SUPPLEMENTARY INFORMATION

Microbial characterization of inocula

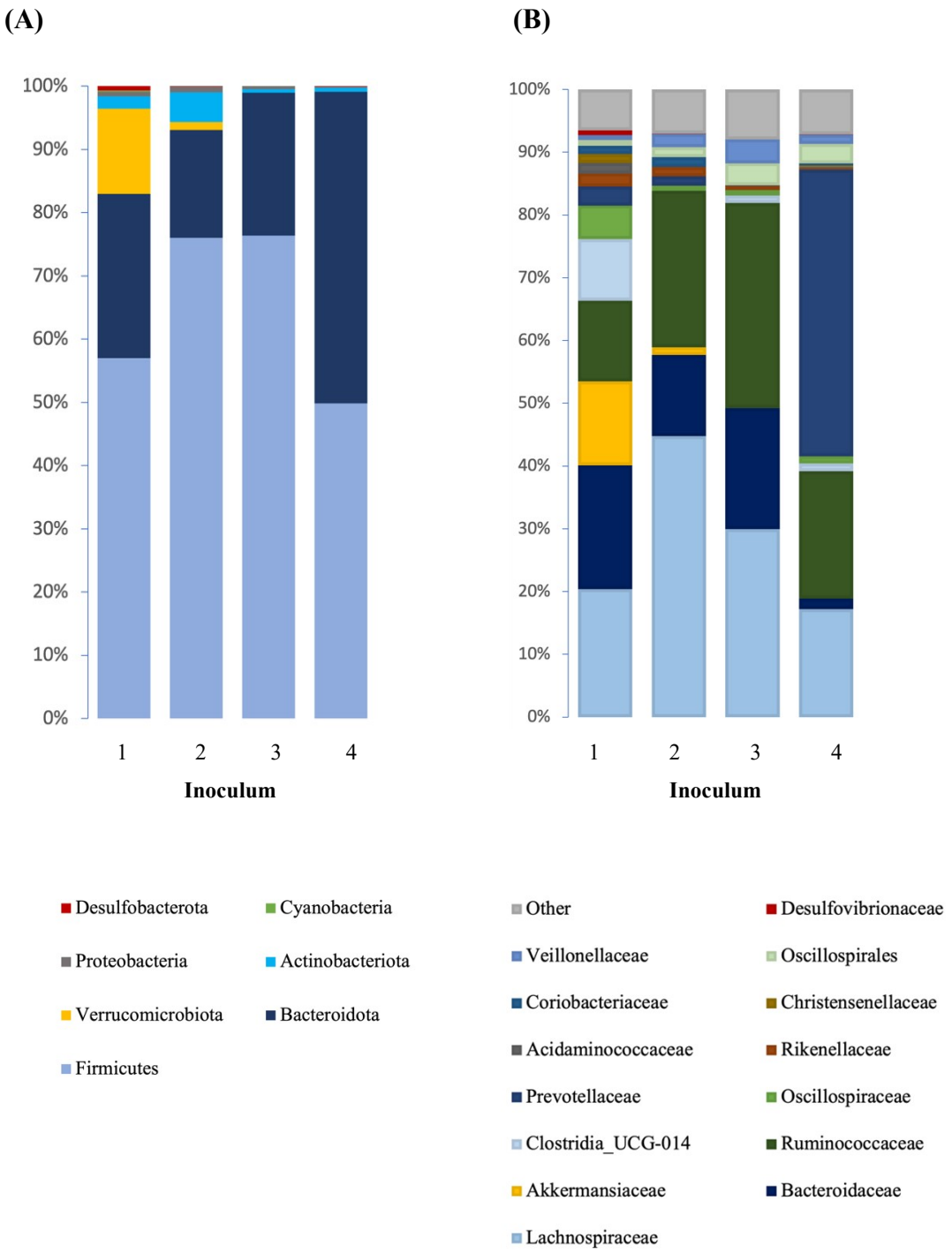
The primers 341F (5'- CCTACGGGNGGCWGCAG) and 785R (5'- GACTACHVGGGTATCTAATCC) that target the V3-V4 region of the 16S rRNA gene (Klindworth et al., 2013), with an extra wobble position in the reverse primer to make it more universal, were used to target total bacteria. The DNA extracts had a DNA concentration of 20 ng μL^{-1}, and were free of RNA, which was validated with agarose gel electrophoresis. The PCR mix included 1 µL of DNA extract, 15 pmol of both the forward primer 341F 5'- NNNNNNNNNTCCTACGGGNGGCWGCAG and reverse primer 785R 5'- NNNNNNNNNNTGACTACHVGGGTATCTAAKCC (Klindworth et al., 2013), 20 µL volume of MyTaq buffer containing 1.5 units MyTaq DNA polymerase (Bioline) and 2 µL of BioStabII PCR Enhancer (Sigma). For each sample, the forward and reverse primers had the same unique 10-nt barcode sequence. The PCR contained an initial predenaturation step for 2 min at 96 °C, followed by 20 cycles using the following parameters: 96°C for 15 s, 50°C for 30 s, 70°C for 90 s. The PCR products were purified using Ampure XP beads, according to the manufacturer's instructions, to remove primer dimer and other small mispriming products, followed by an additional purification on MinElute columns (Qiagen). Finally, about 100 ng of each purified amplicon pool DNA was used to construct Illumina libraries by means of adaptor ligation using the Ovation Rapid DR Multiplex System 1-96 (NuGEN). Illumina libraries were pooled and size selected by preparative gel electrophoresis.

