

Electronic supplementary Information



Figure S1. Image of the FFP. The FFP is presented as a dry granulated product, with an average particle size ranging from 4 to 12 mm with a moisture content of 12.8% and a pH of 4.4. FFP: fermented food product.

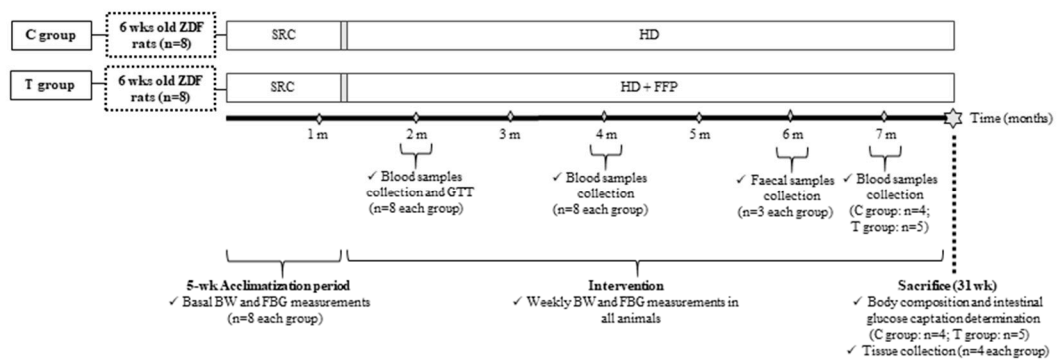


Figure S2. Experimental design. BW: body weight; FBG: fasting blood glucose; FFP: fermented food product; GTT: glucose tolerance test; HD: hypercaloric diet; SRC: standard rodent chow.

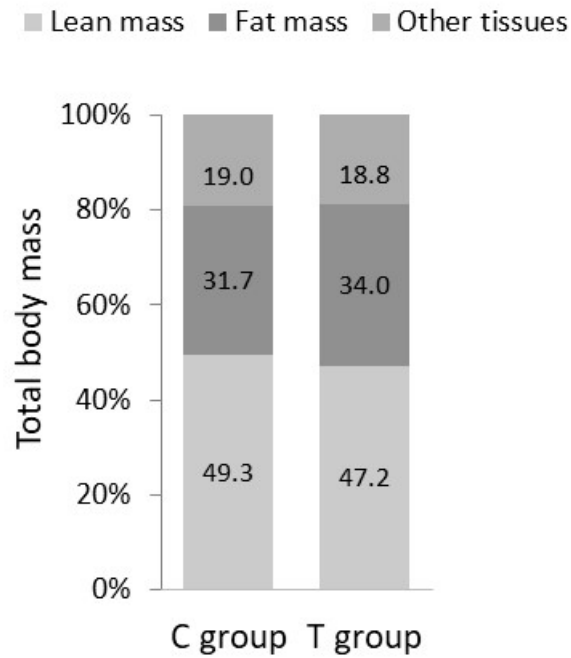


Figure S3. Body composition at the time of sacrifice measured by nuclear magnetic resonance (NMR).

The results are expressed as relative contribution of fat mass, lean mass and other tissues. No statistical differences were observed between C and T group in lean mass (49.3 ± 3.9 vs. 47.2 ± 7.7 % respectively; $p=0.641$), fat mass (31.7 ± 3.5 vs. 34.0 ± 8.4 % respectively; $p=0.630$) and other tissues (19.0 ± 5.6 vs. 18.8 ± 3.5 % respectively; $p=0.947$).

Table S1. Culturable and viable counts determined in the FFP. CFU: colony-forming unit; FFP: fermented food product.

<u>Media and conditions</u>	<u>Target microorganisms</u>	<u>Viable counts (CFU/g)</u>
Trypticase soy agar, 37°C for 24-48h, aerobiosis	Total bacteria	2.0×10^5
Man, Rogosa and Sharpe agar, 37°C for 24-48h, anaerobiosis	Lactobacilli	4.6×10^7
Potato dextrose agar, 25°C for 2-4 days, aerobiosis	Yeast and fungi	1.0×10^5

Table S2. Composition of FFP and ENVIGO TD.06416 hypercaloric diet (per 100 g of product). FFP: fermented food product.

