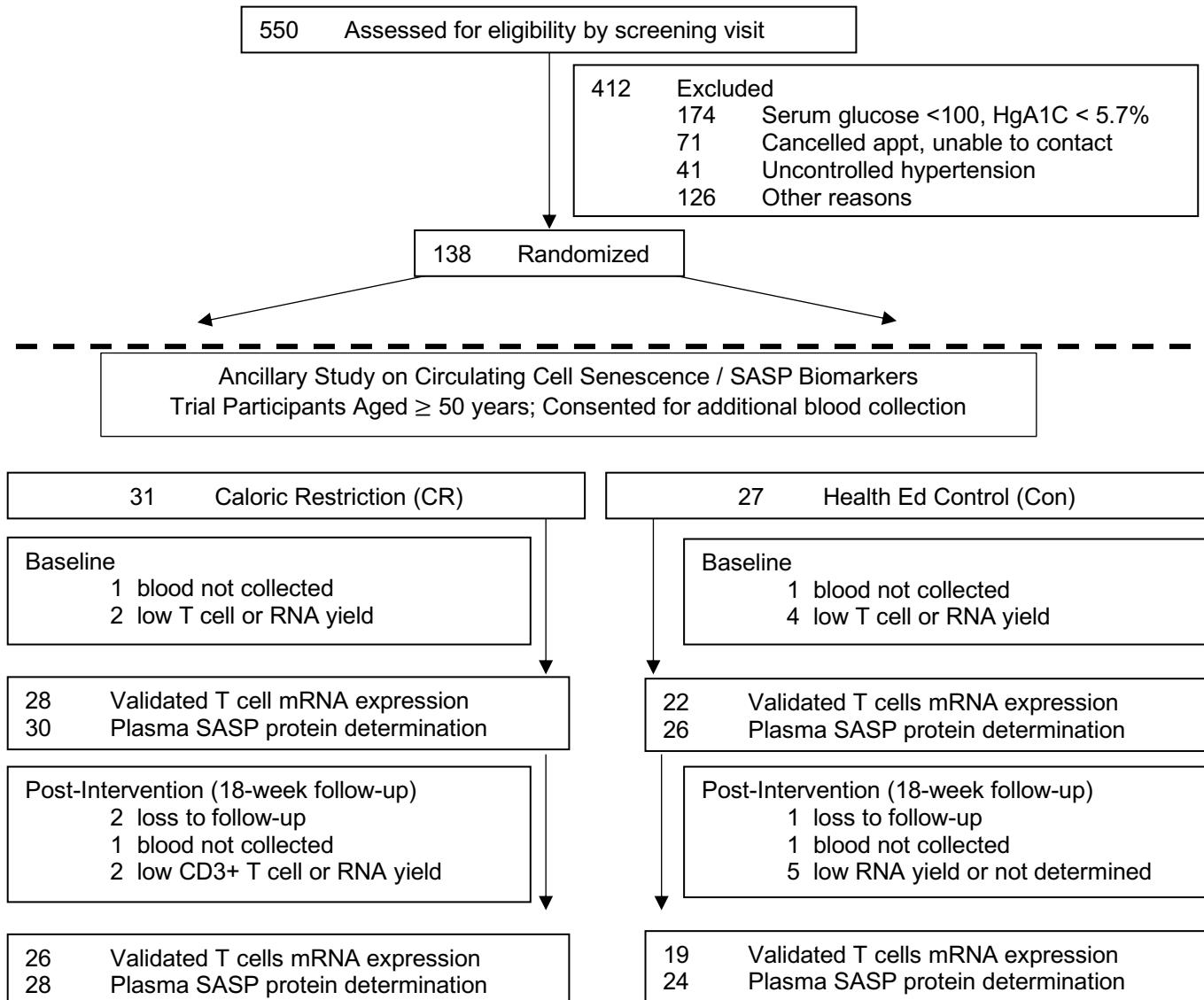
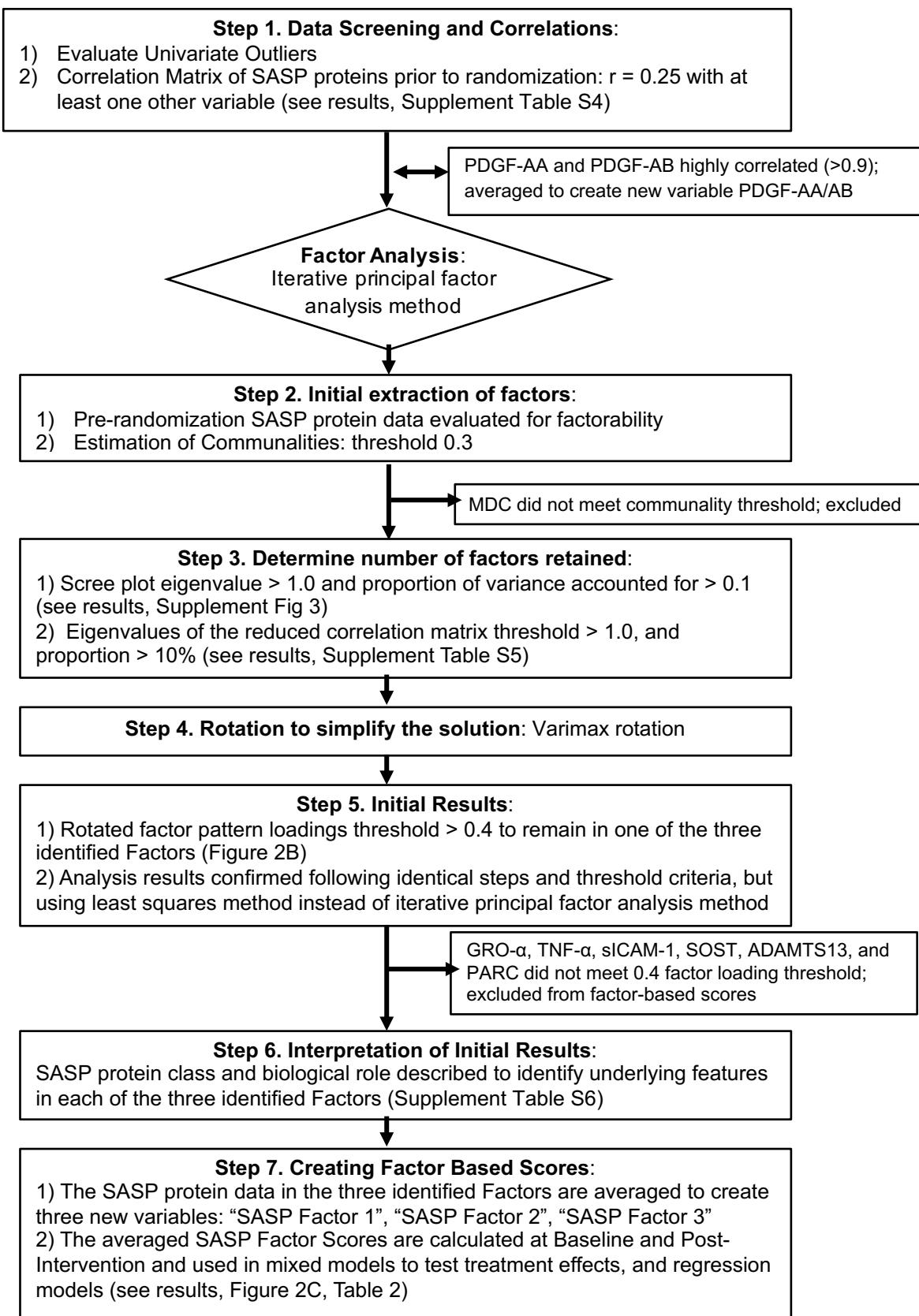


