Supplementary Information (SI) for Food & Function.

Supplementary Materials for

Multi-omics-guided discovery: Yeast Protein alleviates glucocorticoid-induced muscle atrophy through dual activation of IGF-1/PI3K/Akt/FOXO and CaMKK/AMPK signaling pathways

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This PDF file includes:

Supplementary Text
Figs. S1 to S6
Tables S1 to S4 (Tables S2 to S4 are provided in spreadsheet format via hyperlinks: Supplementary Table 2.xlsx; Supplementary Table 3.xlsx; Supplementary Table 4.xlsx)

Supplemental Figures

Fig. S1.

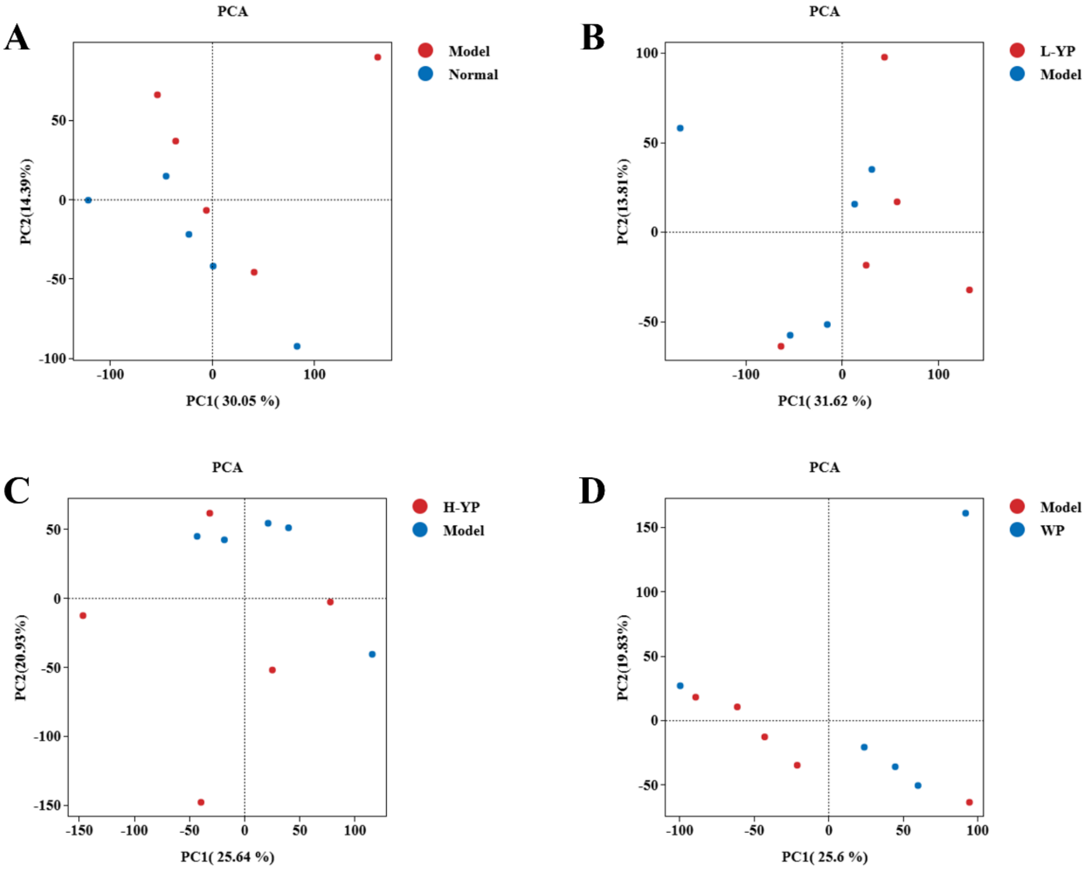


Figure S1. PCA map of the quadriceps transcriptome. (A)Normal vs. Model. (B) Model vs. L-YP. (C) Model vs. H-YP. (D) Model vs. WP.

Fig. S2.

