

# Short chain fatty acids and microbiota metabolites attenuate ghrelin receptor signaling

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Running title: Microbiota metabolites attenuate ghrelin receptor signaling

34 **Abstract**

35 The gastrointestinal microbiota is emerging as a unique and inexhaustible source for metabolites  
36 with potential to modulate G-Protein-coupled receptors (GPCRs). The ghrelin receptor (GHSR-  
37 1a), is a GPCR expressed throughout both the gut and the brain, with a crucial role in  
38 maintaining energy balance and metabolism as well as in central modulation of food intake,  
39 motivation, reward and mood. To date, no studies have investigated the potential of the  
40 gastrointestinal microbiota and its metabolites to modulate GHSR-1a signaling. Here we  
41 investigate the effects of short-chain fatty acids (SCFAs), lactate, and different commensal  
42 bacterial supernatants on GHSR-1a signaling, using calcium mobilization and imaging assays,  
43 receptor internalization,  $\beta$ -arrestin recruitment, and further downstream mTOR, ERK 1/2 and  
44 eEF2 signaling. We identify, for what is to our knowledge the first time, a potent effect of  
45 microbiota-derived metabolites on GHSR-1a signaling with potential significant consequences  
46 for host metabolism and physiology. We suggest a novel route of communication between the  
47 gut microbiota and the host via modulation of GHS-R-1a receptor signaling. Together, this study  
48 highlights, the vast and emerging therapeutic potential in the exploration of the microbiota  
49 metabolome in the specific targeting of key GPCRs, with pleiotropic actions that span both the  
50 central nervous system and periphery.

51 **Keywords:** Ghrelin, GHSR-1a, Microbiota, SCFA, Lactate, Probiotics

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## 56 **Introduction**

57 Recent evidence is positioning the gut microbiota as a rich source for bioactive metabolites able  
58 to specifically target G-protein coupled receptor (GPCR) within the gut brain axis (1–6). These  
59 studies not only reveal the gut microbiome as a rich reservoir to mine ligands with a high  
60 potential to modulate several GPCRs, but also provide a targeted platform to identify the  
61 molecular mechanism by which gut microbiota can manipulate its host. Here, we investigate the  
62 potential of microbiota derived metabolites to modulate the growth hormone secretagogue  
63 receptor (GHSR-1a), also known as the ghrelin receptor. The ghrelin receptor is ubiquitously  
64 expressed throughout the gut-brain axis, and represents a major therapeutic target for several  
65 different disorders ranging from metabolic and eating disorders, including obesity, diabetes and  
66 cachexia, to affective disorders, including anxiety and depression, to even cancer (7–9). The  
67 peripheral and central effects of GHSR-1a signaling, are mediated by the endogenous ligand,  
68 ghrelin, a 28-amino acid peptide hormone, which is synthesized and secreted from the stomach  
69 (10). The gut microbiome has been demonstrated to play a crucial role in a plethora of host  
70 functionalities, many of which are overlapping with the therapeutic areas for which the GHSR-1a  
71 is being investigated, including metabolism, obesity, mood disorders and stress-vulnerabilities  
72 (11, 12). Moreover, the GHSR-1a is expressed throughout the small and large intestine (13),  
73 making it a likely target for the direct interaction with the gut microbiota and microbiota-derived  
74 metabolites, such as short chain fatty acids (SCFAs). Evidence suggests that SCFAs are able to  
75 reach the brain, highlighting the potential to modulate both peripheral and central functions  
76 mediated by GPCRs (14–17). Interestingly, a recent study showed that gut-microbiota derived  
77 acetate was able to stimulate ghrelin secretion and obesity (18) and a few studies have shown

78 changes in circulating ghrelin levels when the microbiota is altered, reinforcing a potential  
79 association of the gut microbiota with the ghrelinergic system (19–21).

80 The pleiotropic physiological effects of the ghrelinergic system are both down to the prevalent  
81 distribution of the GHSR-1a and likely also due to its complex intracellular signaling, involving  
82 G-protein–dependent and –independent pathways, high basal constitutive activity and biased  
83 modulation of GHSR-1a signaling (22). Indeed, G-protein–dependent signaling of the GHSR-1a  
84 includes G $\alpha$ q-dependent activation of Phospholipase C (PLC), inositol trisphosphate (IP3) and  
85 calcium release as well as G $\alpha$ i-dependent activation of phosphatidylinositol 3-kinase (PI3K)  
86 while G-protein-independent signaling involves the recruitment of  $\beta$ -arrestin leading to receptor  
87 internalization (22). As a result, binding of ghrelin to GHSR-1a can trigger the activation of  
88 protein kinase C (PKC), AMP-activated protein kinase (AMPK), mammalian Target of  
89 Rapamycin (mTOR) and extracellular signal–regulated kinases (ERK) 1/2 signaling, stimulating  
90 pro-synthetic pathways and gene expression, cellular metabolism and proliferation (22–24).

91 To date, no studies have investigated the potential of gut microbial components to modulate  
92 GHSR-1a signaling in spite of its central role in gut-brain axis signaling. Therefore, in this study,  
93 we investigate different bacterial-derived metabolites from different bacterial strains, most of  
94 them belonging to the most common species often used as probiotics, *Bifidobacterium* spp. and  
95 *Lactobacillus* spp., for their capability to modulate the GHSR-1a. Regarding bacterial  
96 metabolites, we focus on SCFAs (acetate, propionate and butyrate) and lactate, because these  
97 represent some of the most common gut microbiota-derived metabolites and have been shown to  
98 exert multiple effects on host physiology including modulation of cell homeostasis, neuronal  
99 activity and immune system phenotype (11, 25, 26). SCFAs are of particular interest as they  
100 constitute the major products from bacterial fermentation of dietary fiber in the gut (27). They

101 are present at high levels (mM) in the gut lumen (25), where they maintain gut health and play a  
102 key role in promoting intestinal epithelial barrier integrity and mucus production, and protect  
103 against intestinal inflammation (28). Some studies have also shown that SCFAs influence  
104 gastrointestinal motility (29, 30). Moreover, it has recently been demonstrated that SCFAs may  
105 influence brain function via interactions with GPCRs or histone deacetylases exerting humoral  
106 effects, indirect hormonal and immune pathways and neural routes (28).

107 To address the complexity of GHSR-1a signaling, we used human embryonic kidney cells  
108 (Hek293a), engineered in-house to stably express the human GHSR-1a, and tested selected  
109 bacterial supernatants along with SCFAs and lactate for their capacity to modulate inositol  
110 phosphate, mTOR, ERK1/2 and the recently identified as a ghrelin target Eukaryotic Translation  
111 Elongation Factor 2 (eEF2) signaling pathways, as well as  $\beta$ -arrestin recruitment and GHSR-1a  
112 internalization. Furthermore, we probed bacterial supernatants and SCFAs for their capacity to  
113 alter constitutive GHSR-1a signaling (in the absence of ghrelin) and ghrelin-induced activity of  
114 the GHSR-1a.

## 115 **Methods**

### 116 **Short chain fatty acids (SCFAs) and lactate preparation**

117 SCFA (sodium acetate, sodium propionate and sodium butyrate) and lactate (Sigma-Aldrich,  
118 USA) were dissolved in assay medium (HBSS containing 20mM HEPES) and pH was adjusted  
119 to 7.4 with NaOH 1 M prior to filtration through 0.2  $\mu$ m membrane filters. All compounds were  
120 previously tested for cytotoxic effects in order to establish a safe dose (supporting **Figure S1**).  
121 Final doses were as follows: SCFA were tested at 1 mg/mL (acetate: 17 mM; propionate: 13.7

122 mM; butyrate: 11.5 mM) and lactate at 0.3 mg/mL (3.3 mM), which corresponds with the  
123 physiological concentration range as can be found in the gut lumen (28)).

#### 124 **Bacterial strains supernatants preparation**

125 Different bacterial strains (*B. longum* APC1472, *B. breve* APC6331, *L. rhamnosus* DPC6118, *L.*  
126 *gasseri* DPC6106, *L. brevis* DPC6108 and *P. avidum* APC6544) from the APC Microbiome  
127 Institute and Teagasc Research Center (Cork, Ireland), were maintained in anaerobic culture  
128 conditions in Man Rogosa Sharpe (MRS) agar medium (Difco Laboratories, USA) (for  
129 *Bifidobacterium* strains the medium was supplemented with cysteine hydrochloride (0.05%  
130 w/v)). A single colony from each strain was inoculated in MRS broth medium and incubated  
131 overnight under anaerobic conditions at 37°C. A subculture was carried out by adjusting the  
132 OD<sub>600</sub> to 0.05 and incubated overnight under anaerobic conditions at 37°C for 15 hours approx.  
133 Bacterial cell pellets were collected by centrifugation at 4500 g for 15 min at 4°C, washed twice  
134 in assay medium (1x Hanks balanced salt solution (HBSS) containing 20mM HEPES) (Gibco,  
135 UK) and incubated for 4 hours under culture conditions in assay medium. Finally, bacterial  
136 supernatants were collected by centrifugation at 4500 g for 15 min at 4°C, passed through a 0.2  
137 µm membrane filter (Minisart®, Fisher Scientific, USA) and pH adjusted to 7.4 with NaOH 1 M.  
138 All supernatants were diluted 1:2 in assay medium. Suitability of assay medium to prepare  
139 bacterial supernatants containing microbial-derived metabolites was validated by gas  
140 chromatography analysis of SCFAs (for details see supplementary information and **Figure S2**).

#### 141 **Hek-GHSR-1a-EGFP cell culture**

142 Human embryonic kidney cells (Hek293a) (Invitrogen, Ireland) were transfected with a plasmid  
143 construct expressing the human GHSR-1a receptor with a C-terminal enhanced green fluorescent

144 protein (EGFP) tag and cultured in high glucose Dulbecco's modified Eagle's medium (DMEM,  
145 Invitrogen) containing 10% heat-inactivated fetal bovine serum (FBS) (Sigma-Aldrich), 1% non-  
146 essential amino acids (NEAA) (Gibco) and 300 ng/ $\mu$ l G418 (Calbiochem, Merck KGaA, UK) at  
147 culture conditions (37°C and 5% CO<sub>2</sub> in a humidified atmosphere) as previously described (31).  
148 Cells were grown to a confluence of >85% and subsequently split to a lower density for  
149 continued culturing.

