Supplementary Table 1

PSMB1 Resequencing Primers (for amplification)

Rxn	Forward or Reverse	Primer Location	Region Amplified by the Primer Pair	Primer Sequence	Primer Name
1^3	F	5'FR (-1252)	5' FR & Exon1	CGAACCGTCAGAAAAGAGTACAA	Rxn1Fm
	R	I1 (71)		TGACTCCTAAATAGGCTTCAGCA	Rxn3Rm
4	F	I1 (-74)	Exon 2	ACTATGGAGCATTCTTCTATTTGTAGG	Rxn4Fm
	R	I2 (171)		GACTGCACATTAAATTATTAGGAAACA	Rxn4Rm
5	F	I2 (-127)	Exon 3	GGGTGACTGTTTGTCCCATTA	Rxn5F
	R	I3 (195)		TGCTGCTGTTTCACATTATGC	Rxn5R
6	F	I3 (-145)	Exon 4	CTGTGTTGGTTGATCATGAAGG	Rxn6F
	R	I4 (219)		TAGCAAAATAACTGGCTGCTCA	Rxn6R
7	F	I4 (-110)	Exon 5	TAGCCAAGGTGATAGTCCGTTT	Rxn7F
	R	I5 (191)		AGGCAGAACACAGAGAGAGACC	Rxn7R
8	F	I5 (-78)	Exon 6	GGGTATTGGAAGAAACTTGAACC	Rxn8Fm
	R	3'FR (918)		ATAGAAAAGGGTGGGAAAAATGA	Rxn8Rm

PSMB2 Resequencing Primers (for amplification)

Rxn	Forward or Reverse	Primer Location	Region Amplified by the Primer Pair	Primer Sequence	Primer Name
1^3	F	5'FR (-1126)		CTCCCATTGGTTTGTAGGAATATC	Rxn1Fm
	R	I1 (95)		TCAGATCCTCCCTGGTACTTATTC	Rxn3Rm
4	F	I1 (-151)		TTTTGATCCATAGTTTGTTGAATTGT	Rxn4F
	R	I2 (223)		TACAAAGAGAAAAATCACGTGAAGAC	Rxn4R
5	F	I2 (-161)		GAGGAAAGGGACTAGAGTAGGATTG	Rxn5F
	R	I3 (156)		GCACAAAGACATTGGACTTAAGAAT	Rxn5R
6^7	F	I3 (7112)		AATGGGAAAGAATATGTAGGAAAGG	Rxn6F
	R	I3 (8160)		AAATGACCACTAAAAACAGAACAGC	Rxn7R
8	F	I3 (-127)		ATTGTGATTTACTCAGTTGCTGCT	Rxn8F
	R	I4 (190)		ACTTACATCAGCTTTTGGAAGACC	Rxn8R
9	F	I4 (-161)		GAGTAAGTTGATTGCAGGCTAGAAG	Rxn9F
	R	I5 (140)		GGTAGCAACTTCACATCTGGTTAGT	Rxn9R
10	F	I5 (-137)		CAACTGCCTCCAGTAGAATATCAGT	Rxn10F
	R	3'FR (921)		TATGAAAGAGCTAGTTGGAAAGGAA	Rxn10R

PSMB5 Resequencing Primers (for amplification)

Rxn	Forward or Reverse	Primer Location	Region amplified by the Primer pair	Primer Sequence	Primer Name
1^3	F	5'FR (-1018)	5' FR & Exon1	AGCAGGAGGCAACATTTCATA	Rxn1Fm
	R	I1 (403)		TCATGCCAGTTTCAGTTACCC	Rxn3Rm
4	F	I1 (-84)	Exon 2	TTTGGATTGATGCAAAAAGAAGT	Rxn4Fm
	R	I2 (85)		ACCAAGCCCTTTAATTCATCTGT	Rxn4Rm
5^6	F	I2 (-31)	Exon 3	TTTTTCCTGCTAACCTCATCTCC	Rxn5Fm
	R	3'FR (1461)		ACTACTGCTTTCACAGCCACTTC	Rxn6Rm

