

1 **The associations between bitter and fat taste sensitivity, and dietary fat intake: Are they**
2 **impacted by genetic predisposition?**

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21
22 **Abstract**

23 A relationship between bitter and fat taste sensitivity, *CD36* rs1761667 and *TAS2R38*
24 has been demonstrated. However, research is scarce and does not take diet into account. This
25 study aimed to explore associations between genetics, fat and bitter taste sensitivity and dietary
26 fat intake in healthy UK adults. A cross-sectional study was carried out on 88 Caucasian
27 participants (49 females and 39 males aged 35 ± 1 years; body mass index 24.9 ± 0.5 kg/m²).
28 Bitter taste sensitivity was assessed using phenylthiocarbamide (PTC) impregnated strips and
29 the general Labelled Magnitude Scale. Fat taste sensitivity was assessed by the Ascending
30 Forced Choice Triangle Procedure and dietary intake with a semi-quantitative food frequency
31 questionnaire. Genotyping for rs713598, rs1726866, rs10246939 and rs1761667 was
32 performed. Participants with *TAS2R38* PAV/PAV diplotype perceived PTC strips as more
33 bitter than groups carrying AVI haplotypes (AVI/AVI, $p = 1 \times 10^{-6}$; AVI/AAV, $p = 0.029$).
34 *CD36* rs1761667 was associated with fat taste sensitivity ($p = 0.008$). A negative correlation
35 between bitter taste sensitivity and saturated fat intake was observed ($r_s = -0.256$, $p = 0.016$).
36 When combining the *CD36* genotypes and *TAS2R38* diplotypes into one variable, participants
37 carrying both *TAS2R38* AVI haplotype and *CD36* A allele had a higher intake of saturated fat
38 compared to carriers of *CD36* GG genotype or *TAS2R38* PAV/PAV and PAV/AAV diplotypes
39 (13.8 ± 0.3 vs 12.6 ± 0.5 %TEI, $p = 0.047$) warranting further exploration in a larger cohort.

40 **Keywords:**
41 Taste Perception, Diet, rs1761667, CD36, TAS2R38

42
43 **Abbreviations:**

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45 BMI – body mass index; CD36 - cluster of difference 36; FFQ – food frequency questionnaire;
46 FTS – fat taste sensitivity; long-chain fatty acids – LCFA; MUFA - monounsaturated fatty
47 acid; PROP - 6-n-propylthiouracil; PTC – phenylthiocarbamide; PUFA - polyunsaturated fatty
48 acid; SFA – saturated fatty acid; SNP - single nucleotide polymorphism; TEI – total energy
49 intake.

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56 **1. Introduction:**

57 Taste sensitivity is an important factor in dietary habit development (Karmous et al., 2018).
58 The five defined human tastes are sweet, sour, bitter, salty and umami (Ikeda, 1909), with a
59 potential sixth taste, fat taste (“oleogustus”) recognised recently (Mattes, 2010). The
60 consumption of large amounts of dietary fat constitutes an unhealthy dietary pattern (World
61 Health Organisation (WHO), 2020). Differing taste sensitivity thresholds, which can impact
62 dietary fat consumption, may influence this unhealthy dietary pattern (Duffy & Bartoshuk,
63 2000; Graham et al., 2021). Research has identified genetic predisposition to all six tastes
64 (Melis et al., 2020), although these have scarcely been studied together.

65 A wealth of research has reported a clear disparity in the ability to detect bitter compounds
66 such as phenylthiocarbamide (PTC) and 6-n-propylthiouracil (PROP); a disparity which may
67 be affected by genetics. More specifically, bitter taste sensitivity follows a bimodal distribution,
68 with distinct phenotypes being either non-taster or taster.

69 To date, various candidate genes have been associated with PROP taste sensitivity, such as
70 the taste receptors from the taste receptor 2 family and the gustin gene, *carbonic anhydrase VI*,
71 (*CA6*) (Melis et al., 2013; Roura et al., 2015). *The bitter taste receptor 2 member 38 (TAS2R38)*
72 is the most researched receptor to date regarding PROP or PTC taste sensitivity. It contains
73 three coding single nucleotide polymorphisms (SNPs): rs713598 (Pro49Ala), rs1726866
74 (Ala262Val), and rs10246939 (Val296Ile). These may explain more than 70% of bimodal
75 distribution in PTC taste sensitivity (Kim et al., 2003; Risso et al., 2016). They also create
76 common taster Pro-Ala-Val (PAV) and non-taster Ala-Val-Ile (AVI) haplotypes, observed in
77 over 90% of the Caucasian population (Kim, Wooding, Ricci, Jorde, & Drayna, 2005). In
78 addition, rare haplotypes such as Ala-Ala-Val (AAV), Ala-Ala-Ile (AAI), Pro-Ala-Ile (PAI)
79 and Pro-Val-Ile (PVI) have been identified and may be associated with intermediate
80 sensitivities to PTC and PROP (Risso et al., 2016; Tepper et al., 2008).

81 Research on genetic determinants of PROP/PTC taste sensitivity has mostly been
82 conducted in Caucasian populations (North Americans or Europeans) that are more likely to
83 be carriers of the non-taster *TAS2R38* AVI haplotype compared to African or Asian populations
84 (Risso et al., 2016). Consequently, Caucasians have also been identified as having lower PROP
85 taste sensitivity than the two above-mentioned populations (Williams et al., 2016; Yang et al.,
86 2020).

87 Regarding dietary intake, lower bitter taste sensitivity has been associated with higher
88 acceptance and intake of foods with a bitter taste (brassica vegetables, spinach, coffee) (Akella
89 et al., 1997; Drewnowski et al., 1998, 1999), as well as a higher preference for sweet and fatty

90 tasting foods (Duffy & Bartoshuk, 2000), however, these findings are not consistent across
91 studies (O'Brien et al., 2013; Timpson et al., 2005). Nevertheless, the association between
92 bitter taste sensitivity and intake of foods other than those containing bitter tasting compounds,
93 suggests an interaction with other taste modalities. Considering a larger proportion of bitter
94 non-taster genotypes and phenotypes in Caucasians and the fact these may be associated with
95 diets high in sugar and fat, further research is warranted in this population.

