Diversity In Intestinal Microorganisms Contributes To The Bodysize Difference In Chinese Horses And Ponies

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Research

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Abstract

Background: Intestinal microbiota communities can reflect the digestion and metabolism of the host, as well as the appearance of the host. In China, there are various excellent horse and pony breeds with rich diversity in wither height. However, little is known about the community structure of the intestinal microbiota in horses, let alone the profound effects it causes.

Results: Here in, we generated 16S rRNA sequences of intestinal microorganisms from 118 Chinese horses including Guanzhong horse, Debao pony, and Ningqiang pony. We found that the intestinal microbiota of horses is full of diversity, and *Firmicutes*, *Bacteroidetes*, and *Spirochaetes*, which is consistent with the special structure of the horse digestive tract. Interestingly, the abundance of *Firmicutes* and *Bacteroidetes* at the phylum level, showed a strong correlation with horse height, with R values of 0.82 and -0.86 respectively. Moreover, at the genus level, *Coprococcus*, *Streptococcus*, *Treponema*, and *Prevotella* demonstrated higher significance in terms of height, the prediction of PICRUSt2 function and multiple analyses of the metabolic pathways, and additionally, the metabolic pathways of energy intake and utilization were significantly enriched in horses relative to ponies ($P<0.01$). Notably, flora colonization in mouse littermates contributed to their broad development compared to the control group.

Conclusions: Compared with ponies, the intestinal microbiota enabled better cellulose decomposition and energy uptake in horses; Thus horses could get more energy from food to meet their higher demand for larger body development than ponies. Therefore, our study helps to understand the gut microbiota patterns across equine breeds, which has the potential to advance approaches aimed at personalized microbial modifications in horse breeding.

Full Text

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Tables

Table 1 Proportions of Firmicutes and Bacteroidetes and the F/B ratios of DB, NQ, and GZ.

Groups	Relative abundance of Firmicutes	Relative abundance of Bacteroidetes	Firmicutes/Bacteroidetes (F/B) ratios
	(Mean values ± SD)	(Mean values ± SD)	
DB	48.74%±10.21%	46.93%±10.95%	1.038±0.55
NQ	51.60%±6.92%	39.83%±7.29%	1.364±0.402
GZ	77.59%±4.06%	11.65%±3.17%	6.658±1.282**

**:P<0.01,compared with DB and NQ.

Supplemental Data

Figure S1 is not available with this version.