<u>Components</u>	<u>FFP</u>	<u>TD.06416</u>
Calories (kcal)	467.6	510.0
Fats (%)	2.4	10.2
Proteins (%) (Nx6.25)	44.5	20.0
Carbohydrates (%)	53.1	69.8

Table S3. Body fat weight for rats in C and T groups.

No statistical significant differences between groups were found in the weight of the different fats. The results are expressed as the mean value \pm SD. g: grams.

	<u>C group</u>	<u>T group</u>
Body fat (g)	147.3 \pm 42.0	163.6 \pm 77.5
Body fat BW ⁻¹ (%)	31.7 \pm 3.5	34.0 \pm 8.4
Retroperitoneal fat (g)	16.3 \pm 6.5	28.5 \pm 16.1
Epididimal (g)	9.5 \pm 1.7	13.5 \pm 4.0
Mesenteric fat (g)	4.6 \pm 0.7	5.1 \pm 2.1
Subcutaneous fat (g)	15.5 \pm 5.3	24.7 \pm 12.1
Brown fat (g)	0.4 \pm 0.2	0.9 \pm 0.4

Table S4. Follow-up of lipid profile in ZDF rats. Means in the same column with different letters A, B or C and the same row with different letters a or b differ significantly ($p < 0.05$). n=8 animals/group. Data are expressed as mean \pm SD. ZDF: Zucker diabetic fatty; TC: serum total cholesterol; HDL-C: high-density lipoprotein cholesterol; LDL-C: low-density lipoprotein cholesterol; TG: triglycerides.

	Time (month)	C group	T group
TC (mg dL ⁻¹)	0	155.3 \pm 11.7 ^{Aa}	143.3 \pm 10.8 ^{Aa}
	2	395.1 \pm 55.6 ^{BCa}	353.9 \pm 95.2 ^{Ba}
	4	380.5 \pm 35.3 ^{Ba}	342.1 \pm 77.6 ^{Ba}
	7	478.4 \pm 61.2 ^{Ca}	424.7 \pm 147.0 ^{Ba}
LDL-C (mmol L ⁻¹)	0	0.5 \pm 0.1 ^{Aa}	0.3 \pm 0.1 ^{Ab}
	2	2.2 \pm 0.6 ^{Ba}	1.5 \pm 1.2 ^{Ba}
	4	2.4 \pm 0.5 ^{Ba}	2.1 \pm 0.9 ^{Ba}
	7	3.4 \pm 0.8 ^{Ca}	2.9 \pm 2.0 ^{Ba}
HDL-C (mmol L ⁻¹)	0	2.8 \pm 0.5 ^{Aa}	2.5 \pm 0.4 ^{Aa}
	2	6.5 \pm 0.7 ^{Ba}	5.4 \pm 2.0 ^{Ba}
	4	6.5 \pm 0.8 ^{Ba}	6.5 \pm 1.3 ^{Ba}
	7	6.3 \pm 2.1 ^{Ba}	7.2 \pm 2.1 ^{Ba}
TG (mg dL ⁻¹)	0	223.4 \pm 44.8 ^{Aa}	311.5 \pm 95.7 ^{Ab}
	2	530.1 \pm 129.0 ^{Ba}	585.9 \pm 135.3 ^{Ba}
	4	531.3 \pm 162.4 ^{Ba}	481.9 \pm 90.2 ^{Ba}
	7	791.0 \pm 267.4 ^{Ba}	452.7 \pm 148 ^{ABb}

Table S5. List of bacteria species and OTUs which were identified exclusively in the C group.

