

Supplemental Information

AUTOPHAGOPATHIES: FROM AUTOPHAGY GENE POLYMORPHISMS TO PRECISION MEDICINE FOR HUMAN DISEASES Iris Grosjean and Barnabé Roméo *et al.*

Supplementary tables

Table S1. List of autophagy-related genes and regulators investigated in this study.

<ul style="list-style-type: none"> ULK1 ULK2 ATG13 RB1CC1 ATG101 SMCR8 TBC1D14 WDR41 C9orf72 <p style="text-align: center;">I. ULK1/2 complex</p>	<ul style="list-style-type: none"> PIK3C3/VPS34 PIK3R4/VPS15 BECN1 ATG14 UVRAG <hr/> <ul style="list-style-type: none"> AMBRA1 MCL1 NRBF2 RUBCN RUBCNL SH3GLB1/BIF-1 VMP1 <p style="text-align: center;">II. PtdIns3K complex</p>	<ul style="list-style-type: none"> ATG2A ATG2B ATG9A ATG9B WIPI1 WIPI2 WDR45B WDR45 ZFYVE1/DFCP1 <p style="text-align: center;">III. ATG9 complex</p>	<ul style="list-style-type: none"> ATG5 ATG7 ATG10 ATG12 ATG16L1 ATG16L2 <hr/> <ul style="list-style-type: none"> TP53INP2 <p style="text-align: center;">IV. ATG12 conj</p>	<ul style="list-style-type: none"> EGR1 MAP1LC3A MAP1LC3B MAP1LC3B2 MAP1LC3C GABARAP GABARAPL1 GABARAPL2 GABARAPL3 ATG3 ATG4A ATG4B ATG4C ATG4D <p style="text-align: center;">V. LC3 conjugation system</p>	<ul style="list-style-type: none"> CALCOCO2 DRAM1 FUNDC1 NBR1 NCOA4 NUFIP1 NIPSNAP1 NIPSNAP2 OPTN SQSTM1 TAX1BP1 TOLLIP UBQLN2 WDFY3/ALFY <p style="text-align: center;">VI. Autophagy receptors</p>
<ul style="list-style-type: none"> LAMP1 LAMP2 CHMP2B 					

Tables S2-S7. Association between common genetic polymorphisms in the autophagy-related genes and human diseases (risk, prognosis, theragnosis). ATG SNP (single-nucleotide polymorphism) and their functional annotation (promoter, 5', 3', missense mutations, transcription factor, and miRNA binding sites) were retrieved using PubMed, litvar [1], HaploReg [2,3], and GTEX [4] (eQTLs).

Table S2. ULK1/2 complex.

Table S3. PtdIns3K Complex.

Table S4. ATG9 system.

Table S5. LC3-conjugation system.

Table S6. ATG12-conjugation system.

Table S7. Autophagy receptors.



Related to theragnosis (side effects, toxicity, efficacy), overall survival (OS), and progression-free survival (PFS).



Related to bacterial infection or



viral infection or



parasite infection



Related to air pollution or



coal exposure, or



smoking.



Related to aging



Related to autoimmune and autoinflammatory diseases.

Abbreviations: ALS-FTD, amyotrophic lateral sclerosis, and frontotemporal dementia; Alt, alternate allele; ccRCC, clear cell renal cell carcinoma; CD, Crohn disease; exp, expression; (eQTL): eQTL in different tissue of that affected by the disease; HCC, hepatocellular carcinoma; HNSCC, head and neck squamous cell carcinoma; LD, linkage disequilibrium; MAF, minor allele frequency in European (Eur) or Asian (As) populations; NPC, nasopharyngeal carcinoma; NSCLC, non-small cell lung cancer; Ref, reference allele; SLE, systemic lupus erythematosus.

Table S2. *ULK1/2* complex – AUTOPHAGY.

Gene	SNP (rs)	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX	
<i>ULK1</i> NM_003565.1 93 eQTL	rs9481	A	G	86%	10	 TUBERCULOSIS [5] Protective	Asians	3'UTR	(eQTL)	
	rs7138581	G	C	13%	5	 RISK and SEVERITY	Asians	3'UTR	(eQTL)	
	rs12297124	G	T	8%	4	 TUBERCULOSIS [6] Protective	Asians	Intronic	(eQTL) ↑ exp[6]	
	rs7300908	C	T	2% As 8%	1		Asians	Intronic	(eQTL) ↑ exp[6]	
	rs4964879	G	A	10%	1	 ANKYLOSING SPONDYLITIS [7] Protective	Asians	Intronic	eQTL- Nerve	
	rs11246867	G	A	6%	23	 Age-related MACULAR DEGENERATION [8] Theragnostic (anti-VEGF)	Europeans	5' <i>ULK1</i>		
	rs3088051	T	C	29%	1			 CROHN DISEASE [9] Complications	Oceania	3'UTR
	rs7488085	T	G	6%	23	 CROHN DISEASE [9] Protective	Oceania	Intronic	(eQTL)	
	rs10902469	G	C			 ASTHMA [10]		Americans	Intronic	(eQTL)
	rs10902472	C	T			 ASTHMA [10]		Americans	Intronic	(eQTL)
	rs7487166	A	G	81%	12	 ANKYLOSING SPONDYLITIS [7]	Asians	Intronic	(eQTL)	
	rs9652059	T	C			 ASTHMA [10]	Americans	synonymous	eQTL - colon	
	rs11616018	C	T			 CROHN DISEASE [9] Weak association	Oceania			
	rs7953348	C	T			 CROHN DISEASE [9] Weak association	Oceania	Intronic	(eQTL)	
						 NON SMALL CELL LUNG CANCER (NSCLC) [11] Theragnostic (Platinum-based chemotherapy)	Asians			

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX	
ULK1 NM_003565.1 93 eQTL	rs12303764	T	G	36%	1	 CROHN DISEASE [9,12] NSCLC [11] Theragnostic (platinum-based chemotherapy)	Europeans, and Oceanians Asians	Intronic	eQTL - colon	
	CANCERS. Thirty-six missense somatic mutations of <i>ULK1</i> are co-occurring with mutations in a large number of ULK1 interactors or substrates. Of the mutations, 50% in the ULK1 kinase domain are predicted to affect protein stability and kinase activity (S184F, D102N, and A28V). Consistently, <i>ULK1</i> acts as an oncogene in gastric cardiac adenocarcinoma. Silencing <i>ULK1</i> can significantly suppress cancer cell proliferation, migration and invasion [13,14].									
	rs55815560	C	T	1%	1	 SCHIZOPHRENIA [15] A highly heritable psychiatric disorder, combining these 4 SNPs. No variant was individually statistically significant	Europeans	MISSENSE S665L		
	rs145279005	C	T	1%	1			MISSENSE A705V		
	rs145451295	C	T	1%	2			MISSENSE T242I		
rs188342389	C	T	0%	6	Intron <i>MMP17</i> missense					
ULK2 NM_014683 1450 eQTL	rs281357	T	C	64%	1	PARKINSON DISEASE [16]	American GWAS	Intronic	eQTL-Nerve	
	rs281366	C	T	3%	3	 ACUTE LYMPHOBLASTIC LEUKEMIA [17] Theragnostic (asparaginase-associated pancreatitis)	Europeans	5' <i>ULK2</i>	(eQTL)	
ATG13 NM_014741 4655 eQTL	rs7484002	A	G	17%	130	 ↑ DNA damage [18]	Asians	Intronic	eQTL- Skin ↓ exp [18]	
	rs10838611	G	C	57%	2	 BREAST CANCER (TNBC) [19] Theragnostic (asparaginase-associated pancreatitis)	Asians	3'-UTR		
	rs4565870	T	C	30%	5	SELECTIVE IMMUNOGLOBULIN A DEFICIENCY [20]	European GWAS		eQTL	
	rs35619591	G	A	1%	1	 TYPE 2 DIABETES [21] Insulin processing	European American GWAS	MISSENSE G433R		
RB1CC1/FIP200 NM_014781 68 eQTL	rs1129660	A	G	21%	19	 COLORECTAL CANCER [22] Bad theragnosis (anti-VEGF)	Europeans	synonymous		
	SCHIZOPHRENIA Rare duplications of the <i>RB1CC1</i> gene is enriched in European patients [23,24]									

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
SMCR8 NM_144775 1,354 eQTL	rs1563634	T	C	67%	12	BREAST CANCERS [25]	Europeans	5' <i>SMCR8</i>	eQTL-Breast
	rs8080966	C	T	31%	81	CHILDHOOD APRAXIA OF SPEECH [26]	American GWAS	MISSENSE P524L	eQTL- Brain
	rs12939757	A	G			NEURAL TUBE DEFECTS [27] Low maternal folate intake	Americans	3' <i>SMCR8</i>	eQTL- Brain
	rs921986	C	T			OVARIAN CANCER [28]	American GWAS	3' <i>SMCR8</i>	eQTL- ovary
	rs12952556	T	C					3' <i>SMCR8</i>	eQTL- ovary
TBC1D14 NM_020773 746 eQTL	rs10804990	G	A	62%	3	CORONARY HEART DISEASE [29]	American GWAS	Intronic	eQTL- Artery
WDR41 NM_018268 10007 eQTL ULK1 partner	rs163016	A	T	40%	41	MYOPIA [30]	World	Intronic	(eQTL)
	rs163030	A	C	48%	83	CAUDATE VOLUME [31] Brain region implicated in common neurological and psychiatric disorders	American GWAS	Intronic	eQTL - Brain
	rs163035	A	G					Intronic	eQTL - Brain
	rs335636	A	G					Intronic	eQTL - Brain
	rs335632	C	T	1%	1	HEART eQTL [32]	Genome-wide eQTL mapping Europeans		eQTL
	rs33204	C	T	40%	28	MYOPIA [30]	World	MISSENSE V326I	(eQTL)
	rs10514104	T	C	18%	14	 Age-related HEARING IMPAIRMENT [33]	European GWAS	Intronic	eQTL - Brain ↓ exp [33]

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
<i>C9orf72</i> NC_000009.12 6048 eQTL ULK1 partner	rs774359	T	C	27%	81	ALS-FTD [34–36] PROSTATE CANCER [37]	European GWAS American European GWAS	3'UTR	eQTL - Brain
	rs2814707	C	T			ALS-FTD [34–36] SYSTEMIC LUPUS ERYTHEMATOSUS (SLE) [38] high serum IFNK (type I IFN)	European GWAS American World GWAS	5' <i>C9orf72</i>	eQTL - Brain
	rs3849942	T	C			ALS-FTD [39] PROSTATE CANCER [37]	American GWAS European GWAS	3' <i>C9orf72</i>	eQTL - Brain
	rs3849943	C	T	75%	1	ALS [40]	European GWAS	3' <i>C9orf72</i>	eQTL - Brain
	rs2282241	C	A	43%	6	ALS-FTD [39]	American GWAS	Intronic	eQTL - Brain
	rs2492816	G	A	42%	8	ALS [41]	Europeans	Intronic	(eQTL)
	rs3849944	T	C	47%	10	SLE [38] high serum IFNK	World GWAS	3' UTR	(eQTL)
	rs10812615	T	C			FTD [42]	Oceania GWAS	Intronic	eQTL - Brain
	rs10812616	T	A			Intronic	eQTL - Brain		
	rs10122902	G	A	16%	9	ALS [43] PROSTATE CANCER [37]	Americans European GWAS	synonymous	(eQTL)
	rs10757665	T	C	25%	25	PROSTATE CANCER [37]	European GWAS	Intronic	(eQTL)
	rs10967991	C	T			SCHIZOPHRENIA [44]	American GWAS	5' <i>C9orf72</i>	(eQTL)
	rs12686452	T	C	21%	7	♀ SLE [38] high serum IFNK	World GWAS	Intronic	(eQTL)
	rs17769294	T	C	11%	10	ALS [43] FTD [42]	Oceania GWAS Americans	MISSENSE N207S	(eQTL)

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
IRGM NM_001145805 1645 eQTL	rs4958843	T	C	9%	168	 TUBERCULOSIS [45] ↓ RISK	Middle East	5' <i>IRGM</i>	eQTL – Lung ↑ exp [45]
	rs1000113	C	T			CROHN DISEASE [46] Adult-onset	Europeans	Intron	eQTL
	rs10065172	C	T			 CROHN DISEASE [47–51]	Europeans, Asians Americans	Synonymous MIR196 binding seed ↑ IRGM [52]	Lung, Colon, Blood ↑ exp [47,52] ↓ exp [48,51,53] = exp [54]
						 GRAVE DISEASE [55]	Asians		
						 ANKYLOSING SPONDYLITIS [56] rs4958846C-rs10065172C: RISK rs4958846T-rs10065172C: protective	Asians		
						 SLE [57]	Asians		
	rs11749391	T	C			 SEPSIS [53] ↑ mortality	Asians		
						 TUBERCULOSIS [54,58,59] ↓ RISK (<i>population-specific</i> , Asians)	Asians		
	rs11747270	A	G			 CROHN DISEASE [60]	GWAS (Europe, America, Australia)	eQTL Blood	
	rs11747270	A	G			 PERIODONTITIS [61]	Europeans	Intron	(eQTL)
 CROHN DISEASE [62] <i>Not population-specific</i> [63]				Europeans					
 ULCERATIVE COLITIS* <i>*do not exhibit Hardy-Weinberg equilibrium</i>				Indian* [63] Asians					
rs13361189	T	C	 ARTHRITIS (CD comorbidity) [64]	Asians					
			 CROHN DISEASE [47,48,51,65] ↑ CD colitis (LTF/lactoferrin and TNF)	Americans, Europeans					
			 SLE [57]	Asians					
			 GASTRIC CANCER [66] ↓ RISK x <i>H. pylori</i>	Asians					
rs13361189	T	C	 GLIOMA [67] ↑ IFNG ↑ IL4	Asians					
			GRAVE DISEASE [55]	Asians					

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funcn Annot	eQTL GTEX
IRGM NM_001145805 1645 eQTL	rs13361189	T	C	9%	168	 LEPROSY [68] ↑ <i>Mycobacterium leprae</i> ↑ IFNG and IL4	Asians	5'UTR	eQTL - Blood
						PERIODONTITIS [61]	Europeans		
						NON-ALCOHOLIC FATTY LIVER DISEASE [69,70] CD comorbidity	Asians Europeans		
						 TUBERCULOSIS [58] ↓ RISK rs10065172 rs10051924 rs13361189 >TCC	Asians		
	rs7714584	A	G			CROHN DISEASE [71]	European GWAS	Intron	(eQTL)
	rs72553867	C	A	4%	120	CROHN DISEASE [72]	Asians	MISSENSE T94I	
	rs9637876	C	T	9%	163	 TUBERCULOSIS [73]	Africans	5'UTR	eQTL - lung ↑ exp [73]
						CROHN DISEASE [63]	Indians		
	rs4958846	T	C			 TUBERCULOSIS [45,59,74] ↓ RISK	Middle East, and Asians	5' <i>IRGM</i>	eQTL - Lung ↓ exp
	rs4958847	G	A	13%	51	 CROHN DISEASE <i>population-specific (not in Asians) [64]</i>	Europeans	Intronic	eQTL - colon
						NON-ALCOHOLIC FATTY LIVER DISEASE (NAFLD) [75] CD comorbidity ↑ RISK rs4958847- rs13361189	Americans		
						 ARTHRITIS [64] ↓ RISK	Asians		
						GASTRIC CANCER [66,76] ↓ RISK	Asians, and Europeans		
						 GRAVE DISEASE [55]	Asians		
rs10059011	A	C	54%	1	METASTATIC CLEAR CELL RENAL CELL CARCINOMA ccRCC RISK [77]	Europeans	5'UTR	(eQTL)	
					 TUBERCULOSIS [73]	Africans			

Table S3. PtdIns3K Complex – AUTOPHAGY_LAP.

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEx
PIK3C3/ VPS34 NM_002647 3755 eQTL	rs3813065	C	T	14%	42	SLE [78] Altered ERAP2 exp (MHC-I peptide processing enzyme) ↑ IFNA1	American GWAS	5' <i>PIK3C3</i>	eQTL – Blood ↓ Promoter
						SCHIZOPHRENIA [79] BIPOLAR DISORDER [79] ↑ the binding of a POU-type transcription factor	Middle East		
	rs52911	G	A	34%	47	ESOPHAGEAL SQUAMOUS CELL CARCINOMA [80,81] Protective	Asians, and Americans	Intronic	eQTL - Esophagus
	rs1941526	C	T	20%	83	ALZHEIMER DISEASE [82]	American GWAS	Intronic	eQTL - Nerve
	rs76692125	G	A	4%	1	PANCREATIC CANCER [83] RISK	European GWAS	Intronic	eQTL – Blood ↓ mRNA
	rs2162440 rs7235755	A A	G G	79%	25	GASTRIC CANCER [84,85] (GASTRIC CARDIA ADENOCARCINOMA) associated with shorter telomeres	European GWAS Asian	3' <i>PIK3C3</i> (5' <i>MIR4318</i>)	
PIK3R4/ VPS15 NM_014602 263 eQTL	rs10934954	C	T	20%	176	COLORECTAL CANCER [86]	Europeans	Intronic	eQTL - Colon
	rs2200368	A	G			 Age-related	American GWAS	Intronic	(eQTL)
	rs11713445	G	A			MACULAR DEGENERATION [87]		Intronic	(eQTL)
BECN1 NM_003766 157 eQTL	rs10512488	G	A	21%	1	TYPE 2 DIABETES [88] NON-HODGKIN LYMPHOMA [89]	European GWAS, and study	Intronic	eQTL - Blood
	rs11552193	C	T	0%	1	NSCLC [90]	World	3'UTR	miRNA Sites
	rs60221525	C	A	6%	1	MACHADO-JOSEPH DISEASE/ SPINOCEREBELLAR ATAXIA TYPE 3 [91] RISK Neuroprotective	Europeans	3' <i>BECN1</i>	↑ exp [91]
	rs116943570	A	C	0%	1			3' <i>BECN1</i>	

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEx
ATG14 NM_014924 8192 eQTL – C I	rs8015211	T	C	35%	53	PROSTATE CANCER [92] aggressivity not validated in an independent study	American GWAS	Intronic	eQTL Prostate
	rs8003279	A	G				NSCLC [11] Theragnosis (Platinum): Good	Asians	Synonymous
	rs17742719	G	T	18%	8				Intronic
	rs1009647	G	A	27%	9	 NSCLC Theragnosis (Platinum) [11] TESTICULAR GERM CELL TUMOR [93]	Asians European GWAS	5' ATG14	(eQTL)
UVRAG NM_003369 1790 eQTL Autophagosome maturation – C II	rs80191572	A	G	5%	1	 MULTIPLE SCLEROSIS [94] Theragnosis (Copaxone)	World GWAS	Intronic	(eQTL)
	rs7111334	C	T	8%	3	 RHEUMATOID ARTHRITIS [95] RISK	Asians	Intronic	(eQTL)
	rs7933235	A	G	8%	97	 VITILIGO [96] LD with rs7118567 MISSENSE P10H	Asians	Intronic	
	rs1458836	C	T					5' UVRAG	eQTL - Skin
	rs7116263	C	G	8%	9	CANCER : Etoposide-induced cytotoxicity [97]	Americans	Intronic	(eQTL)
	rs17134573	G	A	3%	154	CARDIOVASCULAR DISEASES Blood lipid, body mass index [98]	American GWAS	Intronic	(eQTL)
	rs594826	G	A	6%	3			Intronic	
AMBRA1 NM_017749.3 148 eQTL	rs11038913	T	C	8%	1	ARTERY DISEASE [99] associated with blood proinsulin levels	European GWAS	Intronic	eQTL - Artery
	rs3802890	A	G	31%	1	♀ AUTISM [100] protective	Europeans	Intronic	(eQTL) ↓ mRNA
	rs7130141	C	T	17%	113	SCHIZOPHRENIA [101,102]	European, and Asian GWAS	Intronic	eQTL - Brain
	rs7112229	C	T					Intronic	
	rs61882743	C	G					Intronic	
	rs12574668	C	A					Intronic	
rs11819869	C	T	Intronic						

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
MCL1 NM_008562.3 402 eQTL Inhibitor of BECN1	rs1258188045	C	G, T	0%	1	MEGALENCEPHALIC LEUKOENCEPHALOPATHY [103]	Europeans	MISSENSE R84C	
	rs9803935	T	G	56%	36	 HNSCC [104] x Human papillomavirus (HPV16)-associated oro-pharyngeal type x SMOKING	Americans	5' <i>MCL1</i>	(eQTL)
	rs3738485	C	G			COLORECTAL CANCER [105] Metastasis	Western Asians	5' <i>MCL1</i>	(eQTL)
	rs961581226	C	A	0%	1	 TUBERCULOSIS [106]	Asians	5' <i>MCL1</i>	
	rs3831987	CC	21mer	0%	1	LUNG CANCER in NON-SMOKER [107] Protective BREAST CANCER [108] Protective	Asians	5' <i>MCL1</i>	↑ exp
NRBF2 NM_030759 1679 eQTL C-I	rs10995190	G	A	14%	11	MAMMOGRAPHIC DENSITY [109] Putative Enhancer. BREAST CANCER Risk Locus Regulates NRBF2 Expression	European, and Asian GWAS	ZNF365 Intronic	
	rs10509168	T	C	52%	4			ZNF365 Intronic	
RUBCNL NM_025113 2581 eQTL	rs1408184	C	T	34%	72	ALZHEIMER DISEASE [110]	Europeans	MISSENSE G152R	eQTL -Brain
	rs2478046	G	A	14%	61	 ALS [111]	Europeans	3' <i>RUBCNL</i>	eQTL -Nerve
SH3GLB1/BIF-1 NM_016009 849 eQTL	rs263436	G	A	24%	35	TYPE 2 DIABETES [112]	European GWAS	intronic	
VMP1 NM_030938 272 eQTL Partner of PI3K C-I	rs1295925	T	C	71%	32	BREAST CANCER [113] Protective OSTEOSARCOMA [114] Protective - TP53 transcriptional binding site	Asians	Intronic	eQTL -Breast

Table S4. ATG9 system – AUTOPHAGY.

