Kemp et al Fig S1

Figure S2. The effect of surgery on GDF-15 in the circulation of wasting and non-wasting patients.
Surgery increased GDF-15 in both wasting and non-wasting patients with maximal GDF-15 found on day 1.
Circulating GDF-15 was higher at all time points in wasting patients compared to non-wasting patients .

Figure S2

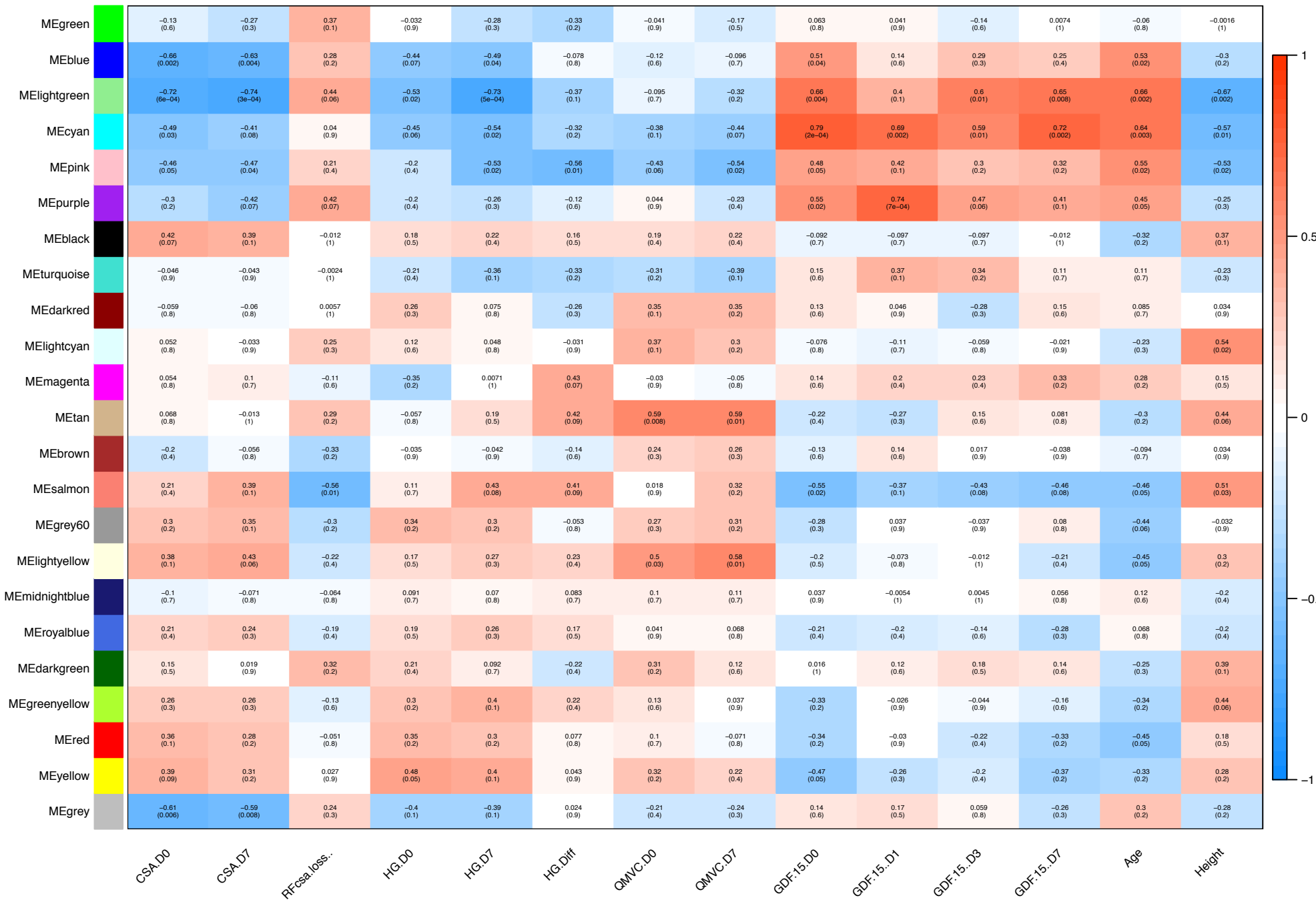**biweight correlation module trait relationships day 0**

Figure S3. Whole genome co-expression network analysis (WGCNA) of plasma metabolites before surgery. Day 0 plasma metabolite levels were grouped using WGCNA then compared with physiological parameters and circulating GDF-15 levels (quantified by ELISA. Red demonstrates positive correlation and blue shows negative correlation. R and p Values calculated using robust biweight mid-correlation are shown in the appropriate box.

