

Supplementary Materials

Table S1. Diet composition.

	STD ^a -C/-FG	STD ^a - ω 3/-FG+ ω 3	^b HFHS-C/-FG	^b HFHS- ω 3/-FG+ ω 3
Flour (g)	1000 ^a	1000 ^a	1000 ^b	1000 ^b
Porcine gelatin (g)	25	25	25	25
Soybean lecithin (g)	6	6	22	22
Oil (mL)	19 mL soybean	19 mL EPA:DHA 1:1	24 mL soybean	24 mL EPA:DHA 1:1
Protein (% weight)	16.4	16.4	21.7	21.7
Fat (% weight)	6.2	6.2	24.1	24.1
Carbohydrates (% weight)	46.6	46.6	45.0	45.0
Total energy density (kcal/g)	3.1	3.1	4.8	4.8

^aTeklad Global 14% Protein Rodent Maintenance Diet (Envigo, IN, USA). ^bTD.08811 45% Kcal Fat Diet (Envigo, IN, USA). STD (standard diet), HFHS (high-fat high-sucrose diet), ω 3 (supplementation with fish oil); FG (supplementation with D-Fagomine).

Table S2. Fatty acid composition of each diet (chow + supplement). Results are expressed as a percentage of total fatty acids (mg/100mg of Total FA).

FATTY ACIDS	STD-C/-FG	STD- ω 3/-FG+ ω 3	HFHS-C/-FG	HFHS- ω 3/-FG+ ω 3
14:00	0.0	0.1	11.5	11.6
16:00	14.8	14.6	32.2	32.0
16:1 ω 7	0.0	0.1	1.7	1.7
18:00	2.9	2.9	13.7	13.7
18:1 ω 9	20.5	20.3	26.4	26.2
18:1 ω 7	0.0	0.0	0.7	0.7
18:2 ω 6	58.6	57.8	9.7	8.7
20:00	n.d.	0.0	n.d.	0.0
18:3 ω 3	2.9	2.9	1.1	1.1
20:1 ω 9	0.0	0.0	0.0	0.0
18:4 ω 3	0.0	0.0	0.0	0.0
20:2 ω 6	0.0	0.0	0.0	0.0
20:3 ω 6	n.d.	0.0	n.d.	0.0
20:4 ω 6	0.0	0.0	0.0	0.0
22:1 ω 11	0.0	0.0	0.0	0.0
22:1 ω 9	0.0	0.0	0.0	0.0
20:4 ω 3	0.0	0.0	0.0	0.0
20:5 ω 3	0.0	0.4	0.0	0.5
24:1 ω 9	0.0	0.0	0.0	0.0
22:5 ω 3	0.0	0.1	0.0	0.1
22:6 ω 3	0.0	0.4	0.0	0.6
ω 3	3.3	3.2	1.6	1.4
ω 6	58.8	58.9	10.4	10.6
ω 6/ ω 3	17.8	18.4	6.5	7.6
SFAs	17.5	18.3	59.4	60.5
MUFAs	21.1	20.3	29.3	28.4
PUFAs	61.1	61.0	10.8	10.7
EPA/DHA	-	1/1	-	1/1.2

¹ STD (standard diet), HFHS (high-fat high-sucrose diet), ω 3 (supplementation with fish oil); FG (supplementation with D-Fagomine); SFAs (saturated fatty acids); MUFAs (monounsaturated fatty acids); PUFAs (polyunsaturated fatty acids); EPA (eicosapentaenoic fatty acid); DHA (docosahexaenoic fatty acid).

Table S3. Carbonylated proteins identified by nanoLC-MS/MS in kidney. Carbonylation index calculated for each protein in each diet are also showed. Protein Spot No. refers to the numbered spots in 2D gels shown in Figure S2.

