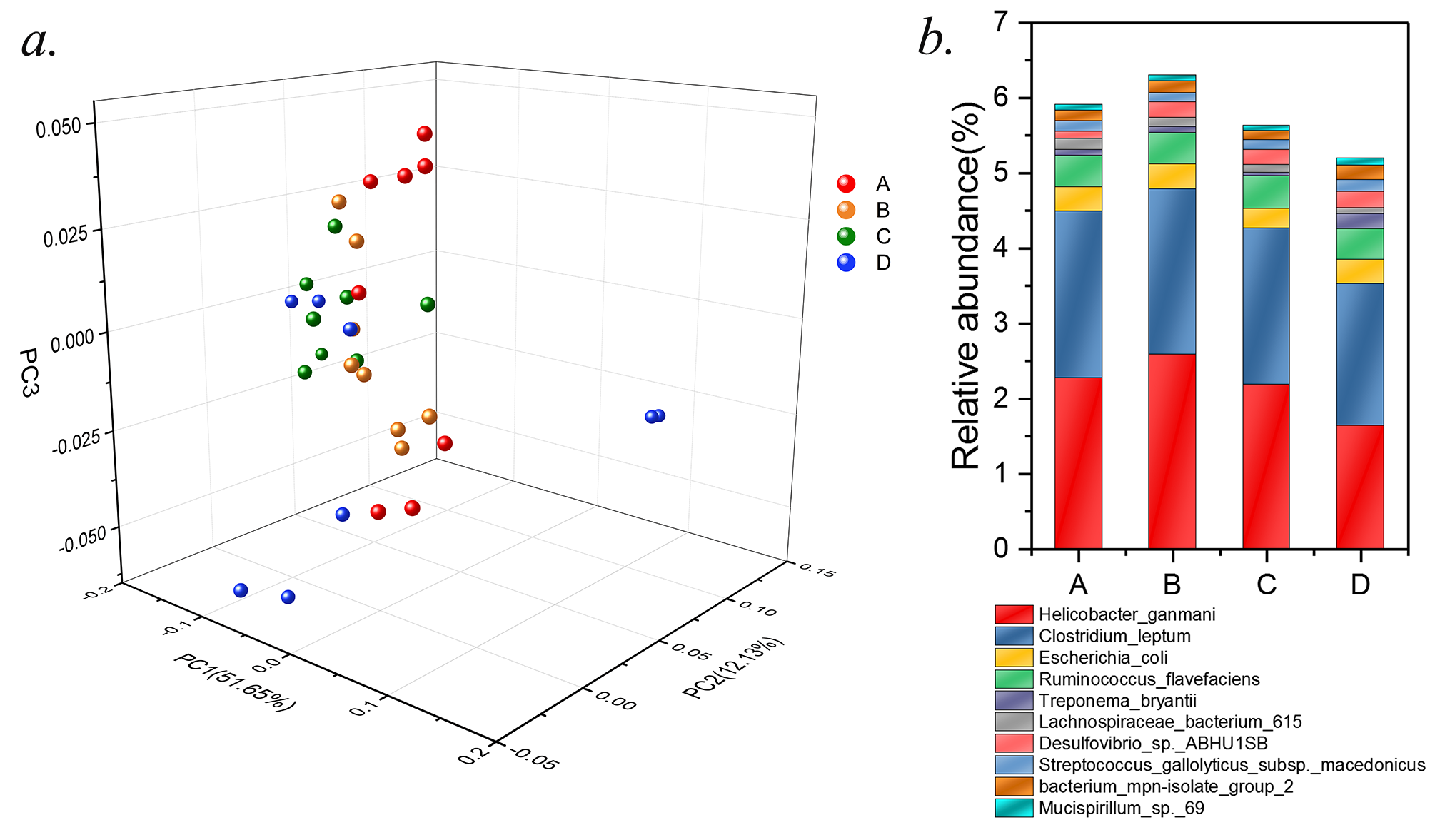
**TableS1** Effects of ethanolamine on alpha diversity and abundance of colonic microbiota

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | Control | Increased Ethanolamine | | |  |
| Indices | A(0μM) | B(250μM) | C(500μM) | D(1000μM) | P-value |
| Observed\_species | 1157.6±12.54 | 1151.4±11.45 | 1148.9±10.13 | 1151.6±24.22 | 0.982 |
| Shannon | 7.96±0.03 | 7.98±0.03 | 7.83±0.07 | 7.89±0.10 | 0.335 |
| Simpson | 0.9903±0.000a | 0.9905±0.001a | 0.9867±0.002b | 0.9869±0.002bc | 0.072 |
| Chao1 | 1250.2±15.28 | 1227.5±14.67 | 1236.0±11.48 | 1229.51±25.56 | 0.805 |
| ACE | 1247.82±15.02 | 1230.72±14.06 | 1238.45±10.85 | 1230.92±26.21 | 0.887 |

All indices were analyzed by Wilcox test and presented with least squares means ± SEM.Within a row, values without same small letter superscripts differ significantly (P < 0.05).



