Supplementary Table 1: Percentage Species Abunandance in Individual Faecal Samples

	GROUP		Control	Control	Control	Pork	Pork	Pork	Sausage	Sausage	Sausage	Frankfurter	Frankfurter	Frankfurter	MEAN (all samples)
	Species level output from Qiime 2	**Label in Figure 4C**	PN13	PN14	PN15	PN16	PN17	PN18	PN19	PN20	PN21	PN22	PN23	PN24	
1	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Bacteroidaceae;D_5__Bacteroides;D_6__Bacteroides_thetaiotaomicron	Thetaiotaomicron	17.23529	25.57786	6.859517	5.011826	16.23198	22.94605	16.06236	19.40043	23.53271	5.6274155	5.6095688	10.661665	14.56305568
2	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;__;__	Lachnospiraceae	7.42517	12.77909	5.840861	5.140462	7.285231	8.387702	6.226257	10.45234	12.18304	10.822131	8.0882531	4.4439867	8.256210614
3	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Blautia;__	Blautia	11.85878	9.658089	9.073173	7.977924	5.801706	7.68189	3.529165	5.502314	7.949205	9.8827838	6.9705419	7.2259505	7.759293196
4	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae;D_5__uncultured_bacterium;D_6__uncultured_bacterium	Muribaculaceae uncult.	3.910041	3.926034	5.505998	14.09021	9.230656	14.31353	9.488149	11.58105	4.489316	3.1276899	3.1987716	3.9918905	7.237778308
5	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Dubosiella;D_6__Dubosiella_newyorkensis	D. newyorkensis	0.016285	0.019672	0.015008	0.020748	0.069873	0.070321	0.008405	0.024136	0.01981	27.553019	30.25094	28.628425	7.224720019
6	D_0__Bacteria;D_1__Verrucomicrobia;D_2__Verrucomicrobiae;D_3__Verrucomicrobiales;D_4__Akkermansiaceae;D_5__Akkermansia;D_6__uncultured_bacterium	Akkermansia uncult.	0.083054	0.052962	0.065659	7.655919	2.382318	5.053327	7.291141	11.7713	6.175884	9.8833615	12.346547	16.264623	6.585508329
7	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae;D_5__Romboutsia;D_6__uncultured_bacterium	Romboutsia uncult.	13.43843	6.60064	16.98136	11.95485	6.201824	3.748486	4.840309	5.803305	6.630144	0.0831894	0.0800097	0.4282446	6.399232794
8	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae_1;D_5__Clostridium_sensu_stricto_1;D_6__uncultured_bacterium	Clostridium sensu stricto uncult.	2.187897	1.482193	3.610322	6.646749	7.604442	0.01172	2.161708	2.342619	1.758976	2.8994968	3.2270578	3.6677255	3.133408818
9	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium;D_6__uncultured_bacterium	Ruminiclostridium uncult.	4.256913	5.431682	3.06066	1.324536	2.806708	4.958263	1.507816	2.64432	3.532297	1.0109822	0.691801	1.1307827	2.696396755
10	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_9;__	Ruminiclostridium_9	3.295281	3.082417	2.6592	2.596788	1.841718	2.846688	1.698605	2.326291	2.39494	0.575971	0.5115772	0.6147208	2.037016404
11	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__uncultured;D_6__uncultured_bacterium	Lachnospiraceae uncult.	1.828812	2.288736	2.072019	1.75028	1.711533	4.090974	1.223735	1.696624	2.925706	1.3639594	1.1581202	1.1708967	1.940116273
12	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Rikenellaceae;D_5__Alistipes;__	Alistipes	0	0	0.006566	7.788705	15.57223	0.004558	0.002521	0.003549	0	0.0132872	0.0121227	0.0108416	1.951198181
13	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Erysipelatoclostridium;Ambiguous_taxa	Erysipelatoclostridium ambig.	5.168876	1.69253	0.983951	1.999253	0.78479	0.509174	1.559086	3.140529	2.123067	1.9139336	1.8685093	0.6982014	1.870158287
14	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__uncultured;__	Ruminococcaceae uncult.	2.34749	2.53766	2.857116	1.088012	1.074581	3.443112	1.713733	2.433484	2.273348	0.3050278	0.2957934	0.4586012	1.735663257