Spot N°	Protein ID	Gene Name	Avg. Mass	UniProtKB code	STD-C	STD-FG	STD- ω 3	STD-FG+ ω 3	HFHS-C	HFHS-FG	HFHS- ω 3	HFHS-FG+ ω 3
1	Phosphatidylethanolamine-binding protein 1 OS=Rattus norvegicus OX=10116 GN=Pebp1 PE=1 SV=3	Pebp1	20801	P31044 PEBP1_RAT	1.02 ^c (0.01)	1.14 ^c (0.14)	0.97 ^c (0.17)	1.07 ^c (0.25)	1.51 ^{ab} (0.01)	1.58 ^a (0.13)	1.11 ^c (0.02)	1.17 ^{bc} (0.06)
2	Superoxide dismutase [Mn] mitochondrial OS=Rattus norvegicus OX=10116 GN=Sod2 PE=1 SV=2	Sod2	24674	P07895 SODM_RAT	1.88(0.50)	1.86(0.22)	1.94(0.58)	1.85(0.17)	2.03(0.44)	1.97(0.15)	2.12(0.22)	2.03(0.12)
3	Glutathione S-transferase alpha-3 OS=Rattus norvegicus OX=10116 GN=Gsta3 PE=1 SV=3	Gsta3	25319	P04904 GSTA3_RAT	0.36(0.10)	0.38(0.21)	0.37(0.17)	0.34(0.23)	0.38(0.09)	0.35(0.13)	0.38(0.10)	0.37(0.12)
	Glutathione S-transferase P OS=Rattus norvegicus OX=10116 GN=Gstp1 PE=1 SV=2	Gstp1	23439	P04906 GSTP1_RAT								
	Glutathione S-transferase alpha-4 OS=Rattus norvegicus OX=10116 GN=Gsta4 PE=1 SV=2	Gsta4	25510	P14942 GSTA4_RAT								
4	Peroxisomal trans-2-enoyl-CoA reductase OS=Rattus norvegicus OX=10116 GN=Pecr PE=2 SV=1	Pecr	32433	Q9WVK3 PECR_RAT	0.71(0.22)	0.73(0.25)	0.73(0.31)	0.72(0.34)	0.71(0.18)	0.59(0.15)	0.72(0.15)	0.72(0.20)
5	Triosephosphate isomerase OS=Rattus norvegicus OX=10116 GN=Tpi1 PE=1 SV=2	Tpi1	26849	P48500 TPIS_RAT	0.54 ^{abc} (0.13)	0.29 ^c (0.07)	0.37 ^{abc} (0.06)	0.29 ^c (0.08)	0.62 ^a (0.16)	0.35 ^{bc} (0.00)	0.61 ^{ab} (0.02)	0.33 ^c (0.11)
	Electron transfer flavoprotein subunit beta OS=Rattus norvegicus OX=10116 GN=Etfb PE=1 SV=3	Etfb	27687	Q68FU3 ETFB_RAT								
6	Enoyl-CoA delta isomerase 1 mitochondrial OS=Rattus norvegicus OX=10116 GN=Eci1 PE=1 SV=1	Eci1	32254	P23965 ECI1_RAT	0.50 ^{ab} (0.01)	0.36 ^{bc} (0.02)	0.47 ^{abc} (0.05)	0.28 ^c (0.08)	0.57 ^a (0.08)	0.36 ^{bc} (0.03)	0.56 ^a (0.13)	0.44 ^{abc} (0.07)
7	Carbonic anhydrase 2 OS=Rattus norvegicus OX=10116 GN=Ca2 PE=1 SV=2	Ca2	29114	P27139 CAH2_RAT	0.95 ^b (0.06)	0.87 ^b (0.06)	0.90 ^b (0.06)	0.92 ^b (0.18)	1.87 ^a (0.29)	1.70 ^a (0.29)	1.50 ^a (0.19)	1.49 ^a (0.14)
8	Omega-amidase NIT2 OS=Rattus norvegicus OX=10116 GN=Nit2 PE=1 SV=1	Nit2	30701	Q497B0 NIT2_RAT	0.62(0.24)	0.57(0.31)	0.61(0.22)	0.56(0.42)	0.66(0.35)	0.55(0.29)	0.67(0.16)	0.66(0.04)
9	3-hydroxyisobutyrate dehydrogenase mitochondrial OS=Rattus norvegicus OX=10116 GN=Hibadh PE=1 SV=3	Hibadh	35303	P29266 3HIDH_RAT	0.62(0.24)	0.60(0.34)	0.61(0.28)	0.60(0.34)	0.60(0.30)	0.53(0.25)	0.63(0.17)	0.62(0.10)
10	Malate dehydrogenase cytoplasmic OS=Rattus norvegicus OX=10116 GN=Mdh1 PE=1 SV=3	Mdh1	36483	O88989 MDHC_RAT	0.27(0.08)	0.31(0.19)	0.43(0.03)	0.32(0.37)	0.27(0.06)	0.23(0.05)	0.28(0.12)	0.12(0.04)
11	Actin cytoplasmic 1 OS=Rattus norvegicus OX=10116 GN=Actb PE=1 SV=1	Actb	41737	P60711 ACTB_RAT	0.19 ^b (0.04)	0.22 ^{ab} (0.09)	0.21 ^{ab} (0.14)	0.20 ^b (0.08)	0.58 ^a (0.15)	0.56 ^{ab} (0.20)	0.37 ^{ab} (0.22)	0.26 ^{ab} (0.04)
12	Heat shock cognate 71 kDa protein OS=Rattus	Hspa8	70871	P63018 HSP7C_RAT	0.64 ^{ab} (0.26)	0.66 ^{ab} (0.29)	0.63 ^{ab} (0.17)	0.56 ^b (0.20)	1.39 ^a (0.37)	1.16 ^{ab} (0.32)	0.90 ^{ab} (0.35)	0.86 ^{ab} (0.057)