The Mothur software package (v.1.44.3), and guidelines developed by Schloss et al. (2009) were used to process the raw Illumina data using R version 4.1.0 on a x86_64-pc-linux-gnu (64-bit) system. The forward and reverse reads were assembled into contigs by a heuristic approach, taking the Phred quality scores into account. Ambiguous contigs or with unsatisfying overlap were removed, and the remaining sequences were aligned to the mothur formatted silva

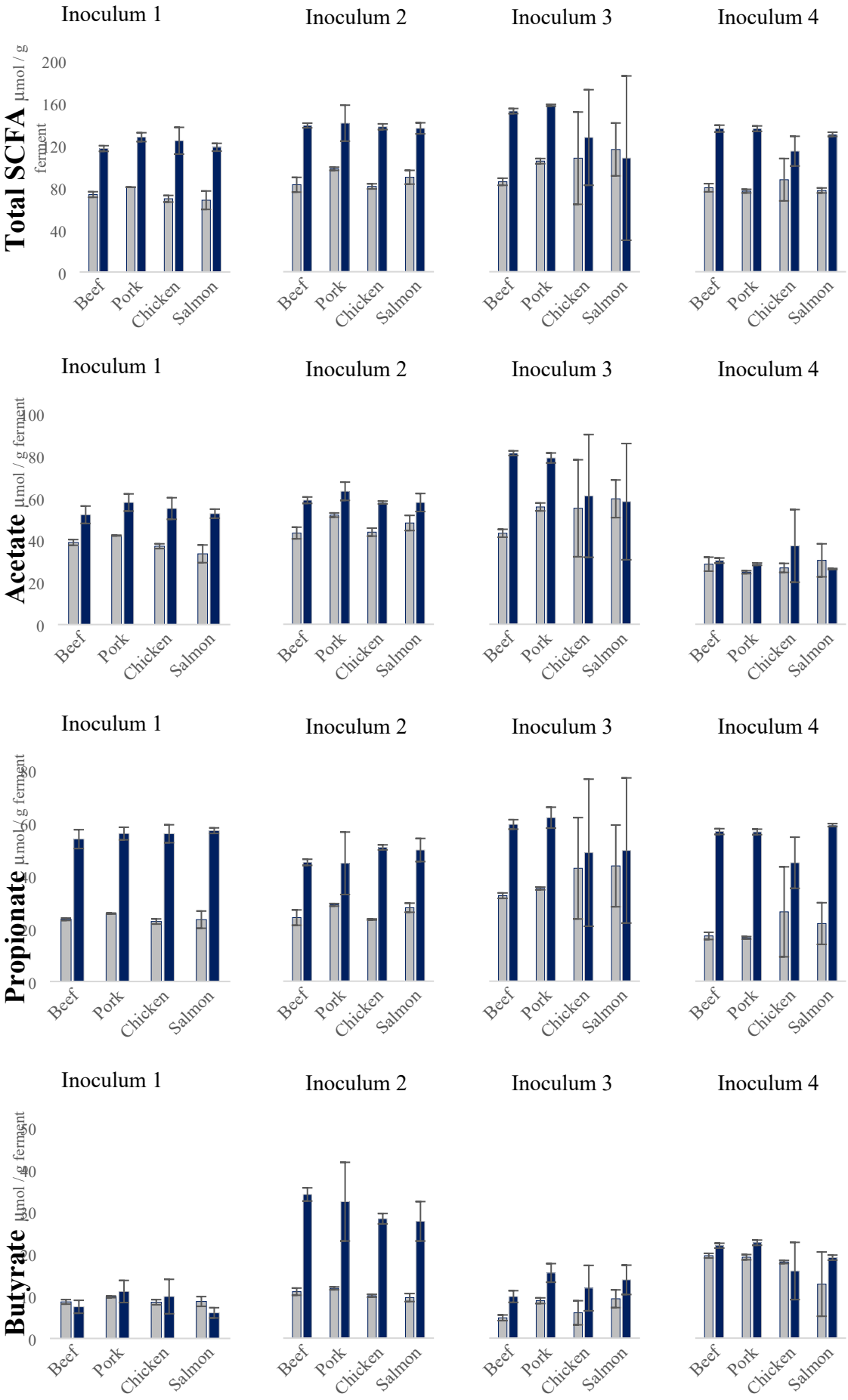
seed v138 database. Those sequences not aligning within the region targeted by the primer set or sequences with homopolymer stretches with a length > 12 bp were removed. The sequences were pre-clustered, allowing mismatch for every 100 bp of sequence. Chimeric sequences were removed with VSEARCH (v2.13.3) (Rognes et al., 2016). Classification of the sequences was carried out by a naïve Bayesian classifier (Wang et al., 2007), using the RDP 16S rRNA gene training set, release 16, with an 85% cut-off for the pseudobootstrap confidence score. Taxa that were annotated as Chloroplast, Mitochondria, unknown, Archaea or Eukarya at the kingdom level were excluded. Sequences were clustered into OTUs with an average linkage, and at a 97% sequence identity, using the OptiClust method (Westcott and Schloss, 2017). If sequences could not be classified at the (super) Kingdom level, they were removed. Representative sequences were picked for each OTU as the most abundant sequence within that OTU.