Gene	variant	Ref	Alt	EUR freq	LD		Disease	Populations	Funct Annot	eQTL GTEX	
ATG2A NM_015104 16 eQTL	rs17146441	C	T	23%	2		CROHN DISEASE [115] Granulomas	Europeans	Intronic	(eQTL)	
	rs188780113	G	A	0%	1		KIDNEY DISEASE [116] RISK of hyperuricemia	Asian GWAS	MISSENSE R478C		
ATG2B NM_018036 318 eQTL	rs3759601	G	C	42%	27		BLADDER CANCER [117] Theragnosis (BCG immunotherapy) European (not in Asian population) [118] ↓ autophagosome formation (macrophages) HNSCC [119] ↑ RISK pharyngeal cancer	Europeans, and Asians	MISSENSE Q1383E	(eQTL)	
ATG9A NM_024085 147 eQTL	rs2382817	A	C	64%	74		INFLAMMATORY BOWEL DISEASE [120]	Europeans	PNKD intron	eQTL – Colon	
ATG9B NM_173681 283 eQTL	rs7830	G	T	36%	1		BLOOD PRESSURE [121] x AIR POLLUTION - urban elderly	Asians	5' <i>ATG9B</i>	eQTL - Artery	
	rs2373929	G	A	46%	1		CORONARY ARTERY DISEASE [122]	Middle East	Intronic	eQTL - Artery	
	rs3763486	T	C	20%	2		SKIN BASAL CELL CARCINOMA [123] STROKE [124]	European GWAS Americans	5' <i>ATG9B</i>	(eQTL)	
	rs3800787	G	C	40%	1		STROKE [124]		Intronic		
	rs3918220	C	G	0%	1			Americans	Intronic		
	rs6464119	T	C	77%	2				Intronic	eQTL - Artery	
	Attributed to NOS3	rs11769158	A	G	88%	1				5' <i>ATG9B</i>	(eQTL)
		rs11760487	G	A	13%	2		BONE DENSITY [125]		Intronic	(eQTL)
		rs12666075	G	T	19%	4			Americans	Intronic	
rs13307588		A	G	94%	2		MYOCARDIAL INFARCTION [126]	Europeans	Intronic	(eQTL)	

Gene	variant	Ref	Alt	EUR freq	LD	Disease Susceptibility	Populations	Funct Annot	eQTL GTEX
WIPI1 NM_017983 1114 eQTL	rs2909207	T	C	76%	27	 Age-adjusted blood medium HDL level [127]	European GWAS	Intronic	(eQTL)
	rs77156594	A	G	0%	1	ANENCEPHALY [128]	Asians	MISSENSE L406P	
	rs146357218	C	T	0%	1			MISSENSE R328Q	
WIPI2 NM_015610 879 eQTL	rs4720530	C	T	55%	1	 OSTEOPOROSIS [129] RISK x Blood lead (Pb) levels in SMOKERS	Asian GWAS	Intronic	(eQTL) – sQTL blood
	DEVELOPMENTAL ABNORMALITIES [130] mental retardation, neurological, psychiatric, skeletal and cardiac abnormalities. homozygous (c.G745A ; pV249M). ↓ Binding of the V231M mutant to ATG16L1 (ATG12–ATG5), ↓ WIPI2 puncta, ↓ LC3 lipidation and ↓ autophagic flux.								
WDR45 NM_007075.3 1206 eQTL	 Neurodegeneration with BRAIN IRON ACCUMULATION [131] BETA-PROPELLER PROTEIN-ASSOCIATED NEURODEGENERATION [132] WDR45 mutations → ↓ autophagy degradation of ferritin → ↑ iron in the brain (basal ganglia), X-linked								
ZFYVE1/DFCP1 NM_021260 1079 eQTL	rs7155380	T	C	45%	25	 ALZHEIMER DISEASE [133] Late-Onset	American GWAS	Intronic	eQTL - Brain/Nerve
	ZFYVE1/DFCP1 (WIPI2 partner) associates with lipid droplets [134].								

Table S5. LC3-conjugation system – AUTOPHAGY_LAP.

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG3 NM_022488 98 eQTL	rs13082005	G	A	40%	4	 NSCLC [11] Theragnosis (Cisplatin)	Asians	Intronic	(eQTL)
ATG4A NM_178270 309 eQTL	rs4036579	A	G	45%	1	 CERVICAL CANCER [135] ↑ HPV INFECTION RISK Transcription factor site	Asians	5' ATG4A	(eQTL)
	rs807182	A	C	45%	1			Intronic	(eQTL)
	rs807181	G	C	45%	2			Intronic	(eQTL)
	rs807183	G	A					Intronic	(eQTL)
	rs807185	A	T	64%	1	LUNG CANCER [136] RISK	Asians	Intronic	(eQTL)
	rs5973822	A	G	6%	1	 CERVICAL CANCER [135] CROHN DISEASE [115] Granulomas OVARIAN CANCER [137]	Asians Europeans	3'UTR miRNA binding site [137]	(eQTL)
	rs7880351	G	C	45%	1	 ccRCC [77] Theragnosis (pazopanib) ↑ OS PFS	Europeans	Intronic	(eQTL)
ATG4B NM_013325.5 1758 eQTL	rs3771570	C	T	13%	21	PROSTATE CANCER [138]	World GWAS	5' ATG4B	(eQTL)
	rs35320439	T	C	33%	1	CROHN DISEASE [139]	European, and Asian GWAS	5' ATG4B	(eQTL)
	rs139302128	C	T	1%	22	ATHEROSCLEROSIS [140] LD with rs138274580 MISSENSE N330S	European GWAS	Intronic	(eQTL)
ATG4C NM_032852 2531 eQTL	rs6670694	G	A	42%	96	 ccRCC [77] Theragnosis (pazopanib) ↑ PFS	Europeans	Intronic	(eQTL)
	rs6683832	G	A	56%	33			CARDIOVASCULAR DISEASE Blood FG (fibrinogen) [141]	European GWAS

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX	
ATG4C NM_032852 2531 eQTL	rs11208029	A	G	14%	109	 TUBERCULOSIS [142]	African GWAS	Intronic	(eQTL)	
	rs6587988	C	T			CARDIOVASCULAR DISEASES [99] Blood lipids (total cholesterol, triglycerides)	European GWAS	Intronic	eQTL - Artery ↓ exp [143]	
	rs11208030	G	A				KASHIN-BECK DISEASE [143]	Asians	Intronic	eQTL – Heart ↓ exp [143]
	rs4409690	G	A						Intronic	(eQTL)
	rs12097658	T	C						Intronic	↓ exp [143]
ATG4D NM_032885 274 eQTL	rs2304165	C	T	15%	16		Europeans	synonymous	(eQTL)	
	rs7248026	T	G	25%	31			CROHN DISEASE [115] ↓ Granulomas	5' <i>ATG4D</i>	(eQTL)
	rs7248036	C	T	40%	5			5' <i>ATG4D</i>	(eQTL)	
	rs10439163	A	G	40%	23			CROHN DISEASE [115] Granulomas CARDIOVASCULAR DISEASE [99] Blood lipids (cholesterol and LDL)	5' <i>ATG4D</i>	eQTL - Heart, Colon
EGR1 NM_001964.2 8 eQTL	rs4902647	C	T	46%	22	 MULTIPLE SCLEROSIS [144]	American GWAS	3' <i>EGR1</i>	(eQTL)	
	rs7729723	A	G	36%	9	 CHRONIC OBSTRUCTIVE PULMONARY DISEASE (COPD) [145,146] x SMOKING	Asians	5' <i>EGR1</i>	(eQTL)	
	rs11743810	C	T	54%	7	SCHIZOPHRENIA [147]	Asians	Intronic	(eQTL)	
GABARAP NM_007278.1 37 eQTL	rs222843	T	C	38%	22	 NICOTINE DEPENDENCE [148] x Smoking-induced disease NICOTINE AND ALCOHOL DEPENDENCE [149]	Asians, and Americans	PROMOTER  (MISSENSE CLDN7)	eQTL - Brain/Nerve ↑ exp [149]	
	rs17710	A	T	15%	2	 NICOTINE DEPENDENCE [148,149]	Americans	3'-UTR	(eQTL)	

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
GABARAPL1 NM_031412	AUTISM spectrum disorder-associated pathways. deletions of GABARAPL1 in autism [150] GABARAPL1 is the most highly expressed gene in the central nervous system among the family.								
GABARAPL2 NM_007285 97 eQTL	rs12599322	G	A	5%	26	 DNA DAMAGE [18]	Asian study	RP11-77K12.8	eQTL
GABARAPL3 NM_028287 15 eQTL	rs6496667	C	A	20%	110	 RHEUMATOID ARTHRITIS [151]	Asian GWAS	5' UTR	(eQTL)
MAP1LC3A NM_181509 27368 eQTL	rs1040747	C	G	36%	43	 CHRONIC Q FEVER [152] <i>x C. burnetii</i> -induced cytokine production - Protective	Europeans	3'UTR	eQTL - Blood
	rs73105013	T	C	9%	1	 Age-related MACULAR DEGENERATION [8]	Europeans	Intronic	(eQTL)
	rs2424994	C	T	15%	1	 CORONARY ARTERY DISEASE [99]	European GWAS	5' UTR	eQTL - Heart
	rs6088521	A	C	49%	1			5' UTR	eQTL - Heart
MAP1LC3B NM_022818 1437 eQTL	rs111626199	C	T	1%	4	ACUTE MYOCARDIAL INFARCTION [153] may abolish the binding sites for GMEB2, and ZBTB7A, ZBTB7B, ZBTB7C, and create the binding sites for GCM1-GCM2	Asians	Promoter	↓ exp [153] (luciferase)
	rs77019223	A	G	9% (1% As)	1			Promoter	↓ exp [153] (luciferase)
	rs8051218	T	C	6%	4	ASTHMA [10]	Americans	Intronic	(eQTL)
	rs7204722	C	T	82%	2			Intronic	(eQTL)
	rs933717	T	C	44%	26	 SLE [154]	Asian GWAS	3' UTR	eQTL – Blood ↑ exp [154]
MAP1LC3C NM_001004343 2 eQTL	rs1776161	G	A	42%	1	UTERINE LEIOMYOMAS [155] Clinical Trial	Americans	Exon1	

Several **cancer-associated mutations in LC3** have been reported that either attenuate its binding to **ATG7** and subsequent lipidation (**LC3B Y113C**) [156] or its interaction and cleavage by **ATG4** (**LC3A R70C/H** [rs778324131](#), **LC3B T113** [rs200708875](#), and **LC3C R76C** [rs776473823](#)) [157]. These **loss-of-function LC3 mutations** could confer tumor-promoting features as they are reducing but not completely blocking autophagy in cells, and thus still support some level of autophagy for the continuous growth of tumor cells at later stages (melanoma/hepatocellular carcinoma) [158,159].

GABARAPs and LC3s have opposite roles in regulating ULK1 for autophagy induction [160]

Mutation of the ULK1 LC3-interacting region that disrupts the Atg8-family protein-ULK1 interaction drastically reduces ULK1 activity, autophagic degradation of SQSTM1, and phagophore formation in response to starvation. Similarly, disruption of the ATG13-Atg8-family protein interaction suppresses ULK1 activity and autophagosome formation. By reconstituting Atg8-family protein-depleted cells with individual Atg8-family members, it has been shown that: **The GABARAP subfamily (GABARAP and GABARAPL1) positively regulates ULK1 activity and autophagosome formation in response to starvation.** In contrast, the LC3 subfamily (LC3B and LC3C) negatively regulates ULK1 activity and phagophore formation.

Table S6. ATG12-conjugation system – AUTOPHAGY_LAP.

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG5 NM_004849.2 509 eQTL	rs490010	A	G	48%	20	 ccRCC [77] Theragnosis (Pazopanib) ↓PFS	Europeans	Intronic	(eQTL)
	rs473543	A	G	44%	12	 BREAST CANCER [161] Theragnosis (Anthracycline and/or taxane) ↑PFS APLASTIC ANEMIA [162] >GG ↓ RISK	Asians	5' ATG5	(eQTL)
	rs506027	T	C			  CROHN DISEASE [163] Theragnosis (anti-TNF) ↑ OS  SEPSIS [164] ↑ TNF IL1B	Europeans, and Asians	5' ATG5 promoter	(eQTL) ↓ exp [164] ↑ exp [165–167]
						ASTHMA [165–167] ↑ neutrophils	Americans, and Asians		
	rs510432	T	C			APLASTIC ANEMIA [162] ↓ RISK	Asians	5' ATG5 promoter	(eQTL) ↓ exp [164] ↑ exp [165–167]
						ASTHMA [165–167] ↑ neutrophils	Americans, and Asians		
						 CROHN DISEASE [163] Theragnosis (anti-TNF) ↑ OS	Europeans		
						 HCC [168] HBV-related diseases	Asians		
						NSCLC EGFR* [169] Theragnosis (gefitinib) ↑ OS PFS	Asians		
						 LUNG FIBROSIS [170] ↓ RISK x COAL	Asians		
			MELANOMA [171] Bad prognosis ↓ tumor-infiltrating lymphocytes			Americans			
			 SEPSIS [164] ↑ TNF IL1B	Asians					

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX	
ATG5 NM_004849.2 509 eQTL	rs2245214	C	G	36%	11	 BLADDER CANCER [117] ↓ autophagy (macrophages) ↓ BCG vaccine-induced trained immunity	Europeans	Intronic	(eQTL)	
						MELANOMA [171] Bad prognosis ↓ tumor-infiltrating lymphocytes	Americans			
						NSCLC [172]	Europeans			
						PAGET DISEASE [173] RISK	Europeans			
	rs671116	A	G	36%	11	 Q FEVER [152] x <i>C. burnetii</i> infection - Protective	Europeans	American GWAS, and Europeans		
						SLE [174,175]	American GWAS, and Europeans			
						SYSTEMIC SCLEROSIS [176]	World GWAS			
	rs633724	C	T	36%	11	 THYROID CANCER [177]	Europeans			
						ESOPHAGEAL SQUAMOUS CELL CARCINOMA (ESCC) [178] >TT Bad prognosis (shorter OS and PFS)	Asians			
	rs573775	G	A	28%	1	ASTHMA [10]	Americans	Intronic		(eQTL) ↑ exp (PBMC) [179]
ASTHMA [167]						Asians				
APLASTIC ANEMIA [162]						Asians				
BEHÇET DISEASE [179] ↓ RISK						Asians				
 SLE [175,180,181] ↑ IFNA IL10						Europeans				
rs548234	C	T	68%	5	 Age-related MACULAR DEGENERATION [8] Protective	Europeans	3' ATG5			
					 HCC [182] x Chronic HBV (Hepatitis B virus) INFECTION	Asian				
					 HBV INFECTION [182] NEUROMYELITIS OPTICA [183] RISK of demyelination ↑T cell exp SLE [176,184] Protective	Asians, and World				

Gene	variant	Ref	Alt	EUR freq	LD		Disease	Populations	Funct Annot	eQTL GTEX
ATG5 NM_004849.2 509 eQTL	rs688810	A	G	22%	1		NSCLC EGFR* [169] Bad theragnosis (gefitinib)	Asians	5' ATG5	(eQTL)
	rs803360	G	C	48%	26		APLASTIC ANEMIA [162] Protective	Asians	Intronic	(eQTL)
	rs3827644	G	C	19%	31		SYSTEMIC SCLEROSIS [176,185]	Eaurpean GWAS, and World GWAS	Intronic	(eQTL)
	rs9372120	T	G				MULTIPLE MYELOMA [186] RHEUMATOID ARTHRITIS [187] SYSTEMIC SCLEROSIS [176]	Eaurpean GWAS, and World GWAS	Intronic	(eQTL)
	rs1322178	C	T				ESOPHAGEAL SQUAMOUS CELL CARCINOMA (ESCC) [178] POOR prognosis	Asians	3'ATG5	eQTL ↑ exp [178]
	rs3804329	A	G			SYSTEMIC SCLEROSIS [176]	World GWAS	intronic	eQTL	
	rs9373839	T	C				CROHN DISEASE [163] Theragnosis (anti-TNF) SYSTEMIC SCLEROSIS [176]	Europeans, World GWAS	Intronic	(eQTL)
	rs6568431	A	C				HBV INFECTION [182] SLE [174,175] ↑ anemia and renal involvement	Asians, Europeans, American GWAS	3' ATG5	↑ exp [182]
	rs6937876	G	A		CEREBRAL PALSY [188] Protective	Asians	↑ plasma level			
	rs12201458	C	A		SLE [57] NEUROMYELITIS OPTICA [183] Protective	Asians				
	rs2299863	T	G	12%	4		ASTHMA [165,166] ↑ ATG5 expression in nasal epithelium.	Americans, and Asians	Intronic	
	rs12212740	G	A	ASTHMA [10,167] Protective	Intronic LD 5' of ATG5					
	rs11751513	C	A	5%	1	ASTHMA [165]	Americans		Intronic	
	rs17067724	A	G	1%	1		HCC [189] RISK	Asians	Intronic RP1-60019.1	
	rs190825454	G	C	0% 1% As	1		ACUTE MYOCARDIAL INFARCTION [153]	Asians	5' ATG5	

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG7 NM_001144912 5828 eQTL	rs8154	T	C	31%	1	 NSCLC (EGFR*) [169] Theragnosis (Gefitinib) BREAST CANCER [190] Bad prognostic ↓ PFS and OS	Asians	Synonymous methylation meQTL [190]	eQTL – Lung ↑ exp [190]
	rs1375206	C	G	60%	36	ASTHMA [167] ↓serum IL8 levels PARKINSON DISEASE [191]	Asians	Intronic	(eQTL)
	rs2594972	A	G			CEREBRAL PALSY [188]	Asians	Intronic	(eQTL sQTL)
	rs2594966	G	A			ISCHEMIC STROKE[192]	Asian GWAS	Intronic	(eQTL sQTL)
	rs2594973	C	G					Intronic	(eQTL sQTL)
	rs2606736	C	T			ccRCC [193] ↓ RISK (> 55 years old)	Asians	Intronic	(eQTL) sQTL – Lung Blood
	rs6442260	G	A					36%	5
	rs1470612	C	T	18%	77	CEREBRAL PALSY [188]	Asians	Intronic	(eQTL)
	rs11706903	C	A			SLE [57]	Asians	Intronic	eQTL blood
	rs2594971	G	A	65%	45	ASTHMA [167] ↓serum IL8 levels	Asians	5' ATG7	(eQTL)
	rs2594975	T	C	51%	1	MYOCARDIAL INFARCTION [194] ↑ binding of transcription factor	Asians	5' ATG7	
	rs7635838	T	C	59%	35	CARDIOVASCULAR DISEASE [99] Blood lipids (HDL)	Europeans	Intronic	(eQTL)
	rs2447607	C	G,T	59%	14	Systolic BLOOD PRESSURE [99]	Europeans	Intronic	eQTL muscle
	rs36117895	T	C	3%	56	HUNTINGTON DISEASE [195]	Europeans	MISSENSE V471A	(eQTL)
rs4684776	T	C	18%	77	ISCHEMIC STROKE [192]	Asian GWAS	Intronic	eQTL	

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG10 NM_001131028 16437 eQTL	rs1864182	C	A	58%	11	BREAST CANCER [196] Protective	Asians	MISSENSE P220H	eQTL - Lung
						NSCLC [197] Poor survival NSCLC EGFR* [169] Theragnosis (gefitinib) ↓ RISK for acquired RESISTANCE. ↑ RISK of primary RESISTANCE	Asians		
						 LUNG FIBROSIS [170] Protective x COAL	Asians		
						MELANOMA [171] ↑ tumor-infiltrating lymphocytes (TILs)	Americans		
	rs1864183	C	T	49%	22	HCC [189]	Asians	MISSENSE T212M	eQTL - Lung
						 HNSCC RISK to develop laryngeal cancer [119] NPC, Bad Theragnosis (radiotherapy) [198]	European, and Asians		
						NSCLC Poor survival[197] Theragnosis (Platinum) [11]	Asians		
						 PAGET DISEASE [173] Protective	Europeans		
						 TUBERCULOSIS [199] ↑ IL8	Asian GWAS		
	rs4703533	C	G	39%	4	 HNSCC NPC [198] Bad Theragnosis (radiotherapy)	Asians	Intronic	
rs10036653	A	T	20%	1	NSCLC [200] ↓ RISK of brain metastasis NSCLC EGFR* [169] Theragnosis (gefitinib) ↓ acquired resistance ↑ PFS ↑ OS	Asians	5' ATG10	eQTL – Lung ↑ OCT4 binding [169]	
rs10514231	C	T	66%	1	BREAST CANCER [196] Protective HCC [189] Protective NSCLC [197] Poor survival HNSCC NPC [198] Bad Theragnosis (radiotherapy)	Asian studies, and GWAS	Intronic	eQTL - Lung, Breast ↑ exp [189]	
rs9447453	C	A	11%	1	 Delayed age of MENOPAUSE [201]	American GWAS	5' ATG10		

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG10 NM_001131028 16437 eQTL	rs324913	T	C	47%	18	 ECZEMA HERPETICUM [202] ↓ IFNG	Americans	Intronic	eQTL - Skin
	rs1485587	A	G				Americans	Intronic	eQTL - Brain
	rs891159	G	A	22%	43	ALZHEIMER DISEASE [203]	American GWAS	Intronic	eQTL - Brain
	rs4703879	A	G						eQTL - Brain
	rs7707921	T	A				European GWAS	Intronic	eQTL - Breast
	rs73134739	T	C				Asian GWAS	Intronic	eQTL - Breast
ATG12 NM_004707 268 eQTL	rs26532	C	A	78%	1	NSCLC [200] RISK of brain metastasis	Asians	Intronic	eQTL - Brain
	rs26537	T	C	40%	5	HNSCC [206] HCC [189]	Asians	Intronic	eQTL ↑ exp [206]
	rs26538	C	T						 NSCLC EGFR* [169] Bad prognosis ↓ PFS LUNG FIBROSIS [170] x COAL - Protective
	rs1058600	C	T	23%	12	 NSCLC [207] Theragnosis (radiotherapy)	Americans	3'UTR	eQTL - Lung
ATG16L1 NM_030803 2507 eQTL	rs2289476	C	A	6%	25	  CROHN DISEASE [208–210] x SMOKING	European, and American GWAS	Intronic	(eQTL)
	rs4663402	A	T	4%	18	HNSCC [206] HCC [189]	Asians	Intronic	eQTL - Esophagus
	rs4663421	G	C						 ♀ ANKYLOSING SPONDYLITIS [211]
	rs6758317	C	T	18%	3	 CROHN DISEASE [64]	Asians	Intronic	
	rs6754677	G	A	62%	8				PROSTATE CANCER [212] Bad prognostic
	rs78835907	G	A	5%	1				