13	norvegicus OX=10116 GN=Hspa8 PE=1 SV=1 Fructose-bisphosphate aldolase B OS=Rattus norvegicus OX=10116 GN=Aldob PE=1 SV=2	Aldob	39618	P00884 ALDOB_RAT	0.31 ^{cd} (0.03)	0.23 ^d (0.05)	0.25 ^d (0.06)	0.24 ^d (0.07)	0.85 ^a (0.13)	0.61 ^b (0.01)	0.50 ^b (0.02)	0.45 ^{bc} (0.02)
14	Aspartate aminotransferase mitochondrial OS=Rattus norvegicus OX=10116 GN=Got2 PE=1 SV=2	Got2	47314	P00507 AATM_RAT	0.79(0.08)	0.75(0.33)	0.75(0.35)	0.71(0.41)	1.17(0.21)	0.97(0.18)	0.83(0.19)	0.83(0.09)
15	Malate dehydrogenase mitochondrial OS=Rattus norvegicus OX=10116 GN=Mdh2 PE=1 SV=2	Mdh2	35684	P04636 MDHM_RAT	0.28(0.16)	0.28(0.23)	0.28(0.11)	0.27(0.11)	0.34(0.06)	0.28(0.05)	0.39(0.18)	0.39(0.10)
16	Glyceraldehyde-3-phosphate dehydrogenase OS=Rattus norvegicus OX=10116 GN=Gapdh PE=1 SV=3	Gapdh	35828	P04797 G3P_RAT	0.36 ^{bc} (0.04)	0.18 ^d (0.10)	0.25 ^{cd} (0.03)	0.17 ^d (0.04)	0.79 ^a (0.01)	0.67 ^a (0.01)	0.46 ^b (0.08)	0.48 ^b (0.07)
17	Hydroxyacyl-coenzyme A dehydrogenase mitochondrial OS=Rattus norvegicus OX=10116 GN=Hadh PE=2 SV=1	Hadh	34448	Q9WVK7 HCDH_RAT	0.46 ^{abc} (0.17)	0.25 ^c (0.03)	0.32 ^{bc} (0.07)	0.32 ^{bc} (0.069)	0.79 ^a (0.09)	0.65 ^{ab} (0.08)	0.56 ^{abc} (0.22)	0.68 ^a (0.16)
18	Hydroxyacid oxidase 2 OS=Rattus norvegicus OX=10116 GN=Hao2 PE=1 SV=2	Hao2	39201	Q07523 HAOX2_RAT	0.38 ^b (0.07)	0.36 ^b (0.15)	0.34 ^b (0.10)	0.34 ^b (0.087)	0.72 ^a (0.09)	0.72 ^a (0.09)	0.49 ^{ab} (0.12)	0.46 ^{ab} (0.10)
19	Aflatoxin B1 aldehyde reductase member 2 OS=Rattus norvegicus OX=10116 GN=Akr7a2 PE=1 SV=2	Akr7a2	40675	Q8CG45 ARK72_RAT	0.64(0.17)	0.61(0.14)	0.65(0.08)	0.57(0.28)	0.69(0.14)	0.65(0.22)	0.52(0.01)	0.54(0.07)
20	Aldo-keto reductase family 1 member A1 OS=Rattus norvegicus OX=10116 GN=Akr1a1 PE=1 SV=2	Akr1a1	36506	P51635 AK1A1_RAT	0.45 ^b (0.14)	0.42 ^b (0.22)	0.21 ^b (0.10)	0.39 ^b (0.14)	1.35 ^a (0.16)	1.30 ^a (0.21)	0.49 ^b (0.15)	0.45 ^b (0.18)
