SUPPLEMENTARY MATERIALS

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Section 1: Derivation and validation of treatment scores

A. The motivation for and concept of treatment scores

Treatment scores were derived as a way of quantifying treatment-associated propensity for late mortality (from health-related causes other than recurrence/progression of the initial cancer) based on the therapeutic exposures that CCSS survivors received for their childhood cancer. Our intention was to augment the formal regression-based inference with a descriptive visualization of data. That is, this summary score permits a graphical evaluation of data with respect to whether, and how much, treatmentassociated propensity for late mortality has declined over time (box plots in Figure 2 within the manuscript), potentially paralleling the temporal reduction in late mortality (exemplified by the red dots in Figure 2).

For example, for certain primary cancer diagnoses, we hypothesized that historical changes (reductions) in treatment exposure over the three decades would result in appreciable reductions in the treatment-related propensity for late mortality (box plots), parallel to the reductions of actual late mortality rates (red dots). Graphing these quantities comparatively allowed visualization of evidence that the treatment changes over time are associated with reduced risk of late mortality. On the other hand, in some childhood cancer types, there may be little change in the treatment-related propensity for late mortality, possibly because no major treatment changes have taken place and/or treatment changes have not resulted in the reduction of propensity for late mortality. Among survivors of such childhood cancer diagnoses, a decline in rates of late mortality over time would suggest that something other than their childhood cancer treatment has contributed to the established reduction in late mortality (e.g., effective follow-up screening or care of severe chronic conditions).

The methodologies used for deriving, validating, and applying the summary treatment score are described in detail below.

B. The derivation of treatment scores

A set of treatment variables that were considered to potentially contribute to the treatment-associated propensity for late mortality were a priori selected for each of the four childhood cancer types where statistically significant reduction in late mortality (from health-related causes) was identified (i.e., Acute Lymphoblastic Leukemia, Astrocytoma, Hodgkin Lymphoma, and Wilms Tumor). Treatment variables were categorized based on clinical relevance by the investigator team. They included:

**Cyclophosphamide Equivalent Dose¹*

The treatment score model was developed using multivariable piecewise exponential models with late mortality (from health-related causes other than recurrence/progression of the initial cancer) as the outcome. For each childhood cancer diagnosis group, we fitted the model with logarithm of person years at risk as an offset (the person years at risk were terminated at death or censoring). The model was of the form:

log (E[Yij]) = log (PYij) + Zijα + Xiβ

where, for the ith survivor in the jth year of attained age, Yij is the Poisson random variable indicating alive/death status, PYij is the person years at risk observed (during the jth year of attained age), Zij is the vector of adjustment variables (age at diagnosis, sex, and attained age in jth year), Xⁱ is the vector of the diagnosis-specific fixed set of treatment variables described above that the survivor received, and α and β are model parameters. The baseline log mortality rate was modeled by a natural cubic spline function of the attained age in Zijα with five knots placed at 10, 20, 30, 40, 45 years old.

The treatment score for a given survivor refers to the estimated partial linear predictor Xî *of health-related late mortality from the treatment portion of the model, i.e., estimated log rate of death, corresponding to the specific set of treatments the survivor has received (Xi), adjusted for age at diagnosis, sex, and attained age.*

C. The validation of treatment scores

To validate the treatment score as a summary scale that measures the propensity for late mortality, we performed an internal validation by splitting the contributing CCSS treatment institutions into two groups by stratified random sampling, and used one group of CCSS institutions for developing the treatment score and the other group for validating it. Specifically, the CCSS institutions were stratified based on their membership to the Pediatric Oncology Group or Children's Cancer Group (the primary legacy treatment consortia to the Children's Oncology Group for the eras in which this analysis takes place) and their patient volumes (approximated by the numbers of CCSS survivors contributed to the cohort). Within each stratum, the institutions were randomly split into the two groups. St. Jude Children's Research Hospital, the largest CCSS institution, was the only exception where the survivors were randomly split into the two groups within the institution.