Figures

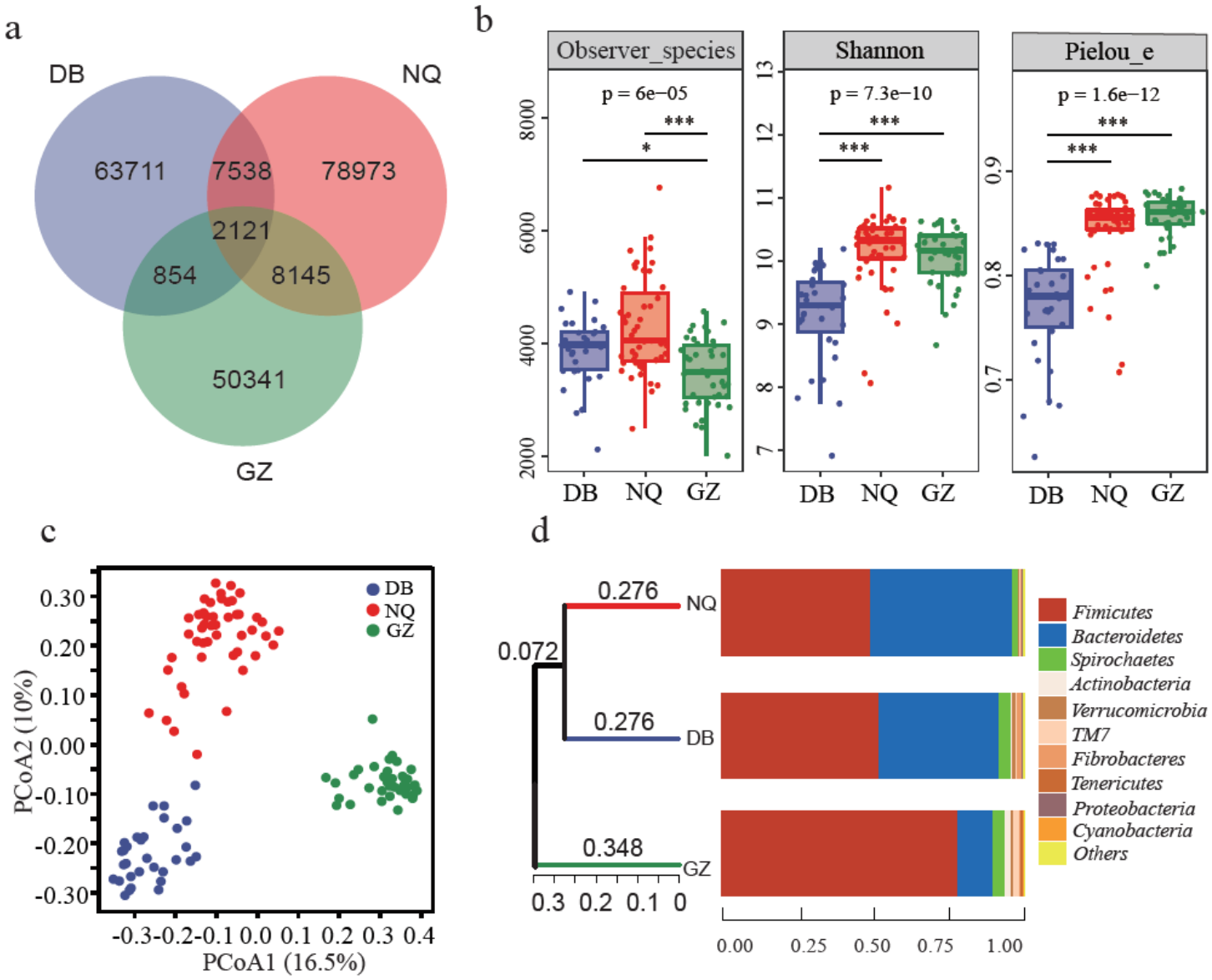

Figure 1

Taxonomic Annotations and Diversity Analysis of Species a Three varieties ASVs statistics Venn diagram. b Alpha diversity analysis maps of fecal microorganisms of three varieties. Each panel corresponds to an alpha diversity index, which is identified in the gray area at its top. In each panel, the Abscissa is the grouping label and the ordinate is the value of the corresponding alpha diversity index. The box plots feature the median (centerline) and interquartile range; the upper and lower edges: the maximum and minimum values (the extreme value within the range of 1.5x IQR); and the point outside the upper and lower edge indicates the outlier. The number under the diversity index label is the P-value of

the Kruskal-Wallis test. When the number of groups is less than or equal to 4 groups, the significant mark of Dunn's test post-test is drawn by default. c PCoA map based on weighted Bray-Curtis distance, each point in the graph represents a sample, and the samples of the same group are represented by the same color. d UPGMA cluster tree based on Bray-Curtis distance of intestinal microorganism structure of three varieties, on the left is UPGMA cluster tree structure, on the right is the relative abundance distribution map of species at the gate level of each sample.

