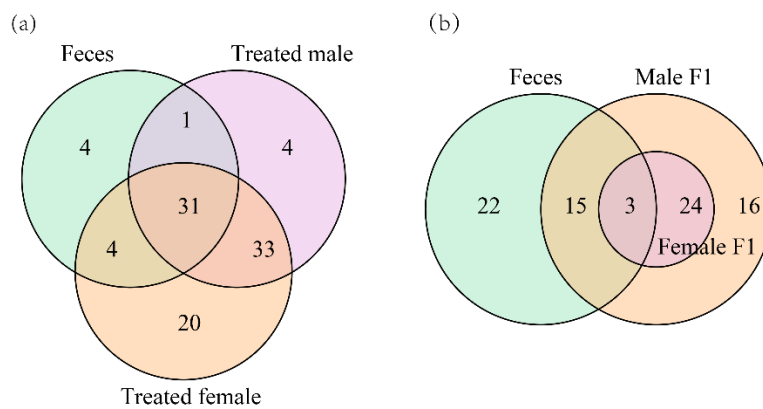


Table S1. Primer Sequences of qRT-PCR used in this study

Gene	Primer sequences (5'→3')	Reference
<i>Sir2</i>	CCGTTACTGAGGAGGAGCTG; GTAGATCGCACACGTCCTTG	[1]
<i>Srl</i>	CTCTTGGAGTCCGAGATCCGCAA; GGGACCGCGAGCTGATGGTT	[1]
<i>InR</i>	AACAGTGGCGGATTTCGGTT; TACTCGGAGCATTGGAGGCAT	[2]
<i>Tor</i>	GCTCAGAGGCGAGAGACAAG; CCAGCTCACGGAGGATAAAG	[3]
<i>Rp49</i>	GACGCTTCAAGGGACAGTATCTG; AAACGCGGTTCTGCATGA	[4]

Table S2. qRT-PCR procedure setting

Step	Time	Temperature
Hot start	2 min	95 °C
PCR reaction	15 s	95 °C
	25 s	55 °C
	35 s	72 °C
melting curve		1 °C / s

Figure S1. Venn diagram of OUT level**Table S3.** Fecal genera that uncolonized in drosophila

Uncolonized fecal genera in treated male group		
	Feces	Male
<i>Veillonella</i>	0.1550%	0.0000%
<i>Bacteroides</i>	0.1133%	0.0000%
<i>Ruminococcaceae</i> UCG-013	0.0817%	0.0000%
<i>uncultured bacterium</i>	0.0133%	0.0000%
<i>Neisseria</i>	0.0017%	0.0000%
Uncolonized fecal genera in treated female group		
Species	Feces	Female
<i>Clostridium sensu stricto 1</i>	0.0217%	0.0000%
<i>Ruminococcaceae</i> UCG-013	0.0817%	0.0000%

<i>Neisseria</i>	0.0017%	0.0000%
Uncolonized fecal genera in female F1		
	Feces	Female F1
<i>Bifidobacterium</i>	76.9050%	0.0000%
<i>Other</i>	14.0300%	0.0000%
<i>Lachnoclostridium</i>	3.2267%	0.0000%
<i>Subdoligranulum</i>	0.6883%	0.0000%
<i>Akkermansia</i>	0.6650%	0.0000%
<i>Escherichia-Shigella</i>	0.4083%	0.0000%
<i>uncultured bacterium</i>	0.3083%	0.0000%
<i>Veillonella</i>	0.1550%	0.0000%
<i>Bacteroides</i>	0.1133%	0.0000%
<i>Peptoclostridium</i>	0.1100%	0.0000%
<i>Intestinibacter</i>	0.1017%	0.0000%
<i>Ruminococcaceae UCG-013</i>	0.0817%	0.0000%
<i>Eggerthella</i>	0.0467%	0.0000%
<i>Erysipelatoclostridium</i>	0.0267%	0.0000%
<i>Clostridium sensu stricto 1</i>	0.0217%	0.0000%
<i>uncultured bacterium</i>	0.0133%	0.0000%
<i>Klebsiella</i>	0.0117%	0.0000%
<i>Proteus</i>	0.0067%	0.0000%
<i>Enterobacter</i>	0.0050%	0.0000%
<i>Neisseria</i>	0.0017%	0.0000%
Uncolonized fecal genera in male F1		
	Feces	Female F1
<i>Escherichia-Shigella</i>	0.4083%	0.0000%
<i>Veillonella</i>	0.1550%	0.0000%
<i>Peptoclostridium</i>	0.1100%	0.0000%
<i>Intestinibacter</i>	0.1017%	0.0000%
<i>Eggerthella</i>	0.0467%	0.0000%
<i>Erysipelatoclostridium</i>	0.0267%	0.0000%
<i>uncultured bacterium</i>	0.0133%	0.0000%
<i>Proteus</i>	0.0067%	0.0000%
<i>Neisseria</i>	0.0017%	0.0000%

Table S4. The exposure of fecal microbes has enriched Male F1 with species that do not exist in the original intestinal bacteria of drosophila

Species	Feces	CK	Male F1
<i>Subdoligranulum</i>	0.6883%	0.0000%	0.0033%
<i>Akkermansia</i>	0.6650%	0.0000%	0.0083%
<i>Bacteroides</i>	0.1133%	0.0000%	0.0117%
<i>Ruminococcaceae UCG-013</i>	0.0817%	0.0000%	0.0067%
<i>Clostridium sensu stricto 1</i>	0.0217%	0.0000%	0.0017%
<i>Klebsiella</i>	0.0117%	0.0000%	0.0083%
<i>Enterobacter</i>	0.0050%	0.0000%	0.0033%

