**Table S1. Individual animals, parasite burden, samples per region, and *Ascaris* intestines included in the microbiome analysis.**

| **Animal ID** | **Infection** | **Worm burden\*** | **Duodenum** | **Jejunum** | **Ileum** | **Cecum** | **Colon** | ***Ascaris* intestines** |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| ***Pig 1*** | + | 5 | 2 | 1 | 2 | 4 | 3 | 5 |
| ***Pig 2*** | + | 187 | 2 | 4 | 0 | 4 | 3 | 7 |
| ***Pig 3*** | + | 42 | 3 | 4 | 2 | 4 | 3 | 8 |
| ***Pig 4*** | + | 0 | 2 | 3 | 2 | 3 | 3 | 0 |
| ***Pig 5*** | + | 1 | 3 | 2 | 2 | 3 | 3 | 1 |
| ***Pig 6*** | - | - | 0 | 0 | 2 | 3 | 3 | 0 |
| ***Pig 7*** | - | - | 0 | 4 | 2 | 3 | 3 | 0 |
| ***Pig 8*** | - | - | 1 | 4 | 0 | 3 | 3 | 0 |
| ***Pig 9*** | - | - | 3 | 4 | 2 | 3 | 3 | 0 |
| ***Pig 10*** | + | 65 | 3 | 3 | 3 | 3 | 3 | 6 |
| ***Pig 11*** | + | 61 | 2 | 1 | 3 | 3 | 3 | 6 |
| ***Pig 12*** | + | 108 | 1 | 3 | 3 | 3 | 3 | 6 |
| ***Pig 13*** | + | 14 | 0 | 1 | 0 | 3 | 2 | 3 |
| ***Pig 14*** | + | 28 | 1 | 0 | 3 | 3 | 3 | 5 |

**\*At the day of dissection. [1]**

**Table S2. Core ASVs by sample type**

| **Tax ID**  **ASV No: Higher taxonomic annotation** | **Jejunum Infected** | **Jejunum Non infected** | ***Ascaris*** |
| --- | --- | --- | --- |
| ASV1:*Clostridium sensu stricto* 1 | X | X | X |
| ASV2:*Lactobacillus* | X | X | X |
| ASV4:*Escherichia-Shigella* | X |  | X |
| ASV5:*Terrisporobacter* | X | X | X |
| ASV6:*Streptococcus* | X | X | X |
| ASV7:*Romboutsia* | X | X | X |
| ASV9:*Turicibacter sanguinis* | X | X | X |
| ASV11:*Prevotella* | X | X | X |
| ASV12:*Succinivibrio* | X | X |  |
| ASV14:Megasphaera | X | X | X |
| ASV17:*Streptococcus alactolyticus* |  | X |  |
| ASV18:*Clostridium sensu stricto* 1 |  |  | X |
| ASV19:Succinivibrionaceae | X | X |  |
| ASV21:*Clostridium sensu stricto* 1 |  |  | X |
| ASV22:*Lactobacillus* | X | X | X |
| ASV24:*Prevotella* | X | X |  |
| ASV25:*Prevotella copri* | X | X | X |
| ASV26:*Anaerovibrio* |  | X |  |
| ASV27:Prevotellaceae | X | X |  |
| ASV28:*Parasutterella* |  | X |  |
| ASV29:*Lactobacillus pontis* | X |  | X |
| ASV30:*Lactobacillus reuteri* | X | X | X |
| ASV31:*Lactobacillus* | X | X |  |
| ASV32:*Prevotella* | X |  |  |
| ASV34:Prevotellaceae | X | X |  |
| ASV35:*Megasphaera* | X | X | X |
| ASV37:*Clostridium s. s.* 1 *butyricum* | X | X |  |
| ASV38:*Anaerovibrio* | X | X |  |
| ASV40:*Lactobacillus* | X |  | X |
| ASV41:*Intestinibacter* | X | X |  |
| ASV42:*Prevotella* | X |  |  |
| ASV44:Prevotellaceae | X |  |  |
| ASV49:Rickettsiales |  |  | X |
| ASV53:*Anaerovibrio* | X |  |  |
| ASV54:*Prevotella* | X | X |  |
| ASV56:*Anaerovibrio* | X | X |  |
| ASV58:*Parasutterella* |  | X |  |
| ASV59:*Prevotella* | X |  |  |
| ASV61:Prevotellaceae | X | X |  |
| ASV62:*Escherichia*-*Shigella* |  |  | X |
| ASV63:*Subdoligranulum* | X | X |  |
| ASV64:Lachnospiraceae | X |  |  |
| ASV71:*Parasutterella* |  | X |  |
| ASV74:Prevotellaceae | X |  |  |
| ASV76:*Prevotella* | X | X |  |
| ASV78:*Prevotella* | X |  |  |
| ASV88:*Blautia* | X | X |  |
| ASV91:*Lactobacillus* | X |  |  |
| ASV131:Clostridia |  | X |  |
| ASV133:*Subdoligranulum* |  | X |  |
| ASV191:*Parasutterella* |  | X |  |
| ASV197:*Bifidobacterium* |  | X |  |