Figure S3

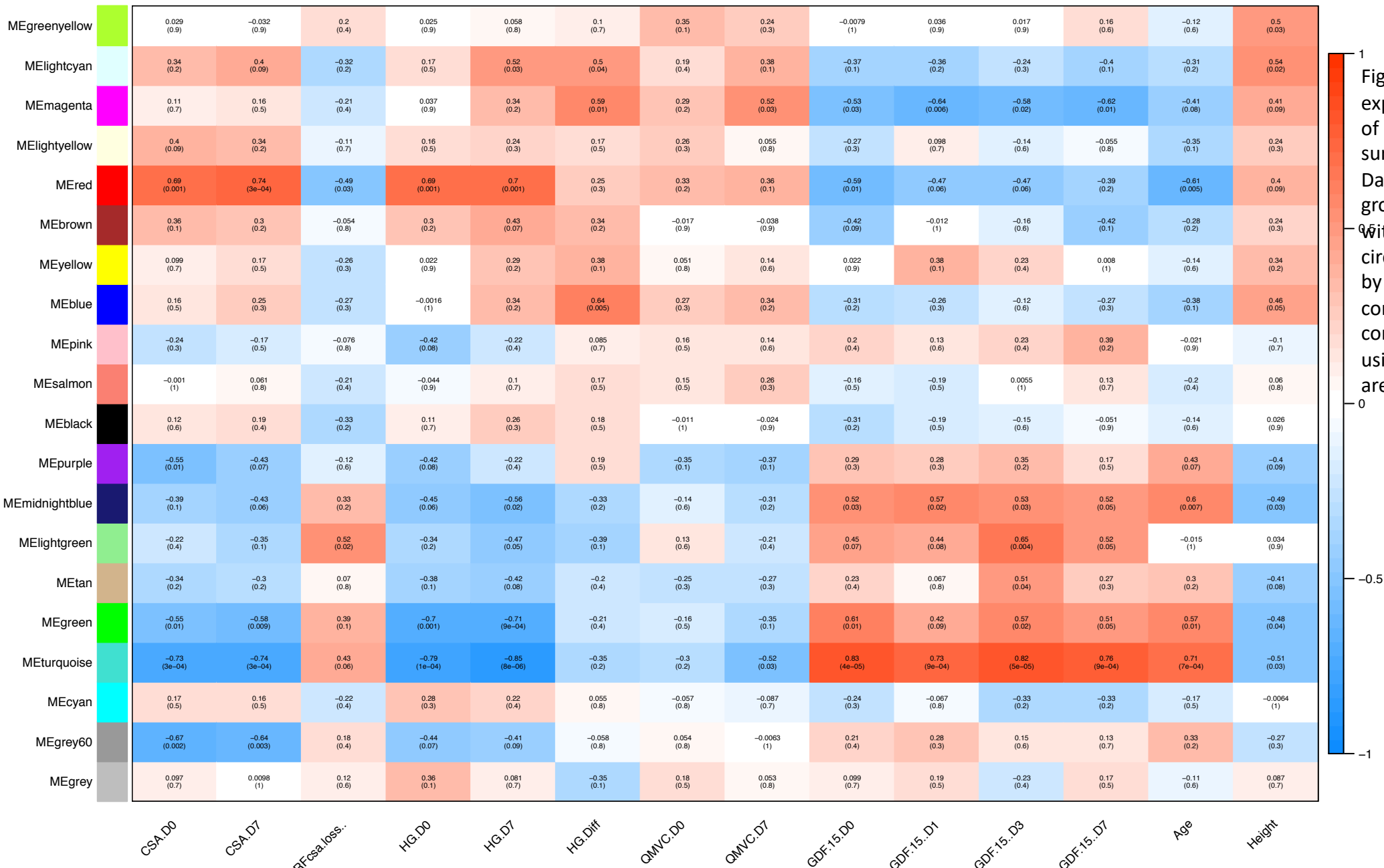# biweight correlation module trait relationships day 1

Figure S4. Whole genome co-expression network analysis (WGCNA) of plasma metabolites 1 day after surgery.
Day 1 plasma metabolite levels were grouped using WGCNA then compared with physiological parameters and circulating GDF-15 levels (quantified by ELISA. Red demonstrates positive correlation and blue shows negative correlation. R and p Values calculated using robust biweight mid-correlation are shown in the appropriate box.