15	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__[Eubacterium]_coprostanoligenes_group;__	Coprostanoligenes	3.330293	2.418873	0.006566	4.489813	1.533539	2.414345	0.339553	0.434449	3.938057	0.0600812	0.0509153	0.0205991	1.586423684
16	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnoclostridium;D_6__uncultured_bacterium	Lachnoclostridium uncult.	1.516138	1.643351	1.665869	1.389269	1.33348	1.157688	0.519415	0.741119	1.213181	2.9959734	2.4334263	1.4256752	1.502882178
17	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_9;D_6__uncultured_bacterium	Ruminiclostridium_9 uncult.	1.33456	1.183333	2.515688	2.165235	1.328332	1.701371	1.022021	1.426868	1.234357	0.1322942	0.1026387	0.1550354	1.191811107
18	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Lactobacillaceae;D_5__Lactobacillus;D_6__Lactobacillus_johnsonii	L. johnsonii	0.045598	0.046153	0.038458	1.543633	0.700206	0.253285	0.090772	0.098674	0.033472	3.6568669	3.973815	3.0866138	1.130628757
19	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Burkholderiaceae;D_5__Parasutterella;D_6__uncultured_bacterium	Parasutterella uncult.	1.606521	0.976023	2.48192	0.498776	0.458223	0.533266	0.49336	0.598433	0.413957	1.1091918	1.171051	2.8459295	1.098887555
20	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__uncultured;__	All others	1.17171	1.384591	1.767172	0.880534	1.171668	0.997513	0.751387	1.443905	1.258265	0.5909913	0.2966016	0.2233377	0.994806326
21	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae;__;__	All others	0.907892	1.075895	0.708182	0.465579	0.166961	0.973421	1.138847	1.426868	0.822449	1.0161815	1.2243908	1.0819953	0.917388525
22	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Intestinimonas;D_6__uncultured_bacterium	All others	0.710028	0.759633	4.177805	0.114528	0.003678	0.003907	0.928728	1.379305	1.129843	0.9896071	0.5277407	0.7144638	0.95327223
23	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Atopobiaceae;D_5__Coriobacteriaceae_UCG-002;D_6__uncultured_bacterium	All others	0.001629	0.003026	0.001876	0.005809	0.008826	0.018882	0.009245	0.018457	0.018444	2.9474463	3.3127248	3.0399948	0.782196711
24	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_UCG-006;__	All others	0.846823	1.035795	0.754144	0.36848	0.472198	0.422576	0.854766	0.989579	1.558828	0.5343763	0.4073221	0.1420254	0.698909274
25	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-014;__	All others	0.225548	0.291294	0.284211	0.029877	0.024272	0.01172	0.103379	0.181021	0.017077	2.721564	3.5858892	0.4564329	0.661023666
26	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;__;__	All others	1.205908	1.120535	1.711831	0.229055	0.326567	0.681721	0.115145	0.30596	0.743893	0.5823257	0.4719764	0.3686156	0.655294409
27	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Sporosarcina;D_6__Sporosarcina_sp._106	All others	0	0.00227	0.002814	0.00166	0	0	7.978652	0.06176	0.01093	0.0127095	0.0064654	0.0032525	0.673376033
28	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Faecalibaculum;D_6__uncultured_bacterium	All others	0	0	9.002823	0	0	0	0	0.00142	0	0	0.0072736	0	0.750959727
29	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Christensenellaceae;D_5__uncultured;D_6__uncultured_bacterium	All others	0.606618	0.259516	0.642523	1.097971	0.600177	0.773528	0.732056	0.856121	1.372343	0.1149631	0.0759688	0.1225105	0.604524535
30	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Oscillibacter;D_6__uncultured_bacterium	All others	0.661173	0.821675	1.816886	0.352712	0.231686	0.319048	0.761473	1.149303	0.463823	0.2709432	0.153554	0.3100708	0.609362168
