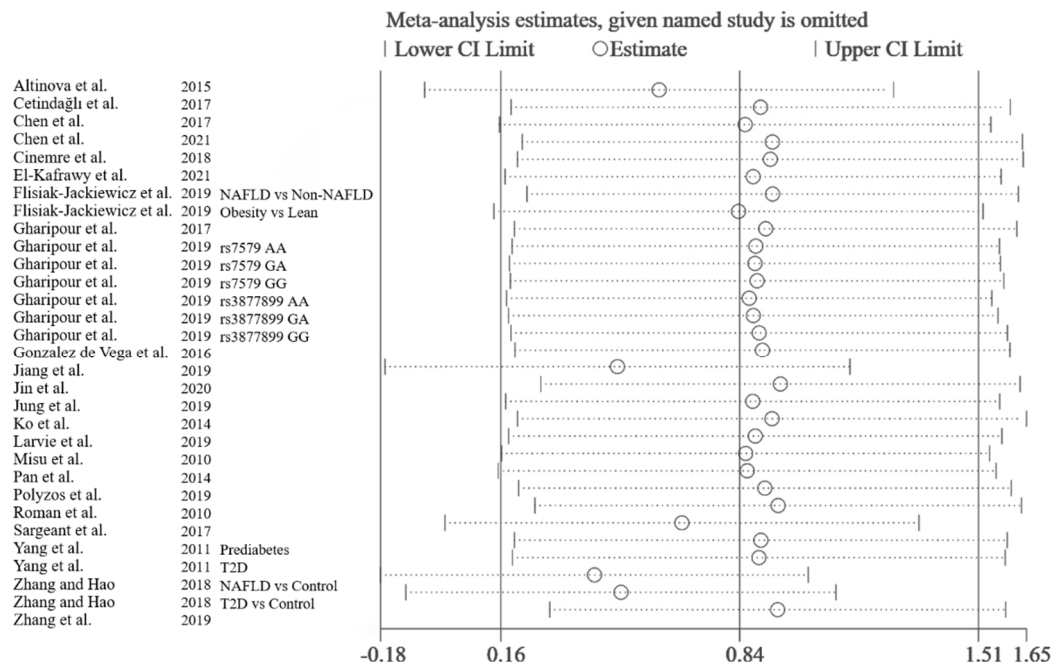**n = 14**

Cetindagli et al., 2017
Cinemre et al., 2018
El-Kafrawy et al., 2021
Flisiak-Jackiewicz et al., 2019
Gharipour et al., 2017
Gharipour et al., 2019
Gonzalez de Vega et al., 2016
Jiang et al., 2019
Jin et al., 2020
Larvie et al., 2019
Misu et al., 2010
Sargeant et al., 2017
Zhang and Hao, 2018
Zhang et al., 2019

Articles reporting correlation coefficients **(n = 13)**

n = 9

Altinova et al., 2015
Chen et al., 2017
Chen et al., 2021
Jung et al., 2019
Ko et al., 2014
Pan et al., 2014
Polyzos et al., 2019
Roman et al., 2010
Yang et al., 2011

