1 Supplementary Figure 1. NRF hotspot mutation and POMP expression levels in cancers (A) 2 Lollipop plots of mutations in NRF2 (top) and NRF3 (bottom). Somatic mutation data from 3 TCGA PanCancer Atlas studies, including 33 tumor types (10976 samples), were analyzed at the 4 cBioPortal for Cancer Genomics (http://cbioportal.org). (B) Dot plots showing POMP gene 5 expression across multiple cancer types and paired normal samples. Red and green dots represent 6 RNA sequencing expression values of patient-matched tumors and adjacent normal tissue 7 archived at TCGA and GTEx database. Red and blue abbreviations at the upper part of each graph 8 indicate a cancer type with significantly higher and lower expression levels of each NRF gene 9 compared to normal samples, respectively (TPM, transcripts per millions; ANOVA, q value 10 cutoff = 0.01). Abbreviations of cancer types were summarized with the numbers of specimens 11 in Supplementary Table 1.

12

13 Supplementary Figure 2. NRF3 induces POMP gene expression and enhances 20S proteasome 14 activity. (A) Endogenous NRF3 protein levels in HCT116 (colorectal carcinoma), H1299 (non-15 small cell lung cancer), LNCaP (prostate adenocarcinoma), A-172 (glioblastoma), T98G 16 (glioblastoma multiforme), U2OS (bone osteosarcoma) and HeLa (cervical adenocarcinoma) cell 17 lines. Endogenous NRF3 protein levels were detected by immunoblotting. (B) Generation of 18 NRF3 knockdown or overexpression cells using HCT116 or H1299 cells. NRF3 and POMP 19 protein levels were detected by immunoblotting. GFP was used as control. (C) NRF3 protein 20 levels in nucleus of H1299-oeNRF3#2 or oeGFP#2 cells. Each cell line was fractionated into the 21 cytoplasmic (C) and nuclear extracts (N), followed by immunobloting. Whole cell extracts were 22 used as input samples. (D) Impact of SDS or ATP on proteasome activity. HCT116 cell extracts 23 were fractionated into 20 fractions, using a 10%-40% glycerol gradient centrifugation, and 24 assayed for Suc-LLVY-AMC (chymotrypsin-like) hydrolysing activity of 20S proteasomes 25 (+SDS/-ATP, black) or 26S proteasomes (-SDS/+ATP, gray). (N = 1) (E) Impact of a 26 proteasome inhibitor MG-132 or a protease inhibitor cocktail (PIC) on protease or proteasome 27 activity. HCT116 cell extracts were fractionated into 20 fractions, using a 10%-40% glycerol 28 gradient centrifugation, and assayed for Suc-LLVY-AMC (chymotrypsin-like) hydrolysing

29 activity under treatment with $1 \times PIC$ (red) (Nacalai Tesque) or 10 μ M MG-132 (blue) (Peptide 30 Institute) in the presence of SDS and the absence of ATP. (N=1) (F) Impact of NRF3 31 overexpression on three types of 20S proteasome activity. The indicated H1299 cell extracts used 32 in Fig. 1D were assayed for Z-GGL-AMC (chymotrypsin-like), Ac-RLR-AMC (trypsin-like), and 33 Z-LLE-AMC (caspase-like) hydrolysing activity of 20S proteasomes (+SDS/-ATP). Mean and 34 individual values are represented as lines and marks, respectively (N=2). The activity in fractions 35 #1-#5 was derived from non-proteasomal proteases. (G) Impact of NRF3 overexpression on 36 mRNA levels of four ATP-independent regulatory complex subunits. mRNA levels of indicated 37 genes in H1299-oeNRF3#2 or oeGFP#2 cells were represented as red or blue bars, respectively. 38 H1299-GFP#2 cells were used as controls. *p < 0.05; n.s., not significant (N = 3, mean \pm SD, t-39 tests) (H) Impact of NRF3 overexpression on mRNA levels of four 20S proteasome assembly 40 chaperones PSMG1-4. Each PSMG mRNA levels H1299-oeNRF3#2 or oeGFP#2 cells were 41 represented as red or blue bars, respectively. H1299-GFP#2 cells were used as controls. *p < 0.0542 $(N = 3, \text{mean} \pm \text{SD}, \text{ANOVA followed by Tukey test})$

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44 Supplementary Figure 3. Impact of NRF3 knockdown in HCT116 p53KO cells on cell fate, 45 POMP expression, proteasome activity and drug resistance. (A) Impact of NRF3 knockdown on 46 Rb and p53 protein levels. HCT116 cells were transfected with indicated siRNA. After 2 d, Rb 47 and p53 proteins were detected by immunostaining. HCT116 p53KO cells were used as controls. 48 Scale bar, 10 µm. (A and B) Representative contour plots of cell-cycle assay in Fig. 4F (A) and 49 cell-cycle assay in Fig. 4G (B). (C) Generation of NRF3 knockdown cells using HCT116 p53KO 50 cells. NRF3 and POMP proteins were detected by immunoblotting. (D) Impact of NRF3 51 knockdown on mRNA levels of POMP in HCT116 p53KO cells. POMP mRNA levels were 52 assessed by RT-qPCR. *p < 0.05 (N = 3, mean \pm SD, ANOVA followed by Tukey test) (E) Impact 53 of NRF3 knockdown on proteasome activity in HCT116 p53KO cells. The indicated cell extracts 54 were fractionated into 20 fractions, using a 10%-40% glycerol gradient centrifugation, and 55 assayed for Suc-LLVY-AMC (chymotrypsin-like) hydrolysing activity of 20S proteasomes 56 (+SDS/-ATP, top) or 26S proteasomes (-SDS/+ATP, bottom). Mean and individual values are 57 represented as lines and marks, respectively (N = 2). The activity in fractions #1–#5 was derived 58 from non-proteasomal proteases. (F) Impact of NRF3 knockdown on the ubiquitin-independent 59 degradation of Rb and p53 proteins in HCT116 p53KO cells. Each protein was detected by 60 immunoblotting after 24 h of treatment with 10 µM TKA-243, a ubiquitin activating enzyme E1 61 inhibitor. DMSO was used as the control. (G) Impact of NRF3 knockdown on mRNA levels of 62 *Rb* in HCT116 p53KO cells. *Rb* mRNA levels were assessed by RT-qPCR. *p < 0.05 (N = 3, 63 mean \pm SD, ANOVA followed by Tukey test) (H) Impact of NRF3 knockdown on the resistance 64 to proteasome inhibitor anticancer agents of HCT116 p53KO cells (left) or HCT116 cells (right). 65 Viabilities of indicated cells were assessed by WST-1 assays after 24 h of treatment with the 66 indicated concentration of BTZ (top) or TAK-243 (bottom) (N = 3, mean \pm SD).

Waku et al., Revised Supplementary Figure 1



Waku et al., Revised Supplementary Figure 2



Waku et al., Revised Supplementary Figure 3



Revised Supplementary Table 1. Abbreviations of cancer types and the numbers of specimens analyzed

Abbreviation	Cancer types	Numbers of specimens (Tumor / Normal)
ACC	Adrenocortical carcinoma	77 / 128
BLCA	Bladder Urothelial Carcinoma	404 / 28
BRCA	Breast invasive carcinoma	1085 / 291
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma	306 / 13
CHOL	Cholangio carcinoma	36/9
COAD	Colon adenocarcinoma	275/349
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma	47 / 337
ESCA	Esophageal carcinoma	182/286
GBM	Glioblastoma multiforme	163/207
HNSC	Head and Neck squamous cell carcinoma	519/44
KICH	Kidney Chromophobe	66 / 53
KIRC	Kidney renal clear cell carcinoma	523 / 100
KIRP	Kidney renal papillary cell carcinoma	286 / 60
LAML	Acute Myeloid Leukemia	173/70
LGG	Brain Lower Grade Glioma	518/207
LIHC	Liver hepatocellular carcinoma	369 / 160
LUAD	Lung adenocarcinoma	483 / 347
LUSC	Lung squamous cell carcinoma	486 / 338
OV	Ovarian serous cystadenocarcinoma	426 / 88
PAAD	Pancreatic adenocarcinoma	179/171
PCPG	Pheochromocytoma and Paraganglioma	182/3
PRAD	Prostate adenocarcinoma	492 / 152
READ	Rectal adenocarcinoma	92/318
SARC	Sarcoma	262/2
SKCM	Skin Cutaneous Melanoma	461 / 558
STAD	Stomach adenocarcinoma	408/211
TGCT	Testicular Germ Cell Tumors	137 / 165
THCA	Thyroid carcinoma	512/337
THYM	Thymoma	118/339
UCEC	Uterine Corpus Endometrial Carcinoma	174/91
UCS	Uterine Carcinosarcoma	57 / 78

Revised Supplementary Table 2. IC50 values with statistics in response to proteasome inhibitors

	H1299					HCT116			HCT116				HCT116-p53KO				
TAK-243	GF	P		NRF3#	/1	GF	-P	NR	F3	shC	ont	shNI	RF3	shC	ont	shN	RF3
	#1	#2	#1	#2	mtPOMP	#1	#2	#1	#2	#1	#2	#1	#2	#1	#2	#1	#2
IC50 (µM, Best-fit values)	0.79	0.52	0.61	0.79	0.68	1.53	1.37	1.45	1.80	1.13	1.02	1.25	1.42	1.81	2.04	1.59	1.62
IC50 (µM, Std. Error)	0.20	0.28	0.12	0.27	0.15	0.25	0.32	0.40	0.36	0.10	0.11	0.25	0.23	0.13	0.33	0.32	0.09
R square (Goodness of Fit)	0.91	0.91	0.92	0.97	0.92	0.94	0.91	0.93	0.94	0.93	0.93	0.85	0.94	0.99	0.98	0.95	1.00

			H1299	Ð		НСТ116 НСТ116 НСТ116-р						-p53KO					
BTZ	GFP		NRF3#1		GFP		NRF3		shCont		shNRF3		shCont		shNRF3		
	#1	#2	#1	#2	mtPOMP	#1	#2	#1	#2	#1	#2	#1	#2	#1	#2	#1	#2
IC50 (µM, Best-fit values)	11.39	15.01	34.13	49.49	12.28	13.82	13.19	52.61	53.28	17.48	24.34	12.49	19.58	72.52	49.63	17.65	16.82
IC50 (µM, Std. Error)	2.01	0.44	2.08	1.36	0.59	1.41	0.57	11.47	6.46	1.36	1.60	1.11	1.60	13.29	5.53	0.61	0.82
R square (Goodness of Fit)	0.99	0.99	0.98	0.99	0.97	0.98	0.98	0.95	0.97	0.97	0.98	0.97	0.99	1.00	0.98	0.99	0.98

