









ORIGINAL RESEARCH

# How Well Do ICD-9-CM Codes Predict True Congenital Heart Defects? A Centers for Disease Control and Prevention-Based Multisite Validation Project

Fred H. Rodriguez III , MD; Cheryl L. Raskind-Hood , MS, MPH; Trenton Hoffman , MS; Sherry L. Farr , PhD; Jill Glidewell, MSN, MPH; Jennifer S. Li , MD; Alfred D'Ottavio , BSE, BEE; Lorenzo Botto, MD; Matthew R. Reeder , MPH; Daphne Hsu , MD; George K. Lui , MD; Anaclare M. Sullivan , MS; Wendy M. Book , MD

**BACKGROUND:** The Centers for Disease Control and Prevention's Surveillance of Congenital Heart Defects Across the Lifespan project uses large clinical and administrative databases at sites throughout the United States to understand population-based congenital heart defect (CHD) epidemiology and outcomes. These individual databases are also relied upon for accurate coding of CHD to estimate population prevalence.

**METHODS AND RESULTS:** This validation project assessed a sample of 774 cases from 4 surveillance sites to determine the positive predictive value (PPV) for identifying a true CHD case and classifying CHD anatomic group accurately based on 57 *International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM)* codes. Chi-square tests assessed differences in PPV by CHD severity and age. Overall, PPV was 76.36% (591/774 [95% CI, 73.20–79.31]) for all sites and all CHD-related *ICD-9-CM* codes. Of patients with a code for complex CHD, 89.85% (177/197 [95% CI, 84.76–93.69]) had CHD; corresponding PPV estimates were 86.73% (170/196 [95% CI, 81.17–91.15]) for shunt, 82.99% (161/194 [95% CI, 76.95–87.99]) for valve, and 44.39% (83/187 [95% CI, 84.76–93.69]) for "Other" CHD anatomic group ( $\chi^2=142.16$ ,  $P<0.0001$ ). *ICD-9-CM* codes had higher PPVs for having CHD in the 3 younger age groups compared with those >64 years of age, ( $\chi^2=4.23$ ,  $P<0.0001$ ).

**CONCLUSIONS:** While CHD *ICD-9-CM* codes had acceptable PPV (86.54%) (508/587 [95% CI, 83.51–89.20]) for identifying whether a patient has CHD when excluding patients with *ICD-9-CM* codes for "Other" CHD and code 745.5, further evaluation and algorithm development may help inform and improve accurate identification of CHD in data sets across the CHD *ICD-9-CM* code groups.

**Key Words:** birth defects ■ congenital heart defects ■ epidemiology ■ surveillance ■ validation

**R**esearch and surveillance of patients with congenital heart defects (CHD) using administrative and clinical data both rely on the diagnostic accuracy of applying *International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM)* and *International Classification of Diseases, Tenth Revision, Clinical Modification (ICD-10-CM)* codes to detect CHD

cases. Administrative data, commonly referred to as claims data, are data created for the purpose of either the billing of health care encounters or record keeping for a health care system or an organization. *ICD* codes captured in administrative data may vary by medical practice, health care system, and region; thus, it is unknown how representative these *ICD* codes are for their intended

Correspondence to: Fred H. Rodriguez III, MD, 2835 Brandywine Rd, Suite 400, Atlanta, GA 30341. Email: [fred.rodriguez@emory.edu](mailto:fred.rodriguez@emory.edu)

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## CLINICAL PERSPECTIVE

### What Is New?

- Four US sites associated with the Centers for Disease Control and Prevention's Surveillance of Congenital Heart Defects Across the Lifespan project validated a sample of 774 cases with *International Classification of Diseases, Ninth Revision, Clinical Modification (ICD-9-CM)* congenital heart disease (CHD) codes to assess true CHD cases.
- The majority of cases were associated with true CHD, though differences in positive predictive value (PPV) were noted based on anatomic complexity and ages of patients.
- Cases with complex CHD codes, multiple CHD codes, and age groups <65 years of age had greater PPV identifying true CHD.

### What Are the Clinical Implications?

- *ICD-9-CM* codes can identify patients with CHD in databases with high PPV for the complex code group, but lower PPV in certain patient groups, particularly those aged >65 years, and with "Other" CHD *ICD* code group.
- When attempting to identify cases with CHD, the presence of >1 CHD code increases the PPV for a true CHD, at the expense of sensitivity.
- Development of algorithms is needed to improve the identification of CHD cases in databases across anatomic code groups and age ranges.

## Nonstandard Abbreviations and Acronyms

<b>CDC</b>	Centers for Disease Control and Prevention
<b>eHR</b>	electronic health record

disease state. In a recent study conducted by Khan et al. (2018), *ICD-9-CM* administrative codes extracted from the electronic health record (eHR) of patients with various types of CHD lesions seen at a large academic health care system were <50% accurate (48.7% [95% CI, 47%–51%]) at classifying those with a true CHD.<sup>1</sup> However, when only patients with moderate or complex CHD anatomy were included, the positive predictive value (PPV) of having CHD increased to 77.2%, (95% CI, 74%–81%). When other factors like younger age, adult CHD, provider type, and ECG, or echocardiogram were documented at the CHD-related encounter, the C-statistic was 0.89 (95% CI, 0.88–0.90).<sup>1</sup> Correctly and consistently applied definitions of CHD may increase the accuracy of CHD

prevalence, health care use, and health outcomes of individuals living with CHD using administrative health care data sets. However, prior studies have demonstrated that some *ICD-9-CM* codes may be associated with false positives and thus do not always reliably identify individuals who truly have CHD.<sup>1–5</sup>

In studies of CHD using publicly available data sets like the National Inpatient Sample and the Kids' Inpatient Database or administrative data sources, a CHD case is typically defined by *ICD-9-CM* codes 745.xx to 747.xx for classification and more recently *ICD-10-CM* codes Q20 to Q28. While the range of these codes is broad and inclusive, this code group contains conditions that are not CHD, and thus, may include individuals who do not have CHD, creating misleading conclusions and misinformation. Furthermore, some codes in the CHD group may code for CHD, but may commonly be used incorrectly, as for "rule out" or normal variants. In particular, individuals with 1 CHD-related *ICD-9-CM* code —745.5— are often misclassified as having CHD. Frequently found in large CHD administrative data sets and commonly included in CHD literature, the *ICD-9-CM* code 745.5 (hereafter referred to as "code 745.5") is used for both secundum atrial septal defect, a true CHD, and patent foramen ovale, a normal variant and not considered a CHD, seen in about 25% of the population.<sup>2</sup>

The current project aims to validate the extent to which CHD-related *ICD-9-CM* codes correctly identify CHD cases in administrative and clinical records by: (1) confirming patients as having a true CHD; and (2) classifying CHD anatomic grouping among those with true CHD. We hypothesized that both individual CHD codes and CHD anatomic groupings would have a high PPV (>80%) for CHD that would vary by anatomic group, but that coding errors would likely include patients who did not truly have a CHD.

## METHODS

This analysis has been replicated by 2 independent analysts. Because of the sensitive nature of the data collected for this study, requests to access the data set from qualified researchers trained in human subject confidentiality protocols may be sent to the Centers for Disease Control and Prevention (CDC) at [jill.glidewell@cdc.hhs.gov](mailto:jill.glidewell@cdc.hhs.gov).

To improve upon CHD classification and as part of the multiyear CDC-sponsored project Surveillance of Congenital Heart Defects Across the Lifespan (CDC-RFA-DD15-1506),<sup>6</sup> 4 sites reviewed the medical records of cases with CHD-related *ICD-9-CM* codes identified from administrative data sources to calculate the PPV of these codes (745.xx–747.xx) in correctly identifying a case with CHD. Cases were ascertained

by the presence of any CHD-related 745.xx to 747.xx *ICD-9-CM* code documented in a health care encounter between January 1, 2011 and December 31, 2013. Inclusion criteria defined a case having the presence of any included *ICD-9-CM* code at any encounter, regardless of how many encounters had CHD *ICD-9-CM* codes. The *ICD-9-CM* codes to define the *ICD* code-based anatomic groups were based on a hierarchy of codes, complex>shunt and valve>shunt or valve>“Other” CHD. The following codes were excluded as they were determined to be reflective of conditions other than true CHD: congenital heart block (746.86), absent/hypoplastic umbilical artery (747.5), pulmonary arteriovenous malformation (747.32), other anomalies of peripheral vascular system (747.6x), and other specified anomalies of circulatory system (747.8x); these codes were also excluded from the definition of CHD in the prior surveillance methods paper.<sup>5,6</sup> Cases with code 745.5 without another included CHD *ICD-9-CM* code were also excluded based on previous studies.<sup>2,3</sup> The Institutional Review Boards from Duke University in North Carolina (NC), Emory University in Georgia (GA), the New York State Department of Health (NY), and University of Utah (UT) approved an analysis of deidentified data to assess PPV of CHD-related *ICD-9-CM* codes.<sup>6</sup> The requirement for informed consent was waived by each site’s respective Institutional Review Board. Eligible codes were classified into 1 of 5 CHD anatomic groups: complex, shunts, valves, shunts and valves, and “Other” CHD or non-specific defects<sup>5–8</sup> (Figure 1 and Data S1). Complex anatomy was based on native anatomy and defined as heart defects characterized by a recognized constellation of multiple specific defects which generally require intervention in the first year of life. Specific defects grouped as “complex” are defined in Data S1.<sup>5,6</sup> A code-based hierarchy was developed such that the presence of a complex code designates the case as complex regardless of additional codes.<sup>6</sup> In the absence of a complex code, the presence of both a shunt and valve code designated “shunt and valve” group inclusion. The absence of complex, shunt or valve codes and only “Other” CHD anatomic group codes designated the case as belonging to the “Other” CHD anatomic group (Figure 1).

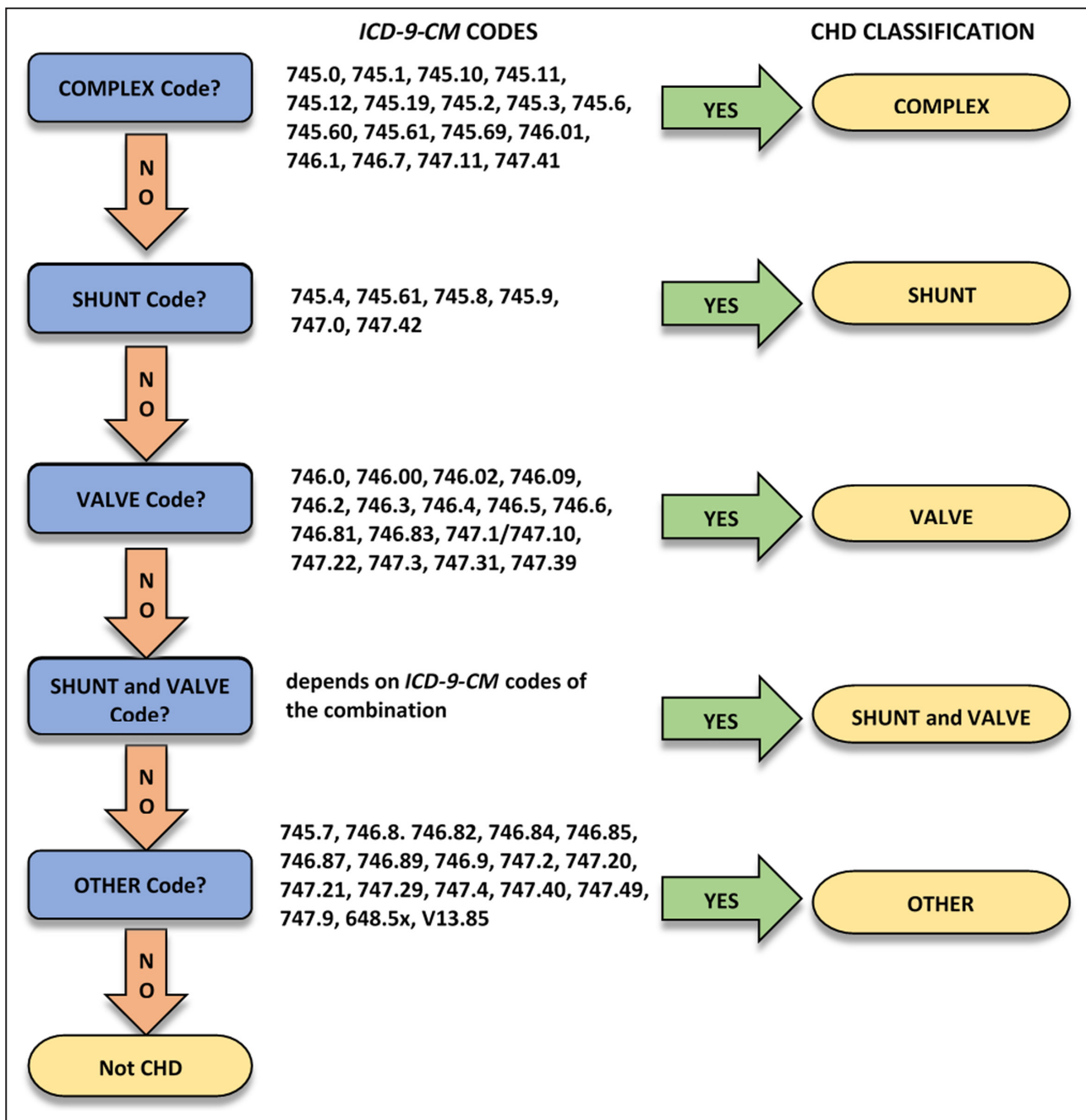
## Data and Procedures

Data from the 4 sites (GA, NC, NY, UT) over a 3-year project period, 2011 to 2013, were used for this validation. A total of 800 cases were planned for the validation study consisting of 200 cases from each of the 4 sites. Each site selected 50 cases from 4 mutually exclusive CHD anatomic groups as defined by the *ICD* code hierarchy (Figure 1) based on native anatomy: complex, shunt, valves, and “Other”, with each group further stratified by age: 1 to 10years, 11 to 19years, 20 to

64years, >64years (GA, NC, NY), or ages 11 to 19years and 20 to 64years (UT). Anatomic groups are described in Figure 1 and Data S1. To ensure a comparable distribution of cases by age, the data set was stratified by age group and a proportion was selected, based on the age distribution of the larger cohort, into each of the 4 mutually exclusive anatomic groups (Figure 2). Only those data sources where medical charts were accessible for review were eligible for inclusion. Cases identified only in administrative data, but without clinical records to review, were excluded. Of the total cases from the larger CHD surveillance project, 69.4% of GA’s cases, 36.7% of NC’s cases, 32.5% of NY’s cases, and 97.6% of UT’s cases were eligible for medical chart review and selection for the validation project.

During medical chart review, clinical investigators at each site supervised the review of predetermined variables abstracted from eHRs and noted the presence/absence of a true CHD based on review of CHD anatomy as determined by: (1) cardiac imaging, (2) clinical diagnosis by an outpatient or inpatient encounter with a pediatric or adult CHD provider, (3) CHD surgery, and (4) autopsy report. Included in this review, clinical investigators evaluated: (1) CHD case (Yes/No), and (2) CHD anatomic group correct (Yes/No). All available information from the eHR (including any data before 2011 or after 2013) was also used to confirm or refute the presence of CHD for each selected case. During chart review, information on type of CHD recorded, number of unique CHD codes per case, diagnostic tests received (ie, echocardiograms, cardiac catheterizations, cardiac surgery), autopsy reports or clinic notes, as well as date of diagnosis and type of provider who made the CHD diagnosis was evaluated. Additionally, demographic information including age, sex, race, and ethnicity was abstracted. With respect to race, small sample size for the “Other” race category necessitated this group be combined with the “unknown” race group (“Other” race includes American Indian/Alaskan Native, Asian, native Hawaiian/Pacific Islander, and multi-racial).

The anatomic group of shunt and valve was excluded before case selection because it was assumed that if the case had codes for both of these anatomic groups, then the case was likely to be a true CHD case. Cases with code 745.5 in isolation or in combination with 746.89 or 746.9 were also excluded given the known poor PPV of these codes to represent a true CHD.<sup>2</sup> A total of 26 cases were excluded from analysis: 12 cases with code 745.5 in isolation or in combination with 746.89 or 746.9 among the sites that were found to be included in error after selection; 5 cases with both a shunt and valve diagnosis that were also erroneously selected for validation; 3 cases that did not have any clinical data to review; 3 cases that were inadvertently reviewed twice; and lastly, 3 cases whose only CHD code(s) were documented during

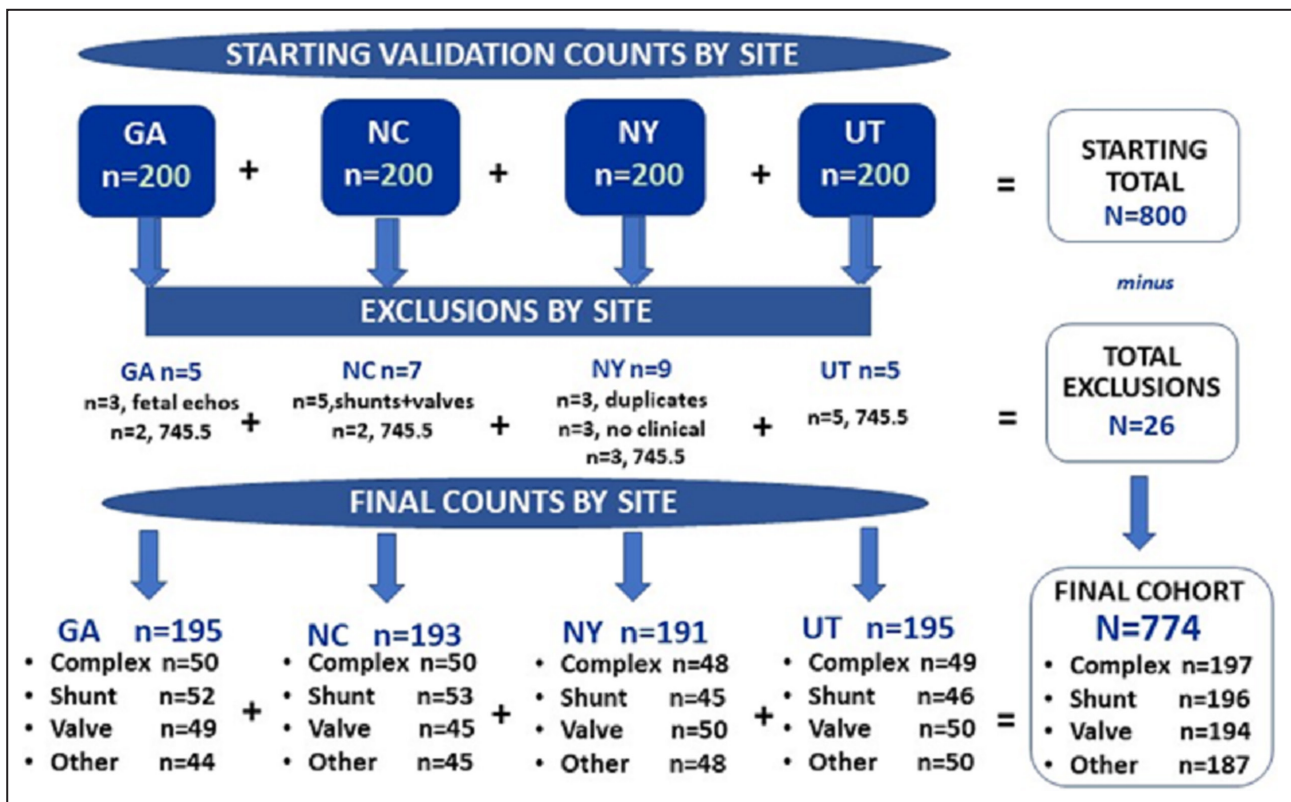


**Figure 1. ICD-9-CM code-based hierarchy for congenital heart defect classification by native CHD anatomy group.**  
 \*Based on hierarchy reported in Ref. [6]. Individuals aged 1 to 64 years with documented congenital heart defects at health care encounters, 5 US surveillance sites, 2011 to 2013. CHD indicates congenital heart defect; and ICD-9-CM, International Classification of Diseases, Ninth Revision, Clinical Modification.

an encounter for a fetal echocardiogram defined by the associated Current Procedural Terminology code (Figure 2). CHD codes occurring during performance of a fetal echocardiogram were excluded based on unpublished data showing that only 2.9% (4 out of 138) of women who had a CHD code solely associated with a fetal echocardiogram encounter actually had a true CHD, whereas the majority of CHD diagnosis codes

documented during fetal echocardiogram encounters are intended for the fetus.

For GA, 200 cases, who resided in 1 of 5 metropolitan-Atlanta counties (Clayton, Cobb, DeKalb, Fulton, Gwinnett) and were seen at least once at 1 of 3 health care systems with records available, were randomly selected for review. For the 1- to 10- and 11- to 19-year-old groups, 13 cases for each CHD anatomic class were



**Figure 2. Cohort constructions and exclusions by site and congenital heart defect type.<sup>†,§</sup>**

<sup>†</sup>ICD-9-CM code 745.5 was omitted from the shunt group as it is used to indicate secundum atrial septal defect and patent foramen ovale, a normal variant. <sup>§</sup>“Other” congenital heart defect anatomic group consists of unspecified defects; congenital heart defect-related ICD-9-CM codes and their assigned CHD anatomic grouping are displayed in Data S1. GA indicates Emory University in Georgia; ICD-9-CM, *International Classification of Diseases, Ninth Revision, Clinical Modification*; NC, Duke University in North Carolina; NY, New York State Department of Health; and UT, Utah.

selected, and for the 20- to 64- and >64-year-old groups, 12 cases for each anatomic class were selected. A total of 195 validated GA cases were retained and contributed to the pooled analyses (Figure 2).

For NC, 200 cases, each with at least 2 encounters, were randomly selected from eHRs at one data source which captured patients with CHD statewide. Similar to GA, 13 cases each for the 1- to 10- and 11- to 19-year-old groups, and 12 cases each for the 20- to 64- and >64-year-old groups were selected for review. A total of 193 validated NC cases were included for pooled analyses with other sites' data (Figure 2).

NY's sample of 200 cases was composed of patients who resided in 1 of 11 counties (Allegany, Bronx, Cattaraugus, Chautauqua, Erie, Genesee, Monroe, Niagara, Orleans, Westchester, Wyoming) in NY and who had a health care encounter at 1 of 2 clinical data sources. NY, like GA and NC, randomly selected 13 cases for each CHD anatomic class for 1- to 10-year-olds and 11- to 19-year-olds, and 12 cases for the 20- to 64-year-olds and >64-year-old groups. A total of 191 NY cases were retained and contributed to pooled analyses (Figure 2).

In UT, data sources included eHRs from 2 health care systems. While 200 CHD cases were randomly selected and stratified by anatomic groupings with 50 in each category, these classes were further stratified by 2 age groupings, 11- to 19-year-olds and 20- to 64-year-olds, with 25 cases each. Although the UT site did not collect data on individuals aged <10 or >64 years, they contributed a total of 195 validated cases to the pooled, multisite data set (Figure 2).

## Statistical Analysis

PPVs for CHD were calculated overall, and by anatomic group, site, and number of unique CHD codes associated with a case. In addition, separate PPV analyses were conducted by sex, race, ethnicity, age group, and anatomic group. For age-specific analyses, since UT did not contribute cases to the youngest age group, 1- to 10-year-olds, or the oldest age group category, >64-year-olds, UT was not included; age-specific analyses included GA, NC, and NY only. For age-specific analyses, PPV was first computed for age groups by sites, and then, also calculated omitting

the “Other” CHD anatomic group, followed by omitting the >64-year-old age group, and finally, by omitting both the “Other” CHD anatomic group and the >64-year-old age group. Analyses for CHD anatomic group proceeded similarly except all 4 sites were included. Lastly, PPVs for having CHD (Yes/No) were calculated for several individual CHD *ICD-9-CM* codes and calculated by number of unique CHD codes.

## RESULTS

**Table 1** shows number of cases by CHD anatomic groups, number of unique CHD-related *ICD-9-CM* codes (single/multiple) recorded in encounters, followed by demographic characteristics of the sample, overall and by site. Slightly over half (51.16%,  $n=396$ ) of the 774 cases were female, and 53.49% ( $n=414$ ) had a single unique CHD-related *ICD-9-CM* code recorded in the medical record. No significant differences were revealed for number of unique *ICD-9-CM* codes by site ( $X^2=7.14$ ,  $P=0.0675$ ) or sex by site ( $X^2=2.77$ ,  $P=0.4278$ ). No significant differences between age groups by site (GA, NC, and NY) in percent of individuals with one CHD-related *ICD-9-CM* code were observed ( $X^2=4.04$ ,  $P=0.6706$ ). Across and by site, however, White race was most prevalent accounting for 66.67% of the sample, followed by Black and other/unknown race, 16.93% and 16.41%, respectively. The contribution of Black cases varied by site, with GA providing almost 40% of the cases, while UT contributed <5% ( $X^2=69.97$ ,  $P<0.0001$ ). The majority of the sample were non-Hispanic (70.03%), and 18.86% of the sample’s ethnicity was unknown ( $X^2=161.38$ ,  $P<0.0001$ ) (**Table 1**).

The PPVs of having a CHD overall, by site, and by anatomic group with “Other” CHD anatomic group status (included/omitted) are seen in **Table 2**. PPV of having a CHD increased  $\approx 10$  percentage points from 76.36% (591/774; [95% CI, 73.20–79.31]) to 86.54% (508/587 [95% CI, 83.51–89.20]) after omitting the “Other” CHD anatomic group ( $X^2=22.28$ ,  $P<0.0001$ ). This pattern was also observed within each site: the increase in PPV ranged from 7.4% for NC (79.79%; 154/193 [95% CI, 73.43–85.22]) to 87.16%; 129/148 [95% CI, 80.68–92.09]) (ns) to 14.6% for NY (70.68%; 135/191 [95% CI, 63.68–77.03] to 85.31%; 122/143 [95% CI, 78.43–90.67]); site-specific Chi-squares are for when “Other” CHD anatomic group was included versus omitted (**Table 2**). When all anatomic groups were combined regardless of whether “Other” CHD anatomic group was included or omitted, significant differences in PPV by site were not observed ( $X^2=5.15$ ,  $P=0.1612$  and  $X^2=0.35$ ,  $P=0.9509$ , respectively) (**Table 2**). However, there was a significant difference in PPV for having a CHD by anatomic group. Of patients with a code for complex CHD, 89.85%

(177/197 [95% CI, 84.76–93.69]) had a CHD (ie, 10.15% (20/197; 95% CI, 6.31–15.24) did not have CHD); corresponding PPV estimates were 86.73% (170/196 [95% CI, 81.17–91.15]) for shunt, 82.99% (161/194 [95% CI, 76.95–87.99]) for valve, and 44.39% (83/187 [95% CI, 84.76–93.69]) for “Other” CHD anatomic group ( $X^2=142.16$ ,  $P<0.0001$ ) (**Table 2**). In **Table S1**, for the complex and shunt categories, all sites reported PPVs >84.00%; for the valve category, UT’s PPV was 76.0% (38/50 [95% CI, 61.83–86.94]) with other sites’ PPVs >80% (89.80%; 44/49 [95% CI, 77.77–96.60]) for GA, 84.44% (38/45 [95% CI, 70.54–93.51]) for NC, and 82.00% (41/50 [95% CI, 68.56–91.42]) for NY. In addition, the PPV of “Other” CHD anatomic group by site ranged from 27.08% (13/48 [95% CI, 15.28–41.85]) in NY to 55.56% (25/45 [95% CI, 40.00–70.36]) in NC (**Table S1**), and when “Other” CHD anatomic group was omitted, PPV for having a CHD did not differ significantly by anatomic group ( $X^2=3.96$ ,  $P=0.1383$ ) (**Table 2**). Lastly, when the PPVs of *ICD-9-CM* codes for correct CHD group assignment were assessed, among patients with  $\geq 1$  complex anatomic codes, 74.62% (147/197 [95% CI, 67.94–80.54]) were confirmed to have complex CHD (ie, 25.4% had a shunt, valve, “Other” CHD anatomic grouping, or no CHD); corresponding PPV estimates for identifying a patient with CHD in the correct CHD group were 84.18% (165/196; 95% CI, 87.31–88.99) for shunt, 80.41% (156/194; 95% CI, 74.12–85.75) for valve, and 29.41% (55/187; 95% CI, 22.99–36.50) for “Other” ( $X^2=168.02$ ,  $P<0.0001$ ) (**Table S2**).

**Table 3** shows PPVs of having a CHD by number of unique CHD-related *ICD-9-CM* codes overall and by anatomic group. Across all anatomic groups, when multiple unique codes were documented across 1 or multiple encounters, PPV was higher, 92.78% (334/360 [95% CI, 90.10–95.45]) compared with when a single CHD code was documented, 62.08% (257/414 [95% CI, 57.40–66.75]) ( $X^2=100.53$ ,  $P<0.0001$ ). This association was seen for anatomically complex CHD ( $X^2=29.88$ ,  $P<0.0001$ ), valve defects ( $X^2=13.05$ ,  $P<0.0001$ ), and the “Other” anatomic group ( $X^2=5.54$ ,  $P=0.019$ ). When >1 unique CHD-related *ICD-9-CM* code appeared in the patient’s eHR, PPV of having a CHD ranged from a low of 73.33% (11/15 [95% CI, 44.90–92.21]) in the “Other” CHD anatomic group to a high of 95.60% (152/159 [95% CI, 91.14–98.21]) in the complex group, compared with a range of 41.86% (72/172 [95% CI, 34.40–49.61]) in “Other” CHD anatomic group to 82.95% (73/88 [95% CI, 75.10–90.13]) in the shunt group for cases with a single CHD code.

