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West, A. L., Miles, E. A., Han, L., Lillycrop, K. A., Napier, J. A., Calder, P. C. and Burdge, G. C. 2021. Dietary Supplementation with Transgenic Camelina sativa Oil Containing 20:5n-3 and 22:6n-3 or Fish Oil Induces Differential Changes in the Transcriptome of CD3+ T Lymphocytes. *Nutrients*. 13 (9), p. 3116. <https://doi.org/10.3390/nu13093116>

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- <https://www.mdpi.com/2072-6643/13/9/3116>

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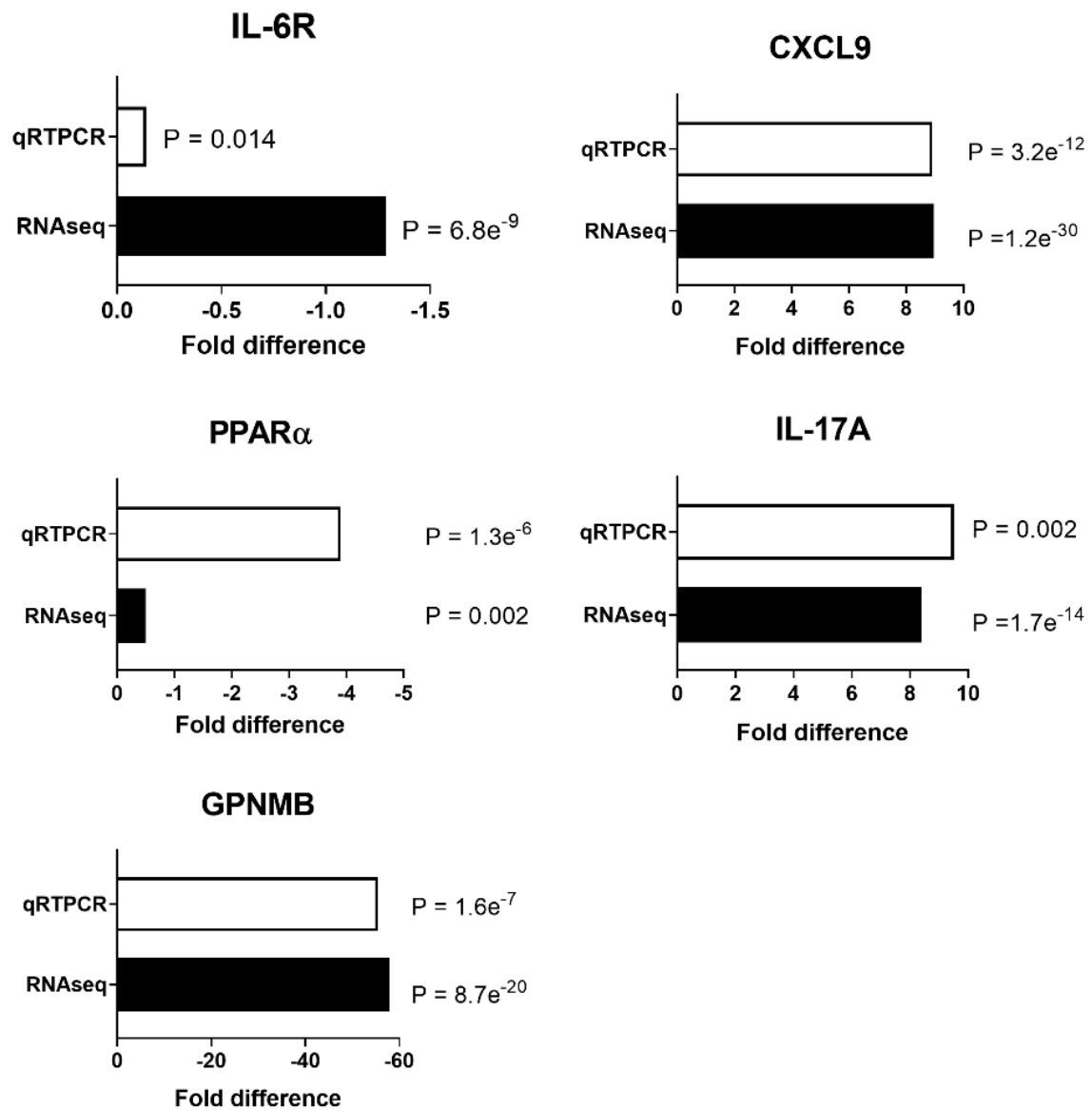
Supplementary online material

