

Supplementary table 1

Characteristics of the patients from whom specimens were used for macrophages isolation, immunohistochemistry or Western blotting

a) IMAC isolation with subsequent mRNA isolation for quantitative PCR

Surgical specimens of six „control“ patients without colonic inflammation were used:

Patient age and gender	Diagnosis	type of surgery
62 yrs, ♂	rectum carcinoma	rectum exstirpation
77 yrs, ♂	rectum carcinoma	rectum resection
82 yrs, ♀	rectum carcinoma	rectum resection
72 yrs, ♂	rectum carcinoma	rectum exstirpation
61 yrs, ♂	colon cancer	laparoscopic resection
75 yrs, ♀	colon cancer	hemicolectomy

IMACs and subsequent IMAC mRNA were further isolated from 5 patient with diverticulitis („inflammatory control“)

Patient age and gender	Diagnosis	type of surgery
66 yrs, ♂	diverticulitis	sigmoid resection
61 yrs, ♂	diverticulitis	sigmoid resection
69 yrs, ♂	diverticulitis	sigmoid resection
65 yrs, ♂	diverticulitis	sigmoid resection
65 yrs, ♂	diverticulitis	lap. sigmoid resection

In addition, IMACs were isolated from eight patients with IBD; three suffering from UC and five from CD

Patient age and gender	Diagnosis	type of surgery
36 yrs, ♀	pancolitis, UC	colectomy
43 yrs, ♂	pancolitis, UC	procto-colectomy
23 yrs, ♂	pancolitis, UC	procto-colectomy
15 yrs, ♂	CD, conglomerate term. ileum	ileo-cecal resection
22 yrs, ♂	CD, conglomerate term. ileum	ileo-cecal resection
52 yrs, ♀	CD, colon stenosis	lap. hemicolectomy
17 yrs, ♀	CD, inflammatory sigmoid stenosis	sigmoid resection
18 yrs, ♀	CD, conglomerate, colon	Colon segment resection

b) Isolation of peripheral blood monocytes with subsequent mRNA isolation for quantitative PCR from 15-14 IBD patients

Patient age and gender	Diagnosis and clinical evaluation of activity	treatment
51 yrs, ♂	CD, active	steroids
30 yrs, ♀	CD, active	steroids
41 yrs, ♀	CD, active	no steroids
44 yrs, ♀	UC, active	no steroids
23 yrs, ♀	CD, active	no steroids
34 yrs, ♂	CD, active	no steroids
60 yrs, ♂	UC, active	no steroids
49 yrs, ♀	UC, remission	steroids
35 yrs, ♂	UC, remission	steroids
38 yrs, ♀	CD, remission	steroids
46 yrs, ♀	CD, remission	no steroids
42 yrs, ♀	CD, remission	no steroids
31 yrs, ♂	CD, remission	no steroids
26 yrs, ♂	CD, remission	no steroids

In addition, blood monocytes were isolated from six healthy donors;

In vitro differentiated macrophages were generated from monocytes of six different voluntary healthy donors.

c) Specimens used for immunohistochemistry

Patient age and gender	Diagnosis	type of surgery
73 yrs, ♂	control	rectum exstirpation
50 yrs, ♀	control	diverticulosis
53 yrs, ♂	control	sigmoid stricture (diverticulitis)
64 yrs, ♀	control	diverticulitis
71 yrs, ♀	control	stricured diverticulitis
60 yrs, ♂	control	left-sided hemicolectomie
48 yrs, ♀	control	lap. sigmoid-resection
27 yrs, ♂	CD	ileo-cecal resection
39 yrs, ♂	CD	ileo-cecal resection
51 yrs, ♀	CD	subtotal colectomy
36 yrs, ♂	CD	stricture, colon segment resection
20 yrs, ♂	CD	colon segment resection, ileo-cecal resection
39 yrs, ♂	CD	colon segment resection, fistula excision
23 yrs, ♂	UC	procto-colectomy
46 yrs, ♂	UC	procto-colectomy
44 yrs, ♂	UC	stricture, colon segment resection
23 yrs, ♂	UC	colectomy
56 yrs, ♀	UC	procto-colectomy
45 yrs, ♂	UC	procto-colectomy

c) Specimens used for protein lysates for Western blots and proteasome activity assays

