Microorganisms and their hosts share the same environment, and microbial metabolic molecules (metabolites) exert crucial effects on host physiology. Environmental factors not only shape the composition of the host’s resident microorganisms, but also modulate their metabolism. However, the exact molecular relationship among the environment, microbial metabolites and host metabolism remains largely unknown. Here, we discovered that environmental methionine tunes bacterial methyl metabolism to regulate host mitochondrial dynamics and lipid metabolism in Caenorhabditis elegans through an endocrine crosstalk involving NR5A nuclear receptor and Hedgehog signalling. We discovered that methionine deficiency in bacterial medium decreases the production of bacterial metabolites that are essential for phosphatidylcholine synthesis in C. elegans. Reductions of diundecanoyl and dilauroyl phosphatidylcholines attenuate NHR-25, a NR5A nuclear receptor, and release its transcriptional suppression of GRL-21, a Hedgehog-like protein. The induction of GRL-21 consequently inhibits the PTR-24 Patched receptor cell non-autonomously, resulting in mitochondrial fragmentation and lipid accumulation. Together, our work reveals an environment–microorganism–host metabolic axis regulating host mitochondrial dynamics and lipid metabolism, and discovers NR5A–Hedgehog intercellular signalling that controls these metabolic responses with critical consequences for host health and survival.

Microorganisms live in close association with eukaryotic organisms across plant and animal kingdoms. Responding to environmental fluctuations, microorganisms quickly alter their transcriptomes, proteomes and biochemical profiles, which modify microorganism-derived metabolites, and consequently contribute to physiological homeostasis and disease susceptibility of the host. To characterize the molecular relationship between environmental inputs, microorganism-derived metabolites and host signalling pathways in regulating host lipid metabolism, we utilized the Escherichia coli–Caenorhabditis elegans system.

C. elegans consume and harbour microorganisms in their gut, and display conserved microorganism–host interactions as in humans. To study whether the same bacteria exposed to different environments exert distinct effects on host lipid metabolism, we cultured wild type (WT) E. coli strain MG1655 in either lysogeny broth (LB) medium or minimal salts (M9) medium. Comparable amounts of LB- and M9-cultured MG1655 (hereafter called MG1655LB and MG1655M9, respectively) were provided to WT C. elegans. We found that C. elegans grown on MG1655M9 have twofold higher fat content levels than those on MG1655LB (Fig. 1a,b), which were quantified using a lipid imaging technique, stimulated Raman scattering (SRS) microscopy, and further confirmed biochemically (Fig. 1b). These changes in fat content levels are independent of developmental exposure (Fig. 1c), and occur rapidly within 24 h of bacterial switch (Supplementary Fig. 1a). The animals on MG1655LB and MG1655M9 have similar pharyngeal pumping, defecation and lipid absorption rates (Supplementary Fig. 1d), indicating indistinguishable food and lipid uptake. Their motilities, lifespan and brood sizes are also similar (Supplementary Fig. 1g), suggesting LB- and M9-cultured bacteria provide comparable levels of support to maintain C. elegans physical activities, somatic maintenance and reproduction. Interestingly, nematode species that are evolutionarily distant from C. elegans, including Pristionchus pacificus, Rhabditis myriophila and Caenorhabditis briggsae, all increase fat content levels when grown on MG1655M9, as compared to those on MG1655LB (Fig. 1d), suggesting a well-conserved environment–bacteria–host metabolic responsive mechanism across different host species.

Next, we found that MG1655M9 are not different from MG1655LB in the levels of caloric content, triacylglycerides or proteins (Supplementary Fig. 2a–c), but show a marginally increased level of carbohydrate content (Supplementary Fig. 2d). However, increasing...
**Figure 1** Bacterial methyl metabolism links host lipid accumulation with environmental methionine availability. (a) Wild-type (WT) *C. elegans* raised on M9-cultured *E. coli* (MG1655<sup>W</sup>) show increased fat content levels compared with those on LB-cultured *E. coli* (MG1655<sup>L</sup>). Lipid storage was visualized using stimulated Raman scattering (SRS) microscopy (a, scale bar, 30 μm). Quantifications based on SRS microscopy and biochemical analyses show similar results (b). **∗∗∗**<i>P</i> < 0.001, Student’s t-test; <i>n</i> = 3 biologically independent experiments. (c) Adult *C. elegans* sufficiently increase or decrease fat content levels 48 h after switching to MG1655<sup>W</sup> or MG1655<sup>L</sup>, respectively. **∗∗∗**<i>P</i> < 0.001, Student’s t-test; <i>n</i> = 3 biologically independent experiments. (d) Different nematode species, *C. elegans*, *C. briggsae*, *R. myriophila* and *P. pacificus* show higher lipid content on MG1655<sup>W</sup> than on MG1655<sup>L</sup>. **∗∗∗**<i>P</i> < 0.001, **∗**<i>P</i> < 0.01, Student’s t-test; <i>n</i> = 3 biologically independent experiments. (e) When cultured in M9 medium supplemented with 20 amino acids (AAs), MG1655<sup>W</sup> fail to induce lipid accumulation in *C. elegans*; while AA supplementation does not alter the effect of MG1655<sup>L</sup>. When supplemented individually, only methionine, but not the other 19 AAs, sufficiently suppresses MG1655<sup>W</sup>-conferring lipid accumulation in *C. elegans*. Without methionine, the other 19 AAs combined cannot exert any suppressing effects. **∗∗∗**<i>P</i> < 0.001, **∗∗**<i>P</i> < 0.01, NS < <i>P</i> < 0.05, one-way ANOVA; <i>n</i> = 3 biologically independent experiments. (f) *C. elegans* raised on MG1655<sup>W</sup> show increased resistance to starvation, compared with those on MG1655<sup>L</sup>. Supplementation of methionine to M9 medium suppresses the starvation resistance conferred by MG1655<sup>W</sup>. **∗∗∗**<i>P</i> < 0.001, log-rank test; <i>n</i> = 120 biologically independent animals. The experiments were independently replicated in the laboratory three times with similar results. Error bars represent standard error. (g-k) Metabolic analyses show the levels of bacterial metabolites in methyl metabolism, including betaine, homocysteine and methionine but not dimethylglycine. **∗∗∗**<i>P</i> < 0.001, **∗∗**<i>P</i> < 0.01, **∗**<i>P</i> < 0.05, Student’s t-test; <i>n</i> = 3 biologically independent experiments. The relationships in *E. coli* methyl cycle are shown in g. (l) MG1655<sup>W</sup>-conferring lipid accumulations in *C. elegans* are suppressed by direct supplementations of betaine, homocysteine and methionine but not dimethylglycine. **∗∗∗**<i>P</i> < 0.001, NS < <i>P</i> < 0.05, two-way ANOVA; <i>n</i> = 3 biologically independent experiments. Error bars represent mean ± standard error of the mean (s.e.m.) unless indicated.
carbohydrate content in MG1655LB by supplementing extra glucose (MG1655LB+Glucose) is not sufficient to increase fat storage in C. elegans (Supplementary Fig. 2e). Therefore, the altered fat storage is less likely due to global nutritional differences between bacteria, but may be actively regulated by functional metabolites derived from bacteria.

