

1 Online Supporting Material

2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39

Healthy and pro-inflammatory gut ecology plays a crucial role in the digestion and tolerance of a novel Gluten Friendly™ bread in celiac subjects: a randomized, double blind, placebo control *in vivo* study

Angelo Andriulli, Antonio Bevilacqua, Orazio Palmieri, Anna Latiano, Rosanna Fontana, Domenica Gioffreda, Stefano Castellana, Tommaso Mazza, Anna Panza, Claudia Menzaghi, Elvira Grandone, Lazzaro di Mauro, Ivana Decina, Michele Tricarico, Daniela Musaico, Markku Mäki, Jorma Isola, Alina Popp, Juha Taavela, Leonardo Petruzzi, Milena Sinigaglia, Maria Rosaria Corbo* and Carmen Lamacchia*

*Correspondence to: carmela.lamacchia@unifg.it and mariarosaria.corbo@unifg.it

This PDF file includes:

FIGURES

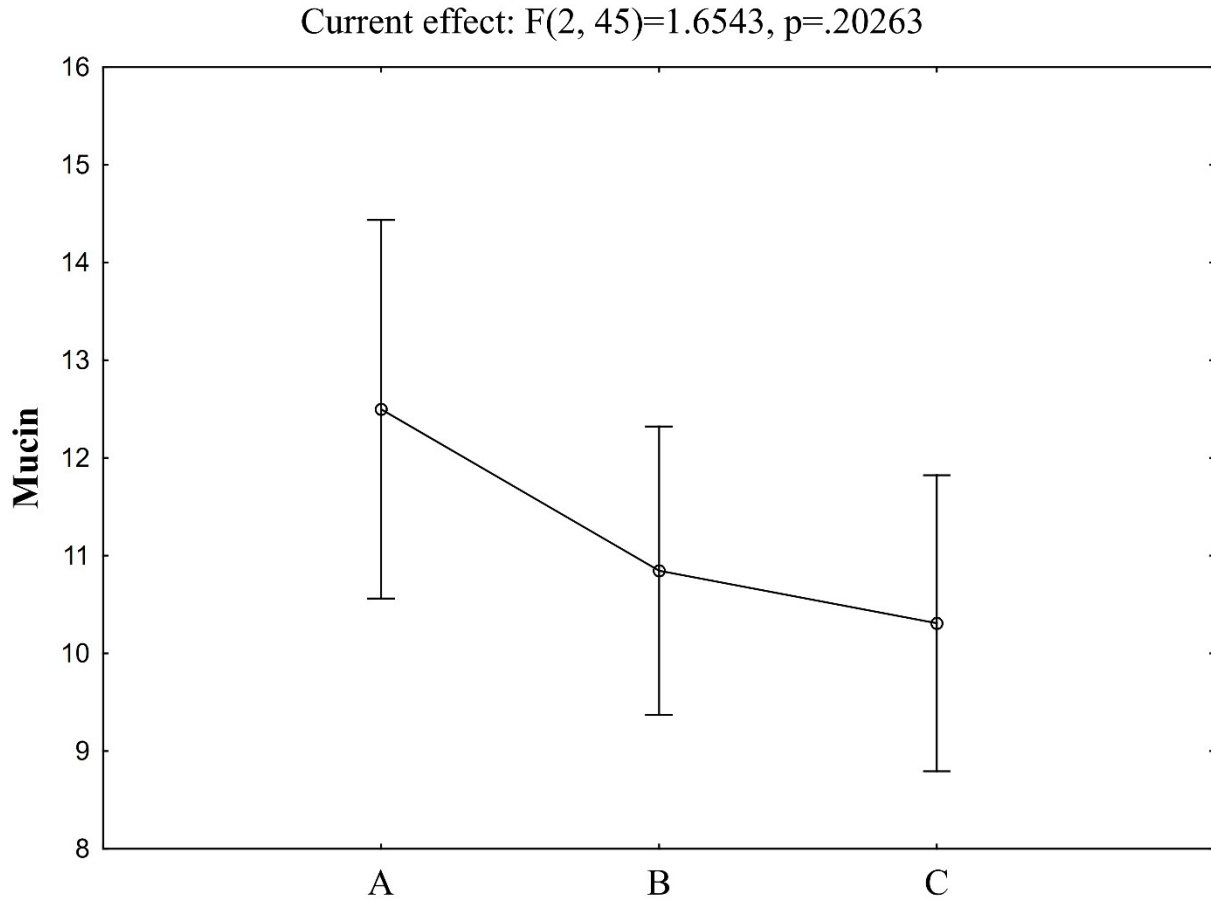
Figs. S1 to S7

TABLES

Tables S1 to S5

40
41

42 **SUPPLEMENTAL FIGURES**



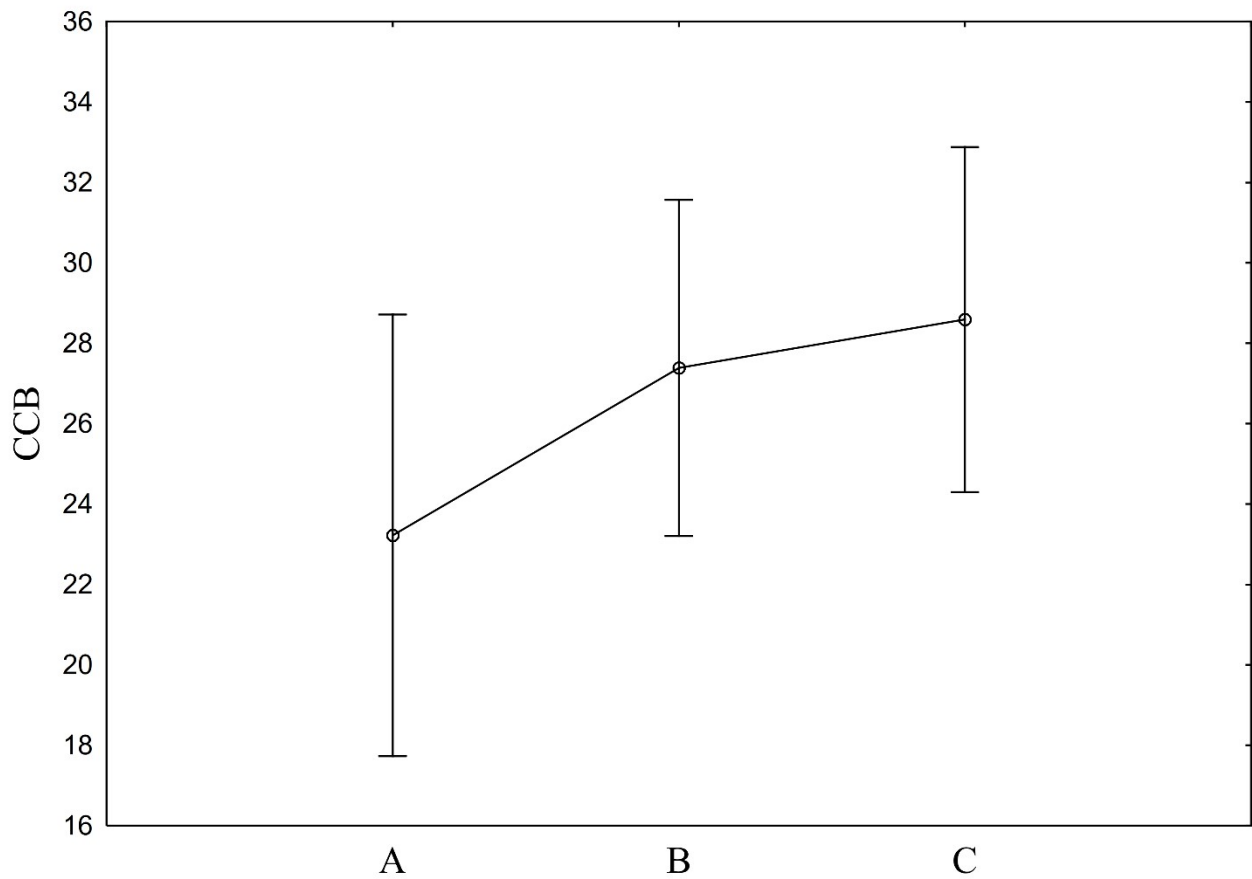
43

44 **Supplemental Figure 1: Mucin 2 at the end of trial in groups A, B and C**

45 Bars denote 95% confidence intervals. A, 0 g of GF daily; B, 3 g of GF daily; C, 6 g of GF daily.
46 Expression of MUC2 in the villus epithelium goblet cells was visualized with anti-MUC2 antibody
47 (Clone BSB-45, REF: BSB 6160, Bio SB Inc., Santa Barbara, CA. Diluted 1:250). The results were
48 reported as number of MUC2+ cells per 100 enterocytes. Measurements were independent of clinical
49 information.