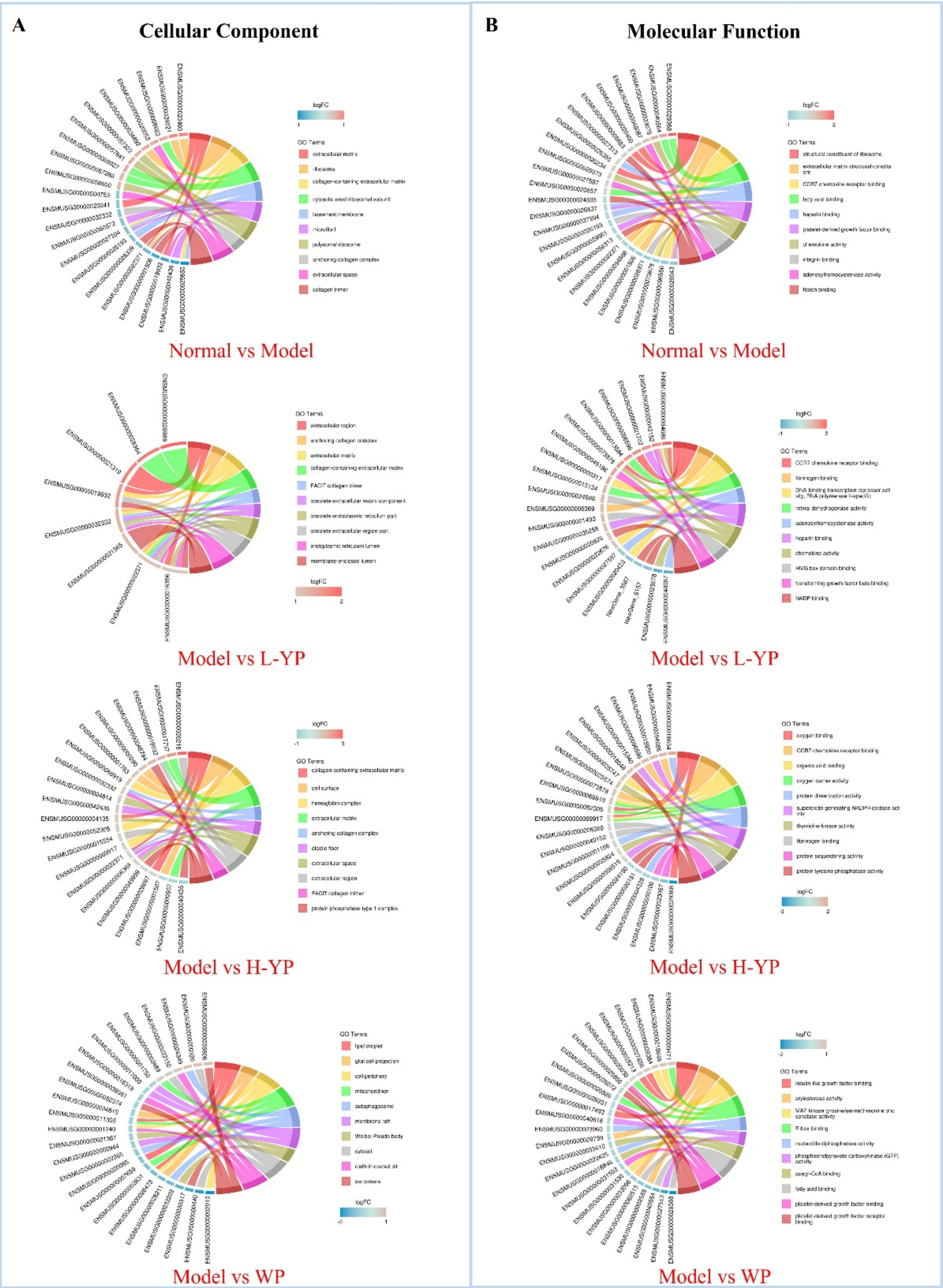


Figure S2. String plot of GO enrichment analysis of the muscle transcriptome. (A) Cellular Component; (B) Molecular Function.

Fig. S3.

