

**Table S1. Effects of the experimental diets on the relative abundance (%) of bacterial orders<sup>1</sup>**

	Diet				SEM	P-Value		
	W-SBM	W-RSM	R-SBM	R-RSM		CER	PM	CER*PM
Jejunum <sup>2</sup>								
<i>Clostridiales</i>	55.5	16.0	71.4	51.9	4.8	0.002	0.001	0.208
<i>Lactobacillales</i>	34.9	70.3	25.3	43.1	4.5	0.024	0.002	0.266
<i>Erysipelotrichales</i>	5.30	1.66	1.40	1.61	0.60	0.086	0.135	0.094
<i>Coriobacteriales</i>	0.158	0.432	0.025	0.050	0.059	0.024	0.179	0.263
<i>Enterobacteriales</i>	0.129	1.30	0.004	0.249	0.181	0.089	0.043	0.176
<i>Bifidobacteriales</i>	0.057	3.24	1.45	2.65	0.593	0.733	0.069	0.402
Colon ascendens								
<i>Clostridiales</i>	44.3	26.0	54.0	38.4	2.6	0.016	< 0.001	0.751
<i>Lactobacillales</i>	32.4	43.1	22.6	22.8	2.8	0.005	0.292	0.309
<i>Bacteroidales</i>	17.5	23.4	18.2	26.1	1.4	0.540	0.014	0.713
<i>Selenomonadales</i>	2.37	2.51	1.60	4.09	0.42	0.626	0.121	0.163
<i>Aeromonadales</i>	1.67	0.610	0.318	1.37	0.328	0.657	0.997	0.115
<i>Erysipelotrichales</i>	0.920	0.764	0.916	2.881	0.325	0.094	0.150	0.092
<i>Coriobacteriales</i>	0.260	1.23	0.257	2.18	0.317	0.442	0.022	0.439
<i>Spirochaetales</i>	0.200	0.082	0.346	0.133	0.043	0.245	0.055	0.573
<i>Bifidobacteriales</i>	0.084	1.37	1.19	0.820	0.331	0.683	0.494	0.223
<i>Gastranaerophilales</i>	0.056	0.486	0.077	0.303	0.065	0.517	0.011	0.414
<i>Desulfovibrionales</i>	0.028	0.081	0.030	0.456	0.100	0.352	0.238	0.356
Faeces								
<i>Clostridiales</i>	50.3	32.9	59.9	39.5	2.7	0.088	< 0.001	0.751
<i>Lactobacillales</i>	32.8	46.7	23.1	28.6	3.3	0.032	0.127	0.509
<i>Bacteroidales</i>	10.6	12.3	11.0	16.3	1.1	0.322	0.123	0.415
<i>Selenomonadales</i>	2.58	2.02	1.56	5.68	0.60	0.252	0.125	0.046
<i>Erysipelotrichales</i>	1.02	0.897	1.04	3.03	0.287	0.047	0.083	0.052
<i>Aeromonadales</i>	0.866	0.371	0.051	0.908	0.220	0.755	0.684	0.134
<i>Spirochaetales</i>	0.671	0.098	0.387	0.179	0.145	0.730	0.189	0.537
<i>Coriobacteriales</i>	0.624	1.77	0.488	3.39	0.357	0.255	0.003	0.179
<i>Bifidobacteriales</i>	0.125	1.83	1.59	1.47	0.415	0.514	0.349	0.279
<i>Desulfovibrionales</i>	0.079	0.186	0.052	0.263	0.024	0.543	< 0.001	0.216
<i>Mollicutes RF39</i>	0.061	0.056	0.049	0.058	0.012	0.844	0.956	0.783
unknown WPS-2	0.055	0.197	0.461	0.227	0.084	0.202	0.785	0.272

W-SBM, wheat/soybean meal; W-RSM, wheat/rapeseed meal; R-SBM, rye/soybean meal; R-RSM, rye/rapeseed meal; SEM, standard error of the mean; CER, cereal; PM, protein meal

<sup>1</sup> Data are presented as means ( $n=11$ );  $P$ -values indicate effects of the factors cereal (CER), protein meal (PM) and their interaction (CER\*PM)

