5-11-2015

The Effect of the Traditional Mediterranean-Style Diet on Metabolic Risk Factors: A Meta-Analysis

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The Effect of the Traditional Mediterranean-Style Diet on Metabolic Risk Factors: A Meta-Analysis

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BS, RD, University of Connecticut, 2013

A Thesis
Submitted in Partial Fulfillment of the Requirements for the Degree of Master of Science
At the University of Connecticut
2015
The Effect of the Traditional Mediterranean-Style Diet on Metabolic Risk Factors: A Meta-Analysis

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Acknowledgments

I would like to express my special appreciation and thanks for my advisor, Dr. Huedo-Medina, as you have been a tremendous mentor for me. I would like to thank you for teaching me invaluable skills in statistics and research. At the beginning of this experience I did not know much about statistics or meta-analysis. You were not only able to make me feel comfortable in this new discipline, but also passionate about my work. Thank you for encouraging me every step of the way. Your advice and mentorship on my research as well as on my career have been priceless. I would also like to thank Dr. Bihuniak for being a wonderful mentor, friend, and role model in both research and life. If it was not for your advice and guidance I would not have ventured on this challenging but rewarding journey to earn my Master’s degree. I would like to thank Dr. Kerstetter and Dr. Kenny for serving as committee members. I would especially like to thank Dr. Kerstetter for providing me with the opportunity to earn my Master’s degree at the University of Connecticut. Thanks to Julia Shook for assisting me with data extraction and always offering a helping hand. I would like to thank all of my SIPED lab mates for all of their advice, friendship, and comic relief. Thank you all for your support throughout the past few years.

A special thanks to my family for their unwavering and unconditional support. I am incredibly grateful to my mother, sister, aunt, uncle, grandmother, and cousins for always believing in me and supporting my career and education goals. I would like to thank all of my close friends for motivating me in times of hardship and understanding and respecting the time I needed to devote to my research. At the end I would like to express appreciation to my beloved and best friend, Chris Darling, who has been my steady rock throughout this journey.
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Abstract

**Importance:** A Mediterranean-style diet has been shown to be effective in improving a variety of disease outcomes, including metabolic risk factors. Such dietary patterns are complex and, thus it is currently unclear as to which components and intervention characteristics are more greatly associated with reducing metabolic syndrome risk.

**Objective:** To obtain overall effect sizes for the metabolic risk factors (waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure) and explain the variability across the current literature based on study design, sample, and diet characteristics.

**Data Sources:** Six electronic databases (PubMed, EMBASE, Web of Science, CINAHL, CAB Direct, and Agricola) were searched from inception until August 4, 2014 using a comprehensive Boolean search strategy.

**Study Selection:** Studies were included if pre- and post- intervention measurements of waist circumference were reported and the traditional Mediterranean-style diet was used as a dietary intervention. Data from 32 studies (N = 3,550) were included.

**Data Extraction and Synthesis:** Independent researchers identified studies that met the inclusion criteria and coded methodological, participant, and intervention characteristics.

**Main Outcomes and Measures:** Weighted mean effect size under random-effects assumptions were obtained and modeled after pooling the individual standardized mean differences for each study on the six metabolic risk factors.
Results: There were significant beneficial effects in favor of the traditional Mediterranean-style diet for waist circumference, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure ($d^+ = -0.58$, 95% CI -0.81 to -0.35; $d^+ = -0.33$, 95% CI -0.69 to -0.19; $d^+ = -0.51$, 95% CI -0.80 to -0.22; $d^+ = -0.74$, 95% CI -1.03 to -0.46; $d^+ = -0.92$, 95% CI -1.41 to -0.43, respectively).

The Mediterranean-style diet was significantly beneficial when, in general the intervention period was longer in duration, the study was conducted in Europe, the study used a behavioral technique, and the study was conducted primarily using small groups.

Conclusions and Relevance: The traditional Mediterranean-style diet had a significant beneficial effect on five of the six metabolic risk factors. This dietary pattern appears to be most successful in reducing metabolic risk when it is recommended for longer periods of time and is implemented using social support.
Introduction

Metabolic syndrome is defined as a group of interrelated risk factors of metabolic origin that appear to directly promote the development of cardiovascular disease (CVD). These metabolic risk factors are also associated with the development of type 2 diabetes mellitus. Underlying risk factors for metabolic syndrome include abdominal obesity, insulin resistance, physical inactivity, aging, hormonal imbalance, and genetic or ethnic predisposition.

Currently, lifestyle therapies such as diet modification and physical activity are first-line interventions to treat the metabolic risk factors. The traditional Mediterranean-style diet (MedSD) is well-known for its cardio-protective benefits and should be considered for prevention and treatment of metabolic syndrome.

The National Cholesterol Education Program’s Adult Treatment Panel III report (NCEP ATPIII) identified six components of metabolic syndrome that are related to CVD: 1) abdominal obesity, 2) atherogenic dyslipidemia, 3) elevated blood pressure, 4) insulin resistance, 5) proinflammatory state, and 6) prothrombotic state. According to the ATP III criteria, a diagnosis of metabolic syndrome can be made when three out of five of the following characteristics are present: 1) abdominal obesity characterized by waist circumference >102 cm for men and >88 cm for women, 2) triglycerides ≥150mg/dL, 3) HDL cholesterol <40 mg/dL for men and <50 mg/dL for women, 4) blood pressure ≥130/≥85 mmHg, and 5) fasting glucose ≥110 mg/dL. Metabolic syndrome is a major health concern in the United States with increasing prevalence. Findings from the Third
National Health and Nutrition Examination Survey (NHANES) suggest that according to the ATP III criteria approximately 34% of adults in the United States have metabolic syndrome⁴. Males and females 40-59 years of age were about three times more likely as those 20-39 years of age to meet the criteria for metabolic syndrome⁴. Males 60 years of age and older were four times as likely and females 60 years of age and older were more than six times as likely as the youngest age group (20-39 years of age) to meet the criteria for metabolic syndrome⁴. With the increasing prevalence of metabolic syndrome, diet modification, particularly adherence to the traditional MedSD, should be considered as a lifestyle change.

The MedSD refers to the dietary habits traditionally followed by people in the countries bordering the Mediterranean Sea². The traditional MedSD puts emphasis on an abundance of food from plant sources, a variety of minimally processed and locally grown foods, and olive oil as the principal source of fat⁵. This dietary pattern also includes daily consumption of low to moderate amounts of cheese and yogurt (low-fat and non-fat versions may be preferable), twice weekly consumption of fish and poultry, consumption of up to seven eggs per week, fresh fruit as dessert, red meat consumption limited to a few times a month, moderate consumption of wine (1 glass/day for women and 1-2 glasses/day for men) and regular physical activity at a level which promotes healthy weight and well-being⁵.
The beneficial role of the MedSD with regard to overall mortality and other chronic diseases is well-established. A 2010 meta-analysis of prospective studies found that adherence to the Mediterranean diet suggests significant protection against major chronic degenerative diseases, a significant reduction in death from any cause, a reduction in the incidence of cardio-and cerebro-vascular diseases, reduction in the incidence of neoplastic diseases, and reduction of the incidence of neurodegenerative diseases\(^2\). In addition, a secondary analysis of the PREDIMED\(^6\) trial concluded that an energy-unrestricted Mediterranean diet may be useful in reducing the risks of central obesity and hyperglycemia in people at high risk of CVD\(^7\). However, there is limited evidence on the effect of a traditional MedSD on metabolic risk factors.

To our knowledge, only one meta-analysis has evaluated literature on the effects of a Mediterranean diet on metabolic syndrome to date\(^8\). This meta-analysis included 35 clinical trials, 2 prospective studies, and 13 cross-sectional studies with a total of 534,906 participants and found an overall beneficial effect of the Mediterranean diet on reducing metabolic syndrome and its components in adults\(^8\). Further, the Scientific Report of the 2015 Dietary Guidelines Advisory Council\(^9\) found dietary characteristics similar to that of a MedSD, including higher intake of vegetables, fruits, seafood, legumes, and nuts; moderate intake of alcohol (among adults); lower consumption of red and processed meat, and low intake of sugar-sweetened foods and drinks\(^9\), to have a positive effect on metabolic syndrome risk factors (i.e., blood pressure and lipid profiles). Taken
together, the findings from the meta-analysis by Kastorini et al.\textsuperscript{3} noted above and the 2015 Dietary Guidelines Advisory Council\textsuperscript{9} clearly support the positive effects of the MedSD on metabolic risk factors. However, it is currently unclear which specific characteristics of these MedSD interventions greatly contribute to significant beneficial effects on the metabolic risk factors such as specific population, location, length of adherence to the MedSD and specific dietary components. Analyzing particular moderators within the current evidence can allow for the development of population specific guidelines to enhance the beneficial effects of the MedSD as well as increase adherence to this dietary pattern.

As mentioned above, CVD risk factors and metabolic syndrome are interrelated such that the diagnostic criteria defining metabolic syndrome encompasses a cluster of health outcomes related to CVD risk. Several systematic reviews and meta-analyses published within the last 10 years that have focused on the MedSD and CVD risk outcomes have reported an overall beneficial effect of the MedSD in reducing CVD risk factors\textsuperscript{10}. Before evidenced-based guidelines for CVD risk reduction can be put into practice, these meta-analyses should undergo a formal evaluation of quality. To address this issue, we recently conducted a review\textsuperscript{10} of methodological quality of systematic reviews and meta-analyses on the MedSD and CVD risk outcomes using an established methodological quality scale (Assessment of Multiple Systematic Reviews\textsuperscript{11}). On average, reviews achieved a low quality score (\textit{Mean} = 7.9±5.10) relative to the
maximum AMSTAR MD score of 20\textsuperscript{10}. Four reviews satisfied at least 80\% of the items possible, suggesting relatively high quality, 3 satisfied at least 45\% of the items, suggesting moderate quality, and the other 13 satisfied less than 45\% of the items, suggesting low quality\textsuperscript{10}. The data from this review suggest that current meta-analyses evaluating the effects of the MedSD on CVD risk do not fully comply with contemporary methodological quality standards. This review provides evidence to support the need for high quality systematic reviews and meta-analyses on the MedSD and various health outcomes that comply with current methodological quality standards.

Given the increasing prevalence of metabolic syndrome, the popularity and relevance of the MedSD, and the reported quality issues of current meta-analyses that have focused on the MedSD, we were interested in evaluating the effects of the traditional MedSD on the following metabolic risk factors: 1) waist circumference, 2) HDL cholesterol, 3) triglycerides, 4) systolic blood pressure, 5) diastolic blood pressure, and 6) fasting blood glucose. The purpose of this work was to conduct a high-quality meta-analysis to evaluate the relationship between the traditional MedSD and metabolic risk factors. This study had three specific aims: 1) to obtain overall effect sizes for each outcome of interest (waist circumference, HDL cholesterol, triglycerides, systolic blood pressure, diastolic blood pressure, and fasting blood glucose), 2) to evaluate the variability/consistency across the current literature on this topic, and 3) to explain
the variability across the current literature on this topic using moderators based on study, sample, and diet characteristics.

Our primary hypothesis is that effects for each outcome will favor the traditional MedSD against baseline (standardized mean difference, $d\neq 0$) with a null hypothesis that the traditional MedSD will have no impact on metabolic risk factors ($d=0$). Our second hypothesis is that the studies will show large and significant variability based on the Q statistic and the $I^2$ index. Lastly, we hypothesized that the variability will be explained using moderators based on sample, diet and study characteristics.

**Methods**

**Literature Search**

The data sources were obtained following the Preferred Reporting Items for Systematic Reviews and Meta-Analyses: The PRISMA Statement guidelines. Original research studies that were published regardless of publication type until August 4, 2014 were included. Language was not restricted. Six computer databases were searched: PubMed, EMBASE (via Scopus), Web of Science, CINAHL, Agricola, and CAB Direct. A comprehensive literature search was conducted with the assistance of the University of Connecticut Health Sciences Librarian (JL) using combinations of Medical Subject Headings and other key words related to the aim of the study. Examples of the key words include: “Mediterranean Diet”, “Mediterranean Style Diet”, adiposity, “metabolic syndrome”, overweight, BMI, “body mas”, “waist
circumference”, obese, obesity, “abdominal fat”, and “weight loss”. The comprehensive search that was conducted for each database can be found in Appendix 1. In addition to the electronic database search, all studies from Kastorini, et al. were screened and four studies overlap in both meta-analyses. The original search focused on obesity outcomes such as weight, BMI, and waist circumference. With the current focus on metabolic risk factors, studies must report pre-and post-intervention data on waist circumference in order to be included in the analysis. Manuscripts that met the following criteria were included: studies that had pre- and post-intervention measurements for at least waist circumference (any other metabolic risk factors were additional) and studies that focused on the Mediterranean diet as a whole dietary pattern. Studies that did not have pre- and post-intervention data on waist circumference, those that focused on particular components of the Mediterranean diet, such as only olive oil, those that included exercise in the intervention, and those that did not report the information in a way that would allow effect sizes to be calculated using the published information were excluded. The relevance of studies was assessed by two independent researchers (MG and JS) with a hierarchical approach on the basis of title, abstract, and full manuscript. The original search resulted in 1,269 abstracts with relevant key words. After screening and hand-searching articles, 32 articles (41 total comparisons) that used the traditional MedSD were included in analysis. Refer to Figure 1 for the PRISMA figure of included and excluded articles. Table 1 provides a description of included
studies. The screening form used by both coders can be found in Appendix 2. A list of excluded articles is available upon request.

**Data Extraction**

A comprehensive and detailed coding form and manual was created by a team of researchers comprised of registered dietitians, a biostatistician, and a physician. The coding form includes approximately 330 variables for each study. Various characteristics were extracted from each study: 1) sample characteristics such as ethnicity, number and proportion of females, location of sample, and recruitment details, 2) intervention characteristics such as length of intervention, diet type, distribution of macronutrients, calorie intake, and participation in dietary counseling, and 3) study design characteristics such as number of interventions, type of control group, experimental conditions, and setting. The coding form was pilot-tested by two independent researchers (MG and JS) and was reviewed by additional experts (JB, JK, AK, TBHM) before being finalized. The coding form can be found in Appendix 3. The coding manual is available upon request. All 32 studies were independently reviewed and coded by two researchers (MG and JS) and disagreements were solved by a third-party expert (TBHM).

**Risk of Bias**

The Cochrane Collaboration’s tool for assessing risk of bias was used to assess risk of bias within individual studies. Raters score items with either a minus sign (“-“) indicating high risk of bias; a plus sign (“+”) indicating moderate risk of bias; or a double plus sign (“++“) indicating low risk of bias for that
parameter. In accordance with these guidelines, we report descriptions of internal and external validity summary ratings categorically, converting these to numerical scores as necessary for the purpose of meta-analytic moderator analysis.

Methodological quality (MQ) rankings have been identified as an under-analyzed element of the data reported in meta-analyses. In this meta-analysis, MQ ratings based on the Cochrane risk of bias scale were entered as one or more possible moderators into the mixed-effects metaregression models.

Statistical Analysis

All descriptive statistics for the included articles were calculated using SAS Version 9.4. All code for this analysis can be found in Appendix 4. Interrater reliability was calculated for all continuous and categorical variables using IBM SPSS Statistics Version 22. The Kappa (κ) coefficient was used to calculate categorical agreement (kappa=0.94, 96.9% agreement) and Pearson’s correlation coefficient was used to calculate continuous agreement (r=1). We tested for asymmetries by using the Begg, Egger, and trim-and-fill statistical tests as well as the funnel plot graphical technique. Publication bias and the remaining statistical tests were calculated using R version 3.1.2 “metafor” package. All code for this analysis can be found in Appendix 5.

Effect sizes (ESs) were calculated for each outcome by calculating the standardized mean change for each sample. The standardized mean change, $d$, is the difference between the post-test and pre-test means for one sample,
divided by the pre-test standard deviation. The standardized mean change allows results from several kinds of designs to be compared or combined directly, eliminating the need to omit studies because of design differences (i.e., between versus within-in group). The effect size index, $d$, follows a normal distribution with a range from negative infinity to positive infinity with zero as the null value. Following Cohen’s classification the magnitude of the standardized $d$ value can be interpreted as 0.25, 0.5, and 0.8 for small, median, and large effects on the outcomes of interest. However, ESs should be interpreted based on their clinical impact depending on the specific outcome and area of research. ESs were calculated using an effect size coding calculator created by Huedo-Medina, et al. This calculator uses a factor that controls for small sample size.

The data extracted to obtain the individual ESs could be means and standard deviations, F-ANOVA, t-test, or mean and standard deviation change. To uphold the assumption of independence, each outcome was analyzed independently when multiple outcomes were reported from the same study. Twenty four studies report at least three outcomes with the most common outcomes being waist circumference, HDL cholesterol, and triglycerides; fifteen studies reported all six outcomes of interest. A multivariate approach for multiple subsamples per study was not followed because no more than five comparisons were available per study. Multiple ESs were obtained from the same study when data was reported separately by participant and diet characteristics. Only two
studies had subsamples based on gender\textsuperscript{31,32}, three studies had multiple subsamples for participant characteristics\textsuperscript{33,34,35}, and one study had subsamples based on different distributions of macronutrients throughout the day\textsuperscript{36}.

Weighted mean effect size by the inverse of the variance of each study was calculated across all studies under random- and fixed-effects assumptions\textsuperscript{37}. The random effects model assumes that the data is coming from different populations and accounts for within and between-study variance\textsuperscript{37}. The fixed effects model assumes that all effect sizes are from the same population and accounts for only within study variance\textsuperscript{37}. To test for heterogeneity, Cochran’s $Q$ and $I^2$ were calculated. $Q$ tests for significance of heterogeneity\textsuperscript{38} whereas $I^2$ calculates the magnitude of heterogeneity with a range from 0\%-100\%\textsuperscript{39}. To evaluate the sources of heterogeneity of the ESs, moderator analysis using weighted mixed-effects models with maximum likelihood estimation of the random-effects weights was performed testing each variable for study, intervention, and participant characteristics independently. Moderator analysis was conducted by using the “mods” command in R. The moving constant technique\textsuperscript{40} was used to produce estimates of the ES ($d+$) at meaningful levels of the moderators and their CIs at different levels of interest. This technique was used to demonstrate results at the maximum and minimum values of significant moderators. Two-sided statistical significance was $p<0.05$. Finally, clinical units of measures were included by transforming arithmetically the standardized ES to its unstandardized version\textsuperscript{41}. 
Results

Analysis of 32 reports shows that out of 3,550 participants, 74% were female with a mean age of 47.19 (SD=11.29). A majority of the studies were conducted in Europe (53.56%) and published in English (97.97%). The included studies varied in design: 37.72% had a non-MedSD comparison group, 10.26% of studies were crossover design, and 33.9% were pre-/post-test only design. The mean publication year was 2010 (SD=2.64) with an 11 year range from 2003-2014. The mean intervention length was 32.4 (SD=45.34) weeks with a range from four to 208 weeks. No significant asymmetries were found using any of the statistical tests or the graphical funnel plot. A summary of the publication bias results can be found in Table 2.

Effect Sizes

The traditional MedSD was found to have a significant beneficial effect on five out of six outcomes of interest. Overall ESs under random-effects assumptions indicate that the traditional MedSD has a significant overall effect on waist circumference, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure ($d_r=-0.58$, 95%CI -0.81 to -0.35; $d_r=-0.33$, 95%CI -0.69 to -0.19; $d_r=-0.51$, 95%CI -0.80 to -0.22; $d_r=-0.74$, 95%CI -1.03 to -0.46; $d_r=-0.92$, 95%CI -1.41 to -0.43, respectively). The null hypothesis regarding significant effects on metabolic risk factors was rejected for a majority of the outcomes of interest. There was not enough evidence to reject the null hypothesis for HDL cholesterol ($d^*=-0.17$, 95%CI -0.08 to 0.42). There is large
heterogeneity between studies with $I^2$ ranging from 93.01%-98.23%. There was enough empirical evidence to reject the null hypothesis for variability between studies. Refer to Table 3 for the overall effect sizes and homogeneity for each of the metabolic risk factors. Please refer to Figures 2-7 for the forest plots for each of the metabolic risk factors.