31	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Carnobacteriaceae;D_5__Atopostipes;D_6__uncultured_bacterium	All others	0	0.001513	0	0	0.015446	0	7.171794	0.026266	0.002049	0.0040439	0	0.0021683	0.601939982
32	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Tyzzerella;D_6__uncultured_bacterium	All others	0.689672	0.62874	0.223242	0.209137	0.522948	0.987095	0.557237	0.653804	0.993907	0.2120174	0.1567867	0.1832237	0.501484054
33	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Staphylococcaceae;D_5__Staphylococcus;D_6__Staphylococcus_lentus	All others	0.013842	0.012862	0.00469	0.00249	0.275816	0.009767	5.729534	0.025556	0.013662	0.0046216	0	0.0195149	0.509363018
34	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_NK4A136_group;__	All others	0.238576	0.165697	0.826369	0.151044	0.094881	0.225287	0.085729	0.149076	0.341549	1.2877024	1.0603305	0.2526101	0.406570771
35	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_UCG-006;D_6__uncultured_bacterium	All others	0.061069	0.113491	0.941741	0.580107	0.466314	0.496152	0.263069	0.332936	0.562872	0.4974032	0.456621	0.0823964	0.404514352
36	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Oscillibacter;D_6__unidentified	All others	0.845194	0.901119	0.083481	0.478028	0.441306	0.69865	0.17566	0.293182	0.212443	0.3148487	0.1147614	0.1940653	0.396061592
37	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Staphylococcaceae;D_5__Staphylococcus;__	All others	0.004886	0.009836	0.005628	0.00415	4.450574	0.007162	0.007564	0.004259	0.002732	0.0034662	0.0129309	0.0054208	0.376550732
38	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Intestinimonas;__	All others	0.364785	0.684729	0.040334	0.253123	0.529568	0.914821	0.181543	0.135588	0.756189	0.0808786	0.0412171	0.0628815	0.337138003
39	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Enterorhabdus;Ambiguous_taxa	All others	0.961632	0.50617	0.146326	1.179302	0.904678	0.108086	0	0	0.144817	0.0017331	0	0	0.329395346
40	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnoclostridium;__	All others	0.25649	0.161914	0.176342	0.242334	0.141954	1.122527	0.208438	0.352813	0.324471	0.0935881	0.2238655	0.0162625	0.276749868
41	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__Turicibacter;__	All others	0.660359	0.500874	0.9333	0.759368	0.16549	0.008465	0.121029	0.18457	0.006148	0.0612366	0.1551703	0.119258	0.306272158
42	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiales_vadinBB60_group;D_5__uncultured_bacterium;D_6__uncultured_bacterium	All others	0.054555	0.354849	0.033768	0.00166	0.008826	0.024091	0.266431	0.434449	0.006148	0.6528056	0.6045177	1.0635645	0.292138743
43	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_5;D_6__uncultured_bacterium	All others	0.349314	0.282214	0.473685	0.3718	0.318476	0.464247	0.189948	0.340035	0.359992	0.0502603	0.076777	0.0617973	0.278212149
44	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Parvibacter;D_6__uncultured_bacterium	All others	0.531707	0.335177	0.573112	0.239844	0.088997	0.223333	0.353001	0.345714	0.409175	0.056615	0.0872833	0.1431096	0.282255602
45	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__uncultured;D_6__uncultured_organism	All others	0	0	0.001876	1.552762	0.630332	0.774179	0	0	0	0.0034662	0	0	0.24688462
46	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__uncultured;D_6__Clostridium_sp._Culture-54	All others	0.238576	0.067338	0.584367	0.506245	0.223595	0.477269	0.189107	0.300991	0.372971	0.009821	0.0016164	0.0249358	0.249736163