Revised Supplementary Table 3. Primer and oligonucleotide sequences

qPCR primer

PSMA1(c6)CCAGGGCAGGATTCACATCTCATTGCGCCCTTTCPSMA2(c2)GCCCCGATTACAGAGTGCTGGACGACACCTGAPSMA3(c7)TGTTGATCGCCATGTGCTGGACGACACCCTGCACCTGAPSMA4(c3)CATTGCTCGGATAGCAACGACTGTGCCCTTCATPSMA5(c5)CTTCAGAGGGTGCCTTACACCGGTCATCACACAACCAPSMA5(c4)ACCCAGGTGCCCTGCTGCCATGCTCTGTCACGACACCAPSMA7(c4)AGTCATGCCCGGATTCCTGCCACCTGCTGTGCCAGGPSMB1(bb)CATGCTACACCCCGCGACTCCGCATGCTCTGTCCAGGPSMB2(b4)CTTCACACCCCGCGAACCTAGGCTGCCAGGTAGTCCAPSMB3(l3)TGGTGGCCACCTTGTTGACAGTGGCCCCTGAATPSMB4(b7)TCTCGGCCGAATGGTATCACATACCGAGGAGCTTPSMB5(l5)CCATGGCCACACTGTTGTGCAGTTGCCGGAAACTPSMB5(l5)CCATGGCCGCAAACCGAATTTTGGGTCCTCGGAACTCPSMB5(l6)CTCCAGGCGGGGAATCATCCCAATGGCCCCCTGAAATPSMB5(l7)CGGCGTGTGCGGTGTGCGGTGATGATCAGGCAGGGAGAACTCPSMC1(RpL2)CGGCTGTGCGGGAAACACGATCAGGCAGCGGGCCAATGAPSMC2(Rpt1)TGGGATTGGCTGGGAAGACGTGCCCACGACAACAGCPSMC3(Rpb3)GCTGTCCAGGCCTGGGAAGACGTGGCCAATGACGCATGAPSMC4(Rp13)GCCGATGCTGGGGAAGACGTGGCCAATGACGCATGAPSMD1(Rpn2)ATCACGAGGGCGCACGAAGCCCACATGAGGTTGTPSMD2(Rpn1)CCCAAGGTGCCTGTTCTGCTGGCCACCACGACTGTPSMD2(Rpn1)CCCAAGGTGCCACAGGCGTGCGCACAGCACGCATGAGPSMD1(Rpn2)ATGCAGGGGGCGCACAGGCCCACACGGCGGCAAAPSMD2(Rpn3)GCTGTGCCAGGTGGAAGACCCCCACAGGGCCACAGPSMD1(Rpn4)GCCAACGCGGCGACAGGGGCCTTGCCGGCACAC<	Target gene	Forward primer	Reverse primer
PSMA2(u2)CCCCCAGATTACAGATTGCTIGGACGAACACCCCTGAPSMA3(u7)TGTGATCGGATTAGCAATGCATGTGGCTTCCATPSMA4(u3)CATTGGCTGGATTAGCAATGCATGTGCCTCCTATPSMA5(u5)CTTCACAGGGTGCCCAGACAGGCTGACCAACACACAPSMA7(u4)AGTCAGTGCGCGGATTCACCCCGTCATCAACACACAPSMB1(b6)CATGCTACAGCCCGGAACCTGGCAGCCGATGATCAPSMB2(g4)CTTCACAGCCCGAACCTGGCAGCCGATGATCAPSMB5(g5)CCATGGCCAACACCTGGCAGCCGATGATCAPSMB5(g5)CCATGGCCACACCCTTGTGCAACGCCGGAACCTPSMB5(g5)CCATGGCCACAACCGAATATCAGGCGGGAACTGCPSMB5(g1)CTGATGGCGGAACTCTCCAATGGCAGAGCTPSMB5(g1)CTGATGGCGGAACACCCATCAGCAGGGGGAACTGCPSMB5(g1)CGGGCTGTGTCGGTGTATGGCCAATGGCAGGACCTPSMC1(Rpt2)CATGGCCACAAACCGAATATCAGGCAGGGGGAACTCPSMC2(Rpt1)TGGGATTGGCTGGGAAGACGTGCCAGAACCACCCACACAPSMC3(Rp5)GCCCACGGGAAGAACGACGCACAGCCACACACACACACACACACACACACACA	PSMA1 (α6)	CCAGGGCAGGATTCATCA	TCTGATTGCGCCCTTTTC
PSMA3(07)TGTTGATCGGCATGTTGGTGGCCACTGTGTCTGCAAPSMA4(03)CATTGGCTGGGATAAGCAATGCATGGGCCTTCCATPSMA5(05)CTTCAQAGGGTGCCCAGACAGCGTGCCACGATGACCACACACAPSMA7(04)AGTCAGTGCGCGAGATCCCTGCCACCTGACTGACCACAGGPSMB1(06)CATGCTACAGCCCTGCTCCAGTGCCAGGTGCCAPSMB2(04)CTTCACACGCCGAAACCTAGGCTGCCAGGTAGGTCAPSMB3(03)TGGTGGCCAACTCTTGTGGCACCCGAGAGGTTAPSMB4(07)TCTCGGCCAAGTGGTGATCCAATGACCAAGGACTGPSMB5(05)CCATGGCGCACATACTCCCAATGGCAACCTTPSMB5(01)CTGAGGCGGACCATACTCCCAATGGCAACCTTPSMB7(02)CGGCTGGTGCGGGTATAGCCAGTTTCCGGACCAAGGGPSMD7(RPI2)CGGCTGGTGCGGAATCATCCCAATGGCAACCCCTTTPSMC1(Rp12)CAGGCCACCAAACCGAATATCAGGCAGGGGGAACTCPSMC3(Rp15)GCCCACGGGACGAAGAGCATCCAAGCACCCCATTAGPSMC4(Rp15)GGAAGACCATGTTGGCAAAGAGGCGACATCAAGGCPSMC3(Rp16)CTCCAGGGCAGTGAAGCGTGCCACAACCCACAACAPSMC3(Rp16)GCCCAGGGACGACACCAAGGCGACATCAAGGCGATTPSMC4(Rp13)GGGAGGTGGAGGACACAAGGCGACATCAAGGCGATTPSMC3(Rp14)CGCAGGCGGTGAAGGCACCCAAAACCCACACAPSMD3(Rpn3)GCTGTGCAGGCGTGTATCCCTGCGGCACACTGAGGTGTPSMD3(Rpn3)GCTGTGCAGGCGTGTACACCCCCAGGCACACGCAAPSMD1(Rpn10)CGGGAGGCGCAGACAGAGCCCACGCGGTAAAPSMD1(Rpn13)CCCCTCGTGGCAGGCGTCCCCGGGCGGGAGGCCCCTTGPSMD1(Rpn13)CCCCCCGGGGGAGGCGCACAGGGCCCACAGCGGTGAAPSMD2(Rpn14)CGCCCCAGGGGGAGACAGGGCCCACAGCCGCTTAG <td>PSMA2 (α2)</td> <td>GCCCCGATTACAGAGTGC</td> <td>TGGACGAACACCACCTGA</td>	PSMA2 (α2)	GCCCCGATTACAGAGTGC	TGGACGAACACCACCTGA
PSMA4 (c3)CATTEGCTGGGATAAGCAATECATETGGCTTCCATPSMA5 (c4)CTTCAGAGGGTGCCCTACACAGGCTGCACTGGCCTAPSMA6 (c4)AGCAGGTGGCCTTACACCGGTCATCACACCACPSMA7 (c4)AGTCAGTGCGCGAGTTCCTGCCACCTGACTGACCACPSMB1 (j6)CATGCTACAGCCCTGTCTGCATGCTCCAGTGATCCAPSMB2 (j4)CTTCACACGCCGAACCTAGGCTGCCAGTGATGCAPSMB3 (j5)TGTGGCCAACCTCTTGTGGCAGCCGAAAGCTPSMB4 (j7)TCTCGGCCAGTGATCCCAATGACGCCCTAAATPSMB5 (j5)CCATGGCCACATGATCTCAATGACGAAGCTPSMB5 (j5)CCATGGCCACAACCGAATTTGGGCAGCATGCPSMB5 (j6)CGCTGTGTGCGCGAATTTGGGCACCATCAPSMB7 (j2)CGGCTGTGCGCGAATTTGGGCTGCCGAATCAPSMC2 (Rpt1)TGGGATTGGCAGAATTTGGGCACCATCAPSMC3 (Rpt5)GCCACGGAGCATACAGCCATGCCATAACAACAGCPSMC4 (Rpt3)GGAAGACCATGTGGCAGACATGCCATACAAACAGCPSMC5 (Rpt4)GCCAGGGCCACAGCACACGCCACGCACAACCACACAPSMD2 (Rpn3)GCTGTGCAGGACACCTCCCCACGGCCACACACACACPSMD3 (Rpn3)GCTGTGCAGGCCACACGCCTGCCCACGCCACGTCATTPSMD4 (Rpn10)CGGCAGGCCGCAGTCCTCCCCCCCAGGCCACCATPSMD7 (Rpn8)ATGCTGCGCGGAGCAGCAACCCCCAAAGCCCCACACCACAPSMD8 (Rpn12)CCCACGGGGCAGCAGCAGCGTGCCCCGGAAGCACACCCACACACACCACACACACAC	PSMA3 (α7)	TGTTGATCGGCATGTTGG	TGGCCACTCTGTCTGCAA
PSMA6 (#5)CTTCAGAGGGTGCCCAGACAGGCTGCACTGTGGCTAPSMA7 (#1)AACCAGGTGGCCTTACACCGGTCATCACACACACAPSMA7 (#4)AGTCAGTGCCGAGTTCCTGCCACCGCGTGACCAPSMB2 (#4)CTTCACAGCCCGAGTACTGGCTGCCAGGTAGGTCTAPSMB3 (#5)TGGTGGCCACCTTGTTGGCAGCCCAGGTAGGTCTAPSMB3 (#7)TCTCGGCCACGTGTATCACATTACCGAGGAGCTPSMB5 (#5)CCATGGCACCTGTGTGAAGGTGGCCCCTGAAATPSMB6 (#7)CTGGGCGCAGTGTATGGCCAGTGCCCGGACTGCPSMB5 (#5)CCATGGCCACATACCCACCATGGCCCCTGAAATPSMB5 (#1)CTGATGGCGGAATCACCCATGGCACATACGGAPSMB7 (#2)CATGGCCACATACGGAATATCAGGCAGGGGGAACTCPSMC1 (Rpl2)CATGGCCACAAACCGAATATCAGGCAGGGGGAACTCPSMC3 (Rpl5)GCCCACGGGCAATACAGCATGCGCACGAACGACACCCCTTTGGPSMC3 (Rpl5)GCCCACGGGGGAAGACGTGCCACGACGCACTGGPSMC4 (Rpl4)GGCAGATCGTGGGTGAAGCGGCCACTGCAAACACACPSMC5 (Rpl6)CTCCAGGCCACGGGGGAAGACGTGCCACCACACACACPSMC6 (Rpl4)GGCAGATCGTGGGTGAAGCGGCGCCACACACACACCACACAPSMD1 (Rpn2)ATTCTAGGAGCCACGCAGGAGCCCCACACACACACACPSMD2 (Rpn1)CCCACGGGCCACCAGACCCCCAAAGCTGCTTPSMD3 (Rpn3)GCTGTGCAGCGCAGCAGGGGAGGTCTCCCCCACACACACAPSMD1 (Rpn4)GCCACCGGCAGCAGACAGGGAGGTCTCCCCCGGTAATPSMD1 (Rpn7)GCAAAGGCCGAGTCAGGCCTCCCCCAGCACACTGGPSMD1 (Rpn7)GCAAAGCCCCGCAGCAGCGCCTCCCCCAGCACACTGGPSMD1 (Rpn7)GCCAACGCCGCAGTCCTCTGCCCACCCGGAGCACACAGPSMD1 (Rpn7)GCCACCGCGCAGCAGCAG	PSMA4 (α3)	CATTGGCTGGGATAAGCA	ATGCATGTGGCCTTCCAT
PSMA6 (a1)AACCAGGGTGGCCTTACACCGGTCATCACACACACCAPSMA7 (a4)AGTCAGTGGCCGAGTCCTGCCACCTGACTGAACCAPSMB1 (b6)CATGCTACAGCCCCTGCTGCAGCTGCACGGGAAGCAPSMB2 (b4)CTTCACAGCCCCTGATAGGCTGCCAGGGAGTCAPSMB3 (b7)TGCTGGCCAACCTCTTGTGCACGCCGAGAGGCATPSMB4 (b7)TCTGGGCCAGCATGATCTCACATACCGAGGAAGCTCPSMB5 (b5)CCATGGCGCACATGATCTCCAATGGCAAAGGACTGCPSMB5 (b1)CTGATGGCGACATGATCATCCCAATGGCAAAGGACTCPSMC1 (Rpl2)CATGGCCACAAACCGAATATCAGGCAAGGGGGAACTCPSMC2 (Rpl1)TGGGATTGGCTGCAGATTTCAGGCAGGGGGGAACTCPSMC3 (Rpl5)GCCACGGAGCATACAGCATGAGCAAGGGGGGATCTPSMC4 (Rpl2)ATGTCAGGAGGGCATGTGGGTGAAGCGGCAGCACTGAGGAGTGGTPSMC5 (Rpl6)CTCCAGGCACTGGGGAAGCGGCAACACCCACAACCPSMD1 (Rpn2)ATGTCAGGAGGCCAGGAAGCCGAAACCGCACATGPSMD2 (Rpn1)CGCAAGTGCTGGGTGAAGCGGCAAAGCTGCATTPSMD3 (Rpn3)GCTGTGCAGGCCGAGTGGAGCCGCAAACCTCACACPSMD3 (Rpn3)GCTGGCAGGCAGCAGGGACCCCAAAGCACCCAAACCCPSMD4 (Rpn12)CACCGGGATGCTGGCTGCCCCGAGGGCAGCAGGPSMD1 (Rpn8)GCTGGCAGGCAGACGGGGCCTCTGCGCAAACCCCAAAPSMD1 (Rpn8)ATCCAGGGGGAGCAGGGCCCTCCGCAAAGCACCCAAAPSMD1 (Rpn8)ATCCAGGGGGAGCAGGGCCCTCCACACGGCGTATTPSMD1 (Rpn9)ATCCTGCGGGAGCAGGGAAGCCCCCACAGGGAGACCTPSMD1 (Rpn13)CCCCCCAGGTGCAGGGGGAGCCGGCCACACAGCGCGGTAAGPSMD1 (Rpn14)CCGCGGGGGGGGGGGGGGGGGCCCCGACAGGGCGGTACAGPSME1 (PA22) <td< td=""><td>PSMA5 (α5)</td><td>CTTCAGAGGGTGCCCAGA</td><td>CAGGCTGCACTGTGGCTA</td></td<>	PSMA5 (α5)	CTTCAGAGGGTGCCCAGA	CAGGCTGCACTGTGGCTA
