

Supplemental Information

**Obesity-Induced Metabolic Stress Leads to Biased
Effector Memory CD4⁺ T Cell Differentiation
via PI3K p110 δ -Akt-Mediated Signals**

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1 **SUPPLEMENTAL INFORMATION**

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3 **SUPPLEMENTAL EXPERIMENTAL PROCEDURES**

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5 ***Determination of abdominal adiposity (android/gynoid ratio)***

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7 Total body DXA scans were acquired using Lunar iDXA (GE Healthcare, Madison,
8 WI). Daily quality control scans were acquired during the study period. All subjects were
9 scanned while wearing a hospital gown with all metal artifacts removed from their body.
10 Trained operators, blinded on patient's identity and clinical history, performed all scans.
11 Patient positioning and data acquisition was conducted in accordance to the operator's
12 manual. Lunar iDXA scans were analyzed with the enCORE software (version 14.0), (GE
13 Healthcare, Madison, WI), (Rothney et al., 2013). Out of total weight, the software allows to
14 discriminate the bone mass, the fat mass and the lean mass. DXA android fat was computed
15 automatically over the DXA android region, a region-of-interest automatically defined by the
16 enCORE software, whose caudal limit is automatically placed at the top of the iliac crest and
17 whose height is set to 20% of the distance from the top of the iliac crest to the base of the
18 skull to define its cephalad limit. DEXA gynoid fat was computed automatically as well, over
19 the DXA gynoid region (percent of fat tissue in inferior half abdominal, glutei and femoral
20 regions); their ratio is automatically determined by the software to give the gender-adjusted
21 measure of abdominal obesity (Rothney et al., 2013).

22

23 ***Lipidomic profile by liquid chromatography-tandem mass spectrometry (LC-MS/MS)***

24

1 All HPLC solvents were MS grade (Carlo Erba); fatty acid internal standards ¹³C-
2 labelled palmitic acid (C16:0) and ¹³C-labelled linoleic acid (C18:2) were purchased from
3 Sigma. Phospholipid standards: C13:0 lysophosphatidylcholines (LPC); C:25:0
4 phosphatidylcholines (PC); C12:0 sphingomyelin (SM); 12:0-13:0 phosphatidylserine (PS);
5 12:0-13:0 phosphatidylinositol (PI); 12:0-13:0 phosphatidylglycerol (PG); 12:0-13:0
6 phosphatidic acid (PA); 12:0-13:0 phosphatidylethanolamine (PE); C12 ceramide (Cer);
7 glucosyl (β) C12 ceramide (GC); lactosyl (β) C12 ceramide (LacCer); C17 mono-sulfo
8 galactosyl-(β)-ceramide (D18:1/17:0; GalCer); were purchased from Avanti Polar Lipids.
9 Quantification of fifteen different fatty acids was performed as previously described
10 (Cermenati et al., 2015). Briefly, samples were homogenized in methanol:acetonitrile (1:1).
11 Aliquots of extracts, after addition of internal standards (¹³C-labelled palmitic and linoleic
12 acids), were subjected to acid hydrolysis and processed as previously described (Cermenati
13 et al., 2015). Fatty acid quantification was performed on a API-4000 triple quadrupole mass
14 spectrometer (AB Sciex) coupled with a HPLC system (Agilent) and CTC PAL HTS auto-
15 sampler (PAL System) using standard curves for each fatty acid analyzed. For the
16 quantification of the different phospholipids, the MS analysis was performed with a flow
17 injection analysis-tandem mass spectrometry (FIA-MS/MS) method. The identity and
18 quantification of the different phospholipids were confirmed using pure standards.
19 Methanolic:acetonitrile extracts were analyzed by a 5 min run in both positive and negative
20 ion mode with a 268 multiple reaction monitoring (MRM) transition in positive mode and 88
21 MRM transition in negative mode. An ESI source connected with an API 4000 triple
22 quadrupole instrument (AB Sciex) was used. The mobile phase was 0.1 % formic acid in
23 MeOH for FIA positive analysis and 5 mM ammonium acetate pH 7 in MeOH for FIA
24 negative. MultiQuant™ software version 3.0.2 was used for data analysis and peak review of
25 chromatograms. Each metabolite level detected was normalized on protein content.

26

27 SUPPLEMENTAL REFERENCES

28

1 Cermenati, G., Audano, M., Giatti, S., Carozzi, V., Porretta-Serapiglia, C., Pettinato, E.,
2 Ferri, C., D'Antonio, M., De Fabiani, E., Crestani, M., *et al.* (2015). Lack of sterol regulatory
3 element binding factor-1c imposes glial Fatty Acid utilization leading to peripheral
4 neuropathy. *Cell metabolism* 21, 571-583.

5 Rothney, M.P., Xia, Y., Wacker, W.K., Martin, F.P., Beaumont, M., Rezzi, S., Giusti, V., and
6 Ergun, D.L. (2013). Precision of a new tool to measure visceral adipose tissue (VAT) using
7 dual-energy X-Ray absorptiometry (DXA). *Obesity (Silver Spring, Md.)* 21, E134-136.

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9 **SUPPLEMENTAL FIGURE AND TABLE LEGENDS**

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11 **Supplemental Figure 1 (related to Figure 1). *In vivo* peritoneal recruitment and**
12 **Rag2KO skin grafts. (A-B)** Schematic of the design **(A)** and timeline **(B)** of the *in vivo*
13 peritoneal recruitment model used in Fig 1A-D. **(C)** Weight gain curves of mice over the 8
14 weeks HFD or CD in C57Bl/6 male recipients and Marilyn female donors. **(D)** Survival curve
15 of C57Bl/6 male skin grafts on HFD or CD Rag2KO female recipients up to 21 days post-
16 transplantation. Also shown is the survival curve following reconstitution of HFD Rag2KO
17 mice with CD4⁺ T cells isolated from Marilyn female mice. **(C-D)** n=3-6 independent mice.
18 **(C)** Values denote mean ± s.e.m. *P<0.05; **P<0.01.

