Supplementary Material*

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* This supplementary material was provided by the authors to give readers further details on their article. The material was reviewed but not copyedited.

SUPPLEMENT 1: CALCULATION OF THE ABBREVIATED LABORATORY-BASED ACUTE PHYSIOLOGY SCORE (abLAPS)

Like the COmorbidity Point Score, version 2 (COPS2)[1], the abLAPS is assigned on a monthly basis to all Kaiser Permanente Northern California adults with a medical record number. The score is a variant of the LAPS score[2,3] except that it uses a 1-month scoring time frame (patients' laboratory records are scanned for the preceding month). The score is used for internal predictive models in combination with the COPS2 because it permits distinguishing between stable and unstable patients. For example, a patient with a COPS2 of 102 is one with a significant comorbidity burden. However, a patient with a COPS2 of 102 and an abLAPS of 12 is a much sicker one than one with an abLAPS of 2. Neither the COPS2 or abLAPS are used as prediction tools directly; rather, they are scalars used in other predictive models or as population descriptors. The table below shows the laboratory tests employed to assign the score and the rule followed when multiple laboratory test results are available over the scoring period. Missing data are imputed to normal (abLAPS subscore = 0).

Laboratory test	Points	Test result to use if multiple tests in time frame
Blood Urea Nitrogen (BUN)		
< 18	0	
18 - 19	4	Select HIGHEST
20 - 39	12	
40 - 79	19	
80+	24	
Creatinine		
< 1.0	0	
1.0 - 1.9	1	Select HIGHEST
2.0 - 3.9	7	
4.0+	5	

Laboratory test	Points	Test result to use if multiple tests in time frame
BUN:Creatinine Ratio (*1000)		
< 25.0	0	Select HIGHEST
25.0 +	6	
Hematocrit		
< 20.0	7	
20.0 - 39.9	5	
40.0 - 49.9	0	Select LOWEST
50.0 - 59.9	6	
60.0+	23	
Arterial pH		
< 7.15	30	
7.15 - 7.24	23	
7.25 - 7.34	16	
7.35 - 7.44	0	Select LOWEST
7.45 - 7.54	11	
7.55 - 7.64	14	
7.65+	14	
Arterial PaCO2		
< 25	5	
25 - 34	12	
35 – 44	0	Select HIGHEST
45 - 54	10	
55 - 64	9	
65+	13	

Laboratory test	Points	Test result to use if multiple tests in time frame
Arterial PaO2		
< 50	13	
50 - 119	0	Select LOWEST
120+	18	
Glucose		
< 40	16	If there is a value < 60, select LOWEST
40 - 59	12	
60 - 199	0	
200 - 349	3	If there are no values < 60, select HIGHEST
350+	3	
Bilirubin		
< 2.0	0	
2.0 - 2.9	10	
3.0 - 4.9	16	Select HIGHEST
5.0 - 7.9	22	
8.0+	32	
Albumin		
< 2.0	23	
2.0 - 2.4	18	Select LOWEST
2.5 - 4.4	0	
4.5+	0	
White blood cell count		
< 2.0	29	
2.0 - 4.9	6	Select LOWEST
5.0 - 12.9	0	
13.0+	15	

Laboratory test	Points	Test result to use if multiple tests in time frame
Troponin		
0	0	
0.01 - 0.19	2	
0.20 - 0.99	6	Select HIGHEST
1.00 - 2.99	18	
3.00 - 5.99	20	
6.00+	25	
Modified Sodium*		
0.0 – 4.9	0	
5.0 - 9.9	6	
10.0 - 15.9	7	Select HIGHEST
16.0 - 48.9	7	
49.0+	10	

* Algorithm to define **Modified Sodium**:

IF SODIUM = 135 to 145, Modified Sodium = 0;
ELSE IF SODIUM < 135, Modified Sodium = $[135 – SODIUM]^2$
ELSE Modified Sodium = $[SODIUM – 145]^2$

REFERENCES

1. Escobar GJ, Gardner MN, Greene JD, Draper D, Kipnis P. Risk-adjusting hospital mortality using a comprehensive electronic record in an integrated health care delivery system. *Med Care.* 2013;51(5):446-453.

2. Escobar G, Greene J, Scheirer P, Gardner M, Draper D, Kipnis P. Risk Adjusting Hospital Inpatient Mortality Using Automated Inpatient, Outpatient, and Laboratory Databases. *Medical Care.* 2008;46(3):232-239.