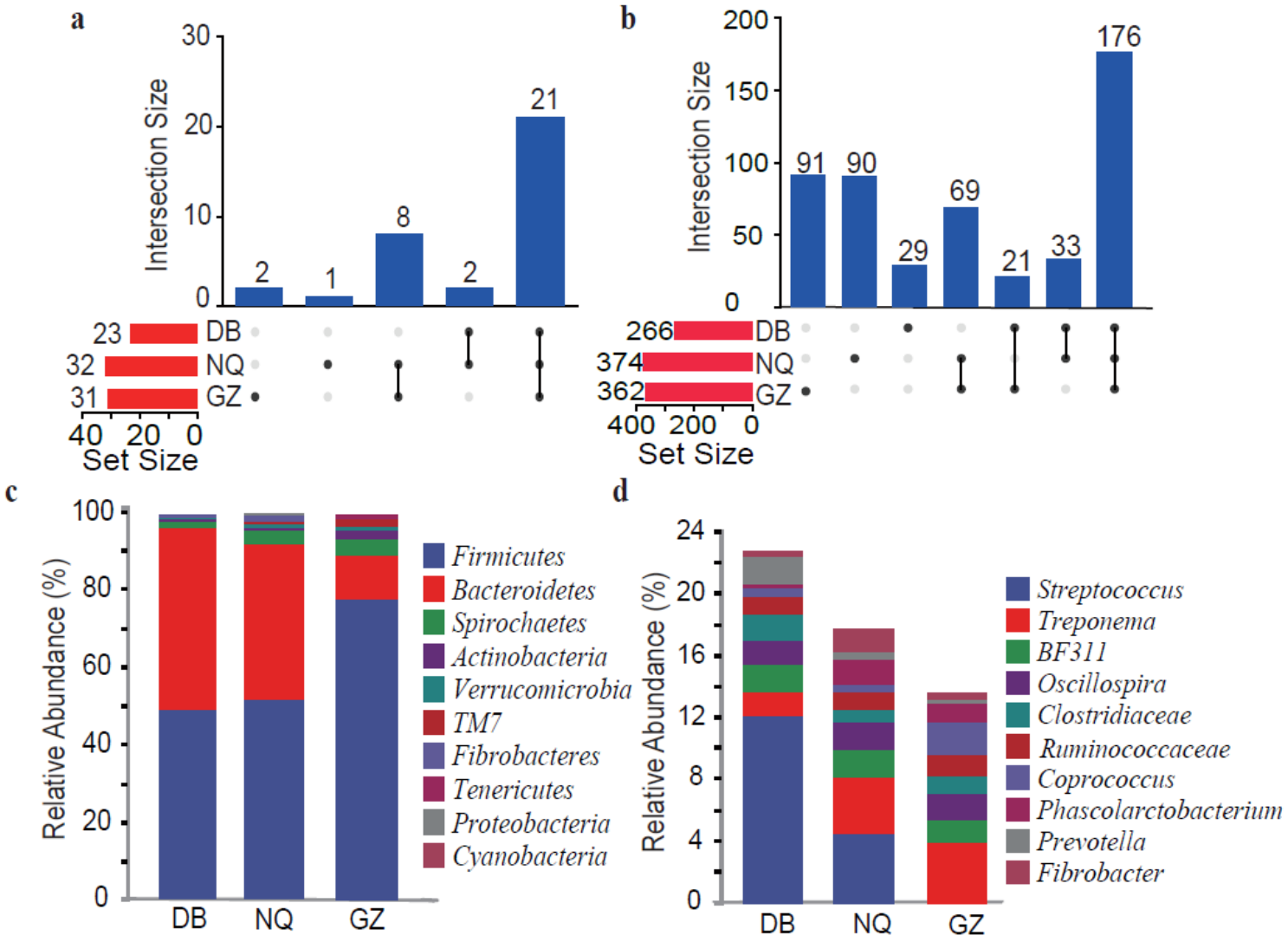

Figure 2

Structure of intestinal flora at the taxonomic level of phyla and genera. a and b is Upset diagrams at the classification level of phyla and genera, respectively. The left side of each graph shows the number of phyla (genera) species, each point in the node matrix at the lower right represents the unique phyla (genera) of the sample statistics of the three varieties, the connection between the nodes represents the common phyla (genera) of the statistically connected set, and the column at the upper right represents the phyla owned by the set corresponding to the connection of the lower node (the histogram of the number of genera). c and d Represent the species abundance map of the three varieties at the phyla and genera level, c is the phyla level abundance map, d is the genera level abundance map.

