Supplemental Appendix A. Distributional summaries of PET textural features, along with MTV and SUV_{max}.

Variable	Label	N	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	Std Deviation	Skewness [1]
Feature1	Tumor MTV	201	1.208	9.925	26.78	67.35	79.35	636.2	103.802	2.97
Feature2	Tumor SUV_{max}	201	3.523	9.459	13.15	14.7	18.36	53.22	7.716	1.368
Feature3	Variance	201	16.42	40.56	48.03	49.06	58.46	91.23	12.99	0.183
Feature4	Skewness	201	-1.909	-0.499	-0.239	-0.22	0.095	0.826	0.454	-0.311
Feature5	Kurtosis	201	-1.266	-0.866	-0.649	-0.531	-0.361	3.339	0.568	2.899
Feature6	Energy	201	0.002	0.003	0.004	0.01	0.006	0.315	0.032	7.11
Feature7	Contrast	201	3.798	19.6	33.26	36.54	48.44	147.3	22.156	1.46
Feature8	Entropy	201	3.247	5.632	5.937	5.805	6.106	6.48	0.477	-2.435
Feature9	Homogeneity	201	0.185	0.267	0.326	0.336	0.384	0.655	0.088	0.776
Feature10	IDM	201	0.103	0.176	0.24	0.253	0.304	0.613	0.097	0.92
Feature11	Correlation	201	-0.022	0.529	0.621	0.61	0.716	0.883	0.15	-0.779
Feature12	SumMean	201	0.011	0.016	0.018	0.018	0.02	0.027	0.003	-0.174
Feature13	Variance2	201	0.014	0.034	0.041	0.043	0.052	0.078	0.013	0.334
Feature14	Dissimilarity	201	1.442	3.171	4.157	4.393	5.375	9.948	1.54	0.64
Feature15	SRE	201	0.466	0.552	0.569	0.565	0.584	0.603	0.024	-1.065
Feature16	LRE	201	2.058	2.28	2.523	2.857	2.845	16.84	1.548	6.671
Feature17	GLN	201	6.821	45.69	146.4	355.3	412.5	5560	585.449	4.415
Feature18	RLN	201	90.96	963	2862	5545	6942	59760	7623.364	2.978
Feature19	RP	201	0.368	0.664	0.692	0.681	0.72	0.75	0.055	-2.328
Feature20	LGRE	201	0.003	0.008	0.012	0.016	0.022	0.091	0.012	2.397
Feature21	HGRE	201	167.1	295.5	349.6	351	407.9	601.7	83.149	0.08
Feature22	SRLGE	201	0.002	0.005	0.007	0.01	0.013	0.055	0.008	2.399
Feature23	SRHGE	201	94.58	167.3	196.1	193.8	222.3	284.4	40.779	-0.308
Feature24	LRLGE	201	0.009	0.021	0.029	0.039	0.044	0.242	0.031	2.99
Feature25	LRHGE	201	349.9	699.3	912.8	1168	1209	16320	1455.334	7.684
Feature26	GLV	201	0.015	0.057	0.082	0.089	0.104	0.365	0.053	2.307
Feature27	RLV	201	0.001	0.008	0.016	0.023	0.031	0.138	0.023	2.606
Feature28	SZE	201	0.457	0.592	0.636	0.641	0.681	0.855	0.073	0.52
Feature29	LZE	201	1.848	6.838	34.2	506.8	179.2	27580	2198.135	9.912
Feature30	GLN2	201	1	5.298	12.78	17.46	23.33	102.5	17.383	2.061
Feature31	ZSN	201	7.5	51.93	106	136.6	175.3	705.1	119.503	1.767
Feature32	ZP	201	0.051	0.238	0.352	0.38	0.519	0.805	0.179	0.383
Feature33	LGZE	201	0.006	0.014	0.019	0.023	0.027	0.093	0.013	2.333
Feature34	HGZE	201	168.7	252.7	277.6	283.8	314	466.1	46.18	0.304
Feature35	SZLGE	201	0.004	0.009	0.013	0.017	0.02	0.086	0.012	2.513
Feature36	SZHGE	201	92.11	139.8	163.1	170.3	189.9	367.2	43.085	1.06