Protein lysates of nine control patients were used

Patient age and gender	Diagnosis	type of surgery
65 yrs, ♀	sigmoid cancer	sigmoid resection
30 yrs, ♀	slow transit obstipation	colectomy
37 yrs, ♀	sigmoid cancer	sigmoid resection
66 yrs, ♂	rectum carcinoma	rectum resection
68 yrs, ♀	cecal adenoma	ileo cecal resection
63 yrs, ♂	IBS with severe pain and obstipation	endoscopic biopsies
34 yrs, ♂	IBS with severe pain and obstipation	endoscopic biopsies
58 yrs, ♀	Rectum carcinoma	rectum resection
67 yrs, ♂	Rectum carcinoma	rectum resection

In addition protein lysates were obtained from 8 patients with IBD:

Patient age and gender	Diagnosis	type of surgery
46 yrs, ♂	UC, mild activity	endoscopic biopsies
19 yrs, ♀	CD with stricture colon transversum	stricture resection
22 yrs, ♂	CD with conglomerate	ileo-cecal resection
42 yrs, ♀	CD with severe inflammation and stricture	ileo-cecal resection
48 yrs, ♀	CD, stricture of anastomosis at ileotransversostomy	stricture resection
33 yrs, ♂	CD mild inflammation	endoscopic biopsies
32 yrs, ♀	CD, stricture	endoscopic biopsies
16 yrs, ♂	CD with conglomerate at terminal ileum	ileo-cecal resection

Supplementary table 2: List of antibodies used

A) Immunohistochemistry

Alexa Flour® 488 goat-anti rabbit IgG (H+L), FITC	Invitrogen, Carlsbad, CA
Alexa Flour® 546 goat-anti mouse IgG (H+L), PE	Invitrogen, Carlsbad, CA
Biotin-SP-conjugated AffiniPure Goat-anti-Mouse IgG	Jackson Immuno Research Laboratories
Goat-anti-Rabbit-IgG, Biotin Conjugate	Sigma-Aldrich
Mouse IgG1, Negative Control	DakoCytomation, Glostrup, Denmark
Mouse-anti-human CD68, Macrophage CLONE KP1	DakoCytomation, Glostrup, Denmark
Rabbit Immunoglobulin Fraction, Negative Control	DakoCytomation, Glostrup, Denmark
UBE2L6 Antibody (N-Term), Purified Rabbit Polyclonal Antibody (Pab)	Abgent, San Diego, USA
Ubiquitin B, Affinity purified Antibody, Rabbit	PTG, ProteinTech Group, Chicago
USP14 Antibody (N-Term), Purified Rabbit Polyclonal Antibody (Pab)	Abgent, San Diego, USA

B) Western Blotting

HRP-goat anti-mouse	Santa Cruz Biotechnology
HRP-goat anti-rabbit	Santa Cruz Biotechnology
Mouse-anti-actin	Chemicon
UBB monoclonal Antibody (M01), clone 1F5, mouse	Abnova Corporation, Taiwan
UBE2A monoclonal Antibody (M01), clone 3D7-E2, mouse	Abnova Corporation, Taiwan
UBE2D2 polyclonal antibody (A01), mouse	Abnova Corporation, Taiwan
UBE2L6 antibody (N-Term), purified rabbit polyclonal antibody (Pab)	Abgent, San Diego, USA
UBE2L6 mouse	Abnova Corporation, Taiwan
Ubiquitin B, affinity purified antibody, rabbit	PTG, ProteinTech Group, Chicago