<sup>2</sup> W-RSM:  $n = 10$  (DNA-extract not amplifiable)

**Table S2. Effects of the experimental diets on the relative abundance (%) of bacterial genera<sup>1</sup>**

	Diet					P-Value		
	W-SBM	W-RSM	R-SBM	R-RSM	SEM	CER	PM	CER*PM
Jejunum <sup>2</sup>								
<i>Clostridium sensu stricto 1</i>	44.3 <sup>a</sup>	3.69 <sup>b</sup>	47.5 <sup>a</sup>	36.4 <sup>a</sup>	3.94	0.005	< 0.001	0.021
<i>Streptococcus</i>	22.8	37.8	22.0	32.5	3.8	0.692	0.101	0.774
<i>Lactobacillus</i>	11.2	31.4	3.01	10.1	3.9	0.050	0.069	0.376
<i>Terrisporobacter</i>	8.00	2.21	15.4	8.73	1.53	0.018	0.033	0.876
<i>Turicibacter</i>	5.23	1.34	1.32	1.56	0.58	0.094	0.099	0.062
<i>Romboutsia</i>	1.81	0.828	1.53	1.52	0.349	0.774	0.493	0.497
<i>Sarcina</i>	0.354	6.74	6.59	4.66	1.828	0.577	0.551	0.269
unknown <i>Streptococcaceae</i>	0.284 <sup>a</sup>	0.049 <sup>b</sup>	0.214 <sup>ab</sup>	0.209 <sup>ab</sup>	0.027	0.360	0.017	0.022
unknown <i>Lactobacillales</i>	0.118	0.037	0.057	0.168	0.030	0.559	0.799	0.111
<i>Intestinibacter</i>	0.113	0.050	0.059	0.056	0.018	0.504	0.357	0.408
<i>Bifidobacterium</i>	0.047	3.20	1.32	2.64	0.555	0.744	0.046	0.404
<i>Olsenella</i>	0.039	0.159	0.015	0.016	0.021	0.037	0.125	0.130
unknown <i>Peptostreptococcaceae</i>	0.035	0.029	0.058	0.072	0.009	0.080	0.805	0.590
Colon ascendens								
<i>Clostridium sensu stricto 1</i>	16.0	1.47	20.2	7.33	1.77	0.085	< 0.001	0.775
<i>Agathobacter</i>	4.20	3.32	4.00	3.38	0.33	0.918	0.273	0.844
<i>Blautia</i>	2.42	2.97	2.71	3.59	0.21	0.280	0.096	0.698
<i>Coprococcus 3</i>	0.778	1.14	1.13	1.21	0.088	0.223	0.214	0.421
<i>Alloprevotella</i>	0.766	0.688	1.05	0.780	0.128	0.481	0.516	0.722
<i>Dorea</i>	0.546	0.891	0.909	1.18	0.116	0.159	0.184	0.879
<i>Intestinibacter</i>	0.484 <sup>a</sup>	0.131 <sup>b</sup>	0.269 <sup>ab</sup>	0.306 <sup>ab</sup>	0.045	0.820	0.069	0.026
<i>Lachnospira</i>	0.455	0.633	0.438	0.698	0.059	0.839	0.071	0.730
<i>Lachnospiraceae NC2004 group</i>	0.350	0.489	0.614	0.362	0.057	0.551	0.622	0.093
<i>Faecalibacterium</i>	0.341	0.793	0.725	2.35	0.311	0.113	0.090	0.333
<i>Coprococcus 1</i>	0.260	0.381	0.308	0.164	0.074	0.578	0.940	0.384
<i>Fusicatenibacter</i>	0.226	0.158	0.154	0.354	0.035	0.366	0.342	0.056
<i>Lachnoclostridium</i>	0.197	0.199	0.140	0.161	0.027	0.403	0.838	0.863
<i>Christensenellaceae R-7 group</i>	0.178	0.061	0.390	0.239	0.071	0.181	0.354	0.908
<i>Anaerovibrio</i>	0.173	0.104	0.237	0.190	0.036	0.319	0.442	0.882
<i>Lachnospiraceae FCS020 group</i>	0.152	0.103	0.073	0.099	0.012	0.069	0.604	0.103
<i>Acidaminococcus</i>	0.142	0.131	0.138	0.105	0.026	0.778	0.678	0.844
<i>Asteroleplasma</i>	0.140	0.245	0.062	0.380	0.067	0.831	0.120	0.428
<i>Catenisphaera</i>	0.136	0.032	0.157	0.345	0.048	0.082	0.657	0.125
<i>Catenibacterium</i>	0.107	0.137	0.133	1.31	0.293	0.313	0.311	0.335
<i>Coprococcus 2</i>	0.097	0.170	0.051	0.067	0.026	0.151	0.389	0.577
<i>Family XIII AD3011 group</i>	0.095	0.045	0.148	0.070	0.013	0.128	0.014	0.594
<i>Bifidobacterium</i>	0.084	1.37	1.19	0.820	0.331	0.683	0.494	0.223
<i>Collinsella</i>	0.071	0.152	0.120	0.418	0.053	0.129	0.069	0.292
<i>Holdemanella</i>	0.067	0.172	0.219	0.392	0.041	0.019	0.075	0.659
<i>Butyricicoccus</i>	0.066	0.033	0.021	0.094	0.011	0.695	0.327	0.013
<i>Acetitomaculum</i>	0.056	0.096	0.145	0.072	0.029	0.583	0.779	0.338
<i>Fournierella</i>	0.045	0.073	0.165	0.106	0.019	0.047	0.675	0.252
<i>Desulfovibrio</i>	0.028	0.081	0.030	0.456	0.100	0.352	0.238	0.356
<i>Intestinimonas</i>	0.020	0.059	0.029	0.046	0.008	0.897	0.078	0.477
<i>Enterorhabdus</i>	0.018	0.040	0.014	0.042	0.006	0.954	0.023	0.779
Faeces								
<i>Streptococcus</i>	26.1	32.7	16.2	18.6	3.1	0.057	0.468	0.729
<i>Clostridium sensu stricto 1</i>	20.3	3.03	27.2	9.39	2.18	0.060	< 0.001	0.944
<i>Lactobacillus</i>	6.54	13.9	6.73	10.0	2.01	0.653	0.199	0.621

