Online Supporting Material

Supplemental Table 1. Semi-purified diet compositions[1]

Diet Constituent (g/kg diet)	Study One Diets				Study Two Diets			
	CO-C	CO-P	FO-C	FO-P	CO	DHA + EPA	EPA	DHA
Casein	200	200	200	200	200	200	200	200
DL-Methionine	3	3	3	3	3	3	3	3
Sucrose	320	320	320	320	440	440	440	440
Corn Starch	220	220	220	220	220	220	220	220
Cellulose	60	0	60	0	60	60	60	60
Pectin	0	60	0	60	0	0	0	0
AIN-76 Mineral Mix[2]	10	10	10	10	10	10	10	10
AIN-76 Salt Mix	35	35	35	35	35	35	35	35
Choline Chloride	2	2	2	2	2	2	2	2
CO	150	150	35	35	30	20	20	20
FO	0	0	115	115	0	0	0	0
EPA	0	0	0	0	0	5	10	0
DHA	0	0	0	0	0	5	0	10
% energy from (n-3) PUFA	0.3	0.3	6.9	7.6	trace	2.5	2.8	2.8

[1]All dry diet constituents were purchased from Bio Serv (Bio Serv, Frenchtown, NJ). Corn oil (CO, Dyets, Madison, WI), fish oil (FO, Omega Protein Inc, Reedville, VA), DHA ethyl ester (>70% pure, Incromega DHA700E SR; Bioriginal Food & Science Corp, Saskatchewan, Canada) and EPA free fatty acid (>95% pure, SLA Pharma, Watford, UK). CO-C (corn oil + cellulose), CO-P (corn oil + pectin), FO-C (fish oil + cellulose) and FO-P (fish oil + pectin).
[2]AIN 76 mineral mix (48).

Supplemental Table 2. Dietary fatty acid composition and % energy

	Study One Diets				Study Two Diets			
	CO-C	CO-P	FO-C	FO-P	CO	DHA + EPA	DHA	EPA
Fatty acid[1]	(g/100g fatty acids)							
14:0	trace[2]	trace	6.9	6.7	trace	trace	trace	trace
16:0	11.6	11.3	18.0	18.4	12.1	8.9	8.9	8.6
16:1(n-7)	trace	trace	8.5	9.0	trace	trace	trace	trace
18:0	1.9	1.8	3.3	3.5	trace	1.4	1.8	1.6
18:1(n-9)	29.1	28.9	14.7	15.1	34.3	15.8	17.8	16.7
18:2(n-6)	55.4	55.8	17.4	17.7	51.4	37.8	33.3	31.7
18:3(n-3)	0.9	0.9	2.5	2.8	trace	0.6	0.7	0.8
20:5(n-3)	trace	trace	9.5	10.9	trace	21.0	36.9	4.4
22:5(n-3)	trace	trace	1.4	1.7	trace	trace	trace	trace
22:6(n-3)	trace	trace	6.2	7.2	trace	12.5	trace	31.6
% Energy from lipid	31.2	31.2	31.2	31.2	7.3	7.3	7.3	7.3
% Energy from (n-3) PUFA	0.3	0.3	6.9	7.6	trace	2.5	2.8	2.8

[1]Only the major fatty acids (> 1g/100 g) are listed
[2]trace, trace amount (< 0.05)