USP14 antibody (N-Term), purified rabbit polyclonal antibody (Pab)	Abgent, San Diego, USA
anti-CD33 mouse IgG1 monoclonal; Clone:P67.6	Miltenyi, Bergisch Gladbach
anti-ATPase 2, rabbit polyclonal	Affinity Research Products, Exeter, UK
anti-beta 2, mouse monoclonal	Affinity Research Products, Exeter, UK
anti-beta 5, rabbit polyclonal	Affinity Research Products, Exeter, UK
anti-MECL-1, rabbit polyclonal	Affinity Research Products, Exeter, UK
anti-beta2i/MECL-1, rabbit polyclonal	Affinity Research Products, Exeter, UK
anti-LMP 7, mouse monoclonal	Affinity Research Products, Exeter, UK
Negative control rabbit immunoglobuline fraction	DakoCytomation, Hamburg
Mouse IgG1 negative control	DakoCytomation, Hamburg
Goat anti-rabbit	Sigma-Aldrich Chemie, Steinheim
Goat anti-mouse	Dianova, Hamburg
Goat anti-rabbit	Santa Cruz Biotechnology, Inc.
Goat anti-mouse	Santa Cruz Biotechnology, Inc.
Mouse anti-actin mouse monoclonal; C4	Chemicon

Supplementary table 3

Primer sequences

Gene checker (integrity of mRNA)

Primer Set	Sequence
GAPDH	5'-TTA GCA CCC CTG GCC AAG G-3' 5'-CTT ACT CCT TGG AGG CCA TG-3'
5'Actin	5'-GCT CAC CAT GGA TGA TGA TAT CGC-3' 5'-GGA GGA GCA ATG ATC TTG ATC TTC-3'
3'Actin	5'-GAA GAT CAA GAT CAT TGC TCC TCC-3' 5'-CTG GTC TCA AGT CAG TGT ACA GG-3'
6K Clathrin	5'-GAC AGT GCC ATC ATG AAT CC-3' 5'-TTT GTG CTT CTG GAG GAA AGA A-3'
2K Clathrin	5'-GCT CAC ATG GGA ATG TTC AC-3' 5'-ATG TTG TCA AAG TTG TCA TAA G-3'

Primers for Taqman® PCR were purchased from MWG (Ebersberg, Germany). A melting temperature of 60°C was chosen. The internal primer was labelled with 5'-FAM and 3'-TAMRA

Primers for proteasomal components

Primer Set	Sequence
ATPase2 for ATPase2 rev ATPase2 probe	5'- CTT TGG TCC ACC CGG TAC AG -3' 5'- CGA ATG AAG CAC GCA TCA GT -3' 5'- AAG ACA CTC TGT GCG CGG GCA GTT -3'
β2 for β2 rev β2 probe	5'- TCG GAC CCC ATA TCA TGT GA -3' 5'- CGC TGG CCC TTC ATG CT -3' 5'- CCT CCT CCT GGC TGG CTA TGA T -3'

β5 for	5′ - GGA AGT GGA GCA GGC CTA TG -3′
β5 rev	5′ - GCA TCT CTG TAG GTG GCT TGG T -3′
β5 probe	5′ - TCT GGC CCG TCG AGC CAT C -3′
MEC1-1 for	5′ - TCT GGG CGC CGA TAC G -3′
MEC1-1 rev	5′ - GGA TCT TCT CGC AGC TCT TGT C -3′
MEC1-1 probe	5′ - CCA CTA ACG ATT CGG TCG TGG C -3′
LMP7 for	5′ - GCC TGC TGG CCA AGG AAT -3′
LMP7 rev	5′ - GCT GCC GAC ACT GAA ATA CGT -3′
LMP7 probe	5′ - CAG GCT GTA CTA TCT GCG AAA TGG A -3′

Primers for ubiquitinylation genes

Primer Set	Sequence
E2A for	5′ - AGA ACC GTT GGA GTC CAA CCT - 3′
E2A rev	5′ - TGG GTT CAT CCA ACA GAG ACT GT - 3′
E2A probe	5′ - TGA TGT GTC TTC CAT TCT AAC ATC C - 3′
E2D2 for	5′ - TTC AAA AGT ACT CTT GTC CAT CTG TTC - 3′
E2D2 rev	5′ - CCG AGC AAT CTC AGG CAC TAA - 3′
E2D2 probe	5′ - CTG TTG TGT GAT CCC AAT CCA GAT GAT CC - 3′
E2L6 for	5′ - TTT GCC TGC CCA TCA TCA G - 3′
E2L6 rev	5′ - CCT CCA GGA CTT GGC AAG TC - 3′
E2L6 probe	5′ - TGA GAA CTG GAA GCC TTG CAC CA - 3′
USP14 for	5′ - CCC ACA GTT TGC CGA GAA AG - 3′
USP14 rev	5′ - CAA TAC TCG CAT CAT TTG TAT CCA A - 3′
USP14 probe	5′ - TGA ACA AGG ACA GTA TCT TCA ACA GGA TGC TAA TG - 3′
UBB for	5′ - GGT GGC TGT TAA TTC TTC AGT CAT G - 3′
UBB rev	5′ - GCA ACG AAA CCT TTA TTA ACA TTT TG - 3′
UBB probe	5′ - TTA CTC TGC ACT ATA GCC ATT TGC CCC AAC TTA A - 3′

