:: SCRIPT AUTHORS ::

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MACHINE LEARNING (ML)

Development of a Machine Learning model for the prognosis of COVID-19 in terms of SEVERITY using laboratory biomarkers. The data are from examinations of patients treated at the Hospital de Clínicas of the Federal University of Paraná

LEGEND:

Sex:

1=Female

2=Male

COVID:

* Total: 35,109 Positive Samples

* Non-Severe (Mild to Moderate): 7,719 samples

* Severe: 27,390 samples

Classification Severity:

* Severe (Serious - Inpatients)

* Non-Severe (Mild to Moderate - Outpatients)

Period of the Samples:

* March 2020 to September 2022

OBJECTIVE:

Develop a Machine Learning model to predict the severity of COVID-19 and identify biomarkers associated with this severity in order to optimize priority in hospital care.

```
# PHASES:
# 1: Import the DataSet
# 2: Import the Pandas library for handling the DataSet
# 3: Remove unnecessary columns (features) from DataSet
# 4: Exploratory Analysis
# 5: Install the Pycaret library to aid Auto-Machine Learn
# 6: Import the Pycaret library
# 7: Perform data pre-processing
# 8: Build and compare models
# 9: Train the best model based on predictive performance metrics
#10: Extract the metrics results from the model
#11: Write conclusions about the best identified model
#12: Save the model to make predictions in real analyzes (Deploy)
```

```
# Phase 1: Import the DataSet

from google.colab import files
uploaded = files.upload()
```

Escolher arquivos COVID19 D…Severity.csv

- **COVID19 DataSetSeverity.csv**(text/csv) - 3610312 bytes, last modified: 26/12/2023 - 100% done

```
Saving COVID19 DataSetSeverity.csv to COVID19 DataSetSeverity.csv
```

```
# Phase 2: Import the Pandas library for handling the DataSet
import pandas as pd
DataSet = pd.read_csv("COVID19 DataSetSeverity.csv")
display (DataSet)
```

	ID	COVID	Age	Sex	Erythrocytes	Haemoglobin	Leukocytes	Mature Neutrophils	Immature Neutrophils	Neutrophils	...	pCO2	pO2	sO2	pH	HCO3 (standard)	HCO3 (actual)	BE(ECF)
0	1	Non-Severe	56	2	2.66	NaN	8.67	NaN	1.0	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	NaN
1	2	Non-Severe	76	1	4.49	NaN	11.84	NaN	6.0	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	NaN
2	3	Non-Severe	56	2	2.98	NaN	8.05	NaN	4.0	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	NaN
3	4	Non-Severe	68	2	4.37	NaN	9.76	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	NaN
4	5	Non-	61	1	4.70	NaN	7.92	NaN	0.0	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	NaN

```
# Phase 3: Remove unnecessary columns (features) from DataSet
DataSetSeverity = DataSet.drop("ID", axis = 1)
display (DataSetSeverity)
```

	COVID	Age	Sex	Erythrocytes	Haemoglobin	Leukocytes	Mature Neutrophils	Immature Neutrophils	Neutrophils	Basophils	...	pCO2	pO2	sO2	pH	HCO3 (standard)	HCO3 (actual)	BE(E
0	Non-Severe	56	2	2.66	NaN	8.67	NaN	1.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
1	Non-Severe	76	1	4.49	NaN	11.84	NaN	6.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
2	Non-Severe	56	2	2.98	NaN	8.05	NaN	4.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
3	Non-Severe	68	2	4.37	NaN	9.76	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
4	Non-Severe	61	1	4.70	NaN	7.92	NaN	0.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	...	
35104	Severe	47	2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
35105	Severe	61	2	3.30	NaN	6.55	NaN	0.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
35106	Severe	47	2	4.06	NaN	8.42	NaN	5.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
35107	Severe	55	2	4.58	NaN	12.15	NaN	8.0	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N
35108	Severe	55	2	NaN	NaN	NaN	NaN	NaN	NaN	NaN	...	NaN	NaN	NaN	NaN	NaN	NaN	N

35109 rows × 51 columns

```
# Phase 4: Exploratory Analysis
## 4.1. DataSet Informations
DataSetSeverity.info()
```

```
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 35109 entries, 0 to 35108
Data columns (total 51 columns):
 #   Column                                       Non-Null Count  Dtype  
---  ------                                       --------------  -----  
 0   COVID                                        35109 non-null  object 
 1   Age                                          35109 non-null  int64  
 2   Sex                                          35109 non-null  int64  
 3   Erythrocytes                                 27977 non-null  float64
 4   Haemoglobin                                  236 non-null    float64
 5   Leukocytes                                   28100 non-null  float64
 6   Mature Neutrophils                           131 non-null    float64
 7   Immature Neutrophils                         23962 non-null  float64
 8   Neutrophils                                  132 non-null    float64
 9   Basophils                                    131 non-null    float64
 10  Eosinophils                                  131 non-null    float64
 11  Lymphocytes                                  28098 non-null  float64
 12  Atypical Lymphocytes                         23837 non-null  float64
 13  Monocytes                                    28098 non-null  float64
 14  Platelets                                    28219 non-null  float64
 15  Prothrombin Time                             8777 non-null   float64
 16  Prothrombin Time – Relation*                 8757 non-null   float64
 17  Prothrombin Time - International Normalized Ratio  8785 non-null   float64
 18  Partial Thromboplastin Time                  2401 non-null   float64
 19  Partial Thromboplastin Time – Relation*      2391 non-null   float64
 20  D-Dimer                                      5102 non-null   float64
 21  Glucose                                      6958 non-null   float64
 22  HbA1c                                        1354 non-null   float64
 23  Total Cholesterol                            1738 non-null   float64
 24  HDL-C                                        1424 non-null   float64
 25  LDL-C                                        1378 non-null   float64
 26  Triglycerides                                1825 non-null   float64
 27  Creatinine                                   26990 non-null  float64
 28  Urea                                         23970 non-null  float64
 29  Potassium                                    24510 non-null  float64
 30  Sodium                                       24427 non-null  float64
 31  Alanine transaminase                         11570 non-null  float64
 32  Aspartate transaminase                       11538 non-null  float64
 33  Albumin                                      7561 non-null   float64
 34  Total Protein                                587 non-null    float64
 35  Globulin                                     587 non-null    float64
 36  Ferritin                                     6185 non-null   float64
 37  C-reactive protein                           15689 non-null  float64
 38  Amylase                                      896 non-null    float64
 39  Lipase                                       907 non-null    float64
 40  Troponin                                     3328 non-null   float64
 41  pCO2                                         272 non-null    float64
 42  pO2                                         269 non-null    float64
 43  sO2                                         267 non-null    float64
 44  pH                                          313 non-null    float64
 45  HCO3 (standard)                             246 non-null    float64
 46  HCO3 (actual)                               272 non-null    float64
 47  BE(ECF)                                     268 non-null    float64
 48  BE(B)                                       271 non-null    float64
 49  CTCO2                                       269 non-null    float64
 50  Procalcitonin                               1922 non-null   float64
dtypes: float64(48), int64(2), object(1)
memory usage: 13.7+ MB
```

```
## 4.2. Install and Import library for Descriptive Statistics
!pip install researchpy
import researchpy as rp
### 1: COVID Feature
rp.summary_cat(DataSetSeverity['COVID'])
```

```
Collecting researchpy
  Downloading researchpy-0.3.5-py3-none-any.whl (33 kB)
Requirement already satisfied: scipy in /usr/local/lib/python3.10/dist-packages (from researchpy) (1.11.4)
Requirement already satisfied: numpy in /usr/local/lib/python3.10/dist-packages (from researchpy) (1.23.5)
Requirement already satisfied: pandas in /usr/local/lib/python3.10/dist-packages (from researchpy) (1.5.3)
Requirement already satisfied: statsmodels in /usr/local/lib/python3.10/dist-packages (from researchpy) (0.14.1)
Requirement already satisfied: patsy in /usr/local/lib/python3.10/dist-packages (from researchpy) (0.5.4)
Requirement already satisfied: python-dateutil>=2.8.1 in /usr/local/lib/python3.10/dist-packages (from pandas->researchpy) (2.8.2)
Requirement already satisfied: pytz>=2020.1 in /usr/local/lib/python3.10/dist-packages (from pandas->researchpy) (2023.3.post1)
Requirement already satisfied: six in /usr/local/lib/python3.10/dist-packages (from patsy->researchpy) (1.16.0)
Requirement already satisfied: packaging>=21.3 in /usr/local/lib/python3.10/dist-packages (from statsmodels->researchpy) (23.2)
Installing collected packages: researchpy
Successfully installed researchpy-0.3.5
```

	Variable	Outcome	Count	Percent
0	COVID	Severe	27390	78.01
1		Non-Severe	7719	21.99

```
### 2: Sex Feature
rp.summary_cat(DataSetSeverity['Sex'])
```

	Variable	Outcome	Count	Percent
0	Sex	2	19504	55.55
1		1	15605	44.45

```
### 3: Biomarkers Features
DescriptiveStat = DataSetSeverity
DataStatistics = DescriptiveStat.drop("COVID", axis = 1)
DataStatistics = DataStatistics.drop("Sex", axis = 1)
for statistical in DataStatistics.columns:
  display(rp.summary_cont(DataStatistics[statistical]))
```

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Age	35109.0	51.6917	20.7704	0.1109	51.4745	51.909

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Erythrocytes	27977.0	3.7228	0.9563	0.0057	3.7116	3.734

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Haemoglobin	236.0	9.2301	2.5486	0.1659	8.9032	9.5569

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Leukocytes	28100.0	18.7901	311.2146	1.8566	15.1511	22.429

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Mature Neutrophils	131.0	51.7206	30.1088	2.6306	46.5162	56.925

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Immature Neutrophils	23962.0	8.2177	9.0723	0.0586	8.1028	8.3326

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Neutrophils	132.0	52.0864	30.2866	2.6361	46.8715	57.3012

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Basophils	131.0	0.3107	0.5819	0.0508	0.2101	0.4113

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Eosinophils	131.0	2.9733	8.0494	0.7033	1.5819	4.3646

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Lymphocytes	28098.0	18.3276	14.7855	0.0882	18.1547	18.5004

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Atypical Lymphocytes	23837.0	0.0842	0.3951	0.0026	0.0792	0.0892

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Monocytes	28098.0	6.8916	4.9824	0.0297	6.8334	6.9499

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Platelets	28219.0	251615.441	156999.4019	934.603	249783.5741	253447.3079

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Prothrombin Time	8777.0	15.4055	8.2819	0.0884	15.2322	15.5788

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Prothrombin Time – Relation*	8757.0	1.408	1.5861	0.0169	1.3748	1.4412

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Prothrombin Time - International Normalized Ratio	8785.0	1.4466	1.8551	0.0198	1.4078	1.4854

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Partial Thromboplastin Time	2401.0	32.9669	13.0154	0.2656	32.4461	33.4878

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Partial Thromboplastin Time – Relation*	2391.0	1.2919	1.547	0.0316	1.2298	1.3539

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	D-Dimer	5102.0	5.7938	66.6974	0.9338	3.9632	7.6244

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Glucose	6958.0	125.1138	72.5043	0.8692	123.4099	126.8177

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	HbA1c	1354.0	6.8219	2.075	0.0564	6.7113	6.9326

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Total Cholesterol	1738.0	169.4873	53.7783	1.29	166.9573	172.0174

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	HDL-C	1424.0	39.9185	14.4876	0.3839	39.1654	40.6716

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	LDL-C	1378.0	101.1627	39.9522	1.0763	99.0514	103.274

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Triglycerides	1825.0	159.7912	121.2147	2.8374	154.2263	165.3562

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Creatinine	26990.0	1.3944	1.469	0.0089	1.3768	1.4119

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Urea	23970.0	65.2884	53.4779	0.3454	64.6113	65.9654

	Variable	N	Mean	SD	SE	95% Conf.	Interval

0	Potassium	24510.0	4.4125	0.7624	0.0049	4.403	4.4221

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Sodium	24427.0	139.3832	4.9508	0.0317	139.3211	139.4453

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Alanine transaminase	11570.0	62.3107	219.867	2.0441	58.304	66.3174

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Aspartate transaminase	11538.0	65.2683	392.5113	3.6542	58.1056	72.4311

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Albumin	7561.0	3.2091	0.774	0.0089	3.1917	3.2266

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Total Protein	587.0	5.7272	1.4442	0.0596	5.6101	5.8442

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Globulin	587.0	2.3336	0.8752	0.0361	2.2626	2.4045

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Ferritin	6185.0	5236.4282	244233.9427	3105.5331	-851.4965	11324.3529

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	C-reactive protein	15689.0	7.5842	7.5281	0.0601	7.4664	7.702

	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Amylase	896.0	123.5301	855.65	28.5853	67.4282	179.6321

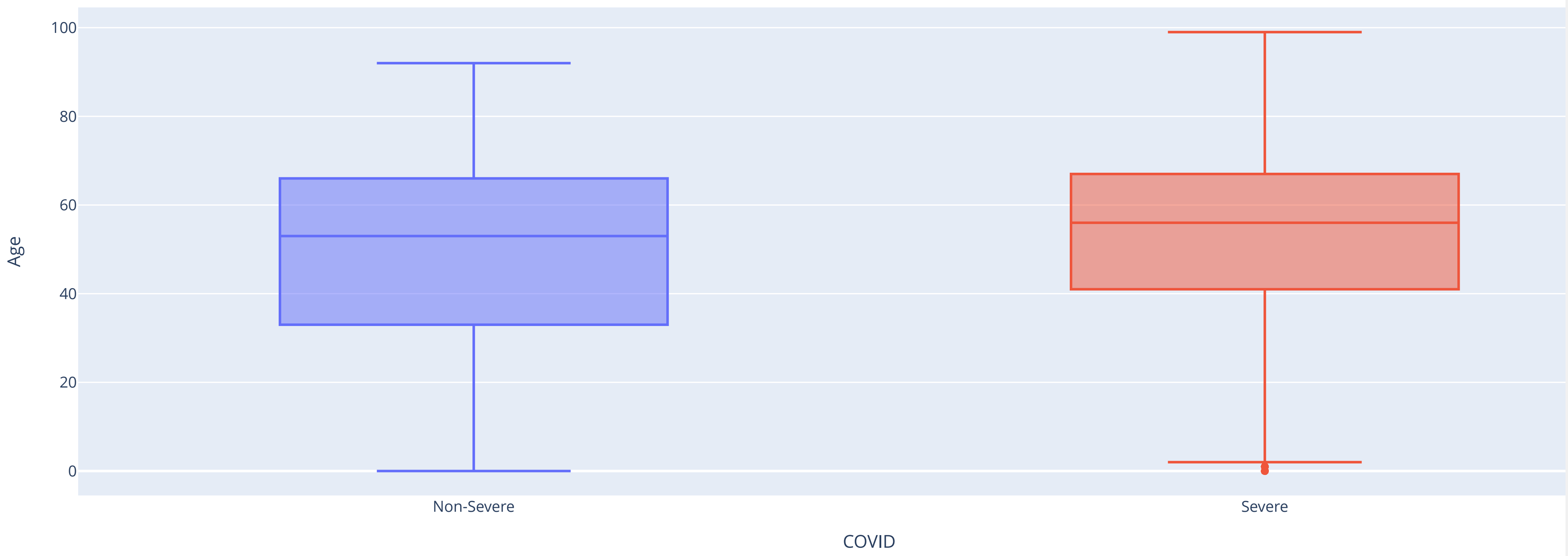
	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Lipase	907.0	189.5899	2348.8678	77.9929	36.5221	342.6576

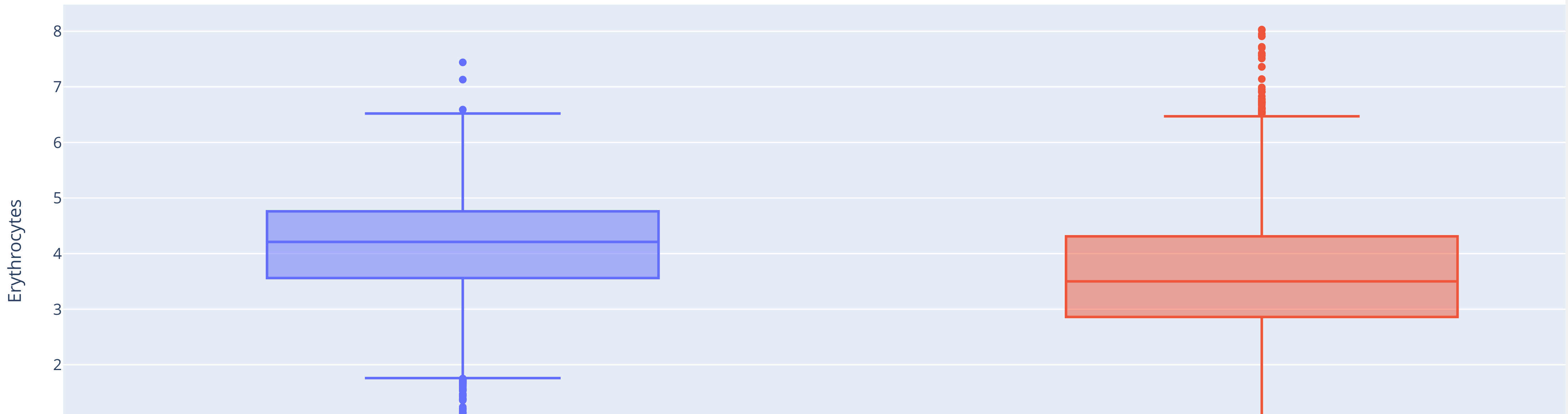
	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	Troponin	3328.0	1789.749	26496.6591	459.3032	889.2037	2690.2943

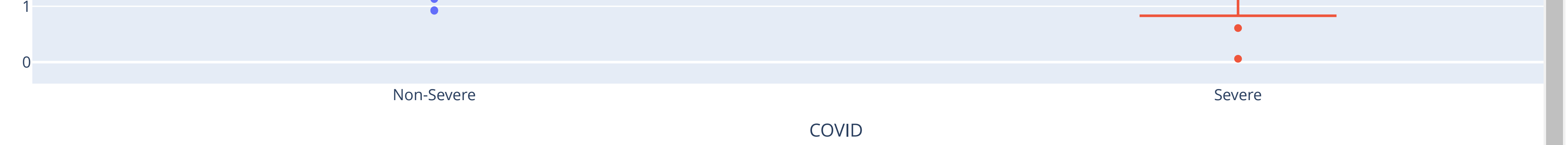
	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	pCO2	272.0	46.0662	18.3158	1.1106	43.8798	48.2526

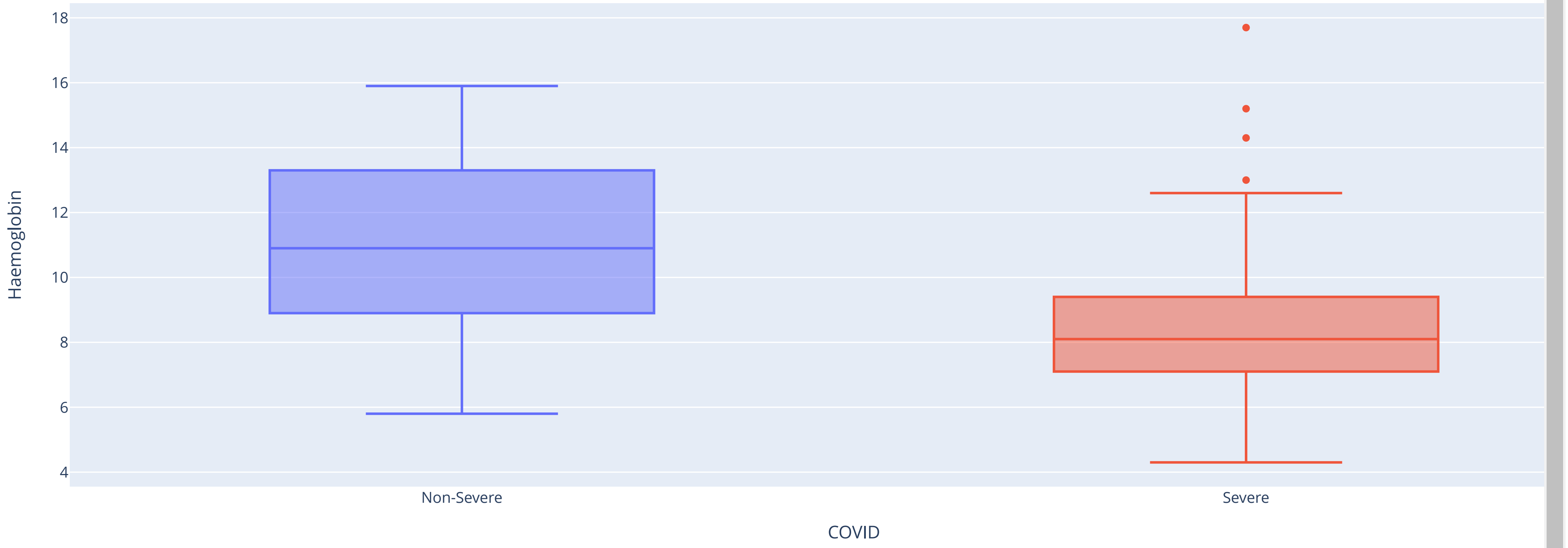
	Variable	N	Mean	SD	SE	95% Conf.	Interval
0	pO2	269.0	79.7353	33.3306	2.0322	75.7342	83.7364

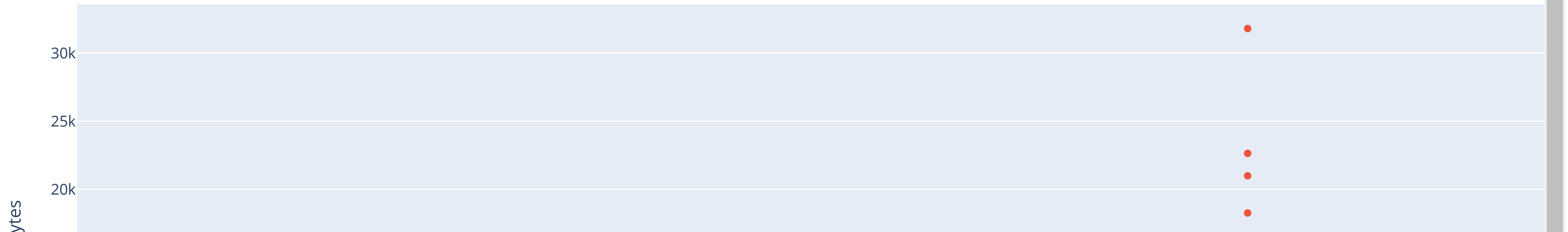
```
## 4.3. Analyzing the variation in biomarker levels between COVID-19 severity samples (SEVERE AND NON-SEVERE)

### 1: Import Plotly library to graphics
import plotly.express as px

### 2: Create Graphics
#      HISTOGRAM
#for biomarker in DataSetSeverity.columns:
#  if biomarker != 'COVID' and biomarker != 'Sex':
#   graphic = px.histogram(DataSetSeverity, x = biomarker, color = "COVID", text_auto = True)
#   graphic.show()

#      BOXPLOT
for biomarker in DataSetSeverity.columns:
    if biomarker != 'COVID' and biomarker != 'Sex':
      graphic = px.box(DataSetSeverity, x = DataSetSeverity.columns[0], y=biomarker, color="COVID")
      graphic.show()
```

