**Supplementary Table S1.** Estimated alpha diversity indices of the faecal microbiota in the dairy calves being supplied essential oil (EO group) or not (CTRL group) during the suckling period.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **Treatment** | **Time point** | **Observed** | **Chao1** | **Ace** | **Shannon** | **Simpson** | **Invsimpson** | **Fisher** |
| Control | T1 | 1027.25 | 1152.918 | 1140.058 | 5.585 | 0.99 | 107.155 | 219.759 |
| EO | T1 | 847.27 | 947.27 | 943.406 | 5.049 | 0.982 | 73.143 | 162.225 |
| Control | T2 | 883.375 | 995.327 | 991.574 | 5.352 | 0.987 | 96.967 | 186.068 |
| EO | T2 | 780.25 | 875.515 | 874.901 | 4.861 | 0.977 | 61.217 | 146.787 |

**Supplementary Table S2**. The core faecal microbiota at the family and phylum level

|  |  |
| --- | --- |
| **Phylum** | **average abundance expressed in %** |
| Firmicutes | 49.21505799 |
| Bacteroidetes | 32.19819766 |
| Proteobacteria | 4.152545955 |
| Verrucomicrobia | 3.096955875 |
| Cyanobacteria | 2.917567392 |
| Euryarchaeota | 2.257383339 |
| Spirochaetes | 1.549456278 |
| Actinobacteria | 1.299001154 |
| Elusimicrobia | 0.9014819117 |
| Fusobacteria | 0.5712724842 |
| Tenericutes | 0.4261650468 |
| Lentisphaerae | 0.3998672588 |
| Kiritimatiellaeota | 0.3962669664 |
| Patescibacteria | 0.2589079844 |
| Epsilonbacteraeota | 0.2175828889 |
| Planctomycetes | 0.07310158929 |
| Excavata | 0.02856753757 |
| Synergistetes | 0.02700219305 |
| Chloroflexi | 0.01142701503 |
| Chlamydiae | 0.00125227562 |
| Fibrobacteres | 0.0009392067147 |

**Supplementary Table S3.** The core faecal microbiota at the genus level

|  |  |
| --- | --- |
| **Genus** | **average abundance expressed in %** |
| Uncultured or unknown | 14.46141372 |
| Bacteroides | 9.283859904 |
| Ruminococcaceae UCG-005 | 8.341205743 |
| Alloprevotella | 6.674889975 |
| Ruminococcaceae UCG-010 | 4.658483535 |
| Faecalibacterium | 4.103801532 |
| Ruminococcaceae UCG-014 | 3.336779714 |
| Prevotella 9 | 3.114969527 |
| Akkermansia | 3.088906438 |
| Blautia | 2.607091508 |
| Alistipes | 2.246747788 |
| Rikenellaceae RC9 gut group | 2.193369331 |
| Prevotella 2 | 1.872863786 |
| Escherichia-Shigella | 1.725877359 |
| Methanobrevibacter | 1.653792962 |
| Phascolarctobacterium | 1.561593809 |
| [Eubacterium] coprostanoligenes group | 1.506650001 |
| Christensenellaceae R-7 group | 1.231148286 |
| Treponema 2 | 1.206494014 |
| Subdoligranulum | 0.9208957876 |
| Elusimicrobium | 0.9014854395 |
| Streptococcus | 0.8855971304 |
| Lachnospiraceae NK4A136 group | 0.8747179434 |
| Roseburia | 0.6617519874 |
| Bifidobacterium | 0.6464898186 |
| Anaerostipes | 0.6437504549 |
| [Ruminococcus] torques group | 0.6273925406 |
| Odoribacter | 0.6261402601 |
| Ruminococcaceae UCG-013 | 0.6022686627 |
| Ruminococcaceae UCG-002 | 0.6021903952 |
| Lachnoclostridium | 0.5859107484 |
| Fusobacterium | 0.5712747198 |
| Prevotellaceae UCG-004 | 0.5348020497 |
| Lactobacillus | 0.5340976419 |
| Barnesiella | 0.4805626496 |
| Tyzzerella 4 | 0.469292125 |
| Collinsella | 0.4410375457 |
| Lachnospiraceae AC2044 group | 0.4390808574 |
| Lachnospiraceae UCG-008 | 0.4363414938 |
| Erysipelotrichaceae UCG-003 | 0.3834326418 |
| Clostridium sensu stricto 1 | 0.3791279275 |
| Ruminiclostridium 9 | 0.3692662184 |
| Lachnospiraceae FCS020 group | 0.368327008 |
| Anaerovibrio | 0.353925782 |
| Methanocorpusculum | 0.3498558703 |
| Sphaerochaeta | 0.3429683275 |
| Parabacteroides | 0.3288801716 |
