

Supplementary Figure Legends

Fig. S1: Hierarchical clustering using bray-curtis as a metric to compare similarity between different gut compartments. Colors indicate different diets and different goat compartments.

Fig. S2: Longitudinal profiles of alpha and beta diversity along with dynamics of two dominant phyla *Bacillota_all* and *Bacteroidota* impacted by diet and gut biogeography. **A.** Analysis of PCoA based on Bray–Curtis dissimilarities between the control (0% / DWOM) and moringa supplemented diet regime (17% / DWM) in each gastrointestinal tract (GIT) region **B.** Alpha diversity (microbial richness) in each gastrointestinal tract (GIT) region of goat fed with DWOM and DWM, respectively. **C.** Boxplots are used to summarize the distribution of *Bacillota_all* and *Bacteroidota* along with their (*Bacillota_all* to *Bacteroidota*) ratios in the goat samples, grouped according to their GIT compartments with respect to diet regimes (DWM and DWOM). Significance is calculated using Wilcoxon test. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$.

Fig. S3: Spatial variation of the relative abundance of bacterial taxa of interest differed between goat fed with control (0% / DWOM) and moringa supplemented (17% / DWM) diet regime in the forestomach (FS) **A.** differential abundance within FS compartment and **B.** differential abundance across all regions of FS compartment. Statistical significance of differences between groups (DWM vs DWOM) for relative abundance was assessed using Wilcoxon test ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$). Diet groups are differentiated by colour in all box plots. RUM_L, rumen liquid fraction; RUM_S, rumen solid fraction, RET, reticulum; OMA, omasum; ABO, abomasum.

Fig. S4: Spatial variation of the relative abundance of bacterial taxa of interest differed between goat fed with control (0% / DWOM) and moringa supplemented (17% / DWM) diet regime in the small intestine (SI). Statistical significance of differences between groups (DWM vs

DWOM) for relative abundance was assessed using Wilcoxon test ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$). Diet groups are differentiated by colour in all box plots. DUO, duodenum; JEJ, jejunum; ILE, ileum.

Fig. S5: Spatial variation of the relative abundance of bacterial taxa of interest differed between goat fed with control (0% / DWOM) and moringa supplemented (17% / DWM) diet regime across all regions of large intestine (LI). Statistical significance of differences between groups (DWM vs DWOM) for relative abundance was assessed using Wilcoxon test ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$). Diet groups are differentiated by colour in all box plots. CEC, cecum; REC, rectum.

Fig. S6: Spatial variation of the relative abundance of bacterial taxa of interest differed between goat fed with control (0% / DWOM) and moringa supplemented (17% / DWM) diet regime across all regions of large intestine (LI). Statistical significance of differences between groups (DWM vs DWOM) for relative abundance was assessed using Wilcoxon test ($*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$). Diet groups are differentiated by colour in all box plots. CEC, cecum; REC, rectum.

Fig. S1

Heatmap visualization showing the expression of 100 genes (rows) across 100 samples (columns). The color scale represents the expression level, ranging from 0.00 (blue) to 0.75 (red). The samples are clustered into two main groups, A and B, based on the dendrogram on the left. The genes are clustered into two main groups, A and B, based on the dendrogram on the top. The color bar on the right indicates the Gltrac2 expression level for each sample.

Legend for Gltrac2 expression levels:

- A_FS-DWM
- A_FS-DWOM
- B_SI-DWM
- B_SI-DWOM
- C_LI-DWM
- C_LI-DWOM

Legend for bray distance:

