

Supplementary Material

Table S1: Corrected P values for Kruskal Wallis test on individual milk samples

Milk		
NPI vs NPO	P value	Higher in
<i>Lactococcus</i>	0.002	NPO
<i>Pseudomonas</i>	0.003	NPO
<i>Acinetobacter</i>	0.008	NPO
<i>Eremococcus</i>	0.012	NPI
<i>Ruminococcus</i>	0.012	NPI
<i>Tumebacillus</i>	0.014	NPO
<i>Prevotella</i>	0.02	NPI
<i>Corynebacteriales</i> uncultured bacterium	0.022	NPI
<i>Ruminococcaceae</i> Incertae Sedis	0.028	NPI
<i>Bacteroidales</i> uncultured bacterium	0.049	NPI
NPI vs PI	P value	Higher in
<i>Pseudomonas</i>	0.035	PI
NPO vs PO	P value	Higher in
uncultured <i>Verrucomicrobia</i> bacterium	0.005	PO
<i>Exiguobacterium</i>	0.009	PO
<i>Pseudomonas</i>	0.011	NPO
DA101 soil group uncultured bacterium	0.013	PO
<i>Bifidobacterium</i>	0.02	NPO
<i>Lactococcus</i>	0.025	NPO
Candidate division TM7 uncultured bacterium	0.027	PO
<i>Lactobacillus</i>	0.03	NPO
<i>Ruminococcaceae</i> Incertae Sedis	0.046	PO
PI vs PO	P value	Higher in
<i>Bifidobacterium</i>	0.001	PI
<i>Eremococcus</i>	0.001	PI
<i>Facklamia</i>	0.001	PI
<i>Alloiococcus</i>	0.001	PI
<i>Atopostipes</i>	0.001	PI
<i>Trichococcus</i>	0.001	PI
<i>Carnobacteriaceae</i> uncultured	0.002	PI
DA101 soil group uncultured <i>Verrucomicrobia</i>	0.002	PO
<i>Corynebacterium</i>	0.003	PI
<i>Exiguobacterium</i>	0.003	PO
DA101 soil group uncultured bacterium	0.003	PO
<i>Lactobacillus</i>	0.004	PI

<i>Ruminococcus</i>	0.009	PI
<i>Flavobacterium</i>	0.009	PO
<i>Massilia</i>	0.012	PO
<i>Sphingomonas</i>	0.014	PO
<i>Psychrobacter</i>	0.019	PI
<i>Prevotella</i>	0.02	PI
<i>Candidatus Saccharimonas</i>	0.02	PI
<i>Variovorax</i>	0.02	PO
<i>Tumebacillus</i>	0.021	PO
<i>Hymenobacter</i>	0.022	PO
<i>Dietzia</i>	0.023	PI
<i>Arthrobacter</i>	0.028	PI
<i>Clostridium sensu stricto 1</i>	0.036	PI

NPI= No prep indoor; NPO=No prep outdoor; PI= Prep indoor; PO= Prep outdoor

Table S2: Corrected P values for Kruskal Wallis test on teat swab samples

Teat		
NPI vs NPO	P value	Higher in
<i>Trichococcus</i>	0.012	NPI
<i>Incertae Sedis</i>	0.013	NPO
<i>Acidimicrobiales</i> uncultured bacterium	0.014	NPO
<i>Peptostreptococcaceae</i> uncultured	0.015	NPO
<i>Marinospirillum</i>	0.02	NPI
<i>Proteiniphilum</i>	0.021	NPI
<i>Erysipelothrix</i>	0.025	NPI
<i>Exiguobacterium</i>	0.025	NPO
<i>Corynebacterium</i>	0.039	NPI
<i>Psychrobacter</i>	0.039	NPI
<i>Arenimonas</i>	0.039	NPO
<i>Betaproteobacteria</i> uncultured bacterium	0.04	NPO
uncultured <i>Mycobacteriaceae</i> bacterium	0.042	NPO
<i>Xanthomonadales</i> uncultured bacterium	0.042	NPO
<i>Eremococcus</i>	0.044	NPI
<i>Blastocatella</i>	0.049	NPO
<i>Verrucomicrobiaceae</i> uncultured	0.049	NPO
<i>Ferruginibacter</i>	0.05	NPO
NPI vs PI	P value	Higher in
<i>Variovorax</i>	0.033	NPI
<i>Bifidobacterium</i>	0.04	PI
<i>Acidimicrobiales</i> uncultured bacterium	0.043	NPI
<i>Devosia</i>	0.043	NPI
NPO vs PO	P value	Higher in
No significant differences	NA	
PI vs PO	P value	Higher in
<i>Proteiniphilum</i>	0.001	PI
<i>Jeotgalicoccus</i>	0.001	PI
<i>Eremococcus</i>	0.001	PI
<i>Facklamia</i>	0.001	PI
<i>Carnobacteriaceae</i> uncultured	0.001	PI
<i>Erysipelothrix</i>	0.001	PI
<i>Marinospirillum</i>	0.001	PI
<i>Blastocatella</i>	0.001	PO
<i>Acidimicrobiales</i> uncultured bacterium	0.001	PO
uncultured <i>Mycobacteriaceae</i> bacterium	0.001	PO
<i>Dyadobacter</i>	0.001	PO
<i>Ferruginibacter</i>	0.001	PO
<i>Devosia</i>	0.001	PO

