Supplementary Figure 3. Impact of age, MOD and fS100A8-A9 on gut metabolic pathway abundances in healthy term infants (related to Figure 2). Abundances of pathways involved in the metabolism of SCFAs were predicted based on 16S rRNA gene sequencing data determined in 240 stool samples collected from 72 human term babies (day 30: n=63, day 90: n=59, day 180: n=62, day 360: n=56). Cuneiform plot (marker direction and hue shows effect direction, marker intensity effect size) of pathway abundances significantly (Spearman or MWU FDR <.1, nested model test FDR <.1) and strongly (absolute Spearman rho or Cliff's delta effect size >.2) impacted by age, MOD or fS100A8-A9 across infancy, when adjusting (nested mixed effects model comparison) for each of the other two variables. Bold markers fulfil significance criteria, gray-edged markers do not and are shown for comparison only