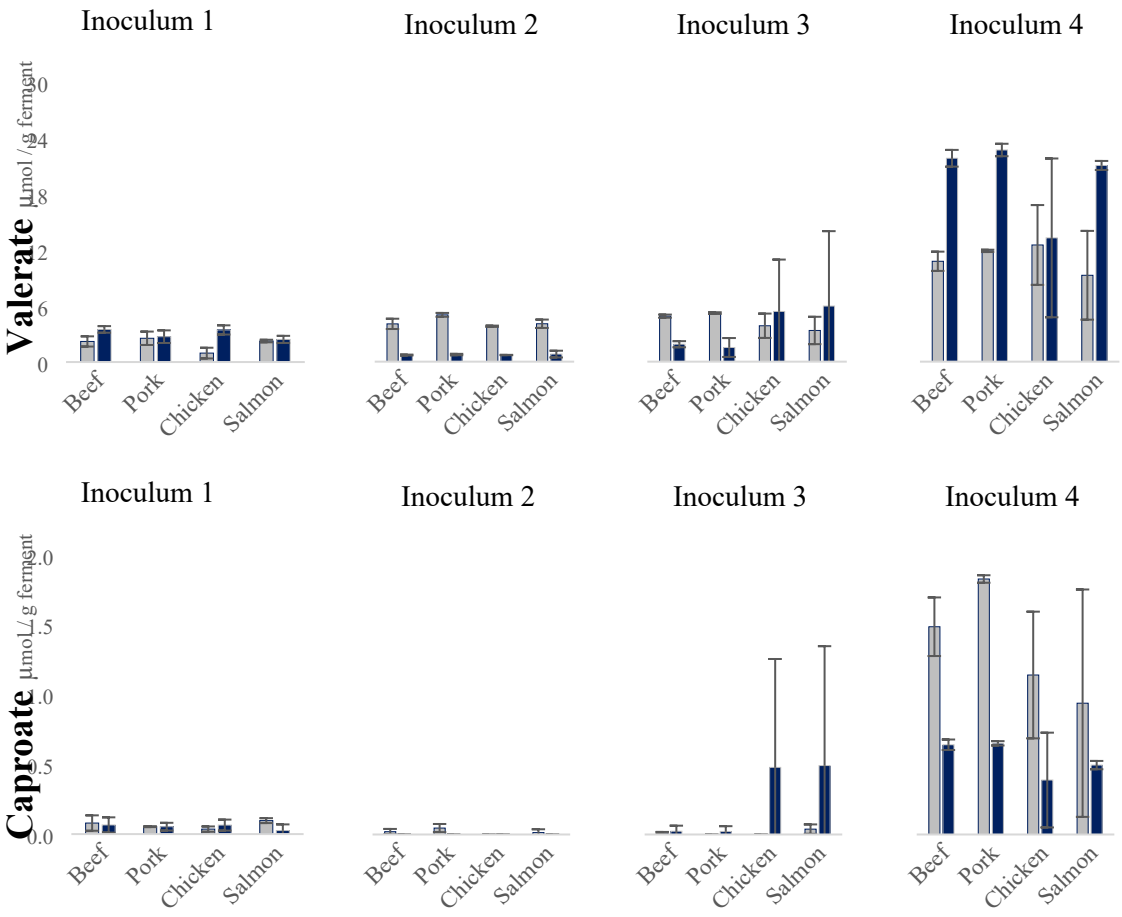
Supplementary Table 1. Composition of the simulated digestive fluids.

