

Table S1 Effects of dietary protein restriction on relative abundance of microbes (Top 10, %) in gut microbiota at the phylum level in gilts and barrows.

Items	High protein diet		Normal protein diet		Low protein diet		SEM	P values		
	Gilts	Barrows	Gilts	Barrows	Gilts	Barrows		Diet	Sex	Diet × Sex
<i>Firmicutes</i>	21.22	26.18	36.40	53.61	50.06	25.60	5.008	0.192	0.940	0.250
<i>Bacteroidetes</i>	27.09	28.70	25.69	17.71	17.12	24.67	1.834	0.248	0.914	0.220
<i>Proteobacteria</i>	19.99	6.704	21.63	12.36	8.827	16.68	1.993	0.618	0.227	0.112
<i>Fusobacteria</i>	15.60 ^a	15.53 ^x	5.486 ^a	5.443 ^y	11.37 ^{ab}	14.50 ^x	1.571	0.022	0.750	0.903
<i>Gracilibacteria</i>	1.912	0.634	3.828	0.401	0.260	1.024	0.704	0.689	0.357	0.483
<i>Actinobacteria</i>	2.250 ^a	4.942 ^x	3.324 ^a	3.098 ^x	5.600 ^a	11.18 ^y	0.745	0.018	0.081	0.293
<i>Spirochaetes</i>	1.092	6.471	0.523	0.995	4.067	1.224	0.680	0.161	0.466	0.071
Unidentified Bacteria	10.62 ^a	8.673 ^x	2.893 ^b	5.765 ^x	1.929 ^b	4.757 ^x	0.815	0.007	0.448	0.380
<i>Synergistetes</i>	0.033 ^a	1.702 ^x	0.022 ^a	0.060 ^y	0.505 ^a	0.191 ^y	0.128	0.028	0.077	0.008
<i>Euryarchaeota</i>	0.001	0.130	0.049	0.019	0.013	0.006	0.020	0.550	0.452	0.209

SEM, standard error of the mean (n = 48, 8 per group).

Mean values with different letters (a, b, and c for gilts; x, y, and z for barrows) or the same letters indicate significant or no statistical difference among diets within the same sex, respectively.

$P < 0.05$ was considered statistically significant.

Table S2 Effects of dietary protein restriction on relative abundance of communities (Top 30, %) in gut microbiota at the genus level in gilts and barrows.

Items	High protein diet		Normal protein diet		Low protein diet		SEM	P values		
	Gilts	Barrows	Gilts	Barrows	Gilts	Barrows		Diet	Sex	Diet × Sex
Unidentified <i>Clostridiales</i>	1.203	7.991	4.591	10.11	14.55	12.97	1.658	0.077	0.288	0.541
<i>Neisseria</i>	14.77	1.384 *	10.71	6.560 ^{NS}	0.869	2.749 ^{NS}	1.224	0.052	0.039	0.043
Unidentified <i>Prevotellaceae</i>	16.59 ^a	4.165 ^{x *}	14.96 ^a	1.598 ^{x *}	1.806 ^b	2.839 ^{x NS}	1.029	0.007	0.000	0.011
<i>Terrisporobacter</i>	0.001	8.739	2.632	5.045	9.423	5.751	1.169	0.379	0.293	0.101
<i>Leptotrichia</i>	15.75 ^a	5.627 ^x	2.957 ^b	3.732 ^x	6.156 ^b	4.645 ^x	1.141	0.033	0.121	0.128
<i>Lactobacillus</i>	0.023	3.566	4.236	8.162	1.241	3.129	1.014	0.167	0.132	0.911
<i>Gracilibacteria</i>	1.693	0.476	4.337	0.458	0.260	0.514	0.599	0.403	0.186	0.384
<i>Fusobacterium</i>	1.179	6.025	2.458	2.465	5.212	2.628	0.691	0.676	0.587	0.089
<i>Spirochaetaceae</i>	0.948	4.889	0.475	0.674	3.719	0.914	0.614	0.288	0.719	0.086
Unidentified Bacteria	9.649 ^a	4.027 ^x	1.579 ^b	2.899 ^x	0.323 ^b	0.951 ^x	0.533	0.000	0.258	0.019

