

Supplementary Information

Influence of developmental diet on adult energy reserves in *Drosophila*

Supplementary figures and tables

Figure S1. Protein content (μg per fly) at eclosion across developmental diets varying in yeast and sugar concentrations. In all groups, protein levels were strongly influenced by developmental diet, with models showing high predictive power (adjusted $R^2 = 0.62\text{--}0.81$). The highest protein content was consistently associated with low sugar ($<5\%$) and intermediate-to-high yeast concentrations, with females generally reaching their peak at slightly higher yeast levels (17–22%) than males (12–20%). On their respective optimal diets, SK flies consistently contained more protein than w^{1118} flies. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S1-2.

Figure S2. Energy content (J per mg protein) at eclosion as a function of sugar concentration in the developmental diet at each yeast level. Each panel shows one combination of yeast level, population, and sex. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S3. Energy content (J per mg protein) at eclosion as a function of yeast concentration in the developmental diet at each sugar level. Each panel shows one combination of sugar level, population, and sex. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S4. Effect of developmental diet on energy reserves (J per fly) at eclosion. Surface plots show the total energy content (J per fly) of newly eclosed flies as a function of yeast and sugar concentrations in the developmental diet. Each surface represents a second-order polynomial fit based on group means. Model fit was robust in all groups, with adjusted R^2 values of 0.59 (w^{1118} males), 0.55 (SK males), 0.65 (w^{1118} females), and 0.82 (SK females). For global statistical analyses, see Tables S6-7.

Figure S5. Energy content (J per mg protein) at eclosion across developmental diets varying in yeast and sugar concentrations. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S3-5.

Figure S6. Energy content (J per fly) at eclosion across developmental diets varying in yeast and sugar concentrations (see also **Figure S5**). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S6-7.

Figure S7. Fat content (μg per mg protein) at eclosion across developmental diets varying in yeast and sugar concentrations. The developmental diet was a strong predictor of fat content in freshly eclosed flies of both sexes, with statistical models for all groups showing strong to very strong fits (Adjusted R^2 ranging from 0.68 to 0.79). High sugar (>20%) developmental diets consistently produce the fattest flies of both sexes. The optimal yeast concentration for maximizing fat was at both low (<5%) and high yeast (>20%) levels. Finally, the w^{1118} genetic line of flies consistently stored more fat than the SK line (see also **Figure S8**). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S8-S9.

Figure S8. Fat content (μg per fly) at eclosion across developmental diets varying in yeast and sugar concentrations. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S10-11.

Figure S9. Glycogen content (μg per mg protein) at eclosion across developmental diets varying in yeast and sugar concentrations. The effect of developmental diet on the glycogen content of freshly eclosed flies was highly genotype-specific, with a strong dietary influence observed in the w^{1118} strain but not in the SK flies. For the w^{1118} strain, developmental diet was a strong predictor

of glycogen stores in both sexes (Adjusted $R^2 = 0.53$ and 0.72), and the highest glycogen content consistently resulted from a developmental diet high in both yeast ($>20\%$) and sugar ($>20\%$). In contrast, the developmental diet had no statistically significant effect on the glycogen content of SK males and was a much weaker and more complex predictor for SK females (see also **Figure S10**). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S12-13.

Figure S10. Glycogen content ($\mu\text{g per fly}$) at eclosion across developmental diets varying in yeast and sugar concentrations. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Table S14-15.

Figure S11. Trehalose content ($\mu\text{g per mg protein}$) at eclosion across developmental diets varying in yeast and sugar concentrations. The developmental diet was a poor predictor of trehalose content in freshly eclosed flies of both sexes. This was confirmed by very weak statistical models across all groups (all Adjusted R^2 values ≤ 0.27), indicating that any visual trends were not statistically robust (see also **Figure S12**). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S16-17.

Figure S12. Trehalose content ($\mu\text{g per fly}$) at eclosion across developmental diets varying in yeast and sugar concentrations. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S18-19.

Figure S13. Glucose content ($\mu\text{g per mg protein}$) at eclosion across developmental diets varying in yeast and sugar concentrations. The effect of developmental diet on glucose levels was complex and depended heavily on both sex and genotype. For males of both genetic strains, the diet had no statistically significant effect on their glucose levels. In contrast, the effect on females was genotype-specific: diet was a considerable predictor of glucose for SK females, with high-sugar ($>20\%$) and intermediate-yeast ($10-17\%$) diets yielding the highest levels. However, diet had no significant impact on the glucose levels of w^{1118} females (see also **Figure S14**). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S20-21.

Figure S14. Glucose content (μg per fly) at eclosion across developmental diets varying in yeast and sugar concentrations. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S22-23.

Figure S15. Protein content (μg per fly) in 10-day-old males. The protein content of 10-day-old adult males was consistently maximized when they developed on a diet with an intermediate yeast concentration (approx. 10-17%). The optimal sugar level, however, varied with genotype and mating status. For the SK flies, the highest protein resulted from developmental diets with low-to-intermediate or intermediate sugar, while for the w^{1118} strain, a low-sugar diet was optimal. Overall, flies from the SK population had higher protein content (peaks of $\sim 75\text{-}80\ \mu\text{g}$) than those from the w^{1118} strain (peaks of $\sim 60\text{-}65\ \mu\text{g}$), and for both genotypes, mated males had lower protein than their virgin counterparts. The statistical models for all groups were moderate (Adjusted R^2 ranging from 0.29 to 0.50), indicating that the developmental diet was a considerable factor in determining final protein content in males. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S26-27.

Figure S16. Protein content (μg per fly) in 10-day-old females. The developmental diet that resulted in the highest protein content in 10-day-old adult females was distinctly different for each genotype and mating status. A shift was observed in the SK population: virgin females had the highest protein ($\sim 130\ \mu\text{g}$) when developed on a high-yeast, high-sugar diet, while mated females had their peak protein ($\sim 155\ \mu\text{g}$) when developed on a balanced intermediate diet. The w^{1118} strain showed a different pattern, with virgins having the most protein ($\sim 90\ \mu\text{g}$) when developed on an intermediate-yeast, low-sugar diet, and mated females having their peak ($\sim 110\ \mu\text{g}$) when developed on a low-yeast, low-sugar diet. The statistical models for these trends were generally weak, indicating that developmental diet is not a consistently strong predictor of final protein content in females. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S26-27.

Figure S17. Energy content (J per mg protein) in 10-day-old w^{1118} flies as a function of sugar concentration in the developmental diet at each yeast level. Each panel shows one combination of yeast level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above

points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S18. Energy content (J per mg protein) in 10-day-old SK flies as a function of sugar concentration in the developmental diet at each yeast level. Each panel shows one combination of yeast level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S19. Energy content (J per mg protein) in 10-day-old w^{1118} flies as a function of yeast concentration in the developmental diet at each sugar level. Each panel shows one combination of sugar level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S20. Energy content (J per mg protein) in 10-day-old SK flies as a function of yeast concentration in the developmental diet at each sugar level. Each panel shows one combination of sugar level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S21. Effect of developmental diet on energy reserves (J per fly) in 10-day-old males. Surface plots show the total energy content (J per fly) of 10-day-old males as a function of yeast and sugar concentrations in the developmental diet. Each surface represents a second-order polynomial fit based on group means. Model fit varied among groups, with adjusted R^2 values of 0.29 (w^{1118} virgins), 0.45 (SK virgins), 0.12 (w^{1118} mated), and 0.36 (SK mated). For global statistical analyses, see Tables S31-32.

Figure S22. Effect of developmental diet on energy reserves (J per fly) in 10-day-old females. Surface plots show the total energy content (J per fly) of 10-day-old females as a function of yeast and sugar concentrations in the developmental diet. Each surface represents a second-order polynomial fit based on group means. Model fit varied across groups, with adjusted R^2 values of 0.25 (w^{1118} virgins), 0.24 (SK virgins), -0.07 (w^{1118} mated), and 0.28 (SK mated). For global statistical analyses, see Tables S31-32.

Figure S23. Energy content (J per mg protein) in 10-day-old males. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Table S28-30.

Figure S24. Energy content (J per fly) in 10-day-old males. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S31-32.

Figure S25. Energy content (J per mg protein) in 10-day-old females. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Table S28-30.

Figure S26. Energy content (J per fly) in 10-day-old females. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S31-32.

Figure S27. Fat content (μg per mg protein) in 10-day-old males. The developmental diet was a key predictor of the fat stored per mg of protein in 10-day-old males for both genotypes, with all statistical models showing moderate to strong fits (Adjusted R^2 ranging from 0.38 to 0.63). For all four groups, the highest values were consistently found in flies that had developed on a low-yeast (<5%) diet. However, the optimal sugar concentration showed a genotype-specific interaction with mating status. For the w^{1118} strain, the developmental optimum was consistently at intermediate sugar (10-15%) for both virgins and mated males. In contrast, for the SK strain, the optimal developmental sugar level was higher for virgins (15-20%) than for mated males (10-15%). Overall, the SK population stored substantially more fat relative to protein than the w^{1118} population (peaks of ~ 650 - 700 $\mu\text{g}/\text{mg}$ vs. ~ 350 - 400 $\mu\text{g}/\text{mg}$), and for both genotypes, mated males stored less than their virgin counterparts. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S33-34.

Figure S28. Fat content (µg per fly) in 10-day-old males. The developmental diet was a key predictor of fat content in 10-day-old males, with all statistical models showing moderate to strong fits (Adjusted R^2 ranging from 0.33 to 0.56). A consistent dietary pattern was observed across both genotypes and mating statuses. The highest fat content was consistently found in flies that developed on a diet with low yeast (<5%) and intermediate sugar (approx. 10-17%). Under these conditions, flies from the SK population stored more fat than those from the w^{1118} population (peaks of ~40-45 µg vs. ~20-25 µg, respectively). For both genotypes, mated males contained less fat than their virgin counterparts. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S35-36.

Figure S29. Fat content (µg per mg protein) in 10-day-old females. The persistent effect of developmental diet on the fat stores of 10-day-old females was complex, with the consequences of mating differing dramatically between the two genotypes. For the w^{1118} strain, the analysis of fat per mg of protein showed that mating obscured the effect of diet. While developmental diet was a considerable predictor for virgins (Adjusted $R^2 = 0.45$), it had no statistically detectable effect in their mated counterparts. In contrast, for the SK flies, both models were statistically weak. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S33-34.

Figure S30. Fat content (µg per fly) in 10-day-old females. Overall, there was no strong persistent effect of the developmental diet on the fat content of 10-day-old females. This was reflected in the statistical models, which were generally weak to non-existent. For three of the four groups (both SK groups and mated w^{1118} females), the models were weak predictors (Adjusted $R^2 \leq 0.35$), with the model for mated w^{1118} flies having no predictive power at all. While developmental diet was a considerable factor for virgin w^{1118} females (Adjusted $R^2 = 0.35$), this was the exception. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S35-36.

Figure S31. Glycogen content (µg per mg protein) in 10-day-old males. In both genotypes, glycogen content per mg protein in 10-day-old males was influenced by the developmental diet, but the patterns and model fits differed substantially. w^{1118} males had their highest glycogen levels under high-yeast (>20–25%) and intermediate-sugar (10–15%) diets. The model fit was moderate

for virgin males (Adj. $R^2 = 0.42$) but poor for mated males (Adj. $R^2 = 0.09$), indicating that developmental diet had a weaker predictive value in the latter group. In the SK population, males consistently showed the highest glycogen levels when developed on low-yeast diets (<5%), with the optimal sugar concentration differing by mating status: virgins peaked at high sugar (>18%), while mated males peaked at low sugar (<5%). The model fit was moderate to good (Adj. $R^2 = 0.44$ and 0.30 for virgins and mated males, respectively). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S37-38.

Figure S32. Glycogen content (μg per fly) in 10-day-old males. The developmental diet that resulted in the highest glycogen content in 10-day-old males differed for each genotype and mating status. For the w^{1118} strain, virgin males had their highest glycogen ($\sim 44 \mu\text{g}$) after developing on a diet of high yeast (>20%) and intermediate sugar (10-15%), a trend supported by a moderate statistical fit (Adjusted $R^2 = 0.40$). Mated w^{1118} males also had lower glycogen levels ($\sim 30 \mu\text{g}$) than virgins, with their peak resulting from a developmental diet of intermediate-to-high yeast (17-22%) and low sugar (5-10%); however, this relationship was very weak statistically (Adjusted $R^2 = 0.14$). For the SK population, virgin males had their highest glycogen content ($\sim 42 \mu\text{g}$) when reared on a developmental diet of low yeast (<5%) and intermediate sugar (approx. 15%). Mated SK males had lower peak glycogen ($\sim 31 \mu\text{g}$), and their maximum was found on a different developmental diet of intermediate yeast (7-12%) and low sugar (<5%). The statistical models for both of these groups were weak (Adjusted $R^2 \leq 0.29$). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S39-40.

Figure S33. Glycogen content (μg per mg protein) in 10-day-old females. The developmental diet that resulted in the highest glycogen per mg of protein in 10-day-old females showed a genotype-specific pattern. The w^{1118} strain consistently had its highest values when developed on a high-yeast (>20%), high-sugar (15-22%) diet. In contrast, for the SK population, the highest values were consistently found in flies that developed on a low-yeast (<5%), low-sugar (<5%) diet, regardless of mating status. For both genotypes, virgin females reached a higher peak value than their mated counterparts. The statistical models were consistently stronger for mated females than for virgins in both strains. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S37-38.

Figure S34. Glycogen content (µg per fly) in 10-day-old females. The persistent effect of developmental diet on the glycogen content of 10-day-old females was fundamentally different for the two genotypes. For the w^{1118} strain, the developmental diet was a strong predictor of glycogen content (Adjusted $R^2 \geq 0.35$). These females consistently had the highest glycogen when developed on diets high in yeast (>17%) and intermediate in sugar (12-17%). For the SK flies, the highest glycogen levels were consistently a consequence of low-sugar (<5%) developmental diets, though the relationship was statistically weak (Adjusted $R^2 \leq 0.33$). The optimal developmental yeast level for this population shifted from intermediate (~10%) in virgins to low (<5%) in mated females. For both genotypes, mated females stored less glycogen than their virgin counterparts. In contrast, Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S39-40.

Figure S35. Trehalose content (µg per mg protein) in 10-day-old males. The developmental diet was a poor predictor of the trehalose per mg protein measured in 10-day-old adult males. The statistical models for all four groups were very weak. Therefore, the trehalose content relative to protein in adult males appears to be largely independent of the yeast and sugar composition of their developmental diet. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S41-42.

Figure S36. Trehalose content (µg per fly) in 10-day-old males. The developmental diet had little to no statistically significant effect on the trehalose content measured in 10-day-old adult males. For three of the four groups analyzed— w^{1118} virgin, w^{1118} mated, and SK virgin males—the statistical models failed, yielding Adjusted R^2 values that indicate no predictive power. The model for the remaining group, mated SK males, was also very weak (Adj. $R^2 = 0.14$). Consequently, the trehalose levels in these adult males appear to be largely independent of the yeast and sugar levels in their developmental diet. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S43-44.

Figure S37. Trehalose content (µg per mg protein) in 10-day-old females. The persistent effects of developmental diet on the trehalose per mg protein measured in 10-day-old adult females were highly genotype-specific. The w^{1118} strain generally showed the highest trehalose per mg protein after development on high-yeast, high-sugar diets. The statistical models for these trends

were generally weak; however, the positive relationship with both yeast and sugar in mated w^{1118} females was the most robustly supported by the analysis (Adj. $R^2 = 0.35$). A distinct pattern was observed in the SK flies, where the optimal developmental diet shifted with mating status: virgin females had the highest values when developed on low-yeast, low-sugar diets, while mated females had the highest values when developed on high-yeast, low-sugar diets. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S41-42.

Figure S38. Trehalose content (μg per fly) in 10-day-old females. The developmental diet was a poor predictor of the trehalose content measured in 10-day-old adult females, as all statistical models were either very weak or failed to show a significant effect (all Adjusted $R^2 \leq 0.18$). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S43-44.

Figure S39. Glucose content (μg per mg protein) in 10-day-old males. A comparative analysis of w^{1118} and SK males reveals that the long-term impact of developmental diet on adult glucose per protein content is strain-dependent. The developmental diet was a weak predictor for w^{1118} males (Adj. R^2 falling from 0.21 to 0.15). For SK males, the developmental diet was consistently moderate predictor of adult glucose per protein levels (Adj. $R^2 \approx 0.40$). They showed differences in relation to mating status: while a low-sugar (<5%) developmental diet was always optimal; the ideal developmental yeast concentration was higher in mated individuals (10-15%). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S45-46.

Figure S40. Glucose content (μg per fly) in 10-day-old males. The analyses of 10-day-old w^{1118} and SK males reveal fundamentally different responses to their developmental diet. The developmental diet that maximized glucose storage was strain-dependent: for w^{1118} males it was a developmental diet of intermediate sugar (~10%) and low yeast (<5%), whereas for SK males of intermediate yeast (10-15%) and low sugar (<5%). The impact of mating also differs between the strains. For w^{1118} males, both virgin and mated individuals show similarly high glucose peaks under their optimal developmental diets. For SK males, however, mated individuals store higher peak glucose levels than virgins (~4.5 μg vs. ~3.5 μg). Finally, the predictive power of the developmental diet varies significantly. For the w^{1118} strain, the diet is a moderately reliable

predictor for virgins (Adj. $R^2 = 0.31$) but becomes a weak predictor for their mated counterparts (Adj. $R^2 = 0.20$). For the SK population, diet is a consistently moderate predictor of final glucose content for both virgin and mated males (Adjusted $R^2 \approx 0.44$ -0.45). Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S47-48.

Figure S41. Glucose content (μg per mg protein) in 10-day-old females. A comparative analysis of w^{1118} and SK females reveals strain-specific differences in the long-term relationship between developmental diet and adult glucose per protein content. For the w^{1118} strain, the developmental diet was a consistently poor predictor of glucose per protein for both virgin and mated individuals (very weak model fits, Adj. $R^2 \approx 0.11$ -0.18). In contrast, for the SK flies, the developmental diet was a very strong predictor of glucose per protein in virgin females (strong model fit, Adj. $R^2 = 0.65$), but its predictive power was lower for mated females (weak-moderate model fit, Adj. $R^2 = 0.31$). The specific developmental diet that resulted in the highest concentration—intermediate yeast (approx. 10%) and low sugar (<5%)—was the same for both virgin and mated females. Mating had no effect on the resulting peak value, which remained consistent at ~ 65 μg per mg protein. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S45-46.

Figure S42. Glucose content (μg per fly) in 10-day-old females. For the w^{1118} strain, the developmental diet was a consistently poor predictor of adult glucose (very weak to weak fits, Adj. R^2 from 0.11 to 0.22). The developmental diet composition that resulted in the highest glucose was high yeast (>20%) for virgins to low yeast (<5%) for mated females. For the SK population, the developmental diet was a better predictor of adult glucose, particularly for virgins (good fit, Adj. $R^2 = 0.55$). The developmental diet composition that produced the highest glucose was intermediate yeast (10-15%) and low sugar (<5%) for both virgin and mated females. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S47-48.

Figure S43. Energy changes (J per mg protein) in w^{1118} flies as a function of sugar concentration in the developmental diet at each yeast level. Each panel shows one combination of yeast level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above

points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S44. Energy changes (J per mg protein) in SK flies as a function of sugar concentration in the developmental diet at each yeast level. Each panel shows one combination of yeast level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S45. Energy changes (J per mg protein) in w^{1118} flies as a function of yeast concentration in the developmental diet at each sugar level. Each panel shows one combination of sugar level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S46. Energy changes (J per mg protein) in SK flies as a function of yeast concentration in the developmental diet at each sugar level. Each panel shows one combination of sugar level, sex, and mating status. Points are individual samples; lines show the quadratic fit. Shaded ribbons are bootstrapped 95% confidence bands (nonparametric, $n = 1000$). Letters above points denote pairwise Welch t-tests with Holm correction per set of comparisons; groups sharing a letter do not differ at $\alpha = 0.05$.

Figure S47. Effect of developmental diet on changes in energy reserves during early adult life in males. Surface plots show the change in total energy content (J per fly) between eclosion and 10 days of age, as a function of yeast and sugar concentrations in the developmental diet. Each surface represents a second-order polynomial fit based on group means. Model fit was moderate to strong, with adjusted R^2 values of 0.62 (w^{1118} virgins), 0.45 (SK virgins), 0.57 (w^{1118} mated), and 0.52 (SK mated). For global statistical analyses, see Tables S54-55.

Figure S48. Effect of developmental diet on changes in energy reserves during early adult life in females. Surface plots show the change in total energy content (J per fly) between eclosion and 10 days of age, as a function of yeast and sugar concentrations in the developmental diet. Each surface represents a second-order polynomial fit based on group means. Model fit was moderate to strong, with adjusted R^2 values of 0.41 (w^{1118} virgins), 0.65 (SK virgins), 0.37 (w^{1118} mated), and 0.74 (SK mated). For global statistical analyses, see Tables S54-55.

Figure S49. Energy changes (J per mg protein) in males — calculated as the difference between energy content in 10-day-old flies and at eclosion. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S51-53.

Figure S50. Energy changes (J per fly) in males — calculated as the difference between energy content in 10-day-old flies and at eclosion. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S54-55.

Figure S51. Energy changes (J per mg protein) in females — calculated as the difference between energy content in 10-day-old flies and at eclosion. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S51-53.

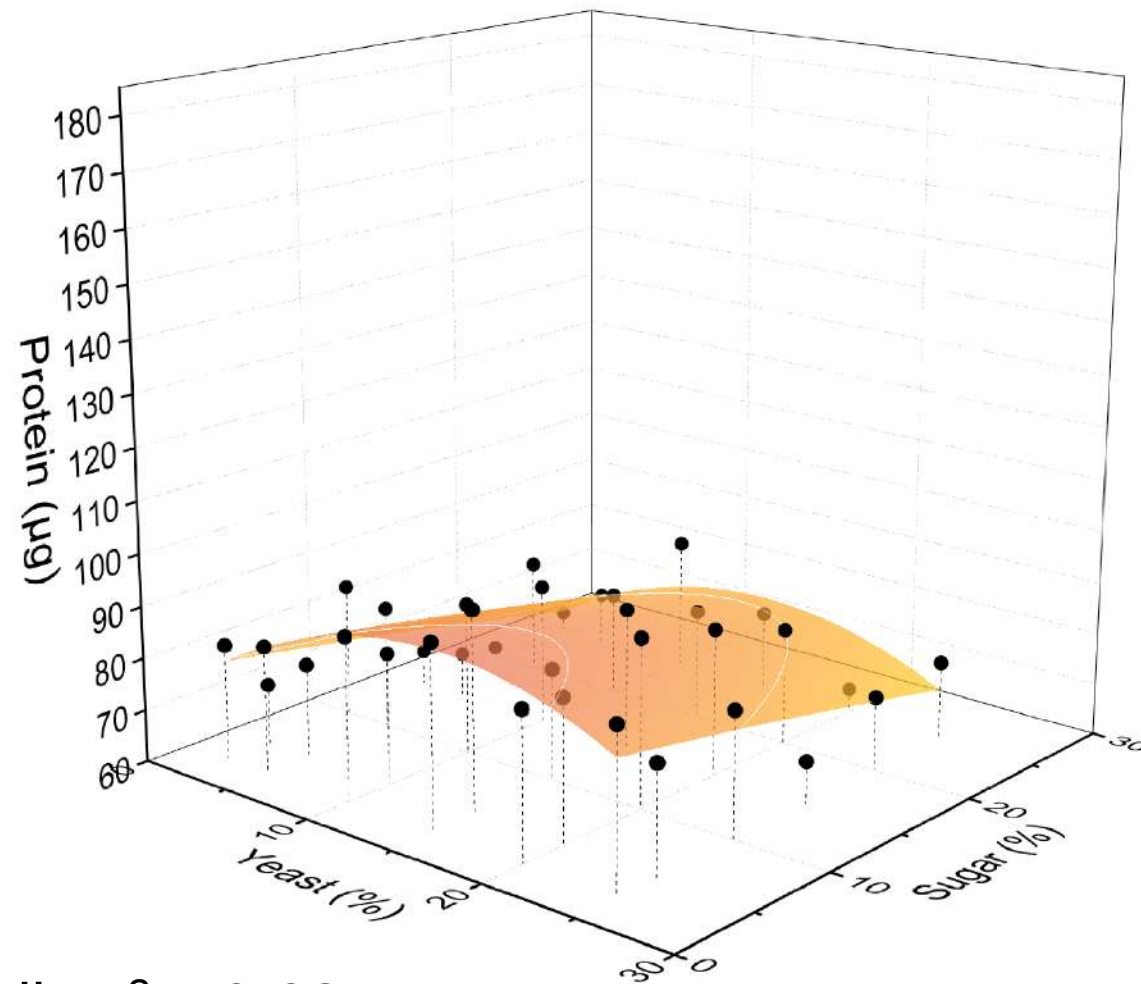
Figure S52. Energy changes (J per fly) in females — calculated as the difference between energy content in 10-day-old flies and at eclosion. Dots represent mean values for each diet combination. For statistical analyses combining all groups, see Tables S54-55.

Figure S1

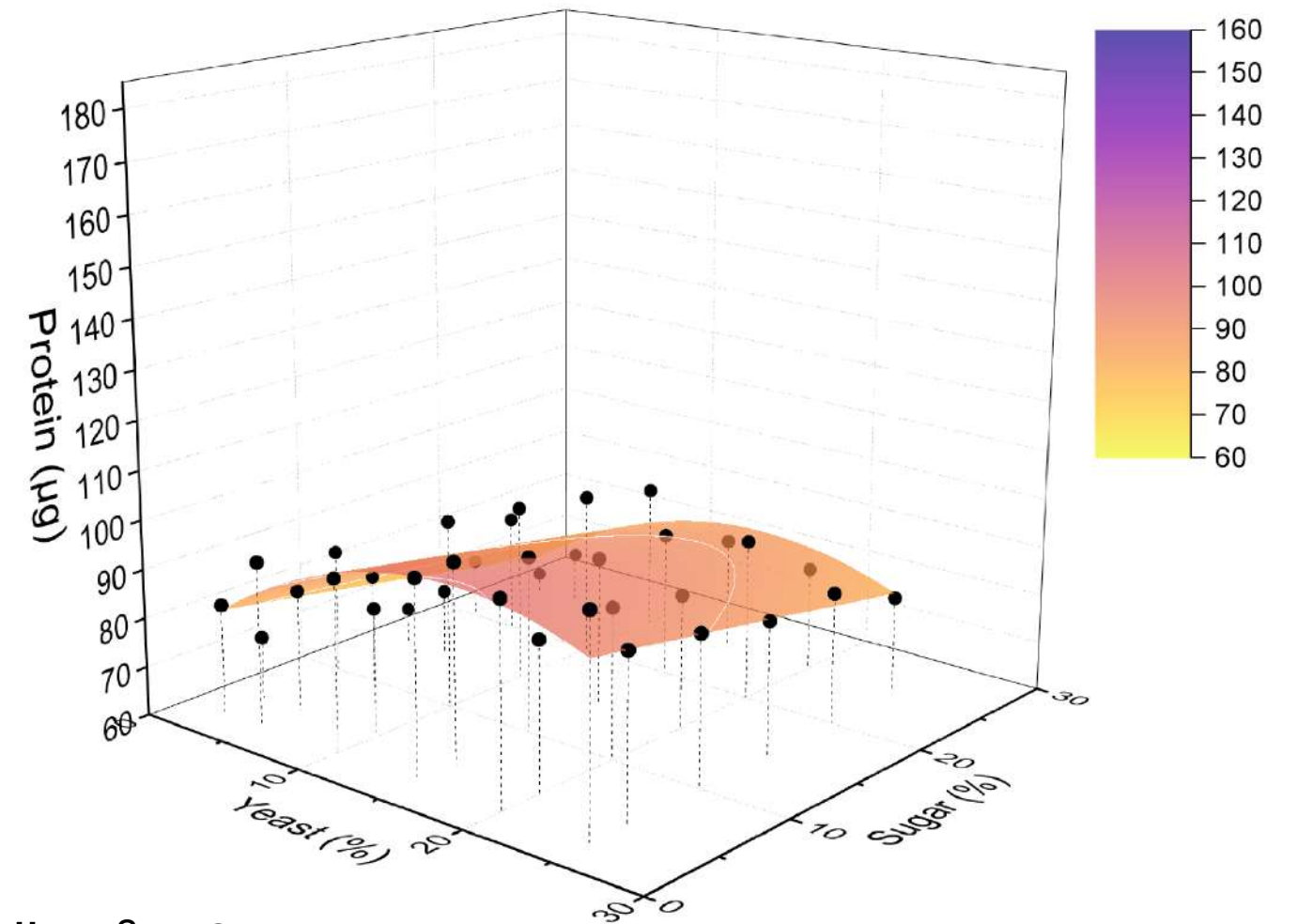
w^{1118}

SK

Males

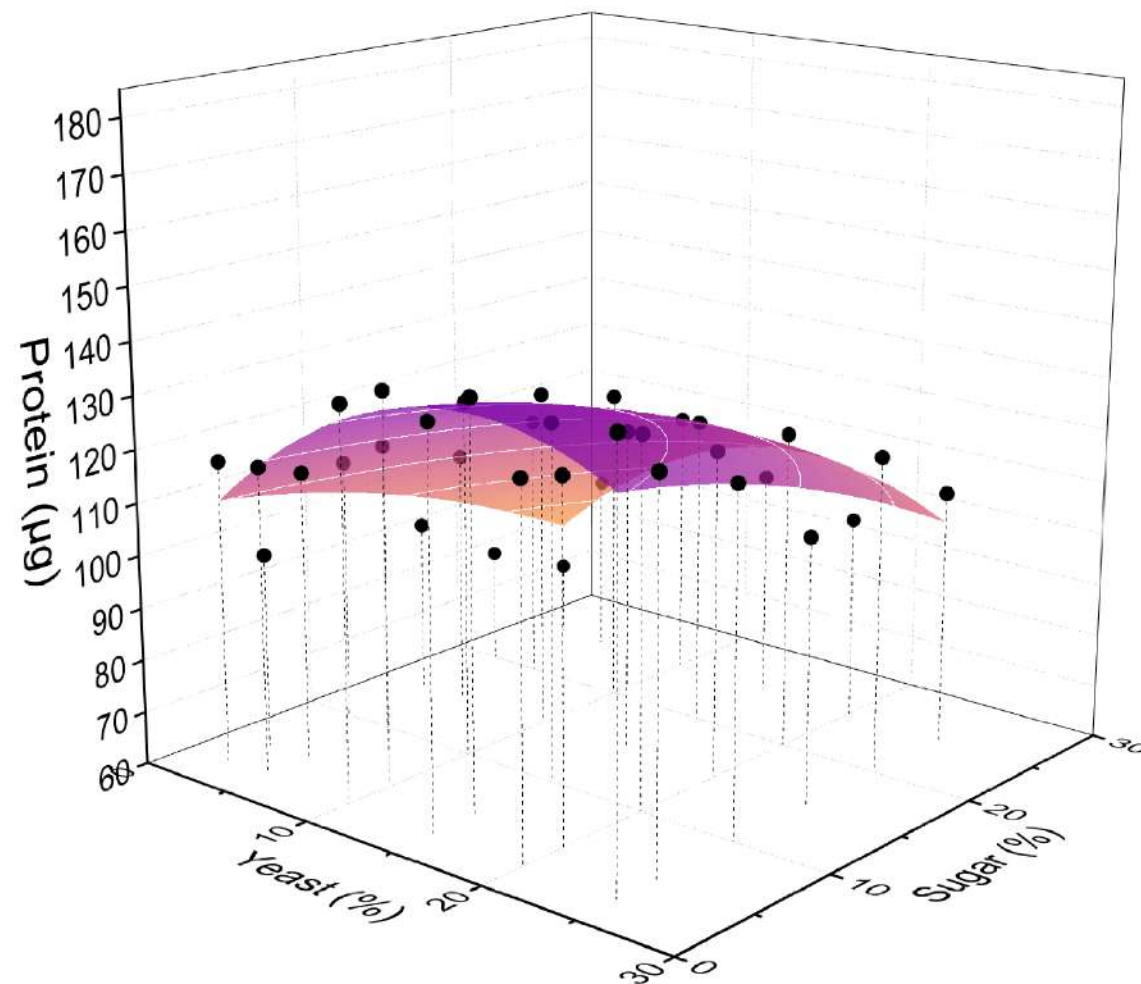


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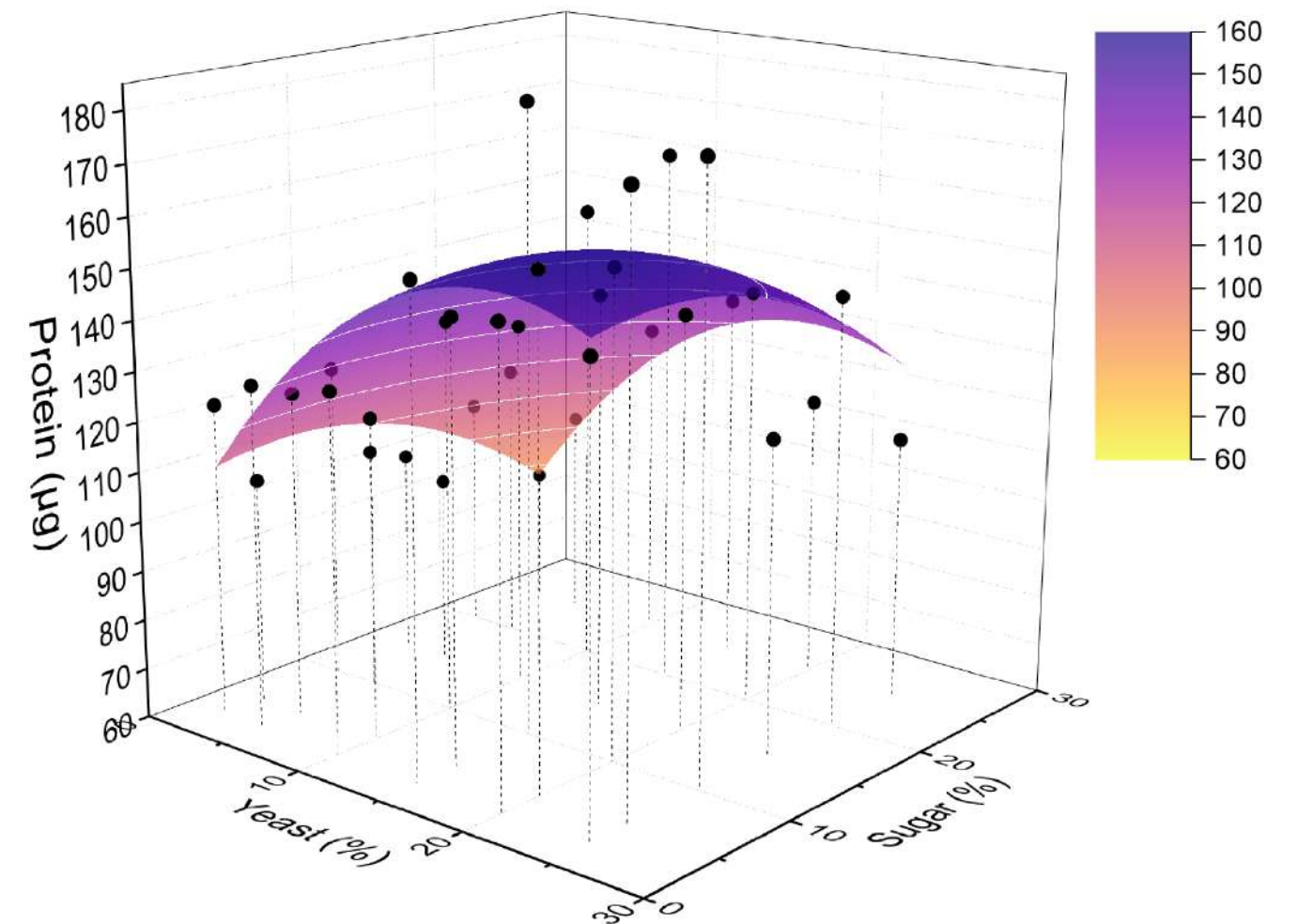


Adj. $R^2 = 0.71$

Females



Adj. $R^2 = 0.81$



Adj. $R^2 = 0.63$

w^{1118}

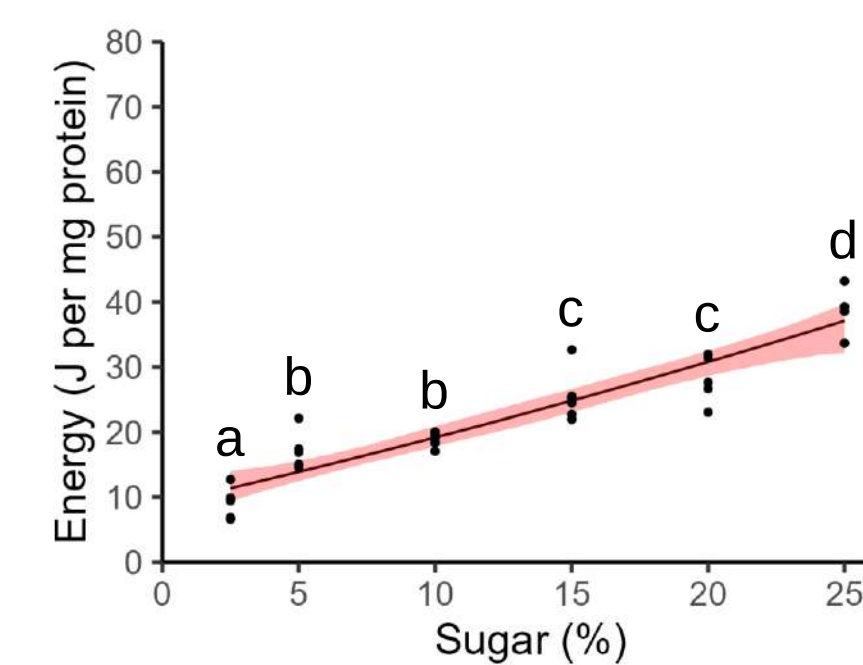
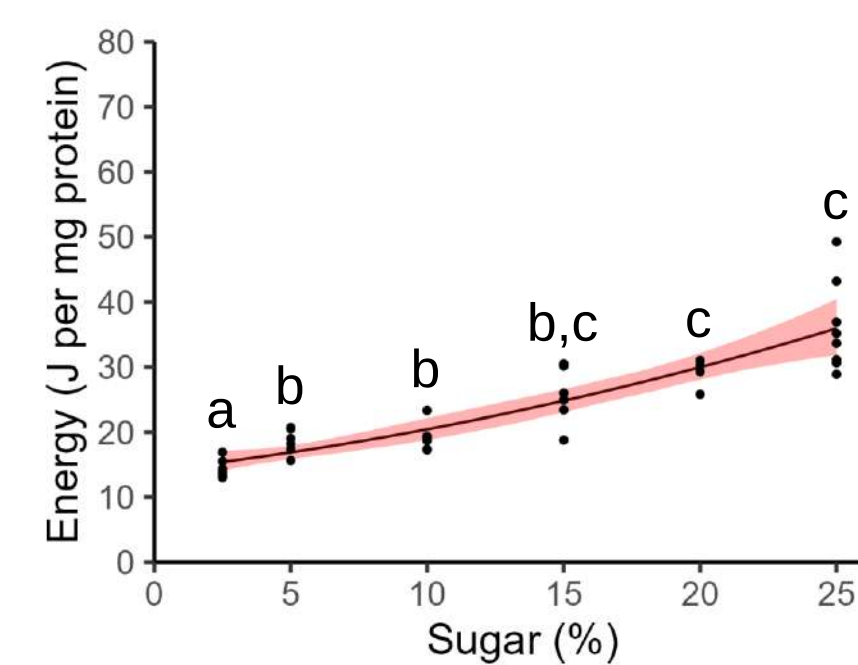
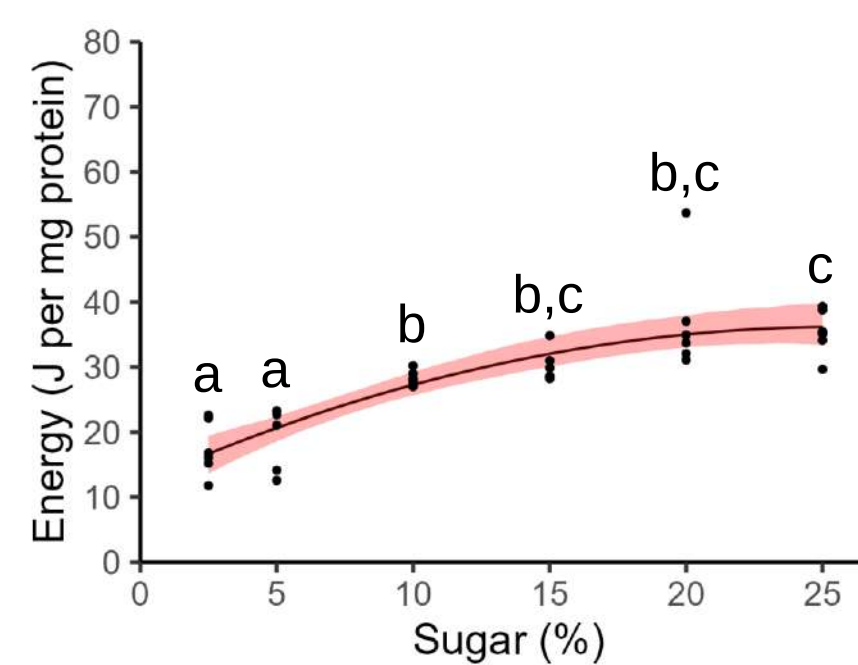
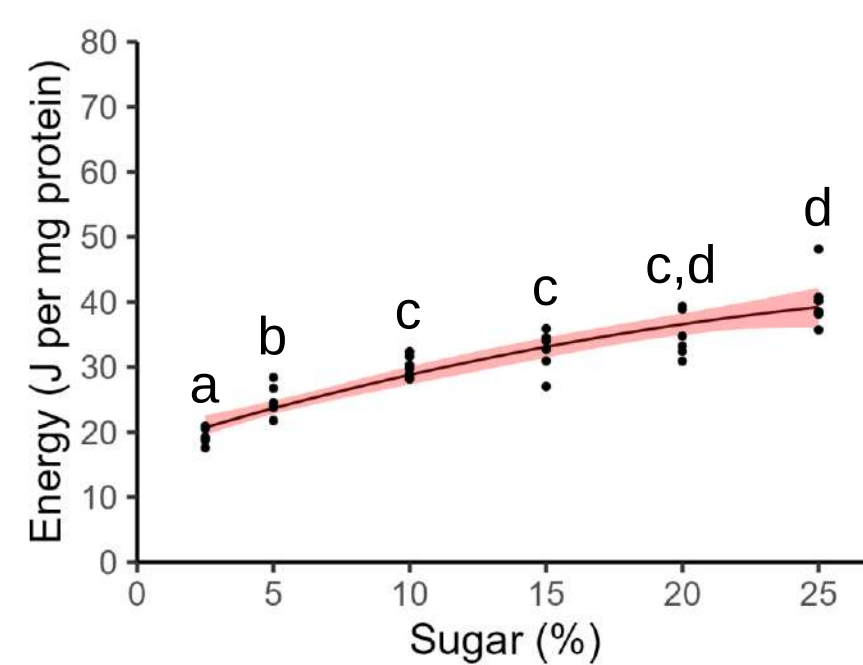
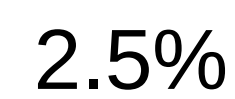
SK

Males

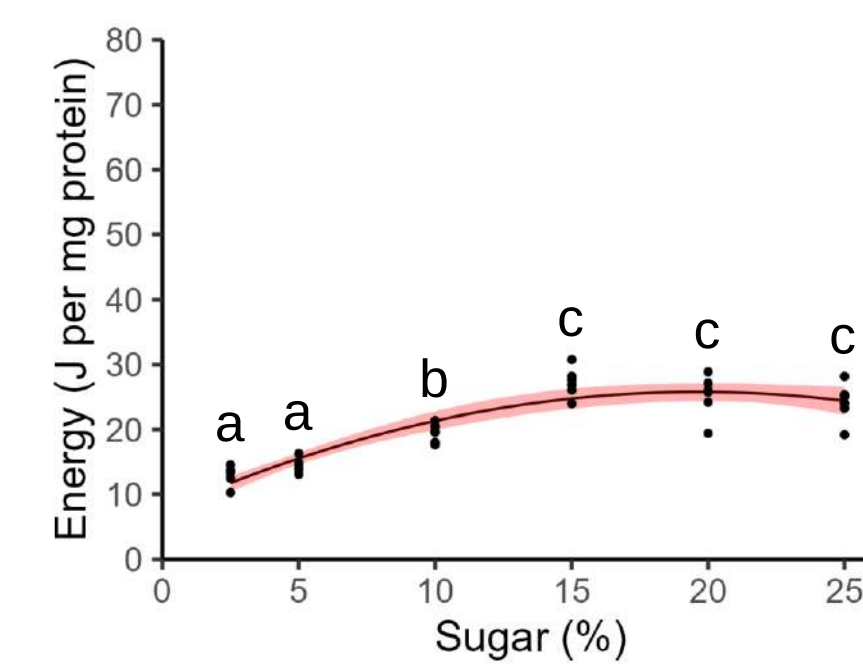
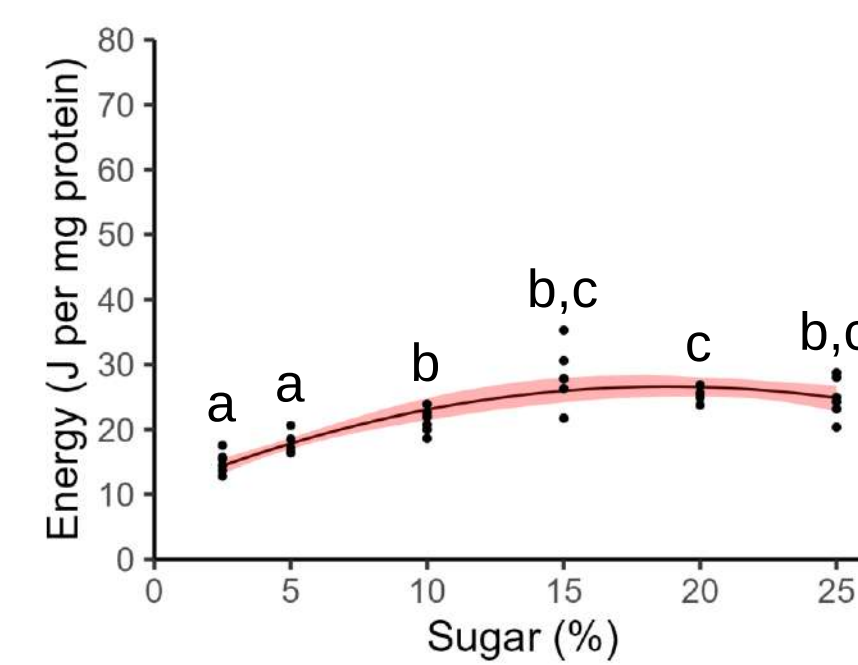
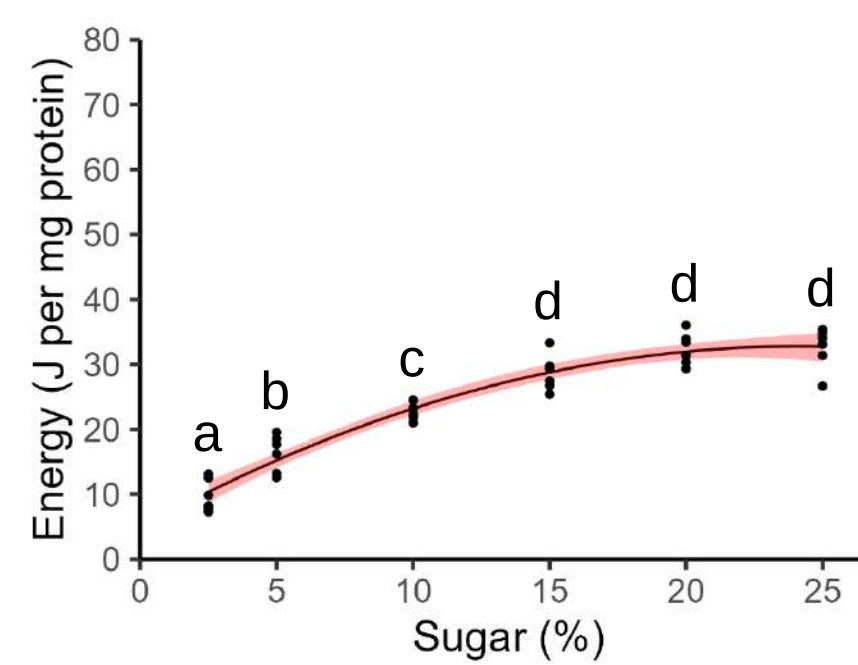
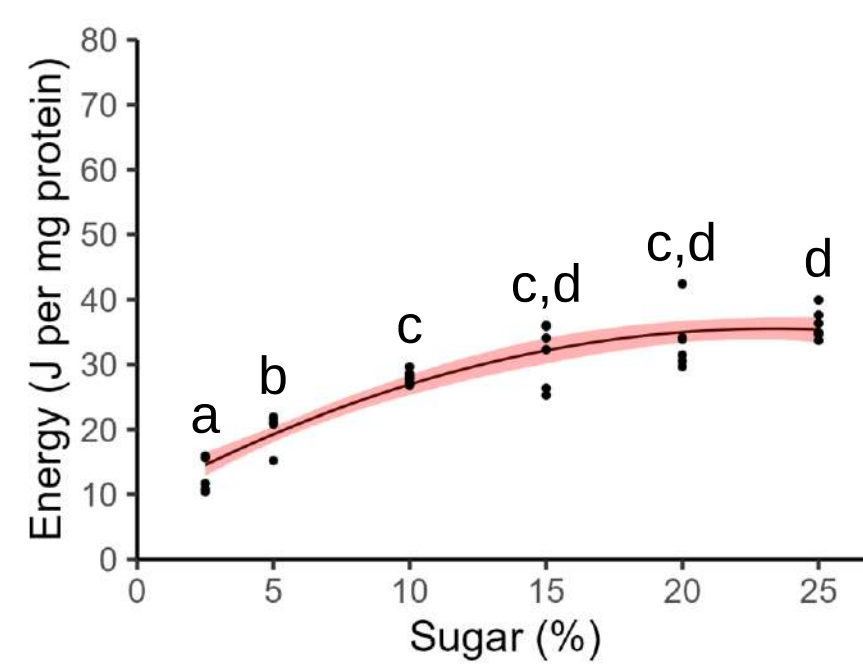
Females

Males

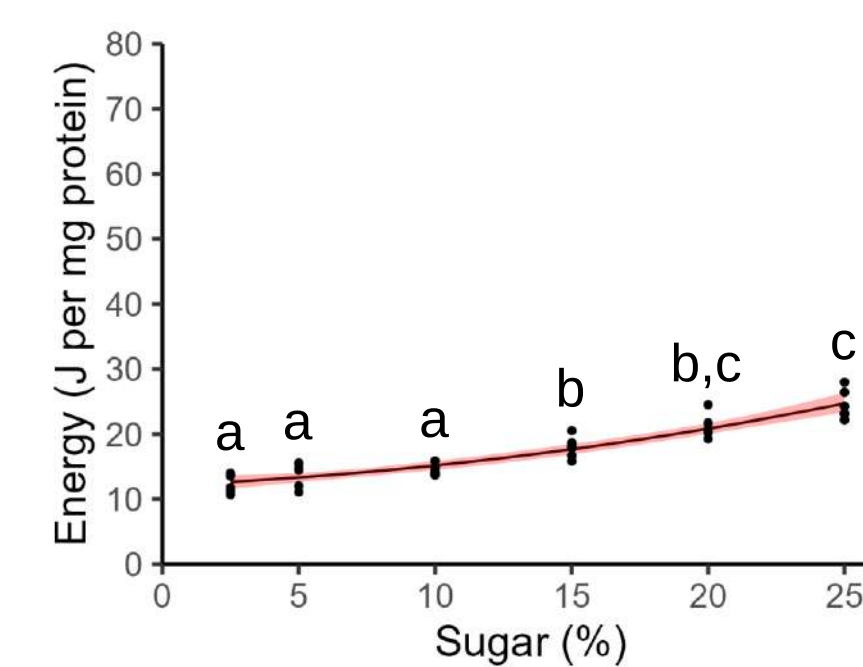
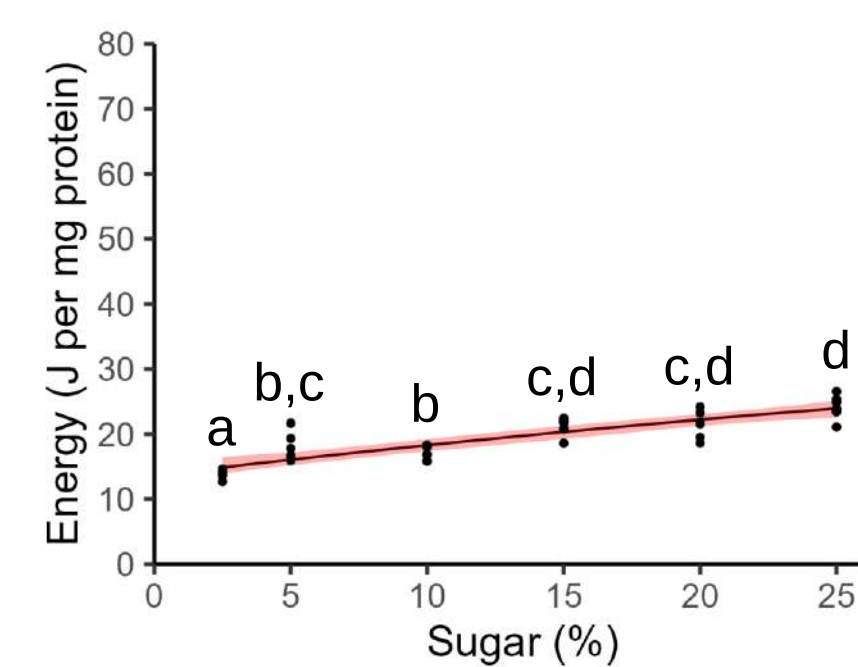
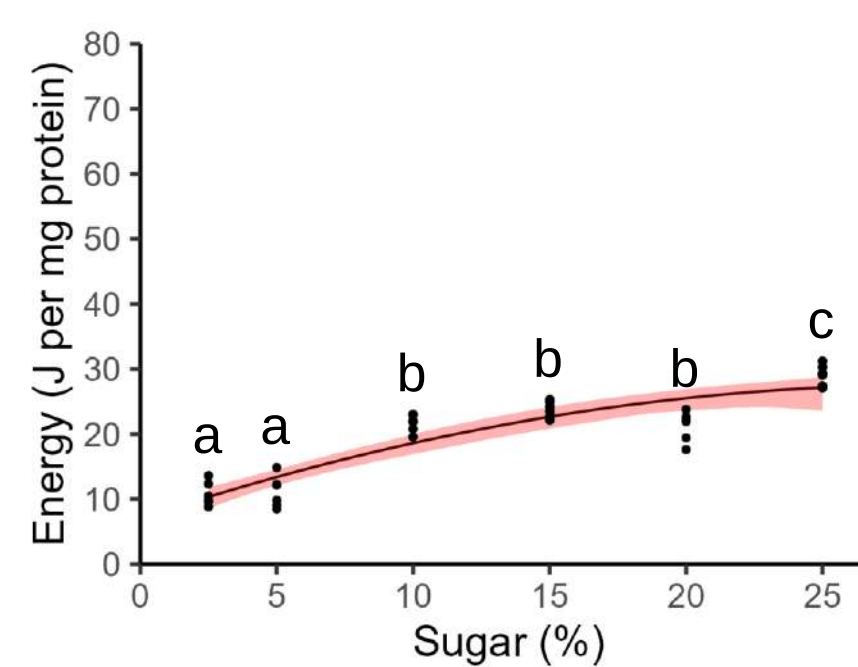
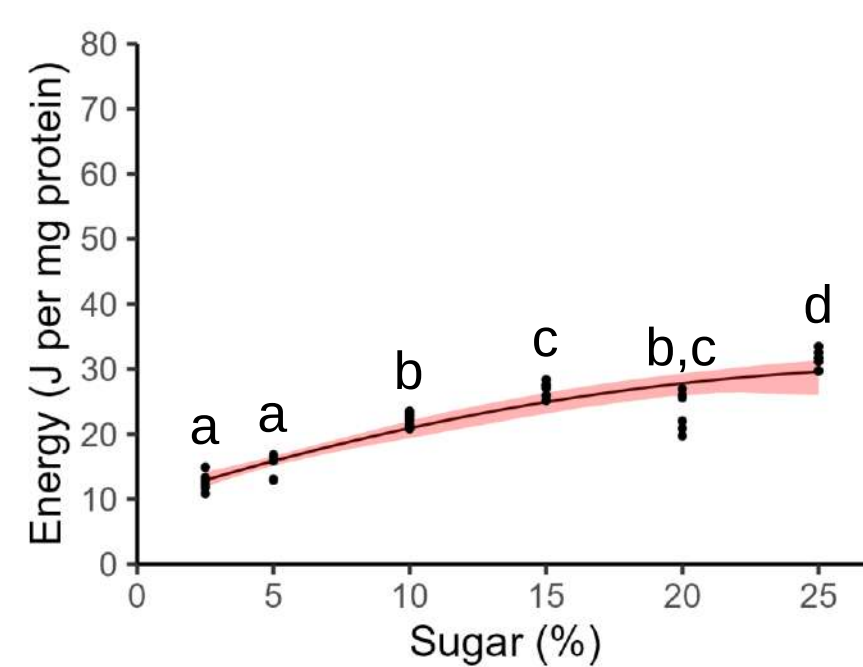
Females



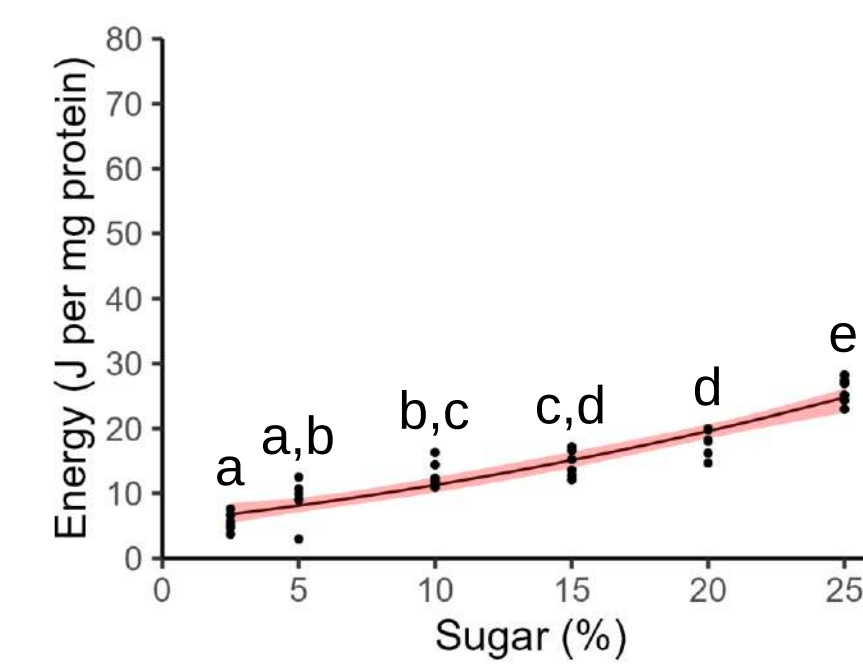
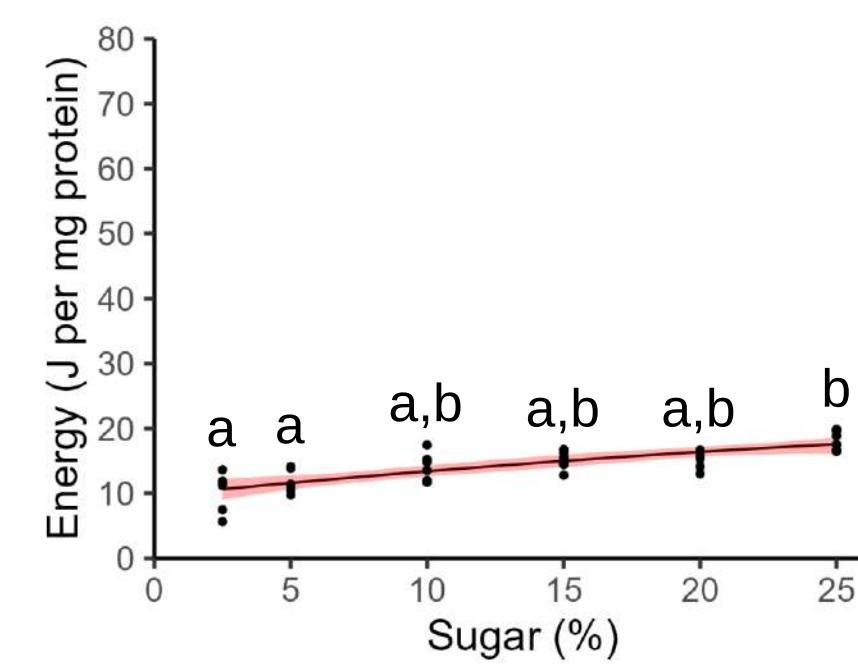
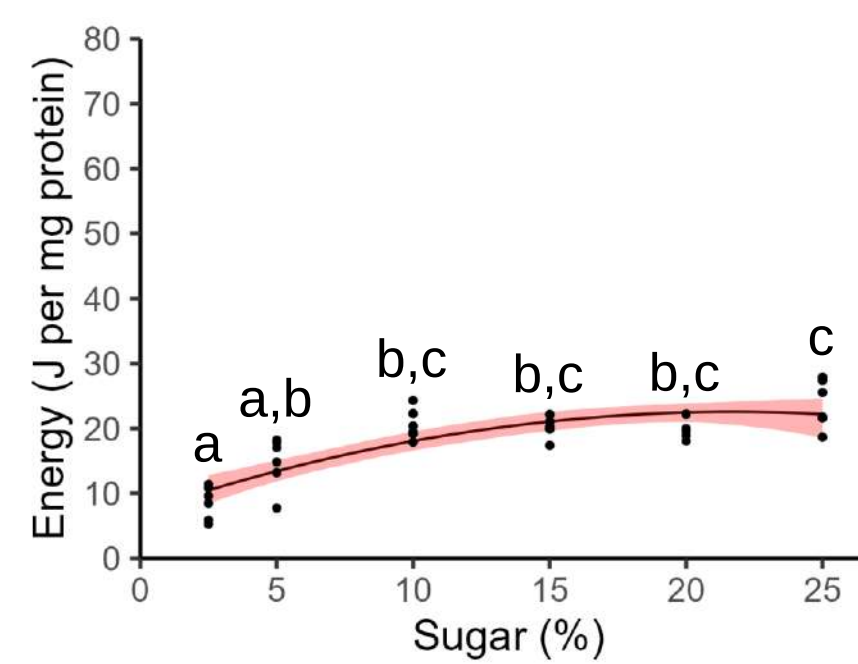
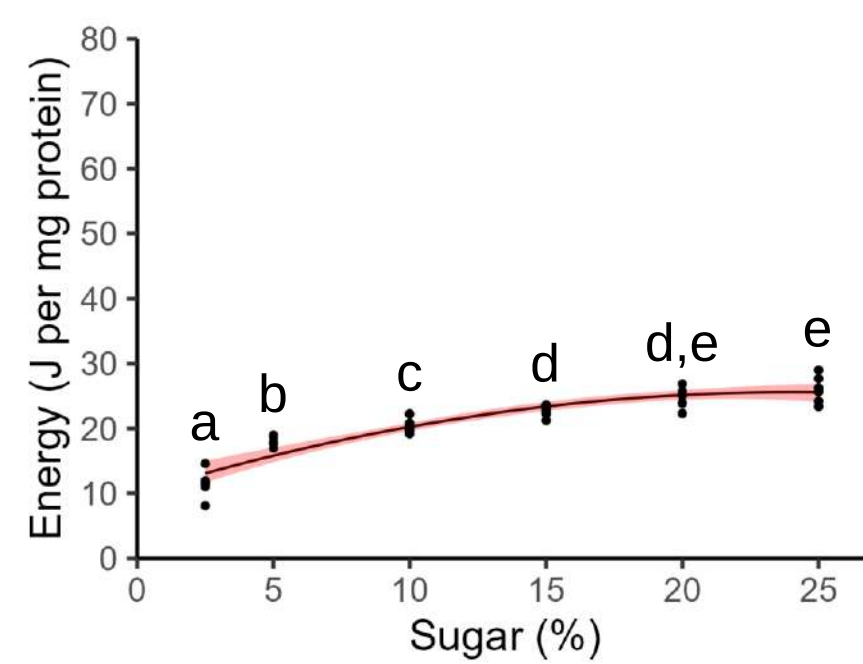
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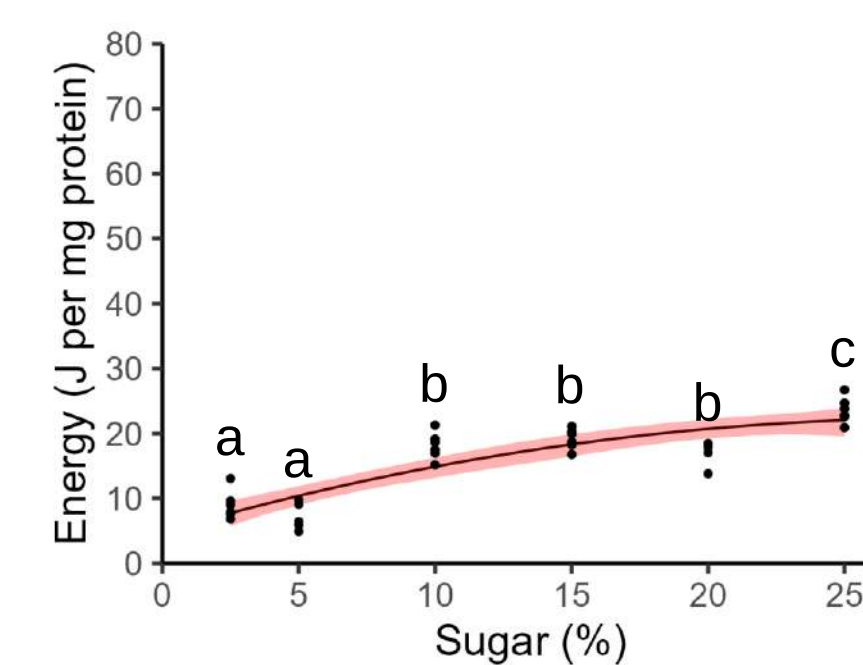
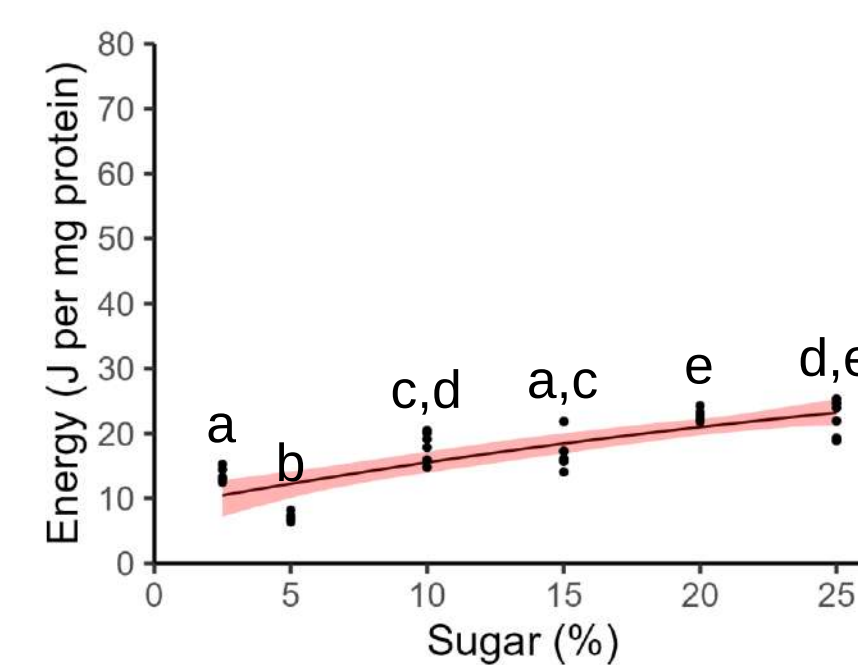
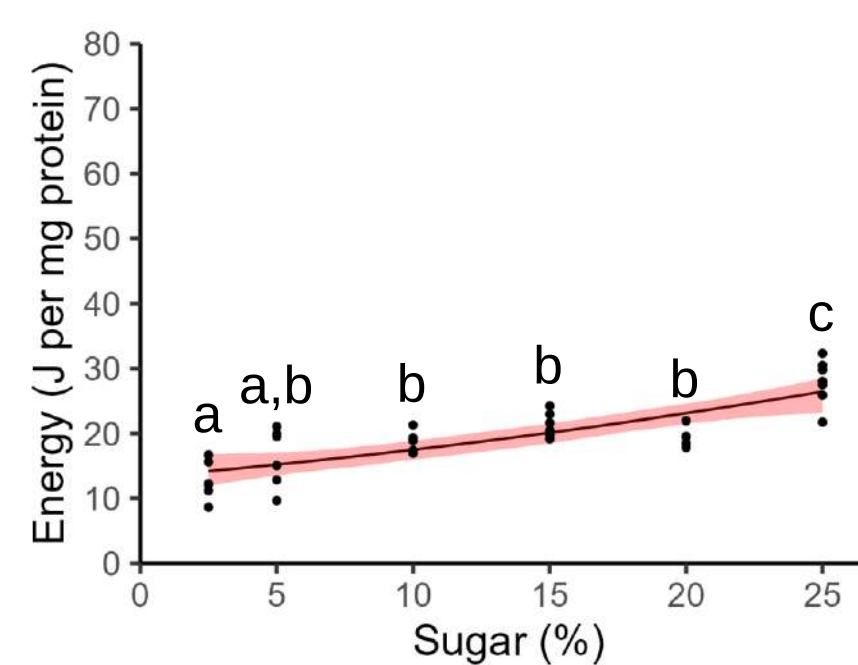
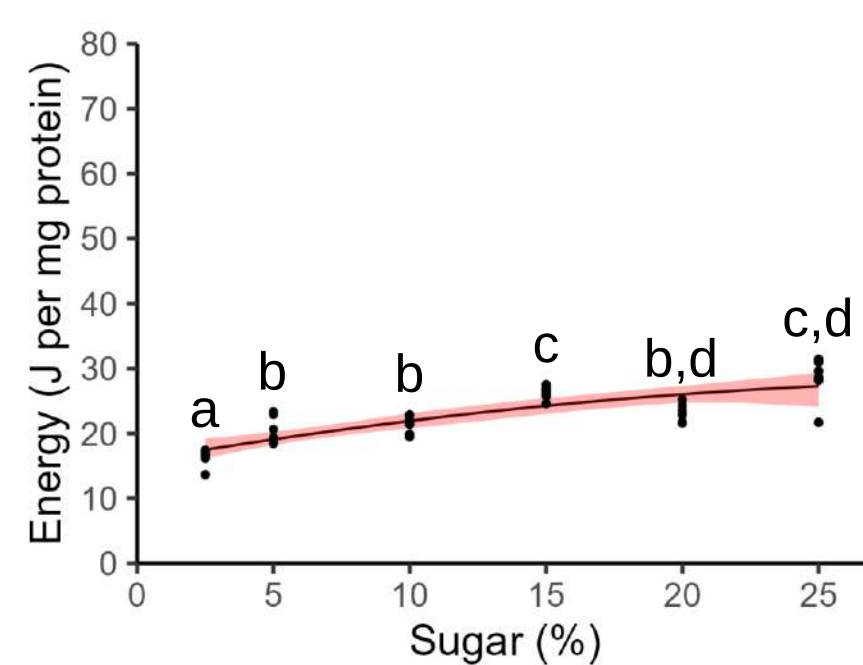
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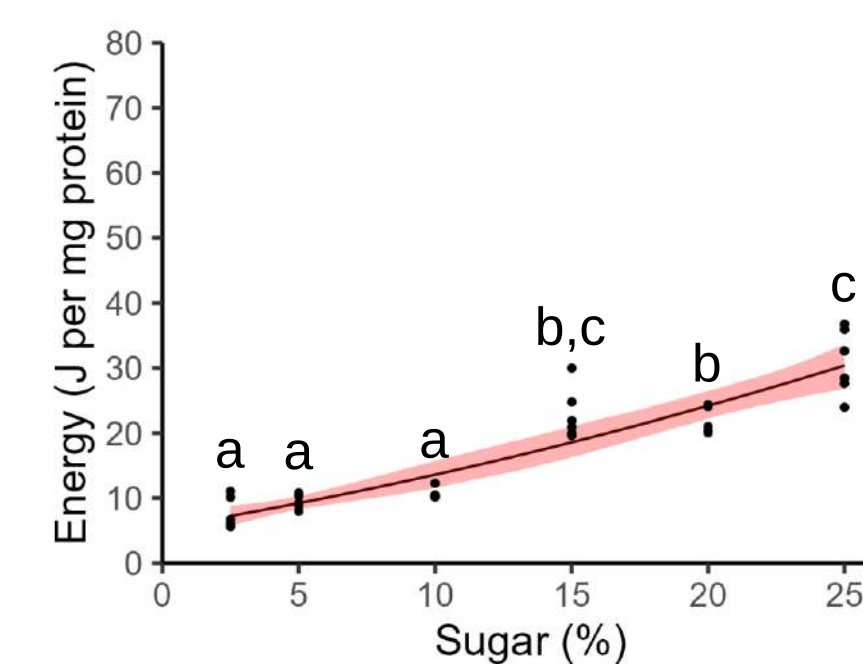
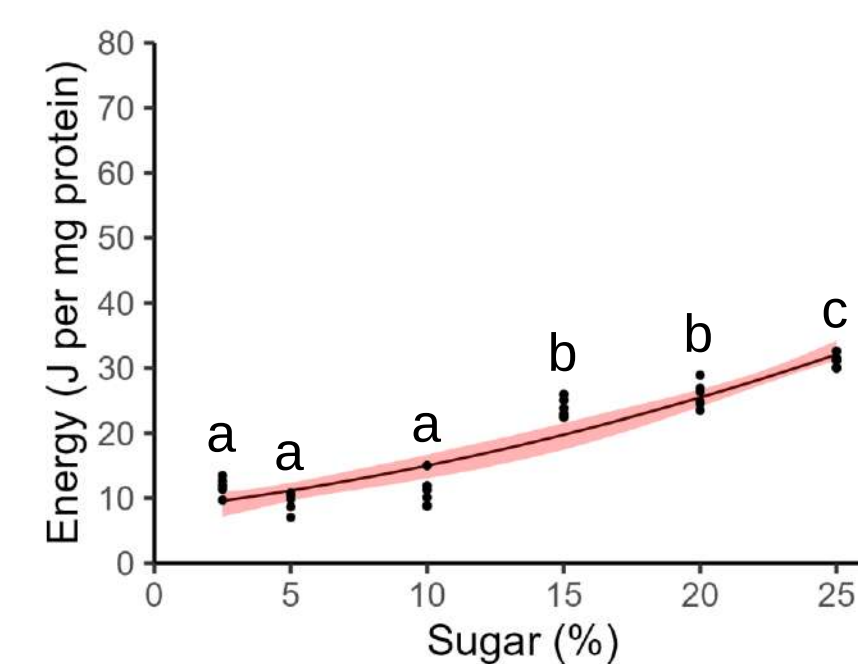
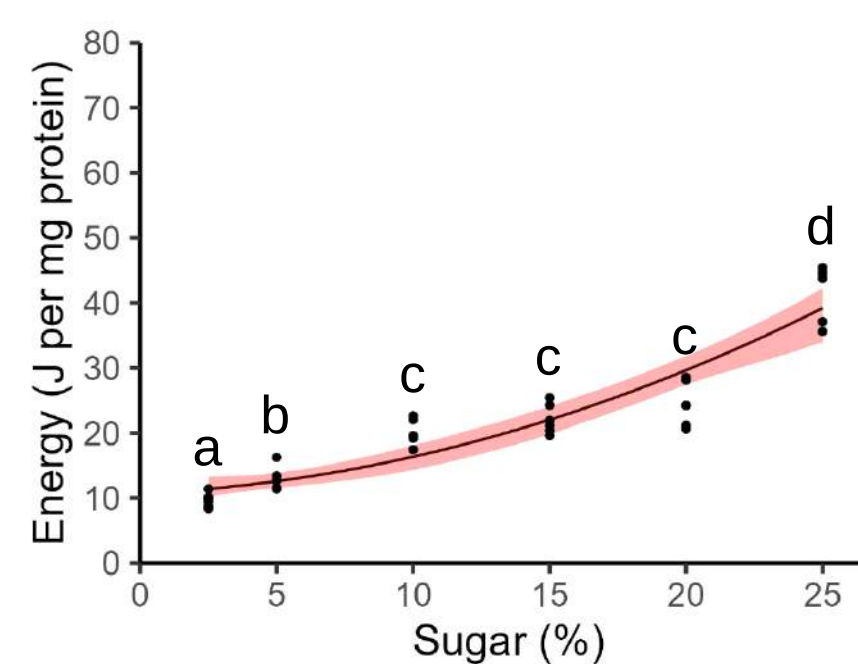
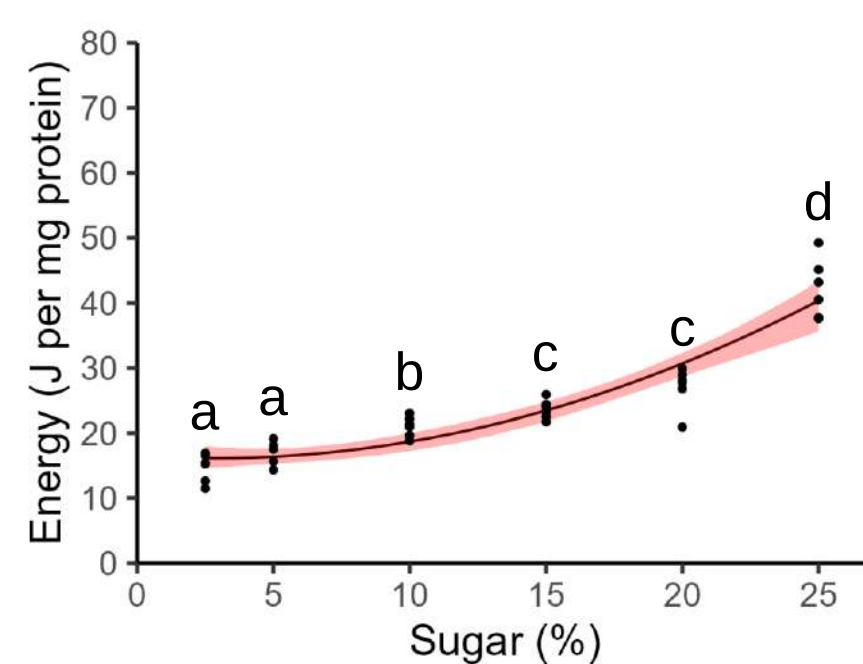


Figure S3.

w^{1118}

SK

SUGAR

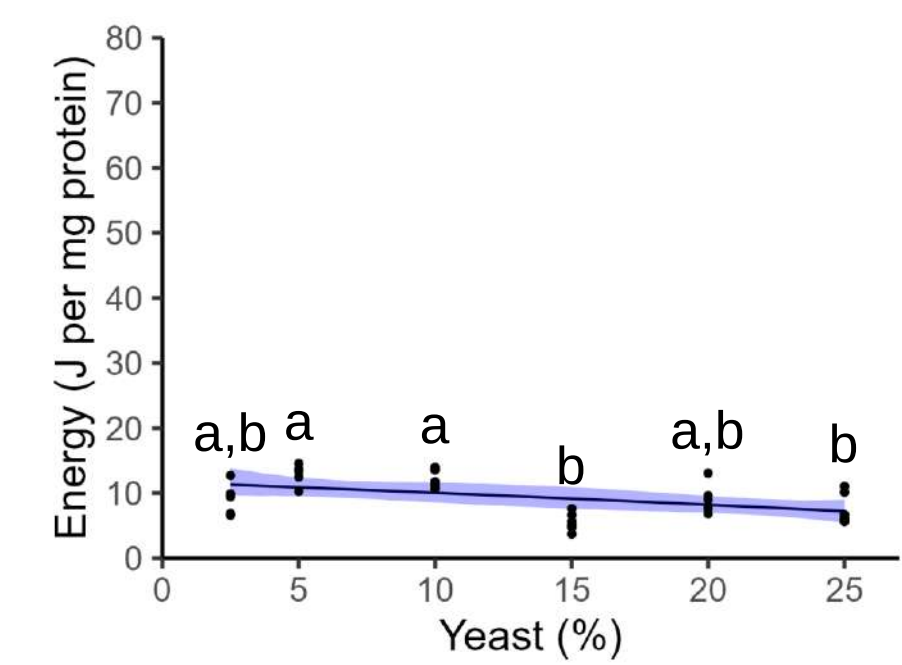
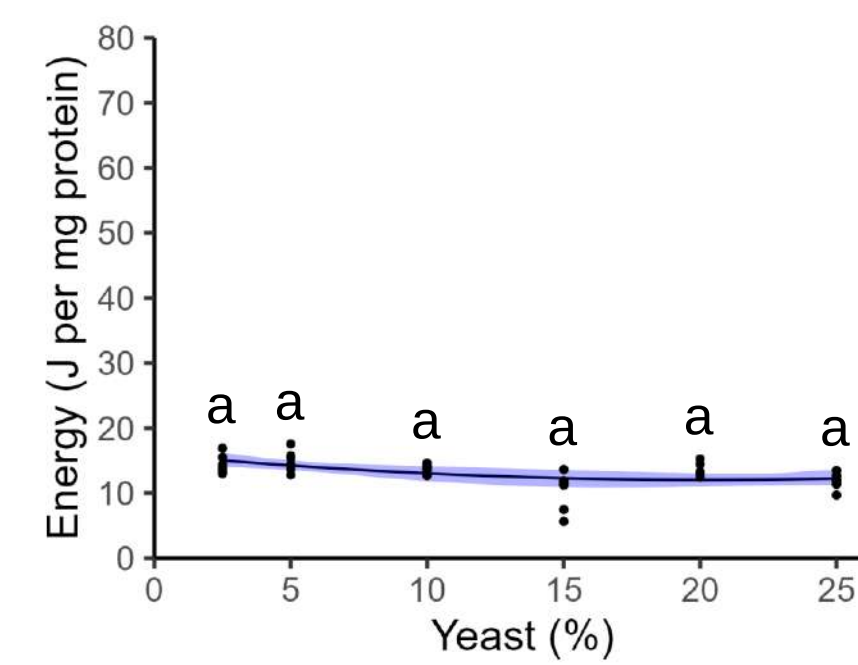
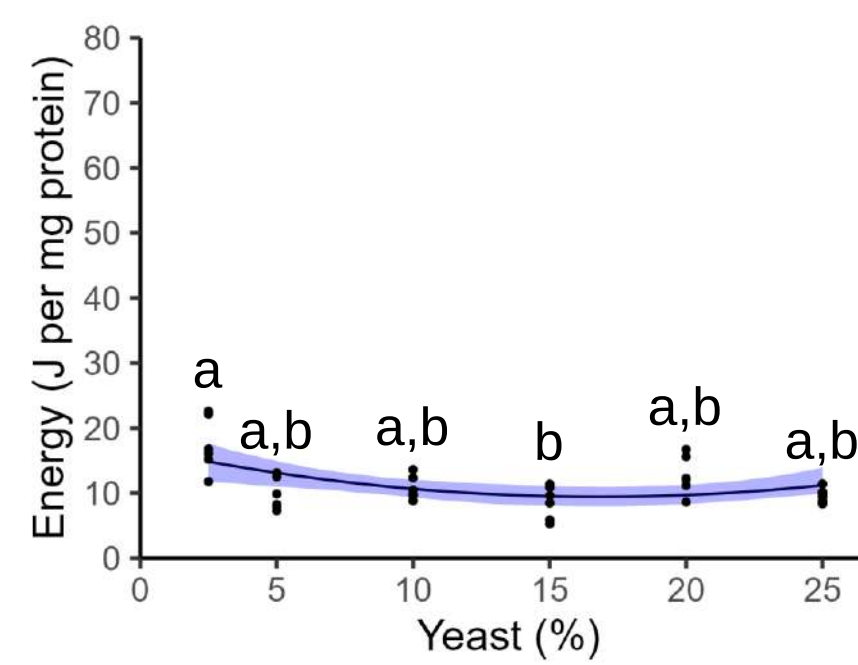
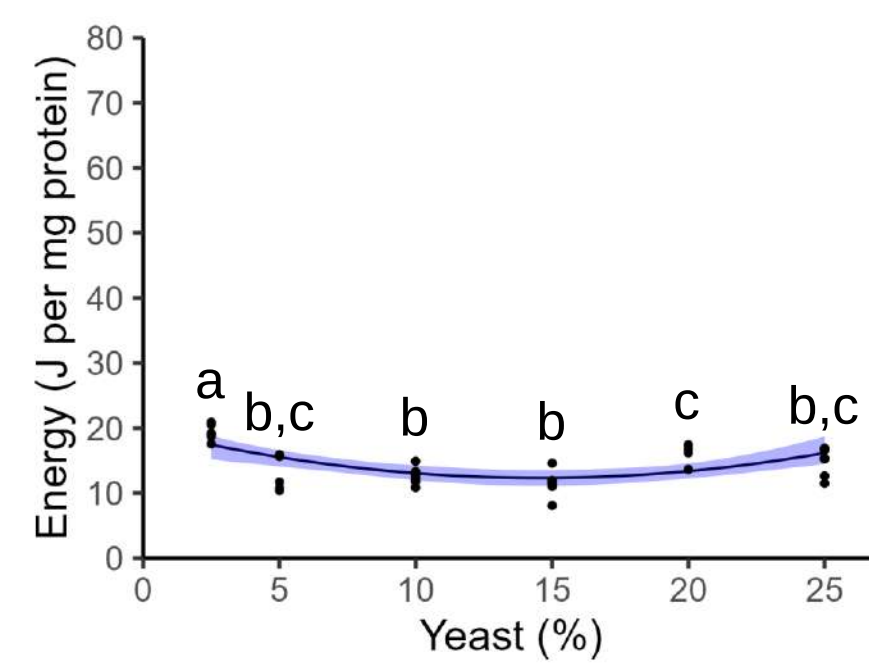
Males

Females

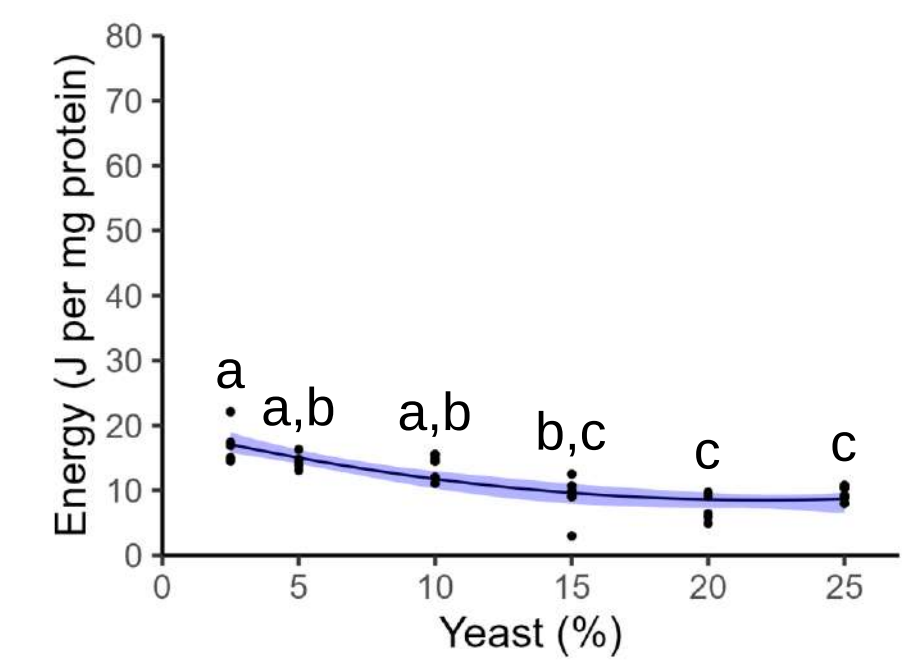
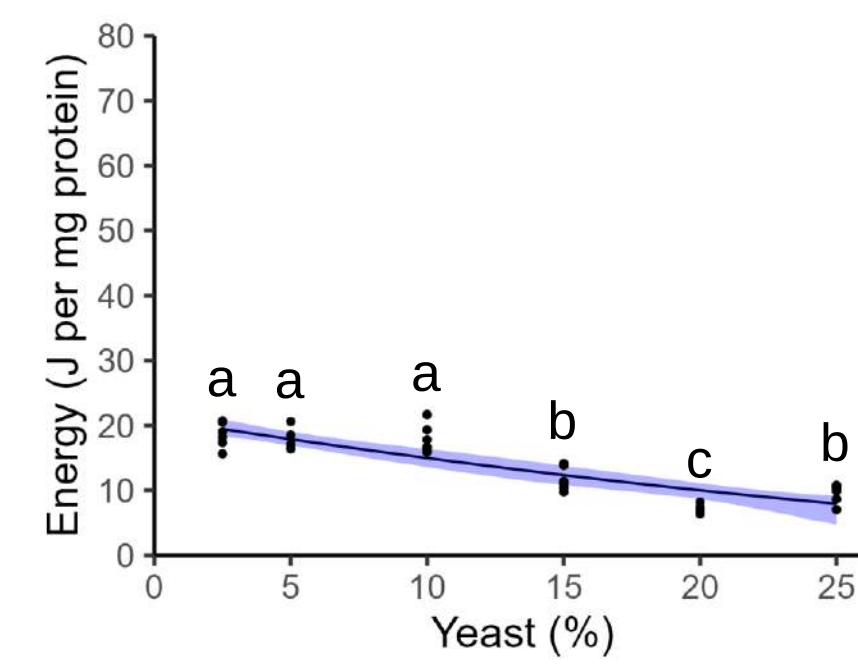
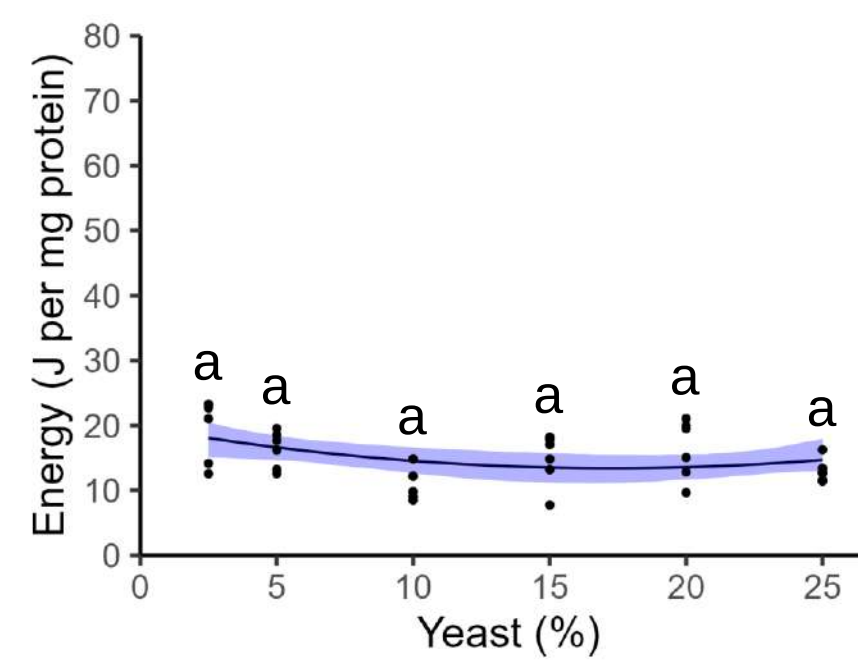
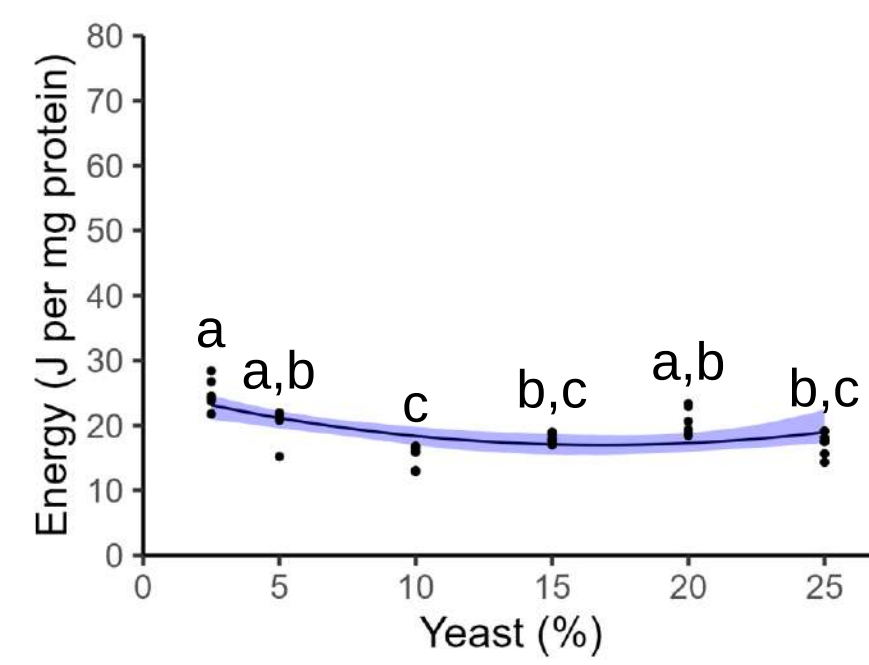
Males

Females

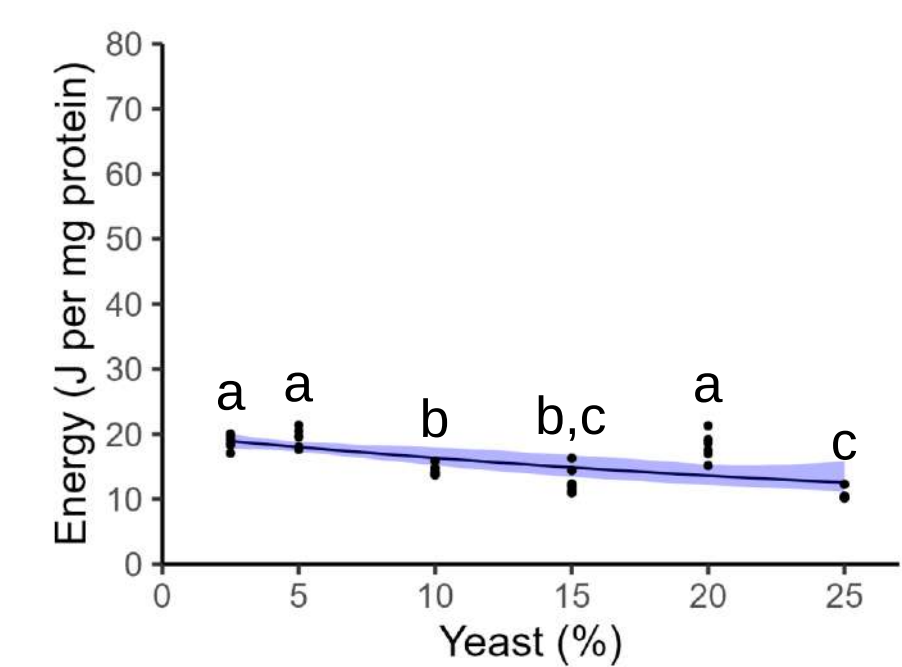
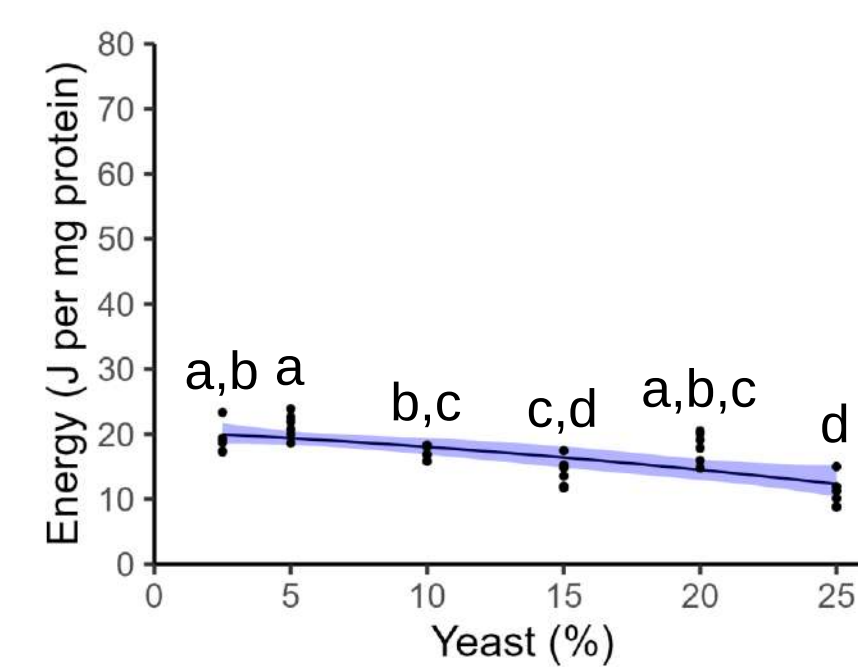
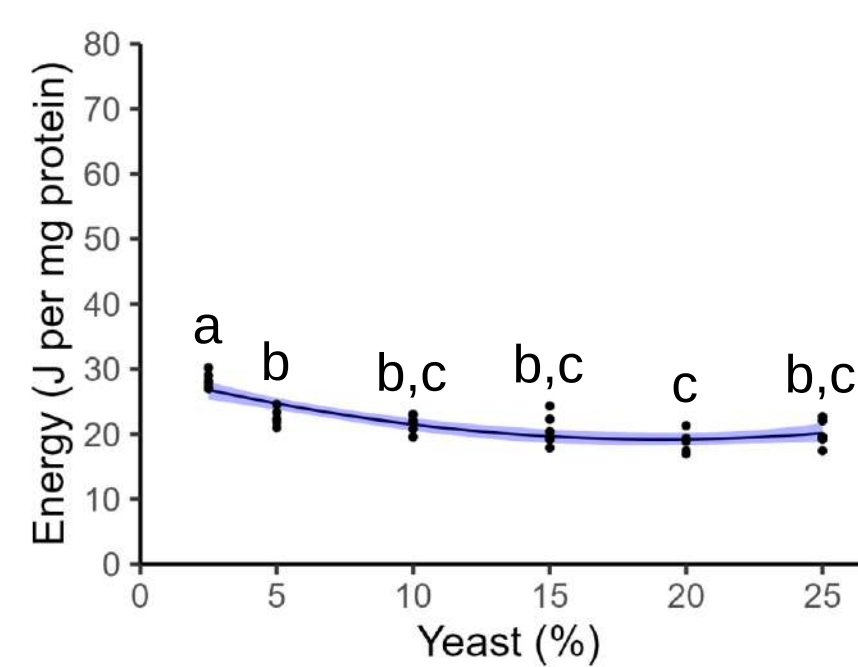
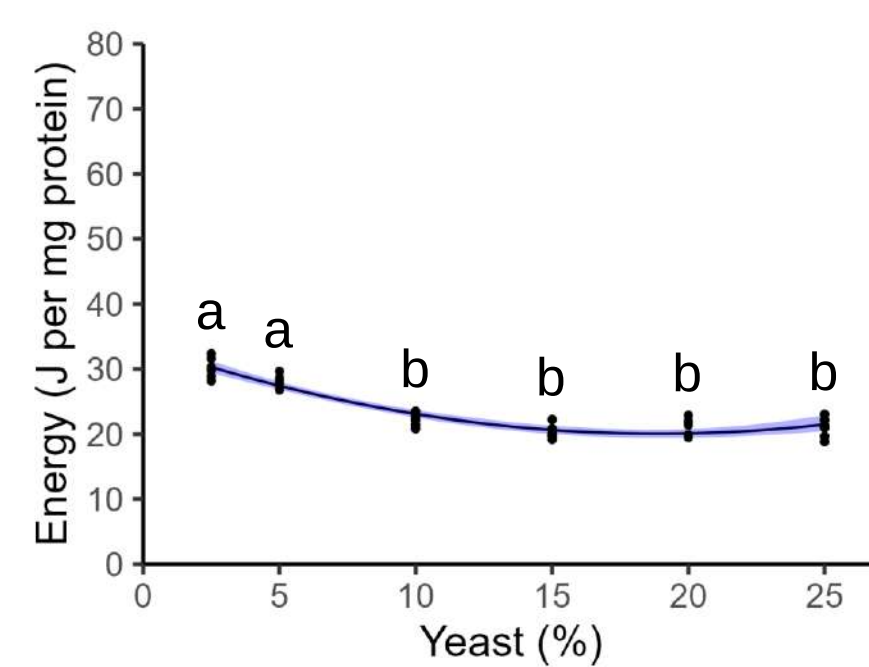
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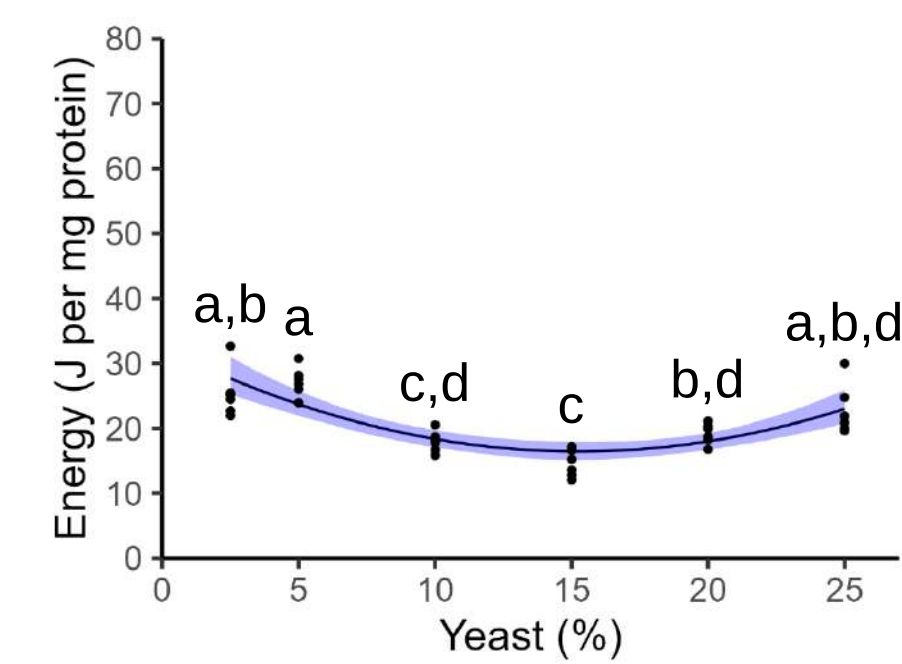
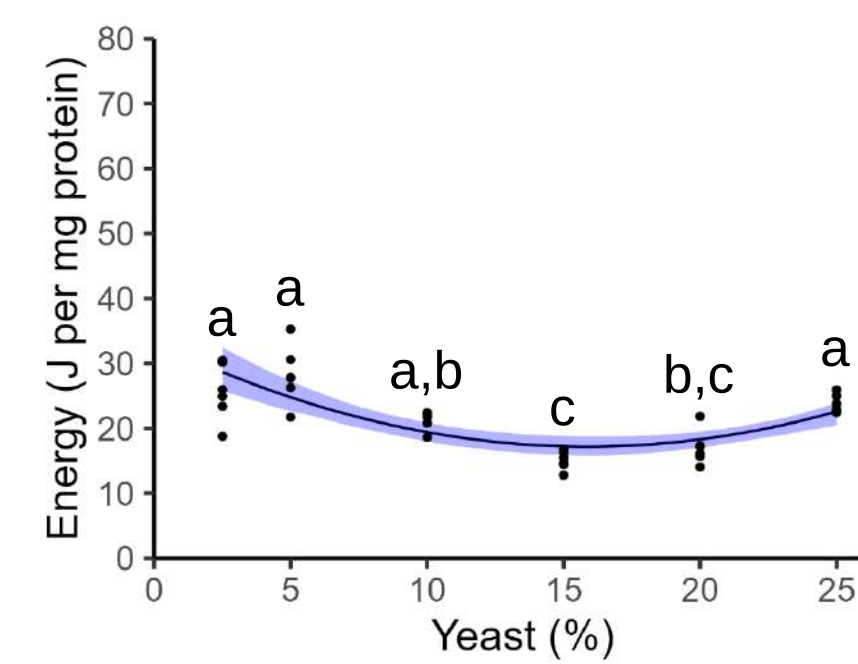
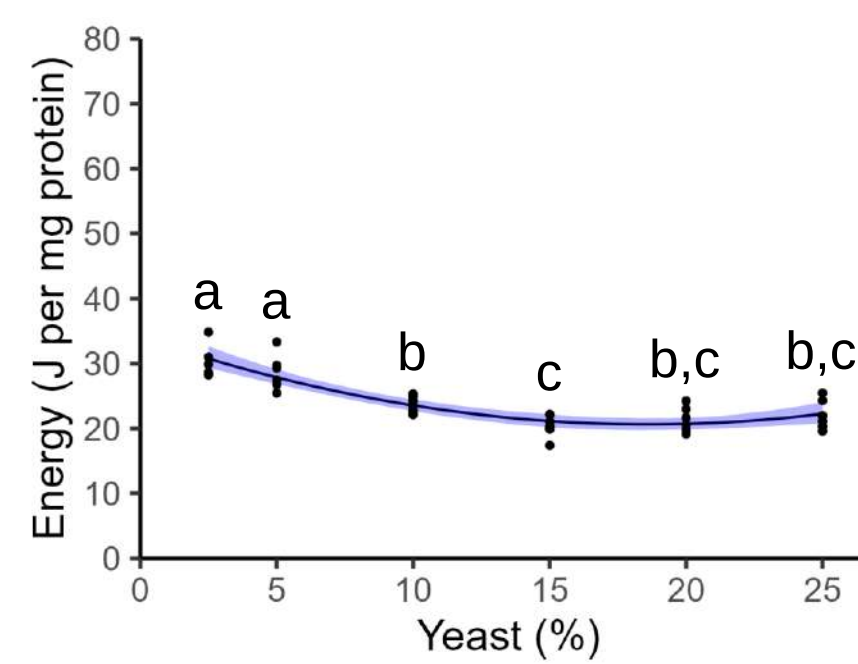
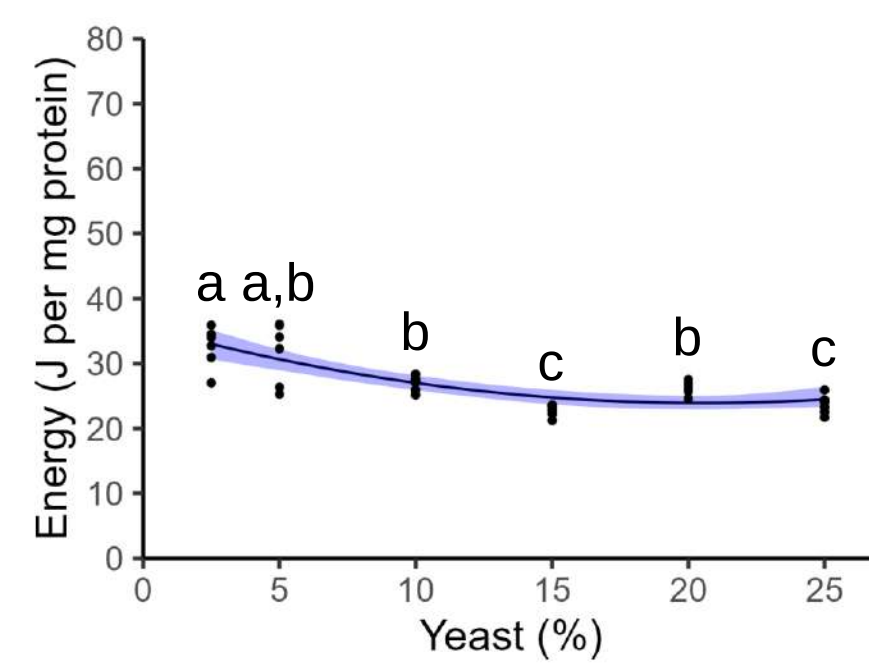
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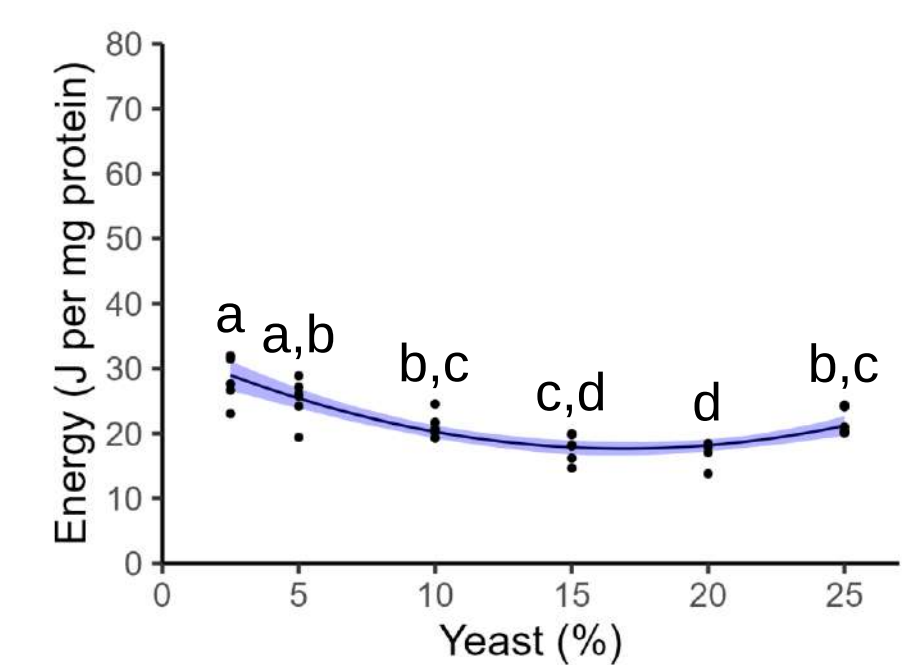
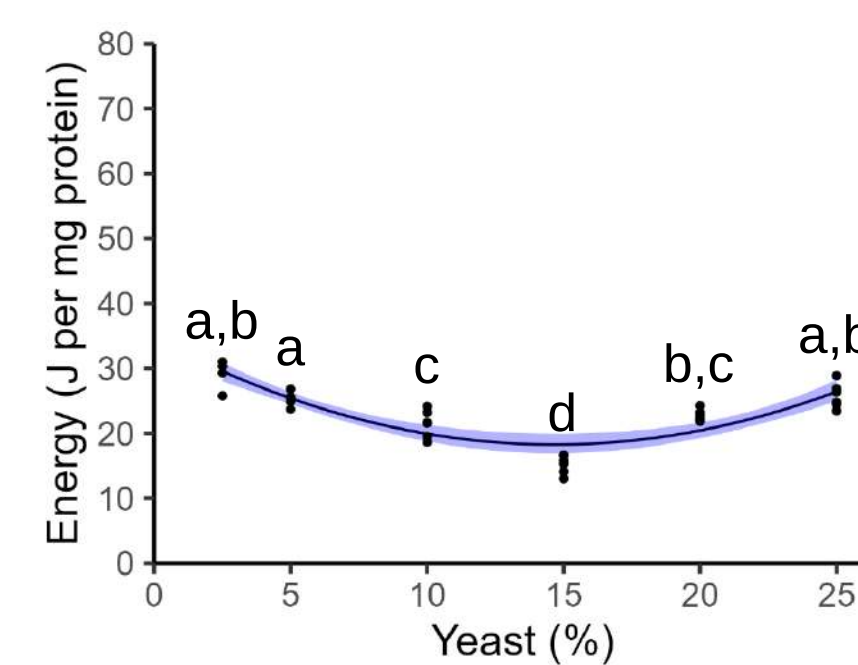
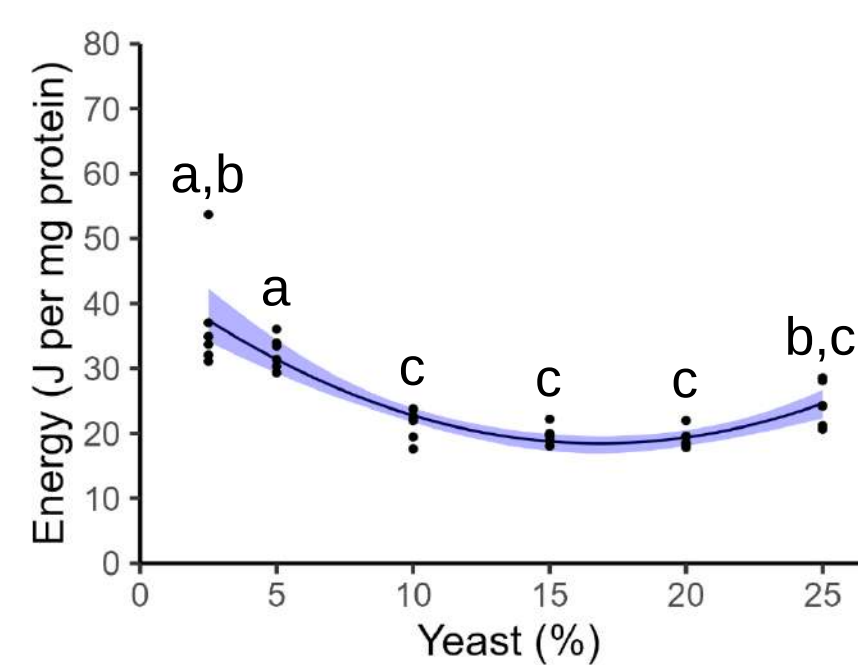
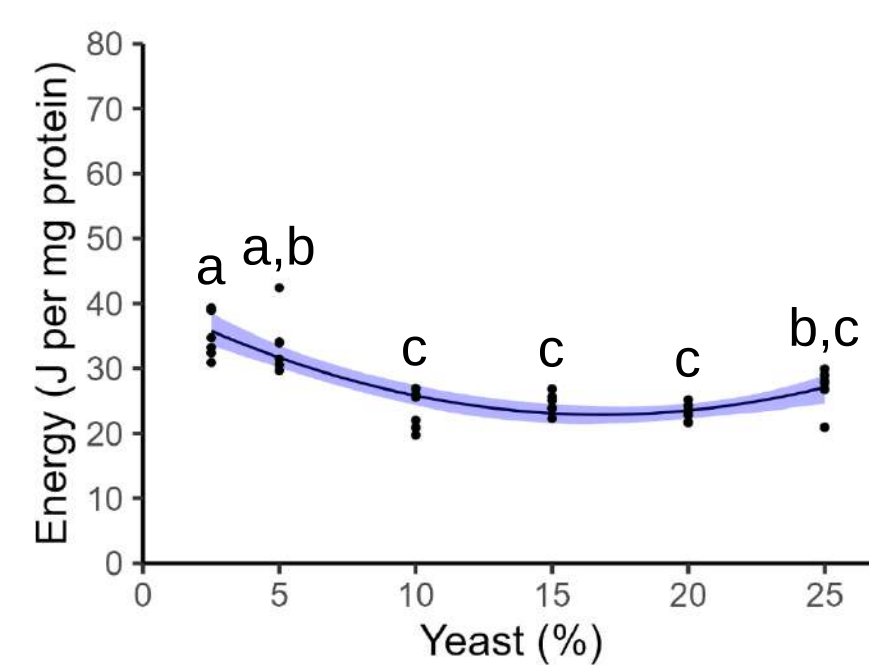
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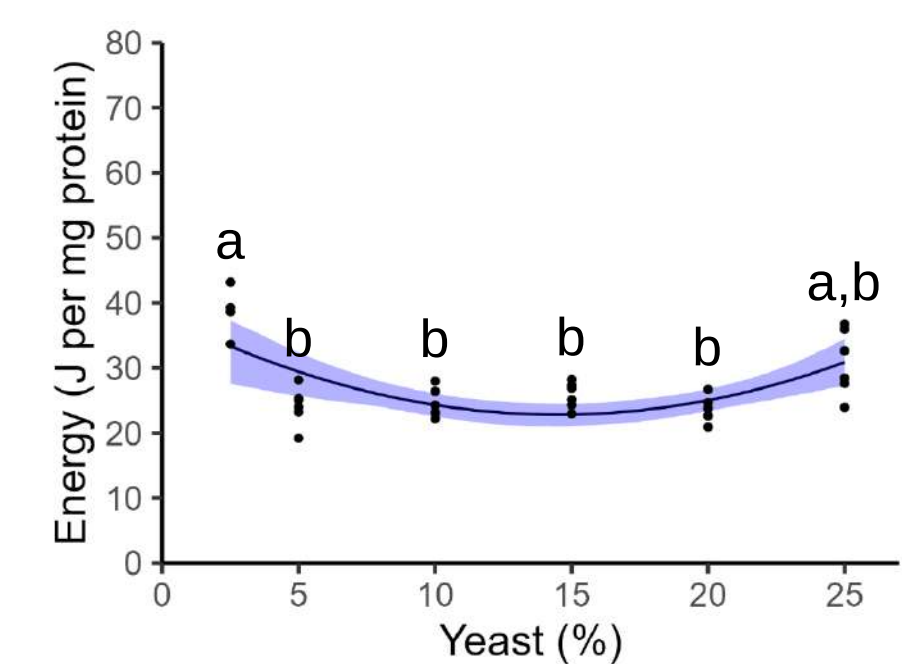
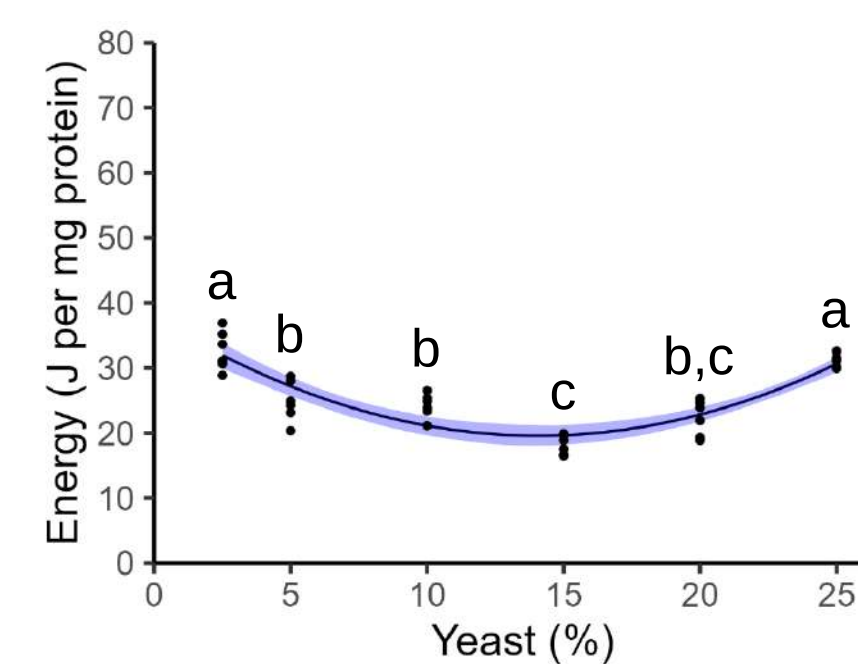
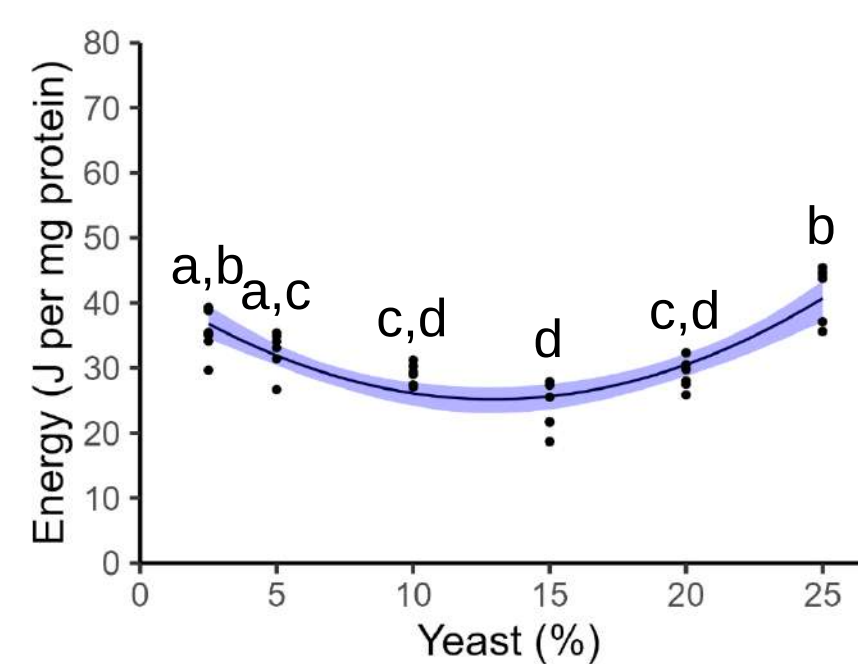
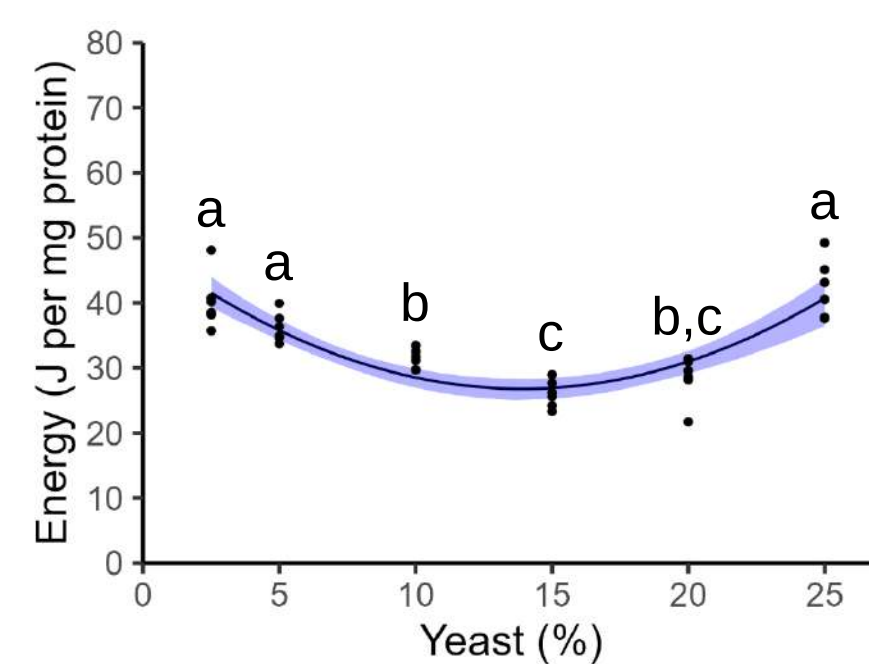


Figure S4.

