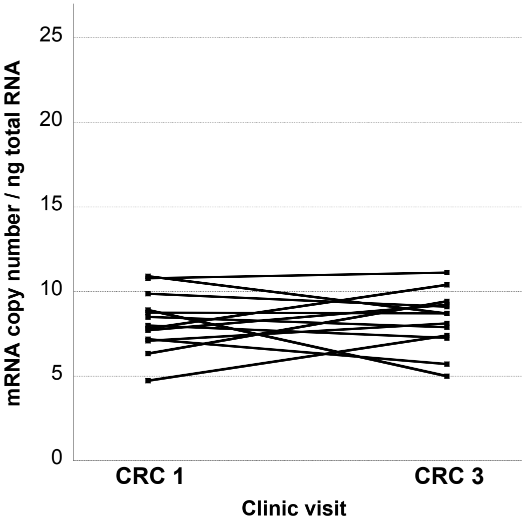
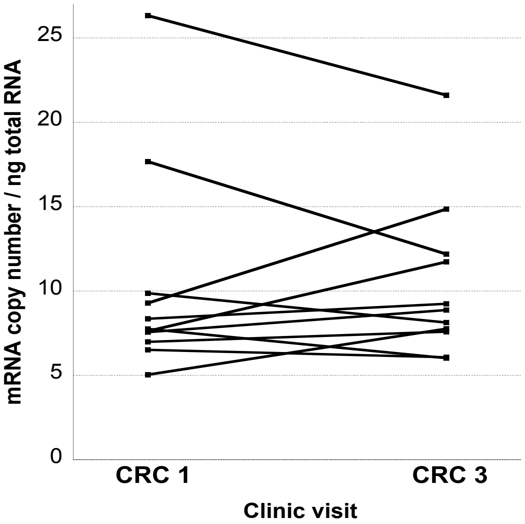
Online Supporting Material

a) *TNFα* expression

control

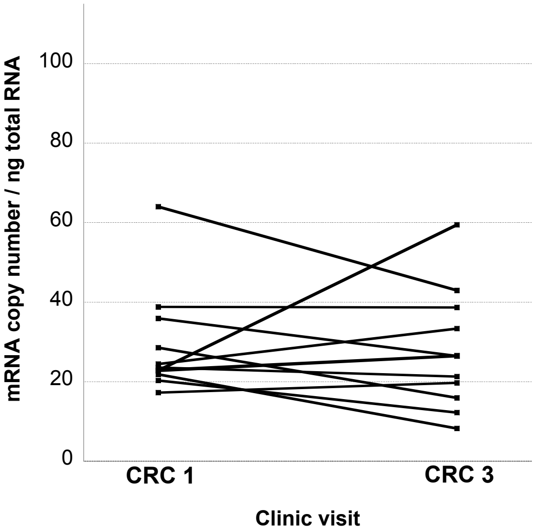


n3 PUFA



b) *IL6* expression

control



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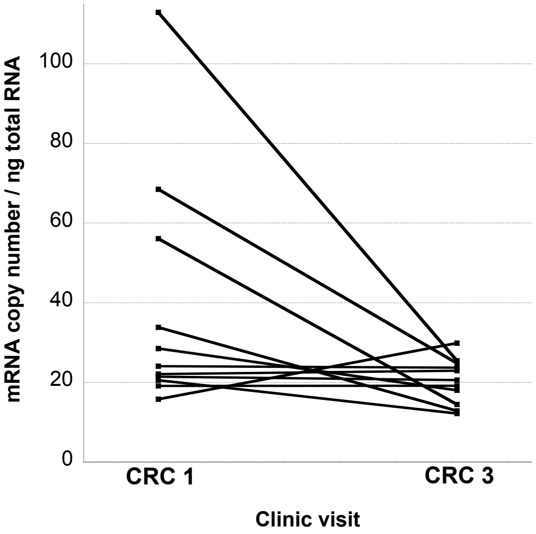