PSMA7 (w4)AGTCAGTGCGCGAGTTCCTGCCACCTGACTGAACCAPSMB1 (j6)CATGCTACAGCCCTGTCGCATGCTCTGTCCAAGGPSMB2 (j4)CTTCACACGCCGAAACCTAGGCTGCACGATGATGCAPSMB3 (j3)TGGTGCCAACTCTTGTGCACTGCCAGATGATCAPSMB4 (j7)TCTCGGCCAACTGATCACACATTACCCAGAGAAGCTPSMB5 (j5)CCATGGCCACTGATCACCACTGGCCAAGATTPSMB5 (j1)CTGATGCGCGGAATCATCCCAATGGCAACGACTGCPSMB7 (j2)CGGCTGTGCGGTGTATGGCCAGTTTCCGGACCTTPSMC1 (Rpt2)CATGGCCACAACCCGAATATCAGGCAGGGGGAACTCAPSMC2 (Rpt3)GCGAGACCATGTGGCAGAATTTGGGTCCTCGGAATCAPSMC3 (Rpt5)GCCCACGGAGAATACAGCATCAGCACAACCCACAACPSMC4 (Rpt8)GGAAGCCATGTGGGAAGACGGCCACTGAGCAAACGCPSMC5 (Rpt6)CTCCAGGCATGGGAGAGACGGCCACTGAGCAACACCACAACAPSMD3 (Rpt3)GCTGTCGCGGCAAGACGGCGCACTGTGTPSMD3 (Rpt1)CCGAGATGCTGCTGATGACCTGGCCCAAAACCTGCTPSMD4 (Rpt10)CGGGATTCTACCACTGGCASTGCGCCCAAAACTGTPSMD6 (Rpt7)GCCACGCGGAGCAGAGAGCAGCTCGCCGGAAACTGTPSMD7 (Rpn8)CCTGCCGCGTCCTTTCGCTGGCGTGCACAAACTGTPSMD1 (Rpn6)ATGCCTGCGGTCACACATACCCCAGGGGGCACCTTTPSMD1 (Rpn12)CCACCCGGAGCAGACGGCAGCCCTGGCCAAAACTGTPSMD1 (Rpn5)TCCAAAGCCCGGTAGCGCCTCGCGTGCCAAAACTGTPSMD1 (Rpn6)ATGCCTGCGGTTCCTGGCGCACACGGGGCCCTTTCCPSMD1 (Rpn13)CCCCTCCTGGGTGAGCAGGGACCTTGCCCAGAGGCCCGTAACCPSME1 (PA28a)CATCCCAGGCGGTAGAGGGCCTCCCACGAGGAGCCCTTTPSME2 (PA22)CGGGAGGCAG	PSMA6 (α1)	AACCAGGGTGGCCTTACA	CCGGTCATCACAAACCA
PSMB1 (βB)CATGCTACAGCCCCTGCTGCATGGCTCTGTCCAAGGPSMB2 (β4)CTTCACACGCCGAAACCTAGGCTGCCAGTAGCGTAAPSMB3 (β3)TGGTGGCCACTGTGTGCAGCCGATGAGGTCTAPSMB4 (β7)TCTCGGCCACATGGTGATCACATAACCGAGAACCTPSMB5 (β5)CCATGGCCACAATCATCCCAATGGCAGGACCATGATPSMB5 (β2)CGGCTGTGTGGGATATACACCCAGTGCCCGAAATCAPSMC1 (Rpt2)CATGGCCACAAACCGAATATCAGGCAGGGGAACTCPSMC2 (Rpt1)TGGAGCTGTGTGGGATACAGCATCAGCACCCCTTTTGGPSMC3 (Rpt5)GCCACGAGGCAATACAGCATCAGCACCCCCTTTGGPSMC5 (Rpt6)GCCACGAGGGGGAAGACGTGCCATGACAACAGCPSMC6 (Rpt4)GGCAGATCGTGGGTGAAGCGCGCACTGAGGACAACAGCPSMC6 (Rpt4)GCCAGGCCTGATGACCTTGGCCAAAACAGCPSMC5 (Rpt6)CTCCAGGCACTGGGGAAGACGTGCCACTGAGGGTTGTPSMD2 (Rpn1)CCCAAGGGCCTGATGACCAGCGACACCCCAACACAPSMD2 (Rpn1)CCCAAGGGCCAGTACTACCCCAGAGCCACACACAPSMD3 (Rpn3)GCTGTGCAGGGCAGACACGGAGGCCCACACACCAPSMD4 (Rpn10)CGGGAGGCCAGACACGGGACGCCCCCAAACTGTPSMD7 (Rpn8)GCTGGCAGGCACACAGGGACCTCTCCCCCGTAATPSMD8 (Rpn12)CCACCCGGGGCAACACGGGACCACCCCCCGGTGCAAACTGTPSMD14 (Rpn13)CCCCTCATGTGCCAGTGGCCCACACAGCACCPSMD14 (Rpn13)CCCTCATGTGCCAGTGGCCCACACAGGGTGCATGAGPSME2 (PA28µ)CAACCACGCGGGTGAGAAAGCCACCCCCGCTTCPSME2 (PA28µ)CGACAACACGCGGGAGACACAGGGGCCTTGCCTTGGPSME3 (PA24)CGACCACCAGGGTGCAGAGATCACCCACACGGGCTGCAAAPSME3 (PA24)CGACCACCACGGGTTG	PSMA7 (α4)	AGTCAGTGCGCGAGTTCC	TGCCACCTGACTGAACCA
PSMB2 (β4)CTTCACACGCCGAAACCTAGGCTGCCAGGTAGTCCAPSMB3 (β3)TGGTGGCCAACTCTTGTGCCAGCCGATGAGTCTAPSMB4 (β7)TCGGGCCACATGATCTGAAGGTGGCCCTGAAATPSMB5 (β1)CTGATGGCGGGATCATCCCATGGCCAGACTGCPSMB7 (β2)CGGCTGTGTGGGTGTATGGCCAGTTTCCGGACCTTPSMC1 (Rpt2)CATGGCCACAACCGAATATCAGGCAGGGGAACTCPSMC2 (Rpt1)TGGGATTGGCTGCAGAATTTTGGGTCCTCCGAATCAPSMC3 (Rpt5)GCCCACGAGCAATACAGCATCAGCACGGGGCATTPSMC3 (Rpt5)GCCCACGGAGCAATACAGCATCAGCACGGGGCATTPSMC4 (Rp13)GGAAGACCATGTGGGAAGACGTGCCATAACAACAGCPSMC5 (Rpt6)CTCCAGGCACTGGGTGAAGCGTGCCATAACAACAGCPSMC5 (Rpt7)GCCAAGGCGCAGCAGAGGCGCACTGACGAACGCAPSMD2 (Rpn1)CCCCAGGGCCTGATGACCTGGCCAAAACGGCACACTTPSMD3 (Rpn3)GCTGTGCAGGGCTTCTCGGTGCGCGCAAACTGTPSMD4 (Rpn10)CGGGATGCTCACGAGGTACCCCAAAAGCGCACACAAPSMD5 (Rpn8)GCTGGCAGGGCAGCAGGGACCCCCCCGAAACTGTPSMD7 (Rpn8)GCTGGCAGGGCAGCAGCAGGAGCTCTCCCCGGTAATPSMD1 (Rpn6)ATCCAGGGGGGAGCAGAGGCCCTCACCCCGAAACTGTPSMD1 (Rpn13)CCCTCATGTCCCAGTTCGCCCCCACAGGGTAATPSMD1 (Rpn13)CCCTCCTGGGTGGAGGTCCCCGGAGGAGCACACCPSME1 (PA28n)CATCCCGGGTGGAGGTCCCCGGAGGAGCACACCPSME2 (PA28)CACCCCACACGGGGAGGAGTGGGCCACACACCACCACCPSME2 (PA28)CGCCAACAGGGGGAGGAGTACCTTCACACACCGGGAGCACACCPSME3 (PA29)CGCAACAAGGCGGTAGATGGGCTGCTGCAGGACACCPSME4 (PA28n)CATCCTGGGTGTCCCTG	PSMB1 (β6)	CATGCTACAGCCCCTGCT	GCATGGCTCTGTCCAAGG
PSMB3 (β3)TGGTGGCCAACTCTTGTGGCAGCCGATGAGGTCTAPSMB4 (β7)TCTCGGCCACATGTGTATCACATAACCGAGGAGCTPSMB5 (β5)CCATGGCACCATGATCTGAAGGTGGCCCTGAAATPSMB5 (β1)CTGATGGCGGGAATCATCCCAATGGCAAAGGACTGCPSMB7 (β2)CGGCTGTGTCGGTGTATGGCCAGTTTCCGGACCTTPSMC2 (Rpt)TGGGATGCGCGCACAACGATCAGGCAGGGGAATCAPSMC3 (Rptb)GCCACGGAGCAATACAGCATCAGCACCCCTTTTGGPSMC4 (Rpt3)GGAAGACCATGTTGGCAAAGAAGATGATGGCAGGTGCATTPSMC5 (Rptb)CTCCAGGCACTGGGGAAGCGTGCCATGACAAACACPSMC6 (Rpt4)GGCAGATCGTGGGTGAAGCGGCCACCACGACACACPSMD1 (Rpn2)ATGTCAGGAGGCCAGCAGAGGCGCACATGAGGGTTGTPSMD2 (Rpn1)CCCAAGGTGCTGATGACCTTGGCCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTTCTCGGTGTGCAGGCCAACCCAAPSMD4 (Rpn10)CGGGATGCTAGAGGCTACCCCAAAGCCACACAAPSMD6 (Rpn7)GCCAAGGCGGATACCTACCCCAAGGCCACACCAAPSMD7 (Rpn8)GCTGGCAGTGCAGAAGGTACCCCAAAGCCACACAAPSMD1 (Rpn7)TCCAAAGGCGGAGTCAGGCCTTGGCTGCACACACCAAPSMD1 (Rpn8)ATGCTGCGGTTTTGGCTGGCAGTCAGPSMD1 (Rpn11)CCGTGCTGGCAGTCAGGCCCCCCGGTAATPSMD13 (Rpn9)ATGCTCTGCGGTTTTGGCGGACGCAGTGTAGGPSME1 (PA280)CATCCCAGTGCCGTGAGATGCGTGGCACACCACCAAPSME1 (PA280)CATCCCAGTGCCGTGAGAGTCCCCACAGGGAGTCAPSME1 (PA280)GCCCAACACAGGGGTGTGGCCAAGAGCCAAACCACCPSME1 (PA280)GCACAAACAGCGCGTGTACACATGGGCATGGCAGTAGAAPSME3 (PA28)CTCCTGTGTGCGCGTTTCT <t< td=""><td>PSMB2 (β4)</td><td>CTTCACACGCCGAAACCT</td><td>AGGCTGCCAGGTAGTCCA</td></t<>	PSMB2 (β4)	CTTCACACGCCGAAACCT	AGGCTGCCAGGTAGTCCA
PSMB4 (β7)TCTCGGCCAGATGGTGATCACATAACCGAGAGACTPSMB5 (β5)CCATGGCACCATGATCTGAAGGTGGCCCCTGAAATPSMB5 (β1)CTGGTGGCGGATCATCCCAATGGCAAAGGACTGCPSMB7 (β2)CGGCTGTGTGGGTGTATGGCCAGTTTCCGGACCTTPSMC1 (Rp12)CATGGCCACAAACCGAATATCAGGCAGGGGGAACTCPSMC3 (Rp15)GCCCACGGAGCATACAGCATCAGCACCCCTTTGGPSMC4 (Rp13)GGAAGACCATGTGGCAAAGAGATGATGGCAGGTGCATTPSMC5 (Rp14)GGCAGCATGGGGAGAGCGGCCACCACAACACAPSMD5 (Rp14)GGCAGATCGTGGGTGAAGCGACGACCCACAACACAPSMD2 (Rp11)CCCAAGGGCCTGATGACCTGGCCAAAGCGCCACTPSMD3 (Rp13)GCTGTCGCAGGGCTCATCTGGTGTGCGCGCAAACCCCACAACAPSMD3 (Rp13)GCTGTCGCAGGCCTGATGACCTGGCCAAAGCGCACACTPSMD4 (Rp10)CGGGATTGCTACGACTGGCAGTGGCGCAAACTCTPSMD5 (Rp12)CCACCCGGATCCTTCTGCTGGCGCAAACCTGTPSMD1 (Rpn3)GCTGCCGCAGGCAGACAGGGACCCTGCCCGGTAATPSMD1 (Rpn5)TCCAAAGGCGAGGCAGACAGGGACCCTGCCCGGTAATPSMD1 (Rpn6)ATGCAGGGAGGCAGACAGGCCTCGCCCCACACTGAPSMD11 (Rpn5)GCAAAAGCAGCCGGTGAGGCCTCACCGGCACACCTPSMD12 (Rpn5)CCCCCACTGGCTCATCTGCCCCACACGGAGCACAGPSMD13 (Rpn9)ATGCTCGCGCTCATCATGGCCCACACGGGAGCACAGPSMD14 (Rpn13)CCCCCCACTGGCTCATCATGGCCCACACGGGAGCACAGPSME1 (Rp15)GAAAAGCACCCGGTGTCCCGGGAGGAGACAGPSME2 (PA28)CACCCCACGGGTGTACCATGGCCACAGGAGCACAAAPSMG2 (PAC2)CCGGGAGGGGGAGACAGGGCCCCCCCTTCTPSME2 (PA28)CACCCCGCGGGGGGAGA	PSMB3 (β3)	TGGTGGCCAACCTCTTGT	GGCAGCCGATGAGGTCTA
PSMB5 (β5)CCATGGCACCATGATCTGAAGGTGGCCCCTGAAATPSMB6 (β1)CTGATGGCGGAATCATCCCAATGGCAAAGGACTGCPSMB7 (β2)CGGCGTGTCGGTGATGGCCAGTTTCCGGACCTPSMC1 (Rpt2)CATGGCCACAAACCGAATATCAGGCAGGGGGAACTCPSMC2 (Rpt1)TGGATTTGGCTGCAGATTTTGGGTCCCCGAATCAPSMC3 (Rpb5)GCCACGGAGCAATACAGCATCAGCACCCCTTTTGGPSMC4 (Rpt3)GGAAGACCATGTGGCAAAGCGTGCCATGACAAACAGCPSMC5 (Rpt4)GCCAGGACGTGGGGGAAGCGGCCCACGACAACCACACACAPSMD5 (Rpn4)GGCAGATCGTGGGTGAAGCGTGCCATGACAAACCACCACAACAPSMD3 (Rpn3)GCTGTCCAGGCCTGATGACCTTGGCCAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGCTTCTCGGTGTCGACGCACACACCACAPSMD3 (Rpn3)GCTGTGCAGGCTGCTTCTGCTGCGAGCCCAAACCCACAPSMD4 (Rpn10)CGGGATTGCTACGACTGGCAGTGCGGCACAACCCAAPSMD8 (Rpn12)CCACCCGGATCCTTCTGCTGGCGGCACAACTGTPSMD9 (Rpn8)GCTGGCAGGCGCAGACAGGGACCTTGCCAGACCACACTGTPSMD1 (Rpn8)ATCCACGGGAGTCAAGCCTCCGGTAACCATTCGPSMD1 (Rpn8)ATCCATCGCGTTTTCGGCGCACACGGCCCCATGACPSMD1 (Rpn8)ATCCCTCGCGTTTTGGCACCACAGGGCGAAGTCAGAPSMD1 (Rpn13)CCCCCCAATGCCCGATGAAAGCCAGCCCGCCTTGCPSME2 (PA28 ₁)CACCCCAGGCGTAGACACCACAGGGAGAGTCAAAPSME2 (PA28 ₁)CACCCCTGCTGTCTGTGGGCACAGAGCCCAAAPSME3 (PA28 ₁)CACCCCCAGGGAGTACACATGGGCAGGAGAGCAAAAPSMG2 (PAC2)CCGGAGAGGCGCGATAAGGTCACCACACCACACCACACPSMG4 (PAC4)CGGACACCCCAGCGTTTCGTTGGGCAGGCAGAAGGCAAAAPSMG2	PSMB4 (β7)	TCTCGGCCAGATGGTGAT	CACATAACCGAGGAAGCT
