

Article

Rumen and Fecal Microbiota Characteristics of Qinchuan Cattle with Divergent Residual Feed Intake

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Supplementary Figures

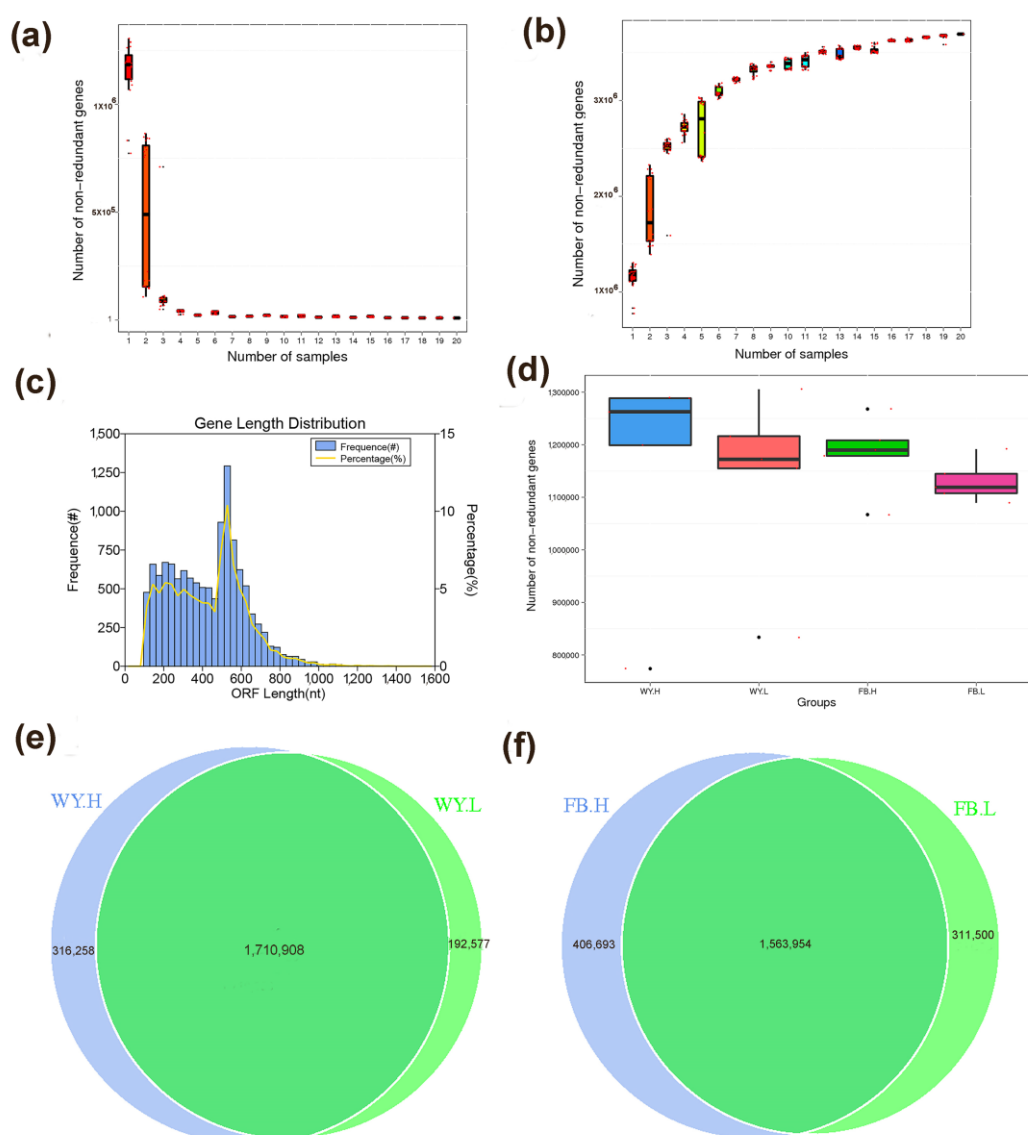


Figure S1. Gene abundance statistics. (a) Core genome sparsity curve; (b) Pan-genome sparsity curve; (c) Gene length distribution plot; (d) Box plot showing the difference in gene numbering

between two groups; (e) Number of shared and unique genes between two groups; (f) Number of shared and unique genes between two groups.

