- 1 Plasma concentrations of advanced glycation end-products and colorectal cancer risk in the
- 2 EPIC study
- 3 Short title: AGEs and colorectal cancer
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- 5 Elom K. Aglago<sup>1</sup>, Casper G. Schalkwijk<sup>2</sup>, Heinz Freisling<sup>1</sup>, Veronika Fedirko<sup>3</sup>, David J. Hughes<sup>4</sup>, Li
- 6 Jiao<sup>5</sup>, Christina C Dahm<sup>6</sup>, Anja Olsen<sup>6,7</sup>, Anne Tjønneland<sup>7,8</sup>, Verena Katzke<sup>9</sup>, Theron Johnson<sup>9</sup>,
- 7 Matthias B. Schulze<sup>10,11</sup>, Krasimira Aleksandrova<sup>11,12</sup>, Giovanna Masala<sup>13</sup>, Sabina Sieri<sup>14</sup>, Vittorio
- 8 Simeon<sup>15</sup>, Rosario Tumino<sup>16</sup>, Alessandra Macciotta<sup>17</sup>, Bas Bueno-de-Mesquita<sup>18</sup>, Guri Skeie<sup>19</sup>, Inger
- 9 Torhild Gram<sup>19</sup>, Torkjel Sandanger<sup>19</sup>, Paula Jakszyn<sup>20,21</sup>, Maria-Jose Sánchez<sup>22, 23, 24, 25</sup>, Pilar
- 10 Amiano<sup>25,26</sup>, Sandra M. Colorado-Yohar<sup>25,27,28</sup>, Aurelio Barricarte Gurrea<sup>25, 29, 30</sup>, Aurora Perez-
- 11 Cornago<sup>31</sup>, Ana-Lucia Mayén<sup>1</sup>, Elisabete Weiderpass<sup>32</sup>, Marc J. Gunter<sup>1</sup>, Alicia K. Heath<sup>33</sup>, Mazda
- 12 Jenab<sup>1</sup>
- 13
- 14 <sup>1</sup>Nutrition and Metabolism Section, International Agency for Research on Cancer, Lyon, France
- <sup>2</sup>Department of Internal Medicine, CARIM School for Cardiovascular Diseases, Maastricht
   University Medical Center, The Netherlands
- <sup>3</sup>Department of Epidemiology, Rollins School of Public Health, Emory University, Atlanta, GA, USA
- 18 <sup>4</sup>Cancer Biology and Therapeutics Group (CBT), Conway Institute, School of Biomolecular and
- 19 Biomedical Science (SBBS), University College Dublin, Ireland
- 20 <sup>5</sup>Department of Medicine, Baylor College of Medicine, Houston, TX, USA
- 21 <sup>6</sup>Department of Public Health, Aarhus University, Denmark
- 22 <sup>7</sup>Danish Cancer Society Research Center, Denmark
- 23 <sup>8</sup>Department of Public Health, University of Copenhagen, Denmark
- <sup>9</sup>Division of Cancer Epidemiology, German Cancer research Center (DKFZ), Heidelberg, Germany
- 25 <sup>10</sup>Department of Molecular Epidemiology, German Institute of Human Nutrition Potsdam-
- 26 Rehbruecke, Nuthetal, Germany
- 27 <sup>11</sup>Institute of Nutrition Science, University of Potsdam, Nuthetal, Germany
- 28 <sup>12</sup>Nutrition, Immunity and Metabolism Department of Nutrition and Gerontology, German Institute of
- 29 Human Nutrition Potsdam-Rehbruecke (DIfE), Nuthetal, Germany
- 30 <sup>13</sup>Cancer Risk Factors and Life-Style Epidemiology Unit, Institute for Cancer Research, Prevention
- 31 and Clinical Network -ISPRO, Florence, Italy
- 32 <sup>14</sup>Epidemiology and Prevention Unit, Fondazione IRCCS Istituto Nazionale dei Tumori di Milano,
- 33 Milano, Italy
- <sup>15</sup>Dipartimento di Salute Mentale e Fisica e Medicina Preventiva, University 'Luigi Vanvitelli',
  Napoli, Italy
- <sup>16</sup>Cancer Registry and Histopathology Department, Provincial Health Authority (ASP 7), Ragusa,
- 37 Italy

- 38 <sup>17</sup>Department of Clinical and Biological Sciences, University of Turin, Italy
- <sup>18</sup>Former senior scientist, Dept. for Determinants of Chronic Diseases (DCD), National Institute for
- 40 Public Health and the Environment (RIVM), PO Box 1, 3720 BA Bilthoven, The Netherlands
- 41 <sup>19</sup>Faculty of Health Sciences, Department of Community Medicine, University of Tromsø, The Arctic
- 42 University of Norway
- 43 <sup>20</sup>Unit of Nutrition and Cancer, Cancer Epidemiology Research Programme, Catalan Institute of
- 44 Oncology, Barcelona, Spain
- 45 <sup>21</sup>Blanquerna School of Health Sciences, Ramon Llull University, Barcelona, Spain
- 46 <sup>22</sup> Escuela Andaluza de Salud Pública (EASP), Granada, Spain
- 47 <sup>23</sup>Instituto de Investigación Biosanitaria ibs.Granada, Granada, Spain
- 48 <sup>24</sup>Department of Preventive Medicine and Public Health, University of Granada, Granada, Spain.
- 49 <sup>25</sup>Centro de Investigación Biomédica en Red de Epidemiología y Salud Pública (CIBERESP), Madrid,
- 50 Spain
- 51 <sup>26</sup>Public Health Division of Gipuzkoa, BioDonostia Research Institute, Donostia-San Sebastian, Spain
- <sup>27</sup>Department of Epidemiology, Murcia Regional Health Council, IMIB-Arrixaca, Murcia, Spain.
- <sup>28</sup>Research Group on Demography and Health, National Faculty of Public Health, University of
- 54 Antioquia, Medellín, Colombia
- 55 <sup>29</sup>Navarra Public Health Institute, Pamplona, Spain.
- <sup>30</sup>Navarra Institute for Health Research (IdiSNA) Pamplona, Spain.
- <sup>31</sup>Cancer Epidemiology Unit, Nuffield Department of Population Health, University of Oxford, UK
- <sup>32</sup>Office of the Director, International Agency for Research on Cancer (IARC), Lyon, France
- <sup>33</sup>Department of Epidemiology and Biostatistics, School of Public Health, Imperial College London,
- 60