unknown.Muribaculacea	5.70	2.64	4.78	4.79	0.62	0.622	0.222	0.219
<i>Terrisporobacter</i>	3.08	0.883	7.77	3.03	0.669	0.004	0.004	0.268
<i>Subdoligranulum</i>	2.73	1.35	1.65	2.01	0.54	0.852	0.646	0.433
<i>Agathobacter</i>	2.15	2.27	1.21	1.30	0.29	0.104	0.861	0.973
<i>Ruminococcaceae</i> UCG-005	2.14	1.56	1.91	1.22	0.20	0.457	0.110	0.888
<i>Prevotella</i> 9	2.11	5.22	2.64	7.13	0.83	0.449	0.022	0.666
unknown <i>Lachnospiraceae</i>	1.81	2.22	1.62	2.66	0.20	0.757	0.076	0.430
unknown <i>Ruminococcaceae</i>	1.71	0.88	1.50	1.09	0.15	0.999	0.042	0.483
<i>Blautia</i>	1.71	2.83	1.78	2.80	0.26	0.974	0.039	0.922
<i>Megasphaera</i>	1.58	0.668	0.643	1.54	0.299	0.955	0.988	0.141
<i>Christensenellaceae</i> R-7 group	1.50	0.450	0.974	0.441	0.184	0.453	0.031	0.468
<i>Ruminococcaceae</i> UCG-002	1.26	1.47	0.913	1.34	0.197	0.558	0.438	0.783
<i>Syntrophococcus</i>	1.15	2.57	0.268	1.34	0.286	0.054	0.024	0.742
<i>Prevotellaceae</i> NK3B31 group	1.14	1.24	1.27	0.538	0.211	0.499	0.464	0.338
<i>Ruminococcaceae</i> NK4A214 group	0.817	1.09	0.974	1.05	0.134	0.831	0.532	0.725
<i>Ruminococcus</i> 2	0.770	0.433	0.317	0.265	0.093	0.098	0.295	0.441
<i>Marvinbryantia</i>	0.766	0.641	0.410	0.586	0.049	0.035	0.787	0.116
<i>Roseburia</i>	0.761	0.734	0.549	0.413	0.123	0.294	0.746	0.829
<i>Treponema</i> 2	0.671	0.098	0.387	0.177	0.145	0.729	0.188	0.538
<i>Phascolarctobacterium</i>	0.581	0.484	0.729	1.10	0.109	0.079	0.519	0.274
<i>Ruminococcaceae</i> UCG-008	0.532	0.153	1.11	0.377	0.077	0.001	< 0.001	0.118
<i>Coprococcus</i> 3	0.525	1.36	0.924	1.59	0.130	0.188	0.003	0.726
<i>Ruminococcus</i> 1	0.494	0.366	0.356	0.283	0.045	0.232	0.274	0.764
<i>Dorea</i>	0.483	0.845	0.637	1.20	0.141	0.367	0.106	0.721
Family XIII AD3011 group	0.468	0.187	0.534	0.289	0.049	0.368	0.007	0.841
<i>Turicibacter</i>	0.441	0.144	0.290	0.133	0.059	0.483	0.054	0.544
<i>Prevotella</i> 7	0.436	0.881	0.135	1.41	0.192	0.758	0.025	0.266
<i>uminococcaceae</i> UCG-014	0.422	0.533	0.554	0.603	0.053	0.356	0.464	0.772