| Ruminococcaceae UCG-009 | 0.3198794054 |
| Romboutsia | 0.3149485508 |
| GCA-900066575 | 0.3039128288 |
| Oscillibacter | 0.27088393 |
| Mailhella | 0.263526782 |
| Faecalitalea | 0.2629006417 |
| Candidatus Saccharimonas | 0.2589089976 |
| Ruminococcus 1 | 0.2528823976 |
| Desulfovibrio | 0.2488124859 |
| Erysipelotrichaceae UCG-004 | 0.2418466755 |
| Megasphaera | 0.2410640001 |
| Ruminococcaceae NK4A214 group | 0.2288542651 |
| Agathobacter | 0.2278367871 |
| Family XIII AD3011 group | 0.2271323794 |
| Ruminobacter | 0.2252539586 |
| Lachnoclostridium 10 | 0.2193056261 |
| Lachnospiraceae UCG-004 | 0.2136703638 |
| Campylobacter | 0.2121832806 |
| [Ruminococcus] gauvreauii group | 0.2089743118 |
| Prevotellaceae UCG-003 | 0.19856473 |
| dgA-11 gut group | 0.1923815949 |
| Prevotella 1 | 0.187685543 |
| Sutterella | 0.1851809819 |
| Prevotellaceae NK3B31 group | 0.1716406988 |
| Ruminococcus 2 | 0.1698405456 |
| Oscillospira | 0.1687448001 |
| Butyricicoccus | 0.1573960079 |
| [Eubacterium] nodatum group | 0.1446384001 |
| Butyricimonas | 0.140803291 |
| Megamonas | 0.1400206157 |
| Prevotellaceae UCG-001 | 0.1152880754 |
| Dorea | 0.1040958182 |
| Intestinibacter | 0.0957994598 |
| Turicibacter | 0.09564292473 |
| Fournierella | 0.095095052 |
| Ruminiclostridium 5 | 0.08687696109 |
| Marvinbryantia | 0.08664215849 |
| Tyzzerella | 0.08656389096 |
| Ruminococcaceae UCG-008 | 0.08484200525 |
| Candidatus Soleaferrea | 0.08124169875 |
| Methanosphaera | 0.08030248836 |
| Parasutterella | 0.07787619485 |
| p-1088-a5 gut group | 0.07310187537 |
| [Eubacterium] oxidoreducens group | 0.07106691952 |
| Lachnospiraceae UCG-010 | 0.06793621822 |
| Lachnospiraceae UCG-001 | 0.06785795069 |
| Intestinimonas | 0.06073560523 |
| Sharpea | 0.05564821562 |
| Ruminococcaceae UCG-004 | 0.05517861042 |
| [Eubacterium] hallii group | 0.05290885198 |
| Terrisporobacter | 0.05251751432 |
| RumEn M2 | 0.04860413769 |
| Succinivibrio | 0.04664744938 |
| Sarcina | 0.04641264678 |
| Negativibacillus | 0.04492556366 |
| Lachnospiraceae NK3A20 group | 0.0447690286 |
| Cellulosilyticum | 0.04124698964 |
| Ruminococcaceae UCG-011 | 0.03952510392 |
| Anaerovorax | 0.03921203379 |
| Ruminiclostridium | 0.03882069613 |
| Coprobacter | 0.03772495067 |
| [Anaerorhabdus] furcosa group | 0.03709881041 |
| Prevotellaceae Ga6A1 group | 0.03568999483 |
| Acetitomaculum | 0.03435944677 |
| Gallibacterium | 0.03373330651 |
| Coprococcus 3 | 0.0317766182 |
| Erysipelatoclostridium | 0.03169835067 |
| [Eubacterium] eligens group | 0.03146354807 |
| Fretibacterium | 0.02700229872 |
| [Eubacterium] brachy group | 0.02645442599 |
| Butyrivibrio | 0.02410640001 |
| Anaerofilum | 0.02410640001 |
| Lachnospiraceae NC2004 group | 0.02363679482 |
| Mycoplasma | 0.0223845143 |
| Defluviitaleaceae UCG-011 | 0.02105396625 |
| Holdemanella | 0.02097569871 |
| Simplicimonas | 0.02066262858 |
| Olsenella | 0.02027129092 |
| Anaerocolumna | 0.02019302339 |
| Dielma | 0.01917554547 |
| [Ruminococcus] gnavus group | 0.01815806754 |
| Lachnospiraceae UCG-006 | 0.01714058962 |
| Veillonella | 0.01682751949 |
| Candidatus Methanomethylophilus | 0.01643618183 |
| Pseudobutyrivibrio | 0.01596657663 |
| Howardella | 0.01494909871 |
| Oribacterium | 0.01471429611 |
| [Acetivibrio] ethanolgignens group | 0.01416642339 |
| Ruminiclostridium 1 | 0.01408815585 |
| Coprococcus 2 | 0.01314894546 |
| Faecalicoccus | 0.01307067793 |