### 150 **Calcium mobilization assay**

151 Changes in intracellular calcium (Ca<sup>2+</sup>) influx were investigated using a FlexStation® 3  
152 multiplate fluorometer (Molecular Devices Corporation, Sunnyvale, CA, USA) as previously  
153 described (32–34). Briefly, Hek-GHSR-1a-EGFP cells were seeded in black 96-well microtiter  
154 plates (2.8\*10<sup>4</sup> cells/well) and maintained at culture conditions. Once the monolayer reached full  
155 confluence (~24 h), cells were incubated for a further ~24h at culture conditions in serum-free  
156 DMEM media. Cells were incubated for 90 min with assay medium (HBSS containing 20mM  
157 HEPES) and 1x Ca<sup>4</sup> dye (Molecular Devices Corporation) (1:1 v/v), according to the  
158 manufacturer's instructions. SCFAs and lactate were dissolved in assay medium as described  
159 above. Finally, compounds were automatically added by the FlexStation® 3 during continuous  
160 fluorescent measurements for a total of 80 sec at 37°C in flex mode with an excitation  
161 wavelength of 485 nm and an emission wavelength of 525 nm. The relative increase in  
162 intracellular calcium [Ca<sup>2+</sup>] was calculated as the difference between maximal and baseline  
163 fluorescence (V<sub>max</sub>-V<sub>min</sub>) and depicted as percentage relative fluorescent units (RFU)  
164 normalized to a maximal response (100% signal) obtained with the GHSR-1a agonist ghrelin  
165 (0.3  $\mu$ M) (Innovagen, Sweden). Background fluorescence was obtained by cells in assay medium  
166 alone and subtracted from RFUs. Exposure to the inverse agonist [D-Arg1, D-Phe5, D-Trp7,9,

167 Leu11]-substance P (SP-analog) (0.5  $\mu$ M) (Tocris, R&D Systems, UK), which also has  
168 antagonist properties, was also carried out. Cells were treated with SCFAs and lactate in the  
169 absence or presence of the agonist ghrelin (0.3  $\mu$ M) in order to study the effects on ghrelin-  
170 independent and ghrelin-dependent responses. Thus, cells were exposed to compounds alone, or  
171 to a combination of compounds with ghrelin (co-treatment) or to a pre-treatment with  
172 compounds during the 90 min of dye incubation before the automatic addition of ghrelin. SCFAs  
173 were tested at 1mg/mL and lactate at 0.3 mg/mL (see sample preparation section above). Wild  
174 type Hek293a cells were included as a control for unspecific calcium responses (see  
175 supplementary information). Data were normalized to the maximum calcium influx obtained  
176 upon treatment with the agonist ghrelin.

#### 177 **Inositol Phosphate assay**

178 Inositol phosphate (IP) accumulation assay was carried out in Hek-GHSR-1a-EGFP cells using  
179 an IP-One Tb assay kit (Cisbio, USA) according to the manufacturer's instructions. Briefly, Hek-  
180 GHSR-1a-EGFP cells were seeded in a 96-well microtiter plate at  $3 \times 10^4$  cells/well and incubated  
181 for 48 hours at culture conditions. For the last 24 hours, the medium was replaced with serum-  
182 free DMEM-high glucose medium. Cells were incubated for 1 hour with samples prepared as  
183 described above in samples preparation section. Untreated cells (cells exposed to assay medium  
184 alone) or cells exposed to ghrelin (0.5  $\mu$ M) or SP-analog (0.5  $\mu$ M) alone were used as controls.  
185 SP-analog (0.5  $\mu$ M), was also included as control. In addition, cells were exposed to samples in  
186 presence of ghrelin in order to elucidate the effects of samples on ghrelin-mediated signaling.  
187 Thus, cells were co-exposed to samples and ghrelin for one hour or to a pre-treatment with  
188 samples for 1 hour followed by exposure to ghrelin for another hour. The ratio of two  
189 fluorescence intensities 665/620 (acceptor/donor) was read in a FlexStation® 3 reader with

190 Cisbio setting recommendations. Data were normalized to the maximum expected IP-one  
191 accumulation obtained upon treatment with the agonist ghrelin.

### 192 **GHSR-1a internalization assay**

193 The potential of SCFAs, lactate and bacterial supernatants to modulate the GHSR-1a was  
194 analyzed by measuring their effect on receptor internalization using Hek-GHSR-1a-EGFP cells  
195 according to previous publications (32–34). Briefly, cells were seeded in a 96-well microtiter  
196 plate at  $3 \times 10^4$  cells/well and incubated for 48 hours at culture conditions. For the last 24 hours  
197 medium was replaced with serum free DMEM-high glucose medium. Cells were exposed to the  
198 same treatments as in IP assay described above. Untreated cells (cells exposed to assay medium  
199 alone) or cells exposed to ghrelin (0.5  $\mu$ M) alone were used as controls. The inverse agonist SP-  
200 analog (0.5  $\mu$ M) was also included as control. Finally, cells were fixed with 4%  
201 paraformaldehyde in phosphate buffer saline (PBS) (Sigma-Aldrich) for 20 min and washed with  
202 1x PBS. Cells were imaged in PBS using the GE Healthcare IN Cell Analyzer 1000 (GE  
203 Healthcare, UK). Receptor GHSR-1a-EGFP trafficking towards the perinuclear region was  
204 quantified by analyzing the EGFP fluorescence intensity using the INCell Analyzer Developer  
205 Toolbox V1.6 software (GE Healthcare) as previously described (33). A total of 15 fields were  
206 taken across 3 independent images in each independent experiment. Data were normalized to the  
207 maximum expected receptor internalization obtained upon treatment with the agonist ghrelin.

### 208 **$\beta$ -Arrestin-1 recruitment analysis**

209 PathHunter® eXpress GHSR-1a U2OS  $\beta$ -Arrestin-1 GPCR Assay (Discoverx, UK) was used to  
210 investigate the effect of SCFAs, lactate and bacterial strains supernatant on GHSR-1a activation  
211 by monitoring  $\beta$ -Arrestin-1 proteins recruitment. The assay was performed according to the

212 manufacturer's protocol with some modifications. Briefly, cells were incubated for 48 hours at  
213 culture conditions. Cells were exposed to same treatments as for the IP assay detailed above.  
214 Finally, detection reagents were added, cells were incubated for 60 min at room temperature and  
215 luminescence was read with the Synergy 2 (Biotek, UK). Data were normalized to the maximum  
216 expected  $\beta$ -Arrestin-1 proteins recruitment obtained upon treatment with the agonist ghrelin (0.5  
217  $\mu$ M).

### 218 **RPPA screening of GHSR-1a signaling pathways activated by ghrelin**

219 A reverse phase protein array (RPPA) (35) of over 300 proteins was conducted by Functional  
220 Proteomics Group of MD Anderson Cancer Centre (University of Texas, USA), as described  
221 (Zhdanov et al, 2019, unpublished). Hek-GHSR-1a-EGFP cells were seeded in a 6-well plate at  
222  $1.0 \times 10^6$  cells/well and incubated for 48 hours at culture conditions. For the last 16 hours, the  
223 medium was replaced with serum free DMEM-high glucose medium. Cells were treated with 0.5  
224  $\mu$ M ghrelin for 1 h. Protein extracts were prepared as described (36) with modifications. Briefly,  
225 cells were lysed in RIPA buffer (ThermoFisher Scientific) with protease and phosphatase  
226 inhibitors' cocktails (cOmplete™ ULTRA and PhosSTOP™ tablets, Roche). After a brief  
227 sonication, the lysates were cleared by centrifugation at 14000 g (15 min, +4°C). Protein yield  
228 was quantified with BCA assay (Pierce), adjusted to 1.0 mg/mL in a dye-free Laemmle buffer  
229 and heated at 95°C for 5 min. Samples were shipped for the analysis on dry ice. Three  
230 independent experiments were performed for RPPA assay. Within each experiment, the signal in  
231 ghrelin-treated cells was normalized to non-stimulated cells. Proteins displaying larger or equal  
232 to 10% change were selected for the construction of Kyoto Encyclopedia of Genes and Genomes  
233 (KEGG) pathways in the Database for Annotation, Visualization and Integrated Discovery  
234 (DAVID) v6.8.

## 235 **Western Blot analysis of mTOR, ERK and eEF2 phosphorylation**

236 Hek-GHSR-1a-EGFP or WT cells were seeded in a 6-well plate at  $2.5 \times 10^6$  cells/well and  
237 incubated for 48 hours at culture conditions. For the last 24 hours, the medium was replaced with  
238 serum free DMEM-high glucose medium. Cells were treated with SCFAs, lactate and bacterial  
239 supernatants (prepared as described above) for 1 h either with or without the addition of agonist  
240 ghrelin (0.5  $\mu$ M). SP-analog (0.5  $\mu$ M) was also included as a control. Additionally, cells were  
241 exposed to a 1 h pre-treatment with SCFAs, lactate, bacterial supernatants and SP-analog,  
242 followed by exposure to ghrelin for another 1 h. Protein extracts were prepared as for the RPPA  
243 analysis. Protein concentration was adjusted to 1.5 – 2.0 mg/mL with 5X Sample Buffer  
244 (Genscript). Western blot analysis was conducted as described (36). Briefly, 50  $\mu$ g of protein  
245 were loaded onto 4-20% Bis-Tris Gels in Tris-MOPS running buffer (Genscript) and wet-  
246 transferred to Immun-Blot® PVDF membrane (BioRad). The membranes were blocked with 5%  
247 BSA, and then incubated overnight at 4°C with primary antibodies against phospho-mTOR  
248 (Ser2448) (Cell Signalling, #2971), phospho-ERK1/2 (Thr202/Tyr204) (Cell Signalling, #9101)  
249 and phospho-eEF2 (Thr56) (Cell Signalling, #2331). Incubation with the HRP-conjugated  
250 secondary antibodies (Sigma) was done in 5% milk for 1 h at room temperature. Protein bands  
251 were visualized using Amersham ECL Prime detection system (GE Healthcare) on the  
252 LAS-3000 Imager (FujiFilm). The membranes were further re-stained against alpha-tubulin as a  
253 loading control (Sigma, T5168). Quantitative analysis was done in ImageJ-Fiji software (NIH).  
254 The density of target protein bands was normalized to alpha-tubulin. Three independent  
255 experiments were performed for each treatment. Within each experiment, the signal in treated  
256 cells was normalized either to non-stimulated control cells (if cells were treated with compounds  
257 in the absence of ghrelin) or to ghrelin-stimulated cells (if cells were treated with compounds in

258 the presence of ghrelin). These values were used for the statistical analysis. Western Blot data  
259 were plotted as Median and IQR (box) with minimal and maximal values as whiskers.

## 260 **Statistical analysis**

261 Data were plotted using GraphPad Prism software (PRISM 5.0; GraphPAD Software Inc., San  
262 Diego, CA, USA) and statistical analysis was performed using SPSS software (IBM SPSS  
263 statistics 22). Normality of the data was tested by Shapiro-Wilk test. Normally distributed data  
264 was analyzed with One-Way ANOVA followed by Dunnett post-hoc test for multiple  
265 comparisons. Non-normally distributed data was analysed with non-parametric multiple  
266 comparisons Kruskal-Wallis test followed by Bonferroni adjustment of p-values. Western blot  
267 data were analyzed with non-parametric Mann-Whitney U test; the Benjamini-Hochberg  
268 adjustment procedure was applied with the false discovery rate (FDR) set at 10% to correct for  
269 multiple testing. \*indicates significant differences vs untreated control (comparisons between  
270 controls and non-ghrelin treated samples) (\* $p \leq 0.05$ , \*\* $p \leq 0.01$ , \*\*\* $p \leq 0.001$ ); \$indicates  
271 significant differences vs ghrelin control (comparisons between samples and ghrelin control)  
272 ( $p \leq 0.05$ , \$\$ $p \leq 0.01$ , \$\$\$ $p \leq 0.001$ ).