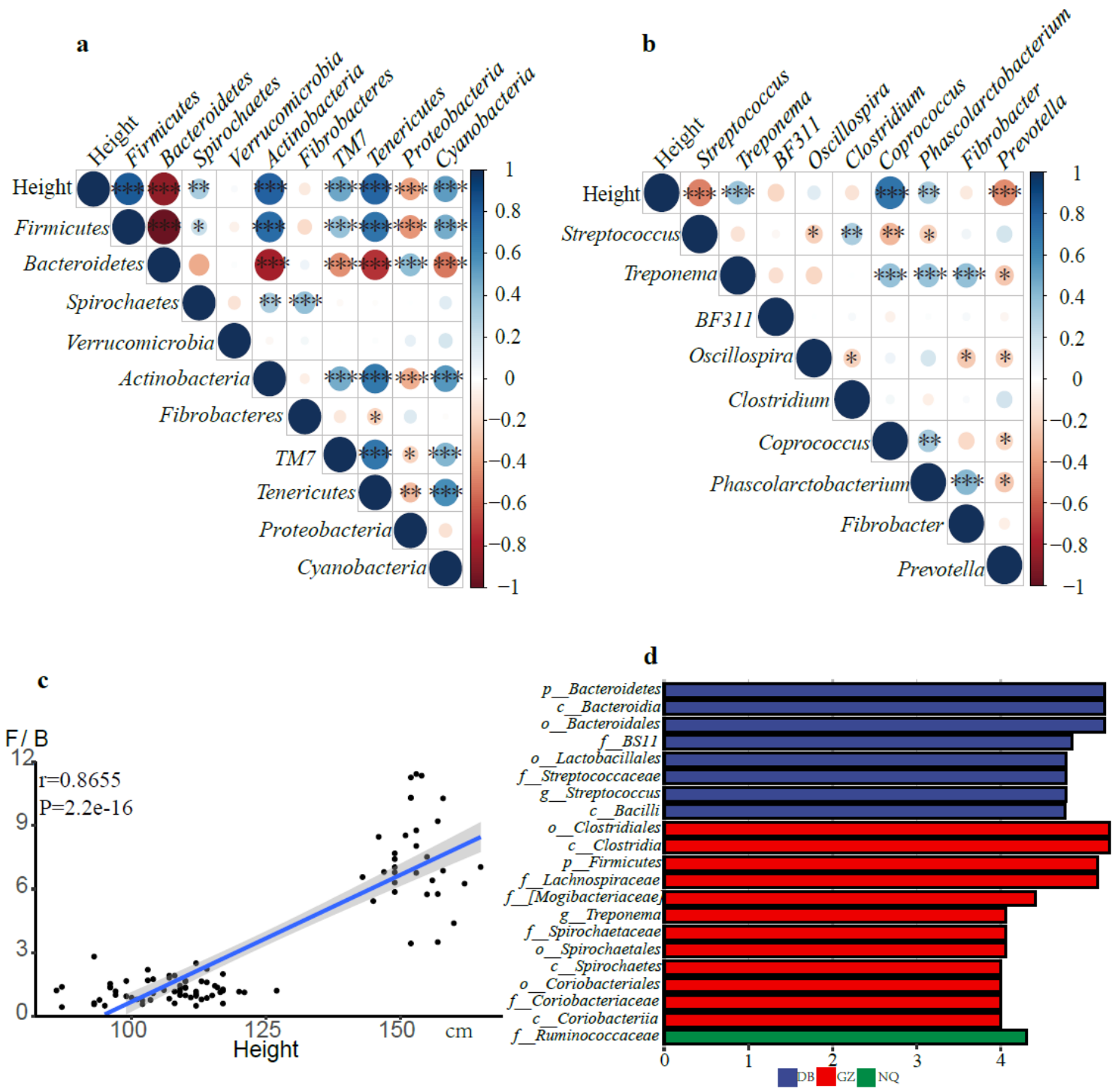

Figure 3

Analysis of the Correlation between Intestinal Microorganisms and Height or the Difference of Microflora a Correlation analysis between different bacterial phyla and height; b Correlation between different bacterial genera and height. The size of the circle in the picture indicates the correlation, the larger the circle, the stronger the correlation. The color of the circle tends to blue indicates a positive correlation, and tends to red indicates a negative correlation(***P<0.001,**P<0.01,*P<005). c Correlation between body height and ratio of Firmicutes to Bacteroidetes. d Bacterial taxa that differed significantly among DB, GZ,

and NQ were identified with linear discriminant analysis (LDA) effect size (LEfSe) using default parameters.