19

20 **Supplemental Figure 2 (related to Figure 2). HFD-induced differentiation of CXCR3⁺-**
21 **LFA1⁺ effector memory-like phenotype in mice and *in vivo* sources of CXCL10. (A-F)**
22 Cell surface staining of CCR7 **(A)**, CD62L **(B)**, CXCR3 **(C)**, LFA1 **(D)**, CD25 **(E)** and CD44
23 **(F)**, in *in vivo*-primed CD4⁺ T cells isolated from pooled lymph nodes of the HFD or CD
24 Marilyn female donor mice used in Fig 1A-D (%). **(G)** Gating strategy defining immune cells
25 tested for expression of CXCL10 in the peritoneal cavity 48 hours after *i.p.* injection of IFN γ
26 (600U/mouse). **(H)** MFI of CXCL10 in the immune cell types defined in G. **(A-F)** n=3-6

1 independent donors. **(H)** n=2 independent mice. **(A-F)** Values denote mean \pm s.e.m.
2 *P<0.05; **P<0.01; *** P<0.001.

3

4 **Supplemental Figure 3 (related to Figure 3). Flow cytometry gating strategy to identify**
5 **CD4⁺ T cell subsets in humans.** Examples of the gating strategy used in an obese **(A)** and
6 a lean **(B)** individual to identify the principal CD4⁺ T cell subsets and some of the T cell
7 subpopulations in the peripheral blood samples of lean, over-weight and obese subjects.

8

9 **Supplemental Figure 4 (related to Figure 3). Body fat distribution association with**
10 **inflammatory T cell subsets and inflammatory mediators. (A-B)** Levels of CRP in the
11 blood of lean, over-weight and obese subjects stratified according to BMI **(A)** and correlation
12 of CRP with effector memory T cells **(B)**. **(C)** Body mass fat distribution of android and
13 gynoid fat within a lean, overweight and obese individual (analysed with body composition by
14 dual-energy X-ray absorptiometry, DEXA). **(D-E)** Correlation of HLADR⁺ **(D)** and CCR5⁺
15 effector memory T cells **(E)** with android/gynoid ratio. **(A-B, D-E)** n=187. ANCOVA, *P<0.05.

16

17 **Supplemental Figure 5 (related to Figure 4). Dendritic cells from HFD-fed mice do not**
18 **affect T cell differentiation. (A)** Dot plots and quantification of *in vitro* proliferation of CFSE-
19 labelled CD4⁺ T cells isolated from pooled lymph nodes of CD Marilyn female mice
20 incubated with CD11c⁺ DC isolated from the spleen of HFD or CD C57Bl/6 male mice for 3
21 days. Undivided and 4th division populations are quantified by dilution of the CFSE-label. **(B)**
22 Dot plots and quantification of *in vivo* proliferation of CFSE-labelled CD4⁺ T cells isolated
23 from pooled lymph nodes of CD Marilyn female *i.v.* injected into C57Bl/6 female recipient
24 mice in combination with CD11c⁺ dendritic cells isolated from the spleen of HFD or CD
25 C57Bl/6 male mice *i.p.* injected for 5 days. Undivided, 1st and 2nd division populations are
26 quantified from the spleen and mesenteric lymph nodes of recipient females by dilution of
27 the CFSE-label. **(C)** Cell surface staining of CD44 and CCR7 in the population of CFSE-
28 labelled CD4⁺ T cells isolated *in vivo* from the spleen and mesenteric lymph nodes of the

1 C57Bl/6 recipient female mice. **(A)** n=3 independent mice (each mouse was tested in
2 triplicate). **(B-C)** n=4 independent mice. Values denote mean \pm s.e.m. *P<0.05; ** P<0.01;
3 ***P<0.001.

4
5 **Supplemental Figure 6 (related to Figures 5 and 6). Mechanistic insights in to**
6 **saturated FA-induced effector memory differentiation of CD4⁺ T cells. (A)** Levels and
7 densitometric quantification of p-Akt (T308), Akt, p-S6 (S235/236) and S6 protein expression
8 in *in vivo*-primed CD4⁺ T cells isolated from mesenteric lymph nodes of CD and HFD mice
9 *i.p.* injected with the PI3K inhibitor IC87114 or left untreated. **(B)** Volcano plot of fatty acids
10 and phospholipids detected in *in vivo*-primed CD4⁺ T cells isolated from mesenteric lymph
11 nodes of CD and HFD mice. Fifteen fatty acids were detected including palmitic acid C16:0;
12 palmitoleic acid C16:1; margaric acid C17:0; stearic acid C18:0; oleic acid C18:1; linoleic
13 acid C18:2; γ -linolenic acid C18:3; arachic acid C20:0; arachidonic acid C20:4;
14 eicosapentaenoic acid C20:5 (EPA); behenic acid C22:0; erucic acid C22:1;
15 docosahexaenoic acid C22:6 (DHA); lignoceric acid C24:0; nervonic acid C24:1. Out of 356
16 phospholipids analyzed (including LysoPC: lysophosphatidylcholine; PC:
17 phosphatidylcholine; PC aa: phosphatidylcholine acyl-acyl; PC ae: phosphatidylcholine acyl-
18 alkyl also known as plasmalogens; PE: phosphatidylethanolamine; PE aa:
19 phosphatidylethanolamine acyl-acyl; PE ae: phosphatidylethanolamine acyl-alkyl also known
20 as plasmalogens; PS: phosphatidylserines; LysoPI: lysophosphatidylinositol; PI:
21 phosphatidylinositol; PG: phosphatidylglycerol; LysoPA: lysophosphatidic acid; PA:
22 phosphatidic acid; SM: sphingomyelin; Cer: ceramide; GCer: glucosyl/galactosyl-ceramide;
23 LacCer: lactosyl-ceramide and gangliosides GM1, GM2 and GM3) 229 different species
24 belonging to different families were detected. The volcano plot displays the relationship
25 between fold-change (expressed as log₂) and significance between the two groups (CD vs.
26 HFD), using a scatter plot view. The y-axis is the negative log₁₀ of p values (a higher value
27 indicates greater significance as indicated by dashed lines) and the x-axis is the difference in
28 levels of metabolites between two experimental groups. Significantly increased metabolites

