

# SUPPLEMENTARY INFORMATION

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Supplementary Table 1 - Allele and genotype frequencies of wild type (A/A) and mutant (G/G) genotypes of ATG16L1 SNP id rs2241880 in all cohorts of EBV transformed B cell lines available in the HapMap project.

Population	Genotype frequencies						Allele frequencies										
	genotype	freq	count	genotype	freq	count	genotype	freq	count	Total	allele	Ref-allele	count	allele	Other-allele	freq	count
ASW (A)	A/A	0.526	30	A/G	0.421	24	G/G	0.053	3	57	A	0.737	84	G	0.263	30	114
CEU (C)	A/A	0.152	17	A/G	0.562	63	G/G	0.286	32	112	A	0.433	97	G	0.567	127	224
CHB (H)	A/A	0.419	57	A/G	0.441	60	G/G	0.14	19	136	A	0.64	174	G	0.36	98	272
CHD (D)	A/A	0.583	63	A/G	0.361	39	G/G	0.056	6	108	A	0.764	165	G	0.236	51	216
GIH (G)	A/A	0.277	28	A/G	0.485	49	G/G	0.238	24	101	A	0.52	105	G	0.48	97	202
JPT (J)	A/A	0.593	67	A/G	0.372	42	G/G	0.035	4	113	A	0.779	176	G	0.221	50	226
LWK (L)	A/A	0.624	68	A/G	0.312	34	G/G	0.064	7	109	A	0.78	170	G	0.22	48	218
MEX (M)	A/A	0.526	30	A/G	0.351	20	G/G	0.123	7	57	A	0.702	80	G	0.298	34	114
MKK (K)	A/A	0.494	77	A/G	0.462	72	G/G	0.045	7	156	A	0.724	226	G	0.276	86	312
TSI (T)	A/A	0.15	15	A/G	0.62	62	G/G	0.23	23	100	A	0.46	92	G	0.54	108	200
YRI (Y)	A/A	0.558	82	A/G	0.367	54	G/G	0.075	11	147	A	0.741	218	G	0.259	76	294

Note: the 'reference' allele is the base observed in the reference genome sequence at this location

**Population descriptors:**

- ASW (A): African ancestry in Southwest USA
- CEU (C): Utah residents with Northern and Western European ancestry from the CEPH collection
- CHB (H): Han Chinese in Beijing, China
- CHD (D): Chinese in Metropolitan Denver, Colorado
- GIH (G): Gujarati Indians in Houston, Texas
- JPT (J): Japanese in Tokyo, Japan
- LWK (L): Luhya in Webuye, Kenya
- MEX (M): Mexican ancestry in Los Angeles, California
- MKK (K): Maasai in Kinyawa, Kenya
- TSI (T): Tuscan in Italy
- YRI (Y): Yoruban in Ibadan, Nigeria

Supplementary Table 2 - Allele and genotype frequencies of indicated SNPs in the CEU cohort of the HapMap project.

chromosome	position	strand	marker id	Gene	alleles	genotyping center/platform	genotyping platform	total allele count	total genotype count
chr5	150208191+		rs10065172	IRGM	C/T	perlegen/Perlegen	Perlegen	118	59
chr9	138389159+		rs10781500	CARD9	C/T	sanger/Illumina_1M	Illumina_1M	226	113
chr9	138383712+		rs10870077	CARD9	C/G	illumina/BeadArray	BeadArray	120	60
chr1	67478546+		rs11209026	IL23R	A/G	sanger/Illumina_1M	Illumina_1M	220	110
chr12	39078567+		rs11564258	MUC19/LRRK2	A/G	broad/AFFY_6.0	AFFY_6.0	226	113
chr2	233848107+		rs2241880	ATG16L1	A/G	sanger/Illumina_1M	Illumina_1M	224	112
chr9	138386317+		rs4077515	CARD9	C/T	sanger/Illumina_1M	Illumina_1M	226	113
chr2	102429801+		rs6708413	IL18RAP	A/G	broad/AFFY_6.0	AFFY_6.0	226	113

Gene	reference homozygote genotype	reference allele	reference allele freq.	reference allele count	reference homozygote genotype frequency	reference homozygote genotype count
IRGM	C/C	C	0.975	115	0.949	56
CARD9	C/C	C	0.513	116	0.248	28
CARD9	C/C	C	0.475	57	0.217	13
IL23R	G/G	G	0.959	211	0.918	101
MUC19/LRRK2	G/G	G	0.973	220	0.947	107
ATG16L1	A/A	A	0.433	97	0.152	17
CARD9	C/C	C	0.518	117	0.257	29
IL18RAP	G/G	G	0.204	46	0.035	4