n = 4
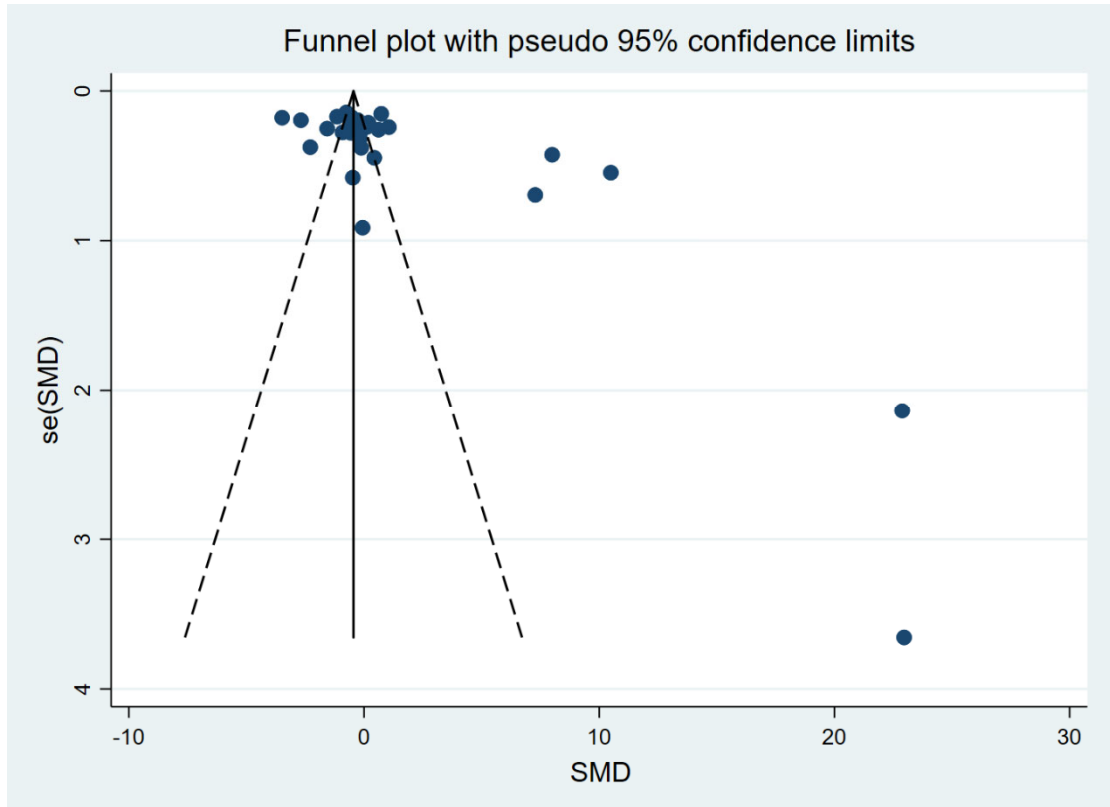
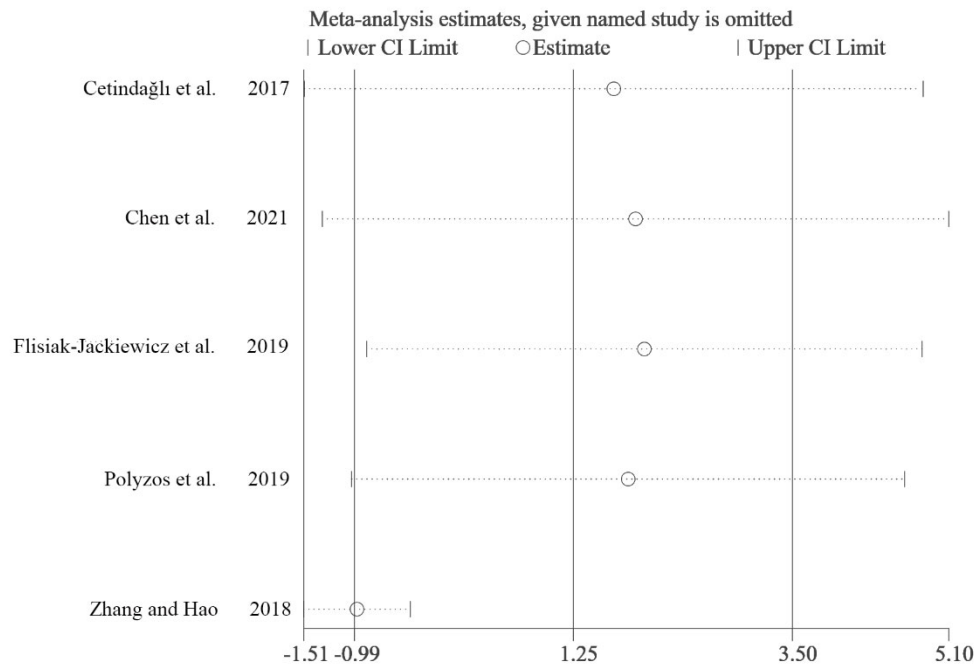Caviglia et al., 2020
di Giuseppe et al., 2017
Fan et al., 2019
Oo et al., 2018

Supplementary Figure S1. Articles reporting the concentrations and/or correlation coefficients of selenoprotein P.

Meta-analysis estimates, given named study is omitted

| Lower CI Limit   ○Estimate | Upper CI Limit

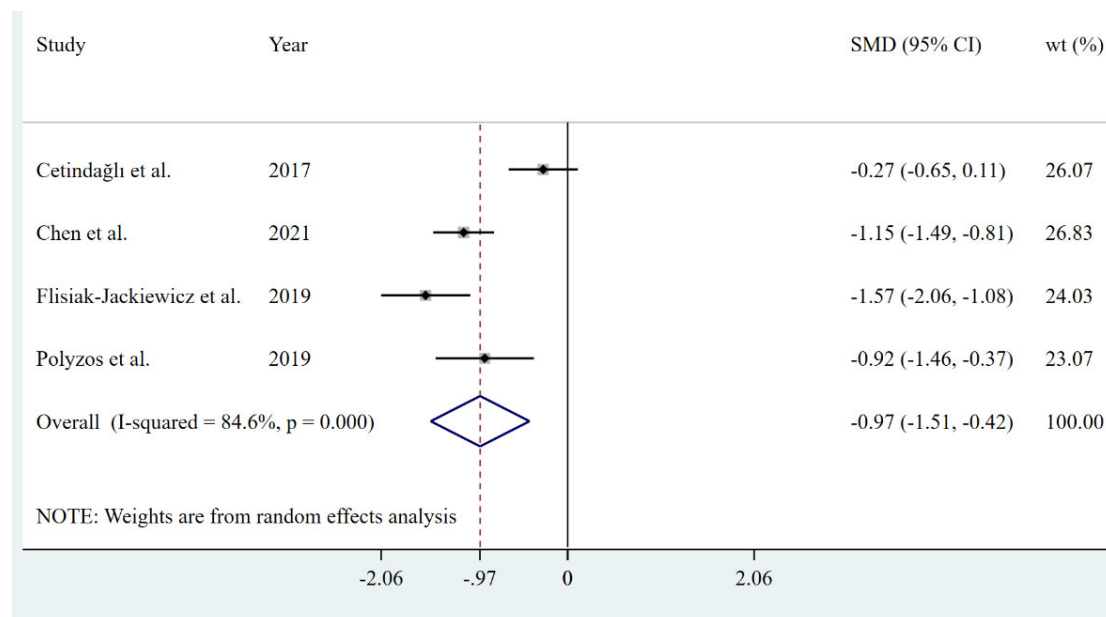|	
Altinova et al.	2015
Cetindağlı et al.	2017
Chen et al.	2017
Chen et al.	2021
Cinemre et al.	2018
El-Kafrawy et al.	2021
Flisiak-Jackiewicz et al.	2019 NAFLD vs Non-NAFLD
Flisiak-Jackiewicz et al.	2019 Obesity vs Lean
Gharipour et al.	2017
Gharipour et al.	2019 rs7579 AA
Gharipour et al.	2019 rs7579 GA
Gharipour et al.	2019 rs7579 GG
Gharipour et al.	2019 rs3877899 AA
Gharipour et al.	2019 rs3877899 GA
Gharipour et al.	2019 rs3877899 GG
Gonzalez de Vega et al.	2016
Jiang et al.	2019
Jin et al.	2020
Jung et al.	2019
Ko et al.	2014
Larvie et al.	2019
Misu et al.	2010
Pan et al.	2014
Polyzos et al.	2019
Roman et al.	2010
Sargeant et al.	2017
Yang et al.	2011 Prediabetes
Yang et al.	2011 T2D
Zhang and Hao	2018 NAFLD vs Control
Zhang and Hao	2018 T2D vs Control
Zhang et al.	2019

