

**Table S1 Autophagy core machinery gene expression analysis**

PSCs/Fibroblasts			
	gene name	fold change	p value
<b>Ulk1 kinase complex</b>	Ulk1	2.76	1.32E-08***
	Ulk2	0.75	0.05
	Atg13	1.95	5.82E-08***
	FIP200	0.21	7.23E-09***
	Atg101	2.1	1.93E-10***
<b>classIII PI3K Complex</b>	PIK3R4	1.17	4.93e-08***
	VPS34	2.12	7.24E-10***
	Becn1	1.07	0.6719372
	atg14	3.13	6.82E-11***
	ambra1	2.7	1.03E-04***
	UVRAG	0.6	0.002**
	SH3GLB1	0.85	2.2e-16***
<b>Atg9 and its cycling</b>	ATG2A	1.47	5.0E-04***
	ATG2B	1.19	0.35
	ATG9A	0.38	4.91E-09***
	ATG9B	1.17	0.054
	WIPI1	0.67	1.6E-04***
	WIPI2	1.28	0.037*
	WIPI3	1.18	0.045*
	WIPI4	1.46	0.0012**
	DFCP1	1.02	0.4927
	VMP1	0.88	3.357e-06***
<b>Atg12 conjugation system</b>	atg12	1.17	0.012
	atg5	1.36	3.1 E-04***
	atg16l	1.32	0.002**
	atg7	1.06	0.27
	atg10	0.79	1.402e-10***
<b>LC3 conjugation system</b>	LC3A	0.38	3.03E-10***
	LC3B	1.37	0.058
	Gabrap	0.16	4.69E-12***
	GabrapL1	0.27	1.17E-09***
	GabrapL2	2.22	1.54E-06***
	Atg3	0.9	0.171
	Atg4A	1.34	0.0068
	Atg4B	0.77	5.99E-05***
	Atg4C	1.16	0.5
	Atg4D	2.87	7.80E-11***