96 In addition to the above, genetic variants in fat taste sensitivity (FTS) have been
97 reported. There have been two candidate genes of focus within human research; the *cluster of*
98 *difference 36 (CD36)* and *G-protein coupled receptor 120 (GPR120)* (Costanzo et al., 2019;
99 Daoudi et al., 2015). There is significant evidence of a link between variants within *CD36* and
100 FTS, specifically the rs1761667 (A/G) SNP. This has been associated with FTS (Daoudi et al.,
101 2015; Pepino et al., 2012; Sayed et al., 2015) and dietary fat intake (Fujii et al., 2019; Pepino
102 et al., 2012; Pioltine et al., 2016; Ramos-Lopez et al., 2016). The *CD36* receptor, a membrane
103 protein belonging to the class B scavenger receptor family located in taste bud cells, has been
104 shown to bind to varying concentrations of saturated and unsaturated long-chain fatty acids
105 (LCFA) (Besnard et al., 2016). To date, it is the only defined fat receptor with a high affinity
106 to LCFA (Khan et al., 2020). Individuals with the A-allele have demonstrated reduced protein
107 levels (Ghosh et al., 2011; Love-Gregory & Abumrad, 2011), and therefore have a higher fat
108 detection threshold (hyposensitive) and consequently cannot taste fat as successfully (Melis et
109 al., 2015; A Sayed et al., 2015). These individuals are likely to consume higher quantities of
110 foods containing fatty acids, potentially leading to weight gain (Besnard et al., 2016), although
111 there is paucity in research and what is available is largely heterogeneous (Tucker et al., 2017).

112 A relationship between bitter and fat taste may be apparent. Prior to the discovery of
113 fat taste and associated receptors, Tepper and Nurse, (1997) described PROP tasters to have a
114 greater ability for oral texture perception through a greater density of trigeminal fibres, thus, a
115 better ability to detect fat. Since this, a relationship between PROP tasters and preference for
116 fat has been demonstrated (Hayes & Duffy, 2007; Tepper & Nurse, 2006). More recently, and
117 in light of this, the *CD36* rs1761667 SNP has been investigated together with PROP taster
118 status and *TAS2R38* haplotypes (Sollai et al., 2019). Although results are consistent regarding
119 the association between fat and bitter taste by both *CD36* rs1761667 and bitter taste *TAS2R38*
120 haplotypes, research is scarce and is yet to be undertaken in a healthy UK cohort
121 comprehensively assessing whether genetic disparities impact dietary intake, alongside taste
122 sensitivity. Therefore, the aim of the current study was to explore the associations between
123 genetics, fat and bitter taste sensitivity and dietary fat intake in healthy UK adults.

124 **2. Methods**

125 **2.1 Study design and participants**

126 The participants were healthy Caucasian adults aged 18-65 years and living in the UK.
127 Participants were recruited via word of mouth and internet postings. Exclusion criteria were
128 pregnancy, breastfeeding, chronic medical conditions, food allergies, smoking, lactose
129 intolerance and intake of any medication that may affect taste perception.

130 At baseline visit, anthropometric measurements including weight (kg), height (m) and waist
131 circumference (cm) were recorded by the research team. Participants provided a 2 mL saliva
132 sample for genotyping and took part in bitter and FTS tests. Participants were asked to refrain
133 from consumption of any food or drink for one hour prior to testing. All participants provided
134 demographic information and completed a food frequency questionnaire (FFQ) administered
135 online (Google Forms).

136 All procedures involving human participants were approved by the St Mary's and Oxford
137 Brookes University Ethics Committees. Written informed consent was obtained from each
138 participant before the baseline data collection, stating they can withdraw from the study at any
139 point. This study is registered as Genetics of Bitter and Fat Taste at ClinicalTrials.gov
140 NCT04038281.

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142 **2.2 Demographic information**

143 Self-reported demographic data (age, sex, ethnicity, income, occupation, and education
144 level) were collected using an online questionnaire (Google Forms).

145

146 **2.3 Anthropometric measurements**

147 Height (m) [Free Standing Height Measure, SECA GmbH & Co., Hamburg, Germany] and
148 weight (kg) [Portable Scale MS-4203, Marsden Weighing Group, Oxfordshire, UK] were
149 recorded by the research team to the second decimal place. Body mass index (BMI) was
150 calculated using the equation: weight (kg)/ height (m²) (World Health Organization, 2018).

151

152 **2.4 Bitter taste sensitivity**

153 The participants rated the intensity of PTC impregnated strip (EISCO labs, Product
154 FSC1031) using the general Labeled Magnitude Scale (gLMS). The gLMS weighted scale
155 labels were: “no sensation” (0), “barely detectable” (1.4), “weak” (6), “moderate” (17),
156 “strong” (35), “very strong” (53), and “the strongest imaginable sensation of any kind” (100)

157 (Roura et al., 2015). Before rating the intensity of the PTC strip, participants were instructed
158 to remember the strongest sensation of any kind they had experienced or the strongest sensation
159 they could imagine happening to them. They were explained these would be deemed as the
160 strongest sensations of any kind on the gLMS scale (Hayes et al., 2013). This was used to guide
161 participants when rating the PTC intensity.

162

163 **2.5 Fat taste sensitivity**

164 The Oral Fatty Acid Threshold Assessment and Ascending Forced Choice Triangle
165 Procedure was carried out to determine each participant's oleic acid (C18:1) detection
166 threshold (FTS). The method used, and standard operating procedure followed, is described in
167 full in Haryono, Sprajcer and Keast, (2014). Briefly, each participant was presented with three
168 cups (30 mL UTH-milk based vehicles) in a random order, two controls (oleic-) and one
169 containing oleic acid (oleic+; 0.02, 0.06, 1, 1.4, 2, 2.8, 3.8, 5, 6.4, 8, 9.8, 12, 20 mM). A
170 participant was required to select the oleic+ solution correctly three times at the same
171 concentration to define their threshold. If they were incorrect at any point, a further three cups
172 were presented, one containing the higher oleic+ concentration and two oleic- solutions.
173 Participants were categorised by their FTS result: hypersensitive tasters have a FTS below 3.8
174 mM, hyposensitive tasters have a FTS above or equal to 3.8 mM and participants who fail to
175 identify the oleic+ sample at the maximum concentration (20 mM) are defined as non-tasters
176 (excluded from analysis) (Haryono et al., 2014; Stewart, Newman, & Keast, 2011).

177 Testing was conducted on one occasion for each participant. Samples were served at room
178 temperature and presented to participants in individual sections within either the St Mary's
179 University Nutrition laboratory or Oxford Brookes University sensory laboratory. Red lighting
180 was used to mask visual differences between the samples, nose clips were worn to inhibit
181 olfactory input, textural differences were avoided with the addition of textural agents (gum
182 Arabic and liquid paraffin), and post-ingestive regulation was followed by the sip-and-spit
183 procedure.

184

185 **2.6 Dietary intake**

186 Habitual dietary intake was assessed with a validated semi-quantitative FFQ (EPIC
187 Norflok). The questionnaires were analysed using the open source, cross-platform tool FFQ
188 EPIC tool for analysis (FETA) (Mulligan et al., 2014) and information on energy and dietary
189 macronutrient intake obtained. More specifically, total carbohydrate, total fat,
190 monounsaturated fatty acid (MUFA), polyunsaturated fatty acid (PUFA), saturated fatty acid

191 (SFA) and total protein were quantified. Intakes of macronutrients were converted into
192 percentage of total energy intake (%TEI) for analyses.