50
51
52
53

Current effect: $F(2, 45)=1.2489, p=.29658$



54

55 **Supplemental Figure 2: Crypt cell proliferation (CB1) at the end of trial in groups A, B and C**

56 Bars denote 95% confidence intervals. A, 0 g of GF daily; B, 3 g of GF daily; C, 6 g of GF daily.

57 Crypt cell proliferation index was determined with anti-Cyclin B1 Ab-4 antibody (Clone GNS11,

58 REF: MS-869-P1, NeoMarkers Inc., Fremont, CA. Diluted 1:100). The results were reported as

59 percentage of proliferating Cyclin B1+ crypt cells. Measurements were independent of clinical

60 information.

61

62

63

64

65

66

67

68

69

70

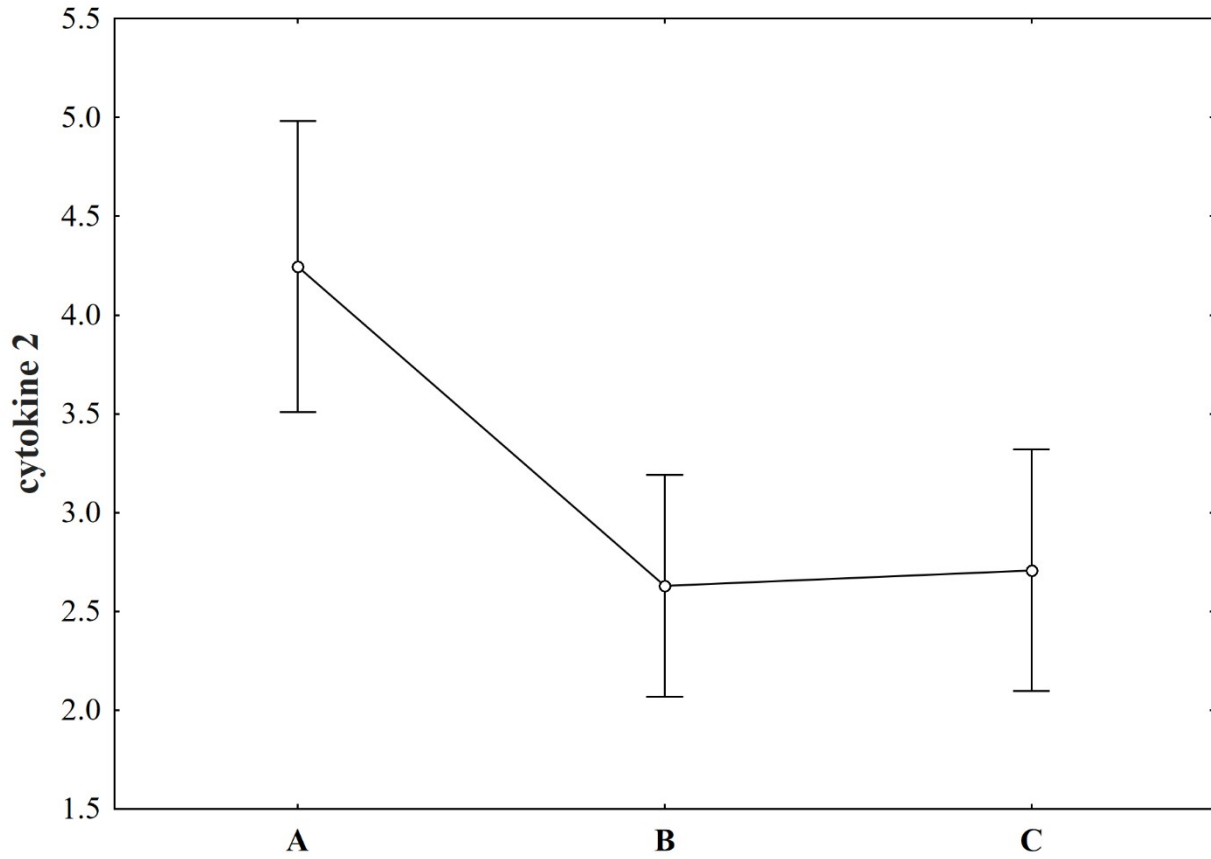
Online Supporting Material

71

72

73 a)