<i>Succinivibrio</i>	0.393	0.179	0.051	0.832	0.181	0.670	0.439	0.178
<i>Oribacterium</i>	0.373	0.690	0.238	0.435	0.060	0.091	0.028	0.597
<i>Lachnospiraceae</i> NK4A136 group	0.332	0.220	0.397	0.231	0.053	0.725	0.203	0.805
<i>Intestinibacter</i>	0.308	0.098	0.264	0.312	0.035	0.206	0.228	0.059
unknown (Family.Prevotellaceae)	0.298	0.391	0.230	0.486	0.059	0.912	0.149	0.495
<i>Lachnospiraceae</i> NC2004 group	0.289	0.335	0.424	0.223	0.042	0.894	0.359	0.147
<i>Olsenella</i>	0.271	0.950	0.148	2.33	0.312	0.291	0.019	0.208
<i>Rikenellaceae</i> RC9 gut group	0.252	0.506	0.438	0.414	0.075	0.759	0.455	0.367
<i>Collinsella</i>	0.226	0.223	0.175	0.423	0.039	0.323	0.110	0.103
<i>Prevotella</i> 2	0.213	0.244	0.226	0.514	0.056	0.198	0.150	0.242
<i>Lachnospiraceae</i> NK3A20 group	0.191	0.249	0.103	0.270	0.050	0.742	0.278	0.598
<i>Coprococcus</i> 1	0.189	0.428	0.231	0.190	0.082	0.560	0.554	0.406
<i>Catenisphaera</i>	0.184	0.048	0.214	0.747	0.092	0.038	0.249	0.056
<i>Lachnospira</i>	0.178	0.354	0.175	0.216	0.048	0.468	0.265	0.488
<i>Mogibacterium</i>	0.172	0.137	0.081	0.131	0.018	0.189	0.840	0.247
<i>Fusicatenibacter</i>	0.148	0.160	0.101	0.366	0.041	0.323	0.087	0.117
<i>Oscillospira</i>	0.147	0.260	0.190	0.149	0.030	0.576	0.551	0.205
<i>Catenibacterium</i>	0.145	0.177	0.167	1.15	0.224	0.272	0.263	0.294
<i>Lachnospiraceae</i> ND3007 group	0.142	0.326	0.283	0.277	0.041	0.577	0.286	0.252
<i>Prevotella</i> 1	0.139	0.579	0.180	0.319	0.096	0.570	0.137	0.435
<i>Solobacterium</i>	0.130	0.082	0.078	0.194	0.025	0.548	0.486	0.099
unknown Family XIII	0.128	0.196	0.068	0.129	0.045	0.494	0.486	0.967
<i>Bifidobacterium</i>	0.125	1.83	1.59	1.47	0.415	0.514	0.349	0.279
<i>Faecalibacterium</i>	0.121	0.535	0.516	0.815	0.088	0.048	0.037	0.731
unknown <i>Veillonellaceae</i>	0.111	0.076	0.025	0.092	0.017	0.288	0.636	0.129
<i>Lachnospiraceae</i> FCS020 group	0.109	0.117	0.096	0.155	0.016	0.694	0.312	0.438

