

Table S1: 232 autophagy regulators from autophagy database HADb (Human Autophagy I

Genelid	Name
55626	autophagy/beclin-1 regulator 1
8542	apolipoprotein L, 1
405	aryl hydrocarbon receptor nuclear translocator
410	arylsulfatase A
411	arylsulfatase B
468	activating transcription factor 4 (tax-responsive enhancer element B67)
22926	activating transcription factor 6
83734	ATG10 autophagy related 10 homolog (<i>S. cerevisiae</i>)
9140	ATG12 autophagy related 12 homolog (<i>S. cerevisiae</i>)
55054	ATG16 autophagy related 16-like 1 (<i>S. cerevisiae</i>)
89849	ATG16 autophagy related 16-like 2 (<i>S. cerevisiae</i>)
23130	ATG2 autophagy related 2 homolog A (<i>S. cerevisiae</i>)
55102	ATG2 autophagy related 2 homolog B (<i>S. cerevisiae</i>)
64422	ATG3 autophagy related 3 homolog (<i>S. cerevisiae</i>)
115201	ATG4 autophagy related 4 homolog A (<i>S. cerevisiae</i>)
23192	ATG4 autophagy related 4 homolog B (<i>S. cerevisiae</i>)
84938	ATG4 autophagy related 4 homolog C (<i>S. cerevisiae</i>)
84971	ATG4 autophagy related 4 homolog D (<i>S. cerevisiae</i>)
9474	ATG5 autophagy related 5 homolog (<i>S. cerevisiae</i>)
10533	ATG7 autophagy related 7 homolog (<i>S. cerevisiae</i>)
79065	ATG9 autophagy related 9 homolog A (<i>S. cerevisiae</i>)
285973	ATG9 autophagy related 9 homolog B (<i>S. cerevisiae</i>)
471	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase
573	BCL2-associated athanogene
9531	BCL2-associated athanogene 3
578	BCL2-antagonist/killer 1
581	BCL2-associated X protein
596	B-cell CLL/lymphoma 2
598	BCL2-like 1
8678	beclin 1, autophagy related
637	BH3 interacting domain death agonist
332	baculoviral IAP repeat-containing 5
57448	baculoviral IAP repeat-containing 6
662	BCL2/adenovirus E1B 19kDa interacting protein 1
664	BCL2/adenovirus E1B 19kDa interacting protein 3
665	BCL2/adenovirus E1B 19kDa interacting protein 3-like
60673	chromosome 12 open reading frame 44
23591	chromosome 17 open reading frame 88
10241	calcium binding and coiled-coil domain 2
10645	calcium/calmodulin-dependent protein kinase kinase 2, beta
821	calnexin
823	calpain 1, (mu/I) large subunit
11132	calpain 10
824	calpain 2, (m/II) large subunit
826	calpain, small subunit 1
834	caspase 1, apoptosis-related cysteine peptidase (interleukin 1, beta, convertase)
836	caspase 3, apoptosis-related cysteine peptidase
837	caspase 4, apoptosis-related cysteine peptidase
841	caspase 8, apoptosis-related cysteine peptidase
6347	chemokine (C-C motif) ligand 2
729230	chemokine (C-C motif) receptor 2
4179	CD46 molecule, complement regulatory protein
1026	cyclin-dependent kinase inhibitor 1A (p21, Cip1)
1027	cyclin-dependent kinase inhibitor 1B (p27, Kip1)
1029	cyclin-dependent kinase inhibitor 2A (melanoma, p16, inhibits CDK4)
8837	CASP8 and FADD-like apoptosis regulator

25978 chromatin modifying protein 2B
 128866 chromatin modifying protein 4B
 1201 ceroid-lipofuscinosis, neuronal 3
 1508 cathepsin B
 1509 cathepsin D
 1514 cathepsin L1
 6376 chemokine (C-X3-C motif) ligand 1
 7852 chemokine (C-X-C motif) receptor 4
 1612 death-associated protein kinase 1
 23604 death-associated protein kinase 2
 1649 DNA-damage-inducible transcript 3
 9077 DIRAS family, GTP-binding RAS-like 3
 10395 deleted in liver cancer 1
 3337 DnaJ (Hsp40) homolog, subfamily B, member 1
 4189 DnaJ (Hsp40) homolog, subfamily B, member 9
 55332 DNA-damage regulated autophagy modulator 1
 9695 ER degradation enhancer, mannosidase alpha-like 1
 1938 eukaryotic translation elongation factor 2
 29904 eukaryotic elongation factor-2 kinase
 1956 epidermal growth factor receptor (erythroblastic leukemia viral (v-erb-b) oncogene homolog
 5610 eukaryotic translation initiation factor 2-alpha kinase 2
 9451 eukaryotic translation initiation factor 2-alpha kinase 3
 1965 eukaryotic translation initiation factor 2, subunit 1 alpha, 35kDa
 1978 eukaryotic translation initiation factor 4E binding protein 1
 1981 eukaryotic translation initiation factor 4 gamma, 1
 2064 v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived on
 2081 endoplasmic reticulum to nucleus signaling 1
 30001 ERO1-like (S. cerevisiae)
 8772 Fas (TNFRSF6)-associated via death domain
 55578 family with sequence similarity 48, member A
 355 Fas (TNF receptor superfamily, member 6)
 2280 FK506 binding protein 1A, 12kDa
 2281 FK506 binding protein 1B, 12.6 kDa
 2353 FBJ murine osteosarcoma viral oncogene homolog
 2308 forkhead box O1
 2309 forkhead box O3
 2548 glucosidase, alpha; acid
 11337 GABA(A) receptor-associated protein
 23710 GABA(A) receptor-associated protein like 1
 11345 GABA(A) receptor-associated protein-like 2
 2597 glyceraldehyde-3-phosphate dehydrogenase
 2773 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
 10399 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
 57120 golgi-associated PDZ and coiled-coil motif containing
 2894 glutamate receptor, ionotropic, delta 1
 2895 glutamate receptor, ionotropic, delta 2
 3065 histone deacetylase 1
 10013 histone deacetylase 6
 9146 hepatocyte growth factor-regulated tyrosine kinase substrate
 3091 hypoxia inducible factor 1, alpha subunit (basic helix-loop-helix transcription factor)
 3326 heat shock protein 90kDa alpha (cytosolic), class B member 1
 3309 heat shock 70kDa protein 5 (glucose-regulated protein, 78kDa)
 3312 heat shock 70kDa protein 8
 26353 heat shock 22kDa protein 8
 3458 interferon, gamma
 3551 inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta
 9641 inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon
 11009 interleukin 24

345611 immunity-related GTPase family, M
 3675 integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)
 3655 integrin, alpha 6
 3688 integrin, beta 1 (fibronectin receptor, beta polypeptide, antigen CD29 includes MDF2, MSK1)
 3691 integrin, beta 4
 3708 inositol 1,4,5-triphosphate receptor, type 1
 2548 glucosidase, alpha; acid
 11337 GABA(A) receptor-associated protein
 23710 GABA(A) receptor-associated protein like 1
 11345 GABA(A) receptor-associated protein-like 2
 2597 glyceraldehyde-3-phosphate dehydrogenase
 2773 guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 3
 10399 guanine nucleotide binding protein (G protein), beta polypeptide 2-like 1
 57120 golgi-associated PDZ and coiled-coil motif containing
 2894 glutamate receptor, ionotropic, delta 1
 2895 glutamate receptor, ionotropic, delta 2
 9711 KIAA0226
 9776 KIAA0652
 22863 KIAA0831
 3799 kinesin family member 5B
 54800 kelch-like 24 (Drosophila)
 3916 lysosomal-associated membrane protein 1
 3920 lysosomal-associated membrane protein 2
 84557 microtubule-associated protein 1 light chain 3 alpha
 81631 microtubule-associated protein 1 light chain 3 beta
 440738 microtubule-associated protein 1 light chain 3 gamma
 5609 mitogen-activated protein kinase kinase 7
 5594 mitogen-activated protein kinase 1
 5595 mitogen-activated protein kinase 3
 5599 mitogen-activated protein kinase 8
 9479 mitogen-activated protein kinase 8 interacting protein 1
 5601 mitogen-activated protein kinase 9
 51360 membrane-bound transcription factor peptidase, site 2
 64223 MTOR associated protein, LST8 homolog (S. cerevisiae)
 64419 myotubularin related protein 14
 2475 mechanistic target of rapamycin (serine/threonine kinase)
 4609 v-myc myelocytomatosis viral oncogene homolog (avian)
 92345 nuclear assembly factor 1 homolog (S. cerevisiae)
 10135 nicotinamide phosphoribosyltransferase
 4077 neighbor of BRCA1 gene 1
 10787 NCK-associated protein 1
 4780 nuclear factor (erythroid-derived 2)-like 2
 4790 nuclear factor of kappa light polypeptide gene enhancer in B-cells 1
 159296 NK2 transcription factor related, locus 3 (Drosophila)
 58484 NLR family, CARD domain containing 4
 4864 Niemann-Pick disease, type C1
 3084 neuregulin 1
 9542 neuregulin 2
 10718 neuregulin 3
 5034 prollyl 4-hydroxylase, beta polypeptide
 5071 Parkinson disease (autosomal recessive, juvenile) 2, parkin
 142 poly (ADP-ribose) polymerase 1
 8682 phosphoprotein enriched in astrocytes 15
 27043 proline, glutamate and leucine rich protein 1
 5195 peroxisomal biogenesis factor 14
 8504 peroxisomal biogenesis factor 3
 5289 phosphoinositide-3-kinase, class 3
 30849 phosphoinositide-3-kinase, regulatory subunit 4