47	D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Bifidobacteriales;D_4__Bifidobacteriaceae;D_5__Bifidobacterium;__	All others	0.027685	0.028751	0.013132	0.149384	0.198588	0.004558	0.013448	0.025556	0.004782	0.4332781	0.6562412	1.7324935	0.273991234
48	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__GCA-900066575;D_6__uncultured_bacterium	All others	0.319187	0.29432	0.429599	0.174281	0.188291	0.375044	0.148764	0.296732	0.245232	0.0849225	0.1179941	0.1474463	0.235151095
49	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Sporosarcina;__	All others	0	0	0	0	0.000736	0	2.886199	0.018457	0	0	0	0	0.242115989
50	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__uncultured;D_6__uncultured_Oscillospira_sp.	All others	0.232062	0.350309	0.091923	0.075522	0.275816	0.353557	0.132795	0.169662	0.311492	0.2380141	0.1737584	0.1073322	0.209353691
51	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__[Eubacterium]_ventriosum_group;__	All others	0.247533	0.177803	0.208234	0.340263	0.126508	0.277376	0.1412	0.191669	0.152331	0.201041	0.2658908	0.1908128	0.210055054
52	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_5;__	All others	0.772726	0.523572	0.166962	0.123657	0.084584	0.213567	0.089931	0.107193	0.101098	0.0958989	0.0743524	0.0542082	0.200645713
53	D_0__Bacteria;D_1__Bacteroidetes;D_2__Bacteroidia;D_3__Bacteroidales;D_4__Muribaculaceae;D_5__mouse_gut_metagenome;D_6__mouse_gut_metagenome	All others	0.293945	0.391922	0.225117	0.121167	0.033098	0.207056	0.305934	0.43019	0.253429	0	0	0.0975747	0.196619426
54	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-010;D_6__uncultured_organism	All others	0.228805	0.198988	0.166962	0.206648	0.083848	0.115899	0.061355	0.128489	0.081289	0.3056055	0.3774195	0.2786301	0.186161424
55	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__A2;D_6__uncultured_bacterium	All others	0.179136	0.345013	0.091923	0.249803	0.231686	0.050136	0.159691	0.149786	0.358626	0.1270949	0.1204186	0.1095005	0.181067724
56	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Planococcaceae;D_5__Sporosarcina;D_6__uncultured_bacterium	All others	0	0.00227	0	0	0.011033	0	2.310472	0.035494	0.004782	0.0051993	0.0113145	0	0.198380381
57	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__[Eubacterium]_xylanophilum_group;D_6__uncultured_bacterium	All others	0.205192	0.214876	0.377072	0.117017	0.034569	0.014325	0.255505	0.333646	0.390732	0.0306183	0.1478967	0.0216833	0.1785943
58	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Staphylococcaceae;D_5__Jeotgalicoccus;__	All others	0	0.003783	0	0	0.017652	0	2.191965	0.008519	0	0.0034662	0	0.0043367	0.185810151
59	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__uncultured;D_6__unidentified	All others	0.263004	0.272379	0.745702	0.012449	0.030156	0.032556	0.074802	0.095834	0.27119	0.1409598	0.0686952	0.112753	0.176706573
60	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_NK4A136_group;D_6__uncultured_bacterium	All others	0.121324	0.12938	0.184784	0.18341	0.075758	0.04688	0.068919	0.24775	0.124324	0.2605445	0.3830767	0.0325249	0.154889525
61	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Angelakisella;__	All others	0.197049	0.187639	0.222304	0.124486	0.189762	0.213567	0.217684	0.298861	0.170091	0.0300406	0	0.0368616	0.157362044
62	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Enterorhabdus;__	All others	0.311045	0.217903	0.496196	0.100419	0.045602	0.088552	0.065557	0.078087	0.407809	0.0635474	0.0379844	0.0119258	0.160385663
63	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-004;D_6__uncultured_bacterium	All others	0.161222	0.139972	0.222304	0.18258	0.096352	0.212264	0.235334	0.181021	0.148915	0.1351828	0.0759688	0.0715548	0.155222514