UK

- 61
- \* To whom correspondence should be addressed.: Mazda Jenab, Address: 150 Cours Albert
  Thomas, 69372 Lyon Cedex 08, Email: jenabm@iarc.fr, Tel: +33 472 73 80 82
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- 66 Data sharing statement: For information on how to submit an application for gaining access to EPIC
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- 68 Disclaimer: Where authors are identified as personnel of the International Agency for Research on
- 69 Cancer / World Health Organization, the authors alone are responsible for the views expressed in this
- 70 article and they do not necessarily represent the decisions, policy or views of the International Agency
- 71 for Research on Cancer / World Health Organization.
- Abbreviations used: AGE, Advanced glycation end-product; BMI, body mass index; CEL, N<sup>ε</sup> (carboxyethyl)lysine; CI, confidence interval; CML, N<sup>ε</sup>-(carboxymethyl)lysine; CRC, colorectal
- 74 cancer; EPIC, European Prospective Investigation into Cancer and Nutrition; IARC, International

- 75 Agency for Research on Cancer; ICD, international classification of diseases; MG-H1, Nδ-(5-hydro-
- 76 5-methyl-4-imidazolon-2-yl)-ornithine; RAGE, receptor for AGE; SD, standard deviation; UPLC-
- 77 MS/MS, ultra-performance liquid chromatography tandem mass-spectrometry

#### 79 Abstract

80 Advanced glycation end-products (AGEs) are a heterogeneous group of compounds formed by the non-enzymatic reaction between amino-acids and reducing sugars, or dicarbonyls as intermediate 81 82 compounds. Experimental studies suggest that AGEs may promote colorectal cancer, but prospective 83 epidemiologic studies are inconclusive. We conducted a case-control study nested within a large European cohort. Plasma concentrations of three protein-bound AGEs: N<sup>ε</sup>-(carboxy-methyl)lysine 84 (CML), N<sup> $\varepsilon$ </sup>-(carboxy-ethyl)lysine (CEL) and N<sup> $\delta$ </sup>-(5-hydro-5-methyl-4-imidazolon-2-yl)-ornithine 85 86 (MG-H1) were measured by ultra-performance liquid chromatography tandem mass-spectrometry in 87 baseline samples collected from 1,378 incident primary colorectal cancer cases and 1,378 matched 88 controls. Multivariable-adjusted odds ratios (ORs) and 95% confidence intervals (CIs) were computed 89 using conditional logistic regression for colorectal cancer risk associated with CML, CEL, MG-H1, 90 total AGEs, and [CEL+MG-H1: CML] and [CEL:MG-H1] ratios. Inverse colorectal cancer risk 91 associations were observed for CML (OR comparing highest to lowest quintile, OR<sub>O5vs.01</sub>=0.40, 92 95%CI:0.27-0.59), MG-H1 (OR<sub>Q5vs.Q1</sub>=0.73, 95%CI:0.53 - 1.00) and total AGEs (OR <sub>Q5vs.Q1</sub>=0.52, 93 95%CI:0.37 - 0.73) whereas no association was observed for CEL. A higher [CEL+MG-H1: CML] 94 ratio was associated with colorectal cancer risk (OR<sub>Q5vs.Q1</sub>=1.91, 95%CI:1.31-2.79). The associations 95 observed did not differ by sex, or by tumour anatomical subsite. Although individual AGEs concentrations appear to be inversely associated with colorectal cancer risk, a higher ratio of 96 97 methylglyoxal-derived AGEs versus those derived from glyoxal (calculated by [CEL+MG-H1: CML] ratio) showed a strong positive risk association. Further insight on the metabolism of AGEs and their 98 dicarbonyls precursors, and their roles in colorectal cancer development is needed. 99

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101 Summary: We evaluated colorectal cancer risk associated with blood levels of major advanced 102 glycation end-products (AGEs). The AGEs examined were mostly associated with lower colorectal 103 cancer risk. The ratio of methylglyoxal-derived versus glyoxal-derived AGEs was positively 104 associated with colorectal cancer.

105

#### 107 Introduction

108 Colorectal cancer (CRC) is the third most common incident cancer and the second leading cause of cancer death globally (1). A substantial body of epidemiologic evidence, particularly from large-scale 109 prospective cohort studies, apportions a considerable contribution of modifiable dietary and lifestyle 110 111 risk factors to CRC development (2-4). Western-type diets tend to promote the formation of 112 Advanced Glycation End-products (AGEs), a heterogeneous class of pro-inflammatory and pro-113 oxidative compounds formed irreversibly by the non-enzymatic combination of amino acids and 114 reducing sugars (5-8). AGEs can also be formed when proteins are glycated by highly reactive 115 dicarbonyls such as glyoxal (GO) and methylglyoxal (MGO) absorbed from the diet, and/or smoking 116 or produced as sugar and lipid metabolism by-products (8,9). GO and MGO have been reported to be 117 over 20,000 times more potent in glycating amino acids, compared to sugars (10,11). As a consequence, most abundant AGEs in the body are derived from GO (N<sup>ε</sup>-(carboxymethyl)lysine; 118 CML) or MGO (N<sup>ε</sup>-(carboxyethyllysine), CEL; and N<sup>δ</sup>-(5-hydro-5-methyl-4-imidazolon-2-yl)-119 120 ornithine, MG-H1) (12-14).

AGEs are thought to affect CRC development by promoting a pro-inflammatory and 121 oxidative environment, primarily via binding to the receptor for AGEs (RAGE), a transmembrane 122 123 protein that belongs to the immunoglobulin superfamily (15). Immunohistochemical expression of AGEs is higher in colon cancer tumours compared to adjacent normal tissues and AGEs have been 124 shown to enhance and promote colon cancer growth in *in vitro* models (16-18). Animal studies show 125 that AGEs can induce sustained inflammation in the colon and promote colon cancer development 126 (19,20). However, two case-control studies nested within prospective studies have reported 127 inconclusive findings for the association between circulating AGEs levels and CRC. In the Women's 128 Health Initiative (WHI) study, Chen et al. (21) found an inverse association between serum CML and 129 CRC in women (Odds ratio (OR)= 0.85, 95%CI:0.49-1.47) while Jiao et al. (22) reported a positive 130 association between circulating CML and CRC risk in male smokers (OR=1.20, 95% confidence 131 interval CI=0.64-2.26) in the Alpha-Tocopherol, Beta-Carotene Cancer Prevention (ATBC) study. 132 These previous investigations focused on CML only, did not include other major AGEs or assess 133

possible differences by sex or tumour anatomical subsite. Furthermore, they detected AGEs by ELISA
kits, which have low specificity and reproducibility (23).