Forward or Reverse			Primer Name
F	3'-FR	AAAGGGGGTACCTGGAAGGGCCTTCAATTGTATCAGTACTT	PSMB5 Acc65I F
R	3'-FR	AAAGGGCTCGAGACTACTGCTTTCACAGCCACTTC	PSMB5 XhoI R

Forward or Reverse			Primer Name
F	Exon1	CGGAC TTGGGGGTTG TGCAGATCTGCT	PSMB5Cys24F
R	Exon1	AGCAGATCTGCACAACCCCCAAGTCCG	PSMB5Cys24R
F	Exon3	GTGGAGCAG GCCTGTGATC TGGCCCGT	PSMB5Cys212F
R	Exon3	ACGGGCCAGATCACAGGCCTGCTCCAC	PSMB5Cys212R
F	Exon3	CA ACCTCTACCA CATGCGGGAGGAT	PSMB5Met238F
R	Exon3	ATCCTCCCGCATGTGGTAGAGGTTG	PSMB5Met238R
F	3'-FR	GTCAAATAAGCCAAGACAGTGGAAGGGAAG	PSMB51094F
R	3'-FR	GTCAAATAAGCCAAGACAGTGGAAGGGAAG	PSMB51094R
F	3'-FR	GCCTGTGTTGCGTCTTTTGTCCA	PSMB51042F
R	3'-FR	TGGACAAAAGACGCAACACAGGC	PSMB51042R

Supplementary Table 1. **Primers for resequencing studies, for creating luciferase constructs and for mutagenesis**. Primers used for *PSMB1*, *PSMB2* and *PSMB5* gene resequencing, for the creation of luciferase constructs and for mutagenesis studies are listed. The nucleotide numbering scheme is that described in the legend for **Table 1**. “U” is upstream, “F” is forward, “R” is reverse, “I” is intron and “UTR” is untranslated region. Acc65I and XhoI restriction sites are underlined in the sequences of primers used to create reporter gene constructs. Primers used to perform mutagenesis to create variant allozyme expression constructs for PSMB5, including PSMB5 Cys24, Cys212 and Met238, are also listed. The nucleotide alteration in each primer is underlined.

Supplementary Table 2

PSMB1 **: Genetic Diversity and Neutrality Test Values**

Population	pi	theta	Tajima D
African-American	6.80 ± 4.27	10.0 ± 3.37	-0.88
Caucasian-American	6.80 ± 4.26	6.26 ± 2.41	0.21
Han Chinese-American	3.71 ± 2.71	5.01 ± 2.08	-0.61
Mexican-American	7.72 ± 4.72	9.39 ± 3.21	-0.48

PSMB2 **: Genetic Diversity and Neutrality Test Values**

Population	pi	theta	Tajima D
African-American	6.91 ± 4.08	12.3 ± 3.72	-1.3
Caucasian-American	0.67 ± 0.82	2.79 ± 1.28	-1.66
Han Chinese-American	1.61 ± 1.40	6.04 ± 2.15	-1.93
Mexican-American	2.05 ± 1.64	7.46 ± 2.51	-1.98

PSMB5 **: Genetic Diversity and Neutrality Test Values**

Population	pi	theta	Tajima D
African-American	5.45 ± 3.68	7.60 ± 2.84	-0.72
Caucasian-American	6.03 ± 3.97	4.84 ± 2.10	0.56
Han Chinese-American	3.15 ± 2.49	4.85 ± 2.11	-0.80
Mexican-American	4.56 ± 3.23	4.15 ± 1.91	0.22

Supplementary Table 2. Estimates of values for π, θ and Tajima's *D* for *PSMB1*, *PSMB2* and *PSMB5* in four ethnic groups. Values are parameter estimate means ± S.E.M. *p*-Values refer to Tajima's *D*.