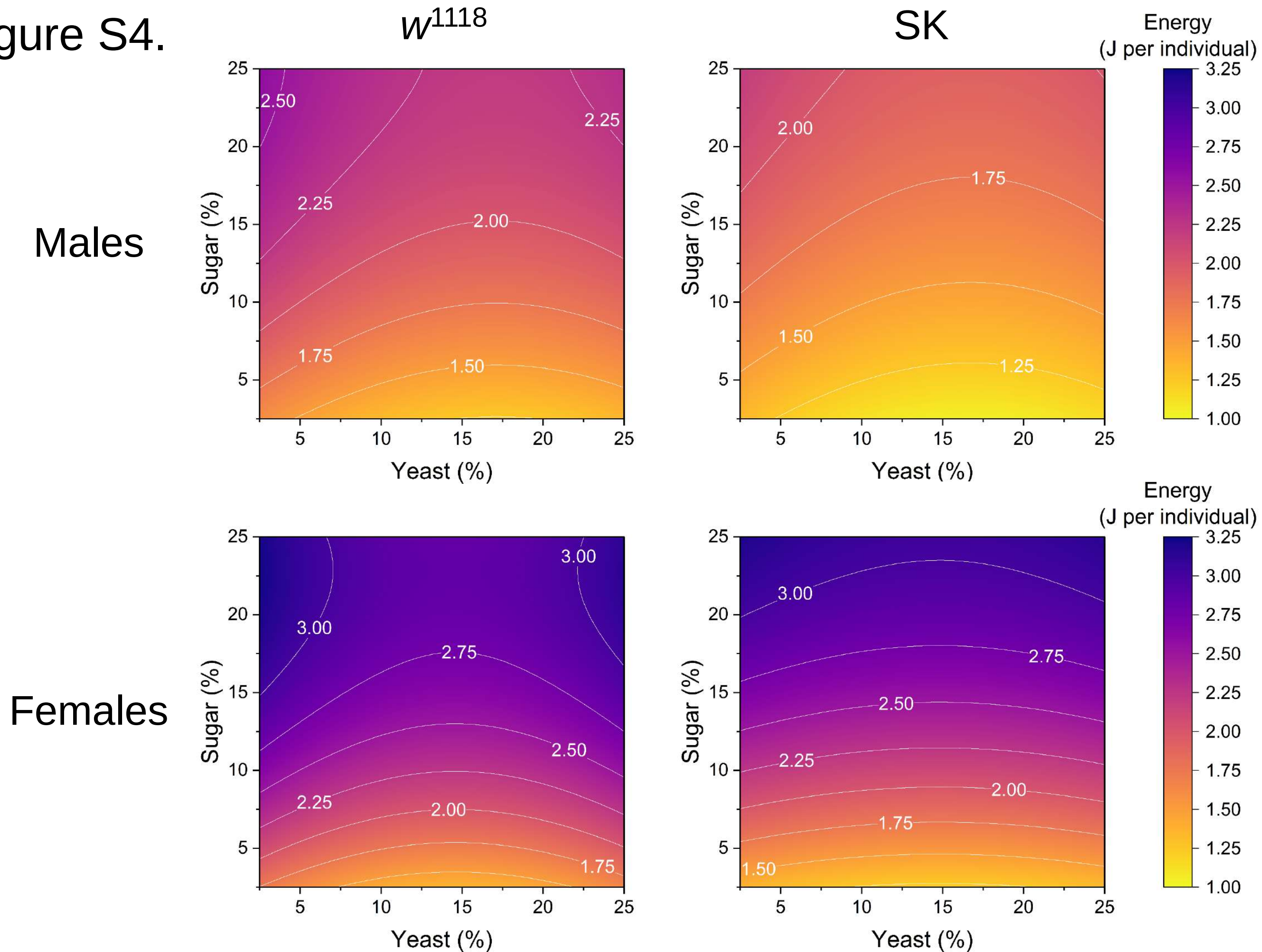
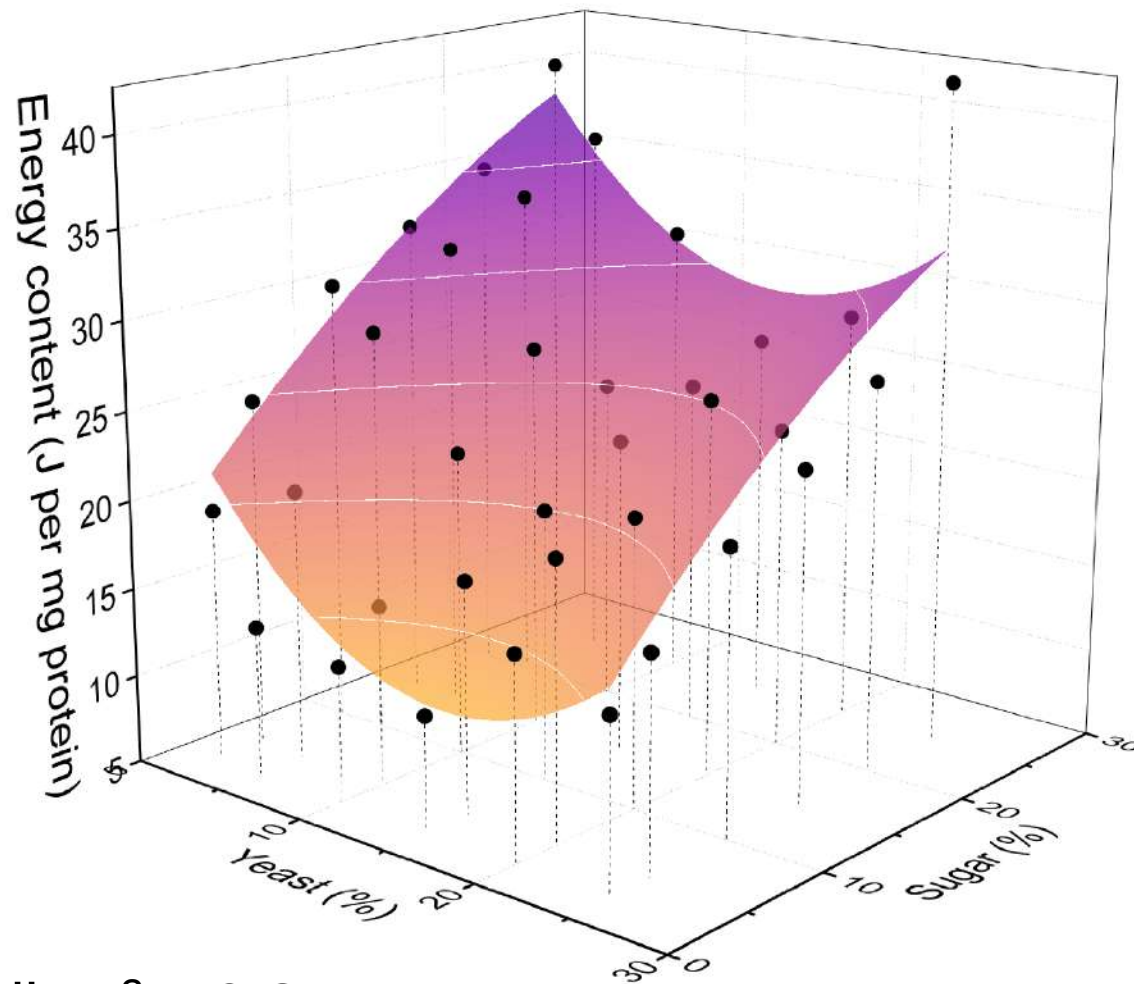


Figure S5

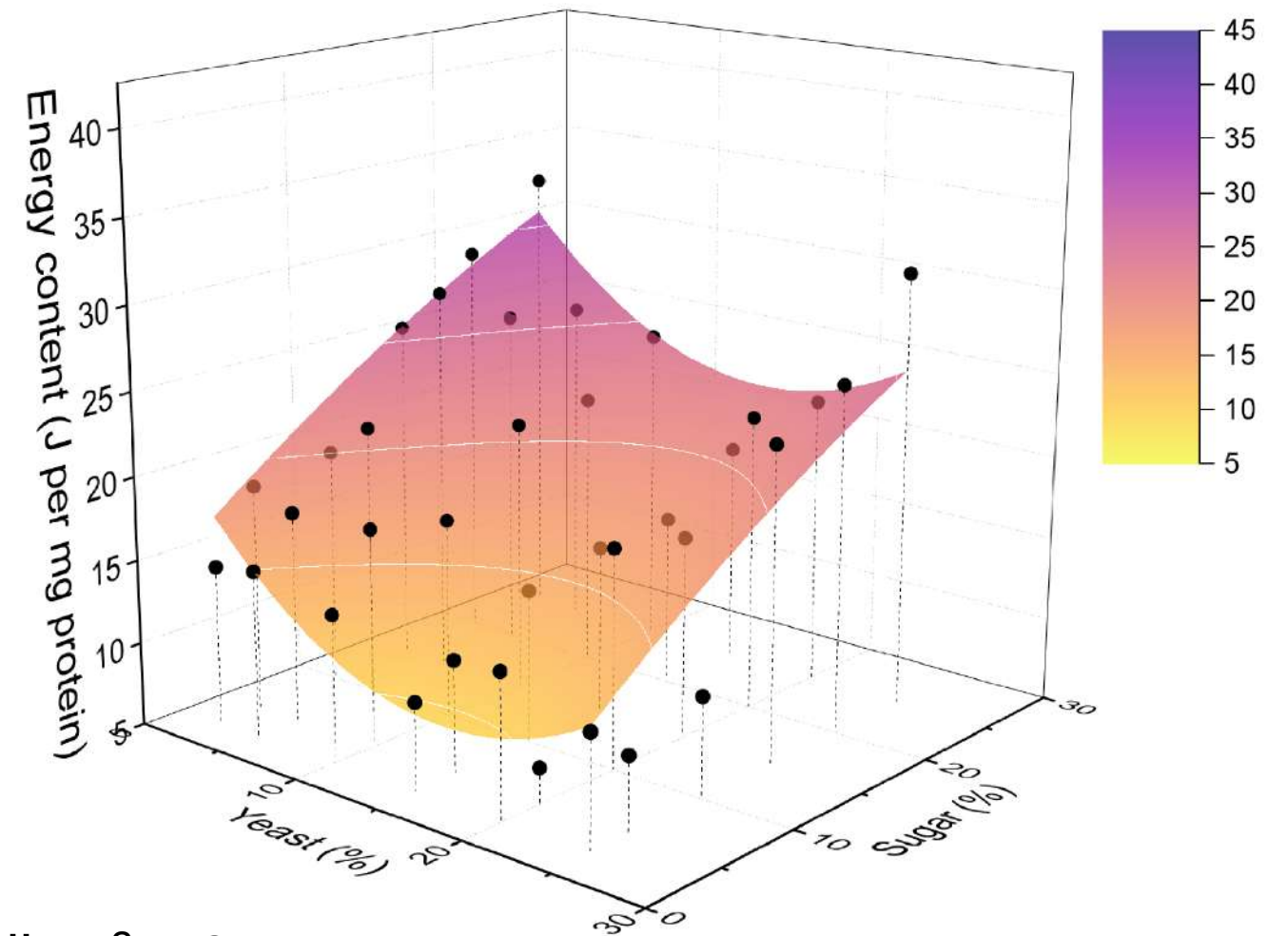
w^{1118}

SK

Males

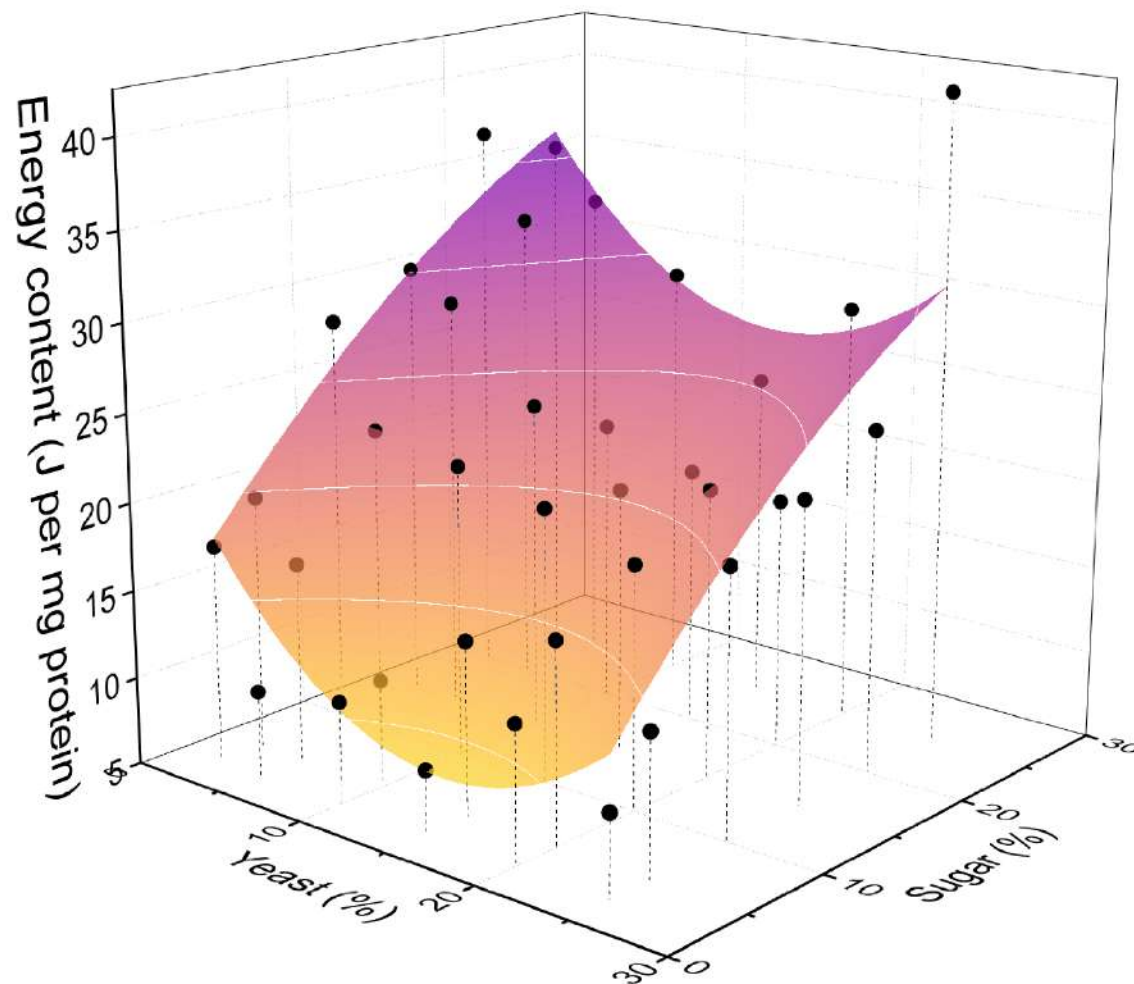


Adj. $R^2 = 0.84$

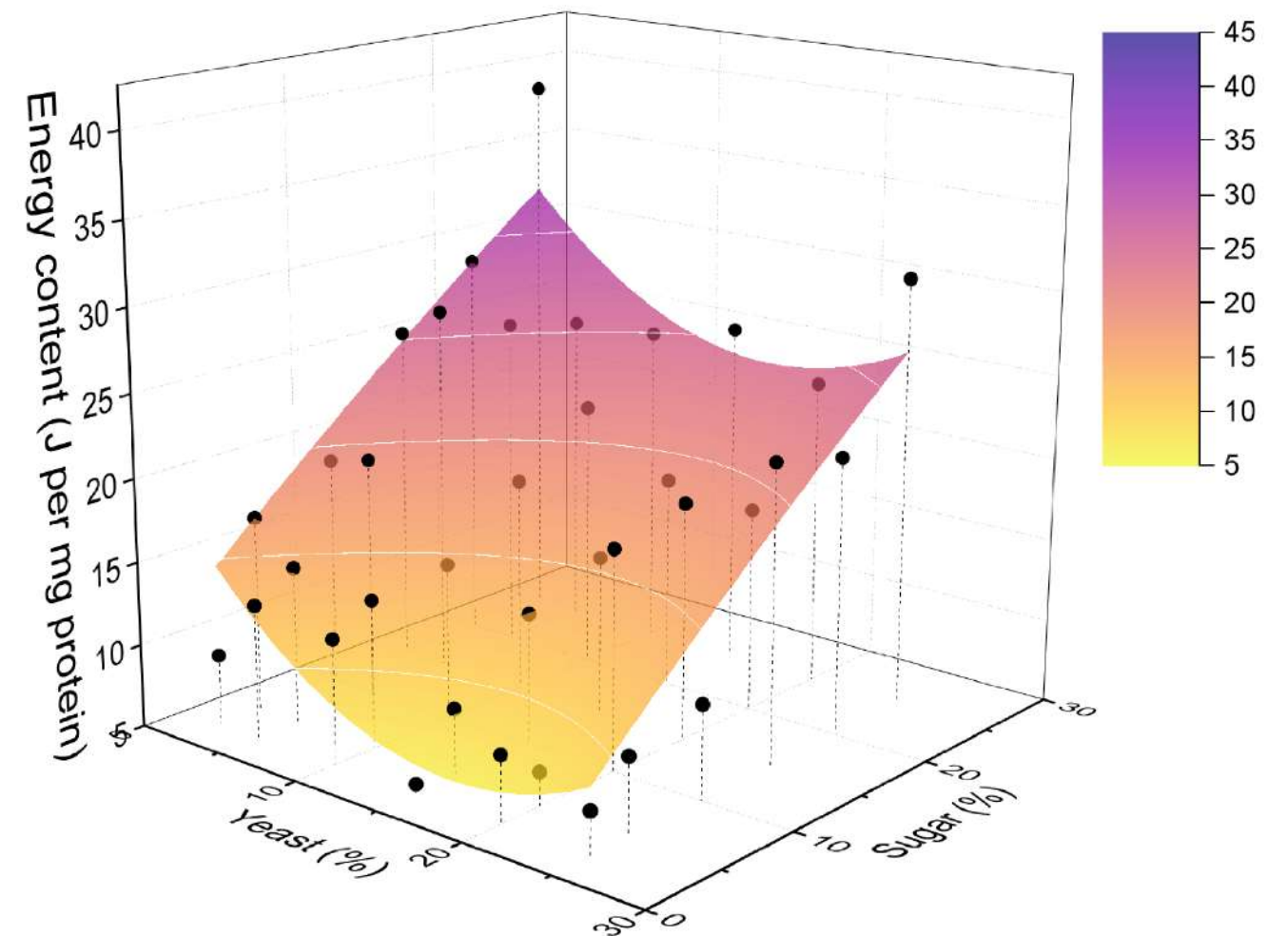


Adj. $R^2 = 0.75$

Females



Adj. $R^2 = 0.82$



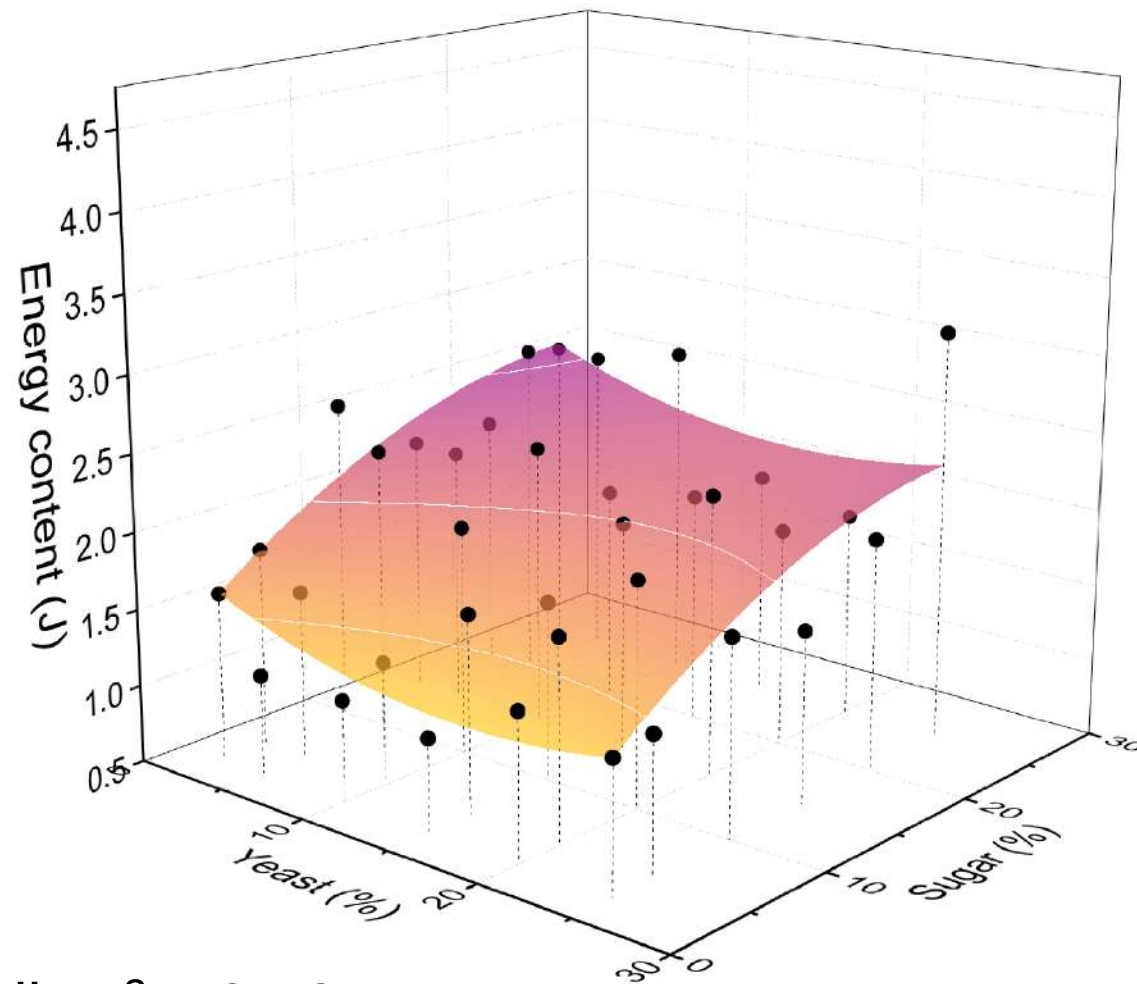
Adj. $R^2 = 0.84$

Figure S6.

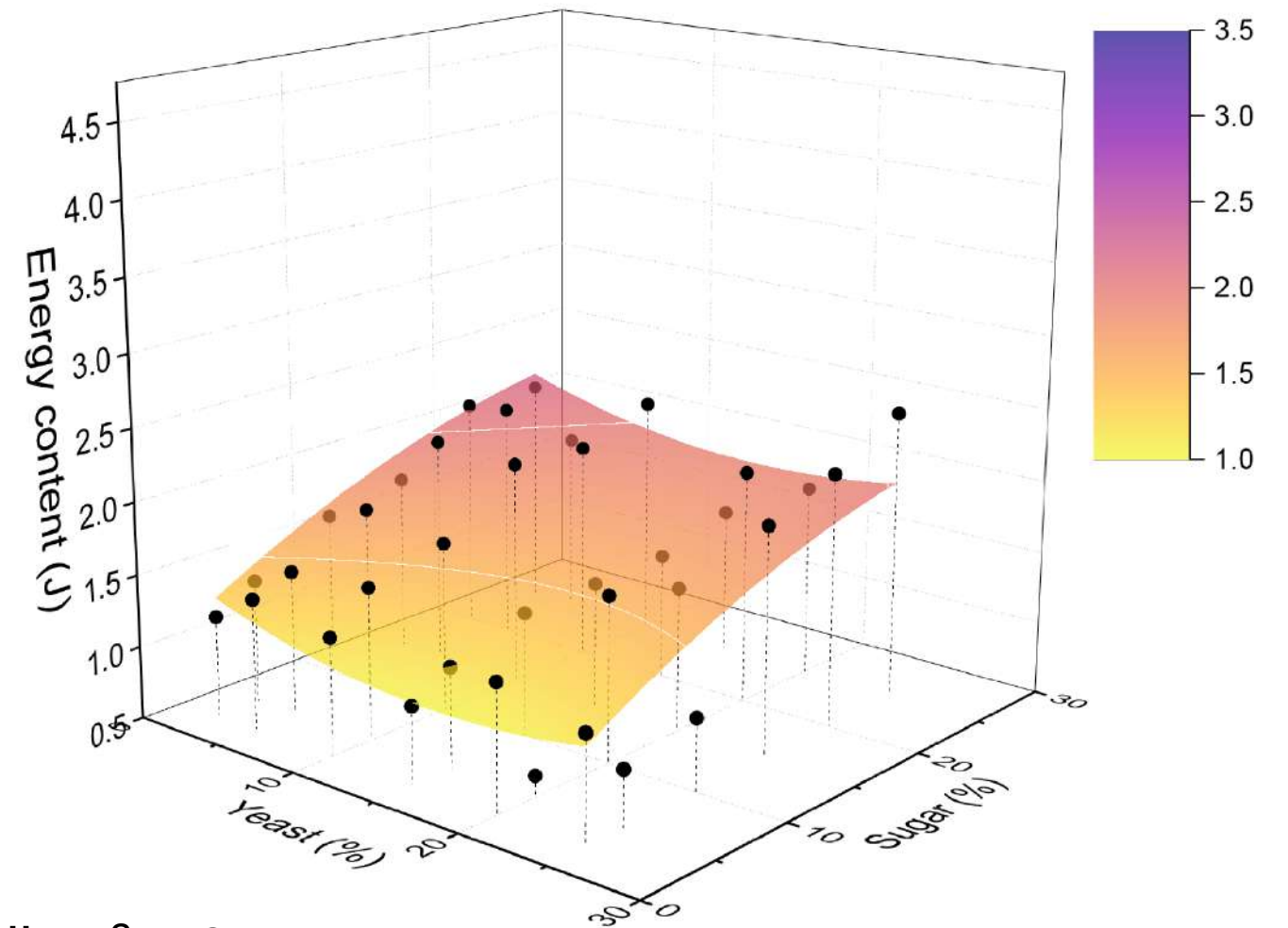
w^{1118}

SK

Males

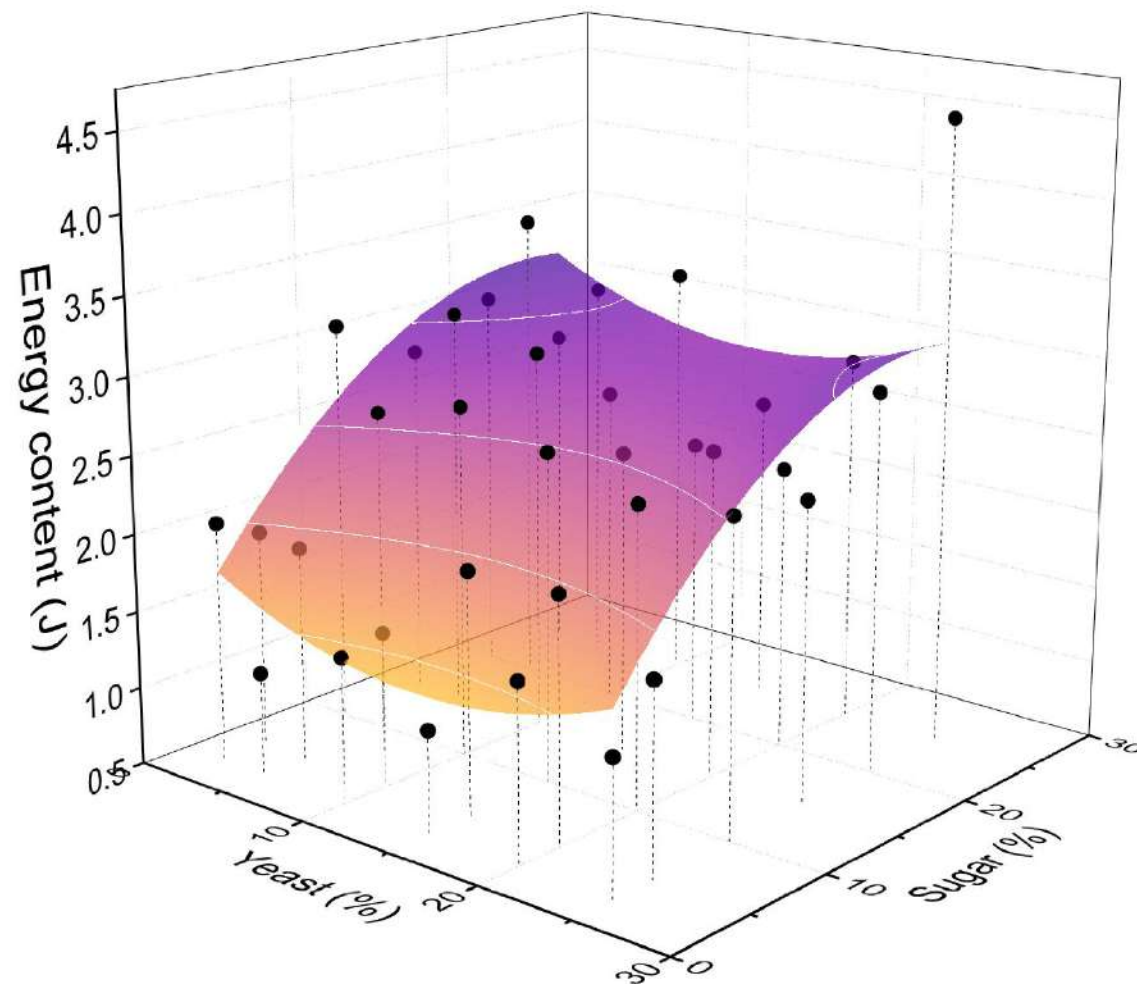


Adj. $R^2 = 0.59$

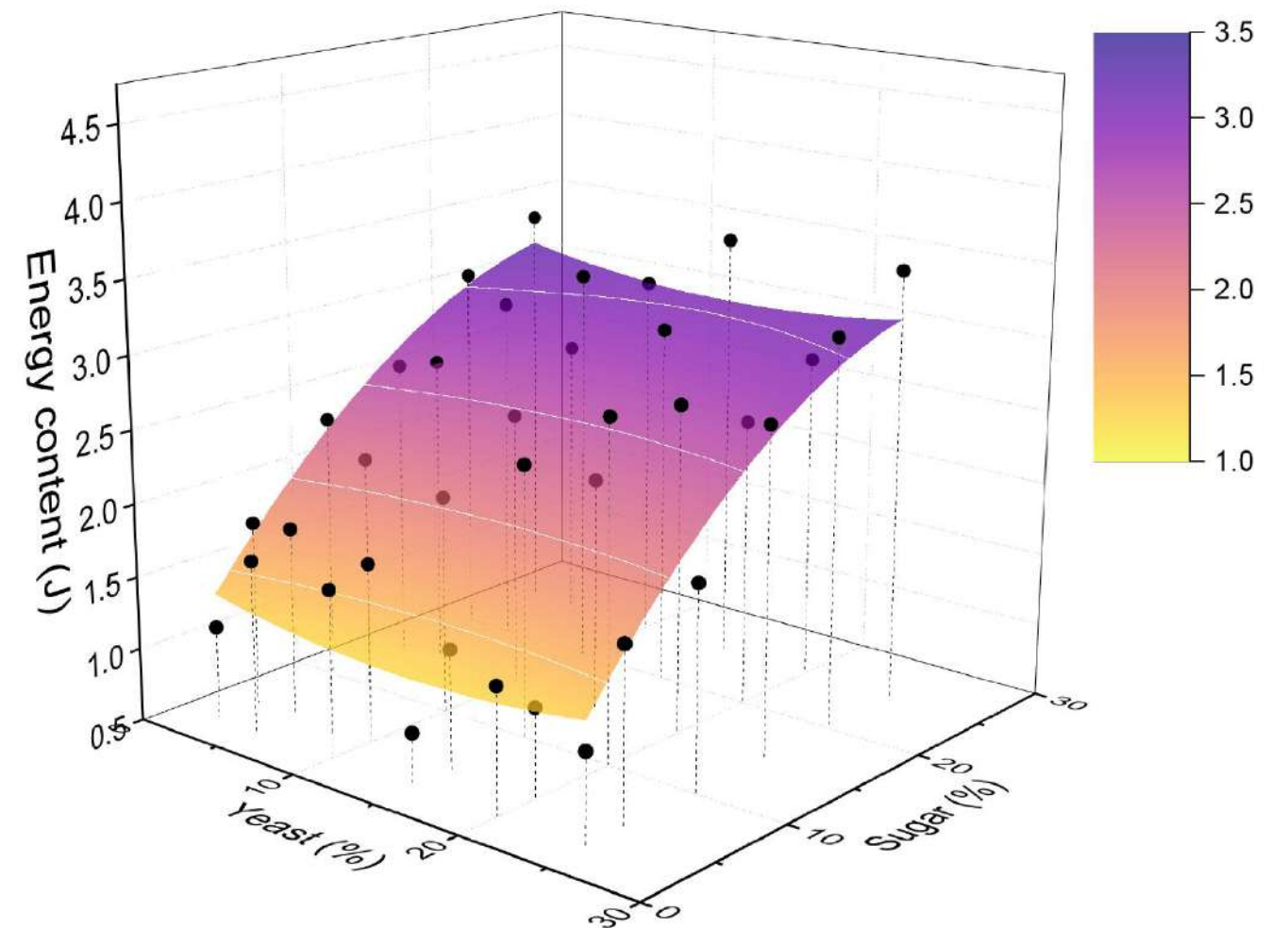


Adj. $R^2 = 0.55$

Females



Adj. $R^2 = 0.65$



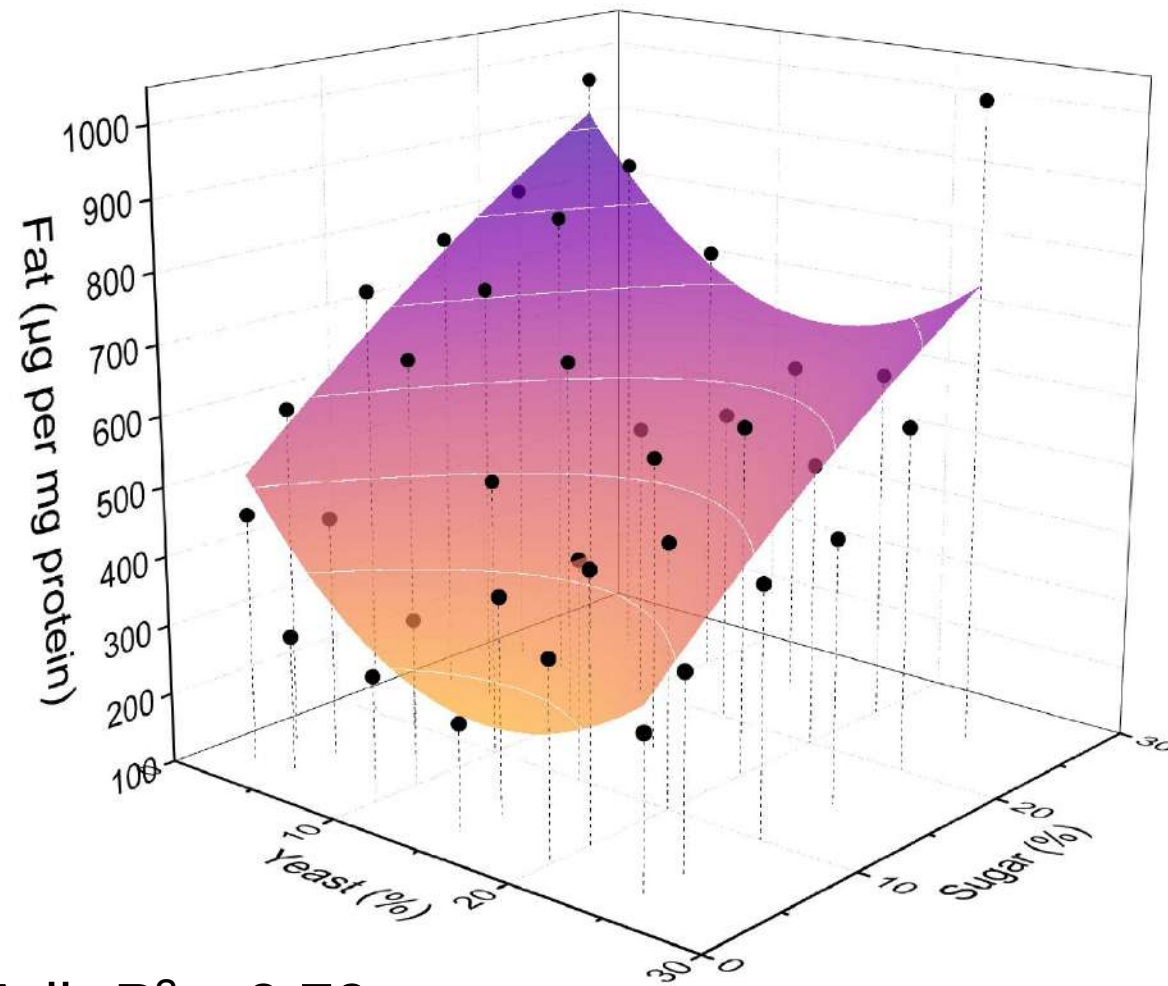
Adj. $R^2 = 0.82$

Figure S7.

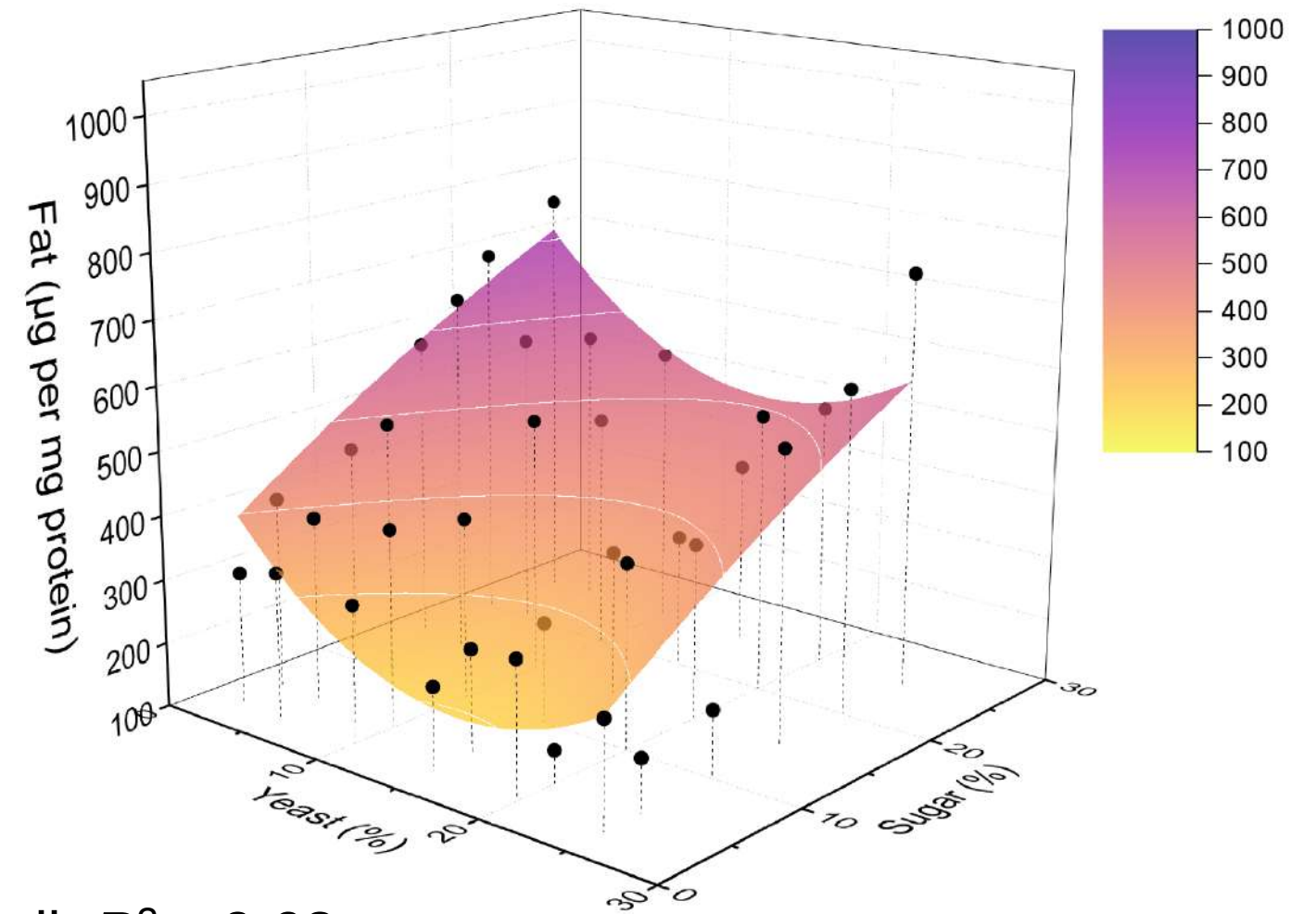
w^{1118}

SK

Males

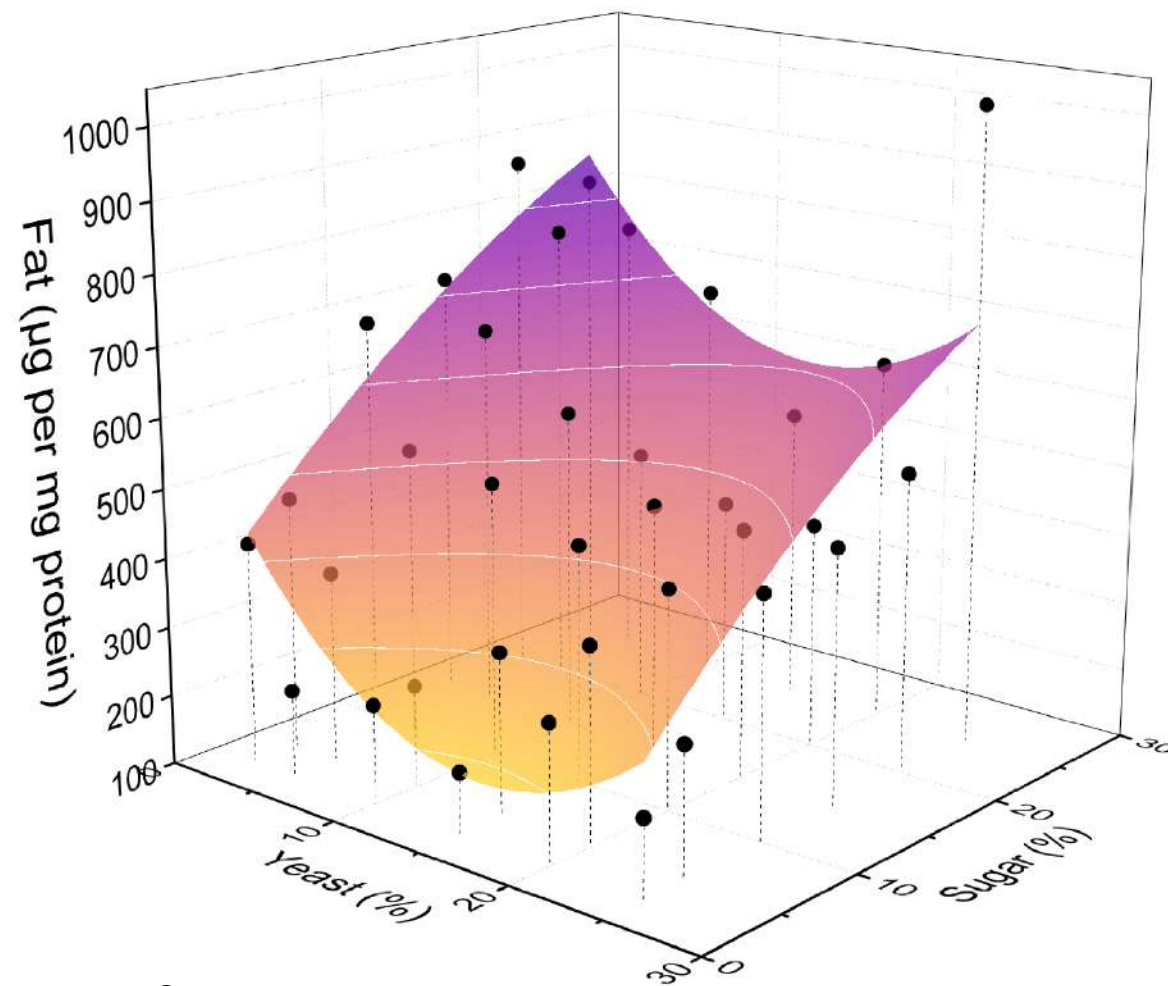


Adj. $R^2 = 0.79$

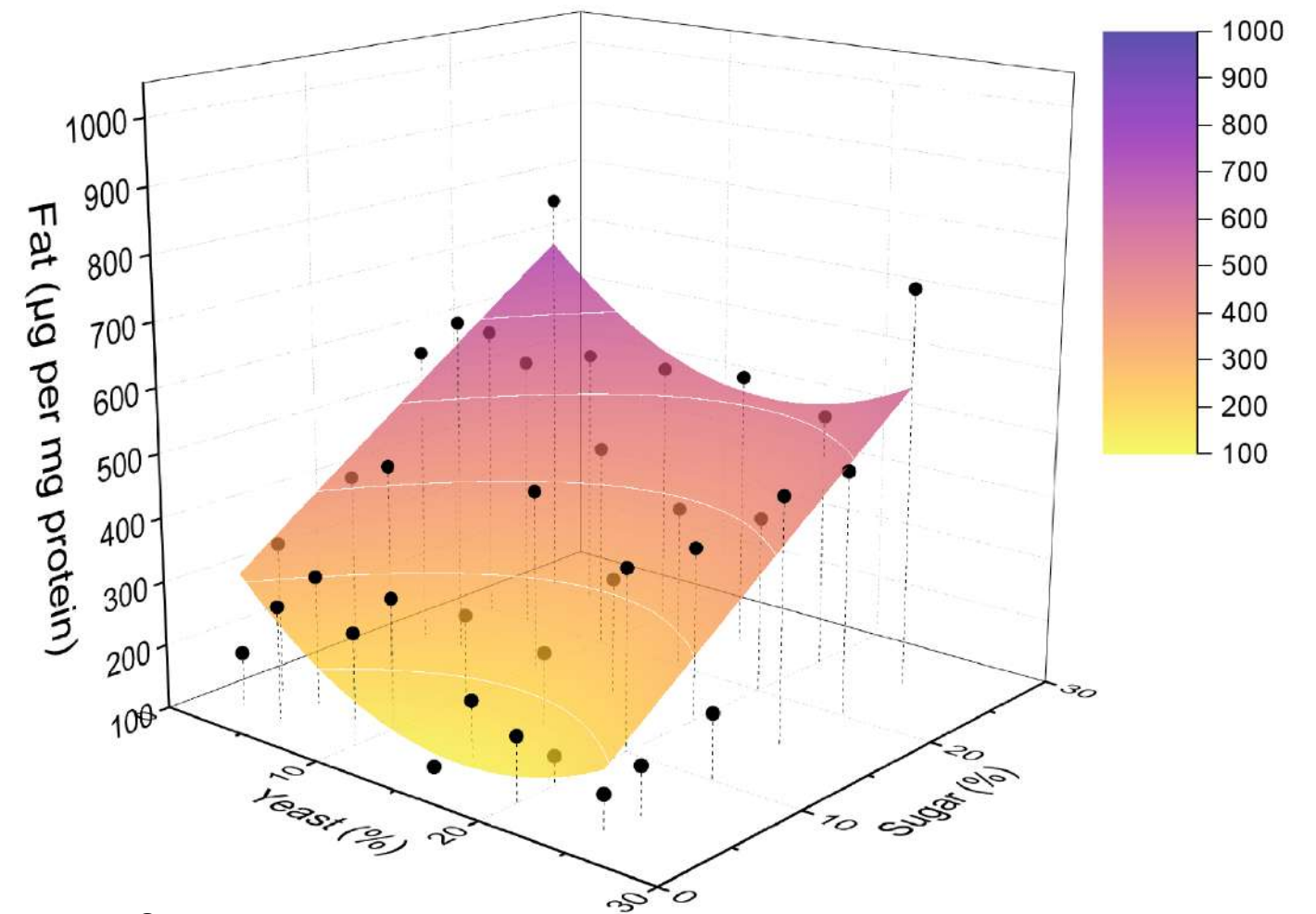


Adj. $R^2 = 0.68$

Females



Adj. $R^2 = 0.78$



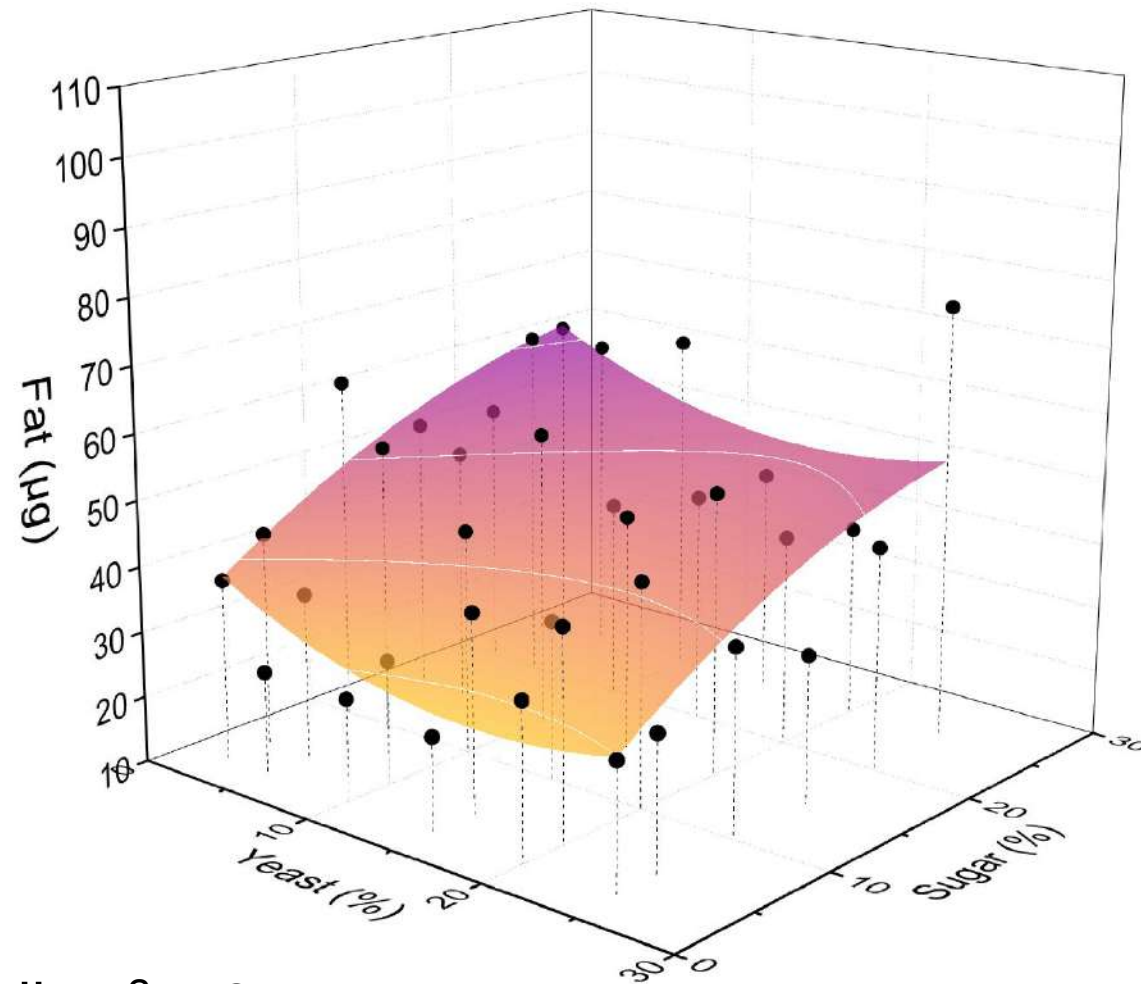
Adj. $R^2 = 0.79$

Figure S8.

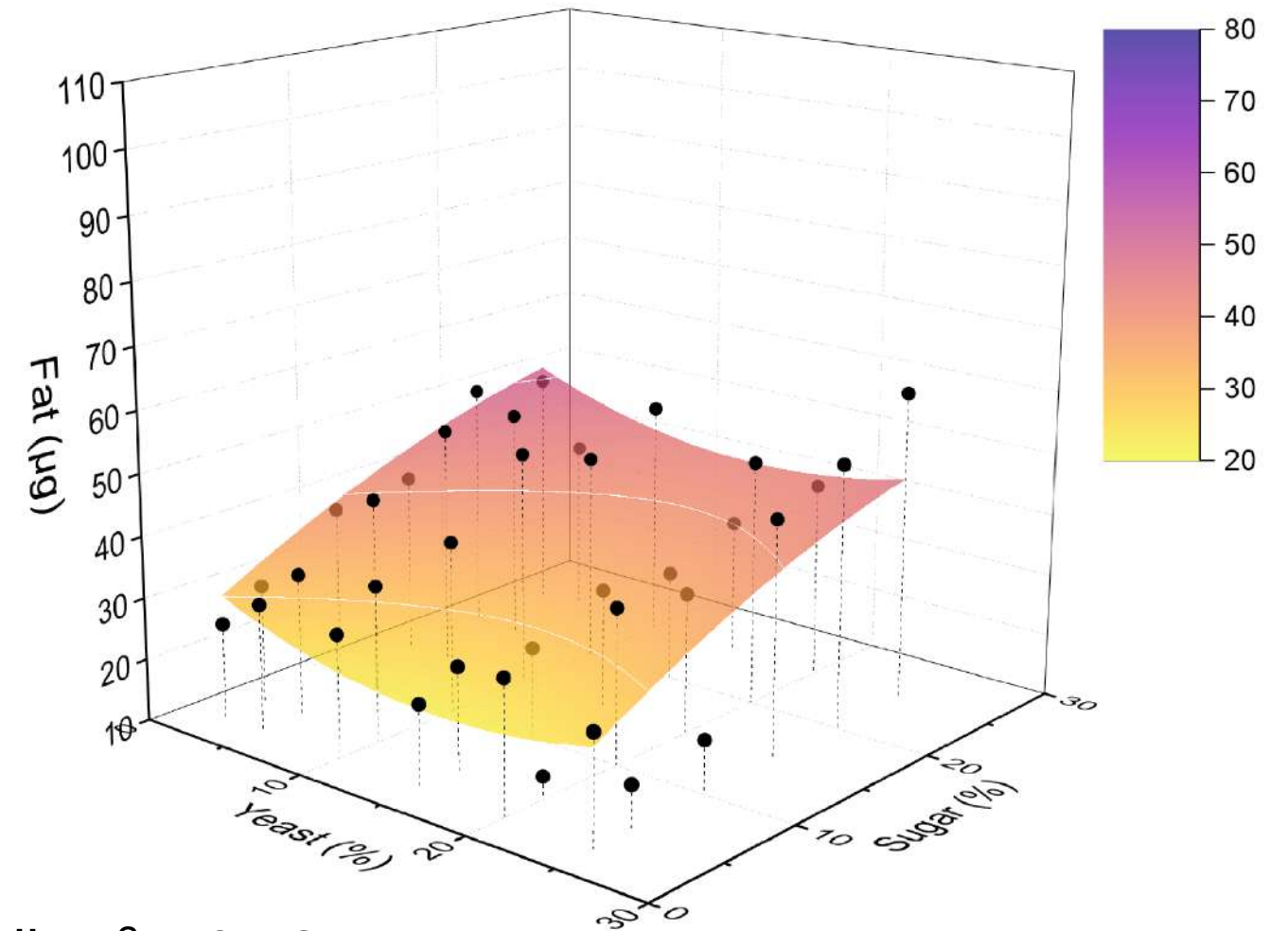
w^{1118}

SK

Males

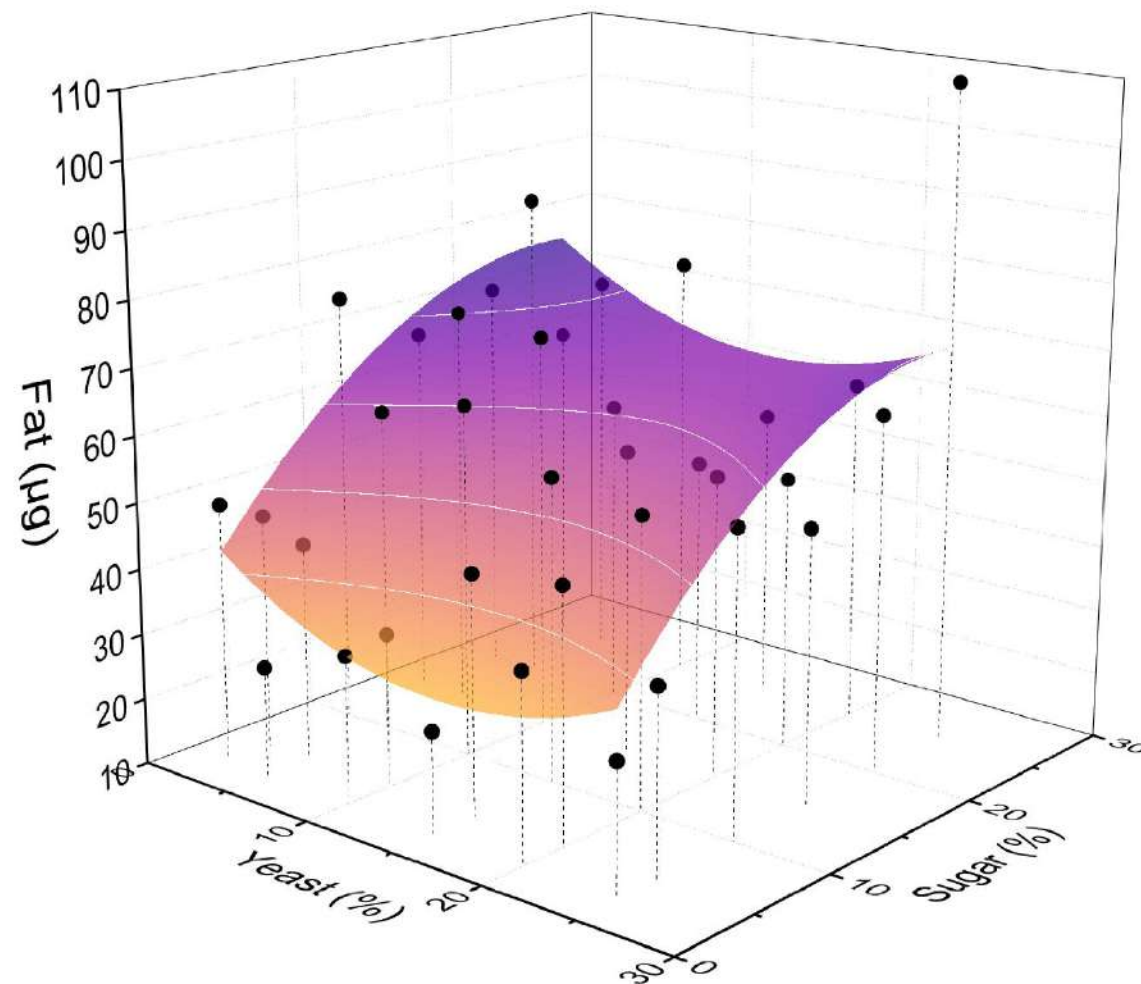


Adj. $R^2 = 0.54$

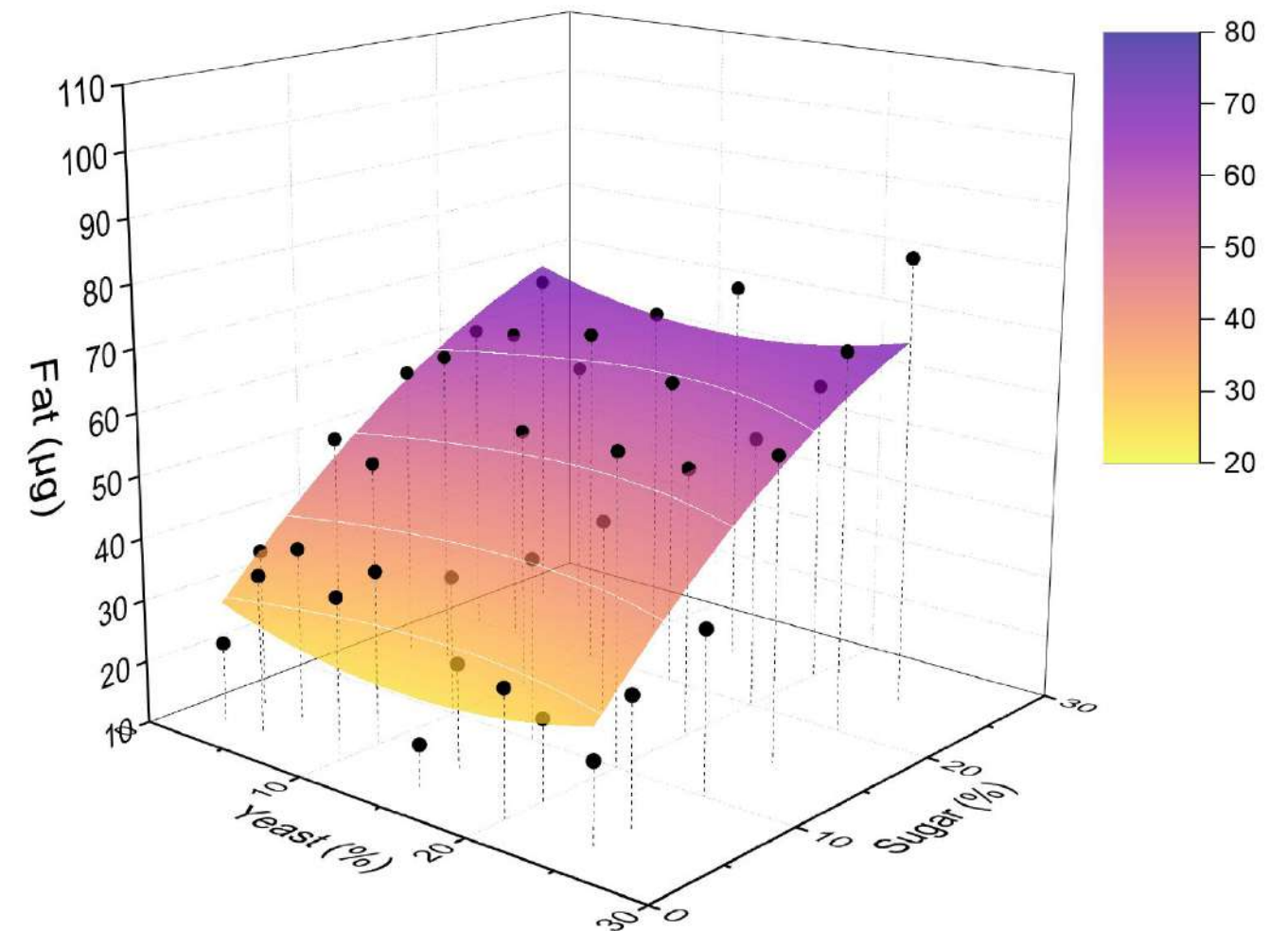


Adj. $R^2 = 0.48$

Females



Adj. $R^2 = 0.58$



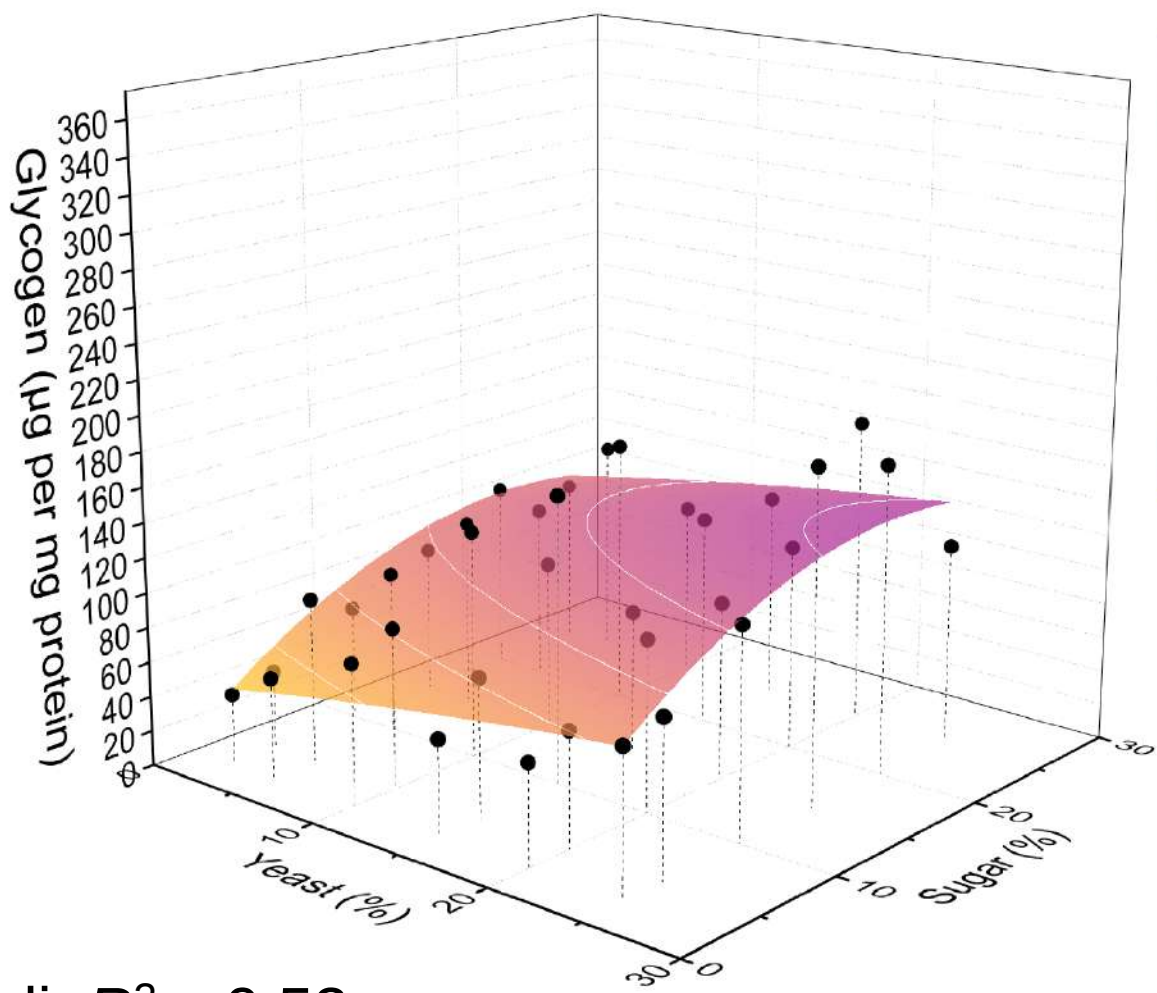
Adj. $R^2 = 0.78$

Figure S9.

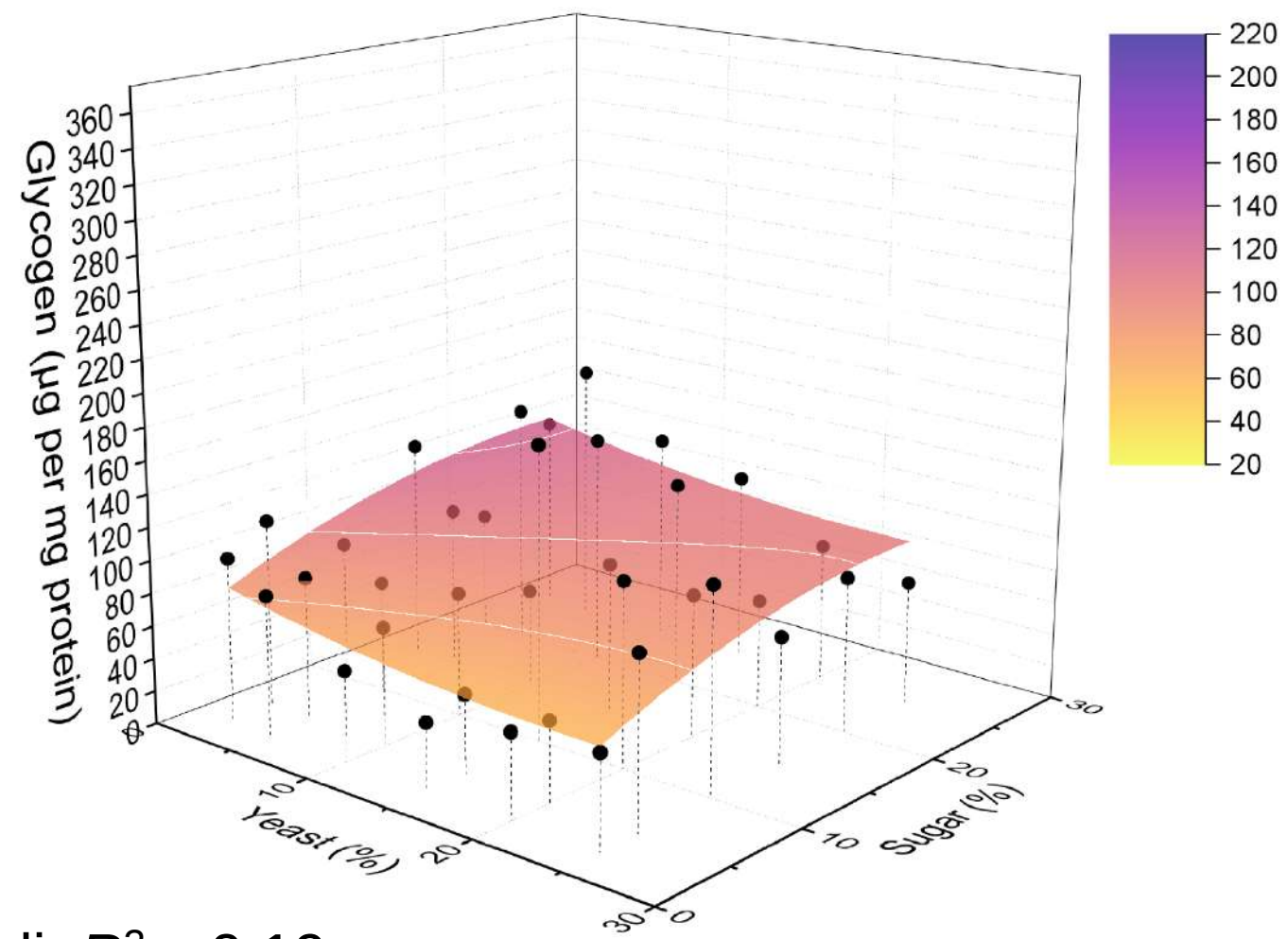
w^{1118}

SK

Males

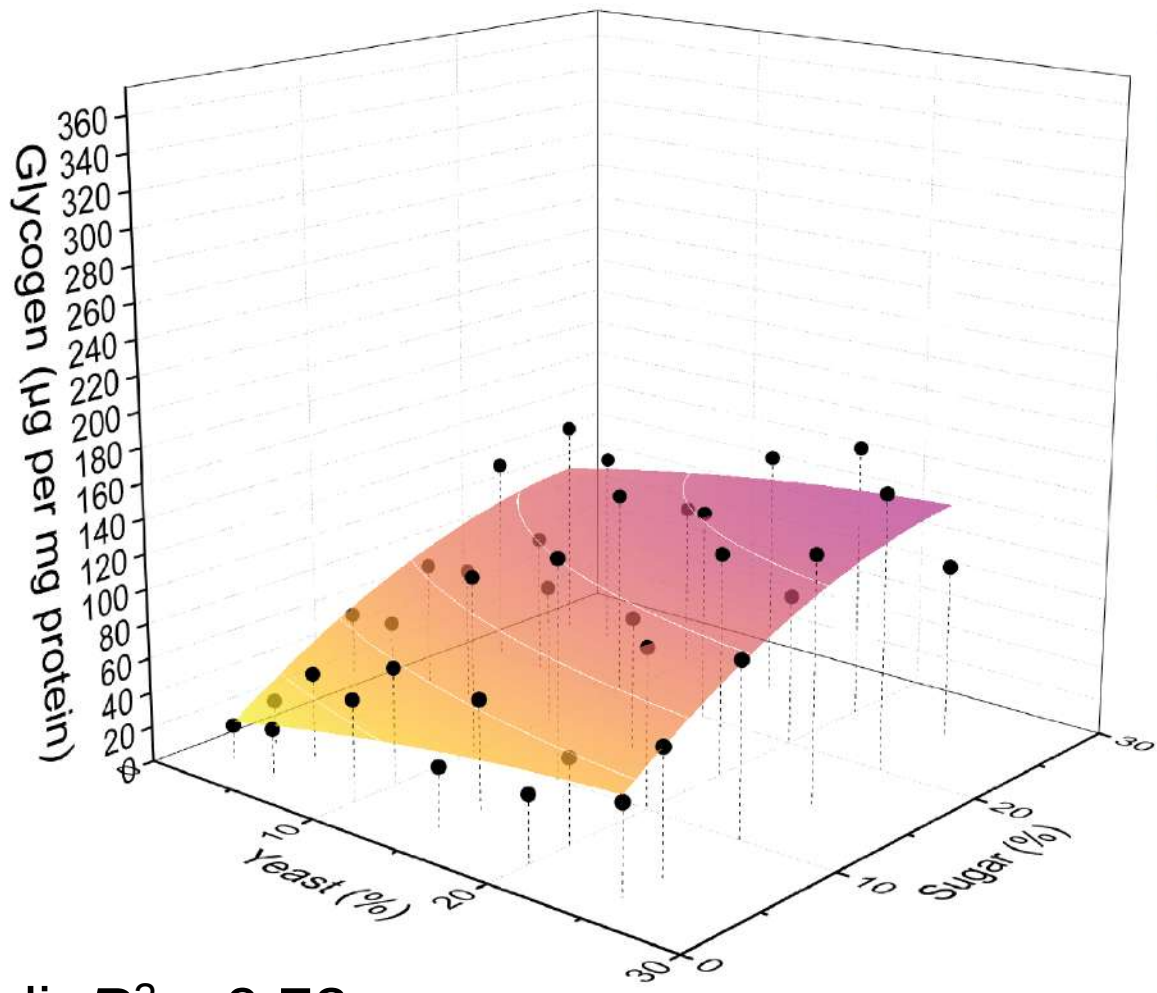


Adj. $R^2 = 0.53$

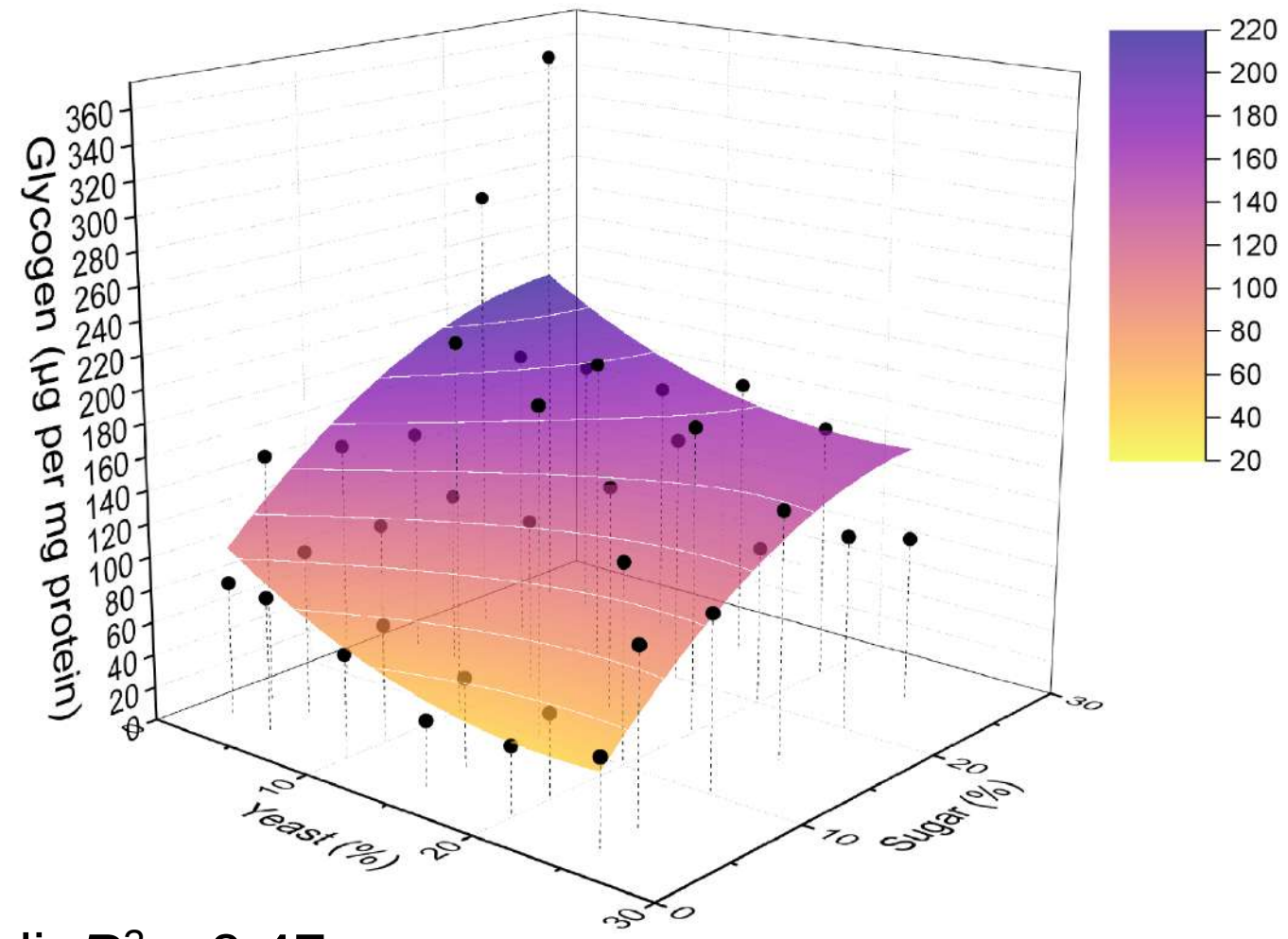


Adj. $R^2 = 0.19$

Females



Adj. $R^2 = 0.72$



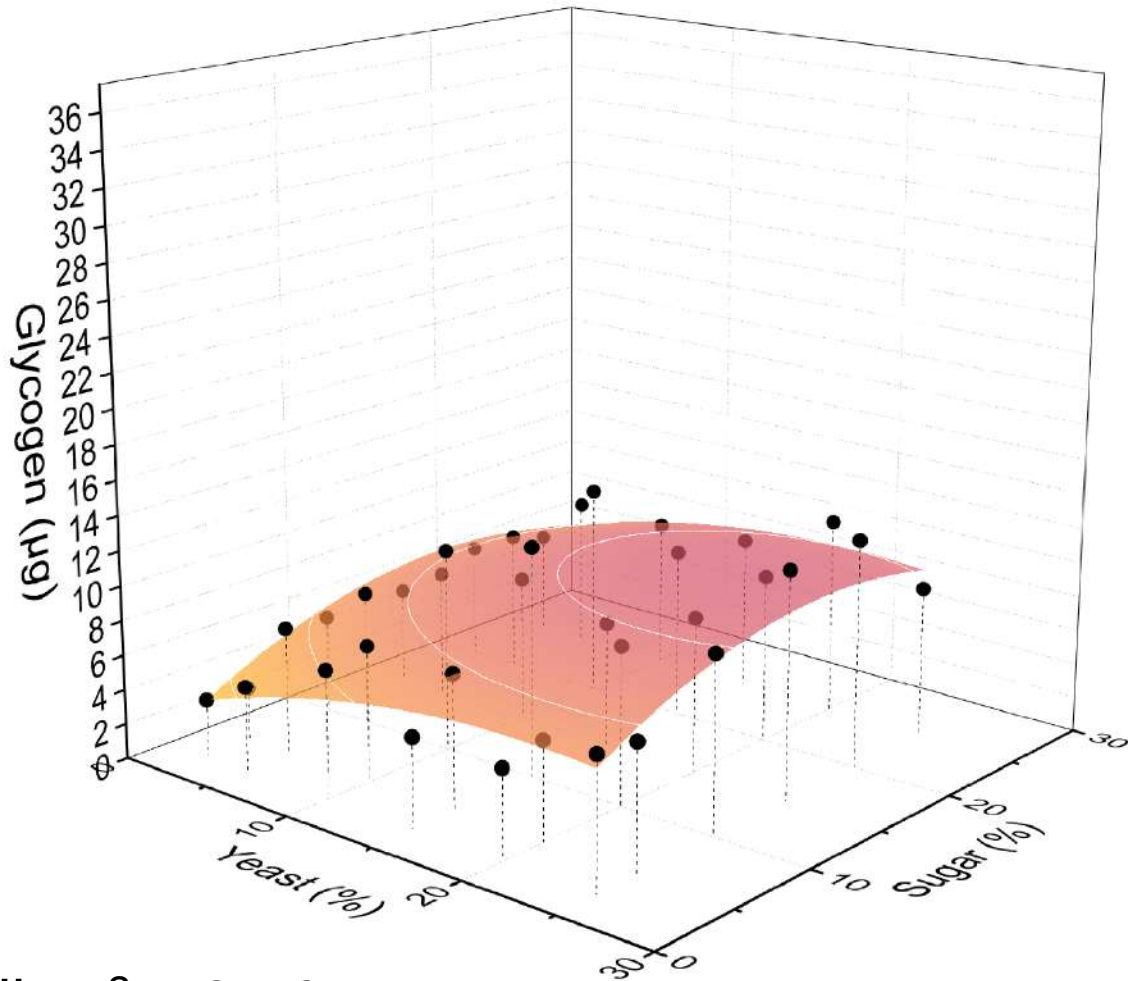
Adj. $R^2 = 0.47$

Figure S10.

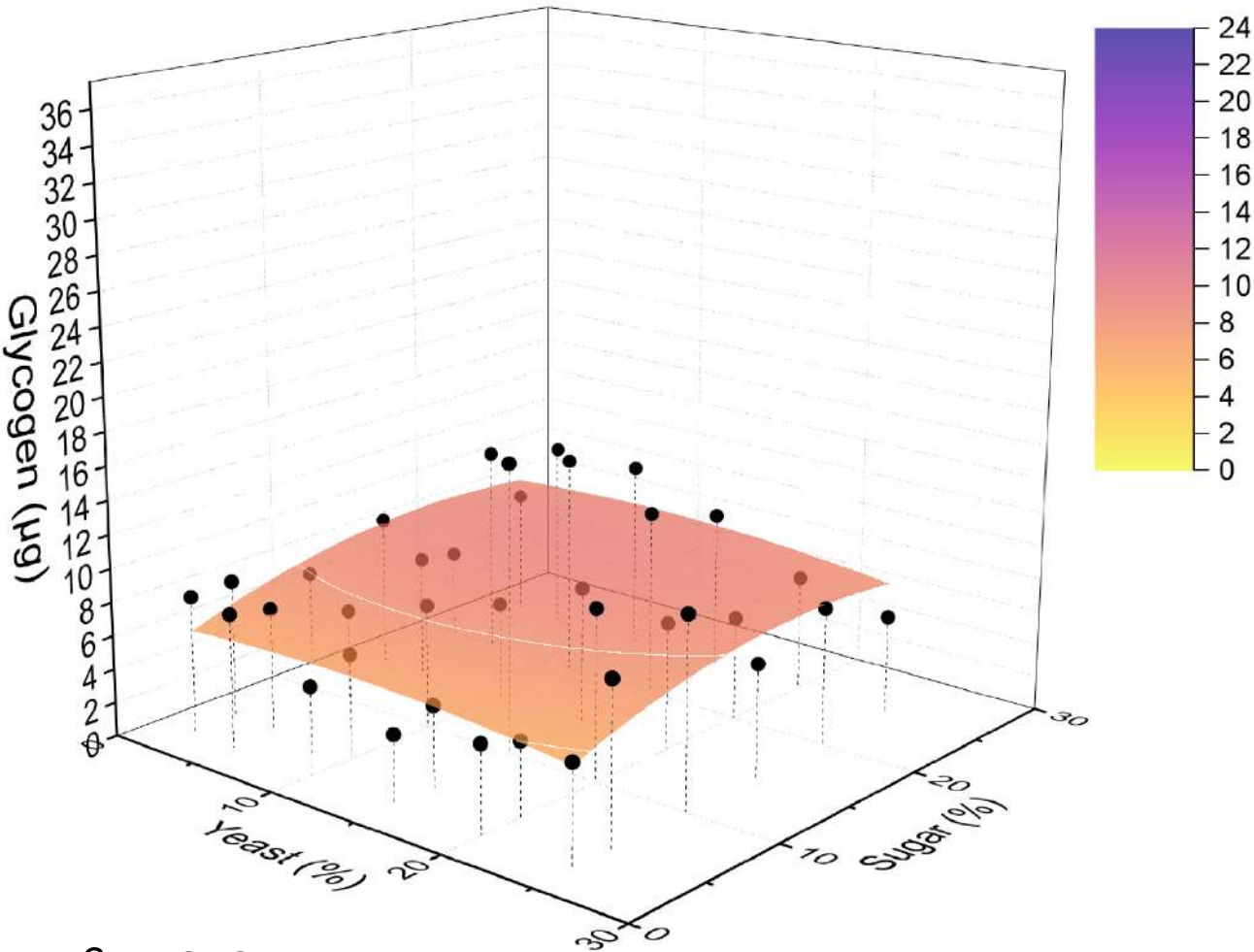
w^{1118}

SK

Males

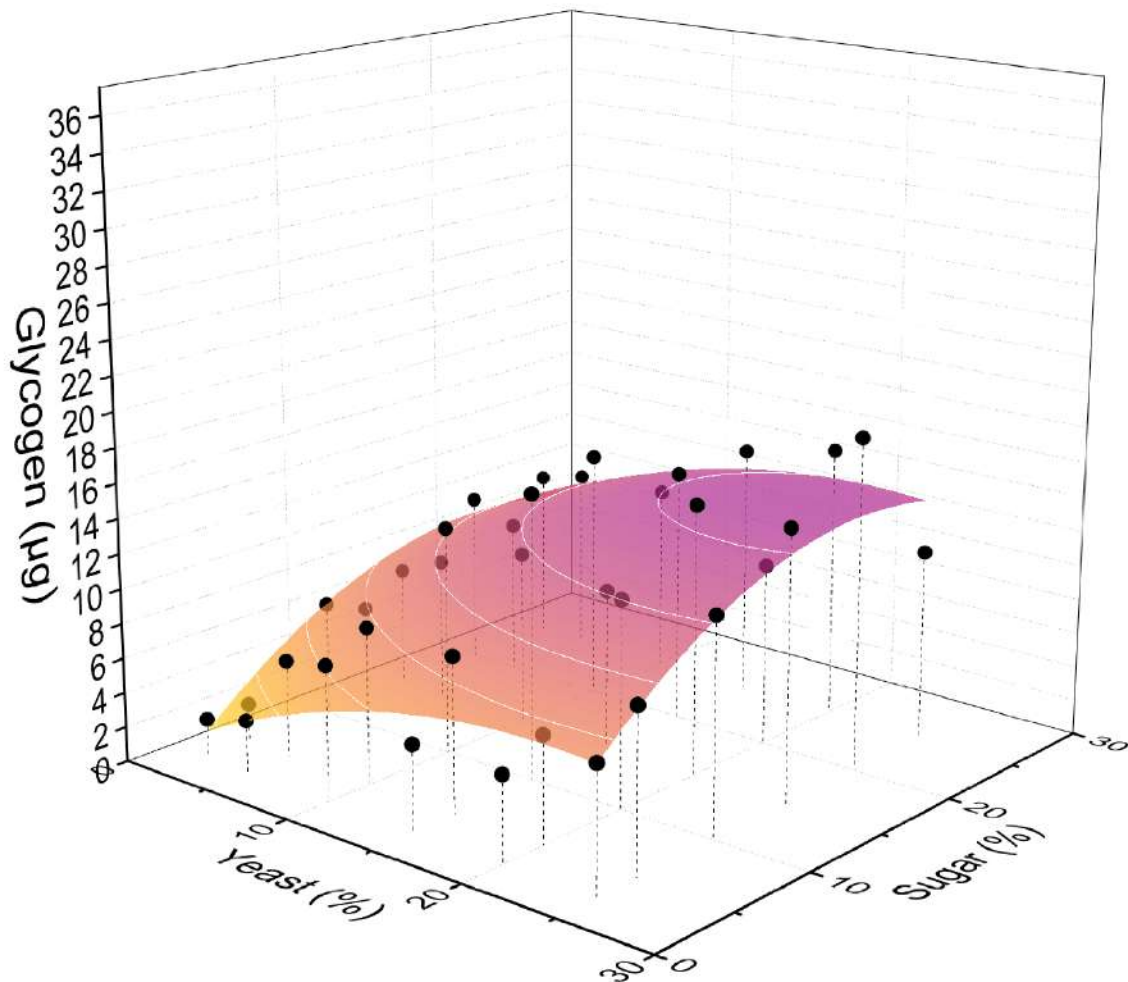


Adj. $R^2 = 0.56$

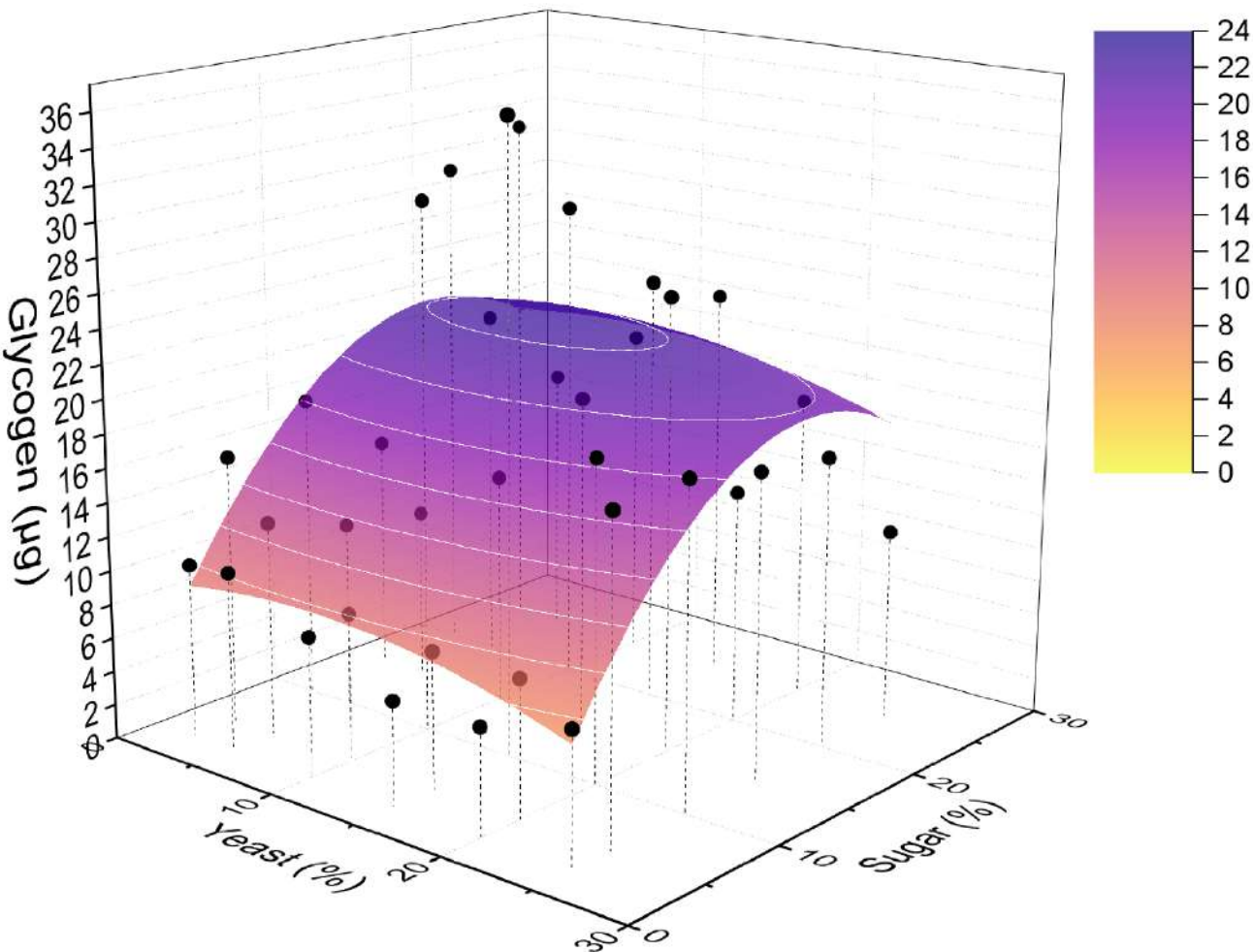


Adj. $R^2 = 0.04$

Females



Adj. $R^2 = 0.71$



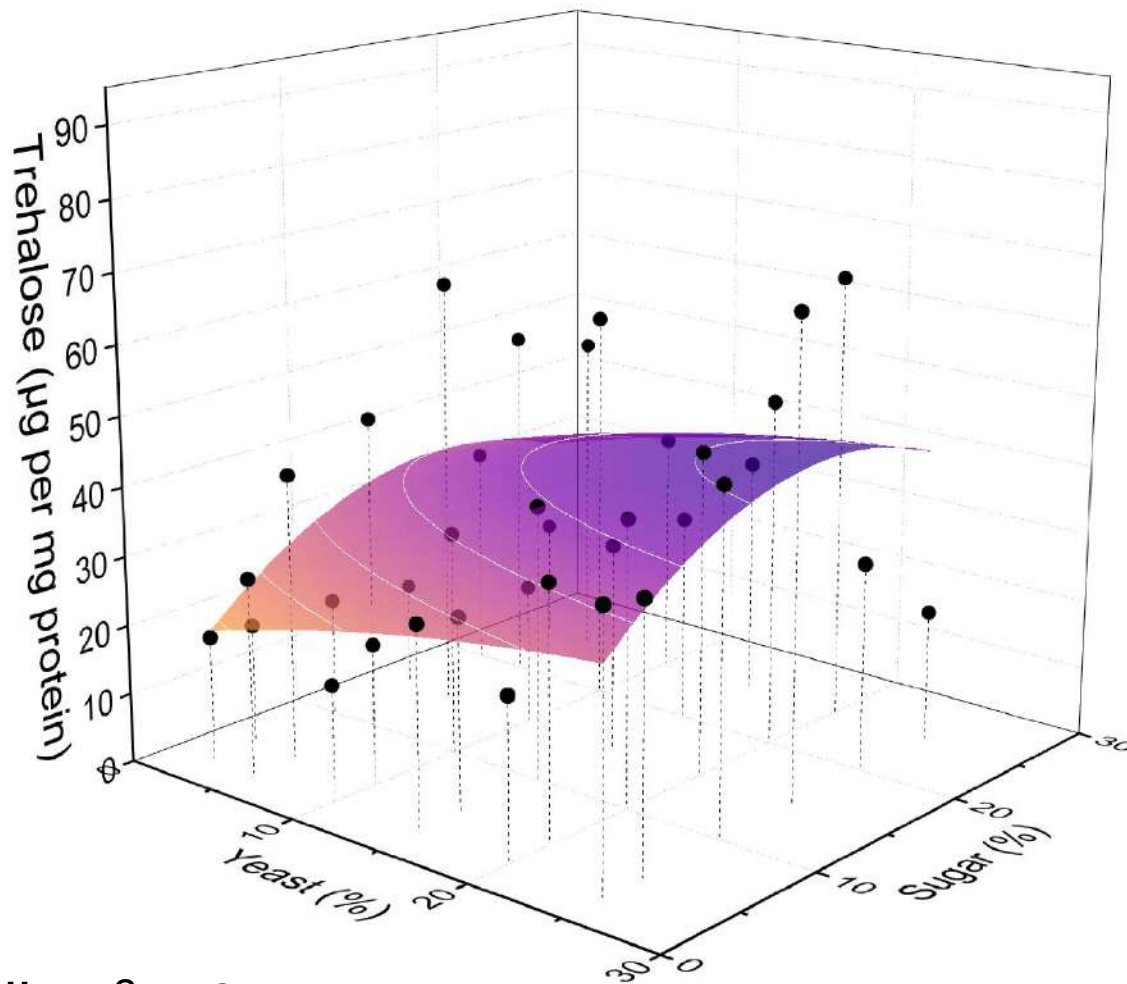
Adj. $R^2 = 0.30$

Figure S11.

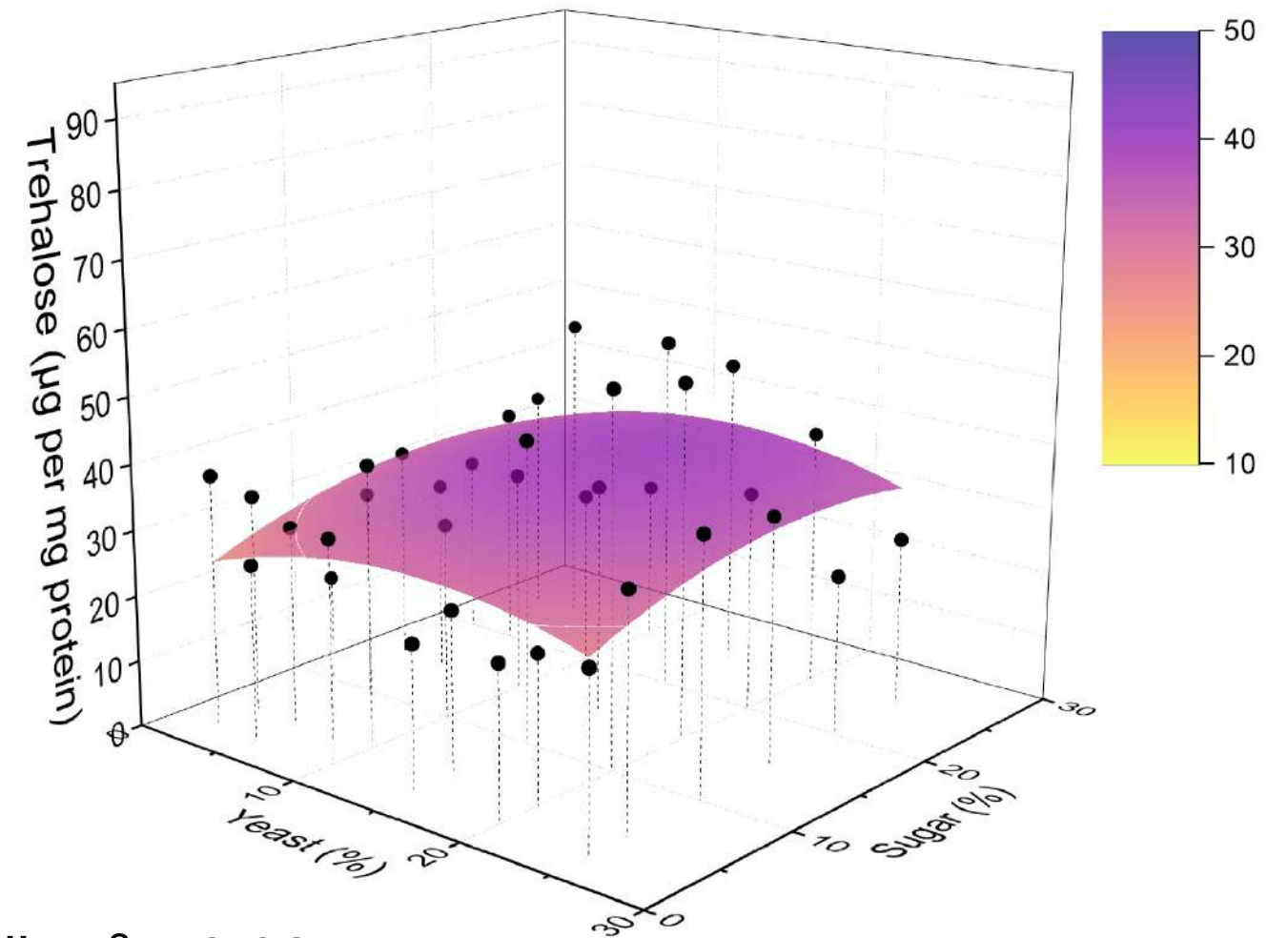
w^{1118}

SK

Males

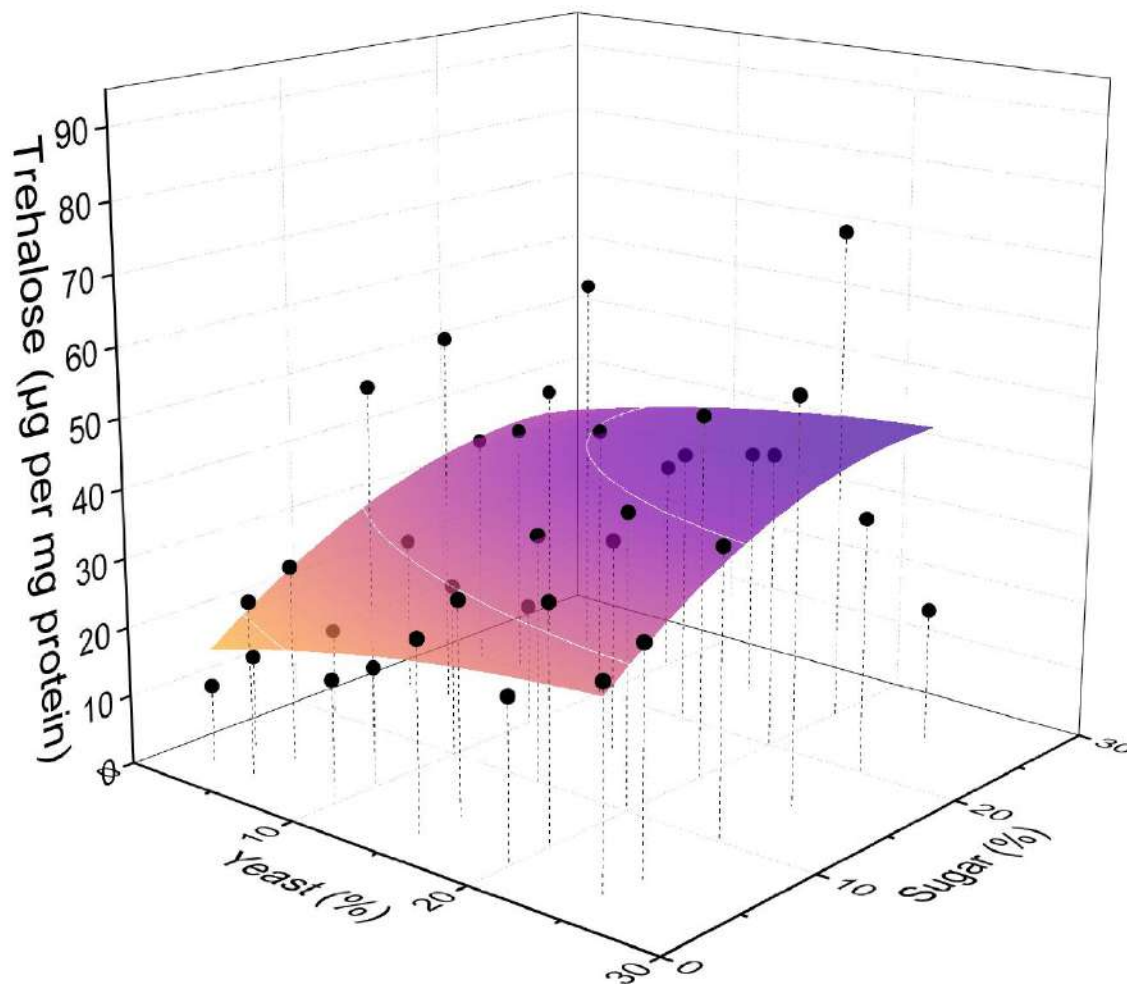


Adj. $R^2 = 0.15$

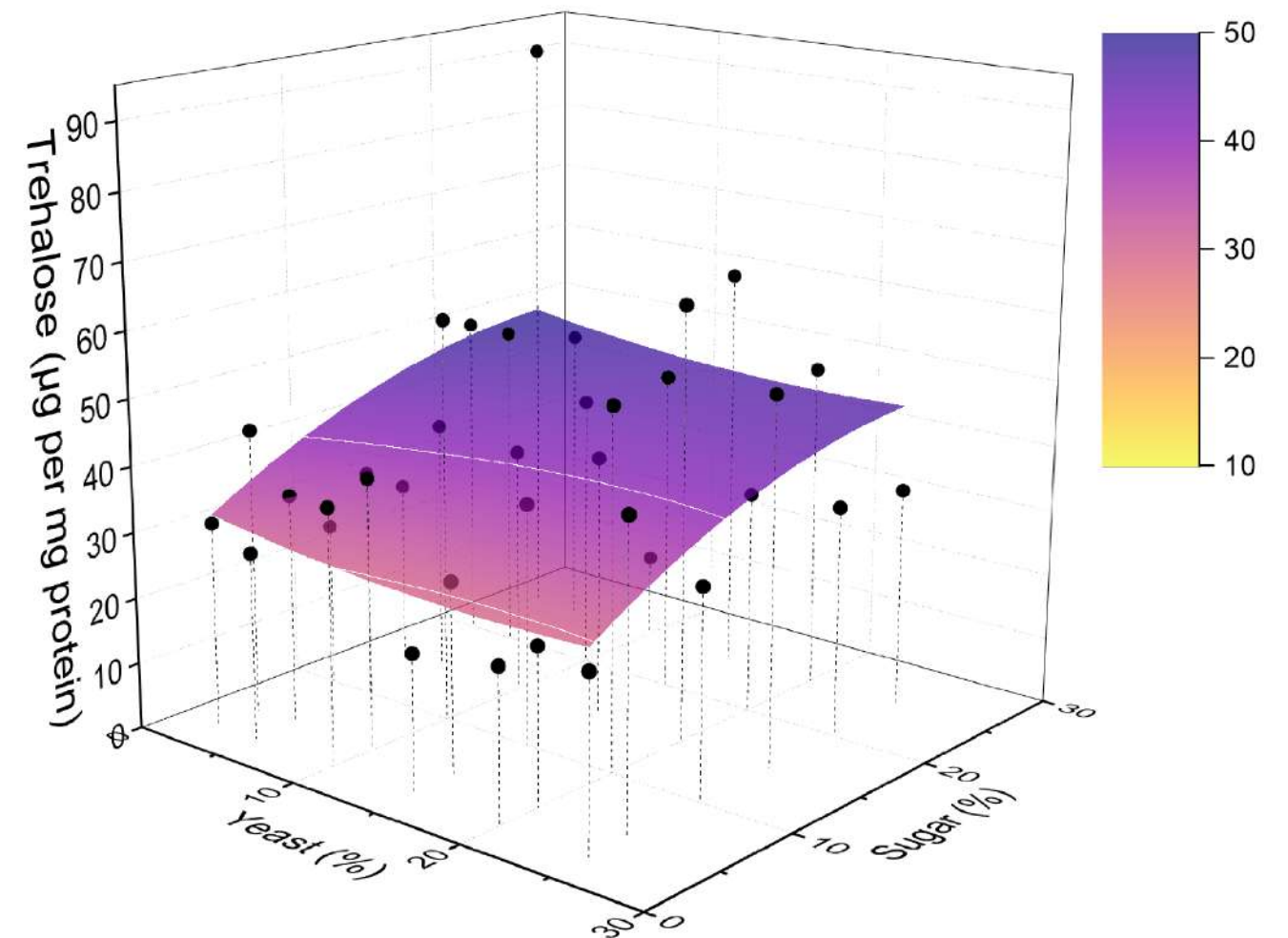


Adj. $R^2 = 0.03$

Females



Adj. $R^2 = 0.27$



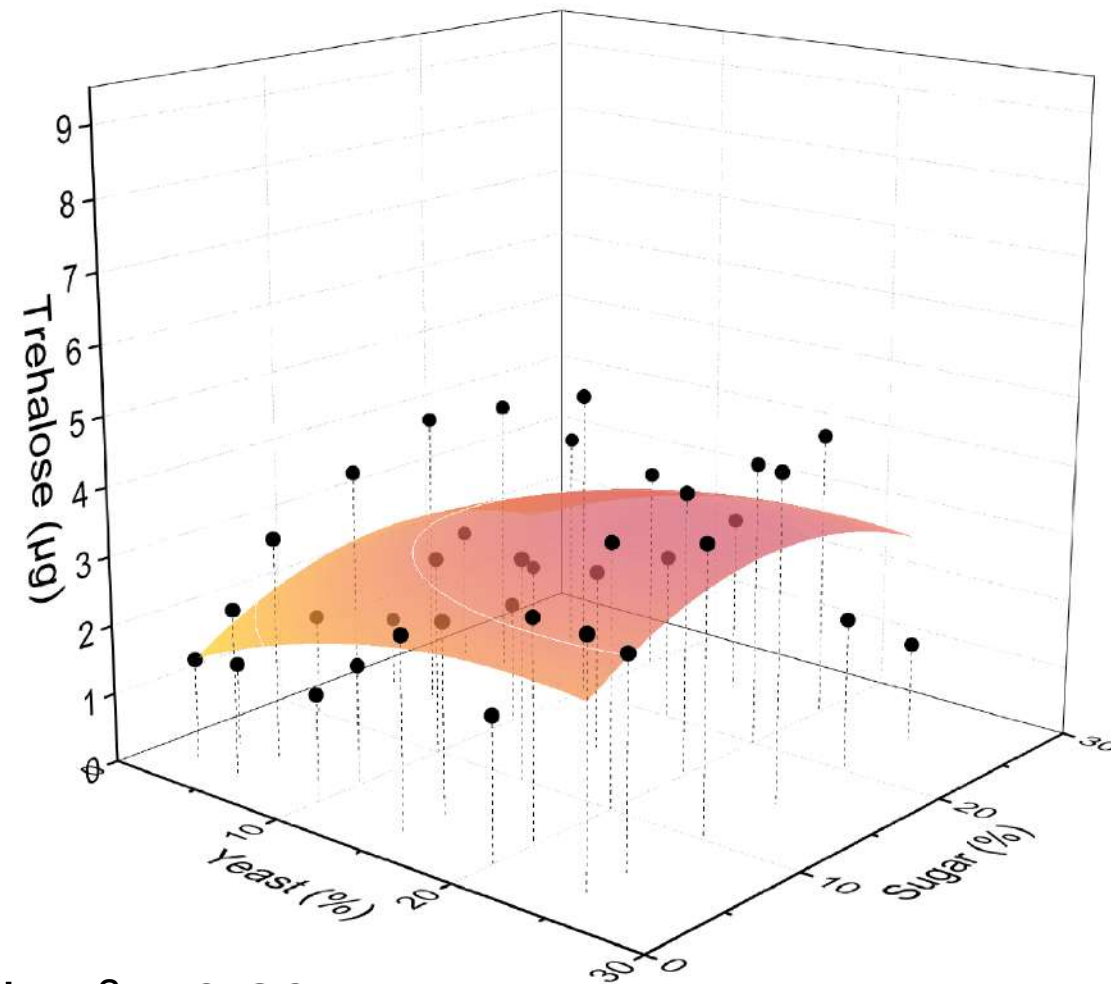
Adj. $R^2 = 0.09$

Figure S12.