Note that the treatment score was not developed for the purpose of predicting individual survivors' deaths. Thus, our validation was not concerned with the score's predictive power for individual survivors' deaths. Rather, we are interested in determining the degree to which stratum defined by treatment scores correlate with mortality risks. We therefore focused our validation of the treatment score's utility on calibration of the treatment-associated propensity for late mortality. Our approach was similar to the methods used for validation of risk calibration for the most widely-used breast cancer risk prediction model developed by Gail et al2-4 and for other risk scores of clinical utility.5,6

Specifically, using one of the two groups of CCSS institutions as the "training dataset", we fitted a treatment score model as described in the previous section. Note that we employed the multiple imputation methodology for missing treatment information, which created 10 complete training datasets. Thus, we fitted the same treatment score model to each of the 10 training datasets and averaged the resulting β parameter estimates to obtain a single trained treatment score model. Using this trained model, the treatment score Xî *was calculated for each survivor of the training institutions based on his/her treatment exposures Xⁱ . We defined treatment score groups by dividing the training institutions' survivors of each childhood cancer type into three groups for Acute Lymphoblastic Leukemia and Hodgkin Lymphoma, where the counts of late mortality from health-related causes were sufficiently large, and two groups for Astrocytoma and Wilms Tumor. The highest treatment score group was defined by a cutoff that approximately placed survivors with the top 20% of treatment scores within each childhood cancer diagnosis group. For Acute Lymphoblastic Leukemia and Hodgkin Lymphoma, the remaining survivors were approximately equally split into two groups by a cutoff of the treatment score (each 40% of the diagnosis*

specific training set). For Astrocytoma, due to having only two binary treatment factors in the model, the cutoff placed approximately half of the survivors in the higher score group.

Using the fixed β parameter estimates from the training model, the treatment scores Xî*'s were also calculated for survivors from the other group of CCSS institutions: these institutions and survivors served as the "validation dataset". Then, they were also grouped into the two or three treatment score groups using the same cutoff values as the training dataset/institutions.*

The table below shows the validation results of the treatment score with respect to the calibration.2-6 Rates of each treatment score group agree well between the survivors of the training institutions and those of the independent validation institutions. This validates the calibration capacity of the treatment score. In addition, we calculated cumulative incidence of late mortality from health-related causes by the training/validation status for each childhood cancer diagnosis group. While cumulative incidence of causespecific mortality has competing risks and even a perfect calibration would not make it equal between the training and validation institutions, the figure below shows reasonably good agreement, further supporting the utility of the treatment score.

Observed rates of late mortality from health-related causes per 10,000 person years in training and validation institutions by treatment score group and childhood cancer type.

Cumulative incidence of late mortality from health-related causes by the training/validation status for each childhood cancer diagnosis group: (A) Acute Lymphoblastic Leukemia; (B) Hodgkin Lymphoma; (C) Wilms Tumor; and (D) Astrocytoma. Black, blue, and red lines are the low-, medium-, and high-risk groups, respectively.

These results validate the derived treatment score as a measure that summarizes treatment-associated propensity for late mortality.

D. The application of treatment scores

The validated treatment scores were standardized within each childhood cancer diagnosis group in order to enhance their interpretability with respect to changes over time. Specifically, we standardized the treatment scores such that those from 1970-1979 had a mean of 0.0 and standard deviation of 1.0 within each childhood cancer diagnosis group. If another time period of survivors (e.g., those from 1980- 1989) had a tendency to have negative/similar/positive values of the standardized treatment score, then that would indicate a decrease/no change/increase in treatment-related propensity for late mortality as compared to 1970-1979.

E. References for Section 1

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Section 2: Multiple imputation of missing treatment information

This section describes the issue of missing treatment information in our analysis of late mortality and our multiple imputation approach.¹

A. The issue of missing treatment information

Treatment information is not complete for a subset of study-eligible survivors in CCSS. This is due to a variety of reasons including: not being able to contact survivors for study recruitment (unsuccessful tracing); passive and active refusal of study participation; participation in the study without consenting to release medical record information; and incomplete treatment records at the treating institutions (primarily partial missing information on some treatment variables).