Figure S4

biweight correlation module trait relationships day 3
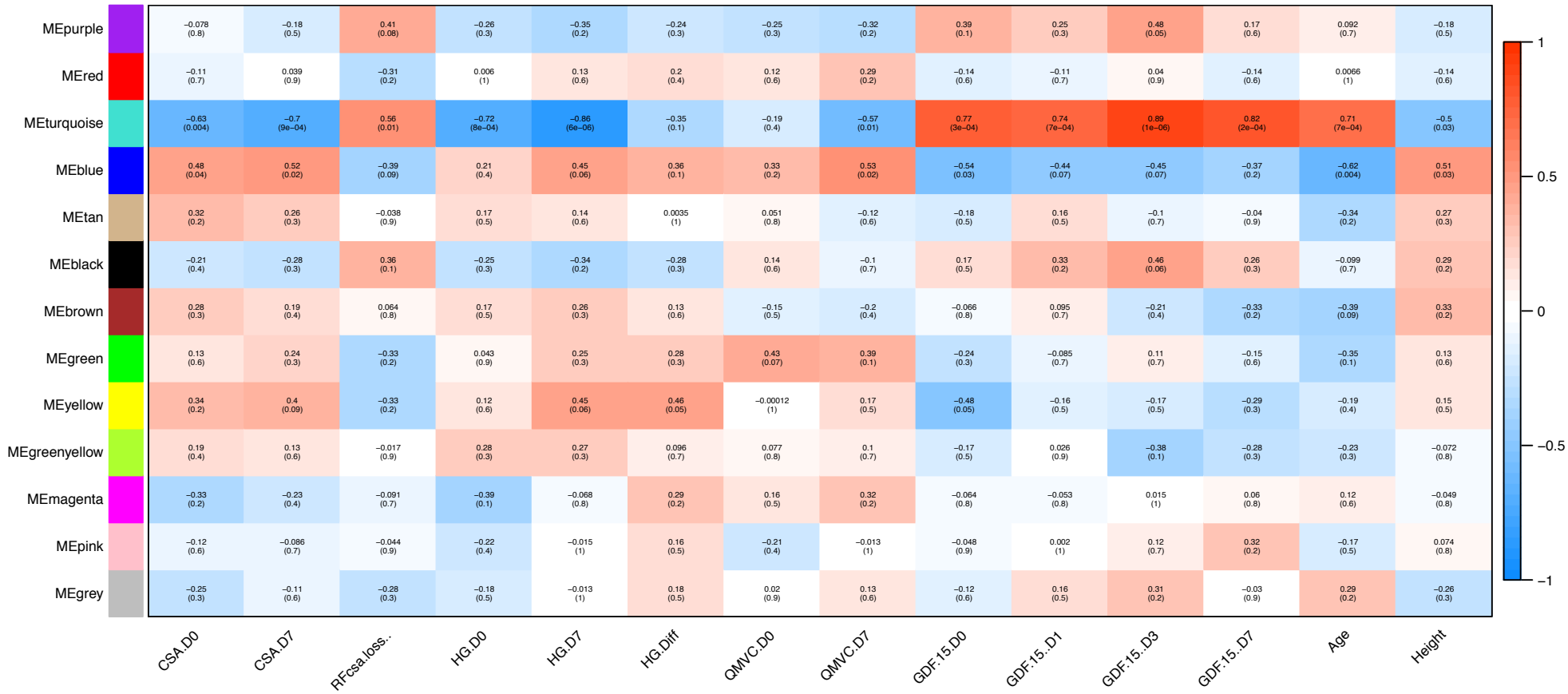
Figure S5. Whole genome co-expression network analysis (WGCNA) of plasma metabolites 3 days after surgery.

Day 3 plasma metabolite levels were grouped using WGCNA then compared with physiological parameters and circulating GDF-15 levels (quantified by ELISA. Red demonstrates positive correlation and blue shows negative correlation. R and p Values calculated using robust biweight mid-correlation are shown in the appropriate box.