We systematically compared metabolite profiles between MG1655LB and MG1655SAMS. Depletion of sucrose, fructose and related metabolites in MG1655SAMS (Supplementary Table 1) suggests increased fermentation; however, C. elegans grown on fermenting MG1655LB did not show increased fat content levels (Supplementary Fig. 2e,f), ruling out the effect of bacterial fermentation on host fat storage. We also detected alterations in the levels of different amino acids (Supplementary Table 1), suggesting that MG1655SAMS adjust their amino acid metabolism in response to environmental amino acid deprivation. Moreover, we found that restoration of amino acids to M9 medium by adding either peptone or casamino acids sufficiently suppresses the increased fat storage in C. elegans on MG1655LB (Supplementary Fig. 1i). Together, these results show that methionine deprivation is the key environmental input that triggers bacterial metabolic alterations, and consequently changes host metabolism.

Interestingly, we found that C. elegans on MG1655SAMS are more resistant to starvation than those on MG1655LB (Fig. 1f), and this survival advantage is fully abrogated when methionine is restored in the environment (Fig. 1f). These results indicate that environmental methionine deprivation reprograms bacterial metabolism and induces ‘anticipatory’ metabolic adaptation in the host to ensure better survival through starvation. The improved survival outcome might be determined simply by increased fat content levels, and/or more complicatedly by secondary metabolic alterations associated with fat storage changes.

Further functional classification of metabolite profiles revealed that MG1655SAMS have reduced levels of all the components in the bacterial methyl cycle, including betaine, homocysteine, dimethylglycine (DMG), and methionine (Fig. 1g–k). We supplemented these metabolites with MG1655SAMS to C. elegans, and found that betaine, homocysteine and methionine, but not DMG, are sufficient to suppress the MG1655SAMS-conferred lipid accumulation (Fig. 1f). Moreover, the supplementation of betaine or homocysteine requires live bacteria to exert their effects on C. elegans (Supplementary Fig. 1j). Together, these results suggest that specific metabolites derived from the bacterial methyl cycle actively regulate fat storage in the host C. elegans.

Methyl metabolism is tightly linked to the synthesis of the universal methyl donor S-adenosylmethionine (SAM) from methionine, a reaction catalysed by S-adenosylmethionine synthetase SAMS-1 (Fig. 2a)13. We found that the C. elegans sams-1(ok3033), sams-1(ok2946), and sams-1(ok2947) mutants have 2–5-fold higher fat content levels than WT worms on MG1655LB, and do not further increase their fat content levels when on MG1655SAMS (Fig. 2b). In addition, direct supplementation of SAM or methionine to WT C. elegans fully suppresses the MG1655SAMS-conferred lipid accumulation, without affecting C. elegans on MG1655LB, and these effects can bypass the requirement of live bacteria (Fig. 2c,d and Supplementary Fig. 1i). As the product of SAMS-1, SAM supplementation directly to C. elegans also rescues the increased fat storage conferred by the sams-1 mutation (Fig. 2d). Therefore, bacterial methyl cycle deficiency leads to a reduction of SAM synthesis, and consequently promotes lipid accumulation in the host.

SAM is required for three tranmethylation steps during phosphatidylcholine (PC) biosynthesis, catalysed by phosphoethanolamine methyltransferases (PMTs; Fig. 2a)14,15. When hindering tranmethylation by RNAi knockdown of pmt-1, we observed a threefold fat content increase in C. elegans on MG1655LB (Fig. 2e). pmt-1 is known to be specifically expressed in hypodermis16. We found that hypodermis-specific RNAi knockdown of pmt-1 sufficiently mimics the effects of the global RNAi knockdown; however, RNAi knockdown of pmt-1 in the intestine has no such effects (Fig. 2e). Furthermore, upon pmt-1 inactivation in hypodermis, methionine supplementation could no longer suppress the MG1655SAMS-conferred lipid accumulation (Fig. 2f), suggesting that responding to bacterial methyl cycle deficiency, reduction of hypodermal PC biosynthesis in C. elegans leads to increased fat storage. In supporting this idea, direct supplementation of diundecanoyl (PC11:0/11:0) or dilauroyl PC (PC12:0/12:0) suppresses the MG1655SAMS-conferred lipid accumulation (Fig. 2g), which does not require live bacteria (Fig. 2h). In contrast, neither dipalmitoyl PC (PC16:0/16:0) nor distearoyl PC (PC18:0/18:0) shows such an effect (Fig. 2g). The requirement of specific PC molecules in this metabolic regulation hints at the involvement of specific receptor(s) for PC signalling transduction.

From screening a series of mutants of nuclear receptors, cell surface receptors and transcription factors (Supplementary Table 2a), we identified that the nhr-25(ku217) mutant shows a twofold fat storage increase when grown on MG1655LB, which is not further enhanced when grown on MG1655SAMS (Fig. 3a,b). nhr-25 encodes an orphan nuclear hormone receptor that belongs to the NHR family, orthologous to mammalian LRH-1 (liver receptor homologue 1) and SF-1 (steroidogenic factor 1)17–19. Although nhr-25 plays a crucial role in C. elegans development18, the observed fat storage changes in the nhr-25(ku217) mutant are not due to developmental deficiency because this temperature-sensitive mutant was kept under permissive temperature throughout development and shifted to non-permissive temperature only at the adult stage. Next, we generated a transgenic strain expressing GFP-fused NHR-25, which restored the difference of fat content levels in the nhr-25 mutant between MG1655LB and MG1655SAMS (Fig. 3b). The GFP fusion revealed the localization of the NHR-25 protein in the nuclei of hypodermal cells (Fig. 3c), which is consistent with previous studies17–19.