| Lachnospiraceae UCG-002 | 0.01260107273 |
| Syntrophococcus | 0.01205320001 |
| Mogibacterium | 0.01166186234 |
| Acetobacter | 0.01166186234 |
| Holdemania | 0.01095745455 |
| Anaeroplasma | 0.01033131429 |
| Peptococcus | 0.01025304676 |
| Candidatus Stoquefichus | 0.01009651169 |
| Eisenbergiella | 0.01001824416 |
| Corynebacterium 1 | 0.009939976629 |
| Fusicatenibacter | 0.009861709097 |
| [Eubacterium] xylanophilum group | 0.009783441564 |
| Ruminiclostridium 6 | 0.009705174032 |
| Lachnospiraceae ND3007 group | 0.009235568837 |
| Papillibacter | 0.008765963642 |
| Pygmaiobacter | 0.008609428577 |
| Flexilinea | 0.007983288316 |
| Pentatrichomonas | 0.007905020784 |
| Ruminococcaceae UCG-003 | 0.007591950654 |
| UBA1819 | 0.007435415589 |
| Cerasicoccus | 0.007357148056 |
| Anaerosporobacter | 0.007357148056 |
| Leuconostoc | 0.006652740264 |
| Hydrogenoanaerobacterium | 0.006652740264 |
| Lachnoclostridium 5 | 0.006496205199 |
| GCA-900066225 | 0.006417937666 |
| Atopobium | 0.006417937666 |
| Saccharofermentans | 0.006339670134 |
| Victivallis | 0.006261402601 |
| Methanimicrococcus | 0.006183135069 |
| Family XIII UCG-001 | 0.006026600004 |
| [Eubacterium] fissicatena group | 0.005556994809 |
| Flavonifractor | 0.005400459743 |
| Sanguibacteroides | 0.005165657146 |
| 28-4 | 0.005165657146 |
| Solobacterium | 0.005009122081 |
| Clostridium sensu stricto 6 | 0.004696051951 |
| Moryella | 0.004539516886 |
| Enterorhabdus | 0.004539516886 |
| Caproiciproducens | 0.004461249353 |
| Arcobacter | 0.004382981821 |
| Caldicoprobacter | 0.004304714288 |
| Erysipelotrichaceae UCG-006 | 0.004226446756 |
| Erysipelotrichaceae UCG-010 | 0.004148179223 |
| Lachnospiraceae UCG-003 | 0.004069911691 |
| Succiniclasticum | 0.003600306496 |
| Jeotgalicoccus | 0.003443771431 |
| Pelistega | 0.003365503898 |
| A2 | 0.003365503898 |
| Coprococcus 1 | 0.003287236366 |
| Bilophila | 0.003287236366 |
| Anaerofustis | 0.003208968833 |
| DNF00809 | 0.003130701301 |
| Acinetobacter | 0.003052433768 |
| [Eubacterium] ruminantium group | 0.002739363638 |
| Dietzia | 0.002739363638 |
| Corynebacterium | 0.002739363638 |
| Methanomicrobium | 0.002582828573 |
| Gordonibacter | 0.00250456104 |
| [Eubacterium] ventriosum group | 0.00219149091 |
| Clostridioides | 0.00219149091 |
| Slackia | 0.002113223378 |
| Lachnospiraceae NK4B4 group | 0.001956688313 |
| Stenotrophomonas | 0.00187842078 |
| Murimonas | 0.001800153248 |
| Eubacterium | 0.001800153248 |
| Catenibacterium | 0.001800153248 |
| Aerosphaera | 0.001721885715 |
| Enterococcus | 0.001643618183 |
| Brevibacterium | 0.001643618183 |
| Serratia | 0.001487083118 |
| [Clostridium] innocuum group | 0.001408815585 |
| Candidatus Methanogranum | 0.001408815585 |
| Fermentimonas | 0.001330548053 |
| Candidatus Methanoplasma | 0.001330548053 |
| Erysipelotrichaceae UCG-008 | 0.00125228052 |
| Chlamydia | 0.00125228052 |
| Ruminococcaceae UCG-001 | 0.001095745455 |
| Coriobacteriaceae UCG-002 | 0.001095745455 |
| Ruminococcaceae UCG-007 | 0.001017477923 |
| Erysipelotrichaceae UCG-009 | 0.001017477923 |
| Lactococcus | 0.0009392103902 |
| Helicobacter | 0.0009392103902 |
| Fibrobacter | 0.0009392103902 |
| Flavobacterium | 0.0008609428577 |
| Facklamia | 0.0008609428577 |
| Lachnospiraceae UCG-009 | 0.0007826753251 |
| Gordonia | 0.0007826753251 |
| Pseudohoeflea | 0.0007044077926 |
| Lachnospiraceae XPB1014 group | 0.0007044077926 |
| Succinivibrionaceae UCG-002 | 0.0006261402601 |