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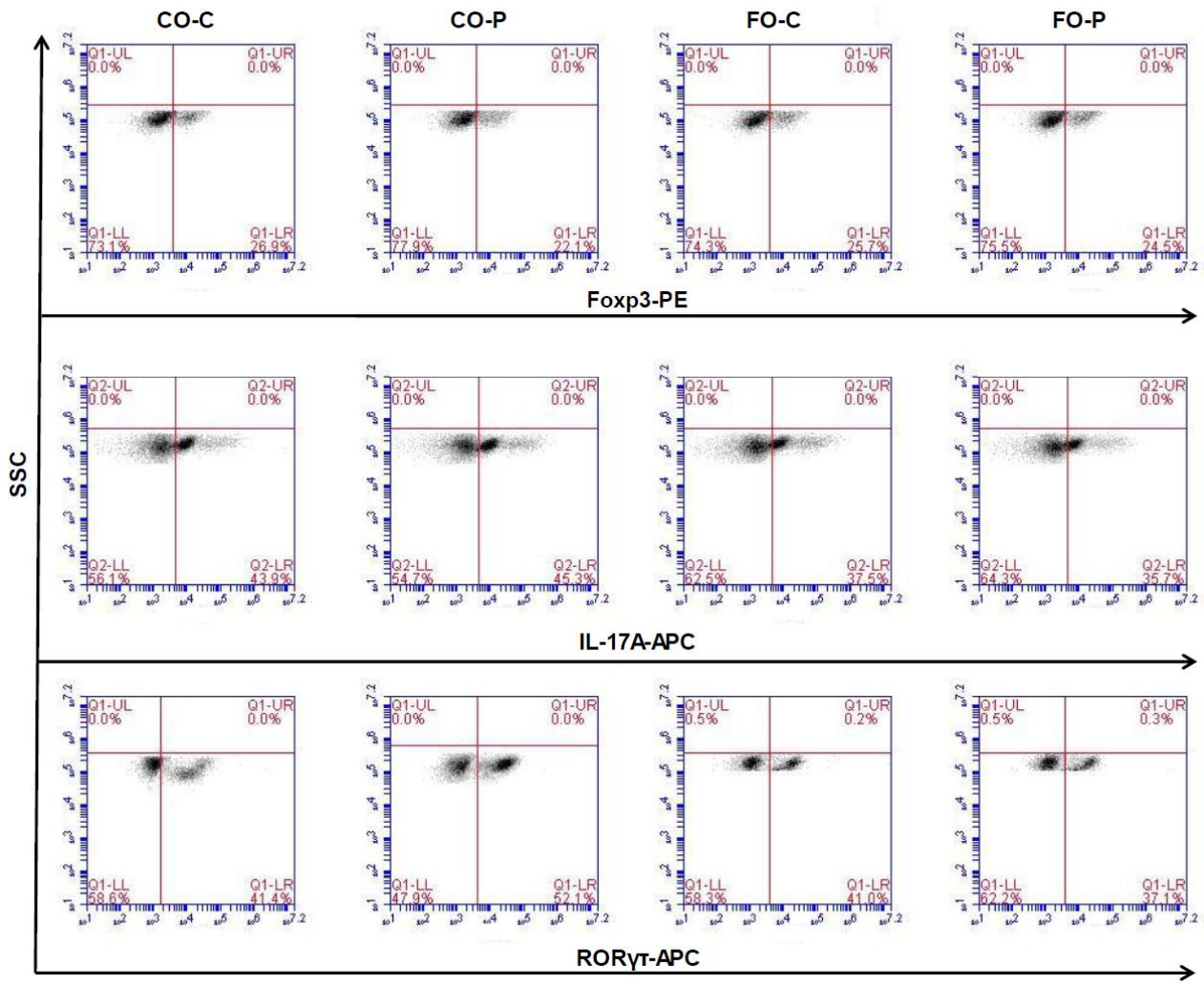
