1. Bar Plot

X axis- Samples

Y axis- FPKM (Fragments Per Kilobase of transcript per Million mapped reads)

The bar plot of FPKM values across different samples reveals a clear variation in gene expression levels, with certain samples showing significantly higher FPKM values compared to others.

1. Box Plot

The lower mean expression of BRAF in ATC could indicate a different regulatory mechanism in these more aggressive tumours, potentially involving other pathways that downregulate BRAF expression or make it less central to ATC progression.

This outlier in ATC might indicate a rare case where BRAF plays a more prominent role in ATC, potentially due to specific mutations or atypical regulatory mechanisms. Further investigation of this outlier, including sequencing to check for mutations, could provide valuable insights into the molecular diversity of ATC and the conditions under which BRAF expression is upregulated in these tumors.

1. Density Plot

This bimodal distribution suggests that there are two subpopulations within the ATC samples regarding BRAF expression. The first peak (between 1.5 and 2.0 FPKM) indicates that a significant portion of ATC tumors have lower BRAF expression levels, while the secondary rise after 3.0 FPKM suggests another group of tumors with higher expression levels. This could reflect heterogeneity within ATC, where different subtypes or stages of the tumor have distinct BRAF expression profiles. The dip at 2.5 FPKM might indicate a transitional phase between these two subpopulations, or it could represent a threshold beyond which BRAF expression becomes more variable.

The flatter peak in PTC suggests a more uniform distribution of BRAF expression across these tumors compared to ATC. This uniformity may indicate that most PTC samples have a moderate level of BRAF expression, which could be consistent with the known role of BRAF mutations in PTC. The fall at 2.75 FPKM might indicate a point where BRAF expression starts to decline in certain PTC samples, possibly due to tumor-specific factors or treatment effects. The rise at 3.5 FPKM suggests a subset of PTC tumors with higher BRAF expression, which might correspond to more aggressive forms or specific molecular subtypes of PTC

1. Heat Map

The heatmap reveals distinct expression patterns for key genes across samples. TP53, NRAS, and HRAS show high expression (red zone), suggesting their critical roles in tumor biology, with TP53 notably lower in two ATC samples, possibly indicating reduced tumor suppressor activity. Conversely, TERT and BRAF exhibit lower expression (white zone) compared to these genes. The varied expression levels highlight molecular heterogeneity within ATC and PTC

1. MAPlot

The MA plot helps to visually assess the quality and significance of differential expression results. Genes with extreme values on the y-axis and large mean values are typically of greatest interest for further biological investigation or validation.

1. Scatter Plot

The positive correlation suggests that in PTC samples, BRAF and NRAS may be co-regulated or part of the same signaling pathway. This could indicate that both genes are contributing to a common oncogenic mechanism in PTC. The co-expression might reflect a synergistic role in tumor development, where the activation of one gene leads to or is associated with the activation of the other.

The negative correlation in ATC samples suggests a more complex regulatory relationship between BRAF and NRAS. This might indicate that in ATC, the activation of one gene might suppress the other, or different mechanisms might be at play compared to PTC. This inverse relationship could reflect differential signaling pathways or compensatory mechanisms in more aggressive or advanced stages of the tumor.

1. Density Plot

The broad distribution after 1.5 FPKM suggests that ATC samples exhibit a wide range of BRAF expression levels, with a concentration of values in the mid to higher FPKM range. The narrowing at 2.5 FPKM indicates a drop in density at this level, suggesting that fewer samples have BRAF expression around this FPKM value. The smaller "belly" above 2.5 FPKM indicates that while there is a range of higher expression values, the distribution is less dense compared to the lower range. This could reflect a heterogeneous expression pattern within ATC samples, where some tumors have very high or very low BRAF expression, but fewer have intermediate levels.

The round "apple" shape indicates a more uniform and broad distribution of BRAF expression levels in PTC samples, with a significant number of samples falling within the 2.0 to 3.0 FPKM range. The narrowing at 3.0 FPKM suggests a slight decrease in density at this point, but the distribution remains relatively broad and stable above 3.0 FPKM. This pattern indicates that PTC samples have a more consistent range of BRAF expression, with fewer extreme values compared to ATC.

1. Volcano Plot

The plot visually represents which genes have significant changes in expression between conditions. Genes far from the x-axis (indicating high fold changes) and high on the y-axis (indicating low p-values) are of particular interest, as they show both large changes in expression and high statistical significance.

The presence of several orange points far to the right suggests that there are multiple genes with significant upregulation

The spread of blue points indicates which genes are significantly reduced and might be involved in pathways that are suppressed or inhibited.