Supplementary table 4: Affymetrix GeneChip® analysis of proteasomal components

For Affymetrix GeneChip® analysis twice mRNA from three control-patients and from three donors for i.v.MACs was pooled and hybridized onto two chips. Affymetrix® analysis showed a significant downregulation of virtually all proteasomal components. There were 46 probe sets for proteasome-subunits representing 35 different genes. For all probe sets a higher expression in i.v.MACs as compared to IMACs was indicated. The ratio signal(i.v.MACs)/signal(IMACs) was between 1.6 and 13.6 with an average of 4.3. Different probe sets for the same mRNA gave similar results. This pointed to a lower mRNA-expression of all proteasomal components in IMACs from normal mucosa as compared with i.v.MACs.

	Gene	Location	Unigene	IMACs Signal 1	IMACs Signal 2	i.v. MAC Signal 1	i.v. MAC Signal 2	Average IMAC	Average i.v. MAC	Ratio (i.v. vs. IMAC
1	proteasome 26S subunit, ATPase, 1	Chr:14q32.11	Hs.4745	382.0	561.0	1267.0	1161.0	471.5	1214.0	2.6
2	proteasome 26S subunit, ATPase, 2	Chr:7q22.1-q22.3	Hs.61153	380.0	491.0	2527.0	1968.0	435.5	2247.5	5.2
3	proteasome 26S subunit, ATPase, 2	Chr:7q22.1-q22.3	Hs.61153	70.0	100.0	289.0	285.0	85.0	287.0	3.4
4	proteasome 26S subunit, ATPase, 3	Chr:11p12-p13	Hs.250758	9.0	35.0	186.0	167.0	22.0	176.5	8.0
5	proteasome 26S subunit, ATPase, 4	Chr:19q13.11-q13.13	Hs.211594	38.0	45.0	92.0	71.0	41.5	81.5	2.0
6	proteasome 26S subunit, ATPase, 6	Chr:14q22.1	Hs.79357	161.0	204.0	626.0	465.0	182.5	545.5	3.0
7	proteasome 26S subunit, non-ATPase, 1	Chr:2q37.1	Hs.3887	132.0	154.0	1001.0	810.0	143.0	905.5	6.3
8	proteasome 26S subunit, non-ATPase, 1	Chr:2q37.1	Hs.3887	75.0	170.0	558.0	415.0	122.5	486.5	4.0
9	proteasome 26S subunit, non-ATPase, 10	Chr:Xq22.3	Hs.433559	114.0	146.0	814.0	841.0	130.0	827.5	6.4
10	proteasome 26S subunit, non-ATPase, 11	Chr:17q11.2	Hs.90744	73.0	80.0	563.0	501.0	76.5	532.0	7.0
11	proteasome 26S subunit, non-ATPase, 12	Chr:17q24.2	Hs.4295	113.0	173.0	607.0	504.0	143.0	555.5	3.9
12	proteasome 26S subunit, non-ATPase, 12	Chr:17q24.2	Hs.4295	48.0	53.0	231.0	219.0	50.5	225.0	4.5
13	proteasome 26S subunit, non-ATPase, 13	Chr:11p15.5	Hs.279554	176.0	229.0	825.0	530.0	202.5	677.5	3.3
14	proteasome 26S subunit, non-ATPase, 13	Chr:11p15.5	Hs.279554	48.0	47.0	157.0	95.0	47.5	126.0	2.7
15	proteasome 26S subunit, non-ATPase, 2	Chr:3q27.3	Hs.74619	231.0	307.0	969.0	804.0	269.0	886.5	3.3
16	proteasome 26S subunit, non-ATPase, 4	Chr:1q21.2	Hs.148495	122.0	193.0	473.0	271.0	157.5	372.0	2.4
17	proteasome 26S subunit, non-ATPase, 4	Chr:1q21.2	Hs.148495	23.0	66.0	319.0	237.0	44.5	278.0	6.2
18	proteasome 26S subunit, non-ATPase, 5	Chr:9q33.3	Hs.193725	98.0	236.0	598.0	442.0	167.0	520.0	3.1
19	Proteasome 26S subunit, non-ATPase, 7	Chr:16q23-q24	Hs.155543	157.0	238.0	488.0	311.0	197.5	399.5	2.0