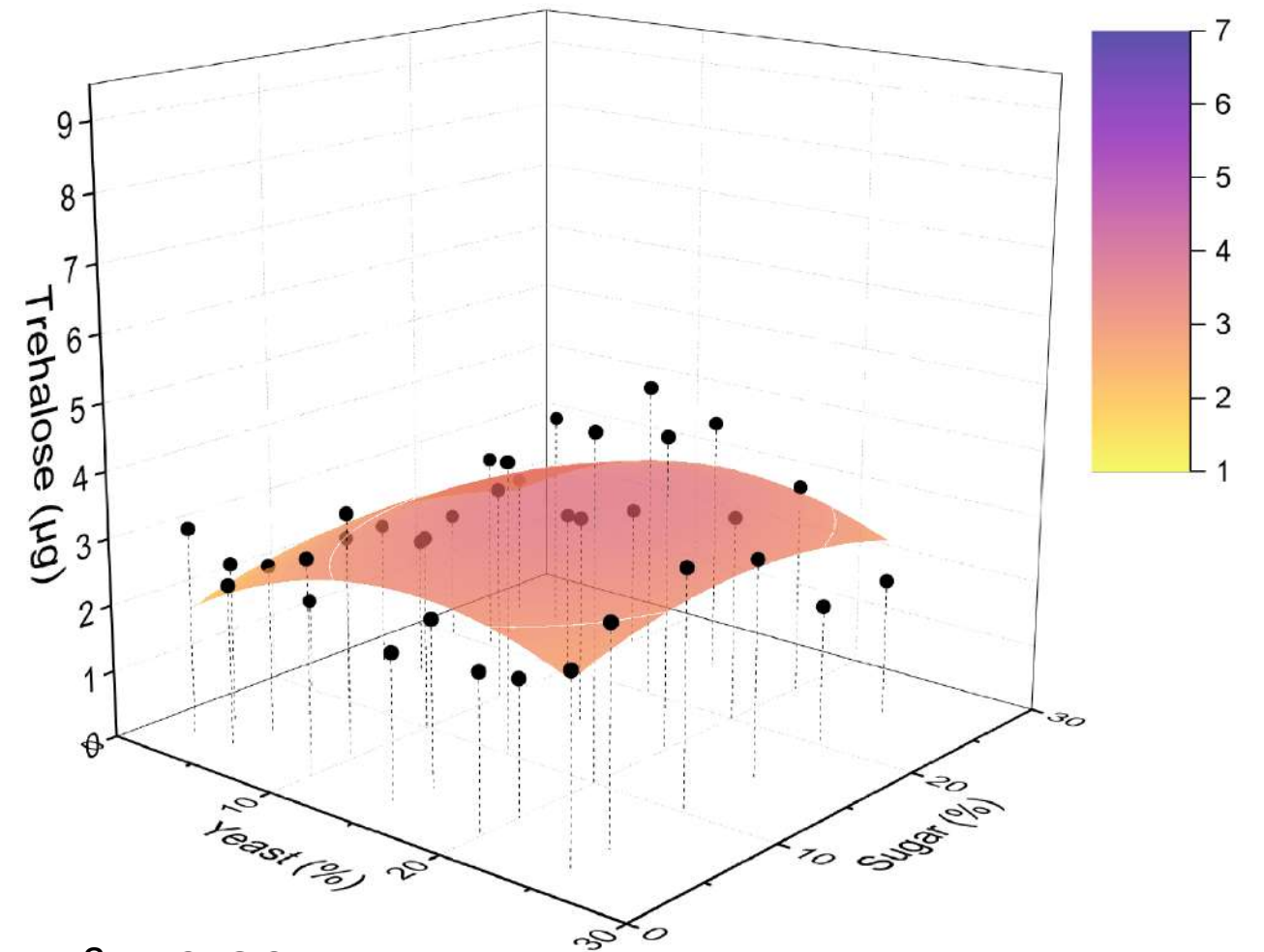
w^{1118}

SK

Males

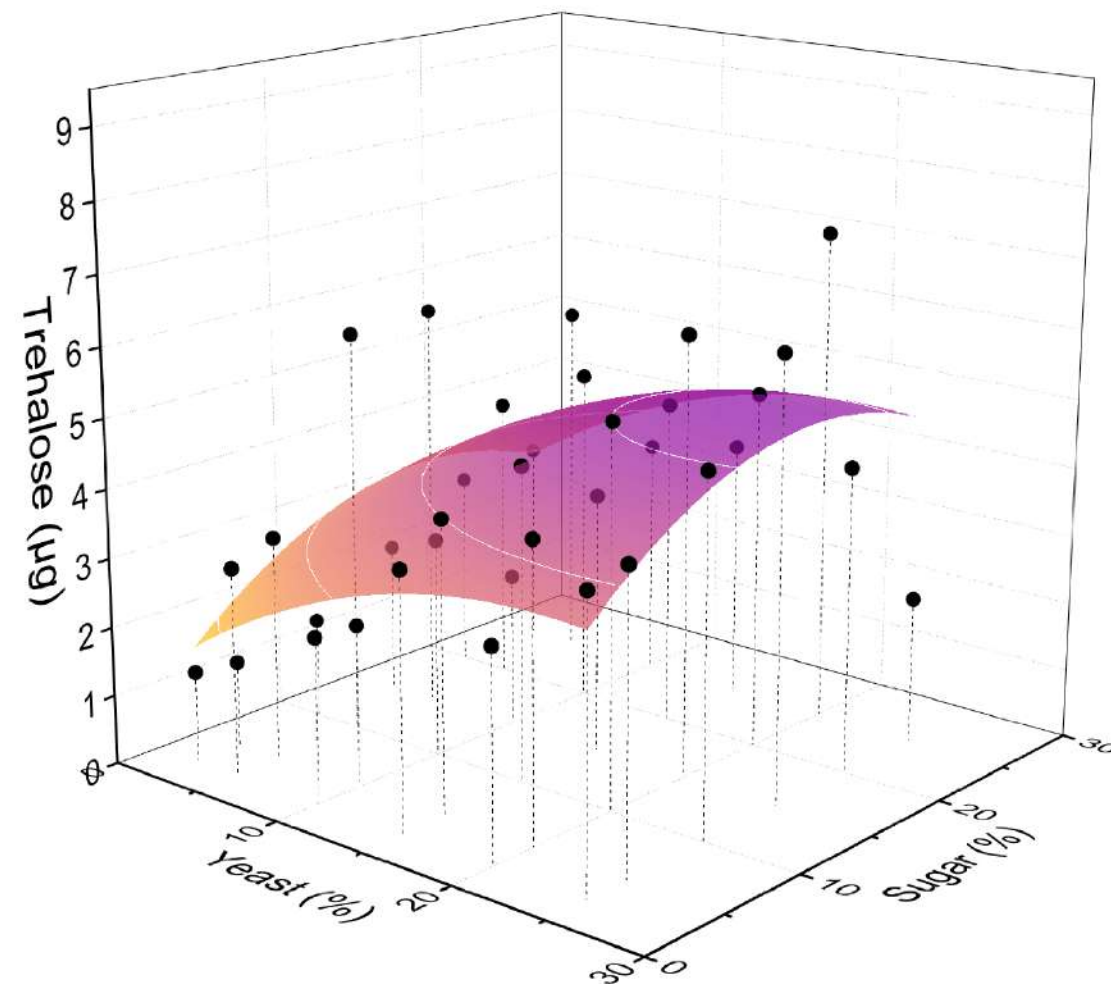


Adj. $R^2 = 0.20$

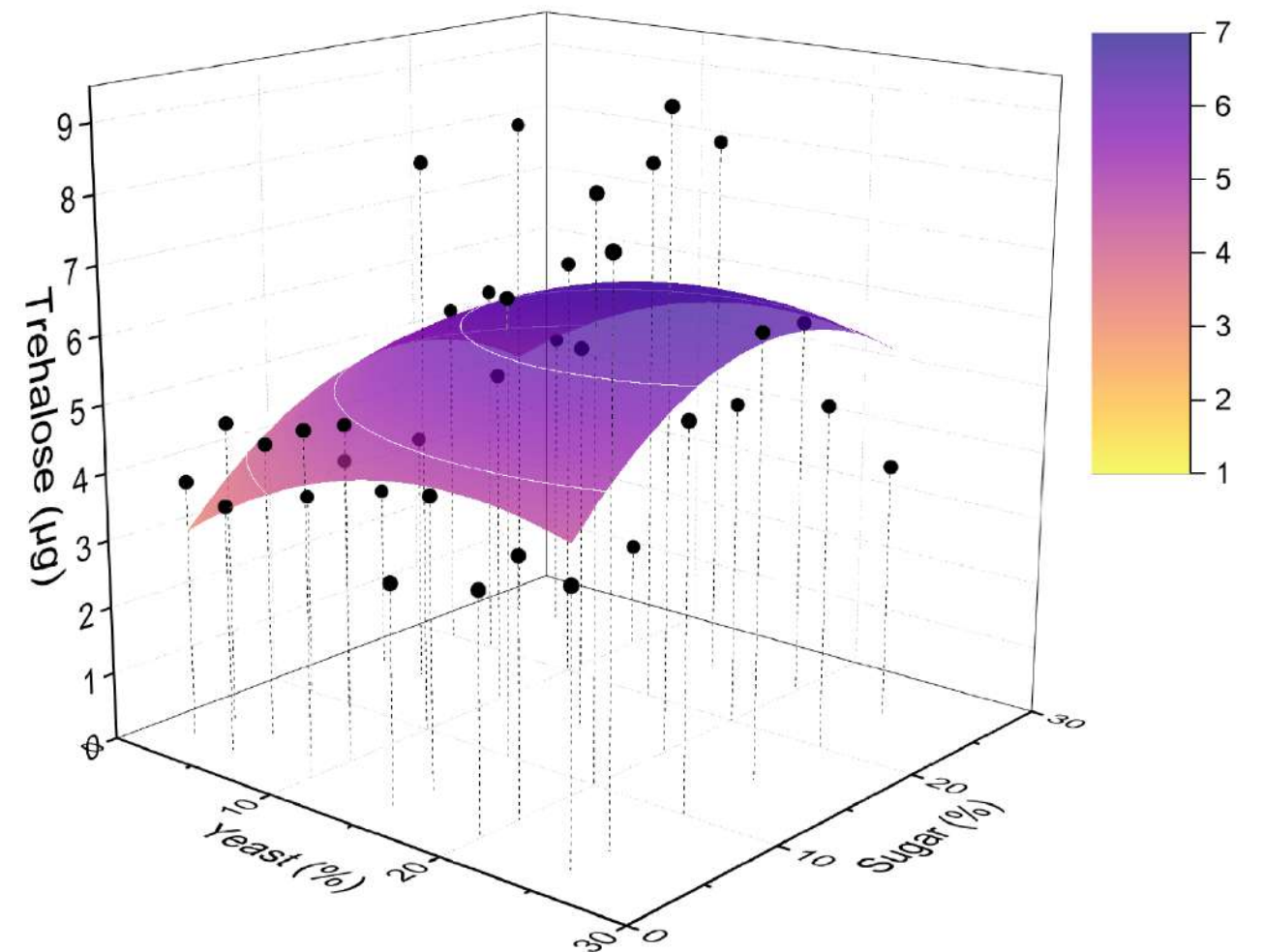


Adj. $R^2 = 0.20$

Females



Adj. $R^2 = 0.32$



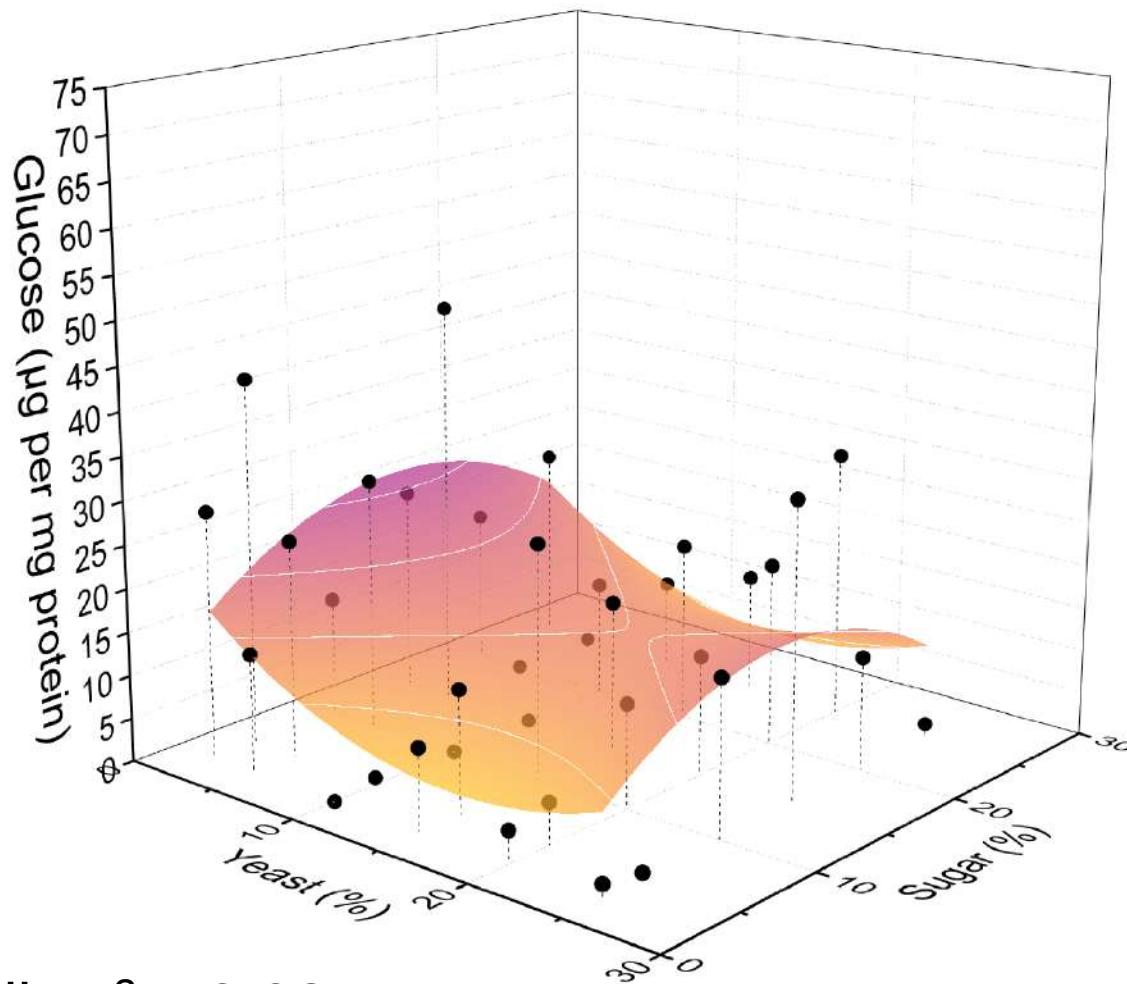
Adj. $R^2 = 0.12$

Figure S13.

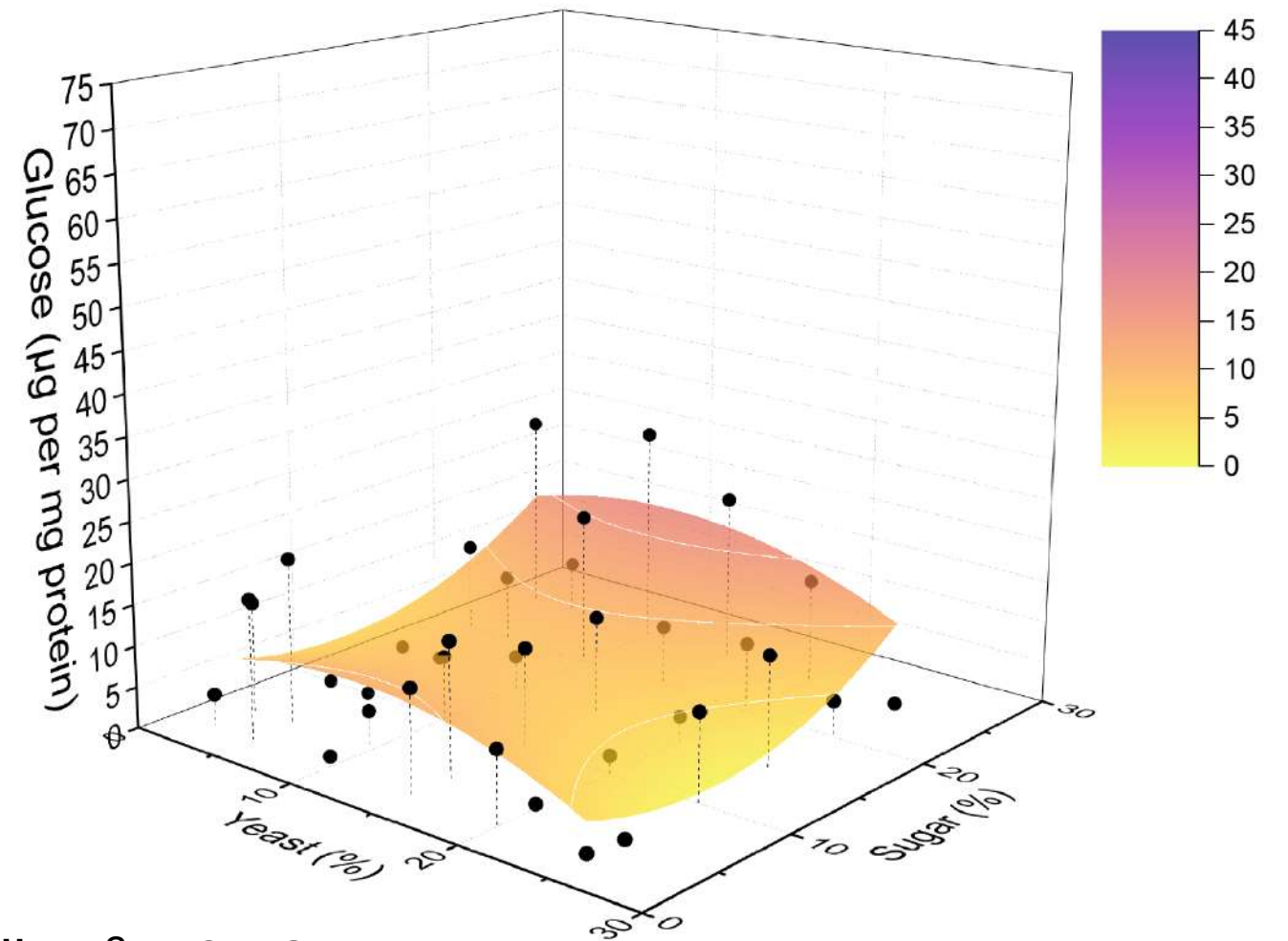
w^{1118}

SK

Males

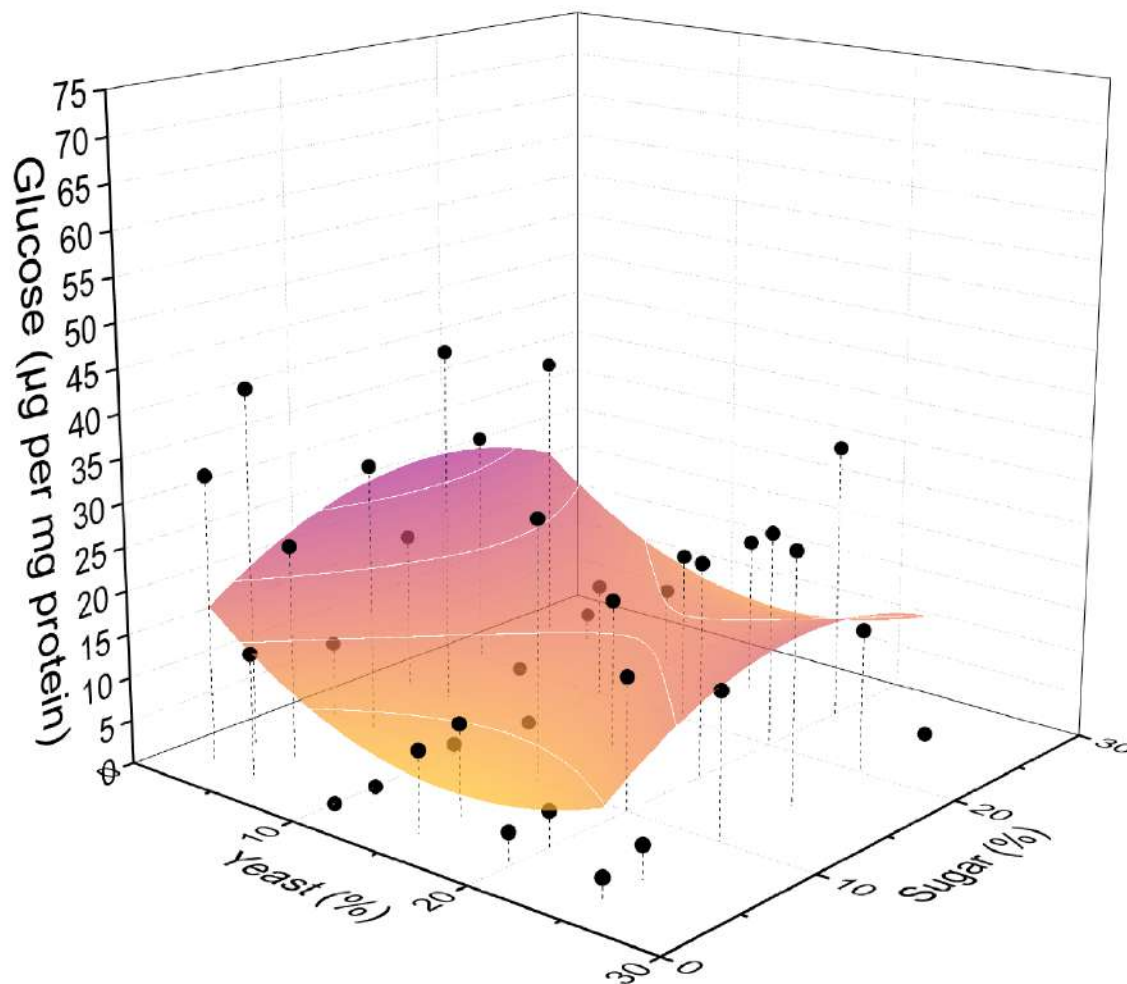


Adj. $R^2 = 0.08$

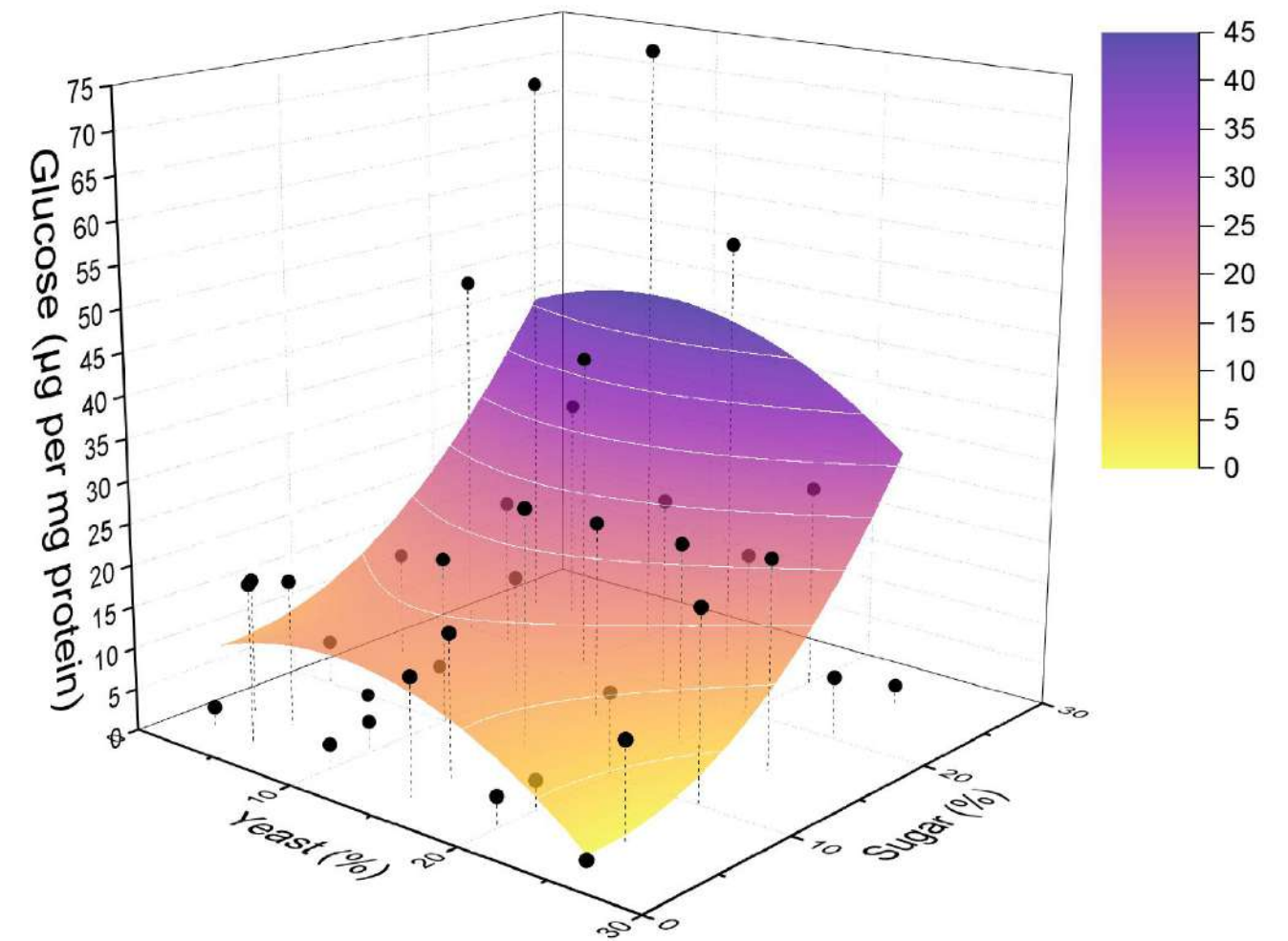


Adj. $R^2 = 0.18$

Females



Adj. $R^2 = 0.08$



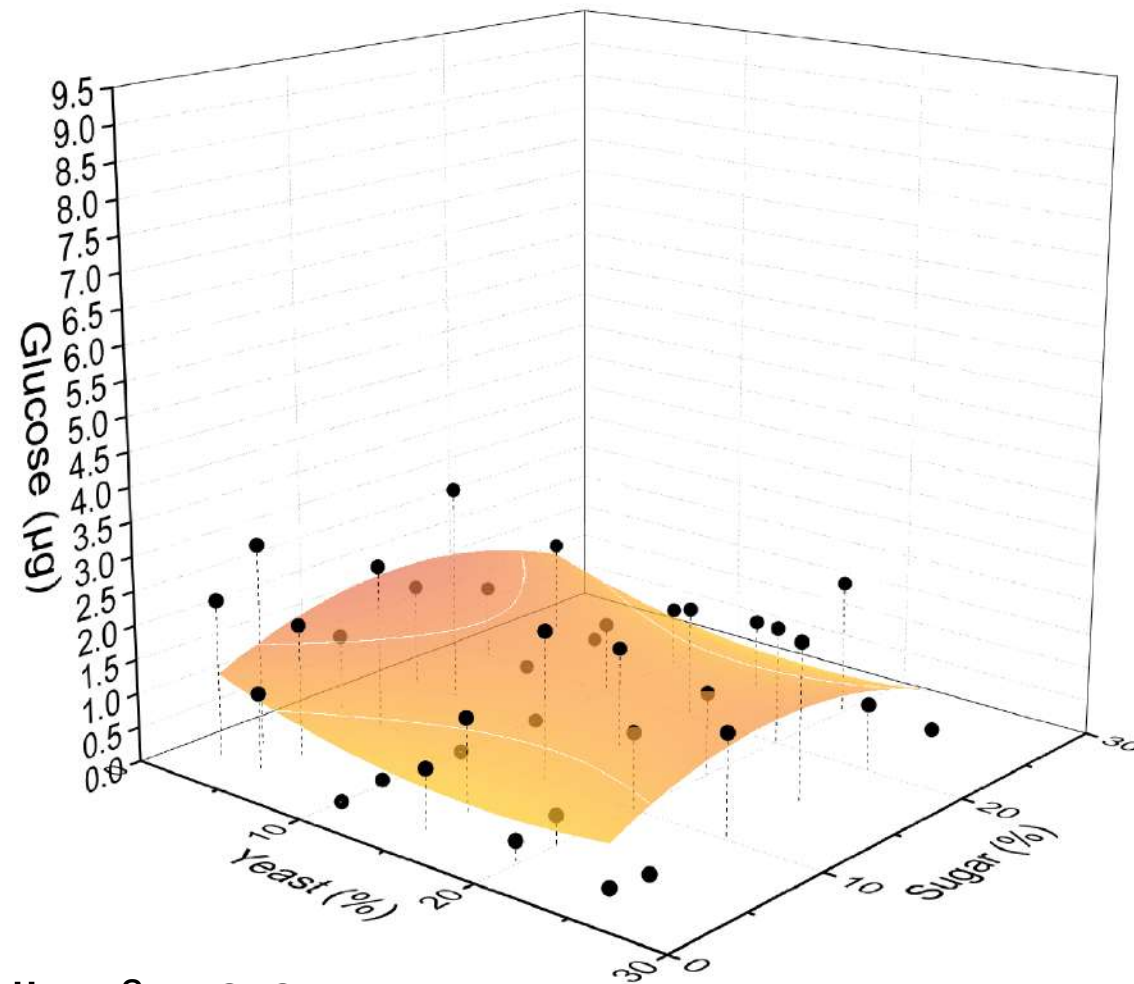
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Figure S14.

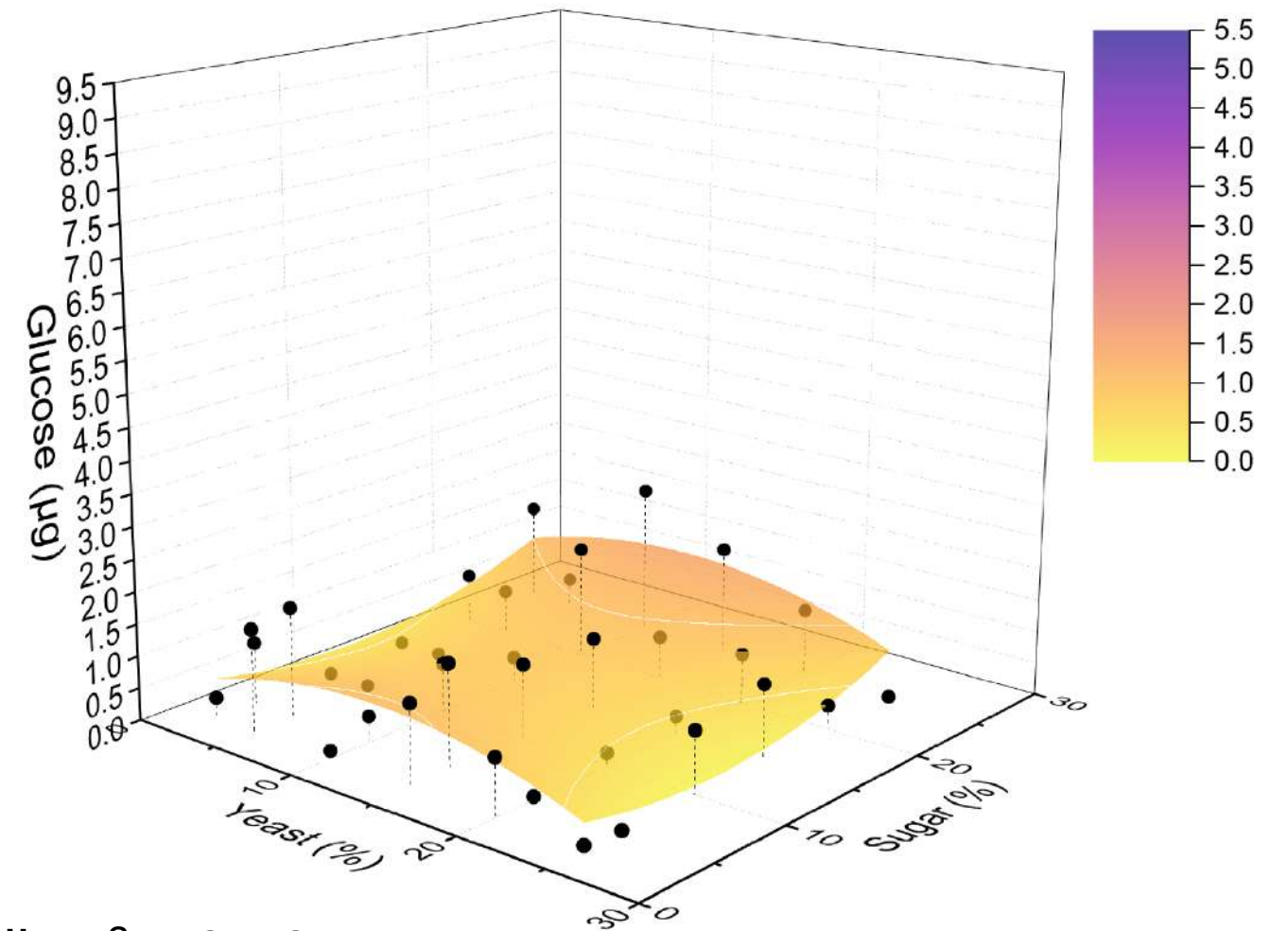
w^{1118}

SK

Males

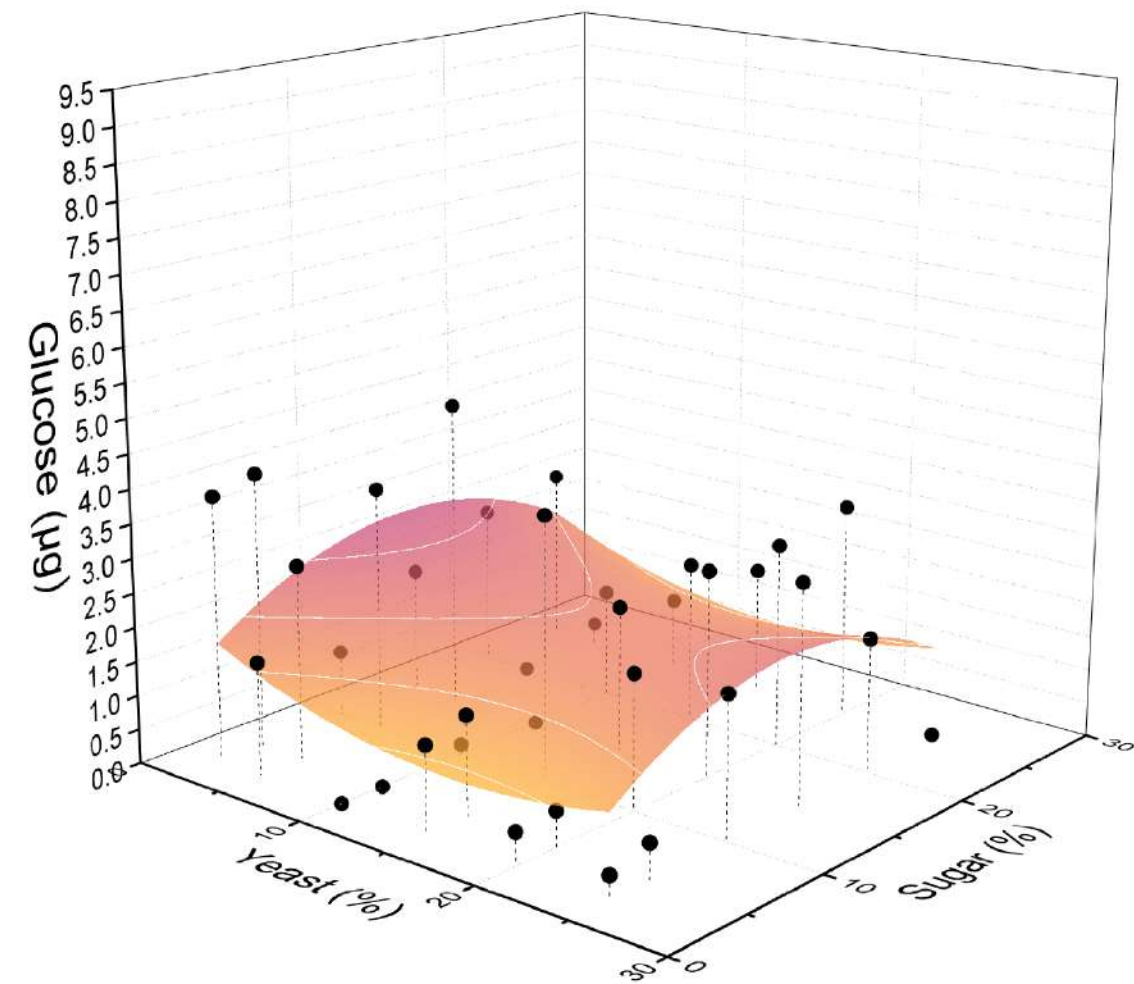


Adj. $R^2 = 0.05$

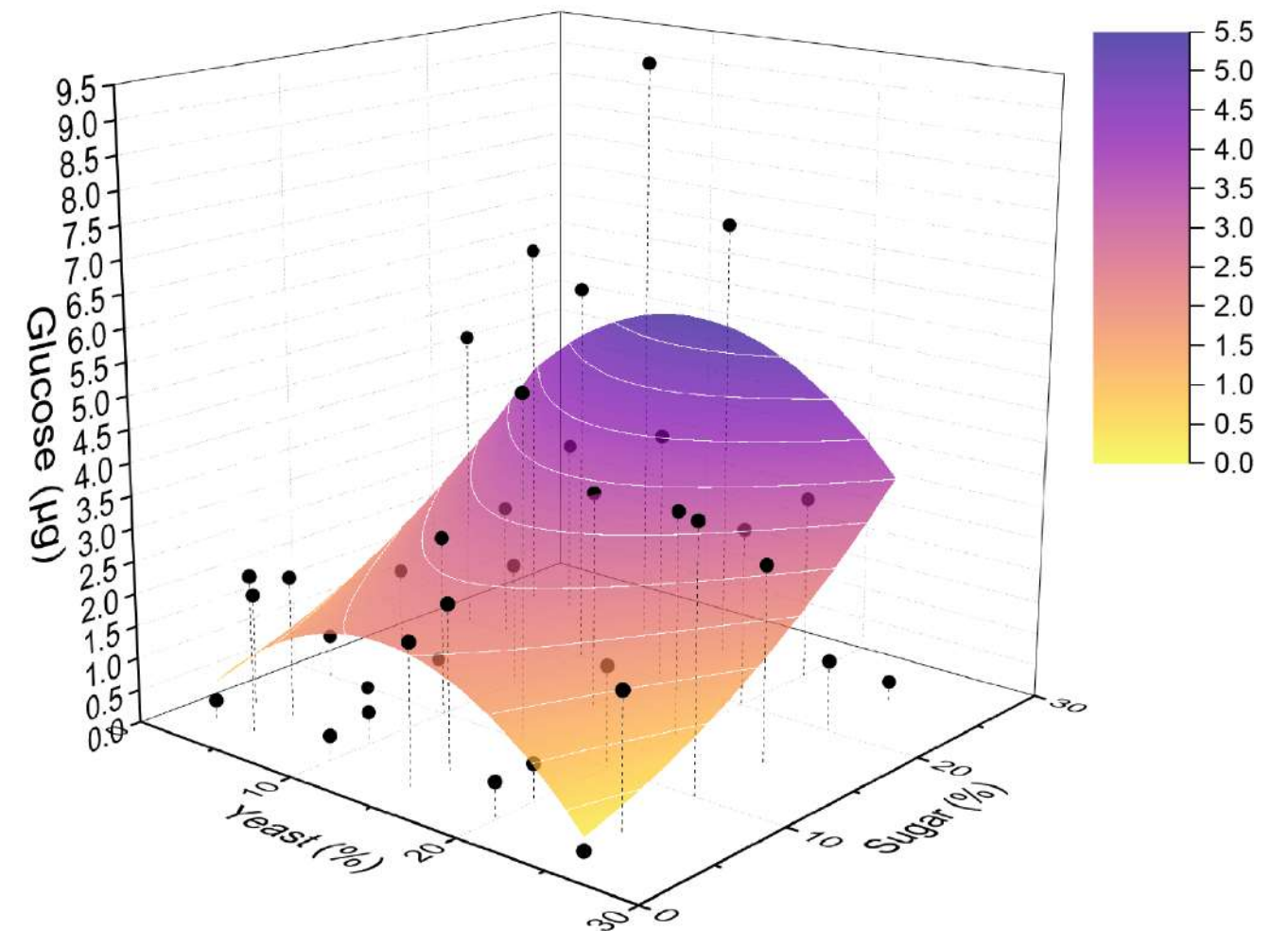


Adj. $R^2 = 0.16$

Females



Adj. $R^2 = 0.02$



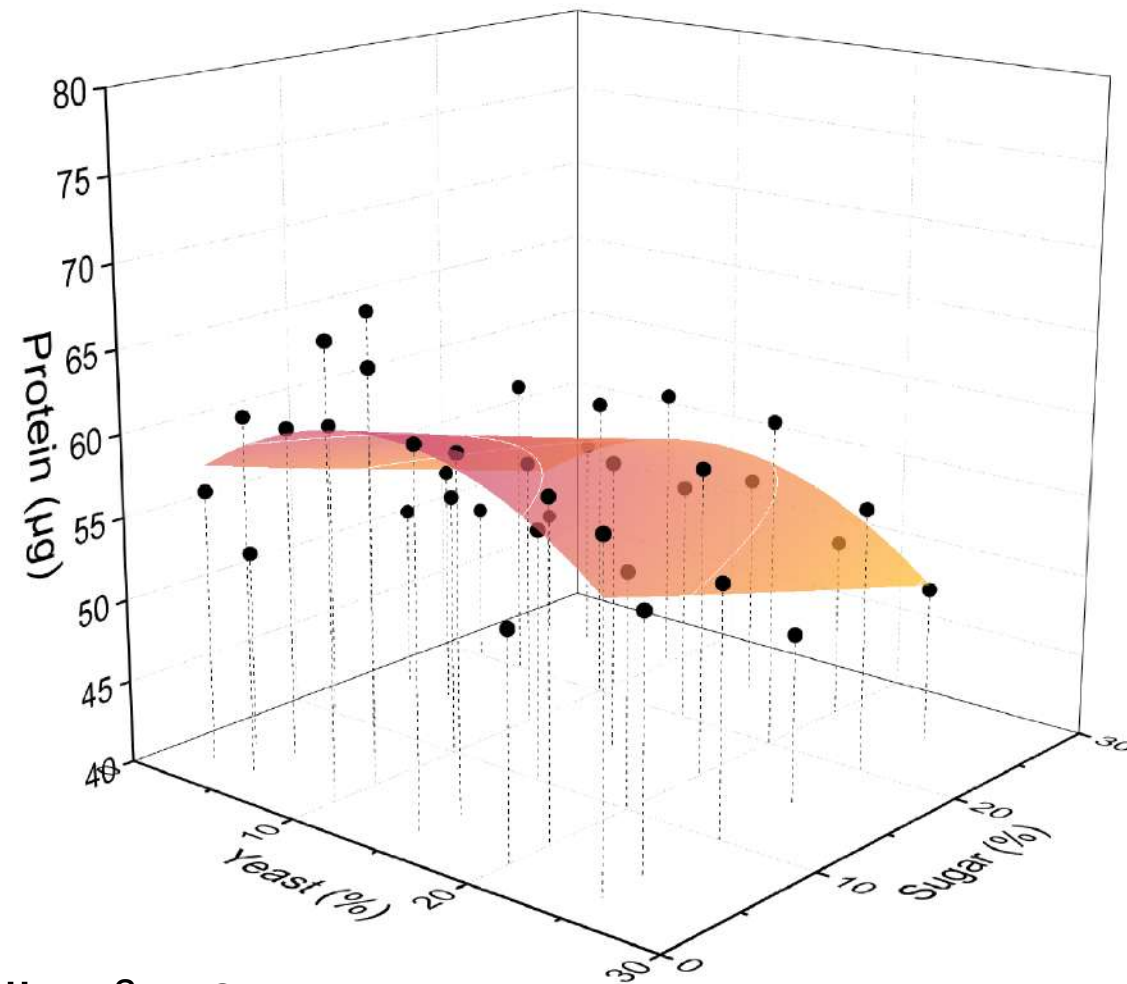
Adj. $R^2 = 0.33$

Figure S15.

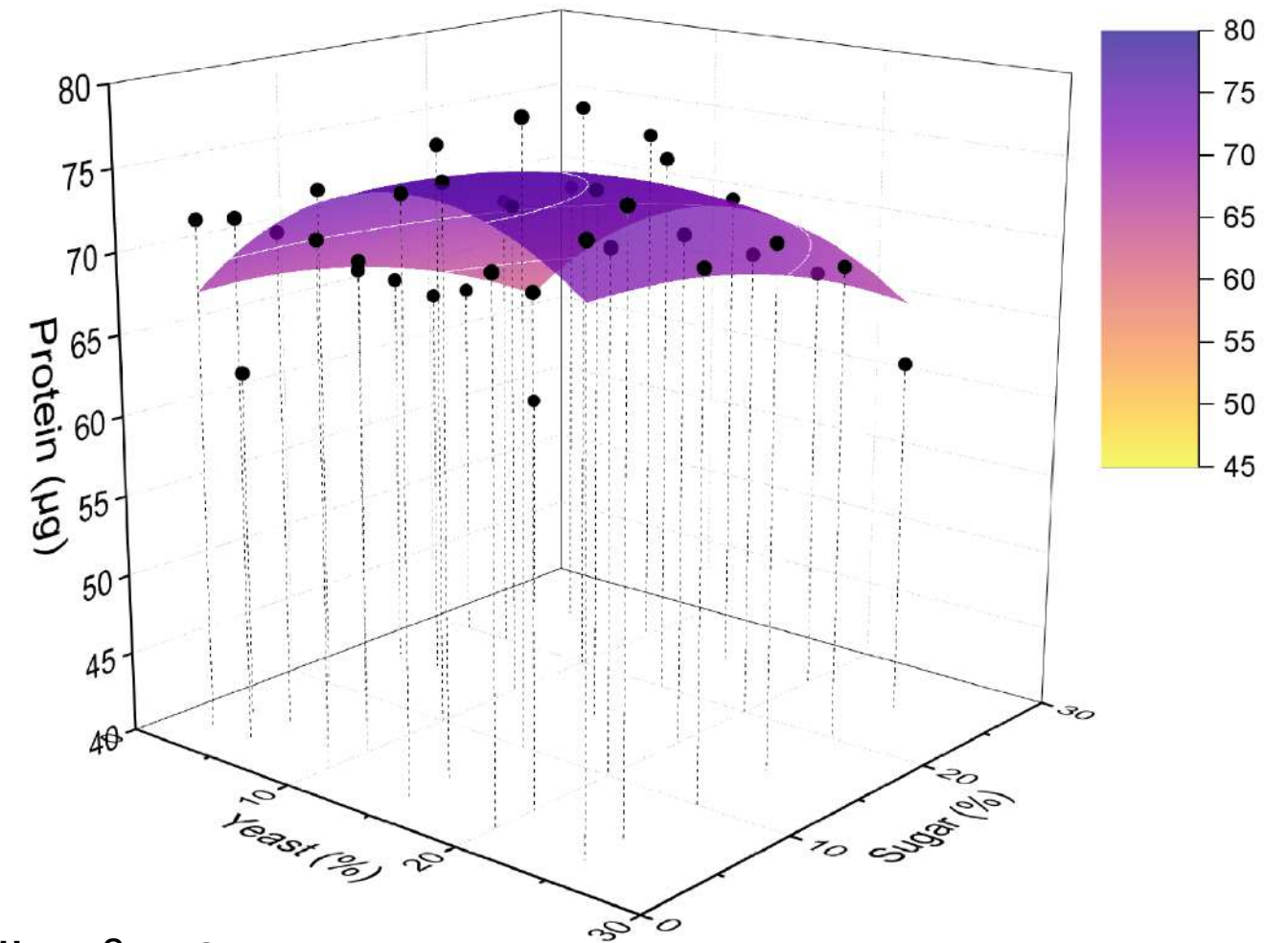
w^{1118}

SK

Virgin
males

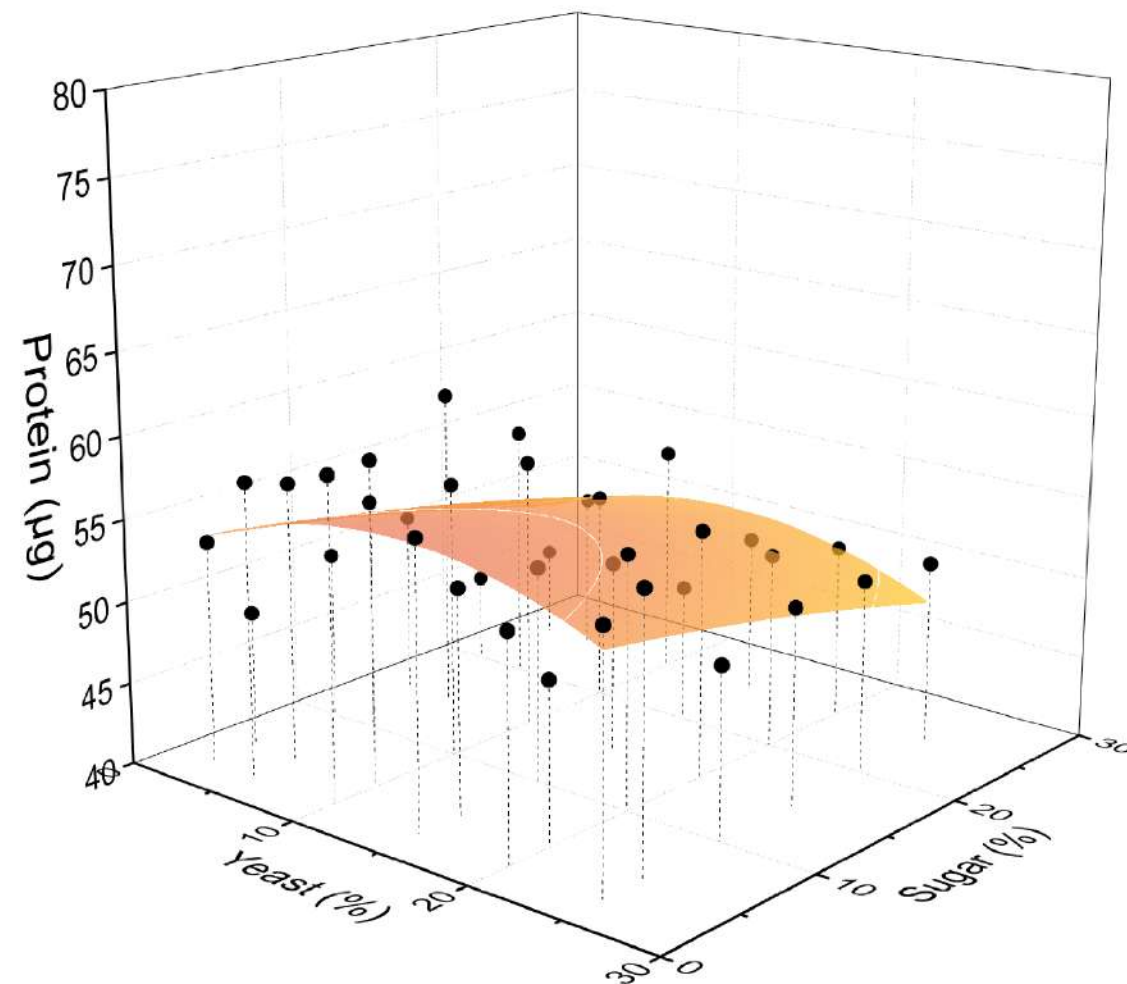


Adj. $R^2 = 0.41$

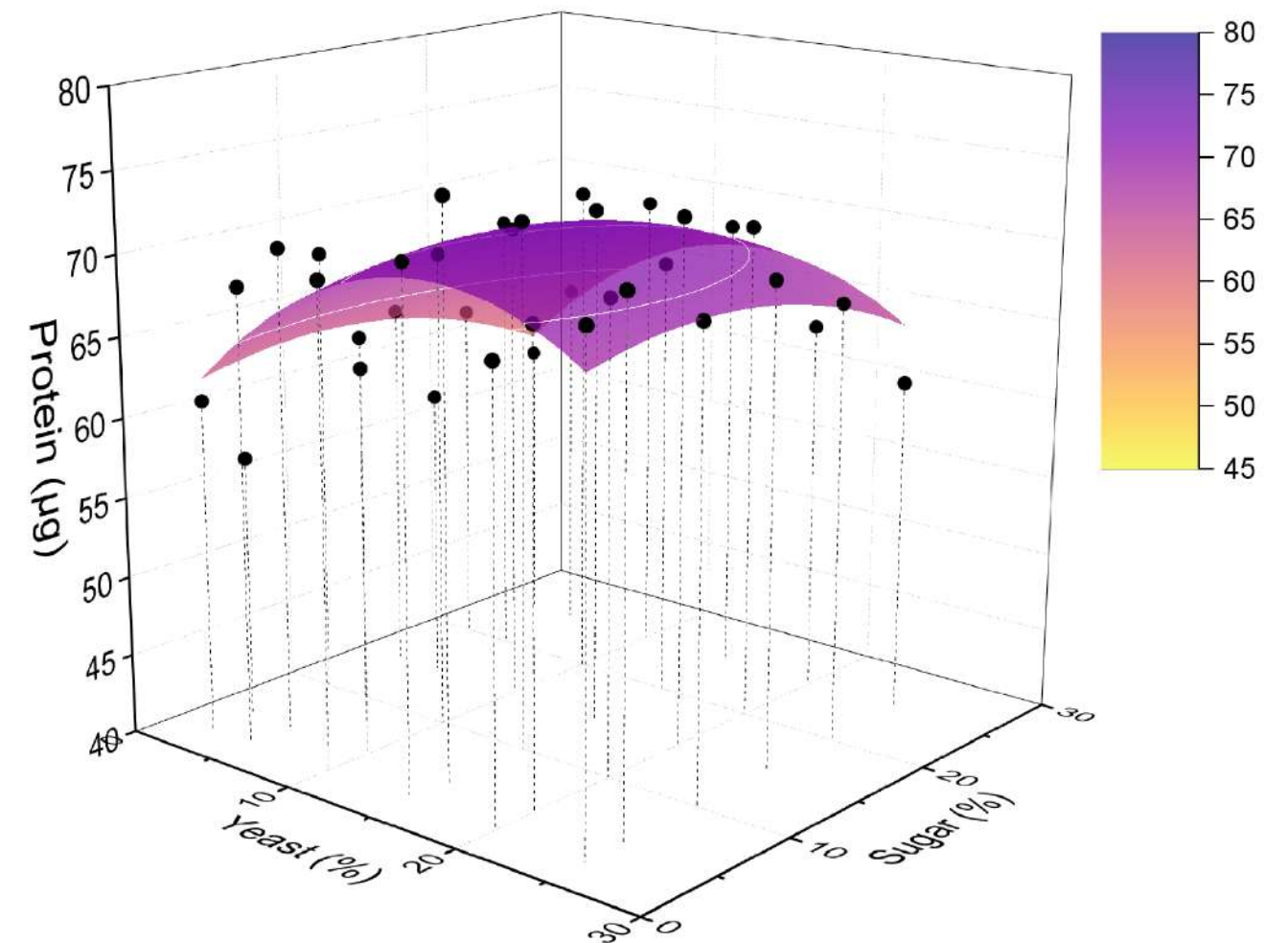


Adj. $R^2 = 0.47$

Mated
males



Adj. $R^2 = 0.29$



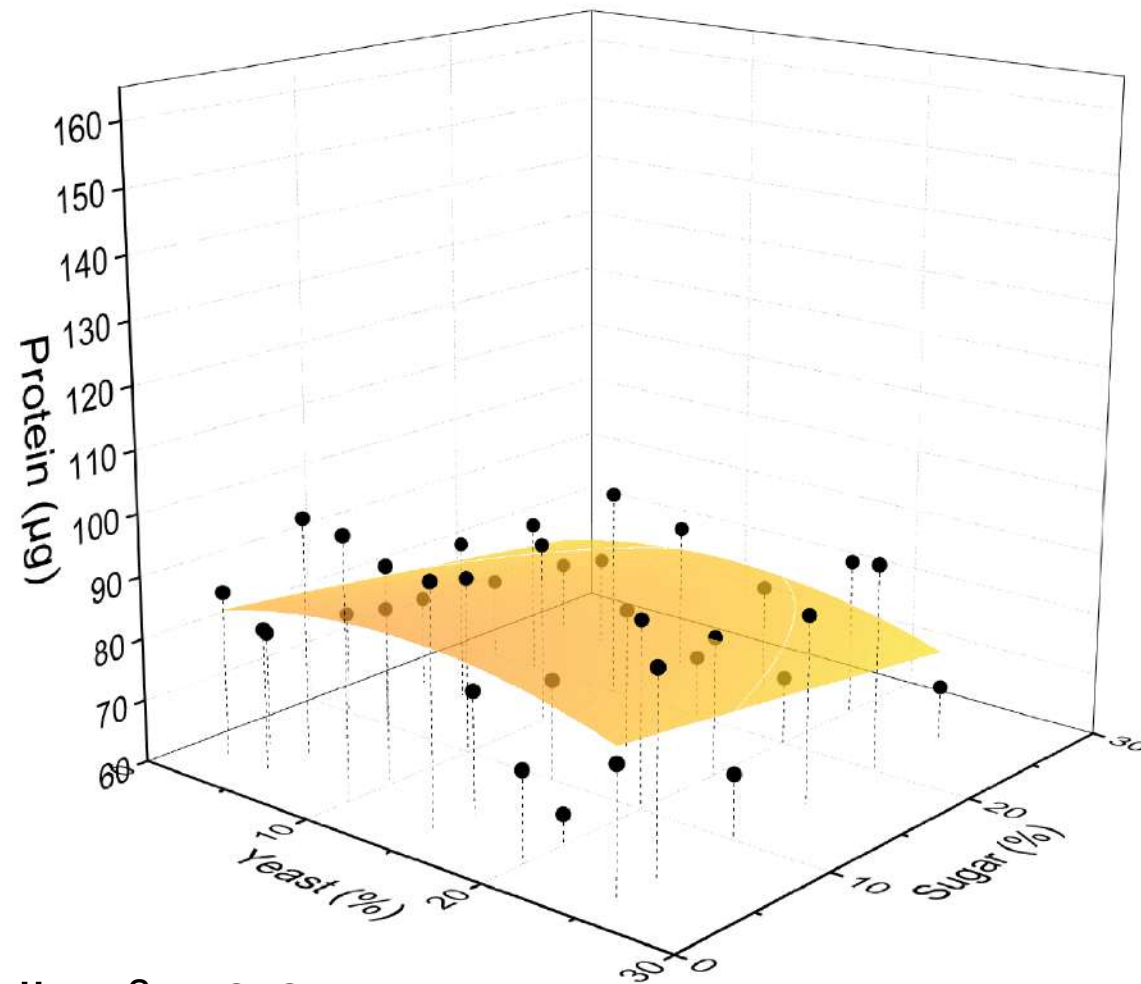
Adj. $R^2 = 0.50$

Figure S16.

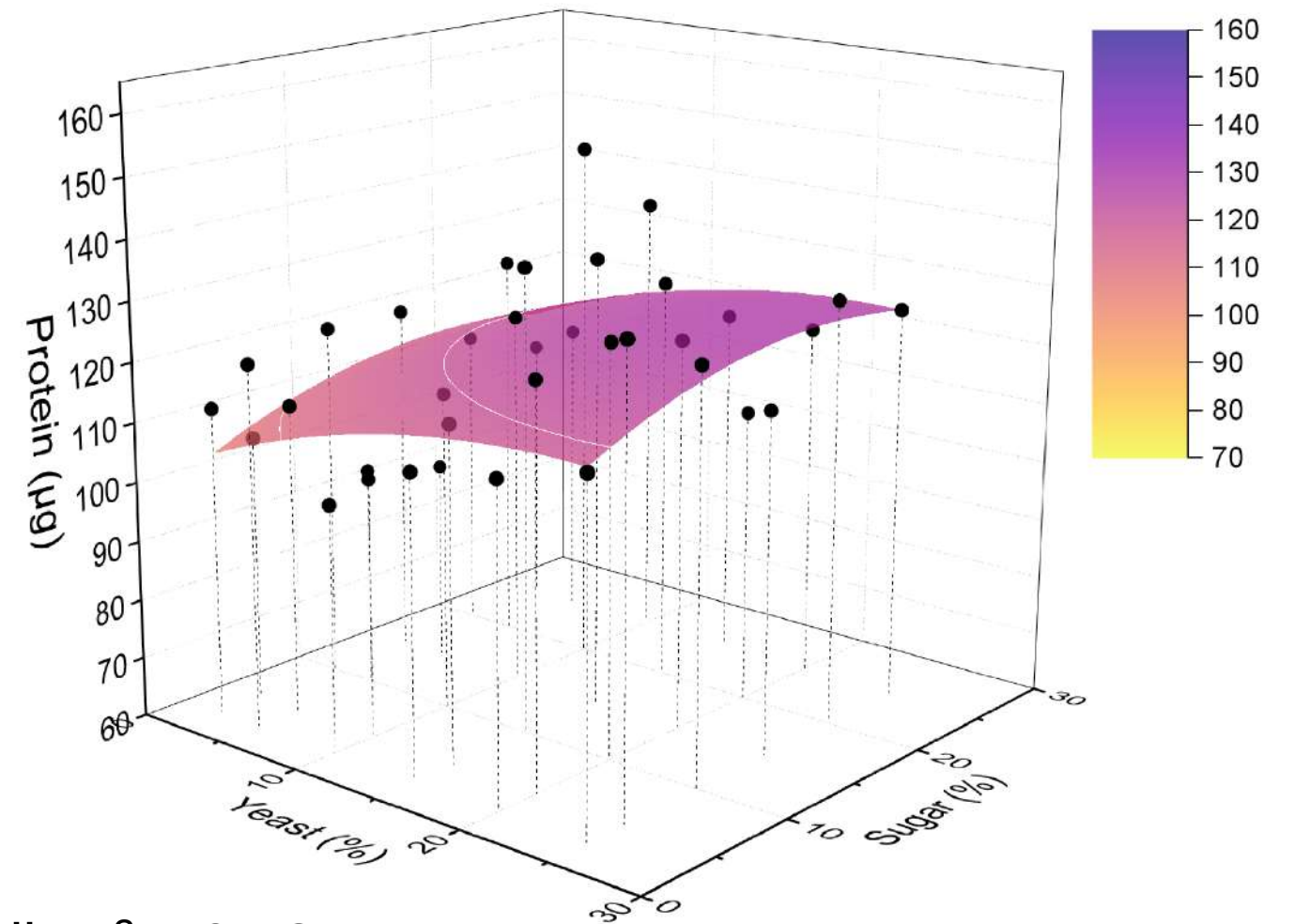
w^{1118}

SK

Virgin
females

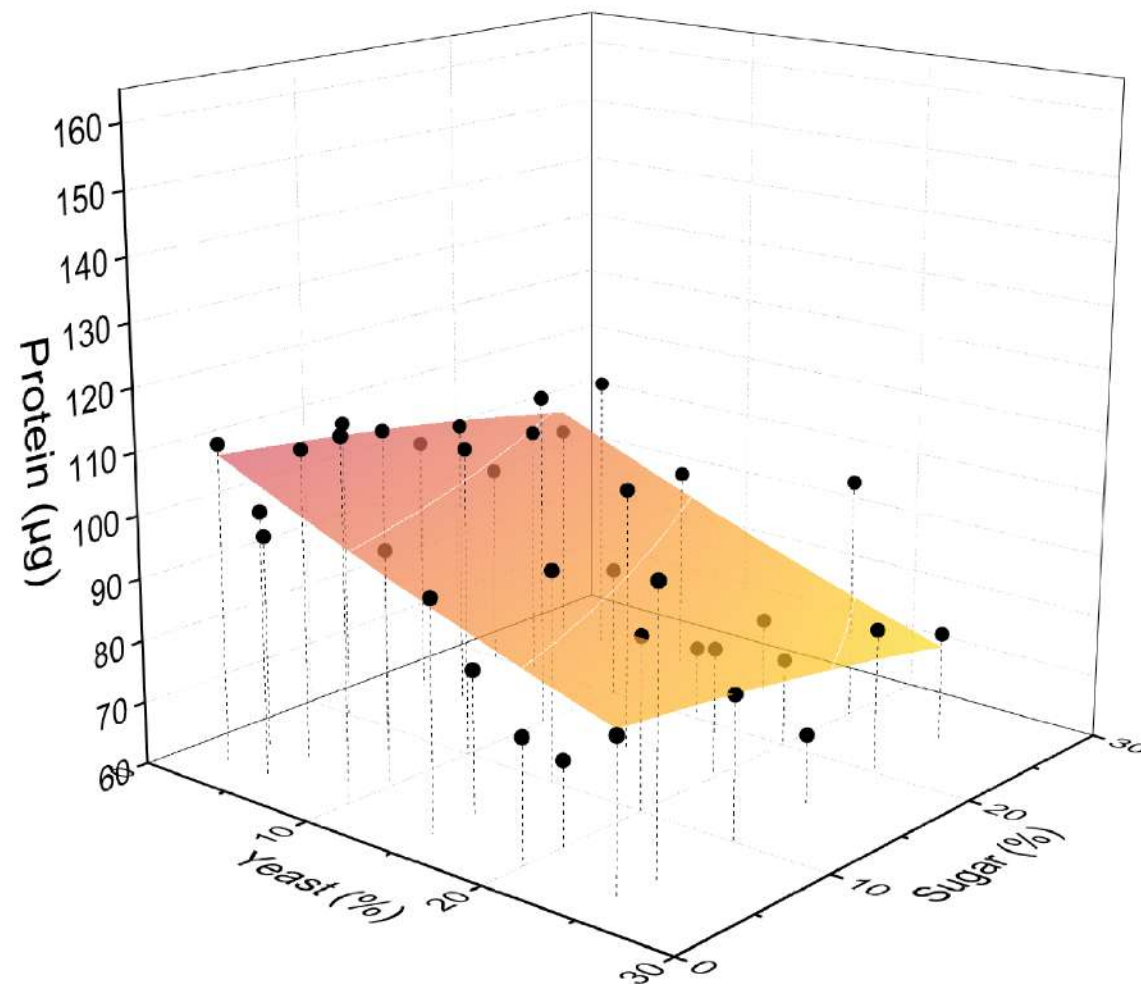


Adj. $R^2 = 0.04$

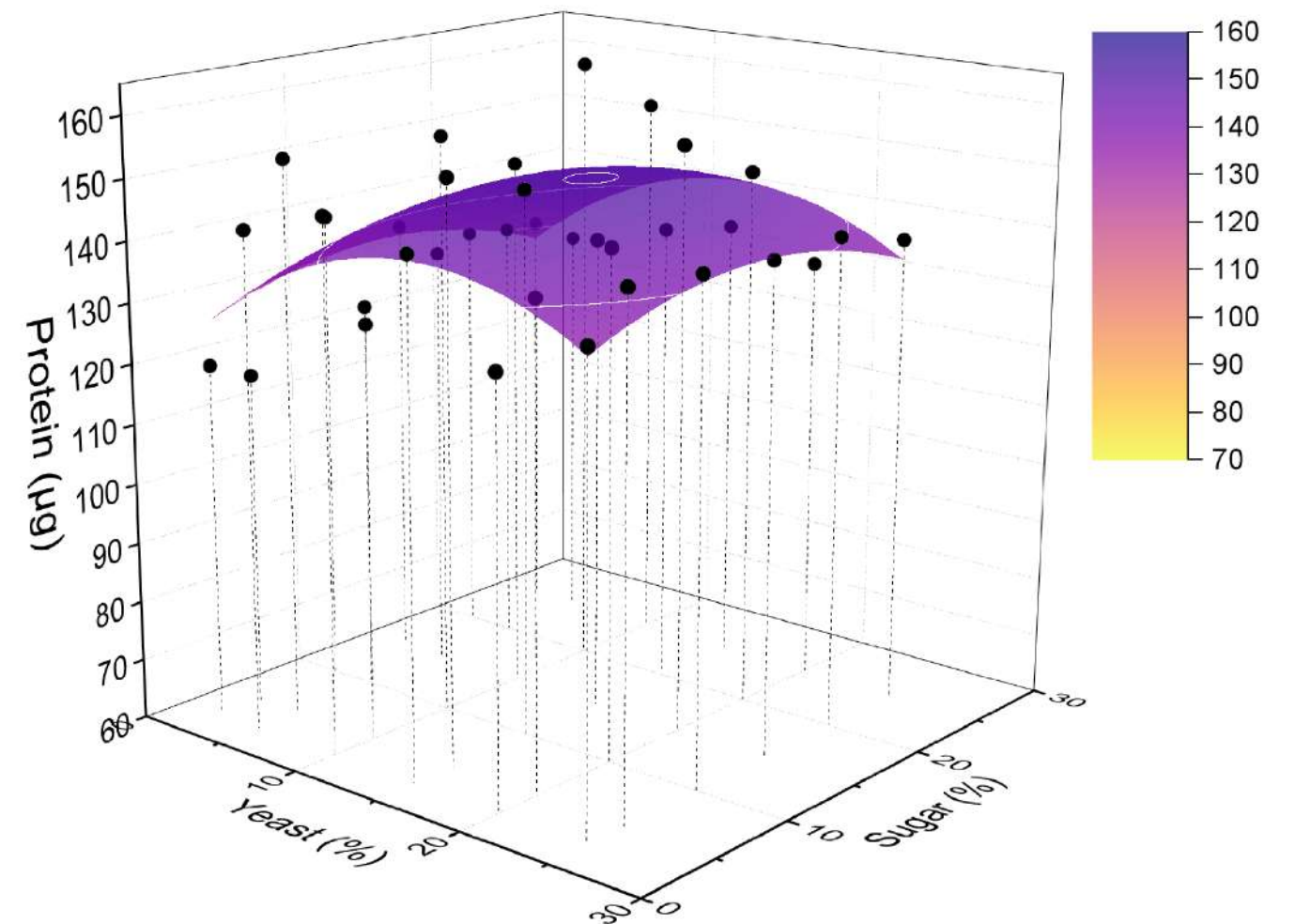


Adj. $R^2 = 0.18$

Mated
females



Adj. $R^2 = 0.40$



Adj. $R^2 = 0.27$

FEMALES

Mated

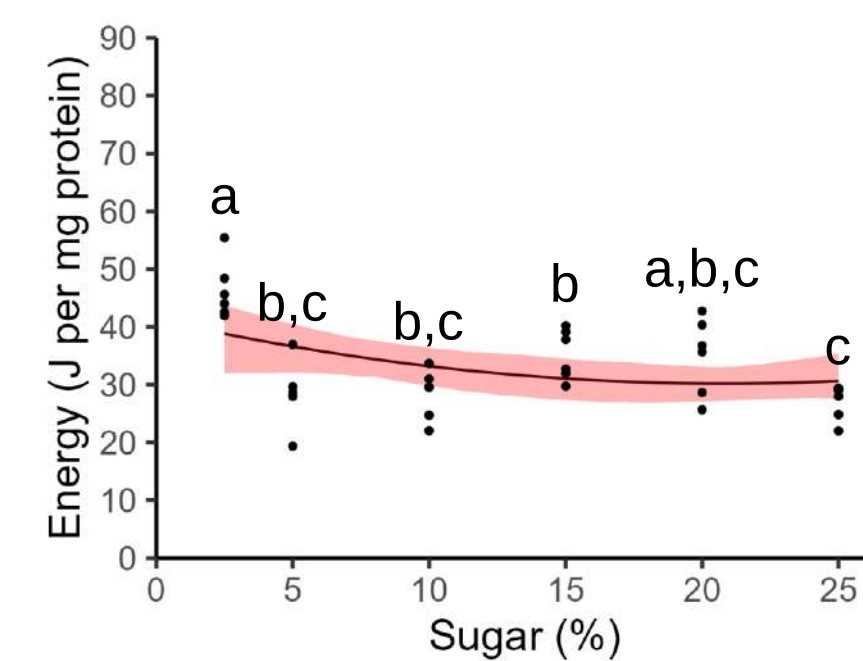


Figure 2 is a scatter plot showing the relationship between Sugar (%) on the x-axis and Energy (J per mg protein) on the y-axis. The x-axis ranges from 0 to 25, and the y-axis ranges from 0 to 90. Data points are plotted for 5, 10, 15, 20, and 25% sugar. A red shaded area represents the confidence interval of the fitted curve. Letters above the data points indicate statistical significance groups: 'a,b' for 5%, 'c' for 10%, 'a,c' for 15%, 'b' for 20%, and 'a,b' for 25%.

Sugar (%)	Energy (J per mg protein)	Significance Group
5	~38	a,b
10	~45	c
15	~42	a,c
20	~35	b
25	~38	a,b

Figure 2 is a scatter plot showing the relationship between Sugar (%) on the x-axis and Energy (J per mg protein) on the y-axis. The x-axis ranges from 0 to 25, and the y-axis ranges from 0 to 90. There are 10 data points, each representing a different strain. A red regression line is fitted to the data, and a pink shaded area represents the confidence interval. The data points are labeled with letters indicating significant differences: 'a, b, c' for 5% sugar, 'a' for 10% sugar, 'b, c' for 15% and 20% sugar, and 'c' for 25% sugar.

Sugar (%)	Energy (J per mg protein)	Significance Group
5	18	a, b, c
5	22	a, b, c
5	25	a, b, c
5	32	a, b, c
5	35	a, b, c
5	48	a, b, c
10	22	a
10	25	a
10	28	a
10	30	a
15	28	b, c
15	38	b, c
20	32	b, c
20	35	b, c
20	42	b, c
25	30	c
25	42	c
25	45	c
25	48	c
25	52	c

Figure 1 is a scatter plot showing the relationship between Energy (J per mg protein) on the y-axis and Sugar (%) on the x-axis. The y-axis ranges from 0 to 90, and the x-axis ranges from 0 to 25. Data points are represented by black dots with vertical error bars. A red line represents the fitted curve, and a red shaded area represents the confidence interval. Letters 'a' are placed above the data points at 2.5%, 5%, 10%, 15%, 20%, and 25% sugar, indicating no significant differences between these groups.

Sugar (%)	Energy (J per mg protein)	Significance
2.5	~35	a
5	~38	a
10	~40	a
15	~42	a
20	~42	a
25	~40	a

Figure 2 is a scatter plot with a fitted quadratic curve showing Energy (J per mg protein) on the y-axis (0 to 90) versus Sugar (%) on the x-axis (0 to 25). Data points are shown for 5%, 10%, 15%, 20%, and 25% sugar concentrations. A red shaded area represents the confidence interval of the fit. Letters 'a' are placed above the data points at 5%, 10%, 15%, and 25% sugar, indicating no significant difference between these groups.

Figure 1 is a scatter plot showing the relationship between Energy (J per mg protein) on the y-axis and Sugar (%) on the x-axis. The y-axis ranges from 0 to 90, and the x-axis ranges from 0 to 25. Data points are represented by black dots with vertical error bars. A red shaded area represents the confidence interval around the black regression line. Letters above the data points indicate statistical significance groups: 'a' for 2.5%, 5%, and 20%; 'a,b' for 10% and 25%; and 'b' for 15%.

Sugar (%)	Energy (J per mg protein)	Significance Group
2.5	~35	a
5	~40	a
10	~50	a,b
15	~50	b
20	~45	a,b
25	~40	a,b

Figure S18.

MALES

FEMALES

YEAST

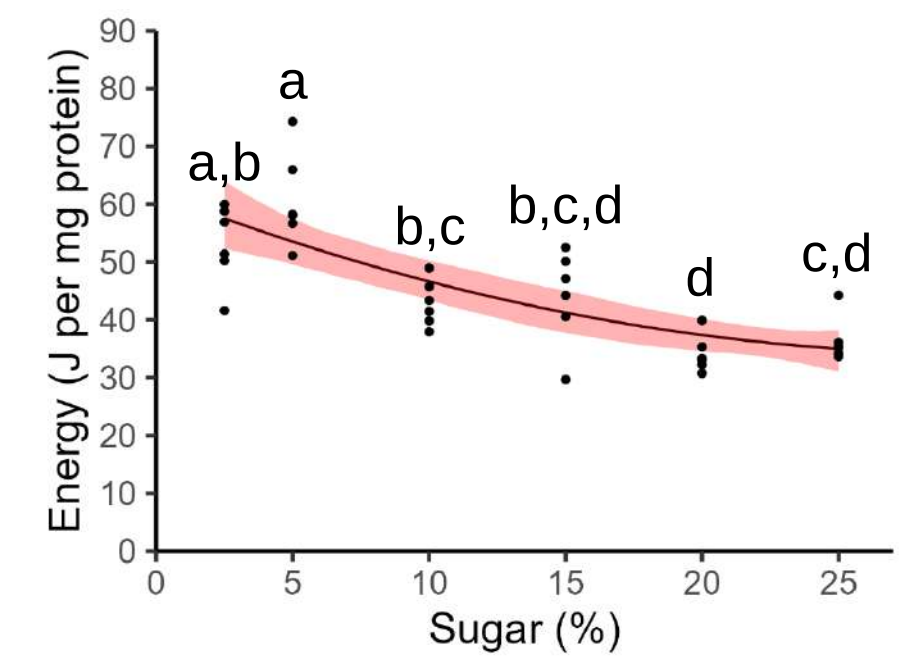
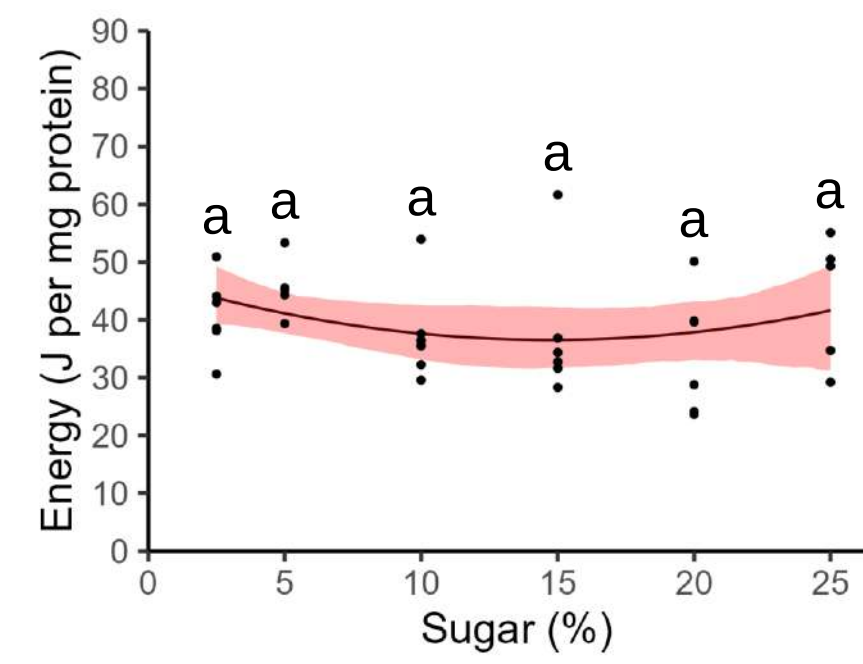
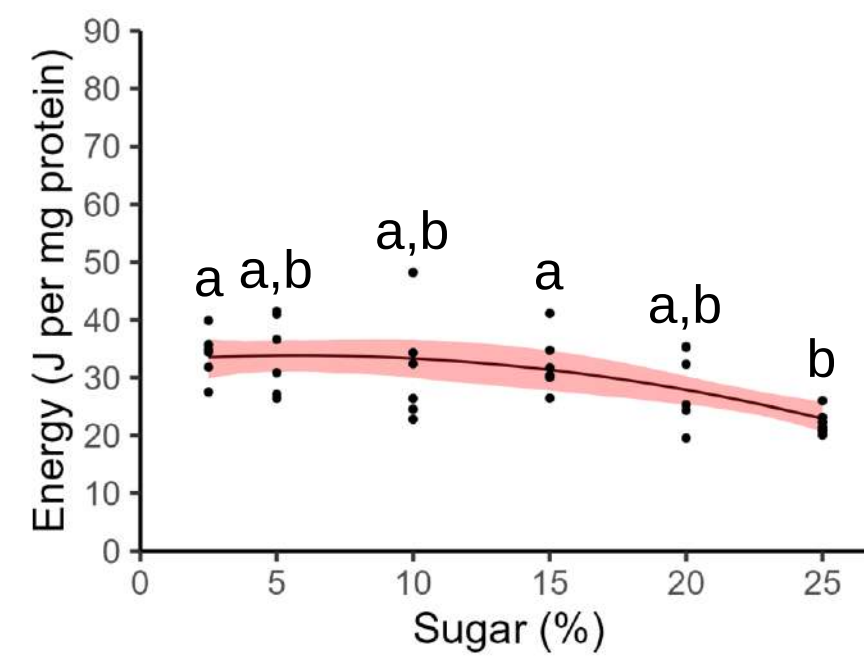
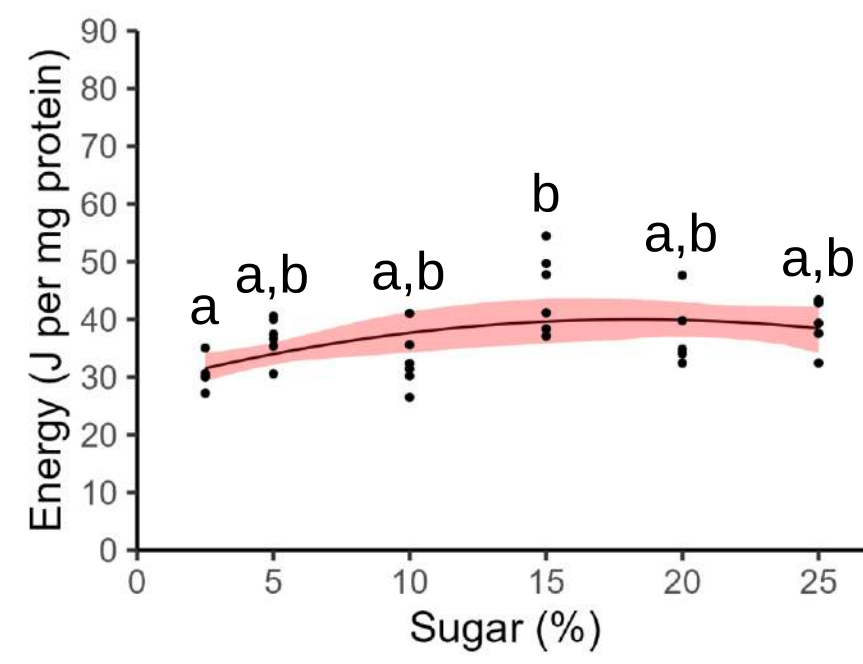
Virgin

Mated

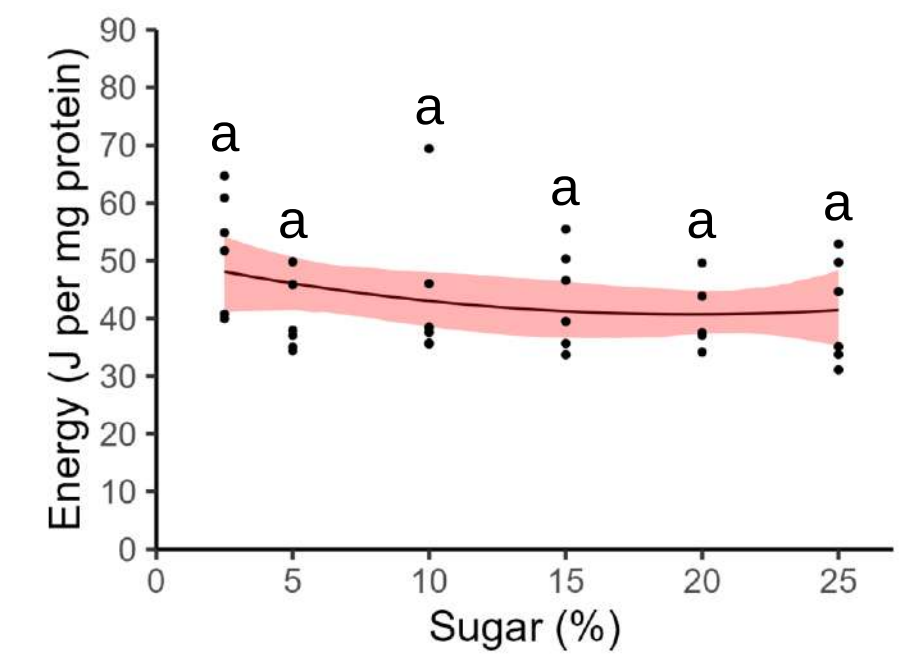
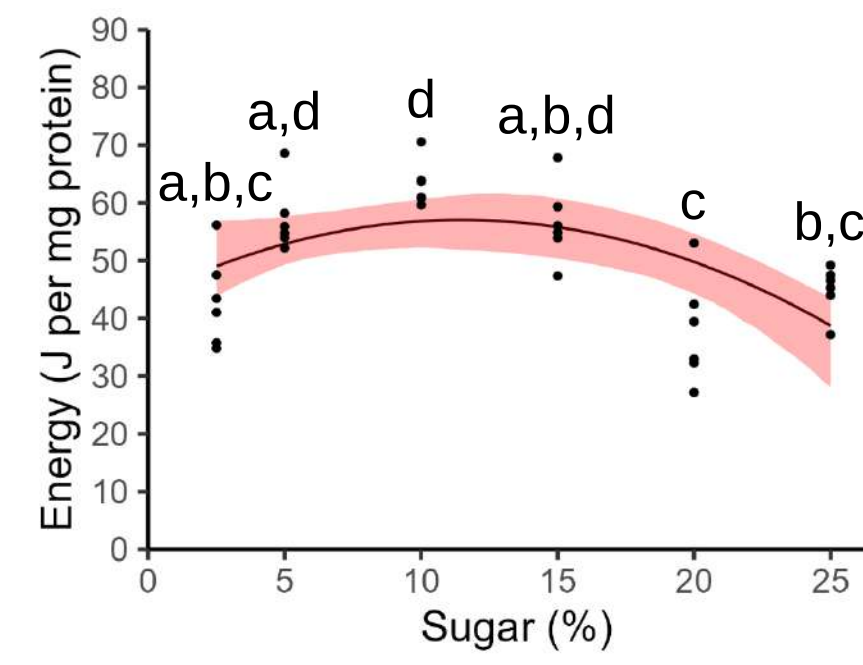
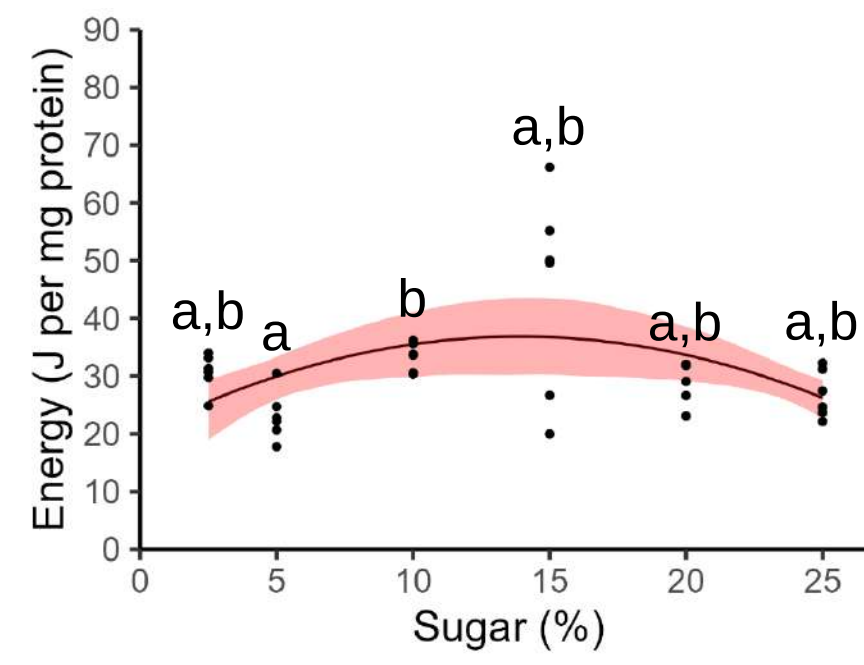
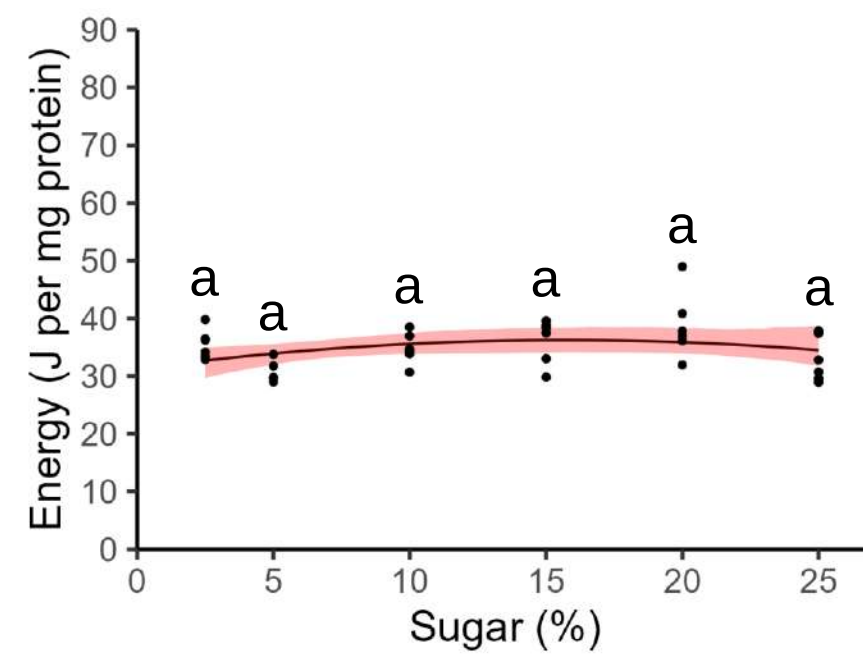
Virgin

Mated

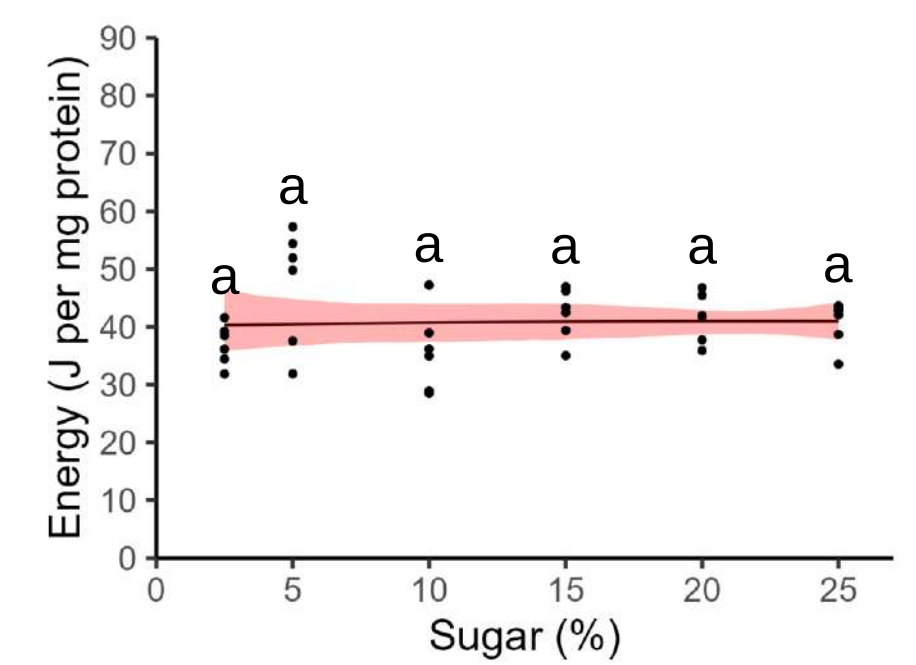
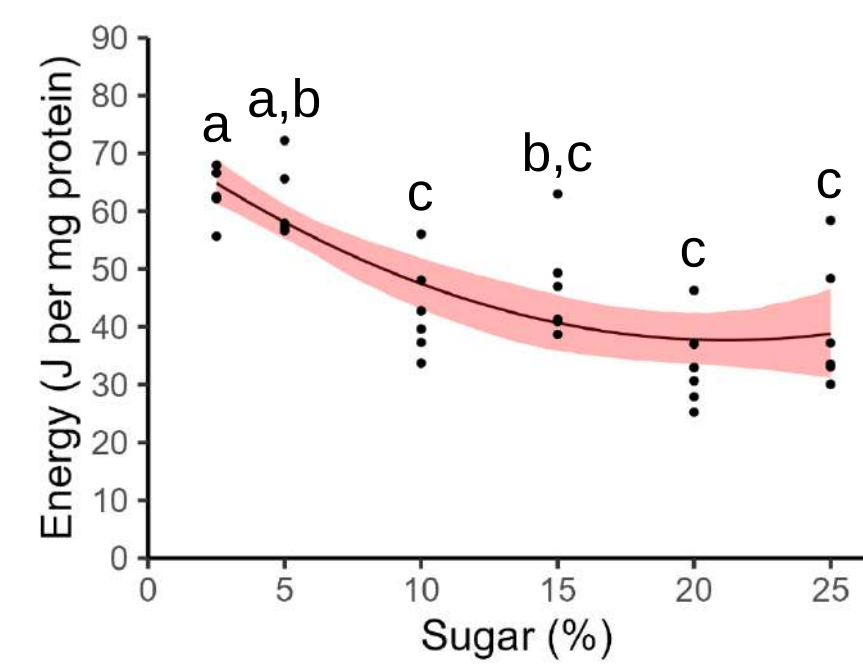
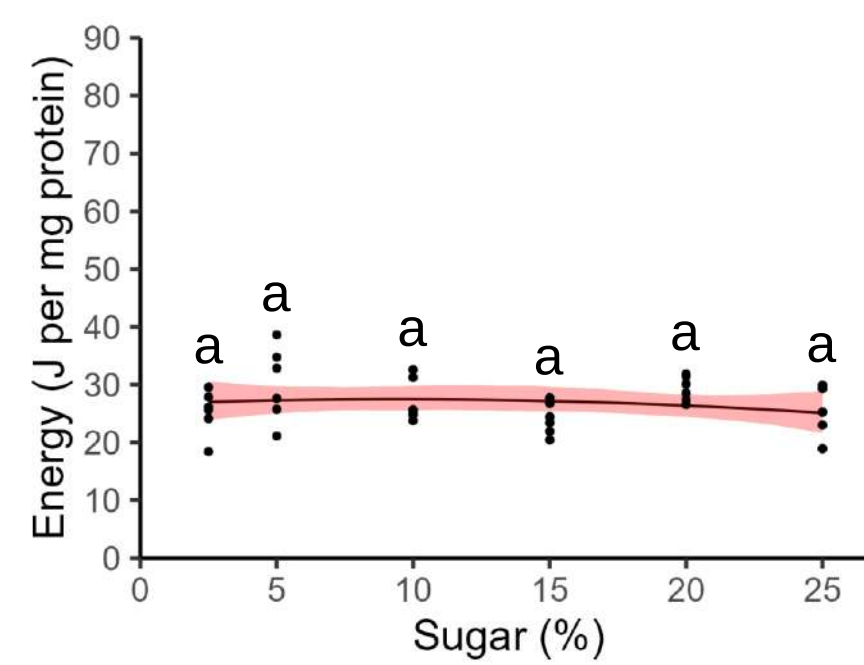
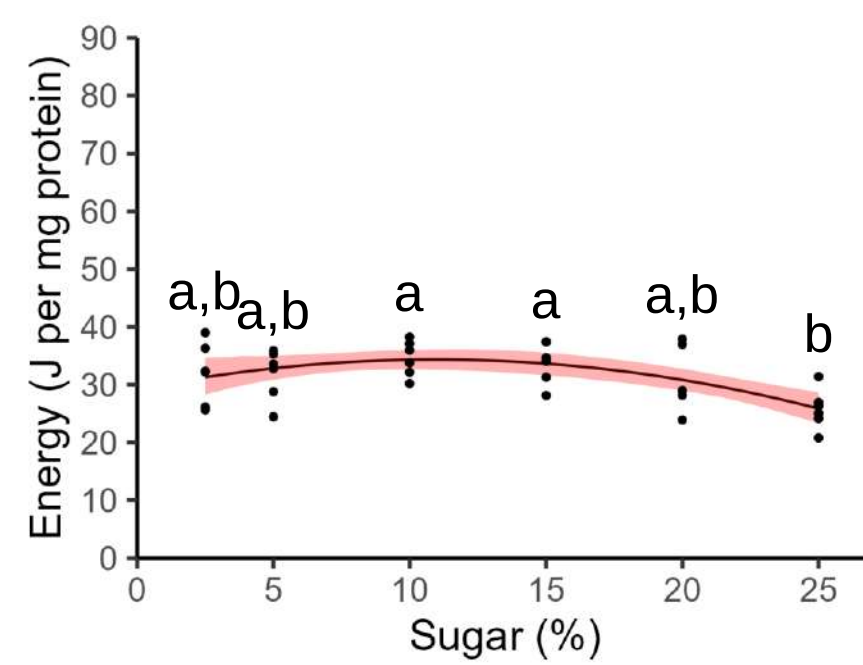
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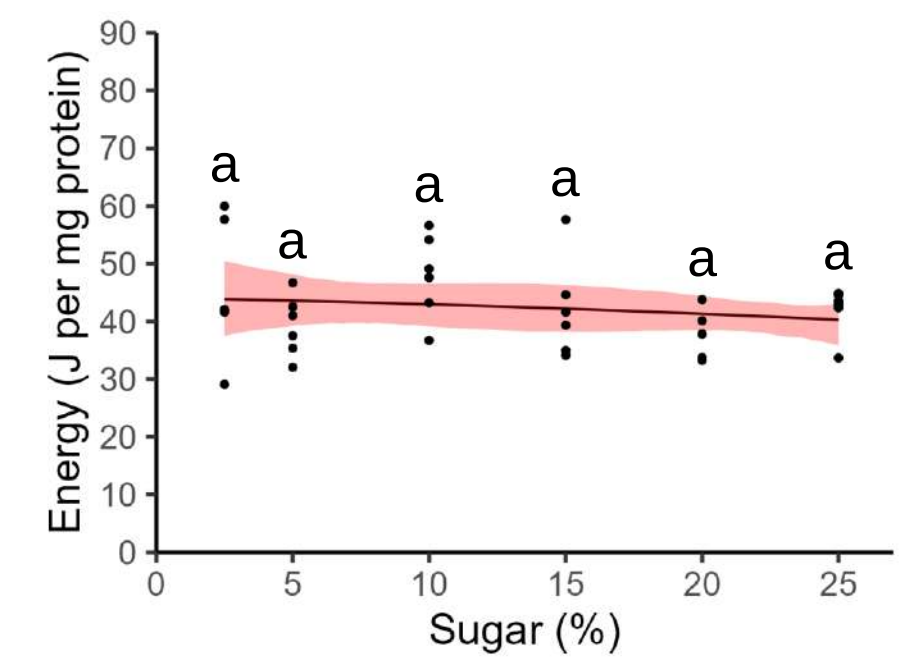
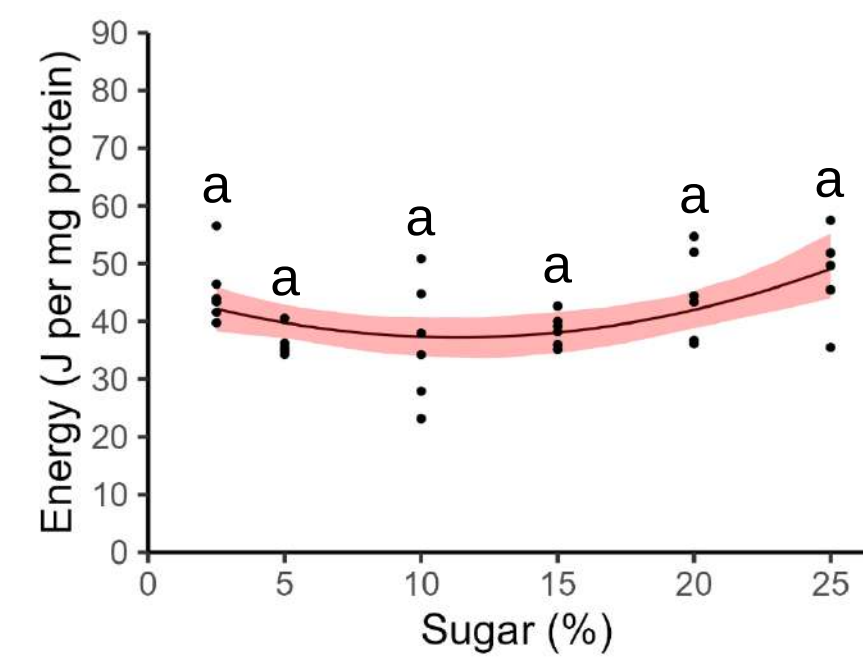
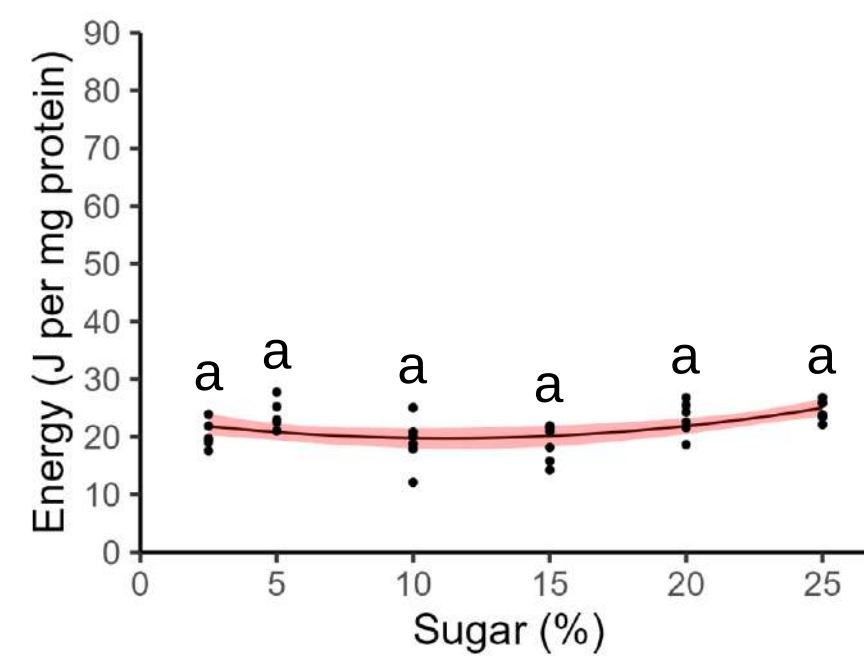
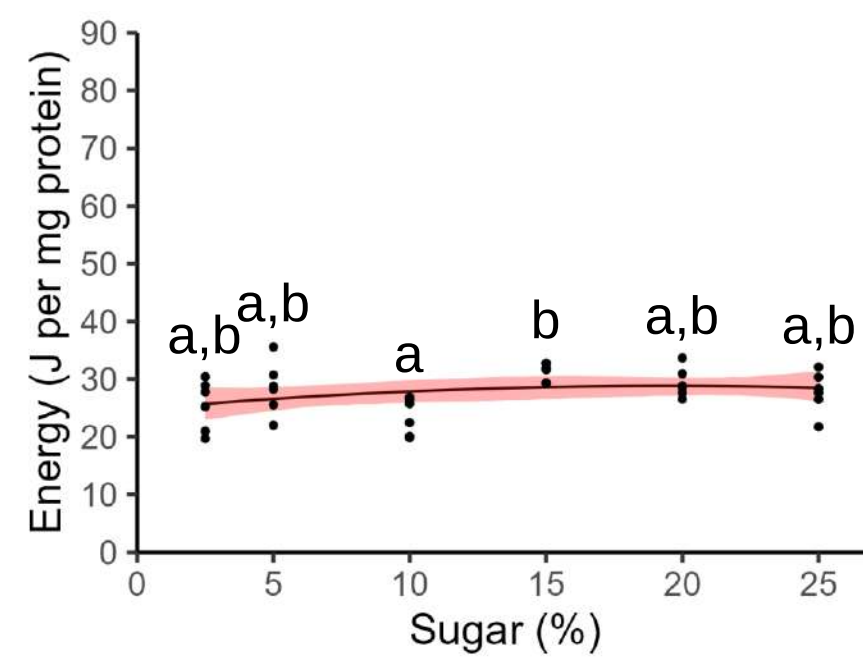
5%



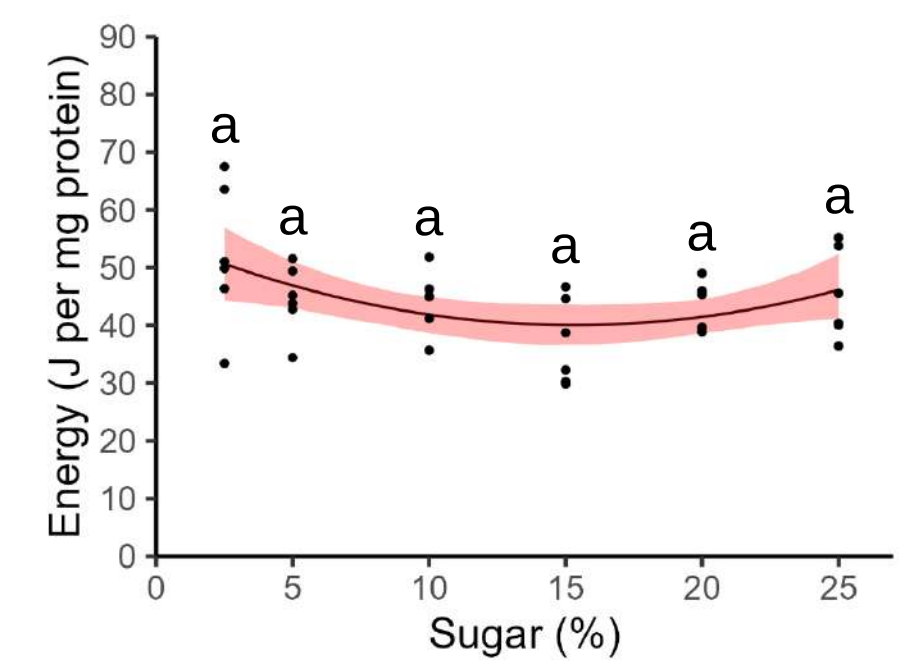
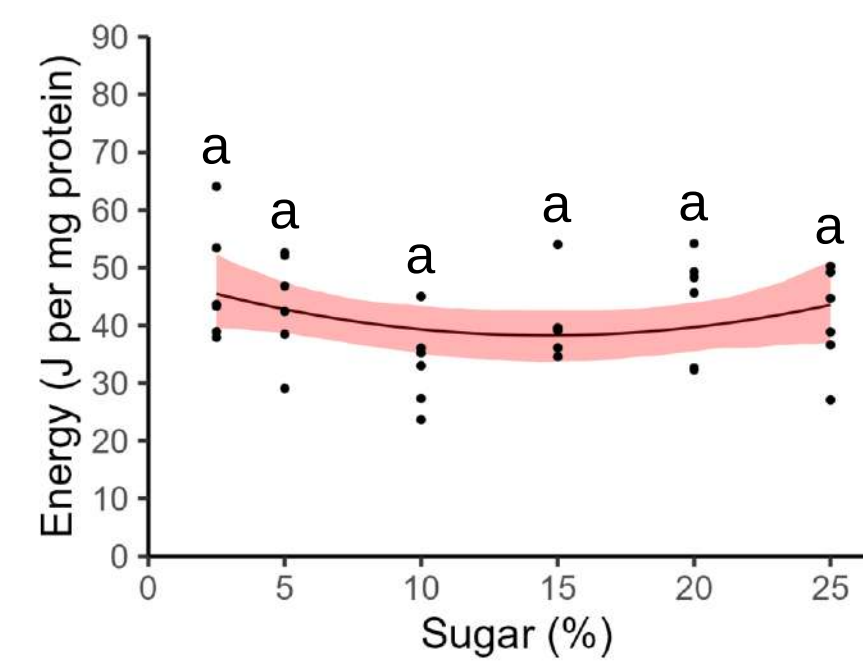
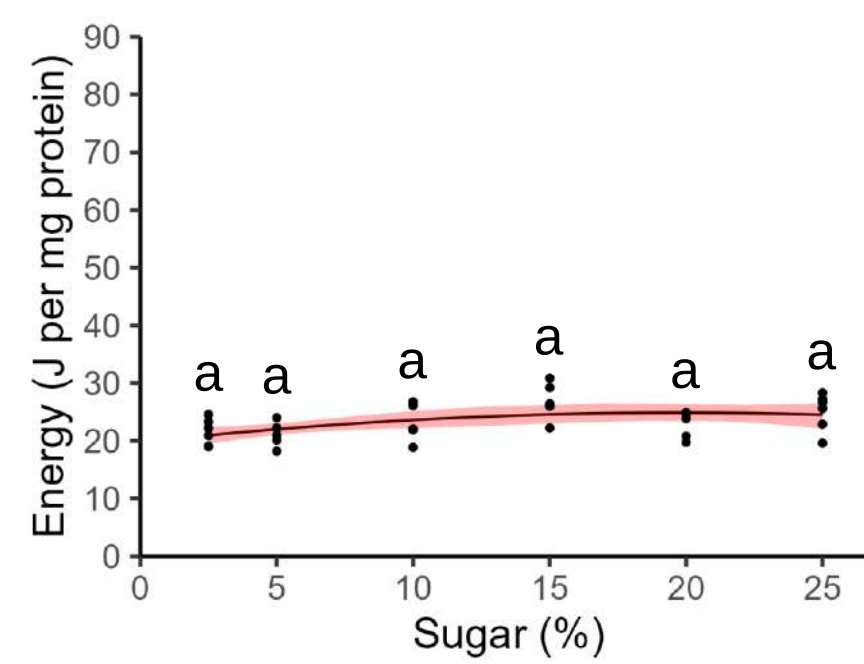
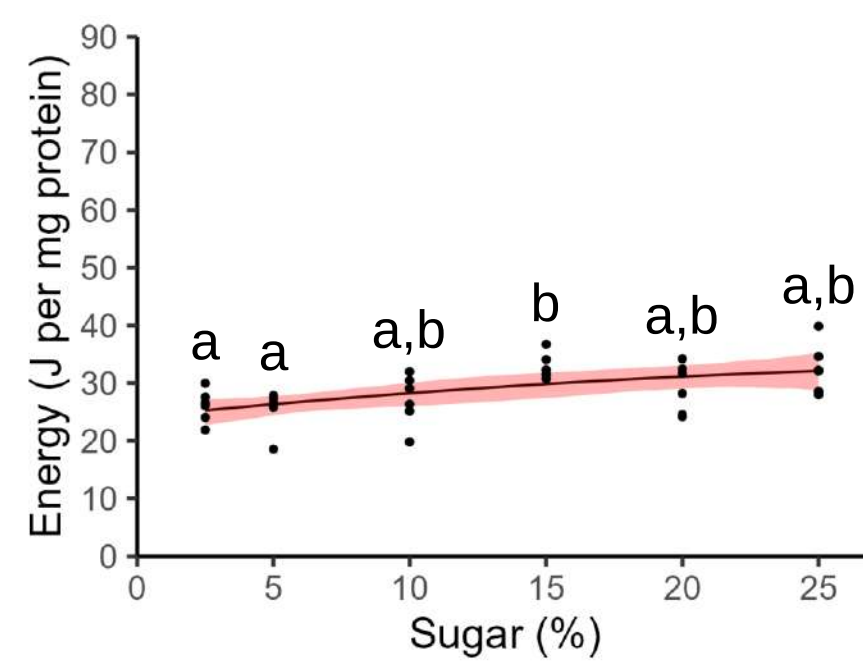
10%



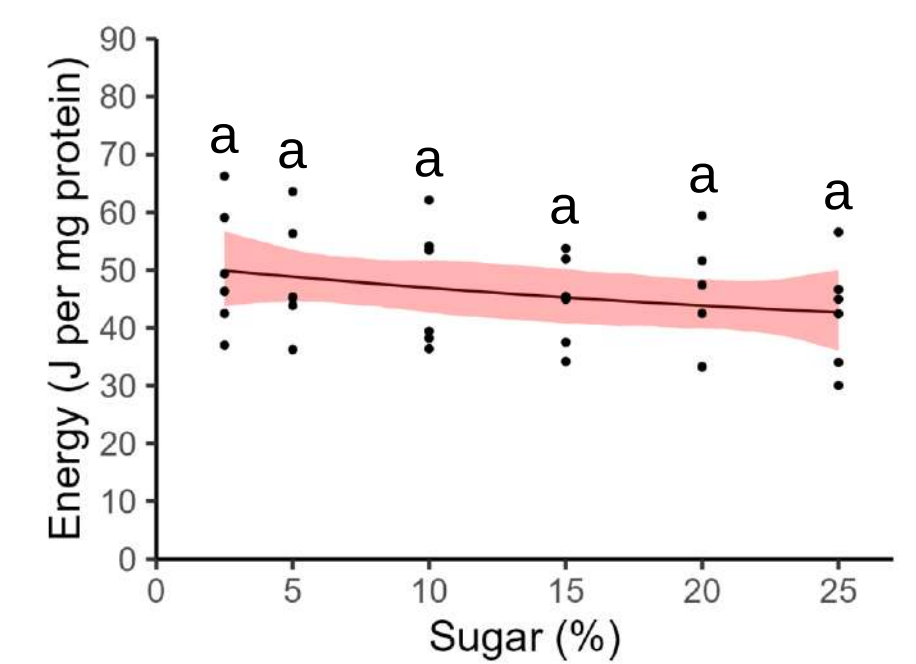
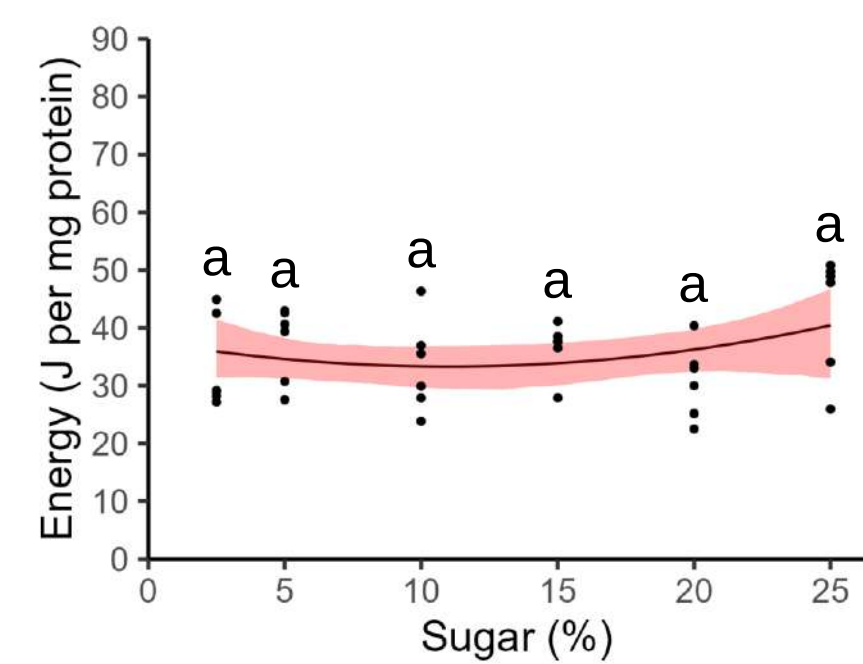
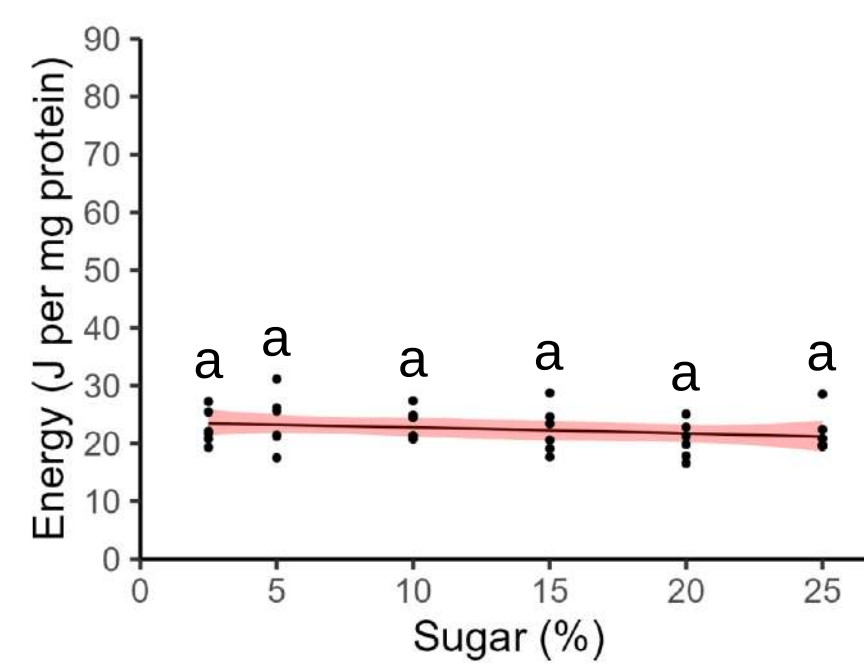
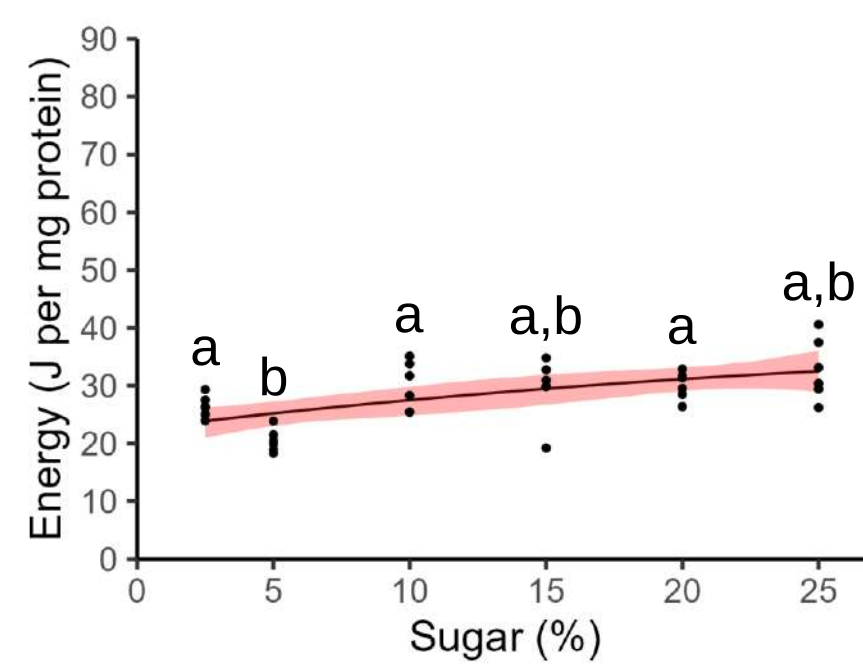
15%



20%



25%



FEMALES

Mated

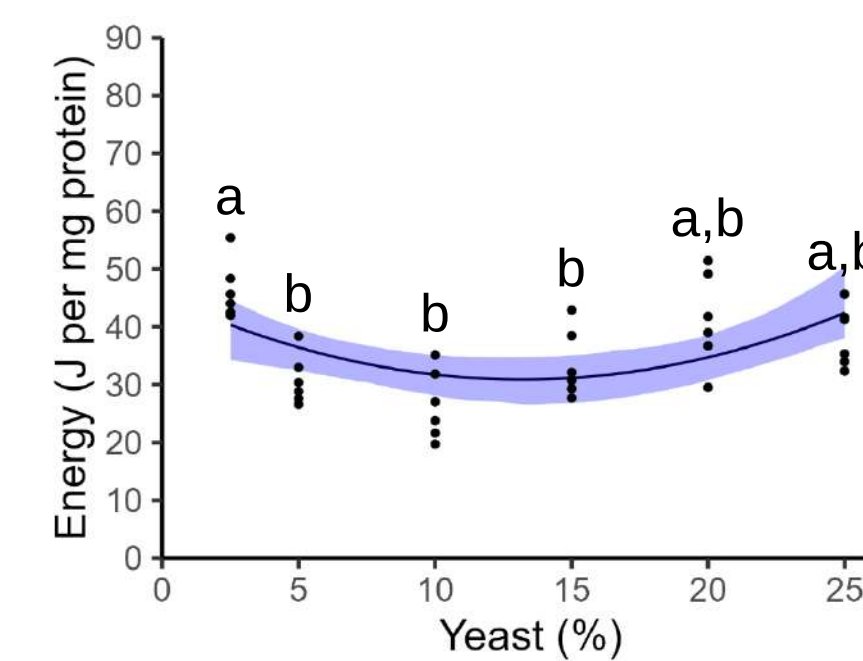


Figure 1 is a scatter plot showing the relationship between Yeast (%) and Energy (J per mg protein). The x-axis represents Yeast (%) from 0 to 25, and the y-axis represents Energy (J per mg protein) from 0 to 90. Data points are shown for 100% yeast (black dots) and 50% yeast (grey dots). A solid line represents the fitted curve, and a shaded area represents the confidence interval. Significance letters (a, b, a,b) are placed above the data points to indicate statistical differences.