3. van Walraven C, Escobar GJ, Greene JD, Forster AJ. The Kaiser Permanente inpatient risk adjustment methodology was valid in an external patient population. *J Clin Epidemiol.* 2010;63(7):798-803.

SUPPLEMENT 2: GEOGRAPHIC ANALYSES

SECTION 1: DESCRIPTION OF SPATIAL CLUSTER METHODOLOGY

Coronavirus infection geographic clusters were identified using the spatial scan statistic *[Kulldorff M. A Spatial Scan Statistic. Commun Stat Theory Methods. 1997;26(6):1481-96.]* and the free SaTScan™ software (https://www.satscan.org/). Clusters identified using the spatial scan statistic can be of any size – although in our implementation no smaller than a single census block group - and are not restricted to those that conform to predefined administrative or political borders. We used the discrete Poisson version of the spatial scan statistic to detect and evaluate geographical clusters with a higher than expected number of coronavirus infections given the underlying population. This is done by gradually scanning a circular variable size window across space, noting the number of observed and expected observations inside each of many thousands of evaluated circles, and calculating the likelihood for each. The circle with the maximum likelihood is the most likely cluster - that is, the cluster least likely to be due to chance. In addition to reporting the most likely cluster, we report secondary clusters that were selected using the Gini index (a measure of statistical dispersion).*[Han J, Zhu L, Kulldorff M, Hostovich S, Stinchcomb DG, Tatalovich Z, et al. Using Gini coefficient to determining optimal cluster reporting sizes for spatial scan statistics. Int J Health Geogr. 2016;15(1):27]* Using Monte Carlo hypothesis testing, the p-value assigned to each cluster is adjusted for the multiple testing inherent in the large number of circles evaluated. We report clusters at a statistical significance level of $p<.05$.

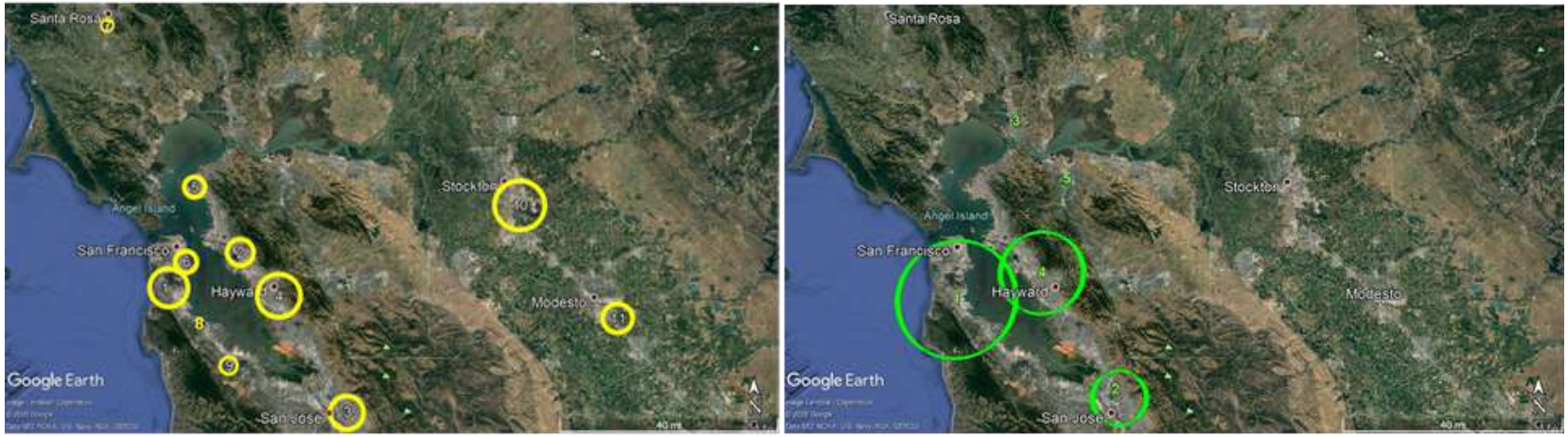
All health plan members included in this study were assigned to census block groups based on their home address as of February 2020. Coronavirus infection and member counts were input to the SaTScan software at the census block group level (with the COVID-19 cases being a subset of the member population.) Due to sparse membership outside the primary service area of KPNC, the spatial analyses were restricted to 17 counties that comprise 96% of the study

population. Spatial analyses were adjusted for age (categorical: 18-40 years, 41-64, and 65+) and sex, and separate analyses were performed on the “low-risk” members (persons with COPS2 ≤10 and abLAPS=0) and all other members.