c) *CD14* expression

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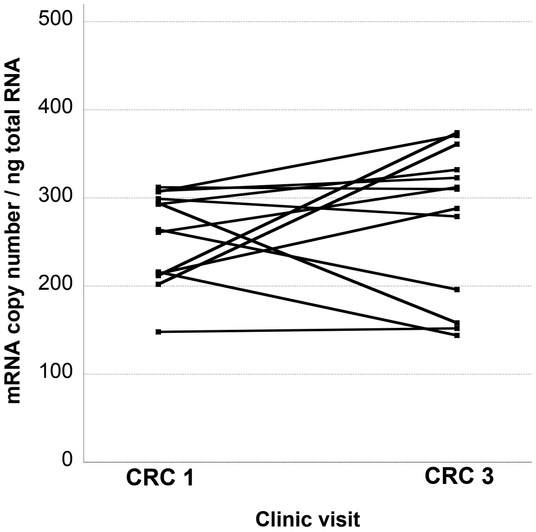

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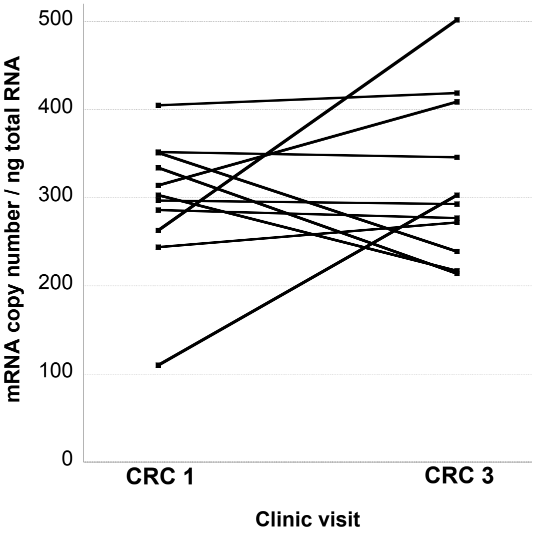
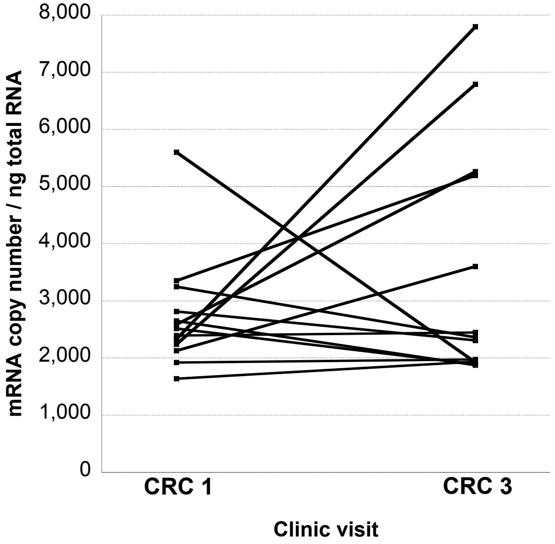