-0.18   0.16   0.84   1.51 1.65

Supplementary Figure S2. Sensitivity analysis of the association between selenoprotein P and metabolic disorders of glucose and lipids. NAFLD, non-alcoholic fatty liver disease; T2D, type 2 diabetes.
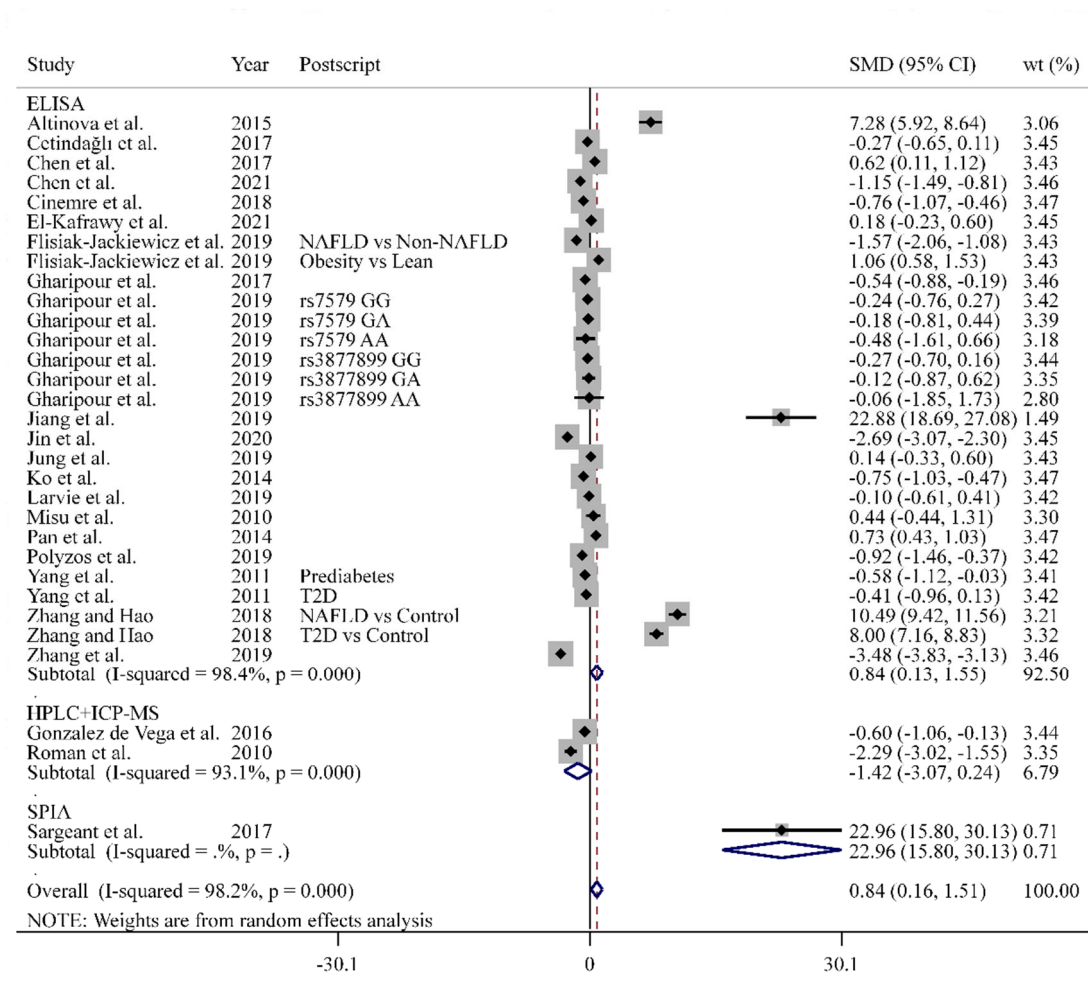
Supplementary Figure S3. Funnel plot of the meta-analysis of the association between selenoprotein P and metabolic disorders of glucose and lipids. SMD, standardized mean difference.
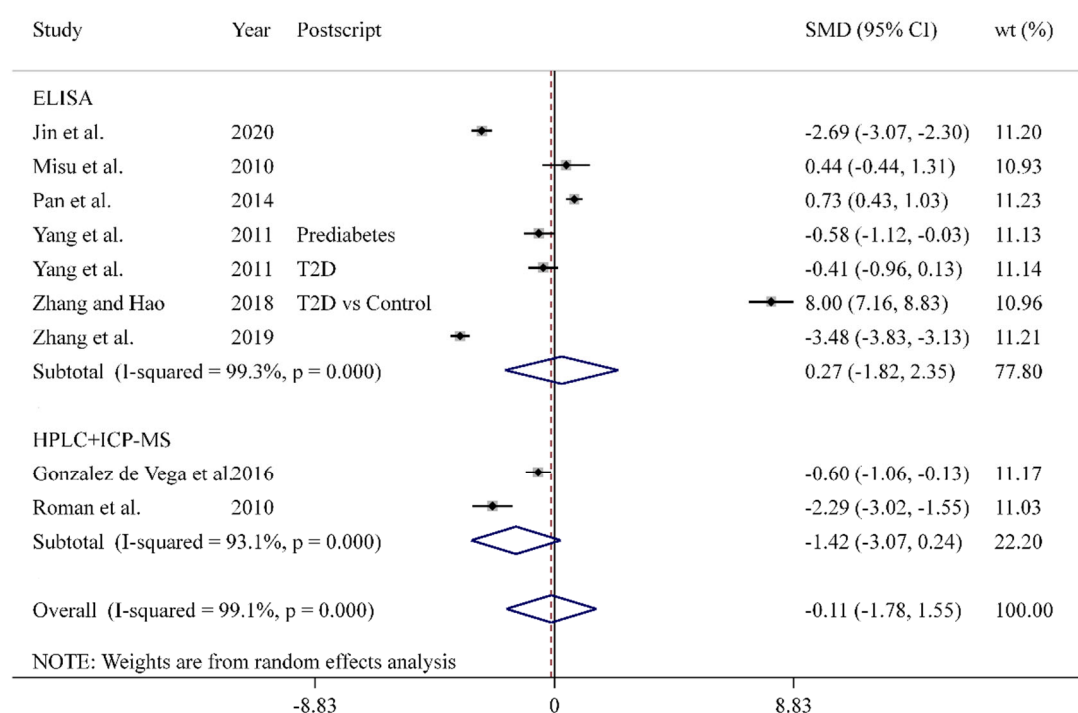

