**Code**

# Prepare the model and get a summary for som1-5

model1 <- glm(disorder~som1 + som2 + som3 + som4 + som5, data = final, family = "binomial")

model1$coef

exp(model1$coef)

summary(model1)

# Prepare the model and get a summary for som6-9

model2 <- glm(disorder~som6 + som7 + som8 + som9, data = final, family = "binomial")

model2$coef

exp(model2$coef)

summary(model2)

# Prepare the model and get a summary for som10-14

model3 <- glm(disorder~som10 + som11 + som12 + som13 + som14, data = final, family = "binomial")

model3$coef

exp(model3$coef)

summary(model3)

**Results**

Call:

glm(formula = disorder ~ som1 + som2 + som3 + som4 + som5, family = "binomial",

data = final)

Deviance Residuals:

Min 1Q Median 3Q Max

-3.3107 -0.2463 0.0000 0.0957 3.0752

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -4.7196 0.5726 -8.242 < 2e-16 \*\*\*

som1 0.5215 0.2351 2.218 0.02656 \*

som2 1.2390 0.2970 4.172 3.02e-05 \*\*\*

som3 0.5441 0.1171 4.648 3.35e-06 \*\*\*

som4 0.5320 0.1468 3.624 0.00029 \*\*\*

som5 2.4536 0.4228 5.804 6.48e-09 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 447.70 on 322 degrees of freedom

Residual deviance: 123.75 on 317 degrees of freedom

AIC: 135.75

Number of Fisher Scoring iterations: 8

Call:

glm(formula = disorder ~ som6 + som7 + som8 + som9, family = "binomial",

data = final)

Deviance Residuals:

Min 1Q Median 3Q Max

-2.34372 -0.62207 0.00045 0.49654 1.86426

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -1.5442 0.2009 -7.685 1.53e-14 \*\*\*

som6 1.9406 0.4662 4.163 3.15e-05 \*\*\*

som7 1.0921 0.2536 4.307 1.66e-05 \*\*\*

som8 1.1669 0.4176 2.794 0.0052 \*\*

som9 1.1918 0.1925 6.190 6.03e-10 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 447.70 on 322 degrees of freedom

Residual deviance: 270.32 on 318 degrees of freedom

AIC: 280.32

Number of Fisher Scoring iterations: 7

Call:

glm(formula = disorder ~ som10 + som11 + som12 + som13 + som14,

family = "binomial", data = final)

Deviance Residuals:

Min 1Q Median 3Q Max

-1.84363 -0.26365 0.00067 0.05370 3.09428

Coefficients:

Estimate Std. Error z value Pr(>|z|)

(Intercept) -4.7789 0.6066 -7.878 3.32e-15 \*\*\*

som10 1.0075 0.3260 3.090 0.0020 \*\*

som11 0.7396 0.3913 1.890 0.0587 .

som12 0.5288 0.3161 1.673 0.0944 .

som13 1.4370 0.2148 6.689 2.24e-11 \*\*\*

som14 1.0204 0.4125 2.474 0.0134 \*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 447.70 on 322 degrees of freedom

Residual deviance: 110.32 on 317 degrees of freedom

AIC: 122.32

Number of Fisher Scoring iterations: 8

**Interpretation**

1. The important features in this model are SOM2-5 as demonstrated by their ‘\*\*\*’ markings and their small p-values. SOM1 is not important for analyzing the disorder as shown by the high p-value.
2. All of the somatic markers 6-9 are important in this model. Only marker 8, with a slightly higher p-value and a marking ‘\*\*’ is of lesser, but still significant, importance.
3. In this model, we see that the order of importance of the markers is 13, 10, 14 and lastly 11 and 12. Marker 13 has a ‘\*\*\*’ marking, 10 is ‘\*\*’, 14 is ‘\*’ and 11/12 are ‘’.
4. In terms of which model is better for predicting the likelihood of the disorder, model 3 is the best, followed closely by model 1 and model 2 in a distant 3rd. The best way to see which is the better predictor of likelihood of the disorder is to see which have the lowest residual deviance and AIC.