<i>Methylobacterium</i>	0.001	PO
<i>Variovorax</i>	0.001	PO
<i>Stenotrophomonas</i>	0.001	PO
<i>Xanthomonas</i>	0.001	PO
DA101 soil group uncultured bacterium	0.001	PO
<i>Corynebacterium</i>	0.002	PI
<i>Ruminococcus</i>	0.002	PI
<i>Psychrobacter</i>	0.002	PI
uncultured Acidobacteria bacterium	0.002	PO
<i>Clavibacter</i>	0.002	PO
<i>Gaiellales</i> uncultured bacterium	0.002	PO
<i>Chitinophagaceae</i> uncultured	0.002	PO
<i>Exiguobacterium</i>	0.002	PO
<i>Sphingomonas</i>	0.002	PO
<i>Betaproteobacteria</i> SC.I.84 uncultured bacterium	0.002	PO
<i>Arenimonas</i>	0.002	PO
<i>Xanthomonadales</i> uncultured bacterium	0.002	PO
DA101 soil group uncultured <i>Verrucomicrobia</i> bacterium	0.002	PO
<i>Verrucomicrobiaceae</i> uncultured	0.002	PO
<i>Bifidobacterium</i>	0.003	PI
<i>Spirochaetaceae</i> uncultured	0.003	PI
Acidobacteria Subgroup 6 uncultured bacterium	0.003	PO
<i>Hymenobacter</i>	0.003	PO
<i>Pedobacter</i>	0.003	PO
WD2101 soil group uncultured bacterium	0.003	PO
<i>Rhizobium</i>	0.003	PO
<i>Chthoniobacter</i>	0.003	PO
<i>Alloiococcus</i>	0.004	PI
<i>Trichococcus</i>	0.004	PI
<i>Rhodococcus</i>	0.004	PO
<i>Bradyrhizobium</i>	0.004	PO
<i>Prevotella</i>	0.005	PI
<i>Brevundimonas</i>	0.005	PO
<i>Massilia</i>	0.005	PO
<i>Spirosoma</i>	0.006	PO
<i>Nocardioides</i>	0.007	PO
<i>Treponema</i>	0.009	PI
<i>Kandleria</i>	0.009	PO
uncultured <i>Parabacteroides</i> sp.	0.011	PI
<i>Blautia</i>	0.011	PI
<i>Halomonas</i>	0.015	PI
<i>Cellvibrio</i>	0.026	PO
<i>Peptostreptococcaceae Incertae Sedis</i>	0.03	PO
<i>Lachnospiraceae</i> uncultured	0.032	PI
<i>Anaerotruncus</i>	0.032	PI