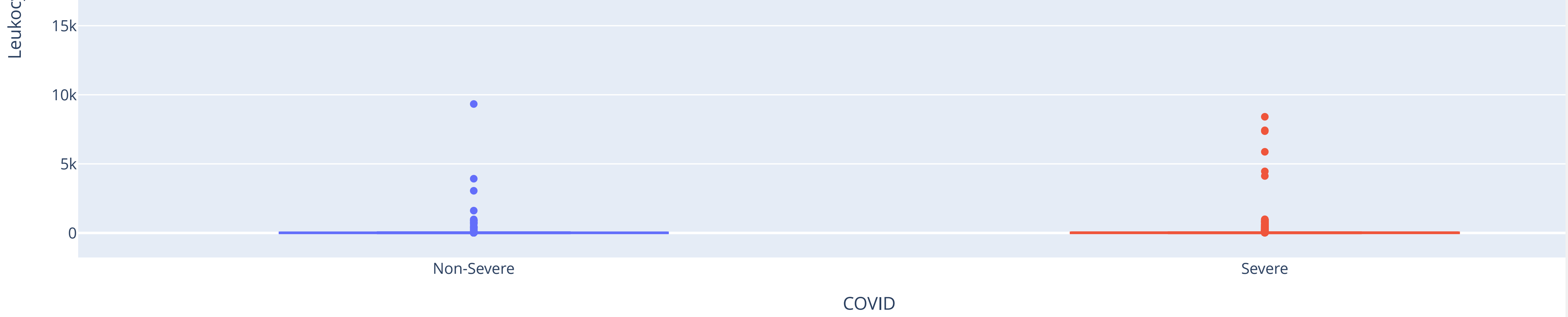

100
80
60
40
20
0
Age
Non-Severe
Severe
COVID

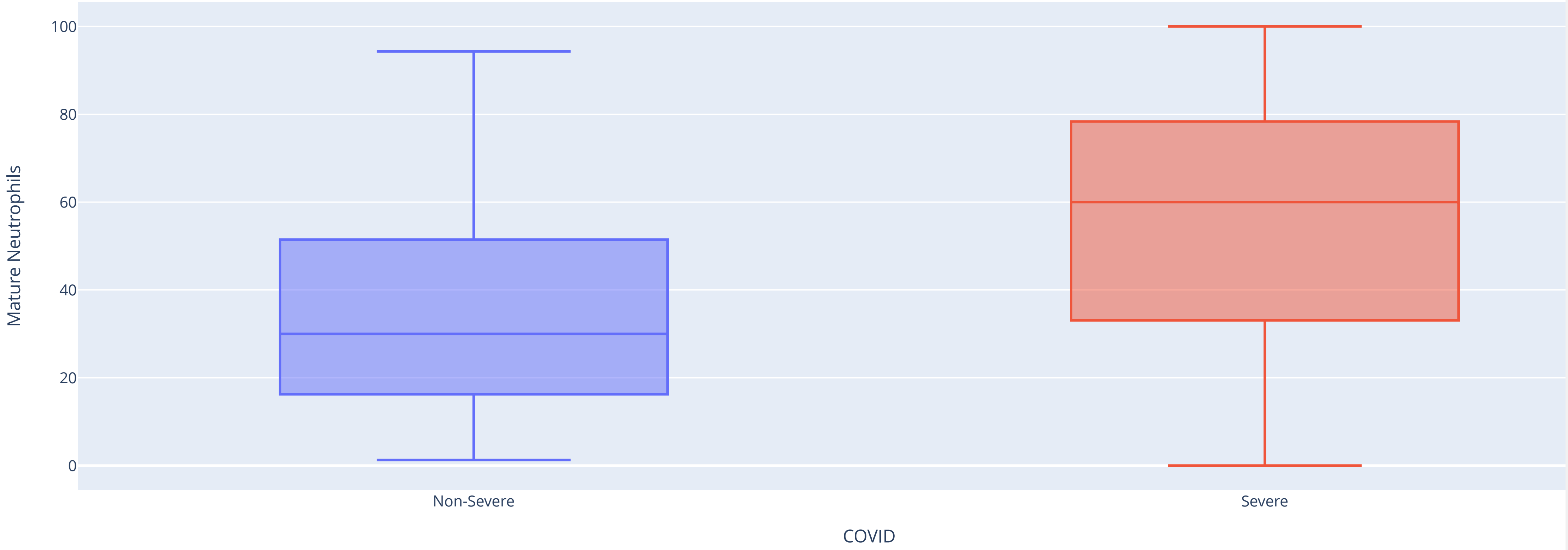

8
7
6
5
4
3
2
Erythrocytes

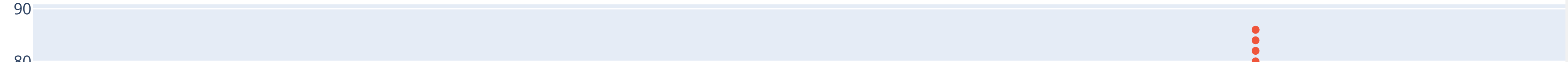

1
0
Non-Severe
Severe
COVID

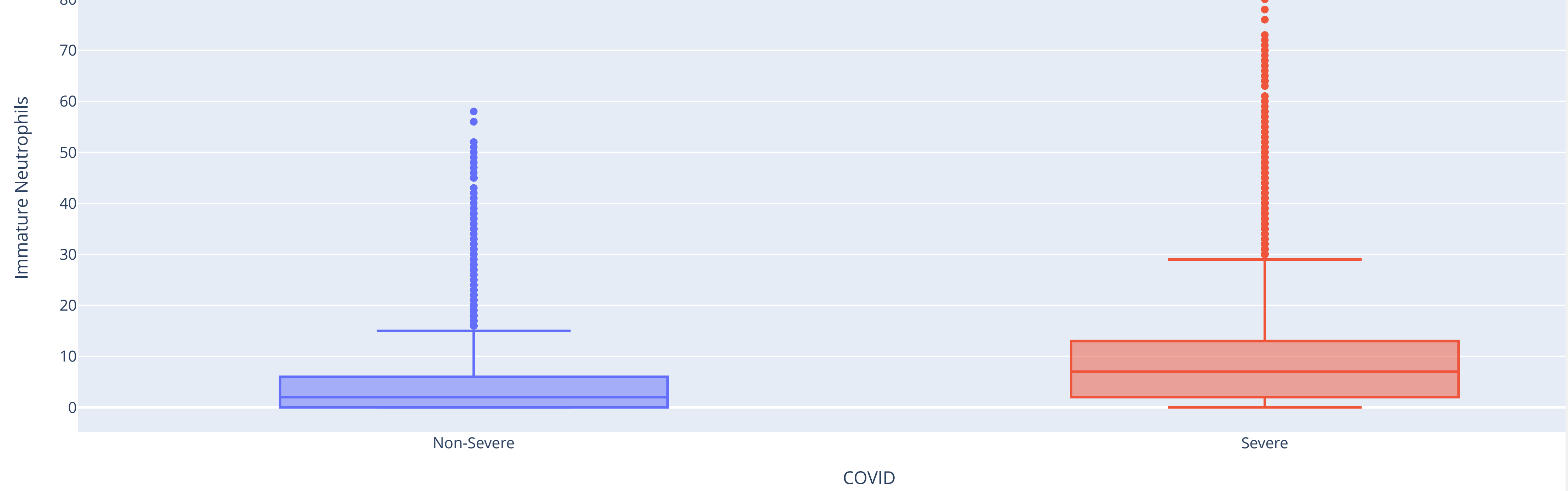

Haemoglobin
18
16
14
12
10
8
6
4
Non-Severe
Severe
COVID

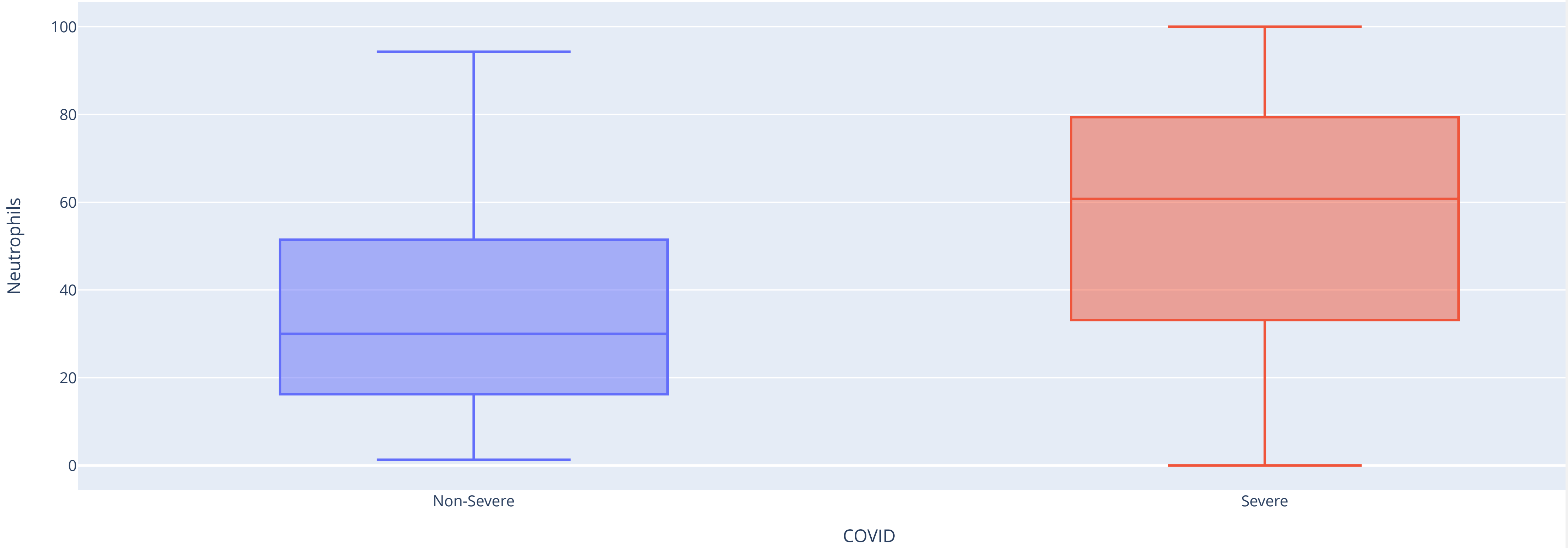

30k
25k
20k
ytes

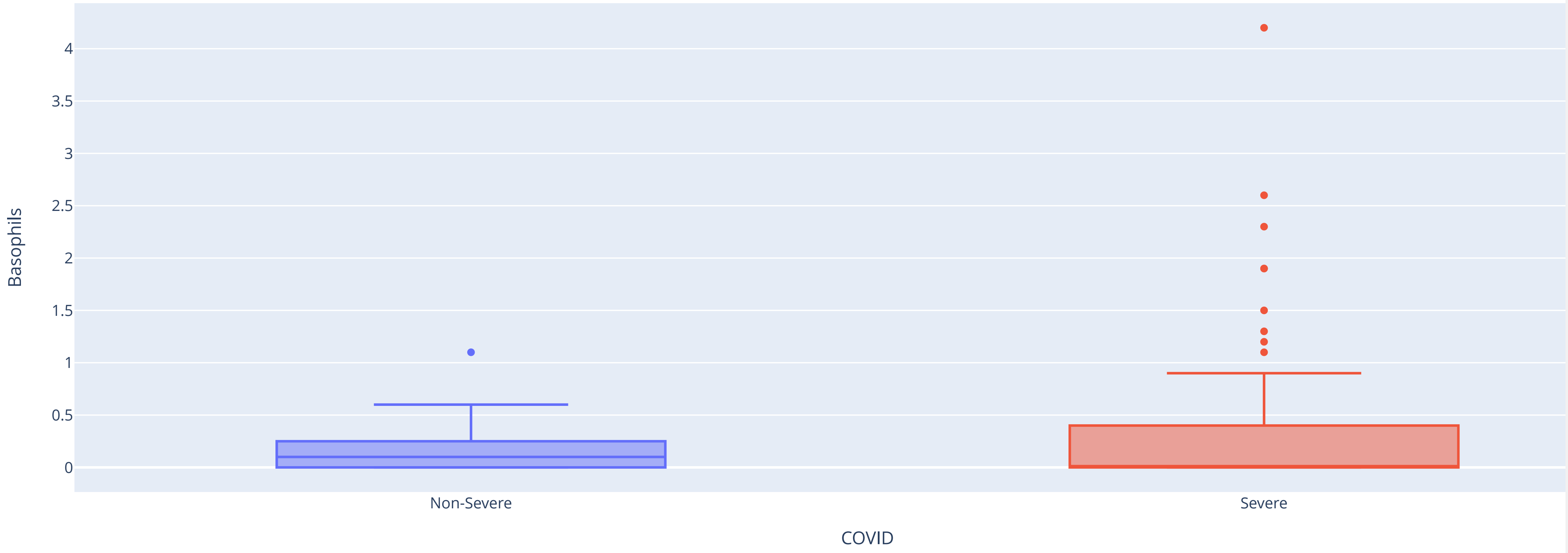

Leukoc
15k
10k
5k
0
Non-Severe
Severe
COVID

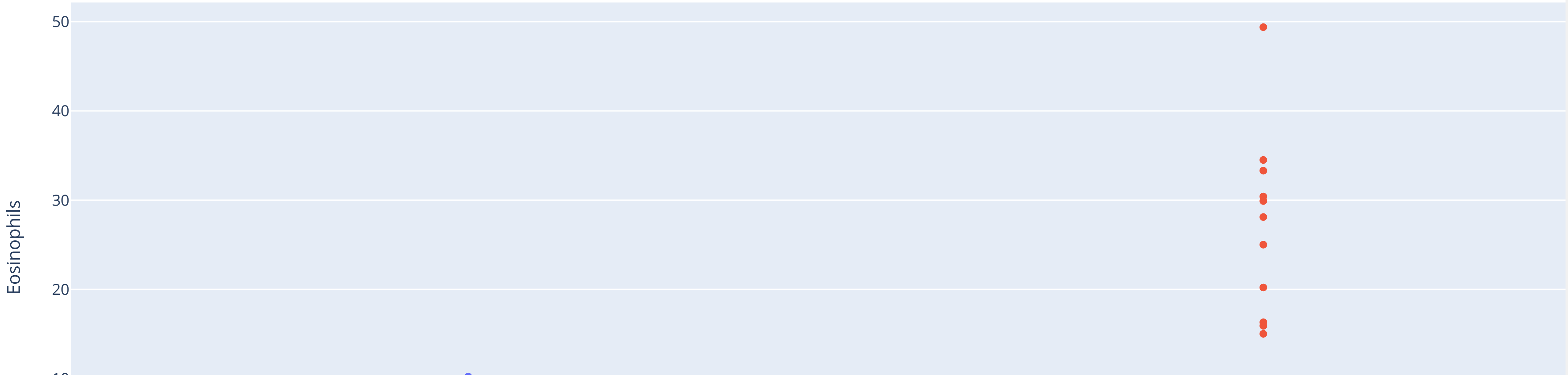

Mature Neutrophils
100
80
60
40
20
0
Non-Severe
Severe
COVID

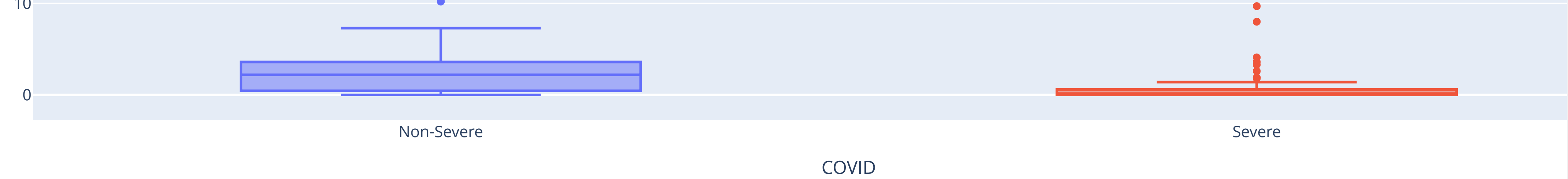

90
80

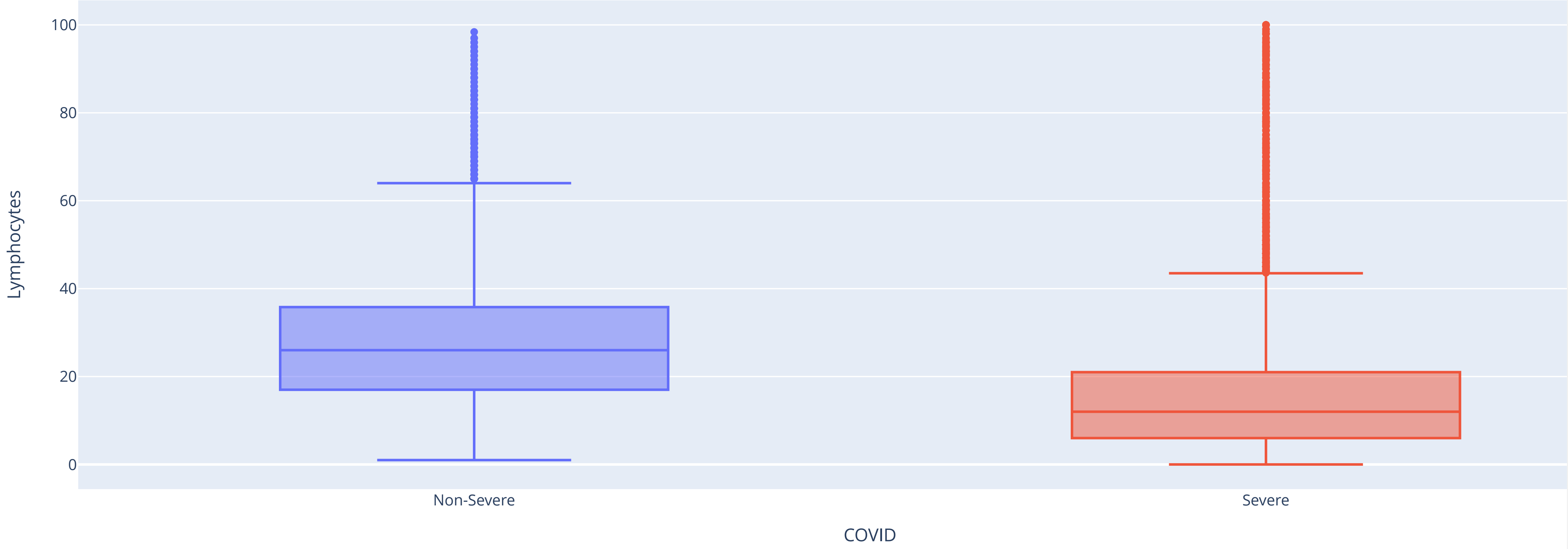

Immature Neutrophils
80
70
60
50
40
30
20
10
0
Non-Severe
Severe
COVID


Neutrophils
100
80
60
40
20
0
Non-Severe
Severe
COVID

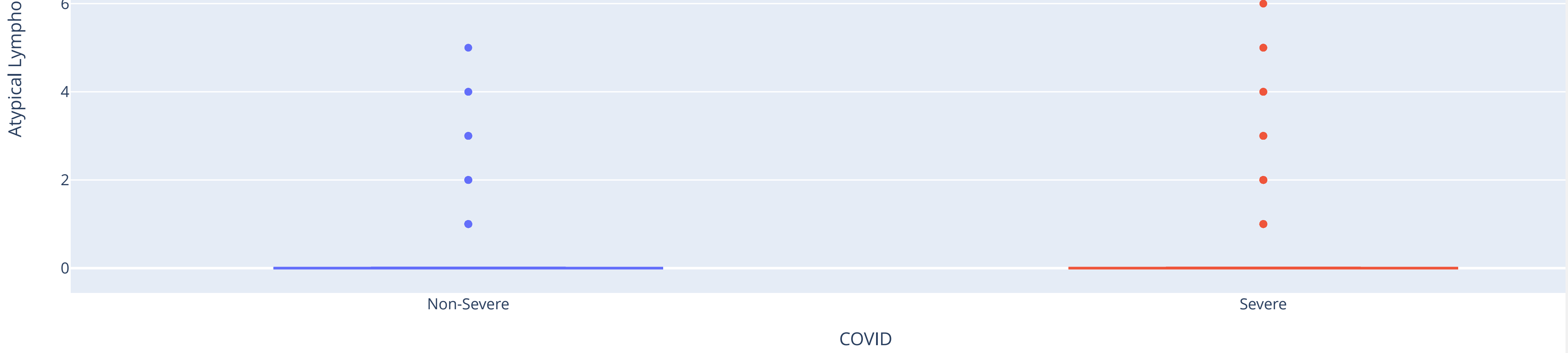

4
3.5
3
2.5
2
1.5
1
0.5
0
Basophils
Non-Severe
Severe
COVID

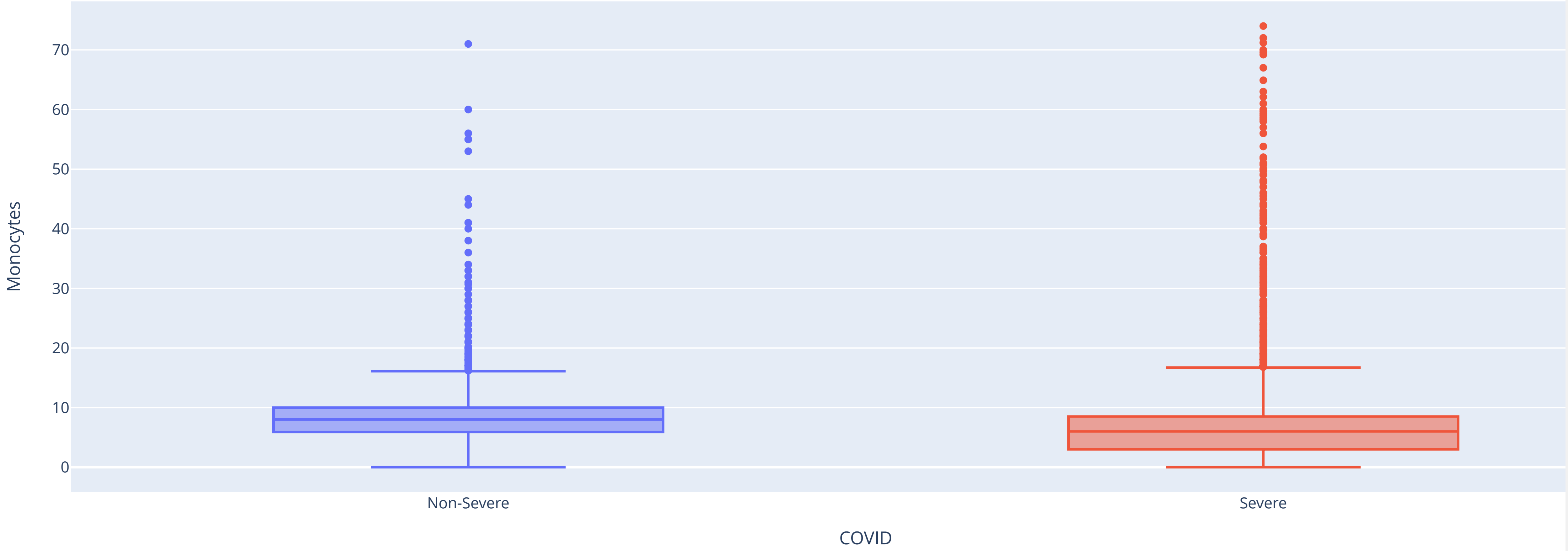

50
40
30
20
Eosinophils

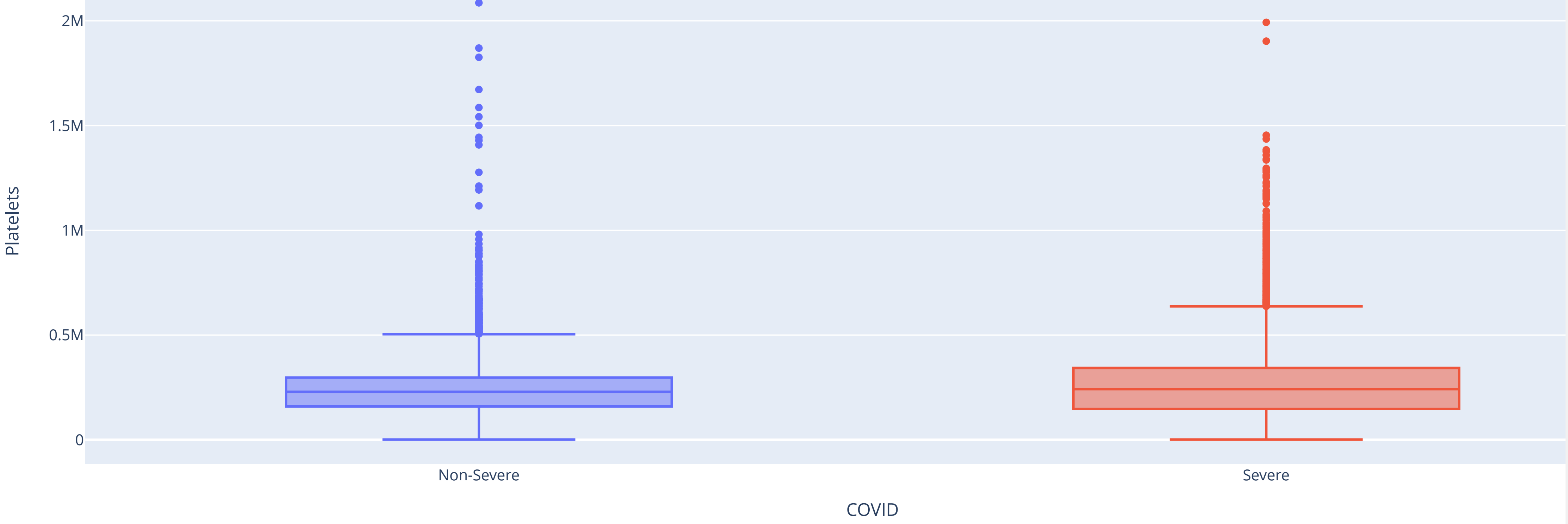

10
0
Non-Severe
Severe
COVID

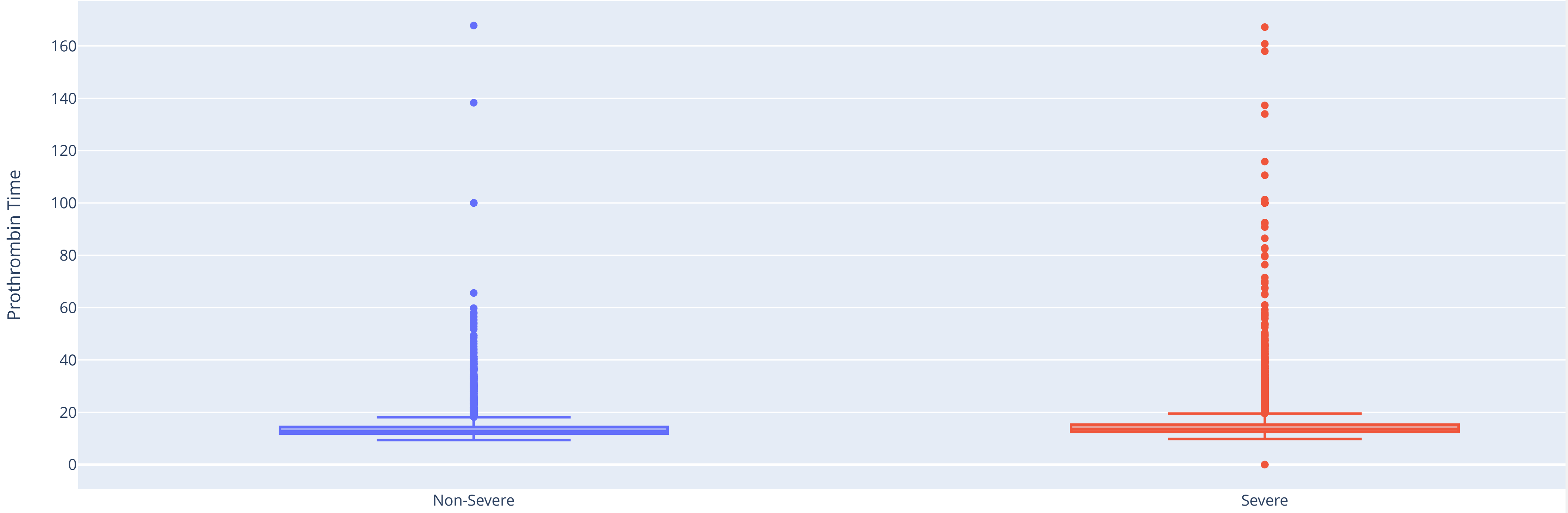

100
80
60
40
20
0
Lymphocytes
Non-Severe
Severe
COVID

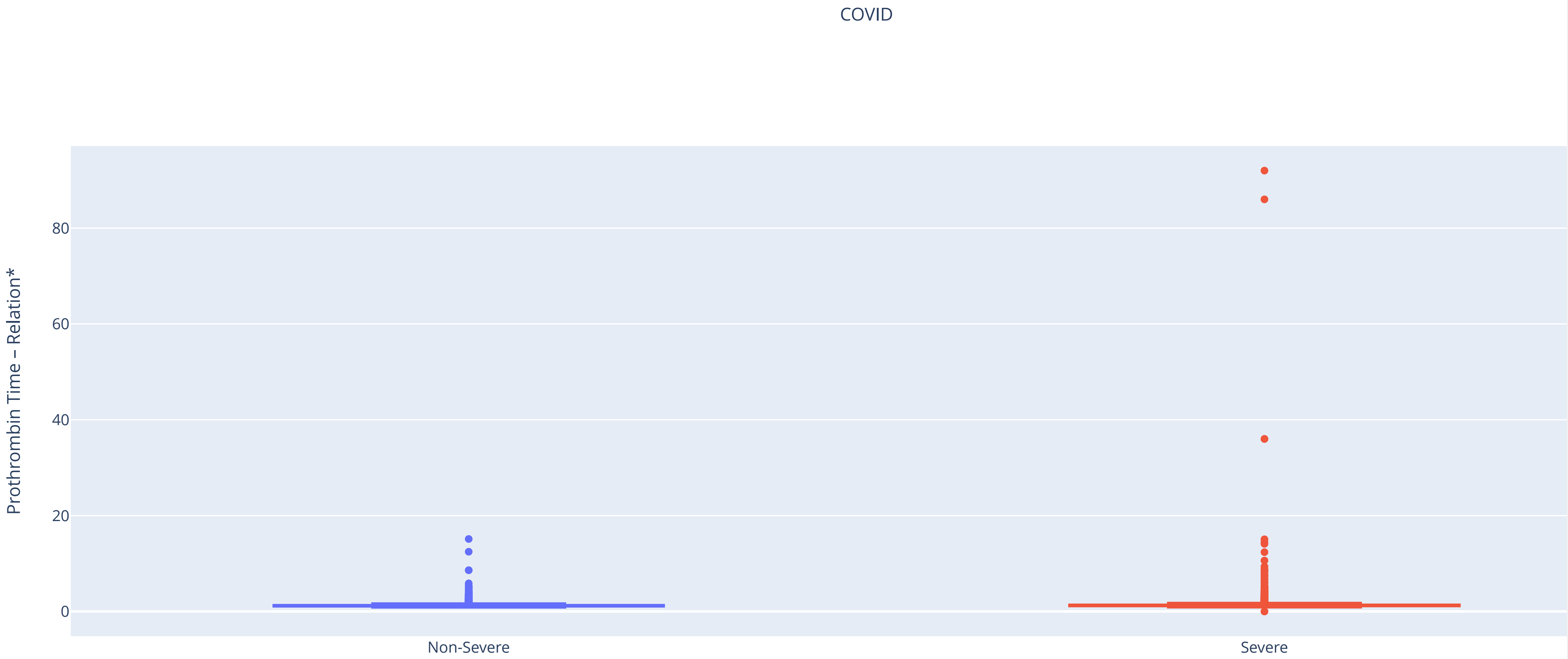
