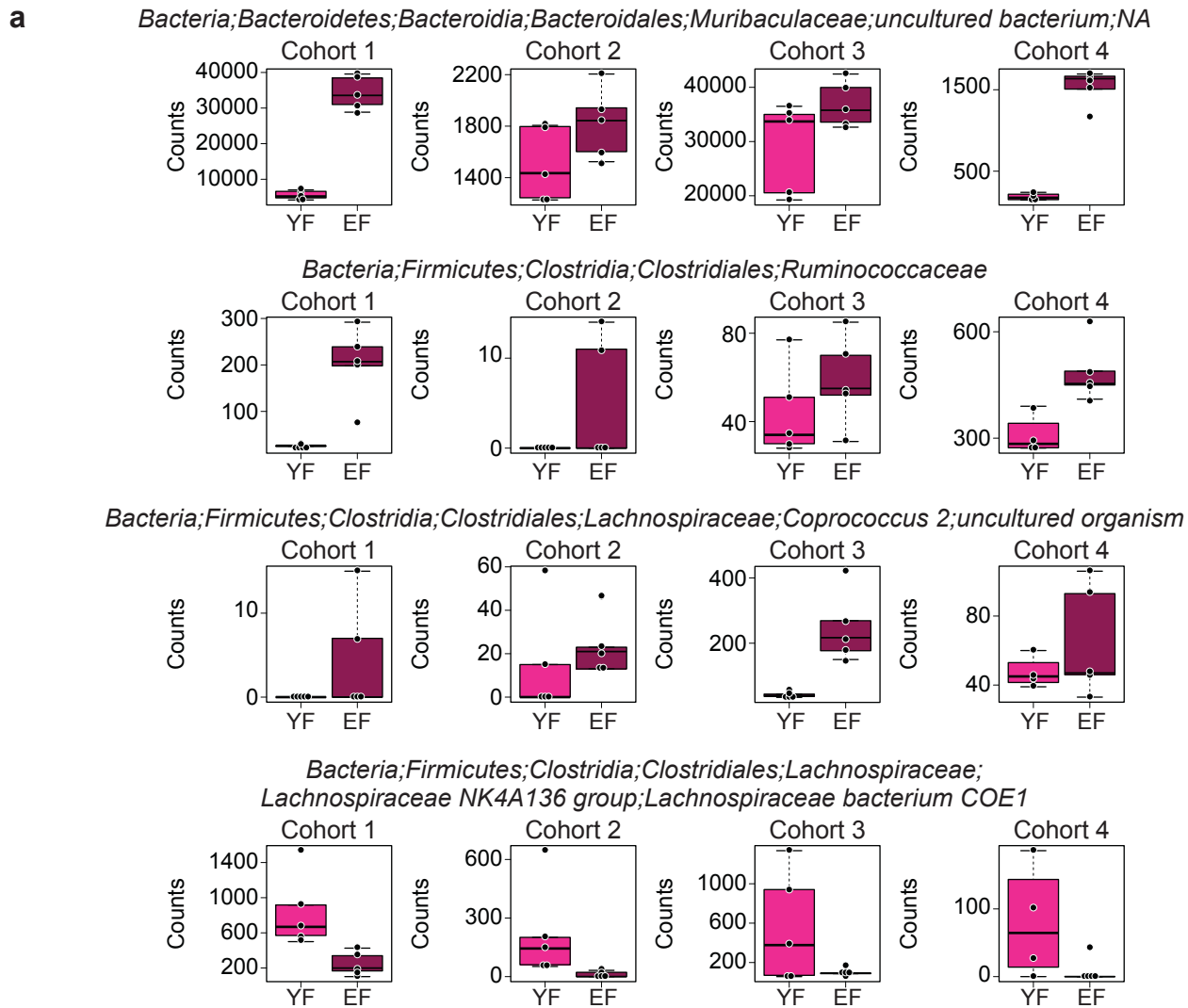


Estropausal gut microbiota transplant improves measures of ovarian function in adult mice