d) *CCL2* expression

control



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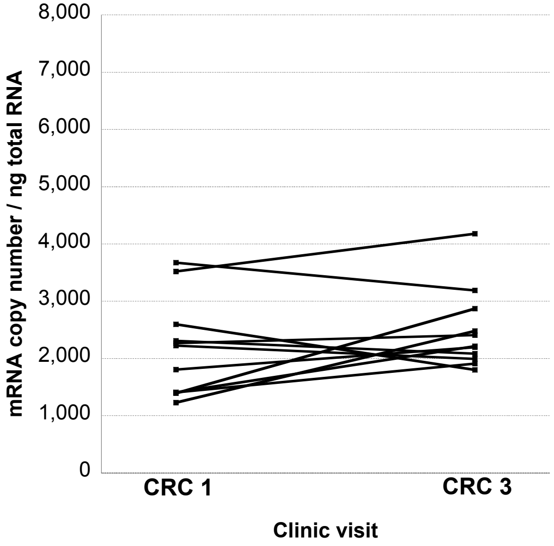
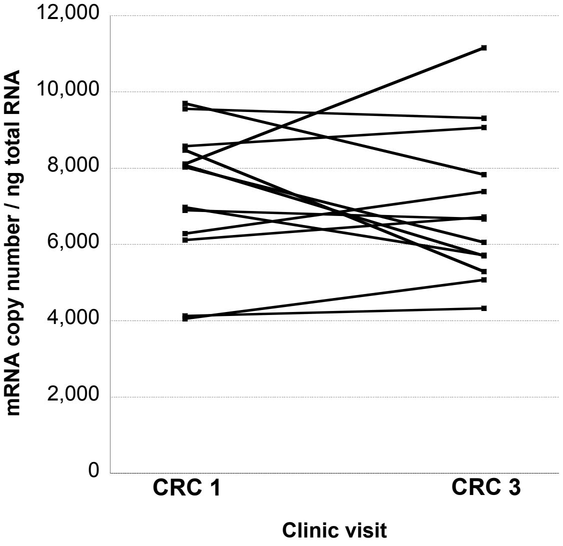


e) *ADIPOQ* expression

control



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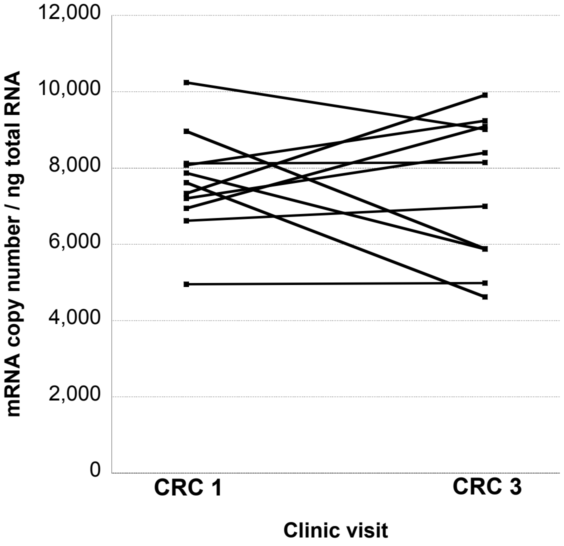
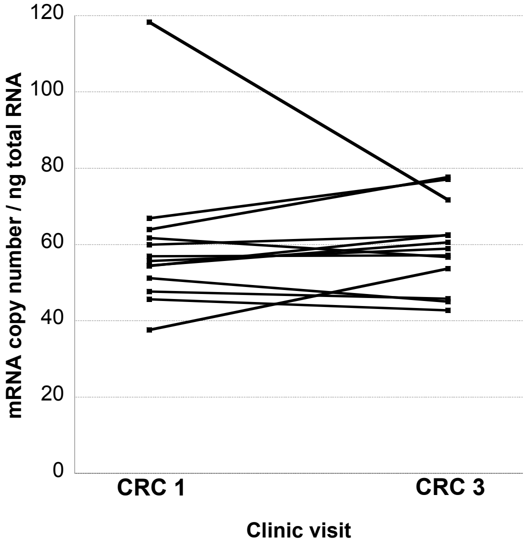