- 0.00
- 0.25
- 0.50
- 0.75

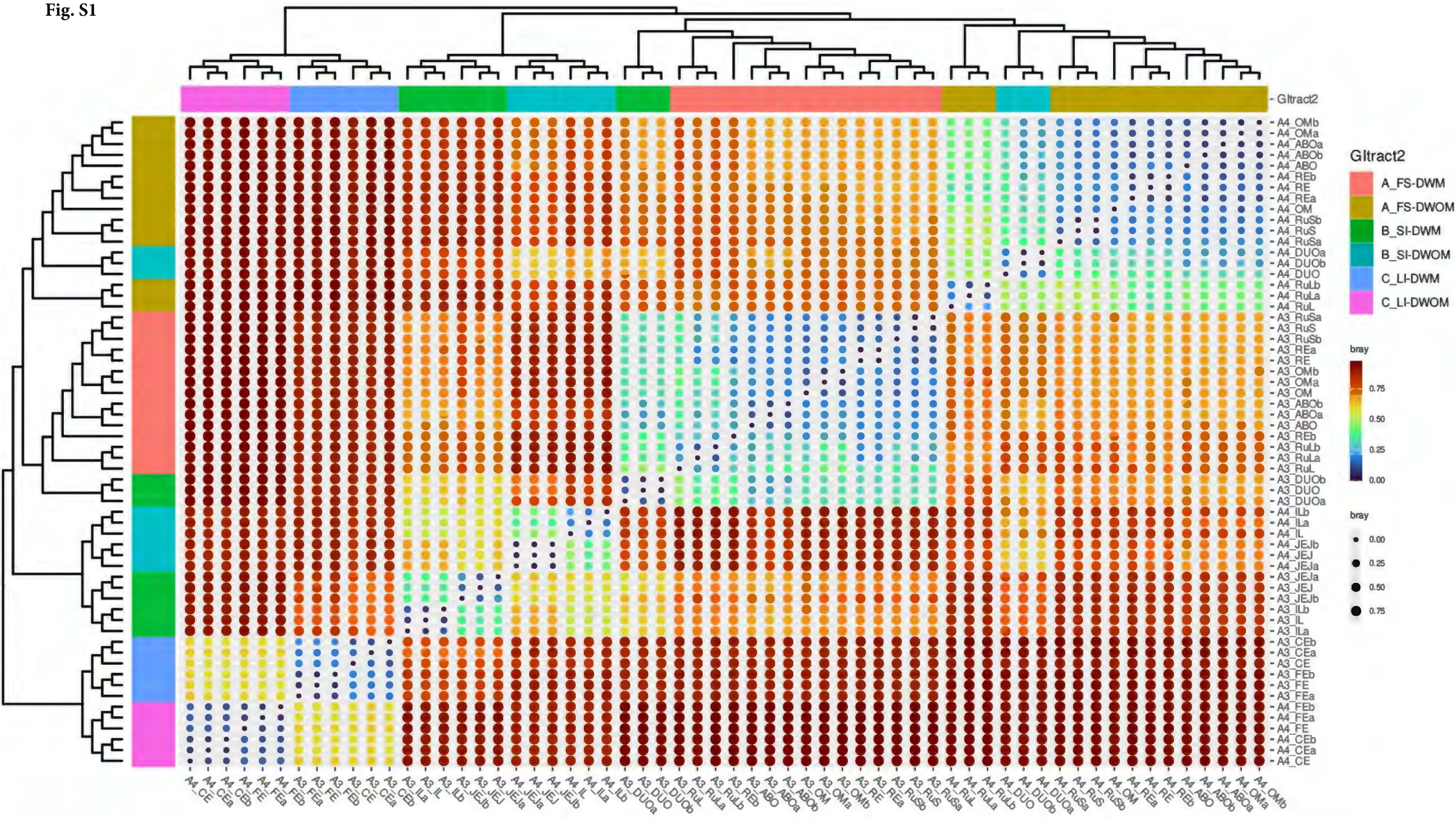


Fig. S2

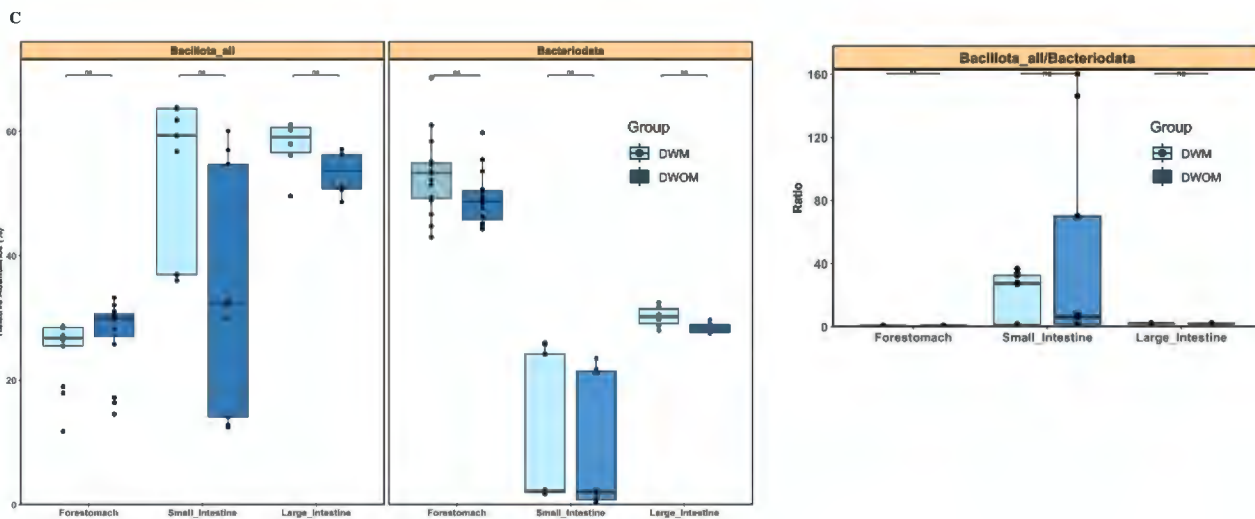