PSMB6 (β1)CTGATGGCGGGAATCATCCCAATGGCAAAGGACTGCPSMB7 (β2)CGGGCTGTGCGGTGTATGGCCAGTTTTCCGGACCTTPSMC1 (Rpt2)CATGGCCACAAACCGAATATCAGGCAGGGGAACTCPSMC2 (Rpt1)TGGGATTTGGCTGCAGATTTTGGGTCCCCGGAATCAPSMC3 (Rpt5)GCCACGGAGCAATACAGCATCAGCACCCCTTTTGGPSMC4 (Rpt3)GGAAGACCATGTTGGCAAAGAGATGATGGCAGGTGCATTPSMC5 (Rpt6)CTCCAGGCACTGGGAGAGCGACGACACCACACACACPSMC6 (Rpt4)GGCAGACTGGGGGGAAGCGACGACACCACACACACPSMD1 (Rpn2)ATGTCAGGAGGCCTGATGACCTTGGCCAAAAGCTGCATPSMD2 (Rpn1)CCCAAGGTGCTGATGACCTTGGCCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTCTTCGGTGTCGACGCAAGCTTTTPSMD4 (Rpn10)CGGGATGCACGAGGTACCTACCCCAAAACCACACACAPSMD6 (Rpn7)GGCAAAGGCCGAGTACCTACCCCAAAACCACACACAAPSMD7 (Rpn8)GCTGGCAGTGCAGAAGGTGCCTGGCTGGCAAAACTGTPSMD1 (Rpn8)ATGCCTGCGGATTCTTTGGCTGGCTGGCAAAACTGTPSMD1 (Rpn8)ATGCCTGCGGATTCCTTTTGGCTGGCTGGAAACCATTGPSMD1 (Rpn8)ATGCCTGCGGGTTCCAATTGCCTCCACACTGACACPSMD1 (Rpn13)CCCCTCATGGCCAGTTCTTCGTGTGCGCCTTTTCPSME1 (Rpn15)GAAAAGCACCCGGTAGAAAGCCACCCAGGGAGACCAAAPSME2 (PA28)CGCAAACAGGTGCAGGTTCCCCGAGGGAAGTCAAAPSME3 (PA28)CGCAACCACCGGGTTTCCGCGCGAGAGGCAAAAPSME3 (PA28)CGCAACCACCGGGTTTCCTTTCGGGGGCCAGAAGGCCAAAPSMG3 (PAC3)GTCTTCTGGGGCAGGATTTCACCACGCGGAGAGCAAAPSMG4 (PAC4)CGGCAGCCGGGGGAGTCCACATGGGGCTGTGGTGGCAGAAPSMG3	PSMB5 (β5)	CCATGGGCACCATGATCT	GAAGGTGGCCCCTGAAAT
PSMB7 (β2)CGGCTGTGCCGGTGTATGGCCAGTTTCCGGACCTTPSMC1 (Rpt2)CATGGCCACAAACCGAATATCAGGCAGGGGAACTCPSMC2 (Rpt1)TGGGATTGGCTGCAGATTTTGGTCCTCCGAATCAPSMC3 (Rpt6)GCCACGGACCATACAGCATCAGCACCCCTTTTGGPSMC4 (Rpt3)GGAAGACCATGTGGCAAAGAAGATGATGGCAAGCAACACACPSMC5 (Rpt6)CTCCAGGCACTGGGAAGACGTGCCATGACAAACAGCPSMC6 (Rpt4)GCCAGTCGTGGTGAAGCGACCACAGAGGGTTGTPSMD2 (Rpn2)ATGTCAGGAGGGCAGCAGAGCGCACATGAGGGTTGTPSMD3 (Rpn3)GCTGTGCAGGGCTTCTTCGGTGTCGACGCCAACTCTTPSMD4 (Rpn10)CGGCATGCTGCAGGGTACTACCCGAAAGCCACACCAAPSMD7 (Rpn8)GCTGCCAGGAGTACCTACCCCAAAGCCACCAAPSMD7 (Rpn8)GCTGCCAGGAGCAGGAGCAGGGAGCTCTGCCCGGTAATPSMD7 (Rpn8)GCTGCCAGGAGGCAGCAGGCAGCTCTGCCCGGTAACTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGCAGCTCTGCCCCGGTAACTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGCAGCCCCACAGGGAGAGCPSMD11 (Rpn13)CCCTCCATGTGCCAGTTCTTCGTGTGCCCCTTTCPSME2 (PA28))CGCAAACGGCGAGGCAGGCCACAGGGGAGGCAGTPSME1 (PA28))CGCAACGGCGGTAGAAAGCCACCCCAGCAGAGTPSME2 (PA28))CGCAACACCCAGCGATTGGGCACAGGCCATAGAGPSME2 (PA28))CGCAACACCCAGCGGTTGCCCCACAGCAGAGTCAAAPSMG2 (PAC2)CCGGAGGAGGCAGAGAGTTCACCACACACCCAAAPSMG4 (PAC4)CGGACTGCTGTCTGTGGGACGTGTGGCAGAAPSMG4 (PAC4)CGGACTGCCGTGTCCTTCTGGGCTGTGTGCCCTTCPSMG4 (PAC4)CGGACTGCCGGGAGAAGAGTCACCCCAGAGGCAGAAAGPSMG4 (PAC4)C	PSMB6 (β1)	CTGATGGCGGGAATCATC	CCAATGGCAAAGGACTGC
PSMC1 (Rpl2)CATGGCCACAAACCGAATATCAGGCAGGGGAACTCPSMC2 (Rpt1)TGGGATTGGCTGCAGATTTTGGGTCCTCCGAATCAPSMC3 (Rpt5)GCCCACGGAGCAATACAGCATCAGCACCCCCTTTTGGPSMC4 (Rpt3)GGAAGACCATGTTGGCAAAGAAGATGATGGCAAGGCGCATTPSMC5 (Rpt4)GCCAGCACTGGGGTGAAGCGTGCCATGACAAACAGCPSMC5 (Rpt4)GCCAGCCCCGATGAGCACCAGAGCGCCCATGACGACACGCPSMD2 (Rpn1)CCCAAGGGCCTCGTGGAGCGCCACATGAGGGTTGTPSMD3 (Rpn3)GCTGTCAGGGCTTCTCGGTGTCGACGCAGCAGCAGPSMD4 (Rpn10)CGGGATGCTACGACGGCCACTGCGCCCAAACCCAAPSMD6 (Rpn7)GCCAGCCAGTGCACGAGCAGCACCCCCAAAAGCCCAAPSMD7 (Rpn8)GCTGGCAGTGCACAAGGTACCCCAAAAGCCCAAACCTGTPSMD7 (Rpn8)GCTGCCAGTGCACAAAGGTACCCCAAAAGCCCAAACCTGTPSMD11 (Rpn6)ATGCAGGAGGCAGACAGGGAGCTCTGGCACAAACCTGPSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD14 (Rpn11)CCGTGCTGGGAGTCCAATTGCCTCCACACTGACCCPSME1 (Rpn13)CCCCCCTGTGCCGGTGAAAGCCCACGGAGAGCACAGPSME2 (PA28µ)CGCAAACAGGTGGAGGTCCCCGGAGGAGACCAAAPSME2 (PA28µ)CGCAAACAGGTGGAGGTCCCCGGAGGAGACCAAAPSME2 (PA28µ)CACCCCCAGCCATGATTGGCACAGAGAGCCCAAAPSMG3 (PAC3)GTCTTCTGGGGCAGTATTGGCACAGAAGACCCAAAPSMG4 (PAC4)CGACCCCCCGGCGATGATGGGCAGTGGAGACAAPSMG3 (PAC3)GTCTTCTGGGGCAGGATTCACCACCCCAGGCAAAPSMG3 (PAC3)GTCTTCTGGGAGCAGAAAGATGGGCTGTGAGAAAGCAAPSMG3 (PAC3)GTCTTCTGGGGCAGGATATGGGCCCATGCCTTGAGAGCAAA	PSMB7 (β2)	CGGCTGTGTCGGTGTATG	GCCAGTTTTCCGGACCTT
PSMC2 (Rpl1)TGGGATTTGGCTGCAGATTTTGGGTCCTCGAATCAPSMC3 (Rpl5)GCCCACGGAGCAATACAGCATCAGCACCCCTTTTGGPSMC4 (Rpl3)GGAAGACCATGTTGGCAAGGAAGATGATGGCAGGGTGATTPSMC5 (Rpl6)CTCCAGGCACTGGGAAGACGACGCACAGCACAACAACAPSMD1 (Rpn2)ATGTCAGGAGGCAGCAGAGCGCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTGATGACCTTGGCCAAAAGCTGCATPSMD4 (Rpn10)CGGGATGCTACGACGAGCACAGCACCCAGGGCCAAAAGCTGCATPSMD5 (Rpn3)GCTGTGCAGGCAGAGCAACCCAGGGCCAAAAGCTGCTPSMD6 (Rpn10)CGGGATGCACAGCAGCAGCAACCCCAGGGCCAAAAGCACCCAAPSMD7 (Rpn8)GCTGGCAGTGCAGAGAGGTACCCCAGGACACCACAPSMD7 (Rpn8)GCTGGCAGTGCAGAAGGTACCCCAGAGCACCCAAPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn13)CCCCTCATGCGGATTTGGCAGCACAGCCCACTGGPSMD14 (Rpn13)CCCTCATGTCCCAGTTCTTCGTGTGCCCCTTTCSHFM1 (Rpn15)GAAAAAGCAGCCGGTAGAAAGCCAGCCCAGGGTCAAGPSME1 (PA28α)CATCCCAGTGCCTGATCCGCCACAGGAGGACAAGTPSME2 (PA28)CGCAACAAGGTGGAGGTCCCCGGAGGAGCAAGTPSME2 (PA28)CGCAACAAGGTGGAGGTCCCGGAAGGCCAAAPSMG2 (PAC2)CGGGAGGAGGATCACAGGGCCCAAAAGGTCCCAAAPSMG2 (PAC2)CGGGAGGAGGATCACAGGGACTGCAGGAGGAGAGTPSMG2 (PAC2)CGGGAGGAGGATCACAGGGCCCAGAAGGCCAAAPSMG2 (PAC2)CGGGAGGAGGATCACAGGGCCCAGAAGGCCAAAPSMG4 (PAC4)CGACTCGCTGTTCCTTTGGGCAGTGAGAGPSMG4 (PAC4)CGACTCGCGGAGAGATTCACCACACGCCGAGAAAPSMG4 (PAC4)<	PSMC1 (Rpt2)	CATGGCCACAAACCGAAT	ATCAGGCAGGGGGAACTC
PSMC3 (Rpl5)GCCACGGAGCAATACAGCATCAGCACCCCTTTTGGPSMC4 (Rpt3)GGAAGACCATGTTGGCAAAGAAGATGATGGCAGGTGCATTPSMC5 (Rpl6)CTCCAGGCATGGGAAGACGTGCCATGACAAACAGCPSMD6 (Rpl4)GGCAGATCGTGGGTGAAGCGACGACAACCCACAACAPSMD1 (Rp12)ATGTCAGGAGGGCAGCAGAGCGCAATGAGGGTTGTPSMD2 (Rpn1)CCCAAGGTGCCTGATGACCTTGGCCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTTCTTCGGTGTCGACGCGCACAAGCTTTPSMD6 (Rpn10)CGGGATGCTACGACTGGCACTGCGCGCCAAAAGCTCTPSMD6 (Rpn12)CCACCCGGATCCTCTCTGCTGGCAGGCCAAACTGTPSMD7 (Rpn8)GCTGGCAGTGCAGAGAGGTACCCCAAAGCACACCAAPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCGGTAATPSMD12 (Rpn5)TCCAAAAGCAGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTGGCAGCACAGGGTGCACCAPSMD14 (Rpn13)CCGTGCTGGAGTTCCAATTGCTTGCGCCCTTTCSHFM1 (Rpn15)GAAAAAGCAGCCGGTAGAAAGCCAGCCCAGGTCAGGTPSME1 (PA28α)CGCAAACAGTGGAGGTCCCCGGAGGAGCAAAGTPSME2 (PA28)CGCAAACAGGTGGAGGTCCCCGGAGGAGGCAGTTPSME2 (PA28)CGCAAACAGCGGAGTATGGCACGAAGGCTCAAAPSMG2 (PAC2)CGGGAGGAGTATCACATGGGATGTGCCCTTCPSMG2 (PAC2)CGGGAGGAGGTATCACATGGGATGTGGCAGAAGPSMG2 (PAC2)CGGGAGGCGAGGAGTTCACCACACGTGGCAAAPSMG2 (PAC2)CGGGAGGCGAGGAGTTCACCACACGTGGACAAPSMG2 (PAC2)CGGGAGGCGAGGAGTTCACCACACGTGGATCCPSMG2 (PAC2)CGGGAGGCGAGGAGTTCACCACACGTGGATCCPSMG2 (PAC2)CGGGAGGCGAGGG	PSMC2 (Rpt1)	TGGGATTTGGCTGCAGAT	TTTGGGTCCTCCGAATCA
PSMC4 (Rpt3)GGAAGACCATGTTGGCAAAGAAGATGATGGCAGGTGCATTPSMC5 (Rpt6)CTCCAGGCACTGGGAAGACGTGCCATGACAAACAGCPSMC5 (Rpt4)GGCAGATCGTGGGTGAAGCGACGACACCCACAACAPSMD1 (Rpn2)ATGTCAGGAGGGCAGCAGAGCGCACATGGAGGGTTGTPSMD2 (Rpn1)CCCAAGGTGCCTGATGACCTTGGCCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCACGGCTCTTCGGTGTCCACCGACGCACTTTPSMD4 (Rpn10)CGGGATTGCTACGACTGGCAGTGCCACAAGCACACAAPSMD5 (Rpn7)GGCAAAGGCCGAGTACCTACCCCAAAGCACACAAPSMD7 (Rpn8)GCTGGCAGTGCAGAGGTACCCCAAAAGCACACAAPSMD1 (Rpn6)ATGCAGGAGGCAGACAGGGAGCTCTGGCTGGCAAACTGTPSMD1 (Rpn6)ATGCAGGGAGGCAGACAGGGACCTCGGCTGGCAAACTGTPSMD13 (Rpn9)ATGCCTGCGGTTTTGGCACCACAGGGTCACTGAPSMD14 (Rpn11)CCGTGCTGGAGTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTGCGCCTTTTCPSME2 (PA28q)CATCCCAGGGGGAGGTAAACCACCCCACTGAGGPSME2 (PA28q)CACCCTCAGGGCAGTGAAGGCACCAGGGAGGACCAAGGPSME2 (PA28q)CGCAAACAGGTGGAGGTCCCGGAGGGAGGTCAAGTPSME2 (PA28q)CGCCAACAGGGGGAGGTATCACATGGGCAAGGGCCAAAPSMG1(PAC1)CCAATCCTCGGCTATCATGGGCCAAGAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCTTCCCATGACACCPSMG3 (PAC3)GTCCTTTGGGGCAGGATTCACCACACCGGCAAAPSMG3 (PAC3)GTCCTTGTGGGCAGGAGTATCACCACACCGGCAAAPSMG3 (PAC3)GCCCTACCTGGGTTCCATGCCTGGGCTGCATGAGPSMG3 (PAC3)GCCCAACAACCCAGCGCTCCCTGGCTGGATGAAAGCAAPSMG3 (P	PSMC3 (Rpt5)	GCCCACGGAGCAATACAG	CATCAGCACCCCTTTTGG