f) *ICAM1* expression

control



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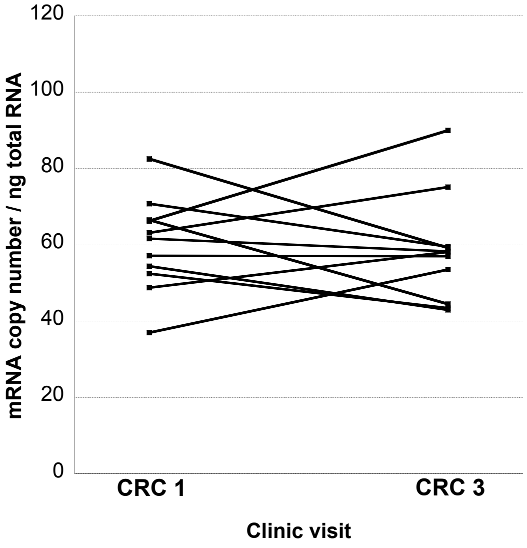
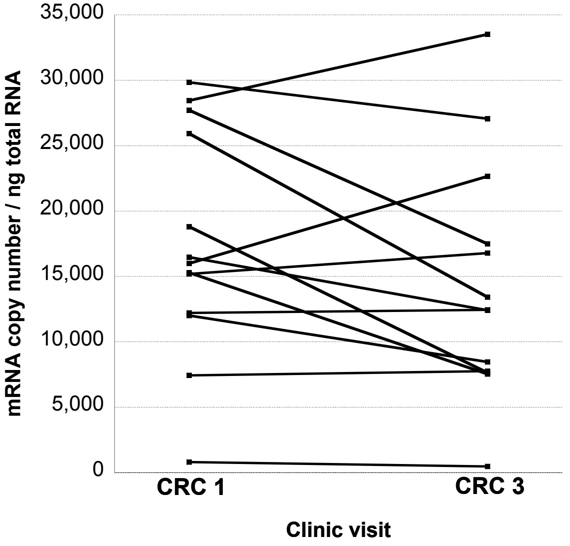


g) *SAA1* expression

control



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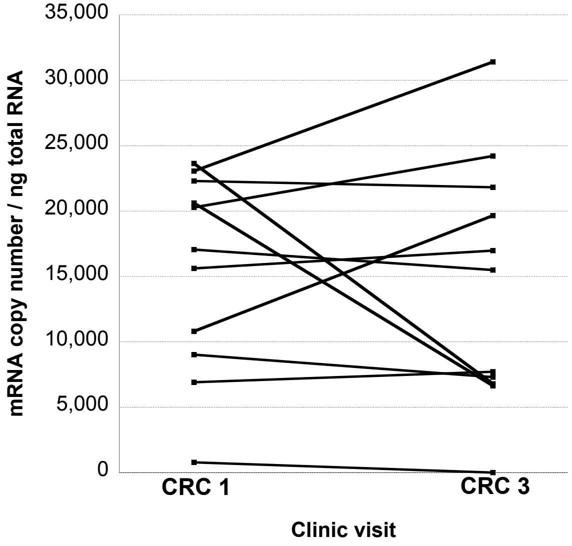
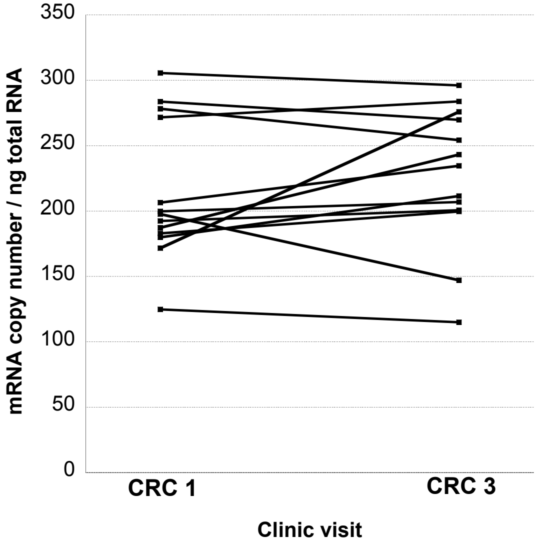