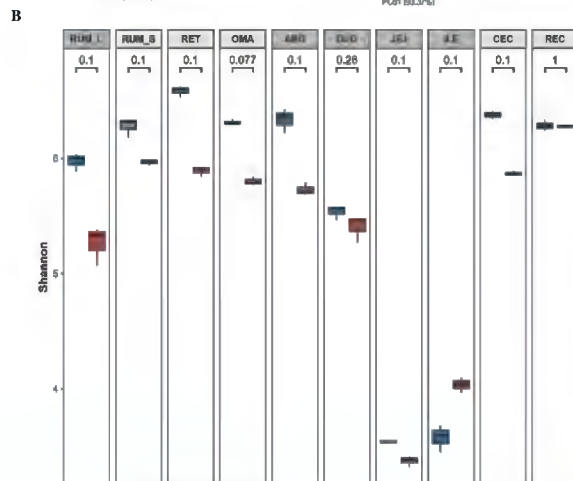
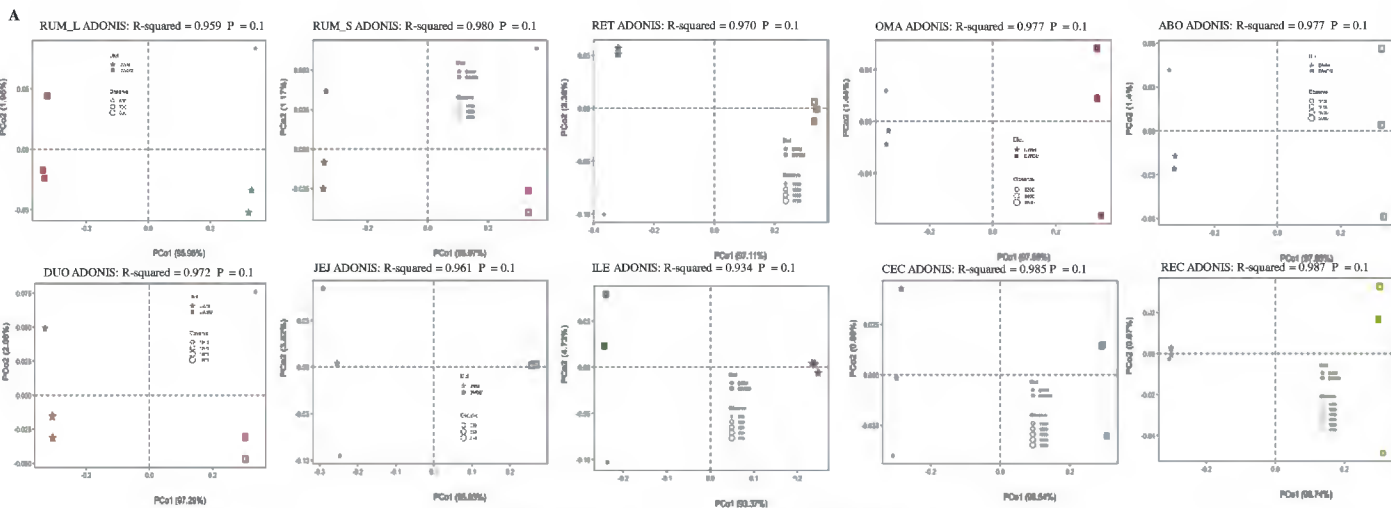
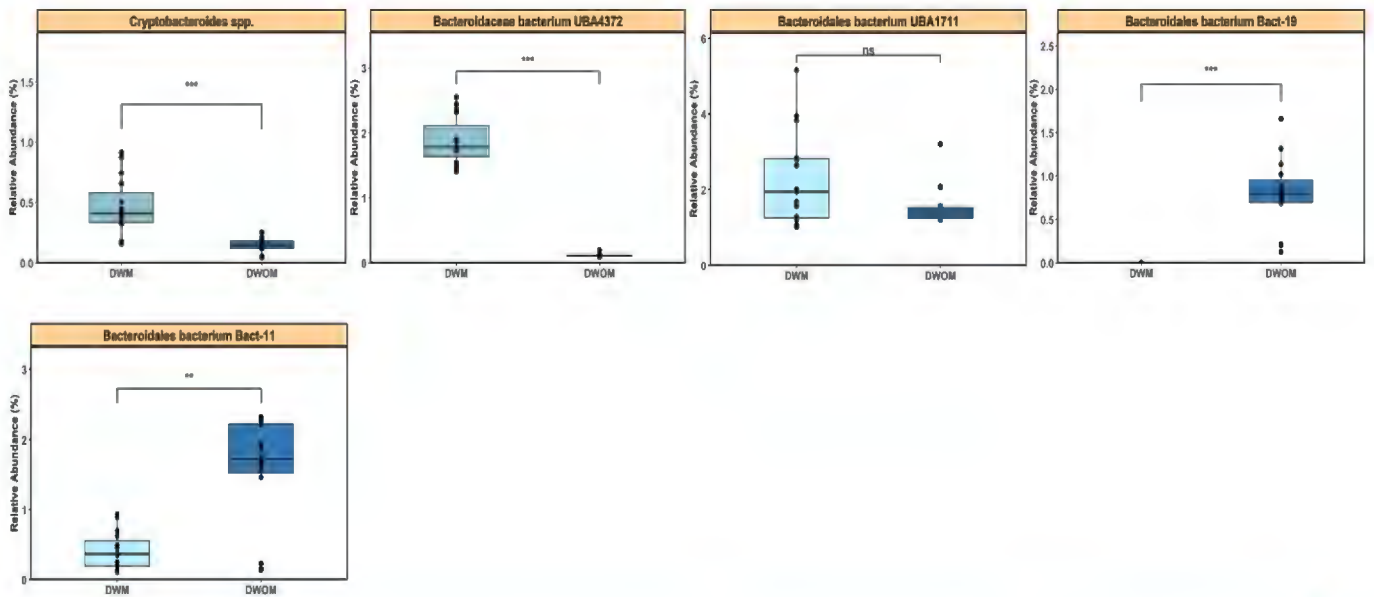