The table below shows the extent of incomplete/missing treatment information in all study-eligible survivors of each diagnosis group for which multiple imputation was used. The percentages of studyeligible survivors with complete treatment information varied from 74% in Astrocytoma to 56% in Hodgkin Lymphoma. Approximately one quarter of survivors in each diagnosis group had treatment information completely missing due to either unsuccessful tracing for study recruitment, passive/active refusal of study participation, or study participation without consenting to release medical record information. The remaining study-eligible survivors had partially missing treatment information with the majority consisting of only one missing treatment variable.

For our late mortality analyses, the outcome (late mortality) data are available for all study-eligible survivors (except Canadian survivors) through the National Death Index, regardless of whether survivors participated in CCSS or not. This complete ascertainment of the outcome variable provides an exceptional opportunity for analyses free of any participation bias. Thus, some of the analyses in this paper that did not use treatment information (e.g., Tables 1 and 2, Figure 1 within the manuscript) were based on the entire study-eligible cohort and free of any participation bias. For the other analyses that utilized treatment information (e.g., Table 3 and Figure 2 within the manuscript), we still used all studyeligible survivors by addressing missing treatment information by a multiple imputation approach, motivated by a special context that applies to pediatric cancer treatment described below.

B. The special context of childhood cancer treatment

The CCSS cohort is hospital-based, consisting of institutions with a long-standing history of specializing in the diagnosis and treatment of children/adolescents with cancer. During the period covered by the CCSS cohort (1970-1999), the great majority of childhood cancer patients seen at CCSS institutions were treated on clinical trial protocols. While some deviations from protocols can take place and some patients may be treated off protocols, treatments a patient receives are largely determined by the protocol the patient is on, or a prior/similar protocol that applies to the patient. Protocols are specific to given childhood cancer diagnoses and, for some diagnoses, they are also specific to patients of certain ages. Given the rare nature of pediatric malignancies, the National Cancer Institute established cooperative clinical trials groups. Pediatric oncologists and other subspecialists involved in the treatment of childhood cancers, have since the 1960s collaborated at a national level to design and conduct protocol-driven clinical trials, while only a select few large pediatric oncology institutions (e.g., St. Jude Children's Research Hospital, Memorial Sloan Kettering Cancer Center, Dana Farber Cancer Center) develop/use their own institution-specific protocols for selected cancer diagnoses. Protocols are modified in successive trials aiming for improvement over current protocols, and therefore evolve over time.

Because of this special context of childhood cancer treatment, the combination of the following 4 variables is strongly indicative of what protocol a survivor might have been treated on and provides an excellent proxy metric for the survivor's treatment exposures: (a) childhood cancer type; (b) institution the survivor was treated at (informing the institution's membership to a specific cooperative oncology consortium; i.e., Children's Oncology Group and its legacy groups consisting of the Pediatric Oncology Group, Children's Cancer Group, National Wilms Tumor Study Group, Intergroup Rhabdomyosarcoma Study Group, Intergroup Ewings Sarcoma Group; or whether it is an institution that develops its own protocols); (c) age at diagnosis; and (d) year of diagnosis. This special context of pediatric oncology, together with the availability of both the outcome and these four variables on the full study-eligible cohort, provides us with an effective analytic approach for addressing missing treatment information through multiple imputation.

C. The multiple imputation approach

We make an assumption of "missing at random",1,2 i.e., conditioned on observed data, whether treatment data of a survivor are missing/incomplete or not does not depend on true (missing/incomplete) treatment itself the survivor had received. This assumption implies that, stratified by the observed data of survivors, the conditional distribution of treatment data within each stratum is equal between survivors with complete treatment information and those without.1,2 While we cannot assess whether the missing at random assumption holds or not directly using the observed data alone, our previous analysis³ with an additional aggregate set of data is consistent with, and supports, this assumption. Specifically, we had collected treatment data of study-eligible non-participants of CCSS in an aggregate form for group comparisons without allowing linkages to individual survivors. We compared participants and study-eligible non-participants of the CCSS study with respect to survivors' demographic and clinical characteristics including treatment modality. This comparison revealed no statistically significant difference between the two groups, in spite of their large sample sizes, in any characteristics including treatment modality, with an exception of vital status. Thus, we felt reasonably *assured to make the missing at random assumption in our analyses, that is, within each stratum formed by the key characteristics (the vital status and the four key variables (a)-(d) above that inform on treatment protocols), all of which are available on the full study-eligible cohort, we assume that missing/incomplete treatment data are due to chance alone.*