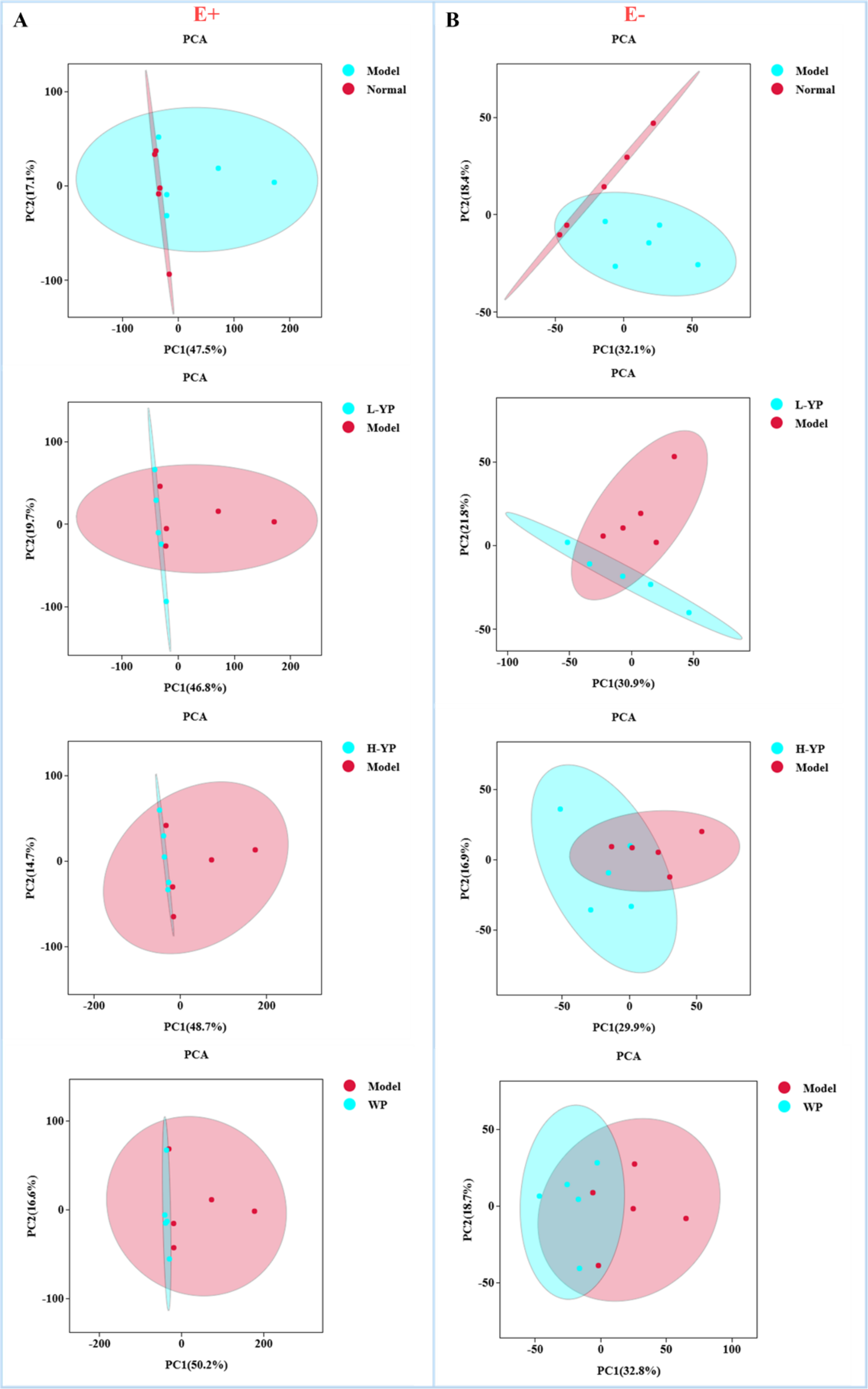
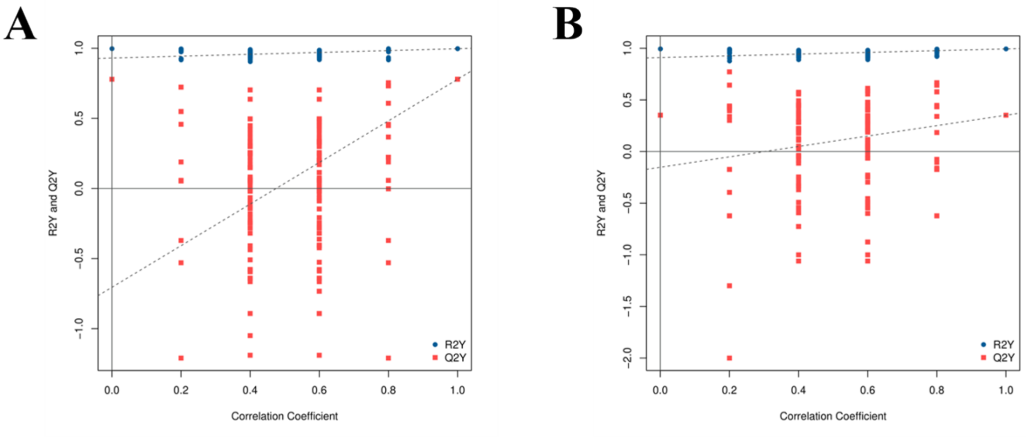