Fig. S3

A



B

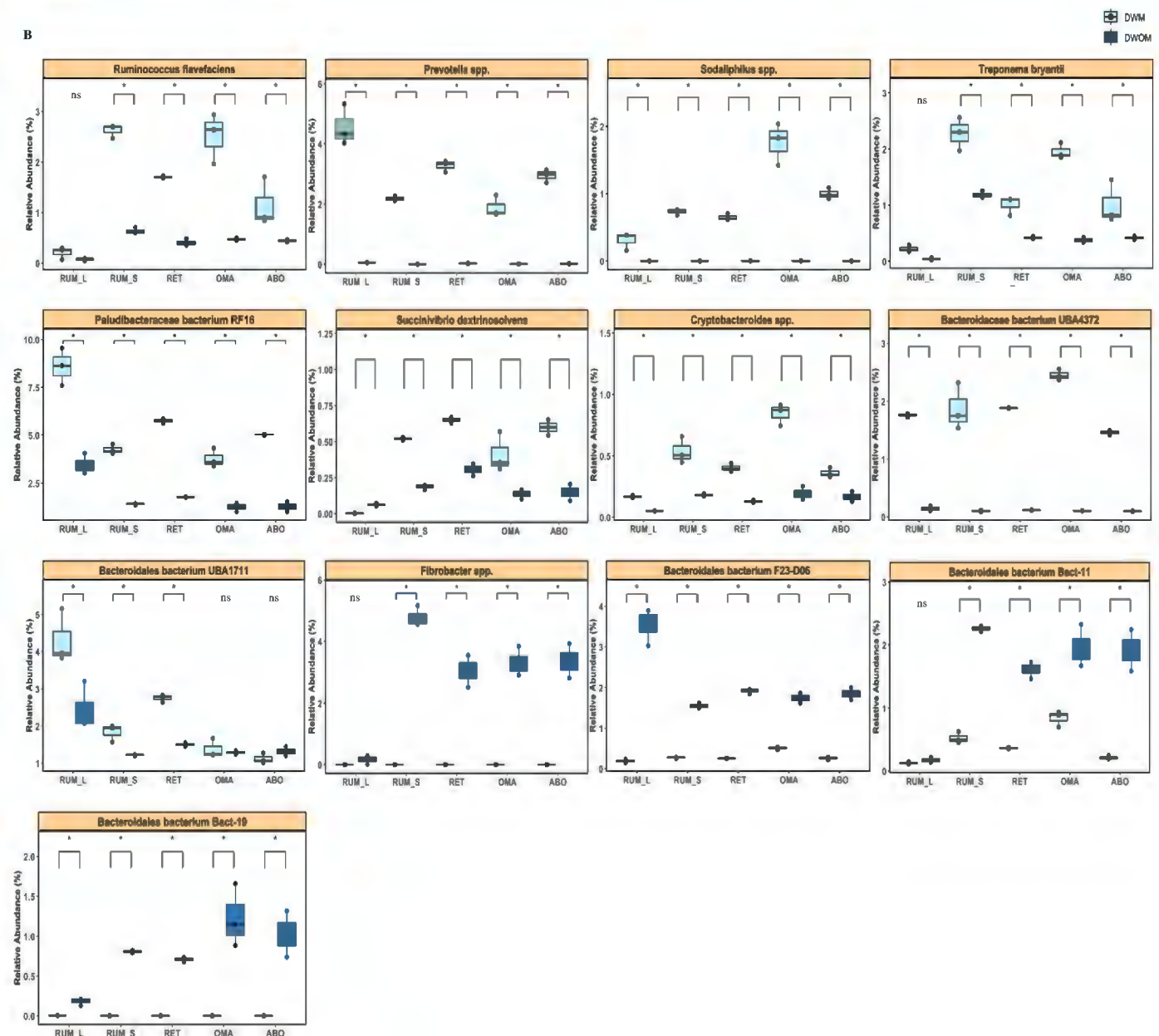