**Table 4** shows PPVs of having a CHD by 4 age groups, 1- to 10-year-olds, 11- to 19-year-olds, 20- to 64-year-olds, and >64-year-olds, by 3 sites (GA, NC, and NY). Compared with age groups  $\leq 64$  years whose PPVs were observed in the mid to lower 80% range

**Table 1. Cases Identified With a Congenital Heart Defect ICD-9-CM Code: Number of Codes and Demographics, Overall and by Sites**

	Overall	Sites*				X <sup>2</sup> † P value
		GA	NC	NY	UT	
CHD anatomic groups						
Noncomplex						
Complex	197	50	50	48	49	
Shunt	196	52	53	45	46	
Valve	194	49	45	50	50	
"Other"†	187	44	45	48	50	
Included in analyses	774	195	193	191	195	
Excluded from data set	26	5	7	9	5	
<b>No. of unique CHD-related ICD-9-CM codes for cases</b>						
Single code	414 (53.49%)	114 (58.46%)	94 (48.70%)	111 (58.12%)	95 (48.72%)	7.14 P=0.0675
Multiple unique codes	360 (46.51%)	81 (41.54%)	99 (51.30%)	80 (41.88%)	100 (51.28%)	
Demographics						
Age group (in y)						
1–10	50 (8.64%)	18 (9.23%)	11 (5.70%)	21 (10.99)	...	4.04 P=0.6706
11–19	156 (26.94%)	52 (26.67%)	52 (26.94%)	52 (27.23%)	...	
20–64	208 (35.92%)	69 (35.38%)	75 (38.86%)	64 (33.51%)	...	
>64	165 (28.50%)	56 (28.72%)	55 (28.50%)	54 (28.27%)	...	
Sex						
Female	396 (51.16%)	105 (53.85%)	94 (48.70%)	91 (47.64%)	106 (54.36%)	2.77 P=0.4278
Male	378 (48.84%)	90 (46.15%)	99 (51.30%)	100 (52.36%)	89 (45.64%)	
Race						
Black	131 (16.93%)	51 (26.15%)	35 (18.13%)	43 (22.51%)	<11 (–)	69.97 P<0.0001
White	516 (66.67%)	102 (52.31%)	139 (72.02%)	111 (58.12%)	164 (84.10%)	
Other§ and unknown	127 (16.41%)	42 (21.54%)	19 (9.84%)	37 (19.37%)	29 (14.87%)	
Ethnicity						
Hispanic	86 (11.11%)	18 (9.23%)	<11 (–)	44 (23.04%)	17 (8.72%)	161.38 P<0.0001†
Non-Hispanic	542 (70.03%)	132 (67.69%)	173 (89.64%)	142 (74.35%)	95 (48.72%)	
Unknown	146 (18.86%)	45 (23.08%)	13 (6.74%)	<11 (–)	83 (42.56%)	

Two numbers of unique CHD-related ICD-9-CM codes (single code, multiple unique codes); 4 age groups (1–10, 11–19, 20–64, >64) for GA, NC, and NY only; UT omitted as cohort does not include 1–10 or >64-year-olds; 2 sexes (male, female); 3 races (Black, White, Other/unknown); and 3 ethnicities (Hispanic, non-Hispanic, unknown). GA indicates Emory University in Georgia; ICD-9-CM, *International Classification of Diseases, Ninth Revision, Clinical Modification*; NC, Duke University in North Carolina; NY, New York State Department of Health; and UT, University of Utah.

\*Site-specific percentages are column percentages; counts <11 not displayed.

†"Other" CHD anatomic group consists of unspecific defects; CHD-related ICD-9-CM codes and CHD anatomic groups are identified in Data S1.

‡X<sup>2</sup> applies to 5 Chi-square analyses, which includes 4 sites: GA, NC, NY, UT, except the X<sup>2</sup> by age which omits UT; 2 number of unique CHD-related ICD-9-CM codes (single code, multiple unique codes); 4 age groups (1–10, 11–19, 20–64, >64) for GA, NC & NY only; UT omitted as cohort does not include 1 to 10 or >64-year-olds; 2 sexes (male, female); 3 races (Black, White, Other/unknown); and 3 ethnicities (Hispanic, non-Hispanic, unknown).

§"Other" race includes American Indian/Alaskan Native, Asian, native Hawaiian/Pacific Islander, and multiracial.

(86.00%; 43/50 [95% CI, 73.26–95.62]) for 1- to 10-year olds, 82.69% (129/156 [95% CI, 75.83–88.27]) for 11- to 19-year-olds, and 84.13% (175/208 [95% CI, 78.45–88.82]) for 20- to 64-year-olds, the PPV for those who were >64 years was significantly lower, 57.58% (95/165 [95% CI, 49.65–65.22]) (X<sup>2</sup>=45.23, P<0.0001). When "Other" CHD anatomic group was omitted, the significant decreasing trend in PPV by age remained, with 95.24% (40/42 [95% CI, 83.84–99.42]) for 1- to 10-year-olds, 94.07% (111/118 [95% CI, 88.16–97.58]) for 11- to

19-year-olds, 93.90% (154/164 [95% CI, 89.07–97.04]) for 20- to 64-year olds, and 66.10% (78/118 [95% CI, 56.81–74.56]) for those >64 years (X<sup>2</sup>=58.82, P<0.0001). Table 4 also reveals the overall PPV of having CHD increased from 76.34% (442/579 [95% CI, 72.66–79.74]) when all 4 age and CHD anatomic groups were included to 94.14% (305/324 [95% CI, 72.66–79.74]) after both "Other" CHD anatomic group and the >64-year-olds were omitted (X<sup>2</sup>=46.04, P<0.0001). However, when the >64-year-olds were excluded regardless of whether or

**Table 2.** PPV\* of ICD-9-CM CHD Codes for Having a CHD Overall, by Site and by CHD Anatomic Group, with “Other”† CHD Anatomic Group Included and Omitted

PPV* for having a CHD, overall					$\chi^2$ † P value
“Other”† CHD included		76.36% 591/774 [73.20–79.31]	22.28 $P < 0.0001$ §		
“Other”† CHD omitted		86.54% 508/587 [83.51–89.20]			
PPV for having a CHD by site					$\chi^2$ † P value
	GA	NC	NY	UT	
“Other”† CHD included	78.46% 153/195 [72.02–84.01]	79.79% 154/193 [73.43–85.22]	70.68% 135/191 [63.68–77.03]	76.41% 149/195 [69.82–82.18]	5.15 $P = 0.1612$
“Other”† CHD omitted	87.42% 132/151 [81.05–92.25]	87.16% 129/148 [80.68–92.09]	85.31% 122/143 [78.43–90.67]	86.21% 125/145 [79.50–91.37]	0.35 $P = 0.9509$
PPV* for having a CHD by anatomic group					$\chi^2$ † P value
Complex	Noncomplex			“Other”† CHD included	“Other”† CHD omitted
	Shunt§	Valve	“Other”†		
89.85% 177/197 [84.76–93.69]	86.73% 170/196 [81.17–91.15]	82.99% 161/194 [76.95–87.99]	44.39% 83/187 [37.14–51.81]	142.16 $P < 0.0001$	3.96 $P = 0.1383$

ICD-9-CM indicates International Classification of Diseases, Ninth Revision, Clinical Modification; NC, Duke University in North Carolina; and PPV, positive predictive value.

\*95% CI presented within brackets for positive predictive values.

† $\chi^2$  - 5 Chi-square analyses that include CHD overall, by site and by anatomic group: Overall CHD status (2: Yes/No) comparing when “Other” CHD anatomic group was included and omitted; by site—separate  $\chi^2$ s conducted when “Other” CHD anatomic group included and omitted: CHD status (2: Yes/No) by site (4: GA, NC, NY, and UT); by anatomic group - separate  $\chi^2$ s conducted when: “Other” CHD anatomic group included: CHD status (2: Yes/No) by anatomic group (4: complex, shunt, valve, and “Other” CHD; and 2) “Other” CHD anatomic group omitted: CHD status (2: Yes/No) by anatomic group (3: complex, shunt, valve).

‡“Other” CHD anatomic group consists of unspecified defects; CHD-related ICD-9-CM codes and assigned CHD anatomic group are displayed in Data S1.

§ICD-9-CM code 745.5 was omitted from the shunt group as it is used to indicate secundum atrial septal defect and patent foramen ovale, a normal variant.

|| $\chi^2$  analyses that revealed significance group differences at the  $P < 0.05$  level or better.

not the “Other” CHD anatomic group was retained in the analysis, no trend in PPV for having a CHD by age was observed (including “Other”:  $X^2 = 0.34$ ,  $P = 0.8451$  and excluding “Other”:  $X^2 = 0.11$ ,  $P = 0.9467$ , respectively). In addition, PPV for having a CHD showed no significant group differences whether “Other” CHD anatomic group was included or omitted for sex ( $X^2 = 1.16$ ,  $P = 0.2809$  and  $X^2 = 1.48$ ,  $P = 0.2238$ , respectively), for race ( $X^2 = 5.62$ ,  $P = 0.0601$  and  $X^2 = 0.35$ ,  $P = 0.8382$ , respectively), or for ethnicity ( $X^2 = 1.24$ ,  $P = 0.5381$  and  $X^2 = 2.84$ ,  $P = 0.24$ , respectively) (Table S3).

PPV of having a CHD for individual ICD-9-CM CHD codes with sufficient case numbers are presented in Table 5. In isolation, tetralogy of Fallot (745.2) had a PPV of 84.2% for having a CHD, ventricular septal defect (745.4) had a PPV of 89.1%, and patent ductus arteriosus had a PPV of 81.3%. However, unspecified anomaly of heart (746.9) had a PPV of 42.2% and other congenital anomaly of heart (746.89) had a PPV of 23.1% for having a CHD. PPV for each of these individual ICD-9-CM CHD-related codes were all  $> 90.0\%$  when multiple unique ICD-9-CM CHD-related codes were identified.

## DISCUSSION

The primary aim of this validation project was to evaluate the PPV of ICD-9-CM codes and a code-based anatomic hierarchy for identifying CHD cases, and secondarily, to assess the PPV of these codes by anatomic groups. Overall, 76.36% of patients with  $\geq 1$  CHD-related ICD-9-CM codes had CHD. Across sites, of those with codes falling into the complex anatomic group, 86.00% to 92.00% had CHD, and only 27.08% to 55.56% of those with codes falling into the “Other” anatomic group had CHD. The PPV of ICD-9-CM codes for CHD was significantly higher for cases aged  $\leq 64$  years (83.82%) compared with those  $> 64$  years (57.58%). Furthermore, for cases aged  $\geq 64$  years, PPV of having CHD by anatomic group revealed a low PPV of 36.17% (17/47 [95% CI, 22.67–49.91]) for the “Other” anatomic group and a high of 73.17% (30/41 [95% CI, 59.61–85.78]) for valve lesions. This is consistent with findings from a previous study assessing the accuracy of code 745.5 to predict true atrial septal defects, in which younger patients, ages 11 to 20 years, were



**Table 3. PPV\* of ICD-9-CM CHD Codes for Having a CHD By Number of Unique CHD Codes and Anatomic Group**

	Single CHD code	Multiple unique CHD codes	$\chi^2$ P value
CHD anatomic group			
Overall	62.08% 257/414 [57.40–66.75]	92.78% 334/360 [90.10–95.45]	100.53 $P<0.0001$
Complex	65.79% 25/38 [48.65–80.37]	95.60% 152/159 [91.14–98.21]	29.88 $P<0.0001$
Shunt <sup>†</sup>	82.95% 73/88 [75.10–90.13]	89.81% 97/108 [82.51–94.80]	1.98 $P=0.1590$
Valve	75.00% 87/116 [66.11–82.57]	94.87% 74/78 [87.39–98.59]	13.05 $P=0.0003$
“Other” <sup>‡</sup>	41.86% 72/172 [34.40–49.61]	73.33% 11/15 [44.90–92.21]	5.54 $P=0.0186$

CHD indicates congenital heart defect; ICD-9-CM, *International Classification of Diseases, Ninth Revision, Clinical Modification*; and PPV, positive predictive value.

\*95% CI presented within brackets [] for positive predictive values.

<sup>†</sup>ICD-9-CM code 745.5 was omitted from the shunt group as it is used to indicate secundum atrial septal defect and patent foramen ovale, a normal variant.

<sup>‡</sup>“Other” CHD anatomic group consists of unspecific defects; CHD-related ICD-9-CM codes and their assigned CHD anatomic grouping are displayed in Data S1.

more likely to have a true atrial septal defect (64.3%) compared with those aged 21 to 40 years (23.7%) or 41 to 64 years (19.0%) ( $P<0.001$ ).<sup>2</sup> Using ICD codes in a “rule-out CHD” manner and incorrect coding for CHD may play a role in the low PPV for older CHD cases. Age-related changes in valve morphology and function may mistakenly be coded as CHD. The “Other” CHD category includes non-specific CHD codes such as “other congenital anomaly of the heart” that may be used inappropriately, for example, when ordering studies to investigate heart murmurs and symptoms of heart failure in older patients.

When examining the accuracy of ICD-9-CM-based native CHD anatomy group, about two thirds of cases across all sites were categorized into the correct anatomic group and the other one-third either did not have CHD or were categorized into the wrong group based on an incorrect code. The PPV of ICD-9-CM codes contained in eHR systems for identifying that a case truly has CHD of the indicated anatomic group ranged from 84.18% for shunt defect codes, excluding 745.5, to 29.41% for the “Other” CHD anatomic code group. Nonspecific codes in the “Other” CHD category may have a low PPV because they may have been used as “rule-out” codes when ordering diagnostic tests or were misused for an acquired heart condition. For example, if a patient has low blood oxygen saturations, then a “rule out CHD” code such as 746.9 (unspecified congenital anomaly of heart) may be used to assess

for CHD. A comparative PPV analysis for case classification revealed a lower PPV for single versus multiple code classification, 62.08% versus 92.78%, respectively (Table 3). While requiring multiple codes for case inclusion may likely avoid “rule out” code misclassification, it often comes at the expense of losing true CHD cases. In this study, relying on multiple codes alone would have resulted in reducing sensitivity by 33.2% (257/774) because 257 single-coded true CHD cases would be excluded. Additionally, reasons for the assignment of an incorrect anatomic group may also include coding errors such as when a code in the 745.xx to 747.xx ICD-9-CM group has a decimal dropped, leading to conversion from 745 to 745.0, a code for truncus arteriosus (745.0), rather than an intended code, for instance 745.4, ventricular septal defect. Misuse of CHD codes may occur in other ways. For example, this study included 3 cases that were coded as “other septal defect” rather than ventricular septal defect. These coding errors highlight that nonspecific CHD ICD-9-CM codes may actually represent specific and true CHD that could have been better captured by a more specific CHD code.

Of the 774 total cases, 414 had a single CHD code and 360 had multiple unique CHD codes. Patients with more than one unique CHD code were more likely to have CHD, and this increase in PPV was significant for the complex and valve anatomic groups. Certain ICD-9-CM codes that frequently occur in combination with other CHD codes had PPVs >90%. For instance, tetralogy of Fallot (745.2) and ventricular septal defect (745.4) all had high PPVs for CHD in combination with other CHD codes.

Prior studies have also examined whether complexity of disease may play a role in the accuracy of coding in administrative data. Steiner et al. (2017) found certain complex CHD codes, such as tetralogy of Fallot and truncus arteriosus, performed well.<sup>9</sup> Khan et al. (2018) found that PPV of moderate or complex CHD codes for CHD was higher compared with simple shunt or valve defects or when coupled with other factors such as age, an encounter with an adult CHD provider, an echocardiogram or ECG compared with noncomplex CHD.<sup>1</sup> The current validation project found that the complex, shunt, and valve groups had higher PPV than the “Other” CHD group, supporting the conclusion that more specific diagnoses have a higher PPV for true CHD.

While this study did not examine sensitivity of administrative databases, other studies have demonstrated poor identification of CHD in state-specific administrative databases for pediatric patients.<sup>3</sup> Cronk et al. (2003) investigated the sensitivity of ICD-9 codes for identifying individuals with CHD in 4 administrative databases in Wisconsin and found that only 57.9% of CHD cases identified at Children’s Hospital

**Table 4. PPV\* of ICD-9-CMCHD Codes† for Having a CHD, Overall and by Age Group, for Three Sites with “Other”‡ CHD Anatomic Group Included and Omitted**

PPV* for having a CHD, for 4 age groups					X <sup>2</sup> †, § P value	
“Other”‡ CHD included		76.34% 442/579 [72.66–79.80]			17.19 P<0.0001	
“Other”‡ CHD omitted		86.65% 383/442 [83.12–89.68]				
PPV* for having CHD by age groups					X <sup>2</sup> †, § P value	
	1–10y	11–19y	20–64y	>64y	All 4 age groups	Three youngest age groups
“Other”‡ CHD included	86.00% 43/50 [73.26–95.62]	82.69% 129/156 [75.83–88.27]	84.13% 175/208 [78.45–88.82]	57.58% 95/165 [49.65–65.22]	45.23 P<0.0001	0.34 P=0.8451
“Other”‡ CHD omitted	95.24% 40/42 [83.84–99.42]	94.07% 111/118 [88.16–97.58]	93.90% 154/164 [89.07–97.04]	66.10% 78/118 [56.81–74.56]	58.82 P<0.0001	0.11 P=0.9467
PPV* for having A CHD, for 3 age groups					X <sup>2</sup> †, ‡ P value	
“Other”‡ CHD included		83.82% 347/414 [79.91–87.23]			18.80 P<0.0001	
“Other”‡ CHD omitted		94.14% 305/324 [90.99–96.43]				

X<sup>2</sup> for having a CHD when all 4 age groups and CHD anatomic groups were included (PPV=76.34%) compared with when >64-year-olds and “Other” CHD anatomic group were omitted (PPV=94.14%) was X<sup>2</sup>=46.04, P<0.0001. CHD indicates congenital heart defect; ICD-9-CM, *International Classification of Diseases, Ninth Revision, Clinical Modification*; and PPV, positive predictive value.

\*95% CI presented within brackets [] for positive predictive values.

†ICD-9-CM code 745.5 was omitted from the shunt group as it is used to indicate secundum atrial septal defect and patent foramen ovale, a normal variant.

‡“Other” CHD anatomic group consists of unspecified defects; CHD-related ICD-9-CM codes and assigned CHD anatomic group are displayed in Data S1.

§UT not included in these analyses as age groups 1–10 and >64 years were not reported.

of Wisconsin were identified by ICD-9 codes and/or a CHD checkbox indicative of the presence of CHD in any state database; a total of 216 cases (57.9%) of the 373 total cases were identified by a CHD ICD-9 code in at least one of the 4 state databases.<sup>10</sup> Almost 62% (231 of 373) had a single CHD diagnosis and 91% (339 of 373) had 1 or 2 CHD diagnoses. Lack of reporting oversight and classification problems were thought to contribute to inadequate identification of CHD from such data sets.

Ideally, constructing an algorithm that utilizes data from administrative and eHRs will help to identify true CHD cases with improved accuracy and sensitivity. Machine learning is one possibility to improve both the PPV and sensitivity of CHD codes for CHD, and specific CHD type, based on ICD codes and other variables from clinical and administrative data sets, using the most predictive factors, while reducing the false negative rate. Restricting analyses to certain ICD codes and age categories may also improve the PPV. As a result of the current findings and previous research,<sup>2,11</sup> researchers may consider excluding the

following codes from administrative data sets to improve the PPV for analyses seeking to study CHD:

- ICD-9-CM and anatomically equivalent ICD-10-CM codes that code for conditions other than heart defects, including congenital heart block (746.86, Q24.6), pulmonary arteriovenous malformation (747.32, Q25.72), absent/hypoplastic umbilical artery (747.5, Q27.0), other anomalies of peripheral vascular system (747.6x, Q27.9), and other specified anomalies of circulatory system (747.8x, Q28.8). These codes were also excluded in the surveillance methodology.<sup>5,6</sup>
- The “Other” CHD anatomic group (as noted in Figure 1 and Data S1) and nonspecific ICD-9-CM codes and the equivalent ICD-10-CM codes including: other specified congenital anomalies of heart 746.8 (Q24.8), obstructive anomalies of heart, not elsewhere classified 746.84, coronary artery anomaly 746.85 (Q24.5), malposition of heart and cardiac apex 746.87 (Q24.0), other specified congenital anomalies of heart 746.89 (Q24.8), unspecified

**Table 5. Positive Predictive Value of Specific CHD ICD-9-CM Codes for Having CHD by Number of Select Unique CHD Codes**

ICD-9-CM code	Description of ICD-9-CM code	CHD anatomic group	Patients, n			PPV for having CHD		
			Single CHD code	Multiple unique CHD codes	Total # with code	Single CHD code	Multiple Unique CHD codes	Total % with code
745.2	Tetralogy of Fallot	Complex	19	53	72	84.2%	94.3%	91.7%
745.4	Ventricular septal defect	Shunt	64	93	157	89.1%	94.6%	92.4%
747.0	Patent ductus arteriosus	Shunt	16	36	52	81.3%	94.4%	90.4%
746.4	Bicuspid aortic valve and congenital aortic valve insufficiency	Valve	61	37	98	82.0%	97.3%	87.8%
746.02	Congenital pulmonary valve stenosis	Valve	10	37	47	100.0%	100.0%	100.0%
746.3	Congenital stenosis of aortic valve	Valve	16	24	40	87.5%	95.8%	92.5%
747.1	Coarctation of aorta	Valve	12	26	38	66.7%	100.0%	89.5%
746.9	Unspecified anomaly of heart	Other	45	89	134	42.2%	94.4%	76.9%
746.89	Other congenital anomaly of heart	Other	26	39	65	23.1%	92.3%	64.6%
V13.65	Personal history of corrected congenital Malformation of heart and circulatory system	Other	11	38	49	54.5%	92.1%	83.7%
746.85	Coronary artery anomaly	Other	26	12	38	61.5%	91.7%	71.1%
746.87	Malposition of heart and cardiac apex	Other	12	15	27	33.3%	93.3%	66.7%
747.29	Other anomaly of aorta	Other	14	12	26	35.7%	91.7%	61.5%

CHD indicates congenital heart defect; ICD-9-CM, *International Classification of Diseases, Ninth Revision, Clinical Modification*; and PPV, positive predictive value.

congenital anomaly of heart 746.9 (Q24.9), other congenital anomalies of aorta 747.2 (Q25.49), anomaly of aorta, unspecified 747.20 (Q25.40), anomalies of aortic arch 747.21, other anomalies of aorta 747.29 (Q25.49), congenital anomalies of great veins 747.4 (Q26.1), anomaly of great veins, unspecified 747.40 (Q26.9), other anomalies of great veins 747.49 (Q26.8), unspecified anomaly of circulatory system 747.9 (Q28.9, personal history of [corrected] congenital malformations of heart and circulatory system V13.65 (Z87.74)

- Patent foramen ovale / atrial septal defect 745.5 / Q21.1 alone or in combination with the “Other” CHD category.

Codes found in combination are likely to be more accurate than an isolated CHD code, though 53% (414/774) of the cases in this validation project had a single unique CHD code. Therefore, it is suggested to avoid excluding cases with single CHD codes from algorithms and analyses; doing so could result in missed cases and lack of generalizability. Additionally, severity of CHD is not indicated by the number of unique CHD codes applied to an individual. It is notable that

eliminating the ICD-9-CM codes above, or eliminating the >64-year-old group, will improve the PPV of CHD, but will also exclude a substantial number of true CHD cases. Certain codes are more likely to identify true CHD cases than others. Even though the vast majority of cases with complex and moderate CHD codes (80%–90%) have CHD, there remains about 1 in 4 or 5 cases who may either not have CHD or have a different severity type than what is coded. Sufficiently detailing how CHD is defined when using administrative data as well as understanding and documenting its limitations will improve the generalizability of the findings to the CHD population.

## LIMITATIONS

The selected cases used in this analysis came from health care centers at locations where records could be reviewed. Thus, there was possible selection bias towards having true CHD, which might overestimate the PPV. However, using data from 2011 to 2013 may lead to an underestimation of PPV compared with more recent years as eHR use has become more standard. Coding

may vary by data source, year, and individuals who document the code (medical versus billing department staff), potentially limiting broad applicability to other data sets. Coding practices vary across both regions and medical centers, which is both a strength and limitation of our paper. Our data set used *ICD-9-CM* codes, which can be mapped to *ICD-10-CM* codes. However, differences in coding practices may vary between the *ICD-9-CM* and *ICD-10-CM* eras, thus making our results not directly applicable to *ICD-10-CM* based data sets. For the individual *ICD-9-CM* codes assessed, the reported PPV is for having CHD (Yes/No) and we were unable to examine PPV for whether the case had the specific CHD documented. We did not have access to false negatives cases in the data available and thus could not calculate sensitivities of CHD *ICD-9-CM* codes.

## CONCLUSIONS

This validation study using data from 4 sites affiliated with the CDC's Surveillance of Congenital Heart Disease Across the Lifespan project revealed that *ICD-9-CM* codes accurately classify patients with true CHD in the majority of cases labeled as complex, shunt, and valve. The PPV of "Other" non-specific CHD *ICD-9-CM* codes was low and may not reflect true CHD. When >1 unique CHD code is associated with a case, the PPV for CHD increases. CHD codes had higher PPV in younger compared with older CHD cases. Further evaluation and algorithm development may help inform and improve the identification of CHD cases when administrative data sets are used.

## ARTICLE INFORMATION

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### Affiliations

Division of Cardiology, Emory University School of Medicine and Emory University Rollins School of Public Health, Atlanta, GA (F.H.R., C.L.R., T.H., W.M.B.); Sibley Heart Center Cardiology, Atlanta, GA (F.H.R.); National Center on Birth Defects and Developmental Disabilities, Centers for Disease Control and Prevention, Atlanta, GA (S.L.F., J.G.); Duke University School of Medicine, Durham, NC (J.S.L., A.D.); Division of Medical Genetics, Department of Pediatrics, University of Utah, Salt Lake City, UT (L.B., M.R.R.); Albert Einstein College of Medicine and The Children's Hospital at Montefiore, Bronx, NY (D.H.); Divisions of Cardiovascular Medicine and Pediatric Cardiology, Stanford University School of Medicine, Palo Alto, CA (G.K.L.); and New York State Department of Health, Bureau of Environmental & Occupational Epidemiology, Albany, NY (A.M.S.).

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### Disclosures

None.

