

The human gut microbiota contributes to Type-2 Diabetes non-resolution 5-years after Roux-en-Y gastric bypass

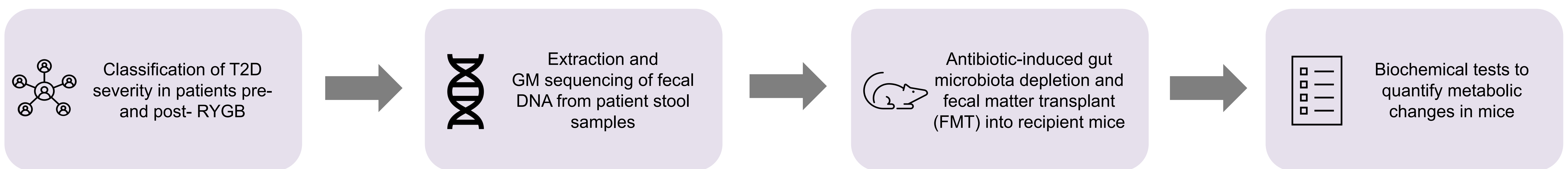
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Introduction

Despite persistent public health efforts, the prevalence of obesity, and associated co-morbidities like type 2 diabetes mellitus (T2DM), have remained on the rise globally¹. Bariatric surgery refers to a collection of surgical procedures performed to manage obesity². For most cases of severe obesity, it is currently the only intervention that can cause major and prolonged weight loss, while improving all obesity related co-morbidities³. However, only 50-60% of bariatric surgery patients undergo T2DM remission (DR) following bariatric surgery⁴. A few parameters have been proposed to predict the likelihood of DR like T2DM severity, and diabetes duration. However, these are not reliably accurate⁵. Some studies have shown that the gut microbiome might have some association with DR rates⁶.

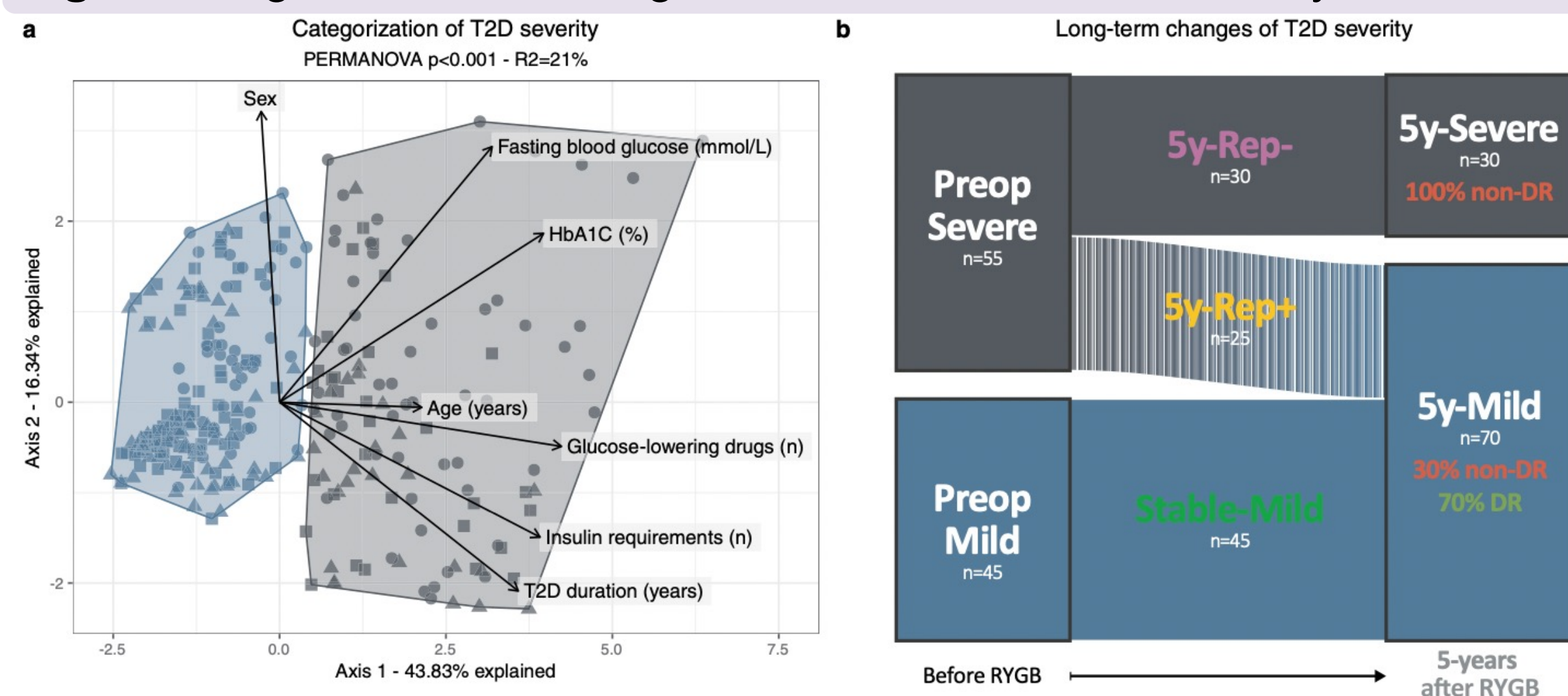
The aim of this study is to support the hypothesis that the gut microbiome can cause metabolic changes in patients that have undergone Roux-en-Y gastric bypass (RYGB), a type of bariatric surgery.

