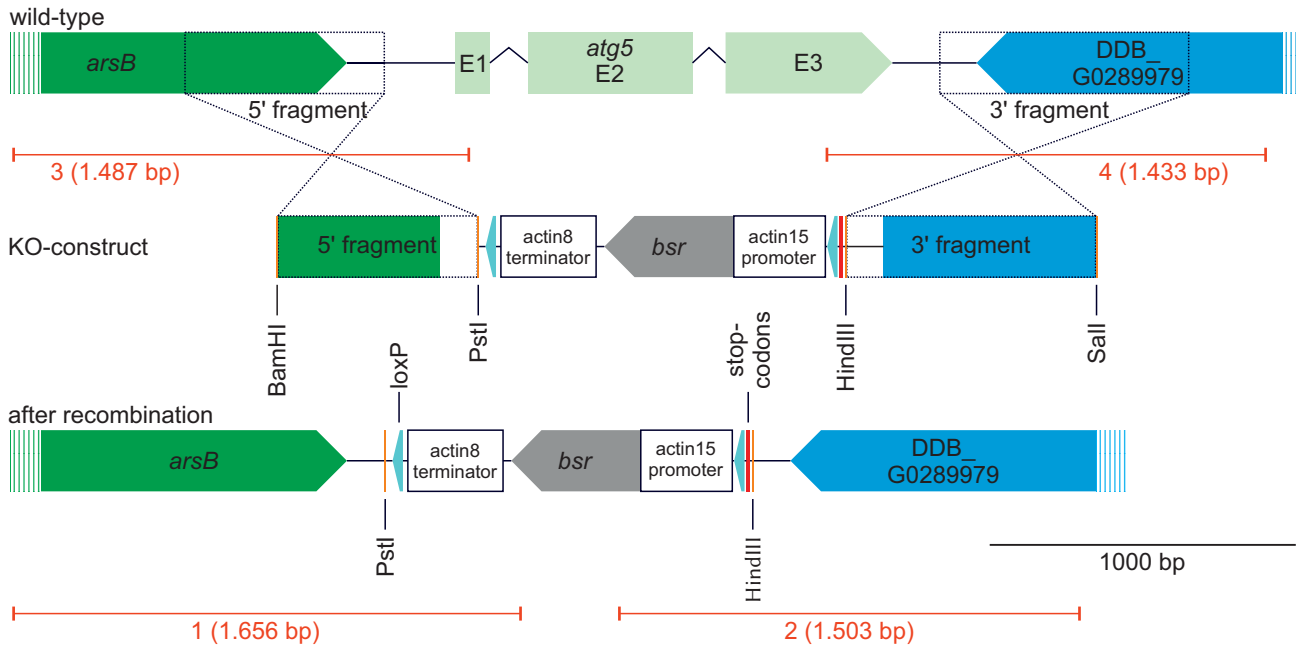
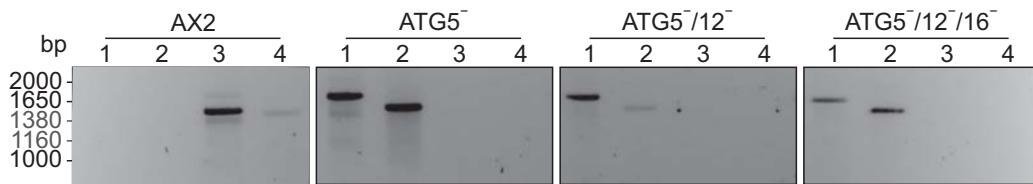


