

Table S1 qRT-PCR results for bovine rotavirus detection in individual calve feces

| Animal no. | Day – 3 | | Day + 1 | | Day + 7 | |
|------------|-----------------------|-----|----------|-----|----------|-----|
| | ¹ Ct value | P/N | Ct value | P/N | Ct value | P/N |
| Healthy 1 | > 35 | - | > 35 | - | > 35 | - |
| Healthy 2 | > 35 | - | > 35 | - | > 35 | - |
| Healthy 3 | > 35 | - | > 35 | - | > 35 | - |
| Rota 1 | > 35 | - | 26.9 | + | 29.3 | + |
| Rota 2 | > 35 | - | 32.2 | + | 34.9 | + |
| Rota 3 | > 35 | - | 24.9 | + | 25.1 | + |

Day – 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

¹Ct value >35 is negative.

Table S2 Individual calves fecal consistency scores in Healthy and Rota groups

| Animal no. | Day – 3 | Day + 1 | Day + 7 |
|------------|---------|---------|---------|
| Healthy 1 | 0 | 1 | 1 |
| Healthy 2 | 1 | 1 | 1 |
| Healthy 3 | 0 | 1 | 1 |
| Rota 1 | 1 | 2 | 2 |
| Rota 2 | 1 | 2 | 3 |
| Rota 3 | 1 | 3 | 3 |

Day – 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

Table S3. Relative abundance ($\geq 0.1\%$) of fecal bacterial phyla, families, and genera between Healthy and Rota groups three days before inoculation

| Measurements | Relative abundance (%) | | SEM | <i>p</i> Value |
|------------------------------------|------------------------|------|------|----------------|
| | Healthy | Rota | | |
| Day – 3 Phyla | | | | |
| Firmicutes | 62.1 | 60.8 | 7.21 | 0.906 |
| Bacteroidota | 28.5 | 22.3 | 6.04 | 1.000 |
| Proteobacteria | 6.05 | 12.7 | 4.04 | 0.663 |
| Actinobacteriota | 2.02 | 3.27 | 1.43 | 0.591 |
| Verrucomicrobiota | 0.73 | 0.92 | 0.42 | 0.663 |
| Fusobacteriota | 0.34 | 0.01 | 0.17 | 1.000 |
| Desulfobacterota | 0.19 | 0.01 | 0.09 | 0.354 |
| Day – 3 Families | | | | |
| Lactobacillaceae | 21.1 | 25.9 | 11.5 | 0.789 |
| Bacteroidaceae | 22.6 | 21.2 | 7.71 | 0.909 |
| Lachnospiraceae | 11.3 | 15.2 | 4.94 | 0.641 |
| Enterobacteriaceae | 5.13 | 8.48 | 3.99 | 0.586 |
| Butyricicoccaceae | 2.67 | 5.72 | 1.86 | 0.328 |
| Coriobacteriaceae | 1.51 | 3.05 | 1.48 | 0.516 |
| Pasteurellaceae | 0.81 | 2.92 | 1.84 | 0.663 |
| Enterococcaceae | 0.93 | 2.89 | 1.45 | 0.420 |
| Tannerellaceae | 0.97 | 1.17 | 0.80 | 0.878 |
| Erysipelatoclostridiaceae | 0.60 | 1.11 | 0.45 | 0.470 |
| Akkermansiaceae | 0.72 | 0.92 | 0.42 | 0.756 |
| Acidaminococcaceae | 1.36 | 0.76 | 0.51 | 0.465 |
| Ruminococcaceae | 18.9 | 0.55 | 7.88 | 0.081 |
| Erysipelotrichaceae | 1.14 | 0.15 | 0.59 | 0.663 |
| Clostridiaceae | 0.01 | 0.12 | 0.04 | 0.354 |
| Oscillospiraceae | 0.27 | 0.01 | 0.01 | 0.077 |
| Rikenellaceae | 0.16 | 0.00 | 0.05 | 0.077 |
| Others | 9.85 | 9.96 | 6.57 | 1.000 |
| Day – 3 Genera | | | | |
| <i>Lactobacillus</i> | 16.5 | 22.0 | 10.5 | 0.731 |
| <i>Bacteroides</i> | 22.6 | 21.2 | 7.71 | 0.909 |
| <i>Escherichia-Shigella</i> | 5.13 | 8.48 | 3.99 | 0.586 |
| <i>Tyzzarella</i> | 3.22 | 6.62 | 2.95 | 0.463 |
| <i>Butyricoccus</i> | 2.67 | 5.72 | 1.86 | 0.328 |
| <i>[Ruminococcus] gnavus group</i> | 1.84 | 4.69 | 2.20 | 0.454 |
| <i>Limosilactobacillus</i> | 4.62 | 3.85 | 2.18 | 0.819 |
| <i>Collinsella</i> | 1.51 | 3.05 | 1.48 | 0.516 |
| <i>Gallibacterium</i> | 0.81 | 2.92 | 1.84 | 0.663 |