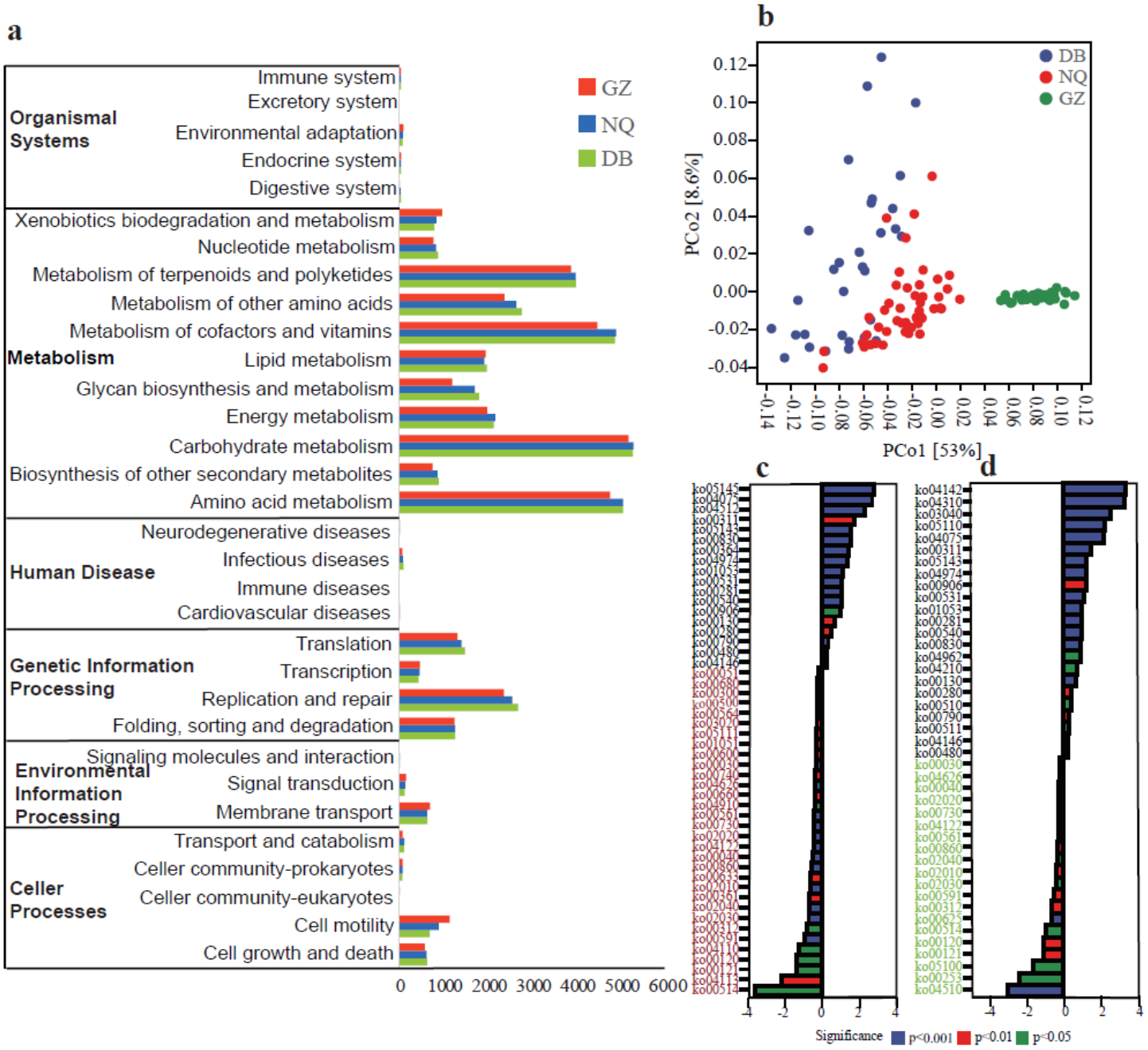

Figure 4

Microbial Gene Functions Prediction on KEGG in DB NQ and GZ Horse by PICRUSt2 a The Abscissa is the abundance or count of the functional pathway (per million KO), the ordinate is the functional pathway of the second classification level of KEGG, and the rightmost is the first level pathway to which the pathway belongs. What shows here is the average abundance of all selected samples. b PCoA based on the Bray–Curtis distances of KEGG modules between DB, NQ, and GZ; c and d In the picture, the transverse axis value logFC (the positive value of log2 (fold change)) represents that the up-regulated group is up-regulated compared with the control group, and the negative value is down-regulated; the vertical