21	Sorbitol dehydrogenase OS=Rattus norvegicus OX=10116 GN=Sord PE=1 SV=4	Sord	38235	P27867 DHSO_RAT	0.51 ^{bcd} (0.09)	0.33 ^{cd} (0.11)	0.30 ^d (0.01)	0.29 ^d (0.01)	0.92 ^a (0.10)	0.70 ^{ab} (0.05)	0.57 ^{bc} (0.14)	0.55 ^{bc} (0.09)
22	Aspartate aminotransferase cytoplasmic OS=Rattus norvegicus OX=10116 GN=Got1 PE=1 SV=3	Got1	46429	P13221 AATC_RAT	0.45 ^c (0.10)	0.44 ^c (0.14)	0.70 ^{bc} (0.01)	0.39 ^c (0.18)	1.09 ^a (0.22)	0.10 ^{ab} (0.12)	0.44 ^c (0.05)	0.43 ^c (0.07)
23	Isocitrate dehydrogenase [NADP] cytoplasmic OS=Rattus norvegicus OX=10116 GN=Idh1 PE=1 SV=1	Idh1	46734	P41562 IDHC_RAT	0.26 ^c (0.09)	0.24 ^c (0.04)	0.55 ^b (0.03)	0.26 ^c (0.06)	0.98 ^a (0.25)	0.46 ^{bc} (0.00)	0.68 ^b (0.08)	0.56 ^b (0.05)
24	Aminoacylase-1A OS=Rattus norvegicus OX=10116 GN=Acy1a PE=1 SV=1	Acy1a	45804	Q6AYS7 ACY1A_RAT	0.48 ^a (0.22)	0.49 ^a (0.29)	0.45 ^a (0.29)	0.46 ^a (0.35)	0.85 ^a (0.22)	0.86 ^a (0.04)	0.65 ^a (0.29)	0.64 ^a (0.10)
25	Aldehyde dehydrogenase mitochondrial OS=Rattus norvegicus OX=10116 GN=Aldh2 PE=1 SV=1	Aldh2	56488	P11884 ALDH2_RAT	0.48 ^a (0.19)	0.42 ^a (0.21)	0.45 ^a (0.29)	0.42 ^a (0.09)	0.71 ^a (0.05)	0.58 ^a (0.03)	0.70 ^a (0.05)	0.53 ^a (0.07)
	4-trimethylaminobutyraldehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh9a1 PE=1 SV=1	Aldh9a1	53653	Q9JLJ3 AL9A1_RAT								
26	Serum albumin OS=Rattus norvegicus OX=10116 GN=Alb PE=1 SV=2	Alb	68731	P02770 ALBU_RAT	0.47 ^{cd} (0.05)	0.39 ^d (0.21)	0.66 ^{abc} (0.06)	0.60 ^{bcd} (0.02)	0.87 ^a (0.02)	0.74 ^{ab} (0.02)	0.42 ^d (0.02)	0.42 ^d (0.07)
27	Protein disulfide-isomerase A3 OS=Rattus norvegicus OX=10116 GN=Pdia3 PE=1 SV=2	Pdia3	56623	P11598 PDIA3_RAT	0.40 ^{abc} (0.08)	0.73 ^a (0.07)	0.38 ^{bc} (0.16)	0.36 ^c (0.13)	0.43 ^{abc} (0.16)	0.36 ^{bc} (0.12)	0.41 ^{abc} (0.17)	0.71 ^{ab} (0.03)
	Alpha-aminoadipic semialdehyde dehydrogenase OS=Rattus norvegicus OX=10116 GN=Aldh7a1 PE=1	Aldh7a1	58749	Q64057 AL7A1_RAT								