Comamonadaceae uncultured

0.047 PO

Atopobium

0.05 PO

NPI= No prep indoor; NPO=No prep outdoor; PI= Prep indoor; PO= Prep outdoor

Table S3: Corrected P values for Kruskal Wallis test on faecal samples

Faeces	P value	Higher in
<i>Prevotella</i>	0.001	Indoor
<i>Bacteroides</i>	0.002	Indoor
<i>Saprospiraceae</i> uncultured	0.002	Indoor
RF16 uncultured bacterium	0.005	Outdoor
<i>Incertae Sedis</i>	0.005	Outdoor
<i>Ruminococcaceae</i> uncultured	0.009	Outdoor
<i>Lachnospiraceae</i> uncultured	0.012	Indoor
<i>Phascolarctobacterium</i>	0.012	Indoor
<i>Sutterella</i>	0.012	Indoor
<i>Ruminobacter</i>	0.012	Indoor
<i>Spirochaetaceae</i> uncultured	0.012	Indoor
uncultured <i>Parabacteroides</i> sp.	0.021	Indoor
<i>Ruminococcus</i>	0.021	Indoor
<i>Treponema</i>	0.021	Indoor
RF9 uncultured bacterium	0.021	Indoor
<i>Peptostreptococcaceae</i> uncultured	0.021	Outdoor
<i>Fibrobacter</i>	0.027	Indoor
<i>Incertae Sedis</i>	0.027	Indoor
<i>Phocaeicola</i>	0.027	Outdoor
<i>Alloprevotella</i>	0.027	Outdoor
<i>Paludibacter</i>	0.036	Outdoor
<i>Prevotellaceae</i> uncultured	0.036	Outdoor
<i>Blautia</i>	0.046	Indoor