MOUTH			**STOMACH**			**SMALL INTESTINE**					
Saliva			Gastric Juice			Duodenal Juice			Bile Juice		
0.900	g	KCl	2.750	g	NaCl	7.010	g	NaCl	5.260	g	NaCl
0.200	g	KSCN	0.270	g	NaH_2PO_4	3.390	g	$NaHCO_3$	5.790	g	$NaHCO_3$
0.900	g	NaH_2PO_4	0.820	g	KCl	0.080	g	KH_2PO_4	0.380	g	KCl
0.570	g	Na_2SO_4	0.400	g	$CaCl_2$ $2H_2O$	0.560	g	KCl	0.150	ml	HCL (37%)
0.300	g	NaCl	0.037	g	NH_4Cl	0.050	g	$MgCl_2$			
1.690	g	$NaHCO_3$	7.500	ml	HCl (37%)	0.180	ml	HCl (37%)			
0.007	g	$NaNO_2$	6.000	ml	Urea	4.000	ml	Urea	10.00	ml	Urea
8.000	ml	Urea	0.020	g	Glucuronic acid	1.000	g	BSA	1.800	g	BSA
0.012	g	Uric acid	0.650	g	Glucose	9.000	g	Pancreatin	30.00	g	Bile
0.290	g	Amylase	0.330	g	Glucosamine -HCl	1.500	g	Lipase	0.222	g	$CaCl_2$
			0.018	g	Ascorbic acid	0.200	g	$CaCl_2$			
			1.000	g	BSA						
			2.500	g	Pepsin						
			3.000	g	Mucin						
			0.011	g	$FeSO_4$ $.7H_2O$						

