|  |  |  |  |
| --- | --- | --- | --- |
| **A** | **Estimate**  | **Std.error**  | **Adj.P.value**  |
| Rheb+ - Co  | 0.4572  | 0.0699  | 0.0000  |
| PTEN- - Co  | 1.0191  | 0.0630  | 0.0000  |
| PTEN-;Rheb+ - Co  | 1.4644  | 0.0589  | 0.0000  |
| PTEN-;Rheb+ - Rheb+  | 1.0072  | 0.0669  | 0.0000  |
| PTEN-;Rheb+ - PTEN-  | 0.4453  | 0.0597  | 0.0000  |

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| **B** | **Estimate**  | **Std.error**  | **Adj.P.value**  |
| Co-0% - 20%  | -0.0851  | 0.0706  | 0.6843  |
| FASN-0% - 20%  | -0.5349  | 0.0694  | 0.0000  |
| Rheb+-0% - 20%  | 0.0247  | 0.0887  | 1.0000  |
| FASN;Rheb+-0% - 20%  | -0.6454  | 0.0629  | 0.0000  |
| PTEN-0% - 20%  | -0.3205  | 0.0719  | 0.0000  |
| FASN-,PTEN-0% - 20%  | -0.2793  | 0.0531  | 0.0000  |
| PTEN-;Rheb+-0% - 20%  | -0.5775  | 0.0705  | 0.0000  |
| FASN-,PTEN-;Rheb+- 0% - 20%  | -0.3034  | 0.0633  | 0.0000  |
| FASN-,PTEN- - FASN-  | 1.0181  | 0.0677  | 0.0000  |
| FASN-;Rheb+ - FASN-  | 0.8428  | 0.0763  | 0.0000  |
| FASN-;Rheb+ - Rheb+  | 0.0021  | 0.0753  | 1.0000  |
| FASN-,PTEN- - PTEN-  | -0.3845  | 0.0593  | 0.0000  |
| FASN-,PTEN-;Rheb+ - PTEN-;Rheb+  | -0.5348  | 0.0513  | 0.0000  |
| PTEN-Ri - PTEN-  | -0.7730  | 0.0750  | 0.0000  |
| FASN-;PTEN-Ri - FASN-;PTEN-  | -1.0254  | 0.0712  | 0.0000  |
| PTEN-Ri - Co  | 0.2461  | 0.0744  | 0.0038  |
| FASN-;PTEN-Ri - Co  | -0.3908  | 0.0743  | 0.0000  |
| PTEN-Ri - FASN;PTEN-Ri  | 0.6369  | 0.0848  | 0.0000  |

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| **C** | **Estimate**  | **Std.error**  | **Adj.P.value**  |
| PFK1i - Co  | -0.0532  | 0.0656  | 1.0000  |
| PKi - Co  | -0.1909  | 0.0661  | 0.0310  |
| LDHi - Co  | -0.0670  | 0.0656  | 1.0000  |
| PDHi - Co  | -0.0659  | 0.0689  | 1.0000  |
| PTEN-PFK1i - PTEN-  | -0.2098  | 0.0657  | 0.0126  |
| PTEN-PKi - PTEN-  | -0.3693  | 0.0662  | 0.0000  |
| PTEN-LDHi - PTEN-  | -0.3690  | 0.0668  | 0.0000  |
| PTEN-PDHi - PTEN-  | -0.2562  | 0.0638  | 0.0006  |
| Rheb+-PFK1i - Rheb+  | 0.0427  | 0.0755  | 1.0000  |
| Rheb+-PKi - Rheb+  | 0.1482  | 0.0660  | 0.1484  |
| Rheb+-LDHi - Rheb+  | 0.0622  | 0.0729  | 1.0000  |
| Rheb+-PDHi - Rheb+  | -0.1623  | 0.0687  | 0.1271  |
|  |

**Table S1:** Statistical tests corresponding to figures S2A (A), 7M (B) and 5M (C). The model tests for the difference in the log ratio of GFP vs. unlabelled clones between pairs of genotypes (Co = control), accounting for larvae and series random effects (see the Methods section). P-values were corrected for multiple testing (Holm-Bonferroni method) and quantify the risk of rejecting the true null hypothesis at the table level.