193

194 **2.7 Single nucleotide polymorphism genotyping**

195 From each participant, a 2 mL saliva sample was collected (SalivaGene Collection Module
196 II; Stratec Molecular GmbH). A stabiliser provided by the manufacturer was added to the saliva
197 sample which was then kept at -20°C until DNA was isolated. Genomic DNA was isolated
198 using a PSP® Saliva-Gene 17 DNA Kit 1011 (Stratec Molecular GmbH) in agreement with
199 the manufacturer procedures. Quality and quantity of the DNA were measured using
200 spectroscopy (Nanodrop, Thermo Fisher, Waltham, MA, USA). Genotyping was then
201 performed using predesigned TaqMan® SNP genotyping assays for the SNPs: rs1761667,
202 rs713598, rs1726866 and rs10246939 and the StepOnePlus thermocycler (Applied Biosystems,
203 CA, USA) with two technical replicates for each sample. The PCR amplification was then
204 completed under the conditions stated by the manufacturer. *TAS2R38* haplotypes, defined by
205 rs713598, rs1726866 and rs10246939, were determined using Haploview software (Barrett et
206 al., 2005).

207

208 **2.8 Statistical analyses**

209 Hardy Weinberg equilibrium was assessed for all SNPs using Chi-square goodness of fit
210 test. Continuous variables are presented as mean \pm standard error of the mean (SEM) or median
211 (interquartile range) and were tested for normality with Shapiro-Wilk test. Categorical
212 variables are presented as absolute (relative) frequencies. Differences in anthropometry,
213 genotype frequencies, bitter and fat taste sensitivity and dietary intake between males and
214 females were tested with an independent samples t-test (with Levene's test for equality of
215 variance), Mann Whitney U or Fisher's Exact test, where appropriate. Individuals who failed
216 to identify the oleic+ solution at 20 mM were defined as non-tasters, therefore have no
217 measurable threshold and were excluded from further analyses on FTS and measurements of
218 dietary intake by *CD36* genotypes, in line with others (Burgess et al., 2018).

219 Spearman's correlation was used to explore the associations between bitter and fat taste
220 sensitivity as continuous variables. Kruskal-Wallis H tests were used to test the difference in
221 bitter taste sensitivity between *TAS2R38* diplotype groups and *CD36* genotypes. Bonferroni
222 adjustment were considered for pairwise comparisons. Mann-Whitney U test was used to
223 analyse the differences in bitter taste sensitivity according to the *TAS2R38* rs713598,
224 rs1726866 and rs10246939. Genotypes were dichotomised into carriers of non-taster (Ala, Val,

225 Ile) and homozygous taster alleles (Pro, Ala, Val). Chi-square or Fisher's Exact test, where
226 appropriate, were used to assess the associations between *CD36* genotypes (AA, AG and GG,
227 and AA/AG and GG), *TAS2R38* diplotypes and FTS categories, and to assess the associations
228 between *CD36* genotypes (AA, AG and GG, and AA/AG and GG) and *TAS2R38* diplotypes.
229 Kruskal-Wallis H test was used to explore the difference in fat taste threshold (mM) between
230 *TAS2R38* diplotypes and *CD36* genotypes with Bonferroni adjustment for
231 multiple comparisons.

232 Spearman's correlation was used to assess the associations between dietary fat intake (total,
233 MUFA, PUFA and SFA) and bitter taste sensitivity, and FTS. One-way analysis of variance
234 (ANOVA) or Kruskal Wallis H, were appropriate, were used to test for differences in dietary
235 intake between *TAS2R38* diplotype groups, and between rs1761667 genotypes (AA, AG and
236 GG). Independent samples t-test (with Levene's test for equality of variance) or Mann Whitney
237 U test, where appropriate, were used to test for differences in dietary intake between rs713598,
238 rs1726866, rs10246939 (carriers of the non-taster and homozygous taster allele), and
239 rs1761667 genotypes (AA/AG and GG) as well as a variable combined of *CD36* genotypes
240 and *TAS2R38* diplotypes (Non-tasters: participants carrying both *TAS2R38* AVI haplotype and
241 *CD36* A allele vs Tasters: carriers of *CD36* GG genotype or *TAS2R38* PAV/PAV and PAV/
242 AAV diplotypes). Participants with AVI/PAV diplotype were grouped with non-tasters
243 considering that larger proportion of our study population carrying this diplotype was deemed
244 a non-taster using the classification by Roura *et al.* (2015) explained below. Finally, two-way
245 ANOVA was conducted to explore the interaction between fat and bitter taster categories on
246 dietary fat intake (total fat, MUFA, PUFA and SFA). For this purpose, PTC ratings were used
247 to categorise the participants into three distinct taster groups. The cut-off criteria were:
248 hyposensitive taster (non-taster) ≤ 15.5 , normal taster > 15.5 , and hypersensitive taster ≥ 51
249 (Roura *et al.*, 2015). Considering a low number of hypersensitive tasters, these were excluded
250 from the analysis. Bonferroni adjustment was used for multiple comparisons.

251 SPSS was used throughout (IBM Corp. Released 2016. IBM SPSS Statistics for Windows,
252 Version 24.0. Armonk, NY: IBM Corp.). All tests were two-tailed, with $p < 0.05$ considered
253 statistically significant.

254

255 3. Results

256

257 3.1 Participant characteristics

258 Participant characteristics are shown in Table 1. Participants were healthy Caucasians (49
259 females (56%) and 39 males (44%)) with mean age 35 ± 1 years and BMI 24.9 ± 0.5 kg/ m².

260 There were no differences in any of the presented variables or genotype frequencies according
261 to sex, therefore males and females were combined in all analyses (data not shown). No
262 differences in BMI were found between genotypes/diplotypes or bitter and fat taster categories
263 (data not shown). Genotype/diplotype frequency of fat non-tasters can be found in
264 Supplementary Table 1.

265 The *TAS2R38* and *CD36* SNPs were in Hardy Weinberg equilibrium ($p = 0.825$, $p = 0.573$,
266 $p = 0.573$ and $p = 0.217$ for the rs713598, rs1726866, rs10246939 and rs1761667 respectively).
267 Haplotype frequencies of *TAS2R38* in the study population were: AVI (53%), PAV (42%) and
268 AAV (5%) and allele frequencies of *CD36* rs1761667 were A (61%) and G (39%).

269

270 **3.2 Taste sensitivity and genetics**

271 There was no correlation between fat and bitter taste sensitivity ($r_s = 0.038$, $p = 0.758$,
272 data not shown, $n = 69$).