65018 PTEN induced putative kinase 1
23645 protein phosphatase 1, regulatory (inhibitor) subunit 15A
5564 protein kinase, AMP-activated, beta 1 non-catalytic subunit
5573 protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
5580 protein kinase C, delta
5588 protein kinase C, theta
5728 phosphatase and tensin homolog
5753 PTK6 protein tyrosine kinase 6
8766 RAB11A, member RAS oncogene family
5861 RAB1A, member RAS oncogene family
53917 RAB24, member RAS oncogene family
83452 RAB33B, member RAS oncogene family
5868 RAB5A, member RAS oncogene family
7879 RAB7A, member RAS oncogene family
5879 ras-related C3 botulinum toxin substrate 1 (rho family, small GTP binding protein Rac1)
5894 v-raf-1 murine leukemia viral oncogene homolog 1
5925 retinoblastoma 1
9821 RB1-inducible coiled-coil 1
5970 v-rel reticuloendotheliosis viral oncogene homolog A (avian)
10287 regulator of G-protein signaling 19
6009 Ras homolog enriched in brain
6198 ribosomal protein S6 kinase, 70kDa, polypeptide 1
57521 regulatory associated protein of MTOR, complex 1
56681 SAR1 homolog A (S. cerevisiae)
5265 serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1
83667 sestrin 2
51100 SH3-domain GRB2-like endophilin B1
23411 sirtuin (silent mating type information regulation 2 homolog) 1 (S. cerevisiae)
22933 sirtuin (silent mating type information regulation 2 homolog) 2 (S. cerevisiae)
8877 sphingosine kinase 1
83985 spinster homolog 1 (Drosophila)
8878 sequestosome 1
6767 suppression of tumorigenicity 13 (colon carcinoma) (Hsp70 interacting protein)
6794 serine/threonine kinase 11
29110 TANK-binding kinase 1
10548 transmembrane 9 superfamily member 1
81671 transmembrane protein 49
157753 transmembrane protein 74
8743 tumor necrosis factor (ligand) superfamily, member 10
7157 tumor protein p53
58476 tumor protein p53 inducible nuclear protein 2
8626 tumor protein p63
7161 tumor protein p73
7248 tuberous sclerosis 1
7249 tuberous sclerosis 2
286319 tumor suppressor candidate 1
8408 unc-51-like kinase 1 (C. elegans)
9706 unc-51-like kinase 2 (C. elegans)
25989 unc-51-like kinase 3 (C. elegans)
9100 ubiquitin specific peptidase 10
7405 UV radiation resistance associated gene
9341 vesicle-associated membrane protein 3 (cellubrevin)
6845 vesicle-associated membrane protein 7
7422 vascular endothelial growth factor A
23001 WD repeat and FYVE domain containing 3
11152 WD repeat domain 45
56270 WDR45-like
55062 WD repeat domain, phosphoinositide interacting 1

26100 WD repeat domain, phosphoinositide interacting 2
53349 zinc finger, FYVE domain containing 1

Database)

Symbol

AMBRA1

APOL1

ARNT

ARSA

ARSB

ATF4

ATF6

ATG10

ATG12

ATG16L1

ATG16L2

ATG2A

ATG2B

ATG3

ATG4A

ATG4B

ATG4C

ATG4D

ATG5

ATG7

ATG9A

ATG9B

ATIC

BAG1

BAG3

BAK1

BAX

BCL2

BCL2L1

BECN1

BID

BIRC5

BIRC6

BNIP1

BNIP3

BNIP3L

C12orf44

C17orf88

CALCOCO2

CAMKK2

CANX

CAPN1

CAPN10

CAPN2

CAPNS1

CASP1

CASP3

CASP4

CASP8

CCL2

CCR2

CD46

CDKN1A

CDKN1B

CDKN2A

CFLAR

CHMP2B
CHMP4B
CLN3
CTSB
CTSD
CTSL1
CX3CL1
CXCR4
DAPK1
DAPK2
DDIT3
DIRAS3
DLC1
DNAJB1
DNAJB9
DRAM1
EDEM1
EEF2
EEF2K
EGFR
EIF2AK2
EIF2AK3
EIF2S1
EIF4EBP1
EIF4G1
ERBB2
ERN1
ERO1L
FADD
FAM48A
FAS
FKBP1A
FKBP1B
FOS
FOXO1
FOXO3
GAA
GABARAP
GABARAPL1
GABARAPL2
GAPDH
GNAI3
GNB2L1
GOPC
GRID1
GRID2
HDAC1
HDAC6
HGS
HIF1A
HSP90AB1
HSPA5
HSPA8
HSPB8
IFNG
IKBKB
IKBKE
IL24

IRGM
ITGA3
ITGA6
ITGB1
ITGB4
ITPR1
GAA
GABARAP
GABARAPL1
GABARAPL2
GAPDH
GNAI3
GNB2L1
GOPC
GRID1
GRID2
KIAA0226
KIAA0652
KIAA0831
KIF5B
KLHL24
LAMP1
LAMP2
MAP1LC3A
MAP1LC3B
MAP1LC3C
MAP2K7
MAPK1
MAPK3
MAPK8
MAPK8IP1
MAPK9
MBTPS2
MLST8
MTMR14
MTOR
MYC
NAF1
NAMPT
NBR1
NCKAP1
NFE2L2
NFKB1
NKX2-3
NLRC4
NPC1
NRG1
NRG2
NRG3
P4HB
PARK2
PARP1
PEA15
PELP1
PEX14
PEX3
PIK3C3
PIK3R4

PINK1
PPP1R15A
PRKAB1
PRKAR1A
PRKCD
PRKCQ
PTEN
PTK6
RAB11A
RAB1A
RAB24
RAB33B
RAB5A
RAB7A
RAC1
RAF1
RB1
RB1CC1
RELA
RGS19
RHEB
RPS6KB1
RPTOR
SAR1A
SERPINA1
SESN2
SH3GLB1
SIRT1
SIRT2
SPHK1
SPNS1
SQSTM1
ST13
STK11
TBK1
TM9SF1
TMEM49
TMEM74
TNFSF10
TP53
TP53INP2
TP63
TP73
TSC1
TSC2
TUSC1
ULK1
ULK2
ULK3
USP10
UVRAG
VAMP3
VAMP7
VEGFA
WDFY3
WDR45
WDR45L
WIP1