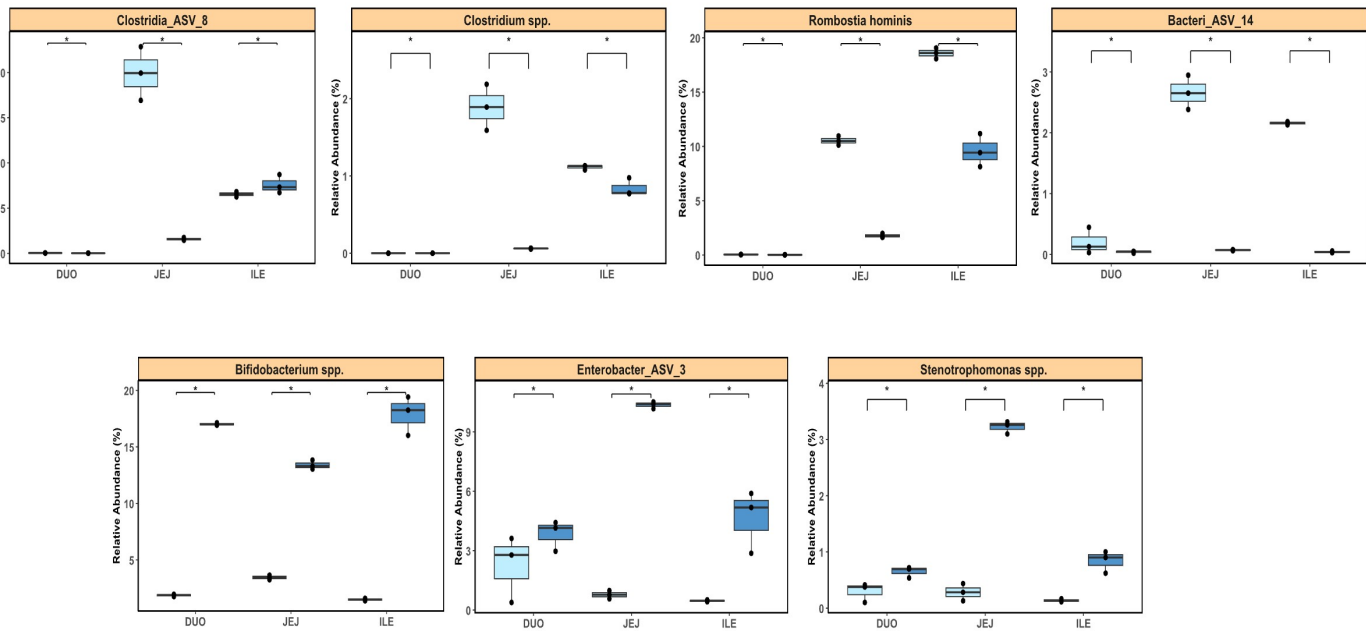
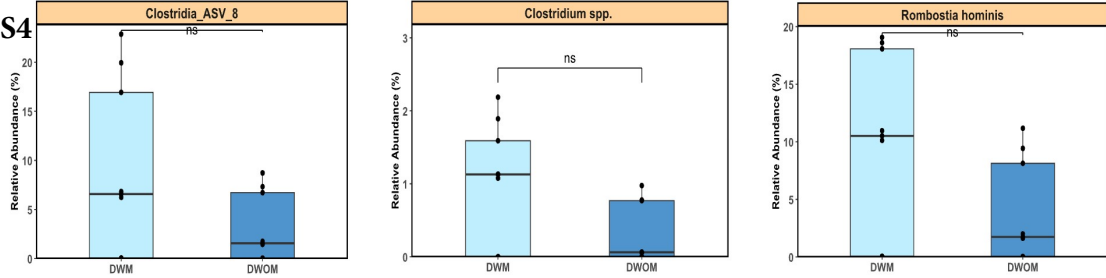
Fig. S4

