

# COVID-19 Baseline Risk Score Analysis Report

## MockCOVE Study

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# Chapter 1

## Disclaimers

- The data presented in the analysis originated from the Moderna Sponsored mRNA-1273-P301 clinical study and are provided to NIAID in accordance with Clinical Trial Agreement between the parties. The study was funded in part by BARDA under Government Contract No. 75A50120C00034
- The preliminary immunogenicity data presented here do not reflect the Sponsors statistical analysis plan and therefore should not be interpreted as a protocol defined read-out of the clinical study.
- These data are not to be disclosed without written permission of Moderna.

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## Chapter 2

# Baseline Risk Score (Proxy for SARS-CoV-2 Exposure)

Table 2.1: Variables considered for risk score analysis.

Variable.Name	Definition	Total.missing.values	Comments
MinorityInd	Baseline covariate underrepresented minority status (1=minority, 0=non-minority)	0/13336 (0.0%)	NA
EthnicityHispanic	Indicator ethnicity = Hispanic (0 = Non-Hispanic)	0/13336 (0.0%)	NA
EthnicityNotreported	Indicator ethnicity = Not reported (0 = Non-Hispanic)	0/13336 (0.0%)	NA
EthnicityUnknown	Indicator ethnicity = Unknown (0 = Non-Hispanic)	0/13336 (0.0%)	NA
Black	Indicator race = Black (0 = White)	0/13336 (0.0%)	NA
Asian	Indicator race = Asian (0 = White)	0/13336 (0.0%)	NA
NatAmer	Indicator race = American Indian or Alaska Native (0 = White)	0/13336 (0.0%)	NA
PacIsl	Indicator race = Native Hawaiian or Other Pacific Islander (0 = White)	0/13336 (0.0%)	NA
Multiracial	Indicator race = Multiracial (0 = White)	0/13336 (0.0%)	NA
Other	Indicator race = Other (0 = White)	0/13336 (0.0%)	NA
Notreported	Indicator race = Not reported (0 = White)	0/13336 (0.0%)	NA
Unknown	Indicator race = unknown (0 = White)	0/13336 (0.0%)	NA
HighRiskInd	Baseline covariate high risk pre-existing condition (1=yes, 0=no)	0/13336 (0.0%)	NA
Sex	Sex assigned at birth (1=female, 0=male)	0/13336 (0.0%)	NA
Age	Age at enrollment in years, between 18 and 85	0/13336 (0.0%)	NA
BMI	BMI at enrollment (kg/m <sup>2</sup> )	0/13336 (0.0%)	NA

Table 2.2: All learner-screen combinations (14 in total) used as input to the Superlearner.

Learner	Screen*
SL.mean	all
SL.glm	all glmnet univar_logistic_pval highcor_random

*Note:*

\*Screen details:

all: includes all variables

glmnet: includes variables with non-zero coefficients in the standard implementation of SL.glmnet that optimizes the lasso tuning parameter via cross-validation

univar\_logistic\_pval: Wald test 2-sided p-value in a logistic regression model  $< 0.10$

highcor\_random: if pairs of quantitative variables with Spearman rank correlation  $> 0.90$ , select one of the variables at random



Figure 2.1: Cross-validated AUC (95% CI) of algorithms for predicting COVID-19 disease status starting 7 days after Day 57.



Figure 2.2: CV-estimated predicted probabilities of COVID-19 disease 7 days after Day 57 by case/control status for top 2 learners, SuperLearner and Discrete SL.



Figure 2.3: ROC curves based off CV-estimated predicted probabilities for the top 2 learners, Superlearner and Discrete SL.

Table 2.3: Weights assigned by Superlearner.

<b>Learner</b>	<b>Screen</b>	<b>Weight</b>
SL.glm	screen_all	0.590
SL.glm	screen_glmnet	0.376
SL.mean	screen_all	0.034
SL.glm	screen_univariate_logistic_pval	0.000
SL.glm	screen_highcor_random	0.000



Table 2.4: Predictors in learners assigned weight  $> 0.0$  by Superlearner.