Yeast (%)	Energy (J per mg protein)	Significance
2.5	18	
2.5	20	
2.5	22	
2.5	24	
2.5	26	
2.5	28	
2.5	30	
2.5	32	
2.5	34	
2.5	36	
2.5	38	
2.5	40	
2.5	42	
2.5	44	
2.5	46	
2.5	48	
2.5	50	
2.5	52	
2.5	54	
2.5	56	
2.5	58	
2.5	60	
2.5	62	
2.5	64	
2.5	66	
2.5	68	
2.5	70	
2.5	72	
2.5	74	
2.5	76	
2.5	78	
2.5	80	
2.5	82	
2.5	84	
2.5	86	
2.5	88	
2.5	90	
5	30	
5	32	
5	34	
5	36	
5	38	
5	40	
5	42	
5	44	
5	46	
5	48	
5	50	
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15	70	
15	72	
15	74	
15	76	
15	78	
15	80	
15	82	
15	84	
15	86	
15	88	
15	90	
2		

Figure 2 is a scatter plot showing the relationship between Yeast concentration (%) and Energy (J per mg protein) for the 2010-2011 season. The x-axis represents Yeast (%) from 0 to 25, and the y-axis represents Energy (J per mg protein) from 0 to 90. Data points are plotted for 2.5%, 5%, 10%, 15%, 20%, and 25% Yeast. A blue shaded area represents the confidence interval, and a black line represents the fitted curve. Letters above the data points indicate statistical significance groups: 'a,b' for 2.5%, 'a' for 5%, 'b' for 10%, 'a,b' for 15%, 'a,b' for 20%, and 'a' for 25%.

Yeast (%)	Energy (J per mg protein)	Significance Group
2.5	~35	a,b
5	~30	a
10	~30	b
15	~35	a,b
20	~40	a,b
25	~50	a

Figure 1 is a scatter plot showing the relationship between Yeast (%) and Energy (J per mg protein). The x-axis represents Yeast (%) from 0 to 25, and the y-axis represents Energy (J per mg protein) from 0 to 90. Data points are shown with vertical error bars. A blue regression line with a shaded confidence interval is fitted to the data. Letters above the data points indicate statistical significance groups: 'a,b' at 2.5%, 'a' at 5%, 'b' at 10% and 15%, 'c' at 20%, and 'c' at 25%.

Yeast (%)	Energy (J per mg protein)	Significance Group
2.5	~32	a,b
5	~35	a
10	~38	b
15	~42	b
20	~48	c
25	~55	c

Figure 2 is a scatter plot showing the relationship between Yeast (%) on the x-axis and Energy (J per mg protein) on the y-axis. The x-axis ranges from 0 to 25, and the y-axis ranges from 0 to 90. Data points are clustered at 5%, 10%, 15%, 20%, and 25% yeast. A blue shaded area represents the confidence interval around the fitted curve. Letters 'a', 'b', and 'a,b' indicate statistical significance groups.

Yeast (%)	Energy (J per mg protein)	Significance Group
3	28	a,b
3	32	a,b
3	35	a,b
3	38	a,b
5	23	a
5	32	a
5	35	a
10	33	a,b
10	38	a,b
10	45	a,b
15	40	b
15	45	b
15	48	b
20	35	a,b
20	48	a,b
20	55	a,b
25	42	b
25	45	b
25	48	b
25	52	b

Figure 2 is a scatter plot showing the relationship between Yeast (%) and Energy (J per mg protein). The x-axis represents Yeast (%) from 0 to 25, and the y-axis represents Energy (J per mg protein) from 0 to 90. Data points are plotted for 5%, 10%, 15%, 20%, and 25% yeast. A blue shaded area represents the confidence interval of the fitted curve. Letters 'a' and 'b' are placed above the data points to indicate statistical significance groups.

Yeast (%)	Energy (J per mg protein)	Significance Group
5	~30	a, b
10	~30	b
15	~35	a, b
20	~40	a, b
25	~45	a, b

FEMALES

Mated

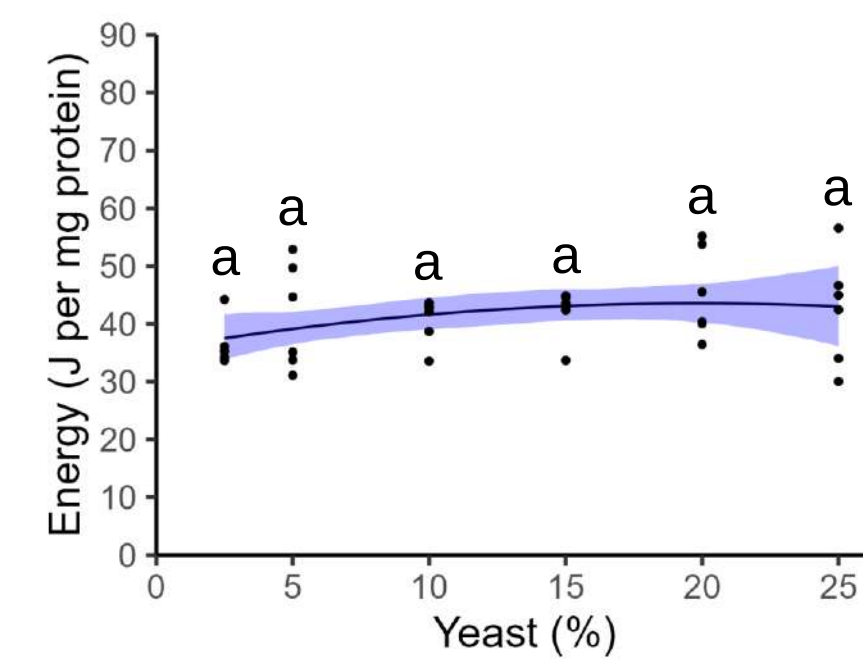
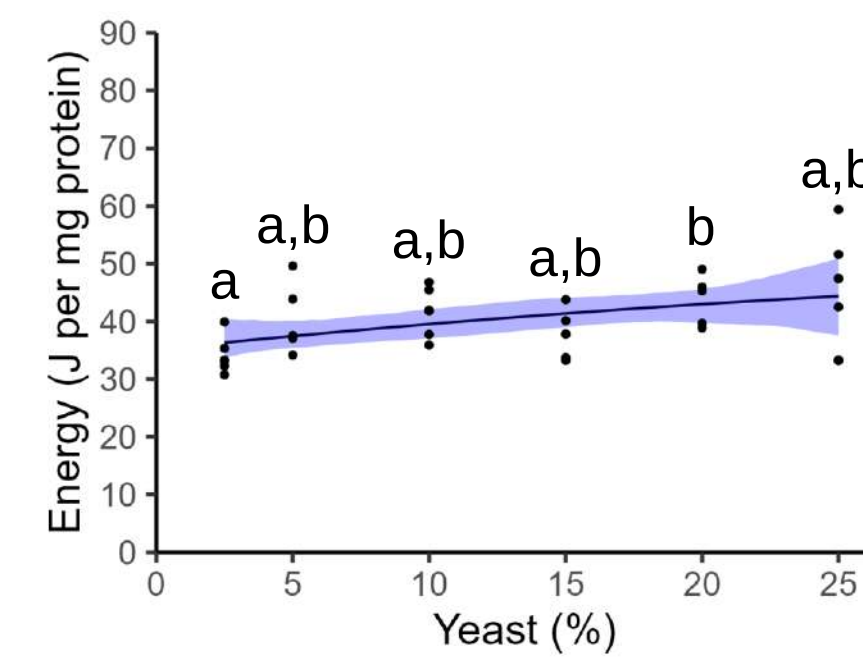
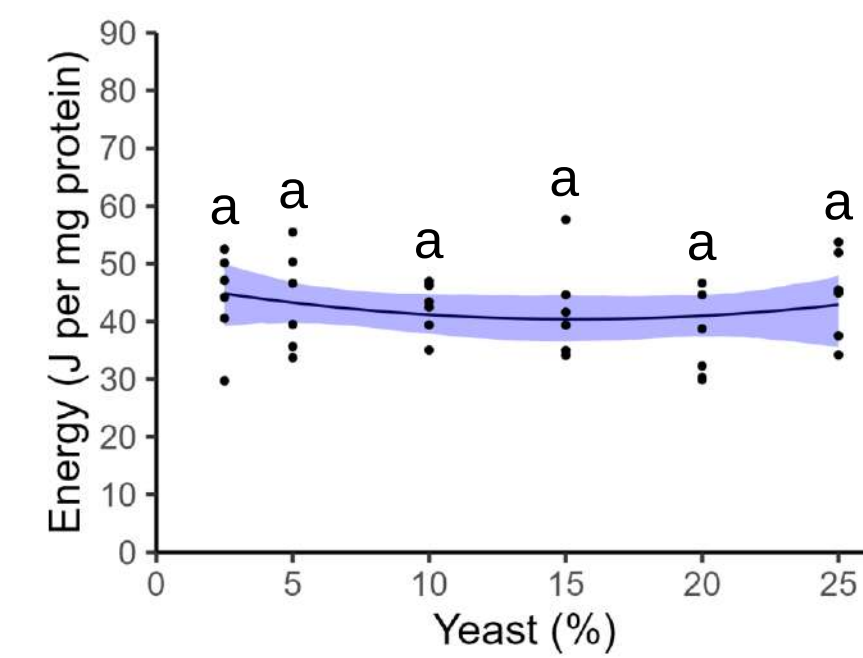
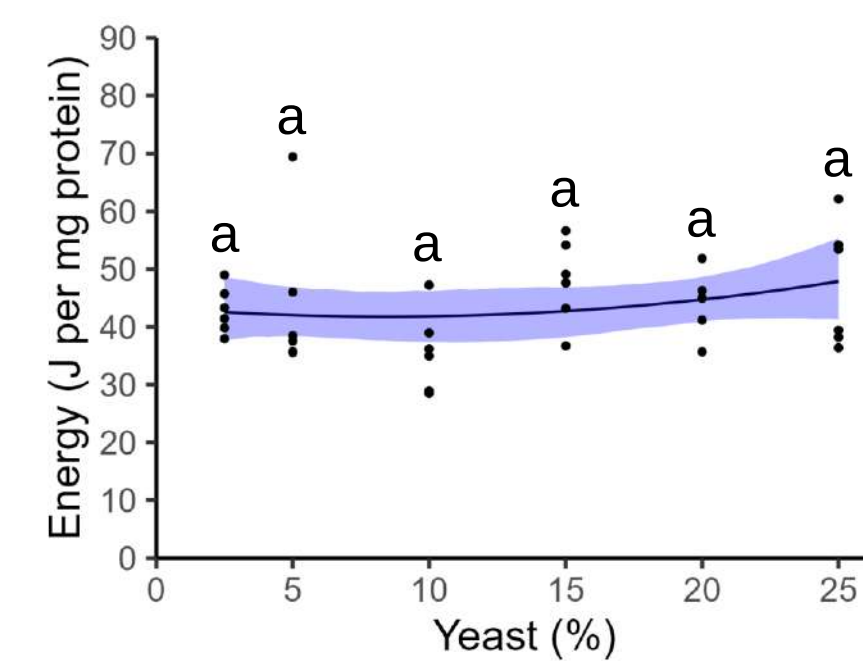
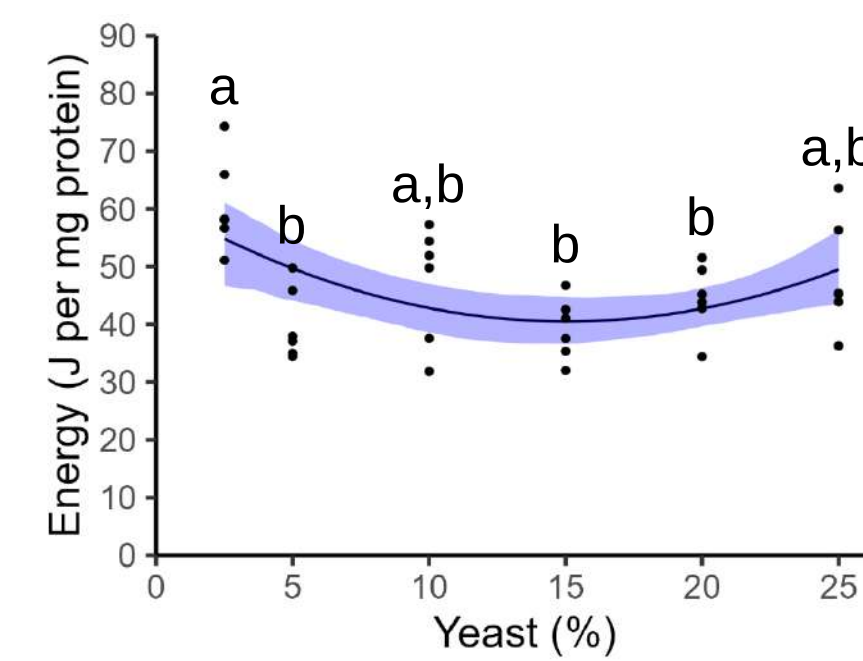
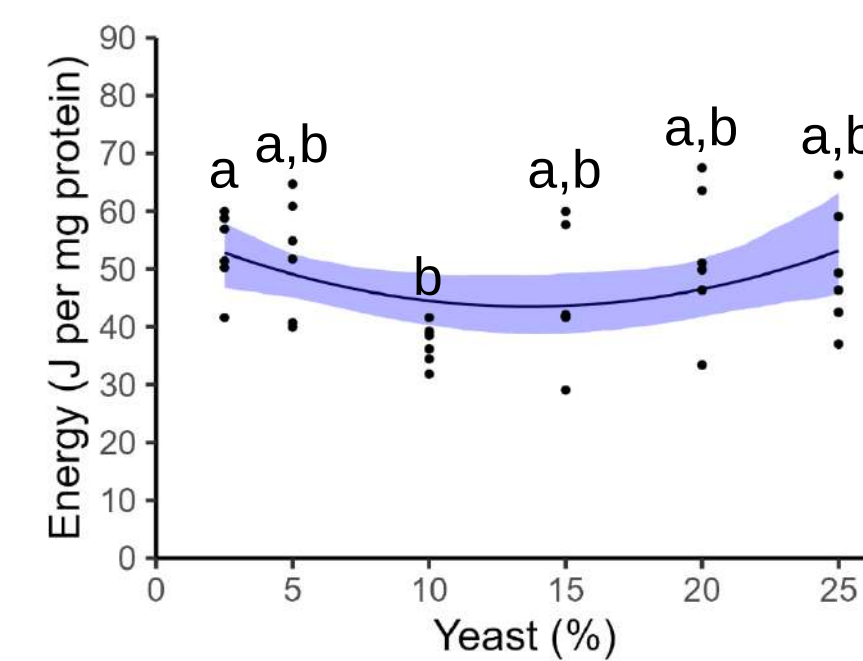
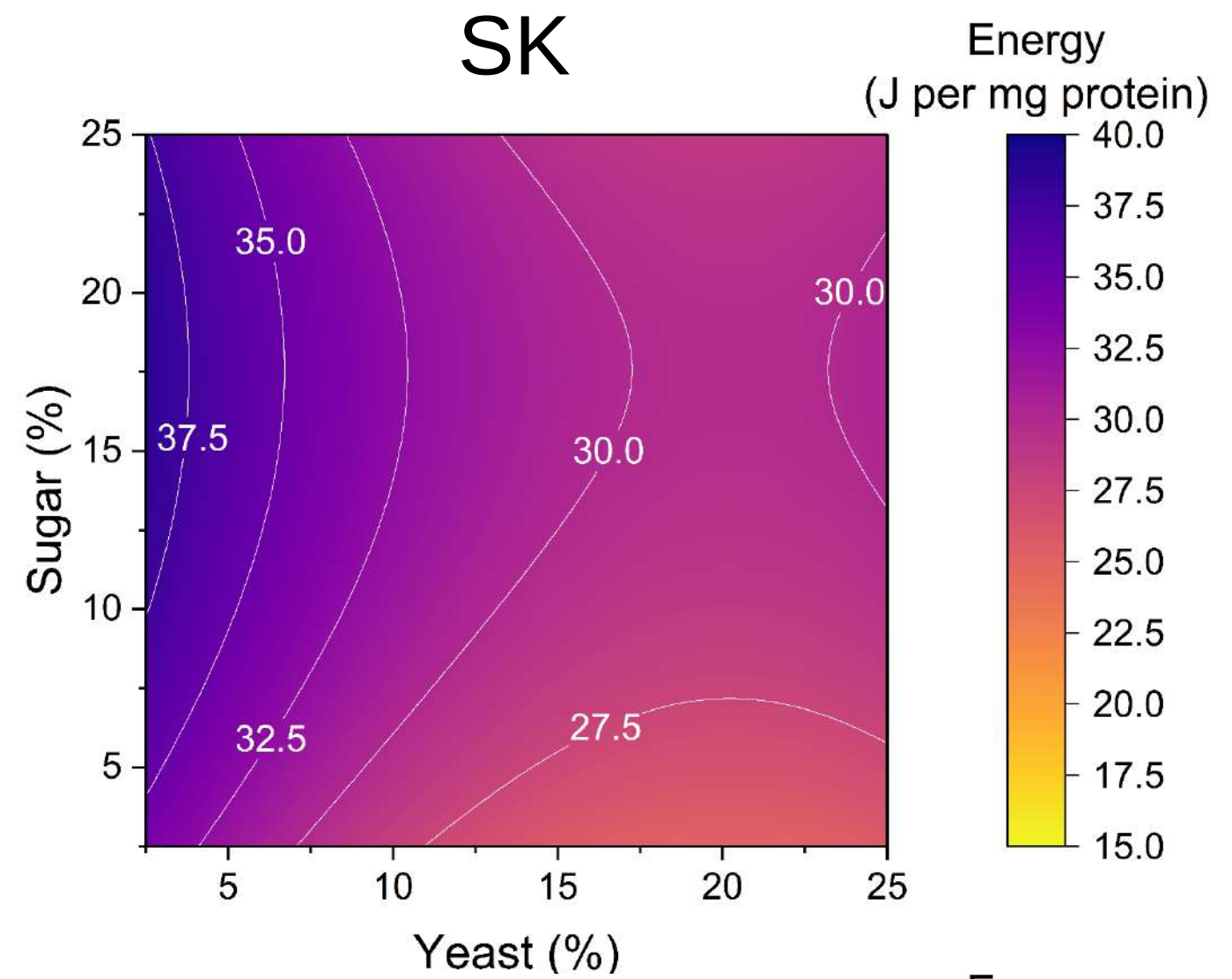
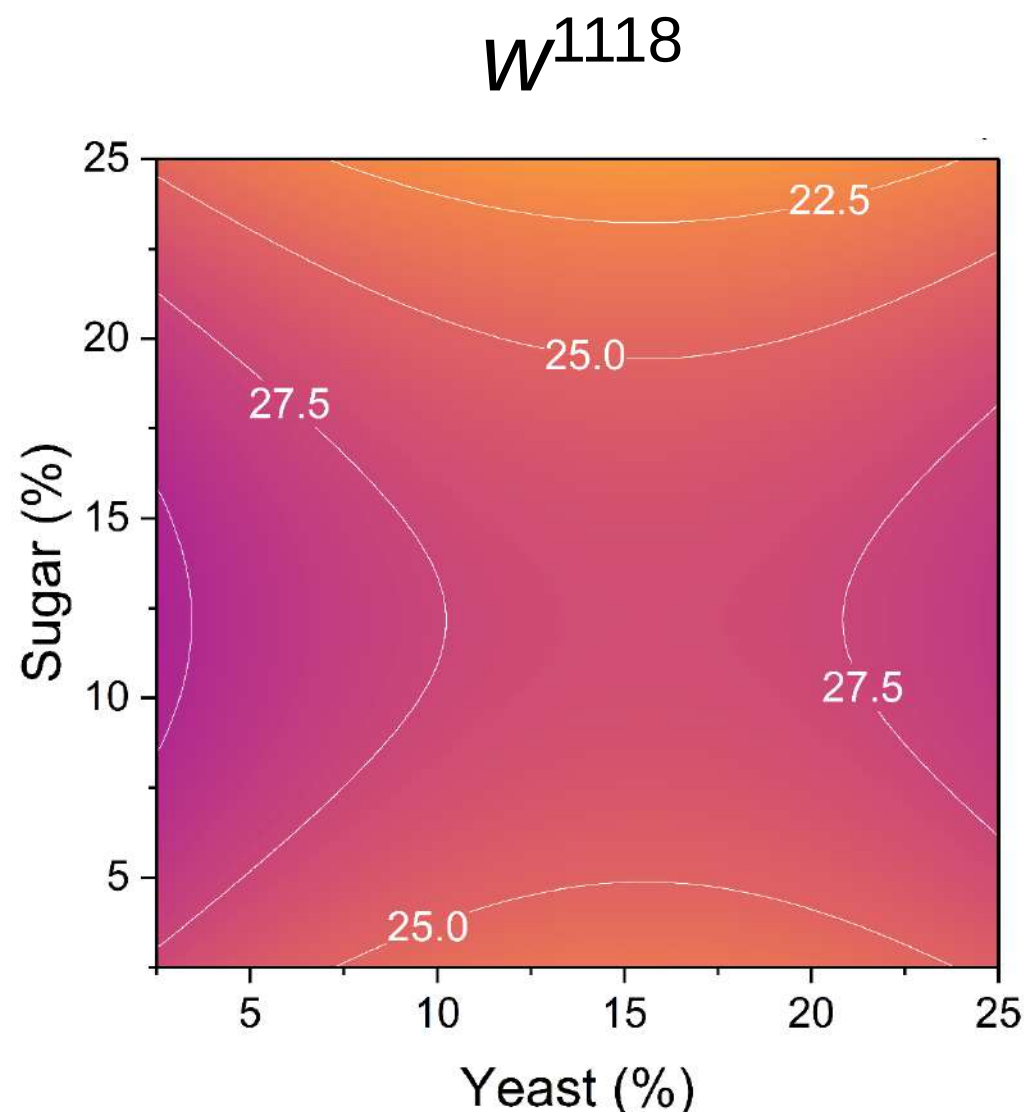


Figure S21.

Virgin
males



Mated
males

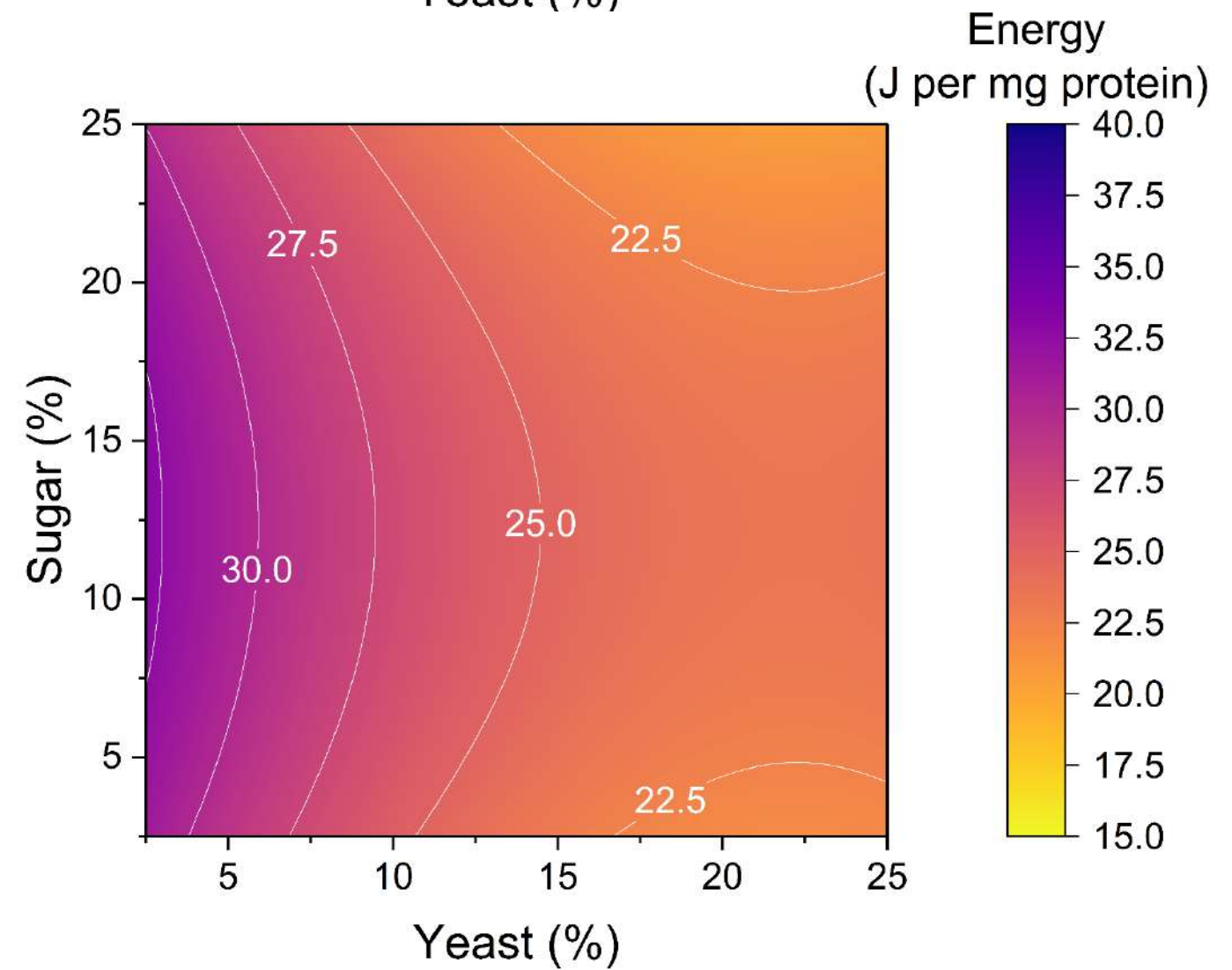
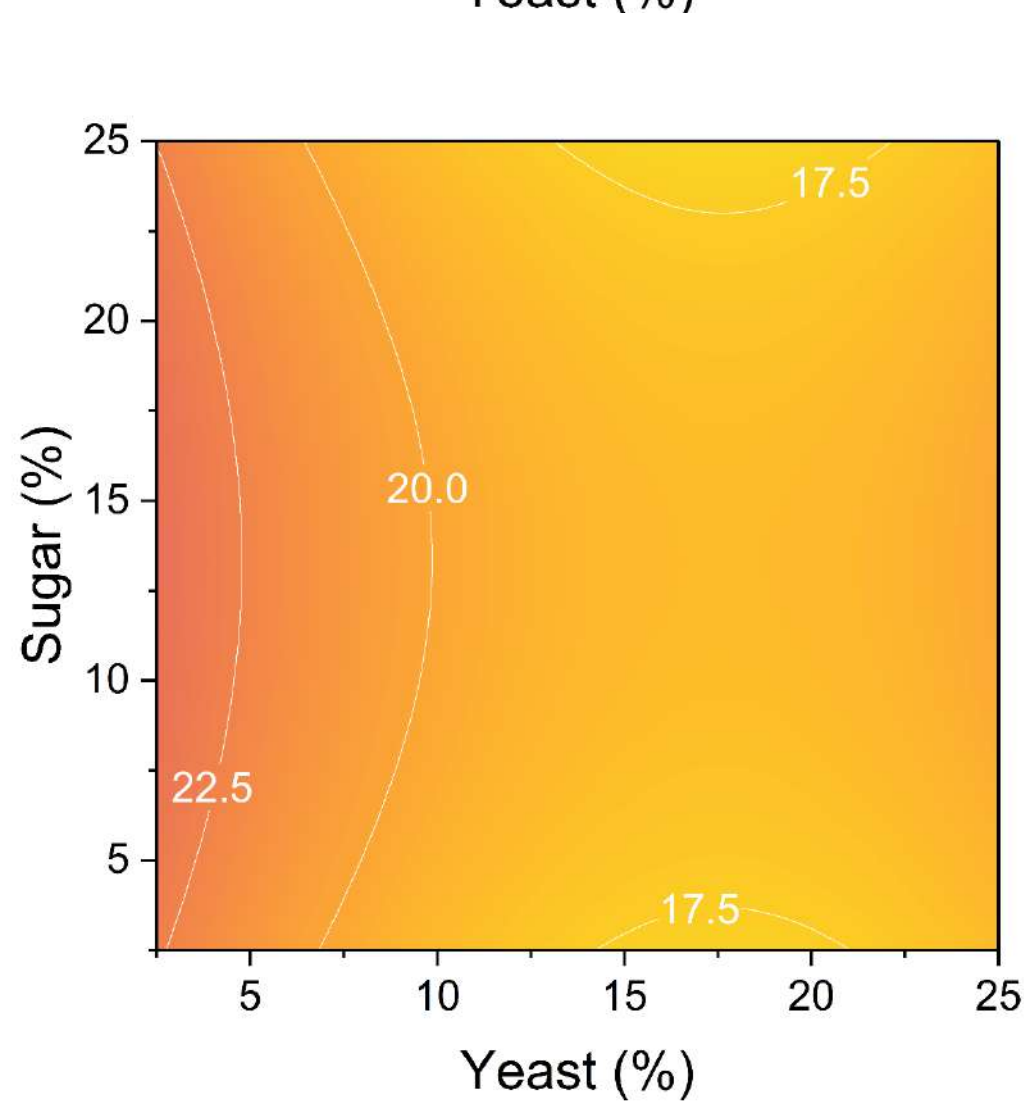
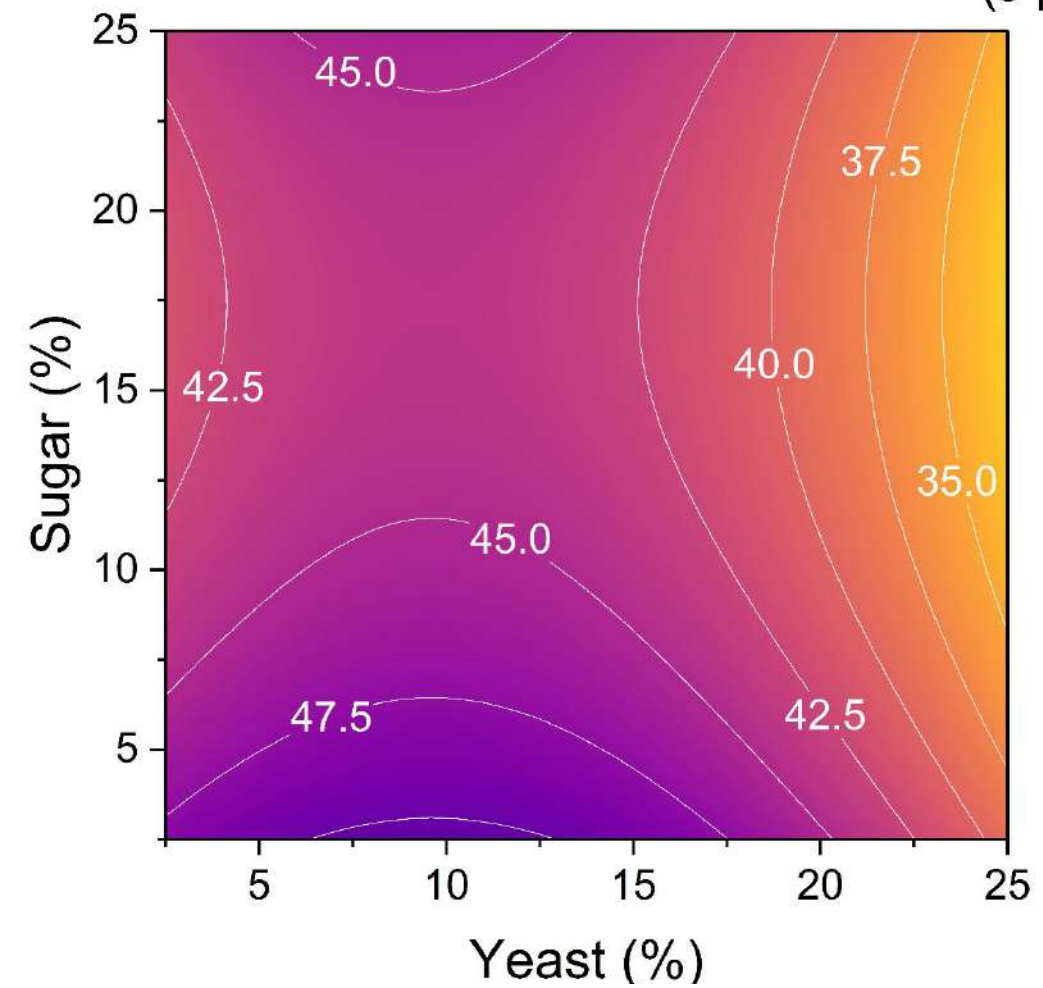
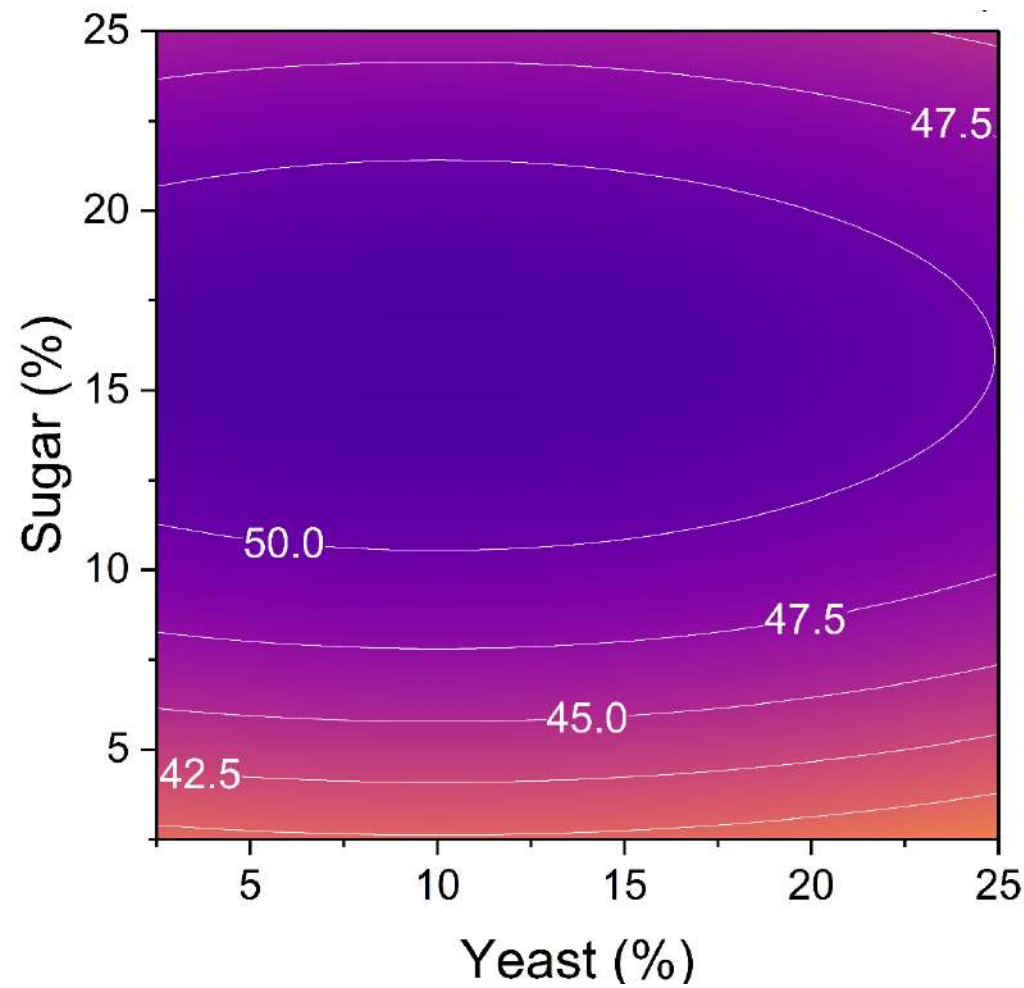


Figure S22.

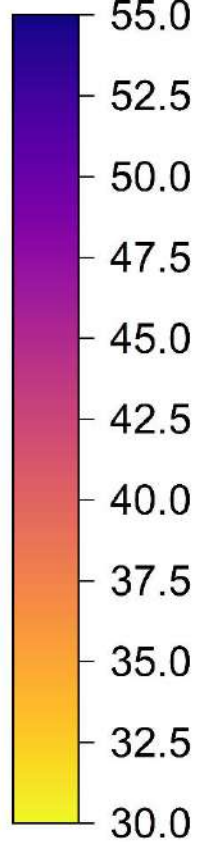
w^{1118}

SK

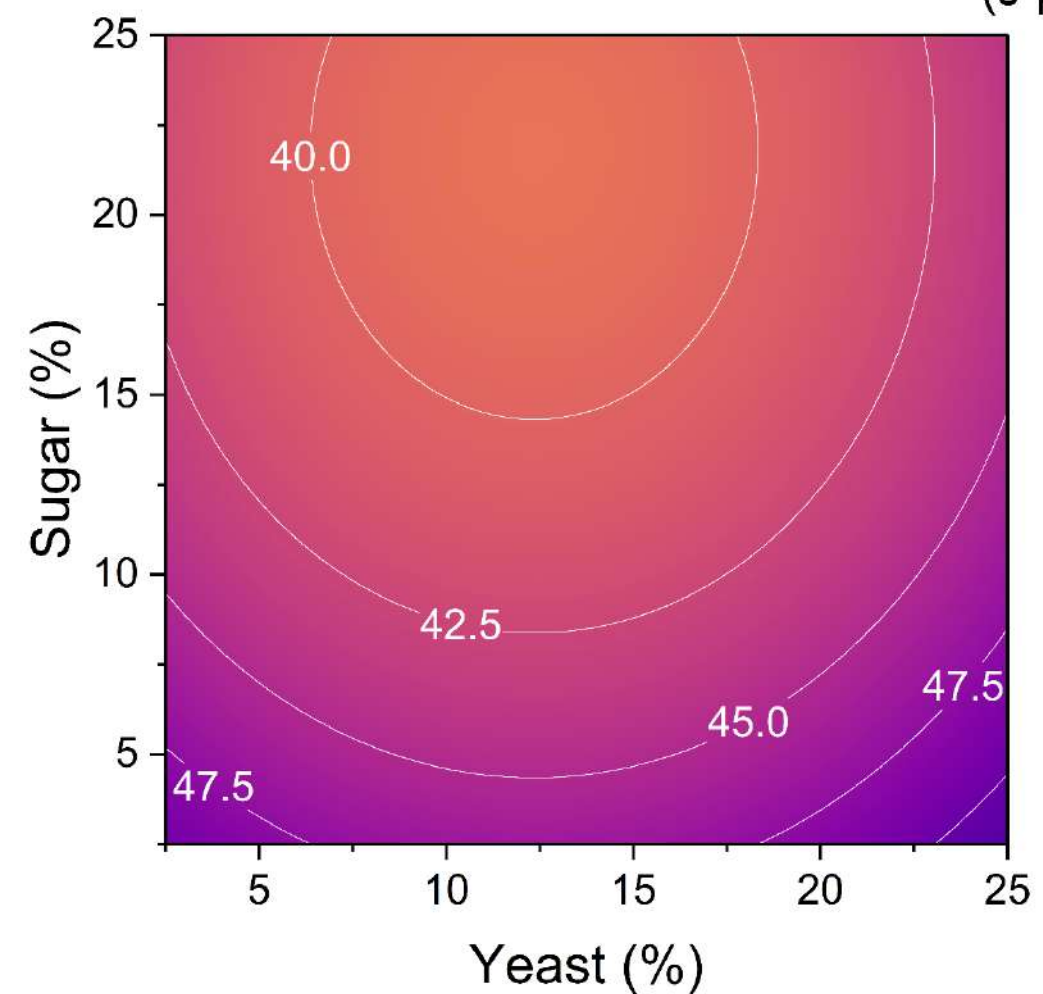
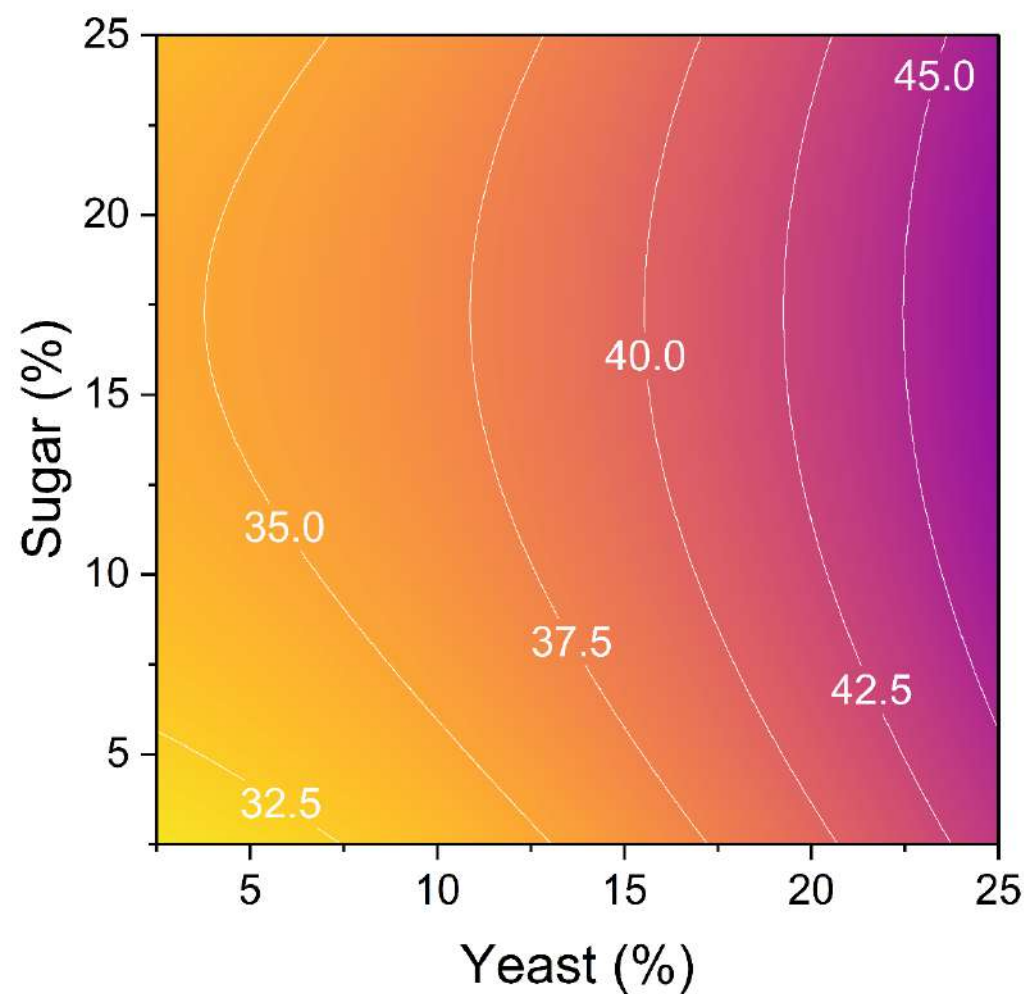
Virgin
females



Energy
(J per mg protein)



Mated
females



Energy
(J per mg protein)

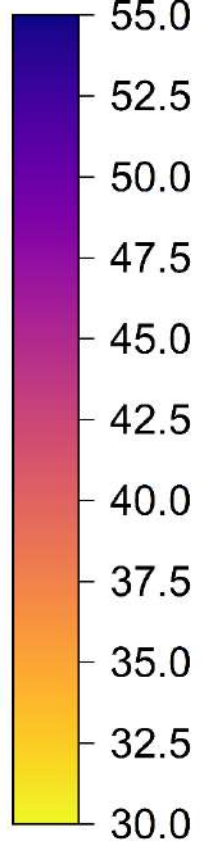
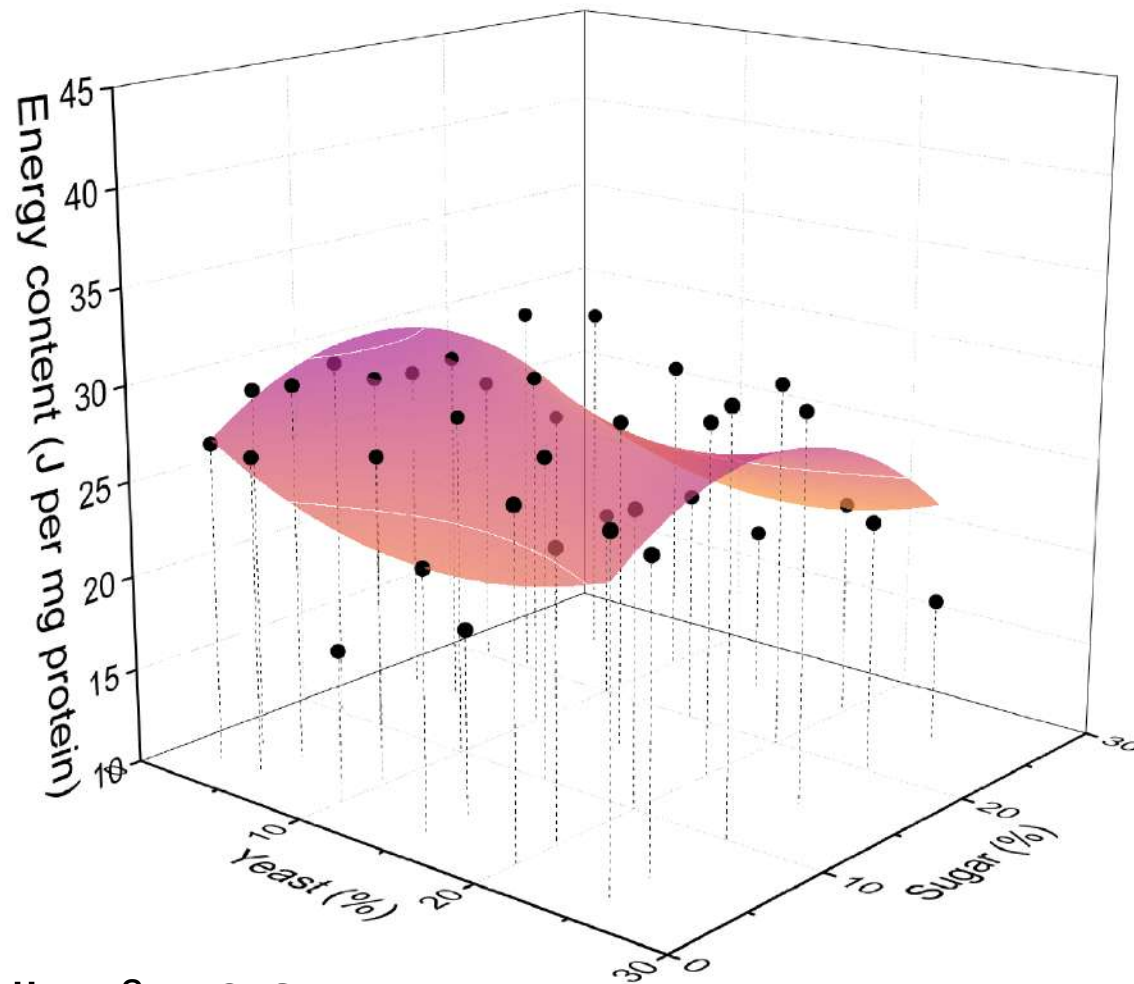


Figure S23.

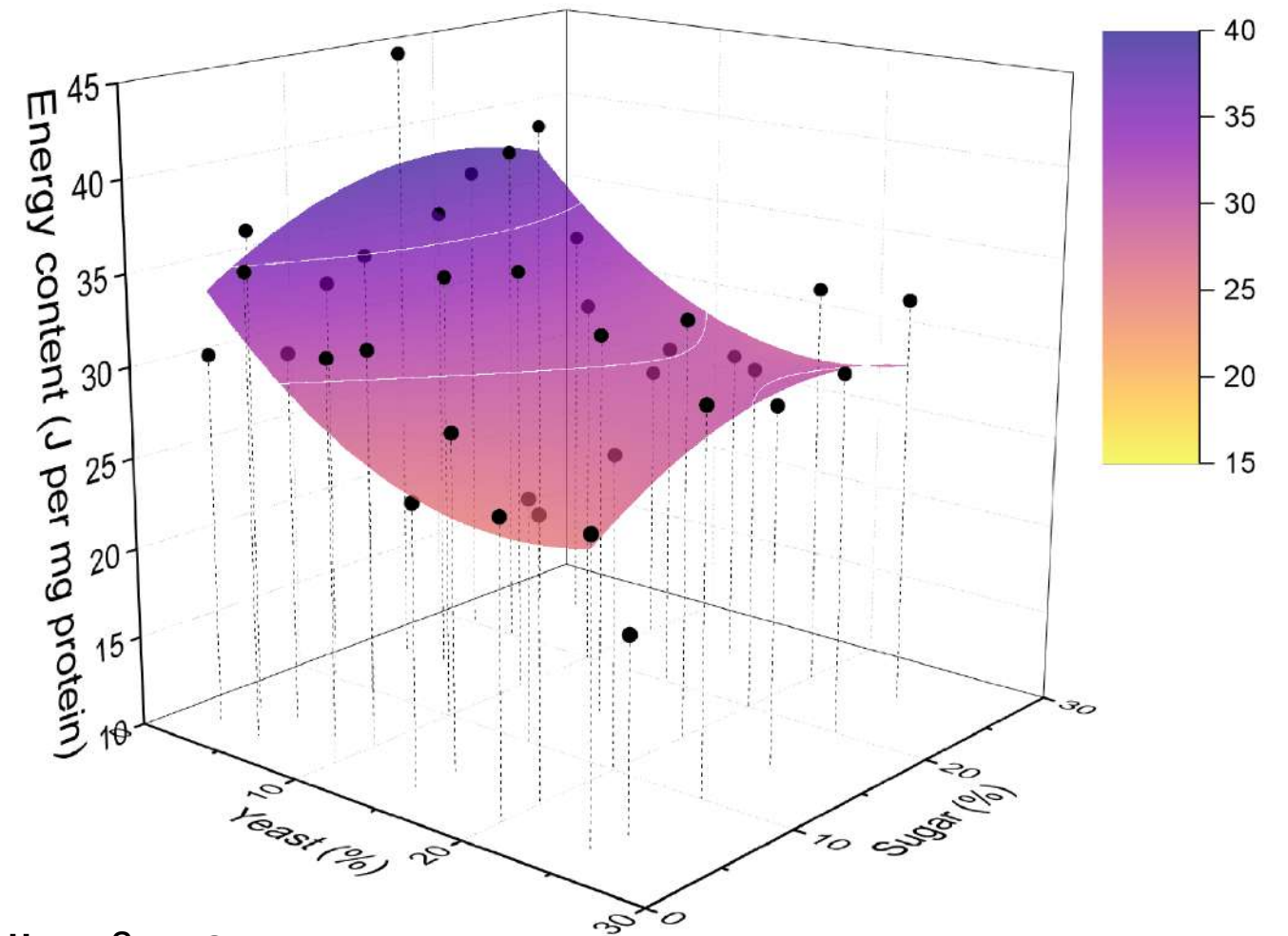
w^{1118}

SK

Virgin
males

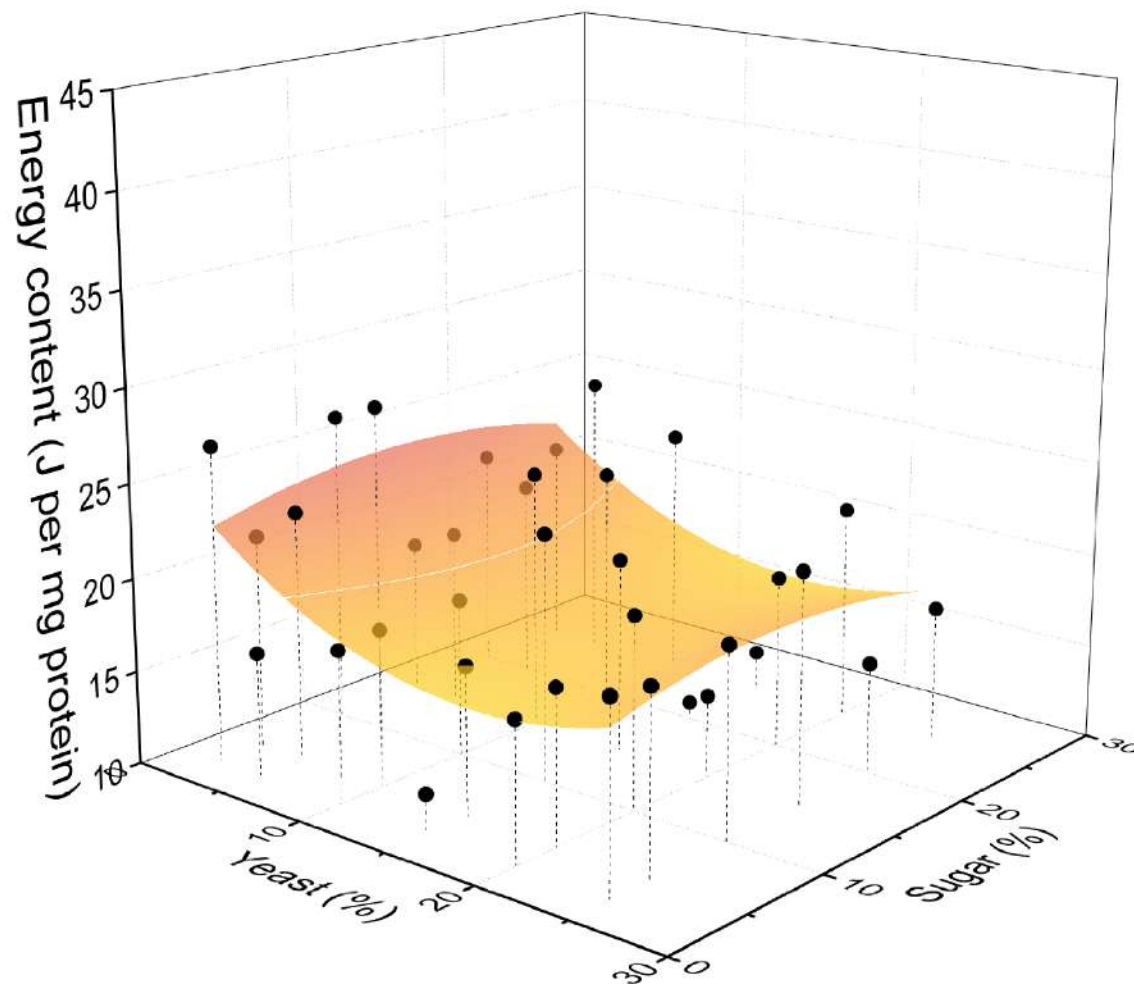


Adj. $R^2 = 0.31$

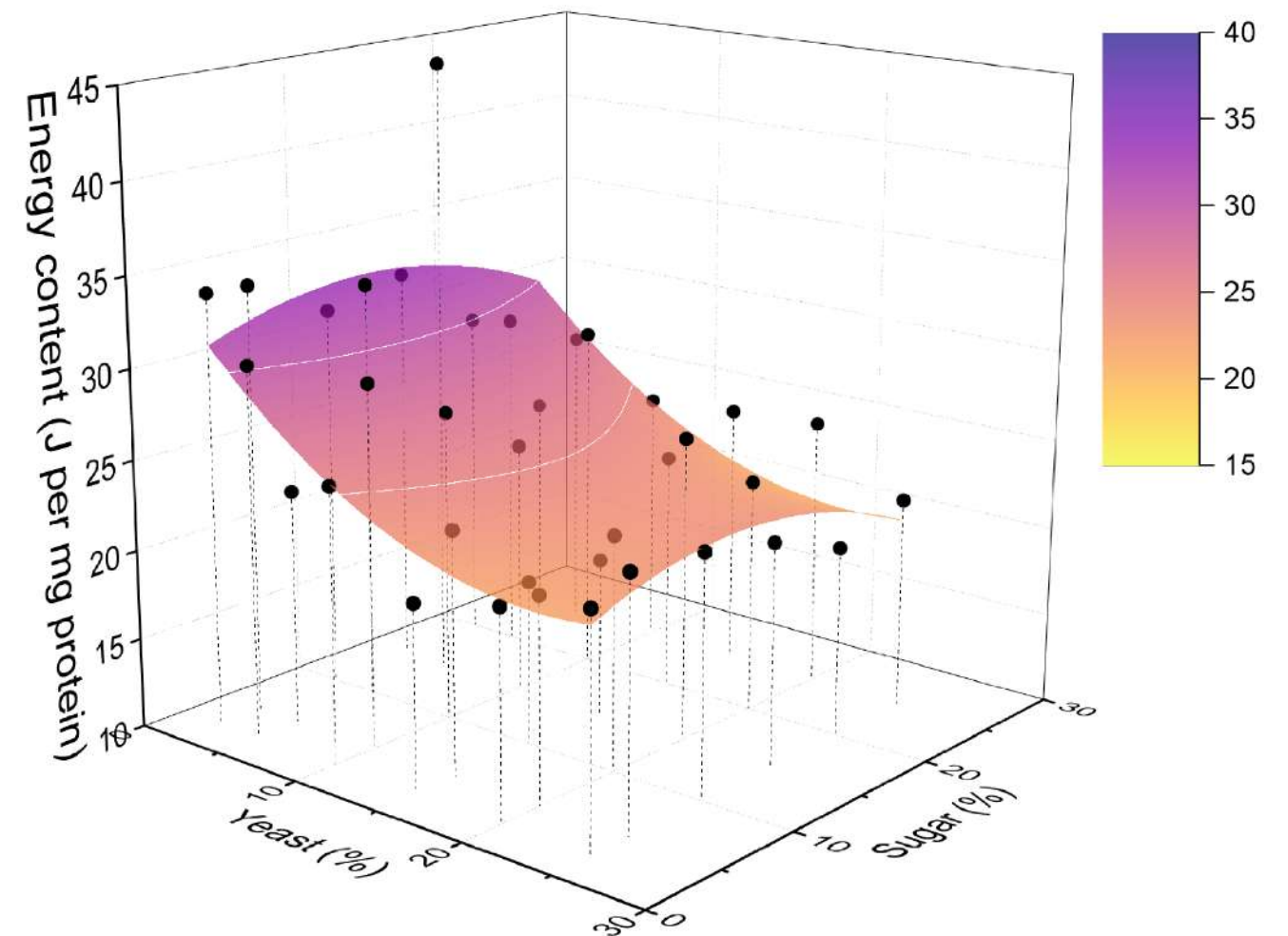


Adj. $R^2 = 0.57$

Mated
males



Adj. $R^2 = 0.18$



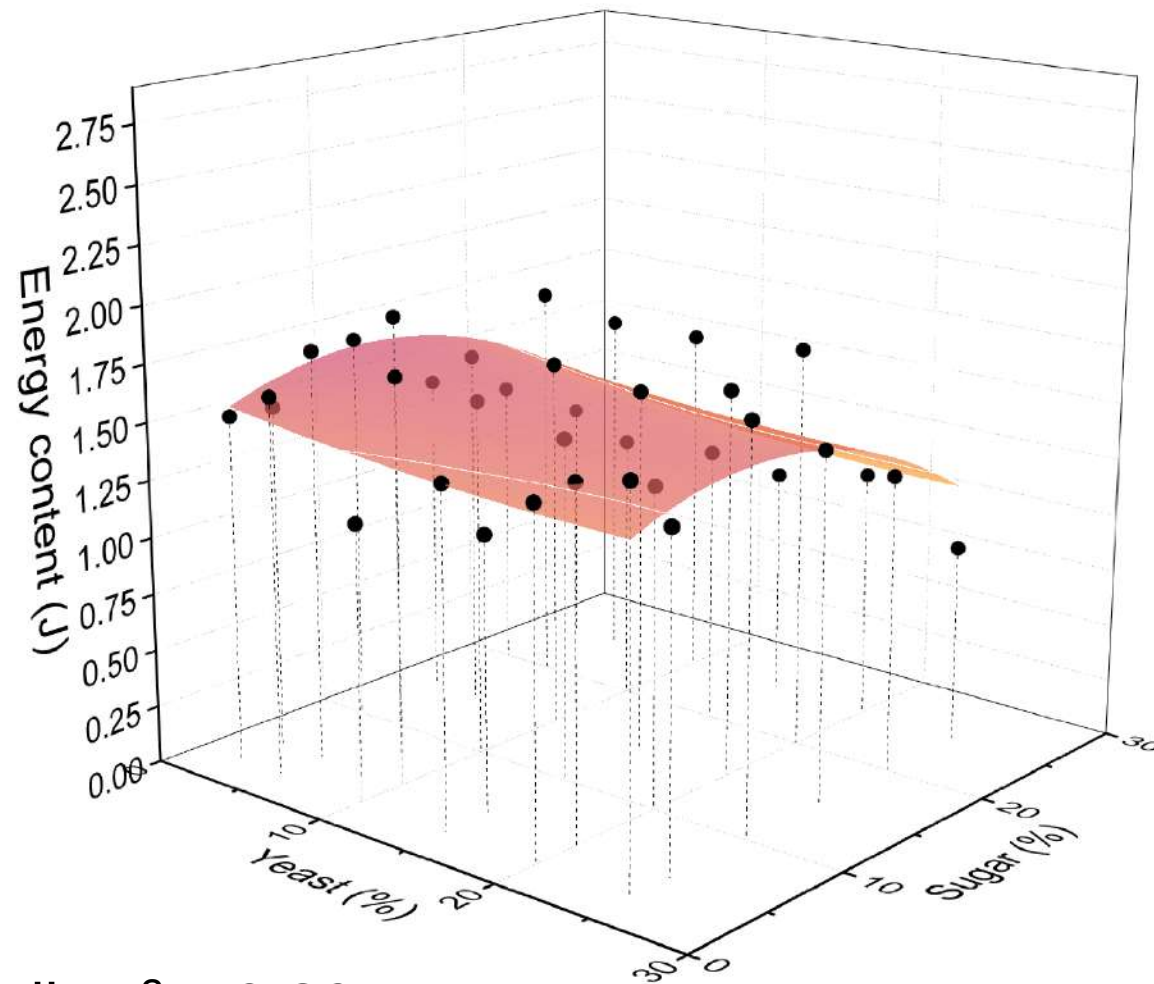
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Figure S24.

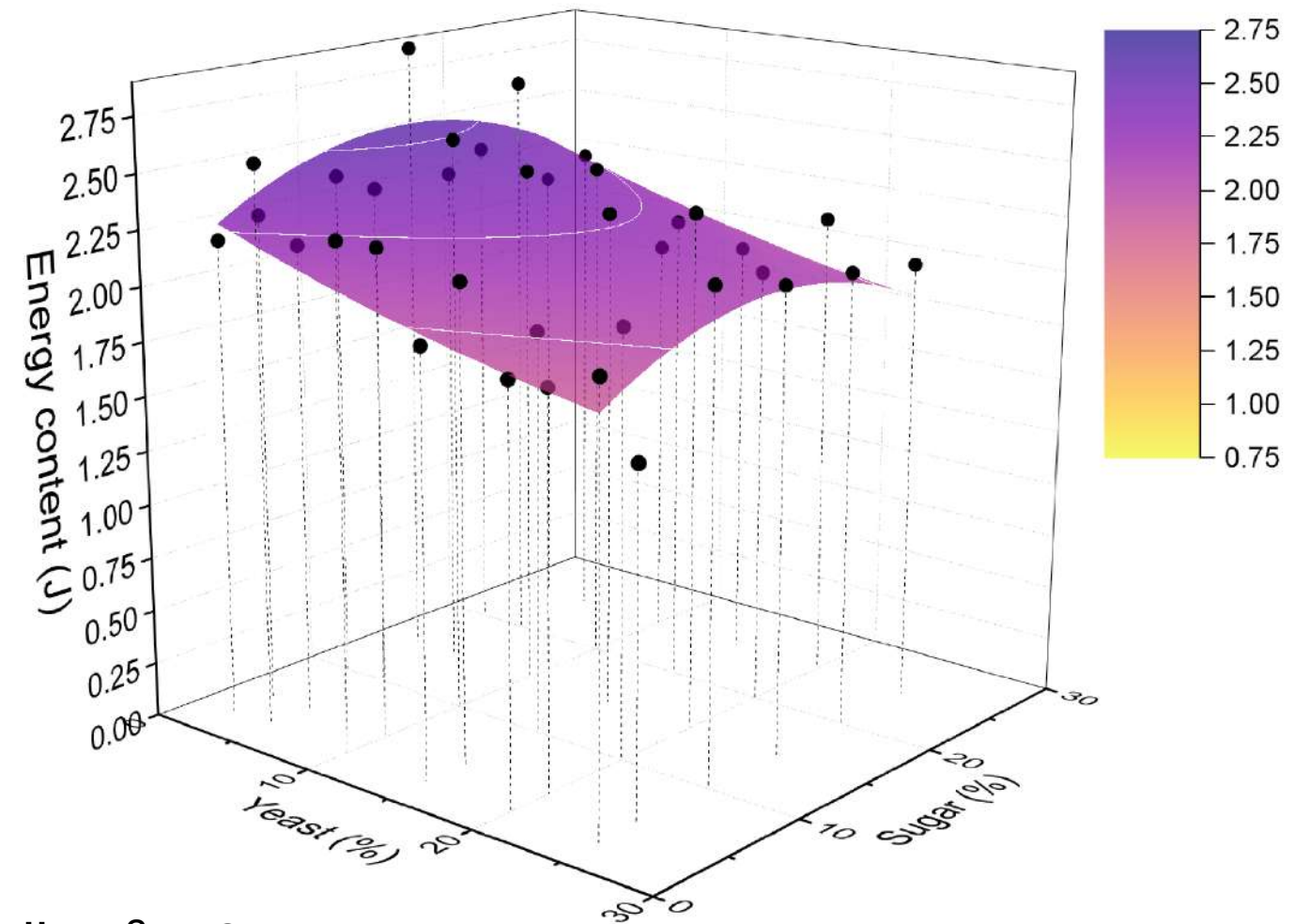
w^{1118}

SK

Virgin
males

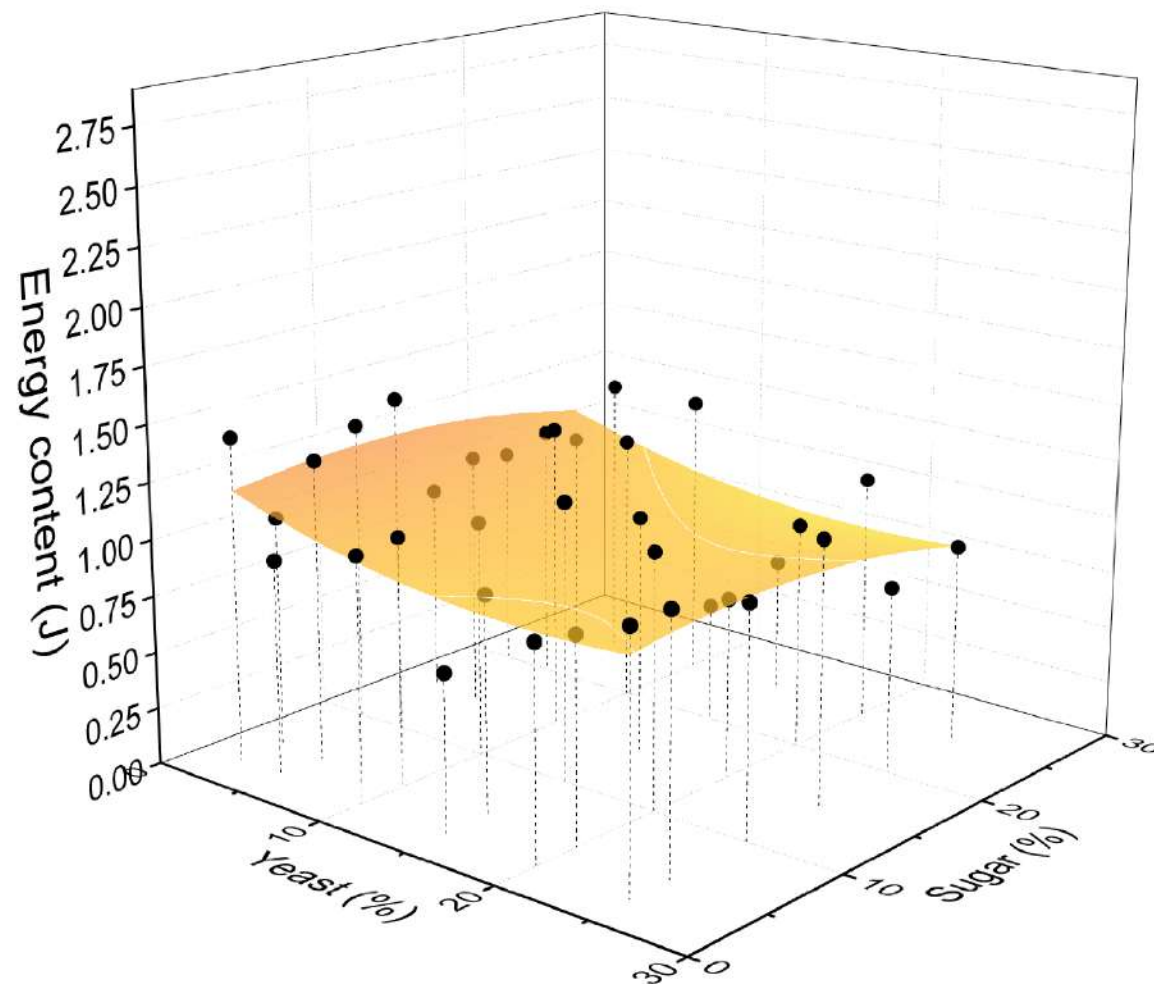


Adj. $R^2 = 0.29$

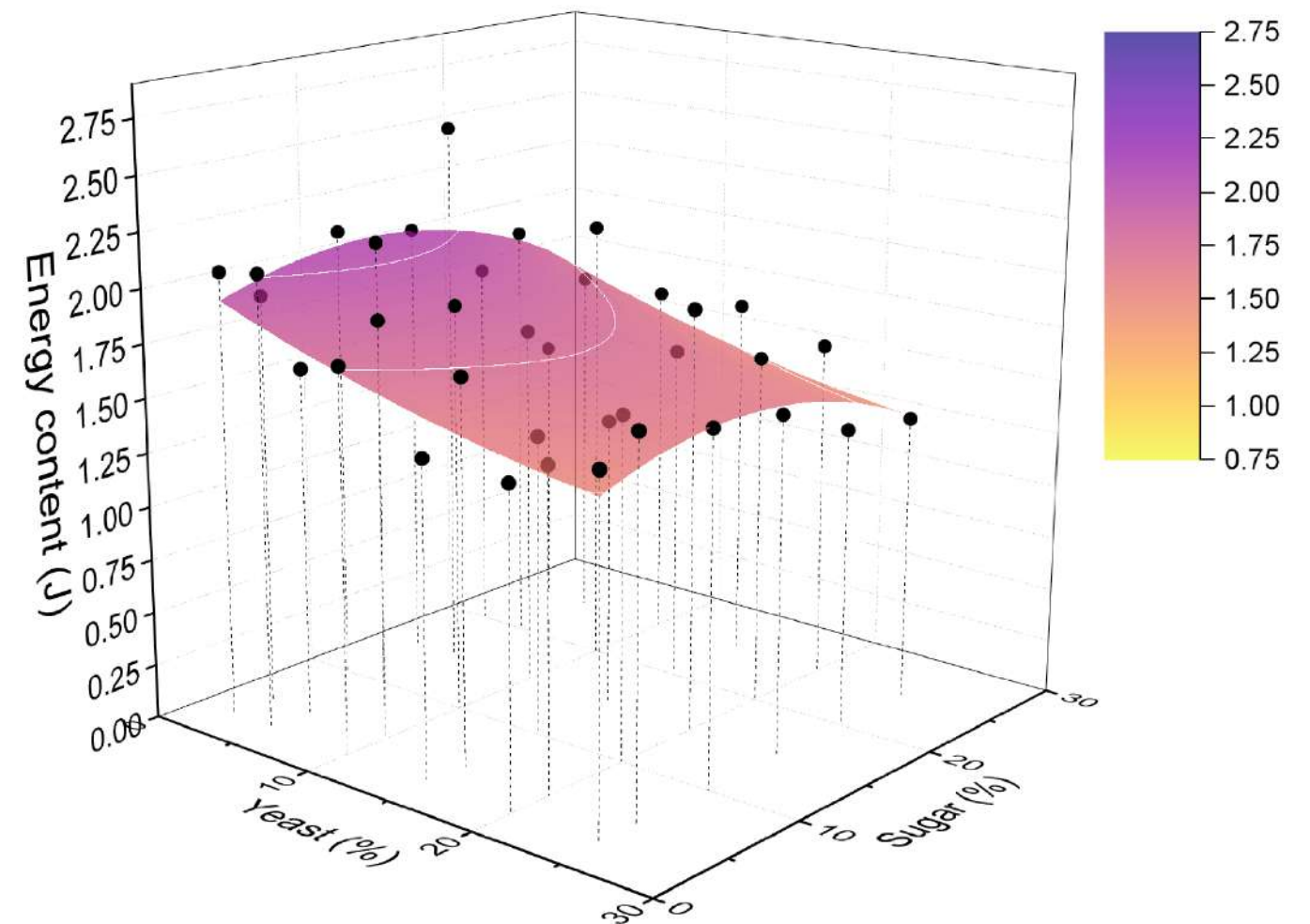


Adj. $R^2 = 0.45$

Mated
males



Adj. $R^2 = 0.12$



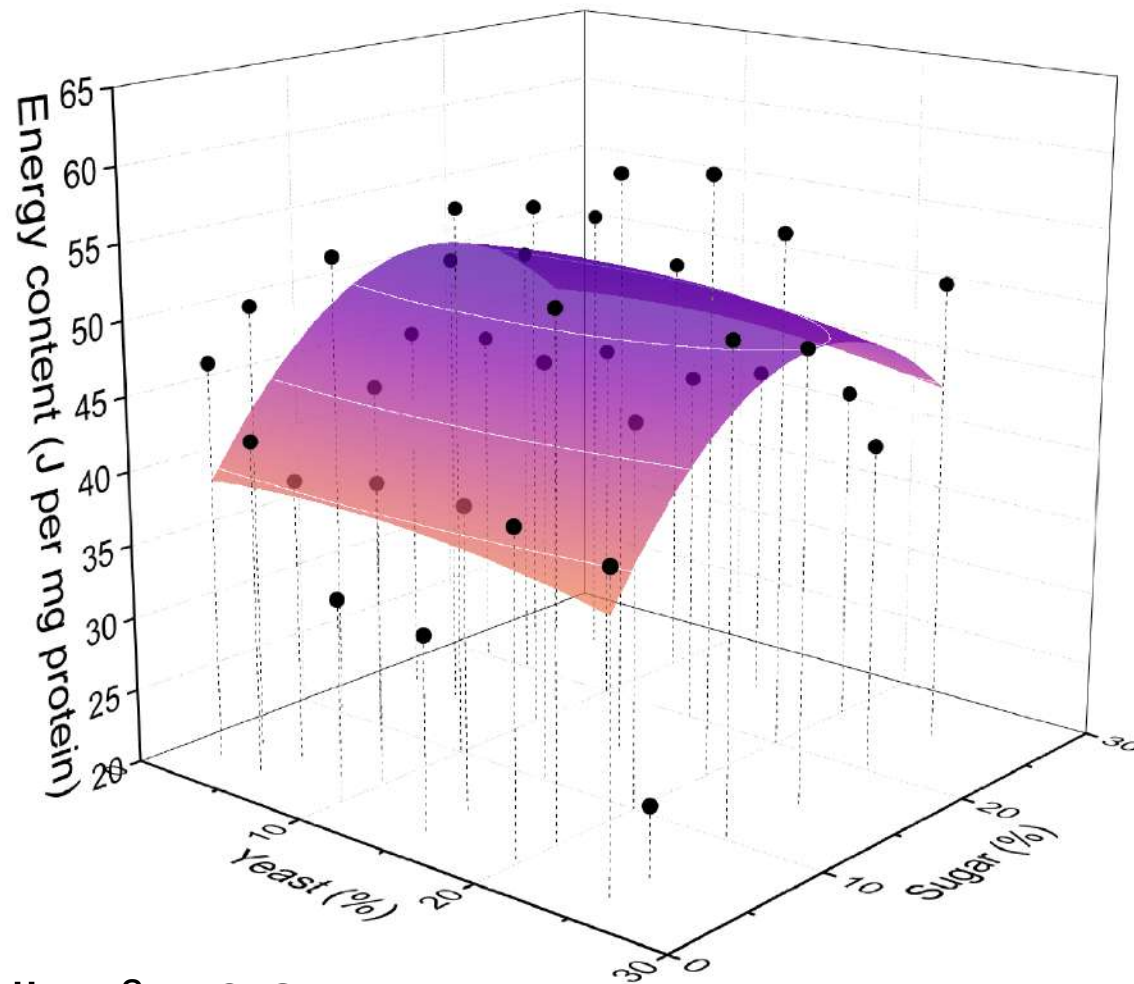
Adj. $R^2 = 0.36$

Figure S25.

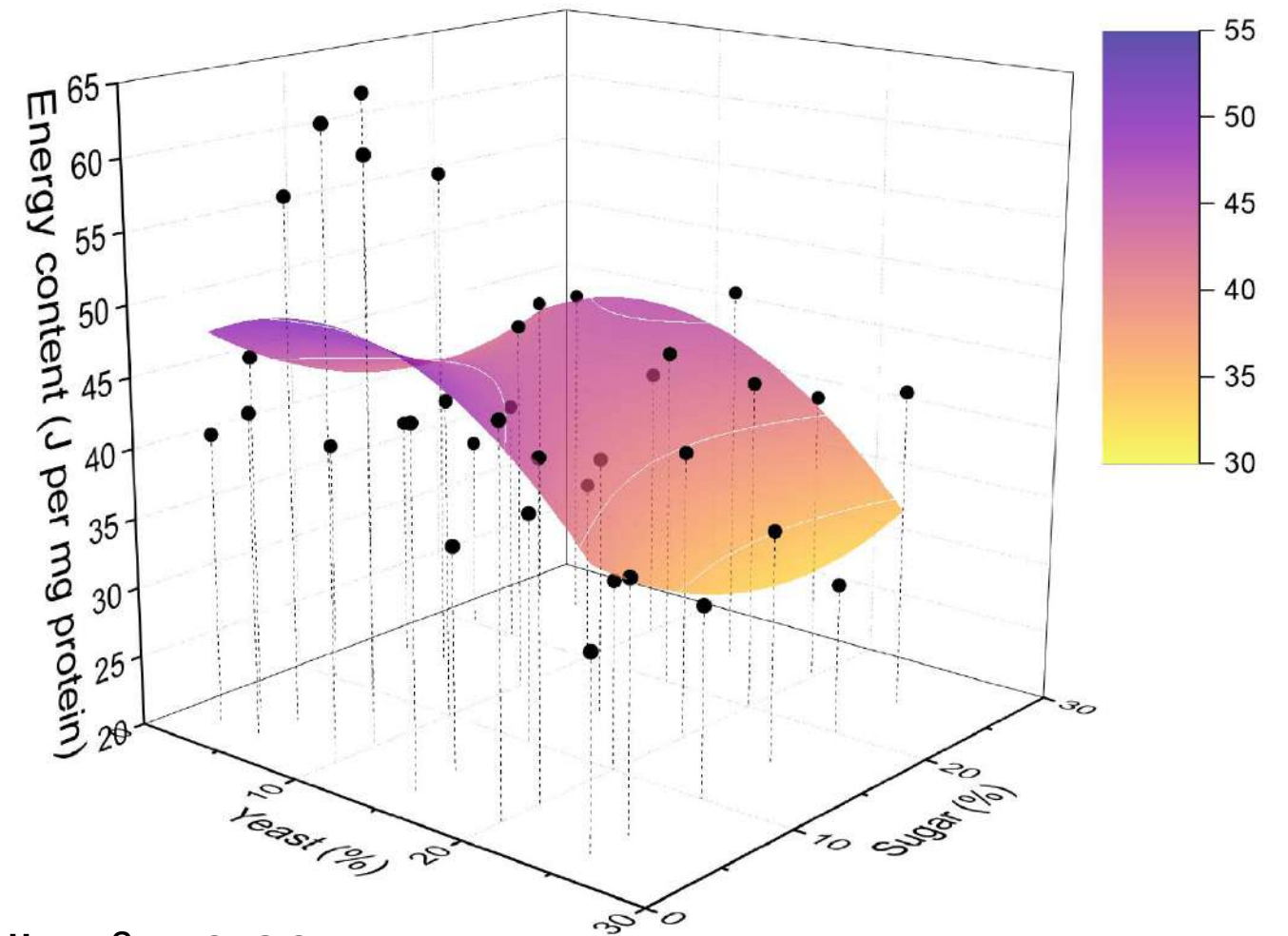
w^{1118}

SK

Virgin
females

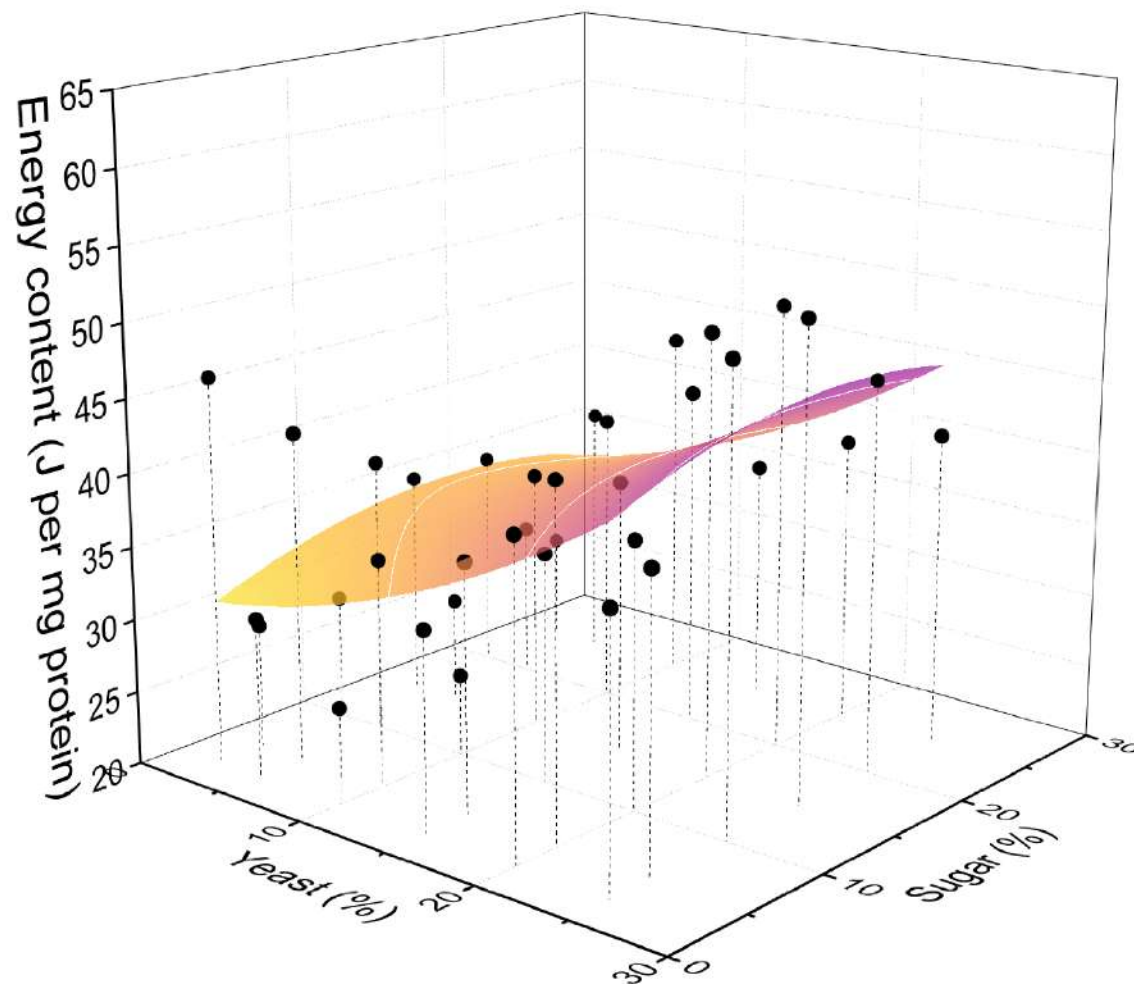


Adj. $R^2 = 0.25$

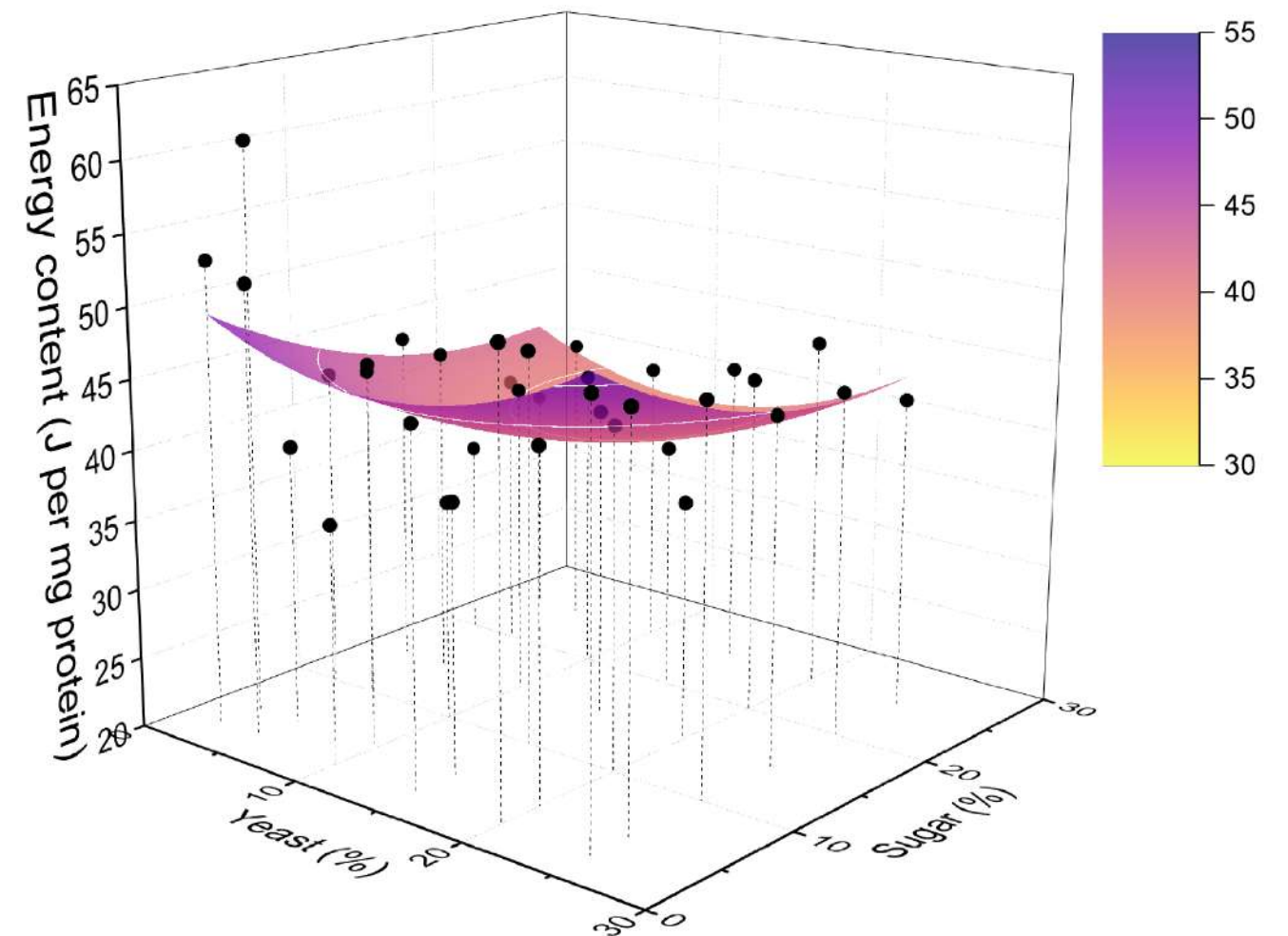


Adj. $R^2 = 0.20$

Mated
females



Adj. $R^2 = 0.34$



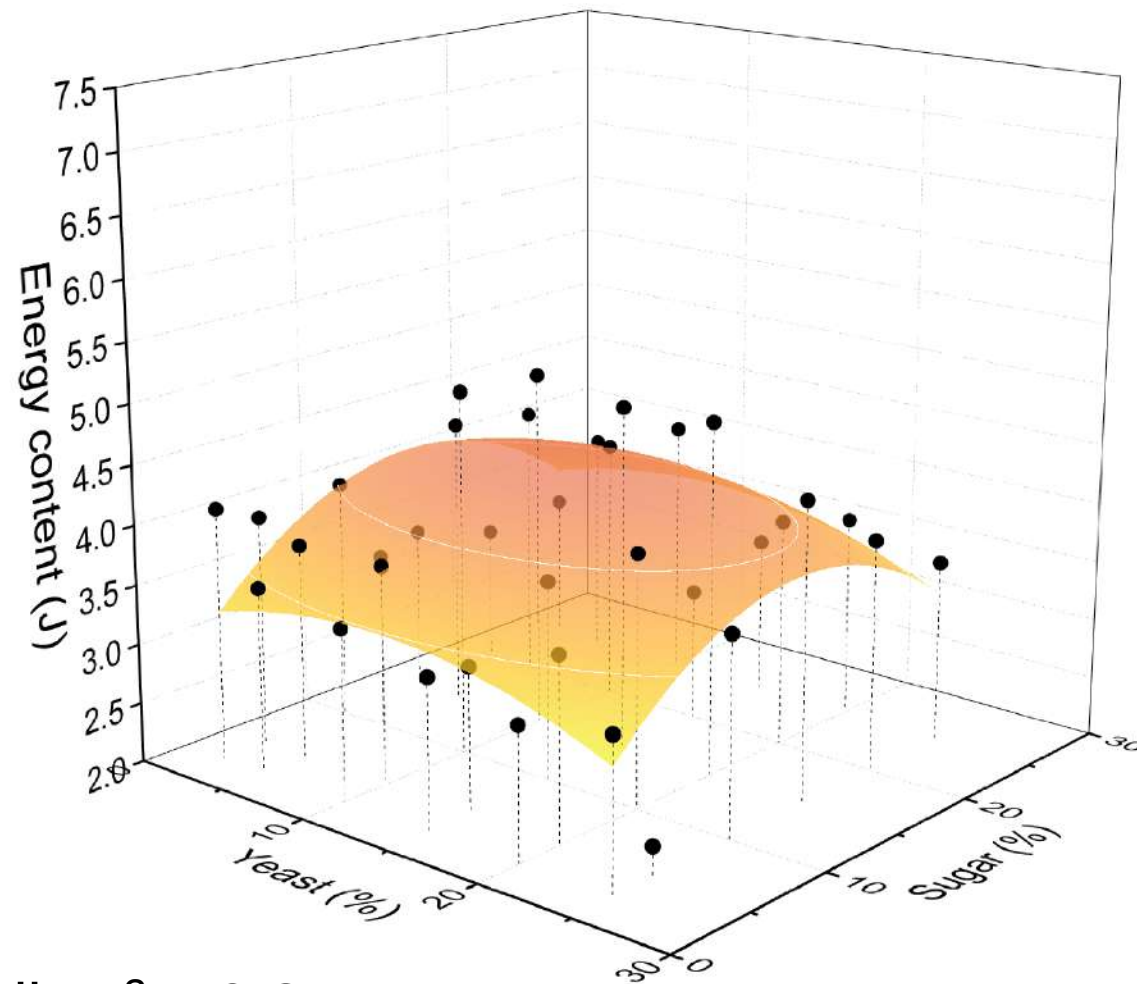
Adj. $R^2 = 0.30$

Figure S26.

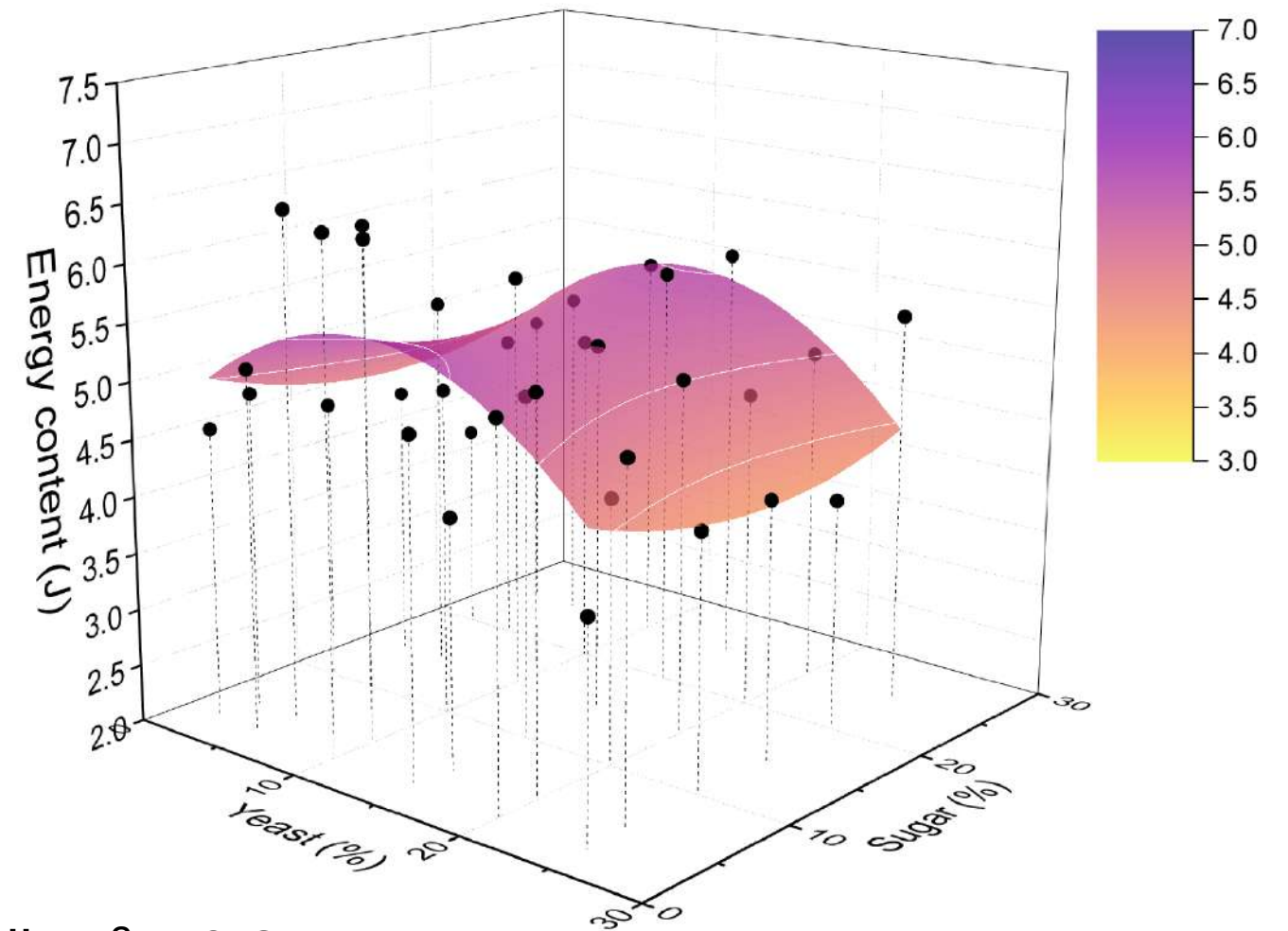
w^{1118}

SK

Virgin
females

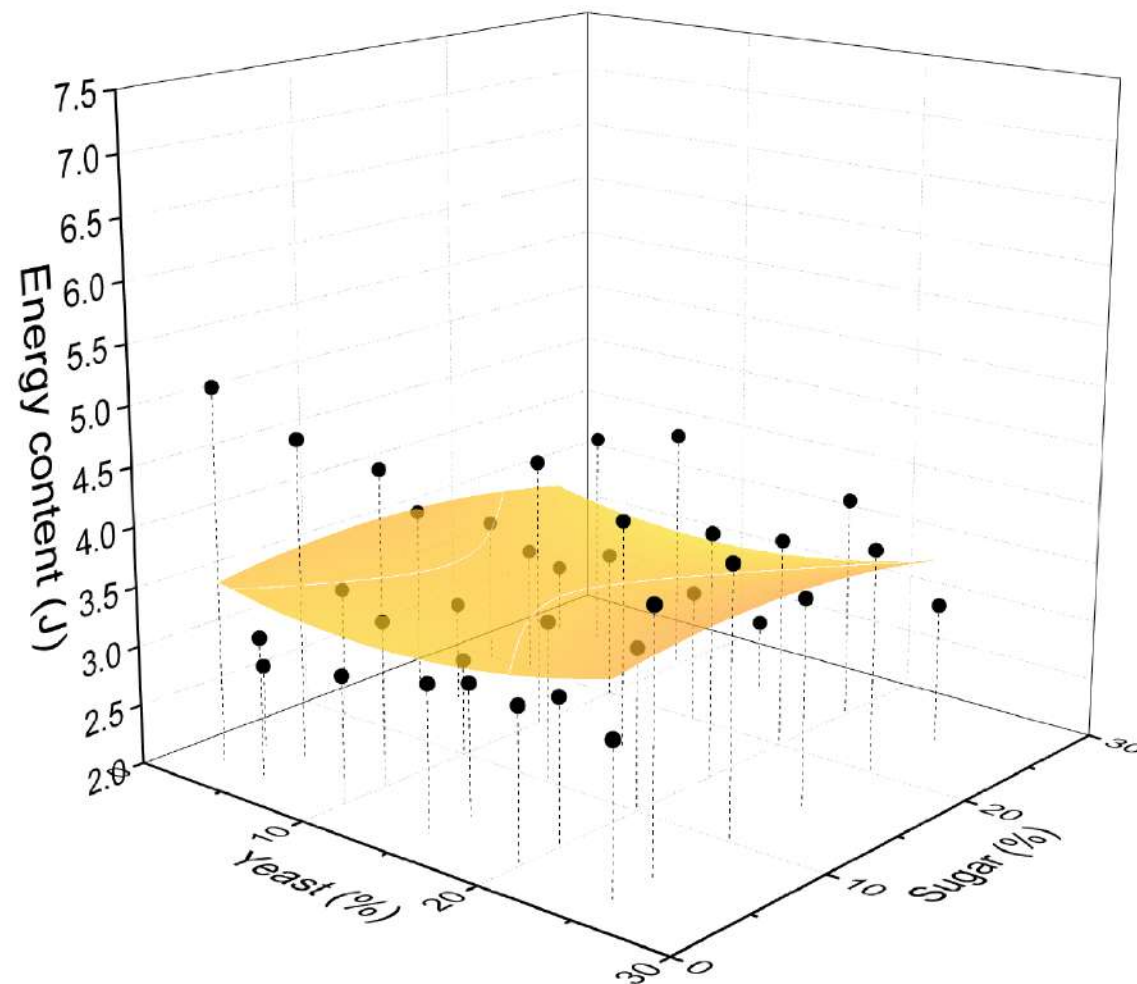


Adj. $R^2 = 0.25$

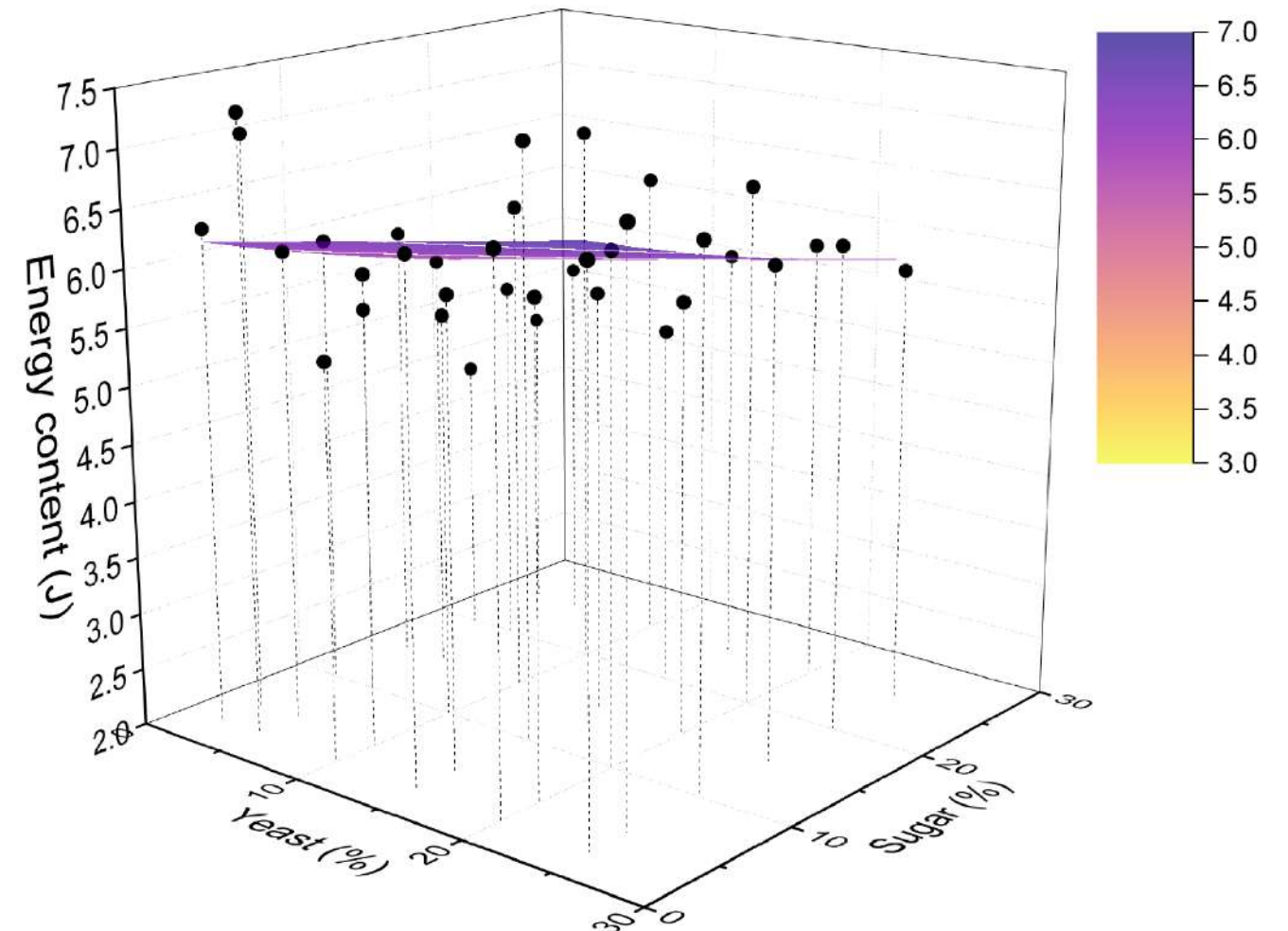


Adj. $R^2 = 0.24$

Mated
females



Adj. $R^2 = -0.07$



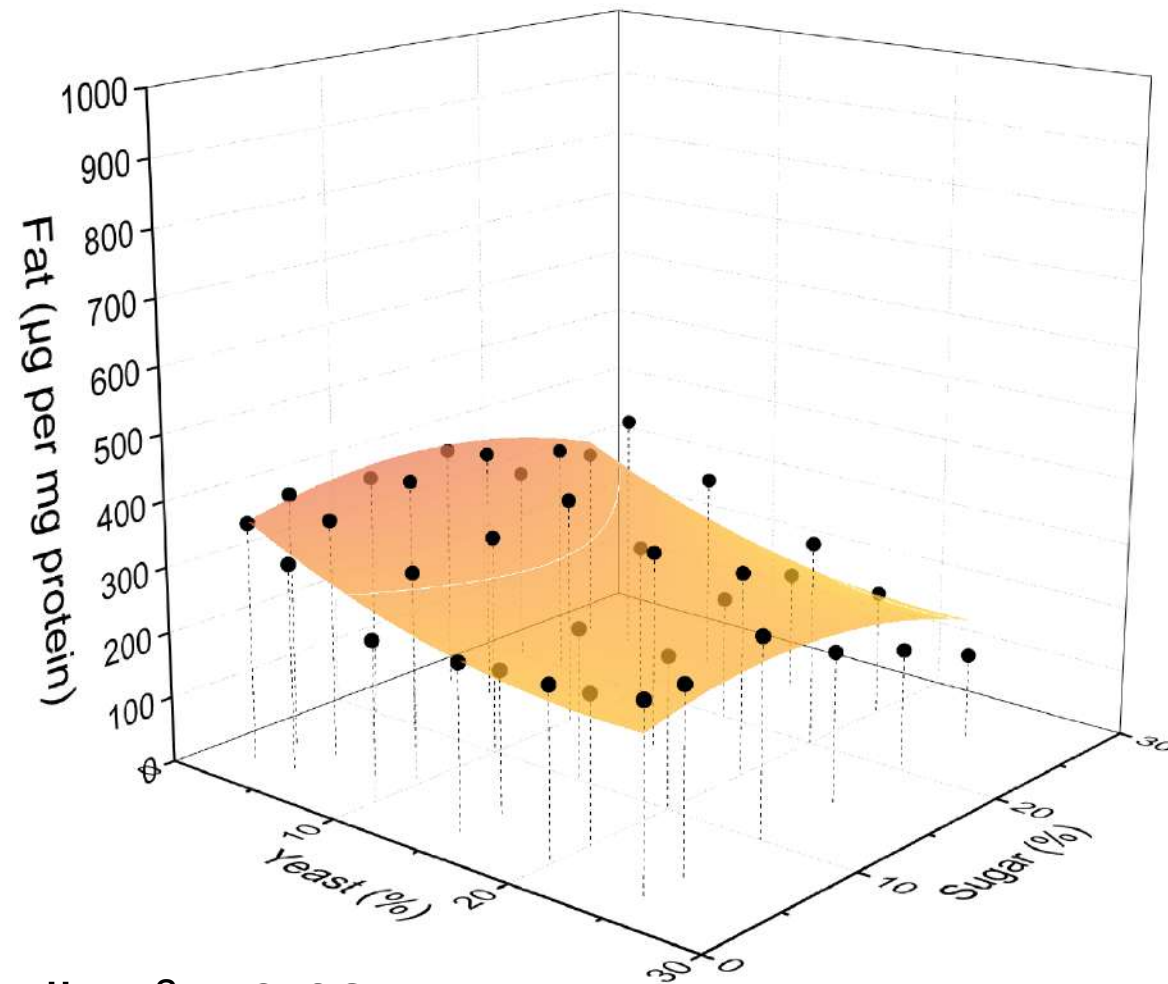
Adj. $R^2 = 0.28$

Figure S27.