Fig. S5

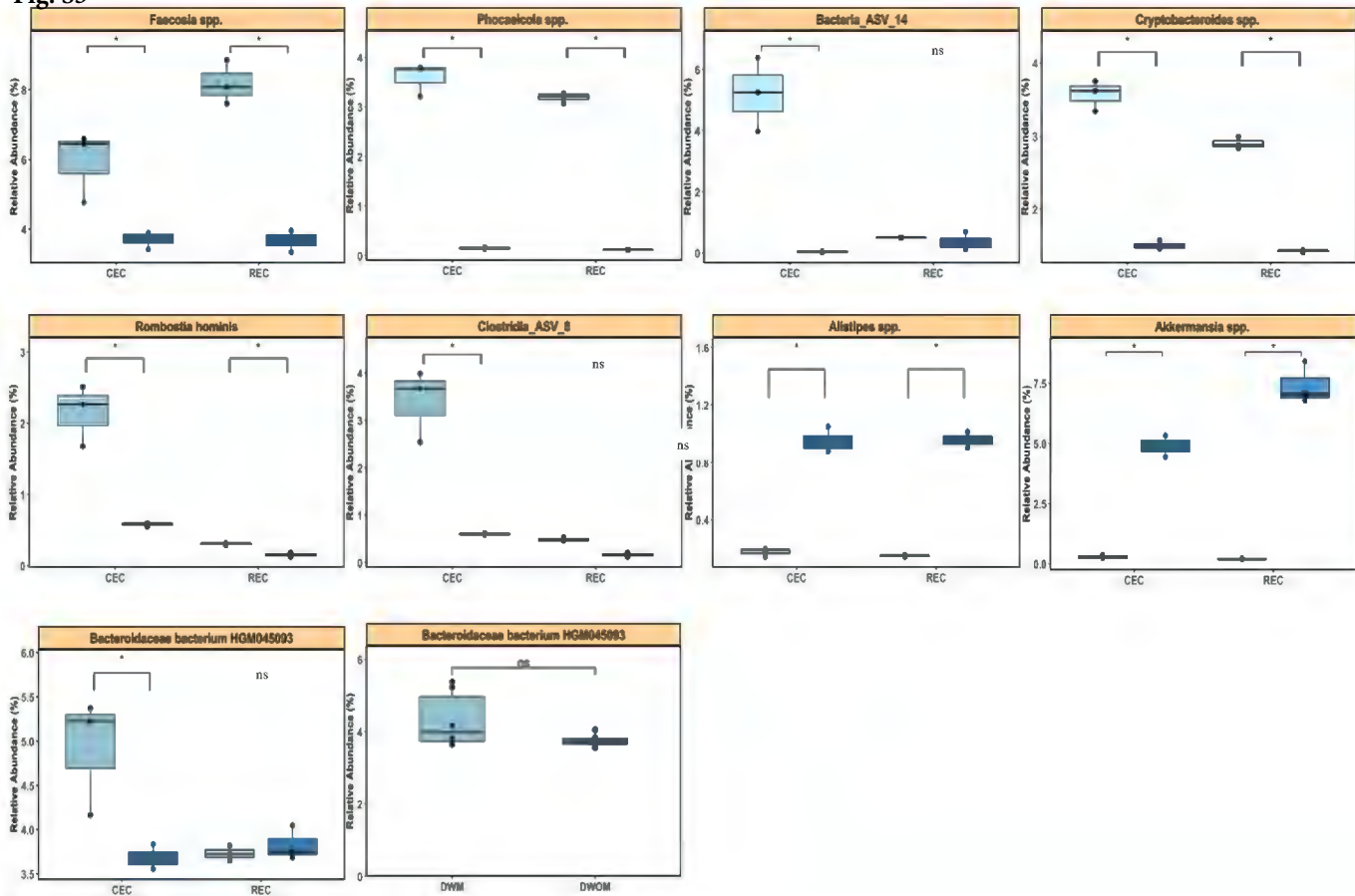
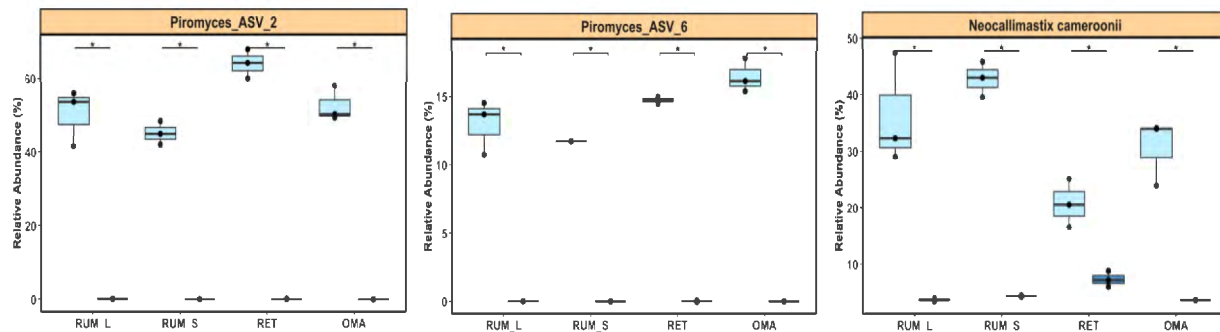
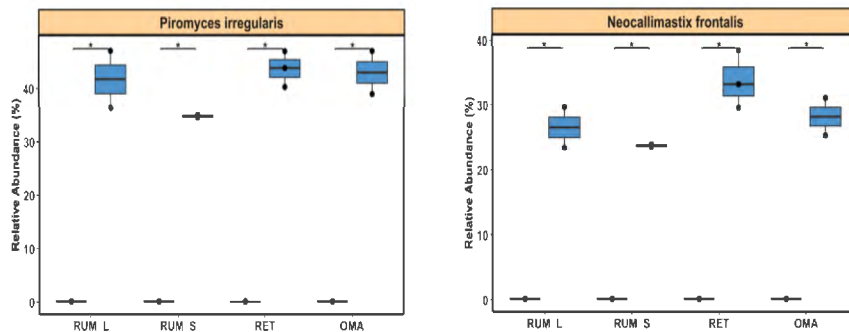