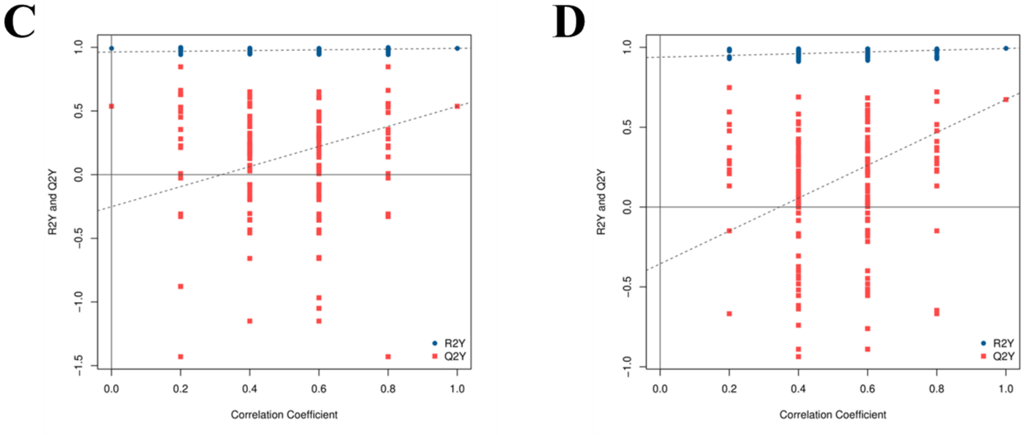
Figure S3. PCA plot of the serum metabolome. (A) Positive ion mode (E+); (B) Negative ion mode (E-)

Fig. S4.



Normal vs Model

Model vs L-YP



Model vs H-YP

Model vs WP

Figure S4 Permutation test diagram of the OPLS-DA model. (A) Normal VS Model (B) Model VS L-YP; (C) Model VS H-YP (D) Model VS WP.

Note: The blue dots and red dots respectively represent the R2Y and Q2Y of the permutation model, and the two dotted lines are the regression lines of the fitting of R2Y and Q2Y. If the slope of the Q2Y fitted regression line is regular, it indicates that the model is meaningful. If the blue dots are generally above the red dots, it suggests that the independence of the modeling training set and the test set is good.

Fig. S5.