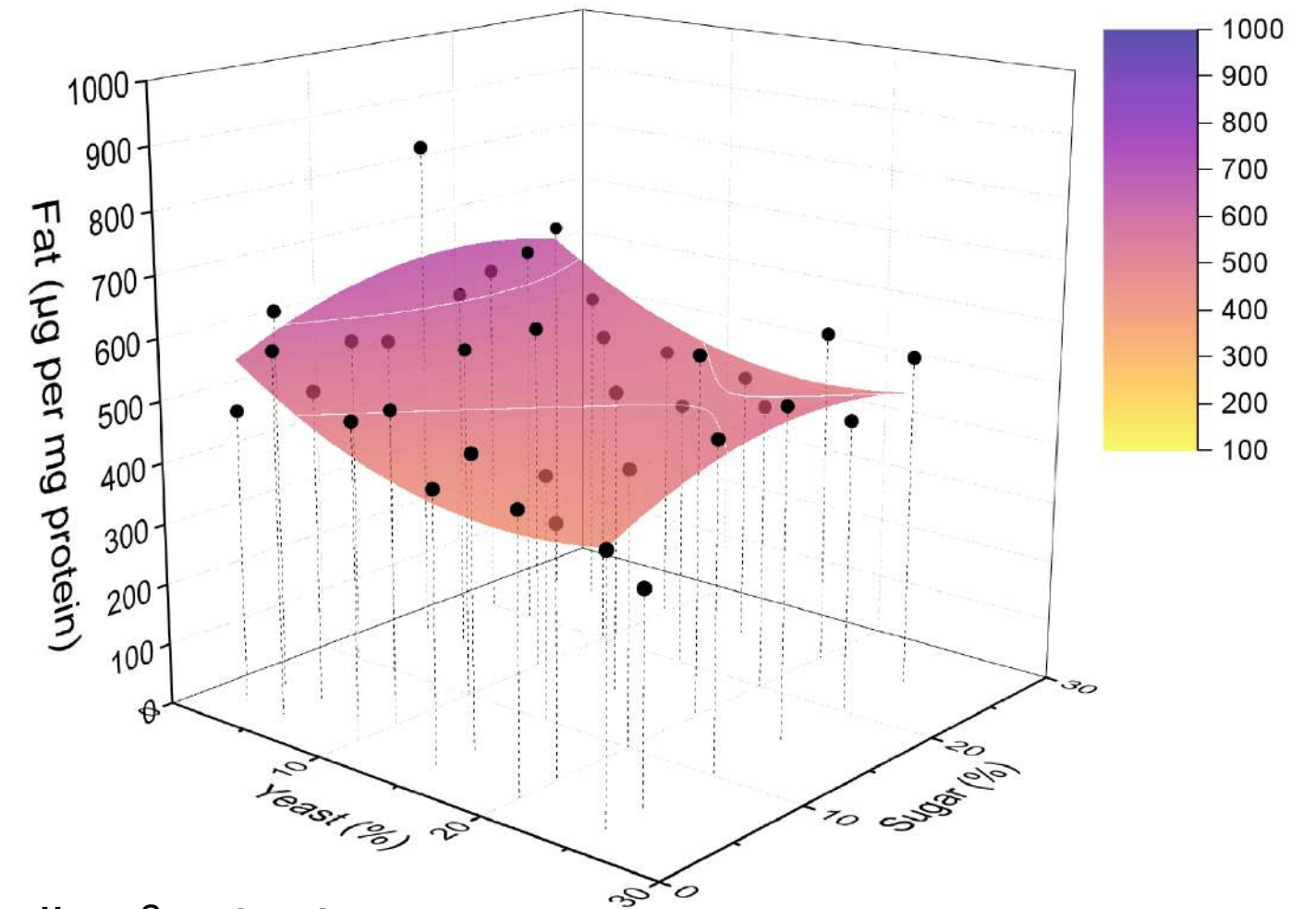
w^{1118}

SK

Virgin
males

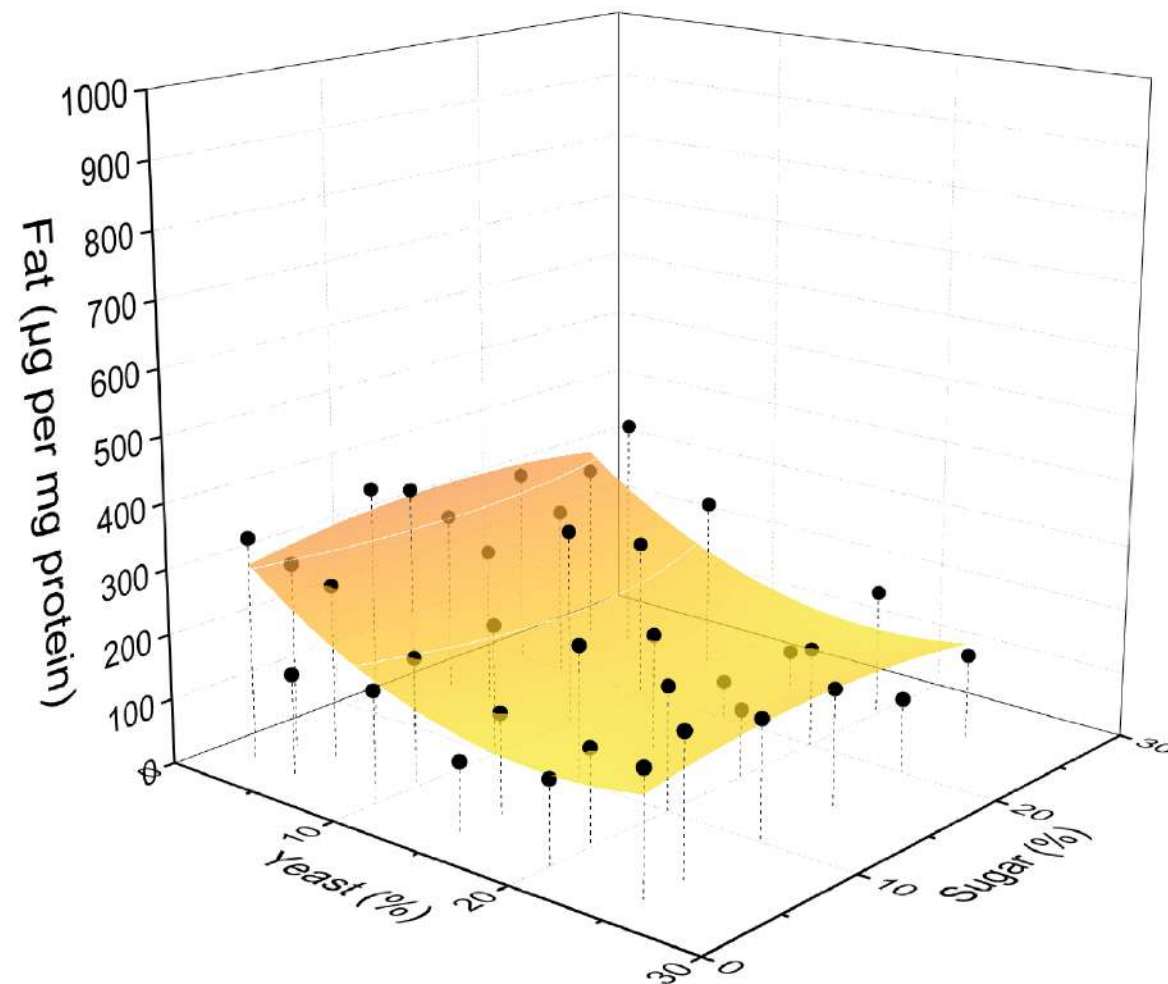


Adj. $R^2 = 0.63$

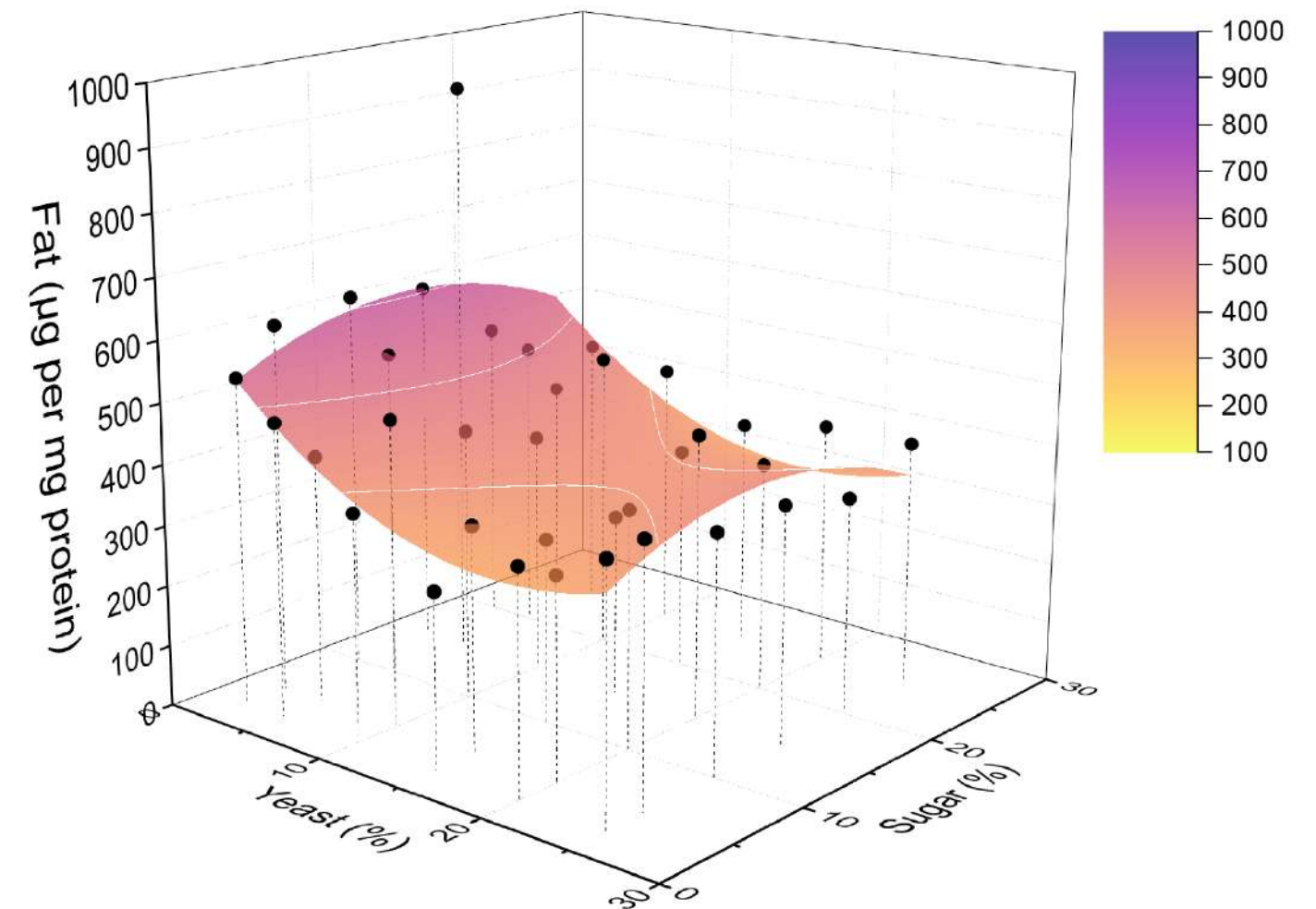


Adj. $R^2 = 0.50$

Mated
males



Adj. $R^2 = 0.56$



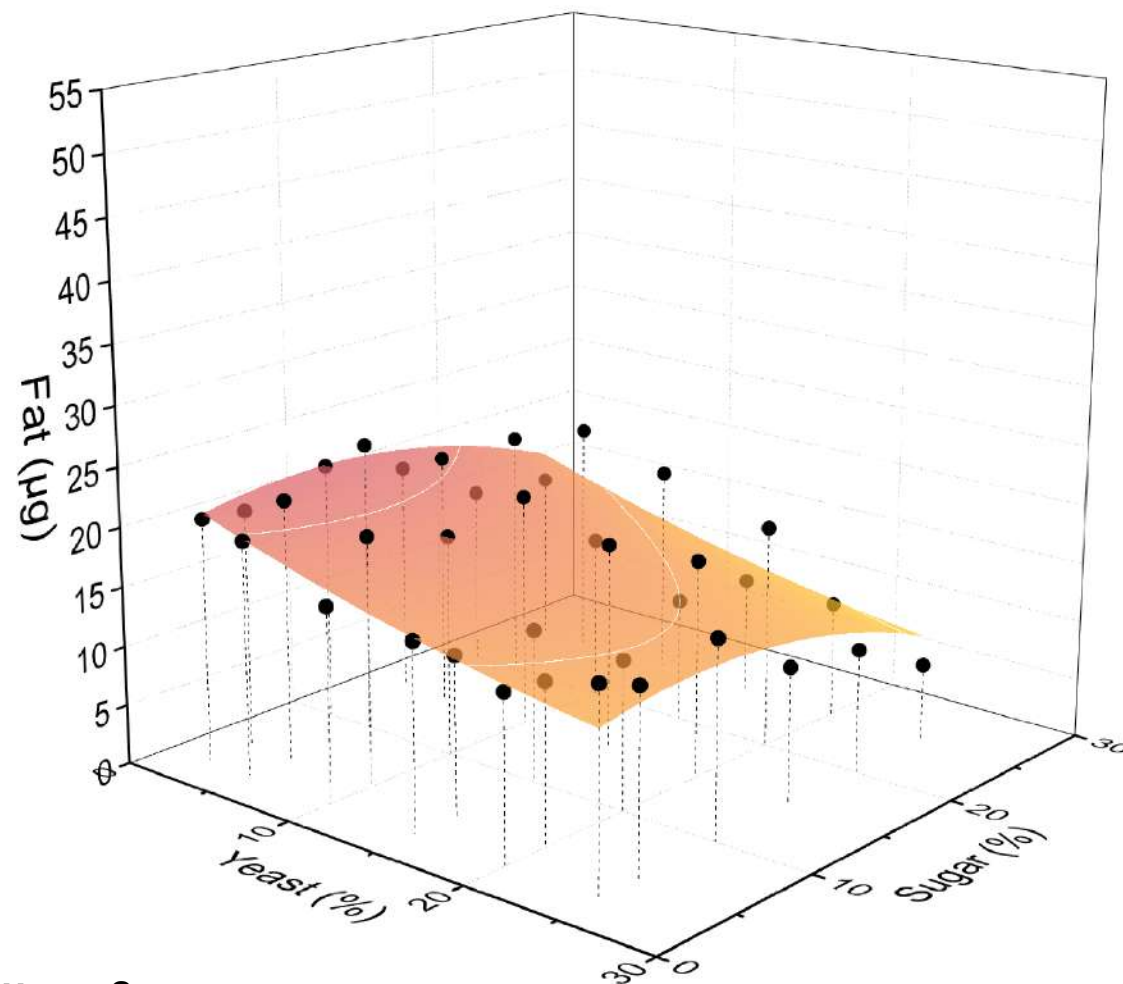
Adj. $R^2 = 0.38$

Figure S28.

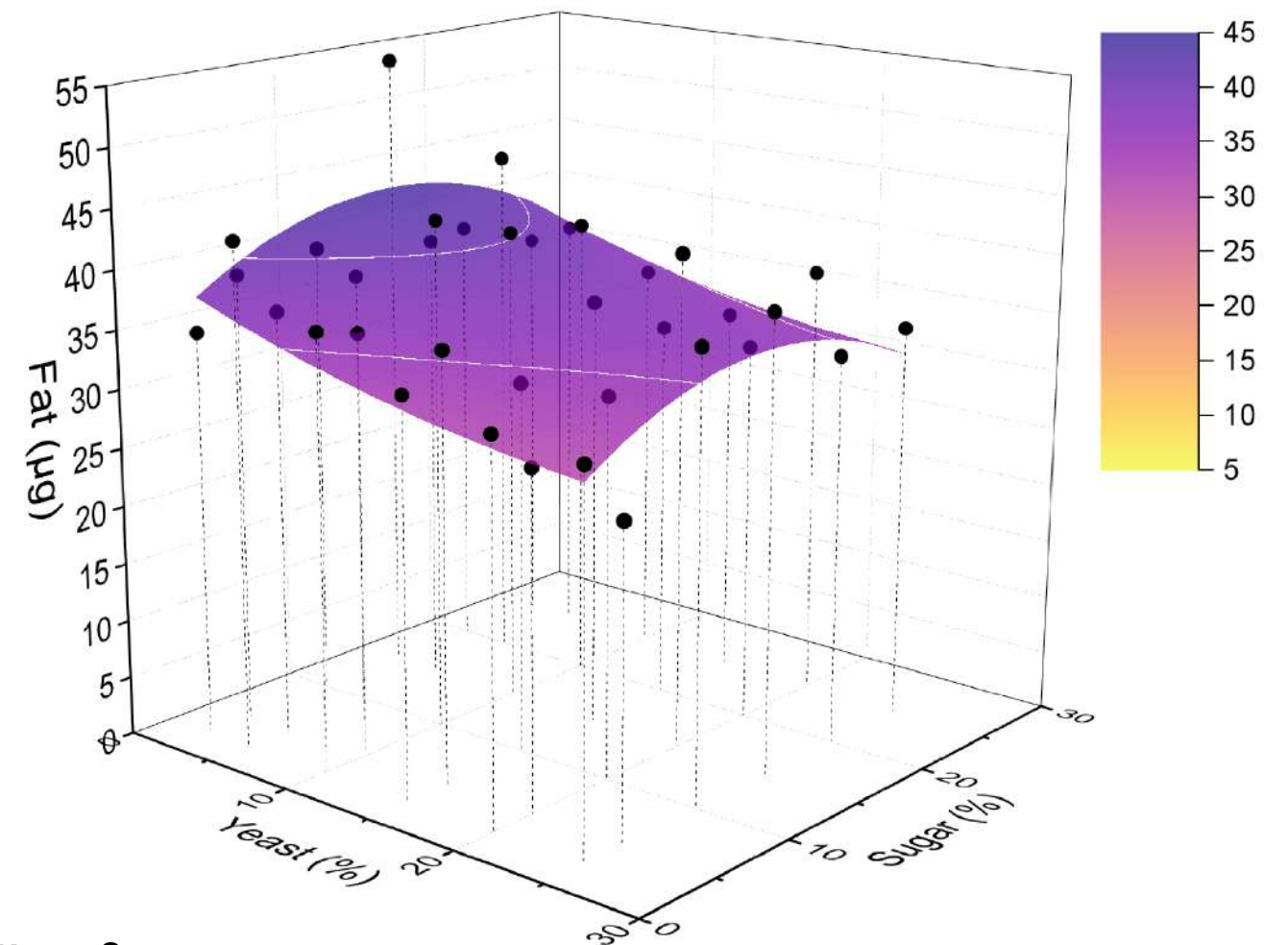
w^{1118}

SK

Virgin
males

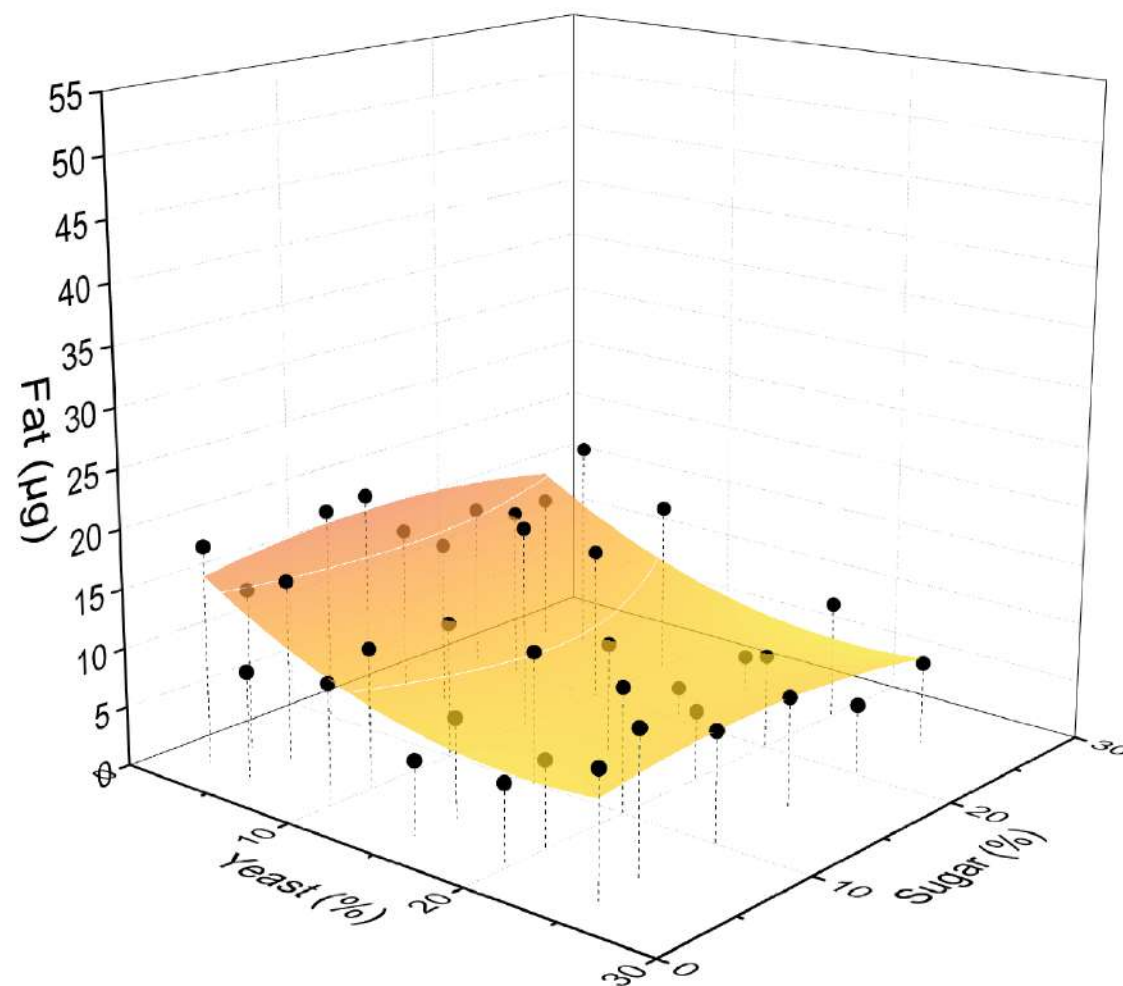


Adj. $R^2 = 0.56$

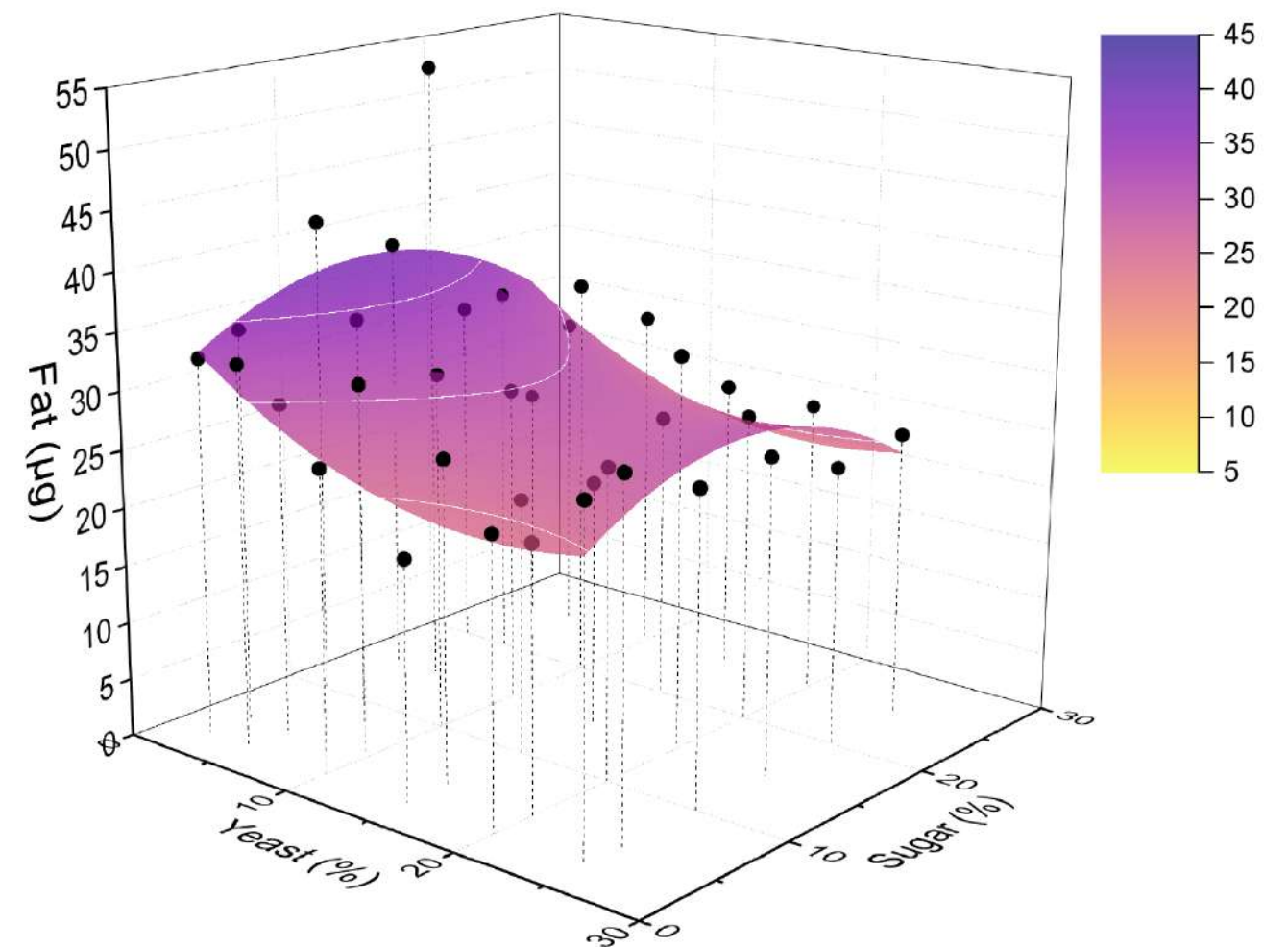


Adj. $R^2 = 0.37$

Mated
males



Adj. $R^2 = 0.49$



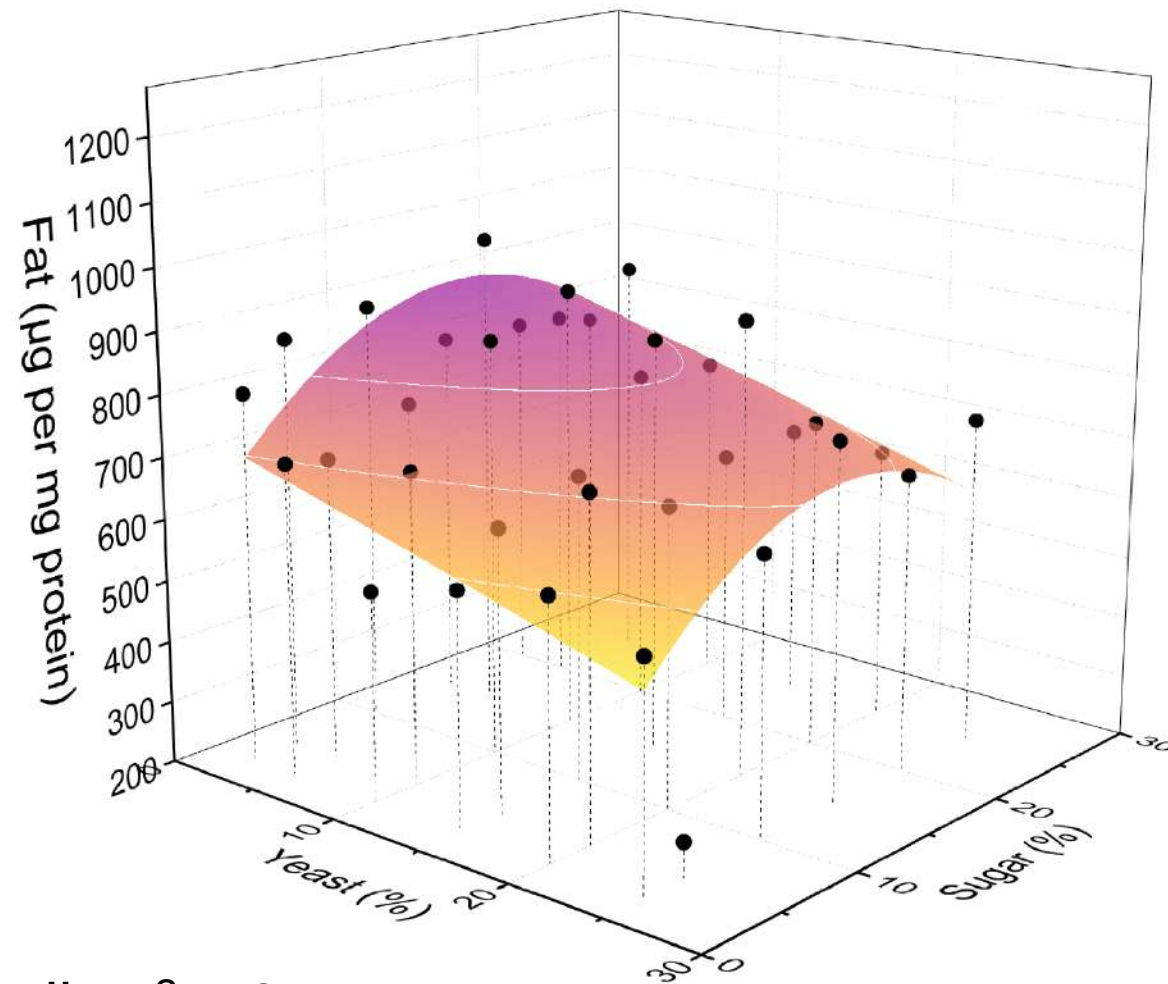
Adj. $R^2 = 0.33$

Figure S29.

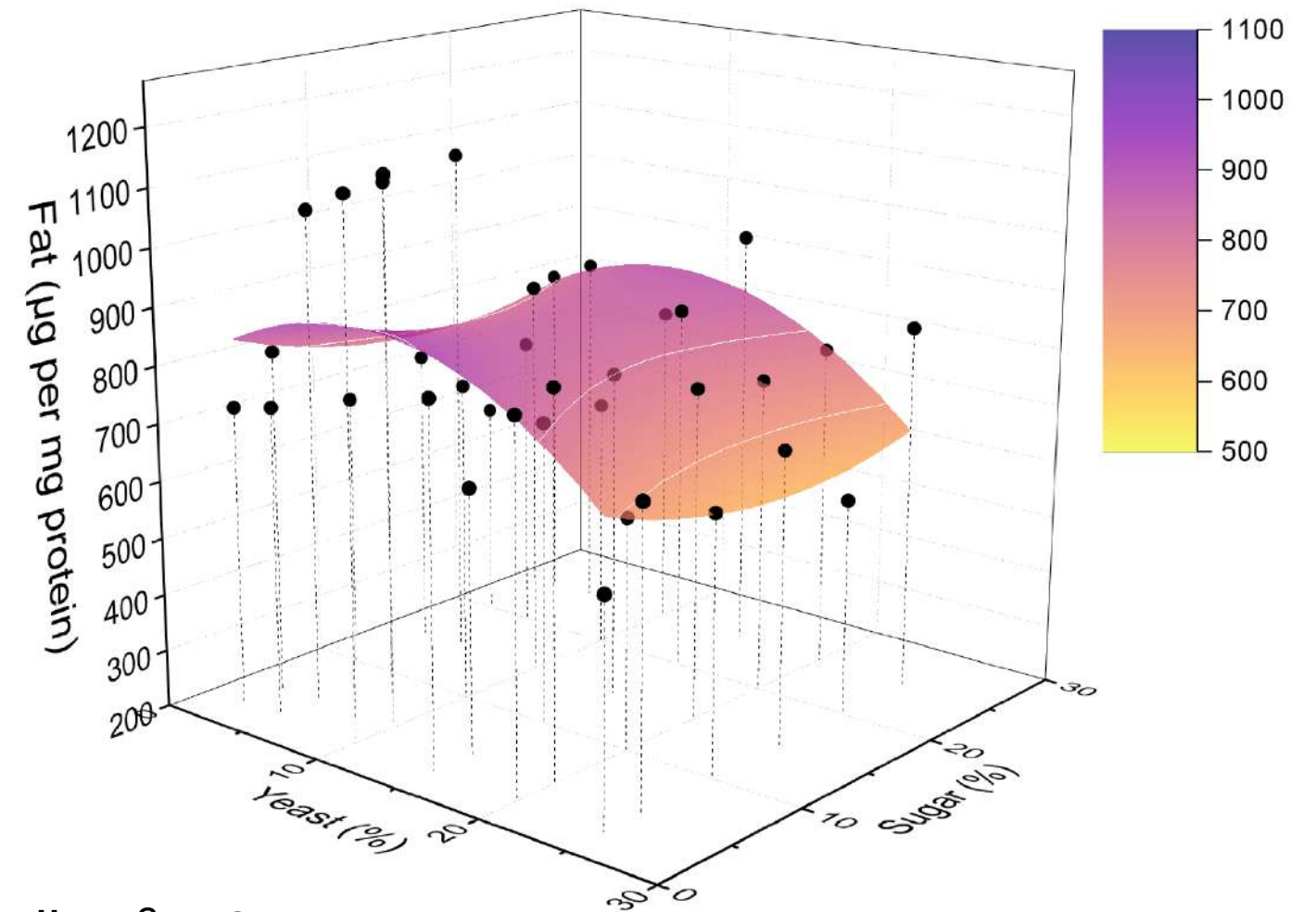
w^{1118}

SK

Virgin
females

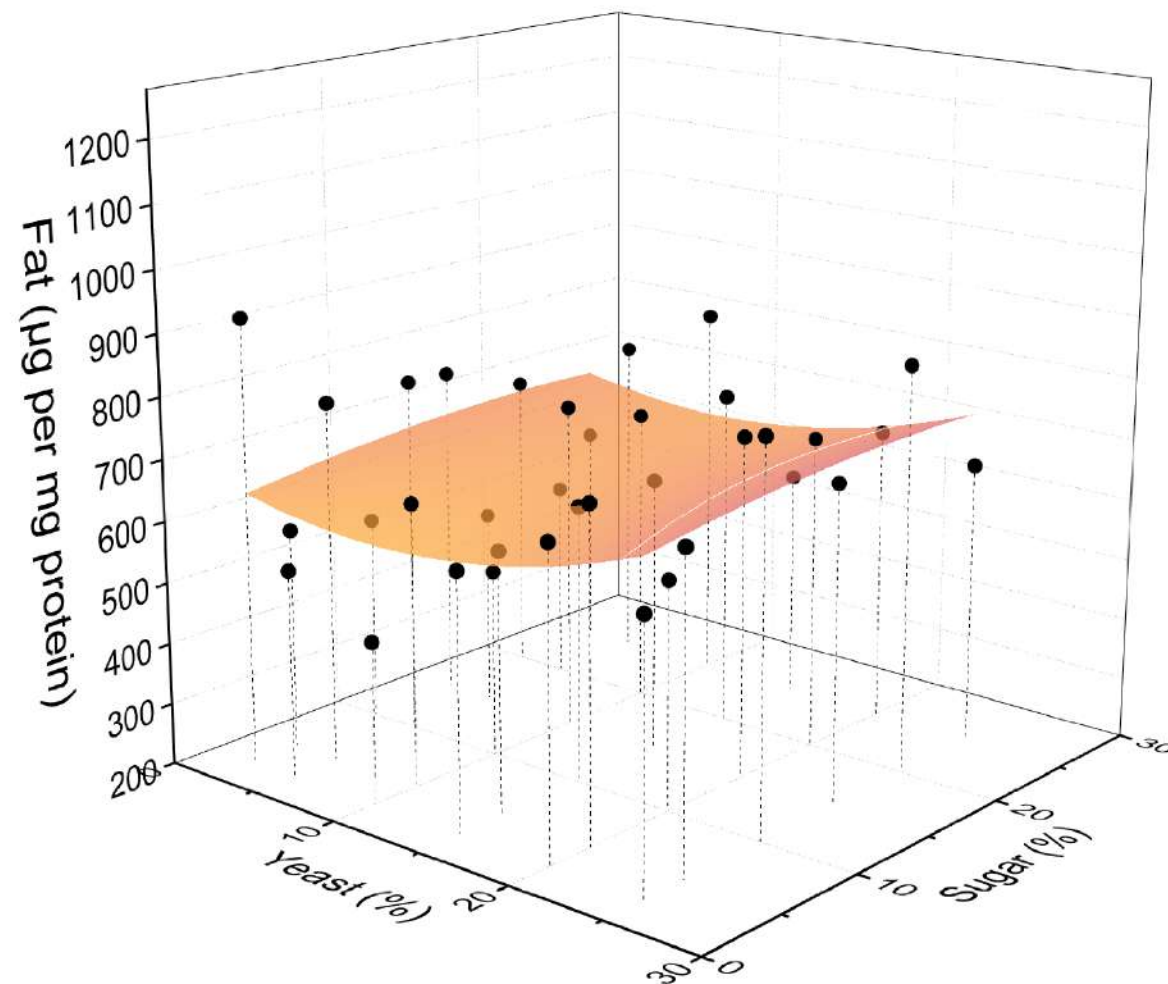


Adj. $R^2 = 0.45$

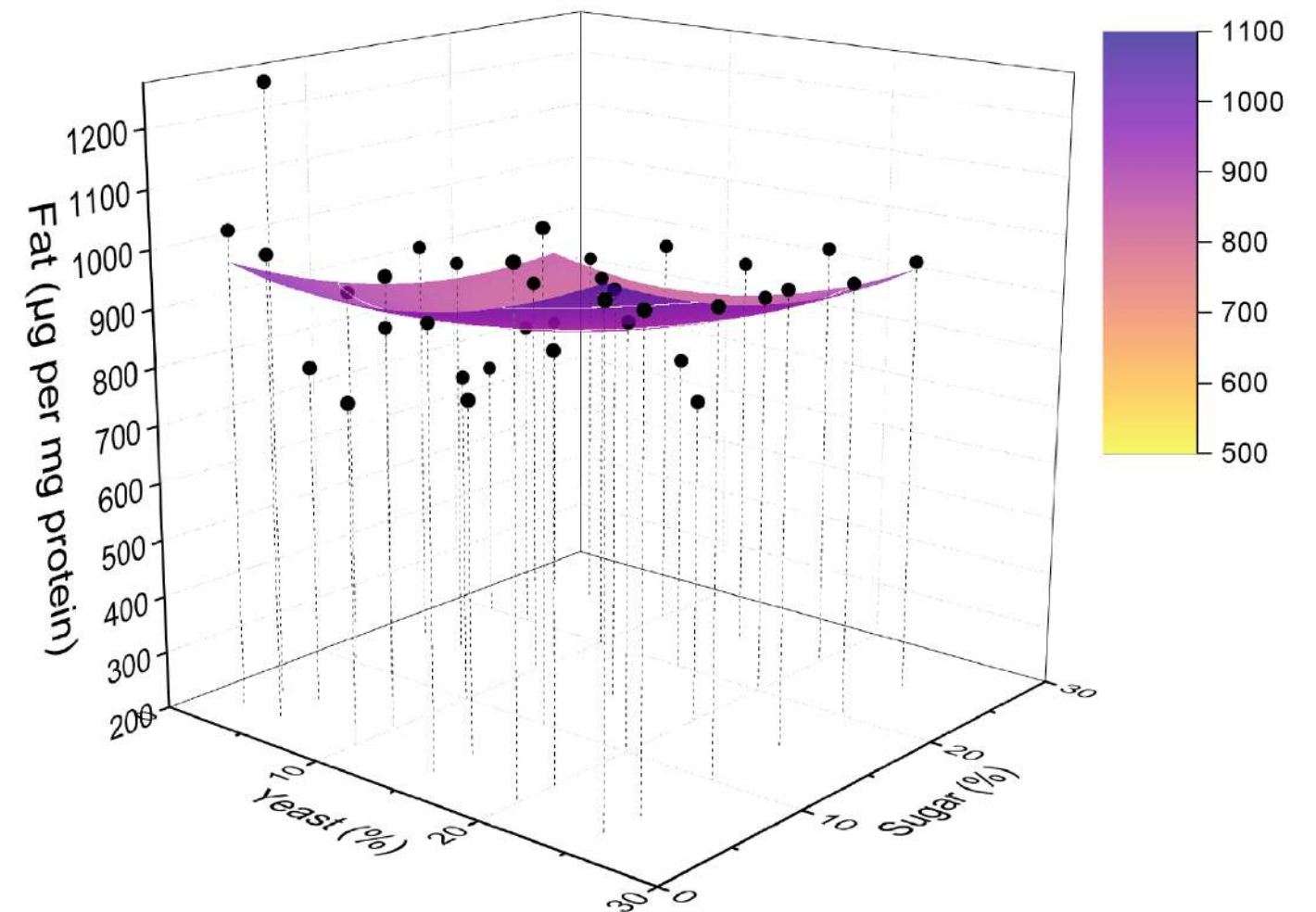


Adj. $R^2 = 0.14$

Mated
females



Adj. $R^2 = -0.01$



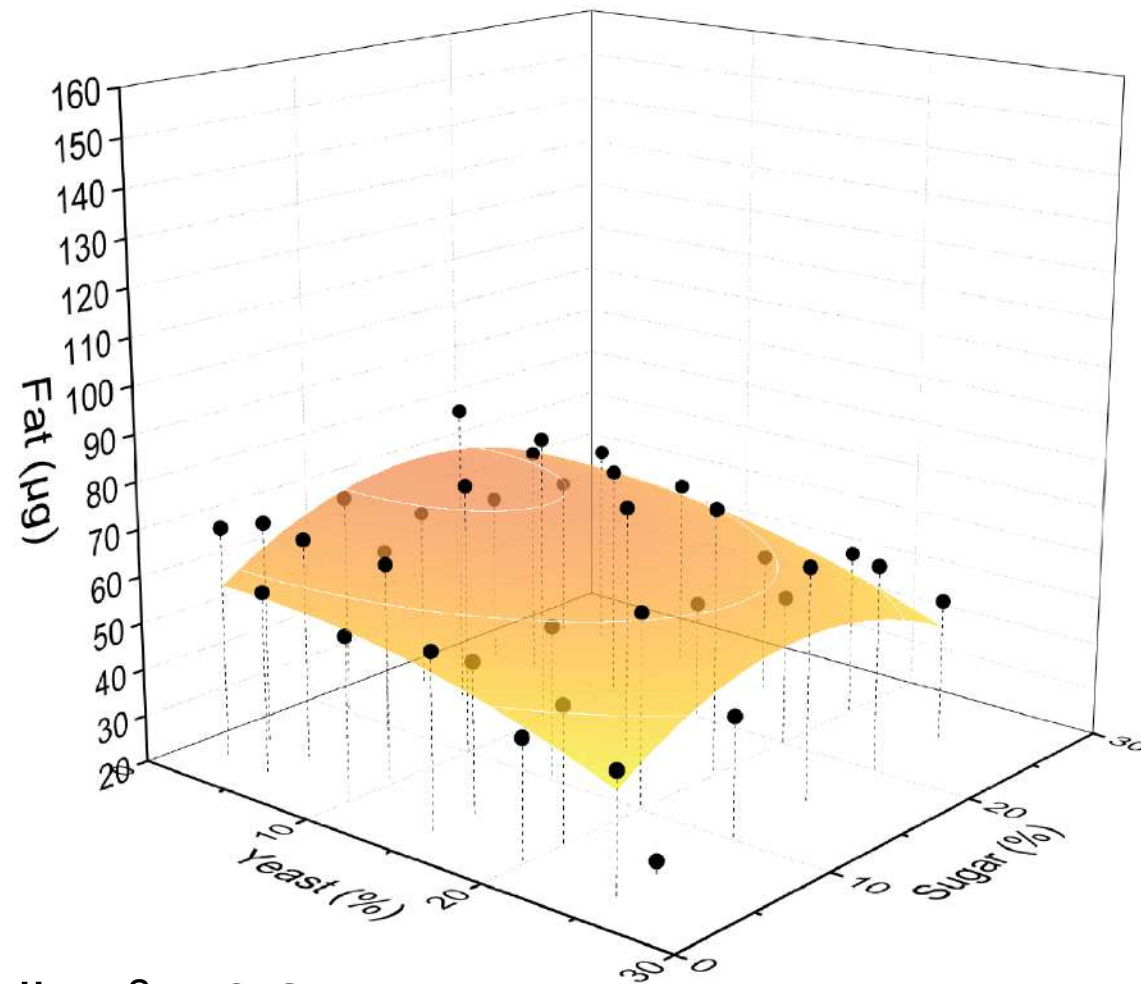
Adj. $R^2 = 0.20$

Figure S30.

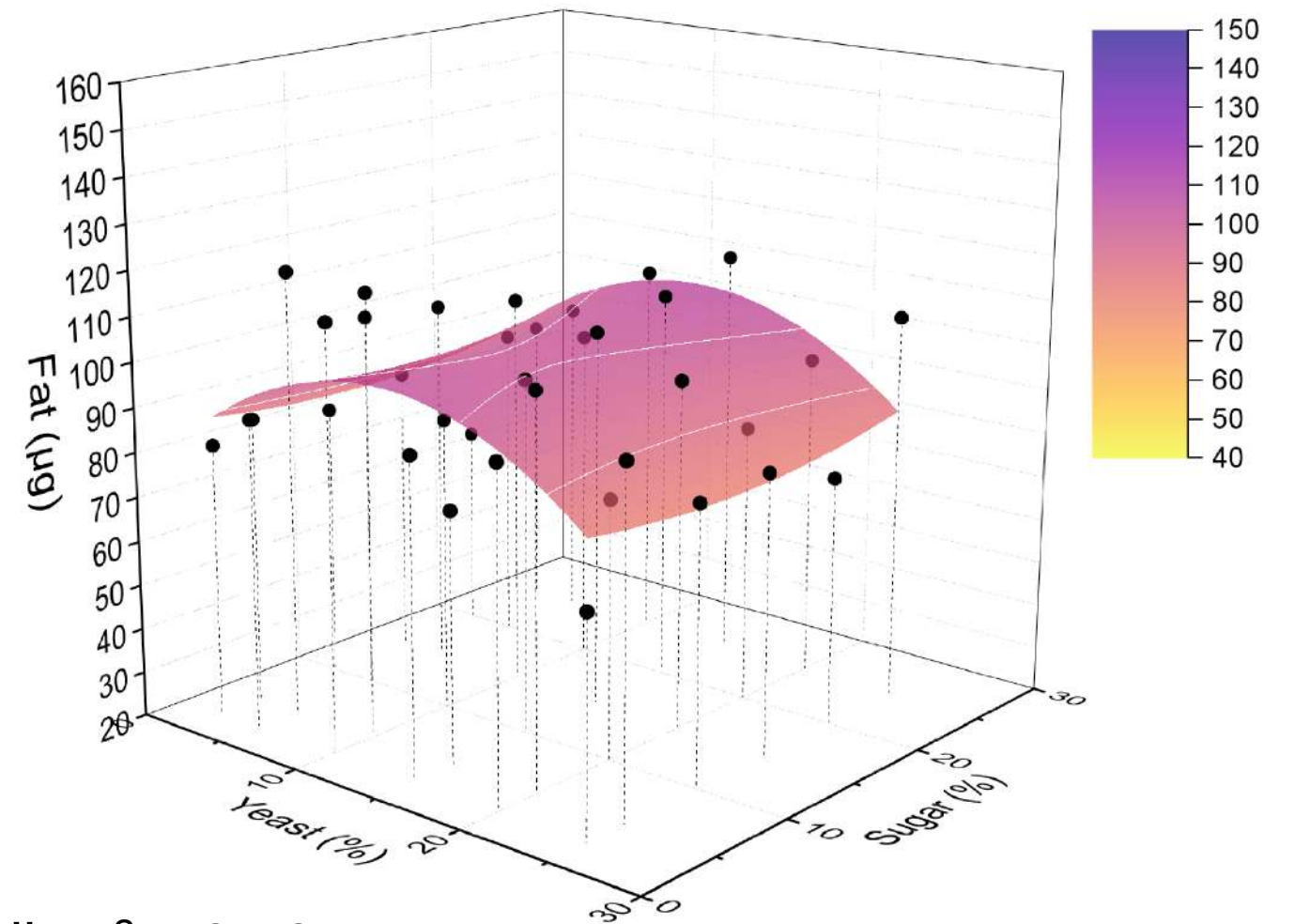
w^{1118}

SK

Virgin
females

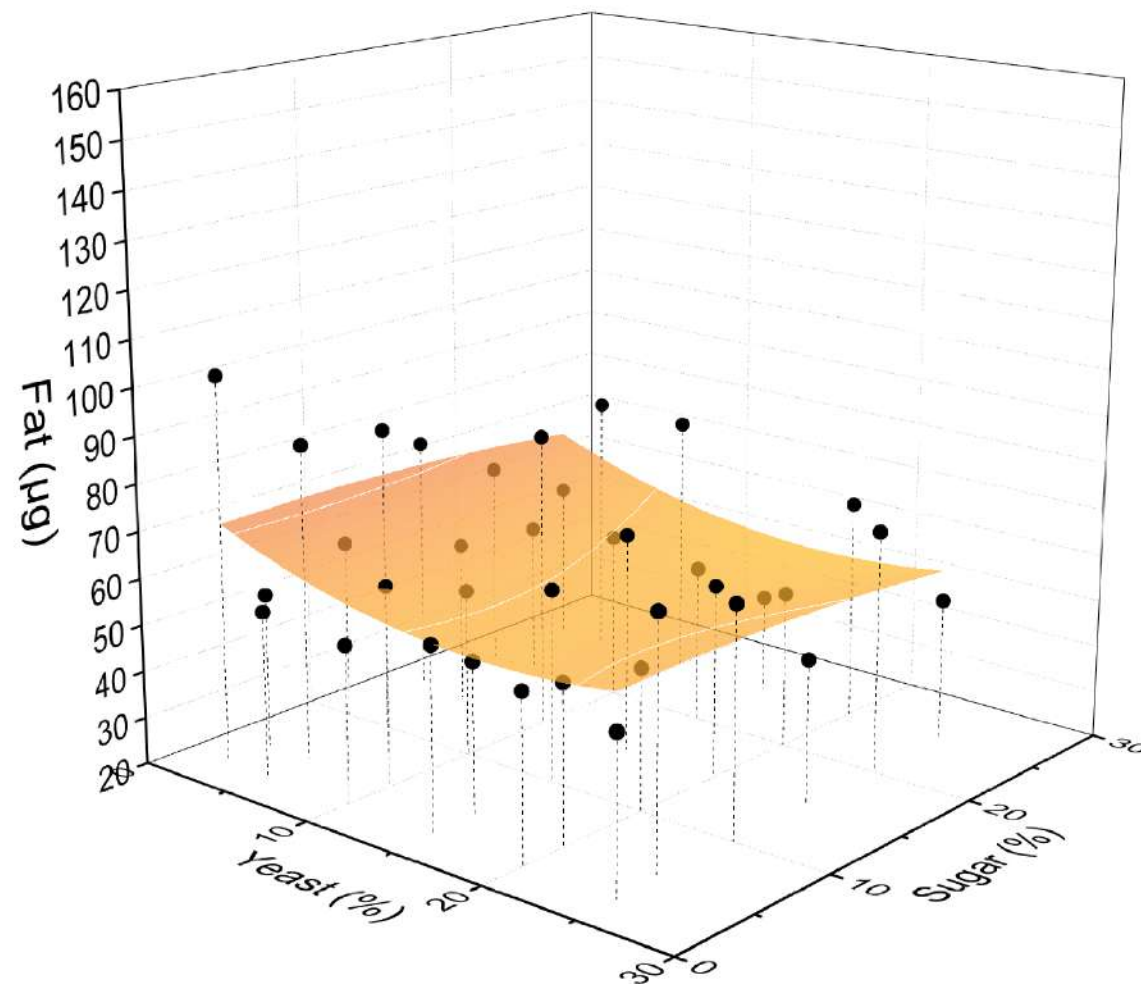


Adj. $R^2 = 0.35$

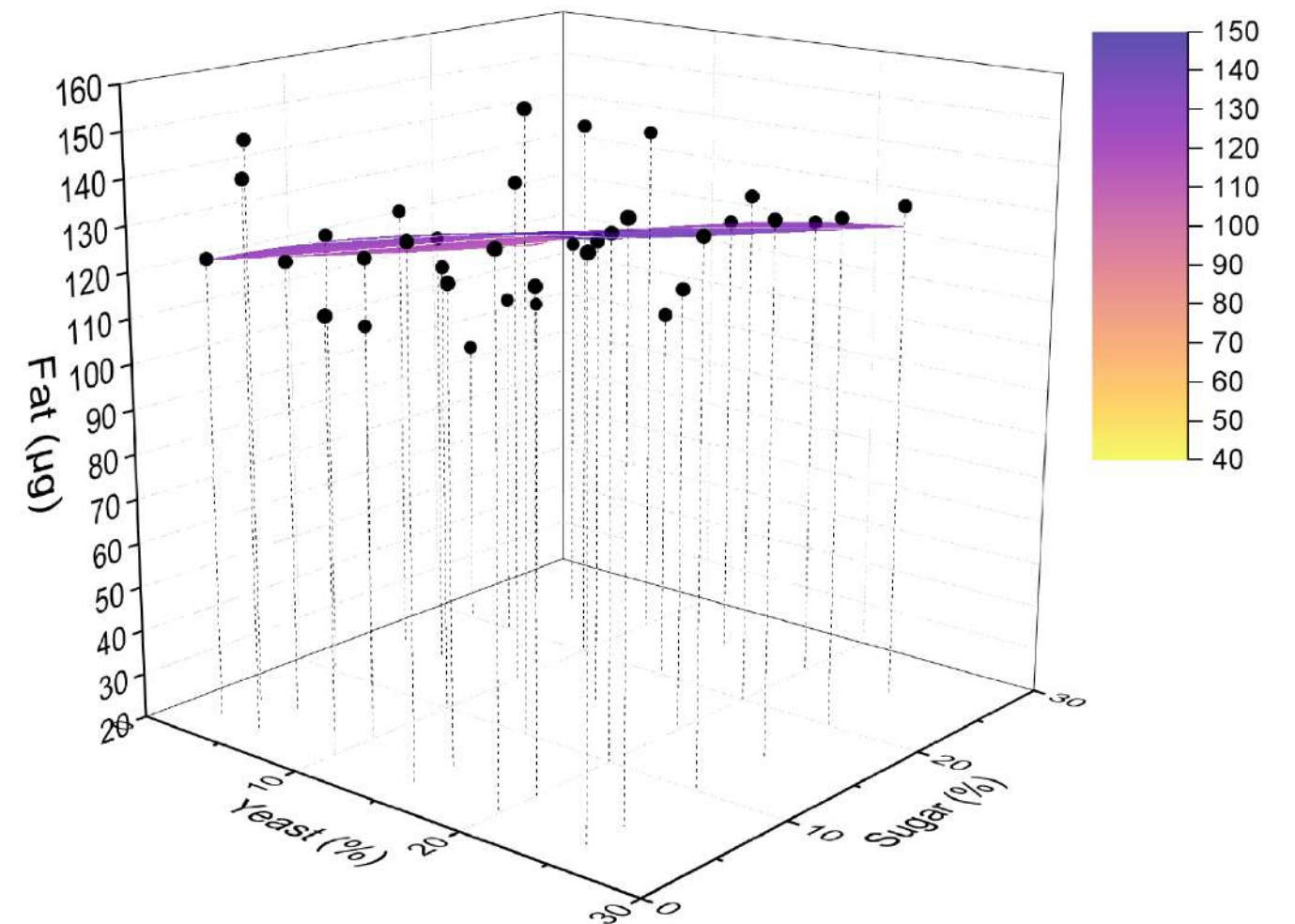


Adj. $R^2 = 0.19$

Mated
females



Adj. $R^2 = 0.02$



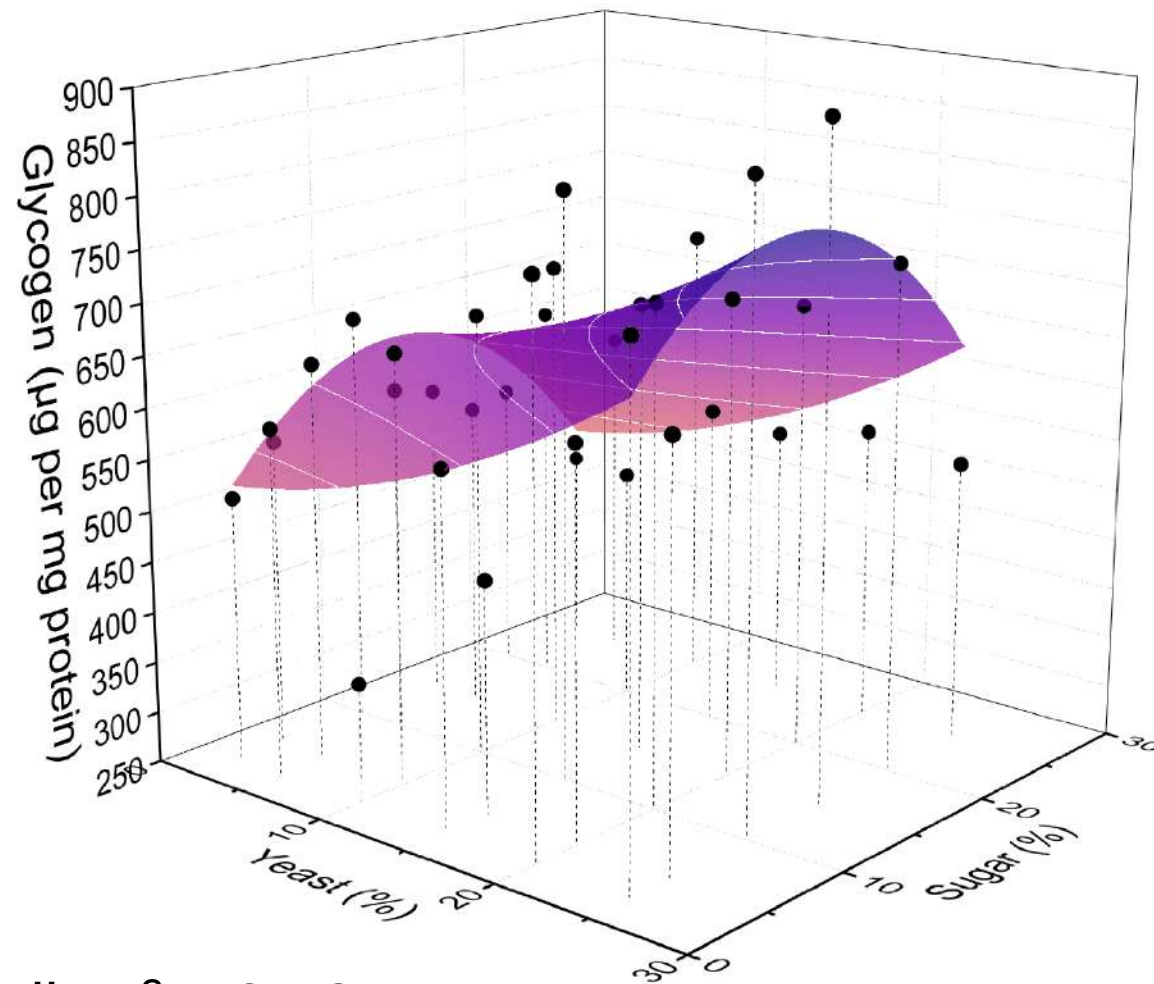
Adj. $R^2 = 0.26$

Figure S31.

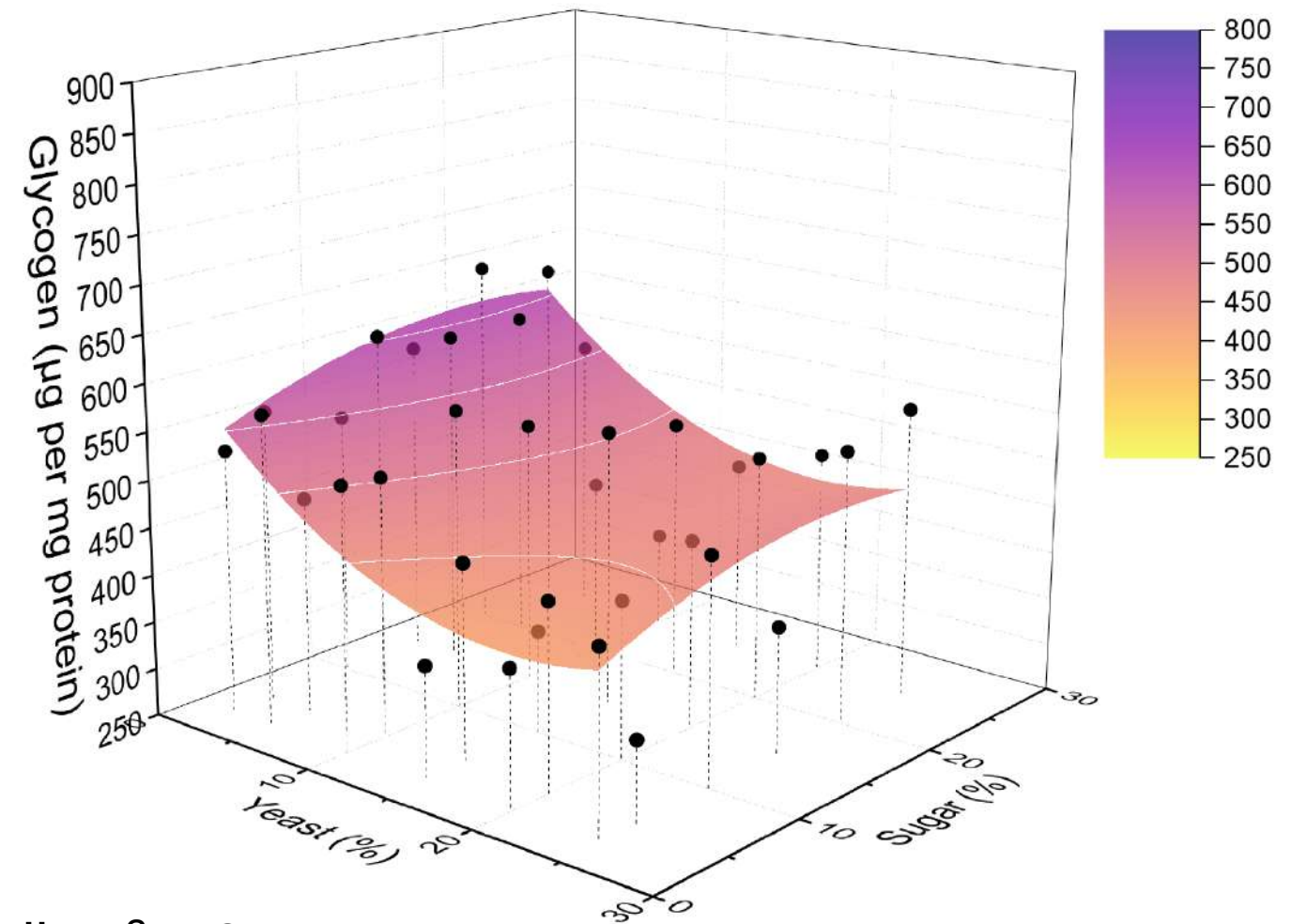
w^{1118}

SK

Virgin
males

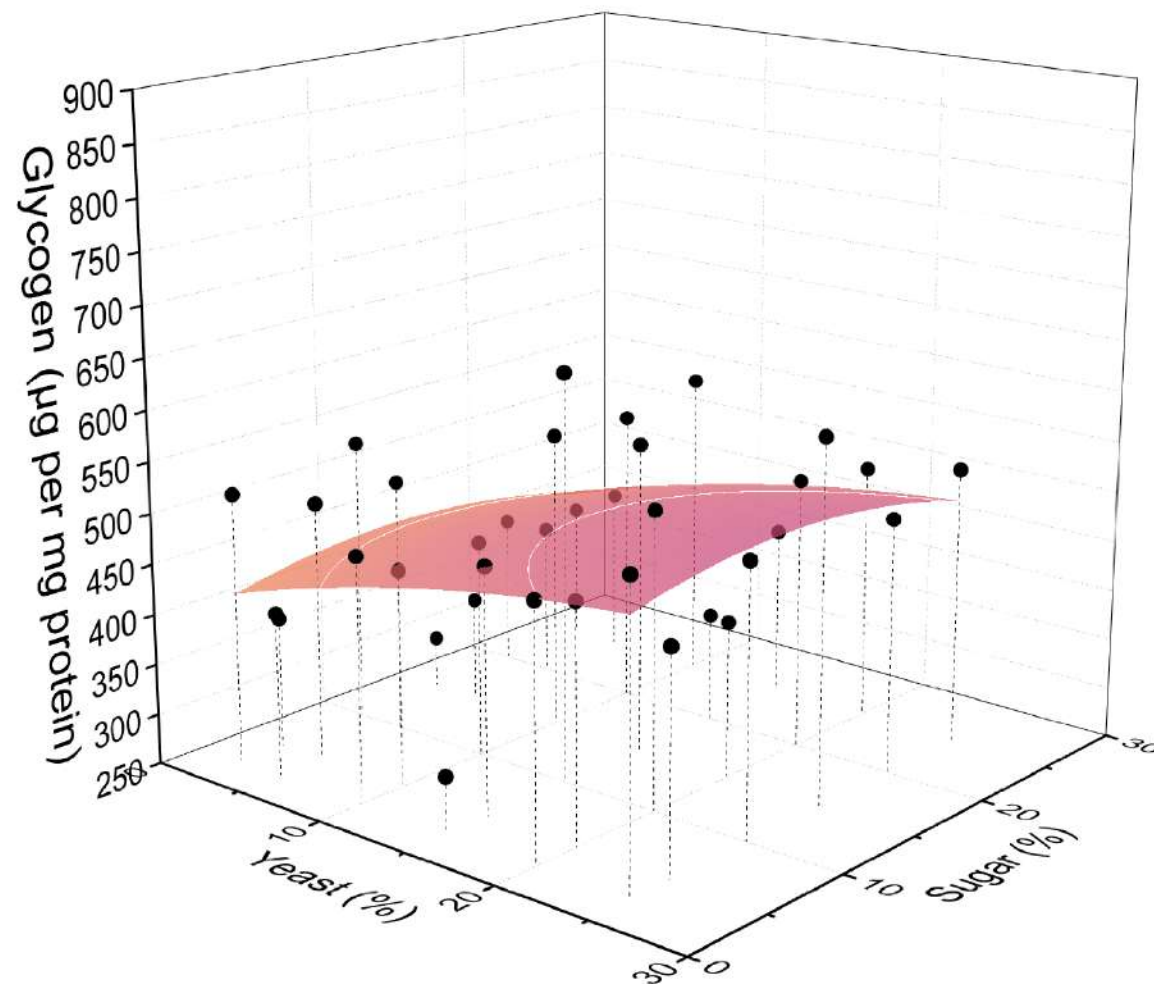


Adj. $R^2 = 0.42$

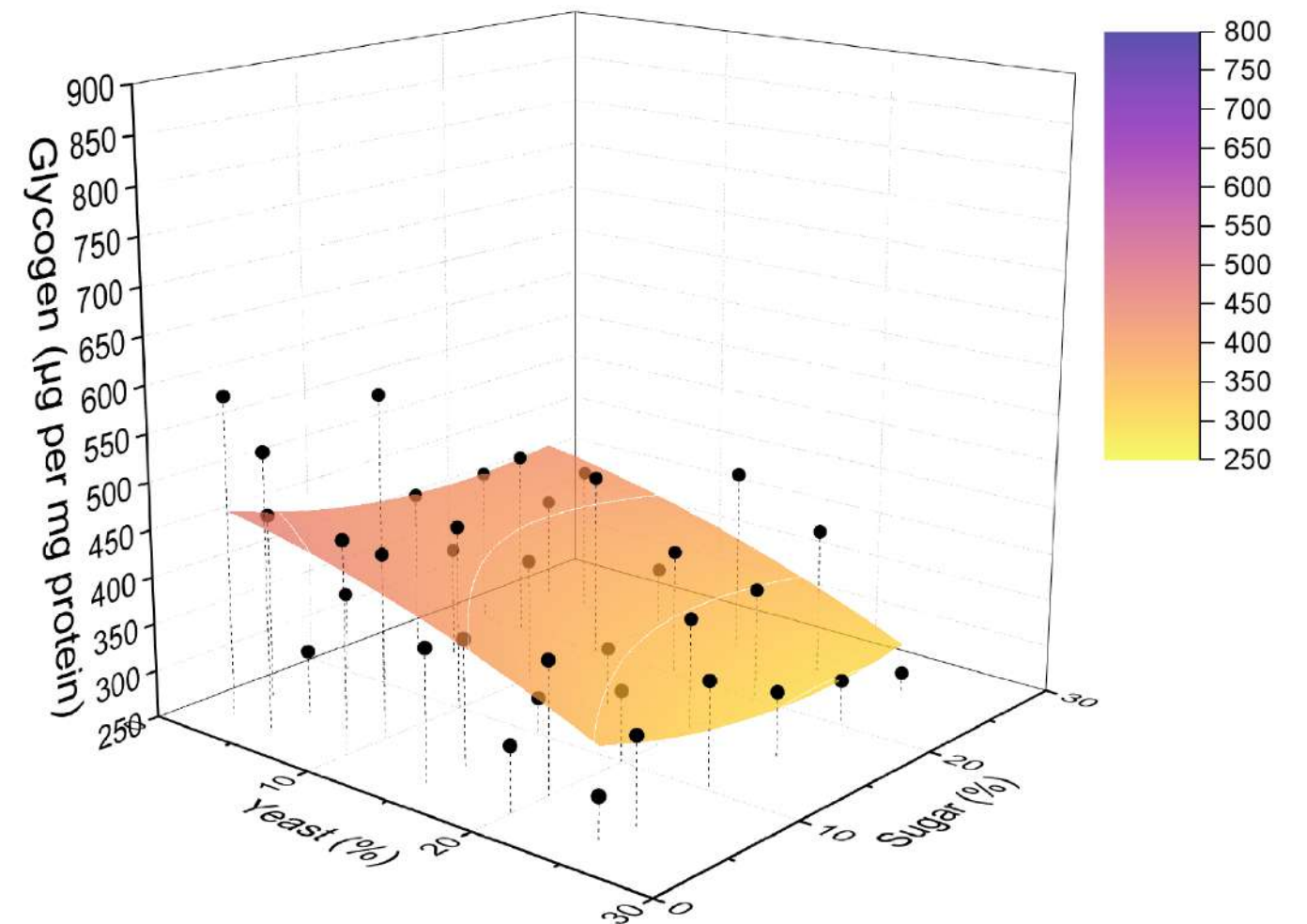


Adj. $R^2 = 0.44$

Mated
males



Adj. $R^2 = 0.09$



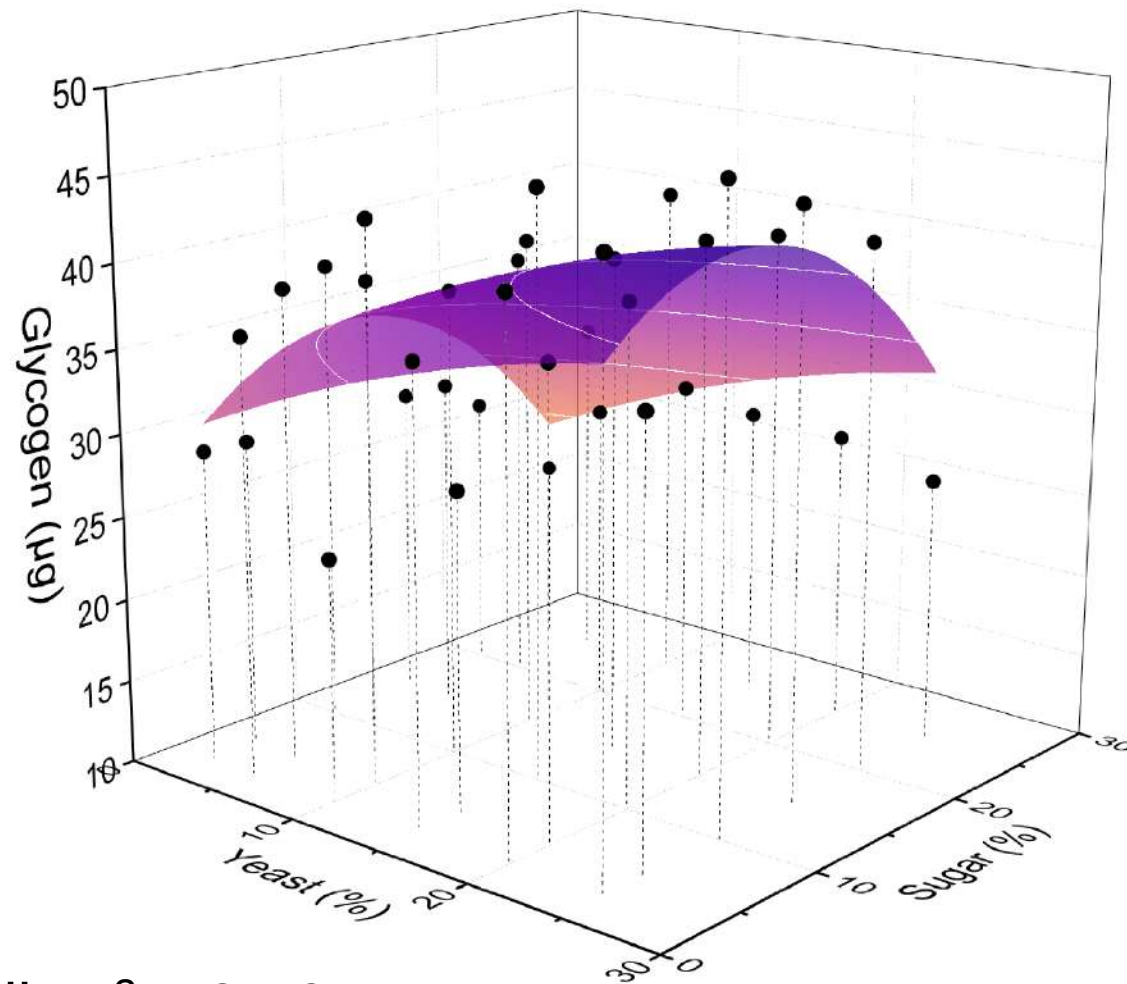
Adj. $R^2 = 0.30$

Figure S32.

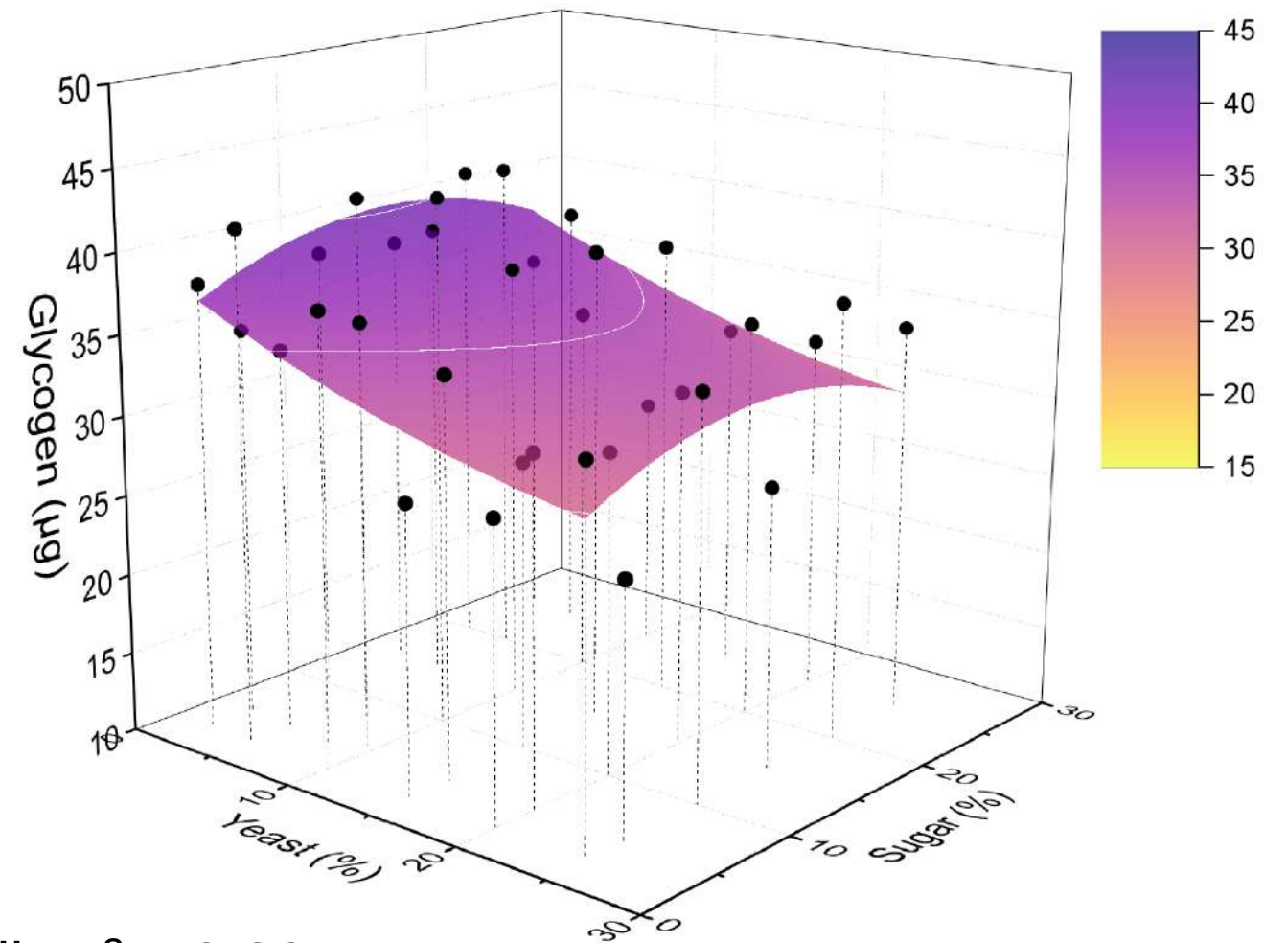
w^{1118}

SK

Virgin
males

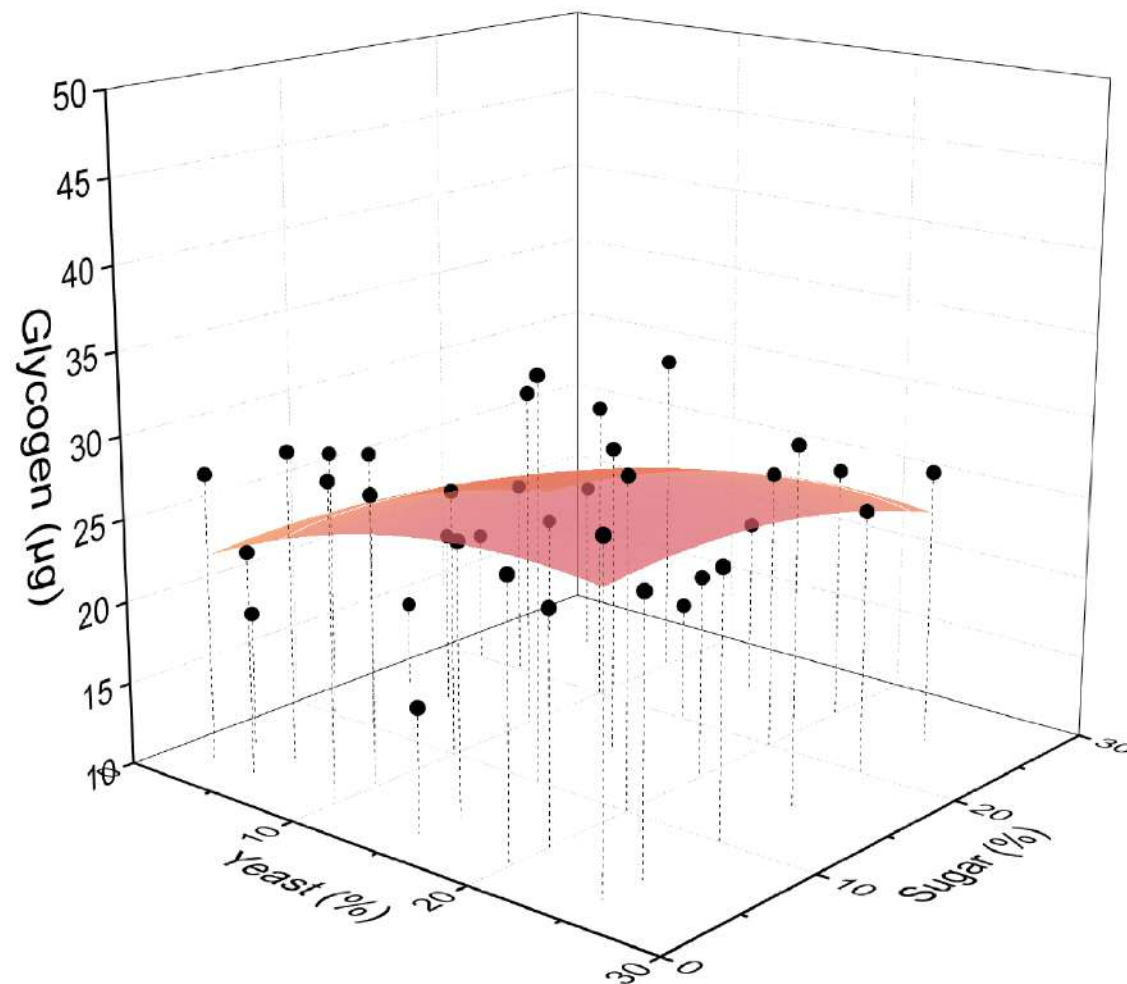


Adj. $R^2 = 0.40$

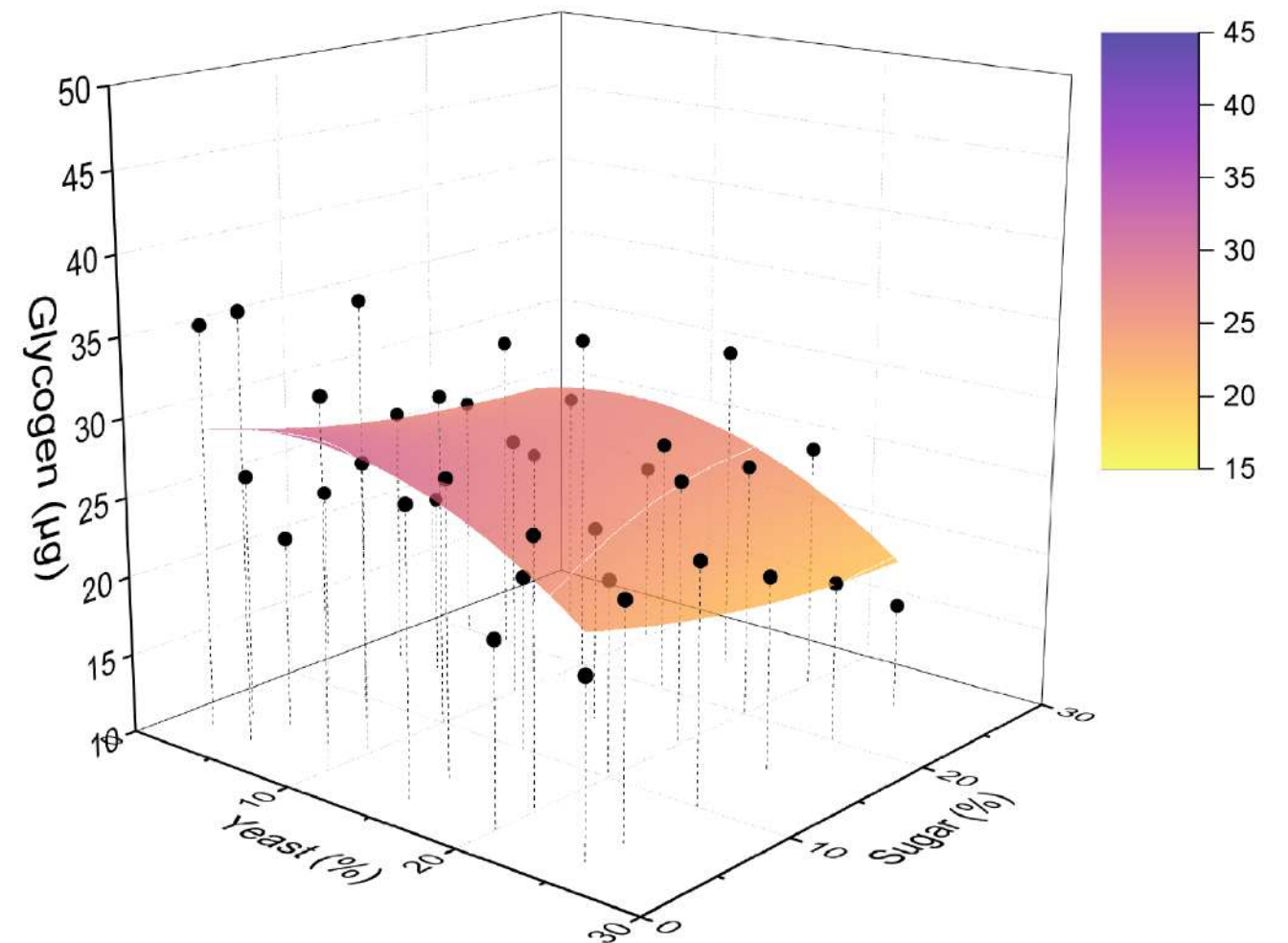


Adj. $R^2 = 0.29$

Mated
males



Adj. $R^2 = 0.14$



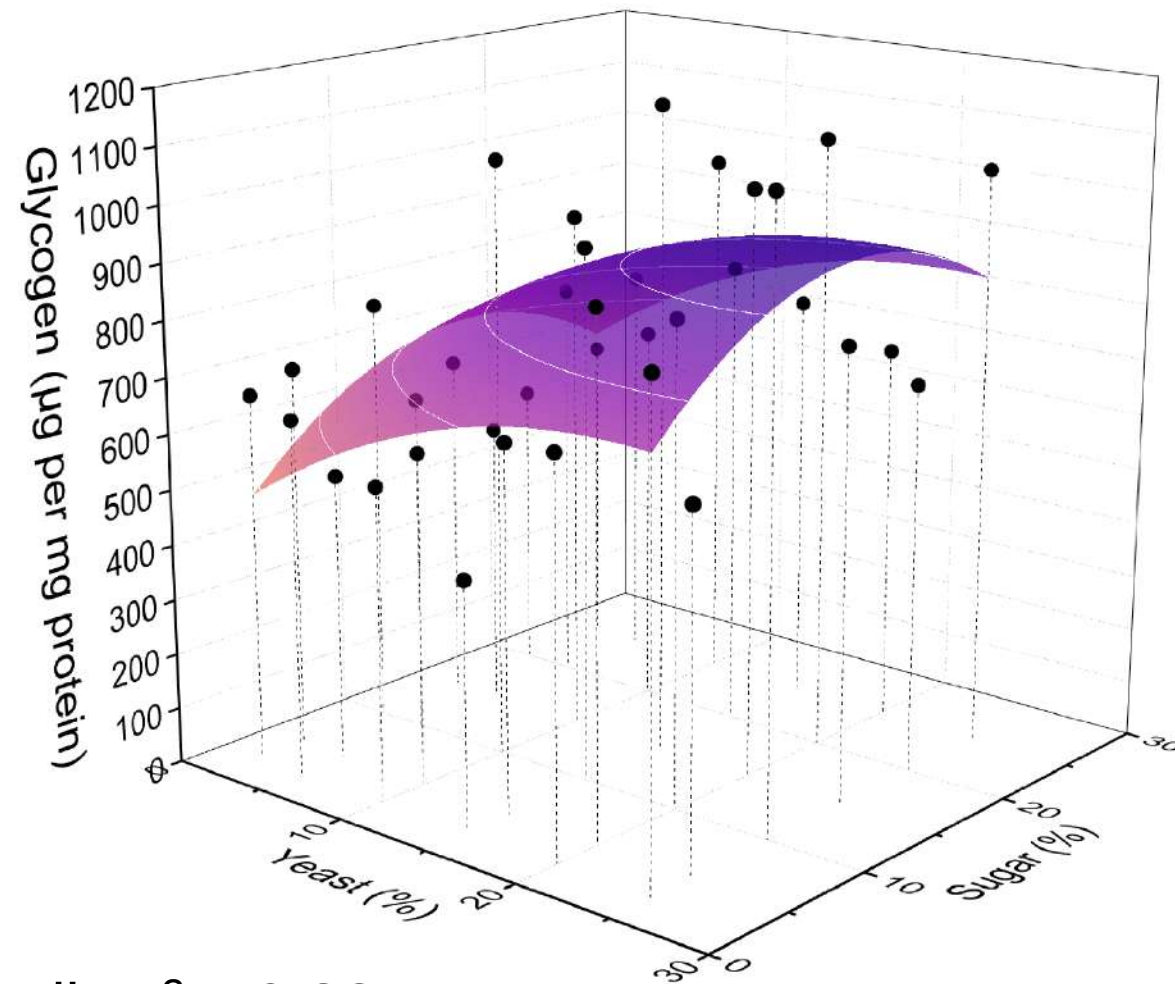
Adj. $R^2 = 0.24$

Figure S33.

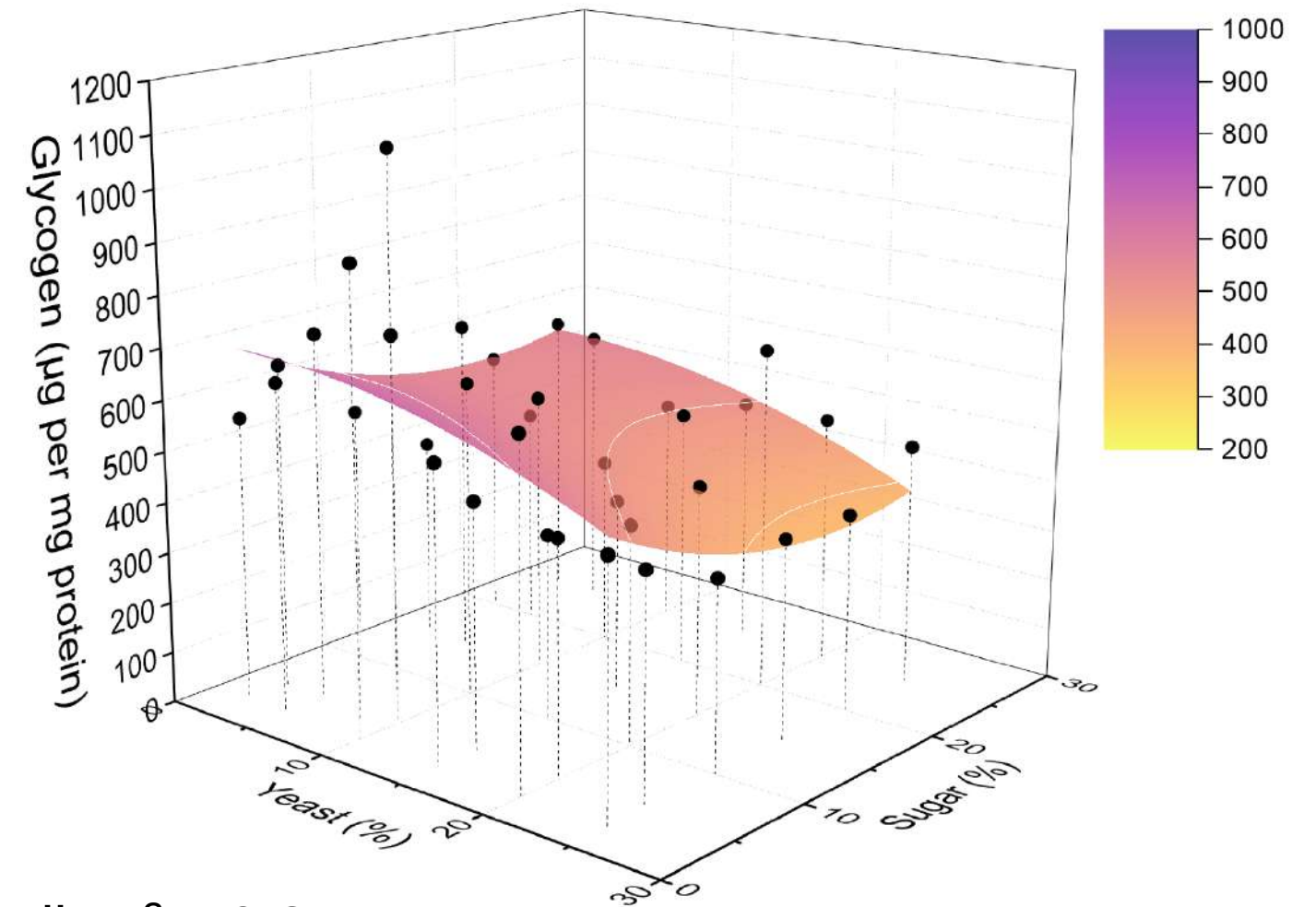
w^{1118}

SK

Virgin
females

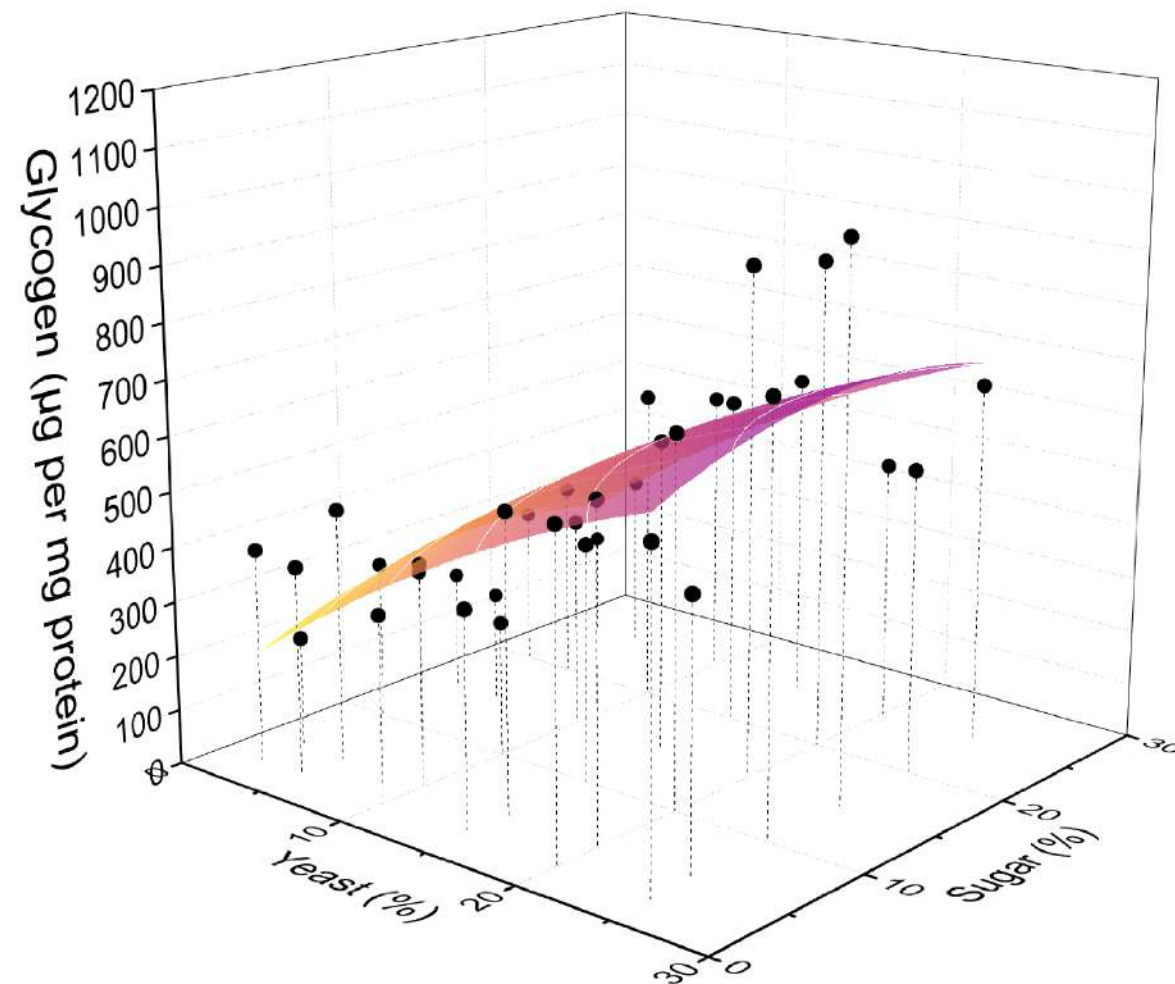


Adj. $R^2 = 0.32$

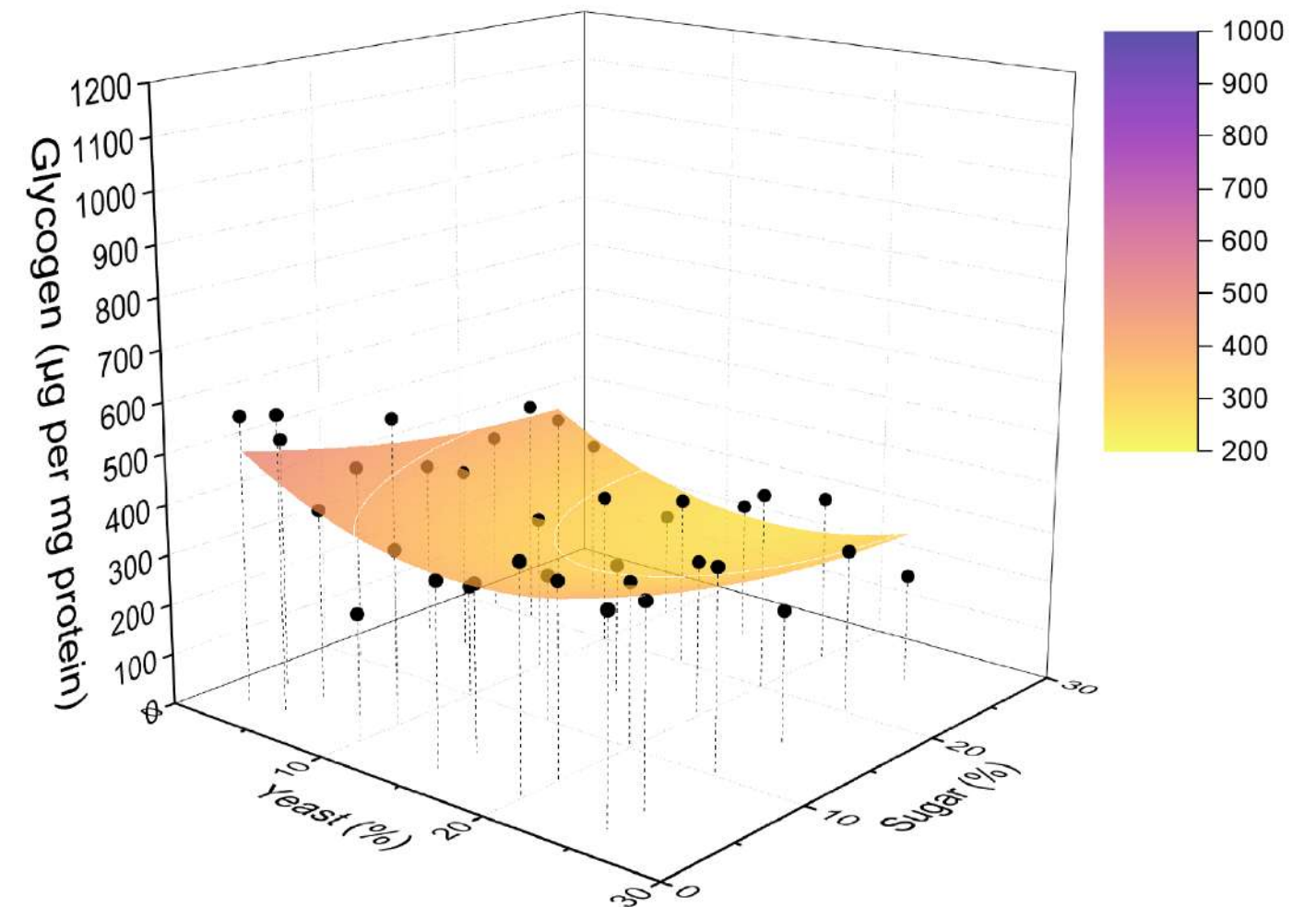


Adj. $R^2 = 0.24$

Mated
females



Adj. $R^2 = 0.61$



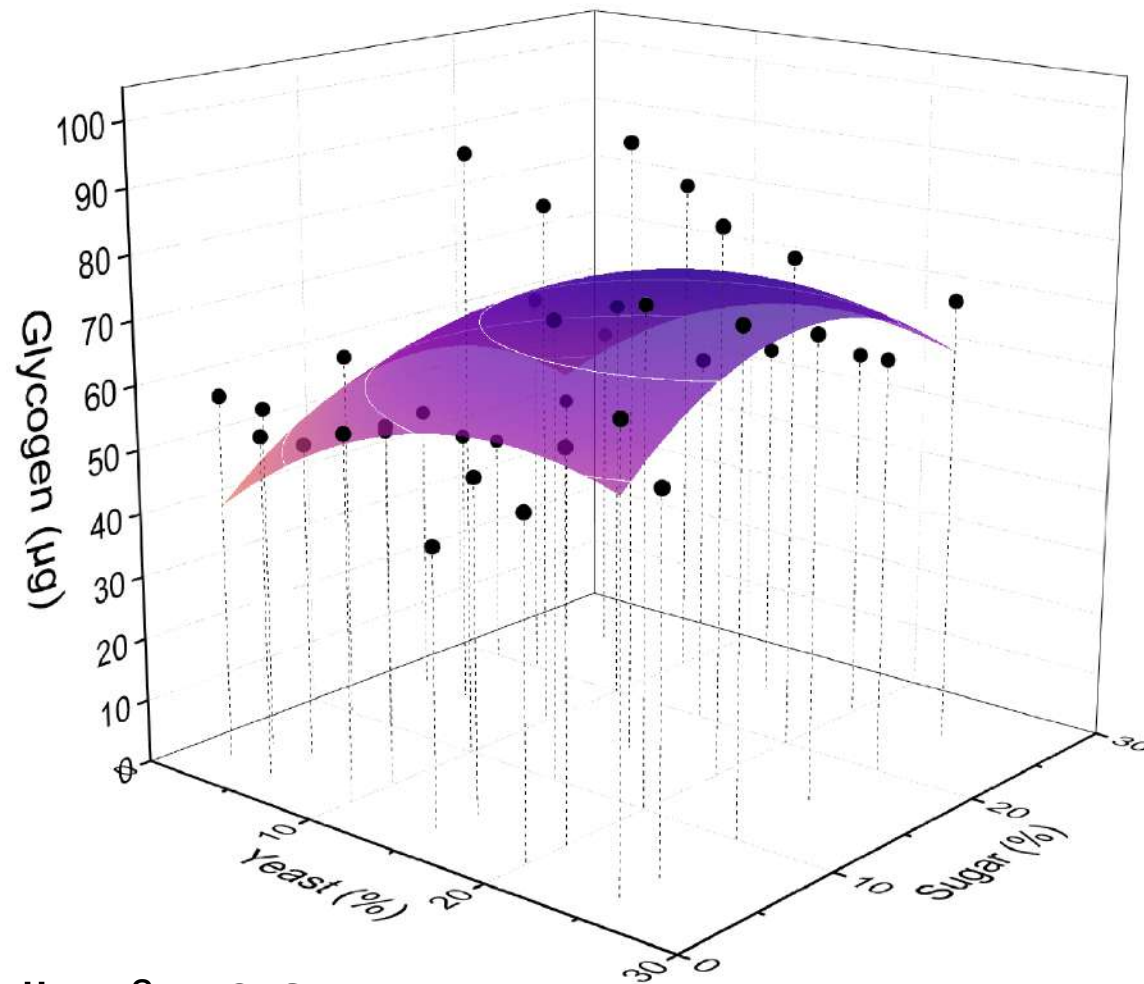
Adj. $R^2 = 0.45$

Figure S34.