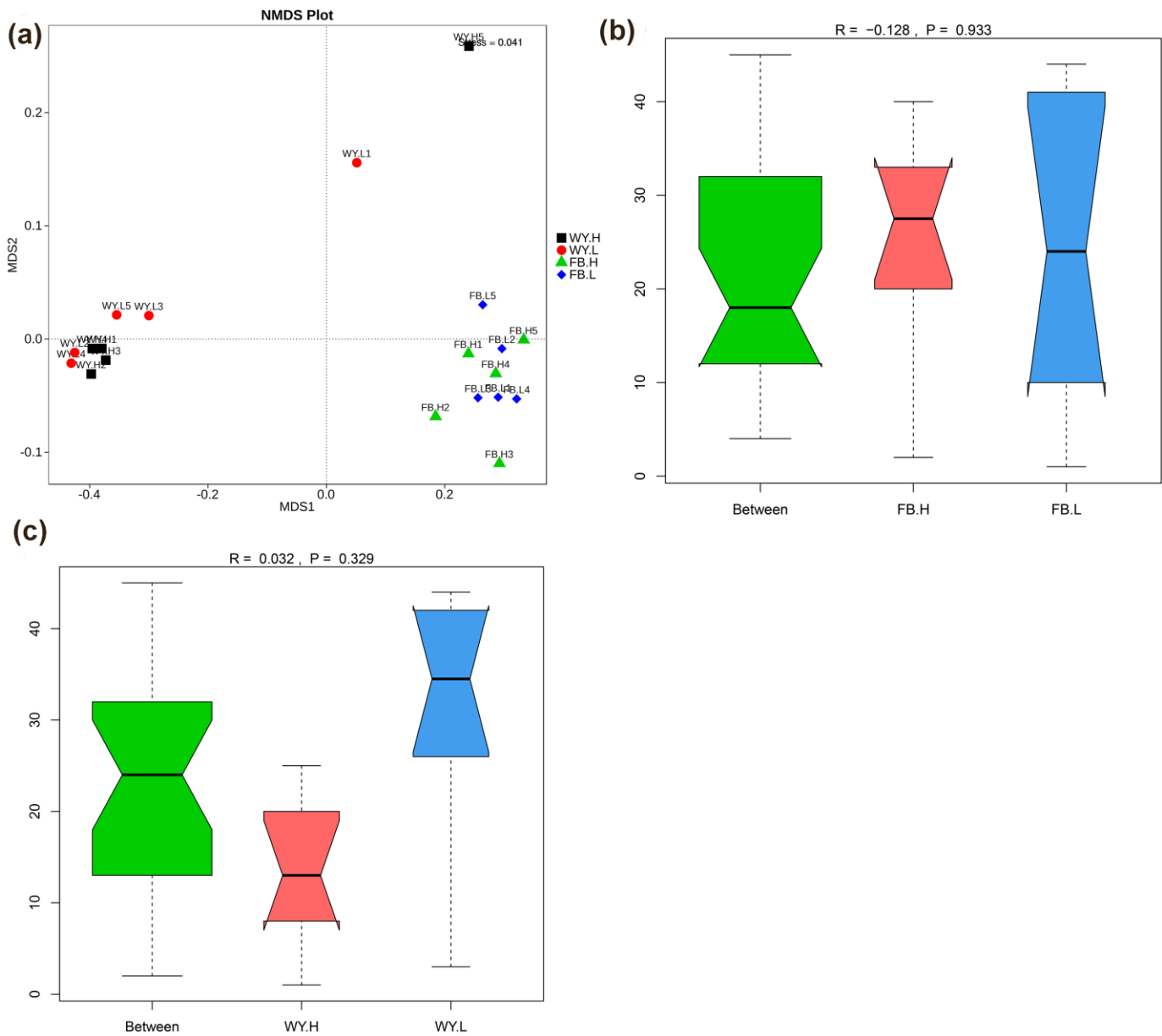


Figure S2. Non-metric multidimensional scaling (NMDS) results. (a) and ANOSIM analysis based on gate-level (b, c).

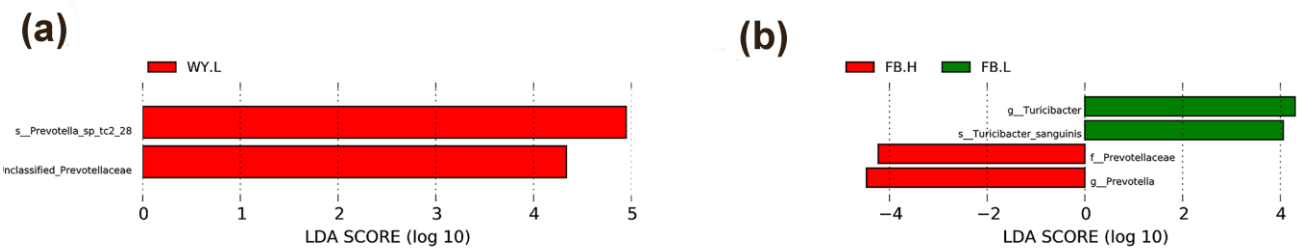


Figure S3. Distribution of linear discriminant analysis (LDA) values and evolutionary branching of divergent species. (a) WY.H VS WY.L; (b) FB.H VS FB.L.