Fig. S6

A



B



Supplementary Table 1: Diet composition

Ingredients	Proportion (%)	Nutrient composition(%)	
		CP	TDN
Maize grains	15	11	90
Bajra grains	20	10	80
Wheat bran	15	10	75
Guar Korma	15	45	70
GNC	7	42	70
MLM	17	24	70
Molasses	5	0	90
Mineral mixture	4	0	0
Salt	2	0	0
Fodder mixture			
Masoor straw	50	5	50
Prosopis cineraria	25	18	55
Gual phalgati	25	12	55
TMR – Fodder mix (60 parts) + concentrate mix (40 parts)			

CP-Crude Protein; TDN-Total Digestible Nutrients; GNC-Groundnut Cake; MLM- Moringa Leaf Meal; TMR-Total Mixed Ration.

Control diet consisted only fodder mixture (CP-10% and 52.5%TDN) whereas moringa supplemented diet consisted Total mixed ration (TMR- with CP-13.57 % CP and 60.57%TDN) having roughage mixture (60 parts) and Concentrate mixture(40 parts) as mentioned in above mentioned Table.

Supplementary Table 2: Animal Details

Animal ID	Sex	Diet Group	Birth Date	Body weight [kg] at 16.01.2022	Body weight [kg] at 02.08.2022	Body weight [kg] at 28.11.2022 (slaughter day)
M952	M	Control	22.9.21	15.2	17.5	21
M953	F	Control	28.9.21	9.4	10.8	14.6
M955	F	Control	30.9.21	12.5	13.7	17.3
P555	M	Control	18.9.21	14.8	16	19.8
P556	F	Control	20.9.21	12.5	15	18.4
P559	M	Control	21.9.21	12.5	16.2	19.5
M947	M	Moringa supplemented	15.9.21	18.6	26.7	31
M949	F	Moringa supplemented	19.9.21	12	22.2	27.8
M956	F	Moringa supplemented	3.10.21	13.3	22.9	28.5
P552	F	Moringa supplemented	14.9.21	17.2	24.2	29.3
P560	M	Moringa supplemented	28.9.21	13.8	Died	-
P567	M	Moringa supplemented	4.10.21	16.8	22	28

Supplementary Table 3: PERMDISP and PERMANOVA results for bacterial communities based on Bray–Curtis distances.