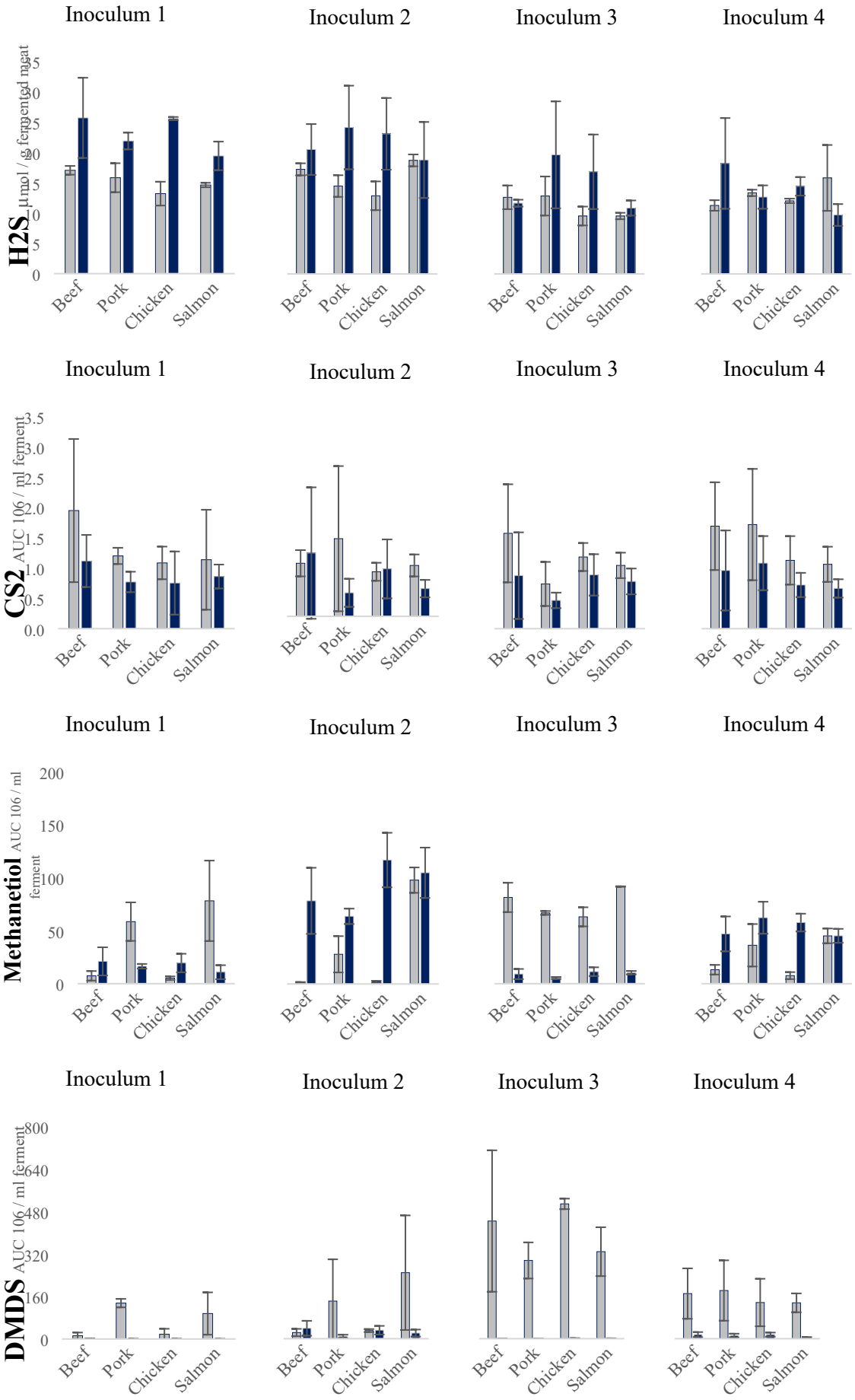


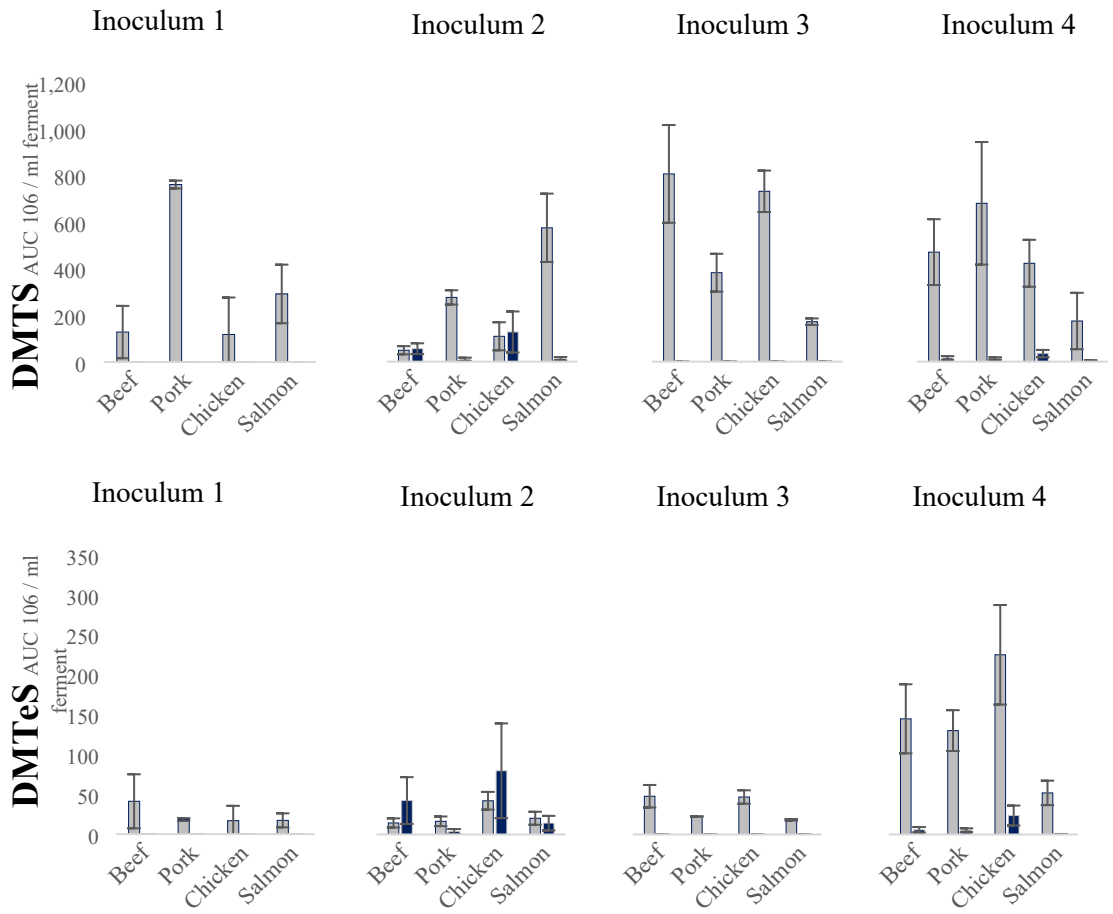
Supplementary Figure 1. Microbial community characterization of inocula at the phylum (A) and family (B) level.