| | | | | |
|-------------------------------------|------|------|------|--------------|
| <i>Enterococcus</i> | 0.93 | 2.89 | 1.45 | 0.420 |
| <i>UG Lachnospiraceae</i> | 0.90 | 2.23 | 1.43 | 1.000 |
| <i>Parabacteroides</i> | 0.97 | 1.17 | 0.80 | 0.878 |
| <i>Erysipelatoclostridium</i> | 0.60 | 1.11 | 0.45 | 0.470 |
| <i>Akkermansia</i> | 0.72 | 0.92 | 0.42 | 0.756 |
| <i>Dorea</i> | 0.82 | 0.91 | 0.61 | 0.930 |
| <i>Phascolarctobacterium</i> | 1.36 | 0.76 | 0.51 | 0.465 |
| <i>Lachnoclostridium</i> | 0.26 | 0.41 | 0.19 | 0.630 |
| <i>Faecalibacterium</i> | 7.24 | 0.39 | 2.98 | 0.081 |
| <i>Blautia</i> | 2.83 | 0.26 | 0.81 | 0.190 |
| <i>Faecalicoccus</i> | 1.14 | 0.15 | 0.59 | 0.663 |
| <i>Clostridium sensu stricto 2</i> | 0.01 | 0.12 | 0.04 | 0.354 |
| <i>Subdoligranulum</i> | 11.1 | 0.11 | 5.09 | 0.077 |
| <i>Fournierella</i> | 0.58 | 0.05 | 0.26 | 0.383 |
| <i>[Ruminococcus] torques group</i> | 1.42 | 0.04 | 0.62 | 0.507 |
| <i>Pseudoflavonifractor</i> | 0.27 | 0.01 | 0.01 | 0.077 |
| <i>Alistipes</i> | 0.16 | 0.00 | 0.05 | 0.077 |
| <i>Others</i> | 9.85 | 9.96 | 6.57 | 1.000 |

Day – 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

SEM: standard error of the mean.

UG: unclassified genus

Table S4. Relative abundance ($\geq 0.1\%$) of fecal bacterial phyla, families, and genera between Healthy and Rota groups post-inoculation day 1