WIP12
ZFYVE1

Table S2: Kaplan-Meier analyses of all 232 autophagy regulators in meta-cohort

characteris	Hazard.Rat	CI95	pvalue	HR(95%CI)
1 AMBRA1	1.016	0.838-1.23	0.870544	1.016(0.838-1.231)
2 APOL1	1.232	1.145-1.32	2.55E-08	1.232(1.145-1.326)
3 ARNT	0.935	0.804-1.08	0.377108	0.935(0.804-1.086)
4 ARSA	0.897	0.799-1.00	0.066201	0.897(0.799-1.007)
5 ARSB	1.113	0.947-1.30	0.193392	1.113(0.947-1.307)
6 ATF4	1.043	0.89-1.222	0.605996	1.043(0.89-1.222)
7 ATF6	0.914	0.783-1.06	0.2532	0.914(0.783-1.067)
8 ATG10	1.06	0.892-1.26	0.507522	1.06(0.892-1.26)
9 ATG16L1	1.126	0.952-1.33	0.16628	1.126(0.952-1.332)
10 ATG2A	0.848	0.739-0.97	0.018849	0.848(0.739-0.973)
11 ATG2B	0.793	0.691-0.91	0.001053	0.793(0.691-0.911)
12 ATG3	1.252	1.042-1.50	0.016184	1.252(1.042-1.503)
13 ATG4A	0.871	0.74-1.026	0.098278	0.871(0.74-1.026)
14 ATG4B	1.114	0.968-1.28	0.131217	1.114(0.968-1.283)
15 ATG5	1.153	1.011-1.31	0.033865	1.153(1.011-1.315)
16 ATG7	1.38	1.161-1.64	0.00026	1.38(1.161-1.64)
17 ATG9A	1.295	1.102-1.52	0.00169	1.295(1.102-1.521)
18 ATIC	1.363	1.196-1.55	3.49E-06	1.363(1.196-1.554)
19 BAG1	0.943	0.846-1.05	0.285899	0.943(0.846-1.051)
20 BAG3	1.166	1.052-1.29	0.003519	1.166(1.052-1.293)
21 BAK1	1.297	1.129-1.49	0.00024	1.297(1.129-1.49)
22 BAX	1.103	0.966-1.26	0.148243	1.103(0.966-1.26)
23 BCL2	0.789	0.686-0.90	0.000871	0.789(0.686-0.907)
24 BCL2L1	1.196	1.06-1.349	0.00367	1.196(1.06-1.349)
25 BID	1.285	1.16-1.425	1.69E-06	1.285(1.16-1.425)
26 BIRC5	1.276	1.196-1.36	1.82E-13	1.276(1.196-1.361)
27 BNIP1	1.114	0.945-1.31	0.199417	1.114(0.945-1.313)
28 BNIP3	1.05	0.971-1.13	0.222256	1.05(0.971-1.136)
29 BNIP3L	0.882	0.782-0.99	0.038024	0.882(0.782-0.993)
30 CALCOO	0.781	0.683-0.89	0.000294	0.781(0.683-0.893)
31 CAMKK2	1.34	1.135-1.58	0.00053	1.34(1.135-1.581)
32 CANX	1.058	0.943-1.18	0.335964	1.058(0.943-1.188)
33 CAPN1	1.122	0.987-1.27	0.079423	1.122(0.987-1.276)
34 CAPN10	0.933	0.812-1.07	0.32202	0.933(0.812-1.071)
35 CAPN2	0.903	0.803-1.01	0.090079	0.903(0.803-1.016)
36 CAPNS1	1.202	1.044-1.38	0.010686	1.202(1.044-1.384)
37 CASP1	0.945	0.87-1.027	0.184249	0.945(0.87-1.027)
38 CASP3	1.155	1.001-1.33	0.04909	1.155(1.001-1.333)
39 CASP4	1.136	1.007-1.28	0.037416	1.136(1.007-1.281)
40 CASP8	1.083	0.95-1.234	0.231303	1.083(0.95-1.234)
41 CCL2	1.009	0.952-1.07	0.752382	1.009(0.952-1.07)
42 CCR2	0.74	0.668-0.81	5.35E-09	0.74(0.668-0.818)
43 CD46	0.942	0.856-1.03	0.216149	0.942(0.856-1.036)
44 CDKN1A	1.249	1.136-1.37	4.11E-06	1.249(1.136-1.372)
45 CDKN1B	0.879	0.779-0.99	0.035385	0.879(0.779-0.991)
46 CDKN2A	1.057	1.009-1.10	0.01856	1.057(1.009-1.107)
47 CFLAR	0.898	0.804-1.00	0.056158	0.898(0.804-1.003)
48 CHMP2B	1.095	0.973-1.23	0.133155	1.095(0.973-1.234)
49 CLN3	0.841	0.741-0.95	0.007335	0.841(0.741-0.954)
50 CTSB	1.178	1.06-1.309	0.002258	1.178(1.06-1.309)
51 CTSD	0.926	0.847-1.01	0.094151	0.926(0.847-1.013)
52 CX3CL1	0.909	0.86-0.962	0.000977	0.909(0.86-0.962)
53 CXCR4	0.944	0.871-1.02	0.15839	0.944(0.871-1.023)
54 DAPK1	0.792	0.717-0.87	4.25E-06	0.792(0.717-0.875)
55 DAPK2	0.718	0.653-0.79	1.43E-11	0.718(0.653-0.791)
56 DDIT3	1.029	0.936-1.13	0.555745	1.029(0.936-1.131)
57 DIRAS3	0.951	0.894-1.01	0.116315	0.951(0.894-1.012)

58	DLC1	0.833	0.772-0.9	3.45E-06	0.833(0.772-0.9)
59	DNAJB1	1.083	0.992-1.18	0.074456	1.083(0.992-1.181)
60	DNAJB9	0.859	0.775-0.95	0.00361	0.859(0.775-0.951)
61	DRAM1	0.818	0.763-0.87	9.49E-09	0.818(0.763-0.876)
62	EDEM1	0.824	0.737-0.92	0.000635	0.824(0.737-0.921)
63	EEF2	0.8	0.69-0.929	0.003381	0.8(0.69-0.929)
64	EGFR	1.005	0.933-1.08	0.886507	1.005(0.933-1.084)
65	EIF2AK2	1.202	1.059-1.36	0.004398	1.202(1.059-1.363)
66	EIF2AK3	0.835	0.739-0.94	0.00375	0.835(0.739-0.943)
67	EIF2S1	1.197	1.06-1.351	0.003619	1.197(1.06-1.351)
68	EIF4EBP1	1.182	1.102-1.26	3.14E-06	1.182(1.102-1.268)
69	EIF4G1	1.239	1.092-1.40	0.000889	1.239(1.092-1.406)
70	ERBB2	0.949	0.862-1.04	0.284249	0.949(0.862-1.045)
71	ERN1	0.895	0.793-1.01	0.070954	0.895(0.793-1.01)
72	FADD	1.358	1.192-1.54	3.98E-06	1.358(1.192-1.546)
73	FAS	0.953	0.876-1.03	0.253205	0.953(0.876-1.035)
74	FKBP1A	1.29	1.131-1.47	0.000143	1.29(1.131-1.471)
75	FKBP1B	1.016	0.934-1.10	0.705443	1.016(0.934-1.106)
76	FOS	0.94	0.892-0.99	0.023359	0.94(0.892-0.992)
77	FOXO1	0.919	0.826-1.02	0.12519	0.919(0.826-1.024)
78	FOXO3	0.958	0.847-1.08	0.494663	0.958(0.847-1.084)
79	GAA	1.028	0.93-1.136	0.587764	1.028(0.93-1.136)
80	GABARAP	0.881	0.733-1.05	0.176006	0.881(0.733-1.058)
81	GABARAPL	1.052	0.951-1.16	0.324884	1.052(0.951-1.163)
82	GABARAPL	0.913	0.788-1.05	0.223825	0.913(0.788-1.057)
83	GAPDH	1.621	1.448-1.81	3.68E-17	1.621(1.448-1.813)
84	GNAI3	1.384	1.203-1.59	5.60E-06	1.384(1.203-1.592)
85	HDAC1	1.23	1.071-1.41	0.003328	1.23(1.071-1.412)
86	HDAC6	0.922	0.796-1.06	0.27773	0.922(0.796-1.068)
87	HGS	1.159	1.019-1.31	0.025075	1.159(1.019-1.318)
88	HIF1A	1.178	1.055-1.31	0.003434	1.178(1.055-1.314)
89	HSP90AB1	1.024	0.915-1.14	0.679182	1.024(0.915-1.147)
90	HSPA5	1.034	0.906-1.18	0.621113	1.034(0.906-1.18)
91	HSPA8	1.168	1.036-1.31	0.011371	1.168(1.036-1.317)
92	HSPB8	0.845	0.783-0.91	1.27E-05	0.845(0.783-0.911)
93	IFNG	1.031	0.955-1.11	0.434815	1.031(0.955-1.112)
94	IKBKB	0.787	0.705-0.87	2.00E-05	0.787(0.705-0.879)
95	IL24	1.021	0.91-1.145	0.728417	1.021(0.91-1.145)
96	ITGA3	1.075	1-1.155	0.050681	1.075(1-1.155)
97	ITGA6	1.203	1.119-1.29	5.84E-07	1.203(1.119-1.294)
98	ITGB1	1.403	1.23-1.601	4.94E-07	1.403(1.23-1.601)
99	ITGB4	1.251	1.169-1.33	9.30E-11	1.251(1.169-1.339)
100	ITPR1	0.818	0.74-0.903	7.73E-05	0.818(0.74-0.903)
101	KIF5B	1.121	0.981-1.28	0.094115	1.121(0.981-1.282)
102	KLHL24	0.923	0.823-1.03	0.169891	0.923(0.823-1.035)
103	LAMP1	0.972	0.86-1.098	0.644712	0.972(0.86-1.098)
104	LAMP2	1	0.891-1.12	0.995281	1(0.891-1.121)
105	MAP1LC3E	0.945	0.808-1.10	0.475597	0.945(0.808-1.105)
106	MAP1LC3C	0.901	0.827-0.98	0.017446	0.901(0.827-0.982)
107	MAP2K7	0.98	0.836-1.15	0.806105	0.98(0.836-1.15)
108	MAPK1	1.139	1.022-1.27	0.019185	1.139(1.022-1.271)
109	MAPK3	0.98	0.842-1.14	0.795344	0.98(0.842-1.141)
110	MAPK8	1.066	0.928-1.22	0.367424	1.066(0.928-1.225)
111	MAPK8IP1	0.913	0.804-1.03	0.159063	0.913(0.804-1.036)
112	MAPK9	0.928	0.814-1.05	0.265647	0.928(0.814-1.058)
113	MBTPS2	1.305	1.097-1.55	0.002694	1.305(1.097-1.554)
114	MLST8	1.018	0.877-1.18	0.812677	1.018(0.877-1.182)
115	MTMR14	0.988	0.816-1.19	0.902709	0.988(0.816-1.197)
116	MTOR	0.952	0.796-1.13	0.590523	0.952(0.796-1.138)