Supplementary Table S1. qRTPCR primers

Gene target	Primer assay
<i>IL6R</i>	Qiagen Hs_IL6R_1_SG QuantiTect Primer Assay (QT00023660)
<i>CXCL9</i>	Qiagen Hs_CXCL9_1_SG QuantiTect Primer Assay (QT00013461)
<i>PPARα</i>	Qiagen Hs_PPARα_1_SG QuantiTect Primer Assay (QT00017451)
<i>IL17A</i>	Qiagen Hs_IL17A_1_SG QuantiTect Primer Assay (QT00009233)
<i>GPNMB</i>	Qiagen Hs_GPNMB_1_SG QuantiTect Primer Assay (QT00036904)
<i>RPL13A</i>	Primer design reference gene assay (HK-SY-hu)
<i>SDHA</i>	Primer design reference gene assay (HK-SY-hu)

Supplementary Table S2. The effect of dietary supplementation with tCSO or FO in the fatty acid composition of PBMCs from the participants subgroups from which T cells were used in RNAseq analysis. Values are mean \pm SEM proportions of total fatty acids (n = 16). There were no significant differences (all $P > 0.05$) between the whole group and the corresponding RNAseq subgroup in the proportions of any fatty acids by Students unpaired t-test.

	Proportions of total fatty acids (%)			
	FO		tCSO	
	Start	End	Start	End
14:0	0.7 \pm 0.1	0.5 \pm 0.1	0.4 \pm 0.1	0.5 \pm 0.1
16:0	20.9 \pm 1.7	19.4 \pm 1.2	19.0 \pm 1.9	18.6 \pm 1.6
16:1n-7	0.3 \pm 0.0	0.2 \pm 0.0	0.3 \pm 0.0	0.2 \pm 0.0
18:0	26.3 \pm 1.4	25.5 \pm 1.0	28.0 \pm 1.6	26.8 \pm 1.3
18:1n-9	14.0 \pm 1.0	16.7 \pm 0.6	14.9 \pm 0.9	15.2 \pm 0.9
18:1n-7	1.5 \pm 0.1	1.4 \pm 0.1	1.4 \pm 0.1	1.2 \pm 0.1
18:2n-6	6.7 \pm 0.5	7.1 \pm 0.2	7.5 \pm 1.0	6.1 \pm 0.4
18:3n-6	0.4 \pm 0.1	0.2 \pm 0.0	0.5 \pm 0.1	0.4 \pm 0.1
18:3n-3	1.0 \pm 0.1	1.1 \pm 0.2	0.8 \pm 0.1	1.1 \pm 0.1
20:0	0.5 \pm 0.1	0.3 \pm 0.0	0.6 \pm 0.2	0.6 \pm 0.2
20:1n-9	1.2 \pm 0.2	1.0 \pm 0.1	1.1 \pm 0.1	0.9 \pm 0.2
20:2n-6	0.6 \pm 0.1	0.3 \pm 0.0	0.6 \pm 0.1	0.4 \pm 0.1
20:3n-6	1.7 \pm 0.1	1.6 \pm 0.2	1.8 \pm 0.2	1.6 \pm 0.2
20:4n-6	17.5 \pm 1.6	18.4 \pm 1.1	16.6 \pm 2.0	18.4 \pm 1.8
20:5n-3	0.7 \pm 0.2	0.9 \pm 0.1	0.9 \pm 0.2	1.2 \pm 0.3
22:5n-3	1.8 \pm 0.2	2.2 \pm 0.2	1.8 \pm 0.3	2.0 \pm 0.3
22:6n-3	2.0 \pm 0.1	2.5 \pm 0.2	2.1 \pm 0.3	2.3 \pm 0.3



Supplementary Figure S1. qRTPCR validation of RNA sequencing assay. Validation of RNAseq analysis of the effect of mitogen stimulation of T lymphocytes by qRTPCR. Values are fold difference between the level of expression of the respective genes in unstimulated and concanavalin A stimulated T cells collected at baseline (n = 16) prior to dietary supplementation. The difference in mRNA expression measured by qRTPCR was calculated by the $\Delta\Delta\text{Ct}$ method [60]. Statistical analyses were by Students paired t test.