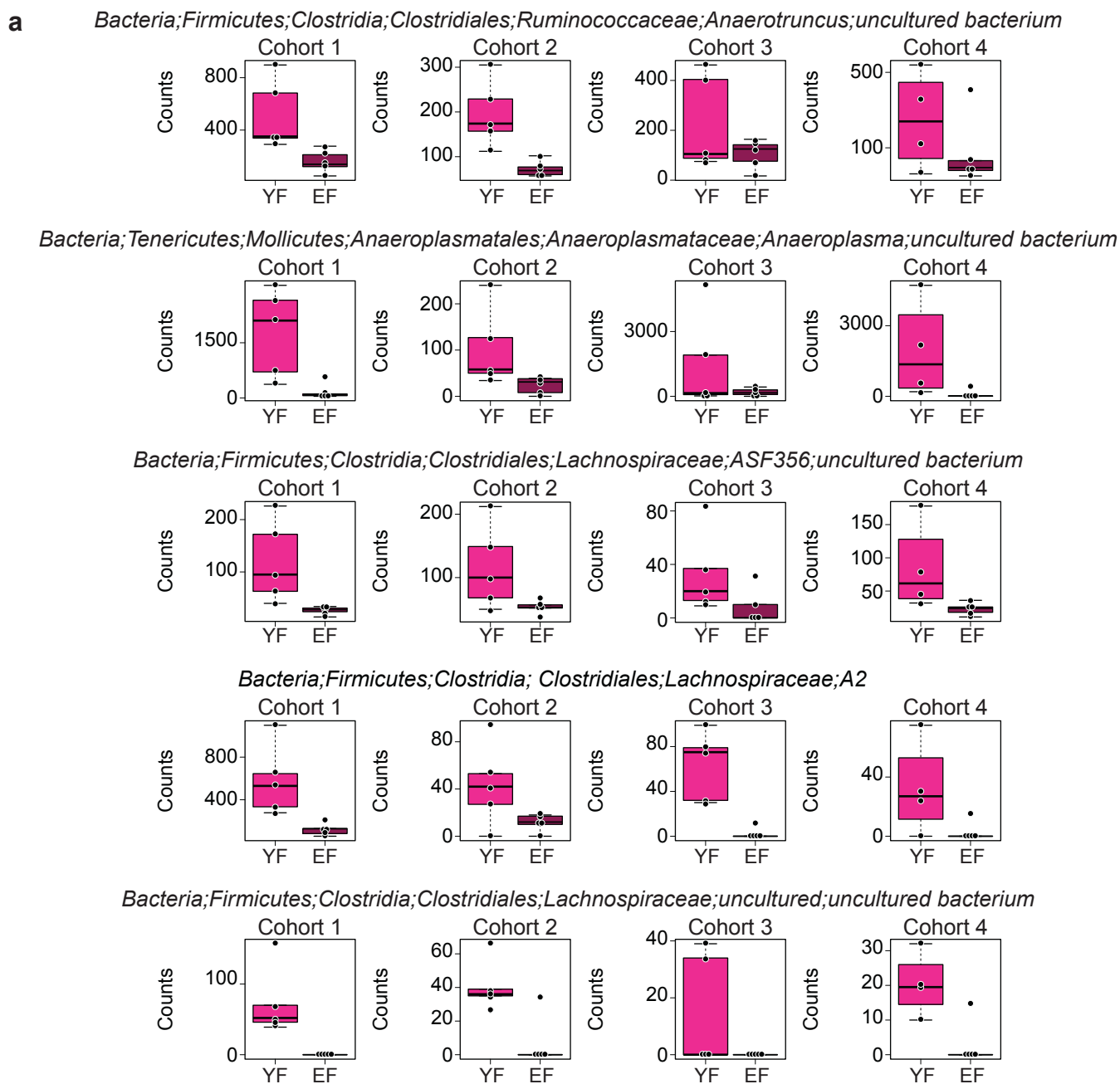
In the format provided by the
authors and unedited