64	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-009;Ambiguous_taxa	All others	0.184835	0.287511	0.232621	0.078841	0.186084	0.298212	0.08825	0.192379	0.196049	0.0277298	0.0266699	0.0379457	0.153094021
65	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family_XIII;D_5__Family_XIII_AD3011_group;__	All others	0.377813	0.236818	0.138822	0.132786	0.127979	0.074227	0.074802	0.105773	0.157796	0.0306183	0.1139532	0.0314407	0.133569051
66	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Anaerotruncus;D_6__uncultured_bacterium	All others	0.088754	0.118787	0.034706	0.149384	0.249338	0.218125	0.076483	0.091575	0.215176	0.0699022	0.1212268	0.0704706	0.125327224
67	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family_XIII;D_5__[Eubacterium]_nodatum_group;__	All others	0.095268	0.052962	0.279521	0.271381	0.163283	0.136084	0.063036	0.076668	0.081289	0.0895441	0.0412171	0.125763	0.123001218
68	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_NK4A136_group;D_6__Clostridiales_bacterium_CIEAF_020	All others	0.789825	0.668841	0	0	0	0	0	0	0	0.0011554	0	0	0.121651763

69	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Marvinbryantia;D_6__uncultured_bacterium	All others	0.029313	0.014376	0.027202	0.027387	0.01471	0.026696	0.222727	0.585655	0.012296	0.2016187	0.1503213	0.0357774	0.112339808
70	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptococcaceae;D_5__uncultured;D_6__uncultured_bacterium	All others	0.145751	0.152078	0.160396	0.114528	0.085319	0.102877	0.08741	0.118551	0.125007	0.0693245	0.076777	0.125763	0.113648376
71	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_5;Ambiguous_taxa	All others	0.03257	0.04237	0.16321	0.051454	0.036776	0.034509	0.045386	0.092995	0.079922	0.308494	0.2295228	0.0585448	0.097979508
72	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-005;__	All others	0.002443	0	0	0.00332	0.001471	0	0.368129	0.670841	0.003415	0.0046216	0	0.1712979	0.10212819
73	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Enterorhabdus;D_6__mouse_gut_metagenome	All others	0.119695	0.053719	0.268265	0.170961	0.09341	0.218125	0.066398	0.094415	0.038937	0.0277298	0.0202045	0.0108416	0.09855832
74	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-013;D_6__uncultured_rumen_bacterium	All others	0.078168	0.08247	0.075039	0.151044	0.084584	0.14585	0.062195	0.113582	0.178288	0.0196419	0.0145472	0.0032525	0.084055187
75	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_NK4A214_group;D_6__uncultured_bacterium	All others	0.157965	0.115004	0.155706	0.134445	0.083848	0.118503	0.045386	0.06176	0.068993	0.0265744	0.0274781	0.0422824	0.086495503
76	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Marvinbryantia;Ambiguous_taxa	All others	0.118881	0.060529	0.151016	0.147724	0.076493	0.073576	0.064717	0.097964	0.120908	0.0340845	0.0533398	0.006505	0.083811461
77	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Adlercreutzia;D_6__uncultured_bacterium	All others	0.144123	0.094576	0.344242	0.148554	0.02133	0.162128	0.030257	0.040463	0.000683	0	0.0024245	0	0.082398421
78	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family_XIII;D_5__[Eubacterium]_brachy_group;D_6__uncultured_bacterium	All others	0.191349	0.072634	0.232621	0.073032	0.046337	0.044927	0.036981	0.070988	0.093584	0.0271521	0.031519	0.0271041	0.079019199
79	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcus_2;__	All others	0	0	0	0.160173	0	0.582099	0	0.00142	0	0.0069324	0.0622298	0	0.067737839
80	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__uncultured_bacterium;D_6__uncultured_bacterium	All others	0.075725	0.072634	0.126629	0.08797	0.051486	0.040369	0.104219	0.128489	0.073091	0.005777	0.0266699	0.0021683	0.06626907