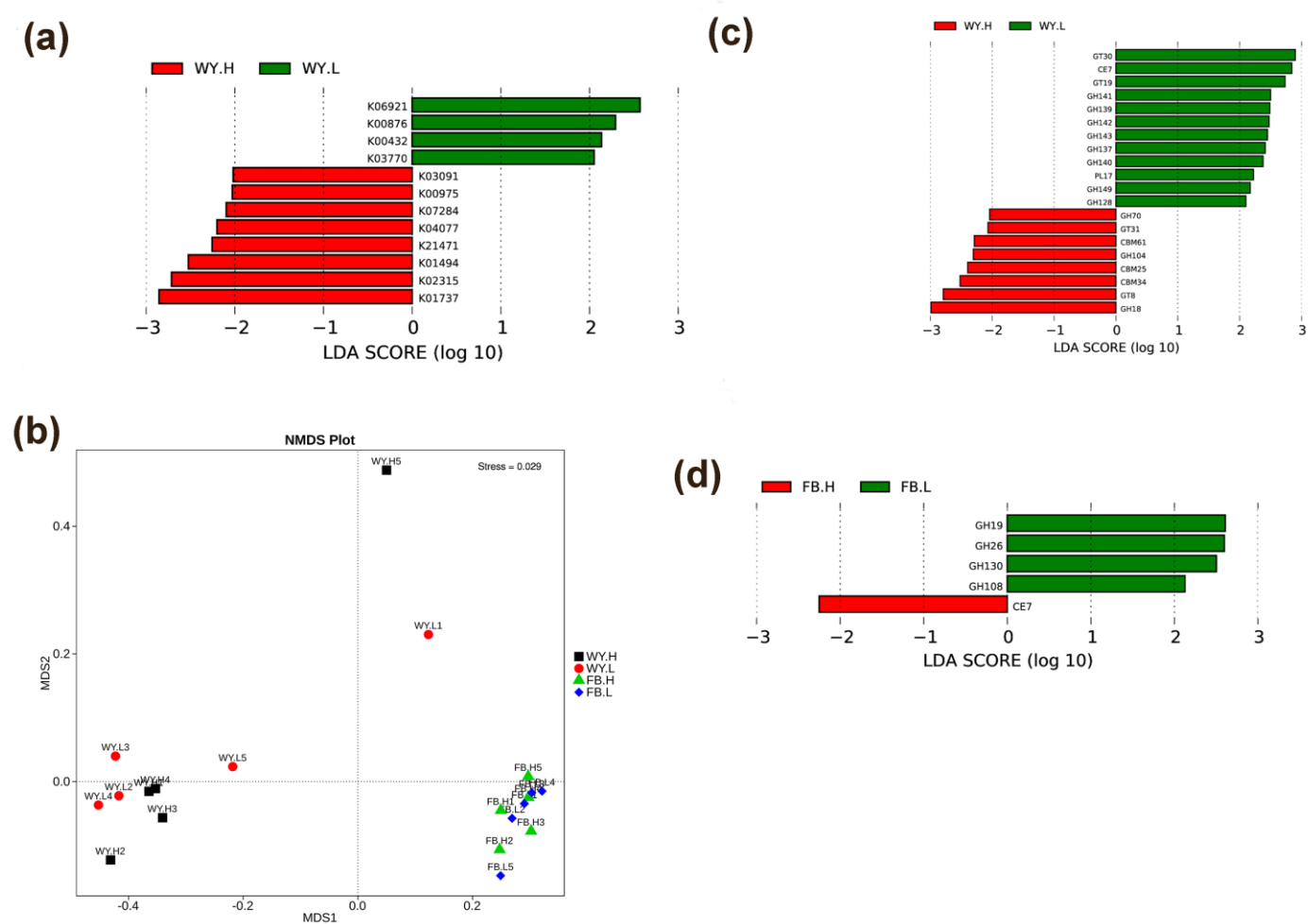


Figure S4. Functional analysis of rumen and fecal microbiota. (a) KEGG analysis of rumen microbiota; (b) NMDS analysis of feces microbiota; (c) KEGG analysis of rumen microbiota (d) KEGG analysis of feces microbiota; Distribution of linear discriminant analysis (LDA) values for different functions: (c) WY.H VS WY.L; (d) FB.H VS FB.L.

