

**Supplementary Table 1** Pearson's correlation between the concentration of metabolites (SCFAs, BCFAs and ammonia) in feces and the top 25 most abundant genus in fecal microbiota. Significant correlations were noted by \* ( $P < 0.05$ ) and \*\* ( $P < 0.01$ )

| Genus                               | Acetate | Propionate | Butyrate | Iso-butyrate | Iso-valerate | Ammonia |
|-------------------------------------|---------|------------|----------|--------------|--------------|---------|
| <i>Megamonas</i>                    | -.427*  | .486*      | -.259    | -.197        | -.080        | .235    |
| <i>Allobaculum</i>                  | .061    | -.374      | .140     | .341         | .109         | -.160   |
| <i>Collinsella</i>                  | -.126   | .165       | -.035    | -.118        | .100         | .232    |
| <i>Prevotella_9</i>                 | -.106   | .217       | -.113    | -.015        | .143         | .358    |
| <i>Anaerovibrio</i>                 | -.262   | .173       | -.213    | -.224        | -.139        | .035    |
| <i>Bacteroides</i>                  | .351    | -.178      | .030     | -.225        | -.380        | -.383   |
| <i>Succinivibrio</i>                | -.142   | -.055      | .470*    | .450*        | .558**       | .343    |
| <i>Blautia</i>                      | .515*   | -.051      | -.009    | .018         | .080         | .142    |
| <i>Holdemanella</i>                 | -.046   | -.335      | .068     | .011         | -.015        | -.235   |
| <i>Alloprevotella</i>               | -.116   | .162       | -.194    | -.074        | -.105        | -.191   |
| <i>Phascolarctobacterium</i>        | .235    | .123       | .021     | .211         | .361         | .341    |
| <i>Escherichia-Shigella</i>         | .397    | -.446*     | .023     | -.249        | -.305        | -.208   |
| <i>Clostridium_sensu_stricto_1</i>  | .114    | -.291      | .176     | .075         | -.157        | -.281   |
| <i>Ruminiclostridium_9</i>          | .085    | -.251      | .158     | -.060        | -.194        | -.372   |
| <i>Fusobacterium</i>                | .331    | -.125      | .055     | -.099        | -.211        | -.206   |
| <i>Lachnoclostridium</i>            | -.051   | .085       | .133     | -.047        | .040         | -.040   |
| <i>Lactobacillus</i>                | .319    | -.221      | .108     | .163         | -.134        | -.345   |
| <i>unidentified_Ruminococcaceae</i> | .202    | -.197      | .061     | -.044        | -.127        | -.276   |
| <i>Parabacteroides</i>              | .189    | -.241      | .064     | -.301        | -.352        | -.220   |
| <i>Romboutsia</i>                   | .519*   | -.390      | .007     | -.273        | -.366        | -.263   |
| <i>unidentified_Lachnospiraceae</i> | -.050   | .116       | -.117    | .041         | .116         | -.023   |
| <i>Lachnospiraceae_UCG-006</i>      | .083    | -.153      | .082     | -.045        | -.158        | -.320   |
| <i>Rikenellaceae_RC9_gut_group</i>  | .413*   | .004       | .154     | -.049        | -.124        | -.214   |
| <i>Streptococcus</i>                | .258    | -.554**    | .084     | -.109        | -.276        | -.379   |