273 As shown in Figure 1, participants carrying PAV/PAV diplotype had higher median
274 ratings of PTC intensity (median (IQR) 31 (30)) compared to participants with AVI haplotype
275 (AVI/AVI, median (IQR) 2 (6) $p = 1 \times 10^{-6}$; AVI/AAV, median (IQR) 4 (14), $p = 0.029$, $n =$
276 88)). Similarly, those classified as AVI/PAV had higher PTC ratings (median (IQR) 9 (24))
277 than those homozygous for AVI haplotype ($p = 0.002$, $n = 88$). Carriers of non-taster alleles
278 for rs713598 (Ala), rs1726866 (Val) and rs10246939 (Ile) had lower ratings of bitterness
279 compared to those homozygous for the taster alleles (Pro, Ala and Val, data not shown).

280 The *CD36* rs1761667 was associated with FTS ($p = 0.008$, $n = 69$) when analysed as
281 three genotype groups (AA, AG and GG). Here, a larger proportion of hyposensitive tasters
282 had the AG genotype (55%), this remained significant after Bonferroni corrections were
283 applied (Figure 1). For exploratory purposes only, non-tasters were included in further
284 analysis, results were consistent ($p = 0.033$; Supplementary Figure 1), however this was
285 no longer significant after Bonferroni correction applied. When genotypes were combined
286 by variant allele (AA/AG, and GG), a larger percentage of participants carrying the A allele
287 (67.2%) were classified as hyposensitive tasters compared to those homozygous for the G
288 allele ($p = 0.013$, $n = 69$, data not shown). Similar was observed when fat taste threshold
289 was treated as a continuous variable (Supplementary Table 3).

290 There was no association between *TAS2R38* diplotypes and *CD36* rs1761667 ($p =$
291 0.622, 0.963, respectively for AA, AG and GG, and AA/AG and GG, $n = 88$). There was also
292 no difference in PTC ratings of bitterness according to *CD36* rs1761667 genotypes ($p = 0.782$,
293 1.000, respectively for AA, AG and GG, and AA/AG and GG, $n = 88$) or *TAS2R38* diplotypes

294 and fat taste categories ($p = 0.384$, $n = 69$). There were no differences in fat taste threshold
295 between *TAS2R38* diplotypes (Supplementary Table 3).

296

297 **3.3 Associations between genetics, taste sensitivity and diet**

298 As shown in Figure 2, the ratings of PTC intensity were negatively correlated with SFA
299 (%TEI) ($r_s = -0.256$, $p = 0.016$, $n = 88$). There were no correlations between bitter taste
300 sensitivity, total fat, MUFA and PUFA intakes. When excluding participants carrying
301 AVI/AVI diplotype, there was no correlation between PTC bitter taste intensity and dietary fat
302 intake ($r_s = -0.229$, $p = 0.069$; $r_s = -0.199$; $p = 0.115$; $r_s = -0.184$; $p = 0.145$; $r_s = -0.166$; $p =$
303 0.191 for total fat, MUFA, PUFA and SFA respectively). Similarly, there were no correlations
304 between fat taste threshold and any of the presented variables (Figure 3, $n = 69$). SFA (%TEI)
305 and total fat (%TEI) ($r_s = 0.656$, $p = 3.9 \times 10^{-12}$) and total fat (%TEI) and energy intake (kcal) (r_s
306 $= 0.225$, $p = 0.035$) were positively correlated in the total cohort (data not shown).

307 There were no differences in energy and macronutrient intakes according to *TAS2R38*
308 diplotypes (Table 2, $n = 88$) or *CD36* rs1761667 (Table 3, $n = 69$). Similar findings were
309 observed when rare diplotypes AVI/AAV and PAV/AAV were excluded from the analyses
310 (data not shown, $n = 78$). When analysing individual *TAS2R38* SNPs, there was a significant
311 difference in SFA between rs1726866 and rs10246939 genotypes. Those carrying the non-
312 taster allele for both SNPs (Val and Ile) had higher intake compared to participants
313 homozygous for the taster allele (Ala and Val), both 13.6 ± 0.3 vs 12.1 ± 0.6 %TEI, $p = 0.032$,
314 $n = 88$. When combining the *CD36* genotypes and *TAS2R38* diplotypes into one variable,
315 participants carrying both *TAS2R38* AVI haplotype and *CD36* A allele had a higher SFA intake
316 compared to carriers of *CD36* GG genotype or *TAS2R38* PAV/PAV and PAV/AAV diplotypes
317 (13.8 ± 0.3 vs 12.6 ± 0.5 %TEI, $p = 0.047$, Supplementary table 2, $n = 88$). Similar was observed
318 when only *TAS2R38* combined diplotypes were compared (AVI/AVI, AVI/AAV, AVI/PAV
319 vs PAV/PAV, PAV/AAV, data not shown).

320 Finally, results of the two-way ANOVA showed no interaction between fat (hypo and
321 hyper) and bitter (non-taster and taster) taster categories on total fat ($p = 0.111$), MUFA ($p =$
322 0.474), PUFA ($p = 0.220$) and SFA ($p = 0.218$). There were also no main effects of bitter taste
323 category on total fat ($p = 0.311$), MUFA ($p = 0.457$), PUFA ($p = 0.688$) and SFA ($p = 0.224$).
324 Similarly, there were no main effects of fat taste category on total fat ($p = 0.186$), MUFA ($p =$
325 0.406), PUFA ($p = 0.145$) and SFA ($p = 0.702$, Figure 4).

326

327

328 4 Discussion

329 The aim of this study was to explore the associations between genetics, taste sensitivity
330 (bitter and fat), and dietary fat intake in healthy UK adults. We have demonstrated a difference
331 in bitter taste sensitivity between *TAS2R38* diplotypes and an association between *CD36*
332 rs1761667 and FTS. We did not find an association between *TAS2R38* and FTS, and *CD36*
333 rs1761667 and bitter taste sensitivity. When analysing dietary intake, although there was no
334 association between either *TAS2R38* diplotypes or *CD36* rs1761667 and dietary intake, we did
335 observe a difference in SFA according to *TAS2R38* rs1726866 and rs10246939 genotypes and
336 a negative correlation between bitter taste sensitivity and SFA. Finally, we did not observe an
337 interaction between bitter and fat taste phenotypes on dietary fat intake. However, when
338 combining the *CD36* genotypes and *TAS2R38* diplotypes into one variable, participants
339 carrying both *TAS2R38* AVI haplotype and *CD36* A allele had a higher intake of saturated fat
340 compared to carriers of *CD36* GG genotype or *TAS2R38* PAV/PAV and PAV/AAV diplotypes.

341

342 4.1 The associations between *TAS2R38*, bitter taste and diet

343 We observed differences in the PTC ratings of bitterness according to *TAS2R38* diplotype
344 groups. Participants with PAV/PAV diplotype had higher ratings than those carrying AVI
345 haplotype and participants classified as AVI/PAV had higher ratings than those homozygous
346 for AVI haplotype. This is in line with previous research where AVI haplotype was associated
347 with bitter non-taster and PAV with a bitter taster phenotype (Bufe et al., 2005; Kim et al.,
348 2005; Tepper, 2008).

