

## **Supporting information**

### **The Rumen Specific Bacteriome in Dry Dairy Cows and Its Possible Relationship with Phenotypes**

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Table content

**Table S1.** PCR conditions.....2

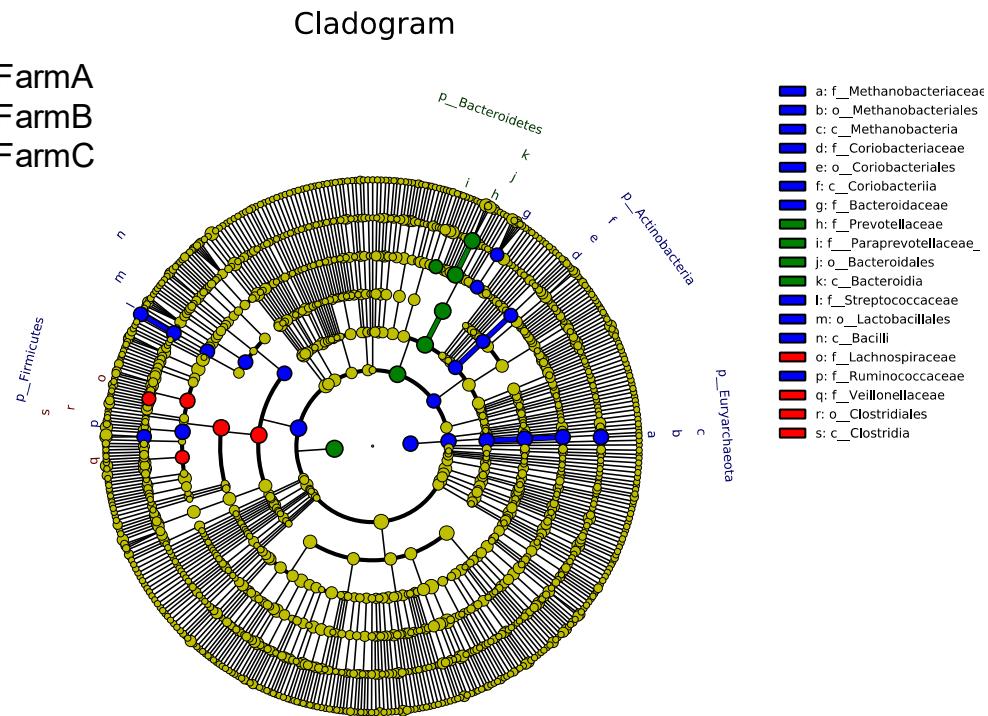
**Figure S1.** Linear discriminant analysis (LDA) effect size of the OTUs with significant differences in abundance in rumen samples from regional farms. (A) Taxonomic cladogram of 16S rRNA sequences. (B) LDA scores of biomarkers in the rumen samples from different regions. The OTUs with LDA scores (log 10) higher than 4 were considered biomarkers for each group. Relative abundance of (C) Bacteroidaceae, Coriobacteriaceae, Lachnospiraceae, Methanobacteriaceae, Paraprevotellaceae, Prevotellaceae, Ruminococcaceae, Streptococcaceae, and Veillonellaceae.....3

**Table S1.** PCR conditions

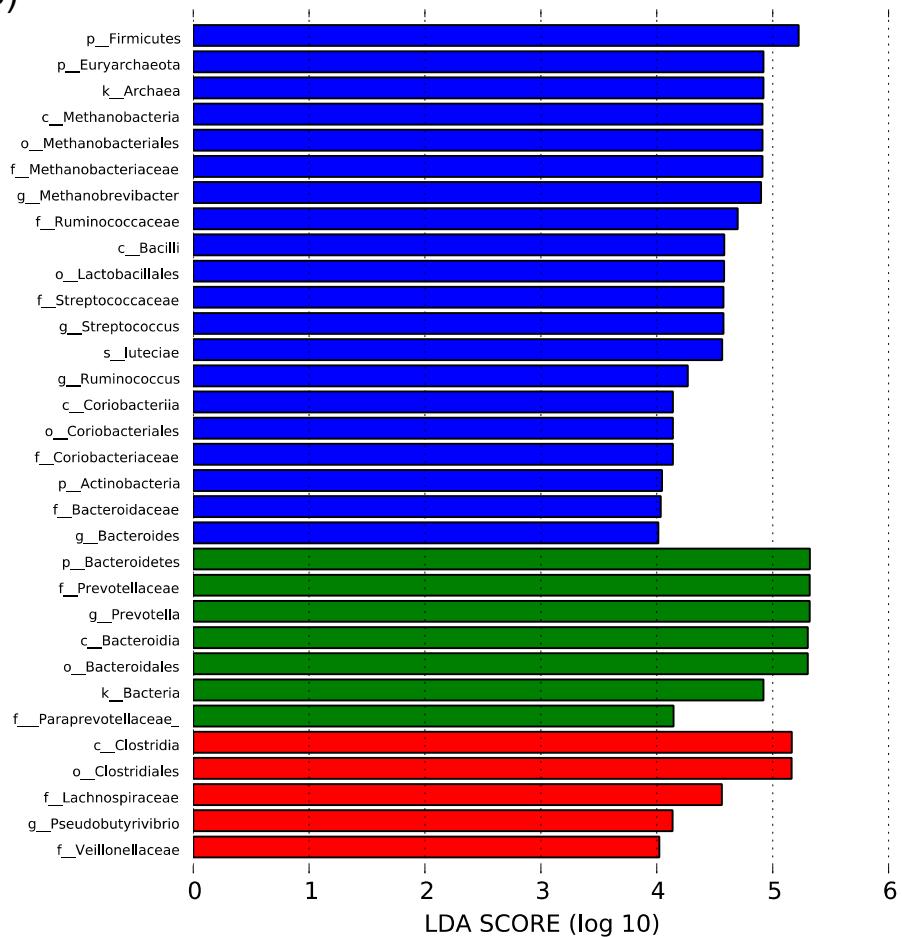
PCR condition	Temperature (°C)	Time
Thermocycler	95	2 min
Denaturing	95	15 sec
Annealing	50	20 sec
Extension	68	45 sec
Amplification 12 cycles (Annealing temperature decrease 0.5 °C every 1 cycle)		
Denaturing	95	15 sec
Annealing	44	20 sec
Extension	68	45 sec
Amplification 28 cycles		
Elongation	68	5 min