h) *CD206* expression

control



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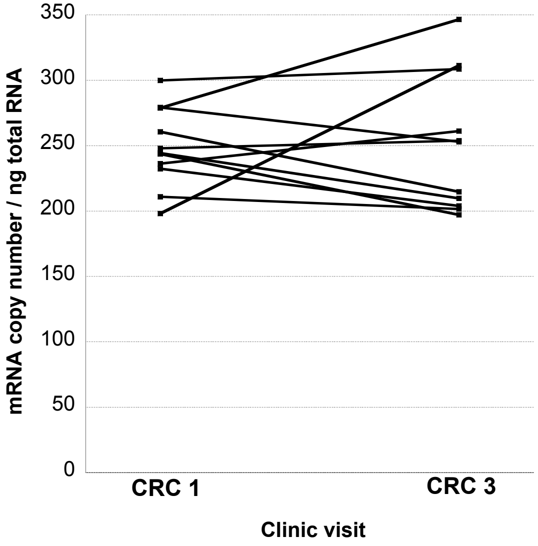
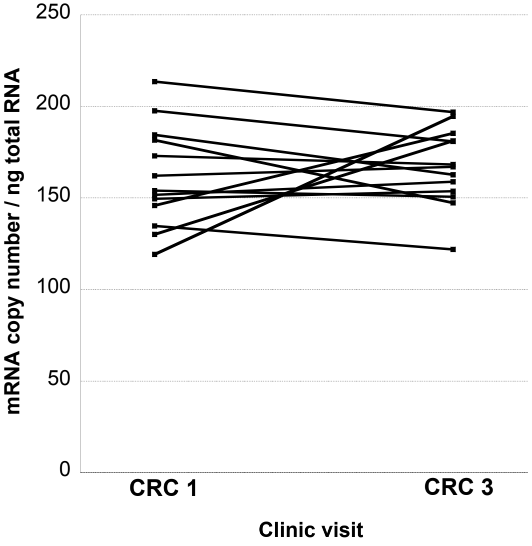


i) *TLR4* expression

control



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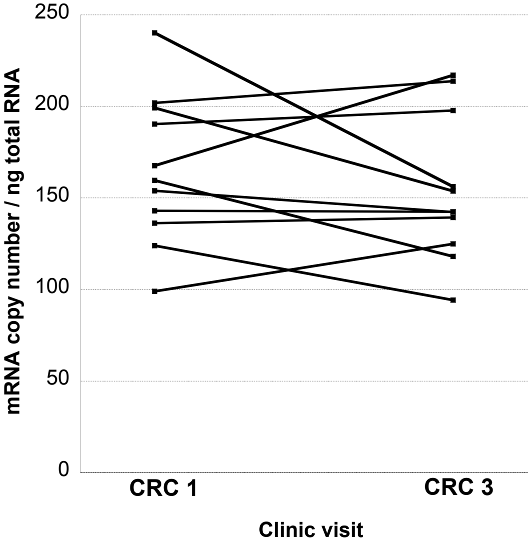
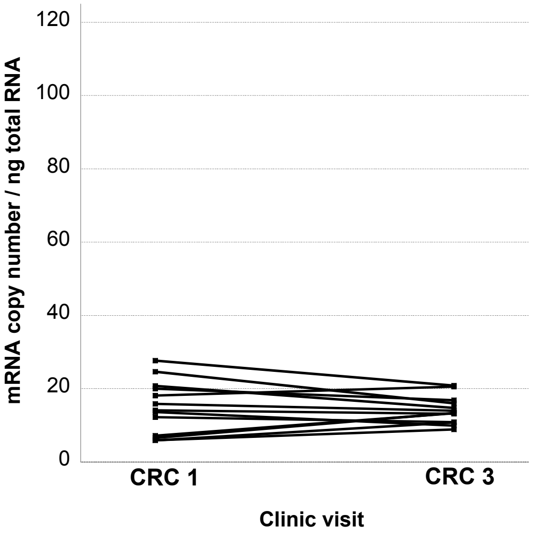