### Supplemental Material

Data S1  
Tables S1–S3

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# Supplemental Materials

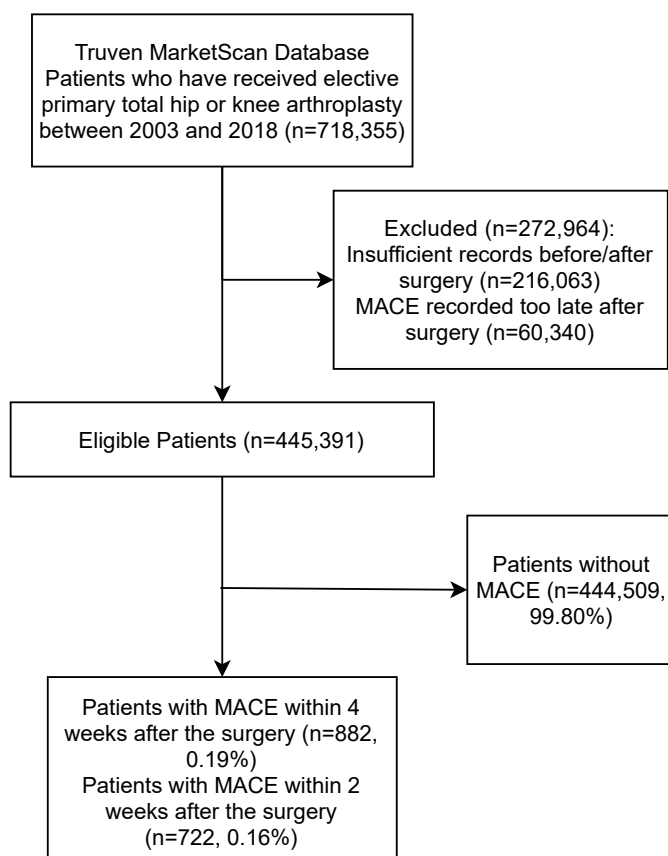


Fig. S1: CONSORT diagram conforming to the CONSORT-AI Extension guidelines stated at [https://doi.org/10.1016/S2589-7500\(20\)30218-1](https://doi.org/10.1016/S2589-7500(20)30218-1)

TABLE S1: Inclusion/Exclusion, Positive/Control Criteria & Cohort Definitions

	<b>Definitions</b>
Inclusion/Exclusion Criteria	Age 45 - 95
	Has total hip/knee CPT codes (See Table S2) in medical history and length of history available before cardiac event spans $\geq 1$ year
	Has a myocardial infarction or a cardiac arrest <sup>‡</sup> (See Table S4 for list of target codes used to identify cardiac event in diagnostic history) 4 weeks (2 weeks considered in secondary analysis) after surgery (positive cohort)
	Has 0.5 yr of medical history available after surgery (control)
Positive & Control Cohorts	<b>Positive Cohort:</b> At least one code for cardiac event (Table S4 )
	<b>Control Cohort:</b> No code on cardiac event within 26 weeks of surgery

TABLE S2: Current Procedural Terminology (CPT) codes for total hip/knee replacement used

CPT code	description
27130	Total Hip Replacement/Resurfacing
27132	Total Hip Replacement/Resurfacing
81.51	Total hip replacement
0SR9	Replacement: Hip Joint, Right
0SRB	Replacement: Hip Joint, Left
27442	Knee Total Replacement - (Arthroplasty)
27443	Knee Total Replacement - (Arthroplasty)
27445	Knee Total Replacement - (Arthroplasty)
27446	Knee Total Replacement - (Arthroplasty)
27447	Knee Total Replacement - (Arthroplasty)
81.54	Total knee replacement
0SRC	Replacement: Knee Joint, Right
0SRD	Replacement: Knee Joint, Left

TABLE S3: Codes used to determine RCRI

Description	Constituent Codes (*NDC: National Drug Code)
History of Heart Failure	ICD9 codes: 428.0, 428.1, 428.20, 428.21, 428.22, 428.23, 428.30, 428.31, 428.32, 428.33, 428.40, 428.41, 428.42, 428.43, 428.9, 428.2, 428.3, 428.4; ICD10 codes: I50.1, I50.20, I50.21, I50.22, I50.23, I50.30, I50.31, I50.32, I50.33, I50.40, I50.41, I50.42, I50.43, I50.810, I50.811, I50.812, I50.813, I50.814, I50.82, I50.83, I50.84, I50.89, I50.9, I50.2, I50.3, I50.4, I50.8, I50.81
History of Cerebrovascular Disease	ICD9 codes: 430, 431, 432.0, 432.1, 432.9, 433.00, 433.01, 433.10, 433.11, 433.20, 433.21, 433.30, 433.31, 433.80, 433.81, 433.90, 433.91, 434.00, 434.01, 434.10, 434.11, 434.90, 434.91, 435.0, 435.1, 435.2, 435.3, 435.8, 435.9, 436, 437.0, 437.1, 437.2, 437.3, 437.4, 437.5, 437.6, 437.7, 437.8, 437.9, 438.0, 438.10, 438.11, 438.12, 438.13, 438.14, 438.19, 438.20, 438.21, 438.22, 438.30, 438.31, 438.32, 438.40, 438.41, 438.42, 438.50, 438.51, 438.52, 438.53, 438.6, 438.7, 438.81, 438.82, 438.83, 438.84, 438.85, 438.89, 438.9, 432, 433, 434, 435, 437, 438, 433.0, 433.1, 433.2, 433.3, 433.8, 433.9, 434.0, 434.1, 434.9, 438.1, 438.2, 438.3, 438.4, 438.5, 438.8; ICD10 codes: I60.00, I60.01, I60.02, I60.10, I60.11, I60.12, I60.2, I60.3, I60.4, I60.5, I60.6, I60.7, I60.8, I60.9, I61.0, I61.1, I61.2, I61.3, I61.4, I61.5, I61.6, I61.8, I61.9, I62.00, I62.01, I62.02, I62.03, I62.1, I62.9, I63.00, I63.011, I63.012, I63.013, I63.019, I63.02, I63.031, I63.032, I63.033, I63.039, I63.09, I63.10, I63.111, I63.112, I63.113, I63.119, I63.12, I63.131, I63.132, I63.133, I63.139, I63.19, I63.20, I63.211, I63.212, I63.213, I63.219, I63.22, I63.231, I63.232, I63.233, I63.239, I63.29, I63.30, I63.311, I63.312, I63.313, I63.319, I63.321, I63.322, I63.323, I63.329, I63.331, I63.332, I63.333, I63.339, I63.341, I63.342, I63.343, I63.349, I63.39, I63.40, I63.411, I63.412, I63.413, I63.419, I63.421, I63.422, I63.423, I63.429, I63.431, I63.432, I63.433, I63.439, I63.441, I63.442, I63.443, I63.449, I63.49, I63.50, I63.511, I63.512, I63.513, I63.519, I63.521, I63.522, I63.523, I63.529, I63.531, I63.532, I63.533, I63.539, I63.541, I63.542, I63.543, I63.549, I63.59, I63.6, I63.81, I63.89, I63.9, I65.01, I65.02, I65.03, I65.09, I65.1, I65.21, I65.22, I65.23, I65.29, I65.9, I65.99, I66.01, I66.02, I66.03, I66.09, I66.11, I66.12, I66.13, I66.19, I66.21, I66.22, I66.23, I66.29, I66.3, I66.8, I66.9, I67.0, I67.1, I67.2, I67.3, I67.4, I67.5, I67.6, I67.7, I67.81, I67.82, I67.83, I67.841, I67.848, I67.850, I67.858, I67.89, I67.9, I68.0, I68.2, I68.8, I69.00, I69.010, I69.011, I69.012, I69.013, I69.014, I69.015, I69.018, I69.019, I69.020, I69.021, I69.022, I69.023, I69.028, I69.031, I69.032, I69.033, I69.034, I69.039, I69.041, I69.042, I69.043, I69.044, I69.049, I69.051, I69.052, I69.053, I69.054, I69.059, I69.061, I69.062, I69.063, I69.064, I69.065, I69.069, I69.090, I69.091, I69.092, I69.099, I69.093, I69.098, I69.10, I69.110, I69.111, I69.112, I69.113, I69.114, I69.115, I69.118, I69.119, I69.120, I69.121, I69.122, I69.123, I69.128, I69.131, I69.132, I69.133, I69.134, I69.139, I69.141, I69.142, I69.143, I69.144, I69.149, I69.151, I69.152, I69.153, I69.154, I69.159, I69.161, I69.162, I69.163, I69.164, I69.165, I69.169, I69.190, I69.191, I69.192, I69.193, I69.198, I69.20, I69.210, I69.211, I69.212, I69.213, I69.214, I69.215, I69.218, I69.219, I69.220, I69.221, I69.222, I69.223, I69.228, I69.231, I69.232, I69.233, I69.234, I69.239, I69.241, I69.242, I69.243, I69.244, I69.249, I69.251, I69.252, I69.253, I69.254, I69.259, I69.261, I69.262, I69.263, I69.264, I69.265, I69.269, I69.290, I69.291, I69.292, I69.293, I69.298, I69.30, I69.310, I69.311, I69.312, I69.313, I69.314, I69.315, I69.318, I69.319, I69.320, I69.321, I69.322, I69.323, I69.328, I69.331, I69.332, I69.333, I69.334, I69.339, I69.341, I69.342, I69.343, I69.344, I69.349, I69.351, I69.352, I69.353, I69.354, I69.359, I69.361, I69.362, I69.363, I69.364, I69.365, I69.369, I69.390, I69.391, I69.392, I69.393, I69.398, I69.80, I69.810, I69.811, I69.812, I69.813, I69.814, I69.815, I69.818, I69.819, I69.820, I69.821, I69.822, I69.823, I69.828, I69.831, I69.832, I69.833, I69.834, I69.839, I69.841, I69.842, I69.843, I69.844, I69.849, I69.851, I69.852, I69.853, I69.854, I69.859, I69.861, I69.862, I69.863, I69.864, I69.865, I69.869, I69.890, I69.891, I69.892, I69.893, I69.898, I69.90, I69.910, I69.911, I69.912, I69.913, I69.914, I69.915, I69.918, I69.919, I69.920, I69.921, I69.922, I69.923, I69.928, I69.931, I69.932, I69.933, I69.934, I69.939, I69.941, I69.942, I69.943, I69.944, I69.949, I69.951, I69.952, I69.953, I69.954, I69.959, I69.961, I69.962, I69.963, I69.964, I69.965, I69.969, I69.990, I69.991, I69.992, I69.993, I69.998, I60, I61, I62, I63, I65, I66, I67, I68, I69, I60.0, I60.1, I60.3, I60.5, I62.0, I63.0, I63.1, I63.2, I63.3, I63.4, I63.5, I63.8, I65.0, I65.2, I66.0, I66.1, I66.2, I67.8, I69.0, I69.1, I69.2, I69.3, I69.8, I69.9, I63.01, I63.03, I63.11, I63.13, I63.21, I63.23, I63.31, I63.32, I63.33, I63.34, I63.41, I63.42, I63.43, I63.44, I63.51, I63.52, I63.53, I63.54, I67.84, I67.85, I69.01, I69.02, I69.03, I69.04, I69.05, I69.06, I69.09, I69.11, I69.12, I69.13, I69.14, I69.15, I69.16, I69.19, I69.21, I69.22, I69.23, I69.24, I69.25, I69.26, I69.29, I69.31, I69.32, I69.33, I69.34, I69.35, I69.36, I69.39, I69.81, I69.82, I69.83, I69.84, I69.85, I69.86, I69.89, I69.91, I69.92, I69.93, I69.94, I69.95, I69.96, I69.99
History of Ischemic Heart Disease	ICD9 codes: 410.00, 410.01, 410.02, 410.10, 410.11, 410.12, 410.20, 410.21, 410.22, 410.30, 410.31, 410.32, 410.40, 410.41, 410.42, 410.50, 410.51, 410.52, 410.60, 410.61, 410.62, 410.70, 410.71, 410.72, 410.80, 410.81, 410.82, 410.90, 410.91, 410.92, 411.0, 411.1, 411.81, 411.89, 412, 413.0, 413.1, 413.9, 414.00, 414.01, 414.02, 414.03, 414.04, 414.05, 414.06, 414.07, 414.10, 414.11, 414.12, 414.19, 414.2, 414.3, 414.4, 414.8, 414.9, 410, 411, 413, 414, 410.0, 410.1, 410.2, 410.3, 410.4, 410.5, 410.6, 410.7, 410.8, 410.9, 411.8, 414.0, 414.1; ICD10 codes: I20.0, I20.1, I20.8, I20.9, I21.01, I21.02, I21.09, I21.11, I21.19, I21.21, I21.29, I21.3, I21.4, I21.9, I21.A, I21.A9, I22.0, I22.1, I22.2, I22.8, I22.9, I23.0, I23.1, I23.2, I23.3, I23.4, I23.5, I23.6, I23.7, I23.8, I24.0, I24.1, I24.8, I24.9, I25.10, I25.110, I25.111, I25.118, I25.119, I25.2, I25.3, I25.41, I25.42, I25.5, I25.6, I25.700, I25.701, I25.708, I25.709, I25.710, I25.711, I25.718, I25.719, I25.720, I25.721, I25.728, I25.729, I25.730, I25.731, I25.738, I25.739, I25.750, I25.751, I25.758, I25.759, I25.760, I25.761, I25.768, I25.769, I25.790, I25.791, I25.798, I25.799, I25.810, I25.811, I25.812, I25.82, I25.83, I25.84, I25.89, I25.9, I20, I21, I22, I23, I24, I25, I21.0, I21.1, I21.2, I21.A, I25.1, I25.4, I25.7, I25.8, I25.11, I25.70, I25.71, I25.72, I25.73, I25.75, I25.76, I25.79, I25.81
Pre-operative creatinine > 2 mg/dL / 176.8 µmol/L - Approximated by History of Chronic Kidney Disease	ICD9 codes: 585.3, 585.5, 585.6, 585.4; ICD10 codes: N18.30, N18.31, N18.32, N18.4, N18.5, N18.6, N18.3
Pre-operative treatment with Insulin	NDC* codes: 08881242112, 08881250305, 54868582400, 08881750023, 08881242120, 08881250313, 38396043277, 08881250321, 00169369619, 08881520665, 08881242138, 36652040218, 56151171101, 08881520673, 08496275501, 08881250354, 08496275511, 08881250362, 08080810055, 36652040276, 00002831101, 08080040028, 08080040029, 08080040030, 08396800100, 38396043377, 08881750130, 36652040318, 00002831517, 56151171201, 08881750155, 08881512597, 36652400801, 36652400802, 36652400803, 36652400804, 36652400805, 36652400806, 36652400807, 36652400808, 68258889903, 08881103025, 36652040376, 96295010494, 96295010495, 96295010496, 96295010497, 96295010498, 08881512647, 08396800200, 38396043477, 57515008218, 08881750239, 56151171301, 08881750254, 55948009710, 08881250545, 57515008258, 36652400901, 36652400902, 36652400903, 36652400904, 36652400905, 08080032010, 36652400906, 36652400907, 36652400908, 59060183302, 08881512738, 08881512746, 08396800300, 54569165101, 08881701166, 54569165102, 38396076339, 08881701174, 54274048310, 08290328888, 38396043577, 08222073150, 08881750338, 08222032195, 96295010629, 36652040518, 08881676624, 96295010643, 08881906005, 96295010645, 08881676632, 08881701216, 00002821001, 08881701224, 59060183402, 08881512811, 08080032110, 08222073198, 36652040576, 89134072202, 00002831501, 08396800400, 54569165200, 54569165202, 08881512852, 54274048410, 08881512860, 38396043677, 51927368100, 36652040618, 08881512878, 08881906104, 57515082180, 08080327114, 08080032210, 36652040676, 08881750510, 52297086578, 08881512944, 08287126003, 08287126004,

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Pre-operative treatment with Insulin (contd.)

NDC\* codes: 08287126005, 08396800500, 08881701364, 08415003129, 08415003130, 08287126014, 08287126015, 08287126016, 38396043777, 08287126021, 08287126026, 08287126027, 08287126028, 08287126029, 36652040718, 08222073358, 08881512977, 08881701406, 08080622112, 00002841501, 00888160813, 0822073396, 08290009652, 08080032310, 08881513025, 68258898501, 36652040776, 08881513033, 89134072402, 08396800600, 08326300250, 08474935900, 08881513058, 38396043877, 11845026407, 36652040818, 08080827012, 59060183702, 08474010278, 68258898601, 08881513132, 08881750700, 36652040876, 54868361900, 08396800700, 08881750718, 08881513157, 38396043977, 08222032591, 08222073556, 08881608201, 08881608202, 08881608203, 08881513207, 08222073594, 08080032510, 08881513223, 08474010378, 08881513231, 11917001487, 11917001489, 11917001492, 54569255700, 54569255701, 08396800800, 08881513249, 08881120037, 08881513256, 76300084010, 00169001771, 38396044077, 08290329403, 08290329405, 08290329406, 08290329407, 08290329408, 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Pre-operative treatment  
with Insulin

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TABLE S4: ICD codes for myocardial infarction used to identify positive cohort

ICD code	description
I46.8	Cardiac arrest due to other underlying condition
I21	ST elevation (STEMI) myocardial infarction involving left main coronary artery
410.72	Subendo infarct subseq
I21.01	ST elevation (STEMI) myocardial infarction involving left main coronary artery
410.01	AMI anterolateral init
I21.4	Non-ST elevation (NSTEMI) myocardial infarction
I21.A9	Other myocardial infarction type
I21.A1	Myocardial infarction type 2
410.61	True post infarct init
I21.3	ST elevation (STEMI) myocardial infarction of unspecified site
410.8	AMI NEC unspecified
410.42	AMI inferior wall subseq
427.5	Cardiac arrest
I46	Cardiac arrest due to underlying cardiac condition
I46.2	Cardiac arrest due to underlying cardiac condition
410	AMI anterolateral unspec
410.71	Subendo infarct initial
410.11	AMI anterior wall init
410.12	AMI anterior wall subseq
410.7	Subendo infarct unspec
I21.21	ST elevation (STEMI) myocardial infarction involving left circumflex coronary artery
410.4	AMI inferior wall unspec
410.21	AMI inferolateral init
410.82	AMI NEC subsequent
410.9	AMI NOS unspecified
410.2	AMI inferolateral unspec
I21.9	Acute myocardial infarction unspecified
I46.9	Cardiac arrest cause unspecified
410.1	AMI anterior wall unspec
410.02	AMI anterolateral subseq
410.51	AMI lateral NEC initial
410.52	AMI lateral NEC subseq
410.92	AMI NOS subsequent
I21.02	ST elevation (STEMI) myocardial infarction involving left anterior descending coronary artery
I21.19	ST elevation (STEMI) myocardial infarction involving other coronary artery of inferior wall
410.81	AMI NEC initial
410.41	AMI inferior wall init
410.31	AMI inferopost initial
410.62	True post infarct subseq
I21.09	ST elevation (STEMI) myocardial infarction involving other coronary artery of anterior wall
410.0	AMI anterolateral unspec
410.5	AMI lateral NEC unspec
410.6	True post infarct unspec
410.3	AMI inferopost unspec
410.91	AMI NOS initial
410.32	AMI inferopost subseq
I21.11	ST elevation (STEMI) myocardial infarction involving right coronary artery
410.22	AMI inferolateral subseq
I21.29	ST elevation (STEMI) myocardial infarction involving other sites

TABLE S5: Number of diagnostic codes encountered in dataset

gender	Number of codes	Number of unique codes
M	4879398	17554
F	7753318	19209
Total	12632716	36763

TABLE S6: CCoR phenotypes and maximum number of unique ICD codes defining CCoR phenotypes

CCoR phenotype	count of ICD codes in definition (Table S7)
Allergic	191
Cardiovascular	2017
CNS	765
Development	820
Digestive	1317
Endocrine	237
Frailty	557
Health-Services	501
Hematologic	429
Hypertension	80
Immune	1546
Infections-Bacterial	409
Infections-Fungal-and-Other	784
Infections-General	3612
Infections-Respiratory	712
Injuries	53265
Integumentary	1457
Metabolic	373
Musculoskeletal	7533
Neoplastic	3022
Ophthalmological	3401
Otic	856
PNS	394
Psychiatric	1478
Reproductive	2675
Respiratory	724



