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

Marissa L. Garcia

University of Connecticut - Storrs, marissa.garcia@uconn.edu

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

Marissa Lee Garcia

BS, RD, University of Connecticut, 2013

A Thesis

Submitted in Partial Fulfillment of the

Requirements for the Degree of

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University of Connecticut

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APPROVAL PAGE

Masters of Science Thesis

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

Presented by
Marissa Lee Garcia, BS, RD

Major Advisor _____
Tania B. Huedo-Medina, PhD

Associate
Advisor _____
Jessica D. Bihuniak, PhD, RD

Associate
Advisor _____
Jane Kerstetter, PhD, RD

Associate
Advisor _____
Anne Kenny, MD

University of Connecticut
2015

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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)¹. These metabolic risk factors are also associated with the development of type 2 diabetes mellitus¹. Underlying risk factors for metabolic syndrome include abdominal obesity, insulin resistance, physical inactivity, aging, hormonal imbalance, and genetic or ethnic predisposition¹. Currently, lifestyle therapies such as diet modification and physical activity are first-line interventions to treat the metabolic risk factors¹. The traditional Mediterranean-style diet (MedSD) is well-known for its cardio-protective benefits² and should be considered for prevention and treatment of metabolic syndrome.

The National Cholesterol Education Program's Adult Treatment Panel III report (NCEP ATP III)³ 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 state³. 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 ≥ 150 mg/dL, 3) HDL cholesterol <40 mg/dL for men and <50 mg/dL for women, 4) blood pressure $\geq 130/\geq 85$ mmHg, and 5) fasting glucose ≥ 110 mg/dL³. 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 cerebrovascular diseases, reduction in the incidence of neoplastic diseases, and reduction of the incidence of neurodegenerative diseases². In addition, a secondary analysis of the PREDIMED⁶ 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 CVD⁷. 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 date⁸. 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 adults⁸⁸. Further, the Scientific Report of the 2015 Dietary Guidelines Advisory Council⁹ 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 drinks⁹, 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.⁸ noted above and the 2015 Dietary Guidelines Advisory Council⁹ 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 factors¹⁰. 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 review¹⁰ 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 Reviews¹¹). On average, reviews achieved a low quality score ($Mean = 7.9 \pm 5.10$) relative to the

maximum AMSTAR_{MD} score of 20¹⁰. 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 quality¹⁰. 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 Statement¹² 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 mass”, “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.⁸ 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 studies¹³. 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-analyses¹⁴. 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 9.4¹⁵. All code for this analysis can be found in **Appendix 4**. Inter-rater reliability was calculated for all continuous and categorical variables using IBM SPSS Statistics Version 22¹⁶. The Kappa (κ) coefficient was used to calculate categorical agreement¹⁷ ($\kappa=0.94$, 96.9% agreement) and Pearson's correlation coefficient was used to calculate continuous agreement¹⁸ ($r=1$). We tested for asymmetries by using the Begg¹⁹, Egger²⁰, and trim-and-fill²¹ statistical tests as well as the funnel plot²² graphical technique. Publication bias and the remaining statistical tests were calculated using R version 3.1.2²³ "metafor" package²⁴. All code for this analysis can be found in **Appendix 5**.

Effect sizes (ESs) were calculated for each outcome by calculating the standardized mean change²⁵ 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 deviation²⁵. 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^{25,26} (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 interest¹⁷. 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.²⁷. This calculator uses a factor that controls for small sample size²⁸.

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^{29,30}. Only two

studies had subsamples based on gender^{31,32}, three studies had multiple subsamples for participant characteristics^{33,34,35}, and one study had subsamples based on different distributions of macronutrients throughout the day³⁶.

Weighted mean effect size by the inverse of the variance of each study was calculated across all studies under random- and fixed-effects assumptions³⁷. The random effects model assumes that the data is coming from different populations and accounts for within and between-study variance³⁷. The fixed effects model assumes that all effect sizes are from the same population and accounts for only within study variance³⁷. To test for heterogeneity, Cochran's Q and I^2 were calculated. Q tests for significance of heterogeneity³⁸ whereas I^2 calculates the magnitude of heterogeneity with a range from 0%-100%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 technique⁴⁰ was used to produce estimates of the ES ($d+$) at meaningful levels of the moderators and their CI s 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 version⁴¹.

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 ($d^r=0.17$, 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; $d_{TG}=-0.71$, 95%CI: -1.08, -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; $d_{TG}=-0.13$,

95%CI:-0.75, 0.48; $d_{FBG}=-0.18$, 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 ($R_{WC}^2=25.19\%$, $p=0.002$; $R_{HDL}^2=49.12\%$, $p<0.0001$; $R_{TG}^2=33.71\%$, $p=0.0008$; $R_{FBG}^2=32.81\%$, $p=0.0015$; $R_{SBP}^2=29.09\%$, $p<0.001$ 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 ($d_{WC}=-1.14$, 95%CI:-1.51, -0.77; $d_{HDL}=0.79$, 95%CI:0.46, 1.13; $d_{TG}=-0.99$, 95%CI:-1.37, -0.06; $d_{FBG}=-1.13$, 95%CI:-1.58, -0.67; $d_{SBP}=-1.36$, 95%CI:-1.84, -0.88; $d_{DBP}=-1.32$, 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 ($d_{WC}=-0.34$, 95%CI:-0.58, -0.09; $d_{SBP}=-0.51$, 95%CI:-0.79, -0.23; $d_{DBP}=-0.77$, 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 ($R_{WC}^2=45.1\%$, $p<0.0001$; $R_{HDL}^2=37.03\%$, $p=0.0015$; $R_{TG}^2=23.74\%$, $p=0.014$; $R_{FBG}^2=39.48\%$, $p=0.0005$ 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 ($R_{DBP}^2 = 67.72\%$, $p < 0.0001$, ; $R_{DBP}^2 = 72.57\%$, $p < 0.0001$; $R_{DBP}^2 = 71.86\%$, $p < 0.0001$ 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^{8,42}, duration of study⁸, study design⁴², and study quality^{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 PRISMA¹² 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-analyses¹⁰. 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 higher¹⁰.

We found that reviews published in higher IPP journals scored significantly higher in total methodological quality¹⁰. 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_{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 index¹⁰. 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.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 levels⁸. 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.⁸ 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-IR⁸. Significant associations were found for all of the above outcomes as well as waist circumference for interventions with more than or equal to 66 participants⁸. 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 glucose⁸. Lastly, studies of high quality were significantly associated with greater effects on HDL cholesterol, triglycerides, systolic blood pressure, diastolic blood pressure, and HOMA-IR⁸. 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.⁸ 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 analysis⁸. 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.⁸ 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 MedSD⁹. 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 lipids⁹. 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 drinks⁹. 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 al⁴⁴. 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 interventions⁴⁵. 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.