Supplementary Figure S4. Sensitivity analysis of the selenoprotein P level in non-alcoholic fatty liver disease or healthy control patients.

Study	Year		SMD (95% CI)	wt (%)
Cetindağlı et al.	2017		-0.27 (-0.65, 0.11)	26.07
Chen et al.	2021		-1.15 (-1.49, -0.81)	26.83
Flisiak-Jackiewicz et al.	2019		-1.57 (-2.06, -1.08)	24.03
Polyzos et al.	2019		-0.92 (-1.46, -0.37)	23.07
Overall (I-squared = 84.6%, p = 0.000)			-0.97 (-1.51, -0.42)	100.00

NOTE: Weights are from random effects analysis
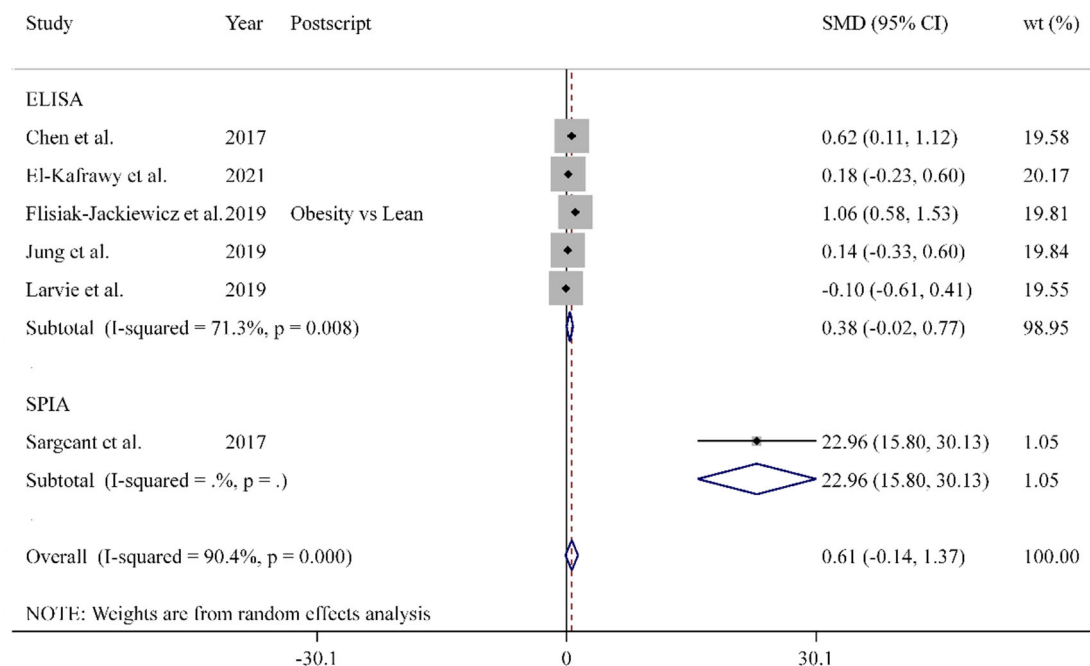
-2.06   -.97   0   2.06

Supplementary Figure S5. Forest plot of the selenoprotein P level in non-alcoholic fatty liver disease or healthy control patients after the exclusion of one study. For each study, the length of a line parallel to the horizontal axis represents the corresponding range of the 95% CI for the adjusted SMD of the central estimate, a black diamond centered in a grey square on the line indicates the effect estimate, and the size of the grey square represents the weight. The vertical dashed line represents the summary SMD, with its 95% CI represented by the width of a hollow diamond. CI, confidence interval; SMD, standardized mean difference; wt, weight.