**Fig.S1** Dose-effects of ethanolamine in altering the composition of colonic microbiota of weaning rats.

a.Weighted principal coordinate analyses (PCoA) plot of sample Bray Curtis distance. b.The most abundant top 10 species of colonic microbiota driven by ethanolamine in the weaning model.

Table S2 Results of Adonis analysis of colonic microbiota driven by different level of ethanolamine

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Vs\_group | Df | SumsOfSqs | MeanSqs | F.Model | R2 | Pr(>F) |
| B-A | 1(14) | 0.05773(0.34622) | 0.057728(0.024730) | 2.3343 | 0.14291(0.85709) | 0.008 |
| B-C | 1(14) | 0.03609(0.38416) | 0.03609(0.02744) | 1.3152 | 0.08588(0.91412) | 0.16 |
| B-D | 1(14) | 0.09585(0.54752) | 0.095854(0.039108) | 2.451 | 0.14899(0.85101) | 0.002 |
| A-C | 1(14) | 0.10098(0.35846) | 0.100980(0.025604) | 3.9439 | 0.21979(0.78021) | 0.001 |
| A-D | 1(14) | 0.13555(0.52181) | 0.135552(0.037272) | 3.6368 | 0.20621(0.79379) | 0.001 |
| C-D | 1(14) | 0.05147(0.55975) | 0.051470(0.039982) | 1.2873 | 0.08421(0.91579) | 0.331 |

Data were analyzed by R software with related packages.

**TableS3** Compositional changes of colonic microbiota driven by ethanolamine treatments at species level

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | | Control | | Ethanolamine | | | | | |  | |
| Taxonomy (%) | | A(0μM) | | B(250μM) | | C(500μM) | | D(1000μM) | | P-value | |
| *Helicobacter\_ganmani* | 0.022721 | | 0.025855 | | 0.021833 | | 0.016341 | | 0.423 | |
| *Clostridium\_leptum* | 0.022166 | | 0.021989 | | 0.020779 | | 0.018854 | | 0.094 | |
| *Escherichia\_coli* | 0.003216 | | 0.003334 | | 0.002585 | | 0.003236 | | 0.877 | |
| *Ruminococcus\_flavefaciens* | 0.004193 | | 0.004157 | | 0.004368 | | 0.004148 | | 0.986 | |
| *Treponema\_bryantii* | 0.000775 | | 0.000751 | | 0.000487 | | 0.001913 | | 0.153 | |
| *Lachnospiraceae\_bacterium\_615* | 0.001483 | | 0.001277 | | 0.001003 | | 0.000799 | | 0.472 | |
| *Desulfovibrio\_sp.\_ABHU1SB* | 0.000941 | | 0.0021 | | 0.002059 | | 0.002259 | | 0.214 | |
| *Streptococcus\_gallolyticus\_subsp.\_macedonicus* | 0.001397 | | 0.001205 | | 0.001239 | | 0.001517 | | 0.914 | |
| *bacterium\_mpn-isolate\_group\_2* | 0.00138 | | 0.001515 | | 0.001289 | | 0.001937 | | 0.374 | |
| *Mucispirillum\_sp.\_69* | 0.000787 | | 0.000814 | | 0.000691 | | 0.000946 | | 0.857 | |
| *Clostridium\_sp.\_ASF356* | 0.001699a | | 0.001543a | | 0.001416ab | | 0.000989b | | 0.001 | |
| *Eubacterium\_sp.\_14-2* | 0.001236a | | 0.000396b | | 0.000406b | | 0.000682ab | | 0.003 | |
| *bacterium\_ic1340* | 0.000943 | | 0.000869 | | 0.00096 | | 0.000953 | | 0.965 | |
| *Lactobacillus\_amylovorus* | 0.000703 | | 0.000523 | | 0.000643 | | 0.000526 | | 0.807 | |
| *Helicobacter\_ganmani* | 0.022721 | | 0.025855 | | 0.021833 | | 0.016341 | | 0.228 | |

Data were analyzed by One-way ANOVA followed by Turkey multiple comparison test and present with the relative abundance of specific taxonomy. Within a row, values without same small letter superscripts differ significantly (P < 0.05).