The aim of the present study was to examine the associations between pre-diagnostic protein-136 bound circulating levels of CML, CEL, and MG-H1 measured using ultra-performance liquid 137 138 chromatography tandem mass spectrometry (UPLC-MS/MS) and CRC risk in the European 139 Prospective Investigation into Cancer and Nutrition (EPIC) cohort. The rationale for the selection of 140 these three AGEs is threefold: they are considered as the most abundant in the body, they have very 141 well characterized chemical structures, and they are derived from specific pathways of formation with 142 CML being mainly derived from GO whereas CEL and MG-H1 are mainly derived from MGO. For 143 CML and CEL, lysine is the amino-acid of the glycation site, whereas it is arginine for MG-H1. At the 144 cellular level, the MGO-lysine adduct CEL is predominantly formed in the cytosol through the glycation of cytosol proteins whereas the MGO-arginine adduct MG-H1 is equally found in cytosol, 145 histone, and mitochondria proteins (24). We hypothesised that protein-bound concentrations of these 146 AGEs would be associated with a higher CRC risk. We also examined CRC risk associated with the 147 148 ratios of AGEs from specific dicarbonyls similar to the [CEL:MG-H1] ratio assessed in previous 149 studies (25,26), as a potential index of the chemical origin of the AGEs. Although MGO glycates 150 amino acids to CEL and MG-H1, both these MGO-derived AGEs have different promoting factors as they are produced from lysine and arginine, respectively. Thus, we applied the ratio of [CEL:MG-H1] 151 as a proxy of the potential differential glycating activities of MGO in the body. 152

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# 154 Materials and methods

155 Study population and data collection

We conducted a nested case-control study within the European Prospective Investigation into Cancer and Nutrition (EPIC) cohort, an ongoing multicentre prospective study with participants recruited from 23 centres constellated in 10 European countries (Denmark, France, Germany, Greece, Italy, the Netherlands, Norway, Spain, Sweden, and the United Kingdom) (27). A total of 521,324 participants were recruited into EPIC between 1992 and 2000. Detailed data on lifestyle, dietary and sociodemographic factors were collected at baseline from all the participants. Body weight and standing 162 height were measured by trained health professionals using standardized protocols. Lifestyle variables such as smoking, physical activity, and the level of education were collected using a validated, 163 164 standardized questionnaire. Information on the highest attained educational level was categorized as 165 none, primary, technical and professional, secondary, or higher (college or university). Smoking was 166 collected as status (current, past, never), by type of products (cigarettes, cigars, pipe), intensity 167 (number of cigarettes), and duration (in years of smoking). Information on past smoking habits and 168 the years since quitting smoking was collected in former smokers. Physical activity was defined 169 according to the Cambridge physical activity definitions: inactive (sedentary job plus no recreational 170 activity), moderately inactive (sedentary job with < 0.5 h recreational activity daily/or standing job 171 with no recreational activity), moderately active (sedentary job with 0.5 to 1 h recreational activity 172 daily/ or standing job with 0.5 h recreational activity daily/ or physical job with no recreational activity) or active (sedentary job with >1 h recreational activity daily/or standing job with >0.5 h 173 174 recreational activity daily/or physical job with at least some recreational activity/or heavy manual job) (28). Blood samples were collected and are stored in liquid nitrogen  $(-196^{\circ}C)$  in biobank facilities 175 176 located at the International Agency for Research on Cancer (IARC), or in local biobanks in Denmark (-150°C) and Sweden (-80°C at Malmö and Umeå) until analysis. Informed consent was obtained 177 178 from all the participants. The EPIC study was approved by the IARC Ethical Committee and the local ethics committees pertaining to each participating centre. 179

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181 Follow-up for CRC incidence and vital status

Vital status (98.4% complete) was ascertained on a regular basis using record linkage with centralised 182 183 regional cancer registries (Denmark, Italy, the Netherlands, Norway, Spain, Sweden, and UK) or via a combination of methods including use of health insurance records, connection with cancer and 184 pathology registries, and active follow-up through participants and their close relatives (France, 185 Germany, and Greece). Incident CRC cases were ascertained according to the classification by the 186 International Classification of Diseases for Oncology (ICD-O, codes C18-C20). Colon cancer 187 included tumours in the proximal site (C18.0-C18.5: from cecum to splenic flexure) or the distal 188 189 segment (C18.6-C18.7: from descending colon down to sigmoid colon), while rectal cancer included

190 tumours that occurred from the recto-sigmoid junction (C19) down to the rectum (C20). Tumours that 191 arose in the anus and in the anal canal (C21) were not included in this analysis.

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193 Nested case-control design study

194 A total of 1,416 incident CRC cases were identified and matched on 1:1 ratio to controls by incidence 195 density sampling from all cohort members alive and free of cancer at the time of diagnosis of the 196 index case. Cases were selected sequentially in the order of date of diagnosis and based on sufficient 197 biological sample availability. The following matching criteria were applied: age at blood collection 198 ( $\pm 1$  year), sex, recruiting centre, time of the day at blood collection ( $\pm 3$  hours), fasting status at blood 199 collection (<3, 3-6, and >6 hours); and additionally, among women by menopausal status (pre-200 menopause, perimenopause, and post-menopause), and hormone replacement therapy (HRT) use at 201 time of blood collection (yes/no). We excluded subjects within incomplete matched case sets (i.e. a 202 case without a control or vice versa, n=12), and 26 cases and their matched controls from Greece due 203 to unforeseen data restriction issues. Thus, the final data analysis included 1,378 CRC cases and their 204 matched controls.