Study	Year	Postscript	SMD (95% CI)	wt (%)
ELISA				
Altinova et al.	2015		7.28 (5.92, 8.64)	3.06
Cetindağlı et al.	2017		-0.27 (-0.65, 0.11)	3.45
Chen et al.	2017		0.62 (0.11, 1.12)	3.43
Chen et al.	2021		-1.15 (-1.49, -0.81)	3.46
Cinemre et al.	2018		-0.76 (-1.07, -0.46)	3.47
El-Kafrawy et al.	2021		0.18 (-0.23, 0.60)	3.45
Flisiak-Jackiewicz et al.	2019	NAFLD vs Non-NAFLD	-1.57 (-2.06, -1.08)	3.43
Flisiak-Jackiewicz et al.	2019	Obesity vs Lean	1.06 (0.58, 1.53)	3.43
Gharipour et al.	2017		-0.54 (-0.88, -0.19)	3.46
Gharipour et al.	2019	rs7579 GG	-0.24 (-0.76, 0.27)	3.42
Gharipour et al.	2019	rs7579 GA	-0.18 (-0.81, 0.44)	3.39
Gharipour et al.	2019	rs7579 AA	-0.48 (-1.61, 0.66)	3.18
Gharipour et al.	2019	rs3877899 GG	-0.27 (-0.70, 0.16)	3.44
Gharipour et al.	2019	rs3877899 GA	-0.12 (-0.87, 0.62)	3.35
Gharipour et al.	2019	rs3877899 AA	-0.06 (-1.85, 1.73)	2.80
Jiang et al.	2019		22.88 (18.69, 27.08)	1.49
Jin et al.	2020		-2.69 (-3.07, -2.30)	3.45
Jung et al.	2019		0.14 (-0.33, 0.60)	3.43
Ko et al.	2014		-0.75 (-1.03, -0.47)	3.47
Larvie et al.	2019		-0.10 (-0.61, 0.41)	3.42
Misu et al.	2010		0.44 (-0.44, 1.31)	3.30
Pan et al.	2014		0.73 (0.43, 1.03)	3.47
Polyzos et al.	2019		-0.92 (-1.46, -0.37)	3.42
Yang et al.	2011	Prediabetes	-0.58 (-1.12, -0.03)	3.41
Yang et al.	2011	T2D	-0.41 (-0.96, 0.13)	3.42
Zhang and Hao	2018	NAFLD vs Control	10.49 (9.42, 11.56)	3.21
Zhang and Hao	2018	T2D vs Control	8.00 (7.16, 8.83)	3.32
Zhang et al.	2019		-3.48 (-3.83, -3.13)	3.46
Subtotal (I-squared = 98.4%, p = 0.000)			0.84 (0.13, 1.55)	92.50
HPLC+ICP-MS				
Gonzalez de Vega et al.	2016		-0.60 (-1.06, -0.13)	3.44
Roman et al.	2010		-2.29 (-3.02, -1.55)	3.35
Subtotal (I-squared = 93.1%, p = 0.000)			-1.42 (-3.07, 0.24)	6.79
SPIA				
Sargeant et al.	2017		22.96 (15.80, 30.13)	0.71
Subtotal (I-squared = .%, p = .)			22.96 (15.80, 30.13)	0.71
Overall (I-squared = 98.2%, p = 0.000)			0.84 (0.16, 1.51)	100.00

NOTE: Weights are from random effects analysis

-30.1   0   30.1

Supplementary Figure S6. Subgroup analysis based on the selenoprotein P detection method for total participants. For each study, the length of a line parallel to the horizontal axis represents the corresponding range of the 95% CI for the adjusted SMD of the central estimate, a black diamond centered in a grey square on the line indicates the effect estimate, and the size of the grey square represents the weight. The vertical dashed line represents the summary SMD with its 95% CI represented by the width of a hollow diamond. CI, confidence interval; ELISA, enzyme-linked immunosorbent assay; HPLC, high-performance liquid chromatography; ICP-MS, inductively coupled plasma-mass spectrometry; NAFLD, non-alcoholic fatty liver disease; SMD, standardized mean difference; SPIA, sol particle homogeneous immunoassay; T2D, type 2 diabetes; wt, weight.