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG16L1 NM_030803 2507 eQTL	rs2241880	A	G	53%	71	 CARDIOVASCULAR DISEASE [213] RISK in postmenopausal women <i>Carotid intima-media thickness</i>	South Americans	MISSENSE T300A	eQTL - Colon Thyroid
						 LUNG CANCER Good prognosis ↓ metastasis [200] x SMOKING – Protective [214] NSCLC EGFR* Bad theragnosis (Gefitinib) [169]	Asians, and Europeans		
						COPD [182]	Asians		
						 CROHN DISEASE [64,208–210,215] x SMOKING LD with 11 other pubmed cited rs: [216] rs10210302 , rs6752107 , rs6431654 , rs6431660 , rs12994997 , rs3828309 , rs2289474 , rs2289472 , rs2241879 , rs3792109 , rs1045100	European GWAS American GWAS and Asians		
						 x BISPHENOL A levels are correlated with systemic CD inflammatory response with dysbiotic microbiota [217]	European		
						PREMATURE DELIVERY [218]	Europeans		
						 UROPATHOGENIC <i>E. coli</i> [219] Protective	Americans		
						 HBV INFECTION [220]	South Asians		
						 BURULI ULCER [221,222] x <i>Mycobacterium ulcerans</i> Protective	African study, and GWAS		
						RHEUMATOID ARTHRITIS [223] <i>ATG16L1</i> rs2241880 x <i>ATG16L2</i> rs11235604 (C/T) <i>ATG16L1</i> rs6758317 x <i>ATG16L2</i> rs11235604 (C/T)	Asians		
						PSORIASIS [224]	Europeans		
						PAGET DISEASE RISK [173]	Europeans		
BREAST CANCER RISK [225]	Africans								
THYROID CANCER [226] Protective ↓ RISK, Good prognosis	Europeans								

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
ATG16L1 NM_030803 2507 eQTL	rs2241880	A	G	53%	71	HNSCC (Oral) [119]	Europeans	MISSENSE T300A	eQTL - Colon Thyroid
						MELANOMA [171] >GG Good prognosis (earlier stage), >AG Younger age	Americans		
COLORECTAL CANCER ↑ RISK [227] Good prognosis (↑ survival, ↓ metastasis) ↑ IFN (indep. of autophagy, MAVS dep)[228]						Europeans Americans			
 GASTRIC CANCER [66,229] x H. Pylori INFECTION Good Prognosis ↑ tumor apoptosis [230]						Asians- Europeans Americans			
	rs13005285	T	G	66%	8	 HCC [231] (Comorbidity HCC and cirrhosis) RISK-based surveillance in cirrhosis. Protective: HBV -related HCC [232]	Europeans Asians		
						PSORIASIS [224]	Europeans	Intronic	eQTL - Skin
ATG16L2 NM_033388 222 eQTL	rs10751215	T	C	47%	33	 Metastatic ccRCC [77] NSCLC Theragnosis (radiotherapy) [207] ↑ ATG16L2 ↓ autophagosome ↑ inflammation	Europeans	Intronic	(eQTL)
	rs10898880	C	A				Americans	5' ATG16L2	(eQTL) ↑ exp [207]
	rs11605818	A	G	2%	1	 SLE [233]	European GWAS	Intronic	
	rs11235604	C	T	0% As 10%	1	  CROHN DISEASE [234–236] Protective SLE [237–239] with IgA nephropathy or lupus nephritis NSCLC EGFR* [169] Bad Theragnosis (Gefitinib) CORONARY ARTERY DISEASE [240] RHEUMATOID ARTHRITIS [223]	Asian GWAS Asian GWAS Asians	MISSENSE R220W <i>Asian-specific</i>	↓ exp
	rs11235667	A	G	0% As 11%	1	SLE [239] YY1, and FOXA binding sites	Asian GWAS	3' ATG16L2	
CHMP2B NM_014043 7278 eQTL	rs1002765	G	A	11%	1	  ATROPHIC GASTRITIS [241] precancerous x <i>H. pylori</i> INFECTION GASTRIC CANCER [241] x H. pylori INFECTION	Asians	 Intronic not specific MIR4795	(eQTL)

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
CHMP2B NM_014043 7278 eQTL	rs63751126	A	C	0%	1	ALS [242] 	Europeans	MISSENSE Q206H	
	rs63751048	C	T	0%	1		FRONTOTEMPORAL DEMENTIA [243] protein-truncating mutation	Europeans	NONSENSE
	rs63750652	G	A,C	0%	1	splice acceptor			
	rs63750653	G	T	0%	1	MISSENSE N148T			
LAMP1 NM_005561 74 eQTL	rs9577229	C	T	0%	1	TUBERCULOSIS [199] 	Asian GWAS	MISSENSE A204V	(eQTL)
	rs12871648	A	C	33%	1	PARKINSON DISEASE [244]	American GWAS	Intronic	
LAMP2 NM_015104 820 eQTL	rs727504953	G	A	0%	1	DANON DISEASE [245] cardiomyopathy, skeletal myopathy, and intellectual disability	Asians	MISSENSE G93R	↓ exp [245]

Table S7. AUTOPHAGY RECEPTORS

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEx
CALCOCO2 NM_00583 1311 eQTL	rs8074034	A	G	49%	26	GLIOBLASTOMA [246] pediatric	European GWAS	Intronic	eQTL - Brain
	rs550510	G	A	18%	14	 MULTIPLE SCLEROSIS: Protective [247] ↑ mitophagy ↑ binding with LC3C (LIR motif) ↓ INFLAMMATION (TNF release from B cells)	Europeans	MISSENSE G140E	eQTL-sQTL blood Brain
	rs2303015	T	C	4%	75	 BACTERIAL PERITONITIS [248] in patients with alcoholic cirrhosis  CROHN DISEASE [249]	Europeans European GWAS	MISSENSE V272A	eQTL - Colon
DRAM1 NM_018370 4677 eQTL induces the formation of the phagophore by binding SQSTM-1 [250,251]	rs7955890	C	T	11%	40	 NSCLC [11] Theragnostic (Platinum) ↑ PFS	Asians	Intronic	eQTL - Lung
	rs17032060	G	A	1%	24			3'UTR	
	rs77694286	A	G	1%	24			 TYPE 2 DIABETES [252] higher protein intake	European GWAS
NBR1 NM_005899 10,959 eQTL	rs17599948	G	C	6%	6	 PROSTATE CANCER [253] progression to lethal cancer after radiotherapy BREAST CANCER [254] Rare <i>BRCA1</i> 3'UTR SNPs NOT SPECIFIC. Common <i>NBR1</i> , <i>NBR2</i> , <i>BRCA1</i>	Americans	Intronic	eQTL – Breast, Prostate
NCOA4 NM_005437 1231 eQTL FERRITINOPHAGY	rs10740051	G	A	27%	8	PROSTATE CANCER [255] Coactivator for AR (androgen receptor) NCOA4 was recently identified as a cargo receptor for ferritin-based lysosomal degradation. NCOA4 depletion can eliminate iron accumulation and thus weaken ferroptosis. Cancer cells are susceptible to ferroptosis. Lower NCOA4 expression in ccRCC is associated with disease progression and poor prognosis, as well as impaired immune infiltration (CD8+ T cells) [256,257]	African Americans	Intronic	(eQTL – sQTL)
	rs10761581	T	G	43%	7			MISSENSE F8V	(eQTL – sQTL)
NUFIP1 NM_012345 144 eQTL RIBOPHAGY	rs17066364	G	C	3% (13% As)	61	 OBESITY [258]	Asians	Intronic LD with 5'	
	rs114280567	G	A	0% (6% As)	2	 ASTHMA [259] x DIISOCYANATE occupational exposure	European GWAS	3'	

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
OPTN NM_021980 473 eQTL	rs3829923	C	T	34%	3	GLAUCOMA [260]	Europeans	Promoter	
	rs10796021	TT	T,TC	44%	1			CCDC3	
	rs7921853	T	G	51%	1			Intronic	(eQTL)
	rs765884	T	C	28%	13			Intronic	(eQTL)
	rs11258194	T	A	3%	2	 GLAUCOMA [261] DIABETIC RETINOPATHY [262]	Asians	MISSENSE M98K	
	rs2234968	G	A	26%	4	GLAUCOMA [261]	Americans, and Asians	synonymous	(eQTL)
	rs10906308	G	A	22%	18	GLAUCOMA [263]	Americans	Intronic	
	rs825411	A	G	54%	4	 PAGET DISEASE [264]	European GWAS	Intronic	(eQTL)
	rs1561570	T	C	50%	3			Intronic	(eQTL)
	rs76647957	A	C	27%	3	PAGET DISEASE [265] Splicing (exon 5 skipping) → Truncated protein.	Americans	intronic	(sQTL)
	rs2234968	G	A					synonymous	(sQTL)
	rs10906303	A	G					intronic	(eQTL)
	Rare mutations or dysregulation of optineurin can cause several neurodegenerative diseases , including: amyotrophic lateral sclerosis, (rs267606929 E478G rs267606928 Q398X ↓ Ub binding), frontotemporal dementia (rs377219791 A481V, UBD, Q235*), glaucoma, (rs28939688 E50K, Insoluble Optineurin, Retinal ganglion cell apoptosis, rs75654767 R545Q Ub binding affected, rs373425395 H486R), Huntington disease, as well as inflammatory digestive disorders such as Crohn disease (reduced expression in macrophages. Innate immunity compromised) [266]								
SQSTM1 NM_003900 339 eQTL	rs10277	T	C	50%	9	 Age-related MACULAR DEGENERATION [8] Theragnosis (anti-VEGF)	Europeans	3'UTR	(eQTL)
<i>SQSTM1</i> amplification on chr.5q is linked to clear cell renal cell carcinoma [267]. Rare germinal <i>SQSTM1</i> mutations are associated with neurodegenerative diseases , such as ALS-FTD [268], Parkinson disease, and also Paget disease of bone, metabolic diseases, obesity, and insulin resistance [269,270]									
TAX1BP1 NM_006024 860 eQTL	rs11540483	T	A,C	11%	51	HNSCC [271]	South Americans	MISSENSE L307I	(eQTL)
	rs10214930	G	A	21%	20	HYPOSPADIAS [272]	European GWAS	Intronic	
Gain of <i>TAX1BP1</i> in 7p15.2-1 was associated with larger hepatocellular carcinoma size and positivity of HCV antibody [273]									

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX		
TOLLIP NM_019009 608 eQTL	rs5743890	T	C	14%	1	PULMONARY FIBROSIS [274,275] ↑ mortality RISK ↓ Expression	European-American GWAS	intronic	(eQTL)		
	rs111521887	C	G	20%	4					intronic	(eQTL)
	rs5743894	T	C							intronic	(eQTL)
	rs5743867	G	A	92%	18	 SEPSIS [276] ↓ RISK >CC ↓ Secretion of TNF and IL6.  HIV INFECTION [277] TUBERCULOSIS [278]	Asians	intronic	TOLLIP AS1 eQTL Lung ↑ exp [276] (PBMCs)		
	rs5743899	C	T	79%	1	 HIV INFECTION [277] RHINOVIRUS INFECTION [279,280] x AIR quality  TUBERCULOSIS [278] >CC RISK for progression.  LEISHMANIASIS [281]	Asians Europeans Asians Amazonians	intronic			
	rs3750920	C	T	46%	1	 LEISHMANIASIS [281] MALARIA [283] LEPROSY [284] TUBERCULOSIS [282] Protection PULMONARY FIBROSIS [285] Theragnosis (N-acetylcysteine) : Good [286]	Amazonians Amazonians Mexicans Asians European GWAS Americans	synonymous	(eQTL) ↑ exp [282] (monocytes)		
	rs3793964	T	C	67%	1	 LEPROSY [287] >TT ↑ RISK ↑ <i>IL1RN</i> exp (monocytes) Potential therapeutic target for IL1-dependent diseases.	Asians	intronic	(eQTL) ↑ exp [287] (monocytes)		
	rs3829223	C	T	52%	3	PULMONARY FIBROSIS [285]	European GWAS	intronic	eQTL		

Gene	variant	Ref	Alt	EUR freq	LD	Disease	Populations	Funct Annot	eQTL GTEX
TOLLIP NM_019009 608 eQTL	rs3168046	G	A	47%	3	PULMONARY FIBROSIS [285] LUNG GRAFT DYSFUNCTION [288] ↑SERPINE1/PAI1 plasma levels	European GWAS American GWAS	3'-UTR	eQTL/sQTL
	rs5744034	A	G	20%	5	PULMONARY FIBROSIS [285]	European GWAS 	3'-UTR LD RP11-532E4.2 missense	(eQTL)
	rs5743854	G	C	88%	3	 TUBERCULOSIS: Theragnosis (BCG VACCINATION) [289] ↓ TOLLIP mRNA expression (monocyte) After M. tuberculosis infection, TOLLIP-deficient monocytes ↑ IL6, ↓ bacterial replication. The TOLLIP-deficiency >G/G ↓ BCG-specific T-cell responses and ↑ susceptibility to tuberculosis infection. Activating TOLLIP may provide a novel adjuvant strategy for BCG vaccination	Americans, and South Africans	Promoter	TOLLIP AS1 eQTL
WDFY3 NM_014991 347 eQTL	rs76117213	G	A	1%	1	ALZHEIMER DISEASE [290]	American GWAS	Intronic	
	rs17009220	G	C	6%	1			Intronic	
Heterozygous, mostly <i>de novo</i> variants in WDFY3 result in a mild NEURODEVELOPMENTAL delay (intellectual disability, autism/hyperactivity disorder) and opposing effects on brain size [291]: Loss-of-function variants (truncating and missense) causing haploinsufficiency lead to MACROCEPHALY . In contrast, variants in the PH-domain of WDFY3 leads to MICROCEPHALY, via dysregulation of the WNT-pathway . Proliferating cortical neural progenitors highly express WDFY3, further supporting a role for this molecule in the regulation of neurogenesis.									

A

LUNG DISEASES

ASTHMA

ULK1 rs7487166, rs9652059, rs11616018, rs10902472 RISK
ATG5 rs573775, rs12201458, rs12212740, rs633724 RISK
ATG5 rs510432 ↑ exp (promoter), rs11751513
ATG7 rs2594971, rs1375206 RISK
MAP1LC3B rs8051218, rs7204722 RISK
NUFIP1 rs114280567
TOLLIP rs5743899 RHINOVIRUS INFECTION (RV) x AIR quality

TUBERCULOSIS

ULK1 rs7300908 RISK, rs12297124 ↓ RISK x INFECTION
ULK1 rs7138581 3'-UTR ↓ RISK, ↑ Severity
ULK1 rs9481 3'-UTR ↑ RISK
IRGM rs4958843, rs4958846 eQTL prom ↓ RISK ↓ exp
IRGM rs10065172 eQTL miR-196 ↓ RISK ↓ exp
IRGM rs10052068, rs10059011 ↓ RISK
IRGM rs10051924, rs13361189, rs9637876
MCL1 rs961581226
ATG4C rs11208029
ATG10 rs1864183
TOLLIP rs5743867, rs5743899, rs3750920
TOLLIP rs5743899, rs5743854 THERAGNOSIS (BCG VACCINATION)
LAMP1 rs9577229

LUNG FIBROSIS

ATG5 rs510432 RISK x COAL
ATG10 rs1864182 ↓ RISK x COAL
ATG12 rs26538 ↓ exp ↓ RISK x COAL
TOLLIP rs5744034, rs3168046, rs3793964, rs3829223
TOLLIP rs5743890, rs111521887, rs5743894
TOLLIP rs3750920 THERAGNOSIS (N-acetylcysteine)

LUNG GRAFT DYSFUNCTION

TOLLIP rs3168046

COPD

ATG16L1 rs2241880 >A ↑ RISK x SMOKING
ERG1 rs7729723 >G ↑ RISK x SMOKING

NICOTINE DEPENDENCE

GABARAP rs222843 RISK
GABARAP rs17710

LUNG CANCER

ULK1 rs7953348, rs12303764 THERAGNOSTIC (platinum)

MCL1 rs3831987 (non-smoker) PROTECTIVE

BECN1 rs11552193

ATG14 rs17742719, rs8003279,
 rs10099647 THERAGNOSTIC (platinum)

ATG5 rs2245214 RISK
ATG5 rs688810 THERAGNOSIS (gefatinib)
ATG5 rs510432 THERAGNOSIS (gefatinib)

ATG7 rs8154 (EGFR*) PROTECTIVE

ATG10 rs10036653 RISK of brain metastasis
ATG10 rs1864183, rs1864182 rs10514231 RISK
ATG10 rs1864183 THERAGNOSIS (platinum)
ATG10 rs10036653 THERAGNOSIS (gefatinib)
ATG10 rs1864182 THERAGNOSIS (gefatinib)

ATG12 rs26532 RISK (brain metastasis)
ATG12 rs26538 THERAGNOSIS (gefatinib)
ATG12 rs1058600

ATG16L1 rs2241880 PROTECTIVE (brain metastasis)

ATG16L1 rs2241880 (EGFR*) RISK
ATG16L2 rs11235604 THERAGNOSIS (gefatinib)
ATG16L2 rs10898880 THERAGNOSIS (radiotherapy) ↑ exp

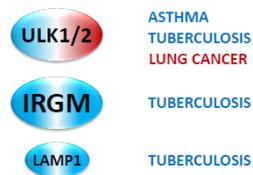
ATG3 rs13082005 THERAGNOSIS (platinum)
ATG4A rs807185 RISK

DRAM rs7955890 rs17032060 THERAGNOSIS



B

ULK1/2 complex



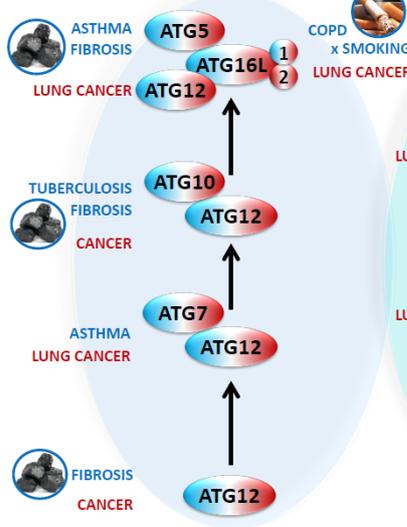
PtdIns3K complex-I



Receptors



ATG12-conj.



LC3-conj. system

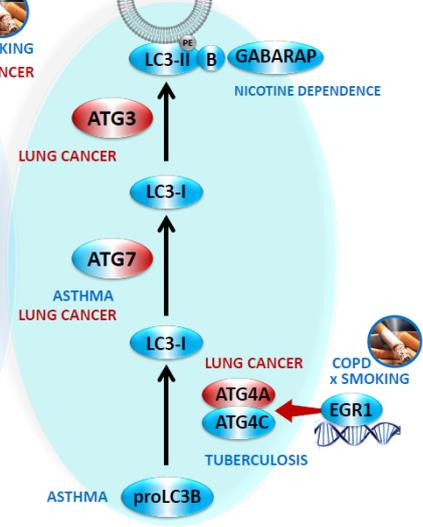


Figure S1. Autophagy deficiency in human lung diseases. (A) Summary of autophagy-related gene variations. (B) Steps of the autophagy pathway affected by SNPs. (C) Phenotypes of autophagy-deficient mouse models [146, 292-306]. CSE, cigarette smoke exposure. (Continued on next page).

C

<i>ulk1/2^{-/-}</i> (DKO)	RESPIRATORY distress [292] Death within 24 h of birth
<i>atg5^{-/-}</i>	
<i>atg4b^{-/-}</i>	LUNG FIBROSIS (tunicamycin [293], (bleomycin) [294]) ↑ inflammation (neutrophil infiltration)
<i>atg5^{ff} or atg7^{ff}</i> <i>Myeloid Cell-Specific</i>	LUNG FIBROSIS [295] ↑ IL18 (bleomycin)
<i>egr1</i> KO	Smoke-induced COPD [146] <i>egr1</i> KO ↓ ATG4B expression ↓ LC3B conversion
<i>map1lc3b^{-/-}</i>	Smoke-induced COPD [296] LUNG FIBROSIS Upon aging (bleomycin) [297]
<i>becn1^{-/-}</i> <i>Lung-Specific, Conditional</i>	LETHAL RESPIRATORY INSUFFICIENCY [298] ↓ Lung development (branching)
Silencing <i>Fundc1</i>	Smoke-induced COPD [299] Cigarette smoke (CSE) COPD mice ↑ FUNDC1. Silencing <i>Fundc1</i> → ↓ IL6 TNF ↓ CSE-induced mitophagy cell apoptosis. ↑ COPD lung function
<i>tollip^{-/-}</i>	ASTHMA [300-302] TOLLIP is a negative regulator of innate immunity: It prevents pulmonary neutrophil recruitment in response to allergen stimulation (house dust mite), bacterial commensal infection, or rhinovirus infection, three contributors of asthma exacerbations. <i>tollip</i> -KO mice experience increased neutrophil recruitment, which exacerbates asthma.
<i>Atg16l1</i> ΔWD LAP deficient	Lethal infection by INFLUENZA A virus [303] fulminant pneumonia , lung inflammation and high mortality
<i>Becn1^{+/-}</i>	LUNG ADENOCARCINOMAS [304,305]
<i>sh3glb1^{-/-}</i>	SMALL CELL LUNG CARCINOMAS [306]

Figure S1 (Continued). Autophagy deficiency in human lung diseases. (A) Summary of autophagy-related gene variations. (B) Steps of the autophagy pathway affected by SNPs. (C) Phenotypes of autophagy-deficient mouse models [146, 292-306]. CSE, cigarette smoke exposure.

