

Table S1 . ATG16L1 T300A frequency with respect to ethnicity

Ethnicity	n	ATG16L1 genotypic frequency			Allelic frequency	
		AA	AG	GG	A allele	G allele
European American (CEU)	224	0.15	0.56	0.29	0.43	0.58
SW American res. African Ancestry (ASW)	98	0.49	0.45	0.06	0.71	0.29
CA res. Mexican Ancestry (MEX)	100	0.52	0.36	0.12	0.7	0.3
Luhya, Kenyan (LWK)	178	0.63	0.32	0.06	0.79	0.21
Yoruban (YRI)	226	0.55	0.36	0.09	0.73	0.27
Japanese (JPT)	172	0.62	0.35	0.04	0.79	0.21
Han Chinese (CHB)	86	0.4	0.44	0.16	0.62	0.38

*NCBI dbSNP and HapMap data

Table S2: Association of ATG16L1 genotype with clinicopathologic characteristics in colon and rectal cancers

Factor	African Americans			Caucasians			<i>P</i>
	ATG16L1 genotype	AA	AG	GG	AA	AG	
Genootypic frequency	92 (45%)	83 (41%)	27 (13%)	65 (28%)	123 (47%)	72 (28%)	<0.001*
Age	mean ± SD	66.5 ± 12.4	68.1 ± 11.7	68.7 ± 11.5	61.0 ± 15.9	63.9 ± 13.5	60.1 ± 13.1
Sex	Male	42 (46%)	29 (35%)	14 (52%)	0.19	39 (60%)	73 (59%)
	Female	50 (54%)	54 (65%)	13 (48%)	26 (40%)	50 (41%)	38 (53%)
Grade	I	15 (16%)	13 (16%)	4 (15%)	0.96	11 (17%)	20 (16%)
	II	58 (63%)	55 (68%)	17 (63%)	38 (57%)	61 (50%)	41 (57%)
	III	18 (17%)	13 (13%)	5 (15%)	5 (16%)	10 (24%)	4 (21%)
	Unk	3 (3%)	4 (5%)	2 (7%)	6 (10%)	12 (1%)	4 (6%)
AJCC stage	Stage I	17 (18%)	16 (19%)	6 (22%)	0.74	18 (27%)	22 (18%)
	Stage II	25 (27%)	25 (30%)	11 (41%)	20 (30%)	41 (33%)	22 (31%)
	Stage III	29 (32%)	27 (33%)	8 (30%)	19 (30%)	35 (28%)	27 (38%)
	Stage IV	19 (21%)	12 (14%)	2 (7%)	6 (10%)	21 (17%)	6 (8%)
	Unk	2 (2%)	3 (4%)	0 (0%)	2 (3%)	4 (3%)	2 (3%)
Anatomic site	Colon	78 (85%)	71 (86%)	24 (85%)	0.5	44 (67%)	73 (59%)
	Rectum	14 (15%)	10 (12%)	3 (11%)	20 (32%)	50 (41%)	40 (56%)
	Unk	0 (0%)	2 (%)	0 (0%)	1 (2%)	0 (0%)	0 (0%)
Follow-up months		38.2 ± 34.9	39.1 ± 33.0	58.1 ± 44.5	0.03*	34.7 ± 33.7	41.6 ± 37.0
						42.7 ± 37.2	0.37*
							0.76*

Data represented as n (%). Categorical variables analyzed by chi-square test.

**Analysis of race as the independent variable with respect to indicated factor

*One-way ANOVA

Table S3. Association of ATG16L1 genotype with tumor clinicopathology in colon cancer

