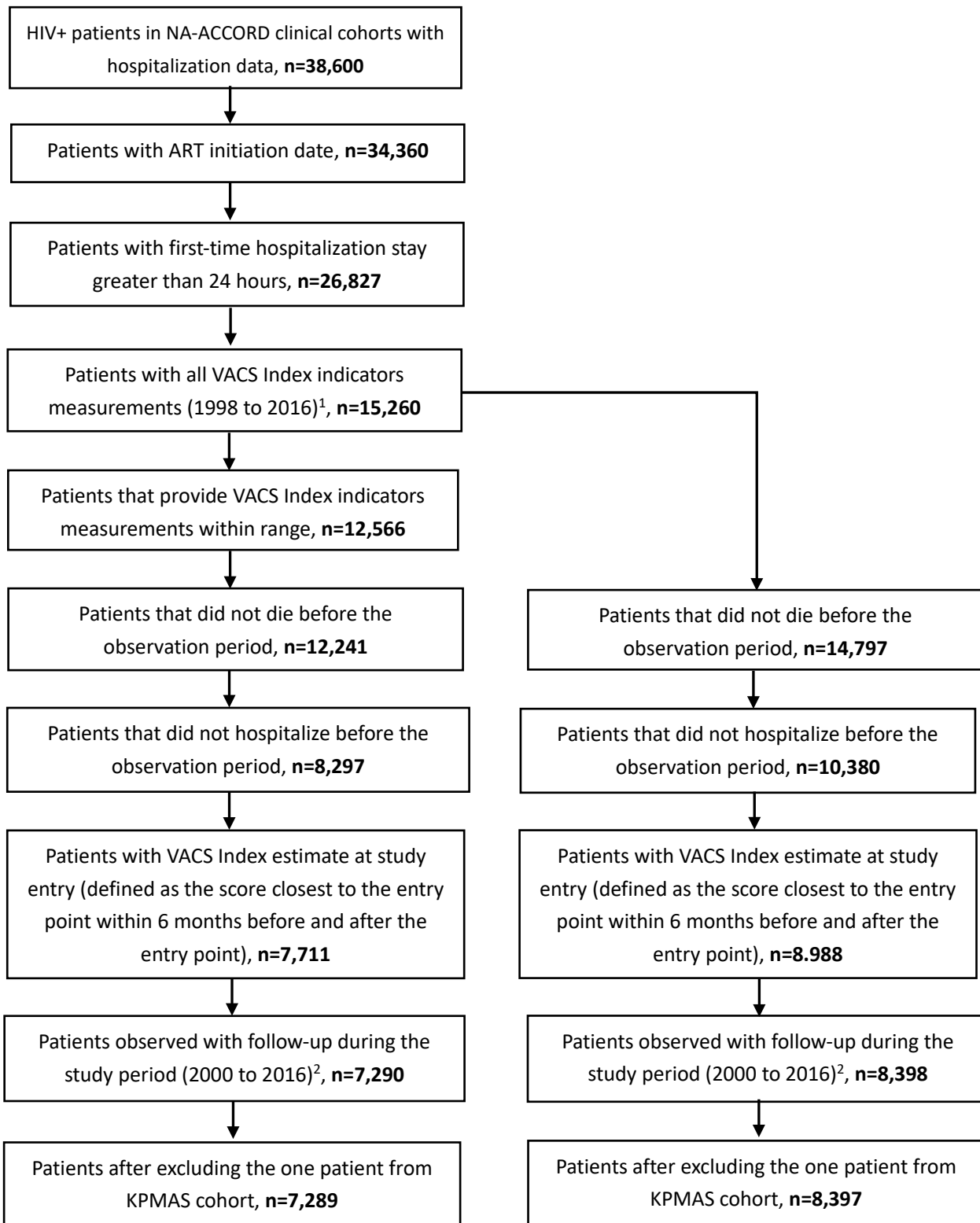


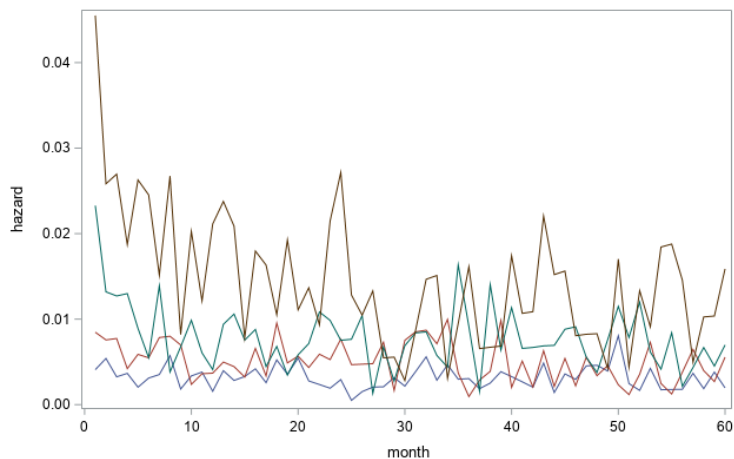
**Supplement Figure 1.** Flowchart of the selection of study population (n=7,289) from the source population (n=38,600). The main track represents the selection of the patients in the primary analyses, and the derivative track represents the selection of the patients in the sensitivity analyses.



<sup>1</sup>Patients were excluded in this step mostly due to missing albumin data.

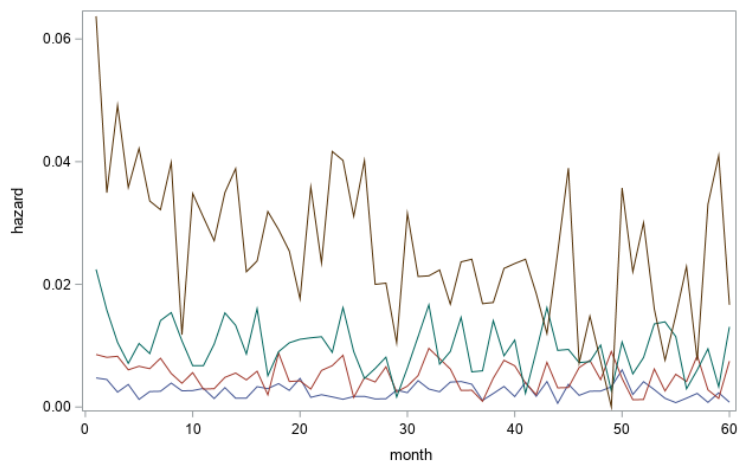
<sup>2</sup>Only one patient in Kaiser Permanente Mid-Atlantic States (KPMAS) Cohort was eligible so we chose to exclude the patient.

**Supplement Figure 2.** Observed hazard of hospitalization by parameterizations of VACS Index. A. hazard by categories of study entry VACS Index (<42, 42-53, 53-64,  $\geq 64$ ); B. hazard by categories of time-updated VACS Index (<43, 43-55, 55-68,  $\geq 68$ ); C. hazard by categories of cumulative VACS Index (<78, 78-124, 124-187,  $\geq 187$ ).