Current effect: $F(2, 43)=7.1268, p=.00212$



74

75

76

77

78

79

80

81

82

83

84

85

86

87

88

89

90

91

92

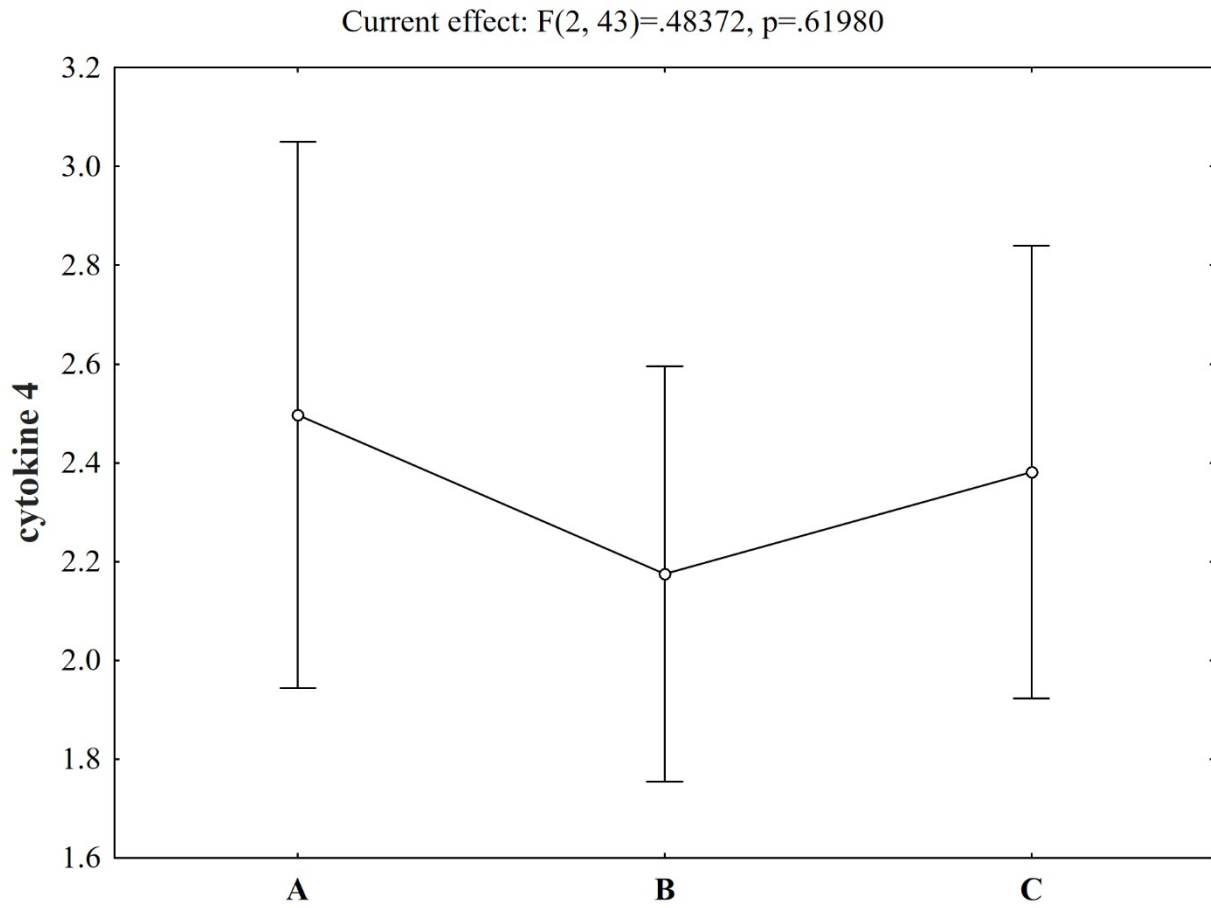
93

94

95

Online Supporting Material

96
97
98
99
100 b)
101
102
103
104

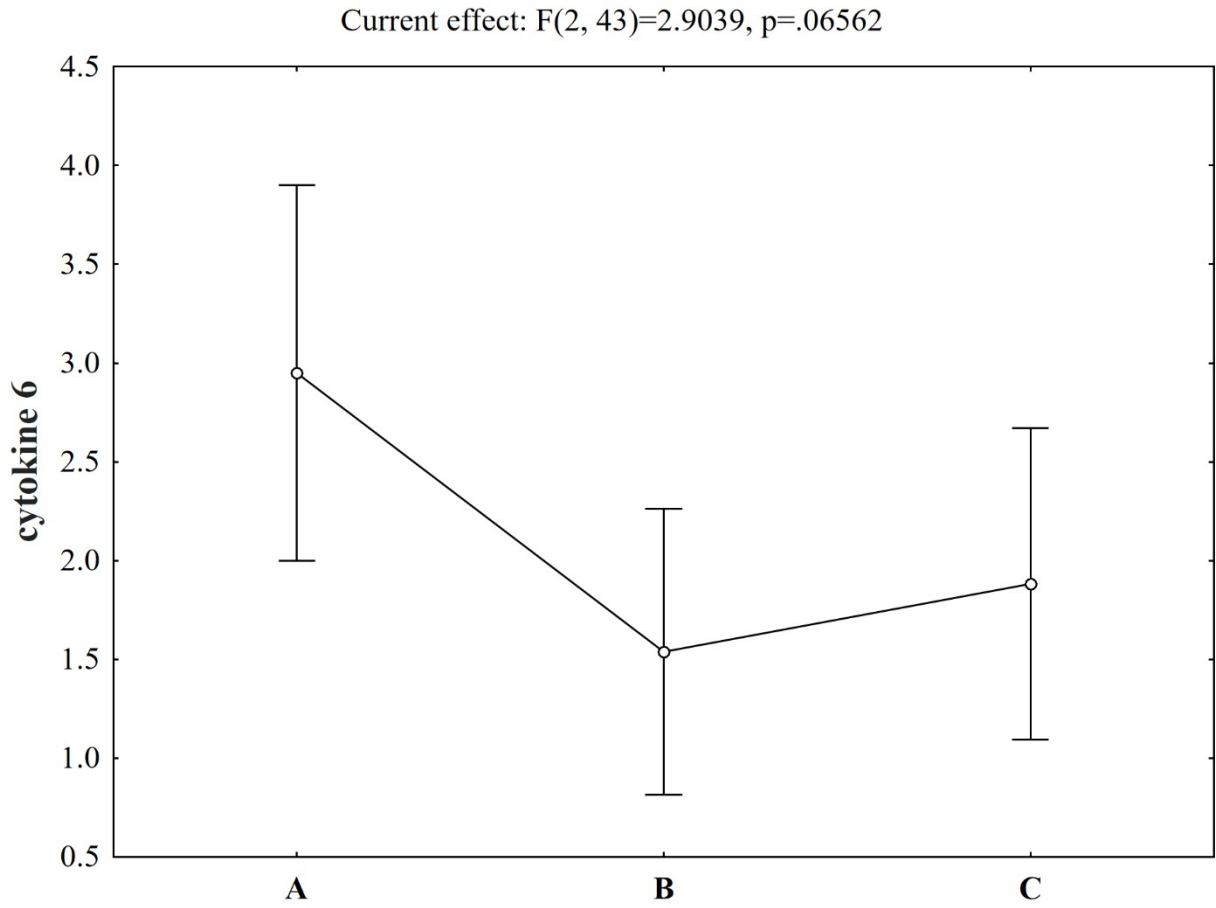


105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121

Online Supporting Material

122
123
124
125
126
127
128
129

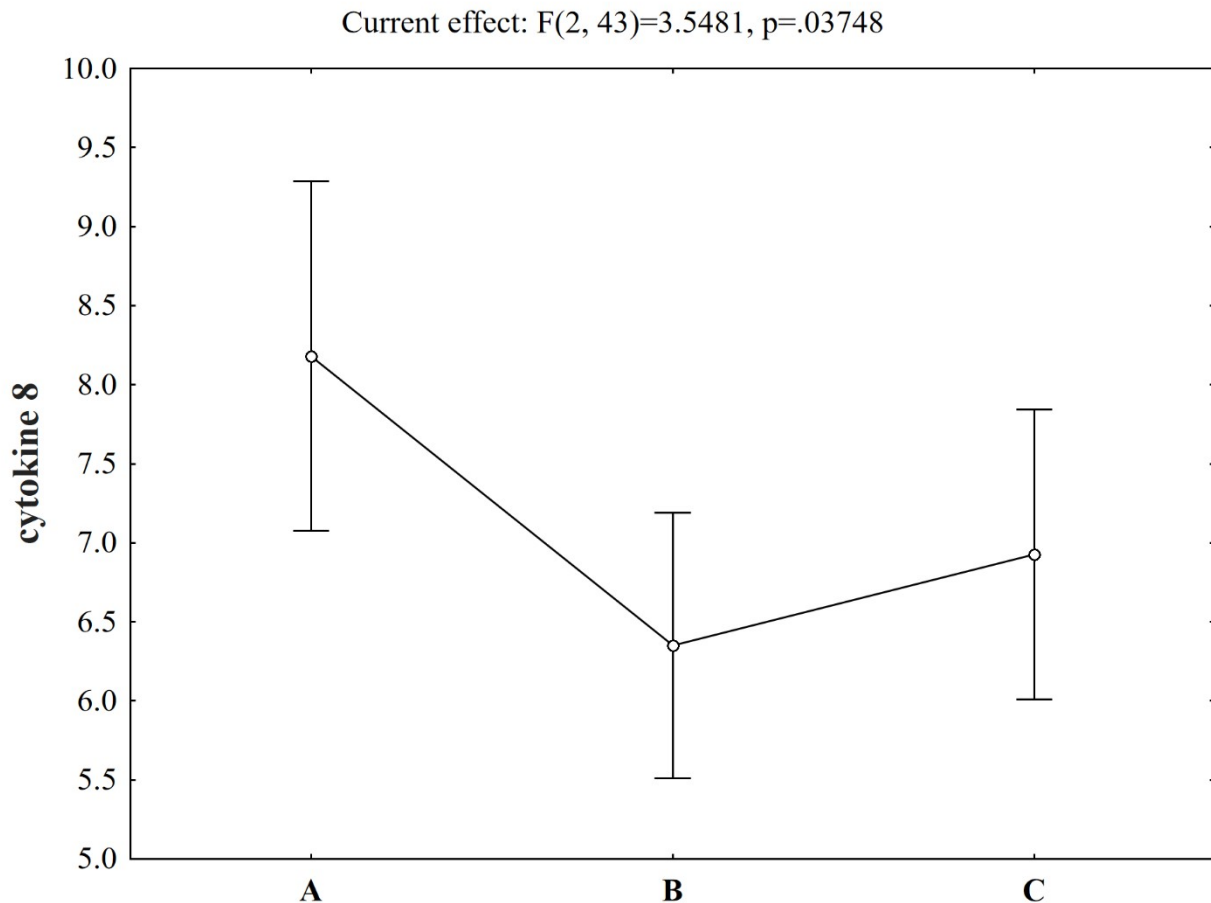
c)



130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147

Online Supporting Material

148
149
150
151
152
153
154 d)
155
156
157



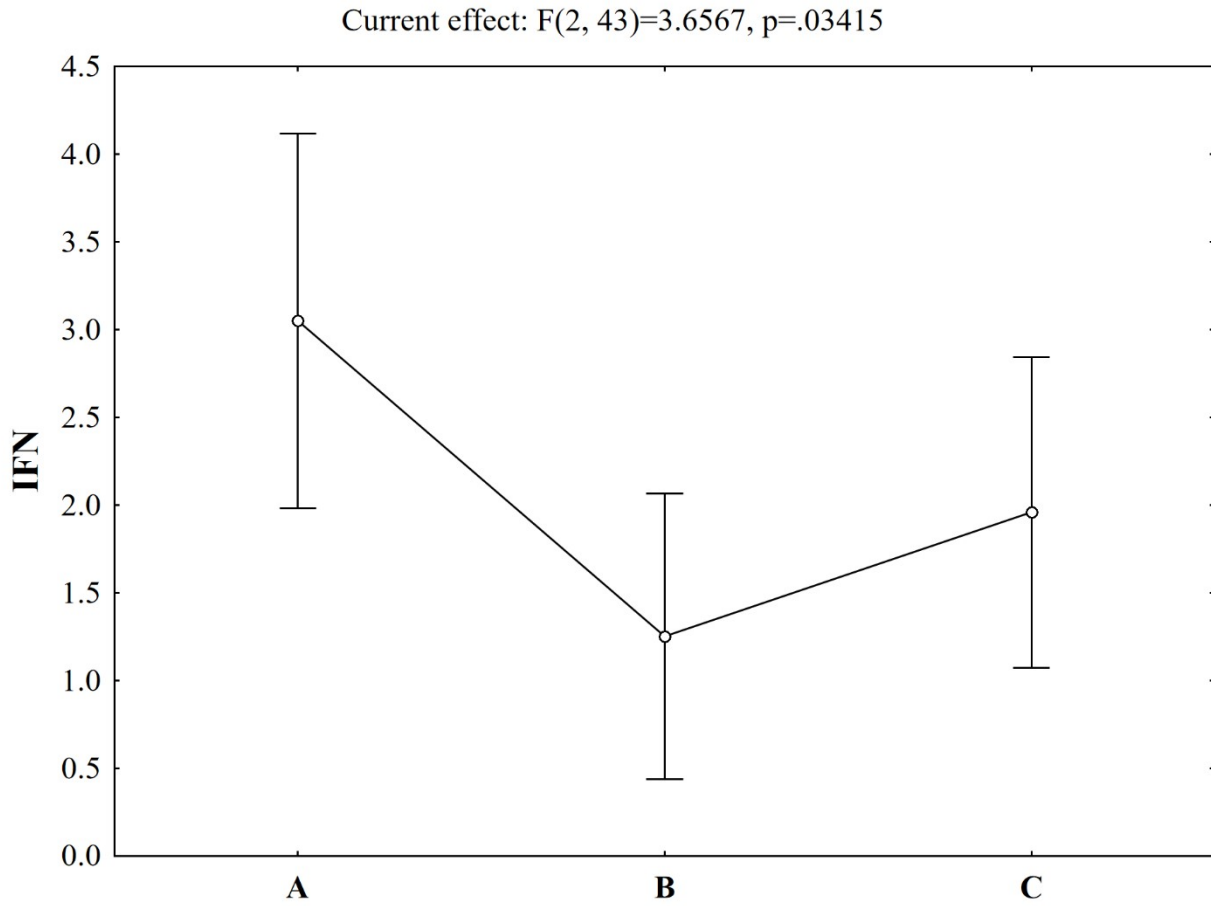
158
159
160 **Supplemental Figure 3: Production of Cytokine 2, 4, 6 and 8 at the end of trial in groups A, B**
161 **and C**