349 In addition to the associations between genetics and taste perception, we also observed
350 an inverse association between bitter taste sensitivity and SFA. Moreover, SFA was positively
351 associated with total fat intake in our study population. This negative association between bitter
352 taste sensitivity and dietary fat intake is in line with previous research reporting higher
353 preference and intake of dietary fat in bitter non-tasters compared to tasters (Choi & Chan,
354 2015; Duffy, 2004; Tepper & Nurse, 1998). Considering that total fat intake was positively
355 associated with energy intake, a higher intake of SFA may be an indicator of a more energy
356 dense pattern of dietary intake. Since we did not explore dietary patterns, this warrants further
357 research in a similar study population.

358 The mechanism behind the association between bitter taste sensitivity and dietary fat
359 intake is not entirely clear. It may be that interaction between bitter and fat taste perception
360 exists and this will be discussed later. Considering that the correlation between bitter taste
361 sensitivity and SFA was no longer significant once participants with AVI/AVI diplotype were

362 excluded, this association appears to be driven by genetic predisposition. In this sense,
363 *TAS2R38* is expressed in the gastrointestinal tract where it may regulate the release of satiety
364 hormones and influence the postprandial response to nutrients (Dotson et al., 2010; Rozengurt,
365 2006). We observed a higher intake of SFA in carriers of the non-taster alleles (Val and Ile) for
366 the rs1726866 and rs10246939 compared to those homozygous for the taster allele (Ala and
367 Val). Similar was observed when *TAS2R38* diplotypes were combined into carriers of the non-
368 taster AVI haplotype and compared to those carrying PAV/PAV or PAV/AAV diplotype. The
369 fact that we did not observe a similar difference in SFA when *TAS2R38* diplotypes were
370 analysed as separate groups may be due to a smaller sub-group sample size when splitting
371 participants into these; this warrants further investigation in a larger sample size study.
372 Interestingly, Dotson *et al.*, (2010) observed an increased eating disinhibition in carriers of the
373 rs1726866 Val, non-taster, allele in their population of Amish women. The authors did not
374 explore dietary intake, however the associations between saturated, total fat and energy intake
375 in our study population suggest that *TAS2R38* may be associated with both eating behaviour,
376 such as eating disinhibition, and a more energy dense dietary pattern. There are number of
377 proposed mechanisms including impaired release of satiety hormones (glucagon-like peptide
378 1 (GLP-1), insulin) and increased levels of leptin in carriers of the non-taster alleles that warrant
379 further investigation.

380 Besides the potential effects of *TAS2R38* intestinal expression on hormone signalling,
381 genetic variations in the *CA6* gene may provide an explanation for the association between
382 bitter taste sensitivity and dietary fat intake. Lower fat intake, as %TEI, was observed in UK
383 individuals carrying the AA genotype of the *CA6* rs2274333 compared to heterozygous AG
384 individuals (Shen et al., 2017). This genotype has been associated with greater bitter taste
385 sensitivity (i.e. PROP super-taster status), through greater fungiform papillae density in AA
386 genotypes compared to homozygous GG genotypes (Melis et al., 2013). Considering that
387 greater fungiform papillae density has also been associated with improved FTS (Zhou et al.,
388 2020), there may be an interaction between *TAS2R38* and *CA6* on dietary fat intake in our study
389 population. These interactions require further research in a similar study population.

390 Finally, due to the cross-sectional nature of the present study, it is not possible to
391 determine the direction of the association between bitter taste sensitivity and dietary fat intake.
392 Besides the possibility that lower bitter taste sensitivity leads to a higher fat intake, the opposite
393 may also be correct. Jeon *et al.* (2008) suggested that a low-cholesterol diet, likely low in
394 saturated fat, increases the sensitivity of intestinal bitter taste signalling system making the gut
395 more responsive to the presence of bitter tasting compounds. Further intervention studies are,

396 therefore, warranted to explore the cause-and-effect relationship between bitter taste and
397 dietary fat intake.

398

399

400 **4.2 The associations between *CD36* rs1761667, fat taste and diet**

401 Furthermore, we observed that the A allele of *CD36* rs1761667 was associated with
402 FTS, specifically a larger percentage of participants carrying the A allele were classified as
403 hyposensitive tasters. This is in line with previous research (Burgess et al., 2018; Chmurzynska
404 et al., 2020; Keller et al., 2012; Melis et al., 2015; Mrizak et al., 2015; Pepino et al., 2012;
405 Amira Sayed & Khan, 2015) and supports that LCFA evoke calcium signalling in gustatory
406 cells expressing *CD36* (El-Yassimi et al., 2008), and that lower protein levels may be related
407 to the A allele hindering ability to detect fat. To date, although research is supportive towards
408 an association between rs1761667 and FTS findings are largely heterogeneous, specifically,
409 regarding ethnicity, which has been shown to modify responses to taste sensitivity (El-Sohemy
410 et al., 2007). Only Melis *et al.*, (2015); Burgess *et al.*, (2018) and Sollai *et al.*, (2019)
411 investigated a Caucasian cohort, similar to ours. Chmurzynska *et al.*, (2020) states recruitment
412 was carried out in Poland, but otherwise does not specify ethnicity of participants. Our results
413 corroborate Melis *et al.*, (2015), and Sollai *et al.*, (2019) but contrast, Burgess *et al.*, (2018)
414 who reported no association between rs1761667 genotype and FTS or perception of fat in the
415 Caucasian sub-group. Results may differ to ours due to Burgess *et al.*, (2018) having a lower
416 sample size (n = 36) than us (n = 69) and Melis *et al.*, (2015) (n = 64), and thus may have
417 resulted in a type II error. Overall, it is evident the *CD36* rs1761667 A-allele may hinder ability
418 to detect fat in Caucasian participants, although research is scarce. Here it is important to state
419 that other factors may lead to differing taste sensitivity levels alongside rs1761667 genotype.
420 This includes both mechanistic factors, for example rs1527483, another SNP on the *CD36* gene
421 that has been associated with instantaneous orosensory fat taste sensitivity (Plesnik *et al.*
422 *al.*, 2018), and interactions between FTS and other tastes, which will be discussed below.
423 Further, an additional factor to consider are fat non-tasters, despite constituting a
424 comparatively small percentage of the population it is unclear whether this sub-population are
425 associated with the same genetic pattern demonstrated by us and others (Burgess et al., 2018;
426 Chmurzynska et al., 2020; Keller et al., 2012; Melis et al., 2015; Mrizak et al., 2015;
427 Pepino et al., 2012; Amira Sayed & Khan, 2015). Such genotypic conclusions cannot yet be
428 drawn since many excluded non-tasters from their analysis (Bajit et al., 2020; Burgess et al.,
429 2018; Karmous et al., 2018; Melis et al., 2020) due to no measurable threshold when
undertaking the forced choice triangle

430 method and a small sub-sample. We have included data for the fat non-tasters in our genetic
431 analysis to aid future research comparisons.

