

1 **Additional file 4**

Response (Gene expression vs. Fat intake)	Proximal			Middle			Distal		
	Gene (count)	Relative %	GOBP (count)	Gene (count)	Relative %	GOBP (count)	Gene (count)	Relative %	GOBP (count)
Linear	1219	48.18	6	1439	50.03	16	366	50.76	3
Logarithmic	719	28.42	7	443	15.40	11	45	6.24	-
Exponential	148	5.85	2	461	16.03	17	121	16.78	6
Quadratic	212	8.38	-	326	11.34	-	85	11.79	-
Cubic	232	9.17	1	207	7.20	-	104	14.42	4

2

3 **Table A4: Count of genes that responded in a significant, dose-dependent way to fat intake (model**
4 **selection based on AIC).** We identified the significant responses in three sections of small intestine (limma
5 library, adjusted p-value < 0.1). Differential gene expression was modelled as either a linear or nonlinear
6 (i.e., logarithmic, exponential, quadratic or cubic) function of dietary fat intake. For each section, we
7 reported the percentage of genes per response type (%) and the number of significant GO terms (Biological
8 Processes - GOBP; hypergeometric test, adjusted p-value < 0. 1). Only GOBP terms with, at least, six
9 differentially expressed genes (in the whole small intestine) have been taken into account. Outcomes
10 obtained by using AIC for model selection were coherent with the trends reported in the manuscript (i.e.,
11 model selection based on the lowest p-value; see Table 1). In particular, with AIC we found: (I) the
12 prevalence of linear-responding genes in all intestine sections; (II) the decreasing relative importance of the
13 logarithmic response when moving from the proximal to the distal section (while the opposite pattern
14 holds for the exponential response); (III) the marginal relevance of other response types (i.e., quadratic and
15 cubic functions).