A

RISK FACTORS

BLOOD LIPIDS

WIP1 rs2909207 (HDL) eQTL
UVRAG rs17134573
ATG4C rs6587988 (cholesterol, triglycerides)
ATG4D rs10439163 (cholesterol, LDL)
ATG7 rs7635838 (HDL)

ATHEROSCLEROSIS

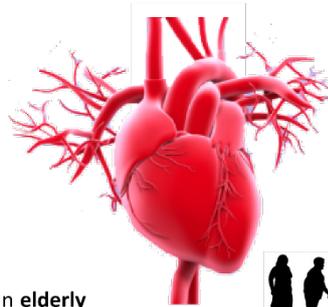
ATG4B rs139302128
ATG4C rs6683832 Blood fibrinogen
ATG16L1 rs2241880 RISK ♀

BLOOD PRESSURE and heart rate

ATG7 rs2447607
ATG9B rs7830 x **AIR POLLUTION** urban elderly

TYPE 2 DIABETES

ATG2B rs4905480
AMBRA1 rs110389913
BECN1 rs10512488
DRAM1 rs77694286
SH3GLB1 rs263436
ATG13 rs35619591



CORONARY ARTERY DISEASE (CAD)

TBC1D14 rs10804990
ATG9B rs2373929
ATG16L2 rs11235604
MAP1LC3A rs2424994, rs6088521

ACUTE MYOCARDIAL INFARCTION

ATG5 rs190825454
ATG7 rs2594975
ATG9B rs13307588
MAP1LC3B rs111626199, rs77019223

STROKE

ATG7 rs2594966, rs2594973, rs4684776
ATG9B rs3800787, rs11769158, rs6464119, rs3918220, rs3763486 (attributed to NOS3)

Q FEVER x *C. burnetii* infection

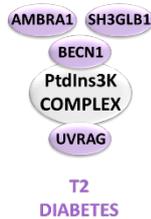
ATG5 rs2245214 Protective
MAP1LC3A rs1040747

B

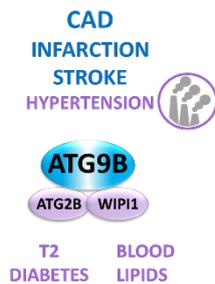
ULK COMPLEX



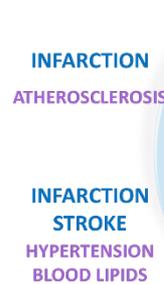
PtdIns3K COMPLEX



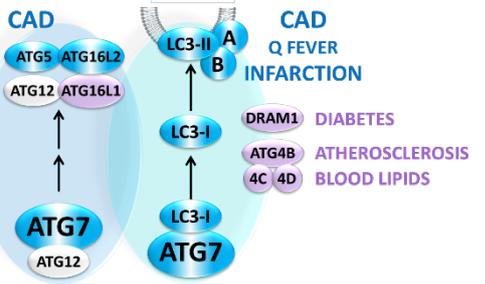
ATG9A SYSTEM



ATG12 CONJ.



LC3 CONJ.



C

<i>atg13</i> ^{-/-}	HEART defect [307] embryonic lethality
<i>rb1cc1</i> ^{-/-}	HEART defect [308] embryonic lethality
<i>atg5</i> ^{fl/fl} <i>Cardiac-specific</i>	Age-related CARDIOMYOPATHY [309] ↑ left ventricular dimension ↓ fractional shortening
<i>uvrag</i> ^{-/-}	Age-related CARDIOMYOPATHY [310] ↑ inflammation
<i>fbxo32/atrogin1</i> ^{-/-}	CARDIOMYOPATHY [311] myocardial remodeling, ↓ diastolic function, arrhythmias → fails to degrade CHMP2B, resulting in autophagy impairment

Figure S2. Autophagy deficiency in human cardiovascular diseases. (A) Summary of autophagy-related gene variations. (B) Steps of the autophagy pathway affected by SNPs. (C) Phenotypes of autophagy-deficient mouse models [307-311]. CAD, coronary artery disease.

A

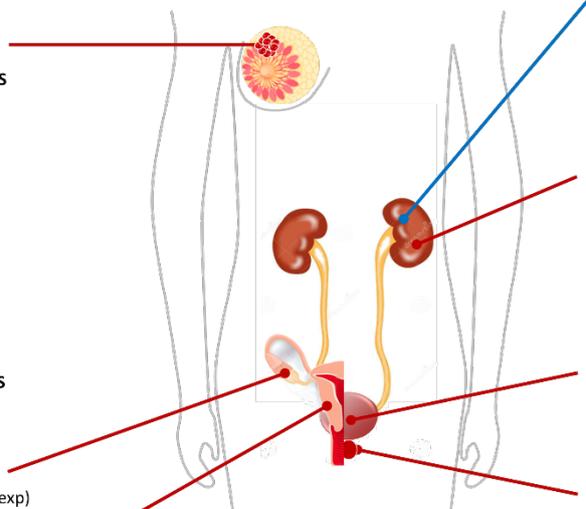
MENOPAUSE
ATG10 rs9447453 Delayed age

BREAST CANCER
ATG13 rs10838611 THERAGNOSIS
ATG16L1 rs2241880 RISK
SMCR8 rs1563634 RISK
MCL1 rs3831987 RISK
NRBF2 rs10995190 RISK
NRBF2 rs10509168 RISK
VMP1 rs1295925 RISK
ATG10 rs1864182 RISK
ATG10 rs10514231 RISK
ATG10 rs7707921 RISK
ATG10 rs73134739 RISK
ATG7 rs8154 PROGNOSIS
ATG5 rs473543 THERAGNOSIS
NBR1 rs1759948 RISK

OVARIAN CANCER
ATG4A rs5973822 (eQTL, miRNA, ↑exp)
SMCR8 rs921986, rs12952556 eQTLs

CERVICAL CANCER
ATG4A rs5973822 (eQTL, miRNA, ↑)
ATG4A rs807181, rs807182 x HPV INFECTION RISK
ATG4A rs807183 (eQTL, ↓exp) x HPV RISK

UTERINE LEIOMYOMAS
MAP1LC3C rs1776161



KIDNEY DISEASE
ATG2A rs188780113 MISSENSE R478C RISK
ATG16L1 rs2241880 MISSENSE T300A
UROPATHOGENIC E. coli
Protective

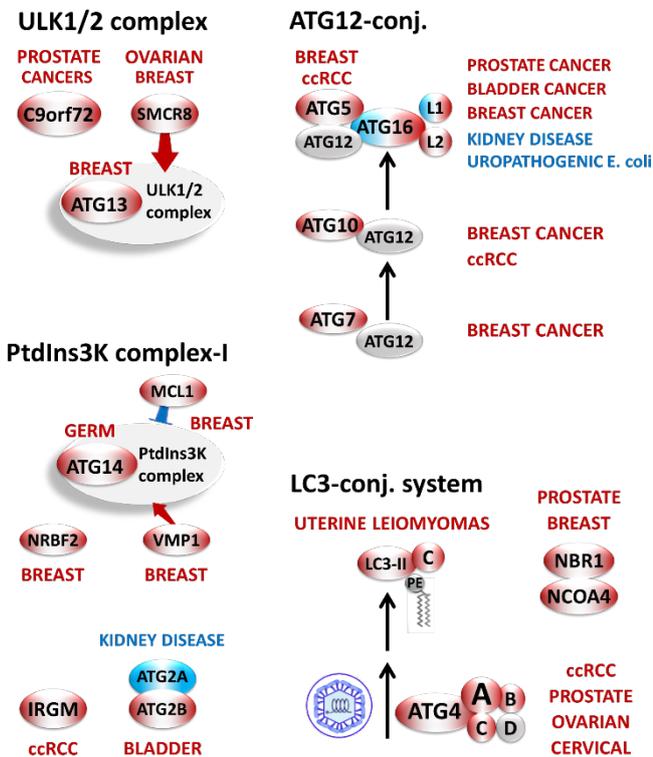
ccRCC
ATG4A rs7880351 THERAGNOSIS (pazopanib)
ATG4C rs6683832 THERAGNOSIS (pazopanib)
 rs6670694
ATG5 rs490010 THERAGNOSIS (pazopanib)
ATG7 rs2606736
ATG16L2 rs10751215 PROGNOSIS
IRGM rs10059011 RISK

BLADDER CANCER
ATG2B rs3759601 THERAGNOSIS (BCG)
ATG5 rs2245214 THERAGNOSIS (BCG)

PROSTATE CANCER
ATG4B rs3771570
ATG16L1 rs78835907 PROGNOSIS
C9orf72 rs774359, rs3849942
 rs10122902, rs10757665
ATG14 rs8015211 PROGNOSIS eQTL
NCOA4 rs10740051, rs10761581
NBR1 rs1759948 THERAGNOSIS (radiotherapy)
 attributed to BRCA1

TESTICULAR GERM CELL TUMOR
ATG14 rs1009647

B



C

<i>atg5</i> ^{-/-} Kidney specific	ACUTE KIDNEY INJURY [312,313] Cisplatin- and ischemia-reperfusion-induced
<i>atg7</i> ^{-/-}	KIDNEY DISEASE AND AGING [314]
<i>atg5</i> ^{+/+}	KIDNEY DISEASE AND AGING [314]
<i>atg16l1</i>	URINARY TRACT INFECTION [315]
<i>Atg16l1</i> ^{T300A}	URINARY TRACT UPEC INFECTION [315] Protection: ↑ vesicle trafficking, ↓ infection. Independent of autophagy or proinflammatory cytokine responses. ↑ expression of RAB33B, which interacts with ATG16L1, as RAB27B and RAB11A → UPEC exocytosis
<i>optn</i> ^{-/-}	E. Coli-INDUCED PERITONITIS [316]
<i>Becn1</i> ^{+/-} or <i>atg7</i> ^{-/-} Ovary specific	REDUCED FERTILITY [317]
<i>atg16l1</i> ^{+/+} Uterus specific	REDUCED FERTILITY [318] Endometrial decidualization
SQSTM1 shRNA	ccRCC growth [267] addictive to SQSTM1 gene gain and overexpression (in vitro and in vivo)
<i>atg7</i> ^{+/+} <i>pten</i> ^{+/+} Inducible prostate specific	PROSTATE CANCER [319] <i>atg7</i> KO delays <i>pten</i> -deficient prostate tumor progression (evidence of ER stress)
<i>Becn1</i> ^{+/-} Becn1 ^{F121A} (KI/KI)	BREAST CANCER [304, 320–322] ↑ ERBB2/HER2-driven tumorigenesis ERBB2/HER2 interacts with BECN1 and inhibits autophagy Somatic Allelic loss of BECN1 is observed in over 50% of human breast cancers
<i>rb1cc1</i> ^{-/-} <i>Rb1cc1</i> ^{+/+} Breast specific	BREAST CANCER [323]
<i>rb1cc1</i> ^{+/+}	OVARIAN CANCER [324] hyperplasia of epidermis (acanthosis)
<i>Becn1</i> ^{+/-}	EARLY OVARIAN TUMORS [325]

Figure S3. Autophagy deficiency in breast and urogenital diseases. (A) Summary of autophagy-related gene variations. (B) Steps of the autophagy pathway affected by SNPs. (C) Phenotypes of autophagy-deficient mouse models [267, 304, 312–325]. UPEC, uropathogenic *E. coli*

Supplementary information references

- [1] Allot A, Peng Y, Wei C-H, et al. LitVar: a semantic search engine for linking genomic variant data in PubMed and PMC. *Nucleic Acids Res.* 2018 Jul 2;46(W1):W530–W536. doi:10.1093/nar/gky355. PubMed PMID: 29762787.
- [2] Ward LD, Kellis M. HaploReg: a resource for exploring chromatin states, conservation, and regulatory motif alterations within sets of genetically linked variants. *Nucleic Acids Res.* 2012 Jan 1;40(D1):D930–D934. doi:10.1093/nar/gkr917. PubMed PMID: 22064851.
- [3] Ward LD, Kellis M. HaploReg v4: systematic mining of putative causal variants, cell types, regulators and target genes for human complex traits and disease. *Nucleic Acids Res.* 2016 Jan 4;44(D1):D877-81. doi:10.1093/nar/gkv1340. PubMed PMID: 26657631.
- [4] Carithers LJ, Ardlie K, Barcus M, et al. A novel approach to high-quality postmortem tissue procurement: The GTEx project. *Biopreserv Biobank.* 2015 Oct 20;13(5):311–319. doi:10.1089/bio.2015.0032. PubMed PMID: 26484571.
- [5] Zhang R-R, Liang L, Chen W-W, et al. *ULK1* polymorphisms confer susceptibility to pulmonary tuberculosis in a Chinese population. *Int J Tuberc Lung Dis.* 2019 Feb 1;23(2):265–271. doi:10.5588/ijtld.18.0174. PubMed PMID: 30808462.
- [6] Horne DJ, Graustein AD, Shah JA, et al. Human *ULK1* variation and susceptibility to Mycobacterium tuberculosis infection. *J Infect Dis.* 2016 Oct 15;214(8):1260–1267. doi:10.1093/infdis/jiw347. PubMed PMID: 27485354.
- [7] Zhang X, Han R, Wang M, et al. Association between the autophagy-related gene *ULK1* and ankylosing spondylitis susceptibility in the Chinese Han population: a case–control study. *Postgrad Med J.* 2017 Dec 1;93(1106):752–757. doi:10.1136/postgradmedj-2017-134964. PubMed PMID: 28667165.
- [8] Paterno JJ, Koskela A, Hyttinen JMT, et al. Autophagy genes for wet age-related macular degeneration in a Finnish case-control study. *Genes (Basel).* 2020 Nov 6;11(11):1318. doi:10.3390/genes11111318. PubMed PMID: 33172148.
- [9] Morgan AR, Lam W-J, Han D-Y, et al. Association analysis of *ULK1* with Crohn's Disease in a New Zealand population. *Gastroenterol Res Pract.* 2012 Mar 20;715309. doi:10.1155/2012/715309. PubMed PMID: 22536218.
- [10] Poon AH, Chouiali F, Tse SM, et al. Genetic and histologic evidence for autophagy in asthma pathogenesis. *J Allergy Clin Immunol.* 2012 Feb;129(2):569–571. doi:10.1016/j.jaci.2011.09.035. PubMed PMID: 22040902.
- [11] Wang S, Song X, Zhao X, et al. Association between polymorphisms of autophagy pathway and responses in non-small cell lung cancer patients treated with platinum-based chemotherapy. *Yi chuan.* 2017 Mar 20;39(3):250–262. doi:10.16288/j.ycz.16-294. PubMed PMID: 28420621.

- [12] Henckaerts L, Cleynen I, Brinar M, et al. Genetic variation in the autophagy gene *ULK1* and risk of Crohn's disease. *Inflamm Bowel Dis*. 2011 Jun;17(6):1392–1397. doi:10.1002/ibd.21486. PubMed PMID: 21560199.
- [13] Kumar M, Papaleo E. A pan-cancer assessment of alterations of the kinase domain of *ULK1*, an upstream regulator of autophagy. *Sci Rep*. 2020 Sep 10;10(1):14874. doi:10.1038/s41598-020-71527-4. PubMed PMID: 32913252.
- [14] Zheng Y, Xie M, Zhang N, et al. miR-1262 suppresses gastric cardia adenocarcinoma via targeting oncogene *ULK1*. *J Cancer*. 2021 Jan 1;12(4):1231–1239. doi:10.7150/JCA.46971. PubMed PMID: 33442421.
- [15] Al Eissa MM, Fiorentino A, Sharp SI, et al. Exome sequence analysis and follow up genotyping implicates rare *ULK1* variants to be involved in susceptibility to schizophrenia. *Ann Hum Genet*. 2018 Mar 17;82(2):88–92. doi:10.1111/ahg.12226. PubMed PMID: 29148569.
- [16] Fung H-C, Scholz S, Matarin M, et al. Genome-wide genotyping in Parkinson's disease and neurologically normal controls: first stage analysis and public release of data. *Lancet Neurol*. 2006 Nov;5(11):911–916. doi:10.1016/S1474-4422(06)70578-6. PubMed PMID: 17052657.
- [17] Wolthers BO, Frandsen TL, Baruchel A, et al. Asparaginase-associated pancreatitis in childhood acute lymphoblastic leukaemia: an observational Ponte di Legno Toxicity Working Group study. *Lancet Oncol*. 2017 Sep;18(9):1238–1248. doi:10.1016/S1470-2045(17)30424-2. PubMed PMID: 28736188.
- [18] Li Z, Xin J, Chen W, et al. Genetic variants in autophagy associated genes are associated with DNA damage levels in Chinese population. *Gene*. 2017 Aug;414–419. doi:10.1016/j.gene.2017.05.017. PubMed PMID: 28512061.
- [19] Liu B, An T, Li M, et al. The association between early-onset cardiac events caused by neoadjuvant or adjuvant chemotherapy in triple-negative breast cancer patients and some novel autophagy-related polymorphisms in their genomic DNA: a real-world study. *Cancer Commun*. 2018 Dec 4;38(1):71. doi:10.1186/s40880-018-0343-7. PubMed PMID: 30514381.
- [20] Bronson PG, Chang D, Bhangale T, et al. Common variants at *PVT1*, *ATG13-AMBRA1*, *AHI1* and *CLEC16A* are associated with selective IgA deficiency. *Nat Genet*. 2016 Nov;48(11):1425–1429. doi:10.1038/ng.3675. PubMed PMID: 27723758.
- [21] Huyghe JR, Jackson AU, Fogarty MP, et al. Exome array analysis identifies new loci and low-frequency variants influencing insulin processing and secretion. *Nat Genet*. 2013 Feb 23;45(2):197–201. doi:10.1038/ng.2507. PubMed PMID: 23263489.
- [22] Berger MD, Yamauchi S, Cao S, et al. Autophagy-related polymorphisms predict hypertension in patients with metastatic colorectal cancer treated with FOLFIRI and bevacizumab: Results from TRIBE and FIRE-3 trials. *Eur J Cancer*. 2017 May;13–20. doi:10.1016/j.ejca.2017.02.020. PubMed PMID: 28347919.

- [23] Errichiello E, Giorda R, Gambale A, et al. *RB1CC1* duplication and aberrant overexpression in a patient with schizophrenia: further phenotype delineation and proposal of a pathogenetic mechanism. *Mol Genet Genomic Med*. 2021 Jan 19;9(1):e1561. doi:10.1002/mgg3.1561. PubMed PMID: 33340270.
- [24] Degenhardt F, Priebe L, Meier S, et al. Duplications in *RB1CC1* are associated with schizophrenia; identification in large European sample sets. *Transl Psychiatry*. 2013 Nov 26;e326. doi:10.1038/tp.2013.101. PubMed PMID: 26151896.
- [25] Broberg K, Huynh E, Engström KS, et al. Association between polymorphisms in *RMI1*, *TOP3A*, and *BLM* and risk of cancer, a case-control study. *BMC Cancer*. 2009 Dec 11;9(1):140. doi:10.1186/1471-2407-9-140. PubMed PMID: 19432957.
- [26] Peter B, Wijsman EM, Nato AQ, et al. Genetic candidate variants in two multigenerational families with childhood apraxia of speech. *PLoS One*. 2016 Apr 27;11(4):e0153864. doi:10.1371/journal.pone.0153864. PubMed PMID: 27120335.
- [27] Etheredge AJ, Finnell RH, Carmichael SL, et al. Maternal and infant gene-folate interactions and the risk of neural tube defects. *Am J Med Genet*. 2012 Oct;158A(10):2439–2446. doi:10.1002/ajmg.a.35552. PubMed PMID: 22903727.
- [28] Kelemen LE, Sellers TA, Schildkraut JM, et al. Genetic variation in the one-carbon transfer pathway and ovarian cancer risk. *Cancer Res*. 2008 Apr 1;68(7):2498–2506. doi:10.1158/0008-5472.CAN-07-5165. PubMed PMID: 18381459.
- [29] Yao L, Zhong W, Zhang Z, et al. Classification tree for detection of single-nucleotide polymorphism (SNP)-by-SNP interactions related to heart disease: Framingham Heart Study. *BMC Proc*. 2009 Dec 15;S83. doi:10.1186/1753-6561-3-s7-s83. PubMed PMID: 20018079.
- [30] Li Y-J, Guggenheim JA, Bulusu A, et al. An international collaborative family-based whole-genome linkage scan for high-grade myopia. *Invest Ophthalmol Vis Sci*. 2009 Jul 1;50(7):3116–3127. doi:10.1167/iovs.08-2781. PubMed PMID: 19324860.
- [31] Stein JL, Hibar DP, Madsen SK, et al. Discovery and replication of dopamine-related gene effects on caudate volume in young and elderly populations (N=1198) using genome-wide search. *Mol Psychiatry*. 2011 Sep 19;16(9):927–937. doi:10.1038/mp.2011.32. PubMed PMID: 21502949.
- [32] Koopmann TT, Adriaens ME, Moerland PD, et al. Genome-wide identification of expression quantitative trait loci (eQTLs) in human heart. *PLoS One*. 2014 May 20;9(5):e97380. doi:10.1371/journal.pone.0097380. PubMed PMID: 24846176.
- [33] Van Laer L, Huyghe JR, Hannula S, et al. A genome-wide association study for age-related hearing impairment in the Saami. *Eur J Hum Genet*. 2010 Jun 13;18(6):685–693. doi:10.1038/ejhg.2009.234. PubMed PMID: 20068591.