1 are shown by blue dots while red dots represented those decreased. **(C)** Representative
2 fluorescence images of the aggregation of CTxB signal. **(D)** Levels and densitometric
3 quantification of p-Akt (S473) and Akt protein expression in CD4⁺ T cells isolated from
4 pooled lymph nodes of mice, then activated with plate bound anti-CD3 (0.5µg/ml,
5 ebioscience) and anti-CD28 (2.5µg/ml, ebioscience) for 6hrs in the presence or absence of
6 the Akt activator SC79 (500 nM). **(E)** Levels and densitometric quantification of p-Akt (T308)
7 and Akt protein expression in *in vivo*-primed CD4⁺ T cells isolated from mesenteric lymph
8 nodes of CD mice *i.p.* injected with the Akt activator SC79 or left untreated. **(A, D-E)** Each
9 lane shows data from independent mouse samples. **(B)** n=3 independent mice. Values
10 denote mean ± s.e.m. *P<0.05; **P<0.01.

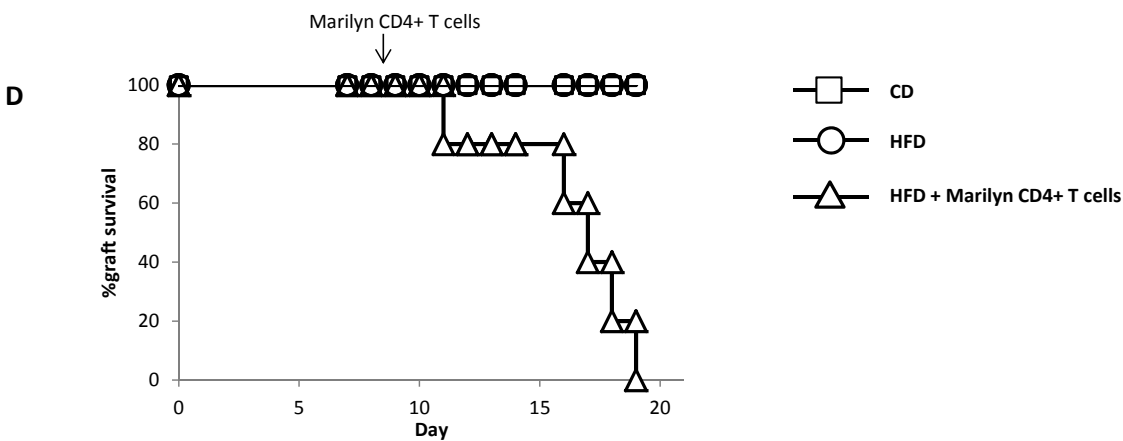
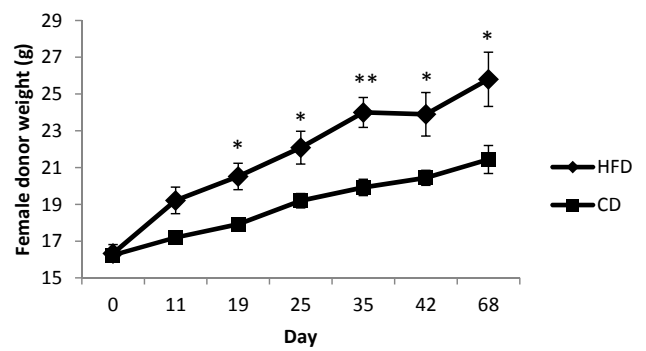
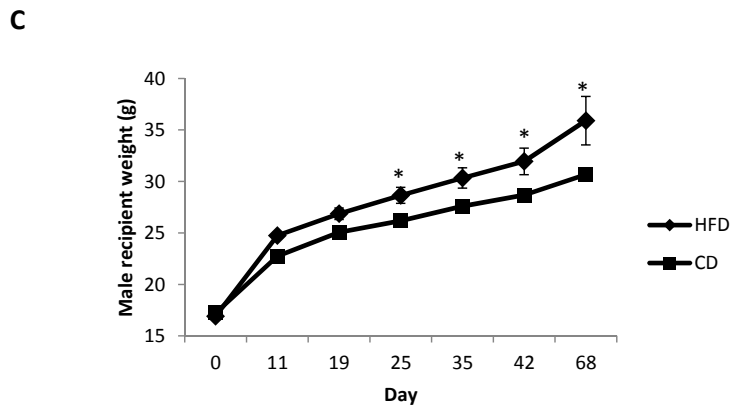
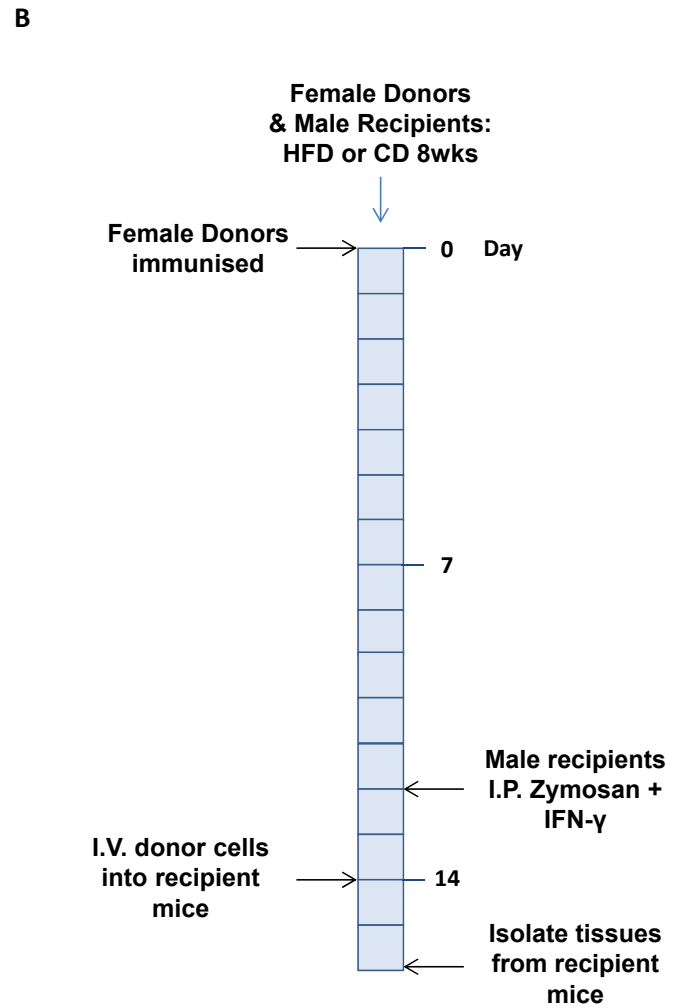
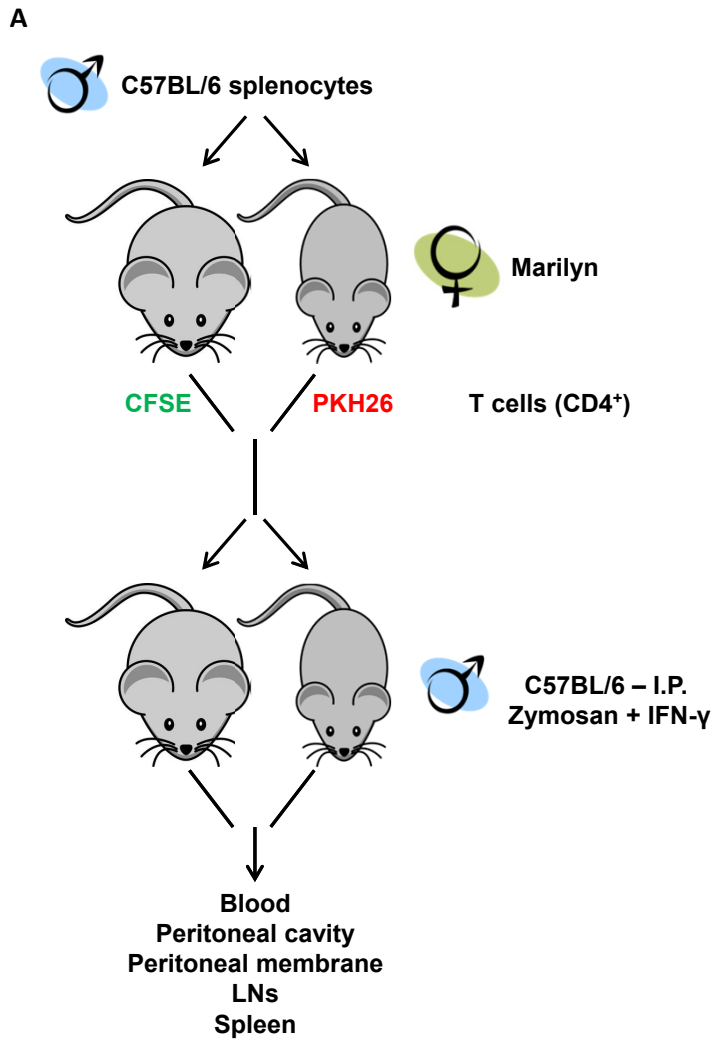
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12 **Supplemental Table 1 (related to Figure 3). Parameters analysed in the n=1,172**
13 **subjects selected.** All the variables were non-normally distributed (Kolmogorov-Smirnov
14 test). Median (Interquartile-Range, IQR) are presented for each variable across subjects
15 divided into lean (BMI< 25 Kg/m²), overweight (BMI≥ 25 Kg/m²) and obese (BMI < 30
16 Kg/m²). Grubb's test was performed for detection of outliers (below and above 1.5*IQR) for
17 each distribution. P is derived from Analysis of covariance (ANCOVA) adjusting for age,
18 gender and therapies.

