Experiment and find the differences between the two cohorts in disease category (purple Alzheimer subject, green normal subject).

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| **SLC26A3**  This gene shows a higher median expression level in AD subjects than in normal subjects, indicating potential upregulation in Alzheimer’s disease. Although there is overlap in the expression range between AD and normal cohorts, the boxplot suggests that AD subjects tend to have higher expression levels overall. | **RASGEF1B**  The expression of **RASGEF1B** appears to be similar between AD and normal cohorts, with a slight tendency for higher expression in normal subjects. Both cohorts exhibit a similar range of expression, and there’s a relatively large overlap, suggesting this gene may not be significantly differentially expressed between the two groups. | **LINGO1**  This gene has comparable expression levels across AD and normal subjects, with overlapping ranges and median values. The lack of significant difference between cohorts implies that **LINGO1** might not be a strong marker for distinguishing AD from normal brain samples. |
| **PDE4DIP**  **PDE4DIP** shows a higher median expression in AD subjects, with the AD cohort having a slightly higher expression range than the normal cohort. Although there is some overlap, the data suggests a possible upregulation of **PDE4DIP** in Alzheimer’s disease, making it a candidate for further investigation. | **LINC01609**  The expression distribution of **LINC01609** is relatively similar between AD and normal cohorts, with both groups showing a high degree of variability and several outliers. The median expression levels are close, which indicates that this gene may not exhibit significant differential expression between the two groups. | **PHYHIP**  The expression of **PHYHIP** is notably higher in AD subjects compared to normal subjects, as evidenced by a higher median and range in the AD cohort. This suggests that **PHYHIP** may be upregulated in Alzheimer’s disease, making it a potentially important gene to explore in the context of disease progression and pathology. |

In summary, **SLC26A3**, **PDE4DIP**, and **PHYHIP** appear to be upregulated in Alzheimer’s disease subjects, as they show higher median expression levels compared to the normal group. These genes could be associated with Alzheimer’s pathology and may be worth further investigation to understand their roles in disease mechanisms. Conversely, **RASGEF1B**, **LINGO1**, and **LINC01609** do not display substantial differences in expression between AD and normal subjects, suggesting they may not be strongly associated with Alzheimer’s disease.

Experiment with subjects of different ages (57 - 89) in development stage category.

![A group of numbers and graphs

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| **SLC26A3**  The expression of **SLC26A3** shows an increasing trend with age, with older subjects (around 80–89 years) having higher expression levels than younger subjects. This gradual increase suggests that **SLC26A3** may be upregulated as individuals age. This pattern could indicate a potential role for **SLC26A3** in aging-related processes or age-associated changes in brain function. | **RASGEF1B**  The expression levels remain relatively consistent across age groups, with only slight fluctuations. There is no significant increase or decrease as age advances, which implies that **RASGEF1B** expression is stable across the age spectrum in this dataset. This stability suggests that **RASGEF1B** may not be directly influenced by age-related factors, making it potentially less relevant in the context of aging. | **LINGO1**  The expression of **LINGO1** exhibits noticeable variation among age groups, with some higher expression in older age groups. Although the differences are not as pronounced as with **SLC26A3**, there is a slight upward trend in older subjects. This pattern suggests that **LINGO1** may have a mild association with age-related processes, possibly contributing to cellular or molecular changes occurring in the aging brain. |
| **PDE4DIP**  Similar to **SLC26A3**, **PDE4DIP** also shows increased expression in older subjects. The increase is gradual, but subjects aged 80 years and above display the highest expression levels. The consistent rise in **PDE4DIP** expression across age groups hints at an age-related upregulation, potentially indicating a role in aging or neurodegeneration. | **LINC01609**  **LINC01609** expression remains low and consistent across all age groups, showing minimal fluctuation. The lack of variability suggests that **LINC01609** may not be affected by age and could be regulated independently of aging-related processes. This stability across ages implies that **LINC01609** is not a significant marker for age-related gene expression changes. | **PHYHIP**  The expression of **PHYHIP** exhibits slight age-related variability, but the changes are not as pronounced as with **SLC26A3** or **PDE4DIP**. Although there is a mild increase in expression with age, the differences are small, suggesting that **PHYHIP** might only be marginally influenced by aging factors. |

In summary, **SLC26A3** and **PDE4DIP** show an age-related increase in expression, with higher levels in older subjects. This trend suggests these genes could play a role in aging processes or age-associated changes in the brain. **LINGO1** and **PHYHIP** display slight increases in expression with age, though these changes are not as strong, making their age-related associations less certain. **RASGEF1B** and **LINC01609**, however, remain relatively stable across the age groups, suggesting that these genes may not be influenced by aging factors.

Experiment with gender cohorts (sex = male vs. female)

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| **SLC26A3**  The expression levels of **SLC26A3** are quite similar between male and female subjects, with both groups showing comparable median values and interquartile ranges. This indicates that there is no significant gender-based difference in the expression of **SLC26A3**. | **RASGEF1B**  Like **SLC26A3**, **RASGEF1B** expression shows minimal variation between genders. The median expression and the spread of values appear nearly identical for both males and females, suggesting that gender does not significantly influence **RASGEF1B** expression levels. | **LINGO1**  **LINGO1** expression levels also appear similar across both genders. Both male and female subjects show a similar distribution of values, with overlapping interquartile ranges and comparable medians, indicating a lack of gender-based variation. |
| **PDE4DIP**  The expression levels of **PDE4DIP** show slight variation between males and females, with females having a slightly higher median expression. However, the overall distribution remains similar, and this difference may not be statistically significant. **PDE4DIP** expression, therefore, does not show a strong gender-dependent difference. | **LINC01609**  **LINC01609** expression shows a consistent pattern between genders, with both male and female groups displaying very low expression levels. Outliers are present, but they appear equally in both male and female distributions, indicating no notable gender influence on **LINC01609** expression. | **PHYHIP**  The expression pattern of **PHYHIP** is similar to **LINC01609**, with both genders showing low expression levels overall. There are outliers, but these do not appear to be gender-specific, and the median and interquartile ranges are nearly identical.. |

In summary, none of the six genes—**SLC26A3**, **RASGEF1B**, **LINGO1**, **PDE4DIP**, **LINC01609**, and **PHYHIP**—show significant gender-based differences in expression. For most genes, the median values, spread, and overall distribution of expression levels are nearly identical between male and female subjects. This suggests that the expression of these particular genes is not strongly influenced by gender.

The lack of significant gender-based differences in the expression levels of these genes implies that any variations observed in other analyses, such as those related to age or disease state, are likely not confounded by gender. This information can be useful in studies focusing on Alzheimer’s or other age-related conditions, as it indicates that the expression of these genes may be influenced more by disease state or age than by gender. This consistency across genders may simplify the analysis of these genes in broader studies by reducing the need to control for gender as a variable.