| Measurements | Relative abundance (%) | | SEM | <i>p</i> Value |
|----------------------------|------------------------|-------|-------|----------------|
| | Healthy | Rota | | |
| Day + 1 Phyla | | | | |
| Firmicutes | 62.2 | 67.4 | 13.9 | 0.823 |
| Verrucomicrobiota | 6.11 | 11.4 | 7.07 | 1.000 |
| Proteobacteria | 10.2 | 9.92 | 7.65 | 0.663 |
| Bacteroidota | 10.3 | 5.13 | 4.19 | 0.437 |
| Fusobacteriota | 0.13 | 4.69 | 2.38 | 1.000 |
| Actinobacteriota | 10.5 | 1.23 | 2.28 | 0.064 |
| Desulfobacterota | 0.00 | 0.23 | 0.12 | 1.000 |
| Campylobacterota | 0.48 | 0.00 | 0.24 | 1.000 |
| Synergistota | 0.07 | 0.00 | 0.03 | 0.505 |
| Day + 1 Families | | | | |
| Streptococcaceae | 10.2 | 39.9 | 11.3 | 0.151 |
| Lactobacillaceae | 1.47 | 20.05 | 10.5 | 0.383 |
| Akkermansiaceae | 2.67 | 11.4 | 6.90 | 0.825 |
| Enterobacteriaceae | 8.50 | 7.44 | 6.61 | 0.663 |
| Fusobacteriaceae | 0.13 | 4.69 | 2.38 | 1.000 |
| Bacteroidaceae | 7.63 | 4.56 | 4.46 | 0.652 |
| Enterococcaceae | 7.38 | 2.11 | 2.58 | 0.256 |
| Clostridiaceae | 12.0 | 1.84 | 3.94 | 0.383 |
| Pasteurellaceae | 0.62 | 1.58 | 1.05 | 0.663 |
| Lachnospiraceae | 3.60 | 0.33 | 1.27 | 0.383 |
| Tannerellaceae | 1.36 | 0.33 | 0.76 | 0.643 |
| Acidaminococcaceae | 0.22 | 0.29 | 0.21 | 0.839 |
| Peptostreptococcaceae | 0.01 | 0.26 | 0.11 | 0.354 |
| Coriobacteriaceae | 1.86 | 0.11 | 0.83 | 0.184 |
| Erysipelatoclostridiaceae | 0.51 | 0.10 | 0.20 | 0.383 |
| Bifidobacteriaceae | 8.53 | 0.03 | 2.42 | 0.190 |
| Ruminococcaceae | 7.03 | 0.00 | 2.85 | 0.184 |
| Butyricicoccaceae | 5.07 | 0.00 | 2.06 | 0.077 |
| Chlamydiaceae | 3.43 | 0.00 | 1.67 | 0.197 |
| Prevotellaceae | 0.98 | 0.00 | 0.34 | 0.064 |
| Others | 16.8 | 4.92 | 5.60 | 0.190 |
| Day + 1 Genera | | | | |
| <i>Streptococcus</i> | 10.2 | 39.9 | 11.29 | 0.151 |
| <i>Limosilactobacillus</i> | 0.85 | 11.46 | 6.04 | 0.383 |
| <i>Akkermansia</i> | 2.67 | 11.41 | 6.90 | 0.825 |
| <i>Ligilactobacillus</i> | 0.62 | 8.59 | 4.47 | 0.383 |

| | | | | |
|------------------------------------|-------|------|------|--------------|
| <i>Escherichia-Shigella</i> | 8.50 | 7.44 | 6.61 | 0.663 |
| <i>Fusobacterium</i> | 0.13 | 4.69 | 2.38 | 1.000 |
| <i>Bacteroides</i> | 7.63 | 4.56 | 4.46 | 0.652 |
| <i>Enterococcus</i> | 7.38 | 2.11 | 2.58 | 0.256 |
| <i>Clostridium sensu stricto 1</i> | 11.86 | 1.73 | 3.91 | 0.383 |
| <i>Gallibacterium</i> | 0.62 | 1.58 | 1.05 | 0.663 |
| <i>Parabacteroides</i> | 1.36 | 0.33 | 0.76 | 0.643 |
| <i>Phascolarctobacterium</i> | 0.22 | 0.29 | 0.21 | 0.839 |
| <i>Peptostreptococcus</i> | 0.01 | 0.26 | 0.11 | 0.354 |
| <i>Blautia</i> | 0.47 | 0.19 | 0.26 | 1.000 |
| <i>[Ruminococcus] gnavus group</i> | 3.06 | 0.13 | 1.05 | 0.184 |
| <i>Clostridium sensu stricto 2</i> | 0.10 | 0.11 | 0.05 | 0.663 |
| <i>Collinsella</i> | 1.86 | 0.11 | 0.83 | 0.184 |
| <i>Erysipelatoclostridium</i> | 0.51 | 0.10 | 0.20 | 0.383 |
| <i>Bifidobacterium</i> | 8.53 | 0.03 | 2.42 | 0.190 |
| <i>Ruminococcus</i> | 0.21 | 0.00 | 0.05 | 0.184 |
| <i>Butyricicoccus</i> | 5.07 | 0.00 | 2.06 | 0.077 |
| <i>Chlamydia</i> | 3.43 | 0.00 | 1.67 | 0.197 |
| <i>Fournierella</i> | 0.86 | 0.00 | 0.26 | 0.197 |
| <i>Faecalibacterium</i> | 5.95 | 0.00 | 2.80 | 0.197 |
| <i>Alloprevotella</i> | 0.98 | 0.00 | 0.34 | 0.064 |
| <i>Others</i> | 16.9 | 4.93 | 5.59 | 0.190 |

Day – 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

SEM: standard error of the mean.