10
8
cytes

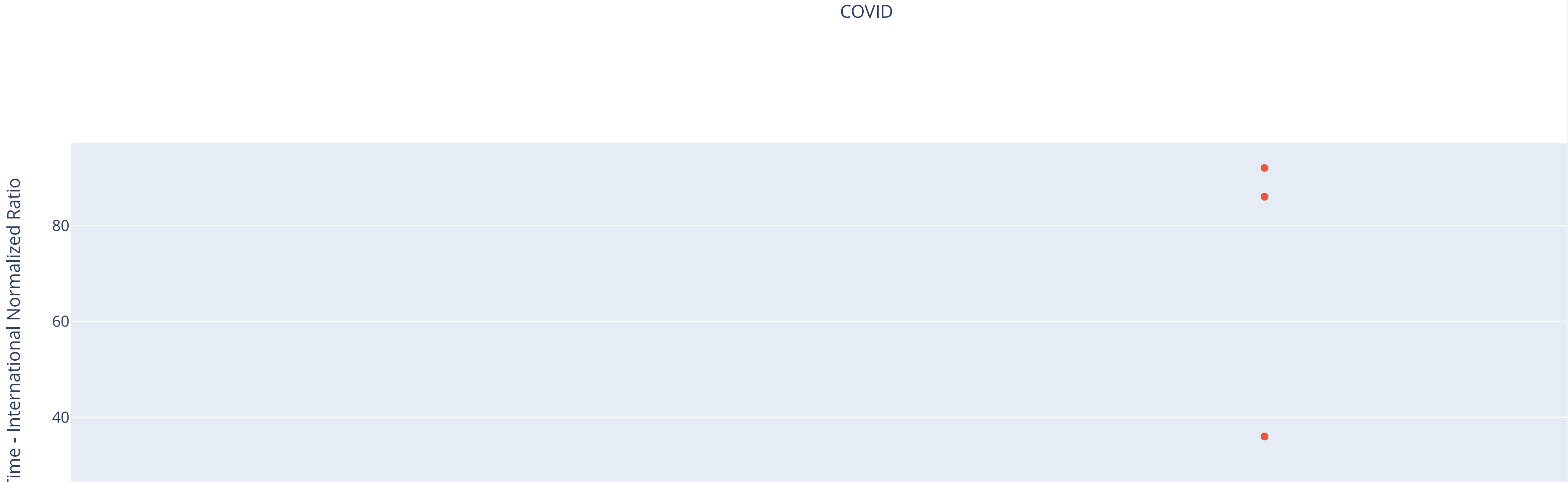

Atypical Lympho
6
4
2
0
Non-Severe
Severe
COVID

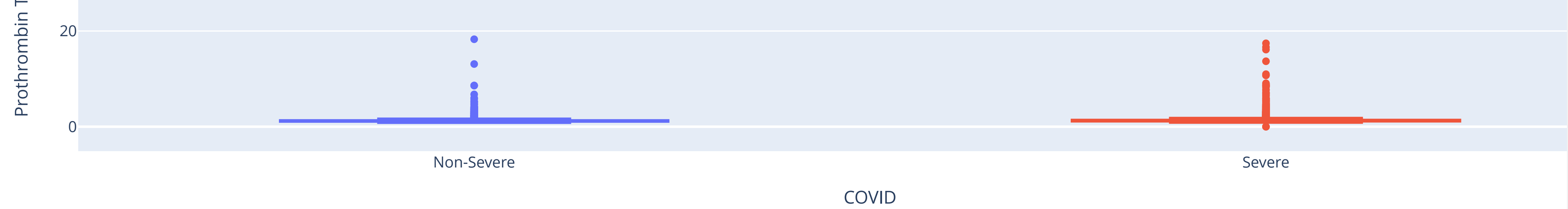

Monocytes
70
60
50
40
30
20
10
0
Non-Severe
Severe
COVID

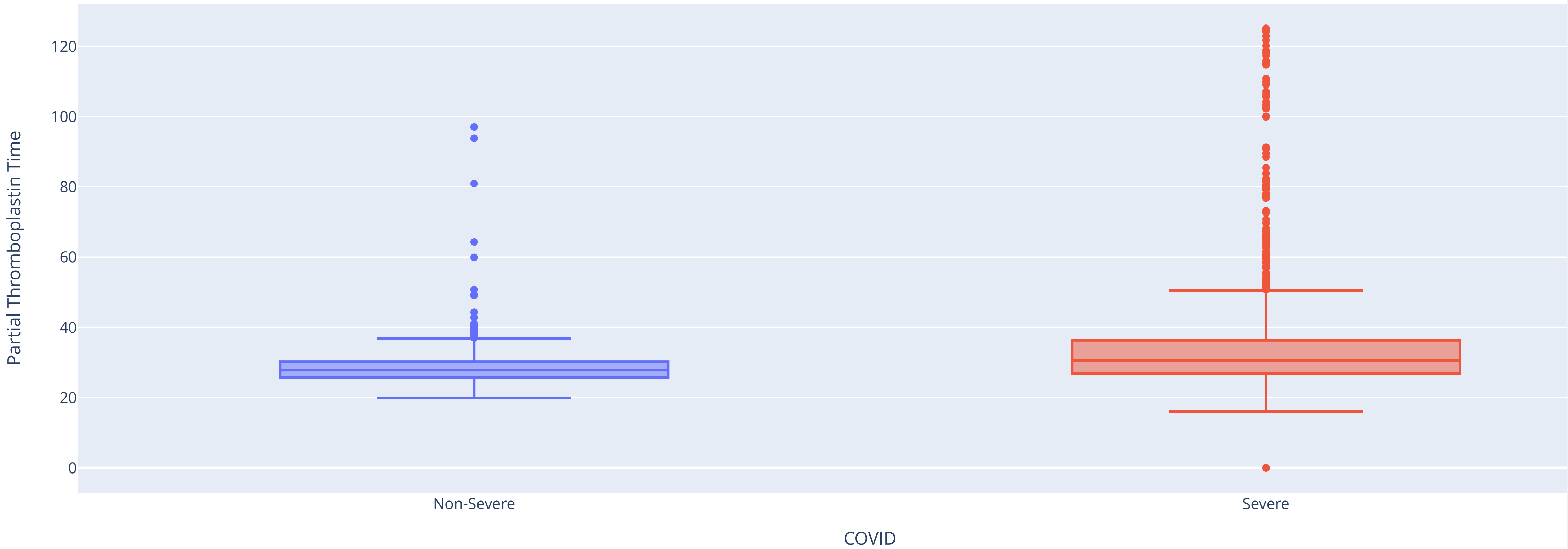

2M
1.5M
1M
0.5M
0
Platelets
Non-Severe
Severe
COVID

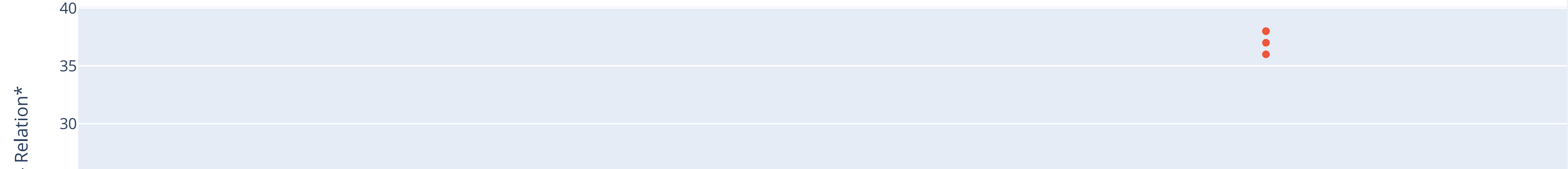

160
140
120
100
80
60
40
20
0
Prothrombin Time
Non-Severe
Severe

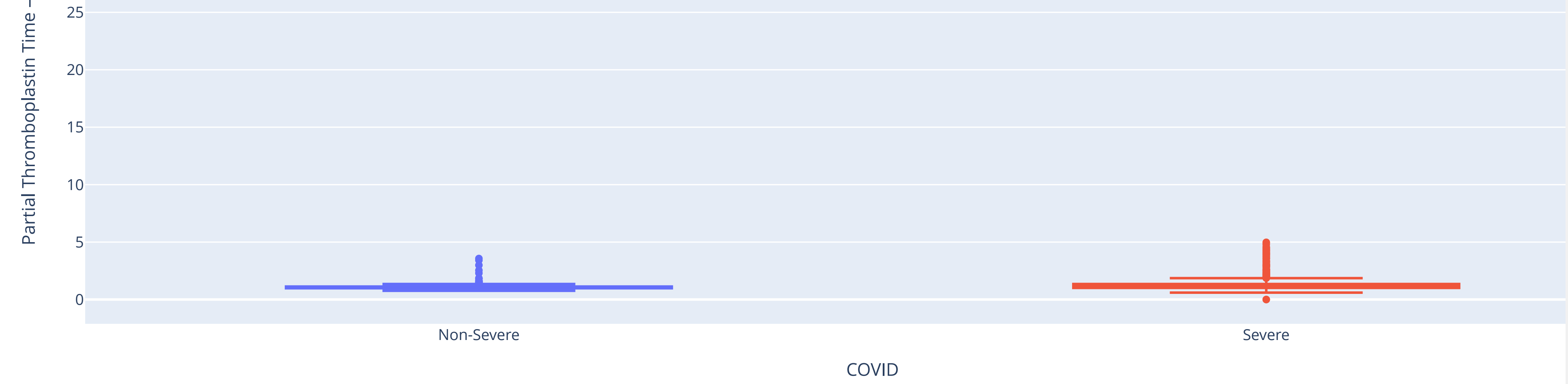

COVID
Prothrombin Time – Relation*
80
60
40
20
0
Non-Severe
Severe

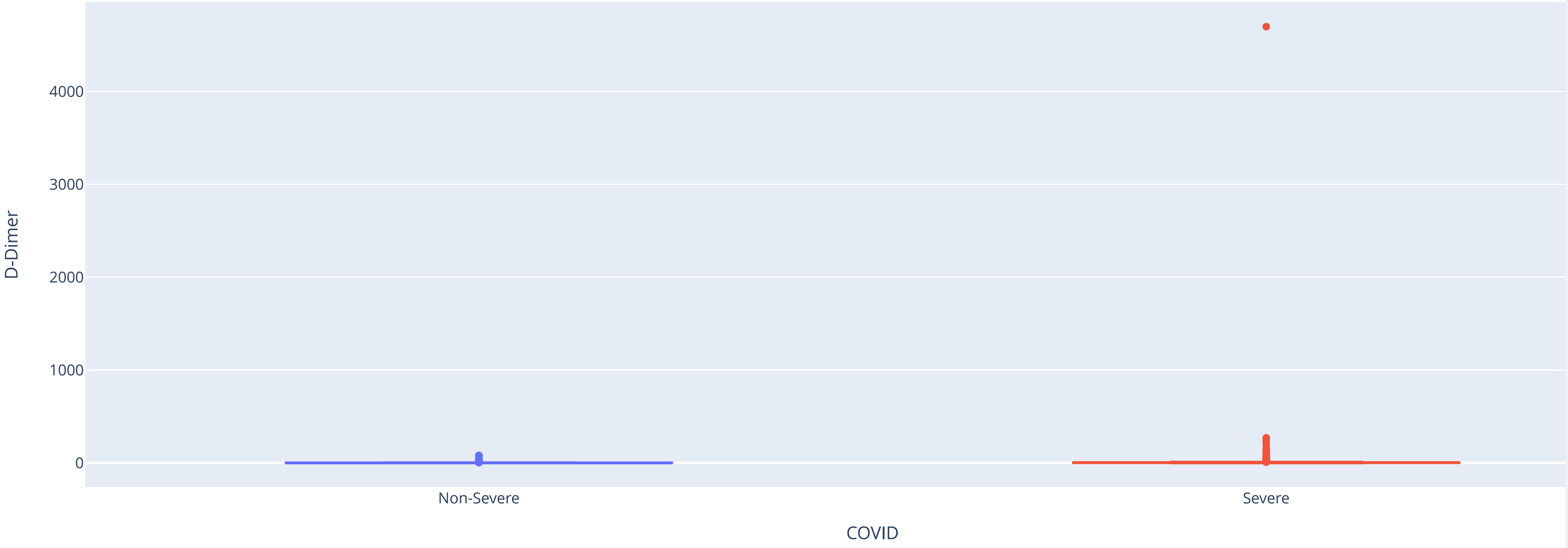

COVID
ime - International Normalized Ratio
80
60
40

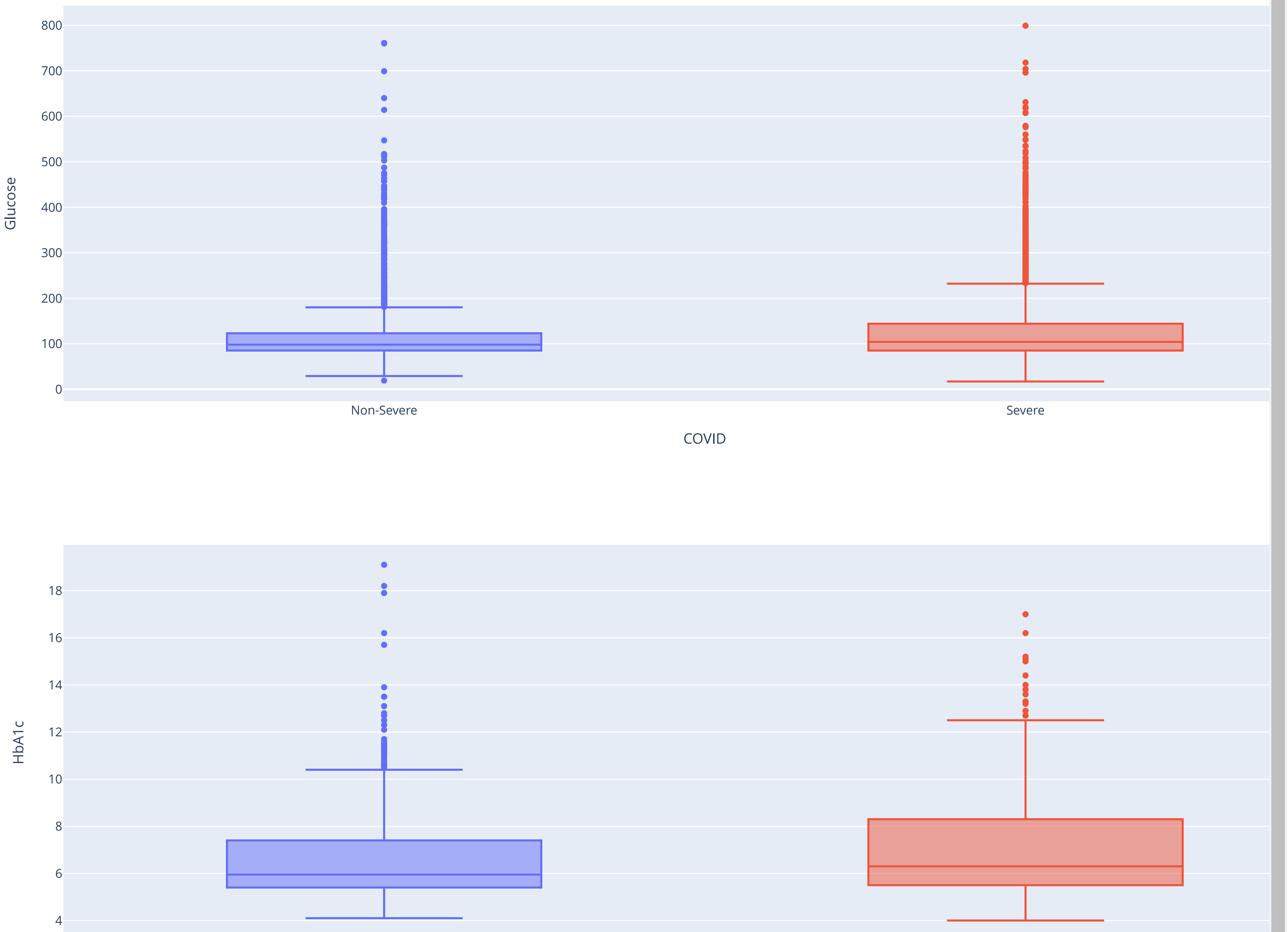

Prothrombin T
20
0
Non-Severe
Severe
COVID


Partial Thromboplastin Time
120
100
80
60
40
20
0
Non-Severe
Severe
COVID

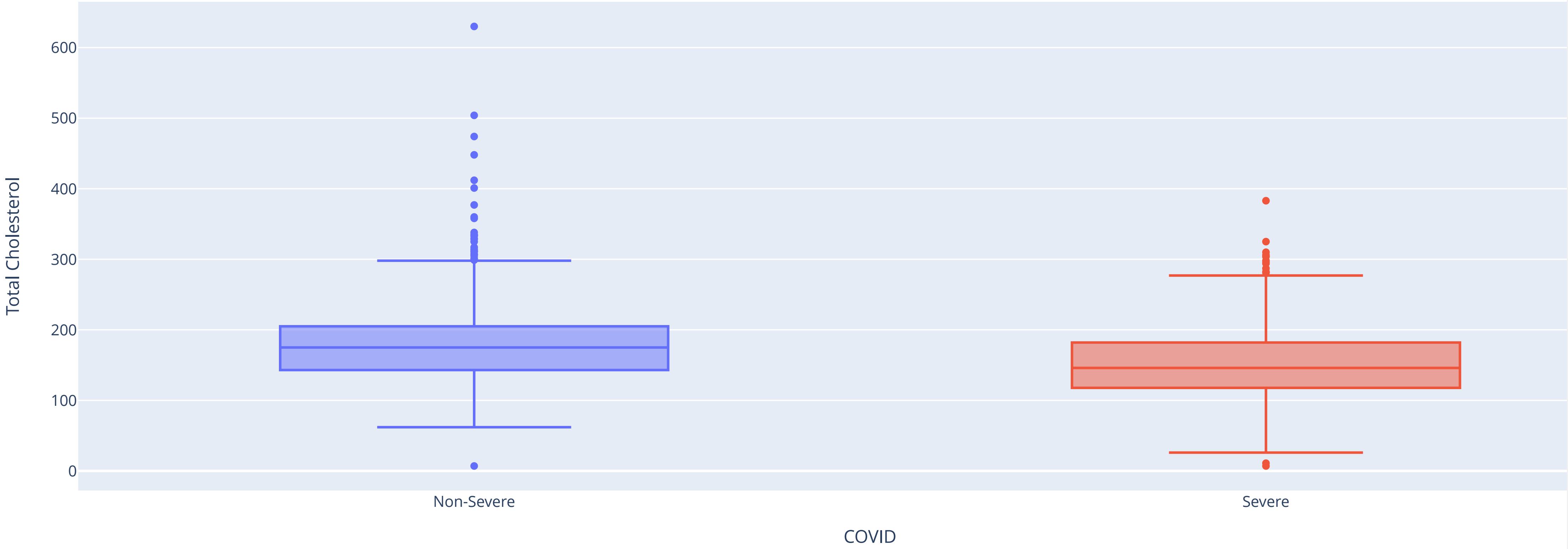

Relation*
40
35
30

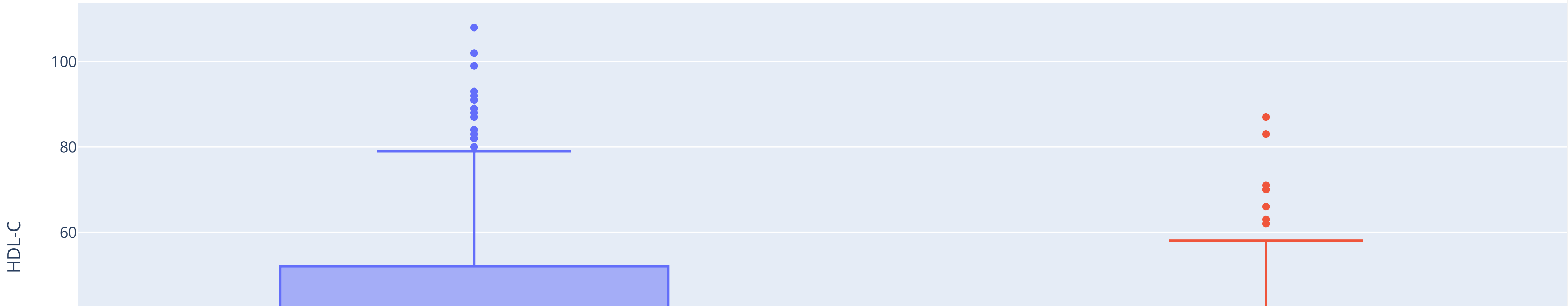

Partial Thromboplastin Time –
25
20
15
10
5
0
Non-Severe
Severe
COVID

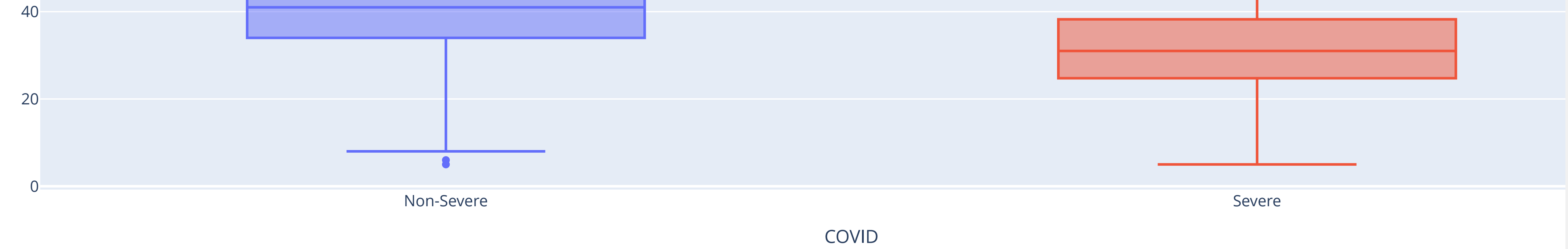

D-Dimer
4000
3000
2000
1000
0
Non-Severe
Severe
COVID

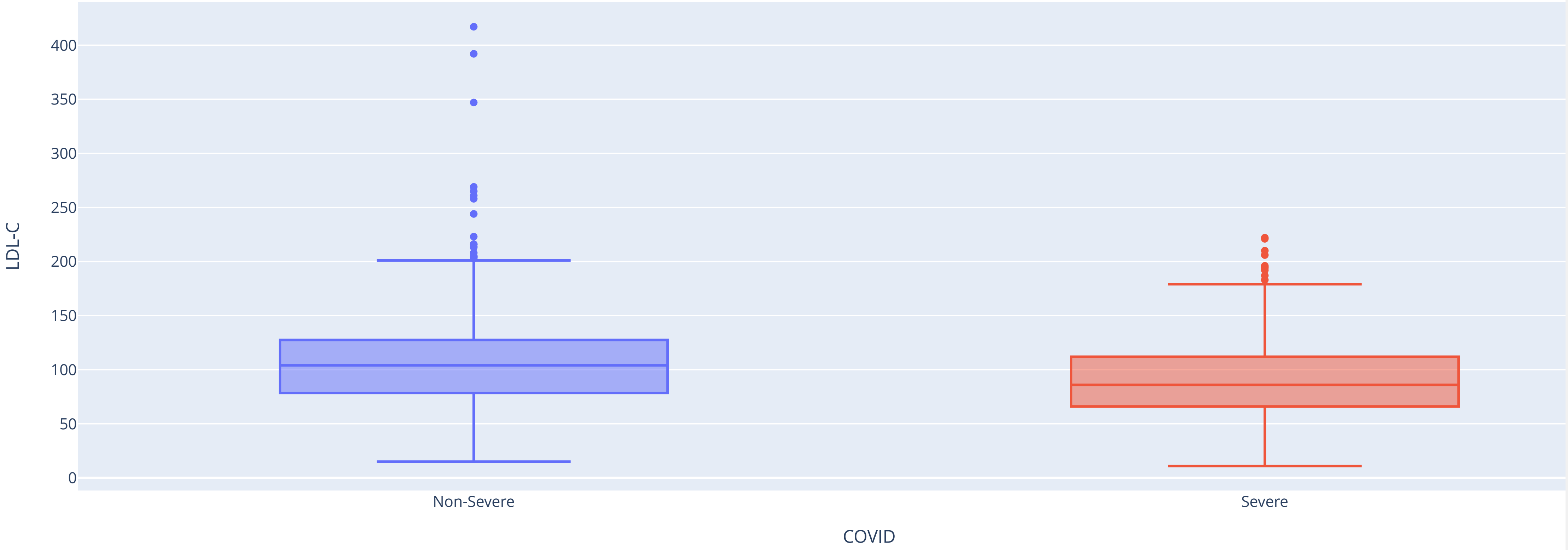

800
700
600
500
400
300
200
100
0
Glucose
Non-Severe
Severe
COVID
18
16
14
12
10
8
6
4
HbA1c

