Supplementary Table 4: The association of the 26S proteasome and tumor progression/metastasis

Note: the associateion between cancer and the 26S proteasome genes has been manually checked in PubMed

a) GSE2514 (Lung cancer, 20 tumor and 19 normal samples; 25 out of
43 26S proteasome genes were mapped on the microarray platform. FWER p-value: 0.02)

Entrez GeneID	Gene Symbol	RANK METRIC SCORE*	Genes have been reported in cancer
10213	PSMD14	0.288528293	
5710	PSMD4	0.165639699	Kim et al., Mol Cancer Res., 6:426, 2008
5713	PSMD7	0.147187442	
5721	PSME2	0.130215749	
5717	PSMD11	0.128598183	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5704	PSMC4	0.123157509	
5706	PSMC6	0.115970835	
5716	PSMD10	0.112173758	Mayer et al., Biochem Society Transaction, 34:746, 2006
5700	PSMC1	0.0898761	Kim et al., Mol Cancer Res., 6:426, 2008
5701	PSMC2	0.081513479	Cui et al., Proteomics, 6:498, 2005
5709	PSMD3	0.071682706	
5719	PSMD13	0.071118504	
7415	VCP	0.060464829	
9861	PSMD6	0.055711303	Ren et al., Oncogene, 19:1419, 2000
5720	PSME1	0.052469168	
5714	PSMD8	0.047414459	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5702	PSMC3	0.046327863	Pollice et al., JBC, 279:6345, 2003
6184	RPN1	0.043426223	
55559	UCHL5IP	0.041885283	
5705	PSMC5	0.041615516	
5715	PSMD9	0.033147983	
5711	PSMD5	0.030562362	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
10197	PSME3	0.015149679	Roessler et al., Molecular & Cellular Proteomics 5:2092, 2006
5718	PSMD12	-0.00983229	Cui et al., Proteomics, 6:498, 2005
9491	PSMF1	-0.069156095	

*Positive rank metric score represent that a gene is highly expressed in tumors.

b) GSE2514 (Bladder cancer, 46 tumor and 14 normal samples; 24 out of

43 26S proteasome genes were mapped on the microarray platform. FWER p-value: 0.03)

Entrez GeneID	Gene Symbol	RANK METRIC SCORE*	Genes have been reported in cancer
5709	PSMD3	0.452427298	
6184	RPN1	0.336738378	
5714	PSMD8	0.329777062	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5706	PSMC6	0.317771047	
10213	PSMD14	0.316393554	
9491	PSMF1	0.277954847	
5702	PSMC3	0.264383167	Pollice et al., JBC, 279:6345, 2003
5713	PSMD7	0.24622044	
10197	PSME3	0.234897956	Roessler et al., Molecular & Cellular Proteomics 5:2092, 2006
5718	PSMD12	0.232518911	Cui et al., Proteomics, 6:498, 2005
5705	PSMC5	0.229539841	
9861	PSMD6	0.228058025	Ren et al., Oncogene, 19:1419, 2000
5721	PSME2	0.197215706	
5704	PSMC4	0.188023791	
5701	PSMC2	0.180720001	Cui et al., Proteomics, 6:498, 2005
5719	PSMD13	0.170107812	
7415	VCP	0.16829586	
5716	PSMD10	0.164572522	Mayer et al., Biochem Society Transaction, 34:746, 2006
5710	PSMD4	0.159759447	Kim et al., Mol Cancer Res., 6:426, 2008
5717	PSMD11	0.118186161	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5700	PSMC1	0.113268174	Kim et al., Mol Cancer Res., 6:426, 2008
5720	PSME1	0.102744684	
5711	PSMD5	-0.028071675	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5715	PSMD9	-0.060938448	

*Positive rank metric score represent that a gene is highly expressed in tumors.

c) 295-set (Breast cancer, 79 "bad" and 216 "good" tumors; 20 out of
43 26S proteasome genes were mapped on the microarray platform. FWER p-value: 0.02)

Entrez GeneID	Gene Symbol	RANK METRIC SCORE*	Genes have been reported in cancer
5713	PSMD7	**0.386086971**	
5714	PSMD8	**0.214990646**	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5702	PSMC3	**0.193814263**	Pollice et al., JBC, 279:6345, 2003
5704	PSMC4	**0.191395864**	
5701	PSMC2	**0.170957178**	Cui et al., Proteomics, 6:498, 2005
5706	PSMC6	**0.163528755**	
55559	UCHL5IP	**0.140605494**	
5719	PSMD13	**0.127183944**	
10197	PSME3	**0.112150006**	Roessler et al., Molecular & Cellular Proteomics 5:2092, 2006
5711	PSMD5	**0.103415385**	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5709	PSMD3	**0.091733046**	
5700	PSMC1	**0.0707700699567794**	Kim et al., Mol Cancer Res., 6:426, 2008
5715	PSMD9	**0.065294839**	
7415	VCP	**0.05195912**	
5716	PSMD10	**0.047902003**	Mayer et al., Biochem Society Transaction, 34:746, 2006
9491	PSMF1	**0.043100398**	
5717	PSMD11	**0.037049145**	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5718	PSMD12	-0.014596398	Cui et al., Proteomics, 6:498, 2005
9861	PSMD6	-0.028772237	Ren et al., Oncogene, 19:1419, 2000
5720	PSME1	-0.040304024	

*Positive rank metric score represent that a gene is highly expressed in "bad" tumors.

* 295 set was take from Chang et al., 2005, PNAS, 102: 3738-43

d) GSE3494 (Breast cancer, 55 "bad" and 181 "good" tumors; 25 out of

43 26S proteasome genes were mapped on the microarray platform. FWER p-value: 0.02)

Entrez GeneID	Gene Symbol	RANK METRIC SCORE*	Genes have been reported in cancer
5709	PSMD3	0.052529093	
5702	PSMC3	0.042976808	Pollice et al., JBC, 279:6345, 2003
5714	PSMD8	0.040342595	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
6184	RPN1	0.036762998	
5713	PSMD7	0.034858033	
5704	PSMC4	0.0318074	
9491	PSMF1	0.02755018	
5705	PSMC5	0.024967447	
10213	PSMD14	0.023421973	
5706	PSMC6	0.023351779	
5718	PSMD12	0.023061328	Cui et al., Proteomics, 6:498, 2005
5716	PSMD10	0.022846168	Mayer et al., Biochem Society Transaction, 34:746, 2006
5721	PSME2	0.022409894	
5700	PSMC1	0.019591264	Kim et al., Mol Cancer Res., 6:426, 2008
7415	VCP	0.019304439	
55559	UCHL5IP	0.017730551	
5719	PSMD13	0.013845699	
5717	PSMD11	0.010386987	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
9861	PSMD6	0.00930169	Ren et al., Oncogene, 19:1419, 2000
5701	PSMC2	0.006858337	Cui et al., Proteomics, 6:498, 2005
10197	PSME3	0.006222811	Roessler et al., Molecular & Cellular Proteomics 5:2092, 2006
5710	PSMD4	0.003250213	Kim et al., Mol Cancer Res., 6:426, 2008
5711	PSMD5	0.001267459	Deng et al., Breast Cancer Research and Treatment, 104:1067, 2007
5715	PSMD9	-0.002555721	
5720	PSME1	-0.011888376	

*Positive rank metric score represent that a gene is highly expressed in "bad" tumors.