

## SUPPLEMENTARY MATERIALS

### MNA-score per sarcopenia classification

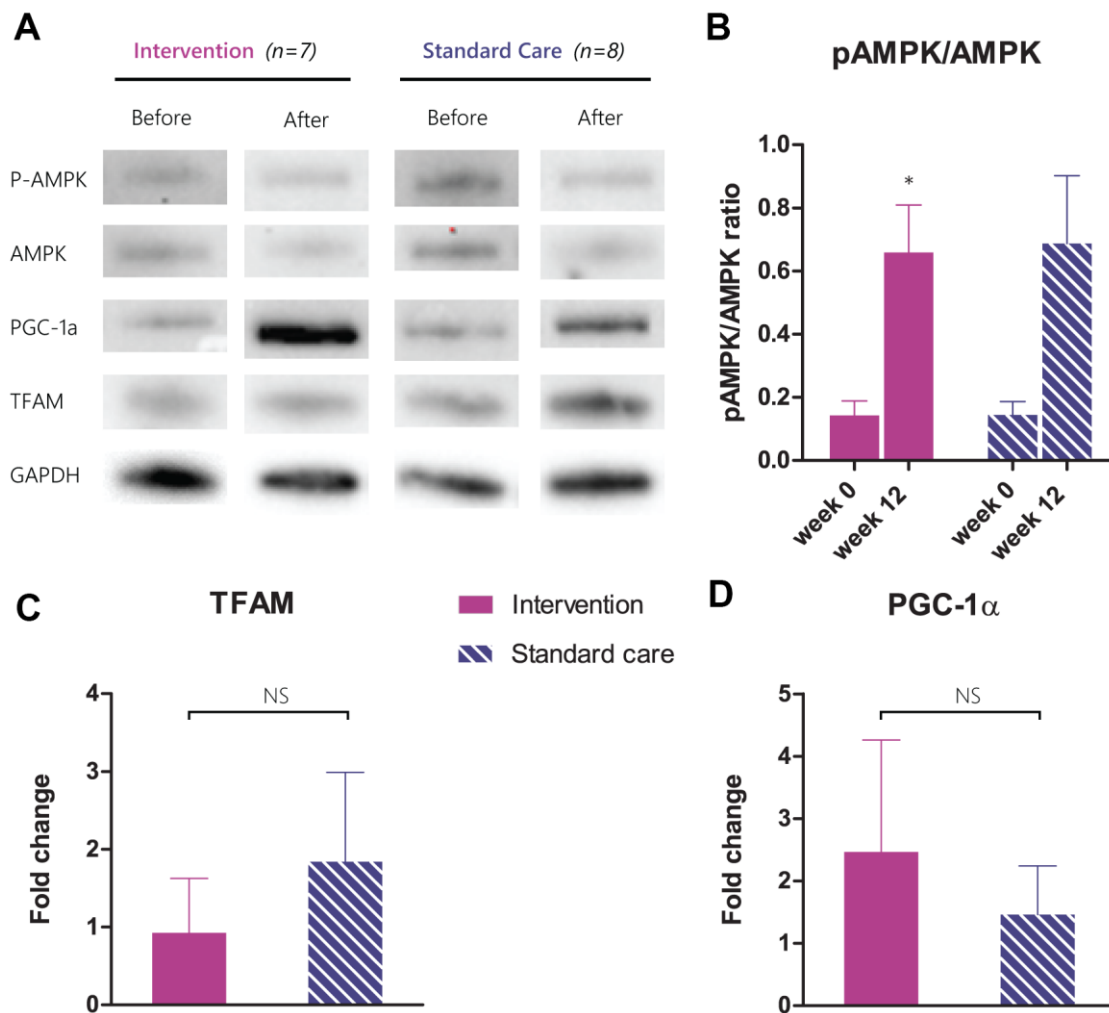
**Supplementary Table 1. Mean MNA-score per EWGSOP2 (Cruz-Jentoft et al., 2019) sarcopenia classification.**

	<b>Mean MNA-score</b>	<b>SD</b>	<b>N-total</b>	<b>N Novel supplement arm</b>	<b>N Standard supplement arm</b>
No Sarcopenia	9.89	1.306	47	25	22
Sarcopenia Probable	9.22	1.649	27	12	15
Sarcopenia Confirmed	9.67	1.155	3	1	2
Sarcopenia Severe	8.60	2.302	5	3	2
Total	9.59	1.515	82	41	41

## Protein expression

Both treatments upregulated the expression of proteins that induce mitochondrial biogenesis (see Figure). Activation of AMPK increased significantly in the novel supplement group ( $P=0.031$ ) compared to the

standard supplement group ( $P=0.125$ ) (Figure 4B). TFAM and PGC-1 $\alpha$  expressions were not differentially upregulated between the two groups (Figures 4C, 4D,  $P=0.603$  and  $P=0.685$  for between treatment differences in TFAM and PGC-1 $\alpha$  fold changes, respectively).



**Supplementary Figure 1. Effects of the two treatments on expression levels of proteins involved in mitochondrial pathways (n=15).** Representative captures from western blots (A), of which quantification (mean plus standard error bar) is presented in (B–D): pAMPK/AMPK ratios per treatment arm and per measurement time (B), fold change between week 0 and 12 in arbitrary units of TFAM (C) and PGC-1 $\alpha$  (D) expression. All protein densities were normalised against GAPDH expression. \*, significant ( $P<.05$ ) within-group change from baseline to week 12.