

SUPPLEMENTARY MATERIAL

corresponding to:

***Dictyostelium* as model for studying
ubiquitination and deubiquitination**

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TABLE S1: *Dictyostelium discoideum* Ubiquitin and Ubiquitin like family members

UBLs/Ub members		ID
UBLs	SUMO	DDB_G0286189
	<i>NEDD8</i>	DDB_G0278711
	<i>ATG12</i>	DDB_G0282929
	<i>ATG8a</i>	DDB_G0286191
	<i>ATG8b</i>	DDB_G0290491
	<i>UFM</i>	DDB_G0295709
	<i>URM</i>	DDB_G0283737
	<i>FAU</i>	DDB_G0273743
Ubiquitin	<i>Ubl5</i>	DDB_G0284205
	<i>UbqA</i>	DDB_G0282295
	<i>UbqD</i>	DDB_G0286907
	<i>UbqF</i>	DDB_G0289449
	<i>UbqG</i>	DDB_G0282369
	<i>UbqH</i>	DDB_G0279721
	<i>UbqI</i>	DDB_G0291928
	<i>UbqJ</i>	DDB_G0269458
	<i>UbqK</i>	DDB_G0280585
	<i>UbqN</i>	DDB_G0292984
	<i>UbqO</i>	DDB_G0292908
	<i>UbqB</i>	DDB_G0280755
<i>UbqC</i>	DDB_G0276765	

TABLE S2: *Dictyostelium discoideum* E1 ubiquitin conjugation members

Ub/Ubl	E1 Activating enzyme ID
Ubq	DDB_G0293306 DDB_G0268496
SUMO	DDB_G0279641 DDB_G0286919
NEDD8	DDB_G0283891 DDB_G0287965
ATG8	DDB_G0271096
ATG12	DDB_G0271096
URM	DDB_G0267980
FAT10	DDB_G0277047
ISG15	DDB_G0270272
UFM	DDB_G0293306
FAU	N.A.
Ubl5	N.A.

TABLE S3: *Dictyostelium discoideum* members of DUB family

DUBs members		ID	D.d. gene name	H.s. gene orthologs
Cys-dependent proteases	<i>USP</i>	DDB_G0268872	N.A.	USP49, USP44
		DDB_G0284381	N.A.	USP11, USP4, USP15
		DDB_G0291239	ubpA	USP5, USP13
		DDB_G0276443	N.A.	USP7
		DDB_G0275021	ubpB	USP10
		DDB_G0290453	usp12	USP12
		DDB_G0271264	N.A.	USP14
		DDB_G0293770	N.A.	USP11, USP4, USP15
		DDB_G0274207	N.A.	USP45, USP16
		DDB_G0271798	N.A.	USP51
		DDB_G0275415	N.A.	N.A.
		DDB_G0271348	N.A.	USP38
		DDB_G0270416	N.A.	similar to H. sapiens USP37 and USP26
		DDB_G0278929	N.A.	USP39
		DDB_G0289611	N.A.	USP40
		DDB_G0274827	N.A.	USP42, USP36
		DDB_G0274795	N.A.	USP48
		DDB_G0292290	N.A.	SENP1
		DDB_G0278795	senp8	SENP8
		DDB_G0293508	N.A.	SENP7
	DDB_G0289557	N.A.	SENP7	
	<i>JOSEPHIN</i>	DDB_G0269646	N.A.	JOSD1, JOSD1
	<i>UCH</i>	DDB_G0292046	N.A.	USP47
		DDB_G0269694	pan2	PAN2
		DDB_G0282007	uch1	UCHL1
		DDB_G0285527	uch2	UCHL5
		DDB_G0282463	N.A.	N.A.
	<i>OTU</i>	DDB_G0277251	N.A.	N.A.
		DDB_G0285907	N.A.	OTUD5
		DDB_G0267906	N.A.	OTUD3
		DDB_G0279375	N.A.	OTUD6B
		DDB_G0271346	yod1	YOD1
		DDB_G0284757	N.A.	N.A.
DDB_G0271346		yod1	YOD1	
<i>MINDY</i>	DDB_G0269770	N.A.	MINDY1, MINDY2	
	DDB_G0281445	N.A.	MINDY1, MINDY2	
<i>ZUP1</i>	+	N.A.	UFSP2	
Metallo-isopeptidase	<i>JAMM/MPN</i>	DDB_G0284597	csn5	COPS5
		DDB_G0293180	csn6	COPS6
		DDB_G0272566	psmD14	PSMD14
		DDB_G0284037	DG1039	STAMPB
		DDB_G0293254	eif3f	EIF3F
		DDB_G0279633	psmD7	PSMD7
		DDB_G0281153	eif3H	EIF3H
		DDB_G0277927	mybH	MYSM1
		DDB_G0274229	prpf8	PRPF8

TABLE S4: *Dictyostelium discoideum* Ubiquitin Binding Domain containing proteins.