**Moderator Analysis**

Moderator analysis was conducted in order to use the descriptive variables to account for some of the variability between studies. Studies included in this meta-analysis varied in some characteristics in regard to study design, population, and dietary intervention. In regards to study characteristics, marginally significant associations were found for study region ($R^2_{WC}=2.9\%, p=0.23$; $R^2_{HDL}=16.69\%, p=0.08$; $R^2_{TG}=4.42\%, p=0.28$; $R^2_{FBG}=3.5\%, p=0.33$ for waist circumference, HDL cholesterol, triglycerides, and fasting blood glucose, respectively). Studies conducted in Europe showed significant beneficial effects from the traditional MedSD intervention on four of the metabolic risk factors ($d_{wc}=-0.82$, 95%CI: -1.12, -0.51; $d_{HDL}=0.55$, 95%CI: 0.21, 0.89; $d_{TG}=-0.75$, 95%CI: -1.15, -0.35; $d_{FBG}=-0.75$, 95%CI: -1.15, -0.35 for waist circumference, HDL cholesterol, triglycerides, and fasting blood glucose, respectively), whereas those studies conducted in the United States did not result in significant effect sizes ($d_{wc}=-0.33$, 95%CI: -0.88, -0.21; $d_{HDL}=-0.10$, 95%CI: -0.59, 0.39; $d_{FBG}=-0.13$, 95%CI: -0.88, 0.62).
95% CI: -0.75, 0.48; \( d_{\text{FBG}} = -0.18 \), 95% CI: -0.96, 0.60 for waist circumference, HDL cholesterol, triglycerides, and fasting blood glucose, respectively).

Significant associations were found for study design for five of the six metabolic risk factors (\( R^2_{\text{WC}} = 25.19\% \), \( p = 0.002 \); \( R^2_{\text{HDL}} = 49.12\% \), \( p < 0.0001 \); \( R^2_{\text{TG}} = 33.71\% \), \( p = 0.0008 \); \( R^2_{\text{FBG}} = 32.81\% \), \( p = 0.0015 \); \( R^2_{\text{SBP}} = 29.09\% \), \( p < 0.001 \) for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, and systolic blood pressure, respectively). Studies using a comparison intervention group design (i.e., a different type of diet) had more beneficial significant effect sizes (\( d_{\text{WC}} = -1.14 \), 95% CI: -1.51, -0.77; \( d_{\text{HDL}} = 0.79 \), 95% CI: 0.46, 1.13; \( d_{\text{TG}} = -0.99 \), 95% CI: -1.37, -0.66; \( d_{\text{FBG}} = -1.13 \), 95% CI: -1.58, -0.67; \( d_{\text{SBP}} = -1.36 \), 95% CI: -1.84, -0.88; \( d_{\text{DBP}} = -1.32 \), 95% CI: -2.27, -0.36 for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure, respectively) compared to those studies using a traditional pre-/post-design or a crossover design (\( d_{\text{WC}} = -0.34 \), 95% CI: -0.58, -0.09; \( d_{\text{SBP}} = -0.51 \), 95% CI: -0.79, -0.23; \( d_{\text{DBP}} = -0.77 \), 95% CI: -1.34, -0.19 for waist circumference, systolic blood pressure, and diastolic blood pressure, respectively).

Studies with a higher Impact per Publication (IPP) value showed more significant beneficial effects for four out of six of the metabolic risk factors (\( R^2_{\text{WC}} = 45.1\% \), \( p < 0.0001 \); \( R^2_{\text{HDL}} = 37.03\% \), \( p = 0.0015 \); \( R^2_{\text{TG}} = 23.74\% \), \( p = 0.014 \); \( R^2_{\text{FBG}} = 39.48\% \), \( p = 0.0005 \) for waist circumference, HDL cholesterol, triglycerides, and fasting blood glucose, respectively). A predictive model was performed in order to determine the magnitude of effect for the minimum and maximum IPP score (0
and 16.104). There were significant associations for IPP value for four outcomes of interest ($B_{wc}= -0.11, p<0.0001; B_{HDL}=0.07, p=0.002; B_{TG}=-0.06, p=0.01; B_{FBG}=-0.08, p=0.0005$ for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, respectively). In the predictive model, the maximum IPP score resulted in more significant beneficial effect sizes than the minimum IPP score.

The length of the intervention (in weeks) significantly explains between 26.2% and 53.32% of the variability between studies for the following outcomes: waist circumference, HDL cholesterol, triglycerides, fasting blood glucose and systolic blood pressure. The meta-regression plots for these analyses are represented in Figures 8-13. A predictive model was performed in order to determine the magnitude of effect for the minimum and maximum lengths of intervention (4 and 208 weeks). There was a significant association for length of intervention for all six outcomes of interest ($B_{wc}=-0.01, p<0.0001; B_{HDL}=0.009, p<0.0001; B_{TG}=-0.008, p=0.006; B_{FBG}=-0.009, p<0.001; B_{SBP}=-0.007, p=0.005; B_{DBP}=-0.009, p=0.09$ for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure, respectively). The longer the length of the intervention, the more significant the beneficial effect in favor of the traditional MedSD. These results are presented in Table 4.

Additional significant or marginally significant intervention characteristics include the use of a behavioral technique and dietary interventions conducted primarily in small groups. Whether or not a behavioral technique was used...
during the intervention (i.e., positive reinforcement or self-monitoring) explained between 2.26% and 14.18% of the variability between studies. The use of a behavioral technique resulted in marginally significant or significant beneficial effects in all of the outcomes of interest ($d_{wc} = -0.73$, 95% CI: -1.08, -0.38; $d_{HDL} = 0.50$, 95% CI: 0.12, 0.89; $d_{TG} = -0.79$, 95% CI: -1.21, -0.37; $d_{FBG} = -0.88$, 95% CI: -1.34, -0.43; $d_{SBP} = -1.12$, 95% CI: -1.56, -0.68; $d_{DBP} = -1.63$, 95% CI: -2.35, -0.85 for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure, respectively) compared to the effects when there was no behavioral technique used ($d_{wc} = -0.41$, 95% CI: -0.71, -0.11; $d_{HDL} = -0.08$, 95% CI: -0.42, 0.25; $d_{TG} = -0.27$, 95% CI: -0.59, 0.60; $d_{FBG} = -0.31$, 95% CI: -0.69, 0.07; $d_{SBP} = -0.54$, 95% CI: -0.92, -0.17; $d_{DBP} = -0.53$, 95% CI: -1.16, 0.11 for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure, respectively).

The level of intervention or supervision during the study (i.e., primarily one-on-one or small groups) resulted in significant associations ($R_{WC}^2 = 16.12\%$, $p=0.014$; $R_{HDL}^2 = 22.31\%$, $p=0.012$; $R_{TG}^2 = 25.64\%$, $p=0.006$; $R_{FBG}^2 = 19.01\%$, $p=0.004$; $R_{SBP}^2 = 30.73\%$, $p=0.004$) for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure, respectively. Interventions consisting of small groups saw significant beneficial effects for all six outcomes ($d_{wc} = -1.15$, 95% CI: -1.61, -0.68; $d_{HDL} = 0.64$, 95% CI: 0.23, 1.05; $d_{TG} = -1.03$, 95% CI: -1.46, -0.59; $d_{FBG} = -1.04$, 95% CI: -1.52, -
0.56; $d_{SBP} = -1.42, 95\% CI: -1.91, -0.94$, $d_{DBP} = -1.54, 95\% CI: -2.43, -0.65$ for waist circumference, HDL cholesterol, triglycerides, fasting blood glucose, systolic blood pressure, and diastolic blood pressure, respectively) compared to the significant effects for two outcomes for those interventions that were primarily one-on-one ($d_{wc} = -0.54, 95\% CI: -0.88, -0.20$; $d_{SBP} = -0.46, 95\% CI: -0.83, -0.09$ for waist circumference and systolic blood pressure respectively).

Multiple variables were significant moderators only for diastolic blood pressure ($R^2_{DBP} = 67.72\%, p<0.0001$; $R^2_{DBP} = 72.57\%, p<0.0001$; $R^2_{DBP} = 71.86\%, p<0.0001$ for number of females, total sample size, and sample size of the intervention group) resulting in significant associations ($B_{DBP} = -0.004, p<0.0001$; $B_{DBP} = -0.004, p<0.0001$; $B_{DBP} = -0.005, p<0.0001$, for number of females, total sample size, and sample size of the intervention group, respectively).

In regards to specific components of the traditional MedSD interventions, the following characteristics were not significant moderators for any of the metabolic risk factors: carbohydrate intake $\geq 50\%$ of calories, saturated fat intake $<10\%$ of calories, total fat intake $<30\%$ of calories, and protein intake $\geq 15\%$ of calories. However, following these specific macronutrient proportions resulted in more beneficial effects in favor of the traditional MedSD compared to carbohydrate intake $<50\%$ of calories, saturated fat intake $\geq 10\%$ of calories, total fat intake $\geq 30\%$ of calories, and protein intake $<15\%$ of calories. In addition to the specific macronutrient proportions of the dietary intervention, whether or not dietary compliance was assessed and whether or not the participants engaged in
dietary counseling were also analyzed as moderators. There was no significant association for either of these variables. There was a significant trend in favor of the MedSD intervention in those interventions that assessed dietary compliance as well as those that included dietary counseling as part of the intervention.

Participant characteristics, in particular the presence or absence of certain disease states, were also analyzed as moderators. These variables included the presence or absence of cardiovascular disease, type II diabetes mellitus, metabolic syndrome, and overweight obesity. None of these variables were significant moderators, however certain trends should be noted. Participants with metabolic syndrome that followed the traditional MedSD had more significant beneficial effects on five out of six of the metabolic risk factors than those participants without metabolic syndrome. Conversely, in this model, effects were more beneficial in favor of the MedSD in participants without cardiovascular disease and without type II diabetes mellitus than those participants with these diseases for all outcomes except HDL cholesterol. Overweight/obese participants saw greater effects for waist circumference, however, those without overweight/obesity saw greater effects for triglycerides. All of the aforementioned effects were favorable, however no significant moderation was found for these variables. Results from the moderator analysis can be found in Table 4. Lists of non-significant moderators and moderators that did not have enough information reported to be analyzed can be found in Table 5 and Table 6, respectively.
Risk of Bias

Risk of bias was unclear for random sequence generation, allocation, blinding, incomplete outcome data, selective reporting, and other potential sources of bias. Moderator analysis was not significant for any of the risk of bias parameters. Low risk of bias was found in 28.1% of articles for random sequence generation and 9.3% of the articles had low risk of bias for allocation concealment. 9.3% of the articles had low risk of bias and 6.3% of the articles had high risk of bias for blinding of participants and personnel. Blinding of outcome assessment had 9.3% low risk of bias and 9.3% high risk of bias. Incomplete outcome data in the short-term and long-term both resulted in 6.3% of articles with high risk of bias. No high or low risk of bias was reported for selective reporting. 15.6% of articles had low risk of bias for other bias whereas 3.1% had high risk of bias for other bias. Refer to Figure 14 for a Risk of Bias Summary.

Discussion

The present meta-analysis of 32 intervention trials found that the traditional MedSD has significant beneficial effects on five out of six of the metabolic risk factors: waist circumference, triglycerides, fasting blood glucose, systolic blood pressure and diastolic blood pressure. The significant heterogeneity between studies was partly attributed to the location of the studies, the length of the intervention, and the IPP value of the journal where the study was published. To our knowledge, this is the first meta-analysis to evaluate the
effects of the Mediterranean diet on metabolic syndrome, that meets 100% of the AMSTAR criteria.

Our findings that a traditional MedSD is beneficial in reducing the risk of CVD-associated metabolic parameters complements and extends previous work in this area. Several recent systematic reviews and meta-analyses published on the MedSD and CVD risk have reported similar positive effects on waist circumference, triglycerides, systolic blood pressure, diastolic blood pressure, and fasting blood glucose. These studies also found similar significant positive associations in moderator analysis for studies conducted in Mediterranean countries\textsuperscript{8,42}, duration of study\textsuperscript{8}, study design\textsuperscript{42}, and study quality\textsuperscript{8,43}. However, we found that in general the meta-analyses and systematic reviews included in this analysis possessed limitations in methodological quality, impacting the ability to draw conclusions from their findings.

In our recent review of methodological quality we used an established methodological quality scale, AMSTAR, to evaluate the quality of 20 meta-analyses and systematic reviews on the MedSD and CVD risk. This review also assessed the relationship between review quality and IPP value of the journal where the article had been published. The PRISMA\textsuperscript{12} guidelines were used to extract scientific literature from eight computer databases using a comprehensive Boolean search strategy. Databases were searched until November 7, 2013 and 20 reports were coded and included in analysis. Included reports were published between 2006 and 2013. Five of the reports were meta-analyses, 11 were systematic reviews, and four were both systematic reviews
and meta-analyses\textsuperscript{10}. Four of the included studies reviewed moderation patterns and found that the MedSD effect was positive for different CVD risk outcomes when, in general: 1) the effect was based on larger samples, 2) the samples were more physically active, 3) the study was conducted in a Mediterranean country, 4) the study period was longer in duration, and 5) study quality was rated higher\textsuperscript{10}.

We found that reviews published in higher IPP journals scored significantly higher in total methodological quality\textsuperscript{10}. Those reviews with higher quality scores tended to report moderator analysis and homogeneity inference test and did not have language restrictions in their search. There were three positively significant associations between the IPP value and AMSTAR\textsubscript{MedSD} aspects: 1) use of duplicate study selection and data extraction, 2) using appropriate statistics to combine findings, and 3) using and justifying an appropriate effect size index\textsuperscript{10}. Given these results, we felt it was imperative to follow all current methodological quality standards while conducting our current meta-analysis on the traditional MedSD and metabolic risk factors. As noted above, for this current meta-analysis, we were successful in meeting 100\% of the AMSTAR criteria and in using moderator analysis to explain some of the variability between studies.

To our knowledge, there has only been one previously published meta-analysis on the effects of the Mediterranean diet on metabolic syndrome. This 2011 meta-analysis by Kastorini, et al.\textsuperscript{8} included 35 clinical trials, 2 prospective
studies, and 13 cross-sectional studies with a total of 534,906 participants. They found that overall, adherence to the Mediterranean diet was associated with a beneficial effect in regard to waist circumference, HDL cholesterol, triglycerides, and fasting glucose levels; overall, adherence to a Mediterranean diet was not associated with beneficial effect in regard to systolic and diastolic blood pressure levels. However, in the present meta-analysis, significant beneficial effects were found for waist circumference, triglycerides, fasting blood glucose, systolic blood pressure and diastolic blood pressure, but not HDL cholesterol.

Using sensitivity analysis, Kastorini, et al. found significant associations for studies conducted in a Mediterranean country and those studies lasting longer than three months in duration for the following outcomes: HDL cholesterol, triglycerides, systolic blood pressure, diastolic blood pressure, glucose, and HOMA-IR. Significant associations were found for all of the above outcomes as well as waist circumference for interventions with more than or equal to 66 participants. Recommendation of physical activity was significantly associated with HDL cholesterol, triglycerides, systolic blood pressure, diastolic blood pressure, and HOMA-IR, whereas no recommendation of physical activity was significantly associated with systolic blood pressure, diastolic blood pressure, and glucose. Lastly, studies of high quality were significantly associated with greater effects on HDL cholesterol, triglycerides, systolic blood pressure, diastolic blood pressure, and HOMA-IR. In the present meta-analysis, significant beneficial associations were found for studies conducted in Europe, studies of
longer duration, studies using a behavioral technique, studies with a comparison
intervention group, studies with a higher IPP value, and studies conducted
primarily in groups for most of the metabolic risk factors. Our current sample of
studies did not report enough baseline physical activity information to analyze
that variable as a moderator. Interventions that included exercise were excluded
from this meta-analysis as that was considered a “MedSD plus” intervention
because it was not looking solely at the effects of the dietary intervention. For
the Kastorini, et al. meta-analysis, the literature search was limited to those
manuscripts published in English and to three computer databases. Small
literature searches of only a few key terms at a time were conducted rather than
one comprehensive literature search. Clinical trials with lack of randomization,
lack of a control diet group, comparison of the Mediterranean diet against the
Mediterranean diet plus an additional intervention, or intervention without
inclusion of all of the components of a Mediterranean diet were excluded from
analysis. For the present meta-analysis language was not restricted for the
literature search, a comprehensive literature search was performed using six
electronic databases, and studies without comparison groups or with a lack of
randomization were not excluded. The present meta-analysis and the meta-
analysis by Kastorini, et al. greatly contribute to the scientific literature in support
of the traditional MedSD and can assist with the creation and implementation of
evidence-based dietary guidelines for those samples that would most benefit
from this dietary pattern using the moderator analysis that has been conducted.
The Scientific Report of the 2015 Dietary Guidelines Advisory Council analyzed the scientific evidence of three healthy dietary patterns, one of which is the MedSD\textsuperscript{9}. This report summarizes the information from large, high-quality randomized control trials related to the effects of the MedSD on multiple health outcomes such as blood pressure and blood lipids\textsuperscript{9}. The Dietary Guidelines Advisory council found that there were common characteristics among dietary patterns associated with positive health outcomes. Some of these characteristics were similar to those of the traditional MedSD such as higher intake of vegetables, fruits, seafood, legumes, and nuts; moderate intake of alcohol (among adults); lower consumption of red and processed meat, and low intake of sugar-sweetened foods and drinks\textsuperscript{9}. This reports highlights the significance and importance of current, high-quality research on the MedSD.

**Practical Applications**

The results of this meta-analysis provide researchers and health professionals with several immediate applications. The moderator analysis conducted in this meta-analysis demonstrates the importance of intervention trials reporting as much detailed information about participant and intervention characteristics as possible. Having this information would make more moderator analysis possible allowing for more specific dietary recommendations to be created for any dietary pattern, but especially the traditional MedSD. This meta-analysis is influential in the fields of dietetics and nutrition as both assessment of dietary compliance and the use of a behavioral technique were two moderators
with positive trends in favor of the MedSD. The significant association in beneficial effects agrees with weight loss interventions conducted by Gokee-LaRose, et al. Registered dietitians should be a vital component of any dietary intervention trial in order to enhance beneficial effects on the outcomes of interest. More significantly beneficial effects were found in those studies that primarily use a small group intervention compared to one-on-one interventions, which supports previous findings in dietary intervention studies that use small group interventions. Most importantly, the results of this meta-analysis agree with most of the current systematic reviews and meta-analyses on the Mediterranean diet.

**Study Limitation and Strengths**

This meta-analysis has several limitations and strengths. There is still significant heterogeneity between the studies that is unexplained which is a limitation for this study. Multiple variables did not have enough data reported to test for moderation effects. The data reported in our sample of studies did not allow us to control for different types and duration of exercise in which participants may have been engaging. Our last limitation is possible ecological fallacy, as we did not have the raw data from the included studies, we should be cautious interpreting the group results as individual effects. There are multiple strengths for this meta-analysis. We used a comprehensive literature search in six electronic databases and an inclusive and comprehensive coding form and manual was created and used for data extraction. We performed moderation
analysis on all variables that reported enough data to do so. To our knowledge, this is the first meta-analysis to find significant associations with the use of behavioral techniques and small group interventions. Lastly, we were able to use the moving constant technique and a predictive model to calculate the effect size at significant values of each significant moderator and transform that effect size into the clinical unit of measure.