Because we adjusted for age and sex, within each of the stratified analyses (by “low-risk” and “all other” members), the resulting clusters are not attributable to the age and sex makeup of the member population in those clusters. However, other “neighborhood” factors such as crowding, presence of multi-generational households, and types of employment, could be some of the reasons for the existence of these clusters. We chose not to adjust for Neighborhood Deprivation Index in the spatial analyses so we could identify areas with higher-than-expected coronavirus infection rates without “adjusting away” for the broad socio-economic factors that are measured by the NDI.

SECTION 2 (FIGURE): CORONAVIRUS INFECTION CLUSTERS AMONG PATIENTS WITH AND WITHOUT COMORBIDITIES

Results of geographic clustering (spatial scanning) analyses when cohort was restricted to low risk (N = 2 765 338, left panel) and all other (N = 716 378, right panel) Kaiser Foundation Health Plan members. In the low risk cohort (patients without comorbidities, left panel), our methodology identified 11 clusters with a total of 327 438 members, 84% of whom were non-White, while those not in a cluster were 58% non-White. Among the remaining non-low risk members (right panel), our methodology identified 5 clusters with a total of 129 144 members, 66% of whom were non-White, while those not in a cluster were 43% non-White. Sections 3-5, below, provide a breakdown of underlying population composition where clusters were identified as well as marginal probabilities for different racial groups



SECTION 3: TABLE SHOWING RACIAL COMPOSITION OF SPATIAL CORONAVIRUS INFECTION CLUSTERS IN LOW RISK COHORT*

Race/ethnicity	All members	Members in a cluster	Members not in a cluster
N	2,655,517	327,438	2,328,079
White	1,034,243 (39%)	53,376 (16%)	980,867 (42%)
Black/African American	160,062 (6%)	25,577 (8%)	134,485 (6%)
Hispanic	556,880 (21%)	113,131 (35%)	443,749 (19%)
Asian	530,730 (20%)	86,242 (26%)	444,488 (19%)
Other/unknown race	373,602 (14%)	49,112 (15%)	324,490 (14%)

FOOTNOTES

* Spatial analyses were restricted to KPNC members residing in one of the following 17 counties, which comprised 95% of the study population: Alameda, Contra Costa, El Dorado, Fresno, Madera, Marin, Napa, Placer, Sacramento, San Francisco, San Joaquin, San Mateo, Santa Clara, Solano, Sonoma, Stanislaus, Yolo. The spatial analysis among low-risk KPNC members identified 11 spatial clusters. The p value for the Chi-square comparing members in a cluster to those not in a cluster is < 0.001.

SECTION 4: RACIAL COMPOSITION OF SPATIAL CORONAVIRUS INFECTION CLUSTERS IN NON-LOW RISK COHORT*

Race/ethnicity	All members	Members in a cluster	Members not in a cluster
N	698,155	129,144	569,011
White	368,387 (53%)	43,899 (34%)	324,488 (57%)
Black/African American	57,967 (8%)	13,232 (10%)	44,735 (8%)
Hispanic	111,370 (16%)	25,822 (20%)	85,548 (15%)
Asian	110,407 (16%)	36,216 (28%)	74,191 (13%)
Other/unknown race	50,024 (7%)	9,975 (8%)	40,049 (7%)

FOOTNOTES

* Spatial analyses were restricted to KPNC members residing in one of the following 17 counties, which comprised 95% of the study population: Alameda, Contra Costa, El Dorado, Fresno, Madera, Marin, Napa, Placer, Sacramento, San Francisco, San Joaquin, San Mateo, Santa Clara, Solano, Sonoma, Stanislaus, Yolo. The spatial analysis among non low-risk KPNC members identified 5 spatial clusters. The p value for the Chi-square comparing members in a cluster to those not in a cluster is < 0.001.