20	proteasome 26S subunit, non-ATPase, 8	Chr:19q13.13	Hs.78466	77.0	132.0	264.0	320.0	104.5	292.0	2.8
21	proteasome 26S subunit, non-ATPase, 9	Chr:12q24.31-q24.32	Hs.5648	101.0	142.0	339.0	322.0	121.5	330.5	2.7
22	proteasome activator subunit 2 (PA28 beta)	Chr:14q11.2	Hs.433810	704.0	734.0	1250.0	1066.0	719.0	1158.0	1.6
23	proteasome activator subunit 3 (PA28 gamma; Ki)	Chr:17q12-q21	Hs.152978	121.0	186.0	770.0	451.0	153.5	610.5	4.0
24	proteasome activator subunit 3 (PA28 gamma; Ki)	Chr:17q12-q21	Hs.152978	35.0	54.0	259.0	141.0	44.5	200.0	4.5
25	proteasome subunit, alpha type, 1	Chr:11p15.1	Hs.82159	520.0	786.0	2419.0	2361.0	653.0	2390.0	3.7
26	proteasome subunit, alpha type, 1	Chr:11p15.1	Hs.82159	443.0	450.0	2638.0	2441.0	446.5	2539.5	5.7
27	proteasome subunit, alpha type, 1	Chr:11p15.1	Hs.82159	277.0	541.0	1741.0	1256.0	409.0	1498.5	3.7
28	proteasome subunit, alpha type, 2	Chr:7p13	Hs.181309	162.0	186.0	510.0	427.0	174.0	468.5	2.7
29	proteasome subunit, alpha type, 3	Chr:14q23	Hs.432428	43.0	86.0	630.0	497.0	64.5	563.5	8.7
30	proteasome subunit, alpha type, 4	Chr:15q24.1	Hs.251531	254.0	335.0	823.0	707.0	294.5	765.0	2.6
31	proteasome subunit, alpha type, 5	Chr:1p13	Hs.76913	140.0	200.0	747.0	836.0	170.0	791.5	4.7
32	proteasome subunit, alpha type, 6	Chr:14q13	Hs.74077	385.0	494.0	1999.0	1820.0	439.5	1909.5	4.3
33	proteasome subunit, alpha type, 7	Chr:20q13.33	Hs.233952	158.0	175.0	1068.0	989.0	166.5	1028.5	6.2
34	proteasome subunit, alpha type, 7	Chr:20q13.33	Hs.233952	40.0	35.0	149.0	181.0	37.5	165.0	4.4
35	proteasome subunit, beta type, 1	Chr:6q27	Hs.75748	237.0	329.0	713.0	647.0	283.0	680.0	2.4
36	proteasome subunit, beta type, 2	Chr:1p34.2	Hs.432607	177.0	219.0	1265.0	1224.0	198.0	1244.5	6.3
37	proteasome subunit, beta type, 3	Chr:17q12	Hs.82793	198.0	200.0	530.0	403.0	199.0	466.5	2.3
38	proteasome subunit, beta type, 4	Chr:1q21	Hs.89545	625.0	726.0	1401.0	1507.0	675.5	1454.0	2.2
39	proteasome subunit, beta type, 4	Chr:1q21	Hs.89545	90.0	146.0	478.0	494.0	118.0	486.0	4.1
40	proteasome subunit, beta type, 5	Chr:14q11.2	Hs.261927	117.0	178.0	1445.0	1460.0	147.5	1452.5	9.8
41	proteasome subunit, beta type, 6	Chr:17p13	Hs.77060	246.0	190.0	615.0	513.0	218.0	564.0	2.6
42	proteasome subunit, beta type, 7	Chr:9q34.11-q34.12	Hs.433434	138.0	193.0	723.0	767.0	165.5	745.0	4.5
43	proteasome subunit, beta type, 8 (large multifunctional protease 7)	Chr:6p21.3	Hs.180062	217.0	258.0	859.0	622.0	237.5	740.5	3.1
44	proteasome subunit, beta type, 8 (large multifunctional protease 7)	Chr:6p21.3	Hs.180062	26.0	95.0	941.0	738.0	60.5	839.5	13.9
45	proteasome subunit, beta type, 9 (large multifunctional protease 2)	Chr:6p21.3	Hs.381081	203.0	301.0	766.0	621.0	252.0	693.5	2.8
46	proteasome activator 200 kDa	Chr:2p16.1	Hs.112396	40.0	85.0	278.0	240.0	62.5	259.0	4.1