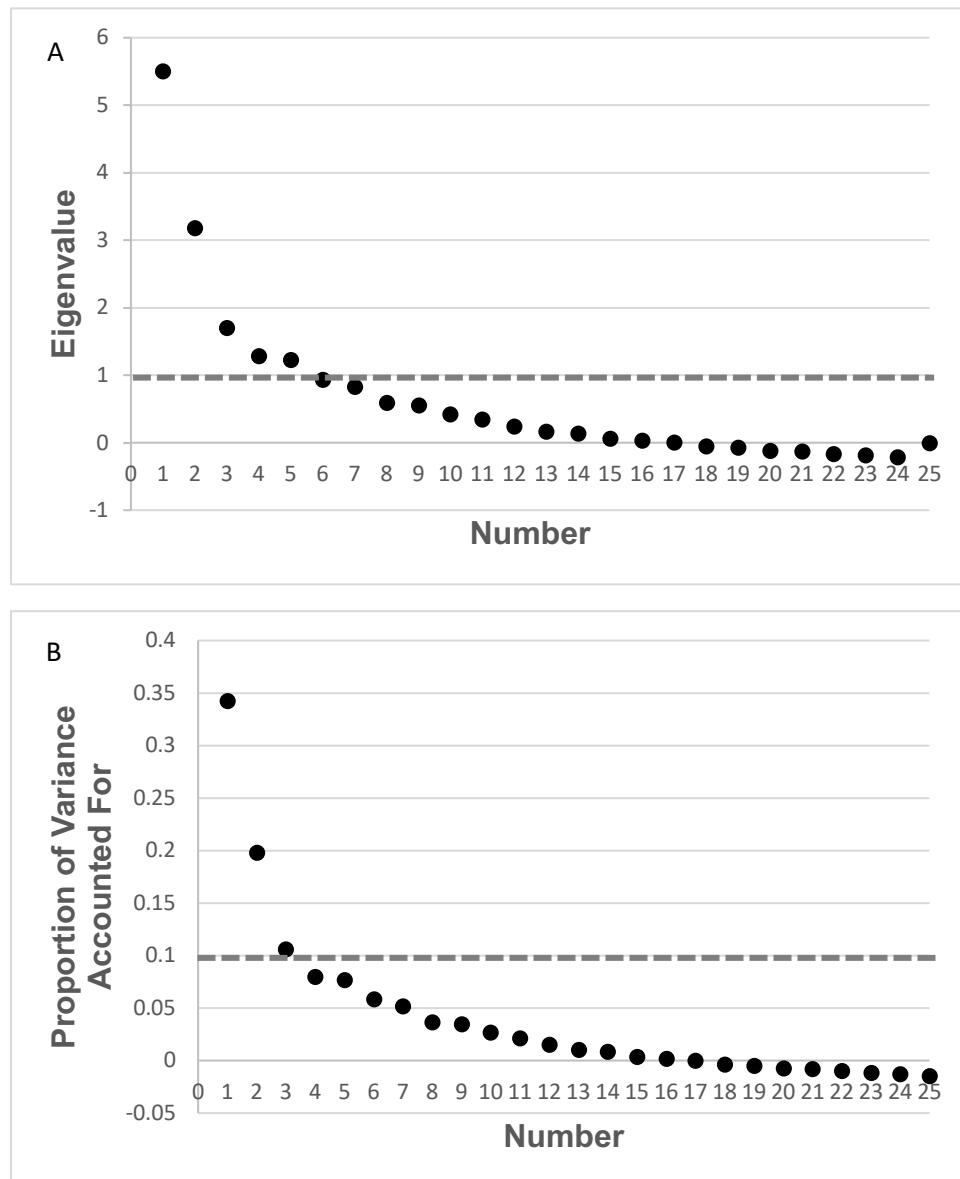
Supplemental Figure 1. Flow of Participants through NCT02869659 and SASP Biomarker Ancillary.



