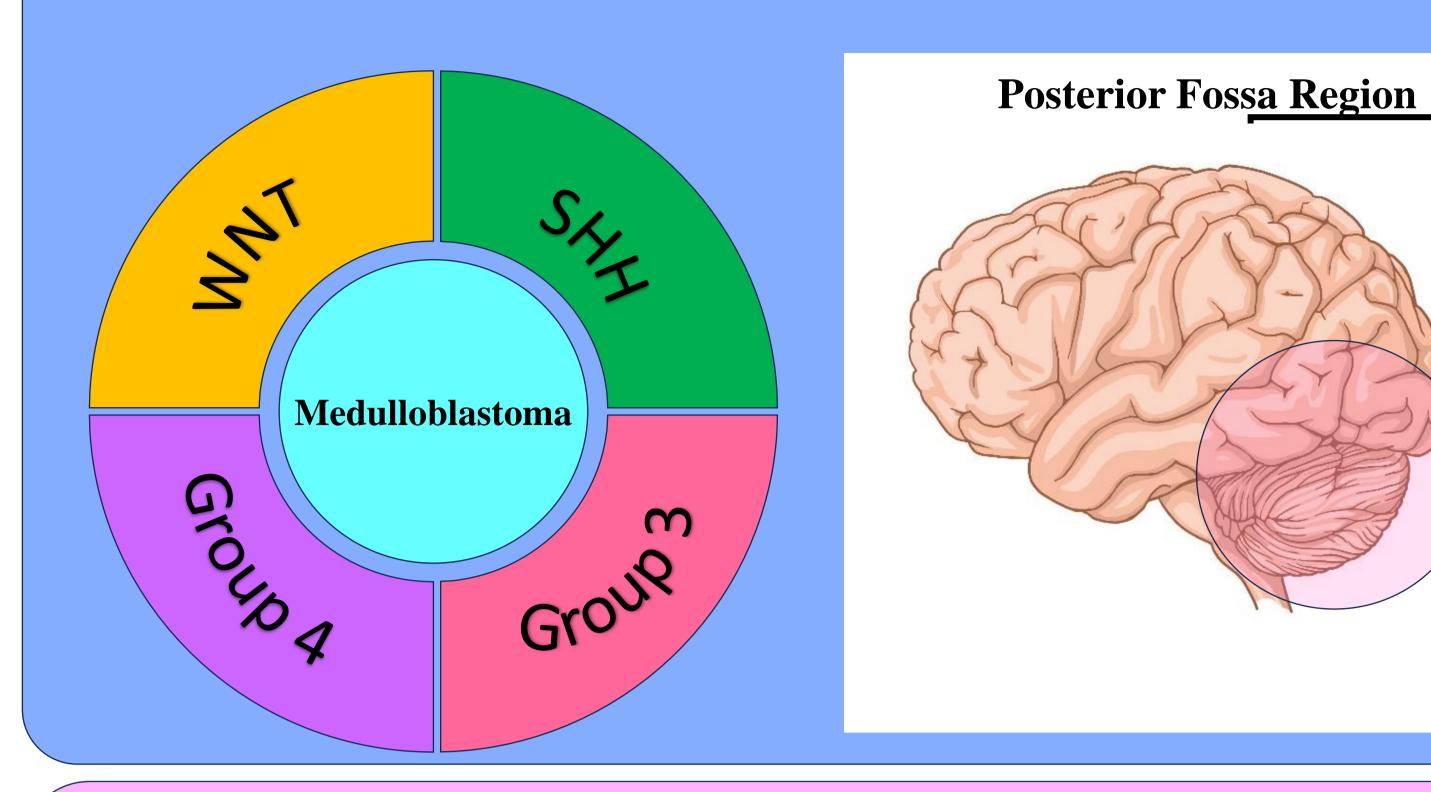
Transcriptomics Landscape of Medulloblastoma: Identifying the Significant Molecular Signals in Subgroup Classification