117 MYC	1.112	1.041-1.18	0.00169	1.112(1.041-1.188)
118 NAMPT	1.064	1.001-1.13	0.044633	1.064(1.001-1.131)
119 NBR1	1.049	0.905-1.21	0.524248	1.049(0.905-1.218)
120 NCKAP1	1.168	1.013-1.34	0.032044	1.168(1.013-1.347)
121 NFE2L2	0.982	0.861-1.12	0.786335	0.982(0.861-1.12)
122 NFKB1	0.929	0.807-1.06	0.302367	0.929(0.807-1.069)
123 NPC1	0.922	0.816-1.04	0.195101	0.922(0.816-1.042)
124 NRG1	1.029	0.921-1.15	0.615086	1.029(0.921-1.15)
125 NRG2	0.93	0.76-1.138	0.480048	0.93(0.76-1.138)
126 P4HB	1.216	1.06-1.394	0.005119	1.216(1.06-1.394)
127 PARP1	1.058	0.919-1.21	0.432852	1.058(0.919-1.218)
128 PEA15	1.127	0.987-1.28	0.077423	1.127(0.987-1.288)
129 PELP1	1.007	0.871-1.16	0.929497	1.007(0.871-1.163)
130 PEX14	0.939	0.797-1.10	0.448887	0.939(0.797-1.106)
131 PEX3	0.935	0.817-1.07	0.334541	0.935(0.817-1.071)
132 PIK3C3	1.006	0.849-1.19	0.947962	1.006(0.849-1.191)
133 PIK3R4	0.908	0.749-1.10	0.3273	0.908(0.749-1.101)
134 PINK1	0.876	0.76-1.009	0.067119	0.876(0.76-1.009)
135 PPP1R15A	0.959	0.873-1.05	0.385139	0.959(0.873-1.054)
136 PRKAB1	0.799	0.713-0.89	9.99E-05	0.799(0.713-0.894)
137 PRKAR1A	0.937	0.832-1.05	0.289218	0.937(0.832-1.056)
138 PRKCD	0.767	0.676-0.87	3.60E-05	0.767(0.676-0.87)
139 PRKCQ	0.885	0.791-0.99	0.032956	0.885(0.791-0.99)
140 PTEN	1.064	0.925-1.22	0.385156	1.064(0.925-1.223)
141 PTK6	1.099	1.023-1.18	0.009779	1.099(1.023-1.18)
142 RAB11A	1.225	1.081-1.38	0.001535	1.225(1.081-1.389)
143 RAB1A	1.166	1.005-1.35	0.043207	1.166(1.005-1.354)
144 RAB33B	0.833	0.716-0.97	0.018391	0.833(0.716-0.97)
145 RAB5A	1.246	1.067-1.45	0.005344	1.246(1.067-1.454)
146 RAB7A	1.379	1.145-1.66	0.000718	1.379(1.145-1.662)
147 RAC1	1.287	1.112-1.49	0.00071	1.287(1.112-1.49)
148 RAF1	0.875	0.735-1.04	0.13437	0.875(0.735-1.042)
149 RB1	1.007	0.88-1.153	0.914911	1.007(0.88-1.153)
150 RB1CC1	0.964	0.857-1.08	0.549679	0.964(0.857-1.086)
151 RELA	1.178	0.997-1.39	0.054502	1.178(0.997-1.393)
152 RGS19	1.022	0.904-1.15	0.73236	1.022(0.904-1.155)
153 RHEB	1.055	0.916-1.21	0.454487	1.055(0.916-1.216)
154 RPS6KB1	1.12	0.969-1.29	0.126343	1.12(0.969-1.294)
155 SAR1A	1.289	1.122-1.48	0.000327	1.289(1.122-1.481)
156 SERPINA1	0.997	0.953-1.04	0.882809	0.997(0.953-1.042)
157 SH3GLB1	1.332	1.165-1.52	2.82E-05	1.332(1.165-1.523)
158 SIRT1	0.8	0.707-0.90	0.000413	0.8(0.707-0.905)
159 SIRT2	0.786	0.669-0.92	0.003505	0.786(0.669-0.924)
160 SPHK1	1.229	1.147-1.31	5.50E-09	1.229(1.147-1.318)
161 SQSTM1	1.01	0.907-1.12	0.850178	1.01(0.907-1.126)
162 ST13	0.96	0.848-1.08	0.51463	0.96(0.848-1.086)
163 STK11	0.899	0.786-1.02	0.119653	0.899(0.786-1.028)
164 TBK1	1.179	1.025-1.35	0.021074	1.179(1.025-1.357)
165 TM9SF1	1.045	0.906-1.20	0.54703	1.045(0.906-1.206)
166 TNFSF10	0.982	0.92-1.048	0.576154	0.982(0.92-1.048)
167 TP53	0.992	0.902-1.09	0.863668	0.992(0.902-1.091)
168 TP63	0.98	0.915-1.05	0.57616	0.98(0.915-1.051)
169 TP73	0.93	0.819-1.05	0.262984	0.93(0.819-1.056)
170 TSC1	0.881	0.763-1.01	0.082816	0.881(0.763-1.017)
171 TSC2	0.872	0.767-0.99	0.036617	0.872(0.767-0.992)
172 ULK1	1.053	0.935-1.18	0.394337	1.053(0.935-1.185)
173 ULK2	0.801	0.7-0.915	0.001139	0.801(0.7-0.915)
174 USP10	1.089	0.934-1.27	0.276065	1.089(0.934-1.271)
175 UVRAG	0.909	0.784-1.05	0.210058	0.909(0.784-1.055)

176 VAMP3	0.999	0.869-1.14	0.98899	0.999(0.869-1.149)
177 VAMP7	0.997	0.884-1.12	0.957272	0.997(0.884-1.124)
178 VEGFA	1.27	1.175-1.37	1.68E-09	1.27(1.175-1.372)
179 WDFY3	0.892	0.781-1.01	0.09229	0.892(0.781-1.019)
180 WDR45	0.817	0.692-0.96	0.017291	0.817(0.692-0.965)
181 WIP1	1.045	0.925-1.18	0.475725	1.045(0.925-1.181)
182 WIP2	1.089	0.937-1.26	0.26499	1.089(0.937-1.266)

Table S3: all DEGs between the two Atclusters

gene	logFC	AveExpr	t	P.Value	adj.P.Val	B
1 TMEM173	-1.26152	5.975408	-15.6594	2.80E-45	5.78E-41	92.0347
2 NAPSB	-1.46972	3.699747	-14.4646	7.06E-40	7.30E-36	79.76305
3 TMEM119	-1.34325	3.746328	-13.9642	1.15E-37	7.93E-34	74.73846
4 CD4	-1.2181	5.211456	-13.7285	1.23E-36	6.38E-33	72.39866
5 MFAP4	-1.79756	5.305178	-13.6635	2.37E-36	9.78E-33	71.75633
6 GAS7	-1.03584	2.514286	-13.595	4.69E-36	1.62E-32	71.08069
7 RASSF2	-1.01074	2.886797	-13.5728	5.86E-36	1.73E-32	70.86229
8 ARHGDI	-1.04177	7.831379	-13.5463	7.63E-36	1.97E-32	70.60147
9 CD37	-1.34618	5.070262	-13.497	1.25E-35	2.86E-32	70.11799
10 ARHGAP3	-1.03561	3.356019	-13.3406	5.88E-35	1.01E-31	68.58696
11 PODN	-1.31445	3.95012	-13.3073	8.18E-35	1.30E-31	68.26204
12 SPARCL1	-1.23674	5.816138	-13.084	7.38E-34	9.53E-31	66.09325
13 PTGDS	-1.78414	6.226466	-13.0572	9.59E-34	1.10E-30	65.83456
14 AOC3	-1.33874	4.076053	-12.9605	2.47E-33	2.55E-30	64.90119
15 C7	-2.07836	4.213026	-12.9263	3.45E-33	3.40E-30	64.5722
16 A2M	-1.30979	7.755283	-12.8699	5.97E-33	5.61E-30	64.03067
17 IL16	-1.04519	3.324508	-12.7307	2.31E-32	1.91E-29	62.69922
18 SELPLG	-1.06964	4.189691	-12.6374	5.68E-32	4.12E-29	61.81092
19 HLA.DPB1	-1.45877	8.157953	-12.627	6.28E-32	4.32E-29	61.71209
20 CELF2	-1.08284	3.549113	-12.6225	6.55E-32	4.37E-29	61.66935
21 CIITA	-1.19808	3.31123	-12.518	1.79E-31	1.09E-28	60.67863
22 HLA.DOA	-1.44401	4.1987	-12.5109	1.92E-31	1.13E-28	60.61086
23 SLCO2B1	-1.25718	4.451268	-12.4653	2.97E-31	1.66E-28	60.18066
24 SLC34A2	-2.24987	8.300537	-12.4575	3.20E-31	1.72E-28	60.10682
25 CX3CL1	-1.74811	4.491483	-12.4559	3.25E-31	1.72E-28	60.09155
26 NAPSA	-2.87237	9.296016	-12.4392	3.81E-31	1.97E-28	59.93435
27 SPN	-1.06165	2.703594	-12.4256	4.34E-31	2.19E-28	59.8058
28 SASH3	-1.05699	3.59127	-12.4083	5.12E-31	2.46E-28	59.64259
29 CD74	-1.36868	11.51898	-12.3949	5.82E-31	2.73E-28	59.51652
30 DOCK2	-1.00221	3.133288	-12.378	6.84E-31	3.14E-28	59.35741
31 SYNE1	-1.0985	4.1834	-12.3294	1.09E-30	4.78E-28	58.90135
32 RPS6KA2	-1.08859	4.424941	-12.2847	1.66E-30	6.74E-28	58.48256
33 LSP1	-1.13275	5.606312	-12.275	1.82E-30	7.25E-28	58.39133
34 FRZB	-1.09038	2.524748	-12.2367	2.62E-30	1.02E-27	58.03304
35 JAML	-1.19959	3.791684	-12.2079	3.45E-30	1.32E-27	57.76372
36 FCMR	-1.05209	3.080767	-12.191	4.04E-30	1.52E-27	57.60676
37 PRELP	-1.34266	3.656484	-12.1891	4.11E-30	1.52E-27	57.58875
38 SLIT3	-1.20571	2.310896	-12.1414	6.46E-30	2.30E-27	57.14409
39 PLD4	-1.08378	2.051876	-12.0901	1.05E-29	3.44E-27	56.66722
40 ROS1	-1.77924	3.245294	-12.0839	1.11E-29	3.53E-27	56.60981
41 ITGAL	-1.10794	3.370154	-12.0419	1.65E-29	5.09E-27	56.22018
42 PARVG	-1.0377	3.800194	-12.0296	1.85E-29	5.55E-27	56.10615
43 PAPLN	-1.0004	3.025518	-11.9871	2.76E-29	8.04E-27	55.71344
44 ADGRF5	-1.68047	4.949497	-11.9769	3.04E-29	8.43E-27	55.61925
45 TPSAB1	-1.71118	4.852625	-11.9758	3.07E-29	8.43E-27	55.60889
46 ELN	-1.64615	4.763539	-11.9638	3.43E-29	8.98E-27	55.49818
47 HLA.DMA	-1.20859	7.259471	-11.9578	3.63E-29	9.38E-27	55.44292
48 LTBP2	-1.2608	4.673334	-11.9384	4.36E-29	1.05E-26	55.26302
49 ABI3BP	-1.34114	3.264953	-11.9054	5.93E-29	1.39E-26	54.95917
50 HLA.DPA1	-1.42543	8.291302	-11.8883	6.96E-29	1.59E-26	54.80154
51 COLEC12	-1.26449	2.900478	-11.8701	8.24E-29	1.82E-26	54.63479
52 EVI2B	-1.04629	4.084858	-11.7678	2.14E-28	4.51E-26	53.69662
53 ADA2	-1.08732	4.772012	-11.7482	2.56E-28	5.30E-26	53.5169
54 CD93	-1.00377	3.746115	-11.7342	2.92E-28	5.97E-26	53.38951
55 ST3GAL5	-1.34501	5.168563	-11.7078	3.73E-28	7.56E-26	53.14805
56 NCKAP1L	-1.06992	3.471657	-11.6652	5.53E-28	1.07E-25	52.76053
57 TNS1	-1.12173	4.764036	-11.586	1.15E-27	2.12E-25	52.04066