UBD		D.d. Gene ID	D.d. gene name	H.s. gene orthologs
α -Helix	UIM	DDB_G0292696	colA	N.A.
		DDB_G0270358	ubxd7	UBXN7
		DDB_G0283893	N.A.	UBR4
		DDB_G0274349	N.A.	N.A.
		DDB_G0275775	psmD4	PSMD4
	UBM	DDB_G0285063	N.A.	N.A.
	UBX	DDB_G0270358	ubxd7	UBXN7
		DDB_G0268260	N.A.	ZFAND2B
		DDB_G0279285	N.A.	ASPSCR1
		DDB_G0280423	N.A.	FAF2
		DDB_G0276057	N.A.	UBXN1
		DDB_G0274349	N.A.	N.A.
		DDB_G0291259	N.A.	N.A.
		DDB_G0268746	N.A.	UBXN4
		DDB_G0269774	N.A.	N.A.
		DDB_G0289369	N.A.	ZFAND2B
		DDB_G0293498	nsf11c	UBXN2B, NSFL1C
		UBA	DDB_G0291239	ubpA
	DDB_G0292304		mrkA	MARK3, MARK2, MARK4, MARK1
	DDB_G0288187		ddi1	DDI2, DDI1
	DDB_G0286357		rcbA	RAD23A, RAD23B
	DDB_G0267452		ubqln	UBQLN2, UBQLN4, UBQLN1
	DDB_G0285063		N.A.	N.A.
	DDB_G0289571		N.A.	N.A.
	DDB_G0287783		N.A.	UBAC2
	DDB_G0278981		N.A.	ARIH1
	DDB_G0270098		p62	NBR1
	DDB_G0268764		N.A.	N.A.
	DDB_G0267516		N.A.	DHX9, DHX57, DHX29, DHX36
	DDB_G0276057		N.A.	UBXN1
	CUE	DDB_G0280455	ascc2	ASCC2
		DDB_G0285763	N.A.	RNF14
DDB_G0283769		HBS1	HBS1L	
DDB_G0275209		N.A.	N.A.	
DDB_G0270388		N.A.	N.A.	
DDB_G0268232		N.A.	N.A.	
DDB_G0274365		N.A.	CUEDC1	
VHS	DDB_G0290163	tom1	HGS, TOM1L2	
Zn-Finger	ZnfUBP	DDB_G0291239	ubpA	USP5, USP13
		DDB_G0270200	N.A.	BRAP
	ZnfA20	DDB_G0276881	N.A.	ZFAND6
		DDB_G0267788	N.A.	N.A.

Other	SH3	DDB_G0291131	N.A.	SH3D21
	PFU	DDB_G0291003	N.A.	PLAA
	JAB/MPN	DDB_G0293254	EIF3F	EIF3F
		DDB_G0293180	CSN6	COPS6
		DDB_G0290227	NPLOC4	NPLOC4
		DDB_G0284597	CSN5	COPS5
		DDB_G0284037	DG1039	STAMBP
		DDB_G0281153	EIF3H	EIF3H
		DDB_G0279633	PSMD7	PSMD7
		DDB_G0277927	MYB1	MYSM1
		DDB_G0268048	N.A.	EMC8, EMC9
		DDB_G0272566	PSMD14	PSMD14
		DDB_G0274229	PRPF8	PRPF8
PH	GLUE	DDB_G0282045	VPS36	VPS36
	PRU	DDB_G0272624	ADRM1-1	ADRM1
Ubiquitin conjugation	UBC	DDB_G0289021	UBE2S	UBE2S
		DDB_G0281725	UBE2M	UBE2M, UBE2F
		DDB_G0278775	UBE2C	UBE2C
		DDB_G0275787	UBE2A	UBE2A, UBE2B
		DDB_G0274313	N.A.	N.A.
		DDB_G0277267	UBE2N	UBE2N
		DDB_G0287693	UBE2I	UBE2I
		DDB_G0284009	CDC34	CDC34, UBE2R2
		DDB_G0291199	UBE2T	UBE2T
		DDB_G0290629	N.A.	UBE2O
		DDB_G0290547	N.A.	UBE2D1, UBE2D3, UBE2D2, UBE2D4
		DDB_G0288697	N.A.	N.A.
		DDB_G0288381	N.A.	N.A.
		DDB_G0288345	N.A.	CDC34, UBE2R2
		DDB_G0282783	N.A.	N.A.
		DDB_G0281833	N.A.	UBE2E1, UBE2E3, UBE2E2
		DDB_G0280347	N.A.	UBE2G2, UBE2G1
		DDB_G0280091	N.A.	UBE2H
		DDB_G0271726	N.A.	UBE2G2, UBE2G1
	UEV	DDB_G0286797	N.A.	TSG101

