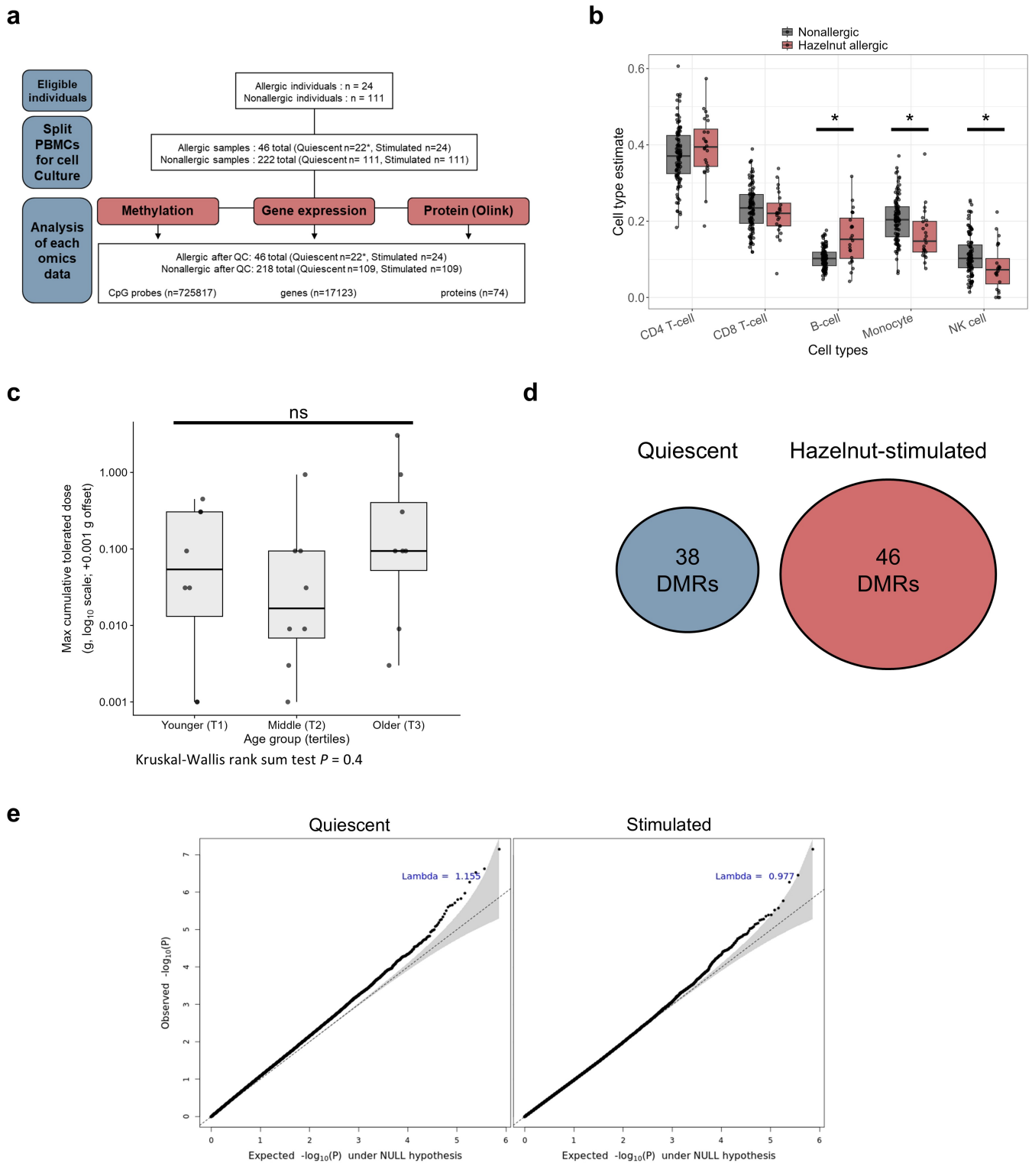


Figure E1 Overview of the cohort and samples, estimated cell composition, association analysis of age and OFC eliciting dose, and case-control methylation DMR and genomic inflation data (a) Flow diagram illustrating differences between “individual” and “sample” numbers during the workflow. * indicates a loss of two samples due to low cell number after thawing. In such cases, the stimulated cell culture conditions were prioritised and there were fewer quiescent samples. (b) Estimated cell composition using DNA methylation data. Significance determined by a Wilcoxon rank-sum test between hazelnut allergic and nonallergic groups is denoted by asterisks ($P < 0.05$). (c) Relationship between age and the maximum tolerated dose during OFC in the allergic cohort. Age was stratified into tertiles. For plotting and statistical purposes, the maximum tolerated dose was converted to a logarithmic scale (log10). The dose 0 grams was offset to 0.001g to allow for successful conversion. (d) Number of DMRs detected in each analysis. Overlapping DMRs not show. (e) Quantile-quantile (QQ) plot showing the observed versus expected p-values of the DNA methylation analysis for the quiescent (left) and stimulated (right) probes. OFC = oral food challenge; QC = quality control; DMR = differentially methylated region.