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Metadata Exploratory Report

Code **▼**

Project: Differential Gene Expression and Methylation in Vaping LatinX Youth

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Center for Innovative Design & Analysis

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1 Background

The data presented in this report are part of a study aimed to assess differential gene expression and methylation in vaping versus non-vaping LatinX youths in Pueblo and Denver, CO. Pulmonary function data were also obtained in order to better understand the impacts of vape use on pulmonary function. To assess differential gene expression and methylation, nasoepithelial swabs were obtained from each participating subject. Pulmonary function is assessed using PFTs (Pulmonary Function Tests) and Impulse Oscillometry (IOS).

2 Study Population

This data set consists of samples taken from 51 people ages 12-17 from the Pueblo, Denver, and Aurora, CO areas. Subjects were asked to identify as 'LatinX' or 'Non-latinX'.

3 Methods

Include the verision of R you are using

3.1 Clinical Data Pocessing

This is a great summary of what you've done, it includes the important bits and describes how you used the other variables

- Subjects are dichotomized to those that used a vaping device in the last 6 months and those who have not based on the variables 'ever_vape', 'vape_days', and 'last_vape'. Six Month Vape Status could not be confirmed for one individual. Any analyses including Six Month Vape Status will have a sample size of n = 50 assuming no other missing values. Vaping status is self-reported. Previous analyses showed n = 12 participants had vaped in the last 6 months. This analysis will use n = 13 participants who had vaped in the last 6 months. One participant (SID = 111) reported that they had used a vaping device 5 out of the last 30 days, but did not respond to 'last_vape'. They were falsely labeled as "NA" in previous analyses.
- Subjects' geographic location (City) is grouped by their reporting recruiting center.

So we will also want a sentence about our lung function measures. It might just be that normality was visually inspected using histograms, but we might not have a noramlity assumption for this measures to pass

3.2 Gene-Count Processing

Key Pt: Filtering parameters (genes were measured in at least X samples or the like)

Key Pts; verisions of annotation (ensembl in this case), verision of packages (DESeg2 and RUVSe

Library Size:

Gene of average

Gene counts were quantified using Ensembl annotation for GrCh 38 ver. 86 (pulled 08/23/2017). Genes were filtered to only include those with an average of 10 reads per sample.

average of 10 reads per sample.

NORMALIZATION BIT: To correct for batch and other technical effects Removal of Unwanted Variance with empirically derived control gene (RUVg) was used. Empirical genes were identified by first making the data Gaussian by performing a variance stabilizing transformation (VST), and then subsetting the quartile of least variable genes across all samples. This was 3,992 genes or 25% of 15,970. 3 nuisance factors were chosen to be removed

Technical effects: Subsetting the qualitie of using this method (k=3).

Normalization: TRANSFORMATION: Gene expression values were VST using the R package DESeq2 ver 1.28.1. (VST is equivalent to Rlog when size estimates vary little between subjects as was in this case).

4 Descriptive Statistics Just relabel as results

Aim to always start with a sentence. Here just state the number of subjects you have after cleaning the data and if any outliers were detected (which no).

Table 1: Clinical Data

		Did Not Vape in Last 6 Months (N=37)	Vaped in Last 6 Months (N=13)	Total (N=50)	p value
Gender I wou	uld prefer to include sex ov	er gender, we are conserned more about accounting for	biological differences, not necessarly gender	identity differences	0.475 ¹
Female		20 (54.1%)	5 (38.5%)	25 (50.0%)	
Male		16 (43.2%)	8 (61.5%)	24 (48.0%)	
Non-Binary		1 (2.7%)	0 (0.0%)	1 (2.0%)	
Age Include units so Age (yrs)					0.663 ²
Mean (SD)		14.6 (1.4)	14.8 (1.4)	14.6 (1.4)	
Range		12.0 - 17.0	13.0 - 17.0	12.0 - 17.0	
Grade					0.457 ³
7th		3 (8.1%)	0 (0.0%)	3 (6.0%)	
8th		8 (21.6%)	4 (30.8%)	12 (24.0%)	
Freshman	Use 9th, 10th, 11th an		3 (23.1%)	17 (34.0%)	
Sophomore	Freshman and sophor used in college so whi to be clear	nore ect are also le it's obvious better 4 (10.8%)	2 (15.4%)	6 (12.0%)	
Junior		4 (10.8%)	2 (15.4%)	6 (12.0%)	
Senior		4 (10.8%)	2 (15.4%)	6 (12.0%)	