**Conclusion**

The results of the present meta-analysis suggest that adherence to the traditional MedSD can have significant beneficial effects on waist circumference, triglycerides, fasting blood glucose, systolic blood pressure and diastolic blood pressure with a positive trend for HDL cholesterol. In addition, the Mediterranean-style diet was significantly beneficial for different metabolic risk factors when, in general the intervention period was longer in duration, the study was conducted in Europe, the study was published in a journal with higher Impact per Publication value, the study included a comparison intervention, the study used a behavioral technique, and the study was conducted primarily using small groups. More high-quality intervention studies are needed to evaluate the relationship between the traditional MedSD and metabolic risk factors in order to provide more detailed information for moderator analysis. This high quality meta-analysis on the effect of the traditional MedSD on metabolic risk factors significantly contributes to the current body of scientific literature in favor of MedSD.
References


15. SAS Institute Inc. SAS 9.4 guide to software updates.

16. IBM Corp. IBM SPSS statistics for windows. 2013.


Figure 1. PRISMA Figure Outlining the Process of Study Identification, Screening, Eligibility, and Inclusion

- Records identified through electronic database searches after removing duplicates (n=1,269):
  - PubMed (n=431)
  - EMBASE via Scopus (n=515)
  - Web of Science (n=890)
  - CINAHL (n=25)
  - Agricola (n=123)
  - CAB Direct (n=423)

- Records screened (n=1,269): Duplicate screening (MG and JIS)

- Full text reports assessed for eligibility (n=777):
  - Records excluded by title and abstract (n=1,196):
    - Full text reports excluded, with reasons (n=31):
      - Used the same database as other sources (n=7)
      - Did not report data on an outcome of interest (n=1)
      - Did not provide sufficient evidence to calculate effect sizes (n=8)
      - Did not have pre/post data on waist circumference (n=15)
      - Not on the Traditional Mediterranean Diet (n=14)

- Reports included in the analysis (n=32)
<table>
<thead>
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<th>Study</th>
<th>Country</th>
<th>N</th>
<th>% F</th>
<th>Age</th>
<th>Diseases</th>
<th>Recruitment</th>
<th>Dietary Assessment</th>
<th>Type of Diet</th>
<th>Duration (weeks)</th>
<th>Control</th>
<th>Outcome</th>
</tr>
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<tbody>
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<td>Aizawa, et al. (2009)</td>
<td>Canada</td>
<td>63</td>
<td>51%</td>
<td>53.9</td>
<td>PDM, PHTN</td>
<td>Physician referral</td>
<td>Group, unsupervised</td>
<td>MD</td>
<td>24</td>
<td>No carotid artery stiffness</td>
<td>Carotid artery stiffness</td>
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<tr>
<td>Bedard, et al. (2012)</td>
<td>Canada</td>
<td>67</td>
<td>NR</td>
<td>39</td>
<td>Ob (57%)</td>
<td>NR</td>
<td>Individual, supervised</td>
<td>MD</td>
<td>8</td>
<td>Non-Ob</td>
<td>CVDRF</td>
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<td>Bekkouche, et al. (2014)</td>
<td>Algeria</td>
<td>86</td>
<td>NR</td>
<td>52</td>
<td>MS (67%)</td>
<td>Hospital</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>12</td>
<td>No MS, healthy</td>
<td>IR, OS, Inflam.</td>
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<td>Netherlands</td>
<td>60</td>
<td>NR</td>
<td>52.5</td>
<td>Ob (100%)</td>
<td>NR</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>10</td>
<td>High SFA diet; High MUFA diet</td>
<td>Serum lipids, IS</td>
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<tr>
<td>Calatayud, et al. (2011)</td>
<td>Spain</td>
<td>98</td>
<td>56%</td>
<td>8.6</td>
<td>Ob (52%)</td>
<td>NR</td>
<td>NR</td>
<td>MD</td>
<td>52</td>
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<td>WT loss</td>
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<td>Connolly, et al. (2011)</td>
<td>Great Britain</td>
<td>206</td>
<td>42%</td>
<td>60.4</td>
<td>CVD or CVDRF (100%)</td>
<td>Hospital, physician referral</td>
<td>Individual, unsupervised</td>
<td>MD</td>
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<td>Corbalan, et al. (2009)</td>
<td>Spain</td>
<td>140</td>
<td>82%</td>
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<td>Clinic referral</td>
<td>Individual, unsupervised</td>
<td>HMD</td>
<td>34</td>
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<td>WT</td>
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<td>Italy</td>
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<td>43.9</td>
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<td>Research database</td>
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<td>Regular diet</td>
<td>IIEF score</td>
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<tr>
<td>Study</td>
<td>Country</td>
<td>N</td>
<td>%</td>
<td>Sex (BMI)</td>
<td>Age (mean)</td>
<td>Study Design</td>
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<td>Group Type</td>
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<td>59</td>
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<td>MD</td>
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<td>215</td>
<td>51%</td>
<td>NIDDM</td>
<td>52.2</td>
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<td>HMD</td>
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<td>LF Diet</td>
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<td>77</td>
<td>100%</td>
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<td>47</td>
<td>Individual, unsupervised</td>
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<td>12</td>
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<td>Canada</td>
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<td>46.7</td>
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<td>MD</td>
<td>24</td>
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<td>89</td>
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<td>MS</td>
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<td>LGMD-MF</td>
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<td>MS RF</td>
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<td>Kolomvotsou, et al. (2013)</td>
<td>Greece</td>
<td>90</td>
<td>48%</td>
<td>Ob</td>
<td>50.4</td>
<td>Individual, unsupervised</td>
<td>Greek MD</td>
<td>8</td>
<td>Regular diet</td>
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<td>Spain</td>
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<td>58</td>
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<td>Maestranza Diesel Group, supervised</td>
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<td>82</td>
<td>48%</td>
<td>Ob (100%)</td>
<td>Hospital</td>
<td>Individual, unsupervised</td>
<td>Greek MD</td>
<td>8 Regular Diet Endo func</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Richard, et al. (2011)</td>
<td>Canada</td>
<td>26</td>
<td>0%</td>
<td>MS (100%)</td>
<td>NR</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>35 Western Diet CVDRF</td>
<td></td>
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</tr>
<tr>
<td>Rubenfire, et al. (2011)</td>
<td>United States</td>
<td>126</td>
<td>68%</td>
<td>MS (100%)</td>
<td>Physician referral</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>12 None WT, BP, TG, serum glucose</td>
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<td></td>
<td></td>
</tr>
<tr>
<td>Ryan, et al. (2013)</td>
<td>Australia</td>
<td>12</td>
<td>50%</td>
<td>NAFLD (100%)</td>
<td>Hospital</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>6 LF diet WT, IS</td>
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<tr>
<td>Sanchez-Benito, et al.</td>
<td>Spain</td>
<td>158</td>
<td>87%</td>
<td>OverWT (100%)</td>
<td>Pharmacy office</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>26 None BMI, BP, cholesterol</td>
<td></td>
<td></td>
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</tr>
<tr>
<td>Year</td>
<td>Location</td>
<td>N</td>
<td>%</td>
<td>Condition</td>
<td>Type</td>
<td>Unit of Measurement</td>
<td></td>
<td></td>
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<td>------</td>
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<td>--------------------</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2012</td>
<td>United States</td>
<td>129</td>
<td>100%</td>
<td>OverWT (100%)</td>
<td>Individual, unsupervised</td>
<td>MD</td>
<td>16</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2012</td>
<td>Romania</td>
<td>223</td>
<td>50%</td>
<td>NIDDM (100%)</td>
<td>Group, unsupervised</td>
<td>HMD</td>
<td>52</td>
<td></td>
<td></td>
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<tr>
<td>2020</td>
<td>South Africa</td>
<td>12</td>
<td>25%</td>
<td>MS (100%)</td>
<td>Group, unsupervised</td>
<td>MD with red wine</td>
<td>8</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2000</td>
<td>England</td>
<td>176</td>
<td>78%</td>
<td>Hypercholesterolemia (100%)</td>
<td>Group, unsupervised</td>
<td>MD</td>
<td>12</td>
<td></td>
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</tr>
</tbody>
</table>

**Note.** N, number of participants at baseline; F, females; NR, not reported; OWT, Overweight; Ob, Obesity; MD, Mediterranean Diet; PDM, Pre-diabetes mellitus; PHTN, Pre-hypertension; HMD, Hypocaloric Mediterranean diet; CVDRF, Cardiovascular Disease risk factors; MS, Metabolic Syndrome; Endo dys, endothelial dysfunction; OS, oxidative stress; NIDDM, Non-insulin Dependent Diabetes; FFMD, Fast food Mediterranean Diet; FF Cons, Fast food consumption; IR, insulin resistance; Inflam, Inflammation; SFA, saturated fatty acid; IS, Insulin Sensitivity; CHD, Coronary Heart Disease; ED, Erectile Dysfunction; IIEF, International Index of Erectile Function; FSD, Female Sexual Dysfunction; FSFI, Female Sexual Function Index; Endo Func., endothelial function; Vas Infl, vascular inflammation; MDN, Mediterranean Diet with nuts; MDO, Mediterranean Diet with olive oil; EPC, endothelial progenitor cell; OC, serum osteocalcin; P1NP, procollagen type 1 N-terminal propeptide; LGMD-MF, Low-Glycemic Mediterranean Diet with Medical Food; MS RF, Metabolic Syndrome Risk Factors; AO, antioxidant; HRQoL, Health-related quality of life; WC, waist circumference; IHD, ischaemic heart disease; IGT, impaired glucose tolerance; KEMEPHY, Ketogenic Mediterranean Diet with phytoextracts; OSAS, Obstructive Sleep Apnea Syndrome; TBARS, thiobarbituric acid reacting substances; TAC, total antioxidant capacity; HMDC, Hypocaloric Mediterranean Diet High Cereal; HMDV, Hypocaloric Mediterranean Diet High Vegetable; BP, blood pressure; TG, serum triglycerides; Inflam Bio, inflammatory biomarkers; MyPyramid for P&B, USDA MyPyramid Diet for Pregnant and Breastfeeding Women; BLS, Bright Liver Score; FVII, activated factor VII; HLF Diet, Hypocaloric Low Fat Diet; MI, Myocardial Infarction

**Note on Dietary Assessment column:**

- **Individual**: A dietitian performed a dietary assessment, providing individualized needs for caloric intake and recommendations, for each participant.
- **Group**: The study provided general dietary recommendations for the participants, such as a range of servings of certain food groups, calories based on gender, as opposed to tailoring diets to individual needs based on weight and height.
- **Supervised**: Participants consumed foods in a supervised setting, where the researchers had control over participant food choices and quantity of food served.
- **Unsupervised**: Participants' food consumption was unsupervised by researchers, such as eating at home.
<table>
<thead>
<tr>
<th>Outcome</th>
<th>s</th>
<th>Egger'</th>
<th>Begg's</th>
</tr>
</thead>
<tbody>
<tr>
<td>WC</td>
<td>5</td>
<td>p=0.64</td>
<td>p=0.001</td>
</tr>
<tr>
<td>HDL</td>
<td>5</td>
<td>p=0.96</td>
<td>p=0.56</td>
</tr>
<tr>
<td>TG</td>
<td>2</td>
<td>p=0.21</td>
<td>p=0.125</td>
</tr>
<tr>
<td>FBG</td>
<td>9</td>
<td>p=0.79</td>
<td>p=0.016</td>
</tr>
<tr>
<td>SBP</td>
<td></td>
<td>p=0.34</td>
<td>p=0.027</td>
</tr>
<tr>
<td>DBP</td>
<td>3</td>
<td>p=0.60</td>
<td>p=0.032</td>
</tr>
</tbody>
</table>

*Note: WC, waist circumference; HDL, HDL cholesterol; TG, triglycerides, FBG, fasting blood glucose; SBP, systolic blood pressure; DBP, diastolic blood pressure*
Table 3. Summary of Results, Overall Effect Sizes and Homogeneity

<table>
<thead>
<tr>
<th>Outcome</th>
<th>k</th>
<th>d+ (95% CI)</th>
<th>Homogeneity of d’s</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Fixed-Effects</td>
<td>Random-Effects</td>
</tr>
<tr>
<td>WC</td>
<td>45</td>
<td>-0.41 (-0.45 to -0.38)*</td>
<td>-0.54 (-0.75 to -0.33)*</td>
</tr>
<tr>
<td>HDL</td>
<td>40</td>
<td>0.15 (-0.02 to 0.32)</td>
<td>0.15 (-0.02 to 0.32)</td>
</tr>
<tr>
<td>TG</td>
<td>38</td>
<td>-0.27 (-0.31 to -0.22)*</td>
<td>-0.34 (-0.51 to -0.16)*</td>
</tr>
<tr>
<td>FBG</td>
<td>33</td>
<td>-0.36 (-0.41 to -0.32)*</td>
<td>-0.42 (-0.51 to -0.19)*</td>
</tr>
<tr>
<td>SBP</td>
<td>30</td>
<td>-0.61 (-0.65 to -0.57)*</td>
<td>-0.62 (-0.64 to -0.19)*</td>
</tr>
<tr>
<td>DBP</td>
<td>30</td>
<td>-0.68 (-0.73 to -0.63)*</td>
<td>-0.78 (-1.22 to -0.34)*</td>
</tr>
</tbody>
</table>

Note: WC, waist circumference; HDL, HDL cholesterol; TG, triglycerides, FBG, fasting blood glucose; SBP, systolic blood pressure; DBP, diastolic blood pressure; * indicates a significant effect; k represents the number of interventions for each outcome included in the analysis; Q represents Cochran’s Q indicating significance of heterogeneity; I² represents the magnitude of heterogeneity; p-value represents the significance of heterogeneity.
### Table 4. Significant Moderator Analysis Results

<table>
<thead>
<tr>
<th>Variable</th>
<th>Outcome</th>
<th>Category</th>
<th>k</th>
<th>d+ (95% CI)</th>
<th>R²</th>
<th>p-value</th>
<th>Clinical Unit of Measure</th>
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</thead>
<tbody>
<tr>
<td></td>
<td>Study Characteristics</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Region</td>
<td>WC</td>
<td>Europe</td>
<td>23</td>
<td>(-1.12 to -0.51)</td>
<td>2.90%</td>
<td>0.23</td>
<td>-8.32 cm</td>
</tr>
<tr>
<td></td>
<td>US</td>
<td></td>
<td>7</td>
<td>(-0.59 to 0.39)</td>
<td>2.90%</td>
<td>0.23</td>
<td>-3.41 cm</td>
</tr>
<tr>
<td>HDL</td>
<td>Europe</td>
<td></td>
<td>13</td>
<td>(0.21 to 0.89)</td>
<td>16.69%</td>
<td>0.08</td>
<td>1.65 mmol/L</td>
</tr>
<tr>
<td></td>
<td>US</td>
<td></td>
<td>6</td>
<td>(-0.59 to 0.39)</td>
<td>16.69%</td>
<td>0.08</td>
<td>-0.31 mmol/L</td>
</tr>
<tr>
<td>TG</td>
<td>Europe</td>
<td></td>
<td>12</td>
<td>(-1.08 to -0.35)</td>
<td>4.42%</td>
<td>0.28</td>
<td>-24.89 mmol/L</td>
</tr>
<tr>
<td></td>
<td>US</td>
<td></td>
<td>4</td>
<td>(-0.75 to 0.48)</td>
<td>4.42%</td>
<td>0.28</td>
<td>-4.69 mmol/L</td>
</tr>
<tr>
<td>FBG</td>
<td>Europe</td>
<td></td>
<td>12</td>
<td>(-1.15 to -0.35)</td>
<td>3.50%</td>
<td>0.33</td>
<td>-0.23 mmol/L</td>
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<tr>
<td></td>
<td>US</td>
<td></td>
<td>3</td>
<td>(-0.96 to 0.60)</td>
<td>3.50%</td>
<td>0.33</td>
<td>-0.06 mmol/L</td>
</tr>
<tr>
<td>SBP</td>
<td>Europe</td>
<td></td>
<td>13</td>
<td>(-1.54 to 0.53)</td>
<td>0.00%</td>
<td>0.68</td>
<td>-3.17 mmol/L</td>
</tr>
<tr>
<td></td>
<td>US</td>
<td></td>
<td>4</td>
<td>(-1.38 to 0.43)</td>
<td>0.00%</td>
<td>0.68</td>
<td>-1.54 mmol/L</td>
</tr>
<tr>
<td>DBP</td>
<td>Europe</td>
<td></td>
<td>13</td>
<td>(-2.56 to 0.90)</td>
<td>0.00%</td>
<td>0.79</td>
<td>-2.97 mmol/L</td>
</tr>
<tr>
<td></td>
<td>US</td>
<td></td>
<td>4</td>
<td>(-1.95 to 1.07)</td>
<td>0.00%</td>
<td>0.79</td>
<td>-1.03 mmol/L</td>
</tr>
<tr>
<td>Metric</td>
<td>Study Design</td>
<td>WC</td>
<td>HDL</td>
<td>TG</td>
<td>FBG</td>
<td>SBP</td>
<td>DBP</td>
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<td>--------------</td>
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<td>MedSD vs. Other Diet</td>
<td>13</td>
<td>9</td>
<td>8</td>
<td>7</td>
<td>7</td>
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<tr>
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<td>Pre/Post or Crossover</td>
<td>-1.14</td>
<td>0.79</td>
<td>-0.34</td>
<td>-1.58</td>
<td>-1.36</td>
<td>-1.32</td>
</tr>
<tr>
<td></td>
<td></td>
<td>(-1.51 to -0.77)</td>
<td>(0.46 to 1.13)</td>
<td>(-1.37 to -0.60)</td>
<td>(-1.58 to -0.67)</td>
<td>(-1.84 to -0.88)</td>
<td>(-2.27 to -0.36)</td>
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<tr>
<td></td>
<td></td>
<td>25.19%</td>
<td>49.12%</td>
<td>33.71%</td>
<td>32.81%</td>
<td>29.09%</td>
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<td></td>
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<td>0.001</td>
<td>&lt;0.0001</td>
<td>0.0008</td>
<td>0.002</td>
<td>0.003</td>
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<td></td>
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<td>-11.63 cm</td>
<td>2.37 mmol/L</td>
<td>-34.65 mmol/L</td>
<td>0.41 mmol/L</td>
<td>-4.45 mmHg</td>
<td>-3.09 mmHg</td>
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<tr>
<td></td>
<td>Impacted per Publication Metric WC</td>
<td>0 (minimum)</td>
<td>0 (minimum)</td>
<td>16.104 (maximum)</td>
<td>16.104 (maximum)</td>
<td>0 (minimum)</td>
<td>0 (minimum)</td>
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<tr>
<td></td>
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<td>39</td>
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<td>39</td>
<td>27</td>
</tr>
<tr>
<td></td>
<td></td>
<td>(-0.42 to 0.06)</td>
<td>(-0.35 to 0.18)</td>
<td>(-2.49 to -1.36)</td>
<td>(-1.34 to -0.19)</td>
<td>(-0.42 to 0.06)</td>
<td>(-0.35 to 0.18)</td>
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<tr>
<td></td>
<td></td>
<td>45.10%</td>
<td>37.03%</td>
<td>45.10%</td>
<td>0.00%</td>
<td>0.00%</td>
<td>0.00%</td>
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<tr>
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<td>&lt;0.0001</td>
<td>0.002</td>
<td>&lt;0.0001</td>
<td>0.34</td>
<td>0.34</td>
<td>0.34</td>
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<tr>
<td></td>
<td></td>
<td>-1.84 cm</td>
<td>-0.24 mmol/L</td>
<td>-19.58 cm</td>
<td>-1.89 cm</td>
<td>-19.58 cm</td>
<td>-2.88 mmol/L</td>
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### Intervention Characteristics

<table>
<thead>
<tr>
<th>Variable</th>
<th>Length of intervention (in weeks)</th>
<th>WC</th>
<th>HDL</th>
<th>TG</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>4 weeks (minimum)</td>
<td>41</td>
<td>28</td>
<td>26</td>
</tr>
<tr>
<td></td>
<td>4 weeks (maximum)</td>
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<td>28</td>
<td>26</td>
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<td></td>
<td>208 weeks (minimum)</td>
<td>41</td>
<td>41</td>
<td>26</td>
</tr>
<tr>
<td></td>
<td>208 weeks (maximum)</td>
<td>41</td>
<td>41</td>
<td>26</td>
</tr>
<tr>
<td>Length of intervention (in weeks)</td>
<td>4 weeks (minimum)</td>
<td>41</td>
<td>-0.29</td>
<td>-0.03</td>
</tr>
<tr>
<td></td>
<td>4 weeks (maximum)</td>
<td>41</td>
<td>-0.12</td>
<td>1.78</td>
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<tr>
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<td>208 weeks (minimum)</td>
<td>41</td>
<td>-3.28 to -1.57</td>
<td>-0.33 to 0.09</td>
</tr>
<tr>
<td></td>
<td>208 weeks (maximum)</td>
<td>41</td>
<td>-1.11 to 2.46</td>
<td>1.11 to 2.46</td>
</tr>
<tr>
<td></td>
<td>208 weeks (minimum)</td>
<td>26</td>
<td>-0.45 to 0.04</td>
<td>-0.45 to 0.04</td>
</tr>
<tr>
<td></td>
<td>208 weeks (maximum)</td>
<td>26</td>
<td>-1.73</td>
<td>-1.73</td>
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</tbody>
</table>

| TG       | 0 (minimum)                      | 25 | -0.19 | -1.09 |
|          | 16.104 (maximum)                 | 25 | -1.09 | -38.15 mmol/L |
| FBG      | 0 (minimum)                      | 23 | -1.44 | -0.44 mmol/L |
|          | 16.104 (maximum)                 | 23 | -1.44 | -0.44 mmol/L |
| SBP      | 0 (minimum)                      | 25 | -1.13 | -1.79 mmHg |
|          | 16.104 (maximum)                 | 25 | -1.13 | -1.79 mmHg |
| DBP      | 0 (minimum)                      | 25 | -1.74 | 1.47 mmHg |
|          | 16.104 (maximum)                 | 25 | -1.74 | 1.47 mmHg |