81	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-014;D_6__uncultured_bacterium	All others	0.16855	0.255733	0.114435	0	0.001471	0.003256	0.002521	0	0.002049	0.0271521	0.0880915	0.0271041	0.057530268
82	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;D_5__Enterorhabdus;D_6__uncultured_bacterium	All others	0.11481	0.125597	0.066597	0.024897	0.019859	0.016929	0.010926	0.017037	0.017761	0.0947435	0.1147614	0.0162625	0.05334834
83	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__A2;__	All others	0.086311	0.0401	0.484003	0.005809	0.005149	0	0	0.008519	0.003415	0.0306183	0.0282863	0.0401141	0.061027018
84	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Burkholderiaceae;D_5__Parasutterella;__	All others	0.140866	0.074147	0.213862	0.028217	0.02133	0.037765	0.028576	0.070988	0.044401	0	0	0	0.055012701
85	D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae;__;__	All others	0.020356	0.035561	0	0.066393	0.035305	0.062507	0.130274	0.108612	0.056014	0.0179088	0.0121227	0.0216833	0.047228046
86	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_FCS020_group;D_6__uncultured_bacterium	All others	0.043155	0.046153	0.030016	0.00332	0.019123	0.031254	0.031938	0.054661	0.090169	0.0716353	0.0210126	0.0303566	0.039399442
87	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiales_vadinBB60_group;Ambiguous_taxa;Ambiguous_taxa	All others	0.030127	0.200501	0.011256	0	0.009562	0	0.005883	0.009938	0.064894	0.0485271	0.0646543	0.0401141	0.040454768
88	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Oscillibacter;__	All others	0.024428	0.062798	0.267327	0.004979	0.05737	0.021487	0.004202	0.00071	0.008197	0.0103987	0.022629	0.0151783	0.041642046
89	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae;D_5__Pseudomonas;__	All others	0.013028	0.011349	0.019698	0.019918	0.025007	0.00586	0.005043	0.009938	0.017761	0.0387062	0.2707399	0.0195149	0.038046914
90	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__GCA-900066225;Ambiguous_taxa	All others	0.072468	0.057502	0.045961	0.072202	0.047808	0.067065	0	0	0.064894	0.0115541	0	0	0.036621329
91	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__uncultured;D_6__uncultured_bacterium	All others	0.017099	0.012862	0.03283	0.015768	0.027949	0.117201	0.068919	0.075248	0.041669	0	0.0105063	0.006505	0.035546444
92	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__GCA-900066225;D_6__uncultured_bacterium	All others	0.058626	0.08247	0.094737	0.012449	0.010297	0.007162	0.024374	0.031945	0.050549	0.0265744	0.0290944	0.0184308	0.037225738
93	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Roseburia;D_6__uncultured_bacterium	All others	0.052112	0.024211	0.00469	0.015768	0.02133	0.064461	0.028576	0.044723	0.021176	0.0121318	0.1074878	0.0314407	0.035675633
94	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Defluviitaleaceae;D_5__Defluviitaleaceae_UCG-011;__	All others	0	0	0	0.032366	0.07208	0	0.030257	0.057501	0.045084	0.0647029	0.054148	0.0292724	0.032117668
95	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Streptococcaceae;D_5__Streptococcus;__	All others	0	0	0.002814	0.043155	0.062518	0	0.027736	0.070279	0.049183	0.041017	0	0.0227674	0.026622452
96	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Acetatifactor;Ambiguous_taxa	All others	0.088754	0.081714	0.033768	0.016598	0.008091	0.024742	0.011767	0.022716	0.028007	0.0046216	0.0024245	0.0108416	0.027836984