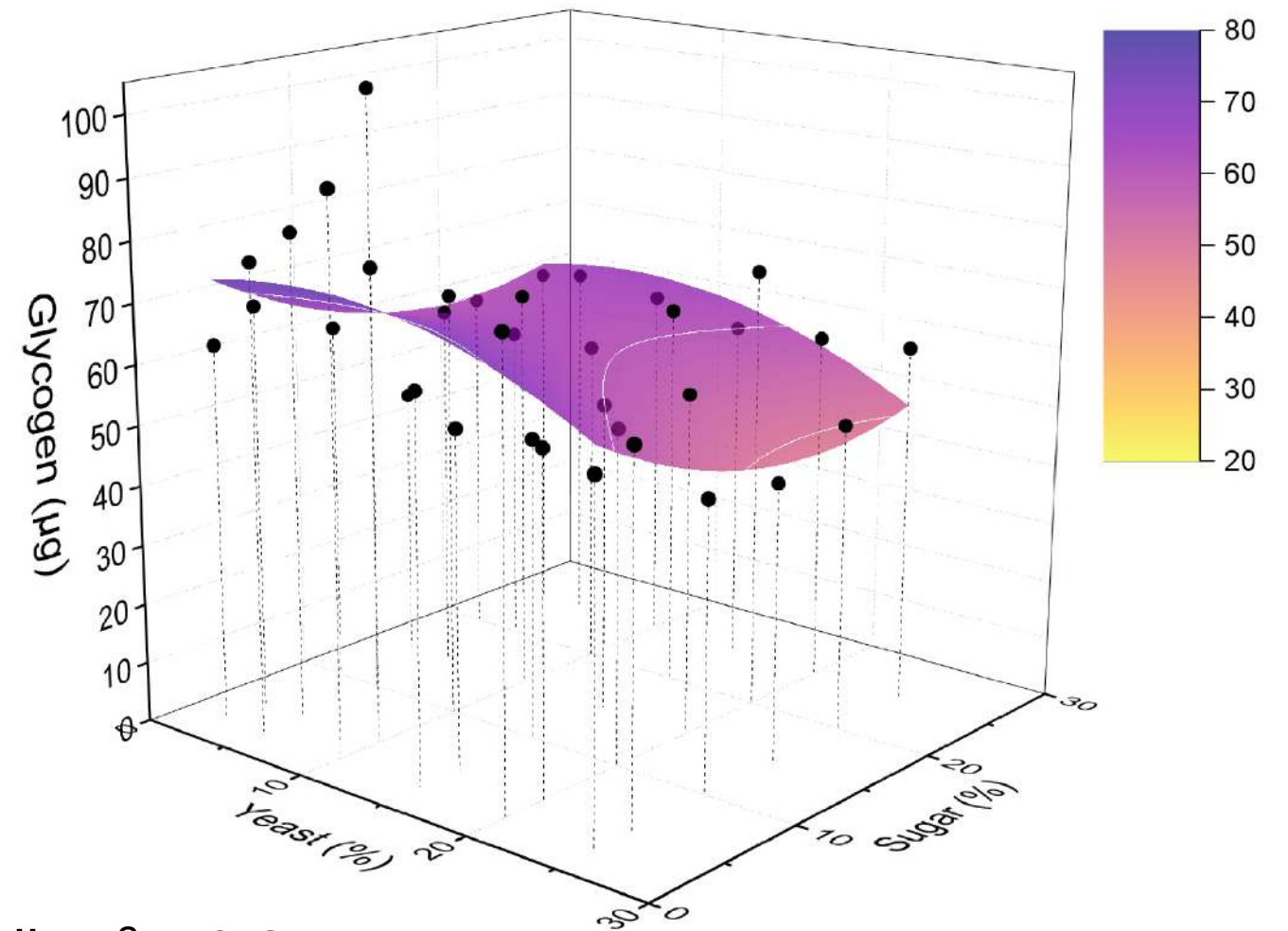
w^{1118}

SK

Virgin
females

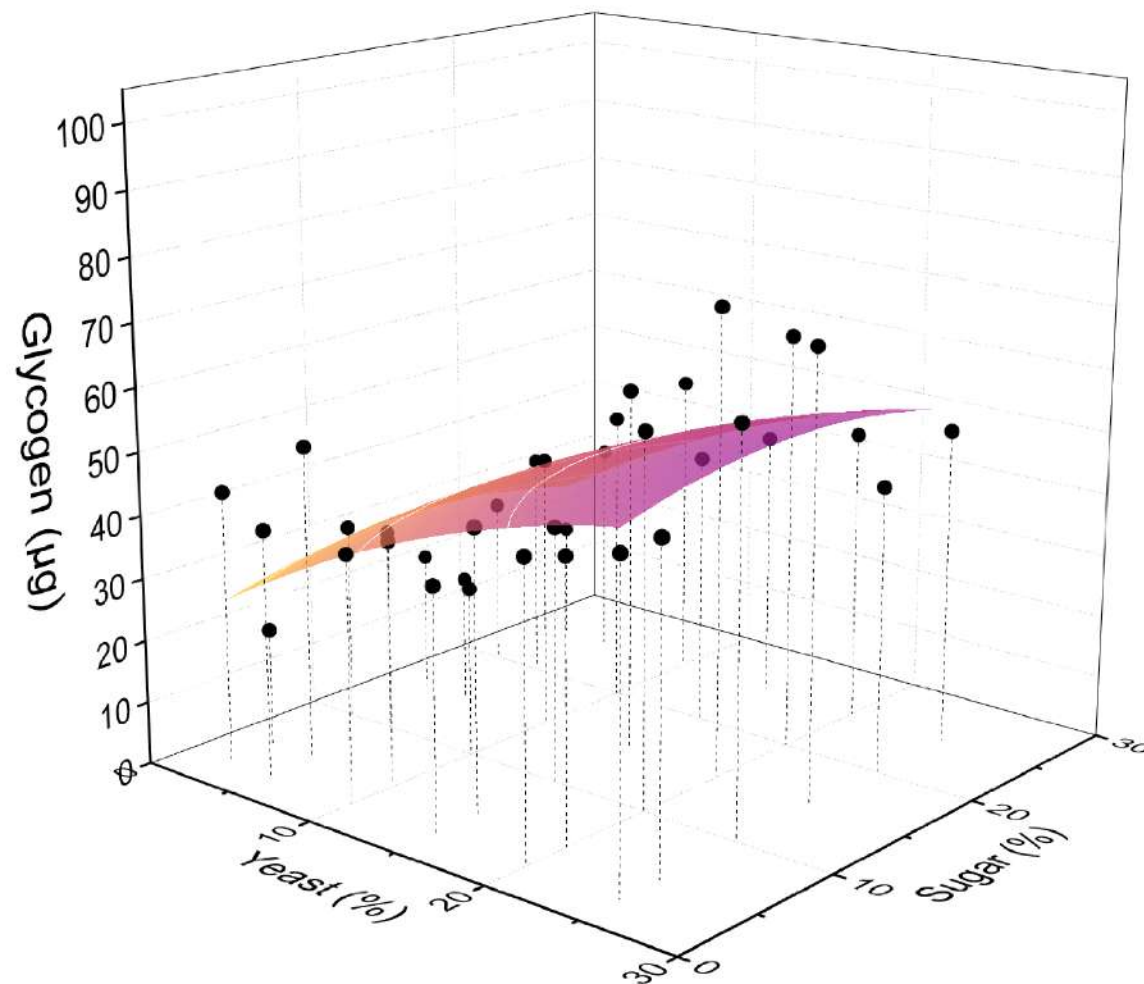


Adj. $R^2 = 0.35$

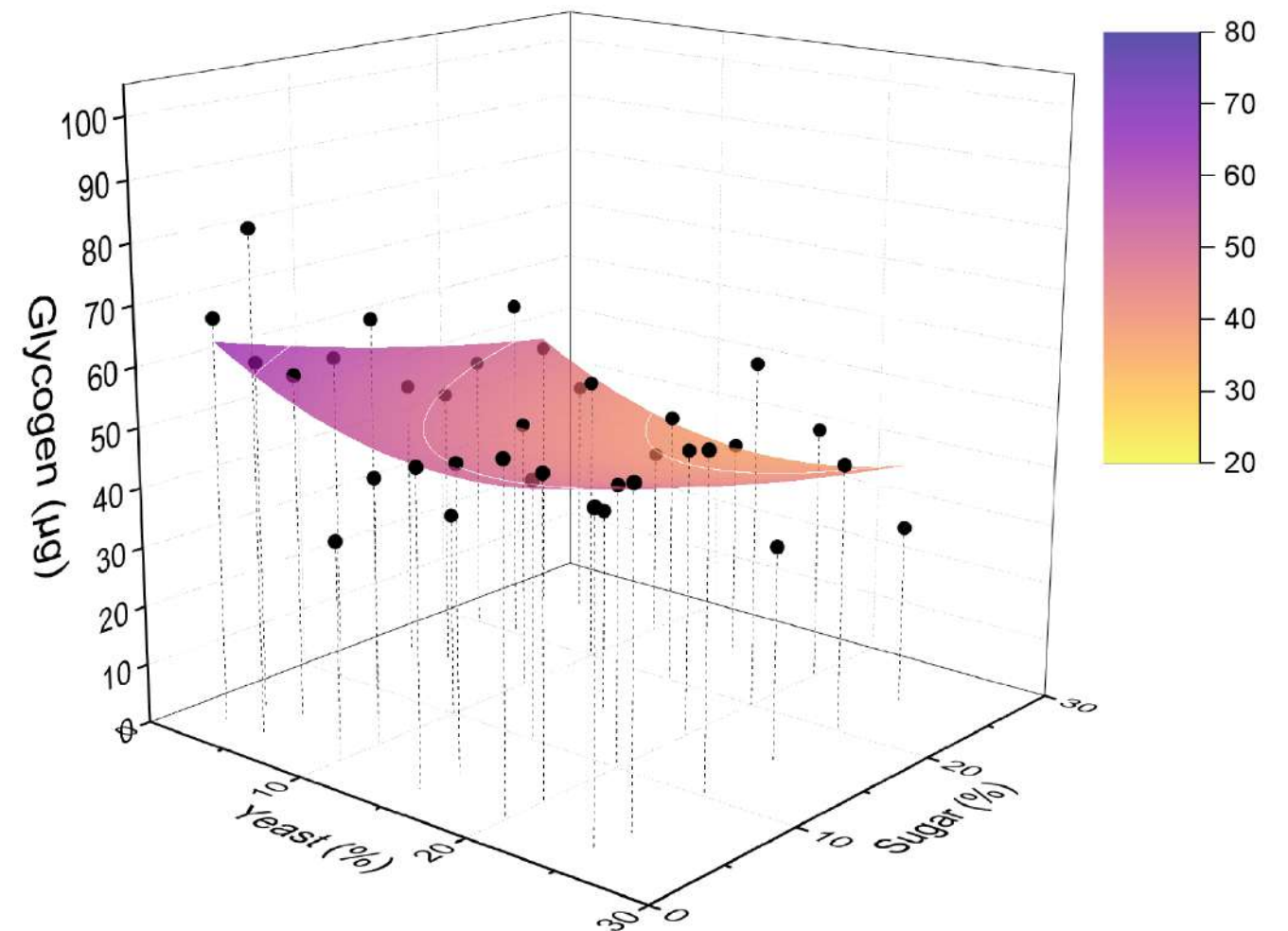


Adj. $R^2 = 0.24$

Mated
females



Adj. $R^2 = 0.53$



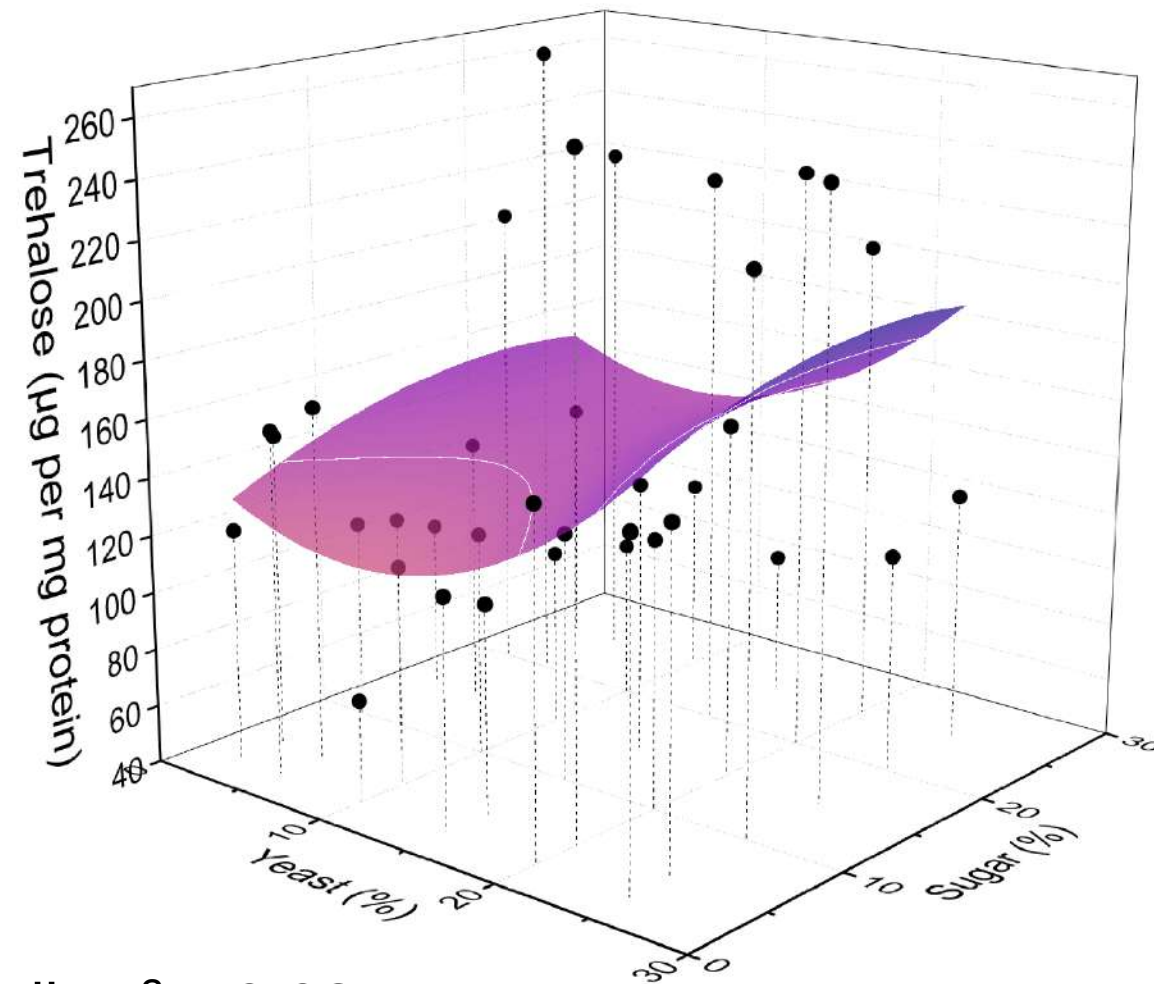
Adj. $R^2 = 0.33$

Figure S35.

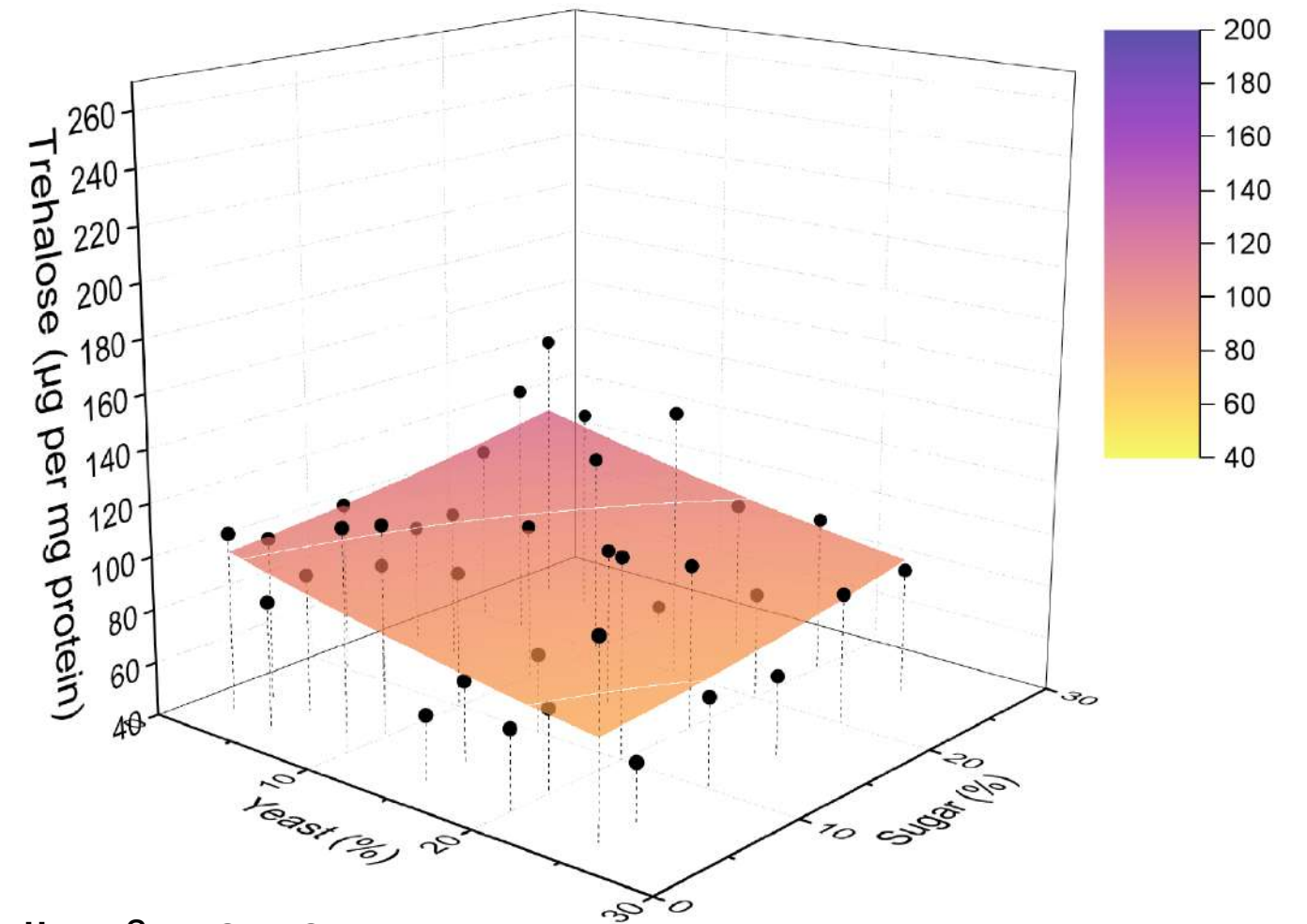
w^{1118}

SK

Virgin
males

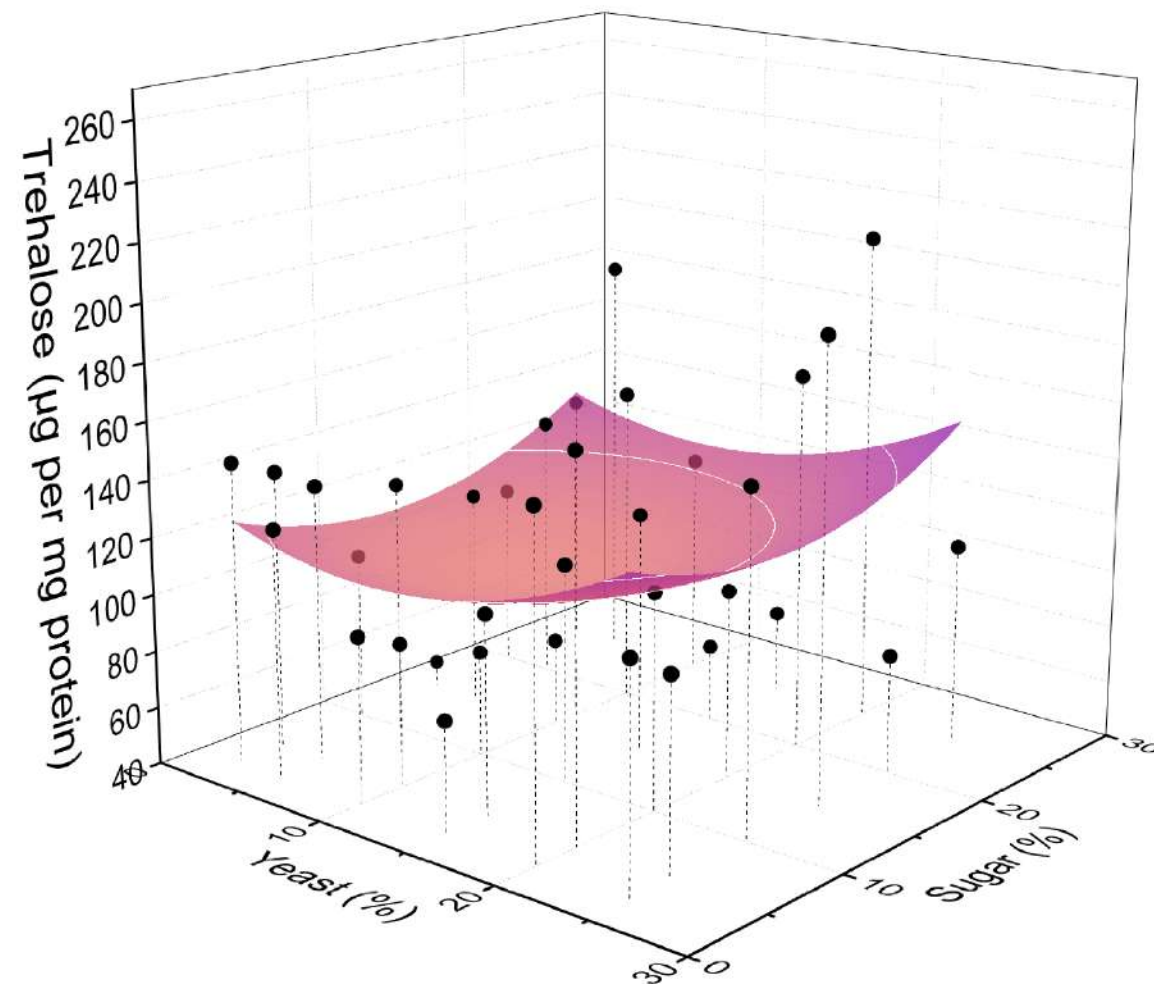


Adj. $R^2 = 0.02$

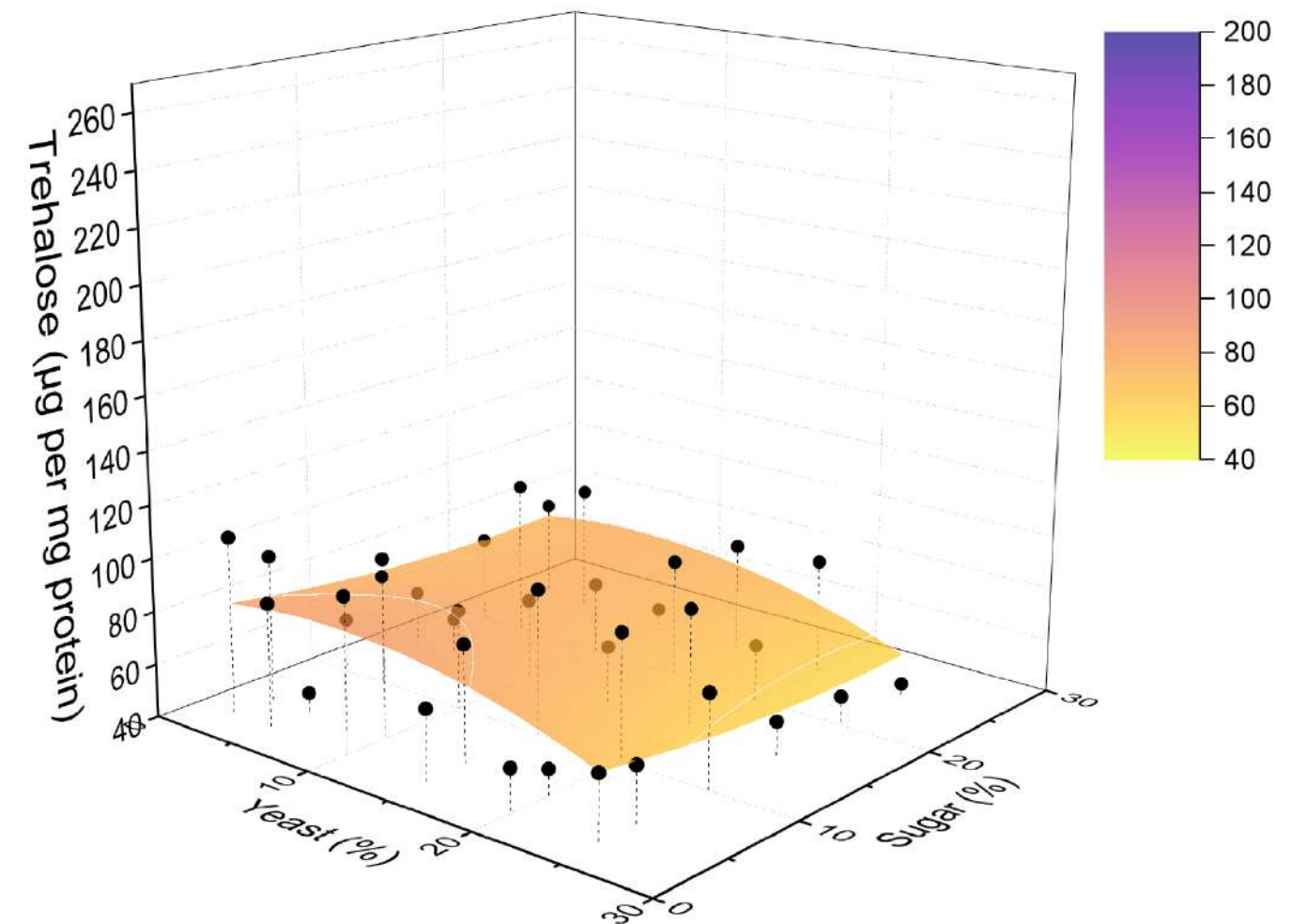


Adj. $R^2 = 0.10$

Mated
males



Adj. $R^2 = -0.01$



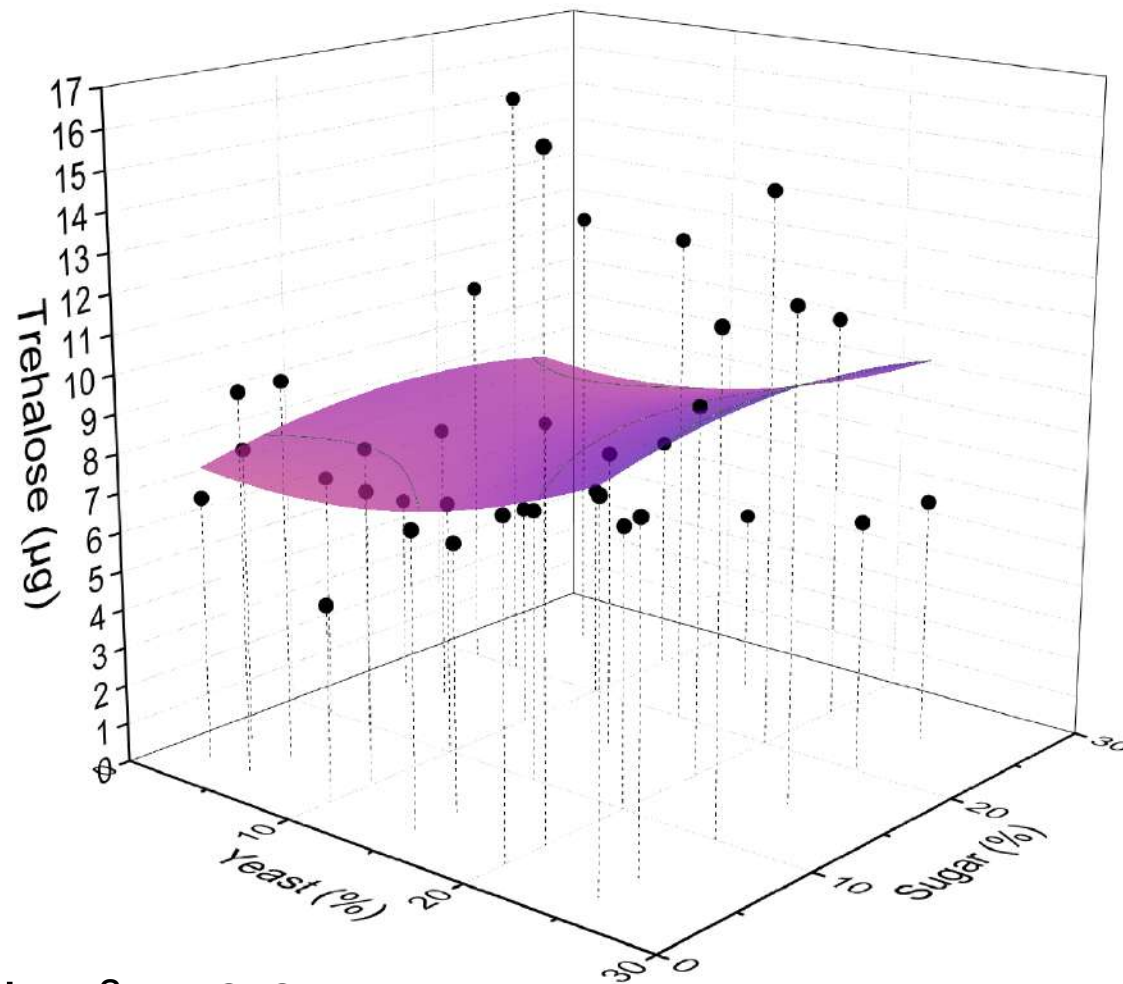
Adj. $R^2 = 0.11$

Figure S36.

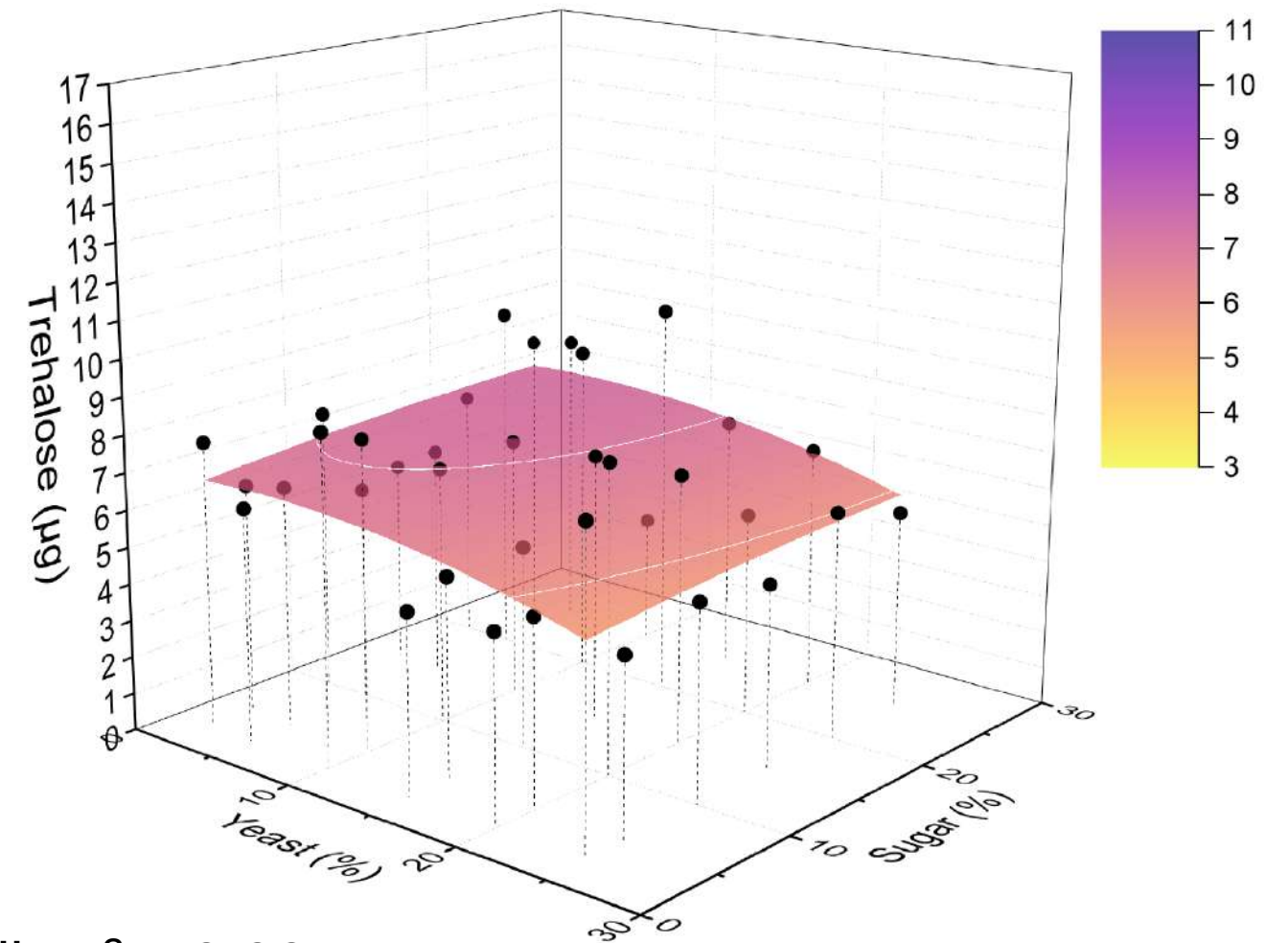
w^{1118}

SK

Virgin
males

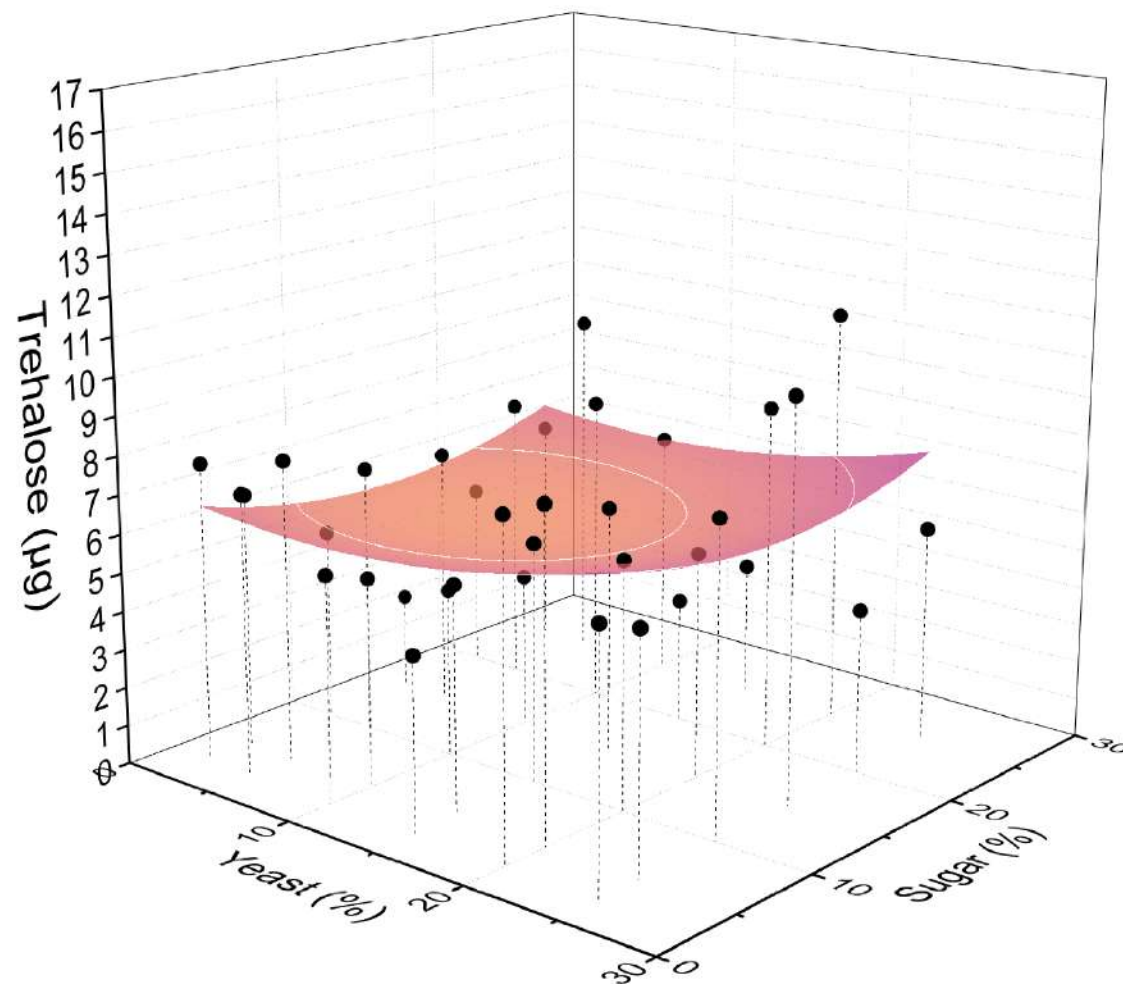


Adj. $R^2 = -0.04$

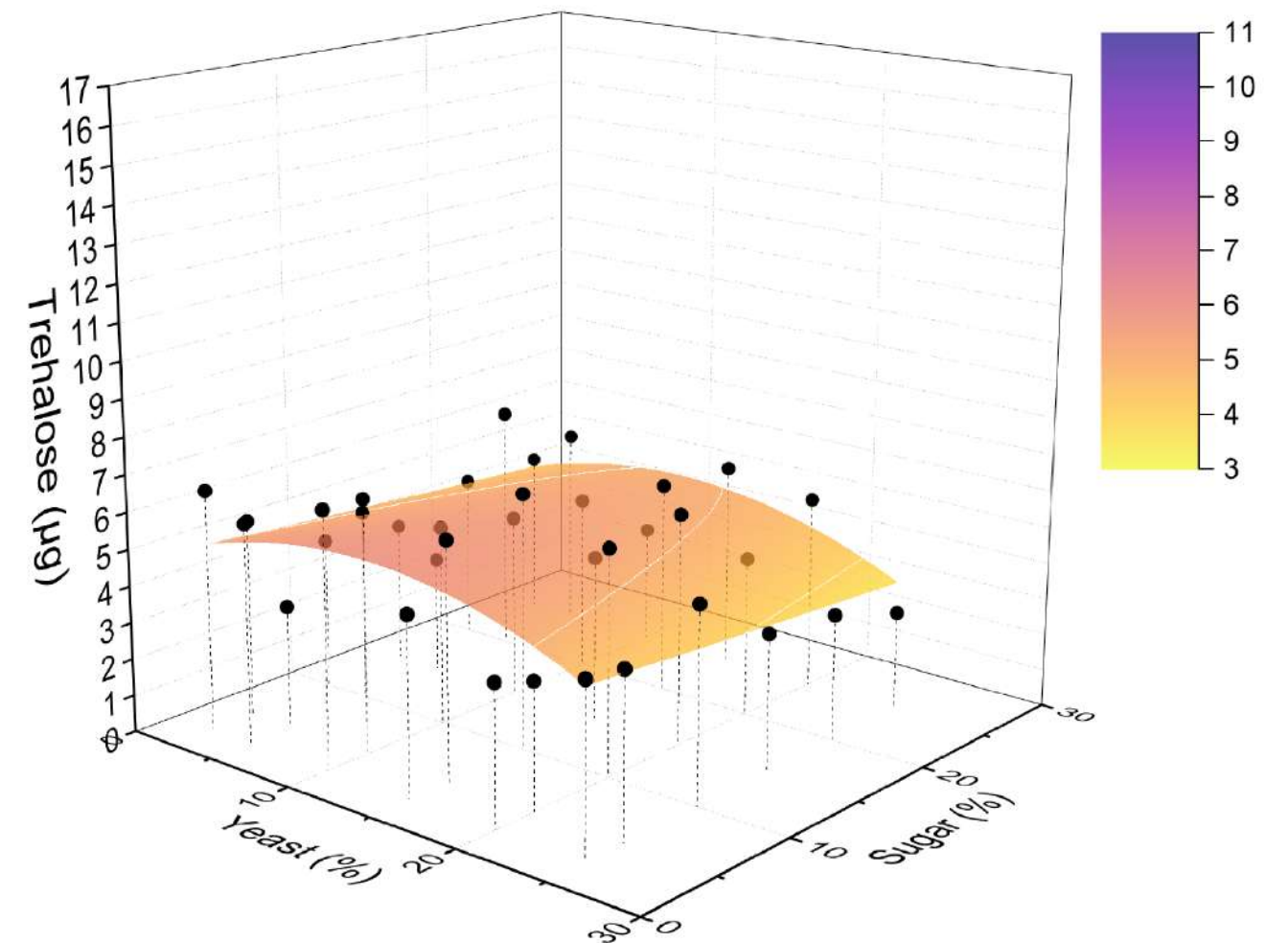


Adj. $R^2 = 0.00$

Mated
males



Adj. $R^2 = -0.03$



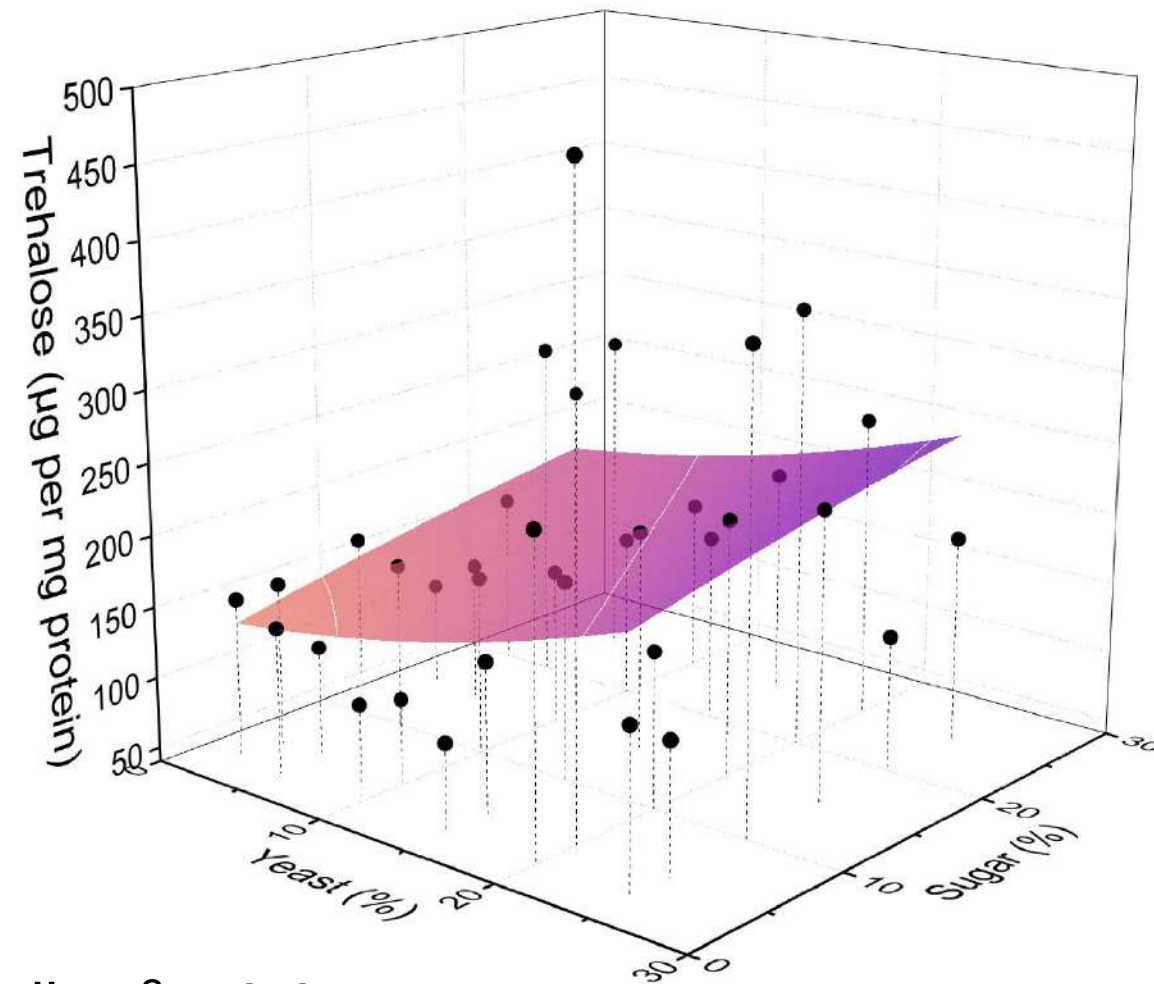
Adj. $R^2 = 0.14$

Figure S37.

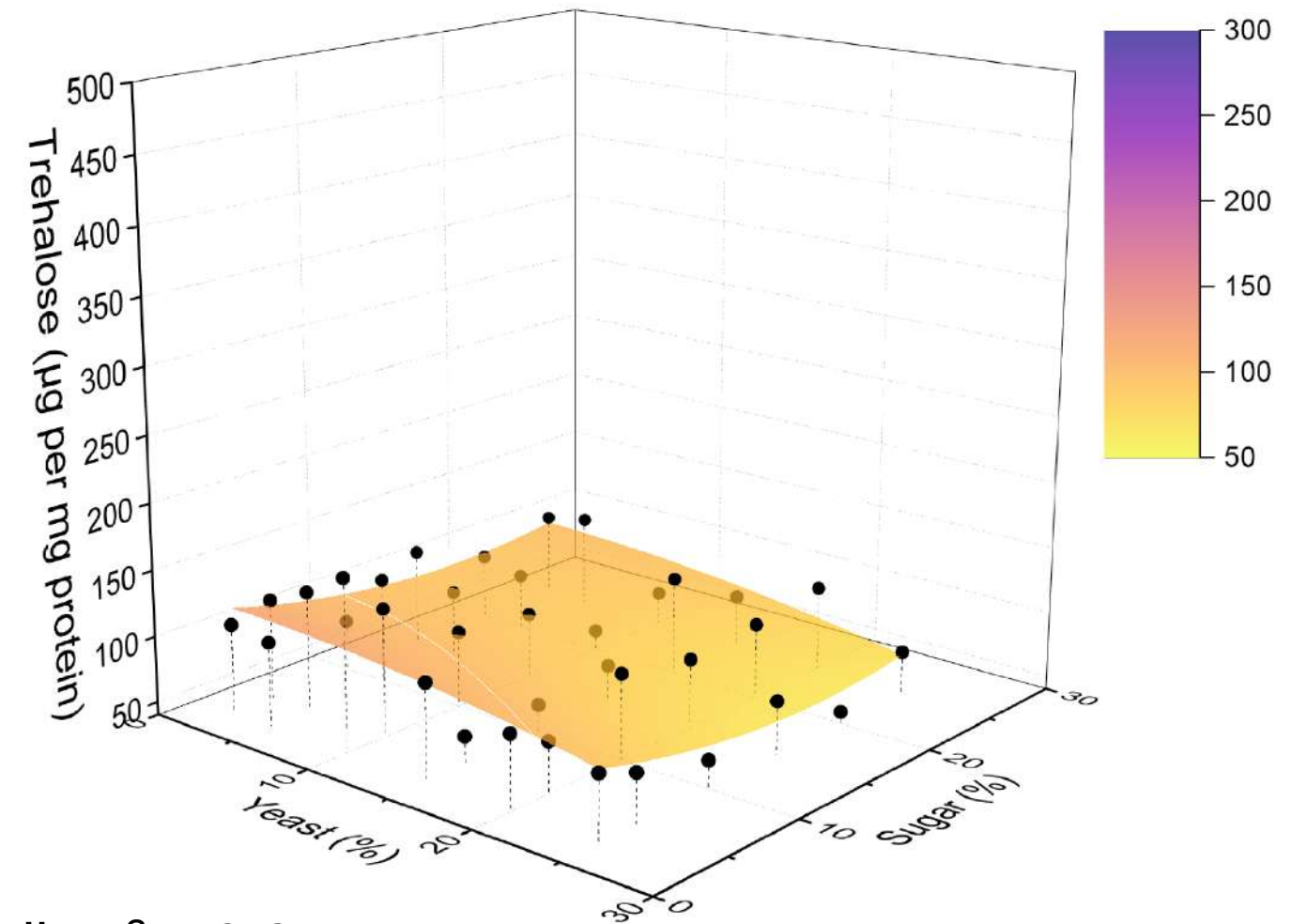
w^{1118}

SK

Virgin
females

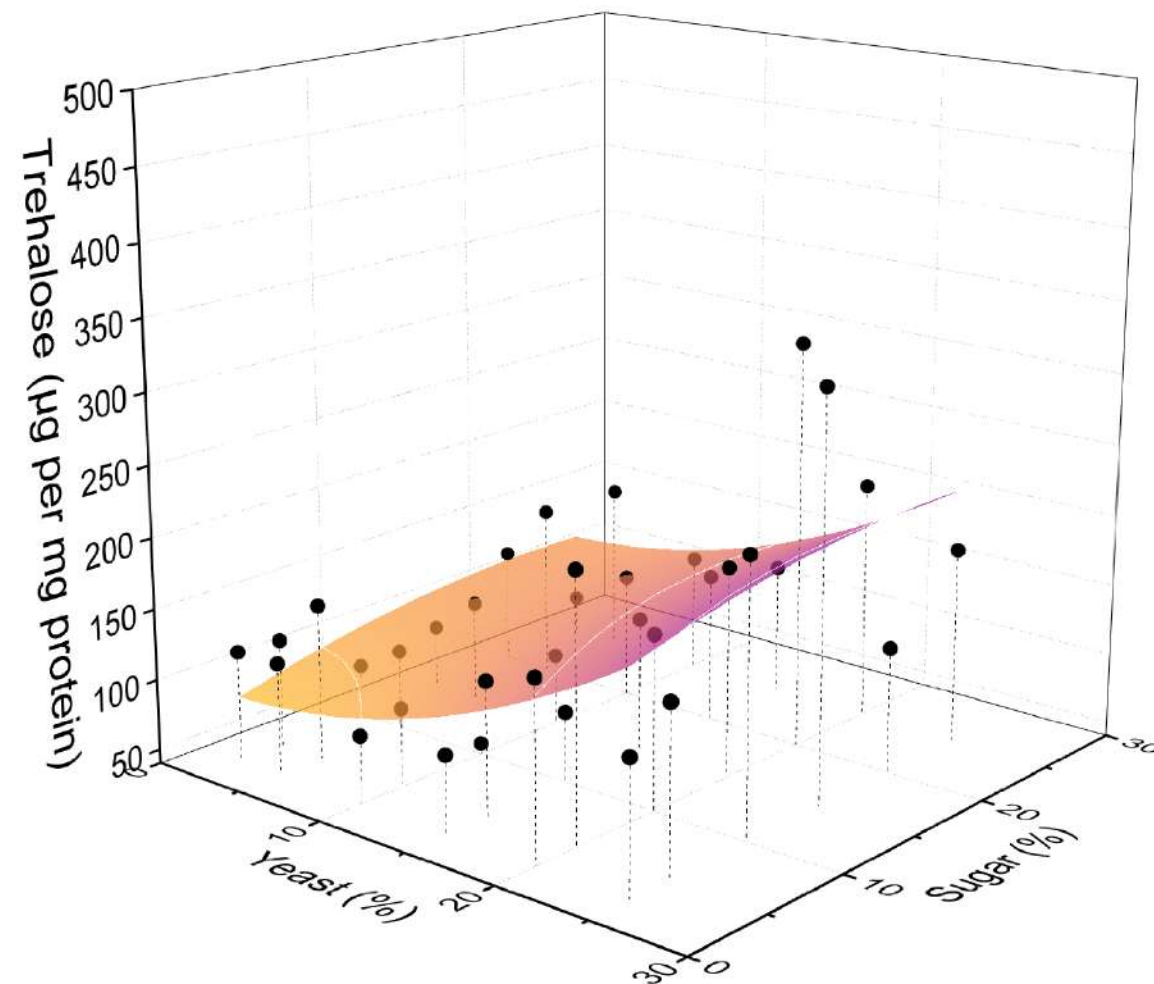


Adj. $R^2 = 0.04$

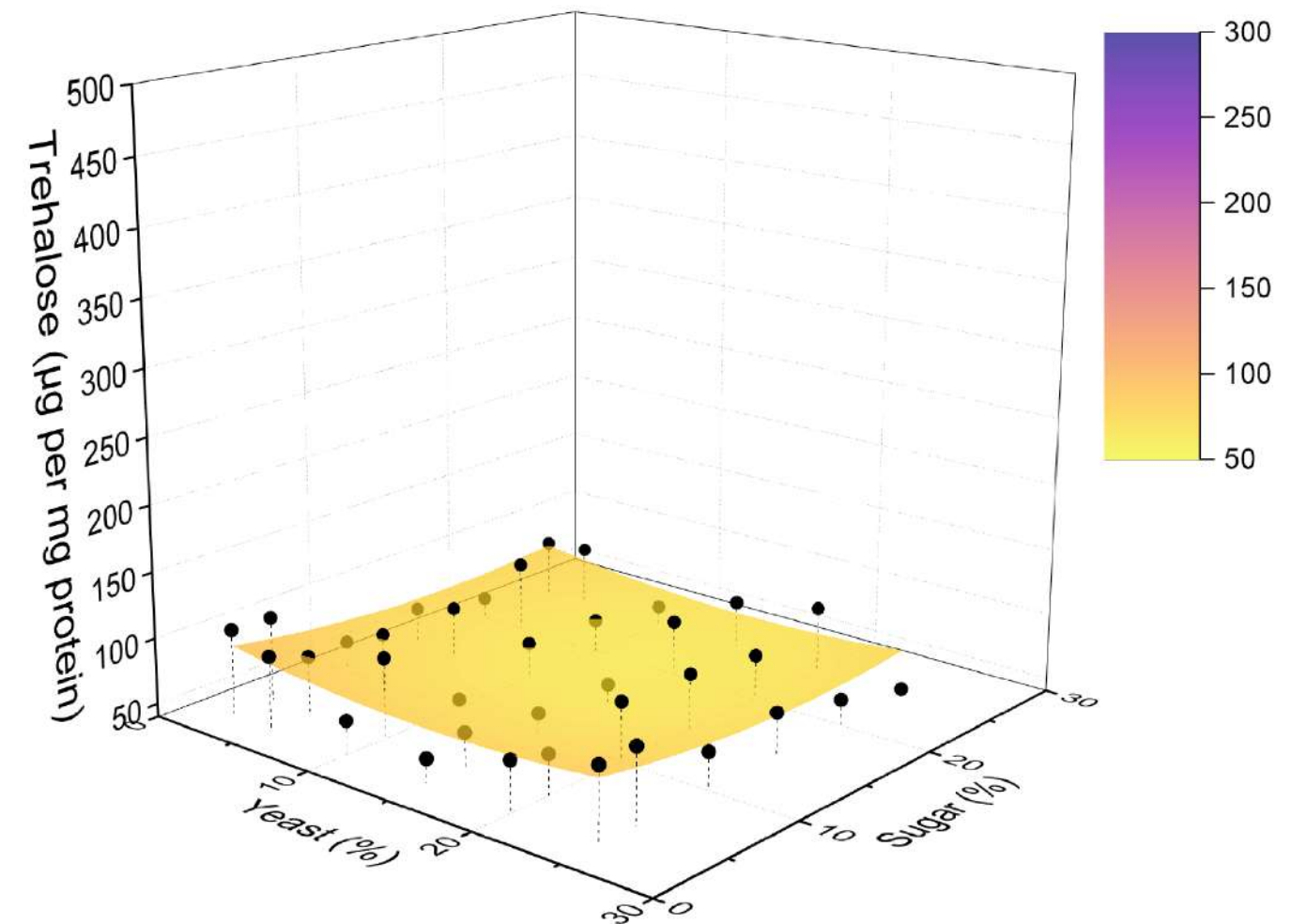


Adj. $R^2 = 0.25$

Mated
females



Adj. $R^2 = 0.35$



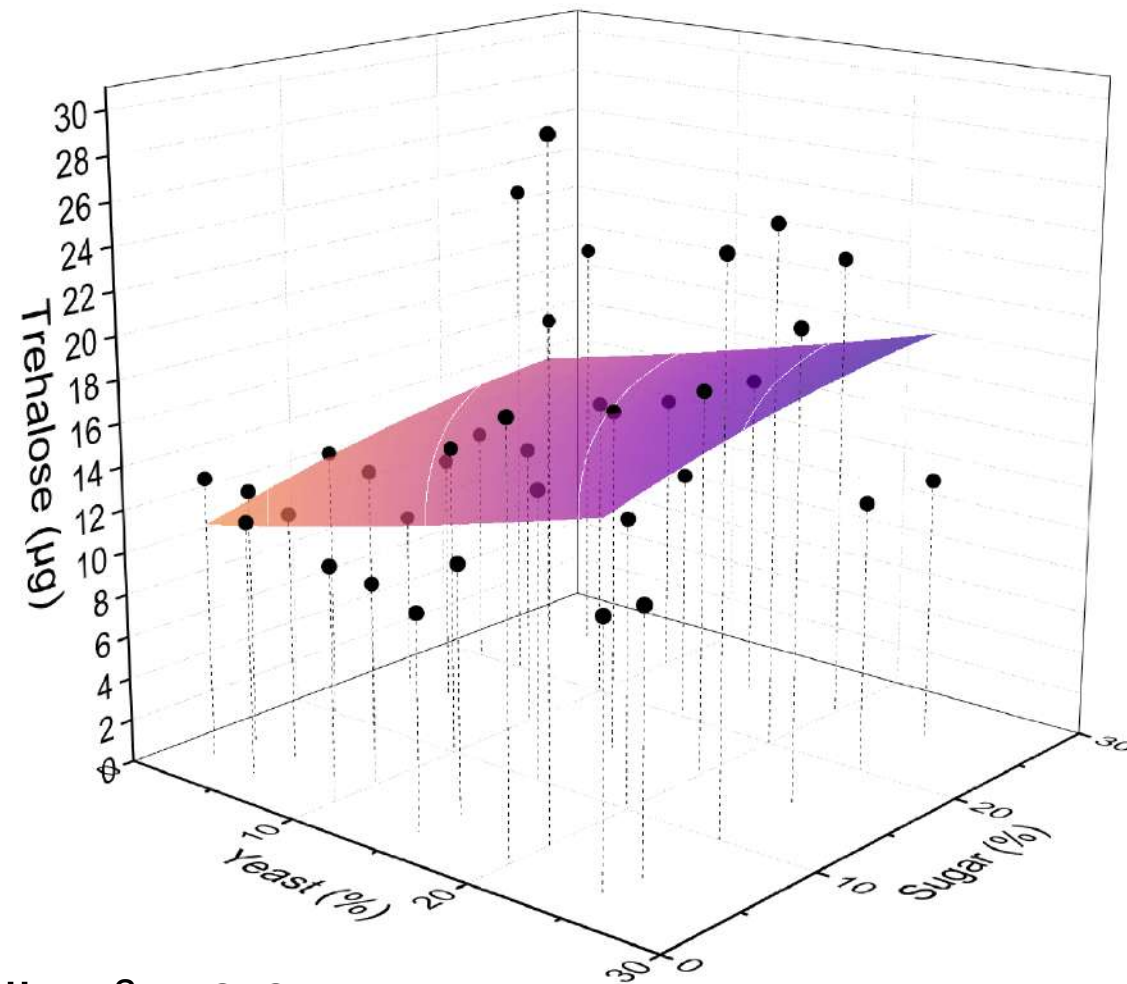
Adj. $R^2 = 0.12$

Figure S38.

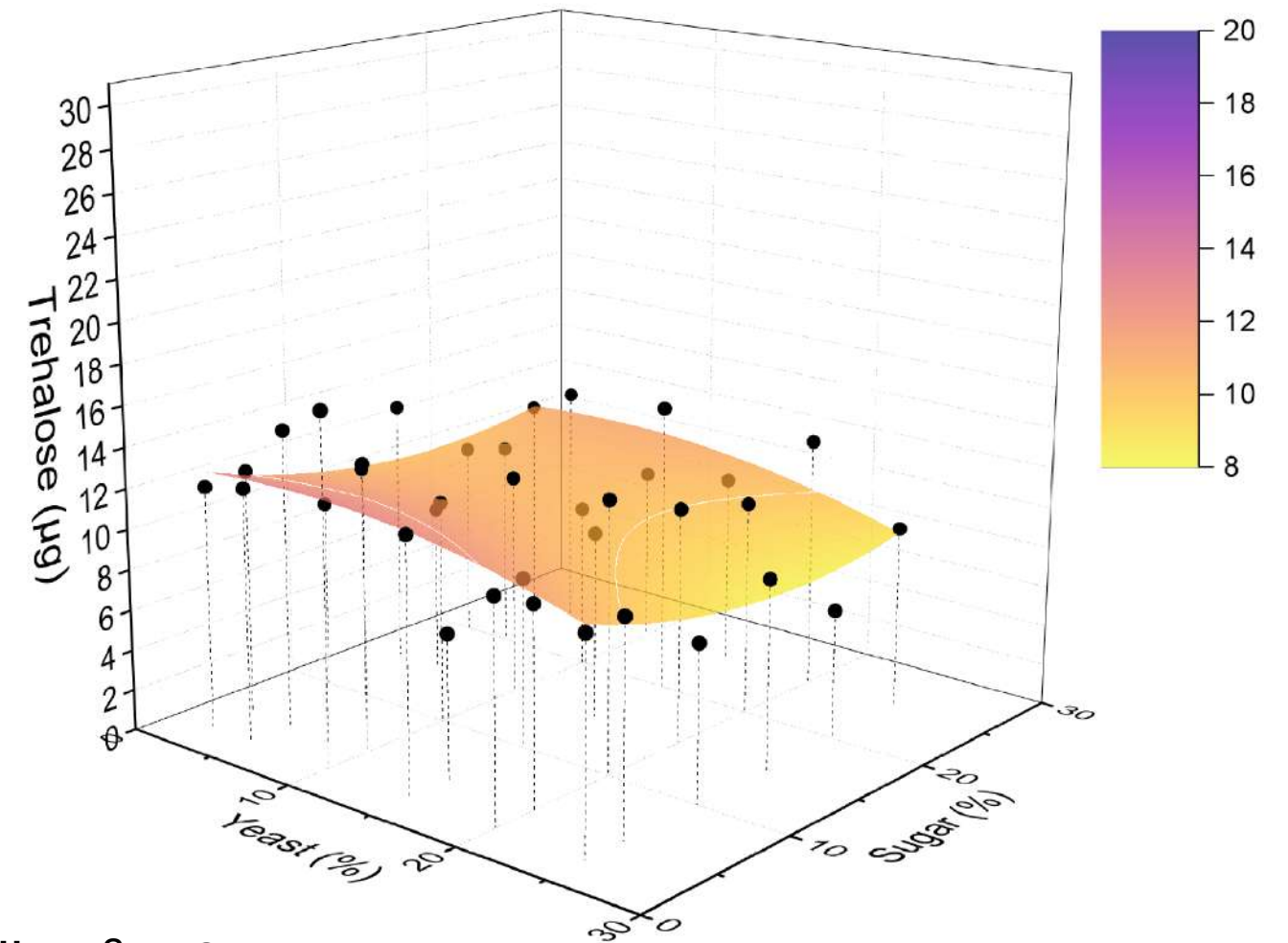
w^{1118}

SK

Virgin
females

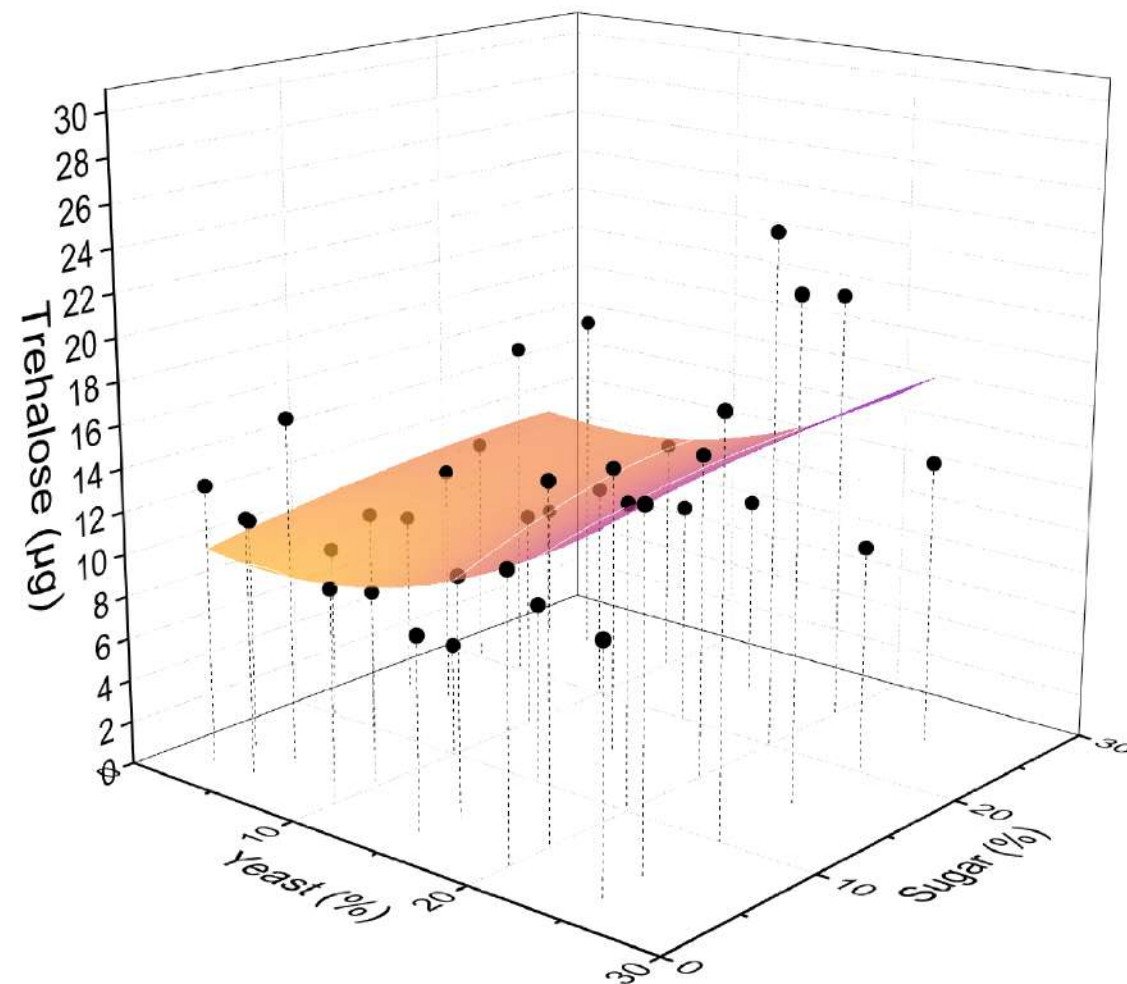


Adj. $R^2 = 0.07$

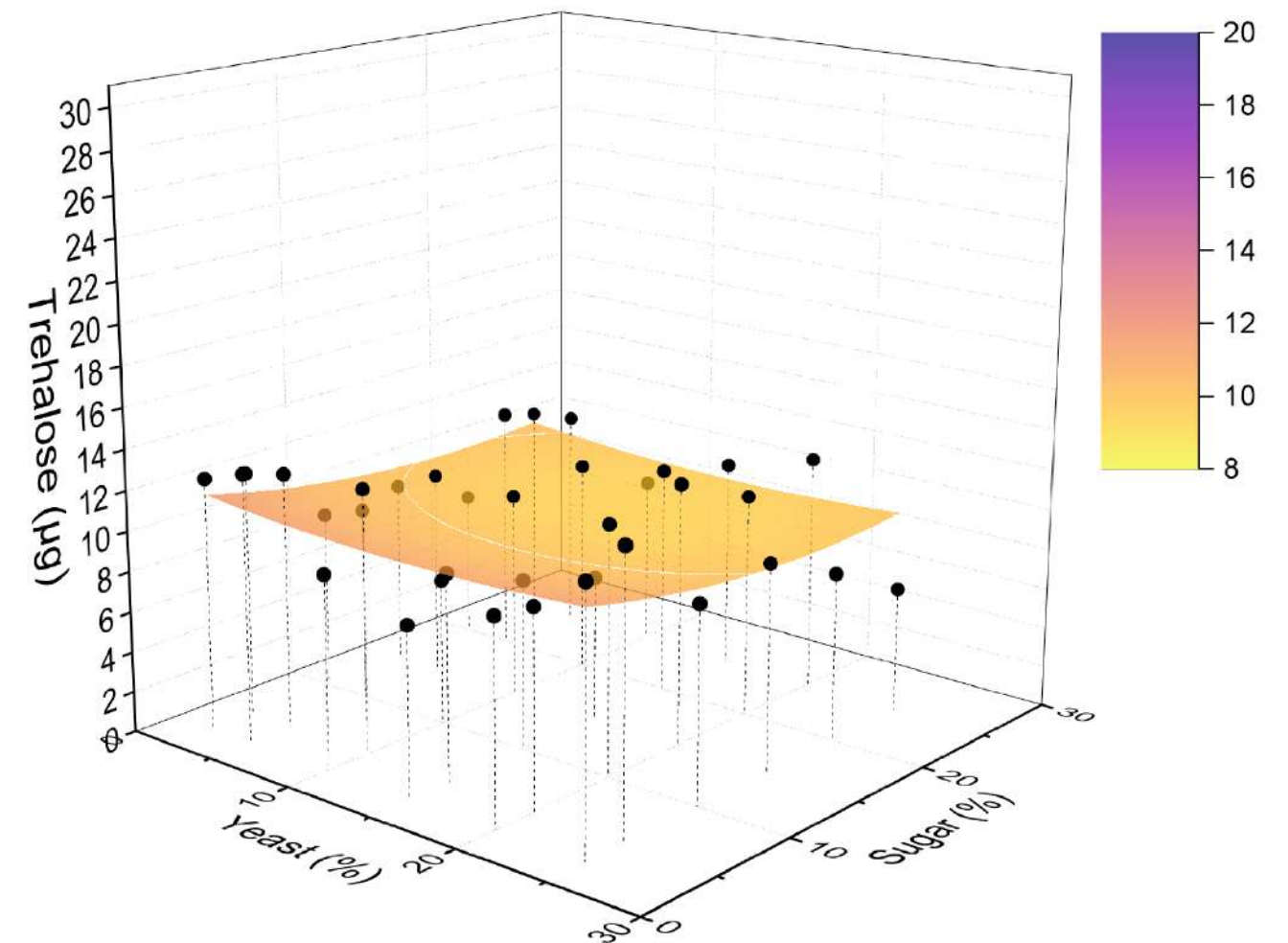


Adj. $R^2 = 0.17$

Mated
females



Adj. $R^2 = 0.18$



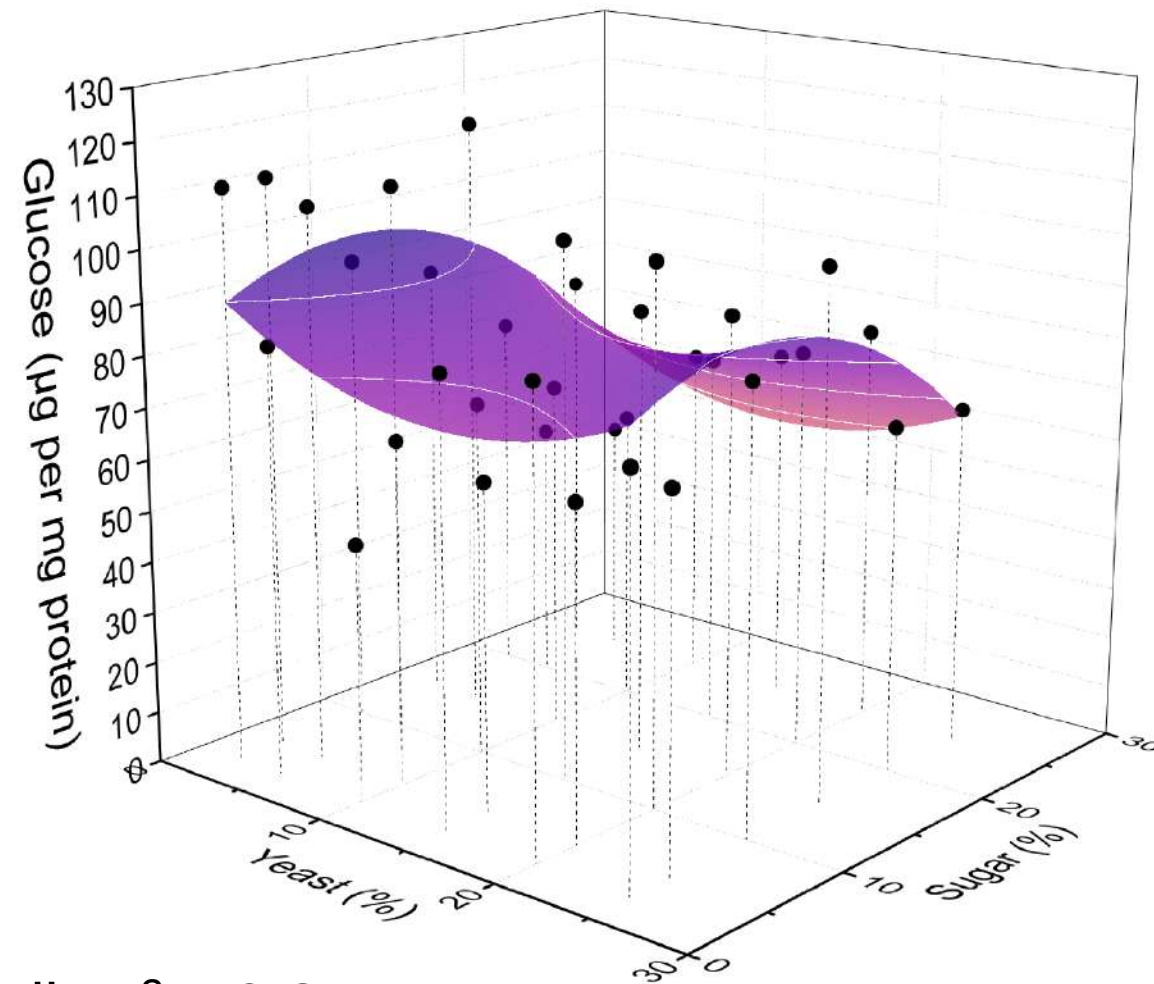
Adj. $R^2 = 0.01$

Figure S39.

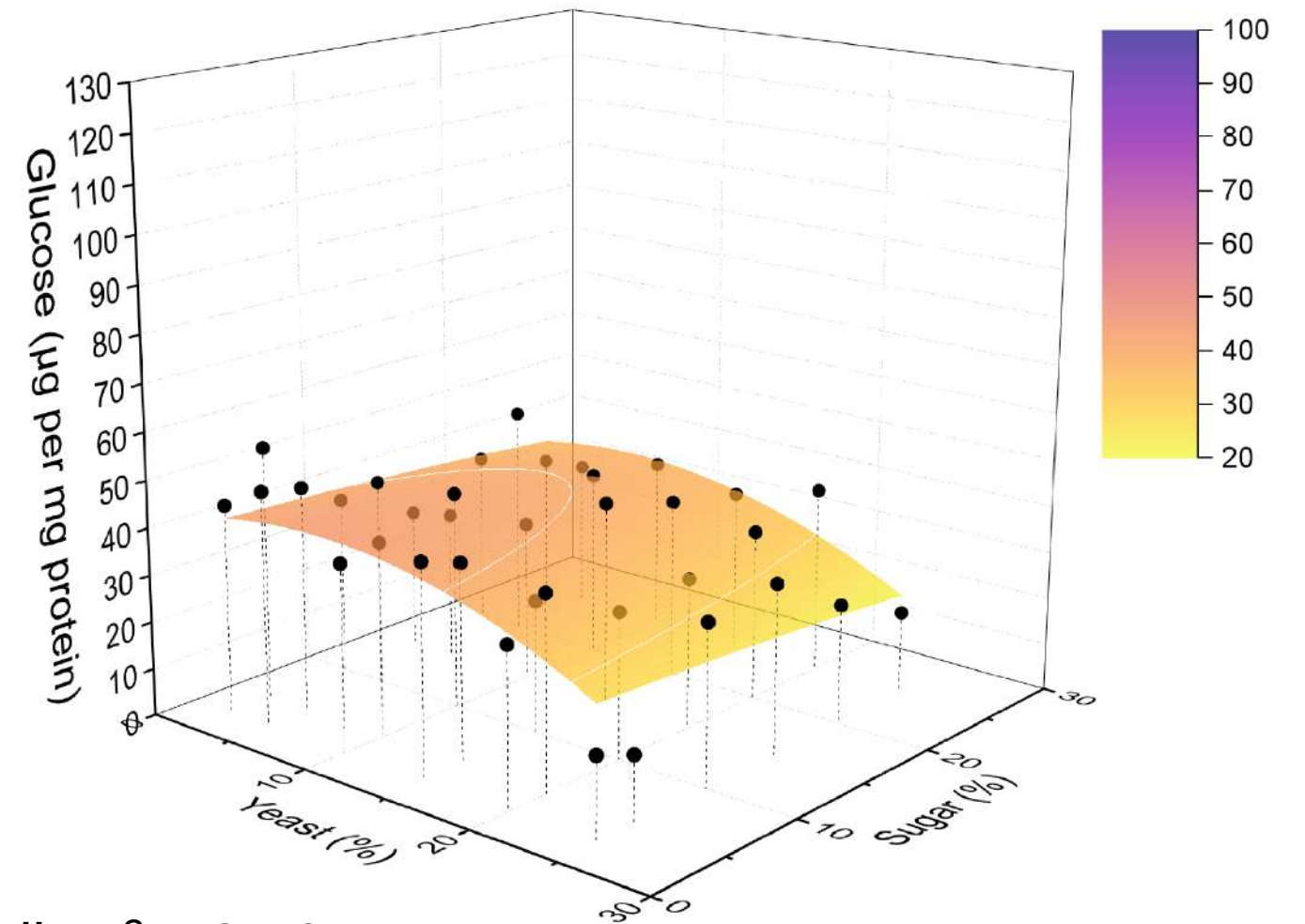
w^{1118}

SK

Virgin
males

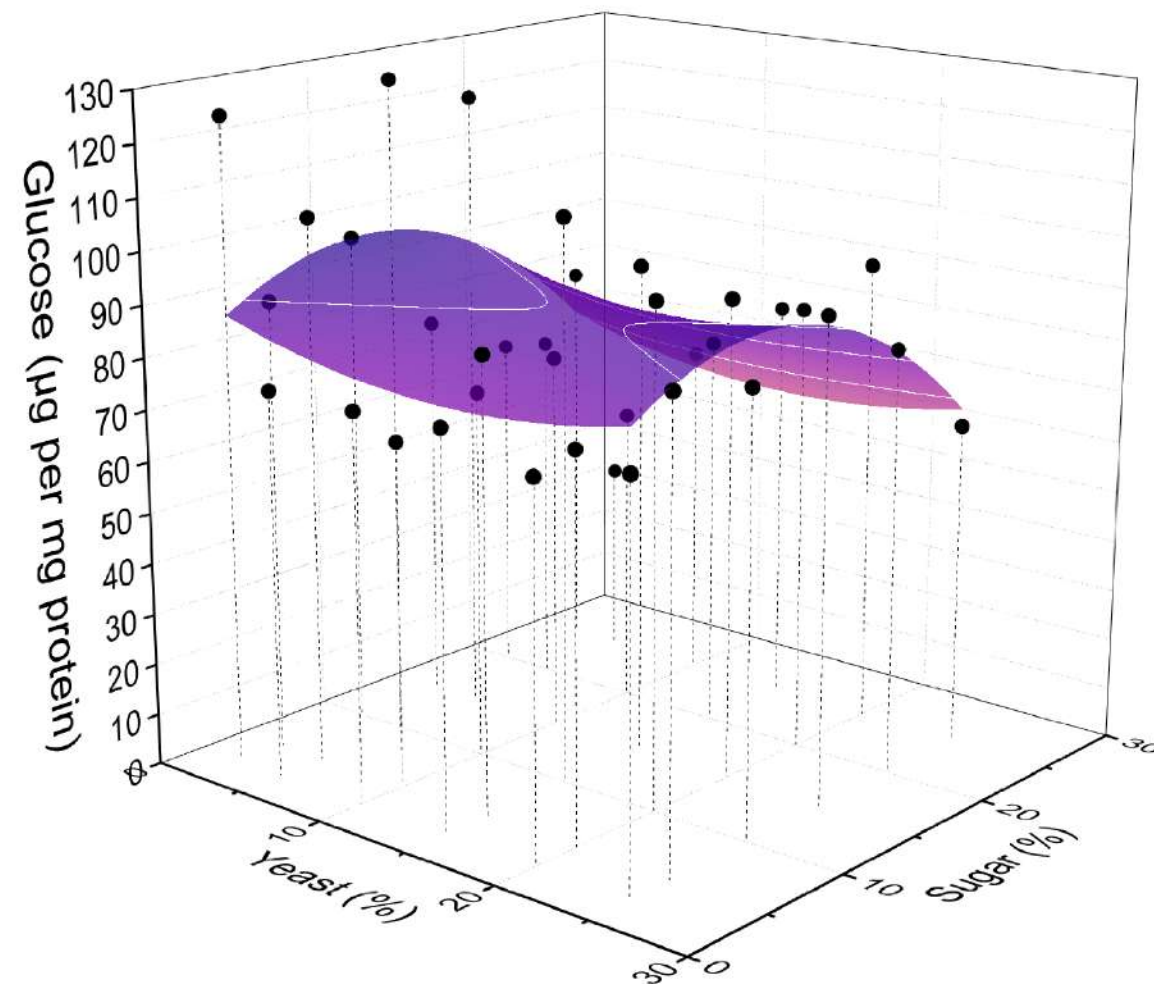


Adj. $R^2 = 0.21$

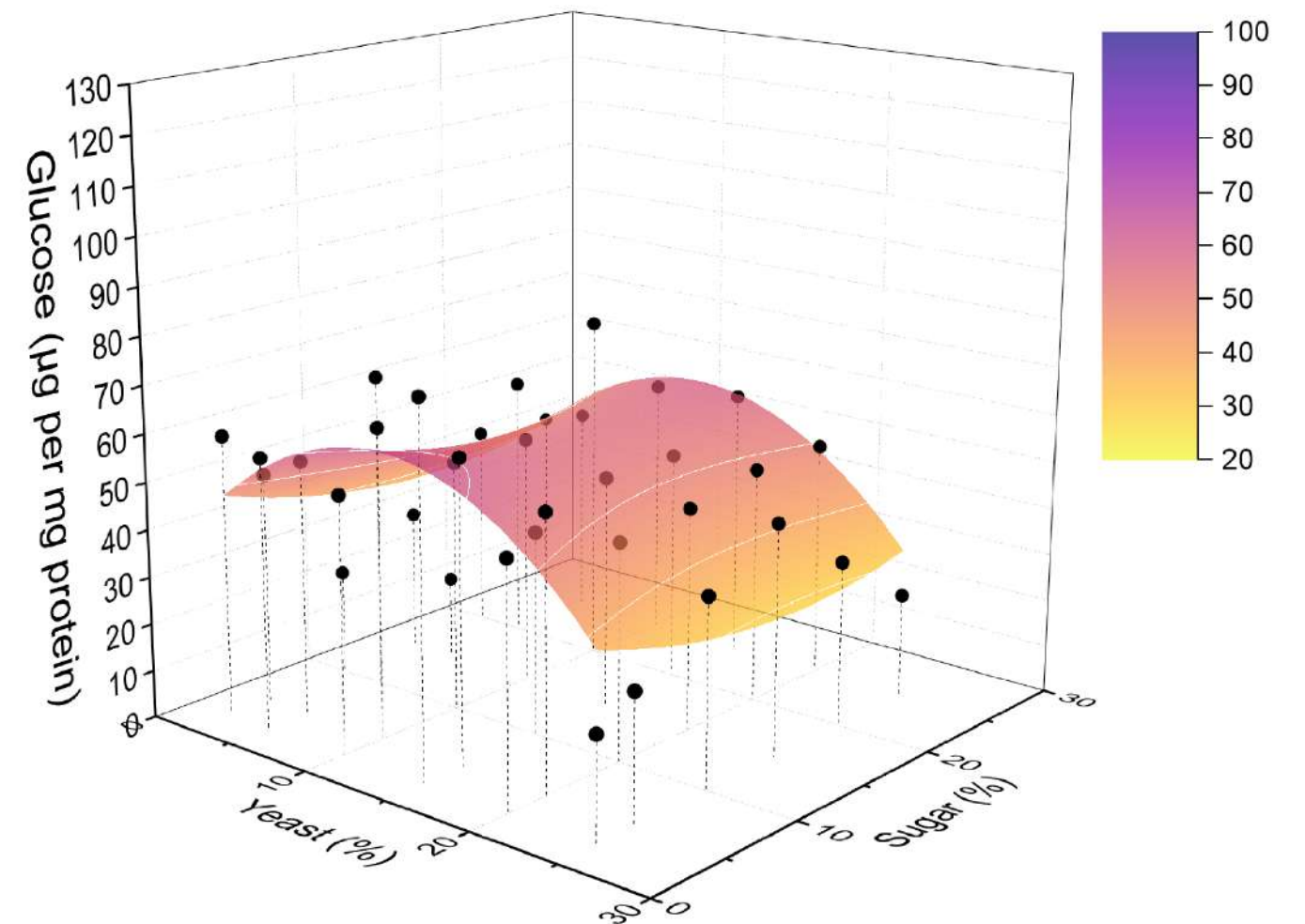


Adj. $R^2 = 0.40$

Mated
males



Adj. $R^2 = 0.15$



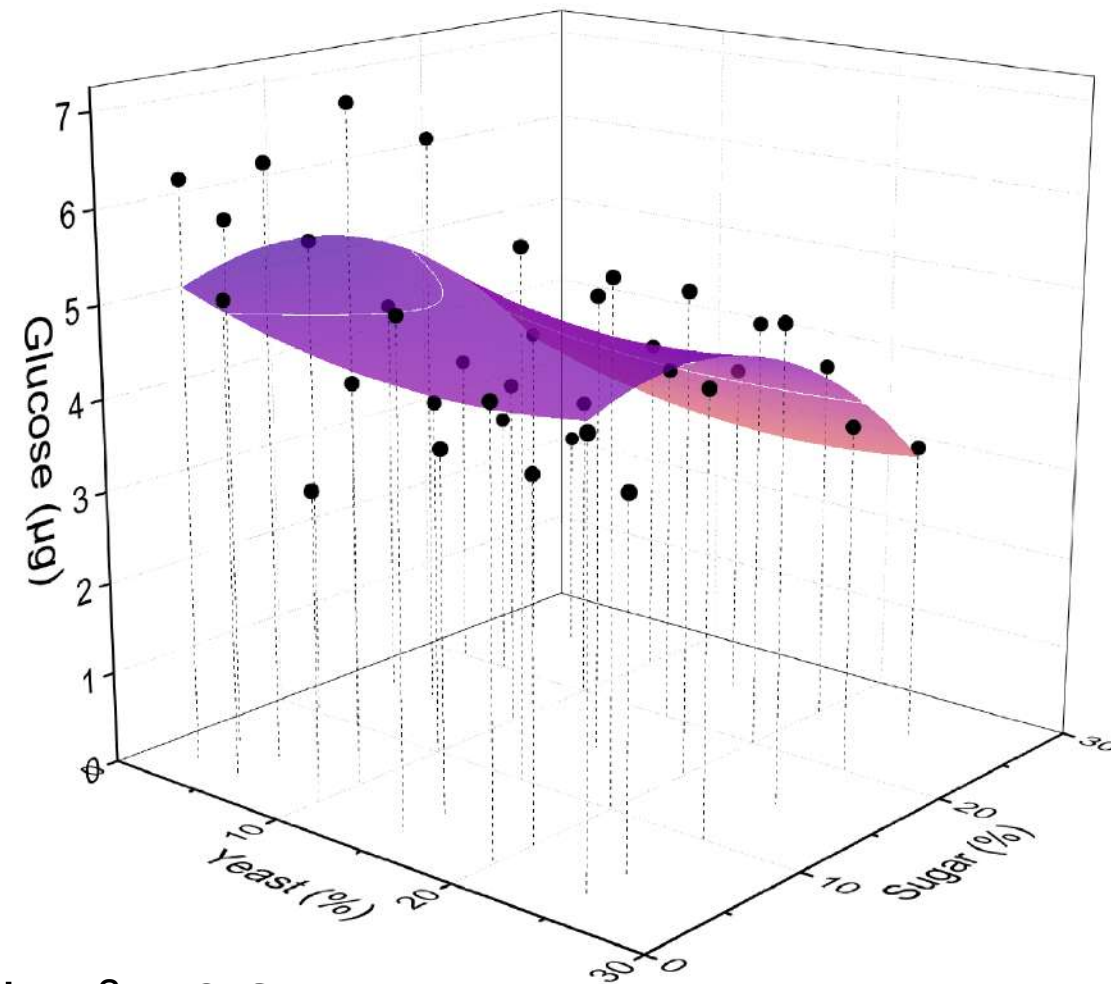
Adj. $R^2 = 0.40$

Figure S40.

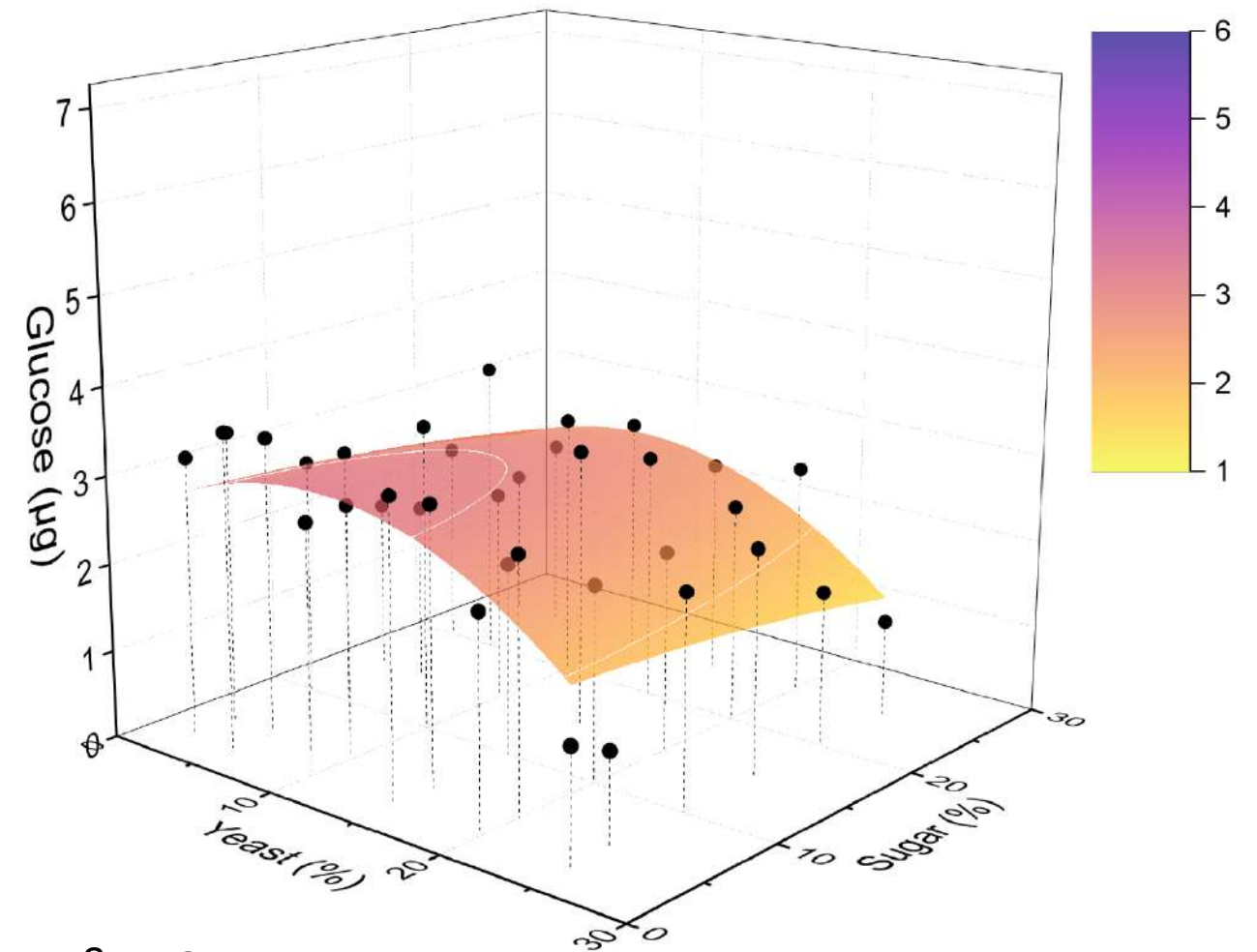
w^{1118}

SK

Virgin
males

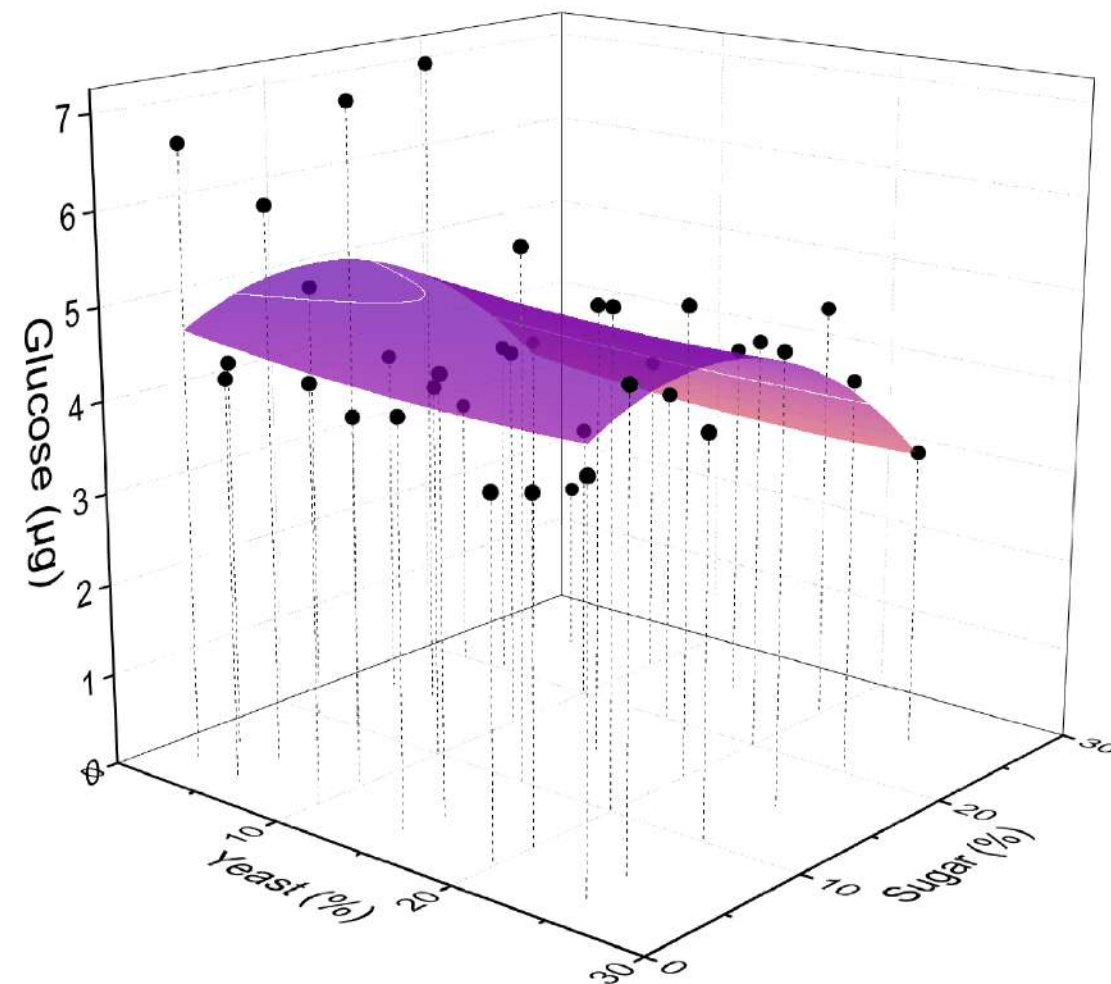


Adj. $R^2 = 0.31$

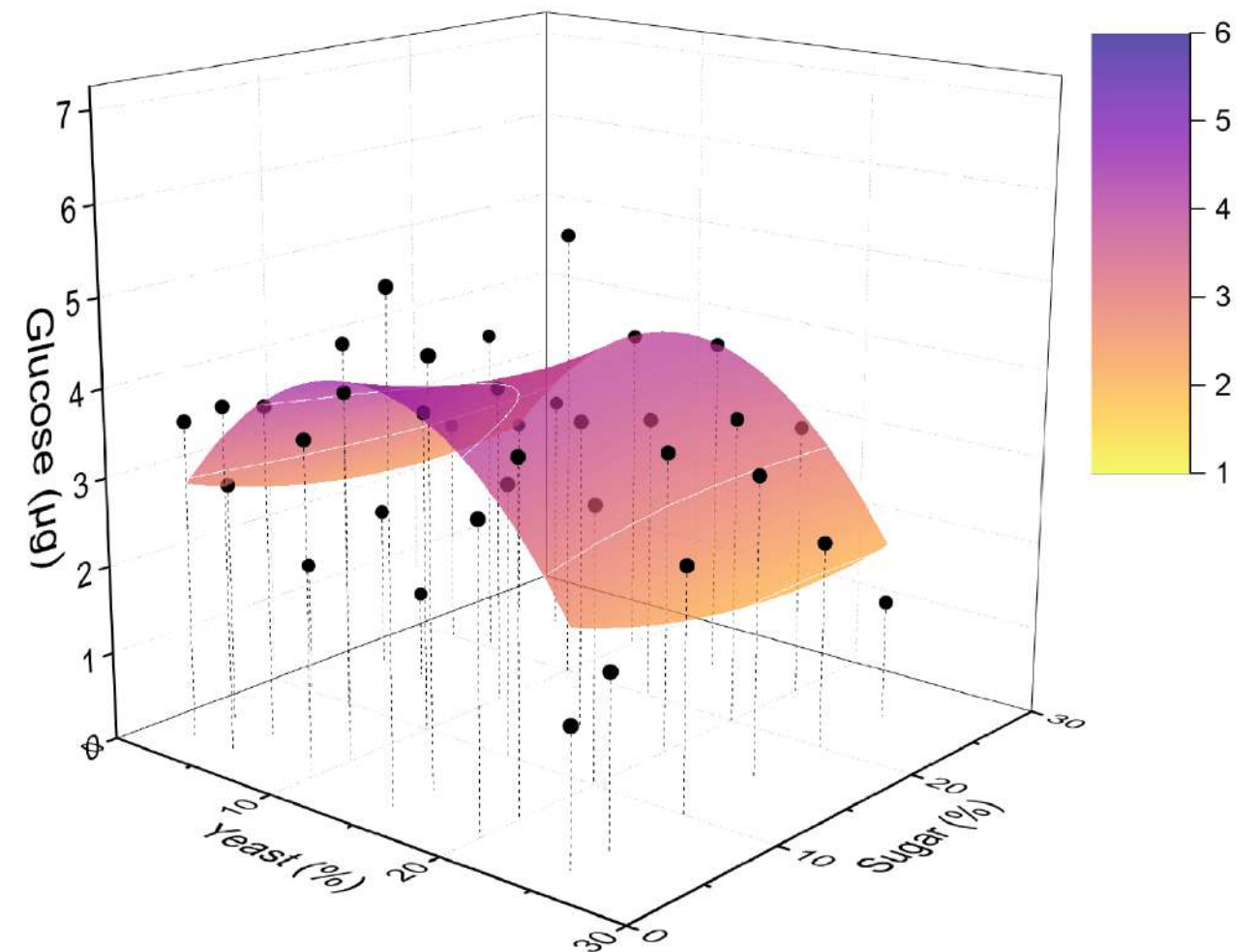


Adj. $R^2 = 0.44$

Mated
males



Adj. $R^2 = 0.20$



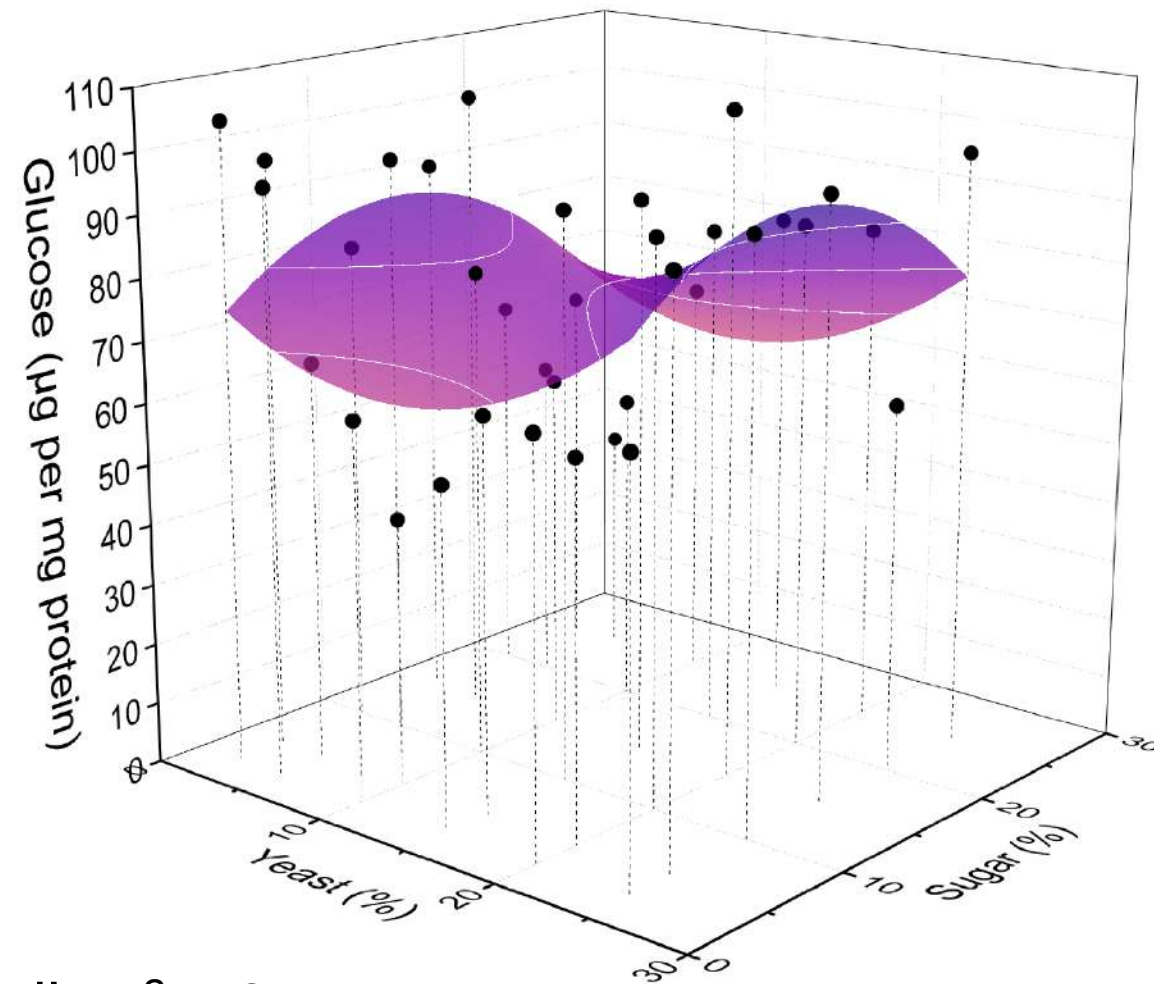
Adj. $R^2 = 0.45$

Figure S41.

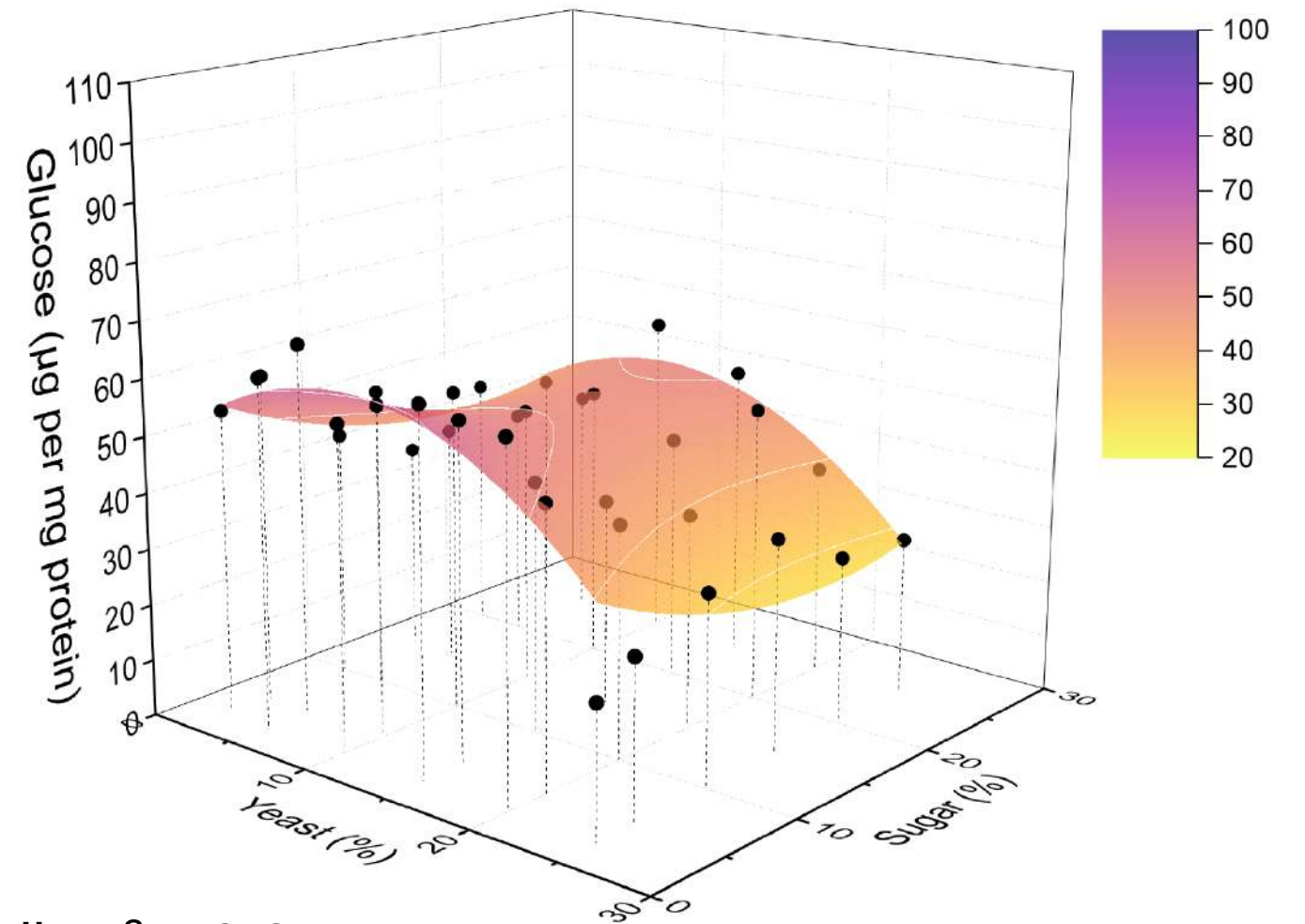
w^{1118}

SK

Virgin
females

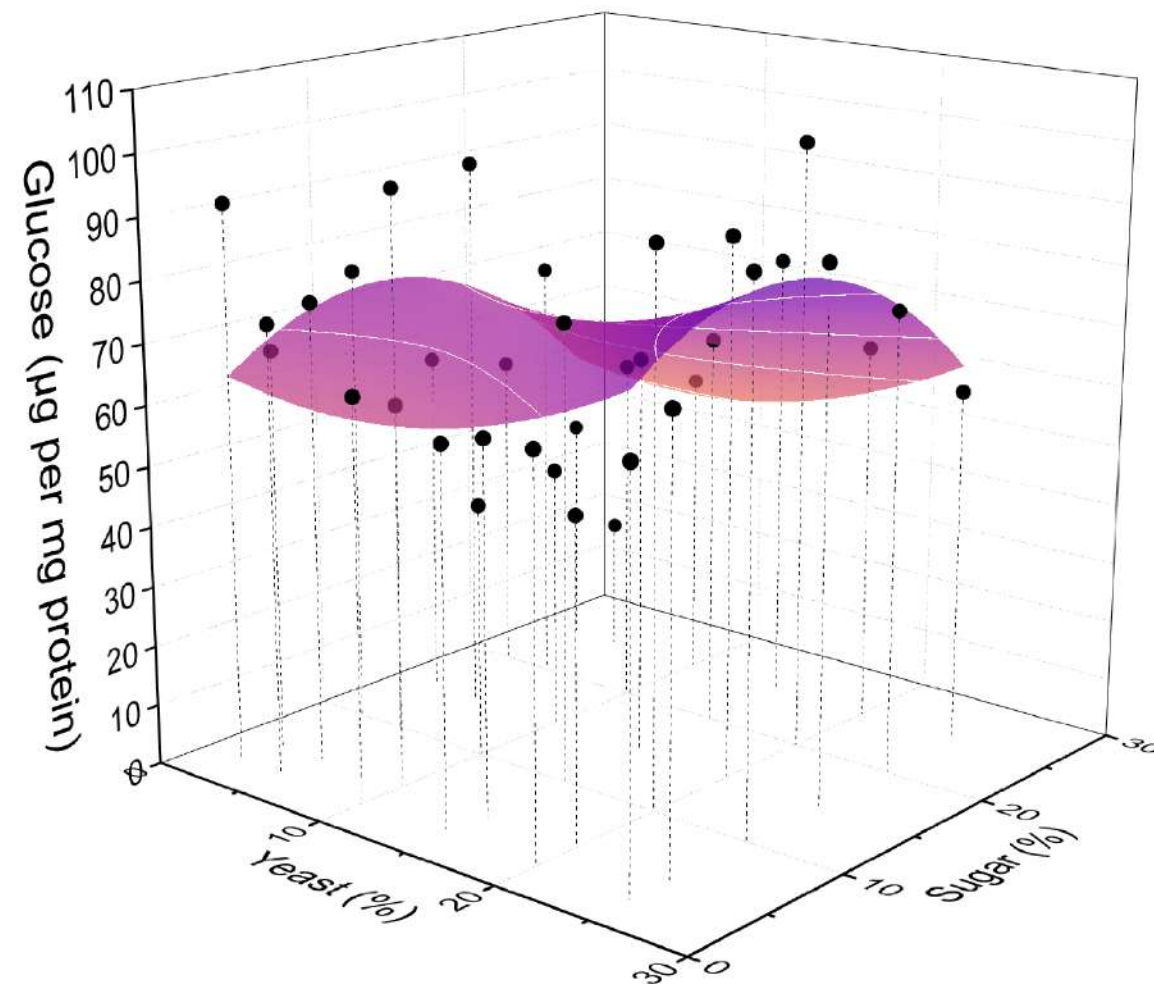


Adj. $R^2 = 0.11$

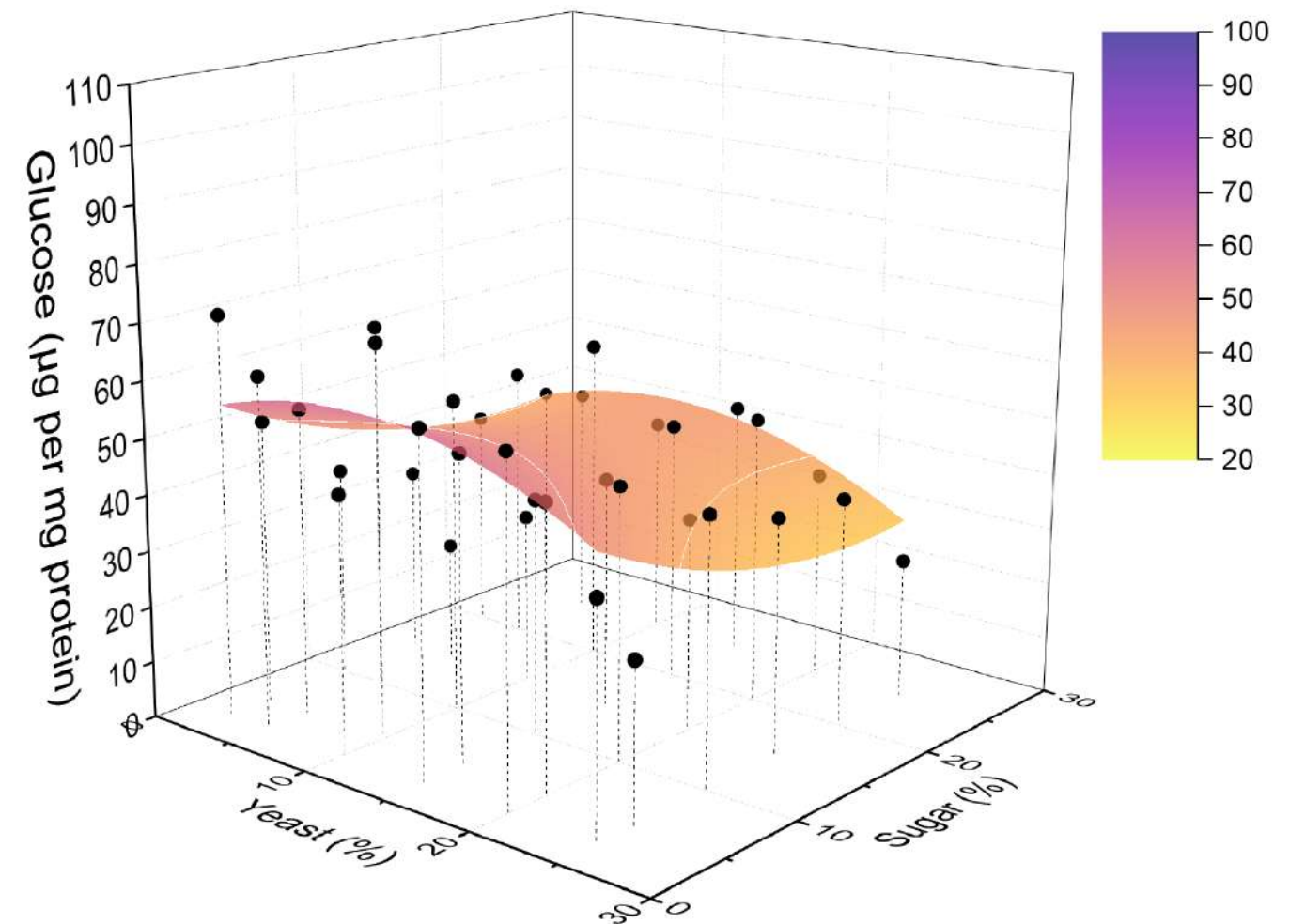


Adj. $R^2 = 0.65$

Mated
females



Adj. $R^2 = 0.18$



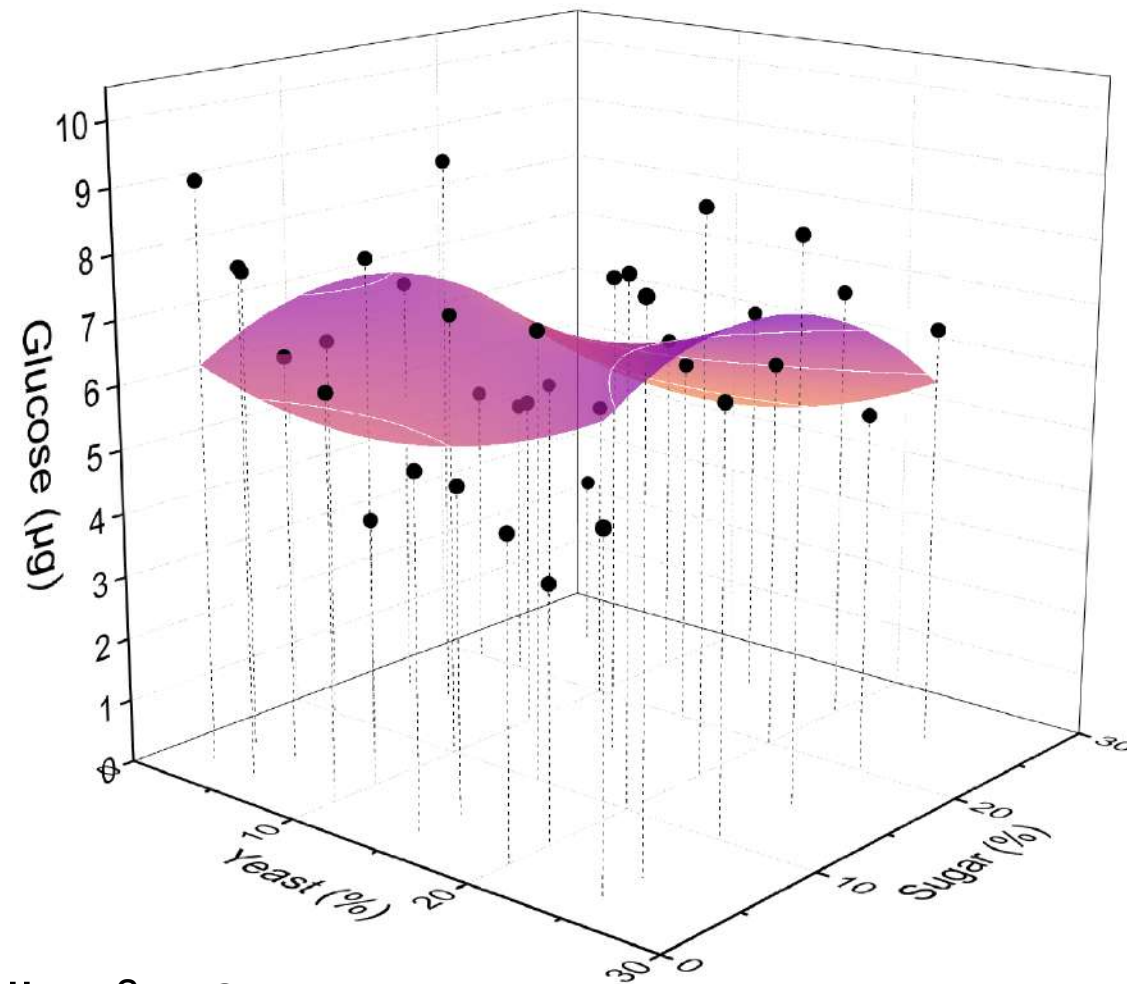
Adj. $R^2 = 0.31$

Figure S42.