Inoculum 1
Inoculum 2
Inoculum 3
Inoculum 4
Total SCFA µmol / g ferment
Acetate µmol / g ferment
Propionate µmol / g ferment
Butyrate µmol / g ferment
Beef
Pork
Chicken
Salmon

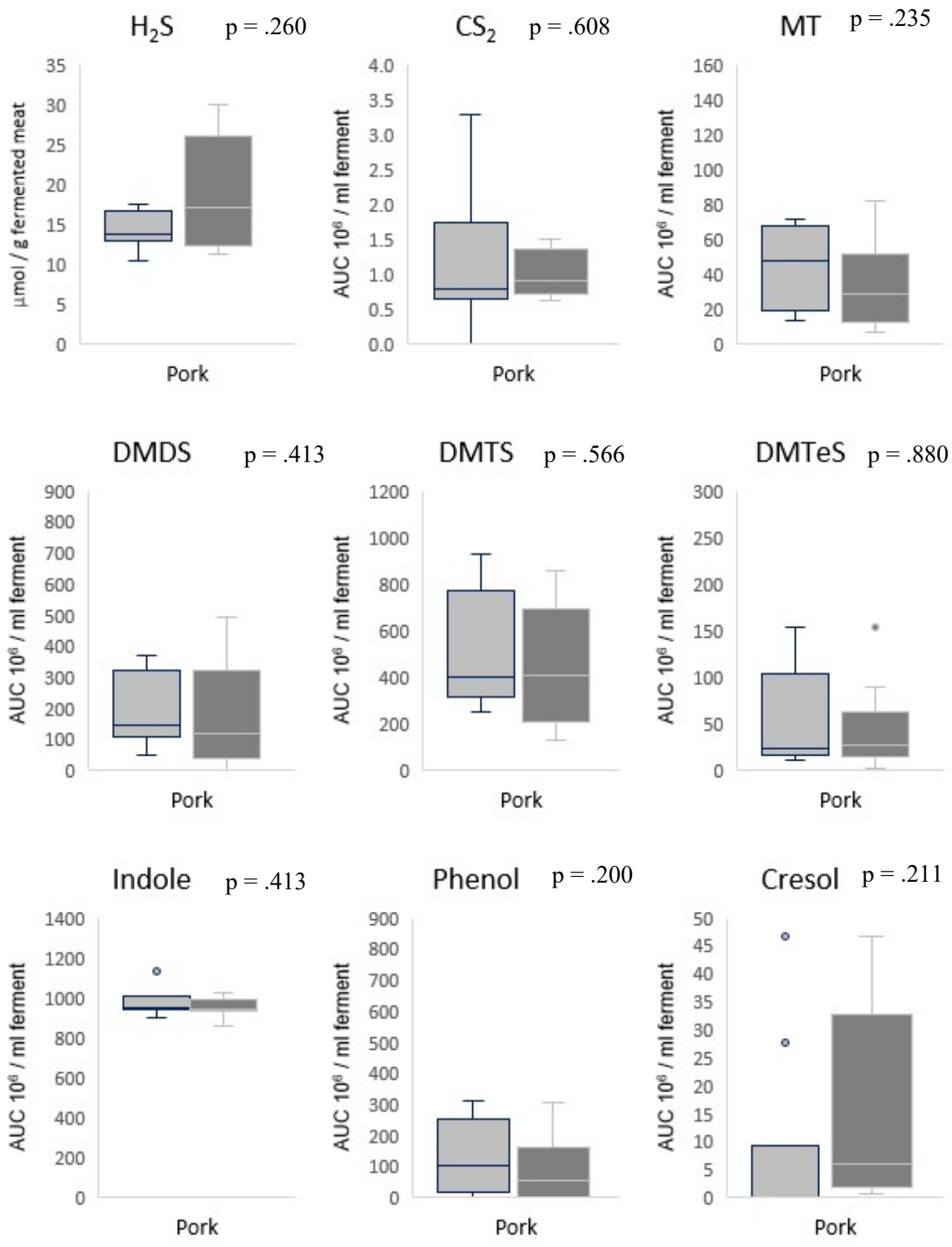


Supplementary Figure 2. Levels of SCFA in ferments of muscle sources with (■) or without FOS (□) for the different inocula.