- [34] Laaksovirta H, Peuralinna T, Schymick JC, et al. Chromosome 9p21 in amyotrophic lateral sclerosis in Finland: a genome-wide association study. *Lancet Neurol.* 2010 Oct;9(10):978–985. doi:10.1016/S1474-4422(10)70184-8. PubMed PMID: 20801718.
- [35] Liu X, He J, Gao F-B, et al. The epidemiology and genetics of Amyotrophic lateral sclerosis in China. *Brain Res.* 2018 Aug 15;121–126. doi:10.1016/j.brainres.2018.02.035. PubMed PMID: 29501653.
- [36] Ferrari R, Mok K, Moreno JH, et al. Screening for *C9ORF72* repeat expansion in FTLD. *Neurobiol Aging.* 2012 Aug;33(8):1850.e1-11. doi:10.1016/j.neurobiolaging.2012.02.017. PubMed PMID: 22459598.
- [37] Williams KA, Lee M, Hu Y, et al. A systems genetics approach identifies *CXCL14*, *ITGAX*, and *LPCAT2* as novel aggressive prostate cancer susceptibility genes. *PLoS Genet.* 2014 Nov 20;10(11):e1004809. doi:10.1371/journal.pgen.1004809. PubMed PMID: 25411967.
- [38] Harley ITW, Niewold TB, Stormont RM, et al. The role of genetic variation near interferon-kappa in systemic lupus erythematosus. *J Biomed Biotechnol.* 2010 Jul 15;706825. doi:10.1155/2010/706825. PubMed PMID: 20706608.
- [39] Karch CM, Wen N, Fan CC, et al. Selective genetic overlap between amyotrophic lateral sclerosis and diseases of the frontotemporal dementia spectrum. *JAMA Neurol.* 2018 Jul 1;75(7):860–875. doi:10.1001/jamaneurol.2018.0372. PubMed PMID: 29630712.
- [40] Fogh I, Ratti A, Gellera C, et al. A genome-wide association meta-analysis identifies a novel locus at 17q11.2 associated with sporadic amyotrophic lateral sclerosis. *Hum Mol Genet.* 2014 Apr 15;23(8):2220–2231. doi:10.1093/hmg/ddt587. PubMed PMID: 24256812.
- [41] Jones AR, Woollacott I, Shatunov A, et al. Residual association at *C9orf72* suggests an alternative amyotrophic lateral sclerosis-causing hexanucleotide repeat. *Neurobiol Aging.* 2013 Sep;34(9):2234.e1-7. doi:10.1016/j.neurobiolaging.2013.03.003. PubMed PMID: 23587638.
- [42] Luty AA, Kwok JBJ, Thompson EM, et al. Pedigree with frontotemporal lobar degeneration-motor neuron disease and Tar DNA binding protein-43 positive neuropathology: genetic linkage to chromosome 9. *BMC Neurol.* 2008 Aug 29;8(1):32. doi:10.1186/1471-2377-8-32. PubMed PMID: 18755042.
- [43] Harms MB, Cady J, Zaidman C, et al. Lack of *C9ORF72* coding mutations supports a gain of function for repeat expansions in amyotrophic lateral sclerosis. *Neurobiol Aging.* 2013 Sep;34(9):2234.e13-9. doi:10.1016/j.neurobiolaging.2013.03.006. PubMed PMID: 23597494.
- [44] Wason JMS, Dudbridge F. Comparison of multimarker logistic regression models, with application to a genomewide scan of schizophrenia. *BMC Genet.* 2010 Dec 9;11(1):80. doi:10.1186/1471-2156-11-80. PubMed PMID: 20828390.
- [45] Bahari G, Hashemi M, Taheri M, et al. Association of *IRGM* polymorphisms and susceptibility to pulmonary tuberculosis in Zahedan, Southeast Iran.

ScientificWorldJournal. 2012 Sep 23;950801. doi:10.1100/2012/950801. PubMed PMID: 23049477.

- [46] Latiano A, Palmieri O, Cucchiara S, et al. Polymorphism of the *IRGM* gene might predispose to fistulizing behavior in crohn's disease. *Am J Gastroenterol*. 2009 Jan;104(1):110–116. doi:10.1038/ajg.2008.3. PubMed PMID: 19098858.
- [47] McCarroll SA, Huett A, Kuballa P, et al. Deletion polymorphism upstream of *IRGM* associated with altered *IRGM* expression and Crohn's disease. *Nat Genet*. 2008 Sep 24;40(9):1107–1112. doi:10.1038/ng.215. PubMed PMID: 19165925.
- [48] Prescott NJ, Dominy KM, Kubo M, et al. Independent and population-specific association of risk variants at the *IRGM* locus with Crohn's disease. *Hum Mol Genet*. 2010 May 1;19(9):1828–1839. doi:10.1093/hmg/ddq041. PubMed PMID: 20106866.
- [49] Parkes M, Barrett JC, Prescott NJ, et al. Sequence variants in the autophagy gene *IRGM* and multiple other replicating loci contribute to Crohn's disease susceptibility. *Nat Genet*. 2007 Jul 6;39(7):830–832. doi:10.1038/ng2061. PubMed PMID: 17554261.
- [50] Brest P, Corcelle EA, Cesaro A, et al. Autophagy and Crohn's disease: at the crossroads of infection, inflammation, immunity, and cancer. *Curr Mol Med*. 2010 Jul;10(5):486–502. doi:10.2174/156652410791608252. PubMed PMID: 20540703.
- [51] Ajayi TA, Innes CL, Grimm SA, et al. Crohn's disease *IRGM* risk alleles are associated with altered gene expression in human tissues. *Am J Physiol Gastrointest Liver Physiol*. 2019 Jan 1;316(1):G95–G105. doi:10.1152/ajpgi.00196.2018. PubMed PMID: 30335469.
- [52] Brest P, Lapaquette P, Souidi M, et al. A synonymous variant in *IRGM* alters a binding site for miR-196 and causes deregulation of *IRGM*-dependent xenophagy in Crohn's disease. *Nat Genet*. 2011 Mar;43(3):242–245. doi:10.1038/ng.762. PubMed PMID: 21278745.
- [53] Kimura T, Watanabe E, Sakamoto T, et al. Autophagy-related *IRGM* polymorphism is associated with mortality of patients with severe sepsis. *PLoS One*. 2014 Mar 13;9(3):e91522. doi:10.1371/journal.pone.0091522. PubMed PMID: 24626347.
- [54] King KY, Lew JD, Ha NP, et al. Polymorphic allele of human *IRGM1* is associated with susceptibility to tuberculosis in African Americans. *PLoS One*. 2011 Jan 21;6(1):e16317. doi:10.1371/journal.pone.0016317. PubMed PMID: 21283700.
- [55] Yao Q, Zhu Y, Wang W, et al. Polymorphisms in autophagy-related gene *IRGM* are associated with susceptibility to autoimmune thyroid diseases. *Biomed Res Int*. 2018 Jun 11;2018(1):7959707. doi:10.1155/2018/7959707. PubMed PMID: 29992164.

- [56] Xia Q, Wang M, Yang X, et al. Autophagy-related *IRGM* genes confer susceptibility to ankylosing spondylitis in a Chinese female population: A case-control study. *Genes Immun.* 2017 Jan;18(1):42–47. doi:10.1038/gene.2016.48. PubMed PMID: 28031552.
- [57] Zhou X, Lu X, Lv J, et al. Genetic association of *PRDM1-ATG5* intergenic region and autophagy with systemic lupus erythematosus in a Chinese population. *Ann Rheum Dis.* 2011 Jul;70(7):1330–1337. doi:10.1136/ard.2010.140111. PubMed PMID: 21622776.
- [58] Lu Y, Li Q, Peng J, et al. Association of autophagy-related *IRGM* polymorphisms with latent versus active tuberculosis infection in a Chinese population. *Tuberculosis (Edinb).* 2016 Mar;47–51. doi:10.1016/j.tube.2016.01.001. PubMed PMID: 26980495.
- [59] Xie H, Li C, Zhang M, et al. Association between *IRGM* polymorphisms and tuberculosis risk: A meta-analysis. *Medicine (Baltimore).* 2017 Oct;96(43):e8189. doi:10.1097/MD.00000000000008189. PubMed PMID: 29068986.
- [60] Ellinghaus D, Jostins L, Spain SL, et al. Analysis of five chronic inflammatory diseases identifies 27 new associations and highlights disease-specific patterns at shared loci. *Nat Genet.* 2016 May;48(5):510–518. doi:10.1038/ng.3528. PubMed PMID: 26974007.
- [61] Folwaczny M, Tsekeri E, Glas J. A haplotypic variant at the *IRGM* locus and rs11747270 are related to the susceptibility for chronic periodontitis. *Inflamm Res.* 2018 Feb 5;67(2):129–138. doi:10.1007/s00011-017-1101-z. PubMed PMID: 28983640.
- [62] Peter I, Mitchell AA, Ozelius L, et al. Evaluation of 22 genetic variants with Crohn's Disease risk in the Ashkenazi Jewish population: a case-control study. *BMC Med Genet.* 2011 May 6;12(1):63. doi:10.1186/1471-2350-12-63. PubMed PMID: 21548950.
- [63] Baskaran K, Pugazhendhi S, Ramakrishna BS. Association of *IRGM* gene mutations with inflammatory bowel disease in the Indian population. *PLoS One.* 2014 Sep 5;9(9):e106863. doi:10.1371/journal.pone.0106863. PubMed PMID: 25191865.
- [64] Kee BP, Ng JG, Ng CC, et al. Genetic polymorphisms of *ATG16L1* and *IRGM* genes in Malaysian patients with Crohn's disease. *J Dig Dis.* 2020 Jan 13;21(1):29–37. doi:10.1111/1751-2980.12829. PubMed PMID: 31654602.
- [65] Rufini S, Ciccacci C, Di Fusco D, et al. Autophagy and inflammatory bowel disease: Association between variants of the autophagy-related *IRGM* gene and susceptibility to Crohn's disease. *Dig Liver Dis.* 2015 Sep;47(9):744–750. doi:10.1016/j.dld.2015.05.012. PubMed PMID: 26066377.
- [66] Castaño-Rodríguez N, Kaakoush NO, Goh K-L, et al. Autophagy in *Helicobacter pylori* infection and related gastric cancer. *Helicobacter.* 2015 Oct;20(5):353–369. doi:10.1111/hel.12211. PubMed PMID: 25664588.

- [67] Ge J, Li L, Jin Q, et al. Functional *IRGM* polymorphism is associated with language impairment in glioma and upregulates cytokine expressions. *Tumour Biol.* 2014 Aug 24;35(8):8343–8348. doi:10.1007/s13277-014-2091-x. PubMed PMID: 24859836.
- [68] Yang D, Chen J, Shi C, et al. Autophagy gene polymorphism is associated with susceptibility to leprosy by affecting inflammatory cytokines. *Inflammation.* 2014 Apr 22;37(2):593–598. doi:10.1007/s10753-013-9773-1. PubMed PMID: 24264476.
- [69] Lin Y-C, Chang P-F, Lin H-F, et al. Variants in the autophagy-related gene *IRGM* confer susceptibility to non-alcoholic fatty liver disease by modulating lipophagy. *J Hepatol.* 2016 Dec;65(6):1209–1216. doi:10.1016/j.jhep.2016.06.029. PubMed PMID: 27417217.
- [70] Simon TG, Deng X, Liu C, et al. The immunity-related GTPase M rs13361189 variant does not increase the risk for prevalent or incident steatosis; results from the Framingham Heart Study. *Liver Int.* 2019 Jun 17;39(6):1022–1026. doi:10.1111/liv.14039. PubMed PMID: 30597691.
- [71] Franke A, McGovern DPB, Barrett JC, et al. Genome-wide meta-analysis increases to 71 the number of confirmed Crohn's disease susceptibility loci. *Nat Genet.* 2010 Dec;42(12):1118–1125. doi:10.1038/ng.717. PubMed PMID: 21102463.
- [72] Moon CM, Shin D-J, Kim SW, et al. Associations between genetic variants in the *IRGM* gene and inflammatory bowel diseases in the Korean population. *Inflamm Bowel Dis.* 2013 Jan;19(1):106–114. doi:10.1002/ibd.22972. PubMed PMID: 22508677.
- [73] Intemann CD, Thye T, Niemann S, et al. Autophagy gene variant *IRGM* -261T contributes to protection from tuberculosis caused by *Mycobacterium tuberculosis* but not by *M. africanum* strains. *PLoS Pathog.* 2009 Sep 11;5(9):e1000577. doi:10.1371/journal.ppat.1000577. PubMed PMID: 19750224.
- [74] Yuan L, Ke Z, Ma J, et al. *IRGM* gene polymorphisms and haplotypes associate with susceptibility of pulmonary tuberculosis in Chinese Hubei Han population. *Tuberculosis (Edinb).* 2016 Jan;58–64. doi:10.1016/j.tube.2015.10.014. PubMed PMID: 26786655.
- [75] Simon TG, Van Der Sloot KWJ, Chin SB, et al. *IRGM* gene variants modify the relationship between visceral adipose tissue and NAFLD in patients with Crohn's disease. *Inflamm Bowel Dis.* 2018 Sep 15;24(10):2247–2257. doi:10.1093/ibd/izy128. PubMed PMID: 29788077.
- [76] Burada F, Plantinga TS, Ioana M, et al. *IRGM* gene polymorphisms and risk of gastric cancer. *J Dig Dis.* 2012 Jul;13(7):360–365. doi:10.1111/j.1751-2980.2012.00602.x. PubMed PMID: 22713085.
- [77] Santoni M, Piva F, De Giorgi U, et al. Autophagic gene polymorphisms in liquid biopsies and outcome of patients with metastatic clear cell renal cell carcinoma.

Anticancer Res. 2018 Oct 1;38(10):5773–5782.
doi:10.21873/anticanres.12916. PubMed PMID: 30275199.

- [78] Kariuki SN, Franek BS, Mikolaitis RA, et al. Promoter variant of *PIK3C3* is associated with autoimmunity against Ro and Sm epitopes in African-American lupus patients. *J Biomed Biotechnol.* 2010 Jul 4;826434. doi:10.1155/2010/826434. PubMed PMID: 20671926.
- [79] Stopkova P, Saito T, Papolos DF, et al. Identification of *PIK3C3* promoter variant associated with bipolar disorder and schizophrenia. *Biol Psychiatry.* 2004 May 15;55(10):981–988. doi:10.1016/j.biopsych.2004.01.014. PubMed PMID: 15121481.
- [80] Ng D, Hu N, Hu Y, et al. Replication of a genome-wide case-control study of esophageal squamous cell carcinoma. *Int J cancer.* 2008 Oct 1;123(7):1610–1615. doi:10.1002/ijc.23682. PubMed PMID: 18649358.
- [81] Hu N, Wang C, Hu Y, et al. Genome-wide association study in esophageal cancer using GeneChip mapping 10K array. *Cancer Res.* 2005 Apr 1;65(7):2542–2546. doi:10.1158/0008-5472.CAN-04-3247. PubMed PMID: 15805246.
- [82] Shulman JM, Chipendo P, Chibnik LB, et al. Functional screening of Alzheimer pathology genome-wide association signals in *Drosophila*. *Am J Hum Genet.* 2011 Feb 11;88(2):232–238. doi:10.1016/j.ajhg.2011.01.006. PubMed PMID: 21295279.
- [83] Zhao L-L, Liu H-L, Luo S, et al. Associations of novel variants in *PIK3C3*, *INSR* and *MAP3K4* of the ATM pathway genes with pancreatic cancer risk. *Am J Cancer Res.* 2020 Jul 1;10(7):2128–2144. PubMed PMID: 32775006.
- [84] Mangino M, Richards JB, Soranzo N, et al. A genome-wide association study identifies a novel locus on chromosome 18q12.2 influencing white cell telomere length. *J Med Genet.* 2009 Jul 1;46(7):451–454. doi:10.1136/jmg.2008.064956. PubMed PMID: 19359265.
- [85] Zhang N, Zheng Y, Liu J, et al. Genetic variations associated with telomere length confer risk of gastric cardia adenocarcinoma. *Gastric Cancer.* 2019 Nov 21;22(6):1089–1099. doi:10.1007/s10120-019-00954-8. PubMed PMID: 30900102.
- [86] Abulí A, Fernández-Rozadilla C, Giráldez MD, et al. A two-phase case-control study for colorectal cancer genetic susceptibility: candidate genes from chromosomal regions 9q22 and 3q22. *Br J Cancer.* 2011 Sep 6;105(6):870–875. doi:10.1038/bjc.2011.296. PubMed PMID: 21811255.
- [87] SanGiovanni JP, Lee PH. AMD-associated genes encoding stress-activated MAPK pathway constituents are identified by interval-based enrichment analysis. *PLoS One.* 2013 Aug 5;8(8):e71239. doi:10.1371/journal.pone.0071239. PubMed PMID: 23940728.
- [88] Hamet P, Haloui M, Harvey F, et al. *PROX1* gene CC genotype as a major determinant of early onset of type 2 diabetes in slavic study participants from

- Action in Diabetes and Vascular Disease: Preterax and Diamicon MR Controlled Evaluation study. *J Hypertens*. 2017 May;S24–S32. doi:10.1097/HJH.0000000000001241. PubMed PMID: 28060188.
- [89] Schuetz JM, Daley D, Graham J, et al. Genetic variation in cell death genes and risk of non-Hodgkin lymphoma. *PLoS One*. 2012 Feb 7;7(2):e31560. doi:10.1371/journal.pone.0031560. PubMed PMID: 22347493.
- [90] Sabarinathan R, Wenzel A, Novotny P, et al. Transcriptome-wide analysis of UTRs in non-small cell lung cancer reveals cancer-related genes with SNV-induced changes on RNA secondary structure and miRNA target sites. *PLoS One*. 2014 Jan 8;9(1):e82699. doi:10.1371/journal.pone.0082699. PubMed PMID: 24416147.
- [91] Kazachkova N, Raposo M, Ramos A, et al. Promoter variant alters expression of the autophagic *BECN1* gene: implications for clinical manifestations of Machado-Joseph disease. *Cerebellum*. 2017 Dec;16(5–6):957–963. doi:10.1007/s12311-017-0875-4. PubMed PMID: 28699106.
- [92] FitzGerald LM, Kwon EM, Conomos MP, et al. Genome-wide association study identifies a genetic variant associated with risk for more aggressive prostate cancer. *Cancer Epidemiol Biomarkers Prev*. 2011 Jun;20(6):1196–1203. doi:10.1158/1055-9965.EPI-10-1299. PubMed PMID: 21467234.
- [93] Litchfield K, Levy M, Orlando G, et al. Identification of 19 new risk loci and potential regulatory mechanisms influencing susceptibility to testicular germ cell tumor. *Nat Genet*. 2017 Jul;49(7):1133–1140. doi:10.1038/ng.3896. PubMed PMID: 28604728.
- [94] Ross CJ, Towfic F, Shankar J, et al. A pharmacogenetic signature of high response to Copaxone in late-phase clinical-trial cohorts of multiple sclerosis. *Genome Med*. 2017 May 31;9(1):50. doi:10.1186/s13073-017-0436-y. PubMed PMID: 28569182.
- [95] Kim H-K, Lee W-Y, Kwon J-T, et al. Association of ultraviolet radiation resistance-associated gene polymorphisms with rheumatoid arthritis. *Biomed reports*. 2014 Jan;2(1):117–121. doi:10.3892/br.2013.185. PubMed PMID: 24649081.
- [96] Jeong T-J, Shin M-K, Uhm Y-K, et al. Association of *UVRAG* polymorphisms with susceptibility to non-segmental vitiligo in a Korean sample. *Exp Dermatol*. 2010 Aug;19(8):e323-5. doi:10.1111/j.1600-0625.2009.01039.x. PubMed PMID: 20163458.
- [97] Bleibel WK, Duan S, Huang RS, et al. Identification of genomic regions contributing to etoposide-induced cytotoxicity. *Hum Genet*. 2009 Mar;125(2):173–180. doi:10.1007/s00439-008-0607-4. PubMed PMID: 19089452.
- [98] Kathiresan S, Manning AK, Demissie S, et al. A genome-wide association study for blood lipid phenotypes in the Framingham Heart Study. *BMC Med Genet*. 2007 Sep 19;S17. doi:10.1186/1471-2350-8-S1-S17. PubMed PMID: 17903299.

- [99] Portilla-Fernandez E, Ghanbari M, van Meurs JBJ, et al. Dissecting the association of autophagy-related genes with cardiovascular diseases and intermediate vascular traits: A population-based approach. *PLoS One*. 2019 Mar 25;14(3):e0214137. doi:10.1371/journal.pone.0214137. PubMed PMID: 30908504.
- [100] Mitjans M, Begemann M, Ju A, et al. Sexual dimorphism of *AMBRA1*-related autistic features in human and mouse. *Transl Psychiatry*. 2017 Oct 10;7(10):e1247. doi:10.1038/tp.2017.213. PubMed PMID: 28994820.
- [101] Rietschel M, Mattheisen M, Degenhardt F, et al. Association between genetic variation in a region on chromosome 11 and schizophrenia in large samples from Europe. *Mol Psychiatry*. 2012 Sep;17(9):906–917. doi:10.1038/mp.2011.80. PubMed PMID: 21747397.
- [102] Li Z, Chen J, Yu H, et al. Genome-wide association analysis identifies 30 new susceptibility loci for schizophrenia. *Nat Genet*. 2017 Nov 1;49(11):1576–1583. doi:10.1038/ng.3973. PubMed PMID: 28991256.
- [103] Brožová K, Krásničanová H, Rusina R. Megalencephalic leukoencephalopathy with subcortical cysts without macrocephaly: A case study of comorbid Turner's syndrome. *Clin Neurol Neurosurg*. 2019 Sep;105400. doi:10.1016/j.clineuro.2019.105400. PubMed PMID: 31302377.
- [104] Zhou Z, Sturgis EM, Liu Z, et al. Genetic variants of *NOXA* and *MCL1* modify the risk of HPV16-associated squamous cell carcinoma of the head and neck. *BMC Cancer*. 2012 May 1;12(1):159. doi:10.1186/1471-2407-12-159. PubMed PMID: 22548841.
- [105] Mhaidat NM, Amawi H, Alzoubi KH. Correlation between *BCL2* and *MCL1* single nucleotide polymorphisms and chemotherapy response in Jordanian patients with colorectal cancer. *Curr Pharm Biotechnol*. 2021 Jul 3;22(5):646–653. doi:10.2174/1389201021666200703200126. PubMed PMID: 32619164.
- [106] Shin HD, Cheong HS, Park BL, et al. Common *MCL1* polymorphisms associated with risk of tuberculosis. *BMB Rep*. 2008 Apr 30;41(4):334–337. doi:10.5483/bmbrep.2008.41.4.334. PubMed PMID: 18452656.
- [107] Jiang Y, Wang W, Wang J, et al. Functional regulatory variants of *MCL1* contribute to enhanced promoter activity and reduced risk of lung cancer in nonsmokers: implications for context-dependent phenotype of an antiapoptotic and antiproliferative gene in solid tumor. *Cancer*. 2012 Apr 15;118(8):2085–2095. doi:10.1002/cncr.26502. PubMed PMID: 21887682.
- [108] Wang S, Jiang Y, Liu J, et al. Revisiting the role of *MCL1* in tumorigenesis of solid cancer: gene expression correlates with antiproliferative phenotype in breast cancer cells and its functional regulatory variants are associated with reduced cancer susceptibility. *Tumour Biol*. 2014 Aug;35(8):8289–8299. doi:10.1007/s13277-014-2108-5. PubMed PMID: 24852432.
- [109] Darabi H, McCue K, Beesley J, et al. Polymorphisms in a putative enhancer at the 10q21.2 breast cancer risk locus regulate *NRBF2* expression. *Am J Hum*