Study	Year	Postscript		SMD (95% CI)	wt (%)
ELISA					
Jin et al.	2020			-2.69 (-3.07, -2.30)	11.20
Misu et al.	2010			0.44 (-0.44, 1.31)	10.93
Pan et al.	2014			0.73 (0.43, 1.03)	11.23
Yang et al.	2011	Prediabetes		-0.58 (-1.12, -0.03)	11.13
Yang et al.	2011	T2D		-0.41 (-0.96, 0.13)	11.14
Zhang and Hao	2018	T2D vs Control		8.00 (7.16, 8.83)	10.96
Zhang et al.	2019			-3.48 (-3.83, -3.13)	11.21
Subtotal (I-squared = 99.3%, p = 0.000)				0.27 (-1.82, 2.35)	77.80
HPLC+ICP-MS					
Gonzalez de Vega et al.	2016			-0.60 (-1.06, -0.13)	11.17
Roman et al.	2010			-2.29 (-3.02, -1.55)	11.03
Subtotal (I-squared = 93.1%, p = 0.000)				-1.42 (-3.07, 0.24)	22.20
Overall (I-squared = 99.1%, p = 0.000)				-0.11 (-1.78, 1.55)	100.00
NOTE: Weights are from random effects analysis					

-8.83   0   8.83

Supplementary Figure S7. Subgroup analysis based on the selenoprotein P detection method for T2D. For each study, the length of a line parallel to the horizontal axis represents the corresponding range of the 95% CI for the adjusted SMD of the central estimate, a black diamond centered in a grey square on the line indicates the effect estimate, and the size of the grey square represents the weight. The vertical dashed line represents the summary SMD with its 95% CI represented by the width of a hollow diamond. CI, confidence interval; ELISA, enzyme-linked immunosorbent assay; HPLC, high-performance liquid chromatography; ICP-MS, inductively coupled plasma-mass spectrometry; SMD, standardized mean difference; T2D, type 2 diabetes; wt, weight.

Study	Year	Postscript	SMD (95% CI)	wt (%)
ELISA				
Chen et al.	2017		0.62 (0.11, 1.12)	19.58
El-Kafrawy et al.	2021		0.18 (-0.23, 0.60)	20.17
Flisiak-Jackiewicz et al.	2019	Obesity vs Lean	1.06 (0.58, 1.53)	19.81
Jung et al.	2019		0.14 (-0.33, 0.60)	19.84
Larvie et al.	2019		-0.10 (-0.61, 0.41)	19.55
Subtotal (I-squared = 71.3%, p = 0.008)			0.38 (-0.02, 0.77)	98.95
SPIA				
Sargeant et al.	2017		22.96 (15.80, 30.13)	1.05
Subtotal (I-squared = .%, p = .)			22.96 (15.80, 30.13)	1.05
Overall (I-squared = 90.4%, p = 0.000)			0.61 (-0.14, 1.37)	100.00
NOTE: Weights are from random effects analysis				

-30.1   0   30.1

Supplementary Figure S8. Subgroup analysis based on the selenoprotein P detection method for obesity. For each study, the length of a line parallel to the horizontal axis represents the corresponding range of the 95% CI for the adjusted SMD of the central estimate, a black diamond centered in a grey square on the line indicates the effect estimate, and the size of the grey square represents the weight. The vertical dashed line represents the summary SMD with its 95% CI represented by the width of a hollow diamond. CI, confidence interval; ELISA, enzyme-linked immunosorbent assay; SMD, standardized mean difference; SPIA, sol particle homogeneous immunoassay; wt, weight.

Supplementary Table S1. Characteristics of the included studies (with indicators and correlation coefficients supplementing Table 1).

Study [a]	Disease	n		Level [b]		Indicator	Correlation coefficient [c]
		Case	Control	Case	Control		
*Altinova et al., 2015[8]	GD	30	35	6.2 (4.5–8.2) ♦	7.9 (4.5–10.7) ♦	HDLC	0.43$^{€}$
						BMI	−0.28$^{€}$
*Caviglia et al., 2020[9]	NAFLD	57			T3: 11.8	HOMA-IR	0.26$^{€}$
						FPG	−0.05$^{€}$
						FIns	0.28$^{€}$
#Cetindağlı et al., 2017[10]	NAFLD	93	37	1574.2 ± 972.1 ♠	232.7 ± 371.05 ♠	–	–
*Chen et al., 2017[11]	OW/OB	34	29	52.3 ± 39.1 ♠	14.5 ± 12.8 ♠	TG	0.48$^{£}$
						TC	0.37$^{£}$
						LDLC	0.35$^{£}$
						BMI	0.55$^{£}$
						HOMA-IR	0.37$^{£}$
						FIns	0.36$^{£}$
#Chen et al., 2021[12]	NAFLD	79	79	13.4 ± 7.0 ♠	11.1 ± 7.1 ♠	TG	0.175$^{£}$
						TC	0.184$^{€}$
						HDLC	−0.001$^{€}$
						LDLC	0.16$^{£}$
						BMI	0.287$^{£}$
						HOMA-IR	−0.019$^{€}$
						FPG	0.15$^{€}$
#Cinemre et al., 2018[13]	GD	86	90	35.29 ± 3.00 ♣	46.98 ± 4.59 ♣	–	–
*di Giuseppe et al.,	MetS	Q1: 225; Q2: 227;			Q1: 2.86 (1.96–3.70) ♦;	TG	−0.3$^{€}$