Development	<p>520.4 742.59 764.96 743.66 750.19 M26.36 756.11 749.01 748.1 524.33 740.740 751.252 35 741.0 743.53 524.79 748.5 752.42 589.0 Q18.1 Q26.2 Q93.4 756.98 743.43 744.21 Q63.8 753.23 750.4 P92 N13.70 746.82 747.40 743.57 743.41 742.5 742.743 34 741.4 524.35 744.82 Q05.2 M26.9 Q55.63 Q10.1 752.43 748.3 756.16 M26.89 744.31 593.71 M26.221 M26.72 313.23 Q31.1 743.49 F94.0 750.24 747.41 Q35.7 Q23.0 Q15.8 Q61.3 749.1 Q16.9 759.0 743.12 750.27 749.03 747.49 Q61.8 P92.4 743.65 750.21 Q20.0 Q87.81 Q64.4 758.5 764.03 524.73 Q17.1 756.13 524.31 743.8 Q18.4 Q27.8 520.8 743.64 Q21.2 741.9 751.61 Q76.5 Q27.7 Q05.7 Q61.01 746.87 Q10.0 Q25.4 Q36.9 M26.06 752.36 743.11 764.91 Q28.3 747 756.14 743.39 759.89 746.6 753.12 750 750.10 Q62.31 M26.39 750.6 Q51.4 Q56.3 Q24.8 747.82 745.7 752.65 750.16 749.02 Q28.8 P05.14 743.35 Q10.9 Q64.9 P05.08 749.23 742.9 747.10 756.12 Q16.4 743.44 K00.4 P05.15 Q22.5 747.20 745.19 751.4 764.07 Q05.1 Q51.3 N28.83 M26.56 Q21.1 744.8 M26.220 747.8 N13.722 Q23.2 752.40 Q00.1 Q87.1 Q06.4 764.92 P05.06 524.56 743.46 Q55.22 745.11 744.0 Q93.4 751.2 K00.2 M26.52 Q76.49 752.89 Q52.12 746.0 Q99.2 E30.1 P92.2 M26.54 745.12 Q02 753.10 745.8 Q33.4 Q24.2 764.12 Q24.6 754.0 315.8 744.89 307.6 Q55.23 750.1 759.4 M26.73 Q00.2 Q40.8 752.64 M26.211 593.7 Q64.10 758.32 Q33.6 524.3 Q26.5 Q18.2 055.64 746.5 P05.9 764.00 744 752.34 752.9 Q43.4 524.57 758.1 747.2 315.9 Q13.4 759.3 524.22 Q16.2 315.4 743.63 752.51 Q27.9 745.3 524.32 743.54 Q20.1 F93.9 Q12.0 746.8 524.8 P05.18 748.61 P92.9 Q42.9 Q52.0 743.56 742.1 Q20.8 Q89.3 524.21 Q51.0 749.20 753.3 Q18.7 315 Q51.811 747.3 Q03.8 748.60 744.09 Q61.9 Q93.81 745.69 741.92 759.2 Q05.8 746.2 747.81 750.29 741.02 Q76.0 744.04 743.36 764.24 P92.8 P05.10 749.11 Q12.4 524.55 Q54.4 746.4 520.1 743.59 764.10 Q37.8 M26.33 313.2 P05.13 524.7 P92.01 745.61 752.11 P05.16 M26.34 Q24.3 751.5 524.74 Q06.2 746.0 Q21.9 752.49 745.4 758.31 752.33 K00.0 E30.0 750.15 307.7 758.1 746.1 Q04.8 764.1 Q10.6 744.23 759.9 764.17 764.90 Q14.0 Q13.0 764.99 593.70 Q43.0 753.21 P05.07 744.05 745.6 Q98.4 744.47 Q52.9 750.3 743.45 Q33.9 764.97 753.7 741.93 764 Q23.1 Q30.0 747.1 752.6 Q15.0 593.73 741.91 M26.79 742.51 524.81 Q51.818 764.21 Q33.0 743.1 Q22.0 Q10.7 Q51.5 752.69 752.1 Q22.1 748.6 Q12.1 750.8 F93.8 Q36.0 745.0 751.8 752.4 Q34.9 747.83 747.21 754.1 746.84 753.5 520.9 524.30 747.60 747.61 R62.51 K00.9 743.52 742.2 Q12.9 753.0 Q51.6 743.9 743.5 759.7 Q89.7 744.03 743.03 753.22 Q38.0 Q38.3 759.81 M26.23 745.9 M26.24 744.02 524.82 P92.5 Q01.9 751.60 Q26.8 Q17.0 Q91.9 524.20 Q97.1 764.20 Q52.3 Q13.5 Q38.4 752.8 752.3 M26.4 746.3 M26.55 747.22 520 743.62 741.00 M26.57 749.04 744.9 Q17.8 756.2 758.4 Q45.1 M26.32 F98.0 P92.6 P05.12 Q17.2 524.26 524.50 748 P92.09 743.2 P05.05 741 756.4 Q10.3 N27.0 747.9 309.21 Q05.0 745 P92.3 Q14.1 742.3 Q62.39 752.47 Q51.810 Q17.3 740.2 Q14.2 Q11.1 589.1 746.09 Q45.9 743.10 747.89 K00.5 751.0 Q15.9 Q64.39 750.11 Q68.0 750.13 Q62.10 749.24 751.9 313.8 743.42 Q77.1 750.26 Q22.2 744.83 524.5 593.0 259.1 747.4 744.01 524.29 744.5 524.53 K00.6 Q04.3 Q92.8 Q12.3 752.44 752.0 751.69 Q89.1 764.08 743.6 764.15 F88 315.5 748.69 589.9 Q11.2 Q55.8 752.7 764.16 747.42 743.33 744.81 Q25.2 741.01 Q62.12 Q05.5 Q89.4 744.24 Q13.3 Q95.0 P05.02 N27.1 313.9 Q38.5 748.4 742.4 744.43 Q38.0 Q54.9 P05.01 524 Q99.9 749.12 758.9 758.33 764.11 753.8 Q07.9 745.5 748.0 747.63 589 758.6 P05.17 764.05 Q38.6 Q26.3 Q26.9 M26.70 524.34 747.0 Q20.5 M26.59 764.02 Q06.8 743.20 Q00.0 764.29 M26.213 Q33.1 752.5 Q76.419 Q91.3 K00.1 764.28 751.4 746.02 M26.25 524.70 748.8 Q43.3 743.58 Q35.9 749.10 Q21.0 752.2 N13.729 752.63 753.17 Q18.5 Q89.2 R62.50 M26.212 Q16.1 Q61.4 Q20.5 524.24 747.62 747.11 749.2 524.37 764.95 743.22 744.22 741.03 Q24.4 Q22.3 M26.82 744.84 Q16.0 Q24.5 753.1 259.748 748.2 752.46 747.64 764.25 764.01 Q39.5 524.72 756.17 743.21 756.15 750.23 Q51.820 Q38.1 Q18.8 Q60.2 P92.1 524.59 750.25 750.5 749.00 752.39 M26.50 752.45 744.3 743.32 F93.0 Q45.8 313.89 758.81 750.0 Q64.4 Q96.9 742 746.85 743.30 313 743.06 Q14.8 R62.7 743.3 Q05.4 751.6 746.89 758.39 749.25 R62.52 752.19 N13.721 752.52 744.1 Q76.2 764.04 Q16.3 745.2 P05.04 748.9 764.14 764.94 520.7 749.21 753.19 750.7 Q25.0 764.27 F98.1 752.31 Q20.4 P05.03 Q91.7 759.83 746.81 743.48 749.0 Q50.01 524.9 Q10.1 745.10 M55.029 K00.2 P60.2 K92 K80.20 K08.122 579.1 532.91 K03.9 K19.317 K36.5 R19.310 K70.61 577.1 K50.919 K25.9 533.30 K35.2 534.2 K51.1 K63.89 K37 K57.40 533.91 K51.919 K05.212 K92.81 K13.79 R19.36 K62.1 K52.831 K51.40 531.0 K51.312 K50.812 K91.2 532.51 787.4 K40.40 K04.01 P77.3 K90.0 K22.3 K84 532.9 K64.4 K50.911 K69 K74.2 K92.9 K03 K64.1 R19.06 K08.119 K27.9 K57.30 K01 K08.414 K08.530 K21 K43.1 534.60 K08.0 K05.30 K80.44 562.12 K27.3 K56.699 K11.23 K50.118 R19.11 531.2 K13.1 K08.9 534.00 530.5 K11.9 527.8 K40.30 569.44 K62.3 K22.7 K08.433 K55.042 K70.30 K64.0 K94.01 K65 R10.2 533.31 K04.99 577.8 K34.2 K08.22 K41.41 K00.9 568.89 K41 K30 K08.52 K76.4 E16.9 K80.19 K02.7 K70.0 578.1 K27.6 K25.7 J86.0 K86 K94.39 K10 K05.323 P78.82 569.41 K32 K29.71 K04.3 K91.0 K58.8 K69.04 787 K57.12 K08.23 K95.89 K60.3 787.7 K26.9 K28.2 K14.1 K00 533.51 K08.494 K57.20 456.2 K04.90 K52.29 K56.0 K28.0 K13.23 530.82 K42 531.41 K29 R19.30 K27 K80.31 K59.01 777.2 R14.2 R14 R19.07 R10.824 534.9 K51.80 K22.10 R11.12 R18.8 K55.069 K28.4 787.21 K31.0 K55.21 K51.913 K38.8 R19.7 K46.0 K55.8 K80.51 K63.1 K57.31 536.1 K85.80 K85.30 K56.50 537.84 K94.29 532.31 534.30 K52.22 K40 R10.84 K73.2 K81.1 K80.66 K71.4 530.84 K40.10 K59.8 K71 K85.9 K80.0 K50.814 527.2 787.23 K54 K08.431 532.40 569.85 531.31 564.01 K97.83 569.87 R11.0 K14.3 537 K62.5 564.09 R14.3 K51.314 K22 K86.1 K91.5 K05.211 K71.50 K08.104 530.9 534.51 K74.1 534.70 K80.11 K62.89 K76.3 K89 R13 K19 K62.6 569.2 K31.1 K65.2 K91.31 532.71 K11.5 K60.4 K57.21 K08.422 K71.9 K51.514 K59.39 K41.10 K08.531 K03.81 K75.3 K51.411 530.11 531.01 K22.9 K72 K64 K08.423 K28.5 K29.01 K08.21 534.40 K31.89 530.2 K27.5 K51.512 K29.41 K22.4 K27.1 K02.61 R10.821 K51.518 K85.10 537.89 K73 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787.24 R19.32 K28.7 K05.329 532.3 533.90 534.10 579 K04.7 K22.11 K10.062 K08.199 K33 K59.00 787.22 K86.3 R19.33 R19.12 K14.2 K03.3 K82 531.41 K29 R19.30 K27 K80.31 K59.01 777.2 R14.2 R14 R19.07 R10.824 534.9 K51.80 K22.10 R11.12 R18.8 K55.069 K28.4 787.21 K31.0 K55.21 K51.913 K38.8 R19.7 K46.0 K55.8 K80.51 K63.1 K57.31 536.1 K85.80 K85.30 K56.50 537.84 K94.29 532.31 534.30 K52.22 K40 R10.84 K73.2 K81.1 K80.66 K71.4 530.84 K40.10 K59.8 K71 K85.9 K80.0 K50.814 527.2 787.23 K54 K08.431 532.40 569.85 531.31 564.01 K97.83 569.87 R11.0 K14.3 537 K62.5 564.09 R14.3 K51.314 K22 K86.1 K91.5 K05.211 K71.50 K08.104 530.9 534.51 K74.1 534.70 K80.11 K62.89 K76.3 K89 R13 K19 K62.6 569.2 K31.1 K65.2 K91.31 532.71 K11.5 K60.4 K57.21 K08.422 K71.9 K51.514 K59.39 K41.10 K08.531 K03.81 K75.3 K51.411 530.11 531.01 K22.9 K72 K64 K08.423 K28.5 K29.01 K08.21 534.40 K31.89 530.2 K27.5 K51.512 K29.41 K22.4 K27.1 K02.61 R10.821 K51.518 K85.10 537.89 K73 K27.2 K38 558 536 536.8 541.0 K94.03 K86.0 K57.13 533.4 K28.9 K38.1 K93 K51.011 R10.826 K50.818 456.1 K51.912 K08.20 568.82 K61.0 579.2 K14.9 K82.1 K06.8 K08.50 R19.6 K51.2 718 565.0 K52.89 R13.19 K51.911 568.81 P76.1 K57.11 558.41 K08.424 K55.021 R10.812 K91.72 K50.013 K70.9 K51.219 K59.09 K94.21 K05.312 531.60 K09.1 777.6 R15.0 K29.0 562.13 K91.83 K56.691 K05.11 K31.83 K60.0 K08.414 K55.032 K13.70 536.0 K08.101 K51.812 568.9 K44.0 K34 K55.039 R16 564.9 K65.0 K12 K04.02 K08.55 P78.1 K08.192 532.30 543 K71.0 K65.3 K08.59 K66.9 K35.89 560.3 K80.70 577.2 K31.84 K08.499 K41.21 P78.83 K14.6 K08.111 K41.00 K65.1 K86.8 568.0 K26 K51.311 K38.0 K76.81 787.91 K29.51 K07 K94.11 K38.9 578.9 K03.89 K55.049 543.9 K85.31 K52.82 R19.02 K08.82 566 R10.30 565.1 K14.0 K85.22 531.90 K29.90 527.4 K94.10 K80.80 527.6 K08.409 K72.91 K49 R10.13 R19.05 532.6 K12.2 K41.01 K60.1 K29.00 K55.9 R15.9 K66.0 K08.124 K08.421 K02.63 K04.1 K26.0 K56.69 R18.0 K91 K51.811 K28.1 787.6 542 568 777.50 K85.11 K12.0 K52.839 531.71 530.4 K90.2 K26.3 P76.0 K31.6 787.24 R19.32 K28.7 K05.329 532.3 533.90 534.10 579 K04.7 K22.11 K10.062 K08.199 K33 K59.00 787.22 K86.3 R19.33 R19.12 K14.2 K03.3 K82 531.41 K29 R19.30 K27 K80.31 K59.01 777.2 R14.2 R14 R19.07 R10.824 534.9 K51.80 K22.10 R11.12 R18.8 K55.069 K28.4 787.21 K31.0 K55.21 K51.913 K38.8 R19.7 K46.0 K55.8 K80.51 K63.1 K57.31 536.1 K85.80 K85.30 K56.50 537.84 K94.29 532.31 534.30 K52.22 K40 R10.84 K73.2 K81.1 K80.66 K71.4 530.84 K40.10 K59.8 K71 K85.9 K80.0 K50.814 527.2 787.23 K54 K08.431 532.40 569.85 531.31 564.01 K97.83 569.87 R11.0 K14.3 537 K62.5 564.09 R14.3 K51.314 K22 K86.1 K91.5 K05.211 K71.50 K08.104 530.9 534.51 K74.1 534.70 K80.11 K62.89 K76.3 K89 R13 K19 K62.6 569.2 K31.1 K65.2 K91.31 532.71 K11.5 K60.4 K57.21 K08.422 K71.9 K51.514 K59.39 K41.</p>
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Frailty	<p>290 S88.911A F31.76 S98.919 333.82 897.3 F10.951 296.34 294.10 295.54 295.03 G24.02 295.53 295.33 298.2 295.52 296.32 S71.029A 295.70 331.7 891.2 S71.109A G24.01 296.21 295.80 F33.9 292.12 336.0 G24.3 G90.59 F19.94 S91.329 333.5 292.2 331.0 296.16 337.09 F28 296.81 295.34 F31.77 S81.829A 336.2 295.01 295.30 S98.912A 292.11 E75.23 291.3 F10.982 F44.89 S76.929A F10.159 G89.22 G32.0 292.89 296.25 331.89 F06.8 293.89 296.56 G90.09 296.22 334.2 F24 295.64 S88.912 333.81 G89.0 298.4 330.9 F31.63 G11.4 F06.4 295.91 333.3 G89.29 335.19 F23 295.24 F84.0 G31.81 F32.1 F31.30 295.84 G25.89 333.1 897.7 299.81 S98.019A 295.15 332.0 F29 F32.0 293.0 295.13 332 296.64 891.1 S98.019 335.21 F19.97 F30.3 335.23 297.3 333.6 338.28 299.10 F32.9 296.03 333.79 295 290.11 291.0 296.62 F10.239 S98.119 331 F30.2 R52 338.12 297 299.01 G12.9 S86.929A 295.23 S71.029 295.11 299.00 295.12 G10 290.13 337.9 G80.3 296.30 296.33 F33.2 F84.3 296 333.89 296.11 335.8 G25.0 F30.13 F31.73 F20.89 296.42 333 337 298 296.06 G31.09 G25.81 296.40 335.22 G90.529 F32.3 G12.8 F31.2 895 290.43 295.63 292 338.19 S71.129A 333.71 S91.129A 337.01 295.35 334.9 296.89 295.25 S88.119A S91.329A 290.9 331.5 F20.1 331.83 F20.0 293.81 G25.3 S76.929 295.94 295.85 290.41 337.29 291 G31.01 S98.912 298.1 S88.911 296.61 335.24 G32.81 G90.01 294.9 338.0 F04 G31.1 G25.82 291.4 892.0 295.73 334 895.0 F01.50 296.45 G20 290.42 891.0 G25.61 295.43 338.22 338 295.61 S81.009 338.11 S71.109 F84.9 F06.0 333.72 G25.83 F30.12 890.2 F31.32 G23.8 891 S78.119A G95.89 331.4 F31.62 296.53 F31.81 338.21 333.99 F10.27 295.02 G25.9 298.9 330 S78.119 F25.9 G21.11 S71.129 291.89 299 S91.129 294.11 296.63 296.7 296.12 295.41 F10.99 295.93 G89.4 F03.90 290.8 295.81 G90.9 295.60 295.40 F02.80 333.2 S98.119A G25.5 896.3 293.1 296.35 G89.21 F20.2 295 45 291.2 890 333.92 335.11 335.9 295.62 F31.60 F33.3 333.93 296.23 331.11 295.05 F01.51 F31.74 296.44 335.20 294 F05 897.2 337.20 296.52 296.10 296.51 333.85 295.44 G11.3 299.80 334.1 S98.911 291.81 295.75 291.1 295.71 296.04 293.84 296.13 296.41 337.00 G89.11 S71.009 S98.911A 331.2 897.0 299.91 291.5 893.1 F32.8 297.9 894.0 330.3 F32.4 G91.1 333.84 F32.5 295.82 S88.919A 296.26 330.8 F30.8 G95.0 331.81 S98.919A S91.309A 295.21 331.19 338.29 895.1 331.3 297.1 F10.929 338.3 G90.519 892 G24.1 G30.9 G95.9 G99.2 295.10 295.90 295.92 S88.919 295.83 292.83 F02.81 331.82 333.90 F31.31 292.82 G93.89 F15.920 296.15 335.10 G12.1 S88.119 F22 293.9 337.22 F06.30 336 299.90 330.1 296.43 F39 335 291.9 334.3 G11.0 892.1 897.1 897.5 893.0 295.95 297.8 F33.1 333.0 333.83 897 F84.8 G12.0 336.1 337.1 292.84 G31.89 F11.182 295.42 290.10 296.66 296.90 337.21 333.4 296.00 F19.921 G91.0 296.02 296.14 G91.2 F31.13 290.3 295.72 894.1 296.82 296.36 290.0 G31.8 897.6 F31.9 F34.8 290.42 G89.12 F30.10 F19.939 332.1 337.3 334.8 897.4 F32.2 896 G12.29 297.2 F31.78 G31.84 291.82 290.12 G12.21 295.55 296.24 293.83 334.4 G94 331.9 G24.5 F20.81 F31.61 334.0 296.20 G21.0' F19.950 S91.309 292.0 F06.1 294.8 G99.0 G89.18 F33.41 335.29 298.3 299.11 294.0 S81.009A S96.929 292.85 295.32 G31.9 890.1 298.8 338.4 S96.929A 896.2 896.1 298.0 F20.5 F33.42 296.65 S78.019A F31.75 893 297.0 S91.109 295.31 296.80 296.46 F19.951 892.2 333.91 296.05 F31.11 F31.5 F10.231 S88.912A F10.50 893.2 330.0 E75.4 296.55 F19.99 F10.96 295.20 G95.19 295.22 295.04 S71.009A 292.9 894.2 F31.64 890.0 G24.9 292.81 G93.9 295.50 S91.109A S81.829 296.60 G12.22 F19.96 S78.019 G11.1 F06.2 F30.11 896.0 296.54 296.50 335.0 295.51 F30.21 290.20 G24.4 F20.9 336.3 894 338.18 F31.10 G90.4 G89.3 G89.28 293.82 293 F11.159 333.94 330.2 295.65 336.8 S86.929 290.40 F30.4 295.00 G24.8 F93.0 G90.7 F31.4 296.99 336.9 F31.12 295.74 296.01 296.31 G11.9</p>
Health-Services	<p>V58.49 V12.50 Z79.2 Z28.3 V04.5 V77.2 Z01.89 V06.3 V10.52 Z00.8 V12.49 V02.61 V70.8 Z93.52 V15.05 Z76.89 V03.89 V71.5 Z41.3 V03.2 V06.0 V22.60 V58.0 V15.1 Z22.31 Z11.59 V18.3 V15.02 V58.30 V72.9 Z82.49 V13.69 V53.7 V57.3 V03.6 V17.4 Z87.898 V12.01 V58.78 V77.0 Z02.1 Z71.3 Z48.01 V71.1 V06.1 V02.51 V01.84 Z41.8 V54.19 V31.01 V64.2 Z38.1 S92.302 V64.00 Z51.11 V07.0 R13.10 V15.01 S59.101 V04.81 V59.9 Z09 V05.9 V01.79 Z02.81 V68.9 Z09.148 200.00 V80.2 V12.61 Z13.0 Z13.5 V67.59 V05.2 V09.0 V54.12 S92.302D V12.59 Z82.5 Z46.82 V54.89 291.012 Z11.8 V68.89 V17.49 V15.83 Z13.9 200.111 Z01.20 V02.2 Z72.820 Z22.50 V06.9 V76.3 V48.9 V72.7 V65.49 V67.4 V07.9 V74.8 V44.1 Z23 V54.09 V58.9 V55.4 Z91.011 V81.6 V77.99 V41.1 Z91.010 V61.29 Z91.038 V55.1 Z28.82 S72.471 S72.471D V29.3 Z87.19 Z48.812 V58.43 Z48.810 V70.2 V55.8 V81.5 Z76.2 Z48.813 Z47.89 V45.51 V41.0 V06.5 Z91.81 Z46.6 V13.02 Z97.3 V07.8 V71.2 V43.1 V75.7 Z13.220 Z01.110 V31.00 Z68.51 Z11.1 Z13.21 V58.74 V72.11 Z01.10 Z38.30 V82.5 V03.3 V41.6 Z45.2 Z11.6 V12.60 Z51.0 Z38.69 V13.7 V78.9 V71.7 V54.10 V54.9 Z11.2 Z55.9 Z39.1 V61.20 V44.52 V70.9 V33.01 V74.9 V05.8 V40.9 Z01.12 Z22.1 V75.9 Z53.29 V29.8 V49.75 Z43.1 S72.011 Z20.9 V54.01 S02.8xxD V20.31 Z13.4 V72.82 Z20.6 V20.32 F69 V12.09 V21.9 V05.4 Z96.1 V18.0 V30.0 Z86.79 V66.5 V04.82 V58.11 V67.9 V21.8 Z71.9 Z43.0 V02.3 V81.4 Z63.9 Z48.03 V67.2 V58.89 V15.09 V04.4 V78.3 V14.3 Z43.8 Z04.41 S42.101 V68.09 V53.6 V54.16 V20.1 298.89 Z16.11 V77.7 Z72.4 Z47.2 Z83.2 V63.81 V53.2 V15.86 V81.2 Z46.9 Z13.228 V85.52 V12.51 V77.6 V54.13 V03.5 V55.0 V07.1 V72.85 V54.15 V67.00 V72.1 Z00.3 Z86.718 V15.5 V61.8 Z85.830 Z86.59 V73.89 P00.2 V72.19 Z46.2 V09.1 Z20.811 Z79.01 Z04.9 Z51.89 V49.2 S52.90x V79.9 V71.81 Z85.528 V82.6 V01.7 V44.0 V19.6 V04.6 V06.2 Z38.31 V45.89 V72.84 V85.51 V77.3 V34.01 V65.43 V65.40 V69.1 Z22.330 H57.9 V04.0 Z77.9 V72.6 V07.39 V01.5 V71.9 V39.01 V12.6 V72.83 V58.82 V78.0 V78.8 V58.31 Z68.53 V44.2 V03.82 V85.54 Z76.1 V20.0 V58.69 Z13.89 Z01.810 V72.2 V70.0 Z48.00 V70.5 Z13.83 Z01.812 V45.2 Z88.3 V70.4 V06.4 V58.73 V05.1 V58.61 V72.31 Z52.9 Z00.110 Z87.01 Z03.89 Z83.3 V19.8 V15.89 Z87.440 V02.4 V49.5 Z86.69 V72.0 S59.101D V01.9 Z20.3 V10.81 Z13.29 Z01.00 V25.01 V13.9 S52.90xD V50.2 Z38.00 Z93.0 V78.1 V02.59 Z03.6 V72.69 V57.89 V02.9 V58.62 V67.51 V74.1 Z68.54 V79.3 Z79.891 V68.1 V07.2 V30.2 Z93.2 V58.32 Z08 V69.4 Z43.4 Z87.798 Z87.09 Z91.018 Z71.1 V04.8 V04.2 Z86.11 V77.1 V76.12 Z22.8 V15.88 V29.0 V61.9 Z12.31 V82.9 Z38.01 V03.1 V02.0 V54.11 Z62.1 Z01.411 Z63.8 298.89 S72.011D Z60.3 V16.3 V71.02 V71.89 V01.89 Z98.2 Z71.89 V14.1 V20.2 Z02.9 V58.81 V70.1 V18.19 V24.1 V65.5 V15.06 R68.89 V80.3 V79.8 Z51.81 V06.8 V72.5 Z89.519 V58.71 V30.01 V40.3 V71.4 V58.83 Z13.828 V19.1 Z12.6 V04.3 V19.2 V53.90 V29.9 V07.31 V12.00 V57.1 Z78.9 Z13.1 V77.91 Z68.52 V65.9 V72.62 V70.3 Z77.011 V14.0 V01.1 Z02.89 Z82.2 Z01.818 Z80.3 Z46.89 V05.3 V02.51 Z72.63 Z04.71 V12.79 V17.5 V72.12 Z13.88 V05.0 V30.1 Z86.19 Z00.2 V15.03 V53.09 V72.60 Z76.0 Z30.011 V04.89 V03.9 Z04.3 V85.53 P00.9 V21.0 Z20.1 V58.3 Z84.89 Z93.1 V49.89 Z88.1 V40.1 V62.4 V21.2 V82.3 Z02.79 V72.81 S42.101D S02.8xx V41.2 Z48.02 V39.00 V67.09 V65.8 V65.3 Z20.89 Z22.0 Z11.9 Z04.6 Z46.1 Z00.129 Z16.10 Z83.49 V50.3 Z28.9 Z88.0 V71.09 Z13.6 P00.89 Z97.5 V02.1 V82.89 Z01.811 V57.21 V06.6 Z41.2 V64.05</p>
Hematologic	<p>D68.59 P59.29 D72.822 P58.42 P52.5 D50.0 P61.2 280.8 P57.0 P50.8 P52.0 282.69 286.0 774.5 D69.2 P50.0 P10.0 281.8 D57.411 D51.0 287.8 286.7 282.5 287.32 774.1 289.51 D55.9 P59 772.14 282.60 280.9 D53.8 D57.211 D59.9 284.8 D61.811 D59.2 D59.6 282.1 D73.81 P52 D61.09 287.3 281.0 282.42 773.4 P50.1 283.11 287.5 286.1 D68.318 D64 773.5 D68.8 285.21 776.4 772.3 D72.820 284.1 P51.8 D63.0 283 P61.5 D78.02 D59.1 772.9 P59.9 283.10 D50.9 D59 D68.311 D53 P10.8 D78.34 D75.81 D72.9 D57 P10 287.39 776.3 D58.9 P10.1 286.4 D74.0 287.31 D55.8 D75.0 285.29 D68.61 D78.81 D72.810 D69.9 D55.2 D60.0 D52 P55.0 D73.0 282.61 D59.5 P54.6 D53.0 285.1 285.22 289 D64.1 289.82 D59.0 D78.33 P61.0 D63 284.0 D61.1 D74.8 P54.2 289.81 281.9 D64.2 D76.3 776.7 P58.0 P58 D57.412 P58.41 773.0 772.13 D64.3 D61.9 D53.1 D68.52 D72.828 D75 P60 P52.8 D52.1 D60 P58.8 283.1 P57 D70.0 D78 D58.1 D69.49 289.59 P61.1 281.3 282.49 D68.32 283.9 D58.0 286.5 P52.4 D69.3 D73.9 D68.51 D57.80 774.31 D57.819 286.3 D78.21 284.81 D73.1 D77 282.68 P10.3 D56.4 D68.0 D73.89 D78.12 D58 284.2 D55 D76.2 P61.8 776.6 282.7 776.1 D53.9 289.52 D57.811 D56.2 D75.9 284.9 P52.6 287.30 D72.829 D68 772.6 287.0 D52.8 282.62 D68.69 776.0 774.4 D72.825 286.2 D57.812 P54.4 284.09 P61 D72.819 284.89 D73.2 282.40 D57.20 284.01 D68.2 D72.0 P58.9 D75.89 D55.3 D61.82 D56 P54.1 773 D53.2 282.9 D56.8 776.9 D69.41 772.4 P56.0 D60.9 D78.11 P59.0 286.9 D78.32 281.1 285.8 D52.9 P50.3 287.41 D57.212 289.8 287.33 D72.823 D72.824 282.64 P54.3 P55.9 D59.3 D58.2 D60.8 D70.4 D51.9 D69.42 P59.8 P61.4 D64.4 D69.1 P57.8 D75.82 D69.6 287.1 P58.2 280.0 P58.5 P56.99 P61.6 772 P50.2 D56.1 P50.4 D70.3 P52.21 284.19 D78.01 282.2 D70.8 D51.1 D50.8 D61.818 D51.8 D57.02 D57.1 D75.1 287.2 774.0 P51.9 774 D69.51 P54.8 P58.1 282.41 285.2 D56.3 P54 D72.818 287.9 P55 P61.9 P55.8 772.8 D54 D52.0 773.3 282.6 D73 D61.2 772.0 774.2 284.12 D78.22 282.8 287.4 D64.9 D55.1 P59.3 P52.22 D74 P54.0 D70 280.1 287.49 287 D76.1 D78.89 289.7 P52.1 D72 D50.1 289.89 D72.1 P56.90 281.2 772.2 286.6 772.11 289.4 D68.1 D59.4 D69.0 D73.4 D58.8 P52.9 D67 P59.1 776.8 D59.8 289.9 283.19 284.11 D61.3 D51.3 D61.89 D66 D57.40 283.0 D71 D56.0 281.4 D61.01 772.10 D69 284 P56 772.12 D51 774.6 D56.5 285 P10.4 D78.31 D63.1 D70.9 P54.5 D72.821 D57.219 P59.20 D57.3 D51.2 D64.89 P61.3 P50.9 772.5 D69.59 285.3 P54.9 D68.4 P55.1 285.9 776.2 289.50 D73.5 282.3 D62 282 776.5 D72.89 282.63 P57.9 D61 D57.00 D63.8 P51.0 D70.2 D74.9 P58.3 P52.3 D56.9 D55.5 D57.419 776 D68.62 D69.8 D68.312 D70.1 289.83 774.7 D64.81 773.2 774.39 D64.0 P50.5 P50 P53 D61.810 774.30 D76 P51 289.5 D73.3 773.1 D60.1 D68.9 P10.9 D65 P10.2 D50 D57.01</p>
Hypertension	<p>404.00 403.00 I15.9 403.11 404.0 402.00 404.10 I11.9 401. 403.0 I13.10 403.90 405.9 I16.1 402.10 402.1 404. 403.1 I15.2 404.11 404.03 403.9 404.1 405.09 404.91 I15.0 401.1 405.0 405.91 403.10 404.12 40311 404.9 404.13 I13.11 I12 I16.0 403 401 402.91 404.02 405.1 I10 I15.1 402.0 I15.8 405.99 405 I13.0 402. I12.9 402.01 I16 403. 404.93 401.9 I11 404 405.19 I12.0 404.01 403.01 403.91 405.01 405. 402 I15 I13 404.90 I14 402.90 404.92 402.9 402.11 I16.9 I13.2 404.04 405.11 401.0 I11.0</p>

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Infections-General	<p>041.4 017.10 B02.21 055 098.14 042.9 B09 011.80 569.5 B69 136.4 A19 078.0 057.8 A50.09 017.81 590.3 083.8 016.4 013.83 003.8 B67 341.21 372.05 016.32 380.12 015.62 017.20 466.1 380.2 001.1 001 A52.10 B94.2 H70.009 B35.0 A92.8 017.44 017.82 123.1 115.00 016.71 B74.8 T79.A12S 081 016.60 011.8 B02.24 T50.A15A A05 B60.12 T50.A25D A04.9 B33.23 T50.A11A 682.6 098.41 B35.2 116.2 N37 018.92 040.89 A77.0 117.7 095.8 045.1 A07.4 A63 B08.1 018.01 070.3 B88.2 M90.869 482.42 A85.1 005.9 041.10 015.5 375.30 A39.83 016.36 013.53 B96.81 011.93 488.11 041.04 A48.51 B26.1 A73 A08.32 B43.1 A18.4 B65.0 A41.02 T80.A19D 018.85 B16.9 066 B87.89 060.1 182.B29 324.9 P36.2 012.85 685 B50.0 A27 A66.5 070.70 A66.1 B02.2 T50.A93A P35.1 A48 100 B17.9 590.1 058.1 079.3 130.1 B06.00 B42.89 112 017.9 B60.0 T50.A22D B74.4 B52.9 046.2 077.9 381.1 086.0 483 056.01 A54.41 016.24 062.4 A83.9 K67 B97.11 449 085.0 007.8 013.62 A92.9 P36.39 T50.A9A5 016.1 011.5 J05.10 466.0 A50.07 B00.82 015.61 B81.3 017.76 012.81 B08.010 015.04 771.3 A30.9 063.8 016.93 A52.05 B02.0 A22.2 059.22 041.03 008.69 011.23 381.0 A06.9 380.1 083.1 A28.2 A36.85 B46.0 013.14 070.52 B77.0 082.40 054.1 482.89 112.89 A02.0 T50.B12S 010.02 032.2 A18.54 B27.82 B73.00 008.5 047 036.42 T80.A10D M79.A21 B45.2 A08.39 681.0 111.0 T50.A25A B40.3 B48.3 375.31 094.1 017.33 014 J31.0 038.4 G00.3 B83.1 045.23 011.43 045.01 T50.B94 041.83 071 015.21 B43.0 016.53 048 094.8 472.1 016.04 010.94 073.7 A96.9 017.4 079.52 015.12 127.8 016.14 T80.A11S A00.1 097.9 A07 011.64 A66.3 038.49 039 100.81 137.3 136.3 382.2 B57 006.0 038.42 A51.45 B87 B95.7 771.1 H70.209 483.8 012.1 A36.9 010.01 063.9 J15.20 B97.89 420.91 B26.85 B45.8 081.2 074.22 A88.0 014.06 042.0 567.3 115.13 B55.1 016.54 016.35 B35.1 573.3 053.13 A37 015.75 079.2 J18.9 N11.8 008.45 056 A52.06 A54.83 A23.1 093.81 A53.0 424.90 A54.84 I40.0 H10.239 A48.52 A49.2 112.84 013.23 0141 099.55 051.0 004.9 093.20 B14 B24 373.4 011.72 B79 098.39 M89.619 T50.B93 A80.9 091.1 A32 A17.82 031.0 M90.879 043.1 488.1 A51.9 J09.X3 A87.2 123.4 G00.9 A21.3 B40.0 B97.4 066.49 A02.24 038.0 B06.01 A48.8 017.06 730.76 421.1 098.5 094.83 020.9 001.9 115.9 015.66 A02.22 A50.03 B37.7 026.0 077.98 482.8 730.75 117.2 055.0 A93 A77.8 A04.5 A01.05 B02.32 003.21 A53.9 322.1 B48.0 B56.9 A44.1 098.50 015.70 B17.2 B67.99 H60.399 098.59 T50.A94 T50.B95D G03.9 A01.2 123 039.1 077.4 682.2 P35.2 T50.B15D B31 017.66 A80.39 A81.09 381.3 B87.81 B60.19 B32 038.12 074 321.2 131.9 012.8 A43.8 B57.42 131.8 015.92 482.2 A07.0 T50.A13D 125 011.90 072.2 060.9 014.05 027.9 101 B30.9 A06.1 320.2 B97.5 484.8 A41.9 130.0 013.90 078.19 T50.B12 084.8 040.2 102.2 A25.0 B57.2 123.5 I31.2 J15.5 B27.81 099.59 B08.72 M86.9 005.2 094.82 H59.42 112.2 T79.A11 139.1 J85.1 003.9 008.43 003.0 A82.9 480.3 A08.2 083.2 123.9 070.43 878.4 078.1 B38.4 B40.1 B00.89 034.0 A51.5 012.01 B71 006.4 513 J17 074.3 A56.4 A18.12 A77.49 B95.8 132.9 B55.2 011.15 017 008.42 T50.B93D L03.039 B77.81 126.0 A56.09 077.3 B95.4 484.5 323.71 682 074.0 008.49 B17.11 010.05 A66.8 A85.2 B48.4 B96.5 A51.31 054.42 011.41 A52.8 132.2 A50.45 A04.7 A77.9 B46.5 006.5 115.04 009 A39.82 B37.42 011.0 B08.09 054.73 A44.8 012.84 P36 B85.0 383.21 059.0 040 126.8 T50.B95S 771.0 074.23 323.51 685.0 A26.0 382.01 B01.2 B83.4 A42.82 B00.7 B67.69 015.7 038.41 B94.1 421.0 021.1 098.86 A68 T50.B15A A49.02 T50.A21D 013.22 A32.7 B58.2 124 099.49 B67.32 012.0 B87.3 070.1 B08.03 132.1 016.55 111.2 T50.A25 090.7 A36.81 A41.53 018.80 A81.01 B69.1 A21.1 098.82 I30.9 002 102.9 016.94 J04.30 A19.8 050.0 017.65 A18.18 A50.43 B93 023.0 A92.5 103 B74.2 032.1 121.8 B85.4 A18.59 A59.02 015.22 A40.3 392 T50.B16D T80.A19S B82.9 A52.15 T50.A93 A30.1 B42.0 053.11 376.00 B48.1 018.04 137.0 033.9 130.5 045.9 131.09 A05.1 A19.9 A77.1 A02.9 T50.A11 125.1 590.01 011.46 A82 028.0 A39.4 139 A99 016.0 041.0 070.0 008.04 B18.1 015.73 B78.7 B34.0 P36.10 B44.1 B39.0 077 095 383.22 A93.0 381.4 062.3 036.89 326 B82 046.72 422.91 099 102.0 154.85 B08.79 016.31 372.03 057.0 013.51 B37.81 T50.B94A 017.73 464.30 T79.A29A A50.9 A54.03 A52.71 730.78 A30.2 J31.2 A02.20 010.8 372.30 A26.8 012.33 008.67 B96.3 B43.9 018.84 A18.52 B58.3 I31.4 A79.89 046.8 T50.B96A B10.89 039.4 B97.81 B05.3 091.8 686.1 115.19 B81.8 B42.81 T50.A95S I38 A69.20 013.96 A06.81 015.2 B05.81 126 070.20 010.84 A93.1 041.82 A56.3 A65 085.9 054.40 093.89 015.54 016.42 084.7 464.31 B05.0 111.9 030.2 A48.1 008.64 072.1 H62.40 B10.82 A06.89 055.1 052 J12.81 466.11 T50.B95 007.2 A38.1 060 A31.1 B34.3 372.04 026.9 M72.6 016.12 027.1 590.2 P39.2 126.9 110.2 011.35 095.1 480.9 013.13 B44.81 004.8 A20.3 013.65 013.8 052.8 I82.A21 382.00 B76.9 A18.10 013.54 A68.0 M89.60 A56.19 116.0 041.43 A52.09 320.82 B25.1 J12.1 A17 036.8 091.3 M89.639 001.0 074.1 A41.3 A03.8 B02.7 B43.8 B97.30 018.96 682.5 682.0 372.20 B87.4 072.9 018.81 J16.0 G03.0 A83.0 041.12 J15.6 321.3 B37.89 012.16 391.2 018.9 B57.41 B58.09 070.5 K65.2 045.03 A98.8 070 095.4 G02 A66.9 T50.B14D 053.29 B33.0 A48.2 031.8 P39.0 099.41 A06.6 A31.9 114.2 J03.90 065.1 730.99 H05.029 A55 A50.7 H67.9 047.8 017.3 054.41 050.2 127.0 016 B34 018.94 011.34 033 056.0 115.11 121.3 A42.81 A24.1 079.50 B76.0 T50.A93D 072.71 099.51 015.95 A15.9 012.10 059.12 B07.0 T50.A13S B96.29 017.34 B00.2 B60.13 P35.9 078.2 049.8 121.9 B44 598 103.0 A05.0 H04.309 021.0 041.8 B22 B02.31 730.74 014.81 012.83 372.21 011 B91 A77.2 B58.01 J15.9 T50.B13D 015.51 054.49 B33.3 026 A54.33 A29 053.21 A51.39 682.4 488.09 321 T50.A12S T50.A22S 088.0 032.85 A00.9 008.8 073.8 730.79 A80.4 B42.9 A41 A71.9 A80.1 093.23 567 039.8 A06.0 H04.429 P37.0 015.23 B78 112.82 041.02 115.92 A41.52 B88.0 B96 022.2 A36.89 A52.9 B35.9 I31.8 A38.8 013.92 I82.B23 H66.90 015.94 M05.1 391 B46.4 017.86 A02.5 A17.83 122 B90.2 B19.11 T50.A96A T80.A11D A43.0 A74.81 016.51 056.80 A18.39 472.0 102 099.5 A67.0 H70.229 323.4 J09.X9 117.4 015.71 A80.0 B47.1 041.5 126.2 J21.8 484.7 I33.0 016.13 B95 016.95 054.71 043.2 422.93 045.10 128.8 B57.1 059.10 B57.0 091.4 038.2 016.61 021 567.31 B65.8 079.81 B37.81 730.91 018.86 B65.3 372.0 B02.23 B39.5 A48.0 B18.8 482.0 381.10 005.3 017.6 464.50 A50.6 P37.8 T50.A96 A52.11 B67.39 H04.339 T50.A14A 039.3 421 T50.A24S B16.1 B51.0 I09.2 053.19 015.56 T79.A22A T80.A19 A52 G05.4 051.2 A44 B33 079 A67.1 380.10 T79.A12D B27 053.22 103.2 771.5 A37.80 B27.19 I82.B11 018.8 A22.0 A18.83 A40.0</p>
Infections-Respiratory	<p>017.10 013.95 017.86 A17.83 J12.9 013.42 016.51 011.80 J15.1 017.83 017.42 A18.39 A19 010.91 J09.X9 017.81 015.71 017.30 013.83 J03.00 T50.A16D A15.8 016.32 017.20 015.62 017.31 B25.0 J20.6 482.32 J21.8 017.02 484.7 016.13 012.31 016.95 017.44 017.82 016.71 013.61 016.60 T50.A15A 011.33 011.84 018.93 016.61 011.10 485 015.50 018.92 018.86 J01.21 J12.3 017.70 482.0 018.01 464.50 011.31 J11.82 482.42 010.06 014.01 J01.20 016.36 J15.8 015.56 T80.A19 013.53 010.14 A19.0 011.93 013.44 A18.4 A17.9 017.22 T50.A15D J20.9 J03 017.80 T80.A19D 011.91 018.85 A18.83 013.06 016.03 012.85 A17.89 J18.1 012.21 015.01 482.82 011.42 462 017.32 J20.0 482.31 017.74 015.14 012.00 J01.10 487.1 012.06 483 012.86 017.93 J09.X1 011.30 016.24 J02.0 J15.212 016.73 010.11 016.66 J10.81 013.62 016.30 480.0 A18.6 013.10 016.34 017.25 017.13 A18.02 J05.10 466.0 013.01 J11.00 015.61 J06.0 010.85 017.76 012.81 015.04 480 010.11 70 A18.13 015.05 016.93 A19.2 013.80 012 A15 016.05 488 A18.85 015.53 011.23 012.04 J01.00 016.45 015.11 013.14 482.89 010.02 A18.54 013.93 J10.08 J01.41 011.96 J07 011.26 015.10 J11.08 018.05 466 J05.0 461.8 017.33 014 015.55 011.43 011.01 013.46 015.21 015.26 016.53 015.20 012.03 011.92 J10.00 016.04 013.60 J21 010.15 J01.01 010.94 010.04 461.2 J15.7 015.12 J02.9 464.51 016.14 017.41 018.82 013.52 011.64 011.83 J85.0 A18.09 482.1 J11.1 482.84 011.24 011.04 J15.3 483.8 010.01 010.83 J15.20 J20.1 A15.0 017.63 J22 016.90 013.26 A19.1 010.16 014.06 016.92 016.35 016.54 010.96 J00 015.75 016.91 J18.9 T50.A16 012.35 016.01 015.76 017.92 A18.31 010.93 012.13 018.95 016.21 T79.A19 013.23 016.41 012.14 482.49 014.85 011.72 017.01 A17.82 J10 488.1 011.71 487.0 J09.X3 T50.A16A 013.66 011.53 013.55 015.83 A17.81 J01.80 015.74 J12.89 B44.0 J18.8 464 482.83 017.06 A18.89 016.65 011.14 J10.01 015.66 J11.2 017.90 013.31 012.34 018.91 J08 010.80 J20.5 A16 I82.A19 011.76 017.24 011.50 013.20 016.16 016.50 015.03 015.65 012.32 015.70 016.52 A15.5 461 016.44 A18.14 015.52 A22.1 011.82 A18.53 460 J01.11 486 017.66 480.8 464.10 J02.8 012.30 J10.89 J21.9 J85.3 012.23 016.76 017.84 016.02 465 015.92 482.2 014.03 J16.8 014.05 011.90 J18.2 018.83 A17.0 017.40 484.8 013.45 464.20 013.90 014.00 J11.83 013.11 011.54 482.41 017.56 J15.5 012.22 463 J08.0 015.90 013.12 011.20 T79.A19S 013.81 013.33 J85.1 480.3 J01.40 015.85 012.02 013.43 016.74 017.94 010.95 017.64 461.3 011.95 012.01 016.46 A15.6 513 J18 011.65 J17 013.21 A18.12 J01.31 A17.1 011.15 015.84 017 013.00 016.63 014.04 013.40 011.94 A18 J01.91 484.5 J06.9 J20.4 464.00 461.1 010.05 012.36 010.86 A18.50 J03.80 011.41 015.15 J01.30 016.33 483.1 T79.A19D 013.32 012.84 012.05 017.52 011.06 J01.90 010.12 015 013.15 J14 011.45 J15.211 J09.X2 016.20 015.02 013.04 J01.81 014.86 011.05 013.82 487.8 015.16 011.66 A18.15 J10.82 017.53 010.90 M79.A19 017.43 013.22 012.11 J03.91 J12.0 J21.1 484.6 A18.2 017.15 J01 011.00 013.03 017.16 J12.2 016.55 J15 016.70 018.80 488.0 013.41 013.25 017.04 016.94 011.32 013.64 J04.30 J09 465.9 A19.8 017.65 A18.18 J03.01 480.2 A18.51 012.20 016.72 J15.29 016.40 010.13 016.00 A18.59 015.22 016.75 018.00 017.51 513.1 T80.A19S 013.86 015.00 A18.82 017.50 018.04 018.06 013.85 A18 011.55 A19.9 J20.2 015.06 011.22 011.46 011.73 J06 017.62 010.03 013.30 010 017.60 015.73 017.05 012.25 017.46 016.10 T50.A15S 012.82 J04.2 016.31 013.51 A16 011.33 J12 017.73 017.91 464.30 018.03 010.10 A037.91 016.43 013.16 010 481 017.35 A18.17 015.86 011.56 J20.8 T50.A16S 011.52 017.72 010.00 011.36 015.82 012.33 011.03 483.0 A15.4 018.84 013.35 A18.52 011.51 012.24 018 J11.89 J03.81 J15.0 013.96 G40.A19 010.84 017.95 010.92 015.54 464.21 016.42 464.31 016.25 A48.1 011.63 464.01 464.4 012.12 T50.A15 J05.0 513.0 015.60 J20 011.11 484 466.11 011.25 013 J12.81 017.23 015.96 016.12 013.63 484.3 461.0 017.03 011.35 480.9 J04.10 013.13 017.12 013.65 015.63 015.80 015.93 A18.10 A18.7 T79.A19A 013.54 J04.11 482 016.62 011.75 A17 J12.1 016.56 J10.83 017.36 011.13 J10.1 011.85 016.64 018.96 011.61 015.91 015.64 482.81 018.81 J16.0 013.05 J20.7 011.86 015.81 J15.6 017.71 012.16 A15.7 011.40 013.50 J02 018.90 016.26 013.91 J15.4 017.14 482.39 A18.32 482.9 A18.11 J03.90 016.11 015.24 465.8 011.60 010.82 487 017.96 013.94 012.26 013.34 016 017.55 018.94 011.34 011.21 014.82 018.02 015.95 J20.3 017.26 017.00 A15.9 012.10 017.54 J11.81 013.56 015.72 013.02 017.34 016.15 J10.2 012.15 011.74 480.1 J05.11 011.44 017.45 014.83 015.13 017.11 014.84 A80.01 010.81 466.19 J11 015.25 A18.84 016.06 016.23 017.21 014.81 A18.16 012.83 J85.2 014.80 017.75 011.16 484.1 011 017.61 J15.9 017.62 015.51 011.12 463 J05 J04.31 A18.03 J85 016.96 482.40 012.80 013.24 013.84 J04 464.11 011.62 J19 017.85 014.02 J21.0 015.23 011.81 T80.A19A J13 013.92 461.9 015.94 011.02 465.0</p>