j) *PAI1* expression

control



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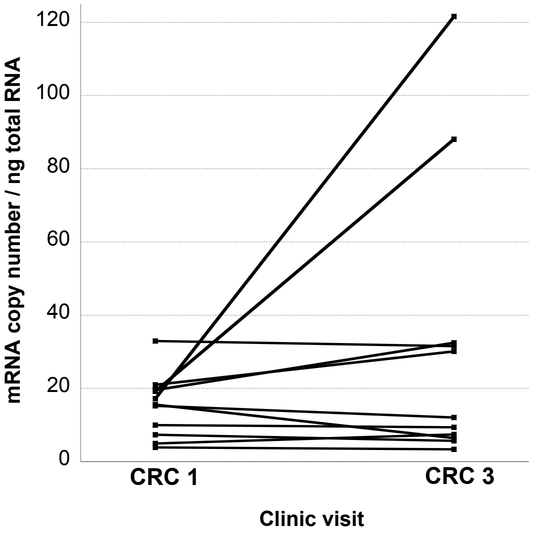
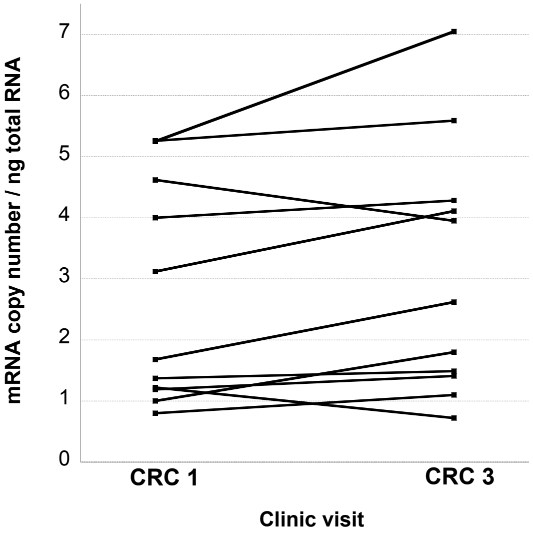


k) *NOS2* expression

control



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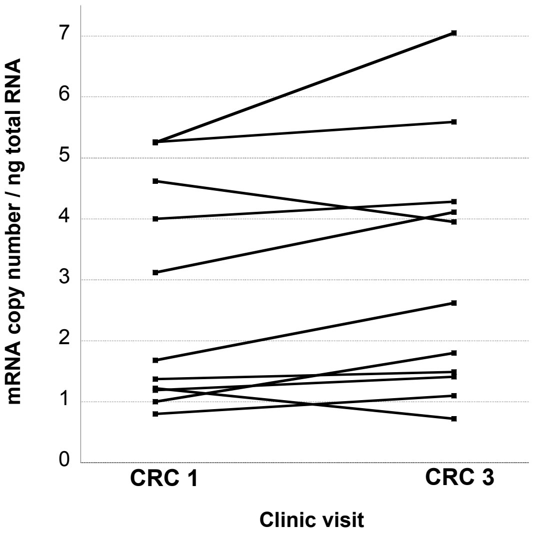
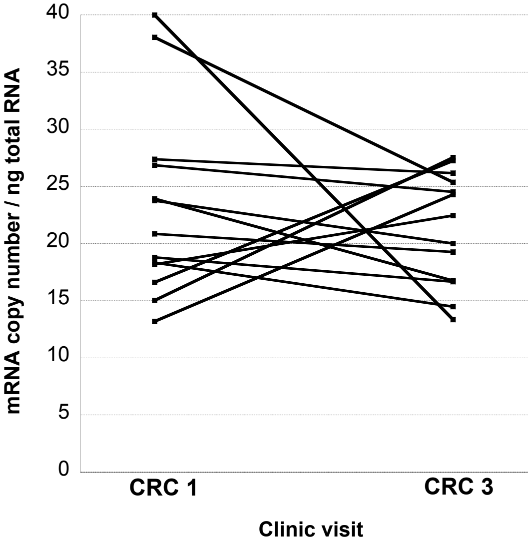