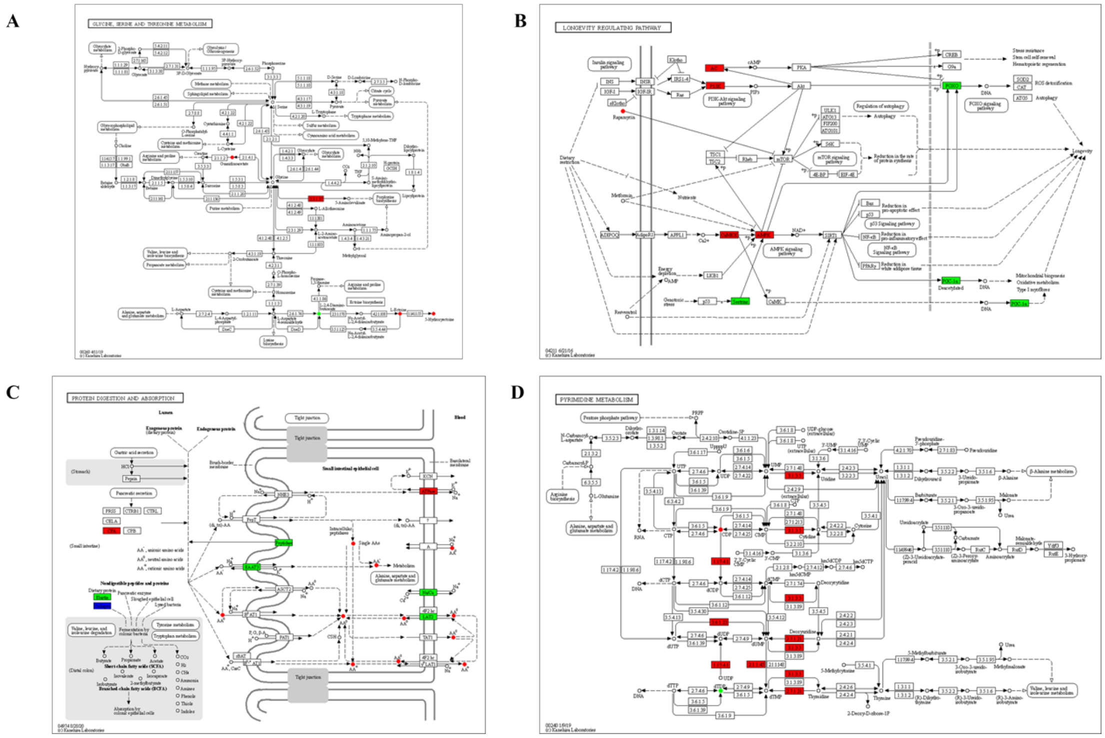


Figure S5 Effects of H-YP on Glycine, serine and threonine metabolism (A) Protein digestion and absorption (C), Longevity Regulating Pathway (B), Pyrimidine metabolism (D) pathway.

Note: The boxes in the figure represent gene products, and the circles represent metabolites; The gene products/metabolites in the red/green background boxes belong to the differential genes/metabolites detected this time. Among them, red indicates up-regulated genes/metabolites and green indicates down-regulated genes/metabolites. All the gene products with blue background boxes belong to both up-regulated and down-regulated genes/metabolites.

Fig. S6.