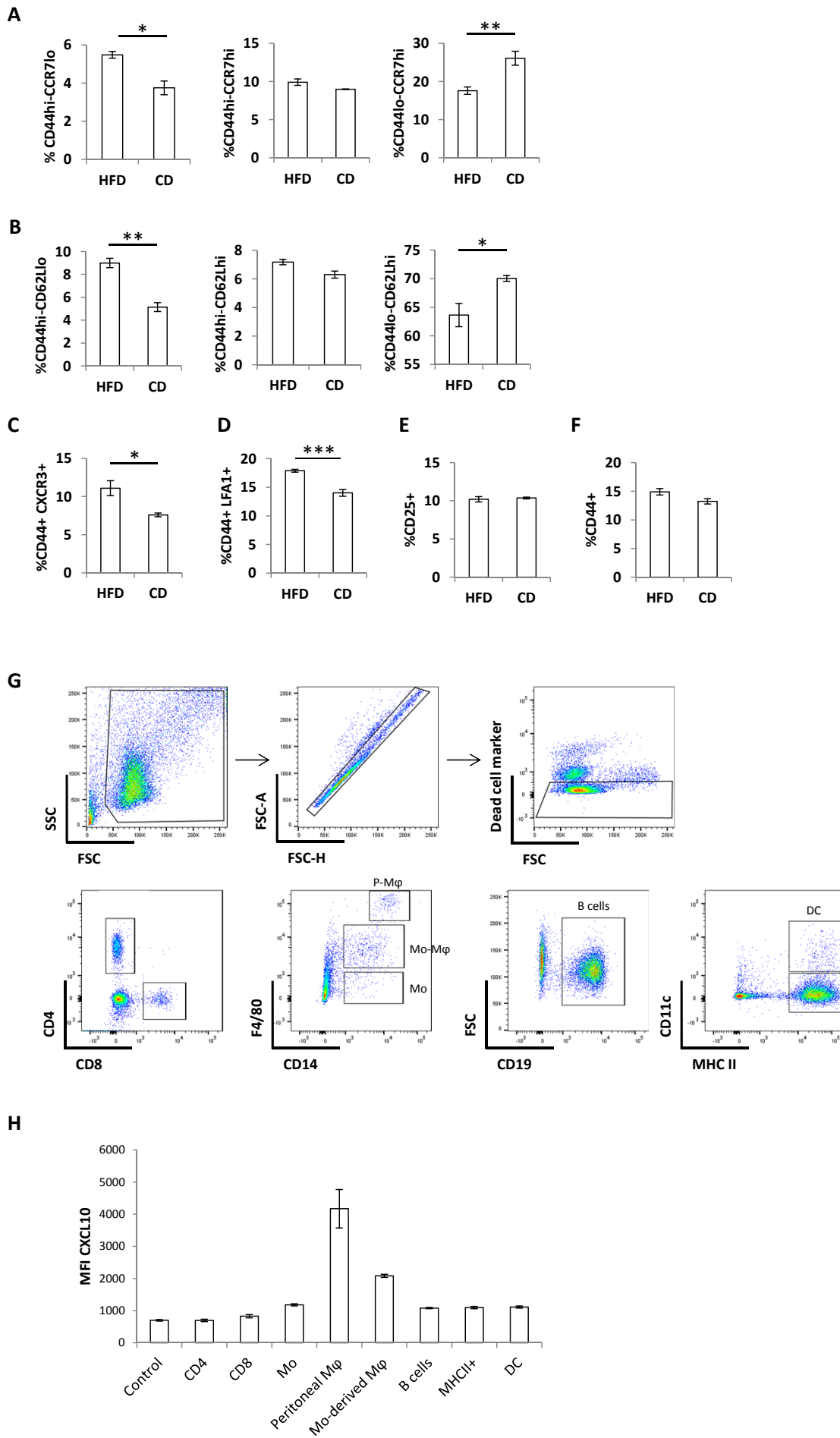
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20 **Supplemental Table 2 (related to Figures 1, 2 and 4-7). Nutrients and caloric**
21 **composition of diets: HFD, CD, PED and PCD.**