Supplemental Figure 2. Factor Analysis Flow Chart



Supplemental Figure 3. Scree plot of preliminary eigenvalues (A) and proportion of the variance accounted for (B) for inclusion in exploratory factor analysis with threshold for factor retention marked by dashed line on plot. Based on threshold criteria eigenvalue >1 and proportion of variance >0.1 criteria three factors are retained.



SUPPLEMENTAL TABLES

Table S1. Intervention effect on metabolic function and physical performance in the cell senescence/ SASP ancillary to VEGGIE at baseline and 18 weeks post-intervention of caloric restriction (CR) or health education control (Con).

	Intervention Group (unadjusted)			Intervention Effect (adjusted)
	CR	Control	Unadjusted	Adjusted
	est. mean ±SE	est. mean ±SE	p-value ¹	p-value ²
Body weight (kg)				p<0.001*
Baseline	101.1 ± 2.5	105.6 ± 2.8	0.24	
Post-intervention	90.3 ± 2.5	106.1 ± 2.8	<0.001*	
Change	-10.8 ± 0.9	+0.5 ± 0.9	<0.001*	
BMI (kg/m²)				p<0.001*
Baseline	36.20 ±0.95	37.91 ±1.04	0.23	
Post-intervention	32.23 ±0.95	37.88 ±1.04	<0.001*	
Change	-3.97 ±0.32	-0.03 ±0.35	<0.001*	
Waist Circumference (cm)				p<0.001*
Baseline	110.8 ± 1.8	113.7 ± 2.1	0.30	
Post-intervention	100.35 ± 1.9	114.6 ± 2.1	<.0001 *	
Change	-10.4 ± 0.90	+1.0 ± 0.95	<0.001*	
Fasting insulin (mIU/L)				p=0.03*
Baseline	14.56 ±2.26	21.87 ±2.37	0.03*	
Post-intervention	9.56 ±2.23	25.31 ±2.45	<0.001*	
Change	-5.00 ±2.57	+3.44 ±2.73	0.03*	
HbA1c (%)				p<0.001*
Baseline	5.74 ± 0.06	5.75 ± 0.07	0.93	
Post-intervention	5.54 ± 0.06	5.75 ± 0.07	0.04*	
Change	-0.20 ± 0.03	-0.01 ± 0.04	0.0002*	
HOMA-IR (index)				p =0.03*
Baseline	3.87 ± 0.61	5.88 ± 0.65	0.03*	
Post-intervention	2.53 ± 0.61	6.80 ± 0.67	<0.001*	
Change	-1.33 ± 0.68	+0.93 ± 0.73	0.03*	
Creatinine (mg/dL)				p 0=.41
Baseline	0.857 ± 0.03	0.837 ± 0.03	0.65	
Post-intervention	0.849 ± 0.03	0.804 ± 0.03	0.33	
Change	-0.008 ± 0.02	-0.033 ± 0.02	0.39	
LDL Cholesterol (mg/dL)				p =1.0
Baseline	114.7 ± 5.3	111.4 ± 5.8	0.68	
Post-intervention	109.4 ± 5.4	106.0 ± 5.9	0.67	
Change	-5.3 ± 4.0	-5.4 ± 4.4	0.98	
Total Cholesterol (mg/dL)				p =0.58
Baseline	189.6 ± 6.4	185.8 ± 7.0	0.69	
Post-intervention	177.8 ± 6.4	177.5 ± 7.0	0.98	
Change	-11.8 ± 4.5	-8.2 ± 4.9	0.59	
Systolic BP (mmHg)				p =0.21
Baseline	130.3 ± 2.7	128.8 ± 2.9	0.71	
Post-intervention	122.1 ± 2.7	125.9 ± 3.0	0.35	