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206 Laboratory analyses of AGEs

Plasma concentrations of protein-bound AGEs were determined with Ultra Performance Liquid 207 208 Chromatography tandem Mass Spectrometry (UPLC-MS/MS) as previously described (29,30). In brief, protein-bound CML, CEL and MG-H1 were extracted from plasma using butanolic 209 hydrochloric acid. The individual AGEs were quantified by calculating the area ratio of each 210 unlabelled peak area to the corresponding internal standard. The sum of AGEs ( $\Sigma$ AGEs, in nmol/L) 211 was calculated by summing up the circulating concentrations of CML, CEL and MG-H1 for each 212 subject. We further calculated the ratios of the AGEs considering their dicarbonyl intermediates: 213 MGO-derived:GO derived (i.e. CEL+MG-H1 divided by CML) (Figure 1). We also calculated the 214 ratio of [CEL:MG-H1] to assess the influence of the relative abundance of lysine-sourced MGO-215 216 derived AGEs (CEL) vs. arginine-sourced MGO-derived AGEs (MG-H1).

218 Statistical analysis

219 Means, standard deviations or frequencies were calculated for all variables. Multivariable conditional logistic regression was used to estimate ORs and 95% CIs for CRC risk associated with circulating 220 levels of protein-bound CML, CEL, MG-H1,  $\Sigma$ AGEs, as well as [CEL+MG-H1):CML] (i.e MGO:GO 221 222 AGEs), and [CEL:MG-H1]. For each main outcome variable (measured biomarker or calculated 223 ratio), quintile cut-points were determined based on the distribution in controls. We ran two models: 224 model 1 was conditioned on the matching factors; model 2 was further adjusted for body mass index 225 (BMI, continuous), height (continuous), highest attained education level (none, primary, technical and 226 professional, secondary, higher), physical activity (inactive, moderately inactive, moderately active, 227 active), smoking status/duration/intensity (never; current smokers 1-<=15, 16-<=25, >26 cigarettes/day; former smokers <=10, 11-<=20, >20 years, occasional), and baseline intake levels of 228 229 energy (continuous, kcal/day), alcohol, red and processed meats, dietary fibre, and dairy products (all 230 as continuous variables and as g/day). Tests for trend were run by using the median value of each quintile included in the model as continuous variables. Separate sub-group analyses were run by sex 231 232 and anatomical sub-sites of CRC site (colon, rectal). The heterogeneity of the associations by sex, across anatomical sub-sites and in various sub-groups was assessed using the likelihood ratio test. We 233 234 assessed the AGEs-CRC association by sub-groups of type-2 diabetes (yes/no; self-reported at baseline) and obesity (defined as BMI  $\geq$  30 kg/m<sup>2</sup>). The potential bias of reverse causality in the 235 AGEs-CRC association was assessed by excluding cases diagnosed within the first two years. All the 236 analyses were conducted using Stata 14.0 (StataCorp, College Station, TX, USA). Two-sided P-237 values <0.05 were statistically significant. 238

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## 240 Results

Selected baseline characteristics of the study participants are shown in Table 1. Compared to controls,
cases had higher BMI, and higher intakes of alcohol and red and processed meats, and lower intakes
of fruits, vegetables, and dairy products. In addition, cases tended to be less physically active
compared to controls.

The associations of individual and combined AGEs, and their various ratios calculated based 245 on pathway of AGEs derivation are shown in Table 2. No statistically significant association was 246 247 observed between CEL and CRC risk (OR comparing highest to lowest quintile, OR<sub>O5vs.01</sub>=0.88, 248 95%CI:0.64-1.19,  $P_{\text{trend}}=0.580$ ), whereas inverse associations for CRC were observed for both CML 249 (OR<sub>Q5vs.Q1</sub>=0.40, 95%CI:0.27-0.59, P<sub>trend</sub><0.001) and MG-H1 (OR<sub>Q5vs.Q1</sub>=0.73, 95%CI:0.53-1.00,  $P_{\text{trend}}=0.016$ ). A near 50% lower odds for developing CRC was observed for  $\Sigma AGEs$  (OR<sub>O5vs.O1</sub>=0.52, 250 251 95%CI:0.37-0.73,  $P_{\text{trend}} < 0.001$ , mostly driven by CML and MG-H1. The ratio of [(CEL+MG-H1): 252 CML] was associated with an increased risk or CRC (OR<sub>Q5vs.Q1</sub>=1.91, 95%CI:1.31 - 2.79, 253  $P_{\text{trend}} = 0.004$ ).

We did not observe significant heterogeneity by sex or by tumour anatomical subsites for individual AGEs,  $\Sigma$ AGEs, and [CEL+MG-H1):CML] (**Table 3**). Analyses stratified by baseline diabetes status and by obesity as indicated by BMI $\geq$  30 kg/m<sup>2</sup> showed that [(CEL+MG-H1):CML] was associated with higher CRC risk in diabetic vs. non-diabetic subjects, and in obese vs. non-obese subjects (**Table 4**). The inverse associations observed with individual AGEs and for  $\Sigma$ AGEs were more prominent in obese individuals compared to non-obese ones.

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#### 261 Discussion

In this study, we found that higher circulating levels of protein-bound CML, MG-H1 and ΣAGEs, but
not CEL, were associated with a lower risk of CRC. We also observed that higher concentrations of
MGO-derived AGEs relative to GO-derived AGEs were associated with higher CRC risk.

The inverse associations observed between the AGEs concentrations evaluated in our study 265 and CRC risk contrast with our hypothesis that these AGEs contribute to colorectal carcinogenesis. 266 Specifically, for CML it is noteworthy that Jiao et al. (22) also reported similar inverse associations as 267 268 observed in our study. However, their study was based on a sub-population of male, Finnish smokers and applied an ELISA-based methodology to assess relative differences of CML between cancer cases 269 and controls. Unfortunately, ELISA methods have limited reproducibility and do not differentiate 270 between protein-bound and free fractions of circulating AGEs. Our initial hypothesis for positive 271 272 AGEs-CRC risk association was based on evidence from experimental studies indicating that AGEs are DNA-damaging and can directly induce sustained inflammation in colon tissues through binding
with RAGE (17,19,31). We chose to analyze protein-bound AGEs because these are specifically
recognized by RAGE (32-34).

