Table S1. 10-fold cross-validation procedure

Divide the training set randomly into 10 parts of approximately equal size. Let m denote the number of most significant genes to calculate a gene score and q the q-th percentile to dichotomize the score.

Given (m, q), where m and q are in reasonable ranges, repeat the following steps:

(1) <u>Train the model with 9 parts of the training set</u>: First select differentially expressed genes with a 0.005 p-value cutoff, order the selected genes by univariate association with survival, then calculate the gene score based on the top m genes and calculate the q-th percentile of this score, which we denote by w.
(2) <u>Test the model with the remaining part</u>: Calculate gene scores using the top m genes identified in step 1 and dichotomize the scores at w obtained from step 1.
(3) <u>Repeat step 1–2 10 times:</u> Every sample in the training set is now assigned a label of 0 or 1. Compute the log rank test between group 0 and 1 and record the p-value.

 Select the best combination of (m, q) that gives the lowest p-value.

Table S2.1. P values regarding gene expression changes 48 hours after administration of bortezomib (Bz), dexamethasone (Dex), thalidomide (Thal), lenalidomide (Len), and melphalan (Mel)

Gene symbol	P values re Bz	P values re Dex	P values re Thal	P values re Len	P values re Mel
PSMA7	0.0001	0.0786	0.9314	0.6567	0.3136
PSMB2	0.0000	0.0638	0.5994	0.7235	0.0067
PSMB3	0.0059	0.8810	0.8071	0.1495	0.1171
PSMC4	0.0002	0.7125	0.9530	0.3164	0.2970
PSMC5	0.0007	0.9406	0.6600	0.4765	0.0750
PSMD14	0.0000	0.4206	0.8290	0.4682	0.0402
PSMD2	0.0008	0.7275	0.7783	0.1120	0.2004
PSMB4	0.0001	0.4902	0.1411	0.0193	0.7144
PSMD4	0.0000	0.1962	0.4422	0.9393	0.8847
SDC1	0.1728	0.5477	0.8025	0.5247	0.8680
DKK1	0.2213	0.4411	0.0000	0.0001	0.9125

Table S2.2. Mean and standard deviation regarding gene expression changes 48 hours after administration of bortezomib (Bz), dexamethasone (Dex), thalidomide (Thal), lenalidomide (Len), and melphalan (Mel)

Gene symbol	Mean change after Bz	SE of change after Bz	Mean change after Dex	SE of change after Dex	Mean change after Thal	SE of change after Thal	Mean change after Len	SE of change after Len	Mean change after Mel	SE of change after Mel
PSMA7	0.21	0.05	-0.33	0.18	0.02	0.17	-0.10	0.23	-0.07	0.06
PSMB2	0.17	0.04	-0.14	0.07	-0.03	0.05	-0.02	0.05	-0.16	0.06
PSMB3	0.13	0.05	-0.01	0.06	0.02	0.07	-0.09	0.06	-0.08	0.05
PSMC4	0.16	0.04	0.02	0.06	0.00	0.06	-0.07	0.06	-0.07	0.07
PSMC5	0.17	0.05	0.00	0.05	0.02	0.05	0.04	0.05	-0.09	0.05
PSMD14	0.23	0.04	-0.07	0.08	-0.02	0.09	-0.06	0.09	-0.12	0.06
PSMD2	0.13	0.04	0.01	0.03	-0.01	0.04	-0.08	0.05	-0.06	0.05
PSMB4	0.17	0.04	0.04	0.06	-0.07	0.05	-0.10	0.04	-0.02	0.04
PSMD4	0.19	0.04	0.07	0.05	-0.04	0.06	0.00	0.06	-0.01	0.08
SDC1	-0.07	0.05	-0.04	0.06	-0.02	0.08	-0.06	0.10	-0.01	0.05
DKK1	0.10	0.08	0.18	0.23	1.22	0.27	1.44	0.27	0.01	0.10