162 Bars denote 95% confidence intervals. A, 0 g of GF daily; B, 3 g of GF daily; C, 6 g of GF daily. a)
163 cytokine 2; b) cytokine 4; c) cytokine 6; d) cytokine 8. The premixed multiplex beads of the Bio-Plex
164 human cytokine Human 27-Plex Panel (Bio-Rad Laboratories, Milan, Italy) was used in presence of
165 30 μ l of plasma. All the plasma samples and standards were run in duplicate, and fluorescent signals
166 were read by using Biorad 200 system (Bio-Rad). Cytokines were analyzed by means of one-way
167 analysis of variance (ANOVA) and Tukey's test, or through the nonparametric test of Friedman if
168 data distribution did not show a normal trend. The critical level of P was set to 0.05

169

Online Supporting Material

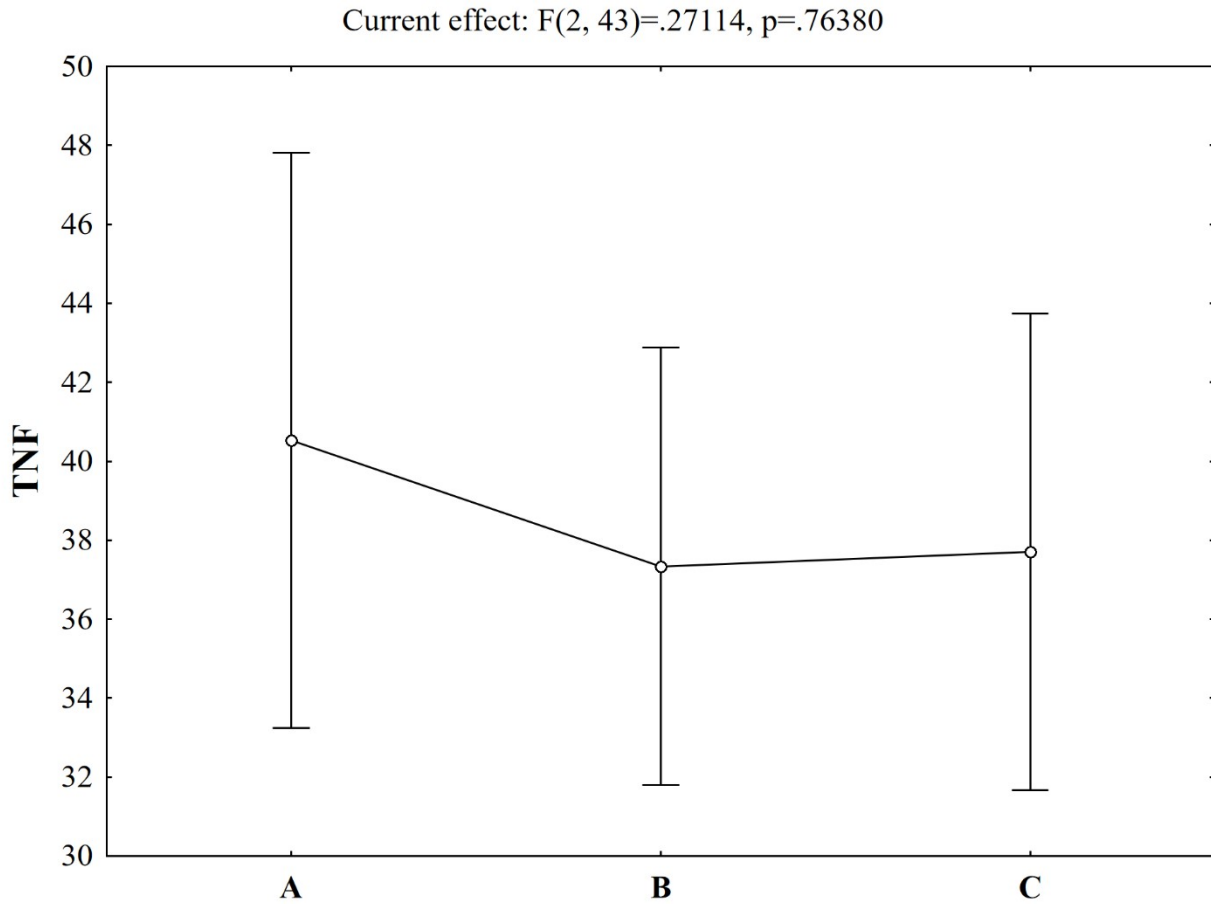
170
171 a)
172
173
174



175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195

Online Supporting Material

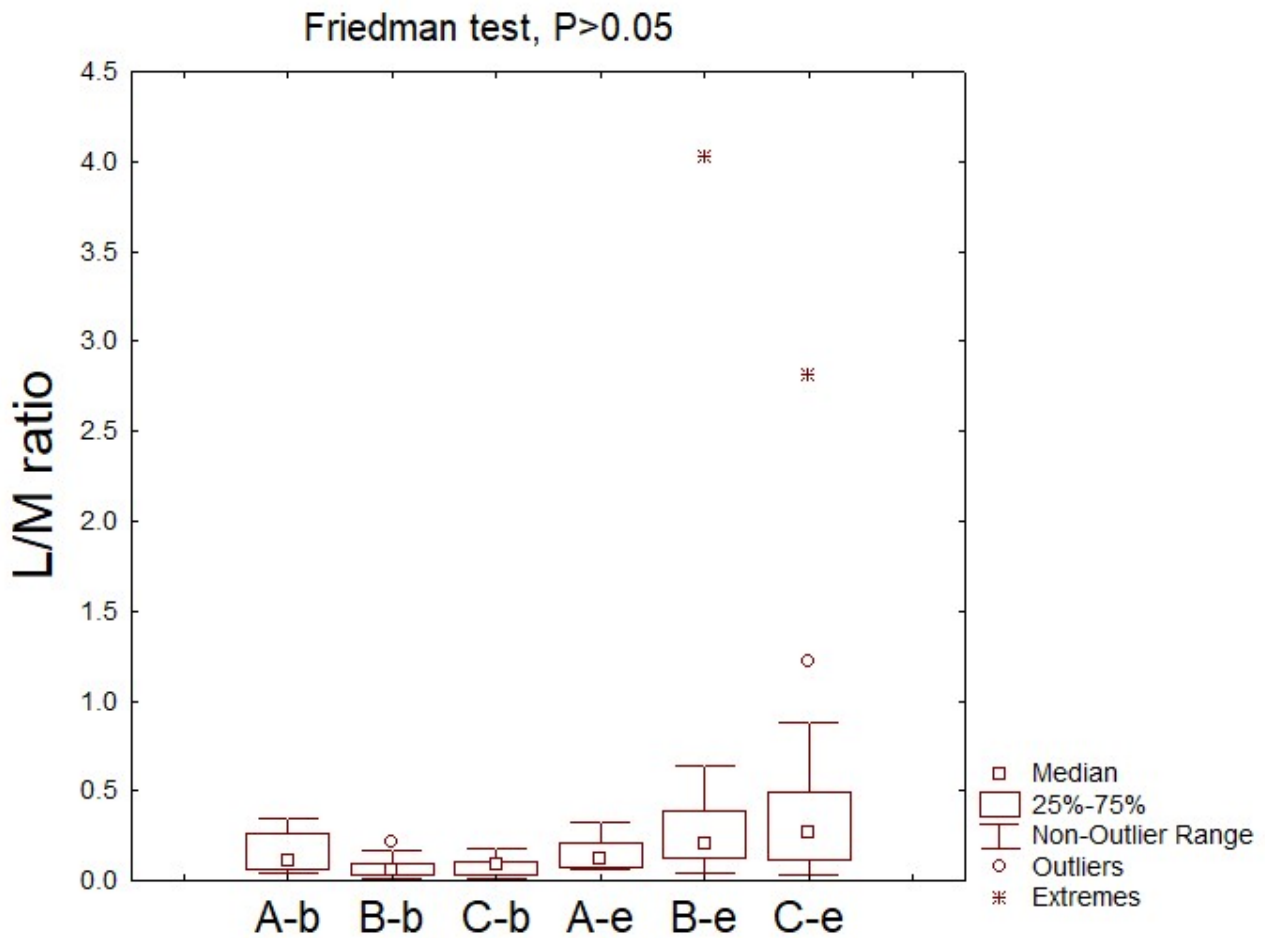
196
197
198
199 b)
200



201
202
203 **Supplemental Figure 4: Production of IFN and TNF at the end of trial in groups A, B and C;**
204 Bars denote 95% confidence intervals. A, 0 g of GF daily; B, 3 g of GF daily; C, 6 g of GF daily. a)
205 IFN; b) TNF. The premixed multiplex beads of the Bio-Plex human cytokine Human 27-Plex Panel
206 (Bio-Rad Laboratories, Milan, Italy) was used in presence of 30 μ l of plasma. All the plasma samples
207 and standards were run in duplicate and fluorescent signals were read by using Biorad 200 system
208 (Bio-Rad). Cytokines were analyzed by means of one-way analysis of variance (ANOVA) and
209 Tukey's test, or through the nonparametric test of Friedman if data distribution did not show a normal
210 trend. The critical level of P was set to 0.05.