276 We assessed CML, CEL and MG-H1 because they are thought to be the most abundant AGEs 277 in the body and although there is evidence that they have harmful pro-inflammatory and pro-oxidative 278 effects, their relationship with the colonic mucosa may be very complicated. The colonic mucosa may be exposed to a variety of other AGEs, both exogenously from the diet and those produced 279 280 endogenously within the body and colonic milieu. Similar to endogenous AGEs, dietary AGEs may 281 increase the body AGEs pool, interact directly with the colon mucosal and increase the risk for obesity (35). Some researchers have classified AGEs into two categories of "non-toxic" and "toxic" 282 283 (36-38). This categorization still requires much further evidence, but it is noteworthy that we have 284 previously shown an increased risk of rectal cancer with higher circulating levels of glyceraldehyde-285 derived AGEs (39), that have been categorized as "toxic" (6,36). Another speculative explanation of our observations is that circulating AGEs concentration may not be reflective of their levels in 286 287 colorectal tissues where they may accumulate. There is a paucity of supportive data for this assertion, 288 and little is known about whether the concentration and actions of specific AGEs may differ between 289 tissues. Van Heijst et al. (40) observed varying AGEs levels from an immunohistochemical expression of CML and the MGO-derived AGE argpyrimidine in various human tumours (muscle, 290 colon, breast and larynx) suggesting that separate AGEs impact tissues differently. Therefore, relevant 291 studies focusing on the functions, effects, and the interactions of CML, CEL and MG-H1 and 292 additional AGEs within normal and cancerous colonic tissues are warranted. 293

The positive association observed with the ratio of MGO-derived AGEs:GO-derived AGEs and CRC risk suggests that the conditions that may lead to more MGO-AGEs vs. GO-AGEs may be important in CRC development. This result may implicate that higher circulating MGO versus GO may be of greater importance in CRC development than AGEs. Both MGO and GO are mainly detoxified through the glyoxalase (GLO) system and by other enzymes such as aldo-keto reductases and dicarbonyl and L-xylulose reductase (41,42). Compared to GO, MGO is more reactive (43) but is rapidly and efficiently detoxified, mainly in the liver (42). This may possibly explain the higher CRC 301 risk observed with MGO-AGE-GO-AGEs in obese individuals. Obesity is often associated with a degree of liver steatosis and decreased liver function and could possibly explain lower clearance of 302 MGO with spillover into the circulation. It can be speculated that in the presence of a "competition" 303 between the production and the detoxification of dicarbonyls, MGO and its derived AGEs may be 304 305 harmful to the colon tissue, and sustain systemic inflammation, compared to GO and derived AGEs -306 but this requires further investigation. Diabetes has been associated with a higher risk of CRC (44). 307 Because diabetes is associated with poor glycaemic control, hyperglycaemia, and enhanced 308 production of AGEs, one would expect that the AGEs-CRC association is higher in subjects with 309 diabetes compared to those without. Additional studies should explore whether CRC risk associated 310 with diabetes could be partially mediated through AGEs. Likewise, future studies may also explore to 311 which extent treatment for diabetes may mitigate endogenous AGEs production and possibly CRC 312 risk.

313 It is also noteworthy that dicarbonyls and some AGEs derived from them display hormetic properties, where lower levels are associated with beneficial health outcomes while higher levels are 314 315 deleterious. Hormetic effects have been reported for lower levels of MGO which have been showed to 316 prevent tumour growth, whereas higher levels promote tumour expansion (45). Surprisingly, it has 317 been reported that another MGO-derived AGE, MG-H3, has anti-oxidative properties comparable with those of ascorbic acid (46). There is substantial evidence showing that the deleterious effects of 318 AGEs are dependent upon the level of RAGE activity. In RAGE knockout mice, cancer development 319 is greatly reduced, suggesting that the cancer-promotive and pro-inflammatory effects of AGEs are 320 necessarily expressed in the presence of RAGE (47,48). Interestingly, there is mounting evidence 321 showing that soluble RAGE (sRAGE), a free circulating isoform of RAGE, is inversely associated 322 with CRC (21,49). The knowledge of AGEs metabolism and CRC need to be expanded, and 323 324 additional studies are needed to better understand the role of dicarbonyls, and derived AGEs in the aetiology of CRC. 325

This study has several strengths, including the quantitative measurement of CEL, CML and MG-H1 by a state-of-the-art UPLC-MS/MS instrumental method. UPLC-MS/MS could be considered the gold standard method for the analysis of AGEs in plasma. UPLC-MS/MS could be used to 329 accurately and precisely measure specific AGEs in both free and protein-bound forms. The major known drawback of using UPLC-MS/MS is its relatively higher cost and the necessity for trained 330 331 personnel (23,50). Additional strengths include the prospective design, the large sample size, and the ability to conduct analyses stratified by sex, and by anatomical subsite (colon vs rectum). A limitation 332 333 to our study is that we lack information on other AGEs produced from MGO including other MGOderived hydroimidazolone (MG-Hs) such as MG-H2, MG-H3 and MG-H4, Nd-(4-carboxy-4,6-334 335 dimethyl5,6-dihydroxy-1,4,5,6-tetrahydropyrimidin-2-yl)-ornithine (THP), argpyrimidine and 336 crosslinking dimer MOLD (8), which may all have roles in CRC development. Another limitation is 337 the use of plasma AGEs levels which are dependent on kidney and liver functions; hence they may 338 not represent tissue levels. Further research is required to determine how circulating AGEs measures 339 in the same individual may relate to levels in colon tumour and normal colon tissues. Therefore, our 340 assessment of AGEs in CRC development is far from complete, even though we analysed three major 341 AGEs compounds. Also, our findings show that circulating measures of AGEs are likely to have differential associations with CRC, indicating that their posited detrimental properties may not be 342 343 equivalent or that they vary in their pro-inflammatory capacity. More study is required on the 344 individual and interactive roles of AGEs in the development of cancers and other chronic diseases. A 345 deeper assessment of the qualitative pathways of AGEs production and their cumulative roles in cancer development may shed more insight into this fascinating topic. An additional limitation of this 346 347 nested case-control study is the fact that blood samples and lifestyle factors were collected at baseline and may not necessarily reflect changes over time. 348

In conclusion, in this large, comprehensive prospective study CML and MG-H1 are inversely 349 associated with CRC risk, contrary to our initial hypothesis. However, we observed a significantly 350 higher CRC risk with higher ratio of MGO-derived:GO-dervied AGEs. Our observations highlight the 351 complexity of the proposed roles of AGEs in CRC development and suggest that AGEs levels may 352 not be interpreted alone, but in consideration of their chemical origins. Additional studies examining 353 toxic dicarbonyl AGEs precursor compounds in CRC development, and assessing the role of AGEs in 354 355 the colonic milieu and within normal and tumorigenic colonic tissues are required. In addition, the 356 development of laboratory instrumental methodologies for the assessment of a larger number of AGEs

- 357 would aid greatly in better defining the roles of this diverse family of compounds in health and
- 358 disease.