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Injuries

S06.9X4S T84.490D T63 S63.621D S82.232C S65.391S T85.614 S25.809D T85.398 S72.346 S83.011A S60.212A S66.526D T80.59X S52.232D S53.266A S32.115P S56.822 S86.391D T63.614D T50.992S S61.221S S19.9XxA 943.23 T23.179 S71.131 T80.410S S93.129 T40.0X2 T81.83XS S72.436R S75.633D T24.591D S82.01 S72.91XK T24.031D S36.533A S56.196S T22.232A T24.332D S92.355K S59.129 S31.112 T78.3XX S66.120A T81.516 S21.442D S62.043P 803.50 S63.232S T53.0X4A S92.123A S66.020D S72.019A T63.511S S82.864R T65.831S S63.857D T14.157 T40 T84.620 S22.040K S56.892D S72.441A T56.1X1D T83.85X T53.7X3 S68.123A T47.1X6S T26.71XA S14.4XX S89.002D T53.1X1 S62.307S T65.213S S82.242M T22.741A S62.023D T46.6X1 S32.131K S52.515C T65.0X3S S46.012A S52.265C S92.221B S65.111A S06.1X1A S60.461 S61.549D S36.814.03 S24.151A S50.811A T62.1X1S S42.446P S52.264G T24.491A S52.042A S92.599K S06.4X9A S92.416D T20.411A T81.507D S12.600B S82.492P S21.351S T45.1X4S S32.000 T75.4XX T82.391 T43.623 S36.290 T54.3X1S S42.209K S56.334D S59.222 S99.829S S09.19XD S34.22XD S63.652A 942.45 S32.471A T40.3X2 S60.444D S82.146S S82.822K S50.10X T83.022S S56.128S S05.91XD S82.874Q S42.111D S25.402A T82.322 S62.614S S86.929S S90.464D S74.00XA T65.4X2 T61.784D S83.30X S32.456S T53.93X T24.501A S37.69XA S37.091D S63.022D S80.849S T46.991S S61.021 T49.0X5 S90.411D S30.826 T63.834 S64.494A S42.033D S32.058D S42.191D S52.332C S31.110S S82.871M T43.4X5S S95.911S 861.20 S20.309A S01.01X S13.171D S72.366M S82.154B T79.5XXA T83.69XS S09.90X S00.252S S83.096S S01.90XA S72.031K S63.439A S06.365 T50.292 T25.139 S09.312A T50.211D S37.031 S82.426A S82.022K S95.809 S12.300K S35.338S S92.244D T23.799 T28.412 S82.254 S62.312 T22.022S S02.118B S06.6X2D S60.940S S31.20XA T17.408D S09.312D S52.399F S62.251K T63.071D S82.464Q S52.243J S82.465Q S82.401N T49.8X6A 914.3 S55.212 S59.102K T86.23 S96.899 S22.050S S41.112D S50.11XA S52.272M S72.416C S82.876G S22.039D S42.144G S63.227A S66.518A S72.416S T85.511A T48.4X4 S82.034R T20.69XD S82.62XP S42.112B S52.244 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Integumentary

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Metabolic	<p>269 E83.30 270.5 P71.4 276.7 264.1 712.38 M1A.9xx0 274.82 E71.42 278.02 274.19 278.01 276.69 263.8 712.86 E72.8 268.1 275.40 274.03 712.28 M10.30 E66.2 783.1 E74.9 E71.41 270.8 712.19 E83.59 E87.70 M11.80 E50.7 E88.1 275.42 E67.0 260 M10.9 E46 274 E72.20 M11.88 276.3 712.84 E83.50 P19.0 264.3 E50.8 278.2 275.1 E50.1 M11.20 E83.81 R63.4 775.9 277.81 268 712.36 277.88 E83.40 E53.9 271.9 P71.3 E87.1 M11.879 270.7 E52 D84.1 273.9 266.2 264.4 265.1 274.8 712.1 M11.249 712.8 M11.849 277.82 E72.9 M11.269 712.16 E50.4 712.88 M10.40 M11.28 269.9 E88.9 264.9 268.0 E55.9 278.0 712.85 266.9 277.9 E75.21 712.3 712.15 E50.6 712.27 712.97 277.8 P72.8 M11.859 278.3 264.0 278.03 G93.9 E53.0 E16.1 271.3 251.0 775.89 E70.0 P71.1 E51.11 P70.1 275.5 P70.4 277.7 272.3 712.15 E50.6 277.87 712.39 274.81 712.96 712.10 274.02 E87.8 712.90 E15 273.8 R63.0 271.2 E66.9 277.86 266.0 E53.8 E64.3 263.1 278 E87.0 272.5 E66.3 712.32 E67.1 262 712.92 M11.9 M11.29 712.31 272.1 P19.1 P71.8 M11.279 712.95 277.85 E65 E88.40 775.81 783.22 E61.4 783.2 263.2 269.0 261 E83.89 P71 M11.829 P74.0 E74.12 274.89 E70.21 E72.03 712.11 E50.2 M11.869 712.80 P19.9 E50.5 264.6 712.13 275.49 E16.2 E54 E67.8 712.83 276.8 278.4 775.7 712.37 E78.3 270.2 270.4 E53.1 E83.52 M83.9 269.2 269.1 783.21 712.33 M1A.00x E87.4 E87.5 P70.3 268.2 271.8 E87.3 M11.259 E76.01 E87.2 266.1 P71.2 E88.01 E55.0 251.2 266 273.4 274.00 272.2 275.01 275.8 712.98 E56.8 E56.1 E74.21 E44.1 272.7 712.91 263.9 E88.81 E78.89 E78.9 712.34 269.3 274.01 263.0 P70.9 712.22 277.2 E74.39 263 E67.3 276.6 E88.09 E50.3 E72.10 R63.5 E43 P19 265 275.9 264.5 E66.01 E83.00 E80.0 E88.89 712.18 E83.118 275.4 E63.8 264 274.10 277.5 275.3 712.94 712.12 E44.0 E40 M11.819 276.2 274.0 E51.8 276.0 E79.8 274.1 267 E83.9 712.23 276.9 272.4 P71.0 G93.89 712.2 712.87 E83.51 P70.2 271.1 276.4 E45 712.93 277.89 P84 P71.9 M11.89 E87.6 E41 712.17 265.0 E78.2 272.9 277.6 274.9 276.0 E56.9 E70.40 E83.110 M11.229 268.9 712.25 272 270 930.2 271 712.35 M11.839 264.2 275.09 712.30 276.1 R63.6 264.8 277.1 270.9 P70 712.21 278.8 272.6 712.9 275.03 M10.00 270.3 270.1 E88.3 E50.0 N20.0 775.8 P70.0 E63.9 E71.50 278.00 712.29 E74.4 274.11 E83.10 712.24 275.2 E78.1 P70.8 712.99 330.3 712.82 712.81 M11.219 M1A.9xx E50.9 251.1 E78.5 E78.6 272.8 P19.2 E71.318 264.7 E71.0 783.0 712.26 712.20 269.8 M1A.00x1 P72.9 265.2 M11.239 712.14 275.41 278.1</p>
Musculoskeletal	<p>553.9 M84.574D Q67.5 M84.442S M70.30 M25.761 M46.87 550.00 M60.231 M71.829 M85.622 M84.675A M84.753D M08.429 733.20 M84.472 M60.239 M84.346K 727.6 M12.332 735.1 M84.550K M62.241 M71.062 M66.219 M05.051 M24.275 552 M67.479 755.67 M89.322 M27.59 M25.842 M80.821S M84.753A M84.573P M54.02 718.80 M53.86 M85.58 Q65.00 733.43 717.41 M24.174 718.9 M85.012 M48.58XG M15.9 M10.452 M41.22 M20.21 M84.522K M16.10 M23.041 M66.211 M19 M13.822 M24.231 717.82 M90.871 M87.035 M48.57XK M96.679 M21.40 M32.12 M93.841 718.82 M46.96 M65.341 M11.10 M25.222 M67.279 M80.019S 719.99 M66.172 M84.462K M84.442K M96.639 M80.011S M08.231 K43.7 M08.849 M23.007 M11.212 M48.02 M84.619G M65.171 M67.229 M66.272 M60.819 719.90 M11.049 M84.553A M85.812 M89.312 719.70 M06.811 M12.449 M45.0 M79.4 M26.03 M24.075 M86.151 P13 M24.676 M99.77 M84.651 M10.329 M89.752 M23.91 M05.271 755.30 M80.052 M05.842 M80.829 M96.662 M00.232 M80.069A M85.311 M63 M93.94279 M08.839 718.47 M77.30 M80.012G M05.372 M15.4 M62.511 719.04 M89.542 M84.561S M84.572 M94.9 736.05 551.01 M08.469 M94.0 M71.129 M80.011P M69.9 M07.649 M67.832 M05.519 M25.642 M84.533D M54.15 M05.069 M62.59 M84.662K M24.031 M20.001 M90.551 M60.031 M05.60 M61.146 M24.651 M41.112 M93.811 719.12 M89.619 M08.911 M14.879 M08.3 M05.69 M00.162 M05.722 756.55 M05.431 M18.32 M70.951 M80.859G 730.39 M92.12 M48.43X M65.852 M26.00 M23.052 M24.572 M40.14 M80.079D M86.542 M05.049 M65.261 M65.011 M84.663P M60.172 M05.811 M11.822 M71.562 M85.321 M99.21 M67.971 733.1 M84.364P M02.10 M60.074 M83.1 M35.9 M97.42XS M12.529 M05.879 M87.032 M46.38 754.5 M90.672 M50.23 719.50 M85.859 737.21 M12.9 M84.452S M84.443 M11.869 719.45 M93.879 M36.3 719.25 M89.49 M76.899 M08.929 M71.869 M89.042 M70.21 M87.334 M10.451 M26.23 M85.00 M06.831 727 M80.831 M90.852 M76.42 M89.28 M65.332 M86.661 M23.631 M50.823 M75.00 M05.479 M84.379 M10.321 M86.021 M61.129 M79.0 M84.569K M61.229 Q79.4 M08 M62.441 M66.811 M06.859 M54 M45.1 M84.571G M84.672D M23.005 M47.13 M84.612S M84.542 M67.272 K08.23 M12.379 M24.839 M10.019 M89.439 M48.51XS M89.30 M25.149 M22.3X2 M89.061 719.20 M84.756D 552.3 M60.831 717.0 M89.08 M32.11 M90.861 M42.09 M54.13 M12.519 M92.291 M93.851 719.83 M23.212 M71.80 M87.838 M06.059 M84.462A M99.43 M66.842 M23.322 722.30 M84.663K M01.X51 M07.60 M24.376 M80.069P M20.031 M72.2 767.5 M61.161 M02.361 M00.811 M26.213 M87.861 M84.673 M85.071 M84.475A M84.519P M99.18 M71.552 M24.575 M43.04 M12.579 717.8 M89.78 M12.219 M84.639 M84.563P M89.165 M60.261 M80.00X 730.37 M34.1 K40.10 P11.3 M26.82 M84.322G M84.564 M62.85 M51.05 718.89 M88.88 M05.121 M05.10 M84.674D M84.342D M89.571 M80.872A M84.841 M23.352 M71.051 M93.969 M99.01 M63.869 M48.061 M02.122 M21.379 Q65.30 719.92 M21.221 M25.361 M87.29 M84.359P M90.511 M72.0 M11.032 M85.639 M60.262 M80.00XP M84.350A 524.07 M94.261 718.41 M86.432 M54.81 M84.459 M10.422 M84.446K M84.572S M23.009 M06.4 M72.6 M87.263 729.39 M14.659 M87.274 M41.41 M84.750A M84.639A M84.672S 719.49 M91.10 M99.00 722.72 M14.621 M61.59 M67.942 M80.869G M89.032 M24.562 359.5 M60.019 M76.61 M24.371 M87.850 M92.219 M84.432G M13.841 M80.822 M84.474D M85.331 719.16 M25.051 M84.353S M94.229 718.73 M19.032 M84.38XK 717.83 M80.031 M84.632K M94.232 M90.532 737.41 M84.575 M10.349 M86.621 M21.859 M60.20 M61.512 M93.022 M84.649 M10.159 M71.811 M05.762 718.76 M23 M84.669D M48.8X5 719.91 M87.037 M52 M10.022 M84.511P M62.011 M26.31 M47.23 718.4 M31.0 M25.641 M11.219 M65.872 M24.112 M65.141 M21.331 M84.757 M20.092 M80.851D M27.0 M87.151 M99.08 M05.742 M70.971 M97 M84.534S M08.412 M43.8X8 736.02 M84.632A M87.011 M24.021 M61.461 M21.629 718.84 M40.56 M84.369G M87.378 M06.849 M89.157 732.8 M66.89 553.03 M92.299 M42.00 M71.572 M35.8 M02.152 755.65 726.70 M89.8X9 M12.822 M80.042K M84.433G M88.832 M67.411 M23.307 M24.7 M05.759 M67.864 M61.412 M54.08 M10.169 M84.434K M18.50 M24.276 M62.89 M84.833 Q65.4 M40.00 M02.022 M85.329 M60.259 733.10 754.81 M80.80XG M90.542 K08.20 M11.019 718.97 M71.121 756.53 M21.029 M62.131 M26.221 M25.129 M34.82 M86.261 M80.042S M86.462 M47.016 736.75 M46.81 G71.19 727.49 M61.071 M71.21 M02.18 M11.152 M80.829K M12.039 M13.131 M88.841 M85.48 M87.833 M84.361 M60.839 M84.350G M84.422G M19.079 M54.9 718.77 M23.003 M80.852S M60.073 M87.031 M71.479 M61.022 M05.321 719.19 M06.022 M84.352D M34.83 M62.419 M11.051 M84.369K M60.821 M90.551.29 M76.891 M66.352 M67.451 M86.061 M24.171 M86.079 M05.429 M97.42XD K44.0 M60.112 M90.552 M06.051 M05.552 M47.28 M08.48 M12.249 M84.439P M00.221 M85.332 M11.021 M85.029 M76.12 M26.52 M86.442 M84.334S M84.576P M13.112 M10.112 M86.252 M94.1 727.3 M85.342 M85.879 524.06 M85.821 M10.359 M84.475S M12.532 717.7 M27.62 M26.73 M43.01 M12.861 M60.869 M84.459A M17.5 M85.061 M48.55XD M88.839 M76.892 M19.022 M80.861A M84.321S M65.311 M80.852P M96.843 524.1 M80.019G M93.839 737.34 M84.632P M90.811 M18.11 M43.20 M24.673 717.81 M14.629 M61.032 M05.461 M85.052 M24.642 M67.89 M89.163 721 M35 M87.20 M99.41 M05.169 M84.575K M08.40 732 M05.349 M42.9 M08.80 M84.434A M86.559 M12.852 M70.11 M51.25 M94.221 M96.5 M25.28 M66.351 M84.345S M84.752S 526.69 M07.611 M87.261 M70.969 719.17 738.7 M84.312P M33.93 M66.371 M84.662A M48.54XS M89.124 Q65.1 M86.039 M65.821 M25.075 718.0 M84.532A M67.841 M75.52 M80.00XD M17.31 M11.142 M66.311 M01.X22 M65.062 M84.652S M80.019A M89.162 M60.046 M32.9 M84.631D M87.132 M23.8X2 M84.552P 722.6 M43.4 M87.271 M84.542D Q67.7 M05.631 726.7 M62.58 M84.751 719.77 M84.671P M96.65 M99.31 M26.06 M62.529 M62.28 M12.121 M60.032 736.22 M71.862 M79.609 M87.00 M05.49 M48.34 M25.039 M24.232 M92.9 M20.42 M80.859P M90.579 M62.459 M20.039 M99.33 733.82 754.44 736.29 M06.321 M84.753P M60.279 M80.861P M84.433D M26.24 M33.02 M80.029G M11.221 M84.443A M65.121 M06.011 M25.531 M21.239 553.2 727.0 M66.852 M86.469 M70.869 M01.X39 M50.221 M84.662S M99.47 M80.052D M84.839 754.42 M10.072 M87.135 M31.31 M87.076 M19.229 M85.842 738.9 M12.361 M79.3 M48 M05.222 M48.56XD 719.56 M84.353A M77.00 M80.851S M80.051D M24.271 735.4 M84.362G M86.569 M80.862K M63.842 526 M80.069D 717.40 M80.88XK 736.0 M87.077 M92.30 M02.211 M25.532 737.29 754.59 733.94 726.8 M67.371 M85.572 M41.30 M08.229 M05.351 M05.512 M42 M25.229 M02.39 754.60 M42.13 M25.871 719.64 717.5 M06.272 Q66.3 M66.132 M61.239 M66.839 M08.042 M21.061 M93.952 M89.462 M96.661 M25.142 M86.8X3 M85.421 M10.131 M91.42 M89.321 M25.419 M71.451 M87.339 M70.911 524.12 M61.00 754.6 M06 M84.451G M86.329 M89.221 M80.052G M89.359 M05.712 M84.758 M86.659 M40.37 718.18 M24.451 M60.061 M47.25 M01.X32 M05.562 M84.476K 726.72 M97.02XD M14.669 M80.052P M87.236 M85.422 M86.172 M89.339 M80.822A M21.539 718.08 M41.43 M84.434 M05.672 754.7 M84.431P M85.839 M05.052 M67.829 M84.663D M75.32 M90.859 M87.363 M12.369 M84.476S M12.062 M80.019 M06.331 755.35 M12.079 M60.162 M84.532 M84.633D M99.16 M06.09 M24.312 M95.4 M90.662 K45.8 M46.05 M08.012 M11.272 M61.19 M46.24 M84.671 M84.673D M48.8X9 M79.9 M84.755S M12.39 M84.58XA 736.73 M21.511 M00.271 M21.162 M66.329 M47.14 M84.443P 719.01 M05.741 M66.331 M84.659G M67.429 M20.22 M80.831P M84.431A M60.045 M25.339 M60.242 M20.62 724.01 M19.279 M48.56XG M65.172 M48.41XG K08.26 M71.821 M06.012 M66.322 M12.09 M66.369 M86.279 M47.813 M11.271 550.11 M12.462 M54.14 M05.122 M79.645 M71.039 M89.231 M87.372 M62.449 M11.111 M05.862 M92.01 Q72.10 M47.24 M99.42 M43.22 M20.10 M06.341 M33.29 736.72 M56 M71.819 M86.452 M65.28 M00.842 M50.80 M79 755.33 550.93 M80.039K M00.152 M25.271 M66.122 718.93 M50.120 M84.68XP M89.59 737.39 M25.772 M19.141 553.00 M65.151 M05.022 M80.811A M70.89 718.83 M10.011 M10.261 M90.50 M11.061 M89.158 M19.039 M86.132 M16.7 M84.350D M41.07 524.63 M46.1 M15.0 M12.131 M89.272 M93.832 M48.31 D48.1 M11.18 M05.771 M35.6 M12.141 M24.652 M87.029 M61.171 M33.11 524.61 M25.08</p>