Change	-8.2 ± 2.8	-2.9 ± 3.1	0.21	
Diastolic BP (mmHg)				p =0.03
Baseline	75.3 ± 1.5	72.6 ± 1.6	0.22	
Post-intervention	70.7 ± 1.5	73.6 ± 1.7	0.20	
Change	-4.6 ± 1.8	$+1.1 \pm 1.9$	0.03	

1 Unadjusted comparison

2 Models were adjusted for age, gender, and race

Table S2. Intervention effect on circulating CD3+ T Cell expression of biomarkers related to cell senescence ($p16^{INK4a}$, $p21^{CIP1/WAF1}$) and cell death/ apoptosis (BCL2L, BAK1) at baseline and 18 weeks post-intervention in cell senescence/ SASP biomarker ancillary to VEGGIE, in unadjusted and age, sex, race adjusted models. Data are estimated means and standard error and change as difference of least squares means; intervention effect as mixed model Type 3 tests of fixed effects F-statistic and p-value. Simple linear regression was used to test if change in T cell gene expression significantly predicted % change in weight with intervention (R^2 , p-value shown).

	Intervention Group (unadjusted)			Intervention Effect (adjusted)	Regression, Δ Exp with % Change Weight
	CR	Control	Unadjusted	Adjusted	
	est. mean \pm SE	est. mean \pm SE	p-value ¹	p-value ²	R^2 F-, p-values
$p16^{INK4a}$					
Baseline	10.35 \pm 0.15	10.15 \pm 0.18	0.394	p =0.451	R^2 = 0.001 p = 0.87
Post-intervention	10.40 \pm 0.16	10.35 \pm 0.18	0.828		
Change	+0.049 \pm 0.14	+0.20 \pm 0.15	0.467		
$p21^{CIP1/WAF1}$					
Baseline	12.32 \pm 0.20	12.02 \pm 0.22	0.317	p =0.693	R^2 = 0.022 p = 0.38
Post-intervention	12.51 \pm 0.20	12.32 \pm 0.22	0.547		
Change	+0.18 \pm 0.23	+0.30 \pm 0.25	0.738		
BCL2L					
Baseline	16.47 \pm 0.07	16.39 \pm 0.089	0.490	p =0.884	R^2 = 0.005 p = 0.69
Post-intervention	16.45 \pm 0.09	16.35 \pm 0.10	0.486		
Change	-0.02 \pm 0.12	-0.037 \pm 0.13	0.934		
BAK1					
Baseline	15.03 \pm 0.26	15.38 \pm 0.30	0.386	p =0.198	R^2 = 0.002 p = 0.82
Post-intervention	14.88 \pm 0.32	14.53 \pm 0.34	0.468		
Change	-0.15 \pm 0.39	-0.85 \pm 0.43	0.240		

1 Unadjusted comparison

2 Models were adjusted for age, gender, and race

Table S3. Intervention effect and bivariate correlations (Spearman rank) on log-transformed plasma SASP biomarkers at baseline and 18 weeks post-intervention in cell senescence/ SASP biomarker ancillary to VEGGIE study. Data are estimated means and standard error and change as difference of least squares means; intervention effect as mixed model Type 3 tests of fixed effects p-value. Simple linear regression was used to test if change in SASP protein significantly predicted % change in weight with intervention (R^2 , p-value). * $p \leq 0.05$.