**Figure S1.**

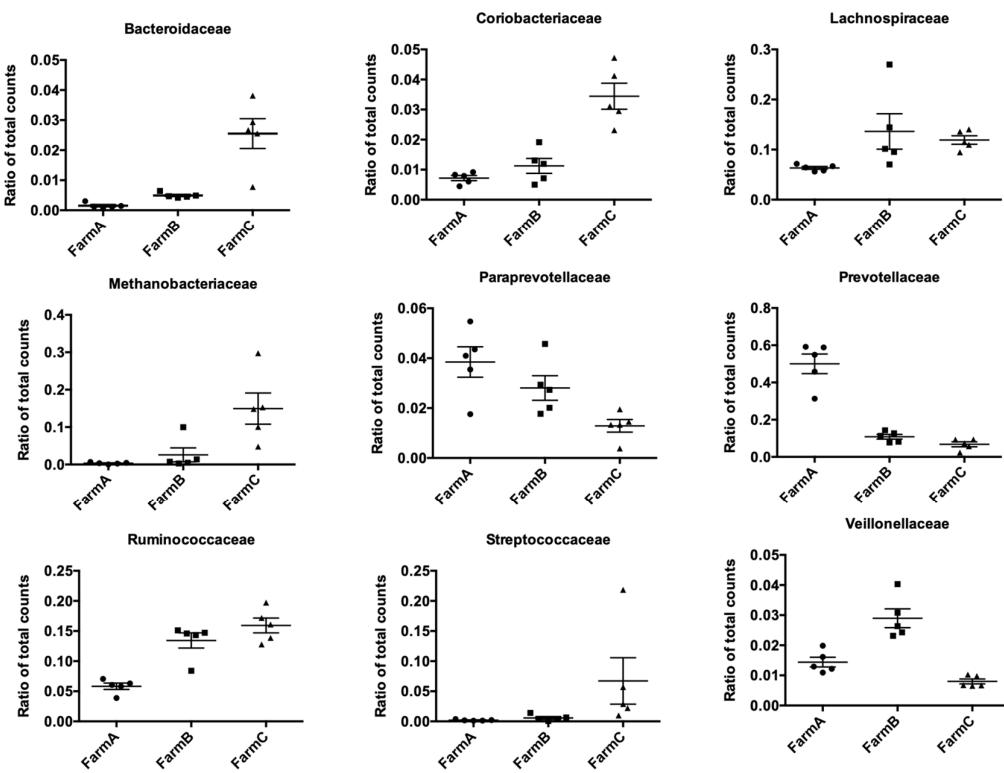
(A)



(B)



(C)



**Figure S1.** Linear discriminant analysis (LDA) effect size of the OTUs with significant differences in abundance in rumen samples from regional farms. (A) Taxonomic cladogram of 16S rRNA sequences. (B) LDA scores of biomarkers in the rumen samples from different regions. The OTUs with LDA scores ( $\log_{10}$ ) higher than 4 were considered biomarkers for each group. Relative abundance of (C) Bacteroidaceae, Coriobacteriaceae, Lachnospiraceae, Methanobacteriaceae, Paraprevotellaceae, Prevotellaceae, Ruminococcaceae, Streptococcaceae, and Veillonellaceae.