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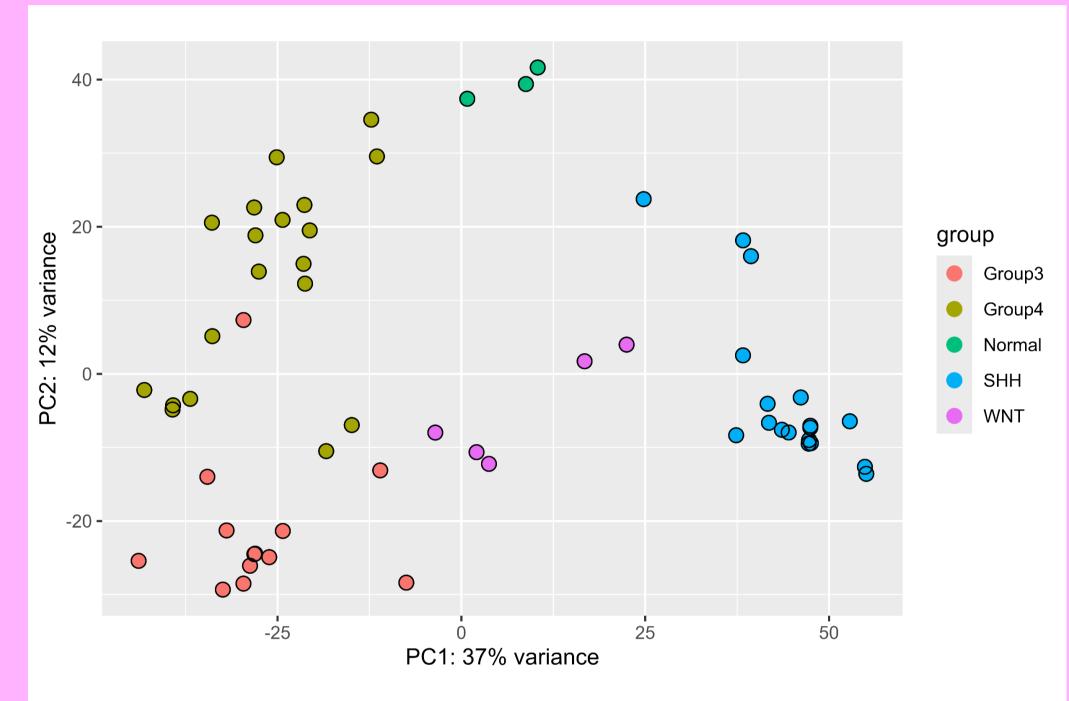
Introduction

Medulloblastoma is one type of central nervous system tumor among children. 70 % of the patients are juveniles; hence, it is also known as "**Pediatric Brain Cancer**." The Tumor Occurs at the **Posterior Fossa** region of the brain. It has four subgroups. In my current study, I am using RNA sequencing data from GEO (**GSE164677**).