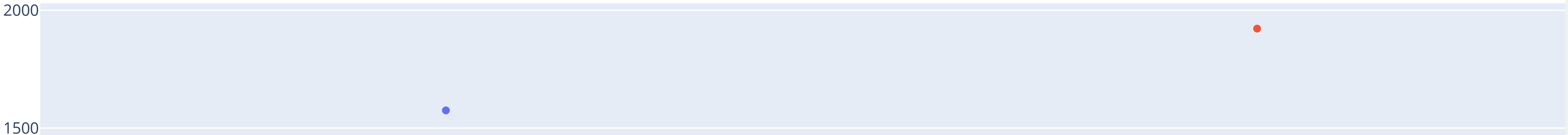
Non-Severe
Severe
COVID

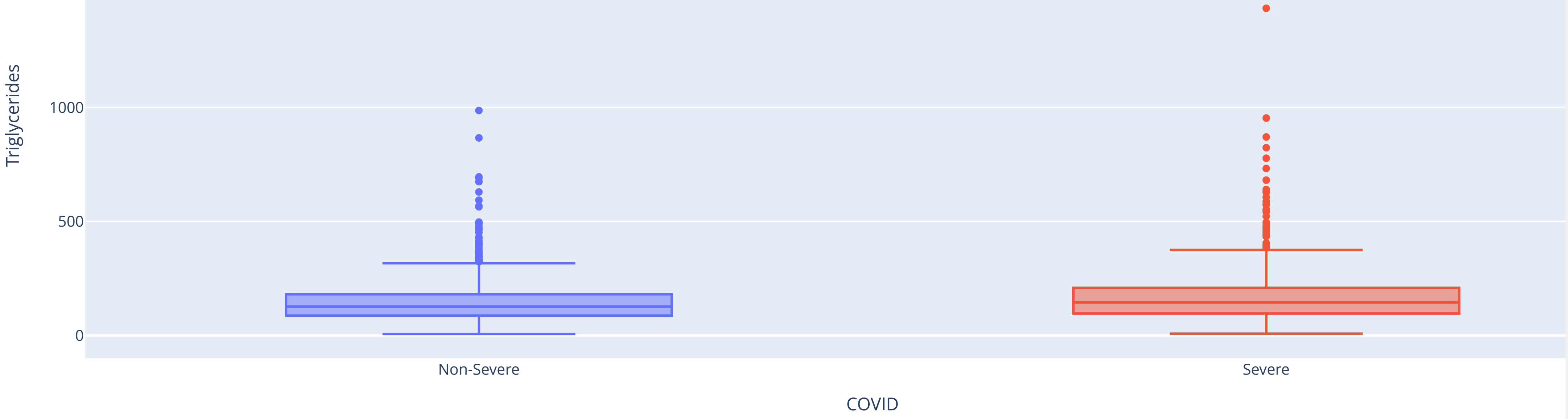

Total Cholesterol
600
500
400
300
200
100
0
Non-Severe
Severe
COVID

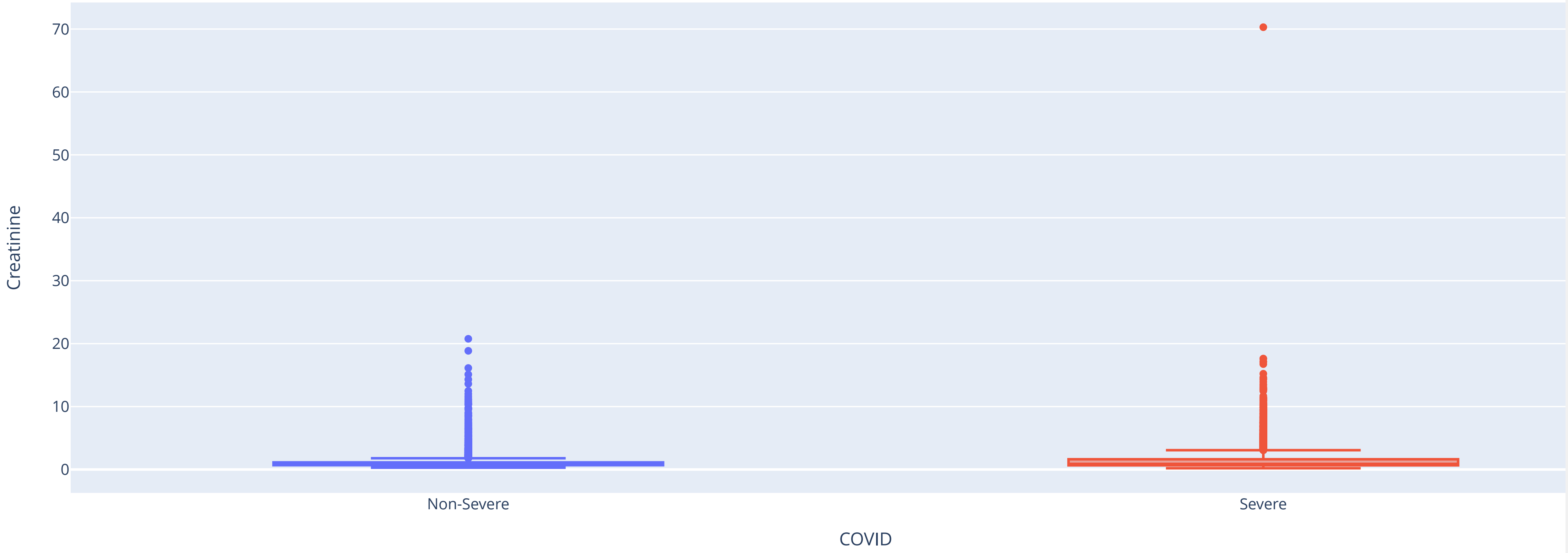

HDL-C
100
80
60

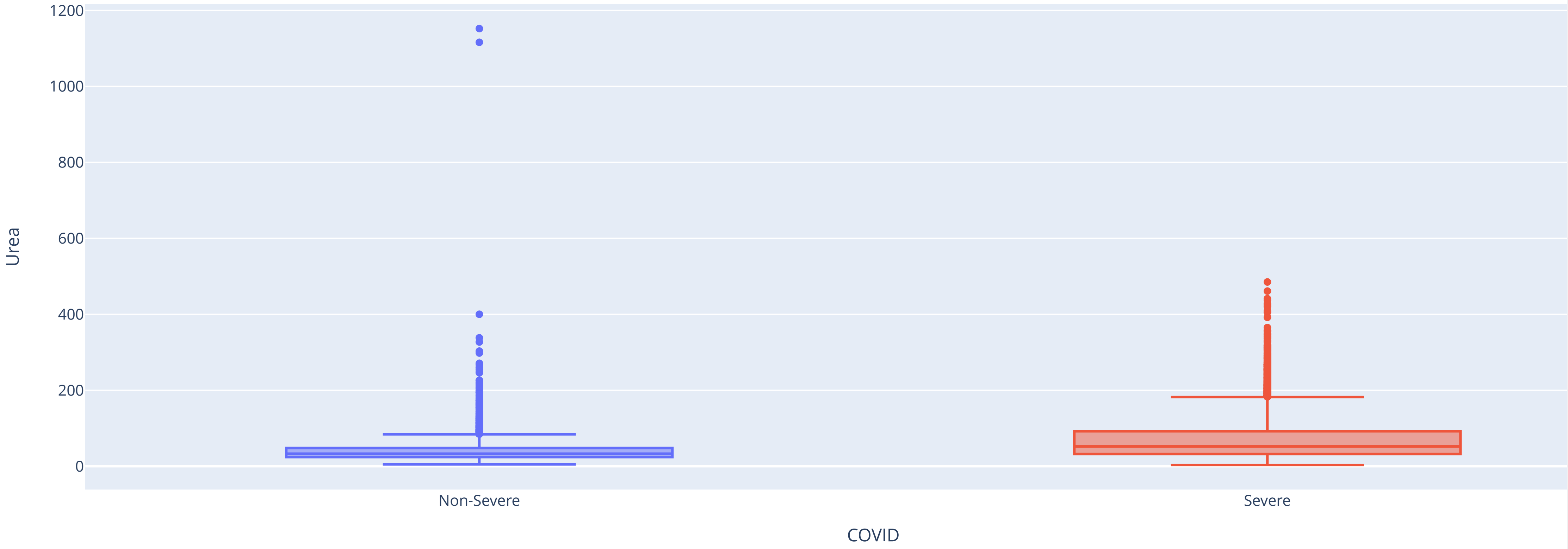

40
20
0
Non-Severe
Severe
COVID

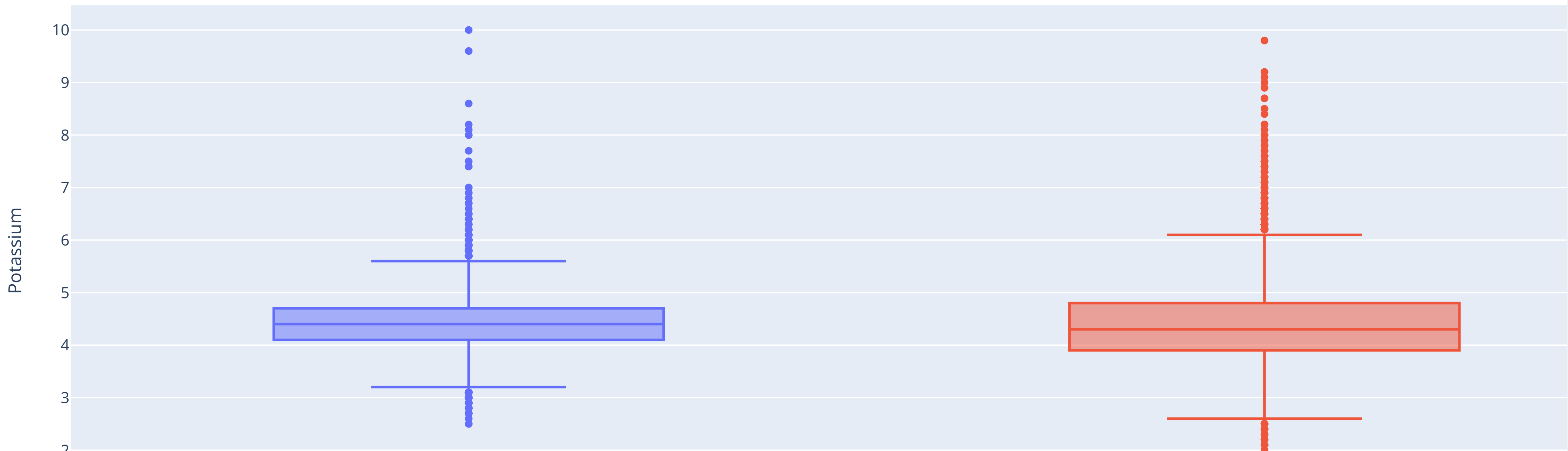

400
350
300
250
200
150
100
50
0
LDL-C
Non-Severe
Severe
COVID

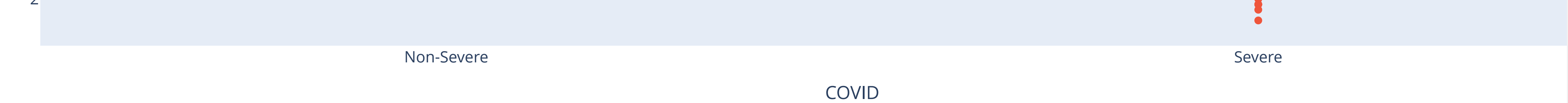

2000
1500

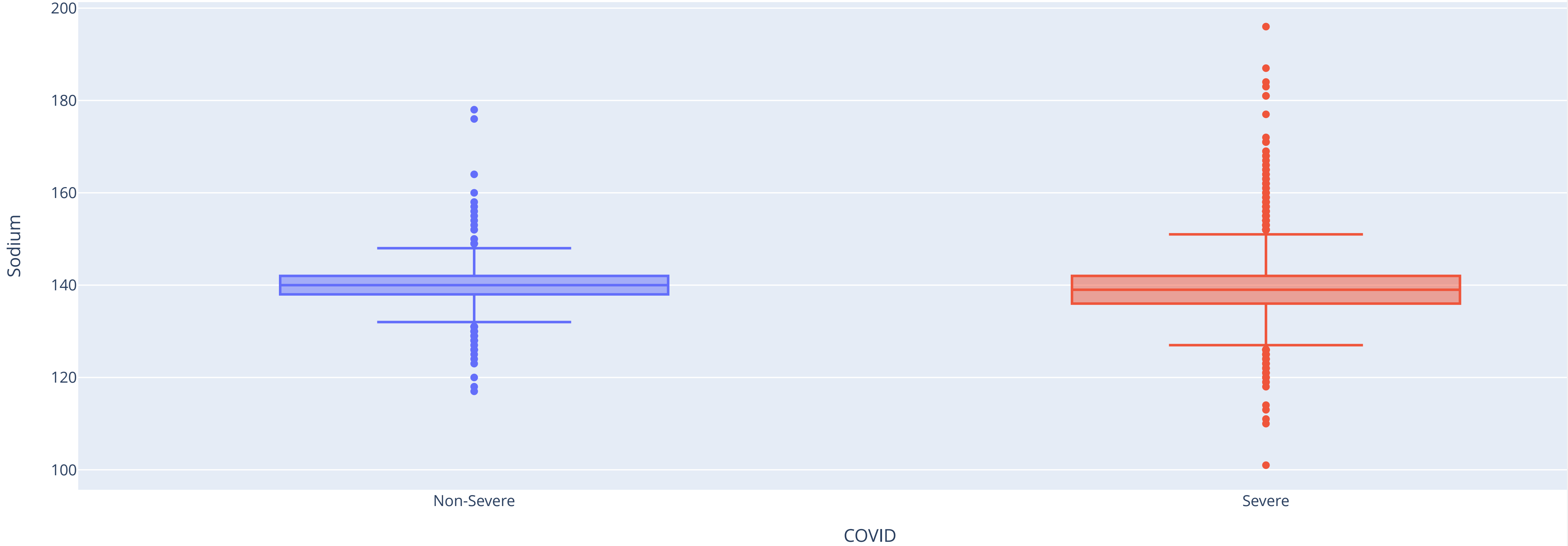

Triglycerides
1000
500
0
Non-Severe
Severe
COVID

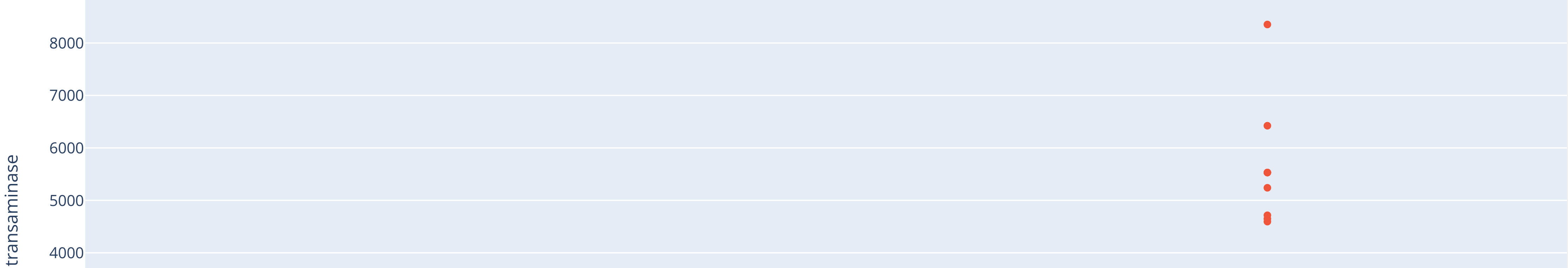

Creatinine
70
60
50
40
30
20
10
0
Non-Severe
Severe
COVID

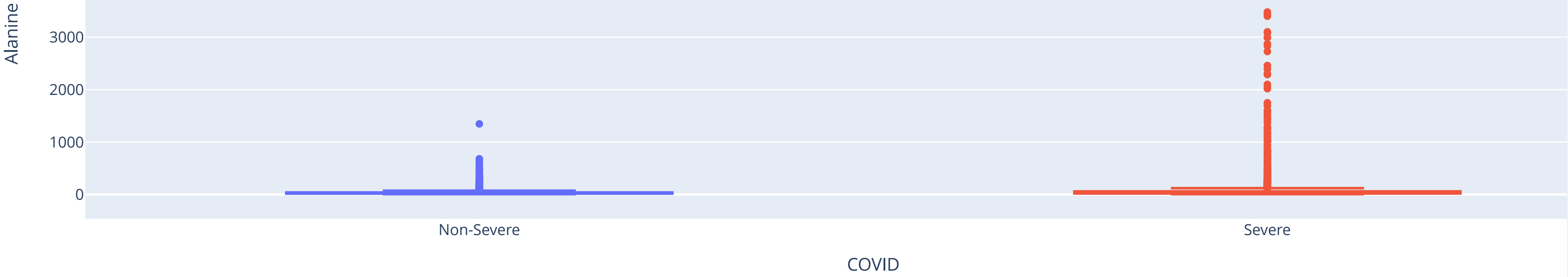

1200
1000
800
600
400
200
0
Urea
Non-Severe
Severe
COVID

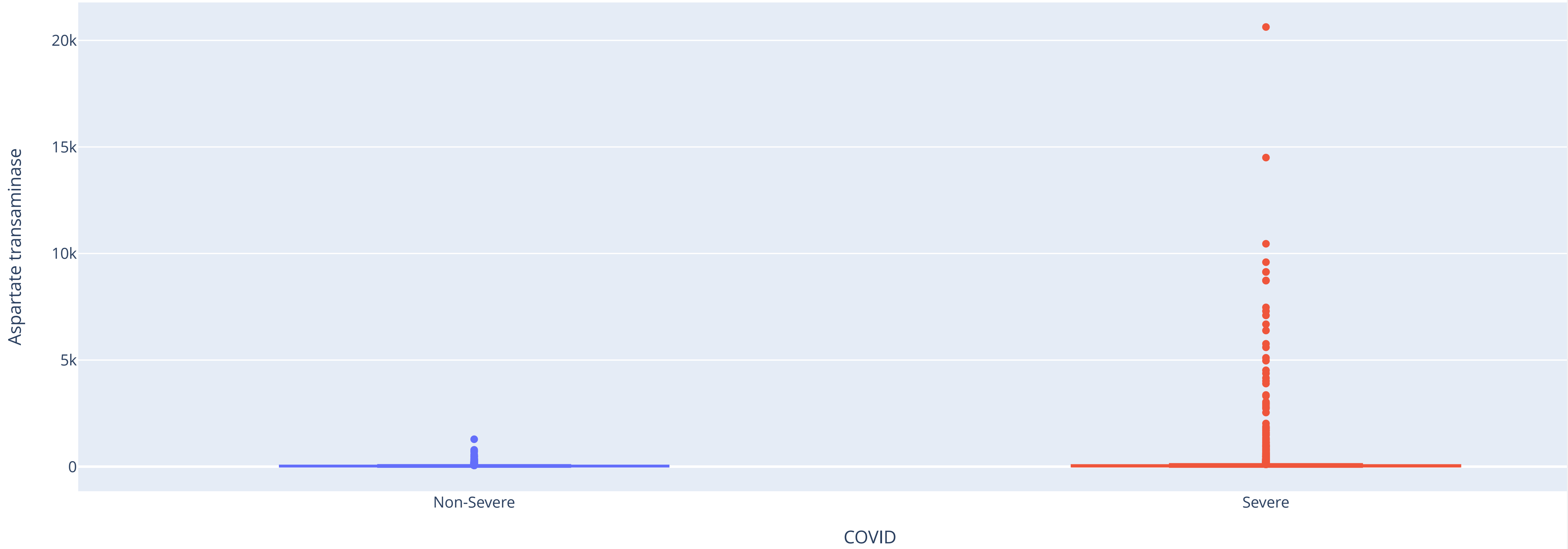

10
9
8
7
6
5
4
3
2
Potassium

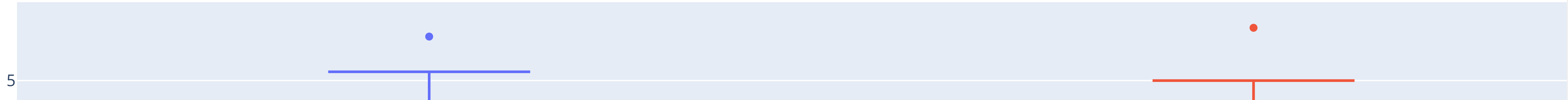

2
Non-Severe
Severe
COVID

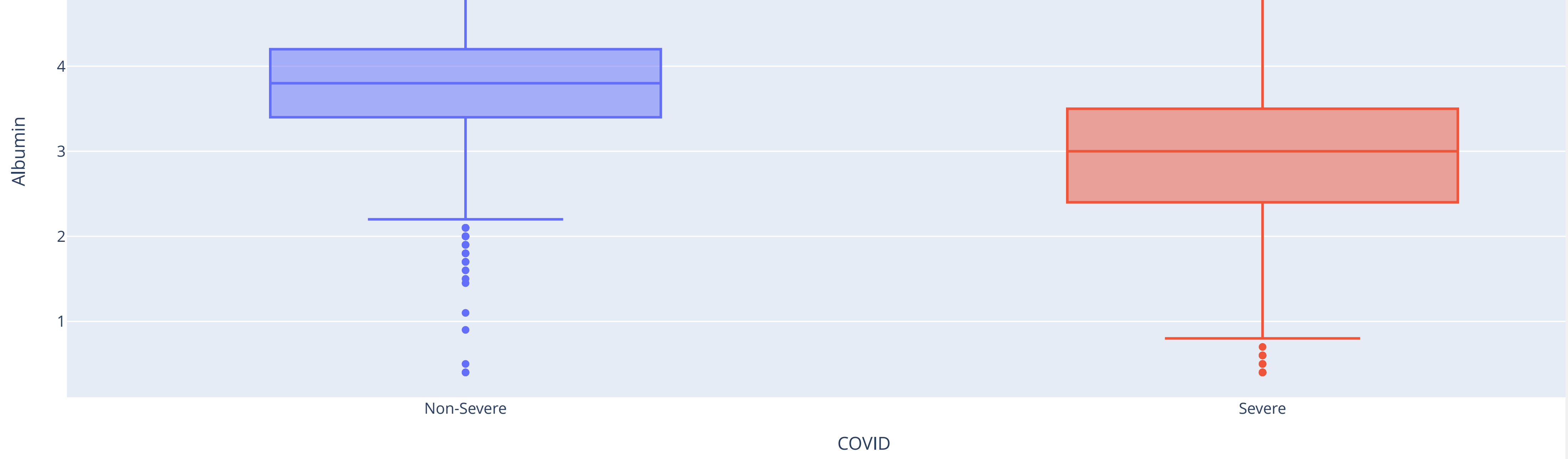

200
180
160
140
120
100
Sodium
Non-Severe
Severe
COVID

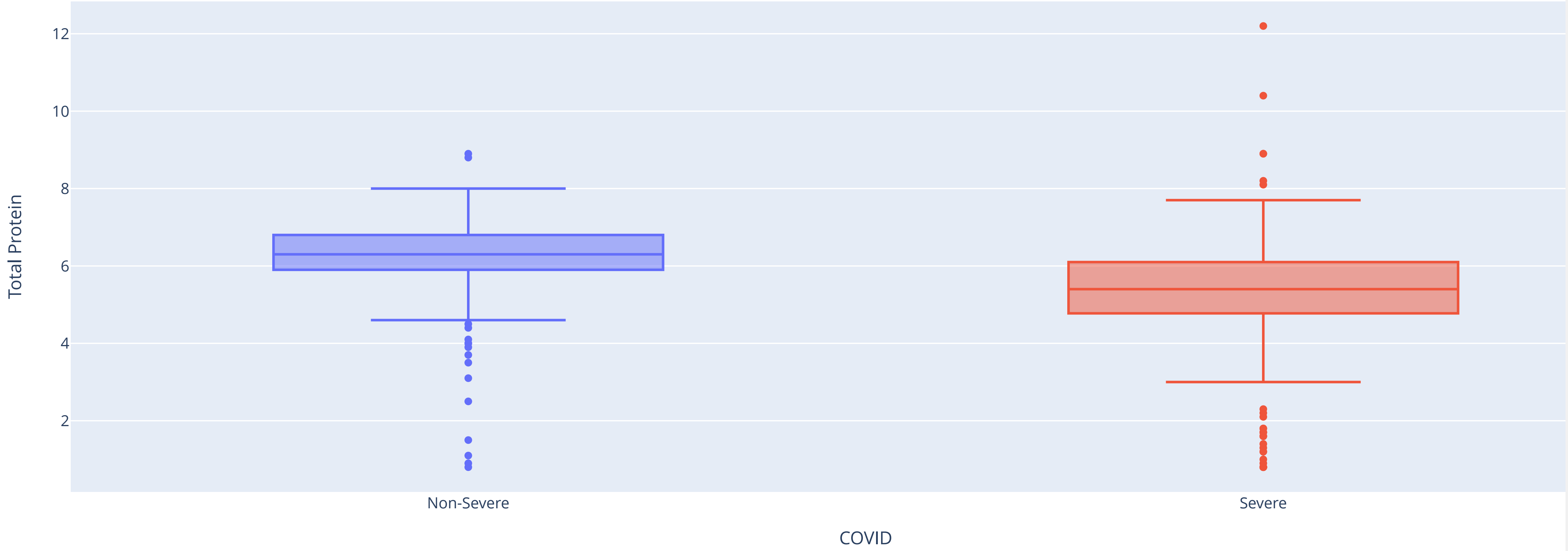

8000
7000
6000
5000
4000
transaminase

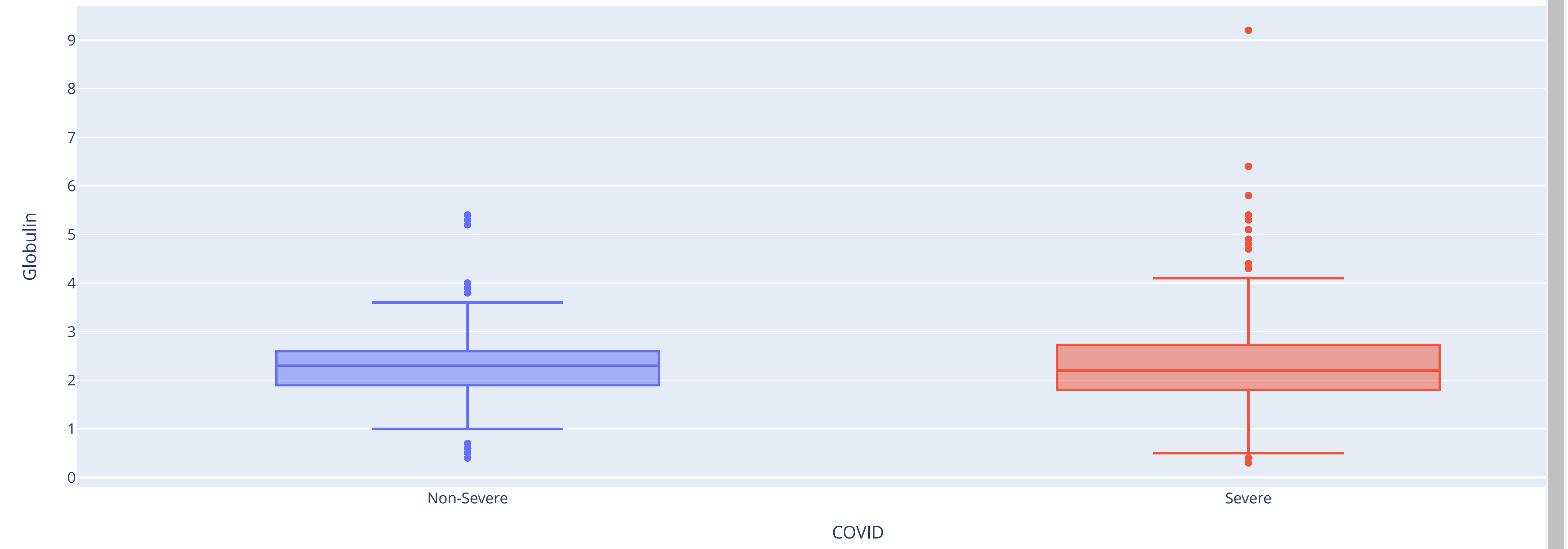

Alanine
3000
2000
1000
0
Non-Severe
Severe
COVID

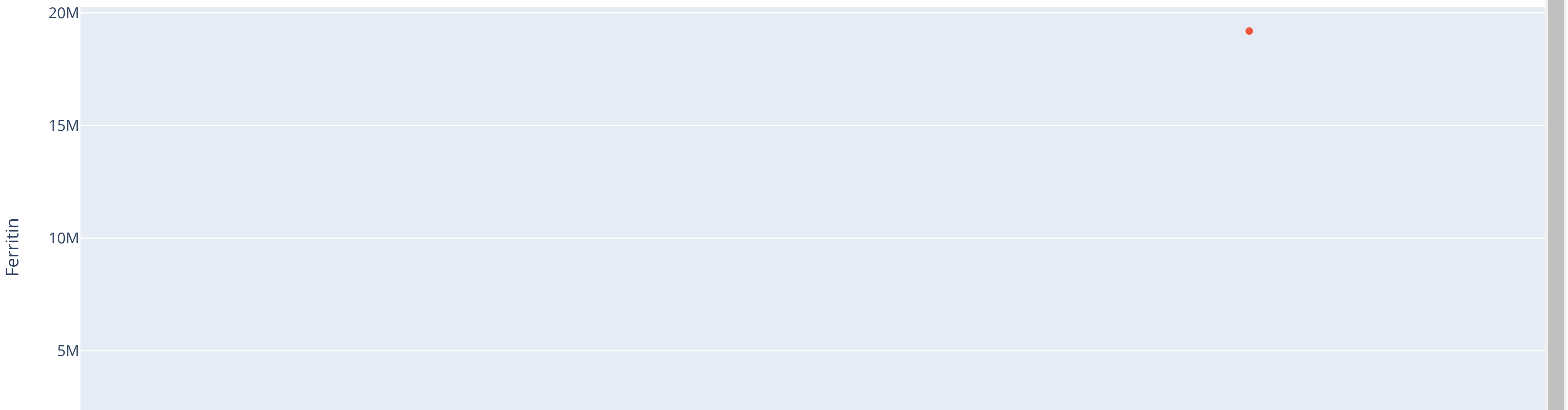

Aspartate transaminase
20k
15k
10k
5k
0
Non-Severe
Severe
COVID

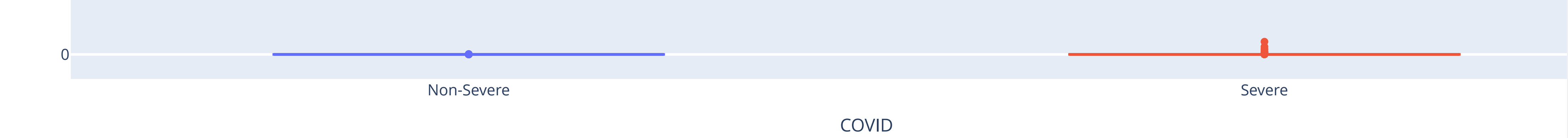

5

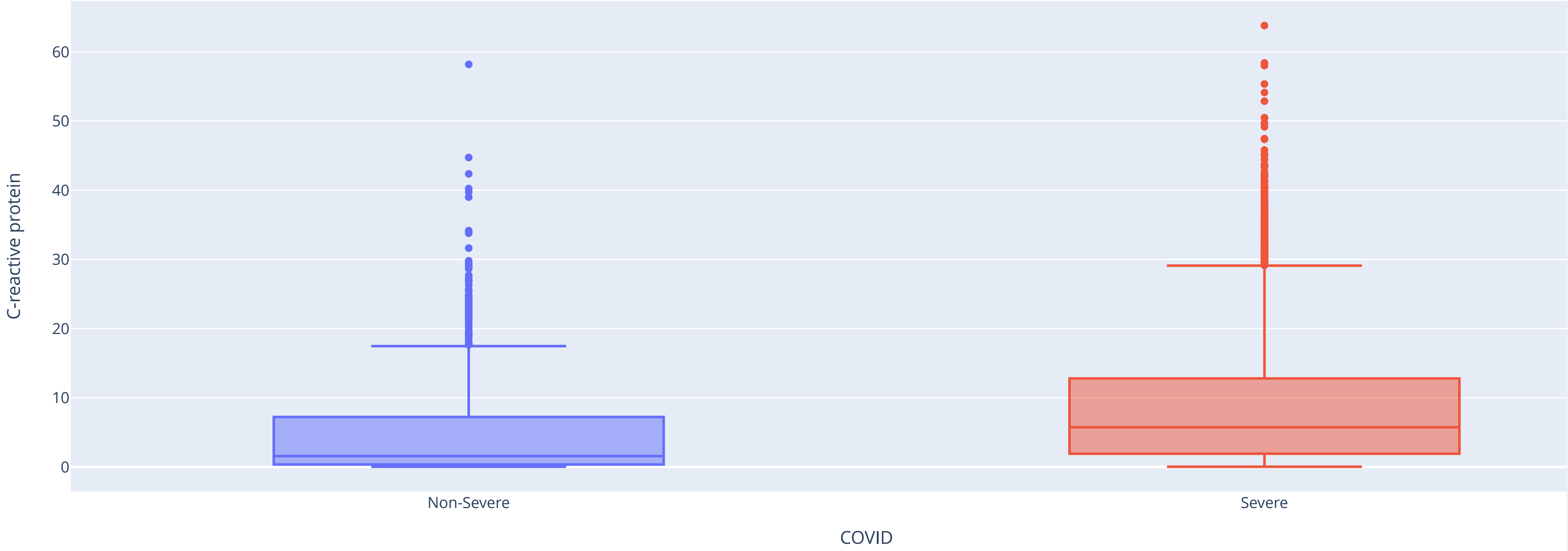

Albumin
4
3
2
1
Non-Severe
Severe
COVID

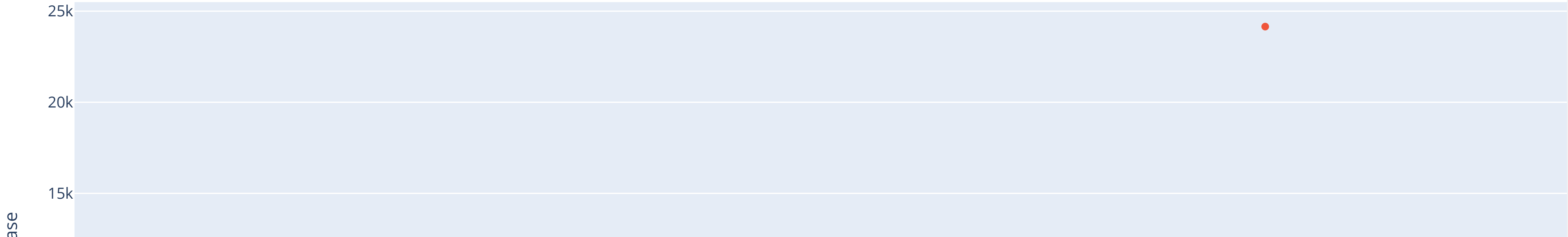

Total Protein
12
10
8
6
4
2
Non-Severe
Severe
COVID

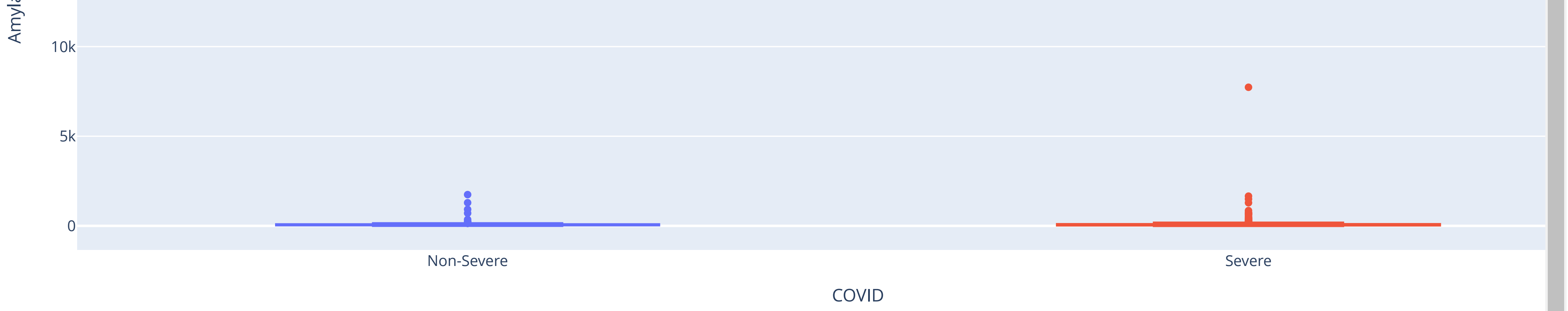

Globulin
9
8
7
6
5
4
3
2
1
0
Non-Severe
Severe
COVID

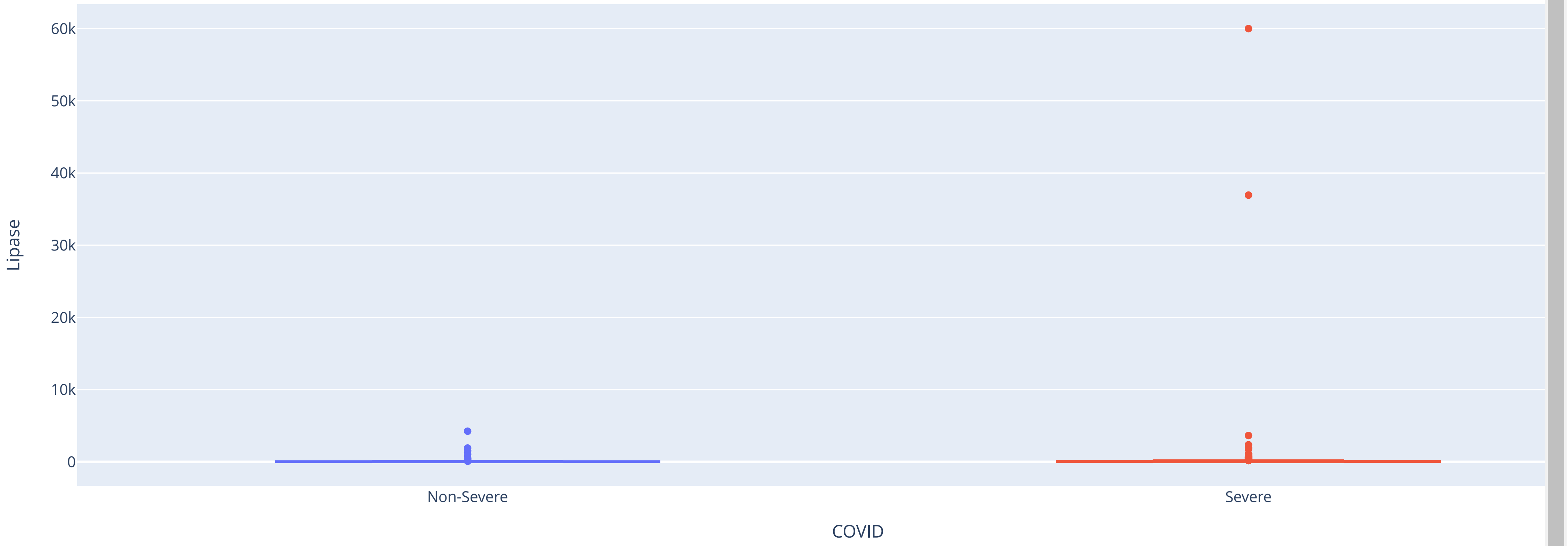

Ferritin
20M
15M
10M
5M

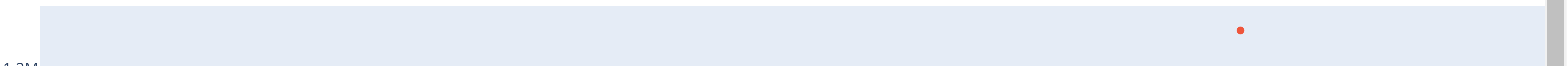

0
Non-Severe
Severe
COVID

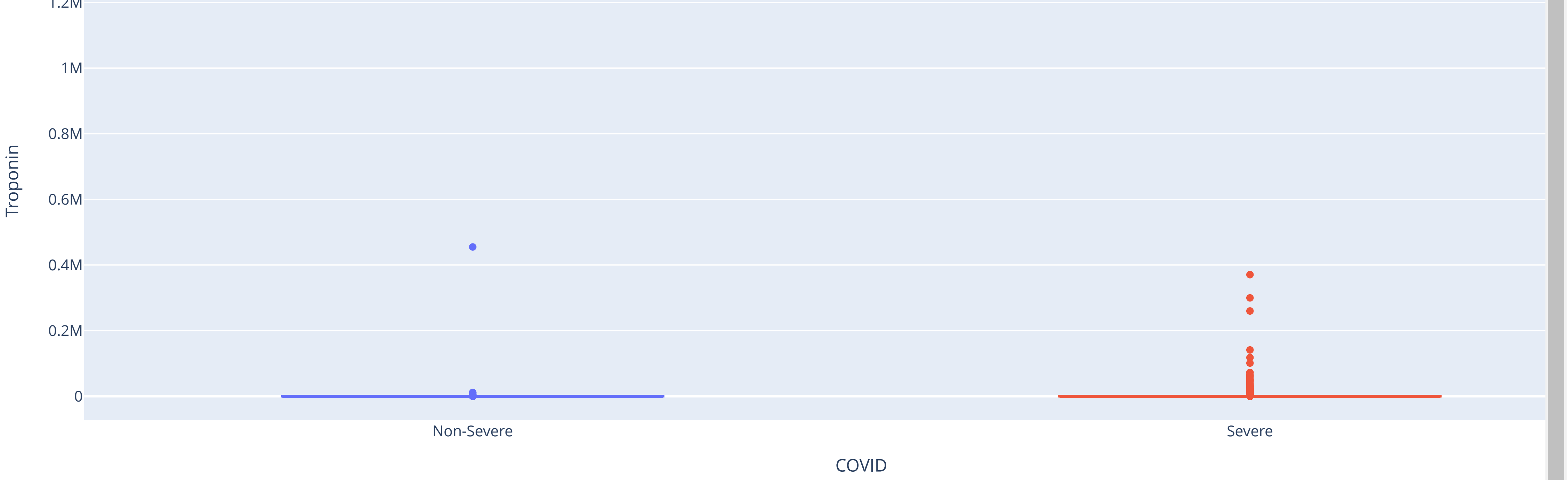

C-reactive protein
60
50
40
30
20
10
0
Non-Severe
Severe
COVID

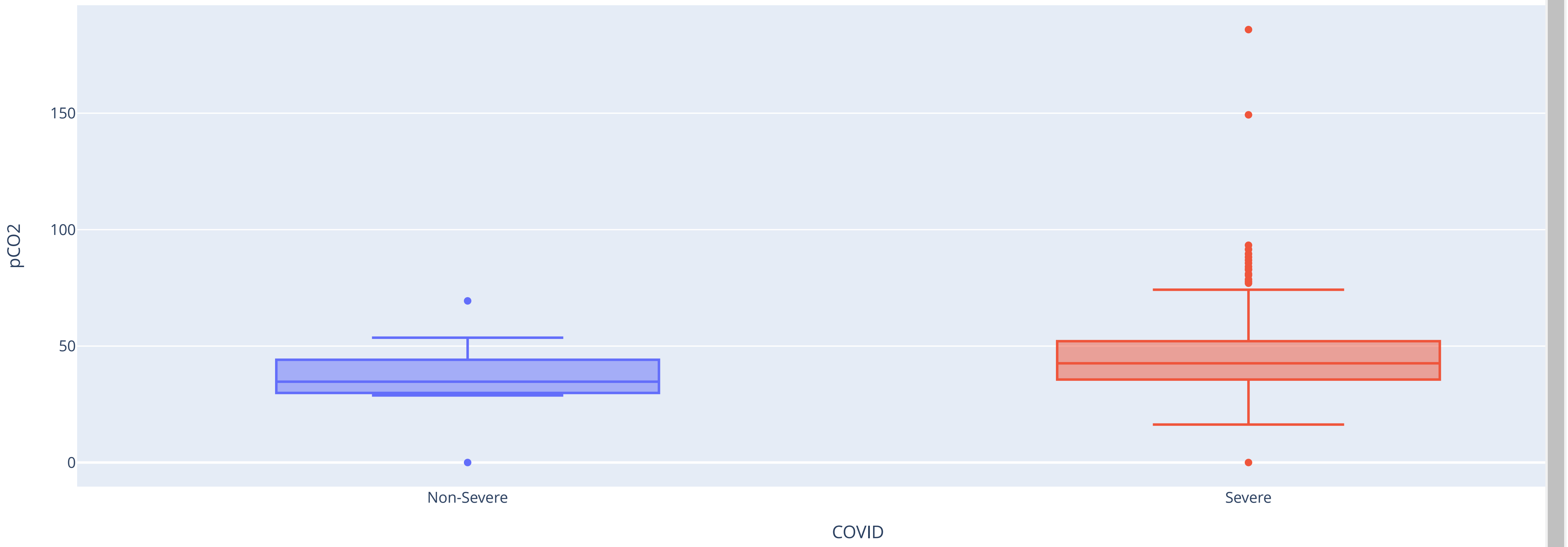

25k
20k
15k
ase

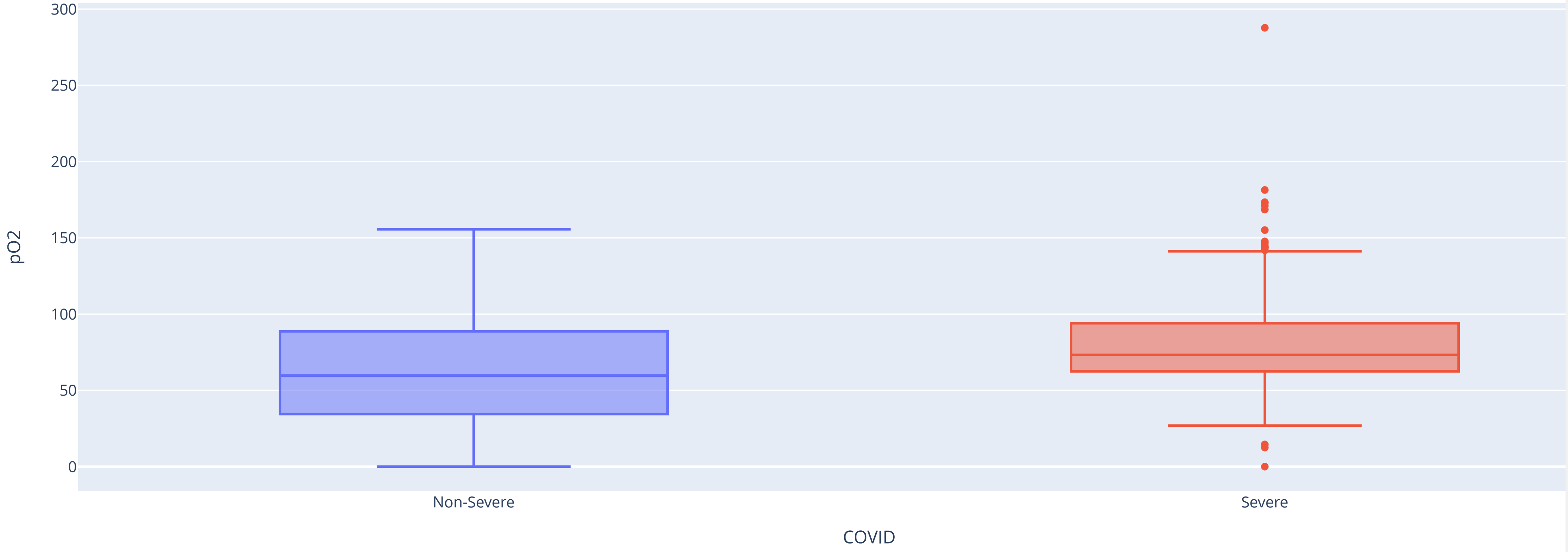

Amyla
10k
5k
0
Non-Severe
Severe
COVID

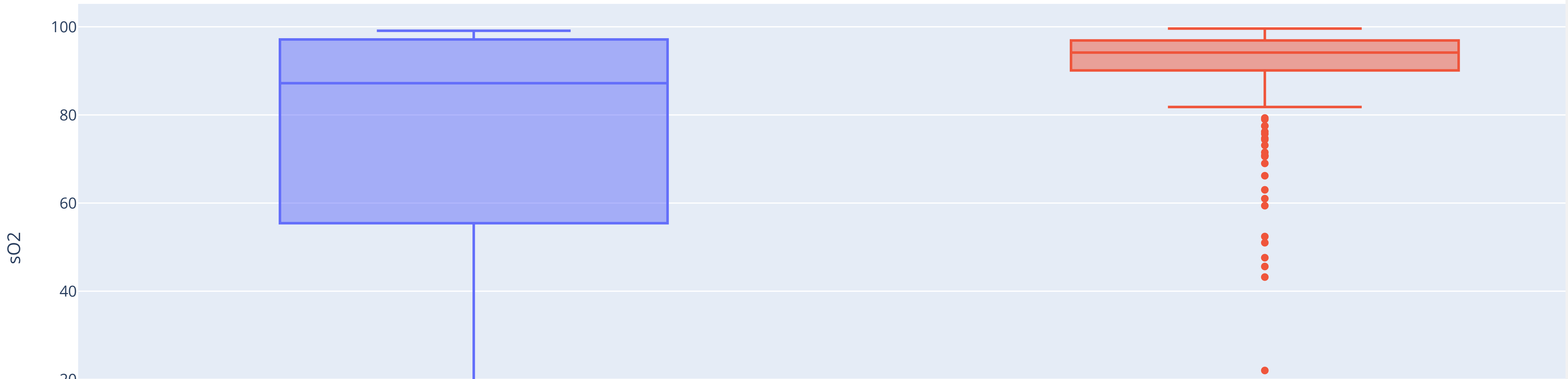

Lipase
60k
50k
40k
30k
20k
10k
0
Non-Severe
Severe
COVID

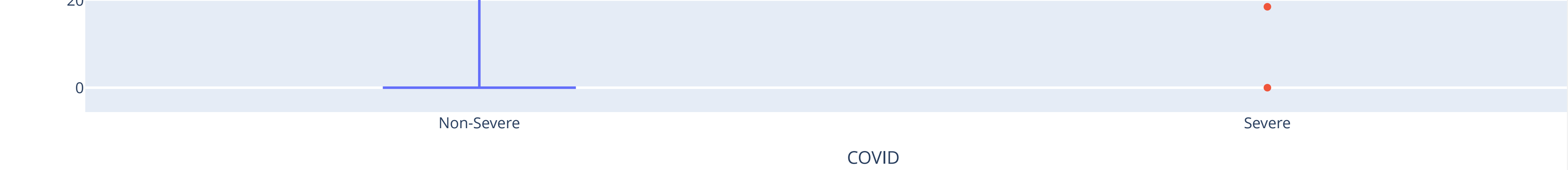


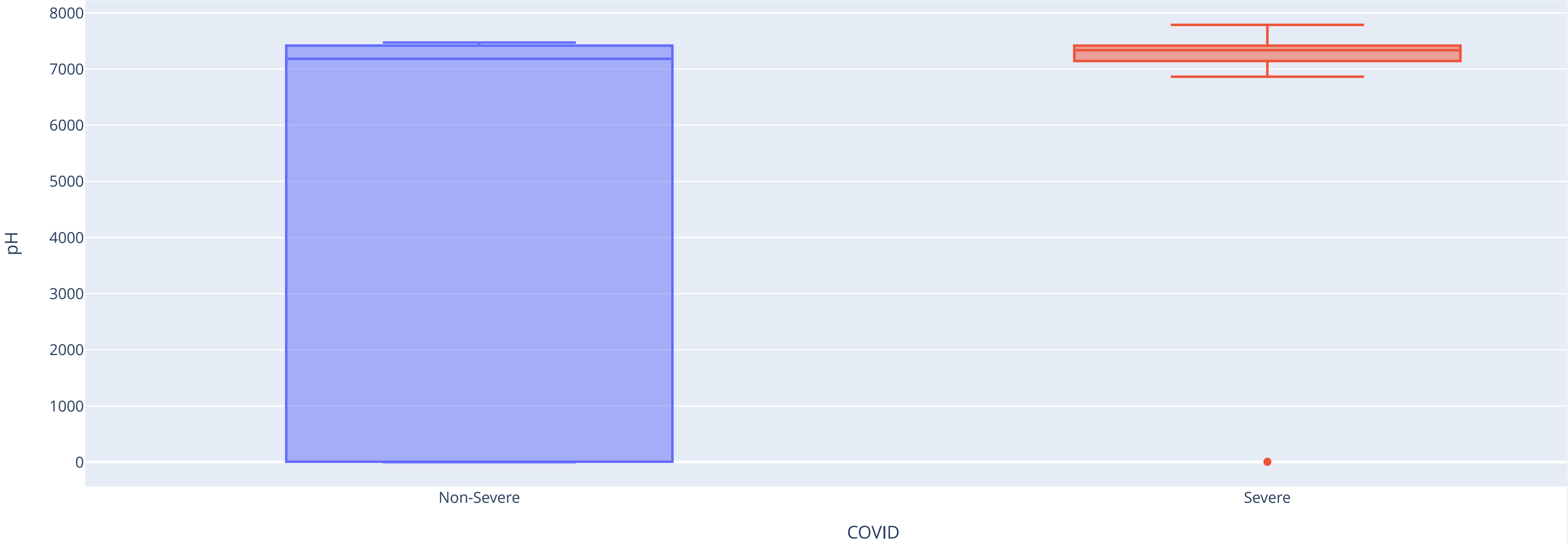

1.2M
1M
0.8M
0.6M
0.4M
0.2M
0
Troponin
Non-Severe
Severe
COVID

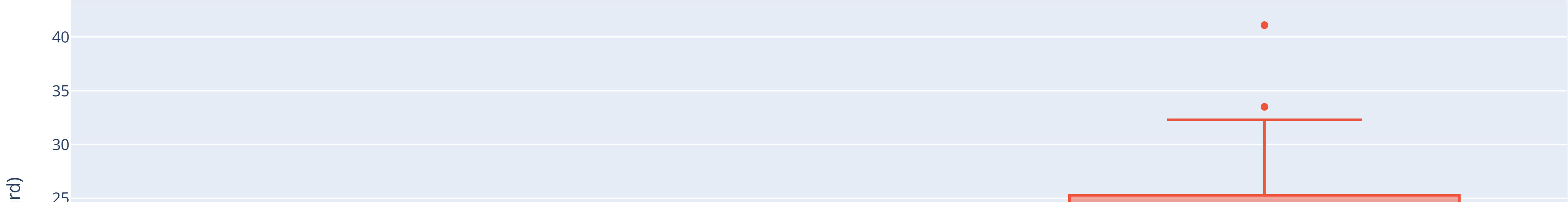

150
100
50
0
pCO2
Non-Severe
Severe
COVID

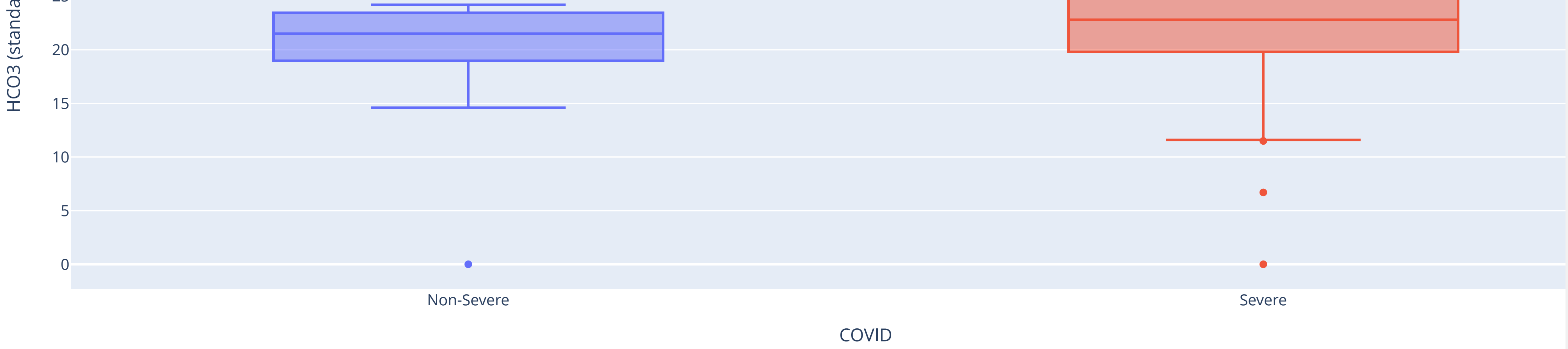

300
250
200
150
100
50
0
pO2
Non-Severe
Severe
COVID

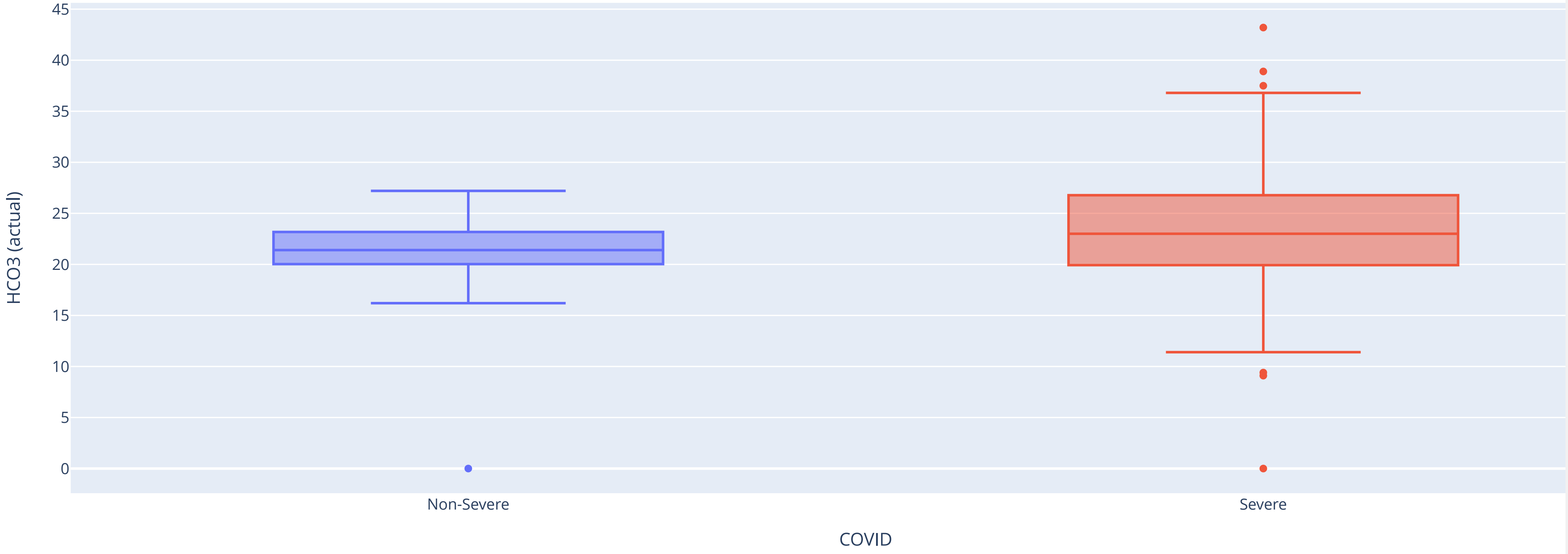

100
80
60
40
20
sO2

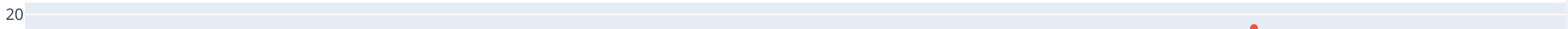

20
0
Non-Severe
Severe
COVID

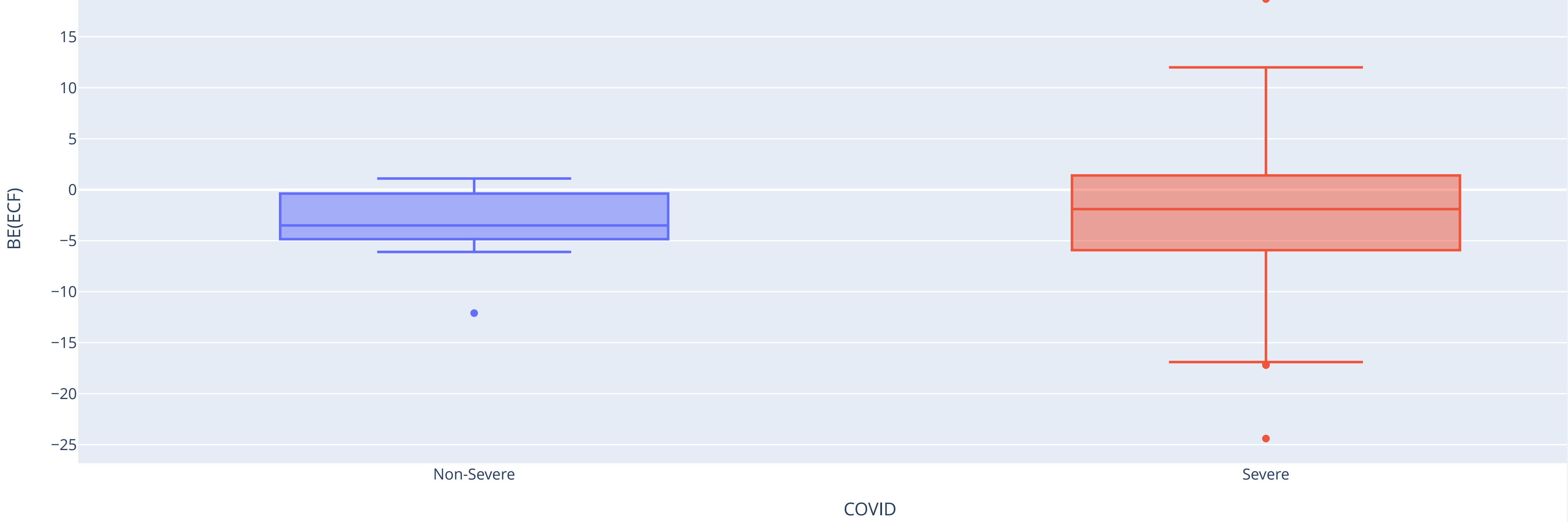

8000
7000
6000
5000
4000
3000
2000
1000
0
pH
Non-Severe
Severe
COVID

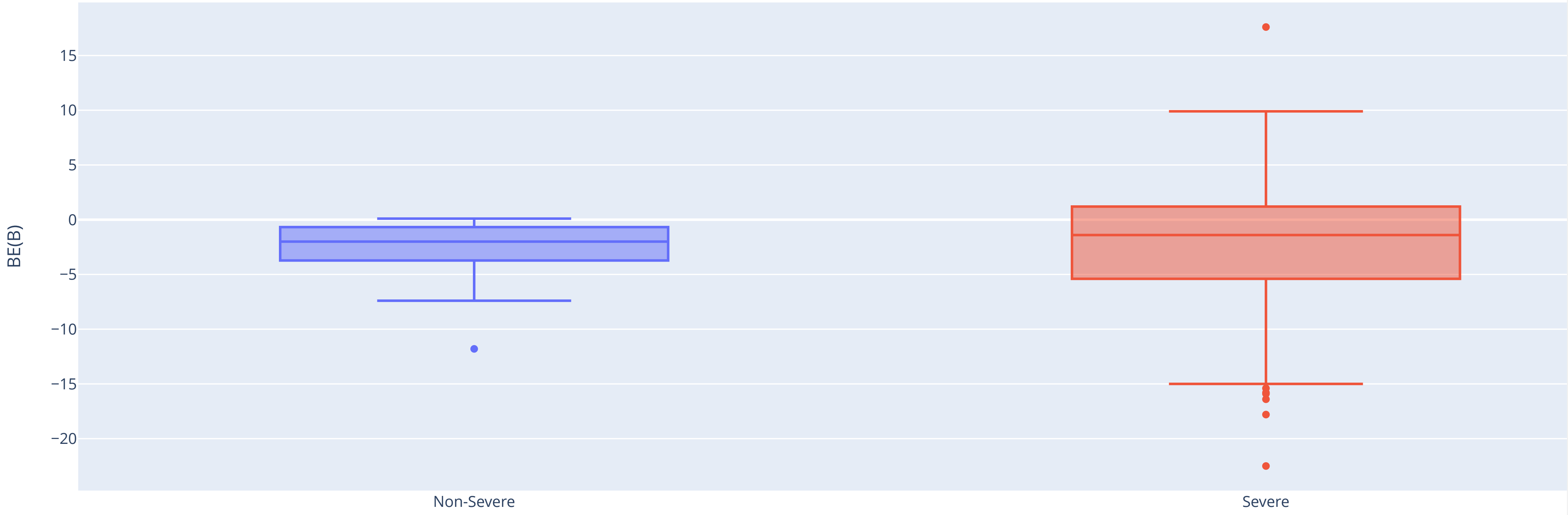

40
35
30
25
rd)

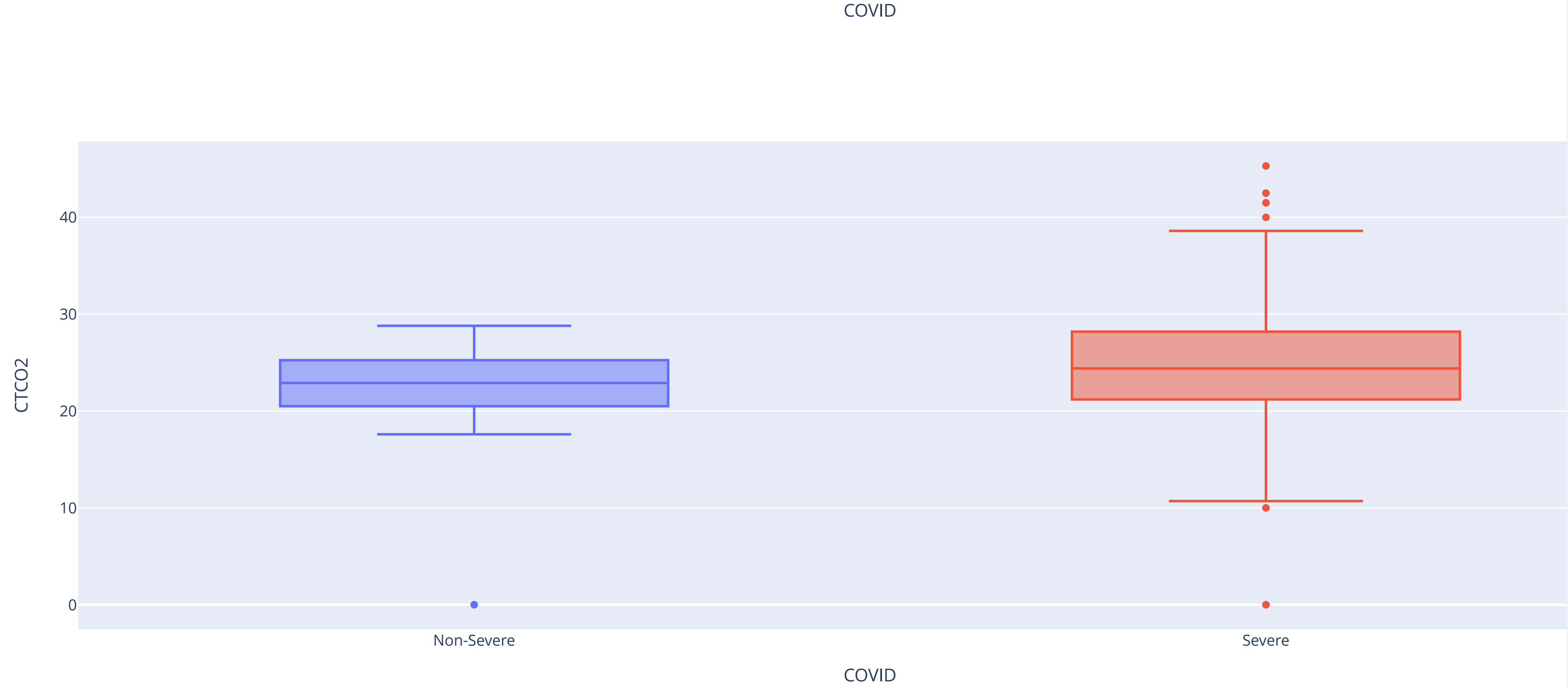

HCO3 (standa
20
15
10
5
0
Non-Severe
Severe
COVID

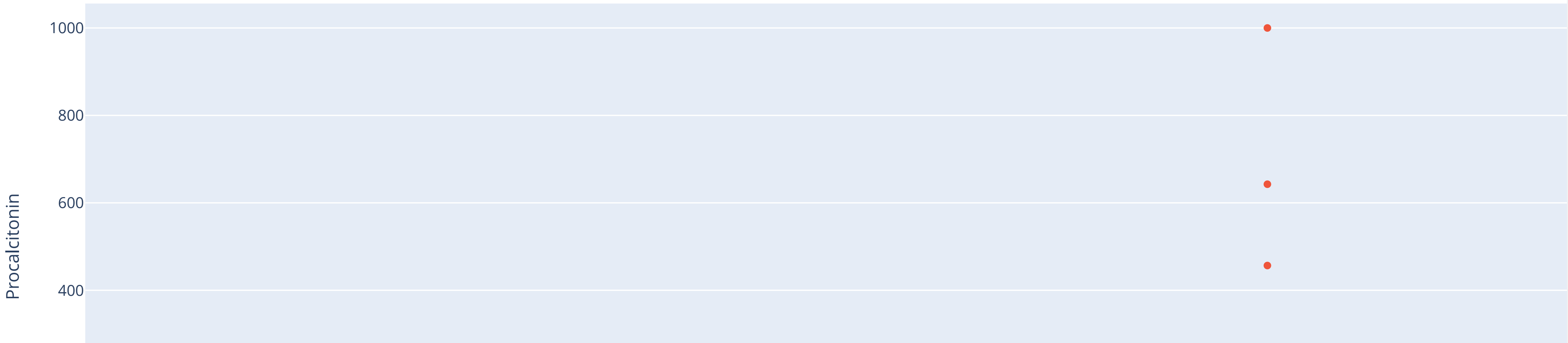

HCO3 (actual)
45
40
35
30
25
20
15
10
5
0
Non-Severe
Severe
COVID


20


15
10
5
0
−5
−10
−15
−20
−25
BE(ECF)
Non-Severe
Severe
COVID


15
10
5
0
−5
−10
−15
−20
BE(B)
Non-Severe
Severe


COVID
40
30
20
10
0
CTCO2
Non-Severe
Severe
COVID


1000
800
600
400
Procalcitonin

```
