

# Gene Analysis of Schizophrenia Patient Samples

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## Summary

TBF

## Introduction

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## Methods

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## Preview of Data

The data used is from the Emani et al. (2024) set of cohorts, with its samples. The raw data of the annotated expression matrices can be found [here](#). All the samples come from the prefrontal cortex (PFC). The metadata contains the information of the following 12 cohorts:

1. CMC
2. DevBrain
3. Girgenti-multiome
4. IsoHuB
5. LIBD
6. Ma\_et\_al (Ma et al. 2022)
7. MultiomeBrain
8. PTSDBrainomics
9. SZBDMulti-Seq
10. ROSMAP
11. UCLA-ASD
12. Velmeshev\_et\_al (Velmeshev et al. 2019)

However, because no annotated matrices were provided for the ROSMAP cohort, these were filtered out from the metadata.

This is an overview of each cohort:

Table 1: Each cohort with the total patients studied, the mean of the age of death, and disease studied.

Cohort	Patients	Mean_Age	Disorder_studied
CMC	100	71	Schizophrenia
DevBrain	16	29	Williams Syndrome, ASD
Girgenti-snMultiome	19	49	None
IsoHuB	4	22	None
LIBD	10	50	None
Ma_et_al	2	57	None
MultiomeBrain	21	42	Schizophrenia, Bipolar Disorder
PTSDBrainomics	19	47	MDD, PTSD
SZBDMulti-Seq	72	65	Bipolar Disorder, Schizophrenia
UCLA-ASD	52	23	ASD
Velmeshev_et_al	27	18	ASD

From Table 1, we can see that the CMC cohort has the biggest number of patient samples with 100 samples, followed by SZBDMulti-seq with 72. Ma\_et\_al has the smallest size, with only 2 samples. CMC and SZBDMulti-seq also have the highest mean of age of death at 71

years and 65 years respectively. Velmeshev\_et\_al has the lowest one, at 18 years. A variety of diseases are studied in these cohorts, with some cohorts studying none. These diseases include schizophrenia, autism spectrum disorder (ASD), bipolar disorder, major depressive disorder (MDD), post-traumatic stress disorder (PTSD), and Williams Syndrome.

Table 2: Number of patients per condition per cohort.

Cohort	Disorder	Number_of_Patients
CMC	Control	53
CMC	Schizophrenia	47
DevBrain	ASD	9
DevBrain	Control	4
DevBrain	Williams Syndrome	3
Girgenti-snMultiome	Control	19
IsoHuB	Control	4
LIBD	Control	10
Ma_et_al	Control	2
MultiomeBrain	Bipolar Disorder	10
MultiomeBrain	Control	5
MultiomeBrain	Schizophrenia	6
PTSDBrainomics	Control	9
PTSDBrainomics	MDD	4
PTSDBrainomics	PTSD	6
SZBDMulti-Seq	Bipolar Disorder	24
SZBDMulti-Seq	Control	24
SZBDMulti-Seq	Schizophrenia	24
UCLA-ASD	ASD	27
UCLA-ASD	Control	25
Velmeshev_et_al	ASD	13
Velmeshev_et_al	Control	14

Table 2 indicates the number of patients per condition in each cohort. The CMC cohort has the highest numbers, with 53 control samples and 47 schizophrenia samples. The UCLA-ASD is second, with 27 ASD samples and 25 control samples.

It must be noted that many patients’ age at death was marked as “89+”. In order to determine the age distribution and the mean age of death, these values were converted to “89”. The number of samples that were marked as “89+” from the Schizophrenia cohorts is in Table 3.

Table 3: Number of patients annotated as “89+” in Schizophrenia cohorts.

Cohort	Disorder	Plus89_patients
CMC	Control	9
CMC	Schizophrenia	5
SZBDMulti-Seq	Bipolar Disorder	1
SZBDMulti-Seq	Control	1
SZBDMulti-Seq	Schizophrenia	2

The age distribution of each condition per cohort was also examined.

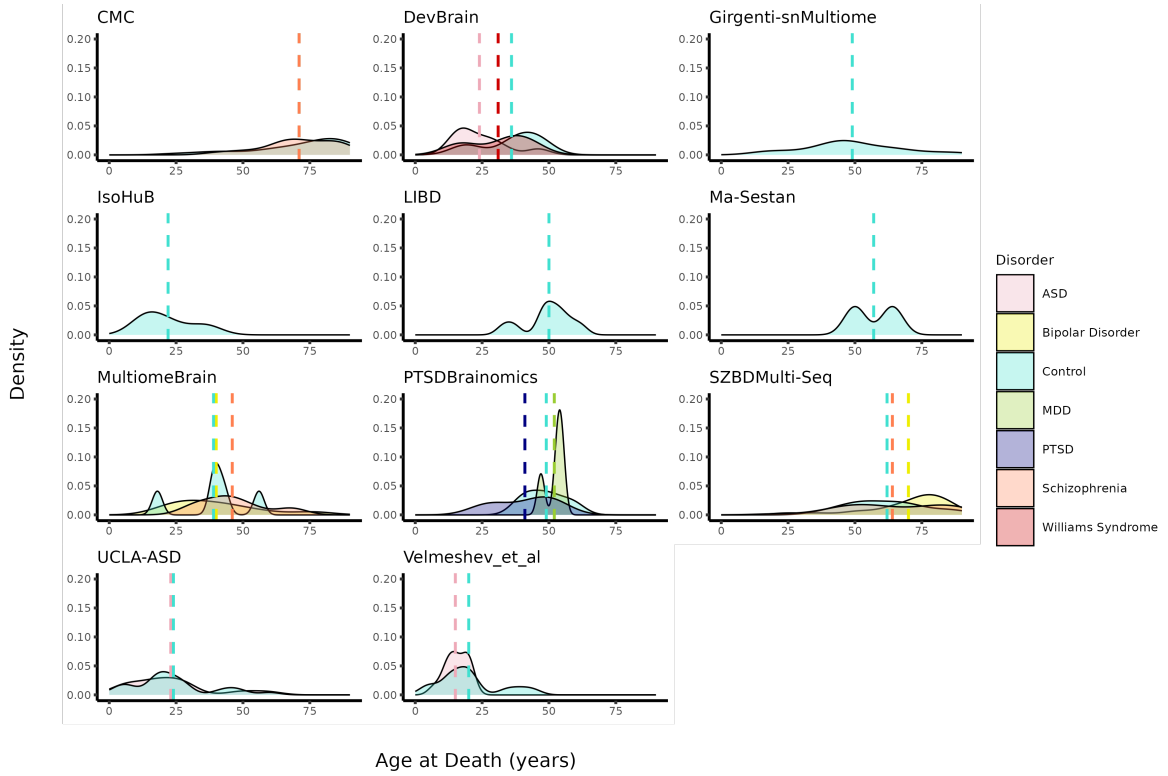


Figure 1: Age distribution in each cohort.

In Figure 1, the dotted vertical lines are the mean of the age at death for each condition.

## References

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