l) *NOS3* expression

control



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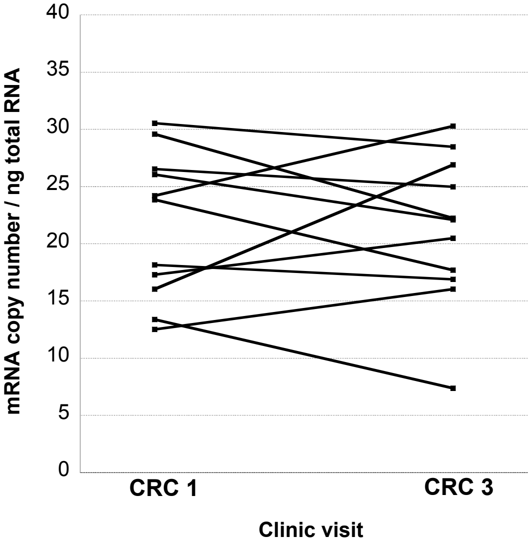
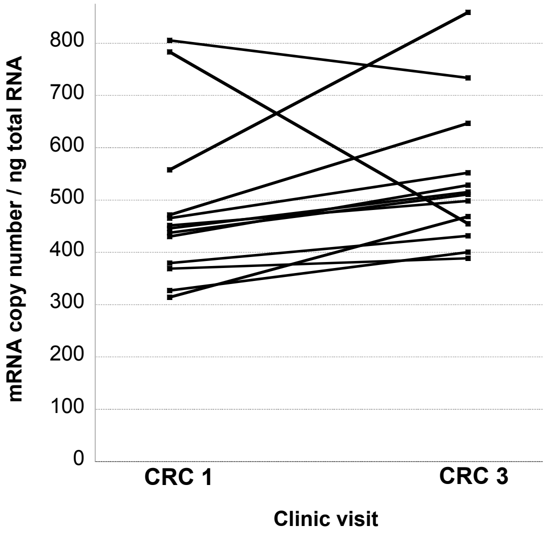


m) *HAS2* expression

control



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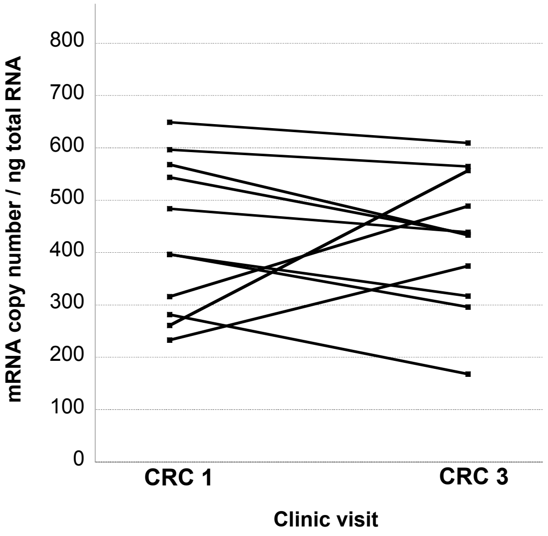

Supplemental Figure 1. Individual change in adipose tissue gene expression in overweight to moderately obese men and women after 14 weeks of control or n3 PUFA-enriched diet treatment. Data presented are mRNA copy number per ng total RNA at baseline (CRC 1) and again at the end of the intervention (CRC3) for panels a) *TNFα*, b) *IL6*, c) *CD14*, d) *CCL2*, e) *ADIPOQ*, f) *ICAM1*, g) *SAA1*, h) *CD206*, i) *TLR4*, j) *PAI1*, k) *NOS2*, l) *NOS3*, m) *HAS2*. Samples were batch analyzed and normalized based on three housekeeping genes.