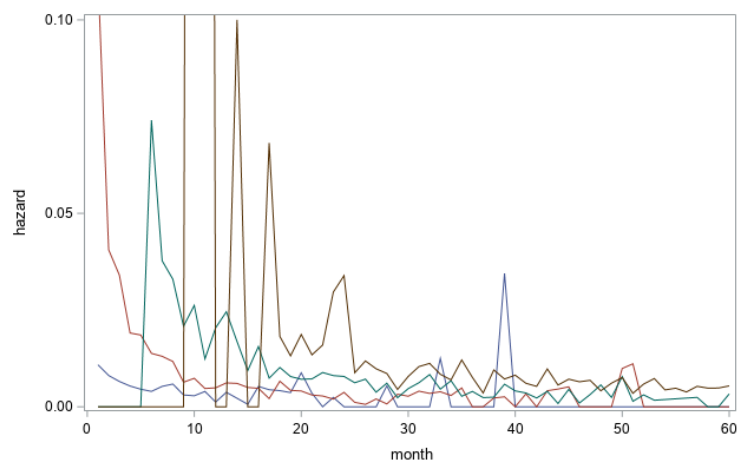
A

entry\_score\_cat — <42 — 42-53 — 53-64 —  $\geq 64$



B

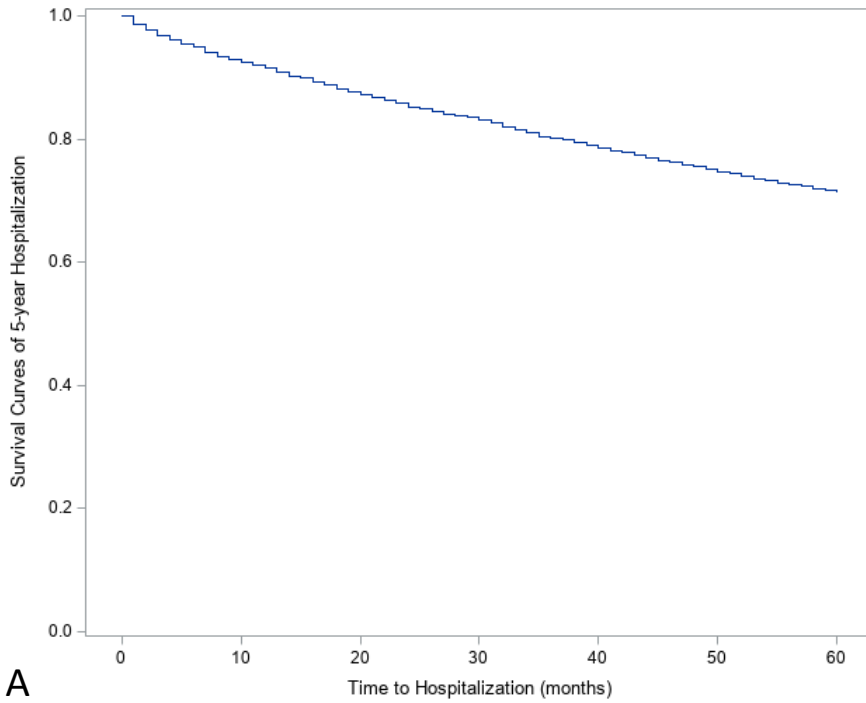
updated\_score\_cat — <43 — 43-55 — 55-68 —  $\geq 68$



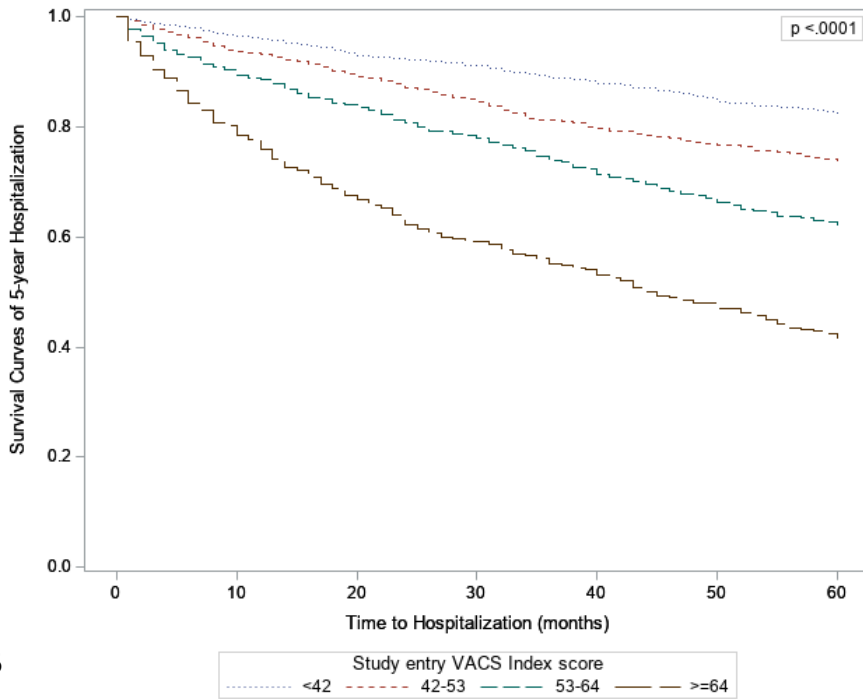
C

cumulative\_score\_cat — <78 — 78-124 — 124-187 —  $\geq 187$

**Supplement Figure 3.** Kaplan-Meier curves for hospitalization-free survival within five years. A. Overall Kaplan-Meier curve for hospitalization-free survival within five years. B. Kaplan-Meier curve for hospitalization-free survival within five years by categories of study entry VACS Index. Study entry VACS Index separated into quartiles with approximately equal number of hospitalizations within each category.