	CR	Control	Adjusted mixed model	Regression, Δ Exp with % Change Weight
	est. mean \pm SE	est. mean \pm SE	p-value	R^2 p-values
Activin A				
Baseline	5.43 \pm 0.06	5.42 \pm 0.07	p<.0001*	$R^2 = 0.384$
Post-intervention	5.18 \pm 0.06	5.40 \pm 0.07	p = 0.937	p<0.001*
Change	-0.24 \pm 0.03*	-0.02 \pm 0.04	p =0.018	
ADAMTS13				
Baseline	13.78 \pm 0.07	13.80 \pm 0.08	p=0.021*	$R^2 = 0.130$
Post-intervention	13.79 \pm 0.07	13.69 \pm 0.08	p =0.887	p = 0.010*
Change	+0.01 \pm 0.03	-0.11 \pm 0.04*	p =0.345	
Eotaxin				
Baseline	4.53 \pm 0.09	4.52 \pm 0.09	p=0.831	$R^2 = 0.010$
Post-intervention	4.50 \pm 0.09	4.52 \pm 0.10	p =0.965	p = 0.46
Change	-0.02 \pm 0.06	-0.003 \pm 0.06	p =0.922	
Fas				
Baseline	8.57 \pm 0.08	8.87 \pm 0.08	p=0.031*	$R^2 = 0.049$
Post-intervention	8.47 \pm 0.08	8.83 \pm 0.08	p =0.013	p = 0.12
Change	-0.10 \pm 0.03*	-0.03 \pm 0.03	p =0.002	
GDF15				
Baseline	6.16 \pm 0.07	6.35 \pm 0.07	p=0.216	$R^2 = 0.056$
Post-intervention	6.14 \pm 0.07	6.37 \pm 0.07	p =0.060	p = 0.09
Change	-0.02 \pm 0.03	+0.03 \pm 0.03	p =0.019*	
Gro-α				
Baseline	4.41 \pm 0.052	4.48 \pm 0.06	p= 0.103	$R^2 = 0.072$
Post-intervention	4.35 \pm 0.053	4.50 \pm 0.06	p =0.356	p = 0.06
Change	-0.06 \pm 0.031	+0.02 \pm 0.03	p =0.066	
sICAM-1				
Baseline	12.31 \pm 0.15	12.21 \pm 0.17	p= 0.002*	$R^2 = 0.307$
Post-intervention	12.23 \pm 0.15	12.22 \pm 0.17	0.640	p<0.001*
Change	-0.08 \pm 0.02*	+0.02 \pm 0.02	0.976	
MCP-1				
Baseline	4.83 \pm 0.08	4.84 \pm 0.08	p= 0.301	$R^2 = 0.034$
Post-intervention	4.80 \pm 0.08	4.89 \pm 0.08	p =0.959	p = 0.20
			p =0.430	

Change	-0.04 ± 0.05	+0.05 ± 0.06		
MMP1				
Baseline	4.66 ± 0.10	4.74 ± 0.12	p = 0.084	R² = 0.084
Post-intervention	4.49 ± 0.11	4.70 ± 0.12	p = 0.588	p = 0.039*
Change	-0.16 ± 0.08*	-0.05 ± 0.08	p = 0.036	
MMP2				R ² = 0.008
Baseline	12.62 ± 0.05	12.62 ± 0.05	p = 0.300	p = 0.532
Post-intervention	12.61 ± 0.05	12.68 ± 0.05	p = 0.978	
Change	-0.01 ± 0.05	+0.07 ± 0.05	p = 0.301	
MMP7				R ² = 0.001
Baseline	7.72 ± 0.09	7.76 ± 0.10	p = 0.562	p = 0.790
Post-intervention	7.66 ± 0.09	7.65 ± 0.10	p = 0.784	
Change	-0.06 ± 0.05	-0.11 ± 0.06	p = 0.936	
MMP9				R ² = 0.001
Baseline	11.27 ± 0.09	11.19 ± 0.10	p = 0.361	p = 0.852
Post-intervention	11.40 ± 0.09	11.19 ± 0.10	p = 0.513	
Change	+0.13 ± 0.09	+0.21 ± 0.13	p = 0.116	
MPO				R ² = 0.028
Baseline	10.43 ± 0.06	10.44 ± 0.06	p = 0.855	p = 0.238
Post-intervention	10.46 ± 0.06	10.47 ± 0.06	p = 0.993	
Change	+0.02 ± 0.04	+0.04 ± 0.05	p = 0.881	
OPN				R ² = 0.019
Baseline	10.29 ± 0.07	10.40 ± 0.08	p = 0.6196	p = 0.339
Post-intervention	10.31 ± 0.07	10.39 ± 0.08	p = 0.275	
Change	+0.02 ± 0.05	-0.01 ± 0.05	p = 0.450	
PAI-1 / Serpin				R ² = 0.125
Baseline	10.35 ± 0.12	10.49 ± 0.13	p = 0.054*	p = 0.011
Post-intervention	9.97 ± 0.12	10.41 ± 0.13	p = 0.393	
Change	-0.36 ± 0.11*	-0.08 ± 0.12	p = 0.017	
PARC				R ² = 0.053
Baseline	10.99 ± 0.08	10.87 ± 0.09	p = 0.556	p = 0.103
Post-intervention	11.02 ± 0.08	10.86 ± 0.09	p = 0.326	
Change	+0.03 ± 0.05	-0.01 ± 0.05	p = 0.196	
PDGF-AA				R ² = 0.026
Baseline	7.19 ± 0.19	7.23 ± 0.20	p = 0.888	p = 0.257
Post-intervention	7.12 ± 0.19	7.13 ± 0.21	p = 0.876	
Change	-0.07 ± 0.13	-0.01 ± 0.14	p = 0.955	
PDGF-AB				R ² = 0.018
Baseline	5.95 ± 0.20	6.00 ± 0.21	p = 0.758	p = 0.342
Post-intervention	5.90 ± 0.20	5.89 ± 0.22	p = 0.864	
Change	-0.05 ± 0.14	-0.12 ± 0.15	p = 0.967	
RAGE				R ² = 0.006
Baseline	7.10 ± 0.08	7.22 ± 0.09	p = 0.378	p = 0.599
Post-intervention	7.05 ± 0.08	7.22 ± 0.09	p = 0.305	
			p = 0.159	