Factor		AA	AG	GG	P
Race	Caucasian	42 (35%)	73 (51%)	40 (63%)	<0.001
	African American	78 (65%)	71 (49%)	24 (37%)	
Grade	I	21 (18%)	25 (17%)	8 (13%)	0.96
	II	70 (58%)	85 (59%)	40 (63%)	
	III	23 (19%)	27 (19%)	14 (22%)	
	Unk	6 (5%)	7 (5%)	2 (3%)	
AJCC stage	Stage I	27 (23%)	28 (19%)	12 (19%)	0.32
	Stage II	30 (25%)	45 (31%)	25 (39%)	
	Stage III	37 (31%)	38 (26%)	21 (33%)	
	Stage IV	23 (19%)	31 (22%)	5 (8%)	
	Unk	3 (3%)	2 (1%)	1 (2%)	
Stage IV	Stage I-III	97 (81%)	113 (78%)	59 (92%)	0.05
	Stage IV	23 (19%)	31 (22%)	5 (8%)	
Follow-up months		39.2 ± 37.9	41.9 ± 36.8	53.8 ± 45.3	*0.048

Data represented as n(%). Categorical variables analyzed by chi-squared test

*One-way ANOVA

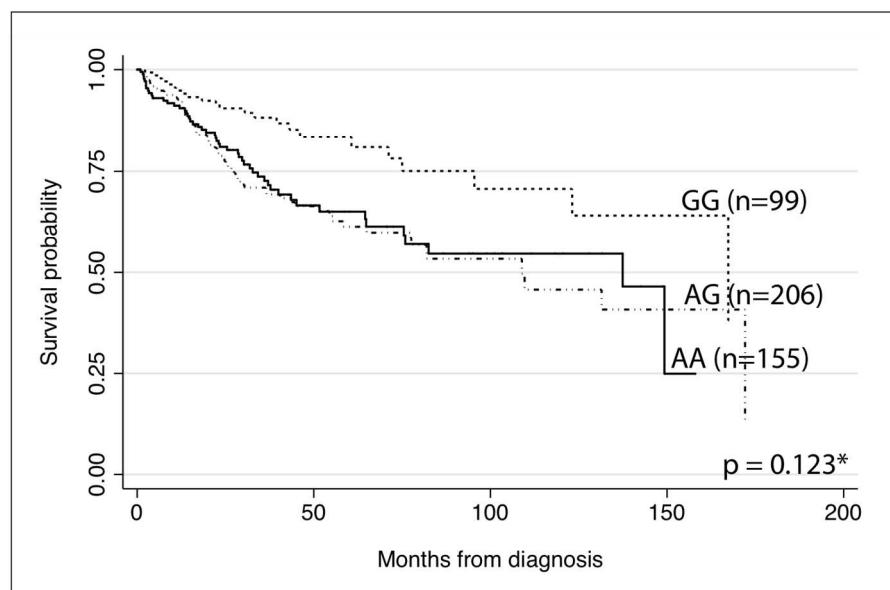
Table S4. Cox regression analysis of prognostic factors with respect to overall survival

Factor	n	Univariate		Multivariate	
		HR (95% CI)	P	HR (95% CI)	P
Age	460	1.0 (1.0-1.0)	<0.001	1.0 (1.0-1.0)	<0.001
Gender	Male	235	1†	—	—
	Female	227	1.0 (0.75-1.5)	0.79	—
Race	Caucasian	260	1†	1†	—
	African American	202	1.5 (1.1-21.0)	0.012	1.7 (1.2-2.5) 0.007
AJCC stage	Stage I	94	1†	1†	—
	Stage II	144	1.6 (0.87-3.1)	0.12	1.3 (0.7-2.6) 0.38
	Stage III	145	2.4 (1.3-4.4)	0.004	1.9 (1.0-3.7) 0.04
	Stage IV	66	12.9 (7.0-24.0)	<0.001	11.8 (6.1-22.9) <0.001
Grade	I	75	1†	1†	—
	II	270	1.9 (1.0-3.3)	0.04	1.4 (0.75-2.5) 0.32
	III	86	3.0 (1.6-5.7)	0.001	2.2 (1.1-4.4) 0.02
Location	Colon	330	1†	1†	—
	Rectum	129	0.51 (0.32-0.82)	0.005	1.3 (0.74-2.1) 0.4
ATG16L1	AA	157	1†	1†	—
Genotype	AG	206	0.85 (0.59-1.2)	0.39	0.88 (0.6-1.3) 0.51
	GG	99	0.55 (0.34-0.90)	0.017	0.73 (0.43-1.2) 0.22