Study [a]	Disease	n		Level [b]		Indicator	Correlation coefficient [c]
		Case	**Control**	**Case**	**Control**		
2017[14]		Q3: 228; Q4: 225			Q2: 4.52 (3.87–5.98) ♦;	TC	0.09[ϵ]
					Q3: 6.05 (5.32–8.47) ♦;	HDLC	0.41[ϵ]
					Q4: 11.72 (8.07–15.79) ♦	LDLC	–0.01[ϵ]
						FPG	–0.15[ϵ]
						HbA1c	–0.13[ϵ]
*El-Kafrawy et al., 2021[15]	OW/OB	50	40	16.18 ± 3.99 ♣	4.25 ± 4.27 ♣	–	–
*Fan et al., 2019[16]	T2D and NAFLD	T2D and NAFLD: 79; T2D: 61		T2D and NAFLD: 1341.11 ± 290.51 ♣; T2D: 755.77 ± 184.90 ♣		TG	–0.149[£]
						TC	–0.106[£]
						HDLC	0.054[£]
						LDLC	0.218[£]
						BMI	0.152[£]
						HOMA-IR	0.613[£]
						FPG	0.03[£]
						FIns	0.018[£]
*Flisiak-Jackiewicz et al., 2019[17]	NAFLD	34	52	19449.5 (13327–28058) ♦	21629 (10369.5–27976) ♦	–	–
	Obesity	86	24	21421 (11566–28058) ♦	5411 (1618–15135) ♦	–	–
*Gharipour et al., 2017[18]	MetS	65	71	41.8 ± 6.57 ♣	81.5 ± 15.2 ♣	–	–
#Gharipour et al., 2019[19]	MetS	rs7579 GG: 29	30	55.52 ± 16.78 ♣	109.48 ± 29.78 ♣	–	–
		rs7579 GA: 18	22	36.65 ± 7.41 ♣	59.80 ± 22.06 ♣	–	–
		rs7579 AA: 8	5	29.45 ± 1.97 ♣	26.65 ± 2.51 ♣	–	–
		rs3877899 GG: 40	44	40.37 ± 8.44 ♣	83.91 ± 21.33 ♣	–	–
		rs3877899 GA: 15	13	56.92 ± 23.34 ♣	86.42 ± 40.99 ♣	–	–

Study [a]	Disease	n		Level [b]		Indicator	Correlation coefficient [c]
		Case	Control	Case	Control		
		rs3877899 AA: 2	3	29.70 ± 4.1 ♠	81.95 ± 107.03 ♠	–	–
[#]Gonzalez de Vega et al., 2016[20]	T2D	78	24	41.9 ± 12.6 ♠	50.5 ± 19.1 ♠	–	–
[#]Jiang et al., 2019[21]	GD	30	30	4.85 ± 1.02 ♠	2.43 ± 1.04 ♠	–	–
[#]Jin et al., 2020[22]	DN	100	100	673.18 ± 86.94 ♠	973.84 ± 132.27 ♠	–	–
[*]Jung et al., 2019[23]	OW/OB	35	35	2.3 ± 0.1 ♠	1.5 ± 0.1 ♠	BMI	0.506£
[*]Ko et al., 2014[24]	MetS	94	116	16.7 ± 2.2 ♥	28.6 ± 2.0 ♥	TG	–0.322£
						TC	–0.038£
						HDLC	0.217£
						BMI	–0.342£
						HOMA-IR	–0.222£
						FPG	0.038£
						FIns	–0.238£
[*]Larvie et al., 2019[25]	OW/OB	32	27	352.13 (276, 446) ♥	360.77 (290, 450) ♥	–	–
[*]Misu et al., 2010[26]	T2D	12	9	6.7 ± 0.9 ♠	5.1 ± 1.7 ♠	–	–
[*]Oo et al., 2018[27]	HG	76		Baseline: 2.51 ± 0.52 ♠		TG	0.004€
						BMI	–0.042€
						HOMA-IR	–0.041€
						FPG	0.194€
						HbA1c	0.113€
						FIns	–0.079€
				4-year follow-up: 3.81 ± 0.60 ♠		BMI	–0.021€
						HOMA-IR	–0.14€
						FPG	0.303€

Study [a]	Disease	n		Level [b]		Indicator	Correlation coefficient [c]
		Case	Control	Case	Control		
						HbA1c	0.164^{ϵ}
						FIns	-0.205^{ϵ}
*Pan et al., 2014[28]	T2D	156	64	3.77 ± 1.79 ♣	2.34 ± 2.30 ♣	TG	$0.239^{\pounds}$
						HDLC	$-0.344^{\pounds}$
						BMI	$0.42^{\pounds}$
						HOMA-IR	$0.445^{\pounds}$
						FPG	$0.202^{\pounds}$
						FIns	$0.401^{\pounds}$
*Polyzos et al., 2019[29]	NAFLD	31	27	SS: 4.2 ± 0.3 ♣;	5 ± 0.2 ♣	BMI	-0.42^{ϵ}
				Borderline NASH: 4.1 ± 0.4 ♣;		HOMA-IR	-0.43^{ϵ}
				Definite NASH: 3.0 ± 0.5 ♣		FPG	-0.45^{ϵ}
						FIns	-0.38^{ϵ}
*Roman et al., 2010[30]	T2D	40	15	58 ± 9 ♣	56 ± 8 ♣	TG	0.1^{ϵ}
						TC	$0.07^{\pounds}$
						HDLC	0.07^{ϵ}
						BMI	-0.06^{ϵ}
						FPG	0.02^{ϵ}
						HbA1c	-0.08^{ϵ}
*Sargeant et al., 2017[31]	OW/OB	11	11	2.81 ± 0.30 ♣	3.01 ± 0.39 ♣	–	–
*Yang et al., 2011[32]	T2D	40	20	1032.4 (495.9–2149.4) ♦;	62.0 (252.5–694.5) ♦	TG	0.343^{ϵ}
						TC	0.07^{ϵ}
	PD	40		867.3 (516.3–1582.7) ♦		HDLC	-0.168^{ϵ}
						LDLC	0.064^{ϵ}