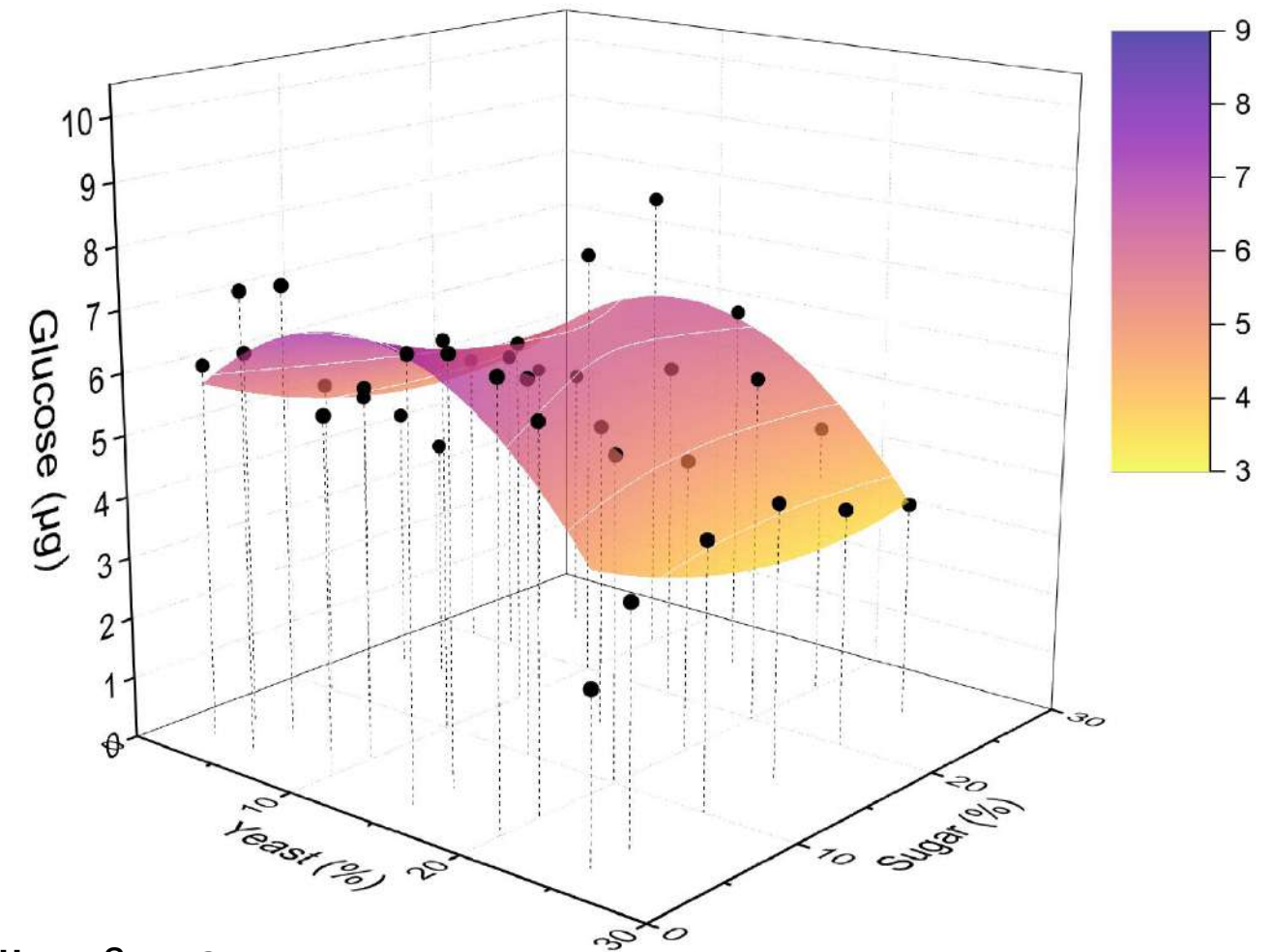
w^{1118}

SK

Virgin
females

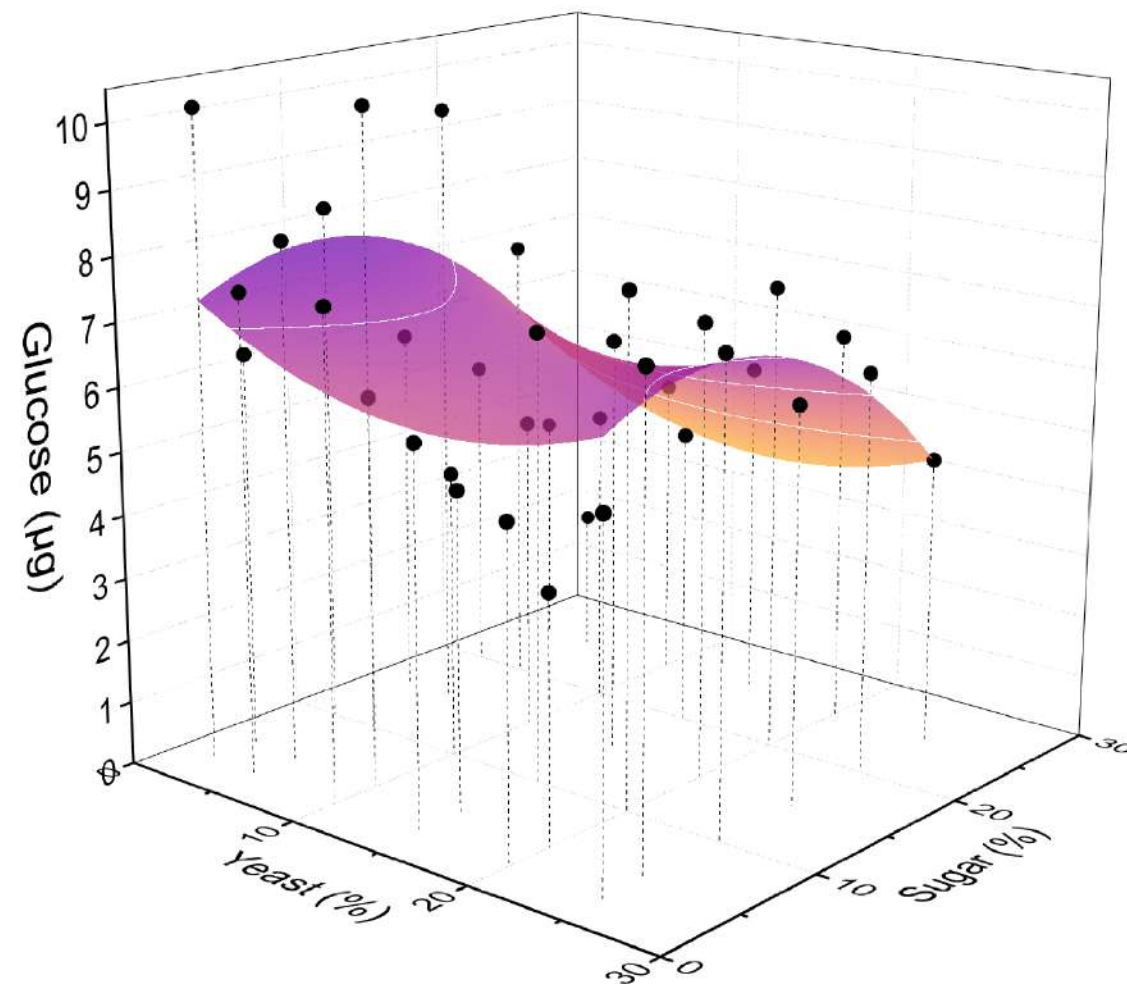


Adj. $R^2 = 0.11$

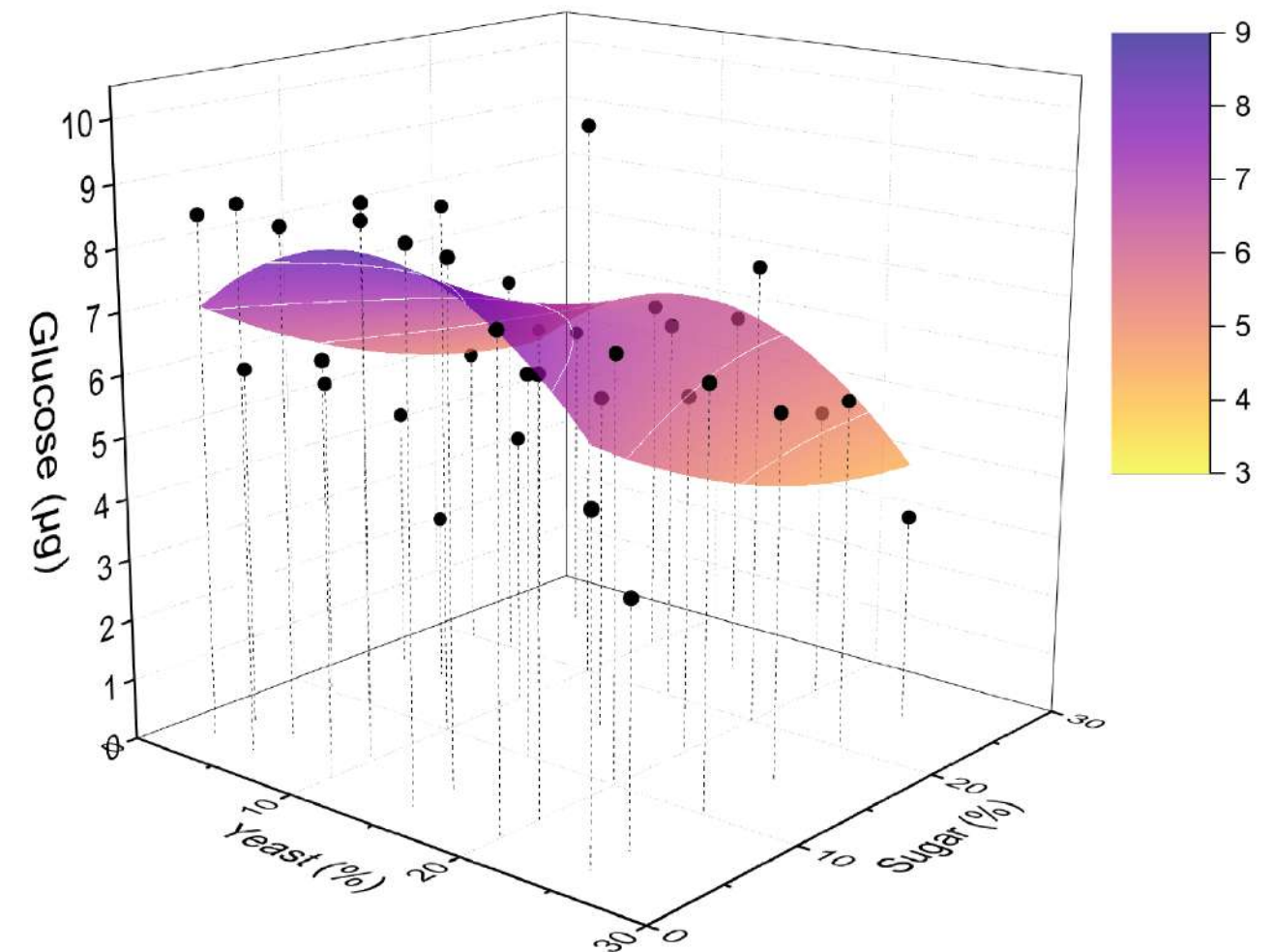


Adj. $R^2 = 0.55$

Mated
females



Adj. $R^2 = 0.22$



Adj. $R^2 = 0.33$

FEMALES

Mated

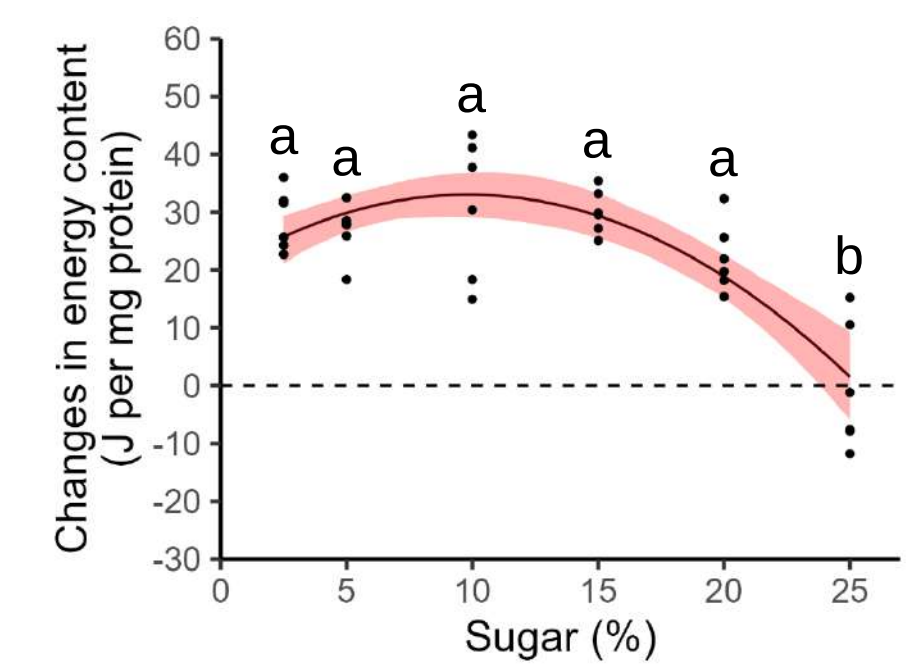
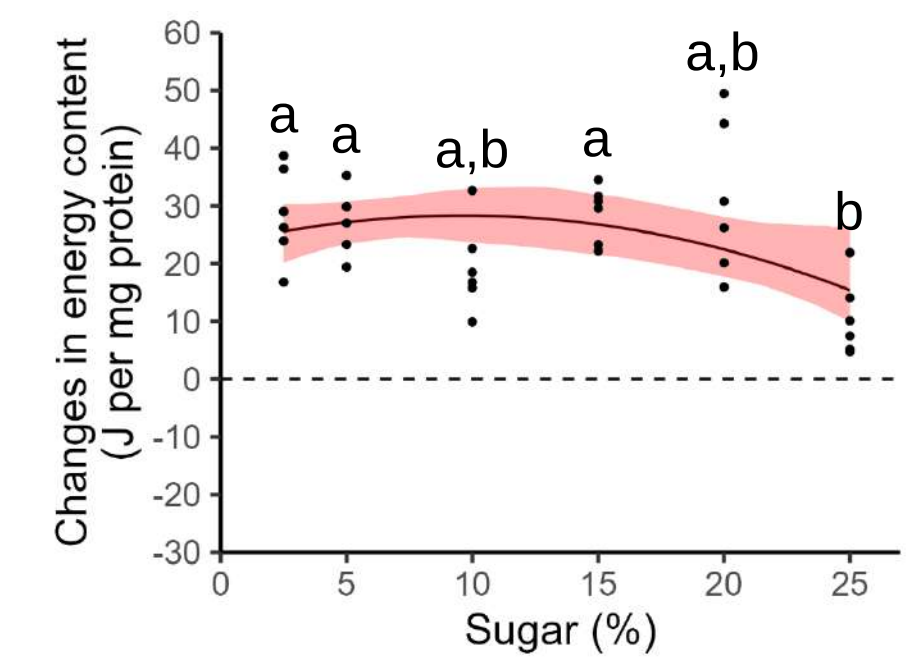
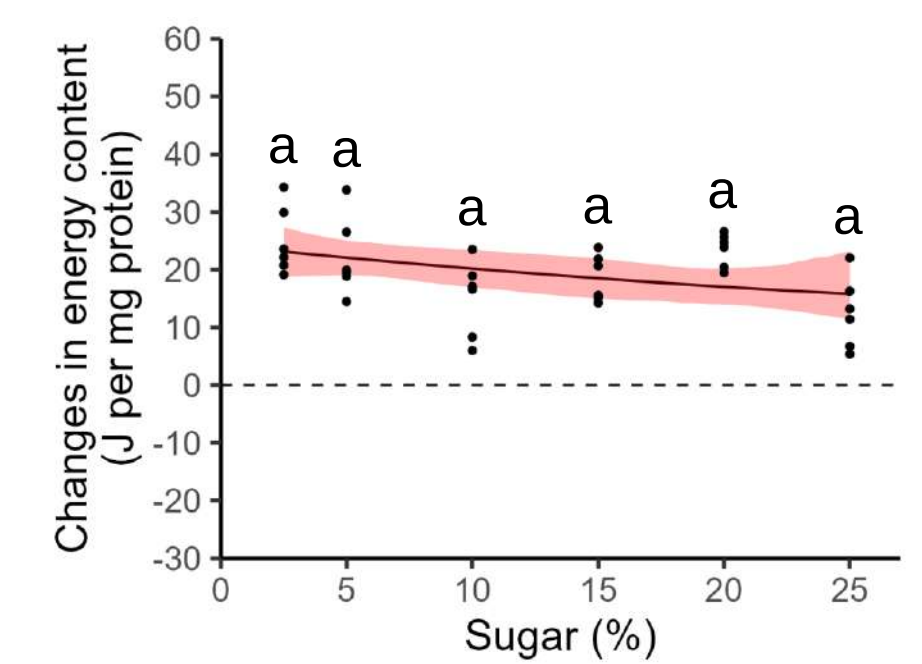
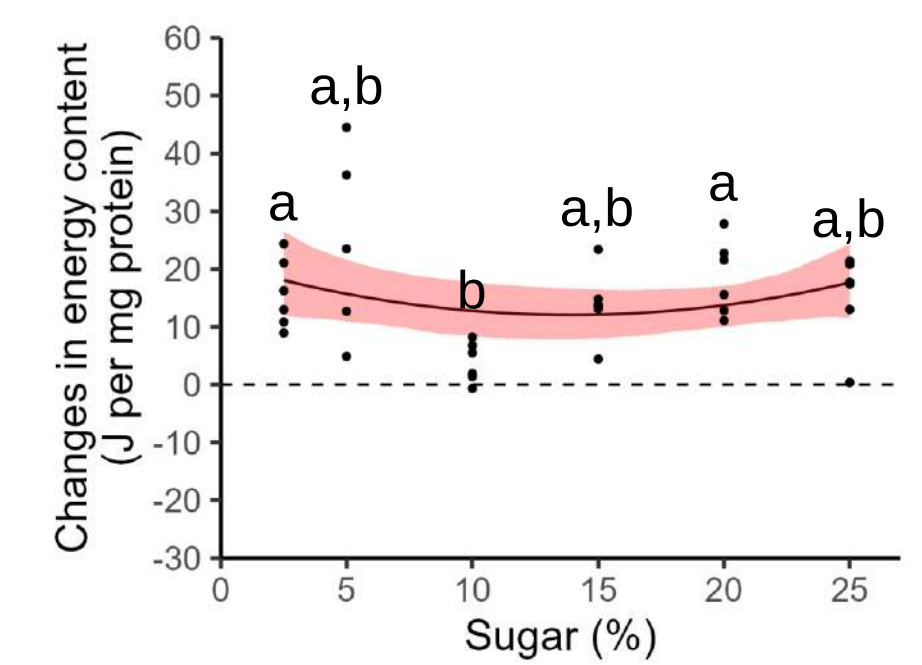
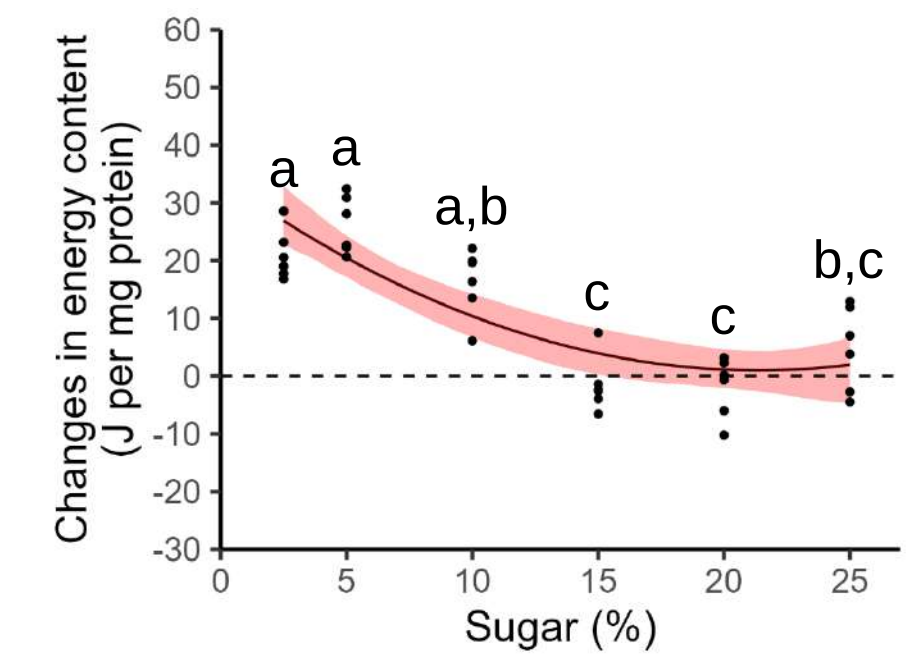
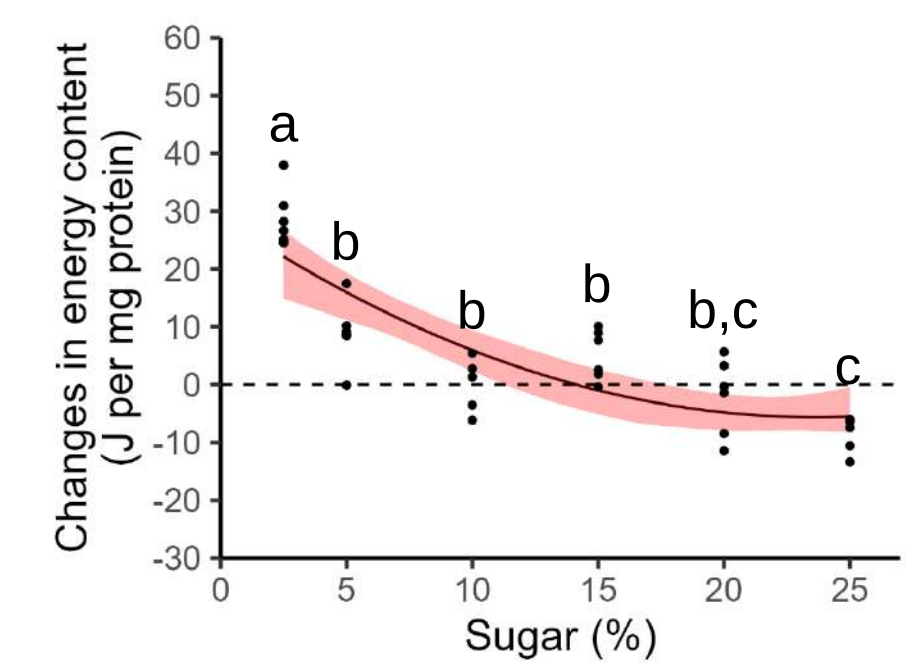


Figure S44.

MALES

FEMALES

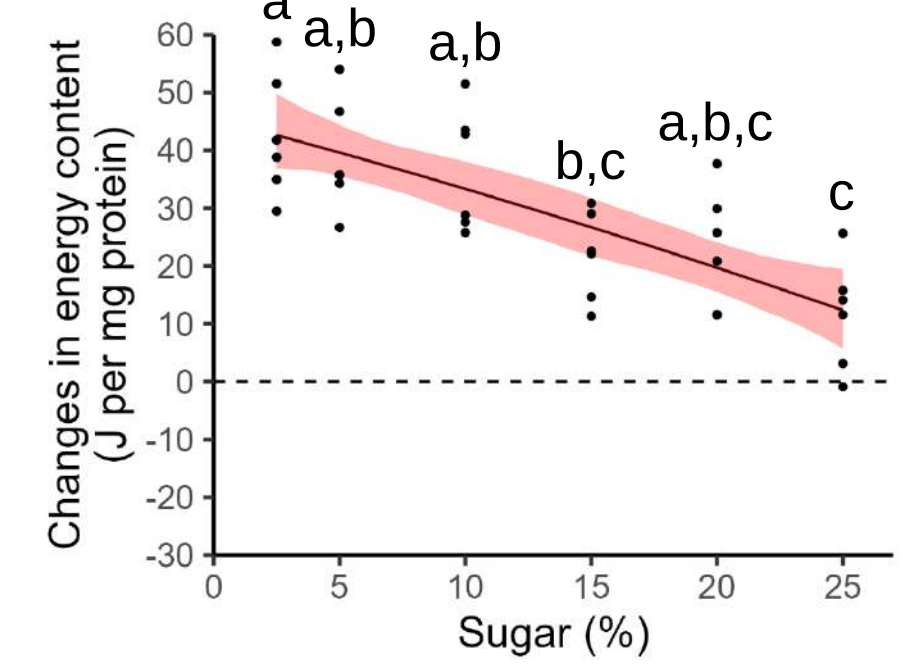
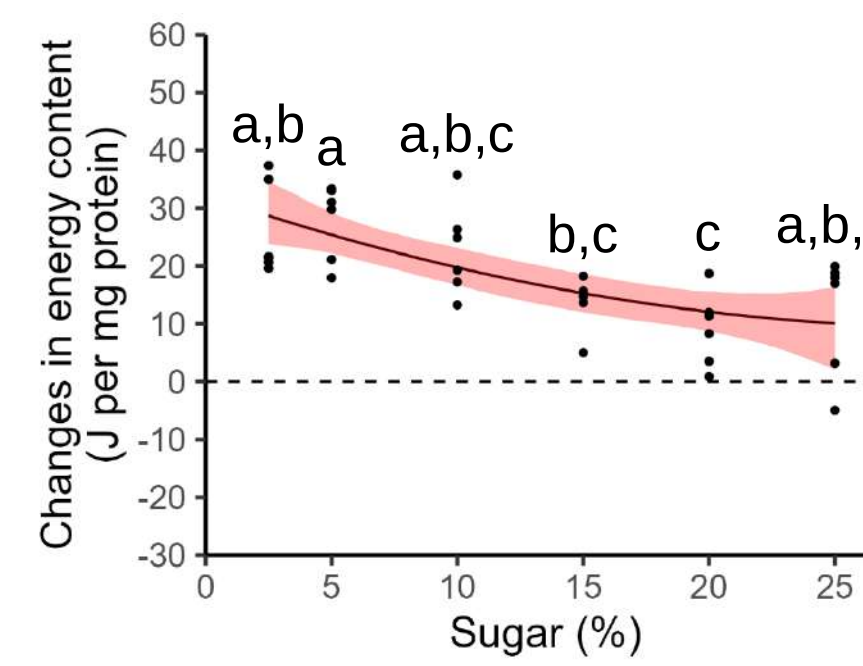
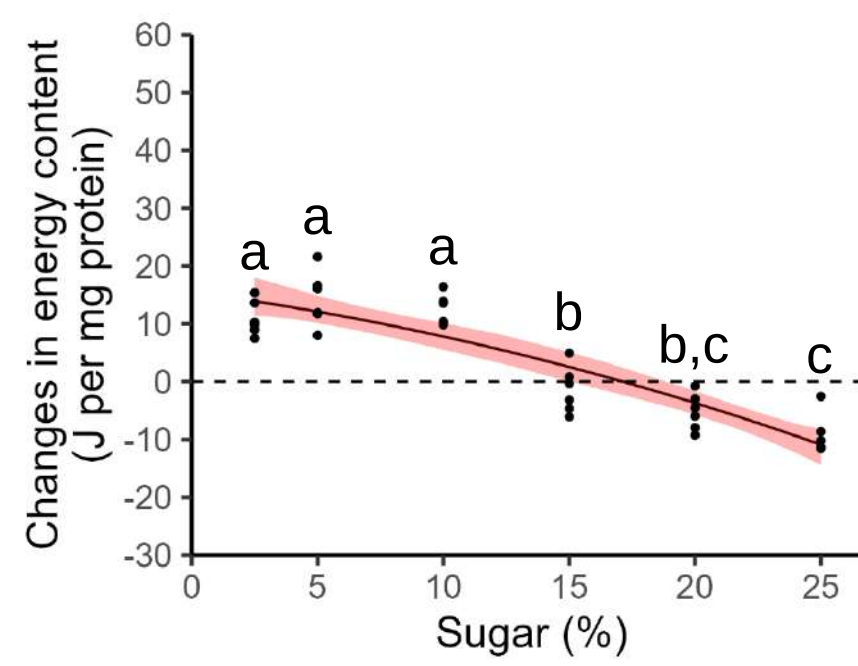
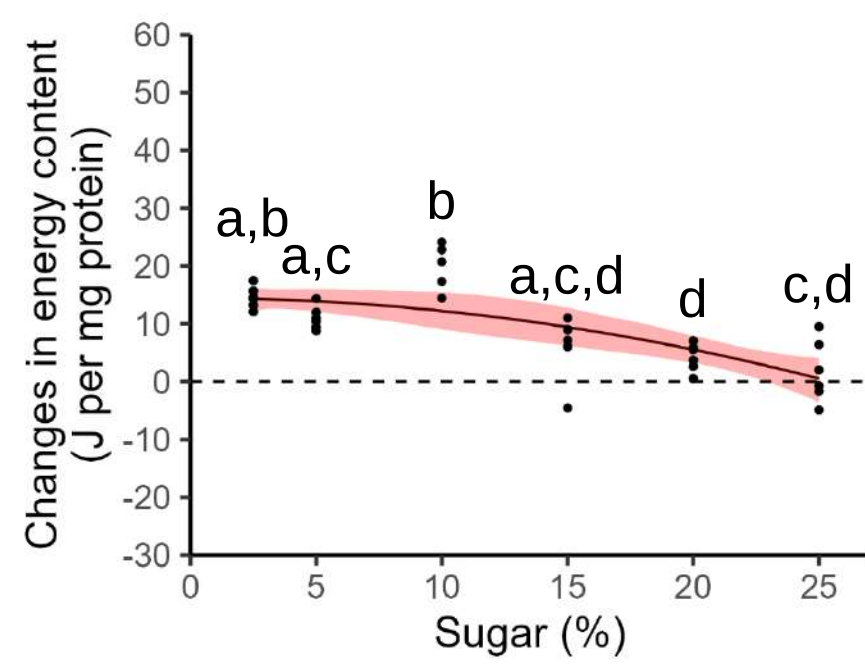
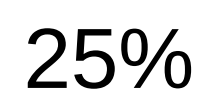
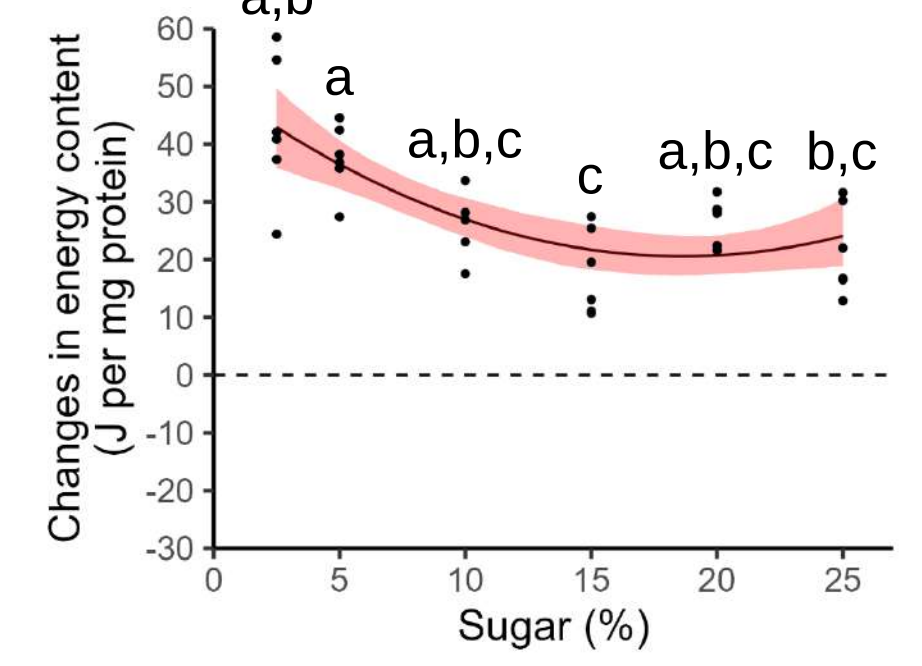
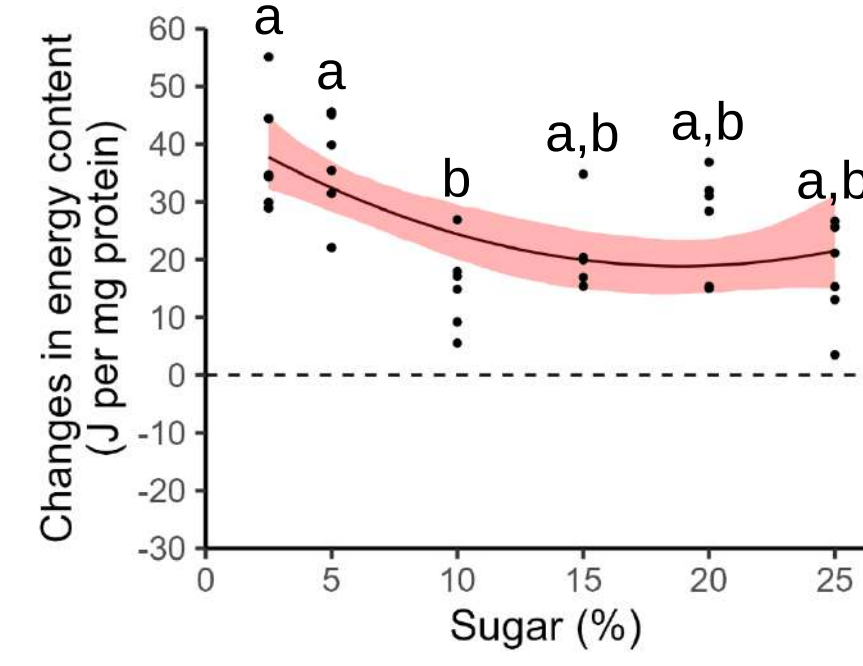
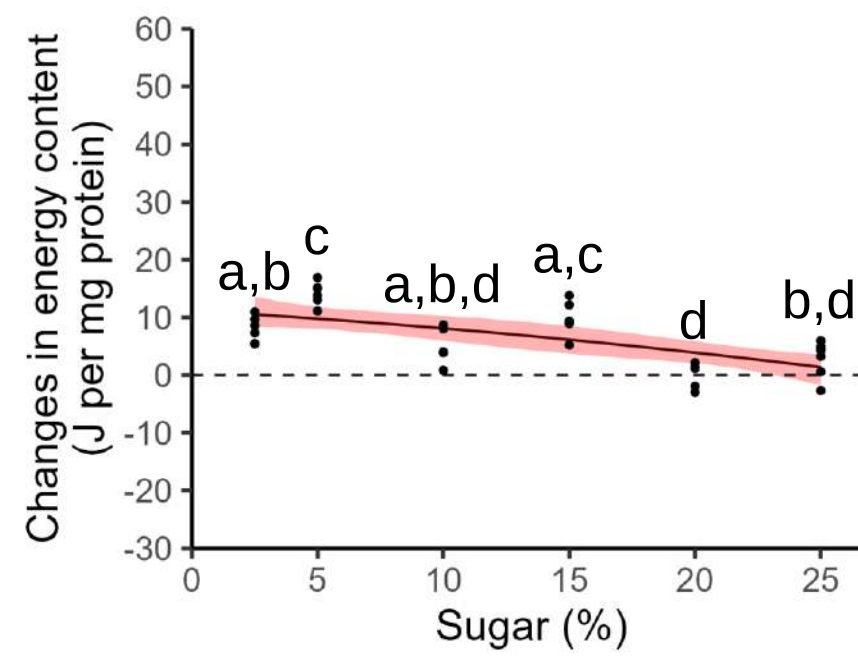
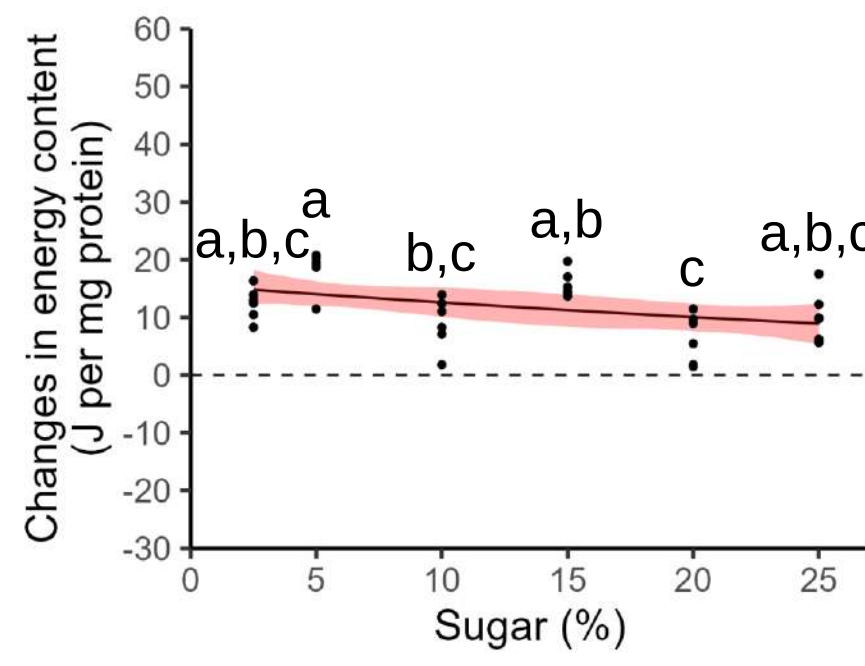
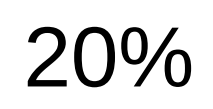
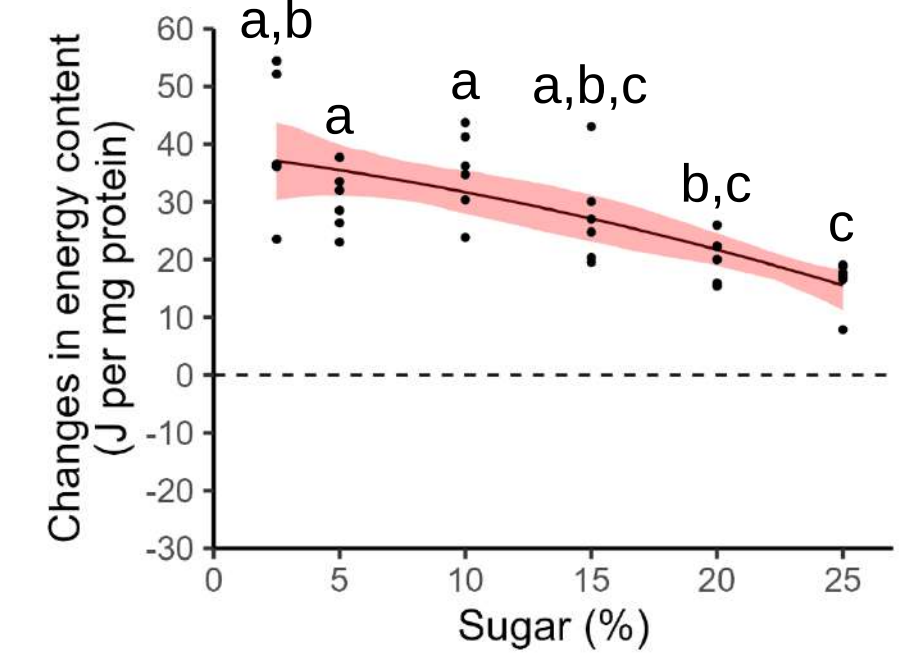
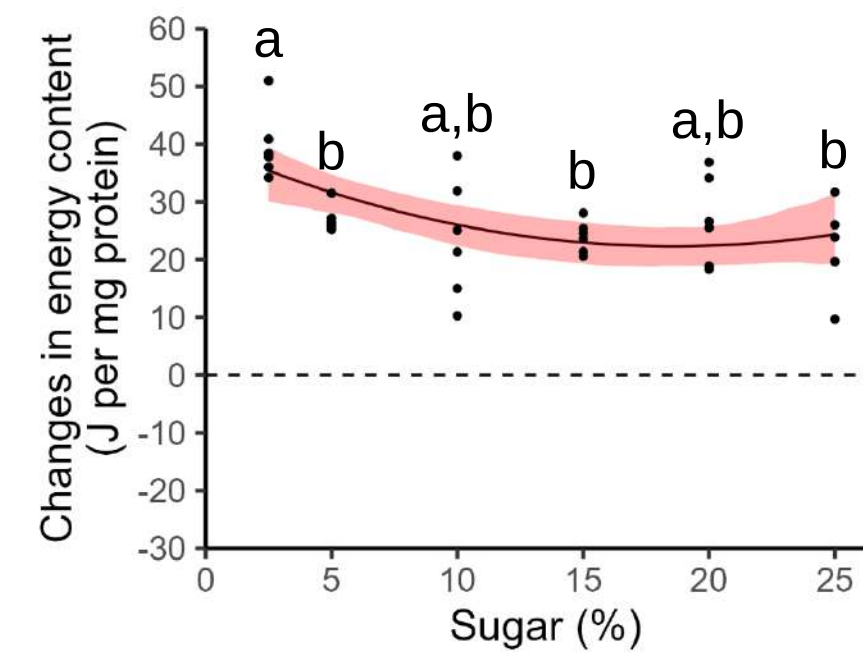
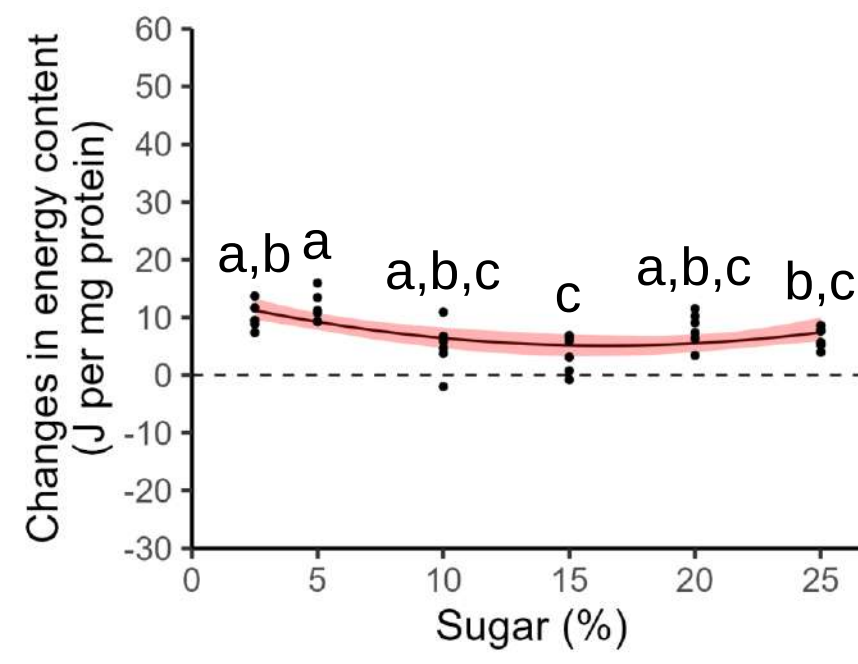
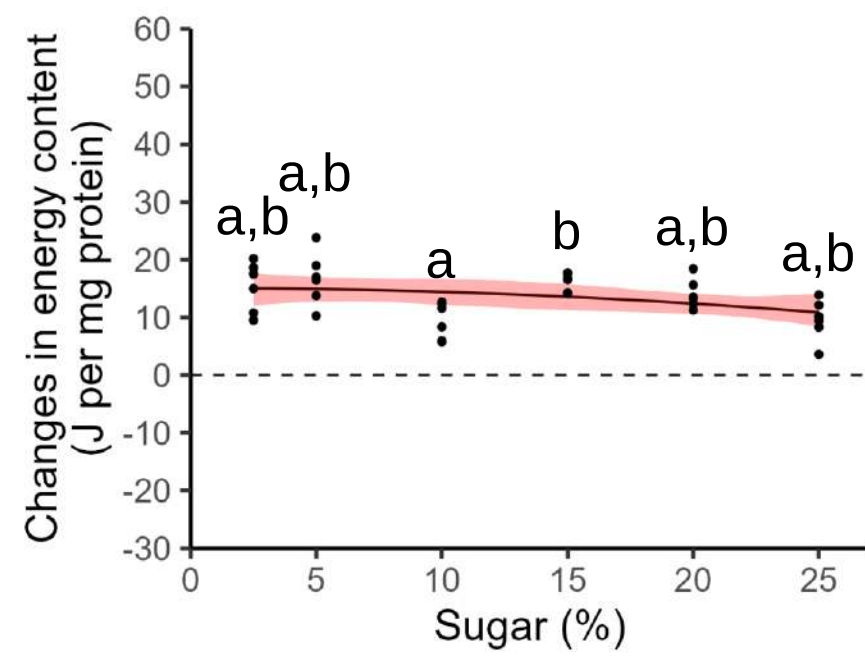
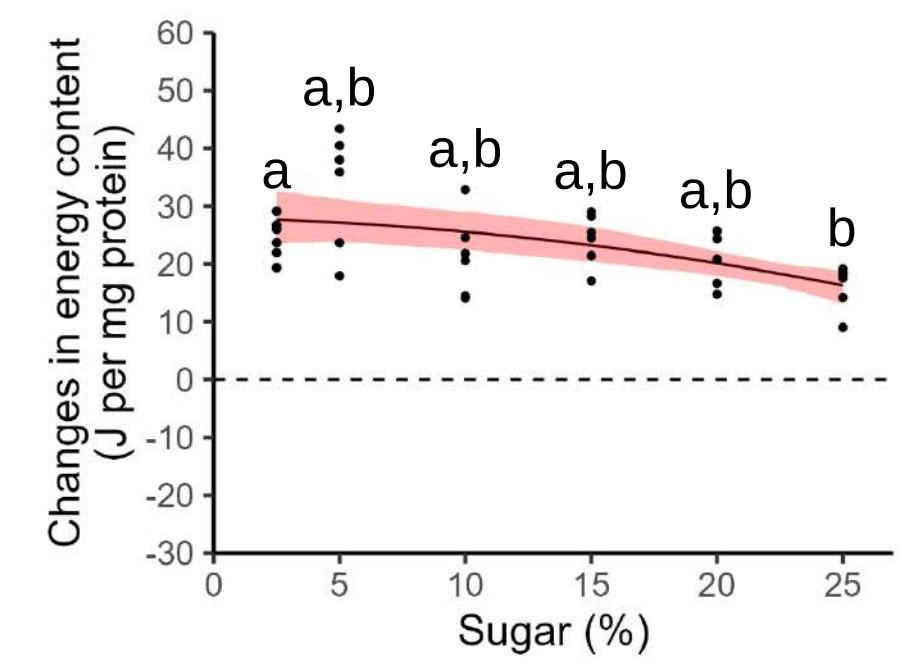
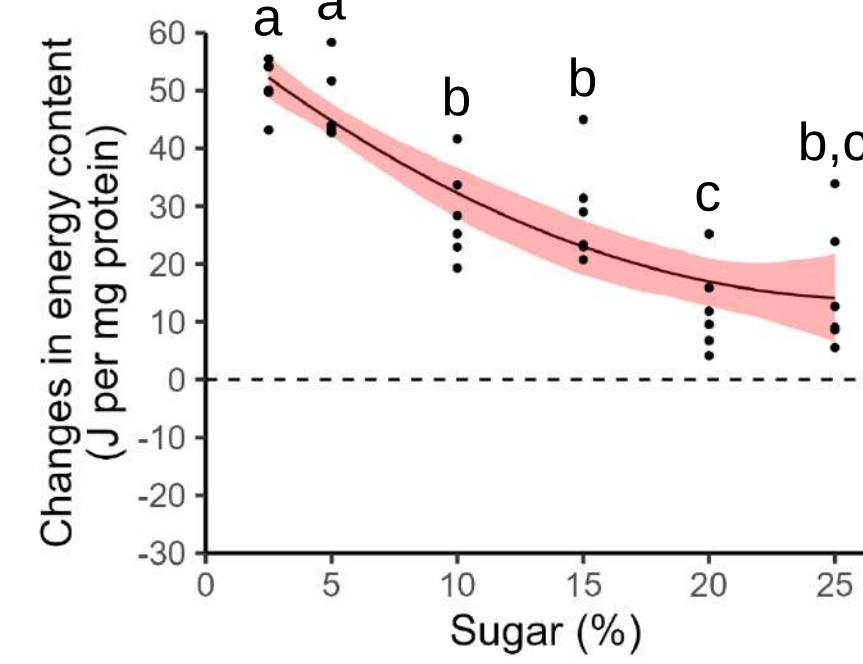
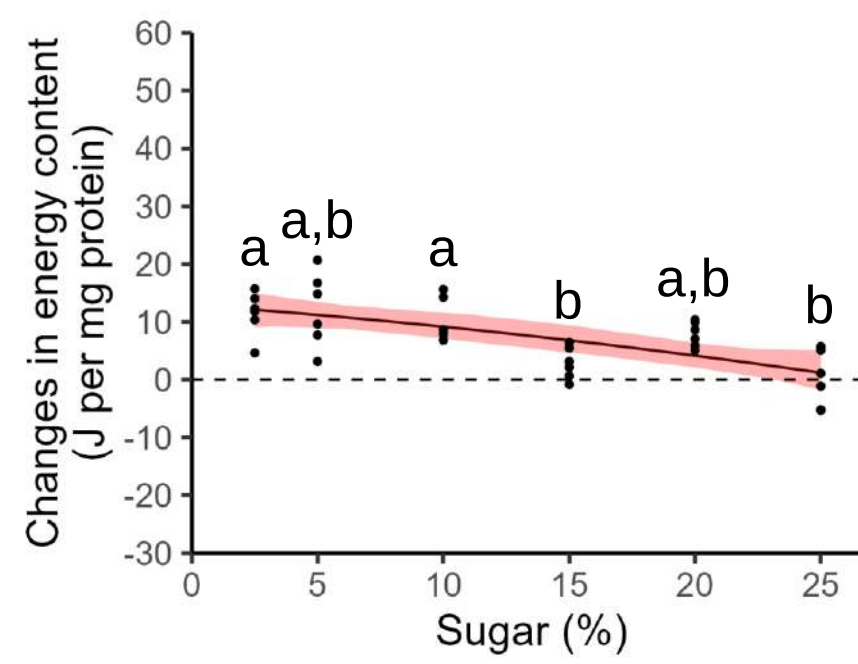
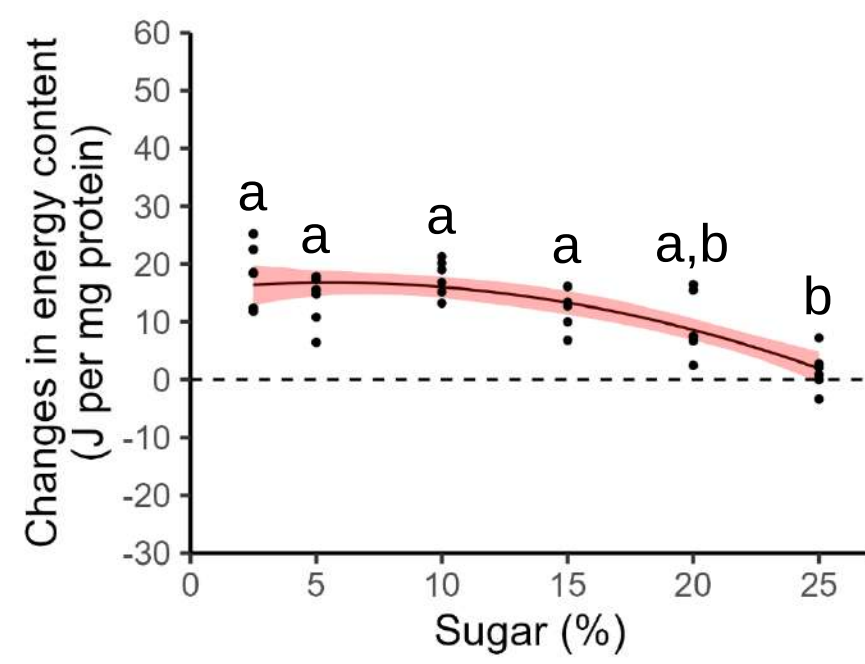
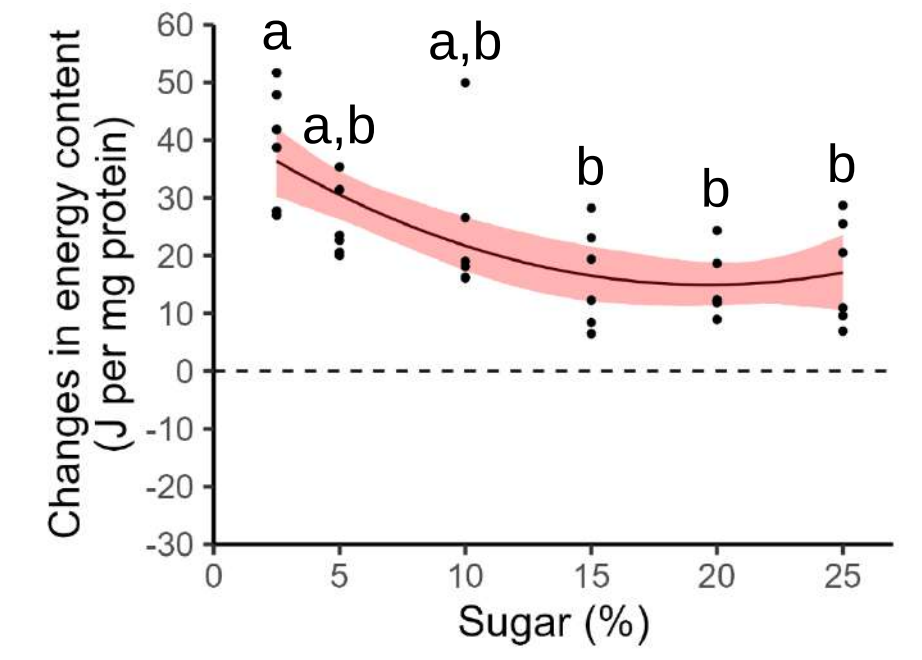
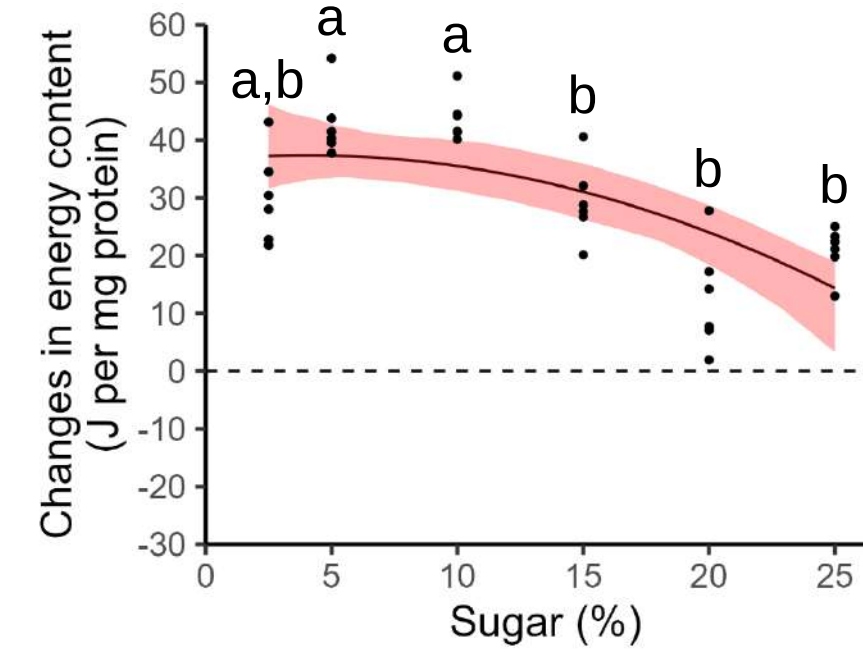
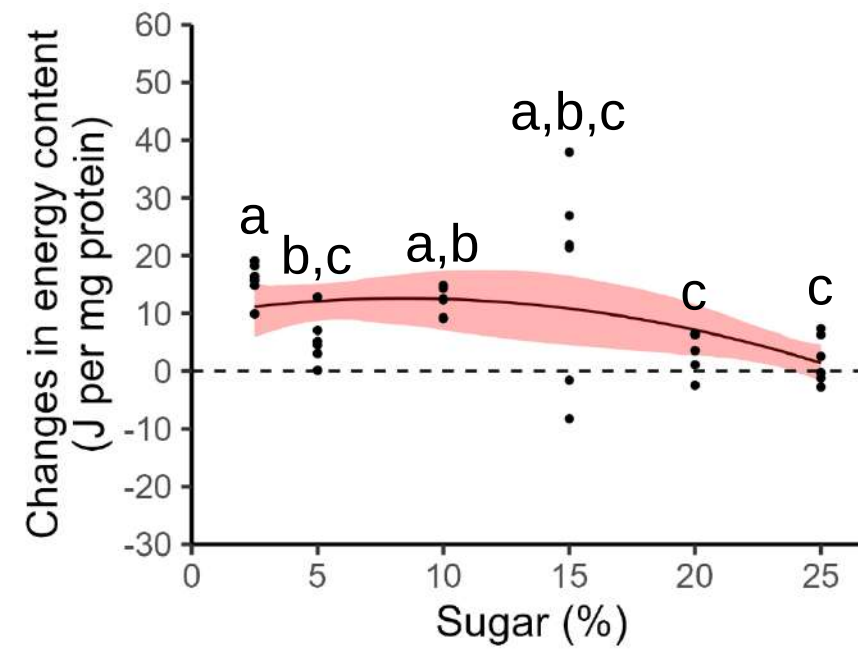
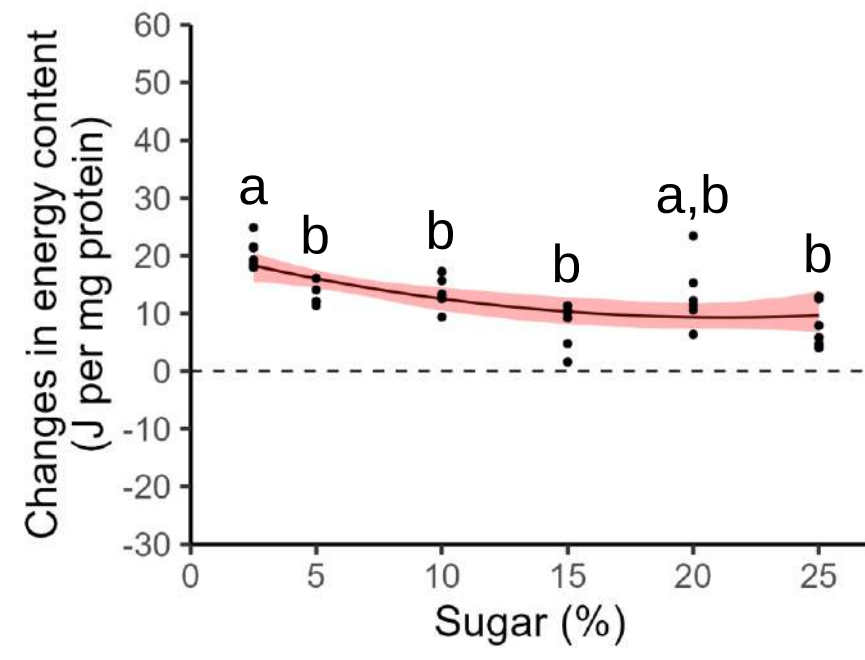
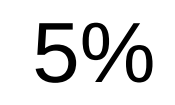
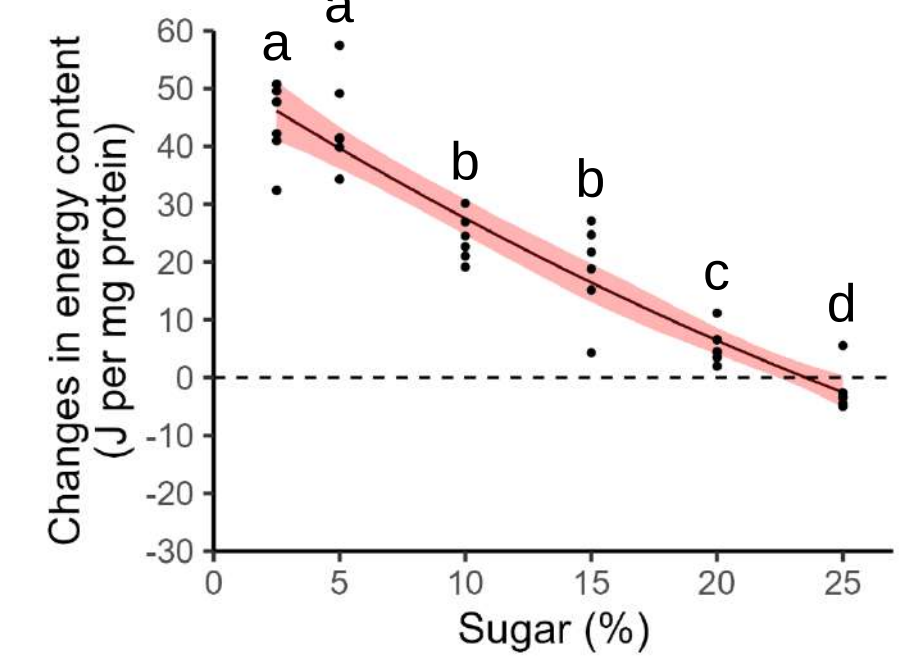
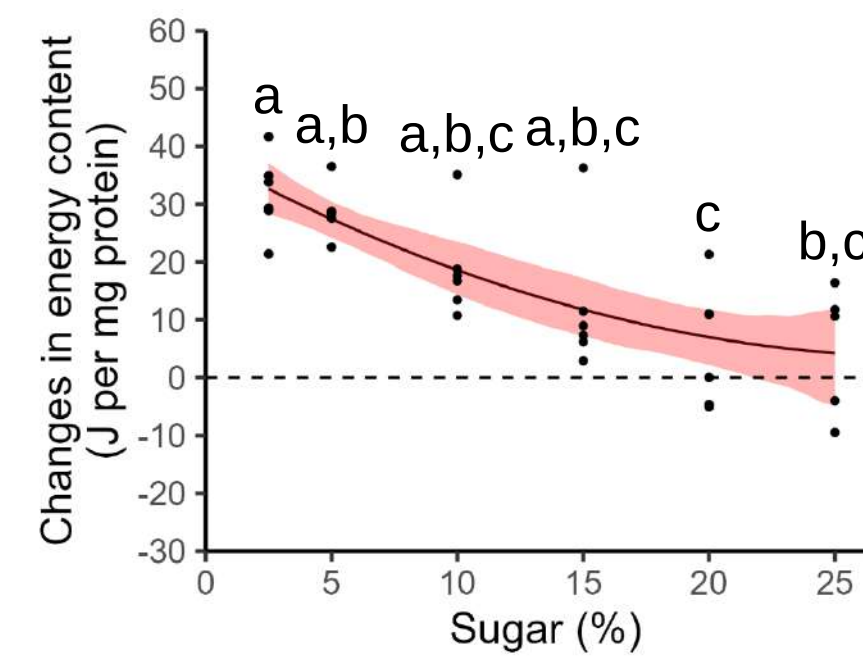
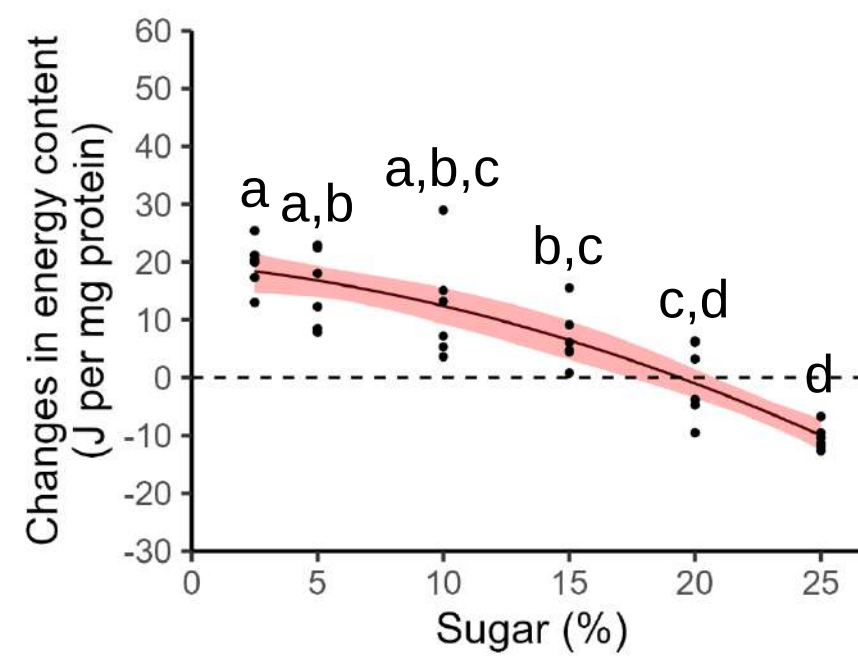
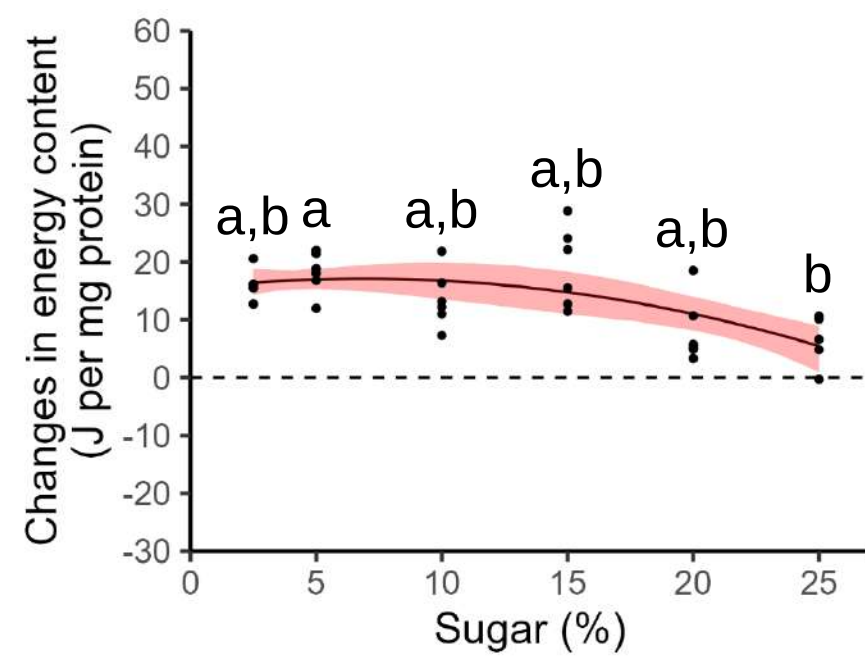
YEAST

Virgin

Mated

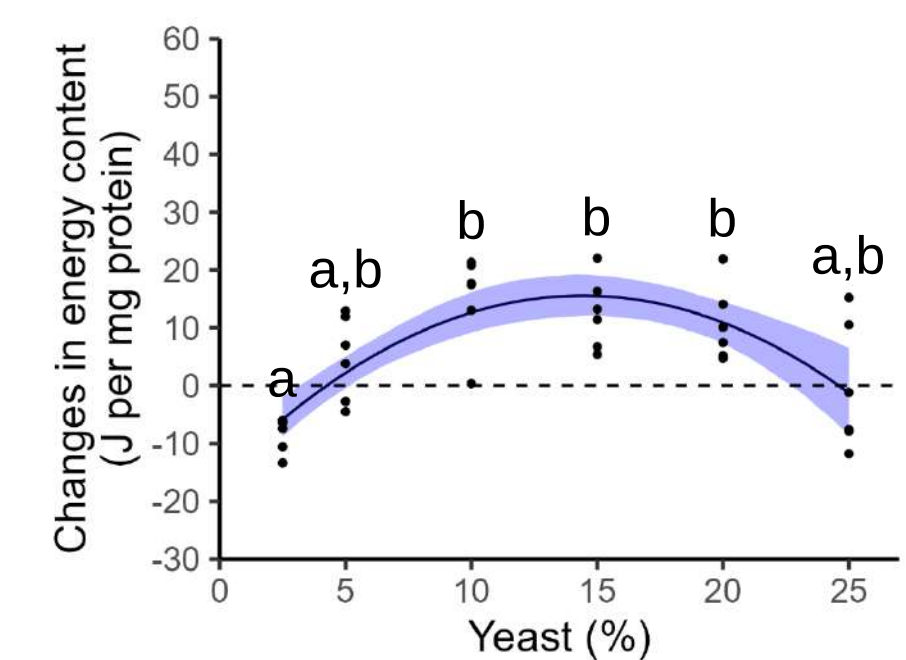
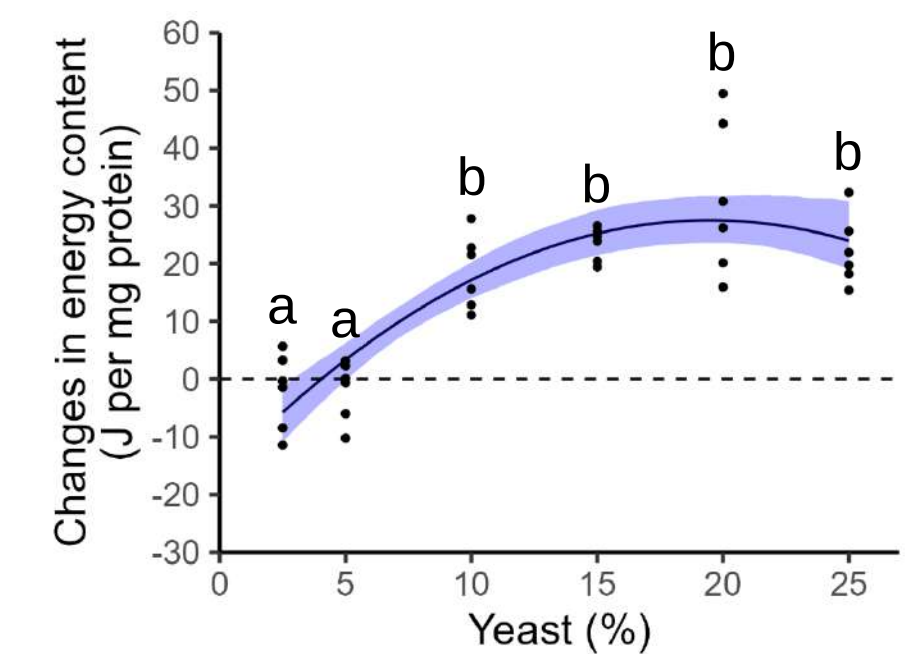
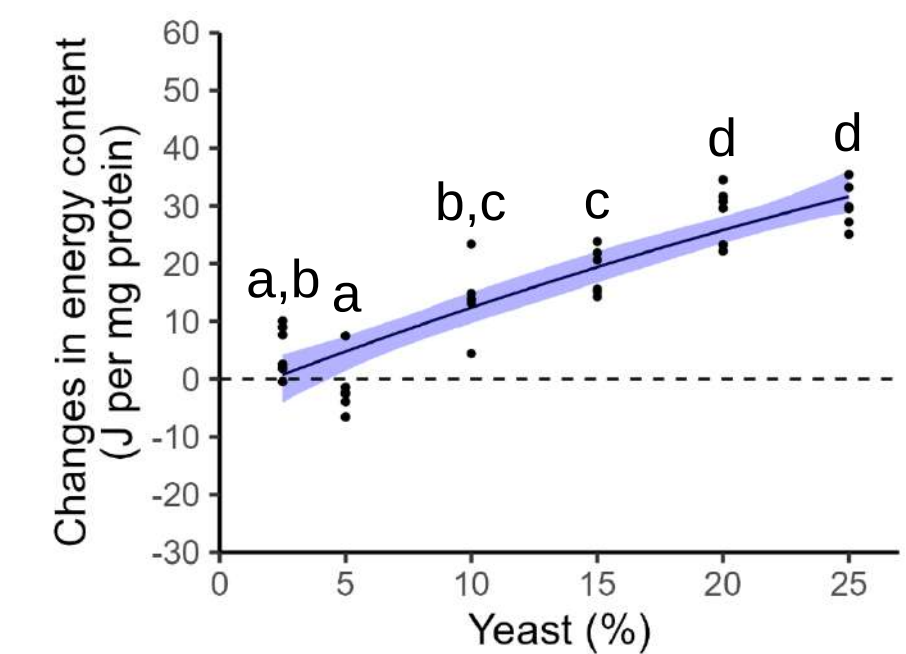
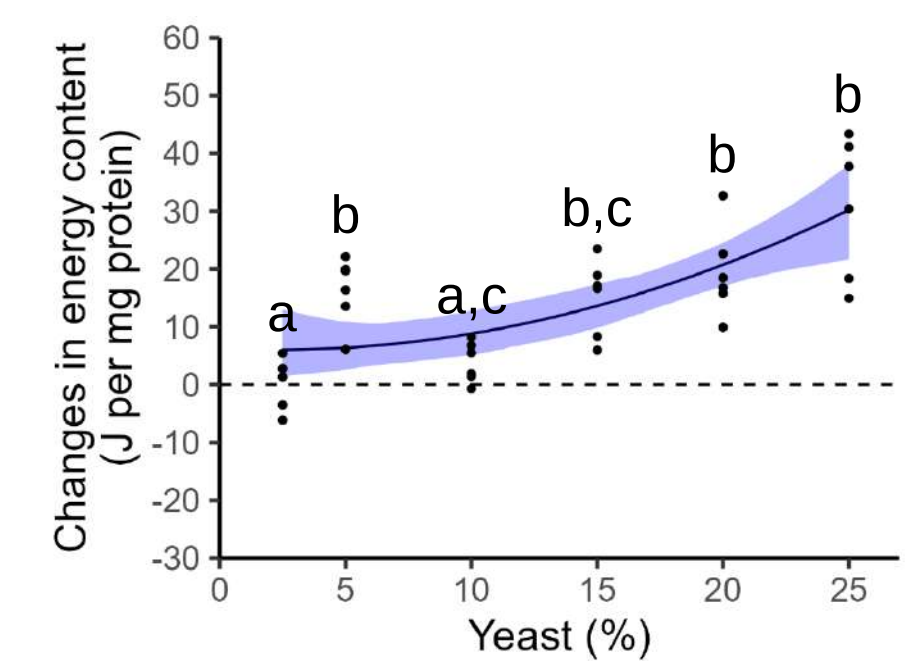
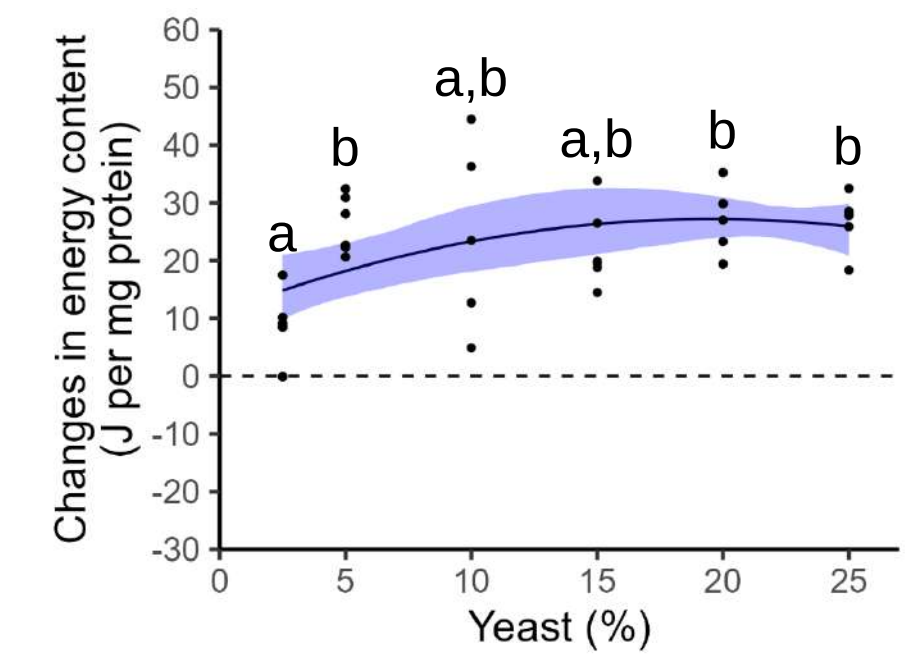
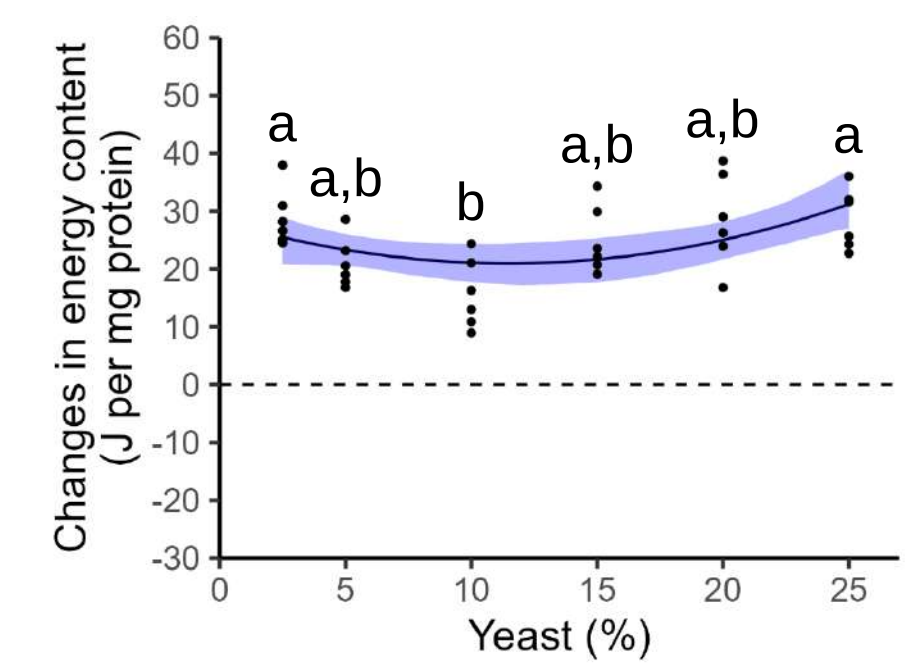
Virgin

Mated



FEMALES

Mated



FEMALES

Mated

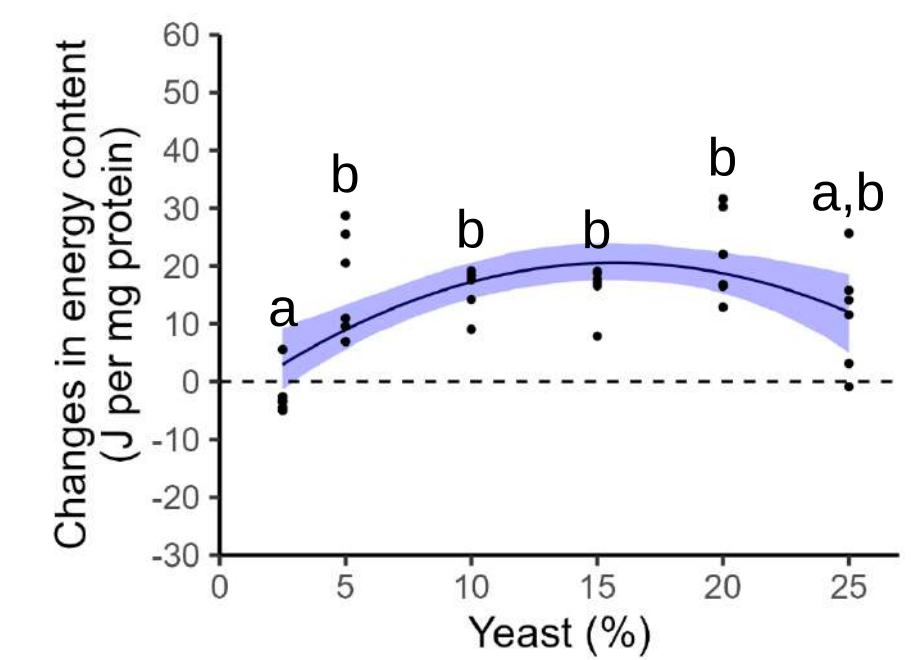
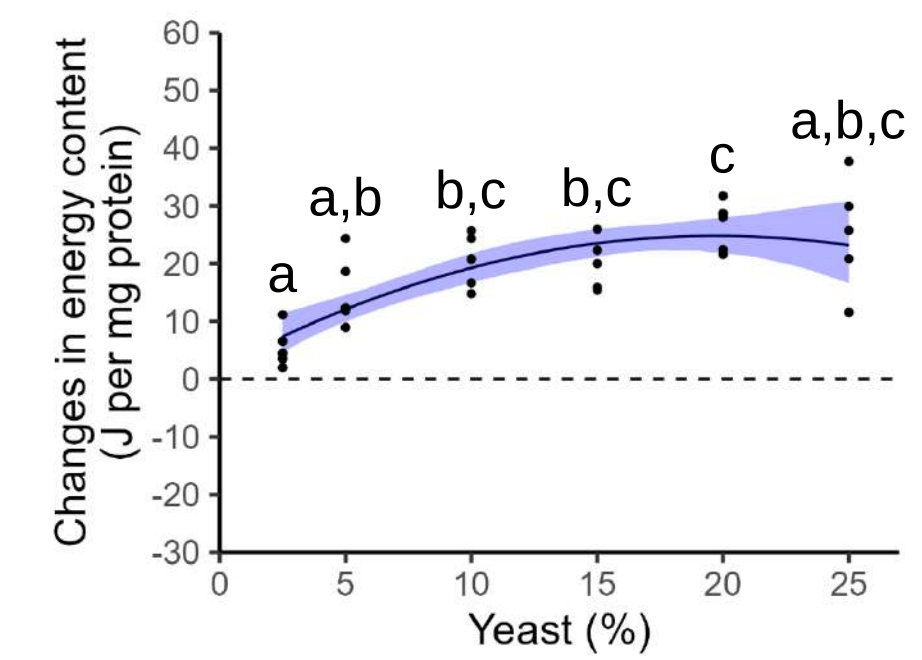
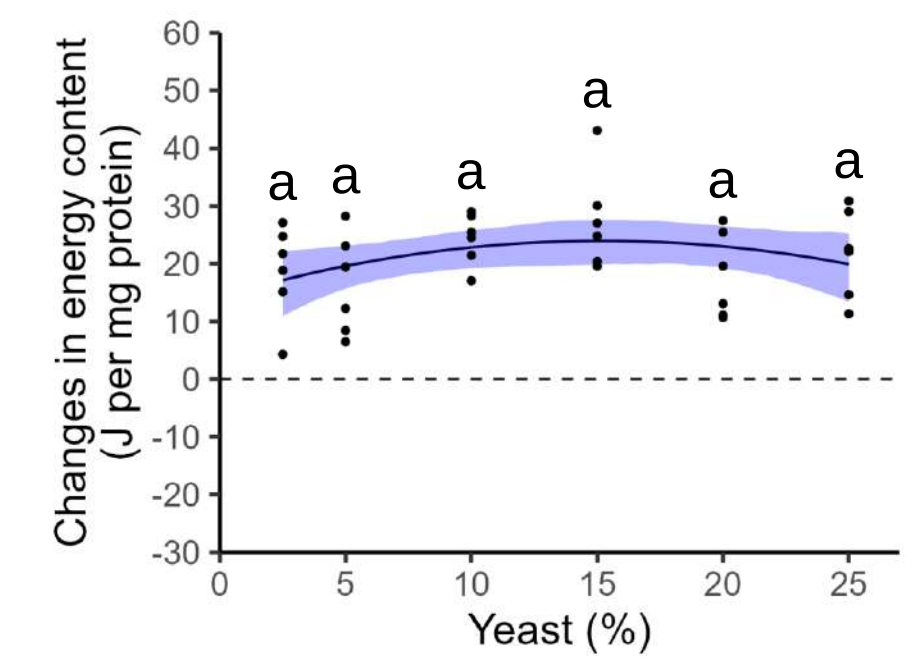
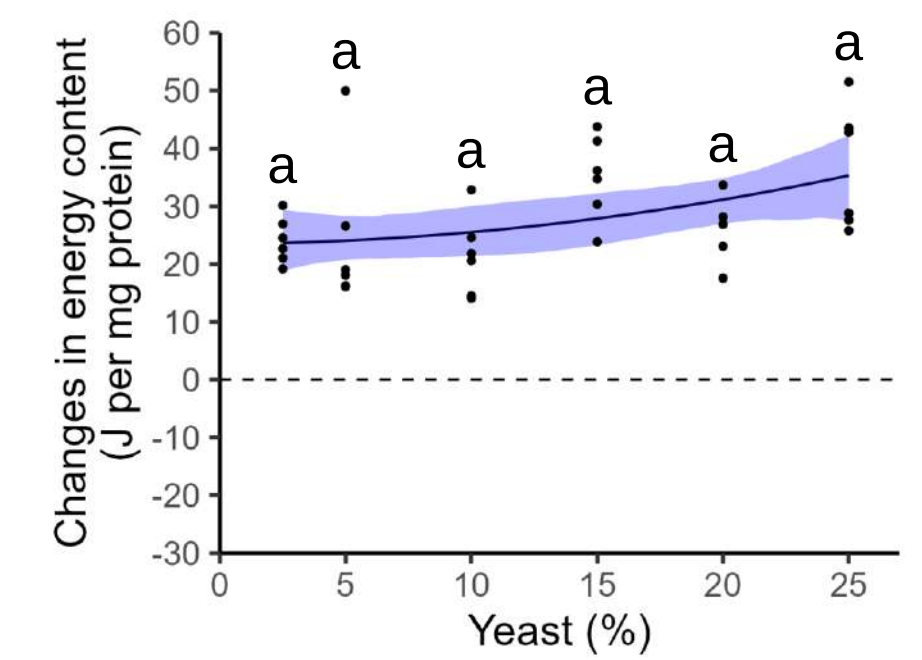
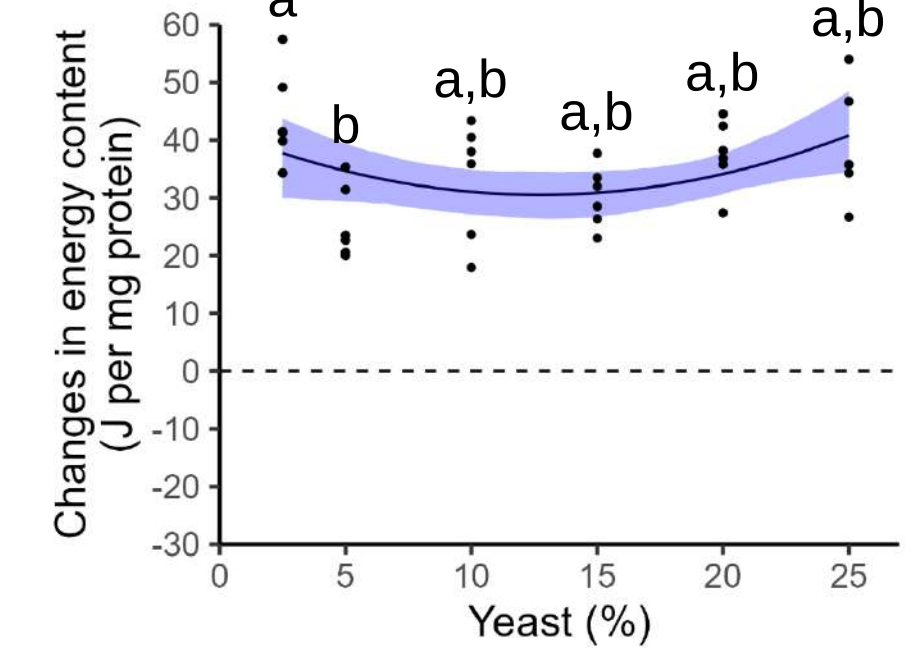
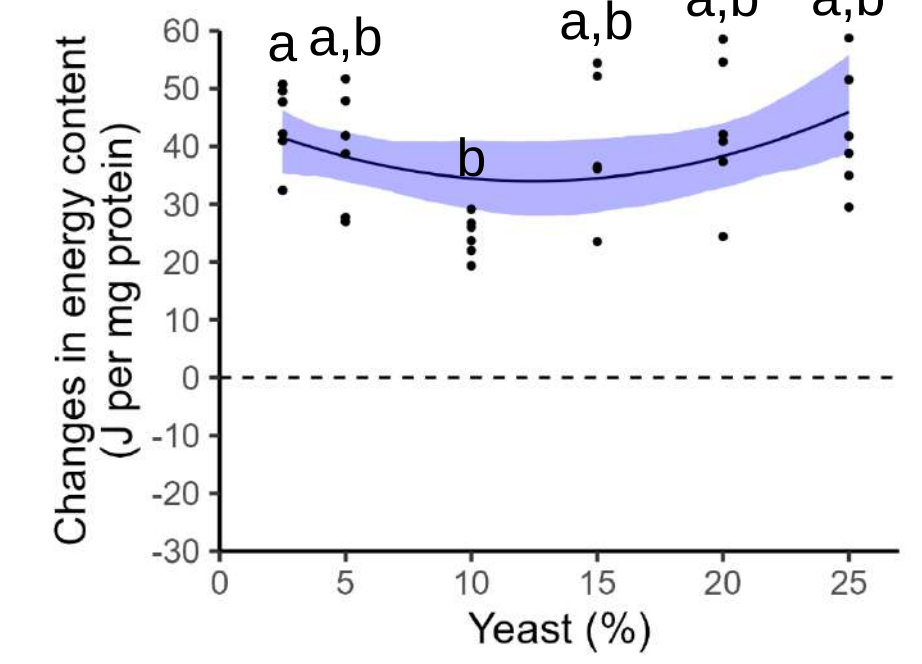


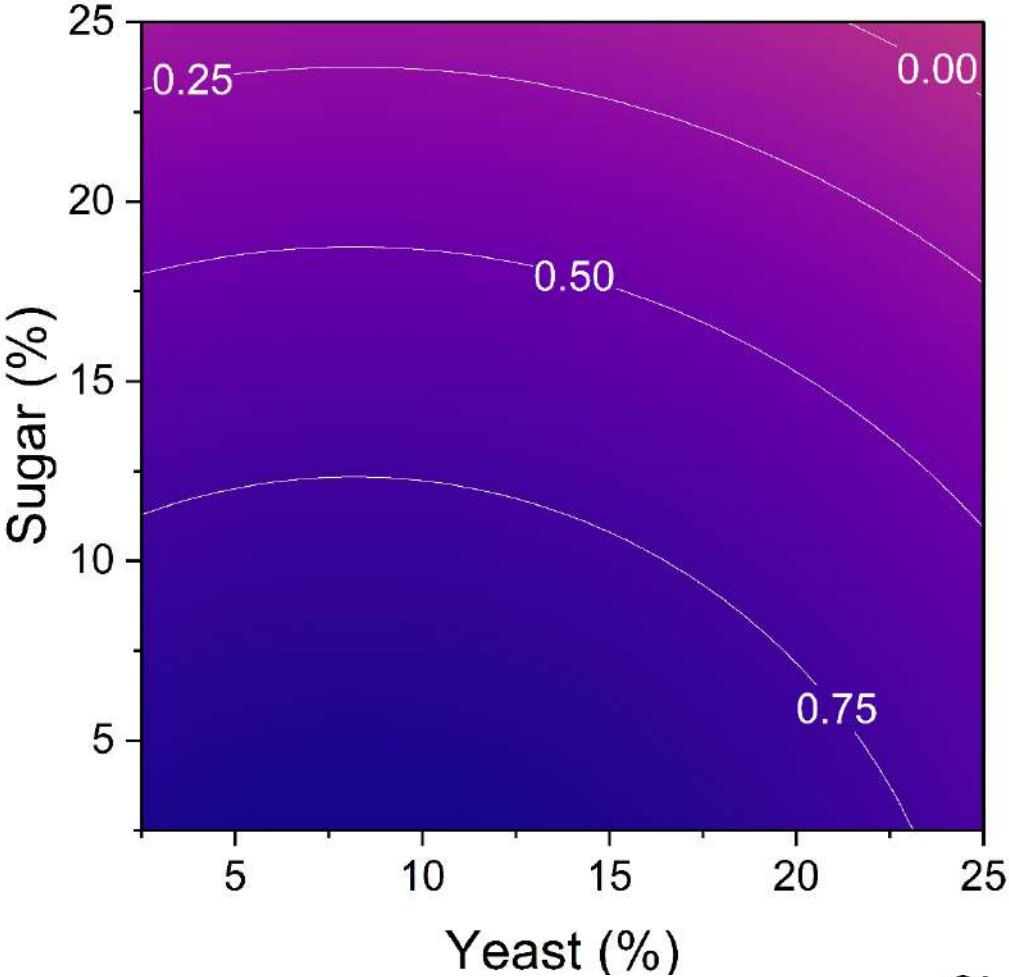
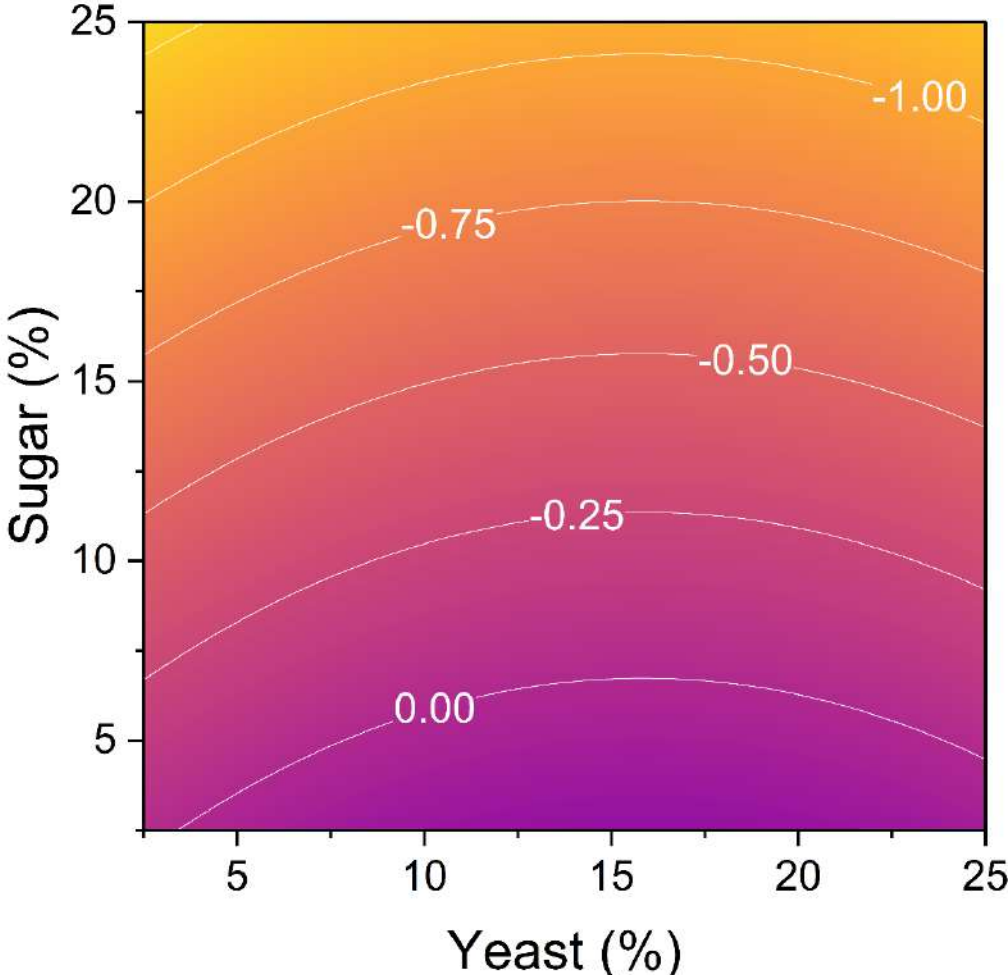
Figure S47.

w^{1118}

SK

Changes in energy
content (J)

Virgin
males



Mated
males

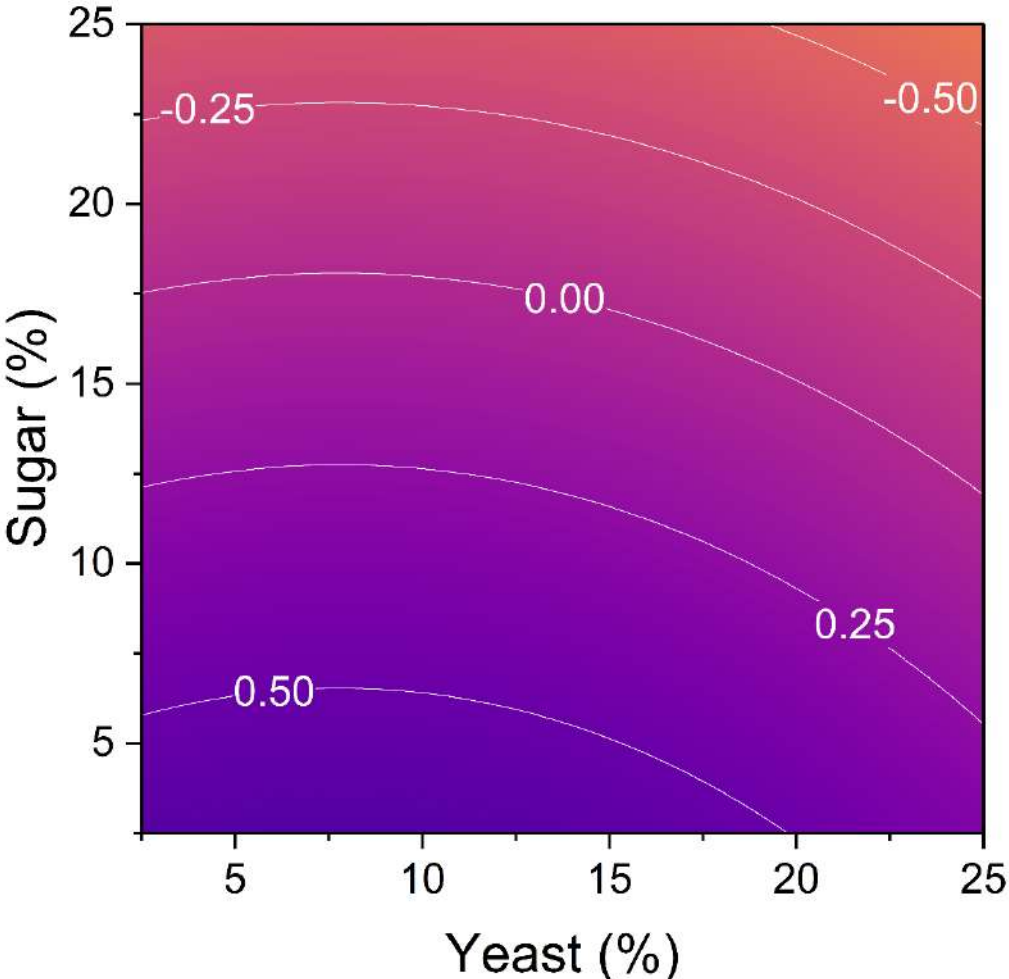
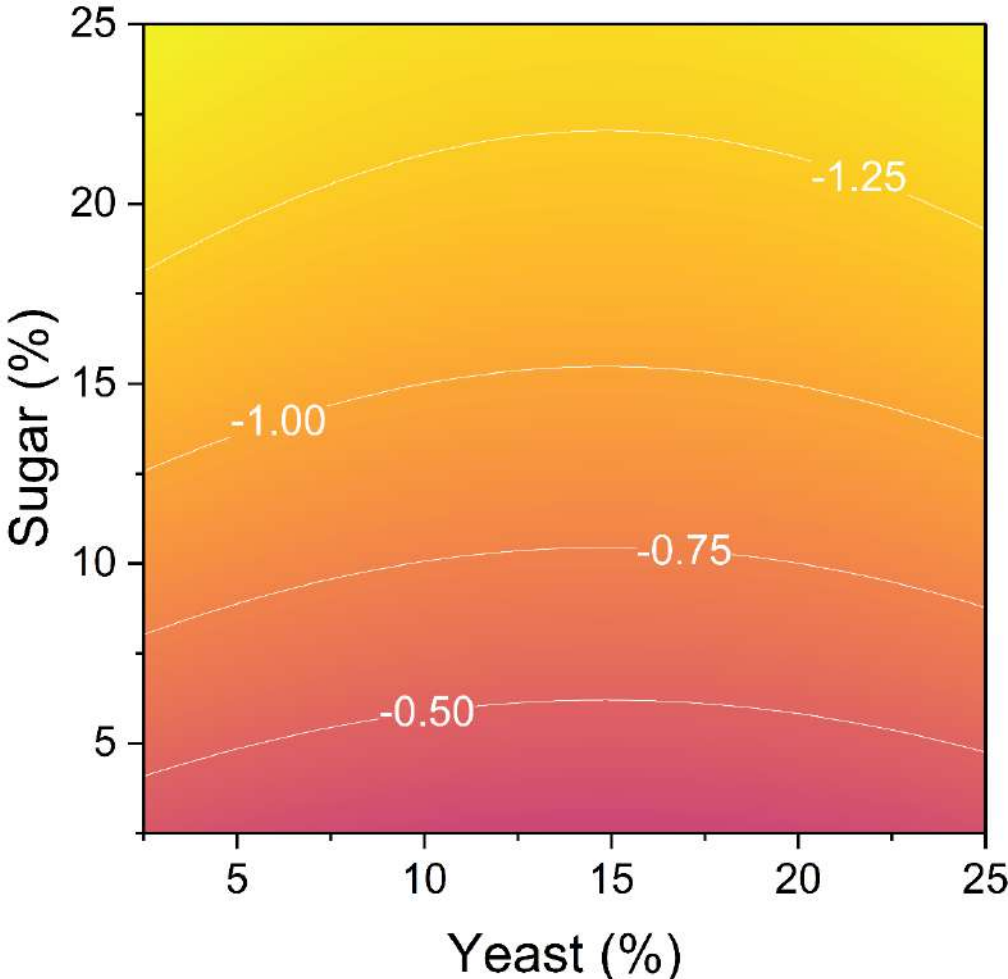


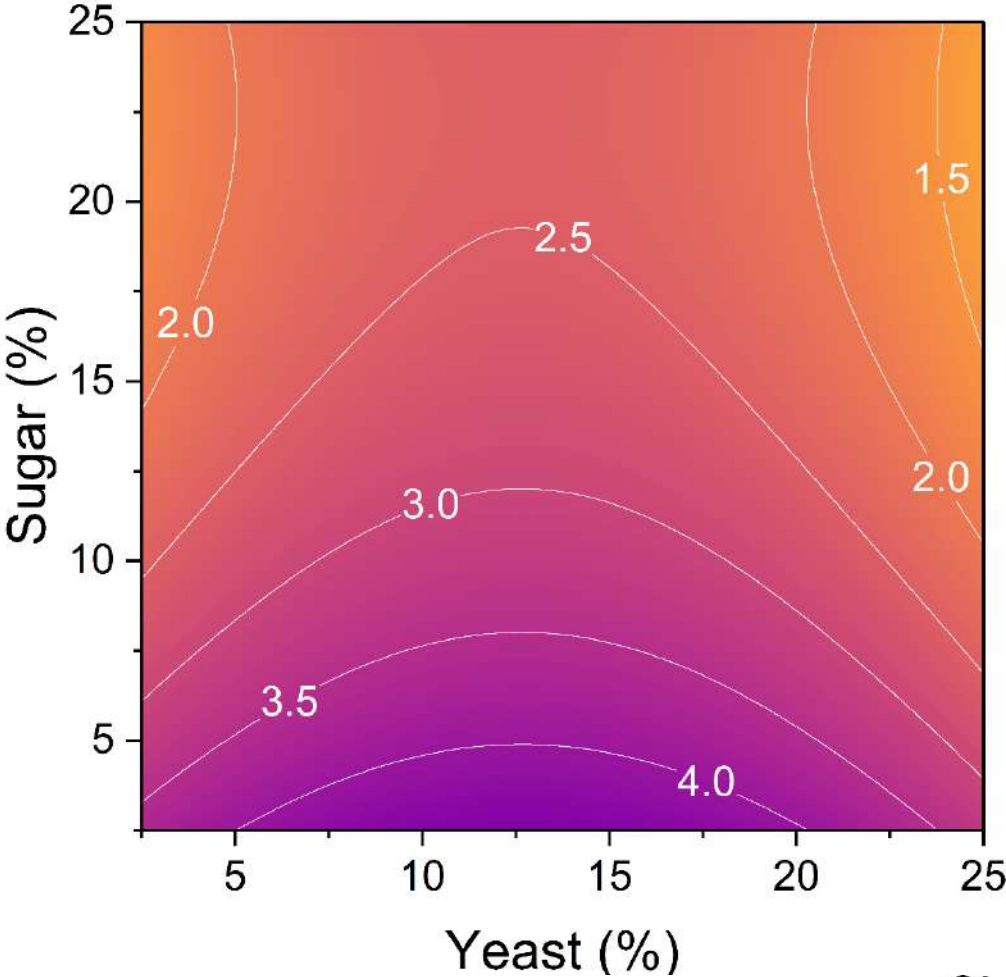
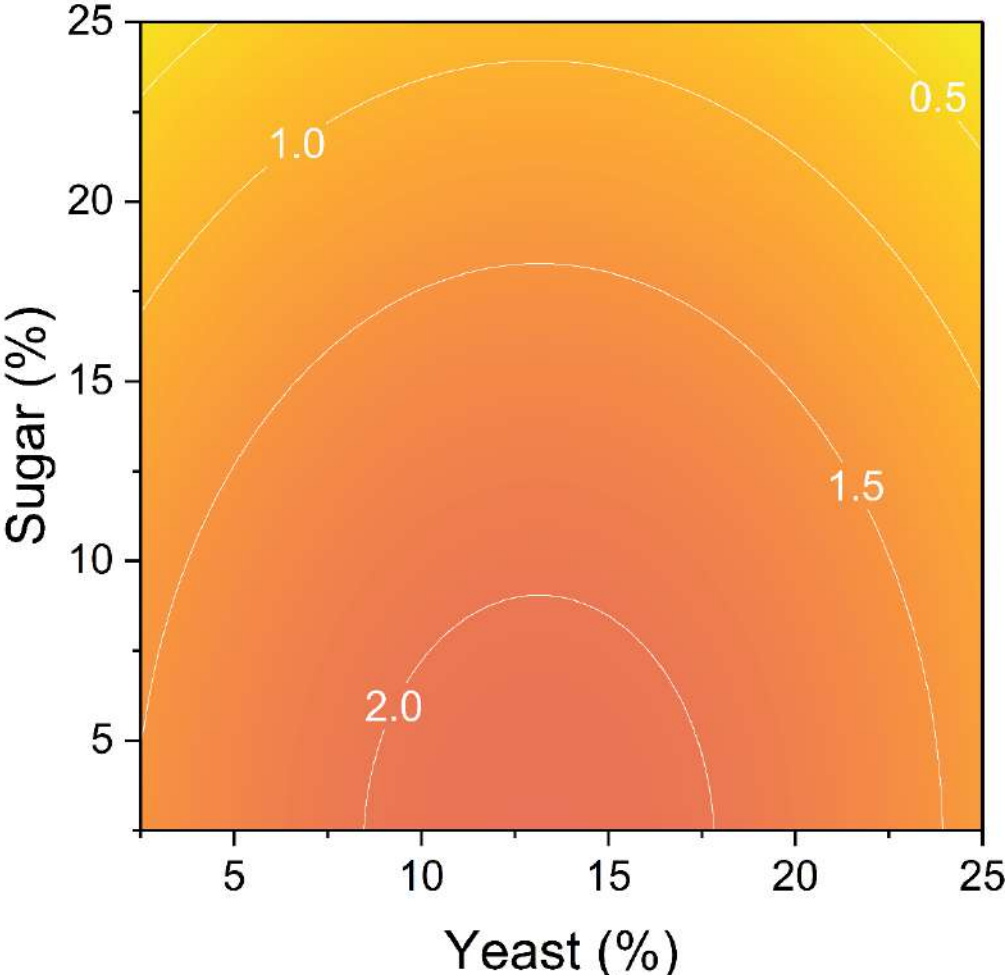
Figure S48.

w^{1118}

SK

Changes in energy
content (J)

Virgin
females



Mated
females

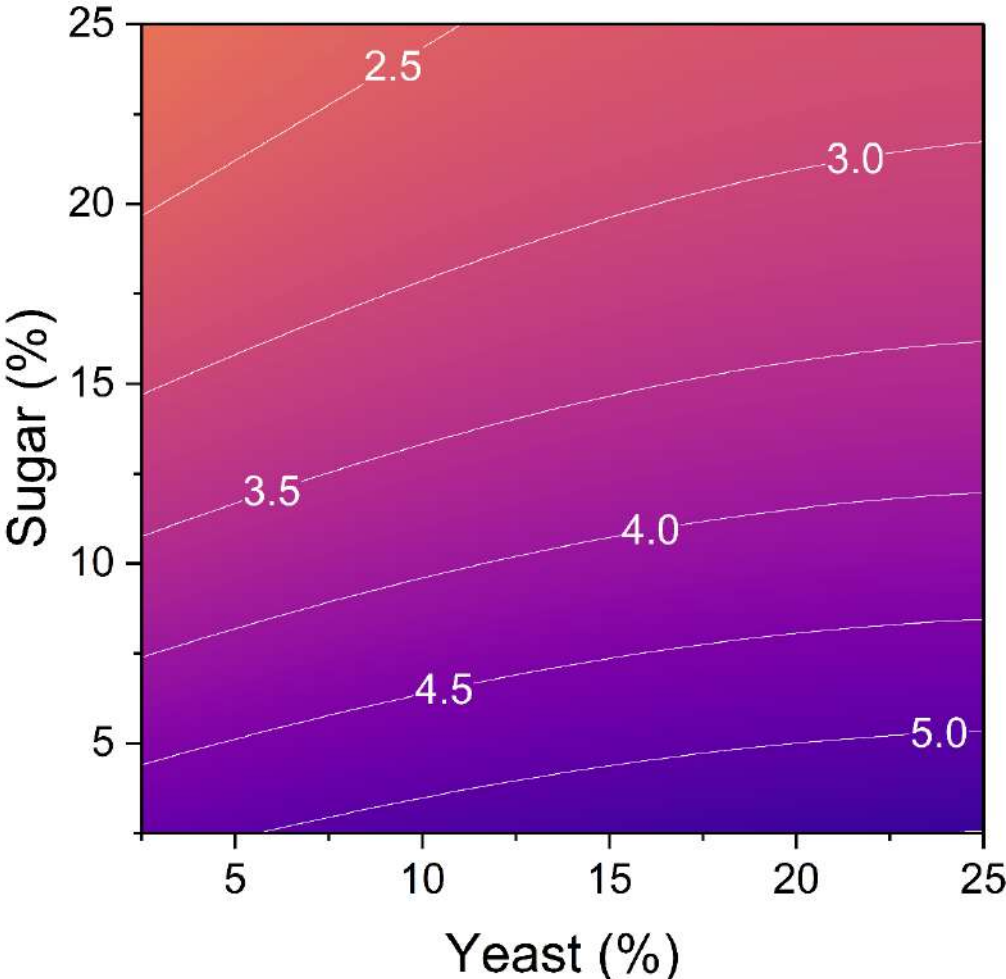
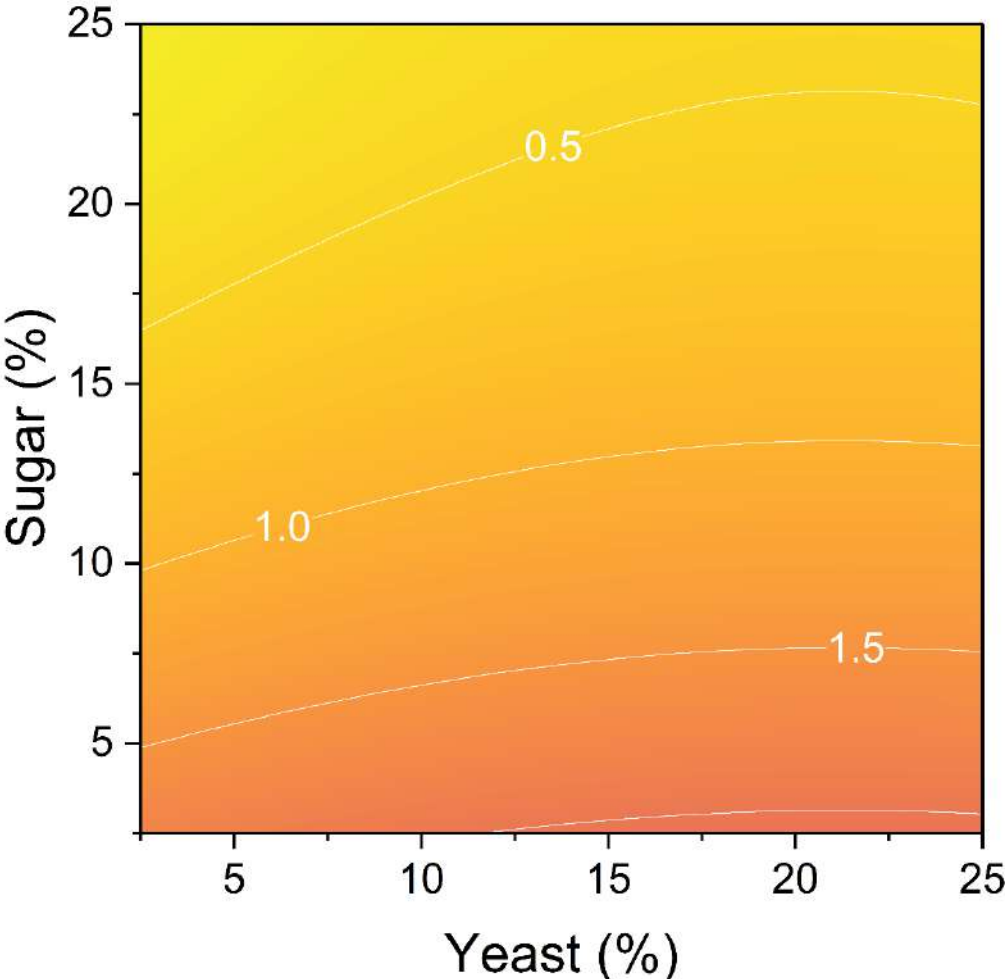
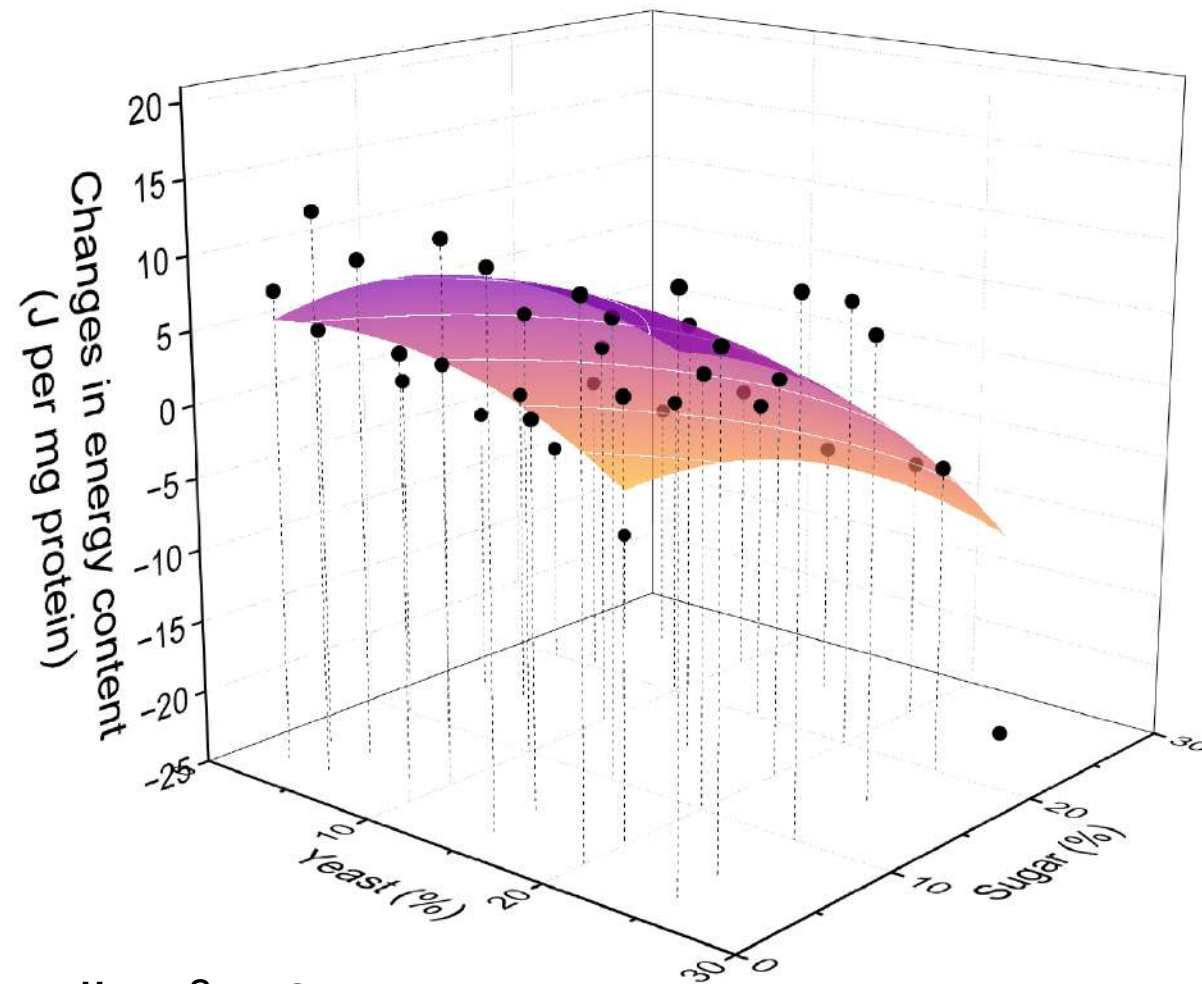


Figure S49.

