

Figure S7.1 . PCA organisation of transcript data (41780 features) after PC1 (46%) and PC 2 (26%).

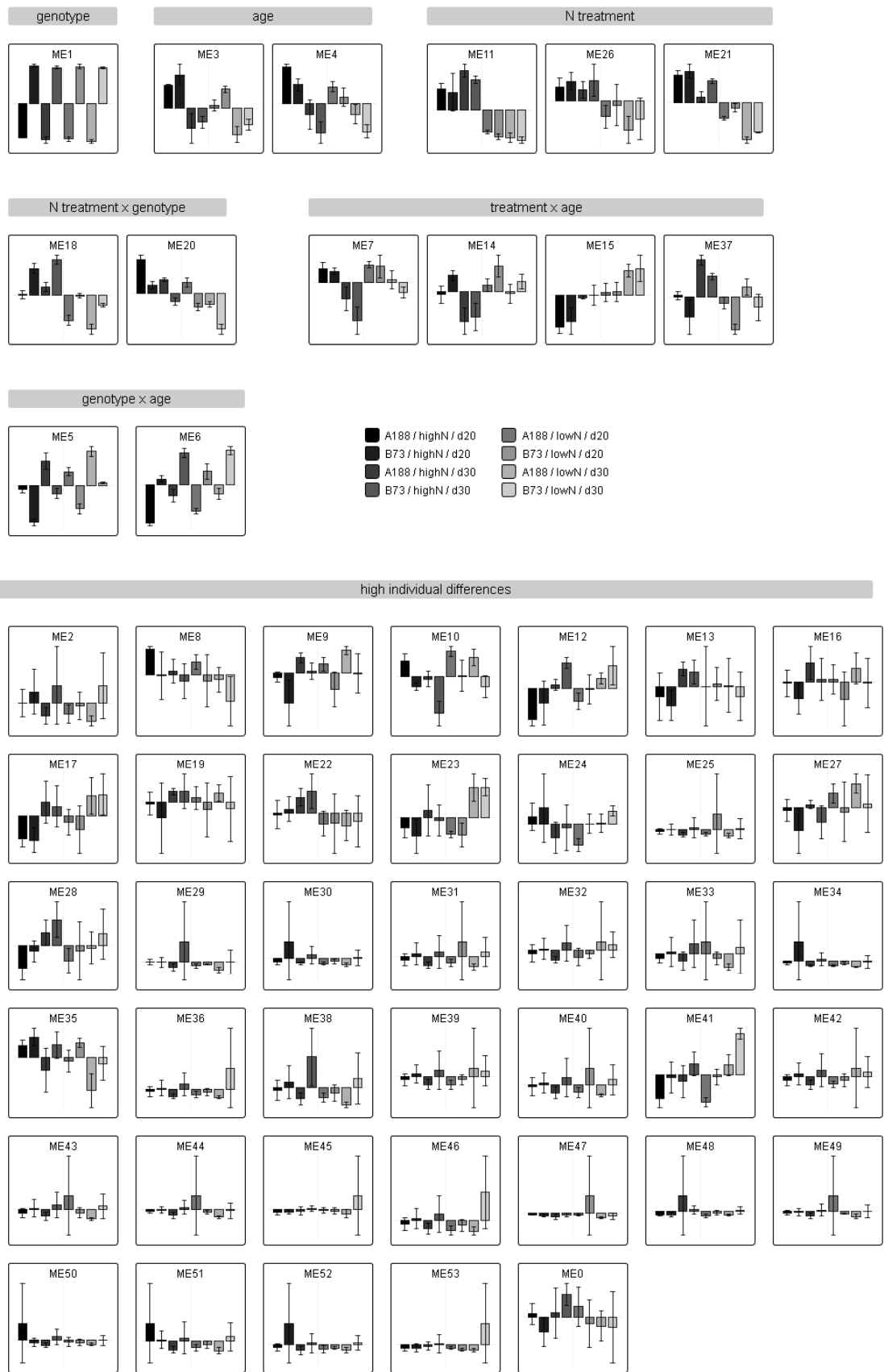


Figure S7.2. Overview of expression pattern in ME modules (eigengene). The modules are sorted according to influence by experimental parameter: N treatment, age and genotype. Module pattern were calculated using WGCNA of individual sample, graphs show average data from 4 replicats.