58	FMO2	-1.25617	2.97927	-11.567	1.37E-27	2.42E-25	51.86837
59	ALOX5	-1.18774	4.529621	-11.5294	1.93E-27	3.33E-25	51.52814
60	SERPING1	-1.00033	7.727873	-11.4768	3.13E-27	5.13E-25	51.05269
61	CCR7	-1.0423	2.148343	-11.4245	5.04E-27	8.15E-25	50.58202
62	SPI1	-1.11691	4.985115	-11.4159	5.46E-27	8.75E-25	50.50457
63	ACKR1	-1.49378	3.01343	-11.4133	5.59E-27	8.89E-25	50.48113
64	IRF8	-1.05579	3.291536	-11.411	5.71E-27	9.01E-25	50.46064
65	ITGB2	-1.24473	6.206803	-11.3927	6.74E-27	1.04E-24	50.29622
66	CD22	-1.12462	2.141064	-11.3902	6.90E-27	1.06E-24	50.27361
67	ACE	-1.00342	4.138346	-11.3885	7.00E-27	1.06E-24	50.25871
68	CSF1R	-1.12151	4.397087	-11.2945	1.65E-26	2.38E-24	49.41669
69	INMT	-1.47815	3.156856	-11.2767	1.93E-26	2.70E-24	49.25807
70	HMCN1	-1.09713	2.686863	-11.2617	2.22E-26	3.07E-24	49.12418
71	SSC5D	-1.05429	2.733527	-11.2362	2.79E-26	3.80E-24	48.89692
72	MOXD1	-1.1505	3.811641	-11.2253	3.08E-26	4.17E-24	48.79945
73	DPYSL2	-1.00275	5.05104	-11.2148	3.39E-26	4.55E-24	48.7058
74	TMPRSS2	-1.55581	4.939405	-11.201	3.84E-26	5.09E-24	48.58363
75	MEGF6	-1.15593	3.351486	-11.1773	4.76E-26	6.18E-24	48.37256
76	C1orf162	-1.00029	4.442053	-11.164	5.36E-26	6.80E-24	48.25516
77	TRIM22	-1.04032	5.088739	-11.1639	5.36E-26	6.80E-24	48.25396
78	HCLS1	-1.01111	5.095891	-11.1495	6.11E-26	7.55E-24	48.12585
79	CPA3	-1.51197	3.487625	-11.128	7.41E-26	9.01E-24	47.93603
80	CISH	-1.08059	4.554014	-11.1099	8.72E-26	1.04E-23	47.77542
81	HLA.DRA	-1.2943	10.16674	-11.1004	9.50E-26	1.13E-23	47.69151
82	SLC15A3	-1.04694	5.89639	-11.0556	1.42E-25	1.60E-23	47.29542
83	SCN7A	-1.00065	1.564559	-11.0534	1.45E-25	1.63E-23	47.27612
84	AL365361.	-1.08117	1.889931	-10.9965	2.41E-25	2.63E-23	46.77539
85	AQP1	-1.86342	6.681851	-10.9866	2.63E-25	2.86E-23	46.68788
86	SNX30	-1.03312	3.227753	-10.9548	3.49E-25	3.72E-23	46.4095
87	ADH1B	-1.99984	3.385362	-10.9157	4.95E-25	5.14E-23	46.06619
88	RHEX	-1.09672	2.145396	-10.9085	5.28E-25	5.45E-23	46.00328
89	ITGAM	-1.08707	3.022443	-10.8893	6.26E-25	6.31E-23	45.83537
90	TXNIP	-1.06051	7.894655	-10.8828	6.63E-25	6.65E-23	45.77845
91	PLCB2	-1.00097	3.803716	-10.8429	9.44E-25	8.93E-23	45.43037
92	MNDA	-1.08264	3.515298	-10.8427	9.46E-25	8.93E-23	45.42889
93	CCL19	-1.75451	4.832755	-10.7409	2.32E-24	2.06E-22	44.54372
94	MGP	-1.25371	8.099553	-10.7398	2.35E-24	2.06E-22	44.53418
95	MGLL	-1.13547	5.600292	-10.6926	3.55E-24	3.07E-22	44.12635
96	LAIR1	-1.06551	4.432761	-10.6728	4.23E-24	3.63E-22	43.95461
97	C4B	-1.42277	6.346425	-10.6661	4.48E-24	3.83E-22	43.89739
98	CCL14	-1.58529	3.75136	-10.6597	4.74E-24	4.04E-22	43.84165
99	ALOX5AP	-1.22871	5.562996	-10.658	4.81E-24	4.08E-22	43.8272
100	VWF	-1.06475	4.976943	-10.6562	4.89E-24	4.13E-22	43.81145
101	LY86	-1.03018	3.426833	-10.6544	4.97E-24	4.17E-22	43.79657
102	SFTPA2	-3.24124	8.790396	-10.6326	6.01E-24	4.99E-22	43.60879
103	ICAM1	-1.29977	6.994123	-10.5904	8.69E-24	7.08E-22	43.24536
104	DLC1	-1.21452	3.565265	-10.5814	9.40E-24	7.57E-22	43.16807
105	SGPP2	-1.24033	4.425099	-10.5757	9.88E-24	7.92E-22	43.11907
106	HLA.DRB1	-1.44988	8.650994	-10.569	1.05E-23	8.32E-22	43.06147
107	MYH11	-1.42983	3.954354	-10.542	1.33E-23	1.03E-21	42.83036
108	IL7R	-1.15358	3.576347	-10.538	1.37E-23	1.06E-21	42.79615
109	TPSB2	-1.69611	4.664157	-10.5379	1.37E-23	1.06E-21	42.7953
110	TNXB	-1.24805	2.906702	-10.5328	1.44E-23	1.10E-21	42.75141
111	SIGLEC1	-1.02094	2.504853	-10.5306	1.46E-23	1.11E-21	42.7325
112	OLR1	-1.29328	3.580497	-10.5224	1.57E-23	1.19E-21	42.6623
113	HLA.DQB2	-1.84751	4.688924	-10.5215	1.58E-23	1.19E-21	42.65508
114	C1orf116	-1.58709	5.237127	-10.51	1.75E-23	1.31E-21	42.55676
115	C4A	-1.3698	6.320902	-10.4785	2.30E-23	1.67E-21	42.28791
116	CYP27A1	-1.08001	4.833635	-10.4471	3.02E-23	2.12E-21	42.01997