## 273 **Results**

### 274 **Effects of SCFAs and lactate on ghrelin receptor signaling**

275 Hence, we investigated their capability to modulate GHSR-1a signaling by testing their effects  
276 on GHSR-1a-mediated intracellular calcium influx in our well establish *in vitro* screening  
277 platform using Hek293a cells stably overexpressing this receptor. Cells were exposed to SCFAs  
278 (acetate, propionate and butyrate) and lactate (at 1 mg/mL and 0.3 mg/mL respectively), or to  
279 SP-analog (0.5  $\mu\text{M}$ ) in presence or absence of the endogenous ligand ghrelin (0.3  $\mu\text{M}$ ). First,

280 calcium mobilization was analyzed on Hek293a WT cells without overexpression of the GHSR-  
281 1a, to control and rule out any potential unspecific responses mediated by SCFAs. No effects  
282 were observed on Hek293a WT cells (Supporting **Figure S3**). As expected, exposure to ghrelin  
283 (0.3  $\mu$ M) led to a significantly ( $p \leq 0.001$ ) increased calcium influx compared to untreated cells  
284 (**Figure 1A**). Exposure to SCFAs, lactate or to SP-analog in the absence of the agonist ghrelin,  
285 did not lead to any significant change in intracellular calcium influx compared to untreated cells,  
286 indicating that none of these compounds act as agonist of the GHSR-1a (**Figure 1A**). However,  
287 when cells were exposed to propionate, butyrate or lactate in presence of ghrelin (co-treatment),  
288 a significant decrease ( $p \leq 0.001$ ,  $p \leq 0.05$  and  $p \leq 0.001$  respectively) in ghrelin-mediated calcium  
289 influx was observed (**Figure 1A**). Exposure to acetate also showed a strong trend ( $p = 0.06$ )  
290 towards reduced ghrelin-mediated calcium influx. The inverse agonist SP-analog did not  
291 demonstrate an antagonist effect on GHSR-1a-mediated calcium mobilization (**Figure 1A**).  
292 Interestingly, when cells were exposed to SCFAs or lactate for 1 hour prior to the addition of  
293 ghrelin (pre-treatment), no antagonist effect could be observed on GHSR-1a-mediated calcium  
294 influx (**Figure 1A**). In contrast, pre-treatment with SP-analog led to a significantly ( $p \leq 0.001$ )  
295 increased ghrelin-mediated calcium influx (**Figure 1A**) as previously described (32, 34). The  
296 intracellular calcium release from the endoplasmic reticulum stores (ER) is characteristic of the  
297 activation of G $\alpha$ q protein coupled receptors, and it is triggered by D-myo-inositol (1,4,5) tri-  
298 phosphate (IP3) following the activation of phospholipase C  $\beta$  (PLC- $\beta$ ) and second messengers  
299 diacyl glycerol (DAG) (37). The lifetime of IP3 is very short (less than 30 sec), and rapidly  
300 degraded to IP2 and then IP1 (38, 39). Therefore, to further investigate the effects of SCFAs and  
301 lactate on GHSR-1a-mediated calcium signaling, IP1 accumulation assay was also carried out in  
302 these cells (**Figure 1B**). Exposure to the agonist ghrelin (0.5  $\mu$ M) led to a significantly increased

303 IP1 accumulation indicating activation of the GHSR-1a (**Figure 1B**). Treatment with the inverse  
304 agonist SP-analog for one hour in the absence of ghrelin decreased significantly ( $p \leq 0.001$ ) the  
305 accumulation of IP1 compared to untreated cells (**Figure 1B**), which is in agreement with  
306 previous publications (40, 41). Lactate showed the same effect as SP-analog ( $p \leq 0.05$ ) and  
307 decreased IP1 accumulation, indicating its potential to act as an inverse agonist for this specific  
308 pathway (**Figure 1B**). However, exposure to SCFAs did not affect IP1 accumulation, although in  
309 the case of butyrate, a non-significant reduction ( $p = 0.07$ ) was observed towards a reduction of  
310 IP1 accumulation compared to untreated cells (**Figure 1B**). In addition, none of the SCFAs nor  
311 lactate were able to modulate IP1 accumulation in the presence of ghrelin. Finally, using calcium  
312 imaging, it was also shown that the SCFAs, acetate, butyrate and to a lesser extent, propionate,  
313 were able to inhibit ghrelin-mediated calcium response either when following a co-treatment or  
314 after a pre-treatment for 1 hour prior to the addition of ghrelin (Supporting **Figure S4**). This is in  
315 line with the calcium mobilization assay (**Figure 1A**).

316 The GHSR-1a has a very high ligand-independent constitutive activity (~50%) (41–43) and, as  
317 a consequence of this high basal activity, is internalized into endosomes. This is a mechanism to  
318 prevent receptor overstimulation, which following  $\beta$ -arrestin recruitment, desensitizes and  
319 internalization the GHSR-1a and marks it for degradation or recycling back to the membrane  
320 (44). Therefore, we next investigated the effect of bacterial metabolites and supernatants on  
321 GHSR-1a internalization. Treatment with ghrelin (0.5  $\mu\text{M}$ ) for one hour led to a significantly  
322 ( $p \leq 0.001$ ) increased internalization compared to untreated cells (**Figure 2A, 2B**). In contrast,  
323 exposure to SP-analog (0.5  $\mu\text{M}$ ) showed a level of GHSR-1a internalization below ( $p \leq 0.05$ ) the  
324 basal levels observed in untreated cells, which is characteristic of inverse agonists (45) (**Figure**  
325 **2A, 2B**). Interestingly, exposure to acetate (1 mg/mL) also showed inverse agonist properties on

326 this signaling pathway as it significantly ( $p \leq 0.01$ ) reduced GHSR-1a internalization compared to  
327 untreated cells (**Figure 2A, 2B**). No effects were observed when cells were treated with the other  
328 bacterial-derived metabolites used here (**Figure 2A, 2B**). In order to elucidate if SCFAs or  
329 lactate may have antagonist activity, ghrelin-mediated receptor internalization was also  
330 investigated in the presence of these compounds. Remarkably, compounds showed capability to  
331 inhibit ghrelin-mediated receptor internalization (**Figure 2A, 2B**) either when cells were exposed  
332 to these compounds and ghrelin for 1 hour (SP-analog:  $p \leq 0.001$ ; acetate:  $p \leq 0.001$ ; propionate:  
333  $p \leq 0.01$ ; lactate:  $p \leq 0.001$ ) or when cells were first pre-treated with these compounds for one hour  
334 followed by addition of ghrelin for another hour (acetate:  $p \leq 0.001$ ; propionate:  $p \leq 0.01$ ; butyrate:  
335  $p \leq 0.05$ ; lactate:  $p \leq 0.001$ ) (**Figure 2A, 2B**), indicating potential GHSR-1a antagonist properties,  
336 as seen in calcium mobilization assays also (**Figure 1**). Finally, SCFA and lactate-mediated  
337 effects on  $\beta$ -arrestin-1 recruitment, which is one of the main proteins involved in the endocytosis  
338 process (42), were also investigated (**Figure 2C**). Exposure to the agonist ghrelin ( $0.5 \mu\text{M}$ ) for  
339 one hour led to significantly ( $p \leq 0.01$ ) increased  $\beta$ -arrestin-1 recruitment compared to untreated  
340 cells (**Figure 2C**). However, exposure to the inverse agonist SP-analog at  $0.5 \mu\text{M}$  did not show  
341 any effect but it did block ghrelin-mediated  $\beta$ -arrestin-1 recruitment when incubated as a co-  
342 treatment with ghrelin for one hour (**Figure 2C**). Pre-treatment with acetate showed a  
343 potentiation effect ( $p \leq 0.001$ ) of ghrelin-mediated  $\beta$ -arrestin-1 recruitment while lactate and  
344 ghrelin co-treatment led to a significant reduction in ghrelin-mediated  $\beta$ -arrestin-1 recruitment at  
345 the tested concentrations (**Figure 2C**). Exposure to propionate and butyrate did not show any  
346 effect (**Figure 2C**).

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## 349 **Effects of bacterial supernatants on ghrelin receptor signaling**

350 Next, we aimed to elucidate whether SCFAs and/or lactate-producing bacterial strains may have  
351 effects on GHSR signaling similar to those observed when testing these compounds directly on  
352 the cells. Hence, six supernatants from different bacterial strains, most of these belonging to  
353 common probiotic genus such as *Bifidobacterium* and *Lactobacillus*, were investigated. We first  
354 tested their effects on the GHSR internalization assay. We identified a bacterial strain,  
355 *Bifidobacterium longum* APC1472, that was able to reduce ( $p \leq 0.001$ ) the basal levels of GHSR-  
356 1a internalization with a similar efficacy than the inverse agonist SP-analog (**Figure 3A, 3B**).  
357 Moreover, this strain also showed a strong ( $p \leq 0.001$ ) inhibition of ghrelin-mediated GHSR-1a  
358 internalization (**Figure 3A, 3B**). In contrast, another *Bifidobacterium* strain, *Bifidobacterium*  
359 *breve* APC6331, did not show capability to reduce basal levels of receptor internalization, but  
360 was able to inhibit ghrelin-mediated GHSR-1a internalization either when added together with  
361 ghrelin (co-treatment,  $p \leq 0.001$ ) or when added 1 hour prior addition of ghrelin (pre-treatment,  
362  $p \leq 0.01$ ). *Lactobacillus* strains (*Lactobacillus rhamnosus* DPC6118, *Lactobacillus gasseri*  
363 DPC6106 and *Lactobacillus brevis* DPC6108) were, overall, less active towards GHSR signaling  
364 compared to the *Bifidobacterium* strains. Thus, the only significant effect observed was an  
365 inhibition of ghrelin-mediated receptor internalization when cells were exposed to ghrelin and  
366 the supernatants from the strains *L. rhamnosus* DPC6118 (co-treatment,  $p \leq 0.001$ ) and *L. gasseri*  
367 DPC6106 (co-treatment,  $p \leq 0.05$ ) (**Figure 3A, B**). Propionate-producing bacterial strain,  
368 *Propionibacterium avidum* APC6544, was also able to inhibit ghrelin-mediated internalization in  
369 both assay settings (co-treatment,  $p \leq 0.001$ ; pre-treatment,  $p \leq 0.01$ ) (**Figure 3A, B**). The most  
370 active strains, *B. longum* APC1472, *B. breve* APC6331, *L. rhamnosus* DPC6118 *P. avidum*  
371 APC6544, were selected for further investigations. In contrast to the internalization assay, the

372 effects observed on  $\beta$ -arrestin-1 recruitment were less prominent (**Figure 3C**). Here, the only  
373 observed effect was an inhibition of ghrelin-mediated  $\beta$ -arrestin-1 recruitment after pre-treatment  
374 with bacterial strains supernatants (*B. longum* APC1472:  $p \leq 0.001$ ; *B. breve* APC6331:  $p \leq 0.05$ , *L.*  
375 *rhamnosus* DPC6118:  $p \leq 0.05$ ; *P. avidum* APC6544:  $p \leq 0.05$ ). In terms of calcium signaling, only  
376 *L. rhamnosus* DPC6118 showed a significant ( $p \leq 0.05$ ) increased ghrelin-mediated IP1  
377 accumulation when exposed to cells together with ghrelin for 1 hour (co-treatment) (**Figure 3D**).