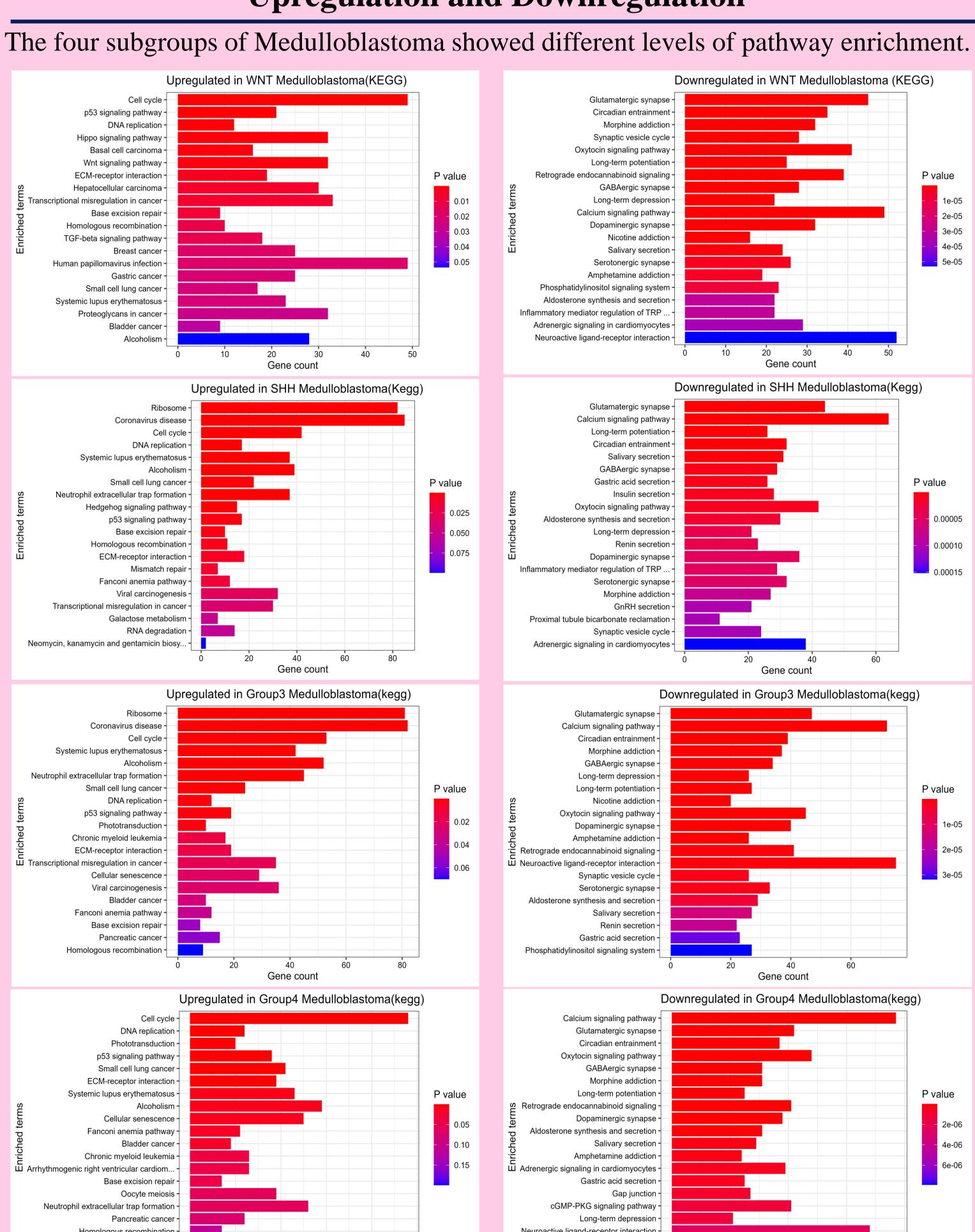


Different Subgroups of Medulloblastoma Form Different Clusters

The PCA plot showed that the four subgroups, e.g., WNT, SHH, Group 3, Group 4, and control samples, are forming different clusters.