117	LGALS9	-1.03552	6.751306	-10.4441	3.10E-23	2.16E-21	41.99409
118	TLR2	-1.06368	3.445448	-10.4383	3.26E-23	2.25E-21	41.94466
119	VIPR1	-1.08407	2.724182	-10.4293	3.52E-23	2.42E-21	41.86815
120	DCN	-1.18818	7.688772	-10.3909	4.91E-23	3.25E-21	41.54232
121	OSCAR	-1.00085	2.882764	-10.3596	6.43E-23	4.22E-21	41.27687
122	COL14A1	-1.24775	3.285186	-10.3547	6.71E-23	4.37E-21	41.23541
123	GPC4	-1.15763	4.527761	-10.3484	7.08E-23	4.57E-21	41.18197
124	GGTLC1	-2.00185	3.113784	-10.3239	8.74E-23	5.58E-21	40.97492
125	SLC22A31	-1.95596	5.554889	-10.3066	1.01E-22	6.39E-21	40.82869
126	HLA.DQA1	-1.65818	6.875028	-10.3042	1.03E-22	6.50E-21	40.80854
127	SFTPA1	-3.17975	8.339292	-10.2846	1.22E-22	7.54E-21	40.64306
128	SPON1	-1.11049	3.279265	-10.2812	1.26E-22	7.73E-21	40.61451
129	SLCO2A1	-1.17878	3.912497	-10.2588	1.53E-22	9.27E-21	40.42525
130	SPOCK2	-1.07173	3.842701	-10.2265	2.01E-22	1.19E-20	40.15397
131	ABCA3	-1.60369	4.835362	-10.2262	2.02E-22	1.19E-20	40.1516
132	CAVIN2	-1.17587	3.51303	-10.2103	2.31E-22	1.35E-20	40.0178
133	MRC1	-1.36659	3.711277	-10.1536	3.75E-22	2.16E-20	39.54283
134	PTPRC	-1.07803	4.158517	-10.1099	5.43E-22	3.07E-20	39.17861
135	SELL	-1.07373	3.18861	-10.0848	6.72E-22	3.71E-20	38.96894
136	ITIH5	-1.07905	2.118975	-10.0178	1.18E-21	6.28E-20	38.41319
137	LTB	-1.18658	4.390148	-9.97838	1.65E-21	8.56E-20	38.08668
138	HLA.DMB	-1.09728	6.588805	-9.97324	1.72E-21	8.92E-20	38.04417
139	MFSD4A	-1.52663	3.509611	-9.96728	1.81E-21	9.30E-20	37.99492
140	MS4A7	-1.00179	3.899866	-9.96658	1.82E-21	9.34E-20	37.98918
141	FOLR2	-1.1623	4.271689	-9.92482	2.58E-21	1.29E-19	37.64479
142	ATP13A4	-1.61255	3.255137	-9.92151	2.66E-21	1.32E-19	37.6175
143	FAM20A	-1.08214	5.005483	-9.89783	3.24E-21	1.59E-19	37.42272
144	COL8A1	-1.17395	4.661476	-9.88688	3.55E-21	1.73E-19	37.33278
145	KCNK5	-1.18149	3.942215	-9.87949	3.77E-21	1.82E-19	37.27207
146	MARCO	-1.64709	4.618881	-9.86557	4.24E-21	2.04E-19	37.15785
147	TIMP3	-1.12688	6.43284	-9.85045	4.81E-21	2.30E-19	37.03391
148	CD1C	-1.10912	2.070897	-9.84173	5.17E-21	2.46E-19	36.96251
149	DMBT1	-2.21448	3.751612	-9.84109	5.20E-21	2.47E-19	36.95727
150	NKX2.1	-1.57017	5.821701	-9.83346	5.54E-21	2.62E-19	36.89474
151	NFIX	-1.09881	4.164527	-9.8218	6.10E-21	2.87E-19	36.79937
152	SCTR	-1.72949	3.016704	-9.78608	8.21E-21	3.79E-19	36.50763
153	CD52	-1.086	6.794894	-9.75269	1.08E-20	4.89E-19	36.23555
154	ITGBL1	-1.10236	4.214622	-9.71081	1.53E-20	6.80E-19	35.89522
155	CCL22	-1.0621	2.305997	-9.69104	1.80E-20	7.92E-19	35.73492
156	FBLN5	-1.02875	4.357377	-9.6758	2.04E-20	8.92E-19	35.61152
157	FXYD1	-1.14101	2.826121	-9.67176	2.11E-20	9.20E-19	35.57877
158	ISLR	-1.08708	5.018855	-9.60306	3.72E-20	1.57E-18	35.02421
159	MYO1G	-1.20681	3.481139	-9.60193	3.75E-20	1.59E-18	35.01509
160	SLC15A2	-1.05114	2.640739	-9.59946	3.83E-20	1.61E-18	34.99517
161	CEACAM6	-1.9303	8.723896	-9.59368	4.01E-20	1.68E-18	34.94863
162	PIGR	-2.4194	5.98623	-9.58701	4.24E-20	1.77E-18	34.89504
163	CYP2B7P	-1.9531	5.04792	-9.58411	4.34E-20	1.80E-18	34.87169
164	LMO3	-1.60162	4.861895	-9.5708	4.84E-20	2.00E-18	34.76469
165	NDNF	-1.493	4.135809	-9.56686	5.00E-20	2.06E-18	34.733
166	CHIT1	-1.91464	4.490941	-9.52762	6.89E-20	2.78E-18	34.41829
167	C8orf34.AS	-1.18014	1.808444	-9.51887	7.39E-20	2.96E-18	34.34825
168	CDH11	-1.1439	4.693523	-9.50213	8.47E-20	3.36E-18	34.21431
169	SFTA3	-1.79789	6.667144	-9.5021	8.48E-20	3.36E-18	34.21407
170	C16orf89	-2.21841	6.396278	-9.48003	1.01E-19	3.98E-18	34.0378
171	CDC42EP1	-1.03361	5.813262	-9.45585	1.23E-19	4.78E-18	33.84493
172	F13A1	-1.24653	3.504185	-9.43219	1.50E-19	5.74E-18	33.65658
173	DPP4	-1.56559	4.574101	-9.42727	1.56E-19	5.93E-18	33.61746
174	CD1E	-1.05692	1.743991	-9.42538	1.58E-19	6.01E-18	33.60243
175	PTPN13	-1.19779	2.949912	-9.41582	1.71E-19	6.46E-18	33.52646

176 MALL	-1.25252	6.65944	-9.40883	1.81E-19	6.82E-18	33.47099
177 CTSH	-1.24117	8.952259	-9.40081	1.93E-19	7.25E-18	33.40727
178 CXCL12	-1.02407	4.032725	-9.35722	2.74E-19	1.01E-17	33.06199
179 CTSE	-2.27464	5.506812	-9.32253	3.62E-19	1.32E-17	32.78794
180 TREM2	-1.06136	4.574254	-9.32134	3.66E-19	1.33E-17	32.77853
181 CYBB	-1.12031	4.482851	-9.30357	4.22E-19	1.52E-17	32.63848
182 SCNN1B	-1.36667	4.426831	-9.30237	4.26E-19	1.53E-17	32.629
183 RAB7B	-1.09765	3.104985	-9.29066	4.68E-19	1.67E-17	32.53676
184 EFEMP1	-1.08823	5.455919	-9.28952	4.72E-19	1.68E-17	32.5278
185 CFAP221	-1.20163	2.704797	-9.28	5.09E-19	1.80E-17	32.4529
186 FAM189A2	-1.02859	2.530838	-9.2593	6.01E-19	2.10E-17	32.29028
187 SOD3	-1.00025	4.636622	-9.24248	6.88E-19	2.37E-17	32.15829
188 CSF3R	-1.26424	4.270791	-9.1937	1.01E-18	3.36E-17	31.77649
189 HLF	-1.13911	2.124761	-9.11212	1.94E-18	6.02E-17	31.14124
190 MMP2	-1.05891	6.771078	-9.08784	2.35E-18	7.15E-17	30.95295
191 SFTPB	-2.46904	10.59871	-9.05915	2.94E-18	8.83E-17	30.73089
192 COL6A3	-1.04222	6.198938	-9.05522	3.04E-18	9.06E-17	30.70051
193 RASGRF1	-1.30686	2.256959	-9.01578	4.14E-18	1.21E-16	30.3962
194 RNASE1	-1.27488	9.23243	-9.00101	4.65E-18	1.35E-16	30.28245
195 LRRK2	-1.3688	3.023734	-8.96835	6.00E-18	1.72E-16	30.03151
196 NPC2	-1.00455	9.357375	-8.95801	6.51E-18	1.86E-16	29.95219
197 ALOX15B	-1.52689	3.815848	-8.9273	8.27E-18	2.33E-16	29.71692
198 SFTPD	-2.05198	6.161598	-8.90396	9.92E-18	2.76E-16	29.53862
199 DES	-1.17289	2.336145	-8.90341	9.96E-18	2.77E-16	29.53437
200 RHOBTB2	-1.05276	4.74675	-8.89726	1.05E-17	2.90E-16	29.48745
201 XKRX	-1.14836	2.287133	-8.89682	1.05E-17	2.90E-16	29.48411
202 FCGBP	-1.30892	2.545659	-8.82605	1.82E-17	4.83E-16	28.94566
203 ACSL5	-1.08089	5.694252	-8.8208	1.89E-17	5.01E-16	28.90583
204 IL33	-1.01055	3.122688	-8.81812	1.93E-17	5.10E-16	28.88551
205 EGR1	-1.13648	5.811774	-8.80829	2.08E-17	5.49E-16	28.81105
206 FHL1	-1.079	3.715733	-8.79961	2.23E-17	5.84E-16	28.74526
207 SFTA2	-1.69933	8.28793	-8.79509	2.31E-17	6.03E-16	28.71108
208 AGER	-1.7382	4.409595	-8.79359	2.33E-17	6.09E-16	28.69974
209 NRGN	-1.30861	4.173371	-8.77416	2.71E-17	7.02E-16	28.55287
210 C4BPA	-1.92198	5.602401	-8.75412	3.16E-17	8.13E-16	28.40163
211 SCGB1A1	-3.07151	5.644401	-8.74192	3.47E-17	8.90E-16	28.30964
212 B3GNT8	-1.09127	3.497209	-8.7197	4.12E-17	1.05E-15	28.14238
213 AMY1C	-1.86638	4.13237	-8.71964	4.12E-17	1.05E-15	28.14193
214 CHRDL1	-1.14032	2.344765	-8.71759	4.19E-17	1.06E-15	28.12651
215 SUS2	-1.71444	4.635487	-8.69741	4.88E-17	1.22E-15	27.97497
216 CLEC3B	-1.09342	3.862284	-8.6599	6.51E-17	1.58E-15	27.69386
217 SHE	-1.07649	2.60349	-8.64611	7.23E-17	1.74E-15	27.59075
218 PRODH	-1.6782	4.843949	-8.63601	7.81E-17	1.87E-15	27.51537
219 CAPN8	-1.50718	5.226647	-8.6242	8.54E-17	2.03E-15	27.4272
220 ALPL	-1.56897	4.708794	-8.46475	2.85E-16	6.26E-15	26.24609
221 B3GNT7	-1.21675	4.398691	-8.46182	2.91E-16	6.36E-15	26.22458
222 ATP11A	-1.01567	5.35649	-8.45047	3.17E-16	6.86E-15	26.14115
223 SORCS2	-1.01743	2.124744	-8.4442	3.32E-16	7.16E-15	26.09508
224 MS4A1	-1.24124	2.307679	-8.43593	3.54E-16	7.55E-15	26.03441
225 SFTPC	-3.31529	7.46349	-8.42554	3.82E-16	8.12E-15	25.95819
226 TMEM130	-1.13673	2.130585	-8.38469	5.19E-16	1.07E-14	25.65928
227 PARM1	-1.11825	4.957132	-8.35256	6.59E-16	1.34E-14	25.425
228 CYP4B1	-1.80233	4.35172	-8.33977	7.24E-16	1.46E-14	25.33187
229 RRAD	-1.24885	3.763147	-8.30513	9.37E-16	1.85E-14	25.08028
230 TROAP	1.05064	3.483081	8.298861	9.81E-16	1.93E-14	25.03487
231 C1QC	-1.00221	7.369124	-8.25219	1.38E-15	2.65E-14	24.69739
232 CXCL17	-1.51376	7.729339	-8.249	1.42E-15	2.71E-14	24.67434
233 SCGB3A1	-2.57205	6.693819	-8.22713	1.67E-15	3.14E-14	24.5167
234 MUC21	-1.87282	3.609285	-8.18365	2.29E-15	4.24E-14	24.20429