Table S5. Relative abundance ($\geq 0.1\%$) of fecal bacterial phyla, families, and genera between Healthy and Rota groups post-inoculation day 7

| Measurements | Relative abundance (%) | | SEM | <i>p</i> Value |
|------------------------------------|------------------------|-------|------|----------------|
| | Healthy | Rota | | |
| Day + 7 Phyla | | | | |
| Firmicutes | 74.29 | 78.73 | 6.28 | 1.000 |
| Actinobacteriota | 25.33 | 12.70 | 6.45 | 0.280 |
| Bacteroidota | 0.12 | 3.35 | 1.56 | 0.507 |
| Verrucomicrobiota | 0.01 | 2.93 | 1.47 | 1.000 |
| Proteobacteria | 0.19 | 2.06 | 0.87 | 0.663 |
| Fusobacteriota | 0.01 | 0.21 | 0.11 | 1.000 |
| Euryarchaeota | 0.04 | 0.01 | 0.03 | 1.000 |
| Day + 7 Families | | | | |
| Lachnospiraceae | 49.1 | 44.3 | 18.1 | 0.862 |
| Streptococcaceae | 9.94 | 14.03 | 5.83 | 0.650 |
| Bifidobacteriaceae | 23.9 | 11.8 | 6.90 | 0.307 |
| Enterococcaceae | 0.43 | 8.16 | 2.22 | 0.081 |
| Clostridiaceae | 2.23 | 4.03 | 2.73 | 1.000 |
| Enterobacteriaceae | 0.15 | 1.07 | 0.45 | 0.663 |
| Erysipelatoclostridiaceae | 3.02 | 0.43 | 1.23 | 0.383 |
| Coriobacteriaceae | 0.81 | 0.37 | 0.41 | 1.000 |
| Erysipelotrichaceae | 0.11 | 0.37 | 0.19 | 0.825 |
| Eubacteriaceae | 0.08 | 0.17 | 0.07 | 0.418 |
| Eggerthellaceae | 0.04 | 0.16 | 0.07 | 0.349 |
| Erysipelotrichaceae | 0.07 | 0.09 | 0.06 | 0.849 |
| Veillonellaceae | 0.11 | 0.01 | 0.03 | 0.354 |
| Others | 9.95 | 15.0 | 11.1 | 1.000 |
| Day + 7 Genera | | | | |
| <i>Limosilactobacillus</i> | 37.7 | 19.9 | 13.7 | 0.424 |
| <i>Streptococcus</i> | 9.94 | 14.0 | 5.83 | 0.650 |
| <i>Lactobacillus</i> | 4.62 | 12.3 | 4.98 | 0.375 |
| <i>Ligilactobacillus</i> | 6.46 | 11.91 | 5.19 | 0.508 |
| <i>Bifidobacterium</i> | 23.9 | 11.8 | 6.90 | 0.663 |
| <i>Enterococcus</i> | 0.43 | 8.16 | 2.22 | 0.081 |
| <i>Clostridium sensu stricto 1</i> | 2.23 | 4.03 | 2.73 | 1.000 |
| <i>Escherichia-Shigella</i> | 0.15 | 1.07 | 0.45 | 0.663 |
| <i>Collinsella</i> | 0.81 | 0.37 | 0.41 | 1.000 |
| <i>Turicibacter</i> | 0.04 | 0.28 | 0.16 | 1.000 |
| <i>Sharpea</i> | 2.95 | 0.26 | 1.15 | 0.190 |
| <i>Eubacterium</i> | 0.08 | 0.17 | 0.07 | 0.418 |
| <i>Erysipelatoclostridium</i> | 0.07 | 0.17 | 0.09 | 0.469 |

| | | | | |
|------------------------|------|------|------|-------|
| <i>Paraeggerthella</i> | 0.04 | 0.16 | 0.07 | 0.354 |
| <i>Acetitomaculum</i> | 0.34 | 0.10 | 0.19 | 0.825 |
| <i>Megasphaera</i> | 0.11 | 0.01 | 0.03 | 0.354 |
| Others | 10.1 | 15.2 | 11.2 | 1.000 |

Day – 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

SEM: standard error of the mean.