97	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_NK4A136_group;Ambiguous_taxa	All others	0.07084	0.071878	0.034706	0.009129	0.011768	0	0.026055	0.022716	0.079239	0	0	0.0043367	0.027555625
98	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__GCA-900066575;__	All others	0.0114	0.006809	0	0.032366	0.022065	0.013022	0.033619	0.051822	0.012979	0.0358177	0.0193963	0.0748073	0.026175326
99	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiales_vadinBB60_group;__;__	All others	0.008957	0.043127	0.008442	0	0.019859	0.005209	0	0.004259	0.007514	0.0346622	0.0274781	0.0563765	0.017990269
100	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-013;__	All others	0.024428	0.010592	0.031892	0.008299	0.005149	0.012371	0.010926	0.023426	0	0.0127095	0.0598052	0.0162625	0.01798835
101	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae;D_5__Enterococcus;__	All others	0.034199	0.018915	0.005628	0.077182	0.028685	0.020836	0	0.00213	0.005465	0.0069324	0.0072736	0	0.017270377
102	D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rhizobiales;D_4__Beijerinckiaceae;D_5__Methylobacterium;__	All others	0.002443	0.003026	0	0.006639	0	0	0	0	0	0.0190642	0.153554	0	0.015393889
103	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Harryflintia;D_6__uncultured_bacterium	All others	0.006514	0.024968	0.01407	0.007469	0.016917	0.031254	0.010086	0.018457	0.022542	0.009821	0	0.0075891	0.014140545
104	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-005;Ambiguous_taxa	All others	0.008143	0.015889	0.016884	0.009129	0.005884	0.001953	0.005883	0.015617	0.014345	0.0398616	0.013739	0.0173466	0.013722885
105	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Anaerotruncus;D_6__uncultured_organism	All others	0	0	0	0.050625	0.077964	0.035811	0	0	0	0	0	0	0.013700009
106	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Roseburia;__	All others	0.0114	0.010592	0.043148	0.024897	0.015446	0.013673	0.005043	0.022716	0.011613	0.0028885	0.0080818	0.0032525	0.014395889
107	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae_1;D_5__Candidatus_Arthromitus;D_6__uncultured_bacterium	All others	0.122952	0.037074	0	0	0	0	0	0	0	0	0	0	0.013335492
108	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Butyricicoccus;D_6__uncultured_bacterium	All others	0.004071	0.001513	0	0.008299	0	0.033207	0.014288	0.014908	0.021859	0.0184865	0.0169718	0.006505	0.011675722
109	D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Mollicutes_RF39;__;__;__	All others	0.030942	0.033291	0.021574	0	0	0	0	0	0	0.0127095	0.0193963	0.0119258	0.010819804
110	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Family_XIII;D_5__Family_XIII_AD3011_group;D_6__uncultured_bacterium	All others	0.013842	0.027238	0.007504	0.009129	0.011768	0.010418	0.009245	0.009938	0.007514	0.0034662	0	0.0021683	0.009352616
111	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__ASF356;D_6__uncultured_bacterium	All others	0	0.012106	0	0	0	0	0.010926	0.024846	0.002049	0	0.054148	0.0119258	0.009666745
112	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiales_vadinBB60_group;D_5__uncultured_Clostridia_bacterium;D_6__uncultured_Clostridia_bact	All others	0	0.015889	0.001876	0	0	0	0.004202	0	0	0.0225305	0.0266699	0.0477032	0.009905889
113	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcus_1;__	All others	0.004071	0.006809	0.005628	0	0	0.002604	0	0.005679	0.004782	0.0190642	0.0468744	0.0032525	0.008230416
114	D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Lactobacillaceae;D_5__Lactobacillus;D_6__Lactobacillus_reuteri	All others	0	0	0	0.08963	0.018388	0	0	0	0	0	0	0	0.009001503