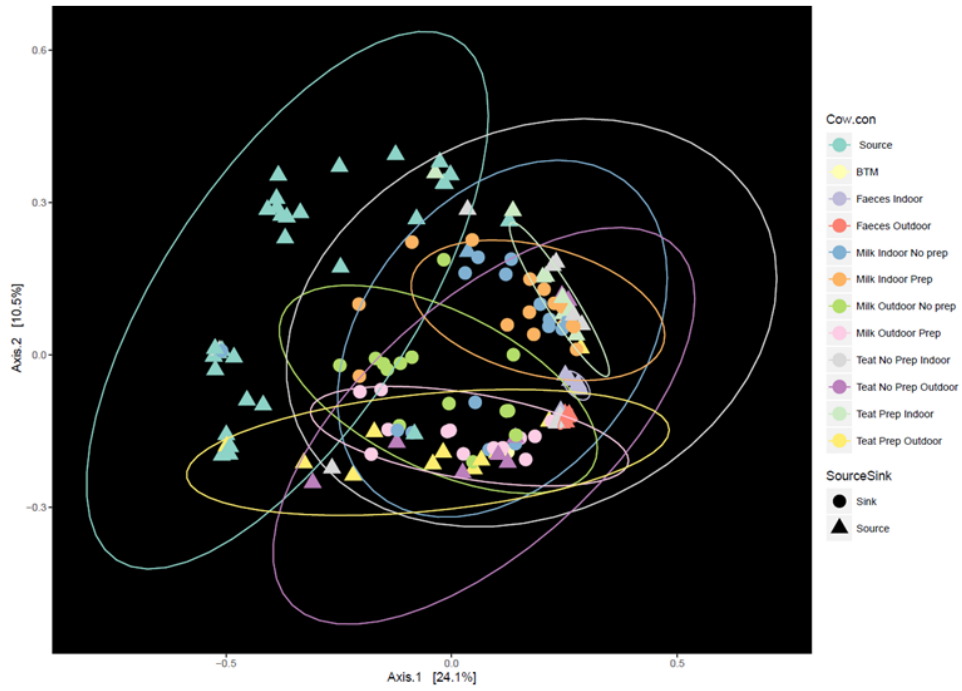
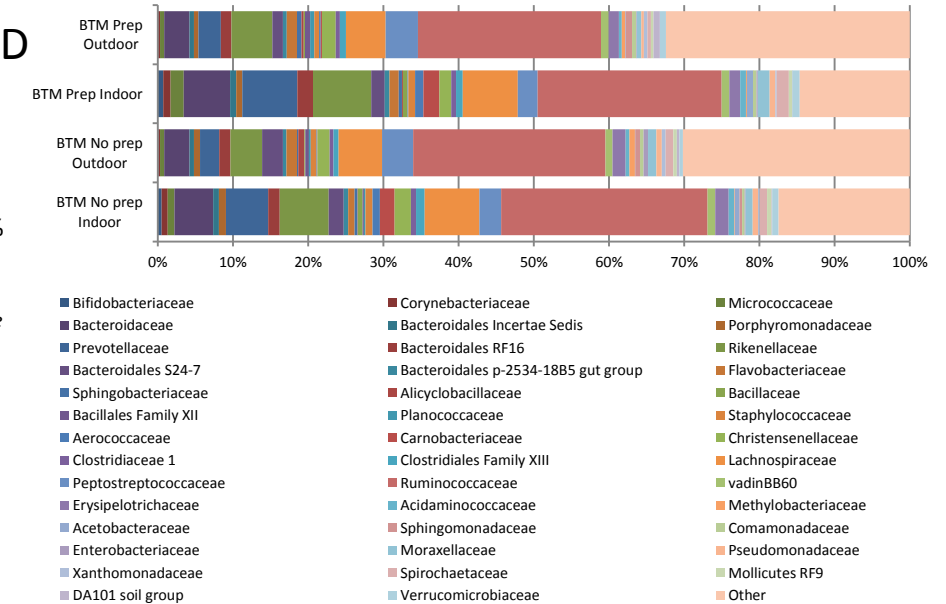
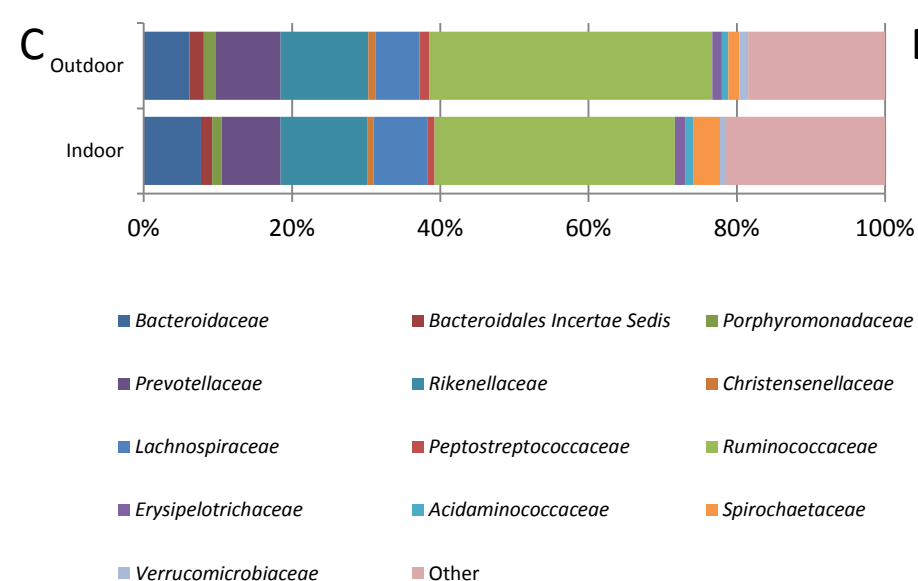
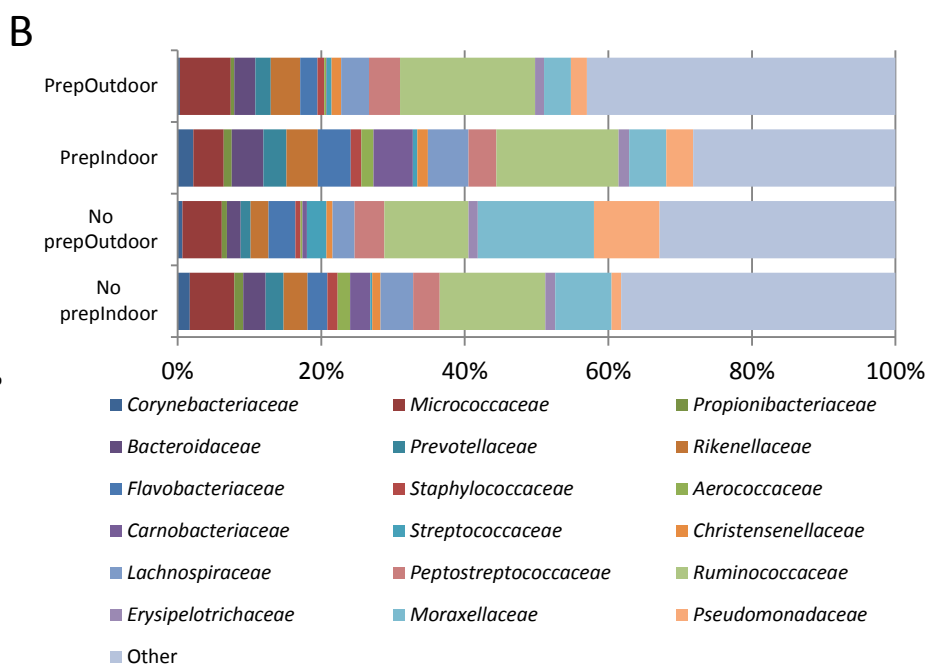
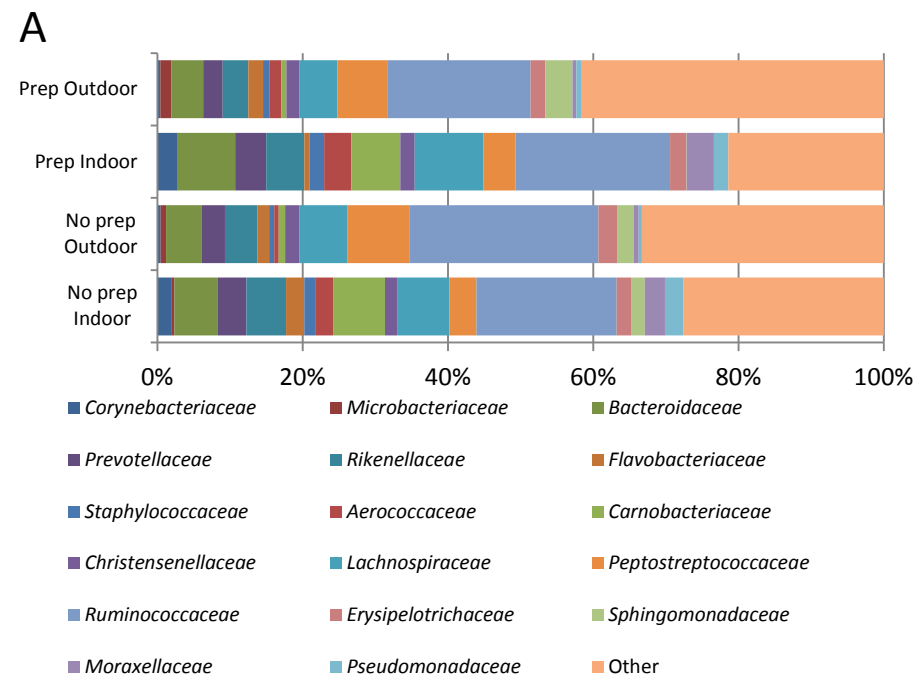
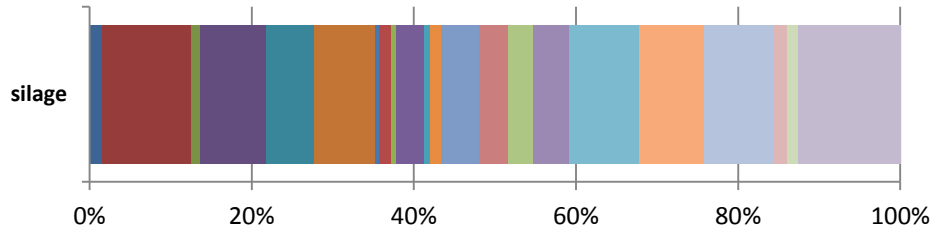