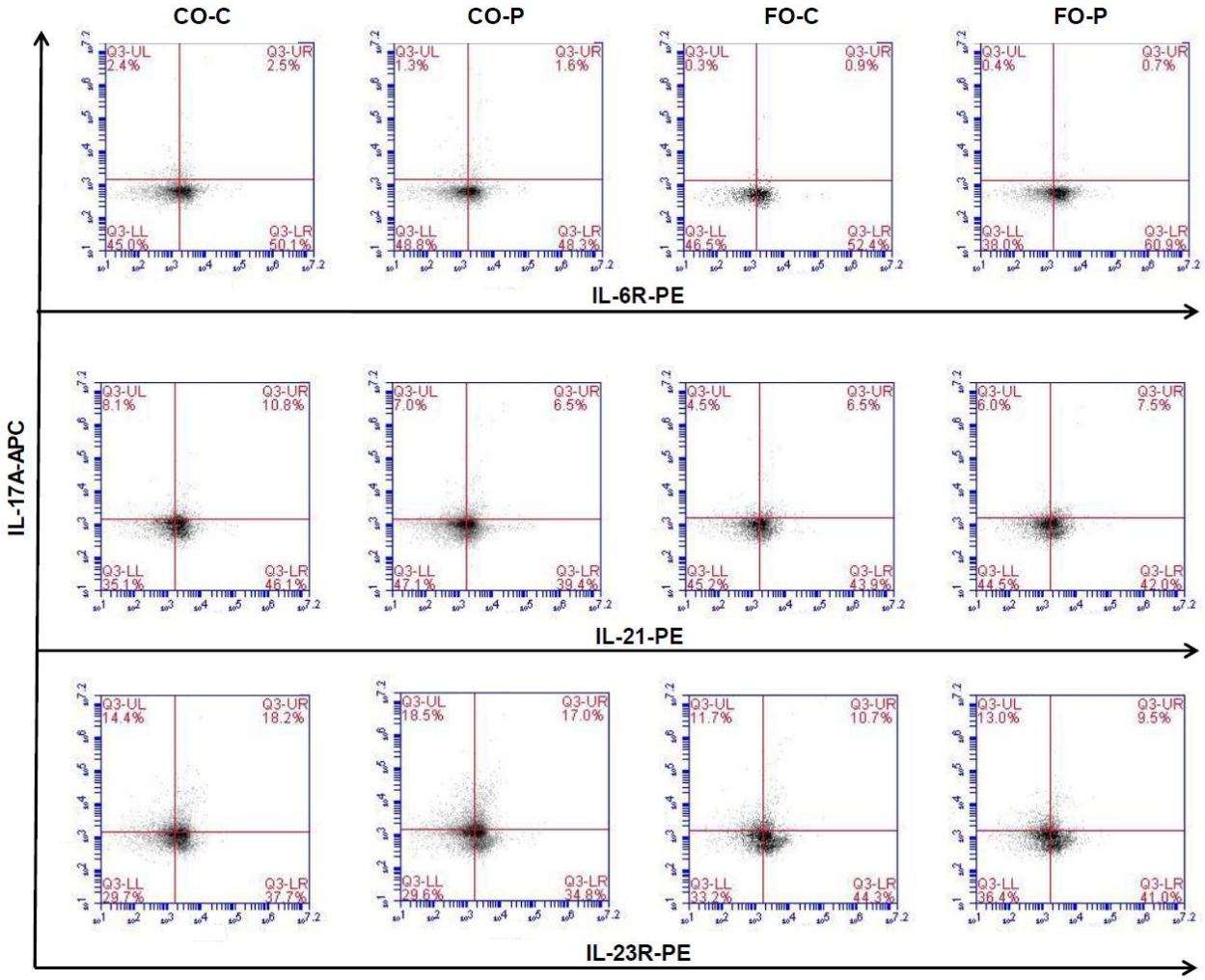
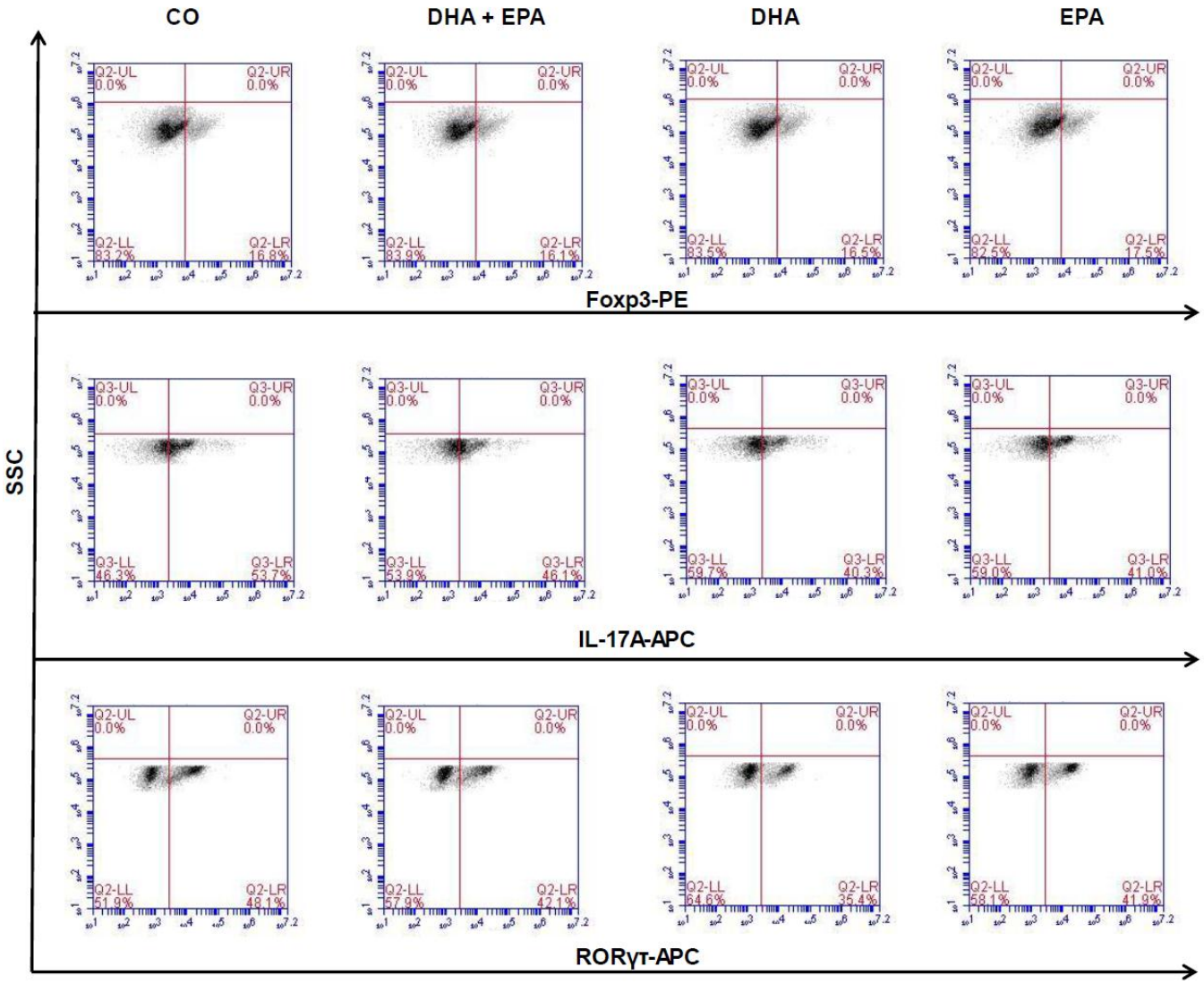