432 It has been stated that a reduced ability to taste fat may lead to greater consumption
433 (Besnard *et al.*, 2016). Despite the association found between *CD36* rs1761667 and FTS, we
434 did not observe a difference in dietary intake (total energy, carbohydrate, protein, fat, MUFA,
435 PUFA or SFA). Our findings may be influenced by the majority of our population carrying at
436 least one A allele (81%). To our knowledge, only Graham *et al.*, (2021) and our study assess
437 rs1761667 genotype and dietary intake on a solely Caucasian healthy cohort. Similarly, Pepino
438 *et al.*, (2012) reported no association between genotype and diet, using a mixture of Caucasian
439 and African American (n = 21) participants. Others have reported that the rs1761667 A allele
440 is associated with a higher dietary fat intake. For example, Ramos-Lopez *et al.*, (2016) reported
441 that in participants with chronic hepatitis C the AA genotype is associated with a higher total
442 fat intake (%TEI) and higher SFA (%TEI) ($p < 0.05$), using a 3-day dietary food record. No
443 differences between MUFA and PUFA were found. Similarly, Fujii *et al.*, (2019), using
444 Japanese (n = 495) participants demonstrated the AA genotype was significantly associated
445 with higher total fat, SFA, MUFA, PUFA, omega-3 and -6 intake ($p < 0.05$), using a short FFQ.
446 In contrast to this, and contradicting mechanisms associated to the A allele causing a reduced
447 protein expression (Melis *et al.*, 2017), Pioltine *et al.*, (2016) reported the A allele was
448 associated with a decreased intake of total fat (g/day), PUFA and MUFA (% kcal and g/day),
449 fatty foods (portion and g/day), and vegetable oils (mL/day) in Brazilian children and
450 adolescents with obesity, using two 24-hour dietary recalls. It is evident that research regarding
451 dietary intake and rs1761667 genotype is highly heterogeneous, preventing any clear
452 conclusion from being drawn. This warrants further research in an ethnically homogenous,
453 healthy cohort of adults or children, similar to our own, with consistent dietary collection
454 methods.

455

456 **4.3 Potential interactions between fat and bitter taste**

457 In our study population bitter and FTS were not correlated. Also, we found neither an
458 association between *TAS2R38* diplotypes and FTS nor *CD36* rs1761667 and bitter taste
459 sensitivity. Our findings contradict other research, reporting an association between the two
460 tastes (Melis *et al.*, 2015; Sollai *et al.*, 2019). Melis *et al.*, (2015), using 64 Italian participants,
461 displayed that perception of fatty acids was associated with rs1761667 *CD36* and that AVI/AVI
462 participants exhibited a 5-fold higher oleic acid threshold than their PAV/PAV counterparts.
463 Later, Sollai *et al.*, (2019), reported similar results but using electrophysiological recordings

464 from the tongue in response to oleic acid in a sample of 35 Italian adults. Similar results have
465 been reported by Karmous *et al.*, (2018), who also displayed a correlation between fat and bitter
466 taste, however in a non-Caucasian (Tunisian) population and by Melis *et al.*, (2020) in patients
467 with inflammatory bowel disease. The fact we did not observe similar associations may be
468 attributed to our study population being UK based and having different allele and haplotype
469 frequencies compared to populations such as Tunisians explored by Karmous *et al.*, (2018).
470 Furthermore, differences in methods of taste sensitivity measurement between studies may also
471 explain discrepancies in results.

472 None of the aforementioned studies explored the dietary intake of participants. In this
473 sense, we observed an association between genetic predisposition to bitter taste, bitter taste
474 sensitivity and dietary fat intake, where non-tasters have a higher intake of SFA than tasters.
475 Although we did not observe an interaction between bitter and fat taste categories on dietary
476 fat intake, we observed a higher intake of SFA in participants carrying both non-taster *CD36*
477 allele (A) and *TAS2R38* haplotype (AVI) compared to those carrying either taster *CD36*
478 genotype (GG) or *TAS2R38* haplotype (PAV/PAV and PAV/AAV). This may suggest that
479 genetic predisposition to hyposensitivity to both fat and bitter taste leads to an increased dietary
480 fat intake, and supports previously observed interactions between the two tastes (Karmous *et*
481 *al.*, 2018; Melis *et al.*, 2015, 2020; Sollai *et al.*, 2019). It may also corroborate proposed
482 mechanisms whereby *TAS2R38* may be involved in the textural perception of fat, whereas
483 *CD36* may determine the chemosensory detection of fat (Keller, 2012). Considering that higher
484 SFA intake was also observed in carriers of *TAS2R38* haplotype (AVI) compared to those
485 carrying PAV/PAV or PAV/AAV diplotypes it may be that *TAS2R38* is driving these
486 differences. Due to the small sample in our study, we were not able to determine exact
487 contribution of *TAS2R38* diplotypes and *CD36* rs1761667 in explaining SFA using regression
488 analysis. These results should therefore be considered hypothesis generating and replicated in
489 a larger cohort.

490

491 **4.4 Strengths and limitations**

492 Besides the fact we comprehensively investigated the associations between genetics, taste
493 and diet, a strength of this study is an ethnically homogenous population enabling a more valid
494 interpretation of genetic association results. However, our population was not homogenous
495 regarding sex, Barragán *et al.*, (2018) reported that sex differences exist in ability to taste.
496 There were no differences between sexes found in any of the variables tested however future
497 research should endeavour to recruit a sex specific cohort or have a sample large enough for

498 sex-specific analyses. Our sample size, although in line with other published research
499 (Karmous et al., 2018; Melis et al., 2015, 2020; Sollai et al., 2019), was low regarding subgroup
500 analysis (Grimaldi *et al.*, 2017). This limits the conclusions that can be drawn and results
501 should be replicated in a larger sample size study.

502 Moreover, in future studies repeated testing of FTS should be considered. Although some
503 have demonstrated FTS is reproducible (Newman & Keast, 2013), others have demonstrated
504 improvement, specifically within the hypersensitive tasters, over time (Tucker & Mattes,
505 2013).

506 Furthermore, the use of PTC filter strips may result in misclassification of participants into
507 bitter tasters and non-tasters (Lawless, 1980). However, more recently, the use of PROP or
508 PTC paper strip has been shown as a valid method to explore genetic predisposition to PTC
509 taste sensitivity (Khataan et al., 2010) and we have used these ratings as a continuous variable
510 in the majority of our analyses. Furthermore, the gLMS may also be more reliable when
511 repeated on multiple occasions (Hayes et al., 2008) and this should be considered in future
512 research. Nevertheless, participants were instructed on the use of the scale, which has been
513 employed in similar studies exploring genetics and bitter taste sensitivity (Yang et al., 2020).