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Neoplastic	<p>C21.2 C05.8 D04.20 C81.30 202.64 172.5 C93.21 D46.C 277.84 C44.301 229 C60.0 C75.3 C44.691 D28.2 C66.9 D37.030 160.0 C91.0 D07.69 D3A.023 173.01 233.30 C34.01 C85.80 D44.4 C45.0 203.0 217 D41.8 209.3 273.3 C44.292 D30.8 229.9 194.9 D06.0 237.2 171.9 202.53 173.41 D29.22 206.2 151.5 C44.112 D38.5 D27.1 C45.7 600.1 D02.4 D07.2 C45.1 210.5 201.72 174 C16.8 155.2 C85.29 155.1 C57.12 192 D44.12 C50.122 C82.02 140 C81.77 149.8 C91.01 C25.8 201.50 237.3 C81.40 C08.9 C84.42 140.6 C83.19 152 186.0 198.8 D23.12 181 146.1 C44.622 211.1 C66.1 202.55 C78.6 200.50 C91.40 236.7 195.0 C96.2 196.0 196.6 173.92 C49 216.8 205.11 D23.21 198.7 206.82 C93.32 189.2 193 D05.01 173.9 140.1 200 200.21 C44.92 233.9 C46.4 C26.0 236.6 C84.07 C44.199 202.2 238.74 228.03 C10.2 D3A.020 C82.44 229.0 C83.72 150 235 C62.00 C33 202.31 D46 C78.7 144.9 188.6 C85.21 C50.422 218.1 C73 C06.80 C69.62 D31.00 D36.13 C76.41 172.2 201.74 187 172.9 173.82 161 D25.1 C44.82 C50.129 C48.8 200.16 175.0 D35 C25.9 C81.04 C84.44 204.10 C44.310 205.32 C49.0 182.C29 C50.629 200.55 C49.8 D41.00 D05.82 204.81 D48.4 203.1 C81.90 C38.3 C68.8 623.7 209.34 208.91 239.5 C83.86 185 164.0 164.1 C82.46 151.8 201.0 C34.82 235.8 C84.13 198.0 203 202.06 C51.2 200.48 157.1 624.3 D42.1 C34.2 D21.4 204.90 205.91 C44.721 C69.40 164 C82.28 200.5 D01.49 C90.11 C49.A4 C43.60 D02.21 C44.219 C84.08 D30.00 772.32 D15 C74.01 206.92 C83.13 C7A.020 C81.35 D23.61 202.42 160.1 D31.50 143.1 D31.32 C62.10 200.54 202.43 C81.99 C81.21 D36.10 D35.01 C84.A3 D10.4 C82.23 209.65 C72.21 C90.20 D05.00 C22.1 213.1 Q85.00 D24 173.52 202.11 C34.31 173.6 D13.7 D03.70 190.3 201.08 D15.0 C76.50 D12.6 D41.21 D3A.098 D26.0 184.1 208.2 C84.Z4 C84.10 225.4 C83.79 D39.9 C82.34 145.4 C69.01 C79 201.75 C84.A2 C41 143.9 C84.A9 A214.4 D42.02 208.8 227.4 206.1 C15.9 C91.Z1 200.37 C17.3 C83.05 207.2 600.9 C50.222 D01 623.0 C81.20 209.13 D06.7 C09 201.73 C90 C88.8 200.30 C83.02 C84.00 C40.22 C92.30 201.58 202.57 155 C50.619 D47.Z9 200.72 C82.94 170.2 C30 215.8 C40.00 C83.51 C92.41 201.94 204.8 173.32 173.91 E31.22 C50.311 D13.5 200.65 207.21 Z15.01 201.6 C16.6 C50.911 206.81 D31.10 D37.6 D07.60 C60.2 C82.24 C82.89 C43.39 C69.11 C82.21 D31.91 C76.51 D05.12 C83.34 C44.319 159.0 232.4 C84.61 C44.41 201.52 D03.4 C92.61 153 237.70 D21.9 D21.5 D38.2 D30.11 D18.03 209.11 233.39 D22.30 201.54 173.59 C48 209.30 C67.9 C72 C7A.00 C82.88 C16.0 C25 C18.2 C18.4 D23.72 189 C88.0 D05.02 C24.8 C68.1 C76.40 C60.1 121.47 C47.20 C82.33 C84.A5 D28.9 C91.92 201.1 205.80 C49.A2 C51.8 C78.01 600.20 D16.5 216.0 228.0 C44.91 149.9 C93.90 153.0 C46.50 20.10 199.1 D31.01 203.50 C82.81 223.81 622.1 233.6 C50.82 202.83 C44.01 C82.38 C83.91 C92.92 N60.89 C91.92 C47.112 C26.9 228.00 144.8 220 D12.5 759.5 C85.25 624.01 D03.62 D20.20 209.50 216.9 239.7 C84.Z2 C50.922 190.0 C44.399 C85.96 C85 201.07 D28.7 207.0 157.9 D3A.00 152.2 201.96 205.01 D43 C85.27 C82.30 201.28 D09.10 C91.41 C64.9 C22.4 238.76 224.5 C50.511 186 202.52 203.10 C7A.092 201.60 209.52 D41.0 C13.1 224.3 C84.04 C81.78 C90.00 D31.12 D01.3 C7B.02 209.31 157.5 C50.611 D12.1 236.99 D09.22 D17.0 202.85 C22.0 C77.9 D37.01 D06.1 D37.5 231.2 224 209.61 C84.97 C50.812 C00.0 C50.019 C84.72 173.4 222.0 C7A.022 D10.39 205 C81.32 C83.01 C83.77 227.6 C79.32 D23.0 200.27 C85.95 621.30 C90.10 C10 200.31 C79.11 C18.8 N60.49 C89 C91.Z2 C72.9 209.02 200.67 140.5 C13.2 203 D31.40 235.5 D07.39 238 C29 C92.A2 D08 C54.0 D17.22 182.C23 153.7 C81.05 C41.9 C00 183.3 D04.61 202.38 C06 174.4 D17.71 N40.1 D09.20 225.2 C44.500 D16.6 C84.A7 C82.95 C81.39 233.1 141 188.4 C69.42 C82.93 202.01 C83.02 C82.01 C65.1 239.4 192.8 202.6 C46 142.2 C49.3 218.2 200.2 C42.0 C30.3 C63.9 C81.33 C96 209.6 C87 202.86 192.9 C90.02 C82.25 202.76 600.00 C50.621 212.7 201.44 153.9 C82.61 203.11 202.97 208.01 D37 C55 C82.49 D21.10 208.12 D48.9 C22.3 C44.609 201.10 C54.1 160.9 C13 D31 C82.39 C84.01 197.7 600.0 175 C84.66 D01.2 D29.20 D35.9 D36.17 D39.2 C88.9 198 C56.9 D14.2 156 E31.21 200.68 C84.64 600.2 D37.9 239.9 C81.25 C85.16 C92.02 C44.529 D31.41 D12.3 227.1 212.8 221.0 C44.90 C50.111 C81.48 C84.92 C53.8 209.20 174.1 C00.8 202.16 237.7 205.82 C56 Q85.03 C84.45 173.70 151.4 D23.71 C83.18 C92.22 C81.78 205.30 239.2 C96.29 C10.8 200.11 C99 602.3 D16.4 C16.3 C50.829 C71.8 C92.31 200.78 C71.5 230.6 190.1 202.14 C82.16 201.00 C69.52 D12.9 173.89 D15.9 205.8 202.28 D29.21 D19 C87.57 C84.62 C03.8 C81.70 C94.01 C81.08 D02 214.8 C60.8 C83.06 C13.9 231.8 C72.59 C90.32 C50 187.8 D14.1 202.88 C85.1 9 202.81 C83.36 C44.509 C44.619 D04.0 D26.9 D37.8 214.3 C25.0 C46.2 182.8 C75.5 D07.30 200.38 C70.9 D15.2 188 C84.A1 C44.391 C84.02 202.26 173.81 C81.4 C91 D29.31 C94.6 C57 202.4 200.34 C85.1 218 236.9 173.11 C18.7 C31.3 201.25 C14.8 D22.22 D35.5 C71.6 C90.21 C43.62 C49.6 236.5 188.0 C31 C22.9 C50.212 C57.7 C93.02 171.0 201.76 C00.5 C25.1 213.4 200.57 C82.64 C84.98 D35.3 D49.512 C67.1 D04.10 C83.14 C75.9 200.3 200.23 200.26 161.0 C78.1 200.7 C82.85 D21.2 C83.75 D21.1 200.83 200.43 C57.4 D10.7 146.5 D49 C44.510 C57.11 238.0 C50.021 196.3 D46.A D16.31 C78.39 569.0 D39 161.2 C25.3 C30.0 C01 D31.31 D36.14 201.46 C94.81 140.4 150.3 C91.A2 D16.02 D13.2 C47.10 C26.1 160.8 D23.10 173.8 D37.1 C44.701 C11 D25 C66.8 C94.00 D17.24 D09 74 C02.9 C91.61 C28 205.02 D21.0 171.6 C17.9 210.9 174.0 D21 C67.4 C50.821 C49.5 173.7 C92.11 209.73 C84.67 C74 C70.05 219 181.8 C06.9 202.75 200.80 224.9 C84.73 C88.2 D17.79 201.21 208.90 152.1 D03 147.8 186.9 C50.622 198.6 229.9 C49.A5 D22.62 203.80 C40.32 C63.9 C81.33 C96 209.6 C87 202.86 C43.30 207.01 D35.1 164.8 238.73 201.62 C96.21 D04.71 171.4 201.41 C91.60 182.21 206.80 189.8 208.21 C82.03 D03.52 D18.09 C25.7 162.0 C80 202.72 C82.41 C82.62 173.39 C72.41 202.00 C03.9 229.8 173.40 224.4 213.3 216.3 C09.14 C83.83 C16.4 C75.4 202.05 C44.191 213 200.13 D41.11 C69.50 192.1 200.75 D13.1 D48.3 C00.2 C80.0 C81.09 C83.89 195.8 C93.Z0 N40.0 C30 C92.A0 C00.1 C34.10 200.1 174.2 173.71 158.0 D07.61 C81.41 C81.91 156.1 C84.12 C92.4 D00.07 221 D35.6 225.9 624.6 233.31 D19.1 C91.A0 C05.0 192.3 211.4 C82.45 160.3 622.10 211.5 C7A.011 D10.0 204.0 C81.42 201.26 D23.30 C02 201.91 C40.90 C78.02 C43.21 C44.222 C91.62 239.3 237.71 239.6 230.8 202.8 232.0 C44.89 C81.12 C7A.021 C96.2 200.01 202.51 N69.3 173.09 D27.9 156.9 C94.82 148.0 197.4 D36.7 202.02 C03.0 189.9 201.53 205.0 D00.02 273.1 199 200.85 E71.448 C50.121 202.20 D48.2 C62.02 149.1 C83.00 C50.321 173.99 D44.2 173.1 C22.7 D44.6 208 C82.56 157.0 170.7 D24.1 D14 C71.4 600.90 C85.98</p>
Ophthalmological	<p>H34.8332 H50.812 H10.439 H35.111 H53.043 364.5 H50.32 H44.812 H01.112 H05.243 H26.493 H10.221 377.62 362.89 H49.43 H18.811 364.71 375.13 365.59 365.89 370.3 H40.51X H44.21 370.24 375.14 H25.23 H17.00 H47.631 H05.342 H21.323 H50.811 H59.022 364.8 H21.229 H20.022 H02.134 H15.022 H46.02 H47.211 H31.111 H59.322 H35.3133 H11.032 H11.432 H16.072 H40.10x2 371.73 370.03 H11.10 362.31 H02.734 H44.753 369.3 H16.142 H40.63X H33.051 H18.739 369.05 360.8 H31.092 H52.532 H18.892 H17.03 H04.223 H01.133 371.20 H27.112 H44.621 H20.813 H53.033 367.20 369.08 372.9 H02.871 H40.1310 H40.51X H15.091 H40.302 H01.023 H31.303 H26.119 H40.1114 H54.2X1 368.31 H15.813 H35.463 H05.812 H26.103 H40.011 372.4 364.53 H10.511 H39 H40.1192 375.22 H20.012 H31.022 H35.052 H40.149 362.9 H40.241 363.70 H34.812 H53.003 H26.069 H18.833 H18.223 H16.132 H47.312 H47.333 H01.019 H21.342 H02.30 H20.821 H40.53X3 H02.104 H02.839 H05.031 H59.343 H16.061 H16.071 H34.02 377.10 371.45 371.60 H18.623 369.75 H02.209 H33.102 369.60 H50.50 371.51 H40.032 H40.2214 H33.22 H05.53 H05.813 H44.649 H54.1224 H02.439 369.66 H40.409 H40.51X1 H40.10x H02.054 H34.00 H50.15 H18.55 H15.821 H44.511 H49.813 H40.53X0 372.56 H02.136 H21.1X9 H53.023 H04.123 H02.89 H18.422 H31.123 H02.036 H20.021 374.54 368.412 H40.60X3 H46.9 368.12 H57.13 H25.811 360.40 H40.62X4 371.58 369.01 H10.413 H16.309 H26.042 H44.431 H49.02 H53.031 362.6 H11.152 H35.439 362.36 H44.131 H35.3114 H26.123 H40.42X3 H53.132 H53.133 366.19 H40.1111 H08 H44.2C2 H53.433 H05.023 H50.69 H04.541 360.34 H04.212 H05.263 H11.133 H31.411 H18.232 H30.111 371.54 H04.023 H40.61X H35.172 H02.203 362.24 H33.032 H40.32X4 H44.112 377.52 H21.319 H20.22 H02.409 H10.12 H15.812 366.10 H18.9 H52.201 H50.022 H11.423 H34.813 H54.60 H57.051 H18.062 H40.63X H44.2A3 H44.539 366.10 H27.133 368.16 H40.233 H30.133 H43.813 H00.023 H02.109 H18.712 H57.8 371 H47.149 H15.129 H40.62X1 H10.239 377.32 H00.011 H44.723 H10.223 H40.139 H18.312 H35.322 H49.01 371.0 H02.735 374.87 H30.012 H02.123 H44.2C3 H10.413 H44.2E2 366.1 369.62 H27.119 H31.21 H47.323 H53.422 364.7 H16.051 371.56 H35.079 H41.312 H53.039 H15.052 H40.13612 H00 H30.009 H40.20X2 H01.002 H40.04 365.21 H34.819 375.54 H02.043 H44.449 H34 H18.713 362.85 364.59 H44.629 H46.12 H47.032 H40.159 364.63 H02.006 H40.822 H21.219 H44.022 H35.3290 368.41 H05.339 377.11 H05.269 H11.063 H54.1152 360.81 H05.52 366.04 H52.13 H53.429 362.77 369.61 369.10 H01.013 H02.879 367.9 365.04 H32.413 H11.242 H30.91 H11.019 H02.239 H30.029 H35.10 H40.43X1 H59.312 371.11 368.2 H04.149 H18.022 376.42 H40.41X2 368.8 H15.819 H05.262 H00.16 H01.014 H47.142 365.63 368.10 H01.113 H55.81 374.85 H05.423 H21.521 H40.053 H54.0X4 362.70 H02.61 H10.231 H51.22 H35.013 H34.8131 369.65 H52.12 370.40 H21.352 H35.3232 H15.123 H02.832 369.24 H57.11 H59.42 369.02 H50.611 H44.441 H31.009 H34.8392 H54.414 H15.841 376.5 374.13 H16.121 379.14 H35.359 H44.811 H54.1141 H47.611 376.21 H04.432 H05.219 H40.123 H21.262 H34.832 H44.702 H0.13 H40.221 H43.392 H40.1412 H01.129 H44.652 H02.863 H40.50X H02.304 H30.101 H16.212 H59.88 H21.532 H01.125 H31.129 H40.33X3 H22 H33.029 H02.721 362.10 H00.401 362.3 360.44 H40.52X4 H02.013 H21.40 H07 H30.129 372.8 375.15 H21.232 H01.016 H31.029 365.05 H40.1491 H53.59 H35.3121 365.6 362.32 367.2 H11.212 H44.622 H05.021 H50.312 H16.032 H02.516 362.14 H40.1123 H43.312 372.6 H33.193 H44.732 H04.551 H43.03 377.72 H44.512 H33.322 379.25 H05.231 H47 H50.30 H21.301 H21.343 H59.211 H40.42X2 H16.323 366.20 H40.62X2 H10.411 H20.042 H04.013 H15.102 H35.411 H16.019 367.5 371.3 H40.1193 H59.319 H18.812 H35.019 H47.013 H02.432 H40.1291 H53.142 H21.333 H54.512 H10.021 369.04 362.16 369.72 H02.875 H30.021 H43.01 365.72 H59.813 368.55 362.74 H31.311 H30.103 H47.219 363.56 H02.833 H40.1194 H00.035 H04.211 H47.393 371.24 379.32 H02.025 H02.204 H15.832 376.41 H18.052 H52.209 H16.332 H40.51X4 H43 H40.52X1 H11.422 H40.1423 H40.60X H52.203 369.0 374.89 H02.849 374.12 H40.50X0 H54.8 H40.043 H44.611 365.60 A18.59 362 368.34 H50.011 H59.021 369.71 367.0 362.15 H11.32 H18.319 H11.131 H53.483 H02.59 H35.3291 H40.30X2 H44.529 H35.319 H40.40X2 H11.052 374.5 H16.391 H21.263 366.42 366.18 H16.129 H40.1221 H18.419 362.29 368.47 H21 365.23 376.40 H18.819 H21.321 H40.63X1 H30.21 H50.00 H33.052 379.21 H02.514 H40.1121 H47.42 H53.411 H15.019 H05 H54.40 372.55 H40.1120 H35.113 H05.011 H59.222 370.44 H33.192 H59.333 362.61 362.17 H02.522 H02.119 H10.812 H59.323 H54.0X45 H18.039 H43.02 H35.722 366.09 H21.313 H04.523 H21.551 H05.033 H54.62 H54.42A H58 H04.332 H10.502 H34.829 365.31 H42 367.1 H30.013 375.57 H21.303 H47.20 H02.864 H20.032 H26.062 377.3 H52.223 H31.002 H40.2292 H44.623 H44.821 H27.03 H04.012 H16.013 H34.833 372.62 H02.055 H02.114 H30.121 H27 377.33 369.9 H16.223 H16.213 H18.829 363.72 H35.723 H25.041 H44.2E3 H44.012 H34.10 H16.221 H40.069 H02 363.55 H04.202 H16.131 369.06 H31.9 H35.3222 H34.822 H35.3293 H47.512 H44.413 H20.21 H16.331 368.62 H35.371 H40.41X3 H21.312 H33.331 H16.012 364.89 H05.412 H00.024 H11.001 H40.1210 H30.893 H26.499 H31.429 H47.12 377.24 H35.3120 H40.1130 H18.719 371.9 364.52 H40.1322 372.34 H11.411 H16.073 H10.232 H11.242 376.43 H35.81 H35.712 H01.025 H11.069 362.65 379.13 H01.123 H35.373 H16.122 H40.2220 H43.811 H31.409 362.1 H34.213 H02.815 H01.029 H44.533 H52.521 H21.242 H44.422 H02.714 366 H34.8191 H34.8391 H35.53 H21.89 H01.001 377.41 H49.33 H31.321 H44.023 H16.052 369.17 370.21 H16.249 H55.09 H26.051 H18.061 H21.223 H25.11 H30.032 H59.362 H53.10 H04.321 H40.1234 H02.12 H11.111 H04.119 H40.1113 H04.031 H21.213 375.52 H26.491 H21.1X1 H40.2292 H06.011 H26.033 H43.20 H15.041 368.9 362.50 H35.349 H15.89 H52.229 H51.8 364.64 H02.829 H00.039 H18.322 H40.42X1 H40.812 H50.42 H02.816 H02.034 H05.029 H21.561 372.42 H40.40X3 H40.823 H50.53 H34.8312 H35.151 H40.10X3 370.20 H59.361 H16.429 H31.423 362.4 H02.105 H40.023 H35.3193 H11.033 367.8 H14 H20.052 H11.142 H40.1324 H18.031 H02.851 H46.10 H50.54 H02.712 365.43 H15.092 H40.42X0 H53.2 H18.011 H11.119 H40.62X0 H44.309 H05.252 H10.422 H35.3131 H40.811 H02.004 H53.55 H10.521 H21.309 H15.012 H40.833 H44.2E1 H50.141 H26.039 H02.115 H31.121 377.0 H16.201 H35.3112 H20.9 H57.09 H52 368.53 H40.1133 H52.202 H40.132 H40.52X3 H05.10 H54.413 374.51 H05.012 H40.1223 H11.829 365.32 377.03 H40.1432 368.32 371.05 H11.431 H01.124 368.30 H34.233 366.4 379 H10.819 H53.129 H02.731 H02.205 H04.429 H49.32 371.02 H53.15 H40.1422 H04 H02.234 H40.022 H33.011 H35.732 H44.391 366.23 H30.9 H50.17 H16.139 368.52 H44.793 H11.059 H18.449 H18.231 H05.823 H18.032 H35.352 H26.049 H04.129 H10.30 H02.811 H11.113 H02.212 H11.439 366.2 H05.3292 H35.441 H40.10X0 H35.023 376.51 H31.103 H43.391 H02.016 H35.3110 H05.253 H05.821 H40.219 H05.409 H53.021 H21.329 H04.439 365.11 H17 H48.11 368.3 372.54 361.3 H54.52A H25.093 H02.145 H44.522 H04.132 H11.022 H04.552 H16.041 H44.722 H54.415A H38 H40.1213 H01.121 363.9 H02.403 H40.40X0 H35.461 363.35 H18.793 376.8 H35.3223 H43.393 H48 H18.52 H34.8390 H40.51X3 H40.339 H47.11 H01.022 H05.811 H40.141 H04.301 H31.422 H15.823 H21.503 375.69 H40.009 H01.146 H57.052 H30.139 H44.601 H26.411 H27.132 H18.899 366.41 H54.61 H20.819 H54.424A 370.34 H33.129 H21.1X3 H02.019 H26.112 H44.323 374.41 H05.221 363.33 366.43 H18.421 H5</p>



Reproductive	<p>764.96 O41.91x O70.0 628.0 646.03 O31.30x 634.91 608.22 679.10 662.11 O35.0xxO P24.21 O13.9 656.01 'O34.00 P57.0 649.7 662.00 669.82 656.23 663.60 618.0 670.2 O34.529 671.80 O03.32 646.51 771.8 E28.2 668.03 674.80 651.2 653.50 661.1 629.9 N82.5 676.32 661.21 646.93 763.9 O36.010 659.90 673.34 649.03 660.33 669.0 674.02 656.13 O92.5 675.11 668 659.10 674.50 N89.4 P07.24 669.50 660.20 661.1 602.2 O00.1 O99.350 N88.0 A48.51 660.31 O22.91 611.72 O01.9 651.50 661.2 648.51 642.53 634.50 O98.03 604.0 679.14 O35.4xxO 665.24 651.71 P35.1 655.70 O99.215 676 P91.63 773.4 767.0 616.51 671.10 O91.219 653.3 664.44 O72.0 669.94 670.8 761.7 673.11 P51.8 660.03 658.40 O00.0 651.7 765.27 671.90 O99.815 663.2 663.01 771.3 302.73 647.8 665.61 N70.93 611.0 O34.41 'O34.01 N64.2 631.0* 652.73 642.23 762 666.3 640.83 763 764.92 P05.06 N85.4 652 618.00 O36.61xO O03.4 671.04 674.32 642.54 673.22 O75.89 N64.89 625.5 O48.0 'O33.5xxO 765.10 652.40 O42.00 764.12 O91.22 679.01 608.24 653.90 647.44 O41.91xO 647.84 643.81 630.0 762.4 659.30 656.4 651.20 669.6 O72.2 654.62 650.0 N64.3 649.60 O71.9 642.13 648.81 659.91 771.1 P01.0 654.93 603.9 654.14 670.80 674.52 768.1 O26.21 O33.5xxO 665.54 661.41 E23.0 602.1 'O33.9 652.50 O92.111 P03.0 O87.4 N88.8 642.92 N60.19 614.4 653.43 648.94 O99.330 O22.31 644.2 659.50 O71.3 646.3 760.70 651.21 'O33.6x 669.8 651.11 652.13 O91.12 762.6 614 660.43 O22.40 O32.6xx 760.61 653.4 E29.1 765.08 765.05 679 P00.1 656.93 647.01 P24.10 760.76 669.24 648.0 N48.6 N43.1 643.8 659.53 O69.2xx 647.10 651.23 N94.819 629.1 764.10 649.41 641.13 655.31 765.18 774.31 642.63 671.51 659.93 616.11 672.00 607 665.20 661.00 644.0 O41.1090 O35.4xx O41.90x 625.6 607.85 639.2 O99.419 O69.1xx 671.23 671.1 N81.2 664.8 O11.9 O83.8 O99.341 665.60 604 656.31 661.23 655.33 669.00 656.7 653.70 614.7 646.8 661 646.14 620.1 645.03 O92.3 648.02 765.16 625.71 663.6 655.9 664.00 N71.0 651.31 768 O99.845 620.8 626.1 P35.2 656.41 652.90 646.54 P08.1 648.93 O22.00 662.1 655.1 N82.8 649.62 654.90 607.82 N80.9 O98.619 625.0 674.84 O31.31xO R10.2 618 O41.8X90 647.20 653.80 679.02 648.52 O10.111 768.0 606.9 668.11 656.30 629.89 669.10 N89.6 670.10 642.93 N80.3 642.1 628 O86.0 660.93 630 646.01 N80.5 655.40 647.63 652.23 N92.4 P07.21 N94.818 656.71 765.02 O89.1 P03.6 O63.1 764.2 P56.0 N85.6 646.10 O23.91 654.03 670.32 654.33 P24.81 610.1 768.9 N81.12 648.73 652.10 O87.3 P50.3 654.52 662.30 761.3 O36.60xO P03.89 669.1 P05.05 N94.810 658.01 O14.02 O60.12xO N48.89 N95.2 O69.9xx 643.23 663.83 O88.23 673.0 771.0 626.5 665.6 659.70 662.23 667.14 647.50 648.14 P59.8 647.60 673.30 661.0 651.00 646.82 N83.4 674.90 669.51 620.4 765.07 670.2 627.6 639.6 659.1 639.53 664.01 659.33 664.01 660.90 666.12 O41.8X1 N49.9 N71.9 653.71 N51 O26.879 O22.10 P22.0 624.5 665.0 P52.21 654.01 O99.03 647.61 665.9 634.31 669.91 O35.8xxO O08.0 P24.30 659.33 N81.6 646.0 P24.31 675.04 658.21 674.10 N92.1 676.33 O88.019 669.04 676.1 668.23 668.80 665.81 762.8 654.54 763.4 O90.4 653.91 O25.2 670.84 647.64 766.21 674.3 659.60 P05.17 648.83 676.60 665.30 651.03 647.32 651.0 659.01 668.83 N46.9 767.5 610.0 668.2 675.23 661.40 642.33 768.3 644.03 N76.0 622.9 O92.6 O36.90x O88.311 654.00 656.00 601.8 668.04 P91.62 O99.340 761.4 765.03 659.3 652.6 648.43 674.9 669.43 643.93 O36.111 647.31 F52.32 647.3 O92.011 642.03 664.40 P11.3 608.8 668.22 641.80 O90.81 659.23 641.30 667 663.23 658.80 608.86 626.9 O66.1 665.64 O88.119 N64.1 P07.18 676.81 N92.2 N48.9 O03.7 O69.2xxO O99.13 O08.6 657.0 673.00 664.81 N73.3 643.01 633.10 641.9 634.62 647.9 622 O99.280 N73.9 649.30 674.20 626.7 671.40 669.83 N41.9 651.6 647.04 764.04 E28.39 764.14 671.20 764.94 642.72 649.73 765.28 774.6 767.4 663.51 647.14 653.60 E29.9 671.3 642.52 649.2 'O34.10 673.24 660.13 648.84 O86.12 649.6 O33.2 O36.8190 769 673.21 671.33 663.10 O41.8X10 O98.219 642.62 N64.59 N94.6 764.93 P03.4 772.5 604.99 641.23 663.90 O98.519 768.2 O26.893 669.90 668.12 648.41 674.00 646.4 651.63 627.4 O60.12x 669.5 634.22 665.40 674.64 639 O03.80 765.15 654.9 664.54 633.80 645.2 P39.0 616.1 O03.31 667.1 765 N64.4 649.11 N93.0 676.50 651.5 648.40 649.53 634.82 O99.345 O32.1xxO 665.83 O91.011 O30.029 653.61 O40.1xxO O36.819 676.01 O35.9xxO 657.01 660.53 O03.83 647.43 663.43 P00.9 N43.3 774.39 773.2 664.11 653.10 608.3 623.6 O22.8X1 631 634.42 658.4 N83.9 654.84 774.30 639.8 768.5 651.73 763.84 766.1 607.1 648.80 O12.01 N46.029 669.40 O99.111 N41.8 773.1 763.89 602.8 633.8 618.7 674.4 621.6 O35.9xx 643.00 O26.849 634 664.04 764.23 611.4 O61.0 646.84 764.09 654.43 O35.3xxO O31.11x 620.3 P01.7 656.83 E28.8 634.32 665.14 655.91 658.03 658.91 664.84 665.44 O91.02 611.5 647.62 607.2 665.3 N60.09 654.4 764.98 P03.819 658.10 666.10 O71.2 O66.5 N44.00 664.3 E28.0 O09.40 'O33.8 668.20 646.11 O71.02 642.60 656.51 678.10 P07.01 N85.3 659.4 O86.81 648.70 N94.9 O36.011 O82 614.1 652.01 O43.101 767.6 774.1 666.22 629 662.01 P01.2 O42.10 654.51 O36.1190 642.24 771.5 763.2 764.03 617.5 652.93 633.00 760.63 O66.9 O34.511 665.70 669.03 651.30 O33.3xx 642.4 660.10 649.12 675.80 N44.02 608.83 O36.829 602 O03.34 646.64 645.01 N90.9 616.4 653.6 N81.9 O36.91x 670.0 676.52 671.54 661.01 770.15 640.91 653.5 665.1 666.2 648.54 760.77 676.93 N61 611.7 P01.8 675.8 644.20 O34.21 656.33 765.11 618.83 608.9 627.3 P35.0 654.63 678.1 647.53 647.83 671.11 652.2 765.14 653.9 760.2 O43.019 611.71 P05.14 666.1 617.8 671.02 O91.23 O40.0 O86.4 665.82 665.11 N75.0 651.83 O64.0xx 676.61 655.01 764.07 O26.619 O32.4xxO O40.1xx 768.4 O26.41 671.82 671.9 648.1 601.4 641.21 P08.0 656.63 654.74 O76 652.41 675.20 653.00 O03.9 676.42 658.90 O98.019 642.43 659.20 661.90 660.73 658.9 641.01 641.00 676.51 N43.2 P24.80 675.660 O41.1010 625.9 618.04 664.14 N88.3 647.13 O65.5 666.14 648.72 676.11 O90.9 607.83 648.9 763.1 661.93 642.34 P02.2 653.03 760.4 655.7 674.2 O22.11 778.81 764.00 674.2 661.10 P12.2 O30.201 646.9 667.12 765.09 633.0 770.86 620.7 O24.911 679.11 646.63 640.03 653.53 653.81 762.1 O99.019 P00.7 654.10 676.60 773.0 668.90 761.6 676.53 649.42 646.20 656.2 658 P05.18 651.91 O75.3 664.51 768.7 P07.00 P58.8 614.3 666.04 652.11 634.3 648.60 659.43 E29.0 653.11 N92.3 O03.39 667.02 649.00 646.42 E28.310 P04.0 O34.40 640.8 642.31 O22.51 641.81 O98.511 P02.9 675.92 764.24 626 P05.10 647.6 641.0 643.90 760.64 603.8 P05.13 639.4 620.6 667.00 O98.911 N97.2 P05.16 674.04 621.0 649.10 664.9 663.33 623.9 761.8 P10.3 652.31 N94.1 346.4 624.0 P27.0 607.89 O25.10 O31.30xO O65.9 O64.9xx 646.12 673.02 O36.8910 O90.5 767.19 670.764 17 652.60 764.99 642.90 634.1 N90.4 N90.89 648.8 618.1 633.01 646.13 642.5 664.60 641.33 O66.40 646.81 764 669.70 O25.3 O69.0xxO 665.01 646.60 O98.119 659.80 674.92 760.9 772.6 O90.3 664.61 621.1 663.61 608.20 774.4 P13.0 N95.8 N80.0 634.12</p>
	Respiratory