Methods



Results

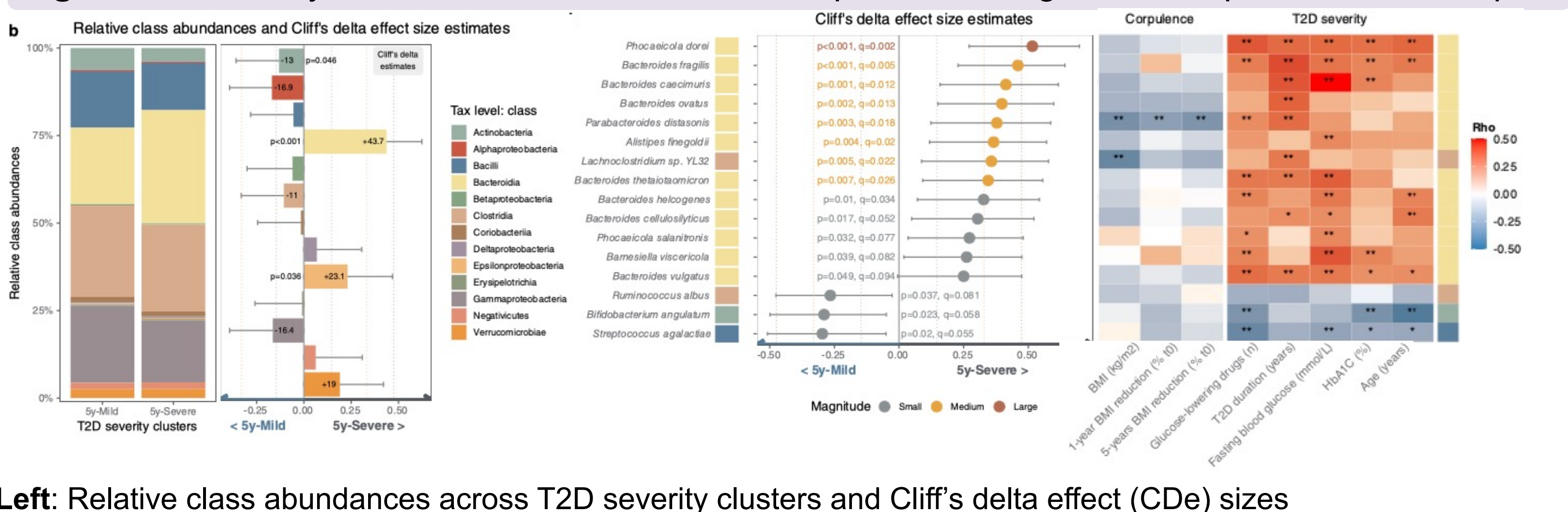
Fig 1: Categorization and long-term evolution of T2D severity after RYGB



Left: Patients' principal component analysis (PCA) projection according to their T2D severity (mild – blue, severe – grey) at all time points (● initial, ▲ 1y, ■ 5y). Arrows show association between clinical variables and T2D severity.