**Table S4** Ethanolamine altered microbial functions of microbiota in weaning rats’ colons.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | Control | Increased Ethanolamine | | |  |  |
| Observation Ids | A(0μM) | B(250μM) | C(500μM) | D(1000μM) | Effect size | p-values |
| Amino sugar and nucleotide sugar metabolism | 1.3577 | 1.3709 | 1.3803 | 1.3820 | 0.4755 | 0.0110 |
| Arginine and proline metabolism | 1.2311 | 1.2309 | 1.2264 | 1.2149 | 0.3739 | 0.0482 |
| Starch and sucrose metabolism | 0.9116 | 0.9375 | 0.9307 | 0.9403 | 0.3954 | 0.0355 |
| Galactose metabolism | 0.6633 | 0.6905 | 0.6932 | 0.6944 | 0.5223 | 0.0043 |
| Propanoate metabolism | 0.5256 | 0.5084 | 0.4997 | 0.4985 | 0.5903 | 0.0042 |
| Fatty acid biosynthesis | 0.4880 | 0.4763 | 0.4728 | 0.4673 | 0.4336 | 0.0189 |
| Drug metabolism - other enzymes | 0.3274 | 0.3370 | 0.3426 | 0.3435 | 0.4822 | 0.0113 |
| Sulfur relay system | 0.2323 | 0.2219 | 0.2150 | 0.2139 | 0.4706 | 0.0114 |
| Benzoate degradation | 0.2310 | 0.2267 | 0.2188 | 0.2169 | 0.3935 | 0.0355 |
| Plant-pathogen interaction | 0.1804 | 0.1784 | 0.1736 | 0.1752 | 0.3977 | 0.0389 |
| Naphthalene degradation | 0.1366 | 0.1366 | 0.1349 | 0.1335 | 0.3814 | 0.0427 |
| Tetracycline biosynthesis | 0.1365 | 0.1298 | 0.1245 | 0.1202 | 0.5504 | 0.0075 |
| Lysine degradation | 0.1337 | 0.1269 | 0.1251 | 0.1226 | 0.5395 | 0.0069 |
| Glycosphingolipid biosynthesis - globo series | 0.1171 | 0.1278 | 0.1327 | 0.1291 | 0.4475 | 0.0175 |
| Limonene and pinene degradation | 0.1028 | 0.0970 | 0.0959 | 0.0948 | 0.5370 | 0.0044 |
| Nitrotoluene degradation | 0.0998 | 0.0921 | 0.0883 | 0.0882 | 0.3967 | 0.0378 |
| Insulin signaling pathway | 0.0803 | 0.0816 | 0.0791 | 0.0777 | 0.3959 | 0.0367 |
| Butirosin and neomycin biosynthesis | 0.0756 | 0.0780 | 0.0785 | 0.0781 | 0.5365 | 0.0038 |
| Ethylbenzene degradation | 0.0531 | 0.0513 | 0.0511 | 0.0492 | 0.4577 | 0.0146 |
| Electron transfer carriers | 0.0282 | 0.0262 | 0.0246 | 0.0249 | 0.3729 | 0.0475 |
| N-Glycan biosynthesis | 0.0243 | 0.0245 | 0.0269 | 0.0273 | 0.3917 | 0.0355 |
| Primary bile acid biosynthesis | 0.0224 | 0.0243 | 0.0240 | 0.0234 | 0.4340 | 0.0199 |
| Secondary bile acid biosynthesis | 0.0224 | 0.0242 | 0.0240 | 0.0233 | 0.4397 | 0.0185 |
| Metabolism of xenobiotics by cytochrome P450 | 0.0201 | 0.0183 | 0.0162 | 0.0165 | 0.4413 | 0.0189 |
| Drug metabolism - cytochrome P450 | 0.0198 | 0.0181 | 0.0161 | 0.0162 | 0.4316 | 0.0188 |
| Renal cell carcinoma | 0.0098 | 0.0086 | 0.0080 | 0.0075 | 0.5380 | 0.0054 |
| alpha-Linolenic acid metabolism | 0.0085 | 0.0073 | 0.0067 | 0.0061 | 0.5271 | 0.0042 |
| G protein-coupled receptors | 0.0001 | 0.0001 | 0.0001 | 0.0001 | 0.4761 | 0.0119 |

Data were analyzed by One-way ANOVA followed by Turkey multiple comparison test and p-values were corrected with Benjamin FDR to filter out potential false positive results and improve the veracity.