TABLE S8: Feature Definitions (Total number of features used: 380)

Feature name	Explanation	T <sub>1</sub> -features
<b>feature</b> scores relative to phenotype score	Mean p-score of <b>feature</b> codes within sequence divided by general p-score of <b>feature</b>	26
<b>feature</b> scores relative to whole score	Mean p-score of <b>feature</b> codes within sequence divided by mean p-score of all codes in the record	26
aggregation score	aggregation of the p-scores in the record	13
high scores proportion	proportion of codes with very high p-scores among all codes in the record	1
low scores proportion	proportion of codes with very low p-scores among all codes in the record	1
dynamics of mean score	mean p-score of second half of the record divided by mean p-score of first half of the record	1
dynamics of geometric mean score	geometric mean p-score of second half of the record divided by mean p-score of first half of the record	1
dynamics of st.dev score	standard deviation of p-scores of second half of the record divided by standard deviation of p-scores of first half of the record	1
dynamics of score range	range of p-scores of second half of the record divided by range of p-scores of first half of the record	1
dynamics of score skew	skew of p-scores of second half of the record divided by skew of p-scores of first half of the record	1
aggregation relative to phn score	aggregation of all <b>feature</b> 's mean scores divided by corresponding general p-score of <b>feature</b>	9
aggregation relative to whole score	aggregation of all <b>feature</b> 's mean scores divided by mean p-score of all codes in the record	9
predicted risk from pfsa model	predicted risk from pfsa model	1
predicted risk from seq model	predicted risk from seq model	1
predicted risk from pscore model	predicted risk from pscore model	1
predicted risk from rare model	predicted risk from rare model	1
age at screening	Patient age at the moment of the screening	1
<b>feature</b> proportion	Ratio of number of weeks with the codes of a given phenotype to the total number of weeks in sequence	26
<b>feature</b> prevalence	Ratio of number of weeks with the codes of a given phenotype to the number of weeks with any diagnosis code recorded	26
<b>feature</b> first incident	Time interval from observation date to the first phenotype code, normalized by record length	26
<b>feature</b> last incident	Time interval from observation date to the last phenotype code, normalized by record length	26
<b>feature</b> mean position	Mean time position of phenotype codes in the record, normalized by record length	26
<b>feature</b> streak	Length of the longest uninterrupted subsequence of weeks with the codes of a given phenotype recorded	26
Max/Mean/Std/Range intermission	Maximum/Mean/Standard Deviation/Range of the lengths of subsequences of consequent weeks with codes	4
Max/Mean/Std cluster	Maximum/Mean/Standard Deviation of the lengths of subsequences of consequent weeks without codes	3
Max/Std/Range prevalence	Maximum/Standard Deviation/Range of the phenotype prevalences	3
Density of DX Record	Proportion of weeks in a record observed where at least one DX code was recorded	1
<b>feature</b>	Sequence Likelihood Defect for a given phenotype	26
<b>feature</b> neg llk	Negative LogLikelihood score for a given phenotype	26
<b>feature</b> pos llk	Positive LogLikelihood score for a given phenotype	26
<b>feature</b> llk ratio	Ratio of Positive to Negative LogLikelihood score for a given phenotype	26
Mean $\Delta$	Mean Sequence Likelihood Defect	1
Std. deviation $\Delta$	Range of Sequence Likelihood Defects	1
Range $\Delta$	Standard Deviation of Sequence Likelihood Defects	1
Mean neg llk	Mean Negative LogLikelihood score	1
Range neg llk	Range of Negative LogLikelihood score	1
Std. deviation neg llk	Standard Deviation of Negative LogLikelihood score	1
Mean pos llk	Mean Positive LogLikelihood score	1
Range pos llk	Range of Positive LogLikelihood score	1
Std. deviation pos llk	Standard Deviation of Positive LogLikelihood score	1
Mean llk ratio	Mean LogLikelihood score ratio	1
Range llk ratio	Range of LogLikelihood score ratio	1
Std. deviation llk ratio	Standard Deviation of LogLikelihood score ratio	1
high scores proportion	proportion of codes with very high p-scores among all codes in the record	1
low scores proportion	proportion of codes with very low p-scores among all codes in the record	1

\* $\Delta$ : Sequence Likelihood Defect (See Methods)

† neg llk: loglikelihood of observed sequence being generated by the model inferred from control (See Methods)

‡ pos llk: loglikelihood of observed sequence being generated by the model inferred from positive (See Methods)

TABLE S9: Proportion of 0's, 1's and 2's on average in trinary encodings with 95% CI

cohort	sex	proportion of 0	proportion of 1	proportion of 2
control	Female	0.879 ± 0.002	0.013 ± 0.001	0.106 ± 0.002
control	Male	0.891 ± 0.003	0.012 ± 0.001	0.095 ± 0.003
positive	Female	0.858 ± 0.040	0.015 ± 0.013	0.126 ± 0.038
positive	Male	0.873 ± 0.037	0.014 ± 0.012	0.111 ± 0.035
TOTAL	Female	0.879 ± 0.002	0.013 ± 0.001	0.106 ± 0.002
TOTAL	Male	0.891 ± 0.002	0.012 ± 0.001	0.095 ± 0.002

TABLE S10: Out-of-sample performance achieved (mean AUC) when training dataset is balanced (Note: performance degrades as we attempt to train with more balanced data, e.g., downsampling ratio of 1 is the case where we sample the control cohort to use only as many patients as in the positive cohort)

sex	downsampling ratio	all patients	age 65+ years	age < 65 years	frail
Female	1	0.755	0.715	0.694	0.732
Female	2	0.756	0.723	0.700	0.736
Female	5	0.768	0.735	0.727	0.752
Female	10	0.781	0.750	0.737	0.769
Female	20	0.772	0.750	0.728	0.759
Female	40	0.790	0.760	0.743	0.772
Male	1	0.724	0.665	0.690	0.721
Male	2	0.743	0.701	0.698	0.746
Male	5	0.754	0.708	0.722	0.761
Male	10	0.751	0.711	0.718	0.757
Male	20	0.759	0.718	0.725	0.759
Male	40	0.759	0.714	0.729	0.759

TABLE S11: Cohort Sizes

sex	cardiac event within week	$n_{\text{positive}}$	$n_{\text{control}}$	$n_{\text{high risk}}$	$n$
M	2	385	185528	146782	185913
M	4	464	185528	146782	185992
F	2	337	258981	204170	259318
F	4	418	258981	204170	259399
	Total	882	444509	350952	445391



TABLE S12: Out-of-sample predictive performance to predict MACE 4 weeks after surgery in sub-cohorts with pre-existing conditions

Pre-existing phenotype	Female CCoR	Female RCRI	Male CCoR	Male RCRI
Allergic	0.77	0.71	0.81	0.78
CNS	0.80	0.67	0.89	0.75
Cardiovascular	0.78	0.69	0.80	0.67
Development	0.77	0.83	0.86	0.68
Digestive	0.81	0.73	0.80	0.71
Endocrine	0.80	0.69	0.80	0.67
Frailty	0.78	0.69	0.85	0.73
Health Services	0.81	0.71	0.83	0.71
Hematologic	0.80	0.72	0.85	0.74
Hypertension	0.77	0.68	0.80	0.66
Immune	0.81	0.71	0.82	0.70
Infections Fungal and Other	0.80	0.76	0.84	0.68
Infections General	0.80	0.75	0.84	0.68
Infections Respiratory	0.76	0.64	0.83	0.63
Injuries	0.79	0.73	0.84	0.69
Integumentary	0.78	0.69	0.80	0.72
Metabolic	0.80	0.70	0.82	0.70
Musculoskeletal	0.81	0.71	0.83	0.70
Neoplastic	0.87	0.75	0.78	0.68
Ophthalmological	0.79	0.69	0.76	0.65
Otic	0.79	0.75	0.84	0.62
PNS	0.80	0.70	0.84	0.73
Psychiatric	0.85	0.74	0.89	0.72
Reproductive	0.80	0.70	0.82	0.79
Respiratory	0.81	0.70	0.83	0.67

TABLE S13: Out-of-sample predictive performance in sub-cohorts stratified by age

age	gender	auc CCoR	auc RCRI	n <sub>positive</sub>	n <sub>control</sub>
45 - 55	F	0.59	0.58	3	9056
45 - 55	M	0.89	0.79	5	7027
55 - 65	F	0.80	0.66	31	27256
55 - 65	M	0.78	0.63	39	20244
65 - 75	F	0.81	0.73	34	14235
65 - 75	M	0.73	0.58	31	9635
75 - 85	F	0.70	0.65	25	8515
75 - 85	M	0.79	0.71	36	5164
85 - 95	F	0.80	0.67	8	1578
85 - 95	M	0.75	0.48	12	847

TABLE S14: Out-of-sample\* performance for predicting MACE with 4 weeks of Hip or Knee Arthroplasty (Primary Endpoint) at 99% Specificity: CCoR vs. RCRI\*\*

sex	cohort	model	sensitivity	PPV	acc	LR+	LR-	AUC
Female	< 65	RCRI	0.01±0.02	0.008±0.000	0.987±0.006	0.04±0.1	1.00±0.02	0.639±0.039
Female	< 65	CCoR	0.14±0.06	0.047±0.004	0.987±0.006	14.12±1.1	0.87±0.06	0.775±0.035
Male	< 65	RCRI	0.07±0.03	0.025±0.003	0.987±0.000	7.42±0.8	0.94±0.03	0.682±0.034
Male	< 65	CCoR	0.15±0.06	0.065±0.003	0.987±0.006	19.94±0.9	0.85±0.06	0.783±0.030
Female	65+	RCRI	0.03±0.01	0.012±0.002	0.987±0.000	3.39±0.5	0.97±0.01	0.664±0.028
Female	65+	CCoR	0.09±0.06	0.036±0.004	0.987±0.006	10.70±1.1	0.92±0.06	0.771±0.025
Male	65+	RCRI	0.03±0.01	0.011±0.001	0.987±0.006	3.17±0.4	0.98±0.00	0.661±0.026
Male	65+	CCoR	0.09±0.05	0.031±0.002	0.987±0.006	9.09±0.6	0.92±0.05	0.762±0.023
Female	all patients	RCRI	0.05±0.01	0.016±0.003	0.987±0.000	4.67±0.8	0.96±0.01	0.688±0.023
Female	all patients	CCoR	0.13±0.01	0.044±0.007	0.987±0.006	13.19±2.1	0.88±0.01	0.801±0.019
Male	all patients	RCRI	0.05±0.01	0.019±0.002	0.987±0.000	5.44±0.7	0.95±0.01	0.705±0.020
Male	all patients	CCoR	0.12±0.05	0.042±0.001	0.987±0.006	12.44±0.3	0.89±0.05	0.802±0.018
Female	frail***	RCRI	0.03±0.00	0.009±0.002	0.987±0.006	2.59±0.6	0.98±0.00	0.670±0.028
Female	frail	CCoR	0.11±0.03	0.036±0.002	0.987±0.000	10.36±0.7	0.90±0.03	0.791±0.025
Male	frail	RCRI	0.06±0.04	0.020±0.002	0.987±0.006	5.91±0.7	0.95±0.04	0.727±0.027
Male	frail	CCoR	0.15±0.03	0.050±0.002	0.987±0.000	15.02±0.7	0.86±0.03	0.810±0.024
Female	high risk****	RCRI	0.02±0.00	0.008±0.001	0.987±0.006	2.19±0.3	0.99±0.00	0.581±0.029
Female	high risk	CCoR	0.07±0.03	0.026±0.002	0.987±0.000	7.73±0.6	0.94±0.03	0.737±0.026
Male	high risk	RCRI	0.03±0.01	0.010±0.001	0.987±0.006	2.91±0.3	0.98±0.00	0.617±0.026
Male	high risk	CCoR	0.09±0.05	0.033±0.002	0.987±0.006	9.61±0.7	0.92±0.05	0.729±0.024
Female	low risk†	CCoR	0.22±0.04	0.071±0.004	0.987±0.000	21.81±1.3	0.79±0.04	0.765±0.036
Male	low risk	CCoR	0.11±0.04	0.042±0.003	0.987±0.000	5.96±0.9	0.90±0.04	0.766±0.032

Abbreviations, AUC, area under the receiver operating characteristic curve; CCoR, Cardiac Co-Morbidity Risk Score; LR+, positive likelihood ratio; LR-, negative likelihood ratio; NPV, negative predictive value; PPV, positive predictive value; acc, accuracy; RCRI, Revised Cardiac Risk Index

\*50% (n=445391) of cohort used for validation

\*\*Because of insufficient availability of relevant laboratory data in the Truven dataset, presence of at least one diagnostic code for chronic kidney disease stage III or higher in the medical record in the year before the date of arthroplasty was used as a surrogate for the RCRI condition, serum creatinine concentration > 2.0mg/dL (to convert to micromoles per liter, multiply by 88.4).

\*\*\*Frail subcategory was defined by codes specified in Table S7

\*\*\*\*Low risk subcohort comprises patients with RCRI score 0. High risk patients have RCRI score > 0.

†No RCRI performance logged for low-risk patients, since their RCRI score is zero.

TABLE S15: Out-of-sample\* performance for predicting MACE with 2 weeks of Hip or Knee Arthroplasty (Secondary Endpoint) at 99% Specificity: CCoR vs. RCRI\*\*

sex	cohort	model	sensitivity	PPV	acc	LR+	LR-	AUC
Female	< 65	RCRI	0.01±0.02	0.009±0.000	0.987±0.006	0.04 ± 0.1	1.00±0.02	0.647 ± 0.044
Female	< 65	CCoR	0.11±0.01	0.073±0.023	0.987±0.006	22.87 ± 8.5	0.90±0.01	0.787 ± 0.039
Male	< 65	RCRI	0.09±0.02	0.032±0.009	0.987±0.000	9.33 ± 2.8	0.92±0.02	0.688 ± 0.037
Male	< 65	CCoR	0.14±0.04	0.056±0.004	0.987±0.000	16.83 ± 1.3	0.87±0.04	0.797 ± 0.033
Female	65+	RCRI	0.04±0.04	0.013±0.002	0.987±0.006	3.66 ± 0.6	0.97±0.03	0.671 ± 0.030
Female	65+	CCoR	0.10±0.03	0.041±0.002	0.987±0.000	12.08 ± 0.7	0.91±0.04	0.787 ± 0.027
Male	65+	RCRI	0.03±0.00	0.010±0.001	0.987±0.000	2.79 ± 0.4	0.98±0.00	0.667 ± 0.028
Male	65+	CCoR	0.09±0.03	0.032±0.002	0.987±0.000	9.32 ± 0.6	0.92±0.03	0.780 ± 0.025
Female	all patients	RCRI	0.05±0.01	0.018±0.003	0.987±0.000	5.17 ± 0.9	0.96±0.01	0.692 ± 0.025
Female	all patients	CCoR	0.14±0.06	0.048±0.001	0.987±0.006	14.48 ± 0.3	0.87±0.06	0.809 ± 0.021
Male	all patients	RCRI	0.05±0.01	0.018±0.002	0.987±0.000	5.15 ± 0.7	0.96±0.01	0.710 ± 0.022
Male	all patients	CCoR	0.14±0.02	0.047±0.007	0.987±0.000	13.98 ± 2.1	0.87±0.02	0.813 ± 0.019
Female	frail***	RCRI	0.03±0.01	0.012±0.003	0.987±0.000	3.43 ± 0.9	0.98±0.01	0.676 ± 0.032
Female	frail	CCoR	0.12±0.03	0.041±0.009	0.987±0.000	11.78 ± 2.7	0.89±0.03	0.807 ± 0.027
Male	frail	RCRI	0.06±0.01	0.020±0.003	0.987±0.000	5.82 ± 0.9	0.95±0.01	0.736 ± 0.029
Male	frail	CCoR	0.17±0.03	0.059±0.009	0.987±0.000	17.76 ± 3.0	0.84±0.03	0.825 ± 0.025
Female	high risk****	RCRI	0.02±0.03	0.008±0.001	0.987±0.006	2.35 ± 0.4	0.99±0.02	0.584 ± 0.032
Female	high risk	CCoR	0.08±0.00	0.029±0.006	0.987±0.006	8.45 ± 1.9	0.93±0.01	0.742 ± 0.028
Male	high risk	RCRI	0.03±0.03	0.009±0.001	0.987±0.006	2.69 ± 0.4	0.98±0.02	0.628 ± 0.028
Male	high risk	CCoR	0.09±0.02	0.033±0.007	0.987±0.000	9.66 ± 2.3	0.92±0.02	0.737 ± 0.026
Female	low risk†	CCoR	0.28±0.07	0.092±0.002	0.988±0.006	28.78 ± 0.7	0.72±0.07	0.779 ± 0.040
Male	low risk	CCoR	0.12±0.04	0.047±0.004	0.987±0.000	6.78 ± 1.1	0.89±0.05	0.793 ± 0.035

Abbreviations, AUC, area under the receiver operating characteristic curve; CCoR, Cardiac Co-Morbidity Risk Score; LR+, positive likelihood ratio; LR-, negative likelihood ratio; NPV, negative predictive value; PPV, positive predictive value; acc, accuracy; RCRI, Revised Cardiac Risk Index

\*50% (n=445391) of cohort used for validation

\*\*Because of insufficient availability of relevant laboratory data in the Truven dataset, presence of at least one diagnostic code for chronic kidney disease stage III or higher in the medical record in the year before the date of arthroplasty was used as a surrogate for the RCRI condition, serum creatinine concentration > 2.0mg/dL (to convert to micromoles per liter, multiply by 88.4).

\*\*\*Frail subcategory was defined by codes specified in Table S7

\*\*\*\*Low risk subcohort comprises patients with RCRI score 0. High risk patients have RCRI score > 0.

†No RCRI performance logged for low-risk patients, since their RCRI score is zero.

TABLE S16: Statistical significance of CCoR AUC > RCRI AUC (\* denotes significance at 95% level, \*\* denotes significance at 99% level)

sex	model	weeks after surgery	RCRI auc	CCoR auc	p value	significance
Female	all patients	2	0.692	0.809	0.010	**
		4	0.688	0.801	0.007	**
	frail <sup>†</sup>	2	0.676	0.807	0.017	*
		4	0.670	0.791	0.014	*
	high risk <sup>‡</sup>	2	0.584	0.742	0.005	**
		4	0.581	0.737	0.003	**
	65+	2	0.671	0.787	0.020	*
		4	0.664	0.771	0.020	*
	< 65	2	0.647	0.787	0.036	*
		4	0.639	0.775	0.028	*
Male	all patients	2	0.710	0.813	0.010	*
		4	0.705	0.802	0.009	**
	frail	2	0.736	0.825	0.045	*
		4	0.727	0.810	0.042	*
	high risk	2	0.628	0.737	0.017	*
		4	0.617	0.729	0.011	*
	65+	2	0.667	0.780	0.017	*
		4	0.661	0.762	0.019	*
	< 65	2	0.688	0.797	0.047	*
		4	0.682	0.783	0.042	*

<sup>†</sup>Frail subcategory was defined by codes specified in Table S7

<sup>‡</sup>Low risk subcohort comprises patients with RCRI score 0. High risk patients have RCRI score > 0.

TABLE S17: Out-of-sample performance achieved using only PFSA component of the CCoR model (Note: the performance is significantly degraded, with all p-values < 0.01.)

sex	prediction horizon	AUC
Female	2 weeks	0.696 ± 0.082
Female	4 weeks	0.698 ± 0.074
Male	2 weeks	0.679 ± 0.074
Male	4 weeks	0.656 ± 0.067

## SUPPLEMENTAL METHODS

### A. Time-series Modeling of Diagnostic History

Individual diagnostic histories can have long-term memory [52], implying that the order, frequency, and comorbid interactions between diseases are important for assessing the future risk of our target phenotype. We analyze patient-specific diagnostic code sequences by first representing the medical history of each patient as a set of stochastic categorical time-series — one each for a specific group of related disorders — followed by the inference of stochastic models for these individual data streams. These inferred generators are from a special class of Hidden Markov Models (HMMs), referred to as Probabilistic Finite State Automata (PFSA) [53]. The inference algorithm we use is distinct from classical HMM learning, and has important advantages related to its ability to infer structure, and its sample complexity (See Supplementary text, Section VI). We infer a separate class of models for the positive and control cohorts, and then the problem reduces to determining the probability that the short diagnostic history from a new patient arises from the positive as opposed to the control category of the inferred models.

### B. Inference & Event Periods

We train our predictive pipeline with all diagnostic codes that are recorded in the past 26years from the point at which a prediction is made. This period from which we use data to train our pipeline is called the “inference window”. Our aim is to make predictions on the occurrence of the target diagnostic codes at 2year from the end of the inference window. For patients in the control cohort, we make sure that no target code appears for 26years after the end of the inference window. Additionally, when making predictions further into the future (upto 4 years, as described in the main text), we always make sure that the control group has no target codes for 1 year after the predicted time of diagnosis, i.e., if we are making a prediction of a diagnosis 4 years in future, then control group patients are chosen to have no diagnosis in at least next 5 years.

### C. Step 1: Partitioning The Human Disease Spectrum

We begin by partitioning the human disease spectrum into 26non-overlapping categories. Each category is defined by a set of diagnostic codes from the International Classification of Diseases, Ninth Revision (ICD9) (See Table SI-S7 for description of the categories used in this study). For this study, we ended up using 4879398 and 7753318 diagnostic codes for males and females respectively (17554 and 19209 unique codes) spanning both ICD9 and ICD10 protocols (using ICD10 General Equivalence Mappings (GEMS) [54] equivalents where necessary), from a total 445391 patients. Transforming the diagnostic histories to report only the broad categories reduces the number of distinct codes that the pipeline needs to handle, thus improving statistical power. Our categories largely align with the top-level ICD9 categories, with small adjustments, e.g. bringing all infections under one category irrespective of the pathogen or the target organ. We do not pre-select the phenotypes; we want our algorithm to seek out the important patterns without any manual curation of the input data. For each patient, the past medical history is a sequence  $(t_1, x_1), \dots, (t_m, x_m)$ , where  $t_i$  are timestamps and  $x_i$  are ICD9 codes diagnosed at time  $t_i$ . We map individual patient history to a three-alphabet categorical time series  $z^k$  corresponding to the disease category  $k$ , as follows. For each week  $i$ , we have:

$$z_i^k = \begin{cases} 0 & \text{if no diagnosis codes in week } i \\ 1 & \text{if there exists a diagnosis of category } k \text{ in week } i \\ 2 & \text{otherwise} \end{cases} \quad (1)$$

The time-series  $z^k$  is observed in the inference period. Thus, each patient is represented by 43 mapped trinary series.

### D. Step 2: Model Inference & The Sequence Likelihood Defect $\Delta$

The mapped series, disease-category, and perioperative cardiac event diagnosis-status are considered to be independent sample paths, and we want to explicitly model these systems as specialized HMMs (PFSAs). We model the positive and the control cohorts and each disease category separately, ending up with a total of 104 HMMs at the population level (26 categories, 2 perioperative cardiac event status categories: positive and control, and 2 sexes). Each of these inferred models is a PFSA; a directed graph with probability-weighted edges, and acts as an optimal generator of the stochastic process driving the sequential appearance of the three letters

(as defined by Eq. (1)) corresponding to disease category, and perioperative cardiac event status-type (See Section VI in the Supplementary text for background on PFSA inference).

To reliably infer the perioperative cardiac event status-type of a new patient, i.e, the likelihood of a diagnostic sequence being generated by the corresponding perioperative cardiac event status-type model, we generalize the notion of Kullbeck-Leibler (KL) divergence [55] between probability distributions to a divergence  $\mathcal{D}_{\text{KL}}(G||H)$  between ergodic stationary categorical stochastic processes [56]  $G, H$  as:

$$\mathcal{D}_{\text{KL}}(G||H) = \lim_{n \rightarrow \infty} \frac{1}{n} \sum_{x:|x|=n} p_G(x) \log \frac{p_G(x)}{p_H(x)} \quad (2)$$

where  $|x|$  is the sequence length, and  $p_G(x), p_H(x)$  are the probabilities of sequence  $x$  being generated by the processes  $G, H$  respectively. Defining the log-likelihood of  $x$  being generated by a process  $G$  as :

$$L(x, G) = -\frac{1}{|x|} \log p_G(x) \quad (3)$$

The cohort-type for an observed sequence  $x$  — which is actually generated by the hidden process  $G$  — can be formally inferred from observations based on the following provable relationships (See Supplementary Text Section VI, Theorem 6 and 7):

$$\lim_{|x| \rightarrow \infty} L(x, G) = \mathcal{H}(G) \quad (4a)$$

$$\lim_{|x| \rightarrow \infty} L(x, H) = \mathcal{H}(G) + \mathcal{D}_{\text{KL}}(G||H) \quad (4b)$$

where  $\mathcal{H}(\cdot)$  is the entropy rate of a process [32]. Importantly, Eq. (4) shows that the computed likelihood has an additional non-negative contribution from the divergence term when we choose the incorrect generative process. Thus, if a patient is eventually going to be diagnosed with perioperative cardiac event, then we expect that the disease-specific mapped series corresponding to her diagnostic history be modeled by the PFSA in the positive cohort. Denoting the PFSA corresponding to disease category  $j$  for positive and control cohorts as  $G_+^j, G_0^j$  respectively, we can compute the *sequence likelihood defect* (SLD,  $\Delta^j$ ) as:

$$\Delta^j \triangleq L(G_0^j, x) - L(G_+^j, x) \rightarrow \mathcal{D}_{\text{KL}}(G_0^j||G_+^j) \quad (5)$$

With the inferred PFSA models and the individual diagnostic history, we estimate the SLD measure on the right-hand side of Eqn. (5). The higher this likelihood defect, the higher the similarity of diagnosis history to that of women with perioperative cardiac event.

### E. Step 3: Risk Estimation Pipeline With Semi-supervised & Supervised Learning Modules

The risk estimation pipeline operates on patient specific information limited to the available diagnostic history in the inference period, and produces an estimate of the relative risk of perioperative cardiac event, with an associated confidence value. To learn the parameters and associated model structures of this pipeline, we transform the patient specific data to a set of engineered features, and the feature vectors realized on the positive and control sets are used to train a gradient-boosting classifier [57]. The complete list of 380 features used is provided in Table 6.

We need two training sets: one to infer the models, and one to train the classifier with features derived from the inferred models. Thus, we do a random 3-way split of the set of unique patients into *feature-engineering* (25%), *training* (25%) and *test* (50%) sets. We use the feature-engineering set of ids first to infer our PFSA models (*unsupervised model inference in each category*), which then allows us to train the gradient-boosting classifier using the training set and PFSA models (*classical supervised learning*), and we finally execute out-of-sample validation on the test set. Fig. 1c in the main text shows the top 20 features ranked in order of their relative importance (relative loss in performance when dropped out of the analysis).

## I. THRESHOLD SELECTION ON ROC CURVE

Once the ROC curve has been computed, we must choose a decision threshold to trade-off true positive rate and false positive rate. In situations where the number of negatives vastly outnumber the number of positives (which is the case in our problem), it is better to base this trade-off on a measure that is independent of the number of true negatives. The two popular measures considered in the literature are accuracy and the F1-score:

$$\text{accuracy} = \frac{t_p + t_n}{t_p + f_p + f_n + t_n} \quad (6)$$

$$\text{F1} = \frac{2t_p}{2t_p + f_p + f_n} \quad (7)$$

The F1-score is the same as accuracy where the number of true negatives is the same as the number of true positives, thus partially correcting for the class imbalance.

The selection of the threshold may also be dictated by the current practice of ensuring high specificities in screening tests. Thus, a relevant clinically operating point is the one corresponding to 95% specificity, which is highlighted in Fig. 1a.

## II. NOTE ON RECIEVER OPERATING CHARACTERISTICS (ROC) AND PRECISION-RECALL CURVES

The ROC curve is a plot between the False Positive rate (FPR) and the True Positive Rate (TPR), and the area under the ROC curve (AUC) is often used as a measure of classifier performance. For the same of completeness, we introduce the relevant definitions:

In the following  $P$  denotes the total number of positive samples (number of patients who are eventually diagnosed), and  $N$  denotes the total number of negative samples (number of patients in the control group).