<table>
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<tr>
<th>Interv</th>
<th>Length of intervention (in weeks)</th>
<th>WC</th>
<th>HDL</th>
<th>TG</th>
</tr>
</thead>
<tbody>
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<td>Length of intervention (in weeks)</td>
<td>4 weeks (minimum)</td>
<td>41</td>
<td>28</td>
<td>26</td>
</tr>
<tr>
<td></td>
<td>4 weeks (maximum)</td>
<td>41</td>
<td>28</td>
<td>26</td>
</tr>
<tr>
<td></td>
<td>208 weeks (minimum)</td>
<td>41</td>
<td>41</td>
<td>26</td>
</tr>
<tr>
<td></td>
<td>208 weeks (maximum)</td>
<td>41</td>
<td>41</td>
<td>26</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Length of intervention (in weeks)</th>
<th>WC</th>
<th>HDL</th>
<th>TG</th>
</tr>
</thead>
<tbody>
<tr>
<td>4 weeks (minimum)</td>
<td>41</td>
<td>-0.52 to -0.08</td>
<td>37.73%</td>
</tr>
<tr>
<td>4 weeks (maximum)</td>
<td>41</td>
<td>-2.42</td>
<td>37.73%</td>
</tr>
<tr>
<td>208 weeks (minimum)</td>
<td>41</td>
<td>-3.28 to -1.57</td>
<td>37.73%</td>
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<tr>
<td>208 weeks (maximum)</td>
<td>41</td>
<td>-1.11 to 2.46</td>
<td>37.73%</td>
</tr>
<tr>
<td>4 weeks (minimum)</td>
<td>26</td>
<td>-0.33 to 0.09</td>
<td>53.32%</td>
</tr>
<tr>
<td>4 weeks (maximum)</td>
<td>26</td>
<td>1.78</td>
<td>53.32%</td>
</tr>
<tr>
<td>208 weeks (minimum)</td>
<td>26</td>
<td>-0.45 to 0.04</td>
<td>33.05%</td>
</tr>
<tr>
<td>208 weeks (maximum)</td>
<td>26</td>
<td>-1.73</td>
<td>33.05%</td>
</tr>
<tr>
<td>Variable</td>
<td>4 weeks (minimum)</td>
<td>4 weeks (maximum)</td>
<td>208 weeks (minimum)</td>
</tr>
<tr>
<td>----------</td>
<td>------------------</td>
<td>------------------</td>
<td>---------------------</td>
</tr>
<tr>
<td>FBG</td>
<td>-0.21 (-0.46 to 0.04)</td>
<td>-2.20 (-2.99 to -1.42)</td>
<td>-0.49 (-2.91 to -1.08)</td>
</tr>
<tr>
<td>SBP</td>
<td>-0.49 (-0.79 to -0.19)</td>
<td>-1.99 (-2.91 to -1.08)</td>
<td>-1.21 (-4.14 to -0.63)</td>
</tr>
<tr>
<td>DBP</td>
<td>-0.64 (-1.21 to -0.07)</td>
<td>-0.64 (-2.39)</td>
<td>-2.39 (-4.14 to -0.63)</td>
</tr>
<tr>
<td>WC</td>
<td>-0.54 (-0.79 to -0.29)</td>
<td>-0.52 (-1.91 to 0.86)</td>
<td>-0.52 (-1.91 to 0.86)</td>
</tr>
<tr>
<td>HDL</td>
<td>0.28 (-0.07 to 0.64)</td>
<td>0.28 (-2.61)</td>
<td>0.28 (-2.61)</td>
</tr>
<tr>
<td>TG</td>
<td>-1.20 mmHg</td>
<td>-1.20 mmHg</td>
<td>-1.20 mmHg</td>
</tr>
<tr>
<td>FBG</td>
<td>-0.16 mmHg</td>
<td>-0.16 mmHg</td>
<td>-0.16 mmHg</td>
</tr>
<tr>
<td>SBP</td>
<td>-2.26 mmHg</td>
<td>-2.26 mmHg</td>
<td>-2.26 mmHg</td>
</tr>
<tr>
<td>DBP</td>
<td>-5.51 cm</td>
<td>-5.51 cm</td>
<td>-5.51 cm</td>
</tr>
<tr>
<td>HDL</td>
<td>0.84 mmol/L</td>
<td>0.84 mmol/L</td>
<td>0.84 mmol/L</td>
</tr>
<tr>
<td>TG</td>
<td>-71.05 mmol/L</td>
<td>-71.05 mmol/L</td>
<td>-71.05 mmol/L</td>
</tr>
<tr>
<td>FBG</td>
<td>-0.15 mmol/L</td>
<td>-0.15 mmol/L</td>
<td>-0.15 mmol/L</td>
</tr>
<tr>
<td>SBP</td>
<td>-3.11 mmHg</td>
<td>-3.11 mmHg</td>
<td>-3.11 mmHg</td>
</tr>
<tr>
<td>Measure</td>
<td>Sample Size</td>
<td>Value (Mean ± SD)</td>
<td>Change (95% CI)</td>
</tr>
<tr>
<td>---------</td>
<td>-------------</td>
<td>-------------------</td>
<td>-----------------</td>
</tr>
<tr>
<td>DBP</td>
<td>0 (minimum)</td>
<td>25</td>
<td>-0.55 (±0.58)</td>
</tr>
<tr>
<td></td>
<td>1,154 (maximum)</td>
<td>25</td>
<td>-0.59 (±0.59)</td>
</tr>
<tr>
<td>WC</td>
<td>12 (minimum)</td>
<td>41</td>
<td>-0.51 (±0.51)</td>
</tr>
<tr>
<td></td>
<td>1,406 (maximum)</td>
<td>41</td>
<td>-0.15 (±0.15)</td>
</tr>
<tr>
<td>HDL</td>
<td>12 (minimum)</td>
<td>28</td>
<td>-0.17 (±0.51)</td>
</tr>
<tr>
<td></td>
<td>1,406 (maximum)</td>
<td>28</td>
<td>-0.49 (±5.29)</td>
</tr>
<tr>
<td>TG</td>
<td>12 (minimum)</td>
<td>26</td>
<td>-0.52 (±0.17)</td>
</tr>
<tr>
<td></td>
<td>1,406 (maximum)</td>
<td>26</td>
<td>-0.49 (±0.49)</td>
</tr>
<tr>
<td>FBG</td>
<td>12 (minimum)</td>
<td>24</td>
<td>-0.69 (±0.69)</td>
</tr>
<tr>
<td></td>
<td>1,406 (maximum)</td>
<td>24</td>
<td>-0.72 (±0.72)</td>
</tr>
<tr>
<td>SBP</td>
<td>12 (minimum)</td>
<td>26</td>
<td>-0.99 (±0.99)</td>
</tr>
<tr>
<td></td>
<td>1,406 (maximum)</td>
<td>26</td>
<td>-0.39 (±0.39)</td>
</tr>
<tr>
<td>DBP</td>
<td>12 (minimum)</td>
<td>26</td>
<td>-0.59 (±0.59)</td>
</tr>
<tr>
<td></td>
<td>1,406 (maximum)</td>
<td>26</td>
<td>-0.59 (±0.59)</td>
</tr>
</tbody>
</table>

Total sample size

Sample size of intervention group

<table>
<thead>
<tr>
<th>Measure</th>
<th>Value (Mean ± SD)</th>
<th>Change (95% CI)</th>
<th>Effect Size</th>
<th>Significance</th>
<th>Value (Maximum)</th>
<th>Difference</th>
</tr>
</thead>
<tbody>
<tr>
<td>WC</td>
<td>11 (minimum)</td>
<td>41</td>
<td>-0.34 (±0.34)</td>
<td>-0.85 to -0.34</td>
<td>0.00%</td>
<td>0.91</td>
</tr>
<tr>
<td>Measure</td>
<td>Minimum</td>
<td>Maximum</td>
<td>Percentage</td>
<td>Value</td>
<td>Percentage</td>
<td>Value</td>
</tr>
<tr>
<td>----------------</td>
<td>---------</td>
<td>---------</td>
<td>------------</td>
<td>-------</td>
<td>------------</td>
<td>------------</td>
</tr>
<tr>
<td>HDL</td>
<td>11</td>
<td>28</td>
<td>0.00%</td>
<td>0.55</td>
<td>0.91</td>
<td>6.9 mmol/L</td>
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<tr>
<td>TG</td>
<td>11</td>
<td>26</td>
<td>0.00%</td>
<td>0.34</td>
<td>0.55</td>
<td>146.3 mmol/L</td>
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<tr>
<td>FBG</td>
<td>11</td>
<td>24</td>
<td>0.00%</td>
<td>0.93</td>
<td>0.55</td>
<td>0.16 mmol/L</td>
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<td>SBP</td>
<td>11</td>
<td>26</td>
<td>0.00%</td>
<td>0.74</td>
<td>0.74</td>
<td>-2.39 mmHg</td>
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<tr>
<td>DBP</td>
<td>11</td>
<td>26</td>
<td>71.86%</td>
<td>&lt;0.0001</td>
<td>&lt;0.0001</td>
<td>-1.15 mmHg</td>
</tr>
<tr>
<td>61.6 years</td>
<td>23</td>
<td>26</td>
<td>71.86%</td>
<td>&lt;0.0001</td>
<td>&lt;0.0001</td>
<td>-13.89 mmHg</td>
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<tr>
<td>WC</td>
<td>No</td>
<td>24</td>
<td>2.26%</td>
<td>0.17</td>
<td>0.17</td>
<td>-4.18 cm</td>
</tr>
<tr>
<td></td>
<td>Yes</td>
<td>16</td>
<td>2.26%</td>
<td>0.17</td>
<td>0.17</td>
<td>-7.45 cm</td>
</tr>
<tr>
<td>HDL</td>
<td>No</td>
<td>16</td>
<td>14.18%</td>
<td>0.03</td>
<td>0.03</td>
<td>-0.24 mmol/L</td>
</tr>
<tr>
<td></td>
<td>Yes</td>
<td>11</td>
<td>14.18%</td>
<td>0.03</td>
<td>1.5 mmol/L</td>
<td></td>
</tr>
</tbody>
</table>

Use of a behavioral technique
<p>| Level of intervention or supervision during the study |  |  |  |  |  |  |
|------------------------------------------------------|---|---|---|---|---|
| Primarily one-on-one | Yes | 16 | (-0.59 to 0.60) | 9.97% | 0.05 | -9.45 mmol/L |
| Primarily one-on-one | No | 9 | (-1.21 to -0.37) | 9.97% | 0.05 | -27.65 mmol/L |
| Small groups | Yes | 13 | (-0.69 to 0.07) | 11.94% | 0.06 | -0.09 mmol/L |
| Small groups | No | 9 | (-1.34 to -0.43) | 11.94% | 0.06 | -0.27 mmol/L |
| Small groups | Yes | 10 | (-1.56 to -0.68) | 11.98% | 0.05 | -3.66 mmHg |
| Small groups | No | 9 | (-1.16 to 0.11) | 13.48% | 0.03 | -1.24 mmHg |
| Small groups | Yes | 15 | (-0.92 to -0.17) | 11.98% | 0.05 | -1.77 mmHg |
| Small groups | Primarily one-on-one | 19 | (-0.88 to -0.20) | 16.12% | 0.01 | -5.51 cm |
| Small groups | Primarily one-on-one | 9 | (-1.61 to -0.68) | 16.12% | 0.01 | -11.73 cm |
| Small groups | Primarily one-on-one | 12 | (-0.49 to 0.27) | 22.31% | 0.01 | -0.33 mmol/L |
| Small groups | No | 9 | (0.23 to 1.05) | 22.31% | 0.01 | 1.92 mmol/L |
| Small groups | Yes | 12 | (-0.50 to 0.20) | 25.64% | 0.006 | -5.25 mmol/L |
| Small groups | Primarily one-on-one | 7 | (-1.46 to -0.59) | 25.64% | 0.006 | -36.05 mmol/L |
| Small groups | Primarily one-on-one | 10 | (-0.61 to 0.22) | 19.01% | 0.03 | -0.06 mmol/L |</p>
<table>
<thead>
<tr>
<th></th>
<th>Small groups</th>
<th>Primarily one-on-one</th>
<th>( k )</th>
<th>( R^2 )</th>
<th>WC</th>
<th>HDL</th>
<th>TG</th>
<th>FBG</th>
<th>SBP</th>
<th>DBP</th>
</tr>
</thead>
<tbody>
<tr>
<td>SBP</td>
<td>7 (-1.04)</td>
<td>(-1.52 to -0.56)</td>
<td>19.01%</td>
<td>0.03</td>
<td>-0.32 mmol/L</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>13 (-0.46)</td>
<td>(-0.83 to -0.09)</td>
<td>30.73%</td>
<td>0.005</td>
<td>-1.50 mmHg</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>7 (-1.42)</td>
<td>(-1.91 to -0.94)</td>
<td>30.73%</td>
<td>0.005</td>
<td>-4.64 mmHg</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>13 (-0.34)</td>
<td>(-1.02 to 0.34)</td>
<td>13.86%</td>
<td>0.05</td>
<td>-0.79 mmHg</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>7 (-1.54)</td>
<td>(-2.43 to -0.65)</td>
<td>13.86%</td>
<td>0.05</td>
<td>-3.60 mmHg</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Note: WC, waist circumference; HDL, HDL cholesterol; TG, triglycerides, FBG, fasting blood glucose; SBP, systolic blood pressure; DBP, diastolic blood pressure; \( k \) is the number of interventions included in the analysis for each outcome; \( R^2 \) indicates the percentage of heterogeneity that the moderator accounts for; Clinical Unit of Measure was calculated using a predictive model and an added metic transformation using the effect sizes for each outcome and category.
Table 5. Non-Significant Moderators

<table>
<thead>
<tr>
<th>Non-Significant Moderators</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proportion of females</td>
</tr>
<tr>
<td>Proportion of participants with any type of disease</td>
</tr>
<tr>
<td>Number of participants with any type of disease</td>
</tr>
<tr>
<td>Proportion of participants taking any type of medication</td>
</tr>
<tr>
<td>Number of participants taking any type of medication</td>
</tr>
<tr>
<td>Type of medication use</td>
</tr>
<tr>
<td>Experimental setting</td>
</tr>
<tr>
<td>Number of participants who dropped out of the intervention</td>
</tr>
<tr>
<td>Length of counseling sessions</td>
</tr>
<tr>
<td>Number of counseling sessions</td>
</tr>
<tr>
<td>Specific type of diet</td>
</tr>
<tr>
<td>Publication Year</td>
</tr>
<tr>
<td>Language of publication</td>
</tr>
<tr>
<td>Recruitment type/Specific population</td>
</tr>
<tr>
<td>Proportion of carbohydrate intake (&lt;50% or ≥50%)</td>
</tr>
<tr>
<td>Proportion of saturated fat intake (&lt;10% or ≥10%)</td>
</tr>
<tr>
<td>Proportion of total fat intake (&lt;30% or ≥30%)</td>
</tr>
<tr>
<td>Mean Age of the Sample</td>
</tr>
<tr>
<td>Proportion of protein intake (&lt;15% or ≥15%)</td>
</tr>
<tr>
<td>Assessment of dietary compliance</td>
</tr>
<tr>
<td>Participation in dietary counseling</td>
</tr>
<tr>
<td>Population with cardiovascular disease</td>
</tr>
<tr>
<td>Population with Type II Diabetes Mellitus</td>
</tr>
<tr>
<td>Population with Metabolic Syndrome</td>
</tr>
<tr>
<td>Population with overweight/obesity</td>
</tr>
</tbody>
</table>
**Table 6.** Moderators that were Unable to be analyzed due to lack of Reported Information

<table>
<thead>
<tr>
<th>Moderators Unable to be Analyzed</th>
</tr>
</thead>
<tbody>
<tr>
<td>Oral contraceptive/hormone-replacement therapy</td>
</tr>
<tr>
<td>Proportion of participants who smoke</td>
</tr>
<tr>
<td>Number of participants that smoke</td>
</tr>
<tr>
<td>Supplement use</td>
</tr>
<tr>
<td>Alcohol intake</td>
</tr>
<tr>
<td>Number of alcoholic drinks/week</td>
</tr>
<tr>
<td>Type of alcohol consumption</td>
</tr>
<tr>
<td>Amount of exercise/week</td>
</tr>
<tr>
<td>Type of exercise</td>
</tr>
<tr>
<td>Was dietary adherence monitored</td>
</tr>
<tr>
<td>Were medications part of the intervention</td>
</tr>
<tr>
<td>Total calories consumed on the intervention diet</td>
</tr>
<tr>
<td>Dietary sodium intake</td>
</tr>
<tr>
<td>Dietary potassium intake</td>
</tr>
<tr>
<td>Unsaturated fat intake</td>
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<tr>
<td>Saturated fat intake</td>
</tr>
<tr>
<td>Cholesterol intake</td>
</tr>
<tr>
<td>Fiber intake</td>
</tr>
<tr>
<td>Servings of vegetables recommended</td>
</tr>
<tr>
<td>Servings of dairy recommended</td>
</tr>
<tr>
<td>Servings of wine recommended</td>
</tr>
<tr>
<td>Servings of fish recommended</td>
</tr>
<tr>
<td>Servings of olive oil recommended</td>
</tr>
<tr>
<td>Servings of legumes recommended</td>
</tr>
<tr>
<td>Servings of meat recommended</td>
</tr>
<tr>
<td>Servings of poultry recommended</td>
</tr>
<tr>
<td>Medication use</td>
</tr>
</tbody>
</table>
Figure 2. Forest Plot for Waist Circumference

Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.
Figure 3. Forest Plot for HDL

<table>
<thead>
<tr>
<th>Author(s) and Year</th>
<th>Favors Baseline</th>
<th>HDL</th>
<th>Favors Intervention</th>
<th>d[95%CI]</th>
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</thead>
<tbody>
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<td>Azzma et al 2009.10</td>
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<tr>
<td>Godard et al 2012.1</td>
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<tr>
<td>Rou et al 2010.10</td>
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</tr>
<tr>
<td>Espinardo et al 2005.3</td>
<td></td>
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<td></td>
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<tr>
<td>Espinardo et al 2004.3</td>
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</tr>
<tr>
<td>Jones et al 2013</td>
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<td>Lanier et al 2012.10</td>
<td></td>
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<td>Leighten et al 2009.3</td>
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<tr>
<td>Lamara et al 2010.6</td>
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<td></td>
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</tr>
<tr>
<td>Lumbarde et al 2012.4</td>
<td></td>
<td></td>
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<tr>
<td>Lumbarde et al 2012.4</td>
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<tr>
<td>Kaidia et al 2003.3</td>
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<tr>
<td>Richard et al 2011.3</td>
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<td>Bialditch et al 2011.3</td>
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<td>Radmore et al 2011.3</td>
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<td>Radmore et al 2011.3</td>
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<tr>
<td>Timar et al 2013</td>
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<tr>
<td>van Velden, et al 2007.2</td>
<td></td>
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</tbody>
</table>

Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.
Figure 4. Forest Plot for Triglycerides

Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.
**Figure 5. Forest Plot for Fasting Blood Glucose**