coordinates are different pathway labels; different colors show the degree of significance. c Indicates the tertiary differential metabolic pathway between DB and GZ, d Indicates the tertiary differential metabolic pathway between NQ and GZ.

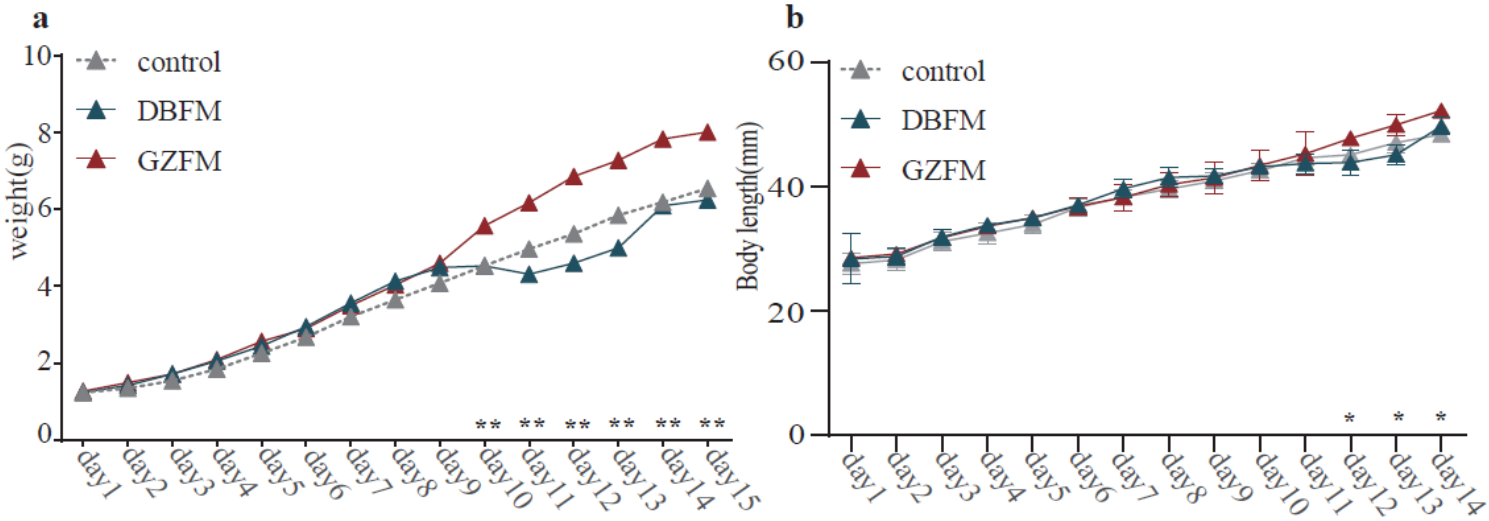

Figure 5

Changes of Body Weight and Body Length in Mice a Indicates the change of body weight of the three groups of mice in 15 days. b Indicates the change of body length of the three groups of mice in 14 days.(**:P<0.01,GZ compared with DB and control. *:P<0.05, GZ compared with DB and control.)

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- tableS1.xlsx
- tableS2.xlsx
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