Under the missing at random assumption, the following multiple imputation approach we employed provides valid statistical inference. For a given survivor with incomplete treatment information, we borrow sets of actual treatments from 10 survivors randomly selected from a pool of survivors with complete treatment information who match with the survivor in question on the key characteristics above. The 10 sets of treatments reflect the range and uncertainty of plausible sets of treatments the survivor in question had received based on the key characteristics. This is a hot-deck imputation method⁴ and we applied Approximate Bayesian Bootstrap to make it properly reflect the entire uncertainty associated with missing data.2,5 Specifically, for each survivor in question, we first bootstrapped the pool of the matched survivors with complete treatment information and then applied the hot-deck imputation above to draw 10 samples by simple random sampling with replacement from the bootstrapped matched pool. This approach is "proper" in the sense of reflect the entire uncertainty1,2 and preserves the combination structures of various treatments that are actually used in clinical practice, i.e., imputation is multivariate. This results in 10 complete datasets are then analyzed one by one with an identical statistical method (e.g., piecewise exponential regression) whose results are expected to differ to some degree depending on the range and uncertainty captured across the 10 imputations. A specific standard statistical method1,2 is used to summarize and provide a single set of results from the 10 sets of results accounting for the uncertainty of each quantity of interest (e.g., a parameter) within each of, and between, the 10 analyses.

The key characteristics on which a pool of survivors with complete treatment information were matched with a survivor with incomplete treatment information depended on the degree of the incompleteness. If a survivor was missing all treatment information, the key characteristics to match were the 4 variables (a)-(d) and the vital status. If a survivor was missing partial treatment information, we additionally matched on all available treatment variables.

D. Sensitivity analysis assessing impact of the imputation

We employed the multiple imputation to reduce potential bias and more properly reflect the level of uncertainties associated with the incomplete treatment data. We conducted a sensitivity analysis using only survivors with complete treatment information, with a caveat that this complete-data-only analysis is potentially biased.1,2

The table below shows results from Table 3 in the manuscript with and without imputation. While individual parameter estimates of relative rates associated with treatment era are slightly different, their overall direction and magnitude of change when therapy is included in the model remained unchanged in each diagnosis group in the complete-data-only analysis. Thus, our main result of Table 3 (described at the end of Results section of the manuscript) is robust with respect to our use of the multiple imputation.

**all models adjusted for sex, age at diagnosis and attained age, ¹ Adjusted for cranial RT dose, anthracycline dose, epipodophyllotoxin and steroid exposure, ² adjusted for chest-directed radiotherapy dose, anthracycline dose, cyclophosphamide equivalent dose and splenectomy,* ³adjusted for abdominal RT dose and anthracycline dose, ⁴adjusted for cranial RT dose and any chemotherapy (yes/no).

E. References for Section 2

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Figure 1. Cumulative all-cause, recurrence/progression and health-related cause late mortality among five-year survivors of childhood cancer by decade for specific childhood cancers

Figure S2. Among five-year survivors, (A) percentage receiving radiotherapy and (B) mean cumulative dose of anthracycline chemotherapy by decade and by primary cancer diagnosis.

Figure S3. Among five-year survivors, box plots providing median cumulative anthracycline dose along with $25th$ and $75Th$ percentiles by decade and by primary cancer diagnosis.