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# 520 FIGURES LEGENDS

- **Figure 1:** Schematic representation of the formation of the AGEs and the rationale for the calculation
- 522 of the ratios
- 523 Abbreviations: AGE, advanced glycation end-product; CML, N $^{\epsilon}$ -carboxy-methyllysine; CEL, N $^{\epsilon}$ -
- 524 carboxy-ethyllysine; GO, glyoxal; MG-H1,  $N^{\delta}$ -(5-hydro-5-methyl-4-imidazolon-2-yl)-ornithine;
- 525 MGO, methylglyoxal
- 526 AGEs are absorbed from the diet or formed during the Maillard reactions from the Amadori or Heyns
- 527 products and from the glycating actions of dicarbonyls such as MGO and GO. CML is derived from
- 528 GO whereas MG-H1 and CEL are derived from MGO.
- 529

530	Table 1: Selected baseline demographic and lifestyle	characteristics	of study participants by
531	colorectal cancer status,		
		Cases	Controls $(n=1.378)$

,	Cases (1.378)	Controls (n=1,378)
Women, %	51.7	51.5
Anthropometry, mean (SD)		
BMI, kg/m <sup>2</sup>	26.7±4.25	26.2±3.74
Waist circumference, cm	90.4±13.0	88.3±12.1
Waist-to-hip ratio	$0.88{\pm}0.10$	$0.87{\pm}0.10$
Lifestyle variables, n (%)		
Smoking status frequency and intensity		
Never	542 (39.8)	514 (37.9)
Current, 1 - 15 cig/day	139 (10.2)	129 (9.51)
Current, 16-25 cig/day	94 (6.91)	87 (6.40)
Current, 26+ cig/day	23 (1.69)	20 (1.47)
Former, quit <= 10 years	129 (9.48)	139 (10.3)
Former, quit 11-20 years	123 (9.04)	144 (10.6)
Former, quit 20+ years	177 (13.0)	166 (12.2)
Current, pipe/cigar/occasional	102 (7.49)	125 (9.22)
Physical activity		
Inactive	361 (25.9)	327 (23.3)
Moderately inactive	448 (32.1)	457 (32.6)
Moderately active	311 (22.3)	284 (20.3)
Active	263 (18.9)	314 (22.4)
Highest education level attained		× /
None	66 (4.85)	68 (5.01)
Primary school completed	490 (36.0)	453 (33.4)
Technical/professional school	343 (25.2)	324 (23.9)
Secondary school	184 (13.5)	217 (16.0)
Higher education	244 (17.9)	247 (18.2)
Dietary intake, mean (SD)		
Energy, Kcal/day	2127±609	2124±620
Alcohol, g/day	$17.0\pm22.1$	$15.4 \pm 19.7$
Red and processed meats, g/day	87.6±53.1	85.1±52.0
Fruits and vegetables, g/day	396±233	421±248
Cereals, g/day	216±121	216±119
Dairy products, g/day	331±251	351±244
Fish and products, g/day	$28.2 \pm 28.8$	29.6±30.6
Sugar, cakes and confectionaries, g/day	$48.7 \pm 66.6$	$48.7 \pm 68.9$
Fats, g/day	28.3±15.6	27.9±16.0
Protein, g/day	89.3±27.9	90.3±27.5
AGEs Biomarkers, mean (SD)		
CML, nmol/l	2719±1046	2855±107 5
CEL, nmol/l	1475±772	1475±740

MGH1, nmol/l	1056±259	1079±262
ΣAGEs, nmol/l	5250±1488	5411±1470
CEL:MG-H1	$1.45 \pm 0.79$	$1.43 \pm 0.75$
(CEL+MG-H1): CML	$1.01{\pm}0.39$	$0.98 \pm 0.38$

Frequencies may not add up to 100% due to missing data Abbreviations: AGE, Advanced glycation end products; BMI, Body mass index; CML, Nε-carboxymethyl-lysine; CEL, Nε-carboxyethyl-lysine; MG-H1, Nδ-(5-hydro-5-methyl-4-imidazolon-

2-yl) ornithine

	Quintile 1	Quintile 2	Quintile 3	Quintile 4	Quintile 5	$P_{\text{trend}}$
CML						
Range, nmol/L	<2014	2014-<2401	2401-<2805	2805-<3505	≥3505	
Cases/controls	302/276	338/276	280/275	247/276	211/275	
Model 1 <sup>*</sup>	1.00 (Ref.)	0.96 (0.75 - 1.23)	0.74 (0.57 - 0.97)	0.58 (0.44 - 0.78)	0.37 (0.26 - 0.52)	<0.001
Model 2 <sup>†</sup>	1.00 (Ref.)	0.97 (0.75 - 1.26)	0.79 (0.59 - 1.04)	0.63 (0.46 - 0.86)	0.40 (0.27 - 0.59)	<0.001
CEL						
Range, nmol/L	<986	986-<1234	1234-<1478	1478-<1807	≥1807	
Cases/controls	272/276	270/276	286/276	290/275	260/275	
Model 1 <sup>*</sup>	1.00 (Ref.)	0.96 (0.74 - 1.23)	1.02 (0.78 - 1.33)	1.01 (0.76 - 1.33)	0.89 (0.66 - 1.19)	0.605
Model 2 <sup>†</sup>	1.00 (Ref.)	0.98 (0.76 - 1.27)	1.04 (0.79 - 1.37)	1.04 (0.78 - 1.39)	0.88 (0.64 - 1.19)	0.580
MG-H1						
Range, nmol/L	<872	872-<974	974-<1082	1082-<1248	≥1248	
Cases/controls	309/276	308/275	260/276	256/274	244/276	
Model 1 <sup>*</sup>	1.00 (Ref.)	0.94 (0.73 - 1.20)	0.75 (0.58 - 0.97)	0.71 (0.54 - 0.93)	0.68 (0.50 - 0.91)	0.002
Model 2 <sup>†</sup>	1.00 (Ref.)	0.97 (0.75 - 1.25)	0.79 (0.61 - 1.03)	0.77 (0.58 - 1.02)	0.73 (0.53 - 1.00)	0.016
ΣAGEs, nmol/L						
Range, nmol/L	<4284	4284-<4848	4848-<5414	5414-<6306	≥6306	
Cases/controls	334/276	315/276	275/276	219/276	235/274	
Model 1 <sup>*</sup>	1.00 (Ref.)	0.89 (0.70 - 1.14)	0.73 (0.56 - 0.95)	0.52 (0.39 - 0.68)	0.48 (0.35 - 0.65)	<0.001
Model 2 <sup>†</sup>	1.00 (Ref.)	0.93 (0.72 - 1.19)	0.76 (0.58 - 1.00)	0.54 (0.41 - 0.73)	0.52 (0.37 - 0.73)	<0.001
CEL:MG-H1						
Range	< 0.89	0.89-<1.15	1.15-<1.43	1.43-<1.81	≥1.81	
Cases/controls	247/276	274/276	263/275	295/275	298/275	
Model 1 <sup>*</sup>	1.00 (Ref.)	1.09 (0.85 - 1.40)	1.09 (0.83 - 1.42)	1.27 (0.96 - 1.68)	1.33 (0.98 - 1.80)	0.047
Model 2 <sup>†</sup>	1.00 (Ref.)	1.13 (0.87 - 1.47)	1.08 (0.82 - 1.42)	1.27 (0.95 - 1.70)	1.26 (0.91 - 1.73)	0.139
(CEL+MG-H1): CML						
Range	< 0.66	0.66-<0.86	0.86-<1.02	1.02-<1.24	≥1.24	
Cases/controls	233/276	279/276	263/275	280/275	322/275	