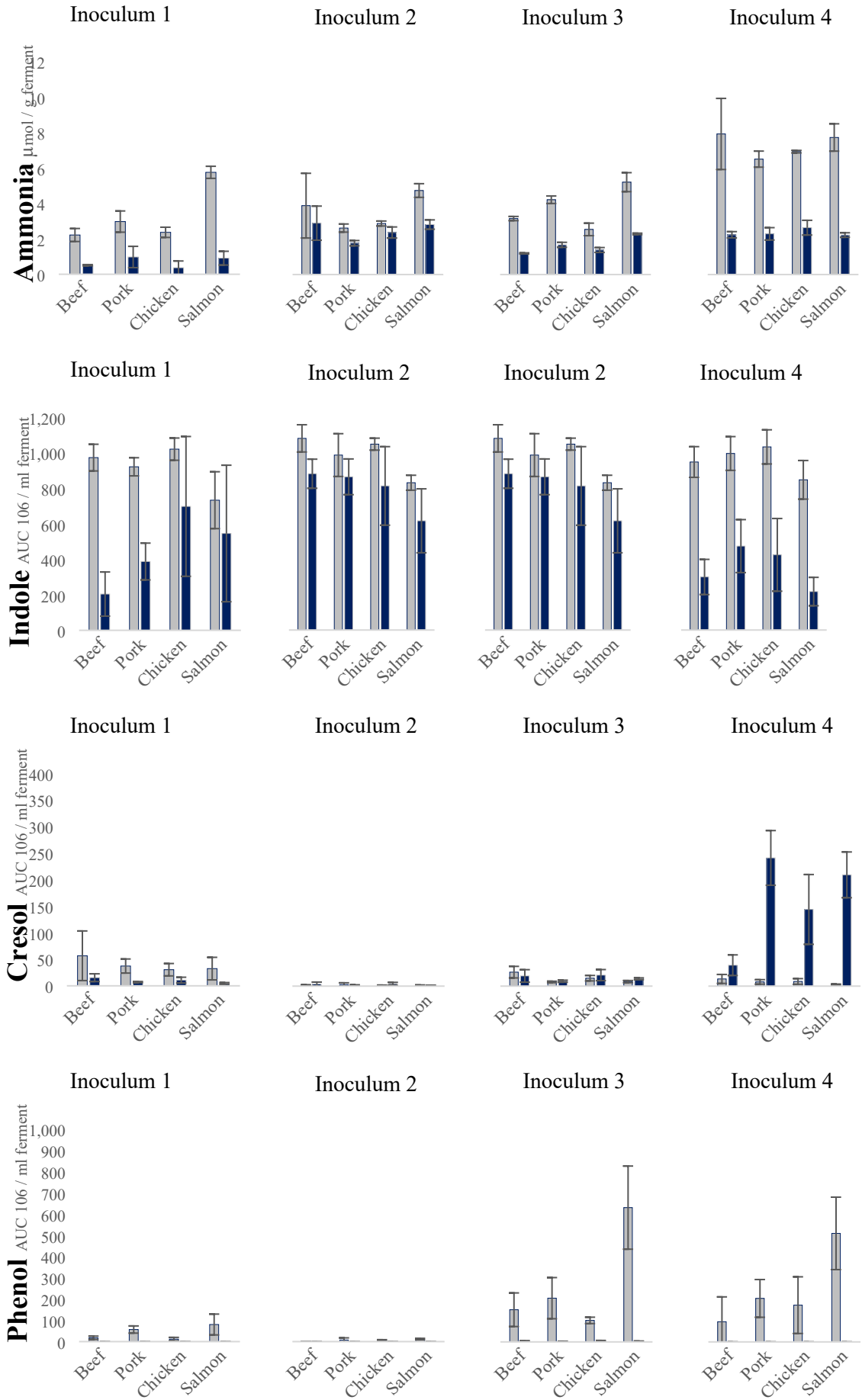

Inoculum 1
Inoculum 2
Inoculum 3
Inoculum 4
H2S µmol / g fermented meat
CS2 AUC 106 / ml ferment
Methanetiol AUC 106 / ml ferment
DMDS AUC 106 / ml ferment
Beef
Pork
Chicken
Salmon