Supplemental Figure 1 (related to Figure 1)



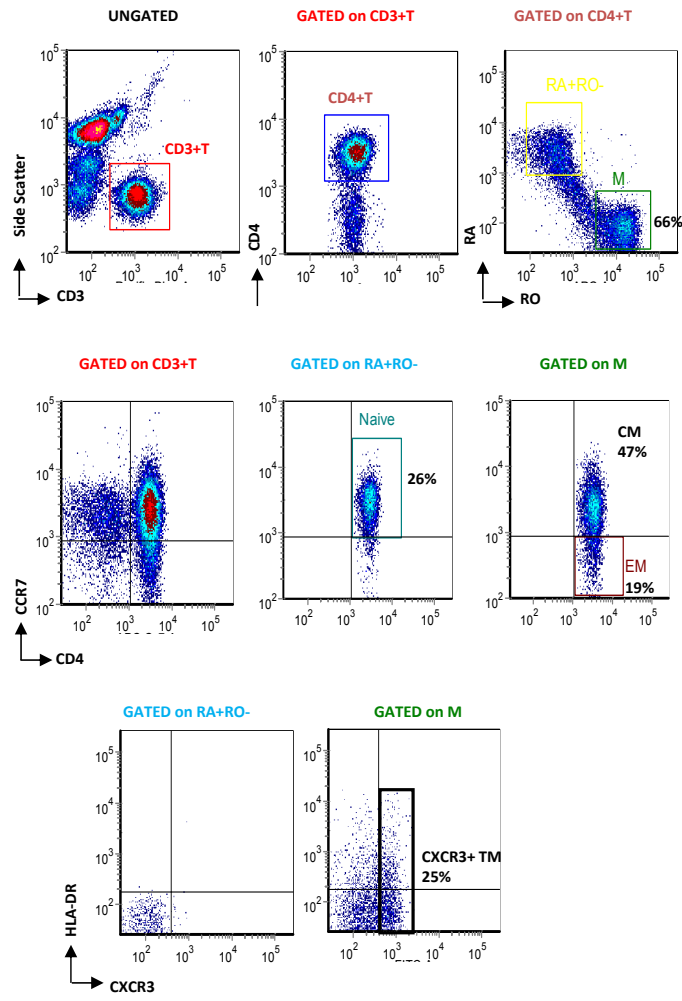
Supplemental Figure 2 (related to Figure 2)



Supplemental Figure 3 (related to Figure 3)