## Insights:
## In general, the levels of all biomarkers varied between SEVERE and NON-SEVERE samples for COVID-19.
## In general, SEVERE samples for COVID-19 had altered laboratory measurements compared to NON-SEVERE samples for COVID-19.
## SEVERE samples for COVID-19 demonstrate changes in laboratory measurements.
## All variables are important for analyzing the two groups of samples.
## The differences between the groups show that an in-depth study of supervised Machine Learning is justifiable.
```

```
# Phase 5: Install the Pycaret library to aid Auto-Machine Learn
!pip install pycaret
```

```
    Requirement already satisfied: pycaret in /usr/local/lib/python3.10/dist-packages (3.2.0)
    Requirement already satisfied: category-encoders>=2.4.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (2.6.3)
    Requirement already satisfied: cloudpickle in /usr/local/lib/python3.10/dist-packages (from pycaret) (2.2.1)
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    Requirement already satisfied: imbalanced-learn>=0.8.1 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.10.1)
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    Requirement already satisfied: ipython>=5.5.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (7.34.0)
    Requirement already satisfied: ipywidgets>=7.6.5 in /usr/local/lib/python3.10/dist-packages (from pycaret) (7.7.1)
    Requirement already satisfied: jinja2>=1.2 in /usr/local/lib/python3.10/dist-packages (from pycaret) (3.1.2)
    Requirement already satisfied: joblib>=1.2.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.3.2)
    Requirement already satisfied: kaleido>=0.2.1 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.2.1)
    Requirement already satisfied: lightgbm>=3.0.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (4.1.0)
    Requirement already satisfied: markupsafe>=2.0.1 in /usr/local/lib/python3.10/dist-packages (from pycaret) (2.1.3)
    Requirement already satisfied: matplotlib<=3.6,>=3.3.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (3.6.0)
    Requirement already satisfied: nbformat>=4.2.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (5.9.2)
    Requirement already satisfied: numba>=0.55.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.58.1)
    Requirement already satisfied: numpy<1.27,>=1.21 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.23.5)
    Requirement already satisfied: pandas<2.0.0,>=1.3.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.5.3)
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    Requirement already satisfied: psutil>=5.9.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (5.9.5)
    Requirement already satisfied: pyod>=1.0.8 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.1.2)
    Requirement already satisfied: requests>=2.27.1 in /usr/local/lib/python3.10/dist-packages (from pycaret) (2.31.0)
    Requirement already satisfied: schemdraw==0.15 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.15)
    Requirement already satisfied: scikit-learn<1.3.0,>=1.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.2.2)
    Requirement already satisfied: scikit-plot>=0.3.7 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.3.7)
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    Requirement already satisfied: sktime!=0.17.1,!=0.17.2,!=0.18.0,<0.22.0,>=0.16.1 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.21.1)
    Requirement already satisfied: statsmodels>=0.12.1 in /usr/local/lib/python3.10/dist-packages (from pycaret) (0.14.1)