unknown <i>Streptococcaceae</i>	0.101	0.052	0.098	0.063	0.013	0.884	0.118	0.796
<i>Intestinimonas</i>	0.096	0.120	0.043	0.075	0.019	0.211	0.468	0.914
<i>Ruminococcaceae</i> UCG-010	0.088	0.125	0.076	0.094	0.022	0.643	0.557	0.842
<i>Ruminococcaceae</i> UCG-013	0.084	0.021	0.077	0.069	0.016	0.520	0.266	0.389
<i>Desulfovibrio</i>	0.079	0.186	0.052	0.263	0.024	0.543	< 0.001	0.216
<i>Prevotellaceae</i> UCG-003	0.078	0.033	0.176	0.097	0.018	0.022	0.075	0.622
<i>Ruminococcaceae</i> UCG-004	0.076	0.050	0.152	0.077	0.016	0.110	0.116	0.440
<i>Lachnoclostridium</i>	0.069	0.181	0.065	0.091	0.018	0.170	0.051	0.217
<i>Holdemanella</i>	0.069	0.236	0.227	0.314	0.039	0.128	0.102	0.598
<i>Shuttleworthia</i>	0.067	0.792	0.334	0.045	0.151	0.427	0.471	0.098
unknown <i>Mollicutes</i> RF39	0.061	0.056	0.049	0.058	0.012	0.844	0.956	0.783
unknown <i>WPS-2</i>	0.055	0.197	0.461	0.227	0.084	0.202	0.785	0.272
<i>Ruminiclostridium</i> 9	0.054	0.072	0.056	0.058	0.010	0.745	0.626	0.697
<i>Alloprevotella</i>	0.049	0.250	0.352	0.153	0.045	0.246	0.994	0.027
<i>Ruminiclostridium</i> 5	0.048	0.039	0.076	0.054	0.008	0.167	0.304	0.682
unknown <i>Atopobiaceae</i>	0.044	0.361	0.055	0.345	0.035	0.959	< 0.001	0.796
<i>Fournierella</i>	0.043	0.061	0.105	0.088	0.016	0.164	0.986	0.582
<i>Sarcina</i>	0.027	0.090	1.35	0.438	0.158	0.005	0.137	0.089
<i>Candidatus_Soleaferrea</i>	0.027	0.051	0.054	0.085	0.012	0.199	0.233	0.885
unknown <i>Bacteroidales</i>	0.024	0.107	0.077	0.145	0.024	0.345	0.120	0.879
<i>Acetitomaculum</i>	0.022	0.152	0.017	0.105	0.023	0.555	0.018	0.643
unknown <i>Erysipelotrichaceae</i>	0.021	0.061	0.034	0.006	0.011	0.353	0.779	0.132
<i>Enterorhabdus</i>	0.017	0.093	0.050	0.123	0.012	0.151	0.001	0.936
unknown <i>Coriobacteriales</i>	0.017	0.089	0.017	0.076	0.011	0.768	0.004	0.750

*W-SBM*, wheat/soybean meal; *W-RSM*, wheat/rapeseed meal; *R-SBM*, rye/soybean meal; *R-RSM*, rye/rapeseed meal; *SEM*, standard error of the mean; *CER*, cereal; *PM*, protein meal

<sup>1</sup> Data are presented as means ( $n=11$ );  $P$ -values indicate effects of the factors cereal (*CER*), protein meal (*PM*) and their interaction (*CER\*PM*)

<sup>2</sup> *W-RSM*:  $n = 10$  (DNA-extract not amplifiable)

<sup>a, b</sup> Values within a row with different superscripts differ significantly at  $P \leq 0.05$  (Tukey Test)