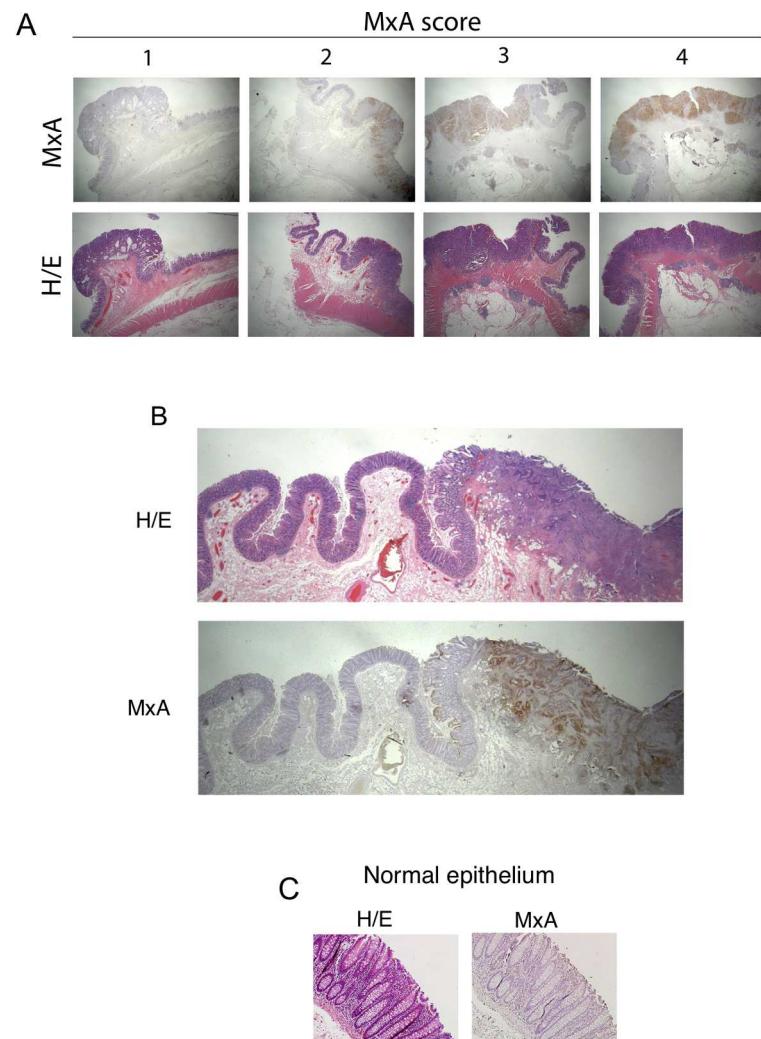
Hazard ratios (HR) and 95% confidence intervals (95% CI) were obtained from univariate and multivariate Cox regression analysis