Fat content levels are tightly balanced between the processes of lipid storage (synthesis and incorporation) and lipid mobilization (lipolysis and oxidation). We applied a chemical imaging method coupling deuterium-tracing and SRS microscopy20 to monitor these two processes in vivo. We found that, compared to those on MG1655LB, C. elegans on MG1655SAMS display an increased rate of lipid storage (Fig. 3d) and a decreased rate of lipid mobilization (Fig. 3e). Interestingly, we found that the nhr-25 mutant on MG1655LB show a low rate of lipid mobilization similar to WT worms on MG1655SAMS (Fig. 3e), but does not affect the rate of lipid storage (Fig. 3d).
Specific phosphatidylcholines mediate host lipid metabolic responses. (a) A diagram of phosphatidylcholine (PC) biosynthesis via transmethylation. S-adenosyl methionine (SAM), synthesized by S-adenosyl methionine synthetase (SAMS-1) from methionine, acts as a methyl donor for the phosphoethanolamine N-methyltransferases like PMT-1 to synthesize phosphocholine from phosphoethanolamine. Phosphocholine is the precursor for PC synthesis. (b) C. elegans sams-1(ok3033), sams-1(ok2947) and sams-1(ok2946) mutants show increased fat content levels compared to WT when on MG1655L8, and the fat content levels of the mutants on MG1655L8 and MG1655pmt-1 mutants are not significantly different. ***P < 0.001, NS P > 0.05, Student's t-test. *P < 0.05, two-way ANOVA; n = 3 biologically independent experiments. (c) Direct supplementation of SAM (1 mg ml⁻¹) to C. elegans suppresses MG1655pmt-1-conferring lipid accumulation. ***P < 0.001, NS P > 0.05, Student's t-test. *P < 0.05, two-way ANOVA; n = 3 biologically independent experiments. (d) With bacteria killed by carbenicillin (60μg ml⁻¹), direct supplementation of SAM suppresses lipid accumulations in WT C. elegans conferred by MG1655pmt-1 and in the sams-1(ok3033) mutant. ***P < 0.001, **P < 0.01, *P < 0.05, NS P > 0.05, two-way ANOVA; n = 3 biologically independent experiments. (e) Global RNAi knockdown of pmt-1 increases fat content to similar levels in C. elegans on MG1655L8 and MG1655pmt-1. Hypodermal but not intestinal RNAi knockdown of pmt-1 sufficiently increases fat content levels. ***P < 0.001, NS P > 0.05, One-way ANOVA; n = 3 biologically independent experiments. (f) Upon hypodermis-specific RNAi knockdown of pmt-1, supplementation of methionine to M9 medium fails to suppress MG1655pmt-1-conferring lipid accumulation. ***P < 0.001, NS P > 0.05, one-way ANOVA; n = 3 biologically independent experiments. (g) Direct supplementation of PC11:0/11:0 or PC12:0/12:0 suppresses MG1655pmt-1-conferring lipid accumulation. ***P < 0.001, Student's t-test. **P < 0.01, ***P < 0.001, two-way ANOVA; n = 3 biologically independent experiments. (h) With bacteria killed by carbenicillin (60μg ml⁻¹), direct supplementation of PC11:0/11:0 or PC12:0/12:0 suppresses MG1655pmt-1-conferring lipid accumulations in C. elegans. **P < 0.01, NS P > 0.05, Student's t-test. ***P < 0.001, two-way ANOVA; n = 3 biologically independent experiments. Error bars represent mean ± s.e.m.
Figure 3 PCs act on NHR-25 to regulate host lipid metabolic responses. (a) SRS microscopic images show that the *C. elegans nhr-25(ku217)* mutant has higher levels of fat content than WT on MG1655\(^{18}\), but does not have further increased fat content levels on MG1655\(^{18}\). Scale bar, 50 μm. The experiments were independently replicated in the laboratory three times with similar results. (b) Restoring nhr-25 expression completely suppresses the increased lipid storage in the *nhr-25(ku217)* mutant on MG1655\(^{18}\), without affecting the fat content levels of the *nhr-25(ku217)* mutant on MG1655\(^{18}\) or WT on either MG1655\(^{18}\) or MG1655\(^{18}\). ***P < 0.001, NS P > 0.05, Student’s t-test. ***P < 0.001, two-way ANOVA; n = 3 biologically independent experiments. (c) GFP-fused NHR-25 proteins are enriched in the nuclei of hypodermal cells. Yellow arrowheads highlight hypodermal seam cells. Scale bar, 10 μm. The experiments were independently replicated in the laboratory three times with similar results. (d) The rates of lipid storage in WT and *nhr-25(ku217)* mutant *C. elegans* on MG1655\(^{18}\) are faster than those in *C. elegans* on MG1655\(^{18}\). **P < 0.01, Student’s t-test; n = 3 biologically independent experiments. (e) In WT *C. elegans*, the rate of lipid mobilization is faster on MG1655\(^{18}\) than on MG1655\(^{18}\); however, this increased lipid mobilization is abrogated in the *nhr-25(ku217)* mutant on MG1655\(^{18}\), **P < 0.05, Student’s t-test; n = 3 biologically independent experiments. (f) RNAi knockdown of nhr-25 increases fat content levels in *C. elegans* raised on MG1655\(^{18}\) and blocks the effect of methionine in suppressing MG1655\(^{18}\)-conferred lipid accumulation. ***P < 0.001, NS P > 0.05, one-way ANOVA; n = 3 biologically independent experiments. (g) The effects of PC11:0/11:0 and PC12:0/12:0 on suppressing lipid accumulation are fully abrogated in the *nhr-25(ku217)* mutant. NS P > 0.05, two-way ANOVA; n = 3 biologically independent experiments. (h-j) In HeLa cells transfected with GAL4-DBD/NHR-25-LBD fusion constructs and UAS-luciferase reporters, administration of PC11:0/11:0 (h) or PC12:0/12:0 (i), but not PC18:0/18:0 (j), activates NHR-25-LBD to induce luciferase expression. ***P < 0.001, NS P > 0.05, Student’s t-test; n = 5 biologically independent wells (h); n = 6 biologically independent wells (j). The experiments were independently replicated in the laboratory three times with similar results. Error bars represent mean ± s.e.m.
Figure 4 Endocrine crosstalk of NHR-25 and Hedgehog signalling regulates host lipid metabolic responses by tuning mitochondrial dynamics. (a) The nhr-25(ku217) mutant increases the expression of a Hedgehog-like gene, grr-21. N = 4 biologically independent experiments. (b) Global or hypodermis-specific, but not intestine-specific RNAi knockdown of grr-21 suppresses MG1655<sup>−</sup>-conferred lipid accumulation. N = 3 biologically independent experiments. (c) Global or intestine-specific RNAi knockdown of a patched-related receptor, ptr-24, increases fat content in C. elegans raised on MG1655<sup>−</sup> to the level as on MG1655<sup>+</sup>. RNAi knockdown of ptr-24 in the intestine, in contrast to their filamentous mitochondrial network (raised on MG1655<sup>−</sup> C. elegans), does not affect fat content levels in C. elegans. (d) C. elegans raised on MG1655<sup>−</sup> exhibit fragmented mitochondria in the intestine, in contrast to their filamentous mitochondrial network on MG1655<sup>+</sup>. Methionine supplementation to M9 medium suppresses MG1655<sup>−</sup>-conferred mitochondrial fragmentation. Hypodermal mitochondrial morphology is not affected by bacterial conditions. Mitochondrial morphologies in the intestine and hypodermis were visualized by confocal microscopy in raxls51[Pges-1::mitoGFP] and raxls49[Pcol-12::mitoGFP] adults, respectively. Scale bar, 10 μm. (e) The drp-1(tm1108) mutation, which inhibits mitochondrial fission, suppresses the MG1655<sup>−</sup>-conferred lipid accumulation. In contrast, the fzo-1(tm1133) mutation, which inhibits mitochondrial fusion, does not affect fat content levels in C. elegans on either MG1655<sup>−</sup> or MG1655<sup>+</sup>. N = 3 biologically independent experiments. (f) Global or intestine-specific, but not hypodermis-specific RNAi knockdown of drp-1 suppresses MG1655<sup>−</sup>-conferred lipid accumulation. N = 3 biologically independent experiments. (g) Compared to WT, the nhr-25(ku217) mutant has increased mitochondrial fragmentation when raised on MG1655<sup>−</sup> (P < 0.001, χ² test), but has the WT level of fragmentation when on MG1655<sup>+</sup> (P > 0.05, χ² test). RNAi knockdown of drp-1 abrogates nhr-25-conferred mitochondrial fragmentation. Scale bar, 3 μm. N = 70 biologically independent cells. (h) The drp-1(tm1108) mutation suppresses the nhr-25(ku217)-conferred lipid accumulation. N = 3 biologically independent experiments. (i) RNAi knockdown of grr-21 suppresses mitochondrial fragmentation conferred by MG1655<sup>+</sup> or by the nhr-25(ku217) mutation (P < 0.001, χ² test). RNAi knockdown of ptr-24 induces mitochondrial fragmentation in the WT C. elegans raised on MG1655<sup>+</sup> (P < 0.001, χ² test), but does not further increase mitochondrial fragmentation conferred by MG1655<sup>+</sup> or by the nhr-25(ku217) mutation. N = 60 biologically independent cells. ***P < 0.001, **P < 0.01, Student's t-test; ###P < 0.001, *P < 0.01, two-way ANOVA; error bars represent mean ± s.e.m.
PC biosynthesis and NHR-25 in hypodermal cells (Figs 2e, 3h–j), suggesting a direct binding between NHR-25 LBD and
ligand-binding domain (LBD) fusion proteins and the UAS-luciferase reporter. We found that PC11:0/11:0 and PC12:0/12:0, but not
PC11:0/12:0 or PC12:0/12:0 supplementation fails to suppress the MG1655\textsuperscript{LB}–conferred lipid accumulation (Fig. 4e).
However, the mutant defective in \textit{drp-1}, encoding the \textit{C. elegans} homologue of yeast Dnm1p and mammalian DRP1 required
for mitochondrial fission\textsuperscript{21}, completely suppresses the MG1655\textsuperscript{LB}–conferred lipid accumulation (Fig. 4e). These findings suggest
that mitochondrial fragmentation is necessary for the MG1655\textsuperscript{LB}–conferred fat content increase, but under the MG1655\textsuperscript{LB} condition, it is not
sufficient to induce lipid accumulation. More importantly, consistent with the tissue-specific alterations in mitochondrial architecture
(Fig. 4d), we demonstrated that intestine-specific RNAi knockdown of \textit{drp-1} suppresses the MG1655\textsuperscript{LB}–conferred lipid accumulation
as the global RNAi knockdown does; however, hypodermis-specific \textit{drp-1} RNAi knockdown has no such an effect (Fig. 4e).
Therefore, the induction of mitochondrial fission in the intestine is specifically responsible for the increased lipid accumulation conferred by bacterial metabolic inputs.