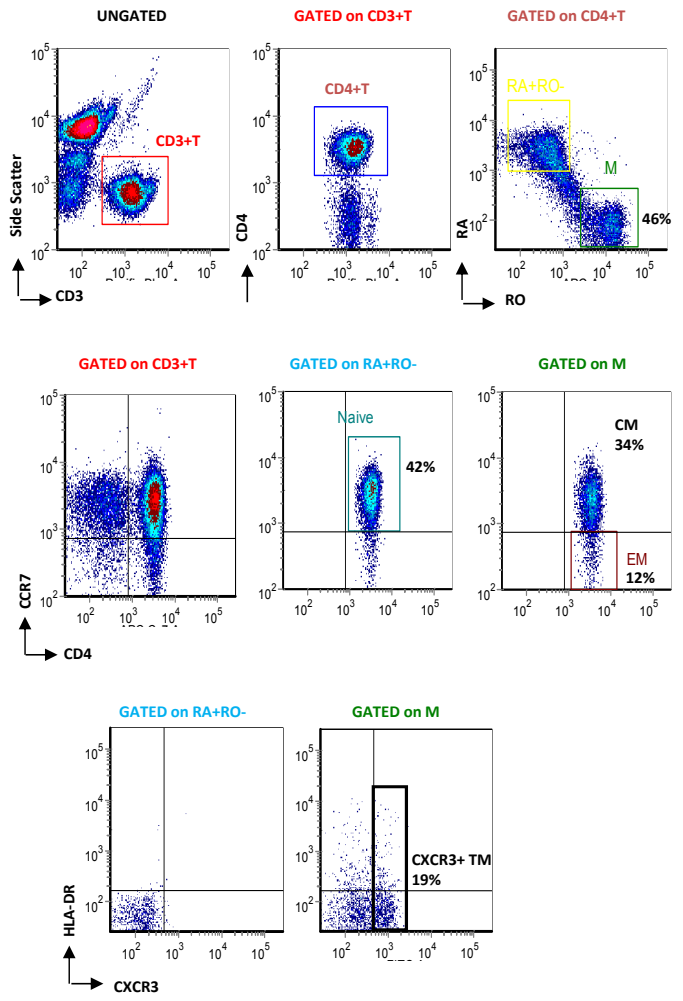
A

BMI 35, Female, 59 years



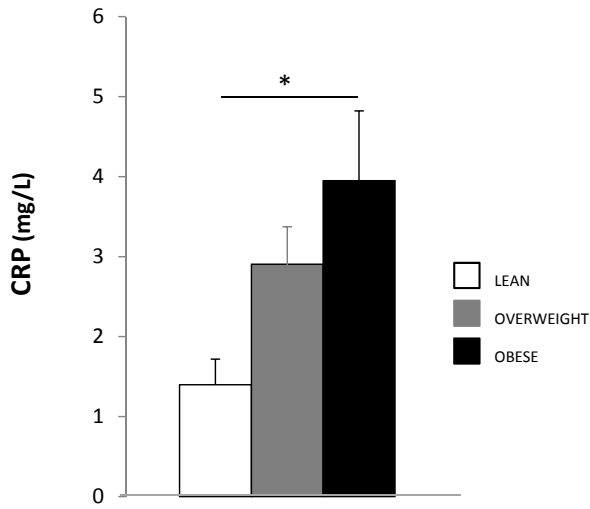
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BMI 24, Female, 61 years

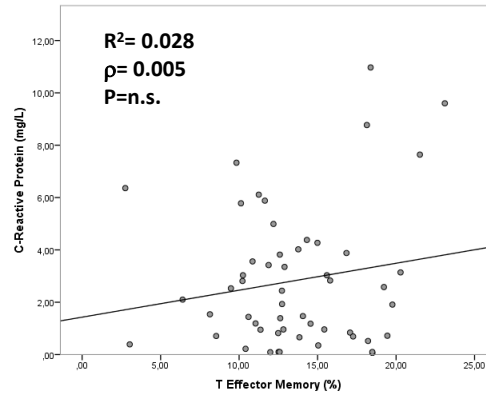


Supplemental Figure 4 (related to Figure 3)

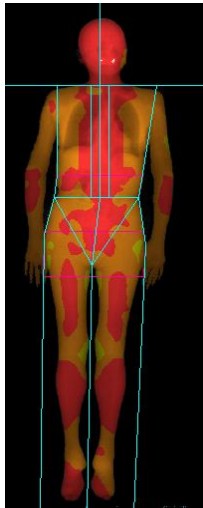
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B

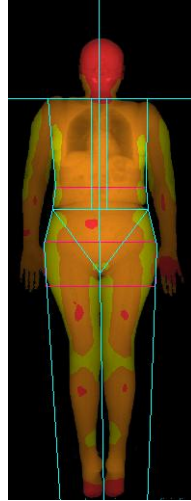


C



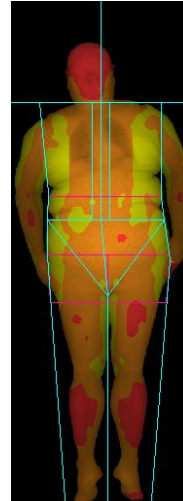
LEAN

Female 66 years
BMI: 19.2 Kg/m²
Android fat: 25.2%
Gynoid fat: 36.4 %
A/G_r: 0.69



OVERWEIGHT

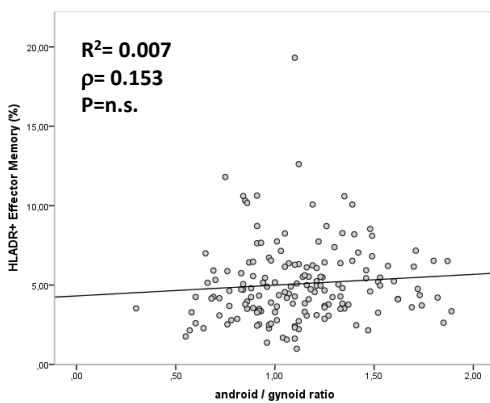
Female 66 years
BMI: 26.2 Kg/m²
Android fat: 51.2%
Gynoid fat: 54.3 %
A/G_r: 0.94



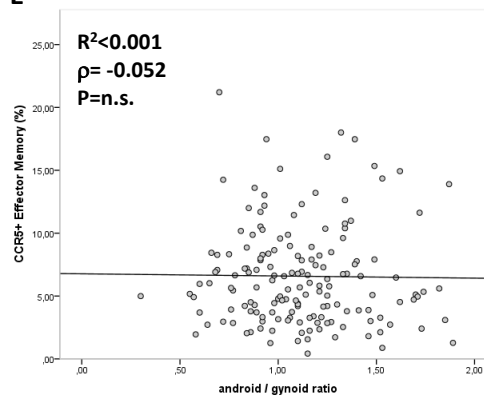
OBESE

Female 66 years
BMI: 37.8 Kg/m²
Android fat: 63.4%
Gynoid fat: 52.4 %
A/G_r: 1.21