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

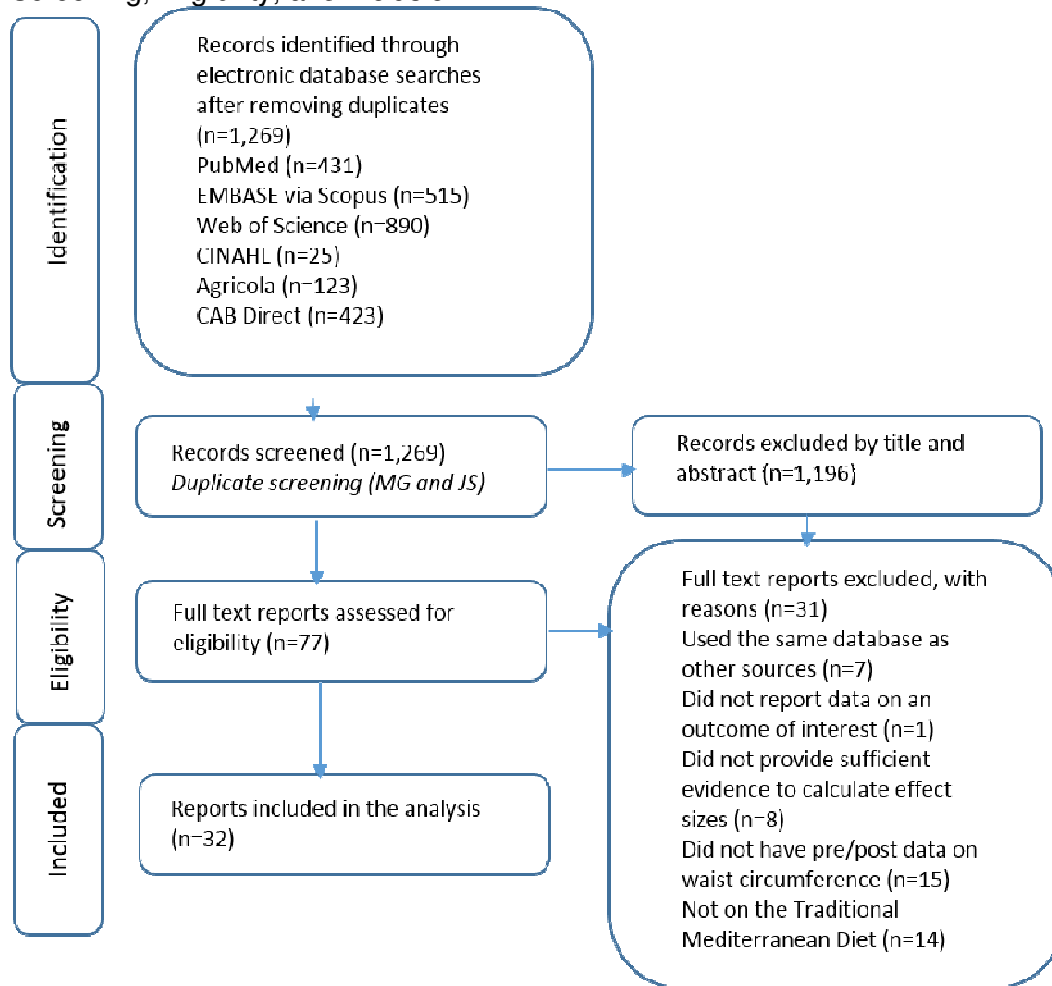


Table 1. Description of Included Studies

Study	Country	N	% F	Age	Diseases	Recruitment	Dietary Assessment	Type of Diet	Duration (weeks)	Control	Outcome
Aizawa, et al. (2009) ⁴⁶	Canada	63	51%	53.9	PDM PHTN	Physician referral	Group, unsupervised	MD	24	No carotid artery stiffness	Carotid artery stiffness
Bedard, et al. (2012) ⁴⁷	Canada	67	NR	39	Ob (57%)	NR	Individual, supervised	MD	8	Non-Ob	CVDRF
Bekkouche, et al. (2014) ⁴⁸	Algeria	86	NR	52	MS (67%)	Hospital	Individual, unsupervised	MD	12	No MS, healthy	IR, OS, Inflamm.
Bos, et al. (2010) ⁴⁹	Netherlands	60	NR	52.5	Ob (100%)	NR	Individual, unsupervised	MD	10	High SFA diet; High MUFA diet	Serum lipids, IS
Calatayud, et al. (2011) ⁵⁰	Spain	98	56%	8.6	Ob (52%)	NR	NR	MD	52	None	WT loss
Connolly, et al. (2011) ⁵¹	Great Britain	206	42%	60.4	CVD or CVDRF (100%)	Hospital, physician referral	Individual, unsupervised	MD	16	None	CVDRF
Corbalan, et al. (2009) ⁵²	Spain	1406	82%	39	Ob (100%)	Clinic referral	Individual, unsupervised	HMD	34	None	WT
Esposito, et al. (2006) ⁵³	Italy	65	0%	43.9	MS, ED (100%)	Research database	Individual, unsupervised	MD	24	Regular diet	IIEF score

Esposito, et al. (2007) ⁵⁴	Italy	59	100%	41.9	MS, FSD (100%)	Research Database	Individual, unsupervised	MD	24	Regular Diet	FSFI score
Esposito, et al. (2004) ⁵⁵	Italy	180	45%	43.9	MS (100%)	Clinic	Group, unsupervised	MD	104	Regular Diet	Endo func, Vas Infl
Esposito, et al. (2009) ⁵⁶	Italy	215	51%	52.2	NIDDM (100%)	Clinic	Group, unsupervised	HMD	208	LF Diet	Glycemic control
Goulet, et al. (2003) ⁵⁷	Canada	77	100%	47	None, healthy	Newspaper ad.	Individual, unsupervised	MD	12	None	Serum lipid, WT
Goulet, et al. (2007) ⁵⁸	Canada	77	100%	46.7	None, healthy	Newspaper ad.	Individual, unsupervised	MD	24	None	WT
Jones, et al. (2011) ⁵⁹	United States	89	100%	47.5	MS (100%)	NR	Individual, unsupervised	LGMD-MF	12	LGMD, no MF	MS RF
Kolomvotsou, et al. (2013) ⁶⁰	Greece	90	48%	50.4	Ob (100%)	Hospital	Individual, unsupervised	Greek MD	8	Regular diet	AO intake, plasma AO capacity
Landaeta-Diaz, et al. (2013) ⁶¹	Spain	45	67%	58	Ob, MS (100%)	Hospital	Individual, unsupervised	HMD with exercise	12	HMD without exercise	HRQoL
Leighton, et al. (2009) ⁶²	Chile	145	0%	39	MS (24%)	Maestranza Diesel	Group, supervised	MD	52	None	MS RF
Lerman, et al. (2010) ⁶³	United States	24	83%	54.4	MS and high LDL-C (100%)	Previous study by Lerman	NR	LGMD-MF	12	LGMD, no MF	Plasma lipids

Lindeberg, et al. (2007) ⁶⁴	Sweden	29	0%	61	IHD, IGT, NIDDM	Hospital	Individual, unsupervised	MD	12	Paleolithic Diet	WT, serum glucose
Llaneza, et al. (2010) ⁶⁵	Spain	116	100%	56.4	IR (100%)	Hospital	Group, unsupervised	MD, soy supplement	104	MD, no supp	IR
Lombardo, et al. (2014) ⁶⁶	Italy	42	100%	46.3	Ob (100%)	Hospital	Individual, unsupervised	HMD	12	HMD	WT
Papandreou, et al. (2012) ⁶⁷	Greece	40	NR	41.5	Ob, OSAS (100%)	University Medical School	Group, unsupervised	HMD	26	Prudent Diet	OSAS
Papandreou, et al. (2012) ⁶⁸	Greece	21	NR	41.5	Ob, OSAS (100%)	University Medical School	Group, unsupervised	HMD	26	Prudent Diet	TBARS
Rallidis, et al. (2009) ⁶⁹	Greece	82	48%	50.4	Ob (100%)	Hospital	Individual, unsupervised	Greek MD	8	Regular Diet	Endo func
Richard, et al. (2011) ⁷⁰	Canada	26	0%	49.4	MS (100%)	NR	Individual, unsupervised	MD	35	Western Diet	CVDRF
Rubenfire, et al. (2011) ⁷¹	United States	126	68%	51	MS (100%)	Physician referral	Individual, unsupervised	MD	12	None	WT, BP, TG, serum glucose
Ryan, et al. (2013) ⁷²	Australia	12	50%	55	NAFLD (100%)	Hospital	Individual, unsupervised	MD	6	LF diet	WT, IS
Sanchez-Benito, et al.	Spain	158	87%	48	OverWT (100%)	Pharmacy office	Individual, unsupervised	MD	26	None	BMI, BP, cholesterol

(2012)⁷³

Stendall-Hollis, et al. (2013) ⁷⁴	United States	129	100%	29.7	OverWT (100%)	Magazine, hospital, Craigslist	Individual, unsupervised	MD	16	MyPyramid for P&B	WT, Inflamm Bio
Timar, et al. (2013) ⁷⁵	Romania	223	50%	55	NIDDM (100%)	Diabetes Center	Group, unsupervised	HMD	52	Diabetic Diet	Glycemic control, CVDRF
Van Velden, et al. (2007) ⁷⁶	South Africa	12	25%	46	MS (100%)	NR	Group, unsupervised	MD with red wine	8	MD without red wine	CVDRF
Wardle, et al. (2000) ⁷⁷	England	176	78%	53	Hypercholesterolemia (100%)	Hospital	Group, unsupervised	MD	12	LF Diet, Regular Diet	Serum cholesterol

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; Inflamm, 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; Inflamm 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 2. Publication Bias

Outcome	s	Publication Bias	
		Egger'	Begg's
WC	5	p=0.64	p=0.001
HDL	5	p=0.96	p=0.56
TG	2	p=0.21	p=0.125
FBG	9	p=0.79	p=0.016
SBP		p=0.34	p=0.027
DBP	3	p=0.60	p=0.032

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

Outcome	k	d+ (95% CI)		Homogeneity of d's		
		Fixed-Effects	Random-Effects	Q	I ² (%)	p-value
		-0.41	-0.54			
WC	45	(-0.45 to -0.38)*	(-0.75 to -0.33)*	425.29	96.37	<0.0001
		0.15	0.15			
HDL	40	(0.09 to 0.19)*	(-0.02 to 0.32)	304.48	91.1	<0.0001
		-0.27	-0.34			
TG	38	(-0.31 to -0.22)*	(-0.51 to -0.16)*	251.41	91.49	<0.0001
		-0.36	-0.42			
FBG	33	(-0.41 to -0.32)*	(-0.64 to -0.19)*	292.85	94.67	<0.0001
		-0.61	-0.62			
SBP	30	(-0.65 to -0.57)*	(-0.89 to -0.35)*	600.44	97.07	<0.0001
		-0.68	-0.78			
DBP	30	(-0.73 to -0.63)*	(-1.22 to -0.34)*	2633.41	98.51	<0.0001