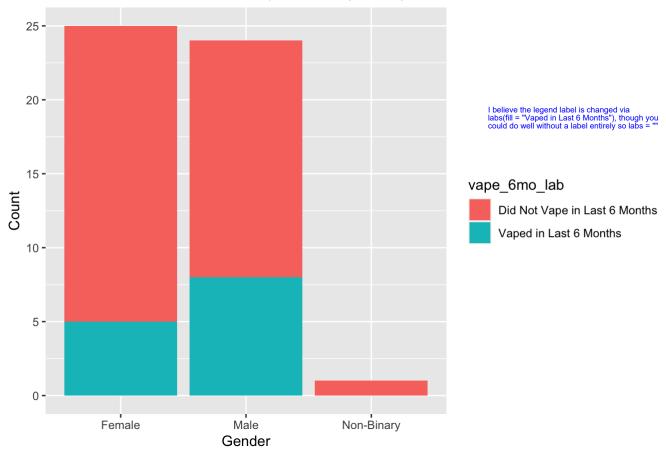
		Did Not Vape in Last 6 Months (N=37)	Vaped in Last 6 Months (N=13)	Total (N=50)	p value
City Maybe since you grouped based on reporting recruitment center, put recruiting center over city here					
Aurora		16 (43.2%)	0 (0.0%)	16 (32.0%)	
CommCity/Denver		11 (29.7%)	1 (7.7%)	12 (24.0%)	
Pueblo		10 (27.0%)	12 (92.3%)	22 (44.0%)	
Ethnicity					0.135 ¹
LatinX		23 (62.2%)	11 (84.6%)	34 (68.0%)	
Non-LatinX		14 (37.8%)	2 (15.4%)	16 (32.0%)	
FEV1/FVC	Include FEV1 as its own measure as we	H			0.494 ²
N-Miss		10	12	22	
Mean (SD)		0.8 (0.1)	0.7 (NA)	0.8 (0.1)	
Range		0.5 - 1.0	0.7 - 0.7	0.5 - 1.0	
R5					0.0072
N-Miss		1	0	1	
Mean (SD)		4.0 (0.9)	5.0 (1.3)	4.3 (1.1)	
Range		2.0 - 6.1	3.7 - 7.6	2.0 - 7.6	
X20					0.0072
N-Miss		4	2	6	
Mean (SD)		0.1 (0.6)	0.7 (0.9)	0.2 (0.7)	
Range		-1.1 - 2.4	-1.0 - 2.3	-1.1 - 2.4	

- 1. Pearson's Chi-squared test
- 2. Linear Model ANOVA
- 3. Trend test for ordinal variables

4.1 Figures

So figures would just be built into the results, so this doesn't really need a header. And again just add a sentence here, you could talk about which of the values above were significantly different between our groups and if you can what that means.