    Requirement already satisfied: tbats>=1.1.3 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.1.3)
    Requirement already satisfied: tqdm>=4.62.0 in /usr/local/lib/python3.10/dist-packages (from pycaret) (4.66.1)
    Requirement already satisfied: xxhash in /usr/local/lib/python3.10/dist-packages (from pycaret) (3.4.1)
    Requirement already satisfied: yellowbrick>=1.4 in /usr/local/lib/python3.10/dist-packages (from pycaret) (1.5)
    Requirement already satisfied: wurlitzer in /usr/local/lib/python3.10/dist-packages (from pycaret) (3.0.3)
    Requirement already satisfied: patsy>=0.5.1 in /usr/local/lib/python3.10/dist-packages (from category-encoders>=2.4.0->pycaret) (0.5.4)
```

```
Requirement already satisfied: packaging in /usr/local/lib/python3.10/dist-packages (from deprecation>=2.1.0->pycaret) (23.2)
Requirement already satisfied: threadpoolctl>=2.0.0 in /usr/local/lib/python3.10/dist-packages (from imbalanced-learn>=0.8.1->pycaret) (3.2.0)
Requirement already satisfied: zipp>=0.5 in /usr/local/lib/python3.10/dist-packages (from importlib-metadata>=4.12.0->pycaret) (3.17.0)
Requirement already satisfied: setuptools>=18.5 in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (67.7.2)
Requirement already satisfied: jedi>=0.16 in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (0.19.1)
Requirement already satisfied: decorator in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (4.4.2)
Requirement already satisfied: pickleshare in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (0.7.5)
Requirement already satisfied: traitlets>=4.2 in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (5.7.1)
Requirement already satisfied: prompt-toolkit!=3.0.0,!=3.0.1,<3.1.0,>=2.0.0 in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (3.0.43)
Requirement already satisfied: pygments in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (2.16.1)
Requirement already satisfied: backcall in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (0.2.0)
Requirement already satisfied: matplotlib-inline in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (0.1.6)
Requirement already satisfied: pexpect>4.3 in /usr/local/lib/python3.10/dist-packages (from ipython>=5.5.0->pycaret) (4.9.0)
Requirement already satisfied: ipykernel>=4.5.1 in /usr/local/lib/python3.10/dist-packages (from ipywidgets>=7.6.5->pycaret) (5.5.6)
Requirement already satisfied: ipython-genutils~=0.2.0 in /usr/local/lib/python3.10/dist-packages (from ipywidgets>=7.6.5->pycaret) (0.2.0)
Requirement already satisfied: widgetsnbextension~=3.6.0 in /usr/local/lib/python3.10/dist-packages (from ipywidgets>=7.6.5->pycaret) (3.6.6)
Requirement already satisfied: jupyterlab-widgets>=1.0.0 in /usr/local/lib/python3.10/dist-packages (from ipywidgets>=7.6.5->pycaret) (3.0.9)
Requirement already satisfied: contourpy>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib<=3.6,>=3.3.0->pycaret) (1.2.0)
Requirement already satisfied: cycler>=0.10 in /usr/local/lib/python3.10/dist-packages (from matplotlib<=3.6,>=3.3.0->pycaret) (0.12.1)
Requirement already satisfied: fonttools>=4.22.0 in /usr/local/lib/python3.10/dist-packages (from matplotlib<=3.6,>=3.3.0->pycaret) (4.46.0)
Requirement already satisfied: kiwisolver>=1.0.1 in /usr/local/lib/python3.10/dist-packages (from matplotlib<=3.6,>=3.3.0->pycaret) (1.4.5)
```

```
#Phase 6: Import the Pycaret library