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| --- | --- | --- | --- |
|  | **Effect**  | **Std.Err.**  | **Adj.Pvalue**  |
| FASN- - Co  | -0.177  | 0.521  | 0.7336  |
| PTEN- - Co  | 0.714  | 0.482  | 0.2772  |
| Rheb+ - Co  | 4.119  | 0.874  | 0.0000  |
| TOR2L1 - Co  | -3.816  | 0.756  | 0.0000  |
| TORΔP - Co  | -4.628  | 1.221  | 0.0005  |
| TOR2L19 - Co  | -4.652  | 0.946  | 0.0000  |
|  |

**Table S2:** Statistical test corresponding to Figure 2M of the difference in frequency between MARCM clones to control. The model is a mixed effect, generalized linear model considering frequencies as binomial data and genotype as a fixed effect, while larvae / series were random effects. P-values were adjusted for multiple testing by a Holm-Bonferroni correction.

|  |
| --- |
| Mass, Males  |
|  | **Effect**  | **Std..Err.**  | **Adj..Pvalue**  |
| 0%: PTEN - Co  | 0.0077  | 0.0257  | 0.7653  |
| 0%: Rheb - Co  | 0.0584  | 0.0238  | 0.0295  |
| 20%: PTEN - Co  | 0.2392  | 0.0236  | 0.0000  |
| 20%: Rheb - Co  | 0.2241  | 0.0249  | 0.0000  |

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| --- |
| Mass, Females  |
|  | **Effect**  | **Std..Err.**  | **Adj..Pvalue**  |
| 0%: PTEN - Co  | 0.0591  | 0.0351  | 0.1879  |
| 0%: Rheb - Co  | 0.0107  | 0.0315  | 0.7347  |
| 20%: PTEN - Co  | 0.2357  | 0.0358  | 0.0000  |
| 20%: Rheb - Co  | 0.3197  | 0.0320  | 0.0000  |

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| --- |
| Protein  |
|  | **Effect**  | **Std..Err.**  | **Adj..Pvalue**  |
| 0%: PTEN - Co  | 2.5869  | 1.6555  | 0.3937  |
| 0%: Rheb - Co  | -0.2045  | 1.6555  | 0.9027  |
| 20%: PTEN - Co  | 7.3687  | 1.6555  | 0.0007  |
| 20%: Rheb - Co  | 1.5259  | 1.6555  | 0.7317  |

|  |
| --- |
| TAG  |
|  | **Effect**  | **Std..Err.**  | **Adj..Pvalue**  |
| 0%: PTEN - Co  | 6.7269  | 3.2213  | 0.1427  |
| 0%: Rheb - Co  | -2.0102  | 3.2213  | 0.5385  |
| 20%: PTEN - Co  | 23.1160  | 3.2213  | 0.0000  |
| 20%: Rheb - Co  | 5.5236  | 3.2213  | 0.1986  |

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| --- |
| Glycogen  |
|  | **Effect**  | **Std..Err.**  | **Adj..Pvalue**  |
| 0%: PTEN - Co  | -0.8275  | 0.3703  | 0.0370  |
| 0%: Rheb - Co  | -1.6765  | 0.3703  | 0.0006  |
| 20%: PTEN - Co  | -1.3188  | 0.3903  | 0.0060  |
| 20%: Rheb - Co  | -1.8334  | 0.3903  | 0.0006  |