514 The present study explored the associations between PTC taste sensitivity as a proxy for
515 bitter taste sensitivity and *TAS2R38* receptor as its determinant. PTC is however, only one of
516 the many bitter tasting compounds and may not be a predictor of general bitter taste sensitivity.
517 There are number of TAS2R bitter taste receptors that are activated by different bitter tasting
518 compounds such as caffeine, quinin and saccharin requiring further investigation to gain a more
519 comprehensive understanding of bitter taste variability and its effects on dietary intake (Roura
520 et al., 2015).

521 Lastly, self-reported dietary intake data, collected via validated FFQ, may be prone to
522 misreporting (Shim, Oh and Kim, 2014). However, to improve accuracy, we selected a
523 population specific FFQ (UK) and expressed macronutrients as % TEI which may improve
524 accuracy of comparisons made (Macdiarmid and Blundell, 1998). Also, although the FFQ used
525 is a validated method to collect dietary consumption over the previous 12 months and has been
526 calibrated using a 24-hour dietary recall, dietary intake may vary over time and FTS has been
527 shown to alter after only weeks of dietary modification (Costanzo et al., 2019; Newman et al.,
528 2016). Therefore, future studies should consider the use of multiple 24-hour dietary recalls to
529 collect dietary intake information.

530
531

532 **5 Conclusion**

533 Overall, we confirmed that *TAS2R38* haplotypes determine bitter taste sensitivity and
534 *CD36* rs1761667 is associated with fat taste sensitivity. Lower sensitivity to bitter taste may
535 also lead to a higher dietary intake of fat. Considering the lack of association between bitter
536 taste sensitivity and SFA when excluding participants carrying *TAS2R38* non-taster AVI/AVI
537 diplotype, this appears to be mainly driven by genetic predisposition. Although we did not
538 observe an interaction between bitter and fat taste categories on dietary fat intake, we observed
539 a higher intake of SFA in participants carrying both non-taster *CD36* allele (A) and *TAS2R38*
540 haplotype (AVI) compared to those carrying either taster *CD36* genotype (GG) or *TAS2R38*
541 diplotype (PAV/PAV and PAV/AAV). This may suggest that genetic predisposition to
542 hyposensitivity to both fat and bitter taste leads to an increased dietary fat intake. Nevertheless,
543 it warrants further research in a larger cohort employing repeated measurements of bitter and
544 FTS and a combination of dietary consumption methods such as FFQ and 24-hour recalls.
545

Acknowledgements

We are grateful to the EPIC-Norfolk Study team for the use of the EPICFFQ software. EPIC-Norfolk is supported by programme grants from the Medical Research Council UK (G9502233, G0300128) and Cancer Research UK (C865/A2883).

Declaration of Interest

Yiannis Mavrommatis is a shareholder for Nell Health, a lifestyle genotyping company. Leta Pilic is serving on advisory board of DNAfuel LTD.

Funding Sources

The authors did not receive external funding for the research.

Author Contributions

546 **Catherine Anna-Marie Graham and Leta Pilic:** Conceptualization, Methodology,
547 Validation, Formal analysis, Investigation, Data curation, Writing – original draft,
548 Visualisation **Ella Mcgrigor:** Investigation, Data Curation **Megan Brown:** Investigation,
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553 Writing – Review and Editing **Yiannis Mavrommatis**: Conceptualization, Methodology,
554 Validation, Writing – Review and Editing, Supervision.
555 All authors have approved the final article.

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557

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814 **Tables****Table 1.** Participant characteristics (n = 88, n = 69). Data presented as mean ± SEM, median (IQR) or absolute (relative) frequencies

	All participants (n = 88)	Fat-tasters only* (n = 69)
Age (years)	35 ± 1	34.7 ± 1.7
BMI (kg/m²)	24.9 ± 0.5	25.0 ± 0.6
18.5-24.9 kg/m ² n (%)	49 (56)	41 (59)
≥25.0 kg/m ² n (%)	39 (44)	28 (41)
Sex n (%)		
Female	49 (56)	40 (58)
Male	39 (44)	29 (42)
Bitter taste intensity rating m (IQR)	6 (18.5)	8 (27.5)
Fat taste category n (%)		
Hyposensitive	42 (48)	42 (48)
Hypersensitive	27 (31)	27 (31)
Non-taster	19 (21)	-
Energy (kcal)	1656 ± 79	1709 ± 94
Carbohydrate (%TEI)	43.6 ± 0.8	44.4 ± 0.9
Protein (%TEI)	19.3 ± 0.3	19.2 ± 0.4
Total fat (%TEI)	37.5 ± 0.6	37.2 ± 0.7
MUFA (%TEI)	14.1 ± 0.3	14.1 ± 0.4
PUFA (%TEI)	6.6 ± 0.2	6.7 ± 0.3
SFA (%TEI)	13.3 ± 0.2	13.1 ± 0.3

815 *Body mass index (BMI), Interquartile range (IQR), Median (m), Monounsaturated fatty acids (MUFA),*
816 *Polyunsaturated fatty acids (PUFA), Saturated fatty acids (SFA), Total energy intake (TEI). **
817 *Participants with a defined fat taste threshold.*

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Table 2. Energy and macronutrient intakes according to *TAS2R38* diplotypes (n = 88). Data presented as mean ± SEM (One-way ANOVA)

	PAV/PAV (n = 13)	AVI/PAV (n = 41)	AVI/AVI (n = 24)	PAV/AAV (n = 3)	AVI/AAV (n = 7)	p-value
Energy (kcal)	1794 ± 224	1683 ± 137	1512 ± 89	1458 ± 100	1814 ± 289	0.666
Protein (%TEI)	20.4 ± 0.7	19.2 ± 0.6	19.0 ± 0.7	20.7 ± 2	18.9 ± 1.8	0.735
CHO (%TEI)	45.1 ± 1.5	43.2 ± 1.3	42.3 ± 1.6	48.3 ± 4.5	44.9 ± 2.9	0.631
Total fat (%TEI)	35.2 ± 1.4	37.9 ± 1.1	38.4 ± 1.3	34.0 ± 4.2	37.4 ± 1.3	0.493
SFA (%TEI)	12.5 ± 0.7	13.5 ± 0.4	14.2 ± 0.6	10.0 ± 0.6	12.9 ± 0.6	0.082
MUFA (%TEI)	13.2 ± 0.6	14.4 ± 0.5	14.4 ± 0.6	14.0 ± 2.5	14.4 ± 0.5	0.613
PUFA (%TEI)	6.2 ± 0.3	6.8 ± 0.4	6.6 ± 0.3	6.7 ± 0.7	6.6 ± 0.5	0.928

821 *Carbohydrate (CHO), Monounsaturated fatty acids (MUFA), Polyunsaturated fatty acids (PUFA),*
 822 *Saturated fatty acids (SFA), Taste 2 receptor member 38 (TAS2R38), Total energy intake (TEI).*
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Table 3. Energy and macronutrient intakes according to *CD36* rs1761667 (n=69). Data presented as mean ± SEM. Kruskal-Wallis, Independent T-test or Man Whitney U test where appropriate.