Table S6. Predicted KEGG hierarchies (orthologs, modules, and pathways) between Healthy and Rota groups

| Measurements | Relative abundance (%) | | SEM | <i>p</i> Value |
|----------------|------------------------|------|------|----------------|
| | Healthy | Rota | | |
| Day – 3 | | | | |
| KEGG orthologs | 4987 | 4647 | 181 | 0.274 |
| KEGG pathways | 127 | 126 | 8.21 | 0.191 |
| KEGG modules | 243 | 250 | 5.49 | 0.258 |
| Day + 1 | | | | |
| KEGG orthologs | 4897 | 5065 | 253 | 0.713 |
| KEGG pathways | 136 | 139 | 7.01 | 0.783 |
| KEGG modules | 140 | 126 | 5.44 | 0.497 |
| Day + 7 | | | | |
| KEGG orthologs | 4633 | 4371 | 525 | 0.759 |
| KEGG pathways | 246 | 234 | 6.26 | 0.957 |
| KEGG modules | 232 | 228 | 13.6 | 0.874 |

Day – 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

SEM: standard error of the mean.

KEGG: Kyoto Encyclopedia of Genes and Genomes.

Table S7. Differentially abundant KEGG modules between Healthy and Rota groups, which were detected using LEfSe with an LDA effect size > 2.

| KEGG modules | Dominance | Treatment | | SEM | LDA | p Value | Description |
|--------------|-----------|-----------|------|------|-------|---------|---|
| | | Healthy | Rota | | | | |
| Day – 3 | | | | | | | |
| M00176 | Healthy | 0.24 | 0.12 | 0.03 | 3.003 | 0.050 | Assimilatory sulfate reduction, sulfate => H2S |
| M00922 | Healthy | 0.25 | 0.02 | 0.06 | 3.093 | 0.050 | CMP-Neu5Ac biosynthesis |
| M00923 | Healthy | 0.14 | 0.01 | 0.03 | 2.954 | 0.050 | UDP-L-FucNAc biosynthesis |
| M00895 | Rota | 0.73 | 0.82 | 0.02 | 2.881 | 0.050 | Thiamine biosynthesis, prokaryotes, AIR (+ DXP/glycine) => TMP/TPP |
| M00899 | Rota | 0.74 | 0.92 | 0.03 | 3.095 | 0.050 | Thiamine salvage pathway, HMP/HET => TMP |
| Day + 1 | | | | | | | |
| M00061 | Healthy | 0.56 | 0.17 | 0.08 | 3.337 | 0.050 | D-Glucuronate degradation, D-glucuronate => pyruvate + D-glyceraldehyde 3P |
| M00133 | Healthy | 0.34 | 0.10 | 0.03 | 3.223 | 0.050 | Polyamine biosynthesis, arginine => agmatine => putrescine => spermidine |
| M00135 | Healthy | 0.26 | 0.05 | 0.06 | 3.098 | 0.050 | GABA biosynthesis, eukaryotes, putrescine => GABA |
| M00308 | Healthy | 0.94 | 0.74 | 0.04 | 3.092 | 0.050 | Semi-phosphorylative Entner-Doudoroff pathway, gluconate => glycerate-3P |
| M00345 | Healthy | 0.83 | 0.58 | 0.07 | 3.208 | 0.050 | Formaldehyde assimilation, ribulose monophosphate pathway |
| M00631 | Healthy | 0.54 | 0.17 | 0.08 | 3.300 | 0.050 | D-Galacturonate degradation (bacteria), D-galacturonate => pyruvate + D-glyceraldehyde 3P |
| M00651 | Healthy | 0.20 | 0.14 | 0.01 | 2.792 | 0.050 | Vancomycin resistance, D-Ala-D-Lac type |
| M00845 | Healthy | 0.81 | 0.71 | 0.04 | 3.063 | 0.050 | Arginine biosynthesis, glutamate => acetylcitrulline => arginine |
| M00878 | Healthy | 0.16 | 0.09 | 0.02 | 2.859 | 0.050 | Phenylacetate degradation, phenylacetate => acetyl-CoA/succinyl-CoA |
| M00892 | Healthy | 0.91 | 0.53 | 0.14 | 3.315 | 0.050 | UDP-N-acetyl-D-glucosamine biosynthesis, eukaryotes, glucose => UDP-GlcNAc |
| M00032 | Rota | 0.15 | 0.19 | 0.01 | 3.022 | 0.050 | Lysine degradation, lysine => saccharopine => acetoacetyl-CoA |
| M00126 | Rota | 0.61 | 0.75 | 0.03 | 3.053 | 0.050 | Tetrahydrofolate biosynthesis, GTP => THF |
| M00129 | Rota | 0.34 | 0.47 | 0.04 | 3.000 | 0.050 | Ascorbate biosynthesis, animals, glucose-1P => ascorbate |
| M00150 | Rota | 0.23 | 0.62 | 0.09 | 3.363 | 0.050 | Fumarate reductase, prokaryotes |
| M00168 | Rota | 0.33 | 0.63 | 0.11 | 3.219 | 0.050 | CAM (Crassulacean acid metabolism), dark |
| M00346 | Rota | 0.66 | 0.74 | 0.03 | 2.849 | 0.050 | Formaldehyde assimilation, serine pathway |