OTU1562|NN=Clostridium_glycolicum_AY007244|D=96.5

Clostridium_celatum
OTU1634|NN=Blautia_stercoris_HM626177|D=94.7
OTU407|NN=Soleaferrea_massiliensis_JX101688|D=87.4
Clostridium_methylpentosum
OTU270|NN=Dorea_massiliensis_JX101687|D=94.1
OTU1336|NN=Clostridium_methylpentosum_Y18181|D=91.5_2
OTU997|NN=Catabacter_hongkongensis_AB671763|D=82.9
OTU566|NN=Clostridium_hathewayi_EF408243|D=97
Abiotrophia_para-adiacens
Citrobacter_werkmanii
Staphylococcus_schleiferi
OTU1353|NN=Clostridium_citroniae_DQ279737|D=92.5
OTU1178|NN=Papillibacter_cinnamivorans_AF167711|D=89.4
OTU307|NN=Sphingobacterium_multivorum_KF535155.1|D=91.3
OTU1282|NN=Roseburia_faecis_AY804149|D=92.8
Abiotrophia_defectiva
OTU1739|NN=Enterobacter_cancerogenus_JN644583|D=96.9
OTU1347|NN=Eubacterium_dolichum_AB649277|D=77.1
OTU1201|NN=Blautia_glucerasea_AB588023|D=94.1
Propionibacterium_acidipropionici
OTU155|NN=Sphingomonas_panni_AJ575818|D=96.7
OTU1006|NN=Eubacterium_rectale_AY804151|D=93.3
Candidatus_Stoquefichus_massiliensis
Blastococcus_massiliensis
OTU1222|NN=Clostridium_sporosphaeroides_CLORR16SAD|D=91.2

Table S6. List of bacteria species and OTUs which were identified exclusively in the T group.