Change	-0.05 ± 0.04	-0.17 ± 0.12		
RANTES				
Baseline	9.38 ± 0.19	9.02 ± 0.21	p=0.147	R ² = 0.017
Post-intervention	9.40 ± 0.20	8.73 ± 0.21	p =0.214	p = 0.355
Change	+0.01 ± 0.14	-0.67 ± 0.29	p =0.026	
SOST				
Baseline	6.39 ± 0.12	6.56 ± 0.13	p=0.112	R ² = 0.057
Post-intervention	6.45 ± 0.12	6.50 ± 0.13	p =0.343	p = 0.090
Change	+0.06 ± 0.05	-0.06 ± 0.18	p =0.751	
TNFR1				
Baseline	6.71 ± 0.05	6.78 ± 0.05	p<0.001*	R ² = 0.387
Post-intervention	6.61 ± 0.05	6.78 ± 0.05	p =0.347	p<0.001*
Change	-0.11 ± 0.02*	+0.001 ± 0.02	p =0.017	
TNFRII				
Baseline	7.82 ± 0.06	7.92 ± 0.06	p = 0.017*	R ² = 0.107
Post-intervention	7.75 ± 0.06	7.96 ± 0.06	p =0.250	p = 0.019*
Change	-0.07 ± 0.03*	+0.04 ± 0.03	p =0.020	
TNF-Alpha				
Baseline	0.98 ± 0.09	1.11 ± 0.09	p = 0.086	R ² = 0.087
Post-intervention	0.95 ± 0.09	1.18 ± 0.09	p =0.291	p = 0.036*
Change	-0.03 ± 0.04	+0.07 ± 0.04	p =0.069	
uPAR				
Baseline	5.93 ± 0.07	6.03 ± 0.07	p = 0.071	R ² = 0.105
Post-intervention	5.84 ± 0.07	6.04 ± 0.07	p =0.286	p = 0.020*
Change	-0.08 ± 0.03*	+0.01 ± 0.03	p =0.050	
VEGF				
Baseline	3.42 ± 0.12	3.49 ± 0.13	p = 0.087	R ² = 0.110
Post-intervention	3.27 ± 0.12	3.43 ± 0.13	p =0.714	p = 0.018*
Change	-0.25 ± 0.08*	-0.06 ± 0.09	p =0.078	

Table S4. Correlation Matrix (absolute value of Pearson r) between log transformed SASP factors. Color to reflect strength of association as criteria for inclusion in exploratory factor analysis.