Supplementary Fig. 1



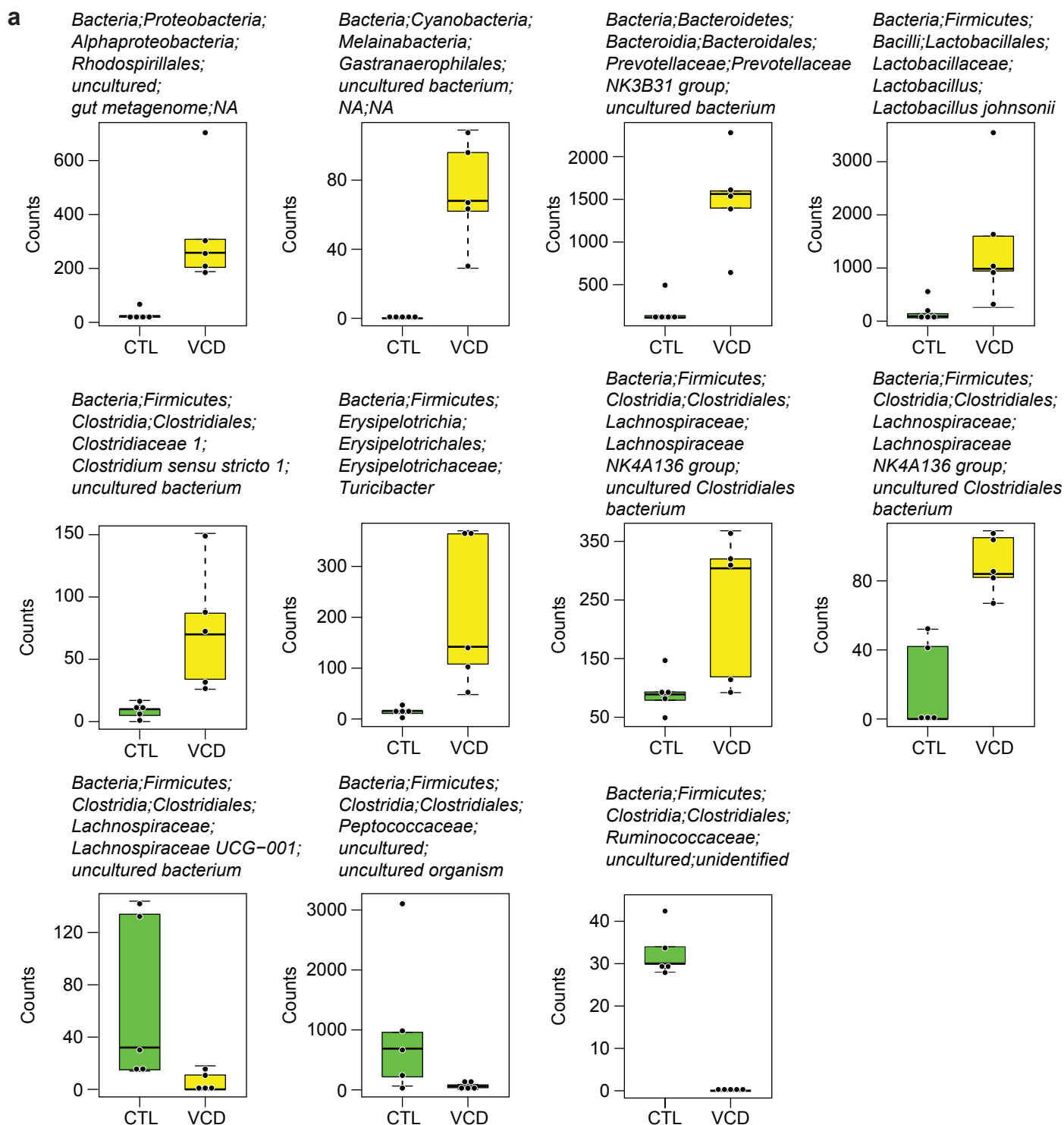
Supplementary Fig. 1: Characterization of fecal microbial profiles of young and estropausal female mice. a, Boxplots of base abundance of differentially abundant microbial genera. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown. YF: Young female; EF: Estropausal female.