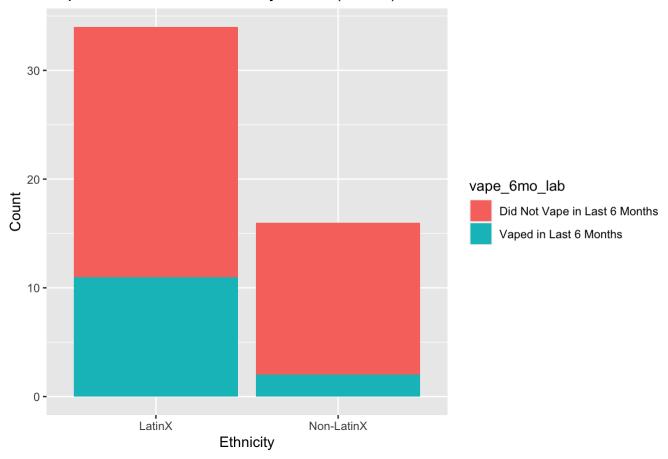
Vaped in the last 6 months by Gender (n = 50)



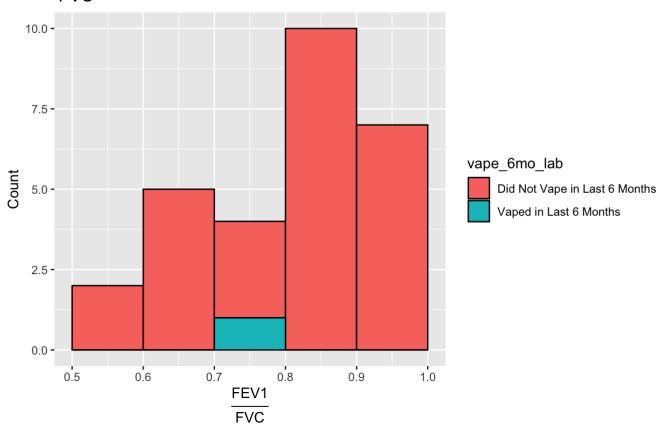
Code

Try to have a sentence for each figure. It helps justify why you have it. If you can't find a sentence to justify maybe it needs some additional information added to it

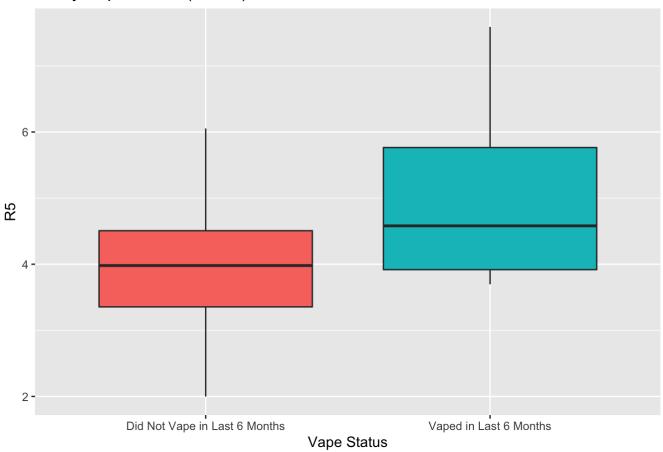
Vaped in the last 6 months by Latino (n = 50)



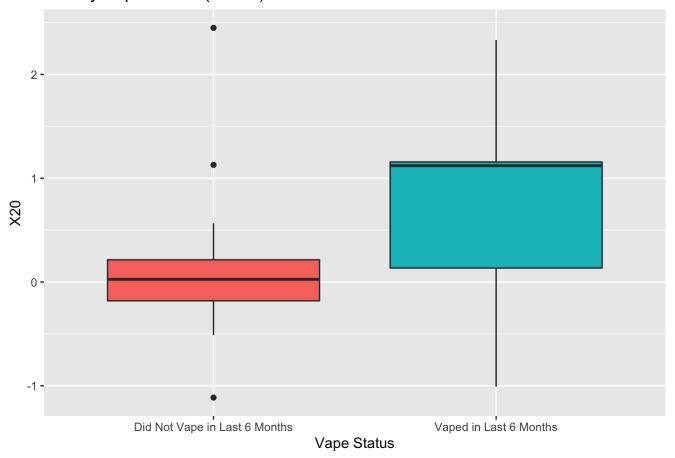








X20 by Vape Status (n = 44)



5 Notes

6 Questions

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