- Genet. 2015 Jul 2;97(1):22–34. doi:10.1016/j.ajhg.2015.05.002. PubMed PMID: 26073781.
- [110] Gómez-Ramos A, Podlesniy P, Soriano E, et al. Distinct X-chromosome SNVs from some sporadic AD samples. *Sci Rep.* 2015 Dec 9;5(1):18012. doi:10.1038/srep18012. PubMed PMID: 26648445.
- [111] Cronin S, Tomik B, Bradley DG, et al. Screening for replication of genome-wide SNP associations in sporadic ALS. *Eur J Hum Genet.* 2009 Feb;17(2):213–218. doi:10.1038/ejhg.2008.194. PubMed PMID: 18987618.
- [112] Manduchi E, Williams SM, Chesi A, et al. Leveraging epigenomics and contactomics data to investigate SNP pairs in GWAS. *Hum Genet.* 2018 May;137(5):413–425. doi:10.1007/s00439-018-1893-0. PubMed PMID: 29797095.
- [113] Chen W, Zhang Y, Zhu Y, et al. Association between genetic variants in p53 binding sites and risks of breast cancer in Chinese population. *Zhonghua Liu Xing Bing Xue Za Zhi.* 2016 Aug 10;37(8):1063–1068. doi:10.3760/cma.j.issn.0254-6450.2016.08.002. PubMed PMID: 27539333.
- [114] Zhang J, Kai L, Zhang W, et al. Association between genetic variants in p53 binding sites and risks of osteosarcoma in a Chinese population: a two-stage case-control study. *Cancer Biol Ther.* 2018 Jun 18;19(11):994–997. doi:10.1080/15384047.2018.1456607. PubMed PMID: 29595404.
- [115] Brinar M, Vermeire S, Cleyne I, et al. Genetic variants in autophagy-related genes and granuloma formation in a cohort of surgically treated Crohn's disease patients. *J Crohns Colitis.* 2012 Feb;6(1):43–50. doi:10.1016/j.crohns.2011.06.008. PubMed PMID: 22261526.
- [116] Yamada Y, Sakuma J, Takeuchi I, et al. Identification of *C21orf59* and *ATG2A* as novel determinants of renal function-related traits in Japanese by exome-wide association studies. *Oncotarget.* 2017 Jul 11;8(28):45259–45273. doi:10.18632/oncotarget.16696. PubMed PMID: 28410202.
- [117] Buffen K, Oosting M, Quintin J, et al. Autophagy controls BCG-induced trained immunity and the response to intravesical BCG therapy for bladder cancer. *PLoS Pathog.* 2014 Oct 30;10(10):e1004485. doi:10.1371/journal.ppat.1004485. PubMed PMID: 25356988.
- [118] Zang Z, Lim YK, Chan YH, et al. Polymorphism in autophagy gene *ATG2B* is not associated with bladder cancer recurrence after intravesical Bacillus Calmette-Guerin (BCG) immunotherapy in Asian patients. *Urol Oncol Semin Orig Investig.* 2021 Apr;39(4):238.e1–e7. doi:10.1016/j.urolonc.2020.11.015. PubMed PMID: 33250346.
- [119] Fernández-Mateos J, Seijas-Tamayo R, Klain JCA, et al. Analysis of autophagy gene polymorphisms in Spanish patients with head and neck squamous cell carcinoma. *Sci Rep.* 2017 Jul 31;7(1):6887. doi:10.1038/s41598-017-07270-0. PubMed PMID: 28761177.

- [120] Meddens CA, Harakalova M, van den Dungen NAM, et al. Systematic analysis of chromatin interactions at disease associated loci links novel candidate genes to inflammatory bowel disease. *Genome Biol.* 2016 Nov 30;17(1):247. doi:10.1186/s13059-016-1100-3. PubMed PMID: 27903283.
- [121] Kim K-N, Kim JH, Jung K, et al. Associations of air pollution exposure with blood pressure and heart rate variability are modified by oxidative stress genes: A repeated-measures panel among elderly urban residents. *Environ Health.* 2016 Mar 25;15(1):47. doi:10.1186/s12940-016-0130-3. PubMed PMID: 27015811.
- [122] Mehrabi Pour M, Nasiri M, Kamfiroozie H, et al. Association of the *ATG9B* gene polymorphisms with coronary artery disease susceptibility: A case-control study. *J Cardiovasc Thorac Res.* 2019 Jun 25;11(2):109–115. doi:10.15171/jcvtr.2019.19. PubMed PMID: 31384404.
- [123] Zhang M, Liang L, Xu M, et al. Pathway analysis for genome-wide association study of basal cell carcinoma of the skin. *PLoS One.* 2011 Jul 28;6(7):e22760. doi:10.1371/journal.pone.0022760. PubMed PMID: 21829505.
- [124] MacClellan LR, Howard TD, Cole JW, et al. Relation of candidate genes that encode for endothelial function to migraine and stroke: the Stroke Prevention in Young Women study. *Stroke.* 2009 Oct;40(10):e550-7. doi:10.1161/STROKEAHA.109.557462. PubMed PMID: 19661472.
- [125] Cho K, Demissie S, Dupuis J, et al. Polymorphisms in the endothelial nitric oxide synthase gene and bone density/ultrasound and geometry in humans. *Bone.* 2008 Jan;42(1):53–60. doi:10.1016/j.bone.2007.09.051.
- [126] Carreras-Torres R, Kundu S, Zanetti D, et al. Genetic risk score of *NOS* gene variants associated with myocardial infarction correlates with coronary incidence across Europe. *PLoS One.* 2014 May 7;9(5):e96504. doi:10.1371/journal.pone.0096504. PubMed PMID: 24806096.
- [127] Chasman DI, Paré G, Mora S, et al. Forty-three loci associated with plasma lipoprotein size, concentration, and cholesterol content in genome-wide analysis. *PLoS Genet.* 2009 Nov 20;5(11):e1000730. doi:10.1371/journal.pgen.1000730. PubMed PMID: 19936222.
- [128] Wang L, Ren A, Tian T, et al. Whole-Exome Sequencing Identifies Damaging de novo Variants in Anencephalic Cases. *Front Neurosci.* 2019 Nov 29;1285. doi:10.3389/fnins.2019.01285. PubMed PMID: 31849593.
- [129] Lee H-S, Park T. Nuclear receptor and VEGF pathways for gene-blood lead interactions, on bone mineral density, in Korean smokers. *PLoS One.* 2018 Mar 8;13(3):e0193323. doi:10.1371/journal.pone.0193323. PubMed PMID: 29518117.
- [130] Jelani M, Dooley HC, Gubas A, et al. A mutation in the major autophagy gene, *WIPI2*, associated with global developmental abnormalities. *Brain.* 2019 May 1;142(5):1242–1254. doi:10.1093/brain/awz075. PubMed PMID: 30968111.

- [131] Kruer MC, Boddaert N. Neurodegeneration with brain iron accumulation: a diagnostic algorithm. *Semin Pediatr Neurol*. 2012 Jun;19(2):67–74. doi:10.1016/j.spen.2012.04.001. PubMed PMID: 22704259.
- [132] Gregory A, Kurian MA, Haack T, et al. Beta-Propeller Protein-Associated Neurodegeneration. 2017 Feb. In: Adam MP, Ardinger HH, Pagon RA, et al., editors. *GeneReviews®* [Internet]. Seattle (WA): University of Washington, Seattle; 1993-2022; PubMed PMID: 28211668.
- [133] Lee JH, Cheng R, Graff-Radford N, et al. Analyses of the National Institute on Aging Late-Onset Alzheimer's Disease Family Study: implication of additional loci. *Arch Neurol*. 2008 Nov;65(11):1518–1526. doi:10.1001/archneur.65.11.1518. PubMed PMID: 19001172.
- [134] Gao G, Sheng Y, Yang H, et al. DFCP1 associates with lipid droplets. *Cell Biol Int*. 2019 Jul 10;43(12):1492–1504. doi:10.1002/cbin.11199. PubMed PMID: 31293035.
- [135] Mao J, Wu L, Wang W, et al. Nucleotide variation in *ATG4A* and susceptibility to cervical cancer in Southwestern Chinese women. *Oncol Lett*. 2018 Mar 20;15(3):2992–3000. doi:10.3892/ol.2017.7663. PubMed PMID: 29435029.
- [136] He Q, Lu Y, Hu S, et al. An intron SNP rs807185 in *ATG4A* decreases the risk of lung cancer in a southwest Chinese population. *Eur J Cancer Prev*. 2016 Jul;25(4):255–258. doi:10.1097/CEJ.000000000000174. PubMed PMID: 26061994.
- [137] Song F-J, Chen K-X. Single-nucleotide polymorphisms among microRNA: big effects on cancer. *Chin J Cancer*. 2011 Jun;30(6):381–391. doi:10.5732/cjc.011.10142. PubMed PMID: 21627860.
- [138] Eeles RA, Olama AA Al, Benlloch S, et al. Identification of 23 new prostate cancer susceptibility loci using the iCOGS custom genotyping array. *Nat Genet*. 2013 Apr;45(4):385–391, 391e1-2. doi:10.1038/ng.2560. PubMed PMID: 23535732.
- [139] Liu JZ, van Sommeren S, Huang H, et al. Association analyses identify 38 susceptibility loci for inflammatory bowel disease and highlight shared genetic risk across populations. *Nat Genet*. 2015 Sep 20;47(9):979–986. doi:10.1038/ng.3359. PubMed PMID: 26192919.
- [140] Franceschini N, Giambartolomei C, de Vries PS, et al. GWAS and colocalization analyses implicate carotid intima-media thickness and carotid plaque loci in cardiovascular outcomes. *Nat Commun*. 2018 Dec 3;9(1):5141. doi:10.1038/s41467-018-07340-5. PubMed PMID: 30510157.
- [141] Yang Q, Kathiresan S, Lin J-P, et al. Genome-wide association and linkage analyses of hemostatic factors and hematological phenotypes in the Framingham Heart Study. *BMC Med Genet*. 2007 Sep 19;S12. doi:10.1186/1471-2350-8-S1-S12. PubMed PMID: 17903294.

- [142] Daya M, van der Merwe L, van Helden PD, et al. Investigating the role of gene-gene interactions in TB susceptibility. *PLoS One*. 2014 Apr 28;10(4):e0123970. doi:10.1371/journal.pone.0123970. PubMed PMID: 25919455.
- [143] Wu C, Wen Y, Guo X, et al. Genetic association, mRNA and protein expression analysis identify *ATG4C* as a susceptibility gene for Kashin-Beck disease. *Osteoarthr Cartil*. 2017 Feb;25(2):281–286. doi:10.1016/j.joca.2016.09.019. PubMed PMID: 27742532.
- [144] Shepard CJ, Cline SG, Hinds D, et al. Breakdown of multiple sclerosis genetics to identify an integrated disease network and potential variant mechanisms. *Physiol Genomics*. 2019 Nov 1;51(11):562–577. doi:10.1152/physiolgenomics.00120.2018. PubMed PMID: 31482761.
- [145] Chen C-Z, Ou C-Y, Wang R-H, et al. Association of *Egr-1* and autophagy-related gene polymorphism in men with chronic obstructive pulmonary disease. *J Formos Med Assoc*. 2015 Aug;114(8):750–755. doi:10.1016/j.jfma.2013.07.015. PubMed PMID: 24012056.
- [146] Chen Z-H, Kim HP, Sciruba FC, et al. *Egr-1* regulates autophagy in cigarette smoke-induced chronic obstructive pulmonary disease. *PLoS One*. 2008 Oct 2;3(10):e3316. doi:10.1371/journal.pone.0003316. PubMed PMID: 18830406.
- [147] Hu T-M, Chen S-J, Hsu S-H, et al. Functional analyses and effect of DNA methylation on the *EGR1* gene in patients with schizophrenia. *Psychiatry Res*. 2019 May;276–282. doi:10.1016/j.psychres.2019.03.044. PubMed PMID: 30952071.
- [148] Lou X-Y, Ma JZ, Sun D, et al. Fine mapping of a linkage region on chromosome 17p13 reveals that *GABARAP* and *DLG4* are associated with vulnerability to nicotine dependence in European-Americans. *Hum Mol Genet*. 2007 Jan 15;16(2):142–153. doi:10.1093/hmg/ddl450. PubMed PMID: 17164261.
- [149] Cui W-Y, Seneviratne C, Gu J, et al. Genetics of GABAergic signaling in nicotine and alcohol dependence. *Hum Genet*. 2012 Jun;131(6):843–855. doi:10.1007/s00439-011-1108-4. PubMed PMID: 22048727.
- [150] Griswold AJ, Ma D, Cukier HN, et al. Evaluation of copy number variations reveals novel candidate genes in autism spectrum disorder-associated pathways. *Hum Mol Genet*. 2012 Aug 1;21(15):3513–3523. doi:10.1093/hmg/dds164. PubMed PMID: 22543975.
- [151] Okada Y, Terao C, Ikari K, et al. Meta-analysis identifies nine new loci associated with rheumatoid arthritis in the Japanese population. *Nat Genet*. 2012 May;44(5):511–516. doi:10.1038/ng.2231.
- [152] Jansen AFM, Schoffelen T, Bleeker-Rovers CP, et al. Genetic variations in innate immunity genes affect response to *Coxiella burnetii* and are associated with susceptibility to chronic Q fever. *Clin Microbiol Infect*. 2019 May;25(5):631.e11-e15. doi:10.1016/j.cmi.2018.08.011. PubMed PMID: 30616015.

- [153] Zhang Y, He X, Li J, et al. Functional genetic variant in *ATG5* gene promoter in acute myocardial infarction. *Cardiol Res Pract*. 2020 Apr 21;9898301. doi:10.1155/2020/9898301. PubMed PMID: 32377431.
- [154] Qi Y, Zhou X, Nath SK, et al. A rare variant (rs933717) at *FBXO31-MAP1LC3B* in Chinese ss associated with systemic lupus erythematosus. *Arthritis Rheumatol*. 2018 Feb;70(2):287–297. doi:10.1002/art.40353. PubMed PMID: 29044928.
- [155] Aissani B, Wiener H, Zhang K. Multiple hits for the association of uterine fibroids on human chromosome 1q43. *PLoS One*. 2013 Mar 14;8(3):e58399. doi:10.1371/journal.pone.0058399. PubMed PMID: 23555580.
- [156] Nuta GC, Gilad Y, Gershoni M, et al. A cancer associated somatic mutation in *LC3B* attenuates its binding to E1-like ATG7 protein and subsequent lipidation. *Autophagy*. 2019 Mar 4;15(3):438–452. doi:10.1080/15548627.2018.1525476. PubMed PMID: 30238850.
- [157] Costa JR, Prak K, Aldous S, et al. Autophagy gene expression profiling identifies a defective microtubule-associated protein light chain 3A mutant in cancer. *Oncotarget*. 2016 Jul 5;7(27):41203–41216. doi:10.18632/oncotarget.9754. PubMed PMID: 27256984.
- [158] Sanborn JZ, Chung J, Purdom E, et al. Phylogenetic analyses of melanoma reveal complex patterns of metastatic dissemination. *Proc Natl Acad Sci U S A*. 2015 Sep 1;112(35):10995–11000. doi:10.1073/pnas.1508074112. PubMed PMID: 26286987.
- [159] Awan F, Obaid A, Ikram A, et al. Mutation-structure-function relationship based integrated strategy reveals the potential impact of deleterious missense mutations in autophagy related proteins on hepatocellular varcinoma (HCC): A comprehensive informatics approach. *Int J Mol Sci*. 2017 Jan 11;18(1):139. doi:10.3390/ijms18010139. PubMed PMID: 28085066.
- [160] Grunwald DS, Otto NM, Park J-M, et al. GABARAPs and LC3s have opposite roles in regulating ULK1 for autophagy induction. *Autophagy*. 2020 Jun;16(4):600–614. doi:10.1080/15548627.2019.1632620. PubMed PMID: 31208283.
- [161] Li M, Ma F, Wang J, et al. Genetic polymorphisms of autophagy-related gene 5 (*ATG5*) rs473543 predict different disease-free survivals of triple-negative breast cancer patients receiving anthracycline- and/or taxane-based adjuvant chemotherapy. *Chin J Cancer*. 2018 Dec 31;37(1):4. doi:10.1186/s40880-018-0268-1. PubMed PMID: 29382381.
- [162] You Y, Huo J, Huang J, et al. Contribution of autophagy-related gene 5 variants to acquired aplastic anemia in Han-Chinese population. *J Cell Biochem*. 2019 Feb 14;120(7):11409–11417. doi:10.1002/jcb.28418. PubMed PMID: 30767262.
- [163] Deželak M, Repnik K, Koder S, et al. A prospective pharmacogenomic study of Crohn's disease patients during routine therapy with anti-TNF- α Drug adalimumab: Contribution of *ATG5*, *NFKB1*, and *CRP* genes to

- pharmacodynamic variability. *OMICS*. 2016 May;20(5):296–309. doi:10.1089/omi.2016.0005. PubMed PMID: 27096233.
- [164] Shao Y, Chen F, Chen Y, et al. Association between genetic polymorphisms in the autophagy-related 5 gene promoter and the risk of sepsis. *Sci Rep*. 2017 Aug 24;7(1):9399. doi:10.1038/s41598-017-09978-5. PubMed PMID: 28839236.
- [165] Martin LJ, Gupta J, Jyothula SSSK, et al. Functional variant in the autophagy-related 5 gene promoter is associated with childhood asthma. *PLoS One*. 2012 Apr 20;7(4):e33454. doi:10.1371/journal.pone.0033454. PubMed PMID: 22536318.
- [166] Zeki AA, Yeganeh B, Kenyon NJ, et al. Autophagy in airway diseases: a new frontier in human asthma? *Allergy*. 2016 Jan;71(1):5–14. doi:10.1111/all.12761. PubMed PMID: 26335713.
- [167] Pham D Le, Kim S-H, Losol P, et al. Association of autophagy related gene polymorphisms with neutrophilic airway inflammation in adult asthma. *Korean J Intern Med*. 2016 Mar 1;31(2):375–385. doi:10.3904/kjim.2014.390. PubMed PMID: 26701229.
- [168] Li N, Fan X, Wang X, et al. Autophagy-related 5 gene rs510432 polymorphism is associated with hepatocellular carcinoma in patients with chronic hepatitis B virus infection. *Immunol Invest*. 2019 May;48(4):378–391. doi:10.1080/08820139.2019.1567532. PubMed PMID: 30907204.
- [169] Yuan J, Zhang N, Yin L, et al. Clinical implications of the autophagy core gene variations in advanced lung adenocarcinoma treated with gefitinib. *Sci Rep*. 2017 Dec 19;7(1):17814. doi:10.1038/s41598-017-18165-5. PubMed PMID: 29259263.
- [170] Yuan J, Han R, Esther A, et al. Polymorphisms in autophagy related genes and the coal workers' pneumoconiosis in a Chinese population. *Gene*. 2017 Oct 20;36–42. doi:10.1016/j.gene.2017.08.017. PubMed PMID: 28844669.
- [171] White KAM, Luo L, Thompson TA, et al. Variants in autophagy-related genes and clinical characteristics in melanoma: a population-based study. *Cancer Med*. 2016 Nov 22;5(11):3336–3345. doi:10.1002/cam4.929. PubMed PMID: 27748080.
- [172] Nikseresht M, Shahverdi M, Dehghani M, et al. Association of single nucleotide autophagy-related protein 5 gene polymorphism rs2245214 with susceptibility to non-small cell lung cancer. *J Cell Biochem*. 2018 Sep 22;120(2):1924–1931. doi:10.1002/jcb.27467. PubMed PMID: 30242869.
- [173] Usategui-Martín R, García-Aparicio J, Corral-Gudino L, et al. Polymorphisms in autophagy genes are associated with paget disease of bone. *PLoS One*. 2015 Jun 1;10(6):e0128984. doi:10.1371/journal.pone.0128984. PubMed PMID: 26030385.
- [174] Gateva V, Sandling JK, Hom G, et al. A large-scale replication study identifies *TNIP1*, *PRDM1*, *JAZF1*, *UHRF1BP1* and *IL10* as risk loci for systemic lupus

- erythematosus. *Nat Genet.* 2009 Nov 18;41(11):1228–1233. doi:10.1038/ng.468. PubMed PMID: 19838195.
- [175] Ciccacci C, Perricone C, Alessandri C, et al. Evaluation of *ATG5* polymorphisms in Italian patients with systemic lupus erythematosus: contribution to disease susceptibility and clinical phenotypes. *Lupus.* 2018 Aug;27(9):1464–1469. doi:10.1177/0961203318776108. PubMed PMID: 29759048.
- [176] Mayes MD, Bossini-Castillo L, Gorlova O, et al. Immunochip analysis identifies multiple susceptibility loci for systemic sclerosis. *Am J Hum Genet.* 2014 Jan 2;94(1):47–61. doi:10.1016/j.ajhg.2013.12.002. PubMed PMID: 24387989.
- [177] Plantinga TS, van de Vosse E, Huijbers A, et al. Role of genetic variants of autophagy genes in susceptibility for non-medullary thyroid cancer and patients outcome. *PLoS One.* 2014 Apr 16;9(4):e94086. doi:10.1371/journal.pone.0094086. PubMed PMID: 24739953.
- [178] Yang PW, Hsieh MS, Chang YH, et al. Genetic polymorphisms of *ATG5* predict survival and recurrence in patients with early-stage esophageal squamous cell carcinoma. *Oncotarget.* 2017 Oct 31;8(53):91494–91504. doi:10.18632/oncotarget.20793. PubMed PMID: 29207660.
- [179] Zheng M, Yu H, Zhang L, et al. Association of *ATG5* gene polymorphisms with Behçet's disease and *ATG10* gene polymorphisms with VKH syndrome in a Chinese Han population. *Invest Ophthalmol Vis Sci.* 2015 Dec 30;56(13):8280–8287. doi:10.1167/iovs.15-18035. PubMed PMID: 26747760.
- [180] Alonso-Perez E, Suarez-Gestal M, Calaza M, et al. Lack of replication of higher genetic risk load in men than in women with systemic lupus erythematosus. *Arthritis Res Ther.* 2014 Jun 19;16(3):R128. doi:10.1186/ar4585. PubMed PMID: 24946689.
- [181] López P, Alonso-Pérez E, Rodríguez-Carrio J, et al. Influence of *Atg5* mutation in SLE depends on functional *IL-10* genotype. *PLoS One.* 2013 Oct 18;8(10):e78756. doi:10.1371/journal.pone.0078756. PubMed PMID: 24205307.
- [182] Li N, Fan X, Wang X, et al. Genetic association of polymorphisms at the intergenic region between *PRDM1* and *ATG5* with hepatitis B virus infection in Han Chinese patients. *J Med Virol.* 2020 Aug 1;92(8):1198–1205. doi:10.1002/jmv.25629. PubMed PMID: 31729038.
- [183] Cai P-P, Wang H-X, Zhuang J-C, et al. Variants of autophagy-related gene 5 are associated with neuromyelitis optica in the Southern Han Chinese population. *Autoimmunity.* 2014 Dec;47(8):563–566. doi:10.3109/08916934.2014.929668. PubMed PMID: 24953774.
- [184] Dang J, Li J, Xin Q, et al. Gene-gene interaction of *ATG5*, *ATG7*, *BLK* and *BANK1* in systemic lupus erythematosus. *Int J Rheum Dis.* 2016 Dec;19(12):1284–1293. doi:10.1111/1756-185X.12768. PubMed PMID: 26420661.