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

Significant Moderator Analysis Results							
Variable	Outcome	Category	k	d+ (95% CI)	R ²	p-value	Clinical Unit of Measure
Study Characteristics							
Region	WC	Europe	23	-0.82 (-1.12 to -0.51)	2.90%	0.23	-8.32 cm
		US	7	-0.33 (-0.59 to 0.39)	2.90%	0.23	-3.41 cm
	HDL	Europe	13	0.551 (0.21 to 0.89)	16.69%	0.08	1.65 mmol/L
		US	6	-0.01 (-0.59 to 0.39)	16.69%	0.08	-0.31 mmol/L
	TG	Europe	12	-0.71 (-1.08 to -0.35)	4.42%	0.28	-24.89 mmol/L
		US	4	-0.13 (-0.75 to 0.48)	4.42%	0.28	-4.69 mmol/L
	FBG	Europe	12	-0.75 (-1.15 to -0.35)	3.50%	0.33	-0.23 mmol/L
		US	3	-0.181 (-0.96 to 0.60)	3.50%	0.33	-0.06 mmol/L
	SBP	Europe	13	-0.97 (-1.54 to 0.53)	0.00%	0.68	-3.17 mmol/L
		US	4	-0.47 (-1.38 to 0.43)	0.00%	0.68	-1.54 mmol/L
	DBP	Europe	13	-1.27 (-2.56 to 0.90)	0.00%	0.79	-2.97 mmol/L
		US	4	-0.44 (-1.95 to 1.07)	0.00%	0.79	-1.03 mmol/L

Study Design	WC	MedSD vs. Other		-1.14				
		Diet	13	(-1.51 to -0.77)	25.19%	0.001	-11.63 cm	
	HDL	Pre/Post or		-0.34				
		Crossover	27	(-0.58 to -0.09)	25.19%	0.001	-3.47 cm	
	HDL	MedSD vs. Other		0.79				
		Diet	9	(0.46 to 1.13)	49.12%	<0.0001	2.37 mmol/L	
	TG	Pre/Post or		-0.12				
		Crossover	19	(-0.35 to 0.102)	49.12%	<0.0001	-0.36 mmol/L	
	FBG	MedSD vs. Other		-0.99				
		Diet	8	(-1.37 to -0.60)	33.71%	0.0008	-34.65 mmol/L	
	SBP	Pre/Post or		-0.20				
		Crossover	18	(-0.45 to 0.05)	33.71%	0.0008	-7.11 mmol/L	
DBP	MedSD vs. Other		-1.13					
	Diet	7	(-1.58 to -0.67)	32.81%	0.002	-0.41 mmol/L		
DBP	Pre/Post or		-0.26					
	Crossover	17	(-0.55 to 0.03)	32.81%	0.002	-0.08 mmol/L		
DBP	MedSD vs. Other		-1.36					
	Diet	7	(-1.84 to -0.88)	29.09%	0.003	-4.45 mmHg		
DBP	Pre/Post or		-0.51					
	Crossover	19	(-0.79 to -0.23)	29.09%	0.003	-1.67 mmHg		
DBP	MedSD vs. Other		-1.32					
	Diet	7	(-2.27 to -0.36)	0.00%	0.34	-3.09 mmHg		
DBP	Pre/Post or		-0.77					
	Crossover	19	(-1.34 to -0.19)	0.00%	0.34	-1.8 mmHg		
Impact per Publication Metric	WC	0 (minimum)	39	(-0.42 to 0.06)	45.10%	<0.0001	-1.84 cm	
		16.104 (maximum)	39	(-2.49 to -1.36)	45.10%	<0.0001	-19.58 cm	
	HDL	0 (minimum)	27	(-0.35 to 0.18)	37.03%	0.002	-0.24mmol/L	
		16.104 (maximum)	27	0.96	37.03%	0.002	-2.88 mmol/L	

				(0.44 to 1.49)			
				-0.19			
TG	0 (minimum)	25		(-0.49 to 0.11)	23.74%	0.013	-6.65 mmol/L
				-1.09			
	16.104 (maximum)	25		(-1.66 to -0.53)	23.74%	0.013	-38.15 mmol/L
				-0.14			
FBG	0 (minimum)	23		(-0.46 to 0.18)	39.48%	0.0005	-0.04 mmol/L
				-1.44			
	16.104 (maximum)	23		(-2.00 to -0.87)	39.48%	0.0005	-0.44 mmol/L
				-0.55			
SBP	0 (minimum)	25		(-0.88 to -0.21)	11.11%	0.16	-1.79 mmHg
				-1.13			
	16.104 (maximum)	25		(-1.77 to -0.48)	11.11%	0.16	-3.69 mmHg
				-0.63			
DBP	0 (minimum)	25		(-1.27 to 0.01)	3.89%	0.16	1.47 mmHg
				-1.74			
	16.104 (maximum)	25		(-2.98 to -0.49)	3.89%	0.16	-4.07 mmHg

Intervention Characteristics

Length of intervention (in weeks)	WC	4 weeks						
		(minimum)	41		(-0.52 to -0.08)	37.73%	<0.0001	-3.04 cm
	HDL	208 weeks						
		(maximum)	41		(-3.28 to -1.57)	37.73%	<0.0001	-24.71 cm
	TG	4 weeks						
		(minimum)	28		(-0.33 to 0.09)	53.32%	<0.0001	-0.36 mmol/L
TG	208 weeks							
	(maximum)	28		(1.11 to 2.46)	53.32%	<0.0001	5.34 mmol/l	
TG	4 weeks							
	(minimum)	26		(-0.45 to 0.04)	33.05%	0.0006	-7.14 mmol/L	
TG	208 weeks							
	(maximum)	26		(-2.50 to -0.97)	33.05%	0.0006	-60.65 mmol/L	

Number of Females	FBG	4 weeks (minimum)	24	-0.21 (-0.46 to 0.04)	50.45%	<0.0001	-0.065 mmol/L
		208 weeks (maximum)	24	-2.20 (-2.99 to -1.42)	50.45%	<0.0001	-0.68 mmol/L
	SBP	4 weeks (minimum)	26	-0.49 (-0.79 to -0.19)	26.15%	0.005	-1.62 mmHg
		208 weeks (maximum)	26	-1.99 (-2.91 to -1.08)	26.15%	0.005	-6.51 mmHg
	DBP	4 weeks (minimum)	26	-0.64 (-1.21 to -0.07)	6.84%	0.09	-1.49mmHg
		208 weeks (maximum)	26	-2.39 (-4.14 to -0.63)	6.84%	0.09	-5.58 mmHg
	WC	0 (minimum)	38	-0.54 (-0.79 to -0.29)	0.00%	0.98	-5.51 cm
		1,154 (maximum)	38	-0.52 (-1.91 to 0.86)	0.00%	0.98	-5.30 cm
	HDL	0 (minimum)	27	0.28 (-0.07 to 0.64)	0.00%	0.48	0.84 mmol/L
		1,154 (maximum)	27	-2.61 (-10.47 to 5.25)	0.00%	0.48	-1.20 mmol/L
	TG	0 (minimum)	25	-0.40 (-0.77 to -0.03)	0.00%	0.74	-14.0 mmol/L
		1,154 (maximum)	25	-2.03 (-11.42 to 7.35)	0.00%	0.74	-71.05 mmol/L
	FBG	0 (minimum)	23	-0.53 (-0.86 to -0.21)	0.00%	0.96	-0.16 mmol/L
		1,154 (maximum)	23	-0.49 (-1.9 to 0.92)	0.00%	0.96	-0.15 mmol/L
	SBP	0 (minimum)	25	-0.69 (-0.99 to -0.39)	0.00%	0.73	-2.26 mmHg
		1,154 (maximum)	25	-0.95	0.00%	0.73	-3.11 mmHg

		1,154 (maximum)	41	-0.51 (-1.91 to 0.89)	0.00%	0.91	-5.20 cm
	HDL	11 (minimum)	28	0.09 (-0.29 to 0.46)	0.00%	0.55	0.27 mmol/L
		1,154 (maximum)	28	2.3 (-4.69 to 9.31)	0.00%	0.55	6.9 mmol/L
	TG	11 (minimum)	26	-0.31 (-0.68 to 0.06)	0.00%	0.34	-10.85 mmol/L
		1,154 (maximum)	26	-4.18 (-11.8 to 3.45)	0.00%	0.34	-146.3 mmol/L
	FBG	11 (minimum)	24	-0.51 (-0.83 to -0.19)	0.00%	0.93	-0.16 mmol/L
		1,154 (maximum)	24	-0.57 (-1.95 to 0.81)	0.00%	0.93	-0.18 mmol/L
	SBP	11 (minimum)	26	-0.73 (-1.04 to -0.41)	0.00%	0.74	-2.39 mmHg
		1,154 (maximum)	26	-0.97 (-2.36 to 0.42)	0.00%	0.74	-3.17 mmHg
	DBP	11 (minimum)	26	-0.49 (-0.78 to -0.20)	71.86%	<0.0001	-1.15 mmHg
		1,154 (maximum)	26	-5.94 (-7.24 to -4.64)	71.86%	<0.0001	-13.89 mmHg
		61.6 years (maximum)	23	-0.32 (-1.05 to 0.41)	0.85%	0.21	-1.05 mmHg
Use of a behavioral technique	WC	No	24	-0.41 (-0.71 to -0.11)	2.26%	0.17	-4.18 cm
		Yes	16	-0.73 (-1.08 to -0.38)	2.26%	0.17	-7.45 cm
	HDL	No	16	-0.08 (-0.42 to 0.25)	14.18%	0.03	-0.24 mmol/L
		Yes	11	0.50	14.18%	0.03	1.5 mmol/L