SECTION 5: MARGINAL PROBABILITIES FOR DIFFERENT RACIAL GROUPS IN GEOGRAPHIC CLUSTERS

Race/ethnicity	Infection Main findings	Among high risk members; NDI not included in model	Among high risk members; NDI included in model	Infection Main findings	Among low risk members; NDI not included in model	Among low risk members; NDI included in model
White	1.00	1.00	1.00	1.00	1.00	1.00
Black/African American	2.01 (1.75 - 2.31)	1.90 (1.53 - 2.36)	1.70 (1.36 - 2.13)	2.01 (1.75 - 2.31)	1.96 (1.63 - 2.35)	1.80 (1.50 - 2.16)
Hispanic	3.93 (3.59 - 4.30)	3.01 (2.57 - 3.53)	2.78 (2.36 - 3.27)	3.93 (3.59 - 4.30)	3.94 (3.53 - 4.41)	3.67 (3.72 - 4.11)
Asian	2.19 (1.98 - 2.42)	1.40 (1.15 - 1.69)	1.37 (1.14 - 1.66)	2.19 (1.98 - 2.42)	2.02 (1.78 - 2.29)	2.02 (1.78 - 2.29)
Other	1.57 (1.38 - 1.78)	1.62 (1.27 - 2.08)	1.57 (1.23 - 2.02)	1.57 (1.38 - 1.78)	1.51 (1.30 - 1.76)	1.47 (1.26 - 1.71)
In-cluster	-	2.69 (2.37 - 3.06)	2.74 (2.41 - 3.12)	-	2.70 (2.48 - 2.94)	2.53 (2.32 - 2.76)

SUPPLEMENT TABLE 1: STUDY SAMPLE CHARACTERISTICS, BY RISK GROUPING *

	Low risk	Medium risk	High risk
N	2,765,338	369,530	346,848
General characteristics[†]			
Age (median, Q1 – Q3)	42.0 (30.0 - 55.0)	63.0 (48.0 - 72.0)	70.0 (60.0 - 79.0)
% male	1,338,921 (48.4%)	169,008 (45.7%)	168,189 (48.5%)
Neighborhood deprivation index (median, Q1-Q3)	-0.370 (-0.867 to 0.227)	-0.416 (-0.876 to 0.176)	-0.355 (-0.829 to 0.249)
CCI score ≥ 4 (%)	1,926 (0.1%)	15,606 (4.2%)	119,600 (34.5%)
Elixhauser score ≥ 6 (%)	49,249 (1.8%)	44,714 (12.1%)	153,201 (44.2%)
COPS2 ≥ 65 (%)	0 (0%)	0 (0%)	85,043 (24.5%)
abLAPS ≥ 10 (%)	0 (0%)	15,645 (4.2%)	37,015 (10.7%)
Racial composition			
% White	1,083,275 (39.2%)	190,452 (51.5%)	190,143 (54.8%)
% Black/African American	162,930 (5.9%)	28,483 (7.7%)	30,268 (8.7%)
% Hispanic	578,640 (20.9%)	61,399 (16.6%)	53,064 (15.3%)
% Asian	537,731 (19.4%)	62,568 (16.9%)	48,796 (14.1%)
% Other/unknown race	402,762 (14.6%)	26,628 (7.2%)	24,577 (7.1%)
Testing and incidence[‡]			
% tested	2.15	3.31	5.61
Positive test rate (%)	4.47	3.76	2.91
Incidence	96.2	124.8	162.9
Outcomes[§]			
Hospitalization rate	13.2	38.7	84.2
Admission to ICU	4.4	11.9	23.1
Intermittent mandatory ventilation	4.2	11.6	22.2
Inpatient death	0.98	5.14	14.13
Death during study period	1.08	7.58	29.12

FOOTNOTES

* Using the COPS2 and abLAPS, we grouped patients into low, medium, and high risk groups as follows. The low risk group was defined as consisting of those patients with the lowest possible scores (COPS2 <11 and abLAPS = 0). After removing these patients, we divided the remaining patients using (a) the upper and lower half of the abLAPS distribution and (b) terciles for the rest of the COPS2 distribution, as shown in the figure below.

<table>
<tr><td colspan="2" rowspan="2">Patients with COPS2 ≥ 11
or abLAPS ≥ 1</td><td colspan="3">COPS2</td></tr>
<tr><td>COPS2
0 to 14</td><td>COPS2
15 to 31</td><td>COPS2
32 to 555</td></tr>
<tr><td rowspan="2">abLAPS</td><td>abLAPS 0</td><td colspan="2" rowspan="2">Medium risk</td><td rowspan="2"></td></tr>
<tr><td>abLAPS 1 to 164</td></tr>
<tr><td colspan="3"></td><td>High risk</td></tr>
</table>

† See main text for details and citations on the neighborhood deprivation index, Charlson Comorbidity Index (CCI) score, Elixhauser score, COPS2, and abLAPS.

‡ Denominator for testing is entire population; denominator for positive test rate is members who were ever tested. Incidence is per 100,000 members.

§ All rates are per 100,000 members; ICU = intensive care unit.

