http://dx.doi.org/10.2106/JBJS.M.00062

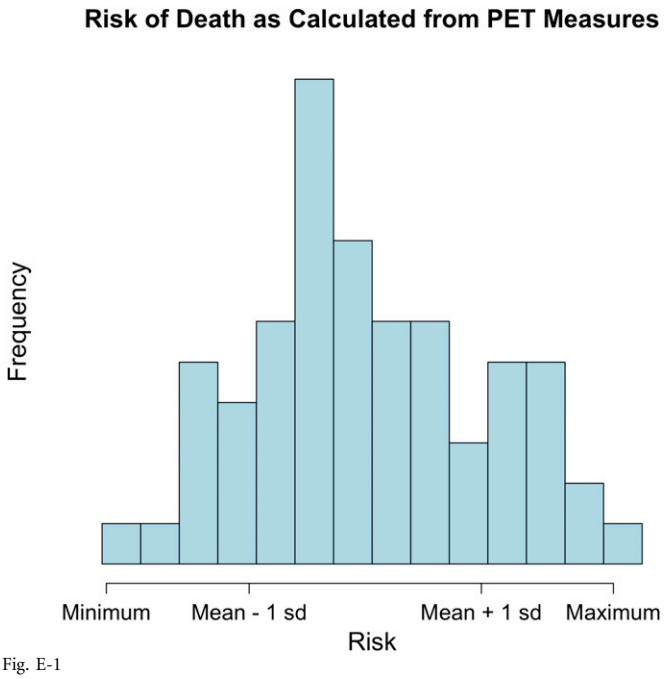

Fig. E-1

Histogram of calculated risk values for the patient group. The risk for each patient was calculated from the PET contributions to the multivariate patient survival model summarized in Table III. sd = standard deviation.

