**SUPPLEMENTARY TABLES**

**Supplementary Table 1. Mouse demographic information.**

| Mouse ID | Genotype | Sex | Weight | Transcriptomics | Metabolomic |
|----------|----------|-----|--------|----------------|-------------|
| 10722    | Null     | M   | 14.01  | x              |             |
| 10723    | Null     | M   | 13.46  | x              |             |
| 10724    | Null     | M   | 13.4   |                | x           |
| 10727    | WT       | M   | 26.22  | x              | x           |
| 10728    | WT       | M   | 27.34  |                |             |
| 10729    | WT       | M   | 25.99  | x              | x           |
| 10713    | WT       | F   | 27.63  | x              | x           |
| 10714    | WT       | F   | 27.03  | x              | x           |
| 10715    | WT       | F   | 26.44  | x              | x           |
| 10717    | Null     | F   | 12.07  | x              | x           |
| 10718    | Null     | F   | 13.96  |                |             |
| 10720    | Null     | F   | 12.31  | x              | x           |

Please browse Full Text version to see the data of Supplementary Tables 2–8.

**Supplementary Table 2. FPKM transcriptomic data.**

**Supplementary Table 3. Raw positive ion mode metabolomics data.**

**Supplementary Table 4. Raw negative ion mode metabolomics data.**

**Supplementary Table 5. RNAseq linear model pvalues.**

**Supplementary Table 6. Gene ontology pathways up or down regulated in GHRH-KO mice.** Note GHRH-KO mice have elevated gene transcript abundances of mitochondria and amino acid metabolism genes.

**Supplementary Table 7. Positive ionization mode metabolite linear model pvalues.**

**Supplementary Table 8. Negative ionization mode metabolite linear model pvalues.**
### Supplementary Table 9. Significantly enriched metabolic pathways in blood serum.

| Variable-Ionization mode | Pathway                              | Significantly different metabolites | Metabolites in pathway | Adjusted p-value |
|--------------------------|--------------------------------------|-------------------------------------|------------------------|------------------|
| Genotype-Positive        | Nicotine degradation III              | 4                                   | 8                      | 0.014            |
|                          | Serotonin degradation                 | 3                                   | 5                      | 0.018            |
|                          | Ceramide biosynthesis                 | 2                                   | 2                      | 0.027            |
|                          | Mineralocorticoid biosynthesis        | 2                                   | 2                      | 0.027            |
|                          | Glutathione redox reactions I         | 2                                   | 2                      | 0.027            |
|                          | Glutathione redox reactions II        | 2                                   | 2                      | 0.027            |
|                          | Nicotine degradation IV               | 3                                   | 7                      | 0.042            |
| Sex-Positive             | CMP-N-acetylneuraminate biosynthesis I| 2                                   | 3                      | 0.007            |
|                          | Serotonin degradation                 | 2                                   | 4                      | 0.009            |

Differentially regulated metabolic pathways for genotype and sex were identified by the program mummichog. Enriched pathways were only discovered in the positive ionization mode.