Variable	Label	N	Min.	1st Qu.	Median	Mean	3rd Qu.	Max.	Std Deviation	Skewness [1]
Feature37	LZLGE	201	0.023	0.091	0.17	2.556	0.738	96.62	10.008	6.605
Feature38	LZHGE	201	382.2	2322	13330	244600	64560	11740000	1044198.852	8.18
Feature39	GLV2	201	0	0.001	0.003	0.015	0.013	0.265	0.035	4.488
Feature40	ZSV	201	0	0	0	0	0	0.002	0	3.836
Feature41	Coarseness	201	0.001	0.005	0.012	0.024	0.03	0.165	0.029	2.175
Feature42	Contrast2	201	0.021	0.158	0.252	0.372	0.414	4.657	0.522	5.927
Feature43	Busyness	201	0.016	0.08	0.156	0.285	0.334	3.253	0.387	3.787
Feature44	Complexity	201	297.1	680.9	909.7	939.4	1134	2147	329.896	0.629
Feature45	Strength	201	0.334	1.952	4.244	8.657	9.736	53.11	10.757	2.094

[1] This corresponds to the statistic $(\frac{n-1}{n})^{3/2} m_3 / m_2^{3/2}$. A negative value indicates a left-skewed distribution. A positive value indicates a right-skewed distribution, with larger values indicating a greater degree of skewness[19].

Supplemental Appendix B. Bootstrap internal validation of model performance (1000 iterations).

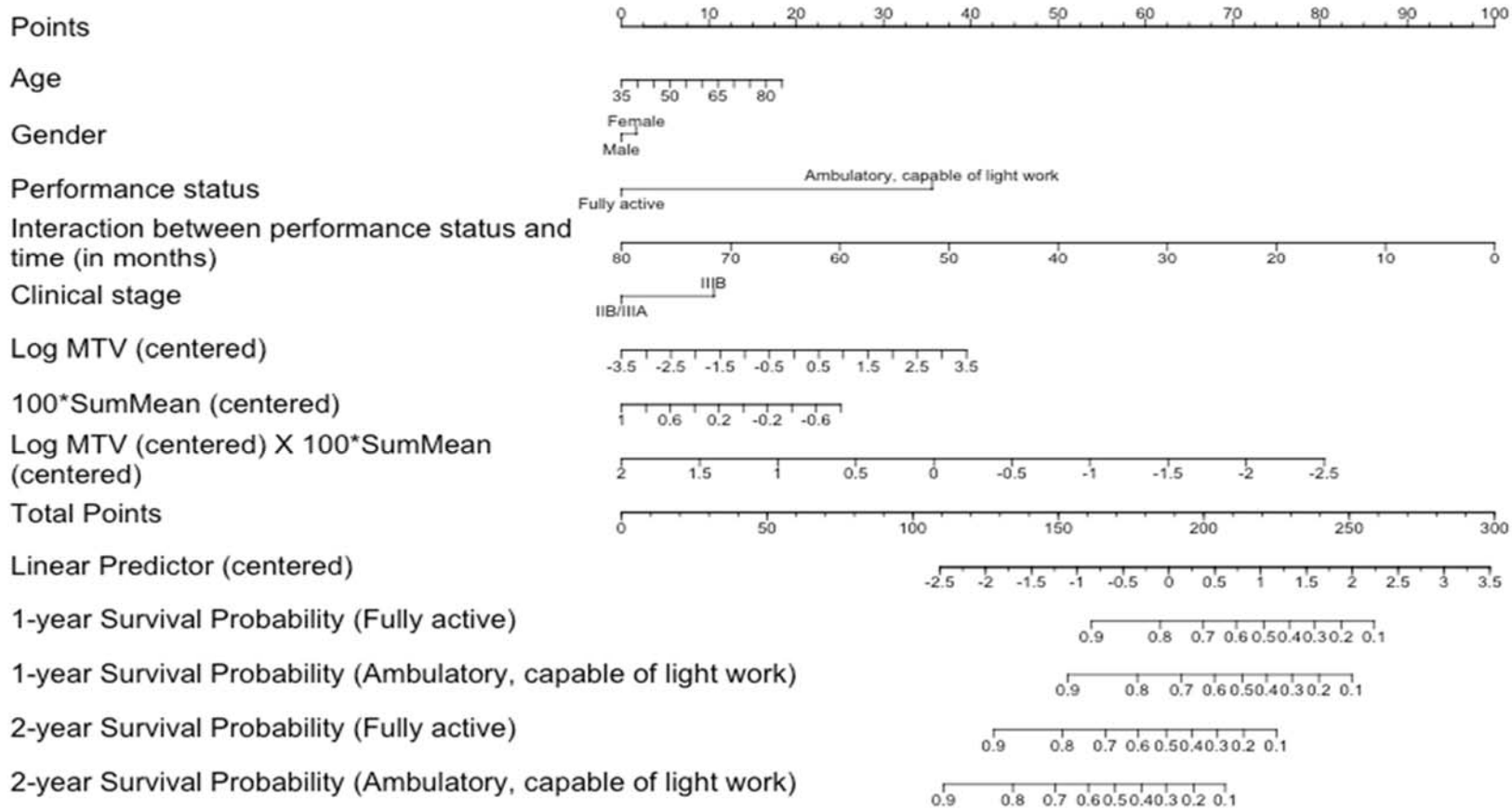
	Original (i.e. sample) C-statistic	Optimism	Final C-statistic	95% bootstrap confidence interval of final C-statistic
Clinical factors only*	0.62	0.02	0.60	(0.56, 0.64)
Clinical factors + MTV**	0.63	0.02	0.61	(0.57, 0.65)
Clinical factors + MTV + SumMean***	0.65	0.02	0.63	(0.59, 0,67)