Supplementary Fig. 2



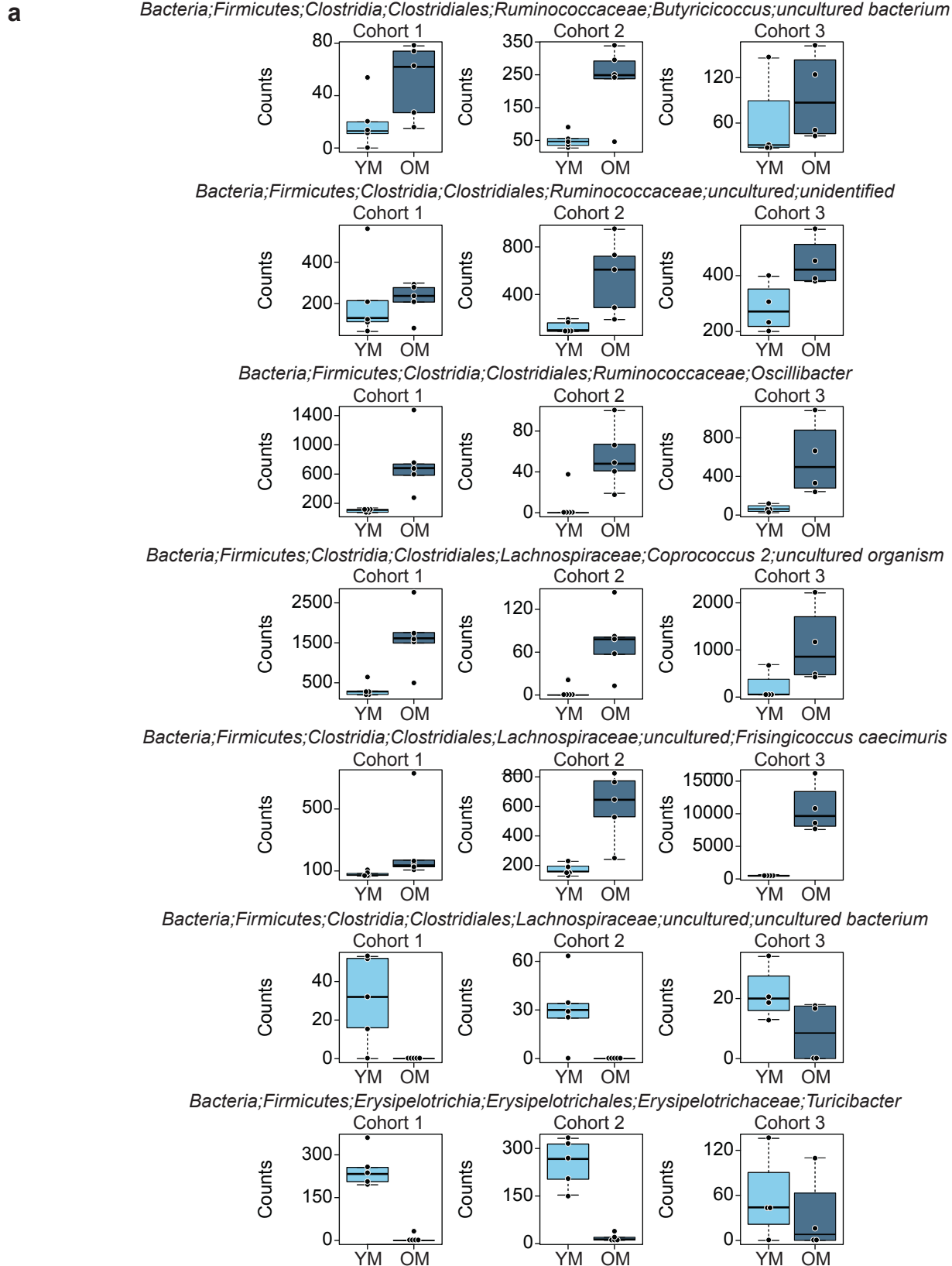
Supplementary Fig. 2: Characterization of fecal microbial profiles of young and estropausal female mice. a, Boxplots of base abundance of differentially abundant microbial genera. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown. YF: Young female; EF: Estropausal female.