211
212
213
214
215
216
217

218
219
220
221



222
223
224
225

226 **Supplemental Figure 5: Lactulose/Mannitol ratio in groups A, B and C.**

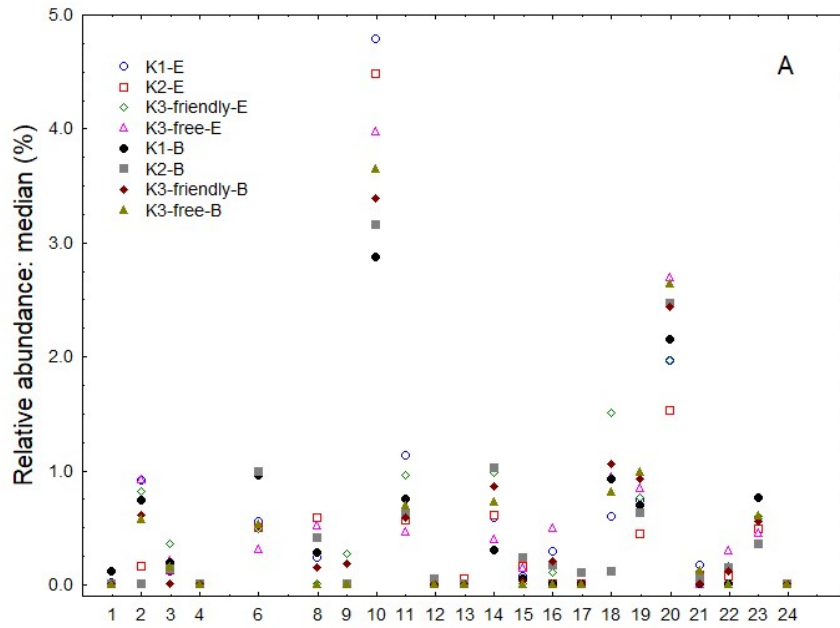
227 A, 0 g of GF daily; B, 3 g of GF daily; C, 6 g of GF daily. Data were expressed as the ratio between
228 the concentration of Lactulose [mg/L] and Mannitol [mg/L]; the letters b and e stand for before and
229 at the end of the trial.

230 Gut permeability was analyzed by the nonparametric test of Friedman. The critical level of P was
231 set to 0.05.

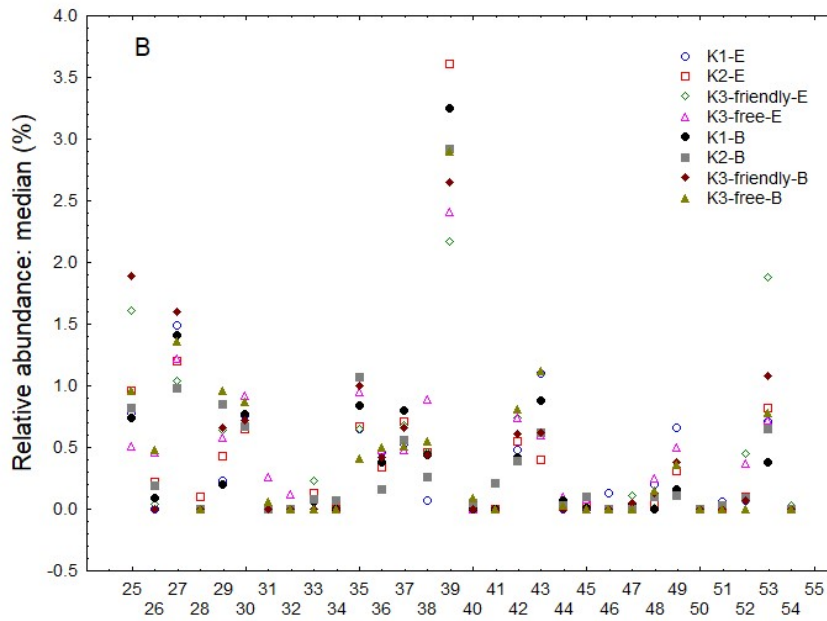
232
233
234
235
236
237
238
239

240

Online Supporting Material



241
242



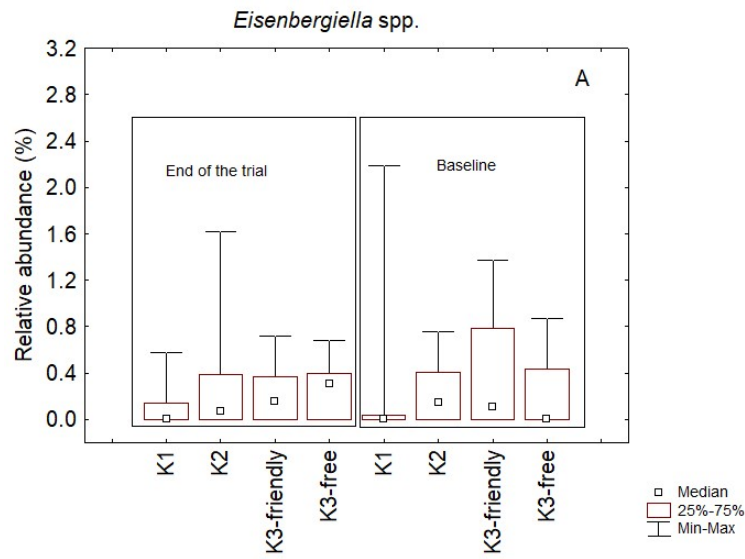
243
244

245 **Supplemental Figure 6:** Overview of some representative genera in cluster 1 (K1), cluster 2 (K3),
246 subjects of cluster 3 receiving Gluten Friendly (K3-friendly) and subjects of cluster 3 receiving
247 Gluten free (K3-free). The letters E and B indicate the end of the trial or the baseline (beginning)
248 The scatter plot represents the median of each group. For the meaning of the number see supplemental
249 table S5

250

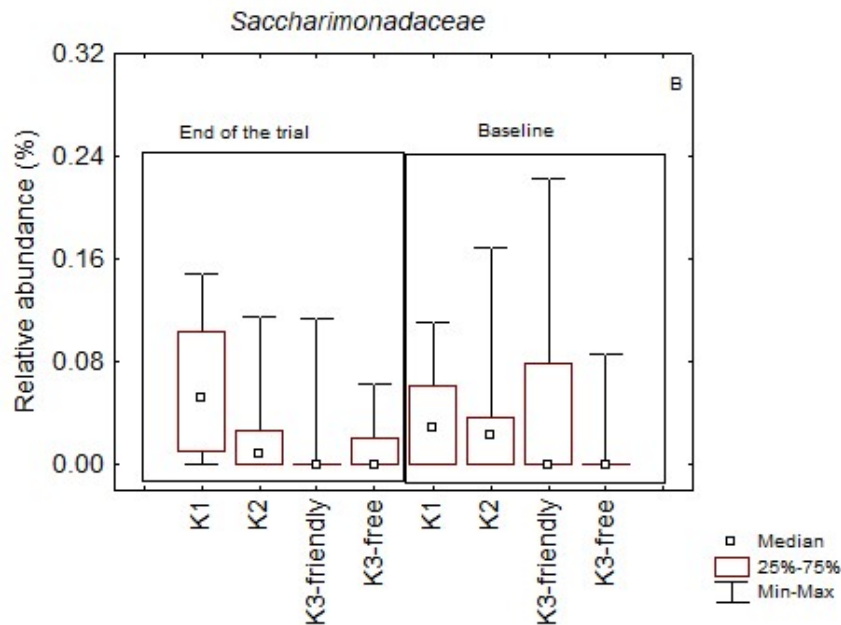
251

Online Supporting Material



252

253



254

255 **Supplemental Figure 7:** Overview of *Eisenbergiella* (A) and *Saccharimonadaceae* (B) in cluster 1
256 (K1), cluster 2 (K3), subjects of cluster 3 receiving Gluten Friendly (K3-friendly) and subjects of
257 cluster 3 receiving Gluten free (K3-free) at the baseline and after the trial.