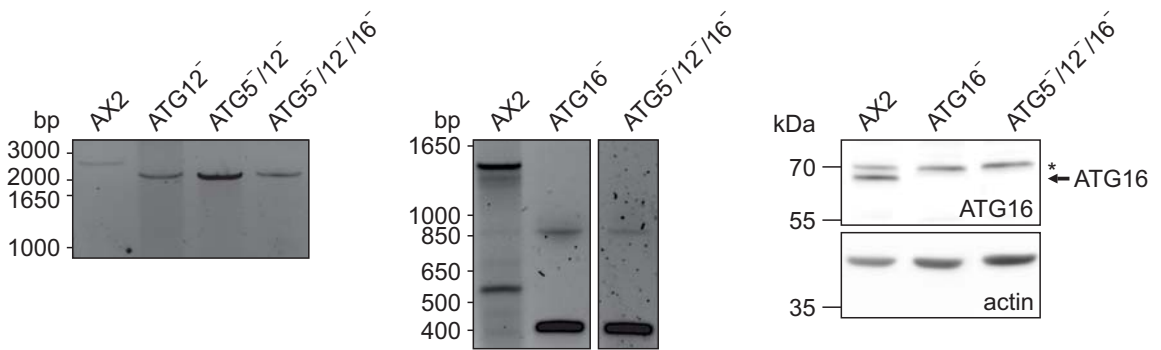
A



B



C



α - - - - - α β - - - - - β β - - - - - β α - - - - -
Ubiquitin-like domain
D. discoideum -MSSFD^EEDIKRSI^WEGKIP^IIVFTLS^PDDL^TSHLS^PSP^SY^TTLMA^PRNS^YF^PLIT^SSLV^KDY^FFS 59
C. elegans - - - -MDYE^VCRK^VWESH^VPC^QFTL^QSSGG^T-HGE^PL^PPFY^TML^PR^FSY^LALA^IQ^KVL^SSE^N 55
D. melanogaster - -MAH^DRE^VL^RMI^WEG^QIG^ICFQAD^RDEI^VG-^IKPE^PF^YLM^IS^RLS^YLP^LV^TDK^VR^KY^FFS 57
D. rerio MIMAD^DK^DVL^RD^VW^FGRI^PAC^FFTLS^PDET^TE-REA^EP^YYLL^PR^VSY^LTL^VT^DK^VKK^HFL 59
H. sapiens - -MTD^DK^DVL^RD^VW^FGRI^PTC^FFTLY^QDEI^TE-REA^EP^YYLL^PR^VSY^LTL^VT^DK^VKK^HFL 57
- - - - -

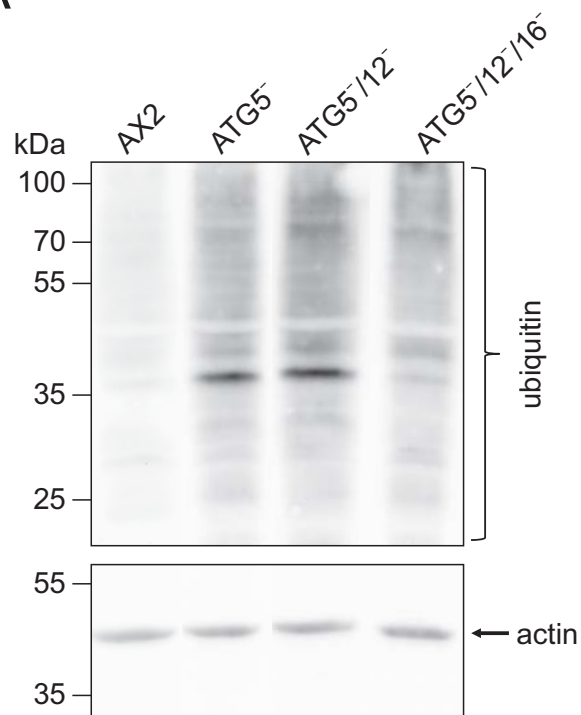
α β - - β β - β α - - - - - α β - - β
D. discoideum SSTL⁻-VLL^DEM^WLE^YRG^IPL^KWH^LPIG^VLYD^TIVG^{...}IIME^QPY^WNI^VVH^FQ^SY^FDR 167
C. elegans RRDDG^EK^VHSD^KM^WLEH^NG^IPL^KMY^IPIG^VIYD^QANL^{...}-DS^ILE^II^VRT^SQ^PEP⁻ 110
D. melanogaster RYIS⁻AEH^QDGA^VW^FDFN^GTPL^RLH^YPIG^VLYD^LLHP^{...}-DST^PW^CL^TI^HFS^KF^EED 112
D. rerio KVMK⁻AED⁻VEE^MW^FEHE^GTPL^KWH^YPIG^VLFD^LHA⁻...-SAL^PWN^IT^VH^FKN^FFE^Q 112
H. sapiens KVMR⁻QED⁻ISE^IW^FEY^ECTPL^KWH^YPIG^LLFD^LLA⁻...-SAL^PWN^IT^VH^FKS^FFE^K 110
- - - - -