Table S5 Function and phenotype summary of the Ub-system components in the *Dictyostelium*

GENE NAME	FUNCTION	PHENOTYPE	REF.
SRCP1	Responsible for suppression of (polyQ) aggregation.	An accumulation of polyubiquitinated protein and polyQ proteins was observed in <i>scrp1</i> null mutants. SRCP1 is necessary for the resistance	(1)
XpF	Involved in DNA double-strand repair by homologous recombination	Aberrant vegetative growth; increased sensitivity to cisplatin	(2, 3)
<i>prp19</i>	Could be relevant for the ubiquitination of NF- κ B activating protein	N.A.	(4)
PsmE3	Activator subunit of the 20S proteasome	N.A.	(5)
RasG	Undergoes ubiquitination	Aberrant cytokinesis and decreased protein modification.	(6)
TOM1	Sorting of ubiquinated proteins to the MVB formation machinery.	Decreased rate of endocytosis	(7)
ATG12	Binds ATG5 and ATG16 then associates with ATG5-ATG12 to form a complex which acts as an E3 ligase during autophagosome formation	Cell viability;endocytosis; autophagosome maturation	(8)
HephA	Regulate cAMP sensitivity and suppress TORC2 deficiency	Delayed aggregation; increased response to cAMP	(9)
MIP1	Ubiquinate the MAP kinase kinase	Decreased chemotaxis to cAMP ; increased aggregate size	(10) (11)
MEK1	Phosphorylate the MAP kinase Erk1 (erkA) and it is regulated by sumoylation and ubiquination	Abolished chemotaxis to cAMP; decreased aggregate size; precocious development.	(10)
ubpA	Specific for unanchored poly-Ub chains	Abolished aggregation.	(12)
ubc	Catalyse the covalent attachment of ubiquitin to target proteins	Development arrests at mound stage; multiple tips.	(13)
NosA	Remove a specific set of proteins to ensure developmental progression	Developmental arrest at the tight-aggregate stage; aberrant protein modification.	(14, 15)
cblA	Act as a positive regulator of STATc tyrosine phosphorylation, dephosphorylating STATc.	Aberrant signal transduction; slugs tend to break; basal disc is missing.	(16)
<i>hfnA</i>	Regulate the activity of filamin complexes.	Decreased slug size; increased phototaxis; increased slug migration; aberrant cell patterning.	(17)
CulB	Regulate prestalk cell	Aberrant slug formation; decreased	(18)

	differentiation in <i>Dictyostelium</i> by ubiquitin-mediated protein degradation	fruiting body size; decreased sporulation; multiple tips in mound.	
CSN	Required for cell proliferation and development	N.A.	(19)
MEKK □	Its stability is under the control of ubiquitin system.	Abnormal cell-type patterning with an enrichment of a prestalk compartment (pst0); reduction in pre-spore population.	(20)
rbrA	Required for cell type proportioning in differentiation	Decreased phototaxis; decreased sorting to prestalk region; decreased sporulation; development arrests at slug stage;	(21)
ubpB	deubiquinate <i>MEKK</i> □;	Aberrant sorus morphology; precocious development	(20)
SKP1	Component of the SCF ubiquitin ligase complex.	Aberrant fruiting body morphology.	(22-25)
ATG16	Expansion of autophagosomal membrane.	Aberrant fruiting body morphology; aberrant slug formation; decreased spore viability; decreased catalytic activity; increased cell death; increased protein modification; multiple tips in mound aberrant phagosome maturation; decreased pinocytosis.	(26)
FbxA	Component of SCF ubiquitin ligase complex.	Aberrant fruiting bodies and decreased sporulation.	(27-29) (27, 30)
SonA	Soppressor of NosA	N.A.	(14)
Hsp101	Promotes thermotolerance.	N.A.	(31)
Ubiquitin	Protein degradation/PTM	N.A.	(32, 33)
SUMO	Protein degradation/PTM	N.A.	(10)

S6-Fig 4 legend abbreviation.

Xpf (Xeroderma pigmentosum, complementation group F); TOM1 (Target Of Myb1) ATG12 (AuTopgaGy 12); UbpA (ubiquitin carboxyl-terminal hydrolase A) HectPH1; SUMO (Small Ubiquitin-related Modifier); MIP1 (MEK Interactin protein 1); SCF complex (SCF E3 ubiquitin ligase complex); CNF (subunit of the COP9 signalosome); HfnA (Hect ubiquitin ligase with N-terminal filamin domain); rbrA (Ring Between Ring A); CblA (Casitas B lineage Lymphoma); UbcB (UBiquitin Conjugating B); UbpB (Ubiquitin Hydrolase B); Ub (ubiquitin).

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