**Definition 1.** *True positive rate, true negative rate, false positive rate, positive predictive value (PPV), and prevalence ( $\rho$ ) are defined as:*

$$TPR = \frac{t_p}{P} = \frac{t_p}{t_p + f_n} \quad (8)$$

$$TNR = \frac{t_n}{N} = \frac{t_n}{t_n + f_p} \quad (9)$$

$$FPR = 1 - TNR \quad (10)$$

$$PPV = \frac{t_p}{t_p + f_p} \quad (11)$$

$$\rho = \frac{P}{N + P} \quad (12)$$

where as before  $t_p, t_n, f_p, f_n$  are true positives, true negatives, false positives, and false negatives respectively.

Note that TPR is also referred to as **recall** or **sensitivity**, and PPV is also referred to as **precision**. True negative rate is also known as **specificity**.

A **precision-recall curve**, or a PPV-sensitivity curve is a plot between PPV and TPR.

Denoting sensitivity by  $s$ , and specificity by  $c$ , it follows that:

$$PPV = \frac{t_p/P}{t_p/P + (f_p/N)(N/P)} = \frac{TPR}{TPR + ((N - t_n)/N)(N/P)} \quad (13)$$

$$\Rightarrow PPV = \frac{s}{s + (1 - c)(\frac{1}{\rho} - 1)} \quad (14)$$

Thus, we note that for a fixed specificity and sensitivity, the PPV depends on prevalence. Indeed, it is clear from the above argument that PPV decreases with decreasing prevalence, and vice versa.

## III. EFFECT OF CLASS IMBALANCE

ROC curves are generally assumed to be robust to class imbalance. Note that if we assume that patient outcomes are independent (which is well-justified in the case of a non-communicable condition, particularly in large databases), then  $t_p$  should scale linearly with the total number of positives  $P$ , implying:

$$TPR = \frac{t_p}{P} = \frac{t'_p}{P'} \quad (15)$$

implying that with different sizes of the set of positive samples (or negative samples), the ROC curve remains unchanged. In particular, note that even if the prevalence is very small (say 0.01%), we cannot cheat to boost the AUC by labeling all predictions as negative, or stating that risk is always zero: in that case, our  $P$  is very small, but our  $t_p = 0$  strictly, implying that our  $TPR = 0$ , thus leading to a zero AUC. We can cheat to boost the accuracy (See the previous section), but not the AUC.

Note that while relative class sizes or imbalance does not affect the ROC (under the assumption that true positives and true negatives scale with the number of positives and negatives), very small absolute sample sizes might still result in poor performance of the model.

The precision-recall curves do get affected by class imbalance, or the prevalence, as shown by Eq (14). However, in diagnostic analysis, they are important since we are generally less interested in the number of true negatives; the ratio of false positives to the total number of positive recommendations by the algorithm is much more relevant, i.e., the PPV or the precision.

## IV. GENERATING PFSA MODELS FROM SET OF INPUT STREAMS WITH VARIABLE INPUT LENGTHS

Our PFSA reconstruction algorithm [53] is distinct from standard HMM learning. We do not need to pre-specify structures, or the number of states in the algorithm, and all model parameters are inferred directly from data. Additionally, we can operate either with 1) a single input stream, or 2) a set of input streams of possibly varying lengths which are assumed to be different and independent sample paths from the unknown stochastic generator we are trying to infer. At an intuitive level, we use the input data to infer the length of histories one must remember to estimate the current state, and predict futures for the process being modeled. Thus, we do not step through the symbol streams with a pre-specified model structure, and avoid the need to have equal-length inputs. More details of the algorithm are provided in the next section.

The ability to model a set of input streams of varying lengths is particularly important, since medical histories of different patients are typically of different lengths.

## V. PROBABILISTIC FINITE STATE AUTOMATA INFERENCE

### A. Probabilistic Finite-State Automaton

Let  $\Sigma$  be a finite alphabet of symbols with size  $|\Sigma|$ . The set of sequences of length  $d$  over  $\Sigma$  is denoted by  $\Sigma^d$ . The set of finite but unbounded sequences over  $\Sigma$  is denoted by  $\Sigma^*$ , the Kleene star operation [58], i.e.  $\Sigma^* = \bigcup_{d=0}^{\infty} \Sigma^d$ . We use lower case Greek, for example  $\sigma$  or  $\tau$ , for symbols in  $\Sigma$ , and lower case Latin, for example  $x$  or  $y$ , for sequences of symbols, i.e.  $x = \sigma_1 \sigma_2 \dots \sigma_n$ . We use  $|x|$  to denote the length of  $x$ . The empty sequence is denoted by  $\lambda$ .

We denote the set of strictly infinite sequences over  $\Sigma$  by  $\Sigma^\omega$ , and the set of strictly infinite sequences having  $x$  as prefix by  $x\Sigma^\omega$ . Let  $\mathcal{S} = \{x\Sigma^\omega : x \in \Sigma^*\} \cup \{\emptyset\}$ , we can verify that  $\mathcal{S}$  is a semiring [59] over  $\Sigma^\omega$ . We use  $\mathcal{F}$  to denote the sigma algebra generated by  $\mathcal{S}$ .

**Definition 2** (Stochastic Process over  $\Sigma$ ). *A stochastic process over a finite alphabet  $\Sigma$  is a collection of  $\Sigma$ -valued random variables  $\{X_t\}_{t \in \mathbb{N}}$  indexed by positive integers [56].*

We are specifically interested in processes in which the  $X_t$ s are not necessarily independently distributed.

**Definition 3** (Sequence-Induced Measure and Derivative). *For a process  $\mathcal{P}$ , let  $\Pr_{\mathcal{P}}(x)$  or simply  $\Pr(x)$  denote the probability  $\mathcal{P}$  producing a sample path prefixed by  $x$ . The **measure**  $\mu_x$  **induced by a sequence**  $x \in \Sigma^*$  is the extension [59] to  $\mathcal{F}$  of the premeasure defined on the semiring  $\mathcal{S}$  given by*

$$\forall x, y \in \Sigma^*, \mu_x(y\Sigma^\omega) \triangleq \frac{\Pr(xy)}{\Pr(x)}, \text{ if } \Pr(x) > 0 \quad (16)$$

*For any  $d \in \mathbb{N}$ , the **d-th order derivative** of a sequence  $x$ , written as  $\phi_x^d$ , is defined to be the marginal distribution of  $\mu_x$  on  $\Sigma^d$ , with the entry indexed by  $y$  denoted by  $\phi_x^d(y)$ . The first-order derivative is called the **symbolic derivative** and is denoted by  $\phi_x$  for short.*

**Definition 4** (Probabilistic Nerode Equivalence and Causal States [60]). *For any pair of sequences  $x, y \in \Sigma^*$ ,  $x$  is equivalent to  $y$ , written as  $x \sim y$ , if and only if either  $\Pr(x) = \Pr(y) = 0$ , or  $\mu_x = \mu_y$ . The equivalence class of a sequence  $x$  is denoted by  $[x]$  and is called a **causal state** [61]. The cardinality of the set of causal states is called the **probabilistic Nerode index**, or the Nerode index for simplicity.*

We can see from the definition that causal states captures how the history of a process influences its future. Since the probabilistic Nerode equivalence is right invariant, it gives rise naturally to a automaton structure introduced below.

**Definition 5** (Probabilistic Finite-State Automaton (PFSA)). *A PFSA  $G$  is defined by a quadruple  $(Q, \Sigma, \delta, \tilde{\pi})$ , where  $Q$  is a finite set,  $\Sigma$  is a finite alphabet,  $\delta : Q \times \Sigma \rightarrow \Sigma$  is called the transition map, and  $\tilde{\pi} : Q \rightarrow \mathbf{P}_\Sigma$ , where*



$\mathbf{P}_\Sigma$  is the space of probability distributions over  $\Sigma$ , is called the transition probability. The entry of  $\tilde{\pi}(q)$  indexed by  $\sigma$  is denoted by  $\tilde{\pi}(q, \sigma)$ .

**Definition 6** (Transition and Observation Matrices). The transition matrix  $\Pi$  is the  $|Q| \times |Q|$  matrix with the entry indexed by  $q, q'$ , written as  $\pi_{q,q'}$ , satisfying

$$\pi_{q,q'} \triangleq \sum_{\{\sigma \in \Sigma | \delta(q, \sigma) = q'\}} \tilde{\pi}(q, \sigma) \quad (17)$$

and the observation matrix  $\tilde{\Pi}$  is a  $|Q| \times |\Sigma|$  matrix with the entry indexed by  $q, \sigma$  equaling  $\tilde{\pi}(q, \sigma)$ .

We note that both  $\Pi$  and  $\tilde{\Pi}$  are stochastic, i.e. non-negative with rows summing up to 1.

**Definition 7** (Extension of  $\delta$  and  $\tilde{\pi}$  to  $\Sigma^*$ ). For any  $x = \sigma_1 \dots \sigma_k$ ,  $\delta(q, x)$  is defined recursively by

$$\delta(q, x) \triangleq \delta(\delta(q, \sigma_1 \dots \sigma_{k-1}), \sigma_k) \quad (18)$$

with  $\delta(q, \lambda) = q$ , and  $\tilde{\pi}(q, x)$  is defined recursively by

$$\tilde{\pi}(q, x) \triangleq \prod_{i=1}^k \tilde{\pi}(\delta(q, \sigma_1 \dots \sigma_{i-1}), \sigma_i) \quad (19)$$

with  $\tilde{\pi}(q, \lambda) = 1$ .

**Definition 8** (Strongly Connected PFSA). We say a PFSA is strongly connected if the underlying directed graph is strongly connected [62]. More precisely, a PFSA  $G = (Q, \Sigma, \delta, \tilde{\pi})$  is strongly connected if for any pair of distinct states  $q$  and  $q' \in Q$ , there is an  $x \in \Sigma^*$  such that  $\delta(q, x) = q'$ .

We assume all PFSA in the discussions in the sequel are strongly connected if not specified otherwise. For strongly connected PFSA  $G$ , there is a unique probability distribution over  $Q$  that satisfies  $\mathbf{v}^\top \Pi = \mathbf{v}^\top$ . This is the **stationary distribution** [63], [64] of  $G$  and is denoted as  $\wp_G$ , or  $\wp$  if  $G$  is understood.

**Definition 9** ( $\Gamma$ -Expression). We can encode the information contained in  $\delta$  and  $\tilde{\pi}$  by a set of  $|Q| \times |Q|$  matrices  $\Gamma = \{\Gamma_\sigma | \sigma \in \Sigma\}$ , where

$$\Gamma_\sigma |_{q,q'} \triangleq \begin{cases} \tilde{\pi}(q, \sigma) & \text{if } \delta(q, \sigma) = q', \\ 0 & \text{if otherwise.} \end{cases} \quad (20)$$

$\Gamma_\sigma$  is called **event-specific transition matrix**, with the event being that  $\sigma$  is current the output.  $\Gamma_\sigma$  can also be extended to arbitrary  $x \in \Sigma^*$  by defining  $\Gamma_x = \prod_{i=1}^k \Gamma_{\sigma_i}$  with  $\Gamma_\lambda = I$ .

**Definition 10** (Sequence-Induced Distribution on States). For a PFSA  $G = (Q, \Sigma, \delta, \tilde{\pi})$  and a distribution  $\wp_0$  on  $Q$ , the **distribution on  $Q$  induced by a sequence  $x$**  is given by  $\wp_{G, \wp_0}^\top(x) = \left[ \wp_0^\top \Gamma_x \right]$  with  $\wp_{G, \wp_0}(\lambda) = \wp_0$ . The entry indexed by  $q \in Q$  of the vector  $\wp_{G, \wp_0}(x)$  is written as  $\wp_{G, \wp_0}(x, q)$ . When  $\wp_0 = \wp_G$ , the stationary distribution of  $G$ , we write  $\wp_{G, \wp_0}(x)$  as  $\wp_G(x)$ , or simply as  $\wp(x)$ , if  $G$  is understood.

**Definition 11** (Stochastic Process Generated by a PFSA). Let  $G = (Q, \Sigma, \delta, \tilde{\pi})$  be a PFSA and let  $\wp_0$  be a distribution on  $Q$ , the  $\Sigma$ -valued stochastic process  $\{X_t\}_{t \in \mathbb{N}}$  generated by  $G$  and  $\wp_0$  satisfies that  $X_1$  follows the distribution  $\wp_0$  and  $X_{t+1}$  follows the distribution  $\wp_{G, \wp_0}(X_1 \dots X_t)$  for  $t \in \mathbb{N}$ .

For the rest of this paper, we will assume  $\wp_0 = \wp_G$  if not specified otherwise. We can show that, when initialized with  $\wp_G$ , the process generated by a PFSA  $G$  is stationary and ergodic. We also note the, for the process generate by  $G$ , we have  $\phi_x = \wp_G(x)^\top \tilde{\Pi}$ . Since  $\wp_G(\lambda) = \wp_G$ , the symbolic derivative of the empty sequence  $\phi_\lambda$  is the stationary distribution on the symbols.

**Definition 12** (Synchronizable PFSA and Synchronizing Sequence). A **synchronizing sequence** is a finite sequence that sends an arbitrary state of the PFSA to a fixed state [65]. To be more precise, let  $G = (Q, \Sigma, \delta, \tilde{\pi})$  be a PFSA, we say a sequence  $x \in \Sigma^*$  is a synchronizing sequence to a state  $q \in Q$  if  $\delta(q', x) = q$  for all  $q' \in Q$ . A PFSA is **synchronizable** if it has at least one synchronizing sequence. Given a sample path generated by a PFSA, we say the PFSA is **synchronized** if a synchronizing sequence transpires in the sample path.

**Definition 13** (Equivalence and Irreducibility). Two PFSA  $G$  and  $H$  are **equivalent** if they generate the same stochastic process. A PFSA  $G$  is said to be **irreducible**, if there is not another PFSA with smaller state set that is equivalent to  $G$ .

**Definition 14**. Consider a PFSA  $G$  over state set  $Q$ . For a give  $\varepsilon > 0$ , we say a sequence  $x$  is a  $\varepsilon$ -synchronizing sequence to a state  $q \in Q$  if

$$\|\wp_G(x) - \mathbf{e}_q\|_\infty \leq \varepsilon. \quad (21)$$

---

**Algorithm 1: GenESeSS**

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**Data:** A sequence  $x$  over alphabet  $\Sigma$ ,  $0 < \varepsilon < 1$   
**Result:** State set  $Q$ , transition map  $\delta$ , and transition probability  $\tilde{\pi}$   
/\* **Step One: Approximate  $\varepsilon$ -synchronizing sequence** \*/

- 1 Let  $L = \lceil \log_{|\Sigma|} 1/\varepsilon \rceil$ ;
- 2 Calculate the **derivative heap**  $\mathcal{D}_\varepsilon^x$  equaling  $\{\hat{\phi}_y^x : y \text{ is a sub-sequence of } x \text{ with } |y| \leq L\}$ ;
- 3 Let  $\mathcal{C}$  be the convex hull of  $\mathcal{D}_\varepsilon^x$ ;
- 4 Select  $x_0$  with  $\hat{\phi}_{x_0}^x$  being a vertex of  $\mathcal{C}$  and has the highest frequency in  $x$ ;
- /\* **Step Two: Identify transition structure** \*/
- 5 Initialize  $Q = \{q_0\}$ ;
- 6 Associate to  $q_0$  the **sequence identifier**  $x_{q_0}^{\text{id}} = x_0$  and the probability vector  $d_{q_0} = \hat{\phi}_{x_0}^x$ ;
- 7 Let  $\tilde{Q}$  be the set of states that are just added and initialize it to be  $Q$ ;
- 8 **while**  $\tilde{Q} \neq \emptyset$  **do**
- 9     Let  $Q_{\text{new}} = \emptyset$  be the set of new states;
- 10    **for**  $(q, \sigma) \in \tilde{Q} \times \Sigma$  **do**
- 11     Let  $x = x_q^{\text{id}}$  and  $d = \hat{\phi}_{x\sigma}^x$ ;
- 12     **if**  $\|d - d_{q'}\|_\infty < \varepsilon$  **for some**  $q' \in Q$  **then**
- 13        Let  $\delta(q, \sigma) = q'$ ;
- 14     **else**
- 15        Let  $Q_{\text{new}} = Q_{\text{new}} \cup \{q_{\text{new}}\}$  and  $Q = Q \cup \{q_{\text{new}}\}$ ;
- 16        Associate to  $q_{\text{new}}$  the sequence identifier  $x_{q_{\text{new}}}^{\text{id}} = x\sigma$  and the probability vector  $d_{q_{\text{new}}} = d$ ;
- 17        Let  $\delta(q, \sigma) = q_{\text{new}}$ ;
- 18     Let  $\tilde{Q} = Q_{\text{new}}$ ;
- 19 Take a strongly connected subgraph of the labeled directed graph defined by  $Q$  and  $\delta$ , and denote the vertex set of the subgraph again by  $Q$ ;
- /\* **Step Three: Identify transition probability** \*/
- 20 Initialize counter  $N[q, \sigma]$  for each pair  $(q, \sigma) \in Q \times \Sigma$ ;
- 21 Choose a random starting state  $q \in Q$ ;
- 22 **for**  $\sigma \in \Sigma$  **do**
- 23     Let  $N[q, \sigma] = N[q, \sigma] + 1$ ;
- 24     Let  $q = \delta(q, \sigma)$ ;
- 25 Let  $\tilde{\pi}(q) = \llbracket (N[q, \sigma])_{\sigma \in \Sigma} \rrbracket$ ;
- 26 **return**  $Q, \delta, \tilde{\pi}$ ;

---

While there exists PFSA that is not synchronizable, we can show that an irreducible PFSA always has an  $\varepsilon$ -synchronizing sequence for some state  $q$  for arbitrarily small  $\varepsilon > 0$ . Moreover, we can show that as length increases, sequences produced by PFSA become uniformly  $\varepsilon$ -synchronizing. These two are the underpinning properties for the inference algorithm of PFSA (See Alg. 1), because they imply that  $\phi_x$  can be used to approximate  $\tilde{\pi}(q)$  if  $x$  are properly prefixed and long enough.

**Definition 15** (Joint  $\varepsilon$ -Synchronizing Sequence). *Let  $G$  and  $H$  be two PFSA over state sets  $Q_G$  and  $Q_H$ , respectively. For a fixed  $\varepsilon$ , a sequence  $x$  is said to be **jointly  $\varepsilon$ -synchronizing** to  $(q, r) \in Q_G \times Q_H$  if  $x$  is  $\varepsilon$ -synchronizing to  $q$  and to  $r$  simultaneously. We define*

$$\Sigma_{\varepsilon, (q, r)}^d \triangleq \{x \in \Sigma^d : x \text{ jointly } \varepsilon\text{-synchronizing to } (q, r)\} \quad (22)$$

**Definition 16** (Joint Pair of States). *Let  $G$  and  $H$  be two PFSA over state sets  $Q_G$  and  $Q_H$ , respectively. Define*

$$p_G(q, r) \triangleq \lim_{d \rightarrow \infty} p_G \left( \Sigma_{\varepsilon, (q, r)}^d \right) \quad (23)$$

*A pair of states  $(q, r) \in Q_G \times Q_H$  is called a **G-joint pair** of states if  $p_G(q, r) > 0$ . We also define*

$$Q_G \triangleq \{(q, r) \in Q_G \times Q_H : (q, r) \text{ is a G-joint pair}\} \quad (24)$$

The inference algorithm for PFSA is called **GenESeSS** for Generator Extraction Using Self-similar Semantics. With an input sequence  $x$  and a hyperparameter  $\varepsilon$ , **GenESeSS** outputs a PFSA in the following three steps: 1) approximate an almost synchronizing sequence; 2) identify the transition structure of the PFSA; 3) calculate the transition probabilities of the PFSA. See Alg. 1 [53] for details.

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**Algorithm 2:** Log-likelihood

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**Data:** A PFSA  $G = (\Sigma, Q, \delta, \tilde{\pi})$  and a sequence  $x$  over alphabet  $\Sigma$

**Result:** Log-likelihood  $L(x, G)$  of  $G$  generating  $x$

- 1 Calculate the state transition matrix  $\Pi$  and observation  $\tilde{\Pi}$ ;
  - 2 Calculate the stationary distribution over states  $\wp_G$  of  $G$  from  $\Pi$ ;
  - 3 Calculate the stationary distribution of alphabet  $\phi_\lambda^\top = \wp_G^\top \tilde{\Pi}$ ;
  - 4 Initialize  $\mathbf{p}$  by  $\wp_G$  and  $\mathbf{q}$  by  $\phi_\lambda$ ;
  - 5 Let  $L = 0$ ;
  - 6 **for**  $i$  from 1 to  $|x|$  **do**
  - 7     Let  $\sigma$  be the  $i$ -th entry of  $x$ ;
  - 8     Let  $L = L - \log \mathbf{q}|_\sigma$ ;
  - 9     Let  $\mathbf{p}^\top = \llbracket \mathbf{p}^\top \Gamma_\sigma \rrbracket$  where  $\Gamma_\sigma$  is defined in 9;
  - 10    Let  $\mathbf{q}^\top = \mathbf{p}^\top \tilde{\Pi}$ ;
  - 11 **return**  $L/|x|$ ;
- 

## VI. THEORETICAL DEVELOPMENT OF SEQUENCE LIKELIHOOD DEFECT

**Definition 17** (Entropy Rate and KL Divergence). *By entropy rate of a PFSA, we mean the entropy rate of the stochastic process generated by the PFSA [32]. Similarly, by KL divergence of two PFSA, we mean the KL divergence between the two processes generated by them [66]. More precisely, we have*

$$\mathcal{H}(G) = - \lim_{d \rightarrow \infty} \frac{1}{d} \sum_{x \in \Sigma^d} p(x) \log p(x) \quad (25)$$

and the KL divergence

$$\mathcal{D}_{KL}(G \parallel H) = \lim_{d \rightarrow \infty} \frac{1}{d} \sum_{x \in \Sigma^d} p_G(x) \log \frac{p_G(x)}{p_H(x)} \quad (26)$$

whenever the limits exist.

**Theorem 1** (Closed-form Formula for Entropy Rate and KL Divergence). *The entropy rate of a PFSA  $G = (\Sigma, Q, \delta, \tilde{\pi})$  is given by*

$$\mathcal{H}(G) = \sum_{q \in Q} \wp_G(q) \cdot h(\tilde{\pi}(q)) \quad (27)$$

where  $h(\mathbf{v})$  is the based-2 entropy of the probability vector  $\mathbf{v}$ .

Consider two PFSA  $G = (Q_G, \Sigma, \delta_G, \tilde{\pi}_G)$  and  $H = (Q_H, \Sigma, \delta_H, \tilde{\pi}_H)$  with  $\mu_G$  being absolutely continuous with respect to  $\mu_H$ . Let  $Q_c$  be the set of  $G$ -joint pairs of states, we have

$$\mathcal{D}_{KL}(G \parallel H) = \sum_{(q,r) \in Q_c} p_G(q, r) \mathcal{D}_{KL}(\tilde{\pi}_G(q) \parallel \tilde{\pi}_H(r)) \quad (28)$$

**Definition 18** (Log-likelihood). *Let  $x \in \Sigma^d$ , the log-likelihood [32] of a PFSA  $G$  generating  $x$  is given by*

$$L(x, G) = -\frac{1}{d} \log p_G(x) \quad (29)$$

The calculation of log-likelihood is detailed in Alg. 2.

**Theorem 2** (Convergence of log-likelihood). *Let  $G$  and  $H$  be two reduced PFSA, and let  $x \in \Sigma^d$  be a sequence generated by  $G$ . Then we have*

$$L(x, H) \rightarrow \mathcal{H}(G) + \mathcal{D}_{KL}(G \parallel H) \quad (30)$$

in probability as  $d \rightarrow \infty$ .

*Proof.* We first notice that

$$\sum_{x \in \Sigma^d} p_G(x) \log \frac{p_G(x)}{p_H(x)} = \sum_{x \in \Sigma^{d-1}} \sum_{\sigma \in \Sigma} p_G(x) \wp_G(x) \tilde{\Pi}_G \Big|_\sigma \log \frac{p_G(x) \wp_G(x) \tilde{\Pi}_G \Big|_\sigma}{p_H(x) \wp_H(x) \tilde{\Pi}_H \Big|_\sigma} \quad (31)$$

$$= \sum_{x \in \Sigma^{d-1}} p_G(x) \log \frac{p_G(x)}{p_H(x)} + \underbrace{\sum_{x \in \Sigma^{d-1}} p_G(x) \sum_{\sigma \in \Sigma} \wp_G(x) \tilde{\Pi}_G \Big|_\sigma \log \frac{\wp_G(x) \tilde{\Pi}_G \Big|_\sigma}{\wp_H(x) \tilde{\Pi}_H \Big|_\sigma}}_{\mathcal{D}_d} \quad (32)$$

By induction, we have  $\mathcal{D}_{\text{KL}}(G \parallel H) = \lim_{d \rightarrow \infty} \frac{1}{d} \sum_{i=1}^d D_i$ , and hence by Cesàro summation theorem [67], we have  $\mathcal{D}_{\text{KL}}(G \parallel H) = \lim_{d \rightarrow \infty} D_d$ . Let  $x = \sigma_1 \sigma_2 \dots \sigma_n$  be a sequence generated by  $G$ . Let  $x^{[i-1]}$  is the truncation of  $x$  at the  $(i-1)$ -th symbols, we have

$$-\frac{1}{n} \sum_{i=1}^n \log \varrho_H \left( x^{[i-1]} \right) \tilde{\Pi}_H \Big|_{\sigma_i} = \underbrace{\frac{1}{n} \sum_{i=1}^n \log \frac{\varrho_G \left( x^{[i-1]} \right) \tilde{\Pi}_G \Big|_{\sigma_i}}{\varrho_H \left( x^{[i-1]} \right) \tilde{\Pi}_H \Big|_{\sigma_i}}}_{A_{x,n}} - \underbrace{\frac{1}{n} \sum_{i=1}^n \log \varrho_G \left( x^{[i-1]} \right) \tilde{\Pi}_G \Big|_{\sigma_i}}_{B_{x,n}} \quad (33)$$

Since the stochastic process  $G$  generates is ergodic, we have

$$\lim_{n \rightarrow \infty} A_{x,n} = \lim_{d \rightarrow \infty} D_d = \mathcal{D}_{\text{KL}}(G \parallel H) \quad (34)$$

and  $\lim_{n \rightarrow \infty} B_{x,n} = \mathcal{H}(G)$ .  $\square$

## VII. PIPELINE OPTIMIZATION: HYPER-TRAINING, TRAINING, & VALIDATION

Our pipeline comprises a network of individually trained light gradient boosting machine (LGBM) [32] classifiers that focus on complementary aspects of the problem, and operate on different categories of input features as described next. Importantly, some of these features need to be generated non-trivially from the raw data, and these *feature generators* have parameters that need to be trained as well (or comprise models that need to be inferred). We call this inference of the feature-generators as **hyper-training**. Importantly, this is different from the more common notion of hyper-parameters. Hyper-parameters are one or more variables whose scalar values are commonly tuned by grid-search or via some meta-heuristics to optimize classifiers, whereas hyper-training produces generators of features, not simply a set of numbers.

### *Hyper-training & Training*

*Trinary Quantization of Medical Histories:* The medical histories are mapped into trinary disease-phenotype-specific data-streams to enable generation of some of the features described below, as outlined in Section -C (Step 1).

*Feature Categories:* The features used in the pipeline maybe categorized as follows:

*PFSA scores:* The PFSA scores are computed on the basis of the inferred PFSA models as described in the previous sections. The generation of the PFSA models from the trinary data-streams is the first hyper-training step. These scores consist of the negative and positive log-likelihood of a phenotype-specific quantized medical history being generated by the PFSA models for the positive cohort and the control cohort of sex-stratified patients, and the corresponding sequence likelihood defects (See SI-Section -D). Recall that PFSAs are specialized HMMs, and these measures encode the dynamics of the underlying processes, and are sensitive to the ordering, and frequency of the codes at the resolution of the disease phenotypes. Also, recall that diseases phenotypes are broad categories of diagnostic codes, and that we generate PFSA models for each category, and separately for the sexes and the positive cohort and the control cohorts).

*Prevalence scores (p-scores):* The p-scores focus on individual diagnostic codes, and we create a dictionary of the ratio of relative prevalence of each code (relative to the set of all codes present) in the positive category (for each sex) to the control category. This is the second hyper-training step. In the later steps of the pipeline, we use dictionary look ups to map codes to their p-scores, and also their aggregate measures such as mean, median, and variance to train a downstream LGBM.

*Rare scores:* These scores consist of a subset of p-scores which correspond to codes with particularly high and low relative prevalences ( $p\text{-score} > 2$  or  $< .5$ ). Thus, this feature category depends on the p-score dictionary generated in the second hyper-training step.

*Sequence scores:* Sequence scores are relatively straight-forward statistical measures such as mean, median, variance, time since last occurrence etc.. on the trinary phenotype-specific sex-stratified histories. No hyper-training is required for the generation of the sequence features.

Thus we require three splits of the training dataset. The first split is used to carry out hyper-training of the PFSA models and the p-score dictionary. The second split is used to train the score-category specific LGBMs, one for each feature category. And the third split is used to train the final LGBM that takes inputs from the outputs of the four LGBMs in the previous layer.

### *Validation*

In validation, or actual prediction of patient fate, we use the trinary mapping, generate the features using the PFSA models and the p-score dictionary, and calculate the raw-risk via the trained LGBM network. The relative score is then obtained by a choice of the operating point reflecting the specificity/sensitivity trade-off discussed before.