	Activin A	ADAMTS13	Eotaxin	Fas	GDF15	GroAlpha	ICAM1	MCP1	MMP1	MMP2	MMP7	MMP9	MPO	OPN	PAI1	PARC	PDGF AA/AB	RAGE	RANTES	SOST	TNFa	TNFR1	TNFRII	uPAR
ADAMTS13	0.10																							
Eotaxin	0.15	0.22																						
Fas	0.20	0.02	0.03	0.34																				
GDF15	0.41	0.00	0.03	0.34																				
GRO-a	0.04	0.06	0.24	0.27	0.21																			
ICAM1	0.11	0.01	0.16	0.04	0.01	0.21																		
MCP1	0.20	0.25	0.55	0.07	0.07	0.15	0.12																	
MMP1	0.28	0.05	0.03	0.20	0.27	0.39	0.24	0.23																
MMP2	0.50	0.08	0.29	0.03	0.16	0.25	0.36	0.23	0.39															
MMP7	0.43	0.11	0.10	0.07	0.20	0.17	0.07	0.19	0.32	0.35														
MMP9	0.12	0.01	0.48	0.15	0.15	0.26	0.21	0.13	0.11	0.10	0.21													
MPO	0.30	0.12	0.15	0.05	0.35	0.15	0.20	0.24	0.04	0.19	0.21	0.29												
OPN	0.23	0.04	0.26	0.30	0.20	0.26	0.29	0.25	0.33	0.32	0.05	0.13	0.13											
PAI1	0.29	0.22	0.69	0.07	0.10	0.25	0.16	0.40	0.15	0.25	0.03	0.35	0.13	0.18										
PARC	0.01	0.18	0.09	0.16	0.17	0.15	0.03	0.00	0.00	0.10	0.07	0.09	0.37	0.09	0.14									
PDGF AA/AB	0.19	0.25	0.78	0.04	0.13	0.38	0.15	0.33	0.21	0.17	0.04	0.45	0.02	0.14	0.77	0.14								
RAGE	0.26	0.13	0.04	0.02	0.20	0.01	0.03	0.42	0.23	0.25	0.26	0.22	0.22	0.05	0.13	0.13	0.09							
RANTES	0.15	0.18	0.48	0.16	0.01	0.25	0.02	0.09	0.05	0.03	0.13	0.27	0.05	0.02	0.59	0.05	0.75	0.44						
SOST	0.24	0.12	0.23	0.05	0.03	0.09	0.03	0.15	0.07	0.22	0.08	0.05	0.09	0.11	0.22	0.17	0.12	0.12	0.03					
TNF-a	0.11	0.20	0.16	0.11	0.03	0.20	0.33	0.29	0.23	0.23	0.03	0.13	0.21	0.23	0.26	0.14	0.11	0.20	0.16	0.08				
TNFR1	0.29	0.24	0.05	0.28	0.33	0.17	0.22	0.37	0.48	0.24	0.17	0.03	0.36	0.37	0.03	0.11	0.10	0.56	0.22	0.12	0.31			
TNFRII	0.21	0.21	0.06	0.24	0.37	0.27	0.28	0.27	0.47	0.28	0.01	0.08	0.27	0.34	0.19	0.14	0.09	0.24	0.12	0.10	0.31	0.65		
uPAR	0.25	0.08	0.39	0.34	0.41	0.40	0.26	0.29	0.49	0.28	0.20	0.35	0.36	0.39	0.27	0.19	0.44	0.19	0.20	0.03	0.17	0.40	0.19	
VEGF	0.15	0.18	0.57	0.05	0.31	0.26	0.10	0.38	0.28	0.15	0.01	0.42	0.10	0.14	0.55	0.05	0.77	0.16	0.48	0.08	0.10	0.29	0.12	0.44

Table S5. Eigenvalues of the reduced correlation matrix; Total 9.70, Average 0.39.

	Eigenvalue	Proportion	Cumulative
1	5.29	0.55	0.55
2	2.99	0.31	0.85
3	1.43	0.15	1.00
4	0.98	0.10	1.10
5	0.93	0.10	1.20
6	0.66	0.07	1.26
7	0.57	0.06	1.32
8	0.34	0.04	1.36
9	0.24	0.03	1.38
10	0.15	0.02	1.40
11	0.06	0.01	1.41
12	-0.01	0.00	1.41
13	-0.04	0.00	1.40
14	-0.10	-0.01	1.39
15	-0.15	-0.02	1.38
16	-0.16	-0.02	1.36
17	-0.20	-0.02	1.34
18	-0.26	-0.03	1.31
19	-0.31	-0.03	1.28
20	-0.36	-0.04	1.24
21	-0.40	-0.04	1.20
22	-0.42	-0.04	1.16
23	-0.48	-0.05	1.11
24	-0.49	-0.05	1.06
25	-0.58	-0.06	1.00

Table S6. SASP factors presented according to factor loading. SASP measures can be classed generally as soluble signaling factors (cytokines, chemokines, and growth factors), soluble receptors or ligands, and proteases and regulators (MMP's and other enzymes), with further subclass or type, and biological role.