Supplementary table 5:

For Affymetrix GeneChip® analysis twice mRNA from three control-patients and from three donors for i.v.MACs was pooled and hybridized onto two chips. Affymetrix® analysis showed a significant downregulation of the ubiquitinylation machinery in IMACs.

Out of 64 probe sets representing 42 genes the majority had clearly a higher signal in i.v.MACs. Only for ubiquitins B and C which showed a high signal in both i.v.MACs and IMACs this was not observed. Ubiquitin D, ubiquitin carrier protein and some other probe sets showed a very low signal making the results not reliable.

	Gene	Location	Unigene	IMACs Signal 1	IMACs Signal 2	i.v. MAC Signal 1	i.v. MAC Signal 2	Average IMAC	Average i.v. MAC	Ratio (i.v. vs. IMAC)
1	ubiquitin activating enzyme E1-like protein	Chr:3p25.2	Hs.278607	38.0	98.0	360.0	257.0	68.0	308.5	4.5
2	ubiquitin associated protein 1	Chr:9p22-p21	Hs.75425	135.0	153.0	445.0	397.0	144.0	421.0	2.9
3	ubiquitin associated protein 2	Chr:9p13.2	Hs.14953	84.0	78.0	185.0	169.0	81.0	177.0	2.2
4	ubiquitin B	Chr:17p12-p11	Hs.356190	7087.0	7084.0	3491.0	3547.0	7085.5	3519.0	0.5
5	ubiquitin C	Chr:12q24.3	Hs.183704	3998.0	4982.0	4544.0	4436.0	4490.0	4490.0	1.0
6	ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase)	Chr:4p14	Hs.76118	24.0	49.0	668.0	552.0	36.5	610.0	16.7
7	ubiquitin carboxyl-terminal esterase L3 (ubiquitin thiolesterase)	Chr:13q21.33	Hs.77917	30.0	18.0	222.0	176.0	24.0	199.0	8.3
8	ubiquitin carrier protein	Chr:19q13.43	Hs.174070	37.0	37.0	18.0	18.0	37.0	18.0	0.5
9	ubiquitin D	Chr:6p21.3	Hs.44532	108.0	159.0	10.0	2.0	133.5	6.0	4.5e-2
10	ubiquitin protein ligase	Chr:12q24.12	Hs.17639	35.0	91.0	205.0	156.0	63.0	180.5	2.9
11	ubiquitin protein ligase E3A	Chr:15q11-q13	Hs.180686	155.0	102.0	361.0	251.0	128.5	306.0	2.4
12	ubiquitin protein ligase E3A	Chr:15q11-q13	Hs.180686	61.0	135.0	442.0	324.0	98.0	383.0	3.9
13	ubiquitin protein ligase E3A	Chr:15q11-q13	Hs.180686	68.0	84.0	407.0	233.0	76.0	320.0	4.2
14	ubiquitin specific protease 10	Chr:16q24.1	Hs.78829	81.0	109.0	69.0	73.0	95.0	71.0	0.7
15	ubiquitin specific protease 10	Chr:16q24.1	Hs.78829	64.0	125.0	315.0	269.0	94.5	292.0	3.1
16	ubiquitin specific protease 12	Chr:5q33-q34	Hs.42400	216.0	250.0	1218.0	804.0	233.0	1011.0	4.3
17	ubiquitin specific protease 12	Chr:5q33-q34	Hs.42400	22.0	28.0	21.0	6.0	25.0	13.5	0.5
18	ubiquitin specific protease 13 (isopeptidase T-3)	Chr:3q26.2-q26.3	Hs.85482	47.0	96.0	77.0	51.0	71.5	64.0	0.9