Figure S5

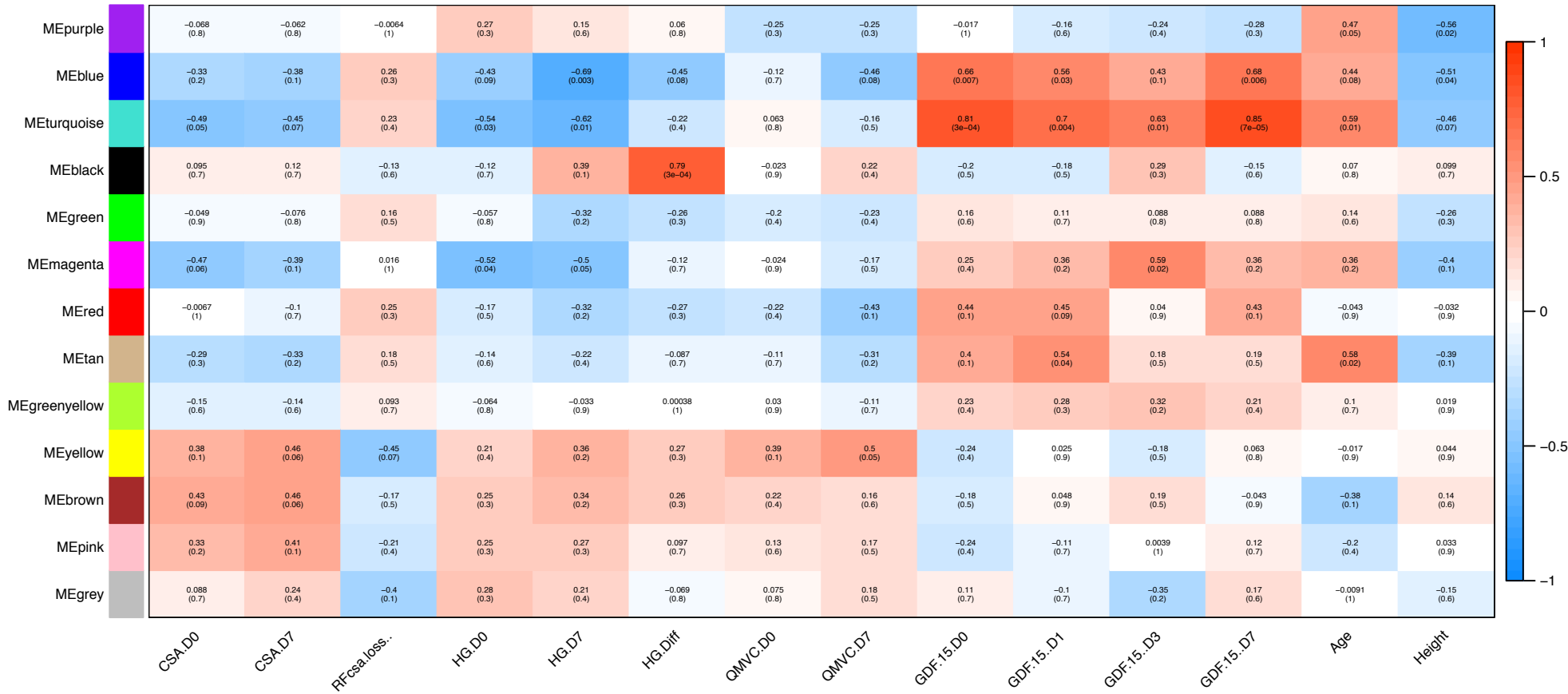**biweight correlation module trait relationships day 7**