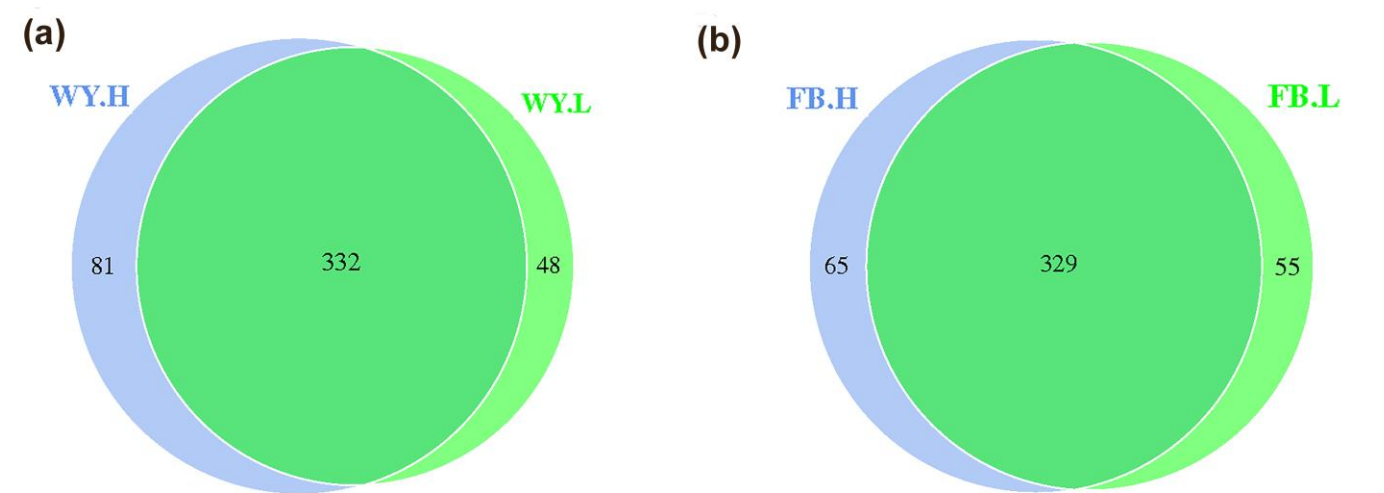


Figure S5. Venn diagram of resistance gene box among the two groups. (a) WY.H VS WY.L; (b) FB.H VS FB.L.

Supplementary Tables

Table S1. 43 differentially expressed genes in intestinal transcriptome at different RFIs.

Gene Name	log2 (Foldchange)	P-Value	FDR	Style
<i>LOC781720</i>	3.0956	0.0000	0.0000	up
<i>LOC100847574</i>	4.4684	0.0000	0.0000	up
<i>LOC781256</i>	-5.1688	0.0000	0.0000	down
<i>MRPL23</i>	-0.9338	0.0000	0.0000	down
<i>GCSAML</i>	2.3837	0.0000	0.0000	up
<i>ACOT2.1</i>	-3.4098	0.0000	0.0001	down
<i>RARRES1</i>	-1.2230	0.0000	0.0002	down
<i>MFI2</i>	-1.5617	0.0000	0.0003	down
<i>LOC509961</i>	-1.1876	0.0000	0.0008	down
<i>LOC539876</i>	-1.2169	0.0000	0.0014	down
<i>PRDX4</i>	-0.6009	0.0000	0.0014	down
<i>CPA3</i>	1.8477	0.0000	0.0017	up
<i>LOC407163</i>	-6.6653	0.0000	0.0017	down
<i>TH</i>	1.6242	0.0000	0.0021	up
<i>FETUB</i>	4.9362	0.0000	0.0024	up
<i>EAF2</i>	-0.9485	0.0000	0.0032	down
<i>HPD</i>	-2.1522	0.0000	0.0044	down
<i>LOC508441</i>	1.7676	0.0000	0.0046	up
<i>ISL1</i>	1.0655	0.0000	0.0046	up
