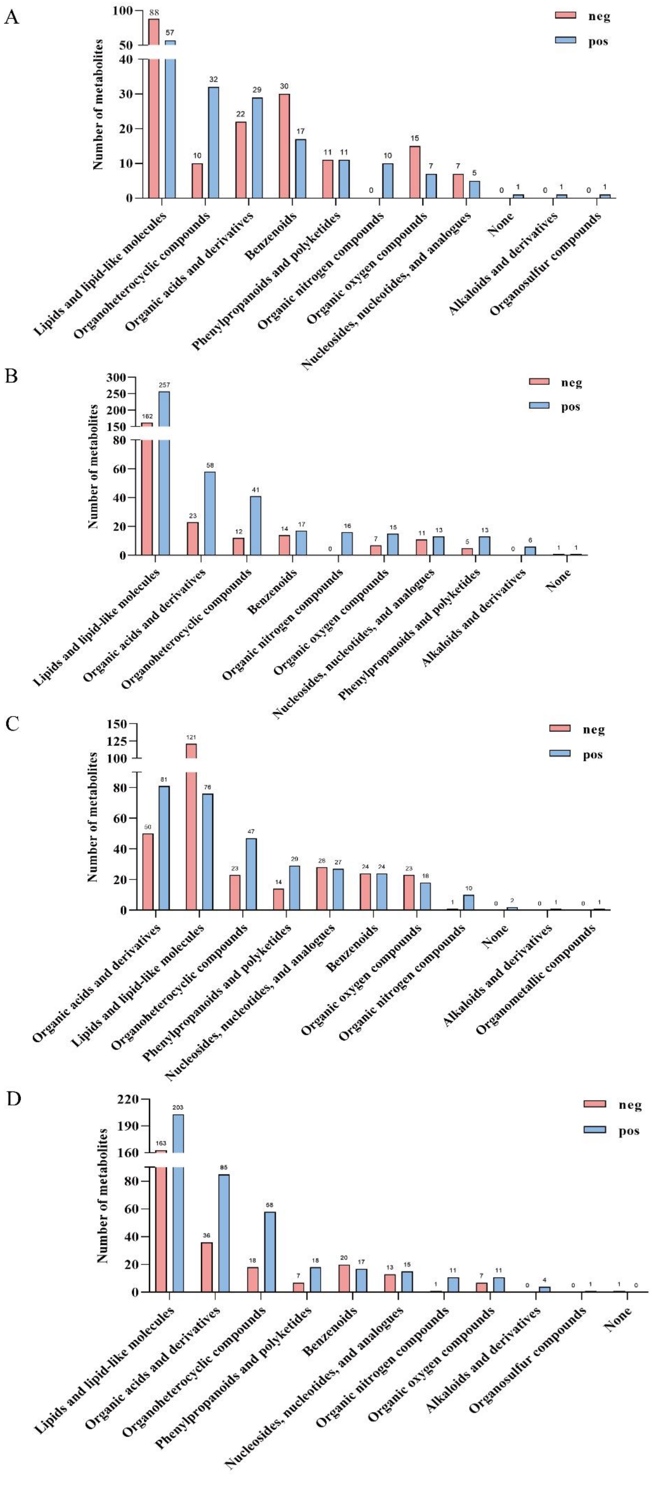
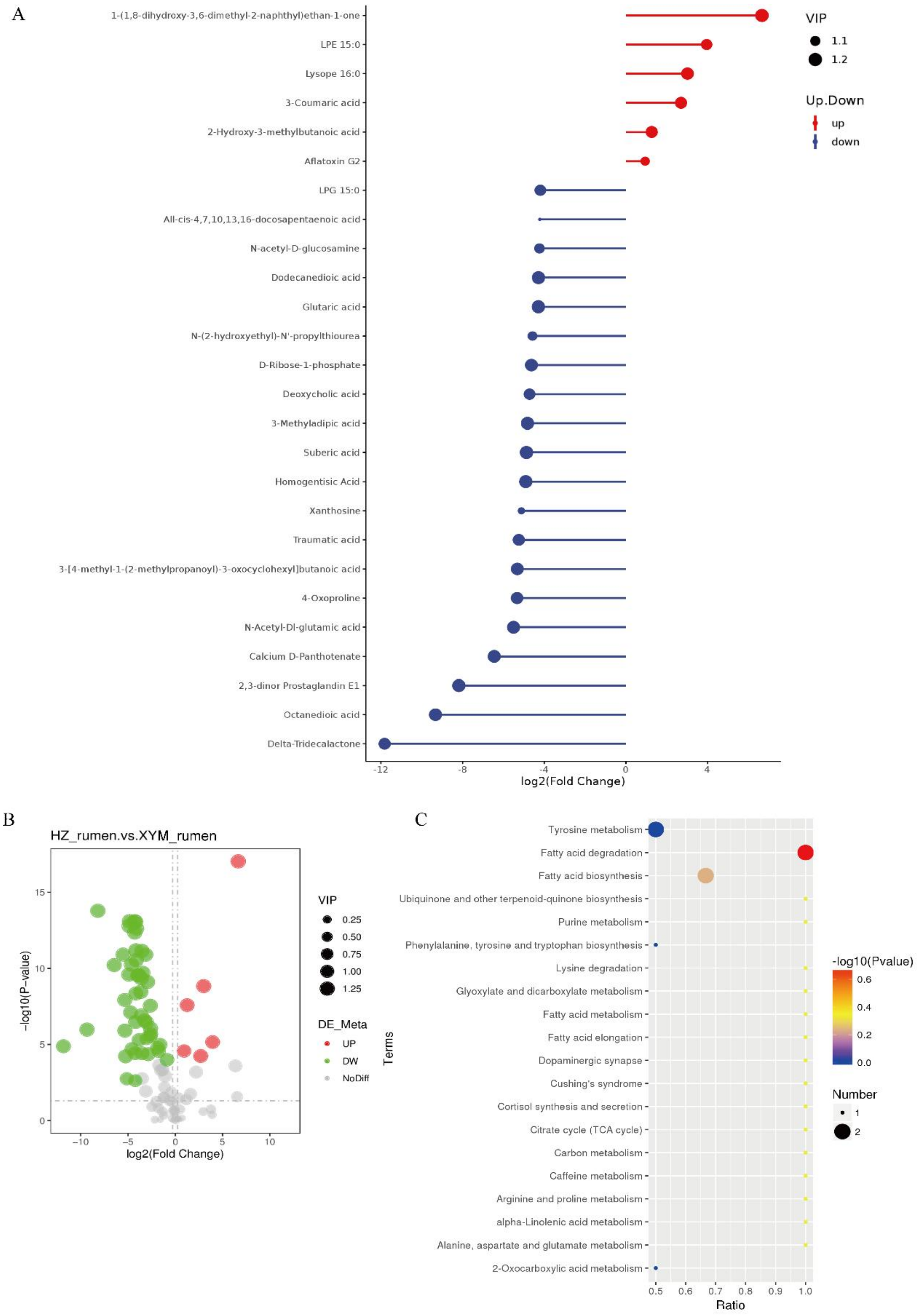