### 378 **Effects of SCFAs and lactate on ghrelin-induced mTOR and ERK signaling**

379 According to gene expression and functional analyses, Hek293a cells are often considered as a  
380 neural cell lineage (46). On the other hand, the pattern of protein phosphorylation induced by  
381 ghrelin can vary even for closely related neuronal cells. Therefore, before addressing the  
382 question how SCFA modulate the effect of ghrelin on intracellular signaling, we selected the best  
383 responders to ghrelin treatment in our Hek-GHSR-1a-EGFP cell line, using the RPPA analysis.  
384 Among 340 proteins tested (both total and phosphorylated), 42 were affected by 1 h treatment  
385 with ghrelin (Supporting **Table S1**). This data helped to build a cumulative map of ghrelin-  
386 induced signaling based on KEGG pathways analysis, which was conducted using DAVID v6.8  
387 online bioinformatics resource (**Figure 4**). We found that pro-synthetic pathways were overall  
388 activated upon ghrelin-mediated GHSR-1a signaling stimulation, while processes up-regulating  
389 apoptosis, autophagy and cell cycle control, were inhibited. In particular, mTOR (including  
390 mTOR, Akt, Rictor, S6K) and ERK1/2 (including ERK1/2, Raf, RSK) pathways, the hallmarks  
391 of the signaling response to ghrelin, were activated in Hek-GHSR-1a-EGFP cells (**Figure 4**;  
392 **Supporting Figures S5, S6**). Hence, phosphorylation levels of mTOR and ERK were selected as  
393 signaling readouts for further analysis, together with phosphorylation status of eEF2, which has  
394 been recently shown to be involved in ghrelin-dependent increase in protein synthesis (Zhdanov

395 et al, 2019, under review). Using Western blotting analysis, we examined effects of SP-analog,  
396 SCFAs and lactate on ghrelin-mediated mTOR signaling activation. Treatment with ghrelin  
397 increased ( $p \leq 0.01$ ) p-mTOR levels compared to untreated cells (**Figure 5A**, middle and lower  
398 panel). However, none of the tested compounds affected mTOR phosphorylation in either the  
399 presence or the absence of ghrelin. Next, stimulation with ghrelin induced a dramatic increase  
400 ( $p \leq 0.01$ ) in ERK1/2 phosphorylation levels (**Figure 5B**, middle and lower panel). While SP-  
401 analog itself demonstrated a negative effect ( $p \leq 0.01$ ) on the activity of ERK, all three SCFAs  
402 increased ERK1/2 phosphorylation, suggesting pre-disposition of cells to a stronger response to  
403 ghrelin (**Figure 5B**, upper panel). Indeed, when applied to cells together with or prior to ghrelin  
404 addition, acetate and propionate significantly ( $p \leq 0.05$ ) potentiated the effect of ghrelin on  
405 ERK1/2 phosphorylation (**Figure 5B**, middle and lower panel). In cells pre-treated with butyrate  
406 or lactate, ghrelin was able to increase ( $p \leq 0.05$ ) p-ERK1/2 levels (**Figure 5B**, lower panel).  
407 Treatment with ghrelin activated eEF2 by decreasing ( $p \leq 0.05$ ) its phosphorylation levels (**Figure**  
408 **5C**, middle and lower panel). Unlike ghrelin, SP-analog ( $p \leq 0.01$ ) and lactate ( $p \leq 0.05$ ), when  
409 acting alone, inhibited eEF2 by increasing its phosphorylation (**Figure 5C**, upper panel).  
410 Moreover, ghrelin was unable to re-activate eEF2 in the presence of lactate (**Figure 5C**, middle  
411 and lower panel) (**Figure 5C**, middle and lower panel). SCFAs did not change eEF2  
412 phosphorylation and did not modulate the effect of ghrelin on it. Unexpectedly, SP-analog  
413 potentiated ( $p \leq 0.01$  and  $p \leq 0.05$  for co-treatment and pre-treatment respectively) the decrease in  
414 p-eEF2 levels induced by ghrelin (**Figure 5C**, middle and lower panel).

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## 418 **Effects of bacterial supernatants on ghrelin-induced mTOR and ERK signaling**

419 Bacterial strains supernatants were also tested as potential modulators of the effect of ghrelin on  
420 mTOR, ERK and eEF2 phosphorylation in Hek-GHSR-1a-EGFP cells (**Figure 6**). While  
421 exposure to ghrelin led to significant ( $p \leq 0.01$ ) increased levels of p-mTOR (**Figure 6A**, middle  
422 and lower panel), none of the supernatants nor SP-analog showed any effect on this pathway  
423 signaling (**Figure 6A**). SP-analog showed a strong inhibition ( $p \leq 0.01$ ) of ERK1/2  
424 phosphorylation compared to untreated cells (**Figure 6B**, upper panel) and a significant  
425 reduction ( $p \leq 0.05$ ) of ghrelin-mediated ERK1/2 phosphorylation when added together with  
426 ghrelin (**Figure 6B**, middle panel). Exposure to *L. rhamnosus* supernatant led to a significant  
427 reduction ( $p \leq 0.05$ ) on ghrelin-mediated ERK1/2 phosphorylation when doing either co-treatment  
428 or pre-treatment prior ghrelin addition (**Figure 6B**, middle and lower panel). The opposite effect  
429 was observed following pre-treatment with *B. longum* and *B. breve* supernatants. Here, the  
430 ghrelin-mediated activation of ERK was significantly enhanced ( $p \leq 0.05$ ) compared to cells  
431 treated with ghrelin alone, as demonstrated by increased p-ERK1/2 levels (**Figure 6B**, middle  
432 and lower panel). Finally, increased p-eEF2 levels were observed following exposure to SP-  
433 analog ( $p \leq 0.01$ ) and *P. avidum* supernatant (**Figure 6C**, upper panel). Exposure to SP-analog  
434 potentiated ghrelin-mediated reduction in p-eEF2 levels either in co-treatment ( $p \leq 0.01$ ) or  
435 following pre-treatment prior to ghrelin addition ( $p \leq 0.05$ ) (**Figure 6C**, middle and lower panel).  
436 Strikingly, the attenuating effect of ghrelin on eEF2 phosphorylation was blocked following pre-  
437 treatment with the four bacterial strain supernatants (**Figure 6C**).

## 438 Discussion

439 The ghrelinergic system, through the activation of the GHSR-1a, is crucial for a diversity of  
440 peripheral functions ranging from gastric motility, gut hormones secretion, glucose and lipid  
441 metabolism, pancreatic function, immune function, cardiac output, to even bone formation (8,  
442 47–54). Moreover, ghrelin and the GHSR-1a also modulate several signaling processes in the  
443 brain, such as appetite regulation, reward and neuropeptide release (including growth hormone,  
444 adrenocorticotrophic hormone, cortisol, and prolactin), mood, memory, learning, and stress  
445 response (7, 9, 54–58). Interestingly, changes in circulating levels of ghrelin have been linked to  
446 changes in gut microbiota composition, suggesting that the ghrelinergic system may be under  
447 regulation of the gut commensal microbes (20, 21). Here, we show, to our knowledge for the  
448 first time, that bacteria-derived SCFAs (acetate, propionate and butyrate) and lactate, as well as  
449 bacterial supernatants of the *Bifidobacterium* and *Lactobacillus* genera, are able to affect GHSR-  
450 1a signaling. Butyrate, propionate, acetate and lactate were all able to inhibit ghrelin-mediated  
451 calcium mobilization in cells expressing the GHSR-1a (**Figure 1A and Figure S4**). This points  
452 to an important novel functionality for microbiota-derived SCFAs in gut-brain axis signaling and  
453 demonstrates the potential of commensal bacteria metabolites as key components of host  
454 interactions through the modulation of host GPCR signaling. In line with this, is the recent  
455 finding that bacteria-derived N-acyl amides fatty acids can mimic human GPCR signaling  
456 molecules also (2). In addition, a forward chemical genetic screen, recently demonstrated an  
457 orthogonal approach to uncover biologically relevant host-microbiota metabolome interactions  
458 (1). They screened the human microbiota metabolome against the GPCRome and showed that  
459 bacterial metabolites can indeed function as agonists for GPCRs, reinforcing the potential  
460 powerful effect that commensal gut microbes can exert on host physiology. Moreover, SCFA

461 have already been shown to be able to modulate the free fatty acid receptor 2 (FFAR2) and  
462 FFAR3, which are also GPCRs (60). They are mainly expressed in the periphery but evidences  
463 exist for FFAR3 to be also expressed in the central (CNS) and peripheral nervous system (PNS)  
464 (28). Indeed, the effect of SCFAs on appetite suppression via the vagus nerve has been suggested  
465 to be mediated by their interaction with the FFAR3 receptor present in nodose ganglion neuros  
466 (61). Together, these findings suggest that SCFAs may indeed affect the central and peripheral  
467 nervous system via modulation of GPCR signaling within the gut-brain axis (28).

468 Interestingly, in our assay, the antagonistic activity of SCFAs on GHSR-1a-induced calcium  
469 influx were not observed when cells were pre-treated with SCFAs before addition of ghrelin  
470 (**Figure 1A**). Likewise, calcium imaging also demonstrated that the inhibitory effect of the  
471 SCFAs was less pronounced when cells were pretreated with SCFAs compared to the inhibitory  
472 effect observed upon simultaneous addition of SCFAs and ghrelin (Supplementary **Figure S4**).  
473 This may suggest that during the pre-incubation time, bacterial-derived metabolites are used as  
474 energy source and become exhausted (57). Moreover, the inhibitory effect of SCFAs on ghrelin-  
475 mediated signaling was not observed when looking at IP accumulation (**Figure 1B**). This  
476 discrepancy in calcium mobilization and IP1 accumulation assays may be explained by the  
477 source of calcium measured in these two different assays. Indeed, the IP1 accumulation assay  
478 measures calcium release from endoplasmic reticulum (ER) only (38, 39). In contrast, the  
479 calcium mobilization assays measure the total intracellular calcium influx, derived from both the  
480 ER stores as well as calcium influx produced by the direct interaction of GPCRs with calcium  
481 channels (63, 64). This may suggest that SCFAs specifically inhibit GHSR-1a-mediated  
482 modulation of calcium channels. This inhibitory effect may have significant relevance for  
483 neuronal function as constitutive and agonist-dependent GHSR-1a activation has previously been

484 shown to inhibit voltage-gated calcium channels CaV2.1 and CaV2.2 currents in rat and mouse  
485 hypothalamic neurons leading to inhibitory effects on depolarization (65, 66). In addition, all  
486 SCFAs and lactate also showed inhibitory effects on subsequent ghrelin-mediated GHSR-1a  
487 internalization, reinforcing their potential as attenuators of ghrelin-mediated GHSR-1a  
488 trafficking (**Figures 2A, 2B**). Moreover, acetate showed capability to decrease the basal levels of  
489 receptor internalization, indicating inverse agonist properties. Overall, this was in accordance  
490 with what we observed with the bacterial strains supernatants (**Figure 3**), where *B. longum*  
491 APC1472 was the most active strain since its supernatant showed both a decrease in the high  
492 basal GHSR-1a internalization and a complete inhibition of ghrelin-mediated receptor  
493 internalization which correlates with its higher content in acetate (**Figure S3**) and indicates a  
494 potent inhibition of ghrelinergic signaling. Interestingly, a positive correlation was observed  
495 between acetate content in bacterial supernatants that showed an inhibitory effect on GHSR-1a  
496 internalization (unpublished data). In contrast, while SP-analog was equally able to decrease  
497 basal internalization, it was unable to block ghrelin-mediated receptor internalization.  
498 Interestingly, pre-incubation with acetate or bacterial strains supernatants potentiated the ghrelin-  
499 mediated  $\beta$ -arrestin recruitment while co-treatment with lactate inhibited it (**Figures 2C, 3C**). No  
500 others effects were observed with the others bacterial metabolites. The observed differences in  $\beta$ -  
501 arrestin recruitment may also suggest involvement of  $\beta$ -arrestin independent GHSR-1a  
502 internalization via interactions with other proteins like  $\mu$ -AP2 (41, 43).