				(0.12 to 0.89)			
	TG	No	16	-0.27 (-0.59 to 0.60)	9.97%	0.05	-9.45 mmol/L
		Yes	9	-0.79 (-1.21 to -0.37)	9.97%	0.05	-27.65 mmol/L
	FBG	No	13	-0.31 (-0.69 to 0.07)	11.94%	0.06	-0.09 mmol/L
		Yes	9	-0.88 (-1.34 to -0.43)	11.94%	0.06	-0.27 mmol/L
	SBP	No	15	-0.54 (-0.92 to -0.17)	11.98%	0.05	-1.77 mmHg
		Yes	10	-1.12 (-1.56 to -0.68)	11.98%	0.05	-3.66 mmHg
	DBP	No	15	-0.53 (-1.16 to 0.11)	13.48%	0.03	-1.24 mmHg
		Yes	10	-1.63 (-2.35 to -0.85)	13.48%	0.03	-3.81 mmHg
Level of intervention or supervision during the study	WC	Primarily one-on-one	19	-0.54 (-0.88 to -0.20)	16.12%	0.01	-5.51 cm
		Small groups	9	-1.15 (-1.61 to -0.68)	16.12%	0.01	-11.73 cm
	HDL	Primarily one-on-one	12	-0.11 (-0.49 to 0.27)	22.31%	0.01	-0.33 mmol/L
		Small groups	9	0.64 (0.23 to 1.05)	22.31%	0.01	1.92 mmol/L
	TG	Primarily one-on-one	12	-0.15 (-0.50 to 0.20)	25.64%	0.006	-5.25 mmol/L
		Small groups	7	-1.03 (-1.46 to -0.59)	25.64%	0.006	-36.05 mmol/L
	FBG	Primarily one-on-one	10	-0.19 (-0.61 to 0.22)	19.01%	0.03	-0.06 mmol/L

	Small groups	7	-1.04 (-1.52 to -0.56)	19.01%	0.03	-0.32mmol/L
SBP	Primarily one-on-one	13	-0.46 (-0.83 to -0.09)	30.73%	0.005	-1.50 mmHg
	Small groups	7	-1.42 (-1.91 to -0.94)	30.73%	0.005	-4.64 mmHg
DBP	Primarily one-on-one	13	-0.34 (-1.02 to 0.34)	13.86%	0.05	-0.79 mmHg
	Small groups	7	-1.54 (-2.43 to -0.65)	13.86%	0.05	-3.60 mmHg

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; R² indicates the percentage of heterogeneity that the moderator accounts for; Clinical Unit of Measure was calculated using a predictive model and an added metric transformation using the effect sizes for each outcome and category.

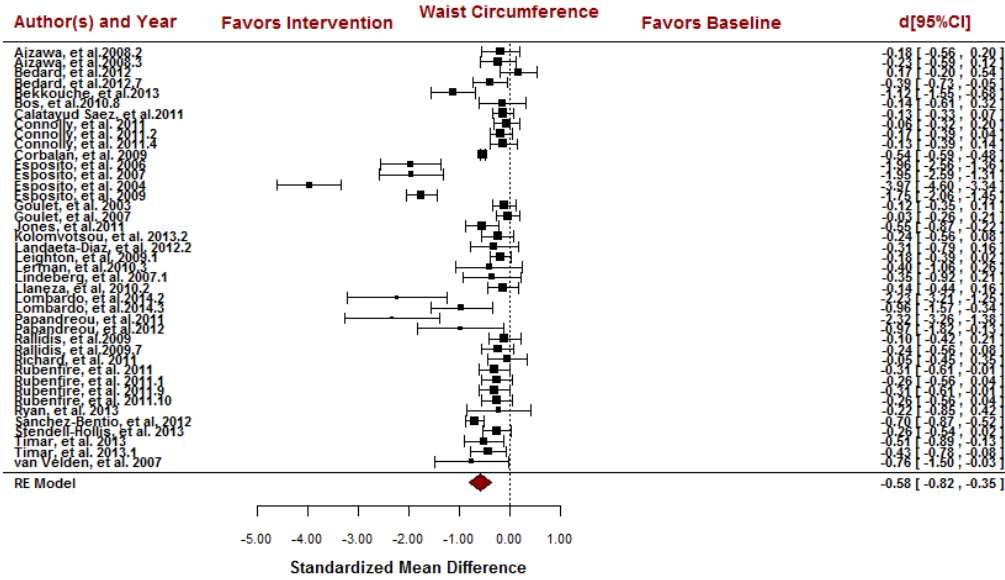
Table 5. Non-Significant Moderators

Non-Significant Moderators
Proportion of females
Proportion of participants with any type of disease
Number of participants with any type of disease
Proportion of participants taking any type of medication
Number of participants taking any type of medication
Type of medication use
Experimental setting
Number of participants who dropped out of the intervention
Length of counseling sessions
Number of counseling sessions
Specific type of diet
Publication Year
Language of publication
Recruitment type/Specific population
Proportion of carbohydrate intake (<50% or ≥50%)
Proportion of saturated fat intake (<10% or ≥10%)
Proportion of total fat intake (<30% or ≥30%)
Mean Age of the Sample
Proportion of protein intake (<15% or ≥15%)
Assessment of dietary compliance
Participation in dietary counseling
Population with cardiovascular disease
Population with Type II Diabetes Mellitus
Population with Metabolic Syndrome
Population with overweight/obesity

Table 6. Moderators that were Unable to be analyzed due to lack of Reported Information

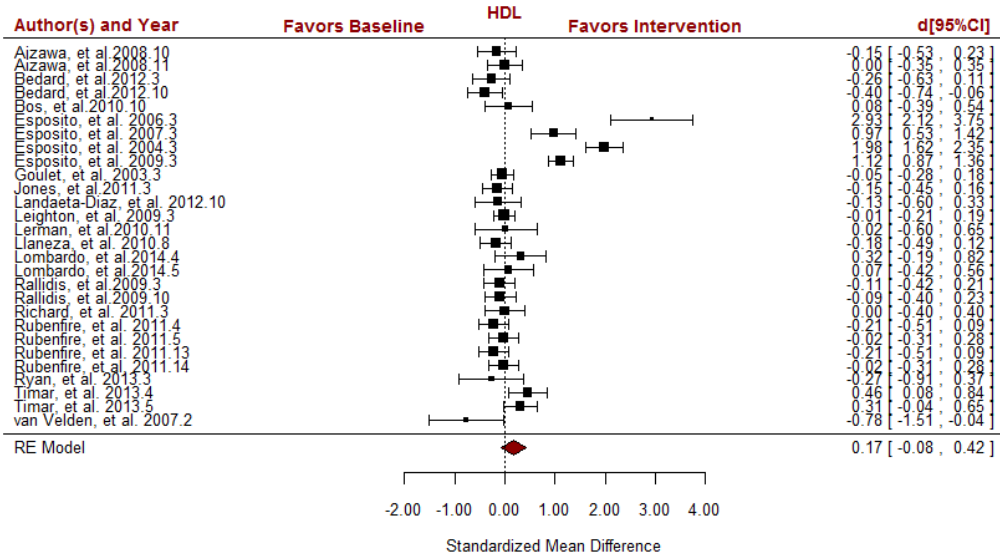
Moderators Unable to be Analyzed
Oral contraceptive/hormone-replacement therapy
Proportion of participants who smoke
Number of participants that smoke
Supplement use
Alcohol intake
Number of alcoholic drinks/week
Type of alcohol consumption
Amount of exercise/week
Type of exercise
Was dietary adherence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

Figure 2. Forest Plot for Waist Circumference



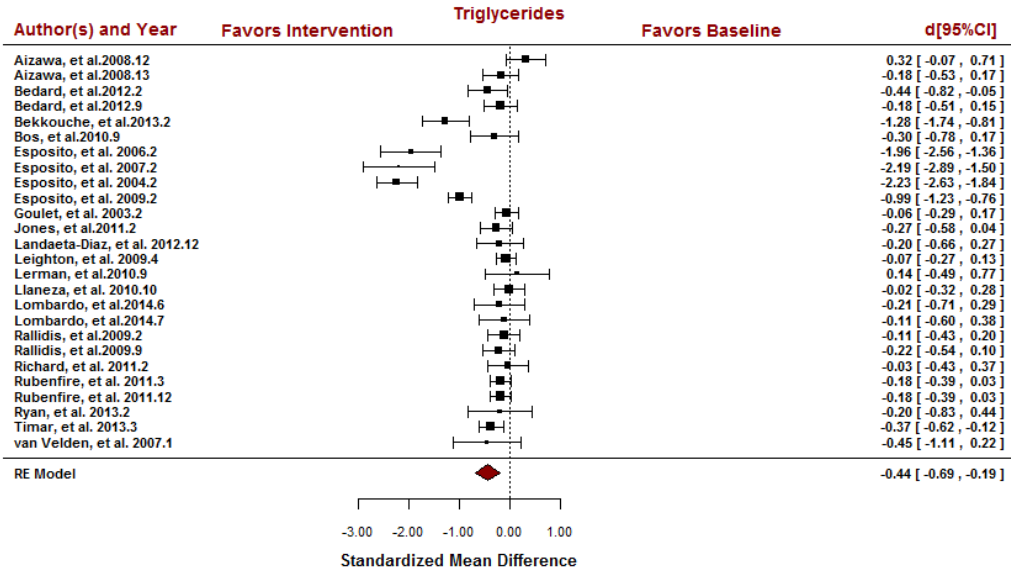
Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (Cis); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.