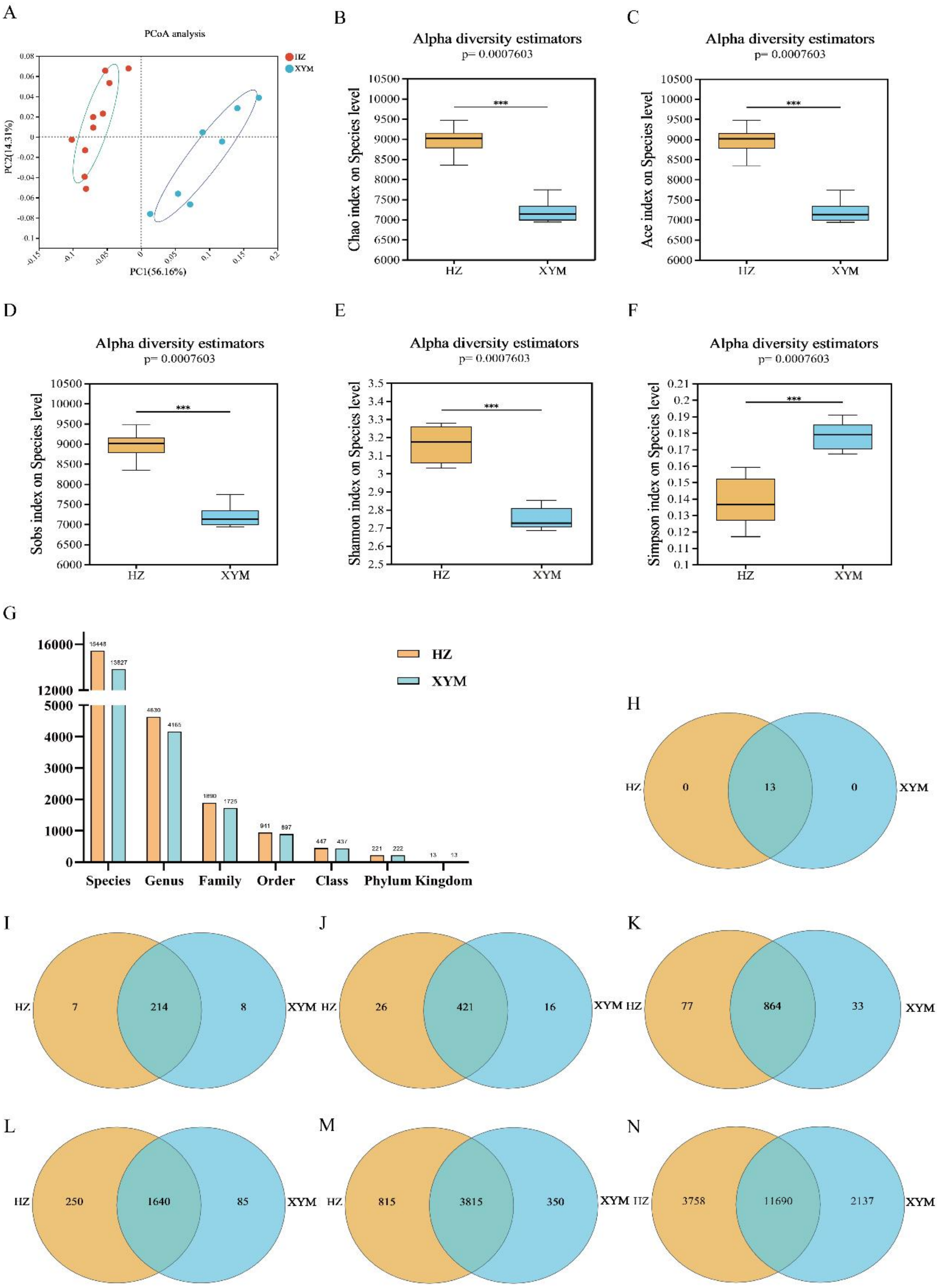