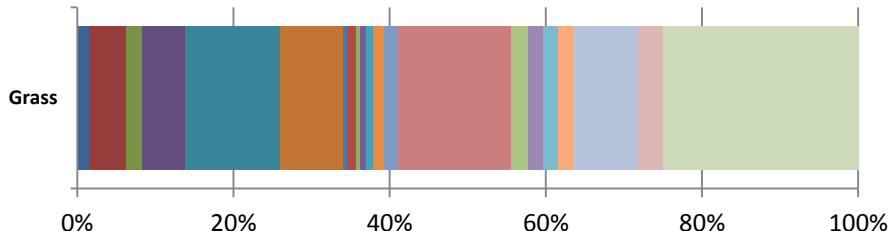
Fig S1: Bray-Curtis PCoA of all samples coloured by farming practice and shaped based on source or sink. The cyan colour indicates environmental samples (soil, bedding, grass and silage).



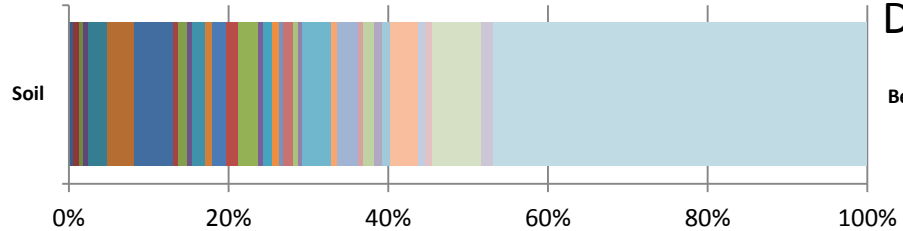
Supplementary Figure 2: Family present in (A) teat surface samples, (B) individual milk samples, (C) faecal samples and (D) BTM samples