- [185] Martin J-E, Assassi S, Diaz-Gallo L-M, et al. A systemic sclerosis and systemic lupus erythematosus pan-meta-GWAS reveals new shared susceptibility loci. *Hum Mol Genet.* 2013 Oct 1;22(19):4021–4029. doi:10.1093/hmg/ddt248. PubMed PMID: 23740937.
- [186] Mitchell JS, Li N, Weinhold N, et al. Genome-wide association study identifies multiple susceptibility loci for multiple myeloma. *Nat Commun.* 2016 Jul 1;7(1):12050. doi:10.1038/ncomms12050. PubMed PMID: 27363682.
- [187] Terao C, Raychaudhuri S, Gregersen PK. Recent advances in defining the genetic basis of rheumatoid arthritis. *Annu Rev Genomics Hum Genet.* 2016 Aug 31;17(3):273–301. doi:10.1146/annurev-genom-090314-045919. PubMed PMID: 27216775.
- [188] Xu J, Xia L, Shang Q, et al. A variant of the autophagy-related 5 gene is associated with child cerebral palsy. *Front Cell Neurosci.* 2017 Dec 18;407. doi:10.3389/fncel.2017.00407. PubMed PMID: 29326554.
- [189] Shen M, Lin L. Functional variants of autophagy-related genes are associated with the development of hepatocellular carcinoma. *Life Sci.* 2019 Oct 15;235(4):116675. doi:10.1016/j.lfs.2019.116675. PubMed PMID: 31340167.
- [190] Zhou J, Hang D, Jiang Y, et al. Evaluation of genetic variants in autophagy pathway genes as prognostic biomarkers for breast cancer. *Gene.* 2017 Sep 5;549–555. doi:10.1016/j.gene.2017.06.053. PubMed PMID: 28669927.
- [191] Zhao X, Chen Y, Wang L, et al. Associations of *ATG7* rs1375206 polymorphism and elevated plasma *ATG7* levels with late-onset sporadic Parkinson's disease in a cohort of Han Chinese from southern China. *Int J Neurosci.* 2020 Dec;130(12):1206–1214. doi:10.1080/00207454.2020.1731507. PubMed PMID: 32065549.
- [192] Lee T-H, Ko T-M, Chen C-H, et al. A genome-wide association study links small-vessel ischemic stroke to autophagy. *Sci Rep.* 2017 Nov 9;7(1):15229. doi:10.1038/s41598-017-14355-3. PubMed PMID: 29123153.
- [193] Wang Z, Tao L, Xue Y, et al. Association of *ATG7* polymorphisms and clear cell renal cell carcinoma risk. *Curr Mol Med.* 2019 Jan;19(1):40–47. doi:10.2174/1566524019666190227202003. PubMed PMID: 30827239.
- [194] Zhang P, Zhang J, Zhang Y, et al. Functional variants of the *ATG7* gene promoter in acute myocardial infarction. *Mol Genet genomic Med.* 2018 Nov;6(6):1209–1219. doi:10.1002/mgg3.508. PubMed PMID: 30407747.
- [195] Metzger S, Saukko M, Van Che H, et al. Age at onset in Huntington's disease is modified by the autophagy pathway: implication of the V471A polymorphism in *Atg7*. *Hum Genet.* 2010 Oct;128(4):453–459. doi:10.1007/s00439-010-0873-9. PubMed PMID: 20697744.
- [196] Qin Z, Xue J, He Y, et al. Potentially functional polymorphisms in *ATG10* are associated with risk of breast cancer in a Chinese population. *Gene.* 2013 Sep 25;527(2):491–495. doi:10.1016/j.gene.2013.06.067. PubMed PMID: 23850577.

- [197] Xie K, Liang C, Li Q, et al. Role of *ATG10* expression quantitative trait loci in non-small cell lung cancer survival. *Int J cancer*. 2016 Oct 1;139(7):1564–1573. doi:10.1002/ijc.30205. PubMed PMID: 27225307.
- [198] Yang Z, Liu Z. Potentially functional variants of autophagy-related genes are associated with the efficacy and toxicity of radiotherapy in patients with nasopharyngeal carcinoma. *Mol Genet Genomic Med*. 2019 Dec 8;7(12):e1030. doi:10.1002/mgg3.1030. PubMed PMID: 31692259.
- [199] Songane M, Kleinnijenhuis J, Alisjahbana B, et al. Polymorphisms in autophagy genes and susceptibility to tuberculosis. *PLoS One*. 2012 Aug 6;7(8):e41618. doi:10.1371/journal.pone.0041618. PubMed PMID: 22879892.
- [200] Li Q, Zhou X, Huang T, et al. The Thr300Ala variant of *ATG16L1* is associated with decreased risk of brain metastasis in patients with non-small cell lung cancer. *Autophagy*. 2017 Jun 3;13(6):1053–1063. doi:10.1080/15548627.2017.1308997. PubMed PMID: 28441070.
- [201] Bae H, Lunetta KL, Murabito JM, et al. Genetic associations with age of menopause in familial longevity. *Menopause*. 2019 Oct;26(10):1204–1212. doi:10.1097/GME.0000000000001367. PubMed PMID: 31188284.
- [202] Howell MD, Gao P, Kim BE, et al. The signal transducer and activator of transcription 6 gene (*STAT6*) increases the propensity of patients with atopic dermatitis toward disseminated viral skin infections. *J Allergy Clin Immunol*. 2011 Nov;128(5):1006–1014. doi:10.1016/j.jaci.2011.06.003. PubMed PMID: 21762972.
- [203] Briones N, Dinu V. Data mining of high density genomic variant data for prediction of Alzheimer's disease risk. *BMC Med Genet*. 2012 Jan 25;13(1):7. doi:10.1186/1471-2350-13-7. PubMed PMID: 22273362.
- [204] Dorling L, Kar S, Michailidou K, et al. The relationship between common genetic markers of breast cancer risk and chemotherapy-induced toxicity: a case-control study. *PLoS One*. 2016 Jul 8;11(7):e0158984. doi:10.1371/journal.pone.0158984. PubMed PMID: 27392074.
- [205] Guo X, Lin W, Bao J, et al. A comprehensive cis-eQTL analysis revealed target genes in breast cancer susceptibility loci identified in genome-wide association studies. *Am J Hum Genet*. 2018 May 3;102(5):890–903. doi:10.1016/j.ajhg.2018.03.016. PubMed PMID: 29727689.
- [206] Song X, Yuan Z, Yuan H, et al. *ATG12* expression quantitative trait loci associated with head and neck squamous cell carcinoma risk in a Chinese Han population. *Mol Carcinog*. 2018 Aug;57(8):1030–1037. doi:10.1002/mc.22823. PubMed PMID: 29637616.
- [207] Wen J, Liu H, Wang L, et al. Potentially functional variants of *ATG16L2* predict radiation pneumonitis and outcomes in patients with non-small cell lung cancer after definitive radiotherapy. *J Thorac Oncol*. 2018 May;13(5):660–675. doi:10.1016/j.jtho.2018.01.028. PubMed PMID: 29454863.

- [208] Kang J, Kugathasan S, Georges M, et al. Improved risk prediction for Crohn's disease with a multi-locus approach. *Hum Mol Genet.* 2011 Jun 15;20(12):2435–2442. doi:10.1093/hmg/ddr116. PubMed PMID: 21427131.
- [209] Rioux JD, Xavier RJ, Taylor KD, et al. Genome-wide association study identifies new susceptibility loci for Crohn disease and implicates autophagy in disease pathogenesis. *Nat Genet.* 2007 May;39(5):596–604. doi:10.1038/ng2032. PubMed PMID: 17435756.
- [210] Liu T, Kern JT, VanDussen KL, et al. Interaction between smoking and ATG16L1T300A triggers Paneth cell defects in Crohn's disease. *J Clin Invest.* 2018 Nov 1;128(11):5110–5122. doi:10.1172/JCI120453. PubMed PMID: 30137026.
- [211] Li X, Chen M, Zhang X, et al. Single nucleotide polymorphisms of autophagy-related 16-like 1 gene are associated with ankylosing spondylitis in females: a case-control study. *Int J Rheum Dis.* 2018 Jan;21(1):322–329. doi:10.1111/1756-185X.13183. PubMed PMID: 28952203.
- [212] Huang C-Y, Huang S-P, Lin VC, et al. Genetic variants of the autophagy pathway as prognostic indicators for prostate cancer. *Sci Rep.* 2015 Sep 14;5(1):14045. doi:10.1038/srep14045. PubMed PMID: 26365175.
- [213] Orsatti CL, Sobreira ML, Sandrim VC, et al. Autophagy-related 16-like 1 gene polymorphism, risk factors for cardiovascular disease and associated carotid intima-media thickness in postmenopausal women. *Clin Biochem.* 2018 Nov;12–17. doi:10.1016/j.clinbiochem.2018.09.006. PubMed PMID: 30236831.
- [214] Al-Ali R, Fernández-Mateos J, González-Sarmiento R. Association of autophagy gene polymorphisms with lung cancer. *Gene Reports.* 2017 Jun;74–77. doi:10.1016/j.genrep.2017.02.001.
- [215] Tsianos VE, Kostoulas C, Gazouli M, et al. *ATG16L1* T300A polymorphism is associated with Crohn's disease in a Northwest Greek cohort, but *ECM1* T130M and *G290S* polymorphisms are not associated with ulcerative colitis. *Ann Gastroenterol.* 2020 Jan-Feb;33(1):38–44. doi:10.20524/aog.2019.0434. PubMed PMID: 31892796.
- [216] Lauriola M, Ugolini G, Rivetti S, et al. *IL23R*, *NOD2/CARD15*, *ATG16L1* and *PHOX2B* polymorphisms in a group of patients with Crohn's disease and correlation with sub-phenotypes. *Int J Mol Med.* 2011 Mar;27(3):469–477. doi:10.3892/ijmm.2010.591. PubMed PMID: 21206965.
- [217] Linares R, Fernández MF, Gutiérrez A, et al. Endocrine disruption in Crohn's disease: Bisphenol A enhances systemic inflammatory response in patients with gut barrier translocation of dysbiotic microbiota products. *FASEB J.* 2021 Jul;35(7):e21697. doi:10.1096/fj.202100481R. PubMed PMID: 34085740.
- [218] Liassides C, Papadopoulos A, Siristatidis C, et al. Single nucleotide polymorphisms of Toll-like receptor-4 and of autophagy-related gene 16 like-1 gene for predisposition of premature delivery: A prospective study. *Medicine (Baltimore).* 2019 Oct;98(40):e17313. doi:10.1097/MD.00000000000017313. PubMed PMID: 31577725.

- [219] Wang C, Bauckman KA, Ross ASB, et al. A non-canonical autophagy-dependent role of the *ATG16L1* T300A variant in urothelial vesicular trafficking and uropathogenic *Escherichia coli* persistence. *Autophagy*. 2019 Mar;15(3):527–542. doi:10.1080/15548627.2018.1535290. PubMed PMID: 30335568.
- [220] Sharma A, Kaur S, Duseja A, et al. The autophagy gene *ATG16L1* (T300A) variant is associated with the risk and progression of HBV infection. *Infect Genet Evol*. 2020 Oct;104404. doi:10.1016/j.meegid.2020.104404. PubMed PMID: 32526369.
- [221] Manry J, Vincent QB, Johnson C, et al. Genome-wide association study of Buruli ulcer in rural Benin highlights role of two LncRNAs and the autophagy pathway. *Commun Biol*. 2020 Apr 20;3(1):177. doi:10.1038/s42003-020-0920-6. PubMed PMID: 32313116.
- [222] Capela C, Dossou AD, Silva-Gomes R, et al. Genetic variation in autophagy-related genes influences the risk and phenotype of Buruli ulcer. *PLoS Negl Trop Dis*. 2016 Apr 29;10(4):e0004671. doi:10.1371/journal.pntd.0004671. PubMed PMID: 27128681.
- [223] Mo JJ, Zhang W, Wen QW, et al. Genetic association analysis of *ATG16L1* rs2241880, rs6758317 and *ATG16L2* rs11235604 polymorphisms with rheumatoid arthritis in a Chinese population. *Int Immunopharmacol*. 2021 Apr;107378. doi:10.1016/j.intimp.2021.107378. PubMed PMID: 33529915.
- [224] Douroudis K, Kingo K, Traks T, et al. Polymorphisms in the *ATG16L1* gene are associated with psoriasis vulgaris. *Acta Derm Venereol*. 2012 Jan;92(1):85–87. doi:10.2340/00015555-1183. PubMed PMID: 21879234.
- [225] El-Amir MI, Wahman MM, Khaled HA, et al. Role of *ATG16L1* (rs2241880) and Interleukin 10 (rs1800872) polymorphisms in breast cancer among Egyptian patients. *Egypt J Immunol*. 2020 Jan;27(1):65–76. PubMed PMID: 33180389.
- [226] Huijbers A, Plantinga TS, Joosten LAB, et al. The effect of the *ATG16L1* Thr300Ala polymorphism on susceptibility and outcome of patients with epithelial cell-derived thyroid carcinoma. *Endocr Relat Cancer*. 2012 May 3;19(3):L15-8. doi:10.1530/ERC-11-0302. PubMed PMID: 22302078.
- [227] Nicoli ER, Dumitrescu T, Uscatu CD, et al. Determination of autophagy gene *ATG16L1* polymorphism in human colorectal cancer. *Rom J Morphol Embryol*. 2014;55(1):57–62. PubMed PMID: 24715166.
- [228] Grimm WA, Messer JS, Murphy SF, et al. The Thr300Ala variant in *ATG16L1* is associated with improved survival in human colorectal cancer and enhanced production of type I interferon. *Gut*. 2016 Mar;65(3):456–464. doi:10.1136/gutjnl-2014-308735. PubMed PMID: 25645662.
- [229] Burada F, Ciurea ME, Nicoli R, et al. *ATG16L1* T300A polymorphism is correlated with gastric cancer susceptibility. *Pathol Oncol Res*. 2016 Apr;22(2):317–322. doi:10.1007/s12253-015-0006-9. PubMed PMID: 26547861.

- [230] Ma C, Storer CE, Chandran U, et al. Crohn's disease-associated *ATG16L1* T300A genotype is associated with improved survival in gastric cancer. *EBioMedicine*. 2021 May;103347. doi:10.1016/j.ebiom.2021.103347. PubMed PMID: 33906066.
- [231] Reuken PA, Lutz P, Casper M, et al. The *ATG16L1* gene variant rs2241880 (p.T300A) is associated with susceptibility to HCC in patients with cirrhosis. *Liver Int*. 2019 Dec;39(12):2360–2367. doi:10.1111/liv.14239. PubMed PMID: 31484215.
- [232] Wisetsathorn S, Tantithavorn V, Hirankarn N, et al. Gene polymorphisms of autophagy machinery and the risk of hepatitis B virus-related hepatocellular carcinoma in a Thai population. *ScienceAsia*. 2017 Dec;43(6):362. doi:10.2306/scienceasia1513-1874.2017.43.362.
- [233] Ramos PS, Williams AH, Ziegler JT, et al. Genetic analyses of interferon pathway-related genes reveal multiple new loci associated with systemic lupus erythematosus. *Arthritis Rheum*. 2011 Jul;63(7):2049–2057. doi:10.1002/art.30356. PubMed PMID: 21437871.
- [234] Yang S-K, Hong M, Zhao W, et al. Genome-wide association study of Crohn's disease in Koreans revealed three new susceptibility loci and common attributes of genetic susceptibility across ethnic populations. *Gut*. 2014 Jan;63(1):80–87. doi:10.1136/gutjnl-2013-305193. PubMed PMID: 23850713.
- [235] Oh SH, Baek J, Kim KM, et al. Is whole exome sequencing clinically practical in the management of pediatric Crohn's disease? *Gut Liver*. 2015 Nov 23;9(6):767–775. doi:10.5009/gnl15176. PubMed PMID: 26503572.
- [236] Ma T, Wu S, Yan W, et al. A functional variant of *ATG16L2* is associated with Crohn's disease in the Chinese population. *Color Dis*. 2016 Nov;18(11):O420–O426. doi:10.1111/codi.13507. PubMed PMID: 27611316.
- [237] Sun C, Molineros JE, Looger LL, et al. High-density genotyping of immune-related loci identifies new SLE risk variants in individuals with Asian ancestry. *Nat Genet*. 2016 Mar;48(3):323–330. doi:10.1038/ng.3496. PubMed PMID: 26808113.
- [238] Molineros JE, Yang W, Zhou X, et al. Confirmation of five novel susceptibility loci for systemic lupus erythematosus (SLE) and integrated network analysis of 82 SLE susceptibility loci. *Hum Mol Genet*. 2017 Mar 15;26(6):1205–1216. doi:10.1093/hmg/ddx026. PubMed PMID: 28108556.
- [239] Lessard CJ, Sajuthi S, Zhao J, et al. Identification of a systemic lupus erythematosus risk locus spanning *ATG16L2*, *FCHSD2*, and *P2RY2* in Koreans. *Arthritis Rheumatol*. 2015 May;68(5):n/a-n/a. doi:10.1002/art.39548. PubMed PMID: 26663301.
- [240] Ishigaki K, Akiyama M, Kanai M, et al. Large-scale genome-wide association study in a Japanese population identifies novel susceptibility loci across different diseases. *Nat Genet*. 2020 Jul;52(7):669–679. doi:10.1038/s41588-020-0640-3. PubMed PMID: 32514122.

- [241] Xu Q, Wu Y, Li Y, et al. SNP-SNP interactions of three new pri-miRNAs with the target gene PGC and multidimensional analysis of *H. pylori* in the gastric cancer/atrophic gastritis risk in a Chinese population. *Oncotarget*. 2016 Apr 26;7(17):23700–23714. doi:10.18632/oncotarget.8057. PubMed PMID: 26988755.
- [242] Parkinson N, Ince PG, Smith MO, et al. ALS phenotypes with mutations in *CHMP2B* (charged multivesicular body protein 2B). *Neurology*. 2006 Sep 26;67(6):1074–1077. doi:10.1212/01.wnl.0000231510.89311.8b. PubMed PMID: 16807408.
- [243] Skibinski G, Parkinson NJ, Brown JM, et al. Mutations in the endosomal ESCRTIII-complex subunit *CHMP2B* in frontotemporal dementia. *Nat Genet*. 2005 Aug;37(8):806–808. doi:10.1038/ng1609. PubMed PMID: 16041373.
- [244] Pankratz N, Wilk JB, Latourelle JC, et al. Genomewide association study for susceptibility genes contributing to familial Parkinson disease. *Hum Genet*. 2009 Jan;124(6):593–605. doi:10.1007/s00439-008-0582-9. PubMed PMID: 18985386.
- [245] Xu J, Wang L, Liu X, et al. A novel *LAMP2* p.G93R mutation associated with mild Danon disease presenting with familial hypertrophic cardiomyopathy. *Mol Genet genomic Med*. 2019 Oct;7(10):e00941. doi:10.1002/mgg3.941. PubMed PMID: 31464081.
- [246] Qu H-Q, Jacob K, Fatet S, et al. Genome-wide profiling using single-nucleotide polymorphism arrays identifies novel chromosomal imbalances in pediatric glioblastomas. *Neuro Oncol*. 2010 Feb;12(2):153–163. doi:10.1093/neuonc/nop001. PubMed PMID: 20150382.
- [247] Di Rita A, Angelini DF, Maiorino T, et al. Characterization of a natural variant of human *NDP52* and its functional consequences on mitophagy. *Cell Death Differ*. 2021 Aug;28(8):2499–2516. doi:10.1038/s41418-021-00766-3. PubMed PMID: 33723372.
- [248] Lutz P, Krämer B, Kaczmarek DJ, et al. A variant in the nuclear dot protein 52kDa gene increases the risk for spontaneous bacterial peritonitis in patients with alcoholic liver cirrhosis. *Dig Liver Dis*. 2016 Jan;48(1):62–68. doi:10.1016/j.dld.2015.09.011. PubMed PMID: 26493630.
- [249] Ellinghaus D, Zhang H, Zeissig S, et al. Association between variants of *PRDM1* and *NDP52* and Crohn's disease, based on exome sequencing and functional studies. *Gastroenterology*. 2013 Aug;145(2):339–347. doi:10.1053/j.gastro.2013.04.040. PubMed PMID: 23624108.
- [250] Zhang X-D, Qi L, Wu J-C, et al. DRAM1 regulates autophagy flux through lysosomes. *PLoS One*. 2013 May 17;8(5):e63245. doi:10.1371/journal.pone.0063245. PubMed PMID: 23696801.
- [251] Galavotti S, Bartesaghi S, Faccenda D, et al. The autophagy-associated factors DRAM1 and p62 regulate cell migration and invasion in glioblastoma stem cells. *Oncogene*. 2013 Feb 7;32(6):699–712. doi:10.1038/onc.2012.111. PubMed PMID: 22525272.