http://dx.doi.org/10.2106/JBJS.M.00062

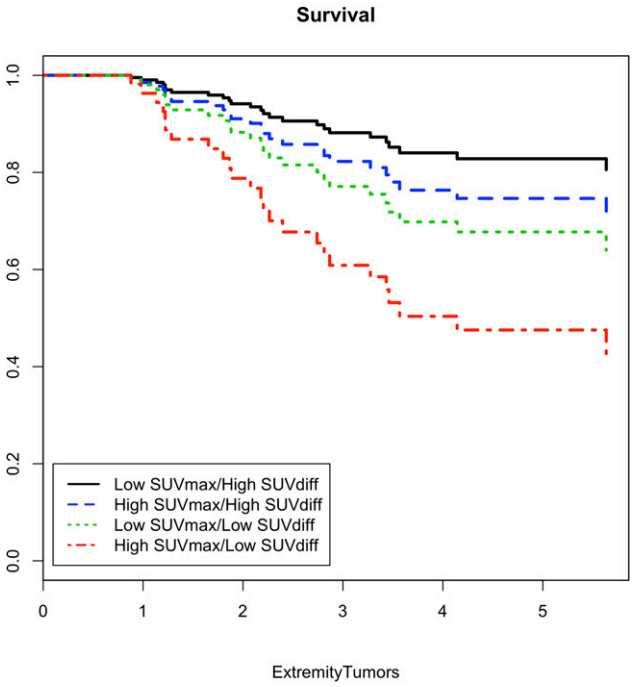

Fig. E-2A

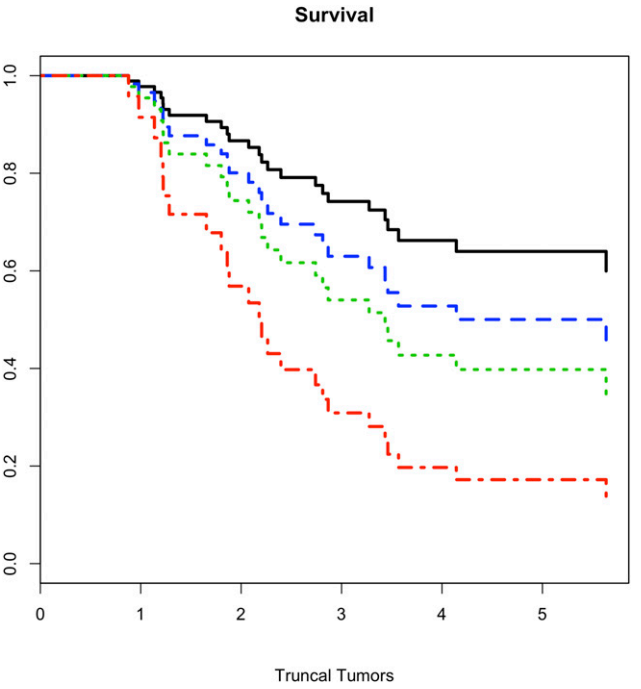

Fig. E-2B

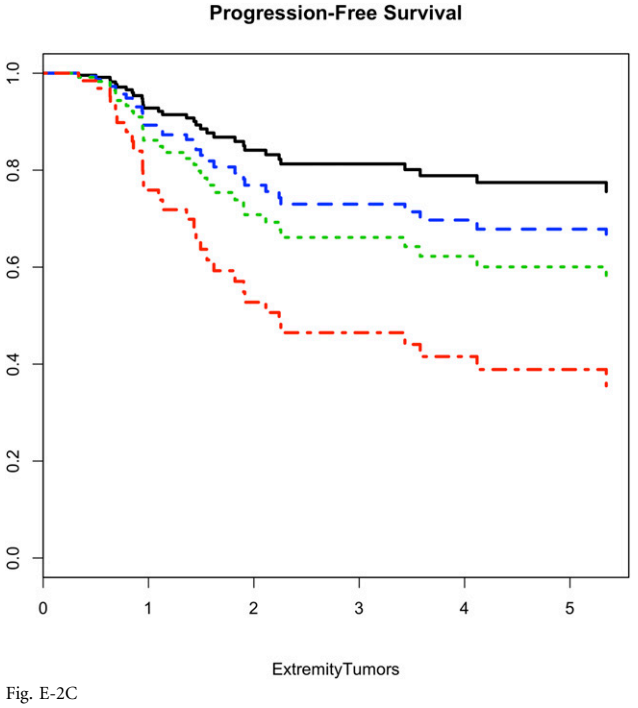

Fig. E-2C

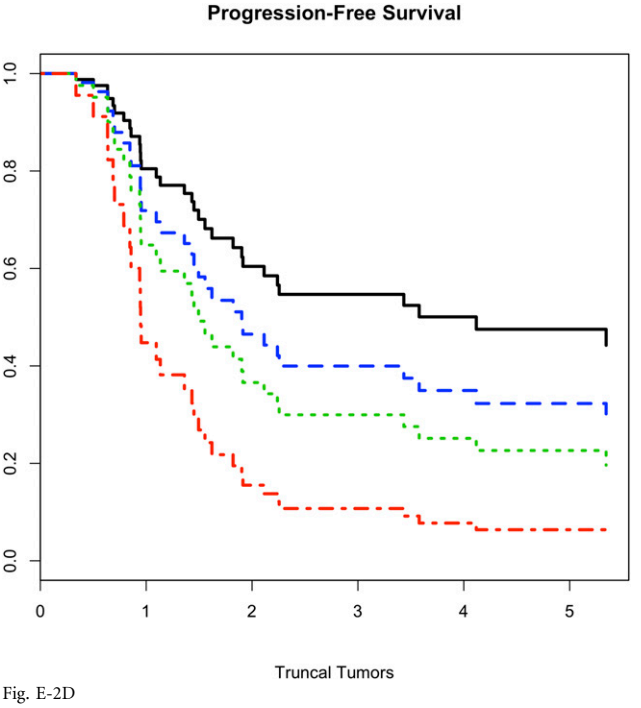

Fig. E-2D

Figs. E-2A through E-2F Predicted patient survival, progression-free survival, and local progression-free survival curves for patients with tumors located in the extremities (Figs. E-2A, E-2C, and E-2E) and trunk (Figs. E-2B, E-2D, and E-2F). The risk group key in Fig. E-2A applies to all six figures. The four risk groups are defined by high vs. low pre-therapy SUVmax and high vs. low SUVdiff. These curves are based on the multivariate models described in the Results section (Tables III, V, and VII), and each curve is adjusted for the model predictions for representative patients (mean values) in that group. ''High'' and ''low'' SUVmax are defined as above and below the median of the SUVmax variable.