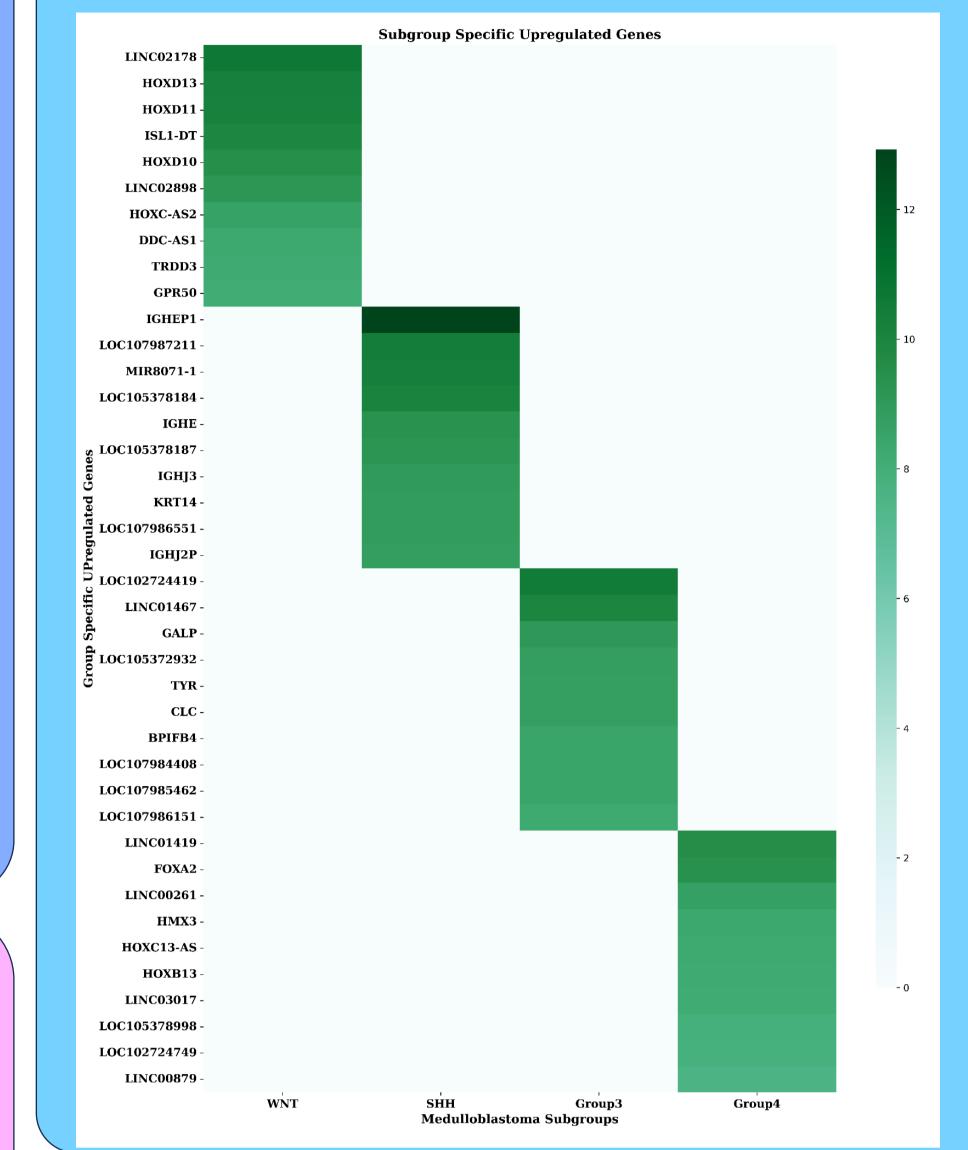


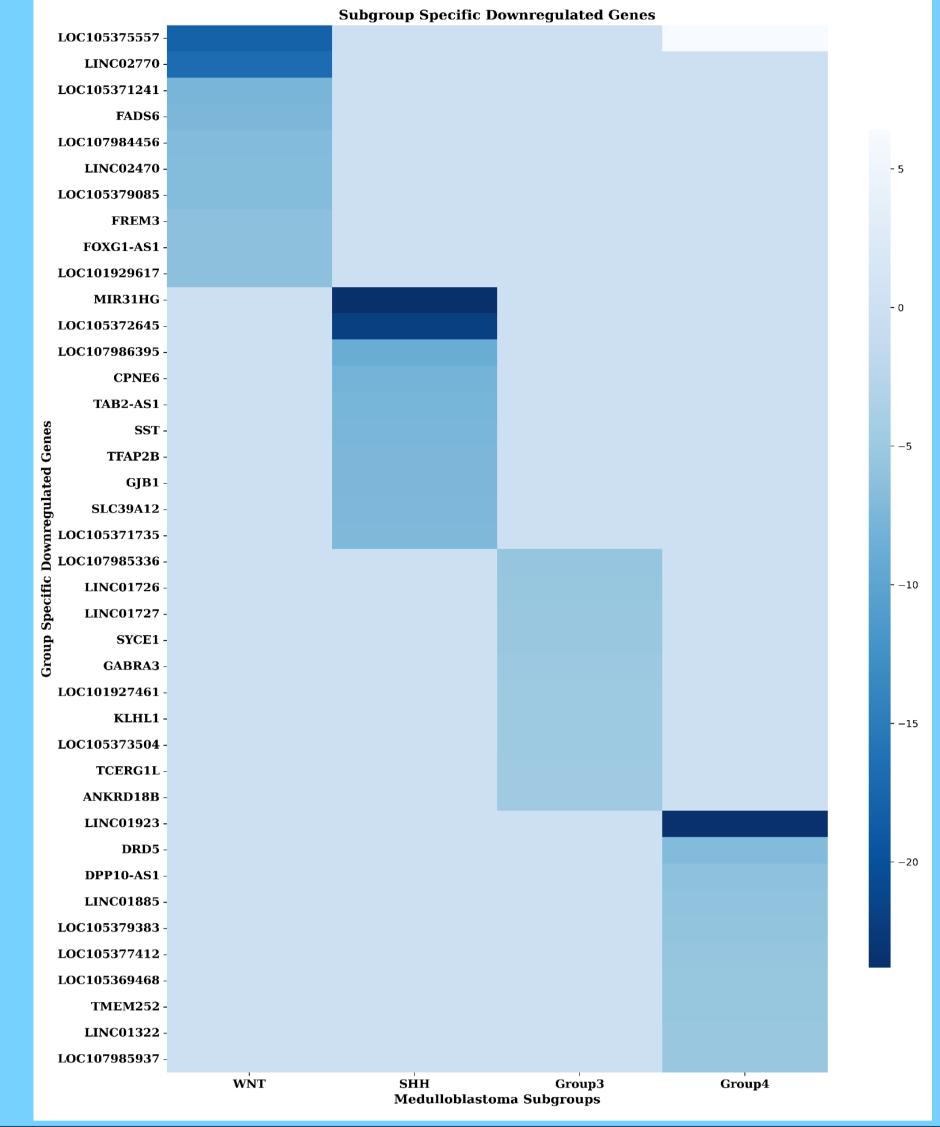
KEGG Pathway Enrichment Analysis Showed Different Pathway Upregulation and Downregulation