PERMDISP						
	Df	SS	MS	F-value	N.per	P-value
Diet						
Groups	1	0.01307	0.01307	0.5402	999	0.471*
Residuals	58	1.37866	0.02377			
Gut part						
Groups	19	1.0363	0.05454	1.516	999	0.134*
Residuals	39	1.4031	0.03597			
PERMANOVA						
	Df	SS	MS	PseudoF	R ²	P-value
Main Effects						
Diet	1	2.9970	2.9970	20.1615	0.13981	0.001*
Gut part	9	9.0727	1.0081	6.7814	0.42324	0.001*
Interaction terms						
Diet x gut part	9	3.5693	0.3966	2.6679	0.16651	0.001*
Residuals	41	5.7974	0.1487		0.27045	
Total	59	21.4364	0.3696		1.00000	

*Statistical significance ($P < 0.05$). Permutations $n = 999$.

Abbreviations: Df, degrees of freedom; SS, sum of squares; MS, mean sum of squares.

$n = 27$ samples per experimental group (originating from 3 replicates per diet with 9 gut regions and rumen was divided into two fractions; liquid and solid, so finally 60 samples). For more information, see Material and Method section.

Supplementary Table 6: PERMDISP and PERMANOVA results for protozoa especially ciliate communities in different compartments of forestomach (FS) based on Bray–Curtis distances.

PERMDISP						
	Df	SS	MS	F-value	N.per	P-value
Diet						
Groups	1	0.036028	0.036028	3.5674	999	0.078*
Residuals	28	0.282778	0.009751			
Gut part						
Groups	4	0.045285	0.011321	1.9384	999	0.1352*
Residuals	25	0.146016	0.005840			

PERMANOVA						
	Df	SS	MS	PseudoF	R ²	P-value
Main Effects						
Diet	1	0.32905	0.32905	35.496	0.22370	0.001*
Gut part	4	0.42504	0.10626	11.463	0.28895	0.001*
Interaction terms						
Diet x gut part	4	0.53147	0.13287	14.333	0.36131	0.001*
Residuals	20	0.18540	0.00927		0.12604	
Total	29	1.47096	0.05072		1.00000	

*Statistical significance ($P < 0.05$). Permutations $n = 999$.

Abbreviations: Df, degrees of freedom; SS, sum of squares; MS, mean sum of squares.

$n = 15$ samples per experimental group (originating from 3 replicates per diet with 4 forestomach regions and rumen was divided into two fractions; liquid and solid, so finally 30 samples). For more information, see Material and Method section.

Supplementary Table 7: PERMDISP and PERMANOVA results for anaerobic gut fungi (AGF) communities in different compartments of forestomach (FS) based on Bray–Curtis distances.

PERMDISP						
	Df	SS	MS	F-value	N.per	P-value
Diet						
Groups	1	0.064791	0.064791	14.15	999	0.001077*
Residuals	22	0.100738	0.004579			
Gut part						
Groups	7	0.062604	0.008944	0.6881	999	0.681*
Residuals	16	0.207944	0.012997			

PERMANOVA						
	Df	SS	MS	PseudoF	R ²	P-value
Main Effects						
Diet	1	4.9756	2.9970	173.2738	0.85073	0.098*
Gut part	3	0.1998	1.0081	2.3195	0.03416	0.105*
Interaction terms						
Diet x gut part	3	0.2138	0.3966	2.4813	0.03655	0.089*
Residuals	16	0.4594	0.1487		0.07856	
Total	23	5.8487	0.3696		1.00000	

*Statistical significance ($P < 0.05$). Permutations $n = 999$.

Abbreviations: Df, degrees of freedom; SS, sum of squares; MS, mean sum of squares.

$n = 12$ samples per experimental group (originating from 3 replicates per diet with 3 forestomach regions and rumen was divided into two fractions; liquid and solid, so finally 24 samples; We have not included abomasum in the anaerobic gut fungi (AGF) community analysis because no amplification was obtained when amplified using AGF specific primer pair). For more information, see Material and Method section.