Strikingly, host NHR-25/GRL-21/PTR-24 signalling regulates mitochondrial architecture in response to bacterial metabolic inputs. The \textit{nhr-25} mutant exhibits a highly fragmented mitochondrial architecture in the intestine regardless of bacterial conditions (Fig. 4g), and inactivation of \textit{drp-1} suppresses mitochondrial fragmentation (Fig. 4g) and increased lipid accumulation in the \textit{nhr-25} mutant (Fig. 4h). Thus, NHR-25 regulates fat storage through tuning mitochondrial fission–fusion dynamics in the intestine. Moreover, RNAi knockdown of \textit{grl-21} reduces the levels of intestinal mitochondrial fragmentation conferred by MG1655\textsuperscript{LB} and by the \textit{nhr-25} mutation (Fig. 4i); and conversely RNAi knockdown of \textit{ptr-24} promotes mitochondrial fragmentation in \textit{C. elegans} grown on MG1655\textsuperscript{LB}, but cannot further enhance the effect conferred by MG1655\textsuperscript{LB} or by the \textit{nhr-25} mutation (Fig. 4i).

In summary, our results reveal the molecular mechanism by which bacterial metabolic activities link environmental variations with host

\begin{figure}[h]
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\caption{Summary model. Environmental methionine regulates the bacterial methyl cycle, which generates substrates for SAM synthesis in the host. SAM acts as the methyl donor for PC biosynthesis in the hypodermis. Specific PC molecules activate NHR-25, which suppresses the expression of a Hedgehog-related gene, \textit{grl-21}. Reduction of \textit{grl-21} cell non-autonomously liberates the Patched receptor PTR-24 from inhibiting mitochondrial fission. In contrast, under the methionine-deficient environment, low NHR-25 activity leads to highly expressed \textit{grl-21}, which antagonistically represses PTR-24 to promote severe mitochondria fragmentation and excessive lipid accumulation.

Together, these results suggest that NHR-25 functions specifically in the hypodermis and regulates intestinal lipid mobilization cell non-autonomously.

When examining whether NHR-25 transduces specific PC signals to regulate fat metabolic responses, we found that methionine, PC11:0/11:0 or PC12:0/12:0 supplementation fails to suppress the MG1655\textsuperscript{LB}–conferred lipid accumulation in the \textit{nhr-25} mutant (Fig. 3f,g). Next, to confirm direct interactions between the PCs and NHR-25, we conducted transactivation assays by transfecting HeLa cells with constructs of GAL4 DNA-binding domain (DBD)/NHR-25 ligand-binding domain (LBD) fusion proteins and the UAS-luciferase reporter. We found that PC11:0/11:0 and PC12:0/12:0, but not PC18:0/18:0, induce luciferase levels in dose-dependent manners (Fig. 3h–j), suggesting a direct binding between NHR-25 LBD and PC11:0/11:0 or PC12:0/12:0. Considering functional specificities of both PC biosynthesis and NHR-25 in hypodermal cells (Figs 2e and 3c), we conclude that reductions in the levels of hypodermal PCs decrease NHR-25 activation cell-autonomously, and NHR-25 subsequently regulates lipid metabolic responses, primarily in the intestine, via a cell non-autonomous mechanism.

We next investigated how NHR-25 regulates lipid metabolic changes cell non-autonomously. From comparing RNA-seq profiles of \textit{C. elegans} on different bacteria and ChiP-seq profiles of NHR-25, we identified 188 candidate genes that are not only differentially regulated between \textit{C. elegans} exposed to MG1655\textsuperscript{LB} and MG1655\textsuperscript{LB}, but also contain NHR-25 binding sites in promoter regions or gene bodies (Supplementary Fig. 3 and Supplementary Table 3a). Among them, 11 genes encode secreted proteins and express in the hypodermis, and were further examined for their expression levels in the \textit{nhr-25} mutant versus WT (Supplementary Table 3b) and their effects on fat storage. We discovered that \textit{grl-21}, encoding a Hedgehog-like protein, is induced 10-fold transcriptionally in the \textit{nhr-25} mutant (Fig. 4a and Supplementary Table 3b), and either global or hypodermal but not intestinal RNAi knockdown of \textit{grl-21} completely abrogates the MG1655\textsuperscript{LB}–conferred lipid accumulation (Fig. 4b). In search of Patched receptor(s), which is antagonized by the Hedgehog-like protein, we screened 15 Patched homologues in \textit{C. elegans} (Supplementary Table 2b,c). We discovered that RNAi knockdown of the Patched gene \textit{ptr-24} increases lipid accumulation in \textit{C. elegans} on MG1655\textsuperscript{LB} (Fig. 4c and Supplementary Table 2b), and intestine-specific RNAi knockdown of \textit{ptr-24} sufficiently mimics this effect (Fig. 4c). Together, these results suggest that NHR-25 controls \textit{grl-21} transcription in the hypodermis, and GRL-21 inhibits the intestinal PTR-24 receptor to regulate fat storage cell non-autonomously.

