

| Isolate ID                | Species              | Host (mouse strain)                | Duration of colonisation | Source                    | Bacterial genotype           |
|---------------------------|----------------------|------------------------------------|--------------------------|---------------------------|------------------------------|
| EG <sub>F1</sub> -LV1     | <i>E. gallinarum</i> | SPF (NZW x BXSb)<br>F <sub>1</sub> | unknown                  | liver                     | See Supplementary Table 1    |
| EG <sub>F1</sub> -FE4     | <i>E. gallinarum</i> | SPF (NZW x BXSb)<br>F <sub>1</sub> | unknown                  | faeces                    | reference genome             |
| EG <sub>mono6</sub> -LV1  | <i>E. gallinarum</i> | Monocolonised<br>C57BL/6           | 3 months                 | liver                     | <i>manY/lacE/ypdA</i> mutant |
| EG <sub>mono6</sub> -LV10 | <i>E. gallinarum</i> | Monocolonised<br>C57BL/6           | 3 months                 | liver                     | <i>immR</i> mutant           |
| EG <sub>mono7</sub> -FE2  | <i>E. gallinarum</i> | Monocolonised<br>C57BL/6           | 3 months                 | faeces                    | <i>walK/manX</i> mutant      |
| EG <sub>mock</sub> -LV1   | <i>E. gallinarum</i> | Mock community<br>C57BL/6          | 7 weeks                  | liver                     | <i>immR</i> mutant           |
| EG <sub>mock</sub> -FE1   | <i>E. gallinarum</i> | Mock community<br>C57BL/6          | 7 weeks                  | faeces                    | <i>mga</i> mutant            |
| EG <sub>SPF1</sub> -SIM1  | <i>E. gallinarum</i> | SPF C57BL/6                        | 1.5 years                | small intestine<br>mucosa | <i>spxA</i> mutant           |
| EG <sub>SPF2</sub> -SIM2  | <i>E. gallinarum</i> | SPF C57BL/6                        | 1.5 years                | small intestine<br>mucosa | <i>yxdM</i> mutant           |
| EG <sub>SPF1</sub> -FE1   | <i>E. gallinarum</i> | SPF C57BL/6                        | 1.5 years                | faeces                    | <i>norD/yocH</i> mutant      |
| LR <sub>mono</sub> -LV1   | <i>L. reuteri</i>    | Monocolonised<br>C57BL/6           | 3 months                 | liver                     | <i>lacS/greA/ccpA</i> mutant |
| LR <sub>mono</sub> -FE7   | <i>L. reuteri</i>    | Monocolonised<br>C57BL/6           | 3 months                 | faeces                    | <i>peg257*</i> mutant        |
| BF <sub>mono1</sub> -SIM5 | <i>B. fragilis</i>   | Monocolonised<br>C57BL/6           | 3 months                 | small intestine<br>mucosa | <i>susC</i> mutant           |
| BF <sub>mono2</sub> -SIM8 | <i>B. fragilis</i>   | Monocolonised<br>C57BL/6           | 3 months                 | small intestine<br>mucosa | <i>peg3916**</i> mutant      |
| BF <sub>mono1</sub> -FE6  | <i>B. fragilis</i>   | Monocolonised<br>C57BL/6           | 3 months                 | faeces                    | <i>rscC</i> mutant           |

\**peg257* gene is annotated by RAST to encode a protein contains gram positive anchor domain.

\*\**peg3916* gene is annotated by RAST to encode an uncharacterized MFS-type transporter.

### Supplementary Table 7 | Metadata of select bacterial strains used in this study.