Supplemental Figure 1. Representative dot plots depicting the detection of T cell subsets by intracellular expression of Treg and Th17 cell markers. Dietary groups (see Materials and Methods) are shown at the top of each column. Purified splenic $CD4^+$ T cells were gated based on side scatter (SSC, y axis) versus the specific marker for each T cell subset (x axis). Tregs were identified as Foxp3-PE^+ cells (top row). Th17 cells were identified by expression of either the signature cytokine IL-17A-APC^+ cells (middle row) or by expression of the signature transcription factor RORγt-APC^+ cells (bottom row). Flow cytometric analysis was conducted using an Accuri C6 flow cytometer (Accuri Cytometers). CO-C, corn oil + cellulose; CO-P, corn oil + pectin; FO-C, fish oil + cellulose and FO-P, fish oil + pectin



Supplemental Figure 2. Representative dot plots depicting the detection of polarized Th17 cells co-expressing surface cytokine receptors. Dietary groups are shown at the top of each column (see Materials and Methods). The percentage of splenic Th17 cells co-expressing specific cytokine receptors was determined by intracellular detection of the Th17 cell signature cytokine IL-17A-APC$^+$ cells (y axis) versus cytokine receptor surface expression (x axis). IL-17A-APC$^+$/IL-6R-PE$^+$ cells (top row), IL-17A-APC$^+$/IL-21R-PE$^+$ cells (middle row), IL-17A-APC$^+$/IL-23R-PE$^+$ cells (bottom row). Flow cytometric analysis was conducted using an Accuri C6 flow cytometer (Accuri Cytometers). CO-C, corn oil + cellulose; CO-P, corn oil + pectin; FO-C, fish oil + cellulose; FO-P, fish oil + pectin.



Supplemental Figure 3. Representative dot plots depicting the detection of T cell subsets by intracellular expression of Treg and Th17 cell markers. Dietary groups (see Materials and Methods) are shown at the top of each column. Purified splenic $CD4^+$ T cells were gated based on side scatter (SSC, y axis) versus the specific marker for each T cell subset (x axis). Tregs were identified as Foxp3-PE^+ cells (top row). Th17 cells were identified by expression of either the signature cytokine IL-17A-APC^+ cells (middle row) or by expression of the signature transcription factor RORγt-APC^+ cells (bottom row). Flow cytometric analysis was conducted using an Accuri C6 flow cytometer (Accuri Cytometers).