258 The box accounts for the interquartile range (from quartile 1 to quartile 3; 25-75%), while the
259 whiskers indicate the minimum and the maximum of the population.

260

Online Supporting Material

261
262
263
264
265
266
267
268
269
270
271

SUPPLEMENTAL TABLES

Supplemental Table 1: Gluten Friendly does not induce Gastrointestinal Symptom

Gastrointestinal Symptom Rating Scale (GSRS) and Bristol Stool Chart. Median and quartiles are shown in brackets.

	Week 1	Week 2	Week 4	Week 8	Week 12
Group A					
Bristol Stool Chart	3.5 (3-4)	4 (4-4)	4 (4-4)	4 (3.5-4)	4 (3-4)
Abdominal pain	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Bloating	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Flatulence	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Group B					
Bristol Stool Chart	3.5 (2.75-4)	3.5 (2.5-4)	4 (3-4)	3.5 (3-4)	3.5 (3-4)
Abdominal pain	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Bloating	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Flatulence	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Group C					
Bristol Stool Chart	3.75 (3-4)	4 (3-4)	3.5 (3-4)	4 (3-4)	4 (3.38-4)
Abdominal pain	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Bloating	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)
Flatulence	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)	0 (0-0)

272
273
274
275
276
277
278
279
280

Online Supporting Material

281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324

Supplemental Table 2: Mean values of the categorical predictors of k-means

	K1	K2	K3
VH/CrD	-1.07	-1.28	-0.10
IEL	97.80	46.22	13.52
G12	53	27	9
CB1	16.88	20.01	-3.12
MUC2	-13.15	-23.80	15.23

VH, VH/CrD
IEL, IEL increase (%)
G12, detection of 33-mer peptide (%)
CB1, increase of CB1 (%)
MUC2, increase of MUC2 (%)

325
326
327
328

Supplemental Table 3: Subjects included in the clusters of k-means

K 1 15 individuals: 7 from C 6 from B 2 from A	K 2 11 individuals: 5 from C 6 from B	K3 22 individuals: 6 from C 7 from B 9 from A
1C	4C	5C
2C	7C	6C
3C	8C	10C
9C	12C	11C
13C	18C	15C
14C	3B	16C
17C	5B	1B
2B	7B	6B
4B	17B	9B
8B	18B	13B
10B	19B	14B
11B		15B
12B		16B
2A		1A
3A		4A
		5A
		6A
		7A
		8A
		9A
		10A
		11A

329
330
331
332
333
334
335
336
337
338
339

Online Supporting Material

340
341

342

343

344 **Supplemental Table 4: Evaluation of pro-inflammatory score at baseline**

345

1 found
0 not found

***Slackia Sutterella* score (%)**

K1	1	1	100
K1	0	1	50
K1	0	1	50
K1	0	1	50
K1	0	0	0
K1	0	0	0
K1	0	1	50
K1	0	1	50
K1	0	1	50
K1	1	1	100
K1	0	0	0
K1	0	0	0

500

***Slackia Sutterella* score (%)**

K2	1	1	100
K2	0	0	0
K2	1	0	50
K2	0	0	0
K2	1	1	100
K2	1	0	50
K2	0	1	50
K2	0	0	0
K2	0	0	0
K2	0	1	50

400

***Slackia Sutterella* score (%)**

K3 Friendly	1	0	50
K3 Friendly	0	1	50
K3 Friendly	0	1	50
K3 Friendly	0	0	0
K3 Friendly	0	0	0
K3 Friendly	0	0	0
K3 Friendly	0	0	0
K3 Friendly	0	0	0
K3 Friendly	0	0	0
K3 Friendly	0	0	0
K3 Friendly	0	0	0

K3 Friendly	0	0	0
K3 Friendly	1	0	0

150

***Slackia Sutterella* score (%)**

K3 free	0	0	0
K3 free	0	1	50
K3 free	0	0	0
K3 free	0	0	0
K3 free	0	0	0
K3 free	0	1	50
K3 free	0	0	0

100

346

	individuals	sum of scores	standaradized score
K 1	12	500	41.67
K 2	10	400	40.00
K3 Friendly	13	150	11.54
K3 free	7	100	14.29

347

348

349

350

351

Online Supporting Material

352

353

354 **Supplemental Table 5: Relative abundance of some target genera at the baseline and the end of the trial in cluster 1 (K1), cluster 2 (K3),**
 355 **subjects of cluster 3 receiving Gluten Friendly (K3-friendly) and subjects of cluster 3 receiving Gluten free (K3-free).**

356 The letters E and B indicate the end of the trial or the baseline (beginning). 1Q: quartile 1; 3Q; quartile 3. The numbers on the first row should be used
 357 to read figures in S6

		1	2	3	4	5	6	8	9	10	11	12	13	14	15	16
		<i>Sutterella</i>	<i>Bifidobacterium</i>	<i>Collinsella</i>	<i>Slackia</i>	<i>Bacteroides</i>	<i>Barnesiella</i>	<i>Butyrivimonas</i>	<i>Paraprevotella</i>	<i>Alistipes</i>	<i>Parabacteroides</i>	<i>Enterococcus</i>	<i>Lactobacillus</i>	<i>Streptococcus</i>	<i>Christensenellaceae R-7 group</i>	<i>Clostridium sensu stricto</i>
K1-E	median	0.019	0.918	0.110	0.000	21.912	0.552	0.232	0.000	4.790	1.135	0.003	0.000	0.586	0.066	0.293
	1Q	0.000	0.548	0.000	0.000	11.372	0.005	0.000	0.000	1.992	0.573	0.000	0.000	0.362	0.000	0.000
	3Q	0.261	1.363	0.349	0.319	36.752	2.129	0.706	0.566	7.380	1.437	0.399	0.000	0.875	0.330	0.632
	min	0.000	0.105	0.000	0.000	7.379	0.000	0.000	0.000	0.000	0.157	0.000	0.000	0.183	0.000	0.000
	max	2.037	2.227	0.566	0.503	55.692	11.453	1.431	2.503	13.784	2.405	0.801	0.016	1.400	0.538	0.954
K2-E	median	0.000	0.153	0.125	0.000	19.367	0.496	0.589	0.000	4.477	0.567	0.006	0.045	0.603	0.154	0.000
	1Q	0.000	0.000	0.000	0.000	16.854	0.000	0.000	0.000	1.312	0.181	0.000	0.000	0.466	0.000	0.000
	3Q	0.561	0.782	0.460	0.328	38.095	4.039	0.842	0.546	7.065	0.794	0.275	0.181	1.116	0.468	0.762
	min	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.071	0.000	0.000
	max	1.425	5.184	1.082	0.641	55.826	9.475	1.017	3.550	14.992	1.940	0.816	1.684	3.101	1.096	1.632
K3-friendly-E	median	0.000	0.815	0.350	0.000	23.215	0.485	0.000	0.272	3.155	0.956	0.020	0.000	0.982	0.000	0.103
	1Q	0.000	0.336	0.000	0.000	12.690	0.018	0.000	0.000	1.579	0.247	0.000	0.000	0.552	0.000	0.000
	3Q	0.025	1.420	0.697	0.000	38.299	1.817	0.316	1.120	4.962	1.382	0.420	0.178	1.239	0.400	0.856
	min	0.000	0.000	0.000	0.000	7.908	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.249	0.000	0.000
	max	0.472	6.231	1.324	0.287	50.604	8.446	0.817	4.336	18.396	1.979	2.096	0.739	3.133	1.955	1.123
K3-free-E	median	0.000	0.925	0.215	0.000	15.919	0.307	0.520	0.000	3.979	0.462	0.000	0.000	0.394	0.149	0.502
	1Q	0.000	0.611	0.000	0.000	13.696	0.000	0.000	0.000	3.073	0.156	0.000	0.000	0.238	0.048	0.000
	3Q	0.000	1.333	0.578	0.000	21.292	2.129	0.741	0.000	6.774	0.804	0.182	0.000	1.824	0.772	0.990
	min	0.000	0.000	0.000	0.000	13.517	0.000	0.000	0.000	2.840	0.000	0.000	0.000	0.226	0.000	0.000
	max	1.071	2.634	0.579	0.000	56.335	2.183	1.096	0.336	9.037	0.962	0.298	0.045	2.490	1.092	1.274
K1-B	median	0.113	0.738	0.187	0.000	21.970	0.962	0.278	0.000	2.875	0.751	0.000	0.000	0.304	0.052	0.000
	1Q	0.000	0.193	0.000	0.000	12.620	0.006	0.000	0.000	2.061	0.238	0.000	0.000	0.154	0.000	0.000
	3Q	0.466	1.113	0.308	0.000	37.742	1.614	0.477	0.612	3.645	0.839	0.040	0.033	0.711	0.256	0.326
	min	0.000	0.000	0.000	0.000	9.057	0.000	0.000	0.000	0.383	0.048	0.000	0.000	0.000	0.000	0.000
	max	0.699	3.071	0.443	0.411	57.927	2.212	1.226	1.876	5.013	1.098	1.159	0.544	1.070	2.541	1.138
K2-B	median	0.000	0.000	0.140	0.000	24.301	0.989	0.407	0.000	3.157	0.623	0.048	0.000	1.027	0.232	0.171
	1Q	0.000	0.000	0.000	0.000	13.245	0.000	0.000	0.000	1.040	0.096	0.000	0.000	0.276	0.000	0.000
	3Q	0.390	0.588	0.254	0.327	32.074	2.099	0.803	0.298	5.195	0.907	0.311	0.032	1.653	0.974	0.362
	min	0.000	0.000	0.000	0.000	5.045	0.000	0.000	0.000	0.118	0.008	0.000	0.000	0.000	0.000	0.000
	max	0.669	0.667	1.127	1.275	39.512	3.581	1.943	2.089	6.372	1.769	0.835	0.652	3.958	2.242	0.593
K3-friendly-B	median	0.000	0.605	0.000	0.000	24.406	0.513	0.150	0.180	3.388	0.584	0.000	0.000	0.859	0.022	0.197
	1Q	0.000	0.069	0.000	0.000	14.662	0.000	0.000	0.000	2.032	0.080	0.000	0.000	0.447	0.000	0.000
	3Q	0.000	0.873	0.424	0.000	30.005	1.020	0.725	0.581	5.910	0.773	0.191	0.044	2.236	0.153	1.005
	min	0.000	0.000	0.000	0.000	7.401	0.000	0.000	0.000	0.134	0.000	0.000	0.000	0.000	0.000	0.000
	max	0.493	1.850	0.788	0.531	36.979	4.340	1.221	9.831	8.455	2.193	0.801	1.548	9.434	0.920	1.878
K3-free-B	median	0.000	0.575	0.161	0.000	22.024	0.532	0.000	0.000	3.645	0.695	0.000	0.000	0.729	0.000	0.000
	1Q	0.000	0.371	0.134	0.000	19.471	0.000	0.000	0.000	2.952	0.401	0.000	0.000	0.386	0.000	0.000
	3Q	0.015	0.998	0.328	0.000	33.458	0.790	0.819	0.000	3.992	0.891	0.560	0.071	1.189	0.197	0.051
	min	0.000	0.311	0.000	0.000	13.038	0.000	0.000	0.000	1.502	0.030	0.000	0.000	0.000	0.000	0.000
	max	0.365	1.819	0.431	0.000	54.808	2.086	1.139	0.580	4.992	1.256	0.721	0.542	2.354	0.488	0.451