D

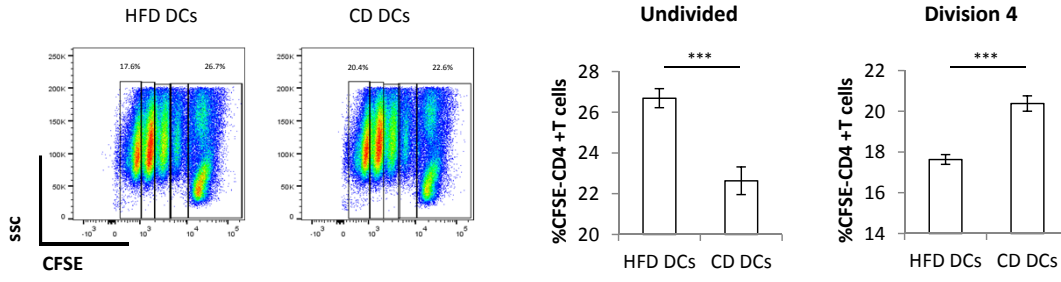


E

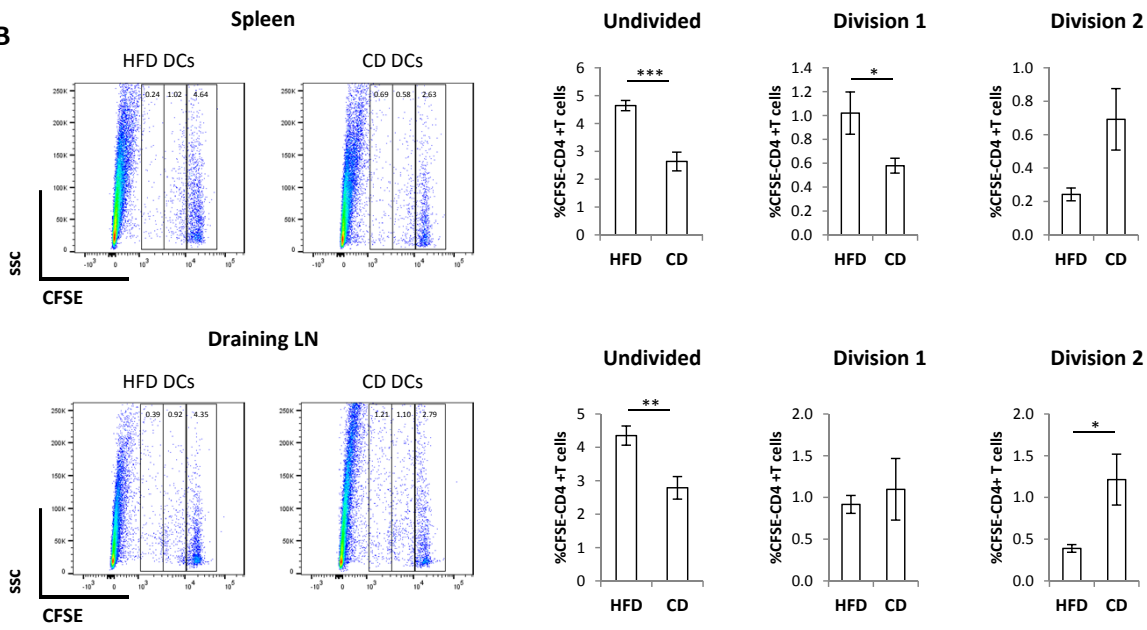


Supplemental Figure 5 (related to Figure 4)

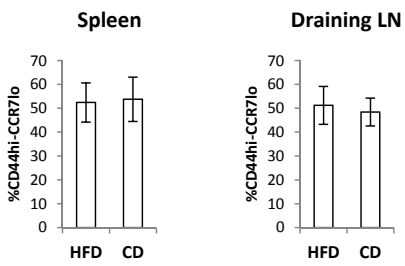
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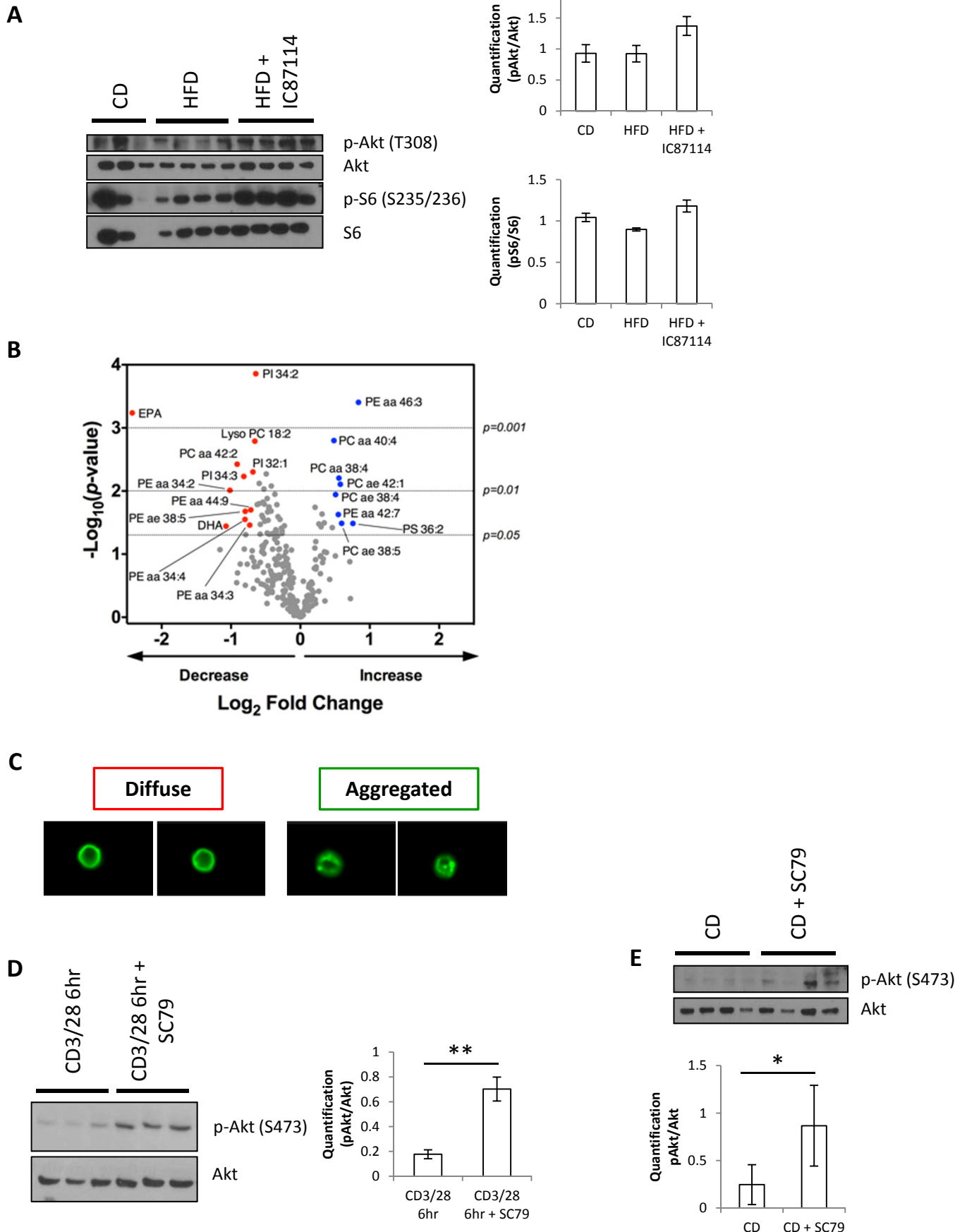
B