**Table S3. Permutational analysis of variance for bacterial taxa composition in different gastrointestinal compartments from *Ascaris* infected pigs**

|  | **Df** | **Sums of squares** | **Mean Sqs** | ***F*-Model** | **R2** | **Pr(>*F*)** |
| --- | --- | --- | --- | --- | --- | --- |
| *Host-Parasite* | 1 | 3.8043 | 3.804 | 26.286 | 0.157 | 0.001\*\*\* |
| *Compartment* | 4 | 3.3525 | 0.838 | 5.791 | 0.138 | 0.001\*\*\* |
| *Individual* | 9 | 5.8167 | 0.646 | 4.466 | 0.240 | 0.001\*\*\* |
| **Residuals** | 78 | 11.2888 | 0.145 | - | 0.465 | - |
| **Total** | 92 | 24.2623 | - | - | 1.000 | - |

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Significance codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1, Df: Degrees of freedom, *F*-Model: *pseudo F*-test statistic, R2: Variance explained and *p* value based on 999 permutations.

**Table S4. Permutational analysis of variance for bacterial taxa composition in jejunum and *Ascaris* from infected pigs**

|  | **Df** | **Sums of squares** | **Mean Sqs** | ***F*-Model** | **R2** | **Pr(>*F*)** |
| --- | --- | --- | --- | --- | --- | --- |
| *Host-Parasite* | 1 | 1.1339 | 1.133 | 9.212 | 0.093 | 0.001\*\*\* |
| *Individual* | 8 | 5.5563 | 0.695 | 5.643 | 0.454 | 0.001\*\*\* |
| **Residuals** | 45 | 5.5388 | 0.123 | - | 0.453 | - |
| **Total** | 54 | 16.2289 | - | - | 1.000 | - |

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Significance codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1, Df: Degrees of freedom, *F*-Model: *pseudo F*-test statistic, R2: Variance explained and *p* value based on 999 permutations.

**Table S5. Permutational analysis of variance for bacterial taxa composition in different gastrointestinal compartments from *Ascaris* infected and non-infected pigs**

|  | **Df** | **Sums of squares** | **Mean Sqs** | ***F*-Model** | **R2** | **Pr(>*F*)** |
| --- | --- | --- | --- | --- | --- | --- |
| *Compartment* | 4 | 4.790 | 1.198 | 9.330 | 0.314 | 0.001\*\*\* |
| *Infection Status* | 1 | 1.046 | 1.046 | 8.153 | 0.069 | 0.001\*\*\* |
| *Individual* | 12 | 3.749 | 0.312 | 2.434 | 0.246 | 0.001\*\*\* |
| **Residuals** | 44 | 5.648 | 0.128 | - | 0.371 | - |
| **Total** | 61 | 15.233 | - | - | 1.000 | - |

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Significance codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1, Df: Degrees of freedom, *F*-Model: *pseudo F*-test statistic, R2: Variance explained and *p* value based on 999 permutations.