115	D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Mollicutes_RF39;D_4__uncultured_bacterium;D_5__uncultured_bacterium;D_6__uncultured_bacterium	All others	0.007328	0.027994	0.013132	0.013279	0.022065	0	0	0	0	0	0	0	0.006983205
116	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__uncultured;D_6__Clostridium_sp._Culture-27	All others	0	0	0.04221	0.009129	0.005149	0.003256	0	0.00284	0	0.005777	0.0121227	0.0054208	0.007158565
117	D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae;D_5__Escherichia-Shigella;__	All others	0.001629	0.003783	0.003752	0.00249	0	0	0.001681	0	0	0.005777	0.0573807	0	0.006374326
118	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Acetatifactor;__	All others	0.007328	0.010592	0.045961	0.00249	0.005884	0.001953	0.001681	0.00284	0	0	0	0	0.006560827
119	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__uncultured;D_6__uncultured_Clostridiales_bacterium	All others	0.008143	0.014376	0.027202	0	0	0	0	0.006389	0	0	0.0096981	0	0.005483905
120	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_UCG-001;D_6__uncultured_bacterium	All others	0.001629	0.00454	0.003752	0.00332	0.002207	0	0.001681	0.011358	0.005465	0.0092433	0.0048491	0	0.004003542
121	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospiraceae_NK4A136_group;D_6__Lachnospiraceae_bacterium_A4	All others	0	0	0	0	0	0	0	0.004259	0	0	0.0064654	0.0140941	0.002068239
122	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Lachnospira;__	All others	0	0	0	0	0	0	0.005883	0.009228	0	0	0	0.0021683	0.001440014
123	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_5;D_6__uncultured_organism	All others	0.003257	0.006053	0	0	0	0	0	0	0	0.0023108	0	0	0.00096839
124	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;D_5__uncultured;D_6__uncultured_bacterium	All others	0	0	0	0	0	0	0	0	0	0	0.0105063	0.0021683	0.001056221
125	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminococcaceae_UCG-014;D_6__uncultured_rumen_bacterium	All others	0	0	0	0	0	0	0	0.007099	0.001366	0	0	0	0.00070542
126	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_6;D_6__uncultured_bacterium	All others	0	0	0	0	0	0	0	0	0	0	0.0072736	0	0.000606134
127	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae;D_5__Tyzzerella_3;D_6__uncultured_bacterium	All others	0	0	0	0	0	0.003907	0	0	0	0	0	0	0.000325559
128	D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae;D_5__Ruminiclostridium_6;__	All others	0	0	0	0	0.001471	0	0	0	0	0	0	0	0.000122585
129	D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Anaeroplasmatales;D_4__Anaeroplasmataceae;D_5__Anaeroplasma;D_6__uncultured_bacterium	All others	0	0	0	0	0	0	0	0.00142	0	0	0	0	0.000118314
130	D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae;__;__	All others	0	0	0	0	0	0	0	0	0	0	0	0	0
		TOTAL (each sample)	100	100	100	100	100	100	100	100	100	100	100	100	

Supplementary Table 2: Proximal nutritional analysis of the modified chow diets consumed in the study.

Analyte / Diet	Frankfurter	Pork	Sausage	Control
Sodium nitrate mg/Kg	24.6	31.9	<21	25.3
Potassium nitrate mg/Kg	29.3	38	<25	30.1
Sodium nitrite mg/Kg	<22.5	<22.5	<22.5	<22.5
Potassium nitrite mg/Kg	<27.7	<27.7	<27.7	<27.7
Fat g/100g	8.4	6.2	8.2	3.5
Moisture g/100g	9.3	8.3	8.3	7
Ash g/100g	2.9	2.7	2.7	2.6
Sodium g/100g	0.26	0.11	0.21	0.11
Sodium chloride g/100g	0.65	0.28	0.53	0.28
Total sugars g/100g	44.6	47.4	46	51.7
Nitrogen (mg/Kg) g/100g	3	3.41	2.98	2.85
Protein g/100g	18.8	21.3	18.6	17.8
Monounsaturated fatty acids g/100g	2.35	3.13	3.84	1.81
Polyunsaturated fatty acids g/100g	2.5	0.25	0.27	0.25
Saturated fatty acids g/100g	2.18	2.55	3.73	1.28
Dietary fibre g/100g	5	6.3	6.3	7.1
Carbohydrate g/100g	55.6	55.2	55.9	62
Energy kcal/100g	383	374	385	362