SV=2													
28	Glutamate dehydrogenase 1 mitochondrial OS=Rattus norvegicus OX=10116 GN=Glud1 PE=1 SV=2	Glud1	61416	P10860 DHE3_RAT	0.43 ^{abc} (0.03)	0.27 ^{cd} (0.09)	0.33 ^{bcd} (0.12)	0.23 ^d (0.12)	0.62 ^a (0.04)	0.49 ^{ab} (0.01)	0.46 ^{abc} (0.04)	0.41 ^{bcd} (0.01)	
29	Alanine--glyoxylate aminotransferase 2 mitochondrial OS=Rattus norvegicus OX=10116 GN=Agxt2 PE=1 SV=2	Agxt2	57201	Q64565 AG_RAT	0.38(0.08)	0.37(0.07)	0.41(0.19)	0.40(0.17)	0.40(0.08)	0.38(0.02)	0.41(0.11)	0.40(0.02)	
30	Retinal dehydrogenase 1 OS=Rattus norvegicus OX=10116 GN=Aldh1a1 PE=1 SV=3	Aldh1a1	54459	P51647 AL1A1_RAT	0.75 ^a (0.09)	0.55 ^a (0.39)	0.62 ^a (0.14)	0.63 ^a (0.36)	1.17 ^a (0.21)	1.06 ^a (0.03)	0.81 ^a (0.08)	0.78 ^a (0.22)	
31	Succinyl-CoA:3-ketoacid coenzyme A transferase 1 mitochondrial OS=Rattus norvegicus OX=10116 GN=Oxct1 PE=1 SV=1	Oxct1	56204	B2GV06 SCOT1_RAT	0.60 ^a (0.12)	0.38 ^a (0.06)	0.41 ^a (0.06)	0.34 ^a (0.04)	0.71 ^a (0.25)	0.40 ^a (0.04)	0.69 ^a (0.20)	0.69 ^a (0.15)	
	Dihydrolipoyl dehydrogenase mitochondrial OS=Rattus norvegicus OX=10116 GN=Dld PE=1 SV=1	Dld	54038	Q6P6R2 DLDH_RAT									
	Methylmalonate-semialdehyde dehydrogenase [acylating] mitochondrial OS=Rattus norvegicus OX=10116 GN=Aldh6a1 PE=1 SV=1	Aldh6a1	57808	Q02253 MMSA_RAT									
32	Catalase OS=Rattus norvegicus OX=10116 GN=Cat PE=1 SV=3	Cat	59757	P04762 CATA_RAT	0.46 ^b (0.16)	0.31 ^b (0.16)	0.26 ^b (0.09)	0.27 ^b (0.08)	0.89 ^a (0.16)	0.60 ^{ab} (0.09)	0.51 ^b (0.11)	0.51 ^b (0.10)	
	Triokinase/FMN cyclase OS=Rattus norvegicus OX=10116 GN=Tkfc PE=1 SV=1	Tkfc	59444	Q4KLZ6 TKFC_RAT									
33	Acyl-coenzyme A synthetase ACSM2 mitochondrial OS=Rattus norvegicus OX=10116 GN=Acsm2 PE=2 SV=2	Acsm2	64145	O70490 ACSM2_RAT	0.71 ^b (0.25)	0.66 ^b (0.26)	0.56 ^b (0.49)	0.65 ^b (0.40)	2.06 ^a (0.21)	1.40 ^{ab} (0.25)	1.04 ^b (0.17)	0.75 ^b (0.24)	
	Transketolase OS=Rattus norvegicus OX=10116 GN=Tkt PE=1 SV=1	Tkt	67644	P50137 TKT_RAT									
34	Aconitate hydratase mitochondrial OS=Rattus norvegicus OX=10116 GN=Aco2 PE=1 SV=2	Aco2	85433	Q9ER34 ACON_RAT	0.49(0.00)	0.50(0.24)	0.51(0.16)	0.53(0.41)	0.54(0.13)	0.63(0.08)	0.53(0.27)	0.54(0.07)	
35	Serotransferrin OS=Rattus norvegicus OX=10116 GN=Tf PE=1 SV=3	Tf	76395	P12346 TRFE_RAT	0.22 ^{ab} (0.14)	0.19 ^{ab} (0.04)	0.21 ^{ab} (0.10)	0.19 ^b (0.04)	0.35 ^{ab} (0.08)	0.45 ^a (0.11)	0.35 ^{ab} (0.09)	0.34 ^{ab} (0.08)	
36	Cytoplasmic aconitate hydratase OS=Rattus norvegicus OX=10116 GN=Aco1 PE=1 SV=1	Aco1	98127	Q63270 ACOC_RAT	0.14(0.01)	0.16(0.08)	0.18(0.14)	0.16(0.12)	0.16(0.03)	0.30(0.07)	0.15(0.06)	0.16(0.17)	