<i>Streptococcus</i>	9.826 ^a	0.910 ^{x *}	12.34 ^a	0.840 ^{x *}	1.833 ^b	3.102 ^{x NS}	0.541	0.011	0.000	0.000
<i>Alloprevotella</i>	5.576	0.718 [*]	2.502	1.309 ^{NS}	1.122	1.521 ^{NS}	0.362	0.122	0.013	0.015
<i>Capnocytophaga</i>	0.965	2.940 ^{NS}	1.174	5.984 ^{NS}	1.994	3.522 ^{NS}	0.642	0.590	0.037	0.532
<i>Faecalibacterium</i>	0.023	0.152	0.573	2.067	0.157	0.173	0.326	0.236	0.407	0.592
<i>Porphyromonas</i>	2.998	5.284	2.540	0.961	3.073	1.588	0.456	0.095	0.777	0.155
<i>Prevotella</i>	2.571	2.658	3.921	1.315	1.409	1.637	0.373	0.393	0.312	0.228
<i>Haemophilus</i>	1.898 ^{ab}	0.023 ^{x *}	4.799 ^a	0.283 ^{x *}	0.064 ^b	0.160 ^{x NS}	0.268	0.002	0.000	0.004
<i>Campylobacter</i>	0.684	2.181 [*]	1.318	3.171 ^{NS}	1.355	1.930 ^{NS}	0.306	0.536	0.038	0.681
<i>Dialister</i>	0.056	0.263	0.033	1.454	0.067	0.051	0.222	0.404	0.233	0.372
<i>Corynebacterium</i>	0.041	1.522 [*]	0.042	1.775 [*]	1.636	2.986 ^{NS}	0.320	0.109	0.022	0.970
Unidentified <i>Ruminococcaceae</i>	1.227	2.359	1.123	2.771	2.540	3.319	0.326	0.314	0.076	0.862
<i>Turicibacter</i>	0.001	1.491	0.129	1.229	1.280	0.762	0.233	0.819	0.147	0.189
<i>Agathobacter</i>	0.009	0.262	0.195	1.329	0.308	0.420	0.199	0.437	0.217	0.531

<i>Comamonas</i>	0.091	0.772	0.099	0.504	0.630	1.493	0.243	0.400	0.188	0.928
<i>Rothia</i>	0.568	0.137	2.126	0.095	0.472	0.855	0.216	0.364	0.116	0.080
<i>Subdoligranulum</i>	0.002	0.383	0.666	1.858	0.744	0.413	0.211	0.124	0.333	0.347
<i>Romboutsia</i>	0.005	1.419	0.707	2.407	2.632	2.342	0.293	0.058	0.116	0.335
Unidentified <i>Lachnospiraceae</i>	0.085	0.301	0.407	1.267	0.618	0.474	0.159	0.268	0.336	0.436
<i>Actinomyces</i>	1.087	0.841	0.716	0.698	0.579	1.061	0.187	0.855	0.847	0.721
<i>Bacteroides</i>	0.050	0.394	0.073	0.787	0.171	0.220	0.124	0.700	0.144	0.552

SEM, standard error of the mean (n = 48, 8 per group).

Barrow mean values with * or NS indicate significant or no statistical difference from gilts at the same protein level, respectively; mean values with different letters (a, b for gilts; x for barrows) or the same letters indicate significant or no statistical difference among diets within the same sex, respectively.

$P < 0.05$ was considered statistically significant.

Table S3 Effects of dietary protein restriction on relative abundance of microbes (Top 10, %) in gut microbiota at the species level in gilts and barrows.

Items	High protein diet		Normal protein diet		Low protein diet		SEM	P values		
	Gilts	Barrows	Gilts	Barrows	Gilts	Barrows		Diet	Sex	Diet × Sex
<i>Prevotella_melaninogenica</i>	8.446 ^a	0.041 ^{x *}	10.81 ^a	0.011 ^{x *}	0.119 ^b	0.032 ^{x NS}	0.823	0.029	0.000	0.028
<i>Clostridium_disporicum</i>	0.004	5.109	2.250	7.685	9.663	7.877	1.054	0.064	0.173	0.298
<i>SR1_bacterium_oral_taxon_875</i>	0.353	0.004	3.322	0.058	0.000	0.003	0.536	0.377	0.268	0.401
<i>Neisseria_subflava</i>	7.796	0.673 [*]	8.074	2.889 ^{NS}	0.044	1.740 ^{NS}	0.765	0.051	0.026	0.058
<i>Leptotrichia_sp_oral_clone_EI013</i>	7.738 ^a	0.003 ^{x *}	1.001 ^b	0.001 ^{x NS}	0.001 ^b	0.012 ^{x NS}	0.456	0.002	0.003	0.002
<i>Streptococcus_gallolyticus_subsp_macedonicus</i>	0.012	0.512	3.807	0.279	1.309	2.378	0.506	0.300	0.523	0.142
<i>Candidatus_Saccharibacteria_bacterium_UB2523</i>	0.032 ^a	3.285 ^{x *}	0.016 ^a	0.013 ^{y NS}	0.134 ^a	0.426 ^{y NS}	0.267	0.035	0.033	0.031
<i>Prevotella_nanceiensis</i>	0.793 ^{ab}	0.001 ^{x *}	2.629 ^a	0.003 ^{x NS}	0.002 ^a	0.002 ^{x NS}	0.210	0.042	0.010	0.042
<i>Haemophilus_parainfluenzae</i>	1.523 ^{ab}	0.019 ^{x *}	4.264 ^b	0.250 ^{x *}	0.041 ^a	0.115 ^{x NS}	0.248	0.003	0.001	0.006
<i>Campylobacter_showae</i>	0.197	1.491 [*]	0.293	2.533 ^{NS}	0.544	1.147 ^{NS}	0.269	0.614	0.014	0.468

SEM, standard error of the mean (n = 48, 8 per group).

Barrow mean values with * or NS indicate significant or no statistical difference from gilts at the same protein level, respectively; mean values with different letters (a, b for gilts; x, y for barrows) or the same letters indicate significant or no statistical difference among diets within the same sex, respectively.

$P < 0.05$ was considered statistically significant.