Supplementary Fig. 3



Supplementary Fig. 3: Differential abundance analysis of 16S amplicon sequencing data of VCD cohort female mice. a, Boxplots of base abundance of differentially abundant microbial genera between control and VCD-injected female mice. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown.

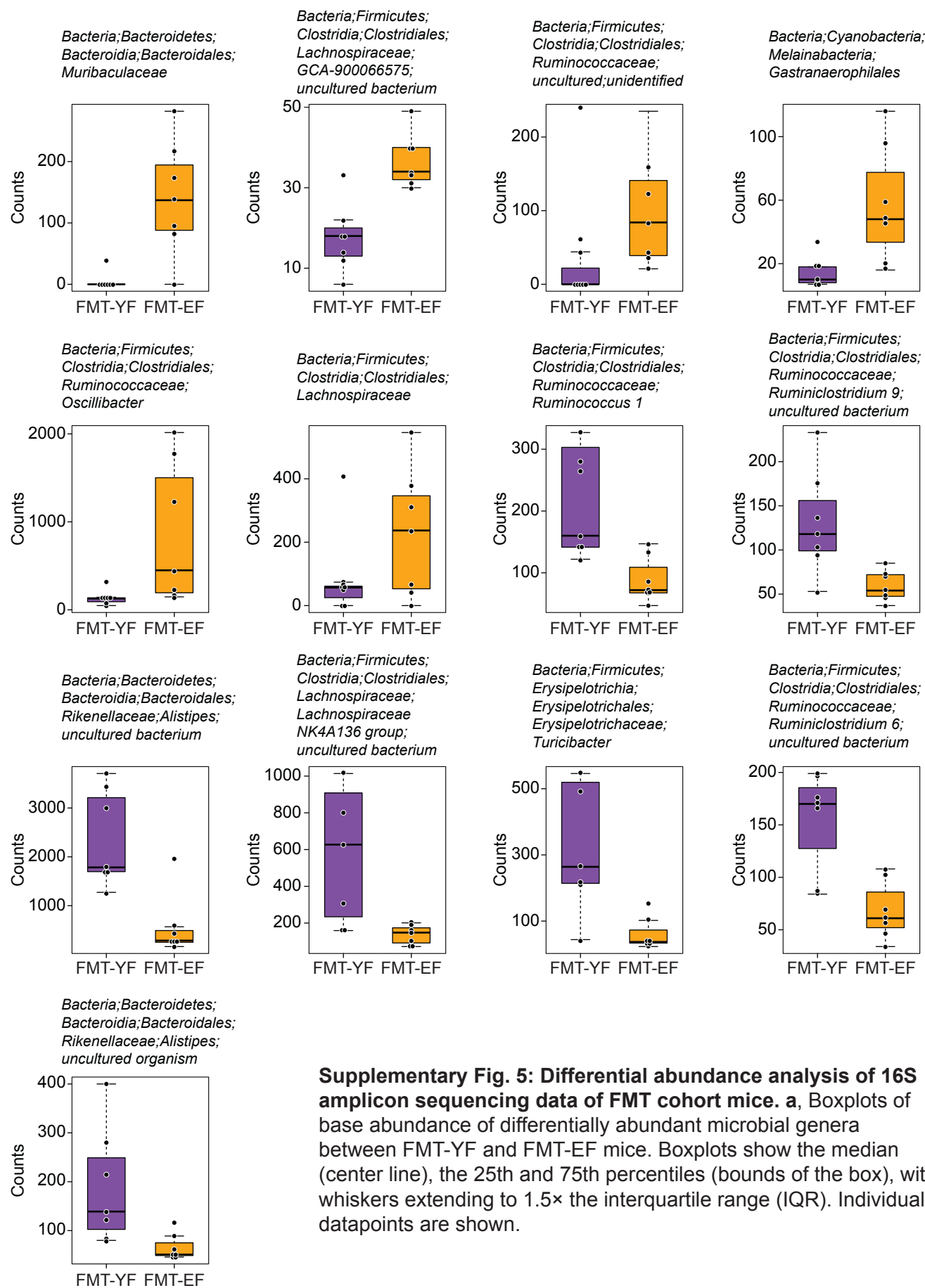
Supplementary Fig. 4



Supplementary Fig. 4: Differential abundance analysis of 16S amplicon sequencing data of young and old male mice. **a**, Boxplots of base abundance of differentially abundant microbial genera between young and old male mice. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown.