503 In agreement with previously published data, the results of RPPA analysis (**Figure 4**) showed  
504 that activation of GHSR-1a strongly affects the pattern of cellular protein phosphorylation (67,  
505 68). This suggests that ghrelin-induced signaling cascades may affect transcription and  
506 translation factors such as NFkB, ERK, mTOR and eEF2. Thus, we next investigated effects of

507 SCFAs on the phosphorylation and activation of these factors. In our experimental conditions,  
508 phosphorylation of mTOR, a master-regulator of protein synthesis and the key responder to  
509 ghrelin treatment, remained unaffected by SCFA, lactate or bacterial supernatants (**Figures 5A,**  
510 **6A**). A possible explanation is the fact that mTOR lies on a crossroad of many positive and  
511 negative regulatory pathways (69), which could compensate for each other, suggesting that all  
512 tested metabolites and, particularly, bacterial supernatants of unknown composition may trigger  
513 numerous pathways. In contrast, ERK1/2 demonstrated a strong response following SCFAs  
514 exposure, and increased ERK phosphorylation (in agreement with (70)), as well as increased  
515 ghrelin-mediated ERK activation was observed, with acetate and propionate as the most effective  
516 mediators (**Figure 5B**). This demonstrates, that the interplay between ghrelin and SCFAs is  
517 complicated and further detailed analysis is warranted, including various timing and  
518 concentration ranges. We believe that signaling pathways involving ERK, and in particular,  
519 upstream kinases driving ERK1/2 phosphorylation, are the most important targets for further  
520 analysis of SCFA / ghrelin crosstalk.

521 The effects of bacterial supernatants were more ambiguous, most likely because they represent  
522 complex cocktails containing SCFAs and / or lactate among other bioactive molecules. In  
523 general, being neutral towards ERK phosphorylation on their own, bacterial supernatants  
524 decreased or tended to decrease the effect of ghrelin when added together with ghrelin (co-  
525 treatment). Exposure to supernatants from *Bifidobacterium* spp. for 1hour prior addition of  
526 ghrelin potentiated the effect of ghrelin on p-ERK levels, in contrast to that of *L. rhamnosus*  
527 DPC6118 (**Figure 6B, lower panel**). Further analysis is required to reveal actual driving forces  
528 of these effects at molecular levels.

529 As we have recently shown, mTOR/p70S6K and, potentially, ERK/RSK axes are involved in  
530 ghrelin-induced activation of e-EF2 (via inhibition of its only kinase eEF2K) with a sequential  
531 rapid activation of protein synthesis (Zhdanov et al, 2019, under review). The eEF2K activity is  
532 regulated by numerous factors (e.g. AMPK, ERK, mTOR, Ca<sup>2+</sup>), which are triggered by ghrelin  
533 and many other stimuli, with an unknown outcome for eEF2 phosphorylation when they applied  
534 in combinations. Here we observed no effect of SCFAs on ghrelin-driven activation on eEF2,  
535 while lactate suppressed it (**Figure 5C**). Similarly, only lactate acted as an inhibitor of eEF2  
536 phosphorylation when used alone. While we cannot fully explain these phenomena, together with  
537 the observed differences between effects of SCFAs and lactate on IP1 and  $\beta$ -arrestin (**Figures**  
538 **1B, 2C**), they may suggest that lactate can trigger unique signaling and metabolic pathways. On  
539 the other hand, phosphorylation status of eEF2 is very sensitive to any stress or metabolic  
540 perturbation imposed to cells, and therefore pre-treatment with lactate, as well as with bacterial  
541 supernatants (**Figure 6C**) could alter metabolic equilibrium in the treated cells.

542 In this study, the analysis of mTOR, ERK and eEF2 phosphorylation status suggests that SCFAs,  
543 lactate and bacterial supernatants mediate ghrelin-dependent signaling cascades through the  
544 GHSR-1a, which can rapidly affect cellular functions and gene expression at the mRNA  
545 translation level (exemplified by eEF2). Moreover, RPPA analysis showed that a one-hour  
546 treatment with ghrelin activates a number of transcriptional factors (e.g. FOXO, NFkB, c-Jun)  
547 (**Figure 4, Table S1**), which in turn can trigger a slower gene expression response, acting at  
548 DNA transcription level. Future analysis of these factors is of a particular interest for biological  
549 models with a long-term / steady increase in ghrelin levels (e.g. cancer).

550 In conclusion, we have identified for the first time the ability of bacterial-derived metabolites  
551 (i.e. butyrate, propionate, acetate and lactate) and bacterial strain supernatants to affect the

552 complex signaling cascades of ghrelin-mediated GHSR-1a activation. Together, these results  
553 highlight the promising therapeutic potential of the gastrointestinal microbiota as an extensive  
554 source for metabolites targeting specific GPCRs within the gut-brain axis, affecting both the  
555 central nervous system and periphery. Further investigation is needed to clarify the mechanism at  
556 molecular levels following SCFA-mediated modulation of the ghrelinergic system and the  
557 functional consequences on energy balance, metabolism, food intake, motivation, reward and  
558 mood. Together, this study highlights the promising potential of the gastrointestinal microbiota  
559 and its metabolites in the development of novel therapeutic strategies to treat several metabolic  
560 and affective disorders involving GHSR-1a signaling.

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#### 565 **Author Contributions**

566 HS, JFC, CTF, BLR, AVG and TGD were involved in the conception of the research; CTF,  
567 AVG, AVZ, SW and SA performed experiments and analyzed data; CTF, HS and AVG wrote  
568 the manuscript; and BLR, DBP, CS and PR contributed with reagents and analytical tools. HS  
569 led the conception of all experiments, supervised the work and edited the manuscript.

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803 **Figure Legends**

804

805 **Figure 1. SCFAs and lactate effects on calcium signaling in Hek-GHSR-1a-EGFP cells.** (A)

806 Intracellular calcium influx and (B) inositol phosphate (IP) accumulation in Hek cells stably  
807 overexpressing the GHSR-1a. Cells were exposed to the endogenous ligand ghrelin (0.3  $\mu$ M,  
808 ghrl), GHSR-1a inverse agonist, [D-Arg1, D-Phe5, D-Trp7,9, Leu11]-substance P (0.5  $\mu$ M, SP-  
809 analog), SCFAs (1 mg/mL) or lactate (0.3 mg/mL) following different treatments: SCFAs/lactate  
810 alone (1 h incubation), co-treatment with ghrelin (1 hour incubation) or pre-treatment with  
811 SCFAs/lactate (1 hour) before ghrelin addition (1 hour). Untreated cells and cells exposed to  
812 ghrelin alone were included as controls. Graphs represent the mean  $\pm$  SEM from at least three  
813 independent experiments with each sample performed at least in duplicate. Data is depicted as a  
814 percentage of maximal response as elicited by the positive control ghrelin. \* $p \leq 0.05$  vs untreated  
815 control (comparisons between controls and non-ghrelin treated samples); \$ $p \leq 0.05$  vs ghrelin  
816 control. For incubation times and statistical details for each assay see methods section.

817

818 **Figure 2. SCFAs and lactate effects on GHSR-1a internalization.** (A) Representative images

819 are depicted following different treatments: SCFAs/lactate alone (1 h incubation), co-treatment  
820 with ghrelin (1 hour incubation) or pre-treatment with SCFAs/lactate (1 hour) before ghrelin  
821 addition (1 hour) and (B) their quantified fluorescence intensity (15 pictures per treatment) of  
822 perinuclear GHSR-1a-EGFP receptor. (C)  $\beta$ -arrestin-1 recruitment analysis expressed as relative  
823 light units (RLU). Graphs represent the mean  $\pm$  SEM from at least 2 independent experiments  
824 with each treatment performed in triplicates. Untreated control (assay buffer), ghrelin (0.5  $\mu$ M),  
825 inverse agonist, [D-Arg1, D-Phe5, D-Trp7,9, Leu11]-substance P (0.5  $\mu$ M, SP-analog), SCFAs

826 (1 mg/mL) and lactate (0.3 mg/mL). \* $p \leq 0.05$  vs untreated control (comparisons between  
827 controls and non-ghrelin treated samples);  $p \leq 0.05$  vs ghrelin control. For statistical details, see  
828 methods section.

829

830 **Figure 3. Bacterial strains supernatants effects on GHSR-1a signaling.** (A) Representative  
831 images are depicted following different treatments: bacterial supernatants alone (1 h incubation),  
832 co-treatment with ghrelin (1 hour incubation) or pre-treatment with supernatants (1 hour) before  
833 ghrelin addition (1 hour) and (B) their quantified fluorescence intensity (15 pictures per  
834 treatment) of perinuclear GHSR-1a-EGFP receptor from at least 5 independent experiments with  
835 each treatment performed in triplicates. (C)  $\beta$ -arrestin-1 recruitment analysis expressed as  
836 relative light units (RLU) from 2 independent experiments with each treatment performed in  
837 triplicates. Graphs represent the mean  $\pm$  SEM. Untreated control (assay buffer), ghrelin (ghrl, 0.5  
838  $\mu$ M), inverse agonist [D-Arg1, D-Phe5, D-Trp7,9, Leu11]-substance P (SP-analogue, 0.5  $\mu$ M)  
839 and diluted bacterial strain supernatants (1:2 v/v in assay buffer; bacterial strains: *B. longum*  
840 APC1472, *B. breve* APC6331, *L. rhamnosus* DPC6118, *L. gasseri* DPC6106, *L. brevis* DPC6108  
841 and *P. avidum* APC6544). \* $p \leq 0.05$  vs untreated control (comparisons between controls and  
842 non-ghrelin treated samples);  $p \leq 0.05$  vs ghrelin control. For statistical details see methods  
843 section.

844

845 **Figure 4. GHS-R1a-mediated activation of mTOR and ERK1/2 signalling pathway induced**  
846 **by ghrelin in Hek293a-GHSR-1a-EGFP cells.** Stimulation of GHSR-1a with agonist ghrelin  
847 (0.5  $\mu$ M) induced numerous changes in protein expression and phosphorylation levels (see also  
848 Suppl. Table X for details); many of the observed changes merged as components of mTOR and

849 ERK1/2 signalling network. The pathway network was constructed in the Database for  
850 Annotation, Visualization and Integrated Discovery (DAVID) based on the results of RPPA  
851 analysis.