Figure 3. Forest Plot for HDL



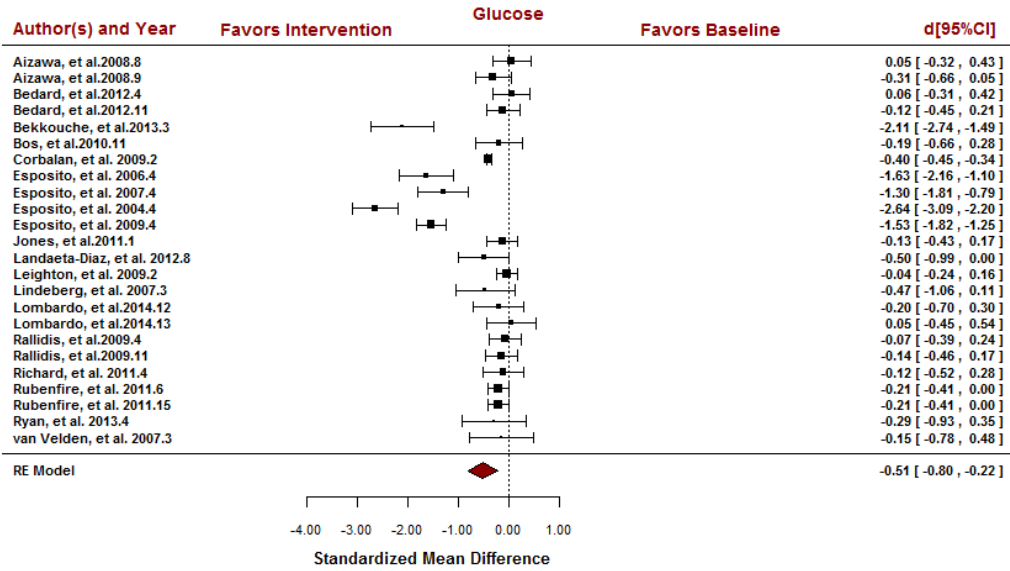
Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (CIs); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.

Figure 4. Forest Plot for Triglycerides



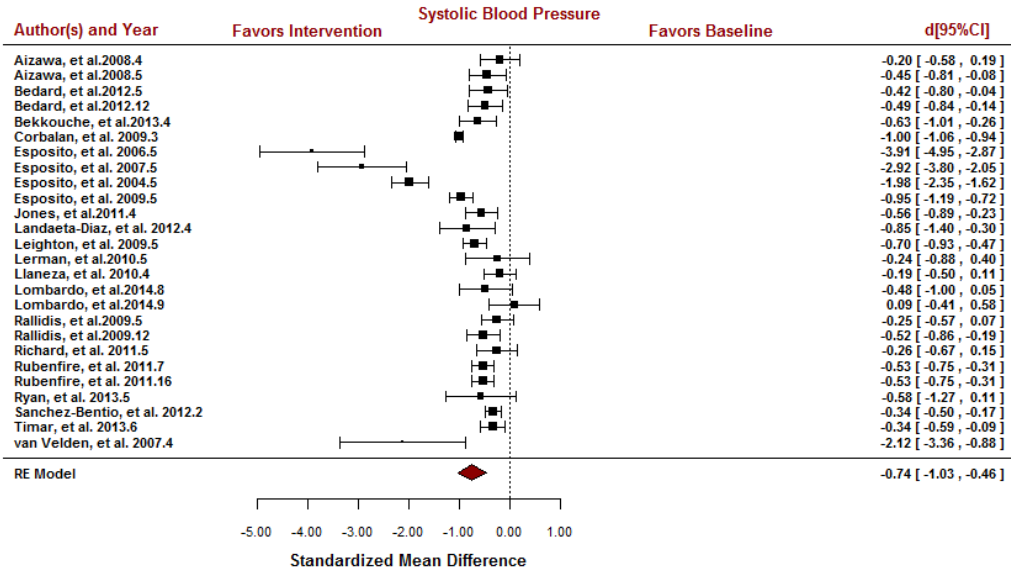
Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (Cis); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.

Figure 5. Forest Plot for Fasting Blood Glucose



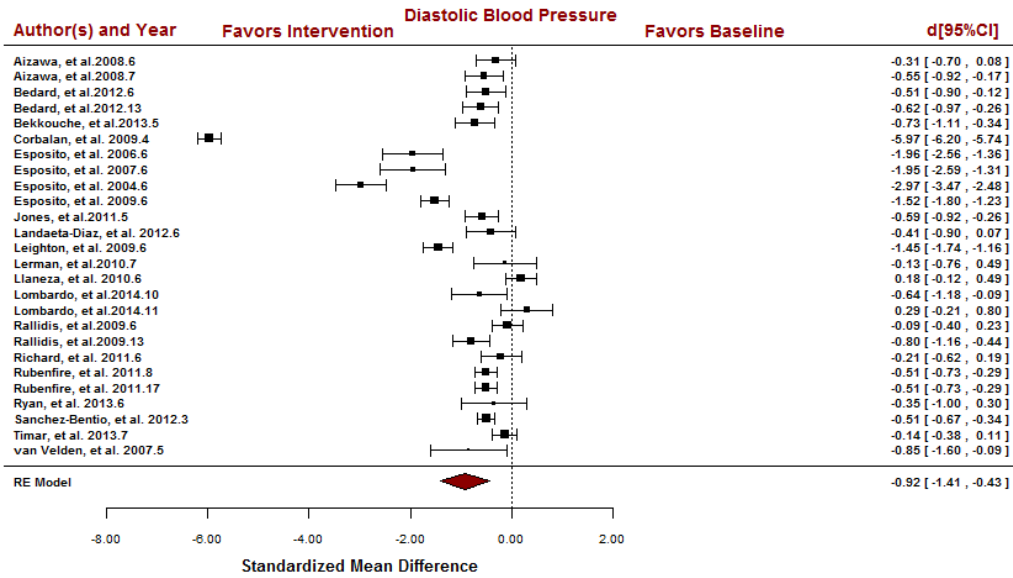
Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (Cis); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.

Figure 6. Forest Plot for Systolic Blood Pressure



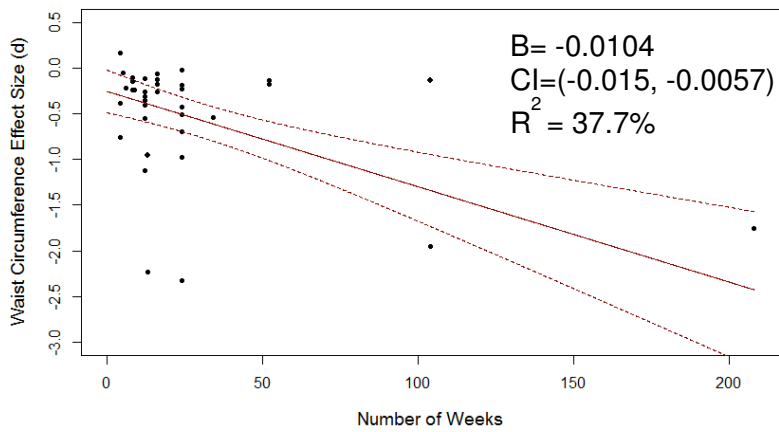
Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (Cis); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.

Figure 7. Forest Plot for Diastolic Blood Pressure



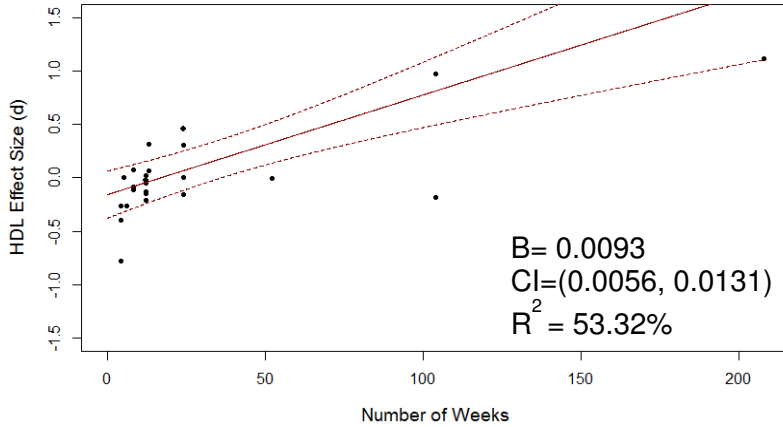
Note: Squares represent point estimates for each individual study; extended line shows 95% confidence intervals (Cis); dotted line represents the null value of zero; diamond represents the weighted mean effect size for the outcome.