	Total	1970-1979	1980-1989	1990-1999	Alive	Dead
All Survivors*	34033	9416	13181	11436	30075	3958
Sex						
Male	18983 (55.8%)	5198 (55.2%)	7354 (55.8%)	6431 (56.2%)	16628 (55.3%)	2355 (59.5%)
Female	15050 (44.2%)	4218 (44.8%)	5827 (44.2%)	5005 (43.8%)	13447 (44.7%)	1603 (40.5%)
Race/Ethnicity						
Non-Hispanic white	21781 (64.0%)	5628 (59.8%)	8332 (63.2%)	7821 (68.4%)	19575 (65.1%)	2206 (55.7%)
Non-Hispanic black	2022 (5.9%)	242 (2.6%)	658 (5.0%)	1122 (9.8%)	1817 (6.0%)	205 (5.2%)
Hispanic	2287 (6.7%)	296 (3.1%)	688 (5.2%)	1303 (11.4%)	2094 (7.0%)	193 (4.9%)
Others	2057 (6.0%)	161 (1.7%)	$706(5.4\%)$	1190 (10.4%)	1849 (6.1%)	208 (5.3%)
Unknown	5886 (17.3%)	3089 (32.8%)	2797 (21.2%)	$0(0.0\%)$	4740 (15.8%)	1146 (28.9%)
Age at Diagnosis (years)						
$0 - 4$	13463 (39.6%)	3660 (38.9%)	5468 (41.5%)	4335 (37.9%)	12319 (41.0%)	1144 (28.9%)
$5-9$	7826 (23.0%)	2204 (23.4%)	2993 (22.7%)	2629 (23.0%)	6950 (23.1%)	876 (22.1%)
$10-14$	7144 (21.0%)	1903 (20.2%)	2670 (20.3%)	2571 (22.5%)	6185 (20.6%)	959 (24.2%)
$15 - 20$	5600 (16.5%)	1649 (17.5%)	2050 (15.6%)	1901 (16.6%)	4621 (15.4%)	979(24.8%)
Survival after diagnosis (years)						
$5-9$	4210 (12.4%)	695 (7.4%)	716(5.4%)	2799 (24.5%)	2349(7.8%)	1861 (47.0%)
$10-14$	6298 (18.5%)	316 (3.4%)	323 (2.5%)	5659 (49.5%)	5523 (18.4%)	775 (19.6%)
15-19	5285 (15.5%)	224 (2.4%)	2083 (15.8%)	2978 (26.0%)	4758 (15.8%)	527 (13.3%)
20-24	$\overline{6721}$ (19.8%)	240 (2.5%)	6481 (49.2%)	$0(0.0\%)$	6343 (21.1%)	$\overline{378}$ (9.5%)
25-29	5964 (17.5%)	2386 (25.3%)	3578 (27.1%)	$0(0.0\%)$	5692 (18.9%)	272 (6.9%)
30-34	4051 (11.9%)	4051 (43.0%)	$0(0.0\%)$	$0(0.0\%)$	3924 (13.0%)	127 (3.2%)
\geq 35	1504 (4.4%)	1504 (16.0%)	$0(0.0\%)$	$0(0.0\%)$	1486 (4.9%)	18 (0.5%)
Diagnosis						
Leukemia	10199 (30.0%)	2982 (31.7%)	4485 (34.0%)	2732 (23.9%)	9019 (30.0%)	1180 (29.8%)
Acute lymphoblastic leukemia	8500 (25.0%)	2652 (28.2%)	3881 (29.4%)	1967 (17.2%)	7557 (25.1%)	943 (23.8%)
Acute myeloid leukemia	1222 (3.6%)	196 (2.1%)	438 (3.3%)	588 (5.1%)	1101 (3.7%)	$121(3.1\%)$
Other leukemia	$477(1.4\%)$	134 (1.4%)	166 (1.3%)	$177(1.5\%)$	361 (1.2%)	116 (3.0%)
Hodgkin lymphoma	4332 (12.7%)	1597 (17.0%)	1465 (11.1%)	1270 (11.1%)	3647 (12.1%)	685 (17.3%)
Non-Hodgkin lymphoma	2837 (8.3%)	705 (7.5%)	1100 (8.3%)	1032 (9.0%)	2621 (8.7%)	216 (5.5%)
