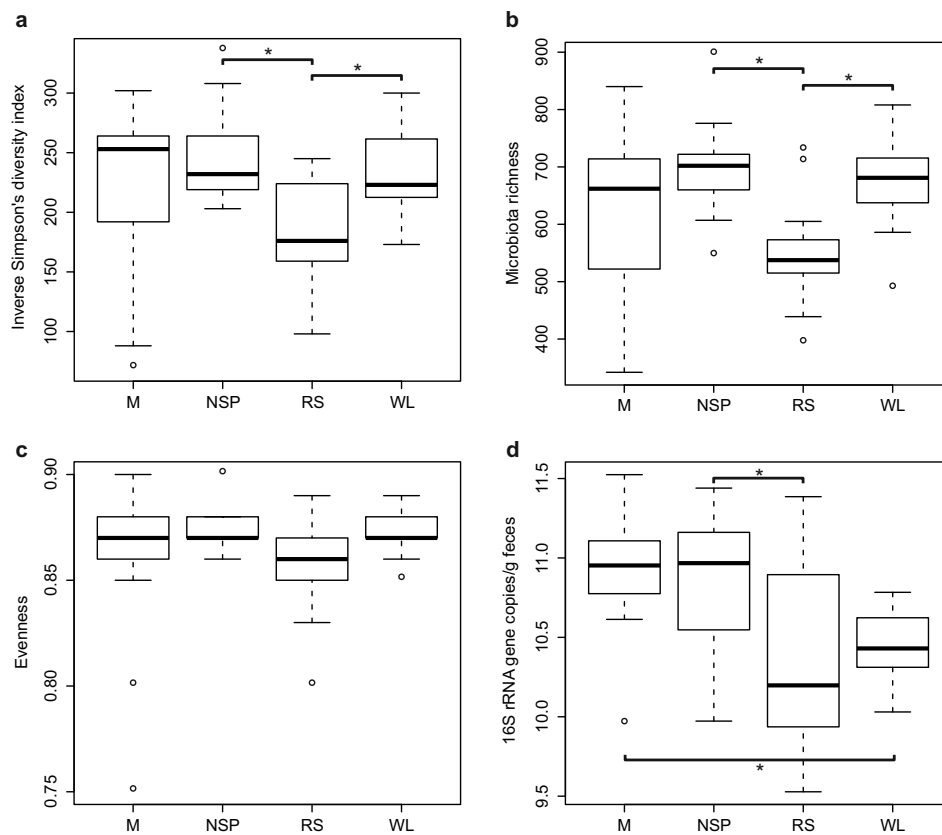
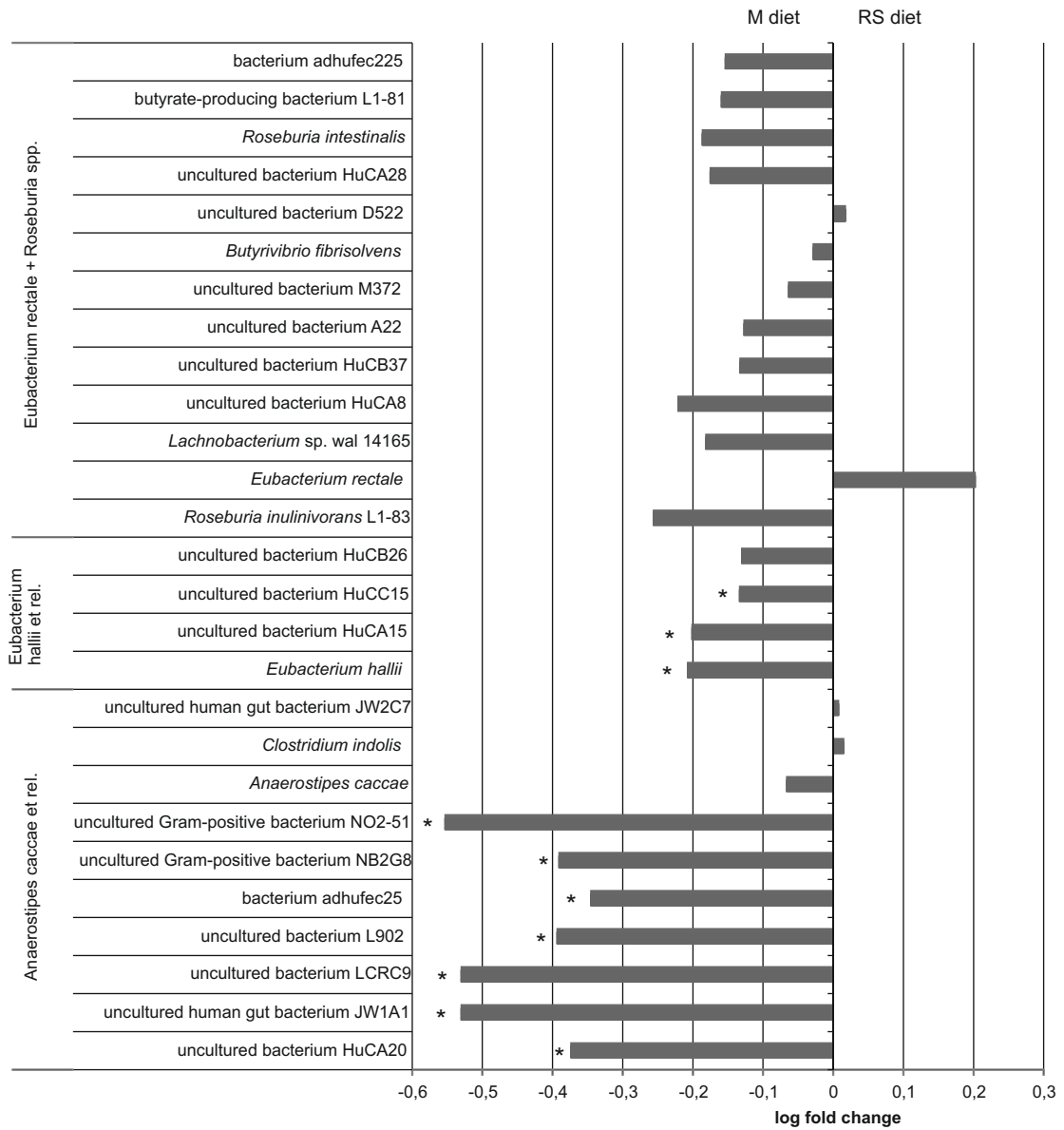