α - - - - - α α - - - - - α α - - - - -
Helix-rich domain
D. discoideum ILLR^CPN^IES^VRT^YY^KN^VLKEAN^FIKQGD^ITK^INN^LIN^IQ^SN^DLWD^GLK⁻-SHD^YDK^FW^S 225
C. elegans -QFQ^MVDR^DMM^EAM^FMQ^NIK^EAD^YLK^TKAE⁻IT^KN^MM^KDES^AQL^WRS^VCN^IP^DN^FDEF^WT 168
D. melanogaster MLV^KLNS^KEL^LESH^YMS^CLKEAD^VLK^HRGL⁻VIS^AMQ^KKD^HN^QLWL^GL^V-NEK^FD^QFWA 169
D. rerio DLLH^CSTNS^VIEAH^FMSC^IKEAD^ALK^HKG^Q-VIN^DMQ^KKD^HK^QLWM^GL^Q-NDK^FD^QFWA 169
H. sapiens DLLH^CPSK^DAEIA^EAF^FMSC^MKEAD^ALK^HKS^Q-VIN^EMQ^KKD^HK^QLWM^GL^Q-NDR^FD^QFWA 167
- - - - -

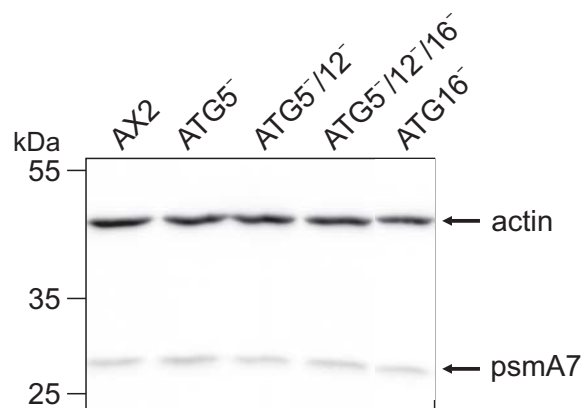
- - - α β - - - β β - β β - β α - - - - - α
Ubiquitin-like domain
D. discoideum VNKK^LIPN⁻-SNKE^YK^NIPI^RL^II^NY--KPPI^QELI^PVFDEN^LVEL^TLEN^LFSR^IPY... 338
C. elegans IVQ^KLMETS⁻EGNE^FFAH^IPLR^VYV^KN--QAFK^QALITAK^HPDG^SLR^TIGEAV^SDVLS... 227
D. melanogaster VNRR^LMEPY^GDLE^SFK^NIPL^RIY^TD-DDFT^YTQ^KLIS^PISV^GGQ^KKS^LADLMA^EL--... 227
D. rerio MNR^KLMEY^PTEEG^GFRY^IPFRI^YQTMS^DRP^FIQT^LFRP^VSSE^GQAL^TIGD^LLKEL--... 231
H. sapiens INR^KLMEY^PAEENG^FRY^IPFRI^YQT^TTER^PFIQ^KLFRP^VAADG^QLHT^LIGD^LLKEV--... 229
- - - - -