Lipid metabolism is tightly linked to mitochondrial dynamics, which is governed by the balance between organelar fusion and fission. Although there are no significant differences in the levels of mitochondrial DNA content between \textit{C. elegans} on MG1655\textsuperscript{LB} and MG1655\textsuperscript{LB} (\textit{P} > 0.05, Supplementary Fig. 1j), we found that \textit{C. elegans} on MG1655\textsuperscript{LB} show excessive mitochondrial fragmentation in the intestine, in contrast to \textit{C. elegans} on MG1655\textsuperscript{LB} that have mitochondria composed of a tubular and filamentous network (Fig. 4d). Interestingly, methionine supplementation compromises the MG1655\textsuperscript{LB}–conferred mitochondrial fragmentation in the intestine (Fig. 4d). On the other hand, mitochondrial architecture in the hypodermis shows no obvious differences, irrespective of bacterial conditions (Fig. 4d). Furthermore, we found that the mutation of \textit{drp-1}, encoding the \textit{C. elegans} homologue of yeast Dnm1p and mammalian DRP1 required for mitochondrial fission\textsuperscript{21}, completely suppresses the MG1655\textsuperscript{LB}–conferred lipid accumulation (Fig. 4e). However, the mutant defective in \textit{fzo-1}, encoding the \textit{C. elegans} mitofusin required for mitochondrial fusion\textsuperscript{22} (Supplementary Fig. 1k), still increases fat content levels when exposed to MG1655\textsuperscript{LB} (Fig. 4e). These findings suggest that mitochondrial fragmentation is necessary for the MG1655\textsuperscript{LB}–conferred fat content increase, but under the MG1655\textsuperscript{LB} condition, it is not sufficient to induce lipid accumulation. More importantly, consistent with the tissue-specific alterations in mitochondrial architecture (Fig. 4d), we demonstrated that intestine-specific RNAi knockdown of \textit{drp-1} suppresses the MG1655\textsuperscript{LB}–conferred lipid accumulation as the global RNAi knockdown does; however, hypodermis-specific \textit{drp-1} RNAi knockdown has no such an effect (Fig. 4e). Therefore, the induction of mitochondrial fission in the intestine is specifically responsible for the increased lipid accumulation conferred by bacterial metabolic inputs.

In summary, our results reveal the molecular mechanism by which bacterial metabolic activities link environmental variations with host
fat metabolism, and elucidate the crucial roles of NR5A family nuclear receptor and Hedgehog signalling in regulating mitochondrial dynamics and fat metabolism (Fig. 5). The endosome crosstalk coordinating phospholipid (hypodermis) and neutral lipid (intestine) metabolism highlights the complexity of metabolic adaptation responses at the whole organism level.

Interestingly, although methionine and its associated 1-carbon metabolism have been linked to SREBP-mediated lipogenesis23, SREBP plays a negligible role in the metabolic adaptation responses to different bacterial environments (Supplementary Table 2a). Instead, our findings demonstrate a close link between mitochondrial architecture and bacterial inputs during host metabolic adaptation, and methionine serves as a crucial cue mediating this connection. Bearing in mind that mitochondria and bacteria are evolutionary relatives and share some of the similar mechanisms for chemical communication24,25, it would be interesting to further elucidate the roles of mitochondria in bacteria–host interactions for improving host fitness. □

METHODS

Methods, including statements of data availability and any associated accession codes and references, are available in the online version of this paper.

Note: Supplementary Information is available in the online version of the paper.

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AUTHOR CONTRIBUTIONS

C.-C.J.L. and M.C.W. wrote the manuscript. C.-C.J.L. and M.C.W. conceived and designed the study. C.-C.J.L. conducted the experiments.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

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We thank J. Mello (Harvard Medical School, USA) for providing strains JM45 and JM43, J. Mamrsh (Caltech, USA) for providing MH155 strain, HeLa cells and discussion, G. Ruvkun (Harvard Medical School, USA) for providingdaf-16(mgDF47), J. J. Wang (University of Wisconsin-Madison, USA) for providingMG1655 bacteria and discussion, J. Sowa and I. Neve for providing OP50 RNAi bacteria, K. H. L. Mak for providing strain raxkls49, W. Dang and H. Liu for biochemical support, Y. Yu and A. S. Mutlu for the SRS support, A. Dervisefendic, H. D. Oakley and P. Slay for maintenance support, H. Liang and L. Han for RNA-seq bioinformatic support, C. Herman, D. Moore, A. Yu, A. Folick and S. Choi for discussions, and H. Dierick, C. Herman and C.-L. F. Li for critical reading of the manuscript. We appreciate the NRBP (Japan) and the CGC (USA) for providing mutant strains. The CGC is funded by NIH Office of Research Infrastructure Programs (P40 OD010440). This work was supported by grants from HHMI (M.C.W.) and National Institute of Health (R01AG045183, R01AT009050, DP1DK113644, M.C.W.), and in part by a training fellowship from the Burroughs Wellcome Fund—The Houston Laboratory and Population Science Training Program in Gene-Environment Interaction of the University of Texas Health Science Center at Houston (BWF Grant 1008200, C.-C.J.L.).

AUTHOR CONTRIBUTIONS

C.-C.J.L. and M.C.W. wrote the manuscript. C.-C.J.L. and M.C.W. conceived and designed the study. C.-C.J.L. conducted the experiments.

COMPETING FINANCIAL INTERESTS

The authors declare no competing financial interests.

LETTERS
METHODS

Nematode strains and generation of transgenic lines. *Caenorhabditis elegans* wild type (N2), *Caenorhabditis briggsae* wild isolate (PBB862), *Pristionchus pacificus* wild isolate (PS5312), *Rhabditis myophilus* wild isolate (*DF5020*, *S.1400 (zh1313hsp-6::GFP); rnc14::DTn10 [rnc14::DTn10 laczgA::T7pol camFRT] (nhr-25[ka217]) X, RB2240 (sams-1(ok3033) X), VC2224 (sams-1(ok9247) X), VC2428(sams-1ok9246) X), CU6372 (dpy-1(15sa10) IV), CU5991 (fzo-1(15sa113) II), CB383 (bpl-1(ep176) III), CB1655 (nhr-80(10ml1) III), STE68 (nhr-49[2041] I), A8A6 (daf-12[2rh26; 2rh31] X), LT121 (dvl-1[870] V), CB1372 (daf-7[4;3723] III), DR63 (daf-7[6nts3] III), DR40 (daf-7[404] IV), GR1321 (pfh-7[2800] II), FI1106 (nhr-64[7406] I), STE69 (nhr-66[ok4040] IV), STE71 (nhr-17[gk796] V), AES01 (nhr-8[k1068] IV), VCI320 (nhr-123[gk777] VII), RR2085 (nhr-72[ok2571] I), RR1661 (nhr-85[ok2901] I), VCI120 (nhr-17[gk509] X), RB1201 (nhr-181[ok1250] V), FX977 (nhr-83[7977] V), FV1804 (nhr-226[15804] IV), VX1375 (nhr-42[4;3715] V), VC2192 (pitr-7[37177] X), and VC2193 (pitr-3[10636] I) were obtained from the Caenorhabditis Genetics Center. The strain nhr-139(n33770), ptr-3(n379422), ptr-16(n7951), and ptr-23(n37562) was obtained from National BioResource Project (Japan). The strain daf-16(mg416) was a gift from G. Ruvkun. The strains JM45 (nld-1[2e12]; Is[pape-1-RDE-1::unc54 3’UTR; Pmyo-2::RFP3]) and JM43 (nld-1[2e12]; Is[pape-2-RDE-1::unc54 3’UTR; Pmyo-2::RFP3]) were gifts from J. Mello.