SUPPLEMENT TABLE 2: RISK GROUPINGS BASED ON COPS2 AND abLAPS*

	White	Black / African American	Hispanic	Asian	Other	Overall
N	1,463,870	221,681	693,103	649,095	453,967	3,481,716
Low risk	1,083,275 (74.0%)	162,930 (73.5%)	578,640 (83.5%)	537,731 (82.8%)	402,762 (88.7%)	2,765,338 (79.4%)
Medium risk	190,452 (13.0%)	28,483 (12.8%)	61,399 (8.9%)	62,568 (9.6%)	26,628 (5.9%)	369,530 (10.6%)
High risk	190,143 (13.0%)	30,268 (13.7%)	53,064 (7.7%)	48,796 (7.5%)	24,577 (5.4%)	346,848 (10.0%)

FOOTNOTES

Comorbidity groupings are the same as Table 1, above.

SUPPLEMENT TABLE 3: PREVALENCE OF ELIXHAUSER COMORBIDITIES IN THE STUDY COHORT*

	All	White	Black/African American	Hispanic	Asian	Other/Unknown race
N	3,481,716	1,463,870	221,681	693,103	649,095	453,967
Congestive heart failure	1.2%	1.6%	2.1%	0.8%	0.7%	0.7%
Valvular disease	0.7%	1.0%	0.7%	0.4%	0.5%	0.4%
Pulmonary circulation disorders	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%
Peripheral vascular disease	7.6%	10.6%	8.4%	5.2%	5.4%	4.0%
Depression	3.6%	4.7%	4.7%	3.6%	1.8%	2.3%
Paralysis	0.5%	0.6%	1.0%	0.4%	0.4%	0.3%
Other neurological disorders	2.2%	3.1%	2.8%	1.7%	1.3%	1.3%
Chronic pulmonary disease	6.9%	8.4%	10.2%	6.5%	4.9%	4.3%
Diabetes without chronic complications	6.8%	5.8%	10.0%	8.3%	8.1%	4.4%
Diabetes with chronic complications	6.0%	5.5%	8.9%	6.7%	6.7%	3.8%
Hypothyroidism	3.9%	5.3%	2.3%	3.2%	3.1%	2.3%
Renal failure	3.1%	3.9%	5.3%	2.2%	2.6%	1.8%
Liver disease	2.5%	2.3%	2.5%	2.6%	3.5%	1.3%
Chronic peptic ulcer disease	0.1%	0.1%	0.1%	0.1%	0.1%	0.1%
HIV and AIDS	0.1%	0.2%	0.3%	0.1%	0.0%	0.1%
Lymphoma	0.2%	0.3%	0.3%	0.2%	0.1%	0.1%
Metastatic cancer	0.5%	0.7%	0.6%	0.3%	0.4%	0.2%
Solid tumor without metastasis	1.6%	2.2%	2.0%	1.1%	1.3%	0.7%
Rheumatoid arthritis/collagen vascular diseases	1.1%	1.4%	1.5%	1.1%	0.8%	0.7%
Coagulation deficiency	0.6%	0.7%	0.7%	0.5%	0.4%	0.3%
Obesity	5.9%	6.4%	11.0%	7.9%	2.7%	3.4%

	All	White	Black/African American	Hispanic	Asian	Other/Unknown race
Weight loss	0.6%	0.7%	1.1%	0.4%	0.4%	0.3%
Fluid and electrolyte disorders	1.4%	1.6%	2.2%	1.2%	1.1%	0.8%
Blood loss anemia	0.4%	0.3%	0.6%	0.5%	0.5%	0.2%
Deficiency anemias	2.4%	2.3%	4.9%	2.6%	2.4%	1.5%
Alcohol abuse	0.7%	1.0%	0.8%	0.6%	0.2%	0.4%
Drug abuse	0.5%	0.7%	0.9%	0.5%	0.1%	0.3%
Psychoses	3.2%	4.7%	3.6%	2.5%	1.3%	2.0%
Hypertension (any)	16.1%	18.5%	25.0%	13.5%	15.1%	9.1%

FOOTNOTES

* Rates are based on methodology of Elixhauser et al. (1998)