C



Supplemental Figure 6 (related to Figures 5 and 6)



Supplemental Table 1 (related to Figure 3)

	LEAN (N= 370)	OVERWEIGHT (N= 552)	OBESE (N= 250)	P
Age (yrs)	<i>67 (46-78)</i>	<i>68 (52-78)</i>	<i>70 (56-78)</i>	< 0.001
Gender (men/women)	<i>111/259</i>	<i>281/271</i>	<i>90/160</i>	
BMI (Kg/m²)	<i>22.90 (20.20-24.60)</i>	<i>27.10 (25.30-29.10)</i>	<i>32.10 (30.40-37.43)</i>	< 0.001
Total cholesterol (mg/dL)	<i>207.00 (162.00-250.00)</i>	<i>201.00 (155.00-250.00)</i>	<i>198.00 (151.00-243.00)</i>	0.279
HDL-C (mg/dL)	<i>67.00 (48.80-90.00)</i>	<i>57 (42-81)</i>	<i>57 (40-73)</i>	< 0.001
Triglycerides (mg/dL)	<i>77 (50-139.4)</i>	<i>96 (56-163)</i>	<i>99 (64-182)</i>	< 0.001
LDL-C (Friedewald Formula)	<i>119.2 (81.56-158.8)</i>	<i>118.20 (80.92-167.48)</i>	<i>118.80 (77.26-158.72)</i>	0.714
ApoA-I (mg/dL)	<i>165 (125.8-179)</i>	<i>154 (115.7-175)</i>	<i>151 (115-174)</i>	< 0.001
Apo-B (mg/dL)	<i>99 (83-131)</i>	<i>101 (79.6-134)</i>	<i>99 (81-128)</i>	0.712
Fasting glucose levels (mg/dL)	<i>88 (75-104)</i>	<i>93 (80-114)</i>	<i>100 (84-133)</i>	< 0.001
Total leukocytes (x10³ U/L)	<i>5.71 (4.33-8.20)</i>	<i>6.36 (4.74-8.80)</i>	<i>6.39 (4.71-8.82)</i>	< 0.001
Neutrophils (x10³ U/L)	<i>3.31 (2.12-5.12)</i>	<i>3.56 (2.43-5.39)</i>	<i>3.59 (2.38-5.33)</i>	0.010
Lymphocytes (x10³ U/L)	<i>1.78 (1.13-2.55)</i>	<i>1.92 (1.36-2.73)</i>	<i>1.95 (1.32-2.77)</i>	< 0.001
Monocytes (x10³ U/L)	<i>0.49 (0.34-0.75)</i>	<i>0.56 (0.39-0.80)</i>	<i>0.55 (0.38-0.81)</i>	0.002
Eosinophils (x10³ U/L)	<i>0.12 (0.05-0.27)</i>	<i>0.15 (0.07-0.33)</i>	<i>0.16 (0.07-0.33)</i>	0.062
Basophils (x10³ U/L)	<i>0.03 (0.01-0.05)</i>	<i>0.03 (0.01-0.05)</i>	<i>0.03 (0.05)</i>	0.668

Supplemental Table 2 (related to Figures 1, 2 and 4-7)

	High Fat diet (HFD)	Chow diet (CD)	Palmitate- enriched diet (PED)	Palmitate- control diet (PCD)
Fat (%)	34.9	9.1	25.2	4.2
Cholesterol, ppm	301	200	0	0
Linoleic Acid (%)	4.7	2.32	3.86	1.89
Linolenic Acid (%)	0.39	0.21	0.29	0.29
Arachidonic Acid (%)	0.06	0.02	0	0
Omega-3 Fatty Acids (%)	0.39	0.32	0.29	0.21
Total Saturated (%)	13.68	2.72	10.05	0.39
Total Mono-saturated (%)	14	2.88	10.38	1.56
Polyunsaturated (%)	-	-	4.38	2.07
Energy (kcal/g)²	5.1	3.56	4.83	3.78
Protein (%)	18.1	23	13	16.7
Fat (%)	61.6	22	47	10
Carbohydrate (%)	20.3	55	40	73.3