Table S1 Analysis of similarity (ANOSIM) of gut microbiota composition in SD rats

Groups	R	*P*.value	Dissimilarity	Permutation
Females-F VS Males-F	0.14	0.06	Bray-curtis	999
Females-J VS Males-J	0.25	0.02	Bray-curtis	999

F stands for fecal samples; J stands for jejunal samples, n=10 per group

Table S2 Permutational multivariate analysis of variance (PERMANOVA) of gut microbiota composition in SD rats.

Groups	Df	SumsOfSqs	F.Model	R2	*P*.value
Females-F VS Males-F	1	0.29	1.95	0.10	0.049
Females-J VS Males-J	1	0.63	3.07	0.15	0.02

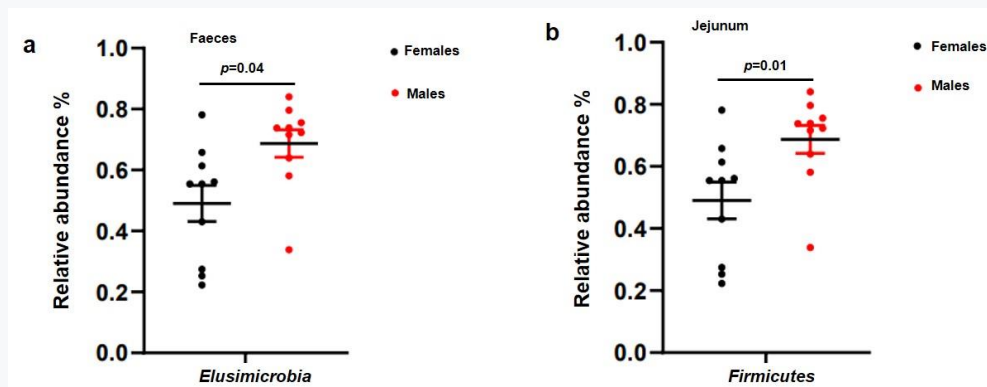F stands for fecal samples; J stands for jejunal samples, n=10 per group.

Fig. S1 Relative abundances distributions per group for the taxa (at phylum level). In faeces or jejunum, the individuals are grouped by Females, Males, n=10 per group, *P* values from Mann–Whitney U test. .shown for the bacterial taxonomic rank of phylum.

Table S3 The influence of sex on the structure of intestinal microflora

Samples	Taxonomy (Family or Genus)	Relative abundance (%, Mean values±SD, n=10)		*p*-value (adjusted)*
		Females	Males	
Faeces	*Alloprevotella*	**0.04±0.04**	0.01±0.04	0.002
	Elusimicrobium	0.01±0.01	**0.030±0.01**	0.04
	Helicobacter	**0.01±0.01**	0.001±0.001	0.01
	Lachnospiracea_incertae_sedis	0.001±0.001	**0.01±0.003**	0.0005
	Desulfovibrionaceae	**0.003±0.003**	0.001±0.001	0.02
Jejunum	*Anaerorhabdus*	0.002+0.002	**0.01±0.004**	0.03
	Blautia	0.05±0.06	**0.12±0.10**	0.04
	Corynebacterium	0.002+0.005	**0.01±0.01**	0.02
	Roseburia	**0.01±0.02**	0.0002±0.0003	0.01
	Rothia	**0.32±0.24**	0.10±0.16	0.01
	Lachnospiraceae	0.005±0.006	**0.01±0.01**	0.04
	Coriobacteriaceae	0.007±0.01	**0.03±0.03**	0.02

* *p* value were adjusted using Benjamini-Hochberg FDR