PSMC5 (Rpt6)CTCCAGGCACTGGGAAGACGTGCCATGACAAACAGCPSMC6 (Rpt4)GGCAGATCGTGGGTGAAGCGACGACAACCCACAACAPSMD1 (Rpn2)ATGTCAGGAGGGCACCAGAGCGCACATGAGGGTTGTPSMD2 (Rpn1)CCCAAGGTGCCTGATGACCTTGGCCAAAGGCGCATPSMD3 (Rpn3)GCTGTGCAGGGCTTCTCGGTGTCGGCGCCAAACTCTTPSMD4 (Rpn10)CGGGATGCCAGGTCCTACCCCAAAGGCCCAACTCTTPSMD5 (Rpn7)GGCAAAGGCCGAGTACCTACCCCAAAGGCACACCAAPSMD5 (Rpn12)CCACCCGGATCCTCTTCTGCTGGCTGGCAAAACTGTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn5)TCCAAAGGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCATGGGAGTCCAGTTGCCTCCACACGGACACGPSMD14 (Rpn11)CCGTGCTGGAGTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTTTTCPSME2 (PA28µ)CGCAAACAGGTGGAGGTCCCCGGAGGGAGGCCAAGAGPSME2 (PA28µ)CGCAACAGGTGGAGGTCCCCGGAGGGAGGCCAAAPSME2 (PA28µ)CGCAACCCAGCGATGTGGGCACAGAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCAAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCAAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCAAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCAAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCTACCAGGCAAAPSMG2 (PAC2)CCGGGAGGAGGAGAGTATCACATGGGCTACCAGGCAGAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGCTACAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGAGAGATTCACCACCACACACACAGGCAGAAPSMG2 (PAC2)CC	PSMC4 (Rpt3)	GGAAGACCATGTTGGCAAAG	AAGATGATGGCAGGTGCATT
PSMC6 (Rpt4)GGCAGATCGTGGGTGAAGCGACGACAACCAACAAPSMD1 (Rpn2)ATGTCAGGAGGCAGCAGAGCGCACATGAGGGTTGTPSMD2 (Rpn1)CCCAAGGTGCCTGATGACCTTGGCCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTTCTTCGGTGTCGAGCGACCACTTTPSMD4 (Rpn10)CGGGATTGCTACGACTGGCAGTGCGGCCAAACTGTPSMD7 (Rpn8)GCTGGCAGGCGAGACCTACCCCAAAGCACACCAAPSMD7 (Rpn8)CCTGCCAGGAGCGAGACAGGGAGCTCTGCCGGTAACPSMD8 (Rpn12)CCACCGGATCCTCTTCTGCTGGCTGGCAAACTGTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCGGTAACPSMD12 (Rpn8)CCTCCTGCGGTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGGGTTCCAATTGCCTCACACTGACCACCADRM1 (Rpn13)CCCCTCATGTGCCAGTACAAGCCAGCCCACTTTCGPSME1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGCCACAGGTAGAPSME2 (PA28µ)CGCAAACAGGTGGAGGTCCCCGGAGGAGAGCTTTTPSME2 (PA28µ)CGCAAACAGGTGGAGGTCCCCGGAGAGGAGCCTTTPSME3 (PA28µ)CAGCCTTCGGCTCATCATGGGCCCATGAGAGCCAAAPSME3 (PA28µ)CAGCCTTCGGGTTACAAATGGGATGTGTCCCCTTCPSME4 (PA200)GAAGCACCCAGCGATGTTCACCACAGCAGCACAAAPSME3 (PAC3)GTCCTTCTGGGGCAGGATTCAGCACAGAGCCCAAAAPSMG2 (PAC4)CGGACTGCTGATCAAGTGGGCAAGGCCAAAAAPSMG3 (PAC3)GTCCTTCTGGGGCAGCAGAAAGTCAGGCTTGGATGAAAGCAAPSMG4 (PAC4)CGGACTGCTGCACCTCCTGGGCAAGCCAGAAAPSM53 (PAC3)GTCCTTCTGGGAGAGAAAAGTCAGGCTTGCATGAGAGAPSM53 (PAC4)CGGACACACCACCGCTCTCCTGGGCAAGCACACPSM64 (PAC4) <td< td=""><td>PSMC5 (Rpt6)</td><td>CTCCAGGCACTGGGAAGA</td><td>CGTGCCATGACAAACAGC</td></td<>	PSMC5 (Rpt6)	CTCCAGGCACTGGGAAGA	CGTGCCATGACAAACAGC
PSMD1 (Rpn2)ATGTCAGGAGGGCAGCAGAGCGCACATGAGGGTTGTPSMD2 (Rpn1)CCCAAGGTGCCTGATGACCTTGGCCAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTTCTTCGGTGTCGACGCAGCATCTTPSMD4 (Rpn10)CGGATTGCTACGACTGGCAGTGCGGCCCAAACTCTTPSMD5 (Rpn7)GGCAAAGGCCGAGTACCTACCCCAAAGCCAACACCAAPSMD7 (Rpn8)GCTGGCAGGCAGAGAGGTACCCCAAAAGCACACCAAPSMD8 (Rpn12)CCACCCGGATCCTCTTCTGCTGGCTGGCAAAACTGTPSMD1 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCGGTAATPSMD1 (Rpn7)CCACCGGATCCTGCGGATTCGGCCTCGGTAACCATTCGPSMD1 (Rpn8)ATGCTGCGGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTGCGCCCTCTTTCSHFM1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGCCAGGAGGAGCACTTTPSME2 (PA28 ₀)CGCAAACAGGTGGAGGTCCCCGGAGGGAGGTCAAGTPSME3 (PA28 ₇)CAGCCTTCGGCTCATCATGGGGCCGTTGATCAAAPSME4 (PA20)GAAACACCCAGCGATGTGCACAGAAGAGCCAAAPSMG2 (PAC2)CCGGAAGGAGTATCACATGGGAAGCCCACACPSMG4 (PAC4)CGGACTGCTGTTCCTGTTGGGCAAGGCCAGTAGAGPSMG4 (PAC4)CGGACTGCCAGCAGCAGAAAGTCAGGCCTGTGATGAAGCAAPSM3 (PAC3)GTCCTTCTGGGAGAGCACCACGGGCCAACACACCACCAGCGTGAAACACPSM64 (PAC4)CGGACTGCCAGCAGCAGAAAGTCAGGCTTCCTGAGTGAGAAGAAPSM3 (PAC3)GTCCTTCTGGGAGGCAGAAAAGTCAGGCTTCCTCTAAGCAAAGACPSM64 (PAC4)CGGACTGCCGAGCTGCTACCCTGGGCAG	PSMC6 (Rpt4)	GGCAGATCGTGGGTGAAG	CGACGACAACCCACAACA
PSMD2 (Rpn1)CCCAAGGTGCCTGATGACCTTGGCCAAAAGCTGCATPSMD3 (Rpn3)GCTGTGCAGGGCTTCTTCGGTGTCGACGCAGCTTTTPSMD4 (Rpn10)CGGGATTGCTACGACTGGCAGTGCGGCCAAACTCTTPSMD5 (Rpn7)GGCAAAGCCCAGAGTACCTACCCCAAAAGCACACCAAPSMD8 (Rpn12)CCACCCGGATCCTCTTGCTGGCTGGCAAAACTGTPSMD1 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn7)TCCAAAAGGCGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTTGGCACCACACGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTTCSHE11 (PA28α)CATCCCAGTGCGGAGGTACCCCGGAGGAGACCAGTPSME2 (PA28))CGCAAACAGTGGAGGTCCCCGGAGGGAGACCTTTPSME3 (PA28γ)CAACCCCAGCGATGTGGGCACAGAAGCCCAAAPSME3 (PA28γ)CGCAAACAGTGGAGGTCCCTTGGACACAAGAGTGCAAAPSME3 (PA28γ)CAACCCCAGCGATGTGGGACACAGAGGCCAAAPSME3 (PA28γ)CGCAACAGGTGGAGGATTCACCACACCGAGAGPSME3 (PA28γ)CGCAACAGCAGCAGATTGGGATGTTGTCCCTTCPSMG2 (PAC1)CCAATCCTCGGTTTTCCCTTGGGCAAGGCCAAAAPSMG3 (PAC3)GTCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG3 (PAC3)GTCCTTCTGGGGAGGAGCACAAAGTCAGGCTGTGATGAAAGCAAPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCAGGCTGTGATGAAAGCAAPSMG3 (PAC4)CGGACTCGCTGTCCTGTCCTGGGCACGACACACPSMG3 (PAC4)GGGCCCAACACACCACCTCTCCTGGCTGGTAGAAAGCAAPSMG3 (PAC3)GTCCTTCTGGGGCAGGAAAAGTCAGGCTGGCATCCTGGAAPSMG3	PSMD1 (Rpn2)	ATGTCAGGAGGGCAGCAG	AGCGCACATGAGGGTTGT
PSMD3 (Rpn3)GCTGTGCAGGGCTTCTTCGGTGTCGACGCAGCTTTTPSMD4 (Rpn10)CGGGATTGCTACGACTGGCAGTGCGGCCAAACTCTTPSMD5 (Rpn7)GGCAAAGGCCGAGTACCTACCCCAAAGGCACACCAAPSMD7 (Rpn8)GCTGGCAGTGCAGAAGGTACCCCAAAAGCACACCAAPSMD8 (Rpn12)CCACCCGGATCCTCTTCTGCTGGCTGGCAAAACTGTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGCACTCTGCCCGGTAATPSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGGAACACAGGPSMD13 (Rpn9)ATGCTCTGCGGTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGAGTCCAATTGCGTGCGCCAGTCTCTPSMD14 (Rpn13)CCCCTCATGTCCAGTCTTCGTGTGCGCCCAGTCTTGPSME1 (PA28α)CATCCCAGTGCCTGATCCGCCACAGGGAGACCTTTPSME2 (PA28μ)CGCAAACAGGTGGAGGTCCCCGGAGGAAGTCAAGTPSME3 (PA28μ)CAGCCTTCGGCTCATCATGGGGCCGTTTGATCTTCTPSME3 (PA28μ)CAGCCTCCGGTTTTCGGCACAGAAGCCCAAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGTCCCCTTCPSMG3 (PAC3)GTCCTTCTGGGCAGAGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTGCTGGTTCCTGTTGGCGAAGGCCATAAGGPSMG4 (PAC4)CGGACTGCGGAGAGAAAGTCAGGCTGGTGATGAAGCAApSMG3 (PAC3)GTCCTTCTGGGCAGAAAAGTCAGGCTGTGATGAAAGCAApSMG4 (PAC4)CGGACTGCTGCTGTCCCTGGGCACCCTTGCPSMG4 (PAC4)CGGACTGCTGCAGACAAGATCAGGCTTGAGATGAAGApS3GCCCAAACAACCACAGCTCCTCCTGGGCATCCTGGAAApS4PAC4)GGGACCCTACCTTGCATTAGGGTTGCCTTGAGAGACpS4PAC4)GGGACCCTACCTGCAAATTAGGGCTTCCTTGAGAACAACACTATGCA	PSMD2 (Rpn1)	CCCAAGGTGCCTGATGAC	CTTGGCCAAAAGCTGCAT
PSMD4 (Rpn10)CGGGATTGCTACGACTGGCAGTGCGGCCAAACTCTTPSMD6 (Rpn7)GGCAAAGGCCGAGTACCTACCCAGGGCCACAGTTTTPSMD7 (Rpn8)GCTGGCAGTGCAGAAGGTACCCCAAAAGCACACCAAPSMD8 (Rpn12)CCACCCGGATCCTCTTCTGCTGGCTGGCAAAACTGTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGCACACTGGCAGAGAGPSMD13 (Rpn9)ATGCTCTGCGGTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTCCAATTGCGTGCCCCTCTTTCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTCSHFM1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGCCCAGGCAAGTPSME2 (PA28α)CATCCCAGTGCTGATCCGCCACAGGGAGAGCAAGTPSME3 (PA28q)CAGCCTTCGGCTCATCATGGGCCGTTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGGCACAGAGAGCCAAAPSMG1(PAC1)CCAGTCCTCGGGTTTCTTGGGCAGGAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGATATCACATGGGAAGGCAAACPSMG3 (PAC3)GTCCTTCTGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTGGTGTCCTGTGGCCAAGAAGCAApS3GCCCAACAACACACAGCTCCTCCTGGGCATGAGAGApS3GCCCCACACAACACCAGGTCCGCTGGCGTGATGAAGCAp53GCCCCACAACAACACACACGCTCTCCTGGGCATGAGAp21GGAGACTCTCAGGGTGGAAATTAGGGCTTGCTGTGAGAAACACACAGGAGp21GGAGACTCTAGGGTGGAAATTAGGGCTTCCTTTGGAGAp21GGAGACTCTAGGGTGGAAATCCTACGTGCTCTCTGTGAGACp21GGAGACCCTACAGGTGGAAATCCTACGTGCTCTCTTGAGAGGp21GGAGACCTCAGGGCAGAAATCCTACGTGCTCTCTT	PSMD3 (Rpn3)	GCTGTGCAGGGCTTCTTC	GGTGTCGACGCAGCTTTT