from pycaret import classification
```

```
# Phase 7: Perform data pre-processing
classification_setup = classification.setup(data = DataSetSeverity, target = "COVID")
```

	Description	Value
0	Session id	8801
1	Target	COVID
2	Target type	Binary
3	Target mapping	Non-Severe: 0, Severe: 1
4	Original data shape	(35109, 51)
5	Transformed data shape	(35109, 51)
6	Transformed train set shape	(24576, 51)
7	Transformed test set shape	(10533, 51)
8	Numeric features	50

```
# Phase 8: Build and compare models
models = classification.compare_models()
```

	Model	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC	TT (Sec)
lightgbm	Light Gradient Boosting Machine	0.8808	0.9177	0.8808	0.8757	0.8757	0.6250	0.6314	2.3050
xgboost	Extreme Gradient Boosting	0.8796	0.9153	0.8796	0.8747	0.8751	0.6247	0.6297	0.9890
rf	Random Forest Classifier	0.8786	0.9060	0.8786	0.8732	0.8725	0.6136	0.6220	5.0830
et	Extra Trees Classifier	0.8779	0.9047	0.8779	0.8726	0.8714	0.6098	0.6191	4.6190
gbc	Gradient Boosting Classifier	0.8636	0.8939	0.8636	0.8572	0.8525	0.5460	0.5645	6.4250
ada	Ada Boost Classifier	0.8481	0.8744	0.8481	0.8383	0.8375	0.5024	0.5153	1.5700
dt	Decision Tree Classifier	0.8144	0.7358	0.8144	0.8168	0.8155	0.4656	0.4658	0.7540
lda	Linear Discriminant Analysis	0.8087	0.7927	0.8087	0.7870	0.7780	0.3002	0.3373	0.4800
ridge	Ridge Classifier	0.8029	0.0000	0.8029	0.7818	0.7587	0.2326	0.2909	0.3030
lr	Logistic Regression	0.8011	0.7758	0.8011	0.7755	0.7634	0.2505	0.2942	2.1290
knn	K Neighbors Classifier	0.7882	0.6947	0.7882	0.7582	0.7616	0.2545	0.2740	1.1900
dummy	Dummy Classifier	0.7802	0.5000	0.7802	0.6086	0.6838	0.0000	0.0000	0.2790
svm	SVM - Linear Kernel	0.7059	0.0000	0.7059	0.7054	0.6286	0.0170	0.0361	1.1300
qda	Quadratic Discriminant Analysis	0.4920	0.6480	0.4920	0.7780	0.4170	0.0281	0.0930	0.2750
nb	Naive Bayes	0.2816	0.7064	0.2816	0.7608	0.2069	0.0263	0.0890	0.1950

```
# Phase 9: Train the best model based on predictive performance metrics
# First: The Light Gradient Boosting Machine (lightgbm) model achieved the best performance. We will create the Light Gradient Boosting Machine model
model_lightgbm = classification.create_model("lightgbm")
```

	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
Fold							
0	0.8763	0.9131	0.8763	0.8708	0.8692	0.6016	0.6123
1	0.8869	0.9166	0.8869	0.8825	0.8825	0.6461	0.6516
2	0.8853	0.9168	0.8853	0.8806	0.8803	0.6384	0.6451
3	0.8857	0.9281	0.8857	0.8812	0.8814	0.6436	0.6487
4	0.8747	0.9131	0.8747	0.8691	0.8695	0.6068	0.6127
5	0.8747	0.9128	0.8747	0.8690	0.8692	0.6057	0.6120
6	0.8889	0.9237	0.8889	0.8846	0.8846	0.6527	0.6581
7	0.8873	0.9295	0.8873	0.8833	0.8841	0.6540	0.6569
8	0.8738	0.9100	0.8738	0.8680	0.8681	0.6014	0.6082
9	0.8742	0.9130	0.8742	0.8684	0.8680	0.6000	0.6081
Mean	0.8808	0.9177	0.8808	0.8757	0.8757	0.6250	0.6314
Std	0.0061	0.0066	0.0061	0.0068	0.0070	0.0224	0.0211

```
# Second: The Extreme Gradient Boosting (xgboost) model second the best performance.
model_xgboost = classification.create_model("xgboost")
```

Fold	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
0	0.8788	0.9058	0.8788	0.8735	0.8736	0.6185	0.6247
1	0.8792	0.9149	0.8792	0.8745	0.8755	0.6275	0.6308
2	0.8820	0.9125	0.8820	0.8772	0.8776	0.6319	0.6368

```
# Third: The Random Forest Classifier (rf) model third the best performance.
model_rf = classification.create_model("rf")
```

