

Apc^{Min/+} tumours and normal mouse small intestines show linear metabolite concentration and DNA cytosine hydroxymethylation gradients from pylorus to colon

Basetti Madhu, Santiago Uribe-Lewis, Martin Bachman, Adele Murrell and

John R Griffiths

Supplementary Material

Table S1. Statistical significance of slopes of metabolite gradients between tissues.
 WT = wild-type C57BL/6J, NAdj = normal tissue adjacent to *Apc^{Min/+}* tumours. t-Cho, choline + phosphocholine + glycerophosphocholine; t-Cr, creatine + phosphocreatine.

Metabolite	WT vs NAdj slopes	Tumour vs NAdj slopes
	p-value	p-value
Choline	0.4828	0.0053
Phosphocholine	0.1779	0.2538
Glycero-phosphocholine	0.1329	0.4096
t-Cho	0.0757	0.9489
Creatine	0.2066	0.0382
t-Cr	0.4194	0.0723
Glutamate	0.1963	0.1305
Glycine	0.2855	0.0052
Taurine	0.3301	0.4175
Leucine	0.2604	0.7754
Valine	0.6008	0.6676

Table S2. Statistical significance of Y-intercepts of metabolite gradients between tissues.
 WT = wild-type C57BL/6J, NAdj = normal tissue adjacent to *Apc*^{Min/+} tumours. t-Cho, choline + phosphocholine + glycerophosphocholine; t-Cr, creatine + phosphocreatine.

Metabolite	Y-intercept				
	WT	NAdj	WT vs Nadj p-value	Tumour	Tumour vs Nadj p-value
Choline	1.66	1.60	0.6724	1.22	N/A
Phosphocholine	1.71	1.20	0.0956	1.57	0.22
Glycero-phosphocholine	1.94	1.58	0.9147	2.50	0.0082
t-Cho	5.36	4.26	0.1110	5.27	0.0004
Creatine	2.60	2.19	0.0262	2.28	N/A
t-Cr	2.61	2.34	0.1903	2.71	<0.0001
Glutamate	2.49	2.41	0.0176	4.24	<0.0001
Glycine	1.76	2.12	0.3397	2.38	N/A
Taurine	6.34	7.39	0.0740	7.59	0.4976
Leucine	1.09	1.25	0.7884	1.65	0.0003
Valine	0.73	0.83	0.4637	1.04	0.076

Table S3. Mean concentrations of metabolite in wild type C57BL/6J tissues (WT), normal tissue adjacent to *Apc*^{Min/+} tumours (NAdj) and *Apc*^{Min/+} Tumour tissue. t-Cho, choline + phosphocholine + glycerophosphocholine; t-Cr, creatine + phosphocreatine.

Metabolite	WT v NAdj			NAdj vs Tumour		
	WT	NAdj	t-test	NAdj	Tumour	t-test
	Mean + 1 s.e.m.	Mean + 1 s.e.m.		Mean + 1 s.e.m.	Mean + 1 s.e.m.	
Choline	0.959+ 0.086	1.085+ 0.093	0.3339	1.085+ 0.093	1.081+ 0.050	0.9649
Phosphocholine	1.564+ 0.091	1.377+ 0.095	0.1711	1.377+ 0.095	1.532+ 0.069	0.2110
Glycerophosphocholine	1.965+ 0.090	1.973+ 0.133	0.9581	1.973+ 0.133	2.674+ 0.187	0.0025
t-Cho	4.519+ 0.177	4.204+ 0.178	0.2196	4.204+ 0.178	5.158+ 0.171	0.0003
Creatine	2.025+ 0.078	1.849+ 0.081	0.1321	1.849+ 0.081	2.309+ 0.101	0.0006
t-Cr	2.168+ 0.075	2.044+ 0.083	0.2787	2.044+ 0.083	2.781+ 0.081	<0.0001
Glutamate	2.819+ 0.108	2.423+ 0.102	0.0120	2.423+ 0.102	4.906+ 0.144	<0.0001
Glycine	1.731+ 0.0705	1.846+ 0.126	0.3999	1.846+ 0.126	2.924+ 0.129	<0.0001
Taurine	6.542+ 0.213	7.111+ 0.216	0.0692	7.111+ 0.216	6.808+ 0.253	0.3630
Leucine	0.8692+ 0.055	0.922+ 0.075	0.5621	0.922+ 0.075	1.38+ 0.113	0.0009
Valine	0.5886+ 0.041	0.650+ 0.055	0.3637	0.650+ 0.055	0.777+ 0.074	0.1764

Table S4. Statistical significance of DNA cytosine hydroxymethylation (5hmC) and methylation (5mC) slopes by tissue. 5hmC = hydroxymethylation, 5mC = methylation, WT = wild-type C57BL/6J, NAdj = normal tissue adjacent to Tumour in *Apc*^{Min/+}.

	5hmC			5mC		
	WT	NAdj	Tumour	WT	NAdj	Tumour
Slope	-0.0001	0.0004	0.0002	-0.0008	-0.0014	0.0133
Is slope significantly non-zero? P-values	0.6017	0.0756	0.0499	0.8884	0.8224	0.0819

Table S5. Statistical significance of DNA cytosine hydroxymethylation (5hmC) and methylation (5mC) slopes between tissues. WT = wild-type C57BL/6J, NAdj = normal tissue adjacent to Tumour in *Apc*^{Min/+}.