Figure 8. Meta-Regression Plot for Waist Circumference



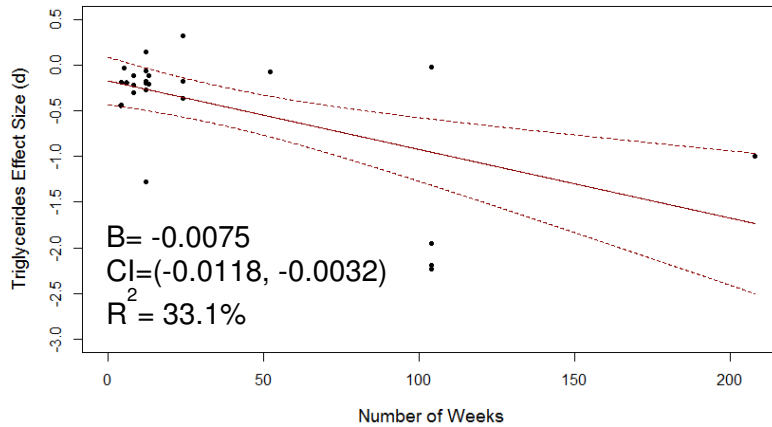
Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; R^2 indicates the percentage of variability accounted for by length.

Figure 9. Meta-Regression Plot for HDL



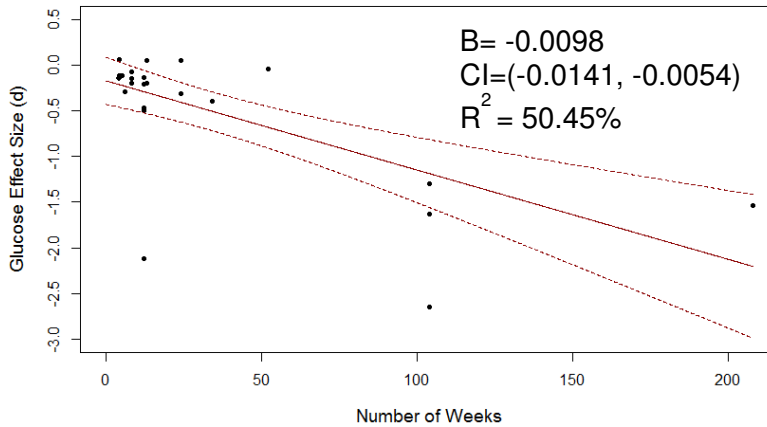
Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; R^2 indicates the percentage of variability accounted for by length.

Figure 10. Meta-Regression Plot for Triglycerides



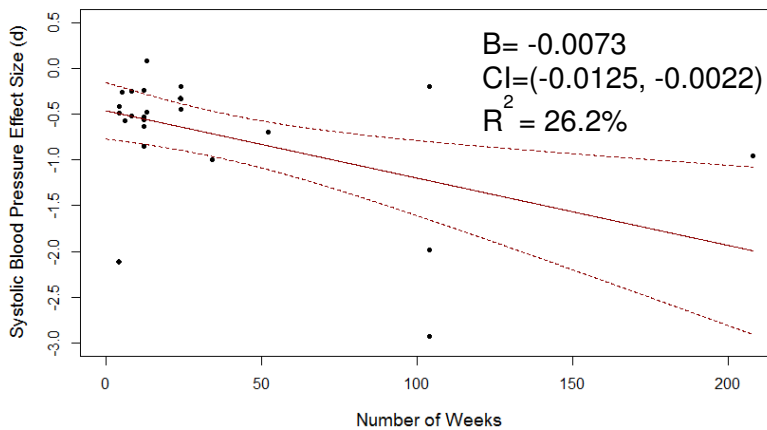
Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; R^2 indicates the percentage of variability accounted for by length.

Figure 11. Meta-Regression Plot for Fasting Blood Glucose



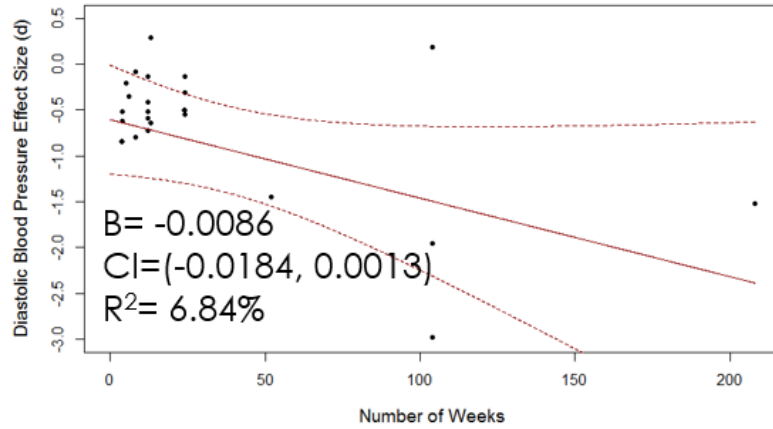
Note: Number of weeks of the intervention is represented on the x-axis; Outcome of interest is represented on the y-axis; B is the unstandardized beta and represents the amount of change in the outcome per week of the intervention; R² indicates the percentage of variability accounted for by length.

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; R² 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.

Figure 14. Risk of Bias

	Random Sequence Generation (selection bias)	Allocation Concealment (selection bias)	Blinding of participants/personnel	Blinding of outcome assessment	Incomplete outcome data (attrition bias) (short term [≤ 6 weeks])	Incomplete outcome data (attrition bias) (long term [> 6 weeks])	Selective reporting (reporting bias)	Other bias
<p>Risk of Bias</p> <p>    </p> <p>Low High Unclear</p>								
Alzawa 2008	?	?	?	?	?	?	?	?
Bedard 2012	?	?	?	?	?	?	?	?
Bekkouché 2013	?	?	?	+	?	?	?	?
Bos 2010	-	?	-	-	?	?	?	?
Calatayud 2011	?	?	?	?	?	?	?	?
Connolly 2011	?	?	?	?	?	?	?	?
Corbalián 2009	?	?	?	?	?	?	?	?
Esposito 2006	?	?	?	?	?	?	?	?
Esposito 2007	?	?	?	?	?	?	?	?
Esposito 2004	-	-	-	-	+	+	?	?
Esposito 2009	-	-	-	-	?	?	?	?
Goulet 2003	?	?	?	?	?	?	?	?
Goulet 2011	?	?	?	?	+	+	?	?
Jones 2011	?	?	?	?	?	?	?	?
Kolomvostou 2013	-	-	?	?	?	?	?	+
Landskets-Diaz 2012	?	?	?	?	?	?	?	-
Leighton 2009	?	?	?	?	?	?	?	?
Lerman 2010	?	?	?	?	?	?	?	?
Lindeberg 2007	?	?	?	?	?	?	?	?
Llaneza 2010	-	?	?	?	?	?	?	?
Lomberdo 2014	?	?	?	?	?	?	?	?
Papandreou 2011	-	?	+	+	?	?	?	-
Papandreou 2012	-	?	+	+	?	?	?	-
Rallidis 2009	-	?	?	?	?	?	?	?
Richard 2011	?	?	?	?	?	?	?	?
Rubentire 2013	?	?	?	?	?	?	?	?
Ryan 2013	?	?	?	?	?	?	?	?
Sanchez-Bentlo 2012	?	?	?	?	?	?	?	?
Stendell-Hollis 2013	-	?	?	?	?	?	?	-
Timar 2013	?	?	?	?	?	?	?	?
Van Velden 2007	?	?	?	?	?	?	?	?
Velasquez-Lopez 2014	?	?	?	?	?	?	?	-

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.

("Mediterranean diet" OR "Mediterranean diets" OR "Mediterranean dietary" OR "Mediterranean style diet" OR "Mediterranean style diets" OR "Diet, Mediterranean"[Mesh]) AND (adiposity OR "metabolic syndrome" OR overweight OR BMI OR "body mass" OR "waist circumference" OR weight [tiab] OR "body weight" OR obese OR obesity OR "abdominal fat" OR "Weight Loss"[Mesh] OR "weight loss" OR "Diet, Reducing"[Mesh]) NOT ("Cross-Sectional Studies"[MeSH Terms] OR "Case Reports"[pt] OR Comment[pt] OR Editorial[pt] OR Letter[pt] OR Review[pt] OR "case control"[ti] OR "case report"[ti] OR "case study"[ti] OR "case series"[ti] OR "Case-Control Studies"[Mesh] OR "Follow-Up Studies"[Mesh] OR "observational study"[ti] OR "prospective cohort"[ti] OR "cohort studies"[Mesh:noexp] OR "cohort study"[ti] OR "Longitudinal Studies"[Mesh:noexp] OR "Follow-Up Studies"[mesh] OR "Retrospective Studies"[mesh] OR "non-randomized"[ti] OR "follow up study"[ti] OR rat[ti] OR rats[ti] OR mice[ti] OR mouse[ti] OR dog[ti] OR dogs[ti] OR cats[ti])

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

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 "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: 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 "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 : 25

5. Agricola years 1970-present

Searched 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

Study ID: _____

Coder: _____

Mediterranean Diet Obesity Meta-Analysis Selection Criteria

Inclusion Criteria Trials MUST match all of these criteria:	Exclusion Criteria Studies CANNOT include any of the following:
<p>Pre- AND Post-intervention weight measurements (at least one of these):</p> <p>Waist Circumference <input type="checkbox"/></p> <p>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.</p> <p><input type="checkbox"/></p>	<p>Survey <input type="checkbox"/></p> <p>Review <input type="checkbox"/></p> <p>Guidelines <input type="checkbox"/></p> <p>Prospective Studies <input type="checkbox"/></p> <p>Epidemiologic Studies <input type="checkbox"/></p> <p>Cross-sectional Studies <input type="checkbox"/></p>

Notes:

Appendix 3. Mediterranean Diet Coding Form (finalized July

2014)

CODER_____ **Coder** (Marissa=1, Julia=2, Other=3)

Study Information

ID_____ **Study ID** (first 3 letters of 1st author's last name & unique ID#: *Pescatello= PÉS001*), _____ (Last name, Yr)

PUB_YR _____ **Publication year** (*consider this missing if unpublished*)

DATA _____ **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*)

LANG _____ **Language of report** 1=English 2=Spanish 3=Japanese
4=Other, specify: _____

SOURCE_____ **Publication Type** 1=journal 2=book 3=thesis/dissertation
4=conference paper 5= unpublished

SCORE_____ **Impact Score of the Journal** (*use ISI Web of Knowledge journal citation reports*)

JOURNAL NAME

PUBMED NAME/ ABBR.