The transgenic strains were generated by gonadal microinjection of DNA mixtures at young adult stage. The integrations of extrachromosomal arrays were induced by gamma irradiation exposures (4,500 rad, 5.9 min) at the L4 stage, and the integrated progeny were backcrossed to N2 at least five times. We generated and used the following transgenic strains: rnaEx[27P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs32[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs3[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs12[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs12[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs12[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs12[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry], raxIs12[P/hr-35::gfp::GFP-nhr-25; Pmyo-2::mcherry]. The strains were incubated in 20°C for both maintenance and experiments, except for experiments containing the temperature-sensitive allele nhr-25[ka217] were shifted to 25°C after development.

Bacteria strains. *E. coli* wild type (MG1655) was a gift from J. Wang. The RNAi competent *E. coli* OP50 strain [res[141-Deln10 lacZ::T7pol camFRT]] was described as described in the literature26.

Culture media, plates and supplementations. MG1655 refers to the bacteria that were inoculated into four tubes, each containing 2 ml of M9 minimal medium for overnight culture (37°C, 220 r.p.m.) and were then followed under SRS at time points of interest. The deuterium diet for two generations, and transferred to a regular diet at the L3 stage, C. elegans were obtained from the Caenorhabditis Genetics Center. The strain nhr-139(n33770), ptr-3(n379422), ptr-16(n7951), and ptr-23(n37562) was obtained from National BioResource Project (Japan). The strain daf-16(mg416) was a gift from G. Ruvkun. The strains JM45 (nld-1[2e12]; Is[pape-1-RDE-1::unc54 3’UTR; Pmyo-2::RFP3]) and JM43 (nld-1[2e12]; Is[pape-2-RDE-1::unc54 3’UTR; Pmyo-2::RFP3]) were gifts from J. Mello.

Measurement of lipid content levels in *C. elegans* by SRS microscopy. *C. elegans* (day-1-old hermaphrodite adults unless indicated, sample size larger than 10 for each of three biological replicates) were anaesthetized in 1% sodium azide in M9 buffer (3 g KH2PO4, 6 g Na2HPO4, 5 g NaCl, 1 ml 1M MgSO4, H2O to 1 litre, sterilized by autoclaving), and mounted on 2% agarose pads sandwiched between glass microscopic slides and coverslips. Images were taken using the SRS system as described in the literature26. In brief, when using a Stokes beam at 1,064 nm and a pump beam at 870 nm. In lipid storage and lipid mobilization rate measurements, deuterium-labelled fat content was traced by examining the Raman signals of CH2 bonds at 2,100 cm−1, which were generated by using a Stokes beam at 1,064 nm and a pump beam at 870 nm. In lipid storage tracing experiments, *C. elegans* were transferred to the deuterium diet at the L3 stage, and imaged under SRS at desired time points until saturation. In lipid mobilization tracing experiments, *C. elegans* were grown on a deuterium diet for two generations, and transferred to a regular diet at the L3 stage, and were then followed under SRS at time points of interest. The deuterium diet was prepared by mixing 2% oleic acid-d34 (Sigma #683582) with MG1655 bacteria, which were cultured from either LB or M9 medium made with deuterium water (D2O, Sigma #151882).

Measurement of lipid content levels in *C. elegans* by biochemical assays. Around 5,000 *C. elegans* (day-1-old adults) were washed off each plate, and divided into two parts for both lipid and protein analyses. For lipid extraction, the *C. elegans* samples were sonicated in an organic solvent made of chloroform : isopropanol : NP-40 (7:11:0.1). The supernatants of the lysates underwent a vacuum-drying step to evaporate the organic solvents, and then were re-dissolved in PBS for TAG assay (Infinity Triglycerides Liquid Stable Reagent, Thermo Scientific, #TR-22421). The values of TAG levels were normalized to the values of protein levels. For protein extraction, the *C. elegans* samples were sonicated in PBS. The supernatants of the lysates were subjected to the Bradford method (Bio-Rad Protein Asssay Dye Reagent Concentrate, #500-0006) to determine protein concentrations.

Physiological measurement in *C. elegans*. Food intake and defecation rates. Videos recording anterior regions of at least 10 individual *C. elegans* (day-1-old hermaphrodite adults) under stereoscope were played in slow motion to calculate the number of defecations per second for all animals. The average fluorescent signals from the first three pairs of intestinal cells were measured using the software ImageJ and were normalized to the exposure times.

Lipid absorption. C1-BODIPY-C12 solution (Life Technologies, D-3823) was added on top of a UV-killed bacteria lawn on NGM or M9 plates at a final concentration of 10 µM, and kept in the dark while being dried in laminar flow hood. *C. elegans* (day-1-old hermaphrodite adults) were transferred onto the C1-BODIPY-C12-containing plates. After the desired times, at least 10 BODIPY-fed *C. elegans* were imaged under an Axioplán2 fluorescence compound microscope (Zeiss) with an Axiocam MRc5 camera (Zeiss), with the ‘auto exposure’ function in the Axiovision imaging software. The average fluorescent signals from the first three pairs of intestinal cells were measured using the software ImageJ and were normalized to the exposure times.

Locomotion activities. *C. elegans* (day-1-old hermaphrodite adults) on freshly seeded bacterial lawns were video recorded using an SMZ1500 stereo microscope (Nikon) connected to a C11440 camera (Hamamatsu). At least 10 individual *C. elegans* were tracked by means of the NIH Elements AR imaging software (Nikon). The moving speed of each of *C. elegans* was calculated by dividing the distance travelled by the elapsed time.

Brood size measurement. More than 15 synchronized L4 hermaphrodite *C. elegans* larvae were transferred to new, individual plates every day until reproduction
cessation. The numbers of hatched progeny were counted across the whole reproductive span to calculate the total brood size for each of individual *C. elegans*. The experiments were performed at 20 °C.

**Lifespan.** Survival, death and censor of more than 100 synchronized hermaphrodite *C. elegans* were recorded every day. Meanwhile, *C. elegans* were transferred to new plates every day until reproductive cessation, and then transferred to new plates every four days to keep providing comparable environmental conditions over time until the population dies off. The experiments were performed at 20 °C.

**Macronutrient and caloric measurements in E. coli.** *E. coli* cultures were seeded onto NGM or M9 plates for at least five biological replicates. After being incubated at 20 °C for three days, the *E. coli* lawns were scraped and collected in distilled deionized water and washed three times. The *E. coli* pellets were pooled and vacuum-dried. Dried weights were measured for normalization.

**Protein.** The protein extraction method was modified from the previous study. *E. coli* samples were re-suspended in TENG-300 buffer (50 mM Tris-HCl pH 7.5, 300 mM NaCl, 1 mM EDTA pH 8.0, 0.5% NP-40, 10% glycerol), PBS and glass beads (100 mM NaCl, 1 mM EDTA pH 8.0, 0.5% NP-40, 10% glycerol), PBS and glass beads were subjected to the Bradford method (Bio-Rad Protein Assay Dye Reagent Concentrate, #500-0006) to determine protein concentrations.