Gene	heterozygote genotype	heterozygote frequency	heterozygote genotype count
IRGM	C/T	0.051	3
CARD9	C/T	0.531	60
CARD9	C/G	0.517	31
IL23R	A/G	0.082	9
MUC19/LRRK2	A/G	0.053	6
ATG16L1	A/G	0.562	63
CARD9	C/T	0.522	59
IL18RAP	A/G	0.336	38

Gene	other homozygote genotype	other allele	other allele freq.	other allele count	other homozygote genotype frequency	other homozygote genotype count
IRGM	T/T	T	0.025	3	0	0
CARD9	T/T	T	0.487	110	0.221	25
CARD9	G/G	G	0.525	63	0.267	16
IL23R	A/A	A	0.041	9	0	0
MUC19/LRRK2	A/A	A	0.027	6	0	0
ATG16L1	G/G	G	0.567	127	0.286	32
CARD9	T/T	T	0.482	109	0.221	25
IL18RAP	A/A	A	0.796	180	0.628	71

**Supplementary Table 3 - NCBI accession IDs and descriptions of ATG16L protein used in multiple sequence analysis by COBAL.**

Accession	Description
NP_110430.5	Homo sapiens ATG16L1a
NP_060444.3	Homo sapiens ATG16L1b
NP_942593.2	Homo sapiens ATG16L1g
NP_001192320.1	Mus musculus ATG16L1a
NP_084122.2	Mus musculus ATG16L1b
NP_001192321.1	Mus musculus ATG16L1g
NP_001102279.2	Rattus norvegicus ATG16L1
NP_001091437.1	Xenopus laevis ATG16L1
NP_001017854.1	Danio rerio ATG16L1
NP_733311.2	Drosophila melanogaster ATG16L1a
NP_733312.2	Drosophila melanogaster ATG16L1b
NP_733313.2	Drosophila melanogaster ATG16L1c
NP_508768.1	Caenorhabditis elegans ATG16L1
AAB70659.1	Dictyostelium discoideum ATG16
NP_001051251.1	Oryza sativa OS03g0746600
NP_013882.1	Saccharomyces cerevisiae ATG16p

**Supplementary Table 4** - *Atg16l1* genotyping of indicated cell lines. RAW264.7 cells are murine, thus presence of the T316A allele (A>G) is not expected.

Cell line	<i>Atg16l1</i> genotype (A=wildtype; G=mutant)
HeLa	A/A
HCT116 Bax <sup>+/+</sup>	A/A
HCT116 Bax <sup>-/-</sup>	A/A
MCF-7	A/G
RAW264.7 (murine)	A/A

<b>ON-TARGETplus, Human CASP3 (Thermo Scientific)</b>	
<i>siRNA</i>	<i>Target Sequence</i>
J-0034307-06	CCGACAAGCUUGAAUUUUAU
J-0034307-08	GAAUUGAUGCGUGAUGUUU
<b>ON-TARGETplus SMARTpool, Human CASP7 (Thermo Scientific)</b>	
<i>siRNA</i>	<i>Target Sequence</i>
J-004407-06	GGGCAAUGCAUCAUAAUA
J-004407-07	GAUCAGGGCUGUAUUGAAG
J-004407-08	UACCGUCCCUUCAGUAA
J-004407-09	CCAGACCGGUCCUGUUUG
<b>Human CASP8 siRNA generated in-house at Genentech, Inc.</b>	
<i>siRNA</i>	<i>Target Sequence</i>
D-003466-02	CAACGACUAUGAAGAAUUC
<b>ON-TARGETplus, Human CASP9 (Thermo Scientific)</b>	
<i>siRNA</i>	<i>Target Sequence</i>
J-003309-05	GAGUCAGGCUCUCCUUUG
J-003309-06	CGGUGAAAGGGAUUUUAUA
<b>ON-TARGETplus Non-targeting siRNA #1 (Thermo Scientific)</b>	
<i>siRNA</i>	<i>Sequence</i>
D-001810-01	UGGUUUACAUGUCGACUAA

**Supplementary Table 5** – siRNA target sequences used in study. Above sequences were pooled at 1:1 ratio for each Caspase indicated. Caspase 3 knockdown was achieved by pooling 2 siRNAs; Caspase 7 knockdown was achieved by using a SMARTpool of 4 siRNAs; Caspase 8 knockdown was achieved by using a single siRNA; Caspase 9 knockdown was achieved by pooling 2 siRNAs.