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| --- |
| Threalose  |
|  | **Effect**  | **Std..Err.**  | **Adj..Pvalue**  |
| 0%: PTEN - Co  | -2.8836  | 0.4507  | 0.0000  |
| 0%: Rheb - Co  | -2.3548  | 0.4507  | 0.0000  |
| 20%: PTEN - Co  | -3.3097  | 0.4750  | 0.0000  |
| 20%: Rheb - Co  | -3.2726  | 0.4750  | 0.0000  |

**Table S3:** Statistical test corresponding to Figure 3.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **A** | **Estimate**  | **Std. error**  | **t value**  | **Pr(>|t|)**  |
| mal,Co,0% vs. mal,Co,10%  | 0.109  | 0.032  | 3.381  | 0.00162  |
| fem,Co,0% vs. fem,Co,10%  | 0.115  | 0.032  | 3.647  | 0.00093  |
| mal,FAS,0% vs. mal,FAS,10%  | 0.098  | 0.031  | 3.141  | 0.00183  |
| fem,FAS,0% vs. fem,FAS,10%  | 0.124  | 0.031  | 3.989  | 0.00033  |
| mal,Co,0% vs. mal,FAS,0%  | 0.241  | 0.033  | 7.425  | 0.00000  |
| fem,Co,0% vs. fem,FAS,0%  | 0.263  | 0.032  | 8.257  | 0.00000  |
| mal,Co,10% vs. mal,FAS,10%  | 0.230  | 0.031  | 7.510  | 0.00000  |
| fem,Co,10% vs. fem,FAS,10%  | 0.272  | 0.031  | 8.884  | 0.00000  |
|  |

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| --- | --- | --- | --- | --- |
| **B** | **Estimate**  | **Std. error**  | **t value**  | **Pr(>|t|)**  |
| mal,Co,0% vs. mal,Co,10%  | 0.045  | 0.034  | 1.346  | 0.30644  |
| fem,Co,0% vs. fem,Co,10%  | 0.093  | 0.034  | 2.762  | 0.02520  |
| mal,FAS,0% vs. mal,FAS,10%  | 0.048  | 0.034  | 1.434  | 0.30644  |
| fem,FAS,0% vs. fem,FAS,10%  | 0.073  | 0.034  | 2.175  | 0.09258  |
| mal,Co,0% vs. mal,FAS,0%  | 0.186  | 0.034  | 5.535  | 0.00000  |
| fem,Co,0% vs. fem,FAS,0%  | 0.276  | 0.034  | 8.216  | 0.00000  |
| mal,Co,10% vs. mal,FAS,10%  | 0.189  | 0.034  | 5.623  | 0.00000  |
| fem,Co,10% vs. fem,FAS,10%  | 0.256  | 0.034  | 7.629  | 0.00000  |
|  |

**Table S4:** (A) Prepupal weight differences (Estimate and standard error, in mg) and (B) Prepupal volume differences (assuming an ellipsoid pupae, volume in mm3) between control and FASN genotypes in absence/presence of sucrose, in males and females. The last column indicate P-values corrected for multiple testing (Holm-Bonferoni correction).

|  |  |  |  |
| --- | --- | --- | --- |
| **A** | **Value**  | **Std. Err**  | **p**  |
| Co -- FASN  | -0.207  | 0.035  | 0.00000  |
| Co -- LDH  | -0.350  | 0.040  | 0.00000  |
| Co -- PDH  | -0.617  | 0.097  | 0.00000  |
| Co -- PFK  | -0.927  | 0.033  | 0.00000  |
| Co -- PK  | -1.171  | 0.031  | 0.00000  |
|  |

|  |  |  |  |
| --- | --- | --- | --- |
| **B** | **Value**  | **Std. Err**  | **p**  |
| Co -- FASN  | -0.053  | 0.026  | 0.04411  |
| Co -- LDH  | -0.412  | 0.037  | 0.00000  |
| Co -- PDH  | -0.337  | 0.034  | 0.00000  |
| Co -- PFK  | -1.221  | 0.024  | 0.00000  |
| Co -- PK  | -1.272  | 0.023  | 0.00000  |
|  |