358

359

	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33
	<i>Ekaziella</i>	<i>Agathobacter</i>	<i>Anaerostipes</i>	<i>Blautia</i>	<i>Coproccoccus 1</i>	<i>Eisenbergiella</i>	<i>Fusicatenibacter</i>	<i>Hungatella</i>	<i>Lachnoclostridium</i>	<i>Lachnospira</i>	<i>Roseburia</i>	<i>Tyzzzeria 4</i>	<i>Eubacterium eligenes group</i>	<i>halii group</i>	<i>ntriosum grovylanophilum</i>		
K1-E	0.000	0.594	0.738	1.968	0.171	0.000	0.486	0.000	0.776	0.000	1.487	0.000	0.228	0.754	0.000	0.000	0.056
	0.000	0.182	0.210	1.715	0.000	0.000	0.299	0.000	0.257	0.000	0.862	0.000	0.000	0.592	0.000	0.000	0.000
	0.018	0.782	1.380	2.925	0.203	0.166	0.951	0.159	2.510	0.357	1.811	0.121	1.228	1.015	0.341	0.078	0.494
	0.000	0.000	0.000	0.347	0.000	0.000	0.000	0.000	0.179	0.000	0.130	0.000	0.000	0.270	0.000	0.000	0.000
	0.062	1.422	1.738	3.445	0.332	0.577	1.542	0.414	4.600	1.540	4.789	0.602	1.825	2.131	0.615	0.466	0.973
K2-E	0.000	0.119	0.440	1.531	0.076	0.072	0.491	0.000	0.952	0.214	1.192	0.091	0.423	0.650	0.000	0.000	0.127
	0.000	0.000	0.296	0.990	0.000	0.000	0.275	0.000	0.552	0.000	0.525	0.000	0.140	0.226	0.000	0.000	0.000
	0.036	0.886	0.991	2.548	0.239	0.406	0.740	0.361	2.481	0.299	2.190	0.600	0.661	0.957	0.331	0.143	0.283
	0.000	0.000	0.000	0.507	0.000	0.000	0.000	0.000	0.254	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.247	2.248	2.375	3.513	0.252	1.615	1.293	1.396	4.111	0.408	5.261	1.563	2.242	1.337	0.658	0.517	0.569
K3-friendly-E	0.000	1.506	0.757	1.959	0.000	0.160	0.599	0.000	1.604	0.035	1.038	0.000	0.636	0.718	0.000	0.000	0.229
	0.000	0.000	0.607	1.807	0.000	0.000	0.345	0.000	0.502	0.000	0.613	0.000	0.121	0.489	0.000	0.000	0.000
	0.000	1.786	1.276	2.534	0.276	0.372	0.880	0.243	2.478	0.608	2.361	0.000	1.380	0.964	0.266	0.515	0.378
	0.000	0.000	0.440	0.686	0.000	0.000	0.000	0.000	0.077	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.028	6.333	1.716	3.299	0.390	0.717	1.341	0.409	2.747	0.835	4.945	0.348	3.373	1.052	0.625	1.557	0.670
K3-free-E	0.000	0.951	0.844	2.697	0.000	0.305	0.450	0.000	0.507	0.455	1.215	0.000	0.577	0.920	0.260	0.113	0.000
	0.000	0.000	0.671	2.376	0.000	0.000	0.253	0.000	0.030	0.000	0.618	0.000	0.000	0.498	0.000	0.000	0.000
	0.491	1.231	1.040	2.836	0.238	0.392	0.781	0.000	3.490	0.493	1.927	0.000	0.890	1.326	0.381	0.448	0.250
	0.000	0.000	0.402	2.081	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.444	0.000	0.000	0.000
	0.589	1.534	1.692	3.001	0.307	0.686	1.660	0.220	4.586	0.739	2.462	0.000	1.999	1.333	0.811	0.552	0.651
K1-B	0.000	0.923	0.694	2.146	0.000	0.000	0.765	0.000	0.734	0.090	1.402	0.000	0.198	0.766	0.000	0.000	0.054
	0.000	0.449	0.309	1.593	0.000	0.000	0.339	0.000	0.220	0.000	0.813	0.000	0.000	0.559	0.000	0.000	0.000
	0.012	1.877	0.969	2.760	0.182	0.053	1.076	0.000	3.446	0.429	2.746	0.000	1.095	0.979	0.340	0.102	0.278
	0.000	0.000	0.000	0.322	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.110	3.550	2.414	3.527	0.341	2.183	1.272	1.068	4.111	2.471	3.672	0.091	1.535	1.512	0.448	0.465	0.856
K2-B	0.103	0.118	0.632	2.465	0.043	0.150	0.351	0.000	0.816	0.188	0.973	0.000	0.847	0.665	0.000	0.000	0.074
	0.000	0.000	0.210	2.240	0.000	0.000	0.121	0.000	0.258	0.000	0.636	0.000	0.354	0.295	0.000	0.000	0.000
	0.344	1.256	0.875	3.620	0.222	0.428	0.541	0.211	1.391	0.822	2.210	0.000	1.344	1.027	0.274	0.105	0.253
	0.000	0.000	0.000	1.723	0.000	0.000	0.000	0.000	0.083	0.000	0.000	0.000	0.000	0.157	0.000	0.000	0.000
	1.871	2.886	1.296	7.940	0.663	0.755	1.140	0.833	5.562	1.458	5.109	0.145	1.825	1.625	0.549	0.597	0.611
K3-friendly-B	0.000	1.060	0.929	2.429	0.000	0.109	0.548	0.000	1.883	0.000	1.599	0.000	0.654	0.718	0.000	0.000	0.000
	0.000	0.000	0.143	1.724	0.000	0.000	0.319	0.000	0.647	0.000	0.940	0.000	0.193	0.312	0.000	0.000	0.000
	0.016	1.221	1.335	4.677	0.311	0.795	0.868	0.000	2.490	0.201	2.348	0.000	1.793	1.164	0.219	0.197	0.112
	0.000	0.000	0.000	0.868	0.000	0.000	0.000	0.000	0.176	0.000	0.394	0.000	0.000	0.000	0.000	0.000	0.000
	0.320	1.866	2.144	6.367	0.542	1.376	0.953	0.506	3.388	1.093	3.393	0.602	4.393	1.866	0.734	1.067	0.468
K3-free-B	0.000	0.819	0.988	2.638	0.127	0.000	0.612	0.000	0.960	0.479	1.357	0.000	0.954	0.862	0.059	0.000	0.000
	0.000	0.316	0.502	1.365	0.000	0.000	0.410	0.000	0.438	0.000	0.445	0.000	0.480	0.709	0.000	0.000	0.000
	0.000	1.271	1.326	3.848	0.252	0.431	0.641	0.223	1.243	0.740	2.683	0.000	1.783	0.984	0.622	0.245	0.262
	0.000	0.000	0.407	0.962	0.000	0.000	0.000	0.000	0.167	0.000	0.000	0.000	0.000	0.311	0.000	0.000	0.000
	0.066	1.584	1.942	4.810	0.309	0.868	1.106	0.283	1.996	0.803	4.844	0.000	2.193	1.061	0.682	0.299	0.420