<table>
<thead>
<tr>
<th>Author(s) and Year</th>
<th>Favors Intervention</th>
<th>Glucose</th>
<th>Favors Baseline</th>
<th>d[95%CI]</th>
</tr>
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<tbody>
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<td>Alzana, et al. 2008.5</td>
<td></td>
<td></td>
<td></td>
<td>0.05 [-0.33, 0.43]</td>
</tr>
<tr>
<td>Alzana, et al. 2008.5</td>
<td></td>
<td></td>
<td></td>
<td>-0.31 [-0.61, 0.05]</td>
</tr>
<tr>
<td>Bedard, et al. 2012.4</td>
<td></td>
<td></td>
<td></td>
<td>0.06 [-0.39, 0.42]</td>
</tr>
<tr>
<td>Bedard, et al. 2012.11</td>
<td></td>
<td></td>
<td></td>
<td>-0.12 [-0.46, 0.21]</td>
</tr>
<tr>
<td>Rebkouchno, et al. 2015.3</td>
<td></td>
<td></td>
<td></td>
<td>-2.11 [-2.74, -1.48]</td>
</tr>
<tr>
<td>Gao, et al. 2015.11</td>
<td></td>
<td></td>
<td></td>
<td>-0.19 [-0.46, 0.28]</td>
</tr>
<tr>
<td>Cortesani, et al. 2009.2</td>
<td></td>
<td></td>
<td></td>
<td>-0.40 [-0.45, 0.36]</td>
</tr>
<tr>
<td>Esposito, et al. 2006.4</td>
<td></td>
<td></td>
<td></td>
<td>-1.03 [-1.64, -0.41]</td>
</tr>
<tr>
<td>Esposito, et al. 2008.4</td>
<td></td>
<td></td>
<td></td>
<td>-1.30 [-1.41, -0.70]</td>
</tr>
<tr>
<td>Esposito, et al. 2004.4</td>
<td></td>
<td></td>
<td></td>
<td>-2.04 [-3.09, -0.99]</td>
</tr>
<tr>
<td>Esposito, et al. 2003.6</td>
<td></td>
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<td></td>
<td>-4.63 [-1.92, -10.25]</td>
</tr>
<tr>
<td>Jones, et al. 2011.1</td>
<td></td>
<td></td>
<td></td>
<td>-1.13 [-0.75, 0.17]</td>
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<td>Landeira, et al. 2012.8</td>
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<td></td>
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<td>-0.39 [-0.99, 0.20]</td>
</tr>
<tr>
<td>Leighton, et al. 2000.2</td>
<td></td>
<td></td>
<td></td>
<td>-0.04 [-0.24, 0.16]</td>
</tr>
<tr>
<td>Lindberg, et al. 2007.3</td>
<td></td>
<td></td>
<td></td>
<td>-0.47 [-0.98, 0.04]</td>
</tr>
<tr>
<td>Lombardo, et al. 2014.12</td>
<td></td>
<td></td>
<td></td>
<td>-0.20 [-0.76, 0.30]</td>
</tr>
<tr>
<td>Lombardo, et al. 2014.13</td>
<td></td>
<td></td>
<td></td>
<td>0.92 [-0.46, 0.30]</td>
</tr>
<tr>
<td>Ballard, et al. 2009.4</td>
<td></td>
<td></td>
<td></td>
<td>0.13 [-0.42, 0.49]</td>
</tr>
<tr>
<td>Ballard, et al. 2010.11</td>
<td></td>
<td></td>
<td></td>
<td>-0.14 [-0.46, 0.17]</td>
</tr>
<tr>
<td>Richard, et al. 2011.4</td>
<td></td>
<td></td>
<td></td>
<td>-0.12 [-0.52, 0.28]</td>
</tr>
<tr>
<td>Rubenstein, et al. 2011.15</td>
<td></td>
<td></td>
<td></td>
<td>-0.21 [-0.41, 0.00]</td>
</tr>
<tr>
<td>Ring, et al. 2013.4</td>
<td></td>
<td></td>
<td></td>
<td>-0.20 [-0.40, 0.30]</td>
</tr>
<tr>
<td>van Volden, et al. 2007.3</td>
<td></td>
<td></td>
<td></td>
<td>-0.15 [-0.28, 0.03]</td>
</tr>
</tbody>
</table>

IE Model: -0.51 [-0.80, -0.22]

**Note:** Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.
Figure 6. Forest Plot for Systolic Blood Pressure

Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.
Figure 7. Forest Plot for Diastolic Blood Pressure

<table>
<thead>
<tr>
<th>Author(s) and Year</th>
<th>Favors Intervention</th>
<th>Favors Baseline</th>
<th>d[95%CI]</th>
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<tbody>
<tr>
<td>Arzoua, et al. 2005.6</td>
<td></td>
<td></td>
<td>0.31 [0.70, 0.88]</td>
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<tr>
<td>Arzoua, et al. 2007.7</td>
<td></td>
<td></td>
<td>0.55 [-0.92, 2.17]</td>
</tr>
<tr>
<td>Bedard, et al. 2011.6</td>
<td></td>
<td></td>
<td>0.81 [-2.20, 3.52]</td>
</tr>
<tr>
<td>Bedard, et al. 2012.6</td>
<td></td>
<td></td>
<td>0.62 [-0.37, 1.22]</td>
</tr>
<tr>
<td>Beskos, et al. 2013.8</td>
<td></td>
<td></td>
<td>0.73 [-1.14, 2.60]</td>
</tr>
<tr>
<td>Corradi, et al. 2000.4</td>
<td></td>
<td></td>
<td>0.57 [-2.03, 2.85]</td>
</tr>
<tr>
<td>Esposito, et al. 2006.6</td>
<td></td>
<td></td>
<td>1.06 [-2.56, 4.66]</td>
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<tr>
<td>Esposito, et al. 2009.6</td>
<td></td>
<td></td>
<td>1.35 [-2.39, 5.11]</td>
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<td>2.97 [-3.47, 9.37]</td>
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<tr>
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<td></td>
<td>1.52 [-0.80, 4.33]</td>
</tr>
<tr>
<td>Jones, et al. 2011.5</td>
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<td>0.50 [-0.92, 2.60]</td>
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<td>Lombardo, et al. 2012.6</td>
<td></td>
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<td>0.41 [0.06, 0.67]</td>
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<td>Longhin, et al. 2000.6</td>
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<td>1.46 [-1.74, 4.65]</td>
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<td>Leon, et al. 2010.6</td>
<td></td>
<td></td>
<td>0.13 [-0.76, 1.01]</td>
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<td>Lienau, et al. 2010.6</td>
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<td>Lombardo, et al. 2014.11</td>
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<td>0.58 [0.01, 1.15]</td>
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<td>Randols, et al. 2009.6</td>
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<td>0.08 [0.40, 0.59]</td>
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<td>0.56 [-1.15, 2.64]</td>
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<td>Randols, et al. 2009.10</td>
<td></td>
<td></td>
<td>0.21 [-0.62, 0.91]</td>
</tr>
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<td>Rubenfire, et al. 2011.6</td>
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<td></td>
<td>0.51 [-0.73, 2.16]</td>
</tr>
<tr>
<td>Rubenfire, et al. 2011.17</td>
<td></td>
<td></td>
<td>0.81 [0.05, 1.62]</td>
</tr>
<tr>
<td>Ryan, et al. 2010.6</td>
<td></td>
<td></td>
<td>0.38 [-0.60, 1.36]</td>
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<td>Sanchez, et al. 2012.3</td>
<td></td>
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<td>0.62 [-0.07, 0.34]</td>
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<tr>
<td>Tenor, et al. 2013.7</td>
<td></td>
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<td>0.41 [-0.03, 0.91]</td>
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<tr>
<td>Van Gelder, et al. 2007.5</td>
<td></td>
<td></td>
<td>0.08 [-1.20, 0.09]</td>
</tr>
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</table>

RE Model: 0.02 [-1.41, 1.45]

Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.
Figure 8. Meta-Regression Plot for Waist Circumference

Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; $R^2$ indicates the percentage of variability accounted for by length.
Figure 9. Meta-Regression Plot for HDL

![Meta-Regression Plot for HDL](image1)

**Note:** Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; $R^2$ indicates the percentage of variability accounted for by length.

Figure 10. Meta-Regression Plot for Triglycerides

![Meta-Regression Plot for Triglycerides](image2)

**Note:** Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; $R^2$ indicates the percentage of variability accounted for by length.
Figure 11. Meta-Regression Plot for Fasting Blood Glucose

Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; $R^2$ indicates the percentage of variability accounted for by length.

Figure 12. Meta-Regression Plot for Systolic Blood Pressure

Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; $R^2$ indicates the percentage of variability accounted for by length.
Figure 13. Meta-Regression Plot for Diastolic Blood Pressure

Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; $R^2$ indicates the percentage of variability accounted for by length.

B = -0.0086
CI = (-0.0184, 0.0013)
$R^2$ = 6.84%
Figure 14. Risk of Bias
Appendix

Appendix 1. Comprehensive Literature Search Strategy

All databases searched until August 4, 2014.

1. PubMed, years 1940s-present

Terms were searched in all fields; however, field labels were used to restrict specific terms/phrases to the Medical Subject Headings [Mesh], publication type [pt] and journal name [ta] fields.


Results: 431

2. EMBASE (via Scopus) years 1823-present

All terms were searched in “Article Title, Abstract, Keywords”. Because of character restrictions in Scopus, this search was run in parts and assembled using the “Search history”.

Limit to Document type: “Article”

{Mediterranean diet} OR {Mediterranean diets} OR {Mediterranean dietary} OR {Mediterranean style diet} OR {Mediterranean style diets}

AND (adiposity OR "weight loss” OR "metabolic syndrome” OR overweight OR BMI OR "body mass” OR "waist circumference” OR weight OR "body weight” OR obese OR obesity OR "abdominal fat”) NOT (in article title) ("Cross-Sectional Studies" OR "Case Reports" OR Comment OR Editorial OR Letter OR Review OR "case control" OR "case report" OR "case study" OR "case series" OR "Follow-Up Study" OR "observational study" OR "prospective cohort" OR "cohort study" OR "Longitudinal Study" OR "Follow-Up Study")
Studies) OR {Retrospective Studies} OR {non-randomized} OR {follow up study} OR rat OR rats OR mice OR mouse OR dog OR dogs OR cats)

Results: 515

3. Web of Science, years 1974-present

All terms were searched in “Topic”.

Limit to Document type: “article”

"Mediterranean diet" OR "Mediterranean diets" OR "Mediterranean dietary" OR "Mediterranean style diet" OR "Mediterranean style diets"

AND

(adiposity OR "weight loss" OR "metabolic syndrome" OR overweight OR BMI OR "body mass" OR "waist circumference" OR weight OR "body weight" OR obese OR obesity OR "abdominal fat")

NOT (in title) ("Cross-Sectional Studies" OR "Case Reports" OR Comment OR Editorial OR Letter OR Review OR "case control" OR "case report" OR "case study" OR "case series" OR "Follow-Up Study" OR "observational study" OR "prospective cohort" OR "cohorts study" OR "Longitudinal Study" OR "Follow-Up Studies" OR "Retrospective Studies" OR "non-randomized" OR "follow up study" OR rat OR rats OR mice OR mouse OR dog OR dogs OR cats)

Results: 890

4. CINAHL

All terms were searched in all fields.

Excluded: MEDLINE Records

Limited to: research articles

"Mediterranean diet" OR "Mediterranean diets" OR "Mediterranean dietary" OR "Mediterranean style diet" OR "Mediterranean style diets"

AND

(adiposity OR "weight loss" OR "metabolic syndrome" OR overweight OR BMI OR "body mass" OR "waist circumference" OR weight OR "body weight" OR obese OR obesity OR "abdominal fat")

NOT (in title) ("Cross-Sectional Studies" OR "Case Reports" OR Comment OR Editorial OR Letter OR Review OR "case control" OR "case report" OR "case study" OR "case series" OR "Follow-Up Study" OR "observational study" OR "prospective cohort" OR "cohorts study" OR "Longitudinal Study" OR "Follow-Up Studies" OR "Retrospective Studies" OR "non-randomized" OR "follow up study" OR rat OR rats OR mice OR mouse OR dog OR dogs OR cats)
Studies" OR "Retrospective Studies" OR "non-randomized" OR "follow up study" OR rat OR rats OR mice OR mouse OR dog OR dogs OR cats)

Results : 25

5. Agricola years 1970-present

Search in “All Fields”

Limited to “academic journals”

"Mediterranean diet" OR "Mediterranean diets" OR "Mediterranean dietary" OR "Mediterranean style diet" OR "Mediterranean style diets"

AND

(adiposity OR "weight loss" OR "metabolic syndrome" OR overweight OR BMI OR "body mass" OR "waist circumference" OR weight OR "body weight" OR obese OR obesity OR "abdominal fat")

NOT (in title) ("Cross-Sectional Studies" OR "Case Reports" OR Comment OR Editorial OR Letter OR Review OR "case control" OR "case report" OR "case study" OR "case series" OR "Follow-Up Study" OR "observational study" OR "prospective cohort" OR "cohort study" OR "Longitudinal Study" OR "Follow-Up Studies" OR "Retrospective Studies" OR "non-randomized" OR "follow up study" OR rat OR rats OR mice OR mouse OR dog OR dogs OR cats)

Results: 123

6. CAB Direct years 1973-present

Limit to Document Type: Journal article

"Mediterranean diet" OR "Mediterranean diets" OR "Mediterranean dietary" OR "Mediterranean style diet" OR "Mediterranean style diets"

AND

(adiposity OR "weight loss" OR "metabolic syndrome" OR overweight OR BMI OR "body mass" OR "waist circumference" OR weight OR "body weight" OR obese OR obesity OR "abdominal fat")

NOT (in title) ("Cross-Sectional Studies" OR "Case Reports" OR Comment OR Editorial OR Letter OR Review OR "case control" OR "case report" OR "case study" OR "case series" OR "Follow-Up Study" OR "observational study" OR "prospective cohort" OR "cohort study" OR "Longitudinal Study" OR "Follow-Up Studies" OR "Retrospective Studies" OR "non-randomized" OR "follow up study" OR rat OR rats OR mice OR mouse OR dog OR dogs OR cats)

Results: 423; TOTAL: 1,269 after removal of duplicates
## Appendix 2. Screening Form

**Mediterranean Diet Obesity Meta-Analysis Selection Criteria**

**Inclusion Criteria**

Trials MUST match all of these criteria:

- **Pre- AND Post-intervention weight measurements** (at least one of these):
  - Waist Circumference

- Mediterranean diet (as a whole, for example, not just olive oil) for at least one of the interventions. Can also be described as Mediterranean-style diet, hypocaloric Mediterranean diet, etc.

**Exclusion Criteria**

Studies CANNOT include any of the following:

- Survey
- Review
- Guidelines
- Prospective Studies
- Epidemiologic Studies
- Cross-sectional Studies

**Notes:**
**Appendix 3. Mediterranean Diet Coding Form** (finalized July 2014)

CODER________ Coder (Marissa=1, Julia=2, Other=3)

**Study Information**

<table>
<thead>
<tr>
<th>Field</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>ID</td>
<td>Study ID (first 3 letters of 1st author’s last name &amp; unique ID#: Pescatello=PES001), (Last name, Yr)</td>
</tr>
<tr>
<td>PUB_YR</td>
<td>Publication year (consider this missing if unpublished)</td>
</tr>
<tr>
<td>DATA</td>
<td>Estimated year of data collection (earliest date for data collection or manuscript submission/publication; if unpublished and date unknown, use year manuscript was acquired; for dissertation or thesis, use year)</td>
</tr>
<tr>
<td>LANG</td>
<td>Language of report 1=English 2=Spanish 3=Japanese 4=Other, specify:</td>
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<td>SOURCE</td>
<td>Publication Type 1=journal 2=book 3=thesis/dissertation 4=conference paper 5=unpublished</td>
</tr>
<tr>
<td>SCORE</td>
<td>Impact Score of the Journal (use ISI Web of Knowledge journal citation reports)</td>
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<td>JOURNAL NAME</td>
<td></td>
</tr>
<tr>
<td>PUBMED NAME/ ABBR.</td>
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</tr>
<tr>
<td>FUNDING SOURCE</td>
<td>1= Gov’nt (i.e., CDC, NIH, etc) 2= Academic/University 3= Private 4= Other</td>
</tr>
<tr>
<td>For all, specify source/grant:</td>
<td></td>
</tr>
<tr>
<td>NOTE_STUDY</td>
<td>study notes (make note of multiple arms; ex. MD vs. low fat vs. low carb + MD vs. CONTROL):</td>
</tr>
</tbody>
</table>

67
**Sample Characteristics** *(proportion: 0.0–1.0) Note: IF ethnicity is reported, ETH_EST will be == 0*

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<tr>
<th>ETH</th>
<th>Ethnicity reported?</th>
<th>1 = yes; 0 = no</th>
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<tbody>
<tr>
<td>PROP_WH</td>
<td>Proportion White; whole #____</td>
<td></td>
</tr>
<tr>
<td>PROP_BLK</td>
<td>Proportion Black/ whole #____</td>
<td></td>
</tr>
<tr>
<td>PROP_ASIAN</td>
<td>Proportion Asian/ whole #____</td>
<td></td>
</tr>
<tr>
<td>PROP_MIX</td>
<td>Proportion Mixed (other)/ whole #____</td>
<td></td>
</tr>
<tr>
<td>PROP_HISP</td>
<td>Proportion Latino/Hispanic/ whole #____</td>
<td></td>
</tr>
<tr>
<td>PROP_CARIB</td>
<td>Proportion Caribbean/ whole #____</td>
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<td>ETH_EST</td>
<td>Assumed ethnicity (0= n/a, 1= White, 2= Asian, 3= Black, 4= Unreported, 5= Hispanic/Latino)</td>
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<th># of Females in Sample; Proportion</th>
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<td># of Females in Sample; Proportion</td>
</tr>
<tr>
<td>NUM_FemiIN2</td>
<td># of Females in Sample; Proportion</td>
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<tr>
<td>NUM_FemiIN3</td>
<td># of Females in Sample; Proportion</td>
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<th>Location of sample <em>(if unreported, use location of first author as estimate of study location)</em></th>
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<td>US_ZIP</td>
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<tr>
<td>3=Canada</td>
<td>4=Europe</td>
</tr>
<tr>
<td>7=Asia <em>(city: Osaka, Japan)</em></td>
<td>8=Australia</td>
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<th>POP</th>
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<td>1=college</td>
<td>2=community</td>
</tr>
<tr>
<td>(senior center, flyers, etc.)</td>
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</table>
3 = clinical/hospital (e.g., cardiac rehab, outpatient clinic, etc.)

**NOTE_RECRUIT**  
Notes on recruitment/ sample location

---

**Risk Characteristics** - report values of baseline data (check methods or descriptive tables)  
*KEEP DATA SEPARATE FOR GROUPS*

**TOTAL_POP**  
Reported as total sample? (1 = yes, 0 = no)  
*if data is collapsed, not separate for groups, chose YES*

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<th>CONTROL / COMPARISON</th>
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<th>IN2 ( n = )</th>
<th>IN3 ( n = )</th>
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<td>( n = ) (total sample)</td>
<td>( n = ) (total sample)</td>
<td>( n = ) (total sample)</td>
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<tr>
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<td>5 = Diabetes</td>
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<td>6 = MetS</td>
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<td>7 = Arthritis</td>
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<td>8 = Dyslipidemia</td>
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<td>9 = Obesity</td>
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<td>10 = Other, specify: _____</td>
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<tr>
<td>11 = Multiple, specify #s: ___________</td>
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**If disease: report**  
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PDF: 69
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<th>Characteristic</th>
<th>CONTROL / COMPARISON n=____ (total sample)</th>
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<th>IN2 n=____ (total sample), specify intervention____</th>
<th>IN3 n=____ (total sample), specify intervention____</th>
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<td>prop. &amp; number if “healthy” denote 0=n/a; if missing=“.”</td>
<td>EASE NumberDisease</td>
<td>ASE NumberDisease</td>
<td>SE NumberDisease</td>
<td>ASE NumberDisease</td>
</tr>
<tr>
<td>Medication use (0=no, 1=yes)</td>
<td>MED</td>
<td>MED</td>
<td>MED</td>
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</tr>
<tr>
<td>If yes, report prop &amp; number; if no meds, use 0=NA (if missing=“.”)</td>
<td>PROP_USE NumberMED</td>
<td>PROP_USE NumberMED</td>
<td>PROP_USE NumberMED</td>
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<td>Medication Type (if no meds=0)</td>
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<td>2= Nitrates</td>
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<td>3= Ca²⁺ Channel Blockers</td>
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<td>4= Angiotension Converting Enzyme (ACE) Inhibitors</td>
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<td>9= Statins</td>
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<td>10=Other, specify:</td>
<td>MED_TYPE</td>
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<tr>
<td>Characteristic</td>
<td>CONTROL / COMPARISON n=_____ (total sample)</td>
<td>IN1 n=_____ (total sample), specify intervention_____ _</td>
<td>IN2 n=_____ (total sample), specify intervention_____ _</td>
<td>IN3 n=_____ (total sample), specify intervention_____ _</td>
</tr>
<tr>
<td>----------------</td>
<td>-------------------------------------------</td>
<td>-------------------------------------------------</td>
<td>-------------------------------------------------</td>
<td>-------------------------------------------------</td>
</tr>
<tr>
<td>11= Multiple, specify:</td>
<td>BP Medication use (1= yes, 0=no) If unreported == “”</td>
<td>BPMedUse</td>
<td>BPMedUse</td>
<td>BPMedUse</td>
</tr>
<tr>
<td>If yes, report prop. &amp; number (if “no”=0, NA; if missing denote=“.”)</td>
<td>BPMedProp BPMedNumber</td>
<td>BPMedProp BPMedNumber</td>
<td>BPMedProp BPMedNumber</td>
<td>BPMedProp BPMedNumber</td>
</tr>
<tr>
<td>If taking meds, is BP controlled? yes= 1, if SBP≤140 OR DBP≤90; no= 0, SBP&gt;140 OR DBP&gt;90 (*if no BP use == NA)</td>
<td>BPControl</td>
<td>BPControl</td>
<td>BPControl</td>
<td>BPControl</td>
</tr>
</tbody>
</table>