 Table 2: ORs and 95%CI for colorectal cancer risk associated with circulating AGEs and their ratios, EPIC study 1992-2012

Model 1 <sup>*</sup>	1.00 (Ref.)	1.49 (1.12 - 1.99)	1.64 (1.19 - 2.27)	1.70 (1.21 - 2.39)	2.14 (1.50 - 3.05)	<0.001
Model 2 <sup>†</sup>	1.00 (Ref.)	1.42 (1.05 - 1.90)	1.54 (1.10 - 2.16)	1.54 (1.08 - 2.19)	1.91 (1.31 - 2.79)	0.004

Abbreviations: AGE, advanced glycation end-product; CI, confidence interval; CML, N<sup> $\epsilon$ </sup>-carboxy-methyllysine; CEL, N<sup> $\epsilon$ </sup>-carboxy-ethyllysine; MG-H1, N<sup> $\delta$ </sup>-(5-hydro-5-methyl-4-imidazolon-2-yl)-ornithine; OR, odds ratio; Quintiles were created based on the distribution in the control group MG-H1 has one missing data, hence MG-H1, CEL:MG-H1 and (CEL+MG-H1): CML have 1,377 cases and 1,377 matched controls \*Model 1 was conditioned on matching factors: age at blood collection (±1 year), sex, recruiting centre, time of the day at blood collection (±3 hours), fasting status at blood collection (<3, 3-6, and >6 hours); and additionally, among women by menopausal status (pre-menopause, perimenopause, and postmenopause), and hormone replacement therapy (HRT) use at time of blood collection (yes/no)

<sup>†</sup>Model 2 model was Model 1 adjusted for BMI (continuous), height (continuous), education (none, primary, technical and professional, secondary, higher education), physical activity (inactive, moderately inactive, moderately active, active), smoking status, duration and intensity (never, 1 - 15 cigarettes/day, 16-25 cigarettes/day, over 26 cigarettes/day, former smokers who quit<10 years, former smokers who quit 11-20 years, former smokers who quit>20 years, current pipe-cigar and occasional smokers), energy intake (continuous), alcohol intake (continuous), processed meat intake (continuous), fibre intake (continuous) and dairy products intake (continuous)

	Colore	ctal cancer	Colo	n cancer	Rect	al cancer	Pheterogeneity by
	Cases/Controls	OR (95% CI)	Cases/Controls	OR (95% CI)	Cases/Controls	OR (95% CI)	subsite
CML, nmol/L							
All	1378/1378	0.75 (0.66 - 0.85)	871/871	0.69 (0.58 - 0.83)	503/503	0.81 (0.66 - 1.00)	0.073
Men	679/679	0.69 (0.57 - 0.83)	404/404	0.66 (0.51 - 0.86)	272/272	0.67 (0.49 - 0.92)	0.162
Women	699/699	0.81 (0.67 - 0.97)	467/467	0.75 (0.59 - 0.96)	231/231	0.90 (0.65 - 1.26)	0.323
$P_{\text{heterogeneity}}$ by sex		0.197		0.223		0.622	
CEL, nmol/L							
All	1378/1378	0.98 (0.88 - 1.08)	871/871	0.98 (0.86 - 1.11)	503/503	1.00 (0.83 - 1.20)	0.986
Men	679/679	1.01 (0.85 - 1.20)	404/404	0.99 (0.77 - 1.25)	272/272	1.10 (0.82 - 1.46)	0.291
Women	699/699	0.97 (0.85 - 1.11)	467/467	1.00 (0.85 - 1.17)	231/231	0.83 (0.61 - 1.12)	0.298
$P_{ m heterogeneity}$ by sex		0.839		0.596		0.129	
MG-H1, nmol/L							
All	1377/1377	0.88 (0.79 - 0.98)	871/871	0.81 (0.71 - 0.93)	503/503	0.99 (0.83 - 1.17)	0.056
Men	678/678	0.83 (0.71 - 0.97)	404/404	0.77 (0.62 - 0.95)	272/272	0.87 (0.68 - 1.13)	0.173
Women	699/699	0.92 (0.80 - 1.07)	467/467	0.87 (0.72 - 1.05)	231/231	1.01 (0.78 - 1.31)	0.346
$P_{\text{heterogeneity}}$ by sex		0.313		0.332		0.701	
ΣAGEs, nmol/L							
All	1377/1377	0.81 (0.72 - 0.91)	871/871	0.76 (0.65 - 0.89)	503/503	0.76 (0.65 - 0.89)	0.144
Men	678/678	0.76 (0.64 - 0.91)	404/404	0.71 (0.55 - 0.91)	272/272	0.81 (0.61 - 1.07)	0.066
Women	699/699	0.85 (0.73 - 1.01)	467/467	0.84 (0.68 - 1.03)	231/231	0.85 (0.62 - 1.15)	0.913
$P_{\text{heterogeneity}}$ by sex		0.233		0.083		0.747	
CEL:MG-H1							
All	1377/1377	1.03 (0.93 - 1.14)	871/871	1.05 (0.93 - 1.19)	503/503	0.99 (0.82 - 1.21)	0.517
Men	678/678	1.10 (0.91 - 1.32)	404/404	1.07 (0.83 - 1.37)	272/272	1.22 (0.87 - 1.70)	0.572
Women	699/699	1.03 (0.90 - 1.17)	467/467	1.08 (0.93 - 1.26)	231/231	0.81 (0.60 - 1.09)	0.175
$P_{\text{heterogeneity}}$ for sex		0.528		0.967		0.110	