<i>ARHGAP15</i>	-0.7072	0.0000	0.0052	down
<i>GRP</i>	1.6598	0.0000	0.0073	up
<i>SLC50A1</i>	-0.7412	0.0000	0.0085	down
<i>TFF2</i>	-0.7987	0.0000	0.0086	down
<i>CHI3L2</i>	-3.4622	0.0000	0.0098	up
<i>TDO2</i>	1.4534	0.0000	0.0098	down
<i>LOC514507</i>	4.7850	0.0000	0.0111	up
<i>VPREB2</i>	-1.9922	0.0000	0.0112	down
<i>LOC104973638</i>	-7.0704	0.0000	0.0112	down
<i>LOC100851913</i>	-2.6272	0.0000	0.0114	down
<i>LOC786867</i>	4.3015	0.0000	0.0143	up
<i>PEBP4</i>	-0.9701	0.0000	0.0170	down
<i>LOC100141266</i>	-1.3293	0.0000	0.0191	down
<i>AQP3</i>	-0.8545	0.0000	0.0206	down
<i>CDH26</i>	3.1660	0.0000	0.0211	up
<i>CHGB</i>	1.3096	0.0000	0.0261	up
<i>FAM3D</i>	-0.5922	0.0001	0.0266	down
<i>CCL5</i>	-0.8184	0.0001	0.0266	down
<i>CCK</i>	1.3095	0.0001	0.0297	up
<i>CCR4</i>	-1.6659	0.0001	0.0314	down
<i>IL17F</i>	-5.5405	0.0001	0.0351	down
<i>CFAP58</i>	-2.5937	0.0001	0.0351	down
<i>ASCL1</i>	2.1796	0.0001	0.0426	up
<i>CD52</i>	-0.8999	0.0001	0.0447	down

Table S2. Significance analysis of production performance of Qinchuan cattle with different RFI (Mean \pm SD).