A



B

**Supplement Table 1.** Range of plausible values and associated VACS Index 2.0 score, setting all other predictors to their median value.

Predictor	Median	Range of plausible values*									
<b>Age (years)</b>											
Value	52	30	35	40	45	50	55	60	65	70	75
Score	**	32	38	41	43	44	45	47	49	53	59
<b>CD4 cell count (cells/ml)</b>											
Value	435	10	100	200	300	400	500	600	700	800	900
Score	**	55	53	51	48	45	43	40	37	34	32
<b>HIV-1 RNA (log copies/mL)</b>											
Value	1.7	1.3	1.5	1.8	2.0	2.5	3.0	3.5	4.0	4.5	5
Score	**	37	41	46	48	51	52	51	50	51	55
<b>Hemoglobin (g/dl)</b>											
Value	14	9	9.5	10	10.5	11	12	13	14	15	16
Score	**	58	58	57	55	54	51	47	44	42	42
<b>FIB-4</b>											
Value	1.34	0.50	1.00	1.45	2.00	3.25	4.00	5.00	6.00	7.00	7.50
Score	**	41	43	45	47	51	53	56	58	60	61
<b>eGFR (ml/min)</b>											
Value	90	0	20	40	60	80	100	120	140	160	180
Score	**	53	51	49	45	44	44	46	51	55	60
<b>Hepatitis C co-infection</b>											
Value	No	Yes									
Score	**	51									
<b>Albumin (g/dl)</b>											
Value	4	2.00	2.25	2.50	2.75	3.00	3.25	3.5	4.00	4.50	5.00
Score	**	65	62	59	57	54	52	49	44	41	39
<b>White blood count (k/ml)</b>											
Value	5.5	2.5	3	4	5	6	7	8	9	10	11
Score	**	43	42	42	43	46	49	51	54	55	55
<b>Body mass index (kg/m2)</b>											
Value	25.3	15	17	18	20	22	24	26	28	30	35
Score	**	62	57	55	51	48	46	44	42	41	41

\*Clinically meaningful values between lowest and highest values used in development model.

\*\*Score = 44 when all values are set to their median and Hepatitis C is set to no.

**Supplement Table 2.** Akaike Information Criterion<sup>a</sup> values for crude and adjusted complementary log-log regression models<sup>b</sup> among men and women.

	Crude	Adjusted
Male, n=6,109		
Study entry VACS Index	14638	14620
Time-updated VACS Index	<b>14230</b>	<b>14229</b>
Cumulative VACS Index	14753	14706
Female, n=1,180		
Study entry VACS Index	3693	3670
Time-updated VACS Index	<b>3596</b>	<b>3589</b>
Cumulative VACS Index	3705	3674

<sup>a</sup>AIC =  $-2(\log\text{-likelihood}) + 2K$ , K is the number of model parameters (the number of variables in the model plus the intercept). Log-likelihood is a measure of model fit. The lower the AIC value, the better the fit.

<sup>b</sup>Adjusted covariates include race/ethnicity, smoking, HIV acquisition risk factor, depression, and calendar year.

**Supplement Table 3.** Akaike Information Criterion<sup>a</sup> values for crude and adjusted complementary log-log regression models<sup>b</sup> among white, Black, and Hispanic.

	Crude	Adjusted
White, n=3,535		
Study entry VACS Index	7923	7923
Time-updated VACS Index	<b>7702</b>	<b>7705</b>
Cumulative VACS Index	7979	7973
Black, n=2,319		
Study entry VACS Index	7586	7557
Time-updated VACS Index	<b>7380</b>	<b>7366</b>
Cumulative VACS Index	7633	7590
Hispanic <sup>c</sup> , n=986		
Study entry VACS Index	2161	2170
Time-updated VACS Index	<b>2098</b>	<b>2108</b>
Cumulative VACS Index	2151	2160

<sup>a</sup>AIC =  $-2(\log\text{-likelihood}) + 2K$ , K is the number of model parameters (the number of variables in the model plus the intercept). Log-likelihood is a measure of model fit. The lower the AIC value, the better the fit.

<sup>b</sup>Adjusted covariates include sex, smoking, HIV acquisition risk factor, depression, and calendar year.

<sup>c</sup>Because of the small sample size among Hispanic, the AIC values before and after adjustment are similar.