**LIFESTYLE VARIABLES**

<table>
<thead>
<tr>
<th>Oral Contraceptive (0=no, 1= yes) OR Hormone replacement therapy</th>
<th>OC_USE HRT_USE</th>
<th>OC_USE HRT_USE</th>
<th>OC_USE HRT_USE</th>
<th>OC_USE HRT_USE</th>
</tr>
</thead>
<tbody>
<tr>
<td>Smokers/smokers (≤6)</td>
<td>SMOKE</td>
<td>SMOKE</td>
<td>SMOKE</td>
<td>SMOKE</td>
</tr>
<tr>
<td>Characteristic</td>
<td>CONTROL / COMPARISON $n=__________$ (total sample)</td>
<td>IN1 $n=_______$ (total sample), specify intervention $_______$</td>
<td>IN2 $n=_______$ (total sample), specify intervention $_______$</td>
<td>IN3 $n=_______$ (total sample), specify intervention $_______$</td>
</tr>
<tr>
<td>---------------------------------------------</td>
<td>-------------------------------------------------------------</td>
<td>---------------------------------------------------------------------------------</td>
<td>---------------------------------------------------------------------------------</td>
<td>---------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>months) (0=no,1=yes ; if missing = “”)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>If yes, report smoker prop. &amp; number</td>
<td>PROP_SM OKE NumberSM OKE</td>
<td>PROP_SM OKE NumberSM OKE</td>
<td>PROP_SM OKE NumberSM OKE</td>
<td>PROP_SM OKE NumberSM OKE</td>
</tr>
<tr>
<td>Nutritional Supplements Permitted? (0=no, 1=yes)</td>
<td>SUPP</td>
<td>SUPP</td>
<td>SUPP</td>
<td>SUPP</td>
</tr>
<tr>
<td>If yes, specify type</td>
<td>TYPE</td>
<td>TYPE</td>
<td>TYPE</td>
<td>TYPE</td>
</tr>
<tr>
<td>Consume Alcohol? (0=no, 1=yes)</td>
<td>ALC</td>
<td>ALC</td>
<td>ALC</td>
<td>ALC</td>
</tr>
<tr>
<td>If yes, how many drinks/week ?</td>
<td>AMT</td>
<td>AMT</td>
<td>AMT</td>
<td>AMT</td>
</tr>
<tr>
<td>If yes, what type of alcohol?</td>
<td>ALCTYPE</td>
<td>ALCTYPE</td>
<td>ALCTYPE</td>
<td>ALCTYPE</td>
</tr>
<tr>
<td>Amount of exercise per week (in min)</td>
<td>EX</td>
<td>EX</td>
<td>EX</td>
<td>EX</td>
</tr>
<tr>
<td>Type of exercise (e.g., cardio, strength training)</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
NOTE_RISK  Notes on risk characteristics relevant to coding

Methods & Design

CON_GRP  Type of control group used
1= random assignment of individuals to conditions including a non-diet control group, specify ____________________
2= random assignment of individuals to conditions including non-diet control session
3= random assignment of individuals to non-MD condition/diet
4= random assignment of individuals to a non-diet control group
5= other, specify: ____________________________________________________________

Experiment/ Intervention Conditions

EXPERIMENT________  INTERVENTIONS/EXPERIMENTAL CONDITION(S)
1= non-diet control/comparison + 1 intervention  2= non-diet control/comparison + 2 interventions
3= non-diet control/comparison + 3 interventions
4= diet control/comparison + 1 intervention  5= diet control/comparison + 2 interventions
6= diet control/comparison + 3 interventions

EXP_SETTING________ Setting of Intervention(s)
1= hospital  2= clinic
3= academic/research lab  4= fitness center, gym
5= Other, specify: ____________________________________________________________
6= multiple, specify: __________________________

DIET_MONITOR________ Was diet adherence monitored? (0= none; 1= yes) If yes, specify:
_____________________________________________________________________

BEHAV_TECH________ Behavioral technique/monitoring system used? (0= none, 1= yes) If yes, specify:
________________________________________________________________________
Examples: positive reinforcement/contingency management, exercise & lifestyle information/lectures; PA logs, etc.

INTER_LVL________ Level of intervention or supervision used in the study
1=primarily 1-on-1  2=small group processes (supervisor & group members)
3=supervised session(s)
4=unsupervised session(s)  5=incentive (payment based on sessions attended)
6=multiply, specify #s:____________________________________

NOTE_EXP & METHODS Notes related to study design & delivery of intervention: ____________________________
### DIET CHARACTERISTICS

<table>
<thead>
<tr>
<th>CONTROL/COMPARISON</th>
<th>IN1</th>
<th>IN2</th>
<th>IN3</th>
</tr>
</thead>
<tbody>
<tr>
<td>LENGTH (in weeks)</td>
<td>LENGTH</td>
<td>LENGTH</td>
<td>LENGTH</td>
</tr>
<tr>
<td>WT Gain/WT Loss</td>
<td>WT Gain/WT Loss</td>
<td>WT Gain/WT Loss</td>
<td>WT Gain/WT Loss</td>
</tr>
<tr>
<td>(1=loss, 2=gain, 3=maintain, 4=unspecified)</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

**PART LOST # of drop outs**

**ADHERENCE (report %) If reported as # of sessions completed, use:==completed sessions x 100**

Were medications used as part of the intervention? (0=no, 1=yes)

If yes, specify

1 = β Blockers  
2 = Nitrates  
3 = Ca²⁺ Channel Blockers  
4 = Angiotensin Converting Enzyme (ACE) Inhibitors  
5 = Diuretics  
6 = Vasodilators  
7 = NSAIDs  
8 = Aspirin  
9 = Statins  
10 = Other, specify:

MEDS

DIET TYPE

(1=MedDiet, 2=low-fat, 3=high protein, 4=low-carb, 5=other, specify)

 Provision of Med Diet Foods? (0=no, 1=yes)

If yes, type and amount:

1 = olive oil (amt:)
2 = nuts (amt:)
3 = fruits (amt:)
4 = fish (amt:)
5 = dairy (amt:)
6 = multiple

Diet specification reported as a distribution of macronutrients? (0=no, 1=yes)

If yes, specify

**KCAL TOTAL BASE (kcal/day)**

**KCAL TOTAL END (kcal/day)**

**KCAL Rx** Prescribed kcals per day

**KCAL REPORT** Reported kcals per day

Energy restriction (kcal or %)

**SOD INTAKE** (mg/day)

**POT INTAKE** (mg/day)

**FAT INTAKE** (g/day)

**Unsaturated: FAT_UNSAT**

**Saturated:**

**FAT SAT**

**Cholesterol: FAT CHOL**
<table>
<thead>
<tr>
<th>Dietary Fiber Intake (g/day)</th>
<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>FIB_INTAKE</td>
<td>--</td>
</tr>
<tr>
<td>Servings/week: Fruit and/or Vegetables</td>
<td>VEG_SER</td>
</tr>
<tr>
<td>Servings/week: Dairy</td>
<td>DAIRY_SER</td>
</tr>
<tr>
<td>Servings/week: Wine</td>
<td>WINE_SER</td>
</tr>
<tr>
<td>Servings/week: Whole Grains</td>
<td>GRAIN_SER</td>
</tr>
<tr>
<td>Servings/week: Fish</td>
<td>FISH_SER</td>
</tr>
<tr>
<td>Servings/week: Olive Oil</td>
<td>OIL_SER</td>
</tr>
<tr>
<td>Servings/week: Nuts</td>
<td>NUTS_SER</td>
</tr>
<tr>
<td>Servings/week: Legumes</td>
<td>LEG_SER</td>
</tr>
<tr>
<td>Servings/week: Red/processed meat</td>
<td>MEAT_SER</td>
</tr>
<tr>
<td>Servings/week: Poultry</td>
<td>POUL_SER</td>
</tr>
</tbody>
</table>

**Dietary Compliance & Counseling**

<table>
<thead>
<tr>
<th>DI_COMPLIANCE</th>
<th>Was Dietary compliance assessed? 0= No; 1= Yes</th>
</tr>
</thead>
<tbody>
<tr>
<td>If yes, specify:</td>
<td>(1=FFQ, 2=Food journal, 3=phone interviewing, 4=24 hr recall, 5=other, specify___)</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Was diet adherence measured pre, during, or post intervention?</th>
<th>(1=pre, 2=during, 3=post, 4=pre,during, and post, 5=pre and post, 6=not reported)</th>
</tr>
</thead>
</table>

<table>
<thead>
<tr>
<th>Is a scale used to measure adherence?</th>
<th>(0=no, 1=yes)</th>
</tr>
</thead>
<tbody>
<tr>
<td>If yes, specify type of scale used</td>
<td></td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>DI_COUNSELING</th>
<th>Participation in dietary counseling? 0= no; 1= yes</th>
</tr>
</thead>
<tbody>
<tr>
<td>If Dietary Counseling was provided, report:</td>
<td></td>
</tr>
<tr>
<td>COUNSEL_HR</td>
<td>hours per week</td>
</tr>
<tr>
<td>COUNSEL_SESS</td>
<td>sessions per week</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>DIET_TOPIC</th>
<th>If Dietary Counseling was provided,</th>
</tr>
</thead>
<tbody>
<tr>
<td>briefly state topics covered</td>
<td></td>
</tr>
<tr>
<td>----------------------------</td>
<td>---</td>
</tr>
<tr>
<td>QoL Was Quality of Life (QoL) assessed? 0=no, 1=yes, if yes, report tool or scale</td>
<td></td>
</tr>
<tr>
<td>NOTE_DIET Report here any notes relevant to the dietary intervention, counseling, implementation, etc.</td>
<td></td>
</tr>
<tr>
<td># of follow-ups</td>
<td></td>
</tr>
<tr>
<td>Interval of follow-ups</td>
<td></td>
</tr>
</tbody>
</table>
Appendix 4. SAS Code

Import Data

To read data set:

```sas
proc print data=midterm;
run;
```

To get mean, range, and standard deviation of certain variables (various dummy codes were created in Excel prior to analysis):

```sas
proc means data=midterm n sum mean max min range std;
   class Diet Article;
run;
```

To calculate percentages for language and region of publication:

```sas
proc freq data=midterm;
run;
```

Age of participants was in a separate spreadsheet (weighted mean and std of age was calculated by hand):

```sas
proc print data=age;
run;
proc means data=age n sum mean max min range std;
run;
```
Appendix 5. R Syntax

Run the Library
Library("metafor")

Overall Effect Sizes

#TMD and WC
model1<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==1), data=Final, method="FE")
model1
model2<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==1), data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model2

#TMD and HDL
model5<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==3), data=Final, method="FE")
model5
model6<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==3), data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model6

#TMD and triglycerides
model7<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==4), data=Final, method="FE")
model7
model8<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==4), data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model8

#TMD and glucose
model9<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==5), data=Final, method="FE")
model9
model10<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==5), data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model10

#TMD and SBP
model11<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==6), data=Final, method="FE")
model11
model12<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==6), data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model12

#TMD and DBP
model13<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==7), data=Final, method="FE")
model13
model14<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==7), data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model14

Forest Plots

#this determines the xleft, xright, ybottom, ytop in the plot in order to use this information to determine where to insert text

#TMD and WC
par("usr")
forest(model2, xlim=c(-10,10), xlab="Standardized Mean Difference", cex=0.8, efac=2, col="dark red", border="black")

op<-par(cex=0.85, font=2, col="black") #to change the size, font, and color of the plot

op<-par(cex=0.85, font=2, col="dark red") #to change the size, the font, and the color of the inserted text in the plot

text (0,45, "Waist Circumference") #the first number indicates where the title starts and the second number how high in the plot
text(c(-4,4),44,c("Favors Intervention", "Favors Baseline")) #here the -8 is telling us the position where favors intervention starts and 7 where the position where
favors baseline starts, and they both are at the 22 height in the plot, if you count
the number of authors are 20, plus the line where RE Model is that is 21 rows, so
the labels Author, and Favors are in line 22

text(-10,44, "Author(s) and Year", pos=4)
text(7.5,44, "d[95%CI]", pos=4)
par(op)

#TMD and HDL
par("usr")
forest(model6, xlim=c(-10,10), xlab="Standardized Mean Difference", cex=0.8,
efac=2, col="dark red", border="black")

op<-par(cex=0.85, font=2, col="black")#to change the size, font, and color of the plot
op<-par(cex=0.85, font=2, col="dark red") #to change the size, the font, and the
color of the inserted text in the plot
text (0,31, "HDL") #the first number indicates where the title starts and the
second number how high in the plot
text(c(-3,3),30,c("Favors Baseline ", "Favors Intervention")) #here the -8 is telling
us the position where favors intervention starts and 7 where the position where
favors baseline starts, and they both are at the 22 height in the plot, if you count
the number of authors are 20, plus the line where RE Model is that is 21 rows, so
the labels Author, and Favors are in line 22

text(-10,30, "Author(s) and Year", pos=4)
text(8,30, "d[95%CI]", pos=4)
par(op)

#TMD and TG
par("usr")
forest(model8, xlim=c(-10,10), xlab="Standardized Mean Difference", cex=0.8,
efac=2, col="dark red", border="black")

op<-par(cex=0.85, font=2, col="black")#to change the size, font, and color of the plot
op<-par(cex=0.85, font=2, col="dark red") #to change the size, the font, and the
color of the inserted text in the plot
text(0.29, "Triglycerides") #the first number indicates where the title starts and
the second number how high in the plot

text(c(-4,4),28,c("Favors Intervention", "Favors Baseline")) #here the -8 is telling
us the position where favors intervention starts and 7 where the position where
favors baseline starts, and they both are at the 22 height in the plot, if you count
the number of authors are 20, plus the line where RE Model is that is 21 rows, so
the labels Author, and Favors are in line 22

text(-10,28, "Author(s) and Year", pos=4)

text(8,28, "d[95%CI]", pos=4)

par(op)

#TMD and FBG

par("usr")

forest(model10, xlim=c(-10,10), xlab="Standardized Mean Difference", cex=0.8,
efac=2, col="dark red", border="black")

op<-par(cex=0.85, font=2, col="black")#to change the size, font, and color of the
plot

op<-par(cex=0.85, font=2, col="dark red") #to change the size, the font, and the
color of the inserted text in the plot

text (0,27, "Glucose") #the first number indicates where the title starts and the
second number how high in the plot

text(c(-4,4),26,c("Favors Intervention", "Favors Baseline")) #here the -8 is telling
us the position where favors intervention starts and 7 where the position where
favors baseline starts, and they both are at the 22 height in the plot, if you count
the number of authors are 20, plus the line where RE Model is that is 21 rows, so
the labels Author, and Favors are in line 22

text(-10,26, "Author(s) and Year", pos=4)

text(8,26, "d[95%CI]", pos=4)

par(op)

#TMD and SBP

par("usr")

forest(model12, xlim=c(-10,10), xlab="Standardized Mean Difference", cex=0.8,
efac=2, col="dark red", border="black")

op<-par(cex=0.85, font=2, col="black")#to change the size, font, and color of the
plot
op<-par(cex=0.80, font=2, col="dark red") #to change the size, the font, and the color of the inserted text in the plot
text (0.29, "Systolic Blood Pressure") #the first number indicates where the title starts and the second number how high in the plot
text(c(-4,4),28,c("Favors Intervention", "Favors Baseline")) #here the -8 is telling us the position where favors intervention starts and 7 where the position where favors baseline starts, and they both are at the 22 height in the plot, if you count the number of authors are 20, plus the line where RE Model is that is 21 rows, so the labels Author, and Favors are in line 22
text(-10,28, "Author(s) and Year", pos=4)
text(8,28, "d[95%CI]", pos=4)
par(op)

#TMD and DBP
par("usr")
forest(model14, xlim=c(-10,10), xlab="Standardized Mean Difference", cex=0.8, efac=2, col="dark red", border="black")

op<-par(cex=0.85, font=2, col="black") #to change the size, font, and color of the plot
op<-par(cex=0.85, font=2, col="dark red") #to change the size, the font, and the color of the inserted text in the plot

text (0.29, "Diastolic Blood Pressure") #the first number indicates where the title starts and the second number how high in the plot
text(c(-4,4),28,c("Favors Intervention", "Favors Baseline")) #here the -8 is telling us the position where favors intervention starts and 7 where the position where favors baseline starts, and they both are at the 22 height in the plot, if you count the number of authors are 20, plus the line where RE Model is that is 21 rows, so the labels Author, and Favors are in line 22
text(-10,28, "Author(s) and Year", pos=4)
text(8,28, "d[95%CI]", pos=4)
par(op)

Publication Bias

#pub bias for med Diet and WC

#Egger's
regtest(model2, model="lm", data=Final)

#Begg's
ranktest(model2, data=Final)

#funnel plot
model2trim=trimfill(model2, data=Final)
funnel(model2trim)

#pub bias for med Diet and HDL
#Egger's
regtest(model6, model="lm", data=Final)

#Begg's
ranktest(model6, data=Final)

#funnel plot
model6trim=trimfill(model6, data=Final)
funnel(model6trim)

#pub bias for med Diet and Triglyceride
#Egger's
regtest(model8, model="lm", data=Final)

#Begg's
ranktest(model8, data=Final)

#funnel plot
model8trim=trimfill(model8, data=Final)
funnel(model8trim)

#pub bias for med Diet and Glucose
#Egger's
regtest(model10, model="lm", data=Final)

#Begg's
ranktest(model10, data=Final)

#funnel plot
model10trim=trimfill(model10, data=Final)
funnel(model10trim)

#pub bias for med Diet and SBP
#Egger's
regtest(model12, model="lm", data=Final)

#Begg's
ranktest(model12, data=Final)

#funnel plot
model12trim=trimfill(model12, data=Final)
funnel(model12trim)

#pub bias for med Diet and DBP
#Egger's
regtest(model14, model="lm", data=Final)

#Begg's
ranktest(model14, data=Final)

#funnel plot
model14trim=trimfill(model14, data=Final)
funnel(model14trim)

Syntax to create subsets

tmdwc<-subset(Final, Diet==1 & Out==1)
tmdhdl<-subset(Final, Diet==1 & Out==3)
tmdtg<-subset(Final, Diet==1 & Out==4)
tmdfbg<-subset(Final, Diet==1 & Out==5)
tmdsbp<-subset(Final, Diet==1 & Out==6)
tmddbp<-subset(Final, Diet==1 & Out==7)

Risk of Bias

#RanSeq-1
model53<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
  mods=~factor(RanSeq)-1, data=Quality, method="REML")
summary(model53)

model54<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
  mods=~factor(RanSeq)-1, data=Quality, method="REML")
summary(model54)

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
  mods=~factor(RanSeq)-1, data=Quality, method="REML")
summary(model55)

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
  mods=~factor(RanSeq)-1, data=Quality, method="REML")
summary(model56)

model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
  mods=~factor(RanSeq)-1, data=Quality, method="REML")
summary(model57)

model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
  mods=~factor(RanSeq)-1, data=Quality, method="REML")
summary(model58)

#RanSeq
model53<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
  mods=~factor(RanSeq), data=Quality, method="REML")
summary(model53)

model54<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
  mods=~factor(RanSeq), data=Quality, method="REML")
summary(model54)

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
  mods=~factor(RanSeq), data=Quality, method="REML")
summary(model55)

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
  mods=~factor(RanSeq), data=Quality, method="REML")
summary(model56)
model57 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==6),
               mods = ~factor(RanSeq), data = Quality, method = "REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==7),
               mods = ~factor(RanSeq), data = Quality, method = "REML")
summary(model58)

# AllCon-1
model53 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==1),
               mods = ~factor(AllCon)-1, data = Quality, method = "REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==3),
               mods = ~factor(AllCon)-1, data = Quality, method = "REML")
summary(model54)

model55 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==4),
               mods = ~factor(AllCon)-1, data = Quality, method = "REML")
summary(model55)

model56 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==5),
               mods = ~factor(AllCon)-1, data = Quality, method = "REML")
summary(model56)

model57 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==6),
               mods = ~factor(AllCon)-1, data = Quality, method = "REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==7),
               mods = ~factor(AllCon)-1, data = Quality, method = "REML")
summary(model58)