PSMD6 (Rpn7)GGCAAAGGCCGAGTACCTACCCAGGGCCACAGTTTTPSMD7 (Rpn8)GCTGGCAGTGCAGAAAGGTACCCCAAAAGCACACCAAPSMD8 (Rpn12)CCACCCGGATCCTCTTCTGCTGGCTGGCAAAACTGTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTGCGCCCTCTTCSHFM1 (Rpn15)GAAAAAGCAGCCGGTAGAAAGCCAGCCCAGTGCTCGGPSME2 (PA28β)CGCAAACAGGTGGAGGTCCCCGGAGGAAGTCAAGTPSME3 (PA28γ)CAGCCTTCGGCTCATCATGGGCCCGTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGCCAACAAGAGCCCAAAPSMG2 (PAC2)CCGGGAGGAGTACACATGGGATGTTGCCCCTTCPSMG3 (PAC3)GTCCTTCGGGCAGGATTCACCACACCTGGCACAAPSMG3 (PAC3)GTGCTTGCGCGCAGTAGCGCCTCCCATGACTTCGPSMG4 (PAC4)CGGACTGCGCAGCAGAAAGTCAGCACAGGCCAAAAPSMG3 (PAC3)GTGACTGCAGCAGGAGTTCGGCTGTCCCATGACTTCGPSMG3 (PAC3)GCCAACAACACCAGCTCTCCTGGGCATGCATGAAGAAPSMG3GCCCAACAACACCAGGTTCCGGCCTGTGTTGGCAGACPSMF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAP53GCCAACAACACCACGCTCTCCTGGGCATCCTTGGAAAP54GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTTTGAAAGCAAP53GCCAACAACACCACACGCTCTCCTGGGCATGCAGAGAPGF3GCCAACAACACCACGGGAAAAGTCAGGCTGCTGTTCTCTGAAAGCAP53GCCAACAACACCACACGCTGCTA	PSMD4 (Rpn10)	CGGGATTGCTACGACTGG	CAGTGCGGCCAAACTCTT
PSMD7 (Rpn8)GCTGGCAGTGCAGAAGGTACCCCAAAAGCACACCAAPSMD8 (Rpn12)CCACCCGGATCCTCTTCTGCTGGCTGGCAAAACTGTPSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTCSHFM1 (Rpn15)GAAAAAGCAGCCGGTAGAAAGCCAGCCCAGTCTTCGPSME2 (PA28q)CATCCCAGTGCTGATCCGCCACAGGGAGGACCTTTPSME2 (PA28q)CGCAAACAGGTGGAGGTCCCCGGAGGGAAGTCAAGTPSME3 (PA28γ)CAGCCTTCGGCTCATCATGGGGCCGTTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGGCACAGAAGGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGCCCTTCPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTGCTGTCTGTTGGCAGGCCGTGAGAGACPSMG3 (PAC3)GTCGCAGCAGCAGAAAGTCAGCAGCTGCAGAAGACAApSMG3 (PAC3)GCCCACAACACACAGCTCTCCTGGGCATGATGAAGCAApSMG3 (PAC3)GCCCACCACCAGCAGTCGGCCTTCCCATGACTTCGPSMG3 (PAC3)GCCCAACAACACAGCTCTCCAGGCGTGTGATGAAAGCAAp53CGCCAACAACACAGCAGCTCCCTGGGCATGCATGAAGACAAp53GCCCAACAACACACAGCTCTCCTGGGCATCCTTGAAGCAAp53GCCCAACAACACCAGGTCCAATTAGGGCTTCCTCTGAAACCAATGCAp21GGAGACTCTCAGGGTGGAAATCCTACGTGCCTCTCTGAAACCTATGCAp24GGAGACTCTCAGGGCGAAAAGATTAGGGCTTCCTCTGAAACCTATGCAp21 <td>PSMD6 (Rpn7)</td> <td>GGCAAAGGCCGAGTACCT</td> <td>ACCCAGGGCCACAGTTTT</td>	PSMD6 (Rpn7)	GGCAAAGGCCGAGTACCT	ACCCAGGGCCACAGTTTT
PSMD8 (Rpn12) CCACCCGGATCCTCTTCT GCTGGCTGGCAAAACTGT PSMD11 (Rpn6) ATGCAGGGAGGCAGACAG GGAGCTCTGCCCGGTAAT PSMD12 (Rpn5) TCCAAAAGGCGGAGTCAG GCCTTCGGTAACCATTCG PSMD13 (Rpn9) ATGCTCTGCGGTTTTTGG CAGCACAGGGTGCATGAG PSMD14 (Rpn11) CCGTGCTGGAGTTCCAAT TGCCTCCACACTGACACC ADRM1 (Rpn13) CCCCTCATGTGCCAGTTC TTCGTGTCGCCCTCTTTC SHFM1 (Rpn15) GAAAAGCAGCCGGTAGA AAGCCAGCCAGTCTTGG PSME2 (PA28α) CATCCCAGTGCTGATCC GCCACAGGGAGAGCACAGT PSME2 (PA28β) CGCAAACAGGTGGAGGTC CCCGGAGGAGAGTCAAGT PSME4 (PA200) GAAAGCACCCAGCGATGT GGGCACTTGCCCAA PSMG1(PAC1) CCATCCCTCGGTTTTC CCTGGCACAACACCAGCCAGAA PSMG3 (PAC3) GTCCTTCTGGGGCAGGAT TCACCACACCTGGCACAC PSMG4 (PAC4) CGGACTGCTGGTCCTGT TGGGCAGTAGAAAGCAA PSMG4 (PAC4) CGGACTGCGAGCAGAAAGA TCAGGCTGTGATGAAAGCAA PSMG4 (PAC4) GGCCCAACACACCAGCTCCT CCTGGGCAGTAGAAGA PSMG4 (PAC4) CGCAACACACCAGCTCCT CTGGGCAGTAGAAGAA PSMG4 (PAC4) GGCCCAACACACCAGCTCCT CTGGGCATCCTGA	PSMD7 (Rpn8)	GCTGGCAGTGCAGAAGGT	ACCCCAAAAGCACACCAA
PSMD11 (Rpn6)ATGCAGGGAGGCAGACAGGGAGCTCTGCCCGGTAATPSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTTCSHFM1 (Rpn15)GAAAAAGCAGCCGGTAGAAAGCCAGCCAGGAGGACCTTTPSME2 (PA28q)CGCAAACAGGTGGAGGTCCCCGGAGGGAAGTCAAGTPSME3 (PA28γ)CAGCCTTCGGCTCATCATGGGCCGTTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGCCACAGAAGGCCAAAPSMG1(PAC1)CCAATCCCTCGGTTTTCCCTTGGACAAGAGCCAAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGTCCCCTTCPSMG3 (PAC3)GTCCTTCTGGGCAGGATTCACCACACTGGCAGAGAPSMG4 (PAC4)CGGACTGCGTGTTCCTGTTGGCAAGGCCAGTAGAGGPSMF3CTGACTGGGAGGCAGCAGAAAGTCAGGCTGTGATGAAAGCAApS3GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTAAACCTATGCAp21GCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGATATAATCCAGTCTGCGTACAGGG	PSMD8 (Rpn12)	CCACCCGGATCCTCTTCT	GCTGGCTGGCAAAACTGT
PSMD12 (Rpn5)TCCAAAAGGCGGAGTCAGGCCTTCGGTAACCATTCGPSMD13 (Rpn9)ATGCTCTGCGGTTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTTCSHFM1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGCCCAGTCTTCGPSME2 (PA28α)CATCCCAGTGCCTGATCCGCCACAGGGAGACTCAAGTPSME2 (PA28β)CGCAAACAGGTGGAGGTCCCCGGAGGAAGTCAAGTPSME3 (PA28γ)CAGCCTCGGCTCATCATGGGCCCGTTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGGCACAGAAGCCCAAAPSMG1(PAC1)CCAATCCCTCGGTTTTTCCCTTGGACAAGAGCCAAAPSMG2 (PAC2)CCGGAAGGAGGTATCACATGGGATGTTGTCCCTTCPSMG3 (PAC3)GTCCTTCTGGGCAGGATTCACCACACCTGGCAACACPSMG4 (PAC4)CGGACTGCAGCAGCAGAAAGATCAGCCTGTGTAGAAGACAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGAGAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGGGAGAp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGGAGAp21GGAGACTCTCAGGGTGAAATCCTACGTGCTCTCTCTAAACCTATGCAp40MAGGCCCAGACTGTGAATCCTACGTGGCTACAGGGHPRTTTCCTTGGTCAGGAGAAAGATCCAGAGGCGTACAGGG	PSMD11 (Rpn6)	ATGCAGGGAGGCAGACAG	GGAGCTCTGCCCGGTAAT
PSMD13 (Rpn9)ATGCTCTGCGGTTTTTGGCAGCACAGGGTGCATGAGPSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTTCSHFM1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGGCCAGGAGGACCTTTPSME1 (PA28α)CATCCCAGTGCCTGATCCGCCACAGGGAGGACCAGTPSME2 (PA28β)CGCAAACAGGTGGAGGTCCCCGGAGGAAGTCAAGTPSME3 (PA28γ)CAGCCTCGGCTCATCATGGGCCCGTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGCCACAGAAGAGCCCAAAPSMG1(PAC1)CCAATCCCTCGGTTTTTCCCTTGGACAAGAGCCAAAPSMG2 (PAC2)CCGGAGGAGGTATCACATGGGATGTTGTCCCTTCPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTCGCTGTTCCTGTTGGGCAAGGCCAGTAGAGPSMF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATGCTTGGAGACp51GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTTTGGAGAp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGAGAGApUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCTTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTCG	PSMD12 (Rpn5)	TCCAAAAGGCGGAGTCAG	GCCTTCGGTAACCATTCG
PSMD14 (Rpn11)CCGTGCTGGAGTTCCAATTGCCTCCACACTGACACCADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTTCSHFM1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGGCCAGTCTTCGPSME1 (PA28α)CATCCCAGTGCCTGATCCGCCACAGGGAGGACCTTTPSME2 (PA28β)CGCAAACAGGTGGAGGTCCCCGGAGGGAAGTCAAGTPSME3 (PA28γ)CAGCCTTCGGCTCATCATGGGCCCGTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGGCACAGAAGCCCAAAPSMG1 (PAC1)CCAATCCCTCGGTTTTCCCTTGGACAAGAGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGTCCCCTTCPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTCGCTGTTCCTGTTGGGCAAGGCCAGAAGAGPSM53GCCCAACAACACCAGCTCCTCCTGGGCATGATGAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTAAACCTATGCATGTTGGTGTGGCAGAACp21GGAGACTCTCAGGGTCGAAAATTAGGGCTTCCTCTGAGAACpUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGAATAATCCAGTCTGGCTTATATCCAACACTTGG	PSMD13 (Rpn9)	ATGCTCTGCGGTTTTTGG	CAGCACAGGGTGCATGAG