852 **Figure 5. Investigation of SCFAs and lactate potential for mTOR/ERK/eEF2 signalling**  
853 **modulation in Hek-GHSR-1a-EGFP cells.** Phosphorylation of mTOR\_Ser2448 (A),  
854 ERK1\_Thr202 (B) and eEF2\_Thr56 (C) was analysed in cells treated with SCFAs/lactate alone  
855 (1 h incubation), co-treatment with ghrelin (1 hour incubation) or pre-treatment with  
856 SCFAs/lactate (1 hour) before ghrelin addition (1 hour). Graphs represent median and IQR (box)  
857 with minimal and maximal values (whiskers) of three independent experiments. Untreated  
858 control (assay buffer), ghrelin (ghrl, 0.5  $\mu$ M), inverse agonist [D-Arg1, D-Phe5, D-Trp7,9,  
859 Leu11]-substance P (SP-analogue, 0.5  $\mu$ M), SCFAs (1 mg/mL) and lactate (0.3 mg/mL). \*  $p \leq$   
860 0.05 vs untreated control and  $p \leq 0.05$  vs ghrelin-treated cells, Mann-Whitney U test.

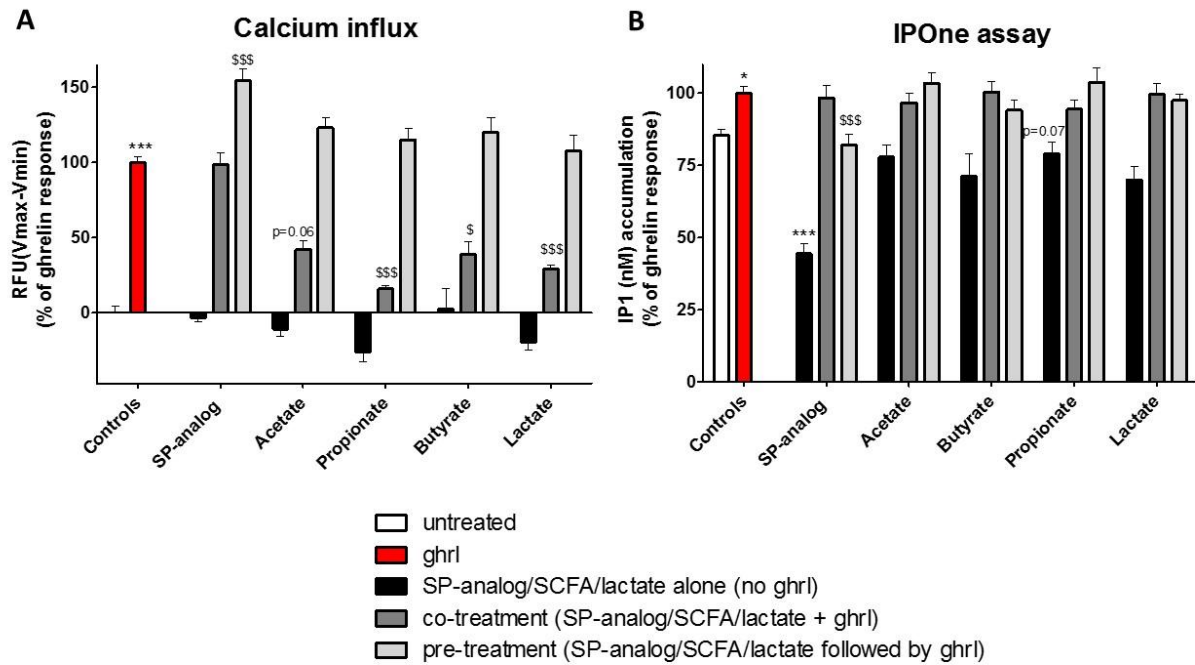
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862 **Figure 6. Investigation of bacterial strain potential for mTOR/ERK/eEF2 signalling**  
863 **modulation in Hek-GHSR-1a-EGFP cells.** Phosphorylation of mTOR\_Ser2448 (A),  
864 ERK1\_Thr202 (B) and eEF2\_Thr56 (C) was analysed in cells following different treatments:  
865 bacterial supernatants alone (1 h incubation), co-treatment with ghrelin (1 hour incubation) or  
866 pre-treatment with supernatants (1 hour) before ghrelin addition (1 hour). Graphs represent  
867 median and IQR (box) with minimal and maximal values (whiskers) of three independent  
868 experiments. Untreated control (assay buffer), ghrelin (ghrl, 0.5  $\mu$ M), inverse agonist [D-Arg1,  
869 D-Phe5, D-Trp7,9, Leu11]-substance P (SP-analogue, 0.5  $\mu$ M) and diluted bacterial strain  
870 supernatants (1:2 v/v in assay buffer; bacterial strains: *B. longum* APC1472, *B. breve* APC6331,

871 *L. rhamnosus* DPC6118, *L. gasseri* DPC6106, *L. brevis* DPC6108 and *P. avidum* APC6544). \*  $p$   
872  $\leq 0.05$  vs untreated control and  $p \leq 0.05$  vs ghrelin-treated cells, Mann-Whitney U test.

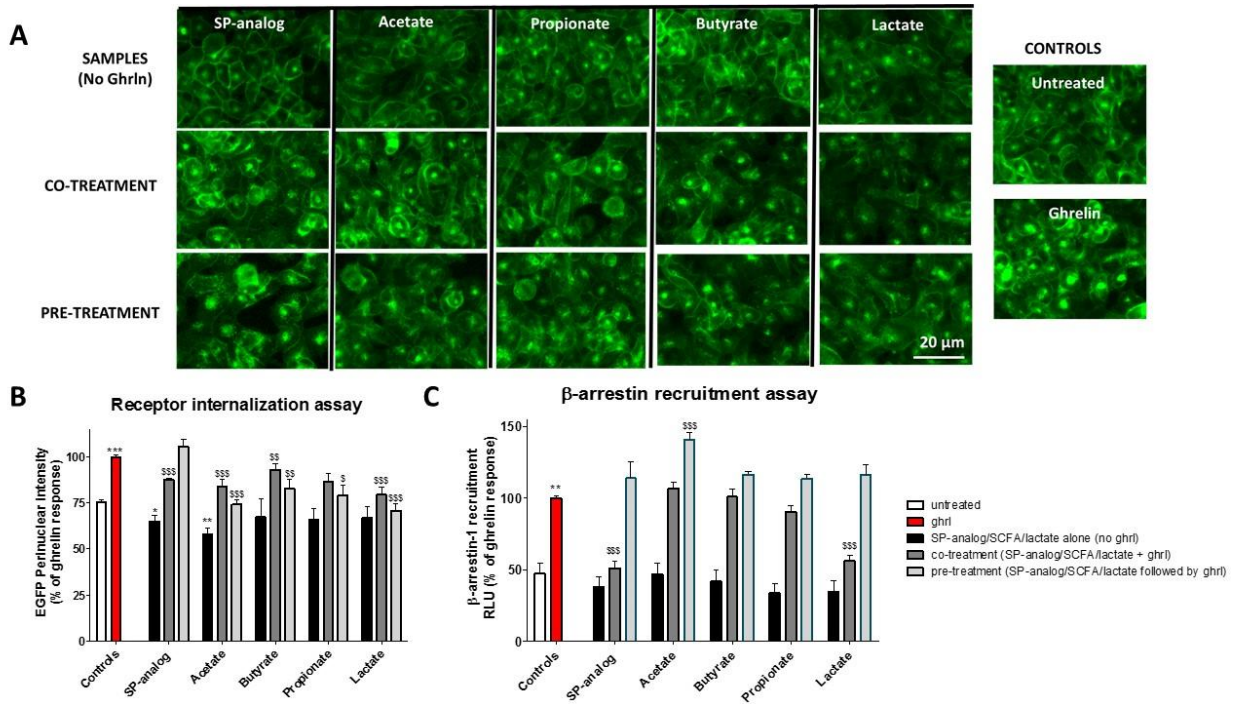
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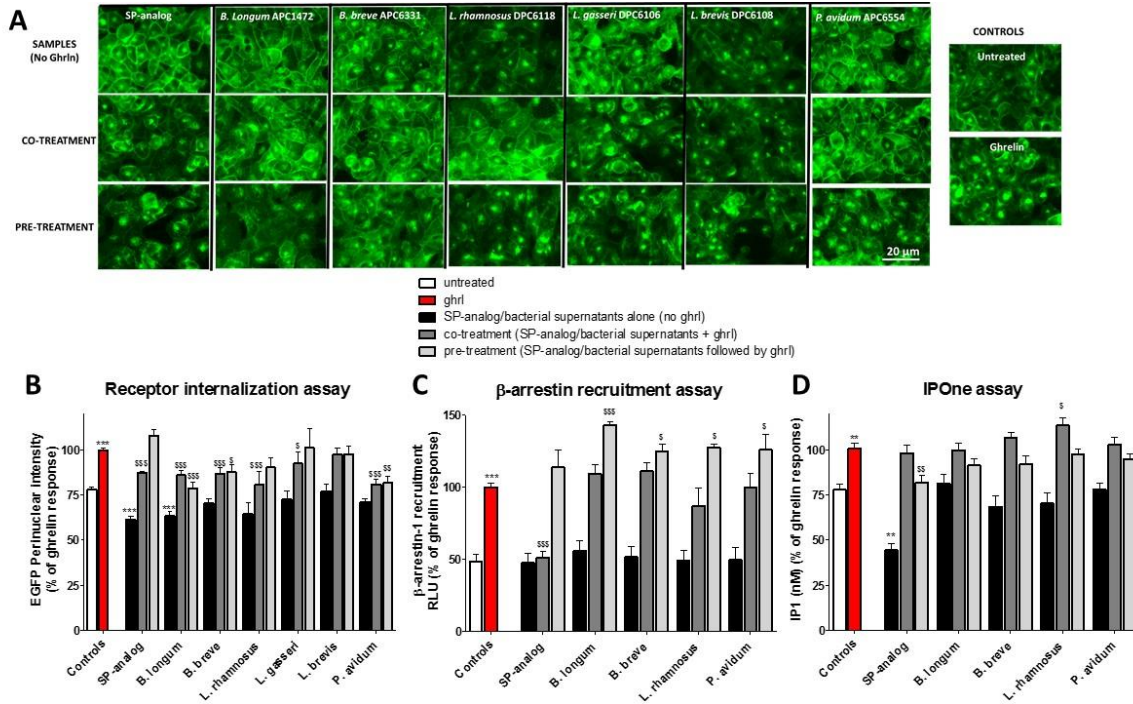
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Figure 3



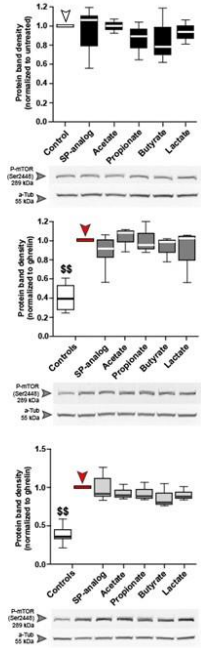
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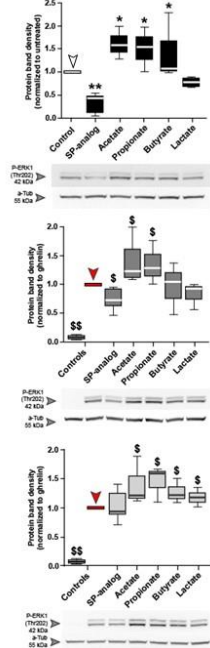
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1011 Figure 5

