Supplementary Tables and Figures

Table S1: Mean, range, and repeatability of percent ratios of amino acids to total amino acid concentration

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| --- | --- | --- | --- |
| Trait | Mean (%) ± SD | Range (%) | Repeatability % |
| Ala:TA | 4.31 ± 0.2 | 3.71 - 4.9 | 13.1 |
| Asp:TA | 13.34 ± 0.77 | 10.91 - 16.9 | 13.1 |
| Arg:TA | 9.38 ± 0.61 | 7.38 - 12.02 | 15.6 |
| Cys:TA | 0.76 ± 0.10 | 0.55 - 1.03 | 15.5 |
| Glu:TA | 15.42 ± 0.85 | 13.01 - 17.85 | 17.5 |
| Gly:TA | 4.32 ± 0.22 | 3.7 - 4.92 | 14.2 |
| His:TA | 2.12 ± 0.33 | 0.64 - 3.2 | 6.5 |
| H-Pro:TA | 10.78 ± 2.78 | 5.33 - 19.91 | 9.6 |
| Ile:TA | 4.29 ± 0.22 | 3.68 - 4.82 | 18.3 |
| Leu:TA | 7.81 ± 0.37 | 6.69 - 8.77 | 19.7 |
| Lys:TA | 4.59 ± 0.66 | 2.72 - 6.14 | 9.9 |
| Met:TA | 0.71 ± 0.06 | 0.58 - 0.94 | 27.0 |
| Phe:TA | 4.45 ± 0.68 | 1.8 - 5.47 | 0.0 |
| Pro:TA | 8.50 ± 1.12 | 6.08 - 11.73 | 10.2 |
| Ser:TA | 4.86 ± 0.26 | 4.18 - 5.64 | 17.6 |
| Thr:TA | 3.64 ± 0.18 | 3.17 - 4.25 | 15.2 |
| Val:TA | 0.74 ± 0.04 | 0.65 - 0.83 | 12.4 |

Chart, polygon

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Figure S1: Histograms of trait distributions fit with density curves for the normal distribution using estimates of the mean and standard deviation

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Figure S2 QQ plots of alanine, valine, leucine, isoleucine, threonine, methionine, lysine, and aspartate fitting the following genome-wide association models from GAPIT: GLM, MLM, MLMM, CMLM, SUPER, FarmCPU, and Blink.

Chart, line chart

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Figure S3: QQ plots of the ratio of glycine, histidine, aspartate, and methionine to total amino acid concentration and digestibility fitting the following genome-wide association models from GAPIT: GLM, MLM, MLMM, CMLM, SUPER, FarmCPU, and Blink

Chart, line chart

Description automatically generated

Figure S4: QQ plots of arginine, cystine, phenylalanine, the ratio of glutamate to total amino acid concentration, and total amino acid concentration fitting the following genome-wide association models from GAPIT: GLM, MLM, MLMM, CMLM, SUPER, FarmCPU, and Blink

Timeline

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Figure S5: Manhattan plots of traits with at least one SNP significantly associated with the trait by multiple models. Different color points represent different GWAS models. Significance thresholds are indicated by dotted and solid grey horizontal lines and correspond to −log(0.05/22,280) and −log(0.01/22,280), respectively (Bonferroni correction). Colored outlines represent pyruvate family amino acids, aspartate family amino acids, and other protein quality traits (Gly, His:TA, PDg). SNP density plots are located above chromosome numbers on a red to green scale of 1 to 50 SNPs per 1 Mb. Grey dashed line boxes indicate significant loci shared across multiple traits.

A picture containing graphical user interface

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Figure S6: Manhattan plots of traits with at least one SNP significantly associated with the trait by any model and TA, which does not have significantly associated SNPs but was included for comparison with ratio traits. Different color points represent different GWAS models. Significance thresholds are indicated by dotted and solid grey horizontal lines and correspond to −log(0.05/22,280) and −log(0.01/22,280), respectively (Bonferroni correction). SNP density plots are located above chromosome numbers on a red to green scale of 1 to 50 SNPs per 1 Mb.