| | | | | | | | |
|---------|---------|------|------|------|-------|-------|---|
| M00793 | Rota | 0.93 | 1.25 | 0.09 | 3.174 | 0.050 | dTDP-L-rhamnose biosynthesis |
| M00840 | Rota | 0.65 | 0.91 | 0.05 | 3.277 | 0.050 | Tetrahydrofolate biosynthesis, mediated by ribA and trpF, GTP => THF |
| M00842 | Rota | 0.59 | 0.84 | 0.04 | 3.186 | 0.050 | Tetrahydrobiopterin biosynthesis, GTP => BH4 |
| M00843 | Rota | 0.59 | 0.84 | 0.04 | 3.186 | 0.050 | L-threo-Tetrahydrobiopterin biosynthesis, GTP => L-threo-BH4 |
| M00899 | Rota | 0.75 | 0.99 | 0.05 | 3.225 | 0.050 | Thiamine salvage pathway, HMP/HET => TMP |
| M00913 | Rota | 0.55 | 0.79 | 0.07 | 3.201 | 0.050 | Pantothenate biosynthesis, 2-oxoisovalerate/spermine => pantothenate |
| Day + 7 | | | | | | | |
| M00017 | Healthy | 1.32 | 1.06 | 0.05 | 3.077 | 0.050 | Methionine biosynthesis, aspartate => homoserine => methionine |
| M00018 | Healthy | 1.25 | 1.08 | 0.04 | 2.792 | 0.050 | Threonine biosynthesis, aspartate => homoserine => threonine |
| M00029 | Healthy | 1.13 | 0.97 | 0.05 | 3.072 | 0.050 | Urea cycle |
| M00526 | Healthy | 1.39 | 1.14 | 0.06 | 2.914 | 0.050 | Lysine biosynthesis, DAP dehydrogenase pathway, aspartate => lysine |
| M00527 | Healthy | 1.39 | 1.14 | 0.06 | 3.026 | 0.050 | Lysine biosynthesis, DAP aminotransferase pathway, aspartate => lysine |
| M00046 | Rota | 0.08 | 0.13 | 0.01 | 3.073 | 0.050 | Pyrimidine degradation, uracil => beta-alanine, thymine => 3-aminoisobutanoate |
| M00117 | Rota | 0.92 | 1.03 | 0.04 | 2.817 | 0.050 | Ubiquinone biosynthesis, prokaryotes, chorismate (+ polyprenyl-PP) => ubiquinol |
| M00373 | Rota | 0.46 | 0.62 | 0.04 | 2.603 | 0.050 | Ethylmalonyl pathway |
| M00530 | Rota | 0.05 | 0.25 | 0.05 | 3.083 | 0.050 | Dissimilatory nitrate reduction, nitrate => ammonia |
| M00880 | Rota | 0.05 | 0.18 | 0.02 | 3.031 | 0.050 | Molybdenum cofactor biosynthesis, GTP => molybdenum cofactor |
| M00899 | Rota | 0.02 | 0.22 | 0.04 | 3.011 | 0.050 | Thiamine salvage pathway, HMP/HET => TMP |
| M00913 | Rota | 0.10 | 0.28 | 0.04 | 2.873 | 0.050 | Pantothenate biosynthesis, 2-oxoisovalerate/spermine => pantothenate |

Day - 3, 3 days before rotavirus inoculation; Day + 1, 1 day post-inoculation; Day + 7, 7 days post-inoculation.

Healthy: non-diarrhea.

Rota: calves inoculated with rotavirus to induce diarrhea.

SEM: standard error of the mean.

KEGG: Kyoto Encyclopedia of Genes and Genomes; LDA: linear discriminant analysis; LEfSe: LDA effect size.