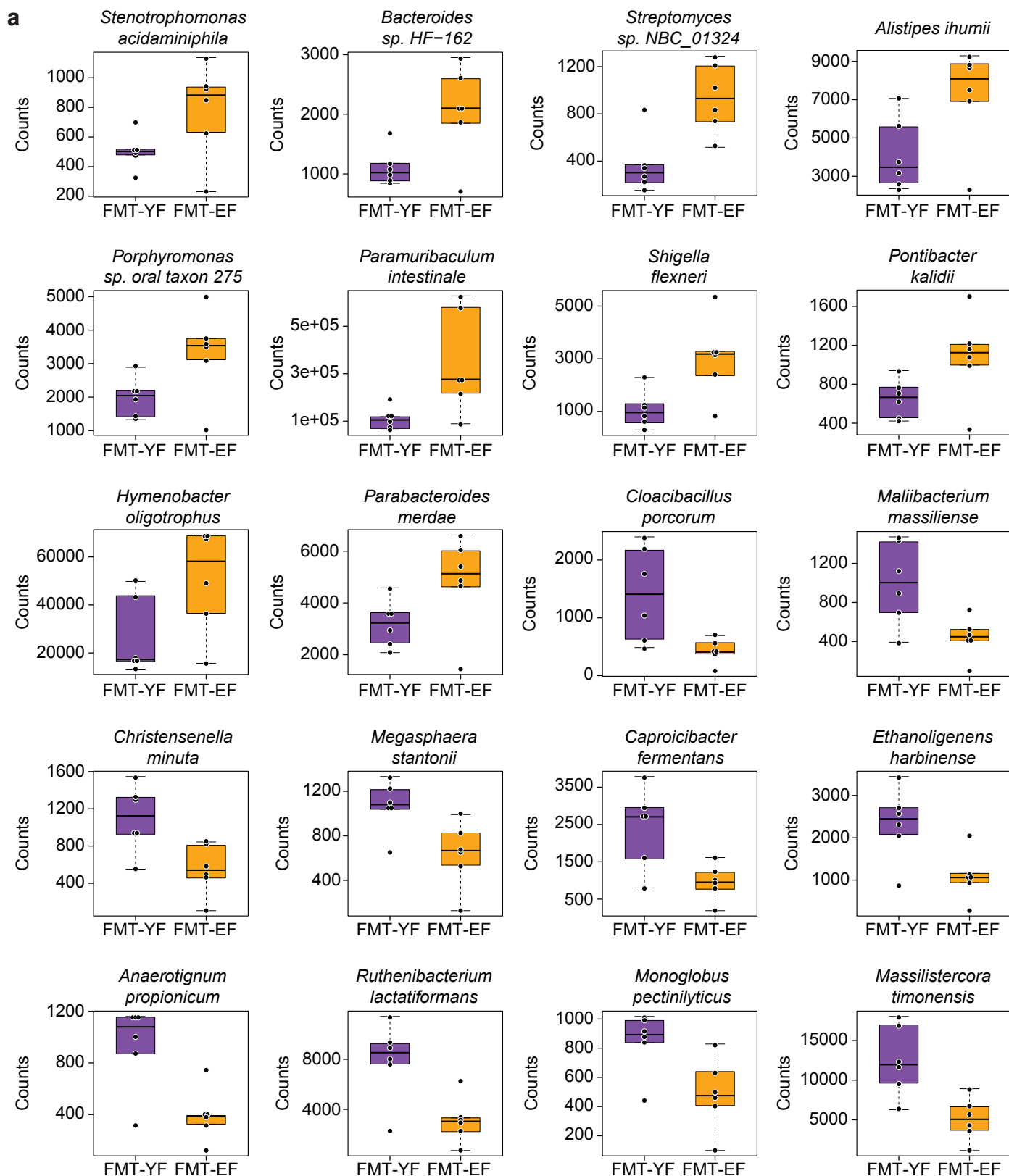
Supplementary Fig. 5

a



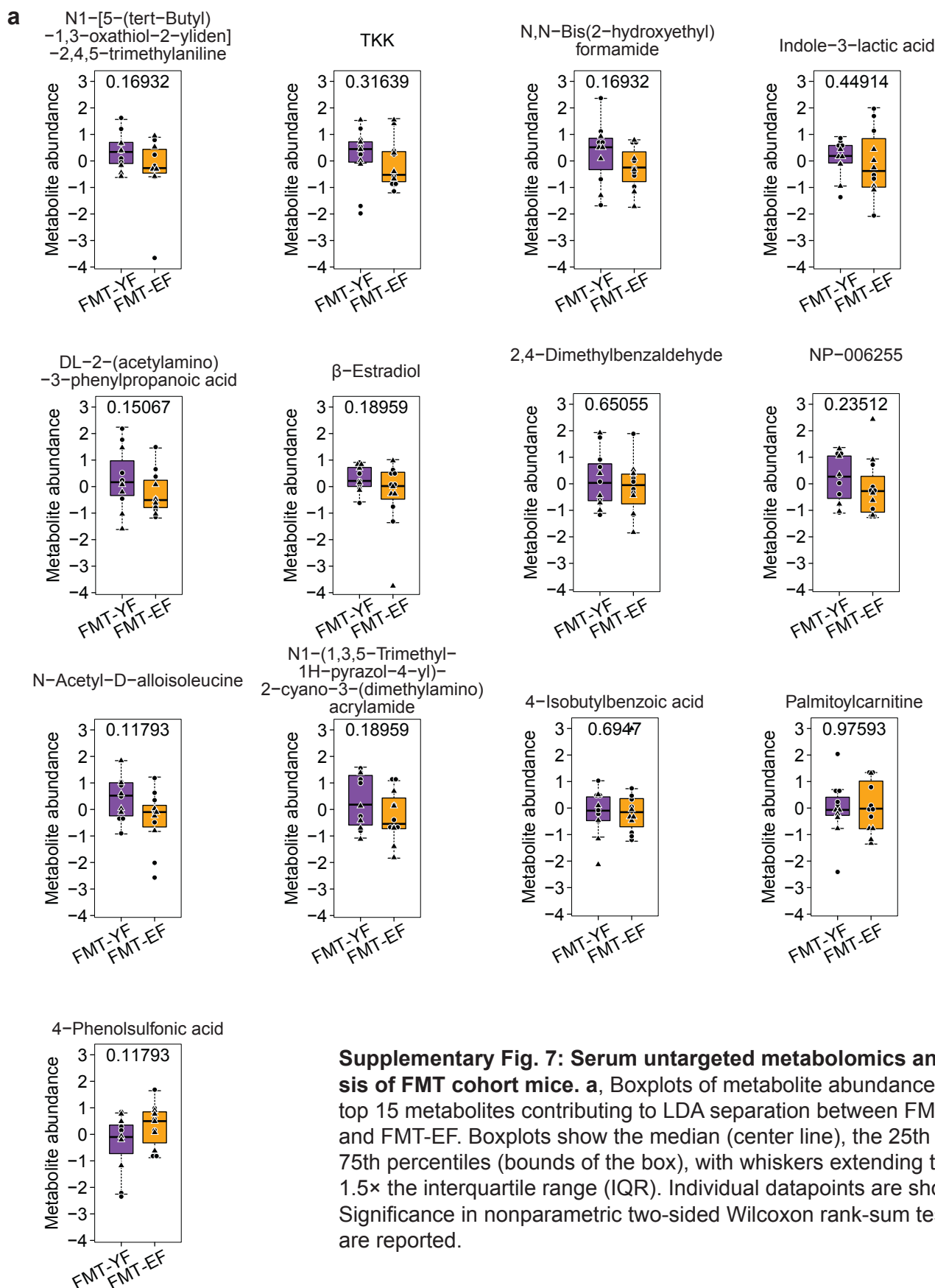
Supplementary Fig. 5: Differential abundance analysis of 16S amplicon sequencing data of FMT cohort mice. a, Boxplots of base abundance of differentially abundant microbial genera between FMT-YF and FMT-EF mice. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown.