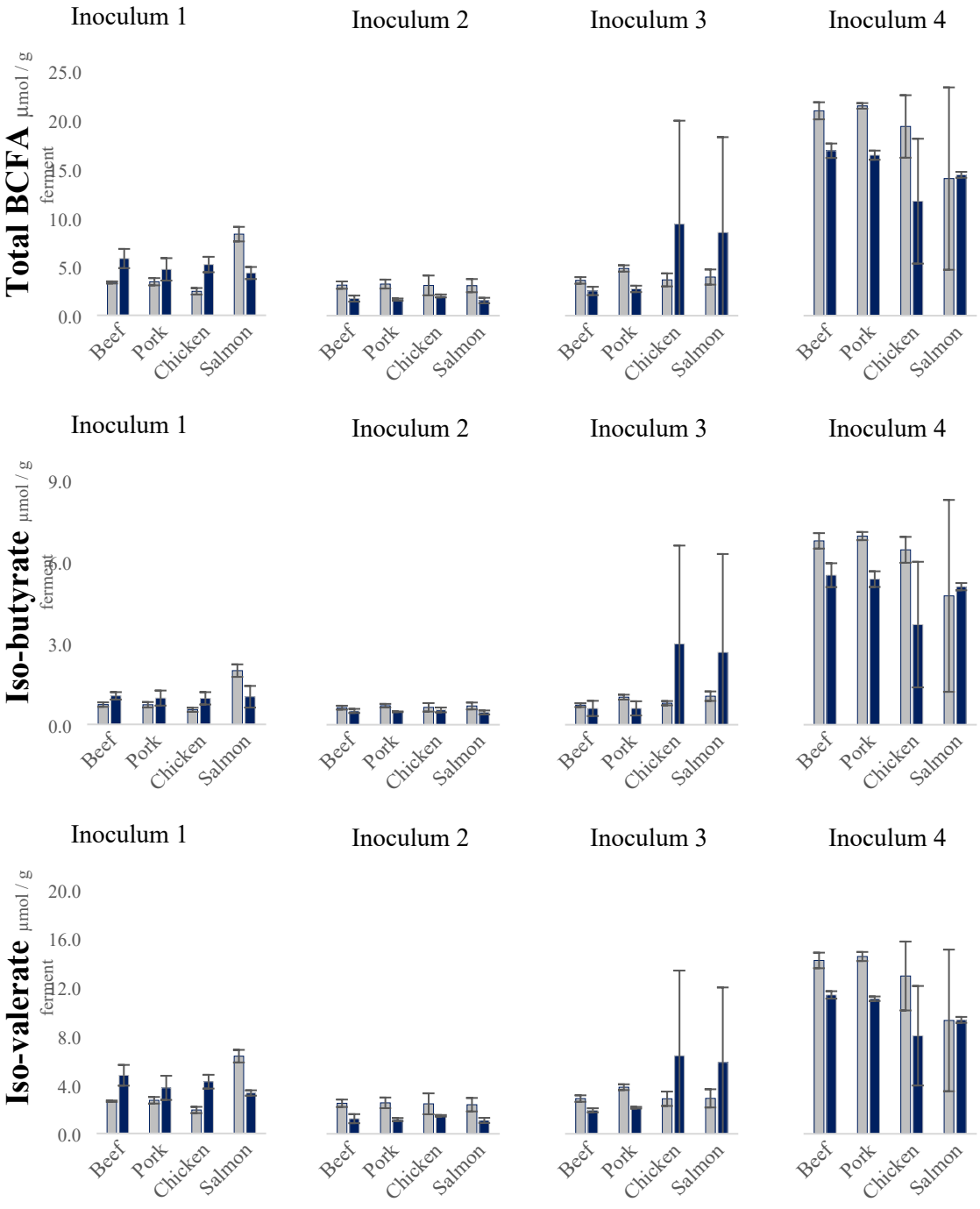


Supplementary Figure 3. Levels of sulfur metabolites in ferments (24h) of muscle sources with ( ) or without FOS ( ) for the different inocula.



Supplementary Figure 4. Levels of sulfur and protein metabolites in ferments of muscle sources with (□) or without (■) mucin.


Inoculum 1
Inoculum 2
Inoculum 3
Inoculum 4
Ammonia µmol / g ferment
0
2
4
6
8
10
12
Beef
Pork
Chicken
Salmon
Inoculum 1
Inoculum 2
Inoculum 2
Inoculum 4
Indole AUC 106 / ml ferment
0
200
400
600
800
1,000
1,200
Beef
Pork
Chicken
Salmon
Inoculum 1
Inoculum 2
Inoculum 3
Inoculum 4
Cresol AUC 106 / ml ferment
0
50
100
150
200
250
300
350
400
Beef
Pork
Chicken
Salmon
Inoculum 1
Inoculum 2
Inoculum 3
Inoculum 4
Phenol AUC 106 / ml ferment
0
100
200
300
400
500
600
700
800
900
1,000
Beef
Pork
Chicken
Salmon



Supplementary Figure 5. Levels of non-sulfur protein fermentation metabolites in ferments of muscle sources with ( ) or without FOS ( ) for the different inocula.

REFERENCES SUPPORTING INFORMATION

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Rognes, T., Flouri, T., Nichols, B., Quince, C., & Mahé, F. (2016). VSEARCH: a versatile open source tool for metagenomics. PeerJ, 4, e2584. https://doi.org/10.7717/peerj.2584

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