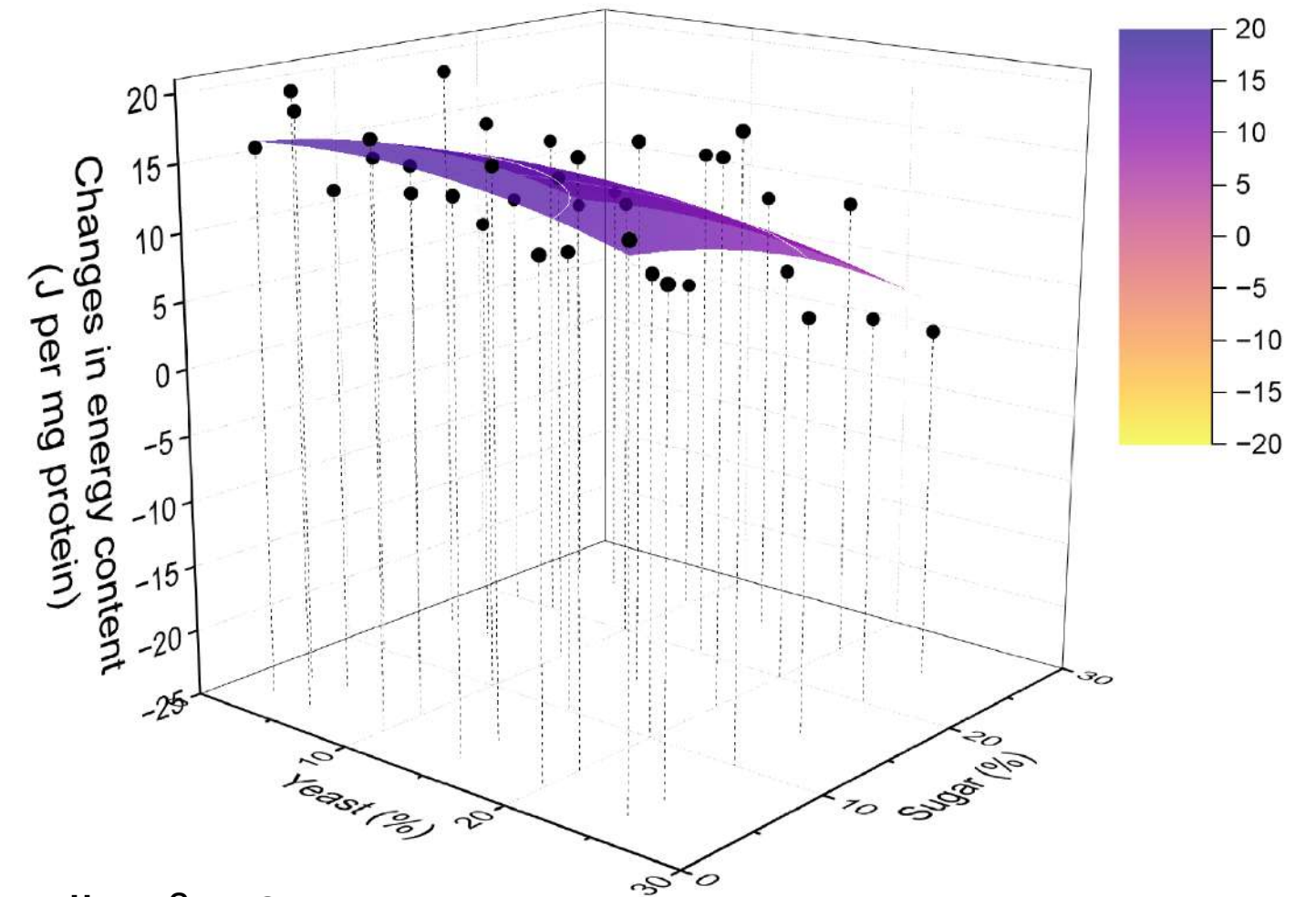
w^{1118}

SK

Virgin
males

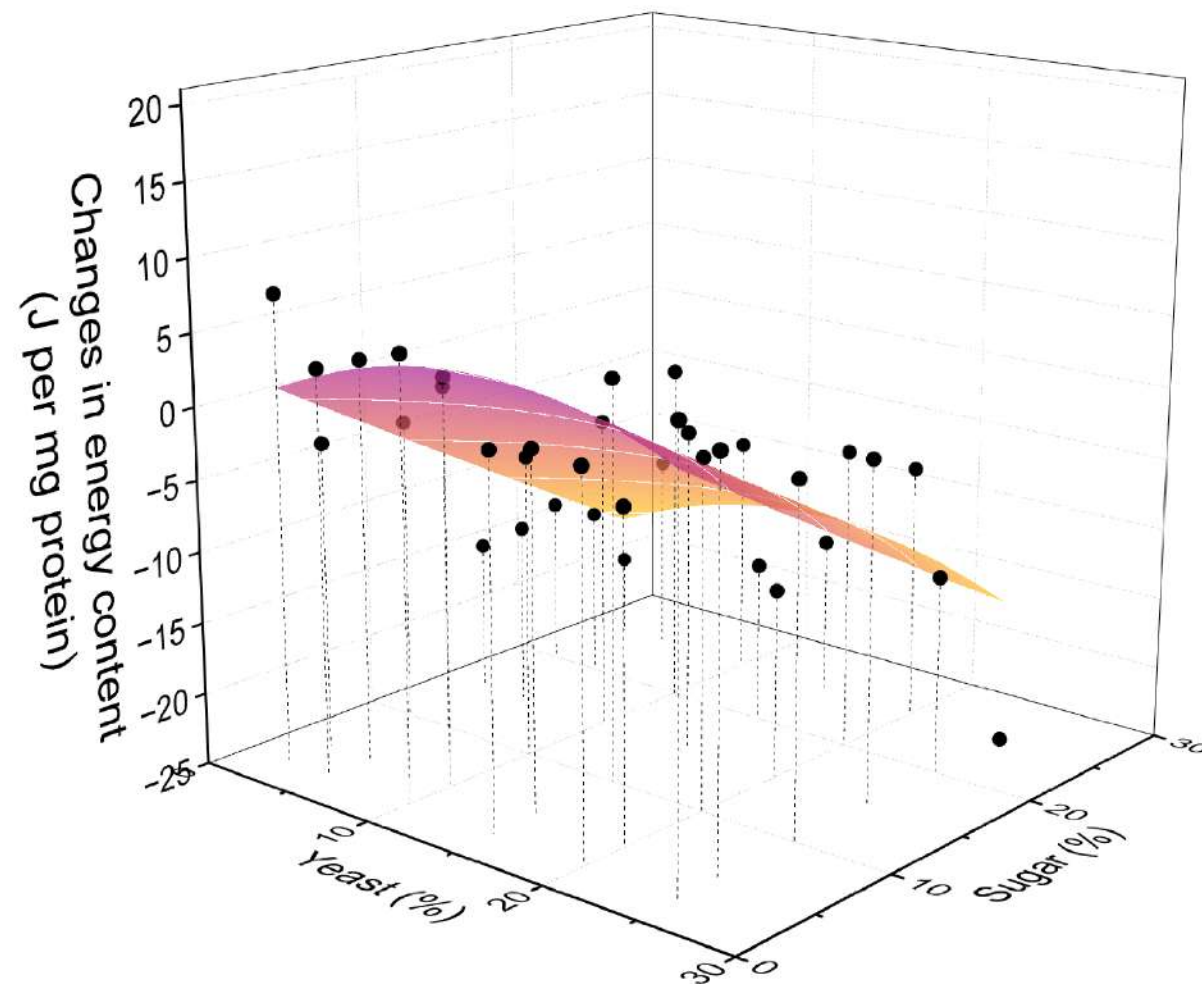


Adj. $R^2 = 0.71$

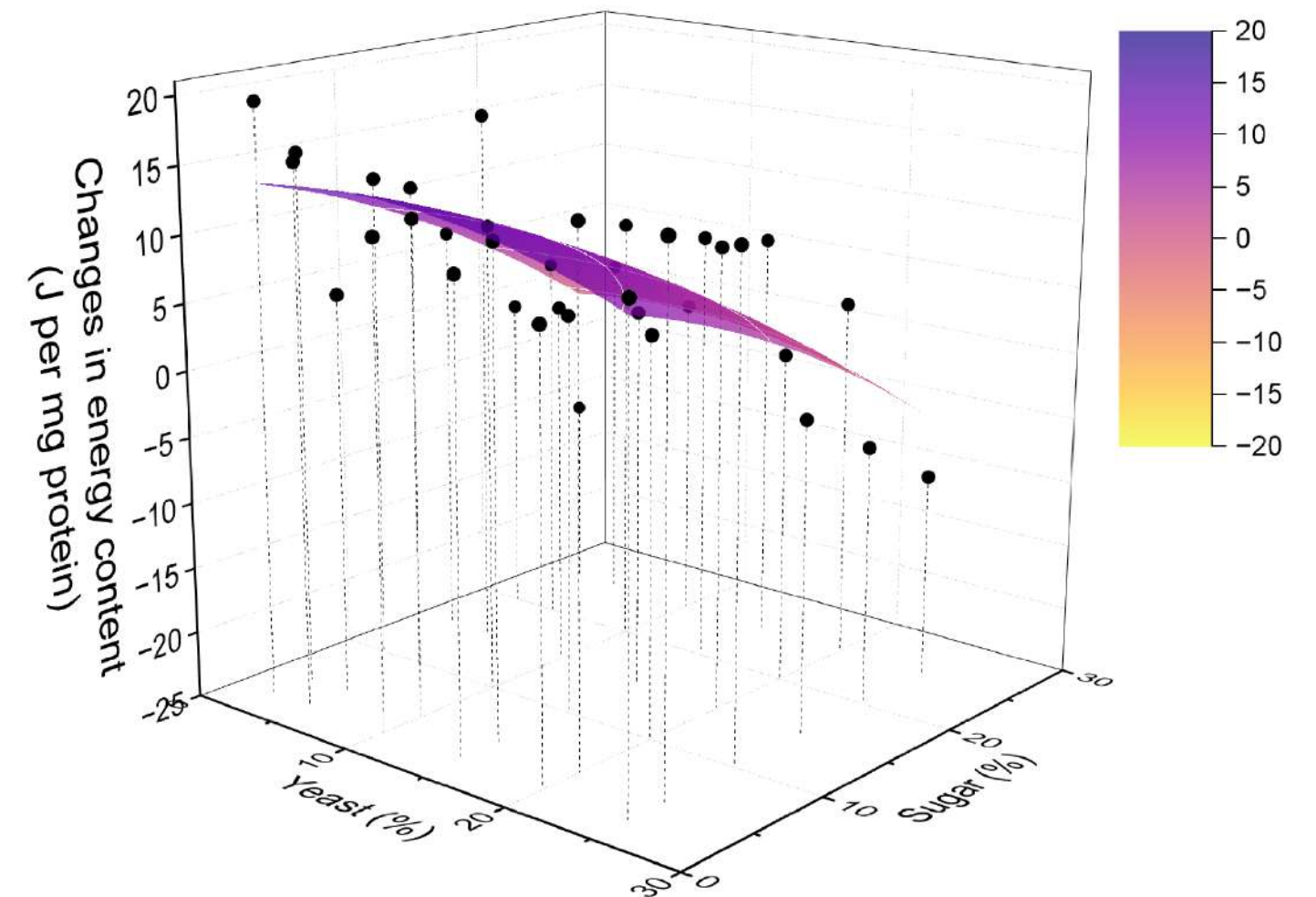


Adj. $R^2 = 0.47$

Mated
males



Adj. $R^2 = 0.65$



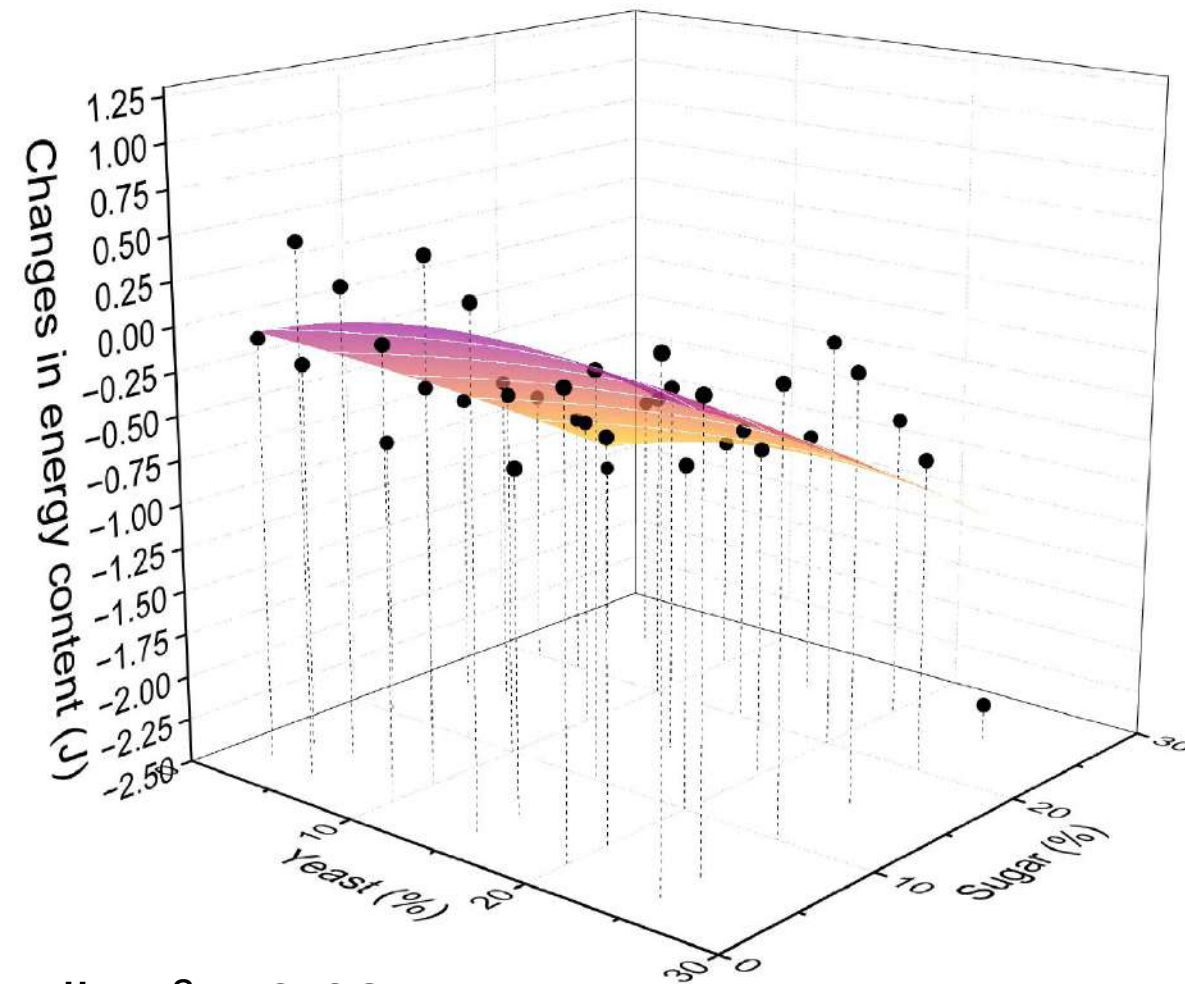
Adj. $R^2 = 0.54$

Figure S50.

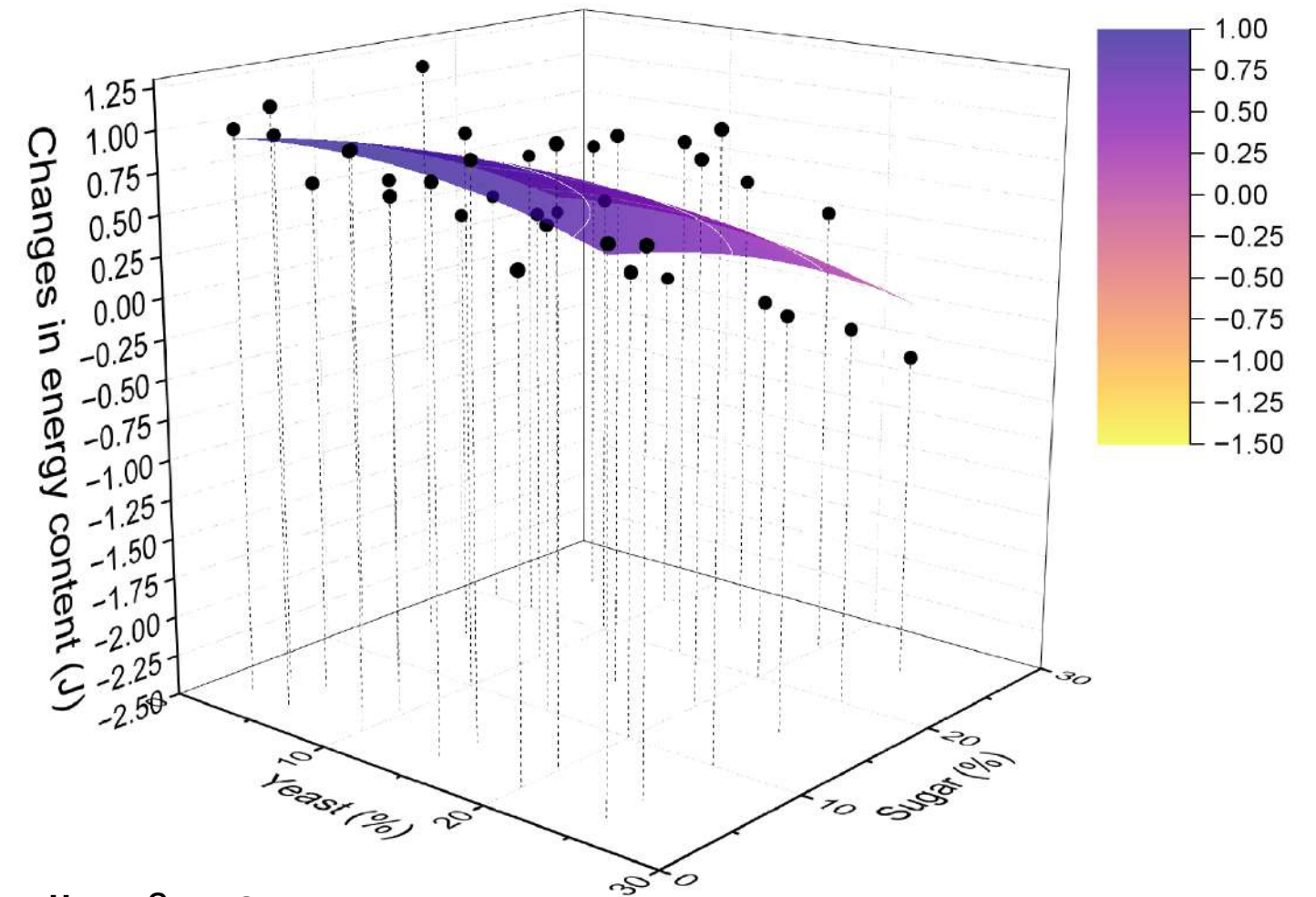
w^{1118}

SK

Virgin
males

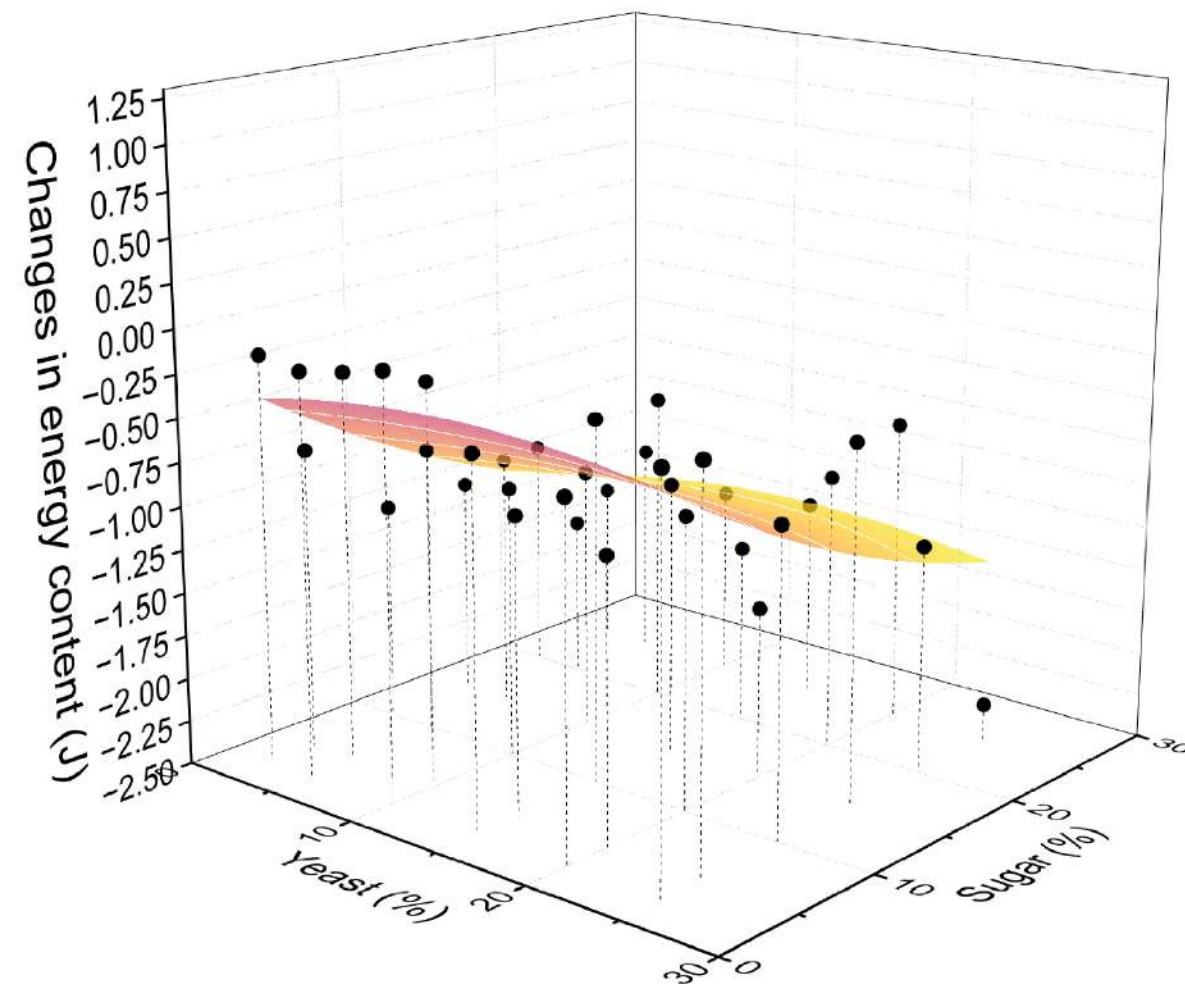


Adj. $R^2 = 0.62$

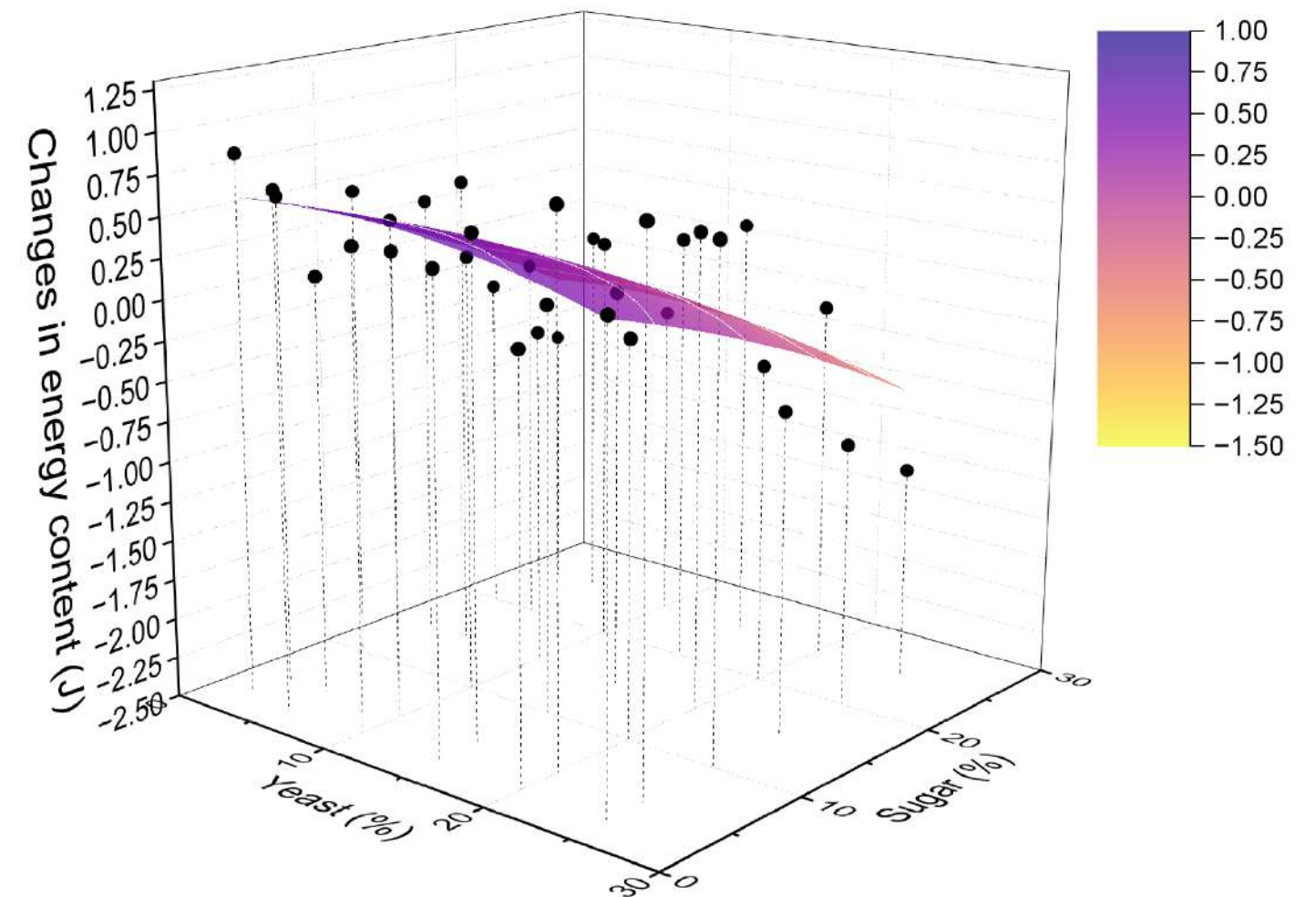


Adj. $R^2 = 0.45$

Mated
males



Adj. $R^2 = 0.57$



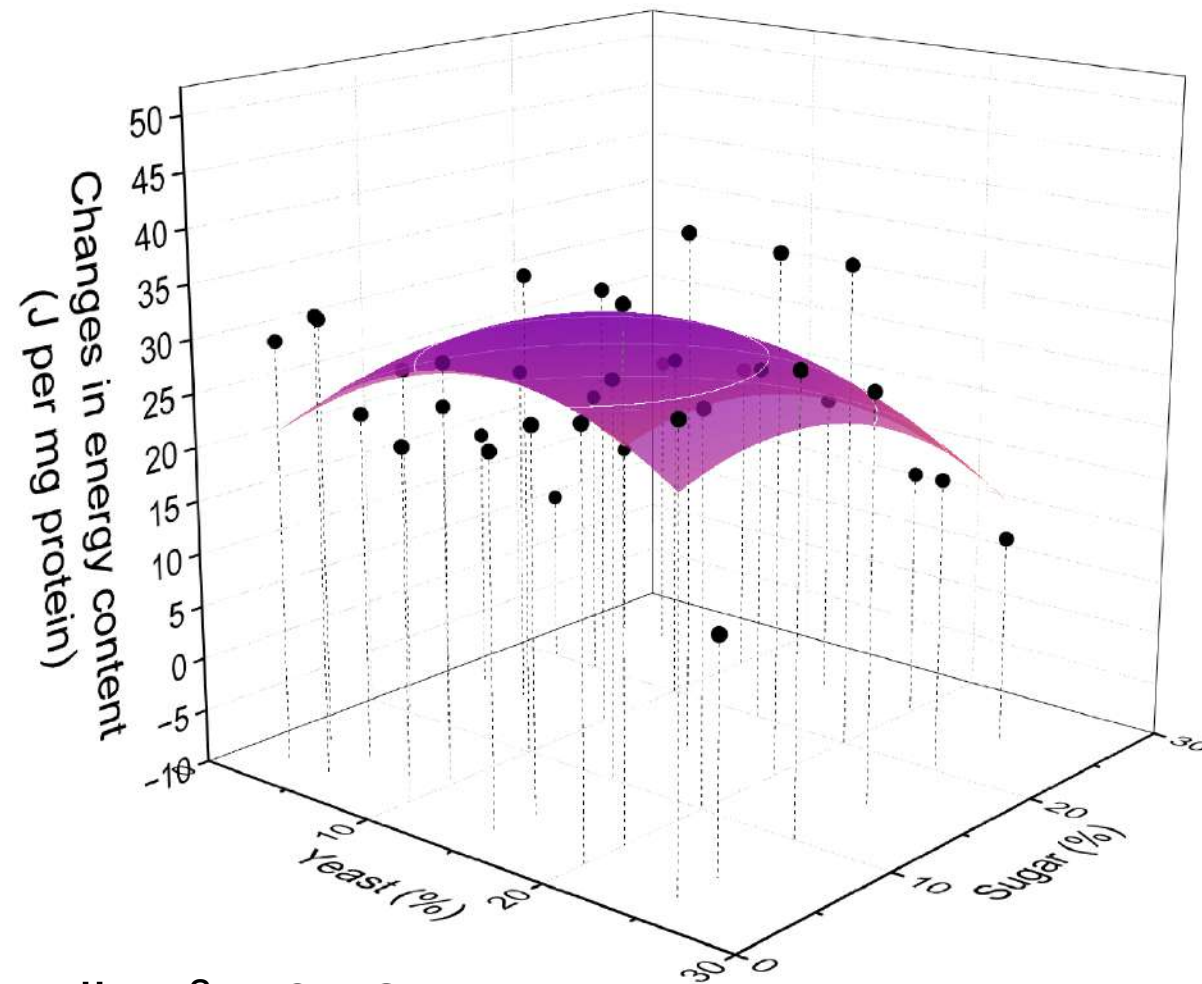
Adj. $R^2 = 0.52$

Figure S51.

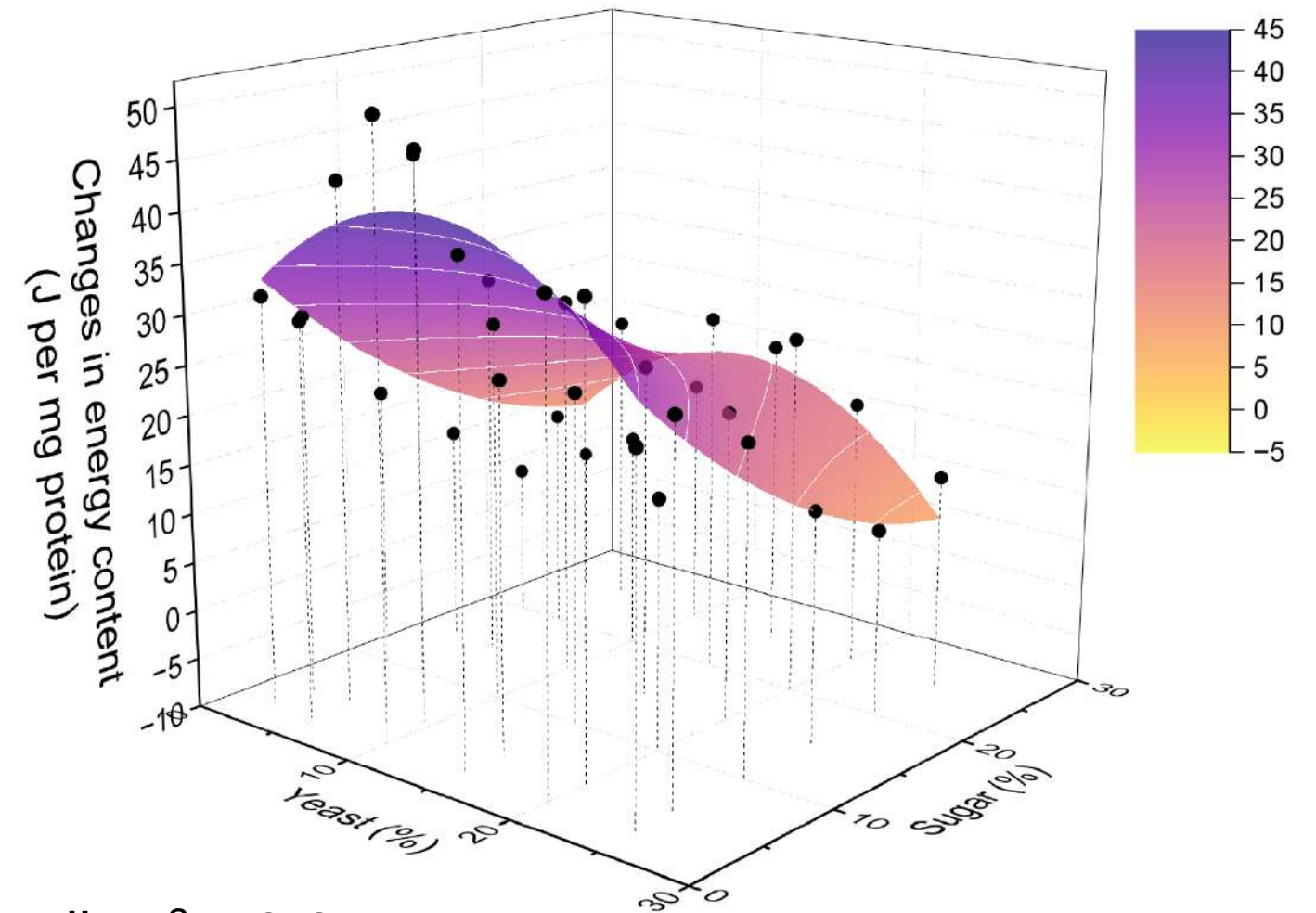
w^{1118}

SK

Virgin
females

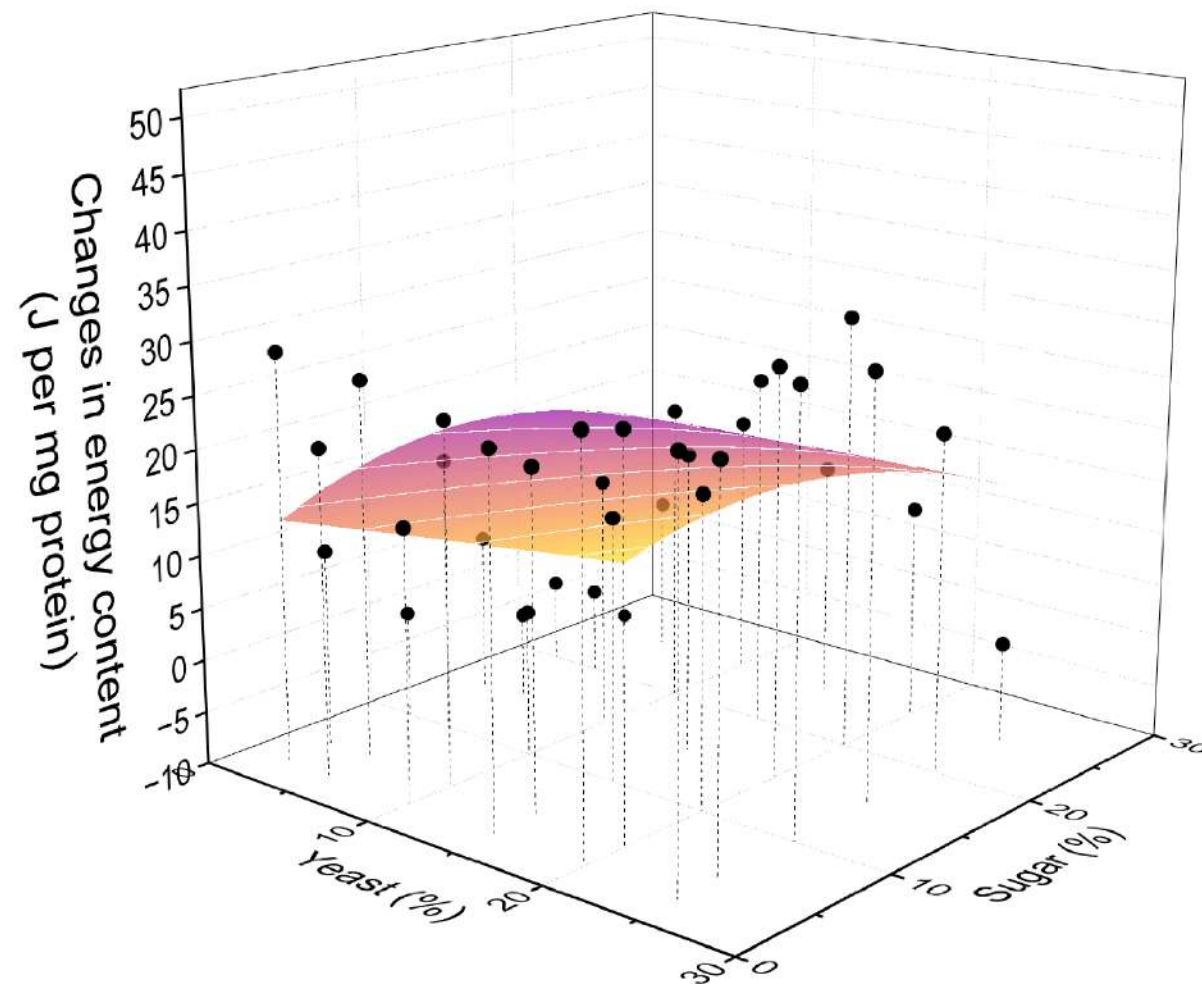


Adj. $R^2 = 0.42$

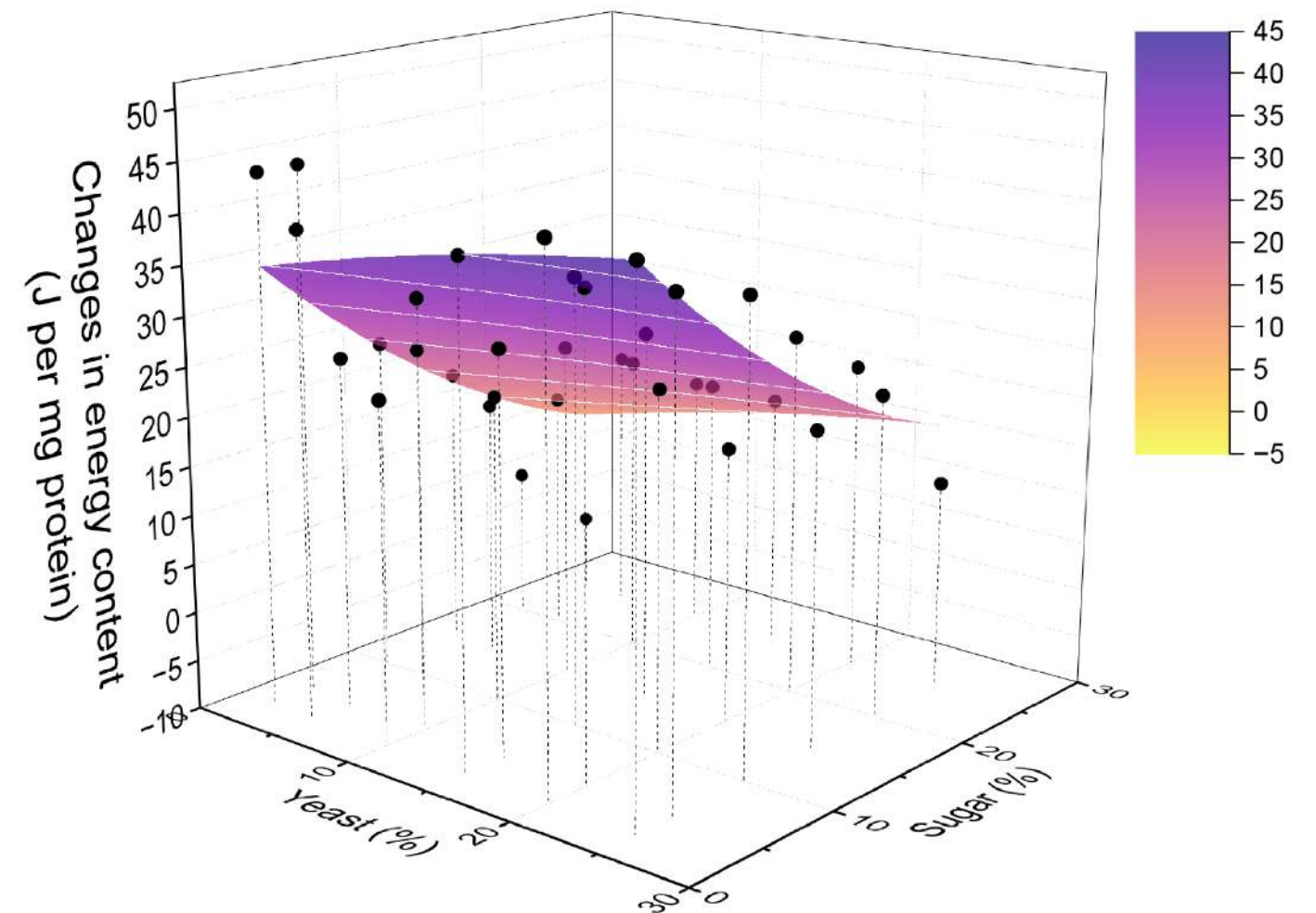


Adj. $R^2 = 0.64$

Mated
females



Adj. $R^2 = 0.55$



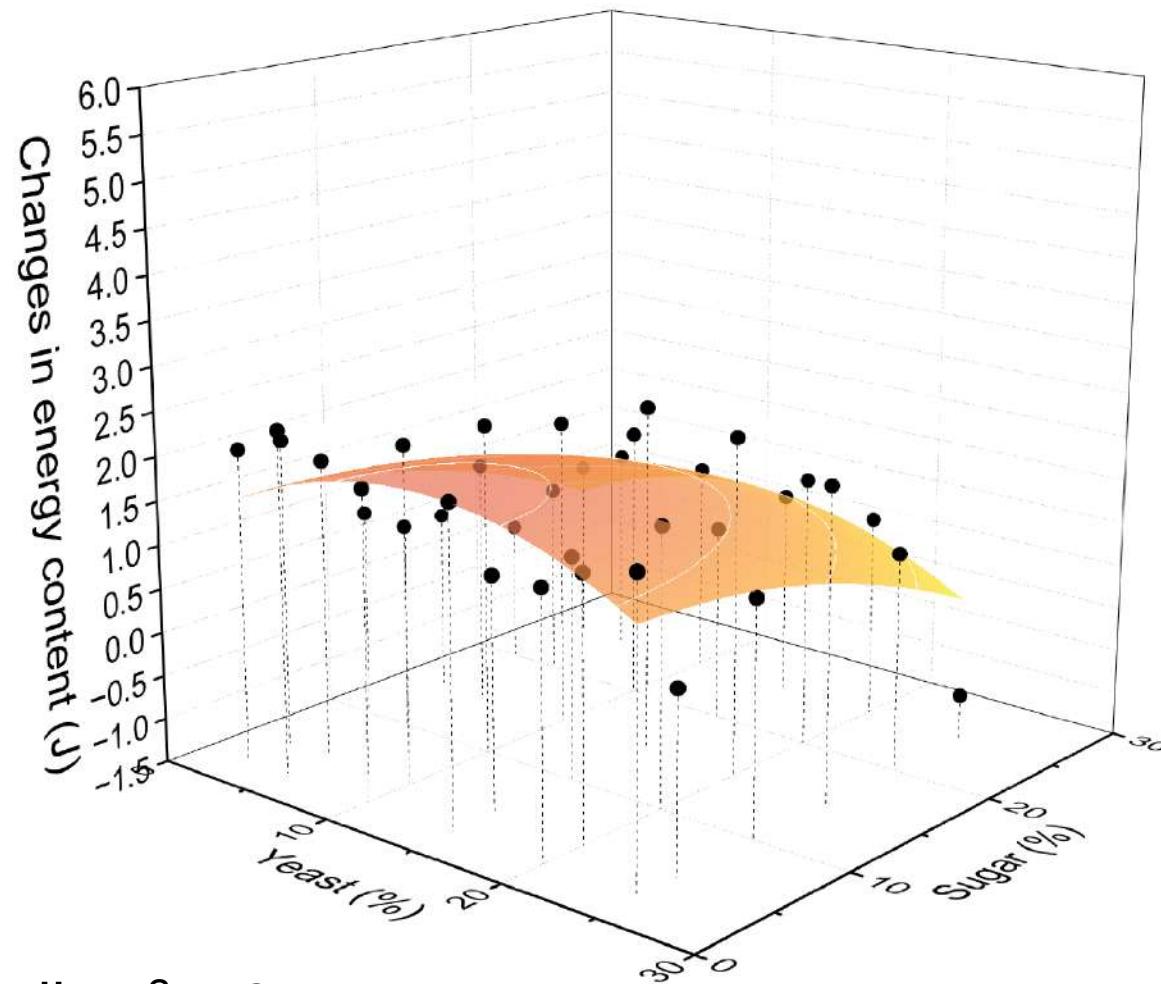
Adj. $R^2 = 0.71$

Figure S52.

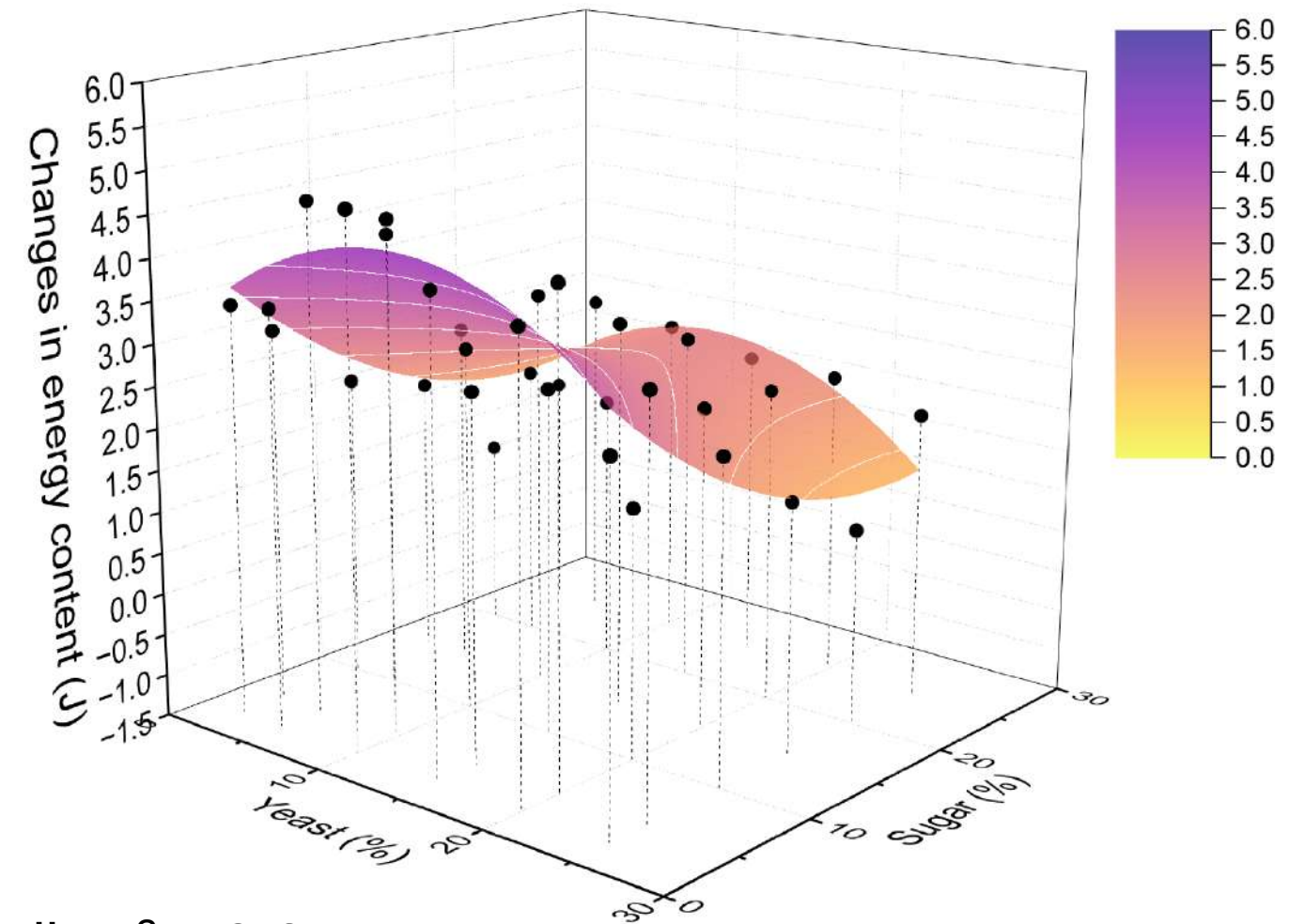
w^{1118}

SK

Virgin
females

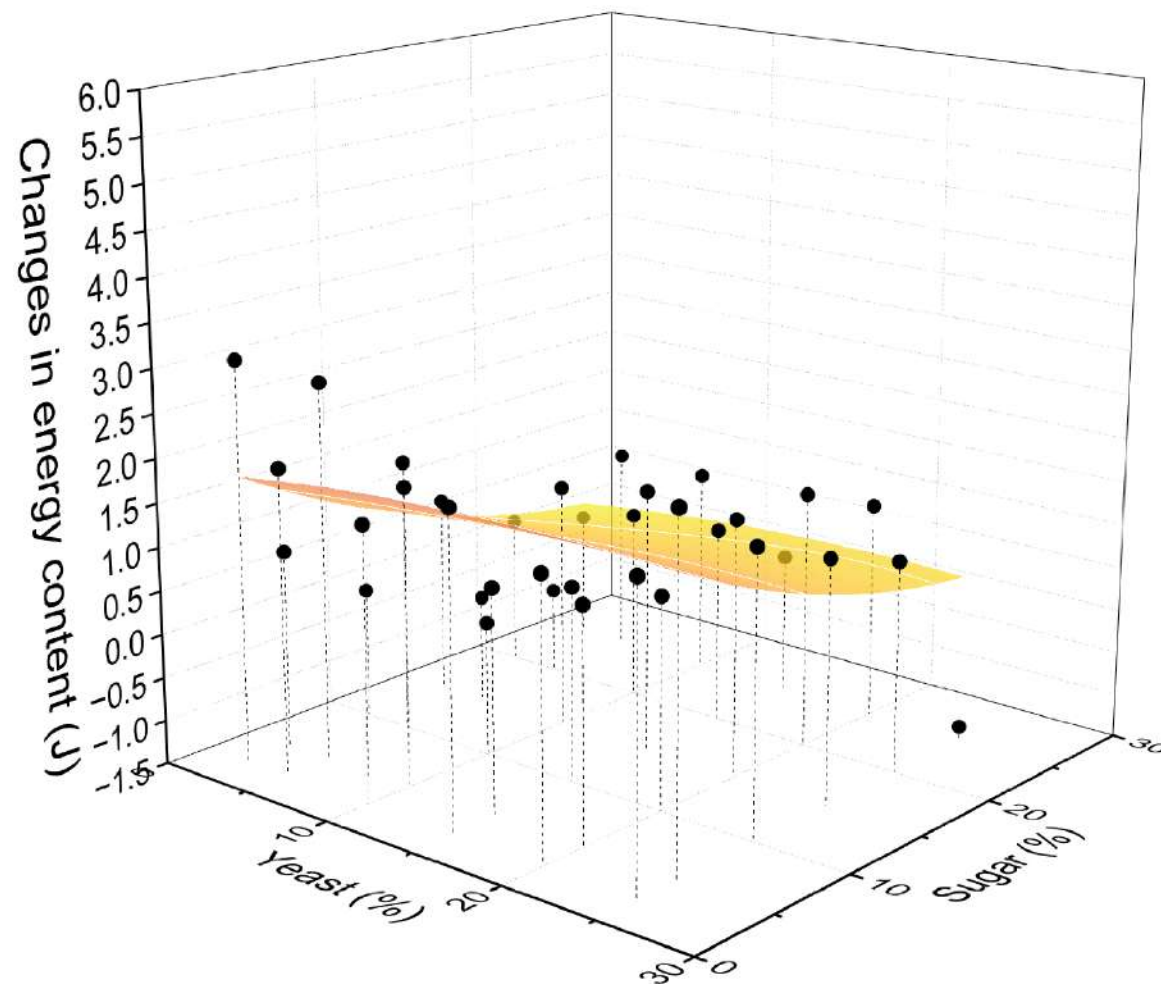


Adj. $R^2 = 0.41$

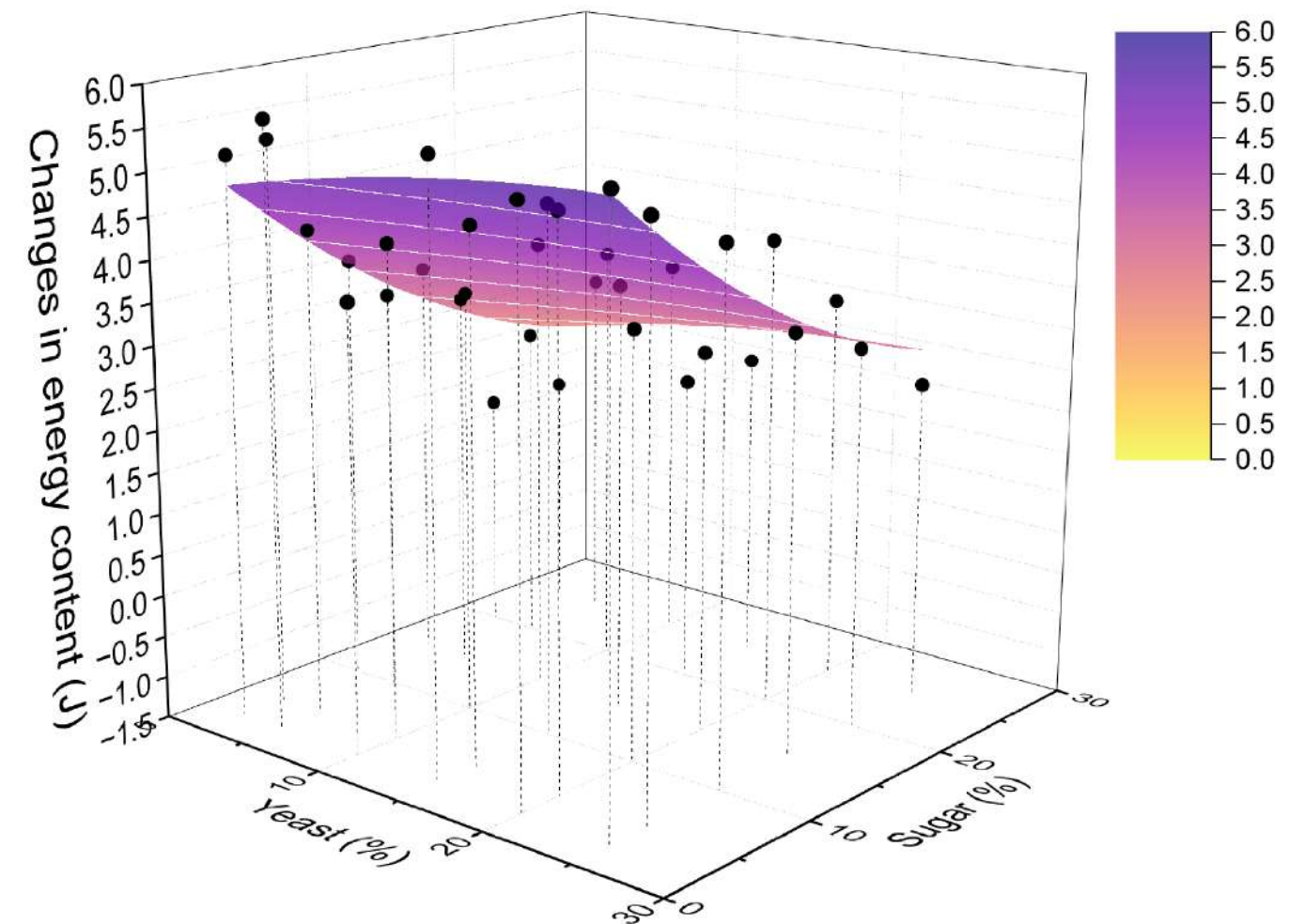


Adj. $R^2 = 0.65$

Mated
females



Adj. $R^2 = 0.37$



Adj. $R^2 = 0.74$

Table S1. Results of multiple linear (polynomial) regression analysis of **protein content (µg per fly) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{9,849} = 554.0$, $p < 0.0001$), with an adjusted R^2 of 0.85.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	23344.2	239.8	< 0.0001
Sex	1	337943.8	3470.9	< 0.0001
Yeast	1	54618.9	561.0	< 0.0001
Sugar	1	37422.9	384.4	< 0.0001
(Yeast) ²	1	31945.1	328.1	< 0.0001
(Sugar) ²	1	1425.3	14.6	0.0001
Sex × Yeast	1	3834.5	39.4	< 0.0001
Population × Yeast	1	2618.4	26.9	< 0.0001
Population × Sugar	1	820.7	8.4	0.0038
Error	849	82663.1	—	—
Total	858	568111.0	—	—

Table S2. Results of generalized linear model (Gamma distribution with log link) of **protein content (µg per fly) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 48.4$, *df* = 9, *p* < 0.0001) and explained ~86% of the null deviance (AIC = 6386.9). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	250.77	< 0.0001
Sex	1	3494.39	< 0.0001
Yeast	1	544.94	< 0.0001
Sugar	1	370.65	< 0.0001
(Yeast) ²	1	306.94	< 0.0001
(Sugar) ²	1	15.73	< 0.0001
Sex × Yeast	1	50.37	< 0.0001
Population × Yeast	1	33.30	< 0.0001
Population × Sugar	1	6.66	0.0099

Table S3. Results of multiple linear (polynomial) regression analysis of **energy content (J per mg protein) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{11,847} = 290.8$, $p < 0.0001$), with an adjusted R^2 of 0.79.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	4339.8	328.8	< 0.0001
Sex	1	938.4	71.1	< 0.0001
Yeast	1	4783.9	362.4	< 0.0001
Sugar	1	29234.1	2214.8	< 0.0001
(Yeast) ²	1	3477.2	263.4	< 0.0001
(Sugar) ²	1	617.5	46.8	< 0.0001
Yeast × Sugar	1	115.9	8.8	0.0031
Sex × Sugar	1	374.2	28.3	< 0.0001
Population × Yeast	1	33.1	2.5	0.11
Population × Sugar	1	16.4	1.2	0.27
Population × Yeast × Sugar	1	100.1	7.6	0.006
Error	847	11179.8	—	—
Total	858	53399.2	—	—

Table S4. Results of generalized linear model (Gamma distribution with log link) of **energy content (J per mg protein) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. The overall model was highly significant (likelihood ratio $\chi^2 = 110.0$, $df = 11$, $p < 0.0001$) and explained ~76% of the null deviance (AIC = 4765.5). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P-value
Population	1	298.62	< 0.0001
Sex	1	77.36	< 0.0001
Yeast	1	321.77	< 0.0001
Sugar	1	1969.63	< 0.0001
(Yeast) ²	1	199.21	< 0.0001
(Sugar) ²	1	85.56	< 0.0001
Yeast $\times$ Sugar	1	24.75	< 0.0001
Sex $\times$ Sugar	1	45.16	< 0.0001
Population $\times$ Yeast	1	9.44	0.0021
Population $\times$ Sugar	1	2.08	0.15
Population $\times$ Yeast $\times$ Sugar	1	12.24	0.0005

Table S5. Results of a 3×3 categorical factorial ANOVA (Yeast: 2.5/10/25%; Sugar: 2.5/10/25%) for **energy content (J per mg protein) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{20,193} = 169.2$, $p < 0.0001$), with an adjusted R^2 of 0.94.

Source of Variation	<i>df</i>	SSQ	<i>F</i>-ratio	<i>P</i>-value
Population	1	1693.3	312.6	< 0.0001
Sex	1	190.8	35.2	< 0.0001
Yeast	2	1062.7	98.1	< 0.0001
Sugar	2	13538.5	1249.1	< 0.0001
Yeast × Sugar	4	908.6	41.9	< 0.0001
Sex × Sugar	2	148.9	13.7	< 0.0001
Population × Yeast	2	173.2	16.0	< 0.0001
Population × Sugar	2	313.0	28.9	< 0.0001
Population × Yeast × Sugar	4	252.5	11.7	< 0.0001
Error	193	1045.5	—	—
Total	213	19374.1	—	—

Table S6. Results of multiple linear (polynomial) regression analysis of **energy content (J per fly) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{10,848} = 182.5$, $p < 0.0001$), with an adjusted R^2 of 0.68.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	12.4	77.1	< 0.0001
Sex	1	65.8	409.4	< 0.0001
Yeast	1	5.1	31.9	< 0.0001
Sugar	1	191.6	1191.5	< 0.0001
(Yeast) ²	1	5.1	31.6	< 0.0001
(Sugar) ²	1	13.6	84.6	< 0.0001
Yeast × Sugar	1	3.0	18.4	< 0.0001
Sex × Yeast	1	0.7	4.3	0.038
Sex × Sugar	1	10.2	63.1	< 0.0001
Population × Sugar	1	0.6	3.8	0.053
Error	848	136.4	—	—
Total	858	429.9	—	—

Table S7. Results of generalized linear model (Gamma distribution with log link) of **energy content (J per fly) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. The overall model was highly significant (likelihood ratio $\chi^2 = 73.9$, *df* = 10, *p* < 0.0001) and explained ~65% of the null deviance (AIC = 945.9). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	86.86	< 0.0001
Sex	1	367.65	< 0.0001
Yeast	1	35.24	< 0.0001
Sugar	1	1140.84	< 0.0001
(Yeast) ²	1	25.30	< 0.0001
(Sugar) ²	1	109.81	< 0.0001
Yeast × Sugar	1	20.17	< 0.0001
Sex × Yeast	1	4.46	0.035
Sex × Sugar	1	30.72	< 0.0001
Population × Sugar	1	6.78	0.009

Table S8. Results of multiple linear (polynomial) regression analysis of **fat content (µg per mg protein) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{11,847} = 241.4$, $p < 0.0001$), with an adjusted R^2 of 0.76.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	3221459	359.1	< 0.0001
Sex	1	773972	86.3	< 0.0001
Yeast	1	3024931	337.2	< 0.0001
Sugar	1	14984855	1670.6	< 0.0001
(Yeast) ²	1	2113521	235.6	< 0.0001
(Sugar) ²	1	223018	24.9	< 0.0001
Yeast × Sugar	1	103491	11.5	0.0007
Sex × Sugar	1	145605	16.2	< 0.0001
Population × Yeast	1	2.8	0.0003	0.99
Population × Sugar	1	5167	0.6	0.45
Population × Yeast × Sugar	1	106230	11.8	0.0006
Error	847	7597367	—	—
Total	858	31415618	—	—

Table S9. Results of generalized linear model (Gamma distribution with log link) of **fat content (µg per mg protein) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 126.2$, *df* = 11, *p* < 0.0001) and explained ~73% of the null deviance (AIC = 10 360.1). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	327.74	< 0.0001
Sex	1	91.46	< 0.0001
Yeast	1	295.76	< 0.0001
Sugar	1	1475.05	< 0.0001
(Yeast) ²	1	176.81	< 0.0001
(Sugar) ²	1	46.12	< 0.0001
Yeast × Sugar	1	26.12	0.0007
Sex × Sugar	1	29.97	< 0.0001
Population × Yeast	1	2.98	0.084
Population × Sugar	1	3.18	0.075
Population × Yeast × Sugar	1	14.56	0.0001

Table S10. Results of multiple linear (polynomial) regression analysis of **fat content (µg per fly) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{12,846} = 122.6$, $p < 0.0001$), with an adjusted R^2 of 0.63.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	13417.2	129.2	< 0.0001
Sex	1	24323.7	234.2	< 0.0001
Yeast	1	5129.8	49.4	< 0.0001
Sugar	1	98753.6	950.8	< 0.0001
(Yeast) ²	1	4359.6	42.0	< 0.0001
(Sugar) ²	1	5169.3	49.8	< 0.0001
Yeast × Sugar	1	2238.2	21.5	< 0.0001
Sex × Yeast	1	365.5	3.5	0.061
Sex × Sugar	1	4195.9	40.4	< 0.0001
Population × Yeast	1	231.1	2.2	0.14
Population × Sugar	1	340.4	3.3	0.071
Population × Yeast × Sugar	1	685.9	6.6	0.010
Error	846	87871.3	—	—
Total	858	240728.9	—	—

Table S11. Results of generalized linear model (Gamma distribution with log link) of **fat content (µg per fly) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 79.1$, *df* = 12, *p* < 0.0001) and explained ~61% of the null deviance (AIC = 6500.0). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	910.49	< 0.0001
Sex	1	209.91	< 0.0001
Yeast	1	135.14	< 0.0001
Sugar	1	50.86	< 0.0001
(Yeast) ²	1	64.41	< 0.0001
(Sugar) ²	1	33.09	< 0.0001
Yeast × Sugar	1	23.33	< 0.0001
Sex × Yeast	1	3.32	0.068
Sex × Sugar	1	21.57	< 0.0001
Population × Yeast	1	0.47	0.49
Population × Sugar	1	7.85	0.0051
Population × Yeast × Sugar	1	7.19	0.007

Table S12. Results of multiple linear (polynomial) regression analysis of **glycogen content (µg per mg protein) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{9,849} = 79.0$, $p < 0.0001$), with an adjusted R^2 of 0.45.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	49021.6	40.4	< 0.0001
Sex	1	1394.6	1.1	0.28
Yeast	1	2007.6	1.7	0.20
Sugar	1	605424.5	499.1	< 0.0001
(Sugar) ²	1	83515.0	68.8	< 0.0001
Yeast × Sugar	1	5637.0	4.6	0.031
Sex × Sugar	1	43938.1	36.2	< 0.0001
Population × Yeast	1	137606.3	113.4	< 0.0001
Population × Sugar	1	4423.8	3.6	0.057
Error	849	1029864.5	—	—
Total	858	1891978.3	—	—

Table S13. Results of generalized linear model (Gamma distribution with log link) of **glycogen content ($\mu\text{g per mg protein}$) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 101.3$, $df = 9$, $p < 0.0001$) and explained ~42% of the null deviance (AIC = 8630.6). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	47.54	< 0.0001
Sex	1	0.59	0.44
Yeast	1	0.22	0.64
Sugar	1	502.89	< 0.0001
(Sugar) ²	1	93.45	< 0.0001
Yeast $\times$ Sugar	1	5.00	0.025
Sex $\times$ Sugar	1	39.09	< 0.0001
Population $\times$ Yeast	1	116.94	< 0.0001
Population $\times$ Sugar	1	6.26	0.012

Table S14. Results of multiple linear (polynomial) regression analysis of **glycogen content (µg per fly) at eclosion**. *df*— degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{11,847} = 79.0$, $p < 0.0001$), with an adjusted R^2 of 0.50.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	1340.8	103.3	< 0.0001
Sex	1	2973.3	229.2	< 0.0001
Yeast	1	719.1	55.4	< 0.0001
Sugar	1	3992.4	307.7	< 0.0001
(Yeast) ²	1	234.7	18.1	< 0.0001
(Sugar) ²	1	1237.4	95.4	< 0.0001
Yeast × Sugar	1	52.7	4.1	0.044
Sex × Yeast	1	31.6	2.4	0.12
Sex × Sugar	1	431.9	33.3	< 0.0001
Population × Yeast	1	1048.4	80.8	< 0.0001
Population × Sugar	1	36.1	2.8	0.096
Error	847	10989.4	—	—
Total	858	22262.7	—	—

Table S15. Results of generalized linear model (Gamma distribution with log link) of **glycogen content ($\mu\text{g per fly}$) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 141.3$, $df = 11$, $p < 0.0001$) and explained ~50% of the null deviance (AIC = 4709.4). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	121.21	< 0.0001
Sex	1	251.85	< 0.0001
Yeast	1	39.79	< 0.0001
Sugar	1	294.74	< 0.0001
(Yeast) ²	1	20.03	< 0.0001
(Sugar) ²	1	111.71	< 0.0001
Yeast $\times$ Sugar	1	6.39	0.012
Sex $\times$ Yeast	1	1.65	0.20
Sex $\times$ Sugar	1	30.95	< 0.0001
Population $\times$ Yeast	1	81.75	< 0.0001
Population $\times$ Sugar	1	3.00	0.083

Table S16. Results of multiple linear (polynomial) regression analysis of **trehalose content (µg per mg protein) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{11,847} = 17.5$, $p < 0.0001$), with an adjusted R^2 of 0.17.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	1781.5	9.3	0.0024
Sex	1	507.3	2.6	0.10
Yeast	1	6052.5	31.6	< 0.0001
Sugar	1	17528.6	91.4	< 0.0001
(Yeast) ²	1	1144.2	6.0	0.015
(Sugar) ²	1	5347.0	27.9	< 0.0001
Yeast × Sugar	1	1409.5	7.4	0.0068
Sex × Sugar	1	1232.5	6.4	0.011
Population × Yeast	1	3830.8	20.0	< 0.0001
Population × Sugar	1	750.8	3.9	0.048
Population × Yeast × Sugar	1	1024.3	5.3	0.021
Error	847	162389.0	—	—
Total	858	199316.0	—	—

Table S17. Results of generalized linear model (Gamma distribution with log link) of **trehalose content ($\mu\text{g per mg protein}$) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 34.8$, $df = 11$, $p = 0.0001$) and explained ~16% of the null deviance (AIC = 7099.6). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	8.27	0.004
Sex	1	2.86	0.091
Yeast	1	24.60	< 0.0001
Sugar	1	123.59	< 0.0001
(Yeast) ²	1	3.78	0.052
(Sugar) ²	1	29.50	< 0.0001
Yeast $\times$ Sugar	1	8.84	0.003
Sex $\times$ Sugar	1	9.13	0.0025
Population $\times$ Yeast	1	21.84	< 0.0001
Population $\times$ Sugar	1	7.33	0.0068
Population $\times$ Yeast $\times$ Sugar	1	5.23	0.022

Table S18. Results of multiple linear (polynomial) regression analysis of **trehalose content (µg per fly) at eclosion**. *df*— degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{12,846} = 46.5$, $p < 0.0001$), with an adjusted R^2 of 0.39.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	99.9	53.9	< 0.0001
Sex	1	472.4	255.0	< 0.0001
Yeast	1	238.1	128.5	< 0.0001
Sugar	1	56.1	30.3	< 0.0001
(Yeast) ²	1	77.6	41.9	< 0.0001
(Sugar) ²	1	88.1	47.5	< 0.0001
Yeast × Sugar	1	16.3	8.8	0.0031
Sex × Yeast	1	7.2	3.9	0.049
Sex × Sugar	1	9.9	5.3	0.021
Population × Yeast	1	14.9	8.1	0.0047
Population × Sugar	1	3.8	2.0	0.16
Population × Yeast × Sugar	1	9.9	5.4	0.021
Error	846	1567.5	—	—
Total	858	2600.8	—	—

Table S19. Results of generalized linear model (Gamma distribution with log link) of **trehalose content (µg per fly) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 89.4$, *df* = 12, *p* < 0.0001) and explained ~34% of the null deviance (AIC = 3104.0). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	47.64	< 0.0001
Sex	1	270.88	< 0.0001
Yeast	1	117.72	< 0.0001
Sugar	1	43.09	< 0.0001
(Yeast) ²	1	40.13	< 0.0001
(Sugar) ²	1	43.56	< 0.0001
Yeast × Sugar	1	12.61	0.0004
Sex × Yeast	1	1.14	0.29
Sex × Sugar	1	7.37	0.0066
Population × Yeast	1	10.73	0.0011
Population × Sugar	1	4.37	0.037
Population × Yeast × Sugar	1	4.90	0.027

Table S20. Results of multiple linear (polynomial) regression analysis of **glucose content (μg per mg protein) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{10,848} = 16.7$, $p < 0.0001$), with an adjusted R^2 of 0.15.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	450.3	4.8	0.029
Sex	1	2511.3	26.9	< 0.0001
Yeast	1	1409.1	15.1	0.0001
Sugar	1	5459.5	58.4	< 0.0001
(Sugar) ²	1	298.8	3.2	0.074
Yeast $\times$ Sugar	1	862.6	9.2	0.0025
Sex $\times$ Sugar	1	891.4	9.5	0.0021
Population $\times$ Yeast	1	169.8	1.8	0.18
Population $\times$ Sugar	1	1097.7	11.7	0.0006
Population $\times$ Yeast $\times$ Sugar	1	2825.7	30.2	< 0.0001
Error	848	79300.9	—	—
Total	858	94892.5	—	—

Table S21. Results of generalized linear model (Gamma distribution with log link) of **glucose content ($\mu\text{g per mg protein}$) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 198.8$, $df = 10$, $p < 0.0001$) and explained ~6% of the null deviance (AIC = 5277.3). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	8.41	0.0037
Sex	1	38.64	< 0.0001
Yeast	1	45.97	< 0.0001
Sugar	1	100.75	< 0.0001
(Sugar) ²	1	13.64	0.0002
Yeast $\times$ Sugar	1	28.37	< 0.0001
Sex $\times$ Sugar	1	13.30	0.0003
Population $\times$ Yeast	1	1.30	0.25
Population $\times$ Sugar	1	10.63	0.0011
Population $\times$ Yeast $\times$ Sugar	1	33.55	< 0.0001

Table S22. Results of multiple linear (polynomial) regression analysis of **glucose content (µg per fly) at eclosion**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. The overall model was statistically significant ($F_{11,847} = 22.2$, $p < 0.0001$), with an adjusted R^2 of 0.21.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	0.1	0.08	0.78
Sex	1	133.6	113.6	< 0.0001
Yeast	1	3.0	2.5	0.11
Sugar	1	50.5	42.9	< 0.0001
(Yeast) ²	1	9.9	8.5	0.0037
(Sugar) ²	1	9.8	8.3	0.0040
Yeast × Sugar	1	12.0	10.2	0.0014
Sex × Sugar	1	14.6	12.5	0.0004
Population × Yeast	1	3.8	3.2	0.073
Population × Sugar	1	17.6	14.9	0.0001
Population × Yeast × Sugar	1	36.8	31.3	< 0.0001
Error	847	995.7	—	—
Total	858	1283.0	—	—

Table S23. Results of generalized linear model (Gamma distribution with log link) of **glucose content ($\mu\text{g per fly}$) at eclosion**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. The overall model was significant (likelihood ratio $\chi^2 = 262.8$, $df = 11$, $p < 0.0001$) and explained $\sim 10\%$ of the null deviance ($AIC = 1782.5$). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	0.34	0.56
Sex	1	168.01	< 0.0001
Yeast	1	16.95	< 0.0001
Sugar	1	57.54	< 0.0001
(Yeast) ²	1	10.32	0.0013
(Sugar) ²	1	8.3	0.0040
Yeast $\times$ Sugar	1	10.2	< 0.0001
Sex $\times$ Sugar	1	11.26	0.0008
Population $\times$ Yeast	1	4.09	0.043
Population $\times$ Sugar	1	14.42	0.0002
Population $\times$ Yeast $\times$ Sugar	1	36.19	< 0.0001

Table S24. Energy-weighted PCA at eclosion – variance explained. PCA on covariance matrix of energy equivalents ($\text{J}\cdot\text{mg}^{-1}$ protein); variables centered, not scaled.

PC	Eigenvalue	Proportion	Cumulative
PC1	60.51	0.9843	0.9843
PC2	0.88	0.0143	0.9986
PC3	0.05	0.0008	0.9993
PC4	0.04	0.0007	1

Table S25. Energy-weighted PCA in 10-day old flies - component loadings. PCA on covariance matrix of energy equivalents ($\text{J}\cdot\text{mg}^{-1}$ protein); variables centered, not scaled.

Metabolite	PC1	PC2	PC3	PC4
Fat	-0.9997	0.0225	-0.0018	0.0020
Glycogen	-0.0222	-0.9773	0.2062	0.0443
Trehalose	-0.0018	-0.1812	-0.9285	0.3241
Glucose	-0.0038	-0.1079	-0.3088	-0.9450

Table S26. Results of multiple linear (polynomial) regression analysis of **protein content (μg per fly) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{14,1707} = 1081.5$, $p < 0.0001$), with an adjusted R^2 of 0.90.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	258187.6	3546.5	< 0.0001
Sex	1	808315.8	11103.2	< 0.0001
Status	1	1362.8	18.7	< 0.0001
Yeast	1	691.9	9.5	0.0021
Sugar	1	6429.3	88.3	< 0.0001
(Yeast) ²	1	7507.7	103.1	< 0.0001
(Sugar) ²	1	637.4	8.8	0.0031
Yeast $\times$ Sugar	1	66.8	0.9	0.34
Sex $\times$ Yeast	1	2335.4	32.1	< 0.0001
Sex $\times$ Sugar	1	2209.2	30.3	< 0.0001
Status $\times$ Yeast	1	801.9	11.0	0.0009
Population $\times$ Yeast	1	7215.0	99.1	< 0.0001
Population $\times$ Sugar	1	3733.9	51.3	< 0.0001
Population $\times$ Yeast $\times$ Sugar	1	597.0	8.2	0.0042
Error	1707	124269.6	—	—
Total	1721	1226520.2	—	—

Table S27. Results of generalized linear model (Gamma distribution with log link) of **protein content ($\mu\text{g per fly}$) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 180.7$, $df = 14$, $p < 0.0001$) and explained ~89% of the null deviance (AIC = 12629.6). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P-value
Population	1	2942.10	< 0.0001
Sex	1	9162.99	< 0.0001
Status	1	60.76	< 0.0001
Yeast	1	5.83	0.016
Sugar	1	45.11	< 0.0001
(Yeast) ²	1	71.45	< 0.0001
(Sugar) ²	1	8.66	0.0033
Yeast $\times$ Sugar	1	0.46	0.50
Sex $\times$ Yeast	1	14.18	0.0002
Sex $\times$ Sugar	1	11.82	0.0006
Status $\times$ Yeast	1	13.43	0.0002
Population $\times$ Yeast	1	94.89	< 0.0001
Population $\times$ Sugar	1	34.75	< 0.0001
Population $\times$ Yeast $\times$ Sugar	1	5.91	0.015

Table S28. Results of multiple linear (polynomial) regression analysis of **energy content (J per mg protein) in 10-day-old flies**. *df*— degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{16,1705} = 175.9$, $p < 0.0001$), with an adjusted R^2 of 0.62.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	6394.9	122.9	< 0.0001
Sex	1	116907.0	2246.9	< 0.0001
Status	1	11141.5	214.1	< 0.0001
Yeast	1	2383.9	45.8	< 0.0001
Sugar	1	19.4	0.4	0.54
(Yeast) ²	1	759.2	14.6	0.0001
(Sugar) ²	1	1002.4	19.3	< 0.0001
Yeast × Sugar	1	545.3	10.5	0.0012
Sex × Yeast	1	3476.6	66.8	< 0.0001
Sex × Sugar	1	0.2	0.0	0.96
Status × Yeast	1	787.7	15.1	0.0001
Status × Sugar	1	190.4	3.7	0.056
Population × Yeast	1	2141.6	41.2	< 0.0001
Population × Sugar	1	494.5	9.5	0.0021
Population × Yeast × Sugar	1	334.6	6.4	0.011
Sex × Yeast × Sugar	1	370.6	7.1	0.0077
Error	1705	88710.3	—	—
Total	1721	235172.9	—	—

Table S29. Results of generalized linear model (Gamma distribution with log link) of **energy content (J per mg protein) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 138.8$, $df = 16$, $p < 0.0001$) and explained ~62% of the null deviance (AIC = –12111.4). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P-value
Population	1	146.29	< 0.0001
Sex	1	2443.41	< 0.0001
Status	1	242.63	< 0.0001
Yeast	1	52.80	< 0.0001
Sugar	1	0.55	0.46
(Yeast) ²	1	19.12	< 0.0001
(Sugar) ²	1	24.08	< 0.0001
Yeast $\times$ Sugar	1	10.45	0.0012
Sex $\times$ Yeast	1	76.80	< 0.0001
Sex $\times$ Sugar	1	0.16	0.69
Status $\times$ Yeast	1	10.07	0.0015
Status $\times$ Sugar	1	4.33	0.038
Population $\times$ Yeast	1	43.29	< 0.0001
Population $\times$ Sugar	1	7.91	0.0049
Population $\times$ Yeast $\times$ Sugar	1	7.61	0.0058
Sex $\times$ Yeast $\times$ Sugar	1	5.73	0.017

Table S30. Results of a 3×3 categorical factorial ANOVA (Yeast: 2.5/10/25%; Sugar: 2.5/10/25%) for **energy content (J per mg protein) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{31,397} = 27.5$, $p < 0.0001$), with an adjusted R^2 of 0.66.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	1240.9	28.3	< 0.0001
Sex	1	25794.7	588.9	< 0.0001
Status	1	2779.9	63.5	< 0.0001
Yeast	2	425.0	4.9	0.0083
Sugar	2	260.9	3.0	0.052
Yeast × Sugar	4	1266.1	7.2	< 0.0001
Sex × Yeast	2	793.2	9.1	0.0001
Sex × Sugar	2	366.7	4.2	0.016
Status × Yeast	2	512.1	5.8	0.0031
Status × Sugar	2	498.5	5.7	0.0037
Population × Yeast	2	445.9	5.1	0.0066
Population × Sugar	2	500.4	5.7	0.0036
Population × Yeast × Sugar	4	2002.4	11.4	< 0.0001
Sex × Yeast × Sugar	4	291.5	1.7	0.16
Error	397	17388.4	—	—
Total	428	54683.8	—	—

Table S31. Results of multiple linear (polynomial) regression analysis of **energy content (J per fly) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{12,1709} = 928.4$, $p < 0.0001$), with an adjusted R^2 of 0.87.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	547.3	1584.3	< 0.0001
Sex	1	3214.6	9305.9	< 0.0001
Status	1	33.3	96.4	< 0.0001
Yeast	1	10.7	30.9	< 0.0001
Sugar	1	2.6	7.4	0.0065
(Sugar) ²	1	11.2	32.5	< 0.0001
Yeast × Sugar	1	4.3	12.4	0.0004
Sex × Yeast	1	12.4	36.0	< 0.0001
Sex × Sugar	1	0.8	2.3	0.13
Status × Yeast	1	1.1	3.1	0.077
Status × Sugar	1	1.4	4.1	0.043
Sex × Yeast × Sugar	1	3.1	8.9	0.0028
Error	1709	590.4	—	—
Total	1721	4438.9	—	—

Table S32. Results of generalized linear model (Gamma distribution with log link) of **energy content (J per fly) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio χ^2 = 543.9, df = 12, p < 0.0001) and explained ~86% of the null deviance (AIC = 3038.4). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	1685.19	< 0.0001
Sex	1	9652.84	< 0.0001
Status	1	121.71	< 0.0001
Yeast	1	34.54	< 0.0001
Sugar	1	8.41	0.0037
(Sugar) ²	1	37.83	< 0.0001
Yeast $\times$ Sugar	1	10.64	0.0011
Sex $\times$ Yeast	1	40.46	< 0.0001
Sex $\times$ Sugar	1	2.72	0.10
Status $\times$ Yeast	1	1.15	0.28
Status $\times$ Sugar	1	4.83	0.028
Sex $\times$ Yeast $\times$ Sugar	1	8.92	0.0028

Table S33. Results of multiple linear (polynomial) regression analysis of **fat content (µg per mg protein) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{16,1705} = 291.5$, $p < 0.0001$), with an adjusted R^2 of 0.73.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	17025013.0	858.5	< 0.0001
Sex	1	69067008.0	3482.6	< 0.0001
Status	1	791382.0	39.9	< 0.0001
Yeast	1	2917152.0	147.1	< 0.0001
Sugar	1	13572.0	0.7	0.41
(Yeast) ²	1	400649.0	20.2	< 0.0001
(Sugar) ²	1	333484.0	16.8	< 0.0001
Yeast × Sugar	1	97742.0	4.9	0.027
Sex × Yeast	1	1266467.0	63.9	< 0.0001
Sex × Sugar	1	304.0	0.0	0.90
Status × Yeast	1	293828.0	14.8	0.0001
Status × Sugar	1	47428.0	2.4	0.12
Population × Yeast	1	116005.0	5.8	0.016
Population × Sugar	1	56505.0	2.8	0.092
Population × Yeast × Sugar	1	150304.0	7.6	0.0060
Sex × Yeast × Sugar	1	222215.0	11.2	0.0008
Error	1705	33813273.0	—	—
Total	1721	126320747.0	—	—

Table S34. Results of generalized linear model (Gamma distribution with log link) of **fat content (µg per mg protein) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 351.6$, *df* = 16, *p* < 0.0001) and explained ~70% of the null deviance (AIC = −1647.4). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i> -value
Population	1	1002.24	< 0.0001
Sex	1	3439.32	< 0.0001
Status	1	73.12	< 0.0001
Yeast	1	190.59	< 0.0001
Sugar	1	1.90	0.17
(Yeast) ²	1	31.14	< 0.0001
(Sugar) ²	1	24.59	< 0.0001
Yeast × Sugar	1	1.55	0.21
Sex × Yeast	1	110.04	< 0.0001
Sex × Sugar	1	0.14	0.71
Status × Yeast	1	3.04	0.081
Status × Sugar	1	1.39	0.24
Population × Yeast	1	16.94	< 0.0001
Population × Sugar	1	0.35	0.55
Population × Yeast × Sugar	1	11.96	0.0005
Sex × Yeast × Sugar	1	11.37	0.0007

Table S35. Results of multiple linear (polynomial) regression analysis of **fat content (µg per fly) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{15,1706} = 826.1$, $p < 0.0001$), with an adjusted R^2 of 0.88.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	368565.2	2716.2	< 0.0001
Sex	1	1273695.7	9386.7	< 0.0001
Status	1	460.3	3.4	0.066
Yeast	1	15474.9	114.0	< 0.0001
Sugar	1	351.1	2.6	0.11
(Sugar) ²	1	3596.4	26.5	< 0.0001
Yeast × Sugar	1	685.7	5.1	0.025
Sex × Yeast	1	5707.8	42.1	< 0.0001
Sex × Sugar	1	237.8	1.8	0.19
Status × Yeast	1	400.0	2.9	0.086
Status × Sugar	1	363.4	2.7	0.10
Population × Yeast	1	7063.0	52.1	< 0.0001
Population × Sugar	1	116.9	0.9	0.35
Population × Yeast × Sugar	1	443.0	3.3	0.071
Sex × Yeast × Sugar	1	1886.4	13.9	0.0002
Error	1706	231490.0	—	—
Total	1721	1912858.9	—	—

Table S36. Results of generalized linear model (Gamma distribution with log link) of **fat content (µg per fly) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 933.6$, *df* = 15, *p* < 0.0001) and explained ~86% of the null deviance (AIC = 13494.6). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	2851.41	< 0.0001
Sex	1	9101.49	< 0.0001
Status	1	27.37	< 0.0001
Yeast	1	157.39	< 0.0001
Sugar	1	2.46	0.12
(Sugar) ²	1	34.84	< 0.0001
Yeast × Sugar	1	1.65	0.20
Sex × Yeast	1	76.91	< 0.0001
Sex × Sugar	1	3.92	0.048
Status × Yeast	1	0.04	0.84
Status × Sugar	1	1.79	0.18
Population × Yeast	1	68.01	< 0.0001
Population × Sugar	1	3.47	0.062
Population × Yeast × Sugar	1	5.20	0.023
Sex × Yeast × Sugar	1	15.19	< 0.0001

Table S37. Results of multiple linear (polynomial) regression analysis of **glycogen content (µg per mg protein) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{12,1709} = 140.7$, $p < 0.0001$), with an adjusted R^2 of 0.49.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	7298426.0	415.7	< 0.0001
Sex	1	104836.0	6.0	0.015
Status	1	13486713.0	768.2	< 0.0001
Yeast	1	416374.0	23.7	< 0.0001
Sugar	1	52854.0	3.0	0.083
(Sugar) ²	1	98620.0	5.6	0.018
Yeast × Sugar	1	242727.0	13.8	0.0002
Sex × Yeast	1	639067.0	36.4	< 0.0001
Status × Yeast	1	256838.0	14.6	0.0001
Status × Sugar	1	68542.0	3.9	0.048
Population × Yeast	1	6452949.0	367.6	< 0.0001
Population × Sugar	1	404641.0	23.0	< 0.0001
Error	1709	30003280.0	—	—
Total	1721	59639250.0	—	—

Table S38. Results of generalized linear model (Gamma distribution with log link) of **glycogen content ($\mu\text{g per mg protein}$) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 124.9$, $df = 12$, $p < 0.0001$) and explained ~49% of the null deviance (AIC = -2063.4). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P -value
Population	1	400.70	< 0.0001
Sex	1	9.53	0.020
Status	1	769.91	< 0.0001
Yeast	1	16.21	< 0.0001
Sugar	1	4.71	0.030
(Sugar) ²	1	5.13	0.024
Yeast $\times$ Sugar	1	18.45	< 0.0001
Sex $\times$ Yeast	1	32.92	< 0.0001
Status $\times$ Yeast	1	15.22	< 0.0001
Status $\times$ Sugar	1	4.95	0.026
Population $\times$ Yeast	1	371.87	< 0.0001
Population $\times$ Sugar	1	25.68	< 0.0001

Table S39. Results of multiple linear (polynomial) regression analysis of **glycogen content (µg per fly) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{13,1708} = 249.2$, $p < 0.0001$), with an adjusted R^2 of 0.65.

Source of Variation	<i>df</i>	SSQ	<i>F</i>-ratio	<i>P</i>-value
Population	1	1330.8	13.8	0.0002
Sex	1	200909.3	2090.2	< 0.0001
Status	1	68296.5	710.5	< 0.0001
Yeast	1	3597.8	37.4	< 0.0001
Sugar	1	2782.4	28.9	< 0.0001
(Yeast) ²	1	1768.8	18.4	< 0.0001
(Sugar) ²	1	1067.0	11.1	0.0009
Yeast × Sugar	1	1763.4	18.3	< 0.0001
Sex × Yeast	1	2271.4	23.6	< 0.0001
Status × Yeast	1	723.6	7.5	0.0061
Status × Sugar	1	605.2	6.3	0.012
Population × Yeast	1	25403.2	264.3	< 0.0001
Population × Sugar	1	538.0	5.6	0.018
Error	1708	164174.2	—	—
Total	1721	475548.8	—	—

Table S40. Results of generalized linear model (Gamma distribution with log link) of **glycogen content (μg per fly) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 211.7$, $df = 13$, $p < 0.0001$) and explained ~67% of the null deviance (AIC = 12717.2). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	13.83	0.0002
Sex	1	2358.73	< 0.0001
Status	1	725.98	< 0.0001
Yeast	1	29.35	< 0.0001
Sugar	1	33.86	< 0.0001
(Yeast) ²	1	19.48	< 0.0001
(Sugar) ²	1	13.58	0.0002
Yeast $\times$ Sugar	1	21.87	< 0.0001
Sex $\times$ Yeast	1	19.38	< 0.0001
Status $\times$ Yeast	1	5.40	0.020
Status $\times$ Sugar	1	7.73	0.0054
Population $\times$ Yeast	1	273.86	< 0.0001
Population $\times$ Sugar	1	6.86	0.0088

Table S41. Results of multiple linear (polynomial) regression analysis of **trehalose content (µg per mg protein) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{12,1709} = 104.5$, $p < 0.0001$), with an adjusted R^2 of 0.42.

Source of Variation	<i>df</i>	SSQ	<i>F</i>-ratio	<i>P</i>-value
Population	1	1335959.6	872.6	< 0.0001
Sex	1	19696.4	12.9	0.0003
Status	1	290176.0	189.5	< 0.0001
Yeast	1	3941.0	2.6	0.11
Sugar	1	510.4	0.3	0.56
(Yeast) ²	1	10788.5	7.0	0.0080
(Sugar) ²	1	5767.2	3.8	0.052
Sex × Yeast	1	18079.9	11.8	0.0006
Status × Yeast	1	10351.0	6.8	0.0094
Status × Sugar	1	6284.8	4.1	0.043
Population × Yeast	1	172396.3	112.6	< 0.0001
Population × Sugar	1	37266.2	24.3	< 0.0001
Error	1709	2616511.7	—	—
Total	1721	4535700.6	—	—

Table S42. Results of generalized linear model (Gamma distribution with log link) of **trehalose content ($\mu\text{g per mg protein}$) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 208.6$, $df = 12$, $p < 0.0001$) and explained $\sim 46\%$ of the null deviance (AIC = -6257.5). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	802.82	< 0.0001
Sex	1	16.76	< 0.0001
Status	1	160.02	< 0.0001
Yeast	1	7.88	0.0050
Sugar	1	1.27	0.26
(Yeast) ²	1	4.68	0.030
(Sugar) ²	1	4.31	0.031
Sex $\times$ Yeast	1	13.17	0.0003
Status $\times$ Yeast	1	4.03	0.045
Status $\times$ Sugar	1	3.46	0.063
Population $\times$ Yeast	1	110.66	< 0.0001
Population $\times$ Sugar	1	23.98	< 0.0001

Table S43. Results of multiple linear (polynomial) regression analysis of **trehalose content (µg per fly) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{10,1711} = 159.9$, $p < 0.0001$), with an adjusted R^2 of 0.48.

Source of Variation	<i>df</i>	SSQ	<i>F</i>-ratio	<i>P</i>-value
Population	1	1587.2	172.1	< 0.0001
Sex	1	11033.2	1196.6	< 0.0001
Status	1	1249.4	135.5	< 0.0001
Yeast	1	66.3	7.2	0.0074
Sugar	1	14.3	1.6	0.21
Sex × Yeast	1	50.0	5.4	0.020
Status × Yeast	1	19.8	2.1	0.14
Status × Sugar	1	42.8	4.6	0.031
Population × Yeast	1	578.2	62.7	< 0.0001
Population × Sugar	1	100.1	10.9	0.0010
Error	1711	15776.3	—	—
Total	1721	30519.2	—	—

Table S44. Results of generalized linear model (Gamma distribution with log link) of **trehalose content (µg per fly) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; *df* — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 221.7$, *df* = 10, *p* < 0.0001) and explained ~50% of the null deviance (AIC = 8713.6). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i>-value
Population	1	198.15	< 0.0001
Sex	1	1094.63	< 0.0001
Status	1	122.93	< 0.0001
Yeast	1	11.69	0.0006
Sugar	1	0.08	0.78
Sex × Yeast	1	5.65	0.017
Status × Yeast	1	1.11	0.29
Status × Sugar	1	4.19	0.041
Population × Yeast	1	64.42	< 0.0001
Population × Sugar	1	14.21	0.0002

Table S45. Results of multiple linear (polynomial) regression analysis of **glucose content ($\mu\text{g per mg protein}$) in 10-day-old flies**. *df*— degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{13,1708} = 148.2$, $p < 0.0001$), with an adjusted R^2 of 0.53.

Source of Variation	<i>df</i>	SSQ	<i>F</i>-ratio	<i>P</i>-value
Population	1	451315.5	1596.7	< 0.0001
Sex	1	1344.4	4.8	0.029
Status	1	1071.7	3.8	0.052
Yeast	1	2717.5	9.6	0.002
Sugar	1	21032.5	74.4	< 0.0001
(Yeast) ²	1	3638.1	12.9	0.0003
(Sugar) ²	1	6136.5	21.7	< 0.0001
Yeast $\times$ Sugar	1	28056.6	99.3	< 0.0001
Sex $\times$ Yeast	1	2638.6	9.3	0.0023
Status $\times$ Yeast	1	2179.6	7.7	0.0055
Population $\times$ Yeast	1	12951.5	45.8	< 0.0001
Population $\times$ Sugar	1	46.6	0.2	0.68
Population $\times$ Yeast $\times$ Sugar	1	5113.4	18.1	< 0.0001
Error	1708	482774.6	—	—
Total	1721	1027407.6	—	—

Table S46. Results of generalized linear model (Gamma distribution with log link) of **glucose content ($\mu\text{g per mg protein}$) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 159.0$, $df = 13$, $p < 0.0001$) and explained ~49% of the null deviance (AIC = –9090.4). Terms for sugar and yeast were mean-centered.

Source of Variation	<i>df</i>	LR χ^2	<i>P</i> -value
Population	1	1627.60	< 0.0001
Sex	1	0.67	0.41
Status	1	10.01	0.0015
Yeast	1	15.87	< 0.0001
Sugar	1	85.56	< 0.0001
(Yeast) ²	1	34.84	< 0.0001
(Sugar) ²	1	16.45	< 0.0001
Yeast $\times$ Sugar	1	89.77	< 0.0001
Sex $\times$ Yeast	1	10.51	0.0012
Status $\times$ Yeast	1	9.88	0.0017
Population $\times$ Yeast	1	69.36	< 0.0001
Population $\times$ Sugar	1	0.21	0.65
Population $\times$ Yeast $\times$ Sugar	1	9.94	0.0016

Table S47. Results of multiple linear (polynomial) regression analysis of **glucose content (μg per fly) in 10-day-old flies**. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{15,1706} = 129.6$, $p < 0.0001$), with an adjusted R^2 of 0.53.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	493.4	260.3	< 0.0001
Sex	1	2388.1	1259.8	< 0.0001
Status	1	54.7	28.9	< 0.0001
Yeast	1	14.8	7.8	0.0052
Sugar	1	245.8	129.7	< 0.0001
(Yeast) ²	1	105.1	55.5	< 0.0001
(Sugar) ²	1	42.1	22.2	< 0.0001
Yeast $\times$ Sugar	1	186.7	98.5	< 0.0001
Sex $\times$ Yeast	1	0.6	0.3	0.56
Sex $\times$ Sugar	1	4.0	2.1	0.15
Status $\times$ Sugar	1	8.7	4.6	0.032
Population $\times$ Yeast	1	23.2	12.2	0.0005
Population $\times$ Sugar	1	8.3	4.4	0.037
Population $\times$ Yeast $\times$ Sugar	1	37.2	19.6	< 0.0001
Sex $\times$ Yeast $\times$ Sugar	1	11.2	5.9	0.015
Error	1706	3233.9	—	—
Total	1721	6919.1	—	—

Table S48. Results of generalized linear model (Gamma distribution with log link) of **glucose content ($\mu\text{g per fly}$) in 10-day-old flies**. LR χ^2 — likelihood ratio chi-square statistic; df — degrees of freedom. “Status” refers to mating status. The overall model was significant (likelihood ratio $\chi^2 = 173.4$, $df = 15$, $p < 0.0001$) and explained ~51% of the null deviance (AIC = 6093.0). Terms for sugar and yeast were mean-centered.

Source of Variation	df	LR χ^2	P-value
Population	1	325.62	< 0.0001
Sex	1	1370.67	< 0.0001
Status	1	40.16	< 0.0001
Yeast	1	9.63	0.0019
Sugar	1	137.20	< 0.0001
(Yeast) ²	1	79.54	< 0.0001
(Sugar) ²	1	28.27	< 0.0001
Yeast $\times$ Sugar	1	88.08	< 0.0001
Sex $\times$ Yeast	1	2.77	0.096
Sex $\times$ Sugar	1	0.02	0.89
Status $\times$ Sugar	1	2.45	0.12
Population $\times$ Yeast	1	21.06	< 0.0001
Population $\times$ Sugar	1	6.37	0.012
Population $\times$ Yeast $\times$ Sugar	1	14.68	0.0001
Sex $\times$ Yeast $\times$ Sugar	1	1.17	0.28

Table S49. Energy-weighted PCA in 10-day old flies – variance explained. PCA on covariance matrix of energy equivalents ($\text{J}\cdot\text{mg}^{-1}$ protein); variables centered, not scaled.

PC	Eigenvalue	Proportion	Cumulative
PC1	119.74	0.8971	0.8971
PC2	12.65	0.0947	0.9918
PC3	0.99	0.0074	0.9992
PC4	0.11	0.0008	1

Table S50. Energy-weighted PCA in 10-day old flies - component loadings. PCA on covariance matrix of energy equivalents ($\text{J}\cdot\text{mg}^{-1}$ protein); variables centered, not scaled.

Metabolite	PC1	PC2	PC3	PC4
Fat	0.9989	0.0460	0.0086	-0.0100
Glycogen	0.0471	-0.9738	-0.2180	0.0437
Trehalose	0.0021	-0.2160	0.9751	0.0496
Glucose	-0.0079	-0.0539	0.0389	-0.9978

Table S51. Results of multiple linear (polynomial) regression analysis of energy change (J per mg protein) — calculated as the difference between energy content in 10-day-old flies and at eclosion. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{14,1707} = 287.5$, $p < 0.0001$), with an adjusted R^2 of 0.70

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	28516.4	426.3	< 0.0001
Sex	1	150294.5	2246.9	< 0.0001
Status	1	10161.1	151.9	< 0.0001
Yeast	1	3629.3	54.3	< 0.0001
Sugar	1	59286.2	886.3	< 0.0001
(Yeast) ²	1	5717.9	85.5	< 0.0001
(Sugar) ²	1	245.8	3.7	0.055
Yeast × Sugar	1	464.9	6.9	0.0085
Sex × Yeast	1	2746.1	41.1	< 0.0001
Sex × Sugar	1	98.0	1.5	0.23
Status × Yeast	1	1419.4	21.2	< 0.0001
Status × Sugar	1	422.7	6.3	0.012
Population × Yeast	1	2729.2	40.8	< 0.0001
Sex × Yeast × Sugar	1	754.9	11.3	0.0008
Error	1707	114182.5	—	—
Total	1721	383425.6	—	—

Table S52. Results of Gaussian linear model (OLS) for **energy change (J per mg protein)**. with MacKinnon–White heteroscedasticity-consistent standard errors (HC3). Reported tests are HC3-robust Type II Wald F-tests. Continuous predictors were mean-centered; quadratic terms use centered variables. The overall model was significant ($F_{14,1707} = 280.95$, $p < 0.0001$), with $R^2 = 0.697$, adj. $R^2 = 0.695$, $\sigma = 8.283$, AIC = 12185.06, $n = 1722$.

Source of Variation	<i>df</i>	<i>F</i> (HC3)	<i>P</i>-value
Population	1	405.63	< 0.0001
Sex	1	2216.08	< 0.0001
Status	1	142.77	< 0.0001
Yeast	1	33.12	< 0.0001
Sugar	1	1055.42	< 0.0001
(Yeast) ²	1	72.00	< 0.0001
(Sugar) ²	1	1.57	0.21
Yeast × Sugar	1	2.72	0.099
Sex × Yeast	1	33.21	< 0.0001
Sex × Sugar	1	12.38	0.0004
Status × Yeast	1	19.58	< 0.0001
Status × Sugar	1	4.73	0.030
Population × Yeast	1	37.44	< 0.0001
Sex × Yeast × Sugar	1	8.09	0.0045

Table S53. Results of a 3×3 categorical factorial ANOVA (Yeast: 2.5/10/25%; Sugar: 2.5/10/25%) for **energy change** (J per mg protein) — calculated as the difference between energy content in 10-day-old flies and at eclosion. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{25,402} = 62.7$, $p < 0.0001$), with an adjusted R^2 of 0.78

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	9002.5	149.1	< 0.0001
Sex	1	34126.7	565.1	< 0.0001
Status	1	2850.9	47.2	< 0.0001
Yeast	2	1358.0	11.2	< 0.0001
Sugar	2	38061.4	315.1	< 0.0001
Yeast × Sugar	4	5745.3	23.8	< 0.0001
Sex × Yeast	2	834.8	6.9	0.0011
Sex × Sugar	2	517.8	4.3	0.014
Status × Yeast	2	675.5	5.6	0.004
Status × Sugar	2	587.8	4.9	0.0082
Population × Yeast	2	81.3	0.7	0.51
Sex × Yeast × Sugar	4	474.3	2.0	0.10
Error	402	24278.7	—	—
Total	427	118997.0	—	—

Table S54. Results of multiple linear (polynomial) regression analysis of energy change (J per fly) — calculated as the difference between energy content in 10-day-old flies and at eclosion. *df* — degrees of freedom; SSQ — sum of squares for each source of variation. “Status” refers to mating status. The overall model was statistically significant ($F_{14,1707} = 477.6$, $p < 0.0001$), with an adjusted R^2 of 0.79.

Source of Variation	<i>df</i>	SSQ	<i>F</i> -ratio	<i>P</i> -value
Population	1	886.4	1660.4	< 0.0001
Sex	1	2160.5	4046.9	< 0.0001
Status	1	13.7	25.6	< 0.0001
Yeast	1	0.6	1.2	0.27
Sugar	1	453.9	850.2	< 0.0001
(Yeast) ²	1	31.7	59.4	< 0.0001
Yeast × Sugar	1	0.5	0.9	0.33
Sex × Yeast	1	2.5	4.8	0.029
Sex × Sugar	1	0.4	0.7	0.41
Status × Yeast	1	3.2	6.0	0.015
Status × Sugar	1	3.2	6.0	0.014
Population × Yeast	1	1.4	2.7	0.10
Population × Sugar	1	4.0	7.5	0.0062
Sex × Yeast × Sugar	1	3.8	7.1	0.0080
Error	1707	911.3	—	—
Total	1721	4480.7	—	—

Table S55. Results of Gaussian linear model (OLS) for **energy change (J per fly)** with MacKinnon–White heteroscedasticity-consistent standard errors (HC3). Reported tests are HC3-robust Type II Wald F-tests. Continuous predictors were mean-centered; quadratic terms use centered variables. The overall model was significant ($F_{14,1707} = 403.45$, $p < 0.0001$), with $R^2 = 0.768$, adj. $R^2 = 0.766$, $\sigma = 0.845$, AIC = 4325.26, $n = 1722$.

Source of Variation	<i>df</i>	<i>F</i> (HC3)	<i>P</i>-value
Population	1	1426.90	< 0.0001
Sex	1	3398.57	< 0.0001
Status	1	2.14	0.14
Yeast	1	0.44	0.51
Sugar	1	718.03	< 0.0001
(Yeast) ²	1	33.19	< 0.0001
Yeast × Sugar	1	0.42	0.52
Sex × Yeast	1	3.29	0.070
Sex × Sugar	1	63.27	< 0.0001
Status × Yeast	1	7.26	0.0071
Status × Sugar	1	6.69	0.0098
Population × Yeast	1	1.37	0.24
Population × Sugar	1	8.27	0.0041
Sex × Yeast × Sugar	1	4.32	0.038

Table S56. Number of samples for each combination of yeast and sugar concentration in the developmental diet used in the analyses of energy stores. Only samples in which all five components—triglycerides (fat), glycogen, trehalose, glucose, and proteins—were successfully quantified are included. These numbers also reflect the samples used for calculating total energy. Samples with missing data for any component were excluded from all analyses.

Population	Age	Group	Yeast	Sugar					
				2.5%	5%	10%	15%	20%	25%
W ¹¹¹⁸	Newly emerged	Males	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Females	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	5	6	6	6
			25%	6	6	6	6	6	6
	10-day-old	Virgin males	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Mated males	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Virgin females	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Mated females	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	5	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
SK	Newly emerged	Males	2.5%	6	6	6	6	4	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Females	2.5%	6	6	6	6	6	4
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
	10-day-old	Virgin males	2.5%	6	6	6	6	6	5
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	5	6	6
			25%	6	6	5	6	6	6
		Mated males	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Virgin females	2.5%	6	5	6	6	6	5
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6
		Mated females	2.5%	6	6	6	6	6	6
			5%	6	6	6	6	6	6
			10%	6	6	6	6	6	6
			15%	6	6	6	6	6	6
			20%	6	6	6	6	6	6
			25%	6	6	6	6	6	6