- [252] Merino J, Dashti HS, Li SX, et al. Genome-wide meta-analysis of macronutrient intake of 91,114 European ancestry participants from the cohorts for heart and aging research in genomic epidemiology consortium. *Mol Psychiatry*. 2019 Dec;24(12):1920–1932. doi:10.1038/s41380-018-0079-4. PubMed PMID: 29988085.
- [253] Sanchez A, Schoenfeld JD, Nguyen PL, et al. Common variation in *BRCA1* may have a role in progression to lethal prostate cancer after radiation treatment. *Prostate Cancer Prostatic Dis*. 2016 Jun;19(2):197–201. doi:10.1038/pcan.2016.4. PubMed PMID: 26926928.
- [254] Pelletier C, Speed WC, Paranjape T, et al. Rare *BRCA1* haplotypes including 3'UTR SNPs associated with breast cancer risk. *Cell Cycle*. 2011 Jan 1;10(1):90–99. doi:10.4161/cc.10.1.14359. PubMed PMID: 21191178.
- [255] Wang Y, Ray AM, Johnson EK, et al. Evidence for an association between prostate cancer and chromosome 8q24 and 10q11 genetic variants in African American men: the Flint Men's Health Study. *Prostate*. 2011 Feb 15;71(3):225–231. doi:10.1002/pros.21234. PubMed PMID: 20717903.
- [256] Mou Y, Wu J, Zhang Y, et al. Low expression of ferritinophagy-related *NCOA4* gene in relation to unfavorable outcome and defective immune cells infiltration in clear cell renal carcinoma. *BMC Cancer*. 2021 Jan 5;21(1):18. doi:10.1186/s12885-020-07726-z. PubMed PMID: 33402128.
- [257] Wu G, Wang Q, Xu Y, et al. A new survival model based on ferroptosis-related genes for prognostic prediction in clear cell renal cell carcinoma. *Aging (Albany NY)*. 2020 Jul 20;12(14):14933–14948. doi:10.18632/aging.103553. PubMed PMID: 32688345.
- [258] Cha S, Yu H, Kim JY. Bone mineral density-associated polymorphisms are associated with obesity-related traits in Korean adults in a sex-dependent manner. *PLoS One*. 2012 Dec;7(12):e53013. doi:10.1371/journal.pone.0053013. PubMed PMID: 23300848.
- [259] Yucesoy B, Kaufman KM, Lummus ZL, et al. Genome-wide association study identifies novel loci associated with diisocyanate-induced occupational asthma. *Toxicol Sci*. 2015 Jul;146(1):192–201. doi:10.1093/toxsci/kfv084. PubMed PMID: 25918132.
- [260] Wolf C, Gramer E, Müller-Myhsok B, et al. Evaluation of nine candidate genes in patients with normal tension glaucoma: a case control study. *BMC Med Genet*. 2009 Sep 15;10(1):91. doi:10.1186/1471-2350-10-91. PubMed PMID: 19754948.
- [261] Park J, Kim M, Park CK, et al. Molecular analysis of myocilin and optineurin genes in Korean primary glaucoma patients. *Mol Med Rep*. 2016 Sep;14(3):2439–2448. doi:10.3892/mmr.2016.5557. PubMed PMID: 27485216.
- [262] Saleem S, Azam A, Maqsood SI, et al. Role of ACE and PAI-1 polymorphisms in the development and progression of diabetic retinopathy. *PLoS One*. 2015 Dec 14;10(12):e0144557. doi:10.1371/journal.pone.0144557. PubMed PMID: 26658948.

- [263] Carbone MA, Chen Y, Hughes GA, et al. Genes of the unfolded protein response pathway harbor risk alleles for primary open angle glaucoma. *PLoS One*. 2011 May 31;6(5):e20649. doi:10.1371/journal.pone.0020649. PubMed PMID: 21655191.
- [264] Albagha OME, Visconti MR, Alonso N, et al. Genome-wide association study identifies variants at *CSF1*, *OPTN* and *TNFRSF11A* as genetic risk factors for Paget's disease of bone. *Nat Genet*. 2010 Jun;42(6):520–524. doi:10.1038/ng.562. PubMed PMID: 20436471.
- [265] Silva IAL, Conceição N, Gagnon É, et al. Effect of genetic variants of *OPTN* in the pathophysiology of Paget's disease of bone. *Biochim Biophys Acta Mol Basis Dis*. 2018 Jan;1864(1):143–151. doi:10.1016/j.bbadis.2017.10.008. PubMed PMID: 28993189.
- [266] Guo Q, Wang J, Weng Q. The diverse role of optineurin in pathogenesis of disease. *Biochem Pharmacol*. 2020 Oct;114:157. doi:10.1016/j.bcp.2020.114157. PubMed PMID: 32687832.
- [267] Li L, Shen C, Nakamura E, et al. *SQSTM1* is a pathogenic target of 5q copy number gains in kidney cancer. *Cancer Cell*. 2013 Dec 9;24(6):738–750. doi:10.1016/j.ccr.2013.10.025. PubMed PMID: 24332042.
- [268] Morgan S, Shatunov A, Sproviero W, et al. A comprehensive analysis of rare genetic variation in amyotrophic lateral sclerosis in the UK. *Brain*. 2017 Jun 1;140(6):1611–1618. doi:10.1093/brain/awx082. PubMed PMID: 28430856.
- [269] Bolland MJ, Tong PC, Naot D, et al. Delayed development of Paget's disease in offspring inheriting *SQSTM1* mutations. *J Bone Miner Res*. 2007 Mar;22(3):411–415. doi:10.1359/jbmr.061204. PubMed PMID: 17181397.
- [270] Collet C, Michou L, Audran M, et al. Paget's disease of bone in the French population: novel *SQSTM1* mutations, functional analysis, and genotype-phenotype correlations. *J Bone Miner Res*. 2007 Feb;22(2):310–317. doi:10.1359/jbmr.061106. PubMed PMID: 17129171.
- [271] Ruiz MT, Balachi JF, Fernandes RA, et al. Analysis of the *TAX1BP1* gene in head and neck cancer patients. *Braz J Otorhinolaryngol*. 2010 Mar-Apr;76(2):193–198. PubMed PMID: 20549079.
- [272] Geller F, Feenstra B, Carstensen L, et al. Genome-wide association analyses identify variants in developmental genes associated with hypospadias. *Nat Genet*. 2014 Sep;46(9):957–963. doi:10.1038/ng.3063. PubMed PMID: 25108383.
- [273] Tanaka Y, Kanai F, Tada M, et al. Gain of *GRHL2* is associated with early recurrence of hepatocellular carcinoma. *J Hepatol*. 2008 Nov;49(5):746–757. doi:10.1016/j.jhep.2008.06.019. PubMed PMID: 18752864.
- [274] Noth I, Zhang Y, Ma S, et al. Genetic variants associated with idiopathic pulmonary fibrosis susceptibility and mortality: a genome-wide association study. *Lancet Respir Med*. 2013 Jun;1(4):309–317. doi:10.1016/S2213-2600(13)70045-6. PubMed PMID: 24429156.

- [275] Bonella F, Campo I, Zorzetto M, et al. Potential clinical utility of *MUC5B* and *TOLLIP* single nucleotide polymorphisms (SNPs) in the management of patients with IPF. *Orphanet J Rare Dis.* 2021 Feb 27;16(1):111. doi:10.1186/s13023-021-01750-3. PubMed PMID: 33639995.
- [276] Song Z, Yin J, Yao C, et al. Variants in the Toll-interacting protein gene are associated with susceptibility to sepsis in the Chinese Han population. *Crit Care.* 2011 Jan 10;15(1):R12. doi:10.1186/cc9413. PubMed PMID: 21219635.
- [277] Wang M-G, Wang J, He J-Q. Genetic association of *TOLLIP* gene polymorphisms and HIV infection: a case-control study. *BMC Infect Dis.* 2021 Jun 21;21(1):590. doi:10.1186/s12879-021-06303-4. PubMed PMID: 34154540.
- [278] Wu S, Huang W, Wang D, et al. Evaluation of *TLR2*, *TLR4*, and *TOLLIP* polymorphisms for their role in tuberculosis susceptibility. *APMIS.* 2018 Jun 20;126(6):501–508. doi:10.1111/apm.12855. PubMed PMID: 29924447.
- [279] Rodrigues AF, Santos AM, Ferreira AM, et al. Year-long rhinovirus infection is influenced by atmospheric conditions, outdoor air virus presence, and immune system-related genetic polymorphisms. *Food Environ Virol.* 2019 Dec;11(4):340–349. doi:10.1007/s12560-019-09397-x. PubMed PMID: 31350695.
- [280] Huang C, Jiang D, Francisco D, et al. Tollip SNP rs5743899 modulates human airway epithelial responses to rhinovirus infection. *Clin Exp Allergy.* 2016 Dec;46(12):1549–1563. doi:10.1111/cea.12793. PubMed PMID: 27513438.
- [281] de Araujo FJ, da Silva LD, Mesquita TG, et al. Polymorphisms in the *TOLLIP* Gene Influence Susceptibility to Cutaneous Leishmaniasis Caused by *Leishmania guyanensis* in the Amazonas State of Brazil. *PLoS Negl Trop Dis.* 2015 Jun 24;9(6):e0003875. doi:10.1371/journal.pntd.0003875. PubMed PMID: 26107286.
- [282] Shah JA, Vary JC, Chau TTH, et al. Human TOLLIP regulates TLR2 and TLR4 signaling and its polymorphisms are associated with susceptibility to tuberculosis. *J Immunol.* 2012 Aug 15;189(4):1737–1746. doi:10.4049/jimmunol.1103541. PubMed PMID: 22778396.
- [283] Brasil LW, Barbosa LRA, de Araujo FJ, et al. *TOLLIP* gene variant is associated with *Plasmodium vivax* malaria in the Brazilian Amazon. *Malar J.* 2017 Mar 13;16(1):116. doi:10.1186/s12936-017-1754-7. PubMed PMID: 28288644.
- [284] Montoya-Buelna M, Fafutis-Morris M, Tovar-Cuevas AJ, et al. Role of Toll-interacting protein gene polymorphisms in leprosy Mexican patients. *Biomed Res Int.* 2013 Nov 4;4:459169. doi:10.1155/2013/459169. PubMed PMID: 24294608.
- [285] Fingerlin TE, Murphy E, Zhang W, et al. Genome-wide association study identifies multiple susceptibility loci for pulmonary fibrosis. *Nat Genet.* 2013 Jun;45(6):613–620. doi:10.1038/ng.2609. PubMed PMID: 23583980.

- [286] Oldham JM, Ma SF, Martinez FJ, et al. TOLLIP, MUC5B, and the response to N-acetylcysteine among individuals with idiopathic pulmonary fibrosis. *Am J Respir Crit Care Med*. 2015 Dec;192(12):1475–1482. doi:10.1164/rccm.201505-1010OC. PubMed PMID: 26331942.
- [287] Shah JA, Berrington WR, Vary JC, et al. Genetic variation in Toll-interacting protein is associated with leprosy susceptibility and cutaneous expression of interleukin 1 receptor antagonist. *J Infect Dis*. 2016 Apr 1;213(7):1189–1197. doi:10.1093/infdis/jiv570. PubMed PMID: 26610735.
- [288] Cantu E, Suzuki Y, Diamond JM, et al. Protein quantitative trait loci analysis identifies genetic variation in the innate immune regulator *TOLLIP* in post-lung transplant primary graft dysfunction risk. *Am J Transplant*. 2016 Mar;16(3):833–840. doi:10.1111/ajt.13525. PubMed PMID: 26663441.
- [289] Shah JA, Musvosvi M, Shey M, et al. A functional Toll-interacting protein variant is associated with bacillus Calmette-Guérin-specific immune responses and tuberculosis. *Am J Respir Crit Care Med*. 2017 Aug 15;196(4):502–511. doi:10.1164/rccm.201611-2346OC. PubMed PMID: 28463648.
- [290] Li QS, Parrado AR, Samtani MN, et al. Variations in the *FRA10AC1* fragile site and 15q21 are associated with cerebrospinal fluid A β 1-42 level. *PLoS One*. 2015 Aug 7;10(8):e0134000. doi:10.1371/journal.pone.0134000. PubMed PMID: 26252872.
- [291] Le Duc D, Giulivi C, Hiatt SM, et al. Pathogenic *WDFY3* variants cause neurodevelopmental disorders and opposing effects on brain size. *Brain*. 2019 Sep 1;142(9):2617–2630. doi:10.1093/brain/awz198. PubMed PMID: 31327001.
- [292] Cheong H, Wu J, Gonzales LK, et al. Analysis of a lung defect in autophagy-deficient mouse strains. *Autophagy*. 2014 Jan 11;10(1):45–56. doi:10.4161/auto.26505. PubMed PMID: 24275123.
- [293] Maciel M, Hernández-Barrientos D, Herrera I, et al. Impaired autophagic activity and *ATG4B* deficiency are associated with increased endoplasmic reticulum stress-induced lung injury. *Aging (Albany NY)*. 2018 Aug 27;10(8):2098–2112. doi:10.18632/aging.101532. PubMed PMID: 30147026.
- [294] Cabrera S, Maciel M, Herrera I, et al. Essential role for the ATG4B protease and autophagy in bleomycin-induced pulmonary fibrosis. *Autophagy*. 2015 Apr 3;11(4):670–684. doi:10.1080/15548627.2015.1034409. PubMed PMID: 25906080.
- [295] Abdel Fattah E, Bhattacharya A, Herron A, et al. Critical role for IL-18 in spontaneous lung inflammation caused by autophagy deficiency. *J Immunol*. 2015 Jun 1;194(11):5407–5416. doi:10.4049/jimmunol.1402277. PubMed PMID: 25888640.
- [296] Chen Z-H, Lam HC, Jin Y, et al. Autophagy protein microtubule-associated protein 1 light chain-3B (LC3B) activates extrinsic apoptosis during cigarette smoke-induced emphysema. *Proc Natl Acad Sci U S A*. 2010 Nov

- 2;107(44):18880–18885. doi:10.1073/pnas.1005574107. PubMed PMID: 20956295.
- [297] Kesireddy VS, Chillappagari S, Ahuja S, et al. Susceptibility of microtubule-associated protein 1 light chain 3 β (*MAP1LC3B/LC3B*) knockout mice to lung injury and fibrosis. *FASEB J.* 2019 Nov;33(11):12392–12408. doi:10.1096/fj.201900854R. PubMed PMID: 31431059.
- [298] Yeganeh B, Lee J, Ermini L, et al. Autophagy is required for lung development and morphogenesis. *J Clin Invest.* 2019 Jun 4;129(7):2904–2919. doi:10.1172/JCI127307. PubMed PMID: 31162135.
- [299] Wen W, Yu G, Liu W, et al. Silencing *FUNDC1* alleviates chronic obstructive pulmonary disease by inhibiting mitochondrial autophagy and bronchial epithelium cell apoptosis under hypoxic environment. *J Cell Biochem.* 2019 Oct;120(10):17602–17615. doi:10.1002/jcb.29028. PubMed PMID: 31237014.
- [300] Habibzay M, Saldana JI, Goulding J, et al. Altered regulation of Toll-like receptor responses impairs antibacterial immunity in the allergic lung. *Mucosal Immunol.* 2012 Sep;5(5):524–534. doi:10.1038/mi.2012.28. PubMed PMID: 22549744.
- [301] Ito Y, Schaefer N, Sanchez A, et al. Toll-interacting protein, Tollip, inhibits IL-13-mediated pulmonary eosinophilic inflammation in mice. *J Innate Immun.* 2018 Mar;10(2):106–118. doi:10.1159/000485850. PubMed PMID: 29393212.
- [302] Dakhama A, Al Mubarak R, Pavelka N, et al. Tollip inhibits ST2 signaling in airway epithelial cells exposed to type 2 cytokines and rhinovirus. *J Innate Immun.* 2020;12(1):103–115. doi:10.1159/000497072. PubMed PMID: 30928973.
- [303] Wang Y, Sharma P, Jefferson M, et al. Non-canonical autophagy functions of ATG16L1 in epithelial cells limit lethal infection by influenza A virus. *EMBO J.* 2021 Mar 15;40(6):e105543. doi:10.15252/embj.2020105543. PubMed PMID: 33586810.
- [304] Qu X, Yu J, Bhagat G, et al. Promotion of tumorigenesis by heterozygous disruption of the beclin 1 autophagy gene. *J Clin Invest.* 2003 Dec 15;112(12):1809–1820. doi:10.1172/JCI20039. PubMed PMID: 14638851.
- [305] Yue Z, Jin S, Yang C, et al. Beclin 1, an autophagy gene essential for early embryonic development, is a haploinsufficient tumor suppressor. *Proc Natl Acad Sci U S A.* 2003 Dec 9;100(25):15077–15082. doi:10.1073/pnas.2436255100. PubMed PMID: 14657337.
- [306] Takahashi Y, Coppola D, Matsushita N, et al. Bif-1 interacts with Beclin 1 through UVRAG and regulates autophagy and tumorigenesis. *Nat Cell Biol.* 2007 Oct;9(10):1142–1151. doi:10.1038/ncb1634. PubMed PMID: 17891140.
- [307] Kaizuka T, Mizushima N. Atg13 is essential for autophagy and cardiac development in mice. *Mol Cell Biol.* 2015 Dec 7;36(4):585–595. doi:10.1128/MCB.01005-15. PubMed PMID: 26644405.

- [308] Gan B, Peng X, Nagy T, et al. Role of FIP200 in cardiac and liver development and its regulation of TNF α and TSC-mTOR signaling pathways. *J Cell Biol.* 2006 Oct 9;175(1):121–133. doi:10.1083/jcb.200604129. PubMed PMID: 17015619.
- [309] Taneike M, Yamaguchi O, Nakai A, et al. Inhibition of autophagy in the heart induces age-related cardiomyopathy. *Autophagy.* 2010 Jul 1;6(5):600–606. doi:10.4161/auto.6.5.11947. PubMed PMID: 20431347.
- [310] Song Z, An L, Ye Y, et al. Essential role for UVRAG in autophagy and maintenance of cardiac function. *Cardiovasc Res.* 2014 Jan 1;101(1):48–56. doi:10.1093/cvr/cvt223. PubMed PMID: 24081163.
- [311] Zaglia T, Milan G, Ruhs A, et al. Atrogin-1 deficiency promotes cardiomyopathy and premature death via impaired autophagy. *J Clin Invest.* 2014 Jun 2;124(6):2410–2424. doi:10.1172/JCI66339. PubMed PMID: 24789905.
- [312] Kaushal GP, Shah S V. Autophagy in acute kidney injury. *Kidney Int.* 2016 Apr;89(4):779–791. doi:10.1016/j.kint.2015.11.021. PubMed PMID: 26924060.
- [313] Jiang M, Wei Q, Dong G, et al. Autophagy in proximal tubules protects against acute kidney injury. *Kidney Int.* 2012 Dec 2;82(12):1271–1283. doi:10.1038/ki.2012.261. PubMed PMID: 22854643.
- [314] Lenoir O, Tharaux P-L, Huber TB. Autophagy in kidney disease and aging: lessons from rodent models. *Kidney Int.* 2016 Nov;90(5):950–964. doi:10.1016/j.kint.2016.04.014. PubMed PMID: 27325184.
- [315] Wang C, Mendonsa GR, Symington JW, et al. Atg16L1 deficiency confers protection from uropathogenic *Escherichia coli* infection in vivo. *Proc Natl Acad Sci U S A.* 2012 Jul 3;109(27):11008–11013. doi:10.1073/pnas.1203952109. PubMed PMID: 22715292.
- [316] Chew TS, O’Shea NR, Sewell GW, et al. Optineurin deficiency in mice contributes to impaired cytokine secretion and neutrophil recruitment in bacteria-driven colitis. *Dis Model Mech.* 2015 Aug 1;8(8):817–829. doi:10.1242/dmm.020362. PubMed PMID: 26044960.
- [317] Gawriluk TR, Hale AN, Flaws JA, et al. Autophagy is a cell survival program for female germ cells in the murine ovary. *Reproduction.* 2011 Jun 11;141(6):759–765. doi:10.1530/REP-10-0489. PubMed PMID: 21464117.
- [318] Oestreich AK, Chadchan SB, Popli P, et al. The autophagy gene Atg16L1 is necessary for endometrial decidualization. *Endocrinology.* 2020 Jan 1;161(1):bqz039. doi:10.1210/endo/bqz039. PubMed PMID: 31875883.
- [319] Santanam U, Banach-Petrosky W, Abate-Shen C, et al. Atg7 cooperates with Pten loss to drive prostate cancer tumor growth. *Genes Dev.* 2016 Feb 15;30(4):399–407. doi:10.1101/gad.274134.115. PubMed PMID: 26883359.
- [320] Liang XH, Jackson S, Seaman M, et al. Induction of autophagy and inhibition of tumorigenesis by beclin 1. *Nature.* 1999 Dec 9;402(6762):672–676. doi:10.1038/45257. PubMed PMID: 10604474.

- [321] Vega-Rubín-de-Celis S, Zou Z, Fernández ÁF, et al. Increased autophagy blocks HER2-mediated breast tumorigenesis. *Proc Natl Acad Sci U S A*. 2018 Apr 17;115(16):4176–4181. doi:10.1073/pnas.1717800115. PubMed PMID: 29610308.
- [322] Aita VM, Liang XH, Murty V V, et al. Cloning and genomic organization of beclin 1, a candidate tumor suppressor gene on chromosome 17q21. *Genomics*. 1999 Jul 1;59(1):59–65. doi:10.1006/geno.1999.5851. PubMed PMID: 10395800.
- [323] Wei H, Wei S, Gan B, et al. Suppression of autophagy by *FIP200* deletion inhibits mammary tumorigenesis. *Genes Dev*. 2011 Jul 15;25(14):1510–1527. doi:10.1101/gad.2051011. PubMed PMID: 21764854.
- [324] Xia H, Wang W, Crespo J, et al. Suppression of *FIP200* and autophagy by tumor-derived lactate promotes naïve T cell apoptosis and affects tumor immunity. *Sci Immunol*. 2017 Nov 17;2(17):139–148. doi:10.1126/sciimmunol.aan4631. PubMed PMID: 29150439.
- [325] Delaney JR, Patel CB, Bapat J, et al. Autophagy gene haploinsufficiency drives chromosome instability, increases migration, and promotes early ovarian tumors. *PLOS Genet*. 2020 Jan 10;16(1):e1008558. doi:10.1371/journal.pgen.1008558. PubMed PMID: 31923184.