Supplementary figure S1: Classification of metabolites in the positive and negative ion modes from rumen fluid and plasma of Xuyi mountain (XYM, n = 7) and Haizi (HZ, n = 10) buffaloes. (A) Rumen fluid from HZ buffalo. (B) Plasma from HZ buffalo. (C) Rumen fluid from XYM buffalo. (D) Plasma from XYM buffalo.



Supplementary figure S2: Differential metabolite identifications of rumen liquids between Xuyi mountain (n = 7) and Haizi (n = 10) buffaloes in the negative ion mode. (A) VIP values and Fold change of metabolites. (B) Volcano plots of differential metabolites based on $\log_2$Fold change and $-\log_{10}$P-value. (C) KEGG pathway enrichment of differential metabolites. The size of the black points indicates the number of differential metabolites enriched.



Supplementary figure S3: Diversity and species compositions of rumen microflora of Xuyi mountain (n = 7) and Haizi (n = 10) buffaloes. (A) PCoA results. Boxplot of the α diversity for (B) Chao, (C) Ace, (D) Sobs, and (E) Shannon index. (G) Histogram of microbial numbers for different classifications. Venn diagram of abundances on (H) Kingdom, (I) phylum, (J) class, (K) order, (L) family, (M) genus, and (N) species levels.

Supplementary table S1: Statistical description of RNA-seq reads of Xuyi mountain (n = 7) and Haizi (n = 10) buffaloes

Sample	Another name	Raw Reads	Clean Reads	Raw Base(G)	Clean Base(G)	Effective (%)	Error (%)	Q20 (%)	Q30 (%)	GC (%)
HZ-1		41904524	40114976	6.29	6.02	95.73	0.03	96.42	90.74	52.88
HZ-2		47367708	45746316	7.11	6.86	96.58	0.03	96.49	90.85	51.69
HZ-3		46566610	44455962	6.98	6.67	95.47	0.03	96.45	90.81	51.77
HZ-4		47423706	44580162	7.11	6.69	94.00	0.03	96.64	91.32	53.45
HZ-5		46259796	44147264	6.94	6.62	95.43	0.03	96.38	90.72	52.94
HZ-6		40701336	38191676	6.11	5.73	93.83	0.03	96.89	91.70	51.37
HZ-7		44632368	41288488	6.69	6.19	92.51	0.03	96.56	90.94	50.37
HZ-8		44610204	42165042	6.69	6.32	94.52	0.03	96.57	91.17	52.72
HZ-9		49114878	46425358	7.37	6.96	94.52	0.03	96.67	91.30	52.82
HZ-10		45213004	43387356	6.78	6.51	95.96	0.03	96.87	91.77	51.14
XY_1	XY-886	50155642	47612758	7.52	7.14	94.93	0.03	96.38	90.86	49.08
XY_2	XY-888	50280842	47775896	7.54	7.17	95.02	0.03	96.38	90.96	51.41
XY_3	XY-884	47218492	45750336	7.08	6.86	96.89	0.03	96.52	91.27	52.60
XY_4	XY-609	52707398	50258002	7.91	7.54	95.35	0.03	96.68	91.55	52.12
XY_5	XY-604	49787924	48038424	7.47	7.21	96.49	0.03	96.42	91.04	52.46
XY_6	XY-801	46495522	45010038	6.97	6.75	96.81	0.03	96.42	91.00	51.78
XY_7	XY-887	46355058	44919194	6.95	6.74	96.90	0.03	96.36	90.90	51.42