**Table S6.** **GLMM to assess impact of infection status on microbial dissimilarity among host microbiomes.**

|  | **Estimate** | **SE** | ***t*-value** | **Var explained** | **Chisq** | ***P*-value** |
| --- | --- | --- | --- | --- | --- | --- |
| **Model: Host-Host microbial dissimilarity** | | | | | | |
| Intercept | 0.7258 | 0.0188 | 38.63 | - | - | - |
| ***Same compartment*** | -0.1478 | 0.0087 | -17.084 | 14.7% | 271.14 | **<0.001\*\*** |
| ***Same individual*** | -0.0797 | 0.0157 | -5.068 | 1.7% | 25.25 | **<0.001\*\*** |
| ***Same infection status*** | -0.0342 | 0.0144 | -2.381 | 0.3% | 4.69 | **0.03\*** |

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Significance codes: ‘\*\*\*’ 0.001, ‘\*\*’ 0.01, ‘\*’ 0.05, SE: Standard error, *t*-value: *t*-test statistic, Chisq: Likelihood ratio Chi-squared statistic and *p-*value

**Table S7. Significant differentially abundant ASV between male and female worms**

|  | **log2Fold**  **Change** | **Phylum** | **Family** | **Genus/Species** |  |
| --- | --- | --- | --- | --- | --- |
| ASV116 | 27.96 | Bacteroidota | Prevotellaceae | *Alloprevotella* | Ascaris Males |
| ASV79 | 27.24 | Bacteroidota | Prevotellaceae | *Prevotellaceae* NK3B31 group | Ascaris Males |
| ASV78 | 26.74 | Bacteroidota | Prevotellaceae | *Prevotella* | Ascaris Males |
| ASV124 | 26.10 | Firmicutes | Lachnospiraceae | *Roseburia* | Ascaris Males |
| ASV259 | 26.04 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Ascaris Males |
| ASV228 | 25.98 | Bacteroidota | Prevotellaceae | *Prevotella* | Ascaris Males |
| ASV73 | 25.85 | Bacteroidota | Prevotellaceae | *Prevotellaceae* NK3B31 group | Ascaris Males |
| ASV210 | 24.90 | Firmicutes | Streptococcaceae | *Streptococcus porcorum* | Ascaris Males |
| ASV108 | 24.85 | Firmicutes | Ruminococcaceae | *Ruminococcus* | Ascaris Males |
| ASV141 | 24.78 | Bacteroidota | Prevotellaceae | *Prevotellaceae* NK3B31 group | Ascaris Males |
| ASV128 | 24.42 | Bacteroidota | Prevotellaceae | *Prevotella* | Ascaris Males |
| ASV133 | 24.41 | Firmicutes | Ruminococcaceae | *Subdoligranulum* | Ascaris Males |
| ASV155 | 24.05 | Firmicutes | Veillonellaceae | *Dialister* | Ascaris Males |
| ASV166 | 23.25 | Bacteroidota | Prevotellaceae | *Prevotellaceae NK3B31 group* | Ascaris Males |
| ASV147 | 21.73 | Fibrobacterota | Fibrobacteraceae | *Fibrobacter* | Ascaris Males |
| ASV156 | -28.84 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Ascaris Females |
| ASV51 | -28.43 | Firmicutes | Peptostreptococcaceae | *Terrisporobacter* | Ascaris Females |
| ASV297 | -26.67 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Ascaris Females |
| ASV138 | -24.52 | Firmicutes | Selenomonadaceae | *Mitsuokella jalaludinii* | Ascaris Females |
| ASV82 | -24.17 | Bacteroidota | Prevotellaceae | *Prevotella* | Ascaris Females |