OTU1073 NN=Barnesiella_intestinihominis_AB370251 D=87.1	OTU42 NN=Ruminococcus_gauvreauii_EF529620 D=88.4
Bacteroides_stercoris	OTU891 NN=Blautia_coccoides_EF025906 D=93.1
Sutterella_stercoricaris	Desulfovibrio_fairfieldensis
Lysinibacillus_massiliensis	OTU523 NN=Barnesiella_intestinihominis_AB370251 D=82_2
Proteus_mirabilis	Neisseria_macacae
OTU975 NN=Bacteroides_fluxus_AB547642 D=96.1	OTU744 NN=Ruminococcus_callidus_X85100 D=91.1
OTU1478 NN=Ruminococcus_flavofaciens_AY349157 D=94	OTU1427 NN=Clostridium_clariflavum_NR_102987.1 D=82.3
OTU69 NN=Oscillibacter_valericigenes_AB238598 D=94.8	OTU523 NN=Barnesiella_intestinihominis_AB370251 D=82
OTU883 NN=Clostridium_lactatifermentans_AY033434 D=90.6	OTU1597 NN=Eubacterium_sulci_AJ006963 D=89.4
Tyzzereella_lactatifermentans	Alistipes_finegoldii
OTU193 NN=Barnesiella_intestinihominis_AB370251 D=85.1	OTU1461 NN=Desulfitobacterium_frappieri_DFU40078 D=84.5
OTU60 NN=Ruminococcus_bromii_DQ882649 D=89.6	Neisseria_elongata
OTU217 NN=Gemmiger_formicilis_GU562446 D=96.5	Lactococcus_garvieae
OTU521 NN=Papillibacter_cinnamivorans_AF167711 D=89.6	OTU1319 NN=Roseburia_intestinalis_AB661435 D=88.7_2
OTU1242 NN=Eubacterium_cellulosolvens_AY178842 D=93.3	OTU1391 NN=Clostridium_clariflavum_NR_102987.1 D=84
OTU815 NN=Pseudomonas_monteilii_GQ284481 D=96.2	OTU1704 NN=Clostridium_sporosphaeroides_CLORR16SAD D=91.6
OTU478 NN=Butyricoccus_pullicaeorum_EU410376 D=91.9	OTU254 NN=Stenotrophomonas_rhizophila_AB539813 D=96.6
OTU267 NN=Parasutterella_excrementihominis_AB370250 D=92.5	OTU661 NN=Blautia_wexlerae_EF036467 D=94.9
OTU779 NN=Lysinibacillus_sphaericus_AJ311894 D=94.4	Pediococcus_damnosus
OTU1337 NN=Desulfovibrio_desulfuricans_DVURRDA D=89	Pseudomonas_oleovorans
OTU1101 NN=Clostridium_lactatifermentans_AY033434 D=94	OTU1116 NN=Clostridium_hathewayi_EF408243 D=93.2
OTU1735 NN=Pseudomonas_monteilii_GQ284481 D=96.6	Blautia_torques
OTU1212 NN=Ruminococcus_lactaris_NR_027579.1 D=87.5	OTU167 NN=Soleaferrea_massiliensis_JX101688 D=88.5
OTU1381 NN=Pseudomonas_fluorescens_KJ161327 D=96.2	OTU570 NN=Ruminococcus_gauvreauii_EF529620 D=91.2_4
OTU655 NN=Clostridium_asparagiforme_AJ582080 D=89.7_2	OTU82 NN=Clostridium_lactatifermentans_AY033434 D=93.1
OTU45 NN=Soleaferrea_massiliensis_JX101688 D=88.7	OTU930 NN=Brevibacillus_agri_AY319301.1 D=78.3
OTU814 NN=Anoxystipes_fissicatena_NR_104800.1 D=92.5_2	Brevundimonas_vesicularis
Odoribacter_laneus	Bacillus_megaterium
Lachnospirillum_indolis	Microbacterium_phyllosphaerae
OTU1508 NN=Eubacterium_rectale_AY804151 D=94.1	Lactococcus_lactis
OTU328 NN=Eubacterium_ventriosum_EUBRRDAB D=94.6	OTU184 NN=Ochrobacterium_anthropi_KC845230 D=79
Bifidobacterium_longum	OTU446 NN=Brachy bacterium_paraconglomeratum_EU660345 D=96.1
OTU522 NN=Melainabacter_A1 D=92.9	Stenotrophomonas_maltophilia
OTU1330 NN=Clostridium_lactatifermentans_AY033434 D=90.5	OTU1064 NN=Leuconostoc_gelidum_KF577567 D=96.8
OTU1119 NN=Soleaferrea_massiliensis_JX101688 D=89.3	Lactobacillus_paracasei
Actinomyces_canis	Butyrivibrio_crossotus
OTU1475 NN=Clostridium_clariflavum_NR_102987.1 D=83	Catabacter_hongkongensis
OTU814 NN=Anoxystipes_fissicatena_NR_104800.1 D=92.5_3	OTU1487 NN=Melainabacter_A1 D=96.1
OTU1570 NN=Clostridium_clariflavum_NR_102987.1 D=79.3	OTU152 NN=Oscillibacter_valericigenes_AB238598 D=94.3
OTU1722 NN=Clostridium_clariflavum_NR_102987.1 D=83.6	OTU1546 NN=Soleaferrea_massiliensis_JX101688 D=87.8
OTU239 NN=Adlercreutzia_equolifaciens_AB306660 D=95	OTU175 NN=Roseburia_hominis_AB661434 D=94.3
OTU444 NN=Ruminococcus_albus_AY445596 D=91.1	OTU287 NN=Coprococcus_catus_AB361624 D=96.2
OTU315 NN=Clostridium_clostridioforme_AY169422 D=91.7	OTU429 NN=Clostridium_methylpentosum_Y18181 D=81.9_2
OTU722 NN=Oscillibacter_valericigenes_AB238598 D=91.6	OTU644 NN=Dorea_massiliensis_JX101687 D=88.1
OTU944 NN=Intestinimonas_butyriciproducens_JX101685.1 D=91.5	OTU821 NN=Massilia_aurea_AM231588 D=96.5
OTU1424 NN=Dorea_formicigenerans_EUBRRDP D=96.7	OTU823 NN=Clostridium_bartlettii_AY438672 D=96.4
OTU1108 NN=Clostridium_bolteae_AJ508452 D=92.8	OTU826 NN=Lactobacillus_vaginalis_GQ422709 D=94
OTU1598 NN=Oscillospira[Pseudoflavonifactor]_capillosus_AY136666 D=90.1	Serratia_marcescens
OTU355 NN=Clostridium_lactatifermentans_AY033434 D=90.6	Streptococcus_parauberis
Psychrobacter_arenosus	Tyzzereella_lactatifermentans
OTU1115 NN=Coprococcus_comes_EF031542 D=95	