FUNDING SOURCE_____ 1= Gov't (i.e., CDC, NIH, etc) 2= Academic/University
3= Private 4= Other

For all, specify source/grant:

NOTE_STUDY_____ **study notes** (*make note of multiple arms; ex. MD vs. low fat vs. low carb + MD vs. CONTROL*): _____

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

ETH _____ **Ethnicity reported?** 1 = yes; 0 = no

PROP_WH _____ Proportion White; whole # _____

PROP_BLK _____ Proportion Black/ whole # _____

PROP_ASIAN _____ Proportion Asian/ whole # _____

PROP_MIX _____ Proportion Mixed (other)/ whole # _____

PROP_HISP _____ Proportion Latino/Hispanic/ whole # _____

PROP_CARIB _____ Proportion Caribbean/ whole # _____

ETH_EST _____ Assumed ethnicity (0= n/a, 1= White, 2= Asian, 3= Black, 4= Unreported, 5= Hispanic/Latino)

NUM_FemCON _____ **# of Females in Sample; Proportion**
(#females/total sample): _____

NUM_FemIN1 _____ **# of Females in Sample; Proportion**
(#females/total sample): _____

NUM_FemIN2 _____ **# of Females in Sample; Proportion**
(#females/total sample): _____

NUM_FemIN3 _____ **# of Females in Sample; Proportion**
(#females/total sample): _____

REGION _____ **Location of sample** (if unreported, use location of first author as estimate of study location)

1=American city: _____ **US_ZIP** _____

2=other US region (city= unreported): _____

3=Canada (city: _____)

4=Europe (city: _____)

5=South/Central America, Mexico, Caribbean (city: _____)

6=Africa (city: _____)

7=Asia (city: Osaka, Japan)
(city: _____)

8=Australia

POP _____ Population 0=not reported 1=school/college 2=community
(senior center, flyers, etc.) _____

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

Characteristic	CONTROL / COMPARISON n=_____ (total sample)	IN1 n=_____ (total sample), specify intervention_____	IN2 n=_____ (total sample), specify intervention_____	IN3 n=_____ (total sample), specify intervention_____
Mean age (years)	AGE	AGE	AGE	AGE
SD for age (years)	AGE_SD	AGE_SD	AGE_SD	AGE_SD
Known disease/ chronic conditions 0= Healthy 3= CVD(s) (i.e., CAD, PAD, HF, MI) 4= Stroke 5= Diabetes 6= MetS 7= Arthritis 8= Dyslipidemia 9= Obesity 10= Other, specify:_____ _____ 11= Multiple, specify #s:_____ _____	DISEASE	DISEASE	DISEASE	DISEASE
If disease: report	PROP_DIS	PROP_DISE	PROP_DISEA	PROP_DISE

Characteristic	CONTROL / COMPARISON n=____ (total sample)	IN1 n=____ (total sample), specify intervention____ –	IN2 n=____ (total sample), specify intervention____ n____	IN3 n=____ (total sample), specify intervention____ –
prop. & number if “healthy” denote 0= n/a; if missing=“.”	EASE NumberDisease	ASE NumberDisease	SE NumberDisease	ASE NumberDisease
Medication use (0=no, 1=yes)	MED	MED	MED	MED
If yes, report prop & number; if no meds, use 0=NA (if missing =“.”)	PROP_USE NumberMED	PROP_USE NumberMED	PROP_USE NumberMED	PROP_USE NumberMED
Medication Type (if no meds= 0) 1= β Blockers 2= Nitrates 3= Ca^{+2} Channel Blockers 4= Angiotension Converting Enzyme (ACE) Inhibitors 5= Diuretics 6= Vasodilators 7= NSAIDs 8= Aspirin 9= Statins 10=Other, specify:	MED_TYPE	MED_TYPE	MED_TYPE	MED_TYPE

Characteristic	CONTROL / COMPARISON n=____ (total sample)	IN1 n=____ (total sample), specify intervention____ —	IN2 n=____ (total sample), specify intervention____ —	IN3 n=____ (total sample), specify intervention____ —
11= Multiple, specify:				
BP Medication use (1= yes, 0=no) <i>If unreported == “.”</i>	BPMedUse	BPMedUse	BPMedUse	BPMedUse
If yes, report prop. & number (if “no”=0, NA; if missing denote=“.”)	BPMedProp BPMedNumber	BPMedProp BPMedNumber	BPMedProp BPMedNumber	BPMedProp BPMedNumber
If taking meds, is BP controlled? yes= 1 , if SBP≤140 OR DBP≤90; no= 0 , SBP>140 OR DBP>90 (*if no BP use == NA)	BPControl	BPControl	BPControl	BPControl
LIFESTYLE VARIABLES				
Oral Contraceptive (0=no, 1=yes) OR Hormone replacement therapy	OC_USE HRT_USE	OC_USE HRT_USE	OC_USE HRT_USE	OC_USE HRT_USE
Smokers/smokers (≤6	SMOKE	SMOKE	SMOKE	SMOKE

Characteristic	CONTROL / COMPARISON n=____ (total sample)	IN1 n=____ (total sample), specify intervention____ —	IN2 n=____ (total sample), specify intervention____ n_____	IN3 n=____ (total sample), specify intervention____ —
months) (0=no, 1=yes ; if missing = “.”)				
If yes, report smoker prop. & number	PROP_SMOKE NumberSMOKE	PROP_SMOKE NumberSMOKE	PROP_SMOKE NumberSMOKE	PROP_SMOKE NumberSMOKE
Nutritional Supplements Permitted? (0=no, 1=yes)	SUPP	SUPP	SUPP	SUPP
If yes, specify type	TYPE	TYPE	TYPE	TYPE
Consume Alcohol? (0=no, 1=yes)	ALC	ALC	ALC	ALC
If yes, how many drinks/week?	AMT	AMT	AMT	AMT
If yes, what type of alcohol?	ALCTYPE	ALCTYPE	ALCTYPE	ALCTYPE
Amount of exercise per week (in min)	EX	EX	EX	EX
Type of exercise (e.g., cardio, strength training)				

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 a non-diet control group

5= other, specify:

Experiment/ Intervention Conditions

EXPERIMENT _____ **INTERVENTIONS/EXPERIMENTAL CONDITION(S)**

1= non-diet control/comparison + 1 intervention
control/comparison + 2 interventions

2= non-diet

3= non-diet control/comparison + 3 interventions

4= diet control/comparison + 1 intervention
+ 2 interventions

5= diet control/comparison

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	CONTROL/ COMPARISON	IN1	IN2	IN3
LENGTH__(in weeks)	LENGTH__	LENGTH__	LENGTH__	LENGTH__
WTGain/WTLoss____ (1=loss, 2=gain, 3=maintain, 4=unspecified)	WTGain/WTLoss____	WTGain/WTLoss____	WTGain/WTLoss____	WTGain/WTLoss____
PART_LOST # of drop outs				
ADHERENCE (report %) If reported as # of sessions completed, use== $(\frac{\text{completed sessions}}{\text{total sessions}} \times 100)$				
Were medications used as part of the intervention? (0=no, 1=yes)	MEDS__	MEDS__	MEDS__	MEDS__
If yes, specify 1= β Blockers 2= Nitrates 3= Ca ⁺² Channel Blockers 4= Angiotension Converting Enzyme (ACE) Inhibitors 5= Diuretics 6= Vasodilators 7= NSAIDs 8= Aspirin 9= Statins 10=Other, specify: 11= Multiple, specify: _____	MED__TYPE	MED__TYPE	MED__TYPE	MED__TYPE
DIET__TYPE (1=MedDiet, 2=low-fat, 3=high protein, 4=low-carb, 5=other, specify)	DIET__TYPE	DIET__TYPE	DIET__TYPE	DIET__TYPE
Provision of Med Diet Foods? (0=no, 1=yes)				
If yes, type and amount ____ 1=olive oi (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 PropCHO____ PropSatFAT____ PropTotFAT____ PropPRO____	PropCHO____ PropSatFAT____ PropTotFAT____ PropPRO____	PropCHO____ PropSatFAT____ PropTotFAT____ PropPRO____	PropCHO____ PropSatFAT____ PropTotFAT____ PropPRO____	PropCHO____ PropSatFAT____ PropTotFAT____ PropPRO____
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 %) KCAL_RES (unit= kcal) OR RES_PERCENT (%)				
SOD_INTAKE (mg/day)				
POT_INTAKE (mg/day)				
FAT_INTAKE (g/day) Unsaturated: FAT_UNSAT Saturated: FAT_SAT Cholesterol: FAT_CHOL	_____ _____ _____	_____ _____ _____	_____ _____ _____	_____ _____ _____