Study [a]	Disease	n		Level [b]		Indicator	Correlation coefficient [c]
		Case	Control	Case	Control		
						BMI	0.259^{ϵ}
						HOMA-IR	0.378^{ϵ}
						FPG	0.335^{ϵ}
						HbA1c	0.264^{ϵ}
[#]Zhang and Hao, 2018[33]	T2D	100	100	3.05 ± 1.20 ♠	2.33 ± 2.30 ♠	–	–
	NAFLD	100	100	4.42 ± 1.80 ♠	2.33 ± 2.30 ♠	–	–
[#]Zhang et al., 2019[34]	T2D	176	142	1811.1 ± 36.3 ♣	1688.2 ± 40.5 ♣	–	–

Note: BMI, body mass index; DN, diabetic nephropathy; ELISA, enzyme-linked immunosorbent assay; FIns, fasting insulin; FPG, fasting plasma glucose; GD, gestational diabetes; HbA1c, hemoglobin A1c; HDLC, high-density lipoprotein cholesterol; HG, hyperglycemia; HOMA-IR, homeostasis model assessment of insulin resistance; HPLC, high-performance liquid chromatography; ICP-MS, inductively coupled plasma-mass spectrometry; LDLC, low-density lipoprotein cholesterol; MetS, metabolic syndrome; NAFLD, non-alcoholic fatty liver disease; NASH, non-alcoholic steatohepatitis; OW/OB, overweight and obesity; PD, prediabetes; SS: simple steatosis; SPIA, sol particle homogeneous immunoassay; T2D, type 2 diabetes; TC, total cholesterol; TG, triglyceride; n, sample size number; -, the data or information were unavailable.

[a] *, cross-sectional study; #, case-control study. [11] adjusted for BMI, age, and sex; [14] adjusted for age, sex, physical activity, education, smoking status, alcohol consumption, and C-reactive protein; [19] adjusted for age, sex, smoking, and nutrition; [24]adjusted for sex, physical activity, sleep duration, paternal education level, high-sensitivity C-reactive protein, homeostasis model assessment of insulin resistance, and alanine aminotransferase; [29] adjusted for age, sex, log (ALT), and WC; [32] adjusted for age and sex; [34] adjusted for BMI.

[b] Data were expressed as quartiles (Q1/2/3/4), tertiles (T1/2/3), medians (interquartile ranges) (♦), means ± SDs (♠), means ± SEs (♣), or geometric means ± SDs (♥) for all subjects or patients vs. controls.

[c] €, Spearman correlation coefficients; £, Pearson correlation coefficients.

Supplementary Table S2. The methodological quality evaluation of the included articles using the modified Newcastle–Ottawa scale

Article	Selection [a,b]			Comparability	Outcome [b]		Score	Quality of study
	Representativeness of samples	Sample size	Ascertainment of exposure		Assessment of the outcome	Statistical test		
Altinova et al., 2015[8]	**		√	√	√	√	9	High
Caviglia et al., 2020[9]	*		√	√c	√	√	7	High
Cetindağli et al., 2017[10]	*	√	√	√	√	√	9	High
Chen et al., 2017[11]	**		√	√	√	√	9	High
Chen et al., 2021[12]	**	√	√	√	√	√	10	High
Cinemre et al., 2018[13]	**	√	√	√c	√	√	9	High
di Giuseppe et al., 2017[14]	**	√	√	√	√	√	10	High
El-Kafrawy et al., 2021[15]	*		√	√	√	√	8	High
Fan et al., 2019[16]	*		√	√	√	√	8	High
Flisiak-Jackiewicz et al., 2019[17]	*		√	–	√	√	6	Moderate
Gharipour et al., 2017[18]	**		√	√	√	√	9	High
Gharipour et al., 2019[19]	*	√	√	√	√	√	9	High
Gonzalez de Vega et al., 2016[20]	**	√	√	–	√	√	8	High
Jiang et al., 2019[21]	*	√	√	√	√	√	9	High
Jin et al., 2020[22]	*	√	√	√	√	√	9	High
Jung et al., 2019[23]	**		√	√	√	√	9	High
Ko et al., 2014[24]	**	√	√	√	√	√	10	High
Larvie et al., 2019[25]	**	√	√	√	√	√	10	High
Misu et al., 2010[26]	*		√	√	√	√	8	High
Oo et al., 2018[27]	**	√	√	–	√	√	8	High

Article	Selection [a,b] Representativeness of samples	Sample size	Ascertainment of exposure	Comparability	Outcome [b] Assessment of the outcome	Statistical test	Score	Quality of study
Pan et al., 2014[28]	**		√	√[c]	√	√	8	High
Polyzos et al., 2019[29]	*		√	√	√	√	8	High
Roman et al., 2010[30]	*		√	√	√	√	8	High
Sargeant et al., 2017[31]		√	√	√	√	√	8	High
Yang et al., 2011[32]	**		√	√	√	√	9	High
Zhang and Hao, 2018[33]	*	√	√	√[c]	√	√	8	High
Zhang et al., 2019[34]	**	√	√	√	√	√	10	High

[a] * moderate and ** high representativeness of sample.

[b] √: Justified and satisfactory sample size, clearly ascertained exposure, comparable subjects in different outcome groups and controlled confounding factors, clearly assessed outcome, or clearly described and appropriate statistical test. - : Controlling of the confounding factors not mentioned.

[c] Only the most important factors were controlled.

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