**Supplementary Table S4.** Differentially abundant genera by time point considering the treatment effect.

|  |  |  |  |
| --- | --- | --- | --- |
| **Genus** | **Time point** | **P-value** | **The behaviour of EO vs. CTRL** |
| Bacteroides | T1 | 0.032 | -0.1082255713 |
| Alloprevotella | T1 | 0.042 | -0.083461477 |
| Faecalibacterium | T1 | 0.042 | -0.07114639098 |
| Ruminococcaceae UCG-014 | T1 | 0.024 | -0.04990262563 |
| Blautia | T1 | 0.004 | -0.04734452235 |
| Prevotella 2 | T2 | 0.028 | -0.04551684 |
| Escherichia-Shigella | T1 | 0.049 | -0.01930628431 |
| Odoribacter | T1 | 0.003 | -0.01601543762 |
| Parabacteroides | T1 | 0.031 | -0.00990739325 |
| Desulfovibrio | T1 | 0.038 | -0.007213628188 |
| Lachnospiraceae UCG-008 | T1 | 0.005 | -0.007191420713 |
| Butyricimonas | T1 | 0.035 | -0.003175830801 |
| Fournierella | T1 | 0.023 | -0.003156335113 |
| Erysipelatoclostridium | T1 | 0.046 | -0.000958589825 |
| Syntrophococcus | T1 | 0.042 | -0.000258443715 |
| Flavonifractor | T1 | 0.044 | -0.0002002584138 |
| Howardella | T2 | 0.023 | -0.0001895123775 |
| [Eubacterium] fissicatena group | T1 | 0.018 | -0.0001574886075 |
| 28-4 | T1 | 0.039 | -0.000135367475 |
| Pentatrichomonas | T1 | 0.039 | -8.19E-05 |
| [Eubacterium] ruminantium group | T1 | 0.014 | 5.14E-05 |
| Caldicoprobacter | T2 | 0.023 | 7.55E-05 |
| Pygmaiobacter | T1 | 0.041 | 0.0001902854863 |
| Ruminiclostridium 1 | T2 | 0.017 | 0.0002197081638 |
| Defluviitaleaceae UCG-011 | T1 | 0.002 | 0.0003010802013 |
| Anaerovorax | T1 | 0.027 | 0.000436225175 |
| Ruminococcaceae UCG-011 | T1 | 0.012 | 0.000572855325 |
| [Eubacterium] brachy group | T1 | 0.008 | 0.00063284201 |
| Cellulosilyticum | T1 | 0.023 | 0.000726269475 |
| Candidatus Soleaferrea | T1 | 0.027 | 0.0008924702675 |
| Prevotellaceae UCG-003 | T1 | 0.005 | 0.002153055325 |
| Mailhella | T1 | 0.014 | 0.003556814265 |
| Ruminobacter | T1 | 0.010 | 0.00361514429 |
| Ruminococcaceae UCG-009 | T1 | 0.020 | 0.003896232625 |
| dgA-11 gut group | T1 | 0.009 | 0.004310734625 |
| Ruminococcaceae UCG-013 | T1 | 0.010 | 0.007547157838 |
| Alistipes | T1 | 0.011 | 0.02473722013 |
| Akkermansia | T1 | 0.003 | 0.04232093193 |