Supplementary Fig. 6



Supplementary Fig. 6: Differential abundance analysis of shotgun metagenomics data of FMT cohort mice. a. Boxplots of base abundance of differentially abundant microbial species between FMT-YF and FMT-EF mice. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown.

Supplementary Fig. 7



Supplementary Fig. 7: Serum untargeted metabolomics analysis of FMT cohort mice. a, Boxplots of metabolite abundances of top 15 metabolites contributing to LDA separation between FMT-YF and FMT-EF. Boxplots show the median (center line), the 25th and 75th percentiles (bounds of the box), with whiskers extending to 1.5× the interquartile range (IQR). Individual datapoints are shown. Significance in nonparametric two-sided Wilcoxon rank-sum tests are reported.

Supplementary Table 1.

Mouse ID	Group	Cohort	Weight (g)	
			Day_0	Day_16
MM051	FMT_YF	1	25	25
MM052	FMT_YF	1	22	22
MM058	FMT_EF	1	27	26
MM059	FMT_EF	1	21	21
MM060	FMT_EF	1	23.5	21
MM061	FMT_YF	1	27.5	26
MM062	FMT_YF	1	26	25.5
MM063	FMT_YF	1	25.5	24
MM064	FMT_YF	1	23.5	23
MM065	FMT_YF	1	24.5	24.5
MM066	FMT_EF	1	26	24.5
MM067	FMT_EF	1	27.5	26
MM068	FMT_EF	1	23.5	23
MM070	FMT_EF	1	23.5	23.5
MM157	FMT_YF	2	24	22
MM158	FMT_YF	2	19	22
MM159	FMT_YF	2	20	20
MM160	FMT_YF	2	20	19
MM161	FMT_YF	2	19	20
MM162	FMT_EF	2	22	23
MM163	FMT_EF	2	20	18
MM164	FMT_EF	2	19	21
MM165	FMT_EF	2	18	18
MM166	FMT_EF	2	19	18

Supplementary Table 1. Weight measurements of FMT cohort.

Supplementary Table 2.

Mouse ID	Group	Estrous cycle staging
MM051	FMT_YF	Estrus
MM052	FMT_YF	Diestrus
MM058	FMT_EF	Estrus
MM059	FMT_EF	Estrus
MM060	FMT_EF	Estrus
MM061	FMT_YF	Estrus
MM062	FMT_YF	Estrus
MM063	FMT_YF	Estrus
MM064	FMT_YF	Proestrus
MM065	FMT_YF	Estrus
MM066	FMT_EF	Estrus
MM067	FMT_EF	Estrus
MM068	FMT_EF	Metestrus
MM070	FMT_EF	Estrus

Supplementary Table 2. Estrous cycle staging data of FMT cohort.