testing. Among the QIs determined appropriate for use we generated a further shortlist by excluding those that were specific to certain patient sub-groups and/or care settings. The shortlist was further reduced by identifying similar/related QIs and retaining the indicator with the highest rating.

Results Our search yielded 7,231 references. Following screening, 35 references met our eligibility criteria and were included in the review. We identified 288 QIs for patients with advanced cancer and/or at the end-of-life. Most evaluated physical aspects of care (n=103, 35.8%) or structure and processes of care (n=109, 37.8%). There was a limited number of QIs relevant to psychosocial (n=18) or spiritual/cultural (n=3) care domains. 27.8% (n=80) of QIs were assessed as appropriate for use; 40.3% (n=116) inappropriate for use, and 31.9% (n=92) had limited testing. Acceptability and validity were the measurement properties with the fewest positive assessments (13.2% and 21.9% respectively). Only 16 QIs (5.6%) reported any benchmarking data. Our shortlist comprised 36 QIs after those specific to patient sub-groups or care settings were excluded. This was further reduced to 15 once duplicate and/or related QIs were removed.

Conclusion Only a small proportion of QIs developed for patients with advanced cancer and/or at the end-of-life have received adequate testing and/or are appropriate for use. Further testing is recommended, particularly with regards to acceptability and validity, as well as research to establish benchmarking data and to expand QIs relevant to psychosocial, cultural and spiritual care domains. To support cancer services in conducting comprehensive and meaningful assessments of quality, we propose 15 QIs, identified from our review as being scientifically sound, applicable across care settings and which collectively evaluate quality across multiple domains of care.

Nutrition/Obesity

OP36 TRANS FATTY ACID BIOMARKERS AND INCIDENT TYPE 2 DIABETES: POOLED ANALYSIS OF 10 PROSPECTIVE COHORT STUDIES IN THE FATTY ACIDS AND OUTCOMES RESEARCH CONSORTIUM (FORCE)

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Background Type 2 diabetes (T2D) is a major risk factor associated with cardiometabolic diseases, and a major contributor towards mortality and morbidity, given its rapidly rising prevalence worldwide. In experimental studies, *trans*-fatty acids (TFAs) exert harmful biologic effects that may affect T2D risk, but findings from observational studies remain inconclusive, especially for biomarkers which provide an objective advantage with less recall bias and estimation errors. By pooling multiple studies, we may also increase generalizability, statistical power, and address potential interactions by subgroups. Therefore, we assessed prospective associations between circulating biomarkers of individual TFAs and incident T2D in a large, diverse sample.

Methods We pooled ten prospective cohort or nested-case-control studies from Australia, Germany, Iceland, UK, and the USA to perform an analysis using harmonized individual level data for TFA biomarkers and incident T2D. Fatty acids (FAs) were measured in plasma phospholipid, red blood cell membrane phospholipid, or total plasma collected between 1990–2008 from 22,711 participants aged ≥18 years without prevalent diabetes. Evaluated TFAs included *trans*-16:1n-9, sum of *trans*-18:1 isomers (*trans*-18:1n6 to *trans*-18:1n12), sum of *trans*-18:2 isomers (*cis*/*trans*-18:2, *trans*/*cis*-18:2, *trans*/*trans*-18:2), and individual *trans*-18:2 isomers. The multivariable-adjusted relative risk or odds ratio was estimated for each cohort by lipid compartments using a pre-specified protocol for definitions of exposures, covariates, and outcomes for statistical analysis. Association estimates were pooled using fixed-effects inverse-variance weighted meta-analysis.

Results During an average maximum of 14 years of follow-up, 2,244 cases of incident T2D were identified. Median levels of TFAs across cohorts were 0.05–0.18% total FAs for *trans*-16:1n-9, 0.09–2.05% for total *trans*-18:1, 0.10–0.73% for total *trans*-18:2, and 0.01–0.36% for individual *trans*-18:2 isomers. In overall pooled analysis, TFAs evaluated per interquintile range were not significantly associated with risk of T2D. Relative risks for individual TFAs were 1.02 (0.78–1.32) for *trans*-16:1n-9, 0.92 (0.79–1.08) for total *trans*-18:1, 1.16 (0.98–1.37) for *trans*/*trans*-18:2, 0.98 (0.79–1.21) for *cis*/*trans*-18:2, 0.93 (0.76–1.14) for *trans*/*cis*-18:2, and 0.90 (0.78–1.04) for total *trans*-18:2. Findings were consistent when TFAs were assessed categorically by study-specific quintiles, and when associations were pooled within lipid compartment (phospholipids or total plasma).

Conclusion We found that biomarker levels of TFAs were not significantly associated with risk of incident T2D in this international pooling project. Findings may reflect no effect of circulating TFA on T2D or be influenced by mixed TFA sources (industrial or ruminant), or to a general decline in TFA exposure during this period. Associations with T2D for higher levels of TFA biomarkers should be investigated.