Table 3: ORs and 95%CI for colorectal cancer risk associated with one standard deviation increase in circulating AGEs and their ratios, by sex and by tumour anatomical subsite, EPIC study 1992-2012

### (CEL+MG-H1): CML

All	1377/1377	1.15 (1.03 - 1.29)	871/871	1.15 (1.00 - 1.32)	503/503	1.17 (0.94 - 1.46)	0.630
Men	678/678	1.34 (1.10 - 1.64)	404/404	1.27 (0.99 - 1.64)	272/272	1.65 (1.12 - 2.44)	0.852
Women	699/699	1.10 (0.95 - 1.27)	467/467	1.15 (0.97 - 1.37)	231/231	0.89 (0.65 - 1.23)	0.292
Pheterogeneity by sex		0.084		0.292		0.065	

Abbreviations: AGE, advanced glycation end-product; CI, confidence interval; CML, N<sup>ε</sup>-carboxy-methyllysine; CEL, N<sup>ε</sup>-carboxy-ethyllysine; MG-H1, N<sup>δ</sup>-(5-hydro-5-methyl-4-imidazolon-2-yl)-ornithine; OR, odds ratio

MG-H1 has one missing data, hence MG-H1, CEL:MG-H1 and (CEL+MG-H1): CML have 1,377 cases and 1,377 matched controls

4 cases of overlapping tumours were considered as colorectal cancer cases, but not classified as colon malignant tumour or rectal one.

\*Models were conditioned on matching factors: age at blood collection ( $\pm 1$  year), sex, recruiting centre, time of the day at blood collection ( $\pm 3$  hours), fasting status at blood collection (<3, 3-6, and >6 hours); and additionally, among women by menopausal status (pre-menopause, peri-menopause, and post-menopause), and hormone replacement therapy (HRT) use at time of blood collection (yes/no) and adjusted for BMI (continuous), height (continuous), education (none, primary, technical and professional, secondary, higher education), physical activity (inactive, moderately inactive, moderately active, active), smoking status, duration and intensity (never, 1 - 15 cigarettes/day, 16-25 cigarettes/day, over 26 cigarettes/day, former smokers who quit<10 years, former smokers who quit 11-20 years, former smokers who quit>20 years, current pipe-cigar and occasional smokers), energy intake (continuous), alcohol intake (continuous), processed meat intake (continuous), fibre intake (continuous) and dairy products intake (continuous)

Table 4: ORs and 95%CI for colorectal cancer risk associated with one standard deviation increase in circulating AGEs and their ratios, stratified by obesity and diabetes status, EPIC study 1992-2012

		Diabetes*			Obese <sup>†</sup>	
			<i>P</i> for			P for
	Yes (n=61)	No (n=1099)	heterogeneity	Yes (n=247)	No (n=1131)	heterogeneity
CML	0.56 (0.25 - 1.25)	0.74 (0.64 - 0.85)	0.486	0.30 (0.19 - 0.47)	0.85 (0.74 - 0.97)	<0.001
CEL	2.07 (0.89 - 4.82)	0.99 (0.88 - 1.10)	0.088	1.01 (0.68 - 1.50)	1.01 (0.90 - 1.12)	0.999
MGH1	1.20 (0.55 - 2.61)	0.87 (0.78 - 0.98)	0.443	0.46 (0.32 - 0.67)	0.96 (0.86 - 1.07)	<0.001
ΣAGEs	1.07 (0.48 - 2.40)	0.81 (0.72 - 0.92)	0.499	0.38 (0.25 - 0.57)	0.90 (0.80 - 1.02)	<0.001
CEL:MG-H1	1.73 (0.78 - 3.84)	1.05 (0.94 - 1.17)	0.228	1.59 (1.11 - 2.27)	1.02 (0.92 - 1.14)	0.019
(CEL+MG-H1): CML	2.94 (1.21 - 7.15)	1.19 (1.05 - 1.35)	0.046	2.36 (1.60 - 3.47)	1.10 (0.98 - 1.24)	<0.001

Abbreviations: AGE, advanced glycation end-product; CI, confidence interval; CML, N<sup> $\epsilon$ </sup>-carboxy-methyllysine; CEL, N<sup> $\epsilon$ </sup>-carboxy-ethyllysine; MG-H1, N<sup> $\delta$ </sup>-(5-hydro-5-methyl-4-imidazolon-2-yl)-ornithine; OR, odds ratio

\*Self-reported history of diabetes at baseline (n missing=218)

<sup>†</sup>Obesity was defined depending on BMI. Obese: BMI>=30 kg/m<sup>2</sup>, non-obese: BMI<30 kg/m<sup>2</sup>

\*Models were conditioned on matching factors: age at blood collection ( $\pm 1$  year), sex, recruiting centre, time of the day at blood collection ( $\pm 3$  hours), fasting status at blood collection (<3, 3-6, and >6 hours); and additionally, among women by menopausal status (pre-menopause, peri-menopause, and post-menopause), and hormone replacement therapy (HRT) use at time of blood collection (yes/no) and adjusted for height (continuous), education (none, primary, technical and professional, secondary, higher education), physical activity (inactive, moderately inactive, moderately active, active), smoking status, duration and intensity (never, 1 - 15 cigarettes/day, 16-25 cigarettes/day, over 26 cigarettes/day, former smokers who quit<10 years, former smokers who quit 11-20 years, former smokers who quit>20 years, current pipe-cigar and occasional smokers), energy intake (continuous), alcohol intake (continuous), processed meat intake (continuous), fibre intake (continuous) and dairy products intake (continuous)



Figure 1