Subgroup Specific Top Upregulated and Downregulated Genes

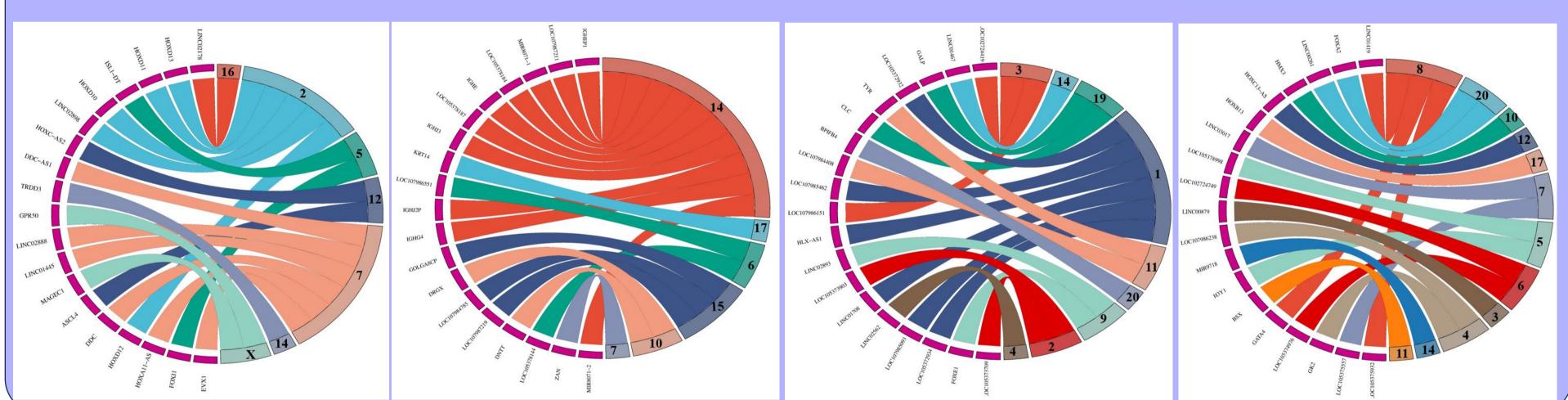
The WNT, SHH, Group 3, and Group 4 Medulloblastoma have shown specific gene markers that are only upregulated or downregulated into that subgroup