SUPPLEMENT TABLE 4: PREVALENCE OF ELIXHAUSER COMORBIDITIES IN HOSPITALIZED PATIENTS*

	All	White	Black/African American	Hispanic	Asian	Other
N	799	206	79	290	162	62
Congestive heart failure	8.6%	15.5%	11.4%	3.8%	4.3%	16.1%
Valvular disease	2.5%	3.4%	3.8%	1.4%	1.9%	4.8%
Pulmonary circulation disorders	0.9%	1.0%	3.8%	0.0%	0.6%	1.6%
Peripheral vascular disease	28.2%	50.0%	39.2%	13.4%	22.8%	24.2%
Depression	5.1%	9.2%	3.8%	3.1%	2.5%	9.7%
Paralysis	3.8%	5.8%	10.1%	1.7%	2.5%	1.6%
Other neurological disorders	10.4%	21.4%	13.9%	2.1%	8.0%	14.5%
Chronic pulmonary disease	16.0%	25.2%	17.7%	13.1%	8.0%	17.7%
Diabetes without chronic complications	24.2%	17.5%	27.8%	26.9%	24.1%	29.0%
Diabetes with chronic complications	25.0%	24.8%	34.2%	22.8%	23.5%	29.0%
Hypothyroidism	7.5%	16.5%	5.1%	4.1%	2.5%	9.7%
Renal failure	14.3%	24.3%	17.7%	7.6%	8.6%	22.6%
Liver disease	7.6%	9.7%	3.8%	8.6%	4.9%	8.1%
Chronic peptic ulcer disease	0.3%	0.5%	0.0%	0.0%	0.6%	0.0%
HIV and AIDS	0.5%	1.0%	1.3%	0.0%	0.0%	1.6%
Lymphoma	1.1%	1.5%	0.0%	0.3%	1.9%	3.2%
Metastatic cancer	1.3%	1.9%	1.3%	0.7%	1.9%	0.0%
Solid tumor without metastasis	3.0%	5.3%	3.8%	1.7%	2.5%	1.6%
Rheumatoid arthritis/collagen vascular diseases	3.9%	5.8%	6.3%	2.1%	1.2%	9.7%
Coagulation deficiency	2.8%	4.9%	0.0%	2.1%	1.2%	6.5%
Obesity	15.4%	15.5%	21.5%	18.6%	6.2%	16.1%
Weight loss	3.4%	5.3%	7.6%	2.1%	1.2%	3.2%

	All	White	Black/African American	Hispanic	Asian	Other
Fluid and electrolyte disorders	6.9%	9.7%	6.3%	4.8%	3.7%	16.1%
Blood loss anemia	2.1%	1.9%	0.0%	3.8%	0.6%	1.6%
Deficiency anemias	12.1%	19.4%	11.4%	10.0%	4.3%	19.4%
Alcohol abuse	1.0%	1.5%	1.3%	0.7%	0.0%	3.2%
Drug abuse	1.6%	4.4%	2.5%	0.7%	0.0%	0.0%
Psychoses	8.0%	16.0%	7.6%	3.8%	4.9%	9.7%
Hypertension (any)	42.6%	51.0%	62.0%	34.8%	33.3%	50.0%

FOOTNOTES

* Rates are based on methodology of Elixhauser et al. (1998)

SUPPLEMENT TABLE 5: MARGINAL PROBABILITIES FOR DIFFERENT RACIAL GROUPS

Race/ethnicity	Marginal probability (%)*					
	Ever Tested	Covid Positive	Hospitalization	LAPS2	Hospital Death	All Death
White	2.59% (2.57%-2.62%)	0.05% (0.05%-0.06%)	18.42% (16.08%-20.76%)	70.76% (66.40%-75.12%)	11.82% (7.98%-15.67%)	4.28% (3.31%-5.24%)
Black/African American	3.08% (3.01%-3.15%)	0.11% (0.10%-0.12%)	23.65% (19.21%-28.09%)	78.74% (72.00%-85.48%)	9.99% (4.14%-15.84%)	4.50% (2.70%-6.31%)
Hispanic	2.93% (2.89%-2.98%)	0.21% (0.20%-0.22%)	23.14% (21.06%-25.22%)	77.43% (73.80%-81.07%)	13.27% (8.74%-17.81%)	4.15% (2.88%-5.43%)
Asian	2.55% (2.51%-2.59%)	0.12% (0.11%-0.13%)	23.68% (20.83%-26.53%)	83.39% (78.68%-88.09%)	11.87% (6.75%-16.98%)	4.74% (3.26%-6.21%)
Other	2.06% (2.02%-2.10%)	0.09% (0.08%-0.09%)	18.76% (14.98%-22.53%)	82.54% (75.06%-90.03%)	9.89% (2.08%-17.70%)	3.80% (1.86%-5.75%

FOOTNOTES

* This is the adjusted probability (absolute risk) of a patient of a given race having the outcome after controlling for all the covariates listed in Table 3 in the main text.