235 FAXDC2	-1.18168	3.804383	-8.15083	2.91E-15	5.28E-14	23.96935
236 FMO5	-1.19975	4.150938	-8.12923	3.41E-15	6.12E-14	23.81508
237 C1QB	-1.02194	7.757725	-8.12405	3.54E-15	6.34E-14	23.77816
238 LTF	-1.74195	4.427352	-8.12251	3.58E-15	6.40E-14	23.76714
239 SELENBP1	-1.1647	6.523852	-8.10365	4.11E-15	7.30E-14	23.63278
240 CCL18	-1.31226	6.472997	-8.09768	4.29E-15	7.61E-14	23.59037
241 HLA.DRB5	-1.58973	6.617762	-8.09241	4.46E-15	7.88E-14	23.55284
242 AQP3	-1.4505	7.510635	-8.06693	5.36E-15	9.35E-14	23.37193
243 CLIC5	-1.0737	2.514942	-8.05531	5.83E-15	1.01E-13	23.28959
244 POPDC3	1.020576	1.021148	8.046516	6.22E-15	1.07E-13	23.2273
245 TMEM100	-1.01843	2.04689	-8.0326	6.87E-15	1.18E-13	23.12884
246 FDCSP	-1.36202	2.546689	-8.02457	7.28E-15	1.24E-13	23.07214
247 CHI3L2	-1.14109	3.380498	-7.97965	1.01E-14	1.69E-13	22.75549
248 VSIG4	-1.01536	4.675607	-7.97766	1.02E-14	1.71E-13	22.74151
249 SLC26A9	-1.38534	2.838763	-7.97007	1.08E-14	1.80E-13	22.68818
250 S100B	-1.14354	3.313008	-7.95945	1.16E-14	1.93E-13	22.6136
251 ZNF750	-1.02728	2.244023	-7.94106	1.33E-14	2.18E-13	22.48464
252 FCER1A	-1.11715	2.134785	-7.90735	1.69E-14	2.73E-13	22.24877
253 AUTS2	-1.00841	3.760908	-7.89708	1.82E-14	2.92E-13	22.17712
254 HLA.DQB1	-1.42873	6.957651	-7.89157	1.89E-14	3.03E-13	22.13866
255 HOPX	-1.41095	7.62922	-7.86985	2.21E-14	3.51E-13	21.98738
256 LRRN4	-1.21085	2.260865	-7.82729	2.99E-14	4.65E-13	21.69188
257 CPAMD8	-1.10642	2.887579	-7.79314	3.80E-14	5.81E-13	21.45572
258 AQP4	-1.46776	3.358634	-7.78936	3.90E-14	5.97E-13	21.42961
259 CH25H	-1.01443	2.695533	-7.77514	4.32E-14	6.54E-13	21.33148
260 FOLR1	-1.62198	6.611132	-7.75572	4.95E-14	7.40E-13	21.19778
261 LAMP3	-1.10182	4.562768	-7.72742	6.04E-14	8.91E-13	21.00343
262 CXCL14	-1.85933	4.570079	-7.72568	6.11E-14	9.00E-13	20.99148
263 FOS	-1.05625	7.045881	-7.71817	6.44E-14	9.45E-13	20.93996
264 HHIP	-1.06599	1.679177	-7.71468	6.60E-14	9.63E-13	20.91608
265 CCL17	-1.16447	2.475887	-7.64846	1.05E-13	1.47E-12	20.46398
266 C3	-1.14621	8.750138	-7.63811	1.13E-13	1.58E-12	20.39361
267 CLIC6	-1.34913	4.7213	-7.61546	1.32E-13	1.83E-12	20.23983
268 HPGD	-1.45812	4.820617	-7.56988	1.81E-13	2.45E-12	19.9315
269 SLC44A4	-1.10672	5.563147	-7.54265	2.18E-13	2.90E-12	19.74801
270 IGHA2	-1.41138	7.587263	-7.46769	3.65E-13	4.69E-12	19.24554
271 MUC1	-1.10026	9.562518	-7.45882	3.88E-13	4.97E-12	19.18634
272 CD79A	-1.13948	4.443891	-7.45172	4.07E-13	5.19E-12	19.13905
273 ADGRF1	-1.56245	3.64797	-7.3996	5.80E-13	7.21E-12	18.79266
274 HLA.DQA2	-1.22999	3.946506	-7.38417	6.44E-13	7.94E-12	18.69044
275 SFRP4	-1.13065	4.436124	-7.37601	6.81E-13	8.33E-12	18.63647
276 PPP1R1B	-1.63814	4.433337	-7.36431	7.37E-13	8.97E-12	18.55919
277 SFTA1P	-1.40369	4.124931	-7.35784	7.70E-13	9.29E-12	18.51649
278 ADGRD1	-1.00028	3.198302	-7.34057	8.65E-13	1.03E-11	18.40267
279 CHI3L1	-1.24119	6.001164	-7.2955	1.17E-12	1.37E-11	18.10662
280 HABP2	-1.26677	2.485464	-7.28953	1.22E-12	1.42E-11	18.0675
281 KCNN4	-1.15184	4.740226	-7.27307	1.36E-12	1.56E-11	17.95981
282 COL10A1	-1.20205	4.494994	-7.26621	1.43E-12	1.63E-11	17.91501
283 HSD17B6	-1.10136	3.460969	-7.2247	1.88E-12	2.11E-11	17.64456
284 MMP7	-1.48243	5.573554	-7.22334	1.90E-12	2.13E-11	17.63567
285 CACNA2D.	-1.26867	2.987408	-7.21803	1.97E-12	2.20E-11	17.60116
286 LYZ	-1.17752	8.297545	-7.19687	2.26E-12	2.50E-11	17.4639
287 IGHA1	-1.33997	11.05672	-7.17233	2.66E-12	2.92E-11	17.30511
288 KRT16P1	-1.20795	2.2151	-7.1544	3.00E-12	3.24E-11	17.18935
289 CD207	-1.1776	1.930337	-7.14516	3.19E-12	3.43E-11	17.12975
290 STEAP4	-1.08476	4.557539	-7.09486	4.44E-12	4.66E-11	16.80665
291 TMEM163	-1.02286	3.889689	-7.06542	5.39E-12	5.61E-11	16.61835
292 APOD	-1.37858	4.900194	-7.03546	6.55E-12	6.71E-11	16.42746
293 PEBP4	-1.4588	3.438587	-7.01242	7.62E-12	7.69E-11	16.28108