360
361
362
363
364
365
366
367
368
369
370

	34	35	36	37	38	39	40	41	42	43	44
	<i>R. gnnavus</i>	<i>R. torques</i>	<i>Intestinibacter</i>	<i>Romboutsia</i>	<i>Butyricoccus</i>	<i>Faecalibacterium</i>	<i>Intestinimonas</i>	<i>Negativibacillus</i>	<i>Oscillibacter</i>	<i>Subdoligranulum</i>	<i>E coproligenes</i>
K1-E	0.000	0.646	0.461	0.529	0.066	2.915	0.000	0.000	0.471	1.091	0.000
	0.000	0.261	0.099	0.263	0.000	1.656	0.000	0.000	0.311	0.786	0.000
	0.179	1.355	0.829	1.271	0.304	3.333	0.305	0.000	1.020	1.620	0.155
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	1.110	2.755	2.450	1.427	1.013	4.322	0.565	0.444	1.134	1.954	1.550
K2-E	0.000	0.666	0.339	0.709	0.459	3.606	0.000	0.000	0.549	0.396	0.017
	0.000	0.515	0.000	0.297	0.037	1.937	0.000	0.000	0.296	0.025	0.000
	0.655	1.017	0.365	1.217	0.992	5.470	0.091	0.405	0.993	1.149	0.167
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.991	1.740	1.363	1.446	1.048	8.319	0.536	0.431	1.512	2.181	0.748
K3-friendly-E	0.000	0.645	0.385	0.676	0.460	2.166	0.000	0.000	0.734	0.606	0.021
	0.000	0.248	0.000	0.083	0.287	1.244	0.000	0.000	0.373	0.000	0.000
	0.338	1.034	0.641	1.006	0.809	2.707	0.204	0.184	1.129	1.324	0.209
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.107	0.000	0.000
	4.861	1.407	1.069	1.801	1.222	4.380	0.294	0.699	1.968	2.488	0.654
K3-free-E	0.000	0.941	0.478	0.476	0.887	2.402	0.000	0.000	0.737	0.595	0.094
	0.000	0.000	0.282	0.382	0.026	1.809	0.000	0.000	0.585	0.052	0.058
	0.000	1.200	0.883	0.577	1.157	3.804	0.058	0.221	0.786	1.003	0.190
	0.000	0.000	0.000	0.000	0.000	0.758	0.000	0.000	0.554	0.025	0.045
	0.000	1.599	1.029	1.411	1.388	4.615	0.287	0.982	1.540	5.028	0.717
K1-B	0.000	0.835	0.377	0.799	0.438	3.242	0.000	0.000	0.416	0.878	0.068
	0.000	0.414	0.213	0.509	0.112	2.245	0.000	0.000	0.226	0.564	0.000
	0.183	1.008	0.699	1.010	0.732	4.171	0.000	0.000	0.949	1.342	0.617
	0.000	0.000	0.000	0.185	0.000	1.536	0.000	0.000	0.000	0.329	0.000
	1.535	2.035	1.190	1.349	1.194	6.138	0.243	0.000	1.191	3.961	1.656
K2-B	0.067	1.062	0.159	0.555	0.255	2.916	0.047	0.209	0.385	0.613	0.027
	0.000	0.633	0.000	0.266	0.007	1.674	0.000	0.000	0.187	0.268	0.005
	0.254	1.173	0.654	1.199	0.590	4.932	0.256	0.503	0.851	2.010	0.245
	0.000	0.127	0.000	0.000	0.000	0.720	0.000	0.000	0.000	0.000	0.000
	0.351	1.414	1.028	1.522	1.208	8.388	0.607	0.587	1.347	3.067	0.593
K3-friendly-B	0.000	0.997	0.415	0.657	0.440	2.644	0.000	0.000	0.602	0.620	0.000
	0.000	0.574	0.155	0.445	0.000	1.613	0.000	0.000	0.297	0.439	0.000
	0.767	1.197	0.632	1.259	0.744	3.031	0.081	0.384	1.024	0.889	0.132
	0.000	0.248	0.000	0.000	0.000	0.403	0.000	0.000	0.000	0.000	0.000
	2.579	1.936	0.872	1.524	1.413	6.062	0.458	0.545	1.778	1.273	0.791
K3-free-B	0.000	0.410	0.496	0.502	0.545	2.897	0.082	0.000	0.803	1.117	0.022
	0.000	0.220	0.434	0.000	0.000	2.286	0.000	0.000	0.000	0.774	0.000
	0.000	0.848	0.609	0.842	0.876	3.646	0.180	0.467	0.985	2.453	0.636
	0.000	0.000	0.163	0.000	0.000	1.760	0.000	0.000	0.000	0.000	0.000
	0.351	1.059	0.618	0.914	1.335	5.014	0.213	0.701	1.301	4.421	0.959

371
372
373
374
375

	45	46	47	48	49	50	51	52	53	54
	<i>Dielma fastidiosa</i>	<i>Turicibacter</i>	<i>colarctobacte</i>	<i>Dialister</i>	<i>Veillonella</i>	<i>Fusobacterium</i>	<i>Saccharimonadaceae</i>	<i>Parasutterella:herichia/Shige</i>	<i>Enterobacteriaceae</i>	
K1-E	0.000	0.127	0.000	0.198	0.659	0.000	0.052	0.065	0.701	0.000
	0.000	0.000	0.000	0.010	0.126	0.000	0.005	0.000	0.243	0.000
	0.103	0.154	0.275	0.483	1.033	0.013	0.107	0.282	1.733	0.044
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.105	0.366	0.725	0.543	1.746	0.052	0.148	0.796	6.094	0.346
K2-E	0.054	0.000	0.000	0.047	0.304	0.000	0.008	0.100	0.821	0.000
	0.016	0.000	0.000	0.000	0.019	0.000	0.000	0.000	0.415	0.000
	0.148	0.134	0.048	0.233	0.970	0.000	0.033	0.531	3.503	0.078
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.231	0.924	0.649	0.331	1.043	0.029	0.116	1.409	15.267	0.165
K3-friendly-E	0.000	0.000	0.107	0.011	0.128	0.000	0.000	0.448	1.876	0.026
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.495	0.000
	0.035	0.103	0.605	0.311	1.079	0.023	0.035	1.525	3.469	0.545
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.109	0.000
	0.297	0.625	0.847	0.561	1.833	0.406	0.114	4.622	13.689	0.732
K3-free-E	0.080	0.000	0.000	0.246	0.493	0.000	0.000	0.369	0.717	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.371	0.000
	0.110	0.058	0.101	0.339	1.103	0.000	0.021	0.818	0.903	0.080
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.174	0.000
	0.218	0.624	0.104	0.514	1.673	0.260	0.062	0.880	1.169	0.240
K1-B	0.006	0.000	0.041	0.000	0.156	0.000	0.029	0.075	0.381	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.136	0.071	0.214	0.213	0.866	0.000	0.065	0.630	1.032	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.358	0.436	0.636	0.471	1.112	0.039	0.110	1.112	10.716	0.465
K2-B	0.097	0.000	0.000	0.098	0.104	0.000	0.022	0.089	0.650	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.367	0.000
	0.279	0.203	0.000	0.378	0.320	0.073	0.038	0.454	3.476	0.041
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.977	0.714	1.048	0.479	0.818	0.216	0.169	1.354	12.195	0.387
K3-friendly-B	0.000	0.000	0.046	0.127	0.372	0.000	0.000	0.061	1.073	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.607	0.000
	0.062	0.133	0.319	0.318	0.712	0.000	0.103	0.554	3.609	0.175
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.331	0.980	0.964	0.451	1.742	0.501	0.222	0.947	33.980	1.069
K3-free-B	0.000	0.000	0.000	0.150	0.354	0.000	0.000	0.000	0.779	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.279	0.000
	0.096	0.000	0.000	0.335	1.196	0.000	0.000	1.223	4.078	0.000
	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
	0.161	0.015	0.290	0.385	1.441	0.295	0.087	1.556	5.905	0.817