Figure S6. Whole genome co-expression network analysis (WGCNA) of plasma metabolites 7 days after surgery.
Day 7 plasma metabolite levels were grouped using WGCNA then compared with physiological parameters and circulating GDF-15 levels (quantified by ELISA. Red demonstrates positive correlation and blue shows negative correlation. R and p Values calculated using robust biweight mid-correlation are shown in the appropriate box.
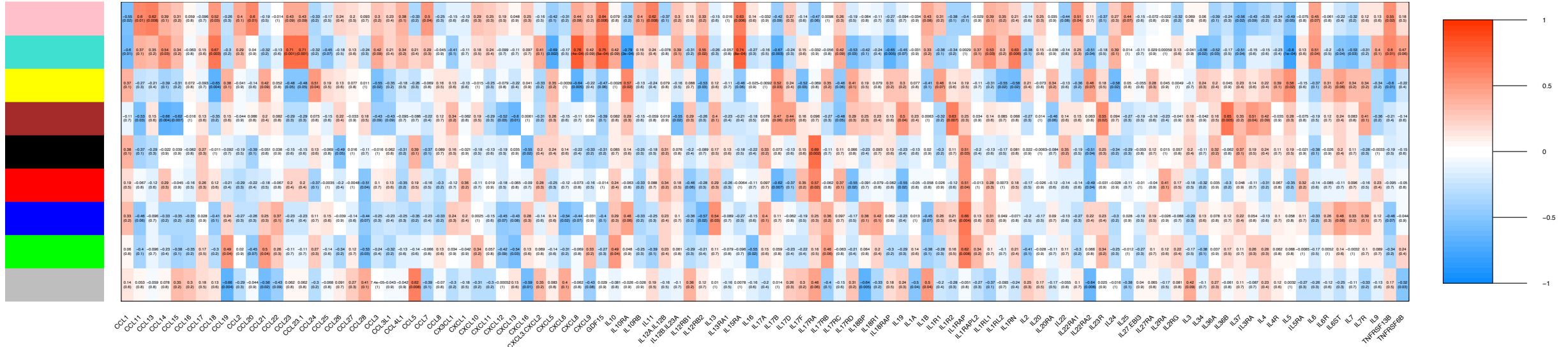
Figure S6

Figure S7. Whole genome co-expression network analysis (WGCNA) of plasma metabolites 1 day after surgery compared to plasma cytokines on the same day and their receptors.

Day 1 plasma metabolite levels were grouped using WGCNA then compared with circulating cytokines quantified by Somascan assay.. Red demonstrates positive correlation and blue shows negative correlation. R and p Values calculated using robust biweight mid-correlation are shown in the appropriate box.

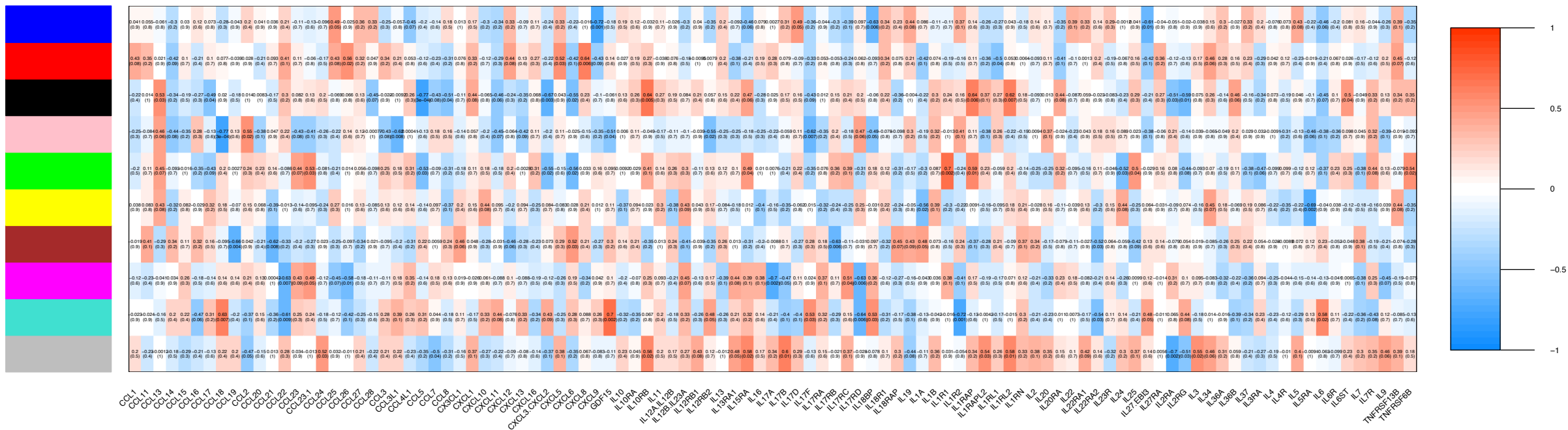Figure S7

biweight correlation module trait rels

Figure S8. Whole genome co-expression network analysis (WGCNA) of plasma metabolites before surgery compared to plasma cytokines on the same day and their receptors.

Day 0 plasma metabolite levels were grouped using WGCNA then compared with circulating cytokines quantified by Somascan assay.. Red demonstrates positive correlation and blue shows negative correlation. R and p Values calculated using robust biweight mid-correlation are shown in the appropriate box.

Figure S8