294	WFDC2	-1.12399	9.31504	-6.96504	1.04E-11	1.02E-10	15.98125
295	KRT16P2	-1.30479	2.603533	-6.95309	1.12E-11	1.09E-10	15.90592
296	VSIG2	-1.31115	3.539861	-6.93998	1.22E-11	1.18E-10	15.82338
297	CD1A	-1.00149	1.771947	-6.93952	1.22E-11	1.19E-10	15.82047
298	CRTAC1	-1.13492	2.927195	-6.93032	1.30E-11	1.25E-10	15.76264
299	SCGB3A2	-2.24493	7.295011	-6.9261	1.33E-11	1.28E-10	15.73614
300	LINC00342	-1.04037	2.757021	-6.89636	1.61E-11	1.54E-10	15.54967
301	HAS3	-1.04682	2.988205	-6.86795	1.94E-11	1.82E-10	15.37222
302	KCNJ15	-1.05478	3.341683	-6.84186	2.29E-11	2.12E-10	15.20973
303	SHISA3	-1.2907	1.824508	-6.70615	5.40E-11	4.72E-10	14.37294
304	CCL13	-1.02151	3.748032	-6.67882	6.42E-11	5.53E-10	14.2061
305	CRYM	-1.25895	3.40609	-6.63649	8.36E-11	7.06E-10	13.94882
306	SCEL	-1.01902	3.846164	-6.63632	8.37E-11	7.06E-10	13.94779
307	HAGLR	-1.01175	3.484488	-6.62159	9.17E-11	7.70E-10	13.85857
308	IGHV3.72	-1.12859	3.173034	-6.61257	9.70E-11	8.11E-10	13.80406
309	HLA.DRB6	-1.01906	4.60553	-6.60076	1.04E-10	8.69E-10	13.73273
310	TNC	-1.17013	5.185894	-6.58533	1.15E-10	9.49E-10	13.63967
311	COMP	-1.18115	3.527647	-6.52684	1.65E-10	1.33E-09	13.28878
312	PCP4L1	-1.25025	3.179602	-6.49551	2.00E-10	1.59E-09	13.10188
313	ICAM4	-1.00813	2.682537	-6.48714	2.10E-10	1.67E-09	13.05204
314	FOSB	-1.27797	3.486596	-6.48651	2.11E-10	1.67E-09	13.04832
315	SERPINA1	-1.17609	8.627531	-6.44591	2.70E-10	2.11E-09	12.80753
316	AQP5	-1.7011	3.725769	-6.44048	2.80E-10	2.17E-09	12.77542
317	COL1A1	-1.00654	8.451696	-6.38665	3.87E-10	2.94E-09	12.45838
318	PLA2G2A	-1.03588	2.07445	-6.31573	5.94E-10	4.34E-09	12.04411
319	JCHAIN	-1.06705	8.139991	-6.23661	9.51E-10	6.72E-09	11.58665
320	MMP28	-1.14191	3.475328	-6.20411	1.15E-09	8.09E-09	11.40013
321	HBA2	-1.14105	5.156282	-6.19616	1.21E-09	8.45E-09	11.35462
322	ADIRF	-1.01924	5.225686	-6.19052	1.25E-09	8.71E-09	11.32243
323	PLAT	-1.04559	4.91362	-6.16133	1.48E-09	1.02E-08	11.15593
324	VSTM2L	-1.11837	4.646878	-6.13464	1.73E-09	1.18E-08	11.00431
325	IL37	-1.25696	1.797374	-6.13185	1.76E-09	1.19E-08	10.98847
326	SLC1A7	-1.25346	2.080881	-6.05123	2.82E-09	1.84E-08	10.5341
327	IGHV3.49	-1.26019	4.531345	-6.03892	3.03E-09	1.97E-08	10.46514
328	SLC6A14	-1.0328	3.804642	-5.93521	5.48E-09	3.43E-08	9.889317
329	VSIG1	-1.24431	2.308214	-5.91468	6.16E-09	3.81E-08	9.77633
330	PLA2G1B	-1.05664	2.304625	-5.91169	6.27E-09	3.87E-08	9.759931
331	AGR3	-1.31601	6.00521	-5.90155	6.64E-09	4.07E-08	9.704242
332	HHLA2	-1.27095	2.003399	-5.86648	8.09E-09	4.88E-08	9.512452
333	IGLV2.18	-1.09433	3.122186	-5.85902	8.44E-09	5.07E-08	9.471768
334	IGLV2.8	-1.16854	5.995763	-5.85366	8.70E-09	5.21E-08	9.442589
335	GLB1L3	-1.0852	1.780859	-5.82025	1.05E-08	6.20E-08	9.261081
336	IGHM	-1.21969	8.387557	-5.78791	1.26E-08	7.33E-08	9.086315
337	IGHV3.74	-1.08629	4.761395	-5.75027	1.55E-08	8.90E-08	8.883966
338	IGHD	-1.42873	4.559447	-5.73677	1.67E-08	9.53E-08	8.811665
339	CHIA	-1.08249	2.235352	-5.72335	1.80E-08	1.02E-07	8.739911
340	IGHV3.30	-1.18641	7.389169	-5.68681	2.20E-08	1.23E-07	8.545364
341	CRABP2	-1.28932	6.675527	-5.68307	2.25E-08	1.25E-07	8.525547
342	CST6	-1.02081	3.675819	-5.68202	2.26E-08	1.26E-07	8.519959
343	CLDN18	-1.27549	2.614264	-5.66411	2.49E-08	1.37E-07	8.425063
344	HBA1	-1.00302	4.216313	-5.61033	3.34E-08	1.80E-07	8.14176
345	IGLV7.46	-1.06596	4.334076	-5.57607	4.03E-08	2.13E-07	7.962466
346	IGHV1.2	-1.2141	5.568701	-5.49999	6.06E-08	3.09E-07	7.56787
347	UCHL1	1.248076	4.865695	5.496939	6.16E-08	3.14E-07	7.552162
348	BPIFB1	-1.50248	4.487896	-5.42598	8.99E-08	4.45E-07	7.188635
349	MS4A15	-1.12922	2.280981	-5.41934	9.31E-08	4.60E-07	7.154815
350	IGHG2	-1.07463	9.339911	-5.38273	1.13E-07	5.49E-07	6.969104
351	IGHV5.51	-1.12333	6.49013	-5.31669	1.59E-07	7.53E-07	6.636939
352	IGLV2.11	-1.0578	6.738018	-5.28359	1.89E-07	8.78E-07	6.471842

353	IGHV4.31	-1.09765	4.215622	-5.22649	2.54E-07	1.15E-06	6.189206
354	IGHV3.11	-1.05686	5.649227	-5.19896	2.92E-07	1.31E-06	6.053896
355	HP	-1.38018	4.699214	-5.17287	3.34E-07	1.48E-06	5.926256
356	IGKV2D.29	-1.09357	4.352216	-5.16847	3.41E-07	1.51E-06	5.904779
357	IGLV1.40	-1.00035	7.606215	-5.12863	4.18E-07	1.82E-06	5.711156
358	IGLV1.44	-1.01522	6.904428	-5.08972	5.08E-07	2.17E-06	5.523345
359	IGLV1.51	-1.02804	7.117748	-5.05984	5.90E-07	2.49E-06	5.380025
360	IGHV3.15	-1.00242	5.920674	-4.9521	1.01E-06	4.06E-06	4.869443
361	IGKV1.17	-1.01654	6.293956	-4.94039	1.06E-06	4.28E-06	4.814562
362	IGKV3.20	-1.00561	9.253149	-4.90176	1.28E-06	5.08E-06	4.63435
363	IGHV3.33	-1.09305	6.529594	-4.85151	1.64E-06	6.35E-06	4.401814
364	IGKV1.16	-1.04288	5.897629	-4.8323	1.80E-06	6.91E-06	4.313453
365	CLDN2	-1.05883	2.236636	-4.79135	2.19E-06	8.26E-06	4.126245
366	CST1	-1.14153	3.961672	-4.66157	4.03E-06	1.44E-05	3.54257
367	SNORD3A	1.00332	6.229234	4.655233	4.15E-06	1.48E-05	3.514452
368	AKR1B10	1.287088	2.534204	4.441586	1.10E-05	3.63E-05	2.586831
369	AKR1C2	1.583792	5.03032	4.440033	1.11E-05	3.65E-05	2.580237
370	CEACAM5	-1.27181	6.23074	-4.23395	2.73E-05	8.36E-05	1.723961
371	SPINK1	-1.37212	6.018074	-4.05248	5.87E-05	0.000168	1.001288
372	PGC	-1.42247	5.170011	-3.80187	0.000161	0.000422	0.05217
373	MSLN	-1.08532	6.106722	-3.48357	0.000538	0.001269	-1.07073

Table S4: Kaplan-Meier analyses of 20 relugators in TCGA cohort

	characteris	HR(95%CI)	pvalue
1	APOL1	1.241(1.09	0.000997
2	ATIC	1.464(1.15	0.001964
3	BAK1	1.484(1.15	0.00187
4	BID	1.215(1.03	0.018374
5	BIRC5	1.196(1.07	0.000913
6	CCR2	0.733(0.61	0.00031
7	CDKN1A	1.19(1.004	0.044383
8	DAPK2	0.76(0.651	0.000505
9	DLC1	0.883(0.79	0.02606
10	DRAM1	0.842(0.74	0.009059
11	EIF4G1	1.505(1.19	0.000656
12	FADD	1.699(1.30	9.75E-05
13	GAPDH	1.594(1.33	3.23E-07
14	GNAI3	1.687(1.21	0.001703
15	ITGA6	1.268(1.13	2.70E-05
16	ITGB1	1.59(1.303	4.95E-06
17	ITGB4	1.177(1.06	0.001386
18	PRKCD	0.762(0.62	0.006472
19	RAC1	1.283(1.06	0.009957
20	SPHK1	1.284(1.12	0.000206