ADRM1 (Rpn13)CCCCTCATGTGCCAGTTCTTCGTGTCGCCCTCTTTCSHFM1 (Rpn15)GAAAAGCAGCCGGTAGAAAGCCAGCCCAGTCTTCGPSME1 (PA28α)CATCCCAGTGCCTGATCCGCCACAGGGAGGACCTTTPSME2 (PA28β)CGCAAACAGGTGGAGGTCCCCGGAGGGAAGTCAAGTPSME3 (PA28γ)CAGCCTTCGGCTCATCATGGGCCGTTTGATCTTCTPSME4 (PA200)GAAAGCACCCAGCGATGTGCCACAGAAGGCCCAAAPSMG1 (PAC1)CCAATCCCTCGGTTTTCCCTTGGACAAGAGCCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGTCCCCTTCPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTGCAGCAGGATCGGCCTCTCCCATGACTTCGPSMF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGCAAATTAGGGCTTCCTGAGACAp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGAAACCTATGCApUMAGGGCCCAGACAGCAGATCCAGAGGCGTACAAGGGHPRTTTCCTTGGTCAGGCAGATATAATCCAGTCTGCCTTATATCCAACACTTGG	PSMD14 (Rpn11)	CCGTGCTGGAGTTCCAAT	TGCCTCCACACTGACACC
SHFM1 (Rpn15) GAAAAAGCAGCCGGTAGA AAGCCAGCCCAGTCTTCG PSME1 (PA28α) CATCCCAGTGCCTGATCC GCCACAGGGAGGACCTTT PSME2 (PA28β) CGCAAACAGGTGGAGGTC CCCGGAGGAAGTCAAGT PSME3 (PA28γ) CAGCCTTCGGCTCATCAT GGGGCCGTTTGATCTTCT PSME4 (PA200) GAAAGCACCCAGCGATGT GGCACAGAAGAGCCCAAA PSMG1(PAC1) CCAATCCCTCGGTTTTC CCTTGGACAAGAGCCCAAA PSMG2 (PAC2) CCGGGAGGAGGTATCACA TGGGATGTTGTCCCCTTC PSMG3 (PAC3) GTCCTTCTGGGGCAGGAT TCACCACACCTGGCAAGAG PSMG4 (PAC4) CGGACTGCCGTGTTCCTGT TGGGCAAGGCCAGTAGAGAG PSMG4 (PAC4) CGGACTGGCAGGAGGAGCAGAAAG TCAGGCTGTGATGAAAGCAA PSMG3 CTGACTGGGAGGCAGGAAAAG TCAGGCTGTGATGAAAGCAA p53 GCCCAACAACACCAGCTCCT CCTGGGCATCCTTGAGAGA p21 GGAGACTCTCAGGGTCGAAA TTAGGGCTTCCTTTGAGAGA p21 GGAGACTCTCAGGGTCGAAA TTAGGGCTTCTCTAAACCTATGCA p21 GGAGACTCTCAGGGTCGAAA TTAGGGCTTCTTAAACCTATGCA p4-actin CCAACCGCGAGAAGAT CCAGGGCGTACAGGG PUMA GGGCCCAGAACTGTGAAGCAT AGGCGCGTACAGGG <	ADRM1 (Rpn13)	CCCCTCATGTGCCAGTTC	TTCGTGTCGCCCTCTTTC
PSME1 (PA28α) CATCCCAGTGCCTGATCC GCCACAGGGAGGACCTTT PSME2 (PA28β) CGCAAACAGGTGGAGGTC CCCGGAGGGAAGTCAAGT PSME3 (PA28γ) CAGCCTTCGGCTCATCAT GGGGCCGTTTGATCTTCT PSME4 (PA200) GAAAGCACCCAGCGATGT GGCACAGAAGCCCCAAA PSMG1(PAC1) CCAATCCCTCGGTTTTTC CCTTGGACAAGAGCCAAA PSMG2 (PAC2) CCGGGAGGAGGTATCACA TGGGATGTTGTCCCCTTC PSMG3 (PAC3) GTCCTTCTGGGGCAGGAT TCACCACACCTGGCAGTAGAG PSMG4 (PAC4) CGGACTCGCTGTTCCTGT TGGGCAAGAAGCAAA PSMF3 CTGACTGGGGAGGCAGAAAAG TCAGGCTGTGATGAAAGCAA PSMG3 (PAC3) GTCCTTCTGGGGCAGGATC GGCCCAAGAAGCAC PSMG4 (PAC4) CGGACTGCGCAGCAGGATC GGCCCAAGAAGCAA PSMF3 CTGACTGGGAGGCAGAAAAG TCAGGCTGTGATGAAAGCAA PSM53 GCCCAACAACACCAGCTCCT CCTGGGCATGCAGAC P53 GCCCAACAACACCAGGTCGAAA TTAGGGCTTCCTCTTGAGAA p21 GGAGACTCTCAGGGTGAAAACT TTAGGGCTTCCTCTTGAAACCTATGCA p24 GGAGACTCTCAGGGAGAAT ACGTGCTCCTCTCTAAACCTATGCA p3-actin CCAACCGCGAGAAGAT ACGTGGCTACAGGG	SHFM1 (Rpn15)	GAAAAAGCAGCCGGTAGA	AAGCCAGCCCAGTCTTCG
PSME2 (PA28β) CGCAAACAGGTGGAGGTC CCCGGAGGGAAGTCAAGT PSME3 (PA28γ) CAGCCTTCGGCTCATCAT GGGGCCGTTTGATCTTCT PSME4 (PA200) GAAAGCACCCAGCGATGT GGCACAGAAGCTCCCAAA PSMG1(PAC1) CCAATCCCTCGGTTTTTC CCTTGGACAAGAGCCAAA PSMG2 (PAC2) CCGGGAGGAGGTATCACA TGGGATGTTGTCCCCTTC PSMG3 (PAC3) GTCCTTCTGGGGCAGGAT TCACCACACCTGGCACACA PSMG4 (PAC4) CGGACTGCTGTTCCTGT TGGGCAAGACTTCG POMP (UMP1) AGGCAGTGCAGCAGGATGA GGCTCTCCCATGACTTCG NRF3 CTGACTGGGAGGCAGAAAAG TCAGGCTGTGATGAAAGCAA p53 GCCCAACAACACCAGCTCCT CCTGGGCATGCAGAC p21 GGAGACTCTCAGGGTCGAAA TTAGGGCTTCCTTTGAAGAGA PUMA GGGCCCAGACTGTGAATCCT ACGTGCTCTCTAAACCTATGCA β-actin CCAACCGCGAGAAGAT CCAGAGGCTACAGGG HPRT TTCCTTGGTCAGGCAGTATAATCC AGTCTGGCTTATATCCAACACTTCG	PSME1 (PA28α)	CATCCCAGTGCCTGATCC	GCCACAGGGAGGACCTTT
PSME3 (PA28γ) CAGCCTTCGGCTCATCAT GGGGCCGTTTGATCTTCT PSME4 (PA200) GAAAGCACCCAGCGATGT GGCACAGAAGCTCCCAAA PSMG1(PAC1) CCAATCCCTCGGTTTTTC CCTTGGACAAGAGCCAAA PSMG2 (PAC2) CCGGGAGGAGGTATCACA TGGGATGTTGTCCCCTTC PSMG3 (PAC3) GTCCTTCTGGGGCAGGAT TCACCACACCTGGCACAC PSMG4 (PAC4) CGGACTCGCTGTTCCTGT TGGGCAAGGCCAGTAGAG POMP (UMP1) AGGCAGTGCAGCAGGATC GCCTCCCCATGACTTCG NRF3 CTGACTGGGAGGCAGAAAAG TCAGGCTGTGATGAAAGCAA p53 GCCCAACAACACCAGCTCCT CCTGGGCATGCTGAGAC p21 GGAGACTCTCAGGGTCGAAA TTAGGGCTTCCTTTGAGAGA p24 GGGCCCAGACTGTGAATCCT ACGTGCTCTCTAAACCTATGCA β-actin CCAACCGCGAGAAGAT CCAGAGCGTACAGGG HPRT TTCCTTGGTCAGGCAGTATAATCC AGTCTGGCTTATATCCAACACTTCG	PSME2 (PA28β)	CGCAAACAGGTGGAGGTC	CCCGGAGGGAAGTCAAGT
PSME4 (PA200) GAAAGCACCCAGCGATGT GGCACAGAAGCTCCCAAA PSMG1(PAC1) CCAATCCCTCGGTTTTC CCTTGGACAAGAGCCAAA PSMG2 (PAC2) CCGGGAGGAGGTATCACA TGGGATGTTGTCCCCTTC PSMG3 (PAC3) GTCCTTCTGGGGCAGGAT TCACCACACCTGGCACACA PSMG4 (PAC4) CGGACTCGCTGTTCCTGT TGGGCAAGGCCAGTAGAG POMP (UMP1) AGGCAGTGCAGCAGGATC GGCTCTCCCATGACTTCG NRF3 CTGACTGGGAGGCAGAAAAG TCAGGCTGTGATGAAAGCAA p53 GCCCAACAACACCAGCTCCT CCTGGGCATCCTTGAGTTCC Retinoblastoma AGGCCCCTACCTTGTAA TGTTGGTGTGGCAGAA p21 GGAGACTCTCAGGGTCGAAA TTAGGGCTTCCTCTTAAACCTATGCA β-actin CCAACCGCGAGAAGAT CCAGAGGCGTACAGGG HPRT TTCCTTGGTCAGGCAGTATAATCC AGTCTGGCTTATATCCAACACTTCG	PSME3 (ΡΑ28γ)	CAGCCTTCGGCTCATCAT	GGGGCCGTTTGATCTTCT
PSMG1(PAC1)CCAATCCCTCGGTTTTCCCTTGGACAAGAGCCAAAPSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGTCCCCTTCPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTCGCTGTTCCTGTTGGGCAAGGCCAGTAGAGPOMP (UMP1)AGGCAGTGCAGCAGGATCGGCTCTCCCATGACTTCGNRF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTGAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	PSME4 (PA200)	GAAAGCACCCAGCGATGT	GGCACAGAAGCTCCCAAA
PSMG2 (PAC2)CCGGGAGGAGGTATCACATGGGATGTTGTCCCCTTCPSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTCGCTGTTCCTGTTGGGCAAGGCCAGTAGAGPOMP (UMP1)AGGCAGTGCAGCAGGATCGGCTCTCCCATGACTTCGNRF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGAGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	PSMG1(PAC1)	CCAATCCCTCGGTTTTTC	CCTTGGACAAGAGCCAAA
PSMG3 (PAC3)GTCCTTCTGGGGCAGGATTCACCACACCTGGCACACPSMG4 (PAC4)CGGACTCGCTGTTCCTGTTGGGCAAGGCCAGTAGAGPOMP (UMP1)AGGCAGTGCAGCAGGTTCGGCTCTCCCATGACTTCGNRF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGAGAAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	PSMG2 (PAC2)	CCGGGAGGAGGTATCACA	TGGGATGTTGTCCCCTTC
PSMG4 (PAC4)CGGACTCGCTGTTCCTGTTGGGCAAGGCCAGTAGAGPOMP (UMP1)AGGCAGTGCAGCAGGTCGGCTCTCCCATGACTTCGNRF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGAGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	PSMG3 (PAC3)	GTCCTTCTGGGGCAGGAT	TCACCACACCTGGCACAC
POMP (UMP1)AGGCAGTGCAGCAGGTTCGGCTCTCCCATGACTTCGNRF3CTGACTGGGAGGCAGAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGAGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	PSMG4 (PAC4)	CGGACTCGCTGTTCCTGT	TGGGCAAGGCCAGTAGAG
NRF3CTGACTGGGAGGCAGAAAAGTCAGGCTGTGATGAAAGCAAp53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	POMP (UMP1)	AGGCAGTGCAGCAGGTTC	GGCTCTCCCATGACTTCG
p53GCCCAACAACACCAGCTCCTCCTGGGCATCCTTGAGTTCCRetinoblastomaAGGCCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTGGAGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	NRF3	CTGACTGGGAGGCAGAAAAG	TCAGGCTGTGATGAAAGCAA
RetinoblastomaAGGCCCCTACCTTGTCATGTTGGTGTTGGCAGACp21GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTGGAGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCAβ-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	p53	GCCCAACAACACCAGCTCCT	CCTGGGCATCCTTGAGTTCC
$p21$ GGAGACTCTCAGGGTCGAAATTAGGGCTTCCTCTTGGAGAPUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCA β -actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	Retinoblastoma	AGGCCCCCTACCTTGTCA	TGTTGGTGTTGGCAGAC
PUMAGGGCCCAGACTGTGAATCCTACGTGCTCTCTCTAAACCTATGCA β -actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	p21	GGAGACTCTCAGGGTCGAAA	TTAGGGCTTCCTCTTGGAGA
β-actinCCAACCGCGAGAAGATCCAGAGGCGTACAGGGHPRTTTCCTTGGTCAGGCAGTATAATCCAGTCTGGCTTATATCCAACACTTCG	PUMA	GGGCCCAGACTGTGAATCCT	ACGTGCTCTCTCTAAACCTATGCA
HPRT TTCCTTGGTCAGGCAGTATAATCC AGTCTGGCTTATATCCAACACTTCG	β-actin	CCAACCGCGAGAAGAT	CCAGAGGCGTACAGGG
	HPRT	TTCCTTGGTCAGGCAGTATAATCC	AGTCTGGCTTATATCCAACACTTCG