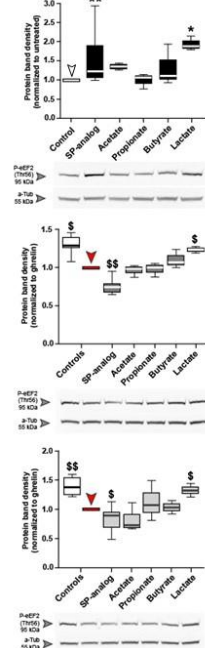
### A mTOR signalling



### B ERK1/2 signalling



### C eEF2 signalling



untreated  
 ghrl  
 SCFA/lactate alone (no ghrl)  
 co-treatment (SCFA/lactate + ghrl)  
 pre-treatment (SCFA/lactate followed by ghrl)

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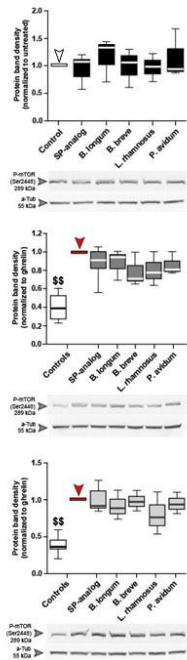
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1028 Figure 6

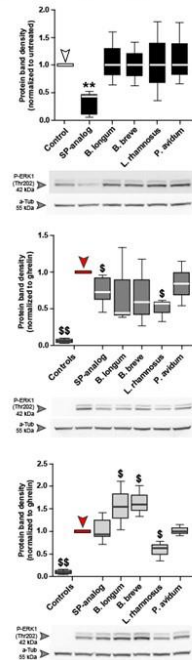
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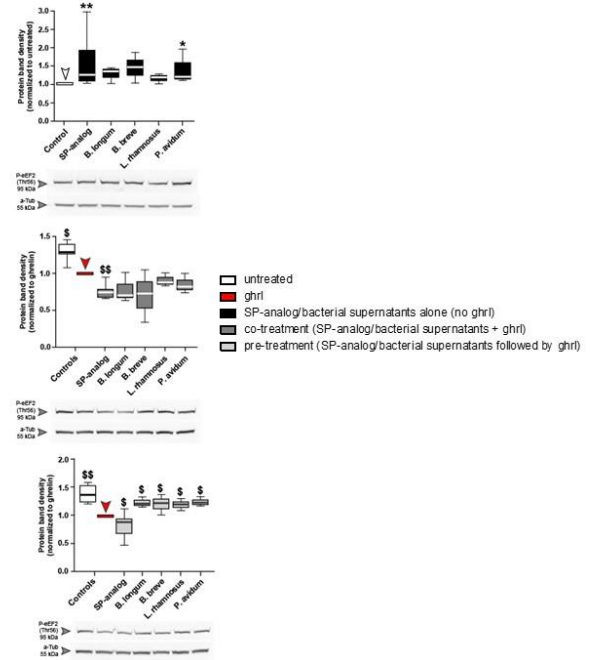
### A mTOR signalling



### B ERK1/2 signalling



### C eEF2 signalling



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## 1 **Supplementary information**

### 2 **Resazurin assay**

3 Cytotoxicity was analyzed using the resazurin assay (R&D systems, Inc.) as previously  
4 described (Torres-Fuentes et al., 2018, 2014). Briefly, Hek293a-GHSR-1a cells were seeded  
5 at  $2.8 \times 10^4$  cells/well and maintained for 48 h at culture conditions. For the last 24 h of this  
6 time period, media was replaced with serum free DMEM media containing 1% NEAA. Cells  
7 were exposed for 4 h to SCFA and lactate at different concentrations containing 10%  
8 resazurin dye. Absorbance was measured at 570 nm. Cell viability was calculated as  
9 percentage of control (cells in 1x Hanks balanced salt solution (Gibco), supplemented with  
10 20 mM HEPES (Sigma-Aldrich)). Values above 90% are not considered cytotoxic.

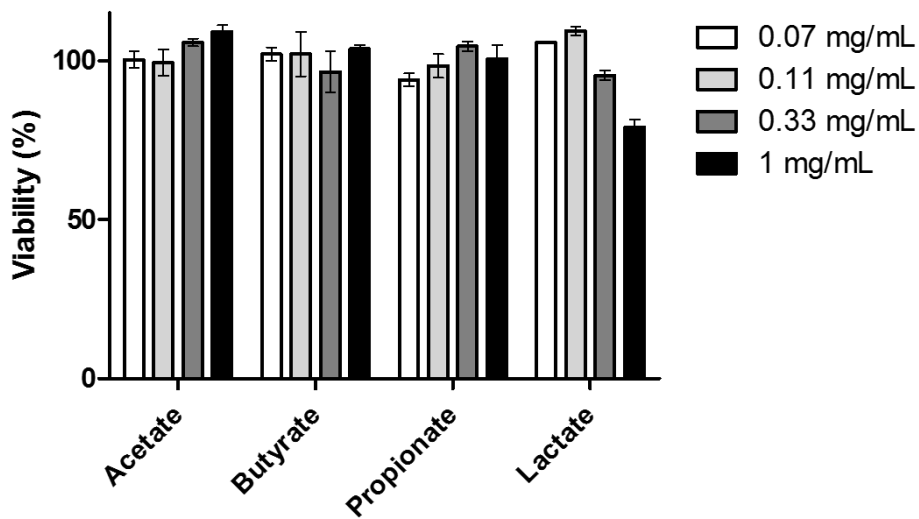
### 11 **Gas chromatography analysis of SCFAs in bacterial supernatants**

12 The concentration of SCFA was analyzed using a Varian 3500 GC flame-ionization system,  
13 fitted with a Nukol-FFAP column (30m x 0.32mm x 0.25mm; Sigma). The initial oven  
14 temperature was set at 100°C for 0.5min, raised to 180°C at 8°C/min and held for 1min, then  
15 increased to 200°C at 20°C/min, and finally held at 200°C for 5min. The temperatures of the  
16 injector and the detector were set at 240 and 250°C, respectively. He gas was used as a carrier  
17 at a flow rate of 1.3 ml/min.(Marques et al., 2015). 270ul of the supernatant was filtered and  
18 transferred to a clear GC vial. 2-Ethylbutyric acid (Sigma) was used as the internal standard  
19 (30 µl). A standard curve was built with different concentrations of a standard mix containing  
20 acetate, propionate, isobutyrate and n-butyrate (Sigma). Peaks were integrated by using the  
21 Varian Star Chromatography Workstation version 6.0 software. All SCFA data are expressed  
22 as mM. Butyrate was not detected in the tested bacterial supernatants.

23 **Calcium imaging**

24 Hek-GHSR-1a-EGFP cells were seeded in 12-well plate at  $2 \times 10^5$  cells/well 48 hours prior to  
25 the assay and maintained at culture conditions. On the day of the assay media was removed  
26 and cells were carefully washed with phosphate buffered saline and incubated for 1 hour at  
27 37°C with 7  $\mu$ M Fura 2-AM (Thermo Fisher Scientific, Massachusetts, United States) in  
28 assay buffer (1x Hanks balanced salt solution, HBSS, containing 20mM HEPES). Following  
29 incubation, Fura 2-AM was removed and replaced with assay buffer. Cells were monitored  
30 using an Olympus BX50W1 set up with a Mercury arc burner (MT20 illumination system,  
31 Cell R, Olympus). An excitation spectrum of 380 nm and 340 nm were recorded with a fixed  
32 emission of 510 nm in a real time following manual pipetting of the compounds. Cells were  
33 exposed to same treatments as per IP assay (see methods section). Pre-treatments were done  
34 during the dye incubation. Regions of interest of single cells were set using a digital  
35 epifluorescent system and its corresponding computer software (Cell R, Olympus). The ratio  
36 of excitation/emission positively correlates to calcium released from intracellular stores. Data  
37 were analyzed using GraphPad Prism software (PRISM 5.0; GraphPAD Software Inc.).

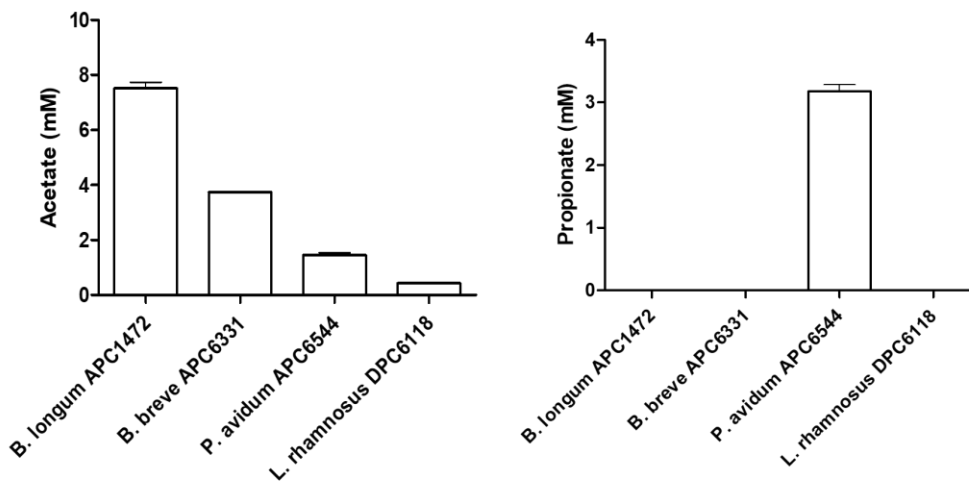
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40 **Figure S1. SCFA and lactate cytotoxicity effects on Hek-GHSR-1a-EGFP cells.** Results  
 41 are expressed as percentage of viability compared to untreated cells (cells in 1x HBSS  
 42 containing 20 mM HEPES). Graph represents the mean  $\pm$  SEM with each treatment in  
 43 triplicate.