β - β α - - - - - α β - - - - β
D. discoideum LLQY^IKATNAEY^KIQGI^QPSL^KSSAV^WLYEH^FGH^PDN^FLYI^VLI^DPSQNNNNNNNNNS^NNY 398
C. elegans STDS^QSEHPP^RLISH^GIDIP^HHT^PLIFAA^KNLS^YPDN^FIHV^VL^LLV^P 275
D. melanogaster - - - - -RRAV^GCRTH^GIDL^HEET^QLQW^MSEHLS^YPDN^FLHLS^VDY^KDV 269
D. rerio - - - - -EPKK^FQVMI^HGIE^PLLET^PIQWL^SEHLS^HPDN^FLHIS^IIPAP^SD 275
H. sapiens - - -EDGE^KKNQVMI^HGIE^PMLE^TELQW^LSEHLS^YPDN^FLHIS^IIPQPT^D 275
- - - - -

A



B



C

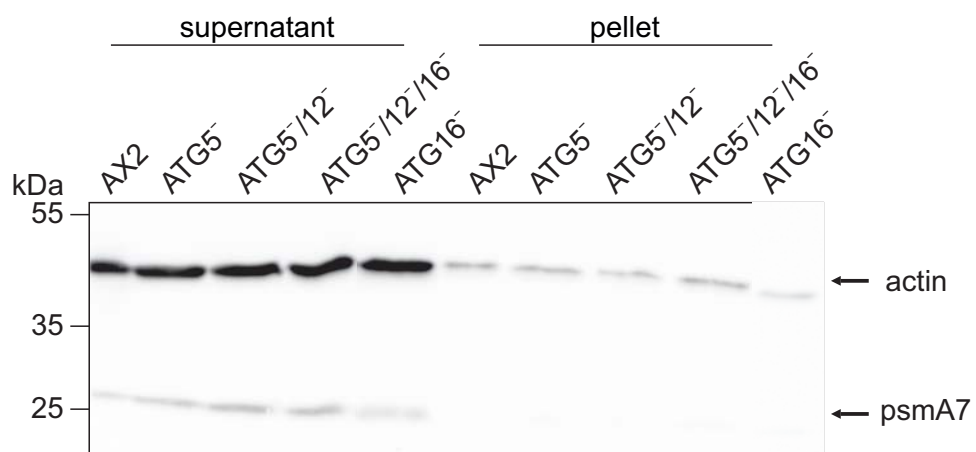


Table S1: Random cell motility of AX2, ATG5⁻, ATG5⁻/12⁻, and ATG5⁻/12⁻/16⁻ cells. Cells starved for four hours were observed in the central channel of an ibidi μ -slide in a TIRF microscope, pictures were taken every 30 sek for 30 min and random cell motility of 20 cells from each strain was calculated with the manual tracking tool of ImageJ. StDev, standard deviation. ns, not significant.

Strain	Velocity [μ m/min]	StDev	Significance versus AX2
AX2	12.53	3.99	-
ATG5 ⁻	11.88	2.49	ns
ATG5 ⁻ /12 ⁻	12.16	2.83	ns
ATG5 ⁻ /12 ⁻ /16 ⁻	10.84	2.72	ns

Table S2: Differential regulation of proteasomal genes in ATG5⁻, ATG5⁻/12⁻, and ATG5⁻/12⁻/16⁻ cells. Genes that are more than 1.5-fold up-regulated in at least two of the mutants are in italic. FC, fold change