Fold	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
0	0.8714	0.9073	0.8714	0.8652	0.8641	0.5865	0.5966
1	0.8824	0.9112	0.8824	0.8776	0.8779	0.6324	0.6377
2	0.8804	0.9024	0.8804	0.8752	0.8749	0.6220	0.6290
3	0.8865	0.9146	0.8865	0.8822	0.8807	0.6384	0.6475
4	0.8808	0.8955	0.8808	0.8757	0.8752	0.6230	0.6305
5	0.8686	0.9034	0.8686	0.8621	0.8602	0.5734	0.5858
6	0.8856	0.9138	0.8856	0.8811	0.8808	0.6405	0.6468
7	0.8873	0.9178	0.8873	0.8829	0.8832	0.6491	0.6539
8	0.8718	0.8931	0.8718	0.8657	0.8642	0.5863	0.5972
9	0.8710	0.9004	0.8710	0.8647	0.8635	0.5843	0.5948
Mean	0.8786	0.9060	0.8786	0.8732	0.8725	0.6136	0.6220
Std	0.0068	0.0079	0.0068	0.0076	0.0082	0.0266	0.0244

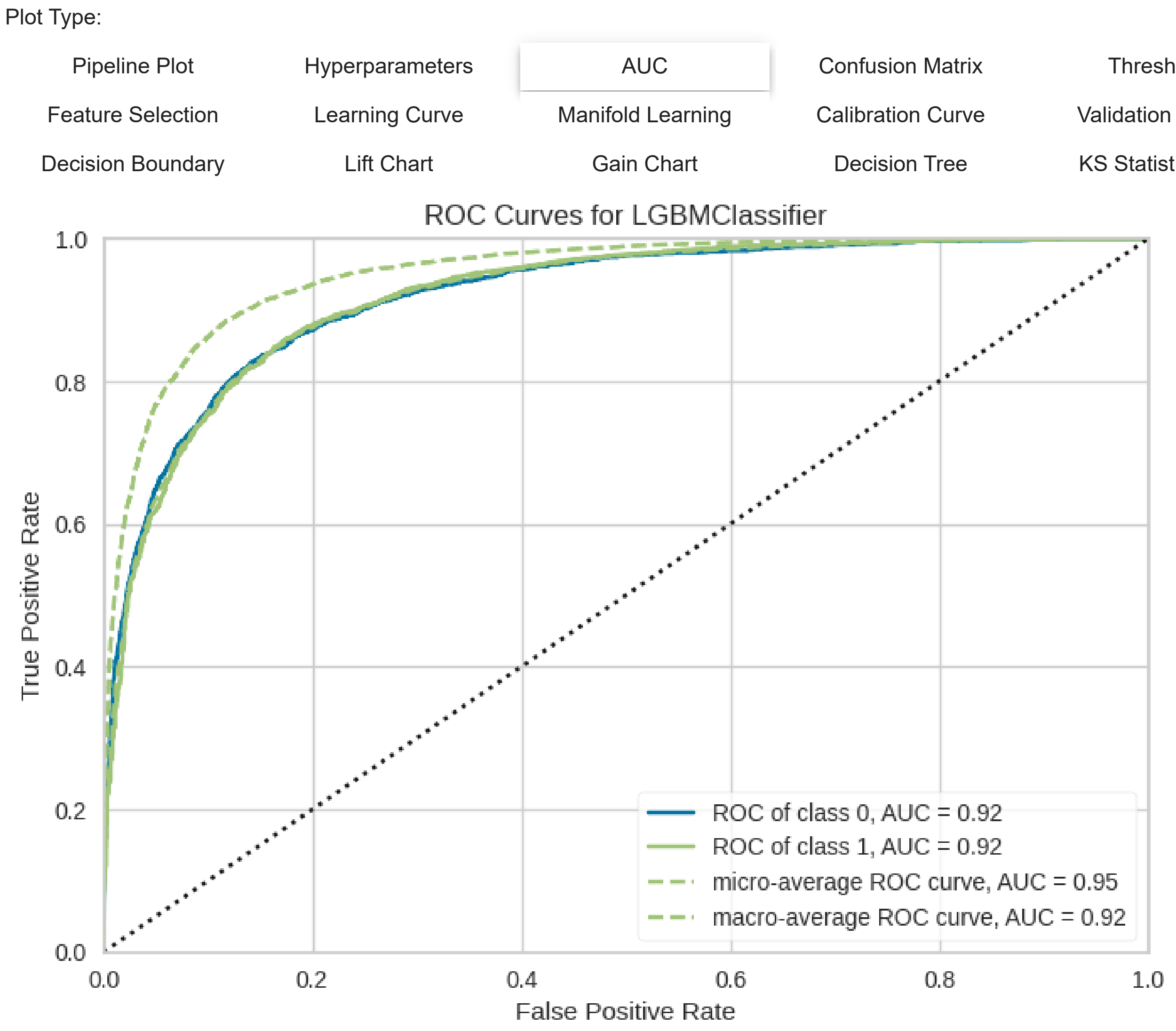
```
# Fourth: The Extra Trees Classifier (et) model fourth the best performance.
model_et = classification.create_model("et")
```

Fold	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
0	0.8694	0.9029	0.8694	0.8629	0.8615	0.5778	0.5889
1	0.8779	0.9055	0.8779	0.8726	0.8729	0.6170	0.6227
2	0.8804	0.9043	0.8804	0.8752	0.8745	0.6198	0.6279
3	0.8873	0.9129	0.8873	0.8832	0.8812	0.6395	0.6496
4	0.8767	0.8945	0.8767	0.8712	0.8707	0.6090	0.6168
5	0.8674	0.9035	0.8674	0.8608	0.8584	0.5672	0.5808
6	0.8828	0.9101	0.8828	0.8779	0.8776	0.6302	0.6370
7	0.8864	0.9134	0.8864	0.8819	0.8815	0.6425	0.6491

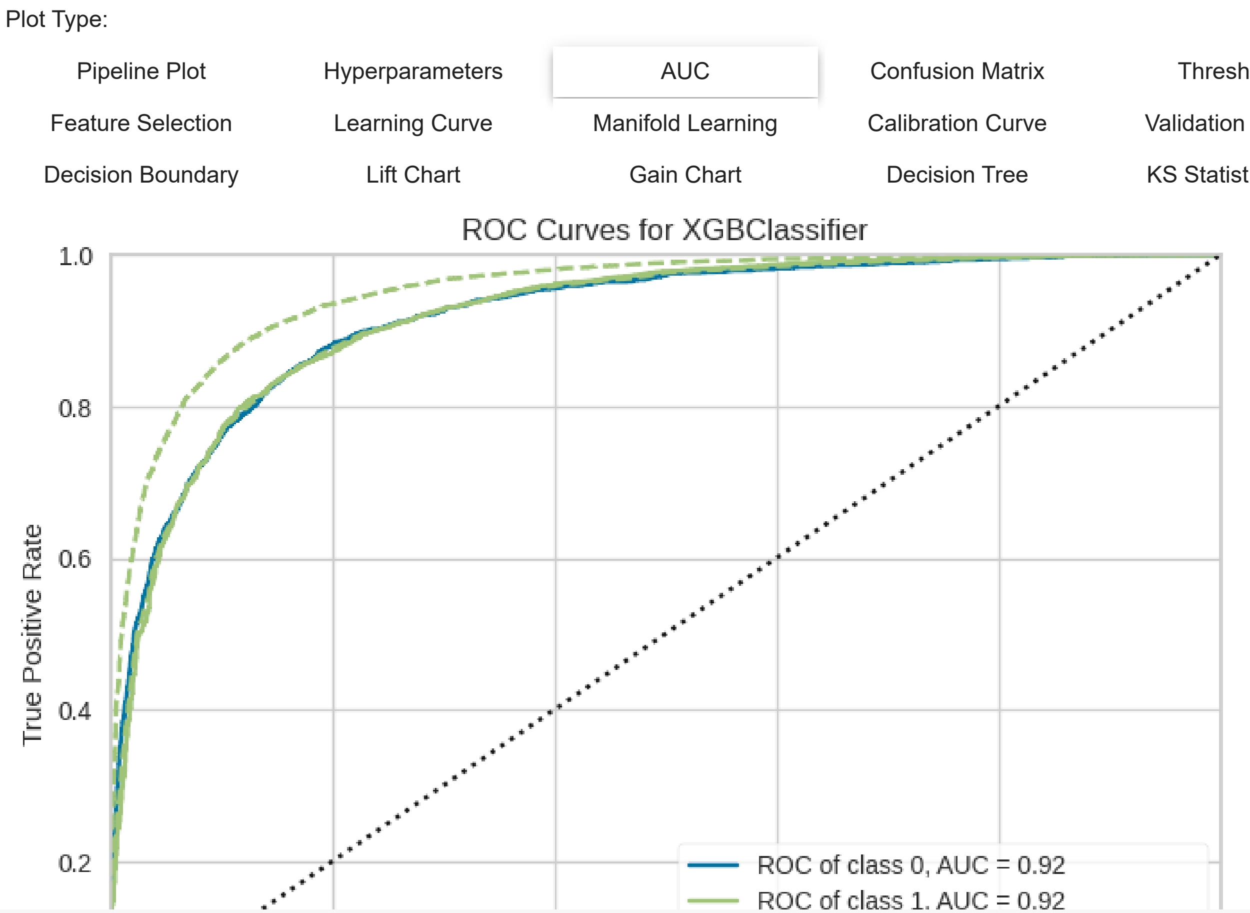
```
# Fifth: The Gradient Boosting Classifier (gbc) model fifth the best performance.
model_gbc = classification.create_model("gbc")
```

Fold	Accuracy	AUC	Recall	Prec.	F1	Kappa	MCC
0	0.8641	0.8834	0.8641	0.8588	0.8514	0.5400	0.5636
1	0.8653	0.8987	0.8653	0.8591	0.8545	0.5521	0.5703
2	0.8621	0.8939	0.8621	0.8554	0.8505	0.5392	0.5583
3	0.8694	0.9031	0.8694	0.8635	0.8599	0.5709	0.5865
4	0.8621	0.8902	0.8621	0.8556	0.8503	0.5386	0.5586
5	0.8592	0.8897	0.8592	0.8519	0.8476	0.5308	0.5494
6	0.8649	0.9025	0.8649	0.8582	0.8547	0.5538	0.5699
7	0.8694	0.9058	0.8694	0.8632	0.8604	0.5727	0.5867
8	0.8641	0.8817	0.8641	0.8578	0.8528	0.5463	0.5654
9	0.8559	0.8903	0.8559	0.8481	0.8431	0.5154	0.5359
Mean	0.8636	0.8939	0.8636	0.8572	0.8525	0.5460	0.5645
Std	0.0039	0.0079	0.0039	0.0045	0.0050	0.0165	0.0147

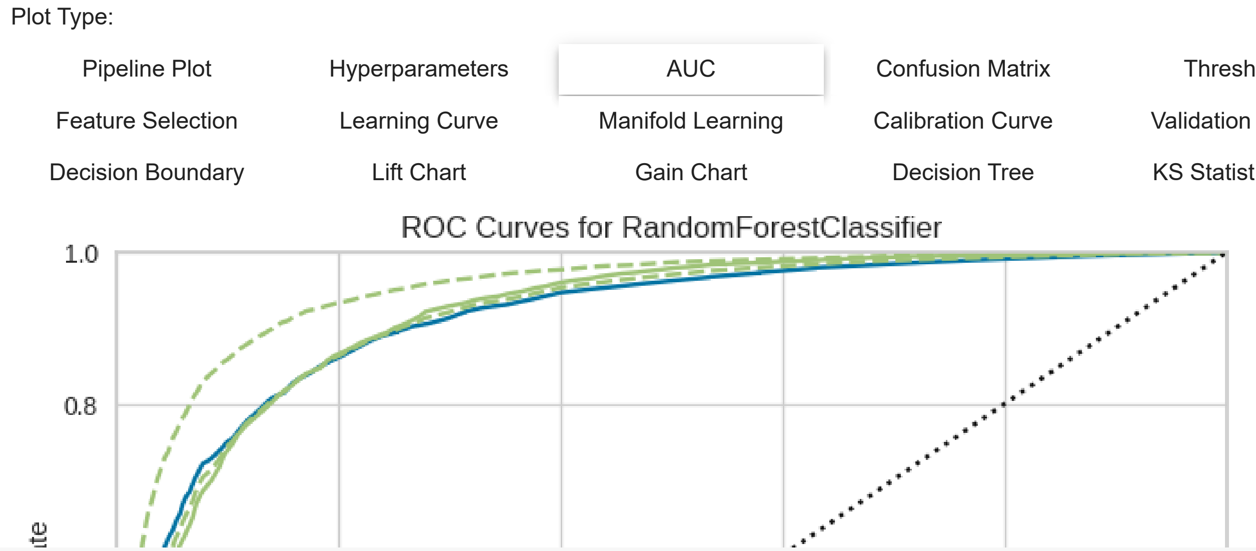
```
# Phase 10: Extract the metrics results from the 5 top models
# First: lightgbm model metrics
classification.evaluate_model(model_lightgbm)
```



```
# Second: xgboost model metrics
classification.evaluate_model(model_xgboost)
```



```
# Third: rf model metrics
classification.evaluate_model(model_rf)
```



```
# Fourth: et model metrics
classification.evaluate_model(model_et)
```

Plot Type:

Pipeline Plot Hyperparameters AUC Confusion Matrix Threshold Precision Recall Prediction Error Class Report

Feature Selection Learning Curve Manifold Learning Calibration Curve Validation Curve Dimensions Feature Importance Feature Importance…

Decision Boundary Lift Chart Gain Chart Decision Tree KS Statistic Plot

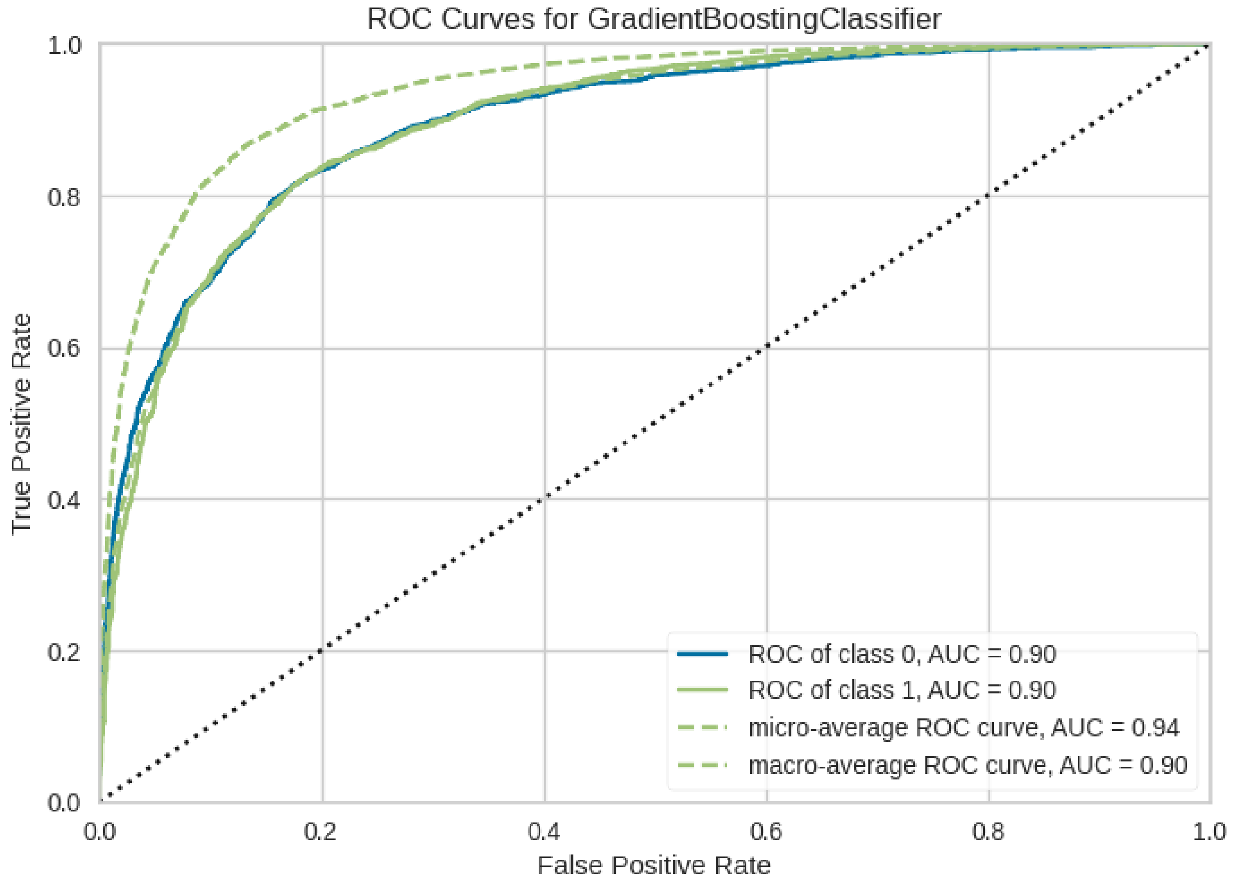
```
# Fifth: gbc model metrics
classification.evaluate_model(model_gbc)
```

Plot Type:

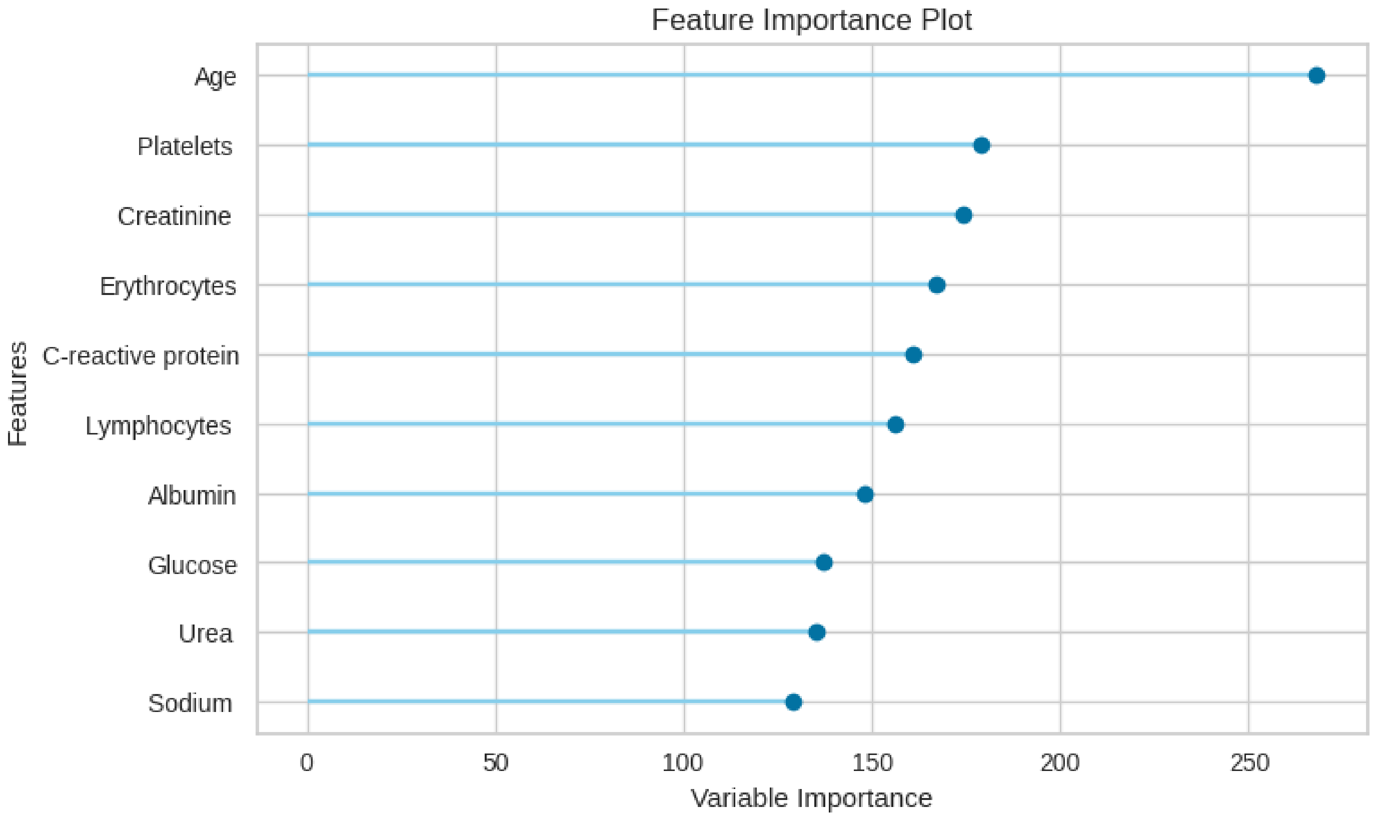
Pipeline Plot Hyperparameters AUC Confusion Matrix Threshold Precision Recall Prediction Error Class Report

Feature Selection Learning Curve Manifold Learning Calibration Curve Validation Curve Dimensions Feature Importance Feature Importance…

Decision Boundary Lift Chart Gain Chart Decision Tree KS Statistic Plot



```
# Plotting only the 10 most important biomarkers for lightgbm model
classification.plot_model(model_lightgbm, plot ="feature")
```



```
# Phase 11: Write conclusions about the best identified model
# Several Machine Learning models were built to predict the diagnosis of COVID-19 using biomarker data from patients with COVID-19
# The Light Gradient Boosting Machine (lightgbm) model had the best predictive performance
# The 5 most important biomarkers for the prognosis of COVID-19, for the samples under study, were: C-reactive protein, Creatinine, Albumin, Lymphocytes and Erythrocytes
# The next step is to develop the App so that the model can be used in Health Institutions.
```

```
# Phase 12: Save the model to make predictions in real analyzes (Deploy)
classification.save_model(model_lightgbm, "BestModel-ML_LightGBM")
```

```
Transformation Pipeline and Model Successfully Saved
(Pipeline(memory=Memory(location=None),
          steps=[('label_encoding',
                  TransformerWrapperWithInverse(exclude=None, include=None,
                                                transformer=LabelEncoder())),
                 ('numerical_imputer',
                  TransformerWrapper(exclude=None,
                                     include=['Age', 'Sex', 'Erythrocytes',
                                              'Haemoglobin ', 'Leukocytes ',
                                              'Mature Neutrophils ',
                                              'Immature Neutrophils',
                                              'Neutrophils ', 'Basophils ',
                                              'Eosinophils ', 'Lym...
                  LGBMClassifier(boosting_type='gbdt', class_weight=None,
                                 colsample_bytree=1.0, importance_type='split',
                                 learning_rate=0.1, max_depth=-1,
                                 min_child_samples=20, min_child_weight=0.001,
                                 min_split_gain=0.0, n_estimators=100, n_jobs=-1,
                                 num_leaves=31, objective=None,
                                 random_state=8801, reg_alpha=0.0,
                                 reg_lambda=0.0, subsample=1.0,
                                 subsample_for_bin=200000, subsample_freq=0))],
          verbose=False),
 'BestModel-ML_LightGBM.pkl')
```