Learner	Screen	Weight	Predictors	Coefficient	Odds.Ratio
SL.glm	screen_all	0.59	(Intercept)	-2.767	0.063
SL.glm	screen_all	0.59	MinorityInd	-0.015	0.985
SL.glm	screen_all	0.59	EthnicityHispanic	-0.013	0.987
SL.glm	screen_all	0.59	EthnicityNotreported	0.046	1.048
SL.glm	screen_all	0.59	EthnicityUnknown	-0.072	0.931
SL.glm	screen_all	0.59	Black	-0.024	0.977
SL.glm	screen_all	0.59	Asian	0.057	1.058
SL.glm	screen_all	0.59	NatAmer	0.007	1.007
SL.glm	screen_all	0.59	PacIsl	-0.025	0.975
SL.glm	screen_all	0.59	Multiracial	-0.052	0.95
SL.glm	screen_all	0.59	Other	0.055	1.056
SL.glm	screen_all	0.59	Notreported	0.005	1.005
SL.glm	screen_all	0.59	Unknown	0.01	1.01
SL.glm	screen_all	0.59	HighRiskInd	-0.019	0.981
SL.glm	screen_all	0.59	Sex	-0.006	0.994
SL.glm	screen_all	0.59	Age	0.824	2.279
SL.glm	screen_all	0.59	BMI	-0.045	0.956
SL.glm	screen_glmnet	0.376	(Intercept)	-2.767	0.063
SL.glm	screen_glmnet	0.376	EthnicityNotreported	0.048	1.049
SL.glm	screen_glmnet	0.376	EthnicityUnknown	-0.071	0.932
SL.glm	screen_glmnet	0.376	Black	-0.035	0.966
SL.glm	screen_glmnet	0.376	Asian	0.05	1.051
SL.glm	screen_glmnet	0.376	Multiracial	-0.064	0.938
SL.glm	screen_glmnet	0.376	Other	0.048	1.049
SL.glm	screen_glmnet	0.376	Age	0.824	2.279
SL.glm	screen_glmnet	0.376	BMI	-0.045	0.956
SL.glm	screen_glmnet	0.376	(Intercept)	-2.767	0.063
SL.glm	screen_glmnet	0.376	EthnicityNotreported	0.048	1.049
SL.glm	screen_glmnet	0.376	EthnicityUnknown	-0.071	0.932
SL.glm	screen_glmnet	0.376	Black	-0.035	0.966
SL.glm	screen_glmnet	0.376	Asian	0.05	1.051
SL.glm	screen_glmnet	0.376	Multiracial	-0.064	0.938
SL.glm	screen_glmnet	0.376	Other	0.048	1.049
SL.glm	screen_glmnet	0.376	Age	0.824	2.279
SL.glm	screen_glmnet	0.376	BMI	-0.045	0.956



Figure 2.4: Superlearner predicted probabilities of COVID-19 disease in vaccinees 7 days after Day 57 by case/control status.



Figure 2.5: ROC curve based off Superlearner predicted probabilities in vaccinees.

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## Chapter 3

# Appendix

- This report was built from the [CoVPN/correlates\\_reporting](https://github.com/CoVPN/correlates_reporting) repository with commit hash 4b4559315cc246c53752aa70432d58d68700d1c5. A diff of the changes introduced by that commit may be viewed at [https://github.com/CoVPN/correlates\\_reporting/commit/4b4559315cc246c53752aa70432d58d68700d1c5](https://github.com/CoVPN/correlates_reporting/commit/4b4559315cc246c53752aa70432d58d68700d1c5)
- The sha256 hash sum of the raw input file, “COVID\_VEtrial\_practicedata\_primarystage1.csv”: 83d0f55d1745ffd42be124d8f9ec9a9903abcc13cd22f95e537542a08b41300a
- The sha256 hash sum of the processed file, “moderna\_mock\_data\_processed.csv”: 28964ce20cfd70a621aff9df412c42b1178d5e749e0f49ddd79fbff2dc7c90a