**TAG.** Lipids were extracted using an organic solvent consisting of chloroform:isopropanol: 3:1 (v/v). The samples were re-suspended in TENG-300 buffer (50 mM Tris-HCl pH 7.5, 300 mM NaCl, 1 mM EDTA pH 8.0, 0.5% NP-40, 10% glycerol), PBS and glass beads (100 mM NaCl, 1 mM EDTA pH 8.0, 0.5% NP-40, 10% glycerol), PBS and glass beads, and then the supernatants were analyzed by mass spectrometry (Thermo Scientific, #TR-22421). The final dried weights were measured for normalization.

**Carbohydrate.** Carbohydrate levels were determined by the anthrone method modified from the previous study. *E. coli* samples were re-suspended in 2.5 M HCl for 3 h to hydrolyze saccharides, and then filter through a 0.2 µm filter. The filtrate was measured for absorbance at 620 nm.

**Colorimetry.** Bacterial colorimetry was performed using an oxygen bomb calorimeter (Parr Model 1541) at the Missouri State Chemical Laboratory. The calorific value of dry bacterial sample was determined by burning in a high-pressure oxygen atmosphere within an oxygen bomb. The released heat of combustion was recorded in a temperature rise in the absorbing medium. The calorific value was calculated by multiplying the temperature changes by the heat capacity, followed by an adjustment using a correction factor for the heat loss.

**Metabolites analysis.** *E. coli* metabolite profiling was performed at Metabolon with five samples each of MG1655 and MG6155. *E. coli* lawns were incubated at 20 °C for three days, and then scraped and collected in distilled deionized water with three times of washing. Each sample contained around 0.1 mg of pooled bacterial pellet. The samples were filtered in liquid nitrogen; the profiling platforms have been described in the previous study. Carbohydrates were identified in this study. A statistical analysis was performed using Welch’s two-sample t-test to identify metabolites that differed significantly between MG1655 and MG6155.

**Transactivation assay in mammalian cells.** The GAL4/UAS system driven luciferase expression in HeLa cells was utilized to measure the transactivation activities of phosphatidylcholines on NHR-25. HeLa cells were cultured in DMEM (Sigma #D5796) with 10% newborn calf serum (Sigma #N4637) and 1% penicillin-streptomycin (Sigma #P0781). When HeLa cells reached 50–70% confluency, lipotransfection of plasmids for expressing GAL4::NHR-25 fusion protein was performed together with FuGENE 6 transfection reagent (Promega #E2692) (2 µl/well) in 24-well plates (1 ml/well). The calibration of activities of phosphatidylcholines on NHR-25 was performed in triplicate for five independent experiments. The DNA content was determined using quantitative real-time polymerase chain reaction (qPCR) analysis of DNA methylation copy number (CPM) and average normalized fluorescence intensities (ANFI). The DNA content was determined using quantitative real-time polymerase chain reaction (qPCR) analysis of DNA methylation copy number (CPM) and average normalized fluorescence intensities (ANFI).

**Confluent microscopy.** Transgenic strains raxEx78[Prhnr-25::eGFP::nhr-25; Pmyo-2::mcherry; lpr-3::Tet-off; lacZ::37pol camFRT], which lacks RNAIII RNAse activity but gains IPTG-inducible T7 RNA polymerase, was transformed into the genome of each of the three biological replicates, and was anaesthetized in 1% sodium azide M9 buffer for starvation challenges. The survivals and deaths were recorded daily. The experiments were performed at 20 °C. The P-values for log rank tests were achieved by using Kaplan–Meier survival analysis.

**RNAi treatments.** The RNAi vectors minipreped from the Ahringer or Vidal library were transformed into the genetic modified OP50 [rnc14::DmTn10 lacZ::37pol camFRT], which lacks RNAIII RNAse activity but gains IPTG-inducible T7 RNA polymerase. The RNAi OP50 colonies were selected by carbenicillin (50 µg ml−1), tetracycline (50 µg ml−1) and chloramphenicol (17 µg ml−1) resistance, and verified by Sanger sequencing. RNAi OP50 bacteria were cultured for 16 ~ 20 h in LB with 25 µg ml−1 carbenicillin, 5 µg ml−1 tetracycline and 17 µg ml−1 chloramphenicol; and the threefold concentrated bacteria cultures were seeded onto RNAi agar plates that contain 1 mM IPTG and 50 µg ml−1 carbenicillin. The plates were incubated at room temperature for one day to induce dsRNA expressions. Approximately 100 synchronized L1 larvae were placed: when reaching adulthood, between approximately 20 and 30 hermaphrodite adults were transferred to new RNAi bacterial plates to lay progeny. The reason for two generations of RNAi treatment was to enhance RNAi efficiency and phenotypic consistency. Synchronized L4 hermaphrodite larvae from the second generation were used as a negative control.
and coverslips. Confocal images were taken using an IX81 microscope (Olympus) connected to an AxioCam ICC3 camera (Zeiss).

Mitochondria morphology measurement. Transgenic strains raxIs51[Pges-1::mitoGFP], nhr-25[ku217], raxIs51[Pges-1::mitoGFP], and raxIs49[Pcol-12::mitoGFP] were imaged in hermaphrodites at the day-3-old adult stage, and presented with single-layer images in anterior regions for consistency. For morphological categorization, if the lengths of majority of mitochondrial filaments in a cell were longer than 4 μm, it would be considered ‘filamented’; if the lengths of majority of mitochondrial filaments in a cell were shorter than 2 μm, it would be considered ‘fragmented’, the rest belonged to the category ‘intermediate’. By using cell as a unit, the accumulated counts of at least 60 cells from each genotype and environmental condition were summed up across biological replicates, and calculated into percentages for bar representations. The χ² test for trend was conducted for statistic analysis.

Fermentation test. Fermentation tests were performed with phenol red as an acidification indicator. Phenol red (Sigma #P3532) was added into the media of E. coli 26. Neve, I., Sowa, J. & Wang, M. C. Modified medium for the oxidation-fermentation test in the identification of marine bacteria. Appl. Environ. Microbiol. 49, 1541–1543 (1985).

RNA extraction and sequencing analysis. Total RNAs were extracted from at least 5,000 young C. elegans adults with Trizol (Life Technologies #15596) followed by column purification (Qiagen #74106). cDNA library and sequencing were carried out by Genomic and RNA Profiling Core at Baylor College of Medicine. Sequence reads were aligned to the C. elegans reference genome (ce10) from UCSC by means of the methods Burrows-Wheeler Aligner (BWA) and Bowtie2/TopHat. By using Cuffdiff, the aligned sequences were mapped to 19,861 of the annotated genes, including 1,632 differentially expressed genes with a change ≥2-fold. Cuffdiff, the aligned sequences were mapped to 19,861 of the annotated genes, including 1,632 differentially expressed genes with a change ≥2-fold. By using cell as a unit, the accumulated counts of at least 60 cells from each genotype and environmental condition were summed up across biological replicates, and calculated into percentages for bar representations. The χ² test for trend was conducted for statistic analysis.

Statistics and reproducibility. In our experimental design, the sample sizes were determined carefully based on experience, although no statistical method was used to predetermine sample sizes. Animal populations were randomized by pipetting in liquid before seeding onto the plates, and picked blindly for phenotypic examinations. From biologically independent experiments/animals/cells/wells, the quantified values that passed the statistical assumption test and showed comparable variances were subjected to appropriate statistical analyses as indicated. The n numbers used to derive statistical analyses are noted in the legends. The numbers of times that experiments were replicated in the laboratory are also noted in the legends, except for Fig. 4d, i, in which the experiments were independently replicated in the laboratory three times with similar results.