¹ Two-way ANOVA analyses were conducted, followed by Tukey HSD's post hoc test. * p<0.05 significant differences given by the factor "diet" (STD and HFHS); § p<0.05 significant differences given by the factor "supplement" (CONTROL, FG, ω-3, FG+ ω-3). Superscript # indicates significant interaction (p<0.05) between the factors diet and supplement. Means with different superscript indicate significant differences (p<0.05) (analyzed by post hoc Tukey HSD).

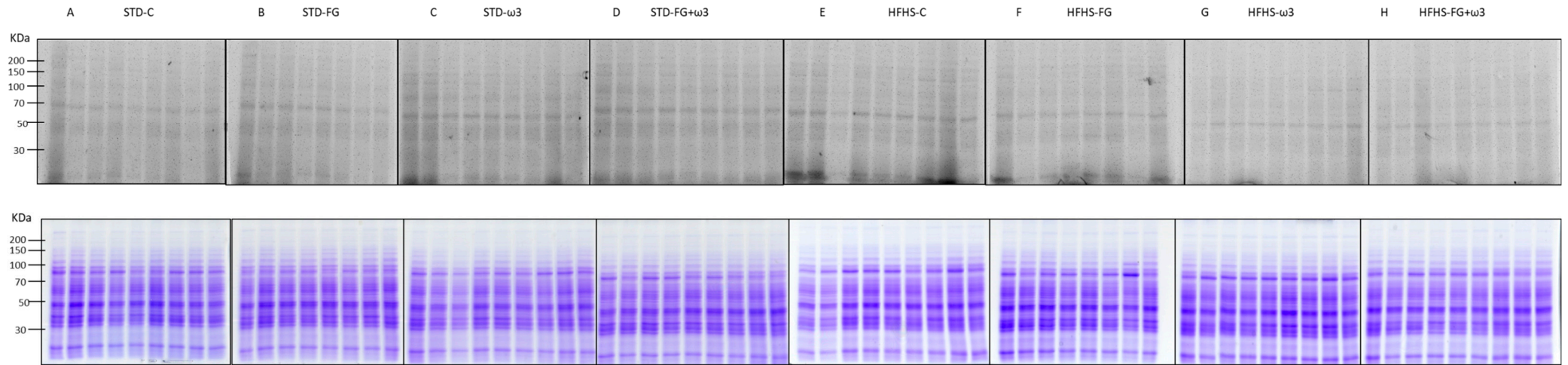


Figure S1. Total proteins carbonylation in rat kidneys. Upper panels show representative images of FTSC-label carbonylated proteins resolved in 1D gels from (A) STD-CONTROL, (B) STD-FG, (C) STD- ω 3, (D) STD-FG+ ω 3, (E) HFHS-CONTROL, (F) HFHS-FG, (G) HFHS- ω 3, (H) HFHS-FG+ ω 3. Lower panels show their corresponding Coomassie stained 1D gels. Images are representatives of three independent labelling experiments performed in triplicates. STD (standard diet), HFHS (high-fat high-sucrose diet), ω 3 (supplementation with fish oil); FG (supplementation with D-Fagomine).