Revised Supplementary Table 3. Continued

ChIP primer

Traget region	Forward primer	Reverse primer
p21-p53RE	GTGGCTCTGATTGGCTTTCTG	CTGAAAACAGGCAGCCCAAG
PUMA-p53RE	GCGAGACTGTGGCCTTGTGT	CGTTCCAGGGTCCACAAAGT
POMP-ARE	CCTCGGAAACGGAAGTGA	ACCATCTTCCGCAGCTCT
POMP-negative locus	GGGCTTTTTGGCCTCTGT	TGGTTGCCCACAAGTCCT
siRNA		
Target gene	Sense	Antisense
siControl	UUCUCCGAACGUGUCACGUTT	ACGUGACACGUUCGGAAATT
siNRF3 #1	GGAUCAAAGUGAUUCUGAUTT	AUCAGAAUCACUUUGAUCCAA
siNRF3 #2	GCAAAGAAGGAAACUCUUATT	UAAGAGUUUCCUUCUUUGCUU
shRNA*		
Target gene	Upper	Lower
shControl	TCGAGGTTCTCCGAACGTGTCACGTT	AGCTTACGCGTAAAAAATTCTCCGAA
	TCAAGAGAACGTGACACGTTCGGAGA	CGTGTCACGTTCTCTTGAAACGTGAC
	ATTTTTACGCGTA	ACGTTCGGAGAACC
shNRF3 #1	TCGAGGGGATCAAAGTGATTCTGATTT	AGCTTACGCGTAAAAAAGGATCAAAG
	CAAGAGAATCAGAATCACTTTGATCC	TGATTCTGATTCTCTTGAAATCAGAAT
	TTTTTTACGCGTA	CACTTTGATCCCC
shNRF3 #2	TCGAGGGCAAAGAAGGAAACTCTTAT	AGCTTACGCGTAAAAAAGCAAAGAAG
	TCAAGAGATAAGAGTTTCCTTCTTTGC	GAAACTCTTATCTCTTGAATAAGAGTT
	TTTTTACGCGTA	TCCTTCTTTGCCC

*These shRNAs have the identical target sequences with siRNAs.

guide RNA

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Name	Upper	Lower
POMP-ARE-gRNA	CACCGTCGGAAACGGAAGTGAGCGG	AAACCCGCTCACTTCCGTTTCCGAC

DNA sequence primer

Name	Forward	Reverse
ChIP region#1 (non-ARE)	TTCTCCTGCTCCCAACAACT	CAGCCTAGGTGACACAGCAA
ChIP region#2 (POMP-ARE)	CCTCGGAAACGGAAGTGA	ACCATCTTCCGCAGCTCT