Right: Long-term trajectories of T2D severity and association with long-term DR. Rep+, good responders; Rep-, poor responders

Fig 2: T2D severity after RYGB is associated with specific GM signatures in patient stool samples

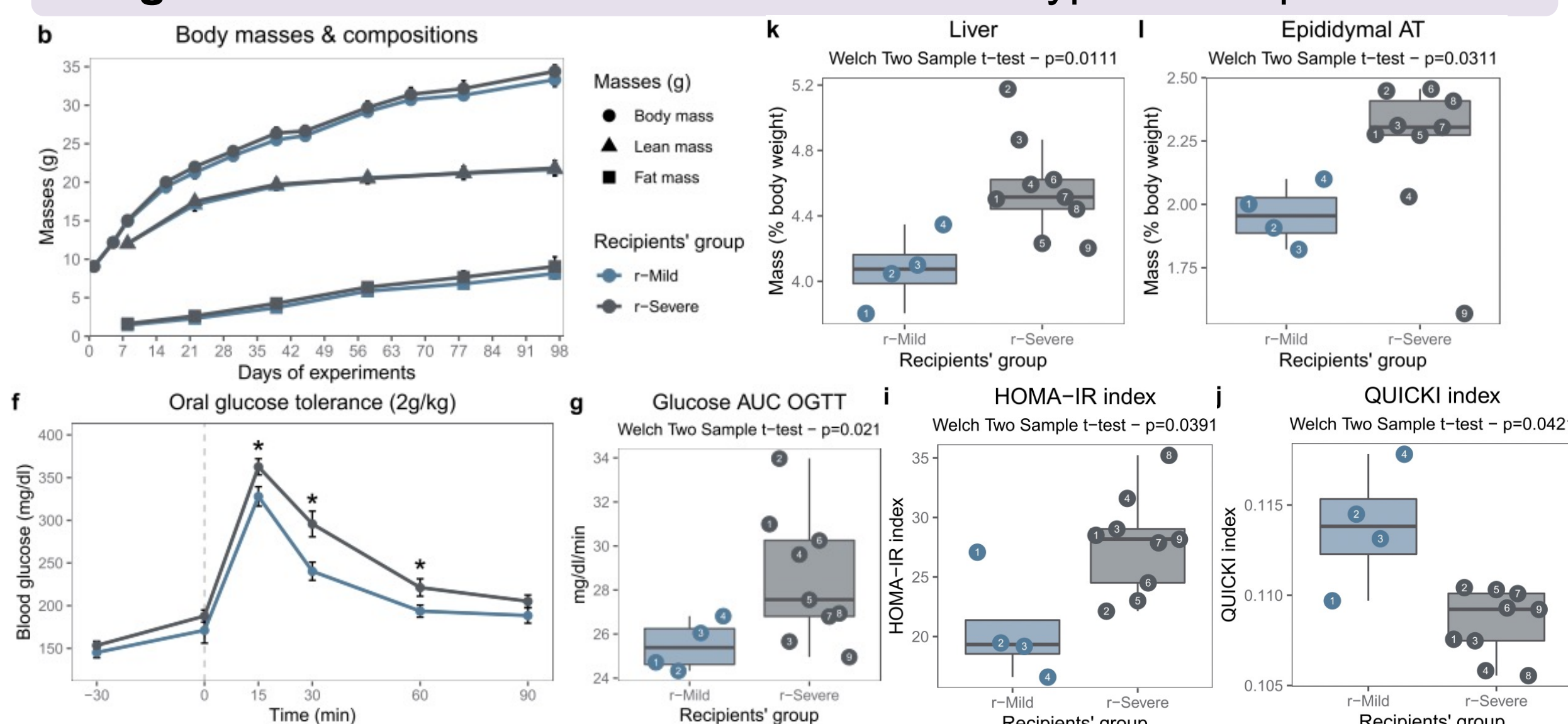


Left: Relative class abundances across T2D severity clusters and Cliff's delta effect (CDe) sizes

Middle: CDe size estimates, showing 13 bacterial genera were significantly more prevalent in 5y-Severe patients (most from *Bacteroides* class), 3 species were more abundant in 5y-Mild patients

Right: Heatmap of Spearman's rank correlations between the 16 species and 5-year clinical variables (*: $p < 0.05$; **: $q < 0.1$), showing association between bacterial species and altered metabolism, related to corpulence and T2D severity