Dietary Fiber Intake (g/day) FIB_INTAKE				
Servings/week: Fruit and/or Vegetables VEG_SER				
Servings/week: Dairy DAIRY_SER				
Servings/week: Wine WINE_SER				
Servings/week: Whole Grains GRAIN_SER				
Servings/week: Fish FISH_SER				
Servings/week: Olive Oil OIL_SER				
Servings/week: Nuts NUTS_SER				
Servings/week: Legumes LEG_SER				
Servings/week: Red/processed meat MEAT_SER				
Servings/week: Poultry POUL_SER				
<i>Dietary Compliance & Counseling</i>				
DI_COMPLIANCE <i>Was Dietary compliance assessed? 0= No; 1= Yes)</i>				
If yes, specify: (1=FFQ, 2=Food journal, 3=phone interviewing, 4=24 hr recall, 5=other,specify___)				
Was diet adherence measured pre, during, or post intervention? (1=pre, 2=during, 3=post, 4=pre,during, and post, 5=pre and post, 6=not reported)				
Is a scale used to measure adherence? (0=no, 1=yes)				
If yes, specify type of scale used _____				
DI_COUNSELING <i>Participation in dietary counseling? 0= no; 1= yes</i>				
<i>If Dietary Counseling was provided, report:</i> COUNSEL_HR <i>hours per week</i> COUNSEL_SESS <i>sessions per week</i>	_____	_____	_____	_____
DIET_TOPIC <i>If Dietary Counseling was provided,</i>				

<i>briefly state topics covered</i>				
QoL Was Quality of Life (QoL) assessed? 0=no, 1=yes, if yes, report tool or scale				
NOTE_DIET Report here any notes relevant to the dietary intervention, counseling, implementation, etc.				
# of follow-ups				
Interval of follow-ups				

Appendix 4. SAS Code

Import Data

To read data set:

```
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):

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

To calculate percentages for language and region of publication:

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

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

```
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-1

```
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

```
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(tmddb$RanSeq)
```

```
table(tmdwc$AllCon)
```

```
table(tmdhdl$AllCon)
```

```
table(tmdtg$AllCon)
```

```
table(tmdfbg$AllCon)
```

```
table(tmdsbp$AllCon)
```

```
table(tmddb$AllCon)
```

```
table(tmdwc$Blinding)
```

```
table(tmdhdl$Blinding)
```

```
table(tmdtg$Blinding)
```

```
table(tmdfbg$Blinding)
```

```
table(tmdsbp$Blinding)
```

```
table(tmddb$Blinding)
```

```
table(tmdwc$Incomp)
```

```
table(tmdhdl$Incomp)
```

```
table(tmdtg$Incomp)
```

```
table(tmdfbg$Incomp)
```

```

table(tmdsbp$Incomp)
table(tmddb$Incomp)
table(tmdwc$Select)
table(tmdhdl$Select)
table(tmdtg$Select)
table(tmdfbg$Select)
table(tmdsbp$Select)
table(tmddb$Select)
table(tmdwc$OtherBias)
table(tmdhdl$OtherBias)
table(tmdtg$OtherBias)
table(tmdfbg$OtherBias)
table(tmdsbp$OtherBias)
table(tmddb$OtherBias)

```

Moderation with Weeks and Metaregression Plot

```

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)))
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$d.ex.,pch= 20, col="black", bg = "black", cex=size,
xlab = "Number of Weeks", #Plotting here the observed values of the subsample
ylab = "Waist Circumference Effect Size (d)", xlim=c(0, 208), ylim=c(-3, 0.5))
lines(seq(0,208,.1), model21pred$pred, col = "dark red")
#Plotting here the regression line and confidence interval of the predictive model

```

```

lines(seq(0,208,.1), model21pred$ci.lb, lty = "dashed", col="dark red")
lines(seq(0,208,.1), model21pred$ci.ub, lty = "dashed", col="dark red")
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$d.ex.,pch= 20, col="black", bg = "black", cex=size,
xlab = "Number of Weeks", #Plotting here the observed values of the subsample
      ylab = "HDL Effect Size (d)",xlim=c(0, 208), ylim=c(-1.5, 1.5))
lines(seq(0,208,.1), model61pred$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", #Plotting here the observed values of the subsample

  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", #Plotting here the observed values of the subsample

  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$w_d.ex.
min= min(wi, na.rm=TRUE)
max= max(wi, na.rm=TRUE)
size= 1.0 + 6.0 * (wi - min)/(max - min)
dietout1= subset(Final,Diet==1 & Out==6) #Here we have to create the
subsample we are working on to just plot the observed values of that below
plot(dietout1$Weeks,dietout1$d.ex.,pch= 20, col="black", bg = "black", cex=size,
xlab = "Number of Weeks", #Plotting here the observed values of the subsample
  ylab = "Systolic Blood Pressure Effect Size (d)",xlim=c(0, 208), ylim=c(-3,
0.5))
lines(seq(0,208,.1), model121pred$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$w_d.ex.
min= min(wi, na.rm=TRUE)
max= max(wi, na.rm=TRUE)
size= 1.0 + 6.0 * (wi - min)/(max - min)
dietout1= subset(Final,Diet==1 & Out==7) #Here we have to create the
subsample we are working on to just plot the observed values of that below
plot(dietout1$Weeks,dietout1$d.ex.,pch= 20, col="black", bg = "black", cex=size,
xlab = "Number of Weeks", #Plotting here the observed values of the subsample

```

```

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)
```

```
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 kcal_tot_in1

```
model6651<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==1), mods=kcal_tot_in1,  
data=MetRisk, method="REML")
```

```
summary(model6651)
```

```
model6653<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3), mods=kcal_tot_in1,  
data=MetRisk, method="REML")
```

```
summary(model6653)
```

```
model6654<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4), mods=kcal_tot_in1,  
data=MetRisk, method="REML")
```

```
summary(model6654)
```

```
model6655<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5), mods=kcal_tot_in1,  
data=MetRisk, method="REML")
```

```
summary(model6655)
```

```
model6656<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6), mods=kcal_tot_in1,  
data=MetRisk, method="REML")
```

```
summary(model6656)
```

```
model6657<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7), mods=kcal_tot_in1,  
data=MetRisk, method="REML")
```

```
summary(model6657)
```

Prop CHO

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

```
summary(model6651)
```

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

```
summary(model6653)
```

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

```
summary(model6654)
```

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

```
summary(model6655)
```

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

```
summary(model6656)
```

```
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

```
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)
```

```
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)
```

```
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)
```

```
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 congrp

```
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_satfat1

```
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(proptotfat_in1), data=Final, method="REML")
```

```
summary(model553)
```

```
model554<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==3),  
mods=~factor(proptotfat_in1), data=Final, method="REML")
```

```
summary(model554)
```

```
model555<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==4),  
mods=~factor(proptotfat_in1), data=Final, method="REML")
```

```
summary(model555)
```

```
model556<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==5),  
mods=~factor(proptotfat_in1), data=Final, method="REML")
```

```
summary(model556)
```

```
model557<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==6),  
mods=~factor(proptotfat_in1), data=Final, method="REML")
```

```
summary(model557)
```

```
model558<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),  
mods=~factor(proptotfat_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
```

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(tmddb$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(tmdsbp$congrp)
```

```
table(tmddbpb$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)
```

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

```
summary(model554)
```

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

```
summary(model555)
```

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

```
summary(model556)
```

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

```
summary(model557)
```

```
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)
```

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

```
summary(model554)
```

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

```
summary(model555)
```

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

```
summary(model556)
```



```
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 interlvi-1

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

```
model993
```

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

```
model994
```

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

model995

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

model996

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

model997

```
model998<-rma(d.ex.,var_d.ex.,subset=(Diet==1 & Out==7),  
mods=~factor(interlv)-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

```
table(tmdwc$region)
```

```
table(tmdhdl$region)
```

```
table(tmdtg$region)
```

```
table(tmdfbg$region)
```

```
table(tmdsbp$region)
```

```
table(tmddb$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=

```

```

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

```

```
"REML", slab= paste(Reference, Year, sep=""))
```

```
model127
```

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

```
model146
```

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

```
model147
```

Min and Max in Intervention 1

```
maxsamp=1154-Final$n_in1
```

```
maxsamp
```

```
minsamp=Final$n_in1-11
```

```
minsamp
```

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

```
model27
```

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

```
model26
```

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

```
model66
```

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

```
model67
```

```
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=maxsamp, 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
```