	Variable	Name	Class	Subclass / Type	Role
Factor 1	PDGF AA/AB	Platelet-Derived Growth Factor	Signaling factors	Growth factor	Proliferation; Chemoattractant; Mitogen
	Eotaxin / CCL11	CC motif chemokine ligand, CCL11	Signaling factors	CC Chemokine	Chemoattractant (eosinophils)
	PAI1	Plasminogen Activator Inhibitor-1	Proteases and regulators	Plasminogen activator system	Serine protease inhibitor (SERPIN) family; Regulate fibrinolytic system
	RANTES	Regulated upon Activation, Normal T Cell Expressed and Secreted	Signaling factors	CC Chemokine	Proinflammatory; Chemoattractant (T cells)
	VEGF	Vascular endothelial growth factor	Signaling factors	Growth factor	Vasculogenesis; Angiogenesis; PDGF subfamily
	MMP9	Matrix Metalloproteinase-9	Proteases and regulators	Enzyme (Matrixin)	Degradation of the extracellular matrix; Gelatinase
Factor 2	TNFRI	Tumor Necrosis Factor Receptor I	Receptors or ligands	TNF Superfamily	Immune cell regulation; Mediate apoptosis
	uPAR	Urokinase-type plasminogen activator receptor	Receptors or ligands	Plasminogen activator system	Wound healing; Proteolysis; Inflammation; Plasminogen activation system
	TNFRII	Tumor Necrosis Factor Receptor II	Receptors or ligands	TNF Superfamily	Wound healing; Immune cell regulation
	MMP1	Matrix Metalloproteinase-1	Proteases and regulators	Enzyme (Matrixin)	Degradation of extracellular matrix; Collagenase
	GDF15	Growth differentiating factor-15	Signaling factors	TGF β Superfamily	Regulation of inflammatory pathways; Apoptosis; cell repair, and cell growth
	OPN	Osteopontin	Signaling factors	Extracellular structural protein	Apoptosis; Bone remodeling; Chemoattractant (neutrophils; macrophage)
	Fas	Fas Ligand	Receptors or ligands	TNF Superfamily	Mediate apoptosis
	MPO	Myeloperoxidase	Proteases and regulators	Leukocyte-derived enzyme	Catalyzes the formation of a number of reactive oxidant species
	GRO α / CXCL1	Growth-regulated protein alpha	Signaling factors	CXC Chemokine	Chemoattractant (neutrophils); Regulation of immune/inflammatory response
	TNF α	Tumor Necrosis Factor-alpha	Signaling factors	TNF Superfamily	Regulation of immune / inflammatory responses; Adipokine
	ICAM1	Intercellular adhesion molecule-1	Receptors or ligands	Immunoglobulin Superfamily	T-cell activation; Regulation of immune /inflammatory responses
Factor 3	ActivinA	Activin A	Signaling factors	TGF β Superfamily	Regulation of proinflammatory responses; Differentiation
	RAGE	Receptor for advanced glycation end products	Receptors or ligands	Immunoglobulin Superfamily	Bind glycoproteins; Pro-inflammatory activation
	MMP7	Matrix Metalloproteinase-7	Proteases and regulators	Enzyme (Matrixin)	Degradation of the extracellular matrix; Wound healing
	MCP1	Monocyte chemoattractant protein	Signaling factors	CC Chemokine / Cytokine	Chemoattractant (monocytes, basophils); Bone degradation
	MMP2	Matrix Metalloproteinase-2	Proteases and regulators	Enzyme (Matrixin)	Degradation of the extracellular matrix; Gelatinase
	SOST	Sclerostin precursor	Signaling factors	Secreted Glycoprotein	Wnt pathway inhibitor; Inhibit bone formation;
	ADAMTS13	A disintegrin and metalloprotease with thrombospondin type motifs	Proteases and regulators	Enzyme (Matrixin)	Cleaves von Willebrand factor (vWF); Blood clotting
	PARC	Parkin-like ubiquitin ligase	Proteases and regulators	E3-ubiquitin ligase; RBR Family	Cytoplasmic anchor in p53-associated protein complexes

Table S7. Intervention effect on circulating SASP factors presented according to factor loading at baseline and 18 weeks post-intervention of CR or health education control. Data are estimated means and standard error and change as difference of least squares means; intervention effect as mixed model Type 3 tests of fixed effects F-statistic and p-value. Simple linear regression was used to test if change in composite SASP Factor scores significantly predicted % change in weight with intervention (R^2 , F-statistic, p-value). * $p \leq 0.05$.

	Intervention Group (unadjusted)			Intervention Effect (adjusted)	Regression, Δ Exp with % Change Weight
	CR	Control	Unadjusted	Adjusted	
	est. mean \pm SE	est. mean \pm SE	p-value ¹	p-value ³	R^2 p-values
SASP Factor 1					
Baseline	7.59 \pm 0.11	7.55 \pm 0.12	0.840		$R^2 = 0.027$
Post-intervention	7.51 \pm 0.11	7.46 \pm 0.12	0.780		$p = 0.248$
Change	-0.077 \pm 0.09	-0.091 \pm 0.093	0.916		
SASP Factor 2				p 0.046*	$R^2 = 0.123$
Baseline	7.57 \pm 0.04	7.69 \pm 0.05	0.065		$p = 0.011^*$
Post-intervention	7.51 \pm 0.04	7.69 \pm 0.05	0.005*		
Change	-0.062 \pm 0.02*	0.002 \pm 0.02	0.048*		
SASP Factor 3				p 0.072	$R^2 = 0.067$
Baseline	7.54 \pm 0.04	7.57 \pm 0.05	0.644		$p = 0.068$
Post-intervention	7.46 \pm 0.05	7.57 \pm 0.05	0.108		
Change	-0.082 \pm 0.03*	0.003 \pm 0.03	0.072		

1 Unadjusted comparison

2 Models were adjusted for age, sex and race

3 Age, sex, and race adjusted comparison to detect intervention effect. F-value and p correspond to Type III fixed effect model for adjusted time \times intervention group interaction in model adjusted for age, sex, and race