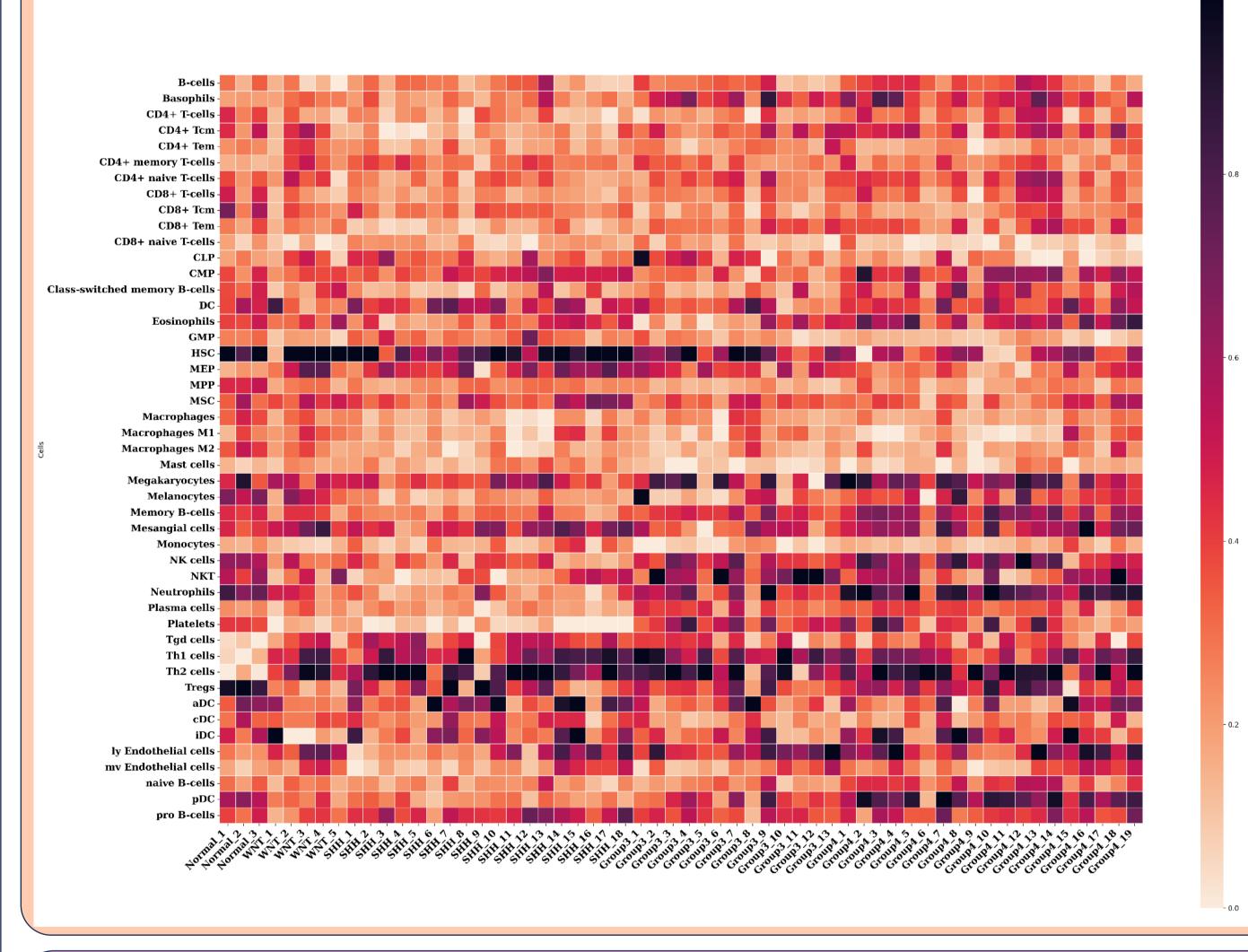
Group-specific Upregulated Genes Showed Different Chromosome Originations

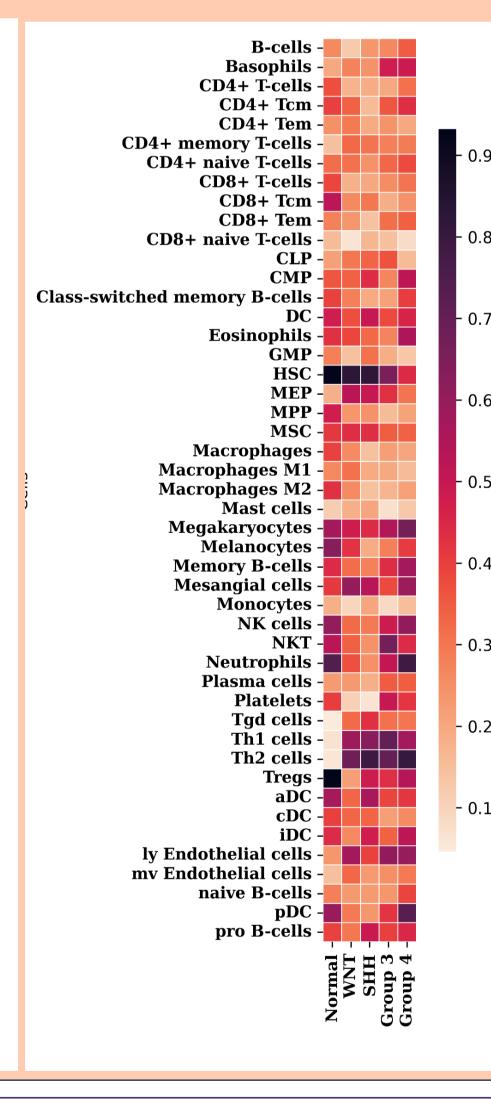
The chord plot below shows that the top 20 unique gene's chromosome or origination



Immune Cell Enrichment Analysis

The four subgroups of Medulloblastoma showed little difference in immune cell abundance.