Gene name	DDB_G ID	ATG5 ⁻		ATG5 ⁻ /12 ⁻		ATG5 ⁻ /12 ⁻ /16 ⁻	
		FC	p-value	FC	p-value	FC	p-value
psmA1	DDB_G0282363	1.02	0.70	1.01	0.84	1.01	0.92
psmA2	DDB_G0292122	1.06	0.16	1.05	0.29	-1.04	0.49
psmA3	DDB_G0267408	1.03	0.65	1.08	0.27	-1.00	0.96
psmA4	DDB_G0280969	-1.01	0.81	-1.01	0.80	-1.07	0.29
psmA5	DDB_G0268538	-1.05	0.35	-1.01	0.90	-1.03	0.66
psmA6	DDB_G0278847	1.01	0.88	1.02	0.69	-1.01	0.89
<i>psmA7</i>	DDB_G0272831	1.56	0.00	1.90	0.00	1.92	0.00
<i>psmB1</i>	DDB_G0272969	1.61	0.00	1.94	0.00	2.02	0.00
psmB2	DDB_G0269472	-1.01	0.79	1.04	0.53	-1.05	0.44
psmB3	DDB_G0269772	1.19	0.01	1.11	0.10	1.10	0.17
psmB4	DDB_G0273163	1.13	0.73	1.11	0.76	1.43	0.31
psmB5	DDB_G0293784	-1.10	0.17	-1.18	0.07	-1.12	0.15
psmB6	DDB_G0267390	1.04	0.42	-1.03	0.65	1.04	0.61
psmB7	DDB_G0283697	-1.17	0.01	-1.09	0.13	-1.04	0.53
psmC1	DDB_G0270784	-1.04	0.57	-1.08	0.36	1.01	0.93
psmC2	DDB_G0276917	-1.07	0.20	-1.06	0.28	-1.03	0.66
psmC3	DDB_G0284415	1.03	0.60	1.01	0.83	-1.01	0.85
psmC4	DDB_G0289003	-1.01	0.77	-1.06	0.19	-1.08	0.11
psmC5	DDB_G0292382	-1.01	0.88	-1.04	0.42	-1.06	0.26
psmC6	DDB_G0284517	-1.01	0.79	-1.04	0.43	-1.06	0.31
psmD1	DDB_G0287953	-1.17	0.00	-1.18	0.00	-1.08	0.13
psmD10	DDB_G0289189	1.20	0.02	1.18	0.08	1.27	0.01
psmD11	DDB_G0281315	-1.01	0.88	-1.03	0.76	-1.02	0.82
psmD12	DDB_G0281051	-1.05	0.30	-1.05	0.48	1.03	0.61
psmD13	DDB_G0285105	-1.10	0.07	-1.08	0.25	-1.03	0.62
<i>psmD14</i>	DDB_G0272566	1.54	0.00	1.83	0.00	1.94	0.00
psmD2	DDB_G0293752	-1.17	0.02	-1.19	0.01	-1.14	0.06
psmD3	DDB_G0288621	-1.08	0.12	-1.10	0.19	-1.02	0.77
psmD4	DDB_G0275755	1.09	0.03	1.11	0.04	1.06	0.26
psmD6	DDB_G0270188	-1.01	0.88	-1.07	0.46	1.02	0.84
psmD7	DDB_G0279633	1.21	0.00	1.16	0.02	1.15	0.05
psmD8	DDB_G0272564	1.03	0.88	1.16	0.55	1.18	0.53
psmD9	DDB_G0275753	-1.57	0.00	1.05	0.49	-1.45	0.00
psmE3	DDB_G0285099	-1.06	0.27	1.06	0.41	1.00	0.96
psmE4	DDB_G0292398	-1.07	0.06	-1.20	0.00	-1.07	0.21
psmF1	DDB_G0282617	1.14	0.03	1.08	0.17	1.07	0.20
psmG1	DDB_G0279769	1.10	0.22	1.13	0.20	1.03	0.66
psmG2	DDB_G0274447	-1.05	0.47	-1.04	0.60	1.04	0.63
psmG3	DDB_G0268522	1.14	0.18	1.21	0.07	1.25	0.01
psmG4	DDB_G0304543	1.10	0.27	1.08	0.38	1.07	0.47