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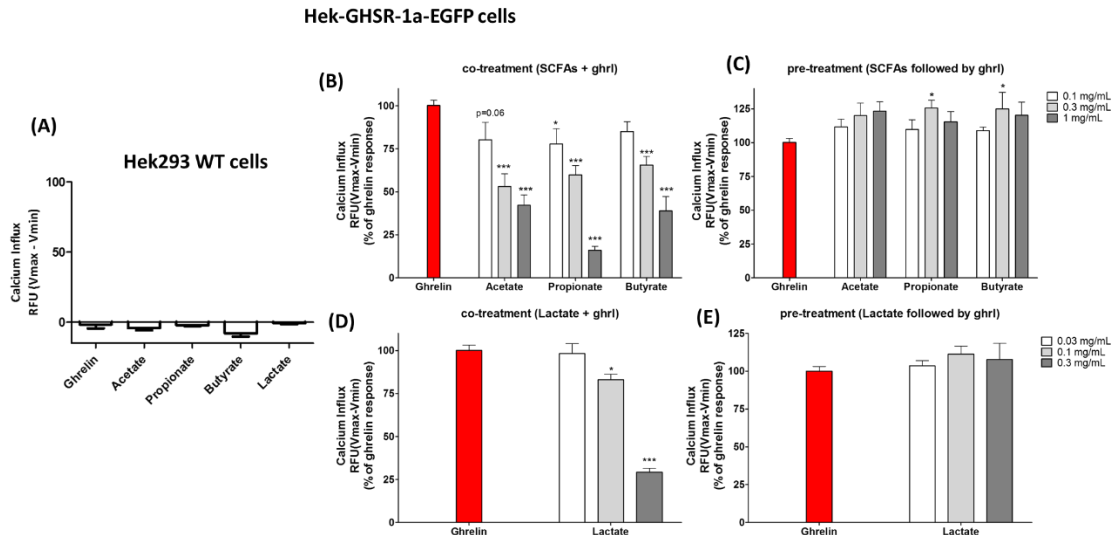


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46 **Figure S2. Bacterial strains supernatants SCFAs analysis by GC.**

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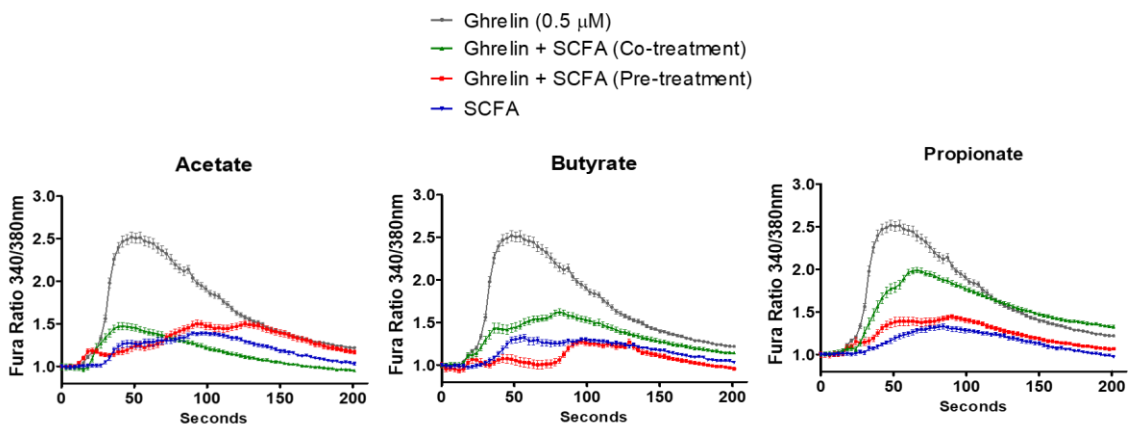
## Calcium influx assay



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50 **Figure S3.** SCFAs and lactate effects on calcium signaling. **(A)** No response was observed  
 51 in Hek293 WT cells. Data is depicted as a percentage of maximal response as elicited by the  
 52 positive control FBS (3.3%). SCFA (1 mg/mL); lactate (0,3 mg/mL). SCFAs **(B, C)** and  
 53 lactate **(D, E)** DRCs in Hek-GHSR-1a-EGFP cells for both assays modes: co-treatment with  
 54 ghrelin (1 hour incubation) or pre-treatment with SCFAs/lactate (1 hour) before ghrelin  
 55 addition (1 hour), Data is depicted as a percentage of maximal response as elicited by the  
 56 positive control ghrelin. Graphs represent the mean  $\pm$  SEM from at least three independents  
 57 experiments with each sample performed in triplicate. \* $p \leq 0.05$  vs ghrelin control.



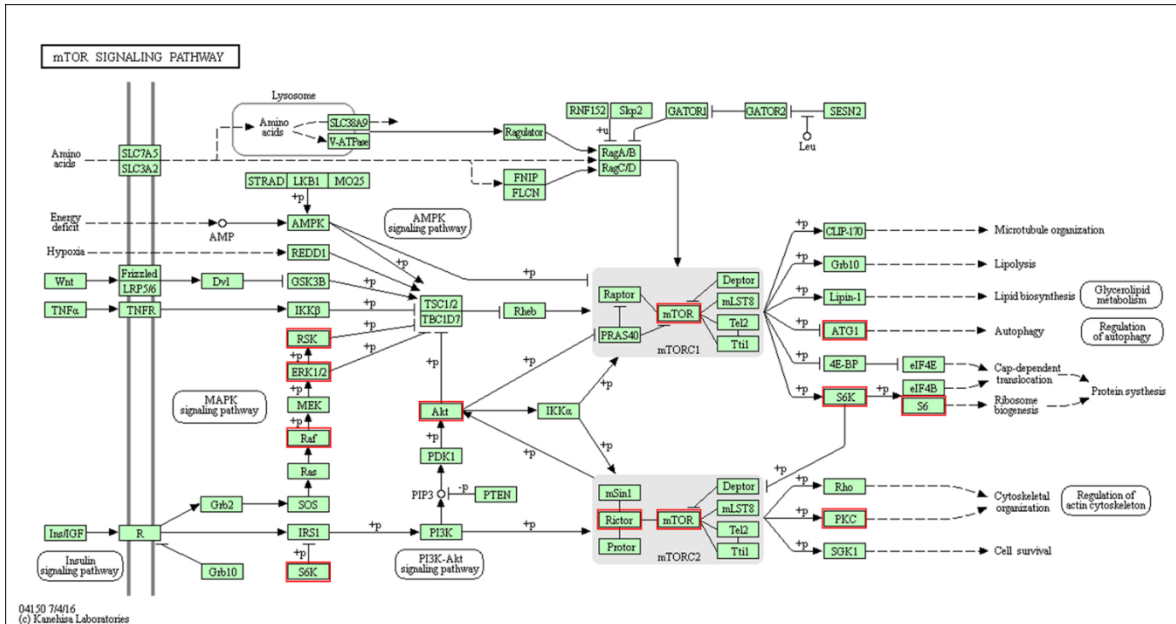
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59 **Figure S4. Calcium imaging analysis in Hek-GHSR-1a-EGFP cells.** Cells were exposed  
 60 to different treatments: the agonist ghrelin (grey bars), co-treatment with ghrelin and SCFAs  
 61 (green), pre-treatment with SCFAs before ghrelin addition (red) or SCFAs alone (blue).  
 62 Graphs represent the mean  $\pm$  SEM from at least four independents experiments. Ghrelin: 0.5  
 63  $\mu$ M; SCFAs: 1 mg/mL

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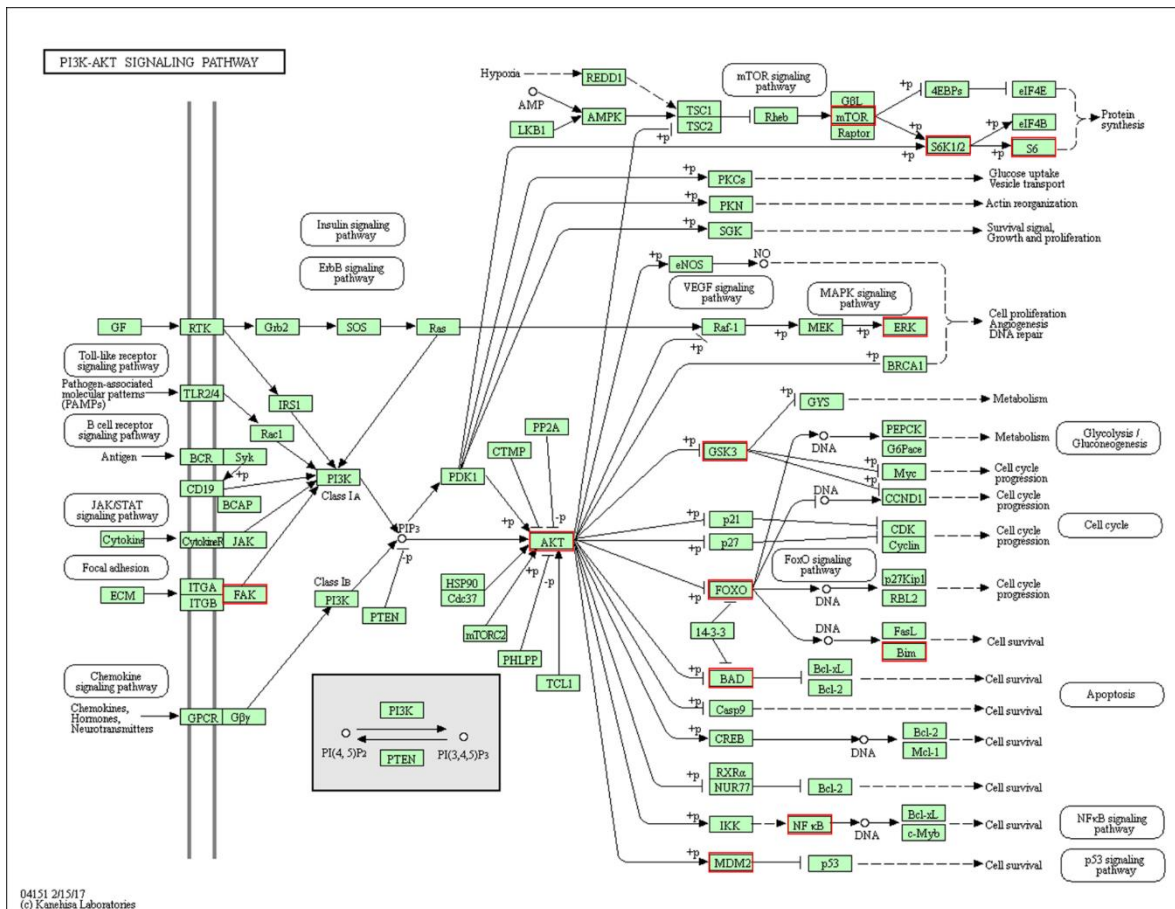
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68 **Figure S5.** GHS-R1a-mediated activation of mTOR & ERK1/2 signalling pathway in Hek293a-GHSR-  
 69 1a-EGFP cells. Cells were treated for 1 h with GHS-R1a agonist ghrelin (0.5  $\mu$ M), and subsequent  
 70 changes in protein expression and phosphorylation levels were screened with RPPA assay. Proteins  
 71 displaying  $\geq 10\%$  change vs. untreated control in three independent experiments (in red rectangles)  
 72 were selected for the construction of KEGG pathways using Functional Annotation Clustering in the  
 73 Database for Annotation, Visualization and Integrated Discovery (DAVID ) v6.8.



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75 **Figure S6. GHS-R1a-mediated activation of PI3K/Akt signalling pathway in Hek293a-GHSR1a-EGFP**  
 76 **cells.** Cells were treated for 1 h with GHS-R1a agonist ghrelin (0.5 μM), and subsequent changes in  
 77 protein expression and phosphorylation levels were screened with RPPA assay. Proteins displaying  
 78 ≥ 10% change vs. untreated control in three independent experiments (in red rectangles) were  
 79 selected for the construction of KEGG pathways using Functional Annotation Clustering in the  
 80 Database for Annotation, Visualization and Integrated Discovery (DAVID) v6.8.

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