19	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	Chr:18p11.32	Hs.75981	284.0	343.0	1346.0	915.0	313.5	1130.5	3.6
20	ubiquitin specific protease 14 (tRNA-guanine transglycosylase)	Chr:18p11.32	Hs.75981	74.0	70.0	517.0	308.0	72.0	412.5	5.7
21	ubiquitin specific protease 15	Chr:12q14	Hs.23168	79.0	126.0	259.0	247.0	102.5	253.0	2.5
22	ubiquitin specific protease 16	Chr:21q22.11	Hs.99819	188.0	319.0	173.0	204.0	253.5	188.5	0.7
23	ubiquitin specific protease 18	Chr:22q11.21	Hs.38260	7.0	8.0	72.0	44.0	7.5	58.0	7.7
24	ubiquitin specific protease 22	Chr:17p11.1	Hs.12064	322.0	415.0	742.0	592.0	368.5	667.0	1.8
25	ubiquitin specific protease 7 (herpes virus-associated)	Chr:16p13.3	Hs.78683	219.0	301.0	825.0	482.0	260.0	653.5	2.5
26	ubiquitin specific protease 8	Chr:15q15.3	Hs.152818	48.0	68.0	188.0	168.0	58.0	178.0	3.1
27	ubiquitin-activating enzyme E1	Chr:Xp11.23	Hs.2055	136.0	215.0	801.0	363.0	175.5	582.0	3.3
28	ubiquitin-activating enzyme E1-like	Chr:3p21	Hs.16695	79.0	216.0	235.0	119.0	147.5	177.0	1.2
29	ubiquitin-activating enzyme E1-like	Chr:3p21	Hs.16695	129.0	149.0	135.0	94.0	139.0	114.5	0.8
30	ubiquitination factor E4A (UFD2 homolog, yeast)	Chr:11q23.3	Hs.75275	111.0	165.0	732.0	513.0	138.0	622.5	4.5
31	ubiquitination factor E4B	Chr:1p36.3	Hs.24594	155.0	164.0	653.0	553.0	159.5	603.0	3.8
32	ubiquitination factor E4B	Chr:1p36.3	Hs.24594	1.0	3.0	53.0	20.0	2.0	36.5	18.3
33	ubiquitin-conjugating enzyme E2 variant 1	Chr:20q13.2	Hs.75875	241.0	348.0	979.0	747.0	294.5	863.0	2.9
34	ubiquitin-conjugating enzyme E2 variant 1	Chr:20q13.2	Hs.75875	99.0	189.0	691.0	534.0	144.0	612.5	4.3
35	ubiquitin-conjugating enzyme E2 variant 2	Chr:8q11.1	Hs.79300	88.0	157.0	354.0	247.0	122.5	300.5	2.5
36	ubiquitin-conjugating enzyme E2, J1	Chr:6q16.1	Hs.184325	143.0	221.0	996.0	805.0	182.0	900.5	4.9
37	ubiquitin-conjugating enzyme E2, J1	Chr:6q16.1	Hs.184325	101.0	196.0	413.0	365.0	148.5	389.0	2.6
38	ubiquitin-conjugating enzyme E2, J1	Chr:6q16.1	Hs.184325	121.0	167.0	509.0	317.0	144.0	413.0	2.9
39	ubiquitin-conjugating enzyme E2, J1	Chr:6q16.1	Hs.184325	49.0	58.0	182.0	206.0	53.5	194.0	3.6
40	ubiquitin-conjugating enzyme E2A	Chr:Xq24-q25	Hs.379466	306.0	388.0	1271.0	1002.0	347.0	1136.5	3.3
41	ubiquitin-conjugating enzyme E2A	Chr:Xq24-q25	Hs.379466	152.0	195.0	226.0	211.0	173.5	218.5	1.3
42	ubiquitin-conjugating enzyme E2B	Chr:5q23-q31	Hs.811	347.0	459.0	432.0	281.0	403.0	356.5	0.9
43	ubiquitin-conjugating enzyme E2B	Chr:5q23-q31	Hs.811	117.0	208.0	660.0	470.0	162.5	565.0	3.5
44	ubiquitin-conjugating enzyme E2D 1	Chr:10q11.2-q21	Hs.129683	15.0	16.0	21.0	2.0	15.5	11.5	0.7