†Reference

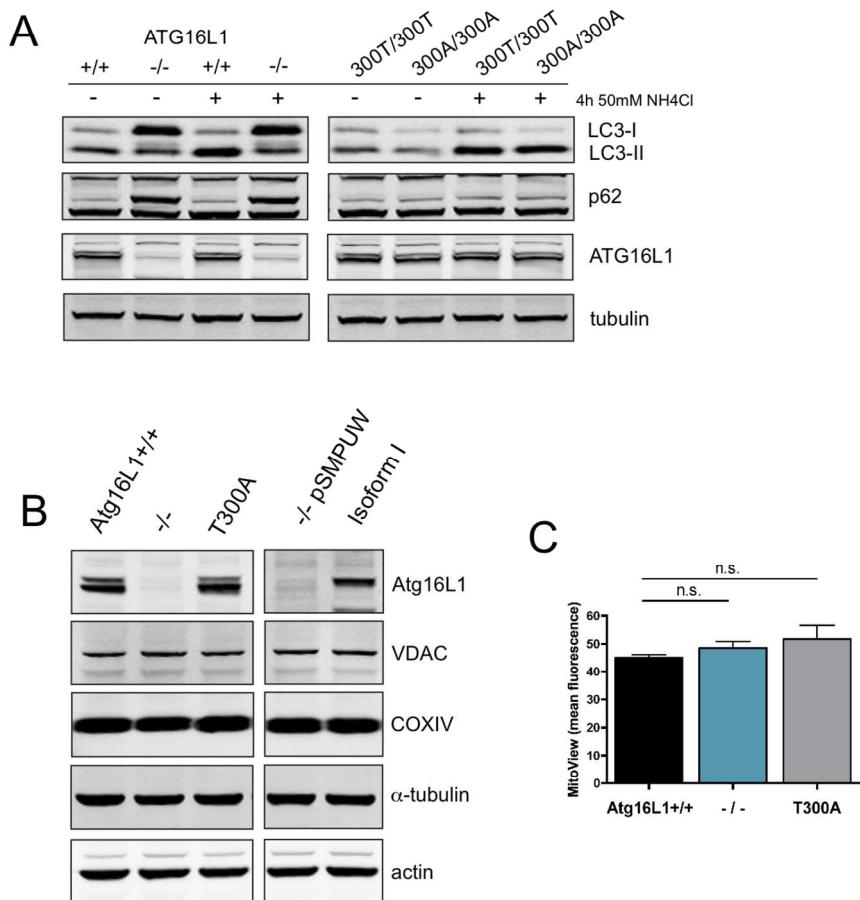
Supplementary Figure 1.



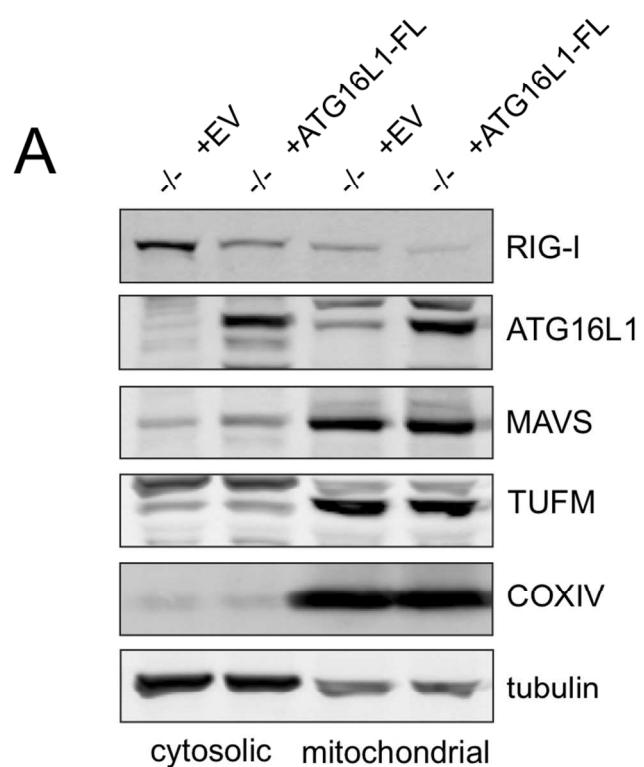
Supplementary Figure 2.



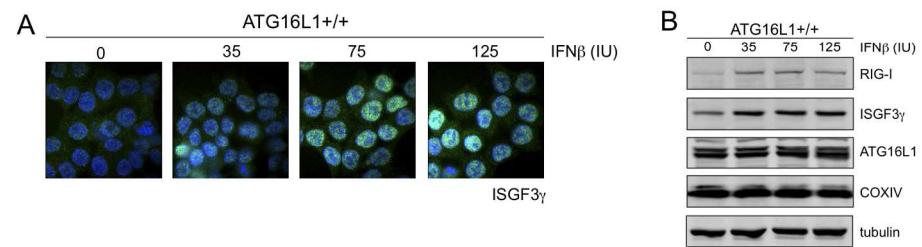
Supplementary Figure 3.



Supplementary Figure 4.



Supplementary Figure 5.



Supplementary Figure 6.