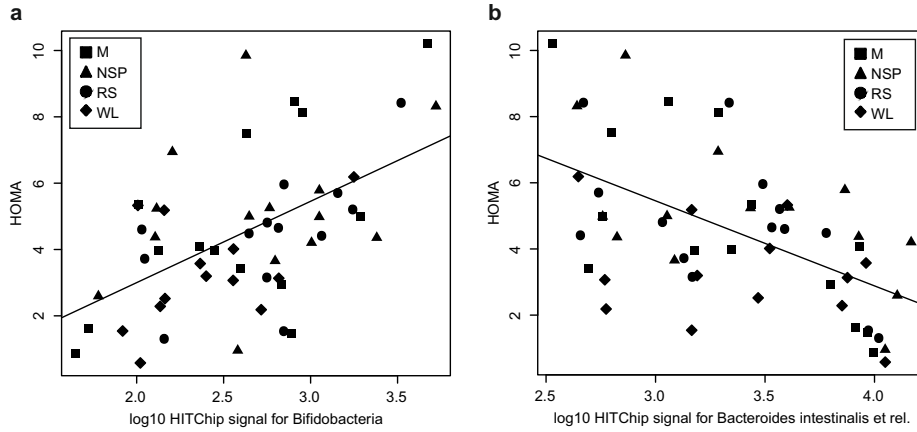
Supplementary Figures 2-6



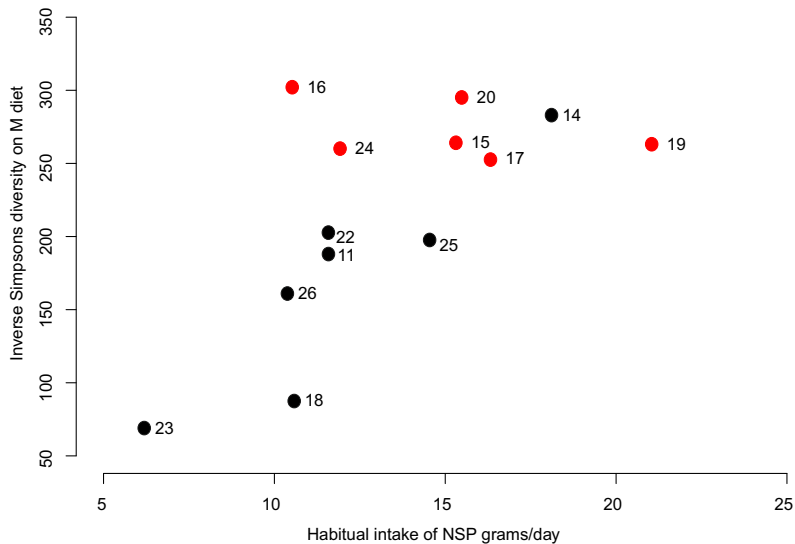
Supplementary Figure S2. Diversity and biomass of the microbiota during dietary shifts. Diversity (a), richness (b) evenness (c) of the microbiota, and the number of total bacteria (d) during different diets. For (d), qPCR data obtained for the last two weeks of each diet (Walker *et al.* (2011) were recalculated here to estimate the counts for bacterial 16S rRNA gene. The boxes extend from 25th percentile to 75th percentile, with a line at the median; the whiskers extent to the highest and lowest values. Diets with statistically significant ($p < 0.05$) difference are indicated with star.



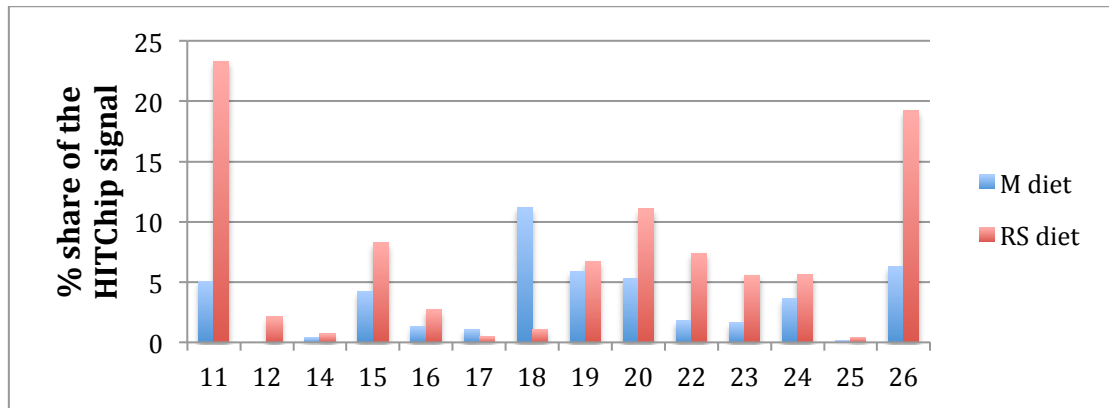
Supplementary Figure S3. Phylotype-level HITChip analysis of bacteria related to *Roseburia intestinalis*, *Eubacterium rectale*, *Eubacterium hallii* and *Anaerostipes caccae* during the RS diet compared to M diet. Stars indicate phylotypes with significant decrease during the RS diet (q-values < 0.05).



Supplementary Figure S4. Significant associations between homeostasis model assessment of insulin resistance (HOMA) and the abundance of a) bifidobacteria and b) bacteria related to *Bacteroides intestinalis*, as detected with HITChip microarray.



Supplementary Figure S5. Associations between the responder status (color), microbiota diversity during the M diet (y-axis), and the habitual intake of NSP fiber (x-axis). The responders are printed in black and non-responders with red, and each volunteer specified by number.



Supplementary Figure S6. Relative abundance of bacteria related to *R. bromii* in the study participants during the M and RS diets as measured with the HITChip microarray. Subject 13 lacked the M-sample. As previously reported based on qPCR (Walker *et al.* 2011), subjects 14 and 25 harboured the lowest levels of R-ruminococci. Both methods target *R. bromii*, the most abundant species of this group, but otherwise slightly differ in their 16S rRNA targets: the HITChip signal derives from *R. bromii* and six related uncultured phylotypes; (uncultured bacterium HuCB2 AJ408987, uncultured bacterium clone Eldhufec230 AY920105, uncultured bacterium clone Eldhufec291 AY920166, uncultured bacterium clone Eldhufec225 AY920100, uncultured bacterium clone Eldhufec291 AY920166, uncultured bacterium cadhufec021h7 AF530298, uncultured bacterium Adhufec014rbh AY471694 (Rajilić-Stojanović *et al.* 2009), while the qPCR primers target six *Ruminococcus* spp. listed in Table S2B.