Name	**The Netherlands Epidemiology of Obesity/ De Nederlandse Epidemiologie van Obesitas (NEO) study**
Description	The NEO study is a prospective, population-based cohort study aimed at investigating pathways leading to obesity-related conditions
Location	Leiden
Lead Institute	Leiden University Medical Centre
Cohort size	6,671 men and women aged 45-65 years, with an oversampling of individuals with a BMI>27 kg/m^2
Start Cohort	Inclusion period 2008-2012
Follow-up	2012 onwards
Variables and Measurement methods	A diverse range of measurements was performed in the NEO study (*see* https://www.lumc.nl/sub/5041/att/1429619 *for complete overview*), questionnaires, urine samples, overview of all medication, medical history, physical examination and blood samples. Blood samples were collected in both the fasting state and after a liquid mixed meal. In addition, several more advanced measurements were performed in subgroups including: • Abdominal fat (subcutaneous and visceral, MRI) • Aortic pulse wave velocity (MRI) • Cardiac function (MRI) • Knee osteoarthritis (knee MRI and questionnaire (KOOS)) • Hepatic triglyceride content measurements by proton-magnetic resonance spectroscopy (^{1}H-MRS) • Indirect calorimetry • Dual-energy X-ray absorptiometry (DEXA-scan) • Actigraphy (ActiWatch) • Accelerometry (Actiheart) • Heart rate variability measurements (Actiheart) • Sidestream darkfield (SDF) imaging of the glycocalyx
Availability and Type of -omic data	Genomic • Illumina HumanCoreExome (n=5,744). Genetic variants from 1000 genome (1KG) project imputation. Illumina HumanCoreExome array contains 547,644 directly genotyped variants, which are composed of all the tag SNPs found on the Illumina HumanCore BeadChip and >240,000 markers on the HumanExome BeadChip which specifically covers exonic regions. Metabolomic data: • Nightingale Health Metabolomics platform in all participants (N = 6,671) • Metabolon Discovery HD4 platform in N = 599 • Biocrates AbsoluteIDQ™p150 kit in N = 526 No Methylation, Transcriptomics, Proteomics, Microbiome
Design paper	De Mutsert et al. 2013
website	www.lumc.nl/org/neo-studie/