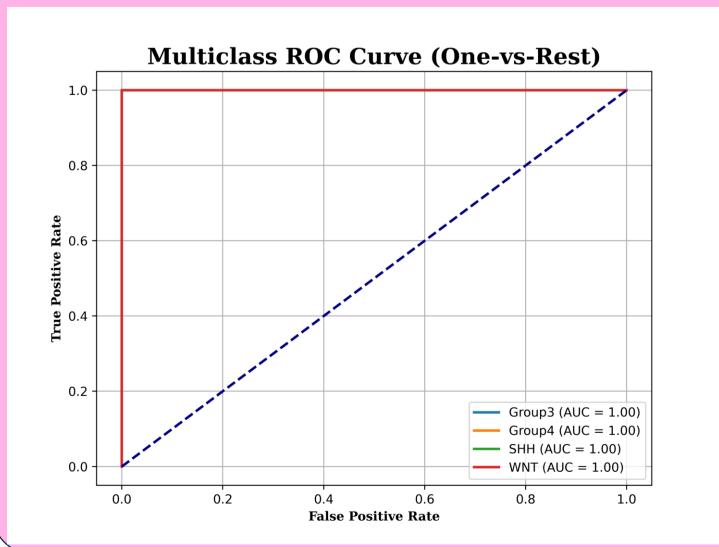


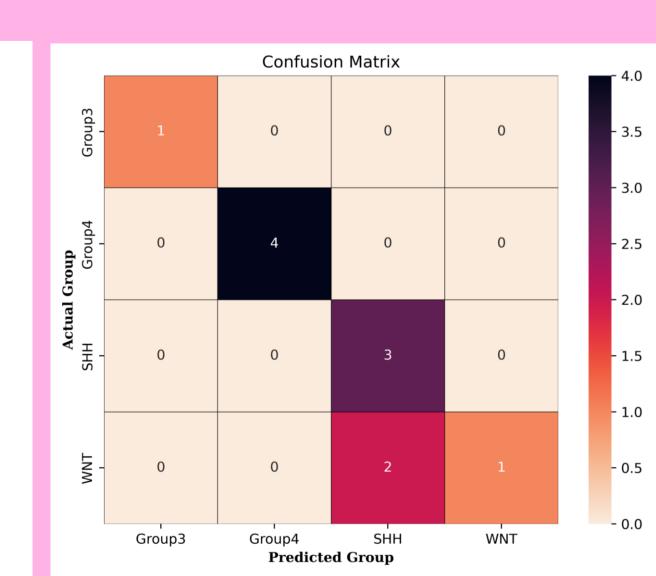


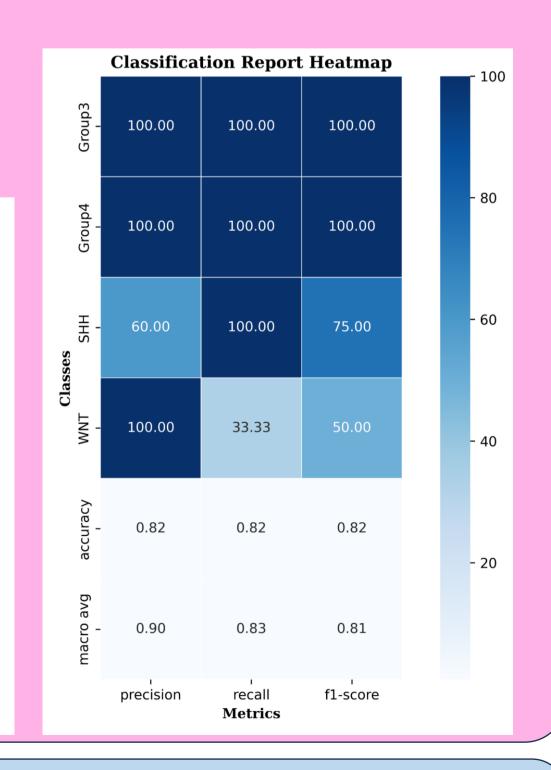
Logistic Regression Based Classification Using the Group-Specific Upregulated Genes

The model had an AUC of 1.0 for all the groups.

The model had an accuracy of about 82 %.







Conclusion

The molecular signals are significant for the subgroup classification of Medulloblastoma and could be helpful in disease diagnosis and treatment.



Progesterone-mediated oocyte maturation -

Mismatch repair