	HRFI Group	LRFI Group	P-Value
Initial body weight(kg)	273.50 \pm 20.28	285.75 \pm 22.32	0.448
Final body weight (kg)	412.50 \pm 35.10	419.25 \pm 28.72	0.776
Average daily gain (kg/d)	1.187 \pm 0.06	1.21 \pm 0.047	0.450
Actual daily feed intake (kg)	11.86 \pm 0.08	10.44 \pm 0.23	0.004
RFI (kg)	0.55 \pm 0.044	−0.84 \pm 0.13	0.006

SD standard deviation.

Table S3. Raw data filtering statistics.

Sample Name	Raw Data	Clean Data	Q20 Content (%)	Q30 Content (%)	GC Content (%)
WY.H1	13,480.62	13,428.48	97.20	91.98	34.19
WY.H2	13,006.87	12,962.35	97.07	91.72	29.27
WY.H3	13,754.91	13,711.80	97.28	92.19	32.36
WY.H4	13,612.34	13,572.89	97.27	92.21	33.16
WY.H5	14,975.90	14,964.36	96.52	90.67	42.92
WY.L1	13,129.56	13,122.49	97.49	92.80	47.48
WY.L2	13,135.14	13,113.61	97.35	92.22	30.36
WY.L3	12,668.74	12,631.11	97.25	92.17	35.38
WY.L4	13,050.74	13,032.51	96.88	91.19	29.32
WY.L5	13,020.91	12,986.51	97.30	92.31	39.72
FB.H1	12,664.17	12,641.64	97.56	92.97	45.66
FB.H2	12,812.16	12,799.09	97.53	92.79	45.33
FB.H3	12,228.62	12,209.60	97.64	93.05	43.28
FB.H4	12,793.23	12,779.56	97.38	92.46	44.27
FB.H5	13,718.24	13,691.41	97.36	92.54	44.12
FB.L1	13,365.36	13,352.09	97.08	91.79	44.42
FB.L2	13,553.91	13,543.11	97.32	92.34	43.34
FB.L3	12,897.86	12,881.15	97.30	92.29	42.97
FB.L4	12,653.89	12,644.64	97.69	93.13	43.87
FB.L5	13,702.14	13,634.43	97.69	93.17	43.12

Table S4. The percent for all phyla in rumen and feces samples.

Species Name	WY-L	WY-H	FB-L	FB-H
<i>Bacteroidetes</i>	15.000%	12.000%	17.000%	16.000%
<i>Firmicutes</i>	14.000%	12.000%	24.000%	25.000%
<i>Euryarchaeota</i>	0.740%	1.100%	0.440%	0.250%
<i>Actinobacteria</i>	0.210%		0.860%	0.860%
<i>Fibrobacteres</i>	0.210%	0.270%	0.200%	0.082%
<i>Spirochaetes</i>	0.210%	0.280%	0.940%	0.910%
<i>Chlamydiae</i>	0.210%	0.790%	0.920%	0.210%
<i>Proteobacteria</i>	0.210%	0.280%	0.400%	0.610%
<i>Verrucomicrobia</i>	0.100%			
<i>Tenericutes</i>	0.110%			
<i>Fusobacteria</i>		0.090%	0.130%	0.032%
<i>Ascomycota</i>		0.090%		

<i>Candidatus_Peregrinibacteria</i>		0.100%		0.046%
<i>Thermodesulfobacteria</i>			0.110%	
<i>Others</i>	69.000%	73.000%	55.000%	56.000%