Note:

Sample: indicates the name of the sample

Raw reads: The number of Raw reads to be sequenced

Clean reads: Number of Clean reads obtained after filtration

Raw bases: The total bases of the Raw data are calculated by multiplying the number of Raw reads by the sequencing length, expressed in G
Clean bases: The total number of bases of the filtered data, in G
Error: Average base sequencing error rate
Q20, Q30: The percentage of bases with Phred values greater than 20 and 30 in the total base
GC: The percentage of GC bases in the total number of bases

Supplementary table S2: Statistical description of reads information of rumen fluid metagenome of Xuyi mountain (n = 7) and Haizi (n = 10) buffaloes

Samples	**Another name**	**Raw Base(G)**	**Clean Base(G)**	**Raw reads**	**Clean reads**	**Optimized reads**	**Clean in raw reads (%)**	**Optimized in raw reads (%)**	**Contigs**	**Q20(%)**	**Q30(%)**	**GC(%)**
HZ_1		7.02	7.01	46809744	46480156	41173098	99.30	87.96	645527	97.29	92.35	46.1
HZ_2		6.75	6.74	45002806	44714296	39068138	99.36	86.81	649893	97.63	93.15	48.47
HZ_3		6.57	6.55	43797022	43460744	38557086	99.23	88.04	618628	97.17	92.11	46.98
HZ_4		7.12	7.1	47459546	47111098	41525212	99.27	87.50	705078	97.26	92.31	46.95
HZ_5		6.69	6.68	44598970	44294866	38866356	99.32	87.15	643852	97.34	92.44	45.65
HZ_6		6.96	6.94	46390734	46049330	39421822	99.26	84.98	632977	97.21	92.16	44.71
HZ_7		7.06	7.05	47099678	46783650	40929726	99.33	86.90	668680	97.13	91.92	45.35
HZ_8		6.41	6.4	42711730	42448490	36963100	99.38	86.54	565249	97.31	92.33	46.12
HZ_9		7.09	7.07	47297486	46968676	38345146	99.30	81.07	670927	97.41	92.66	45.76
HZ_10		7.48	7.42	49862064	49587282	36687788	99.45	73.58	648285	97.39	92.44	42.8
XY_1	XY-886	6.74	6.72	44925686	44553314	40732464	99.17	90.67	657754	96.83	91.66	50.41
XY_2	XY-888	6.78	6.76	45171486	44758120	42290002	99.08	93.62	643492	96.21	90.29	49.8
XY	XY	7.0	7.04	470	465	4340	99.01	92.33	6282	96.	91.	48.

_3	-884	5		09062	41326	5474			41	49	04	65
XY_4	XY-609	6.48	6.47	43232392	42817366	40404850	99.04	93.46	639502	96.31	90.58	49.17
XY_5	XY-604	5.91	5.89	39374082	38984186	36576216	99.01	92.89	529297	96.32	90.66	49.15
XY_6	XY-801	6.64	6.62	44240062	43850414	40203404	99.12	90.88	648909	96.63	91.26	49.91
XY_7	XY-887	6.16	6.15	41081584	40660774	36826216	98.98	89.64	579264	96.39	90.89	49.83

Note:

Sample: indicates the name of the sample

Raw bases: The total bases of the Raw data are calculated by multiplying the number of Raw reads by the sequencing length, expressed in G

Clean bases: The total number of bases of the filtered data, in G

Raw reads: The number of Raw reads to be sequenced

Clean reads: Number of Clean reads obtained after filtration

Optimized reads: Number of optimized sequences after removal from host

Contigs: The number of contigs in the sequence

Q20, Q30: The percentage of bases with Phred values greater than 20 and 30 in the total base

GC: The percentage of GC bases in the total number of bases