45	ubiquitin-conjugating enzyme E2D 1	Chr:10q11.2-q21	Hs.129683	10.0	7.0	44.0	30.0	8.5	37.0	4.4
46	ubiquitin-conjugating enzyme E2D 2	Chr:5q31.3	Hs.108332	185.0	247.0	1008.0	718.0	216.0	863.0	4.0
47	ubiquitin-conjugating enzyme E2D 2	Chr:5q31.3	Hs.108332	44.0	39.0	95.0	67.0	41.5	81.0	2.0
48	ubiquitin-conjugating enzyme E2G 1	Chr:17p13.3	Hs.78563	208.0	297.0	981.0	697.0	252.5	839.0	3.3
49	ubiquitin-conjugating enzyme E2G 1	Chr:17p13.3	Hs.78563	49.0	75.0	424.0	265.0	62.0	344.5	5.6
50	ubiquitin-conjugating enzyme E2G 2	Chr:21q22.3	Hs.192853	45.0	56.0	140.0	94.0	50.5	117.0	2.3
51	ubiquitin-conjugating enzyme E2I	Chr:16p13.3	Hs.432833	258.0	343.0	816.0	691.0	300.5	753.5	2.5
52	ubiquitin-conjugating enzyme E2L 3	Chr:22q11.21	Hs.108104	61.0	72.0	425.0	266.0	66.5	345.5	5.2
53	ubiquitin-conjugating enzyme E2L 3	Chr:22q11.21	Hs.108104	31.0	35.0	242.0	140.0	33.0	191.0	5.8
54	ubiquitin-conjugating enzyme E2L 3	Chr:22q11.21	Hs.108104	4.0	62.0	322.0	236.0	33.0	279.0	8.5
55	ubiquitin-conjugating enzyme E2L 6	Chr:11q12	Hs.169895	270.0	325.0	1728.0	1192.0	297.5	1460.0	4.9
56	ubiquitin-conjugating enzyme E2M	Chr:19q13.43	Hs.406068	16.0	12.0	129.0	92.0	14.0	110.5	7.9
57	ubiquitin-conjugating enzyme E2N	Chr:12q22	Hs.75355	205.0	269.0	454.0	525.0	237.0	489.5	2.1
58	ubiquitin-conjugating enzyme E2N	Chr:12q22	Hs.75355	49.0	128.0	467.0	307.0	88.5	387.0	4.4
59	ubiquitin-like 1 (sentrin)	Chr:2q33	Hs.81424	369.0	435.0	929.0	930.0	402.0	929.5	2.3
60	ubiquitin-like 1 (sentrin)	Chr:2q33	Hs.81424	60.0	121.0	502.0	497.0	90.5	499.5	5.5
61	ubiquitin-like 3	Chr:13q12-q13	Hs.173091	120.0	310.0	776.0	660.0	215.0	718.0	3.3
62	ubiquitin-like 3	Chr:13q12-q13	Hs.173091	45.0	94.0	272.0	194.0	69.5	233.0	3.4
63	ubiquitin-like 4	Chr:Xq28	Hs.76480	35.0	47.0	292.0	187.0	41.0	239.5	5.8
64	ubiquitin-like 5	Chr:19p13.3	Hs.13836	169.0	181.0	436.0	394.0	175.0	415.0	2.4
65	ubiquitin-protein isopeptide ligase (E3)	Chr:7q36.3	Hs.155287	63.0	98.0	644.0	465.0	80.5	554.5	6.9