# AllCon
model53 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==1),
               mods = ~factor(AllCon), data = Quality, method = "REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset = (Diet==1 & Out==3),
               mods = ~factor(AllCon), data = Quality, method = "REML")
summary(model54)
model55 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
     mods=~factor(AllCon), data=Quality, method="REML")
summary(model55)

model56 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
     mods=~factor(AllCon), data=Quality, method="REML")
summary(model56)

model57 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
     mods=~factor(AllCon), data=Quality, method="REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
     mods=~factor(AllCon), data=Quality, method="REML")
summary(model58)

# Blinding

model53 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
     mods=~factor(Blinding)-1, data=Quality, method="REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
     mods=~factor(Blinding)-1, data=Quality, method="REML")
summary(model54)

model55 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
     mods=~factor(Blinding)-1, data=Quality, method="REML")
summary(model55)

model56 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
     mods=~factor(Blinding)-1, data=Quality, method="REML")
summary(model56)

model57 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
     mods=~factor(Blinding)-1, data=Quality, method="REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
     mods=~factor(Blinding)-1, data=Quality, method="REML")
summary(model58)

# Blinding-1
model53 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), 
mods=~factor(Blinding), data=Quality, method="REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), 
mods=~factor(Blinding), data=Quality, method="REML")
summary(model54)

model55 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), 
mods=~factor(Blinding), data=Quality, method="REML")
summary(model55)

model56 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), 
mods=~factor(Blinding), data=Quality, method="REML")
summary(model56)

model57 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), 
mods=~factor(Blinding), data=Quality, method="REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), 
mods=~factor(Blinding), data=Quality, method="REML")
summary(model58)

#Incomp-1
model53 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), 
mods=~factor(Incomp)-1, data=Quality, method="REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), 
mods=~factor(Incomp)-1, data=Quality, method="REML")
summary(model54)

model55 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), 
mods=~factor(Incomp)-1, data=Quality, method="REML")
summary(model55)

model56 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), 
mods=~factor(Incomp)-1, data=Quality, method="REML")
summary(model56)
model57 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
               mods =~ factor(Incomp) - 1, data = Quality, method = "REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
               mods =~ factor(Incomp) - 1, data = Quality, method = "REML")
summary(model58)

# Incomp

model53 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
               mods =~ factor(Incomp), data = Quality, method = "REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
               mods =~ factor(Incomp), data = Quality, method = "REML")
summary(model54)

model55 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
               mods =~ factor(Incomp), data = Quality, method = "REML")
summary(model55)

model56 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
               mods =~ factor(Incomp), data = Quality, method = "REML")
summary(model56)

model57 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
               mods =~ factor(Incomp), data = Quality, method = "REML")
summary(model57)

model58 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
               mods =~ factor(Incomp), data = Quality, method = "REML")
summary(model58)

# Select

model53 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
               mods =~ factor(Select), data = Quality, method = "REML")
summary(model53)

model54 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
               mods =~ factor(Select), data = Quality, method = "REML")
summary(model54)
model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(Select), data=Quality, method="REML")
summary(model55)

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(Select), data=Quality, method="REML")
summary(model56)

model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(Select), data=Quality, method="REML")
summary(model57)

model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(Select), data=Quality, method="REML")
summary(model58)

#Select-1

model53<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=~factor(Select)-1, data=Quality, method="REML")
summary(model53)

model54<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(Select)-1, data=Quality, method="REML")
summary(model54)

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(Select)-1, data=Quality, method="REML")
summary(model55)

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(Select)-1, data=Quality, method="REML")
summary(model56)

model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(Select)-1, data=Quality, method="REML")
summary(model57)

model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(Select)-1, data=Quality, method="REML")
summary(model58)

#OtherBias-1
model53<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=~factor(OtherBias)-1, data=Quality, method="REML"
) summary(model53)

model54<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(OtherBias)-1, data=Quality, method="REML"
) summary(model54)

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(OtherBias)-1, data=Quality, method="REML"
) summary(model55)

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(OtherBias)-1, data=Quality, method="REML"
) summary(model56)

model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(OtherBias)-1, data=Quality, method="REML"
) summary(model57)

model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(OtherBias)-1, data=Quality, method="REML"
) summary(model58)

#OtherBias
model53<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=~factor(OtherBias), data=Quality, method="REML"
) summary(model53)

model54<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(OtherBias), data=Quality, method="REML"
) summary(model54)

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(OtherBias), data=Quality, method="REML"
) summary(model55)

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(OtherBias), data=Quality, method="REML"
) summary(model56)
model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(OtherBias), data=Quality, method="REML")
summary(model57)
model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(OtherBias), data=Quality, method="REML")
summary(model58)

#to get the k for each variable
table(tmdwc$RanSeq)
table(tmdhdl$RanSeq)
table(tmdtg$RanSeq)
table(tmdfbg$RanSeq)
table(tmdsbp$RanSeq)
table(tmddbp$RanSeq)
table(tmdwc$AllCon)
table(tmdhdl$AllCon)
table(tmdtg$AllCon)
table(tmdfbg$AllCon)
table(tmdsbp$AllCon)
table(tmddbp$AllCon)
table(tmdwc$Blinding)
table(tmdhdl$Blinding)
table(tmdtg$Blinding)
table(tmdfbg$Blinding)
table(tmdsbp$Blinding)
table(tmddbp$Blinding)
table(tmdwc$Incomp)
table(tmdhdl$Incomp)
table(tmdtg$Incomp)
table(tmdfbg$Incomp)
Moderation with Weeks and Metaregression Plot

```r
model21 <- rma(d.ex, var_d.ex, subset = (Diet == 1 & Out == 1), mods = Weeks, data = Final, method = "REML", slab = paste(Reference, Year, sep = ","))

model21pred <- predict(model21, newmods = cbind(seq(0, 208, 0.1)))

wi = Final$w_d.ex.
min = min(wi, na.rm = TRUE)
max = max(wi, na.rm = TRUE)
size = 1.0 + 6.0 * (wi - min) / (max - min)
dietout1 = subset(Final, Diet == 1 & Out == 1)  # Here we have to create the subsample we are working on to just plot the observed values of that below

plot(dietout1$Weeks, dietout1$d.ex, pch = 20, col = "black", bg = "black", cex = size, xlab = "Number of Weeks", ylab = "Waist Circumference Effect Size (d)", xlim = c(0, 208), ylim = c(-3, 0.5))
lines(seq(0, 208, 0.1), model21pred$pred, col = "dark red")
```

# Plotting here the observed values of the subsample
# Plotting here the regression line and confidence interval of the predictive model
model21 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=Weeks, data=Final, method="REML", slab=paste(Reference, Year, sep =","))
model21pred <- predict(model21, newmods=cbind(seq(0,208,.1)))
model21

model61 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), mods=Weeks, data=Final, method="REML", slab=paste(Reference, Year, sep =","))
model61pred <- predict(model61, newmods=cbind(seq(0,208,.1)))
wi = Final$w_d.ex.
min = min(wi, na.rm=TRUE)
max = max(wi, na.rm=TRUE)
size = 1.0 + 6.0 * (wi - min)/(max - min)
dietout1 = subset(Final,Diet==1 & Out==3) #Here we have to create the subsample we are working on to just plot the observed values of that below
plot(dietout1$Weeks,dietout1$d.ex.,pch=20, col="black", bg="black", cex=size, xlab = "Number of Weeks", ylab = "HDL Effect Size (d)", xlim=c(0, 208), ylim=c(-1.5, 1.5))
lines(seq(0,208,.1), model61pred$pred, col = "dark red")
#Plotting here the regression line and confidence interval of the predictive model
lines(seq(0,208,.1), model61pred$ci.lb, lty = "dashed", col="dark red")
lines(seq(0,208,.1), model61pred$ci.ub, lty = "dashed", col="dark red")
model61

model81 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=Weeks, data=Final, method="REML", slab=paste(Reference, Year, sep =","))
model81pred <- predict(model81, newmods=cbind(seq(0,208,.1)))
wi = Final$w_d.ex.
min = min(wi, na.rm=TRUE)
max = max(wi, na.rm=TRUE)
size = 1.0 + 6.0 * (wi - min)/(max - min)
dietout1 = subset(Final, Diet==1 & Out==4)  # Here we have to create the
subsample we are working on to just plot the observed values of that below
plot(dietout1$Weeks, dietout1$d.ex., pch=20, col="black", bg="black", cex=size,
xlab = "Number of Weeks", ylab = "Triglycerides Effect Size (d)", xlim=c(0, 208), ylim=c(-3, 0.5))
lines(seq(0,208,.1), model81pred$pred, col= "dark red")
# Plotting here the regression line and confidence interval of the predictive model
lines(seq(0,208,.1), model81pred$ci.lb, lty="dashed", col="dark red")
lines(seq(0,208,.1), model81pred$ci.ub, lty="dashed", col="dark red")
model81

model101 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=Weeks,
data=Final, method="REML", slab=paste(Reference, Year, sep=","))
model101pred <- predict(model101, newmods=cbind(seq(0,208,.1)))
wi = Final$w_d.ex.
min = min(wi, na.rm=TRUE)
max = max(wi, na.rm=TRUE)
size = 1.0 + 6.0 * (wi - min)/(max - min)
dietout1 = subset(Final, Diet==1 & Out==5)  # Here we have to create the
subsample we are working on to just plot the observed values of that below
plot(dietout1$Weeks, dietout1$d.ex., pch=20, col="black", bg="black", cex=size,
xlab = "Number of Weeks", ylab = "Glucose Effect Size (d)", xlim=c(0, 208), ylim=c(-3, 0.5))
lines(seq(0,208,.1), model101pred$pred, col= "dark red")
# Plotting here the regression line and confidence interval of the predictive model
lines(seq(0,208,.1), model101pred$ci.lb, lty="dashed", col="dark red")
lines(seq(0,208,.1), model101pred$ci.ub, lty="dashed", col="dark red")
model101
model121 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6), mods = Weeks, 
data = Final, method = "REML", slab = paste(Reference, Year, sep = ","))
model121pred <- predict(model121, newmods = cbind(seq(0, 208, .1)))

wi = Final$w_d.ex.
min = min(wi, na.rm = TRUE)
max = max(wi, na.rm = TRUE)
size = 1.0 + 6.0 * (wi - min)/(max - min)
dietout1 = subset(Final, Diet == 1 & Out == 6)  # Here we have to create the 
subsmaple we are working on to just plot the observed values of that below
plot(dietout1$Weeks, dietout1$d.ex., pch = 20, col = "black", bg = "black", cex = size,
  xlab = "Number of Weeks", ylab = "Systolic Blood Pressure Effect Size (d)",
  xlim = c(0, 208), ylim = c(-3, 0.5))
lines(seq(0, 208, .1), model121pred$pred, col = "dark red")  
# Plotting here the regression line and confidence interval of the predictive model
lines(seq(0, 208, .1), model121pred$ci.lb, lty = "dashed", col = "dark red")
lines(seq(0, 208, .1), model121pred$ci.ub, lty = "dashed", col = "dark red")

model121

model141 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7), mods = Weeks, 
data = Final, method = "REML", slab = paste(Reference, Year, sep = ","))
model141pred <- predict(model141, newmods = cbind(seq(0, 208, .1)))

wi = Final$w_d.ex.
min = min(wi, na.rm = TRUE)
max = max(wi, na.rm = TRUE)
size = 1.0 + 6.0 * (wi - min)/(max - min)
dietout1 = subset(Final, Diet == 1 & Out == 7)  # Here we have to create the 
subsmaple we are working on to just plot the observed values of that below
plot(dietout1$Weeks, dietout1$d.ex., pch = 20, col = "black", bg = "black", cex = size,
  xlab = "Number of Weeks", ylab = "Systolic Blood Pressure Effect Size (d)",
  xlim = c(0, 208), ylim = c(-3, 0.5))
lines(seq(0, 208, .1), model141pred$pred, col = "dark red")  
# Plotting here the regression line and confidence interval of the predictive model
lines(seq(0, 208, .1), model141pred$ci.lb, lty = "dashed", col = "dark red")
lines(seq(0, 208, .1), model141pred$ci.ub, lty = "dashed", col = "dark red")

model141
ylab = "Diastolic Blood Pressure Effect Size (d)", xlim=c(0, 208), ylim=c(-3, 0.5))
lines(seq(0,208,.1), model141pred$pred, col = "dark red")
#Plotting here the regression line and confidence interval of the predictive model
lines(seq(0,208,.1), model141pred$ci.lb, lty = "dashed", col="dark red")
lines(seq(0,208,.1), model141pred$ci.ub, lty = "dashed", col="dark red")
model141

**Moderation for diseasein1_no**

model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1 ),
mods=(diseasein1_no), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=(diseasein1_no), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=(diseasein1_no), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=(diseasein1_no), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=(diseasein1_no), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=(diseasein1_no), data=Final, method="REML")
summary(model558)

**Moderation for Year**

model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=Year,
data=Final, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=Year,
data=Final, method="REML")
summary(model6653)
model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=Year, data=Final, method="REML")
summary(model6654)
model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=Year, data=Final, method="REML")
summary(model6655)
model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=Year, data=Final, method="REML")
summary(model6656)
model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=Year, data=Final, method="REML")
summary(model6657)

**Moderation for Score**
model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=score, data=Final, method="REML")
summary(model6651)
model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=score, data=Final, method="REML")
summary(model6653)
model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=score, data=Final, method="REML")
summary(model6654)
model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=score, data=Final, method="REML")
summary(model6655)
model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=score, data=Final, method="REML")
summary(model6656)
model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=score, data=Final, method="REML")
summary(model6657)
Moderation for No_FEMin1

model6651<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
mods=No_FEMin1, data=MetRisk, method="REML")

summary(model6651)

model6653<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
mods=No_FEMin1, data=MetRisk, method="REML")

summary(model6653)

model6654<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=No_FEMin1, data=MetRisk, method="REML")

summary(model6654)

model6655<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=No_FEMin1, data=MetRisk, method="REML")

summary(model6655)

model6656<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
mods=No_FEMin1, data=MetRisk, method="REML")

summary(model6656)

model6657<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
mods=No_FEMin1, data=MetRisk, method="REML")

summary(model6657)

Moderation for Prop_FEMin1

model6651<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
mods=Prop_FEMin1, data=MetRisk, method="REML")

summary(model6651)

model6653<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
mods=Prop_FEMin1, data=MetRisk, method="REML")

summary(model6653)

model6654<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=Prop_FEMin1, data=MetRisk, method="REML")

summary(model6654)

model6655<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=Prop_FEMin1, data=MetRisk, method="REML")

summary(model6655)
model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=Prop_FEMin1, data=MetRisk, method="REML")
summary(model6656)

model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=Prop_FEMin1, data=MetRisk, method="REML")
summary(model6657)

**Moderation for n_in1**

model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=n_in1,
data=Final, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=n_in1,
data=Final, method="REML")
summary(model6653)

model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=n_in1,
data=Final, method="REML")
summary(model6654)

model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=n_in1,
data=Final, method="REML")
summary(model6655)

model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=n_in1,
data=Final, method="REML")
summary(model6656)

model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=n_in1,
data=Final, method="REML")
summary(model6657)

**Moderation for n_total**

model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=n_total,
data=MetRisk, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=n_total,
data=MetRisk, method="REML")
summary(model6653)
model6654 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=n_total, data=MetRisk, method="REML")
summary(model6654)

model6655 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=n_total, data=MetRisk, method="REML")
summary(model6655)

model6656 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=n_total, data=MetRisk, method="REML")
summary(model6656)

model6657 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=n_total, data=MetRisk, method="REML")
summary(model6657)

**Moderation for agein1**

model6651 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=agein1, data=Final, method="REML")
summary(model6651)

model6653 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), mods=agein1, data=Final, method="REML")
summary(model6653)

model6654 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=agein1, data=Final, method="REML")
summary(model6654)

model6655 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=agein1, data=Final, method="REML")
summary(model6655)

model6656 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=agein1, data=Final, method="REML")
summary(model6656)

model6657 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=agein1, data=Final, method="REML")
summary(model6657)

**Moderation for disease_in1 prop**
model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=diseasein1_prop, data=Final, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=diseasein1_prop, data=Final, method="REML")
summary(model6653)

model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=diseasein1_prop, data=Final, method="REML")
summary(model6654)

model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=diseasein1_prop, data=Final, method="REML")
summary(model6655)

model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=diseasein1_prop, data=Final, method="REML")
summary(model6656)

model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=diseasein1_prop, data=Final, method="REML")
summary(model6657)

**Moderation for diseasein1_no**

model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=diseasein1_no, data=Final, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=diseasein1_no, data=Final, method="REML")
summary(model6653)

model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=diseasein1_no, data=Final, method="REML")
summary(model6654)

model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=diseasein1_no, data=Final, method="REML")
summary(model6655)
model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=diseasein1_no, data=Final, method="REML")
summary(model6656)

model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=diseasein1_no, data=Final, method="REML")
summary(model6657)

**Moderation for medin1_prop**

model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=medin1_prop, data=MetRisk, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=medin1_prop, data=MetRisk, method="REML")
summary(model6653)

model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=medin1_prop, data=MetRisk, method="REML")
summary(model6654)

model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=medin1_prop, data=MetRisk, method="REML")
summary(model6655)

model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=medin1_prop, data=MetRisk, method="REML")
summary(model6656)

model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=medin1_prop, data=MetRisk, method="REML")
summary(model6657)

**Moderation for medin1_no**

model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=medin1_no, data=MetRisk, method="REML")
summary(model6651)

model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=medin1_no, data=MetRisk, method="REML")
summary(model6653)
summary(model6653)
model6654 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=medin1_no, data=MetRisk, method="REML")
summary(model6654)
model6655 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=medin1_no, data=MetRisk, method="REML")
summary(model6655)
model6656 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=medin1_no, data=MetRisk, method="REML")
summary(model6656)
model6657 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=medin1_no, data=MetRisk, method="REML")
summary(model6657)

**Moderation for kcaltot_in1**

model6651 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=kcaltot_in1, data=MetRisk, method="REML")
summary(model6651)
model6653 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), mods=kcaltot_in1, data=MetRisk, method="REML")
summary(model6653)
model6654 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=kcaltot_in1, data=MetRisk, method="REML")
summary(model6654)
model6655 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=kcaltot_in1, data=MetRisk, method="REML")
summary(model6655)
model6656 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=kcaltot_in1, data=MetRisk, method="REML")
summary(model6656)
model6657 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=kcaltot_in1, data=MetRisk, method="REML")
summary(model6657)
**Prop CHO**

```r
model6651 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
                 mods=propcho_in1, data=Final, method="REML")
summary(model6651)
```

```r
model6653 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
                 mods=propcho_in1, data=Final, method="REML")
summary(model6653)
```

```r
model6654 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
                 mods=propcho_in1, data=Final, method="REML")
summary(model6654)
```

```r
model6655 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
                 mods=propcho_in1, data=Final, method="REML")
summary(model6655)
```

```r
model6656 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
                 mods=propcho_in1, data=Final, method="REML")
summary(model6656)
```

```r
model6657 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
                 mods=propcho_in1, data=Final, method="REML")
summary(model6657)
```

**Moderator for Region 1 and Region 4**

```r
model553 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1 &
                 (region==1 | region==4)), mods=~factor(region), data=Final, method="REML")
summary(model553)
```

```r
model554 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3 &
                 (region==1 | region==4)), mods=~factor(region), data=Final, method="REML")
summary(model554)
```

```r
model555 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4 &
                 (region==1 | region==4)), mods=~factor(region), data=Final, method="REML")
summary(model555)
```

```r
model556 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5 &
                 (region==1 | region==4)), mods=~factor(region), data=Final, method="REML")
summary(model556)
```
model557 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6 &
(region==1 | region==4)), mods=~factor(region), data=Final, method="REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7 &
(region==1 | region==4)), mods=~factor(region), data=Final, method="REML")
summary(model558)

**Moderation for disease_in1**

model553 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1 ),
mods=~factor(disease_in1), data=Final, method="REML")
summary(model553)

model554 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
mods=~factor(disease_in1), data=Final, method="REML")
summary(model554)

model555 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=~factor(disease_in1), data=Final, method="REML")
summary(model555)

model556 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=~factor(disease_in1), data=Final, method="REML")
summary(model556)

model557 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
mods=~factor(disease_in1), data=Final, method="REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
mods=~factor(disease_in1), data=Final, method="REML")
summary(model558)