CNS tumors	6369 (18.7%)	1225 (13.0%)	2294 (17.4%)	2850 (24.9%)	5443 (18.1%)	926 (23.4%)
Astrocytoma	3904 (11.5%)	824 (8.8%)	1410 (10.7%)	1670 (14.6%)	3383 (11.2%)	521 (13.2%)
Medulloblastoma, PNET	1380 (4.1%)	227 (2.4%)	493 (3.7%)	660 (5.8%)	1133 (3.8%)	247 (6.2%)
Other CNS	1085(3.2%)	174 (1.8%)	391 (3.0%)	520 (4.5%)	$927(3.1\%)$	158 (4.0%)
Wilms tumor	3055 (9.0%)	814 (8.6%)	1173 (8.9%)	1068 (9.3%)	2898 (9.6%)	157 (4.0%)
Neuroblastoma	2632 (7.7%)	680 (7.2%)	931 (7.1%)	1021 (8.9%)	2457 (8.2%)	175 (4.4%)
Rhabdomyosarcoma	1679 (4.9%)	549 (5.8%)	614 (4.7%)	516 (4.5%)	1510 (5.0%)	169 (4.3%)
Bone tumors	2930 (8.6%)	864 (9.2%)	1119 (8.5%)	947 (8.3%)	2480 (8.2%)	450 (11.4%)
Ewing sarcoma	997 (2.9%)	279 (3.0%)	381 (2.9%)	337 (2.9%)	813 (2.7%)	184 (4.6%)
Osteosarcoma	1771 (5.2%)	539 (5.7%)	683 (5.2%)	549 (4.8%)	1518 (5.0%)	253 (6.4%)
Other bone tumors	$162(0.5\%)$	46 (0.5%)	$\overline{55}$ (0.4%)	61(0.5%)	$\overline{149} (0.5\%)$	13 (0.3%)
Treatment exposure						
Any radiation						
Yes	19455 (57.2%)	7213 (76.6%)	7587 (57.6%)	4656 (40.7%)	16366 (54.4%)	3089 (78.0%)
No	14578 (42.8%)	2203 (23.4%)	5594 (42.4%)	6780 (59.3%)	13708 (45.6%)	870 (22.0%)
Chest radiation						
Yes	8299 (24.4%)	3073 (32.6%)	3062 (23.2%)	2163 (18.9%)	6715 (22.3%)	1584 (40.0%)
$\rm No$	25734 (75.6%)	6343 (67.4%)	10119 (76.8%)	9273 (81.1%)	23360 (77.7%)	2375 (60.0%)
Chest radiation dose						
None	25734 (75.6%)	6343 (67.4%)	10119 (76.8%)	9273 (81.1%)	23360 (77.7%)	2375 (60.0%)
\geq 1-<20Gy	2230 (6.6%)	$518(5.5\%)$	965 (7.3%)	748 (6.5%)	$1888(6.3\%)$	342 (8.6%)
\geq 20-<30Gy	2189 (6.4%)	765 (8.1%)	679 (5.2%)	745 (6.5%)	1899 (6.3%)	290 (7.3%)
\geq 30Gy	3879 (11.4%)	1790 (19.0%)	$1419(10.8\%)$	671 (5.9%)	2928 (9.7%)	951 (24.0%)
Central nervous system radiation						
Yes	10185 (29.9%)	3655 (38.8%)	4344 (33.0%)	2186 (19.1%)	8457 (28.1%)	1728 (43.7%)
No	23848 (70.1%)	5761 (61.2%)	8837 (67.0%)	9250 (80.9%)	21618 (71.9%)	2230 (56.3%)
Central nervous system radiation						
dose						

Table S1. Demographic and treatment characteristics by treatment era and life status of five-year survivors of childhood cancer

Table S3. Cumulative incidence of all-cause, recurrence/progression, and health-related cause late mortality at 15 years from primary cancer diagnosis

*adjusted for sex and age at diagnosis

Table S8. Cumulative incidence of all cause and cause-specific