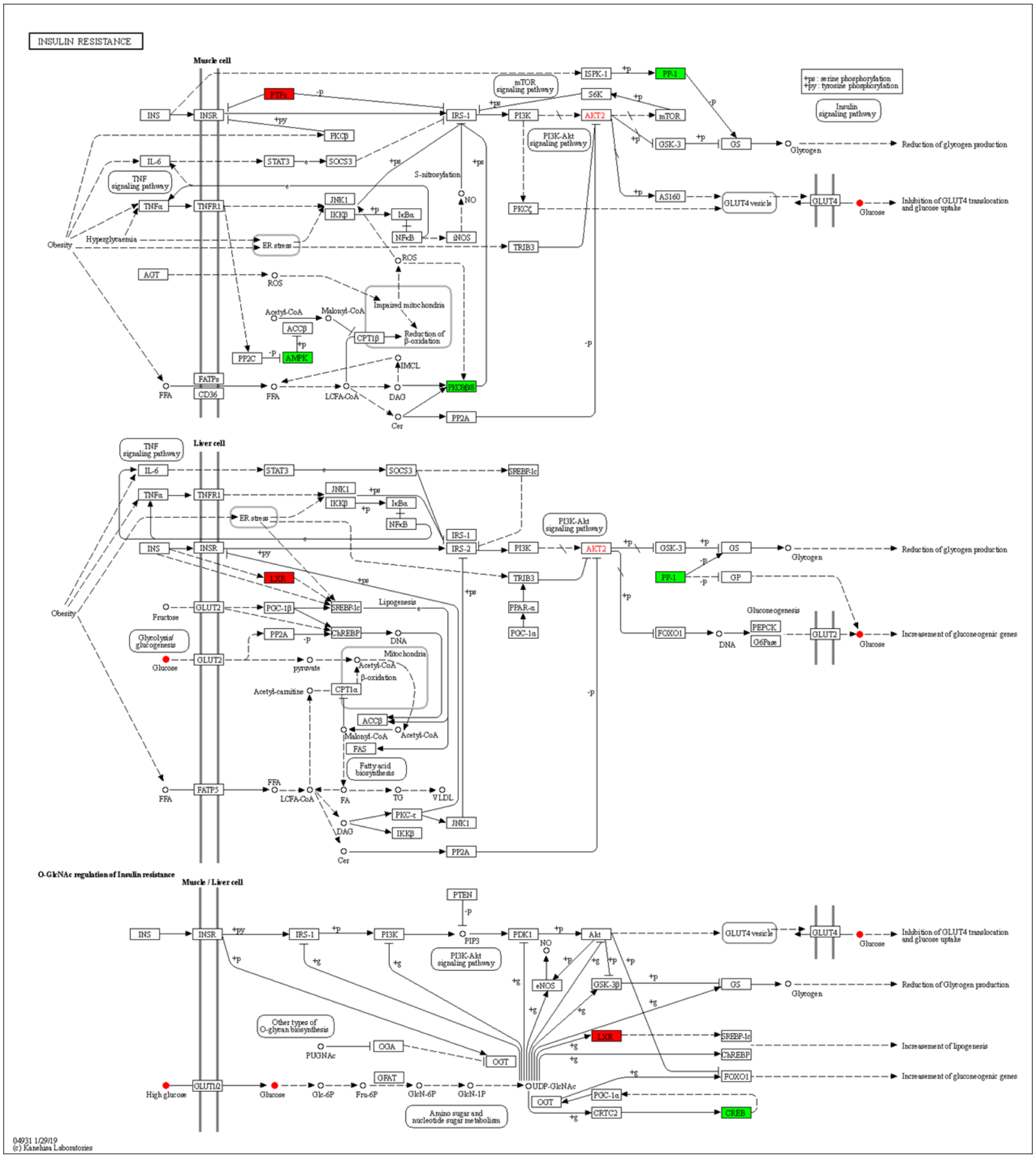


Figure S6 KEGG analysis diagram of the insulin resistance pathway in the normal group vs the model group.

Table S1.

Table S1 Quality control of RNA sequencing in quadriceps femoris specimens.

Group	Samples	Clean reads	Clean bases	Q30 (%)	GC content (%)
Normal	A1	21296930	6363200734	97.97	47.75
	A2	20838015	6215594008	98.42	47.54
	A3	21961644	6534743520	98.47	47.07
	A4	21517435	6421870636	98.22	47.78
	A5	20374490	6070328977	98.26	47.29
Model	B1	19848230	5917079140	97.9	47.98
	B2	20396711	6072124491	98.43	47.72
	B3	22819049	6778679154	97.57	47.3
	B4	21368048	6365695163	97.99	47.42
	B5	21304287	6359696152	98.33	48.75
L-YP	C1	20509743	6114220709	98.29	47.02
	C2	20934744	6231660056	97.91	47.81
	C3	21206714	6323709313	97.76	48.02
	C4	21807904	6493378916	98.21	47.84
	C5	19477018	5807048736	97.47	47.97
H-YP	D1	20788639	6196667355	98.28	47.22
	D2	20622559	6147914834	98.3	47.88
	D3	20473430	6115016491	98.24	47.14
	D4	21515301	6420057923	98.24	47.64
	D5	20211362	6021981906	98.18	48.52
WP	E1	21079026	6294574673	98.46	47.04
	E2	20495979	6109447699	98.49	48.41
	E3	19277481	5751686443	98.4	47.98
	E4	20996794	6274927150	98.34	47.42
	E5	21510017	6425351916	98.12	46.24

Note: Clean reads refer to the total number of pair-end Reads in Clean Data; "Clean bases" refers to the total number of bases in "Clean Data". GC content is the percentage of G and C among the total bases in Clean Data; Q30% is the percentage of bases with a Clean Data quality value greater than or equal to 30.