**Moderation for Supple_in1**

model553 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1 ),
mods=~factor(Supple_in1), data=Final, method="REML")
summary(model553)

model554 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
mods=~factor(Supple_in1), data=Final, method="REML")
summary(model554)
model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(Supple_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(Supple_in1), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(Supple_in1), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(Supple_in1), data=Final, method="REML")
summary(model558)

**Moderation for alcohol_in1**

model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1 ),
mods=~factor(alcohol_in1), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(alcohol_in1), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(alcohol_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(alcohol_in1), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(alcohol_in1), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(alcohol_in1), data=Final, method="REML")
summary(model558)

**Moderation for oc_in1**
model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1 ),
mods=~factor(oc_in1), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(oc_in1), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(oc_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(oc_in1), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(oc_in1), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(oc_in1), data=Final, method="REML")
summary(model558)

Moderation for smoke_in1

model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1 ),
mods=~factor(smoke_in1), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(smoke_in1), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(smoke_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(smoke_in1), data=Final, method="REML")
summary(model556)
model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(smoke_in1), data=Final, method="REML")
summary(model557)
model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(smoke_in1), data=Final, method="REML")
summary(model558)

**Moderation for congpr**

model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=~factor(congrp), data=Final, method="REML")
summary(model553)
model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(congrp), data=Final, method="REML")
summary(model554)
model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(congrp), data=Final, method="REML")
summary(model555)
model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(congrp), data=Final, method="REML")
summary(model556)
model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(congrp), data=Final, method="REML")
summary(model557)
model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(congrp), data=Final, method="REML")
summary(model558)

**Moderation for provision_in1**

model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
mods=~factor(provision_in1), data=Final, method="REML")
summary(model553)
model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(provision_in1), data=Final, method="REML")
summary(model554)
model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(provision_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(provision_in1), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(provision_in1), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(provision_in1), data=Final, method="REML")
summary(model558)

**Moderation for macrodist_in1**

model553<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1 ),
mods=~factor(macrodist_in1), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
mods=~factor(macrodist_in1), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
mods=~factor(macrodist_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
mods=~factor(macrodist_in1), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
mods=~factor(macrodist_in1), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
mods=~factor(macrodist_in1), data=Final, method="REML")
summary(model558)

**Moderation for propcho_in1**
model553<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1 ),
  mods=~factor(propcho_in1), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(propcho_in1), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(propcho_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(propcho_in1), data=Final, method="REML")
summary(model556)

model557<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(propcho_in1), data=Final, method="REML")
summary(model557)

model558<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(propcho_in1), data=Final, method="REML")
summary(model558)

**Moderation for prop_satfatin1**

model553<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1 ),
  mods=~factor(propsatfat_in1), data=Final, method="REML")
summary(model553)

model554<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(propsatfat_in1), data=Final, method="REML")
summary(model554)

model555<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(propsatfat_in1), data=Final, method="REML")
summary(model555)

model556<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(propsatfat_in1), data=Final, method="REML")
summary(model556)
model557 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model558)

**Moderation for proptotfat_in1**
model553 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1 ),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model553)

model554 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model554)

model555 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model555)

model556 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model556)

model557 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
              mods = ~ factor(propsatfat_in1), data = Final, method = "REML")
summary(model558)

**Moderation for proppro_in 1**
model553 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1 ),
              mods = ~ factor(proppro_in1), data = Final, method = "REML")
summary(model553)

model554 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
              mods = ~ factor(proppro_in1), data = Final, method = "REML")
summary(model554)
model555 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=~factor(proppro_in1), data=Final, method="REML")
summary(model555)

model556 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=~factor(proppro_in1), data=Final, method="REML")
summary(model556)

model557 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
mods=~factor(proppro_in1), data=Final, method="REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
mods=~factor(proppro_in1), data=Final, method="REML")
summary(model558)

**Moderation for lang**

model993 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
mods=~factor(lang)-1, data=MetRisk, method="REML")
model993

model994 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
mods=~factor(lang)-1, data=MetRisk, method="REML")
model994

model995 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=~factor(lang)-1, data=MetRisk, method="REML")
model995

model996 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=~factor(lang)-1, data=MetRisk, method="REML")
model996

model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
mods=~factor(lang)-1, data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
mods=~factor(lang)-1, data=MetRisk, method="REML")
model998

**Moderation for pop**
model993<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=~factor(pop)-1, data=MetRisk, method="REML")
model993

model994<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=~factor(pop)-1, data=MetRisk, method="REML")
model994

model995<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=~factor(pop)-1, data=MetRisk, method="REML")
model995

model996<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=~factor(pop)-1, data=MetRisk, method="REML")
model996

model997<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=~factor(pop)-1, data=MetRisk, method="REML")
model997

model998<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=~factor(pop)-1, data=MetRisk, method="REML")
model998

**Moderation for diet_in1**

model993<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=~factor(diet_in1), data=MetRisk, method="REML")
model993

model994<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=~factor(diet_in1), data=MetRisk, method="REML")
model994

model995<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=~factor(diet_in1), data=MetRisk, method="REML")
model995

model996<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=~factor(diet_in1), data=MetRisk, method="REML")
model996

model997<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=~factor(diet_in1), data=MetRisk, method="REML")
model997

model998<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=~factor(diet_in1), data=MetRisk, method="REML")
model998
model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), 
mods=~factor(diet_in1), data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), 
mods=~factor(diet_in1), data=MetRisk, method="REML")
model998

**Moderation for Interlvl**

model553 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1 ), 
mods=~factor(interlvl), data=Final, method="REML")
summary(model553)

model554 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), 
mods=~factor(interlvl), data=Final, method="REML")
summary(model554)

model555 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), 
mods=~factor(interlvl), data=Final, method="REML")
summary(model555)

model556 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), 
mods=~factor(interlvl), data=Final, method="REML")
summary(model556)

model557 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), 
mods=~factor(interlvl), data=Final, method="REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), 
mods=~factor(interlvl), data=Final, method="REML")
summary(model558)

**Moderation for Region-1**

model53 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), 
mods=~factor(region)-1, 
data=Final, method="REML")
model53

model54 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), 
mods=~factor(region)-1, 
data=Final, method="REML")
model54

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=~factor(region)-1, data=Final, method="REML")
model55

model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=~factor(region)-1, data=Final, method="REML")
model56

model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=~factor(region)-1, data=Final, method="REML")
model57

model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=~factor(region)-1, data=Final, method="REML")
model58

**Tables for k of each Region**

table(tmdwc$region)
table(tmdhdl$region)
table(tmdtg$region)
table(tmdfbg$region)
table(tmdsbp$region)
table(tmddbp$region)

**Moderation for congrp-1**

model53<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=~factor(congrp)-1, data=Final, method="REML")
model53

model54<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=~factor(congrp)-1, data=Final, method="REML")
model54

model55<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=~factor(congrp)-1, data=Final, method="REML")
model55
model56<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
  mods=~factor(congrp)-1, data=Final, method="REML")
model56
model57<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),
  mods=~factor(congrp)-1, data=Final, method="REML")
model57
model58<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),
  mods=~factor(congrp)-1, data=Final, method="REML")
model58

Tables for k of each congrp

  table(tmdwc$congrp)
  table(tmdhdl$congrp)
  table(tmdtg$congrp)
  table(tmdfbg$congrp)
  table(tmddsbp$congrp)
  table(tmddbp$congrp)

Moderation for medin1-1

  model993<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1),
    mods=~factor(medin1)-1, data=MetRisk, method="REML")
  model993
  model994<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),
    mods=~factor(medin1)-1, data=MetRisk, method="REML")
  model994
  model995<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),
    mods=~factor(medin1)-1, data=MetRisk, method="REML")
  model995
  model996<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),
    mods=~factor(medin1)-1, data=MetRisk, method="REML")
  model996
model997<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(medin1)-1, data=MetRisk, method="REML")

model997

model998<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(medin1)-1, data=MetRisk, method="REML")

model998

**Moderation for experiment-1**

model993<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(experiment)-1, data=MetRisk, method="REML")

model993

model994<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(experiment)-1, data=MetRisk, method="REML")

model994

model995<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(experiment)-1, data=MetRisk, method="REML")

model995

model996<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(experiment)-1, data=MetRisk, method="REML")

model996

model997<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(experiment)-1, data=MetRisk, method="REML")

model997

model998<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(experiment)-1, data=MetRisk, method="REML")

model998

**Moderation for diet_monitor-1**

model993<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(diet_monitor)-1, data=MetRisk, method="REML")

model993

model994<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(diet_monitor)-1, data=MetRisk, method="REML")

model994
model995<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=~factor(diet_monitor)-1, data=MetRisk, method="REML")
model995

model996<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=~factor(diet_monitor)-1, data=MetRisk, method="REML")
model996

model997<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
mods=~factor(diet_monitor)-1, data=MetRisk, method="REML")
model997

model998<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
mods=~factor(diet_monitor)-1, data=MetRisk, method="REML")
model998

**Moderation for behave-1**

model993<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
mods=~factor(behave)-1, data=MetRisk, method="REML")
model993

model994<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
mods=~factor(behave)-1, data=MetRisk, method="REML")
model994

model995<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
mods=~factor(behave)-1, data=MetRisk, method="REML")
model995

model996<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
mods=~factor(behave)-1, data=MetRisk, method="REML")
model996

model997<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
mods=~factor(behave)-1, data=MetRisk, method="REML")
model997

model998<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
mods=~factor(behave)-1, data=MetRisk, method="REML")
model998

**Moderation for compliance_in1-1**
model993<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(compliance_in1)-1, data=MetRisk, method="REML")
model993
model994<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(compliance_in1)-1, data=MetRisk, method="REML")
model994
model995<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(compliance_in1)-1, data=MetRisk, method="REML")
model995
model996<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(compliance_in1)-1, data=MetRisk, method="REML")
model996
model997<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(compliance_in1)-1, data=MetRisk, method="REML")
model997
model998<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(compliance_in1)-1, data=MetRisk, method="REML")
model998

**Moderation for measure_ad_in1-1**

model993<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(measure_ad_in1)-1, data=MetRisk, method="REML")
model993
model994<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(measure_ad_in1)-1, data=MetRisk, method="REML")
model994
model995<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(measure_ad_in1)-1, data=MetRisk, method="REML")
model995
model996<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(measure_ad_in1)-1, data=MetRisk, method="REML")
model996
model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=~factor(measure_ad_in1)-1, data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=~factor(measure_ad_in1)-1, data=MetRisk, method="REML")
model998

**Moderation for scale_in1-1**

model993 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=~factor(scale_in1)-1, data=MetRisk, method="REML")
model993

model994 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), mods=~factor(scale_in1)-1, data=MetRisk, method="REML")
model994

model995 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=~factor(scale_in1)-1, data=MetRisk, method="REML")
model995

model996 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=~factor(scale_in1)-1, data=MetRisk, method="REML")
model996

model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=~factor(scale_in1)-1, data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=~factor(scale_in1)-1, data=MetRisk, method="REML")
model998

**Moderation for counsel_in1-1**

model993 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=~factor(counsel_in1)-1, data=MetRisk, method="REML")
model993

model994 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), mods=~factor(counsel_in1)-1, data=MetRisk, method="REML")
model994
model995 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(counsel_in1)-1, data=MetRisk, method="REML")
model995

model996 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(counsel_in1)-1, data=MetRisk, method="REML")
model996

model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(counsel_in1)-1, data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(counsel_in1)-1, data=MetRisk, method="REML")
model998

**Moderation for QoL_in1-1**

model993 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(QoL_in1)-1, data=MetRisk, method="REML")
model993

model994 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(QoL_in1)-1, data=MetRisk, method="REML")
model994

model995 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(QoL_in1)-1, data=MetRisk, method="REML")
model995

model996 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(QoL_in1)-1, data=MetRisk, method="REML")
model996

model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(QoL_in1)-1, data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(QoL_in1)-1, data=MetRisk, method="REML")
model998

**Moderation for cho_in1-1**
model993 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
mods = ~factor(cho_in1) - 1, data = MetRisk, method = "REML")
model993

model994 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
mods = ~factor(cho_in1) - 1, data = MetRisk, method = "REML")
model994

model995 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
mods = ~factor(cho_in1) - 1, data = MetRisk, method = "REML")
model995

model996 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
mods = ~factor(cho_in1) - 1, data = MetRisk, method = "REML")
model996

model997 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
mods = ~factor(cho_in1) - 1, data = MetRisk, method = "REML")
model997

model998 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
mods = ~factor(cho_in1) - 1, data = MetRisk, method = "REML")
model998

**Moderation for satfat_in1-1**

model993 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
mods = ~factor(satfat_in1) - 1, data = MetRisk, method = "REML")
model993

model994 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
mods = ~factor(satfat_in1) - 1, data = MetRisk, method = "REML")
model994

model995 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
mods = ~factor(satfat_in1) - 1, data = MetRisk, method = "REML")
model995

model996 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
mods = ~factor(satfat_in1) - 1, data = MetRisk, method = "REML")
model996
model997 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
    mods = ~factor(satfat_in1) - 1, data = MetRisk, method = "REML")

model997

model998 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
    mods = ~factor(satfat_in1) - 1, data = MetRisk, method = "REML")

model998

**Moderation for totfat_in1-1**

model993 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
    mods = ~factor(totfat_in1) - 1, data = MetRisk, method = "REML")

model993

model994 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
    mods = ~factor(totfat_in1) - 1, data = MetRisk, method = "REML")

model994

model995 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
    mods = ~factor(totfat_in1) - 1, data = MetRisk, method = "REML")

model995

model996 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
    mods = ~factor(totfat_in1) - 1, data = MetRisk, method = "REML")

model996

model997 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
    mods = ~factor(totfat_in1) - 1, data = MetRisk, method = "REML")

model997

model998 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
    mods = ~factor(totfat_in1) - 1, data = MetRisk, method = "REML")

model998

**Moderation for pro_in1-1**

model993 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
    mods = ~factor(pro_in1) - 1, data = MetRisk, method = "REML")

model993

model994 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
    mods = ~factor(pro_in1) - 1, data = MetRisk, method = "REML")

model994
model995 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
mods = ~factor(pro_in1)-1, data = MetRisk, method = "REML")
model995

model996 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
mods = ~factor(pro_in1)-1, data = MetRisk, method = "REML")
model996

model997 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
mods = ~factor(pro_in1)-1, data = MetRisk, method = "REML")
model997

model998 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
mods = ~factor(pro_in1)-1, data = MetRisk, method = "REML")
model998

**Moderation for CVD-1**

model553 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1),
mods = ~factor(CVD)-1, data = MetRisk, method = "REML")
summary(model553)

model554 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3),
mods = ~factor(CVD)-1, data = MetRisk, method = "REML")
summary(model554)

model555 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4),
mods = ~factor(CVD)-1, data = MetRisk, method = "REML")
summary(model555)

model556 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 5),
mods = ~factor(CVD)-1, data = MetRisk, method = "REML")
summary(model556)

model557 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6),
mods = ~factor(CVD)-1, data = MetRisk, method = "REML")
summary(model557)

model558 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7),
mods = ~factor(CVD)-1, data = MetRisk, method = "REML")
summary(model558)

**Moderation for DM-1**
model553<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=~factor(DM)-1, data=MetRisk, method="REML")

summary(model553)

code

code

code

model558<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=~factor(DM)-1, data=MetRisk, method="REML")

summary(model558)

**Moderation for MetS-1**

model553<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=~factor(MetS)-1, data=MetRisk, method="REML")

summary(model553)

code

code

code

model558<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=~factor(MetS)-1, data=MetRisk, method="REML")

summary(model558)
model557<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), 
  mods=~factor(MetS)-1, data=MetRisk, method="REML")
summary(model557)
model558<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(MetS)-1, data=MetRisk, method="REML")
summary(model558)

**Moderation for overwtobes-1**
model553<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(overwtobes)-1, data=MetRisk, method="REML")
summary(model553)
model554<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(overwtobes)-1, data=MetRisk, method="REML")
summary(model554)
model555<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4),
  mods=~factor(overwtobes)-1, data=MetRisk, method="REML")
summary(model555)
model556<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5),
  mods=~factor(overwtobes)-1, data=MetRisk, method="REML")
summary(model556)
model557<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6),
  mods=~factor(overwtobes)-1, data=MetRisk, method="REML")
summary(model557)
model558<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7),
  mods=~factor(overwtobes)-1, data=MetRisk, method="REML")
summary(model558)

**Moderation for interlvl-1**
model993<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1),
  mods=~factor(interlvl)-1, data=MetRisk, method="REML")
model993
model994<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3),
  mods=~factor(interlvl)-1, data=MetRisk, method="REML")
model994
model995 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), 
mods=~factor(interlvl)-1, data=MetRisk, method="REML")
model995

model996 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), 
mods=~factor(interlvl)-1, data=MetRisk, method="REML")
model996

model997 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), 
mods=~factor(interlvl)-1, data=MetRisk, method="REML")
model997

model998 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), 
mods=~factor(interlvl)-1, data=MetRisk, method="REML")
model998

Region-1

model53 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), 
mods=~factor(region)-1, data=Final, method="REML")
model53

model54 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), 
mods=~factor(region)-1, data=Final, method="REML")
model54

model55 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), 
mods=~factor(region)-1, data=Final, method="REML")
model55

model56 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), 
mods=~factor(region)-1, data=Final, method="REML")
model56

model57 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), 
mods=~factor(region)-1, data=Final, method="REML")
model57

model58 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), 
mods=~factor(region)-1, data=Final, method="REML")
model58

Tables for k of each region
Moving the constant For Min Weeks and Max Weeks

maxweeks=208-Final$Weeks
maxweeks
minweeks=Final$Weeks-4
minweeks
model23<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=maxweeks, data=Final, method="REML", slab= paste(Reference, Year, sep =","))
model23
model25<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=minweeks, data=Final, method="REML", slab= paste(Reference, Year, sep =","))
model25
model63<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==3), mods=maxweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model63
model65<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==3), mods=minweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model65
model83<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==4), mods=maxweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model83
model85<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==4), mods=minweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model85
model103<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==5), mods=maxweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model103
model105<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==5), mods=minweeks, data=Final, method="REML",slab= paste(Reference, Year, sep=""))
model105
model123<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==6), mods=maxweeks, data=Final, method="REML",slab= paste(Reference, Year, sep=""))
model123
model125<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==6), mods=minweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model125
model143<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==7), mods=maxweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model143
model145<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==7), mods=minweeks, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model145

**Max and Min Total Sample Size**

maxtot=1154-Final$n_tot
maxtot
mintot=Final$n_tot-12
mintot
model107<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==1), mods=mintot, data=Final, method=
model107 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==1), mods=maxtot, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model87 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==3), mods=mintot, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model107 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=mintot, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model106 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=mintot, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model126 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=maxtot, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model127 <- rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=maxtot, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model146 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7), mods = mintot, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

model147 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7), mods = maxtot, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

Min and Max in Intervention 1

maxsamp = 1154 - Final$n_in1

minsamp = Final$n_in1 - 11

model27 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1), mods = minsamp, data = Final, method = "REML", slab = paste(Reference, Year, sep = ","))

model26 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 1), mods = maxsamp, data = Final, method = "REML", slab = paste(Reference, Year, sep = ","))

model66 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3), mods = minsamp, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

model67 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 3), mods = maxsamp, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

model86 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 4), mods = minsamp, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))
model86
model87<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==4), mods=mxsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model87
model106<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=minsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model106
model107<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==5), mods=maxsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model107
model126<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=minsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model126
model127<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==6), mods=maxsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model127
model146<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=minsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model146
model147<-rma(d.ex., var_d.ex., subset=(Diet==1 & Out==7), mods=maxsamp, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model147

Min and Max Age for Intervention

maxage=65-Final$agein1

maxage

minage=Final$agein1-8.8

minage
model27<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=minage, data=Final, method="REML", slab= paste(Reference, Year, sep =","))
model27
model26<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=maxage, data=Final, method="REML", slab= paste(Reference, Year, sep =","))
model26
model66<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==3), mods=minage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model66
model67<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==3), mods=maxage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model67
model86<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==4), mods=minage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model86
model87<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==4), mods=maxage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model87
model106<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==5), mods=minage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model106
model107<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==5), mods=maxage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model107
model126<-rma(d.ex.,var_d.ex.,subset=(Diet==1&Out==6), mods=minage, data=Final, method="REML", slab= paste(Reference, Year, sep=""))
model126
model127 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 6), mods = maxage, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

model127

model146 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7), mods = minage, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

model146

model147 <- rma(d.ex., var_d.ex., subset = (Diet == 1 & Out == 7), mods = maxage, data = Final, method = "REML", slab = paste(Reference, Year, sep = ""))

model147