Table S5. Adonis analysis on genus level in treated male drosophila

	Df	Sums Of Sqs	Mean Sqs	F.Model	R2	Pr(>F)	Sig
Group	1	2.9790	1.48949	6.4819	0.32439	0.001	***
Residuals	27	6.2044	0.22979	0.67561			
Total	29	9.1834	1.00000				

Table S6. Adonis analysis on genus level in treated female drosophila

	Df	Sums Of Sqs	Mean Sqs	F.Model	R2	Pr(>F)	Sig
Group	1	0.5969	0.59694	2.9681	0.10612	0.036	*
Residuals	25	5.0280	0.20112	0.89388			
Total	26	5.6250	1.00000				

Table S7. Relative abundance of intestinal bacterial phyla in male drosophila under the exposure of fecal microorganisms

OTU ID	Feces	D10 CK	D20 CK	D30 CK	D10 Male Treated	D20 Male Treated	D30 Male Treated	Male F1
Actinobacteria	76.95%	0.01%	0.01%	0.00%	0.05%	0.12%	53.21%	0.02%
Bacteroidetes	0.42%	0.00%	0.00%	0.01%	0.00%	0.01%	0.60%	0.04%
Firmicutes	21.51%	1.51%	0.32%	1.21%	15.10%	2.86%	31.27%	0.20%

Table S8. Shannon index of male drosophila group

	Feces	D10 CK	D20 CK	D30 CK	D10 Male Treated	D20 Male Treated	D30 Male Treated	Male F1
shannon	2.54	0.81	0.80	0.87	2.35	2.80	3.61	1.15

Table S9. Shannon index of female drosophila group

	Feces	D10 CK	D20 CK	D30 CK	D10 Female Treated	D20 Female Treated	D30 Female Treated	Female F1
shannon	2.54	1.29	1.26	1.09	1.36	2.41	1.76	0.72

Table S10. Relative abundance of bacteria in fecal samples TOP 20 (male drosophila group)

[illegible]

<i>Intestinibacter</i>	0.00%	0.00%	0.10%	0.00%	0.00%	0.00%	0.00%	0.00%	0.31%	0.00%
<i>Ruminococcaceae UCG-013</i>	0.00%	0.00%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%
<i>Eggerthella</i>	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.00%	0.05%	0.00%
<i>Erysipelatoclostridium</i>	0.00%	0.03%	0.03%	0.00%	0.00%	0.00%	0.00%	0.00%	0.02%	0.00%
<i>Clostridium sensu stricto 1</i>	0.00%	0.02%	0.02%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>uncultured bacterium</i>	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
<i>Klebsiella</i>	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.09%	0.01%

Table S11. Relative abundance of bacteria in fecal samples TOP 20 (female drosophila group)

OTU ID	D0	Abx	Feces	D10 CK	D20 CK	D30 CK	D10 Female Treated	D20 Female Treated	D30 Female Treated	Female F1
<i>Bifidobacterium</i>	0.00%	0.01%	76.91%	0.05%	0.01%	0.00%	0.71%	5.91%	17.57%	0.00%
<i>Other</i>	0.02%	0.79%	14.03%	0.00%	0.00%	0.00%	0.02%	0.13%	0.12%	0.00%
<i>Lachnoclostridium</i>	0.06%	2.74%	3.23%	0.00%	0.00%	0.00%	0.03%	0.35%	0.44%	0.00%
<i>Enterococcus</i>	13.06%	0.08%	2.63%	0.14%	0.79%	0.95%	1.68%	0.21%	0.43%	0.00%
<i>Subdoligranulum</i>	0.00%	0.00%	0.69%	0.00%	0.00%	0.00%	0.00%	0.00%	0.01%	0.00%
<i>Akkermansia</i>	0.00%	0.00%	0.67%	0.00%	0.00%	0.00%	0.03%	0.00%	0.01%	0.00%
<i>Escherichia-Shigella</i>	0.01%	0.33%	0.41%	0.00%	0.00%	0.00%	0.00%	0.09%	3.47%	0.00%
<i>uncultured bacterium</i>	0.00%	0.03%	0.31%	0.00%	0.00%	0.00%	0.00%	0.03%	0.03%	0.00%
<i>Streptococcus</i>	0.01%	0.23%	0.31%	0.02%	0.01%	0.00%	0.00%	0.04%	0.05%	0.00%
<i>Veillonella</i>	0.00%	0.00%	0.16%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Lactobacillus</i>	3.28%	1.27%	0.13%	14.95%	0.76%	0.32%	7.10%	20.81%	76.20%	0.03%
<i>Bacteroides</i>	0.00%	0.16%	0.11%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Peptoclostridium</i>	0.00%	0.00%	0.11%	0.00%	0.00%	0.00%	0.01%	0.11%	0.30%	0.00%
<i>Intestinibacter</i>	0.00%	0.01%	0.10%	0.00%	0.00%	0.00%	0.01%	0.10%	0.39%	0.00%
<i>Ruminococcaceae UCG-013</i>	0.00%	0.03%	0.08%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Eggerthella</i>	0.00%	0.00%	0.05%	0.00%	0.00%	0.00%	0.00%	0.01%	0.04%	0.00%
<i>Erysipelatoclostridium</i>	0.00%	0.13%	0.03%	0.00%	0.00%	0.00%	0.00%	0.01%	0.03%	0.00%
<i>Clostridium sensu stricto 1</i>	0.00%	0.01%	0.02%	0.00%	0.00%	0.00%	0.00%	0.07%	0.01%	0.00%
<i>uncultured bacterium</i>	0.00%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%
<i>Klebsiella</i>	0.01%	0.00%	0.01%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%	0.00%

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