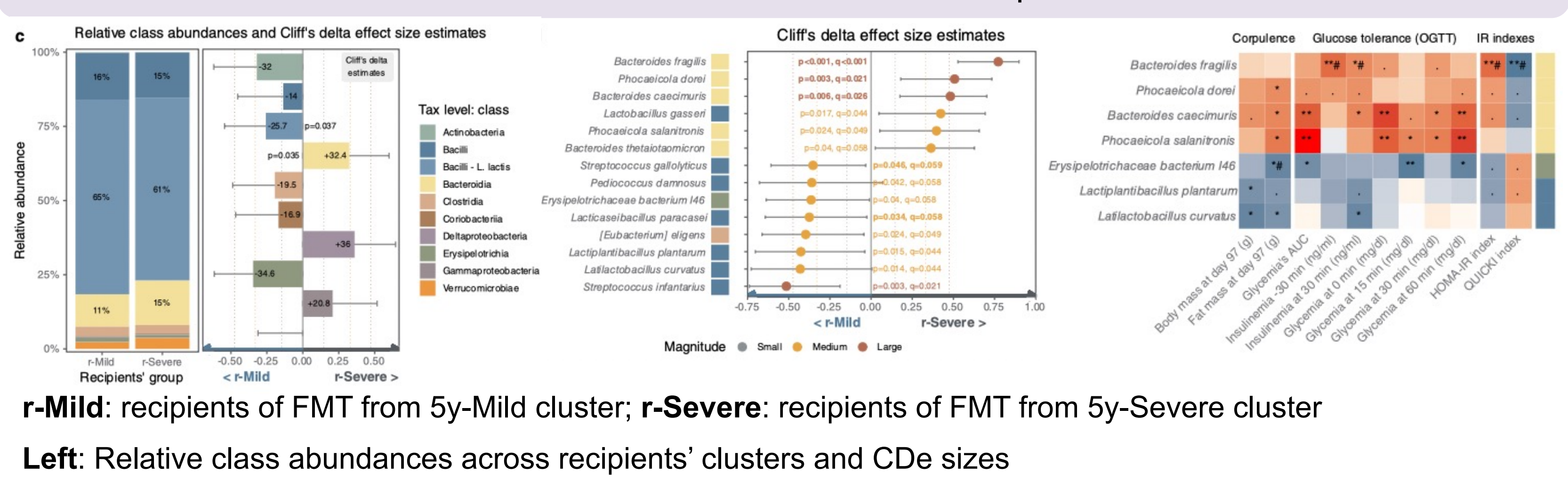
Fig 3: FMT-induced Altered Metabolic Phenotype in Recipient Mice



b: Body masses & compositions; **k:** Liver mass; **l:** Epididymal Adipose Tissue, showing that the body mass and fat mass of the r-Severe group significantly increased more than r-Mild group, indicating **higher corpulence**

f: Blood Glucose Levels during OGTT; **g:** Area under Curve of OGTT; **i:** HOMA-IR index; **j:** QUICKI index, showing that r-Severe group has significantly **poorer glucose tolerance** and is significantly **more insulin resistant** than r-Mild group

Fig 4: Bacterial species from class *Bacteroidia* associated with increased corpulence, glucose intolerance and insulin resistance in recipient mice



r-Mild: recipients of FMT from 5y-Mild cluster; **r-Severe:** recipients of FMT from 5y-Severe cluster

Left: Relative class abundances across recipients' clusters and CDe sizes

Middle: CDe size estimates, showing 8 bacterial species were more prevalent in r-Mild animals (CDe<0), and 6 species in r-Severe animals (CDe>0), of which 5 species belonged to the class *Bacteroidia* and were also more prevalent in humans from the 5y-Severe cluster

Right: Heatmap of Spearman's rank correlations between 6 species and animal's phenotypic variables (*: $p < .05$; **: $q < 0.1$), showing association between bacterial species and altered metabolism, related to corpulence, glucose intolerance (OGTT) and insulin resistance (IR indices)

Key findings

- The *Bacteroidia* class of bacteria was associated with greater T2DM severity and alterations of glucose homeostasis markers.
- The gut microbiome (GM) of good metabolic responders was like that of Stable-Mild patients, suggesting that post RYGB metabolic improvements could be attributed to a partial restoration of a "Mild" GM profile.
- The hallmark GM changes associated with T2DM severity were partially transmittable in mice via FMT and resulted in a change in the recipient mice's metabolism.
- Following transplantation, there were strong similarities between donors and recipient mice's phenotypes, as well as bacterial abundances. This suggests that there is partial involvement of the GM in T2DM severity and persistence after RYGB.

Implications of findings

- Considering that the GM composition plays a role in post bariatric surgery DR, modulating the GM composition, on top of existing therapies, could improve outcomes for post-RYGB patients dramatically.
- However, more studies have to be done to validate the efficacy of GM modulation in reducing DR in post bariatric surgery patients.
- Therefore, a future research question could be whether modulating the GM composition in post bariatric surgery patients could reduce DR rates more significantly compared to conventional therapies.

Conclusion

This study concludes that GM contributes to long-term T2D persistence and severity after RYGB.

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