	WT vs NAdj			NAdj vs Tumour		
	WT slope	NAdj slope	p-value	NAdj slope	Tumour slope	p-value
5hmC	-0.0001	0.0004	0.0869	0.0004	0.0002	0.4429
5mC	-0.0008	-0.0014	0.9485	-0.0014	0.0133	0.1373

Fig S1. Method for obtaining samples for measurements of metabolite concentrations and DNA modifications. An example of a small intestine whole-mount with the gastro-duodenal junction at the top of the left hand mount and the caecum and colon in the right hand mount. The caecum and colon (far right) were not assessed. Tissues from WT and *Apc^{Min/+}* animals were dissected at measured distances from the stomach, and were then used for metabolite and DNA modification analyses.



Dissect
normal tissues
and tumours.

HR-MAS ¹H NMR



Recover tissues
(where possible),
extract DNA.

LC-MS

Fig S2. Plot of metabolite concentrations in WT gut tissues as a measure of tissue dissection order. Small intestine tissues were dissected proximal to distal from the pylorus (top to bottom) or distal to proximal (bottom to top) to assess whether metabolite concentrations would be dependent on time to snap freeze in liquid nitrogen. PC, phosphocholine; GPC, glycerophosphocholine.

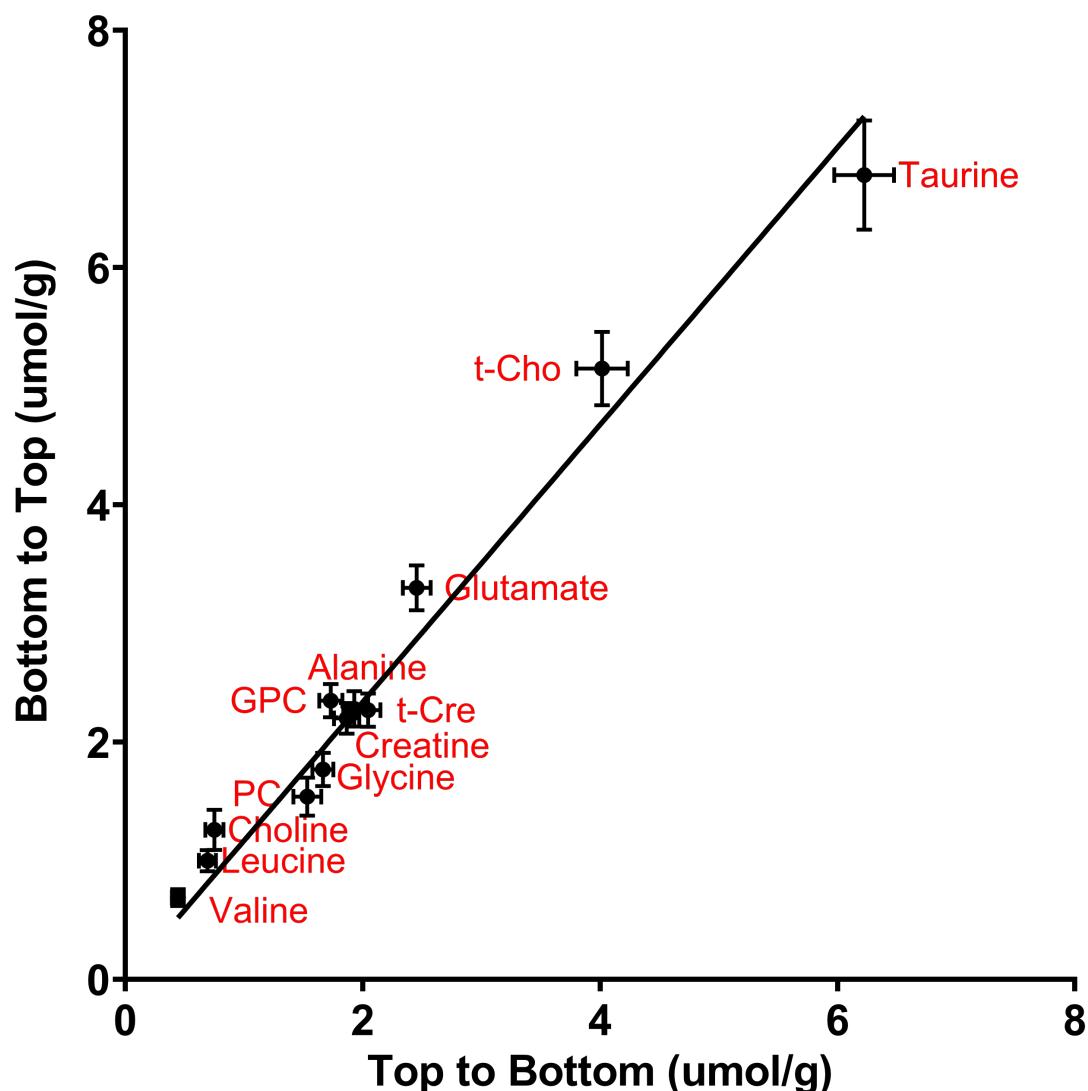


Fig S3. Plot of metabolite concentrations in normal tissue adjacent to tumours (NAdj) and Tumour tissues along the small intestine as a function of distance from pylorus. t-Cho, choline + phosphocholine + glycerophosphocholine; t-Cr, creatine + phosphocreatine.