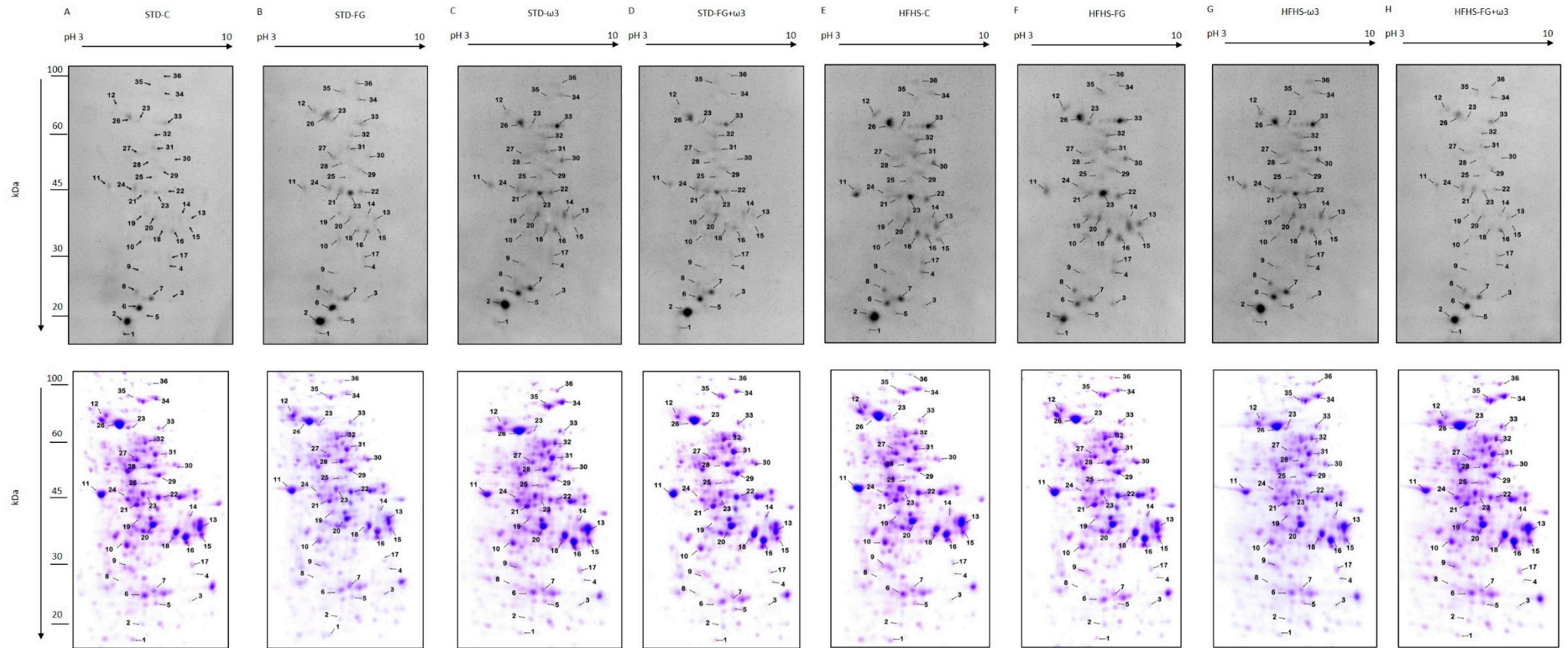


Figure S2. Carbonylated proteins identified in rat kidneys. Upper panels show representative images of FTSC-label carbonylated proteins resolved in 2D gels from (A) STD-CONTROL, (B) STD-FG, (C) STD- ω 3, (D) STD-FG+ ω 3, (E) HFHS-CONTROL, (F) HFHS-FG, (G) HFHS- ω 3, (H) HFHS-FG+ ω 3. Lower panels show their corresponding Coomassie stained 2D gels. Numbered protein spots represent carbonylated proteins confidently identified, and they are listed in Table 5 and Supplementary Table S3. Images are representatives of three independent labelling experiments performed in triplicates. STD (standard diet), HFHS (high-fat high-sucrose diet), ω 3 (supplementation with fish oil); FG (supplementation with D-Fagomine).