**Table S8. Significant differentially abundant ASV between Hosts and parasites (*Ascaris*)**

|  | **log2 Fold**  **Change** | **Phylum** | **Family** | **Genus** |  |
| --- | --- | --- | --- | --- | --- |
| ASV203 | 30.00 | Firmicutes | Lactobacillaceae | *Lactobacillus* | Host |
| ASV197 | 29.72 | Actinobacteriota | Bifidobacteriaceae | *Bifidobacterium* | Host |
| ASV119 | 29.71 | Bacteroidota | Prevotellaceae | *Prevotellaceae UCG-001* | Host |
| ASV350 | 29.45 | Actinobacteriota | Atopobiaceae | *Coriobacteriaceae UCG-002* | Host |
| ASV226 | 28.84 | Firmicutes | Peptococcaceae | *Peptococcus* | Host |
| ASV248 | 28.28 | Firmicutes | Veillonellaceae | *Megasphaera* | Host |
| ASV400 | 28.08 | Firmicutes | Lactobacillaceae | *Lactobacillus* | Host |
| ASV455 | 27.34 | Firmicutes | Peptostreptococcaceae | *Asaccharospora* | Host |
| ASV266 | 26.96 | Actinobacteriota | Bifidobacteriaceae | *Bifidobacterium* | Host |
| ASV462 | 26.78 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Host |
| ASV430 | 26.49 | Firmicutes | Lactobacillaceae | *Lactobacillus* | Host |
| ASV513 | 26.13 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Host |
| ASV1328 | 26.11 | Actinobacteriota | Bifidobacteriaceae | *Pseudoscardovia* | Host |
| ASV426 | 26.00 | Actinobacteriota | Bifidobacteriaceae | *Bifidobacterium* | Host |
| ASV112 | 25.62 | Bacteroidota | Prevotellaceae | *Prevotella* | Host |
| ASV169 | 25.34 | Bacteroidota | Prevotellaceae | *Prevotella* | Host |
| ASV134 | 24.80 | Bacteroidota | Prevotellaceae | *Prevotellaceae NK3B31 group* | Host |
| ASV15 | -30.00 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Ascaris |
| ASV156 | -28.60 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Ascaris |
| ASV84 | -25.12 | Firmicutes | Lachnospiraceae | *Agathobacter* | Ascaris |
| ASV118 | -24.95 | Bacteroidota | Prevotellaceae | *Prevotellaceae NK3B31 group* | Ascaris |
| ASV141 | -24.63 | Bacteroidota | Prevotellaceae | *Prevotellaceae NK3B31 group* | Ascaris |
| ASV116 | -24.37 | Bacteroidota | Prevotellaceae | *Alloprevotella* | Ascaris |
| ASV124 | -24.16 | Firmicutes | Lachnospiraceae | *Roseburia* | Ascaris |
| ASV73 | -23.73 | Bacteroidota | Prevotellaceae | *Prevotellaceae NK3B31 group* | Ascaris |
| ASV212 | -23.69 | Firmicutes | Lactobacillaceae | *Lactobacillus* | Ascaris |
| ASV66 | -23.30 | Firmicutes | Lachnospiraceae | *Lachnospira* | Ascaris |
| ASV259 | -22.52 | Firmicutes | Clostridiaceae | *Clostridium sensu stricto 1* | Ascaris |
| ASV228 | -22.15 | Bacteroidota | Prevotellaceae | *Prevotella* | Ascaris |
| ASV155 | -21.58 | Firmicutes | Veillonellaceae | *Dialister* | Ascaris |
| ASV367 | -21.48 | Firmicutes | Staphylococcaceae | *Staphylococcus* | Ascaris |
| ASV82 | -21.18 | Bacteroidota | Prevotellaceae | *Prevotella* | Ascaris |
| ASV111 | -21.11 | Bacteroidota | Prevotellaceae | *Prevotellaceae NK3B31 group* | Ascaris |
| ASV505 | -21.06 | Firmicutes | Streptococcaceae | *Streptococcus* | Ascaris |
| ASV215 | -20.40 | Firmicutes | Ruminococcaceae | *Ruminococcus* | Ascaris |
| ASV315 | -19.77 | Firmicutes | Lachnospiraceae | *Anaerosporobacter* | Ascaris |
| ASV171 | -11.77 | Proteobacteria | Pseudomonadaceae | *Pseudomonas* | Ascaris |
| ASV4 | -2.65 | Proteobacteria | Enterobacteriaceae | *Escherichia-Shigella* | Ascaris |