OP37 HEREDITARY HAEMOCHROMATOSIS: ASSOCIATIONS WITH MORBIDITY AND IRON SUPPLEMENT USE IN 451,243 UK BIOBANK PARTICIPANTS

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Background Hereditary haemochromatosis (HH) is the most common and probably the most treatable genetic disorder in Europe, but many patients are misdiagnosed or diagnosed too late. HH causes iron overload and is predominantly due to the *HFE* p.C282Y genetic variant. HH is easily prevented and

treated with phlebotomy. We aimed to test *HFE* p.C282Y homozygote associations with prevalent and incident morbidity in the large UK Biobank sample of European descent. We also examined how iron supplement use may affect associations between p.C282Y homozygosity and morbidity.

Methods We studied 451,243 participants of European descent (aged 40 to 70 years) from the UK Biobank. Data were available on prevalent and incident adverse health outcomes from baseline questionnaires and from up to 9.4 years hospital inpatient follow-up (mean 7 years). Participants also reported baseline dietary supplement use. We tested associations between p.C282Y homozygosity, prevalent and incident outcomes, and iron supplement use, using logistic regression and Cox proportional hazard regression, adjusted for age, sex, genotyping array type and genetic principal components.

Results 2,890 participants were p.C282Y homozygotes (0.6%, or 1/156), of whom 7.3% (210/2890) had haemochromatosis diagnosed at baseline, increasing to 15.1% (437/2890) by the end of follow-up. P.C282Y homozygotes had substantial excess prevalent and incident morbidity including haemochromatosis, liver disease, arthritis and diabetes compared to those with no mutations (combined measure of excess incident morbidity; men, HR: 3.37, 95% CI: 2.87–3.97; women, HR: 2.99,95% CI: 2.51–3.55). A sub-analysis of 200,975 older participants (aged 60–70 years) showed that both male and female p. C282Y homozygotes also had an increased likelihood of Fried frailty and chronic pain.

In p.C282Y homozygotes undiagnosed with haemochromatosis, the intake of iron supplements or multivitamins increased the likelihood of frailty (OR: 2.15, 95% CI: 1.22–3.77) and incident osteoarthritis (HR: 1.86, 95% CI: 1.02–3.41)

Conclusion In a large community volunteer sample, *HFE* p. C282Y homozygosity was associated with substantial excess morbidity, frailty and chronic pain in both men and women. In p.C282Y homozygotes undiagnosed with haemochromatosis, taking iron supplements or multivitamins was an additional risk factor for developing morbidity, including frailty and osteoarthritis. Since the p.C282Y associated iron overload can be prevented and treated, these findings suggest there is a need for expanded case finding and screening for hereditary haemochromatosis. It also suggests that warnings and controls on iron containing supplements may be needed.

OP38 PREDICTING THE RISK OF CHILDHOOD OVERWEIGHT AND OBESITY AT 4–5 YEARS USING PREGNANCY AND EARLY LIFE HEALTHCARE DATA

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Background In England, 9.5% of children aged 4–5 years and 20.1% aged 10–11 years are obese, with the prevalence in the most deprived areas being more than twice as that in the least deprived. There is evidence illustrating the developmental origins of obesity, but it focuses on individual risk factors and comes mostly from research birth cohorts which are not necessarily representative of the wider population. There is no system-based early identification of childhood obesity risk at pregnancy stage and onwards.The aim was to develop and validate a risk identification system for childhood obesity using existing routinely collected maternal and early-life population-level healthcare data in Hampshire.

Methods Studying Lifecourse Obesity PrEdictors (SLOPE) study is an anonymised population-based linked cohort of maternal antenatal and delivery records for all births taking place at University Hospital Southampton 2003–2018, and child health records including information on postnatal growth, type of feeding and childhood body mass index (BMI) up to 14 years. Childhood age- and sex- adjusted BMI at 4–5 years was used to define the outcome of overweight and obesity in the models. Logistic regression models together with multivariable fractional polynomials were used to select model predictors and to identify transformations of continuous predictors that best predict the outcome. Predictive accuracy was evaluated by assessing model discrimination and calibration.

Results Childhood BMI was available for approximately 30000 children aged 4–5 years (9% obese). Models were developed in stages, incorporating data collected at first antenatal booking appointment, birth and early life predictors. The area under the curve (AUC) was lowest (0.64) for the model only incorporating maternal predictors from the booking appointment and highest for the model incorporating all factors up to weight at 2 years for predicting outcome at 4–5 years (0.82 for overweight and obesity and 0.89 for obesity excluding overweight). Maternal predictors included BMI, smoking status at first antenatal appointment, age and ethnicity. Early life predictors included birthweight, gender, breastfeeding and weight at 1 or 2 years of age. Although AUC was lower for the booking models, maternal predictors remained consistent across the models, thus high-risk groups could be identified at an early stage with more precise estimation as the child grows.

Conclusion This prediction modelling can be used to identify and quantify clustering of risk for childhood obesity as early as the first trimester of pregnancy, and can strengthen the long-term preventive element of antenatal and early years care.

OP39 DEVELOPMENT OF A SHORT FOOD FREQUENCY QUESTIONNAIRE TO ASSESS DIET QUALITY IN POPULATION STUDIES

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Background Food frequency questionnaires (FFQs) are a popular tool in nutritional epidemiology, enabling estimates of habitual diet in large populations, but are time-consuming to complete. There is an increasing need for a short, accurate dietary tool that characterises healthy dietary patterns for use in observational and interventional research.

Methods The National Diet and Nutrition Survey (NDNS) is a general population national survey. Randomly-selected