A

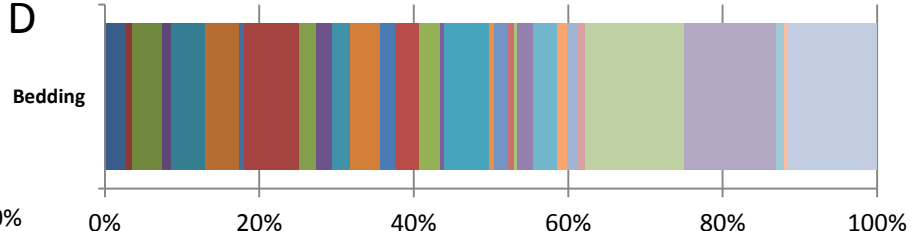
- *Porphyromonadaceae*
- *Prevotellaceae*
- *Cryomorphaceae*
- *Flavobacteriaceae*
- *Sphingobacteriaceae*
- *Bacillaceae*
- *Paenibacillaceae*
- *Planococcaceae*
- *Enterococcaceae*
- *Lactobacillaceae*
- *Ruminococcaceae*
- *Erysipelotrichaceae*
- *Acetobacteraceae*
- *Alcaligenaceae*
- *Comamonadaceae*
- *Campylobacteraceae*
- *Enterobacteriaceae*
- *Moraxellaceae*
- *Pseudomonadaceae*
- *Xanthomonadaceae*
- *Acholeplasmataceae*
- *Other*

B

- *Nocardiaceae*
- *Microbacteriaceae*
- *Micrococcaceae*
- *Cytophagaceae*
- *Flavobacteriaceae*
- *Sphingobacteriaceae*
- *Planococcaceae*
- *Ruminococcaceae*
- *Caulobacteraceae*
- *Aurantimonadaceae*
- *Methylobacteriaceae*
- *Rhizobiaceae*
- *Rickettsiales mitochondria*
- *Sphingomonadaceae*
- *Comamonadaceae*
- *Oxalobacteraceae*
- *Enterobacteriaceae*
- *Moraxellaceae*
- *Pseudomonadaceae*
- *Xanthomonadaceae*
- *Other*

C

- *Acidimicrobiaceae*
- *Microbacteriaceae*
- *Micrococcaceae*
- *Nocardiodiaceae*
- *Cytophagaceae*
- *Flavobacteriaceae*
- *Chitinophagaceae*
- *Saprospiraceae*
- *Sphingobacteriaceae*
- *Family XII*
- *Planococcaceae*
- *Sphingobacteriales env.OPS 17*
- *Ruminococcaceae*
- *Gemmatimonadaceae*
- *Planctomycetaceae*
- *Caulobacteraceae*
- *Bradyrhizobiaceae*
- *Hyphomicrobiaceae*
- *Rhizobiales Incertae Sedis*
- *Xanthobacteraceae*
- *Rhodospirillales Incertae Sedis*
- *Erythrobacteraceae*
- *Sphingomonadaceae*
- *Alcaligenaceae*
- *Comamonadaceae*
- *Oxalobacteraceae*
- *Nitrosomonadaceae*
- *Haliangiaceae*
- *Pseudomonadaceae*
- *Xanthomonadaceae*
- *Opitutaceae*
- *Chthoniobacteraceae*
- *DA101 soil group*
- *Verrucomicrobiaceae*
- *Other*

D

- *Corynebacteriaceae*
- *Micrococcaceae*
- *Bacteroidaceae*
- *Porphyromonadaceae*
- *Prevotellaceae*
- *Rikenellaceae*
- *Cryomorphaceae*
- *Flavobacteriaceae*
- *Sphingobacteriaceae*
- *Bacillaceae*
- *Planococcaceae*
- *Staphylococcaceae*
- *Aerococcaceae*
- *Carnobacteriaceae*
- *Lachnospiraceae*
- *Peptostreptococcaceae*
- *Ruminococcaceae*
- *vadinBB60*
- *Erysipelotrichaceae*
- *Acidaminococcaceae*
- *Comamonadaceae*
- *Idiomarinaceae*
- *Pseudoalteromonadaceae*
- *Chromatiaceae*
- *Enterobacteriaceae*
- *Halomonadaceae*
- *Moraxellaceae*
- *Pseudomonadaceae*
- *Spirochaetaceae*
- *Acholeplasmataceae*
- *Other*

Supplementary Figure 3: Family present in environmental samples, (A) Silage, (B) Grass, (C) Soil and (D) Bedding samples