	AA (n = 29)	AG (n = 29)	GG (n = 11)	AA/AG (n = 58)	p-value¹	p-value²
Energy (kcal)	1803 ± 152	1631 ± 156	1670 ± 150	1717 ± 109	0.416	0.611
Protein (%TEI)	19.1 ± 0.6	19.3 ± 0.7	19.1 ± 0.9	19.2 ± 2.2	0.952	0.786
CHO (%TEI)	44.7 ± 1.4	43.9 ± 1.3	45.2 ± 2.2	44.3 ± 0.9	0.846	0.703
Total fat (%TEI)	36.9 ± 1.3	37.9 ± 1.0	36.0 ± 1.7	37.4 ± 1.7	0.453	0.458
SFA (%TEI)	12.5 ± 0.5	13.8 ± 0.4	12.9 ± 1.0	13.2 ± 0.3	0.156	0.762
MUFA (%TEI)	14.2 ± 0.5	14.2 ± 0.6	13.7 ± 0.7	14.2 ± 0.3	0.869	0.811
PUFA (%TEI)	7.0 ± 0.5	6.5 ± 0.5	6.0 ± 0.3	6.8 ± 0.3	0.514	0.312

Cluster of differentiation 36 (CD36), Carbohydrate (CHO), Monounsaturated fatty acids (MUFA), Polyunsaturated fatty acids (PUFA), Saturated fatty acids (SFA), Total energy intake (TEI), p-value¹ difference in diet between three genotypes (AA, AG, GG), p-value² difference in diet between two genotypes (AA/AG and GG).

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Supplementary Table 1. Genotype/Diplotype Frequency of Fat Non-Tasters (n = 19)

CD36 rs1761667, n (%)	
AA	6 (32)
AG	8 (42)
GG	5 (26)
TAS2R38 Diplotype, n (%)	
PAV/PAV	0 (0)
AVI/PAV	7 (37)
AVI/AVI	10 (53)
PAV/AAV	0 (0)
AVI/AAV	2 (10)

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832 **Supplementary Table 2.** Dietary fat intake and BMI according to *CD36/TAS2R38* combined
833 genotypes/diplotypes (n = 88). Data presented as mean ± SEM. Independent T-test or Man Whitney U
834 test where appropriate.

	Non-taster (n = 58)	Taster (n = 30)	p-value
BMI (kg/m²)	24.7 ± 0.6	25.4 ± 0.9	0.747
Total fat (%TEI)	38.3 ± 0.9	35.9 ± 0.9	0.085
SFA (%TEI)	13.8 ± 0.3	12.6 ± 0.5	0.047
MUFA (%TEI)	14.5 ± 0.4	13.6 ± 0.4	0.290
PUFA (%TEI)	6.8 ± 0.3	6.3 ± 0.2	0.766

835 *Body mass index (BMI), Cluster of differentiation 36 (CD36), Monounsaturated fatty acids (MUFA),*
836 *Polyunsaturated fatty acids (PUFA), Saturated fatty acids (SFA), Taste 2 receptor member 38*
837 *(TAS2R38), Total energy intake (TEI). Non-taster: (AA/AG + AVI/AVI, AVI/PAV, AVI/AAV); Taster:*
838 *(carriers of either GG or PAV/PAV, PAV/AAV).*

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853 **Supplementary Table 3.** Fat taste threshold (mM) according to *CD36* genotypes and
 854 *TAS2R38* diplotypes (n = 69). Data presented as median (IQR), Kruskal-Wallis H test with
 855 Bonferroni adjustment for multiple comparisons*.

	Fat taste threshold (mM)	p-value
<i>CD36</i> genotypes		
GG (n = 11)	2.0 (4.0)	0.019*
AG (n = 29)	5.0 (6.0)	
AA (n = 29)	5.0 (5.4)	
AA/AG (n= 58)	5.0 (6.0)	
<i>TAS2R38</i> diplotypes		
PAV/PAV (n = 13)	5.0 (3.5)	0.732
AVI/PAV (n = 31)	3.8 (7.0)	
AVI/AVI (n = 17)	5.0 (7.4)	
PAV/AAV (n = 3)	6.4 (0.0)	
AVI/AAV (n = 5)	5.0 (11.3)	

856 * *GG* vs *AG* ($p = 0.23$), *GG* vs *AA* ($p = 0.594$), *AA* vs *AG* ($p = 0.190$). Interquartile range (IQR).
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860 **Figure legends**

861 **Figure 1.** Genetics and taste sensitivity

862 (A) *TAS2R38* diplotypes and bitter taste sensitivity; total n = 88, PAV/PAV = 13, AVI/PAV =
 863 41, AVI/AVI = 24, PAV/AAV = 3, AVI/AAV = 7, a: different than PAV/PAV (AVI/AVI, $p =$
 864 1×10^{-6} ; AVI/AAV, $p = 0.029$), b: different than AVI/AVI ($p = 0.002$). Line represents the median
 865 and whiskers min and max values, Kruskal-Wallis H test with Bonferroni adjusted p values.

866 (B) *CD36* rs1761667 and fat taste sensitivity, total n = 69, AA = 29, AG = 29, GG = 11, * $p =$
 867 0.008 , Fischer's Exact test.

868 Cluster of differentiation 36 (*CD36*), Taste 2 receptor member 38 (*TAS2R38*).
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870 **Figure 2.** The correlations between bitter taste sensitivity (PTC intensity rating) and dietary fat
 871 intake (n = 88); Phenylthiocarbamide (PTC), total energy intake (TEI). Spearman's
 872 correlation.

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874 **Figure 3.** The correlations between fat taste threshold and dietary fat intake (n = 69). Oleic
 875 acid concentrations/fat taste threshold was: 0.02, 0.06, 1, 1.4, 2, 2.8, 3.8, 5, 6.4, 8, 9.8, 12 and
 876 20 mM. Total energy intake (TEI). Spearman's correlation.
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878 **Figure 4.** Difference in dietary fat intake according to bitter taster status in A) fat
 879 hypersensitive taster (total n = 27, bitter taster = 9, bitter non-taster = 18) and B) fat
 880 hyposensitive taster group (total n = 40, bitter taster = 14, bitter non-taster = 26).
 881 Error bars represent \pm SEM.

882

883 **Supplementary Figure 1.** *CD36* rs1761667 and fat taste sensitivity; total n = 88, AA =
 884 35, AG = 37, GG = 16, Fischer's Exact test, $p = 0.033$ (no longer significant after
 885 Bonferroni correction applied). Cluster of differentiation 36 (*CD36*).
 886