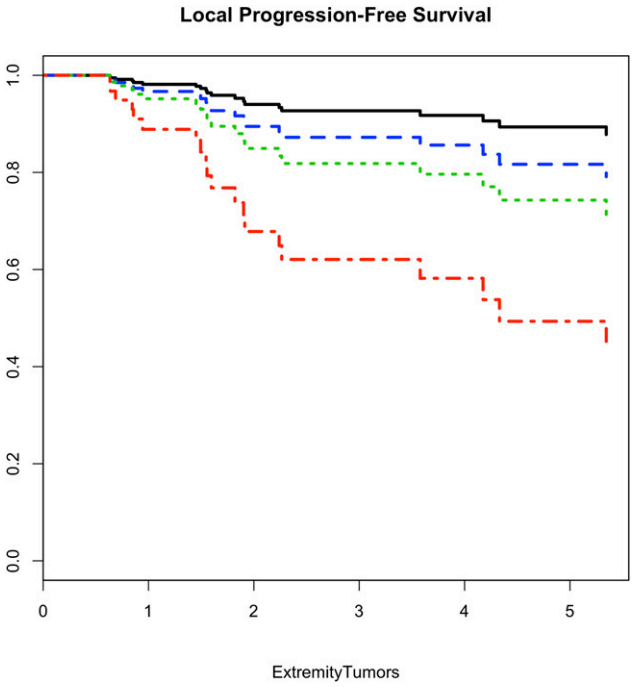

Fig. E-2E

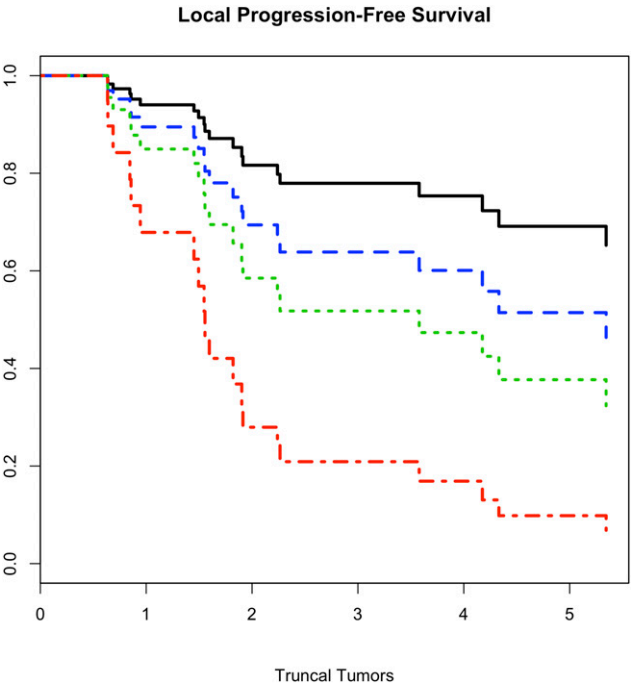

Fig. E-2F

http://dx.doi.org/10.2106/JBJS.M.00062

TABLE E-1 Optimal Model and Chosen Model for Each Outcome

	Full Data Set		Validation Data Set		
Outcome and Model Variables	−2 × Log-Likelihood	C-Statistic	−2 × Log-Likelihood	Concordance Statistic	Akaike Information Criterion
Patient survival					
SUVmax, SUVdiff, site*	178.17	0.69	180.19	0.67	184.17
Progression-free survival					
SUVmax, SUVdiff, site, sex, bone vs. other	212.27	0.74	221.92	0.71	220.27
SUVmax, SUVdiff, site*	219.01	0.71	224.51	0.69	225.01
Local-progression-free survival					
SUVmax, SUVdiff	141.29	0.71	143.47	0.70	145.29
SUVmax, SUVdiff, site*	134.93	0.78	145.37	0.76	140.93

*Chosen model.

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Appendix 1 Model Validation

Akaike Information Criterion (AIC) and cross-validation results for all 255 possible models were considered. Each model included at least one of the eight prognostic variables. Models were then ranked by the leave-out-one cross-validated likelihood (CV) method and concordance statistics; the AIC was also evaluated. Both of these assessments balance the trade-off between the number of parameters used and how well the model fits. The CV method also evaluates subsets of the original data set to assess whether the results are expected to be generalizable to more than this particular original data set. The models with the optimal cross-validated log-likelihoods are shown in Table E-1.

For survival, the cross-validated likelihood values for the 255 models ranged from 180.19 for the best model to 200.55 for the worst model; the corresponding range for the AIC was 181.64 to 195.89. The concordance statistic ranged from 0.76 for the best to 0.15 for the worst. (The model choice was based on the cross-validated likelihood; for readability, the models with the optimal AIC and concordance values are not shown in the table.)

For progression-free survival, the cross-validated likelihood criteria for the 255 models ranged from 221.92 for the best model to 246.22 for the worst; the corresponding range for the AIC was 220.10 to 240.35. The concordance statistic ranged from 0.80 for the best to 0.37 for the worst.

For local progression-free survival, the CV criteria for the 255 models ranged from 143.47 for the best model to 172.62 for the worst; the corresponding range for the AIC was 139.76 to 157.50. The concordance statistic ranged from 0.79 from the best to 0.09 for the worst. ■