Data availability. RNA-seq data that support the findings of this study have been deposited in the NCBI Sequence Read Archive (SRA, http://www.ncbi.nlm.nih.gov/sra) under the BioProject ID PRJNA378539. The accession codes for each of the biological samples are SAMN06551858, SAMN06551859, SAMN06551860, SAMN06551861, SAMN06551862 and SAMN06551863. NHR ChIP-seq data that support the findings of this study are from the modENCODE project under the NCBI BioProject ID PRJNA13758. The extracted datasets generated for this manuscript are provided in Supplementary Table 3a, b. Source data for Fig. 1h–k have been provided as Supplementary Table 1. All other data supporting the findings of this study are available from the corresponding author on request.

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Supplementary Figure 1 Physiological measurements in C. elegans living on MG1655LB and MG1655M9. (a) Adult C. elegans significantly increase or decrease fat content levels within 24 hours of switching to MG1655M9 or MG1655LB, respectively. *p<0.05, **p<0.01, Student’s t-test; n=3 biologically independent experiments. (b) and (c) C. elegans raised on MG1655LB and on MG1655M9 show similar rates of pharyngeal pumping (b) and defecation (c), indicating comparable food intake rate and food retention time. Error bars represent standard deviation (SD). p>0.05, Student’s t-test; n=3 biologically independent experiments. (d) C. elegans raised on MG1655LB and MG1655M9 show indistinguishable rates of lipid absorption, assayed by a lipophilic BODIPY fluorescence dye. p>0.05, Student’s t-test; n=10 biologically independent animals. The box plots were generated to indicate ranges of min to max values, with 25th, 50th and 75th percentiles. (e-g) C. elegans raised on MG1655LB and MG1655M9 show similar levels of mobility (e, p>0.05, Student’s t-test; n=11 biologically independent animals), lifespan (f, p>0.05, Log-rank test; n=100 biologically independent animals), and brood size (g, p>0.05, Student’s t-test; n=18 biologically independent animals). The experiments were independently replicated in laboratory 3 times with similar results. (h) C. elegans raised on E. coli cultured in M9 medium supplemented with either peptone or casamino acids (CAA) show reduced lipid accumulation, compared with those on MG1655M9. **p<0.01, ***p<0.001, Student’s t-test; n=5 biologically independent experiments. (i) With bacteria killed by carbenicillin (60μg/ml), MG1655M9-conferred lipid accumulation in C. elegans can still be significantly suppressed by supplementation of methionine but not betaine or homocysteine. ***p<0.001, **p<0.01, n.s. p>0.05, Student’s t-test. ##p<0.01, n.s. p>0.05, two-way ANOVA; n=3 biologically independent experiments. (j) Mitochondrial DNA copy numbers are not significantly different among C. elegans raised on MG1655LB, MG1655LB+Methionine, MG1655M9, and MG1655M9+Methionine, n.s. p>0.05, one-way ANOVA; n=3 biologically independent experiments. (k) The fzo-1(tm1333) mutant exhibits completely fragmented mitochondrial morphology, p<0.001, Chi-squared test; n=50 biologically independent cells. The experiments were independently replicated in laboratory 3 times with similar results. Error bars represent mean ± standard error of the mean (SEM).
Supplementary Figure 2 Nutritional characterizations in *E. coli* MG1655<sub>LB</sub> and *E. coli* MG1655<sub>M9</sub>. (a) Oxygen bomb calorimetry revealed similar caloric values in MG1655<sub>LB</sub> and MG1655<sub>M9</sub>. (b) and (c) The levels of triacylglycerides (b) and proteins (c) were measured biochemically and found no significant differences between MG1655<sub>LB</sub> and MG1655<sub>M9</sub>. n.s. p>0.05, Student's t-test; n=7 biologically independent experiments (b), n=5 biologically independent experiments (c). (d) MG1655<sub>M9</sub> has a higher level of carbohydrates than MG1655<sub>LB</sub>. *p*<0.05, Student's t-test; n=6 biologically independent experiments. (e) Fermenting MG1655<sub>LB</sub>+glucose (with 0.2% glucose), as verified in (f), is not sufficient to recapitulate MG1655<sub>M9</sub>-conferred lipid accumulation in *C. elegans*. *C. elegans* on MG1655<sub>LB</sub> (without glucose) served as negative controls. n.s. p>0.05, Student's t-test; n=3 biologically independent experiments. (f) In phenol red fermentation tests, MG1655<sub>M9</sub> shows positive fermentation (yellow), but MG1655<sub>LB</sub> shows negative fermentation (red). Addition of glucose (0.2%) to LB is sufficient to drive MG1655<sub>LB</sub>+glucose to undergo fermentation. The experiments were independently replicated in laboratory 3 times with similar results. Error bars represent mean ± SEM.
Supplementary Figure 3 Search of endocrine signaling candidates by bioinformatics. The Venn diagram showing 188 overlapped genes that are differentially regulated between *C. elegans* grown on MG1655<sup>LB</sup> and MG1655<sup>M9</sup> (NCBI BioProject ID PRJNA378539) and are found in NHR-25 ChIP-seq (modENCODE project, NCBI BioProject ID PRJNA13758). The identities of these 188 genes are listed in Supplementary Table 3a.
Supplementary Table Legends

Supplementary Table 1 Comparison of metabolomic profiles between *E. coli* MG1655<sup>LB</sup> and *E. coli* MG1655<sup>M9</sup>. (a) Metabolomic profiling analyses reveal metabolites that are significantly upregulated (64) and downregulated (90) in *E. coli* MG1655<sup>M9</sup> vs. *E. coli* MG1655<sup>LB</sup>, out of total 261 detected bacterial metabolites. The metabolites are categorized by super-pathways and sub-pathways. *p*<0.05, Welch’s *t*-test; *n*=5 biologically independent experiments.

Supplementary Table 2 Summary of candidate screening for the fat metabolic response. (a) List of screened genotypes for fold changes in lipid content levels. (b,c) Lists of screened patched genes that are reported with intestinal expressions according to Wormbase by RNAi knockdowns (b) and genetic mutations (c). N=20 biologically independent animals. The experiments were independently replicated in laboratory 2 times with similar results.

Supplementary Table 3 Search of endocrine signaling candidates by bioinformatics. (a) List of the identities of the 188 genes that are differentially regulated between *C. elegans* grown on MG1655<sup>LB</sup> and MG1655<sup>M9</sup> (NCBI BioProject ID PRJNA378539) and are found in NHR-25 ChIP-seq (modENCODE project, NCBI BioProject ID PRJNA13758), containing 134 genes reported with hypodermal expression according to Wormbase. (b) List of the 11 genes (out of the 188 genes) reported to be secreted according to Wormbase, and the distances of NHR-25 binding regions to their transcription start site (TSS) according to ChIP-seq (modENCODE project, under the NCBI BioProject ID PRJNA13758). The order was prioritized by the levels of mRNA induction in the *nhr-25(ku217)* mutant as compared to WT according to qPCR. NA, not available due to non-specific primer alignments; *n*=4 biologically independent experiments.