*: Age, gender, performance status, performance status x time, clinical stage

**: Age, gender, performance status, performance status x time, clinical stage, log(MTV)

***: Age, gender, performance status, performance status x time, clinical stage, log(MTV), 100xSumMean, log(MTV) x 100xSumMean. This last model is equivalent to that shown in Table 2.

Supplemental Appendix C. Nomogram of the multivariate Cox model presented in Table 2.



The linear predictor (centered) is the linear predictor of the Cox model in Table 2 minus the overall mean of linear predictors (0.9455).

Use: In order to use the above nomogram to estimate the predicted X-year survival probability for a patient, first for each predictor determine the number of points via a straight line to the "Points" line (top row). Next, sum the points over all predictors to arrive at the Total Points. Finally, according to the performance status of the patient, draw a straight line from the "Total Points" line to either the "X-year Survival Probability (Fully active)" line or the "X-year Survival Probability (Ambulatory, capable of light work)" line to determine the predicted probability.

Examples:

A. For a male patient, age 60, with stage IIIB and performance status of 1 (Ambulatory, capable of light work), suppose that the MTV was 100 cm^3 and the SumMean was 0.02. Then log MTV (centered) corresponds to log(100) – 3.293 = 1.312 (where the natural logarithm is used), and 100*SumMean (centered) corresponds to 100*0.02 – 1.809 = 0.191. Then approximating the number of points for each predictor we have:

Age = 9 pts
Gender = 0 pts
Performance status = 35 pts
Interaction between performance status (Ambulatory, capable of light work) and time (@1 year) = 85 pts
Interaction between performance status (Ambulatory, capable of light work) and time (@2 years) =70 pts
Clinical stage = 11 pts
Log MTV (centered) = 27 pts
100*SumMean (centered) = 12 pts
Log MTV (centered) X 100*SumMean (centered) = 31 pts

Total points (@1 year) = 210
Total points (@2 years) = 195

1-year Survival Probability (Ambulatory, capable of light work) = 0.54
2-year Survival Probability (Ambulatory, capable of light work) = 0.23

B. For a patient with identical characteristics to that of example A, but with a performance status of 0 (Fully active). Again, approximating the number of points for each predictor we have:

Age = 9 pts
Gender = 0 pts
Performance status = 0 pts
Interaction between performance status (Fully active) and time (@1 year) = 100 pts
Interaction between performance status (Fully active) and time (@2 years) = 100 pts
Clinical stage = 11 pts
Log MTV (centered) = 27 pts
100*SumMean (centered) = 12 pts
Log MTV (centered) X 100*SumMean (centered) = 31 pts

Total points (@1 year) = 190
Total points (@2 years) = 190

1-year Survival Probability (Fully active) = 0.77
2-year Survival Probability (Fully active) = 0.47