**Table S5 :** Survival analysis for males (A) and females (B) corresponding to Figure 4D.

|  |  |  |  |
| --- | --- | --- | --- |
| **A** | **Effect**  | **Std.Err**  | **Adj.Pvalue**  |
| FASN.0% - Co.0%  | -0.256  | 0.369  | 0.48801  |
| Co.10% - Co.0%  | 1.280  | 0.400  | 0.00410  |
| FASN.10% - Co.0%  | -1.460  | 0.407  | 0.00133  |
| Co.10% - FASN.0%  | 1.536  | 0.373  | 0.00019  |
| FASN.10% - FASN.0%  | -1.204  | 0.381  | 0.00410  |
| FASN.10% - Co.10%  | -2.740  | 0.411  | 0.00000  |
|  |

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| --- | --- | --- | --- |
| **B** | **Value**  | **Std.Err.**  | **Adj.Pvalue**  |
| Asym: Co.10% - Co.0%  | 0.261  | 0.081  | 0.00770  |
| Asym: FASN.0% - Co.0%  | -0.064  | 0.076  | 0.96390  |
| Asym: FASN.10% - FASN.0%  | -0.152  | 0.078  | 0.24840  |
| xmid: Co.10% - Co.0%  | 0.153  | 0.305  | 0.96390  |
| xmid: FASN.0% - Co.0%  | 2.574  | 0.291  | 0.00000  |
| xmid: FASN.10% - FASN.0%  | 3.257  | 0.378  | 0.00000  |
| scal: Co.10% - Co.0%  | -0.038  | 0.034  | 0.96390  |
| scal: FASN.0% - Co.0%  | 0.393  | 0.047  | 0.00000  |
| scal: FASN.10% - FASN.0%  | 0.131  | 0.111  | 0.96390  |
|  |

**Table S6:** Statistical test corresponding to Figure A. (A) Pairwise comparison of pupariation frequencies (logit scale) at Day 15. (B) Coefficients (logistic model with 3 parameters: asymptote (Asym), day at inflection (xmid), and horizontal stretching (scal)) for the pupariation frequency analysis. The model is a non-linear mixed-effect model, with Genotype and Sugar as fixed factors for all three logistic coefficents, and Replicate as a random effect (for Asym and xmid only, due to convergence issues with the full model). The last column indicate P-values corrected for multiple testing (Holm-Bonferoni correction).

|  |  |  |  |
| --- | --- | --- | --- |
|  | **Estimate**  | **Std.error**  | **Adj.P.value**  |
| PTEN- - Co  | 0.9029  | 0.1693  | 0.0000  |
| Rheb+ - Co  | 0.6960  | 0.1631  | 0.0000  |
| 2L1 - Co  | -1.5505  | 0.1855  | 0.0000  |
| 2L1,PTEN- - Co  | 0.2529  | 0.1965  | 0.1982  |
| 2L1;Rheb+ - Co  | -1.3477  | 0.1866  | 0.0000  |
| DP - Co  | -2.4447  | 0.1718  | 0.0000  |
| DP,PTEN- - Co  | -2.1265  | 0.1711  | 0.0000  |
| DP;Rheb+ - Co  | -2.3276  | 0.1690  | 0.0000  |
| 2L19 - Co  | -2.2405  | 0.1741  | 0.0000  |
| 2L19,PTEN- - Co  | -2.0352  | 0.1665  | 0.0000  |
| 2L19;Rheb+ - Co  | -1.6777  | 0.1539  | 0.0000  |
|  |

**Table S7:** Statistical tests corresponding to figure S2C. The model tests for the difference in the log ratio of GFP vs. unlabelled clones between pairs of genotypes (Co = control), accounting for larvae random effects (see the Methods section). P-values were corrected for multiple testing (Holm-Bonferroni method) and quantify the risk of rejecting the true null hypothesis at the table level.